



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:31 AM UTC

PDB ID : 6FTJ / pdb_00006ftj
EMDB ID : EMD-4317
Title : Cryo-EM Structure of the Mammalian Oligosaccharyltransferase Bound to Sec61 and the Non-programmed 80S Ribosome
Authors : Braunger, K.; Becker, T.; Beckmann, R.
Deposited on : 2018-02-22
Resolution : 4.70 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

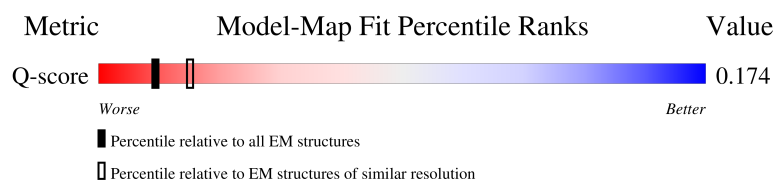
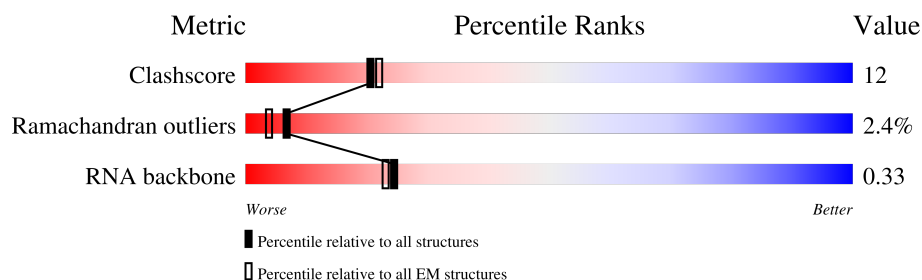
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 (4.20 - 5.20)

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	244	
2	B	394	
3	C	362	
4	D	292	

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Mol	Chain	Length	Quality of chain
5	E	248	
6	F	225	
7	G	241	
8	H	190	
9	I	213	
10	J	169	
11	L	210	
12	M	138	
13	N	203	
14	O	199	
15	P	153	
16	Q	187	
17	R	180	
18	S	175	
19	T	159	
20	U	99	
21	V	131	
22	W	63	
23	X	119	
24	Y	134	
25	Z	135	
26	a	147	
27	b	75	
28	c	94	
29	d	107	

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Mol	Chain	Length	Quality of chain
30	e	128	
31	f	109	
32	g	114	
33	h	122	
34	i	102	
35	j	86	
36	k	69	
37	l	50	
38	m	52	
39	n	23	
40	o	104	
41	p	91	
42	r	136	
43	s	198	
44	t	163	
45	u	3662	
46	v	120	
47	w	156	
48	x	426	
49	y	62	
50	z	29	
51	1	162	
52	2	60	
53	3	120	
54	4	34	

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Mol	Chain	Length	Quality of chain
55	5	696	
56	6	97	
57	7	25	
58	8	80	
59	K	8	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
61	ZN	o	201	-	-	X	-
62	9UB	5	809	-	-	X	-

2 Entry composition [i](#)

There are 62 unique types of molecules in this entry. The entry contains 152111 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3148	2007	591	537	13		

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2884	1814	578	478	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	362	LYS	SER	conflict	UNP G1SVW5
C	363	SER	ASP	conflict	UNP G1SVW5

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	292	Total	C	N	O	S	0	0
			2386	1509	437	426	14		

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	236	Total	C	N	O	S	0	0
			1898	1215	362	318	3		

- Molecule 6 is a protein called Ul30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

- Molecule 7 is a protein called uL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	241	Total	C	N	O	S	0	0
			1934	1233	371	326	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	191	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called Ribosomal protein L10 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	204	Total	C	N	O	S	0	0
			1655	1051	319	272	13		

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1703	1065	354	280	4		

- Molecule 12 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	54	GLN	LYS	conflict	UNP G1TVT6

- Molecule 16 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 24 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	75	Total	C	N	O	S	0	0
			609	378	130	98	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	136	Total	C	N	O	S	0	0
			1094	676	229	183	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	198	Total	C	N	O	S	0	0
			1523	969	265	280	9		

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 45 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 46 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 47 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 48 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	426	Total	C	N	O	S	0	0
			3313	2181	535	576	21		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	?	-	THR	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	MET	deletion	UNP P38377
x	?	-	TYR	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	ASP	deletion	UNP P38377
x	?	-	PRO	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	GLU	deletion	UNP P38377
x	?	-	MET	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	145	SER	ALA	conflict	UNP P38377
x	?	-	SER	deletion	UNP P38377

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Chain	Residue	Modelled	Actual	Comment	Reference
x	?	-	GLY	deletion	UNP P38377
x	?	-	ASN	deletion	UNP P38377
x	?	-	LEU	deletion	UNP P38377
x	?	-	LEU	deletion	UNP P38377
x	?	-	VAL	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	LEU	deletion	UNP P38377
x	?	-	LEU	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	THR	deletion	UNP P38377
x	?	-	TRP	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	ASP	deletion	UNP P38377
x	?	-	THR	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	PRO	deletion	UNP P38377
x	?	-	ALA	deletion	UNP P38377
x	?	-	ARG	deletion	UNP P38377
x	?	-	ALA	deletion	UNP P38377
x	?	-	TYR	deletion	UNP P38377

- Molecule 49 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 50 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	29	Total	C	N	O	S	0	0
			229	157	36	34	2		

- Molecule 51 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1,RPN1.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	1	162	Total	C	N	O	0	0
			882	550	165	167		

- Molecule 52 is a protein called TMEM258.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	2	60	Total	C	N	O	0	0
			300	180	60	60		

- Molecule 53 is a protein called Oligosaccharyltransferase complex subunit OSTC.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	120	Total	C	N	O	S	0	0
			802	529	130	136	7		

- Molecule 54 is a protein called OST4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	34	Total	C	N	O	S	0	0
			268	180	41	45	2		

- Molecule 55 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	644	Total	C	N	O	S	0	0
			5090	3331	819	904	36		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	88	LEU	ILE	conflict	UNP F1PJP5

- Molecule 56 is a protein called DAD1.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	6	97	Total	C	N	O	0	0
			485	291	97	97		

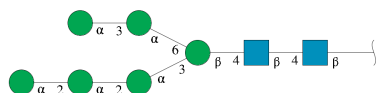
- Molecule 57 is a protein called OST48.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	7	25	Total	C	N	O	0	0
			125	75	25	25		

- Molecule 58 is a protein called RPN2.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	8	80	Total	C	N	O	0	0
			400	240	80	80		

- Molecule 59 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
59	K	8	Total	C	N	O	0	0
			94	52	2	40		

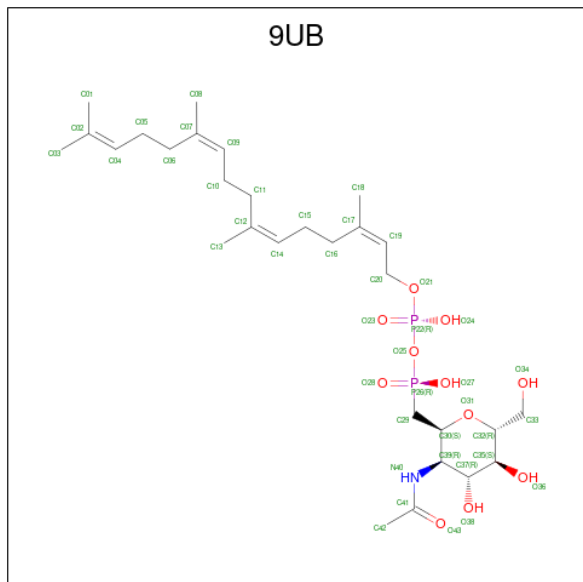
- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	B	1	Total	Mg	0
			1	1	
60	I	1	Total	Mg	0
			1	1	
60	P	1	Total	Mg	0
			1	1	
60	V	1	Total	Mg	0
			1	1	
60	a	1	Total	Mg	0
			1	1	
60	e	1	Total	Mg	0
			1	1	
60	g	1	Total	Mg	0
			1	1	
60	u	145	Total	Mg	0
			145	145	
60	v	5	Total	Mg	0
			5	5	
60	w	2	Total	Mg	0
			2	2	

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
61	g	1	Total Zn 1 1	0
61	j	1	Total Zn 1 1	0
61	m	1	Total Zn 1 1	0
61	o	1	Total Zn 1 1	0
61	p	1	Total Zn 1 1	0

- Molecule 62 is [(2 {S},3 {R},4 {R},5 {S},6 {R})-3-acetamido-6-(hydroxymethyl)-4,5-bis(oxidanyl)oxan-2-yl]methyl-[oxidanyl-[(2 {Z},6 {Z},10 {Z})-3,7,11,15-tetramethylhexadeca-2,6,10,14-tetraenoxylphosphoryl]oxy-phosphinic acid (CCD ID: 9UB) (formula: $C_{29}H_{51}NO_{11}P_2$).

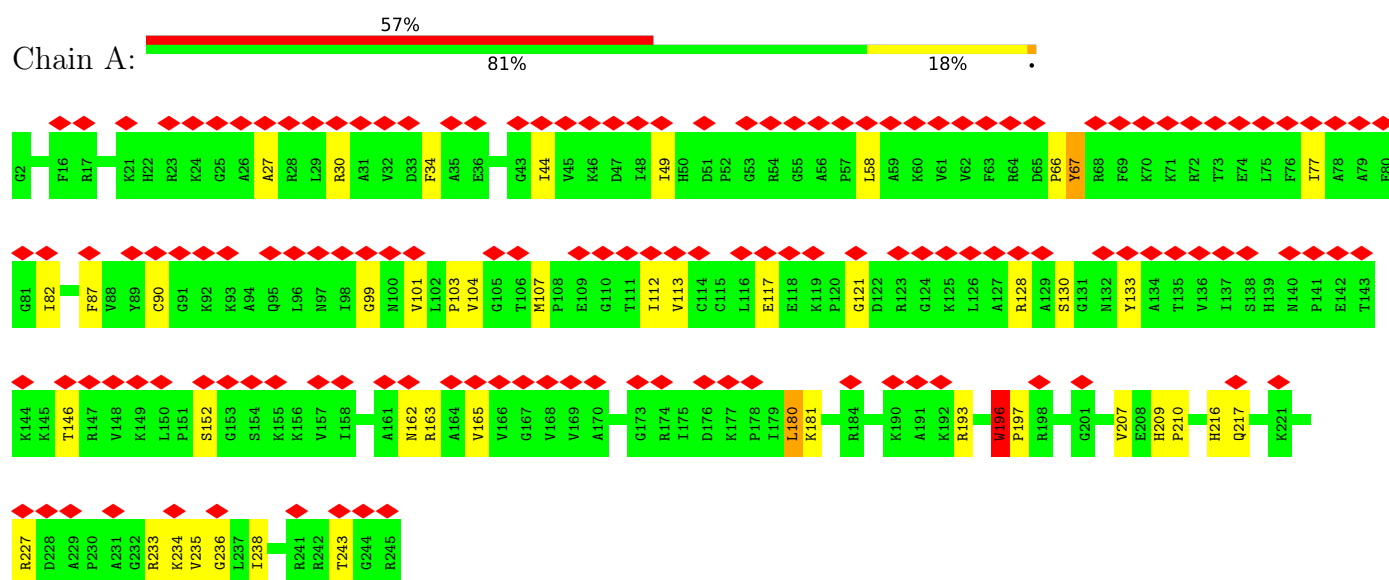


Mol	Chain	Residues	Atoms					AltConf
62	5	1	Total 43	C 29	N 1	O 11	P 2	0

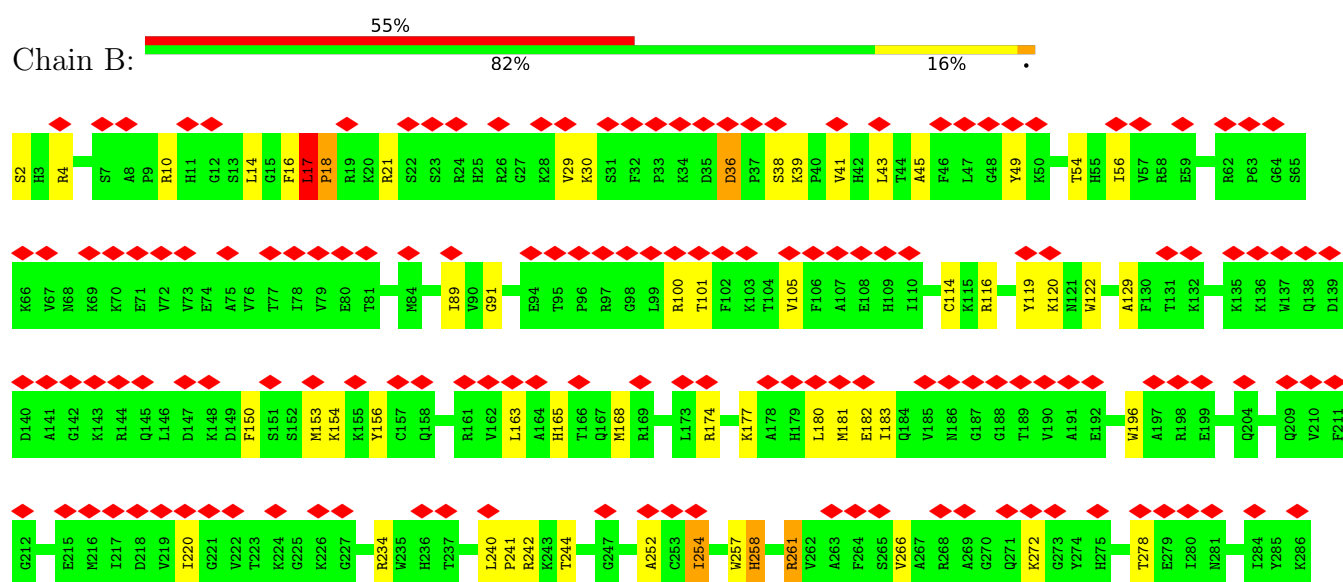
3 Residue-property plots

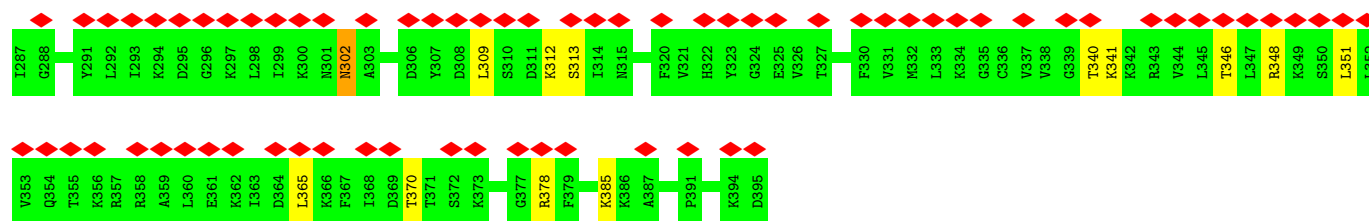
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: uL2

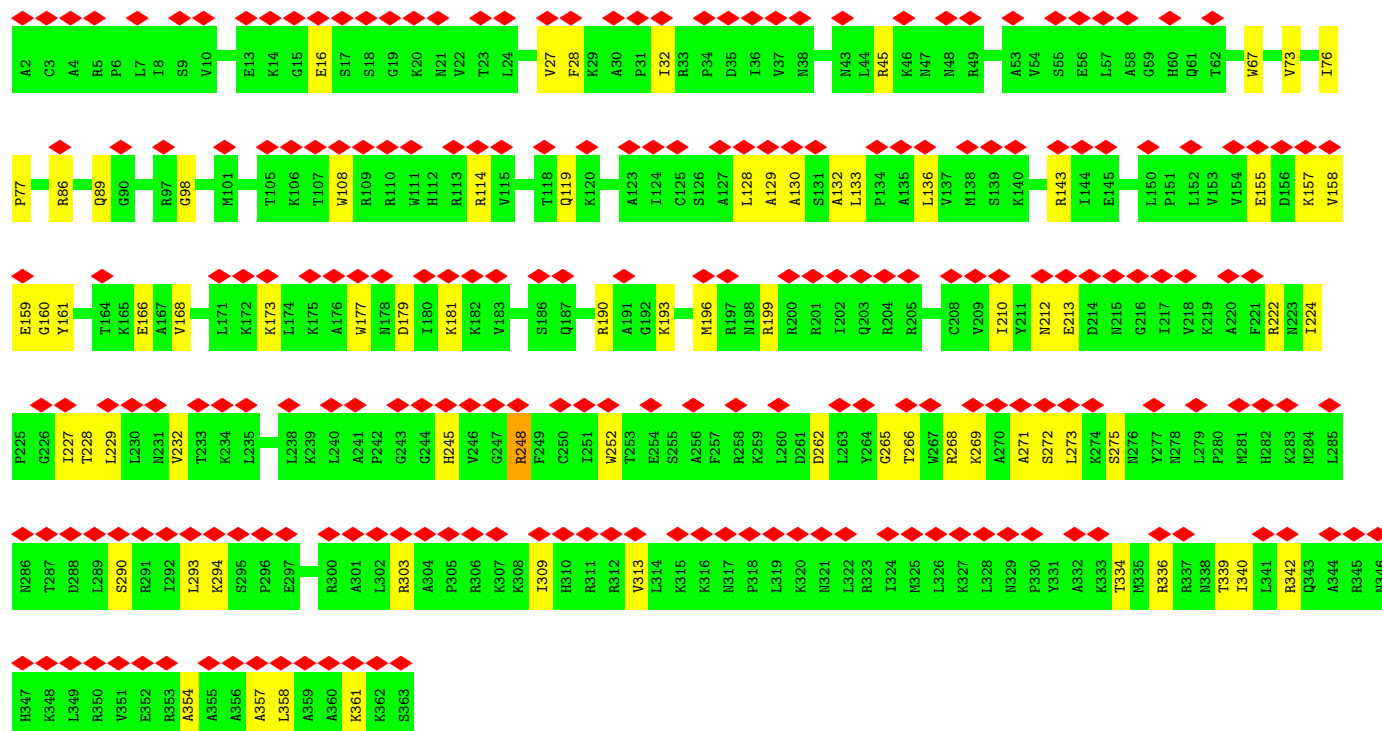
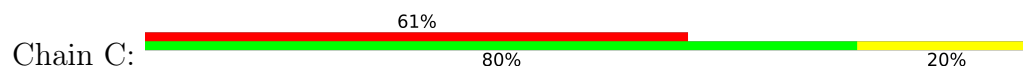


• Molecule 2: uL3

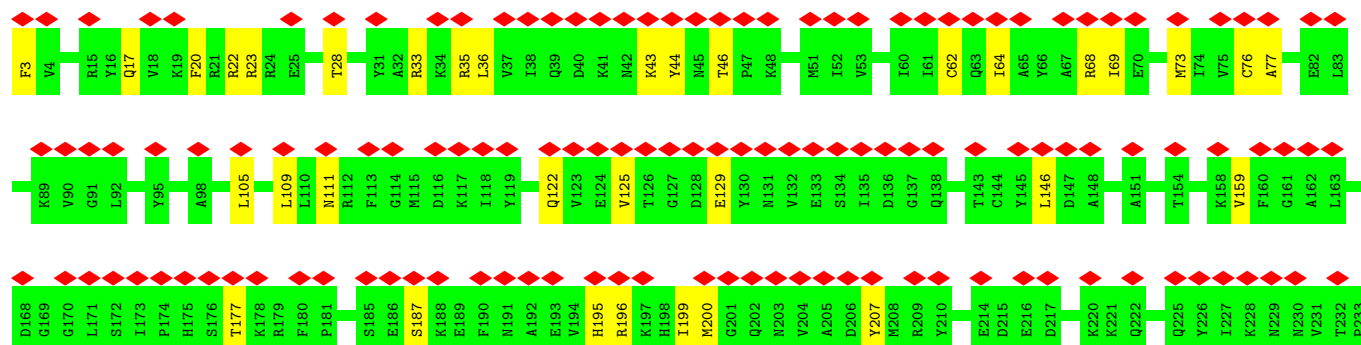
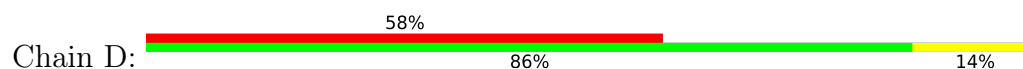


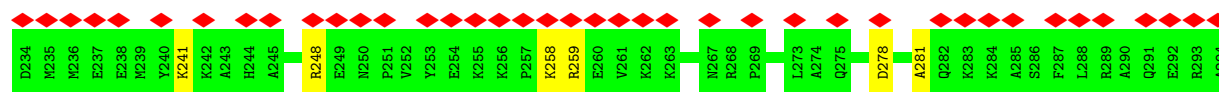


• Molecule 3: Ribosomal protein L4

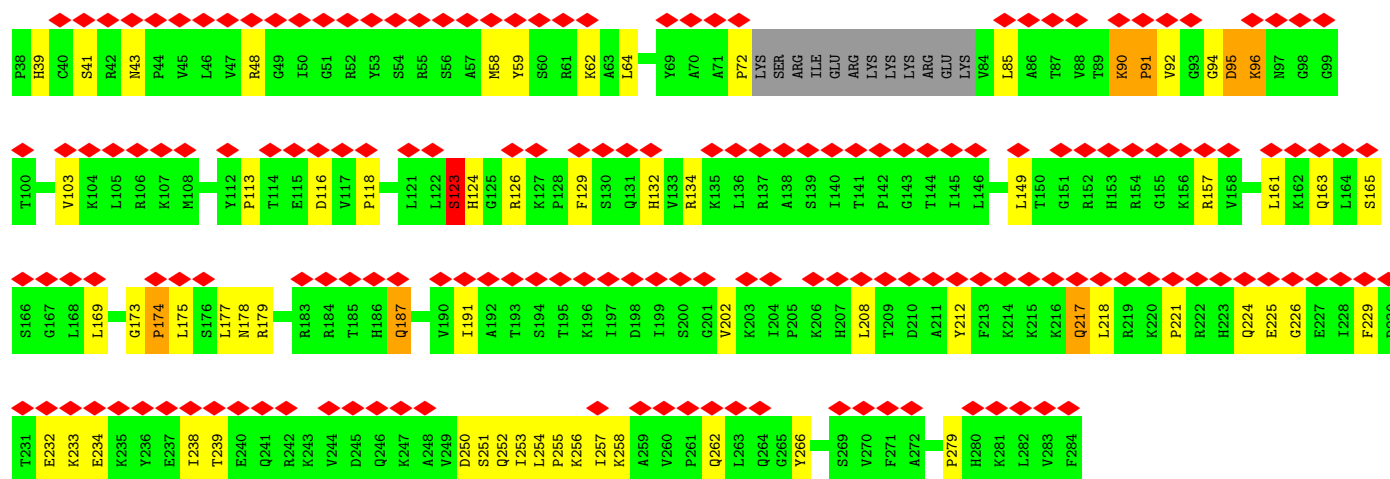


• Molecule 4: 60S ribosomal protein L5

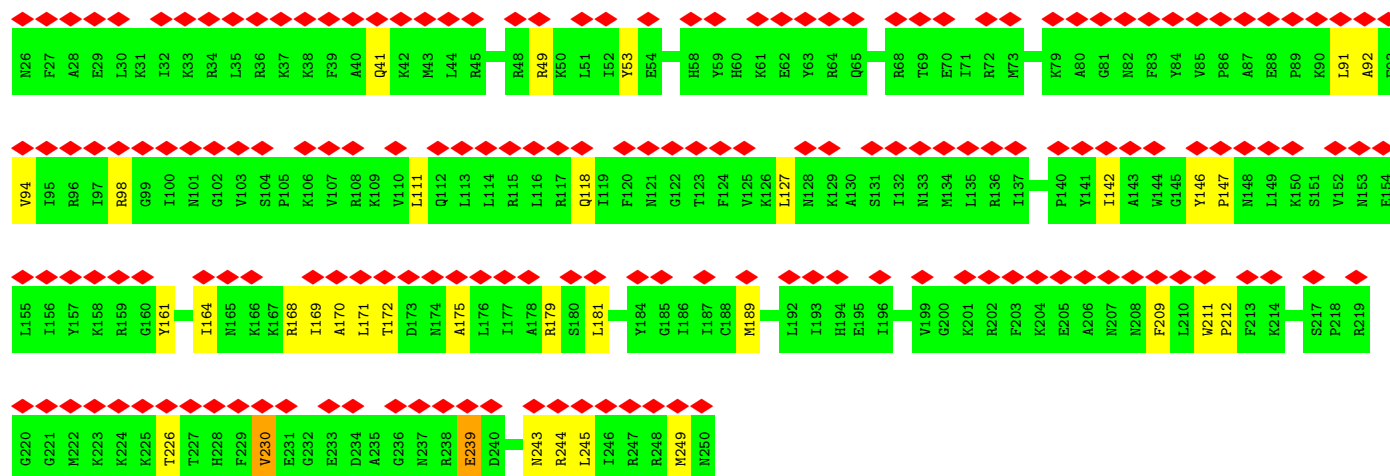
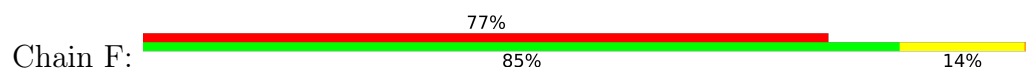




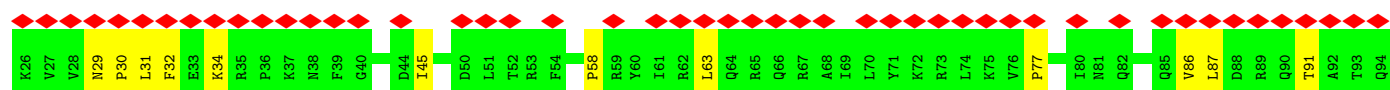
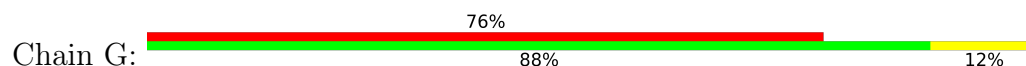
• Molecule 5: 60S ribosomal protein L6

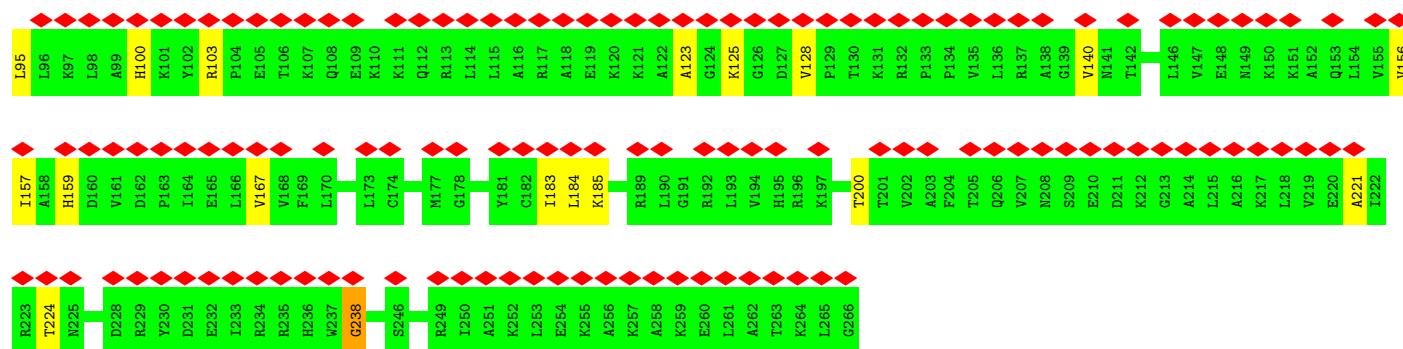


• Molecule 6: Ul30

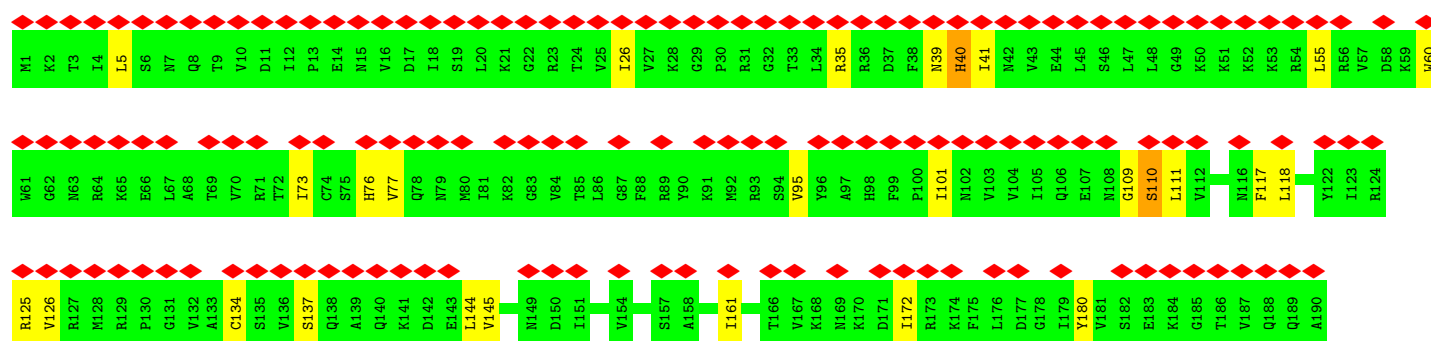
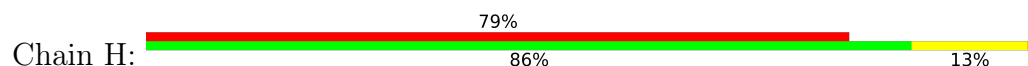


• Molecule 7: uL8

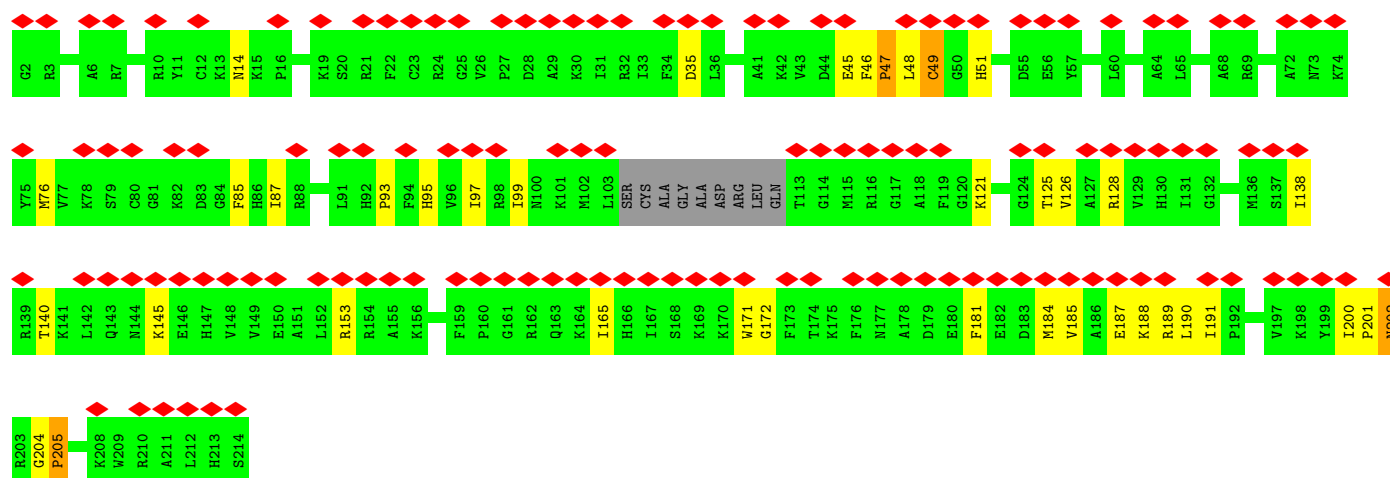
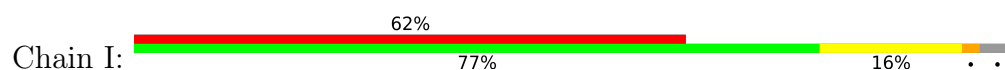




• Molecule 8: uL6

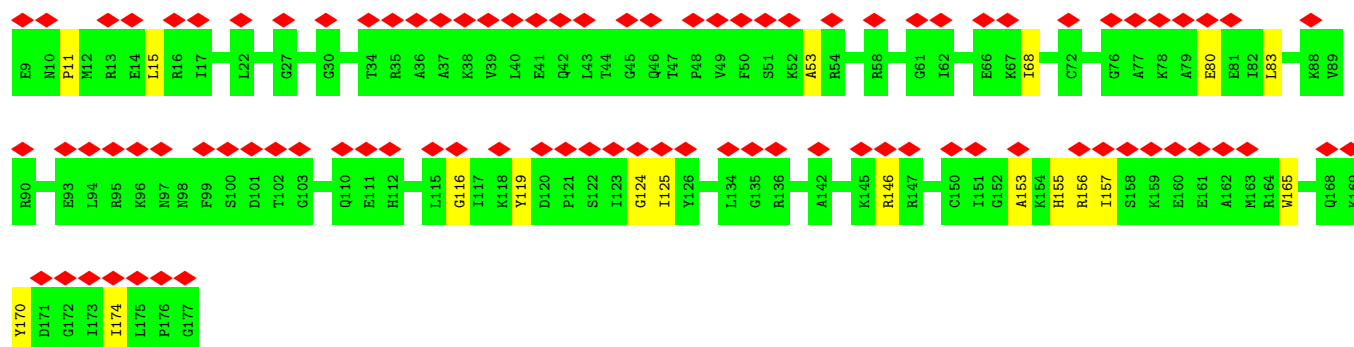


• Molecule 9: Ribosomal protein L10 (Predicted)

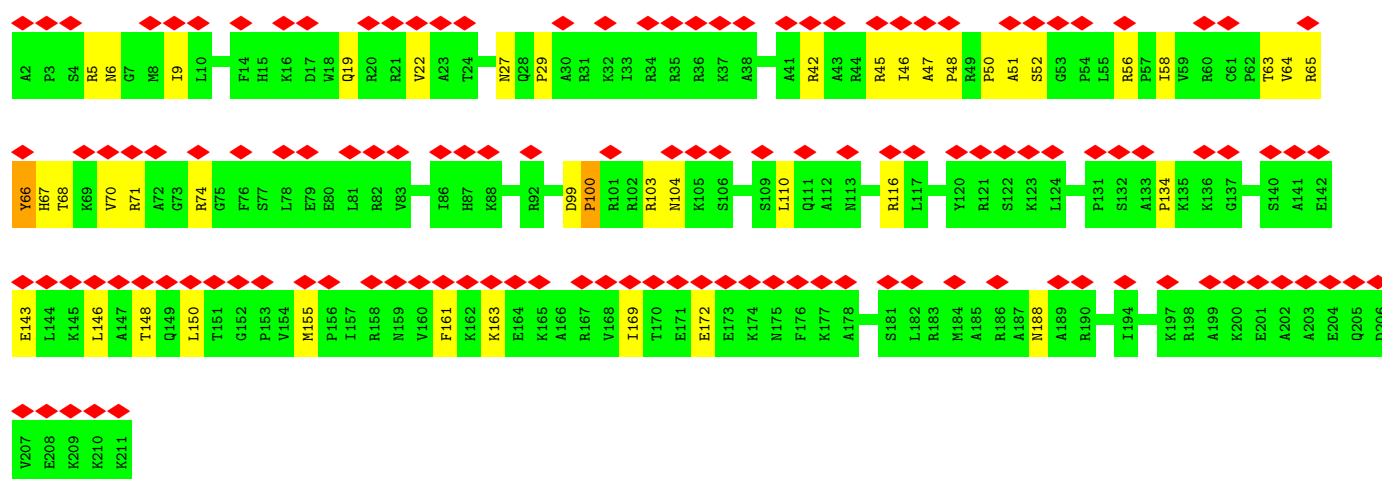


• Molecule 10: Ribosomal protein L11

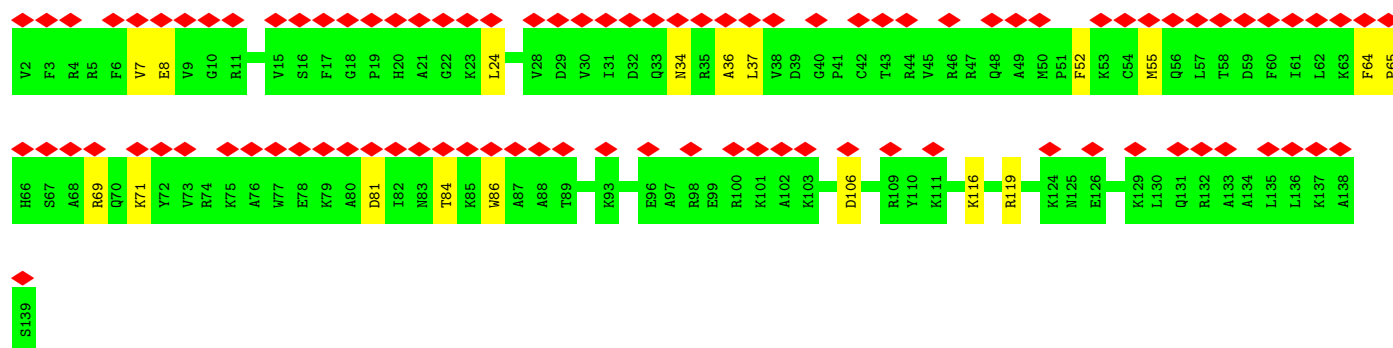
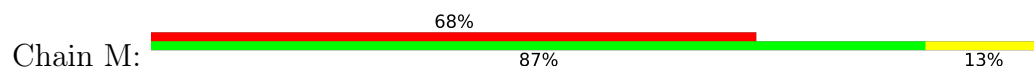




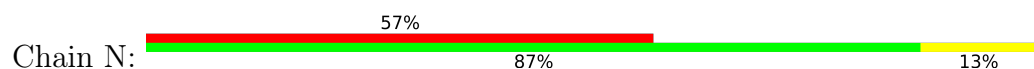
• Molecule 11: eL13

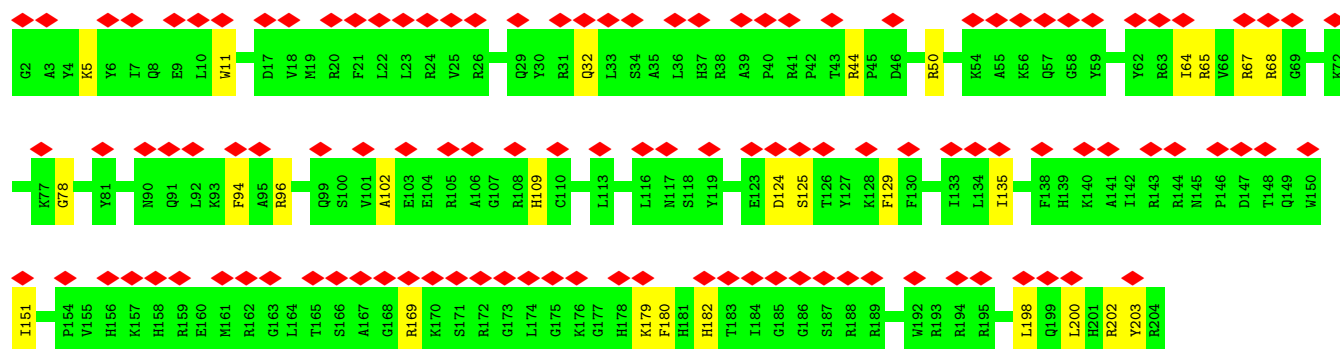


• Molecule 12: Ribosomal protein L14

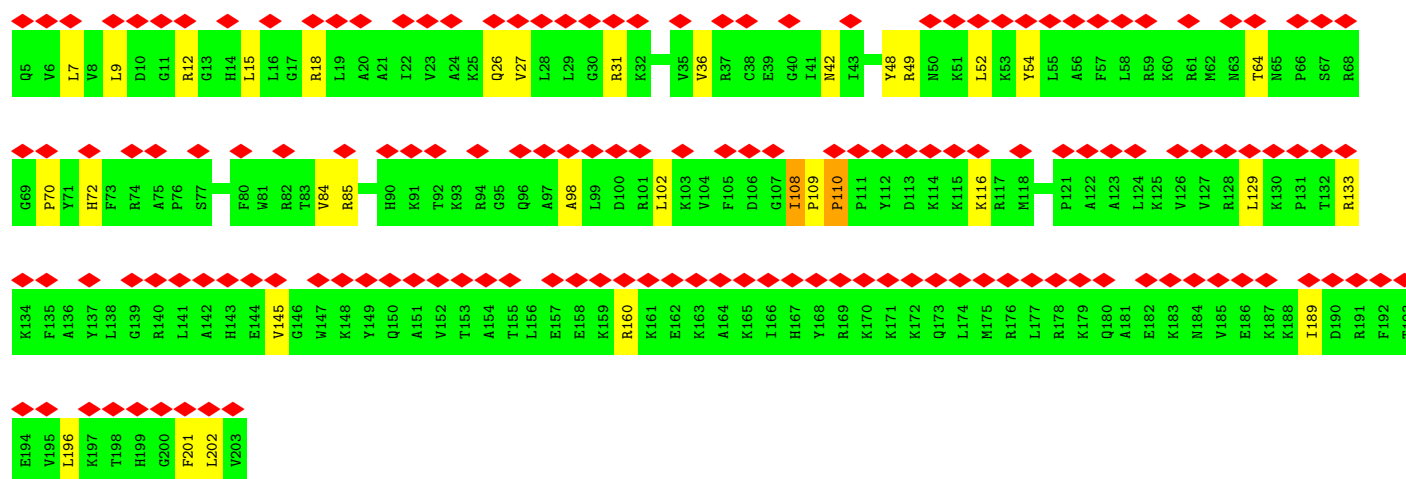
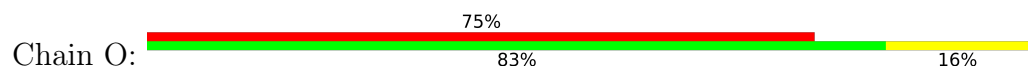


• Molecule 13: Ribosomal protein L15

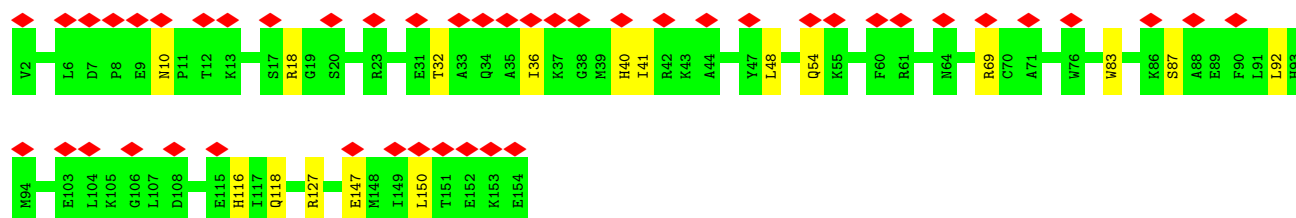
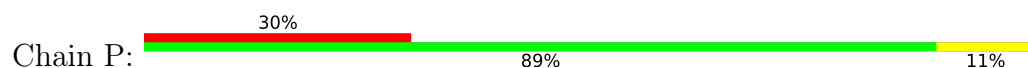




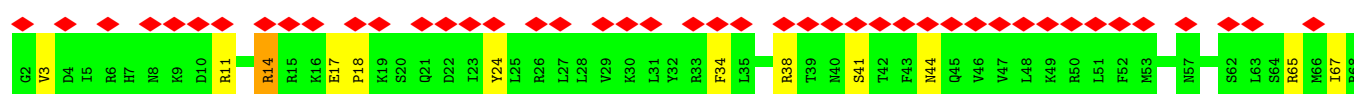
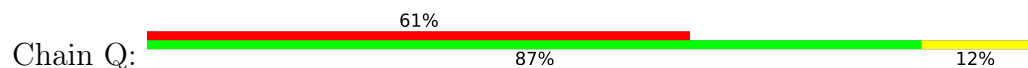
• Molecule 14: uL13

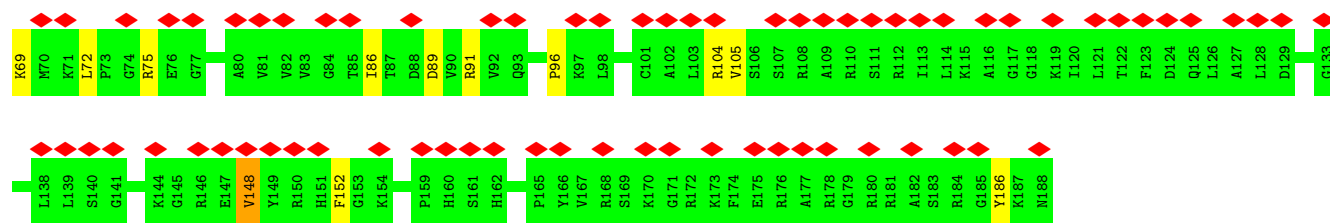


• Molecule 15: uL22

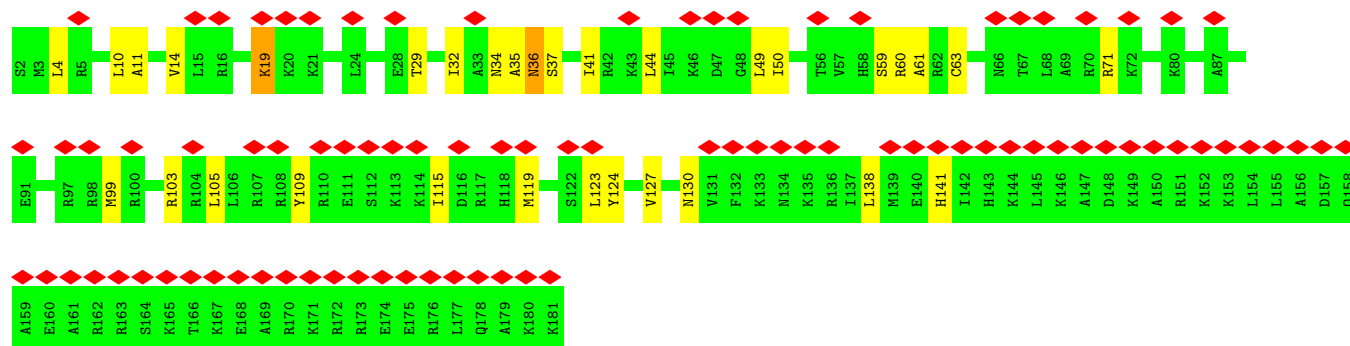
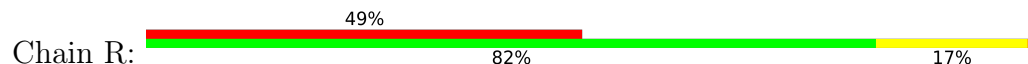


• Molecule 16: uL14

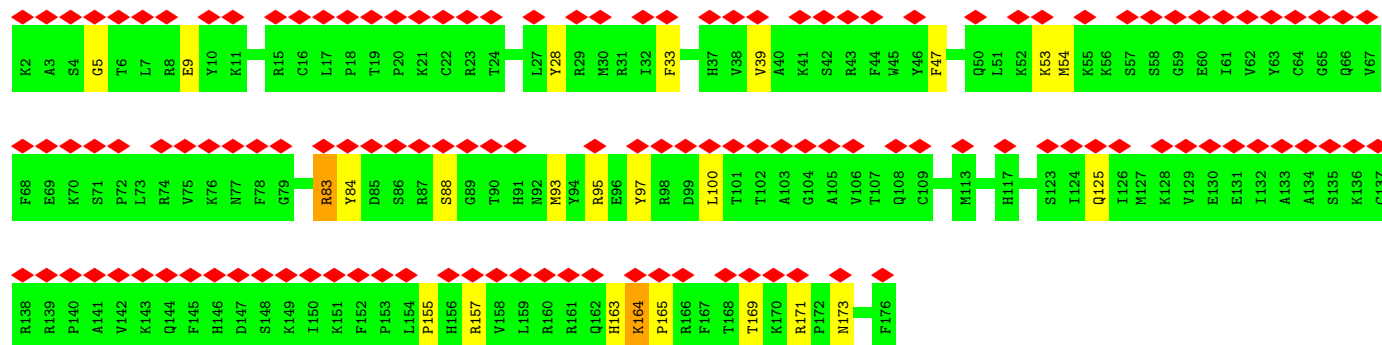
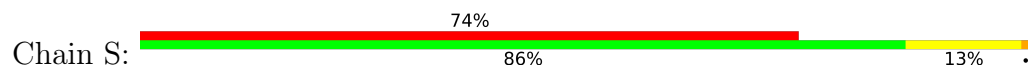




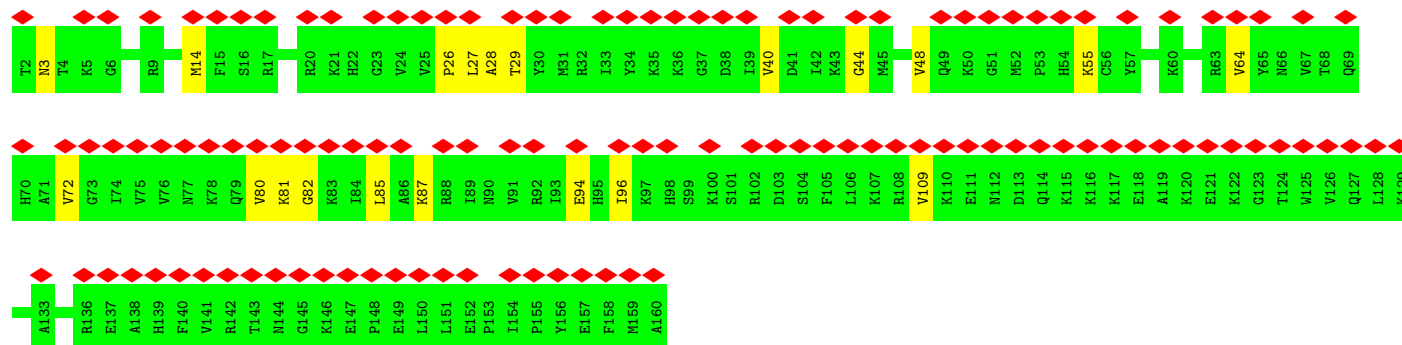
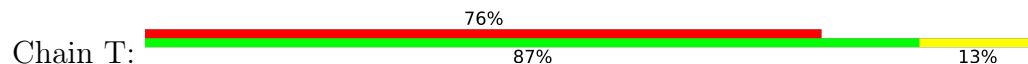
• Molecule 17: eL19



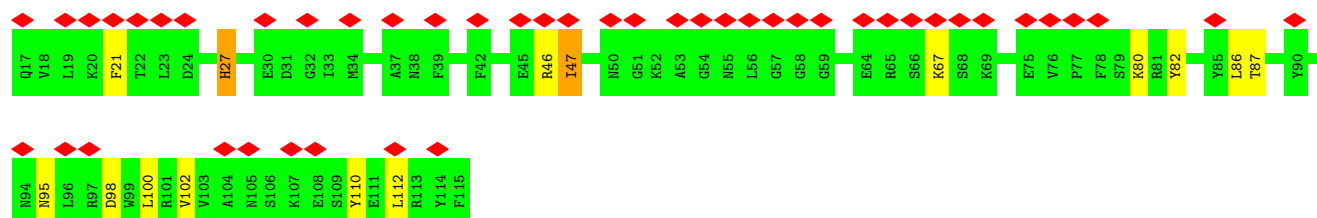
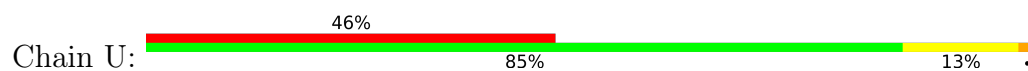
• Molecule 18: eL20



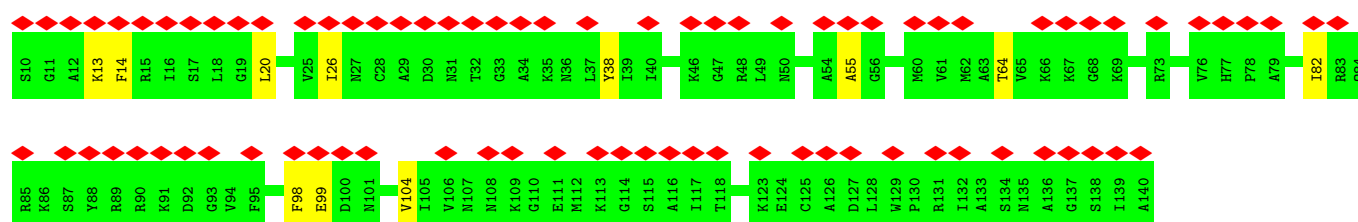
• Molecule 19: eL21



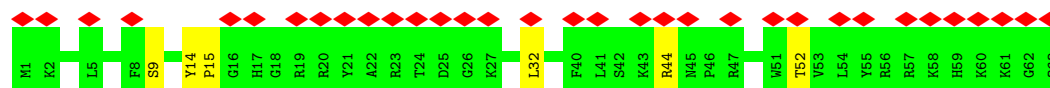
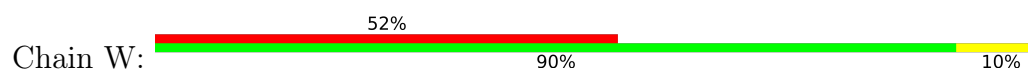
- Molecule 20: Ribosomal protein L22



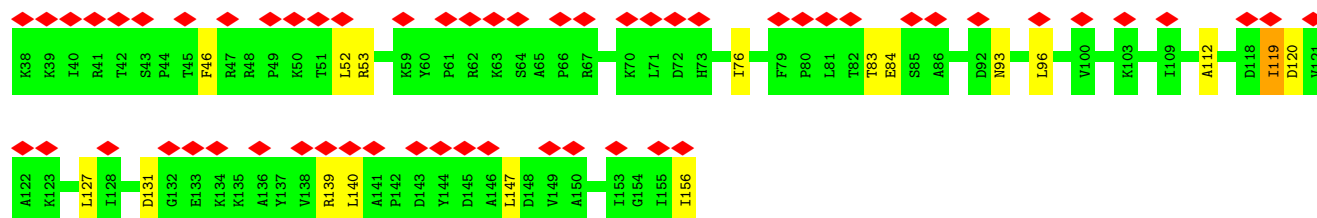
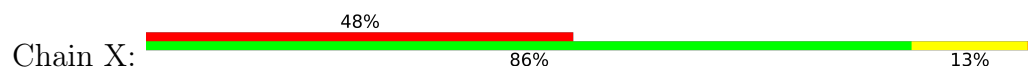
- Molecule 21: uL14



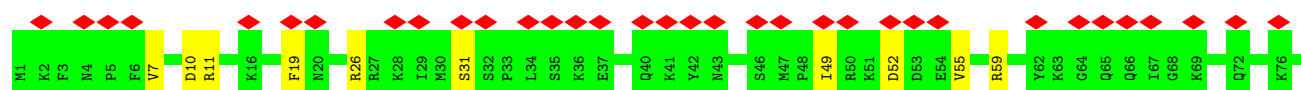
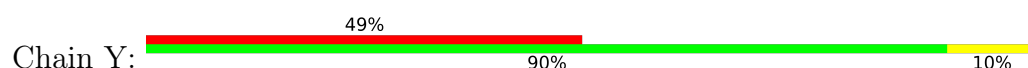
- Molecule 22: Ribosomal protein L24

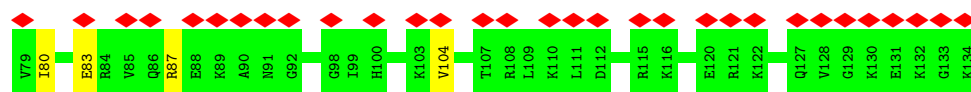


- Molecule 23: uL23

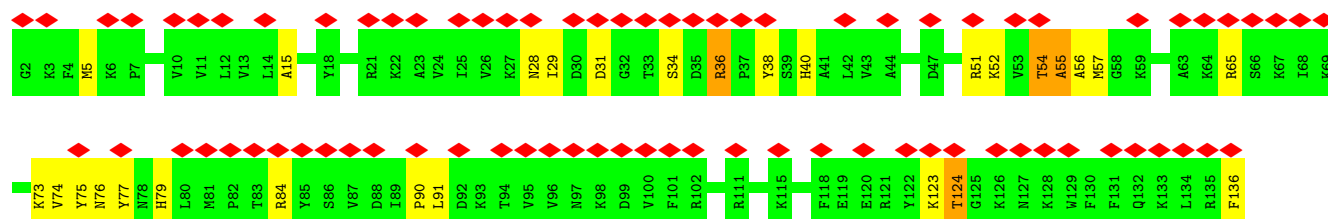
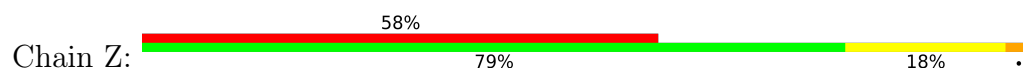


- Molecule 24: Ribosomal protein L26

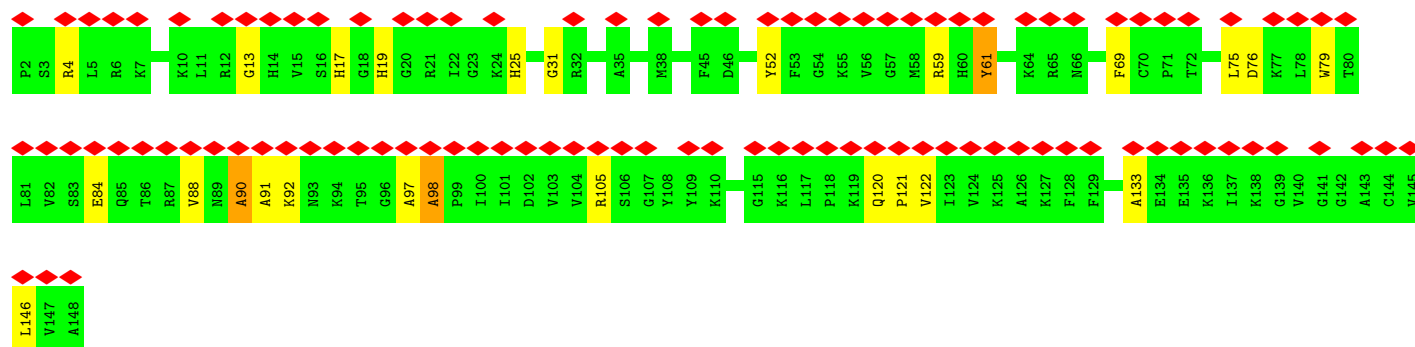
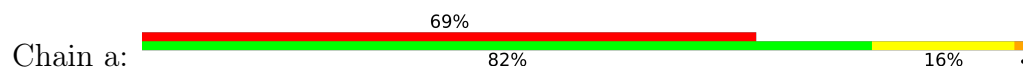




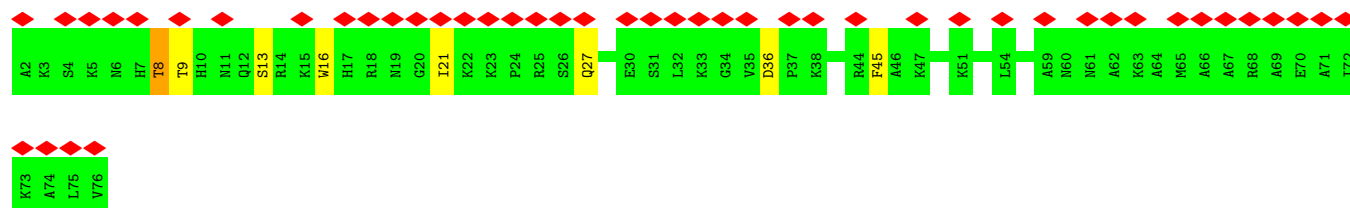
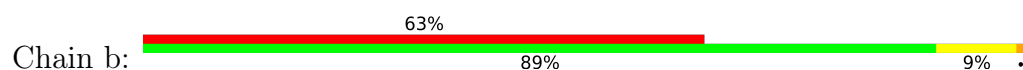
• Molecule 25: 60S ribosomal protein L27



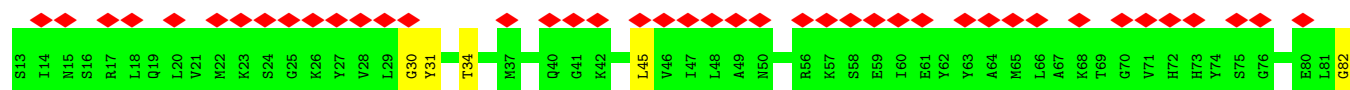
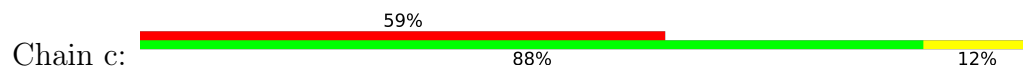
• Molecule 26: uL15

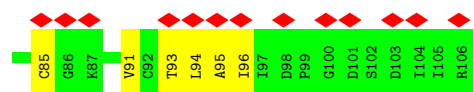


• Molecule 27: 60S ribosomal protein L29

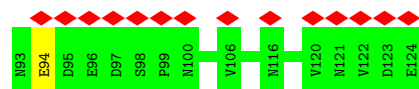
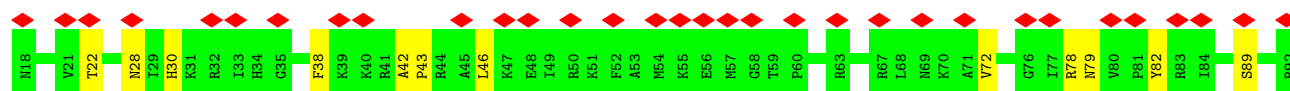
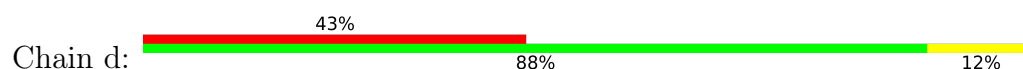


• Molecule 28: eL30

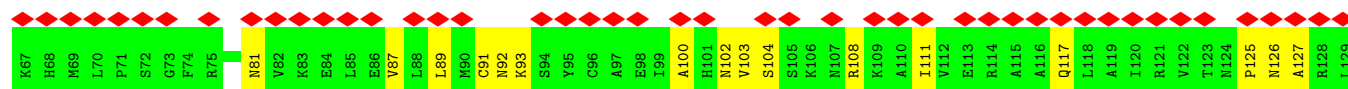
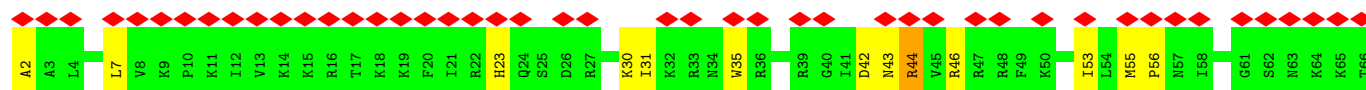
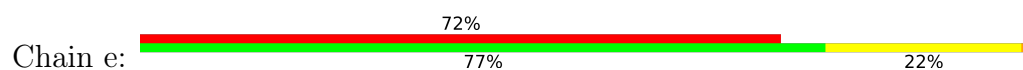




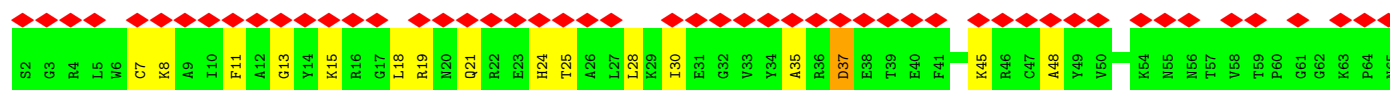
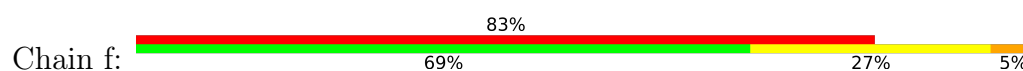
• Molecule 29: eL31



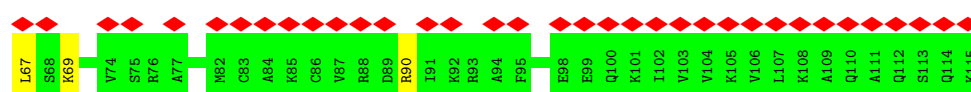
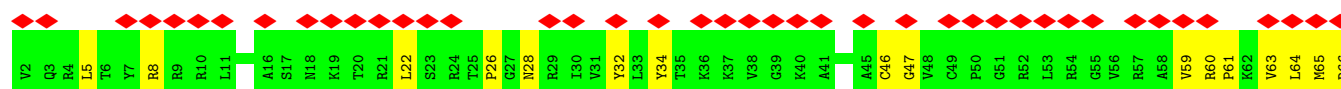
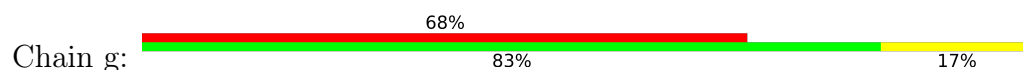
• Molecule 30: eL32



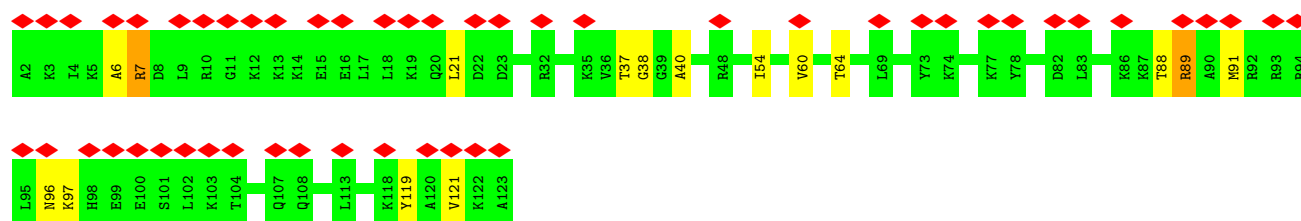
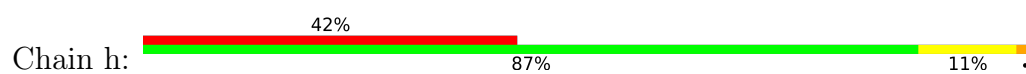
• Molecule 31: eL33



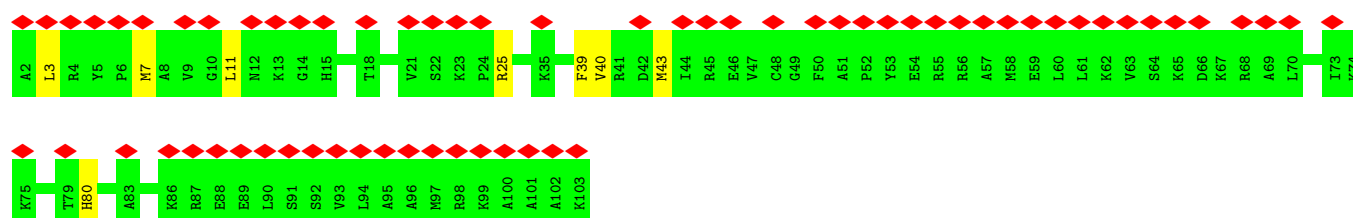
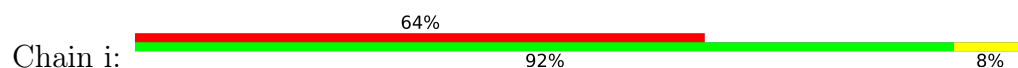
• Molecule 32: eL34



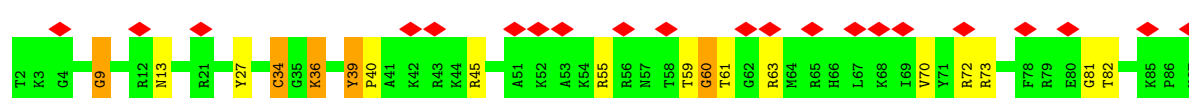
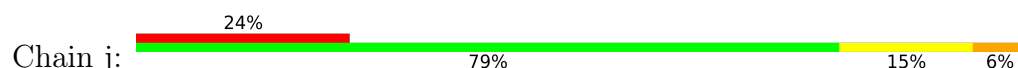
• Molecule 33: uL29



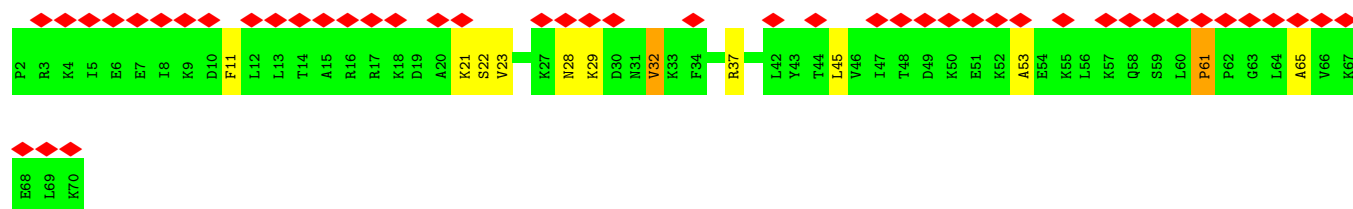
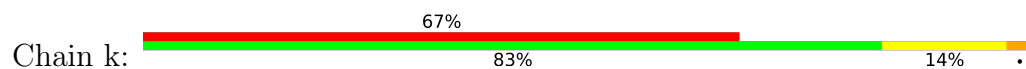
• Molecule 34: 60S ribosomal protein L36



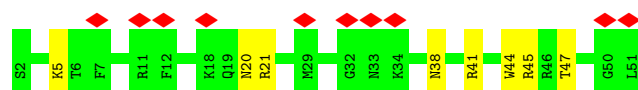
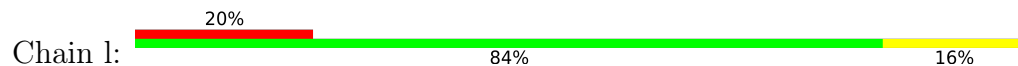
• Molecule 35: Ribosomal protein L37



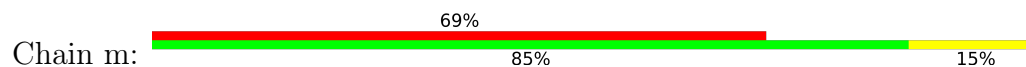
• Molecule 36: eL38

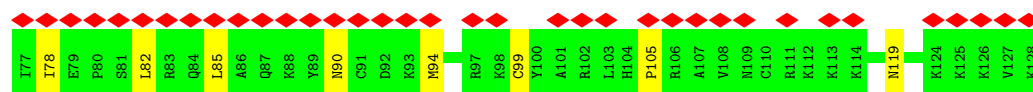


• Molecule 37: eL39



• Molecule 38: eL40

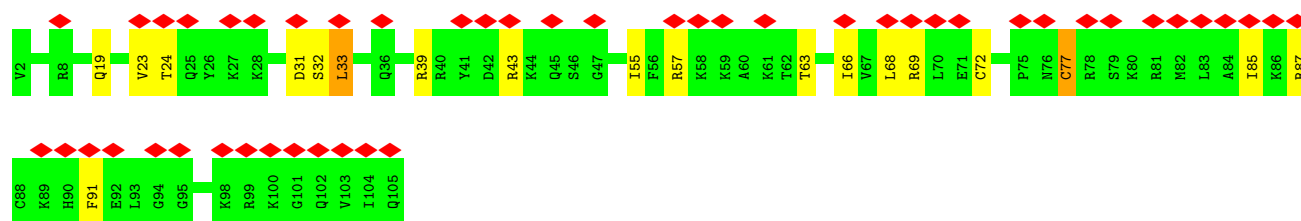
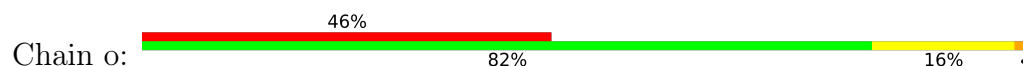




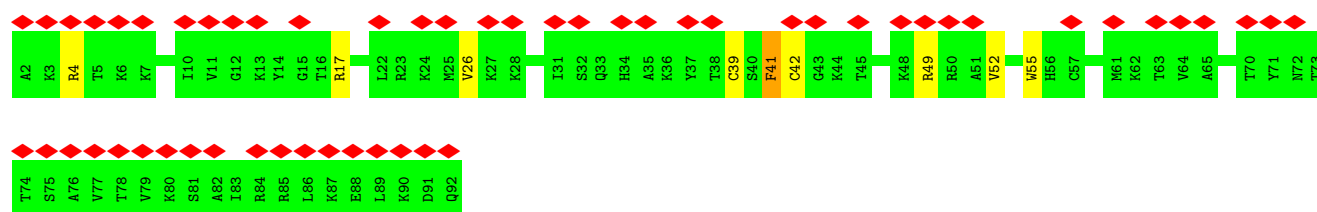
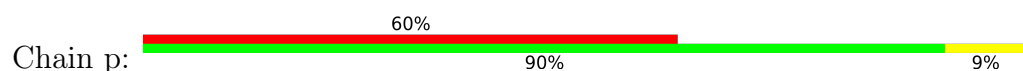
- Molecule 39: 60s ribosomal protein l41



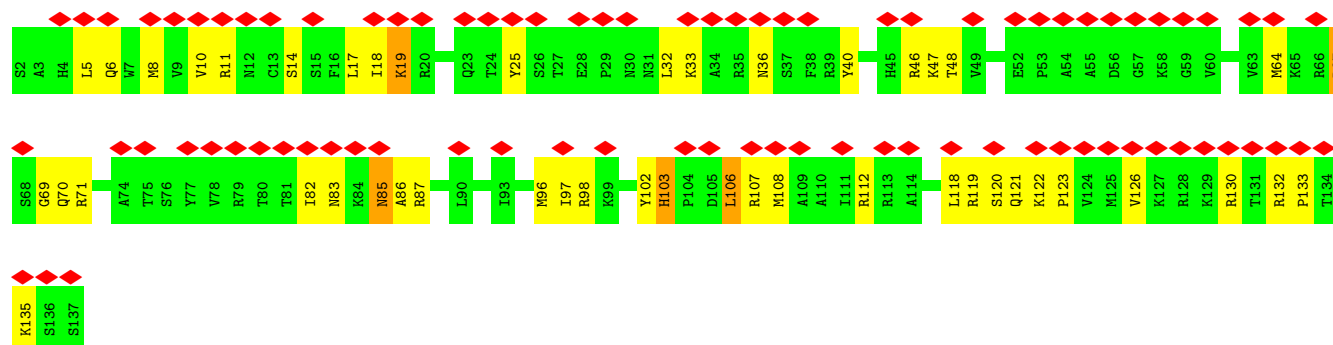
- Molecule 40: eL42



- Molecule 41: Ribosomal protein L37a

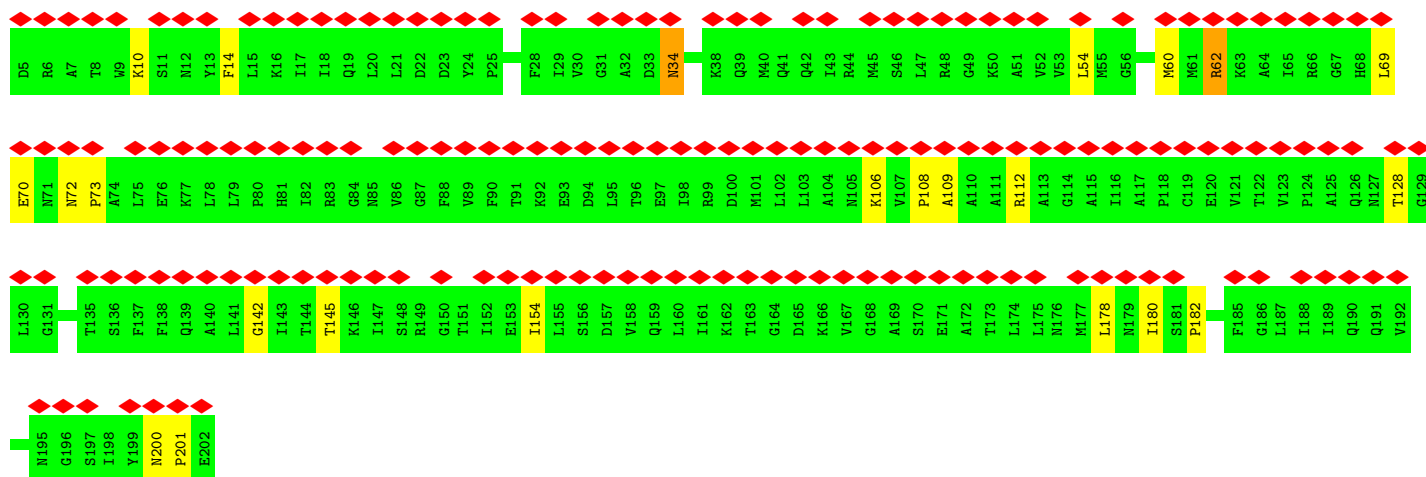


- Molecule 42: eL28



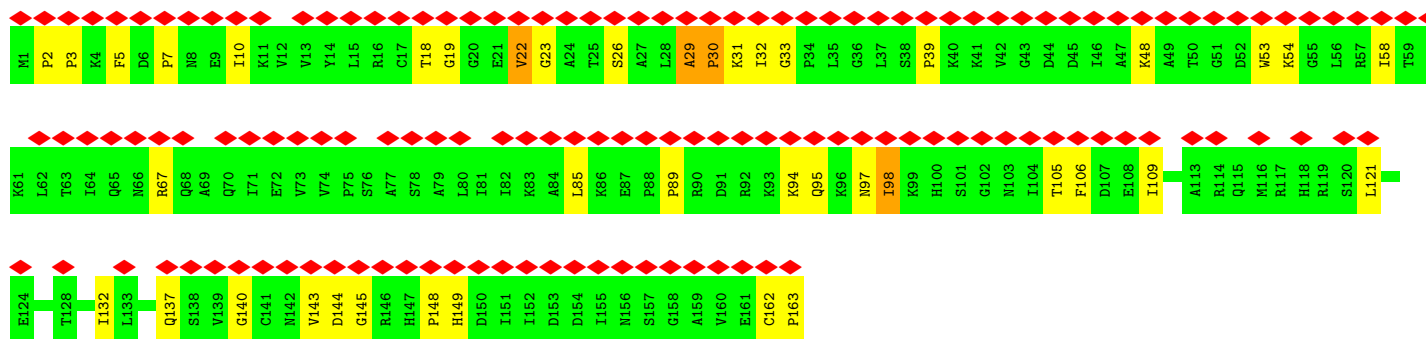
- Molecule 43: 60S acidic ribosomal protein P0

Chain s: 



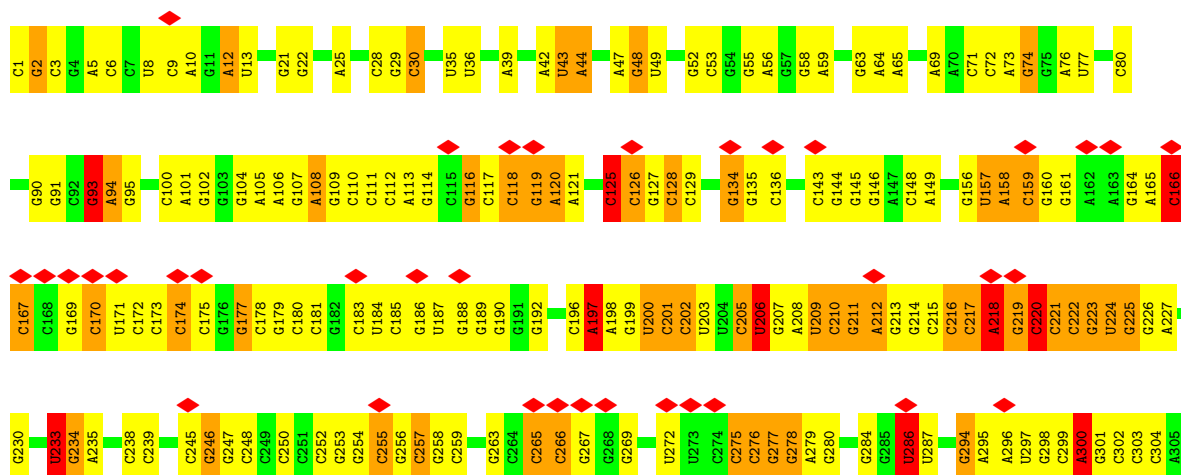
• Molecule 44: Ribosomal protein L12

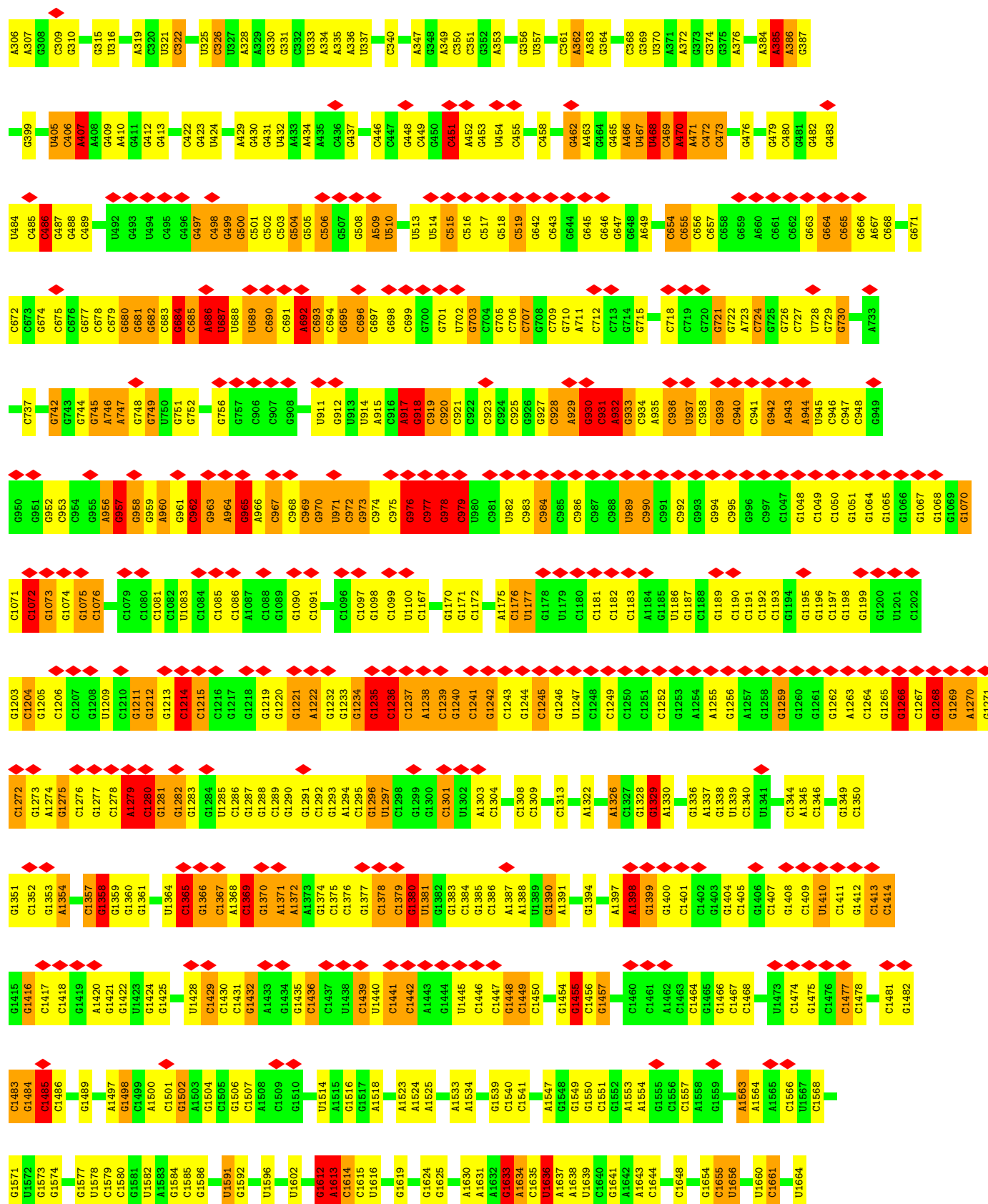
Chain t: 



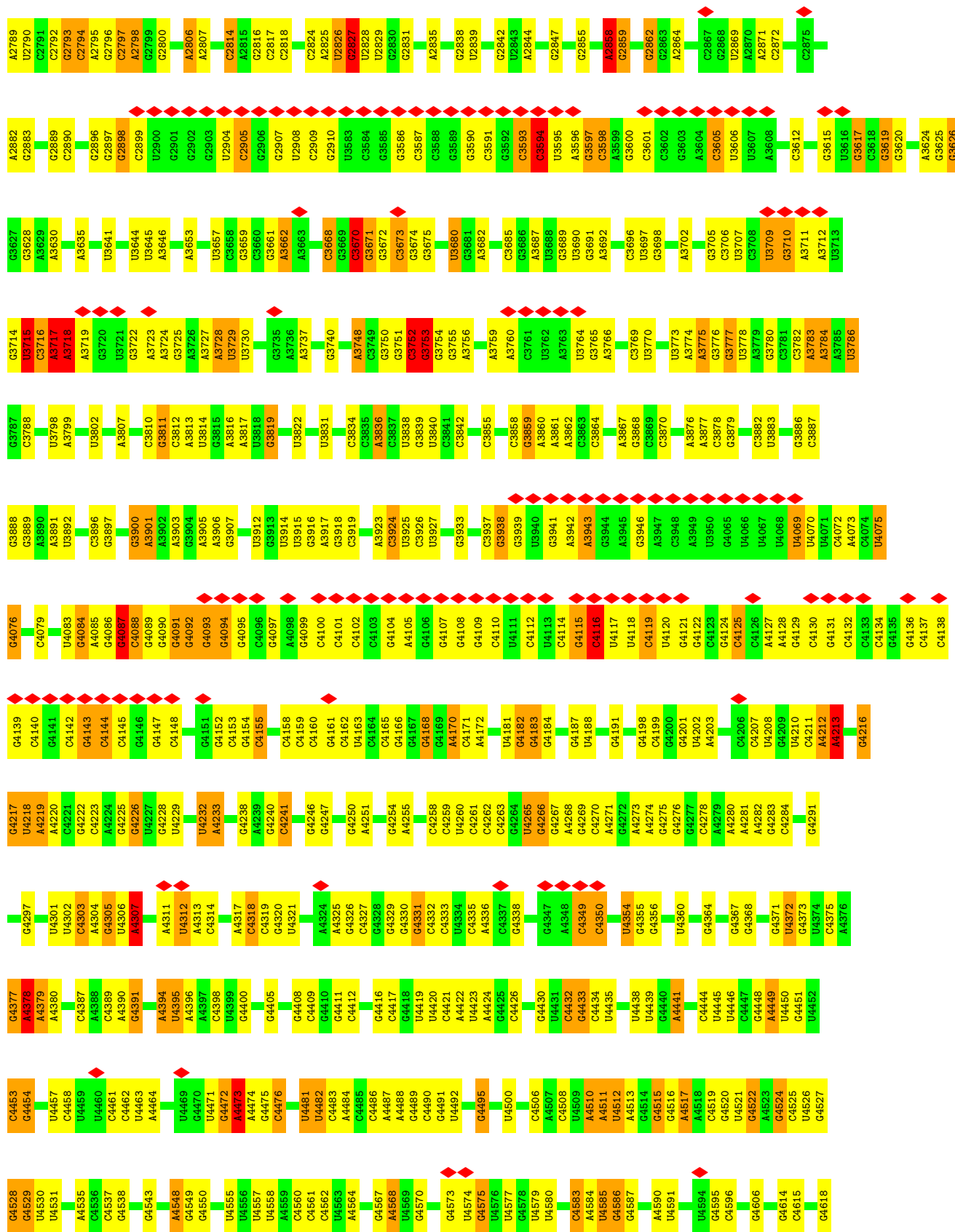
• Molecule 45: 28S rRNA

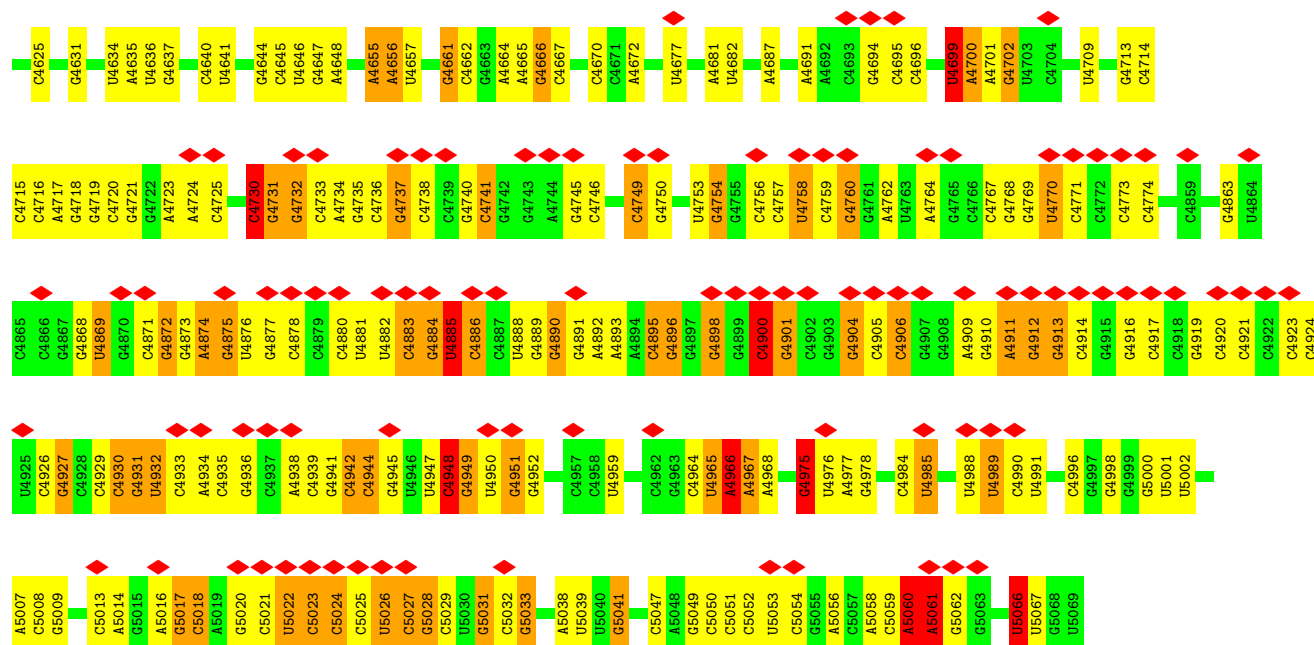
Chain u: 



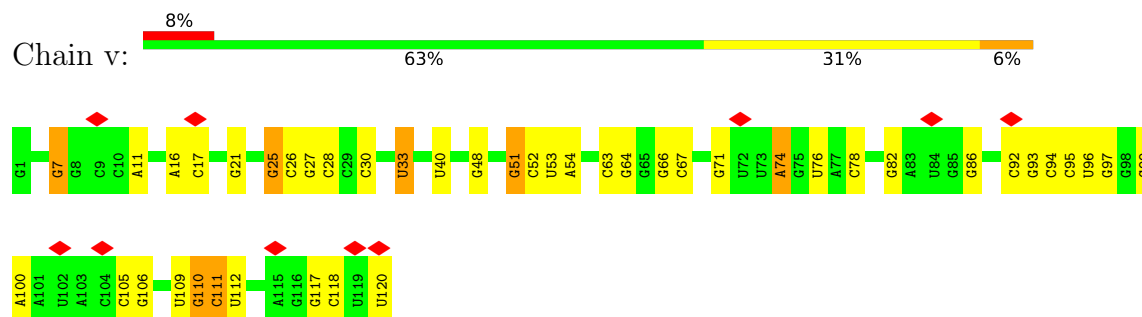




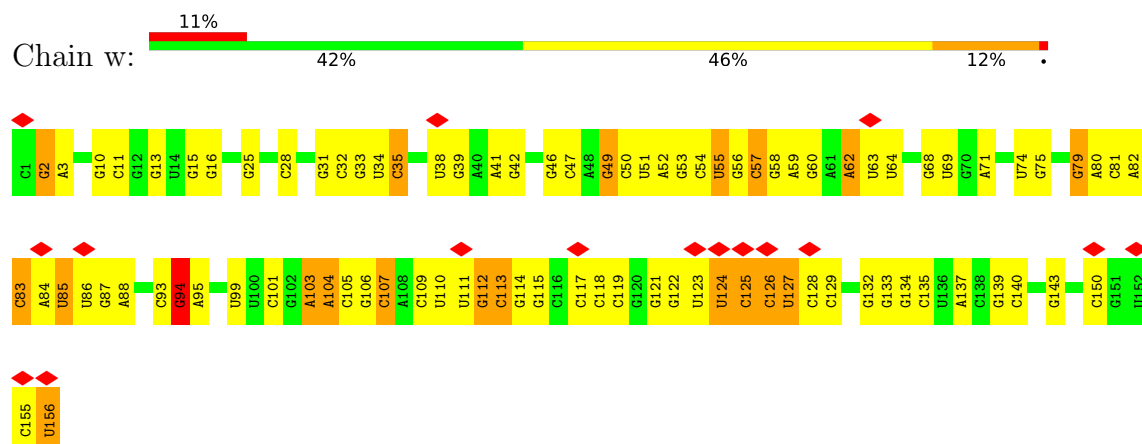




• Molecule 46: 5S ribosomal RNA

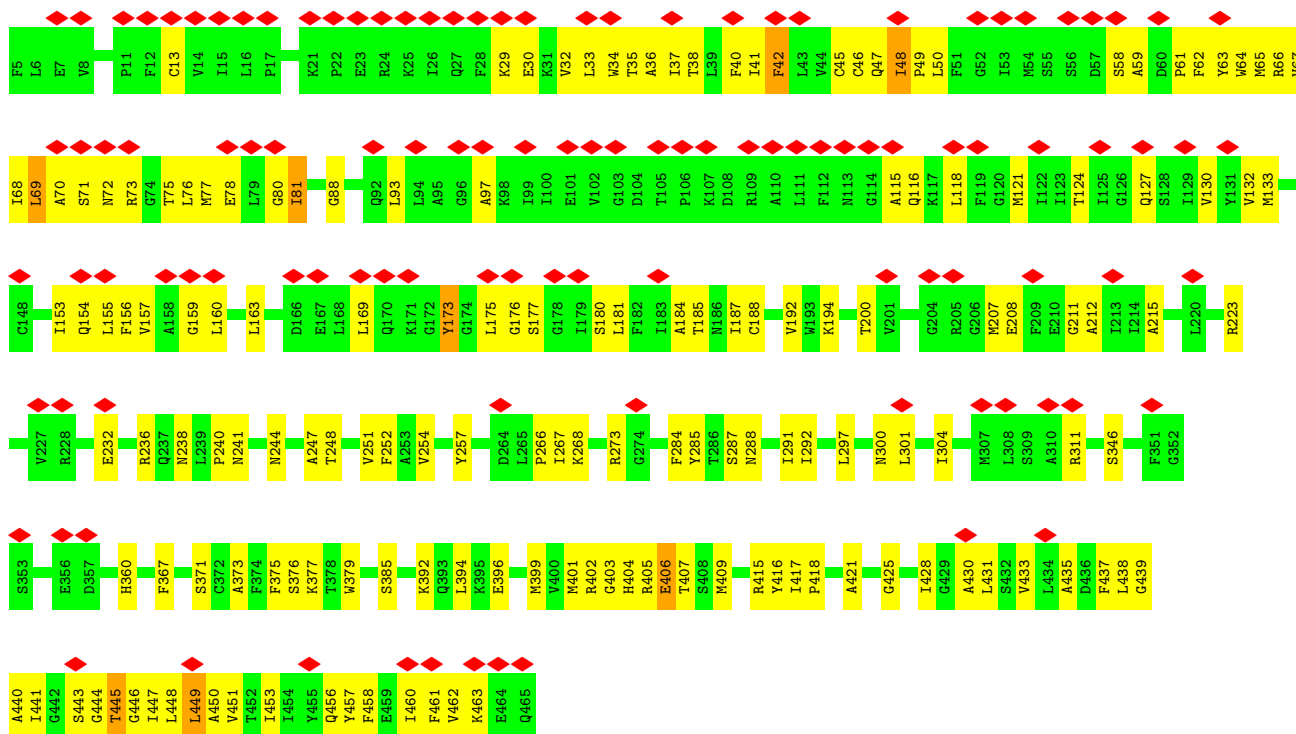


• Molecule 47: 5.8S ribosomal RNA

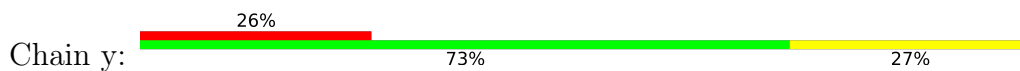


• Molecule 48: Protein transport protein Sec61 subunit alpha isoform 1

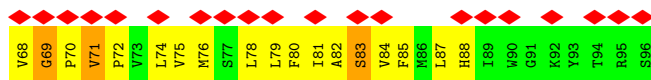




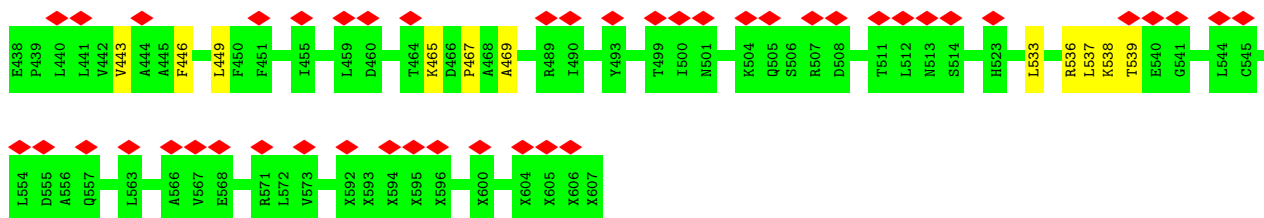
- Molecule 49: Protein transport protein Sec61 subunit gamma



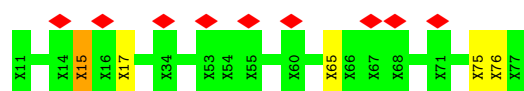
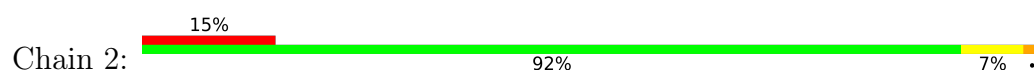
- Molecule 50: Protein transport protein Sec61 subunit beta



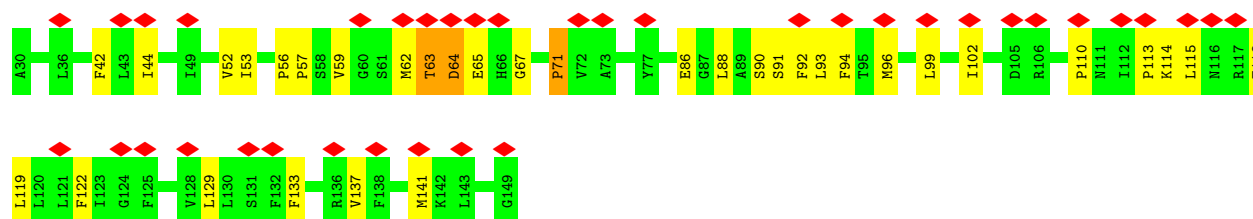
- Molecule 51: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1, RPN1



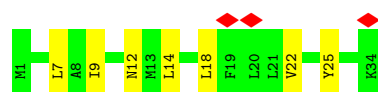
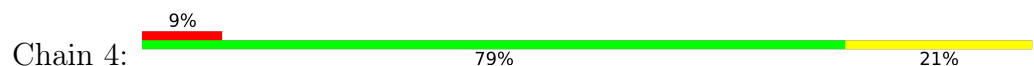
- Molecule 52: TMEM258



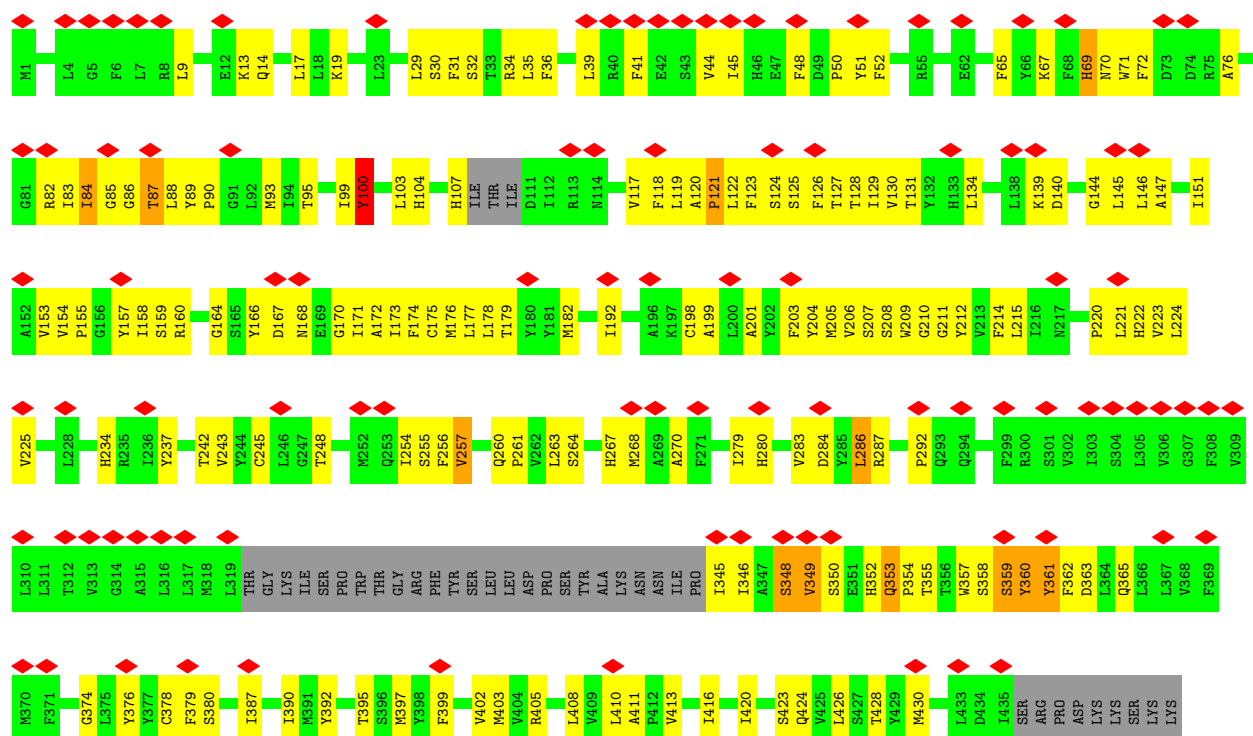
- Molecule 53: Oligosaccharyltransferase complex subunit OSTC

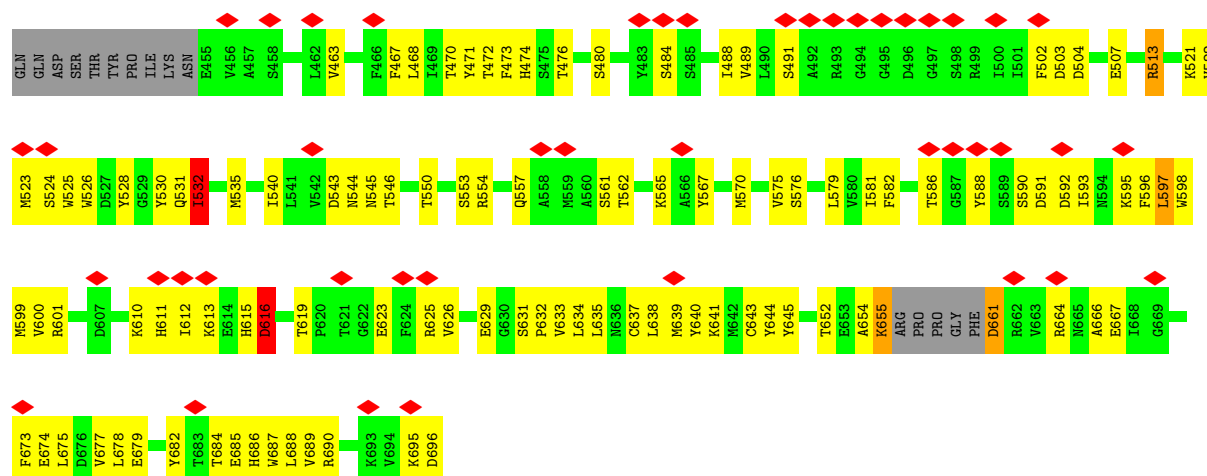


- Molecule 54: OST4

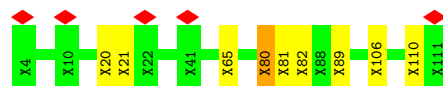
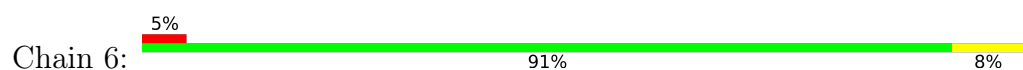


- Molecule 55: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A

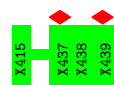




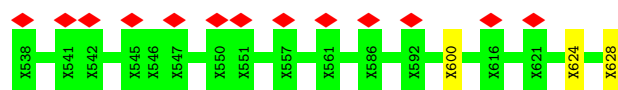
- Molecule 56: DAD1



- Molecule 57: OST48



- Molecule 58: RPN2



- Molecule 59: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	90895	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.291	Depositor
Minimum map value	-0.169	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	596.2, 596.2, 596.2	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1924, 1.1924, 1.1924	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, 9UB, ZN, BMA, NAG, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.63	3/1906 (0.2%)	0.92	2/2556 (0.1%)
2	B	0.53	0/3216	0.93	13/4311 (0.3%)
3	C	0.56	2/2938 (0.1%)	0.96	3/3946 (0.1%)
4	D	0.48	0/2432	0.86	0/3257
5	E	0.65	3/1936 (0.2%)	1.00	7/2600 (0.3%)
6	F	0.51	0/1905	0.87	0/2539
7	G	0.54	0/1967	0.94	2/2647 (0.1%)
8	H	0.52	1/1535 (0.1%)	0.82	2/2063 (0.1%)
9	I	0.56	1/1693 (0.1%)	0.87	3/2260 (0.1%)
10	J	0.48	0/1376	0.85	0/1841
11	L	0.55	1/1734 (0.1%)	0.92	1/2317 (0.0%)
12	M	0.49	0/1158	0.94	1/1547 (0.1%)
13	N	0.58	1/1746 (0.1%)	0.96	3/2338 (0.1%)
14	O	0.54	0/1671	0.95	3/2234 (0.1%)
15	P	0.59	3/1268 (0.2%)	0.91	4/1701 (0.2%)
16	Q	0.54	0/1530	0.89	0/2041
17	R	0.58	2/1524 (0.1%)	0.95	2/2013 (0.1%)
18	S	0.52	0/1493	0.95	2/2002 (0.1%)
19	T	0.55	1/1326 (0.1%)	0.84	1/1770 (0.1%)
20	U	0.52	1/822 (0.1%)	0.77	0/1103
21	V	0.55	0/993	0.88	1/1332 (0.1%)
22	W	0.58	0/541	0.94	2/720 (0.3%)
23	X	0.55	1/993 (0.1%)	0.90	0/1334
24	Y	0.48	0/1132	0.91	1/1504 (0.1%)
25	Z	0.51	0/1130	0.90	3/1507 (0.2%)
26	a	0.52	0/1191	0.97	4/1590 (0.3%)
27	b	0.57	1/619 (0.2%)	0.96	1/818 (0.1%)
28	c	0.49	0/742	0.93	0/996
29	d	0.51	0/903	0.87	0/1216
30	e	0.62	1/1071 (0.1%)	0.98	1/1429 (0.1%)
31	f	0.70	3/895 (0.3%)	1.02	7/1198 (0.6%)
32	g	0.55	1/916 (0.1%)	0.89	1/1220 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.49	0/1021	0.93	1/1348 (0.1%)
34	i	0.57	1/841 (0.1%)	0.94	2/1112 (0.2%)
35	j	0.61	0/720	1.03	1/952 (0.1%)
36	k	0.55	0/575	0.90	1/761 (0.1%)
37	l	0.67	0/454	0.92	0/599
38	m	0.51	0/435	0.90	0/575
39	n	0.55	0/223	0.88	0/284
40	o	0.52	0/864	0.86	0/1140
41	p	0.57	0/718	0.94	1/953 (0.1%)
42	r	0.62	2/1110 (0.2%)	0.98	2/1484 (0.1%)
43	s	0.59	0/1547	0.81	3/2088 (0.1%)
44	t	0.64	0/1257	0.97	3/1697 (0.2%)
45	u	0.44	7/87790 (0.0%)	0.90	299/136937 (0.2%)
46	v	0.38	0/2858	0.77	1/4455 (0.0%)
47	w	0.40	0/3701	0.82	3/5766 (0.1%)
48	x	0.52	0/3383	0.96	9/4584 (0.2%)
49	y	0.47	0/504	0.93	0/673
50	z	0.53	0/236	1.50	5/321 (1.6%)
51	1	0.45	0/757	0.74	1/1052 (0.1%)
53	3	0.53	0/815	1.16	10/1107 (0.9%)
54	4	0.43	0/273	0.68	0/371
55	5	0.80	4/5224 (0.1%)	1.11	28/7093 (0.4%)
All	All	0.50	40/161608 (0.0%)	0.91	440/237302 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	4
3	C	0	2
4	D	0	1
5	E	0	1
7	G	0	1
9	I	0	2
11	L	0	3
17	R	0	1
18	S	0	2
19	T	0	1
20	U	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	Y	0	1
31	f	0	1
42	r	0	2
45	u	0	1
48	x	0	2
52	2	0	1
53	3	0	2
55	5	0	6
56	6	0	5
All	All	0	41

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	5	545	ASN	C-N	-29.89	0.91	1.33
55	5	550	THR	C-N	-28.48	0.96	1.34
45	u	680	G	O3'-P	-26.91	1.20	1.61
45	u	692	A	O3'-P	26.39	2.00	1.61
45	u	1965	G	O3'-P	-18.43	1.33	1.61
55	5	513	ARG	C-N	15.90	1.58	1.33
45	u	472	C	O3'-P	-15.71	1.37	1.61
45	u	197	A	O3'-P	10.55	1.76	1.61
45	u	462	G	O3'-P	-7.39	1.50	1.61
55	5	532	ILE	C-N	6.59	1.43	1.33
19	T	3	ASN	CG-OD1	5.77	1.34	1.23
42	r	6	GLN	CD-OE1	5.50	1.33	1.23
5	E	187	GLN	CD-OE1	5.47	1.33	1.23
32	g	28	ASN	CG-OD1	5.38	1.33	1.23
31	f	24	HIS	ND1-CE1	5.34	1.37	1.32
23	X	93	ASN	CG-OD1	5.33	1.33	1.23
3	C	212	ASN	CG-OD1	5.32	1.33	1.23
3	C	119	GLN	CD-OE1	5.30	1.33	1.23
17	R	34	ASN	CG-OD1	5.29	1.33	1.23
27	b	27	GLN	CD-OE1	5.28	1.33	1.23
15	P	116	HIS	ND1-CE1	5.26	1.37	1.32
17	R	141	HIS	ND1-CE1	5.24	1.37	1.32
45	u	223	G	O3'-P	-5.24	1.53	1.61
34	i	80	HIS	ND1-CE1	5.22	1.37	1.32
30	e	102	ASN	CG-OD1	5.17	1.33	1.23
42	r	83	ASN	CG-OD1	5.17	1.33	1.23
15	P	40	HIS	CD2-NE2	-5.15	1.32	1.37
31	f	21	GLN	CD-OE1	5.15	1.33	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	N	109	HIS	ND1-CE1	5.15	1.37	1.32
15	P	40	HIS	ND1-CE1	5.13	1.37	1.32
20	U	95	ASN	CG-OD1	5.12	1.33	1.23
1	A	216	HIS	ND1-CE1	5.10	1.37	1.32
8	H	76	HIS	ND1-CE1	5.09	1.37	1.32
1	A	216	HIS	CD2-NE2	-5.09	1.32	1.37
31	f	21	GLN	CD-NE2	-5.06	1.22	1.33
5	E	39	HIS	ND1-CE1	5.05	1.37	1.32
5	E	163	GLN	CD-OE1	5.05	1.33	1.23
9	I	95	HIS	ND1-CE1	5.04	1.37	1.32
1	A	162	ASN	CG-OD1	5.04	1.33	1.23
11	L	188	ASN	CG-OD1	5.03	1.33	1.23

All (440) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	5	545	ASN	CA-C-N	-22.05	79.43	121.54
55	5	545	ASN	C-N-CA	-22.05	79.43	121.54
55	5	545	ASN	O-C-N	20.82	146.53	122.79
45	u	680	G	O3'-P-O5'	18.20	131.31	104.00
55	5	550	THR	O-C-N	-14.62	106.30	122.09
3	C	98	GLY	N-CA-C	-13.76	99.01	111.67
45	u	1358	G	C4'-C3'-O3'	13.60	133.39	113.00
45	u	462	G	P-O3'-C3'	-13.35	100.18	120.20
45	u	4975	G	C2'-C3'-O3'	13.14	129.20	109.50
53	3	56	PRO	N-CA-CB	12.96	109.96	103.22
55	5	550	THR	CA-C-N	12.96	139.30	120.38
55	5	550	THR	C-N-CA	12.96	139.30	120.38
45	u	1357	C	C4'-C3'-O3'	12.92	132.38	113.00
55	5	359	SER	N-CA-C	-12.26	97.91	111.28
45	u	47	A	C4'-C3'-O3'	11.98	127.38	109.40
50	z	69	GLY	CA-C-N	11.47	134.18	119.84
50	z	69	GLY	C-N-CA	11.47	134.18	119.84
55	5	349	VAL	N-CA-C	-11.22	94.60	109.30
55	5	532	ILE	O-C-N	-11.04	110.72	121.87
14	O	110	PRO	N-CA-C	10.95	124.06	110.70
55	5	292	PRO	N-CA-CB	10.70	109.74	102.25
45	u	5061	A	C2'-C3'-O3'	10.56	125.34	109.50
45	u	2695	A	C2'-C3'-O3'	10.48	125.22	109.50
55	5	513	ARG	O-C-N	-10.42	108.08	122.46
55	5	257	VAL	N-CA-C	-10.26	93.01	107.99
55	5	350	SER	CA-C-N	-10.25	104.18	121.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	5	350	SER	C-N-CA	-10.25	104.18	121.92
45	u	1485	C	C2'-C3'-O3'	10.19	124.78	109.50
48	x	48	ILE	CA-C-N	10.18	130.11	120.03
48	x	48	ILE	C-N-CA	10.18	130.11	120.03
45	u	2858	A	C4'-C3'-O3'	10.16	128.24	113.00
45	u	1279	A	C2'-C3'-O3'	10.04	124.57	109.50
45	u	2046	G	C2'-C3'-O3'	10.03	124.54	109.50
45	u	3718	A	C4'-C3'-O3'	9.99	127.99	113.00
45	u	215	C	C4'-C3'-O3'	-9.90	98.14	113.00
53	3	94	PHE	N-CA-C	9.85	122.09	111.36
45	u	1365	C	C4'-C3'-O3'	9.58	123.77	109.40
45	u	90	G	C2'-C3'-O3'	9.50	127.95	113.70
45	u	1398	A	C2'-C3'-O3'	9.49	123.74	109.50
45	u	4528	G	C2'-C3'-O3'	9.45	127.88	113.70
55	5	513	ARG	CA-C-N	9.45	134.85	121.71
55	5	513	ARG	C-N-CA	9.45	134.85	121.71
45	u	2123	C	C2'-C3'-O3'	9.45	123.67	109.50
45	u	1239	C	C2'-C3'-O3'	9.41	123.61	109.50
45	u	3888	G	C2'-C3'-O3'	9.39	127.78	113.70
45	u	1847	C	C4'-C3'-O3'	-9.27	99.09	113.00
48	x	48	ILE	N-CA-C	9.26	119.15	108.96
45	u	218	A	C3'-C2'-O2'	9.26	124.58	110.70
45	u	118	C	C4'-C3'-O3'	-9.18	99.23	113.00
45	u	1696	C	C2'-C3'-O3'	9.09	123.13	109.50
45	u	4948	C	C2'-C3'-O3'	9.01	127.22	113.70
45	u	3753	G	N9-C1'-C2'	-9.01	98.49	112.00
50	z	69	GLY	N-CA-C	-9.01	103.78	115.22
45	u	4951	G	C2'-C3'-O3'	8.97	122.95	109.50
45	u	4872	G	C2'-C3'-O3'	8.96	122.94	109.50
45	u	385	A	C4'-C3'-O3'	8.95	122.82	109.40
45	u	220	C	C2'-C3'-O3'	8.92	127.08	113.70
45	u	276	C	C4'-C3'-O3'	-8.90	99.65	113.00
45	u	197	A	P-O3'-C3'	8.87	133.51	120.20
45	u	1211	G	C2'-C3'-O3'	8.87	127.00	113.70
45	u	93	G	C4'-C3'-O3'	8.87	126.30	113.00
45	u	3697	U	C2'-C3'-O3'	8.81	126.91	113.70
45	u	1455	G	C2'-C3'-O3'	8.59	126.59	113.70
45	u	209	U	C4'-C3'-O3'	8.59	125.89	113.00
45	u	2083	C	C4'-C3'-O3'	8.56	125.85	113.00
45	u	930	G	C4'-C3'-O3'	8.35	121.92	109.40
45	u	1969	G	C4'-C3'-O3'	8.32	125.48	113.00
45	u	220	C	N1-C1'-C2'	-8.28	99.58	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	67	TRP	N-CA-C	-8.28	97.42	109.59
45	u	2661	U	C2'-C3'-O3'	8.27	121.91	109.50
45	u	1292	C	C2'-C3'-O3'	8.24	126.06	113.70
45	u	1292	C	C4'-C3'-O3'	-8.20	100.69	113.00
45	u	1755	C	C2'-C3'-O3'	8.19	121.79	109.50
45	u	2068	C	C4'-C3'-O3'	8.06	121.49	109.40
45	u	1410	U	C2'-C3'-O3'	8.04	121.56	109.50
45	u	4975	G	C4'-C3'-O3'	-8.03	97.36	109.40
45	u	275	C	C2'-C3'-O3'	7.97	125.66	113.70
45	u	5060	A	C2'-C3'-O3'	7.95	125.62	113.70
45	u	125	C	C2'-C3'-O3'	7.94	125.61	113.70
45	u	5027	C	C2'-C3'-O3'	7.90	121.35	109.50
45	u	1477	C	C2'-C3'-O3'	7.88	125.52	113.70
45	u	4170	A	C2'-C3'-O3'	7.85	121.27	109.50
45	u	686	A	C4'-C3'-O3'	7.73	120.99	109.40
53	3	71	PRO	N-CA-CB	7.72	110.52	103.34
45	u	5059	C	C2'-C3'-O3'	7.68	125.22	113.70
45	u	2028	C	C2'-C3'-O3'	-7.68	102.18	113.70
45	u	406	C	C2'-C3'-O3'	7.67	125.20	113.70
45	u	48	G	C2'-C3'-O3'	7.64	120.97	109.50
45	u	2116	C	C2'-C3'-O3'	7.58	120.87	109.50
45	u	3718	A	N9-C1'-C2'	-7.58	100.64	112.00
45	u	462	G	O3'-P-O5'	7.54	115.31	104.00
45	u	4699	U	C4'-C3'-O3'	7.54	120.72	109.40
26	a	31	GLY	N-CA-C	-7.52	104.80	111.95
2	B	17	LEU	N-CA-C	7.49	122.86	108.12
45	u	1724	G	C4'-C3'-O3'	7.47	120.61	109.40
45	u	3718	A	C2'-C3'-O3'	-7.43	102.55	113.70
48	x	81	ILE	N-CA-C	-7.41	105.32	112.29
45	u	4075	U	C4'-C3'-O3'	7.40	120.50	109.40
3	C	232	VAL	CB-CA-C	-7.39	102.02	112.22
45	u	3619	G	C4'-C3'-O3'	-7.36	101.96	113.00
45	u	1500	A	C4'-C3'-O3'	-7.33	102.01	113.00
45	u	4965	U	C4'-C3'-O3'	-7.30	102.04	113.00
45	u	1357	C	C2'-C3'-O3'	-7.30	102.75	113.70
2	B	258	HIS	CA-C-N	-7.27	110.75	119.84
2	B	258	HIS	C-N-CA	-7.27	110.75	119.84
45	u	956	A	C4'-C3'-O3'	7.27	120.31	109.40
47	w	94	G	C2'-C3'-O3'	7.27	120.40	109.50
45	u	4730	C	C4'-C3'-O3'	7.26	120.29	109.40
45	u	4666	G	C4'-C3'-O3'	-7.25	102.12	113.00
45	u	2349	A	C4'-C3'-O3'	-7.21	102.19	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	u	917	A	C4'-C3'-O3'	7.21	120.21	109.40
36	k	61	PRO	N-CA-C	7.17	119.44	110.70
45	u	1236	C	C2'-C3'-O3'	7.15	124.43	113.70
55	5	286	LEU	CA-C-N	-7.15	107.89	121.54
55	5	286	LEU	C-N-CA	-7.15	107.89	121.54
45	u	977	C	C2'-C3'-O3'	7.13	124.39	113.70
45	u	1268	G	C4'-C3'-O3'	7.12	120.08	109.40
45	u	3858	C	C4'-C3'-O3'	-7.11	102.34	113.00
45	u	4885	U	C2'-C3'-O3'	7.11	124.36	113.70
45	u	2256	C	C2'-C3'-O3'	7.09	120.13	109.50
15	P	40	HIS	CB-CG-CD2	-7.08	121.99	131.20
45	u	928	C	C2'-C3'-O3'	-7.06	103.11	113.70
48	x	69	LEU	CA-C-N	-7.04	112.09	122.86
48	x	69	LEU	C-N-CA	-7.04	112.09	122.86
21	V	13	LYS	N-CA-C	7.00	118.99	111.36
45	u	3876	A	C2'-C3'-O3'	7.00	120.00	109.50
45	u	2769	U	C4'-C3'-O3'	6.99	119.89	109.40
45	u	1818	G	C2'-C3'-O3'	6.97	124.16	113.70
45	u	2107	C	C2'-C3'-O3'	6.92	119.88	109.50
45	u	1974	U	C4'-C3'-O3'	6.90	119.75	109.40
45	u	223	G	P-O3'-C3'	6.90	130.55	120.20
45	u	1380	G	C1'-C2'-O2'	-6.88	101.47	111.80
45	u	965	G	C2'-C3'-O3'	6.87	119.81	109.50
5	E	39	HIS	CB-CG-CD2	-6.86	122.29	131.20
45	u	692	A	P-O3'-C3'	6.85	130.48	120.20
30	e	42	ASP	N-CA-C	-6.85	98.07	109.24
1	A	216	HIS	CB-CG-CD2	-6.83	122.32	131.20
45	u	4378	A	C2'-C3'-O3'	6.82	119.72	109.50
45	u	3657	U	C2'-C3'-O3'	6.80	123.90	113.70
47	w	124	U	C4'-C3'-O3'	6.76	119.53	109.40
45	u	1474	C	C2'-C3'-O3'	6.73	123.80	113.70
45	u	4115	G	C4'-C3'-O3'	6.73	119.50	109.40
45	u	1969	G	C2'-C3'-O3'	-6.72	103.62	113.70
45	u	2093	A	C2'-C3'-O3'	6.70	119.56	109.50
45	u	2588	C	C2'-C3'-O3'	-6.69	103.67	113.70
15	P	116	HIS	CB-CG-CD2	-6.68	122.51	131.20
45	u	1500	A	C2'-C3'-O3'	6.68	123.72	113.70
55	5	255	SER	N-CA-C	6.68	118.64	111.36
45	u	2632	U	N1-C1'-C2'	6.68	122.02	112.00
45	u	2797	C	N1-C1'-C2'	-6.67	103.99	114.00
45	u	957	G	C2'-C3'-O3'	6.67	119.51	109.50
45	u	4449	A	C4'-C3'-O3'	6.67	119.41	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	u	1835	G	C2'-C3'-O3'	6.67	119.50	109.50
45	u	3670	C	C4'-C3'-O3'	6.65	122.97	113.00
45	u	4548	A	C4'-C3'-O3'	6.64	119.35	109.40
45	u	1	C	C4'-C3'-O3'	6.63	119.35	109.40
17	R	141	HIS	CB-CG-CD2	-6.61	122.60	131.20
45	u	1380	G	C4'-C3'-O3'	6.61	119.31	109.40
5	E	72	PRO	N-CA-CB	6.60	110.26	103.00
45	u	90	G	C4'-C3'-O3'	-6.59	103.11	113.00
45	u	1388	A	C4'-C3'-O3'	-6.59	103.11	113.00
31	f	24	HIS	CB-CG-CD2	-6.59	122.64	131.20
45	u	1672	U	N1-C1'-C2'	6.57	121.85	112.00
7	G	77	PRO	CA-C-N	6.55	126.18	119.56
7	G	77	PRO	C-N-CA	6.55	126.18	119.56
2	B	261	ARG	N-CA-C	-6.55	98.77	108.79
34	i	80	HIS	CB-CG-CD2	-6.55	122.69	131.20
45	u	1282	G	C1'-C2'-O2'	6.54	118.21	108.40
45	u	1369	C	C2'-C3'-O3'	-6.49	103.97	113.70
45	u	2714	G	C4'-C3'-O3'	-6.49	103.27	113.00
45	u	207	G	C2'-C3'-O3'	-6.48	103.98	113.70
2	B	258	HIS	N-CA-C	6.48	124.12	109.81
45	u	4400	G	C4'-C3'-O3'	-6.47	103.29	113.00
45	u	4888	U	C2'-C3'-O3'	6.47	119.21	109.50
45	u	3715	U	C4'-C3'-O3'	6.47	122.71	113.00
44	t	140	GLY	N-CA-C	6.46	120.72	112.83
45	u	4213	A	C4'-C3'-O3'	-6.46	103.31	113.00
45	u	4543	G	C4'-C3'-O3'	-6.45	103.33	113.00
45	u	1975	G	C4'-C3'-O3'	6.44	119.06	109.40
45	u	407	A	C4'-C3'-O3'	-6.40	103.40	113.00
45	u	1848	C	C2'-C3'-O3'	6.40	123.30	113.70
45	u	2395	A	C2'-C3'-O3'	6.40	119.10	109.50
13	N	109	HIS	CB-CG-CD2	-6.40	122.88	131.20
51	1	467	PRO	N-CA-CB	6.40	110.30	103.52
13	N	78	GLY	N-CA-C	-6.39	104.39	110.21
45	u	932	A	C2'-C3'-O3'	6.39	119.09	109.50
45	u	1329	G	C4'-C3'-O3'	6.36	122.55	113.00
45	u	4517	A	C4'-C3'-O3'	-6.36	103.46	113.00
45	u	1697	G	C4'-C3'-O3'	6.36	118.93	109.40
45	u	944	A	C4'-C3'-O3'	-6.35	103.48	113.00
45	u	936	C	C2'-C3'-O3'	6.33	119.00	109.50
8	H	76	HIS	CB-CG-CD2	-6.33	122.97	131.20
45	u	1390	G	C2'-C3'-O3'	6.33	123.19	113.70
55	5	348	SER	N-CA-C	6.31	118.16	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	u	2506	G	C4'-C3'-O3'	6.30	118.85	109.40
24	Y	87	ARG	NE-CZ-NH2	6.29	124.86	119.20
53	3	113	PRO	N-CA-CB	6.29	109.85	103.25
45	u	4211	C	C4'-C3'-O3'	-6.28	103.58	113.00
45	u	2858	A	C1'-C2'-O2'	-6.28	98.98	108.40
18	S	164	LYS	N-CA-C	-6.28	101.08	110.24
44	t	29	ALA	CA-C-N	6.27	127.68	119.84
44	t	29	ALA	C-N-CA	6.27	127.68	119.84
45	u	1613	A	C2'-C3'-O3'	6.27	118.91	109.50
45	u	2266	C	C2'-C3'-O3'	6.27	118.91	109.50
45	u	2429	A	C4'-C3'-O3'	-6.25	103.62	113.00
45	u	1280	C	C4'-C3'-O3'	-6.25	103.63	113.00
45	u	964	A	O4'-C1'-C2'	-6.24	101.36	107.60
45	u	4473	A	C4'-C3'-O3'	-6.24	103.64	113.00
45	u	218	A	C4'-C3'-O3'	-6.23	103.66	113.00
45	u	5024	C	C2'-C3'-O3'	6.22	118.83	109.50
45	u	684	G	C3'-C2'-O2'	6.21	120.02	110.70
45	u	1232	G	C2'-C3'-O3'	6.20	118.80	109.50
45	u	223	G	C1'-C2'-O2'	6.19	117.69	108.40
45	u	978	G	C2'-C3'-O3'	6.18	122.97	113.70
45	u	3593	C	C4'-C3'-O3'	6.18	118.67	109.40
45	u	4084	G	C2'-C3'-O3'	6.17	118.76	109.50
48	x	449	LEU	CA-CB-CG	-6.17	94.69	116.30
55	5	597	LEU	N-CA-C	-6.17	104.55	111.28
45	u	1891	A	C2'-C3'-O3'	6.16	118.75	109.50
45	u	3657	U	C4'-C3'-O3'	-6.16	103.75	113.00
45	u	1329	G	C2'-C3'-O3'	6.15	122.92	113.70
45	u	4144	C	C4'-C3'-O3'	6.11	118.57	109.40
31	f	92	LEU	CA-C-N	6.09	125.98	119.28
31	f	92	LEU	C-N-CA	6.09	125.98	119.28
31	f	93	PRO	N-CA-C	6.08	121.86	113.65
5	E	90	LYS	CA-C-N	6.07	127.43	119.84
5	E	90	LYS	C-N-CA	6.07	127.43	119.84
45	u	4473	A	N9-C1'-C2'	6.07	121.10	112.00
45	u	1969	G	N9-C1'-C2'	-6.06	102.91	112.00
5	E	39	HIS	CB-CG-ND1	6.03	131.75	122.70
22	W	14	TYR	CA-C-N	6.03	127.38	119.84
22	W	14	TYR	C-N-CA	6.03	127.38	119.84
45	u	2474	G	C3'-C2'-O2'	6.03	119.74	110.70
45	u	1965	G	O3'-P-O5'	-6.02	94.97	104.00
45	u	4900	C	C2'-C3'-O3'	6.00	118.50	109.50
45	u	2088	A	C2'-C3'-O3'	5.99	118.48	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	u	3672	G	C2'-C3'-O3'	-5.99	104.72	113.70
9	I	121	LYS	N-CA-C	-5.99	102.34	110.36
50	z	69	GLY	O-C-N	5.99	123.22	121.07
45	u	497	G	C2'-C3'-O3'	-5.97	104.74	113.70
45	u	212	A	N9-C1'-C2'	5.97	120.95	112.00
46	v	96	U	C2'-C3'-O3'	-5.95	104.77	113.70
45	u	3859	G	C4'-C3'-O3'	-5.95	104.07	113.00
45	u	4318	C	C4'-C3'-O3'	-5.95	104.07	113.00
15	P	40	HIS	CB-CG-ND1	5.95	131.62	122.70
45	u	1214	C	C4'-C3'-O3'	5.93	118.30	109.40
2	B	254	ILE	N-CA-C	-5.93	104.55	110.30
45	u	462	G	OP1-P-O3'	-5.92	90.23	108.00
45	u	5049	G	C4'-C3'-O3'	5.92	118.28	109.40
55	5	348	SER	O-C-N	5.91	128.38	122.12
45	u	1357	C	C3'-C2'-O2'	5.86	119.49	110.70
45	u	1457	G	C4'-C3'-O3'	-5.86	104.21	113.00
9	I	95	HIS	CB-CG-CD2	-5.86	123.59	131.20
45	u	1553	A	C4'-C3'-O3'	-5.85	104.22	113.00
45	u	4083	U	C4'-C3'-O3'	-5.85	104.23	113.00
45	u	3753	G	C4'-C3'-O3'	5.84	121.76	113.00
45	u	294	G	C4'-C3'-O3'	-5.83	104.26	113.00
25	Z	36	ARG	CA-C-N	5.82	125.50	119.56
25	Z	36	ARG	C-N-CA	5.82	125.50	119.56
45	u	979	C	C2'-C3'-O3'	5.82	122.43	113.70
45	u	4116	C	C2'-C3'-O3'	5.81	118.22	109.50
45	u	451	C	C2'-C3'-O3'	5.80	118.19	109.50
55	5	353	GLN	CA-C-N	5.78	125.69	119.85
55	5	353	GLN	C-N-CA	5.78	125.69	119.85
45	u	918	G	C2'-C3'-O3'	-5.78	105.03	113.70
45	u	1429	C	C4'-C3'-O3'	-5.77	104.34	113.00
1	A	216	HIS	CB-CG-ND1	5.77	131.36	122.70
45	u	2468	U	C4'-C3'-O3'	5.77	118.05	109.40
45	u	4435	U	C4'-C3'-O3'	-5.75	104.37	113.00
45	u	1633	G	C4'-C3'-O3'	5.75	121.63	113.00
45	u	1636	U	C4'-C3'-O3'	-5.75	104.38	113.00
45	u	497	G	C4'-C3'-O3'	5.74	121.61	113.00
45	u	2427	G	C4'-C3'-O3'	-5.74	104.39	113.00
45	u	4568	A	C4'-C3'-O3'	-5.74	104.39	113.00
45	u	2827	G	C2'-C3'-O3'	-5.73	100.91	109.50
45	u	3864	C	C2'-C3'-O3'	-5.72	105.12	113.70
43	s	200	ASN	CA-C-N	5.71	126.98	119.84
43	s	200	ASN	C-N-CA	5.71	126.98	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	u	4228	G	C4'-C3'-O3'	-5.69	100.86	109.40
45	u	265	C	C4'-C3'-O3'	5.68	117.92	109.40
45	u	2554	U	C4'-C3'-O3'	5.68	121.52	113.00
31	f	24	HIS	CB-CG-ND1	5.68	131.22	122.70
45	u	286	U	N1-C1'-C2'	5.67	120.50	112.00
18	S	83	ARG	NE-CZ-NH2	5.66	124.30	119.20
15	P	116	HIS	CB-CG-ND1	5.66	131.19	122.70
17	R	141	HIS	CB-CG-ND1	5.65	131.18	122.70
45	u	486	C	C2'-C3'-O3'	5.65	122.18	113.70
45	u	1266	G	C2'-C3'-O3'	5.65	122.17	113.70
43	s	72	ASN	N-CA-C	5.64	116.76	109.65
55	5	121	PRO	N-CA-C	-5.64	105.69	113.53
45	u	1912	G	C4'-C3'-O3'	-5.63	104.56	113.00
45	u	664	G	C4'-C3'-O3'	5.62	117.83	109.40
50	z	83	SER	N-CA-C	-5.62	105.16	111.28
45	u	468	U	N1-C1'-C2'	5.61	120.42	112.00
45	u	4656	A	C2'-C3'-O3'	5.61	117.91	109.50
45	u	2251	G	C4'-C3'-O3'	5.60	117.80	109.40
45	u	2858	A	N9-C1'-C2'	-5.60	103.60	112.00
45	u	220	C	C4'-C3'-O3'	-5.59	104.61	113.00
45	u	209	U	C1'-C2'-O2'	5.59	116.79	108.40
45	u	2053	C	C4'-C3'-O3'	-5.59	104.61	113.00
45	u	3717	A	C2'-C3'-O3'	-5.59	105.32	113.70
45	u	4521	U	C4'-C3'-O3'	-5.58	104.63	113.00
45	u	680	G	OP2-P-O3'	-5.57	91.28	108.00
35	j	9	GLY	N-CA-C	5.57	119.62	112.83
45	u	5041	G	C2'-C3'-O3'	-5.55	105.37	113.70
45	u	4655	A	C4'-C3'-O3'	-5.55	104.68	113.00
2	B	16	PHE	CA-C-N	-5.53	116.18	122.26
2	B	16	PHE	C-N-CA	-5.53	116.18	122.26
45	u	1633	G	C2'-C3'-O3'	-5.53	105.41	113.70
45	u	4882	U	C2'-C3'-O3'	5.53	117.79	109.50
45	u	222	C	C1'-C2'-O2'	5.51	116.67	108.40
34	i	80	HIS	CB-CG-ND1	5.51	130.96	122.70
45	u	977	C	C4'-C3'-O3'	-5.50	104.75	113.00
45	u	1477	C	C4'-C3'-O3'	-5.50	104.75	113.00
45	u	1280	C	N1-C1'-C2'	5.49	120.24	112.00
45	u	3673	C	C2'-C3'-O3'	5.49	117.74	109.50
25	Z	54	THR	N-CA-C	5.49	119.28	112.47
45	u	1968	G	C2'-C3'-O3'	-5.49	105.47	113.70
53	3	62	MET	CA-C-N	5.49	132.02	121.54
53	3	62	MET	C-N-CA	5.49	132.02	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	5	172	ALA	N-CA-C	-5.49	105.30	111.28
45	u	2700	G	C4'-C3'-O3'	-5.47	104.79	113.00
13	N	109	HIS	CB-CG-ND1	5.47	130.90	122.70
45	u	3807	A	C4'-C3'-O3'	-5.47	104.80	113.00
45	u	277	G	C4'-C3'-O3'	5.46	117.58	109.40
45	u	2119	C	C2'-C3'-O3'	5.45	117.68	109.50
48	x	63	TYR	N-CA-C	5.44	117.02	111.14
33	h	96	ASN	N-CA-C	5.44	119.39	112.87
45	u	2027	U	C4'-C3'-O3'	5.43	121.15	113.00
27	b	8	THR	N-CA-C	5.43	115.71	108.38
45	u	4375	C	C2'-C3'-O3'	-5.43	105.56	113.70
8	H	76	HIS	CB-CG-ND1	5.42	130.83	122.70
45	u	470	A	O4'-C1'-C2'	-5.42	102.18	107.60
45	u	4331	G	C2'-C3'-O3'	5.41	117.62	109.50
2	B	18	PRO	N-CA-C	-5.41	101.33	112.47
45	u	4965	U	C2'-C3'-O3'	5.41	121.81	113.70
2	B	36	ASP	CA-C-N	-5.40	113.09	119.84
2	B	36	ASP	C-N-CA	-5.40	113.09	119.84
45	u	4998	G	C4'-C3'-O3'	-5.40	104.90	113.00
45	u	1380	G	N9-C1'-C2'	5.38	122.06	114.00
41	p	52	VAL	CB-CA-C	-5.37	103.22	111.71
45	u	1235	G	C2'-C3'-O3'	-5.36	105.66	113.70
53	3	57	PRO	N-CA-C	5.36	123.51	112.47
5	E	217	GLN	N-CA-C	5.35	117.74	110.35
53	3	63	THR	CA-C-N	5.35	131.76	121.54
53	3	63	THR	C-N-CA	5.35	131.76	121.54
45	u	1214	C	C2'-C3'-O3'	5.35	117.53	109.50
2	B	36	ASP	N-CA-C	-5.35	102.85	109.64
45	u	2083	C	C2'-C3'-O3'	-5.35	105.68	113.70
31	f	106	TYR	N-CA-C	5.34	121.62	109.81
45	u	1236	C	C3'-C2'-O2'	5.34	118.71	110.70
45	u	2246	C	C2'-C3'-O3'	5.34	121.71	113.70
45	u	2864	A	C4'-C3'-O3'	-5.33	105.00	113.00
45	u	2546	G	C3'-C2'-O2'	5.33	118.69	110.70
45	u	4938	A	C2'-C3'-O3'	-5.33	105.71	113.70
45	u	1847	C	C2'-C3'-O3'	5.32	121.68	113.70
45	u	2474	G	C2'-C3'-O3'	5.32	121.68	113.70
45	u	2068	C	C2'-C3'-O3'	5.31	117.46	109.50
45	u	5066	U	N1-C1'-C2'	5.30	119.95	112.00
45	u	430	G	C4'-C3'-O3'	-5.30	105.05	113.00
48	x	406	GLU	N-CA-C	5.29	116.73	111.07
45	u	1921	C	C4'-C3'-O3'	5.28	117.32	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	u	4558	U	C4'-C3'-O3'	-5.28	105.08	113.00
45	u	134	G	C4'-C3'-O3'	5.28	117.32	109.40
45	u	3594	C	N1-C1'-C2'	5.27	119.90	112.00
45	u	4087	G	C2'-C3'-O3'	-5.27	105.80	113.70
45	u	1990	A	C2'-C3'-O3'	5.27	121.60	113.70
45	u	1072	C	N1-C1'-C2'	5.27	121.90	114.00
45	u	1725	U	C1'-C2'-O2'	5.27	116.30	108.40
45	u	4966	A	C4'-C3'-O3'	-5.27	105.10	113.00
11	L	99	ASP	N-CA-C	-5.26	102.51	110.50
45	u	2027	U	N1-C1'-C2'	-5.25	104.12	112.00
45	u	4625	C	C4'-C3'-O3'	-5.25	105.13	113.00
45	u	4364	G	C4'-C3'-O3'	-5.24	105.14	113.00
45	u	4966	A	N9-C1'-C2'	5.24	119.86	112.00
26	a	120	GLN	CA-C-N	5.23	125.22	119.89
26	a	120	GLN	C-N-CA	5.23	125.22	119.89
45	u	2257	C	C4'-C3'-O3'	5.23	117.24	109.40
45	u	1358	G	O4'-C1'-C2'	-5.22	102.38	107.60
45	u	989	U	C3'-C2'-O2'	5.21	118.52	110.70
45	u	1648	C	C4'-C3'-O3'	-5.21	105.19	113.00
45	u	4696	C	C4'-C3'-O3'	-5.20	105.19	113.00
32	g	67	LEU	N-CA-C	5.20	117.00	110.24
45	u	2313	A	C3'-C2'-O2'	5.20	118.50	110.70
45	u	976	G	C3'-C2'-O2'	5.20	118.50	110.70
45	u	2260	C	C3'-C2'-O2'	5.20	118.49	110.70
14	O	108	ILE	CA-C-N	5.19	125.73	120.38
14	O	108	ILE	C-N-CA	5.19	125.73	120.38
45	u	300	A	N9-C1'-C2'	5.19	119.79	112.00
45	u	2064	G	C2'-C3'-O3'	5.19	121.49	113.70
45	u	3903	A	C4'-C3'-O3'	-5.19	105.22	113.00
45	u	5022	U	C3'-C2'-O2'	5.18	118.47	110.70
45	u	1428	U	C4'-C3'-O3'	-5.17	105.24	113.00
45	u	1677	U	C4'-C3'-O3'	-5.16	105.25	113.00
19	T	27	LEU	N-CA-C	5.16	119.29	112.89
45	u	206	U	C2'-C3'-O3'	5.16	121.44	113.70
45	u	4307	A	C4'-C3'-O3'	-5.16	105.26	113.00
45	u	4266	G	C2'-C3'-O3'	-5.16	105.97	113.70
42	r	103	HIS	CA-C-N	-5.15	114.31	119.56
42	r	103	HIS	C-N-CA	-5.15	114.31	119.56
47	w	93	C	C4'-C3'-O3'	-5.15	105.28	113.00
5	E	123	SER	N-CA-C	5.14	118.82	112.24
45	u	931	C	C3'-C2'-O2'	5.13	118.40	110.70
45	u	4228	G	C2'-C3'-O3'	5.13	117.19	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	a	61	TYR	N-CA-C	5.12	116.72	111.03
45	u	2422	C	C3'-C2'-O2'	5.12	118.38	110.70
45	u	93	G	C1'-C2'-O2'	-5.11	100.73	108.40
9	I	49	CYS	N-CA-C	5.11	118.67	111.52
45	u	166	C	C4'-C3'-O3'	5.11	120.66	113.00
45	u	2084	C	C4'-C3'-O3'	5.10	117.05	109.40
55	5	87	THR	CA-CB-CG2	5.10	119.17	110.50
45	u	4312	U	C4'-C3'-O3'	-5.09	105.36	113.00
55	5	100	TYR	CA-CB-CG	5.09	123.07	113.90
45	u	962	C	C2'-C3'-O3'	5.09	117.13	109.50
12	M	8	GLU	N-CA-C	-5.08	102.27	110.14
45	u	687	U	C1'-C2'-O2'	5.07	116.00	108.40
45	u	2262	G	C3'-C2'-O2'	5.07	118.30	110.70
45	u	3697	U	C3'-C2'-O2'	5.07	118.30	110.70
45	u	4640	C	C4'-C3'-O3'	-5.07	105.40	113.00
45	u	1804	A	C2'-C3'-O3'	5.06	117.09	109.50
45	u	1848	C	C4'-C3'-O3'	-5.06	105.40	113.00
45	u	1358	G	C2'-C3'-O3'	-5.06	106.11	113.70
53	3	110	PRO	N-CA-CB	5.06	110.10	103.42
31	f	83	MET	N-CA-C	-5.06	103.72	110.55
45	u	4069	U	C3'-C2'-O2'	5.05	118.27	110.70
2	B	101	THR	N-CA-CB	5.05	117.39	109.97
45	u	1898	C	C2'-C3'-O3'	5.04	117.07	109.50
45	u	4888	U	C4'-C3'-O3'	5.04	116.96	109.40
45	u	5026	U	N1-C1'-C2'	5.04	119.56	112.00
45	u	48	G	C4'-C3'-O3'	5.04	116.95	109.40
45	u	4585	U	C4'-C3'-O3'	-5.04	105.45	113.00
45	u	693	C	C2'-C3'-O3'	5.03	121.25	113.70
45	u	486	C	C3'-C2'-O2'	5.03	118.25	110.70
45	u	266	C	C2'-C3'-O3'	-5.03	106.16	113.70
45	u	233	U	C2'-C3'-O3'	5.02	117.04	109.50
45	u	2264	C	C4'-C3'-O3'	-5.02	105.47	113.00
45	u	3752	C	C2'-C3'-O3'	-5.02	106.17	113.70
45	u	2505	C	C4'-C3'-O3'	5.01	116.92	109.40
45	u	1336	G	C2'-C3'-O3'	-5.01	106.18	113.70
45	u	1612	G	C2'-C3'-O3'	5.00	117.01	109.50

There are no chirality outliers.

All (41) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	2	15	UNK	Peptide

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Mol	Chain	Res	Type	Group
53	3	64	ASP	Peptide
53	3	67	GLY	Peptide
55	5	100	TYR	Peptide
55	5	263	LEU	Peptide
55	5	532	ILE	Mainchain
55	5	616	ASP	Peptide
55	5	655	LYS	Peptide
55	5	69	HIS	Peptide
56	6	20	UNK	Peptide
56	6	21	UNK	Peptide
56	6	80	UNK	Peptide
56	6	81	UNK	Peptide
56	6	89	UNK	Peptide
1	A	196	TRP	Peptide
2	B	17	LEU	Peptide
2	B	257	TRP	Peptide
2	B	258	HIS	Peptide
2	B	351	LEU	Peptide
3	C	245	HIS	Peptide
3	C	339	THR	Peptide
4	D	36	LEU	Peptide
5	E	123	SER	Peptide
7	G	238	GLY	Peptide
9	I	188	LYS	Peptide
9	I	202	ASN	Peptide
11	L	27	ASN	Peptide
11	L	46	ILE	Peptide
11	L	66	TYR	Peptide
17	R	19	LYS	Peptide
18	S	163	HIS	Peptide
18	S	164	LYS	Peptide
19	T	26	PRO	Peptide
20	U	27	HIS	Peptide
24	Y	7	VAL	Peptide
31	f	105	LEU	Peptide
42	r	106	LEU	Peptide
42	r	70	GLN	Peptide
45	u	2793	G	Sidechain
48	x	173	TYR	Peptide
48	x	42	PHE	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1868	0	1959	31	0
2	B	3148	0	3267	63	0
3	C	2884	0	3062	46	0
4	D	2386	0	2419	34	0
5	E	1898	0	2035	93	0
6	F	1870	0	1994	27	0
7	G	1934	0	2087	31	0
8	H	1516	0	1597	18	0
9	I	1655	0	1704	42	0
10	J	1353	0	1386	11	0
11	L	1703	0	1820	27	0
12	M	1137	0	1211	18	0
13	N	1701	0	1749	20	0
14	O	1638	0	1777	31	0
15	P	1242	0	1269	13	0
16	Q	1506	0	1623	17	0
17	R	1508	0	1664	19	0
18	S	1454	0	1496	15	0
19	T	1298	0	1366	11	0
20	U	808	0	831	7	0
21	V	979	0	1039	5	0
22	W	528	0	541	5	0
23	X	976	0	1052	37	0
24	Y	1115	0	1205	8	0
25	Z	1107	0	1182	16	0
26	a	1162	0	1209	19	0
27	b	609	0	650	5	0
28	c	732	0	769	7	0
29	d	888	0	930	9	0
30	e	1053	0	1147	29	0
31	f	876	0	912	19	0
32	g	906	0	999	12	0
33	h	1013	0	1147	25	0
34	i	830	0	916	4	0
35	j	705	0	738	16	0
36	k	569	0	637	6	0
37	l	444	0	482	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	429	0	466	9	0
39	n	222	0	264	1	0
40	o	851	0	921	12	0
41	p	708	0	756	7	0
42	r	1094	0	1168	125	0
43	s	1523	0	1577	27	0
44	t	1238	0	1295	10	0
45	u	78486	0	39663	1531	0
46	v	2558	0	1296	27	0
47	w	3314	0	1683	54	0
48	x	3313	0	3433	351	0
49	y	494	0	527	27	0
50	z	229	0	245	62	0
51	1	882	0	485	18	0
52	2	300	0	64	5	0
53	3	802	0	705	79	0
54	4	268	0	285	6	0
55	5	5090	0	4915	427	0
56	6	485	0	104	3	0
57	7	125	0	27	0	0
58	8	400	0	86	2	0
59	K	94	0	79	0	0
60	B	1	0	0	0	0
60	I	1	0	0	0	0
60	P	1	0	0	0	0
60	V	1	0	0	0	0
60	a	1	0	0	0	0
60	e	1	0	0	0	0
60	g	1	0	0	0	0
60	u	145	0	0	0	0
60	v	5	0	0	0	0
60	w	2	0	0	0	0
61	g	1	0	0	0	0
61	j	1	0	0	0	0
61	m	1	0	0	1	0
61	o	1	0	0	2	0
61	p	1	0	0	0	0
62	5	43	0	0	24	0
All	All	152111	0	111915	3173	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (3173) 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)
48:x:29:LYS:HG3	53:3:118:PHE:CE2	1.26	1.68
48:x:157:VAL:CG1	50:z:80:PHE:CD2	1.76	1.65
48:x:66:ARG:HH22	48:x:70:ALA:CA	1.06	1.64
48:x:157:VAL:HB	50:z:80:PHE:CZ	1.28	1.64
53:3:92:PHE:CE1	53:3:96:MET:CE	1.78	1.64
48:x:181:LEU:HD11	48:x:457:TYR:CZ	1.23	1.62
48:x:176:GLY:HA3	48:x:457:TYR:CE1	1.22	1.60
49:y:56:LEU:CD1	53:3:92:PHE:CD2	1.84	1.60
53:3:92:PHE:CZ	53:3:96:MET:CE	1.84	1.59
48:x:157:VAL:CB	50:z:80:PHE:CE2	1.75	1.57
48:x:157:VAL:HG12	50:z:80:PHE:CD2	1.33	1.54
55:5:86:GLY:C	55:5:256:PHE:CZ	1.86	1.53
53:3:92:PHE:CE1	53:3:96:MET:HE2	1.33	1.52
49:y:56:LEU:HD11	53:3:92:PHE:CD2	1.39	1.51
55:5:86:GLY:C	55:5:256:PHE:HZ	1.11	1.50
48:x:157:VAL:CB	50:z:80:PHE:CZ	1.87	1.50
30:e:2:ALA:CB	42:r:130:ARG:NH1	1.75	1.50
33:h:38:GLY:N	48:x:266:PRO:HG3	1.16	1.48
55:5:504:ASP:CB	55:5:688:LEU:HG	1.40	1.47
48:x:66:ARG:HD2	48:x:72:ASN:ND2	1.19	1.46
53:3:92:PHE:CE1	53:3:96:MET:SD	2.09	1.45
55:5:348:SER:HB3	55:5:598:TRP:CZ2	1.53	1.44
55:5:521:LYS:CE	55:5:523:MET:HE2	1.47	1.44
48:x:176:GLY:CA	48:x:457:TYR:CE1	2.01	1.43
48:x:157:VAL:CG1	50:z:80:PHE:CZ	1.94	1.42
55:5:127:THR:CG2	55:5:174:PHE:HD2	1.33	1.41
33:h:38:GLY:CA	48:x:266:PRO:HB3	1.47	1.41
48:x:181:LEU:HD11	48:x:457:TYR:CE1	1.52	1.41
53:3:92:PHE:CD1	53:3:96:MET:HE2	1.56	1.39
33:h:37:THR:C	48:x:266:PRO:HG3	1.47	1.38
55:5:359:SER:O	55:5:363:ASP:CB	1.70	1.38
48:x:61:PRO:O	48:x:65:MET:CB	1.69	1.37
5:E:279:PRO:HG2	31:f:7:CYS:SG	1.65	1.37
55:5:214:PHE:HD1	62:5:809:9UB:C05	1.36	1.37
53:3:92:PHE:CZ	53:3:96:MET:HE1	1.48	1.36
49:y:56:LEU:CD1	53:3:92:PHE:HD2	1.20	1.36
45:u:976:G:H2'	45:u:977:C:O4'	1.25	1.36
55:5:214:PHE:CD1	62:5:809:9UB:C05	2.09	1.34
45:u:216:C:H1'	51:1:536:ARG:CB	1.55	1.34
55:5:590:SER:OG	55:5:591:ASP:N	1.58	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:29:LYS:HE2	53:3:118:PHE:CZ	1.63	1.33
48:x:61:PRO:C	48:x:65:MET:CE	1.98	1.33
55:5:52:PHE:HB2	55:5:530:TYR:CG	1.65	1.32
23:X:156:ILE:HD11	48:x:415:ARG:NH1	1.43	1.31
55:5:87:THR:N	55:5:256:PHE:HZ	1.27	1.31
48:x:181:LEU:CD1	48:x:457:TYR:CZ	2.14	1.30
48:x:66:ARG:CD	48:x:72:ASN:ND2	1.94	1.29
55:5:168:ASN:ND2	62:5:809:9UB:C29	1.95	1.29
55:5:359:SER:O	55:5:363:ASP:HB2	1.14	1.28
45:u:216:C:O2	51:1:536:ARG:HA	1.25	1.28
30:e:2:ALA:HB3	42:r:130:ARG:NH1	0.97	1.27
55:5:127:THR:HG23	55:5:174:PHE:CD2	1.68	1.27
55:5:157:TYR:CE1	55:5:173:ILE:HD13	1.67	1.27
42:r:47:LYS:CG	42:r:102:TYR:HE2	1.49	1.25
45:u:2367:A:N1	45:u:2788:U:O4	1.66	1.25
23:X:84:GLU:N	48:x:403:GLY:O	1.66	1.25
55:5:30:SER:OG	55:5:124:SER:HB3	1.33	1.25
55:5:348:SER:HB3	55:5:598:TRP:CE2	1.71	1.25
50:z:74:LEU:O	50:z:78:LEU:CD1	1.85	1.24
55:5:209:TRP:CZ2	62:5:809:9UB:C19	2.02	1.24
45:u:469:C:O2	45:u:688:U:H1'	1.36	1.24
48:x:435:ALA:O	48:x:441:ILE:CD1	1.85	1.24
5:E:126:ARG:NH1	45:u:712:C:H1'	1.50	1.24
55:5:357:TRP:O	55:5:360:TYR:C	1.80	1.23
48:x:62:PHE:HA	48:x:65:MET:SD	1.79	1.23
48:x:66:ARG:NH2	48:x:70:ALA:HA	0.91	1.23
55:5:175:CYS:SG	55:5:204:TYR:HD2	1.61	1.23
48:x:29:LYS:CE	53:3:118:PHE:HZ	1.52	1.23
48:x:153:ILE:O	48:x:157:VAL:HG23	1.35	1.23
55:5:127:THR:CG2	55:5:174:PHE:CD2	2.20	1.23
45:u:4213:A:N1	45:u:4218:U:O4	1.72	1.22
55:5:214:PHE:HD1	62:5:809:9UB:C06	1.51	1.22
48:x:29:LYS:CG	53:3:118:PHE:CE2	2.22	1.22
55:5:209:TRP:HZ2	62:5:809:9UB:C19	1.28	1.22
5:E:202:VAL:HG13	5:E:256:LYS:NZ	1.55	1.21
23:X:156:ILE:HG21	48:x:416:TYR:OH	1.40	1.21
48:x:244:ASN:ND2	48:x:439:GLY:O	1.74	1.21
33:h:38:GLY:N	48:x:266:PRO:CG	2.05	1.20
33:h:38:GLY:CA	48:x:266:PRO:CB	2.18	1.20
45:u:2468:U:O4	45:u:2473:A:N1	1.73	1.20
12:M:116:LYS:CG	14:O:196:LEU:HD21	1.72	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1929:A:N1	45:u:2054:U:O4	1.75	1.19
48:x:435:ALA:O	48:x:441:ILE:HD13	1.05	1.19
50:z:68:VAL:CG1	50:z:70:PRO:O	1.89	1.19
45:u:1958:A:H5''	45:u:1962:A:O2'	1.03	1.19
45:u:692:A:O3'	45:u:693:C:P	2.00	1.18
48:x:29:LYS:CG	53:3:118:PHE:HE2	1.55	1.18
49:y:56:LEU:HD12	53:3:92:PHE:CE2	1.77	1.18
55:5:590:SER:O	55:5:591:ASP:CB	1.90	1.18
55:5:346:ILE:O	55:5:349:VAL:HG12	1.44	1.18
48:x:46:CYS:SG	48:x:77:MET:HG3	1.81	1.18
55:5:52:PHE:CG	55:5:530:TYR:CZ	2.31	1.18
48:x:124:THR:OG1	48:x:156:PHE:CE1	1.97	1.18
45:u:216:C:C2	51:1:536:ARG:HA	1.78	1.18
9:I:191:ILE:CD1	9:I:200:ILE:HD12	1.74	1.17
55:5:357:TRP:CA	55:5:360:TYR:HB2	1.73	1.17
43:s:14:PHE:CE2	43:s:62:ARG:CD	2.28	1.16
48:x:437:PHE:HD2	48:x:438:LEU:CD2	1.58	1.16
5:E:254:LEU:HD23	5:E:257:ILE:HD11	1.24	1.15
11:L:163:LYS:HE2	45:u:509:A:H4'	1.16	1.15
43:s:14:PHE:CD2	43:s:62:ARG:CD	2.29	1.15
48:x:124:THR:OG1	48:x:156:PHE:HE1	1.26	1.15
48:x:61:PRO:C	48:x:65:MET:SD	2.30	1.15
55:5:71:TRP:O	55:5:83:ILE:CG1	1.95	1.15
49:y:56:LEU:HD12	53:3:92:PHE:CD2	1.70	1.15
5:E:202:VAL:HG13	5:E:256:LYS:HZ2	1.05	1.14
48:x:66:ARG:NH2	48:x:70:ALA:CA	1.76	1.14
55:5:245:CYS:SG	56:6:65:UNK:CB	2.36	1.14
51:1:443:VAL:CG2	52:2:65:UNK:CB	2.27	1.13
23:X:156:ILE:CG2	48:x:416:TYR:OH	1.95	1.13
45:u:1958:A:C5'	45:u:1962:A:O2'	1.96	1.13
42:r:97:ILE:HG21	42:r:107:ARG:HB2	1.19	1.13
45:u:472:C:N3	45:u:473:C:C4	2.16	1.13
55:5:71:TRP:O	55:5:83:ILE:HG12	1.45	1.13
50:z:68:VAL:HG12	50:z:70:PRO:O	1.43	1.12
5:E:59:TYR:CD2	5:E:64:LEU:HD12	1.83	1.12
7:G:156:VAL:HG11	7:G:184:LEU:HD12	1.29	1.12
48:x:443:SER:HB3	48:x:447:ILE:CD1	1.78	1.12
55:5:86:GLY:HA2	55:5:256:PHE:CE1	1.82	1.12
42:r:47:LYS:CG	42:r:102:TYR:CE2	2.33	1.12
42:r:47:LYS:HG2	42:r:102:TYR:HE2	1.07	1.11
48:x:29:LYS:HG3	53:3:118:PHE:CZ	1.83	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:s:14:PHE:CD2	43:s:62:ARG:HD3	1.85	1.11
33:h:38:GLY:HA3	48:x:266:PRO:CB	1.78	1.11
48:x:50:LEU:CD1	50:z:88:HIS:HA	1.80	1.11
55:5:513:ARG:HD2	55:5:535:MET:O	1.46	1.10
55:5:522:VAL:HG11	55:5:532:ILE:HG21	1.18	1.10
48:x:66:ARG:NH1	48:x:69:LEU:O	1.84	1.10
55:5:52:PHE:CB	55:5:530:TYR:CD2	2.35	1.10
55:5:504:ASP:HB2	55:5:688:LEU:HG	1.26	1.10
55:5:601:ARG:HB2	55:5:613:LYS:NZ	1.67	1.10
55:5:357:TRP:HA	55:5:360:TYR:CB	1.82	1.10
55:5:399:PHE:CD1	62:5:809:9UB:C03	2.34	1.10
5:E:226:GLY:N	42:r:135:LYS:HD3	1.65	1.09
55:5:51:TYR:CD2	55:5:531:GLN:HG2	1.86	1.09
55:5:52:PHE:CD1	55:5:530:TYR:CE1	2.39	1.09
55:5:87:THR:N	55:5:256:PHE:CZ	2.11	1.09
23:X:156:ILE:CD1	48:x:415:ARG:HH12	1.63	1.09
50:z:74:LEU:O	50:z:78:LEU:HD13	1.51	1.09
55:5:86:GLY:HA2	55:5:256:PHE:HE1	0.99	1.09
55:5:348:SER:CB	55:5:598:TRP:CZ2	2.35	1.09
5:E:126:ARG:HH11	45:u:712:C:C1'	1.67	1.08
9:I:191:ILE:HD11	9:I:200:ILE:HD12	1.29	1.08
5:E:279:PRO:CG	31:f:7:CYS:SG	2.40	1.08
23:X:156:ILE:CD1	48:x:415:ARG:NH1	2.13	1.08
48:x:121:MET:CE	48:x:156:PHE:CD1	2.36	1.08
48:x:121:MET:HE1	48:x:156:PHE:CD1	1.88	1.08
5:E:126:ARG:NH1	45:u:712:C:C1'	2.15	1.08
5:E:202:VAL:CG1	5:E:256:LYS:NZ	2.17	1.08
55:5:399:PHE:CE1	62:5:809:9UB:C03	2.24	1.08
30:e:2:ALA:CB	42:r:130:ARG:HH11	1.48	1.07
55:5:130:VAL:HG23	55:5:177:LEU:HD12	1.30	1.07
9:I:191:ILE:HD12	9:I:200:ILE:CD1	1.84	1.07
12:M:116:LYS:HG3	14:O:196:LEU:HD21	1.33	1.07
55:5:214:PHE:CD1	62:5:809:9UB:C06	2.35	1.07
9:I:191:ILE:CD1	9:I:200:ILE:CD1	2.33	1.07
53:3:115:LEU:HA	53:3:119:LEU:HD11	1.36	1.07
5:E:202:VAL:CG1	5:E:256:LYS:HZ2	1.68	1.07
33:h:38:GLY:HA2	48:x:266:PRO:HB3	1.30	1.07
48:x:50:LEU:HD12	50:z:88:HIS:HA	1.11	1.07
55:5:175:CYS:SG	55:5:204:TYR:CD2	2.48	1.07
11:L:42:ARG:NH1	11:L:51:ALA:O	1.88	1.06
23:X:84:GLU:H	48:x:403:GLY:C	1.62	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:358:SER:O	55:5:362:PHE:HB3	1.54	1.06
55:5:596:PHE:O	55:5:600:VAL:HG23	1.54	1.06
42:r:118:LEU:HA	42:r:121:GLN:HE21	1.19	1.06
42:r:120:SER:N	42:r:122:LYS:HZ2	1.52	1.06
51:1:443:VAL:HG23	52:2:65:UNK:CB	1.85	1.06
33:h:38:GLY:HA3	48:x:266:PRO:HB3	1.12	1.06
55:5:168:ASN:HD21	62:5:809:9UB:C29	1.62	1.06
43:s:14:PHE:CD2	43:s:62:ARG:HD2	1.91	1.06
53:3:88:LEU:HD22	53:3:88:LEU:H	1.21	1.06
53:3:92:PHE:CZ	53:3:96:MET:SD	2.41	1.05
48:x:157:VAL:HG11	50:z:80:PHE:CD2	1.61	1.05
48:x:181:LEU:HD21	48:x:457:TYR:CD1	1.90	1.05
48:x:437:PHE:HD2	48:x:438:LEU:HD23	1.18	1.05
55:5:504:ASP:HB3	55:5:688:LEU:HG	1.09	1.05
55:5:521:LYS:HE2	55:5:523:MET:HE2	1.33	1.05
55:5:590:SER:C	55:5:591:ASP:CG	2.22	1.05
5:E:62:LYS:HE3	45:u:978:G:OP1	1.57	1.05
55:5:526:TRP:HE3	55:5:544:ASN:HA	1.20	1.05
48:x:47:GLN:H	48:x:75:THR:HB	1.19	1.05
48:x:61:PRO:C	48:x:65:MET:HE3	1.46	1.05
55:5:526:TRP:CE3	55:5:544:ASN:HA	1.92	1.05
48:x:61:PRO:C	48:x:65:MET:HB3	1.81	1.04
48:x:64:TRP:CZ2	48:x:346:SER:HB2	1.91	1.04
45:u:216:C:C1'	51:1:536:ARG:CB	2.35	1.04
48:x:66:ARG:HD2	48:x:72:ASN:CG	1.82	1.04
23:X:156:ILE:OXT	48:x:415:ARG:NH2	1.90	1.04
45:u:2409:U:C4	45:u:2783:A:N1	2.25	1.04
5:E:126:ARG:HH11	45:u:712:C:H1'	0.94	1.04
45:u:471:A:C6	45:u:472:C:C6	2.46	1.04
53:3:42:PHE:HB2	53:3:91:SER:HB2	1.05	1.04
23:X:83:THR:HA	48:x:403:GLY:HA2	1.37	1.03
55:5:399:PHE:CG	62:5:809:9UB:C03	2.19	1.03
43:s:14:PHE:CE1	45:u:1960:A:C2	2.46	1.03
55:5:52:PHE:CD2	55:5:530:TYR:CZ	2.45	1.03
43:s:14:PHE:HE2	43:s:62:ARG:CG	1.72	1.03
53:3:92:PHE:CE2	53:3:96:MET:HE1	1.93	1.03
55:5:175:CYS:HG	55:5:204:TYR:HD2	1.05	1.03
55:5:590:SER:C	55:5:591:ASP:OD1	2.02	1.02
5:E:62:LYS:NZ	45:u:978:G:OP2	1.91	1.02
48:x:157:VAL:HG13	50:z:80:PHE:CE2	1.66	1.02
55:5:359:SER:O	55:5:363:ASP:HB3	1.59	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:97:ILE:CG2	42:r:107:ARG:HB2	1.88	1.02
48:x:176:GLY:CA	48:x:457:TYR:HE1	1.52	1.02
48:x:437:PHE:C	48:x:438:LEU:HD23	1.84	1.02
55:5:504:ASP:CB	55:5:688:LEU:CG	2.37	1.02
9:I:184:MET:HE2	9:I:190:LEU:HG	1.40	1.02
48:x:157:VAL:CB	50:z:80:PHE:HE2	1.35	1.02
55:5:590:SER:O	55:5:591:ASP:HB3	1.59	1.02
48:x:62:PHE:CA	48:x:65:MET:SD	2.47	1.02
45:u:3751:G:C2'	45:u:3752:C:H5'	1.90	1.01
45:u:470:A:C5	45:u:471:A:C8	2.47	1.01
45:u:472:C:C2	45:u:473:C:C5	2.48	1.01
55:5:123:PHE:CG	55:5:171:ILE:HG22	1.96	1.01
5:E:62:LYS:CE	45:u:978:G:P	2.49	1.01
42:r:47:LYS:HD2	42:r:102:TYR:CD2	1.94	1.01
42:r:119:ARG:C	42:r:122:LYS:HZ2	1.68	1.01
55:5:31:PHE:CE2	55:5:121:PRO:HB2	1.96	1.01
55:5:590:SER:O	55:5:591:ASP:CG	2.04	1.01
48:x:42:PHE:HD1	48:x:45:CYS:HB2	1.25	1.00
5:E:225:GLU:C	42:r:135:LYS:HD3	1.85	1.00
33:h:37:THR:C	48:x:266:PRO:CG	2.33	1.00
45:u:205:C:O2'	45:u:2305:U:H5	1.44	1.00
55:5:590:SER:CB	55:5:591:ASP:N	2.23	1.00
48:x:157:VAL:HG13	50:z:80:PHE:HE2	0.91	1.00
48:x:443:SER:HB3	48:x:447:ILE:CG1	1.90	1.00
53:3:92:PHE:HE1	53:3:96:MET:SD	1.60	1.00
55:5:504:ASP:HB3	55:5:688:LEU:CG	1.89	1.00
43:s:14:PHE:HE2	43:s:62:ARG:HG3	1.22	1.00
55:5:52:PHE:HB2	55:5:530:TYR:CD2	1.94	1.00
9:I:184:MET:HE2	9:I:190:LEU:CD1	1.91	1.00
9:I:202:ASN:O	46:v:63:C:C5	2.15	0.99
55:5:123:PHE:CD1	55:5:171:ILE:HG22	1.95	0.99
48:x:443:SER:HB3	48:x:447:ILE:HG13	1.42	0.99
48:x:437:PHE:CD2	48:x:438:LEU:CD2	2.44	0.99
5:E:126:ARG:NH1	45:u:712:C:C2'	2.26	0.99
55:5:279:ILE:O	55:5:283:VAL:HG23	1.62	0.99
55:5:127:THR:HG22	55:5:174:PHE:CD2	1.97	0.99
51:1:443:VAL:HG22	52:2:65:UNK:CB	1.91	0.98
55:5:123:PHE:CD2	55:5:171:ILE:HG22	1.96	0.98
55:5:130:VAL:CG2	55:5:177:LEU:HD12	1.93	0.98
55:5:521:LYS:CE	55:5:523:MET:CE	2.41	0.98
55:5:83:ILE:O	55:5:85:GLY:N	1.96	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:86:GLY:CA	55:5:256:PHE:CE1	2.46	0.98
42:r:47:LYS:CD	42:r:102:TYR:CE2	2.47	0.97
55:5:51:TYR:HD2	55:5:531:GLN:HG2	1.26	0.97
48:x:66:ARG:CZ	48:x:66:ARG:HA	1.94	0.97
45:u:470:A:C6	45:u:471:A:C8	2.52	0.97
50:z:69:GLY:N	50:z:70:PRO:CD	2.25	0.97
55:5:52:PHE:HB2	55:5:530:TYR:CD1	2.00	0.97
5:E:62:LYS:CE	45:u:978:G:OP2	2.13	0.97
10:J:80:GLU:OE2	10:J:170:TYR:OH	1.82	0.96
45:u:77:U:O4	45:u:335:A:N1	1.98	0.96
48:x:437:PHE:CD2	48:x:438:LEU:HD21	2.00	0.96
43:s:14:PHE:CE1	45:u:1960:A:N3	2.33	0.96
23:X:156:ILE:HG21	48:x:416:TYR:HH	1.31	0.96
45:u:1968:G:H1	45:u:2018:C:H42	1.12	0.96
55:5:214:PHE:HA	62:5:809:9UB:C06	1.94	0.96
55:5:348:SER:CB	55:5:598:TRP:CE2	2.48	0.96
48:x:42:PHE:CD1	48:x:45:CYS:HB2	2.00	0.96
48:x:66:ARG:CD	48:x:72:ASN:CG	2.38	0.96
2:B:163:LEU:HD21	2:B:182:GLU:CG	1.95	0.95
45:u:1278:C:H3'	45:u:1279:A:H4'	1.48	0.95
30:e:2:ALA:O	42:r:130:ARG:NH2	1.98	0.95
55:5:127:THR:HG23	55:5:174:PHE:HD2	0.78	0.95
55:5:521:LYS:HE3	55:5:523:MET:HE2	1.46	0.95
45:u:1983:A:N1	45:u:2008:U:O4	2.00	0.95
48:x:61:PRO:O	48:x:65:MET:HB3	0.78	0.95
9:I:184:MET:HE2	9:I:190:LEU:CG	1.95	0.95
45:u:471:A:C5	45:u:472:C:C6	2.55	0.95
45:u:4278:C:HO2'	45:u:4281:A:H8	1.06	0.95
53:3:42:PHE:HB2	53:3:91:SER:CB	1.95	0.95
12:M:116:LYS:HG2	14:O:196:LEU:HD21	1.49	0.95
45:u:1983:A:N1	45:u:2008:U:C4	2.35	0.95
45:u:216:C:O2	51:1:536:ARG:CA	2.13	0.95
45:u:3751:G:O2'	45:u:3752:C:H5'	1.65	0.95
48:x:50:LEU:HD12	50:z:88:HIS:CA	1.97	0.95
45:u:2409:U:O4	45:u:2783:A:N1	1.99	0.95
2:B:163:LEU:CD2	2:B:182:GLU:HG2	1.96	0.94
5:E:126:ARG:NH1	45:u:712:C:O2'	2.00	0.94
55:5:601:ARG:HB2	55:5:613:LYS:HZ2	1.22	0.94
45:u:957:G:H1'	45:u:958:G:OP2	1.67	0.94
48:x:47:GLN:O	48:x:75:THR:CB	2.15	0.94
38:m:99:CYS:HG	61:m:201:ZN:ZN	0.71	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:30:SER:OG	55:5:124:SER:CB	2.13	0.94
42:r:32:LEU:HD11	42:r:106:LEU:HD12	1.48	0.94
45:u:472:C:N4	45:u:473:C:N4	2.16	0.94
55:5:86:GLY:O	55:5:256:PHE:CZ	2.19	0.94
55:5:157:TYR:HE1	55:5:173:ILE:HD13	1.05	0.94
42:r:98:ARG:HH22	42:r:107:ARG:HH12	1.12	0.94
45:u:1958:A:H5''	45:u:1962:A:HO2'	1.21	0.94
48:x:181:LEU:CD1	48:x:457:TYR:CE1	2.40	0.94
55:5:52:PHE:HB3	55:5:530:TYR:CD2	2.01	0.94
33:h:38:GLY:CA	48:x:266:PRO:CG	2.43	0.93
45:u:1929:A:H61	45:u:2054:U:H3	1.10	0.93
55:5:168:ASN:HD22	62:5:809:9UB:C29	1.78	0.93
5:E:126:ARG:HH12	45:u:712:C:C2'	1.80	0.93
55:5:30:SER:HG	55:5:124:SER:HB3	1.12	0.93
55:5:52:PHE:CG	55:5:530:TYR:CE1	2.56	0.93
53:3:42:PHE:CB	53:3:91:SER:HB2	1.98	0.93
48:x:62:PHE:N	48:x:65:MET:SD	2.41	0.93
55:5:178:LEU:HD23	55:5:179:THR:N	1.84	0.93
48:x:46:CYS:HA	48:x:75:THR:OG1	1.69	0.92
40:o:77:CYS:HG	61:o:201:ZN:ZN	0.62	0.92
5:E:279:PRO:HG2	31:f:7:CYS:HG	1.28	0.92
48:x:66:ARG:NE	48:x:72:ASN:HB3	1.83	0.92
45:u:469:C:O2	45:u:688:U:C1'	2.17	0.92
55:5:601:ARG:CB	55:5:613:LYS:NZ	2.32	0.92
45:u:2468:U:N3	45:u:2473:A:N6	2.17	0.92
55:5:590:SER:O	55:5:591:ASP:N	2.03	0.92
4:D:200:MET:HE2	4:D:241:LYS:HE3	1.50	0.92
42:r:47:LYS:HG2	42:r:102:TYR:CE2	1.98	0.92
48:x:66:ARG:NH2	48:x:70:ALA:C	2.26	0.92
55:5:524:SER:OG	55:5:579:LEU:O	1.88	0.92
53:3:93:LEU:HD23	53:3:137:VAL:HG22	1.51	0.91
2:B:163:LEU:CD2	2:B:182:GLU:CG	2.48	0.91
45:u:472:C:C2	45:u:473:C:C6	2.58	0.91
45:u:472:C:C4	45:u:473:C:N4	2.38	0.91
9:I:48:LEU:HD21	9:I:145:LYS:HG2	1.48	0.91
33:h:38:GLY:CA	48:x:266:PRO:HG3	2.00	0.91
42:r:98:ARG:NH2	42:r:107:ARG:NH1	2.17	0.91
30:e:2:ALA:HB3	42:r:130:ARG:CZ	2.01	0.91
55:5:280:HIS:O	55:5:284:ASP:OD2	1.89	0.91
45:u:466:A:C2	45:u:467:U:C5	2.58	0.91
45:u:976:G:C2'	45:u:977:C:O4'	2.17	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:86:GLY:C	55:5:256:PHE:CE1	2.47	0.91
55:5:521:LYS:NZ	55:5:523:MET:HE2	1.86	0.91
42:r:98:ARG:NH2	42:r:107:ARG:HH12	1.66	0.91
23:X:83:THR:HA	48:x:403:GLY:CA	2.01	0.91
50:z:74:LEU:O	50:z:78:LEU:HD12	1.70	0.90
42:r:47:LYS:CD	42:r:102:TYR:CD2	2.54	0.90
42:r:118:LEU:HA	42:r:121:GLN:NE2	1.87	0.90
43:s:14:PHE:CE2	43:s:62:ARG:HG3	2.06	0.90
45:u:1958:A:O2'	45:u:1959:U:H5''	1.71	0.90
55:5:86:GLY:CA	55:5:256:PHE:HE1	1.82	0.90
9:I:191:ILE:HD12	9:I:200:ILE:HD11	1.52	0.90
55:5:52:PHE:CG	55:5:530:TYR:CE2	2.60	0.90
23:X:156:ILE:HD11	48:x:415:ARG:HH12	0.95	0.90
55:5:357:TRP:HA	55:5:360:TYR:HB2	0.92	0.90
2:B:174:ARG:NH1	45:u:4985:U:O2	2.04	0.90
43:s:14:PHE:CE2	43:s:62:ARG:HD3	2.01	0.90
48:x:42:PHE:HE1	48:x:45:CYS:HG	1.12	0.90
43:s:14:PHE:HE1	45:u:1960:A:N3	1.70	0.90
45:u:102:G:O2'	45:u:1381:U:O2'	1.90	0.90
48:x:66:ARG:HH21	48:x:70:ALA:HA	1.34	0.90
42:r:119:ARG:HG3	42:r:122:LYS:HE3	1.54	0.89
43:s:14:PHE:HD2	43:s:62:ARG:CD	1.84	0.89
55:5:345:ILE:HD11	55:5:595:LYS:HD3	1.52	0.89
55:5:130:VAL:HG23	55:5:177:LEU:CD1	2.02	0.89
2:B:156:TYR:CD1	45:u:4909:A:H2'	2.08	0.89
42:r:47:LYS:HB3	42:r:102:TYR:CE2	2.07	0.89
55:5:214:PHE:CE1	62:5:809:9UB:C05	2.55	0.89
42:r:107:ARG:HD2	42:r:108:MET:N	1.87	0.89
45:u:211:G:C2	45:u:212:A:C8	2.60	0.89
5:E:251:SER:O	5:E:255:PRO:CD	2.20	0.89
48:x:176:GLY:N	48:x:457:TYR:CZ	2.41	0.89
53:3:115:LEU:HA	53:3:119:LEU:CD1	2.02	0.89
43:s:14:PHE:HE2	43:s:62:ARG:CD	1.82	0.88
45:u:216:C:C2	51:1:536:ARG:CA	2.57	0.88
5:E:62:LYS:CE	45:u:978:G:OP1	2.21	0.88
50:z:68:VAL:HG13	50:z:70:PRO:O	1.71	0.88
45:u:2433:G:H4'	48:x:268:LYS:HD3	1.55	0.88
45:u:689:U:N3	45:u:690:C:C5	2.42	0.88
48:x:46:CYS:SG	48:x:77:MET:CG	2.60	0.88
55:5:157:TYR:CE1	55:5:173:ILE:CD1	2.55	0.88
55:5:521:LYS:HE2	55:5:523:MET:CE	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:521:LYS:HE3	55:5:523:MET:HB3	1.56	0.88
45:u:205:C:O2'	45:u:2305:U:C5	2.26	0.88
55:5:52:PHE:CZ	55:5:82:ARG:NH1	2.42	0.88
55:5:597:LEU:H	55:5:597:LEU:HD12	1.39	0.88
55:5:31:PHE:CZ	55:5:121:PRO:HB2	1.55	0.87
55:5:590:SER:C	55:5:591:ASP:N	2.33	0.87
55:5:346:ILE:O	55:5:349:VAL:CG1	2.22	0.87
42:r:47:LYS:CB	42:r:102:TYR:CE2	2.58	0.87
48:x:47:GLN:C	48:x:75:THR:HG22	1.99	0.87
42:r:103:HIS:ND1	42:r:106:LEU:HD23	1.89	0.87
7:G:156:VAL:HG11	7:G:184:LEU:CD1	2.05	0.87
5:E:238:ILE:O	5:E:239:THR:OG1	1.93	0.86
43:s:14:PHE:CE2	43:s:62:ARG:HD2	2.06	0.86
11:L:163:LYS:CE	45:u:509:A:H4'	2.05	0.86
23:X:156:ILE:HG13	48:x:415:ARG:CZ	2.04	0.86
45:u:2027:U:O2'	45:u:2028:C:H5'	1.76	0.86
48:x:66:ARG:CZ	48:x:69:LEU:O	2.24	0.86
55:5:31:PHE:CZ	55:5:121:PRO:CB	2.38	0.86
48:x:29:LYS:HE2	53:3:118:PHE:HZ	0.73	0.86
45:u:1279:A:H3'	45:u:1280:C:H5''	1.57	0.86
55:5:118:PHE:O	55:5:121:PRO:HD2	1.76	0.86
5:E:254:LEU:CD2	5:E:257:ILE:HD11	2.05	0.86
48:x:443:SER:CB	48:x:447:ILE:CD1	2.54	0.86
55:5:52:PHE:CB	55:5:530:TYR:CE2	2.58	0.86
45:u:470:A:N6	45:u:471:A:C5	2.44	0.86
42:r:135:LYS:NZ	45:u:451:C:H2'	1.90	0.85
45:u:472:C:C4	45:u:473:C:C4	2.64	0.85
9:I:49:CYS:SG	9:I:51:HIS:NE2	2.48	0.85
42:r:47:LYS:O	42:r:103:HIS:CD2	2.28	0.85
30:e:2:ALA:O	42:r:130:ARG:NH1	2.10	0.85
48:x:47:GLN:O	48:x:75:THR:HB	1.74	0.85
48:x:47:GLN:N	48:x:75:THR:HB	1.91	0.85
4:D:200:MET:HE1	4:D:241:LYS:HG3	1.57	0.85
48:x:42:PHE:HE1	48:x:45:CYS:SG	2.00	0.85
48:x:181:LEU:HD11	48:x:457:TYR:OH	1.76	0.85
5:E:225:GLU:OE2	42:r:135:LYS:N	2.10	0.85
45:u:1279:A:C3'	45:u:1280:C:H5''	2.07	0.85
45:u:1956:A:O2'	45:u:1957:U:H5'	1.77	0.85
55:5:52:PHE:CD2	55:5:530:TYR:CE2	2.63	0.85
30:e:2:ALA:CA	42:r:130:ARG:NH1	2.40	0.84
45:u:1957:U:O2'	45:u:1958:A:C8	2.29	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:181:LEU:CD1	48:x:457:TYR:OH	2.24	0.84
55:5:395:THR:HG23	62:5:809:9UB:C01	2.08	0.84
33:h:37:THR:O	48:x:266:PRO:HD3	1.78	0.84
48:x:153:ILE:O	48:x:157:VAL:CG2	2.23	0.84
48:x:121:MET:HE3	48:x:156:PHE:CD1	2.13	0.84
48:x:176:GLY:N	48:x:457:TYR:OH	2.11	0.84
53:3:53:ILE:HD11	55:5:354:PRO:CG	2.07	0.83
42:r:135:LYS:NZ	45:u:451:C:C2'	2.42	0.83
55:5:544:ASN:O	55:5:546:THR:HG22	1.79	0.83
43:s:14:PHE:HD2	43:s:62:ARG:HD3	1.37	0.83
30:e:2:ALA:O	42:r:130:ARG:CZ	2.27	0.82
55:5:52:PHE:CE2	55:5:530:TYR:OH	2.33	0.82
5:E:62:LYS:HE2	45:u:978:G:P	2.17	0.82
5:E:94:GLY:HA3	45:u:686:A:N7	1.95	0.82
48:x:47:GLN:H	48:x:75:THR:CB	1.92	0.82
53:3:92:PHE:CE2	53:3:96:MET:CE	2.57	0.82
4:D:33:ARG:NH2	46:v:7:G:O3'	2.13	0.82
45:u:472:C:N3	45:u:473:C:C5	2.48	0.82
42:r:119:ARG:O	42:r:122:LYS:HE3	1.80	0.82
55:5:254:ILE:O	55:5:257:VAL:O	1.97	0.82
45:u:470:A:C5	45:u:471:A:N7	2.48	0.81
45:u:1367:C:C2	45:u:1370:G:H2'	2.15	0.81
5:E:62:LYS:HE2	45:u:978:G:OP2	1.79	0.81
55:5:52:PHE:CB	55:5:530:TYR:CG	2.51	0.81
4:D:200:MET:HE1	4:D:241:LYS:CG	2.10	0.81
7:G:87:LEU:HD23	7:G:184:LEU:CD2	2.10	0.81
45:u:690:C:N3	45:u:691:C:C5	2.48	0.81
50:z:71:VAL:HG13	50:z:74:LEU:HD12	1.61	0.81
53:3:53:ILE:CD1	55:5:354:PRO:CG	2.58	0.81
5:E:157:ARG:O	5:E:178:ASN:ND2	2.13	0.81
12:M:81:ASP:OD1	12:M:84:THR:HG23	1.80	0.81
42:r:135:LYS:HD2	42:r:135:LYS:O	1.80	0.81
55:5:157:TYR:OH	55:5:173:ILE:HD12	1.78	0.81
55:5:601:ARG:HB3	55:5:613:LYS:HG3	1.61	0.81
48:x:66:ARG:HH22	48:x:70:ALA:C	1.86	0.81
55:5:513:ARG:CD	55:5:535:MET:O	2.29	0.81
55:5:601:ARG:CB	55:5:613:LYS:HZ2	1.93	0.81
7:G:86:VAL:HG21	7:G:185:LYS:HE3	1.62	0.80
42:r:122:LYS:HB2	42:r:123:PRO:CD	2.10	0.80
45:u:690:C:C2	45:u:691:C:C6	2.69	0.80
55:5:212:TYR:CE2	55:5:257:VAL:HG21	2.16	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:163:LEU:HD21	2:B:182:GLU:HG3	1.61	0.80
7:G:86:VAL:HG12	7:G:87:LEU:N	1.96	0.80
55:5:212:TYR:HE2	55:5:257:VAL:HG21	1.46	0.80
5:E:251:SER:O	5:E:255:PRO:HD2	1.81	0.80
42:r:135:LYS:HZ1	45:u:451:C:H2'	1.45	0.80
45:u:463:A:N1	45:u:692:A:C2	2.49	0.80
45:u:2433:G:H4'	48:x:268:LYS:CD	2.10	0.80
48:x:437:PHE:CD2	48:x:438:LEU:HD23	2.10	0.80
2:B:156:TYR:CE1	45:u:4909:A:H2'	2.16	0.80
23:X:156:ILE:HG23	48:x:416:TYR:OH	1.82	0.80
45:u:1379:C:H4'	45:u:1380:G:O4'	1.81	0.80
48:x:64:TRP:HZ2	48:x:346:SER:HB2	1.41	0.80
45:u:2395:A:O2'	45:u:2806:A:H1'	1.82	0.80
55:5:525:TRP:CE3	55:5:599:MET:HE2	2.17	0.80
53:3:53:ILE:HD11	55:5:354:PRO:HG3	1.62	0.80
45:u:1929:A:N6	45:u:2054:U:H3	1.80	0.79
48:x:47:GLN:N	48:x:75:THR:CB	2.45	0.79
55:5:30:SER:OG	55:5:34:ARG:NH2	2.15	0.79
7:G:87:LEU:HD23	7:G:184:LEU:HD21	1.64	0.79
30:e:2:ALA:C	42:r:130:ARG:HH12	1.90	0.79
45:u:957:G:N2	45:u:959:G:O6	2.15	0.79
55:5:88:LEU:HD12	55:5:256:PHE:HB3	1.63	0.79
9:I:202:ASN:O	46:v:63:C:C4	2.34	0.79
47:w:55:U:O4	47:w:62:A:N1	2.16	0.79
53:3:86:GLU:OE1	55:5:357:TRP:NE1	2.16	0.79
45:u:919:C:N4	45:u:920:C:C4	2.51	0.79
2:B:163:LEU:HD23	2:B:182:GLU:HG2	1.64	0.79
23:X:84:GLU:N	48:x:403:GLY:C	2.32	0.79
48:x:443:SER:HB3	48:x:447:ILE:HD11	1.62	0.79
53:3:141:MET:SD	55:5:357:TRP:HZ3	2.06	0.79
55:5:52:PHE:HZ	55:5:82:ARG:HH11	1.29	0.79
55:5:211:GLY:O	55:5:214:PHE:HB3	1.82	0.79
45:u:4723:A:H2'	45:u:4724:A:C8	2.18	0.79
45:u:212:A:H2'	45:u:213:G:H8	1.47	0.79
45:u:688:U:N3	45:u:689:U:C6	2.50	0.79
48:x:176:GLY:CA	48:x:457:TYR:CZ	2.65	0.79
55:5:178:LEU:HD21	55:5:201:ALA:HB1	1.65	0.79
5:E:279:PRO:CD	31:f:7:CYS:SG	2.71	0.78
45:u:2026:A:C2'	45:u:2027:U:H5'	2.14	0.78
45:u:3751:G:H2'	45:u:3752:C:H5'	1.65	0.78
45:u:1213:G:C6	45:u:1215:C:C2	2.72	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:216:C:H5	45:u:217:C:O2	1.65	0.78
48:x:157:VAL:CG1	50:z:80:PHE:CE2	0.73	0.78
50:z:69:GLY:N	50:z:70:PRO:HD2	1.97	0.78
2:B:163:LEU:HD21	2:B:182:GLU:HG2	1.59	0.78
43:s:14:PHE:CE1	45:u:1960:A:H2	2.02	0.78
48:x:29:LYS:CG	53:3:118:PHE:CZ	2.59	0.78
53:3:53:ILE:CD1	55:5:354:PRO:HG2	2.13	0.78
2:B:36:ASP:OD2	2:B:39:LYS:HE2	1.83	0.78
45:u:2769:U:C2	45:u:2770:C:C5	2.72	0.78
24:Y:59:ARG:NH2	45:u:200:U:O2'	2.17	0.77
42:r:119:ARG:O	42:r:122:LYS:CE	2.32	0.77
45:u:745:G:H2'	45:u:746:A:O4'	1.83	0.77
55:5:52:PHE:HZ	55:5:82:ARG:NH1	1.81	0.77
37:l:21:ARG:HD2	48:x:273:ARG:NH1	1.98	0.77
45:u:77:U:N3	45:u:335:A:N6	2.32	0.77
55:5:122:LEU:HD12	55:5:122:LEU:O	1.83	0.77
55:5:522:VAL:CG1	55:5:532:ILE:HG21	2.09	0.77
55:5:126:PHE:C	55:5:174:PHE:HE2	1.92	0.77
23:X:83:THR:HG22	48:x:403:GLY:O	1.83	0.77
15:P:127:ARG:NH2	45:u:2422:C:OP1	2.17	0.77
48:x:121:MET:HE1	48:x:156:PHE:HD1	1.46	0.77
45:u:504:G:N1	45:u:654:C:C2	2.52	0.77
48:x:248:THR:OG1	48:x:440:ALA:C	2.17	0.77
4:D:35:ARG:HB2	45:u:4325:A:C2	2.20	0.77
42:r:122:LYS:HB2	42:r:123:PRO:HD2	1.66	0.77
45:u:3723:A:H2'	45:u:3724:A:C8	2.20	0.77
48:x:42:PHE:CD1	48:x:45:CYS:CB	2.67	0.77
9:I:191:ILE:HD11	9:I:200:ILE:CD1	2.08	0.76
55:5:524:SER:HG	55:5:579:LEU:C	1.93	0.76
45:u:466:A:C2	45:u:467:U:C6	2.73	0.76
23:X:83:THR:CG2	48:x:403:GLY:O	2.34	0.76
42:r:119:ARG:C	42:r:122:LYS:NZ	2.43	0.76
53:3:93:LEU:O	53:3:133:PHE:CE1	2.39	0.76
55:5:168:ASN:HD21	62:5:809:9UB:P26	2.07	0.76
55:5:345:ILE:CD1	55:5:595:LYS:HD3	2.15	0.76
5:E:226:GLY:N	42:r:135:LYS:CD	2.46	0.76
42:r:119:ARG:HG3	42:r:122:LYS:CE	2.15	0.76
48:x:66:ARG:HD3	48:x:72:ASN:ND2	2.00	0.76
49:y:56:LEU:CG	53:3:92:PHE:CD2	2.69	0.76
52:2:75:UNK:O	52:2:76:UNK:CB	2.33	0.76
9:I:184:MET:CE	9:I:190:LEU:CD1	2.64	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:86:GLY:CA	55:5:256:PHE:CZ	2.69	0.76
33:h:38:GLY:HA3	48:x:266:PRO:CG	2.11	0.76
45:u:209:U:C4	45:u:211:G:C8	2.74	0.76
45:u:2793:G:C6	45:u:2797:C:C4	2.73	0.76
48:x:157:VAL:HG11	50:z:80:PHE:CZ	1.84	0.76
55:5:601:ARG:CB	55:5:613:LYS:HZ3	1.98	0.76
43:s:14:PHE:CE2	43:s:62:ARG:CG	2.57	0.76
55:5:357:TRP:O	55:5:361:TYR:N	2.18	0.76
48:x:47:GLN:C	48:x:75:THR:CG2	2.59	0.75
48:x:443:SER:CB	48:x:447:ILE:HD11	2.16	0.75
45:u:470:A:N6	45:u:471:A:C4	2.55	0.75
45:u:504:G:C2	45:u:654:C:O2	2.39	0.75
53:3:114:LYS:O	53:3:119:LEU:HG	1.85	0.75
45:u:2468:U:C4	45:u:2473:A:N1	2.54	0.75
3:C:159:GLU:OE1	3:C:159:GLU:N	2.20	0.75
42:r:118:LEU:CA	42:r:121:GLN:HE21	1.98	0.75
45:u:211:G:C2	45:u:212:A:N7	2.55	0.75
55:5:357:TRP:O	55:5:360:TYR:CA	2.34	0.75
48:x:64:TRP:CH2	48:x:346:SER:HA	2.22	0.75
55:5:504:ASP:HB2	55:5:688:LEU:CG	2.10	0.75
5:E:202:VAL:CG1	5:E:256:LYS:HZ1	1.97	0.75
48:x:443:SER:N	48:x:447:ILE:HD12	2.02	0.75
50:z:71:VAL:N	50:z:72:PRO:HD2	2.02	0.74
55:5:31:PHE:CD2	55:5:121:PRO:HB2	2.23	0.74
55:5:87:THR:HA	62:5:809:9UB:O38	1.87	0.74
42:r:97:ILE:HG21	42:r:107:ARG:CB	2.11	0.74
45:u:208:A:N1	45:u:233:U:C2	2.55	0.74
50:z:74:LEU:C	50:z:78:LEU:HD13	2.12	0.74
55:5:357:TRP:C	55:5:360:TYR:HB2	2.12	0.74
48:x:64:TRP:CD1	48:x:64:TRP:H	2.06	0.74
3:C:158:VAL:HA	3:C:161:TYR:CE2	2.22	0.74
45:u:688:U:C4	45:u:689:U:C5	2.75	0.74
55:5:72:PHE:HA	55:5:83:ILE:HG12	1.69	0.74
7:G:86:VAL:HG11	7:G:185:LYS:HG2	1.68	0.74
42:r:120:SER:HA	42:r:122:LYS:NZ	2.02	0.74
45:u:1279:A:H3'	45:u:1280:C:C5'	2.18	0.74
55:5:525:TRP:HB2	55:5:592:ASP:OD2	1.88	0.74
9:I:184:MET:CE	9:I:190:LEU:HG	2.16	0.74
55:5:521:LYS:HD2	55:5:575:VAL:HA	1.68	0.74
11:L:116:ARG:NH1	11:L:155:MET:O	2.21	0.73
48:x:66:ARG:HD2	48:x:72:ASN:HD22	0.92	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:590:SER:O	55:5:591:ASP:CA	2.37	0.73
42:r:47:LYS:HD2	42:r:102:TYR:HD2	1.50	0.73
55:5:597:LEU:HD12	55:5:597:LEU:N	2.04	0.73
48:x:444:GLY:O	48:x:446:GLY:N	2.21	0.73
53:3:92:PHE:CG	53:3:96:MET:HE2	2.21	0.73
43:s:10:LYS:NZ	45:u:1960:A:O2'	2.20	0.73
55:5:34:ARG:CZ	55:5:124:SER:OG	2.36	0.73
55:5:525:TRP:CD1	55:5:595:LYS:HD2	2.23	0.73
30:e:2:ALA:CB	42:r:130:ARG:CZ	2.64	0.73
55:5:87:THR:CA	55:5:256:PHE:CZ	2.60	0.73
55:5:468:LEU:O	55:5:471:TYR:HB3	1.89	0.73
55:5:544:ASN:O	55:5:546:THR:CG2	2.36	0.73
45:u:22:G:N2	47:w:35:C:C2	2.56	0.73
45:u:467:U:N3	45:u:468:U:C5	2.56	0.73
45:u:3914:U:H3	45:u:4378:A:N6	1.86	0.73
45:u:2779:C:O2'	47:w:112:G:OP1	2.05	0.73
30:e:117:GLN:O	42:r:122:LYS:HD3	1.88	0.73
42:r:135:LYS:HZ3	45:u:451:C:C2'	2.02	0.72
45:u:212:A:H2'	45:u:213:G:C8	2.24	0.72
55:5:524:SER:OG	55:5:579:LEU:C	2.33	0.72
11:L:161:PHE:CE1	26:a:105:ARG:HG3	2.24	0.72
45:u:1280:C:C4	45:u:1282:G:C6	2.77	0.72
55:5:593:ILE:HD13	55:5:639:MET:HG3	1.70	0.72
53:3:88:LEU:HD22	53:3:88:LEU:N	2.02	0.72
55:5:157:TYR:OH	55:5:173:ILE:CD1	2.37	0.72
55:5:177:LEU:C	55:5:177:LEU:HD13	2.15	0.72
45:u:690:C:C4	45:u:691:C:C5	2.77	0.72
55:5:123:PHE:CD2	55:5:170:GLY:O	2.42	0.72
45:u:1278:C:C3'	45:u:1279:A:H4'	2.18	0.71
45:u:1724:G:H4'	45:u:1725:U:OP2	1.89	0.71
45:u:3914:U:H3	45:u:4378:A:H61	1.37	0.71
48:x:157:VAL:HB	50:z:80:PHE:HZ	0.72	0.71
55:5:257:VAL:HG12	55:5:261:PRO:HD3	1.72	0.71
2:B:261:ARG:HE	45:u:3870:C:H4'	1.55	0.71
5:E:254:LEU:HD22	5:E:258:LYS:HE3	1.72	0.71
45:u:2632:U:H2'	45:u:2633:U:C6	2.25	0.71
2:B:163:LEU:CD2	2:B:182:GLU:HG3	2.17	0.71
45:u:166:C:O2	45:u:166:C:H2'	1.90	0.71
45:u:977:C:C2'	45:u:978:G:H5'	2.20	0.71
53:3:90:SER:OG	55:5:357:TRP:NE1	2.22	0.71
55:5:601:ARG:HB2	55:5:613:LYS:HZ3	1.53	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:120:SER:HA	42:r:122:LYS:HZ3	1.56	0.71
45:u:2026:A:O2'	45:u:2027:U:H5'	1.90	0.71
48:x:157:VAL:CB	50:z:80:PHE:HZ	1.59	0.71
7:G:86:VAL:CG1	7:G:87:LEU:H	2.04	0.71
30:e:2:ALA:CB	42:r:130:ARG:HH12	2.01	0.71
45:u:2367:A:N1	45:u:2788:U:C4	2.57	0.71
48:x:430:ALA:O	48:x:433:VAL:HB	1.91	0.71
5:E:217:GLN:NE2	5:E:233:LYS:HD2	2.05	0.71
3:C:157:LYS:O	3:C:160:GLY:N	2.20	0.71
45:u:516:C:C2	45:u:646:G:N2	2.59	0.71
45:u:977:C:C2	45:u:978:G:C8	2.79	0.71
48:x:176:GLY:N	48:x:457:TYR:CE1	2.58	0.71
30:e:30:LYS:NZ	45:u:2347:A:N3	2.39	0.71
45:u:956:A:H4'	45:u:957:G:OP2	1.89	0.71
7:G:87:LEU:CD2	7:G:184:LEU:HD21	2.20	0.71
33:h:38:GLY:HA2	48:x:266:PRO:CB	2.04	0.71
7:G:156:VAL:CG1	7:G:184:LEU:HD12	2.14	0.70
9:I:191:ILE:CD1	9:I:200:ILE:HD11	2.14	0.70
43:s:34:ASN:OD1	45:u:1969:G:P	2.49	0.70
45:u:4075:U:O2'	45:u:4076:G:H2'	1.91	0.70
48:x:66:ARG:NH2	48:x:69:LEU:O	2.20	0.70
42:r:130:ARG:HD2	42:r:130:ARG:C	2.17	0.70
45:u:723:A:C2	45:u:943:A:N1	2.59	0.70
45:u:1958:A:H4'	45:u:1962:A:H1'	1.72	0.70
30:e:91:CYS:O	30:e:93:LYS:N	2.25	0.70
48:x:47:GLN:O	48:x:75:THR:CG2	2.39	0.70
5:E:62:LYS:HE3	45:u:978:G:P	2.23	0.70
45:u:1279:A:C2'	45:u:1280:C:H5''	2.21	0.70
45:u:4481:U:H2'	45:u:4482:U:C6	2.27	0.70
55:5:601:ARG:HB3	55:5:613:LYS:CG	2.22	0.70
48:x:157:VAL:HG12	50:z:80:PHE:CE2	0.88	0.70
45:u:181:C:N3	45:u:256:G:C2	2.59	0.70
45:u:4371:G:O2'	45:u:4372:U:OP2	2.05	0.70
5:E:251:SER:O	5:E:255:PRO:HD3	1.91	0.70
45:u:499:G:N2	45:u:656:C:C2	2.60	0.70
45:u:2367:A:N6	45:u:2788:U:H3	1.88	0.70
35:j:59:THR:O	47:w:42:G:OP1	2.10	0.70
45:u:211:G:H4'	45:u:234:G:C8	2.27	0.70
48:x:47:GLN:N	48:x:75:THR:HG21	2.07	0.70
48:x:181:LEU:HD21	48:x:457:TYR:CE1	2.26	0.70
45:u:1929:A:N1	45:u:2054:U:C4	2.59	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:2773:G:N2	45:u:2774:C:C2	2.60	0.69
49:y:63:ASN:HD21	53:3:71:PRO:C	2.00	0.69
5:E:225:GLU:C	42:r:135:LYS:CD	2.62	0.69
9:I:187:GLU:OE1	9:I:189:ARG:NE	2.25	0.69
45:u:1991:A:N6	45:u:2003:G:OP1	2.25	0.69
50:z:69:GLY:N	50:z:70:PRO:HD3	2.06	0.69
55:5:52:PHE:CD2	55:5:530:TYR:OH	2.44	0.69
55:5:71:TRP:O	55:5:83:ILE:CD1	2.40	0.69
55:5:157:TYR:CZ	55:5:173:ILE:HD13	2.26	0.69
55:5:521:LYS:HE3	55:5:523:MET:CB	2.23	0.69
45:u:4510:A:O2'	45:u:4511:A:O4'	2.11	0.69
45:u:4901:G:N2	45:u:4921:C:C2	2.60	0.69
48:x:47:GLN:N	48:x:75:THR:CG2	2.56	0.69
53:3:129:LEU:O	53:3:133:PHE:HB3	1.92	0.69
45:u:499:G:C2	45:u:656:C:C2	2.81	0.69
45:u:2367:A:N6	45:u:2788:U:N3	2.40	0.69
48:x:66:ARG:NH2	48:x:66:ARG:HA	2.07	0.69
50:z:79:LEU:C	50:z:79:LEU:HD23	2.18	0.69
45:u:208:A:H3'	45:u:209:U:H5''	1.73	0.69
48:x:42:PHE:CE1	48:x:45:CYS:SG	2.84	0.69
48:x:78:GLU:HG2	48:x:155:LEU:HD22	1.75	0.69
45:u:468:U:O2	45:u:469:C:O4'	2.10	0.69
45:u:482:G:H2'	45:u:483:G:C8	2.27	0.69
55:5:52:PHE:CD1	55:5:530:TYR:CZ	2.73	0.69
55:5:348:SER:HB3	55:5:598:TRP:HZ2	1.44	0.69
9:I:87:ILE:HG12	9:I:138:ILE:HG12	1.74	0.69
45:u:197:A:N1	45:u:225:G:O2'	2.24	0.69
55:5:214:PHE:CA	62:5:809:9UB:C06	2.71	0.69
45:u:469:C:H2'	45:u:470:A:O4'	1.93	0.69
45:u:1635:C:H2'	45:u:1636:U:H5'	1.75	0.69
49:y:53:PHE:HE1	53:3:92:PHE:CE1	2.11	0.69
7:G:86:VAL:HG12	7:G:87:LEU:H	1.55	0.68
45:u:200:U:C4	45:u:238:C:O4'	2.46	0.68
48:x:69:LEU:HB2	48:x:80:GLY:HA2	1.74	0.68
55:5:134:LEU:HD13	55:5:177:LEU:HD21	1.74	0.68
55:5:424:GLN:NE2	55:5:428:THR:OG1	2.26	0.68
55:5:522:VAL:CG1	55:5:532:ILE:HD13	2.22	0.68
23:X:83:THR:C	48:x:403:GLY:O	2.36	0.68
45:u:1367:C:N3	45:u:1369:C:OP2	2.26	0.68
48:x:29:LYS:CE	53:3:118:PHE:CZ	2.44	0.68
55:5:597:LEU:H	55:5:597:LEU:CD1	2.06	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:j:34:CYS:SG	35:j:36:LYS:HB3	2.33	0.68
50:z:78:LEU:HD12	50:z:78:LEU:N	2.07	0.68
55:5:157:TYR:HE1	55:5:173:ILE:CD1	1.94	0.68
23:X:83:THR:CA	48:x:403:GLY:O	2.42	0.68
45:u:465:G:C2	45:u:466:A:C8	2.82	0.68
45:u:1968:G:H1	45:u:2018:C:N4	1.89	0.68
45:u:2526:C:O4'	48:x:405:ARG:NH2	2.26	0.68
48:x:47:GLN:O	48:x:75:THR:HG22	1.93	0.68
55:5:525:TRP:HE1	55:5:595:LYS:HD3	1.58	0.68
4:D:69:ILE:HD11	19:T:28:ALA:HB1	1.75	0.68
39:n:13:LEU:HD11	39:n:17:ARG:CZ	2.23	0.68
45:u:978:G:H2'	45:u:979:C:O4'	1.92	0.68
42:r:118:LEU:HD12	42:r:121:GLN:NE2	2.08	0.68
3:C:271:ALA:O	3:C:272:SER:OG	2.11	0.68
45:u:680:G:C2	45:u:681:G:C8	2.82	0.68
50:z:76:MET:SD	50:z:76:MET:N	2.65	0.68
42:r:122:LYS:HD2	42:r:122:LYS:N	2.09	0.68
45:u:1958:A:O2'	45:u:1959:U:C5'	2.41	0.68
48:x:406:GLU:OE1	48:x:407:THR:N	2.27	0.68
53:3:53:ILE:HD12	55:5:354:PRO:HG2	1.74	0.68
55:5:395:THR:CG2	62:5:809:9UB:C02	2.71	0.68
30:e:2:ALA:CA	42:r:130:ARG:HH12	2.03	0.67
45:u:209:U:C5	45:u:211:G:C8	2.82	0.67
45:u:1358:G:H8	45:u:1358:G:H3'	1.58	0.67
55:5:601:ARG:HH11	55:5:601:ARG:CG	2.07	0.67
4:D:23:ARG:NH2	45:u:4280:A:OP2	2.27	0.67
45:u:166:C:O2	45:u:167:C:H5	1.76	0.67
45:u:504:G:C6	45:u:654:C:N3	2.61	0.67
55:5:52:PHE:HB3	55:5:530:TYR:CE2	2.24	0.67
3:C:210:ILE:HG21	3:C:252:TRP:CZ3	2.30	0.67
48:x:64:TRP:CZ2	48:x:346:SER:CB	2.74	0.67
3:C:313:VAL:HG11	6:F:172:THR:HG21	1.76	0.67
42:r:120:SER:N	42:r:122:LYS:NZ	2.37	0.67
45:u:497:G:N2	45:u:657:C:C2	2.62	0.67
45:u:642:G:N2	45:u:643:C:C2	2.62	0.67
45:u:973:G:N2	45:u:1282:G:O2'	2.28	0.67
45:u:4453:C:C2	45:u:4529:G:C2	2.82	0.67
55:5:220:PRO:O	55:5:223:VAL:HB	1.94	0.67
55:5:395:THR:CG2	62:5:809:9UB:C01	2.72	0.67
45:u:2288:G:N2	45:u:2290:C:C2	2.63	0.67
48:x:64:TRP:CH2	48:x:346:SER:CA	2.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:e:2:ALA:C	42:r:130:ARG:NH1	2.52	0.67
48:x:157:VAL:HG11	50:z:80:PHE:CE2	0.87	0.67
55:5:31:PHE:HZ	55:5:118:PHE:O	1.78	0.67
42:r:123:PRO:HG2	42:r:126:VAL:HB	1.74	0.67
42:r:130:ARG:HD2	42:r:130:ARG:O	1.93	0.67
45:u:1264:C:H2'	45:u:1265:G:O4'	1.95	0.67
55:5:402:VAL:HG23	55:5:403:MET:HG2	1.76	0.67
45:u:166:C:O2	45:u:167:C:C5	2.48	0.67
48:x:45:CYS:HB3	48:x:77:MET:SD	2.34	0.67
55:5:348:SER:HB3	55:5:598:TRP:NE1	2.08	0.67
45:u:217:C:H3'	45:u:218:A:H4'	1.77	0.66
42:r:107:ARG:HD2	42:r:107:ARG:C	2.19	0.66
45:u:2409:U:C4	45:u:2783:A:C2	2.83	0.66
55:5:51:TYR:CE2	55:5:531:GLN:HG2	2.30	0.66
55:5:157:TYR:CZ	55:5:173:ILE:CD1	2.78	0.66
5:E:161:LEU:HD21	5:E:253:ILE:HD11	1.76	0.66
6:F:245:LEU:HD23	6:F:249:MET:HG3	1.77	0.66
8:H:95:VAL:HG22	38:m:82:LEU:HD22	1.76	0.66
50:z:78:LEU:HD12	50:z:78:LEU:H	1.59	0.66
55:5:521:LYS:NZ	55:5:523:MET:CE	2.55	0.66
45:u:22:G:C2	47:w:35:C:N3	2.64	0.66
45:u:471:A:C6	45:u:472:C:C5	2.83	0.66
45:u:1268:G:H4'	45:u:1269:G:OP1	1.95	0.66
45:u:2468:U:H3	45:u:2473:A:N6	1.91	0.66
48:x:48:ILE:HG13	48:x:49:PRO:HD2	1.75	0.66
50:z:72:PRO:O	50:z:76:MET:N	2.27	0.66
5:E:225:GLU:HA	42:r:135:LYS:HE2	1.76	0.66
45:u:723:A:H2	45:u:943:A:N1	1.93	0.66
49:y:56:LEU:HD11	53:3:92:PHE:HD2	0.51	0.66
45:u:691:C:C2	45:u:692:A:C8	2.84	0.66
45:u:3752:C:O2'	45:u:3753:G:OP2	2.09	0.66
48:x:78:GLU:HG2	48:x:155:LEU:CD2	2.25	0.66
10:J:83:LEU:HD12	10:J:170:TYR:CZ	2.31	0.66
45:u:2258:C:O2	45:u:2258:C:H2'	1.96	0.66
45:u:2826:U:H4'	45:u:2827:G:H5'	1.77	0.66
48:x:47:GLN:O	48:x:75:THR:HA	1.96	0.66
55:5:65:PHE:H	55:5:69:HIS:HB3	1.60	0.66
12:M:116:LYS:HG3	14:O:196:LEU:CD2	2.20	0.66
45:u:466:A:N1	45:u:467:U:C4	2.65	0.66
45:u:1957:U:C2'	45:u:1958:A:C8	2.79	0.66
48:x:61:PRO:O	48:x:65:MET:CG	2.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:86:VAL:CG1	7:G:87:LEU:N	2.57	0.65
23:X:156:ILE:CG1	48:x:415:ARG:NH1	2.59	0.65
48:x:176:GLY:HA3	48:x:457:TYR:CZ	2.14	0.65
48:x:438:LEU:HD23	48:x:438:LEU:N	2.03	0.65
55:5:507:GLU:OE2	55:5:685:GLU:HG3	1.96	0.65
45:u:680:G:C4	45:u:681:G:C8	2.85	0.65
45:u:1958:A:H3'	45:u:1958:A:OP2	1.96	0.65
4:D:200:MET:CE	4:D:241:LYS:HE3	2.26	0.65
45:u:1378:C:H3'	45:u:1379:C:C5'	2.26	0.65
48:x:66:ARG:CD	48:x:72:ASN:HD22	1.83	0.65
55:5:528:TYR:CE2	55:5:581:ILE:HD12	2.32	0.65
2:B:120:LYS:N	45:u:4968:A:OP1	2.28	0.65
5:E:59:TYR:CD2	5:E:64:LEU:CD1	2.73	0.65
45:u:1358:G:C6	45:u:1379:C:N3	2.64	0.65
45:u:1359:G:H2'	45:u:1360:G:C8	2.30	0.65
45:u:1635:C:C2'	45:u:1636:U:H5'	2.26	0.65
48:x:346:SER:O	48:x:360:HIS:NE2	2.29	0.65
50:z:71:VAL:CG1	50:z:74:LEU:HD12	2.27	0.65
55:5:178:LEU:HD23	55:5:178:LEU:C	2.21	0.65
11:L:56:ARG:O	11:L:116:ARG:NH2	2.28	0.65
45:u:220:C:H3'	45:u:220:C:OP1	1.96	0.65
48:x:66:ARG:HD2	48:x:72:ASN:CB	2.25	0.65
48:x:78:GLU:OE2	48:x:155:LEU:O	2.14	0.65
2:B:14:LEU:HD23	2:B:17:LEU:HD21	1.77	0.65
25:Z:52:LYS:O	25:Z:65:ARG:NH2	2.29	0.65
42:r:119:ARG:C	42:r:122:LYS:CE	2.70	0.65
45:u:1879:C:O2'	45:u:1891:A:N3	2.29	0.65
10:J:83:LEU:HD12	10:J:170:TYR:OH	1.96	0.65
42:r:47:LYS:HD2	42:r:102:TYR:CE2	2.22	0.65
46:v:30:C:C2	46:v:48:G:N2	2.65	0.65
55:5:50:PRO:HB3	55:5:166:TYR:HB3	1.79	0.65
2:B:254:ILE:HG23	2:B:266:VAL:HG11	1.78	0.65
42:r:32:LEU:CD1	42:r:106:LEU:HD12	2.24	0.65
45:u:1404:G:C2	45:u:1414:C:C2	2.85	0.65
48:x:61:PRO:O	48:x:65:MET:HE3	1.96	0.65
9:I:184:MET:CE	9:I:190:LEU:HD11	2.27	0.64
45:u:1969:G:O2'	45:u:1970:A:H5'	1.97	0.64
45:u:5066:U:H2'	45:u:5067:U:C6	2.32	0.64
2:B:45:ALA:HB3	2:B:183:ILE:HG23	1.79	0.64
9:I:184:MET:HG2	9:I:189:ARG:HD2	1.79	0.64
45:u:1682:A:C2	45:u:1683:U:C2	2.85	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:200:U:O4	45:u:238:C:C1'	2.46	0.64
45:u:206:U:O2	45:u:208:A:C8	2.51	0.64
45:u:986:C:C2	45:u:1068:G:N2	2.65	0.64
45:u:1358:G:H3'	45:u:1358:G:C8	2.32	0.64
45:u:2084:C:H3'	45:u:2085:G:C5'	2.27	0.64
49:y:13:GLN:O	49:y:17:ASP:HB2	1.98	0.64
55:5:167:ASP:OD2	55:5:405:ARG:NH1	2.30	0.64
45:u:976:G:H4'	45:u:976:G:OP1	1.98	0.64
45:u:1957:U:O2'	45:u:1958:A:H8	1.78	0.64
5:E:225:GLU:CA	42:r:135:LYS:HE2	2.28	0.64
45:u:209:U:C5	45:u:211:G:N7	2.66	0.64
45:u:211:G:N3	45:u:212:A:C8	2.66	0.64
45:u:471:A:C2	45:u:472:C:C1'	2.80	0.64
45:u:690:C:N3	45:u:691:C:C6	2.66	0.64
3:C:158:VAL:HA	3:C:161:TYR:CD2	2.33	0.64
26:a:4:ARG:NH2	45:u:2341:A:OP2	2.31	0.64
42:r:135:LYS:HZ1	45:u:451:C:C2'	2.09	0.64
45:u:470:A:C6	45:u:471:A:N9	2.65	0.64
48:x:67:VAL:HG12	48:x:68:ILE:HD13	1.80	0.64
45:u:471:A:C5	45:u:472:C:C5	2.85	0.64
45:u:1380:G:O2'	45:u:1381:U:O2	2.10	0.64
48:x:62:PHE:HB2	48:x:72:ASN:HD22	1.63	0.64
55:5:118:PHE:C	55:5:121:PRO:HD2	2.23	0.64
7:G:86:VAL:HG13	7:G:183:ILE:O	1.98	0.64
45:u:4213:A:N1	45:u:4218:U:C4	2.61	0.64
48:x:47:GLN:O	48:x:75:THR:CA	2.46	0.64
24:Y:59:ARG:NH1	45:u:200:U:C2	2.66	0.63
48:x:444:GLY:O	48:x:445:THR:C	2.40	0.63
28:c:34:THR:OG1	28:c:95:ALA:HB2	1.97	0.63
45:u:1823:G:O3'	45:u:1825:A:P	2.56	0.63
45:u:4579:U:H2'	45:u:4580:U:C6	2.33	0.63
13:N:202:ARG:NH2	45:u:1372:A:OP1	2.32	0.63
33:h:37:THR:O	48:x:266:PRO:CD	2.46	0.63
45:u:167:C:C2	45:u:269:G:N2	2.66	0.63
45:u:3668:C:C2	45:u:3675:G:C2	2.87	0.63
55:5:123:PHE:HZ	55:5:171:ILE:O	1.77	0.63
5:E:279:PRO:HD2	31:f:7:CYS:SG	2.38	0.63
45:u:1213:G:N1	45:u:1215:C:C2	2.67	0.63
55:5:123:PHE:CD1	55:5:171:ILE:CG2	2.71	0.63
5:E:254:LEU:HD23	5:E:257:ILE:CD1	2.13	0.63
30:e:108:ARG:HH22	30:e:127:ALA:HB3	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:65:ARG:NH1	45:u:1502:G:OP1	2.32	0.63
45:u:202:C:C2	45:u:214:G:C2	2.87	0.63
45:u:1550:G:C2	45:u:1579:C:C2	2.86	0.63
45:u:4723:A:C2	45:u:4724:A:C6	2.86	0.63
48:x:48:ILE:CG1	48:x:49:PRO:HD2	2.28	0.63
6:F:161:TYR:CE2	6:F:170:ALA:HB2	2.34	0.63
9:I:204:GLY:O	9:I:205:PRO:C	2.41	0.63
45:u:465:G:C6	45:u:466:A:N7	2.67	0.63
55:5:395:THR:HG23	62:5:809:9UB:C02	2.29	0.63
7:G:87:LEU:CD2	7:G:184:LEU:CD2	2.77	0.63
45:u:22:G:C2	47:w:35:C:C2	2.87	0.63
45:u:1378:C:H3'	45:u:1379:C:H5'	1.81	0.63
45:u:2090:U:P	45:u:2090:U:O4'	2.56	0.63
45:u:2108:G:C6	45:u:2125:C:N4	2.67	0.63
11:L:65:ARG:HG2	11:L:66:TYR:CE2	2.34	0.62
45:u:468:U:O4	45:u:687:U:O4	2.17	0.62
45:u:2268:A:H4'	45:u:2269:C:H5'	1.80	0.62
48:x:42:PHE:CE1	48:x:45:CYS:CB	2.82	0.62
48:x:437:PHE:O	48:x:438:LEU:HD23	1.98	0.62
55:5:51:TYR:HD2	55:5:531:GLN:CG	2.05	0.62
45:u:199:G:C4	45:u:201:C:C5	2.87	0.62
45:u:688:U:C4	45:u:689:U:C6	2.87	0.62
3:C:32:ILE:HD12	3:C:130:ALA:HB2	1.82	0.62
45:u:1983:A:C6	45:u:2008:U:O4	2.52	0.62
45:u:2409:U:O4	45:u:2783:A:C6	2.52	0.62
45:u:3900:G:N2	45:u:4562:C:C2	2.67	0.62
14:O:201:PHE:HB2	14:O:202:LEU:HD13	1.80	0.62
42:r:47:LYS:O	42:r:103:HIS:HD2	1.78	0.62
45:u:200:U:O4	45:u:238:C:H1'	1.98	0.62
45:u:4885:U:H2'	45:u:4886:C:O4'	1.99	0.62
48:x:236:ARG:HH12	48:x:238:ASN:HB2	1.64	0.62
42:r:120:SER:CA	42:r:122:LYS:HZ2	2.13	0.62
45:u:1987:C:O2	45:u:1987:C:H2'	2.00	0.62
45:u:3783:A:H4'	45:u:3784:A:H5''	1.81	0.62
53:3:59:VAL:HA	53:3:71:PRO:HA	1.81	0.62
45:u:470:A:N7	45:u:471:A:N7	2.48	0.62
45:u:1081:C:C2	45:u:1220:G:C2	2.87	0.62
45:u:2547:G:N2	45:u:2548:C:C2	2.68	0.62
4:D:200:MET:CE	4:D:241:LYS:HG3	2.28	0.62
5:E:202:VAL:HG13	5:E:256:LYS:HZ1	1.50	0.62
45:u:504:G:C6	45:u:654:C:C2	2.87	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:2758:G:O2'	45:u:2764:A:N3	2.26	0.62
55:5:175:CYS:HB3	55:5:205:MET:HB2	1.80	0.62
12:M:81:ASP:OD1	12:M:84:THR:CG2	2.47	0.62
42:r:135:LYS:NZ	45:u:451:C:H3'	2.14	0.62
45:u:1983:A:C2	45:u:2008:U:C4	2.87	0.62
48:x:267:ILE:HG21	48:x:399:MET:HB3	1.82	0.62
48:x:443:SER:H	48:x:447:ILE:HD12	1.63	0.62
55:5:488:ILE:HG22	55:5:531:GLN:HE22	1.64	0.62
9:I:204:GLY:O	9:I:205:PRO:O	2.16	0.62
45:u:1186:U:H2'	45:u:1187:G:O4'	2.00	0.62
45:u:3765:G:O2'	45:u:3766:A:C8	2.49	0.62
55:5:71:TRP:O	55:5:83:ILE:HG13	1.98	0.62
55:5:349:VAL:HG11	55:5:352:HIS:HD2	1.62	0.62
2:B:163:LEU:HD23	2:B:182:GLU:CG	2.24	0.61
50:z:71:VAL:N	50:z:72:PRO:CD	2.62	0.61
45:u:1339:U:H2'	45:u:1340:C:C6	2.34	0.61
45:u:1723:A:N1	45:u:1838:A:C2	2.67	0.61
50:z:83:SER:O	50:z:87:LEU:HB2	2.00	0.61
24:Y:49:ILE:HD13	24:Y:80:ILE:HD13	1.82	0.61
45:u:209:U:C5	45:u:211:G:C5	2.89	0.61
45:u:472:C:O2	45:u:473:C:C6	2.52	0.61
45:u:680:G:C2	45:u:681:G:N9	2.68	0.61
45:u:2905:C:C2	45:u:3590:G:N2	2.68	0.61
45:u:969:C:O2'	45:u:970:G:N3	2.31	0.61
5:E:95:ASP:N	45:u:686:A:C8	2.69	0.61
42:r:120:SER:CA	42:r:122:LYS:NZ	2.63	0.61
48:x:288:ASN:HB3	48:x:291:ILE:HB	1.83	0.61
37:l:5:LYS:NZ	45:u:2407:G:N7	2.48	0.61
45:u:77:U:H3	45:u:335:A:N6	1.97	0.61
45:u:977:C:C4	45:u:978:G:N7	2.69	0.61
45:u:1999:A:H1'	45:u:2017:A:N1	2.16	0.61
45:u:2623:A:C2	45:u:2624:G:C5	2.89	0.61
45:u:3723:A:C2	45:u:3724:A:C6	2.88	0.61
45:u:4769:G:H2'	45:u:4770:U:O4'	2.00	0.61
45:u:2127:C:H2'	45:u:2128:G:C8	2.36	0.61
48:x:59:ALA:CB	48:x:65:MET:SD	2.89	0.61
48:x:59:ALA:HB3	48:x:65:MET:SD	2.40	0.61
48:x:66:ARG:CD	48:x:72:ASN:HB3	2.29	0.61
55:5:122:LEU:HD12	55:5:122:LEU:C	2.26	0.61
55:5:525:TRP:NE1	55:5:595:LYS:HD2	2.15	0.61
41:p:39:CYS:SG	41:p:41:PHE:HB2	2.41	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1296:G:H1'	45:u:1297:U:P	2.41	0.61
45:u:1358:G:C8	45:u:1358:G:C3'	2.84	0.61
45:u:1672:U:H2'	45:u:1673:U:C6	2.36	0.61
45:u:3662:A:H61	45:u:3680:U:H3	1.48	0.61
45:u:4411:G:C2	45:u:4432:C:C2	2.89	0.61
48:x:444:GLY:O	48:x:447:ILE:N	2.31	0.61
3:C:114:ARG:CZ	3:C:114:ARG:HB2	2.31	0.61
45:u:472:C:C2	45:u:473:C:C4	2.81	0.61
48:x:61:PRO:O	48:x:65:MET:SD	2.52	0.61
55:5:528:TYR:CZ	55:5:581:ILE:HD12	2.36	0.61
42:r:119:ARG:C	42:r:122:LYS:HE3	2.25	0.60
45:u:181:C:C2	45:u:256:G:N2	2.69	0.60
45:u:1839:U:H2'	45:u:1840:G:O4'	2.00	0.60
45:u:111:C:C2	45:u:331:G:C2	2.89	0.60
45:u:1241:C:N4	45:u:1270:A:O2'	2.34	0.60
45:u:2554:U:H4'	45:u:2555:G:OP1	2.01	0.60
48:x:211:GLY:HA3	48:x:240:PRO:HG2	1.81	0.60
55:5:525:TRP:NE1	55:5:595:LYS:CD	2.64	0.60
45:u:2367:A:C2	45:u:2788:U:O4	2.53	0.60
45:u:2616:C:C2	45:u:2722:G:C2	2.89	0.60
55:5:212:TYR:OH	55:5:257:VAL:HG23	2.01	0.60
45:u:209:U:C4	45:u:211:G:N9	2.68	0.60
45:u:216:C:C5	45:u:217:C:O2	2.52	0.60
45:u:2793:G:C5	45:u:2797:C:N4	2.69	0.60
45:u:3594:C:O2	45:u:3594:C:H2'	2.01	0.60
50:z:78:LEU:CD1	50:z:78:LEU:H	2.14	0.60
55:5:126:PHE:HB3	55:5:174:PHE:CE2	2.36	0.60
3:C:45:ARG:NH2	45:u:2295:C:O2'	2.35	0.60
28:c:85:CYS:SG	28:c:94:LEU:HD22	2.42	0.60
42:r:47:LYS:CD	42:r:102:TYR:HD2	2.07	0.60
45:u:1213:G:C2	45:u:1215:C:O2	2.54	0.60
45:u:5000:G:C2	45:u:5051:C:C2	2.89	0.60
50:z:71:VAL:O	50:z:71:VAL:HG12	2.02	0.60
14:O:18:ARG:NH2	45:u:2057:A:OP1	2.35	0.60
45:u:208:A:C5	45:u:233:U:N3	2.54	0.60
45:u:515:C:C2	45:u:647:G:C2	2.90	0.60
55:5:553:SER:O	55:5:610:LYS:NZ	2.34	0.60
18:S:9:GLU:HG2	18:S:33:PHE:CE2	2.36	0.60
45:u:1957:U:H2'	45:u:1958:A:H8	1.67	0.60
45:u:2045:G:O6	45:u:3870:C:O2'	2.17	0.60
45:u:4207:C:C2	45:u:4226:G:C2	2.90	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:120:ALA:N	55:5:121:PRO:CD	2.65	0.60
18:S:53:LYS:NZ	46:v:74:A:O2'	2.35	0.60
42:r:17:LEU:HD23	42:r:18:ILE:N	2.17	0.60
45:u:4092:G:N2	45:u:4158:C:C2	2.70	0.60
55:5:257:VAL:CG1	55:5:261:PRO:HD3	2.31	0.60
45:u:106:A:H1'	45:u:336:A:C8	2.36	0.60
48:x:66:ARG:HE	48:x:72:ASN:HB3	1.66	0.60
42:r:132:ARG:HE	42:r:133:PRO:HD2	1.67	0.59
45:u:2288:G:N1	45:u:2290:C:C4	2.70	0.59
45:u:2827:G:H2'	45:u:2827:G:N3	2.17	0.59
45:u:4283:G:N2	45:u:4284:C:C2	2.70	0.59
45:u:4892:A:N1	45:u:4927:G:O6	2.35	0.59
48:x:66:ARG:CD	48:x:72:ASN:CB	2.79	0.59
1:A:234:LYS:HG2	1:A:238:ILE:HD12	1.83	0.59
48:x:50:LEU:HD23	48:x:50:LEU:O	2.02	0.59
48:x:160:LEU:HA	48:x:163:LEU:HD12	1.84	0.59
55:5:600:VAL:O	55:5:615:HIS:HE1	1.85	0.59
18:S:84:TYR:CE2	18:S:93:MET:HE3	2.37	0.59
45:u:472:C:H2'	45:u:473:C:C6	2.37	0.59
45:u:1074:G:C2	45:u:1238:A:C2	2.91	0.59
45:u:1268:G:C2	45:u:1270:A:C8	2.90	0.59
45:u:1957:U:C2'	45:u:1958:A:H8	2.14	0.59
48:x:244:ASN:CG	48:x:439:GLY:O	2.44	0.59
48:x:421:ALA:O	48:x:425:GLY:N	2.33	0.59
54:4:7:LEU:HD23	55:5:36:PHE:HB3	1.82	0.59
55:5:357:TRP:O	55:5:360:TYR:O	2.18	0.59
1:A:207:VAL:HG11	45:u:1633:G:C6	2.37	0.59
45:u:2446:C:C2	45:u:2515:G:C2	2.90	0.59
45:u:3617:G:O2'	45:u:3620:G:N7	2.35	0.59
16:Q:104:ARG:NH2	45:u:1353:G:N7	2.51	0.59
45:u:4901:G:C2	45:u:4921:C:N3	2.70	0.59
48:x:244:ASN:O	48:x:440:ALA:HA	2.02	0.59
55:5:286:LEU:O	55:5:287:ARG:CB	2.42	0.59
1:A:196:TRP:O	1:A:197:PRO:C	2.46	0.59
28:c:45:LEU:HD23	28:c:96:ILE:HD12	1.83	0.59
45:u:917:A:C2	45:u:919:C:C5	2.90	0.59
45:u:4441:A:H8	45:u:4441:A:H5''	1.68	0.59
45:u:286:U:H2'	45:u:287:U:C6	2.37	0.59
45:u:466:A:C2	45:u:467:U:C4	2.90	0.59
45:u:4219:A:H2'	45:u:4220:A:C8	2.37	0.59
46:v:30:C:N3	46:v:48:G:C2	2.71	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:83:C:H4'	47:w:85:U:O2	2.03	0.59
48:x:121:MET:HE1	48:x:156:PHE:CG	2.36	0.59
55:5:601:ARG:HB3	55:5:613:LYS:NZ	2.17	0.59
3:C:76:ILE:HG22	3:C:77:PRO:HD2	1.84	0.59
3:C:108:TRP:HZ2	11:L:19:GLN:HE21	1.51	0.59
3:C:114:ARG:NE	45:u:1358:G:O3'	2.36	0.59
3:C:357:ALA:O	3:C:361:LYS:HG3	2.03	0.59
17:R:10:LEU:O	17:R:14:VAL:HG23	2.03	0.59
23:X:83:THR:HA	48:x:403:GLY:O	2.03	0.59
26:a:25:HIS:CG	45:u:1338:G:H22	2.21	0.59
45:u:166:C:O2	45:u:166:C:C2'	2.49	0.59
53:3:92:PHE:CE1	53:3:96:MET:CG	2.86	0.59
45:u:1074:G:N2	45:u:1075:G:C2	2.71	0.59
45:u:1266:G:H5''	45:u:2112:G:C2	2.37	0.59
45:u:1541:C:C2	45:u:1619:G:C2	2.90	0.59
48:x:69:LEU:CB	48:x:80:GLY:HA2	2.33	0.59
55:5:210:GLY:O	62:5:809:9UB:C16	2.50	0.59
45:u:1957:U:H2'	45:u:1958:A:C8	2.38	0.58
48:x:285:TYR:OH	48:x:385:SER:O	2.20	0.58
55:5:525:TRP:CB	55:5:592:ASP:OD2	2.49	0.58
41:p:42:CYS:HA	45:u:2674:A:N6	2.18	0.58
45:u:4757:C:O4'	45:u:4757:C:O2	2.21	0.58
55:5:260:GLN:O	55:5:267:HIS:NE2	2.32	0.58
23:X:156:ILE:CG1	48:x:415:ARG:CZ	2.78	0.58
45:u:113:A:H2'	45:u:114:G:O4'	2.03	0.58
55:5:123:PHE:CZ	55:5:171:ILE:O	2.56	0.58
55:5:504:ASP:OD2	55:5:686:HIS:HB2	2.03	0.58
55:5:530:TYR:CD1	55:5:543:ASP:OD1	2.56	0.58
45:u:463:A:N1	45:u:692:A:H2	2.00	0.58
45:u:3709:U:O2'	45:u:3710:G:O4'	2.21	0.58
48:x:71:SER:HB3	48:x:75:THR:H	1.68	0.58
55:5:525:TRP:HE1	55:5:595:LYS:CD	2.16	0.58
45:u:1358:G:H2'	45:u:1359:G:O4'	2.04	0.58
45:u:2084:C:H3'	45:u:2085:G:H5'	1.84	0.58
45:u:2654:C:C2	45:u:2681:G:N2	2.71	0.58
56:6:106:UNK:O	56:6:110:UNK:N	2.36	0.58
2:B:154:LYS:HB2	2:B:154:LYS:NZ	2.18	0.58
5:E:226:GLY:H	42:r:135:LYS:NZ	2.01	0.58
45:u:3751:G:O2'	45:u:3752:C:C5'	2.47	0.58
48:x:375:PHE:O	48:x:379:TRP:HB2	2.03	0.58
49:y:58:HIS:HA	49:y:61:ILE:HG12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:177:LEU:O	55:5:177:LEU:HD22	2.04	0.58
43:s:34:ASN:OD1	45:u:1968:G:O3'	2.21	0.58
45:u:642:G:N1	45:u:643:C:C4	2.71	0.58
45:u:300:A:C2	45:u:301:G:C5	2.92	0.58
48:x:66:ARG:HD3	48:x:72:ASN:CG	2.26	0.58
33:h:37:THR:C	48:x:266:PRO:CD	2.77	0.58
45:u:216:C:N4	51:1:539:THR:HA	2.18	0.58
7:G:156:VAL:CG1	7:G:184:LEU:CD1	2.78	0.58
45:u:245:C:O2	45:u:245:C:O4'	2.22	0.58
45:u:466:A:N3	45:u:467:U:C6	2.71	0.58
48:x:435:ALA:HB1	48:x:441:ILE:HG21	1.86	0.58
20:U:87:THR:HG23	20:U:102:VAL:HG21	1.85	0.57
45:u:212:A:C2	45:u:213:G:C5	2.91	0.57
45:u:1639:U:N3	45:u:1643:A:O2'	2.37	0.57
45:u:1757:U:H2'	45:u:1758:G:O4'	2.03	0.57
45:u:4754:G:C2	45:u:4880:C:C2	2.92	0.57
48:x:181:LEU:CG	48:x:457:TYR:CE1	2.87	0.57
48:x:185:THR:HG22	49:y:47:MET:HB3	1.86	0.57
55:5:157:TYR:HB2	55:5:411:ALA:HB1	1.85	0.57
55:5:525:TRP:CD1	55:5:592:ASP:OD1	2.57	0.57
1:A:104:VAL:CG1	1:A:146:THR:HG21	2.34	0.57
10:J:83:LEU:CD1	10:J:170:TYR:CZ	2.87	0.57
10:J:119:TYR:HE2	10:J:125:ILE:HD11	1.68	0.57
45:u:472:C:C4	45:u:473:C:C5	2.91	0.57
45:u:1279:A:O3'	45:u:1279:A:OP1	2.22	0.57
45:u:1398:A:O2'	45:u:1399:G:OP2	2.20	0.57
45:u:4975:G:N2	45:u:4984:C:C2	2.72	0.57
1:A:101:VAL:HB	1:A:165:VAL:HG12	1.86	0.57
45:u:919:C:C4	45:u:920:C:C5	2.92	0.57
45:u:3870:C:C2	45:u:3886:G:C2	2.92	0.57
48:x:157:VAL:CG1	50:z:80:PHE:HE2	0.26	0.57
55:5:374:GLY:O	55:5:378:CYS:N	2.36	0.57
3:C:313:VAL:CG1	6:F:172:THR:HG21	2.35	0.57
11:L:71:ARG:NH2	45:u:74:G:O3'	2.37	0.57
48:x:66:ARG:HH21	48:x:70:ALA:CA	2.01	0.57
48:x:392:LYS:O	48:x:396:GLU:HB2	2.04	0.57
45:u:470:A:C6	45:u:471:A:N7	2.70	0.57
45:u:691:C:C2	45:u:692:A:N7	2.72	0.57
45:u:2256:C:O2	45:u:2256:C:H2'	2.04	0.57
47:w:155:C:H2'	47:w:156:U:O4'	2.05	0.57
14:O:7:LEU:HD22	14:O:9:LEU:HD21	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:135:LYS:NZ	45:u:451:C:C3'	2.68	0.57
45:u:976:G:C6	45:u:977:C:C4	2.93	0.57
45:u:1959:U:H1'	45:u:1961:G:C1'	2.35	0.57
48:x:223:ARG:NH1	48:x:232:GLU:OE1	2.38	0.57
53:3:88:LEU:H	53:3:88:LEU:CD2	2.00	0.57
55:5:176:MET:O	55:5:179:THR:HG22	2.04	0.57
55:5:593:ILE:CD1	55:5:639:MET:HG3	2.34	0.57
19:T:80:VAL:HG21	19:T:85:LEU:HD12	1.86	0.57
40:o:66:ILE:HD13	40:o:91:PHE:CE1	2.40	0.57
43:s:14:PHE:HD2	43:s:62:ARG:HH11	1.53	0.57
45:u:199:G:C6	45:u:201:C:N4	2.73	0.57
45:u:976:G:C2	45:u:977:C:C2	2.91	0.57
45:u:1213:G:O6	45:u:1215:C:C4	2.57	0.57
45:u:1280:C:C2	45:u:1282:G:C5	2.92	0.57
47:w:55:U:C4	47:w:62:A:N1	2.72	0.57
48:x:252:PHE:CZ	48:x:451:VAL:HG11	2.39	0.57
55:5:570:MET:HB3	55:5:575:VAL:HG11	1.86	0.57
9:I:184:MET:HE2	9:I:190:LEU:HD12	1.82	0.57
45:u:471:A:C2	45:u:472:C:H1'	2.40	0.57
45:u:1840:G:H3'	45:u:1842:G:P	2.44	0.57
45:u:2367:A:N6	45:u:2798:A:O4'	2.37	0.57
45:u:2408:U:C1'	45:u:2409:U:C5	2.88	0.57
45:u:3751:G:O2'	45:u:3775:A:N6	2.37	0.57
4:D:62:CYS:HB3	4:D:105:LEU:HD22	1.87	0.57
38:m:119:ASN:C	38:m:119:ASN:ND2	2.63	0.57
45:u:470:A:C6	45:u:471:A:C5	2.92	0.57
45:u:2640:G:N7	45:u:2694:G:O6	2.37	0.57
45:u:3593:C:H4'	45:u:3594:C:OP2	2.05	0.57
55:5:71:TRP:O	55:5:83:ILE:HD11	2.05	0.57
55:5:601:ARG:HB3	55:5:613:LYS:CD	2.34	0.57
3:C:114:ARG:CZ	45:u:1358:G:H5''	2.35	0.57
31:f:28:LEU:HG	31:f:101:ILE:HD11	1.85	0.57
45:u:1268:G:C4	45:u:2111:G:C2	2.93	0.56
45:u:463:A:N1	45:u:692:A:N1	2.52	0.56
45:u:469:C:C4	45:u:470:A:C5	2.93	0.56
45:u:680:G:C6	45:u:681:G:N7	2.73	0.56
45:u:687:U:C4	45:u:688:U:C5	2.93	0.56
45:u:2524:U:H5''	45:u:2711:G:C2	2.40	0.56
45:u:4461:C:O2	45:u:4516:G:C2	2.58	0.56
55:5:83:ILE:C	55:5:85:GLY:N	2.62	0.56
3:C:336:ARG:O	3:C:340:ILE:HG12	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:m:119:ASN:C	38:m:119:ASN:HD22	2.12	0.56
45:u:209:U:O4	45:u:211:G:H1'	2.05	0.56
45:u:370:U:C6	45:u:1637:A:C2	2.93	0.56
45:u:422:C:C2	47:w:13:G:C2	2.94	0.56
45:u:516:C:N3	45:u:646:G:C2	2.74	0.56
45:u:707:C:C2	45:u:1291:G:C2	2.92	0.56
45:u:2409:U:C5	45:u:2783:A:C2	2.93	0.56
45:u:3641:U:H5	45:u:3646:A:N7	2.04	0.56
45:u:4260:U:H2'	45:u:4261:C:C6	2.40	0.56
49:y:63:ASN:ND2	53:3:71:PRO:O	2.38	0.56
53:3:92:PHE:HE1	53:3:96:MET:CG	2.18	0.56
55:5:522:VAL:HG11	55:5:532:ILE:HD13	1.88	0.56
14:O:18:ARG:NH1	45:u:2053:C:O3'	2.39	0.56
45:u:216:C:N4	51:1:538:LYS:O	2.38	0.56
48:x:175:LEU:HD23	48:x:460:ILE:HG22	1.86	0.56
48:x:428:ILE:O	48:x:431:LEU:HB3	2.05	0.56
2:B:181:MET:HE2	2:B:183:ILE:HG12	1.88	0.56
6:F:91:LEU:HD22	6:F:92:ALA:N	2.20	0.56
6:F:146:TYR:CE2	6:F:239:GLU:HB3	2.41	0.56
11:L:42:ARG:HG3	11:L:45:ARG:HH12	1.69	0.56
11:L:161:PHE:CD1	26:a:105:ARG:HD2	2.40	0.56
17:R:60:ARG:NH1	17:R:63:CYS:SG	2.79	0.56
45:u:665:C:O2	45:u:665:C:H2'	2.05	0.56
45:u:680:G:N2	45:u:681:G:H1'	2.19	0.56
45:u:1485:C:O2	45:u:1485:C:O4'	2.23	0.56
48:x:64:TRP:CD1	48:x:64:TRP:N	2.73	0.56
45:u:471:A:N6	45:u:472:C:C5	2.73	0.56
45:u:1278:C:C6	45:u:1279:A:H1'	2.40	0.56
46:v:66:G:C2	46:v:67:C:C2	2.93	0.56
45:u:4101:C:C2	45:u:4109:G:C2	2.94	0.56
46:v:30:C:C2	46:v:48:G:C2	2.94	0.56
54:4:22:VAL:HG11	55:5:146:LEU:HB3	1.88	0.56
55:5:153:VAL:HA	55:5:158:ILE:HD11	1.88	0.56
55:5:349:VAL:O	55:5:349:VAL:HG13	2.06	0.56
55:5:601:ARG:HH11	55:5:601:ARG:HG3	1.71	0.56
45:u:465:G:N2	45:u:466:A:H1'	2.21	0.56
15:P:48:LEU:HD12	15:P:92:LEU:HD13	1.87	0.56
19:T:64:VAL:HG13	19:T:72:VAL:HG13	1.88	0.56
45:u:685:C:O2	45:u:685:C:C2'	2.53	0.56
45:u:1279:A:C3'	45:u:1280:C:C5'	2.78	0.56
45:u:1365:C:H4'	45:u:1366:G:OP1	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1404:G:N2	45:u:1414:C:C2	2.74	0.56
45:u:2258:C:O2	45:u:2258:C:C2'	2.54	0.56
16:Q:69:LYS:O	16:Q:75:ARG:NH1	2.39	0.56
17:R:10:LEU:HB3	17:R:41:ILE:HD13	1.88	0.56
44:t:30:PRO:O	44:t:32:ILE:N	2.38	0.56
45:u:181:C:N4	45:u:256:G:C6	2.74	0.56
45:u:211:G:N2	45:u:212:A:C8	2.74	0.56
45:u:1269:G:C6	45:u:2111:G:N2	2.74	0.56
45:u:2773:G:N1	45:u:2774:C:C4	2.73	0.56
53:3:93:LEU:HB3	53:3:133:PHE:HE1	1.71	0.56
3:C:158:VAL:HG22	3:C:161:TYR:HE2	1.71	0.55
7:G:86:VAL:HG22	7:G:183:ILE:HG22	1.87	0.55
37:l:21:ARG:CD	48:x:273:ARG:NH1	2.56	0.55
42:r:47:LYS:CD	42:r:102:TYR:HE2	1.94	0.55
45:u:471:A:C6	45:u:472:C:N1	2.74	0.55
45:u:1968:G:O2'	45:u:1969:G:O5'	2.20	0.55
45:u:2547:G:N1	45:u:2548:C:C4	2.75	0.55
45:u:4416:G:N2	45:u:4417:C:C2	2.74	0.55
48:x:121:MET:CE	48:x:156:PHE:HD1	2.04	0.55
15:P:36:ILE:HD12	15:P:48:LEU:HD11	1.88	0.55
18:S:28:TYR:CD2	18:S:54:MET:HE1	2.41	0.55
45:u:1483:C:O2	45:u:1483:C:O4'	2.23	0.55
46:v:82:G:C2	46:v:95:C:C2	2.94	0.55
48:x:50:LEU:HD11	50:z:88:HIS:HA	1.85	0.55
48:x:301:LEU:HD23	48:x:304:ILE:HD12	1.87	0.55
55:5:127:THR:N	55:5:174:PHE:HE2	2.03	0.55
45:u:497:G:C2	45:u:657:C:C2	2.94	0.55
45:u:1279:A:C2	45:u:1280:C:C2	2.95	0.55
45:u:1743:A:C5	45:u:1744:U:C5	2.95	0.55
45:u:3612:C:H1'	45:u:5016:A:C8	2.41	0.55
55:5:90:PRO:HA	55:5:93:MET:HE3	1.89	0.55
55:5:525:TRP:CD2	55:5:599:MET:HE2	2.41	0.55
1:A:82:ILE:HD11	1:A:99:GLY:HA3	1.89	0.55
11:L:47:ALA:HB3	11:L:48:PRO:HD3	1.87	0.55
45:u:471:A:C2	45:u:472:C:O4'	2.59	0.55
45:u:472:C:H42	45:u:473:C:N4	2.03	0.55
45:u:1959:U:H1'	45:u:1961:G:N9	2.21	0.55
45:u:4717:A:H2'	45:u:4718:G:O4'	2.07	0.55
58:8:624:UNK:O	58:8:628:UNK:N	2.40	0.55
3:C:168:VAL:HG13	3:C:177:TRP:CZ3	2.41	0.55
45:u:1277:G:N2	45:u:1278:C:C2	2.75	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1975:G:O4'	45:u:1984:A:H1'	2.07	0.55
45:u:2557:G:C2	45:u:2571:C:C2	2.94	0.55
32:g:69:LYS:N	45:u:2769:U:OP1	2.40	0.55
45:u:4524:G:N2	45:u:4525:C:C2	2.75	0.55
19:T:87:LYS:NZ	45:u:4301:U:OP2	2.39	0.55
45:u:470:A:C6	45:u:471:A:C4	2.95	0.55
45:u:4586:G:H8	45:u:4586:G:H5''	1.70	0.55
45:u:5023:C:O2	45:u:5023:C:O4'	2.23	0.55
48:x:181:LEU:HD12	48:x:457:TYR:OH	2.03	0.55
48:x:453:ILE:O	48:x:456:GLN:HG3	2.07	0.55
55:5:127:THR:HA	55:5:174:PHE:CE2	2.42	0.55
45:u:200:U:C5	45:u:238:C:O4'	2.60	0.55
45:u:1360:G:C6	45:u:1361:G:C5	2.94	0.55
45:u:4213:A:H61	45:u:4218:U:H3	1.55	0.55
7:G:156:VAL:HG13	7:G:184:LEU:HG	1.89	0.55
45:u:127:G:N2	45:u:128:C:C2	2.75	0.55
45:u:962:C:OP2	45:u:2264:C:N3	2.40	0.55
45:u:1959:U:H4'	45:u:1961:G:C4'	2.37	0.55
45:u:2256:C:O2	45:u:2256:C:C2'	2.54	0.55
45:u:2408:U:O4'	45:u:2409:U:C5	2.60	0.55
48:x:30:GLU:HG2	48:x:33:LEU:HD12	1.88	0.55
45:u:211:G:C2	45:u:212:A:C5	2.95	0.55
45:u:688:U:O4	45:u:689:U:C5	2.60	0.55
45:u:2688:G:N2	45:u:2689:C:C2	2.75	0.55
45:u:4730:C:O2	45:u:4730:C:O4'	2.25	0.55
48:x:121:MET:HE3	48:x:156:PHE:CE1	2.41	0.55
48:x:437:PHE:C	48:x:437:PHE:CD2	2.86	0.55
55:5:52:PHE:CB	55:5:530:TYR:CD1	2.83	0.55
45:u:919:C:N4	45:u:920:C:C5	2.75	0.54
45:u:937:U:O2	45:u:937:U:H2'	2.07	0.54
45:u:1380:G:H4'	45:u:1381:U:OP1	2.07	0.54
45:u:2481:G:C2	45:u:2498:C:C2	2.94	0.54
2:B:21:ARG:NH2	45:u:4568:A:O3'	2.41	0.54
41:p:41:PHE:O	45:u:2674:A:N6	2.40	0.54
45:u:1371:A:N6	47:w:28:C:O2'	2.40	0.54
48:x:121:MET:O	48:x:124:THR:OG1	2.25	0.54
14:O:36:VAL:HG11	14:O:108:ILE:HD12	1.89	0.54
33:h:119:TYR:C	33:h:119:TYR:CD2	2.86	0.54
45:u:106:A:H2'	45:u:107:G:O4'	2.06	0.54
45:u:211:G:N1	45:u:212:A:C5	2.76	0.54
45:u:516:C:C2	45:u:646:G:C2	2.95	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1249:C:C2	45:u:1262:G:C2	2.95	0.54
45:u:1279:A:H2'	45:u:1280:C:H5''	1.88	0.54
45:u:1398:A:H1'	45:u:1399:G:C8	2.43	0.54
45:u:2028:C:O2'	45:u:2029:A:O5'	2.24	0.54
48:x:292:ILE:HD13	48:x:449:LEU:HB3	1.88	0.54
55:5:525:TRP:CD2	55:5:599:MET:CE	2.90	0.54
30:e:46:ARG:HA	30:e:55:MET:SD	2.48	0.54
45:u:470:A:C4	45:u:471:A:C8	2.95	0.54
45:u:1067:G:H2'	45:u:1068:G:O4'	2.07	0.54
48:x:297:LEU:HD13	48:x:300:ASN:HD22	1.70	0.54
6:F:230:VAL:HA	18:S:39:VAL:HG12	1.89	0.54
23:X:139:ARG:NH2	45:u:2533:C:OP1	2.41	0.54
35:j:59:THR:O	35:j:60:GLY:C	2.50	0.54
45:u:301:G:C6	45:u:302:C:C4	2.96	0.54
45:u:471:A:N6	45:u:472:C:C4	2.75	0.54
45:u:1563:A:C8	45:u:1563:A:O5'	2.60	0.54
55:5:488:ILE:HG13	55:5:489:VAL:HG23	1.87	0.54
42:r:122:LYS:CB	42:r:123:PRO:CD	2.82	0.54
45:u:206:U:O2	45:u:208:A:H8	1.90	0.54
45:u:1664:U:H2'	45:u:1665:C:C6	2.42	0.54
55:5:220:PRO:HG2	55:5:270:ALA:HB1	1.90	0.54
55:5:234:HIS:O	55:5:237:TYR:N	2.39	0.54
45:u:933:G:C2	45:u:940:C:C6	2.95	0.54
45:u:1835:G:O2'	45:u:1836:G:OP2	2.21	0.54
50:z:68:VAL:C	50:z:70:PRO:HD2	2.32	0.54
2:B:91:GLY:HA3	2:B:153:MET:HE3	1.88	0.54
2:B:116:ARG:HD2	2:B:122:TRP:CD2	2.43	0.54
13:N:67:ARG:NH1	45:u:2458:C:OP1	2.41	0.54
17:R:71:ARG:NH1	45:u:3605:C:OP2	2.36	0.54
48:x:66:ARG:HH22	48:x:69:LEU:C	2.15	0.54
50:z:74:LEU:C	50:z:78:LEU:CD1	2.71	0.54
55:5:359:SER:C	55:5:360:TYR:O	2.48	0.54
55:5:397:MET:HA	55:5:410:LEU:HD11	1.89	0.54
55:5:633:VAL:O	55:5:637:CYS:N	2.41	0.54
2:B:163:LEU:HD23	2:B:182:GLU:HA	1.90	0.54
45:u:472:C:O2	45:u:473:C:N1	2.41	0.54
45:u:1751:A:C2	45:u:1780:A:C2	2.95	0.54
45:u:3718:A:H2'	45:u:3719:A:C8	2.43	0.54
46:v:66:G:C6	46:v:67:C:C4	2.95	0.54
48:x:61:PRO:HB2	48:x:65:MET:CB	2.38	0.54
48:x:121:MET:O	48:x:156:PHE:CE1	2.61	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:4:14:LEU:HD22	55:5:29:LEU:HG	1.90	0.54
45:u:210:C:O5'	45:u:210:C:H6	1.91	0.54
45:u:1205:G:N2	45:u:1206:C:C2	2.76	0.54
45:u:1357:C:H5''	45:u:1358:G:OP1	2.08	0.54
55:5:31:PHE:CG	55:5:121:PRO:CB	2.70	0.54
55:5:123:PHE:CD2	55:5:171:ILE:CG2	2.79	0.54
55:5:600:VAL:O	55:5:615:HIS:CE1	2.61	0.54
4:D:129:GLU:HG3	4:D:177:THR:HG21	1.90	0.53
7:G:29:ASN:HB2	7:G:32:PHE:CE2	2.43	0.53
23:X:83:THR:HA	48:x:403:GLY:C	2.32	0.53
45:u:2043:A:O2'	45:u:4461:C:O2	2.25	0.53
45:u:2301:G:N2	45:u:2302:C:C2	2.76	0.53
45:u:4895:C:H1'	45:u:4896:G:C8	2.43	0.53
47:w:15:G:C6	47:w:16:G:N1	2.76	0.53
55:5:357:TRP:O	55:5:360:TYR:CB	2.56	0.53
4:D:200:MET:HE2	4:D:241:LYS:CE	2.33	0.53
15:P:69:ARG:NH2	45:u:4568:A:N3	2.57	0.53
19:T:48:VAL:HG21	19:T:94:GLU:HG2	1.90	0.53
45:u:977:C:N3	45:u:978:G:N7	2.57	0.53
45:u:1430:C:C2	45:u:1455:G:C2	2.96	0.53
45:u:4759:C:H2'	45:u:4760:G:O4'	2.09	0.53
17:R:59:SER:N	45:u:4646:U:OP1	2.42	0.53
32:g:61:PRO:HA	32:g:64:LEU:HD22	1.90	0.53
45:u:209:U:C6	45:u:211:G:N7	2.76	0.53
45:u:2089:G:N3	45:u:2089:G:H2'	2.23	0.53
45:u:2654:C:C2	45:u:2681:G:C2	2.97	0.53
45:u:3816:A:O2'	45:u:3819:G:N3	2.39	0.53
45:u:4138:C:C2	45:u:4147:G:C2	2.96	0.53
45:u:4977:A:H2'	45:u:4978:G:O4'	2.08	0.53
50:z:69:GLY:H	50:z:70:PRO:CD	2.17	0.53
51:1:533:LEU:O	51:1:537:LEU:CB	2.56	0.53
45:u:1213:G:C6	45:u:1215:C:N3	2.77	0.53
45:u:1378:C:OP1	45:u:1379:C:H3'	2.09	0.53
45:u:2768:C:O2	45:u:2768:C:O4'	2.26	0.53
45:u:4635:A:C2	45:u:4664:A:C5	2.96	0.53
55:5:562:THR:HG21	55:5:565:LYS:HD2	1.91	0.53
55:5:641:LYS:NZ	55:5:674:GLU:OE1	2.39	0.53
2:B:156:TYR:CD1	45:u:4909:A:C2'	2.89	0.53
8:H:26:ILE:HB	8:H:35:ARG:HG2	1.91	0.53
31:f:102:ARG:NH2	45:u:4947:U:O4	2.41	0.53
45:u:686:A:C3'	45:u:687:U:H5'	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1468:C:C2	45:u:1498:G:C2	2.96	0.53
45:u:3662:A:N6	45:u:3680:U:H3	2.06	0.53
45:u:4389:C:H2'	45:u:4390:A:C8	2.43	0.53
48:x:62:PHE:N	48:x:65:MET:CE	2.66	0.53
55:5:488:ILE:HG22	55:5:531:GLN:NE2	2.23	0.53
55:5:616:ASP:OD2	55:5:634:LEU:N	2.36	0.53
5:E:202:VAL:HB	5:E:252:GLN:OE1	2.09	0.53
45:u:471:A:N1	45:u:472:C:H1'	2.23	0.53
45:u:746:A:O2'	45:u:747:A:O5'	2.20	0.53
45:u:1668:A:C4	45:u:2282:A:C2	2.96	0.53
45:u:4723:A:C2	45:u:4724:A:C5	2.97	0.53
17:R:35:ALA:O	17:R:37:SER:N	2.41	0.53
45:u:1358:G:O2'	45:u:1359:G:O4'	2.20	0.53
55:5:100:TYR:HB2	55:5:104:HIS:HB2	1.90	0.53
5:E:202:VAL:HG12	5:E:256:LYS:HZ1	1.74	0.53
45:u:1899:G:N2	45:u:1900:C:C2	2.77	0.53
45:u:4583:C:C4	45:u:4718:G:C6	2.97	0.53
48:x:121:MET:O	48:x:156:PHE:HE1	1.91	0.53
55:5:468:LEU:O	55:5:471:TYR:CB	2.56	0.53
13:N:135:ILE:HD12	13:N:151:ILE:HD13	1.90	0.53
23:X:76:ILE:HG21	23:X:112:ALA:HB2	1.91	0.53
25:Z:29:ILE:HG21	25:Z:40:HIS:CE1	2.44	0.53
45:u:973:G:N2	45:u:1282:G:HO2'	2.04	0.53
45:u:1297:U:O4'	45:u:1297:U:OP2	2.27	0.53
45:u:2693:G:C6	45:u:2694:G:N1	2.77	0.53
6:F:244:ARG:NH1	45:u:942:G:OP2	2.41	0.53
8:H:180:TYR:HB2	38:m:85:LEU:HD11	1.90	0.53
11:L:58:ILE:HG23	11:L:70:VAL:CG1	2.39	0.53
45:u:2108:G:C2	45:u:2125:C:N3	2.77	0.53
48:x:443:SER:HB2	48:x:447:ILE:HD11	1.91	0.53
55:5:31:PHE:CZ	55:5:118:PHE:O	2.62	0.53
7:G:34:LYS:O	45:u:4128:A:N3	2.42	0.52
31:f:48:ALA:HB2	31:f:71:TRP:CZ3	2.44	0.52
37:l:44:TRP:CZ3	37:l:45:ARG:HD3	2.44	0.52
45:u:4303:C:O2	45:u:4303:C:O4'	2.26	0.52
47:w:79:G:OP1	49:y:31:LYS:NZ	2.22	0.52
48:x:29:LYS:CD	53:3:118:PHE:CZ	2.92	0.52
49:y:33:PHE:O	49:y:37:ALA:HB2	2.08	0.52
55:5:83:ILE:HD12	55:5:84:ILE:H	1.73	0.52
2:B:89:ILE:HD13	2:B:153:MET:HE1	1.91	0.52
45:u:93:G:O2'	45:u:94:A:O4'	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:472:C:N4	45:u:473:C:H41	2.06	0.52
45:u:1854:G:N2	45:u:4394:A:O4'	2.42	0.52
45:u:2089:G:O2'	45:u:2090:U:OP2	2.25	0.52
45:u:2905:C:C2	45:u:3590:G:C2	2.96	0.52
45:u:4579:U:H2'	45:u:4580:U:O4'	2.08	0.52
45:u:5028:G:C6	45:u:5029:C:N4	2.77	0.52
55:5:31:PHE:CG	55:5:121:PRO:HB2	2.16	0.52
26:a:146:LEU:HD13	34:i:7:MET:HG2	1.91	0.52
40:o:63:THR:O	40:o:87:ARG:NH1	2.43	0.52
45:u:405:U:O2'	45:u:407:A:N7	2.40	0.52
45:u:680:G:N3	45:u:681:G:C8	2.78	0.52
45:u:4213:A:C2	45:u:4218:U:O4	2.57	0.52
47:w:119:C:C2	47:w:132:G:C2	2.98	0.52
55:5:593:ILE:CD1	55:5:639:MET:CG	2.87	0.52
2:B:29:VAL:HG13	2:B:348:ARG:HD3	1.91	0.52
11:L:9:ILE:O	11:L:9:ILE:HG23	2.09	0.52
45:u:256:G:N2	45:u:257:C:C2	2.77	0.52
45:u:707:C:O2	45:u:1291:G:C2	2.63	0.52
45:u:4281:A:C2	45:u:4283:G:C5	2.98	0.52
48:x:247:ALA:O	48:x:251:VAL:HG22	2.09	0.52
55:5:204:TYR:O	55:5:207:SER:OG	2.27	0.52
45:u:12:A:H8	45:u:12:A:H5''	1.75	0.52
45:u:1086:C:C2	45:u:1212:G:C2	2.97	0.52
45:u:1447:C:H2'	45:u:1448:G:O4'	2.08	0.52
45:u:4966:A:H2'	45:u:4967:A:C8	2.45	0.52
48:x:200:THR:HB	48:x:208:GLU:H	1.74	0.52
55:5:83:ILE:C	55:5:85:GLY:H	2.18	0.52
55:5:119:LEU:O	55:5:122:LEU:HB3	2.09	0.52
55:5:130:VAL:HG21	55:5:177:LEU:HD12	1.87	0.52
55:5:160:ARG:HB2	55:5:408:LEU:HD21	1.92	0.52
1:A:34:PHE:CD2	45:u:4087:G:C6	2.98	0.52
2:B:340:THR:OG1	2:B:341:LYS:N	2.43	0.52
12:M:69:ARG:O	12:M:71:LYS:N	2.42	0.52
45:u:52:G:N2	45:u:53:C:C2	2.78	0.52
45:u:2733:C:H2'	45:u:2734:U:O4'	2.10	0.52
48:x:288:ASN:O	48:x:291:ILE:N	2.43	0.52
55:5:203:PHE:HA	55:5:206:VAL:HG12	1.91	0.52
2:B:56:ILE:HG12	2:B:365:LEU:HD22	1.92	0.52
45:u:181:C:C2	45:u:256:G:C2	2.98	0.52
45:u:2108:G:N1	45:u:2125:C:C4	2.77	0.52
45:u:2110:C:C6	45:u:2110:C:OP1	2.62	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:46:CYS:C	48:x:75:THR:HG21	2.34	0.52
50:z:70:PRO:HB2	50:z:72:PRO:HD2	1.92	0.52
45:u:929:A:H3'	45:u:930:G:C5'	2.40	0.52
45:u:1771:U:H2'	45:u:1772:C:O4'	2.10	0.52
45:u:1891:A:O2'	45:u:1892:A:O4'	2.25	0.52
5:E:250:ASP:O	5:E:254:LEU:HB2	2.10	0.52
10:J:53:ALA:HB2	10:J:68:ILE:HD12	1.91	0.52
45:u:671:G:C6	45:u:672:C:C4	2.98	0.52
45:u:986:C:C2	45:u:1068:G:C2	2.97	0.52
45:u:2363:A:C2	45:u:3860:A:C4	2.98	0.52
45:u:3594:C:O2	45:u:3594:C:C2'	2.56	0.52
36:k:22:SER:HA	36:k:65:ALA:HB3	1.91	0.52
42:r:18:ILE:HG23	42:r:25:TYR:HB2	1.92	0.52
42:r:48:THR:N	42:r:102:TYR:OH	2.39	0.52
45:u:687:U:C5	45:u:688:U:C5	2.97	0.52
45:u:689:U:C2	45:u:690:C:C6	2.98	0.52
45:u:1266:G:H5''	45:u:2112:G:N3	2.25	0.52
45:u:1549:G:C2	45:u:1580:C:C2	2.98	0.52
45:u:2505:C:O2	45:u:2505:C:O4'	2.28	0.52
45:u:2517:A:N3	45:u:2539:C:O2'	2.43	0.52
49:y:53:PHE:HE1	53:3:92:PHE:CZ	2.27	0.52
51:1:446:PHE:HA	51:1:449:LEU:HD12	1.92	0.52
55:5:36:PHE:HA	55:5:39:LEU:HB3	1.92	0.52
45:u:300:A:H2'	45:u:301:G:C8	2.45	0.51
45:u:691:C:H2'	45:u:692:A:H8	1.75	0.51
55:5:103:LEU:O	55:5:107:HIS:N	2.43	0.51
9:I:187:GLU:OE1	9:I:189:ARG:CD	2.58	0.51
20:U:46:ARG:O	20:U:47:ILE:C	2.53	0.51
23:X:156:ILE:CD1	48:x:415:ARG:CZ	2.85	0.51
45:u:112:C:C2	45:u:330:G:C2	2.97	0.51
45:u:691:C:H2'	45:u:692:A:C8	2.45	0.51
45:u:2297:G:N2	45:u:2338:C:C2	2.79	0.51
45:u:2525:U:P	45:u:2711:G:H1	2.33	0.51
48:x:41:ILE:O	48:x:45:CYS:N	2.30	0.51
55:5:178:LEU:HD23	55:5:179:THR:CA	2.39	0.51
4:D:122:GLN:O	4:D:248:ARG:NH2	2.43	0.51
4:D:196:ARG:O	4:D:200:MET:HG2	2.10	0.51
30:e:7:LEU:HB2	30:e:93:LYS:HB3	1.92	0.51
44:t:121:LEU:HD22	44:t:132:ILE:HD13	1.92	0.51
45:u:220:C:H2'	45:u:221:C:C6	2.45	0.51
45:u:476:G:N2	45:u:679:C:C2	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:677:G:N2	45:u:678:C:C2	2.77	0.51
45:u:1874:A:H5'	45:u:4218:U:O2	2.10	0.51
45:u:1912:G:N2	45:u:1913:C:C2	2.78	0.51
45:u:3628:G:C2	45:u:3834:C:C2	2.98	0.51
45:u:4441:A:H5''	45:u:4441:A:C8	2.44	0.51
48:x:132:VAL:HG23	48:x:133:MET:HG3	1.91	0.51
48:x:180:SER:HB2	48:x:453:ILE:HD13	1.91	0.51
50:z:84:VAL:O	50:z:88:HIS:HB2	2.09	0.51
2:B:378:ARG:HE	22:W:32:LEU:HD21	1.75	0.51
45:u:2301:G:N1	45:u:2302:C:C4	2.79	0.51
45:u:4305:G:N3	45:u:4305:G:C2'	2.73	0.51
45:u:4913:G:O2'	45:u:4914:C:O4'	2.28	0.51
48:x:130:VAL:HG11	48:x:304:ILE:HG23	1.92	0.51
55:5:221:LEU:O	55:5:224:LEU:HB3	2.11	0.51
55:5:286:LEU:CD2	55:5:286:LEU:N	2.74	0.51
3:C:130:ALA:HB1	3:C:136:LEU:HD12	1.91	0.51
26:a:25:HIS:ND1	45:u:1338:G:N2	2.58	0.51
35:j:63:ARG:NH2	47:w:58:G:N7	2.58	0.51
45:u:2712:G:N2	45:u:2713:C:C2	2.79	0.51
45:u:4338:G:C4	45:u:4372:U:C5	2.98	0.51
47:w:106:G:N2	47:w:107:C:C2	2.79	0.51
48:x:29:LYS:CB	53:3:118:PHE:CE2	2.92	0.51
53:3:53:ILE:CD1	55:5:354:PRO:HG3	2.29	0.51
2:B:36:ASP:OD1	2:B:36:ASP:N	2.44	0.51
5:E:126:ARG:HH12	45:u:712:C:H2'	1.69	0.51
8:H:111:LEU:HD11	8:H:125:ARG:HB2	1.92	0.51
14:O:72:HIS:N	45:u:4586:G:OP1	2.41	0.51
42:r:85:ASN:O	42:r:87:ARG:N	2.44	0.51
45:u:205:C:N3	45:u:209:U:C5	2.79	0.51
45:u:1723:A:N1	45:u:1838:A:N1	2.58	0.51
45:u:1929:A:C2	45:u:2054:U:O4	2.60	0.51
45:u:4735:G:C2	45:u:4736:C:C2	2.98	0.51
2:B:220:ILE:HG12	2:B:278:THR:HG23	1.93	0.51
9:I:76:MET:HG3	9:I:87:ILE:HD11	1.93	0.51
9:I:97:ILE:HD13	9:I:126:VAL:HG11	1.92	0.51
14:O:70:PRO:O	14:O:72:HIS:CE1	2.64	0.51
42:r:119:ARG:CG	42:r:122:LYS:CE	2.88	0.51
43:s:54:LEU:HD23	43:s:60:MET:HE1	1.93	0.51
45:u:43:U:H2'	45:u:44:A:O5'	2.09	0.51
45:u:1412:G:N2	45:u:1413:C:C2	2.79	0.51
45:u:1904:G:C2	45:u:2073:C:C2	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:4966:A:C2	45:u:4967:A:C2	2.99	0.51
48:x:37:ILE:HA	48:x:40:PHE:HD2	1.75	0.51
55:5:645:TYR:O	55:5:690:ARG:NH2	2.43	0.51
23:X:156:ILE:HG13	48:x:415:ARG:NH2	2.26	0.51
48:x:441:ILE:HD12	48:x:444:GLY:HA2	1.93	0.51
5:E:226:GLY:N	42:r:135:LYS:CE	2.74	0.51
45:u:463:A:C2	45:u:692:A:H2	2.29	0.51
45:u:3723:A:C2	45:u:3724:A:C5	2.99	0.51
45:u:4758:U:O2	45:u:4758:U:O4'	2.29	0.51
45:u:4906:C:C2	45:u:4916:G:C2	2.99	0.51
48:x:443:SER:CB	48:x:447:ILE:HD12	2.39	0.51
45:u:1959:U:H4'	45:u:1961:G:C5'	2.41	0.51
45:u:4093:G:C3'	45:u:4094:G:H5'	2.41	0.51
45:u:4281:A:C2	45:u:4283:G:C6	2.99	0.51
45:u:5000:G:N2	45:u:5051:C:C2	2.78	0.51
48:x:248:THR:O	48:x:251:VAL:HG23	2.10	0.51
55:5:212:TYR:HE2	55:5:257:VAL:CG2	2.20	0.51
55:5:345:ILE:HA	55:5:598:TRP:CD1	2.46	0.51
4:D:3:PHE:HB2	45:u:1755:C:C6	2.47	0.50
45:u:224:U:O2	45:u:224:U:O4'	2.27	0.50
45:u:504:G:C2	45:u:654:C:C2	2.99	0.50
45:u:1072:C:O2	45:u:1072:C:C2'	2.60	0.50
45:u:1171:G:C2	45:u:1191:C:C2	2.99	0.50
45:u:1400:G:C6	45:u:1401:C:C4	2.99	0.50
45:u:1822:U:O4'	45:u:1822:U:O2	2.27	0.50
45:u:1960:A:H4'	45:u:1961:G:OP2	2.11	0.50
45:u:2028:C:O2'	45:u:2029:A:C5'	2.60	0.50
45:u:3782:C:C2	45:u:3811:G:N2	2.79	0.50
47:w:125:C:O2	47:w:125:C:O4'	2.29	0.50
2:B:302:ASN:HB2	2:B:313:SER:HA	1.94	0.50
25:Z:5:MET:HG2	25:Z:77:TYR:CE1	2.46	0.50
45:u:1265:G:C2'	45:u:1266:G:H5'	2.41	0.50
45:u:1268:G:C2	45:u:2111:G:N2	2.78	0.50
45:u:1358:G:H2'	45:u:1359:G:H8	1.75	0.50
45:u:1998:A:O2'	45:u:1999:A:O4'	2.30	0.50
45:u:2638:G:C2	45:u:2639:U:C4	2.98	0.50
55:5:413:VAL:HA	55:5:416:ILE:HD12	1.92	0.50
55:5:470:THR:HA	55:5:473:PHE:HD2	1.76	0.50
7:G:95:LEU:HD13	7:G:184:LEU:HD11	1.93	0.50
25:Z:15:ALA:HB3	25:Z:79:HIS:HB3	1.93	0.50
45:u:105:A:C2	45:u:336:A:C8	3.00	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1400:G:C2	45:u:1401:C:C2	2.99	0.50
45:u:1776:A:C6	45:u:1777:C:C4	2.99	0.50
45:u:2297:G:C2	45:u:2338:C:N3	2.79	0.50
5:E:95:ASP:N	45:u:686:A:N7	2.59	0.50
45:u:1736:A:N3	46:v:78:C:O2'	2.42	0.50
45:u:3641:U:C2	45:u:3645:U:C5	2.99	0.50
55:5:528:TYR:CZ	55:5:581:ILE:CD1	2.94	0.50
3:C:334:THR:HG21	6:F:53:TYR:OH	2.11	0.50
12:M:24:LEU:HD11	12:M:86:TRP:CG	2.47	0.50
42:r:47:LYS:HD3	42:r:102:TYR:CD2	2.44	0.50
42:r:122:LYS:N	42:r:122:LYS:CD	2.73	0.50
45:u:222:C:H2'	45:u:223:G:O4'	2.11	0.50
45:u:325:U:H2'	45:u:326:C:C6	2.47	0.50
45:u:471:A:N1	45:u:472:C:C1'	2.74	0.50
45:u:1214:C:H1'	45:u:1215:C:OP2	2.10	0.50
45:u:2028:C:O2'	45:u:2029:A:O4'	2.29	0.50
45:u:2494:U:H2'	45:u:2495:U:O4'	2.12	0.50
45:u:4094:G:H2'	45:u:4095:G:O4'	2.12	0.50
56:6:80:UNK:O	56:6:82:UNK:N	2.45	0.50
5:E:226:GLY:H	42:r:135:LYS:CE	2.25	0.50
17:R:61:ALA:HB2	45:u:2633:U:H5''	1.93	0.50
45:u:1886:G:C2	45:u:1894:C:C2	3.00	0.50
45:u:5031:G:N2	45:u:5032:C:C2	2.80	0.50
48:x:461:PHE:O	48:x:461:PHE:HD1	1.94	0.50
50:z:81:ILE:C	50:z:81:ILE:HD12	2.36	0.50
2:B:4:ARG:HG3	45:u:4458:C:N4	2.27	0.50
2:B:43:LEU:HD13	2:B:196:TRP:CH2	2.46	0.50
25:Z:51:ARG:HB2	25:Z:65:ARG:HD2	1.92	0.50
32:g:60:ARG:HG3	32:g:61:PRO:HD2	1.94	0.50
45:u:77:U:C4	45:u:335:A:N1	2.76	0.50
45:u:466:A:N1	45:u:467:U:C5	2.79	0.50
45:u:1263:A:C6	45:u:1264:C:C4	3.00	0.50
45:u:3717:A:N1	45:u:3933:G:H1'	2.26	0.50
45:u:4389:C:H2'	45:u:4390:A:H8	1.76	0.50
45:u:4462:C:C2	45:u:4515:G:C2	3.00	0.50
5:E:134:ARG:NH1	5:E:165:SER:O	2.45	0.50
45:u:125:C:O2'	45:u:126:C:OP1	2.22	0.50
45:u:462:G:O2'	45:u:463:A:H5'	2.12	0.50
45:u:977:C:H2'	45:u:978:G:O4'	2.12	0.50
45:u:1358:G:C2'	45:u:1359:G:O4'	2.59	0.50
45:u:1983:A:C2	45:u:2010:A:H5''	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:2368:A:N6	45:u:2788:U:O2	2.45	0.50
45:u:4583:C:N4	45:u:4718:G:C6	2.80	0.50
48:x:248:THR:N	48:x:440:ALA:CB	2.38	0.50
48:x:248:THR:N	48:x:440:ALA:CA	2.71	0.50
50:z:75:VAL:HA	50:z:78:LEU:HD13	1.94	0.50
55:5:95:THR:OG1	55:5:204:TYR:OH	2.29	0.50
17:R:109:TYR:HB3	17:R:115:ILE:HG12	1.94	0.50
30:e:108:ARG:NH2	30:e:127:ALA:HB3	2.26	0.50
42:r:47:LYS:HB3	42:r:102:TYR:CZ	2.46	0.50
43:s:14:PHE:CZ	45:u:1960:A:N3	2.79	0.50
45:u:1754:U:O2	45:u:1754:U:O4'	2.30	0.50
45:u:2108:G:N2	45:u:2125:C:C2	2.80	0.50
45:u:2311:C:C2	45:u:2328:G:C2	3.00	0.50
55:5:212:TYR:CE2	55:5:257:VAL:CG2	2.92	0.50
55:5:675:LEU:HD13	55:5:679:GLU:HA	1.94	0.50
23:X:147:LEU:CD2	49:y:20:ARG:HH22	2.25	0.49
42:r:107:ARG:HD2	42:r:108:MET:CA	2.42	0.49
45:u:2752:G:H2'	45:u:2753:G:O4'	2.12	0.49
55:5:126:PHE:C	55:5:174:PHE:CE2	2.82	0.49
55:5:127:THR:N	55:5:174:PHE:CE2	2.80	0.49
55:5:348:SER:CB	55:5:598:TRP:NE1	2.71	0.49
42:r:119:ARG:O	42:r:122:LYS:CD	2.59	0.49
45:u:211:G:N2	45:u:212:A:N9	2.60	0.49
45:u:467:U:C2	45:u:468:U:C6	3.00	0.49
45:u:1400:G:H2'	45:u:1401:C:O4'	2.13	0.49
45:u:1910:G:N2	45:u:1911:C:C2	2.80	0.49
45:u:2588:C:OP1	45:u:2767:U:O2'	2.30	0.49
45:u:4079:C:C2	45:u:4168:G:C2	3.00	0.49
45:u:4579:U:O2	45:u:4580:U:C2	2.65	0.49
45:u:4989:U:O2	45:u:4989:U:O4'	2.30	0.49
48:x:367:PHE:O	48:x:371:SER:OG	2.22	0.49
1:A:180:LEU:HD21	41:p:26:VAL:HG21	1.93	0.49
13:N:169:ARG:NH1	45:u:63:G:OP2	2.41	0.49
17:R:105:LEU:HD12	17:R:138:LEU:HD13	1.94	0.49
42:r:135:LYS:HD2	42:r:135:LYS:C	2.37	0.49
45:u:93:G:H2'	45:u:94:A:C8	2.48	0.49
45:u:971:U:H2'	45:u:972:C:H5'	1.95	0.49
45:u:1613:A:C2	45:u:1630:A:C2	3.00	0.49
45:u:2056:G:C8	45:u:2058:G:C8	3.00	0.49
45:u:2090:U:O4'	45:u:2090:U:OP2	2.30	0.49
45:u:2463:G:N2	45:u:2464:C:C2	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:3752:C:H2'	45:u:3777:G:C8	2.47	0.49
45:u:3914:U:N3	45:u:4378:A:N6	2.48	0.49
45:u:4213:A:N6	45:u:4218:U:H3	2.10	0.49
45:u:4691:A:C2	45:u:4700:A:C4	3.00	0.49
48:x:61:PRO:HB2	48:x:65:MET:HB2	1.93	0.49
48:x:157:VAL:HG12	50:z:80:PHE:CZ	1.99	0.49
48:x:244:ASN:ND2	48:x:439:GLY:C	2.63	0.49
55:5:463:VAL:HG22	55:5:467:PHE:HB2	1.93	0.49
4:D:111:ASN:ND2	4:D:111:ASN:C	2.70	0.49
14:O:54:TYR:CE1	14:O:145:VAL:HG11	2.47	0.49
45:u:975:C:C3'	45:u:976:G:O4'	2.60	0.49
45:u:1167:C:C2	45:u:1195:G:C2	3.00	0.49
45:u:2123:C:O2'	45:u:2124:G:OP2	2.20	0.49
45:u:2257:C:O2'	45:u:2258:C:O5'	2.25	0.49
55:5:123:PHE:CE2	55:5:170:GLY:O	2.54	0.49
55:5:365:GLN:HG3	55:5:474:HIS:CG	2.46	0.49
55:5:619:THR:N	55:5:623:GLU:O	2.32	0.49
3:C:213:GLU:OE1	3:C:213:GLU:N	2.46	0.49
5:E:62:LYS:HE2	45:u:979:C:OP2	2.13	0.49
11:L:9:ILE:HG21	26:a:52:TYR:CE2	2.48	0.49
15:P:54:GLN:HA	15:P:83:TRP:CD1	2.47	0.49
20:U:80:LYS:HD3	20:U:110:TYR:CE2	2.47	0.49
42:r:82:ILE:HD11	42:r:96:MET:HE3	1.94	0.49
45:u:1235:G:H2'	45:u:1236:C:H5'	1.93	0.49
45:u:1245:C:C4	45:u:1269:G:O6	2.66	0.49
45:u:1956:A:C2'	45:u:1957:U:H5'	2.43	0.49
4:D:146:LEU:HD11	4:D:159:VAL:HG11	1.94	0.49
9:I:46:PHE:CD1	9:I:140:THR:HA	2.48	0.49
9:I:181:PHE:O	9:I:185:VAL:HG23	2.12	0.49
45:u:166:C:C2	45:u:167:C:H5	2.30	0.49
45:u:230:G:C2	45:u:239:C:C2	3.01	0.49
45:u:703:G:O6	45:u:706:C:N4	2.45	0.49
45:u:1170:G:C2	45:u:1192:C:C2	3.00	0.49
45:u:1811:G:N2	45:u:1812:C:C2	2.80	0.49
45:u:2477:A:H2'	45:u:2478:C:C6	2.48	0.49
45:u:4099:G:C6	45:u:4100:C:C4	3.01	0.49
45:u:4411:G:C2	45:u:4432:C:O2	2.65	0.49
46:v:71:G:C2	46:v:105:C:C2	3.00	0.49
48:x:64:TRP:H	48:x:64:TRP:HD1	1.58	0.49
55:5:176:MET:HE1	55:5:215:LEU:HD22	1.94	0.49
4:D:68:ARG:HG3	4:D:73:MET:HE3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:195:HIS:CE1	4:D:199:ILE:HD11	2.48	0.49
11:L:66:TYR:O	11:L:68:THR:N	2.46	0.49
21:V:82:ILE:HD12	21:V:104:VAL:HG22	1.93	0.49
23:X:127:LEU:HD12	23:X:127:LEU:C	2.38	0.49
43:s:112:ARG:NH1	45:u:1968:G:OP1	2.45	0.49
45:u:986:C:N3	45:u:1068:G:C2	2.81	0.49
45:u:990:C:C4	45:u:1064:G:C2	3.01	0.49
45:u:1301:C:O4'	45:u:1301:C:O2	2.29	0.49
45:u:1666:C:O2'	45:u:1688:G:OP1	2.21	0.49
45:u:1699:A:N6	45:u:2094:G:O2'	2.46	0.49
45:u:2468:U:O2	45:u:2469:C:C5	2.66	0.49
48:x:181:LEU:CD2	48:x:457:TYR:CE1	2.95	0.49
50:z:79:LEU:C	50:z:79:LEU:CD2	2.85	0.49
53:3:88:LEU:N	53:3:88:LEU:HD13	2.27	0.49
55:5:645:TYR:HD1	55:5:673:PHE:HA	1.77	0.49
5:E:208:LEU:HD12	5:E:208:LEU:O	2.12	0.49
10:J:156:ARG:NH2	46:v:17:C:OP1	2.46	0.49
16:Q:11:ARG:NH2	45:u:1690:C:OP2	2.45	0.49
42:r:47:LYS:O	42:r:103:HIS:NE2	2.45	0.49
44:t:94:LYS:HA	44:t:95:GLN:C	2.38	0.49
45:u:100:C:H2'	45:u:101:A:O4'	2.13	0.49
45:u:465:G:N1	45:u:466:A:C8	2.81	0.49
45:u:956:A:H3'	45:u:957:G:C8	2.48	0.49
45:u:1269:G:C5	45:u:2111:G:C2	3.01	0.49
45:u:1345:A:H2'	45:u:1346:C:C6	2.48	0.49
45:u:1787:A:N3	45:u:4210:U:O2'	2.44	0.49
45:u:1987:C:O2	45:u:1987:C:C2'	2.61	0.49
45:u:2730:U:H2'	45:u:2731:C:C6	2.48	0.49
45:u:4093:G:H3'	45:u:4094:G:H5'	1.95	0.49
45:u:4136:G:C6	45:u:4137:C:C4	3.01	0.49
45:u:4489:G:C6	45:u:4490:C:C4	3.00	0.49
49:y:56:LEU:HG	53:3:92:PHE:CD2	2.47	0.49
51:1:465:LYS:O	51:1:469:ALA:N	2.44	0.49
1:A:44:ILE:HG22	1:A:87:PHE:CD2	2.48	0.49
4:D:258:LYS:O	4:D:259:ARG:HG3	2.13	0.49
5:E:202:VAL:HG12	5:E:256:LYS:NZ	2.17	0.49
45:u:1449:C:H2'	45:u:1450:C:O4'	2.12	0.49
45:u:1726:U:H3	45:u:1836:G:H1	1.61	0.49
45:u:2468:U:C4	45:u:2473:A:N6	2.77	0.49
45:u:4735:G:C6	45:u:4736:C:C4	3.01	0.49
45:u:4932:U:H2'	45:u:4933:C:O4'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:194:LYS:HD2	48:x:240:PRO:HG3	1.94	0.49
2:B:252:ALA:HB3	45:u:4457:U:O2	2.13	0.49
27:b:45:PHE:CE1	45:u:1815:G:N7	2.81	0.49
45:u:1328:G:O2'	45:u:2349:A:OP1	2.31	0.49
45:u:1381:U:O2	45:u:1381:U:O4'	2.28	0.49
45:u:1399:G:H2'	45:u:1400:G:O4'	2.12	0.49
45:u:2726:G:C6	45:u:2727:C:N4	2.81	0.49
32:g:46:CYS:SG	32:g:47:GLY:N	2.85	0.48
45:u:356:G:O2'	47:w:25:G:N3	2.44	0.48
45:u:919:C:N4	45:u:920:C:N4	2.61	0.48
45:u:4767:C:C2	45:u:4868:G:C2	3.01	0.48
50:z:75:VAL:CA	50:z:78:LEU:HD13	2.43	0.48
55:5:31:PHE:O	55:5:35:LEU:HG	2.12	0.48
55:5:645:TYR:HE1	55:5:674:GLU:H	1.59	0.48
1:A:107:MET:SD	1:A:113:VAL:HG11	2.53	0.48
45:u:384:A:C6	45:u:386:A:C6	3.01	0.48
45:u:467:U:N3	45:u:468:U:C6	2.80	0.48
45:u:1279:A:O2'	45:u:1280:C:OP1	2.30	0.48
45:u:1448:G:N2	45:u:1449:C:C2	2.81	0.48
45:u:2026:A:H2'	45:u:2027:U:H5'	1.93	0.48
45:u:3782:C:N3	45:u:3811:G:C2	2.81	0.48
45:u:3896:C:O2	45:u:4564:A:N1	2.46	0.48
45:u:4303:C:O2	45:u:4303:C:O5'	2.32	0.48
45:u:4574:U:H3'	45:u:4575:G:H5''	1.94	0.48
48:x:254:VAL:O	48:x:257:TYR:HB3	2.13	0.48
55:5:84:ILE:HD12	55:5:87:THR:HG23	1.95	0.48
55:5:376:TYR:O	55:5:380:SER:N	2.46	0.48
17:R:44:LEU:HD22	17:R:49:LEU:HD12	1.96	0.48
31:f:79:GLY:O	31:f:81:SER:N	2.45	0.48
45:u:984:C:C2	45:u:1070:G:C2	3.01	0.48
45:u:1878:G:N2	45:u:1879:C:C2	2.81	0.48
45:u:2729:C:H2'	45:u:2730:U:O4'	2.13	0.48
45:u:2909:C:C2	45:u:3586:G:C2	3.01	0.48
45:u:3626:G:C6	45:u:3836:A:C2	3.01	0.48
45:u:3860:A:H61	45:u:4560:C:H5	1.61	0.48
45:u:4129:G:H2'	45:u:4130:C:O4'	2.14	0.48
53:3:92:PHE:CZ	53:3:96:MET:HE2	1.87	0.48
55:5:521:LYS:N	55:5:576:SER:OG	2.45	0.48
2:B:49:TYR:CE1	2:B:168:MET:HE1	2.47	0.48
7:G:100:HIS:HA	7:G:103:ARG:HD2	1.95	0.48
17:R:36:ASN:ND2	48:x:407:THR:CG2	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:a:61:TYR:N	45:u:4354:U:O4	2.46	0.48
43:s:128:THR:HG22	43:s:178:LEU:HD21	1.96	0.48
45:u:300:A:C2	45:u:301:G:C6	3.01	0.48
45:u:505:G:C2	45:u:506:C:C2	3.01	0.48
45:u:1367:C:O2	45:u:1367:C:H2'	2.14	0.48
45:u:3715:U:O2'	45:u:3716:C:O4'	2.28	0.48
45:u:4724:A:C6	45:u:4725:C:C4	3.01	0.48
48:x:437:PHE:CE2	48:x:438:LEU:HD21	2.44	0.48
55:5:361:TYR:O	55:5:365:GLN:NE2	2.45	0.48
55:5:567:TYR:OH	55:5:695:LYS:O	2.32	0.48
2:B:165:HIS:HB3	2:B:180:LEU:HG	1.95	0.48
5:E:254:LEU:O	5:E:258:LYS:HG3	2.13	0.48
11:L:65:ARG:HG2	11:L:66:TYR:CD2	2.48	0.48
13:N:65:ARG:HG3	13:N:129:PHE:CE1	2.49	0.48
16:Q:86:ILE:HB	16:Q:105:VAL:HG13	1.95	0.48
45:u:106:A:O2'	45:u:335:A:N3	2.43	0.48
45:u:1383:G:C5	45:u:1384:C:C4	3.02	0.48
45:u:2539:C:H2'	45:u:2540:C:C6	2.48	0.48
45:u:2557:G:C6	45:u:2558:C:C4	3.01	0.48
48:x:69:LEU:HD22	48:x:81:ILE:HG13	1.95	0.48
55:5:127:THR:HA	55:5:130:VAL:HG22	1.95	0.48
1:A:49:ILE:HG22	1:A:58:LEU:HB2	1.94	0.48
3:C:303:ARG:O	16:Q:38:ARG:NH1	2.42	0.48
5:E:254:LEU:O	5:E:257:ILE:HG12	2.14	0.48
12:M:36:ALA:HB2	12:M:52:PHE:CE1	2.49	0.48
40:o:24:THR:HG23	40:o:69:ARG:HB3	1.94	0.48
45:u:1252:C:C2	45:u:1259:G:C2	3.01	0.48
45:u:1297:U:P	45:u:1297:U:O4'	2.71	0.48
45:u:1448:G:C6	45:u:1449:C:N4	2.82	0.48
45:u:2336:G:C6	45:u:2337:C:C4	3.02	0.48
55:5:31:PHE:CZ	55:5:121:PRO:CG	2.97	0.48
55:5:222:HIS:O	55:5:225:VAL:HB	2.13	0.48
55:5:590:SER:CA	55:5:591:ASP:N	2.76	0.48
2:B:252:ALA:HB1	45:u:4524:G:N3	2.29	0.48
5:E:62:LYS:HE2	45:u:978:G:OP1	2.08	0.48
7:G:32:PHE:CZ	25:Z:55:ALA:HA	2.48	0.48
35:j:45:ARG:NH1	45:u:372:A:O3'	2.46	0.48
45:u:80:C:C2	45:u:104:G:C2	3.01	0.48
45:u:499:G:N3	45:u:499:G:H2'	2.28	0.48
45:u:2336:G:C2	45:u:2337:C:C2	3.01	0.48
45:u:3724:A:N6	45:u:3725:G:C6	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:4489:G:C2	45:u:4490:C:C2	3.02	0.48
45:u:4916:G:C2	45:u:4917:C:C2	3.02	0.48
3:C:193:LYS:HD2	3:C:196:MET:HE3	1.94	0.48
28:c:82:GLY:HA2	28:c:91:VAL:CG1	2.44	0.48
45:u:28:C:C2	45:u:55:G:C2	3.02	0.48
45:u:351:C:C2	47:w:25:G:N2	2.82	0.48
45:u:965:G:N3	45:u:965:G:H2'	2.29	0.48
45:u:2557:G:C2	45:u:2558:C:C2	3.01	0.48
45:u:2844:A:O2'	45:u:4631:G:H4'	2.14	0.48
5:E:254:LEU:N	5:E:255:PRO:HD2	2.28	0.48
9:I:184:MET:HE3	9:I:189:ARG:HB3	1.95	0.48
42:r:118:LEU:HD12	42:r:121:GLN:HE22	1.77	0.48
45:u:499:G:C2	45:u:656:C:N3	2.82	0.48
45:u:1995:G:C2	45:u:1996:C:C2	3.02	0.48
45:u:2519:U:C2	45:u:2520:C:C5	3.01	0.48
45:u:2586:G:C8	45:u:2770:C:H1'	2.49	0.48
45:u:2618:G:N2	45:u:2720:C:C2	2.82	0.48
45:u:5020:G:H2'	45:u:5021:C:O4'	2.13	0.48
48:x:212:ALA:HB3	48:x:215:ALA:H	1.79	0.48
3:C:290:SER:O	3:C:294:LYS:HG2	2.14	0.48
16:Q:67:ILE:HD12	16:Q:96:PRO:HD2	1.96	0.48
28:c:34:THR:HG21	28:c:93:THR:CG2	2.44	0.48
32:g:5:LEU:HD13	32:g:32:TYR:CE2	2.49	0.48
40:o:68:LEU:HD11	40:o:85:ILE:CD1	2.44	0.48
41:p:49:ARG:HB2	41:p:55:TRP:CZ3	2.49	0.48
45:u:472:C:H2'	45:u:473:C:O4'	2.14	0.48
45:u:2627:C:O2	45:u:2627:C:O4'	2.30	0.48
45:u:3714:G:C6	45:u:3715:U:C4	3.02	0.48
45:u:4378:A:O2'	45:u:4379:A:H2'	2.14	0.48
55:5:155:PRO:HA	55:5:158:ILE:HD12	1.95	0.48
55:5:561:SER:HA	55:5:637:CYS:HA	1.96	0.48
5:E:59:TYR:CZ	5:E:64:LEU:HB2	2.49	0.47
8:H:39:ASN:O	8:H:40:HIS:HB3	2.14	0.47
13:N:124:ASP:OD1	13:N:125:SER:N	2.46	0.47
24:Y:52:ASP:OD1	24:Y:52:ASP:N	2.47	0.47
45:u:1176:C:HO2'	45:u:1177:U:C4'	2.26	0.47
45:u:1958:A:H3'	45:u:1958:A:P	2.54	0.47
45:u:4099:G:C2	45:u:4100:C:C2	3.02	0.47
45:u:4492:U:O2'	45:u:4512:U:O2	2.22	0.47
48:x:68:ILE:HD13	48:x:68:ILE:N	2.28	0.47
50:z:79:LEU:HD23	50:z:79:LEU:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:126:PHE:HB3	55:5:174:PHE:CZ	2.49	0.47
55:5:652:THR:O	55:5:655:LYS:NZ	2.46	0.47
2:B:105:VAL:HG11	2:B:150:PHE:CZ	2.49	0.47
42:r:10:VAL:HG13	42:r:14:SER:HB3	1.96	0.47
45:u:199:G:N2	45:u:201:C:C2	2.82	0.47
45:u:508:G:C2	45:u:510:U:C5	3.02	0.47
45:u:671:G:C2	45:u:672:C:C2	3.01	0.47
45:u:689:U:C4	45:u:690:C:C5	3.03	0.47
45:u:967:C:N3	45:u:2254:G:C6	2.83	0.47
45:u:1246:G:H2'	45:u:1247:U:O4'	2.14	0.47
45:u:1872:G:O2'	45:u:4219:A:N3	2.38	0.47
45:u:5020:G:C2	45:u:5021:C:C2	3.02	0.47
55:5:48:PHE:HA	55:5:531:GLN:HE21	1.78	0.47
2:B:234:ARG:HA	2:B:272:LYS:HD2	1.95	0.47
3:C:268:ARG:NH2	45:u:655:C:OP2	2.47	0.47
4:D:64:ILE:HG13	4:D:105:LEU:HD21	1.95	0.47
13:N:5:LYS:HG2	34:i:40:VAL:HG11	1.96	0.47
33:h:88:THR:O	33:h:89:ARG:C	2.57	0.47
42:r:135:LYS:HZ1	45:u:451:C:H3'	1.77	0.47
45:u:977:C:H2'	45:u:978:G:H5'	1.96	0.47
45:u:1383:G:C6	45:u:1384:C:C4	3.02	0.47
45:u:1910:G:C6	45:u:1911:C:N4	2.82	0.47
45:u:2496:G:C2	45:u:2497:C:C2	3.02	0.47
45:u:3938:G:O6	45:u:4172:A:N1	2.48	0.47
45:u:4730:C:O5'	45:u:4731:G:N2	2.47	0.47
45:u:4919:G:C2	45:u:4920:C:C2	3.02	0.47
55:5:14:GLN:HA	55:5:17:LEU:HB2	1.97	0.47
55:5:44:VAL:HG22	55:5:45:ILE:HG13	1.96	0.47
55:5:353:GLN:HB3	55:5:354:PRO:HD2	1.95	0.47
55:5:387:ILE:HA	55:5:390:ILE:HD12	1.96	0.47
6:F:211:TRP:CD1	6:F:212:PRO:HD2	2.50	0.47
37:l:41:ARG:NH1	45:u:2431:A:OP1	2.48	0.47
45:u:298:G:N2	45:u:299:C:C2	2.83	0.47
45:u:1279:A:H2'	45:u:1280:C:C6	2.49	0.47
45:u:1584:G:C6	45:u:1585:C:C4	3.02	0.47
45:u:1661:C:C2	45:u:2345:G:N1	2.82	0.47
48:x:78:GLU:CG	48:x:155:LEU:HD22	2.44	0.47
53:3:92:PHE:HZ	53:3:96:MET:SD	2.23	0.47
55:5:154:VAL:HG13	55:5:157:TYR:HB3	1.95	0.47
2:B:91:GLY:CA	2:B:153:MET:HE3	2.45	0.47
5:E:123:SER:O	5:E:126:ARG:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:124:HIS:NE2	45:u:1282:G:N7	2.63	0.47
9:I:45:GLU:O	9:I:46:PHE:CD1	2.67	0.47
14:O:109:PRO:HB2	14:O:110:PRO:CD	2.43	0.47
17:R:11:ALA:HB1	17:R:50:ILE:HD13	1.96	0.47
20:U:100:LEU:HD22	20:U:112:LEU:HB3	1.96	0.47
27:b:8:THR:OG1	27:b:9:THR:N	2.46	0.47
30:e:35:TRP:CZ2	30:e:56:PRO:HD2	2.50	0.47
32:g:63:VAL:O	32:g:66:ARG:N	2.45	0.47
42:r:119:ARG:O	42:r:122:LYS:HD2	2.15	0.47
45:u:2459:G:N2	45:u:2462:C:OP2	2.47	0.47
45:u:4092:G:C2	45:u:4158:C:C2	3.02	0.47
48:x:69:LEU:HD23	48:x:80:GLY:N	2.29	0.47
48:x:375:PHE:O	48:x:379:TRP:CB	2.62	0.47
50:z:71:VAL:O	50:z:75:VAL:HG23	2.15	0.47
55:5:72:PHE:HA	55:5:83:ILE:CG1	2.42	0.47
2:B:119:TYR:OH	2:B:129:ALA:N	2.48	0.47
5:E:226:GLY:CA	42:r:135:LYS:HD3	2.41	0.47
11:L:65:ARG:HD3	26:a:69:PHE:CD1	2.49	0.47
14:O:84:VAL:HG11	14:O:102:LEU:HD22	1.96	0.47
29:d:38:PHE:CE1	45:u:4634:U:C2	3.03	0.47
45:u:211:G:N2	45:u:212:A:C4	2.83	0.47
45:u:721:G:C2	45:u:948:C:C2	3.03	0.47
45:u:1280:C:N3	45:u:1282:G:C6	2.83	0.47
45:u:4119:C:O2	45:u:4119:C:O4'	2.30	0.47
47:w:56:G:C6	47:w:57:C:C4	3.02	0.47
55:5:99:ILE:HG23	55:5:103:LEU:HD13	1.95	0.47
55:5:146:LEU:HD21	55:5:423:SER:HB2	1.96	0.47
2:B:241:PRO:O	2:B:244:THR:OG1	2.30	0.47
2:B:312:LYS:HD2	2:B:370:THR:HG21	1.97	0.47
9:I:153:ARG:HA	9:I:165:ILE:HD11	1.96	0.47
27:b:13:SER:HA	27:b:16:TRP:CE3	2.49	0.47
29:d:46:LEU:HD12	29:d:72:VAL:HG11	1.97	0.47
45:u:120:A:H2'	45:u:149:A:N6	2.29	0.47
45:u:177:G:C6	45:u:178:C:C4	3.03	0.47
45:u:177:G:C2	45:u:178:C:C2	3.03	0.47
45:u:208:A:C2	45:u:233:U:C2	3.03	0.47
45:u:497:G:C2	45:u:657:C:N3	2.82	0.47
45:u:1189:G:C6	45:u:1190:C:C4	3.02	0.47
45:u:1308:C:H2'	45:u:1309:C:C6	2.49	0.47
45:u:1468:C:C2	45:u:1498:G:N2	2.82	0.47
45:u:1643:A:H2'	45:u:1644:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1957:U:O2'	45:u:1958:A:O4'	2.33	0.47
45:u:2128:G:C6	45:u:2129:C:C4	3.03	0.47
45:u:2618:G:C2	45:u:2720:C:C2	3.03	0.47
45:u:2818:C:OP1	45:u:4655:A:H4'	2.15	0.47
45:u:3586:G:C6	45:u:3587:C:C4	3.02	0.47
45:u:4152:G:N2	45:u:4153:C:C2	2.82	0.47
45:u:4525:C:H2'	45:u:4526:U:O4'	2.15	0.47
48:x:47:GLN:CA	48:x:75:THR:CG2	2.92	0.47
55:5:65:PHE:O	55:5:69:HIS:N	2.47	0.47
55:5:175:CYS:SG	55:5:204:TYR:C	2.97	0.47
55:5:348:SER:O	55:5:349:VAL:C	2.53	0.47
16:Q:186:TYR:CD2	45:u:4307:A:H4'	2.50	0.47
35:j:9:GLY:HA2	45:u:2792:C:O2	2.14	0.47
45:u:484:U:C4	45:u:486:C:C5	3.02	0.47
45:u:505:G:C6	45:u:506:C:C4	3.02	0.47
45:u:1198:G:H2'	45:u:1199:G:C8	2.49	0.47
45:u:2907:G:H2'	45:u:2908:U:O4'	2.15	0.47
45:u:3715:U:H2'	45:u:3716:C:C6	2.49	0.47
45:u:4942:C:O3'	45:u:4944:C:P	2.73	0.47
48:x:69:LEU:HD23	48:x:80:GLY:H	1.78	0.47
49:y:53:PHE:CE1	53:3:92:PHE:CZ	3.03	0.47
4:D:76:CYS:SG	4:D:77:ALA:N	2.87	0.47
11:L:100:PRO:O	34:i:25:ARG:NH2	2.47	0.47
17:R:124:TYR:OH	45:u:2666:U:OP2	2.23	0.47
45:u:77:U:H3	45:u:336:A:N6	2.13	0.47
45:u:211:G:H4'	45:u:234:G:H8	1.76	0.47
45:u:384:A:N6	45:u:386:A:C6	2.83	0.47
45:u:1240:G:C2	45:u:1241:C:C2	3.03	0.47
45:u:2771:G:C6	45:u:2772:C:C4	3.03	0.47
45:u:2858:A:O2'	45:u:2859:G:C8	2.65	0.47
48:x:59:ALA:HB1	48:x:65:MET:SD	2.54	0.47
7:G:58:PRO:HD3	23:X:46:PHE:HD2	1.80	0.47
15:P:32:THR:HG21	15:P:87:SER:HB3	1.96	0.47
23:X:52:LEU:HD22	23:X:53:ARG:N	2.30	0.47
45:u:465:G:C2	45:u:466:A:N9	2.83	0.47
45:u:967:C:OP1	45:u:2254:G:N1	2.48	0.47
45:u:1075:G:C2	45:u:1076:C:C2	3.02	0.47
45:u:1099:C:H2'	45:u:1100:U:O4'	2.15	0.47
45:u:1189:G:C2	45:u:1190:C:C2	3.03	0.47
45:u:1270:A:H2'	45:u:1271:G:O5'	2.15	0.47
45:u:1995:G:C6	45:u:1996:C:C4	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:3597:G:C2	45:u:3598:C:C2	3.03	0.47
45:u:4461:C:C2	45:u:4516:G:C2	3.02	0.47
45:u:4661:G:C6	45:u:4662:C:C4	3.03	0.47
48:x:115:ALA:HA	48:x:118:LEU:HD12	1.97	0.47
53:3:141:MET:HE2	55:5:362:PHE:HB2	1.96	0.47
55:5:126:PHE:O	55:5:129:ILE:HG22	2.16	0.47
4:D:43:LYS:HB3	4:D:46:THR:CG2	2.46	0.46
14:O:160:ARG:NH2	45:u:4759:C:OP1	2.47	0.46
17:R:99:MET:HE3	17:R:127:VAL:HG12	1.96	0.46
21:V:38:TYR:N	21:V:64:THR:O	2.47	0.46
45:u:218:A:N3	45:u:218:A:C2'	2.78	0.46
45:u:2065:G:C6	45:u:2066:C:C4	3.03	0.46
45:u:2814:C:O2	45:u:2814:C:C2'	2.62	0.46
45:u:3586:G:C2	45:u:3587:C:C2	3.03	0.46
45:u:4246:G:N2	45:u:4263:C:C2	2.83	0.46
45:u:4537:C:H2'	45:u:4538:G:C8	2.50	0.46
46:v:117:G:C2	46:v:118:C:C2	3.03	0.46
47:w:127:U:C4	47:w:128:C:C5	3.03	0.46
48:x:37:ILE:HG21	50:z:74:LEU:HD13	1.97	0.46
48:x:181:LEU:HD11	48:x:457:TYR:CE2	2.20	0.46
3:C:161:TYR:CD1	3:C:166:GLU:HB3	2.49	0.46
19:T:64:VAL:HG22	19:T:72:VAL:HG11	1.97	0.46
26:a:59:ARG:NH2	45:u:294:G:O2'	2.48	0.46
45:u:22:G:N1	47:w:35:C:C4	2.83	0.46
45:u:108:A:N1	45:u:333:U:O2'	2.41	0.46
45:u:1541:C:C2	45:u:1619:G:N2	2.82	0.46
45:u:2089:G:HO2'	45:u:2090:U:P	2.38	0.46
45:u:5017:G:C6	45:u:5018:C:C4	3.04	0.46
48:x:177:SER:OG	48:x:180:SER:N	2.36	0.46
48:x:188:CYS:HB3	49:y:48:GLY:HA2	1.96	0.46
55:5:286:LEU:N	55:5:286:LEU:HD22	2.31	0.46
55:5:567:TYR:OH	55:5:696:ASP:O	2.32	0.46
6:F:98:ARG:HH21	6:F:226:THR:HG22	1.80	0.46
14:O:26:GLN:OE1	14:O:31:ARG:NH1	2.48	0.46
30:e:31:ILE:HD11	45:u:2347:A:C5	2.50	0.46
42:r:82:ILE:HD11	42:r:96:MET:CE	2.46	0.46
42:r:118:LEU:CD1	42:r:121:GLN:NE2	2.79	0.46
45:u:120:A:C2	45:u:148:C:O2	2.68	0.46
45:u:984:C:C2	45:u:1070:G:N2	2.84	0.46
45:u:1732:C:C2	45:u:1798:G:C2	3.03	0.46
45:u:2046:G:C2	45:u:2047:A:C2	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:2496:G:C6	45:u:2497:C:C4	3.02	0.46
45:u:3941:G:H2'	45:u:3942:A:O4'	2.15	0.46
48:x:88:GLY:HA2	48:x:116:GLN:HE22	1.79	0.46
55:5:176:MET:HE2	55:5:176:MET:HA	1.97	0.46
55:5:644:TYR:OH	55:5:664:ARG:NH1	2.48	0.46
13:N:68:ARG:CG	45:u:302:C:OP1	2.64	0.46
15:P:41:ILE:HD12	15:P:150:LEU:CD1	2.46	0.46
18:S:47:PHE:HE1	18:S:125:GLN:HG2	1.81	0.46
45:u:499:G:C2	45:u:500:G:C8	3.03	0.46
45:u:1928:C:C4	45:u:2054:U:O2	2.69	0.46
45:u:1984:A:N6	45:u:2011:C:O2'	2.48	0.46
45:u:3717:A:O2'	45:u:3718:A:O4'	2.33	0.46
45:u:3900:G:H5''	45:u:3901:A:H4'	1.97	0.46
6:F:41:GLN:CG	45:u:2095:A:N1	2.79	0.46
18:S:84:TYR:CD1	18:S:84:TYR:C	2.94	0.46
37:l:20:ASN:O	37:l:41:ARG:NE	2.48	0.46
45:u:479:G:N2	45:u:480:C:C2	2.83	0.46
45:u:698:G:N2	45:u:699:C:C2	2.83	0.46
45:u:747:A:C2	45:u:749:G:H1'	2.50	0.46
45:u:1322:A:N6	45:u:4446:U:OP1	2.48	0.46
45:u:2089:G:C6	45:u:2262:G:H2'	2.50	0.46
45:u:2297:G:C2	45:u:2338:C:C2	3.03	0.46
45:u:2569:G:H2'	45:u:2570:U:O4'	2.15	0.46
45:u:2743:A:C2	45:u:2744:A:C4	3.03	0.46
45:u:3600:G:C6	45:u:3601:C:C4	3.04	0.46
45:u:4102:C:C2	45:u:4108:G:C2	3.03	0.46
55:5:14:GLN:HA	55:5:17:LEU:HD13	1.97	0.46
5:E:41:SER:HA	45:u:978:G:H4'	1.97	0.46
12:M:119:ARG:NH2	14:O:189:ILE:HD12	2.31	0.46
14:O:133:ARG:CZ	45:u:1928:C:C4	2.98	0.46
14:O:196:LEU:HB3	14:O:202:LEU:HD22	1.97	0.46
45:u:279:A:OP1	45:u:279:A:H3'	2.15	0.46
45:u:302:C:N4	45:u:303:C:N4	2.64	0.46
45:u:384:A:C6	45:u:386:A:C5	3.04	0.46
45:u:978:G:C6	45:u:979:C:C4	3.04	0.46
45:u:1221:G:O2'	45:u:1222:A:O5'	2.22	0.46
45:u:1826:G:C6	45:u:1827:C:C4	3.04	0.46
45:u:1855:G:C2	45:u:1856:C:C2	3.04	0.46
45:u:2122:G:O2'	45:u:2123:C:P	2.74	0.46
45:u:3662:A:N6	45:u:3680:U:N3	2.57	0.46
45:u:4473:A:C2	45:u:4474:A:C5	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:32:VAL:O	48:x:35:THR:OG1	2.27	0.46
48:x:76:LEU:HD21	48:x:154:GLN:HE21	1.80	0.46
48:x:176:GLY:H	48:x:457:TYR:HH	1.52	0.46
5:E:250:ASP:O	5:E:254:LEU:N	2.46	0.46
8:H:126:VAL:HG11	8:H:161:ILE:HG22	1.97	0.46
11:L:150:LEU:HD22	33:h:121:VAL:CG2	2.46	0.46
33:h:60:VAL:O	33:h:64:THR:HG23	2.16	0.46
42:r:17:LEU:HD21	42:r:19:LYS:HG3	1.97	0.46
45:u:35:U:O2'	45:u:1525:A:N1	2.46	0.46
45:u:691:C:O2	45:u:692:A:C8	2.69	0.46
45:u:917:A:C6	45:u:919:C:N4	2.84	0.46
45:u:1886:G:N2	45:u:1894:C:C2	2.83	0.46
45:u:2743:A:H2'	45:u:2744:A:C8	2.50	0.46
45:u:4737:G:C2	45:u:4738:C:C2	3.04	0.46
47:w:126:C:O2'	47:w:127:U:C5	2.64	0.46
55:5:134:LEU:HD13	55:5:177:LEU:CD2	2.42	0.46
2:B:29:VAL:CG2	2:B:346:THR:HG21	2.46	0.46
4:D:200:MET:HE1	4:D:241:LYS:HG2	1.93	0.46
9:I:202:ASN:N	9:I:202:ASN:OD1	2.49	0.46
25:Z:28:ASN:C	25:Z:29:ILE:HD12	2.41	0.46
25:Z:55:ALA:O	25:Z:57:MET:N	2.49	0.46
29:d:28:ASN:C	29:d:28:ASN:OD1	2.57	0.46
35:j:27:TYR:HA	35:j:34:CYS:HA	1.98	0.46
42:r:132:ARG:NE	42:r:132:ARG:HA	2.31	0.46
45:u:181:C:C4	45:u:256:G:N1	2.84	0.46
45:u:497:G:H3'	45:u:498:C:H5''	1.98	0.46
45:u:680:G:N1	45:u:681:G:C5	2.84	0.46
45:u:705:G:N2	45:u:706:C:C2	2.84	0.46
45:u:751:G:C2	45:u:752:G:N7	2.84	0.46
45:u:1404:G:C6	45:u:1405:C:C4	3.04	0.46
45:u:2065:G:H2'	45:u:2066:C:O4'	2.16	0.46
45:u:2847:G:N2	45:u:3842:C:C2	2.84	0.46
45:u:4283:G:N1	45:u:4284:C:C4	2.84	0.46
45:u:4740:G:C2	45:u:4741:C:C2	3.04	0.46
45:u:4881:U:O2	45:u:4881:U:O4'	2.34	0.46
47:w:71:A:C2	47:w:88:A:H1'	2.50	0.46
47:w:139:G:C6	47:w:140:C:C4	3.02	0.46
55:5:507:GLU:OE2	55:5:685:GLU:CG	2.62	0.46
16:Q:14:ARG:NH2	45:u:2083:C:OP2	2.48	0.46
45:u:1237:C:O2	45:u:1237:C:O4'	2.33	0.46
45:u:1358:G:H2'	45:u:1359:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1591:U:N3	45:u:4555:U:OP1	2.47	0.46
45:u:1613:A:H3'	45:u:1614:C:C5'	2.46	0.46
45:u:2020:U:O2	45:u:2020:U:H2'	2.14	0.46
45:u:3918:G:C6	45:u:3919:C:C4	3.04	0.46
47:w:55:U:N3	47:w:62:A:C2	2.83	0.46
48:x:248:THR:O	48:x:251:VAL:CG2	2.64	0.46
1:A:193:ARG:NH2	45:u:3685:C:OP1	2.48	0.46
7:G:159:HIS:CE1	7:G:185:LYS:HE2	2.51	0.46
16:Q:17:GLU:HB2	16:Q:18:PRO:HD2	1.98	0.46
31:f:45:LYS:HD3	31:f:107:PRO:HD2	1.97	0.46
45:u:726:G:C6	45:u:727:C:N4	2.84	0.46
45:u:918:G:H2'	45:u:918:G:N3	2.31	0.46
45:u:1269:G:C8	45:u:2111:G:C6	3.04	0.46
45:u:1416:G:N2	45:u:1417:C:C2	2.84	0.46
45:u:1448:G:C2	45:u:1449:C:C2	3.04	0.46
45:u:1983:A:C2	45:u:2008:U:O4	2.65	0.46
45:u:1995:G:C6	45:u:1996:C:N3	2.84	0.46
45:u:2245:G:C2	45:u:2246:C:C2	3.04	0.46
45:u:2270:G:C6	45:u:2271:C:C4	3.04	0.46
45:u:2559:G:C6	45:u:2560:C:C4	3.04	0.46
45:u:2698:G:C6	45:u:2699:C:C4	3.03	0.46
45:u:4423:U:O2	45:u:4423:U:O4'	2.34	0.46
45:u:4473:A:H2'	45:u:4474:A:C8	2.51	0.46
53:3:53:ILE:HD12	55:5:354:PRO:CG	2.38	0.46
5:E:169:LEU:HD21	5:E:187:GLN:HG3	1.98	0.45
6:F:41:GLN:HG3	45:u:2095:A:N1	2.31	0.45
45:u:190:G:C2	45:u:252:C:C2	3.04	0.45
45:u:978:G:C2	45:u:979:C:C2	3.05	0.45
45:u:2465:C:H2'	45:u:2466:G:C8	2.51	0.45
45:u:2594:C:C2	45:u:2752:G:C2	3.04	0.45
45:u:3727:A:H2'	45:u:3728:A:C8	2.51	0.45
45:u:4372:U:O2	45:u:4377:G:H1'	2.15	0.45
45:u:4919:G:C6	45:u:4920:C:C4	3.04	0.45
48:x:155:LEU:O	48:x:159:GLY:N	2.49	0.45
53:3:99:LEU:HA	53:3:102:ILE:HD12	1.98	0.45
1:A:209:HIS:CG	1:A:210:PRO:HD2	2.51	0.45
18:S:84:TYR:C	18:S:84:TYR:HD1	2.24	0.45
26:a:79:TRP:CZ2	26:a:122:VAL:HG13	2.51	0.45
40:o:43:ARG:NH2	45:u:294:G:OP2	2.48	0.45
42:r:103:HIS:ND1	42:r:106:LEU:CD2	2.73	0.45
43:s:180:ILE:HG22	43:s:182:PRO:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:216:C:C4	51:l:538:LYS:O	2.69	0.45
45:u:746:A:H4'	45:u:747:A:OP1	2.16	0.45
45:u:751:G:N2	45:u:912:G:C4	2.85	0.45
45:u:1240:G:C6	45:u:1241:C:C4	3.04	0.45
45:u:1855:G:C6	45:u:1856:C:C4	3.04	0.45
45:u:2128:G:C2	45:u:2129:C:C2	3.03	0.45
45:u:4916:G:C6	45:u:4917:C:C4	3.04	0.45
47:w:56:G:C2	47:w:57:C:C2	3.03	0.45
48:x:376:SER:OG	48:x:377:LYS:N	2.50	0.45
1:A:112:ILE:HG23	1:A:133:TYR:CD2	2.51	0.45
42:r:8:MET:HA	42:r:8:MET:HE2	1.97	0.45
45:u:351:C:C2	47:w:25:G:C2	3.04	0.45
45:u:467:U:C4	45:u:468:U:C5	3.05	0.45
45:u:1270:A:H2'	45:u:1271:G:O4'	2.16	0.45
45:u:1279:A:C4	45:u:1280:C:C4	3.04	0.45
45:u:1357:C:O2'	45:u:1358:G:O4'	2.29	0.45
45:u:1379:C:H4'	45:u:1380:G:C8	2.50	0.45
45:u:1549:G:N2	45:u:1580:C:C2	2.84	0.45
45:u:1826:G:C2	45:u:1827:C:C2	3.04	0.45
45:u:1995:G:C5	45:u:1996:C:C4	3.05	0.45
45:u:2315:G:C2	45:u:2325:C:C2	3.05	0.45
45:u:3942:A:H2'	45:u:3943:A:O4'	2.17	0.45
45:u:4773:C:C2	45:u:4863:G:C2	3.04	0.45
46:v:86:G:C2	46:v:92:C:C2	3.03	0.45
48:x:61:PRO:O	48:x:65:MET:CA	2.57	0.45
55:5:151:ILE:HA	55:5:154:VAL:HG12	1.98	0.45
55:5:625:ARG:HH11	55:5:629:GLU:HB3	1.82	0.45
3:C:181:LYS:HD2	45:u:2300:A:N1	2.31	0.45
24:Y:31:SER:OG	45:u:239:C:O3'	2.34	0.45
26:a:75:LEU:HD11	26:a:133:ALA:HA	1.98	0.45
26:a:84:GLU:O	26:a:88:VAL:HG23	2.16	0.45
34:i:39:PHE:O	34:i:43:MET:HB2	2.16	0.45
45:u:994:G:C6	45:u:995:C:C4	3.05	0.45
45:u:2097:U:O2	45:u:2097:U:O4'	2.33	0.45
45:u:2245:G:C6	45:u:2246:C:C4	3.05	0.45
45:u:4644:G:C6	45:u:4645:C:C4	3.05	0.45
45:u:4699:U:C4	45:u:4702:G:C6	3.05	0.45
48:x:38:THR:HG21	48:x:169:LEU:HD11	1.98	0.45
53:3:118:PHE:HD1	53:3:122:PHE:HZ	1.64	0.45
55:5:426:LEU:HG	55:5:430:MET:HE2	1.97	0.45
55:5:601:ARG:CG	55:5:601:ARG:NH1	2.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:240:LEU:HB3	2:B:241:PRO:HD2	1.96	0.45
3:C:86:ARG:HD3	45:u:376:A:OP1	2.16	0.45
4:D:146:LEU:HD11	4:D:159:VAL:CG1	2.47	0.45
5:E:113:PRO:O	42:r:112:ARG:NE	2.50	0.45
14:O:116:LYS:HD3	18:S:169:THR:HG21	1.98	0.45
45:u:1904:G:N2	45:u:2073:C:C2	2.84	0.45
45:u:1925:G:C6	45:u:1926:C:C4	3.05	0.45
45:u:3900:G:C2	45:u:4562:C:N3	2.84	0.45
45:u:4472:G:C6	45:u:4473:A:N7	2.84	0.45
45:u:4740:G:C6	45:u:4741:C:C4	3.04	0.45
48:x:401:MET:H	48:x:409:MET:HE2	1.80	0.45
5:E:174:PRO:O	5:E:177:LEU:N	2.50	0.45
6:F:171:LEU:HB2	6:F:189:MET:HE1	1.98	0.45
14:O:12:ARG:O	18:S:171:ARG:NH2	2.49	0.45
17:R:119:MET:HG3	17:R:123:LEU:HD22	1.97	0.45
45:u:216:C:C2	51:l:536:ARG:O	2.70	0.45
45:u:1196:G:C2	45:u:1197:C:C2	3.05	0.45
45:u:2567:G:C2	45:u:2568:C:C2	3.04	0.45
45:u:3690:U:H2'	45:u:3691:G:O4'	2.17	0.45
45:u:3782:C:C2	45:u:3811:G:C2	3.05	0.45
45:u:4587:G:C2	45:u:4716:C:C2	3.04	0.45
48:x:69:LEU:CD2	48:x:80:GLY:CA	2.95	0.45
48:x:176:GLY:HA2	48:x:457:TYR:CE1	2.31	0.45
48:x:184:ALA:HA	48:x:450:ALA:HB1	1.98	0.45
48:x:373:ALA:O	48:x:376:SER:OG	2.27	0.45
55:5:125:SER:O	55:5:128:THR:HG22	2.17	0.45
55:5:199:ALA:HB2	55:5:243:VAL:HA	1.98	0.45
55:5:280:HIS:O	55:5:284:ASP:CG	2.59	0.45
55:5:345:ILE:CD1	55:5:525:TRP:HE1	2.29	0.45
55:5:654:ALA:HB1	55:5:667:GLU:HG2	1.98	0.45
2:B:100:ARG:NH1	45:u:4911:A:OP2	2.49	0.45
2:B:154:LYS:HB2	2:B:154:LYS:HZ2	1.79	0.45
8:H:95:VAL:HG12	38:m:78:ILE:HD11	1.97	0.45
24:Y:10:ASP:O	24:Y:11:ARG:C	2.59	0.45
31:f:35:ALA:O	31:f:37:ASP:N	2.49	0.45
33:h:88:THR:O	33:h:91:MET:N	2.50	0.45
36:k:37:ARG:NH2	45:u:2537:A:OP2	2.50	0.45
45:u:467:U:H2'	45:u:467:U:O2	2.17	0.45
45:u:1072:C:O2	45:u:1072:C:H2'	2.17	0.45
45:u:1171:G:C6	45:u:1172:C:C4	3.04	0.45
45:u:1959:U:H1'	45:u:1961:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:4183:G:H2'	45:u:4183:G:N3	2.32	0.45
45:u:5001:U:H2'	45:u:5002:U:O4'	2.16	0.45
55:5:52:PHE:CD1	55:5:530:TYR:CD1	3.00	0.45
55:5:175:CYS:SG	55:5:205:MET:N	2.89	0.45
7:G:221:ALA:O	7:G:224:THR:OG1	2.34	0.45
45:u:199:G:C2	45:u:201:C:C2	3.05	0.45
45:u:504:G:O6	45:u:654:C:C4	2.70	0.45
45:u:994:G:C2	45:u:1050:C:C2	3.04	0.45
45:u:1070:G:C6	45:u:1071:C:N4	2.85	0.45
45:u:1365:C:O2	45:u:1366:G:C8	2.69	0.45
45:u:2711:G:H3'	45:u:2712:G:H5''	1.99	0.45
48:x:66:ARG:HA	48:x:66:ARG:NE	2.29	0.45
18:S:83:ARG:HH21	18:S:83:ARG:CG	2.29	0.45
32:g:26:PRO:HG2	45:u:2521:G:O2'	2.17	0.45
45:u:1277:G:N1	45:u:1278:C:C4	2.85	0.45
45:u:1946:G:O2'	45:u:1948:G:OP1	2.24	0.45
45:u:2322:G:C6	45:u:2323:C:C4	3.05	0.45
45:u:2698:G:C2	45:u:2699:C:C2	3.04	0.45
45:u:4136:G:C2	45:u:4137:C:C2	3.04	0.45
45:u:4240:G:C6	45:u:4241:C:C4	3.05	0.45
46:v:27:G:C2	46:v:28:C:C2	3.05	0.45
48:x:78:GLU:OE2	48:x:155:LEU:HD22	2.17	0.45
48:x:177:SER:HG	48:x:180:SER:H	1.58	0.45
5:E:157:ARG:HD3	5:E:266:TYR:CZ	2.52	0.45
5:E:173:GLY:O	5:E:174:PRO:C	2.60	0.45
42:r:17:LEU:HD23	42:r:17:LEU:C	2.42	0.45
45:u:100:C:O2	45:u:100:C:O4'	2.33	0.45
45:u:179:G:C2	45:u:180:C:C2	3.05	0.45
45:u:488:G:N2	45:u:489:C:C2	2.85	0.45
45:u:973:G:N2	45:u:974:C:C2	2.85	0.45
45:u:2715:G:C6	45:u:2716:C:C4	3.05	0.45
45:u:4109:G:C6	45:u:4110:C:C4	3.05	0.45
45:u:4666:G:C6	45:u:4667:C:C4	3.05	0.45
45:u:5017:G:C2	45:u:5018:C:C2	3.04	0.45
55:5:177:LEU:C	55:5:177:LEU:HD22	2.41	0.45
55:5:593:ILE:HD12	55:5:639:MET:HG2	1.99	0.45
6:F:49:ARG:NH1	45:u:974:C:O3'	2.49	0.44
9:I:14:ASN:O	9:I:128:ARG:NH2	2.45	0.44
11:L:74:ARG:NH2	45:u:76:A:N7	2.65	0.44
19:T:80:VAL:O	19:T:82:GLY:N	2.51	0.44
23:X:96:LEU:HG	23:X:140:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z:29:ILE:HD12	25:Z:29:ILE:N	2.32	0.44
30:e:53:ILE:HG22	45:u:437:G:H5'	1.99	0.44
45:u:994:G:C2	45:u:995:C:C2	3.05	0.44
45:u:1639:U:O2	45:u:1639:U:H2'	2.16	0.44
45:u:1823:G:C3'	45:u:1825:A:P	3.05	0.44
45:u:1840:G:C3'	45:u:1842:G:P	3.05	0.44
45:u:2065:G:C2	45:u:2066:C:C2	3.04	0.44
45:u:2659:A:N1	45:u:2672:C:O2'	2.40	0.44
45:u:2898:G:C6	45:u:2899:C:C4	3.05	0.44
45:u:4091:G:N2	45:u:4159:C:C2	2.85	0.44
45:u:4883:C:O2'	45:u:4884:G:P	2.74	0.44
46:v:117:G:C6	46:v:118:C:C4	3.05	0.44
48:x:61:PRO:O	48:x:65:MET:N	2.50	0.44
48:x:69:LEU:HD22	48:x:80:GLY:C	2.42	0.44
48:x:93:LEU:O	48:x:97:ALA:N	2.44	0.44
55:5:182:MET:HB3	55:5:198:CYS:HA	1.98	0.44
9:I:93:PRO:HB2	9:I:125:THR:HB	1.99	0.44
25:Z:54:THR:O	25:Z:56:ALA:N	2.50	0.44
44:t:97:ASN:N	44:t:98:ILE:HA	2.32	0.44
45:u:977:C:O2'	45:u:978:G:H5'	2.17	0.44
45:u:2793:G:H5''	45:u:2794:C:H5''	1.99	0.44
45:u:4147:G:C6	45:u:4148:C:C4	3.05	0.44
45:u:4713:G:C6	45:u:4714:C:C4	3.05	0.44
45:u:4874:A:H3'	45:u:4875:G:C5'	2.47	0.44
45:u:4904:G:N2	45:u:4905:C:C2	2.85	0.44
55:5:31:PHE:CE1	55:5:121:PRO:CD	2.93	0.44
11:L:19:GLN:HA	11:L:22:VAL:HG23	1.99	0.44
26:a:19:HIS:NE2	45:u:1338:G:N2	2.65	0.44
31:f:11:PHE:CE2	31:f:97:ILE:HD13	2.51	0.44
42:r:47:LYS:C	42:r:103:HIS:HD2	2.25	0.44
44:t:85:LEU:HD13	44:t:109:ILE:CG2	2.48	0.44
45:u:278:G:H4'	45:u:279:A:OP2	2.17	0.44
45:u:1098:G:C2	45:u:1099:C:C2	3.05	0.44
45:u:2270:G:C2	45:u:2271:C:C2	3.06	0.44
45:u:2481:G:C6	45:u:2482:C:C4	3.05	0.44
45:u:2594:C:O2	45:u:2752:G:C2	2.71	0.44
45:u:2715:G:C2	45:u:2716:C:C2	3.05	0.44
45:u:3729:U:H2'	45:u:3730:U:C6	2.52	0.44
45:u:4129:G:C6	45:u:4130:C:C4	3.05	0.44
45:u:4451:G:C6	45:u:4522:G:C8	3.05	0.44
46:v:111:C:H2'	46:v:112:U:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:94:G:H5'	47:w:94:G:C8	2.52	0.44
48:x:376:SER:O	48:x:379:TRP:N	2.47	0.44
55:5:131:THR:HG21	55:5:151:ILE:HG12	2.00	0.44
55:5:491:SER:O	55:5:588:TYR:OH	2.32	0.44
2:B:56:ILE:CG1	2:B:365:LEU:HD22	2.47	0.44
2:B:154:LYS:NZ	2:B:154:LYS:CB	2.81	0.44
12:M:37:LEU:HD23	18:S:100:LEU:HD11	1.98	0.44
30:e:23:HIS:HB2	30:e:53:ILE:HD11	1.99	0.44
35:j:9:GLY:HA3	45:u:2800:G:H1'	1.98	0.44
45:u:654:C:O2	45:u:654:C:H2'	2.16	0.44
45:u:1679:A:N1	45:u:4391:G:O2'	2.46	0.44
45:u:2288:G:C2	45:u:2290:C:C4	3.05	0.44
45:u:2609:G:C2	45:u:2731:C:O2	2.70	0.44
45:u:4349:C:H3'	45:u:4350:C:C5'	2.48	0.44
45:u:4749:C:O2	45:u:4749:C:O4'	2.32	0.44
53:3:92:PHE:CD1	53:3:92:PHE:O	2.70	0.44
53:3:93:LEU:C	53:3:133:PHE:CE1	2.95	0.44
55:5:611:HIS:HB3	55:5:612:ILE:HD12	2.00	0.44
3:C:86:ARG:HA	3:C:89:GLN:HG3	2.00	0.44
7:G:30:PRO:HG2	7:G:31:LEU:HD22	2.00	0.44
17:R:99:MET:O	17:R:103:ARG:HB2	2.17	0.44
35:j:13:ASN:OD1	35:j:13:ASN:N	2.50	0.44
41:p:17:ARG:NH2	45:u:1577:G:OP1	2.50	0.44
45:u:686:A:H3'	45:u:687:U:H5'	2.00	0.44
45:u:689:U:C2	45:u:690:C:C5	3.05	0.44
45:u:1744:U:H2'	45:u:1745:G:O4'	2.17	0.44
45:u:2909:C:O2	45:u:3586:G:C2	2.71	0.44
45:u:3670:C:O2'	45:u:3671:G:O4'	2.36	0.44
45:u:4088:C:H2'	45:u:4089:G:C8	2.53	0.44
45:u:4240:G:C2	45:u:4241:C:C2	3.06	0.44
45:u:4320:G:H2'	45:u:4321:U:O4'	2.18	0.44
45:u:5008:C:H2'	45:u:5009:G:O4'	2.16	0.44
47:w:68:G:H2'	47:w:69:U:O4'	2.17	0.44
50:z:69:GLY:H	50:z:70:PRO:HD3	1.76	0.44
55:5:177:LEU:CD1	55:5:177:LEU:C	2.85	0.44
1:A:90:CYS:CB	1:A:101:VAL:HG13	2.47	0.44
1:A:152:SER:OG	45:u:3661:G:N7	2.47	0.44
2:B:261:ARG:HB2	14:O:64:THR:HG21	2.00	0.44
11:L:104:ASN:OD1	11:L:110:LEU:HB2	2.18	0.44
13:N:198:LEU:HD23	13:N:198:LEU:HA	1.94	0.44
33:h:21:LEU:HD11	33:h:54:ILE:HG23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:17:LEU:HD12	42:r:36:ASN:HD21	1.82	0.44
45:u:1241:C:C2'	45:u:1242:G:OP1	2.65	0.44
45:u:1874:A:C5'	45:u:4218:U:O2	2.66	0.44
45:u:4666:G:C2	45:u:4667:C:C2	3.06	0.44
45:u:4754:G:N2	45:u:4880:C:C2	2.86	0.44
45:u:5020:G:C6	45:u:5021:C:C4	3.04	0.44
55:5:32:SER:HA	55:5:35:LEU:HD12	1.99	0.44
55:5:245:CYS:O	55:5:248:THR:OG1	2.35	0.44
2:B:385:LYS:NZ	45:u:5002:U:OP2	2.48	0.44
8:H:117:PHE:CE1	8:H:118:LEU:HD23	2.53	0.44
9:I:47:PRO:HB3	9:I:171:TRP:CE2	2.53	0.44
17:R:99:MET:N	17:R:99:MET:SD	2.91	0.44
45:u:52:G:N1	45:u:53:C:C4	2.86	0.44
45:u:1048:G:C2	45:u:1049:C:C2	3.06	0.44
45:u:2275:G:H8	45:u:2275:G:H5''	1.82	0.44
45:u:2559:G:C2	45:u:2560:C:C2	3.06	0.44
45:u:3900:G:C2	45:u:4562:C:C2	3.06	0.44
45:u:4109:G:C2	45:u:4110:C:C2	3.06	0.44
45:u:4207:C:C2	45:u:4226:G:N2	2.85	0.44
45:u:4482:U:N3	45:u:4483:C:C5	2.86	0.44
45:u:4890:G:C2	45:u:4930:C:C2	3.06	0.44
47:w:134:G:C6	47:w:135:C:C4	3.05	0.44
1:A:207:VAL:HG12	45:u:3919:C:C5'	2.48	0.44
5:E:262:GLN:N	45:u:4930:C:OP1	2.48	0.44
32:g:8:ARG:HB2	32:g:34:TYR:HE2	1.83	0.44
45:u:2:G:C2	45:u:3:C:C2	3.06	0.44
45:u:322:C:O2	45:u:4356:G:C2	2.71	0.44
45:u:952:G:C6	45:u:953:C:C4	3.06	0.44
45:u:1354:A:N1	45:u:1385:G:O2'	2.45	0.44
45:u:2315:G:C2	45:u:2325:C:O2	2.71	0.44
45:u:2457:G:C6	45:u:2458:C:C4	3.06	0.44
45:u:2612:G:C2	45:u:2613:C:C2	3.06	0.44
45:u:2612:G:C6	45:u:2613:C:C4	3.05	0.44
45:u:2738:C:O2'	45:u:2740:U:O2	2.35	0.44
45:u:3600:G:C2	45:u:3601:C:C2	3.06	0.44
45:u:3882:C:H2'	45:u:3883:U:C6	2.53	0.44
45:u:3891:A:H2'	45:u:3892:U:O4'	2.18	0.44
45:u:4142:C:C4	45:u:4143:G:N1	2.86	0.44
45:u:4904:G:C2	45:u:4905:C:C2	3.06	0.44
45:u:5038:A:H2'	45:u:5039:U:O4'	2.18	0.44
48:x:66:ARG:NE	48:x:72:ASN:CB	2.67	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:284:PHE:HB3	48:x:287:SER:HA	1.99	0.44
48:x:461:PHE:O	48:x:461:PHE:CD1	2.70	0.44
55:5:525:TRP:CZ3	55:5:599:MET:HE2	2.52	0.44
55:5:610:LYS:HA	55:5:615:HIS:NE2	2.33	0.44
55:5:688:LEU:HD13	55:5:689:VAL:HG23	1.99	0.44
3:C:224:ILE:HG22	3:C:227:ILE:HD13	1.99	0.44
3:C:262:ASP:O	3:C:271:ALA:O	2.36	0.44
6:F:92:ALA:HB3	6:F:127:LEU:HD21	2.00	0.44
15:P:41:ILE:HD12	15:P:150:LEU:HD13	1.99	0.44
41:p:4:ARG:NH1	45:u:1554:A:OP2	2.51	0.44
44:t:143:VAL:O	44:t:145:GLY:N	2.51	0.44
45:u:43:U:C2'	45:u:44:A:O5'	2.66	0.44
45:u:680:G:C6	45:u:681:G:C5	3.06	0.44
45:u:977:C:C3'	45:u:978:G:H5'	2.46	0.44
45:u:1326:A:OP2	45:u:4445:U:O2'	2.35	0.44
45:u:1691:G:C2	45:u:1692:C:C2	3.06	0.44
45:u:2490:U:O2'	45:u:2491:C:O4'	2.23	0.44
45:u:2654:C:N3	45:u:2681:G:C2	2.86	0.44
45:u:2664:G:N2	45:u:2671:C:C2	2.85	0.44
45:u:2816:G:C6	45:u:2817:C:C4	3.06	0.44
45:u:3861:A:H2'	45:u:3862:A:C8	2.53	0.44
45:u:4216:G:C2'	45:u:4217:G:H5'	2.48	0.44
45:u:5016:A:N6	45:u:5033:G:O2'	2.50	0.44
47:w:10:G:C2	47:w:11:C:C2	3.06	0.44
48:x:450:ALA:HA	48:x:453:ILE:HD12	2.00	0.44
15:P:18:ARG:HA	15:P:147:GLU:HA	1.99	0.43
22:W:44:ARG:HG2	22:W:44:ARG:HH11	1.81	0.43
45:u:217:C:H6	45:u:217:C:H2'	1.67	0.43
45:u:218:A:H1'	45:u:219:G:H8	1.83	0.43
45:u:469:C:N4	45:u:470:A:C6	2.86	0.43
45:u:1064:G:C2	45:u:1065:G:C4	3.06	0.43
45:u:1171:G:C2	45:u:1172:C:C2	3.05	0.43
45:u:1213:G:C6	45:u:1215:C:C4	3.06	0.43
45:u:2021:G:C2	45:u:2022:C:C2	3.06	0.43
45:u:2042:A:N3	45:u:4462:C:O2'	2.49	0.43
45:u:2376:A:H2'	45:u:2377:C:O4'	2.17	0.43
45:u:2468:U:C2	45:u:2473:A:N6	2.85	0.43
45:u:2871:A:H2'	45:u:2872:C:O4'	2.18	0.43
45:u:4232:U:H1'	45:u:4233:A:OP2	2.18	0.43
45:u:4408:G:C6	45:u:4409:C:C4	3.06	0.43
46:v:25:G:C6	46:v:26:C:C4	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:247:ALA:O	48:x:440:ALA:HB3	2.13	0.43
48:x:401:MET:HG2	48:x:409:MET:HE2	2.00	0.43
55:5:30:SER:HG	55:5:34:ARG:HH22	1.66	0.43
6:F:146:TYR:CE2	6:F:239:GLU:CB	3.01	0.43
12:M:116:LYS:HE3	14:O:201:PHE:CE2	2.53	0.43
14:O:27:VAL:CG1	14:O:98:ALA:HB1	2.47	0.43
32:g:5:LEU:HD21	32:g:22:LEU:HD12	2.00	0.43
45:u:476:G:C2	45:u:679:C:C2	3.06	0.43
45:u:723:A:C2	45:u:724:C:C6	3.06	0.43
45:u:1196:G:C6	45:u:1197:C:C4	3.05	0.43
45:u:1358:G:N3	45:u:1359:G:N7	2.66	0.43
45:u:1724:G:C4'	45:u:1725:U:OP2	2.63	0.43
45:u:3705:G:C6	45:u:3706:C:C4	3.06	0.43
45:u:4681:A:H2'	45:u:4682:U:O4'	2.18	0.43
47:w:118:C:C2	47:w:133:G:C2	3.06	0.43
5:E:132:HIS:CE1	45:u:711:A:HI'	2.52	0.43
26:a:97:ALA:O	26:a:98:ALA:HB3	2.18	0.43
45:u:192:G:C2	45:u:250:C:C2	3.05	0.43
45:u:254:G:C2	45:u:255:C:C2	3.06	0.43
45:u:744:G:H2'	45:u:745:G:C8	2.53	0.43
45:u:1265:G:OP1	45:u:2115:G:N1	2.51	0.43
45:u:1268:G:C4	45:u:2111:G:N2	2.86	0.43
45:u:1358:G:O6	45:u:1379:C:N3	2.52	0.43
45:u:1691:G:C6	45:u:1692:C:C4	3.06	0.43
45:u:1846:G:C2	45:u:1847:C:C2	3.07	0.43
45:u:2358:G:H2'	45:u:2359:U:O4'	2.19	0.43
45:u:2682:G:N2	45:u:2683:C:C2	2.85	0.43
45:u:4416:G:N1	45:u:4417:C:C4	2.86	0.43
45:u:4737:G:C6	45:u:4738:C:C4	3.07	0.43
45:u:4919:G:N2	45:u:4920:C:C2	2.87	0.43
48:x:35:THR:OG1	48:x:36:ALA:N	2.50	0.43
48:x:58:SER:HA	48:x:73:ARG:HE	1.83	0.43
48:x:417:ILE:HD13	48:x:417:ILE:HA	1.85	0.43
52:2:15:UNK:O	52:2:17:UNK:N	2.51	0.43
55:5:9:LEU:HG	55:5:13:LYS:HB3	2.00	0.43
55:5:67:LYS:NZ	58:8:600:UNK:H2	2.16	0.43
55:5:345:ILE:HD11	55:5:595:LYS:CD	2.36	0.43
1:A:30:ARG:O	1:A:163:ARG:NH2	2.52	0.43
13:N:68:ARG:HG2	45:u:302:C:OP1	2.18	0.43
17:R:4:LEU:HD22	17:R:32:ILE:HG22	1.99	0.43
26:a:13:GLY:HA2	45:u:1660:U:H3'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:28:ASN:HB3	45:u:4996:C:OP1	2.18	0.43
45:u:218:A:N3	45:u:218:A:H2'	2.32	0.43
45:u:307:A:N3	45:u:310:G:O2'	2.41	0.43
45:u:469:C:C4	45:u:470:A:N7	2.86	0.43
45:u:744:G:H2'	45:u:745:G:H8	1.83	0.43
45:u:1072:C:H1'	45:u:1073:G:C8	2.54	0.43
45:u:1271:G:H3'	45:u:1272:C:H5'	2.00	0.43
45:u:1374:G:C6	45:u:1375:C:C4	3.06	0.43
45:u:1436:C:O5'	45:u:2119:C:N4	2.51	0.43
45:u:1655:C:H2'	45:u:1656:U:H5''	2.00	0.43
45:u:1947:U:O2	45:u:1947:U:H2'	2.17	0.43
45:u:4187:G:H2'	45:u:4188:U:O4'	2.19	0.43
3:C:28:PHE:HA	3:C:129:ALA:HA	2.00	0.43
8:H:55:LEU:HD22	8:H:77:VAL:HG11	2.00	0.43
11:L:29:PRO:CB	45:u:1371:A:H2'	2.49	0.43
16:Q:89:ASP:OD1	16:Q:91:ARG:NH2	2.51	0.43
19:T:85:LEU:HD13	45:u:4305:G:C2	2.53	0.43
29:d:22:THR:HG22	29:d:89:SER:HB2	2.01	0.43
35:j:72:ARG:NH2	47:w:94:G:OP2	2.52	0.43
45:u:1430:C:O2	45:u:1455:G:C2	2.70	0.43
45:u:1912:G:C2	45:u:1913:C:C2	3.07	0.43
45:u:1928:C:N4	45:u:2054:U:O2	2.51	0.43
45:u:2021:G:C6	45:u:2022:C:C4	3.06	0.43
45:u:2050:G:C6	45:u:2051:C:C4	3.07	0.43
45:u:2898:G:C2	45:u:2899:C:C2	3.06	0.43
45:u:4913:G:HO2'	45:u:4914:C:C1'	2.32	0.43
48:x:29:LYS:HG3	53:3:118:PHE:HE2	0.72	0.43
54:4:9:ILE:HA	54:4:12:ASN:HD22	1.83	0.43
55:5:127:THR:CA	55:5:174:PHE:CE2	3.02	0.43
55:5:348:SER:HB2	55:5:598:TRP:CZ2	2.42	0.43
1:A:233:ARG:O	1:A:235:VAL:HB	2.17	0.43
2:B:10:ARG:C	2:B:10:ARG:CD	2.91	0.43
7:G:87:LEU:HD11	7:G:91:THR:HG21	2.01	0.43
21:V:20:LEU:HD13	21:V:26:ILE:HG21	2.01	0.43
40:o:77:CYS:SG	61:o:201:ZN:ZN	1.79	0.43
45:u:1048:G:C6	45:u:1049:C:C4	3.06	0.43
45:u:1270:A:C2'	45:u:1271:G:O5'	2.67	0.43
45:u:1280:C:C2	45:u:1282:G:C4	3.06	0.43
45:u:4129:G:C2	45:u:4130:C:C2	3.06	0.43
45:u:4948:C:H3'	45:u:4949:G:N2	2.33	0.43
45:u:5060:A:O2'	45:u:5061:A:OP1	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:z:83:SER:O	50:z:87:LEU:CB	2.65	0.43
55:5:176:MET:SD	55:5:215:LEU:HD13	2.58	0.43
55:5:378:CYS:HB3	55:5:390:ILE:HD11	1.99	0.43
2:B:378:ARG:NE	22:W:32:LEU:HD21	2.34	0.43
6:F:92:ALA:CB	6:F:127:LEU:HD21	2.49	0.43
13:N:180:PHE:O	13:N:182:HIS:N	2.52	0.43
15:P:118:GLN:NE2	45:u:423:G:N3	2.66	0.43
19:T:14:MET:HE1	19:T:55:LYS:HB2	2.00	0.43
26:a:17:HIS:CE1	45:u:1338:G:H2'	2.53	0.43
45:u:125:C:C2	45:u:145:G:C2	3.06	0.43
45:u:174:C:C2	45:u:263:G:C2	3.07	0.43
45:u:642:G:C2	45:u:643:C:C4	3.06	0.43
45:u:744:G:C2	45:u:921:C:C2	3.06	0.43
45:u:972:C:H2'	45:u:973:G:H8	1.84	0.43
45:u:1280:C:C4	45:u:1282:G:O6	2.72	0.43
45:u:1296:G:C1'	45:u:1297:U:P	3.06	0.43
45:u:2606:G:C2	45:u:2607:C:C2	3.07	0.43
45:u:4090:G:N2	45:u:4160:C:C2	2.86	0.43
45:u:4222:G:C6	45:u:4223:C:C4	3.07	0.43
45:u:4250:G:C2	45:u:4259:C:C2	3.06	0.43
46:v:110:G:C2	46:v:111:C:C2	3.06	0.43
48:x:133:MET:HE2	48:x:311:ARG:HH22	1.83	0.43
48:x:241:ASN:HB3	48:x:244:ASN:HB2	2.01	0.43
55:5:19:LYS:HD3	55:5:145:LEU:HD11	2.01	0.43
1:A:207:VAL:HG12	45:u:3919:C:H4'	2.00	0.43
2:B:43:LEU:HD13	2:B:196:TRP:HH2	1.83	0.43
23:X:119:ILE:HG23	23:X:120:ASP:N	2.33	0.43
27:b:36:ASP:N	27:b:36:ASP:OD1	2.52	0.43
45:u:76:A:C5	45:u:77:U:C5	3.06	0.43
45:u:212:A:C4	45:u:213:G:N7	2.87	0.43
45:u:468:U:O2	45:u:468:U:H2'	2.18	0.43
45:u:686:A:C2'	45:u:687:U:H5'	2.49	0.43
45:u:691:C:N3	45:u:692:A:C5	2.87	0.43
45:u:1959:U:H4'	45:u:1961:G:O4'	2.19	0.43
45:u:2088:A:O2'	45:u:2089:G:P	2.76	0.43
45:u:2256:C:H1'	45:u:2257:C:OP2	2.19	0.43
45:u:2712:G:N1	45:u:2713:C:C4	2.87	0.43
45:u:4731:G:H4'	45:u:4732:G:H5'	1.99	0.43
50:z:82:ALA:HA	50:z:85:PHE:HB3	2.01	0.43
55:5:349:VAL:CG1	55:5:352:HIS:HD2	2.27	0.43
1:A:103:PRO:HA	1:A:163:ARG:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:95:ASP:OD1	5:E:96:LYS:N	2.49	0.43
13:N:94:PHE:CE2	13:N:96:ARG:HB2	2.54	0.43
35:j:81:GLY:O	35:j:82:THR:CG2	2.67	0.43
45:u:156:G:N2	45:u:157:U:O4	2.52	0.43
45:u:1090:G:C2	45:u:1091:C:C2	3.06	0.43
45:u:1404:G:C2	45:u:1405:C:C2	3.06	0.43
45:u:2076:G:C6	45:u:2077:C:C4	3.07	0.43
47:w:134:G:C2	47:w:135:C:C2	3.06	0.43
48:x:458:PHE:CE2	49:y:36:ILE:HG22	2.53	0.43
49:y:33:PHE:O	49:y:37:ALA:CB	2.66	0.43
55:5:139:LYS:HG2	55:5:140:ASP:HB2	2.01	0.43
55:5:177:LEU:HD13	55:5:177:LEU:O	2.19	0.43
5:E:43:ASN:HB3	5:E:58:MET:SD	2.59	0.43
6:F:175:ALA:O	6:F:179:ARG:HB2	2.19	0.43
11:L:163:LYS:NZ	45:u:509:A:H5'	2.34	0.43
22:W:44:ARG:HH11	22:W:44:ARG:CG	2.32	0.43
25:Z:136:PHE:OXT	32:g:90:ARG:NH1	2.51	0.43
36:k:32:VAL:HG11	36:k:53:ALA:HB1	2.00	0.43
45:u:158:A:H5''	45:u:159:C:H2'	1.99	0.43
45:u:179:G:C6	45:u:180:C:C4	3.07	0.43
45:u:202:C:C2	45:u:214:G:N2	2.87	0.43
45:u:301:G:C2	45:u:302:C:C2	3.07	0.43
45:u:1757:U:C2	45:u:1758:G:C8	3.07	0.43
45:u:1942:A:N3	45:u:4432:C:O2'	2.44	0.43
45:u:1959:U:OP1	45:u:1960:A:O3'	2.37	0.43
45:u:2567:G:C6	45:u:2568:C:C4	3.07	0.43
45:u:2703:G:C2	45:u:2704:C:C2	3.06	0.43
45:u:4508:C:N3	45:u:4512:U:H5	2.16	0.43
55:5:379:PHE:HD1	55:5:379:PHE:HA	1.73	0.43
55:5:480:SER:O	55:5:484:SER:OG	2.32	0.43
15:P:118:GLN:HE22	45:u:423:G:H21	1.66	0.42
42:r:46:ARG:HH22	42:r:67:ARG:HH11	1.67	0.42
45:u:258:G:C2	45:u:259:C:C2	3.06	0.42
45:u:687:U:C4	45:u:688:U:C4	3.07	0.42
45:u:1270:A:C5	45:u:1271:G:H1'	2.53	0.42
45:u:1379:C:O2	45:u:1379:C:O4'	2.37	0.42
45:u:1539:G:C6	45:u:1540:C:C4	3.06	0.42
45:u:1755:C:O2	45:u:1755:C:O2'	2.22	0.42
45:u:1811:G:C6	45:u:1812:C:C4	3.07	0.42
45:u:2542:G:C2	45:u:2775:C:C2	3.07	0.42
45:u:4124:G:O2'	45:u:4125:C:OP1	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:4139:G:C6	45:u:4140:C:C4	3.06	0.42
45:u:4147:G:C2	45:u:4148:C:C2	3.07	0.42
45:u:4898:G:N2	45:u:4923:C:C2	2.87	0.42
45:u:4904:G:C6	45:u:4905:C:C4	3.07	0.42
47:w:60:G:N2	47:w:64:U:C2	2.87	0.42
48:x:236:ARG:H	48:x:241:ASN:ND2	2.17	0.42
50:z:71:VAL:H	50:z:72:PRO:HD2	1.83	0.42
55:5:214:PHE:CB	62:5:809:9UB:C06	2.97	0.42
55:5:682:TYR:CE2	55:5:684:THR:HA	2.54	0.42
2:B:2:SER:N	45:u:4517:A:OP2	2.53	0.42
3:C:114:ARG:HB3	13:N:203:TYR:CD1	2.54	0.42
14:O:48:TYR:CE2	14:O:52:LEU:HD11	2.54	0.42
45:u:127:G:C2	45:u:128:C:C2	3.07	0.42
45:u:469:C:N4	45:u:470:A:C5	2.87	0.42
45:u:504:G:H22	45:u:654:C:H1'	1.84	0.42
45:u:681:G:C6	45:u:682:G:C5	3.07	0.42
45:u:689:U:C3'	45:u:690:C:H5''	2.49	0.42
45:u:702:U:H2'	45:u:703:G:H4'	2.01	0.42
45:u:747:A:C2	45:u:918:G:N1	2.87	0.42
45:u:976:G:C6	45:u:977:C:N3	2.88	0.42
45:u:1466:G:N2	45:u:1467:C:C2	2.88	0.42
45:u:1484:G:H2'	45:u:1484:G:N3	2.34	0.42
45:u:1584:G:C2	45:u:1585:C:C2	3.08	0.42
45:u:1811:G:C2	45:u:1812:C:C2	3.07	0.42
45:u:2034:G:C6	45:u:2035:C:C4	3.06	0.42
45:u:2468:U:N3	45:u:2473:A:C6	2.83	0.42
45:u:2468:U:C4	45:u:2473:A:C6	3.07	0.42
45:u:3590:G:N1	45:u:3591:C:C2	2.86	0.42
45:u:3597:G:C6	45:u:3598:C:C4	3.07	0.42
45:u:4713:G:C2	45:u:4714:C:C2	3.08	0.42
47:w:2:G:N3	47:w:2:G:H2'	2.34	0.42
47:w:10:G:C6	47:w:11:C:C4	3.07	0.42
55:5:144:GLY:HA2	55:5:147:ALA:HB3	2.01	0.42
5:E:116:ASP:N	5:E:116:ASP:OD1	2.52	0.42
30:e:81:ASN:HA	30:e:111:ILE:HD11	2.01	0.42
35:j:70:VAL:HG22	35:j:73:ARG:NH2	2.33	0.42
42:r:130:ARG:C	42:r:130:ARG:CD	2.86	0.42
45:u:298:G:C2	45:u:299:C:C2	3.07	0.42
45:u:681:G:C2	45:u:682:G:H1'	2.54	0.42
45:u:742:G:C2	45:u:923:C:C2	3.07	0.42
45:u:1416:G:C6	45:u:1417:C:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1431:C:C2	45:u:1454:G:N2	2.87	0.42
45:u:1550:G:C2	45:u:1579:C:O2	2.72	0.42
45:u:2294:G:N2	45:u:2295:C:C2	2.87	0.42
45:u:2468:U:C2	45:u:2469:C:C5	3.08	0.42
45:u:2481:G:C2	45:u:2482:C:C2	3.07	0.42
45:u:2862:G:N3	45:u:3624:A:H2'	2.34	0.42
48:x:62:PHE:O	48:x:66:ARG:N	2.49	0.42
48:x:431:LEU:HD23	48:x:448:LEU:HD21	1.99	0.42
48:x:441:ILE:HB	48:x:444:GLY:H	1.84	0.42
6:F:92:ALA:HA	6:F:147:PRO:HD3	2.02	0.42
14:O:27:VAL:HG13	14:O:98:ALA:HB1	2.01	0.42
30:e:87:VAL:HG13	42:r:25:TYR:CD1	2.53	0.42
31:f:30:ILE:HD11	31:f:84:VAL:HG11	2.01	0.42
31:f:93:PRO:O	31:f:94:ALA:HB3	2.19	0.42
40:o:19:GLN:NE2	40:o:72:CYS:SG	2.92	0.42
45:u:5:A:C6	45:u:6:C:C4	3.07	0.42
45:u:76:A:C6	45:u:77:U:C5	3.08	0.42
45:u:93:G:O2'	45:u:94:A:O5'	2.37	0.42
45:u:963:G:H2'	45:u:963:G:N3	2.35	0.42
45:u:1234:G:H2'	45:u:1235:G:C8	2.55	0.42
45:u:1925:G:C2	45:u:1926:C:C2	3.06	0.42
45:u:4139:G:C2	45:u:4140:C:C2	3.07	0.42
45:u:4212:A:C2	45:u:4218:U:C5	3.07	0.42
45:u:4462:C:C2	45:u:4515:G:N2	2.88	0.42
48:x:47:GLN:C	48:x:75:THR:CB	2.89	0.42
48:x:69:LEU:HD23	48:x:80:GLY:CA	2.49	0.42
48:x:268:LYS:HG3	48:x:402:ARG:HD2	2.00	0.42
48:x:453:ILE:O	48:x:457:TYR:HB2	2.20	0.42
55:5:34:ARG:NH2	55:5:124:SER:HB3	2.34	0.42
55:5:661:ASP:HB2	55:5:666:ALA:HB3	2.01	0.42
3:C:342:ARG:HG3	3:C:342:ARG:HH11	1.84	0.42
4:D:22:ARG:NH1	4:D:28:THR:OG1	2.53	0.42
4:D:207:TYR:CE1	46:v:33:U:C6	3.08	0.42
5:E:149:LEU:HD11	5:E:191:ILE:HG13	2.02	0.42
9:I:87:ILE:HG12	9:I:138:ILE:CG1	2.45	0.42
9:I:184:MET:CE	9:I:190:LEU:CG	2.78	0.42
24:Y:19:PHE:O	24:Y:26:ARG:NH2	2.52	0.42
44:t:162:CYS:N	44:t:163:PRO:CD	2.83	0.42
45:u:209:U:N3	45:u:211:G:C8	2.88	0.42
45:u:517:C:C2	45:u:645:G:N2	2.88	0.42
45:u:978:G:OP2	45:u:979:C:OP2	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:2052:G:C6	45:u:2053:C:C4	3.08	0.42
45:u:2609:G:N1	45:u:2731:C:C2	2.88	0.42
45:u:2703:G:C6	45:u:2704:C:C4	3.08	0.42
45:u:4213:A:N6	45:u:4218:U:N3	2.61	0.42
45:u:5031:G:C6	45:u:5032:C:C4	3.08	0.42
46:v:93:G:C2	46:v:94:C:C2	3.07	0.42
48:x:187:ILE:HD13	48:x:447:ILE:HA	2.02	0.42
55:5:117:VAL:HG23	55:5:164:GLY:HA2	2.01	0.42
55:5:355:THR:HB	55:5:359:SER:OG	2.20	0.42
2:B:114:CYS:SG	2:B:180:LEU:HD11	2.59	0.42
3:C:161:TYR:HD1	3:C:166:GLU:OE2	2.02	0.42
3:C:354:ALA:O	3:C:358:LEU:HG	2.20	0.42
5:E:48:ARG:NH2	45:u:1281:G:C4	2.88	0.42
12:M:34:ASN:ND2	45:u:1925:G:OP1	2.52	0.42
17:R:4:LEU:HD11	17:R:29:THR:HG23	2.02	0.42
42:r:64:MET:HE1	42:r:102:TYR:CD1	2.54	0.42
44:t:22:VAL:HG13	44:t:48:LYS:HE2	2.00	0.42
45:u:199:G:C2	45:u:201:C:C4	3.07	0.42
45:u:1090:G:C6	45:u:1091:C:C4	3.08	0.42
45:u:1416:G:C2	45:u:1417:C:C2	3.07	0.42
45:u:1431:C:C2	45:u:1454:G:C2	3.06	0.42
45:u:1612:G:N3	45:u:1612:G:C2'	2.83	0.42
45:u:2526:C:N4	45:u:2527:A:N6	2.67	0.42
45:u:2712:G:C2	45:u:2713:C:C2	3.08	0.42
45:u:3753:G:O2'	45:u:3754:G:H5'	2.20	0.42
47:w:53:G:C6	47:w:54:C:C4	3.07	0.42
48:x:207:MET:SD	48:x:207:MET:N	2.89	0.42
48:x:443:SER:HB3	48:x:447:ILE:HD12	1.83	0.42
55:5:29:LEU:HD23	55:5:29:LEU:HA	1.88	0.42
55:5:544:ASN:O	55:5:546:THR:HG23	2.16	0.42
55:5:635:LEU:HA	55:5:640:TYR:CD2	2.54	0.42
4:D:44:TYR:CD1	45:u:1823:G:H4'	2.55	0.42
5:E:225:GLU:HG3	42:r:135:LYS:HE2	1.21	0.42
6:F:164:ILE:HB	6:F:169:ILE:HD12	2.02	0.42
8:H:117:PHE:CZ	8:H:118:LEU:HD23	2.54	0.42
8:H:134:CYS:SG	8:H:144:LEU:HD23	2.59	0.42
11:L:50:PRO:HD2	33:h:119:TYR:HE2	1.85	0.42
14:O:85:ARG:NH2	45:u:3887:C:OP2	2.45	0.42
24:Y:55:VAL:HG13	24:Y:104:VAL:HG13	2.02	0.42
31:f:18:LEU:HD23	31:f:19:ARG:NH1	2.34	0.42
36:k:11:PHE:HB3	36:k:45:LEU:HD22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:l:38:ASN:O	45:u:362:A:N1	2.53	0.42
38:m:94:MET:HG2	38:m:105:PRO:HA	2.01	0.42
45:u:165:A:H3'	45:u:166:C:H6	1.85	0.42
45:u:472:C:N3	45:u:473:C:N3	2.63	0.42
45:u:709:C:H2'	45:u:710:G:O4'	2.20	0.42
45:u:952:G:H2'	45:u:953:C:O4'	2.20	0.42
45:u:1098:G:C6	45:u:1099:C:C4	3.08	0.42
45:u:1806:G:C2	45:u:1807:C:C2	3.08	0.42
45:u:2831:G:C2	45:u:3855:C:C2	3.08	0.42
45:u:3724:A:C6	45:u:3725:G:C5	3.08	0.42
45:u:3868:G:N2	45:u:3900:G:O2'	2.53	0.42
45:u:3870:C:C2	45:u:3886:G:N2	2.87	0.42
45:u:4072:C:H2'	45:u:4073:A:O4'	2.20	0.42
45:u:4094:G:H2'	45:u:4095:G:C1'	2.50	0.42
45:u:4274:A:H2'	45:u:4275:G:C8	2.54	0.42
45:u:4901:G:C2	45:u:4921:C:C2	3.08	0.42
45:u:4920:C:H2'	45:u:4921:C:C6	2.55	0.42
48:x:155:LEU:HA	48:x:155:LEU:HD23	1.63	0.42
2:B:242:ARG:NH2	45:u:1591:U:OP2	2.41	0.42
4:D:111:ASN:C	4:D:111:ASN:HD22	2.28	0.42
5:E:43:ASN:HD22	5:E:43:ASN:C	2.28	0.42
5:E:208:LEU:HA	5:E:212:TYR:HD2	1.84	0.42
6:F:168:ARG:HD2	6:F:211:TRP:CD1	2.55	0.42
19:T:40:VAL:HG13	19:T:96:ILE:HG23	2.01	0.42
35:j:39:TYR:O	35:j:40:PRO:C	2.60	0.42
36:k:23:VAL:HG22	36:k:23:VAL:O	2.20	0.42
43:s:145:THR:HG22	43:s:154:ILE:HG13	2.01	0.42
45:u:689:U:O2	45:u:689:U:H2'	2.20	0.42
45:u:952:G:C2	45:u:953:C:C2	3.07	0.42
45:u:1075:G:C6	45:u:1076:C:C4	3.07	0.42
45:u:1736:A:C2	45:u:1794:A:C4	3.08	0.42
45:u:1755:C:C3'	45:u:1756:U:H5''	2.50	0.42
45:u:1969:G:O2'	45:u:1970:A:C5'	2.66	0.42
45:u:2793:G:C6	45:u:2797:C:N4	2.86	0.42
45:u:3769:C:H2'	45:u:3770:U:O4'	2.20	0.42
45:u:4093:G:C6	45:u:4094:G:N7	2.88	0.42
45:u:4269:G:C2	45:u:4270:C:C2	3.08	0.42
45:u:4326:G:C6	45:u:4327:C:C4	3.07	0.42
45:u:4530:U:H2'	45:u:4531:U:C6	2.55	0.42
45:u:4891:G:C2	45:u:4929:C:C2	3.07	0.42
45:u:4931:G:N3	45:u:4931:G:H2'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:417:ILE:O	48:x:421:ALA:N	2.52	0.42
1:A:196:TRP:CG	1:A:197:PRO:N	2.86	0.42
1:A:243:THR:HG21	45:u:3748:A:O4'	2.20	0.42
2:B:36:ASP:OD2	2:B:39:LYS:CE	2.62	0.42
5:E:225:GLU:HG3	42:r:135:LYS:HE3	1.35	0.42
8:H:5:LEU:HD22	8:H:60:TRP:CH2	2.55	0.42
13:N:179:LYS:O	45:u:298:G:H5'	2.20	0.42
42:r:33:LYS:HD2	42:r:40:TYR:CE2	2.54	0.42
42:r:118:LEU:CB	42:r:121:GLN:HE21	2.32	0.42
45:u:116:G:C2	45:u:117:C:C2	3.08	0.42
45:u:284:G:C2	45:u:304:C:O2	2.73	0.42
45:u:479:G:C2	45:u:480:C:C2	3.07	0.42
45:u:707:C:H42	45:u:1290:G:H1	1.68	0.42
45:u:1075:G:N2	45:u:1076:C:C2	2.88	0.42
45:u:1374:G:C2	45:u:1375:C:C2	3.07	0.42
45:u:4395:U:C6	45:u:4395:U:H5'	2.55	0.42
45:u:4901:G:N1	45:u:4921:C:C4	2.88	0.42
45:u:5028:G:C2	45:u:5029:C:C2	3.07	0.42
47:w:139:G:C2	47:w:140:C:C2	3.08	0.42
48:x:34:TRP:HZ3	50:z:74:LEU:HD11	1.84	0.42
48:x:288:ASN:ND2	48:x:428:ILE:HG13	2.35	0.42
55:5:207:SER:OG	55:5:208:SER:N	2.53	0.42
55:5:420:ILE:O	55:5:424:GLN:N	2.53	0.42
55:5:472:THR:O	55:5:476:THR:OG1	2.27	0.42
10:J:15:LEU:HD11	10:J:157:ILE:HG23	2.01	0.42
19:T:109:VAL:HG13	45:u:1803:G:C6	2.55	0.42
23:X:83:THR:O	48:x:404:HIS:NE2	2.50	0.42
45:u:258:G:C6	45:u:259:C:C4	3.08	0.42
45:u:685:C:O2	45:u:685:C:H2'	2.20	0.42
45:u:1367:C:H1'	45:u:1370:G:C8	2.54	0.42
45:u:1448:G:C6	45:u:1449:C:C4	3.08	0.42
45:u:1557:C:C2	45:u:1571:G:N2	2.87	0.42
45:u:1557:C:C2	45:u:1571:G:C2	3.07	0.42
45:u:2771:G:C2	45:u:2772:C:C2	3.08	0.42
45:u:3590:G:C6	45:u:3591:C:C4	3.07	0.42
45:u:4181:U:O4	45:u:4182:G:C6	2.73	0.42
45:u:4247:G:C2	45:u:4262:C:C2	3.08	0.42
45:u:4283:G:C6	45:u:4284:C:N4	2.88	0.42
45:u:4371:G:C5	45:u:4372:U:C4	3.07	0.42
45:u:4583:C:C2	45:u:4718:G:C2	3.08	0.42
47:w:31:G:C2	47:w:32:C:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:244:ASN:HA	48:x:439:GLY:O	2.20	0.42
48:x:394:LEU:HD23	48:x:394:LEU:HA	1.78	0.42
48:x:418:PRO:O	48:x:421:ALA:HB3	2.20	0.42
55:5:586:THR:HG23	55:5:687:TRP:HZ2	1.85	0.42
2:B:41:VAL:HG21	2:B:196:TRP:CG	2.55	0.41
14:O:15:LEU:HD11	14:O:129:LEU:HD13	2.01	0.41
15:P:36:ILE:CD1	15:P:48:LEU:HD11	2.48	0.41
21:V:20:LEU:HB2	21:V:55:ALA:O	2.19	0.41
27:b:45:PHE:CD1	45:u:1815:G:N7	2.88	0.41
40:o:55:ILE:HD12	40:o:57:ARG:NH2	2.35	0.41
45:u:127:G:C6	45:u:128:C:C4	3.08	0.41
45:u:1075:G:C6	45:u:1076:C:N4	2.88	0.41
45:u:1205:G:C2	45:u:1206:C:C2	3.08	0.41
45:u:1329:G:C8	45:u:1329:G:H3'	2.55	0.41
45:u:1781:U:C4	45:u:1782:U:C5	3.08	0.41
45:u:2313:A:O2'	45:u:2314:G:OP1	2.22	0.41
45:u:2463:G:C2	45:u:2464:C:C2	3.07	0.41
45:u:2606:G:C6	45:u:2607:C:C4	3.08	0.41
45:u:2645:G:C6	45:u:2646:C:C4	3.07	0.41
45:u:4966:A:N1	45:u:4967:A:C6	2.88	0.41
53:3:52:VAL:HG13	53:3:53:ILE:HG13	2.02	0.41
55:5:9:LEU:HD23	55:5:9:LEU:H	1.85	0.41
55:5:677:VAL:HG23	55:5:678:LEU:HG	2.02	0.41
5:E:62:LYS:NZ	45:u:978:G:P	2.83	0.41
6:F:111:LEU:HD23	6:F:111:LEU:HA	1.92	0.41
7:G:157:ILE:HG23	7:G:167:VAL:HG11	2.01	0.41
9:I:49:CYS:HB2	9:I:172:GLY:O	2.21	0.41
20:U:21:PHE:CD1	20:U:80:LYS:HG2	2.55	0.41
25:Z:36:ARG:CD	25:Z:74:VAL:HG11	2.50	0.41
25:Z:38:TYR:CE1	25:Z:76:ASN:OD1	2.73	0.41
29:d:78:ARG:HG2	29:d:78:ARG:HH11	1.83	0.41
45:u:212:A:C2	45:u:213:G:C6	3.08	0.41
45:u:742:G:N2	45:u:923:C:C2	2.88	0.41
45:u:1275:G:C2	45:u:1276:C:C2	3.08	0.41
45:u:1359:G:C5	45:u:1360:G:C5	3.07	0.41
45:u:1484:G:N3	45:u:1484:G:C2'	2.82	0.41
45:u:1615:C:H2'	45:u:1616:U:O4'	2.19	0.41
45:u:1958:A:C4'	45:u:1962:A:O2'	2.63	0.41
45:u:2050:G:C2	45:u:2051:C:C2	3.08	0.41
45:u:2273:G:C2	45:u:2274:C:C2	3.08	0.41
45:u:2311:C:C2	45:u:2328:G:N2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:2661:U:HO2'	45:u:2662:G:P	2.43	0.41
45:u:4131:G:C6	45:u:4132:C:C4	3.08	0.41
45:u:4433:G:C2	45:u:4434:C:C2	3.09	0.41
45:u:4583:C:N3	45:u:4718:G:C2	2.88	0.41
45:u:5031:G:C2	45:u:5032:C:C2	3.09	0.41
47:w:46:G:N2	47:w:47:C:C2	2.88	0.41
48:x:461:PHE:CD1	48:x:461:PHE:C	2.98	0.41
53:3:63:THR:O	53:3:65:GLU:N	2.53	0.41
53:3:118:PHE:HD1	53:3:122:PHE:CZ	2.38	0.41
55:5:71:TRP:C	55:5:83:ILE:HG12	2.35	0.41
55:5:504:ASP:HB3	55:5:688:LEU:CB	2.49	0.41
1:A:107:MET:SD	1:A:113:VAL:CG1	3.09	0.41
3:C:229:LEU:HD22	3:C:229:LEU:N	2.35	0.41
4:D:64:ILE:CD1	4:D:109:LEU:HD22	2.50	0.41
8:H:95:VAL:CG1	38:m:78:ILE:HD11	2.51	0.41
15:P:10:ASN:N	15:P:10:ASN:OD1	2.53	0.41
40:o:39:ARG:NH1	45:u:295:A:OP2	2.52	0.41
45:u:29:G:C2	45:u:30:C:C2	3.08	0.41
45:u:196:C:C2	45:u:246:G:C2	3.08	0.41
45:u:385:A:C2	45:u:386:A:C5	3.08	0.41
45:u:1819:G:H5''	45:u:1819:G:C8	2.55	0.41
45:u:1959:U:O2'	45:u:1960:A:P	2.78	0.41
45:u:2793:G:O6	45:u:2797:C:C5	2.73	0.41
45:u:2889:G:C6	45:u:2890:C:C4	3.08	0.41
45:u:3752:C:O2'	45:u:3753:G:P	2.78	0.41
48:x:157:VAL:CG2	50:z:80:PHE:CE2	2.84	0.41
53:3:90:SER:CB	55:5:357:TRP:CD1	3.03	0.41
55:5:122:LEU:HD11	55:5:126:PHE:CE2	2.56	0.41
55:5:626:VAL:HG11	55:5:664:ARG:CZ	2.50	0.41
9:I:49:CYS:SG	9:I:49:CYS:O	2.78	0.41
18:S:173:ASN:HA	45:u:4762:A:H2	1.86	0.41
31:f:13:GLY:HA2	31:f:97:ILE:CD1	2.50	0.41
33:h:38:GLY:HA3	48:x:266:PRO:CD	2.50	0.41
35:j:55:ARG:NH2	45:u:364:G:O6	2.52	0.41
40:o:31:ASP:O	40:o:33:LEU:N	2.53	0.41
42:r:97:ILE:HG22	42:r:107:ARG:HB2	1.91	0.41
45:u:674:G:C2	45:u:675:C:C2	3.08	0.41
45:u:682:G:H2'	45:u:682:G:N3	2.35	0.41
45:u:975:C:H5''	45:u:976:G:OP2	2.20	0.41
45:u:1203:G:C2	45:u:1204:C:C2	3.08	0.41
45:u:1268:G:O4'	45:u:2111:G:C5	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1277:G:C2	45:u:1278:C:C2	3.08	0.41
45:u:1349:G:C6	45:u:1350:C:C4	3.08	0.41
45:u:1412:G:C2	45:u:1413:C:C2	3.09	0.41
45:u:1721:G:C6	45:u:1722:C:C4	3.08	0.41
45:u:2076:G:C2	45:u:2077:C:C2	3.08	0.41
45:u:2465:C:H2'	45:u:2466:G:O4'	2.20	0.41
45:u:3937:C:H2'	45:u:3938:G:N2	2.35	0.41
45:u:4182:G:H5''	45:u:4183:G:OP2	2.20	0.41
45:u:4305:G:N3	45:u:4305:G:H2'	2.35	0.41
45:u:4349:C:H3'	45:u:4350:C:H5'	2.03	0.41
45:u:4595:G:C6	45:u:4596:C:C4	3.08	0.41
45:u:4911:A:H3'	45:u:4912:G:H5''	2.01	0.41
46:v:27:G:C6	46:v:28:C:C4	3.08	0.41
48:x:127:GLN:HA	48:x:130:VAL:HG12	2.02	0.41
55:5:41:PHE:CZ	55:5:489:VAL:HG11	2.56	0.41
55:5:502:PHE:C	55:5:503:ASP:N	2.78	0.41
55:5:504:ASP:HB3	55:5:688:LEU:CD1	2.49	0.41
2:B:116:ARG:HB3	2:B:177:LYS:HA	2.03	0.41
6:F:118:GLN:HG3	16:Q:3:VAL:HG22	2.03	0.41
8:H:5:LEU:HD13	8:H:60:TRP:CD2	2.56	0.41
13:N:200:LEU:HD23	13:N:200:LEU:HA	1.96	0.41
16:Q:148:VAL:HG13	16:Q:152:PHE:CZ	2.56	0.41
32:g:59:VAL:HG21	32:g:63:VAL:HG11	2.02	0.41
45:u:80:C:C2	45:u:104:G:N2	2.89	0.41
45:u:369:G:N2	45:u:372:A:OP2	2.50	0.41
45:u:479:G:C6	45:u:480:C:C4	3.08	0.41
45:u:1085:C:C2	45:u:1213:G:N1	2.89	0.41
45:u:1466:G:C2	45:u:1467:C:C2	3.09	0.41
45:u:2396:A:N6	45:u:2814:C:O2	2.54	0.41
45:u:3923:A:H2'	45:u:3924:C:C6	2.55	0.41
45:u:4152:G:C2	45:u:4153:C:C2	3.08	0.41
46:v:93:G:C6	46:v:94:C:C4	3.07	0.41
47:w:128:C:C5	47:w:129:C:C5	3.08	0.41
55:5:264:SER:H	55:5:268:MET:HG3	1.85	0.41
55:5:488:ILE:CG2	55:5:531:GLN:NE2	2.84	0.41
2:B:89:ILE:CD1	2:B:153:MET:HE1	2.50	0.41
7:G:58:PRO:CD	23:X:46:PHE:HD2	2.34	0.41
9:I:35:ASP:OD1	9:I:35:ASP:N	2.54	0.41
12:M:55:MET:O	18:S:157:ARG:NH2	2.53	0.41
13:N:64:ILE:HD11	13:N:102:ALA:HA	2.03	0.41
18:S:95:ARG:HD3	18:S:97:TYR:OH	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:169:G:C2	45:u:170:C:C2	3.09	0.41
45:u:209:U:C6	45:u:211:G:C8	3.08	0.41
45:u:216:C:H41	51:1:539:THR:HA	1.86	0.41
45:u:235:A:C2	45:u:238:C:C5	3.08	0.41
45:u:689:U:O2	45:u:690:C:C6	2.73	0.41
45:u:715:G:H1	45:u:953:C:H42	1.68	0.41
45:u:931:C:C2'	45:u:932:A:O5'	2.68	0.41
45:u:1422:G:C2	45:u:1464:C:C2	3.09	0.41
45:u:1633:G:H5'	45:u:1634:A:OP1	2.20	0.41
45:u:1912:G:C6	45:u:1913:C:N4	2.89	0.41
45:u:2547:G:C2	45:u:2548:C:C2	3.09	0.41
45:u:4276:G:N2	45:u:4333:C:C2	2.88	0.41
45:u:4586:G:H5''	45:u:4586:G:C8	2.52	0.41
49:y:61:ILE:HA	49:y:64:ILE:HD12	2.02	0.41
54:4:18:LEU:HD22	55:5:29:LEU:HD12	2.01	0.41
55:5:52:PHE:CB	55:5:530:TYR:CZ	2.89	0.41
55:5:488:ILE:CG2	55:5:531:GLN:HE22	2.33	0.41
3:C:266:THR:HG22	3:C:269:LYS:HB3	2.02	0.41
13:N:11:TRP:CE3	13:N:44:ARG:NH2	2.89	0.41
23:X:156:ILE:HG22	49:y:24:ARG:HE	1.86	0.41
31:f:72:GLY:HA3	31:f:88:PHE:CD2	2.56	0.41
32:g:63:VAL:O	32:g:64:LEU:C	2.63	0.41
33:h:6:ALA:O	33:h:7:ARG:C	2.64	0.41
35:j:59:THR:HG22	47:w:41:A:O2'	2.20	0.41
42:r:135:LYS:HZ1	45:u:451:C:C3'	2.30	0.41
45:u:167:C:C2	45:u:269:G:C2	3.08	0.41
45:u:197:A:H2'	45:u:198:A:C8	2.55	0.41
45:u:216:C:O2	51:1:536:ARG:CB	2.65	0.41
45:u:684:G:HO2'	45:u:685:C:P	2.42	0.41
45:u:684:G:O2'	45:u:685:C:O5'	2.37	0.41
45:u:976:G:H2'	45:u:977:C:C1'	2.37	0.41
45:u:1439:C:O2	45:u:1439:C:O4'	2.39	0.41
45:u:2625:U:C4	45:u:2626:U:C4	3.09	0.41
45:u:4269:G:C6	45:u:4270:C:C4	3.09	0.41
48:x:248:THR:N	48:x:440:ALA:HB1	1.58	0.41
53:3:44:ILE:HD11	55:5:397:MET:HE2	2.02	0.41
53:3:92:PHE:CE1	53:3:96:MET:HG3	2.56	0.41
55:5:70:ASN:HB3	55:5:84:ILE:HG21	2.03	0.41
55:5:76:ALA:HA	55:5:540:ILE:HG22	2.03	0.41
55:5:192:ILE:HG23	55:5:242:THR:HG21	2.02	0.41
55:5:631:SER:HA	55:5:632:PRO:HD3	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:GLU:OE1	1:A:121:GLY:N	2.52	0.41
3:C:190:ARG:NE	3:C:199:ARG:O	2.44	0.41
25:Z:73:LYS:HG2	25:Z:75:TYR:CZ	2.56	0.41
29:d:79:ASN:OD1	29:d:79:ASN:N	2.53	0.41
45:u:28:C:C2	45:u:55:G:N2	2.88	0.41
45:u:303:C:H2'	45:u:304:C:O4'	2.21	0.41
45:u:1264:C:C4	45:u:1265:G:N7	2.88	0.41
45:u:1424:G:H2'	45:u:1425:G:O4'	2.21	0.41
45:u:1441:C:N4	45:u:1442:C:N4	2.69	0.41
45:u:2645:G:C2	45:u:2646:C:C2	3.08	0.41
45:u:3786:U:O4'	45:u:4537:C:O2'	2.36	0.41
45:u:4408:G:C2	45:u:4409:C:C2	3.08	0.41
47:w:56:G:C4	47:w:62:A:C2	3.08	0.41
55:5:209:TRP:NE1	62:5:809:9UB:O27	2.54	0.41
1:A:236:GLY:N	45:u:3687:A:O2'	2.52	0.41
3:C:76:ILE:HG22	3:C:77:PRO:CD	2.51	0.41
3:C:228:THR:OG1	3:C:248:ARG:NH2	2.54	0.41
4:D:43:LYS:O	4:D:46:THR:HG22	2.20	0.41
5:E:157:ARG:NH2	12:M:106:ASP:OD2	2.53	0.41
6:F:181:LEU:HD11	6:F:209:PHE:HB2	2.02	0.41
7:G:140:VAL:HG13	7:G:200:THR:OG1	2.21	0.41
8:H:109:GLY:O	8:H:110:SER:C	2.63	0.41
10:J:15:LEU:HD21	10:J:157:ILE:HD13	2.03	0.41
11:L:146:LEU:HB2	11:L:148:THR:HG22	2.01	0.41
12:M:116:LYS:HG2	14:O:196:LEU:CD2	2.35	0.41
13:N:124:ASP:OD1	45:u:3937:C:O2'	2.37	0.41
16:Q:24:TYR:CE1	42:r:5:LEU:HD13	2.56	0.41
16:Q:41:SER:OG	16:Q:44:ASN:ND2	2.54	0.41
25:Z:123:LYS:O	25:Z:124:THR:HG23	2.20	0.41
26:a:90:ALA:O	26:a:91:ALA:HB3	2.21	0.41
26:a:98:ALA:HB2	26:a:121:PRO:HB2	2.03	0.41
28:c:30:GLY:O	28:c:34:THR:HG22	2.20	0.41
29:d:30:HIS:CG	29:d:82:TYR:CD1	3.09	0.41
30:e:100:ALA:HB3	30:e:103:VAL:HG23	2.02	0.41
30:e:104:SER:HB3	45:u:2303:C:OP1	2.21	0.41
36:k:28:ASN:ND2	45:u:2695:A:OP2	2.50	0.41
44:t:85:LEU:HD13	44:t:109:ILE:HG21	2.03	0.41
45:u:29:G:C6	45:u:30:C:C4	3.09	0.41
45:u:206:U:O2	45:u:206:U:H2'	2.20	0.41
45:u:254:G:C6	45:u:255:C:C4	3.09	0.41
45:u:258:G:N2	45:u:259:C:C2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:462:G:C2'	45:u:463:A:H5'	2.51	0.41
45:u:933:G:C2	45:u:939:G:C2	3.09	0.41
45:u:960:A:N6	45:u:1283:G:O6	2.54	0.41
45:u:976:G:OP1	45:u:976:G:C4'	2.68	0.41
45:u:1205:G:N1	45:u:1206:C:C4	2.89	0.41
45:u:1279:A:C4	45:u:1280:C:N3	2.89	0.41
45:u:1431:C:H2'	45:u:1432:G:O4'	2.20	0.41
45:u:1466:G:C6	45:u:1467:C:C4	3.09	0.41
45:u:1721:G:C2	45:u:1722:C:C2	3.09	0.41
45:u:2052:G:C2	45:u:2053:C:C2	3.09	0.41
45:u:2301:G:C6	45:u:2302:C:C4	3.09	0.41
45:u:2613:C:N4	45:u:2614:C:N4	2.68	0.41
45:u:2623:A:C2	45:u:2624:G:C6	3.08	0.41
45:u:4131:G:C2	45:u:4132:C:C2	3.09	0.41
45:u:4595:G:C2	45:u:4596:C:C2	3.08	0.41
45:u:4661:G:C2	45:u:4662:C:C2	3.09	0.41
45:u:4868:G:H3'	45:u:4869:U:H5''	2.03	0.41
47:w:49:G:C6	47:w:50:C:C4	3.09	0.41
47:w:112:G:C6	47:w:113:C:C4	3.09	0.41
48:x:13:CYS:HB3	48:x:118:LEU:HD21	2.02	0.41
48:x:88:GLY:HA2	48:x:116:GLN:NE2	2.36	0.41
49:y:56:LEU:HD12	53:3:92:PHE:HE2	1.60	0.41
54:4:25:TYR:CE2	55:5:145:LEU:HD12	2.56	0.41
55:5:179:THR:HA	55:5:182:MET:HB2	2.03	0.41
55:5:582:PHE:CE1	55:5:643:CYS:HB3	2.55	0.41
3:C:27:VAL:HG11	3:C:128:LEU:HD13	2.03	0.41
3:C:143:ARG:N	3:C:179:ASP:OD1	2.54	0.41
4:D:17:GLN:O	45:u:4265:U:N3	2.46	0.41
5:E:90:LYS:N	5:E:91:PRO:HD3	2.35	0.41
10:J:53:ALA:HB2	10:J:68:ILE:CD1	2.51	0.41
14:O:42:ASN:OD1	14:O:42:ASN:N	2.54	0.41
23:X:156:ILE:CG2	48:x:416:TYR:HH	2.06	0.41
28:c:31:TYR:HA	28:c:34:THR:HG22	2.02	0.41
45:u:22:G:C2	47:w:35:C:C4	3.09	0.41
45:u:119:G:H3'	45:u:120:A:H5'	2.03	0.41
45:u:119:G:H5''	45:u:119:G:C8	2.56	0.41
45:u:2630:U:O2'	45:u:2632:U:H4'	2.21	0.41
45:u:3717:A:O2'	45:u:3718:A:O5'	2.38	0.41
45:u:4326:G:C2	45:u:4327:C:C2	3.08	0.41
45:u:4473:A:C2	45:u:4474:A:C4	3.09	0.41
46:v:51:G:C2	46:v:52:C:C2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:122:LEU:HD11	55:5:126:PHE:CD2	2.56	0.41
1:A:27:ALA:HB1	1:A:77:ILE:HG13	2.03	0.40
5:E:59:TYR:CE2	5:E:64:LEU:HD12	2.48	0.40
9:I:204:GLY:C	9:I:205:PRO:O	2.64	0.40
16:Q:72:LEU:HB2	16:Q:75:ARG:HD3	2.03	0.40
42:r:47:LYS:HD3	42:r:102:TYR:CE2	2.50	0.40
45:u:368:C:C2	45:u:374:G:C2	3.09	0.40
45:u:933:G:N1	45:u:939:G:N2	2.69	0.40
45:u:1075:G:H2'	45:u:1076:C:C6	2.56	0.40
45:u:1351:G:C2	45:u:1352:C:C2	3.10	0.40
45:u:1412:G:C6	45:u:1413:C:C4	3.09	0.40
45:u:1834:U:O2	45:u:1834:U:H2'	2.20	0.40
45:u:2083:C:H4'	45:u:2084:C:OP2	2.21	0.40
45:u:2273:G:C6	45:u:2274:C:C4	3.10	0.40
45:u:2322:G:C2	45:u:2323:C:C2	3.09	0.40
45:u:2463:G:C6	45:u:2464:C:N4	2.89	0.40
45:u:2517:A:N1	45:u:2518:G:C2	2.89	0.40
45:u:2628:U:C4	45:u:2629:C:C5	3.09	0.40
45:u:2661:U:O2'	45:u:2662:G:O5'	2.40	0.40
45:u:2889:G:C2	45:u:2890:C:C2	3.09	0.40
45:u:3723:A:C2	45:u:3730:U:N3	2.89	0.40
45:u:4201:G:C6	45:u:4202:U:C4	3.09	0.40
45:u:4614:G:C6	45:u:4615:C:C4	3.09	0.40
46:v:16:A:H2'	46:v:17:C:C6	2.56	0.40
47:w:32:C:H2'	47:w:33:G:O4'	2.20	0.40
48:x:462:VAL:O	48:x:463:LYS:C	2.64	0.40
55:5:348:SER:OG	55:5:598:TRP:NE1	2.54	0.40
55:5:392:TYR:CZ	55:5:413:VAL:HG22	2.57	0.40
55:5:554:ARG:HB2	55:5:557:GLN:HE21	1.86	0.40
55:5:638:LEU:HD23	55:5:638:LEU:HA	1.91	0.40
2:B:30:LYS:NZ	45:u:4717:A:OP2	2.49	0.40
3:C:293:LEU:HD22	16:Q:34:PHE:CD2	2.56	0.40
4:D:200:MET:CE	4:D:241:LYS:CE	2.98	0.40
6:F:94:VAL:HG13	6:F:142:ILE:HD12	2.04	0.40
14:O:48:TYR:CE2	45:u:1930:U:C2	3.09	0.40
20:U:87:THR:CG2	20:U:102:VAL:HG21	2.51	0.40
21:V:98:PHE:O	21:V:99:GLU:HB3	2.21	0.40
31:f:15:LYS:HB3	31:f:25:THR:HB	2.03	0.40
35:j:81:GLY:C	35:j:82:THR:HG23	2.46	0.40
45:u:93:G:C2'	45:u:94:A:C8	3.04	0.40
45:u:465:G:N1	45:u:466:A:C5	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:1448:G:C2	45:u:2097:U:C4	3.10	0.40
45:u:1506:G:C2	45:u:1507:C:C2	3.09	0.40
45:u:1932:A:H2'	45:u:1933:G:C8	2.57	0.40
45:u:2862:G:H2'	45:u:3619:G:O6	2.21	0.40
45:u:3705:G:C2	45:u:3706:C:C2	3.09	0.40
45:u:4154:G:C2	45:u:4155:C:C2	3.09	0.40
45:u:4486:C:H2'	45:u:4487:A:O4'	2.21	0.40
46:v:66:G:C6	46:v:67:C:N3	2.89	0.40
47:w:154:G:C2	47:w:155:C:C2	3.09	0.40
49:y:53:PHE:CE1	53:3:92:PHE:CE1	3.01	0.40
53:3:92:PHE:CD2	53:3:96:MET:HE2	2.56	0.40
1:A:181:LYS:HB3	45:u:1577:G:N7	2.36	0.40
3:C:173:LYS:NZ	45:u:218:A:N6	2.69	0.40
6:F:147:PRO:HA	6:F:243:ASN:OD1	2.22	0.40
8:H:137:SER:HB3	8:H:145:VAL:HG23	2.04	0.40
9:I:76:MET:HB3	9:I:85:PHE:CD2	2.56	0.40
12:M:81:ASP:O	12:M:84:THR:OG1	2.32	0.40
20:U:82:TYR:CZ	20:U:86:LEU:HD11	2.56	0.40
22:W:9:SER:HA	22:W:52:THR:HG22	2.04	0.40
31:f:8:LYS:HB3	31:f:100:ARG:CZ	2.52	0.40
45:u:2:G:C6	45:u:3:C:C4	3.09	0.40
45:u:247:G:C2	45:u:248:C:C2	3.09	0.40
45:u:301:G:C5	45:u:302:C:C4	3.08	0.40
45:u:488:G:C6	45:u:489:C:C4	3.09	0.40
45:u:695:G:H3'	45:u:696:C:H5'	2.02	0.40
45:u:730:G:N2	45:u:939:G:N2	2.69	0.40
45:u:751:G:N2	45:u:752:G:C5	2.89	0.40
45:u:971:U:C2'	45:u:972:C:H5'	2.51	0.40
45:u:1573:G:C6	45:u:1574:G:N1	2.89	0.40
45:u:1959:U:C1'	45:u:1961:G:O4'	2.70	0.40
45:u:2316:G:C2	45:u:2317:C:C2	3.10	0.40
45:u:2316:G:C6	45:u:2317:C:C4	3.09	0.40
45:u:2533:C:C2	45:u:2534:C:C5	3.08	0.40
45:u:4395:U:H5'	45:u:4395:U:H6	1.85	0.40
45:u:4411:G:C6	45:u:4412:C:C4	3.10	0.40
45:u:4476:C:O2	45:u:4476:C:O4'	2.39	0.40
45:u:4495:G:C2	45:u:4506:C:C2	3.09	0.40
45:u:4900:C:O2'	45:u:4901:G:P	2.80	0.40
48:x:192:VAL:HG13	49:y:52:PHE:CE1	2.55	0.40
1:A:66:PRO:HG2	1:A:67:TYR:CE2	2.57	0.40
1:A:227:ARG:NH2	45:u:3659:G:O2'	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:278:ASP:O	4:D:281:ALA:HB3	2.20	0.40
7:G:63:LEU:HD12	13:N:32:GLN:HB3	2.02	0.40
8:H:41:ILE:HG12	8:H:73:ILE:CG1	2.52	0.40
10:J:165:TRP:CH2	10:J:170:TYR:HE2	2.39	0.40
13:N:50:ARG:NH2	45:u:279:A:OP2	2.54	0.40
29:d:42:ALA:N	29:d:43:PRO:CD	2.85	0.40
30:e:43:ASN:O	30:e:44:ARG:C	2.63	0.40
40:o:23:VAL:HG13	40:o:68:LEU:HB3	2.04	0.40
45:u:35:U:H5'	45:u:36:U:OP2	2.21	0.40
45:u:482:G:H2'	45:u:483:G:N9	2.36	0.40
45:u:1203:G:C6	45:u:1204:C:C4	3.10	0.40
45:u:1383:G:C2	45:u:1384:C:C2	3.10	0.40
45:u:1732:C:O2	45:u:1798:G:C2	2.75	0.40
45:u:1806:G:C6	45:u:1807:C:C4	3.09	0.40
45:u:2301:G:C2	45:u:2302:C:C2	3.09	0.40
45:u:2463:G:C6	45:u:2464:C:C4	3.10	0.40
45:u:2481:G:N2	45:u:2498:C:C2	2.90	0.40
45:u:2688:G:N1	45:u:2689:C:C4	2.89	0.40
45:u:2882:A:H2'	45:u:2883:G:H5'	2.04	0.40
45:u:4116:C:O2	45:u:4116:C:O2'	2.36	0.40
45:u:4198:G:C5	45:u:4199:C:C5	3.09	0.40
45:u:4453:C:H2'	45:u:4454:G:O4'	2.21	0.40
45:u:4561:C:C2	45:u:4562:C:C5	3.10	0.40
45:u:4664:A:H2'	45:u:4665:A:O4'	2.21	0.40
45:u:4714:C:C5	45:u:4715:C:C5	3.09	0.40
47:w:31:G:C6	47:w:32:C:C4	3.10	0.40
47:w:103:A:C8	47:w:104:A:C8	3.09	0.40
47:w:112:G:C2	47:w:113:C:C2	3.10	0.40
48:x:47:GLN:CA	48:x:75:THR:HG21	2.52	0.40
48:x:406:GLU:OE1	48:x:407:THR:HB	2.21	0.40
1:A:27:ALA:O	1:A:128:ARG:NH2	2.54	0.40
5:E:41:SER:CB	45:u:978:G:H5''	2.51	0.40
5:E:124:HIS:CD2	45:u:1282:G:C5	3.09	0.40
5:E:225:GLU:CA	42:r:135:LYS:CE	2.98	0.40
8:H:172:ILE:HD12	38:m:90:ASN:HB3	2.02	0.40
12:M:64:PHE:HB2	12:M:65:PRO:HD2	2.03	0.40
25:Z:38:TYR:CD1	25:Z:76:ASN:OD1	2.74	0.40
44:t:30:PRO:O	44:t:33:GLY:N	2.49	0.40
45:u:211:G:N1	45:u:212:A:N7	2.70	0.40
45:u:471:A:N1	45:u:472:C:N1	2.69	0.40
45:u:518:G:C6	45:u:519:C:C4	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:674:G:C6	45:u:675:C:C4	3.10	0.40
45:u:680:G:C2	45:u:681:G:C4	3.09	0.40
45:u:941:C:H2'	45:u:942:G:O4'	2.21	0.40
45:u:1349:G:C2	45:u:1350:C:C2	3.10	0.40
45:u:1385:G:C6	45:u:1386:C:C4	3.09	0.40
45:u:1550:G:N1	45:u:1551:C:C2	2.89	0.40
45:u:1981:G:O2'	45:u:1982:G:C8	2.75	0.40
45:u:2058:G:C6	45:u:2059:C:C4	3.09	0.40
45:u:2408:U:H1'	45:u:2409:U:C5	2.56	0.40
45:u:3706:C:H2'	45:u:3707:U:O4'	2.22	0.40
45:u:4472:G:H2'	45:u:4473:A:H5'	2.04	0.40
47:w:106:G:N1	47:w:107:C:C4	2.90	0.40
48:x:69:LEU:HD12	48:x:69:LEU:HA	1.65	0.40
48:x:173:TYR:CZ	48:x:175:LEU:HB2	2.57	0.40
55:5:19:LYS:HE3	55:5:19:LYS:HB2	1.83	0.40
55:5:155:PRO:O	55:5:159:SER:OG	2.25	0.40
55:5:346:ILE:C	55:5:349:VAL:HG12	2.34	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	242/244 (99%)	209 (86%)	28 (12%)	5 (2%)	5	29
2	B	392/394 (100%)	345 (88%)	42 (11%)	5 (1%)	9	41
3	C	360/362 (99%)	322 (89%)	27 (8%)	11 (3%)	3	21
4	D	290/292 (99%)	262 (90%)	25 (9%)	3 (1%)	12	47
5	E	232/248 (94%)	179 (77%)	36 (16%)	17 (7%)	1	11
6	F	223/225 (99%)	204 (92%)	17 (8%)	2 (1%)	14	49
7	G	239/241 (99%)	203 (85%)	31 (13%)	5 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	188/190 (99%)	166 (88%)	19 (10%)	3 (2%)	7	37
9	I	200/213 (94%)	181 (90%)	15 (8%)	4 (2%)	6	31
10	J	167/169 (99%)	147 (88%)	13 (8%)	7 (4%)	2	17
11	L	208/210 (99%)	180 (86%)	16 (8%)	12 (6%)	1	14
12	M	136/138 (99%)	123 (90%)	12 (9%)	1 (1%)	18	55
13	N	201/203 (99%)	181 (90%)	20 (10%)	0	100	100
14	O	197/199 (99%)	184 (93%)	12 (6%)	1 (0%)	24	63
15	P	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
16	Q	185/187 (99%)	169 (91%)	14 (8%)	2 (1%)	11	45
17	R	178/180 (99%)	166 (93%)	9 (5%)	3 (2%)	7	35
18	S	173/175 (99%)	157 (91%)	12 (7%)	4 (2%)	5	28
19	T	157/159 (99%)	139 (88%)	15 (10%)	3 (2%)	6	32
20	U	97/99 (98%)	82 (84%)	11 (11%)	4 (4%)	2	18
21	V	129/131 (98%)	115 (89%)	13 (10%)	1 (1%)	16	53
22	W	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	37
23	X	117/119 (98%)	109 (93%)	6 (5%)	2 (2%)	7	35
24	Y	132/134 (98%)	114 (86%)	17 (13%)	1 (1%)	16	53
25	Z	133/135 (98%)	113 (85%)	13 (10%)	7 (5%)	1	15
26	a	145/147 (99%)	122 (84%)	19 (13%)	4 (3%)	4	24
27	b	73/75 (97%)	67 (92%)	5 (7%)	1 (1%)	9	39
28	c	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
29	d	105/107 (98%)	91 (87%)	13 (12%)	1 (1%)	12	47
30	e	126/128 (98%)	115 (91%)	6 (5%)	5 (4%)	2	18
31	f	107/109 (98%)	94 (88%)	8 (8%)	5 (5%)	2	16
32	g	112/114 (98%)	103 (92%)	8 (7%)	1 (1%)	14	49
33	h	120/122 (98%)	106 (88%)	10 (8%)	4 (3%)	3	21
34	i	100/102 (98%)	92 (92%)	6 (6%)	2 (2%)	6	31
35	j	84/86 (98%)	71 (84%)	8 (10%)	5 (6%)	1	13
36	k	67/69 (97%)	56 (84%)	7 (10%)	4 (6%)	1	13
37	l	48/50 (96%)	40 (83%)	7 (15%)	1 (2%)	5	29
38	m	50/52 (96%)	44 (88%)	6 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	n	21/23 (91%)	21 (100%)	0	0	100	100
40	o	102/104 (98%)	92 (90%)	7 (7%)	3 (3%)	3	23
41	p	89/91 (98%)	80 (90%)	8 (9%)	1 (1%)	11	45
42	r	132/136 (97%)	113 (86%)	12 (9%)	7 (5%)	1	15
43	s	196/198 (99%)	164 (84%)	22 (11%)	10 (5%)	1	15
44	t	161/163 (99%)	102 (63%)	33 (20%)	26 (16%)	0	3
48	x	420/426 (99%)	373 (89%)	46 (11%)	1 (0%)	43	78
49	y	60/62 (97%)	52 (87%)	8 (13%)	0	100	100
50	z	27/29 (93%)	25 (93%)	1 (4%)	1 (4%)	2	19
51	1	134/162 (83%)	129 (96%)	5 (4%)	0	100	100
53	3	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	16	53
54	4	32/34 (94%)	31 (97%)	1 (3%)	0	100	100
55	5	632/696 (91%)	538 (85%)	88 (14%)	6 (1%)	14	49
All	All	8141/8362 (97%)	7150 (88%)	798 (10%)	193 (2%)	7	27

All (193) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	TRP
3	C	273	LEU
5	E	91	PRO
5	E	95	ASP
5	E	118	PRO
5	E	175	LEU
5	E	221	PRO
7	G	45	ILE
7	G	128	VAL
8	H	40	HIS
8	H	110	SER
9	I	47	PRO
11	L	64	VAL
11	L	67	HIS
17	R	36	ASN
18	S	165	PRO
20	U	47	ILE
25	Z	84	ARG
26	a	90	ALA

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Mol	Chain	Res	Type
29	d	94	GLU
30	e	92	ASN
31	f	80	ASN
33	h	7	ARG
36	k	61	PRO
40	o	32	SER
42	r	86	ALA
43	s	62	ARG
43	s	201	PRO
44	t	29	ALA
44	t	30	PRO
44	t	31	LYS
44	t	53	TRP
44	t	89	PRO
44	t	144	ASP
44	t	148	PRO
44	t	149	HIS
48	x	445	THR
55	5	84	ILE
55	5	89	TYR
1	A	217	GLN
2	B	38	SER
2	B	302	ASN
3	C	73	VAL
3	C	155	GLU
3	C	275	SER
4	D	187	SER
5	E	85	LEU
5	E	92	VAL
5	E	174	PRO
5	E	234	GLU
10	J	116	GLY
10	J	155	HIS
11	L	63	THR
11	L	143	GLU
11	L	172	GLU
17	R	130	ASN
18	S	88	SER
19	T	81	LYS
20	U	98	ASP
23	X	131	ASP
25	Z	34	SER

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Mol	Chain	Res	Type
26	a	76	ASP
30	e	44	ARG
34	i	11	LEU
35	j	36	LYS
35	j	39	TYR
42	r	67	ARG
42	r	71	ARG
43	s	70	GLU
43	s	106	LYS
43	s	109	ALA
44	t	5	PHE
44	t	26	SER
44	t	39	PRO
44	t	58	ILE
44	t	106	PHE
55	5	360	TYR
55	5	361	TYR
2	B	18	PRO
3	C	16	GLU
3	C	132	ALA
3	C	248	ARG
5	E	96	LYS
5	E	179	ARG
5	E	232	GLU
6	F	239	GLU
9	I	205	PRO
10	J	11	PRO
10	J	146	ARG
16	Q	14	ARG
17	R	19	LYS
21	V	14	PHE
25	Z	55	ALA
25	Z	124	THR
26	a	92	LYS
30	e	125	PRO
30	e	126	ASN
31	f	37	ASP
31	f	79	GLY
33	h	97	LYS
34	i	3	LEU
36	k	32	VAL
37	l	47	THR

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Mol	Chain	Res	Type
42	r	19	LYS
42	r	85	ASN
43	s	69	LEU
43	s	108	PRO
43	s	142	GLY
44	t	54	LYS
44	t	67	ARG
44	t	105	THR
44	t	137	GLN
53	3	64	ASP
55	5	661	ASP
1	A	180	LEU
2	B	54	THR
5	E	129	PHE
5	E	224	GLN
8	H	101	ILE
11	L	5	ARG
11	L	52	SER
19	T	29	THR
24	Y	83	GLU
25	Z	31	ASP
26	a	98	ALA
30	e	89	LEU
32	g	65	MET
33	h	89	ARG
36	k	29	LYS
41	p	41	PHE
44	t	2	PRO
44	t	18	THR
1	A	130	SER
2	B	309	LEU
4	D	20	PHE
5	E	218	LEU
5	E	229	PHE
7	G	123	ALA
7	G	125	LYS
10	J	153	ALA
11	L	6	ASN
11	L	103	ARG
16	Q	148	VAL
20	U	27	HIS
25	Z	91	LEU

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Mol	Chain	Res	Type
31	f	107	PRO
33	h	40	ALA
35	j	34	CYS
35	j	61	THR
36	k	21	LYS
40	o	77	CYS
42	r	11	ARG
43	s	34	ASN
44	t	7	PRO
55	5	616	ASP
1	A	67	TYR
3	C	222	ARG
3	C	309	ILE
10	J	124	GLY
11	L	100	PRO
11	L	169	ILE
14	O	49	ARG
18	S	5	GLY
20	U	67	LYS
22	W	15	PRO
31	f	106	TYR
35	j	60	GLY
40	o	33	LEU
44	t	10	ILE
44	t	19	GLY
44	t	22	VAL
3	C	133	LEU
9	I	99	ILE
27	b	21	ILE
43	s	73	PRO
4	D	125	VAL
11	L	134	PRO
25	Z	90	PRO
3	C	265	GLY
5	E	103	VAL
6	F	230	VAL
7	G	238	GLY
9	I	201	PRO
19	T	44	GLY
10	J	174	ILE
12	M	7	VAL
18	S	155	PRO

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Mol	Chain	Res	Type
44	t	3	PRO
44	t	98	ILE
23	X	119	ILE
42	r	69	GLY
44	t	23	GLY
50	z	71	VAL

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	u	3647/3662 (99%)	1211 (33%)	0
46	v	119/120 (99%)	20 (16%)	0
47	w	155/156 (99%)	52 (33%)	0
All	All	3921/3938 (99%)	1283 (32%)	0

All (1283) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	u	2	G
45	u	8	U
45	u	9	C
45	u	10	A
45	u	12	A
45	u	13	U
45	u	21	G
45	u	25	A
45	u	30	C
45	u	39	A
45	u	42	A
45	u	43	U
45	u	44	A
45	u	48	G
45	u	49	U
45	u	56	A
45	u	58	G
45	u	59	A
45	u	64	A

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Mol	Chain	Res	Type
45	u	65	A
45	u	69	A
45	u	71	C
45	u	72	C
45	u	73	A
45	u	74	G
45	u	91	G
45	u	93	G
45	u	94	A
45	u	95	G
45	u	108	A
45	u	109	G
45	u	110	C
45	u	116	G
45	u	118	C
45	u	119	G
45	u	120	A
45	u	121	A
45	u	125	C
45	u	126	C
45	u	128	C
45	u	129	C
45	u	134	G
45	u	135	G
45	u	136	C
45	u	143	C
45	u	144	G
45	u	146	G
45	u	157	U
45	u	158	A
45	u	159	C
45	u	160	G
45	u	161	G
45	u	164	G
45	u	166	C
45	u	167	C
45	u	170	C
45	u	171	U
45	u	172	C
45	u	173	C
45	u	174	C
45	u	175	C

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Mol	Chain	Res	Type
45	u	177	G
45	u	183	C
45	u	184	U
45	u	185	C
45	u	186	G
45	u	187	U
45	u	188	G
45	u	189	G
45	u	197	A
45	u	200	U
45	u	201	C
45	u	202	C
45	u	203	U
45	u	205	C
45	u	206	U
45	u	210	C
45	u	211	G
45	u	216	C
45	u	217	C
45	u	218	A
45	u	219	G
45	u	220	C
45	u	221	C
45	u	224	U
45	u	225	G
45	u	226	G
45	u	227	A
45	u	233	U
45	u	234	G
45	u	246	G
45	u	253	G
45	u	255	C
45	u	257	C
45	u	265	C
45	u	266	C
45	u	267	G
45	u	272	U
45	u	275	C
45	u	276	C
45	u	277	G
45	u	278	G
45	u	280	G

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Mol	Chain	Res	Type
45	u	286	U
45	u	296	A
45	u	297	U
45	u	300	A
45	u	306	A
45	u	309	C
45	u	315	G
45	u	316	U
45	u	319	A
45	u	321	U
45	u	322	C
45	u	326	C
45	u	328	A
45	u	334	A
45	u	337	U
45	u	340	C
45	u	347	A
45	u	349	A
45	u	350	C
45	u	353	A
45	u	357	U
45	u	361	C
45	u	362	A
45	u	363	A
45	u	385	A
45	u	386	A
45	u	387	G
45	u	399	G
45	u	405	U
45	u	406	C
45	u	407	A
45	u	409	G
45	u	410	A
45	u	412	G
45	u	413	G
45	u	424	U
45	u	429	A
45	u	431	G
45	u	432	U
45	u	434	A
45	u	446	C
45	u	448	G

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Mol	Chain	Res	Type
45	u	449	C
45	u	451	C
45	u	452	A
45	u	453	G
45	u	454	U
45	u	455	C
45	u	458	C
45	u	466	A
45	u	467	U
45	u	468	U
45	u	469	C
45	u	470	A
45	u	471	A
45	u	473	C
45	u	485	C
45	u	486	C
45	u	487	G
45	u	498	C
45	u	499	G
45	u	500	G
45	u	501	C
45	u	502	C
45	u	503	C
45	u	504	G
45	u	506	C
45	u	509	A
45	u	510	U
45	u	513	U
45	u	514	U
45	u	515	C
45	u	519	C
45	u	649	A
45	u	654	C
45	u	655	C
45	u	663	G
45	u	664	G
45	u	665	C
45	u	666	G
45	u	667	A
45	u	668	C
45	u	681	G
45	u	682	G

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Mol	Chain	Res	Type
45	u	683	C
45	u	684	G
45	u	685	C
45	u	686	A
45	u	687	U
45	u	689	U
45	u	690	C
45	u	692	A
45	u	694	C
45	u	695	G
45	u	696	C
45	u	697	G
45	u	701	G
45	u	703	G
45	u	707	C
45	u	718	C
45	u	721	G
45	u	722	G
45	u	724	C
45	u	728	U
45	u	729	G
45	u	730	G
45	u	737	C
45	u	742	G
45	u	745	G
45	u	746	A
45	u	747	A
45	u	748	G
45	u	749	G
45	u	756	G
45	u	911	U
45	u	914	U
45	u	915	A
45	u	917	A
45	u	918	G
45	u	919	C
45	u	920	C
45	u	925	C
45	u	927	G
45	u	928	C
45	u	929	A
45	u	930	G

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Mol	Chain	Res	Type
45	u	931	C
45	u	932	A
45	u	933	G
45	u	934	C
45	u	935	A
45	u	936	C
45	u	937	U
45	u	938	C
45	u	939	G
45	u	940	C
45	u	942	G
45	u	943	A
45	u	944	A
45	u	945	U
45	u	946	C
45	u	947	C
45	u	957	G
45	u	958	G
45	u	960	A
45	u	961	G
45	u	962	C
45	u	963	G
45	u	964	A
45	u	965	G
45	u	966	A
45	u	967	C
45	u	968	C
45	u	969	C
45	u	970	G
45	u	971	U
45	u	972	C
45	u	973	G
45	u	976	G
45	u	977	C
45	u	978	G
45	u	979	C
45	u	982	U
45	u	983	C
45	u	984	C
45	u	989	U
45	u	990	C
45	u	992	C

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Mol	Chain	Res	Type
45	u	1051	G
45	u	1070	G
45	u	1072	C
45	u	1073	G
45	u	1075	G
45	u	1076	C
45	u	1083	U
45	u	1097	C
45	u	1175	A
45	u	1176	C
45	u	1177	U
45	u	1181	C
45	u	1182	C
45	u	1183	C
45	u	1193	C
45	u	1204	C
45	u	1209	U
45	u	1211	G
45	u	1212	G
45	u	1214	C
45	u	1215	C
45	u	1219	G
45	u	1221	G
45	u	1222	A
45	u	1233	G
45	u	1234	G
45	u	1235	G
45	u	1236	C
45	u	1237	C
45	u	1238	A
45	u	1239	C
45	u	1240	G
45	u	1241	C
45	u	1242	G
45	u	1243	C
45	u	1244	G
45	u	1245	C
45	u	1255	A
45	u	1256	G
45	u	1259	G
45	u	1266	G
45	u	1267	C

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Mol	Chain	Res	Type
45	u	1268	G
45	u	1269	G
45	u	1270	A
45	u	1272	C
45	u	1273	G
45	u	1274	A
45	u	1275	G
45	u	1279	A
45	u	1280	C
45	u	1281	G
45	u	1285	U
45	u	1286	C
45	u	1287	G
45	u	1288	G
45	u	1289	C
45	u	1293	G
45	u	1294	A
45	u	1295	C
45	u	1296	G
45	u	1297	U
45	u	1301	C
45	u	1303	A
45	u	1304	C
45	u	1313	C
45	u	1326	A
45	u	1329	G
45	u	1330	A
45	u	1337	A
45	u	1344	C
45	u	1354	A
45	u	1358	G
45	u	1364	U
45	u	1365	C
45	u	1366	G
45	u	1367	C
45	u	1368	A
45	u	1369	C
45	u	1370	G
45	u	1371	A
45	u	1372	A
45	u	1376	C
45	u	1377	G

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Mol	Chain	Res	Type
45	u	1378	C
45	u	1379	C
45	u	1380	G
45	u	1381	U
45	u	1387	A
45	u	1390	G
45	u	1391	A
45	u	1394	G
45	u	1397	A
45	u	1398	A
45	u	1399	G
45	u	1407	C
45	u	1408	G
45	u	1409	C
45	u	1410	U
45	u	1411	C
45	u	1413	C
45	u	1414	C
45	u	1416	G
45	u	1418	C
45	u	1420	A
45	u	1421	G
45	u	1429	C
45	u	1432	G
45	u	1435	G
45	u	1436	C
45	u	1439	C
45	u	1440	U
45	u	1441	C
45	u	1442	C
45	u	1445	U
45	u	1446	C
45	u	1448	G
45	u	1449	C
45	u	1455	G
45	u	1456	C
45	u	1457	G
45	u	1475	G
45	u	1477	C
45	u	1478	C
45	u	1481	C
45	u	1482	G

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Mol	Chain	Res	Type
45	u	1483	C
45	u	1484	G
45	u	1485	C
45	u	1486	C
45	u	1489	G
45	u	1497	A
45	u	1498	G
45	u	1501	C
45	u	1502	G
45	u	1504	G
45	u	1514	U
45	u	1516	G
45	u	1518	A
45	u	1523	A
45	u	1524	A
45	u	1533	A
45	u	1534	A
45	u	1547	A
45	u	1563	A
45	u	1564	A
45	u	1566	C
45	u	1568	C
45	u	1578	U
45	u	1582	U
45	u	1586	G
45	u	1591	U
45	u	1592	G
45	u	1596	U
45	u	1602	U
45	u	1612	G
45	u	1613	A
45	u	1614	C
45	u	1624	G
45	u	1625	G
45	u	1631	A
45	u	1633	G
45	u	1634	A
45	u	1636	U
45	u	1638	A
45	u	1641	G
45	u	1654	G
45	u	1655	C

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Mol	Chain	Res	Type
45	u	1656	U
45	u	1661	C
45	u	1670	G
45	u	1676	C
45	u	1677	U
45	u	1678	C
45	u	1679	A
45	u	1691	G
45	u	1692	C
45	u	1696	C
45	u	1697	G
45	u	1698	C
45	u	1699	A
45	u	1719	A
45	u	1720	C
45	u	1721	G
45	u	1722	C
45	u	1724	G
45	u	1725	U
45	u	1733	G
45	u	1734	G
45	u	1735	U
45	u	1742	A
45	u	1746	A
45	u	1750	G
45	u	1753	G
45	u	1754	U
45	u	1755	C
45	u	1756	U
45	u	1757	U
45	u	1758	G
45	u	1760	G
45	u	1761	G
45	u	1764	G
45	u	1767	A
45	u	1768	C
45	u	1772	C
45	u	1776	A
45	u	1777	C
45	u	1781	U
45	u	1787	A
45	u	1799	G

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Mol	Chain	Res	Type
45	u	1800	U
45	u	1803	G
45	u	1804	A
45	u	1805	A
45	u	1812	C
45	u	1815	G
45	u	1818	G
45	u	1819	G
45	u	1820	C
45	u	1821	G
45	u	1822	U
45	u	1828	C
45	u	1830	G
45	u	1832	C
45	u	1833	G
45	u	1834	U
45	u	1835	G
45	u	1836	G
45	u	1842	G
45	u	1847	C
45	u	1848	C
45	u	1855	G
45	u	1867	A
45	u	1869	G
45	u	1882	U
45	u	1885	G
45	u	1886	G
45	u	1889	U
45	u	1892	A
45	u	1897	A
45	u	1899	G
45	u	1900	C
45	u	1910	G
45	u	1918	U
45	u	1919	G
45	u	1920	C
45	u	1921	C
45	u	1922	G
45	u	1923	A
45	u	1931	C
45	u	1947	U
45	u	1952	G

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Mol	Chain	Res	Type
45	u	1955	G
45	u	1956	A
45	u	1957	U
45	u	1958	A
45	u	1959	U
45	u	1960	A
45	u	1961	G
45	u	1962	A
45	u	1964	A
45	u	1968	G
45	u	1969	G
45	u	1970	A
45	u	1975	G
45	u	1976	G
45	u	1977	C
45	u	1979	A
45	u	1980	U
45	u	1981	G
45	u	1983	A
45	u	1984	A
45	u	1985	G
45	u	1986	U
45	u	1987	C
45	u	1988	G
45	u	1990	A
45	u	1991	A
45	u	1992	U
45	u	1993	C
45	u	1997	U
45	u	1998	A
45	u	2001	G
45	u	2002	A
45	u	2003	G
45	u	2004	U
45	u	2005	G
45	u	2008	U
45	u	2010	A
45	u	2011	C
45	u	2019	C
45	u	2020	U
45	u	2021	G
45	u	2024	G

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Mol	Chain	Res	Type
45	u	2025	A
45	u	2026	A
45	u	2027	U
45	u	2028	C
45	u	2044	U
45	u	2046	G
45	u	2047	A
45	u	2048	U
45	u	2052	G
45	u	2055	G
45	u	2056	G
45	u	2062	C
45	u	2064	G
45	u	2068	C
45	u	2069	A
45	u	2070	U
45	u	2071	A
45	u	2079	G
45	u	2084	C
45	u	2085	G
45	u	2089	G
45	u	2090	U
45	u	2091	C
45	u	2092	G
45	u	2093	A
45	u	2094	G
45	u	2095	A
45	u	2097	U
45	u	2100	A
45	u	2101	C
45	u	2103	G
45	u	2107	C
45	u	2108	G
45	u	2109	G
45	u	2110	C
45	u	2111	G
45	u	2112	G
45	u	2113	G
45	u	2114	G
45	u	2115	G
45	u	2116	C
45	u	2117	G

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Mol	Chain	Res	Type
45	u	2118	G
45	u	2119	C
45	u	2120	G
45	u	2122	G
45	u	2123	C
45	u	2124	G
45	u	2125	C
45	u	2126	G
45	u	2127	C
45	u	2129	C
45	u	2130	G
45	u	2131	C
45	u	2247	C
45	u	2248	C
45	u	2250	C
45	u	2251	G
45	u	2252	G
45	u	2253	A
45	u	2254	G
45	u	2255	C
45	u	2256	C
45	u	2257	C
45	u	2258	C
45	u	2259	G
45	u	2260	C
45	u	2261	G
45	u	2263	A
45	u	2264	C
45	u	2265	G
45	u	2266	C
45	u	2267	U
45	u	2268	A
45	u	2269	C
45	u	2270	G
45	u	2274	C
45	u	2275	G
45	u	2279	A
45	u	2288	G
45	u	2289	C
45	u	2299	G
45	u	2300	A
45	u	2301	G

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Mol	Chain	Res	Type
45	u	2312	U
45	u	2313	A
45	u	2314	G
45	u	2324	C
45	u	2331	G
45	u	2332	A
45	u	2333	G
45	u	2335	C
45	u	2337	C
45	u	2348	G
45	u	2351	C
45	u	2360	A
45	u	2364	G
45	u	2370	A
45	u	2371	U
45	u	2382	A
45	u	2383	C
45	u	2395	A
45	u	2396	A
45	u	2397	G
45	u	2398	U
45	u	2399	G
45	u	2417	A
45	u	2422	C
45	u	2424	G
45	u	2425	U
45	u	2428	A
45	u	2429	A
45	u	2433	G
45	u	2434	G
45	u	2440	U
45	u	2441	C
45	u	2447	U
45	u	2450	G
45	u	2458	C
45	u	2469	C
45	u	2471	G
45	u	2473	A
45	u	2474	G
45	u	2475	G
45	u	2485	U
45	u	2488	C

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Mol	Chain	Res	Type
45	u	2489	C
45	u	2490	U
45	u	2491	C
45	u	2493	G
45	u	2495	U
45	u	2499	C
45	u	2503	G
45	u	2504	C
45	u	2505	C
45	u	2506	G
45	u	2507	A
45	u	2512	A
45	u	2513	A
45	u	2514	G
45	u	2519	U
45	u	2521	G
45	u	2527	A
45	u	2530	U
45	u	2536	A
45	u	2537	A
45	u	2544	G
45	u	2546	G
45	u	2547	G
45	u	2553	A
45	u	2554	U
45	u	2555	G
45	u	2564	G
45	u	2566	G
45	u	2568	C
45	u	2571	C
45	u	2575	U
45	u	2577	C
45	u	2583	C
45	u	2587	A
45	u	2588	C
45	u	2589	C
45	u	2591	A
45	u	2601	A
45	u	2602	G
45	u	2611	A
45	u	2620	G
45	u	2623	A

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Mol	Chain	Res	Type
45	u	2624	G
45	u	2627	C
45	u	2638	G
45	u	2640	G
45	u	2647	A
45	u	2653	C
45	u	2661	U
45	u	2662	G
45	u	2663	G
45	u	2669	C
45	u	2673	G
45	u	2676	A
45	u	2679	G
45	u	2681	G
45	u	2686	G
45	u	2687	U
45	u	2688	G
45	u	2695	A
45	u	2696	A
45	u	2704	C
45	u	2708	U
45	u	2710	C
45	u	2711	G
45	u	2712	G
45	u	2714	G
45	u	2716	C
45	u	2721	G
45	u	2724	G
45	u	2725	A
45	u	2726	G
45	u	2733	C
45	u	2740	U
45	u	2743	A
45	u	2754	G
45	u	2755	A
45	u	2756	G
45	u	2760	G
45	u	2761	U
45	u	2762	G
45	u	2767	U
45	u	2768	C
45	u	2769	U

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Mol	Chain	Res	Type
45	u	2770	C
45	u	2772	C
45	u	2787	A
45	u	2788	U
45	u	2789	A
45	u	2790	U
45	u	2794	C
45	u	2795	A
45	u	2796	G
45	u	2798	A
45	u	2806	A
45	u	2807	A
45	u	2814	C
45	u	2824	C
45	u	2825	A
45	u	2826	U
45	u	2827	G
45	u	2828	U
45	u	2829	U
45	u	2835	A
45	u	2838	G
45	u	2839	U
45	u	2842	G
45	u	2855	G
45	u	2858	A
45	u	2859	G
45	u	2862	G
45	u	2869	U
45	u	2896	G
45	u	2897	G
45	u	2898	G
45	u	2904	U
45	u	2905	C
45	u	2910	G
45	u	3594	C
45	u	3595	U
45	u	3596	A
45	u	3597	G
45	u	3598	C
45	u	3605	C
45	u	3606	U
45	u	3615	G

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Mol	Chain	Res	Type
45	u	3617	G
45	u	3625	G
45	u	3626	G
45	u	3630	A
45	u	3635	A
45	u	3644	U
45	u	3653	A
45	u	3662	A
45	u	3668	C
45	u	3670	C
45	u	3671	G
45	u	3673	C
45	u	3674	G
45	u	3680	U
45	u	3682	A
45	u	3689	G
45	u	3692	A
45	u	3696	C
45	u	3698	G
45	u	3702	A
45	u	3709	U
45	u	3710	G
45	u	3711	A
45	u	3712	A
45	u	3715	U
45	u	3716	C
45	u	3717	A
45	u	3718	A
45	u	3722	G
45	u	3728	A
45	u	3729	U
45	u	3737	A
45	u	3740	G
45	u	3748	A
45	u	3750	G
45	u	3752	C
45	u	3753	G
45	u	3755	G
45	u	3756	A
45	u	3759	A
45	u	3760	A
45	u	3764	U

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Mol	Chain	Res	Type
45	u	3773	U
45	u	3774	A
45	u	3775	A
45	u	3776	G
45	u	3777	G
45	u	3778	U
45	u	3780	G
45	u	3783	A
45	u	3784	A
45	u	3786	U
45	u	3788	C
45	u	3798	U
45	u	3799	A
45	u	3802	U
45	u	3810	C
45	u	3811	G
45	u	3812	C
45	u	3813	A
45	u	3814	U
45	u	3817	A
45	u	3819	G
45	u	3822	U
45	u	3831	U
45	u	3836	A
45	u	3838	U
45	u	3839	G
45	u	3840	U
45	u	3859	G
45	u	3867	A
45	u	3877	A
45	u	3878	C
45	u	3879	G
45	u	3889	G
45	u	3897	G
45	u	3900	G
45	u	3901	A
45	u	3905	A
45	u	3906	A
45	u	3907	G
45	u	3912	U
45	u	3915	U
45	u	3916	G

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Mol	Chain	Res	Type
45	u	3917	A
45	u	3924	C
45	u	3925	U
45	u	3926	C
45	u	3927	U
45	u	3938	G
45	u	3939	G
45	u	3943	A
45	u	3946	G
45	u	4069	U
45	u	4070	U
45	u	4076	G
45	u	4084	G
45	u	4085	A
45	u	4086	G
45	u	4087	G
45	u	4088	C
45	u	4091	G
45	u	4092	G
45	u	4093	G
45	u	4094	G
45	u	4097	G
45	u	4104	G
45	u	4105	A
45	u	4107	G
45	u	4112	C
45	u	4114	C
45	u	4115	G
45	u	4116	C
45	u	4117	U
45	u	4118	U
45	u	4119	C
45	u	4120	U
45	u	4121	G
45	u	4122	G
45	u	4125	C
45	u	4127	A
45	u	4134	C
45	u	4143	G
45	u	4144	C
45	u	4145	C
45	u	4155	C

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Mol	Chain	Res	Type
45	u	4161	G
45	u	4162	C
45	u	4163	U
45	u	4165	C
45	u	4166	G
45	u	4168	G
45	u	4170	A
45	u	4171	C
45	u	4182	G
45	u	4183	G
45	u	4184	G
45	u	4191	G
45	u	4203	A
45	u	4208	U
45	u	4212	A
45	u	4213	A
45	u	4216	G
45	u	4217	G
45	u	4218	U
45	u	4219	A
45	u	4225	G
45	u	4226	G
45	u	4229	U
45	u	4232	U
45	u	4233	A
45	u	4238	G
45	u	4241	C
45	u	4251	A
45	u	4254	G
45	u	4255	A
45	u	4258	C
45	u	4265	U
45	u	4266	G
45	u	4267	G
45	u	4268	A
45	u	4271	A
45	u	4273	A
45	u	4282	A
45	u	4291	G
45	u	4297	G
45	u	4302	U
45	u	4303	C

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Mol	Chain	Res	Type
45	u	4304	A
45	u	4305	G
45	u	4306	U
45	u	4307	A
45	u	4311	A
45	u	4312	U
45	u	4313	A
45	u	4314	C
45	u	4317	A
45	u	4318	C
45	u	4319	C
45	u	4329	G
45	u	4330	G
45	u	4331	G
45	u	4332	C
45	u	4335	C
45	u	4336	A
45	u	4349	C
45	u	4350	C
45	u	4354	U
45	u	4355	G
45	u	4360	U
45	u	4367	G
45	u	4368	G
45	u	4372	U
45	u	4373	G
45	u	4377	G
45	u	4378	A
45	u	4379	A
45	u	4380	A
45	u	4387	C
45	u	4391	G
45	u	4394	A
45	u	4395	U
45	u	4396	A
45	u	4398	C
45	u	4405	G
45	u	4419	U
45	u	4420	U
45	u	4421	C
45	u	4422	A
45	u	4424	A

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Mol	Chain	Res	Type
45	u	4426	C
45	u	4430	G
45	u	4432	C
45	u	4433	G
45	u	4438	U
45	u	4439	U
45	u	4441	A
45	u	4444	C
45	u	4448	G
45	u	4449	A
45	u	4450	U
45	u	4453	C
45	u	4454	G
45	u	4463	U
45	u	4464	A
45	u	4471	U
45	u	4472	G
45	u	4473	A
45	u	4475	G
45	u	4476	C
45	u	4481	U
45	u	4482	U
45	u	4484	A
45	u	4488	A
45	u	4491	G
45	u	4495	G
45	u	4500	U
45	u	4510	A
45	u	4511	A
45	u	4512	U
45	u	4513	A
45	u	4515	G
45	u	4519	C
45	u	4520	G
45	u	4522	G
45	u	4524	G
45	u	4527	G
45	u	4528	G
45	u	4529	G
45	u	4535	A
45	u	4548	A
45	u	4549	G

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Mol	Chain	Res	Type
45	u	4550	G
45	u	4557	U
45	u	4567	G
45	u	4570	G
45	u	4573	G
45	u	4575	G
45	u	4577	U
45	u	4583	C
45	u	4584	A
45	u	4585	U
45	u	4586	G
45	u	4590	A
45	u	4591	U
45	u	4606	G
45	u	4618	G
45	u	4636	U
45	u	4637	G
45	u	4641	U
45	u	4647	G
45	u	4648	A
45	u	4656	A
45	u	4657	U
45	u	4661	G
45	u	4670	C
45	u	4672	A
45	u	4677	U
45	u	4687	A
45	u	4694	G
45	u	4695	C
45	u	4699	U
45	u	4700	A
45	u	4701	A
45	u	4702	G
45	u	4709	U
45	u	4719	G
45	u	4720	C
45	u	4721	G
45	u	4730	C
45	u	4731	G
45	u	4732	G
45	u	4733	C
45	u	4734	A

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Mol	Chain	Res	Type
45	u	4737	G
45	u	4741	C
45	u	4745	G
45	u	4746	C
45	u	4749	C
45	u	4750	G
45	u	4753	U
45	u	4754	G
45	u	4756	C
45	u	4758	U
45	u	4760	G
45	u	4764	A
45	u	4768	G
45	u	4770	U
45	u	4771	C
45	u	4774	C
45	u	4869	U
45	u	4871	C
45	u	4872	G
45	u	4873	G
45	u	4874	A
45	u	4875	G
45	u	4876	U
45	u	4877	G
45	u	4878	C
45	u	4883	C
45	u	4884	G
45	u	4885	U
45	u	4886	C
45	u	4889	G
45	u	4890	G
45	u	4893	A
45	u	4895	C
45	u	4896	G
45	u	4898	G
45	u	4900	C
45	u	4901	G
45	u	4904	G
45	u	4906	C
45	u	4910	G
45	u	4911	A
45	u	4912	G

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Mol	Chain	Res	Type
45	u	4913	G
45	u	4924	C
45	u	4926	C
45	u	4927	G
45	u	4930	C
45	u	4931	G
45	u	4932	U
45	u	4934	A
45	u	4935	C
45	u	4936	G
45	u	4939	C
45	u	4941	G
45	u	4942	C
45	u	4944	C
45	u	4945	G
45	u	4948	C
45	u	4949	G
45	u	4950	U
45	u	4951	G
45	u	4952	G
45	u	4959	U
45	u	4964	C
45	u	4965	U
45	u	4966	A
45	u	4967	A
45	u	4975	G
45	u	4976	U
45	u	4985	U
45	u	4988	U
45	u	4989	U
45	u	4990	C
45	u	4991	U
45	u	5007	A
45	u	5013	C
45	u	5014	A
45	u	5017	G
45	u	5018	C
45	u	5022	U
45	u	5023	C
45	u	5024	C
45	u	5025	C
45	u	5026	U

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Mol	Chain	Res	Type
45	u	5027	C
45	u	5028	G
45	u	5031	G
45	u	5033	G
45	u	5041	G
45	u	5047	C
45	u	5050	C
45	u	5052	C
45	u	5053	U
45	u	5054	C
45	u	5056	A
45	u	5058	A
45	u	5060	A
45	u	5061	A
45	u	5062	G
45	u	5066	U
46	v	7	G
46	v	11	A
46	v	21	G
46	v	25	G
46	v	33	U
46	v	40	U
46	v	51	G
46	v	53	U
46	v	54	A
46	v	64	G
46	v	74	A
46	v	76	U
46	v	97	G
46	v	99	G
46	v	100	A
46	v	106	G
46	v	109	U
46	v	110	G
46	v	111	C
46	v	120	U
47	w	2	G
47	w	3	A
47	w	34	U
47	w	35	C
47	w	38	U
47	w	39	G

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Mol	Chain	Res	Type
47	w	49	G
47	w	51	U
47	w	52	A
47	w	55	U
47	w	57	C
47	w	59	A
47	w	62	A
47	w	63	U
47	w	74	U
47	w	75	G
47	w	79	G
47	w	80	A
47	w	81	C
47	w	82	A
47	w	83	C
47	w	84	A
47	w	85	U
47	w	86	U
47	w	87	G
47	w	94	G
47	w	95	A
47	w	99	U
47	w	101	C
47	w	103	A
47	w	104	A
47	w	105	C
47	w	107	C
47	w	109	C
47	w	110	U
47	w	111	U
47	w	112	G
47	w	113	C
47	w	114	G
47	w	115	G
47	w	117	C
47	w	121	G
47	w	122	G
47	w	123	U
47	w	124	U
47	w	125	C
47	w	126	C
47	w	127	U

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Mol	Chain	Res	Type
47	w	137	A
47	w	143	G
47	w	150	C
47	w	156	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

8 monosaccharides 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	$\# Z > 2$
59	NAG	K	1	59,55	14,14,15	0.47	0	17,19,21	0.64	0
59	NAG	K	2	59	14,14,15	0.25	0	17,19,21	0.55	0
59	BMA	K	3	59	11,11,12	0.65	0	15,15,17	0.86	1 (6%)
59	MAN	K	4	59	11,11,12	0.82	0	15,15,17	1.62	2 (13%)
59	MAN	K	5	59	11,11,12	0.70	0	15,15,17	1.21	2 (13%)
59	MAN	K	6	59	11,11,12	0.89	1 (9%)	15,15,17	0.96	2 (13%)
59	MAN	K	7	59	11,11,12	1.24	1 (9%)	15,15,17	1.25	2 (13%)
59	MAN	K	8	59	11,11,12	0.67	0	15,15,17	1.02	2 (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
59	NAG	K	1	59,55	-	2/6/23/26	0/1/1/1
59	NAG	K	2	59	-	1/6/23/26	0/1/1/1
59	BMA	K	3	59	-	2/2/19/22	0/1/1/1
59	MAN	K	4	59	-	0/2/19/22	0/1/1/1
59	MAN	K	5	59	-	1/2/19/22	0/1/1/1
59	MAN	K	6	59	-	0/2/19/22	0/1/1/1
59	MAN	K	7	59	-	0/2/19/22	0/1/1/1
59	MAN	K	8	59	-	2/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	K	7	MAN	C2-C3	2.43	1.56	1.52
59	K	6	MAN	O5-C1	-2.00	1.40	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	K	4	MAN	C1-O5-C5	4.45	118.15	112.19
59	K	4	MAN	O2-C2-C3	-3.64	102.62	110.15
59	K	7	MAN	C1-O5-C5	3.25	116.55	112.19
59	K	5	MAN	C1-O5-C5	3.04	116.27	112.19
59	K	5	MAN	O2-C2-C3	-2.96	104.02	110.15
59	K	8	MAN	C1-O5-C5	2.83	115.98	112.19
59	K	6	MAN	O2-C2-C3	-2.41	105.16	110.15
59	K	7	MAN	O3-C3-C2	2.36	114.86	110.05
59	K	3	BMA	C1-O5-C5	2.15	115.07	112.19
59	K	8	MAN	O2-C2-C3	-2.12	105.76	110.15
59	K	6	MAN	C1-O5-C5	2.07	114.96	112.19

There are no chirality outliers.

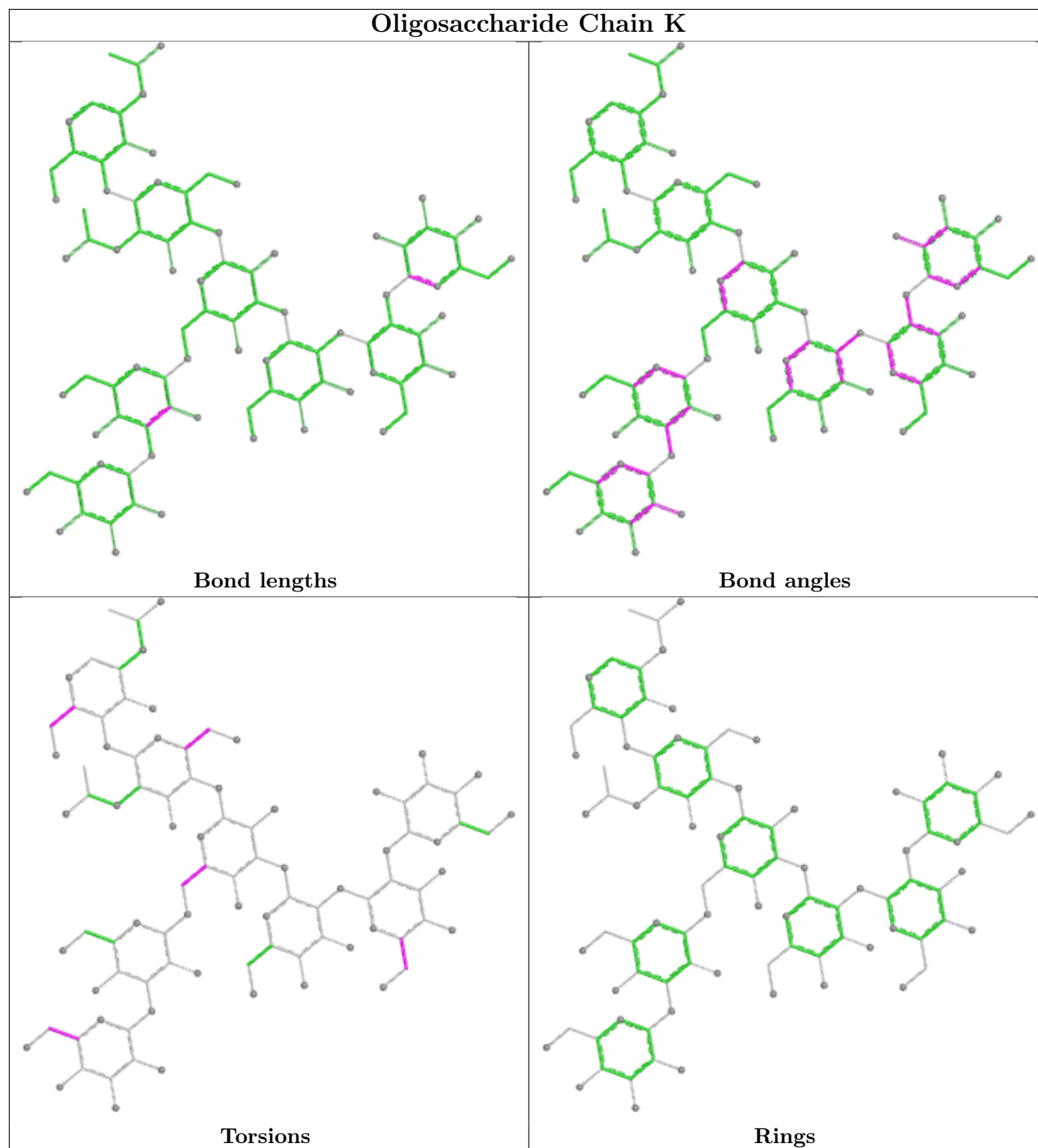
All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	K	3	BMA	C4-C5-C6-O6
59	K	3	BMA	O5-C5-C6-O6
59	K	8	MAN	O5-C5-C6-O6
59	K	8	MAN	C4-C5-C6-O6
59	K	1	NAG	C4-C5-C6-O6
59	K	1	NAG	O5-C5-C6-O6
59	K	5	MAN	O5-C5-C6-O6
59	K	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

Of 165 ligands modelled in this entry, 164 are monoatomic - leaving 1 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	$\# Z > 2$
62	9UB	5	809	-	43,43,43	2.55	10 (23%)	48,59,59	1.64	13 (27%)

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
62	9UB	5	809	-	-	3/39/62/62	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	5	809	9UB	P26-O25	8.09	1.67	1.58
62	5	809	9UB	P22-O25	7.82	1.67	1.59
62	5	809	9UB	P26-C29	6.76	1.91	1.80
62	5	809	9UB	C37-C39	-3.75	1.46	1.53
62	5	809	9UB	C41-N40	3.56	1.45	1.34
62	5	809	9UB	C06-C07	3.01	1.57	1.51
62	5	809	9UB	C11-C12	2.70	1.56	1.51
62	5	809	9UB	C18-C17	2.43	1.56	1.50
62	5	809	9UB	C16-C17	2.39	1.56	1.51
62	5	809	9UB	C20-C19	2.13	1.55	1.49

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	5	809	9UB	C18-C17-C16	4.13	122.39	115.23
62	5	809	9UB	C20-C19-C17	-3.78	120.01	126.20
62	5	809	9UB	C39-N40-C41	-2.68	116.83	123.11
62	5	809	9UB	C01-C02-C03	2.62	120.61	114.59
62	5	809	9UB	C32-O31-C30	2.59	117.72	113.19
62	5	809	9UB	O31-C32-C35	2.46	114.12	109.70
62	5	809	9UB	C15-C14-C12	-2.40	122.14	127.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	5	809	9UB	O27-P26-C29	2.39	111.04	105.69
62	5	809	9UB	C10-C09-C07	-2.38	122.18	127.62
62	5	809	9UB	C08-C07-C06	2.32	119.26	115.23
62	5	809	9UB	C18-C17-C19	-2.21	117.95	123.63
62	5	809	9UB	C13-C12-C11	2.17	118.99	115.23
62	5	809	9UB	C33-C32-C35	-2.06	107.95	113.02

There are no chirality outliers.

All (3) torsion outliers are listed below:

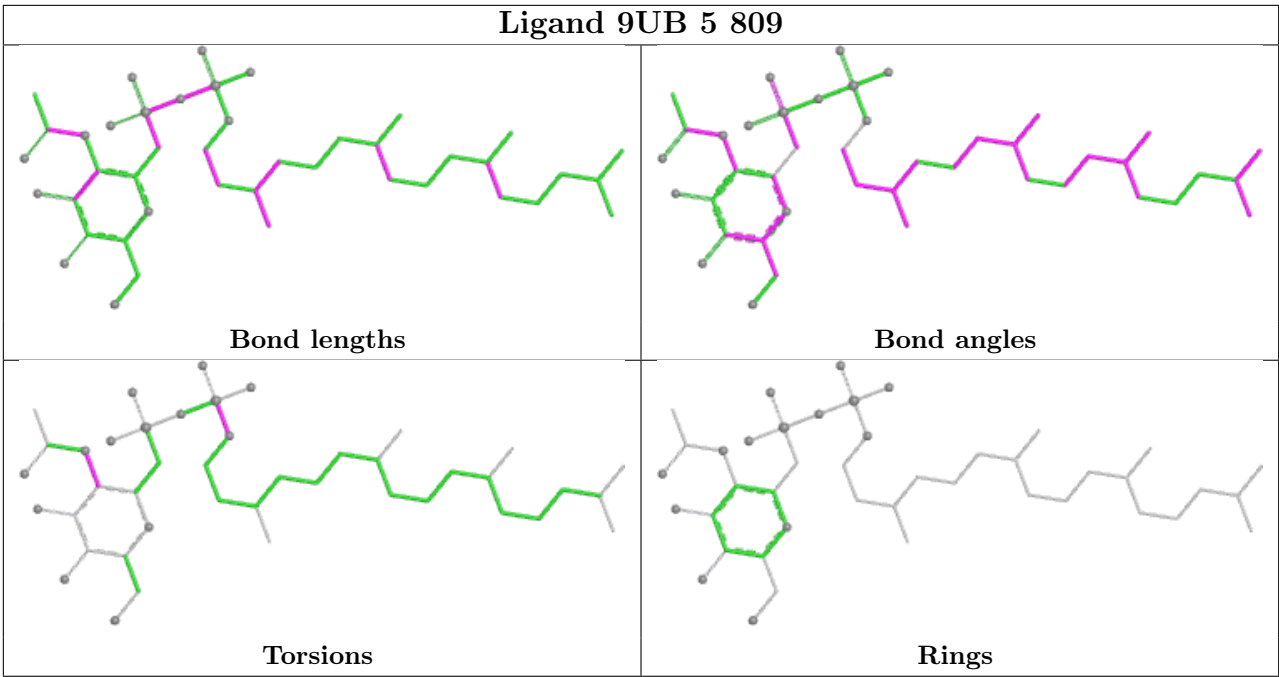
Mol	Chain	Res	Type	Atoms
62	5	809	9UB	C20-O21-P22-O25
62	5	809	9UB	C20-O21-P22-O23
62	5	809	9UB	C30-C39-N40-C41

There are no ring outliers.

1 monomer is involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	5	809	9UB	24	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
45	u	21
55	5	4
58	8	2
56	6	2
48	x	2
51	1	1
52	2	1
42	r	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	4776:G	O3'	4859:C	P	17.95
1	u	757:G	O3'	906:C	P	17.49
1	u	519:C	O3'	642:G	P	16.73
1	u	2910:G	O3'	3583:U	P	16.46

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	566:UNK	C	577:UNK	N	15.56
1	1	573:VAL	C	582:UNK	N	15.25
1	u	2131:C	O3'	2243:C	P	14.50
1	u	3950:U	O3'	4065:G	P	14.39
1	u	997:C	O3'	1047:C	P	13.95
1	6	46:UNK	C	53:UNK	N	13.30
1	2	42:UNK	C	50:UNK	N	12.33
1	8	598:UNK	C	600:UNK	N	11.54
1	6	82:UNK	C	88:UNK	N	10.20
1	x	312:PHE	C	337:PRO	N	9.61
1	u	1051:G	O3'	1064:G	P	8.98
1	x	133:MET	C	145:SER	N	8.39
1	u	1222:A	O3'	1232:G	P	5.15
1	u	2016:C	O3'	2017:A	P	4.53
1	u	1100:U	O3'	1167:C	P	4.42
1	u	1699:A	O3'	1718:C	P	4.00
1	r	121:GLN	C	122:LYS	N	2.97
1	u	1840:G	O3'	1842:G	P	2.91
1	u	4939:C	O3'	4941:G	P	2.80
1	5	502:PHE	C	503:ASP	N	2.78
1	u	4942:C	O3'	4944:C	P	2.73
1	u	1823:G	O3'	1825:A	P	2.56
1	5	590:SER	C	591:ASP	N	2.33
1	u	692:A	O3'	693:C	P	2.00
1	u	197:A	O3'	198:A	P	1.77
1	u	472:C	O3'	473:C	P	1.37
1	u	1965:G	O3'	1966:C	P	1.33
1	u	680:G	O3'	681:G	P	1.20
1	5	550:THR	C	551:HIS	N	0.96
1	5	545:ASN	C	546:THR	N	0.91

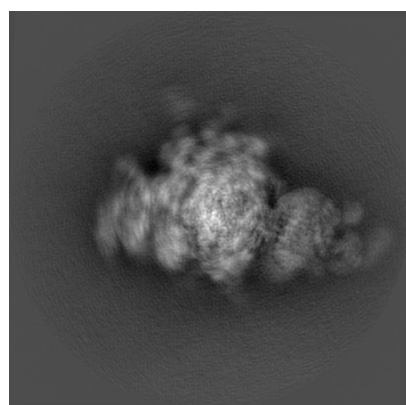
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4317. These allow visual inspection of the internal detail of the map and identification of artifacts.

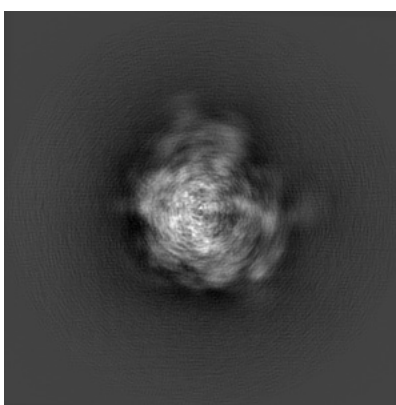
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

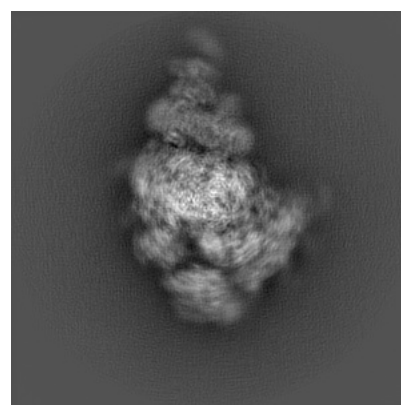
6.1.1 Primary map



X



Y

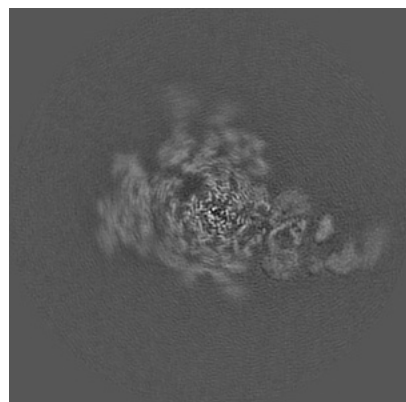


Z

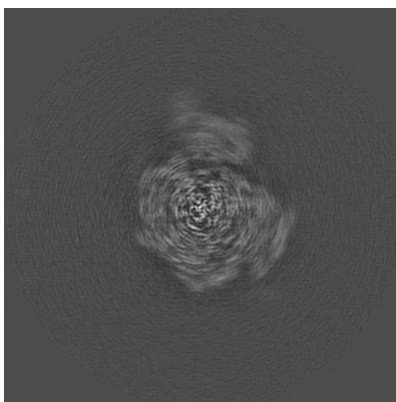
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

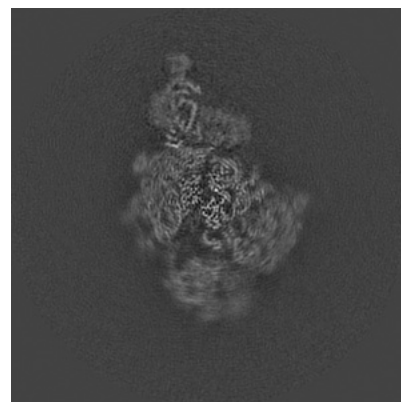
6.2.1 Primary map



X Index: 250



Y Index: 250

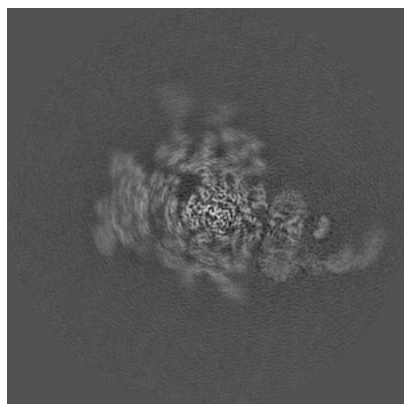


Z Index: 250

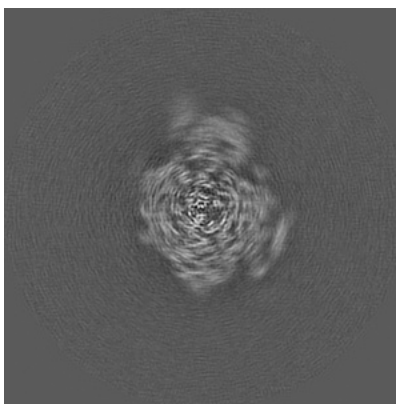
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

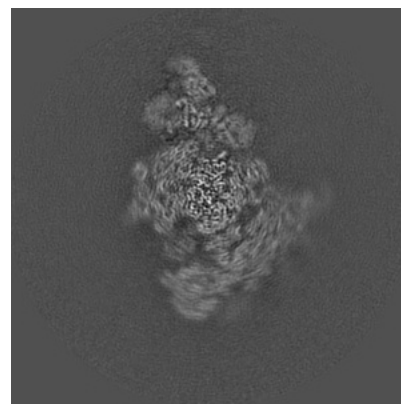
6.3.1 Primary map



X Index: 253



Y Index: 245

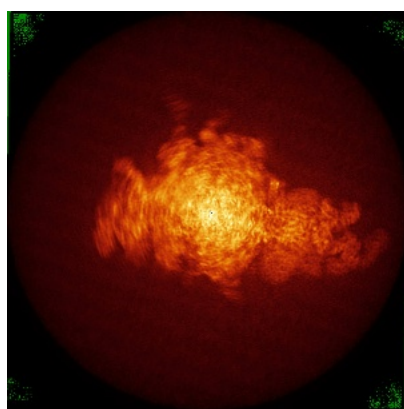


Z Index: 235

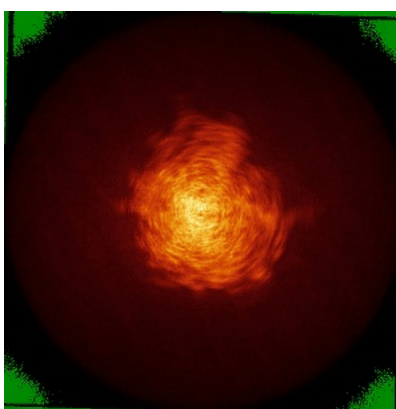
The images above show the largest variance slices of the map in three orthogonal directions.

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

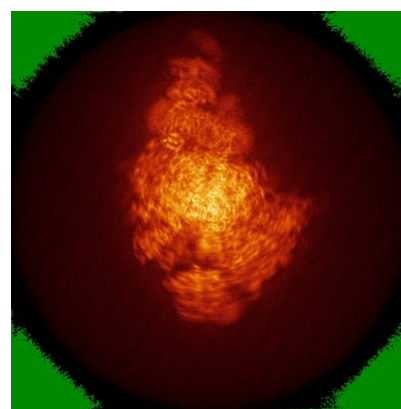
6.4.1 Primary map



X



Y



Z

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 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

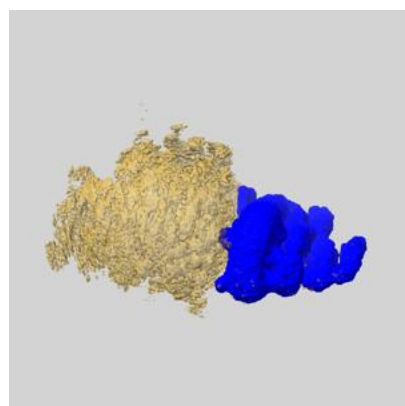
6.6 Mask visualisation [i](#)

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

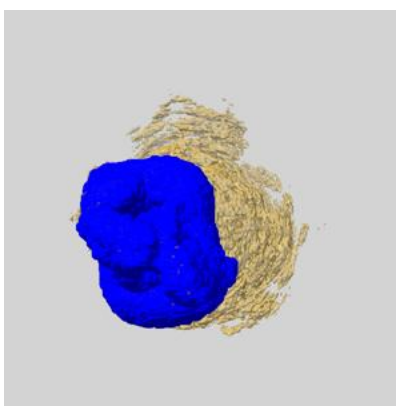
A mask typically either:

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

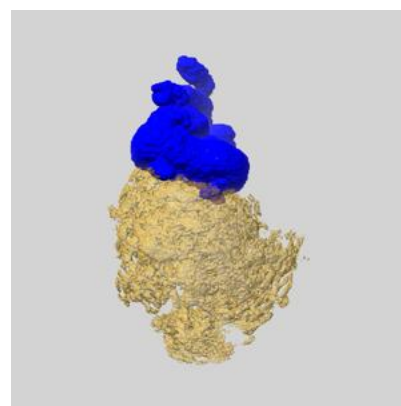
6.6.1 emd_4317_msk_1.map [i](#)



X



Y

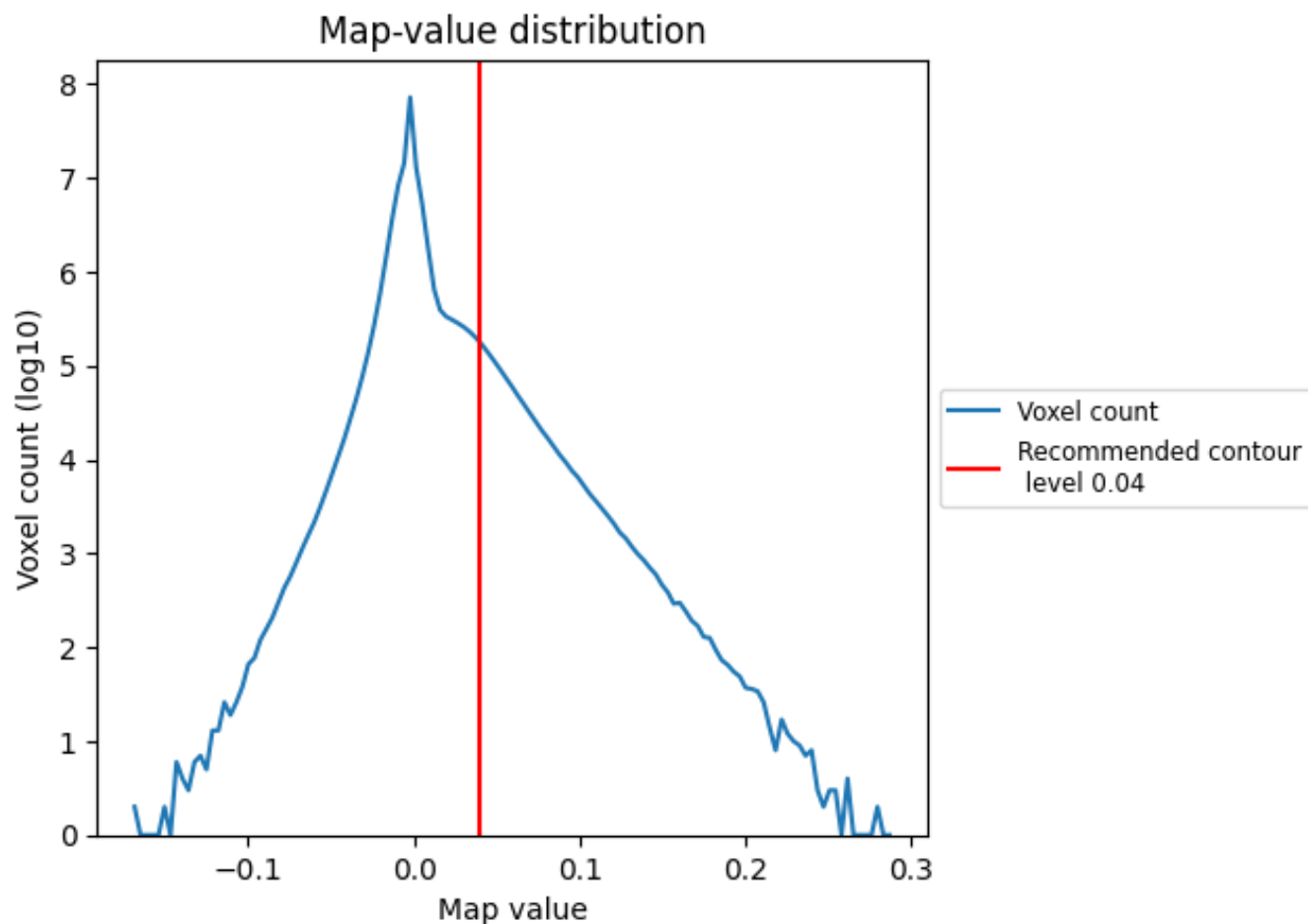


Z

7 Map analysis [i](#)

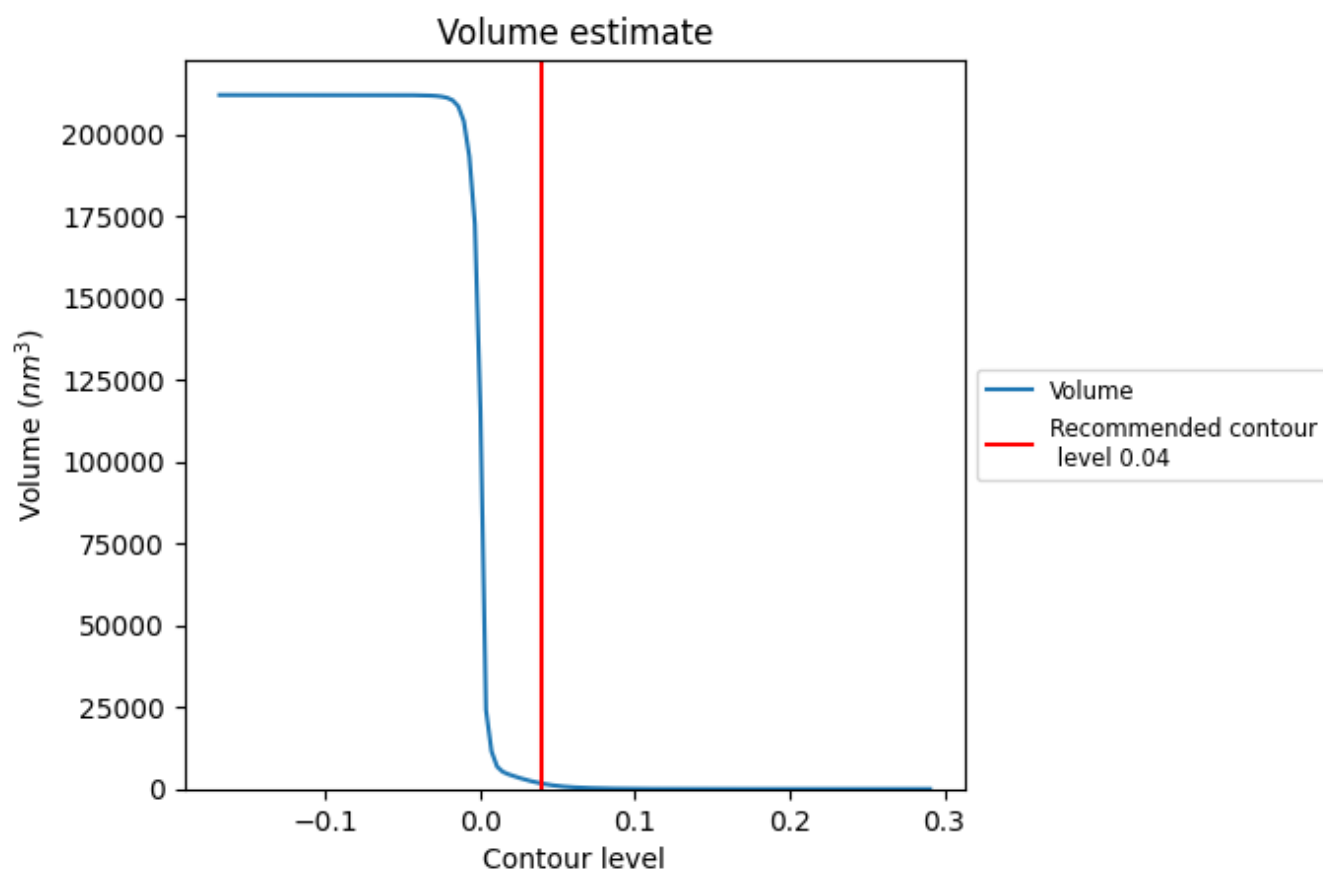
This section contains the results of statistical analysis of the map.

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.

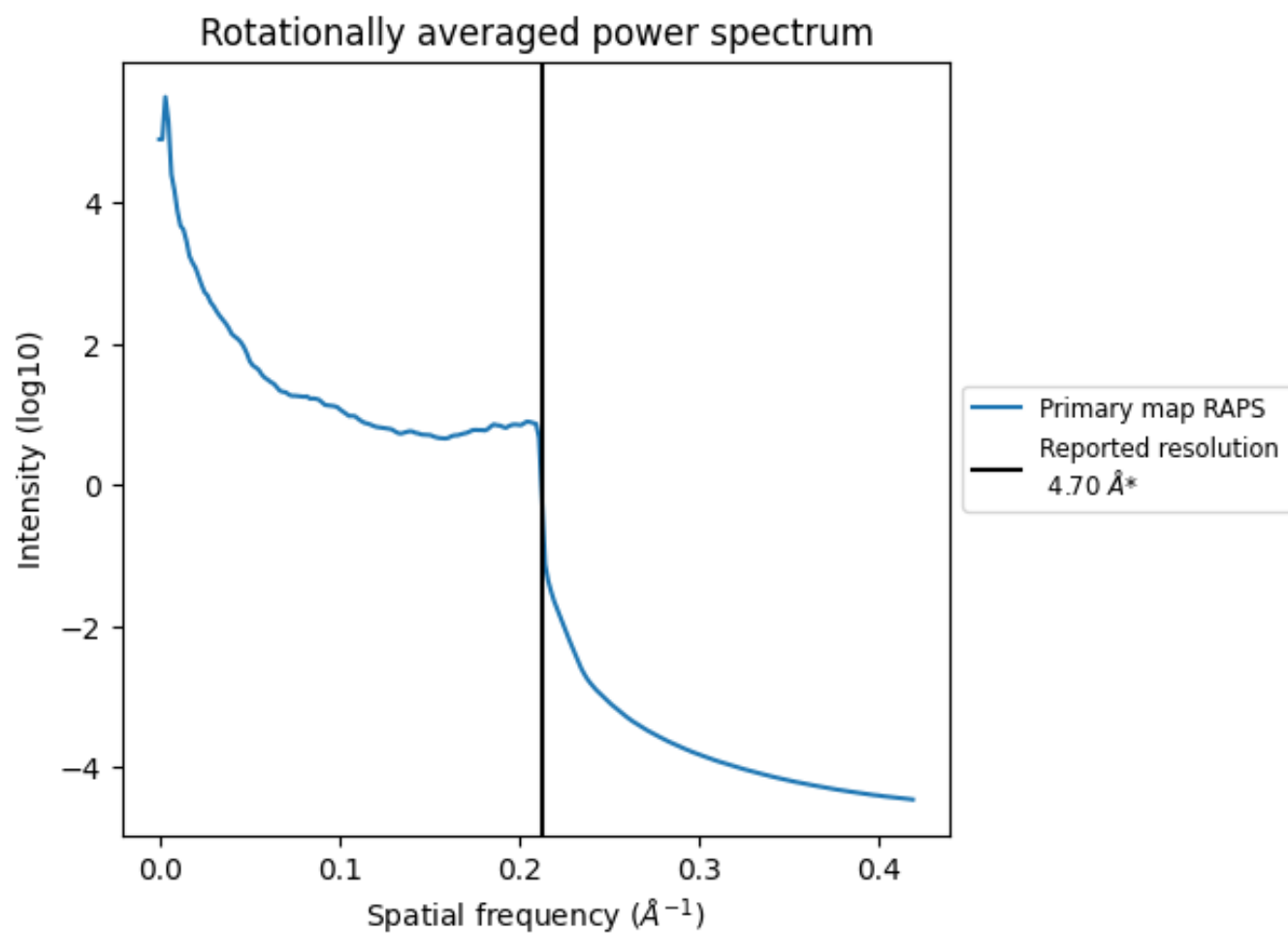
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1641 nm³; this corresponds to an approximate mass of 1482 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 0.213 Å⁻¹

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

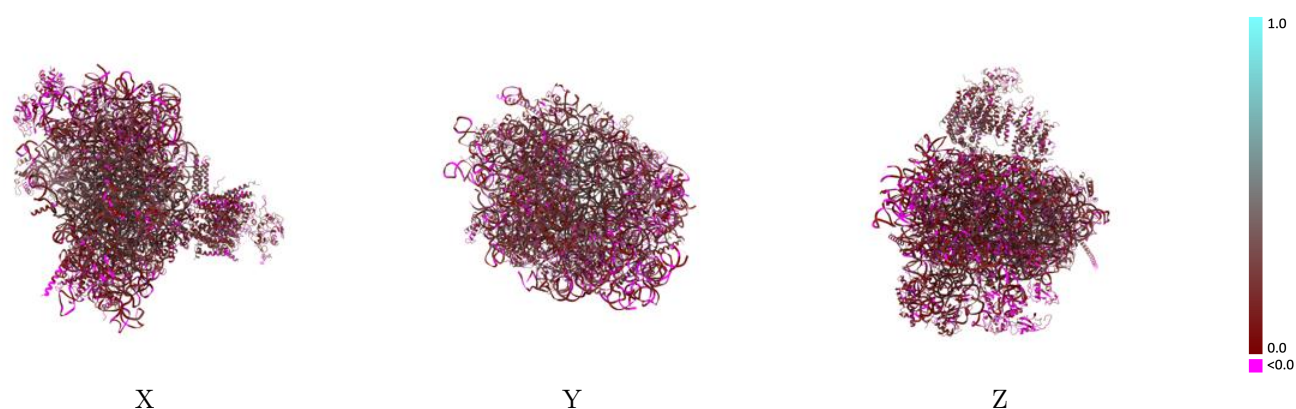
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4317 and PDB model 6FTJ. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)

This section was not generated.

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

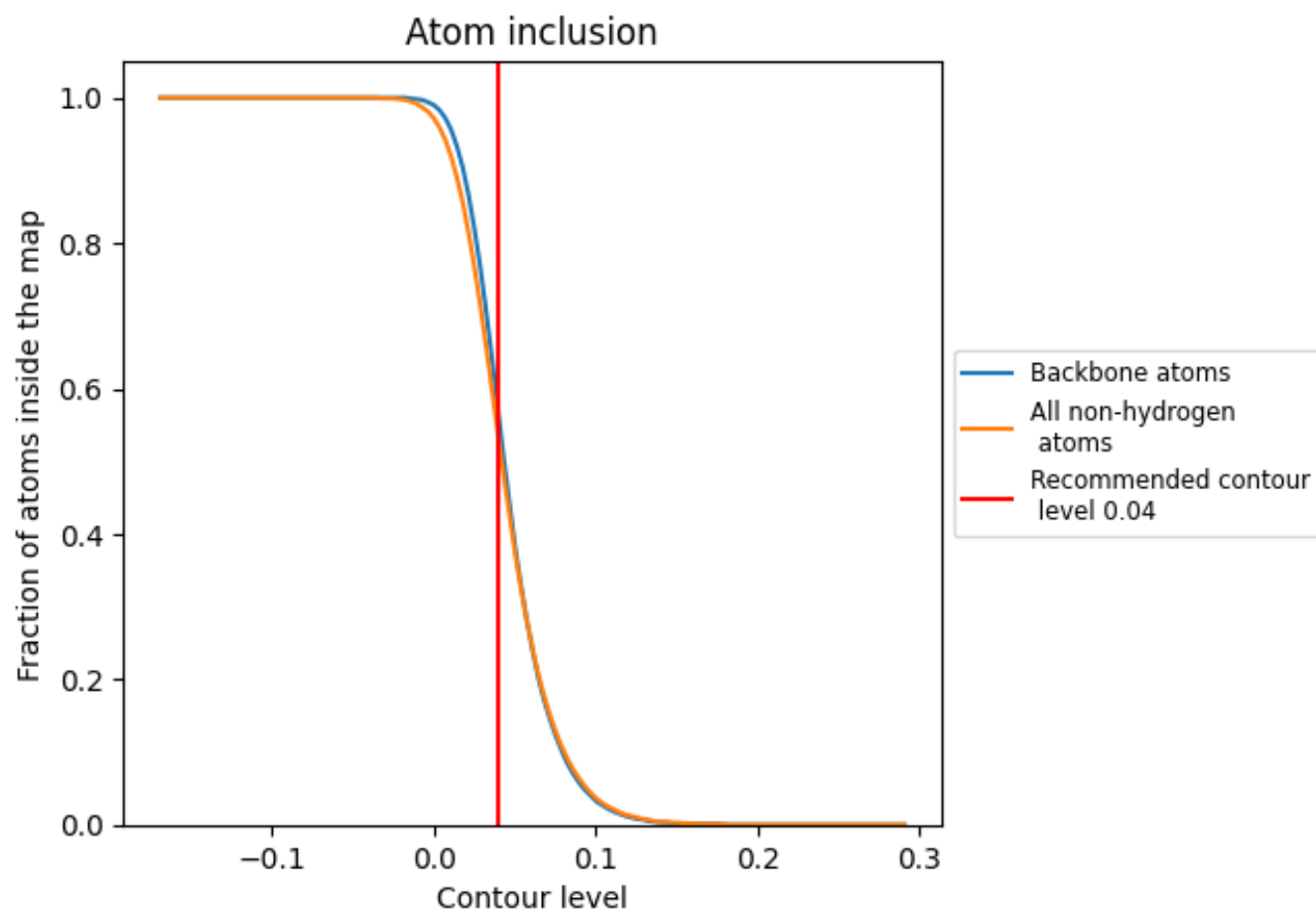


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 53% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5340	 0.1740
1	 0.6550	 0.1980
2	 0.7600	 0.2210
3	 0.5740	 0.1750
4	 0.6090	 0.2080
5	 0.5850	 0.1790
6	 0.8470	 0.2550
7	 0.8160	 0.2140
8	 0.7770	 0.2330
A	 0.3640	 0.1920
B	 0.3700	 0.1570
C	 0.3320	 0.1680
D	 0.3630	 0.1080
E	 0.2450	 0.0940
F	 0.2580	 0.1230
G	 0.2180	 0.1030
H	 0.2080	 0.0760
I	 0.3290	 0.1670
J	 0.3870	 0.1220
K	 0.5210	 0.1490
L	 0.3220	 0.1430
M	 0.2970	 0.1060
N	 0.3930	 0.1800
O	 0.2380	 0.1060
P	 0.5140	 0.2280
Q	 0.3310	 0.1600
R	 0.3910	 0.1490
S	 0.2490	 0.1080
T	 0.2310	 0.1230
U	 0.4110	 0.1380
V	 0.3350	 0.1830
W	 0.3930	 0.1850
X	 0.4090	 0.1880
Y	 0.4170	 0.1650
Z	 0.3620	 0.1310



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Chain	Atom inclusion	Q-score
a	 0.3010	 0.1530
b	 0.3340	 0.1360
c	 0.3160	 0.1520
d	 0.4640	 0.2090
e	 0.2440	 0.1380
f	 0.1830	 0.0770
g	 0.3030	 0.1600
h	 0.4390	 0.1690
i	 0.3370	 0.1660
j	 0.5720	 0.2520
k	 0.3000	 0.1370
l	 0.5580	 0.2660
m	 0.2520	 0.0870
n	 0.4530	 0.1880
o	 0.4210	 0.1890
p	 0.3220	 0.1620
r	 0.3350	 0.1260
s	 0.1440	 0.0380
t	 0.1180	 0.0100
u	 0.6530	 0.1930
v	 0.7110	 0.1640
w	 0.7430	 0.2300
x	 0.5500	 0.1930
y	 0.5620	 0.1960
z	 0.2620	 0.0520