



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 06:35 AM UTC

PDB ID : 6D90 / pdb_00006d90
EMDB ID : EMD-7834
Title : Mammalian 80S ribosome with a double translocated CrPV-IRES, P-site tRNA and eRF1.
Authors : Pisareva, V.P.; Pisarev, A.V.; Fernandez, I.S.
Deposited on : 2018-04-27
Resolution : 3.20 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
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

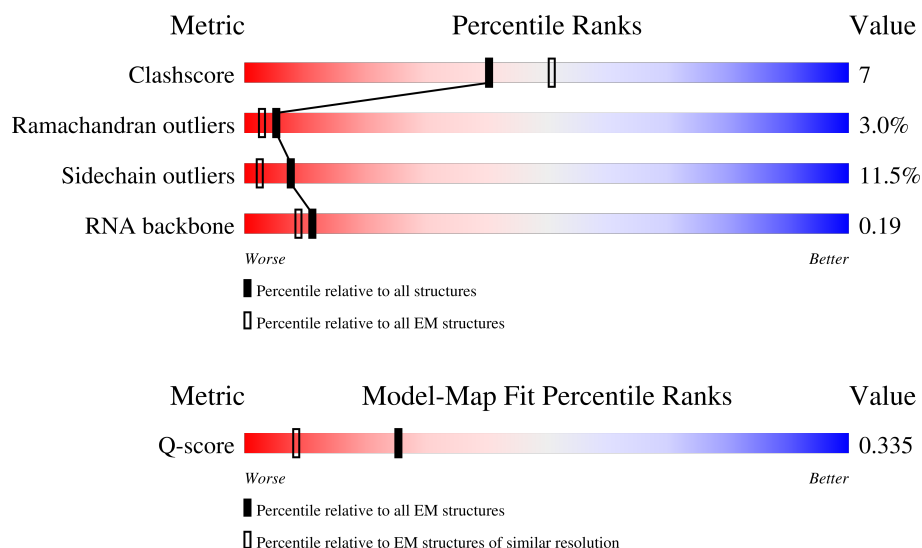
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	257	
2	B	403	
3	C	392	

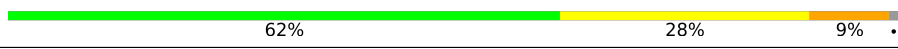
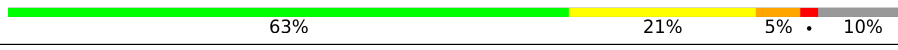
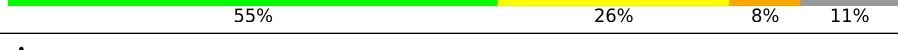
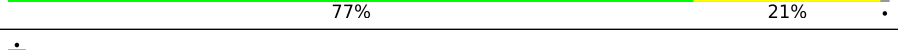
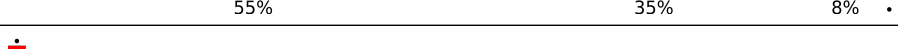
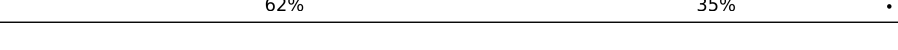
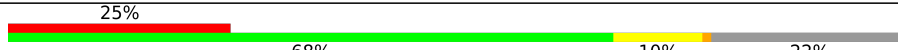
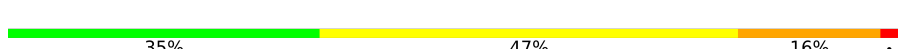
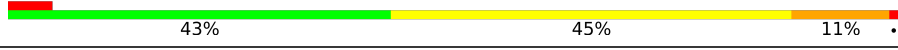
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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	249	
7	G	242	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	198	
13	N	204	
14	O	199	
15	P	184	
16	Q	188	
17	R	181	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	226	
28	c	115	

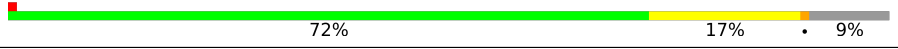
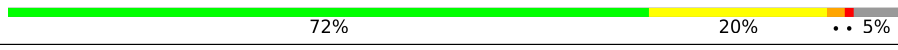
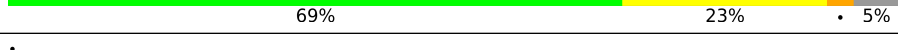
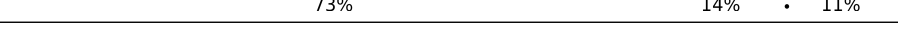
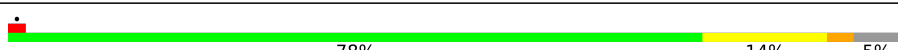
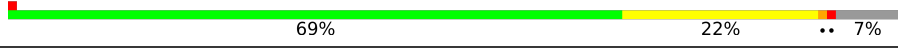
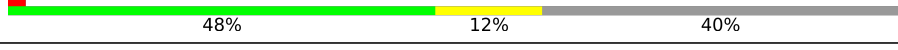
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Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	126	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	52	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	303	
44	t	195	
45	5	3594	
46	7	119	
47	8	151	
48	K	217	
49	2	1697	
50	3	87	
51	BB	295	
52	CC	264	
53	DD	255	

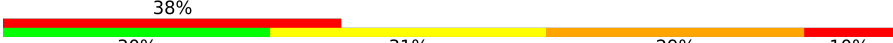
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Mol	Chain	Length	Quality of chain
54	EE	281	
55	FF	263	
56	GG	204	
57	HH	249	
58	II	194	
59	JJ	208	
60	KK	194	
61	LL	149	
62	MM	158	
63	NN	132	
64	OO	151	
65	PP	151	
66	QQ	145	
67	RR	172	
68	SS	135	
69	TT	152	
70	UU	145	
71	VV	119	
72	WW	83	
73	XX	130	
74	YY	143	
75	ZZ	134	
76	aa	125	
77	bb	115	
78	cc	84	

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Mol	Chain	Length	Quality of chain
79	dd	69	
80	ee	56	
81	ff	133	
82	gg	156	
83	hh	317	
84	jj	437	
85	4	194	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 223875 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 Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	239	Total	C	N	O	S	0	0
			1777	1110	361	300	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	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
			2883	1812	577	480	14		

- Molecule 4 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	LYS	-	expression tag	UNP P19949

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 8 is a protein called 60S ribosomal protein L9.

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 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	137	Total	C	N	O	S	0	0
			1130	722	220	181	7		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	PRO	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	PRO	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLY	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12

- 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	198	Total	C	N	O	S	0	0
			1623	1046	318	254	5		

- Molecule 15 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called rL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	6	ARG	LEU	conflict	UNP G1TX70
Q	14	ARG	TRP	conflict	UNP G1TX70
Q	23	ILE	MET	conflict	UNP G1TX70
Q	24	TYR	CYS	conflict	UNP G1TX70
Q	38	ARG	HIS	conflict	UNP G1TX70
Q	57	ASN	LYS	conflict	UNP G1TX70
Q	66	MET	VAL	conflict	UNP G1TX70
Q	74	GLY	ASP	conflict	UNP G1TX70
Q	75	ARG	PRO	conflict	UNP G1TX70
Q	86	VAL	ILE	conflict	UNP G1TX70
Q	110	ARG	HIS	conflict	UNP G1TX70
Q	117	GLY	GLU	conflict	UNP G1TX70
Q	124	ASP	HIS	conflict	UNP G1TX70
Q	150	ARG	GLN	conflict	UNP G1TX70
Q	172	ARG	GLY	conflict	UNP G1TX70
Q	184	ARG	TRP	conflict	UNP G1TX70

- Molecule 17 is a protein called Ribosomal protein L19.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 18 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	1	MET	THR	conflict	UNP G1TTY7
S	18	PRO	-	insertion	UNP G1TTY7
S	19	THR	-	insertion	UNP G1TTY7
S	20	PRO	SER	conflict	UNP G1TTY7
S	22	CYS	SER	conflict	UNP G1TTY7
S	23	ARG	PRO	conflict	UNP G1TTY7
S	24	THR	ALA	conflict	UNP G1TTY7
S	49	SER	LEU	conflict	UNP G1TTY7
S	50	GLN	GLU	conflict	UNP G1TTY7
S	95	ARG	HIS	conflict	UNP G1TTY7
S	101	THR	ILE	conflict	UNP G1TTY7
S	102	THR	MET	conflict	UNP G1TTY7
S	104	GLY	SER	conflict	UNP G1TTY7
S	126	ILE	VAL	conflict	UNP G1TTY7
S	132	ILE	MET	conflict	UNP G1TTY7
S	135	SER	ALA	conflict	UNP G1TTY7
S	136	LYS	ARG	conflict	UNP G1TTY7
S	138	ARG	PRO	conflict	UNP G1TTY7
S	149	LYS	ARG	conflict	UNP G1TTY7
S	151	LYS	ARG	conflict	UNP G1TTY7
S	168	THR	TYR	conflict	UNP G1TTY7
S	169	THR	ALA	conflict	UNP G1TTY7
S	176	PHE	-	insertion	UNP G1TTY7

- 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 eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1

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Chain	Residue	Modelled	Actual	Comment	Reference
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called uL24.

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 eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	98	Total	C	N	O	S	0	0
			761	481	134	140	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 Ribosomal protein L32.

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 Large ribosomal subunit protein 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 eL35.

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		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	3	ARG	GLN	conflict	UNP G1U3J0
k	38	CYS	TYR	conflict	UNP G1U3J0
k	48	THR	MET	conflict	UNP G1U3J0
k	66	VAL	MET	conflict	UNP G1U3J0

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			447	286	96	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 eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called Large ribosomal subunit protein 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 eL43.

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	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	262	LEU	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	266	THR	ALA	conflict	UNP A0A1U7UFL5
s	267	LEU	PHE	conflict	UNP A0A1U7UFL5
s	269	ILE	ALA	conflict	UNP A0A1U7UFL5
s	270	ILE	ASP	conflict	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PHE	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5

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Chain	Residue	Modelled	Actual	Comment	Reference
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PRO	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	272	VAL	ALA	conflict	UNP A0A1U7UFL5
s	273	ARG	ALA	conflict	UNP A0A1U7UFL5
s	274	ASP	ALA	conflict	UNP A0A1U7UFL5
s	275	SER	ALA	conflict	UNP A0A1U7UFL5
s	276	THR	PRO	conflict	UNP A0A1U7UFL5
s	278	ASP	ALA	conflict	UNP A0A1U7UFL5
s	282	ALA	LEU	conflict	UNP A0A1U7UFL5
s	284	GLN	ALA	conflict	UNP A0A1U7UFL5
s	286	SER	ALA	conflict	UNP A0A1U7UFL5
s	290	PRO	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	294	ASN	ASP	conflict	UNP A0A1U7UFL5

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5	3594	Total	C	N	O	P	0	0
			77073	34324	14116	25039	3594		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 48 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	K	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 50 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	87	Total	C	N	O	P	0	0
			1861	829	333	612	87		

- Molecule 51 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	114	THR	ALA	conflict	UNP G1TLT8
BB	235	GLU	ALA	conflict	UNP G1TLT8
BB	252	MET	VAL	conflict	UNP G1TLT8
BB	288	MET	VAL	conflict	UNP G1TLT8

- Molecule 52 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CC	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 53 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DD	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DD	97	PHE	CYS	conflict	UNP G1SWM1
DD	101	SER	ALA	conflict	UNP G1SWM1
DD	141	VAL	LEU	conflict	UNP G1SWM1
DD	181	PRO	LEU	conflict	UNP G1SWM1
DD	191	VAL	-	insertion	UNP G1SWM1
DD	215	MET	LEU	conflict	UNP G1SWM1
DD	271	ASP	ASN	conflict	UNP G1SWM1
DD	274	VAL	MET	conflict	UNP G1SWM1

- Molecule 54 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	EE	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 55 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	FF	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FF	25	GLY	SER	conflict	UNP G1TK17
FF	51	ARG	LYS	conflict	UNP G1TK17
FF	78	THR	ALA	conflict	UNP G1TK17
FF	156	VAL	MET	conflict	UNP G1TK17

- Molecule 56 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	GG	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 57 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	HH	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 58 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	II	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 59 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	JJ	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JJ	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 60 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
60	KK	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 61 is a protein called S10_ plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LL	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 62 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	MM	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 63 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	NN	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 64 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	OO	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 65 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	PP	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 66 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	QQ	115	Total	C	N	O	S	0	0
			956	610	176	163	7		

- Molecule 67 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	RR	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 68 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 69 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	TT	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 70 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	UU	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 71 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	VV	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 72 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	WW	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
WW	3	ASN	SER	conflict	UNP G1TM82
WW	4	ASP	ASN	conflict	UNP G1TM82
WW	33	GLN	PRO	conflict	UNP G1TM82
WW	50	PHE	SER	conflict	UNP G1TM82
WW	75	ALA	SER	conflict	UNP G1TM82
WW	76	ASP	HIS	conflict	UNP G1TM82
WW	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 73 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	XX	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	YY	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	ZZ	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 76 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	aa	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 77 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	bb	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
bb	28	ARG	CYS	conflict	UNP G1TFE8
bb	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 78 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	cc	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 79 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	dd	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 80 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	ee	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ff	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 82 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	gg	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 83 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	hh	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 84 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	jj	416	Total	C	N	O	S	0	0
			3280	2087	559	623	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
jj	183	ALA	GLY	conflict	UNP P62495
jj	184	ALA	GLY	conflict	UNP P62495

- Molecule 85 is a RNA chain called CrPV-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	4	194	Total	C	N	O	P	0	0
			4105	1840	704	1367	194		

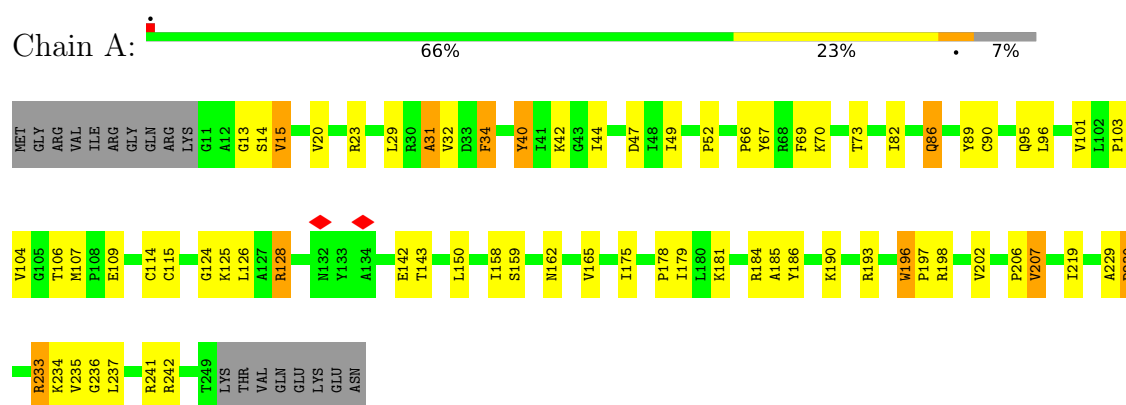
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	?	-	G	deletion	GB KP974707.1
4	6219	C	A	conflict	GB KP974707.1
4	6220	U	C	conflict	GB KP974707.1
4	6222	G	U	conflict	GB KP974707.1

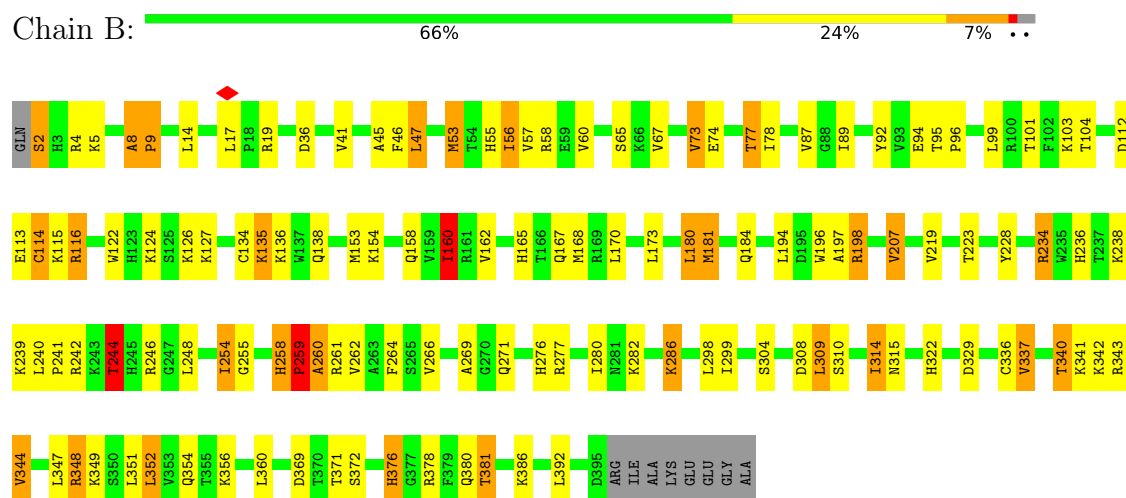
3 Residue-property plots

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

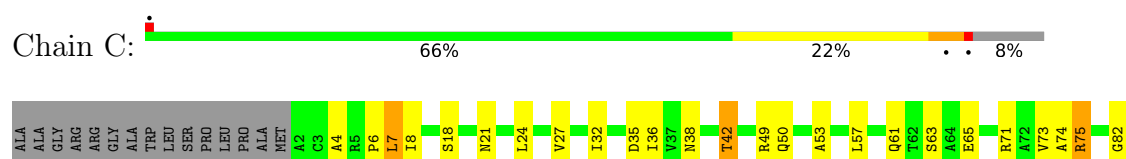
• Molecule 1: Ribosomal protein L8

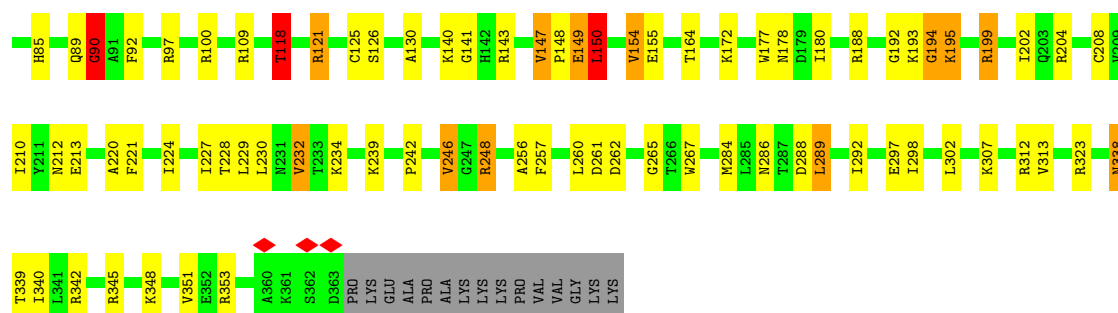


• Molecule 2: uL3



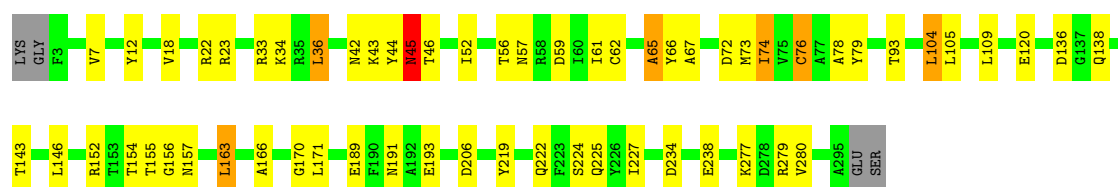
• Molecule 3: Ribosomal protein L4





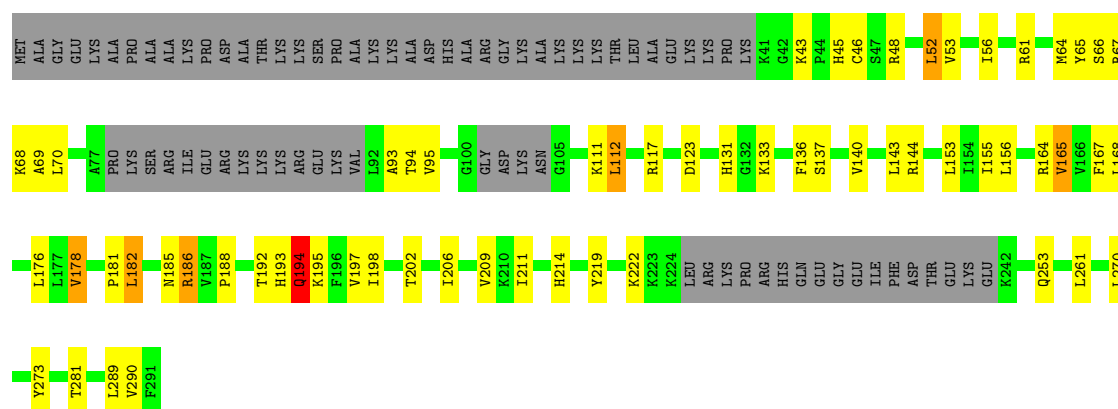
- Molecule 4: Large ribosomal subunit protein uL18

Chain D: 78% 18% ..



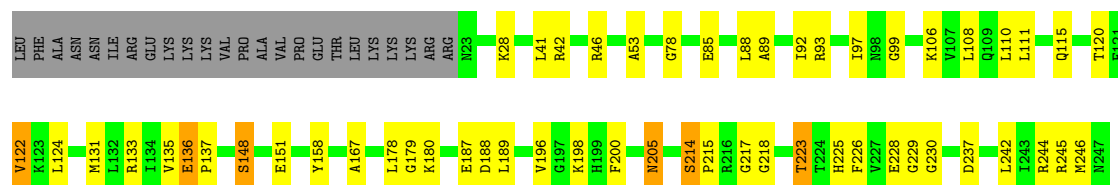
- Molecule 5: 60S ribosomal protein L6

Chain E: 53% 19% • 26%



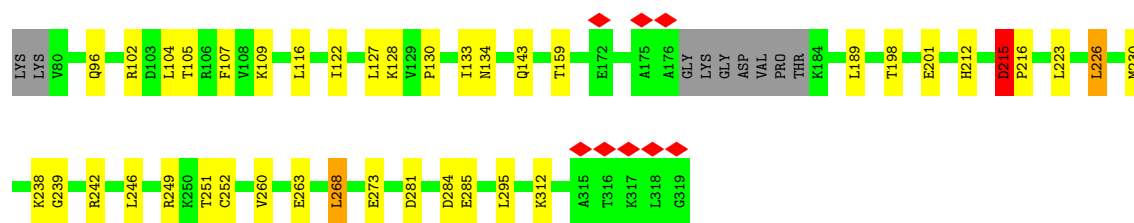
- Molecule 6: uL30

Chain F: 68% 20% • 10%

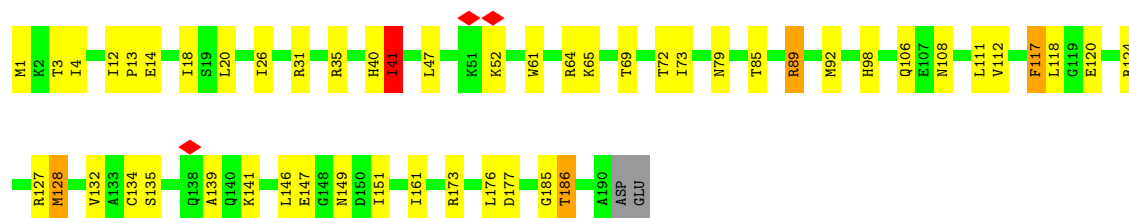


- Molecule 7: eL8

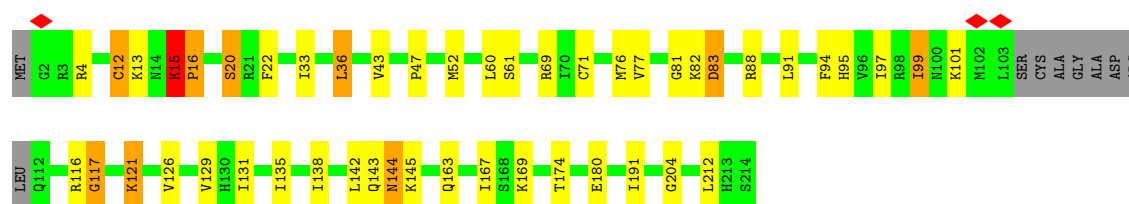
Chain G: 80% 15% ..



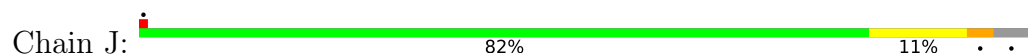
• Molecule 8: 60S ribosomal protein L9



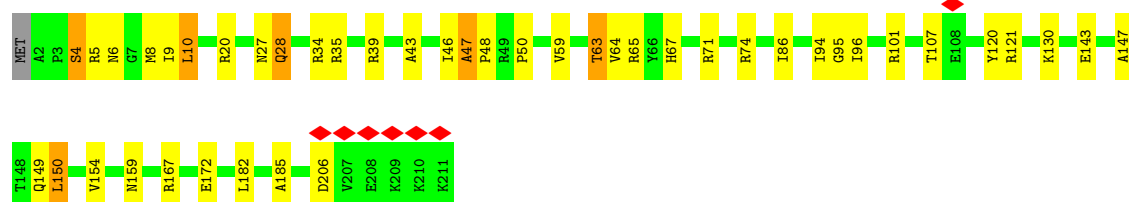
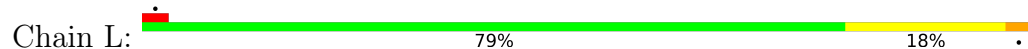
• Molecule 9: 60S ribosomal protein L10



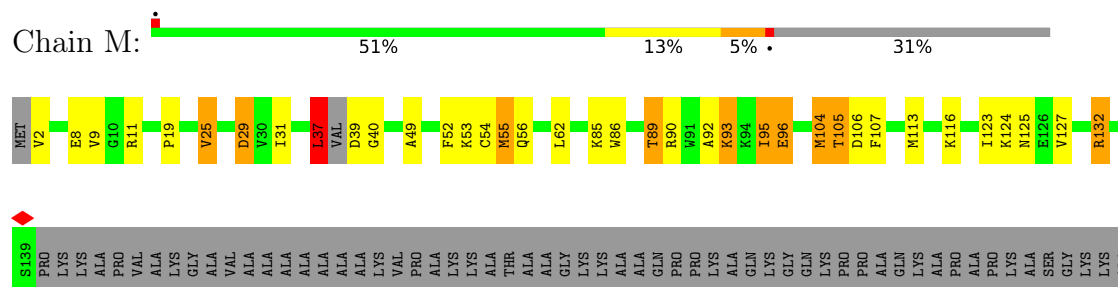
• Molecule 10: Ribosomal protein L11



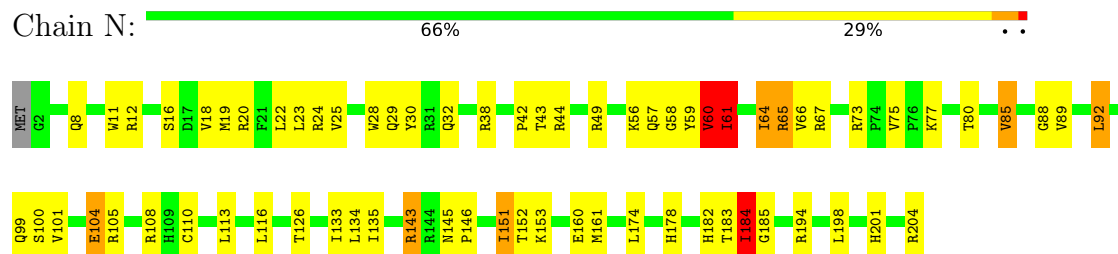
• Molecule 11: eL13



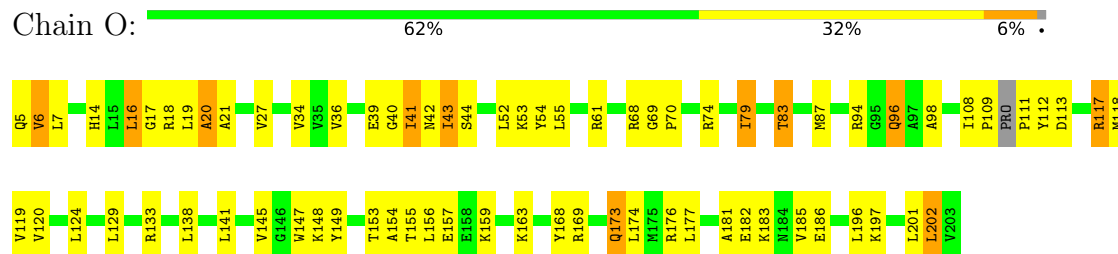
• Molecule 12: Large ribosomal subunit protein eL14



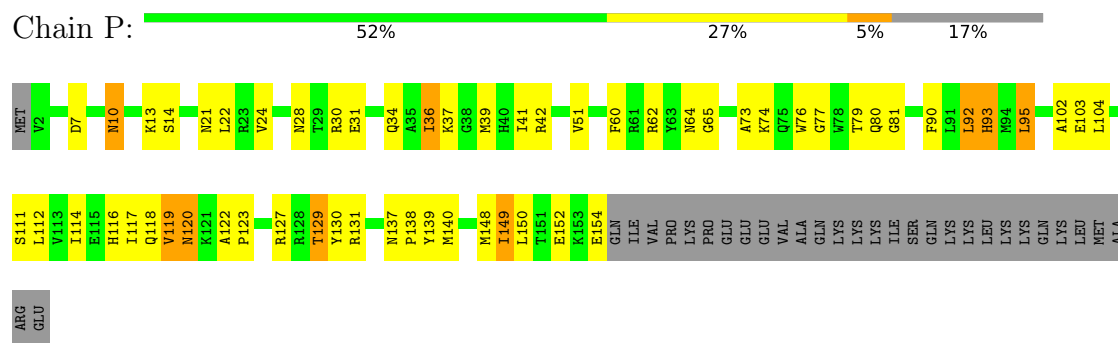
• Molecule 13: Ribosomal protein L15



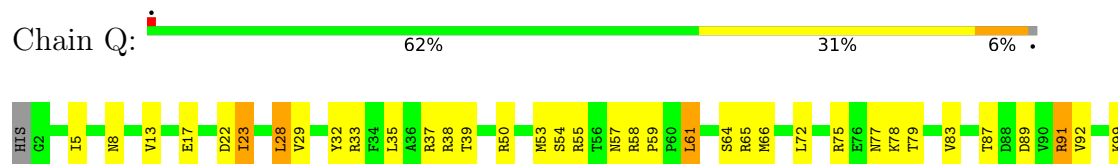
• Molecule 14: uL13

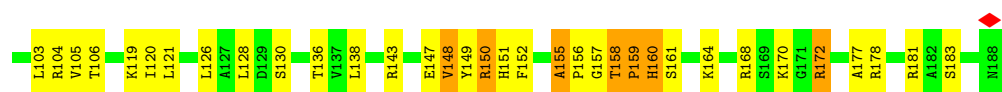


• Molecule 15: Large ribosomal subunit protein uL22



• Molecule 16: rL18





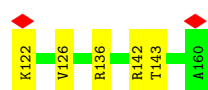
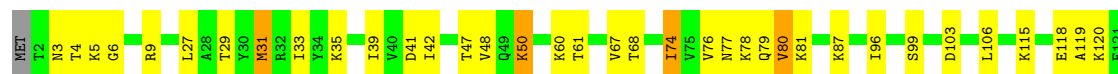
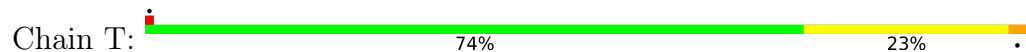
• Molecule 17: Ribosomal protein L19



• Molecule 18: 60S ribosomal protein L18a



• Molecule 19: eL21

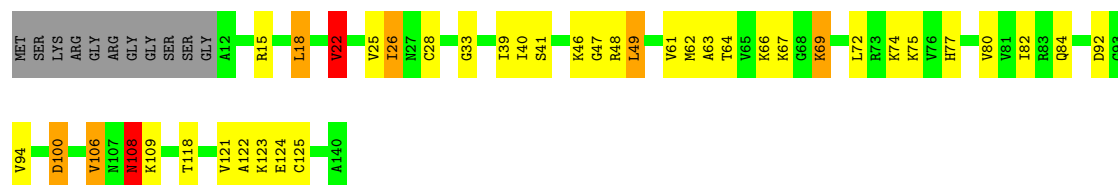


• Molecule 20: eL22

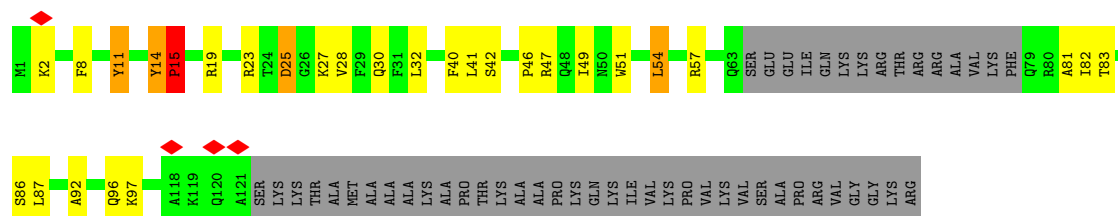


• Molecule 21: Ribosomal protein L23

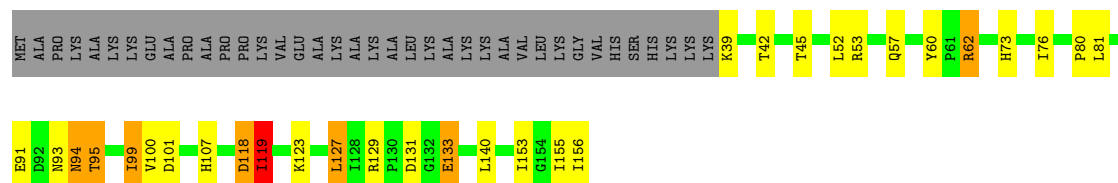




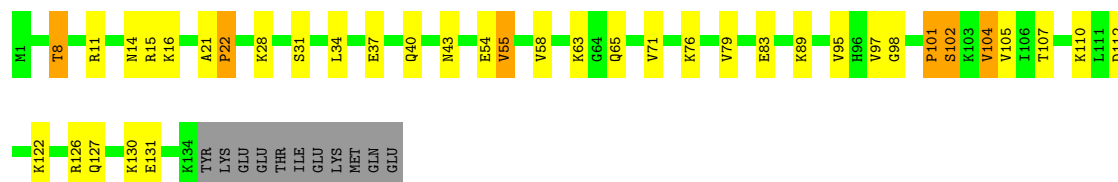
- Molecule 22: eL24



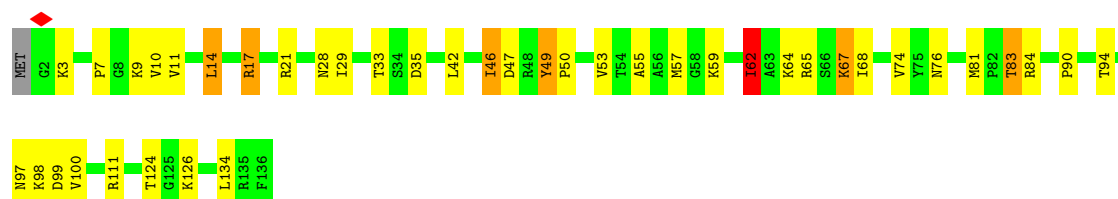
- Molecule 23: eL23



- Molecule 24: uL24

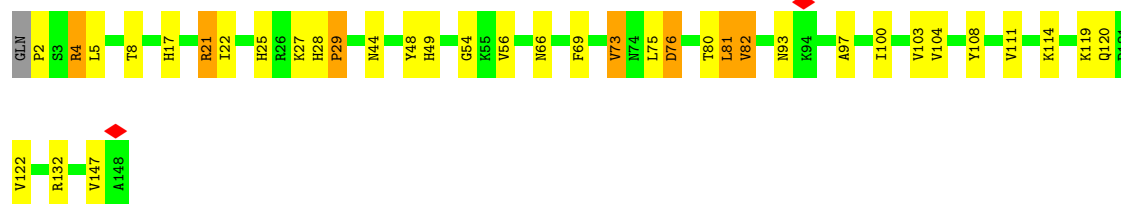


- Molecule 25: 60S ribosomal protein L27



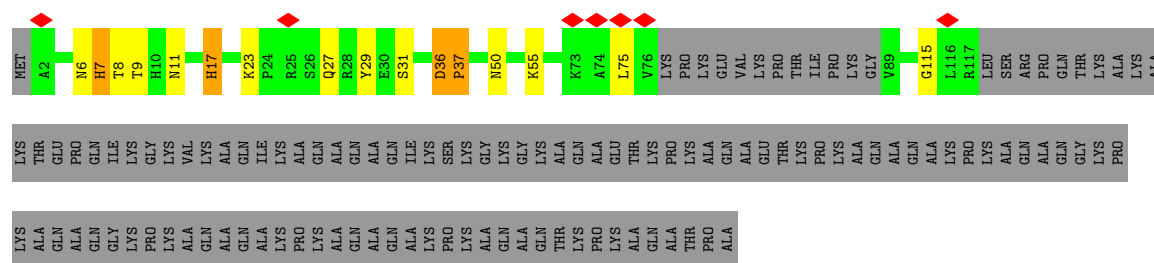
- Molecule 26: uL15

Chain a: 



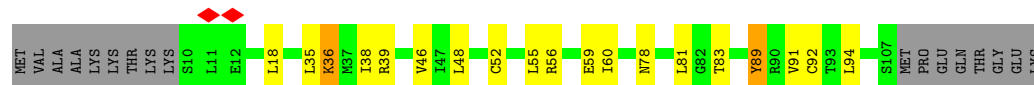
• Molecule 27: eL29

Chain b: 



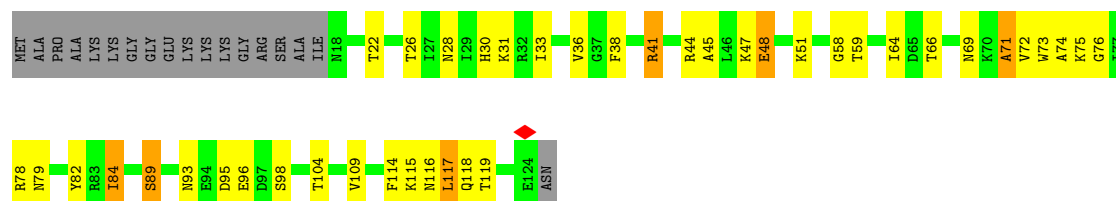
• Molecule 28: eL30

Chain c: 



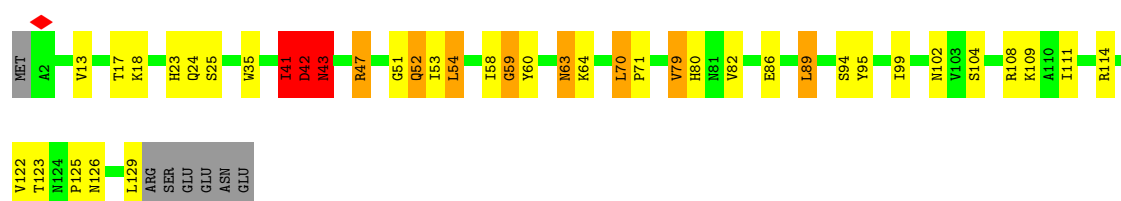
• Molecule 29: eL31

Chain d: 

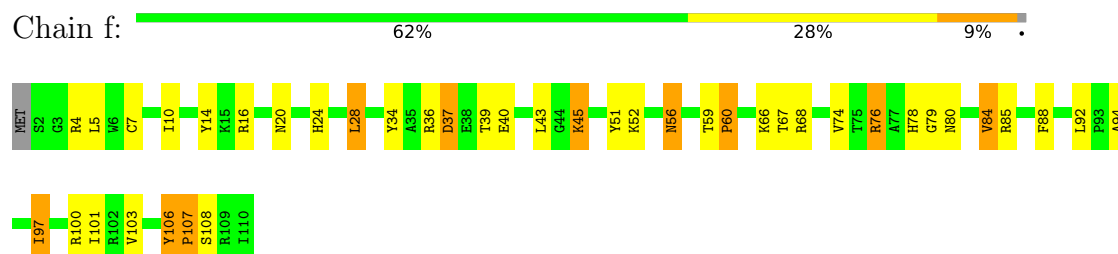


• Molecule 30: Ribosomal protein L32

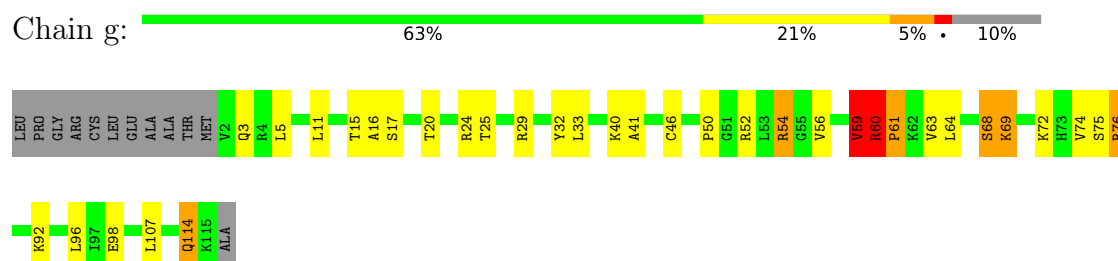
Chain e: 



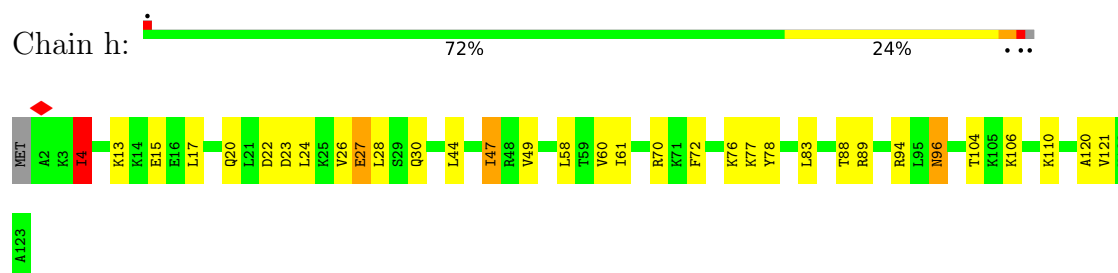
- Molecule 31: eL33



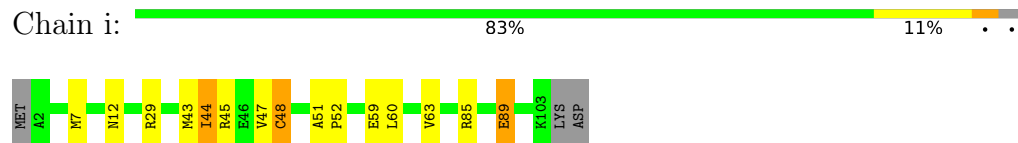
- Molecule 32: Large ribosomal subunit protein eL34



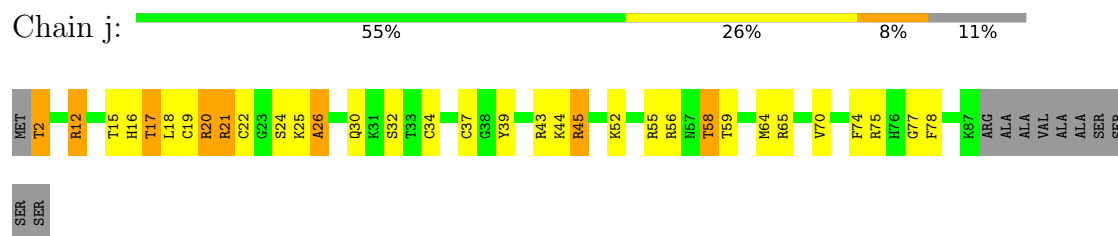
- Molecule 33: eL35



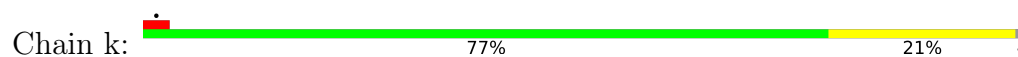
- Molecule 34: 60S ribosomal protein L36

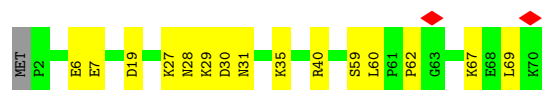


- Molecule 35: Ribosomal protein L37



- Molecule 36: eL38

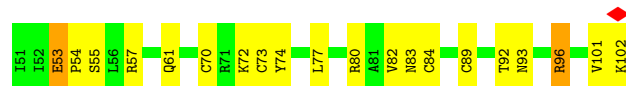




• Molecule 37: eL39



• Molecule 38: eL40



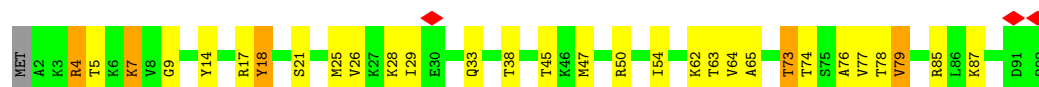
• Molecule 39: eL41



• Molecule 40: Large ribosomal subunit protein eL42



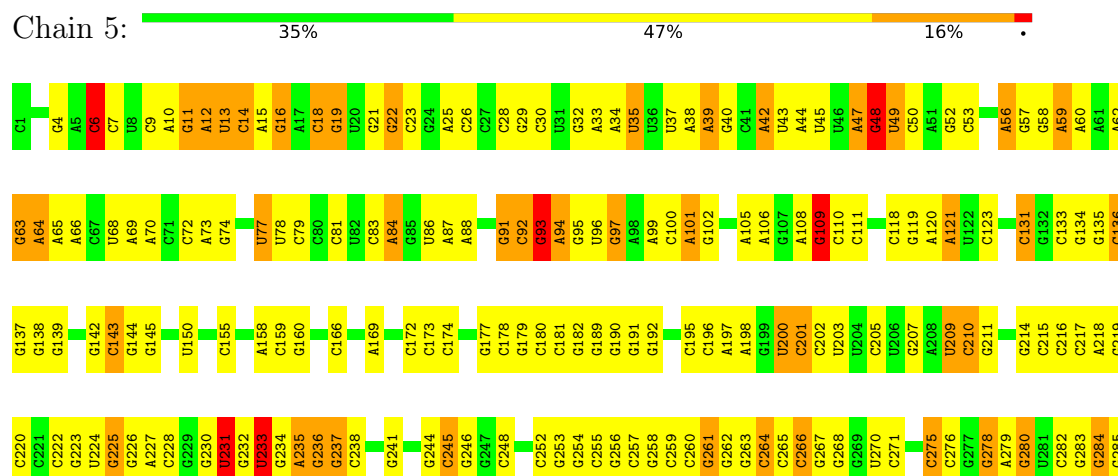
• Molecule 41: eL43



• Molecule 42: eL28



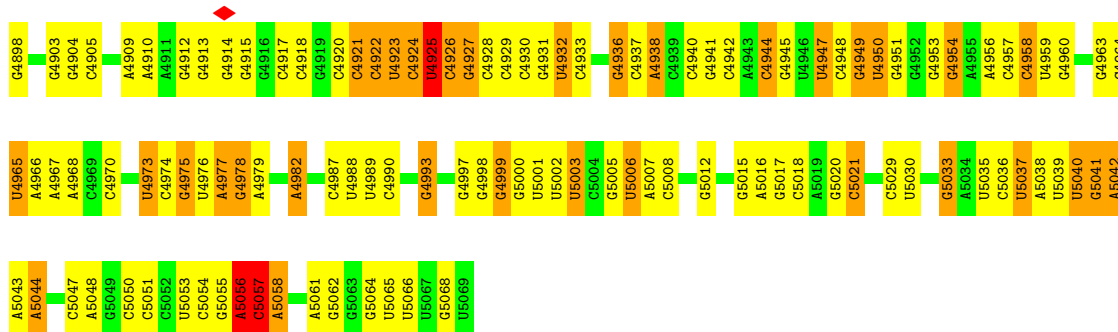
Chain s:



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G1769	A1684	U1616	C1535	G1470	A1391	G1322	G1234	C983	C916	C699	G507	C361
A1770	G1685	U1536	U1537	U1471	A1392	A1522	G1235	C984	A917	C700	G508	A362
G1771	C1686	G1618	A1538	C1472	G1393	G1323	G1236	C985	G918	G701	A509	A363
G1772	U1687	U1539	C1539	U1473	G1394	A1324	C1237	C986	C919	U702	U510	G364
U1773	G1688	U1622	G1539	C1474	G1395	A1325	A1238	C990	C920	C703	U511	U365
U1774	A1689	A1623	G1543	G1475	G1396	A1526	C1239	C990	C921	C704	C516	A366
A1775	G1690	G1624	G1543	C1476	A1397	C1327	G1244	C990	G922A	G437	C517	G369
A1776	C1692	G1625	G1543	C1477	A1398	G1328	G1245	C990	C922B	G438	G518	A295
C1777	U1693	C1546	C1546	C1478	G1399	G1329	G1246	C990	C923	C706	C519	A296
U1778	G1694	A1547	G1548	C1479	G1400	A1330	C1251	C990	C924	A711	C521	U297
U1779	U1695	G1548	G1548	C1481	G1401	C1331	C1252	C990	C925	G712	C522	G298
C1696	C1696	A1554	G1554	G1482	C1402	C1332	C1252	C990	G926	G713	C522	A300
G1720	G1693	G1555	G1555	C1483	G1403	A1333	C1271	C990	C927	G714	C522	G301
G1721	A1634	C1556	G1556	G1484	C1405	A1334	C1272	C990	C928	A711	C522	C302
C1722	C1635	C1557	C1557	C1485	C1405	G1335	C1273	C990	C929	U717	C522	C303
A1723	U1636	A1558	G1558	G1487	C1411C	G1336	C1274	C990	C930	C718	C522	G304
G1724	A1637	A1559	G1559	G1488	G1412	A1337	C1275	C990	A932	C719	C522	A305
U1727	G1640	G1641	G1560	G1489	G1413	U1339	C1276	C990	G933	G722	C522	A306
U1728	A1642	A1643	G1561	G1490	C1414	U1340	C1277	C990	A935	A723	C522	G312
U1729	A1644	C1644	G1562	G1491	G1415	U1341	C1278	C990	G935A	C727	C522	G315
C1732	G1645	C1645	G1563	G1492	G1415	U1341	C1279	C990	C936	U728	C522	U316
G1733	U1649	U1650	G1564	G1493	G1415	U1341	C1280	C990	C937	C729	C522	A319
U1734	G1650	G1651	G1565	G1494	G1415	U1341	C1281	C990	A943	G730	C522	C320
U1735	G1651	G1652	G1566	G1495	G1415	U1341	C1282	C990	A944	G731	C522	A320
A1736	G1652	G1653	G1567	G1496	G1415	U1341	C1283	C990	U945	G732	C522	A321
G1737	G1653	G1654	G1568	G1497	G1415	U1341	C1284	C990	C948	A733	C522	U327
U1738	G1654	G1655	G1569	G1498	G1415	U1341	C1285	C990	C949	G734	C522	U328
U1739	G1655	G1656	G1570	G1499	G1415	U1341	C1286	C990	C950	G735	C522	G331
G1821	G1656	G1657	G1571	G1501	G1415	U1341	C1287	C990	C951	G736	C522	C332
U1822	G1657	G1658	G1572	G1502	G1415	U1341	C1288	C990	C952	G737	C522	U333
G1823	G1658	G1659	G1573	G1503	G1415	U1341	C1289	C990	C953	G738	C522	A334
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A1825	G1660	G1661	G1575	G1505	G1415	U1341	C1291	C990	C955	G740	C522	A336
G1826	G1661	G1662	G1576	G1506	G1415	U1341	C1292	C990	C956	G741	C522	U337
C1827	G1662	G1663	G1577	G1507	G1415	U1341	C1293	C990	C957	G742	C522	A338
G1828	G1663	G1664	G1578	G1508	G1415	U1341	C1294	C990	C958	G743	C522	G403
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G1835	G1669	G1670	G1583	G1513	G1415	U1341	C1299	C990	C963	G748	C522	G409
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G1839	G1676	G1677	G1587	G1517	G1415	U1341	C1303	C990	C967	G752	C522	G343
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G1844	G1686	G1687	G1592	G1522	G1415	U1341	C1308	C990	C972	G757	C522	G415
G1845	G1688	G1689	G1593	G1523	G1415	U1341	C1309	C990	C973	G758	C522	U416
G1846	G1690	G1691	G1594	G1524	G1415	U1341	C1310	C990	C974	G759	C522	G417
G1847	G1692	G1693	G1595	G1525	G1415	U1341	C1311	C990	C975	G760	C522	C351
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G1850	G1698	G1699	G1598	G1528	G1415	U1341	C1314	C990	C978	G763	C522	U354
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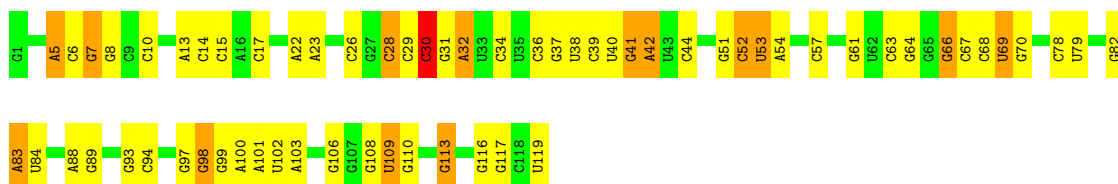
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G3634	G2797	A2725	C2651	G2575	C2437	A2368	G2294	U2084	U2015	G1945	U1876
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C3636	A2799	G2727	C2653	G2577	G2439	C2373	G2301	G2086	A2017	U1948	G1880
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	U2801	C2731	G2655	A2581	C2441	G2375	G2303	G2089	G2023	U1953	U1852
U3641	G2802	G2732	G2656	A2582	U2444	A2376	U2304	U2090	C2024		G1883
A3642	U2803	G2733	A2659	G2583	G2445	C2377	G2305	C2091	A2025	U1957	C1884
A3643	G2804	G2734	G2660	G2584	G2446	G2378	G2306	G2092	A2026	A1958	
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A3663	C2820	G2754	C2676	G2601	G2462	G2394	C2322	A2107	G1902	U1974	
G3664	U2821	A2755	G2677	G2602	U2463	A2395	G2323	G2108	A2043	G1975	
G3665	G2822	G2756	G2678	G2603	G2464	G2397	G2324	A2109	U2044	G1976	
C3666	U2823	A2757	G2679	C2604	G2465	U2398	G2325	G2109	G2045	C1977	
	A2824	G2758	G2680	G2605	G2466	G2399	G2326	G2110	A2046	U1906	
G3669	G2825	G2759	C2681	G2606	G2467		G2327	G2111	A2047	C1978	
G3670	U2826	G2760	U2691	C2607	G2470	G2404	G2328	G2112	U2048	A1979	
C3671	G2827	U2761	U2692		G2471	G2405	G2329	G2113	G2049	U1980	
G3672	U2828	G2762	G2693	A2611	A2472	G2406	G2330	G2114	G2050	U1981	
C3673	U2829	U2763	G2694	G2542	G2473	G2407	A2332	G2115	G2051	G1982	
G3674	G2830	A2764	A2695	A2543	G2474	G2408	G2333	G2116	C2052	A1983	
G3675	C3601	A2765	A2696	G2544	G2475	U2409	G2334	G2117	C2053	A1984	
G3676	A2831	A2766	G2697	U2545	A2476	G2411	G2335	G2118	U2054	G1985	
	A2832	G2767	G2698	G2546	C2477	U2412	G2336	G2119	G2055	U1986	
U3677	A2833	G2768	C2699	G2547	G2478	A2413	G2337	G2120	U2056	C1987	
	A2834	U2769	G2700	C2548	G2479	U2414	C2340	G2121	A2057	G1988	
	A2835	G2770	G2699	G2549	C2482	U2415	U2344			G1989	
	A2836	G2771	U2701	G2550	G2483	G2414					





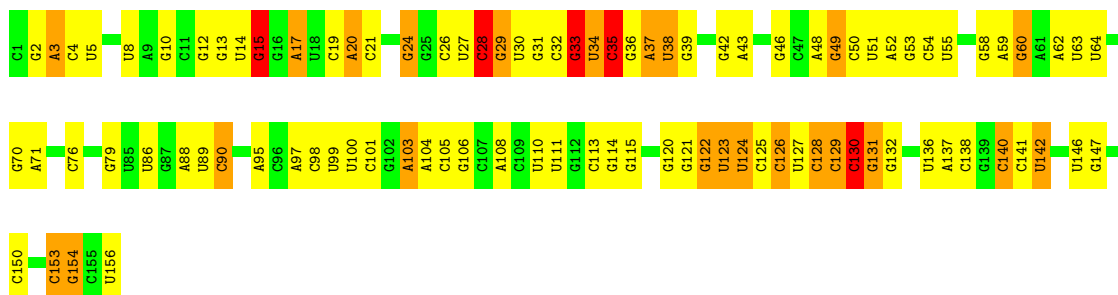
• Molecule 46: 5S rRNA

Chain 7: 47% 40% 12% .



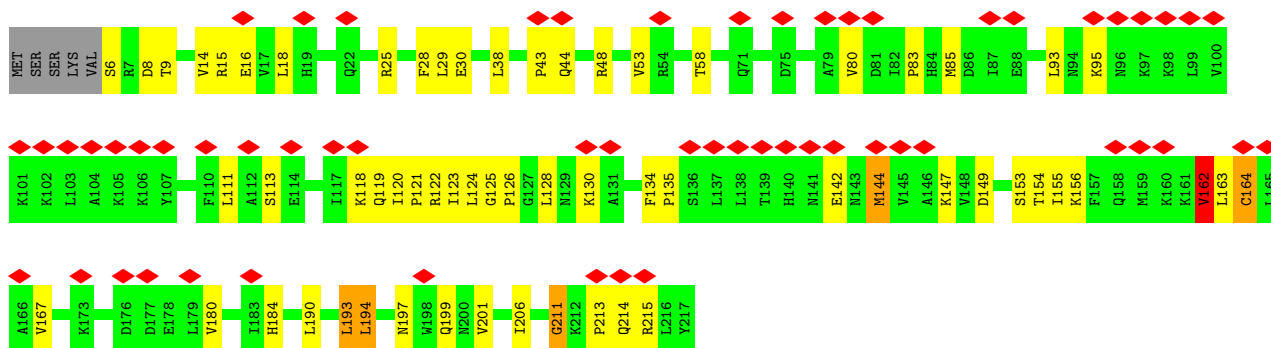
• Molecule 47: 5.8S rRNA

Chain 8: 37% 44% 15% .

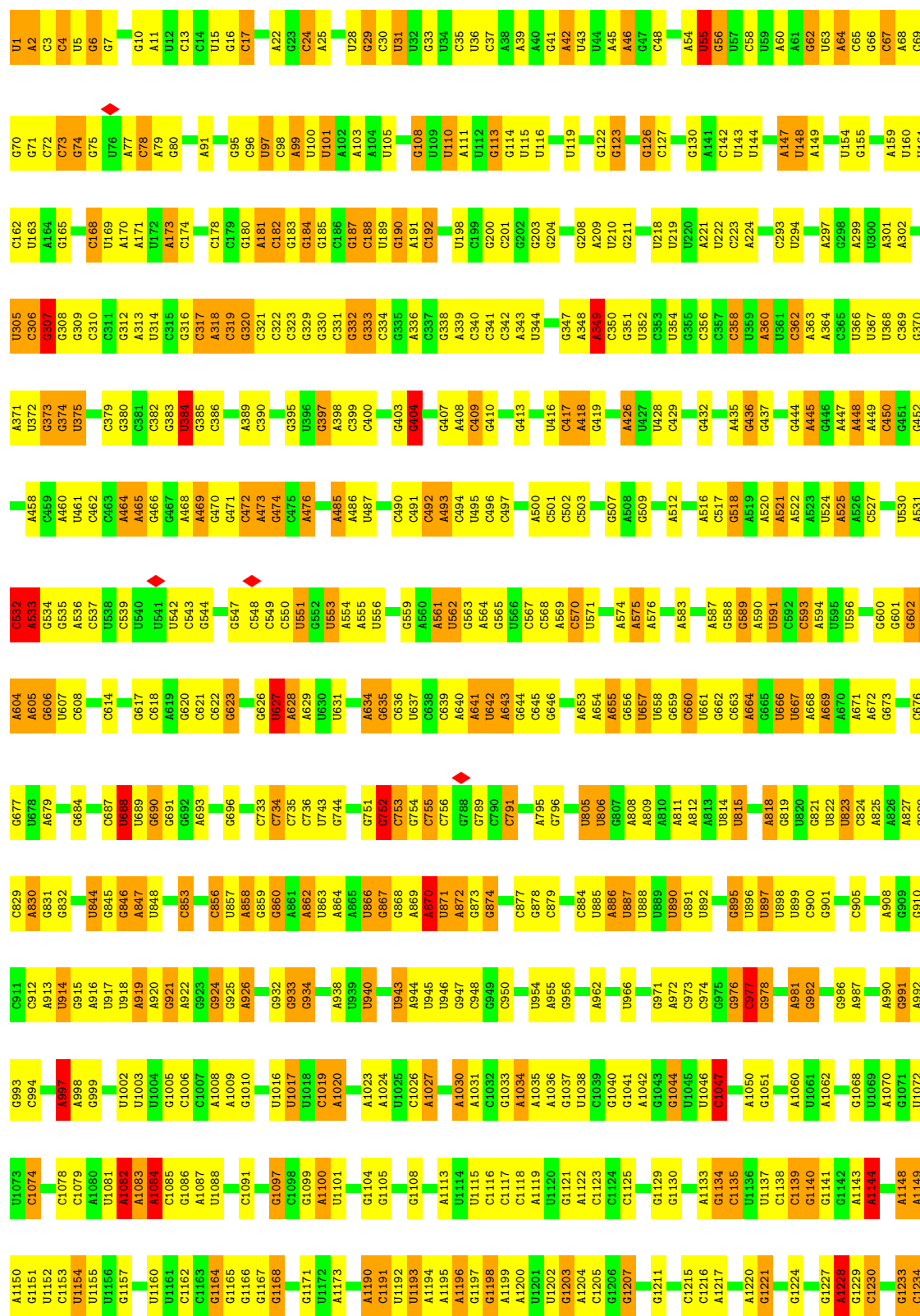
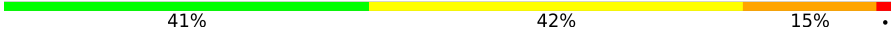


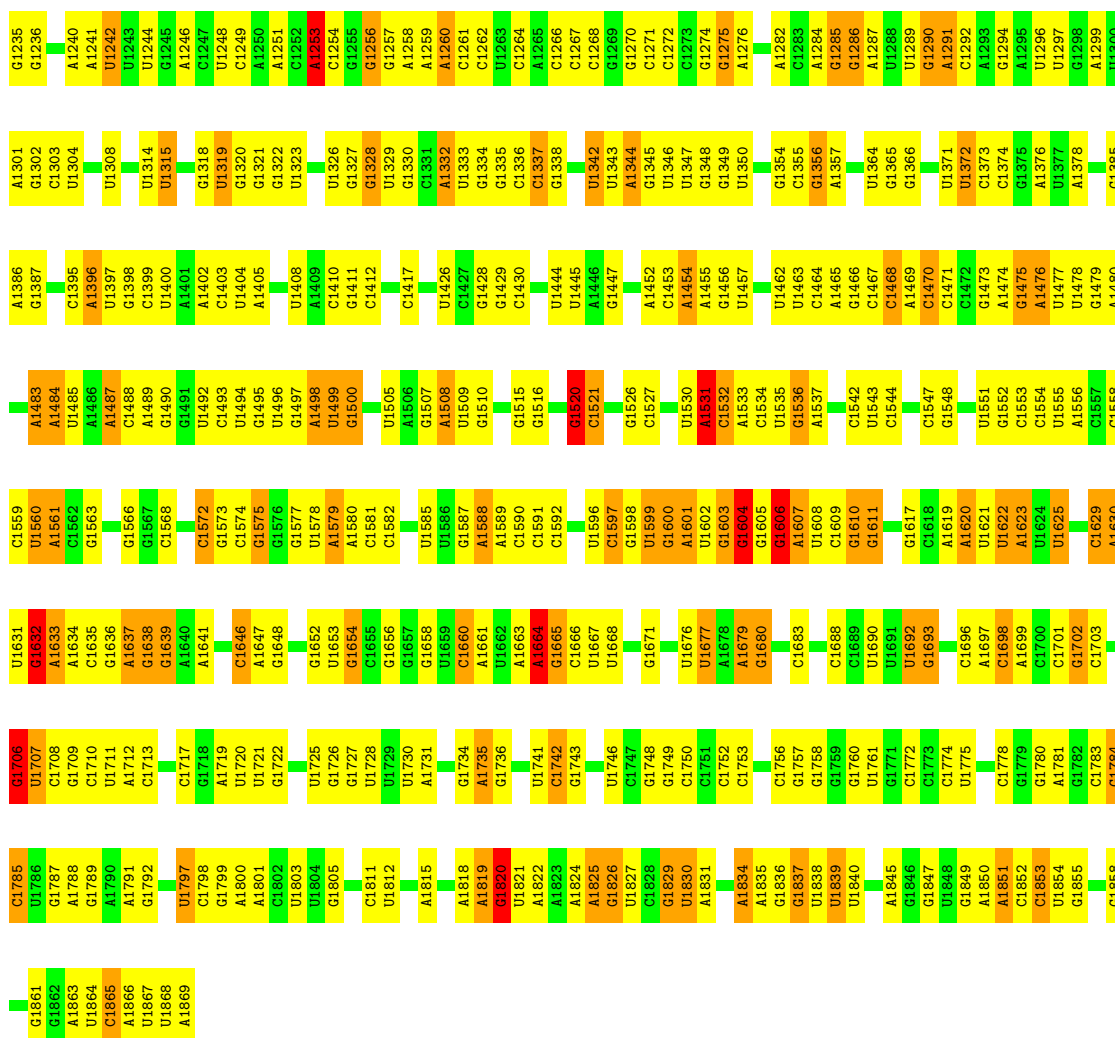
• Molecule 48: Ribosomal protein

Chain K: 27% 69% 26% . .

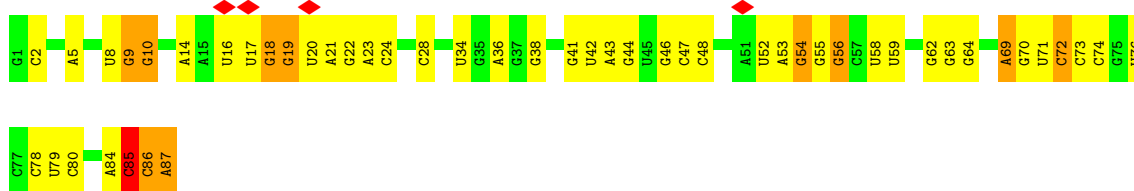
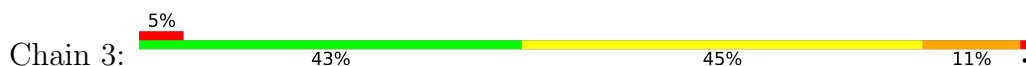


• Molecule 49: 18S rRNA

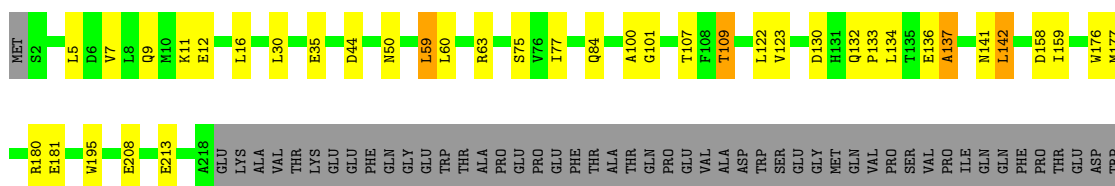
Chain 2: 



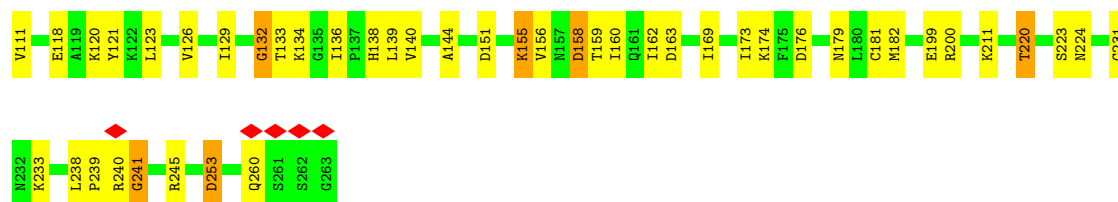
• Molecule 50: P-tRNA



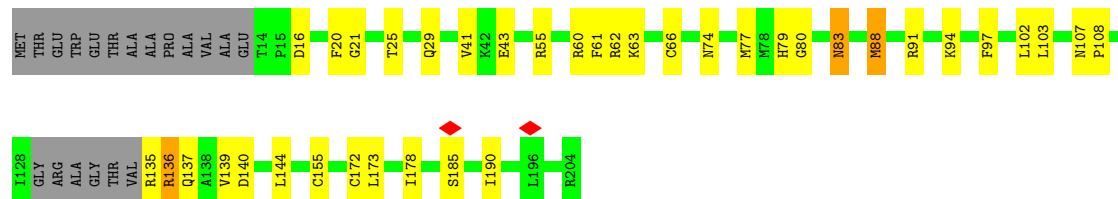
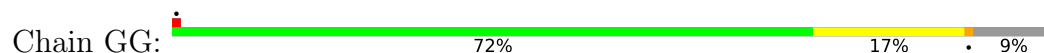
• Molecule 51: Small ribosomal subunit protein uS2



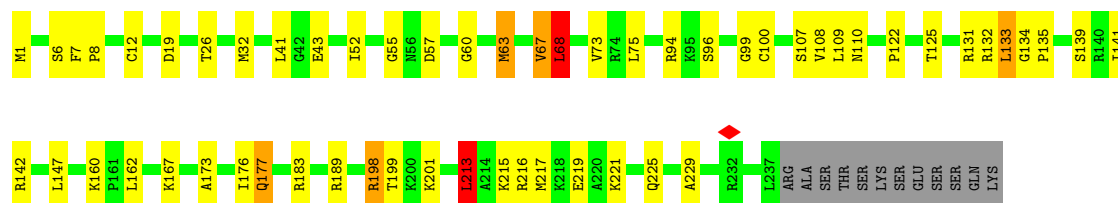
MET	A2	K6	R11	V12	A13	H17	W18	M19	K22	L23	T24	G25	V26	F27	A28	P29	R30	P31	L38	R39	P43	L44	I45	I46	F47	L48	L52	K53	Y54	G58	D59	G67	R68	F69	I70	K71	I72	D73	R77	T78	D79	I80	T81	L101	G107	R108
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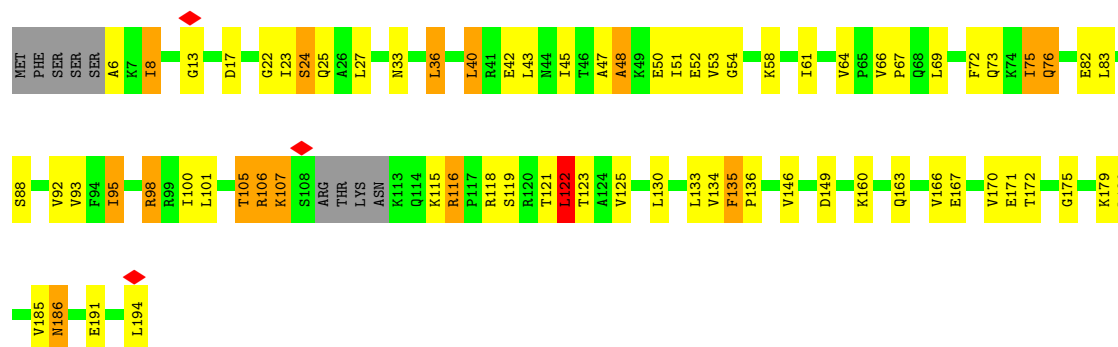
• Molecule 56: Ribosomal protein S5



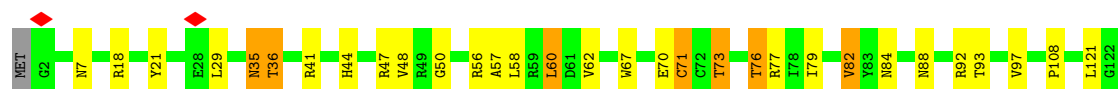
• Molecule 57: 40S ribosomal protein S6



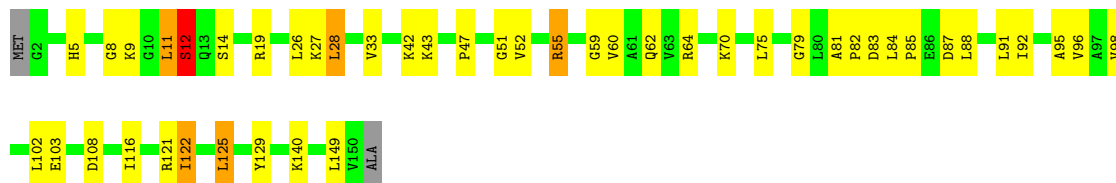
• Molecule 58: 40S ribosomal protein S7



• Molecule 59: 40S ribosomal protein S8



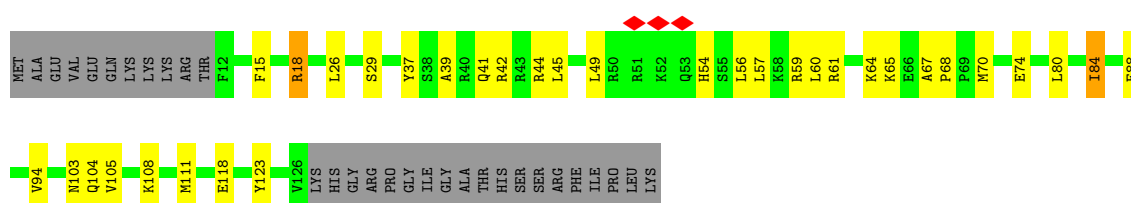
• Molecule 64: Ribosomal protein S13

Chain OO:  68% 26% ..

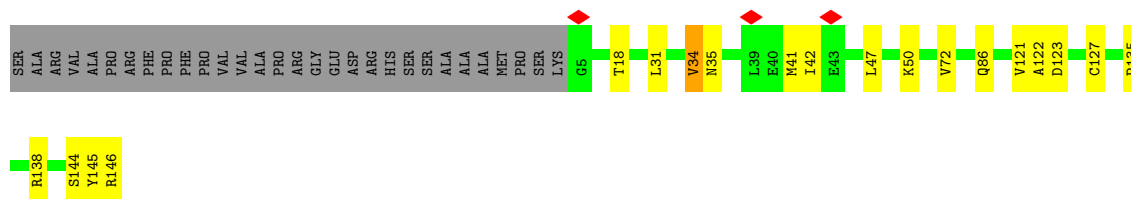
• Molecule 65: Small ribosomal subunit protein uS11

Chain PP:  76% 11% .. 10%

• Molecule 66: uS19

Chain QQ:  56% 22% . 21%

• Molecule 67: Ribosomal protein S16

Chain RR:  72% 10% . 17%

• Molecule 68: eS17

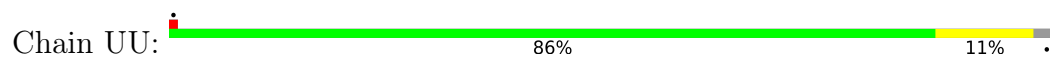
Chain SS:  80% 17% ..

• Molecule 69: uS13

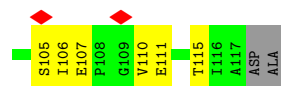
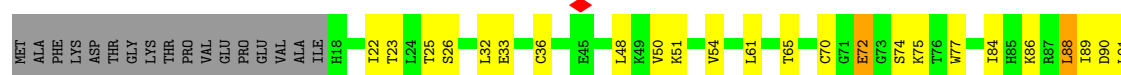
Chain TT:  78% 14% . 5%



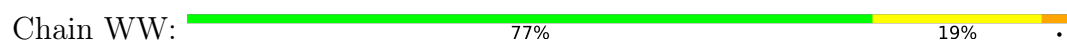
- Molecule 70: eS19



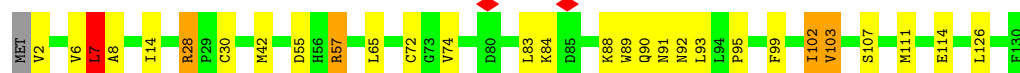
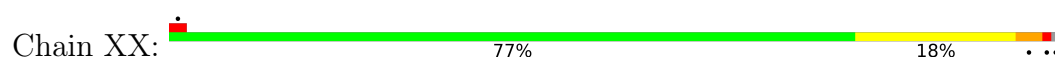
- Molecule 71: uS10



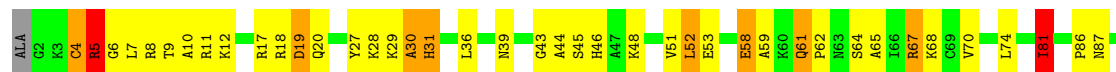
- Molecule 72: 40S ribosomal protein S21



- Molecule 73: Ribosomal protein S15a

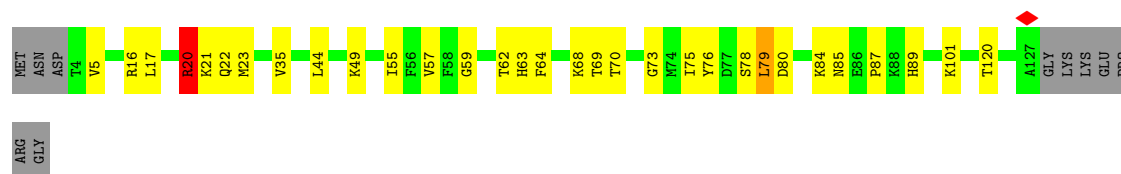


- Molecule 74: Ribosomal protein S23

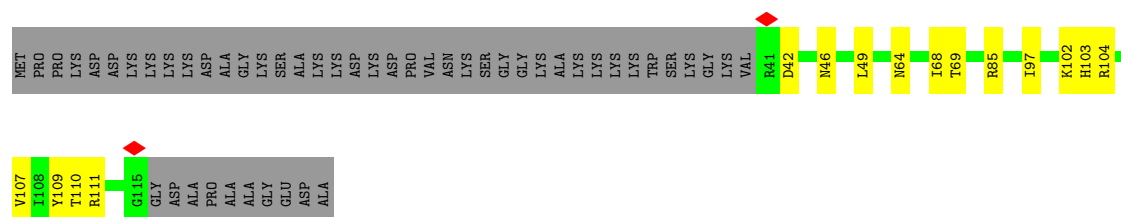


- Molecule 75: 40S ribosomal protein S24

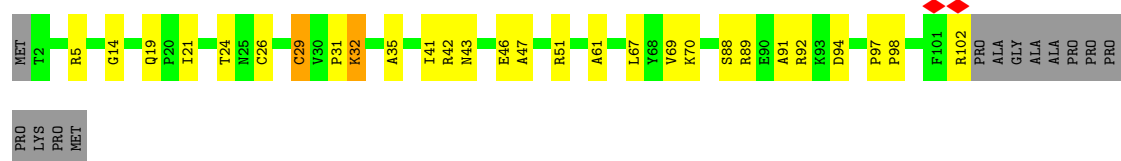




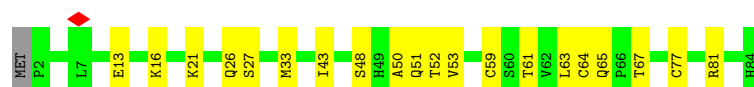
- Molecule 76: eS25



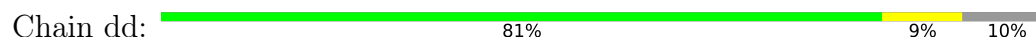
- Molecule 77: 40S ribosomal protein S26



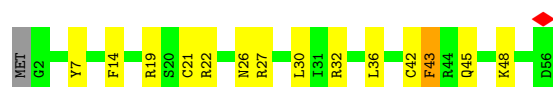
- Molecule 78: 40S ribosomal protein S27



- Molecule 79: Ribosomal protein S28



- Molecule 80: eS29



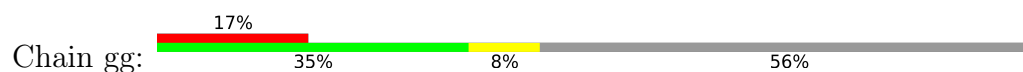
- Molecule 81: 40S ribosomal protein S30



MET GLN PHE VAL ARG ALA GLN LEU HIS THR LEU VAL THR ARG GLU THR VAL ALA GLN ILE LYS ALA HIS VAL ALA SER LEU GLY ILE ALA PRO GLU ASP GLN VAL VAL LEU LEU ALA GLY THR PRO LEU GLU ASP GLU ALA THR LEU GLN CYS GLY VAL GLU

ALA LEU SER THR LEU VAL ALA GLY ARG MET LEU GLY VAL THR LYS VAL H76 H77 H79 H80 H81 H82 H83 H84 H88 H89 H90 H91 H92 H93 H94 H95 H96 H97 H98 H99 H100 H106 H107 H108 H109 H114 H117 H118 H119 H120 H121 H122 H123 H124 H131 H132

• Molecule 82: Ribosomal protein S27a

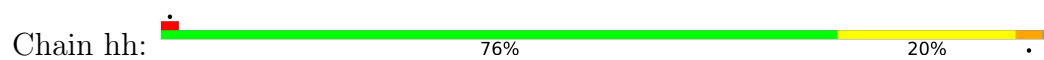


MET GLN PHE VAL LYS THR LEU THR LEU GLY LYS THR ILE THR LEU VAL GLU VAL GLU PRO LYS SER ASP THR ILE THR ASN VAL LYS ALA LYS ILE GLN ASP LYS GLY ILE ARG PRO ASP GLN ARG LEU ILE PHE ALA GLY LYS LEU GLU ASP ARG THR LEU SER ASP TYR ASN

ILE GLN LYS SER THR LEU HIS VAL LEU ARG LYS ARG GLY ALA LYS LYS ARG LYS K83 K84 K85 K86 K87 K88 K89 K90 K91 K92 K95 K96 K97 K98 K99 K100 K101 K102 K103 K104 K105 K106 K107 K108 K109 K110 K111 K112 K113 K114 K115 K116 K117 K124 K125 K126 K127

A128 F150 ASN LYS PRO GLU ASP LYS

• Molecule 83: RACK1

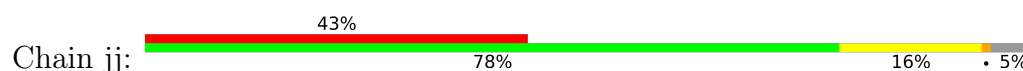


MET T2 G13 H14 N15 I31 S35 R36 D37 K38 T39 W43 L59 R60 H64 F65 L79 S80 G85 T86 L87 R88 T97 V108 L109 L120 L125 D126 K127 T128 I129 T134 V142 Q143 D144 E145 H147 S148 E149 S152 C153 F156

S161 M162 P163 I164 I165 V166 S167 C168 L179 L184 N11 M11 H187 H188 H191 T192 L195 N196 T197 V198 C207 K212 E223 G224 K225 H226 L227 L230 L235 C249 I258 W259 I266 E269 E273 V274 I275 S276 T277 S278 S279 K280 A281 T287 S288 L289

L306 I314 THR ARG

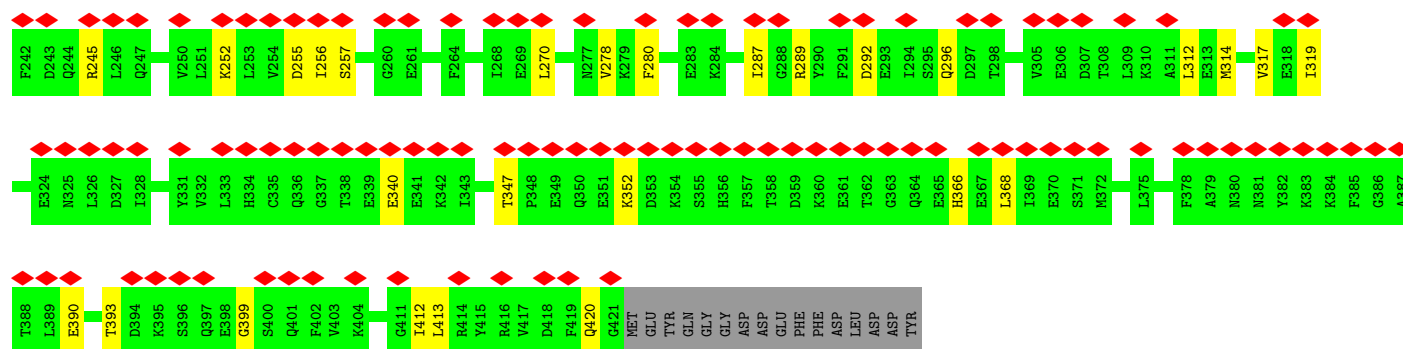
• Molecule 84: Eukaryotic peptide chain release factor subunit 1



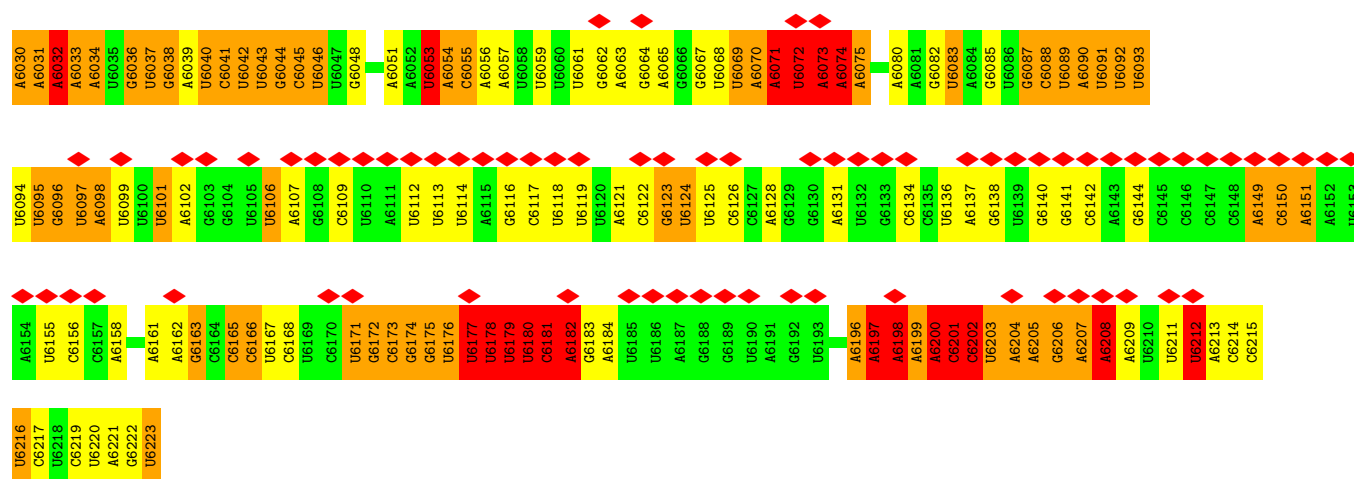
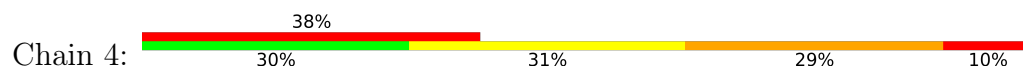
MET ALA ASP ASP PRO A7 A8 R10 R11 V12 E13 I14 W15 K18 K19 S23 L24 A27 T32 S33 H34 I35 S36 L37 R47 V48 N51 L52 A59 I62 K63 S64 R65 R68 L72 T76 S77 Q78 Q79 L82 N86 K87 R88 P89 F90

N91 G92 V95 I100 V101 T102 E103 A104 G105 K108 K118 P119 I120 N121 L124 Y125 L126 C127 D128 H132 A135 L136 L140 S141 D142 D143 S144 K145 F146 G147 F148 I151 D152 G153 S154 G155 A156 L157 F158 Q162 G163 N164 T165 R166 E167 H170 K171 F172

D175 L176 P177 K178 K179 H180 A183 A184 Q185 S186 A187 L188 R189 L193 R194 M195 E196 K197 R198 H199 N200 V202 R203 K204 V205 A206 Q211 L212 F213 T214 S215 G216 D217 K218 V219 G153 G155 A156 F158 Q162 G163 N164 T165 R166 E167 H170 K171 F172



• Molecule 85: CrPV-IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	75654	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.144	Depositor
Minimum map value	-0.061	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1.12	3/1812 (0.2%)	1.17	4/2439 (0.2%)
2	B	1.03	3/3240 (0.1%)	1.21	9/4339 (0.2%)
3	C	1.08	1/2936 (0.0%)	1.18	18/3943 (0.5%)
4	D	0.88	2/2437 (0.1%)	0.97	4/3264 (0.1%)
5	E	0.98	0/1762	1.06	3/2362 (0.1%)
6	F	0.97	1/1911 (0.1%)	1.07	9/2549 (0.4%)
7	G	0.93	0/1910	1.00	3/2569 (0.1%)
8	H	1.01	0/1535	1.09	0/2063
9	I	0.98	2/1702 (0.1%)	1.11	4/2272 (0.2%)
10	J	0.91	0/1385	0.95	3/1852 (0.2%)
11	L	0.96	0/1733	1.03	2/2316 (0.1%)
12	M	1.01	1/1150 (0.1%)	1.07	2/1534 (0.1%)
13	N	1.05	4/1746 (0.2%)	1.23	8/2338 (0.3%)
14	O	1.08	4/1653 (0.2%)	1.15	6/2206 (0.3%)
15	P	1.07	3/1268 (0.2%)	1.15	2/1700 (0.1%)
16	Q	1.05	2/1539 (0.1%)	1.16	9/2054 (0.4%)
17	R	1.00	1/1524 (0.1%)	1.18	2/2013 (0.1%)
18	S	1.03	1/1501 (0.1%)	1.13	4/2012 (0.2%)
19	T	0.99	0/1326	1.06	2/1770 (0.1%)
20	U	0.89	0/823	1.01	2/1104 (0.2%)
21	V	1.08	2/983 (0.2%)	1.24	10/1319 (0.8%)
22	W	0.94	0/873	1.22	5/1158 (0.4%)
23	X	1.05	0/984	1.12	1/1323 (0.1%)
24	Y	0.97	0/1132	1.09	2/1504 (0.1%)
25	Z	0.98	0/1130	1.10	4/1507 (0.3%)
26	a	1.11	2/1191 (0.2%)	1.18	6/1590 (0.4%)
27	b	0.92	0/861	1.03	3/1138 (0.3%)
28	c	0.97	0/771	1.04	0/1034
29	d	1.13	3/903 (0.3%)	1.18	4/1216 (0.3%)
30	e	1.11	3/1071 (0.3%)	1.21	3/1429 (0.2%)
31	f	1.13	0/895	1.25	6/1198 (0.5%)
32	g	1.05	1/916 (0.1%)	1.22	3/1220 (0.2%)
33	h	1.02	1/1021 (0.1%)	1.15	2/1348 (0.1%)
34	i	0.90	0/841	1.04	1/1112 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	1.17	2/720 (0.3%)	1.37	7/952 (0.7%)
36	k	0.91	0/575	1.00	0/761
37	l	1.07	0/459	1.20	2/608 (0.3%)
38	m	1.00	1/435 (0.2%)	1.16	2/575 (0.3%)
39	n	1.12	0/240	1.47	5/305 (1.6%)
40	o	0.91	0/864	0.99	0/1140
41	p	1.05	0/718	1.19	2/953 (0.2%)
42	r	1.06	1/1010 (0.1%)	1.24	5/1354 (0.4%)
43	s	0.92	0/1530	0.85	1/2064 (0.0%)
44	t	0.94	0/1174	0.89	0/1582
45	5	0.62	36/86202 (0.0%)	1.04	604/134412 (0.4%)
46	7	0.54	0/2836	0.92	6/4421 (0.1%)
47	8	0.62	2/3581 (0.1%)	1.02	28/5577 (0.5%)
48	K	0.97	0/1730	0.99	5/2315 (0.2%)
49	2	0.58	7/40502 (0.0%)	0.96	152/63100 (0.2%)
50	3	0.49	0/2079	0.87	5/3238 (0.2%)
51	BB	1.01	2/1747 (0.1%)	0.92	0/2374
52	CC	0.91	1/1756 (0.1%)	1.00	2/2350 (0.1%)
53	DD	0.95	1/1753 (0.1%)	1.15	11/2369 (0.5%)
54	EE	0.90	0/1796	1.04	1/2417 (0.0%)
55	FF	0.95	1/2118 (0.0%)	1.08	1/2849 (0.0%)
56	GG	0.87	0/1492	1.01	1/2005 (0.0%)
57	HH	0.88	0/1946	1.00	3/2590 (0.1%)
58	II	0.95	2/1510 (0.1%)	1.07	2/2022 (0.1%)
59	JJ	0.97	0/1715	1.05	3/2287 (0.1%)
60	KK	0.94	1/1550 (0.1%)	1.07	2/2069 (0.1%)
61	LL	0.98	0/834	1.02	1/1125 (0.1%)
62	MM	1.05	2/1195 (0.2%)	1.13	5/1597 (0.3%)
63	NN	0.82	0/918	0.87	0/1233
64	OO	1.00	1/1226 (0.1%)	1.04	1/1649 (0.1%)
65	PP	0.88	0/1029	0.98	1/1380 (0.1%)
66	QQ	0.89	0/974	1.05	5/1301 (0.4%)
67	RR	0.84	0/1146	0.91	2/1534 (0.1%)
68	SS	0.95	0/1082	0.96	2/1452 (0.1%)
69	TT	0.93	0/1208	0.96	1/1618 (0.1%)
70	UU	0.84	0/1115	0.91	0/1493
71	VV	0.98	1/805 (0.1%)	1.14	3/1081 (0.3%)
72	WW	0.98	0/643	1.04	0/860
73	XX	0.99	0/1051	1.12	2/1406 (0.1%)
74	YY	1.11	0/1116	1.24	9/1490 (0.6%)
75	ZZ	0.89	0/1028	1.07	3/1366 (0.2%)
76	aa	0.90	0/604	0.84	0/810
77	bb	1.03	1/828 (0.1%)	1.09	2/1109 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	cc	0.97	0/665	1.18	4/891 (0.4%)
79	dd	0.92	0/490	0.95	0/656
80	ee	0.87	0/470	0.98	0/623
81	ff	0.89	0/462	1.17	1/607 (0.2%)
82	gg	0.87	0/567	0.89	0/753
83	hh	0.83	0/2492	0.88	4/3391 (0.1%)
84	jj	0.97	0/3333	0.93	2/4483 (0.0%)
85	4	0.54	4/4586 (0.1%)	1.26	65/7136 (0.9%)
All	All	0.78	106/240370 (0.0%)	1.04	1109/352528 (0.3%)

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	4
2	B	0	2
3	C	0	3
12	M	0	1
13	N	0	1
16	Q	0	1
22	W	0	1
23	X	0	1
24	Y	0	1
27	b	0	1
29	d	0	1
30	e	0	1
31	f	0	3
32	g	0	2
35	j	0	1
36	k	0	1
37	l	0	1
40	o	0	1
45	5	0	7
48	K	0	2
49	2	0	3
51	BB	0	1
52	CC	0	1
54	EE	0	1
55	FF	0	3
57	HH	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
65	PP	0	2
69	TT	0	1
73	XX	0	2
74	YY	0	1
81	ff	0	1
83	hh	0	1
85	4	1	4
All	All	1	59

All (106) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	BB	12	GLU	CD-OE2	16.54	1.56	1.25
85	4	6182	A	O3'-P	-10.44	1.45	1.61
85	4	6178	U	C1'-N1	9.53	1.61	1.47
45	5	4520	G	O3'-P	8.86	1.74	1.61
49	2	690	G	O5'-C5'	7.83	1.54	1.42
45	5	1522	G	O3'-P	7.35	1.72	1.61
77	bb	97	PRO	CA-C	7.22	1.56	1.52
45	5	42	A	O3'-P	7.11	1.71	1.61
85	4	6030	A	O3'-P	6.86	1.71	1.61
4	D	45	ASN	N-CA	6.83	1.54	1.46
64	OO	5	HIS	CA-C	6.66	1.62	1.52
49	2	667	U	O3'-P	6.47	1.70	1.61
51	BB	208	GLU	CD-OE2	6.45	1.37	1.25
71	VV	72	GLU	CD-OE2	6.43	1.37	1.25
6	F	133	ARG	N-CA	6.37	1.54	1.46
45	5	1591	U	O3'-P	6.35	1.70	1.61
45	5	2527	A	O3'-P	6.33	1.70	1.61
21	V	40	ILE	N-CA	6.29	1.54	1.46
45	5	2890	C	O3'-P	6.20	1.70	1.61
2	B	244	THR	CA-C	6.19	1.60	1.52
15	P	130	TYR	N-CA	6.11	1.53	1.46
45	5	1339	U	O3'-P	6.04	1.70	1.61
45	5	2441	C	O3'-P	6.04	1.70	1.61
21	V	62	MET	N-CA	6.03	1.53	1.46
45	5	2079	G	O3'-P	6.03	1.70	1.61
45	5	4516	G	O3'-P	6.00	1.70	1.61
45	5	4620	U	O3'-P	-5.98	1.52	1.61
26	a	73	VAL	CA-C	5.96	1.60	1.52
1	A	13	GLY	N-CA	5.95	1.51	1.45
2	B	47	LEU	CA-C	5.95	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	66	PRO	N-CA	-5.90	1.43	1.47
30	e	43	ASN	CA-C	5.90	1.60	1.52
45	5	2593	C	O3'-P	5.78	1.69	1.61
45	5	1917	A	O3'-P	-5.77	1.52	1.61
13	N	67	ARG	CA-C	-5.77	1.45	1.52
35	j	65	ARG	CA-C	5.76	1.60	1.52
45	5	3870	C	O3'-P	5.75	1.69	1.61
45	5	4376	A	O3'-P	5.74	1.69	1.61
3	C	50	GLN	CA-C	-5.69	1.44	1.52
62	MM	75	GLY	N-CA	5.66	1.50	1.45
13	N	30	TYR	N-CA	5.62	1.53	1.45
16	Q	156	PRO	CA-C	-5.61	1.47	1.53
45	5	2044	U	O3'-P	5.56	1.69	1.61
62	MM	101	ARG	CA-C	5.55	1.59	1.53
42	r	117	ILE	CA-C	5.53	1.60	1.52
14	O	79	ILE	CA-CB	5.52	1.60	1.54
4	D	74	ILE	CA-C	-5.51	1.46	1.52
58	II	116	ARG	CA-C	5.48	1.59	1.52
45	5	1506	G	O3'-P	5.47	1.69	1.61
18	S	132	ILE	N-CA	5.46	1.52	1.46
49	2	6	G	O3'-P	5.45	1.69	1.61
47	8	15	G	O3'-P	5.45	1.69	1.61
45	5	1650	A	O3'-P	5.44	1.69	1.61
38	m	73	CYS	N-CA	5.43	1.52	1.46
33	h	4	ILE	CA-CB	5.41	1.59	1.53
14	O	112	TYR	N-CA	5.41	1.54	1.46
29	d	71	ALA	N-CA	5.40	1.52	1.46
45	5	3882	C	O3'-P	5.40	1.69	1.61
49	2	1706	G	O3'-P	-5.36	1.53	1.61
35	j	30	GLN	CA-C	5.36	1.59	1.52
60	KK	39	ASN	CA-C	-5.36	1.46	1.52
45	5	3852	A	O3'-P	5.36	1.69	1.61
45	5	2087	C	O3'-P	-5.33	1.53	1.61
14	O	112	TYR	CA-CB	5.32	1.60	1.53
45	5	3694	U	O3'-P	5.32	1.69	1.61
49	2	1658	G	O3'-P	-5.28	1.53	1.61
45	5	39	A	O3'-P	5.27	1.69	1.61
45	5	5057	C	O3'-P	5.26	1.69	1.61
2	B	116	ARG	CA-C	5.25	1.60	1.52
45	5	2512	A	O3'-P	5.24	1.69	1.61
32	g	60	ARG	CA-C	5.24	1.59	1.52
45	5	4461	C	O3'-P	5.24	1.69	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	d	44	ARG	CA-C	5.22	1.59	1.52
45	5	2577	C	O3'-P	-5.22	1.53	1.61
17	R	39	GLN	N-CA	5.21	1.52	1.46
29	d	51	LYS	N-CA	5.20	1.53	1.46
30	e	79	VAL	N-CA	5.20	1.51	1.46
53	DD	176	LYS	CA-C	5.19	1.58	1.52
45	5	1907	A	O3'-P	5.18	1.69	1.61
45	5	1592	G	O5'-C5'	5.16	1.50	1.42
45	5	2440	U	O3'-P	-5.16	1.53	1.61
45	5	40	G	O3'-P	5.15	1.68	1.61
45	5	1470	G	O3'-P	-5.15	1.53	1.61
13	N	30	TYR	CA-C	5.13	1.59	1.52
30	e	42	ASP	CA-C	5.13	1.59	1.52
45	5	1354	A	O3'-P	5.12	1.68	1.61
14	O	120	VAL	N-CA	5.12	1.50	1.46
49	2	1081	U	O3'-P	5.12	1.68	1.61
1	A	49	ILE	N-CA	5.12	1.52	1.46
85	4	6181	C	C1'-N1	-5.08	1.40	1.48
52	CC	117	TRP	CA-C	-5.07	1.48	1.53
12	M	37	LEU	CA-C	5.07	1.63	1.52
13	N	80	THR	CA-C	-5.06	1.46	1.52
9	I	94	PHE	N-CA	5.05	1.52	1.46
16	Q	8	ASN	CA-C	5.05	1.57	1.52
45	5	2817	C	O3'-P	5.04	1.68	1.61
55	FF	138	HIS	CA-C	5.04	1.58	1.52
58	II	116	ARG	C-N	5.04	1.39	1.33
45	5	350	C	O3'-P	5.03	1.68	1.61
15	P	130	TYR	CA-C	5.03	1.59	1.52
26	a	4	ARG	CA-C	5.02	1.59	1.52
45	5	1905	U	O3'-P	5.02	1.68	1.61
47	8	29	G	O3'-P	-5.01	1.53	1.61
9	I	15	LYS	N-CA	5.01	1.53	1.46
49	2	669	A	O3'-P	5.01	1.68	1.61
15	P	81	GLY	N-CA	5.00	1.50	1.45

All (1109) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6030	A	O3'-P-O5'	33.43	154.14	104.00
85	4	6030	A	P-O3'-C3'	-26.97	79.75	120.20
85	4	6181	C	C4'-C3'-O3'	-23.70	77.45	113.00
45	5	4520	G	C1'-C2'-O2'	-18.58	80.53	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6178	U	C1'-C2'-O2'	17.34	137.81	111.80
85	4	6178	U	C2'-C3'-O3'	15.74	133.11	109.50
45	5	2695	A	C2'-C3'-O3'	14.93	131.90	109.50
85	4	6072	U	N1-C1'-C2'	14.93	134.40	112.00
85	4	6072	U	C2'-C3'-O3'	13.89	134.54	113.70
85	4	6200	A	N9-C1'-C2'	13.39	134.08	114.00
85	4	6177	U	C2'-C3'-O3'	12.99	133.19	113.70
85	4	6071	A	O4'-C1'-C2'	-12.92	94.68	107.60
85	4	6073	A	C2'-C3'-O3'	12.81	132.91	113.70
45	5	4461	C	C4'-C3'-O3'	12.56	131.84	113.00
45	5	48	G	C2'-C3'-O3'	12.55	128.33	109.50
45	5	1358	G	C4'-C3'-O3'	12.44	128.06	109.40
85	4	6178	U	N1-C1'-C2'	12.32	132.49	114.00
45	5	2786	C	C2'-C3'-O3'	-12.14	95.48	113.70
45	5	1914	C	C1'-C2'-O2'	12.12	126.59	108.40
85	4	6054	A	C2'-C3'-O3'	12.02	127.53	109.50
45	5	4516	G	C2'-C3'-O3'	11.98	131.67	113.70
45	5	930	G	C2'-C3'-O3'	11.95	131.63	113.70
45	5	47	A	C4'-C3'-O3'	11.77	127.05	109.40
85	4	6177	U	N1-C1'-C2'	11.28	128.92	112.00
45	5	4463	U	C1'-C2'-O2'	11.03	128.35	111.80
45	5	4515	G	C4'-C3'-O3'	10.81	129.22	113.00
85	4	6030	A	OP1-P-O3'	-10.66	76.00	108.00
49	2	1698	C	C2'-C3'-O3'	10.62	125.43	109.50
45	5	2050	G	C3'-C2'-O2'	10.59	126.58	110.70
45	5	4633	G	C1'-C2'-O2'	-10.46	92.72	108.40
85	4	6071	A	C4'-C3'-O3'	10.44	128.66	113.00
45	5	2046	G	C2'-C3'-O3'	10.40	125.09	109.50
45	5	4520	G	C3'-C2'-O2'	10.39	126.29	110.70
45	5	352	G	C1'-C2'-O2'	-10.29	96.36	111.80
45	5	4394	A	C4'-C3'-O3'	10.29	124.83	109.40
45	5	4516	G	N9-C1'-C2'	10.15	127.22	112.00
49	2	1024	A	C3'-C2'-O2'	10.15	125.93	110.70
45	5	1911	C	N1-C1'-C2'	10.14	127.21	112.00
49	2	870	A	C2'-C3'-O3'	9.98	124.48	109.50
45	5	4523	A	C3'-C2'-O2'	9.97	125.65	110.70
45	5	4949	G	C4'-C3'-O3'	9.93	124.30	109.40
45	5	2032	U	C2'-C3'-O3'	-9.92	98.82	113.70
45	5	2043	A	C1'-C2'-O2'	-9.89	93.57	108.40
45	5	4462	C	C2'-C3'-O3'	9.87	128.50	113.70
45	5	4461	C	C1'-C2'-O2'	9.85	123.17	108.40
45	5	4947	U	C2'-C3'-O3'	9.80	128.40	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6201	C	C4'-C3'-O3'	-9.72	98.41	113.00
13	N	185	GLY	N-CA-C	-9.69	99.24	112.52
45	5	2845	A	C4'-C3'-O3'	-9.61	98.59	113.00
85	4	6071	A	N9-C1'-C2'	9.59	126.38	112.00
45	5	4633	G	C2'-C3'-O3'	-9.58	99.33	113.70
45	5	4514	G	N9-C1'-C2'	9.54	126.31	112.00
45	5	4520	G	C2'-C3'-O3'	9.50	127.95	113.70
85	4	6053	U	C4'-C3'-O3'	9.50	127.25	113.00
45	5	3621	A	C3'-C2'-O2'	9.45	124.88	110.70
85	4	6197	A	N9-C1'-C2'	9.42	126.13	112.00
21	V	47	GLY	N-CA-C	9.32	123.62	110.38
45	5	1291	G	C2'-C3'-O3'	9.29	127.64	113.70
45	5	4516	G	O4'-C4'-C3'	-9.28	94.72	104.00
45	5	4517	A	C2'-C3'-O3'	9.28	127.62	113.70
9	I	121	LYS	N-CA-C	-9.25	99.50	110.13
45	5	2804	C	C1'-C2'-O2'	9.19	122.18	108.40
49	2	13	C	C3'-C2'-O2'	9.16	124.44	110.70
45	5	1835	G	C2'-C3'-O3'	9.11	123.17	109.50
45	5	2440	U	C4'-C3'-O3'	9.07	123.00	109.40
81	ff	118	VAL	N-CA-C	9.05	120.43	110.21
85	4	6073	A	N9-C1'-C2'	9.04	125.56	112.00
45	5	4196	G	C3'-C2'-O2'	9.03	124.24	110.70
45	5	4392	G	C4'-C3'-O3'	-8.95	99.57	113.00
74	YY	61	GLN	CA-C-N	8.94	131.02	119.84
74	YY	61	GLN	C-N-CA	8.94	131.02	119.84
45	5	3706	C	C3'-C2'-O2'	8.93	124.09	110.70
45	5	4660	G	C3'-C2'-O2'	8.88	124.02	110.70
45	5	2533	C	C3'-C2'-O2'	8.85	123.97	110.70
85	4	6182	A	O3'-P-O5'	-8.80	90.80	104.00
85	4	6032	A	C4'-C3'-O3'	8.80	122.60	109.40
45	5	1370	G	C2'-C3'-O3'	8.78	122.67	109.50
26	a	28	HIS	CA-C-N	8.77	130.81	119.84
26	a	28	HIS	C-N-CA	8.77	130.81	119.84
49	2	1652	G	C3'-C2'-O2'	8.76	123.84	110.70
45	5	4187	G	C3'-C2'-O2'	8.72	123.78	110.70
1	A	13	GLY	N-CA-C	8.68	122.36	110.56
85	4	6180	U	N1-C1'-C2'	8.67	125.00	112.00
45	5	1578	U	C2'-C3'-O3'	8.66	126.69	113.70
45	5	1915	C	C1'-C2'-O2'	-8.63	98.86	111.80
45	5	3792	G	C4'-C3'-O3'	-8.58	100.13	113.00
45	5	1358	G	C2'-C3'-O3'	-8.55	96.67	109.50
45	5	1922	G	C3'-C2'-O2'	8.54	123.51	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	1234	G	C2'-C3'-O3'	8.53	122.29	109.50
85	4	6200	A	C2'-C3'-O3'	8.53	122.29	109.50
45	5	69	A	C2'-C3'-O3'	-8.48	100.98	113.70
45	5	2328	G	C4'-C3'-O3'	8.45	125.67	113.00
45	5	4522	G	C3'-C2'-O2'	8.34	123.21	110.70
45	5	4673	U	C4'-C3'-O3'	-8.29	100.57	113.00
2	B	259	PRO	N-CA-C	-8.27	95.44	112.47
45	5	4516	G	C1'-C2'-O2'	8.27	120.80	108.40
47	8	128	C	C4'-C3'-O3'	8.23	125.35	113.00
85	4	6178	U	C5'-C4'-O4'	8.23	121.44	109.10
45	5	1917	A	C2'-C3'-O3'	8.22	126.03	113.70
45	5	1530	G	C3'-C2'-O2'	8.22	123.03	110.70
45	5	969	C	C2'-C3'-O3'	8.21	121.82	109.50
45	5	1872	G	C4'-C3'-O3'	-8.20	100.70	113.00
45	5	3824	A	C3'-C2'-O2'	8.18	122.97	110.70
45	5	3906	A	C2'-C3'-O3'	8.18	121.77	109.50
45	5	4631	G	C1'-C2'-O2'	8.17	120.66	108.40
45	5	1380	G	C4'-C3'-O3'	8.14	121.61	109.40
45	5	4925	U	C2'-C3'-O3'	8.13	121.69	109.50
45	5	1917	A	C1'-C2'-O2'	-8.11	96.23	108.40
32	g	60	ARG	CA-C-N	8.08	130.38	121.00
32	g	60	ARG	C-N-CA	8.08	130.38	121.00
45	5	4432	C	C1'-C2'-O2'	8.04	120.47	108.40
45	5	4699	U	C4'-C3'-O3'	8.04	121.46	109.40
46	7	79	U	C4'-C3'-O3'	-8.03	100.95	113.00
85	4	6201	C	C2'-C3'-O3'	8.03	125.74	113.70
45	5	1670	G	C2'-C3'-O3'	-8.01	101.68	113.70
31	f	108	SER	N-CA-C	8.01	120.65	110.24
45	5	1590	C	C2'-C3'-O3'	-8.00	101.69	113.70
47	8	20	A	C1'-C2'-O2'	7.97	120.36	108.40
45	5	385	A	C4'-C3'-O3'	7.95	121.32	109.40
45	5	4460	U	N1-C1'-C2'	7.92	123.88	112.00
85	4	6074	A	C5'-C4'-C3'	7.91	127.87	116.00
45	5	4459	U	N1-C1'-C2'	7.91	123.86	112.00
45	5	4397	A	C3'-C2'-O2'	7.89	122.53	110.70
45	5	4518	A	C2'-C3'-O3'	-7.89	97.67	109.50
85	4	6074	A	C5'-C4'-O4'	7.87	121.61	109.80
45	5	1353	G	C3'-C2'-O2'	7.86	122.48	110.70
45	5	2347	A	C3'-C2'-O2'	-7.83	102.85	114.60
85	4	6074	A	C4'-C3'-O3'	-7.81	101.29	113.00
45	5	4469	U	C3'-C2'-O2'	7.80	122.40	110.70
85	4	6208	A	C2'-C3'-O3'	7.80	121.20	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	857	U	C4'-C3'-O3'	-7.80	101.31	113.00
45	5	4511	A	C3'-C2'-O2'	7.79	122.38	110.70
45	5	4179	G	C1'-C2'-O2'	7.77	120.05	108.40
45	5	2787	A	N9-C1'-C2'	7.77	123.65	112.00
45	5	1931	C	C2'-C3'-O3'	-7.76	102.06	113.70
78	cc	51	GLN	N-CA-C	7.75	122.68	113.23
45	5	1649	U	C1'-C2'-O2'	7.74	123.42	111.80
85	4	6180	U	O4'-C4'-C3'	-7.74	96.26	104.00
49	2	375	U	C4'-C3'-O3'	-7.70	101.45	113.00
3	C	192	GLY	N-CA-C	7.70	122.76	111.76
49	2	688	U	C2'-C3'-O3'	7.69	121.04	109.50
45	5	2040	A	C1'-C2'-O2'	-7.68	100.28	111.80
22	W	14	TYR	CA-C-N	7.68	129.44	119.84
22	W	14	TYR	C-N-CA	7.68	129.44	119.84
46	7	88	A	C3'-C2'-O2'	7.67	122.20	110.70
65	PP	138	ASP	N-CA-C	7.66	119.78	108.14
45	5	1636	U	C4'-C3'-O3'	-7.64	101.54	113.00
45	5	1332	C	C1'-C2'-O2'	7.63	119.85	108.40
52	CC	161	VAL	N-CA-C	7.63	118.40	110.62
84	jj	62	ILE	CB-CA-C	-7.63	99.83	110.96
49	2	1047	C	C1'-C2'-O2'	7.62	119.83	108.40
9	I	20	SER	N-CA-C	7.61	118.65	108.38
47	8	19	C	C1'-C2'-O2'	-7.61	96.99	108.40
45	5	2631	U	C4'-C3'-O3'	-7.60	101.60	113.00
45	5	1531	U	C4'-C3'-O3'	-7.60	101.60	113.00
45	5	2340	C	C4'-C3'-O3'	-7.59	101.61	113.00
49	2	1579	A	C4'-C3'-O3'	-7.58	101.62	113.00
85	4	6179	U	C5'-C4'-O4'	7.58	121.17	109.80
16	Q	59	PRO	N-CA-C	7.58	119.94	110.70
49	2	1526	G	C3'-C2'-O2'	7.57	122.06	110.70
45	5	1910	G	N9-C1'-C2'	7.56	123.33	112.00
45	5	4462	C	O4'-C4'-C3'	-7.55	96.45	104.00
45	5	2532	C	C2'-C3'-O3'	-7.55	102.38	113.70
35	j	32	SER	N-CA-C	7.54	122.05	112.86
45	5	335	A	N9-C1'-C2'	7.50	123.25	112.00
45	5	375	G	C3'-C2'-O2'	7.49	121.94	110.70
45	5	426	A	N9-C1'-C2'	7.49	123.23	112.00
45	5	3876	A	C2'-C3'-O3'	7.48	120.72	109.50
45	5	1326	A	C4'-C3'-O3'	-7.48	101.78	113.00
45	5	3935	C	C1'-C2'-O2'	7.47	119.61	108.40
45	5	2043	A	N9-C1'-C2'	7.47	123.20	112.00
45	5	3870	C	C2'-C3'-O3'	7.47	124.90	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	1314	C	C2'-C3'-O3'	7.46	120.69	109.50
42	r	10	VAL	N-CA-C	7.46	117.54	110.53
45	5	293	G	C3'-C2'-O2'	7.44	121.87	110.70
25	Z	62	ILE	N-CA-C	-7.42	104.62	111.67
57	HH	176	ILE	N-CA-C	7.42	117.39	106.85
45	5	1462	A	C3'-C2'-O2'	7.41	121.81	110.70
66	QQ	67	ALA	CA-C-N	7.40	128.01	120.38
66	QQ	67	ALA	C-N-CA	7.40	128.01	120.38
45	5	2694	G	C2'-C3'-O3'	7.39	120.59	109.50
49	2	887	U	C4'-C3'-O3'	7.38	120.46	109.40
45	5	2509	C	C3'-C2'-O2'	7.36	121.73	110.70
45	5	4950	U	C2'-C3'-O3'	7.35	120.52	109.50
17	R	38	ARG	N-CA-C	7.33	121.14	111.75
3	C	338	ASN	N-CA-C	-7.32	101.40	110.41
45	5	4345	C	C4'-C3'-O3'	-7.32	102.02	113.00
3	C	82	GLY	N-CA-C	7.32	121.33	110.42
45	5	2468	U	C4'-C3'-O3'	7.32	120.38	109.40
45	5	2551	A	C2'-C3'-O3'	7.32	124.68	113.70
45	5	2549	G	C3'-C2'-O2'	7.32	121.67	110.70
45	5	1322	A	C4'-C3'-O3'	7.31	120.36	109.40
45	5	2740	U	C1'-C2'-O2'	-7.31	100.84	111.80
15	P	130	TYR	N-CA-C	7.30	120.63	108.73
45	5	1900	C	C3'-C2'-O2'	7.29	121.63	110.70
45	5	712	C	C3'-C2'-O2'	7.28	121.62	110.70
1	A	159	SER	N-CA-C	7.25	121.06	112.93
45	5	4242	U	C2'-C3'-O3'	7.25	120.38	109.50
45	5	2440	U	C2'-C3'-O3'	-7.25	98.63	109.50
45	5	332	C	C2'-C3'-O3'	-7.24	102.84	113.70
85	4	6179	U	C5'-C4'-C3'	7.22	126.83	116.00
85	4	6179	U	N1-C1'-C2'	7.21	122.81	112.00
6	F	217	GLY	N-CA-C	-7.20	96.11	113.18
45	5	1534	A	C4'-C3'-O3'	7.19	120.19	109.40
85	4	6202	C	C4'-C3'-O3'	7.17	120.15	109.40
49	2	978	G	C3'-C2'-O2'	7.15	121.43	110.70
45	5	3603	G	C4'-C3'-O3'	7.13	120.10	109.40
45	5	4510	A	C4'-C3'-O3'	-7.13	102.31	113.00
45	5	4386	C	C4'-C3'-O3'	-7.13	102.31	113.00
39	n	8	LYS	N-CA-C	-7.12	102.71	111.40
45	5	4558	U	C4'-C3'-O3'	-7.12	102.32	113.00
45	5	2052	G	C2'-C3'-O3'	7.10	124.35	113.70
7	G	102	ARG	N-CA-C	7.09	118.92	108.14
45	5	418	A	C1'-C2'-O2'	7.09	119.04	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	GG	136	ARG	N-CA-C	7.08	119.98	110.35
35	j	75	ARG	N-CA-C	7.07	121.49	113.01
75	ZZ	20	ARG	N-CA-C	7.06	119.59	108.79
49	2	653	A	C3'-C2'-O2'	7.05	121.28	110.70
45	5	79	C	C3'-C2'-O2'	7.04	121.27	110.70
49	2	24	C	C2'-C3'-O3'	7.04	124.26	113.70
45	5	424	U	C2'-C3'-O3'	-7.04	103.14	113.70
47	8	146	U	C3'-C2'-O2'	7.04	121.25	110.70
14	O	69	GLY	CA-C-N	7.02	128.61	119.84
14	O	69	GLY	C-N-CA	7.02	128.61	119.84
45	5	4569	U	C2'-C3'-O3'	-7.02	103.17	113.70
49	2	596	U	C1'-C2'-O2'	7.01	118.92	108.40
45	5	2089	G	C2'-C3'-O3'	7.01	120.02	109.50
49	2	1152	U	C2'-C3'-O3'	-7.00	103.20	113.70
45	5	1613	A	C2'-C3'-O3'	7.00	120.00	109.50
53	DD	135	GLY	N-CA-C	7.00	125.13	115.27
45	5	4699	U	C2'-C3'-O3'	-6.99	99.02	109.50
45	5	4711	C	C4'-C3'-O3'	-6.99	102.52	113.00
85	4	6151	A	C2'-C3'-O3'	6.99	119.98	109.50
23	X	62	ARG	N-CA-C	6.97	119.48	111.11
45	5	4188	U	C3'-C2'-O2'	6.97	121.15	110.70
45	5	438	G	C3'-C2'-O2'	6.96	121.13	110.70
45	5	2817	C	C3'-C2'-O2'	6.95	121.12	110.70
85	4	6073	A	C1'-O4'-C4'	-6.95	102.95	109.90
45	5	4462	C	C3'-C2'-O2'	6.94	121.11	110.70
45	5	334	A	N9-C1'-C2'	6.94	122.40	112.00
45	5	4176	C	C4'-C3'-O3'	-6.92	102.61	113.00
49	2	1680	G	C3'-C2'-O2'	6.92	121.08	110.70
85	4	6198	A	C4'-C3'-O3'	6.92	123.38	113.00
45	5	2698	G	C1'-C2'-O2'	6.92	118.78	108.40
45	5	2849	A	N9-C1'-C2'	6.92	124.37	114.00
45	5	2603	C	C3'-C2'-O2'	6.91	121.06	110.70
45	5	2328	G	C3'-C2'-O2'	6.90	121.06	110.70
45	5	2809	G	C1'-C2'-O2'	6.90	118.75	108.40
45	5	2742	G	C3'-C2'-O2'	6.90	121.04	110.70
45	5	1906	U	C3'-C2'-O2'	6.88	121.03	110.70
49	2	752	G	C2'-C3'-O3'	6.88	119.82	109.50
26	a	54	GLY	N-CA-C	6.87	119.14	110.96
67	RR	144	SER	N-CA-C	6.86	118.98	108.42
45	5	2420	A	C1'-C2'-O2'	6.82	118.63	108.40
27	b	115	GLY	N-CA-C	6.81	121.96	114.40
49	2	1241	A	C1'-C2'-O2'	6.81	118.62	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	3666	C	C1'-C2'-O2'	-6.80	98.20	108.40
85	4	6200	A	C8-N9-C1'	-6.80	107.30	127.70
45	5	3631	U	C3'-C2'-O2'	6.79	120.89	110.70
62	MM	114	SER	CA-C-N	6.79	128.33	119.84
62	MM	114	SER	C-N-CA	6.79	128.33	119.84
2	B	244	THR	N-CA-C	6.78	120.20	110.24
45	5	418	A	C2'-C3'-O3'	-6.78	103.54	113.70
85	4	6202	C	C2'-C3'-O3'	6.78	119.66	109.50
45	5	280	G	N9-C1'-C2'	6.76	124.15	114.00
45	5	4084	G	C2'-C3'-O3'	6.75	119.62	109.50
45	5	1840	G	C3'-C2'-O2'	6.74	120.80	110.70
45	5	953	C	C1'-C2'-O2'	6.73	118.50	108.40
49	2	991	G	C3'-C2'-O2'	6.73	120.79	110.70
45	5	83	C	C4'-C3'-O3'	-6.72	102.91	113.00
45	5	4238	G	C3'-C2'-O2'	6.72	120.78	110.70
45	5	11	G	C3'-C2'-O2'	6.72	120.78	110.70
34	i	47	VAL	N-CA-C	6.70	118.26	110.62
45	5	1682	A	C3'-C2'-O2'	6.69	120.73	110.70
45	5	2661	U	C4'-C3'-O3'	6.68	119.43	109.40
45	5	1915	C	C3'-C2'-O2'	6.68	124.62	114.60
45	5	4305	G	N9-C1'-C2'	6.68	124.01	114.00
49	2	1688	C	C3'-C2'-O2'	6.67	120.71	110.70
45	5	1853	G	C4'-C3'-O3'	-6.67	103.00	113.00
60	KK	95	ASP	N-CA-C	-6.66	103.94	111.07
45	5	4518	A	C4'-C3'-O3'	6.66	119.39	109.40
85	4	6072	U	O4'-C4'-C3'	-6.66	97.34	104.00
45	5	4127	A	N9-C1'-C2'	6.66	123.99	114.00
45	5	4521	U	C1'-C2'-O2'	6.64	118.37	108.40
45	5	5006	U	C2'-C3'-O3'	6.64	119.47	109.50
21	V	100	ASP	N-CA-C	6.63	117.03	108.34
45	5	2051	C	N1-C1'-C2'	6.63	121.94	112.00
45	5	427	A	C2'-C3'-O3'	6.61	123.62	113.70
45	5	11	G	C4'-C3'-O3'	-6.61	103.09	113.00
45	5	84	A	C2'-C3'-O3'	6.59	119.38	109.50
13	N	153	LYS	N-CA-C	6.59	118.20	109.83
49	2	1082	A	C3'-C2'-O2'	6.59	120.58	110.70
45	5	4697	U	C3'-C2'-O2'	6.58	120.58	110.70
45	5	4170	A	C2'-C3'-O3'	6.58	119.37	109.50
45	5	4376	A	C3'-C2'-O2'	6.58	120.57	110.70
12	M	104	MET	N-CA-C	6.58	119.91	110.24
49	2	1632	G	C1'-C2'-O2'	6.56	121.64	111.80
45	5	4517	A	N9-C1'-C2'	6.55	121.83	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	II	24	SER	N-CA-C	6.55	118.98	111.11
45	5	396	A	C3'-C2'-O2'	6.55	120.52	110.70
45	5	2389	A	C1'-C2'-O2'	6.55	118.22	108.40
45	5	3896	C	C3'-C2'-O2'	6.55	120.52	110.70
45	5	2276	A	C1'-C2'-O2'	6.54	118.22	108.40
45	5	4521	U	C2'-C3'-O3'	-6.54	103.89	113.70
73	XX	28	ARG	CA-C-N	-6.54	113.03	119.90
73	XX	28	ARG	C-N-CA	-6.54	113.03	119.90
45	5	1382	G	C1'-C2'-O2'	6.54	118.20	108.40
45	5	4448	G	C4'-C3'-O3'	6.53	122.80	113.00
64	OO	122	ILE	N-CA-C	-6.53	104.80	110.74
45	5	93	G	C4'-C3'-O3'	-6.53	103.21	113.00
45	5	3868	G	C1'-C2'-O2'	-6.53	102.01	111.80
45	5	4938	A	N9-C1'-C2'	6.53	123.79	114.00
45	5	4975	G	C4'-C3'-O3'	6.52	119.19	109.40
45	5	1534	A	C2'-C3'-O3'	-6.52	99.72	109.50
18	S	84	TYR	N-CA-C	6.52	119.22	108.99
45	5	3876	A	C3'-C2'-O2'	6.52	124.37	114.60
59	JJ	93	THR	N-CA-C	-6.52	100.39	110.10
48	K	211	GLY	N-CA-C	6.51	128.62	113.18
45	5	4125	C	N1-C1'-C2'	6.49	121.74	112.00
62	MM	16	ILE	N-CA-C	6.49	117.46	107.99
35	j	19	CYS	N-CA-C	-6.49	102.17	110.53
45	5	2809	G	C3'-C2'-O2'	-6.49	100.97	110.70
45	5	4649	G	C3'-C2'-O2'	6.49	120.43	110.70
47	8	37	A	C3'-C2'-O2'	6.48	124.31	114.60
85	4	6073	A	C5'-C4'-O4'	6.48	119.51	109.80
18	S	168	THR	N-CA-C	6.47	117.97	108.14
5	E	253	GLN	OE1-CD-NE2	-6.47	116.13	122.60
59	JJ	139	LYS	N-CA-C	6.47	118.78	109.14
45	5	2700	G	C4'-C3'-O3'	-6.47	103.30	113.00
49	2	464	A	C4'-C3'-O3'	6.46	119.10	109.40
45	5	4660	G	C1'-C2'-O2'	-6.46	98.70	108.40
45	5	2440	U	N1-C1'-C2'	-6.46	104.31	114.00
45	5	1667	A	C3'-C2'-O2'	6.46	120.39	110.70
49	2	458	A	C3'-C2'-O2'	6.45	120.38	110.70
4	D	76	CYS	N-CA-C	6.45	118.90	108.32
45	5	1519	C	C2'-C3'-O3'	-6.45	104.03	113.70
45	5	3904	G	C2'-C3'-O3'	6.45	123.37	113.70
49	2	1534	C	C1'-C2'-O2'	6.44	121.47	111.80
13	N	153	LYS	CA-C-N	6.44	126.13	119.82
13	N	153	LYS	C-N-CA	6.44	126.13	119.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	261	G	C4'-C3'-O3'	6.44	122.66	113.00
53	DD	206	SER	N-CA-C	6.44	116.36	107.73
45	5	292	G	C2'-C3'-O3'	-6.43	104.05	113.70
45	5	4161	G	C2'-C3'-O3'	-6.43	104.05	113.70
45	5	2043	A	C3'-C2'-O2'	6.43	120.34	110.70
45	5	1745	G	C4'-C3'-O3'	-6.42	103.37	113.00
49	2	1228	A	C3'-C2'-O2'	6.42	120.33	110.70
45	5	4248	A	C4'-C3'-O3'	6.42	122.63	113.00
45	5	4517	A	P-O5'-C5'	-6.42	111.27	120.90
45	5	1683	U	C4'-C3'-O3'	-6.42	103.38	113.00
45	5	4459	U	C1'-C2'-O2'	6.42	118.02	108.40
68	SS	50	ILE	CB-CA-C	-6.41	103.76	111.97
45	5	4341	C	C2'-C3'-O3'	-6.41	104.08	113.70
62	MM	64	GLY	N-CA-C	6.41	120.46	110.91
11	L	10	LEU	N-CA-C	6.40	118.92	108.55
45	5	2329	U	C3'-C2'-O2'	6.40	120.30	110.70
4	D	65	ALA	N-CA-C	6.40	118.79	109.07
49	2	1227	G	C1'-C2'-O2'	6.39	117.99	108.40
3	C	232	VAL	CB-CA-C	-6.39	103.55	111.92
7	G	215	ASP	CA-C-N	-6.38	111.86	119.84
7	G	215	ASP	C-N-CA	-6.38	111.86	119.84
45	5	979	C	C4'-C3'-O3'	6.38	122.58	113.00
45	5	4603	C	C1'-C2'-O2'	6.38	117.98	108.40
45	5	3648	A	C1'-C2'-O2'	6.38	121.37	111.80
49	2	1148	A	O4'-C1'-C2'	-6.38	99.42	105.80
49	2	1198	G	C4'-C3'-O3'	-6.37	103.45	113.00
45	5	1917	A	C4'-C3'-O3'	-6.37	103.45	113.00
46	7	26	C	C3'-C2'-O2'	6.36	120.25	110.70
45	5	4558	U	C3'-C2'-O2'	6.36	120.23	110.70
16	Q	178	ARG	N-CA-C	6.35	120.52	113.21
45	5	1917	A	C3'-C2'-O2'	6.35	120.23	110.70
49	2	645	C	C3'-C2'-O2'	6.35	120.23	110.70
49	2	1	U	C2'-C3'-O3'	6.34	119.02	109.50
45	5	4176	C	C2'-C3'-O3'	6.34	123.21	113.70
59	JJ	79	ILE	N-CA-C	6.33	117.03	111.90
49	2	1820	G	C3'-C2'-O2'	6.33	120.19	110.70
45	5	3854	C	C2'-C3'-O3'	-6.32	104.22	113.70
49	2	627	U	C2'-C3'-O3'	6.32	123.18	113.70
45	5	4633	G	C3'-C2'-O2'	6.31	120.17	110.70
45	5	2607	C	C3'-C2'-O2'	6.31	120.17	110.70
45	5	2406	G	C3'-C2'-O2'	6.31	120.17	110.70
49	2	445	A	C3'-C2'-O2'	6.31	120.17	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4461	C	N1-C1'-C2'	6.31	121.47	112.00
49	2	1637	A	C2'-C3'-O3'	6.31	118.96	109.50
49	2	1483	A	C3'-C2'-O2'	6.31	120.16	110.70
45	5	1521	C	C3'-C2'-O2'	6.30	120.16	110.70
45	5	2421	G	C4'-C3'-O3'	6.30	118.86	109.40
45	5	1633	G	C4'-C3'-O3'	6.30	122.44	113.00
49	2	533	A	C3'-C2'-O2'	6.29	120.14	110.70
3	C	150	LEU	CA-C-N	6.29	128.97	120.79
3	C	150	LEU	C-N-CA	6.29	128.97	120.79
15	P	81	GLY	N-CA-C	6.29	119.49	111.37
45	5	3854	C	C1'-C2'-O2'	6.29	117.83	108.40
45	5	238	C	C4'-C3'-O3'	-6.28	103.57	113.00
45	5	4175	G	C2'-C3'-O3'	-6.28	104.28	113.70
45	5	4469	U	C2'-C3'-O3'	6.28	123.13	113.70
47	8	37	A	C1'-C2'-O2'	-6.28	102.38	111.80
77	bb	89	ARG	N-CA-C	6.27	118.20	111.36
45	5	2450	G	C3'-C2'-O2'	6.27	120.10	110.70
45	5	3780	G	C4'-C3'-O3'	-6.26	103.61	113.00
45	5	1311	G	C3'-C2'-O2'	6.25	120.08	110.70
29	d	89	SER	N-CA-C	6.24	118.94	108.02
49	2	108	G	C3'-C2'-O2'	6.24	120.06	110.70
49	2	1606	G	C1'-C2'-O2'	6.24	121.16	111.80
45	5	4462	C	N1-C1'-C2'	6.24	121.36	112.00
49	2	110	U	C2'-C3'-O3'	6.24	123.06	113.70
45	5	50	C	C3'-C2'-O2'	6.24	120.06	110.70
45	5	2848	G	C4'-C3'-O3'	6.24	118.75	109.40
45	5	4456	C	C2'-C3'-O3'	6.23	123.05	113.70
45	5	4470	G	C1'-C2'-O2'	6.23	117.74	108.40
22	W	97	LYS	N-CA-C	6.22	118.48	109.84
49	2	1690	U	C3'-C2'-O2'	6.22	120.03	110.70
45	5	2623	A	C2'-C3'-O3'	6.21	123.01	113.70
85	4	6200	A	C4'-C3'-O3'	6.21	118.71	109.40
45	5	4665	A	C4'-C3'-O3'	-6.20	103.70	113.00
2	B	219	VAL	N-CA-C	6.19	117.65	107.24
45	5	372	A	C4'-C3'-O3'	-6.19	103.71	113.00
45	5	1564	A	C3'-C2'-O2'	6.19	119.99	110.70
85	4	6212	U	C2'-C3'-O3'	6.19	118.78	109.50
10	J	102	THR	N-CA-C	-6.18	103.24	111.96
47	8	24	G	C3'-C2'-O2'	6.18	119.97	110.70
3	C	32	ILE	N-CA-C	-6.18	100.73	108.89
6	F	135	VAL	N-CA-C	6.18	117.41	111.91
49	2	642	U	C4'-C3'-O3'	-6.18	103.73	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	3645	U	C2'-C3'-O3'	-6.17	104.44	113.70
45	5	1874	A	C4'-C3'-O3'	-6.17	103.75	113.00
49	2	465	A	C4'-C3'-O3'	6.17	118.65	109.40
45	5	1072	C	C2'-C3'-O3'	6.17	118.75	109.50
33	h	49	VAL	CB-CA-C	-6.16	103.95	112.02
45	5	4936	G	C4'-C3'-O3'	6.16	122.23	113.00
21	V	67	LYS	N-CA-C	6.14	118.07	107.93
60	KK	168	GLY	N-CA-C	6.13	118.42	110.45
45	5	4400	G	C4'-C3'-O3'	-6.13	103.81	113.00
62	MM	119	ASP	N-CA-C	6.13	119.27	107.44
2	B	55	HIS	CB-CA-C	-6.12	97.73	110.40
2	B	344	VAL	N-CA-C	6.12	117.60	108.23
45	5	1622	U	C3'-C2'-O2'	6.12	119.88	110.70
49	2	204	G	C4'-C3'-O3'	6.12	122.17	113.00
49	2	448	A	C4'-C3'-O3'	6.12	118.57	109.40
42	r	10	VAL	CB-CA-C	-6.11	104.01	112.02
49	2	1260	A	C2'-C3'-O3'	-6.11	104.54	113.70
3	C	229	LEU	N-CA-C	-6.11	101.74	110.59
49	2	997	A	C3'-C2'-O2'	6.10	119.85	110.70
45	5	15	A	C1'-C2'-O2'	6.10	117.55	108.40
45	5	4516	G	O5'-C5'-C4'	-6.09	102.36	111.50
45	5	4630	G	C2'-C3'-O3'	6.08	122.83	113.70
45	5	2450	G	C4'-C3'-O3'	6.08	122.12	113.00
45	5	1942	A	N9-C1'-C2'	6.07	121.11	112.00
45	5	2888	G	N9-C1'-C2'	6.07	121.11	112.00
45	5	4622	A	C4'-C3'-O3'	-6.07	103.90	113.00
3	C	154	VAL	N-CA-C	6.06	116.34	108.35
45	5	87	A	C1'-C2'-O2'	6.06	117.49	108.40
45	5	4463	U	C2'-C3'-O3'	6.06	118.58	109.50
49	2	605	A	C3'-C2'-O2'	6.05	119.78	110.70
45	5	2071	A	C3'-C2'-O2'	6.05	119.78	110.70
45	5	2070	U	C2'-C3'-O3'	6.05	118.57	109.50
10	J	26	VAL	N-CA-C	6.05	116.40	111.62
45	5	1323	A	C2'-C3'-O3'	-6.05	104.63	113.70
85	4	6030	A	OP2-P-O3'	-6.05	89.86	108.00
45	5	352	G	C3'-C2'-O2'	6.04	123.67	114.60
45	5	2587	A	C2'-C3'-O3'	6.04	118.57	109.50
49	2	358	C	C3'-C2'-O2'	6.04	119.76	110.70
19	T	27	LEU	N-CA-C	6.04	120.49	113.18
45	5	1515	A	C2'-C3'-O3'	-6.04	104.65	113.70
45	5	2640	G	N9-C1'-C2'	6.04	121.05	112.00
45	5	4491	G	N9-C1'-C2'	6.04	121.05	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	2823	G	C3'-C2'-O2'	6.03	119.75	110.70
45	5	1747	U	C4'-C3'-O3'	-6.03	103.96	113.00
49	2	1190	A	C1'-C2'-O2'	6.02	117.44	108.40
85	4	6071	A	C2'-C3'-O3'	-6.02	104.67	113.70
45	5	4535	A	C3'-C2'-O2'	6.02	119.73	110.70
16	Q	58	ARG	CA-C-N	6.01	126.57	120.38
16	Q	58	ARG	C-N-CA	6.01	126.57	120.38
49	2	976	G	C4'-C3'-O3'	-6.01	103.98	113.00
74	YY	30	ALA	N-CA-C	6.01	117.52	110.97
45	5	1546	C	C4'-C3'-O3'	-6.01	103.99	113.00
45	5	3887	C	C3'-C2'-O2'	6.01	119.71	110.70
45	5	3759	A	C1'-C2'-O2'	6.00	117.40	108.40
6	F	135	VAL	CB-CA-C	-5.99	105.30	112.19
45	5	4460	U	C1'-C2'-O2'	5.99	117.39	108.40
45	5	4507	A	C3'-C2'-O2'	5.99	119.69	110.70
37	1	48	LYS	N-CA-C	5.99	123.07	114.39
49	2	399	C	C4'-C3'-O3'	5.99	118.38	109.40
45	5	449	C	C4'-C3'-O3'	5.98	118.37	109.40
45	5	4305	G	C2'-C3'-O3'	5.98	118.47	109.50
47	8	154	G	C4'-C3'-O3'	-5.97	104.04	113.00
45	5	1636	U	C3'-C2'-O2'	5.97	119.65	110.70
45	5	3781	C	C4'-C3'-O3'	5.97	121.95	113.00
45	5	1455	G	C2'-C3'-O3'	5.97	122.65	113.70
45	5	2434	G	C3'-C2'-O2'	5.97	119.65	110.70
45	5	4287	G	C2'-C3'-O3'	5.97	122.65	113.70
50	3	69	A	N9-C1'-C2'	5.97	122.95	114.00
45	5	4135	G	C3'-C2'-O2'	5.96	119.64	110.70
30	e	95	TYR	N-CA-C	5.96	119.25	109.72
45	5	1904	G	C1'-C2'-O2'	5.96	117.33	108.40
45	5	4687	A	C3'-C2'-O2'	5.96	119.63	110.70
45	5	47	A	C1'-C2'-O2'	5.96	120.73	111.80
49	2	39	A	C3'-C2'-O2'	5.95	119.63	110.70
45	5	222	C	C2'-C3'-O3'	-5.95	104.77	113.70
49	2	1253	A	C2'-C3'-O3'	5.95	118.42	109.50
49	2	1249	C	N1-C1'-C2'	5.94	120.91	112.00
47	8	130	C	C3'-C2'-O2'	5.93	119.60	110.70
45	5	16	G	C3'-C2'-O2'	5.93	119.60	110.70
45	5	3869	C	C1'-C2'-O2'	5.93	117.30	108.40
74	YY	81	ILE	CB-CA-C	-5.93	101.69	110.82
85	4	6071	A	C4'-C3'-C2'	-5.93	96.67	102.60
49	2	604	A	C4'-C3'-O3'	-5.92	104.11	113.00
45	5	275	C	C2'-C3'-O3'	5.92	122.58	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	18	G	C4'-C3'-O3'	5.92	118.28	109.40
13	N	61	ILE	N-CA-C	5.91	116.63	108.12
49	2	940	U	C4'-C3'-O3'	5.91	121.86	113.00
45	5	3606	U	C2'-C3'-O3'	5.91	122.56	113.70
45	5	1616	U	C3'-C2'-O2'	5.91	119.56	110.70
45	5	2836	A	C3'-C2'-O2'	5.91	119.56	110.70
45	5	231	U	C4'-C3'-O3'	-5.90	104.15	113.00
45	5	2351	C	C3'-C2'-O2'	5.90	119.55	110.70
9	I	4	ARG	CA-C-N	5.90	126.09	120.31
9	I	4	ARG	C-N-CA	5.90	126.09	120.31
45	5	2361	G	C2'-C3'-O3'	5.90	118.35	109.50
45	5	2295	C	C1'-C2'-O2'	-5.90	99.56	108.40
57	HH	68	LEU	N-CA-C	5.90	123.36	110.80
21	V	108	ASN	N-CA-C	5.89	119.30	111.75
45	5	2407	G	C4'-C3'-O3'	5.89	118.24	109.40
49	2	28	U	C4'-C3'-O3'	5.89	121.83	113.00
49	2	1620	A	N9-C1'-C2'	5.89	122.83	114.00
45	5	1524	A	C1'-C2'-O2'	5.88	117.22	108.40
45	5	1873	A	C2'-C3'-O3'	-5.88	104.88	113.70
49	2	344	U	C3'-C2'-O2'	5.88	119.52	110.70
45	5	932	A	C4'-C3'-O3'	5.88	118.21	109.40
45	5	1393	G	C4'-C3'-O3'	-5.88	104.19	113.00
45	5	4342	C	C3'-C2'-O2'	5.87	119.51	110.70
49	2	6	G	C2'-C3'-O3'	5.86	122.50	113.70
3	C	204	ARG	N-CA-C	5.86	117.61	110.41
45	5	2290	C	C4'-C3'-O3'	5.86	121.78	113.00
45	5	1573	G	N9-C1'-C2'	5.85	120.78	112.00
45	5	4586	G	C2'-C3'-O3'	5.85	122.48	113.70
45	5	121	A	N9-C1'-C2'	5.85	120.77	112.00
45	5	245	C	C2'-C3'-O3'	5.85	122.47	113.70
45	5	1632	A	C2'-C3'-O3'	-5.84	104.93	113.70
45	5	81	C	C1'-C2'-O2'	5.84	117.16	108.40
45	5	2502	A	C3'-C2'-O2'	5.84	119.46	110.70
45	5	4484	A	C3'-C2'-O2'	5.84	119.46	110.70
47	8	8	U	C3'-C2'-O2'	5.84	119.46	110.70
49	2	524	U	C3'-C2'-O2'	5.84	119.46	110.70
24	Y	65	GLN	N-CA-C	5.83	119.46	112.93
6	F	218	GLY	N-CA-C	5.83	117.75	110.29
45	5	3643	A	C4'-C3'-O3'	-5.83	100.66	109.40
49	2	1520	G	N9-C1'-C2'	5.83	120.74	112.00
37	1	6	THR	CB-CA-C	-5.83	100.19	109.80
45	5	1908	A	C4'-C3'-O3'	-5.82	104.26	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	cc	50	ALA	N-CA-C	5.82	120.54	112.45
45	5	2333	G	C1'-C2'-O2'	5.82	117.13	108.40
49	2	977	C	C3'-C2'-O2'	5.82	119.43	110.70
47	8	17	A	C4'-C3'-O3'	-5.81	104.28	113.00
45	5	19	G	C1'-C2'-O2'	5.81	117.11	108.40
45	5	1587	G	C4'-C3'-O3'	5.81	118.11	109.40
45	5	2064	G	C4'-C3'-O3'	5.81	121.72	113.00
45	5	2421	G	C2'-C3'-O3'	-5.81	100.79	109.50
45	5	1856	C	C3'-C2'-O2'	5.81	119.41	110.70
45	5	4700	A	C3'-C2'-O2'	5.81	119.41	110.70
45	5	2327	G	C4'-C3'-O3'	-5.80	104.30	113.00
45	5	3637	U	C1'-C2'-O2'	5.80	117.10	108.40
45	5	2498	C	C3'-C2'-O2'	5.79	119.39	110.70
45	5	4993	G	C2'-C3'-O3'	-5.79	105.01	113.70
49	2	1228	A	C2'-C3'-O3'	5.79	122.38	113.70
45	5	4232	U	C2'-C3'-O3'	5.78	118.17	109.50
45	5	4488	A	C1'-C2'-O2'	5.78	120.48	111.80
2	B	87	VAL	CB-CA-C	-5.78	104.98	110.70
45	5	3641	U	C2'-C3'-O3'	-5.78	105.03	113.70
49	2	1508	A	C4'-C3'-O3'	5.78	118.06	109.40
45	5	1281	G	C2'-C3'-O3'	-5.77	105.04	113.70
47	8	142	U	C3'-C2'-O2'	5.77	119.36	110.70
45	5	4429	C	C3'-C2'-O2'	5.77	119.36	110.70
45	5	4374	U	C2'-C3'-O3'	5.77	118.16	109.50
49	2	1342	U	C4'-C3'-O3'	5.77	118.06	109.40
45	5	4476	C	C4'-C3'-O3'	-5.77	104.35	113.00
74	YY	31	HIS	N-CA-C	5.77	119.08	112.97
85	4	6178	U	C5'-C4'-C3'	5.76	123.84	115.20
45	5	717	U	C1'-C2'-O2'	5.76	117.04	108.40
45	5	1632	A	C1'-C2'-O2'	5.75	117.03	108.40
45	5	1912	G	N9-C1'-C2'	5.75	120.63	112.00
47	8	15	G	N9-C1'-C2'	5.75	120.62	112.00
45	5	4656	A	C1'-C2'-O2'	-5.75	103.18	111.80
48	K	215	ARG	N-CA-C	5.74	118.98	110.48
45	5	1291	G	C3'-C2'-O2'	5.74	119.31	110.70
74	YY	6	GLY	N-CA-C	5.74	118.64	112.33
45	5	3844	U	C4'-C3'-O3'	5.74	121.61	113.00
49	2	99	A	C3'-C2'-O2'	5.74	119.31	110.70
49	2	1638	G	C3'-C2'-O2'	5.73	119.30	110.70
3	C	257	PHE	N-CA-C	-5.73	104.48	112.45
45	5	2427	G	N9-C1'-C2'	5.73	120.60	112.00
45	5	1307	A	C3'-C2'-O2'	5.73	119.30	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	3647	A	C2'-C3'-O3'	5.73	122.30	113.70
45	5	1909	G	C1'-C2'-O2'	5.73	116.99	108.40
45	5	2815	A	C3'-C2'-O2'	5.73	119.29	110.70
45	5	2052	G	N9-C1'-C2'	5.72	120.58	112.00
45	5	4335	C	C1'-C2'-O2'	5.71	116.97	108.40
49	2	55	U	N1-C1'-C2'	5.71	122.57	114.00
49	2	1625	U	C1'-C2'-O2'	5.71	116.97	108.40
45	5	1780	A	C3'-C2'-O2'	5.71	119.26	110.70
45	5	1392	A	C4'-C3'-O3'	-5.71	104.44	113.00
45	5	3624	A	C2'-C3'-O3'	-5.71	105.14	113.70
42	r	39	ARG	N-CA-C	-5.71	104.70	111.03
45	5	2509	C	C2'-C3'-O3'	5.71	122.26	113.70
85	4	6200	A	C1'-C2'-O2'	5.71	120.36	111.80
45	5	2272	C	C3'-C2'-O2'	5.70	119.26	110.70
45	5	3894	A	C1'-C2'-O2'	5.70	116.96	108.40
6	F	214	SER	CA-C-N	5.70	127.24	120.23
6	F	214	SER	C-N-CA	5.70	127.24	120.23
5	E	222	LYS	N-CA-C	5.70	118.05	110.53
49	2	1164	G	N9-C1'-C2'	5.70	120.55	112.00
45	5	3837	C	C3'-C2'-O2'	5.69	119.24	110.70
52	CC	212	VAL	N-CA-CB	5.69	116.73	110.53
47	8	35	C	C1'-C2'-O2'	5.68	116.92	108.40
50	3	18	G	C2'-C3'-O3'	5.68	118.02	109.50
33	h	44	LEU	N-CA-C	5.68	117.14	111.07
49	2	666	U	C3'-C2'-O2'	5.68	119.21	110.70
49	2	465	A	C2'-C3'-O3'	5.67	118.01	109.50
45	5	4325	A	C3'-C2'-O2'	5.67	119.21	110.70
45	5	2801	U	C3'-C2'-O2'	5.67	119.21	110.70
45	5	108	A	C4'-C3'-O3'	5.67	117.91	109.40
45	5	4414	A	C2'-C3'-O3'	5.67	118.00	109.50
45	5	3840	U	C1'-C2'-O2'	5.66	116.89	108.40
47	8	124	U	C4'-C3'-O3'	5.66	117.89	109.40
48	K	154	THR	N-CA-C	5.66	117.84	110.43
85	4	6073	A	O4'-C4'-C3'	-5.66	98.34	104.00
39	n	3	ALA	N-CA-C	5.66	117.14	110.97
85	4	6180	U	C4'-C3'-O3'	5.65	121.48	113.00
45	5	4174	U	C3'-C2'-O2'	5.65	119.18	110.70
85	4	6180	U	C2'-C3'-O3'	5.65	122.18	113.70
45	5	1650	A	C3'-C2'-O2'	5.65	123.08	114.60
50	3	19	G	C2'-C3'-O3'	5.65	117.97	109.50
45	5	370	U	C2'-C3'-O3'	-5.65	105.23	113.70
42	r	124	VAL	N-CA-C	5.65	116.20	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	32	G	C1'-C2'-O2'	5.64	116.87	108.40
45	5	4391	G	C3'-C2'-O2'	5.64	119.17	110.70
49	2	1834	A	C3'-C2'-O2'	-5.64	106.13	114.60
45	5	2785	C	C2'-C3'-O3'	-5.64	105.24	113.70
5	E	61	ARG	N-CA-C	5.64	119.24	112.93
45	5	1920	C	C2'-C3'-O3'	5.64	117.95	109.50
45	5	2856	C	C4'-C3'-O3'	-5.64	104.55	113.00
24	Y	102	SER	N-CA-C	-5.63	105.52	112.90
31	f	106	TYR	CA-C-N	5.63	126.88	119.84
31	f	106	TYR	C-N-CA	5.63	126.88	119.84
45	5	3689	G	C1'-C2'-O2'	-5.63	99.95	108.40
85	4	6200	A	O4'-C4'-C3'	-5.63	100.47	106.10
45	5	3878	C	C2'-C3'-O3'	5.63	117.94	109.50
45	5	3649	A	C4'-C3'-O3'	-5.62	104.57	113.00
47	8	42	G	C3'-C2'-O2'	5.62	119.13	110.70
78	cc	16	LYS	N-CA-C	-5.62	105.30	111.82
49	2	404	G	C3'-C2'-O2'	5.62	119.13	110.70
45	5	1847	C	C3'-C2'-O2'	5.62	119.13	110.70
45	5	2528	G	N9-C1'-C2'	5.62	120.42	112.00
45	5	3908	A	C2'-C3'-O3'	-5.62	105.28	113.70
45	5	3913	G	C2'-C3'-O3'	5.62	117.92	109.50
48	K	164	CYS	N-CA-C	5.61	117.72	109.24
45	5	60	A	C1'-C2'-O2'	5.61	116.82	108.40
53	DD	200	ARG	N-CA-C	5.61	118.37	110.23
45	5	2271	C	N1-C1'-C2'	5.61	120.42	112.00
18	S	115	ALA	N-CA-C	5.61	117.47	111.36
49	2	1572	C	C4'-C3'-O3'	5.61	121.41	113.00
45	5	961	G	C4'-C3'-O3'	-5.61	104.59	113.00
49	2	1164	G	C2'-C3'-O3'	-5.61	105.29	113.70
49	2	1499	U	C3'-C2'-O2'	5.61	119.11	110.70
45	5	1316	G	C1'-C2'-O2'	5.60	116.80	108.40
45	5	5056	A	C2'-C3'-O3'	-5.60	105.31	113.70
19	T	87	LYS	N-CA-C	5.59	117.60	108.76
45	5	6	C	C3'-C2'-O2'	5.59	119.09	110.70
1	A	107	MET	N-CA-C	5.59	116.03	109.60
45	5	4287	G	C3'-C2'-O2'	5.59	119.09	110.70
49	2	976	G	C3'-C2'-O2'	5.59	119.09	110.70
45	5	2549	G	C2'-C3'-O3'	5.59	122.08	113.70
54	EE	60	GLY	N-CA-C	5.59	120.45	110.95
45	5	4461	C	O4'-C4'-C3'	-5.58	98.42	104.00
45	5	388	A	C3'-C2'-O2'	5.58	119.07	110.70
32	g	20	THR	N-CA-C	5.58	117.10	109.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4514	G	C2'-C3'-O3'	5.57	122.06	113.70
45	5	4620	U	C1'-C2'-O2'	5.57	116.76	108.40
31	f	34	TYR	N-CA-C	5.57	121.32	113.02
49	2	1246	A	C1'-C2'-O2'	5.57	116.75	108.40
45	5	1929	A	C3'-C2'-O2'	5.56	119.04	110.70
45	5	4466	C	C3'-C2'-O2'	5.56	119.05	110.70
45	5	4523	A	C5'-C4'-C3'	5.56	124.34	116.00
85	4	6178	U	C6-N1-C1'	-5.56	104.52	121.20
49	2	561	A	C2'-C3'-O3'	5.56	122.04	113.70
35	j	56	ARG	N-CA-C	-5.56	106.34	113.23
35	j	74	PHE	N-CA-C	5.56	117.03	110.97
45	5	2332	A	C4'-C3'-O3'	5.56	117.74	109.40
45	5	4533	A	C2'-C3'-O3'	-5.55	105.37	113.70
3	C	97	ARG	N-CA-C	-5.55	101.43	110.20
41	p	74	THR	N-CA-C	5.55	117.41	111.36
45	5	2332	A	C2'-C3'-O3'	-5.55	101.17	109.50
53	DD	198	ALA	CA-C-N	5.55	125.53	120.21
53	DD	198	ALA	C-N-CA	5.55	125.53	120.21
49	2	24	C	C4'-C3'-O3'	-5.54	104.69	113.00
45	5	948	C	C3'-C2'-O2'	5.54	119.01	110.70
45	5	3763	A	C2'-C3'-O3'	5.54	122.01	113.70
38	m	96	ARG	CA-C-N	-5.54	114.62	120.66
38	m	96	ARG	C-N-CA	-5.54	114.62	120.66
49	2	1173	A	C1'-C2'-O2'	5.54	116.71	108.40
26	a	29	PRO	N-CA-C	5.54	123.88	112.47
45	5	3876	A	O4'-C4'-C3'	-5.54	100.56	106.10
45	5	4207	C	C2'-C3'-O3'	5.54	122.00	113.70
45	5	2711	G	C2'-C3'-O3'	5.54	117.80	109.50
45	5	4585	U	C1'-C2'-O2'	5.54	116.70	108.40
39	n	9	ARG	N-CA-C	5.53	117.31	111.28
45	5	4534	G	C1'-C2'-O2'	-5.53	100.10	108.40
45	5	1298	C	C4'-C3'-O3'	-5.53	104.71	113.00
45	5	1913	C	N1-C1'-C2'	5.53	120.29	112.00
45	5	4393	G	C4'-C3'-O3'	5.53	117.69	109.40
49	2	349	A	C1'-C2'-O2'	5.53	116.69	108.40
45	5	4469	U	O4'-C4'-C3'	-5.52	98.48	104.00
45	5	4723	A	C2'-C3'-O3'	-5.52	105.42	113.70
58	II	106	ARG	N-CA-C	-5.51	104.29	111.02
45	5	2623	A	C3'-C2'-O2'	5.51	118.97	110.70
85	4	6182	A	OP2-P-O3'	5.51	124.53	108.00
45	5	47	A	C3'-C2'-O2'	-5.51	106.34	114.60
49	2	1196	A	C3'-C2'-O2'	5.50	118.95	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4425	G	C1'-C2'-O2'	5.50	116.64	108.40
49	2	155	G	C3'-C2'-O2'	5.50	118.94	110.70
45	5	1655	C	C1'-C2'-O2'	-5.50	100.16	108.40
53	DD	207	ALA	CA-C-N	5.49	126.71	119.84
53	DD	207	ALA	C-N-CA	5.49	126.71	119.84
45	5	3838	U	C2'-C3'-O3'	-5.48	105.47	113.70
41	p	38	THR	N-CA-CB	5.48	118.81	109.87
45	5	3876	A	C1'-C2'-O2'	-5.48	103.58	111.80
30	e	43	ASN	N-CA-C	5.48	122.47	110.80
45	5	4462	C	C4'-C3'-O3'	5.48	121.22	113.00
45	5	4663	G	C3'-C2'-O2'	5.48	118.92	110.70
45	5	393	U	C3'-C2'-O2'	5.48	118.91	110.70
46	7	5	A	C3'-C2'-O2'	5.47	118.91	110.70
45	5	3871	A	C3'-C2'-O2'	5.47	118.91	110.70
45	5	4380	A	C2'-C3'-O3'	5.47	117.71	109.50
45	5	1591	U	C3'-C2'-O2'	5.47	118.90	110.70
49	2	1171	G	C1'-C2'-O2'	5.47	120.00	111.80
45	5	2655	C	C1'-C2'-O2'	5.47	116.60	108.40
45	5	4623	G	C3'-C2'-O2'	5.47	118.90	110.70
14	O	186	GLU	N-CA-C	5.46	120.91	113.37
45	5	1888	A	C1'-C2'-O2'	5.46	116.59	108.40
45	5	4518	A	C5'-C4'-C3'	5.46	123.39	115.20
49	2	1019	C	C4'-C3'-O3'	-5.46	104.81	113.00
4	D	280	VAL	N-CA-C	5.46	117.45	112.43
48	K	213	PRO	N-CA-C	5.46	119.65	111.14
61	LL	89	ILE	N-CA-C	5.46	116.38	110.21
45	5	1285	U	C4'-C3'-O3'	5.45	121.18	113.00
2	B	160	ILE	N-CA-C	5.45	116.58	108.46
6	F	215	PRO	N-CA-C	5.45	119.06	110.50
21	V	63	ALA	N-CA-C	5.45	118.33	109.06
45	5	3689	G	C3'-C2'-O2'	5.45	118.88	110.70
3	C	199	ARG	N-CA-C	-5.45	99.53	109.56
45	5	2805	C	N1-C1'-C2'	5.45	120.17	112.00
49	2	29	G	C3'-C2'-O2'	5.45	118.87	110.70
45	5	400	A	C1'-C2'-O2'	5.45	116.57	108.40
45	5	2593	C	C3'-C2'-O2'	5.45	118.87	110.70
49	2	525	A	C3'-C2'-O2'	5.45	118.87	110.70
49	2	4	C	C1'-C2'-O2'	5.44	116.56	108.40
55	FF	25	GLY	N-CA-C	5.44	119.47	110.55
21	V	72	LEU	N-CA-C	5.43	117.28	111.36
45	5	1739	G	N9-C1'-C2'	5.43	120.15	112.00
85	4	6073	A	C5'-C4'-C3'	5.43	124.15	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	33	ARG	N-CA-C	-5.43	105.26	111.07
49	2	1622	U	C4'-C3'-O3'	-5.43	101.25	109.40
45	5	4434	C	C2'-C3'-O3'	-5.43	105.56	113.70
53	DD	202	THR	N-CA-C	-5.43	104.40	111.02
45	5	2551	A	C3'-C2'-O2'	5.43	118.84	110.70
45	5	2508	U	C3'-C2'-O2'	5.42	118.84	110.70
45	5	1327	C	C3'-C2'-O2'	5.42	118.83	110.70
45	5	958	G	C2'-C3'-O3'	5.42	117.62	109.50
49	2	1544	C	C2'-C3'-O3'	-5.42	105.58	113.70
49	2	1728	U	C3'-C2'-O2'	5.42	118.82	110.70
49	2	1084	A	C1'-C2'-O2'	5.41	116.52	108.40
45	5	4442	U	C1'-C2'-O2'	5.41	116.52	108.40
45	5	2294	G	C1'-C2'-O2'	-5.41	100.28	108.40
45	5	3614	G	C2'-C3'-O3'	-5.41	105.59	113.70
49	2	1454	A	C2'-C3'-O3'	5.41	117.61	109.50
20	U	109	SER	N-CA-C	5.40	117.18	108.32
45	5	4604	G	C3'-C2'-O2'	5.40	118.80	110.70
45	5	2822	G	C2'-C3'-O3'	-5.40	105.60	113.70
45	5	363	A	C2'-C3'-O3'	5.40	117.59	109.50
49	2	924	G	C1'-C2'-O2'	5.40	116.50	108.40
45	5	4618	G	C3'-C2'-O2'	5.39	118.79	110.70
50	3	85	C	C4'-C3'-O3'	5.39	117.49	109.40
47	8	31	G	C3'-C2'-O2'	5.39	118.79	110.70
49	2	1275	G	C3'-C2'-O2'	5.39	118.79	110.70
77	bb	98	PRO	N-CA-C	5.39	115.65	110.47
49	2	397	G	C3'-C2'-O2'	5.39	118.78	110.70
53	DD	147	VAL	N-CA-C	5.39	116.16	110.72
45	5	14	C	C3'-C2'-O2'	5.38	118.78	110.70
45	5	1503	A	O4'-C4'-C3'	-5.38	100.72	106.10
45	5	3673	C	C4'-C3'-O3'	5.38	117.47	109.40
6	F	205	ASN	N-CA-C	-5.38	106.67	113.18
47	8	60	G	C2'-C3'-O3'	5.38	117.57	109.50
74	YY	5	ARG	N-CA-C	5.38	122.26	110.80
74	YY	39	ASN	CA-C-N	5.38	124.84	119.24
74	YY	39	ASN	C-N-CA	5.38	124.84	119.24
45	5	4516	G	C3'-C2'-O2'	-5.38	102.63	110.70
49	2	553	U	C4'-C3'-O3'	5.38	117.47	109.40
45	5	4715	C	C1'-C2'-O2'	5.38	116.47	108.40
49	2	1474	A	C4'-C3'-O3'	-5.38	104.93	113.00
46	7	14	C	C1'-C2'-O2'	5.38	116.46	108.40
66	QQ	68	PRO	N-CA-C	5.38	117.26	110.70
45	5	4282	A	C4'-C3'-O3'	5.37	117.46	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4625	C	N1-C1'-C2'	5.37	120.06	112.00
49	2	933	G	C1'-C2'-O2'	5.37	116.46	108.40
25	Z	74	VAL	N-CA-C	5.37	115.05	106.88
45	5	2518	G	C1'-C2'-O2'	5.37	116.46	108.40
45	5	2320	G	C4'-C3'-O3'	-5.37	104.95	113.00
45	5	4878	C	C4'-C3'-O3'	5.37	121.05	113.00
45	5	1684	A	C2'-C3'-O3'	-5.37	105.65	113.70
45	5	4867	G	C3'-C2'-O2'	5.37	118.75	110.70
49	2	643	A	C4'-C3'-O3'	5.37	117.45	109.40
26	a	21	ARG	N-CA-C	-5.37	104.32	111.24
49	2	476	A	C2'-C3'-O3'	5.37	121.75	113.70
45	5	3762	U	C3'-C2'-O2'	5.37	118.75	110.70
21	V	26	ILE	N-CA-C	-5.36	100.66	108.97
27	b	37	PRO	N-CA-C	5.36	123.52	112.47
45	5	3603	G	O4'-C4'-C3'	-5.36	100.74	106.10
49	2	1230	C	C4'-C3'-O3'	-5.36	104.96	113.00
83	hh	126	ASP	N-CA-C	-5.36	102.12	110.10
45	5	4071	U	C4'-C3'-O3'	-5.35	104.97	113.00
45	5	236	G	C1'-C2'-O2'	5.35	116.43	108.40
47	8	103	A	C1'-C2'-O2'	5.35	116.42	108.40
18	S	93	MET	N-CA-C	5.34	116.40	108.60
45	5	1876	U	C3'-C2'-O2'	5.34	118.72	110.70
85	4	6106	U	C4'-C3'-O3'	5.34	117.42	109.40
45	5	1874	A	P-O5'-C5'	-5.34	112.89	120.90
45	5	457	G	C4'-C3'-O3'	-5.34	104.99	113.00
49	2	662	G	C4'-C3'-O3'	5.34	117.41	109.40
45	5	4947	U	C4'-C3'-O3'	-5.34	104.99	113.00
57	HH	99	GLY	N-CA-C	5.34	119.37	112.54
45	5	210	C	C2'-C3'-O3'	5.34	117.51	109.50
45	5	4176	C	P-O5'-C5'	-5.34	112.89	120.90
45	5	2390	G	C1'-C2'-O2'	5.33	116.40	108.40
45	5	449	C	C2'-C3'-O3'	5.33	117.50	109.50
45	5	712	C	C1'-C2'-O2'	-5.33	100.41	108.40
45	5	3870	C	C1'-C2'-O2'	5.33	116.39	108.40
45	5	3925	U	C1'-C2'-O2'	5.33	116.39	108.40
49	2	24	C	C3'-C2'-O2'	5.33	118.69	110.70
10	J	113	ILE	N-CA-C	5.32	116.05	110.62
13	N	85	VAL	CB-CA-C	-5.32	102.56	111.29
21	V	22	VAL	N-CA-C	5.32	120.41	109.34
45	5	955	G	C1'-C2'-O2'	5.32	119.78	111.80
45	5	2464	C	C2'-C3'-O3'	-5.32	105.72	113.70
45	5	1913	C	C2'-C3'-O3'	5.32	121.67	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	2468	U	C2'-C3'-O3'	-5.31	101.53	109.50
45	5	4195	G	C2'-C3'-O3'	5.31	117.47	109.50
30	e	25	SER	N-CA-C	-5.31	106.06	112.54
1	A	47	ASP	N-CA-C	5.31	117.15	108.55
45	5	1884	C	C3'-C2'-O2'	5.31	118.66	110.70
66	QQ	118	GLU	N-CA-C	5.31	119.24	112.87
27	b	17	HIS	N-CA-C	5.31	118.85	112.38
45	5	359	A	C3'-C2'-O2'	5.31	118.66	110.70
45	5	3627	G	C3'-C2'-O2'	5.31	118.66	110.70
45	5	1847	C	C4'-C3'-O3'	-5.31	105.04	113.00
45	5	1860	U	C1'-C2'-O2'	5.31	116.36	108.40
45	5	45	U	C2'-C3'-O3'	5.30	121.66	113.70
45	5	1918	U	C3'-C2'-O2'	5.30	118.66	110.70
49	2	297	A	C1'-C2'-O2'	5.30	116.36	108.40
75	ZZ	16	ARG	N-CA-C	-5.30	105.50	111.28
45	5	1880	G	C1'-C2'-O2'	5.30	116.35	108.40
45	5	3915	U	C3'-C2'-O2'	5.30	118.66	110.70
45	5	283	G	C1'-C2'-O2'	5.30	116.35	108.40
49	2	1030	A	C3'-C2'-O2'	5.30	118.65	110.70
45	5	1742	A	C3'-C2'-O2'	5.30	118.65	110.70
45	5	4403	U	C1'-C2'-O2'	5.30	116.34	108.40
49	2	655	A	C4'-C3'-O3'	5.30	117.34	109.40
42	r	18	ILE	CB-CA-C	5.29	117.32	110.12
45	5	4580	U	C3'-C2'-O2'	5.29	118.64	110.70
49	2	101	U	C3'-C2'-O2'	5.29	118.64	110.70
49	2	409	C	C3'-C2'-O2'	5.29	118.64	110.70
71	VV	107	GLU	N-CA-C	5.29	112.98	108.22
45	5	3916	G	N9-C1'-C2'	5.29	119.94	112.00
49	2	1664	A	C4'-C3'-O3'	5.29	117.33	109.40
45	5	4163	U	C4'-C3'-O3'	-5.29	105.07	113.00
26	a	25	HIS	N-CA-C	-5.28	99.90	108.41
49	2	943	U	C3'-C2'-O2'	5.28	118.62	110.70
45	5	397	G	C2'-C3'-O3'	5.28	121.62	113.70
45	5	1394	G	C3'-C2'-O2'	5.28	118.61	110.70
45	5	2068	C	C4'-C3'-O3'	5.28	117.31	109.40
45	5	233	U	C2'-C3'-O3'	5.27	121.61	113.70
45	5	2715	G	C2'-C3'-O3'	5.27	121.61	113.70
25	Z	17	ARG	N-CA-C	5.27	118.49	111.75
47	8	28	C	C3'-C2'-O2'	5.27	118.60	110.70
83	hh	35	SER	N-CA-C	5.27	117.08	109.07
45	5	1462	A	C2'-C3'-O3'	5.27	121.60	113.70
2	B	260	ALA	N-CA-C	5.26	122.01	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4567	G	C2'-C3'-O3'	5.26	121.59	113.70
45	5	4559	A	C2'-C3'-O3'	5.26	121.59	113.70
45	5	4571	A	C4'-C3'-O3'	-5.26	105.11	113.00
49	2	1610	G	C3'-C2'-O2'	5.26	118.59	110.70
45	5	5044	A	C4'-C3'-O3'	-5.26	105.12	113.00
49	2	564	A	C3'-C2'-O2'	5.26	118.59	110.70
45	5	437	G	C3'-C2'-O2'	5.25	118.58	110.70
45	5	1566	C	C3'-C2'-O2'	5.25	118.58	110.70
45	5	2785	C	C1'-C2'-O2'	5.25	116.28	108.40
49	2	485	A	C3'-C2'-O2'	5.25	118.58	110.70
49	2	1484	A	C4'-C3'-O3'	-5.25	105.12	113.00
45	5	1875	C	C1'-C2'-O2'	5.24	116.27	108.40
45	5	2809	G	C4'-C3'-O3'	-5.24	105.14	113.00
13	N	44	ARG	CA-C-N	-5.24	114.22	119.56
13	N	44	ARG	C-N-CA	-5.24	114.22	119.56
45	5	92	C	C2'-C3'-O3'	5.24	117.36	109.50
35	j	52	LYS	N-CA-C	-5.24	106.84	113.18
45	5	1509	C	C3'-C2'-O2'	5.24	118.56	110.70
45	5	109	G	C1'-C2'-O2'	5.23	116.25	108.40
45	5	1523	A	C3'-C2'-O2'	5.23	118.55	110.70
45	5	2517	A	C4'-C3'-O3'	-5.23	105.15	113.00
45	5	4577	U	C3'-C2'-O2'	5.23	118.55	110.70
45	5	4717	A	C3'-C2'-O2'	5.23	118.55	110.70
49	2	1611	G	C3'-C2'-O2'	5.23	118.55	110.70
49	2	1144	A	N9-C1'-C2'	5.23	119.85	112.00
85	4	6178	U	C1'-O4'-C4'	-5.23	104.47	109.70
45	5	1663	C	C2'-C3'-O3'	-5.23	105.86	113.70
45	5	4127	A	C2'-C3'-O3'	-5.22	101.66	109.50
47	8	38	U	C4'-C3'-O3'	5.22	117.24	109.40
45	5	2300	A	C3'-C2'-O2'	5.22	122.43	114.60
47	8	140	C	C1'-C2'-O2'	5.22	116.23	108.40
49	2	532	C	C2'-C3'-O3'	5.22	121.53	113.70
45	5	3672	G	C3'-C2'-O2'	5.22	118.53	110.70
49	2	593	C	C2'-C3'-O3'	-5.22	105.87	113.70
45	5	3902	A	C1'-C2'-O2'	-5.22	100.57	108.40
45	5	2856	C	C2'-C3'-O3'	5.21	121.52	113.70
6	F	223	THR	N-CA-C	5.21	116.96	111.28
45	5	4579	U	C1'-C2'-O2'	5.21	116.22	108.40
45	5	5003	U	C3'-C2'-O2'	5.21	118.52	110.70
47	8	39	G	C2'-C3'-O3'	5.21	117.32	109.50
49	2	1604	G	N9-C1'-C2'	5.21	119.82	112.00
69	TT	127	TRP	N-CA-C	5.21	119.62	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	VV	90	ASP	N-CA-C	5.21	117.14	108.02
45	5	2331	G	C2'-C3'-O3'	5.21	117.31	109.50
49	2	1531	A	C2'-C3'-O3'	-5.21	105.89	113.70
45	5	237	G	C4'-C3'-O3'	-5.20	105.20	113.00
45	5	1578	U	C3'-C2'-O2'	5.20	118.50	110.70
45	5	2510	G	C4'-C3'-O3'	-5.20	105.20	113.00
49	2	867	G	C3'-C2'-O2'	5.20	118.49	110.70
45	5	143	C	C2'-C3'-O3'	-5.19	105.91	113.70
45	5	1235	G	C2'-C3'-O3'	5.19	117.29	109.50
53	DD	93	ILE	CB-CA-C	-5.19	105.23	111.88
45	5	4404	U	C1'-C2'-O2'	5.19	119.58	111.80
45	5	2358	G	C2'-C3'-O3'	5.19	121.48	113.70
45	5	1072	C	C4'-C3'-O3'	5.18	117.18	109.40
45	5	2329	U	N1-C1'-C2'	5.18	119.78	112.00
45	5	4672	A	C2'-C3'-O3'	5.18	121.48	113.70
84	jj	120	ILE	CB-CA-C	-5.18	104.12	111.28
45	5	4218	U	C2'-C3'-O3'	-5.18	105.93	113.70
45	5	4119	C	C2'-C3'-O3'	5.18	121.47	113.70
49	2	113	G	C2'-C3'-O3'	5.18	117.27	109.50
22	W	28	VAL	N-CA-C	5.18	115.49	107.78
45	5	1368	A	C1'-C2'-O2'	5.18	116.16	108.40
49	2	373	G	C3'-C2'-O2'	5.18	118.46	110.70
45	5	2067	C	C4'-C3'-O3'	-5.17	105.24	113.00
45	5	4459	U	O4'-C4'-C3'	-5.17	98.83	104.00
45	5	2289	C	C2'-C3'-O3'	5.17	117.26	109.50
45	5	2830	G	C2'-C3'-O3'	5.17	121.46	113.70
4	D	36	LEU	N-CA-C	5.17	117.71	111.40
29	d	47	LYS	N-CA-C	-5.17	103.65	111.56
45	5	4270	C	C2'-C3'-O3'	-5.17	105.95	113.70
16	Q	130	SER	CA-C-N	5.17	124.61	119.24
16	Q	130	SER	C-N-CA	5.17	124.61	119.24
3	C	118	THR	N-CA-C	5.16	118.44	112.97
45	5	3671	G	N9-C1'-C2'	5.16	119.74	112.00
45	5	83	C	C2'-C3'-O3'	5.16	121.44	113.70
43	s	56	GLY	N-CA-C	5.15	118.27	110.75
45	5	1470	G	C4'-C3'-O3'	-5.15	105.28	113.00
45	5	1936	C	C3'-C2'-O2'	5.15	118.42	110.70
20	U	47	ILE	CB-CA-C	-5.15	103.58	111.71
45	5	319	A	C3'-C2'-O2'	5.15	118.42	110.70
45	5	504	G	C2'-C3'-O3'	5.15	121.42	113.70
45	5	954	C	C1'-C2'-O2'	5.15	116.12	108.40
47	8	99	U	O4'-C1'-C2'	-5.15	102.45	107.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	518	G	O4'-C1'-C2'	-5.15	102.45	107.60
49	2	1749	G	C4'-C3'-O3'	5.14	120.71	113.00
45	5	1953	U	C4'-C3'-O3'	-5.14	105.29	113.00
45	5	1656	U	C2'-C3'-O3'	-5.14	105.99	113.70
66	QQ	123	TYR	N-CA-C	5.14	114.61	107.73
85	4	6072	U	O4'-C1'-C2'	-5.14	102.46	107.60
45	5	4456	C	C3'-C2'-O2'	5.14	118.41	110.70
45	5	1688	G	C2'-C3'-O3'	-5.13	106.00	113.70
45	5	2298	U	C3'-C2'-O2'	5.13	118.40	110.70
45	5	3859	G	C4'-C3'-O3'	-5.13	105.30	113.00
45	5	4973	U	C2'-C3'-O3'	-5.13	106.00	113.70
45	5	2071	A	N9-C1'-C2'	5.13	119.70	112.00
49	2	1072	U	C3'-C2'-O2'	5.13	118.40	110.70
45	5	1905	U	C3'-C2'-O2'	5.13	118.39	110.70
49	2	1667	U	C3'-C2'-O2'	5.13	118.39	110.70
85	4	6200	A	C4-N9-C1'	5.13	141.69	126.30
45	5	445	U	C3'-C2'-O2'	5.13	118.39	110.70
45	5	3902	A	C3'-C2'-O2'	5.12	118.39	110.70
35	j	70	VAL	N-CA-C	-5.12	106.08	110.74
45	5	379	G	C1'-C2'-O2'	5.12	116.08	108.40
45	5	1851	G	C1'-C2'-O2'	5.12	116.08	108.40
3	C	92	PHE	N-CA-C	-5.12	100.11	108.76
16	Q	183	SER	N-CA-C	5.12	119.24	112.89
49	2	307	G	C4'-C3'-O3'	5.12	117.08	109.40
45	5	2858	A	C3'-C2'-O2'	5.11	118.37	110.70
45	5	973	G	C2'-C3'-O3'	-5.11	106.03	113.70
49	2	1634	A	N9-C1'-C2'	5.11	119.67	112.00
45	5	4496	A	C3'-C2'-O2'	5.11	118.36	110.70
45	5	4690	G	C4'-C3'-O3'	-5.11	105.33	113.00
29	d	41	ARG	N-CA-C	5.11	116.54	111.07
45	5	63	G	N9-C1'-C2'	5.11	119.66	112.00
46	7	30	C	C1'-C2'-O2'	5.11	116.06	108.40
49	2	1445	U	C3'-C2'-O2'	5.11	118.36	110.70
22	W	30	GLN	N-CA-C	-5.11	101.38	109.76
45	5	931	C	C2'-C3'-O3'	5.11	121.36	113.70
53	DD	137	VAL	CB-CA-C	-5.11	101.55	110.38
45	5	2792	C	C2'-C3'-O3'	-5.10	106.04	113.70
45	5	78	U	C4'-C3'-O3'	5.10	120.65	113.00
45	5	2417	A	C1'-C2'-O2'	5.10	116.05	108.40
47	8	101	C	C3'-C2'-O2'	5.10	118.36	110.70
49	2	168	C	C1'-C2'-O2'	5.10	116.05	108.40
45	5	1326	A	C1'-C2'-O2'	-5.10	100.75	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4515	G	N9-C1'-C2'	5.10	119.65	112.00
45	5	4629	U	C3'-C2'-O2'	5.10	118.35	110.70
85	4	6200	A	O4'-C1'-N9	5.10	115.85	108.20
39	n	2	ARG	N-CA-C	-5.10	103.31	110.50
45	5	4684	A	C3'-C2'-O2'	5.10	118.34	110.70
47	8	33	G	C3'-C2'-O2'	5.10	118.35	110.70
49	2	384	U	C2'-C3'-O3'	-5.10	106.06	113.70
39	n	6	ARG	N-CA-C	-5.09	104.70	112.04
49	2	1658	G	C4'-C3'-O3'	-5.09	105.36	113.00
14	O	6	VAL	N-CA-C	5.09	115.30	108.17
45	5	374	G	N9-C1'-C2'	5.09	119.64	112.00
49	2	1010	G	C4'-C3'-O3'	-5.09	105.37	113.00
49	2	1837	G	C2'-C3'-O3'	-5.09	106.07	113.70
83	hh	80	SER	N-CA-C	5.09	116.34	107.49
3	C	27	VAL	CB-CA-C	-5.09	105.38	112.04
31	f	67	THR	N-CA-C	5.09	117.59	109.96
49	2	532	C	C3'-C2'-O2'	5.09	118.33	110.70
83	hh	306	LEU	N-CA-C	5.08	116.85	110.24
14	O	117	ARG	CB-CA-C	5.08	119.08	109.37
45	5	2756	G	C3'-C2'-O2'	5.08	118.32	110.70
45	5	4670	C	C4'-C3'-O3'	-5.08	105.38	113.00
45	5	2294	G	C4'-C3'-O3'	-5.08	105.39	113.00
45	5	4513	A	C3'-C2'-O2'	5.08	118.31	110.70
49	2	1515	G	C1'-C2'-O2'	5.08	116.01	108.40
45	5	504	G	C3'-C2'-O2'	5.07	118.31	110.70
45	5	1928	C	C4'-C3'-O3'	5.07	117.01	109.40
45	5	2655	C	C4'-C3'-O3'	-5.07	105.39	113.00
25	Z	9	LYS	N-CA-C	5.07	117.22	110.53
85	4	6178	U	C2-N1-C1'	5.06	132.89	117.70
47	8	142	U	C2'-C3'-O3'	5.06	121.29	113.70
75	ZZ	20	ARG	NE-CZ-NH2	5.06	123.75	119.20
45	5	369	G	C1'-C2'-O2'	5.06	115.99	108.40
29	d	31	LYS	N-CA-C	5.06	119.58	113.41
45	5	1585	C	C3'-C2'-O2'	5.06	118.29	110.70
45	5	2881	A	C1'-C2'-O2'	5.06	115.99	108.40
45	5	4221	C	C2'-C3'-O3'	5.06	117.09	109.50
67	RR	34	VAL	CB-CA-C	-5.06	106.12	111.23
45	5	4648	A	C1'-C2'-O2'	5.06	115.98	108.40
49	2	360	A	C4'-C3'-O3'	5.05	116.98	109.40
49	2	1706	G	C1'-C2'-O2'	5.05	115.98	108.40
85	4	6074	A	C1'-O4'-C4'	-5.05	104.84	109.90
45	5	1362	G	C4'-C3'-O3'	-5.05	105.42	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	224	ILE	N-CA-C	5.05	112.16	107.56
45	5	3654	G	C1'-C2'-O2'	5.05	115.98	108.40
49	2	856	C	C3'-C2'-O2'	5.05	118.28	110.70
17	R	135	LYS	N-CA-C	5.05	118.91	112.34
49	2	1113	A	C4'-C3'-O3'	-5.05	105.42	113.00
45	5	4232	U	C4'-C3'-O3'	5.05	116.97	109.40
45	5	4525	C	C3'-C2'-O2'	5.05	118.27	110.70
45	5	302	C	C2'-C3'-O3'	-5.05	106.13	113.70
45	5	438	G	C2'-C3'-O3'	5.05	121.27	113.70
47	8	21	C	C1'-C2'-O2'	5.05	115.97	108.40
21	V	18	LEU	N-CA-C	5.04	117.71	109.59
45	5	3832	U	C2'-C3'-O3'	-5.04	106.13	113.70
31	f	66	LYS	N-CA-C	5.04	116.47	111.07
45	5	4982	A	C1'-C2'-O2'	5.04	115.97	108.40
45	5	351	C	C3'-C2'-O2'	5.04	118.26	110.70
45	5	2813	A	C4'-C3'-O3'	-5.04	105.44	113.00
45	5	5065	U	C3'-C2'-O2'	5.04	118.26	110.70
49	2	1256	G	C4'-C3'-O3'	-5.04	105.44	113.00
68	SS	18	GLU	N-CA-C	5.04	117.42	111.33
78	cc	43	ILE	N-CA-C	5.04	115.10	107.75
45	5	2062	C	C3'-C2'-O2'	5.04	118.25	110.70
45	5	2463	G	C1'-C2'-O2'	5.04	115.95	108.40
45	5	4612	C	C4'-C3'-O3'	-5.04	105.45	113.00
45	5	1673	U	C4'-C3'-O3'	-5.03	105.45	113.00
11	L	28	GLN	N-CA-C	5.03	120.93	109.81
45	5	2308	A	C4'-C3'-O3'	5.03	120.55	113.00
71	VV	77	TRP	N-CA-C	5.03	116.59	108.34
45	5	2337	C	C3'-C2'-O2'	5.03	118.24	110.70
45	5	2435	G	C3'-C2'-O2'	5.03	118.24	110.70
85	4	6198	A	N9-C1'-C2'	5.03	119.54	112.00
45	5	4216	G	C3'-C2'-O2'	5.02	118.24	110.70
2	B	280	ILE	N-CA-C	5.02	116.13	108.80
45	5	3927	U	C4'-C3'-O3'	-5.02	105.47	113.00
49	2	1244	U	C3'-C2'-O2'	5.02	118.23	110.70
12	M	55	MET	N-CA-C	5.01	116.58	108.41
14	O	41	ILE	CB-CA-C	-5.01	103.79	111.71
45	5	295	A	C1'-C2'-O2'	5.01	115.92	108.40
45	5	2295	C	C2'-C3'-O3'	-5.01	106.18	113.70
45	5	2445	C	C2'-C3'-O3'	-5.01	106.18	113.70
45	5	2580	U	C3'-C2'-O2'	5.01	118.22	110.70
21	V	84	GLN	N-CA-C	5.01	116.81	109.24
45	5	4870	G	C2'-C3'-O3'	5.01	117.02	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	1372	A	C3'-C2'-O2'	5.01	118.22	110.70
45	5	4083	U	C3'-C2'-O2'	5.01	118.22	110.70
49	2	476	A	C3'-C2'-O2'	5.01	118.22	110.70
45	5	3597	G	C4'-C3'-O3'	-5.01	105.49	113.00
45	5	4533	A	C1'-C2'-O2'	-5.01	100.89	108.40
49	2	1097	G	C3'-C2'-O2'	5.01	118.21	110.70
45	5	1378	C	C2'-C3'-O3'	5.00	117.01	109.50
3	C	49	ARG	N-CA-C	-5.00	102.38	110.14
16	Q	23	ILE	N-CA-C	5.00	115.72	110.62
45	5	4438	U	C1'-C2'-O2'	5.00	115.91	108.40
45	5	4518	A	P-O5'-C5'	5.00	128.41	120.90
45	5	4225	G	C4'-C3'-O3'	5.00	120.50	113.00
45	5	4249	G	O4'-C1'-C2'	-5.00	102.60	107.60

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	4	6200	A	C1'

All (59) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
49	2	1604	G	Sidechain
49	2	1606	G	Sidechain
49	2	1632	G	Sidechain
85	4	6071	A	Sidechain
85	4	6181	C	Sidechain
85	4	6197	A	Sidechain
85	4	6200	A	Sidechain
45	5	1911	C	Sidechain
45	5	1912	G	Sidechain
45	5	334	A	Sidechain
45	5	4459	U	Sidechain
45	5	4462	C	Sidechain
45	5	4463	U	Sidechain
45	5	4489	G	Sidechain
1	A	162	ASN	Peptide
1	A	178	PRO	Peptide
1	A	196	TRP	Peptide
1	A	31	ALA	Peptide
2	B	2	SER	Peptide
2	B	258	HIS	Peptide

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Mol	Chain	Res	Type	Group
51	BB	77	ILE	Peptide
3	C	149	GLU	Peptide
3	C	150	LEU	Peptide
3	C	90	GLY	Peptide
52	CC	211	PHE	Peptide
54	EE	153	VAL	Peptide
55	FF	22	LYS	Peptide
55	FF	253	ASP	Peptide
55	FF	78	THR	Peptide
57	HH	213	LEU	Peptide
57	HH	67	VAL	Peptide
48	K	162	VAL	Peptide
48	K	18	LEU	Peptide
12	M	31	ILE	Peptide
13	N	184	ILE	Peptide
65	PP	137	SER	Peptide
65	PP	138	ASP	Peptide
16	Q	155	ALA	Peptide
69	TT	7	GLU	Peptide
22	W	54	LEU	Peptide
23	X	99	ILE	Peptide
73	XX	57	ARG	Peptide
73	XX	88	LYS	Peptide
24	Y	101	PRO	Peptide
74	YY	61	GLN	Peptide
27	b	11	ASN	Peptide
29	d	95	ASP	Peptide
30	e	51	GLY	Peptide
31	f	106	TYR	Peptide
31	f	51	TYR	Peptide
31	f	80	ASN	Peptide
81	ff	117	ASN	Peptide
32	g	107	LEU	Peptide
32	g	60	ARG	Peptide
83	hh	145	GLU	Peptide
35	j	44	LYS	Peptide
36	k	67	LYS	Peptide
37	l	47	THR	Peptide
40	o	61	LYS	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	1777	0	1819	26	0
2	B	3172	0	3310	54	0
3	C	2883	0	3052	46	0
4	D	2391	0	2424	25	0
5	E	1729	0	1887	37	0
6	F	1875	0	1995	21	0
7	G	1879	0	2025	13	0
8	H	1516	0	1597	20	0
9	I	1664	0	1712	15	0
10	J	1362	0	1399	7	0
11	L	1702	0	1820	25	0
12	M	1130	0	1201	19	0
13	N	1701	0	1749	32	0
14	O	1623	0	1771	39	0
15	P	1242	0	1274	33	0
16	Q	1515	0	1634	30	0
17	R	1508	0	1664	26	0
18	S	1462	0	1508	17	0
19	T	1298	0	1366	15	0
20	U	809	0	833	6	0
21	V	969	0	1031	10	0
22	W	860	0	903	11	0
23	X	967	0	1040	12	0
24	Y	1115	0	1205	11	0
25	Z	1107	0	1182	20	0
26	a	1162	0	1209	23	0
27	b	848	0	920	5	0
28	c	761	0	794	5	0
29	d	888	0	930	18	0
30	e	1053	0	1147	25	0
31	f	876	0	912	17	0
32	g	906	0	1002	14	0
33	h	1013	0	1147	19	0
34	i	830	0	916	8	0
35	j	705	0	741	12	0
36	k	569	0	637	2	0
37	l	447	0	480	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	429	0	469	7	0
39	n	239	0	289	5	0
40	o	851	0	924	6	0
41	p	708	0	760	12	0
42	r	994	0	1051	11	0
43	s	1507	0	1564	9	0
44	t	1160	0	1218	10	0
45	5	77073	0	38949	733	0
46	7	2538	0	1286	27	0
47	8	3208	0	1629	50	0
48	K	1705	0	1800	80	0
49	2	36229	0	18306	334	0
50	3	1861	0	939	12	0
51	BB	1710	0	1708	23	0
52	CC	1729	0	1803	12	0
53	DD	1716	0	1806	34	0
54	EE	1768	0	1866	16	0
55	FF	2076	0	2177	26	0
56	GG	1471	0	1522	15	0
57	HH	1923	0	2089	28	0
58	II	1488	0	1582	35	0
59	JJ	1686	0	1772	22	0
60	KK	1525	0	1640	24	0
61	LL	810	0	836	13	0
62	MM	1175	0	1249	10	0
63	NN	908	0	939	7	0
64	OO	1202	0	1289	23	0
65	PP	1016	0	1039	7	0
66	QQ	956	0	1002	15	0
67	RR	1128	0	1195	8	0
68	SS	1068	0	1121	9	0
69	TT	1190	0	1249	13	0
70	UU	1097	0	1130	6	0
71	VV	795	0	862	8	0
72	WW	636	0	637	8	0
73	XX	1034	0	1080	10	0
74	YY	1098	0	1167	22	0
75	ZZ	1011	0	1083	14	0
76	aa	598	0	656	13	0
77	bb	814	0	867	10	0
78	cc	651	0	672	4	0
79	dd	488	0	514	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	ee	459	0	452	6	0
81	ff	457	0	502	16	0
82	gg	555	0	567	3	0
83	hh	2436	0	2392	31	0
84	jj	3280	0	3326	26	0
85	4	4105	0	2053	494	0
All	All	223875	0	167264	2681	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (2681) 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)
85:4:6181:C:C3'	85:4:6182:A:H2'	1.26	1.62
85:4:6176:U:C4	85:4:6177:U:C5	1.76	1.60
85:4:6181:C:H3'	85:4:6182:A:C2'	1.31	1.60
85:4:6198:A:H2'	85:4:6199:A:C5'	1.25	1.58
85:4:6198:A:C2'	85:4:6199:A:H5'	1.12	1.55
85:4:6096:G:N2	85:4:6101:U:C1'	1.71	1.52
85:4:6042:U:C2	85:4:6088:C:H4'	1.46	1.47
85:4:6096:G:N2	85:4:6101:U:N1	1.63	1.43
85:4:6042:U:N3	85:4:6088:C:H4'	1.25	1.41
85:4:6174:G:C5	85:4:6204:A:OP2	1.74	1.38
85:4:6176:U:C4	85:4:6177:U:C6	2.09	1.36
48:K:124:LEU:HD12	85:4:6038:G:C4	1.58	1.35
85:4:6053:U:OP2	85:4:6053:U:C6	1.78	1.34
85:4:6181:C:C5'	85:4:6182:A:OP2	1.76	1.33
85:4:6179:U:C2	85:4:6180:U:C6	2.17	1.33
85:4:6179:U:C4	85:4:6180:U:C4	2.18	1.31
85:4:6206:G:C8	85:4:6207:A:N7	1.99	1.30
48:K:44:GLN:O	85:4:6083:U:C4'	1.80	1.28
85:4:6123:G:O6	85:4:6163:G:H1'	1.11	1.28
48:K:44:GLN:O	85:4:6083:U:H4'	1.15	1.27
85:4:6042:U:N3	85:4:6088:C:C4'	1.97	1.27
48:K:119:GLN:HA	85:4:6037:U:O2'	1.32	1.26
85:4:6042:U:H3	85:4:6088:C:C3'	1.48	1.24
85:4:6176:U:C5	85:4:6177:U:C6	2.26	1.23
85:4:6176:U:O4	85:4:6177:U:C5	1.83	1.23
48:K:124:LEU:HD12	85:4:6038:G:C5	1.75	1.21
48:K:48:ARG:HH12	85:4:6082:G:P	1.63	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6176:U:O4	85:4:6177:U:H5	1.15	1.21
85:4:6179:U:C2	85:4:6180:U:C5	2.29	1.21
85:4:6174:G:C6	85:4:6204:A:OP2	1.95	1.18
85:4:6206:G:N3	85:4:6207:A:N6	1.92	1.17
48:K:126:PRO:HD3	85:4:6087:G:C5'	1.75	1.16
85:4:6096:G:N2	85:4:6101:U:H1'	1.60	1.15
48:K:126:PRO:HG3	85:4:6087:G:OP2	1.45	1.14
85:4:6042:U:N3	85:4:6088:C:O3'	1.81	1.14
85:4:6206:G:H1'	85:4:6207:A:C6	1.81	1.14
48:K:124:LEU:CD1	85:4:6038:G:C4	2.30	1.13
85:4:6071:A:C4	85:4:6072:U:C6	2.36	1.13
48:K:48:ARG:NH1	85:4:6082:G:P	2.21	1.13
85:4:6176:U:C5	85:4:6177:U:H6	1.63	1.13
85:4:6179:U:N3	85:4:6180:U:C4	2.14	1.12
85:4:6096:G:N2	85:4:6101:U:C2	2.18	1.11
85:4:6173:C:H3'	85:4:6174:G:C5'	1.82	1.10
85:4:6071:A:C5	85:4:6072:U:C5	2.40	1.10
85:4:6177:U:C5	85:4:6178:U:C5	2.40	1.09
48:K:48:ARG:NH1	85:4:6082:G:O5'	1.84	1.08
85:4:6042:U:C2	85:4:6088:C:C4'	2.36	1.07
85:4:6123:G:O6	85:4:6163:G:C1'	2.02	1.07
48:K:48:ARG:NH1	85:4:6082:G:OP1	1.86	1.07
48:K:126:PRO:HD2	85:4:6040:U:O4	1.54	1.06
85:4:6173:C:C3'	85:4:6174:G:H5''	1.85	1.06
85:4:6042:U:N3	85:4:6088:C:C3'	2.20	1.05
85:4:6177:U:C6	85:4:6178:U:C6	2.44	1.04
85:4:6178:U:C2	85:4:6179:U:C6	2.45	1.04
48:K:123:ILE:HG23	85:4:6040:U:C6	1.92	1.04
85:4:6179:U:C4	85:4:6180:U:O4	2.11	1.04
85:4:6181:C:H5'	85:4:6182:A:OP2	0.87	1.04
85:4:6176:U:N3	85:4:6177:U:C5	2.25	1.03
85:4:6096:G:C2	85:4:6101:U:C6	2.46	1.03
85:4:6174:G:N7	85:4:6204:A:OP2	1.92	1.03
85:4:6071:A:C2	85:4:6072:U:C2	2.48	1.02
85:4:6030:A:O2'	85:4:6031:A:OP1	1.63	1.01
85:4:6071:A:C6	85:4:6072:U:C4	2.47	1.01
85:4:6069:U:C2'	85:4:6070:A:H8	1.58	1.00
85:4:6176:U:N3	85:4:6177:U:C6	2.28	1.00
85:4:6034:A:N6	85:4:6090:A:N1	2.08	1.00
85:4:6034:A:H2	85:4:6091:U:O4	1.43	0.99
85:4:6042:U:O2	85:4:6088:C:H5'	1.61	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6206:G:C1'	85:4:6207:A:C5	2.45	0.99
85:4:6179:U:N3	85:4:6180:U:C5	2.28	0.99
85:4:6179:U:C4	85:4:6180:U:C5	2.49	0.99
85:4:6053:U:H6	85:4:6053:U:P	1.85	0.98
85:4:6206:G:C4	85:4:6207:A:N6	2.28	0.98
85:4:6198:A:O2'	85:4:6199:A:H5'	1.63	0.98
85:4:6182:A:N1	85:4:6196:A:O2'	1.95	0.98
85:4:6176:U:H2'	85:4:6177:U:C4'	1.94	0.97
85:4:6197:A:C6	85:4:6198:A:C5	2.53	0.97
85:4:6177:U:C5	85:4:6178:U:C6	2.53	0.96
85:4:6198:A:H2'	85:4:6199:A:C4'	1.96	0.96
85:4:6182:A:N6	85:4:6197:A:O4'	1.98	0.96
58:II:61:ILE:HD11	58:II:95:ILE:HD12	1.48	0.96
14:O:79:ILE:HG21	14:O:138:LEU:HD11	1.48	0.95
85:4:6036:G:N2	85:4:6089:U:O4	1.99	0.95
85:4:6097:U:OP1	85:4:6098:A:C6	2.18	0.95
48:K:126:PRO:HD3	85:4:6087:G:H5''	1.49	0.95
85:4:6181:C:H5'	85:4:6182:A:P	2.07	0.95
45:5:2042:A:N3	45:5:4462:C:O2'	1.98	0.95
85:4:6045:C:O2'	85:4:6046:U:O5'	1.85	0.95
85:4:6179:U:C6	85:4:6180:U:C5	2.54	0.95
85:4:6096:G:C2	85:4:6101:U:N1	2.34	0.95
85:4:6206:G:H2'	85:4:6207:A:C4	2.01	0.94
85:4:6176:U:C6	85:4:6177:U:H6	1.85	0.94
58:II:6:ALA:HB2	58:II:25:GLN:HE21	1.30	0.94
85:4:6181:C:C5'	85:4:6182:A:P	2.55	0.94
85:4:6124:U:O4	85:4:6162:A:N6	2.00	0.94
85:4:6198:A:C2'	85:4:6199:A:C5'	2.03	0.94
85:4:6206:G:N9	85:4:6207:A:N7	2.17	0.93
48:K:126:PRO:CD	85:4:6040:U:O4	2.17	0.93
85:4:6034:A:C2	85:4:6091:U:O4	2.21	0.92
85:4:6182:A:H61	85:4:6197:A:C4'	1.83	0.92
85:4:6176:U:H2'	85:4:6177:U:C1'	2.00	0.92
48:K:126:PRO:HD3	85:4:6087:G:H5'	1.51	0.92
85:4:6070:A:O2'	85:4:6172:G:H1'	1.70	0.92
85:4:6206:G:C2'	85:4:6207:A:C4	2.52	0.92
85:4:6198:A:C6	85:4:6199:A:C5	2.57	0.92
45:5:1398:A:H2'	45:5:1399:G:O4'	1.70	0.91
49:2:1606:G:N2	49:2:1633:A:N7	2.17	0.91
85:4:6041:C:N3	85:4:6088:C:OP2	2.03	0.91
85:4:6069:U:C2'	85:4:6070:A:C8	2.50	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:HH:52:ILE:HD11	57:HH:109:LEU:HD22	1.53	0.91
48:K:126:PRO:CG	85:4:6087:G:OP2	2.18	0.91
15:P:64:ASN:HD22	15:P:80:GLN:NE2	1.69	0.91
85:4:6198:A:H3'	85:4:6199:A:H3'	1.53	0.90
85:4:6176:U:C5	85:4:6177:U:C5	2.57	0.90
85:4:6179:U:N1	85:4:6180:U:C5	2.40	0.90
85:4:6176:U:H2'	85:4:6177:U:H4'	1.51	0.90
85:4:6197:A:C5	85:4:6198:A:N7	2.40	0.90
85:4:6176:U:C6	85:4:6177:U:C6	2.59	0.90
85:4:6053:U:OP2	85:4:6053:U:C5	2.24	0.90
85:4:6173:C:H3'	85:4:6174:G:H5''	1.45	0.90
85:4:6206:G:C2'	85:4:6207:A:C5	2.56	0.89
85:4:6173:C:C2'	85:4:6174:G:H5''	2.02	0.89
13:N:116:LEU:HD22	13:N:135:ILE:HD11	1.53	0.89
85:4:6179:U:C5	85:4:6180:U:C5	2.60	0.89
85:4:6182:A:N6	85:4:6197:A:C4'	2.35	0.88
85:4:6198:A:N6	85:4:6199:A:N7	2.21	0.88
85:4:6206:G:C1'	85:4:6207:A:C6	2.57	0.88
85:4:6203:U:O2'	85:4:6204:A:OP2	1.92	0.88
85:4:6206:G:H2'	85:4:6207:A:C8	2.08	0.88
45:5:3924:C:C4	45:5:3925:U:C4	2.62	0.88
85:4:6097:U:OP1	85:4:6098:A:N6	2.07	0.88
85:4:6053:U:OP2	85:4:6053:U:H6	1.22	0.87
85:4:6179:U:N1	85:4:6180:U:C6	2.42	0.87
85:4:6178:U:N3	85:4:6179:U:C5	2.42	0.87
85:4:6199:A:C8	85:4:6200:A:C8	2.63	0.87
85:4:6072:U:H2'	85:4:6073:A:H1'	1.57	0.87
85:4:6096:G:N2	85:4:6101:U:O4'	2.08	0.87
45:5:4461:C:N4	45:5:4515:G:O6	2.08	0.86
48:K:125:GLY:CA	85:4:6087:G:C8	2.57	0.86
48:K:125:GLY:HA3	85:4:6087:G:H5'	1.57	0.86
48:K:124:LEU:HD11	85:4:6038:G:H2'	1.56	0.86
85:4:6179:U:O4	85:4:6180:U:O4	1.93	0.86
85:4:6206:G:C8	85:4:6207:A:C8	2.63	0.86
45:5:4197:G:N1	50:3:86:C:OP2	2.08	0.86
85:4:6046:U:N3	85:4:6082:G:O6	2.08	0.86
85:4:6199:A:H1'	85:4:6200:A:C1'	2.06	0.85
85:4:6198:A:C3'	85:4:6199:A:H3'	2.07	0.84
3:C:232:VAL:HG21	3:C:256:ALA:HB1	1.57	0.84
85:4:6053:U:C6	85:4:6053:U:P	2.66	0.84
85:4:6206:G:H2'	85:4:6207:A:N9	1.92	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:128:MET:HE3	8:H:146:LEU:HD21	1.58	0.84
85:4:6174:G:N2	85:4:6202:C:O2	2.10	0.84
85:4:6042:U:H3	85:4:6088:C:C4'	1.74	0.84
48:K:123:ILE:HG23	85:4:6040:U:H6	1.36	0.84
85:4:6177:U:H3'	85:4:6178:U:H4'	1.59	0.83
48:K:44:GLN:C	85:4:6083:U:H4'	2.04	0.83
85:4:6096:G:N1	85:4:6101:U:C6	2.46	0.83
85:4:6173:C:C3'	85:4:6174:G:C5'	2.50	0.83
53:DD:88:ILE:HD13	53:DD:94:ILE:HD11	1.59	0.83
85:4:6173:C:H2'	85:4:6174:G:H5''	1.61	0.82
85:4:6206:G:N9	85:4:6207:A:C5	2.47	0.82
11:L:150:LEU:HD22	33:h:121:VAL:HG21	1.62	0.82
85:4:6176:U:C2'	85:4:6177:U:H4'	2.08	0.82
48:K:125:GLY:HA2	85:4:6087:G:C8	2.15	0.82
85:4:6176:U:C4	85:4:6177:U:H5	1.49	0.82
85:4:6096:G:O3'	85:4:6098:A:N7	2.13	0.82
13:N:110:CYS:HB3	13:N:113:LEU:HD12	1.62	0.81
85:4:6174:G:N2	85:4:6202:C:C2	2.47	0.81
45:5:2279:A:N7	45:5:2280:G:C2	2.48	0.81
85:4:6069:U:H2'	85:4:6070:A:H8	1.44	0.81
45:5:1666:C:H2'	45:5:1667:A:O4'	1.80	0.81
85:4:6095:U:H5'	85:4:6098:A:OP2	1.80	0.81
85:4:6173:C:O2'	85:4:6174:G:N2	2.13	0.81
48:K:123:ILE:HG23	85:4:6040:U:C5	2.15	0.81
45:5:4461:C:N3	45:5:4515:G:N1	2.26	0.80
85:4:6096:G:N2	85:4:6101:U:C6	2.48	0.80
85:4:6181:C:C2'	85:4:6182:A:H2'	2.10	0.80
85:4:6069:U:C3'	85:4:6070:A:H8	1.93	0.80
85:4:6176:U:C2	85:4:6177:U:C6	2.69	0.80
85:4:6206:G:H1'	85:4:6207:A:C5	2.15	0.80
85:4:6197:A:C5	85:4:6198:A:C8	2.70	0.80
85:4:6199:A:C5	85:4:6200:A:C4	2.70	0.80
48:K:119:GLN:O	85:4:6038:G:P	2.40	0.80
45:5:3611:A:C2	45:5:3612:C:C2	2.69	0.79
85:4:6197:A:C6	85:4:6198:A:C6	2.71	0.79
85:4:6069:U:H2'	85:4:6070:A:C8	2.16	0.79
45:5:4458:C:N4	45:5:4520:G:O6	2.16	0.79
49:2:976:G:H2'	49:2:977:C:C6	2.17	0.78
85:4:6173:C:H3'	85:4:6174:G:H5'	1.64	0.78
35:j:2:THR:OG1	45:5:3642:A:O2'	2.02	0.78
3:C:313:VAL:HG11	6:F:167:ALA:HB3	1.63	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:K:121:PRO:HD2	85:4:6037:U:H2'	1.66	0.78
49:2:96:C:O2	49:2:473:A:O2'	2.00	0.78
49:2:870:A:O2'	49:2:871:U:OP2	2.01	0.78
85:4:6070:A:N3	85:4:6070:A:H2'	1.97	0.78
85:4:6179:U:C6	85:4:6180:U:H5	1.99	0.78
49:2:1139:C:O2	49:2:1140:G:C8	2.36	0.78
85:4:6197:A:N6	85:4:6198:A:N6	2.32	0.78
85:4:6201:C:OP1	85:4:6201:C:H4'	1.84	0.78
85:4:6174:G:C8	85:4:6205:A:C5	2.72	0.78
5:E:153:LEU:HD13	5:E:197:VAL:HG11	1.66	0.78
85:4:6203:U:C2'	85:4:6204:A:OP2	2.31	0.78
85:4:6178:U:C2	85:4:6179:U:C5	2.71	0.78
85:4:6201:C:H3'	85:4:6202:C:C6	2.19	0.77
49:2:1825:A:H1'	85:4:6221:A:N3	1.97	0.77
85:4:6042:U:O2	85:4:6088:C:C5'	2.31	0.77
85:4:6198:A:C6	85:4:6199:A:N7	2.52	0.77
45:5:2639:U:O2'	45:5:2694:G:N1	2.17	0.77
49:2:1610:G:OP2	69:TT:132:ARG:NH1	2.17	0.77
19:T:42:ILE:HD11	19:T:74:ILE:HD11	1.66	0.77
64:OO:28:LEU:HD23	64:OO:33:VAL:HG22	1.67	0.77
85:4:6206:G:O2'	85:4:6207:A:C4	2.38	0.77
48:K:44:GLN:O	85:4:6083:U:C5'	2.33	0.77
48:K:122:ARG:HD2	85:4:6037:U:H5'	1.67	0.76
85:4:6070:A:O2'	85:4:6172:G:C1'	2.34	0.76
85:4:6173:C:H4'	85:4:6173:C:OP1	1.84	0.76
48:K:122:ARG:NH1	85:4:6036:G:H21	1.84	0.76
85:4:6071:A:C4	85:4:6072:U:C5	2.70	0.76
85:4:6198:A:N6	85:4:6199:A:C5	2.54	0.76
16:Q:87:THR:HG22	16:Q:106:THR:HG21	1.68	0.76
5:E:131:HIS:HB2	45:5:972:C:C4	2.21	0.76
49:2:890:U:O4	49:2:897:U:O4	2.03	0.76
45:5:3641:U:H5	45:5:3646:A:N7	1.84	0.76
45:5:4520:G:OP1	45:5:4521:U:OP2	2.03	0.76
45:5:91:G:O6	45:5:93:G:N2	2.19	0.75
85:4:6071:A:C8	85:4:6071:A:H5'	2.22	0.75
8:H:31:ARG:O	8:H:149:ASN:ND2	2.18	0.75
45:5:2311:C:N4	45:5:2312:U:C4	2.55	0.75
45:5:4469:U:O4	45:5:4486:C:N4	2.16	0.75
48:K:119:GLN:CA	85:4:6037:U:O2'	2.24	0.75
45:5:2043:A:H2	45:5:4515:G:N3	1.84	0.74
85:4:6069:U:C3'	85:4:6070:A:C8	2.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6179:U:O2	85:4:6179:U:H2'	1.87	0.74
85:4:6201:C:H3'	85:4:6202:C:H6	1.52	0.74
45:5:5005:G:N2	45:5:5041:G:O2'	2.20	0.74
85:4:6176:U:H2'	85:4:6177:U:H1'	1.69	0.74
85:4:6069:U:H3'	85:4:6070:A:C8	2.22	0.74
85:4:6095:U:C5'	85:4:6098:A:OP2	2.36	0.74
45:5:971(A):G:O5'	45:5:971(A):G:N3	2.21	0.74
85:4:6071:A:C2	85:4:6072:U:N3	2.56	0.74
45:5:1770:A:H2'	45:5:1771:U:O4'	1.86	0.74
48:K:126:PRO:HG3	85:4:6087:G:P	2.28	0.74
75:ZZ:62:THR:HA	75:ZZ:69:THR:HG22	1.69	0.73
85:4:6206:G:H2'	85:4:6207:A:C5	2.21	0.73
49:2:520:A:O2'	49:2:825:A:N3	2.19	0.73
85:4:6041:C:C2	85:4:6088:C:OP2	2.42	0.73
12:M:37:LEU:O	12:M:39:ASP:N	2.22	0.73
85:4:6198:A:O2'	85:4:6199:A:C5'	2.26	0.73
85:4:6200:A:N7	85:4:6204:A:C2	2.57	0.73
49:2:1396:A:O2'	49:2:1398:G:N7	2.22	0.72
85:4:6201:C:H2'	85:4:6202:C:C5	2.24	0.72
45:5:1751:A:C2	45:5:1780:A:C2	2.78	0.72
58:II:8:ILE:HD12	58:II:45:ILE:HB	1.71	0.72
9:I:91:LEU:HD12	9:I:135:ILE:HG23	1.71	0.72
16:Q:105:VAL:HG21	16:Q:120:ILE:HG21	1.70	0.72
48:K:53:VAL:HG11	48:K:190:LEU:HD21	1.71	0.72
49:2:1605:G:H2'	49:2:1606:G:O4'	1.89	0.72
41:p:4:ARG:NH1	45:5:1554:A:OP2	2.22	0.72
42:r:120:SER:O	42:r:122:LYS:N	2.23	0.71
45:5:4470:G:O6	45:5:4471:U:C4	2.43	0.71
85:4:6071:A:C6	85:4:6072:U:C5	2.75	0.71
85:4:6199:A:C4	85:4:6200:A:C4	2.77	0.71
58:II:53:VAL:HG11	58:II:172:THR:HG23	1.72	0.71
48:K:124:LEU:HD12	85:4:6038:G:N9	2.05	0.71
85:4:6071:A:N3	85:4:6072:U:N1	2.38	0.71
85:4:6176:U:H4'	85:4:6176:U:OP1	1.89	0.71
37:l:44:TRP:CZ3	37:l:45:ARG:HG2	2.26	0.71
26:a:21:ARG:NH1	45:5:1317:U:OP1	2.23	0.71
85:4:6198:A:H2'	85:4:6199:A:C3'	2.20	0.70
73:XX:90:GLN:HB3	73:XX:102:ILE:HD11	1.71	0.70
45:5:3873:G:H2'	45:5:3874:G:C8	2.26	0.70
45:5:3924:C:N4	45:5:3925:U:O4	2.24	0.70
48:K:124:LEU:CD1	85:4:6038:G:C5	2.65	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:2757:A:C6	45:5:2758:G:C6	2.80	0.70
85:4:6203:U:H1'	85:4:6205:A:O4'	1.90	0.70
13:N:135:ILE:HD12	13:N:151:ILE:HD12	1.72	0.70
45:5:106:A:C1'	45:5:336:A:H1'	2.22	0.70
60:KK:32:ILE:HG21	81:ff:107:ARG:HG2	1.72	0.70
85:4:6182:A:H61	85:4:6197:A:C5'	2.04	0.70
29:d:59:THR:OG1	29:d:104:THR:OG1	2.09	0.70
37:l:12:PHE:CD2	37:l:51:LEU:HD11	2.27	0.70
49:2:16:G:H2'	49:2:17:C:C6	2.26	0.70
49:2:319:C:H2'	49:2:320:G:C8	2.26	0.70
85:4:6179:U:O2	85:4:6180:U:C6	2.44	0.70
62:MM:82:MET:HB2	62:MM:85:THR:HG23	1.72	0.69
85:4:6197:A:N6	85:4:6198:A:H62	1.90	0.69
4:D:12:TYR:OH	45:5:4265:U:OP1	2.10	0.69
45:5:48:G:O2'	45:5:49:U:OP2	2.09	0.69
74:YY:9:THR:O	74:YY:11:ARG:N	2.24	0.69
59:JJ:82:VAL:HG12	59:JJ:202:ILE:HD13	1.74	0.69
85:4:6073:A:H2'	85:4:6074:A:H1'	1.74	0.69
85:4:6178:U:O3'	85:4:6178:U:OP1	2.10	0.69
85:4:6200:A:N7	85:4:6204:A:N1	2.40	0.69
85:4:6174:G:C6	85:4:6204:A:P	2.85	0.69
85:4:6198:A:C8	85:4:6199:A:H2'	2.28	0.69
35:j:17:THR:OG1	35:j:18:LEU:N	2.20	0.69
13:N:59:TYR:O	13:N:60:VAL:HG23	1.92	0.69
15:P:116:HIS:HB3	15:P:149:ILE:HB	1.74	0.69
48:K:119:GLN:HA	85:4:6037:U:C2'	2.23	0.69
31:f:14:TYR:OH	31:f:94:ALA:HB2	1.93	0.69
85:4:6178:U:H3'	85:4:6179:U:H4'	1.74	0.69
85:4:6179:U:O3'	85:4:6179:U:OP1	2.10	0.69
85:4:6197:A:N7	85:4:6198:A:C8	2.61	0.68
26:a:80:THR:C	26:a:81:LEU:HD23	2.19	0.68
49:2:1660:C:OP2	80:ee:32:ARG:NH1	2.26	0.68
8:H:41:ILE:HG12	8:H:73:ILE:HD11	1.75	0.68
85:4:6045:C:HO2'	85:4:6046:U:C5'	2.07	0.68
66:QQ:61:ARG:O	66:QQ:65:LYS:N	2.27	0.68
85:4:6198:A:C5	85:4:6199:A:C8	2.81	0.68
45:5:4510:A:C6	45:5:4511:A:N1	2.62	0.68
45:5:1291:G:C6	45:5:1292:C:N4	2.62	0.68
85:4:6197:A:C6	85:4:6198:A:N7	2.60	0.68
58:II:52:GLU:HA	58:II:58:LYS:HA	1.76	0.68
85:4:6181:C:OP1	85:4:6181:C:H4'	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:FF:44:LEU:HD22	55:FF:72:ILE:HD11	1.76	0.68
56:GG:74:ASN:HA	56:GG:77:MET:HE2	1.76	0.68
85:4:6197:A:C5	85:4:6198:A:C5	2.81	0.68
17:R:58:HIS:NE2	45:5:4645:C:OP1	2.26	0.67
23:X:119:ILE:HD11	23:X:140:LEU:HD22	1.76	0.67
85:4:6199:A:C4	85:4:6200:A:N9	2.62	0.67
14:O:17:GLY:HA3	45:5:2052:G:O3'	1.94	0.67
26:a:75:LEU:O	26:a:76:ASP:C	2.37	0.67
11:L:35:ARG:NH1	45:5:105:A:O2'	2.26	0.67
85:4:6163:G:H5''	85:4:6163:G:N3	2.08	0.67
85:4:6203:U:O2	85:4:6205:A:H1'	1.95	0.67
4:D:45:ASN:N	4:D:45:ASN:HD22	1.93	0.67
18:S:1:MET:HE2	18:S:121:ALA:HB1	1.75	0.67
45:5:2292:C:N3	45:5:2344:U:O2	2.28	0.67
48:K:121:PRO:HG2	85:4:6037:U:N3	2.09	0.67
49:2:1825:A:C8	85:4:6221:A:C2	2.75	0.67
85:4:6053:U:H3	85:4:6073:A:N6	1.91	0.67
85:4:6201:C:H5'	85:4:6202:C:P	2.34	0.67
4:D:78:ALA:HB1	4:D:104:LEU:HD22	1.75	0.67
48:K:125:GLY:HA3	85:4:6087:G:C5'	2.25	0.67
85:4:6177:U:C5	85:4:6178:U:C4	2.82	0.67
15:P:118:GLN:HE21	15:P:120:ASN:HD21	1.43	0.67
35:j:24:SER:O	35:j:26:ALA:N	2.28	0.67
45:5:4633:G:O2'	45:5:4635:A:OP2	2.13	0.67
64:OO:75:LEU:HB3	64:OO:81:ALA:HB2	1.76	0.67
85:4:6071:A:N1	85:4:6072:U:C4	2.62	0.67
1:A:198:ARG:NH2	45:5:3688:U:OP2	2.27	0.67
45:5:63:G:C4	45:5:333:U:C4	2.83	0.67
85:4:6045:C:O2	85:4:6046:U:C4	2.47	0.67
49:2:1083:A:O2'	49:2:1084:A:OP1	2.11	0.66
8:H:120:GLU:OE1	8:H:124:ARG:NH2	2.28	0.66
60:KK:40:LYS:O	60:KK:41:ARG:C	2.37	0.66
85:4:6063:A:C6	85:4:6207:A:H3'	2.30	0.66
45:5:2793:G:H1	45:5:2797:C:HO2'	1.44	0.66
40:o:24:THR:HA	40:o:93:LEU:HD21	1.75	0.66
45:5:2043:A:C2	45:5:4515:G:N3	2.63	0.66
47:8:13:G:C5	47:8:14:U:C5	2.83	0.66
69:TT:85:ASN:HD21	69:TT:97:GLN:HE22	1.42	0.66
5:E:65:TYR:CD1	5:E:70:LEU:HD12	2.31	0.66
85:4:6071:A:N3	85:4:6072:U:C2	2.63	0.66
85:4:6198:A:N9	85:4:6199:A:H2'	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:jj:62:ILE:HD12	84:jj:68:ARG:HA	1.77	0.66
45:5:1655:C:H2'	45:5:1656:U:H5''	1.78	0.66
45:5:4468:U:O2	45:5:4708:A:N7	2.29	0.66
81:ff:106:LYS:O	81:ff:109:MET:N	2.29	0.66
13:N:38:ARG:NH1	47:8:141:C:OP1	2.28	0.65
45:5:2439:G:N2	45:5:2539:C:O2	2.29	0.65
30:e:41:ILE:O	30:e:42:ASP:C	2.38	0.65
48:K:122:ARG:NH1	85:4:6036:G:N2	2.44	0.65
85:4:6174:G:C8	85:4:6205:A:C6	2.83	0.65
45:5:2549:G:H2'	45:5:2550:G:O4'	1.97	0.65
49:2:627:U:O2'	49:2:628:A:OP2	2.11	0.65
55:FF:181:CYS:SG	55:FF:182:MET:N	2.68	0.65
56:GG:103:LEU:HD23	56:GG:178:ILE:HD13	1.78	0.65
85:4:6097:U:O4	85:4:6098:A:C2	2.50	0.65
85:4:6203:U:O5'	85:4:6203:U:H6	1.79	0.65
55:FF:126:VAL:HG21	55:FF:155:LYS:O	1.96	0.65
10:J:143:ASP:OD1	10:J:144:LYS:N	2.30	0.65
45:5:3654:G:O2'	45:5:3693:U:OP1	2.11	0.65
45:5:3924:C:N3	45:5:3925:U:C4	2.65	0.65
83:hh:109:LEU:HD11	83:hh:125:ARG:HG2	1.79	0.65
85:4:6197:A:C8	85:4:6198:A:C8	2.84	0.65
31:f:28:LEU:HG	31:f:101:ILE:HD11	1.79	0.65
31:f:56:ASN:HD22	31:f:56:ASN:N	1.95	0.65
45:5:4446:U:O2'	45:5:4450:U:OP1	2.15	0.65
45:5:4944:C:O2	45:5:4944:C:C5'	2.45	0.65
49:2:319:C:OP1	49:2:319:C:H4'	1.96	0.65
49:2:639:C:OP1	81:ff:114:ARG:NH2	2.30	0.65
85:4:6198:A:C2'	85:4:6199:A:H3'	2.27	0.65
85:4:6071:A:N9	85:4:6072:U:C6	2.64	0.64
45:5:1872:G:O2'	45:5:4219:A:N3	2.29	0.64
15:P:64:ASN:ND2	15:P:80:GLN:NE2	2.43	0.64
45:5:4485:C:C4	45:5:4486:C:H5	2.14	0.64
29:d:73:TRP:O	29:d:76:GLY:N	2.31	0.64
45:5:3662:A:O4'	45:5:3664:G:C8	2.50	0.64
76:aa:64:ASN:OD1	85:4:6124:U:O2'	2.04	0.64
45:5:319:A:H2'	45:5:320:C:O4'	1.98	0.64
85:4:6180:U:C2	85:4:6181:C:H1'	2.33	0.64
85:4:6197:A:N1	85:4:6198:A:C6	2.65	0.64
35:j:59:THR:O	35:j:64:MET:SD	2.55	0.64
49:2:1780:G:H2'	49:2:1781:A:O4'	1.98	0.64
3:C:210:ILE:CG2	3:C:232:VAL:HG22	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6174:G:OP1	85:4:6202:C:N4	2.30	0.64
5:E:131:HIS:HB2	45:5:972:C:C2	2.32	0.64
17:R:35:ALA:O	17:R:40:GLN:NE2	2.31	0.63
45:5:2752:G:H2'	45:5:2753:G:O4'	1.98	0.63
49:2:1154:U:O2'	53:DD:194:ARG:HD3	1.98	0.63
85:4:6053:U:H3	85:4:6073:A:H61	1.46	0.63
45:5:63:G:C4	45:5:333:U:O4	2.52	0.63
45:5:3924:C:C4	45:5:3925:U:O4	2.51	0.63
49:2:994:C:N4	77:bb:14:GLY:O	2.32	0.63
57:HH:52:ILE:HD11	57:HH:109:LEU:CD2	2.29	0.63
73:XX:6:VAL:O	73:XX:7:LEU:C	2.41	0.63
85:4:6045:C:O2	85:4:6046:U:C5	2.51	0.63
45:5:4338:G:O2'	45:5:4372:U:O4	2.13	0.63
18:S:34:ALA:HB1	18:S:39:VAL:HG23	1.80	0.63
49:2:1144:A:OP1	49:2:1355:C:C5	2.51	0.63
85:4:6071:A:C8	85:4:6071:A:H3'	2.33	0.63
2:B:103:LYS:HB3	2:B:153:MET:HE3	1.79	0.63
30:e:52:GLN:NE2	45:5:1312:A:O2'	2.31	0.63
45:5:3642:A:OP2	45:5:3644:U:OP1	2.16	0.63
29:d:118:GLN:NE2	45:5:4997:G:O2'	2.32	0.63
7:G:212:HIS:NE2	7:G:238:LYS:HG2	2.14	0.63
85:4:6092:U:H4'	85:4:6092:U:OP1	1.98	0.63
8:H:64:ARG:NH2	45:5:4693:C:OP1	2.32	0.63
66:QQ:103:ASN:O	66:QQ:105:VAL:HG23	1.99	0.63
11:L:185:ALA:HB3	34:i:7:MET:HE1	1.81	0.62
45:5:34:A:C2	45:5:35:U:C6	2.87	0.62
47:8:121:G:C6	47:8:122:G:N7	2.67	0.62
45:5:64:A:H61	45:5:334:A:H62	1.46	0.62
49:2:1346:U:O2'	49:2:1485:U:O2'	2.15	0.62
59:JJ:35:ASN:HD22	59:JJ:35:ASN:N	1.96	0.62
85:4:6176:U:H2'	85:4:6177:U:O4'	1.98	0.62
11:L:143:GLU:O	11:L:147:ALA:N	2.33	0.62
17:R:50:ILE:C	17:R:50:ILE:HD12	2.24	0.62
17:R:70:ARG:HG2	17:R:76:MET:HE2	1.80	0.62
17:R:99:MET:O	17:R:101:ILE:N	2.32	0.62
24:Y:21:ALA:HB1	24:Y:22:PRO:CD	2.30	0.62
48:K:122:ARG:HB2	85:4:6037:U:C6	2.34	0.62
49:2:753:C:N4	49:2:791:C:O2'	2.33	0.62
9:I:36:LEU:HD11	9:I:69:ARG:HD3	1.82	0.62
11:L:43:ALA:HA	11:L:46:ILE:HG13	1.80	0.62
15:P:64:ASN:ND2	15:P:80:GLN:HE22	1.97	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:91:G:C6	45:5:93:G:N2	2.68	0.62
45:5:3927:U:O2	45:5:4185:G:C2	2.52	0.62
45:5:4467:A:H2'	45:5:4468:U:O4'	2.00	0.62
85:4:6042:U:C2	85:4:6088:C:C5'	2.82	0.62
12:M:105:THR:HG22	12:M:106:ASP:H	1.64	0.62
45:5:2640:G:N7	45:5:2694:G:O6	2.32	0.62
45:5:4439:U:N3	45:5:4440:G:C8	2.68	0.62
49:2:1825:A:C1'	85:4:6221:A:N3	2.61	0.62
68:SS:31:ASN:O	68:SS:35:CYS:SG	2.57	0.62
30:e:24:GLN:NE2	45:5:1315:C:O5'	2.32	0.62
85:4:6096:G:N1	85:4:6101:U:O4'	2.31	0.62
21:V:80:VAL:HG23	21:V:106:VAL:HG21	1.81	0.62
45:5:973:G:N2	45:5:1282:G:O6	2.33	0.62
48:K:126:PRO:CD	85:4:6087:G:H5''	2.26	0.62
49:2:641:A:C6	49:2:642:U:N3	2.68	0.62
55:FF:18:TRP:CE3	55:FF:46:ILE:HD11	2.34	0.62
56:GG:103:LEU:HD23	56:GG:178:ILE:CD1	2.30	0.62
85:4:6071:A:H3'	85:4:6071:A:H8	1.65	0.62
85:4:6094:U:O5'	85:4:6094:U:H6	1.83	0.62
45:5:63:G:C6	45:5:333:U:C5	2.87	0.62
45:5:2715:G:H2'	45:5:2716:C:C6	2.35	0.62
85:4:6036:G:C2	85:4:6089:U:O4	2.52	0.62
85:4:6074:A:O3'	85:4:6074:A:OP1	2.18	0.62
84:jj:10:ARG:NE	84:jj:14:ILE:HD11	2.14	0.61
14:O:156:LEU:HD13	45:5:4910:A:C4	2.35	0.61
31:f:36:ARG:O	31:f:39:THR:HG22	2.00	0.61
45:5:929:A:N7	45:5:930:G:C2	2.68	0.61
45:5:2411:C:O2'	45:5:2526:C:O2	2.17	0.61
85:4:6197:A:H61	85:4:6198:A:N6	1.97	0.61
4:D:33:ARG:NH2	46:7:8:G:OP1	2.33	0.61
49:2:626:G:C2	85:4:6223:U:C4	2.88	0.61
49:2:1037:G:C6	49:2:1038:U:C5	2.88	0.61
57:HH:215:LYS:O	57:HH:219:GLU:N	2.34	0.61
11:L:150:LEU:HD13	33:h:121:VAL:HG23	1.82	0.61
49:2:1143:A:H2'	49:2:1144:A:C8	2.35	0.61
45:5:4596:C:C4	45:5:4597:U:C4	2.88	0.61
48:K:121:PRO:O	85:4:6088:C:H5	1.83	0.61
48:K:124:LEU:CD1	85:4:6038:G:N3	2.63	0.61
85:4:6161:A:N6	85:4:6162:A:H62	1.99	0.61
85:4:6179:U:C2	85:4:6180:U:N1	2.66	0.61
85:4:6181:C:O2	85:4:6196:A:C2	2.52	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6042:U:C4	85:4:6088:C:O3'	2.53	0.61
85:4:6182:A:H61	85:4:6197:A:H5'	1.66	0.61
5:E:131:HIS:HB2	45:5:972:C:N3	2.14	0.61
49:2:1078:C:C5	49:2:1079:C:C5	2.89	0.61
85:4:6095:U:O5'	85:4:6098:A:OP2	2.19	0.61
85:4:6181:C:C2'	85:4:6182:A:C2'	2.75	0.61
3:C:53:ALA:HB3	47:8:27:U:H4'	1.83	0.61
45:5:1358:G:H4'	45:5:1359:G:OP1	2.00	0.61
46:7:32:A:C4	46:7:41:G:N7	2.69	0.61
49:2:919:A:OP2	64:OO:64:ARG:NH2	2.34	0.61
57:HH:32:MET:HE2	57:HH:63:MET:HG2	1.82	0.61
15:P:64:ASN:HD22	15:P:80:GLN:HE22	1.48	0.61
27:b:6:ASN:O	27:b:7:HIS:CB	2.49	0.61
85:4:6071:A:C4	85:4:6072:U:N1	2.69	0.61
10:J:140:SER:O	10:J:141:ILE:C	2.43	0.60
41:p:76:ALA:HA	41:p:79:VAL:HB	1.82	0.60
45:5:427:A:H2'	45:5:428:G:O4'	2.00	0.60
45:5:1529:G:C2	45:5:1646:A:C2	2.88	0.60
49:2:1535:U:H1'	56:GG:88:MET:HE1	1.83	0.60
85:4:6174:G:N7	85:4:6205:A:C5	2.69	0.60
83:hh:36:ARG:HD2	83:hh:65:PHE:CD2	2.35	0.60
49:2:350:C:HO2'	49:2:383:G:H1	1.49	0.60
49:2:1190:A:H2'	49:2:1191:C:O4'	2.00	0.60
85:4:6175:G:N2	85:4:6202:C:N4	2.49	0.60
85:4:6181:C:O2'	85:4:6182:A:C8	2.51	0.60
85:4:6071:A:C8	85:4:6071:A:C5'	2.85	0.60
85:4:6097:U:C4	85:4:6098:A:C2	2.90	0.60
85:4:6197:A:H8	85:4:6197:A:OP2	1.84	0.60
45:5:977:C:N3	45:5:978:G:C2	2.70	0.60
58:II:121:THR:O	58:II:123:THR:N	2.34	0.60
16:Q:79:THR:CG2	16:Q:136:THR:HG22	2.32	0.60
47:8:27:U:O2'	47:8:28:C:O5'	2.19	0.60
85:4:6171:U:O2'	85:4:6172:G:N2	2.33	0.60
45:5:3879:G:O2'	45:5:3881:G:OP2	2.18	0.60
45:5:5001:U:H2'	45:5:5002:U:O4'	2.01	0.60
47:8:141:C:H2'	47:8:142:U:H6	1.65	0.60
49:2:1608:U:H2'	49:2:1609:C:O4'	2.02	0.60
50:3:86:C:O2'	50:3:87:A:C4	2.53	0.60
78:cc:64:CYS:SG	78:cc:65:GLN:N	2.75	0.60
85:4:6181:C:H2'	85:4:6182:A:O2'	2.01	0.60
45:5:376:A:N6	45:5:377:A:C6	2.70	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:3948:C:O2'	45:5:3949:A:O4'	2.14	0.60
48:K:180:VAL:HG22	48:K:184:HIS:CE1	2.37	0.60
45:5:62:A:N3	45:5:77:U:O2'	2.35	0.59
53:DD:235:ASN:O	53:DD:239:ALA:N	2.33	0.59
85:4:6071:A:C8	85:4:6071:A:C3'	2.84	0.59
2:B:240:LEU:HB2	2:B:248:LEU:HA	1.85	0.59
49:2:73:C:H2'	49:2:74:G:H4'	1.84	0.59
45:5:1395:U:C5	45:5:1396:G:N7	2.71	0.59
45:5:1691:G:C2	45:5:1692:C:C2	2.91	0.59
4:D:62:CYS:HB3	4:D:105:LEU:HD22	1.84	0.59
5:E:193:HIS:O	5:E:195:LYS:N	2.35	0.59
45:5:1279:A:C6	45:5:1281:G:N1	2.70	0.59
49:2:2:A:C2	49:2:418:A:C2	2.91	0.59
49:2:318:A:C2	49:2:333:G:C2	2.90	0.59
76:aa:111:ARG:NH1	85:4:6123:G:H21	2.01	0.59
30:e:42:ASP:OD2	45:5:1317:U:O4	2.21	0.59
49:2:350:C:HO2'	49:2:383:G:N2	1.99	0.59
85:4:6073:A:H3'	85:4:6074:A:H4'	1.85	0.59
4:D:72:ASP:O	46:7:113:G:N2	2.36	0.59
45:5:2590:G:O2'	45:5:2755:A:N6	2.36	0.59
46:7:32:A:C2	46:7:41:G:C6	2.90	0.59
59:JJ:57:ALA:HB1	59:JJ:60:LEU:HD13	1.83	0.59
85:4:6176:U:C2'	85:4:6177:U:H1'	2.31	0.59
85:4:6178:U:C4	85:4:6179:U:C5	2.90	0.59
2:B:77:THR:HG21	2:B:337:VAL:HG22	1.84	0.59
14:O:27:VAL:CG1	14:O:98:ALA:HB1	2.33	0.59
25:Z:49:TYR:HB3	25:Z:50:PRO:CD	2.33	0.59
45:5:705:G:H2'	45:5:706:C:C6	2.37	0.59
49:2:845:G:H2'	49:2:846:G:O5'	2.02	0.59
2:B:276:HIS:O	2:B:277:ARG:HG2	2.02	0.59
16:Q:147:GLU:O	16:Q:149:TYR:N	2.35	0.59
37:l:4:HIS:HA	45:5:2781:G:O2'	2.02	0.59
45:5:963:G:N2	45:5:970:G:O5'	2.36	0.59
45:5:4719:G:H8	45:5:4719:G:O5'	1.86	0.59
47:8:140:C:H2'	47:8:141:C:C6	2.38	0.59
48:K:121:PRO:HG2	85:4:6037:U:C4	2.37	0.59
55:FF:43:PRO:HD2	55:FF:46:ILE:HD12	1.85	0.59
56:GG:136:ARG:HD3	85:4:6212:U:H5'	1.84	0.59
85:4:6070:A:HO2'	85:4:6172:G:C1'	2.13	0.59
85:4:6197:A:H2'	85:4:6198:A:C4'	2.33	0.59
85:4:6199:A:H1'	85:4:6200:A:C4'	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:971(A):G:N3	45:5:971(A):G:P	2.76	0.59
13:N:28:TRP:O	13:N:32:GLN:NE2	2.36	0.58
23:X:93:ASN:HB3	23:X:95:THR:HG23	1.84	0.58
33:h:47:ILE:HG21	47:8:49:G:H5'	1.85	0.58
38:m:74:TYR:O	45:5:4472:G:O2'	2.21	0.58
83:hh:109:LEU:HD11	83:hh:125:ARG:CG	2.32	0.58
85:4:6198:A:HO2'	85:4:6199:A:C5'	2.16	0.58
48:K:194:LEU:HD21	48:K:197:ASN:HB3	1.85	0.58
67:RR:47:LEU:HD23	67:RR:50:LYS:HG3	1.85	0.58
45:5:1325:C:H4'	45:5:1326:A:O5'	2.04	0.58
51:BB:16:LEU:HD22	68:SS:96:ILE:HD12	1.85	0.58
54:EE:70:THR:HG22	54:EE:86:LEU:HD13	1.85	0.58
55:FF:43:PRO:CD	55:FF:46:ILE:HD12	2.33	0.58
77:bb:91:ALA:O	77:bb:92:ARG:C	2.46	0.58
85:4:6181:C:H3'	85:4:6182:A:O2'	1.99	0.58
1:A:202:VAL:HG23	45:5:3689:G:OP1	2.03	0.58
17:R:4:LEU:HD21	17:R:33:ALA:HB2	1.84	0.58
73:XX:8:ALA:HB2	73:XX:74:VAL:HG11	1.85	0.58
80:ee:42:CYS:O	80:ee:43:PHE:C	2.45	0.58
85:4:6179:U:O2	85:4:6180:U:N1	2.36	0.58
11:L:39:ARG:NH2	45:5:1362:G:OP1	2.37	0.58
45:5:2889:G:C2	45:5:3613:U:O2	2.56	0.58
49:2:617:G:OP1	81:ff:82:VAL:HG13	2.03	0.58
51:BB:75:SER:HB3	51:BB:122:LEU:HD12	1.85	0.58
85:4:6096:G:C2	85:4:6101:U:C1'	2.77	0.58
85:4:6197:A:H2'	85:4:6198:A:O4'	2.03	0.58
1:A:236:GLY:H	45:5:3687:A:HO2'	1.52	0.58
28:c:38:ILE:HD11	28:c:46:VAL:HG21	1.85	0.58
45:5:426:A:H2'	45:5:427:A:O4'	2.02	0.58
45:5:4395:U:C6	45:5:4395:U:H5'	2.39	0.58
67:RR:34:VAL:HG12	67:RR:35:ASN:ND2	2.18	0.58
85:4:6055:C:N4	85:4:6056:A:C6	2.71	0.58
2:B:2:SER:O	45:5:4517:A:N7	2.36	0.58
14:O:54:TYR:CE2	14:O:145:VAL:HG11	2.39	0.58
45:5:34:A:C2	45:5:35:U:C5	2.91	0.58
58:II:130:LEU:HA	58:II:133:LEU:HD12	1.85	0.58
85:4:6042:U:C4	85:4:6088:C:H4'	2.28	0.58
85:4:6177:U:C4	85:4:6178:U:C2	2.91	0.58
2:B:134:CYS:SG	2:B:135:LYS:N	2.77	0.58
45:5:33:A:H2'	45:5:34:A:C8	2.38	0.58
45:5:4759:C:O4'	45:5:4759:C:O2	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:93:ARG:CZ	6:F:108:LEU:HD13	2.34	0.58
45:5:1868:A:N1	45:5:4441:A:O2'	2.33	0.58
49:2:870:A:C6	49:2:915:G:C6	2.92	0.58
52:CC:103:MET:HE1	52:CC:212:VAL:HG23	1.85	0.58
3:C:164:THR:HG22	3:C:220:ALA:O	2.04	0.58
18:S:102:THR:HG22	18:S:129:VAL:HG11	1.85	0.58
49:2:1487:A:C6	49:2:1488:C:N4	2.72	0.58
85:4:6071:A:N1	85:4:6072:U:N3	2.51	0.58
1:A:233:ARG:O	1:A:235:VAL:N	2.37	0.57
3:C:340:ILE:HG21	5:E:52:LEU:HD11	1.86	0.57
4:D:45:ASN:N	4:D:45:ASN:ND2	2.50	0.57
13:N:105:ARG:NH1	45:5:2459:G:N7	2.52	0.57
45:5:4502:C:H2'	45:5:4503:A:O4'	2.03	0.57
85:4:6074:A:OP1	85:4:6074:A:H4'	1.90	0.57
85:4:6181:C:C3'	85:4:6182:A:C2'	2.21	0.57
13:N:64:ILE:HD12	13:N:65:ARG:N	2.19	0.57
48:K:124:LEU:HD12	85:4:6038:G:C8	2.40	0.57
66:QQ:39:ALA:HA	66:QQ:42:ARG:HD3	1.86	0.57
83:hh:120:ILE:HD11	83:hh:134:THR:HG22	1.86	0.57
85:4:6070:A:H1'	85:4:6172:G:C8	2.39	0.57
40:o:8:ARG:HE	40:o:23:VAL:HG21	1.67	0.57
45:5:964:A:H2'	45:5:965:G:O4'	2.05	0.57
45:5:3767:C:O2	45:5:3767:C:H2'	2.04	0.57
75:ZZ:84:LYS:HG3	75:ZZ:85:ASN:ND2	2.18	0.57
49:2:1139:C:C2	49:2:1140:G:C8	2.92	0.57
85:4:6073:A:H2'	85:4:6073:A:N3	2.20	0.57
85:4:6171:U:C2'	85:4:6172:G:H21	2.16	0.57
13:N:42:PRO:HB3	13:N:61:ILE:HD13	1.87	0.57
45:5:1322:A:C6	45:5:1326:A:C8	2.93	0.57
53:DD:102:LEU:HD23	53:DD:130:ILE:HD11	1.86	0.57
45:5:1078:A:C2	45:5:1233:G:C2	2.92	0.57
45:5:2724:G:C2	45:5:2726:G:N7	2.72	0.57
57:HH:68:LEU:N	57:HH:100:CYS:SG	2.77	0.57
84:jj:151:ILE:CD1	84:jj:205:VAL:HG11	2.35	0.57
45:5:11:G:H2'	45:5:12:A:H5''	1.87	0.57
45:5:3736:A:O2'	45:5:3932:U:O2'	2.14	0.57
45:5:5020:G:O2'	45:5:5021:C:O5'	2.20	0.57
49:2:1087:A:H4'	49:2:1088:U:OP2	2.05	0.57
71:VV:36:CYS:HB2	71:VV:89:ILE:HD11	1.85	0.57
77:bb:42:ARG:O	77:bb:67:LEU:N	2.38	0.57
9:I:83:ASP:OD1	9:I:83:ASP:N	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:114:PHE:HA	29:d:117:LEU:HD23	1.85	0.57
33:h:26:VAL:O	33:h:30:GLN:NE2	2.37	0.57
45:5:977:C:N4	45:5:978:G:C6	2.73	0.57
48:K:121:PRO:HG2	85:4:6037:U:C2	2.39	0.57
64:OO:81:ALA:HB1	64:OO:82:PRO:HD2	1.87	0.57
2:B:134:CYS:O	2:B:136:LYS:N	2.38	0.57
46:7:68:C:C4	46:7:69:U:C4	2.93	0.57
71:VV:23:THR:HG23	71:VV:88:LEU:HD23	1.87	0.57
16:Q:50:ARG:HA	16:Q:53:MET:HE3	1.87	0.57
16:Q:181:ARG:HH11	26:a:56:VAL:HG21	1.70	0.57
45:5:4944:C:O2	45:5:4944:C:H5''	2.04	0.57
47:8:13:G:C6	47:8:14:U:C4	2.93	0.57
49:2:655:A:C8	49:2:657:U:C6	2.93	0.57
11:L:47:ALA:O	11:L:149:GLN:CD	2.48	0.56
23:X:118:ASP:C	23:X:119:ILE:HG22	2.29	0.56
45:5:33:A:C6	45:5:34:A:C6	2.93	0.56
45:5:1944:A:C6	45:5:1945:G:N7	2.73	0.56
45:5:4265:U:O4'	45:5:4265:U:O2	2.21	0.56
45:5:2304:U:H2'	45:5:2304:U:O2	2.03	0.56
48:K:119:GLN:O	85:4:6037:U:O3'	2.23	0.56
49:2:1665:G:OP1	70:UU:89:PRO:HD2	2.05	0.56
75:ZZ:84:LYS:HE3	75:ZZ:85:ASN:HD22	1.69	0.56
85:4:6178:U:C2'	85:4:6179:U:H1'	2.34	0.56
2:B:56:ILE:HG23	2:B:57:VAL:N	2.20	0.56
14:O:18:ARG:O	14:O:21:ALA:N	2.38	0.56
22:W:51:TRP:O	22:W:51:TRP:HE3	1.88	0.56
35:j:16:HIS:NE2	45:5:1532:G:OP1	2.33	0.56
45:5:2638:G:C2	45:5:2639:U:C4	2.94	0.56
45:5:3819:G:C2	45:5:3820:G:N7	2.73	0.56
48:K:121:PRO:O	85:4:6088:C:C5	2.58	0.56
49:2:384:U:O2'	62:MM:135:SER:C	2.48	0.56
49:2:1335:G:H2'	49:2:1336:C:O4'	2.06	0.56
49:2:1839:U:H2'	49:2:1840:U:C6	2.40	0.56
57:HH:142:ARG:HA	57:HH:147:LEU:HD12	1.86	0.56
85:4:6096:G:C2	85:4:6101:U:O4'	2.58	0.56
85:4:6175:G:H21	85:4:6202:C:N4	2.04	0.56
45:5:422:C:C2	47:8:13:G:N2	2.74	0.56
45:5:986:C:O2	45:5:1069:G:C2	2.59	0.56
45:5:2724:G:N3	45:5:2726:G:N7	2.53	0.56
45:5:3908:A:H2'	45:5:3908:A:N3	2.20	0.56
55:FF:118:GLU:O	55:FF:120:LYS:N	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:hh:168:CYS:SG	83:hh:198:VAL:HG23	2.46	0.56
85:4:6041:C:O2'	85:4:6043:U:OP1	2.15	0.56
45:5:209:U:C4	45:5:233:U:C4	2.93	0.56
49:2:1605:G:C2'	49:2:1606:G:O4'	2.53	0.56
60:KK:46:VAL:HG11	60:KK:106:LEU:HD12	1.88	0.56
85:4:6041:C:O2	85:4:6088:C:OP2	2.23	0.56
3:C:212:ASN:HB2	3:C:256:ALA:HB2	1.87	0.56
45:5:4467:A:N1	45:5:4489:G:O6	2.39	0.56
48:K:48:ARG:NH1	85:4:6082:G:C5'	2.68	0.56
59:JJ:82:VAL:CG1	59:JJ:202:ILE:HD13	2.36	0.56
85:4:6177:U:C2	85:4:6178:U:H1'	2.41	0.56
2:B:89:ILE:HD12	2:B:89:ILE:C	2.30	0.56
2:B:341:LYS:O	2:B:343:ARG:N	2.38	0.56
4:D:154:THR:O	4:D:156:GLY:N	2.38	0.56
6:F:158:TYR:CZ	6:F:167:ALA:HB2	2.41	0.56
45:5:198:A:C2	45:5:237:G:O4'	2.58	0.56
45:5:403:G:C2	45:5:404:U:C5	2.93	0.56
45:5:2076:G:C6	45:5:2077:C:N4	2.74	0.56
5:E:52:LEU:O	5:E:53:VAL:HG23	2.05	0.56
15:P:74:LYS:O	15:P:77:GLY:N	2.35	0.56
17:R:138:LEU:O	17:R:141:HIS:N	2.39	0.56
45:5:422:C:C2	47:8:13:G:C2	2.94	0.56
85:4:6071:A:C8	85:4:6071:A:C4'	2.89	0.56
45:5:3816:A:O2'	45:5:3819:G:N3	2.36	0.56
45:5:4485:C:C4	45:5:4486:C:C5	2.93	0.56
49:2:181:A:C6	49:2:182:C:N4	2.73	0.56
49:2:845:G:C6	49:2:846:G:C2	2.94	0.56
49:2:1473:G:H2'	49:2:1475:G:N2	2.20	0.56
55:FF:11:ARG:N	55:FF:26:VAL:O	2.38	0.56
83:hh:79:LEU:HD11	83:hh:120:ILE:HD13	1.87	0.56
85:4:6071:A:H8	85:4:6071:A:C5'	2.19	0.56
85:4:6149:A:H2'	85:4:6150:C:H4'	1.86	0.56
85:4:6198:A:C6	85:4:6199:A:C8	2.93	0.56
2:B:259:PRO:O	2:B:261:ARG:N	2.35	0.56
29:d:33:ILE:HD11	29:d:41:ARG:HB3	1.86	0.56
33:h:96:ASN:HD22	33:h:96:ASN:N	2.03	0.56
45:5:106:A:H1'	45:5:336:A:H1'	1.88	0.56
51:BB:122:LEU:HD13	51:BB:142:LEU:CD1	2.36	0.56
84:jj:151:ILE:HD11	84:jj:205:VAL:HG11	1.88	0.56
85:4:6199:A:C6	85:4:6200:A:C2	2.94	0.56
6:F:148:SER:OG	6:F:244:ARG:NH1	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:41:ALA:HB3	32:g:52:ARG:HB3	1.88	0.55
63:NN:54:SER:C	63:NN:55:ASN:HD22	2.14	0.55
85:4:6200:A:N6	85:4:6204:A:H2	2.04	0.55
45:5:1291:G:C6	45:5:1292:C:C4	2.94	0.55
49:2:1741:U:H2'	49:2:1742:C:O4'	2.06	0.55
85:4:6045:C:C2	85:4:6046:U:C5	2.94	0.55
85:4:6178:U:O2	85:4:6179:U:C2	2.59	0.55
85:4:6179:U:N3	85:4:6180:U:N3	2.54	0.55
17:R:77:GLY:HA3	45:5:2888:G:OP1	2.06	0.55
35:j:20:ARG:O	35:j:20:ARG:HD3	2.06	0.55
45:5:423:G:C4	47:8:12:G:N2	2.75	0.55
45:5:1360:G:C6	45:5:1361:G:C5	2.94	0.55
45:5:2397:G:C8	45:5:2399:G:C8	2.95	0.55
45:5:4507:A:C2	45:5:4508:C:C2	2.94	0.55
48:K:155:ILE:HD12	48:K:167:VAL:CG2	2.36	0.55
1:A:186:TYR:O	1:A:190:LYS:N	2.40	0.55
43:s:82:ILE:HA	43:s:86:VAL:HG21	1.88	0.55
45:5:264:C:O2'	45:5:266:C:N3	2.29	0.55
45:5:4209:G:H2'	45:5:4210:U:O4'	2.07	0.55
47:8:121:G:C2	47:8:122:G:C8	2.95	0.55
49:2:575:A:N6	49:2:576:A:C6	2.74	0.55
49:2:853:C:O2	49:2:853:C:O4'	2.23	0.55
58:II:185:VAL:C	58:II:186:ASN:OD1	2.50	0.55
85:4:6041:C:N3	85:4:6088:C:H5'	2.21	0.55
85:4:6200:A:H2'	85:4:6201:C:H1'	1.88	0.55
15:P:119:VAL:C	15:P:120:ASN:HD22	2.14	0.55
35:j:21:ARG:NH1	35:j:39:TYR:HA	2.22	0.55
45:5:930:G:N7	45:5:931:C:N3	2.55	0.55
45:5:1958:A:O2'	45:5:2025:A:N1	2.39	0.55
45:5:3688:U:C2	45:5:3689:G:C8	2.95	0.55
49:2:373:G:H4'	62:MM:85:THR:HG21	1.88	0.55
51:BB:59:LEU:HD22	51:BB:181:GLU:HG2	1.87	0.55
59:JJ:67:TRP:CZ2	59:JJ:158:ILE:HD11	2.41	0.55
3:C:342:ARG:O	3:C:345:ARG:N	2.40	0.55
13:N:85:VAL:HG23	45:5:43:U:OP1	2.07	0.55
39:n:23:ARG:NH1	45:5:3807:A:OP2	2.40	0.55
45:5:2693:G:C6	45:5:2694:G:C2	2.95	0.55
45:5:2746:A:C8	45:5:2747:U:C5	2.95	0.55
85:4:6177:U:N1	85:4:6178:U:H1'	2.22	0.55
18:S:161:ARG:HD3	45:5:1921:C:C2	2.42	0.55
25:Z:42:LEU:HD12	25:Z:98:LYS:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:60:ARG:HD3	32:g:61:PRO:HD3	1.89	0.55
49:2:165:G:O4'	57:HH:110:ASN:ND2	2.40	0.55
49:2:752:G:O2'	49:2:753:C:H3'	2.06	0.55
65:PP:146:ARG:HA	77:bb:29:CYS:SG	2.46	0.55
3:C:193:LYS:O	3:C:194:GLY:C	2.50	0.55
5:E:133:LYS:NZ	45:5:713:C:O2	2.39	0.55
18:S:168:THR:OG1	18:S:169:THR:N	2.38	0.55
61:LL:65:ARG:O	61:LL:66:HIS:ND1	2.40	0.55
62:MM:104:LYS:O	74:YY:11:ARG:NH2	2.39	0.55
85:4:6161:A:N6	85:4:6162:A:N6	2.54	0.55
85:4:6171:U:O2'	85:4:6172:G:H5''	2.07	0.55
85:4:6174:G:N7	85:4:6205:A:N7	2.54	0.55
9:I:116:ARG:O	9:I:117:GLY:C	2.50	0.55
26:a:22:ILE:HG23	45:5:1319:U:OP1	2.07	0.55
26:a:82:VAL:HG12	45:5:509:A:O2'	2.06	0.55
45:5:370:U:C6	45:5:1637:A:C2	2.95	0.55
45:5:1840:G:H2'	45:5:1841:C:O4'	2.07	0.55
49:2:912:C:C4	49:2:914:U:O2	2.60	0.55
49:2:1134:G:C2	49:2:1135:C:C2	2.95	0.55
49:2:1332:A:C5	49:2:1500:G:C2	2.94	0.55
66:QQ:57:LEU:HG	66:QQ:80:LEU:HD13	1.89	0.55
45:5:2505:C:O2	45:5:2505:C:O4'	2.23	0.55
45:5:2746:A:H2'	45:5:2747:U:O4'	2.07	0.55
49:2:1046:U:H2'	49:2:1047:C:O4'	2.07	0.55
57:HH:216:ARG:HA	57:HH:219:GLU:HB2	1.88	0.55
66:QQ:108:LYS:HE3	66:QQ:111:MET:HE3	1.89	0.55
83:hh:88:ARG:CD	83:hh:97:THR:HG21	2.35	0.55
85:4:6199:A:N9	85:4:6200:A:N9	2.55	0.55
30:e:52:GLN:CD	30:e:52:GLN:N	2.65	0.54
45:5:4470:G:N1	45:5:4471:U:C2	2.75	0.54
84:jj:78:VAL:HG23	84:jj:95:VAL:HG11	1.89	0.54
45:5:1615:C:H2'	45:5:1616:U:C6	2.42	0.54
45:5:4469:U:H1'	45:5:4708:A:C8	2.42	0.54
47:8:122:G:N2	47:8:128:C:N4	2.56	0.54
49:2:987:A:OP1	77:bb:32:LYS:NZ	2.41	0.54
49:2:1167:G:C2	49:2:1193:U:O2	2.61	0.54
49:2:1285:G:O2'	49:2:1286:G:OP1	2.20	0.54
74:YY:27:TYR:O	74:YY:30:ALA:HB3	2.06	0.54
76:aa:111:ARG:HH11	85:4:6123:G:H21	1.54	0.54
85:4:6199:A:C1'	85:4:6200:A:C1'	2.82	0.54
49:2:1631:U:H2'	49:2:1632:G:O4'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:QQ:18:ARG:NH1	69:TT:90:VAL:HG22	2.21	0.54
85:4:6179:U:H4'	85:4:6179:U:OP1	2.00	0.54
85:4:6197:A:N7	85:4:6198:A:N7	2.55	0.54
5:E:48:ARG:NH2	45:5:981:C:OP2	2.41	0.54
6:F:196:VAL:HG13	6:F:200:PHE:CD1	2.42	0.54
15:P:10:ASN:HD21	15:P:13:LYS:HG2	1.72	0.54
30:e:59:GLY:O	45:5:1900:C:O4'	2.26	0.54
49:2:845:G:H2'	49:2:846:G:O4'	2.08	0.54
49:2:845:G:C2'	49:2:846:G:O5'	2.56	0.54
85:4:6071:A:H2'	85:4:6072:U:C4'	2.37	0.54
85:4:6073:A:N3	85:4:6073:A:C2'	2.70	0.54
85:4:6178:U:O2	85:4:6179:U:N1	2.40	0.54
45:5:1362:G:C2	45:5:1376:C:O2	2.60	0.54
45:5:5020:G:HO2'	45:5:5021:C:C5'	2.21	0.54
57:HH:132:ARG:HB3	57:HH:133:LEU:HD12	1.88	0.54
64:OO:87:ASP:OD1	64:OO:125:LEU:HD11	2.07	0.54
74:YY:27:TYR:O	74:YY:31:HIS:N	2.39	0.54
17:R:154:LEU:HD23	17:R:155:LEU:CD2	2.37	0.54
56:GG:102:LEU:HD22	76:aa:110:THR:HG21	1.89	0.54
85:4:6180:U:OP1	85:4:6180:U:H4'	2.07	0.54
54:EE:21:LEU:CD2	54:EE:48:ILE:HD11	2.38	0.54
66:QQ:94:VAL:HG13	66:QQ:105:VAL:HB	1.89	0.54
76:aa:102:LYS:HB2	76:aa:107:VAL:HG12	1.88	0.54
46:7:38:U:O2'	46:7:42:A:N6	2.32	0.54
49:2:570:C:C5	49:2:571:U:C5	2.96	0.54
85:4:6199:A:H1'	85:4:6200:A:O4'	2.06	0.54
1:A:207:VAL:HG12	45:5:3919:C:H5'	1.90	0.54
8:H:112:VAL:HG21	8:H:128:MET:HE2	1.90	0.54
45:5:2426:U:C4	45:5:2427:G:N7	2.76	0.54
45:5:4353:U:H5'	45:5:4354:U:O2	2.08	0.54
46:7:102:U:H2'	46:7:103:A:O4'	2.08	0.54
52:CC:127:VAL:HG11	52:CC:176:VAL:HG11	1.89	0.54
84:jj:24:LEU:O	84:jj:27:ALA:HB2	2.08	0.54
85:4:6091:U:O2	85:4:6091:U:H2'	2.07	0.54
6:F:111:LEU:HD21	6:F:131:MET:HE2	1.89	0.54
33:h:17:LEU:O	33:h:20:GLN:N	2.41	0.54
45:5:930:G:N7	45:5:931:C:C4	2.76	0.54
45:5:1650:A:H3'	45:5:1651:G:C5'	2.38	0.54
45:5:2011:C:H2'	45:5:2012:A:O4'	2.08	0.54
46:7:32:A:C8	46:7:41:G:C8	2.96	0.54
61:LL:12:TYR:HB3	61:LL:83:LEU:HD21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:LEU:HD13	1:A:150:LEU:HD21	1.89	0.53
1:A:181:LYS:HB3	45:5:1577:G:C5	2.44	0.53
15:P:131:ARG:HD3	15:P:137:ASN:OD1	2.07	0.53
24:Y:43:ASN:ND2	24:Y:127:GLN:HE21	2.06	0.53
33:h:76:LYS:O	45:5:136:C:N4	2.41	0.53
45:5:1398:A:N6	45:5:1419:G:N3	2.56	0.53
45:5:1759:G:C2	45:5:1774:C:O2	2.61	0.53
68:SS:31:ASN:HD21	68:SS:55:THR:CG2	2.21	0.53
85:4:6042:U:O2	85:4:6088:C:C4'	2.55	0.53
13:N:116:LEU:HD23	13:N:133:ILE:HG21	1.89	0.53
22:W:46:PRO:O	22:W:49:ILE:N	2.39	0.53
48:K:123:ILE:HG12	85:4:6040:U:C5'	2.39	0.53
55:FF:31:PRO:HA	55:FF:81:THR:HB	1.90	0.53
60:KK:81:LEU:CD1	60:KK:97:ILE:HD11	2.38	0.53
14:O:16:LEU:HB2	14:O:43:ILE:HG23	1.91	0.53
40:o:81:ARG:C	40:o:82:MET:HE3	2.33	0.53
45:5:3767:C:O2	45:5:3768:U:C6	2.62	0.53
49:2:1139:C:O2	49:2:1139:C:H3'	2.08	0.53
85:4:6073:A:H3'	85:4:6074:A:C4'	2.39	0.53
85:4:6206:G:C2	85:4:6207:A:N6	2.73	0.53
8:H:89:ARG:HG3	8:H:147:GLU:HG3	1.90	0.53
45:5:99:A:H2'	45:5:100:C:O2	2.07	0.53
45:5:2850:A:O2'	45:5:4495:G:OP1	2.26	0.53
45:5:4287:G:H2'	45:5:4288:C:O4'	2.08	0.53
64:OO:52:VAL:O	64:OO:55:ARG:N	2.41	0.53
45:5:2043:A:N1	45:5:4515:G:O2'	2.32	0.53
45:5:4455:G:OP1	45:5:4501:U:H5''	2.09	0.53
58:II:8:ILE:HG23	58:II:8:ILE:O	2.09	0.53
47:8:33:G:H5''	47:8:34:U:OP1	2.09	0.53
60:KK:78:LEU:O	60:KK:82:VAL:HG23	2.08	0.53
84:jj:91:ASN:HA	84:jj:119:PRO:HA	1.90	0.53
85:4:6199:A:C2	85:4:6200:A:N3	2.77	0.53
2:B:114:CYS:SG	2:B:165:HIS:HB3	2.48	0.53
6:F:223:THR:HB	46:7:83:A:C5'	2.39	0.53
26:a:2:PRO:CG	26:a:5:LEU:HD12	2.39	0.53
45:5:1332:C:H2'	45:5:1333:A:C8	2.43	0.53
45:5:1915:C:O2	45:5:1915:C:O5'	2.27	0.53
49:2:925:G:C2	49:2:926:A:C8	2.97	0.53
59:JJ:67:TRP:HZ2	59:JJ:158:ILE:HD11	1.74	0.53
85:4:6053:U:O2	85:4:6073:A:N1	2.42	0.53
14:O:87:MET:HE2	45:5:2051:C:O2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z:28:ASN:C	25:Z:29:ILE:HD12	2.33	0.53
32:g:15:THR:O	32:g:17:SER:N	2.42	0.53
47:8:141:C:H2'	47:8:142:U:C6	2.43	0.53
85:4:6161:A:C5	85:4:6162:A:N7	2.77	0.53
2:B:113:GLU:HA	2:B:116:ARG:HD2	1.91	0.53
20:U:100:LEU:HA	20:U:113:ARG:O	2.09	0.53
25:Z:83:THR:OG1	25:Z:84:ARG:N	2.42	0.53
45:5:4584:A:C2	45:5:4719:G:C4	2.97	0.53
49:2:688:U:O4'	49:2:688:U:O2	2.26	0.53
49:2:755:C:N4	49:2:789:G:O6	2.42	0.53
78:cc:33:MET:HE2	78:cc:48:SER:HA	1.91	0.53
43:s:39:GLN:HE22	43:s:185:PHE:HB2	1.74	0.53
45:5:4:G:N1	47:8:154:G:C6	2.77	0.53
49:2:867:G:C6	49:2:868:G:O6	2.61	0.53
59:JJ:35:ASN:O	59:JJ:36:THR:C	2.52	0.53
3:C:149:GLU:HB3	3:C:150:LEU:HB2	1.90	0.52
4:D:76:CYS:HB3	4:D:109:LEU:HD13	1.91	0.52
17:R:70:ARG:CG	17:R:76:MET:HE2	2.39	0.52
74:YY:45:SER:O	74:YY:46:HIS:CG	2.62	0.52
85:4:6178:U:N1	85:4:6179:U:C6	2.78	0.52
7:G:109:LYS:HG3	45:5:4085:A:C5	2.44	0.52
16:Q:61:LEU:HD21	16:Q:66:MET:HB2	1.90	0.52
45:5:100:C:O2	45:5:100:C:O4'	2.25	0.52
45:5:2693:G:C6	45:5:2694:G:N2	2.77	0.52
49:2:862:A:C4	73:XX:107:SER:HA	2.44	0.52
69:TT:111:LEU:HA	69:TT:114:LEU:HB2	1.92	0.52
85:4:6198:A:N1	85:4:6199:A:C5	2.76	0.52
85:4:6199:A:C5	85:4:6200:A:C5	2.96	0.52
15:P:111:SER:O	15:P:152:GLU:HA	2.09	0.52
21:V:39:ILE:HG23	21:V:61:VAL:CG2	2.40	0.52
29:d:38:PHE:CD2	29:d:78:ARG:HD3	2.44	0.52
32:g:56:VAL:HG13	32:g:72:LYS:HA	1.91	0.52
49:2:187:G:C6	49:2:188:C:C5	2.97	0.52
49:2:1100:A:C2	49:2:1133:A:C2	2.96	0.52
49:2:1129:G:C6	49:2:1130:G:O6	2.63	0.52
55:FF:13:ALA:O	55:FF:39:ARG:NH2	2.42	0.52
83:hh:166:VAL:HG11	83:hh:207:CYS:SG	2.50	0.52
18:S:90:THR:C	18:S:91:HIS:ND1	2.68	0.52
45:5:930:G:C8	45:5:930:G:H3'	2.45	0.52
45:5:973:G:C2	45:5:1282:G:O6	2.62	0.52
45:5:4349:C:O2	45:5:4349:C:O4'	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:4926:C:O2	45:5:4926:C:O4'	2.24	0.52
49:2:1328:G:C6	49:2:1329:U:C4	2.97	0.52
85:4:6097:U:H5''	85:4:6098:A:OP2	2.08	0.52
85:4:6161:A:C6	85:4:6162:A:N7	2.78	0.52
17:R:5:ARG:NH2	45:5:2385:U:OP1	2.42	0.52
30:e:47:ARG:NH1	45:5:1883:G:OP1	2.43	0.52
51:BB:30:LEU:HD21	51:BB:35:GLU:HG2	1.89	0.52
52:CC:103:MET:HE2	52:CC:215:VAL:HG23	1.91	0.52
54:EE:16:ILE:HD11	80:ee:36:LEU:HD23	1.91	0.52
60:KK:84:ILE:HG22	60:KK:150:ARG:HA	1.91	0.52
85:4:6063:A:C5	85:4:6208:A:OP2	2.63	0.52
85:4:6178:U:C2	85:4:6179:U:N1	2.76	0.52
19:T:4:THR:O	19:T:9:ARG:NE	2.43	0.52
42:r:60:VAL:HG21	42:r:118:LEU:HD11	1.92	0.52
45:5:2032:U:H2'	45:5:2033:A:C8	2.44	0.52
45:5:2746:A:C8	45:5:2747:U:C6	2.98	0.52
49:2:688:U:OP2	58:II:123:THR:HG23	2.10	0.52
14:O:16:LEU:HD13	14:O:83:THR:HG21	1.91	0.52
34:i:51:ALA:HB1	34:i:52:PRO:HD2	1.91	0.52
49:2:1858:G:OP2	65:PP:146:ARG:NH2	2.37	0.52
50:3:85:C:O3'	50:3:86:C:H4'	2.09	0.52
52:CC:38:MET:HE3	52:CC:185:VAL:HG11	1.91	0.52
74:YY:48:LYS:HG3	74:YY:101:LEU:HD12	1.91	0.52
3:C:57:LEU:HD12	3:C:61:GLN:NE2	2.25	0.52
9:I:33:ILE:O	9:I:69:ARG:NH2	2.43	0.52
45:5:381:U:O4	45:5:382:G:C6	2.63	0.52
45:5:1795:A:H2'	45:5:1796:U:O4'	2.10	0.52
49:2:350:C:HO2'	49:2:383:G:H22	1.56	0.52
62:MM:69:ARG:HD3	62:MM:69:ARG:N	2.25	0.52
85:4:6042:U:C4	85:4:6088:C:C3'	2.89	0.52
85:4:6042:U:C4	85:4:6088:C:C4'	2.88	0.52
3:C:8:ILE:HG23	3:C:150:LEU:HD21	1.91	0.52
3:C:74:ALA:O	3:C:75:ARG:HB2	2.09	0.52
19:T:47:THR:HG22	45:5:4278:C:OP1	2.10	0.52
45:5:33:A:C2	45:5:34:A:C4	2.97	0.52
45:5:444:G:C6	45:5:445:U:C4	2.98	0.52
45:5:4589:A:N1	45:5:4621:C:O2'	2.39	0.52
49:2:1865:C:O2	49:2:1865:C:O4'	2.27	0.52
69:TT:34:LYS:O	69:TT:99:LEU:O	2.28	0.52
85:4:6055:C:C4	85:4:6056:A:C5	2.98	0.52
85:4:6165:C:H5'	85:4:6166:C:OP2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6206:G:N9	85:4:6207:A:C6	2.77	0.52
85:4:6206:G:O2'	85:4:6207:A:N3	2.32	0.52
45:5:373:G:HO2'	45:5:1645:C:HO2'	1.56	0.52
45:5:1517:G:C2'	45:5:1517:G:N3	2.73	0.52
45:5:1933:G:H2'	45:5:1934:A:C8	2.46	0.52
45:5:2898:G:C2	45:5:3602:C:O2	2.63	0.52
45:5:3676:G:C6	45:5:3677:U:C4	2.98	0.52
53:DD:252:THR:HG22	73:XX:99:PHE:CE1	2.44	0.52
58:II:194:LEU:HD11	64:OO:19:ARG:NH2	2.25	0.52
85:4:6030:A:H2	85:4:6096:G:OP1	1.92	0.52
14:O:133:ARG:NE	45:5:1928:C:N4	2.58	0.51
16:Q:151:HIS:ND1	16:Q:164:LYS:O	2.42	0.51
41:p:17:ARG:HB3	41:p:18:TYR:CD2	2.45	0.51
45:5:444:G:C5	45:5:445:U:C5	2.98	0.51
45:5:1279:A:C5	45:5:1281:G:O6	2.63	0.51
45:5:1932:A:H2'	45:5:1933:G:O5'	2.10	0.51
45:5:1936:C:C5	46:7:84:U:C4	2.98	0.51
45:5:2627:C:O4'	45:5:2627:C:O2	2.26	0.51
45:5:2638:G:C2	45:5:2639:U:C5	2.98	0.51
45:5:4583:C:O2	45:5:4719:G:O6	2.28	0.51
48:K:123:ILE:CG2	85:4:6040:U:C5	2.91	0.51
49:2:981:A:H2'	49:2:982:G:C8	2.45	0.51
49:2:1467:C:H2'	49:2:1468:C:C6	2.44	0.51
52:CC:103:MET:HE1	52:CC:212:VAL:CG2	2.40	0.51
76:aa:97:ILE:HD12	76:aa:109:TYR:CD1	2.44	0.51
85:4:6176:U:C3'	85:4:6177:U:H4'	2.38	0.51
85:4:6179:U:C5	85:4:6180:U:H5	2.14	0.51
2:B:45:ALA:HB1	2:B:181:MET:HE1	1.92	0.51
14:O:44:SER:HB3	14:O:129:LEU:HD21	1.90	0.51
17:R:24:LEU:O	17:R:25:ASP:C	2.52	0.51
21:V:100:ASP:OD1	21:V:100:ASP:N	2.41	0.51
45:5:2693:G:O6	45:5:2694:G:N2	2.43	0.51
45:5:3941:G:C2	45:5:3942:A:C4	2.99	0.51
45:5:4470:G:O6	45:5:4471:U:N3	2.43	0.51
45:5:4630:G:O2'	45:5:4671:C:N3	2.38	0.51
45:5:4691:A:C2	45:5:4700:A:C4	2.98	0.51
49:2:356:C:C2'	49:2:356:C:O2	2.58	0.51
49:2:1229:G:C6	49:2:1230:C:C4	2.98	0.51
49:2:1346:U:HO2'	49:2:1485:U:HO2'	1.50	0.51
59:JJ:44:HIS:CG	59:JJ:58:LEU:HD11	2.45	0.51
63:NN:19:GLN:HE22	63:NN:88:TRP:HB3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:QQ:108:LYS:CE	66:QQ:111:MET:HE3	2.40	0.51
68:SS:31:ASN:HD21	68:SS:55:THR:HG22	1.75	0.51
68:SS:98:VAL:HG21	68:SS:117:LEU:HD22	1.92	0.51
85:4:6063:A:C4	85:4:6208:A:OP2	2.62	0.51
29:d:66:THR:O	29:d:69:ASN:N	2.43	0.51
35:j:58:THR:OG1	35:j:59:THR:N	2.44	0.51
45:5:3672:G:C8	45:5:3672:G:O5'	2.63	0.51
49:2:333:G:H2'	49:2:334:C:O4'	2.10	0.51
49:2:1019:C:H2'	49:2:1020:A:O4'	2.10	0.51
52:CC:65:ARG:O	52:CC:87:ILE:HG22	2.10	0.51
57:HH:7:PHE:CE2	57:HH:125:THR:HG22	2.45	0.51
3:C:7:LEU:HD23	3:C:21:ASN:HD22	1.75	0.51
8:H:176:LEU:HD11	38:m:61:GLN:HE21	1.74	0.51
14:O:44:SER:CB	14:O:129:LEU:HD21	2.40	0.51
16:Q:83:VAL:O	16:Q:83:VAL:HG12	2.11	0.51
45:5:1736:A:H2'	45:5:1737:A:O4'	2.11	0.51
45:5:2266:C:O2'	45:5:2267:U:OP2	2.24	0.51
45:5:2504:C:H2'	45:5:2505:C:C2	2.45	0.51
45:5:2532:C:O2	45:5:2532:C:H2'	2.10	0.51
49:2:677:G:N1	49:2:1027:A:OP2	2.33	0.51
85:4:6182:A:N1	85:4:6196:A:C2'	2.73	0.51
31:f:78:HIS:ND1	31:f:85:ARG:NE	2.58	0.51
49:2:932:G:H2'	49:2:934:G:OP1	2.11	0.51
49:2:1253:A:HO2'	49:2:1666:C:HO2'	1.56	0.51
60:KK:40:LYS:O	60:KK:42:GLU:N	2.44	0.51
74:YY:74:LEU:HD11	74:YY:81:ILE:HD11	1.92	0.51
5:E:193:HIS:O	5:E:194:GLN:C	2.52	0.51
12:M:29:ASP:HB2	12:M:37:LEU:HD12	1.92	0.51
45:5:1867:A:C6	45:5:1868:A:C6	2.98	0.51
51:BB:122:LEU:HD13	51:BB:142:LEU:HD11	1.93	0.51
4:D:61:ILE:HG23	4:D:79:TYR:CD1	2.45	0.51
5:E:167:PHE:CE1	5:E:176:LEU:HD22	2.44	0.51
44:t:98:ILE:HG22	45:5:1978:C:H4'	1.92	0.51
45:5:13:U:O2	45:5:13:U:O4'	2.28	0.51
45:5:752:G:C2'	45:5:753:C:O5'	2.59	0.51
45:5:4476:C:O2	45:5:4476:C:O4'	2.27	0.51
54:EE:1:MET:HE2	54:EE:3:VAL:HG12	1.93	0.51
85:4:6181:C:H2'	85:4:6182:A:C2'	2.40	0.51
3:C:143:ARG:HG3	3:C:178:ASN:HB3	1.92	0.51
15:P:131:ARG:HD3	15:P:137:ASN:CG	2.35	0.51
45:5:4188:U:H2'	45:5:4189:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:K:123:ILE:CG2	85:4:6040:U:C6	2.81	0.51
73:XX:89:TRP:O	73:XX:90:GLN:C	2.54	0.51
85:4:6045:C:C2'	85:4:6046:U:O5'	2.59	0.51
85:4:6178:U:N3	85:4:6179:U:C4	2.78	0.51
85:4:6206:G:C4	85:4:6207:A:C6	2.98	0.51
3:C:210:ILE:HG22	3:C:232:VAL:HG22	1.93	0.51
3:C:302:LEU:HD23	16:Q:39:THR:CG2	2.41	0.51
12:M:37:LEU:HA	12:M:49:ALA:HA	1.93	0.51
22:W:92:ALA:O	22:W:96:GLN:HB2	2.11	0.51
25:Z:49:TYR:HB3	25:Z:50:PRO:HD2	1.93	0.51
32:g:114:GLN:N	32:g:114:GLN:HE21	2.09	0.51
45:5:2386:U:C4	45:5:2387:G:N7	2.78	0.51
45:5:2482:C:N4	45:5:2483:G:O6	2.43	0.51
49:2:318:A:C2	49:2:333:G:N1	2.79	0.51
49:2:380:G:N1	49:2:383:G:OP2	2.43	0.51
49:2:872:A:C5	49:2:874:G:C8	2.99	0.51
58:II:135:PHE:O	58:II:136:PRO:C	2.51	0.51
85:4:6182:A:N6	85:4:6197:A:H4'	2.25	0.51
85:4:6197:A:OP2	85:4:6197:A:H3'	2.10	0.51
5:E:95:VAL:HG23	5:E:112:LEU:HD21	1.92	0.51
13:N:110:CYS:CB	13:N:113:LEU:HD12	2.39	0.51
16:Q:155:ALA:O	16:Q:158:THR:OG1	2.29	0.51
40:o:66:ILE:HD13	40:o:91:PHE:CE1	2.46	0.51
45:5:1612:G:N3	45:5:1612:G:C2'	2.73	0.51
45:5:3611:A:C6	45:5:3612:C:N3	2.79	0.51
53:DD:75:ILE:HG23	53:DD:75:ILE:O	2.11	0.51
58:II:36:LEU:HD12	58:II:40:LEU:HD12	1.92	0.51
83:hh:127:LYS:HE3	83:hh:149:GLU:HA	1.93	0.51
85:4:6177:U:C6	85:4:6178:U:C5	2.82	0.51
1:A:14:SER:OG	1:A:15:VAL:N	2.44	0.50
3:C:38:ASN:O	3:C:42:THR:HG23	2.11	0.50
35:j:45:ARG:NH1	45:5:372:A:O3'	2.43	0.50
45:5:4303:C:O2	45:5:4303:C:O4'	2.29	0.50
49:2:601:G:C6	49:2:602:G:C6	2.99	0.50
49:2:1639:G:N3	50:3:42:U:O2'	2.41	0.50
63:NN:50:CYS:SG	63:NN:51:VAL:N	2.84	0.50
62:MM:88:ILE:HD13	62:MM:111:VAL:HG21	1.93	0.50
72:WW:55:ILE:HD11	72:WW:69:ILE:HG12	1.93	0.50
85:4:6201:C:H5'	85:4:6202:C:OP2	2.10	0.50
6:F:28:LYS:HE3	45:5:965:G:N7	2.27	0.50
45:5:2596:G:C2	45:5:2750:G:C2	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:860:G:OP2	58:II:107:LYS:NZ	2.44	0.50
85:4:6163:G:N3	85:4:6163:G:C5'	2.73	0.50
3:C:8:ILE:HD11	3:C:24:LEU:HD12	1.93	0.50
11:L:47:ALA:HB3	11:L:48:PRO:CD	2.40	0.50
13:N:11:TRP:HA	13:N:19:MET:HE2	1.93	0.50
14:O:176:ARG:O	14:O:177:LEU:HD23	2.11	0.50
15:P:102:ALA:HB2	15:P:112:LEU:HD11	1.94	0.50
33:h:20:GLN:O	33:h:24:LEU:HG	2.11	0.50
45:5:1773:U:C4	45:5:1774:C:N4	2.80	0.50
45:5:3706:C:N4	45:5:3707:U:C4	2.79	0.50
45:5:4772:C:N4	45:5:4864:U:O2	2.44	0.50
49:2:823:U:O5'	49:2:823:U:O2	2.30	0.50
49:2:1589:A:N3	49:2:1653:U:O2'	2.37	0.50
85:4:6046:U:C2	85:4:6082:G:N1	2.80	0.50
4:D:66:TYR:CZ	4:D:73:MET:HE3	2.46	0.50
14:O:5:GLN:HG2	14:O:6:VAL:HG23	1.93	0.50
33:h:72:PHE:CD2	33:h:72:PHE:O	2.65	0.50
33:h:106:LYS:O	33:h:110:LYS:N	2.45	0.50
45:5:106:A:H1'	45:5:336:A:N3	2.27	0.50
45:5:109:G:O6	45:5:110:C:C4	2.64	0.50
45:5:3611:A:C2	45:5:3612:C:O2	2.64	0.50
49:2:1349:G:C5	49:2:1350:U:C4	2.99	0.50
52:CC:120:MET:HE2	52:CC:122:GLU:HG3	1.92	0.50
71:VV:32:LEU:HA	71:VV:110:VAL:HG21	1.93	0.50
83:hh:277:THR:HB	83:hh:281:ALA:HB3	1.93	0.50
85:4:6034:A:H4'	85:4:6034:A:OP1	2.10	0.50
85:4:6203:U:H1'	85:4:6205:A:C1'	2.41	0.50
16:Q:147:GLU:O	16:Q:148:VAL:C	2.54	0.50
23:X:99:ILE:C	23:X:100:VAL:HG23	2.35	0.50
25:Z:76:ASN:ND2	45:5:2656:U:OP1	2.44	0.50
31:f:94:ALA:O	31:f:97:ILE:HG13	2.12	0.50
45:5:106:A:O4'	45:5:336:A:H1'	2.10	0.50
45:5:2097:A:H2'	45:5:2097:A:N3	2.26	0.50
49:2:945:U:C4	49:2:946:U:C4	2.99	0.50
49:2:1600:G:O3'	49:2:1601:A:H4'	2.11	0.50
2:B:95:THR:HB	2:B:96:PRO:HD2	1.93	0.50
2:B:234:ARG:NH1	2:B:271:GLN:O	2.39	0.50
30:e:111:ILE:O	30:e:114:ARG:N	2.45	0.50
45:5:1355:G:C5	45:5:1356:U:C5	3.00	0.50
45:5:4468:U:H3	45:5:4708:A:H62	1.58	0.50
47:8:54:C:C6	47:8:54:C:O5'	2.65	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:339:A:H2'	49:2:340:C:C5	2.46	0.50
49:2:687:C:O2	49:2:687:C:H2'	2.11	0.50
51:BB:59:LEU:N	51:BB:59:LEU:HD23	2.27	0.50
85:4:6176:U:N1	85:4:6177:U:C6	2.79	0.50
45:5:1558:A:H8	45:5:1558:A:O5'	1.94	0.50
49:2:1017:U:O2'	64:OO:51:GLY:C	2.54	0.50
3:C:286:ASN:HB2	3:C:292:ILE:HD11	1.94	0.50
17:R:82:LYS:N	45:5:2812:A:OP1	2.43	0.50
45:5:1984:A:N7	45:5:2010:A:O2'	2.38	0.50
45:5:4485:C:N4	45:5:4486:C:H41	2.09	0.50
45:5:4921:C:OP2	45:5:4922:C:C4	2.65	0.50
48:K:123:ILE:HG12	85:4:6040:U:H5''	1.93	0.50
49:2:173:A:C5	49:2:174:C:C5	3.00	0.50
55:FF:67:GLN:HE21	55:FF:69:PHE:HE2	1.60	0.50
2:B:45:ALA:CB	2:B:181:MET:HE1	2.42	0.49
4:D:166:ALA:HB1	4:D:171:LEU:HD22	1.94	0.49
13:N:8:GLN:HE22	45:5:278:G:H5'	1.76	0.49
17:R:104:ARG:HD2	45:5:2898:G:OP1	2.12	0.49
64:OO:125:LEU:HD22	64:OO:129:TYR:CE2	2.47	0.49
67:RR:86:GLN:HE22	67:RR:122:ALA:HB2	1.77	0.49
85:4:6088:C:H3'	85:4:6088:C:H6	1.76	0.49
85:4:6177:U:C3'	85:4:6178:U:H4'	2.35	0.49
13:N:88:GLY:C	13:N:92:LEU:HD21	2.37	0.49
15:P:122:ALA:HB1	15:P:123:PRO:CD	2.42	0.49
31:f:36:ARG:O	31:f:37:ASP:C	2.55	0.49
45:5:1932:A:C2'	45:5:1933:G:O5'	2.59	0.49
45:5:3605:C:C4	45:5:3606:U:C5	3.00	0.49
45:5:3642:A:OP2	45:5:3644:U:P	2.70	0.49
49:2:403:G:C6	49:2:404:G:C5	3.01	0.49
49:2:655:A:H8	49:2:657:U:H2'	1.77	0.49
49:2:805:U:H2'	49:2:806:U:O4'	2.12	0.49
49:2:1588:A:H2'	49:2:1589:A:H8	1.77	0.49
56:GG:91:ARG:HD2	76:aa:103:HIS:CE1	2.47	0.49
57:HH:1:MET:HE3	57:HH:109:LEU:HD12	1.93	0.49
60:KK:40:LYS:O	60:KK:43:VAL:N	2.42	0.49
3:C:195:LYS:NZ	45:5:2334:C:OP2	2.41	0.49
4:D:219:TYR:CZ	4:D:227:ILE:HD11	2.47	0.49
25:Z:81:MET:HE2	32:g:96:LEU:HD21	1.94	0.49
41:p:21:SER:O	41:p:25:MET:HE3	2.13	0.49
45:5:4892:A:H2'	45:5:4893:A:O4'	2.12	0.49
64:OO:88:LEU:HD11	64:OO:122:ILE:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6174:G:OP1	85:4:6175:G:N3	2.46	0.49
85:4:6178:U:C1'	85:4:6179:U:H1'	2.42	0.49
7:G:104:LEU:O	7:G:105:THR:C	2.56	0.49
8:H:92:MET:SD	8:H:161:ILE:HD11	2.52	0.49
13:N:11:TRP:CZ3	13:N:23:LEU:HD21	2.47	0.49
14:O:19:LEU:O	14:O:20:ALA:C	2.55	0.49
14:O:74:ARG:NH2	45:5:4712:C:OP1	2.45	0.49
44:t:56:LEU:HD11	44:t:82:ILE:HD12	1.94	0.49
48:K:123:ILE:HG12	85:4:6040:U:O5'	2.12	0.49
85:4:6034:A:H2	85:4:6091:U:C4	2.27	0.49
85:4:6197:A:N6	85:4:6198:A:C6	2.80	0.49
2:B:46:PHE:CE2	2:B:207:VAL:HG22	2.47	0.49
2:B:134:CYS:O	2:B:135:LYS:C	2.55	0.49
15:P:10:ASN:O	15:P:10:ASN:OD1	2.30	0.49
49:2:1005:G:H2'	49:2:1006:C:O4'	2.12	0.49
49:2:1853:C:H2'	49:2:1853:C:O2	2.12	0.49
54:EE:72:VAL:HG23	61:LL:20:VAL:HG21	1.95	0.49
59:JJ:76:THR:HG23	59:JJ:108:PRO:HG2	1.95	0.49
25:Z:57:MET:HE1	25:Z:65:ARG:NH2	2.27	0.49
45:5:415:G:C6	47:8:20:A:C2	3.01	0.49
45:5:2279:A:N7	45:5:2280:G:N3	2.60	0.49
45:5:4174:U:O2'	45:5:4175:G:H5'	2.12	0.49
54:EE:169:ASP:O	54:EE:187:LYS:HA	2.13	0.49
7:G:260:VAL:HG11	7:G:268:LEU:HG	1.93	0.49
15:P:74:LYS:NZ	45:5:4970:C:OP1	2.36	0.49
17:R:7:GLN:HG2	17:R:32:ILE:O	2.13	0.49
32:g:5:LEU:HD11	32:g:32:TYR:CZ	2.48	0.49
32:g:40:LYS:NZ	45:5:2601:A:OP1	2.45	0.49
45:5:1279:A:C4	45:5:1281:G:C6	3.01	0.49
45:5:4265:U:H4'	45:5:4266:G:O4'	2.13	0.49
45:5:4277:G:N2	45:5:4332:C:C4	2.81	0.49
48:K:119:GLN:O	85:4:6038:G:OP2	2.29	0.49
48:K:128:LEU:CD1	85:4:6038:G:H1	2.26	0.49
49:2:78:C:OP1	57:HH:173:ALA:HB3	2.13	0.49
49:2:184:G:C6	49:2:185:G:C6	3.00	0.49
53:DD:214:LEU:O	53:DD:215:MET:C	2.56	0.49
58:II:121:THR:O	58:II:122:LEU:C	2.55	0.49
60:KK:63:LEU:HD22	60:KK:67:ASP:OD1	2.13	0.49
75:ZZ:84:LYS:HG3	75:ZZ:85:ASN:HD22	1.76	0.49
81:ff:119:VAL:HG23	81:ff:121:THR:HG23	1.95	0.49
24:Y:43:ASN:HD22	24:Y:127:GLN:HE21	1.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:s:112:ARG:NH1	45:5:1969:G:OP1	2.45	0.49
45:5:454:U:C4	45:5:455:C:N4	2.81	0.49
45:5:2758:G:O2'	45:5:2765:A:N3	2.45	0.49
47:8:27:U:C2'	47:8:28:C:O5'	2.60	0.49
48:K:128:LEU:HD13	48:K:135:PRO:CD	2.43	0.49
49:2:1148:A:H4'	49:2:1149:A:O5'	2.12	0.49
71:VV:32:LEU:O	71:VV:33:GLU:C	2.56	0.49
84:jj:32:THR:O	84:jj:32:THR:OG1	2.30	0.49
85:4:6094:U:H2'	85:4:6095:U:H4'	1.95	0.49
3:C:143:ARG:CG	3:C:178:ASN:HB3	2.43	0.49
4:D:279:ARG:NH2	46:7:61:G:O3'	2.46	0.49
14:O:16:LEU:CB	14:O:43:ILE:HG23	2.42	0.49
14:O:96:GLN:NE2	45:5:3888:G:O6	2.46	0.49
15:P:10:ASN:OD1	15:P:10:ASN:C	2.56	0.49
37:l:17:GLN:O	37:l:18:LYS:C	2.56	0.49
42:r:51:VAL:HB	42:r:113:ARG:HD3	1.94	0.49
45:5:929:A:H2'	45:5:930:G:O4'	2.12	0.49
45:5:4463:U:H3	45:5:4513:A:H61	1.61	0.49
49:2:1563:G:C2	49:2:1573:G:C2	3.01	0.49
72:WW:2:GLN:CD	72:WW:6:GLY:HA2	2.37	0.49
4:D:65:ALA:HB2	4:D:74:ILE:HD13	1.94	0.49
11:L:185:ALA:CB	34:i:7:MET:HE1	2.42	0.49
12:M:52:PHE:CD1	12:M:55:MET:HE2	2.48	0.49
13:N:12:ARG:NH2	45:5:279:A:OP2	2.46	0.49
16:Q:79:THR:HG22	16:Q:136:THR:HG22	1.95	0.49
20:U:38:ASN:O	20:U:42:PHE:N	2.43	0.49
23:X:153:ILE:HD11	23:X:155:ILE:CD1	2.42	0.49
33:h:4:ILE:HG21	33:h:20:GLN:HE22	1.77	0.49
45:5:284:G:H2'	45:5:284:G:N3	2.28	0.49
45:5:2662:G:C2	45:5:2663:G:C4	3.01	0.49
45:5:3659:G:C6	45:5:3660:C:N3	2.81	0.49
47:8:35:C:O2	47:8:35:C:H2'	2.12	0.49
52:CC:103:MET:HG2	52:CC:104:ASP:N	2.28	0.49
64:OO:91:LEU:HD12	64:OO:125:LEU:HD12	1.95	0.49
45:5:2320:G:H2'	45:5:2321:G:C8	2.48	0.48
45:5:2702:C:N3	45:5:2715:G:C6	2.81	0.48
83:hh:156:PHE:HA	83:hh:165:ILE:HG22	1.95	0.48
83:hh:226:HIS:O	83:hh:227:LEU:HD23	2.13	0.48
25:Z:81:MET:HE1	28:c:59:GLU:OE1	2.13	0.48
45:5:1902:G:C5	45:5:2075:G:C2	3.01	0.48
45:5:4653:C:C4	45:5:4654:C:N4	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:K:142:GLU:CD	48:K:144:MET:HE2	2.38	0.48
49:2:562:U:H2'	49:2:563:G:C8	2.47	0.48
49:2:1207:G:N2	85:4:6216:U:O2'	2.46	0.48
49:2:1646:C:OP1	67:RR:138:ARG:NH1	2.43	0.48
71:VV:25:THR:HG22	71:VV:86:LYS:HG3	1.95	0.48
85:4:6053:U:C2	85:4:6073:A:N1	2.81	0.48
85:4:6070:A:N3	85:4:6070:A:C2'	2.74	0.48
3:C:323:ARG:NH2	45:5:977:C:O2	2.46	0.48
18:S:120:ARG:N	18:S:120:ARG:HD2	2.28	0.48
45:5:1314:C:O2'	45:5:1315:C:OP2	2.19	0.48
45:5:4687:A:N1	45:5:4704:C:C5	2.81	0.48
51:BB:5:LEU:C	51:BB:7:VAL:H	2.21	0.48
51:BB:132:GLN:N	51:BB:133:PRO:HD2	2.28	0.48
52:CC:205:TYR:CD2	52:CC:206:PRO:HD2	2.49	0.48
83:hh:88:ARG:HD3	83:hh:97:THR:HG21	1.94	0.48
85:4:6070:A:HO2'	85:4:6172:G:H8	1.49	0.48
31:f:88:PHE:CE1	31:f:92:LEU:HD11	2.49	0.48
41:p:45:THR:O	41:p:45:THR:HG22	2.13	0.48
45:5:1332:C:H2'	45:5:1333:A:H8	1.77	0.48
45:5:2263:A:H2'	45:5:2264:C:C6	2.48	0.48
45:5:3611:A:N1	45:5:3612:C:N3	2.61	0.48
47:8:153:C:N3	47:8:154:G:C5	2.82	0.48
62:MM:16:ILE:HD12	62:MM:16:ILE:O	2.14	0.48
69:TT:46:ARG:NH2	69:TT:52:LEU:HD21	2.28	0.48
84:jj:76:THR:HG23	84:jj:79:GLN:OE1	2.12	0.48
85:4:6095:U:O5'	85:4:6098:A:P	2.70	0.48
31:f:28:LEU:N	31:f:28:LEU:CD1	2.76	0.48
41:p:17:ARG:NH2	45:5:1577:G:OP1	2.42	0.48
44:t:109:ILE:HD13	44:t:133:LEU:HD21	1.95	0.48
49:2:997:A:H2'	49:2:998:A:O4'	2.13	0.48
83:hh:36:ARG:HD2	83:hh:65:PHE:CE2	2.49	0.48
84:jj:35:ILE:HD13	84:jj:127:CYS:SG	2.53	0.48
85:4:6196:A:C5'	85:4:6196:A:C8	2.96	0.48
5:E:69:ALA:HB2	45:5:1071:C:C4	2.48	0.48
14:O:79:ILE:CG2	14:O:138:LEU:HD11	2.32	0.48
25:Z:17:ARG:NH1	45:5:2578:G:N7	2.61	0.48
31:f:45:LYS:HD3	31:f:107:PRO:HD2	1.96	0.48
43:s:59:THR:OG1	45:5:1961:G:O5'	2.30	0.48
45:5:4:G:C6	47:8:154:G:N1	2.82	0.48
45:5:973:G:H2'	45:5:973:G:N3	2.29	0.48
45:5:4619:U:C2	45:5:4620:U:C6	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:8:122:G:C2	47:8:128:C:N4	2.82	0.48
49:2:589:G:N7	49:2:591:U:H2'	2.29	0.48
54:EE:49:ILE:HG23	54:EE:87:TYR:HB2	1.94	0.48
85:4:6203:U:O2'	85:4:6204:A:P	2.71	0.48
2:B:160:ILE:HD13	2:B:194:LEU:HD13	1.95	0.48
9:I:33:ILE:HG21	9:I:36:LEU:HD23	1.96	0.48
11:L:71:ARG:NH1	45:5:102:G:OP1	2.46	0.48
24:Y:21:ALA:HB1	24:Y:22:PRO:HD2	1.94	0.48
45:5:2819:U:H2'	45:5:2820:C:H6	1.79	0.48
49:2:1034:A:C2	49:2:1082:A:C2	3.01	0.48
58:II:43:LEU:HD23	58:II:72:PHE:CE2	2.49	0.48
2:B:347:LEU:O	2:B:348:ARG:HB2	2.14	0.48
20:U:27:HIS:N	20:U:28:PRO:CD	2.77	0.48
45:5:419:A:C2	45:5:420:A:C4	3.02	0.48
45:5:1614:C:N4	45:5:1615:C:N4	2.62	0.48
45:5:1851:G:C6	45:5:1852:U:C4	3.01	0.48
45:5:4513:A:H2'	45:5:4514:G:O4'	2.14	0.48
49:2:1253:A:O2'	49:2:1666:C:O2'	2.29	0.48
17:R:105:LEU:HD21	17:R:139:MET:HE3	1.95	0.48
41:p:73:THR:O	41:p:77:VAL:HG23	2.14	0.48
44:t:59:THR:HG21	45:5:1975:G:N7	2.28	0.48
45:5:4468:U:C2	45:5:4708:A:N7	2.80	0.48
49:2:30:C:N4	49:2:31:U:C4	2.82	0.48
49:2:921:G:C8	78:cc:21:LYS:O	2.67	0.48
50:3:54:G:H2'	50:3:55:G:O4'	2.14	0.48
68:SS:17:ILE:HG22	68:SS:69:ILE:HD11	1.96	0.48
2:B:8:ALA:O	45:5:4492:U:OP2	2.32	0.48
3:C:302:LEU:HD23	16:Q:39:THR:HG23	1.94	0.48
14:O:17:GLY:CA	45:5:2052:G:O3'	2.61	0.48
36:k:28:ASN:O	36:k:29:LYS:C	2.57	0.48
43:s:47:LEU:O	43:s:51:ALA:HB3	2.14	0.48
45:5:335:A:H2'	45:5:336:A:C8	2.49	0.48
45:5:2602:G:O4'	45:5:2742:G:H2'	2.14	0.48
45:5:4931:G:C6	45:5:4932:U:C4	3.02	0.48
47:8:13:G:C6	47:8:14:U:C5	3.01	0.48
49:2:323:C:O2	49:2:329:G:N2	2.35	0.48
55:FF:19:MET:HE3	55:FF:108:ARG:HD3	1.95	0.48
83:hh:36:ARG:O	83:hh:65:PHE:CD1	2.67	0.48
2:B:240:LEU:HB2	2:B:248:LEU:CA	2.43	0.47
32:g:75:SER:O	32:g:76:ARG:HB2	2.14	0.47
45:5:3633:C:N4	45:5:3634:G:O6	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:3757:G:C2	45:5:3768:U:C2	3.01	0.47
45:5:4957:C:H3'	45:5:4958:C:H5''	1.96	0.47
49:2:1469:A:C6	49:2:1470:C:C4	3.01	0.47
64:OO:85:PRO:HG2	64:OO:129:TYR:CE2	2.48	0.47
69:TT:98:VAL:C	69:TT:99:LEU:HD22	2.39	0.47
84:jj:10:ARG:HE	84:jj:14:ILE:HD11	1.79	0.47
2:B:101:THR:HG23	45:5:4724:A:H1'	1.96	0.47
10:J:73:THR:OG1	46:7:39:C:N3	2.46	0.47
12:M:93:LYS:HA	12:M:96:GLU:HG3	1.96	0.47
18:S:117:HIS:O	18:S:118:ARG:C	2.57	0.47
43:s:28:PHE:CE2	43:s:91:THR:HG21	2.49	0.47
45:5:1796:U:C5	45:5:1797:G:C8	3.02	0.47
47:8:121:G:N1	47:8:122:G:N7	2.62	0.47
49:2:374:G:C6	49:2:375:U:C4	3.02	0.47
49:2:492:C:H4'	49:2:493:A:OP1	2.14	0.47
49:2:1531:A:O2'	49:2:1532:C:O4'	2.31	0.47
49:2:1617:G:H2'	49:2:1619:A:OP2	2.14	0.47
85:4:6034:A:C6	85:4:6090:A:N1	2.81	0.47
85:4:6123:G:O6	85:4:6163:G:C2'	2.60	0.47
3:C:8:ILE:HD11	3:C:24:LEU:CD1	2.44	0.47
13:N:104:GLU:HA	13:N:160:GLU:HG3	1.95	0.47
16:Q:89:ASP:OD1	16:Q:91:ARG:NH2	2.47	0.47
17:R:138:LEU:O	17:R:139:MET:C	2.57	0.47
29:d:75:LYS:HB2	29:d:79:ASN:O	2.15	0.47
45:5:1360:G:C5	45:5:1361:G:N7	2.82	0.47
45:5:2085:G:N2	45:5:2086:G:C4	2.82	0.47
45:5:2503:G:C2	45:5:4084:G:C5	3.03	0.47
45:5:2757:A:N6	45:5:2758:G:O6	2.47	0.47
45:5:4269:G:C6	45:5:4270:C:C4	3.02	0.47
48:K:194:LEU:HD21	48:K:197:ASN:CB	2.43	0.47
49:2:925:G:OP1	64:OO:121:ARG:NH2	2.40	0.47
53:DD:141:VAL:HG12	53:DD:142:LYS:N	2.27	0.47
60:KK:108:ARG:HA	60:KK:113:GLN:HE21	1.78	0.47
83:hh:162:ASN:HB3	83:hh:164:ILE:HD12	1.97	0.47
85:4:6201:C:H2'	85:4:6202:C:C6	2.50	0.47
12:M:132:ARG:NH2	45:5:4895:C:C2	2.83	0.47
14:O:109:PRO:C	14:O:111:PRO:HG2	2.39	0.47
16:Q:28:LEU:HD11	16:Q:103:LEU:HD21	1.95	0.47
29:d:28:ASN:C	29:d:28:ASN:OD1	2.57	0.47
45:5:331:G:C2	45:5:332:C:C5	3.02	0.47
45:5:930:G:C8	45:5:930:G:C3'	2.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:1274:A:C2	45:5:1275:G:C4	3.03	0.47
45:5:1314:C:C2	45:5:1315:C:C5	3.03	0.47
45:5:2279:A:C8	45:5:2280:G:N3	2.83	0.47
45:5:2290:C:H1'	45:5:2321:G:N3	2.29	0.47
45:5:2439:G:C6	45:5:2440:U:C4	3.02	0.47
45:5:3656:A:H4'	45:5:3747:A:C6	2.49	0.47
48:K:126:PRO:CB	85:4:6087:G:OP2	2.61	0.47
49:2:445:A:H4'	59:JJ:50:GLY:HA2	1.97	0.47
49:2:806:U:C2	49:2:858:A:C2	3.03	0.47
74:YY:18:ARG:O	74:YY:19:ASP:C	2.56	0.47
80:ee:42:CYS:O	80:ee:45:GLN:N	2.43	0.47
81:ff:79:LEU:N	81:ff:79:LEU:HD12	2.28	0.47
83:hh:88:ARG:HD2	83:hh:97:THR:HG21	1.95	0.47
85:4:6055:C:C5	85:4:6056:A:N7	2.82	0.47
85:4:6200:A:H62	85:4:6204:A:H2	1.61	0.47
4:D:163:LEU:C	4:D:163:LEU:HD12	2.39	0.47
6:F:225:HIS:O	6:F:226:PHE:C	2.57	0.47
38:m:70:CYS:SG	38:m:89:CYS:SG	3.10	0.47
49:2:348:A:C2	49:2:349:A:C4	3.02	0.47
49:2:1372:U:H2'	49:2:1373:C:C6	2.50	0.47
49:2:1531:A:H2'	49:2:1532:C:O4'	2.14	0.47
56:GG:61:PHE:O	56:GG:62:ARG:C	2.57	0.47
59:JJ:62:VAL:HG12	59:JJ:77:ARG:HA	1.97	0.47
74:YY:43:GLY:O	74:YY:44:ALA:HB2	2.14	0.47
1:A:67:TYR:CD1	45:5:4086:G:C2	3.02	0.47
5:E:165:VAL:HB	5:E:178:VAL:HG22	1.97	0.47
11:L:47:ALA:HB3	11:L:48:PRO:HD3	1.96	0.47
26:a:2:PRO:HG2	26:a:5:LEU:HD12	1.96	0.47
45:5:727:C:H2'	45:5:728:U:C6	2.50	0.47
45:5:1371:A:N1	47:8:28:C:O2'	2.47	0.47
45:5:1660:U:O2	45:5:2345:G:H3'	2.14	0.47
45:5:2465:C:H1'	45:5:3672:G:N2	2.29	0.47
45:5:3795:A:O2'	49:2:1719:A:N1	2.46	0.47
45:5:4496:A:C2	45:5:4505:C:O2	2.68	0.47
49:2:360:A:C2	49:2:362:C:C2	3.03	0.47
49:2:634:A:C2	49:2:635:G:N7	2.82	0.47
49:2:818:A:C2	49:2:847:A:C8	3.02	0.47
49:2:1203:G:C6	49:2:1204:A:C6	3.02	0.47
66:QQ:111:MET:HE2	69:TT:117:ILE:O	2.15	0.47
1:A:40:TYR:CD2	1:A:40:TYR:C	2.93	0.47
3:C:289:LEU:HD12	3:C:289:LEU:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:340:ILE:HG21	5:E:52:LEU:CD1	2.44	0.47
14:O:27:VAL:HG12	14:O:98:ALA:HB1	1.95	0.47
23:X:60:TYR:CE2	23:X:62:ARG:NE	2.82	0.47
26:a:73:VAL:CG1	26:a:111:VAL:HG22	2.45	0.47
45:5:6:C:H2'	45:5:7:C:C6	2.50	0.47
45:5:63:G:C5	45:5:333:U:C5	3.02	0.47
45:5:332:C:H2'	45:5:333:U:O5'	2.14	0.47
45:5:699:C:H2'	45:5:700:G:O5'	2.14	0.47
45:5:1360:G:C4	45:5:1361:G:C8	3.03	0.47
45:5:4486:C:H2'	45:5:4487:A:O4'	2.14	0.47
45:5:4953:G:H2'	45:5:4954:G:O4'	2.15	0.47
45:5:4965:U:O2	45:5:4965:U:O4'	2.31	0.47
47:8:29:G:H2'	47:8:30:U:O4'	2.15	0.47
48:K:125:GLY:HA3	85:4:6087:G:C8	2.46	0.47
49:2:886:A:N6	49:2:901:G:N3	2.62	0.47
49:2:1520:G:N2	49:2:1521:C:C4	2.82	0.47
49:2:1599:U:OP2	76:aa:46:ASN:ND2	2.47	0.47
49:2:1664:A:C8	49:2:1666:C:N4	2.82	0.47
49:2:1696:C:O3'	49:2:1702:G:O2'	2.20	0.47
53:DD:103:LYS:O	53:DD:130:ILE:HA	2.14	0.47
54:EE:66:ILE:O	54:EE:70:THR:HG23	2.15	0.47
69:TT:98:VAL:O	69:TT:99:LEU:HD13	2.14	0.47
74:YY:68:LYS:HE3	81:ff:82:VAL:HG22	1.94	0.47
84:jj:146:PHE:CE1	84:jj:278:VAL:HG21	2.50	0.47
5:E:68:LYS:HD3	45:5:980:U:OP2	2.15	0.47
32:g:59:VAL:HG21	32:g:63:VAL:HG11	1.96	0.47
44:t:98:ILE:HG22	45:5:1978:C:H5''	1.97	0.47
49:2:96:C:H2'	49:2:97:U:O4'	2.14	0.47
49:2:98:C:OP2	49:2:426:A:O2'	2.27	0.47
49:2:126:G:H2'	57:HH:199:THR:HG21	1.97	0.47
49:2:223:C:C2	49:2:299:A:C2	3.02	0.47
49:2:305:U:O4	59:JJ:184:ARG:NH1	2.48	0.47
60:KK:143:ASN:C	60:KK:144:ILE:HG13	2.38	0.47
5:E:185:ASN:O	5:E:186:ARG:HB2	2.13	0.47
6:F:178:LEU:O	6:F:180:LYS:N	2.48	0.47
19:T:68:THR:HG22	27:b:36:ASP:HB3	1.95	0.47
23:X:129:ARG:NH2	23:X:133:GLU:OE1	2.48	0.47
45:5:453:G:O2'	45:5:705:G:OP1	2.31	0.47
45:5:1286:C:H2'	45:5:1286:C:O2	2.15	0.47
45:5:1667:A:C6	45:5:2280:G:C8	3.03	0.47
45:5:2311:C:C4	45:5:2312:U:C4	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:2363:A:C2	45:5:3860:A:C4	3.03	0.47
48:K:125:GLY:CA	85:4:6087:G:H8	2.20	0.47
55:FF:132:GLY:N	55:FF:136:ILE:O	2.45	0.47
74:YY:28:LYS:O	74:YY:29:LYS:C	2.56	0.47
85:4:6198:A:H2'	85:4:6199:A:H5'	0.48	0.47
2:B:122:TRP:CE2	2:B:127:LYS:HE3	2.50	0.47
2:B:240:LEU:N	2:B:248:LEU:O	2.43	0.47
6:F:42:ARG:O	6:F:46:ARG:N	2.48	0.47
14:O:196:LEU:O	14:O:197:LYS:C	2.58	0.47
45:5:11:G:C2'	45:5:12:A:H5''	2.45	0.47
45:5:711:A:H2'	45:5:712:C:C6	2.49	0.47
45:5:1691:G:C2	45:5:1846:G:C2	3.03	0.47
45:5:1879:C:C2'	45:5:1880:G:O5'	2.63	0.47
45:5:2622:G:H2'	45:5:2623:A:O4'	2.15	0.47
45:5:4196:G:N1	50:3:86:C:OP1	2.40	0.47
49:2:687:C:C4	58:II:118:ARG:NH2	2.83	0.47
53:DD:233:LEU:O	53:DD:234:GLY:C	2.55	0.47
85:4:6070:A:H3'	85:4:6071:A:H5''	1.97	0.47
3:C:74:ALA:O	3:C:75:ARG:CB	2.63	0.46
5:E:168:LEU:HD13	5:E:211:ILE:HD13	1.97	0.46
8:H:173:ARG:NH1	38:m:101:VAL:HG23	2.30	0.46
11:L:65:ARG:HD2	26:a:69:PHE:CD1	2.50	0.46
45:5:1285:U:N3	45:5:1286:C:C5	2.84	0.46
45:5:3717:A:C6	45:5:3718:A:C6	3.02	0.46
45:5:4399:U:C4	45:5:4400:G:C5	3.03	0.46
45:5:4701:A:N7	45:5:4702:G:C8	2.83	0.46
49:2:42:A:C6	49:2:43:U:C4	3.03	0.46
49:2:1743:G:O2'	49:2:1791:A:N6	2.49	0.46
64:OO:116:ILE:O	64:OO:116:ILE:HG22	2.15	0.46
85:4:6031:A:H1'	85:4:6032:A:C8	2.49	0.46
85:4:6063:A:N6	85:4:6207:A:C5'	2.78	0.46
85:4:6174:G:N7	85:4:6205:A:C8	2.82	0.46
15:P:36:ILE:HA	15:P:39:MET:HE2	1.97	0.46
16:Q:32:TYR:HA	16:Q:35:LEU:HB2	1.97	0.46
45:5:376:A:C6	45:5:377:A:C6	3.03	0.46
45:5:415:G:N1	47:8:20:A:C2	2.84	0.46
45:5:1667:A:N7	45:5:2280:G:N7	2.61	0.46
45:5:2624:G:C5	45:5:2625:U:C5	3.03	0.46
45:5:4687:A:N1	45:5:4704:C:C4	2.83	0.46
49:2:46:A:C2	49:2:473:A:N1	2.84	0.46
49:2:1559:C:H2'	49:2:1560:U:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:HH:55:GLY:N	57:HH:63:MET:SD	2.89	0.46
61:LL:2:LEU:HD12	61:LL:2:LEU:O	2.16	0.46
64:OO:91:LEU:CD1	64:OO:125:LEU:HD12	2.45	0.46
7:G:133:ILE:HD11	13:N:18:VAL:HG13	1.97	0.46
11:L:86:ILE:CD1	11:L:96:ILE:HD13	2.45	0.46
13:N:99:GLN:O	13:N:101:VAL:N	2.48	0.46
26:a:48:TYR:O	26:a:49:HIS:CG	2.68	0.46
29:d:73:TRP:O	29:d:75:LYS:N	2.49	0.46
45:5:4:G:C6	47:8:154:G:C6	3.03	0.46
45:5:981:C:H2'	45:5:982:U:O4'	2.16	0.46
45:5:1420:A:H4'	45:5:1421:G:OP1	2.14	0.46
45:5:4443:C:H1'	45:5:4444:C:H5	1.80	0.46
45:5:4896:G:O2'	45:5:4897:G:H5'	2.15	0.46
47:8:14:U:C4	47:8:15:G:C6	3.03	0.46
49:2:589:G:C2	49:2:591:U:C5	3.04	0.46
49:2:1797:U:C4	49:2:1798:C:C4	3.03	0.46
61:LL:49:MET:HE2	61:LL:52:LEU:HD23	1.97	0.46
85:4:6074:A:H2'	85:4:6074:A:N3	2.29	0.46
14:O:168:TYR:OH	45:5:4768:G:OP1	2.31	0.46
30:e:63:ASN:OD1	30:e:64:LYS:N	2.49	0.46
36:k:35:LYS:NZ	45:5:2695:A:OP1	2.48	0.46
40:o:54:PRO:HB3	45:5:4379:A:C8	2.50	0.46
45:5:750:U:H2'	45:5:751:G:O4'	2.16	0.46
45:5:974:C:C4	45:5:1282:G:C8	3.04	0.46
45:5:1744:U:O4	45:5:1745:G:O6	2.33	0.46
45:5:1804:A:N7	45:5:1833:G:C2	2.84	0.46
45:5:2638:G:N1	45:5:2639:U:C4	2.83	0.46
45:5:3676:G:C5	45:5:3677:U:C5	3.04	0.46
49:2:690:G:H2'	49:2:691:G:O4'	2.14	0.46
51:BB:30:LEU:HD21	51:BB:35:GLU:CG	2.46	0.46
66:QQ:44:ARG:HG2	66:QQ:84:ILE:HD11	1.98	0.46
3:C:154:VAL:HG12	3:C:155:GLU:N	2.31	0.46
14:O:108:ILE:HG23	14:O:108:ILE:O	2.16	0.46
45:5:2279:A:H2'	45:5:2280:G:O4'	2.15	0.46
45:5:3689:G:O2'	45:5:3818:U:OP1	2.34	0.46
45:5:3924:C:C2	45:5:3925:U:C5	3.04	0.46
49:2:450:C:O2	49:2:450:C:O4'	2.33	0.46
49:2:1240:A:H8	49:2:1267:C:O2'	1.98	0.46
49:2:1601:A:N7	49:2:1636:G:N1	2.63	0.46
51:BB:134:LEU:O	51:BB:137:ALA:HB3	2.15	0.46
75:ZZ:20:ARG:HB3	75:ZZ:76:TYR:CD1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:hh:156:PHE:CE2	83:hh:179:LEU:HD11	2.50	0.46
85:4:6199:A:N1	85:4:6200:A:C2	2.83	0.46
2:B:392:LEU:HD22	2:B:392:LEU:N	2.30	0.46
5:E:156:LEU:HD11	5:E:198:ILE:CD1	2.46	0.46
30:e:99:ILE:HG21	30:e:108:ARG:HG3	1.97	0.46
35:j:43:ARG:HG3	45:5:21:G:H5''	1.98	0.46
45:5:1362:G:C2	45:5:1376:C:C2	3.03	0.46
45:5:1759:G:N1	45:5:1774:C:O2	2.49	0.46
45:5:1890:G:C8	45:5:1890:G:O5'	2.69	0.46
45:5:2279:A:N7	45:5:2280:G:N2	2.64	0.46
45:5:2811:G:N1	45:5:2814:C:OP2	2.49	0.46
49:2:472:C:H2'	49:2:473:A:OP2	2.16	0.46
49:2:1839:U:H2'	49:2:1840:U:H6	1.80	0.46
49:2:1853:C:O2	49:2:1854:U:C6	2.69	0.46
58:II:194:LEU:HD11	64:OO:19:ARG:HH22	1.80	0.46
22:W:25:ASP:N	22:W:25:ASP:OD1	2.48	0.46
45:5:1472:C:O2	45:5:1493:G:C2	2.68	0.46
45:5:2655:C:C3'	45:5:2656:U:H5''	2.46	0.46
45:5:2724:G:C6	45:5:2726:G:O6	2.69	0.46
45:5:4475:G:H5''	45:5:4476:C:H5'	1.97	0.46
49:2:752:G:HO2'	49:2:753:C:H3'	1.79	0.46
49:2:806:U:C2	49:2:858:A:H2	2.33	0.46
51:BB:177:MET:O	51:BB:181:GLU:N	2.33	0.46
21:V:39:ILE:HG12	21:V:61:VAL:HG21	1.98	0.46
45:5:735:G:N2	45:5:929:A:N7	2.64	0.46
45:5:1395:U:O5'	45:5:1395:U:H6	1.98	0.46
45:5:4567:G:C2	45:5:4568:A:C8	3.03	0.46
45:5:4921:C:O3'	45:5:4922:C:O4'	2.34	0.46
49:2:1784:G:N2	49:2:1785:C:C2	2.84	0.46
53:DD:65:LYS:CG	53:DD:273:LEU:HD13	2.46	0.46
53:DD:236:PHE:O	53:DD:239:ALA:N	2.49	0.46
85:4:6063:A:N6	85:4:6207:A:H5'	2.30	0.46
11:L:50:PRO:HG3	33:h:121:VAL:HG22	1.97	0.46
16:Q:65:ARG:NH1	45:5:1502:G:OP2	2.49	0.46
27:b:8:THR:OG1	27:b:9:THR:N	2.49	0.46
45:5:376:A:C6	45:5:377:A:C5	3.04	0.46
45:5:1398:A:N6	45:5:1419:G:C2	2.83	0.46
45:5:1612:G:N3	45:5:1612:G:O2'	2.46	0.46
45:5:1910:G:N3	45:5:1917:A:H2	2.13	0.46
45:5:4120:U:H4'	45:5:4121:G:OP2	2.15	0.46
45:5:4125:C:H2'	45:5:4125:C:O2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:4490:C:N3	45:5:4491:G:N7	2.63	0.46
51:BB:130:ASP:HB3	51:BB:133:PRO:HG2	1.97	0.46
64:OO:81:ALA:HB1	64:OO:82:PRO:CD	2.45	0.46
69:TT:50:ILE:HD11	69:TT:67:VAL:HG22	1.98	0.46
75:ZZ:62:THR:HG23	75:ZZ:69:THR:HG22	1.97	0.46
84:jj:312:LEU:HD13	84:jj:317:VAL:HG22	1.97	0.46
85:4:6178:U:H2'	85:4:6179:U:H1'	1.98	0.46
1:A:40:TYR:CD1	45:5:4117:U:C4	3.04	0.46
1:A:69:PHE:CB	45:5:4125:C:C6	2.99	0.46
2:B:314:ILE:HD12	2:B:315:ASN:N	2.31	0.46
2:B:352:LEU:HD21	45:5:4678:G:H5'	1.98	0.46
6:F:122:VAL:O	6:F:122:VAL:HG12	2.17	0.46
9:I:143:GLN:O	9:I:145:LYS:N	2.49	0.46
18:S:78:PHE:CZ	18:S:102:THR:HA	2.51	0.46
24:Y:122:LYS:HG2	45:5:195:C:O3'	2.16	0.46
45:5:1355:G:C6	45:5:1356:U:C4	3.04	0.46
45:5:2076:G:H5''	45:5:2077:C:OP2	2.15	0.46
45:5:2590:G:C2'	45:5:2755:A:H61	2.29	0.46
45:5:2650:G:C6	45:5:2651:C:C4	3.04	0.46
45:5:4562:C:H2'	45:5:4563:U:O4'	2.15	0.46
46:7:32:A:C4	46:7:41:G:C5	3.03	0.46
49:2:532:C:O2'	49:2:533:A:OP1	2.34	0.46
49:2:654:A:C4	49:2:655:A:C2	3.04	0.46
49:2:895:G:O2'	49:2:896:U:O4'	2.22	0.46
49:2:934:G:OP2	49:2:993:G:N2	2.49	0.46
56:GG:102:LEU:HD13	76:aa:110:THR:CG2	2.45	0.46
1:A:82:ILE:HD12	1:A:86:GLN:NE2	2.30	0.45
2:B:197:ALA:O	2:B:198:ARG:C	2.58	0.45
7:G:201:GLU:HG2	7:G:230:MET:HE3	1.98	0.45
21:V:48:ARG:HD3	21:V:49:LEU:O	2.15	0.45
31:f:4:ARG:O	31:f:5:LEU:HD22	2.16	0.45
45:5:34:A:N1	45:5:35:U:C4	2.84	0.45
45:5:86:U:C5	45:5:97:G:N2	2.84	0.45
45:5:235:A:O2'	45:5:237:G:OP2	2.26	0.45
45:5:2288:G:N2	45:5:2290:C:C2	2.84	0.45
45:5:3969:G:O6	45:5:4053:A:C2	2.69	0.45
45:5:4066:U:H2'	45:5:4067:U:O4'	2.16	0.45
45:5:4926:C:H2'	45:5:4927:G:O5'	2.16	0.45
49:2:63:U:H2'	49:2:64:A:H5''	1.98	0.45
49:2:1035:A:H2'	49:2:1036:A:O4'	2.16	0.45
53:DD:191:VAL:HG11	53:DD:236:PHE:CD1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:bb:31:PRO:O	77:bb:32:LYS:C	2.59	0.45
84:jj:126:LEU:HD13	84:jj:132:HIS:ND1	2.30	0.45
2:B:2:SER:N	45:5:4517:A:OP2	2.50	0.45
3:C:292:ILE:O	3:C:298:ILE:HD12	2.16	0.45
6:F:78:GLY:O	19:T:143:THR:HG22	2.16	0.45
6:F:158:TYR:CE1	6:F:167:ALA:HB2	2.52	0.45
15:P:95:LEU:CD1	15:P:148:MET:HE1	2.45	0.45
20:U:72:VAL:HG11	20:U:83:LEU:HD11	1.99	0.45
21:V:108:ASN:HD22	21:V:109:LYS:N	2.14	0.45
30:e:126:ASN:OD1	30:e:126:ASN:N	2.47	0.45
45:5:1278:C:H2'	45:5:1279:A:O5'	2.15	0.45
45:5:2666:U:O2	45:5:2668:G:C8	2.69	0.45
45:5:5041:G:H3'	45:5:5041:G:C8	2.51	0.45
49:2:147:A:H2'	49:2:148:U:C6	2.51	0.45
49:2:1499:U:O2	49:2:1499:U:H2'	2.15	0.45
49:2:1601:A:OP2	49:2:1636:G:O6	2.34	0.45
49:2:1629:C:H2'	49:2:1630:A:O4'	2.16	0.45
49:2:1692:U:H2'	49:2:1693:G:C8	2.51	0.45
50:3:86:C:H2'	50:3:87:A:C2	2.51	0.45
3:C:109:ARG:HA	45:5:1341:U:H5'	1.98	0.45
3:C:298:ILE:HG13	16:Q:128:LEU:HD23	1.99	0.45
8:H:26:ILE:HG22	8:H:35:ARG:HG2	1.98	0.45
8:H:117:PHE:O	8:H:118:LEU:HB2	2.16	0.45
31:f:59:THR:HG22	31:f:60:PRO:HD2	1.97	0.45
45:5:346:G:C4	47:8:29:G:N2	2.85	0.45
45:5:1318:C:H2'	45:5:1319:U:O4'	2.17	0.45
45:5:1330:A:C2	45:5:2357:G:C5	3.04	0.45
45:5:1470:G:N1	45:5:1495:G:N7	2.64	0.45
45:5:1866:U:O4	45:5:1867:A:C6	2.70	0.45
45:5:3699:C:O2'	45:5:3775:A:O2'	2.25	0.45
49:2:67:C:C2	57:HH:162:LEU:HD23	2.52	0.45
49:2:417:C:C2'	49:2:418:A:OP1	2.64	0.45
49:2:664:A:C2	49:2:1164:G:C5	3.04	0.45
49:2:830:A:C2	49:2:845:G:N1	2.85	0.45
50:3:34:U:O2	50:3:36:A:C8	2.69	0.45
53:DD:83:LEU:HD11	72:WW:15:ARG:HG3	1.99	0.45
55:FF:156:VAL:O	55:FF:156:VAL:HG12	2.17	0.45
56:GG:102:LEU:HD13	76:aa:110:THR:HG22	1.97	0.45
58:II:47:ALA:O	58:II:48:ALA:HB2	2.16	0.45
75:ZZ:62:THR:HG23	75:ZZ:69:THR:CG2	2.47	0.45
82:gg:104:LYS:O	82:gg:117:LEU:HD12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6197:A:C4	85:4:6198:A:C8	3.04	0.45
3:C:89:GLN:O	3:C:90:GLY:O	2.34	0.45
5:E:94:THR:HG22	5:E:111:LYS:HG3	1.98	0.45
5:E:131:HIS:HB2	45:5:972:C:C5	2.50	0.45
6:F:148:SER:HG	6:F:244:ARG:HH11	1.59	0.45
14:O:14:HIS:CE1	14:O:119:VAL:HG13	2.51	0.45
24:Y:16:LYS:HE3	47:8:24:G:OP1	2.17	0.45
39:n:1:MET:HB2	49:2:1706:G:H5'	1.99	0.45
45:5:722:G:C2	45:5:723:A:C4	3.03	0.45
45:5:1838:A:C5	45:5:1839:U:C5	3.04	0.45
45:5:3743:G:C2	45:5:3744:G:C8	3.04	0.45
45:5:5015:G:C2	45:5:5033:G:C2	3.04	0.45
48:K:122:ARG:O	85:4:6041:C:N4	2.49	0.45
49:2:1149:A:H2'	49:2:1149:A:N3	2.31	0.45
53:DD:180:VAL:HG11	53:DD:184:VAL:HG22	1.98	0.45
73:XX:89:TRP:O	73:XX:92:ASN:N	2.24	0.45
85:4:6196:A:C8	85:4:6196:A:H5''	2.51	0.45
6:F:106:LYS:O	6:F:110:LEU:HG	2.17	0.45
12:M:123:ILE:O	12:M:127:VAL:N	2.46	0.45
16:Q:172:ARG:NH2	26:a:56:VAL:O	2.47	0.45
24:Y:15:ARG:NH1	45:5:230:G:OP1	2.49	0.45
45:5:1559:G:C2	45:5:1560:A:C4	3.04	0.45
45:5:1894:C:H2'	45:5:1895:G:O5'	2.17	0.45
45:5:2634:C:H2'	45:5:2635:U:H6	1.80	0.45
45:5:2820:C:O2	45:5:2820:C:H2'	2.17	0.45
45:5:3641:U:C5	45:5:3646:A:N7	2.75	0.45
45:5:4075:U:C5	45:5:4169:G:C6	3.04	0.45
49:2:1229:G:C5	49:2:1230:C:C5	3.04	0.45
84:jj:59:ALA:HB3	84:jj:72:LEU:HD21	1.96	0.45
85:4:6182:A:N6	85:4:6197:A:C5'	2.74	0.45
2:B:58:ARG:NH1	2:B:60:VAL:HG22	2.31	0.45
3:C:221:PHE:HB3	3:C:227:ILE:HG21	1.99	0.45
12:M:105:THR:HG22	12:M:106:ASP:N	2.29	0.45
15:P:36:ILE:HG23	15:P:37:LYS:N	2.32	0.45
15:P:73:ALA:O	15:P:74:LYS:C	2.58	0.45
37:l:41:ARG:HG2	37:l:41:ARG:HH11	1.81	0.45
45:5:4382:G:C2'	45:5:4383:U:O5'	2.64	0.45
49:2:589:G:C5	49:2:591:U:H2'	2.52	0.45
49:2:867:G:C6	49:2:868:G:C6	3.04	0.45
49:2:1653:U:H2'	49:2:1654:G:C1'	2.47	0.45
51:BB:16:LEU:HD22	68:SS:96:ILE:CD1	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:NN:64:LEU:O	63:NN:68:LEU:HD13	2.16	0.45
79:dd:50:VAL:HG12	79:dd:51:ARG:O	2.16	0.45
85:4:6199:A:H1'	85:4:6200:A:H4'	1.99	0.45
20:U:45:GLU:C	20:U:45:GLU:CD	2.84	0.45
31:f:28:LEU:HG	31:f:101:ILE:CD1	2.47	0.45
32:g:59:VAL:HG13	32:g:64:LEU:CD1	2.47	0.45
45:5:361:C:C2	45:5:378:A:C2	3.05	0.45
45:5:1752:G:C6	45:5:1753:G:N7	2.85	0.45
45:5:2519:U:H1'	45:5:2520:C:C6	2.52	0.45
45:5:2553:A:C8	45:5:2554:U:C2	3.05	0.45
45:5:2662:G:N2	45:5:2663:G:C4	2.85	0.45
49:2:551:U:O2'	81:ff:117:ASN:OD1	2.34	0.45
49:2:1220:A:N6	49:2:1221:G:C6	2.85	0.45
49:2:1258:A:C4	49:2:1663:A:C2	3.05	0.45
49:2:1607:A:N6	49:2:1632:G:H1'	2.31	0.45
51:BB:176:TRP:O	51:BB:180:ARG:N	2.47	0.45
85:4:6180:U:O2	85:4:6181:C:H1'	2.16	0.45
85:4:6206:G:H1'	85:4:6207:A:N6	2.26	0.45
2:B:380:GLN:C	2:B:381:THR:HG22	2.42	0.45
5:E:165:VAL:CG1	5:E:178:VAL:HG22	2.47	0.45
8:H:132:VAL:HG13	8:H:147:GLU:O	2.16	0.45
9:I:204:GLY:O	46:7:63:C:H3'	2.16	0.45
41:p:5:THR:OG1	45:5:1554:A:OP1	2.33	0.45
43:s:26:LYS:HD2	43:s:95:LEU:HD22	1.99	0.45
45:5:722:G:N2	45:5:723:A:N3	2.64	0.45
45:5:1279:A:C5	45:5:1281:G:C6	3.04	0.45
45:5:4557:U:O5'	45:5:4557:U:H6	1.99	0.45
45:5:5047:C:C2	45:5:5048:A:N7	2.85	0.45
49:2:332:G:O6	57:HH:189:ARG:NH2	2.49	0.45
57:HH:198:ARG:O	57:HH:201:LYS:N	2.49	0.45
67:RR:18:THR:O	67:RR:18:THR:HG22	2.17	0.45
85:4:6171:U:O2'	85:4:6172:G:N3	2.49	0.45
85:4:6177:U:C4	85:4:6178:U:C4	3.05	0.45
11:L:167:ARG:HE	26:a:100:ILE:HD11	1.81	0.45
12:M:92:ALA:HA	12:M:95:ILE:HB	1.99	0.45
14:O:87:MET:HB3	45:5:1913:C:O2'	2.17	0.45
15:P:138:PRO:O	45:5:3860:A:O2'	2.25	0.45
26:a:103:VAL:HG13	26:a:108:TYR:HB2	1.98	0.45
45:5:34:A:C2'	45:5:35:U:O5'	2.65	0.45
45:5:700:G:C6	45:5:701:G:C6	3.05	0.45
45:5:1074:G:C2	45:5:1238:A:C2	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:1584:G:C5	45:5:1585:C:C5	3.05	0.45
45:5:2706:G:C6	45:5:2708:U:OP2	2.70	0.45
45:5:3687:A:C2	45:5:3688:U:C2	3.04	0.45
45:5:4351:U:C4	45:5:4352:U:C5	3.05	0.45
49:2:641:A:H2'	49:2:642:U:O4'	2.16	0.45
49:2:1679:A:H2'	56:GG:60:ARG:HD2	1.99	0.45
50:3:9:G:H3'	50:3:10:G:H5''	1.98	0.45
51:BB:7:VAL:HG21	72:WW:42:VAL:HA	1.98	0.45
54:EE:101:GLN:O	54:EE:104:SER:HB3	2.17	0.45
55:FF:47:PHE:HE1	55:FF:111:VAL:HG22	1.82	0.45
57:HH:75:LEU:O	57:HH:94:ARG:HA	2.16	0.45
5:E:95:VAL:CG2	5:E:112:LEU:HD21	2.47	0.45
8:H:185:GLY:O	8:H:186:THR:HG23	2.17	0.45
9:I:36:LEU:HD11	9:I:69:ARG:CD	2.44	0.45
17:R:15:LEU:HD23	17:R:52:ARG:HB2	1.98	0.45
19:T:39:ILE:HG22	19:T:99:SER:CB	2.47	0.45
34:i:43:MET:HA	34:i:43:MET:HE3	1.99	0.45
45:5:4464:A:H2'	45:5:4464:A:N3	2.31	0.45
45:5:4581:G:C2	45:5:4582:C:C5	3.05	0.45
49:2:1042:A:C2	49:2:1074:C:C2	3.05	0.45
49:2:1270:G:C6	49:2:1271:C:C5	3.04	0.45
49:2:1344:A:H4'	49:2:1345:G:OP1	2.17	0.45
49:2:1610:G:C6	49:2:1611:G:C5	3.05	0.45
54:EE:6:SER:O	54:EE:10:LYS:N	2.49	0.45
81:ff:106:LYS:O	81:ff:107:ARG:C	2.60	0.45
83:hh:212:LYS:HA	83:hh:235:ILE:HG13	1.99	0.45
85:4:6097:U:OP1	85:4:6098:A:C5	2.67	0.45
17:R:49:LEU:N	17:R:49:LEU:HD23	2.32	0.44
23:X:107:HIS:CE1	47:8:130:C:H5'	2.52	0.44
44:t:135:THR:HG22	45:5:1974:U:O4	2.16	0.44
45:5:2311:C:C4	45:5:2312:U:C5	3.05	0.44
45:5:3909:C:O2	45:5:4397:A:C2	2.70	0.44
45:5:4897:G:H2'	45:5:4898:G:O4'	2.16	0.44
49:2:846:G:H5''	49:2:847:A:O5'	2.16	0.44
53:DD:115:GLN:OE1	53:DD:120:GLN:NE2	2.51	0.44
54:EE:126:ILE:HD11	54:EE:134:CYS:SG	2.57	0.44
55:FF:28:ALA:HB1	55:FF:29:PRO:CD	2.47	0.44
59:JJ:202:ILE:HA	59:JJ:205:ARG:HB3	1.97	0.44
85:4:6097:U:OP1	85:4:6097:U:C5	2.70	0.44
85:4:6181:C:C2'	85:4:6182:A:O2'	2.65	0.44
85:4:6200:A:H3'	85:4:6201:C:C4'	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Y:55:VAL:HG13	24:Y:104:VAL:HG22	1.99	0.44
27:b:17:HIS:CG	45:5:1724:G:C5	3.04	0.44
45:5:18:C:O2	45:5:18:C:H2'	2.16	0.44
45:5:92:C:OP2	45:5:4341:C:O2'	2.29	0.44
45:5:983:C:C4	45:5:984:C:C4	3.05	0.44
45:5:1322:A:N7	45:5:1326:A:C5	2.85	0.44
45:5:1673:U:O2'	45:5:4304:A:N7	2.38	0.44
45:5:1739:G:C6	45:5:1740:C:N4	2.85	0.44
45:5:1922:G:C2	45:5:2063:G:C5	3.06	0.44
45:5:3757:G:C5	45:5:3758:U:C5	3.05	0.44
45:5:4362:A:H8	45:5:4362:A:O5'	2.00	0.44
49:2:190:G:C2	49:2:208:G:N1	2.85	0.44
50:3:69:A:N7	50:3:72:C:C4	2.85	0.44
81:ff:77:GLY:HA2	81:ff:81:ARG:HB2	1.99	0.44
83:hh:249:CYS:HA	83:hh:258:ILE:HG22	1.99	0.44
83:hh:266:ILE:HD11	83:hh:269:GLU:HB2	1.99	0.44
85:4:6074:A:H2'	85:4:6075:A:H5'	1.98	0.44
85:4:6097:U:O2	85:4:6097:U:H2'	2.18	0.44
1:A:126:LEU:HD13	1:A:150:LEU:CD2	2.48	0.44
4:D:219:TYR:CE2	4:D:227:ILE:HD11	2.53	0.44
17:R:7:GLN:NE2	17:R:33:ALA:HA	2.32	0.44
24:Y:79:VAL:HG21	24:Y:98:GLY:HA3	1.99	0.44
27:b:6:ASN:O	27:b:7:HIS:HB3	2.16	0.44
45:5:93:G:C2'	45:5:94:A:O5'	2.66	0.44
45:5:214:G:C5	45:5:215:C:C5	3.05	0.44
45:5:227:A:C4	45:5:228:C:C6	3.05	0.44
45:5:1845:U:O2	45:5:1845:U:H2'	2.17	0.44
47:8:123:U:HO2'	47:8:126:C:H5	1.62	0.44
49:2:823:U:O4'	60:KK:140:GLN:NE2	2.51	0.44
49:2:1551:U:O2	49:2:1551:U:O4'	2.34	0.44
51:BB:59:LEU:O	51:BB:63:ARG:N	2.50	0.44
61:LL:26:ASP:OD1	61:LL:28:HIS:N	2.50	0.44
11:L:64:VAL:HA	11:L:67:HIS:CD2	2.53	0.44
21:V:125:CYS:O	21:V:125:CYS:SG	2.75	0.44
33:h:60:VAL:O	33:h:61:ILE:C	2.60	0.44
45:5:360:A:C4	47:8:24:G:H1'	2.52	0.44
45:5:1325:C:O2	45:5:1325:C:O5'	2.36	0.44
45:5:1691:G:N2	45:5:1846:G:N3	2.65	0.44
45:5:2438:A:C2	45:5:2441:C:C5	3.06	0.44
45:5:2590:G:HO2'	45:5:2755:A:N6	2.15	0.44
45:5:4054:C:C6	45:5:4054:C:OP2	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:4135:G:N1	45:5:4150:G:C2	2.86	0.44
45:5:4924:C:C4	45:5:4925:U:O4	2.71	0.44
47:8:3:A:H2'	47:8:4:C:O4'	2.17	0.44
47:8:106:G:H1'	47:8:136:U:O2	2.17	0.44
63:NN:18:LEU:O	63:NN:18:LEU:HD13	2.17	0.44
74:YY:48:LYS:CG	74:YY:101:LEU:HD12	2.48	0.44
2:B:167:GLN:HB3	2:B:170:LEU:HD12	1.99	0.44
3:C:239:LYS:O	3:C:248:ARG:NH1	2.50	0.44
22:W:82:ILE:HG22	22:W:83:THR:N	2.33	0.44
33:h:58:LEU:HB3	47:8:60:G:C8	2.53	0.44
35:j:22:CYS:SG	35:j:34:CYS:SG	3.13	0.44
45:5:319:A:C5	45:5:320:C:C5	3.06	0.44
45:5:1291:G:C5	45:5:1292:C:C4	3.05	0.44
45:5:3873:G:C6	45:5:3874:G:C6	3.06	0.44
49:2:380:G:O6	59:JJ:178:ARG:NH2	2.50	0.44
73:XX:55:ASP:O	73:XX:57:ARG:N	2.47	0.44
82:gg:114:ILE:HD13	82:gg:116:ARG:HE	1.83	0.44
85:4:6071:A:H2'	85:4:6072:U:C5'	2.48	0.44
5:E:206:ILE:O	5:E:206:ILE:HG23	2.17	0.44
13:N:64:ILE:HD11	13:N:66:VAL:HG23	1.99	0.44
16:Q:64:SER:HB3	16:Q:92:VAL:HG11	1.99	0.44
21:V:118:THR:O	21:V:118:THR:HG23	2.17	0.44
30:e:58:ILE:C	30:e:60:TYR:H	2.25	0.44
31:f:56:ASN:N	31:f:56:ASN:ND2	2.64	0.44
45:5:1517:G:N3	45:5:1517:G:H2'	2.32	0.44
45:5:1752:G:C2	45:5:1753:G:C8	3.05	0.44
45:5:3656:A:O4'	45:5:3747:A:C2	2.71	0.44
49:2:62:G:C2	49:2:63:U:C6	3.06	0.44
49:2:168:C:OP1	57:HH:131:ARG:NH2	2.51	0.44
49:2:1825:A:C1'	85:4:6221:A:C4	3.00	0.44
53:DD:241:PHE:O	53:DD:242:ASP:C	2.61	0.44
85:4:6070:A:C2'	85:4:6172:G:H1'	2.47	0.44
85:4:6177:U:C1'	85:4:6178:U:H1'	2.47	0.44
6:F:89:ALA:HB3	6:F:124:LEU:HD21	2.00	0.44
45:5:734:G:O5'	45:5:734:G:H8	2.01	0.44
45:5:2264:C:N4	45:5:2265:G:C6	2.85	0.44
45:5:2438:A:O2'	45:5:2440:U:OP2	2.36	0.44
45:5:2761:U:H4'	45:5:2762:G:O5'	2.18	0.44
45:5:3926:C:O2	45:5:3926:C:H2'	2.17	0.44
45:5:4354:U:O2	45:5:4354:U:O4'	2.35	0.44
48:K:38:LEU:O	48:K:163:LEU:HD21	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1129:G:C6	49:2:1130:G:C6	3.06	0.44
49:2:1290:G:C6	49:2:1291:A:C6	3.06	0.44
49:2:1320:G:H2'	49:2:1321:G:O4'	2.18	0.44
49:2:1330:G:C4	49:2:1492:U:C5	3.06	0.44
51:BB:60:LEU:HD22	51:BB:159:ILE:HD13	2.00	0.44
53:DD:206:SER:HB2	53:DD:224:THR:HG21	1.99	0.44
78:cc:53:VAL:HG23	78:cc:53:VAL:O	2.17	0.44
1:A:229:ALA:HB1	1:A:230:PRO:HD2	2.00	0.44
13:N:143:ARG:HD2	13:N:152:THR:HG21	1.99	0.44
22:W:51:TRP:O	22:W:51:TRP:CE3	2.68	0.44
30:e:79:VAL:HG12	30:e:80:HIS:N	2.33	0.44
41:p:17:ARG:HB3	41:p:18:TYR:CE2	2.53	0.44
45:5:300:A:H2'	45:5:301:G:C8	2.53	0.44
45:5:423:G:C2	47:8:12:G:N3	2.86	0.44
45:5:3642:A:H3'	45:5:3643:A:H2'	1.99	0.44
45:5:4714:C:H5''	45:5:4715:C:OP2	2.17	0.44
45:5:4868:G:C6	45:5:4869:U:C5	3.06	0.44
48:K:44:GLN:O	85:4:6083:U:O4'	2.32	0.44
49:2:29:G:H2'	49:2:30:C:O4'	2.17	0.44
49:2:301:A:C2	59:JJ:73:THR:HG21	2.52	0.44
49:2:814:U:C5	49:2:815:U:C5	3.06	0.44
49:2:1044:G:OP2	49:2:1044:G:O4'	2.34	0.44
49:2:1289:U:OP2	82:gg:95:ARG:NH1	2.51	0.44
49:2:1853:C:C2	49:2:1854:U:C5	3.05	0.44
54:EE:21:LEU:HD21	54:EE:48:ILE:HD11	1.98	0.44
54:EE:52:ALA:O	54:EE:90:LYS:HA	2.18	0.44
55:FF:48:LEU:HD22	55:FF:70:ILE:HD11	1.98	0.44
62:MM:40:ILE:HD11	62:MM:68:ILE:HG13	1.99	0.44
74:YY:58:GLU:OE1	74:YY:59:ALA:N	2.45	0.44
2:B:276:HIS:O	2:B:277:ARG:CG	2.66	0.44
13:N:16:SER:O	13:N:20:ARG:HB2	2.18	0.44
33:h:23:ASP:O	33:h:27:GLU:HB2	2.18	0.44
45:5:1358:G:C8	45:5:1379:C:N4	2.86	0.44
45:5:2724:G:C2	45:5:2726:G:C5	3.06	0.44
45:5:4485:C:N3	45:5:4486:C:C5	2.86	0.44
45:5:4534:G:H2'	45:5:4535:A:O5'	2.18	0.44
45:5:4769:G:N2	45:5:4866:C:C2	2.86	0.44
47:8:28:C:O2'	47:8:29:G:H5'	2.18	0.44
49:2:1498:A:C5	49:2:1499:U:C5	3.06	0.44
49:2:1561:A:C5	49:2:1575:G:C2	3.05	0.44
53:DD:267:GLN:HE22	72:WW:35:ASN:ND2	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:II:105:THR:HB	58:II:107:LYS:N	2.33	0.44
80:ee:21:CYS:SG	80:ee:22:ARG:N	2.91	0.44
3:C:147:VAL:O	3:C:148:PRO:C	2.61	0.43
11:L:47:ALA:O	11:L:149:GLN:NE2	2.51	0.43
20:U:80:LYS:HD3	20:U:110:TYR:CE2	2.53	0.43
26:a:104:VAL:CG2	26:a:147:VAL:HG11	2.48	0.43
45:5:111:C:C2	45:5:331:G:C2	3.06	0.43
45:5:1335:G:O6	45:5:1336:G:C2	2.71	0.43
45:5:2276:A:H2'	45:5:2277:C:O4'	2.17	0.43
45:5:2706:G:C5	45:5:2708:U:OP2	2.71	0.43
45:5:4605:A:N6	84:jj:296:GLN:HA	2.32	0.43
45:5:4977:A:H2'	45:5:4978:G:O4'	2.16	0.43
60:KK:83:ARG:HG2	60:KK:84:ILE:HG23	1.99	0.43
60:KK:110:LEU:O	60:KK:111:GLN:C	2.61	0.43
74:YY:4:CYS:O	74:YY:4:CYS:SG	2.76	0.43
85:4:6074:A:OP1	85:4:6074:A:O2'	2.21	0.43
85:4:6177:U:H5	85:4:6178:U:C5	2.20	0.43
85:4:6206:G:H2'	85:4:6207:A:N7	2.31	0.43
3:C:150:LEU:CD1	42:r:71:ARG:HE	2.32	0.43
4:D:22:ARG:NH1	46:7:7:G:H5''	2.33	0.43
5:E:69:ALA:HB2	45:5:1071:C:C5	2.53	0.43
21:V:33:GLY:HA3	21:V:69:LYS:HG3	2.00	0.43
43:s:26:LYS:HG2	43:s:91:THR:HG23	2.00	0.43
45:5:423:G:C4	47:8:12:G:C2	3.05	0.43
45:5:453:G:H2'	45:5:453:G:N3	2.33	0.43
45:5:1295:U:O2	45:5:1295:U:O4'	2.33	0.43
46:7:28:C:H2'	46:7:29:C:H5'	2.00	0.43
49:2:806:U:N3	49:2:858:A:C2	2.86	0.43
49:2:1168:G:C2	49:2:1192:U:O2	2.71	0.43
49:2:1855:G:OP2	65:PP:147:ARG:NH1	2.51	0.43
54:EE:105:LEU:HD23	54:EE:184:ILE:CG2	2.48	0.43
59:JJ:70:GLU:O	59:JJ:71:CYS:C	2.61	0.43
66:QQ:26:LEU:HD13	66:QQ:88:GLU:HA	2.00	0.43
77:bb:21:ILE:HD12	77:bb:32:LYS:HA	2.00	0.43
83:hh:230:LEU:HD22	83:hh:259:TRP:CD2	2.53	0.43
84:jj:48:VAL:HG12	84:jj:52:LEU:HD12	1.99	0.43
4:D:42:ASN:N	19:T:68:THR:O	2.51	0.43
13:N:56:LYS:O	13:N:58:GLY:N	2.51	0.43
22:W:54:LEU:HD12	22:W:54:LEU:N	2.34	0.43
29:d:71:ALA:O	29:d:72:VAL:C	2.60	0.43
42:r:10:VAL:HA	42:r:13:CYS:SG	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:699:C:C2'	45:5:700:G:O5'	2.67	0.43
45:5:752:G:H2'	45:5:753:C:O5'	2.18	0.43
45:5:1823:G:C6	45:5:1824:G:C6	3.07	0.43
45:5:2803:U:O2	45:5:2803:U:H2'	2.17	0.43
45:5:3736:A:C2'	45:5:3932:U:O2'	2.66	0.43
48:K:6:SER:OG	48:K:197:ASN:O	2.36	0.43
49:2:924:G:C2	49:2:1019:C:O2	2.71	0.43
49:2:1797:U:C4	49:2:1798:C:N4	2.86	0.43
58:II:53:VAL:HG23	58:II:175:GLY:HA3	1.99	0.43
59:JJ:172:LEU:HB3	59:JJ:190:LEU:HD23	2.00	0.43
60:KK:47:LYS:O	60:KK:50:LEU:N	2.51	0.43
66:QQ:94:VAL:O	66:QQ:105:VAL:N	2.51	0.43
81:ff:106:LYS:O	81:ff:108:ARG:N	2.51	0.43
85:4:6034:A:N1	85:4:6090:A:C2	2.86	0.43
85:4:6198:A:C2'	85:4:6199:A:O5'	2.63	0.43
1:A:42:LYS:HD3	1:A:89:TYR:CE1	2.53	0.43
1:A:124:GLY:O	1:A:128:ARG:NH1	2.50	0.43
3:C:130:ALA:HB3	3:C:246:VAL:HG12	2.00	0.43
5:E:168:LEU:HD13	5:E:211:ILE:CD1	2.49	0.43
6:F:92:ILE:HG21	6:F:246:MET:HE1	2.00	0.43
14:O:201:LEU:O	14:O:202:LEU:HD12	2.18	0.43
16:Q:105:VAL:HG11	16:Q:120:ILE:HD13	2.00	0.43
17:R:93:VAL:O	17:R:96:MET:N	2.51	0.43
28:c:35:LEU:HD13	28:c:60:ILE:CD1	2.49	0.43
30:e:41:ILE:O	30:e:43:ASN:N	2.52	0.43
41:p:14:TYR:HE2	41:p:26:VAL:HG11	1.84	0.43
45:5:1398:A:C2'	45:5:1399:G:O4'	2.55	0.43
45:5:1463:C:H2'	45:5:1464:C:O4'	2.18	0.43
45:5:1733:G:C5	45:5:4214:A:C2	3.07	0.43
45:5:2309:G:H2'	45:5:2310:C:O4'	2.18	0.43
45:5:3819:G:C2	45:5:3820:G:C8	3.06	0.43
45:5:3971:G:C2	45:5:4049:U:OP1	2.71	0.43
45:5:4526:U:C5	45:5:4527:G:C6	3.07	0.43
45:5:4998:G:H2'	45:5:4999:G:O4'	2.18	0.43
45:5:5012:G:N2	45:5:5037:U:C2	2.87	0.43
46:7:32:A:C5	46:7:41:G:C8	3.07	0.43
48:K:126:PRO:CD	85:4:6087:G:H5'	2.36	0.43
49:2:306:C:H5''	49:2:307:G:H3'	2.00	0.43
49:2:845:G:O2'	49:2:846:G:H5'	2.18	0.43
49:2:872:A:C6	49:2:874:G:C5	3.07	0.43
49:2:1276:A:O2'	61:LL:51:SER:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1297:U:O4	66:QQ:59:ARG:NH1	2.51	0.43
49:2:1398:G:C2	49:2:1399:C:C6	3.06	0.43
59:JJ:60:LEU:HD23	59:JJ:185:ALA:HB2	2.00	0.43
61:LL:43:LEU:HD12	61:LL:43:LEU:O	2.19	0.43
85:4:6083:U:OP2	85:4:6083:U:C6	2.70	0.43
1:A:103:PRO:O	1:A:106:THR:N	2.51	0.43
2:B:254:ILE:HG22	2:B:255:GLY:N	2.34	0.43
6:F:28:LYS:CE	45:5:965:G:N7	2.81	0.43
22:W:14:TYR:HB3	22:W:15:PRO:HD2	2.00	0.43
39:n:9:ARG:NH2	49:2:1851:A:OP1	2.44	0.43
45:5:430:G:N2	47:8:5:U:C2	2.87	0.43
45:5:1650:A:H3'	45:5:1651:G:H5'	1.99	0.43
45:5:2543:A:C5	45:5:2546:G:N2	2.87	0.43
45:5:2655:C:H3'	45:5:2656:U:H5''	2.01	0.43
45:5:3641:U:OP2	45:5:3646:A:N6	2.48	0.43
45:5:3829:G:C2	45:5:3830:A:C8	3.06	0.43
48:K:8:ASP:CG	48:K:9:THR:N	2.76	0.43
49:2:35:C:N3	49:2:36:U:C5	2.86	0.43
49:2:350:C:O2'	49:2:383:G:N1	2.42	0.43
49:2:1276:A:N6	49:2:1322:G:O4'	2.51	0.43
49:2:1536:G:C2	49:2:1537:A:C5	3.06	0.43
53:DD:75:ILE:HD12	53:DD:265:PRO:HB3	1.99	0.43
53:DD:209:VAL:HB	53:DD:210:PRO:CD	2.48	0.43
57:HH:213:LEU:HD22	57:HH:216:ARG:HB2	1.99	0.43
62:MM:42:LEU:HD13	62:MM:42:LEU:N	2.34	0.43
85:4:6053:U:P	85:4:6053:U:C5	3.07	0.43
1:A:185:ALA:O	1:A:186:TYR:C	2.62	0.43
2:B:17:LEU:O	2:B:19:ARG:N	2.51	0.43
3:C:36:ILE:O	3:C:36:ILE:HG22	2.17	0.43
7:G:130:PRO:O	7:G:134:ASN:HB2	2.19	0.43
23:X:93:ASN:O	23:X:94:ASN:HB2	2.18	0.43
25:Z:55:ALA:HB3	45:5:4129:G:OP2	2.19	0.43
28:c:36:LYS:O	28:c:39:ARG:N	2.51	0.43
28:c:89:TYR:CZ	45:5:2673:G:C6	3.06	0.43
45:5:2081:C:H2'	45:5:2082:G:C8	2.54	0.43
45:5:4468:U:O2	45:5:4708:A:C8	2.71	0.43
45:5:4470:G:C6	45:5:4471:U:C2	3.06	0.43
45:5:4928:C:O2	45:5:4928:C:O4'	2.35	0.43
49:2:62:G:N2	49:2:63:U:H1'	2.33	0.43
49:2:986:G:C8	65:PP:137:SER:O	2.72	0.43
57:HH:213:LEU:CD1	57:HH:217:MET:HE2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:KK:110:LEU:HD22	60:KK:130:ILE:HD11	2.01	0.43
84:jj:317:VAL:HG12	84:jj:413:LEU:HD23	2.00	0.43
85:4:6046:U:N3	85:4:6082:G:C6	2.85	0.43
85:4:6071:A:N7	85:4:6072:U:C5	2.85	0.43
85:4:6088:C:C3'	85:4:6088:C:C6	3.01	0.43
1:A:90:CYS:HB2	1:A:101:VAL:HG13	1.99	0.43
2:B:238:LYS:HG3	2:B:239:LYS:O	2.19	0.43
14:O:156:LEU:HD22	45:5:4910:A:C8	2.54	0.43
16:Q:57:ASN:O	16:Q:143:ARG:NH1	2.52	0.43
22:W:40:PHE:CD2	22:W:40:PHE:C	2.96	0.43
29:d:93:ASN:HD21	29:d:98:SER:N	2.17	0.43
42:r:68:SER:O	42:r:69:GLY:C	2.62	0.43
45:5:285:G:H2'	45:5:286:U:O4'	2.19	0.43
45:5:2664:G:C6	45:5:2665:U:N3	2.87	0.43
48:K:123:ILE:O	85:4:6040:U:H5	2.01	0.43
49:2:54:A:C6	49:2:474:G:C5	3.06	0.43
49:2:171:A:N7	49:2:173:A:C5	2.86	0.43
49:2:293:C:O2	49:2:293:C:H2'	2.18	0.43
49:2:622:C:H2'	49:2:623:G:O5'	2.19	0.43
51:BB:176:TRP:NE1	51:BB:195:TRP:CZ3	2.87	0.43
67:RR:86:GLN:NE2	67:RR:122:ALA:HB2	2.32	0.43
83:hh:166:VAL:HB	83:hh:198:VAL:HG11	2.00	0.43
85:4:6181:C:H3'	85:4:6182:A:C3'	2.30	0.43
30:e:17:THR:HG21	45:5:1301:C:O2'	2.19	0.43
45:5:59:A:C2	45:5:338:A:C2	3.07	0.43
45:5:101:A:C5	45:5:102:G:C8	3.06	0.43
45:5:291:U:C2	45:5:297:U:C4	3.07	0.43
45:5:957:G:N7	45:5:958:G:C6	2.86	0.43
45:5:1279:A:C4	45:5:1281:G:O6	2.72	0.43
48:K:80:VAL:HG21	48:K:147:LYS:HG3	2.01	0.43
49:2:1030:A:C2	49:2:1031:A:N7	2.86	0.43
49:2:1345:G:O6	49:2:1385:G:C6	2.72	0.43
51:BB:84:GLN:HG2	51:BB:100:ALA:HB1	2.00	0.43
51:BB:109:THR:O	53:DD:89:LYS:NZ	2.50	0.43
53:DD:139:LEU:O	53:DD:139:LEU:HD13	2.18	0.43
58:II:42:GLU:O	58:II:43:LEU:HD12	2.19	0.43
74:YY:59:ALA:HB1	74:YY:114:ASP:HB3	2.01	0.43
77:bb:19:GLN:CD	77:bb:19:GLN:N	2.75	0.43
83:hh:39:THR:HG22	83:hh:60:ARG:HG2	2.01	0.43
85:4:6197:A:N1	85:4:6198:A:C5	2.86	0.43
3:C:199:ARG:NH2	45:5:2295:C:OP1	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:48:ARG:O	5:E:64:MET:HE1	2.18	0.43
11:L:182:LEU:HD23	34:i:7:MET:HE3	1.99	0.43
12:M:86:TRP:CD1	12:M:86:TRP:O	2.72	0.43
14:O:124:LEU:HD11	18:S:171:ARG:NH1	2.33	0.43
18:S:33:PHE:CE1	18:S:106:VAL:HG21	2.54	0.43
19:T:103:ASP:OD1	19:T:106:LEU:HD12	2.19	0.43
25:Z:17:ARG:HD3	45:5:2578:G:O6	2.18	0.43
25:Z:59:LYS:HA	25:Z:62:ILE:HB	2.00	0.43
45:5:63:G:C5	45:5:333:U:C4	3.07	0.43
45:5:319:A:H5'	45:5:3727:A:O2'	2.18	0.43
45:5:651:C:H2'	45:5:652:G:O4'	2.19	0.43
45:5:3924:C:C2	45:5:3925:U:C6	3.06	0.43
45:5:4699:U:H4'	45:5:4700:A:OP1	2.19	0.43
47:8:141:C:C2	47:8:142:U:C5	3.07	0.43
47:8:150:C:O2	47:8:150:C:H2'	2.18	0.43
49:2:189:U:O4	49:2:190:G:C2	2.72	0.43
49:2:316:G:C2	49:2:317:C:C2	3.07	0.43
49:2:403:G:C6	49:2:404:G:N7	2.87	0.43
49:2:1734:G:C2	49:2:1799:G:C2	3.07	0.43
63:NN:52:LEU:HD23	63:NN:78:LYS:HG2	2.01	0.43
70:UU:27:LYS:CD	70:UU:110:LEU:HD23	2.49	0.43
72:WW:46:PHE:CE2	72:WW:48:GLY:HA2	2.54	0.43
85:4:6199:A:OP2	85:4:6199:A:H4'	2.19	0.43
3:C:149:GLU:CB	3:C:150:LEU:HB2	2.49	0.43
3:C:338:ASN:O	3:C:339:THR:OG1	2.36	0.43
4:D:157:ASN:OD1	4:D:157:ASN:C	2.62	0.43
7:G:189:LEU:HD11	7:G:246:LEU:HD13	2.00	0.43
17:R:154:LEU:HD23	17:R:155:LEU:HD22	2.00	0.43
32:g:54:ARG:CD	32:g:54:ARG:N	2.81	0.43
42:r:60:VAL:CG2	42:r:118:LEU:HD11	2.48	0.43
45:5:86:U:C5	45:5:97:G:C2	3.07	0.43
45:5:2504:C:H3'	45:5:2505:C:H5''	2.01	0.43
45:5:4243:C:O2	45:5:4243:C:H2'	2.17	0.43
48:K:122:ARG:HB2	85:4:6037:U:H6	1.79	0.43
49:2:340:C:H2'	49:2:341:C:O4'	2.18	0.43
49:2:1196:A:N7	49:2:1197:G:C8	2.86	0.43
49:2:1315:U:O2	49:2:1315:U:O4'	2.34	0.43
49:2:1661:A:OP1	80:ee:19:ARG:NH2	2.43	0.43
49:2:1712:A:C2	49:2:1822:A:C2	3.06	0.43
53:DD:186:GLY:HA3	53:DD:243:ALA:HB2	2.01	0.43
55:FF:158:ASP:OD1	55:FF:158:ASP:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:JJ:57:ALA:HB2	59:JJ:183:GLY:HA2	2.01	0.43
74:YY:11:ARG:O	74:YY:12:LYS:C	2.60	0.43
10:J:43:LEU:HB2	10:J:117:ILE:HD11	1.99	0.42
17:R:99:MET:C	17:R:101:ILE:H	2.27	0.42
26:a:103:VAL:CG1	26:a:108:TYR:HB2	2.48	0.42
37:l:20:ASN:ND2	37:l:41:ARG:NH1	2.67	0.42
38:m:53:GLU:HG3	38:m:54:PRO:HD2	2.01	0.42
38:m:83:ASN:ND2	38:m:93:ASN:HB3	2.34	0.42
39:n:6:ARG:O	39:n:9:ARG:N	2.52	0.42
45:5:291:U:O2	45:5:297:U:C2	2.72	0.42
45:5:1388:A:C6	45:5:1389:U:C4	3.07	0.42
45:5:5000:G:N2	45:5:5051:C:C2	2.87	0.42
46:7:52:C:O2'	46:7:53:U:O4'	2.37	0.42
46:7:70:G:C6	46:7:106:G:C6	3.07	0.42
47:8:153:C:N3	47:8:154:G:C6	2.86	0.42
49:2:1078:C:C5	49:2:1079:C:C4	3.07	0.42
55:FF:52:LEU:HD13	55:FF:54:TYR:CE2	2.54	0.42
57:HH:26:THR:O	57:HH:26:THR:HG22	2.19	0.42
57:HH:177:GLN:HA	57:HH:177:GLN:HE21	1.84	0.42
57:HH:225:GLN:O	57:HH:229:ALA:HB3	2.18	0.42
61:LL:44:HIS:O	61:LL:48:ALA:N	2.49	0.42
71:VV:50:VAL:HG22	71:VV:51:LYS:O	2.19	0.42
84:jj:287:ILE:HD13	84:jj:399:GLY:HA2	2.01	0.42
2:B:299:ILE:HD12	2:B:299:ILE:N	2.34	0.42
14:O:173:GLN:HE21	14:O:176:ARG:HB2	1.84	0.42
26:a:2:PRO:HG3	26:a:5:LEU:HD12	2.02	0.42
40:o:82:MET:HE1	45:5:4346:U:H5'	2.01	0.42
43:s:68:HIS:HB3	43:s:75:LEU:HD12	2.02	0.42
45:5:230:G:C6	45:5:231:U:N3	2.88	0.42
45:5:2757:A:N6	45:5:2758:G:C6	2.87	0.42
45:5:4510:A:C5	45:5:4511:A:N1	2.86	0.42
48:K:124:LEU:HD13	85:4:6038:G:C2	2.54	0.42
49:2:63:U:C2'	49:2:64:A:H5''	2.49	0.42
49:2:468:A:C2	49:2:469:A:C4	3.07	0.42
49:2:993:G:N2	49:2:994:C:C2	2.87	0.42
49:2:1597:C:H4'	49:2:1603:G:O6	2.19	0.42
53:DD:137:VAL:HG21	53:DD:244:ILE:HD11	2.00	0.42
58:II:186:ASN:OD1	58:II:186:ASN:N	2.52	0.42
61:LL:32:HIS:CD2	61:LL:45:VAL:HG21	2.54	0.42
84:jj:225:VAL:HG13	84:jj:252:LYS:HB3	2.01	0.42
85:4:6174:G:H8	85:4:6205:A:C6	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6177:U:C4	85:4:6178:U:N3	2.87	0.42
85:4:6183:G:N2	85:4:6184:A:H1'	2.35	0.42
2:B:56:ILE:CG2	2:B:57:VAL:N	2.82	0.42
3:C:339:THR:HG22	3:C:342:ARG:NH2	2.34	0.42
5:E:156:LEU:HD11	5:E:198:ILE:HG13	2.01	0.42
9:I:81:GLY:O	9:I:82:LYS:C	2.61	0.42
23:X:73:HIS:O	23:X:76:ILE:HG22	2.19	0.42
25:Z:14:LEU:HD21	32:g:92:LYS:HE3	2.01	0.42
25:Z:29:ILE:HG22	25:Z:29:ILE:O	2.19	0.42
26:a:104:VAL:HG21	26:a:147:VAL:HG11	2.00	0.42
30:e:64:LYS:NZ	45:5:2079:G:OP2	2.49	0.42
45:5:972:C:P	45:5:972:C:O4'	2.77	0.42
45:5:4201:G:N2	45:5:4221:C:C4	2.87	0.42
45:5:4510:A:C6	45:5:4511:A:C2	3.07	0.42
64:OO:121:ARG:O	64:OO:125:LEU:HB2	2.20	0.42
65:PP:56:VAL:HG23	65:PP:60:MET:SD	2.59	0.42
71:VV:54:VAL:HB	71:VV:88:LEU:HD12	2.00	0.42
74:YY:51:VAL:HG12	74:YY:52:LEU:N	2.35	0.42
77:bb:69:VAL:HG12	77:bb:70:LYS:N	2.34	0.42
85:4:6030:A:N1	85:4:6095:U:O2'	2.52	0.42
2:B:356:LYS:O	2:B:360:LEU:HD12	2.19	0.42
5:E:181:PRO:O	5:E:182:LEU:C	2.61	0.42
8:H:173:ARG:C	8:H:176:LEU:HD21	2.45	0.42
41:p:64:VAL:HG12	41:p:65:ALA:N	2.34	0.42
45:5:409:G:O2'	45:5:410:A:OP1	2.32	0.42
45:5:1349:G:C5	45:5:1350:C:C5	3.07	0.42
45:5:2393:C:H5''	45:5:2394:G:OP2	2.19	0.42
45:5:2439:G:C2	45:5:2539:C:O2	2.72	0.42
45:5:2478:C:H2'	45:5:2479:G:O4'	2.20	0.42
45:5:4127:A:H4'	45:5:4128:A:OP1	2.19	0.42
45:5:5020:G:C2'	45:5:5021:C:O5'	2.67	0.42
49:2:55:U:H4'	49:2:56:G:OP1	2.19	0.42
49:2:356:C:O2	49:2:356:C:H2'	2.19	0.42
49:2:1303:C:O2	49:2:1303:C:O4'	2.37	0.42
54:EE:119:CYS:O	54:EE:120:TYR:C	2.62	0.42
55:FF:220:THR:HG22	55:FF:224:ASN:HD22	1.83	0.42
57:HH:63:MET:SD	57:HH:63:MET:N	2.89	0.42
58:II:36:LEU:CD1	58:II:75:ILE:HD11	2.49	0.42
64:OO:87:ASP:CG	64:OO:125:LEU:HD11	2.44	0.42
66:QQ:57:LEU:HD11	66:QQ:80:LEU:HD22	2.00	0.42
85:4:6096:G:C2	85:4:6101:U:C2	2.97	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S:1:MET:HE1	18:S:110:TYR:CZ	2.54	0.42
18:S:13:VAL:HG12	18:S:29:ARG:HB2	2.00	0.42
19:T:118:GLU:O	19:T:119:ALA:HB3	2.19	0.42
33:h:96:ASN:N	33:h:96:ASN:ND2	2.65	0.42
46:7:66:G:C2	46:7:67:C:C2	3.08	0.42
47:8:89:U:C4	47:8:90:C:C4	3.07	0.42
49:2:521:A:N6	49:2:522:A:C2	2.87	0.42
49:2:867:G:O6	49:2:868:G:O6	2.37	0.42
49:2:1452:A:C6	49:2:1476:A:C6	3.07	0.42
53:DD:82:TYR:OH	53:DD:162:ILE:HD12	2.19	0.42
68:SS:53:TYR:O	68:SS:57:LEU:N	2.49	0.42
70:UU:27:LYS:HD3	70:UU:110:LEU:HD23	2.01	0.42
2:B:46:PHE:O	2:B:47:LEU:HD12	2.20	0.42
10:J:60:PHE:N	10:J:60:PHE:CD1	2.87	0.42
16:Q:99:LYS:CE	16:Q:121:LEU:HD11	2.49	0.42
30:e:35:TRP:HB3	45:5:2321:G:OP1	2.18	0.42
30:e:70:LEU:CB	30:e:71:PRO:CD	2.97	0.42
31:f:74:VAL:HG13	31:f:84:VAL:HG13	2.02	0.42
45:5:1362:G:N1	45:5:1376:C:N3	2.67	0.42
45:5:2050:G:O2'	45:5:2051:C:H5'	2.20	0.42
45:5:4413:C:N4	45:5:4414:A:N1	2.67	0.42
45:5:4640:C:C4	45:5:4641:U:C4	3.07	0.42
49:2:1399:C:H2'	49:2:1400:U:C6	2.55	0.42
49:2:1820:G:C5	49:2:1821:U:C5	3.07	0.42
52:CC:70:SER:OG	52:CC:71:LEU:N	2.53	0.42
53:DD:88:ILE:HD13	53:DD:94:ILE:CD1	2.40	0.42
62:MM:104:LYS:HE2	74:YY:8:ARG:NH1	2.35	0.42
85:4:6199:A:C4	85:4:6200:A:H1'	2.54	0.42
4:D:67:ALA:HA	4:D:72:ASP:HB3	2.01	0.42
8:H:134:CYS:SG	8:H:135:SER:N	2.92	0.42
16:Q:148:VAL:CG1	16:Q:152:PHE:CZ	3.02	0.42
25:Z:42:LEU:HD11	25:Z:97:ASN:O	2.20	0.42
29:d:45:ALA:O	29:d:48:GLU:N	2.52	0.42
37:l:48:LYS:O	37:l:49:LEU:CB	2.68	0.42
38:m:84:CYS:SG	38:m:89:CYS:SG	3.16	0.42
39:n:7:LYS:O	39:n:7:LYS:CG	2.68	0.42
45:5:225:G:H3'	45:5:226:G:C5'	2.50	0.42
45:5:319:A:C6	45:5:320:C:C4	3.08	0.42
45:5:1296:G:C2	45:5:1297:U:C2	3.08	0.42
45:5:1322:A:C5	45:5:1326:A:N7	2.87	0.42
45:5:2065:G:H2'	45:5:2066:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:2540:C:H2'	45:5:2541:G:O4'	2.19	0.42
45:5:4998:G:C4	45:5:4999:G:C8	3.07	0.42
45:5:5039:U:C4	45:5:5040:U:C5	3.07	0.42
49:2:30:C:C4	49:2:31:U:C5	3.07	0.42
49:2:218:U:H2'	49:2:219:U:H6	1.85	0.42
49:2:1829:G:C6	49:2:1830:U:C4	3.07	0.42
56:GG:94:LYS:O	56:GG:97:PHE:N	2.52	0.42
58:II:23:ILE:O	58:II:27:LEU:HD12	2.19	0.42
58:II:66:VAL:N	58:II:67:PRO:CD	2.83	0.42
64:OO:92:ILE:O	64:OO:95:ALA:HB3	2.20	0.42
67:RR:86:GLN:HE22	67:RR:122:ALA:CB	2.32	0.42
75:ZZ:22:GLN:C	75:ZZ:23:MET:HE3	2.45	0.42
84:jj:289:ARG:NE	84:jj:412:ILE:HD13	2.34	0.42
85:4:6032:A:H1'	85:4:6033:A:N3	2.35	0.42
85:4:6206:G:H8	85:4:6207:A:C8	2.32	0.42
2:B:282:LYS:NZ	2:B:336:CYS:O	2.37	0.42
8:H:69:THR:O	8:H:72:THR:HG22	2.18	0.42
11:L:63:THR:HG21	26:a:66:ASN:HD22	1.85	0.42
13:N:108:ARG:NH2	13:N:161:MET:HE1	2.35	0.42
13:N:183:THR:O	13:N:184:ILE:C	2.61	0.42
26:a:93:ASN:ND2	26:a:97:ALA:HB3	2.34	0.42
30:e:23:HIS:HA	30:e:53:ILE:HD13	2.02	0.42
45:5:22:G:H2'	45:5:23:C:C6	2.54	0.42
45:5:52:G:C2	45:5:53:C:C5	3.08	0.42
45:5:1470:G:N2	45:5:1495:G:C8	2.88	0.42
45:5:2311:C:N4	45:5:2312:U:O4	2.53	0.42
45:5:2459:G:H2'	45:5:2461:G:OP2	2.20	0.42
45:5:3653:A:C2	45:5:3692:A:O4'	2.73	0.42
45:5:3762:U:H2'	45:5:3763:A:C8	2.55	0.42
49:2:436:G:H2'	49:2:437:G:H5'	2.01	0.42
49:2:824:C:C6	60:KK:144:ILE:HD13	2.54	0.42
49:2:1319:U:N3	49:2:1320:G:N7	2.68	0.42
69:TT:58:GLU:OE2	76:aa:49:LEU:HD11	2.20	0.42
83:hh:37:ASP:CG	83:hh:38:LYS:N	2.77	0.42
85:4:6181:C:C2'	85:4:6182:A:C8	3.03	0.42
11:L:167:ARG:NE	26:a:100:ILE:HD11	2.35	0.42
15:P:30:ARG:HD3	15:P:30:ARG:C	2.45	0.42
15:P:129:THR:HB	15:P:139:TYR:HB2	2.02	0.42
18:S:12:VAL:HG22	18:S:64:CYS:SG	2.60	0.42
19:T:115:LYS:HB3	19:T:126:VAL:HG11	2.02	0.42
25:Z:21:ARG:HE	25:Z:47:ASP:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:e:53:ILE:HG22	30:e:54:LEU:N	2.34	0.42
44:t:15:LEU:HD21	44:t:31:LYS:HD3	2.01	0.42
45:5:56:A:C2	45:5:57:G:C4	3.08	0.42
45:5:1529:G:N2	45:5:1646:A:C2	2.88	0.42
45:5:1795:A:H4'	46:7:98:G:N3	2.34	0.42
45:5:2898:G:C2	45:5:2899:C:C2	3.08	0.42
49:2:831:G:C2	49:2:844:U:O2	2.73	0.42
49:2:917:U:H2'	49:2:918:U:O4'	2.20	0.42
49:2:1735:A:N6	49:2:1799:G:O2'	2.52	0.42
55:FF:239:PRO:O	55:FF:241:GLY:N	2.53	0.42
58:II:160:LYS:O	58:II:163:GLN:HB2	2.19	0.42
59:JJ:84:ASN:HD21	59:JJ:97:VAL:CG2	2.32	0.42
1:A:219:ILE:HD11	45:5:3689:G:H5'	2.01	0.42
2:B:41:VAL:HG21	2:B:196:TRP:CG	2.55	0.42
12:M:56:GLN:NE2	45:5:4870:G:C4	2.87	0.42
24:Y:8:THR:HG23	45:5:347:A:OP2	2.19	0.42
45:5:929:A:N6	45:5:930:G:N1	2.68	0.42
45:5:1664:U:H2'	45:5:1665:C:H6	1.85	0.42
45:5:4340:U:C5	45:5:4341:C:C5	3.08	0.42
45:5:4489:G:O4'	45:5:4709:U:H5''	2.20	0.42
45:5:4507:A:C2	45:5:4508:C:N1	2.88	0.42
45:5:4654:C:O2'	45:5:4655:A:H5'	2.20	0.42
49:2:436:G:C2'	49:2:437:G:H5'	2.50	0.42
49:2:1198:G:C6	49:2:1199:A:C6	3.08	0.42
49:2:1234:C:O2	49:2:1234:C:H2'	2.18	0.42
49:2:1328:G:C5	49:2:1329:U:C4	3.08	0.42
58:II:73:GLN:HA	58:II:76:GLN:HB2	2.01	0.42
68:SS:98:VAL:CG2	68:SS:117:LEU:HD22	2.49	0.42
74:YY:67:ARG:NH2	74:YY:114:ASP:OD2	2.53	0.42
75:ZZ:57:VAL:HA	75:ZZ:73:GLY:HA2	2.02	0.42
5:E:67:ARG:NH2	45:5:1070:G:OP2	2.53	0.41
8:H:111:LEU:HD23	8:H:112:VAL:N	2.35	0.41
45:5:386:A:H2	45:5:404:U:O2	2.02	0.41
45:5:1078:A:C2	45:5:1233:G:N1	2.88	0.41
45:5:4650:G:O3'	45:5:5008:C:H4'	2.20	0.41
49:2:660:C:OP2	74:YY:17:ARG:NH1	2.53	0.41
49:2:734:C:H2'	49:2:735:C:C6	2.55	0.41
53:DD:92:GLU:O	53:DD:96:PHE:N	2.49	0.41
58:II:146:VAL:HG12	73:XX:42:MET:HE1	2.01	0.41
70:UU:46:ALA:HB1	70:UU:47:PRO:HD2	2.02	0.41
70:UU:113:VAL:HG23	70:UU:113:VAL:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:XX:103:VAL:HG12	73:XX:126:LEU:HB2	2.02	0.41
83:hh:31:ILE:HG23	83:hh:43:TRP:CD1	2.55	0.41
84:jj:146:PHE:HE1	84:jj:278:VAL:HG21	1.85	0.41
2:B:242:ARG:NH2	45:5:2856:C:O2	2.54	0.41
11:L:48:PRO:HB2	33:h:120:ALA:HB2	2.01	0.41
14:O:147:TRP:CZ2	14:O:149:TYR:O	2.73	0.41
14:O:154:ALA:O	14:O:157:GLU:N	2.51	0.41
15:P:41:ILE:HG23	15:P:42:ARG:HG2	2.02	0.41
18:S:8:ARG:HB2	18:S:34:ALA:O	2.19	0.41
25:Z:46:ILE:HD11	25:Z:49:TYR:CD1	2.55	0.41
34:i:85:ARG:O	34:i:89:GLU:N	2.53	0.41
42:r:106:LEU:O	42:r:107:ARG:C	2.62	0.41
45:5:1391:A:N3	45:5:4364:G:O2'	2.48	0.41
45:5:1529:G:N2	45:5:1646:A:N3	2.68	0.41
45:5:2691:U:H2'	45:5:2692:U:C6	2.54	0.41
45:5:3924:C:C4	45:5:3925:U:C5	3.07	0.41
45:5:4944:C:O2	45:5:4944:C:H5'	2.19	0.41
47:8:129:C:C4	47:8:130:C:N4	2.88	0.41
56:GG:97:PHE:CD1	56:GG:108:PRO:HB3	2.54	0.41
56:GG:185:SER:HA	56:GG:190:ILE:HB	2.02	0.41
60:KK:115:PHE:CD1	60:KK:123:ILE:HG13	2.55	0.41
61:LL:1:MET:HE3	61:LL:3:MET:HG2	2.02	0.41
75:ZZ:87:PRO:HB2	75:ZZ:89:HIS:CD2	2.54	0.41
81:ff:84:LYS:HG2	81:ff:88:GLN:NE2	2.35	0.41
84:jj:100:ILE:C	84:jj:100:ILE:HD12	2.46	0.41
85:4:6179:U:H3'	85:4:6180:U:O4'	2.20	0.41
5:E:273:TYR:OH	12:M:106:ASP:OD2	2.33	0.41
14:O:5:GLN:HE21	14:O:6:VAL:HG23	1.85	0.41
15:P:28:ASN:HD22	15:P:60:PHE:HZ	1.68	0.41
25:Z:67:LYS:C	25:Z:68:ILE:HD12	2.45	0.41
31:f:79:GLY:HA2	45:5:2066:C:O2'	2.19	0.41
42:r:82:ILE:CG2	42:r:89:THR:HG23	2.51	0.41
45:5:2455:G:N2	45:5:2469:C:C5	2.88	0.41
45:5:4051:C:C6	48:K:211:GLY:HA2	2.55	0.41
45:5:4200:G:C6	45:5:4201:G:C4	3.08	0.41
45:5:4201:G:C6	45:5:4202:U:C4	3.08	0.41
45:5:4735:G:O2'	45:5:4736:C:C6	2.72	0.41
45:5:5055:G:C2	45:5:5056:A:C5	3.08	0.41
48:K:121:PRO:CG	85:4:6037:U:C2	3.03	0.41
49:2:403:G:C4	49:2:404:G:C8	3.08	0.41
49:2:1229:G:C5	49:2:1230:C:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1233:G:C5	49:2:1234:C:C5	3.09	0.41
49:2:1597:C:OP2	76:aa:85:ARG:NH1	2.54	0.41
53:DD:66:LEU:O	53:DD:70:VAL:HG23	2.20	0.41
56:GG:139:VAL:HG11	79:dd:27:CYS:SG	2.60	0.41
60:KK:86:VAL:HG12	60:KK:100:LEU:HD11	2.02	0.41
64:OO:11:LEU:O	64:OO:12:SER:CB	2.67	0.41
65:PP:96:LYS:HB3	65:PP:132:VAL:HG21	2.02	0.41
71:VV:22:ILE:CD1	71:VV:91:LEU:HD11	2.50	0.41
85:4:6198:A:C2'	85:4:6199:A:C3'	2.86	0.41
5:E:155:ILE:HD13	5:E:192:THR:HG21	2.02	0.41
5:E:270:LEU:HD13	12:M:107:PHE:CZ	2.54	0.41
7:G:215:ASP:CB	7:G:216:PRO:CD	2.98	0.41
12:M:86:TRP:O	12:M:86:TRP:CG	2.73	0.41
16:Q:159:PRO:O	16:Q:160:HIS:C	2.63	0.41
42:r:32:LEU:HB2	42:r:113:ARG:HD2	2.01	0.41
45:5:1803:G:OP2	45:5:1836:G:H5'	2.19	0.41
45:5:2049:G:O2'	45:5:3884:U:O2'	2.27	0.41
46:7:30:C:C2'	46:7:31:G:O5'	2.69	0.41
48:K:126:PRO:HB3	85:4:6087:G:OP2	2.21	0.41
49:2:122:G:H2'	49:2:123:G:O4'	2.20	0.41
49:2:866:U:H2'	49:2:867:G:O4'	2.20	0.41
51:BB:63:ARG:NH1	72:WW:78:ILE:HG23	2.35	0.41
53:DD:253:PRO:HG3	53:DD:256:TRP:CZ2	2.55	0.41
54:EE:57:ASN:O	54:EE:65:ARG:NH1	2.51	0.41
57:HH:57:ASP:O	57:HH:60:GLY:N	2.52	0.41
58:II:83:LEU:HD13	58:II:92:VAL:HG21	2.03	0.41
74:YY:87:ASN:HB3	74:YY:90:CYS:SG	2.60	0.41
84:jj:319:ILE:HG23	84:jj:390:GLU:HG3	2.02	0.41
1:A:95:GLN:HB2	45:5:4118:U:O4	2.21	0.41
2:B:112:ASP:O	2:B:116:ARG:HG3	2.21	0.41
2:B:378:ARG:HD3	22:W:11:TYR:CE1	2.55	0.41
3:C:140:LYS:NZ	3:C:242:PRO:O	2.52	0.41
13:N:184:ILE:O	13:N:194:ARG:NH1	2.54	0.41
15:P:120:ASN:HD22	15:P:120:ASN:N	2.18	0.41
15:P:140:MET:N	45:5:3860:A:OP1	2.48	0.41
19:T:77:ASN:N	19:T:77:ASN:HD22	2.18	0.41
25:Z:10:VAL:O	25:Z:11:VAL:HG23	2.20	0.41
45:5:448:G:C6	45:5:450:G:C5	3.09	0.41
45:5:1496:G:O5'	45:5:1496:G:H8	2.03	0.41
45:5:1516:G:C6	45:5:1518:A:C4	3.09	0.41
45:5:1667:A:C5	45:5:2280:G:N7	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:1982:G:N2	45:5:2009:A:O2'	2.43	0.41
45:5:3829:G:C2	45:5:3830:A:N7	2.89	0.41
45:5:4510:A:C2'	45:5:4511:A:O5'	2.68	0.41
45:5:4576:U:C4	45:5:4577:U:C4	3.08	0.41
45:5:5043:A:H2'	45:5:5044:A:O4'	2.20	0.41
46:7:66:G:C6	46:7:67:C:C4	3.09	0.41
49:2:374:G:C5	49:2:375:U:C5	3.08	0.41
49:2:606:G:H8	81:ff:131:ASN:HD21	1.69	0.41
49:2:1228:A:H2'	49:2:1229:G:C8	2.56	0.41
58:II:61:ILE:HD12	58:II:93:VAL:HG13	2.01	0.41
64:OO:47:PRO:HG3	64:OO:75:LEU:HD22	2.02	0.41
84:jj:78:VAL:CG2	84:jj:95:VAL:HG11	2.50	0.41
85:4:6067:G:H5'	85:4:6203:U:P	2.61	0.41
85:4:6067:G:OP2	85:4:6202:C:O3'	2.38	0.41
1:A:101:VAL:HB	1:A:165:VAL:HG12	2.01	0.41
4:D:163:LEU:HD12	4:D:163:LEU:O	2.21	0.41
5:E:136:PHE:O	5:E:137:SER:C	2.63	0.41
9:I:20:SER:OG	9:I:22:PHE:N	2.48	0.41
13:N:16:SER:CB	34:i:48:CYS:HB2	2.51	0.41
13:N:146:PRO:HG2	33:h:104:THR:HG23	2.03	0.41
15:P:92:LEU:HD12	15:P:92:LEU:O	2.21	0.41
44:t:109:ILE:HD13	44:t:133:LEU:CD2	2.50	0.41
45:5:1360:G:C6	45:5:1361:G:N7	2.88	0.41
45:5:1643:A:C6	45:5:1644:C:C4	3.08	0.41
45:5:1664:U:H2'	45:5:1665:C:C6	2.56	0.41
45:5:1910:G:N3	45:5:1917:A:C2	2.89	0.41
45:5:3659:G:C2	45:5:3686:G:C2	3.09	0.41
45:5:4729:A:OP2	45:5:5068:G:N2	2.54	0.41
45:5:5041:G:H5'	45:5:5042:A:OP1	2.21	0.41
49:2:114:G:N2	49:2:383:G:C4	2.89	0.41
49:2:123:G:N2	49:2:342:C:C2	2.88	0.41
49:2:417:C:O2'	49:2:418:A:OP1	2.36	0.41
49:2:1242:U:C5	49:2:1520:G:C8	3.09	0.41
49:2:1605:G:H2'	49:2:1606:G:C1'	2.51	0.41
49:2:1623:A:N6	69:TT:132:ARG:HE	2.19	0.41
50:3:9:G:H3'	50:3:10:G:C5'	2.51	0.41
60:KK:78:LEU:O	60:KK:79:ARG:C	2.63	0.41
64:OO:98:VAL:O	64:OO:102:LEU:HD12	2.21	0.41
76:aa:68:ILE:HB	76:aa:109:TYR:HB2	2.03	0.41
85:4:6069:U:H2'	85:4:6070:A:O4'	2.20	0.41
85:4:6092:U:H2'	85:4:6093:U:H5'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6179:U:OP1	85:4:6179:U:C3'	2.68	0.41
85:4:6182:A:H4'	85:4:6183:G:OP1	2.20	0.41
4:D:56:THR:HG22	4:D:57:ASN:N	2.36	0.41
12:M:2:VAL:HG11	45:5:4765:G:OP2	2.20	0.41
18:S:169:THR:OG1	45:5:4875:G:C8	2.66	0.41
30:e:82:VAL:HG22	30:e:111:ILE:HG12	2.02	0.41
45:5:1614:C:C4	45:5:1615:C:N4	2.88	0.41
45:5:2294:G:C4	45:5:2295:C:C5	3.09	0.41
45:5:2436:U:C2	45:5:2783:A:O4'	2.73	0.41
45:5:2439:G:C5	45:5:2440:U:C5	3.08	0.41
45:5:5057:C:H2'	45:5:5058:A:C8	2.55	0.41
48:K:113:SER:HB3	48:K:120:ILE:HD12	2.03	0.41
49:2:1825:A:H1'	85:4:6221:A:C4	2.55	0.41
50:3:55:G:C6	50:3:56:G:C6	3.09	0.41
52:CC:106:THR:O	52:CC:107:ARG:C	2.63	0.41
53:DD:200:ARG:O	60:KK:54:ARG:NH2	2.53	0.41
66:QQ:54:HIS:HA	66:QQ:57:LEU:HD13	2.02	0.41
74:YY:137:LYS:O	74:YY:138:LYS:HG2	2.20	0.41
75:ZZ:21:LYS:N	75:ZZ:75:ILE:O	2.50	0.41
83:hh:85:GLY:HA2	83:hh:108:VAL:HG23	2.02	0.41
85:4:6196:A:O5'	85:4:6196:A:H8	2.02	0.41
85:4:6199:A:N9	85:4:6200:A:C8	2.88	0.41
1:A:34:PHE:CD2	45:5:4087:G:C6	3.08	0.41
2:B:371:THR:O	2:B:372:SER:C	2.63	0.41
9:I:15:LYS:O	9:I:16:PRO:C	2.63	0.41
29:d:41:ARG:HD3	29:d:78:ARG:O	2.21	0.41
41:p:62:LYS:NZ	45:5:4121:G:N7	2.64	0.41
45:5:423:G:C2	47:8:12:G:C2	3.09	0.41
45:5:1592:G:C2	45:5:1604:G:C2	3.09	0.41
45:5:1632:A:H2'	45:5:1632:A:N3	2.35	0.41
45:5:1687:U:O2	45:5:1687:U:H2'	2.19	0.41
45:5:2053:C:O4'	45:5:2057:A:C2	2.74	0.41
45:5:2404:A:N6	45:5:2405:G:C2	2.89	0.41
45:5:2590:G:C2'	45:5:2755:A:N6	2.83	0.41
45:5:4239:A:H2'	45:5:4240:G:O4'	2.20	0.41
45:5:4602:A:C2	45:5:4610:A:C4	3.09	0.41
45:5:4681:A:C6	45:5:4682:U:C2	3.08	0.41
49:2:63:U:H2'	49:2:64:A:C5'	2.50	0.41
52:CC:197:ILE:O	52:CC:198:GLU:C	2.64	0.41
85:4:6198:A:C6	85:4:6199:A:C4	3.07	0.41
85:4:6206:G:C4	85:4:6207:A:N7	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ARG:HA	1:A:52:PRO:HD2	2.03	0.41
2:B:8:ALA:HB1	2:B:9:PRO:CD	2.50	0.41
2:B:57:VAL:HG22	2:B:73:VAL:HG12	2.02	0.41
4:D:67:ALA:HB1	19:T:31:MET:HE1	2.02	0.41
6:F:223:THR:HB	46:7:83:A:H5'	2.02	0.41
9:I:191:ILE:HD11	9:I:212:LEU:HD11	2.02	0.41
10:J:16:ARG:CZ	10:J:16:ARG:HB3	2.50	0.41
14:O:17:GLY:HA3	45:5:2053:C:H5'	2.03	0.41
14:O:40:GLY:O	14:O:41:ILE:C	2.64	0.41
16:Q:150:ARG:O	16:Q:164:LYS:HB3	2.20	0.41
17:R:78:ILE:HA	17:R:81:ARG:HD2	2.03	0.41
19:T:48:VAL:HG12	19:T:50:LYS:O	2.20	0.41
21:V:121:VAL:HG12	21:V:122:ALA:N	2.35	0.41
24:Y:43:ASN:HD22	24:Y:127:GLN:NE2	2.18	0.41
26:a:17:HIS:ND1	26:a:17:HIS:O	2.54	0.41
26:a:119:LYS:NZ	45:5:1419:G:O6	2.40	0.41
30:e:60:TYR:CE1	45:5:1900:C:H4'	2.56	0.41
45:5:929:A:C5	45:5:930:G:C2	3.09	0.41
45:5:2519:U:C2	45:5:2520:C:C5	3.08	0.41
45:5:2520:C:O2	45:5:2640:G:N2	2.54	0.41
45:5:2594:C:O2'	45:5:2595:C:H5'	2.21	0.41
45:5:2605:G:C6	45:5:2735:G:C6	3.09	0.41
45:5:3877:A:N3	45:5:4401:G:O2'	2.48	0.41
45:5:5000:G:C2	45:5:5051:C:C2	3.09	0.41
46:7:108:G:C6	46:7:109:U:C4	3.09	0.41
48:K:149:ASP:O	48:K:153:SER:N	2.53	0.41
49:2:126:G:OP1	57:HH:198:ARG:NH2	2.54	0.41
49:2:301:A:N3	59:JJ:73:THR:CG2	2.84	0.41
49:2:494:C:H2'	49:2:495:U:O4'	2.20	0.41
49:2:626:G:C6	85:4:6223:U:C2	3.09	0.41
49:2:642:U:O4	81:ff:106:LYS:NZ	2.54	0.41
49:2:846:G:C8	55:FF:19:MET:HE1	2.56	0.41
49:2:1100:A:C2	49:2:1101:U:H1'	2.56	0.41
49:2:1139:C:O2	49:2:1139:C:C3'	2.69	0.41
49:2:1290:G:C2	49:2:1291:A:C4	3.09	0.41
49:2:1328:G:C5	49:2:1329:U:C5	3.08	0.41
49:2:1707:U:C5	49:2:1708:C:C4	3.09	0.41
55:FF:133:THR:HG23	55:FF:134:LYS:HG2	2.03	0.41
58:II:43:LEU:HD23	58:II:72:PHE:CD2	2.56	0.41
58:II:167:GLU:HA	58:II:170:VAL:HG23	2.03	0.41
60:KK:144:ILE:HA	60:KK:145:PRO:HD2	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:WW:73:ALA:O	72:WW:74:LYS:C	2.64	0.41
75:ZZ:62:THR:HG22	75:ZZ:63:HIS:H	1.86	0.41
83:hh:223:GLU:O	83:hh:225:LYS:N	2.54	0.41
85:4:6196:A:C5'	85:4:6196:A:H8	2.34	0.41
85:4:6198:A:N6	85:4:6199:A:C6	2.89	0.41
85:4:6198:A:C4	85:4:6199:A:H2'	2.55	0.41
85:4:6199:A:C6	85:4:6200:A:C4	3.09	0.41
85:4:6200:A:C5	85:4:6204:A:C2	3.09	0.41
5:E:53:VAL:HB	5:E:56:ILE:HD12	2.03	0.41
7:G:127:LEU:HD23	13:N:24:ARG:HH11	1.85	0.41
8:H:79:ASN:HD22	8:H:151:ILE:HG21	1.86	0.41
9:I:91:LEU:CD1	9:I:135:ILE:HG23	2.46	0.41
13:N:22:LEU:C	13:N:24:ARG:H	2.29	0.41
15:P:90:PHE:O	15:P:93:HIS:N	2.43	0.41
15:P:127:ARG:O	15:P:139:TYR:HB3	2.21	0.41
23:X:80:PRO:HG2	23:X:155:ILE:CG2	2.51	0.41
29:d:26:THR:HA	29:d:84:ILE:O	2.20	0.41
42:r:23:GLN:C	42:r:24:THR:OG1	2.64	0.41
45:5:972:C:C6	45:5:1281:G:C6	3.09	0.41
45:5:1835:G:O2'	45:5:1836:G:P	2.79	0.41
45:5:2695:A:C5	45:5:2697:A:C5	3.09	0.41
45:5:4418:G:C4	45:5:4421:C:N4	2.88	0.41
45:5:4459:U:H2'	45:5:4460:U:O4'	2.21	0.41
45:5:4596:C:C5	45:5:4597:U:C4	3.08	0.41
55:FF:58:GLY:O	55:FF:59:ASP:C	2.63	0.41
58:II:98:ARG:HD3	58:II:125:VAL:HG22	2.03	0.41
85:4:6161:A:C4	85:4:6162:A:C8	3.09	0.41
85:4:6197:A:C8	85:4:6197:A:OP2	2.70	0.41
2:B:92:TYR:CE1	2:B:101:THR:HB	2.56	0.40
2:B:114:CYS:SG	2:B:180:LEU:HD13	2.61	0.40
3:C:172:LYS:HE3	3:C:177:TRP:CE2	2.56	0.40
11:L:5:ARG:O	11:L:6:ASN:C	2.65	0.40
14:O:133:ARG:CZ	45:5:1928:C:N4	2.84	0.40
15:P:73:ALA:O	15:P:76:TRP:N	2.55	0.40
33:h:70:ARG:HB3	33:h:83:LEU:HD22	2.03	0.40
35:j:34:CYS:SG	35:j:37:CYS:SG	3.19	0.40
45:5:198:A:N1	45:5:237:G:H5'	2.35	0.40
45:5:976:G:C8	45:5:976:G:O5'	2.74	0.40
49:2:191:A:C2'	49:2:192:C:OP1	2.69	0.40
49:2:1709:G:C6	49:2:1826:G:C6	3.10	0.40
49:2:1865:C:OP2	77:bb:5:ARG:NH1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:FF:121:TYR:HA	55:FF:163:ASP:HA	2.03	0.40
59:JJ:35:ASN:N	59:JJ:35:ASN:ND2	2.64	0.40
61:LL:1:MET:HE1	61:LL:43:LEU:HD12	2.03	0.40
70:UU:60:THR:HG23	70:UU:75:MET:CE	2.50	0.40
85:4:6201:C:C5	85:4:6204:A:N1	2.89	0.40
7:G:107:PHE:O	45:5:4085:A:H2'	2.21	0.40
16:Q:148:VAL:HG12	16:Q:152:PHE:CZ	2.56	0.40
19:T:33:ILE:CD1	19:T:35:LYS:HG2	2.52	0.40
29:d:30:HIS:HB2	29:d:82:TYR:HD1	1.87	0.40
32:g:68:SER:O	32:g:69:LYS:C	2.64	0.40
44:t:116:MET:HG3	44:t:132:ILE:HD11	2.01	0.40
45:5:29:G:C6	45:5:30:C:C5	3.09	0.40
45:5:381:U:C4	45:5:382:G:C5	3.09	0.40
45:5:1589:C:H6	45:5:1589:C:O5'	2.04	0.40
45:5:1867:A:N3	45:5:4403:U:O2'	2.54	0.40
45:5:1990:A:H3'	45:5:1991:A:H5''	2.03	0.40
45:5:2811:G:N2	45:5:2813:A:H3'	2.36	0.40
45:5:4454:G:N2	45:5:4455:G:H1'	2.36	0.40
49:2:1044:G:OP2	49:2:1044:G:H8	2.04	0.40
49:2:1531:A:C2'	49:2:1532:C:O4'	2.69	0.40
49:2:1788:A:N6	49:2:1789:G:C6	2.89	0.40
49:2:1853:C:H2'	49:2:1854:U:C6	2.56	0.40
51:BB:122:LEU:HD13	51:BB:142:LEU:HD13	2.04	0.40
69:TT:26:ILE:HG22	69:TT:45:LEU:HD11	2.01	0.40
81:ff:119:VAL:HG23	81:ff:121:THR:CG2	2.51	0.40
83:hh:146:SER:OG	83:hh:147:HIS:N	2.54	0.40
85:4:6034:A:N1	85:4:6090:A:H2	2.20	0.40
10:J:53:ALA:HB2	10:J:68:ILE:HD11	2.03	0.40
12:M:29:ASP:CB	12:M:37:LEU:HD12	2.51	0.40
13:N:73:ARG:NE	13:N:88:GLY:O	2.55	0.40
17:R:26:PRO:O	17:R:27:ASN:C	2.63	0.40
22:W:81:ALA:HB2	22:W:87:LEU:HA	2.02	0.40
23:X:127:LEU:C	23:X:127:LEU:HD12	2.45	0.40
29:d:22:THR:HG22	29:d:89:SER:HB3	2.02	0.40
29:d:59:THR:HG1	29:d:104:THR:HG1	1.53	0.40
30:e:104:SER:O	30:e:108:ARG:HB2	2.20	0.40
37:l:12:PHE:CE2	37:l:51:LEU:HD11	2.56	0.40
45:5:466:A:C2	45:5:468:U:C5	3.10	0.40
45:5:1353:G:O2'	45:5:1503:A:N1	2.54	0.40
45:5:1358:G:N7	45:5:1379:C:N4	2.69	0.40
45:5:1383:G:C5	45:5:1384:C:C4	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:2033:A:N3	45:5:2034:G:C8	2.89	0.40
45:5:4498:U:H2'	45:5:4500:U:OP2	2.20	0.40
47:8:131:G:C6	47:8:132:G:N7	2.89	0.40
49:2:1248:U:O2'	67:RR:145:TYR:HB3	2.21	0.40
49:2:1289:U:O5'	49:2:1289:U:H6	2.04	0.40
65:PP:62:VAL:HG21	65:PP:73:ALA:HB2	2.01	0.40
75:ZZ:79:LEU:O	75:ZZ:80:ASP:C	2.65	0.40
3:C:118:THR:HA	3:C:121:ARG:HB2	2.03	0.40
6:F:53:ALA:HB2	6:F:187:GLU:HG3	2.02	0.40
7:G:215:ASP:HB2	7:G:216:PRO:CD	2.52	0.40
9:I:16:PRO:HA	9:I:95:HIS:HD2	1.86	0.40
11:L:34:ARG:O	11:L:35:ARG:C	2.63	0.40
12:M:123:ILE:O	12:M:127:VAL:HG23	2.21	0.40
14:O:169:ARG:NE	45:5:4860:G:OP1	2.54	0.40
14:O:181:ALA:O	14:O:182:GLU:C	2.63	0.40
16:Q:147:GLU:O	16:Q:150:ARG:N	2.38	0.40
19:T:33:ILE:HD12	19:T:33:ILE:O	2.21	0.40
30:e:53:ILE:HG22	30:e:54:LEU:O	2.21	0.40
30:e:89:LEU:HD12	30:e:89:LEU:C	2.45	0.40
31:f:43:LEU:HD22	31:f:76:ARG:HA	2.04	0.40
34:i:44:ILE:O	34:i:45:ARG:C	2.63	0.40
45:5:200:U:HO2'	45:5:201:C:P	2.45	0.40
45:5:963:G:H22	45:5:970:G:P	2.44	0.40
45:5:2082:G:C6	45:5:2083:C:N4	2.89	0.40
45:5:4428:A:H2'	45:5:4429:C:O4'	2.22	0.40
45:5:4923:U:H2'	45:5:4924:C:C6	2.56	0.40
46:7:32:A:N7	46:7:41:G:C8	2.89	0.40
49:2:55:U:O2	49:2:55:U:C2'	2.70	0.40
49:2:622:C:C4	49:2:623:G:H1'	2.57	0.40
49:2:1104:G:C2	49:2:1129:G:C2	3.09	0.40
49:2:1337:C:H2'	49:2:1338:G:C8	2.57	0.40
49:2:1356:G:O2'	49:2:1357:A:C8	2.73	0.40
49:2:1676:U:H5''	49:2:1677:U:OP2	2.21	0.40
53:DD:216:MET:O	53:DD:217:ALA:C	2.63	0.40
55:FF:18:TRP:HB3	55:FF:46:ILE:HD13	2.03	0.40
58:II:95:ILE:HD13	58:II:180:LEU:HD11	2.03	0.40
60:KK:45:ARG:O	60:KK:49:THR:HG23	2.21	0.40
61:LL:12:TYR:CB	61:LL:83:LEU:HD21	2.50	0.40
75:ZZ:55:ILE:HG23	75:ZZ:75:ILE:HG12	2.02	0.40
81:ff:84:LYS:NZ	81:ff:88:GLN:HE22	2.19	0.40
85:4:6043:U:H1'	85:4:6044:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:MET:HE3	45:5:4626:A:H5'	2.04	0.40
2:B:241:PRO:O	2:B:244:THR:OG1	2.40	0.40
4:D:52:ILE:HD13	46:7:6:C:H4'	2.04	0.40
5:E:45:HIS:ND1	5:E:46:CYS:O	2.49	0.40
7:G:201:GLU:CD	7:G:226:LEU:HD11	2.46	0.40
8:H:127:ARG:C	8:H:128:MET:O	2.64	0.40
11:L:120:TYR:O	11:L:121:ARG:C	2.63	0.40
12:M:39:ASP:CG	12:M:40:GLY:N	2.78	0.40
15:P:116:HIS:CB	15:P:149:ILE:HB	2.48	0.40
16:Q:37:ARG:NE	45:5:2087:C:OP2	2.46	0.40
17:R:89:MET:HA	17:R:90:PRO:HD3	1.95	0.40
18:S:82:LEU:HD22	18:S:126:ILE:HD13	2.03	0.40
44:t:32:ILE:HD13	44:t:42:VAL:HG21	2.04	0.40
45:5:64:A:H61	45:5:334:A:N6	2.14	0.40
45:5:131:C:O2	45:5:138:G:C2	2.73	0.40
45:5:2694:G:H4'	45:5:2695:A:O5'	2.21	0.40
45:5:5041:G:H3'	45:5:5041:G:H8	1.87	0.40
49:2:1149:A:C4	49:2:1151:G:C8	3.10	0.40
49:2:1707:U:C5	49:2:1708:C:C5	3.09	0.40
49:2:1748:G:C2	49:2:1787:G:C2	3.09	0.40
49:2:1819:A:H2'	49:2:1820:G:O4'	2.22	0.40
53:DD:174:ILE:HG23	53:DD:174:ILE:O	2.21	0.40
53:DD:209:VAL:HB	53:DD:210:PRO:HD3	2.04	0.40
57:HH:217:MET:O	57:HH:221:LYS:N	2.54	0.40
60:KK:110:LEU:HD21	60:KK:135:ILE:CD1	2.51	0.40
63:NN:35:ILE:HD13	63:NN:108:CYS:SG	2.61	0.40
83:hh:38:LYS:N	83:hh:38:LYS:CD	2.85	0.40
83:hh:187:ASN:O	83:hh:188:HIS:ND1	2.55	0.40
84:jj:121:ASN:O	84:jj:164:ASN:ND2	2.51	0.40
85:4:6053:U:O2	85:4:6073:A:C2	2.75	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	237/257 (92%)	183 (77%)	45 (19%)	9 (4%)	2	18
2	B	392/403 (97%)	327 (83%)	46 (12%)	19 (5%)	2	14
3	C	358/392 (91%)	298 (83%)	48 (13%)	12 (3%)	3	20
4	D	291/297 (98%)	257 (88%)	29 (10%)	5 (2%)	7	35
5	E	208/291 (72%)	173 (83%)	29 (14%)	6 (3%)	3	24
6	F	223/249 (90%)	193 (86%)	24 (11%)	6 (3%)	4	25
7	G	229/242 (95%)	202 (88%)	25 (11%)	2 (1%)	14	47
8	H	188/192 (98%)	157 (84%)	20 (11%)	11 (6%)	1	10
9	I	201/214 (94%)	171 (85%)	24 (12%)	6 (3%)	3	23
10	J	168/178 (94%)	144 (86%)	20 (12%)	4 (2%)	4	28
11	L	208/211 (99%)	184 (88%)	19 (9%)	5 (2%)	4	28
12	M	133/198 (67%)	108 (81%)	20 (15%)	5 (4%)	2	18
13	N	201/204 (98%)	171 (85%)	25 (12%)	5 (2%)	4	27
14	O	194/199 (98%)	167 (86%)	25 (13%)	2 (1%)	12	45
15	P	151/184 (82%)	123 (82%)	22 (15%)	6 (4%)	2	17
16	Q	185/188 (98%)	154 (83%)	24 (13%)	7 (4%)	2	18
17	R	178/181 (98%)	148 (83%)	24 (14%)	6 (3%)	3	20
18	S	174/176 (99%)	142 (82%)	26 (15%)	6 (3%)	3	20
19	T	157/160 (98%)	128 (82%)	22 (14%)	7 (4%)	2	15
20	U	97/128 (76%)	80 (82%)	14 (14%)	3 (3%)	3	22
21	V	127/140 (91%)	107 (84%)	16 (13%)	4 (3%)	3	22
22	W	102/157 (65%)	87 (85%)	9 (9%)	6 (6%)	1	10
23	X	116/156 (74%)	101 (87%)	11 (10%)	4 (3%)	3	20
24	Y	132/145 (91%)	106 (80%)	23 (17%)	3 (2%)	5	29
25	Z	133/136 (98%)	108 (81%)	21 (16%)	4 (3%)	3	23
26	a	145/148 (98%)	115 (79%)	28 (19%)	2 (1%)	9	39
27	b	100/226 (44%)	86 (86%)	10 (10%)	4 (4%)	2	17
28	c	96/115 (84%)	87 (91%)	9 (9%)	0	100	100
29	d	105/125 (84%)	87 (83%)	13 (12%)	5 (5%)	2	14
30	e	126/135 (93%)	97 (77%)	24 (19%)	5 (4%)	2	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	f	107/110 (97%)	91 (85%)	13 (12%)	3 (3%)	4	25
32	g	112/126 (89%)	91 (81%)	14 (12%)	7 (6%)	1	8
33	h	120/123 (98%)	99 (82%)	19 (16%)	2 (2%)	7	35
34	i	100/105 (95%)	90 (90%)	10 (10%)	0	100	100
35	j	84/97 (87%)	67 (80%)	11 (13%)	6 (7%)	1	6
36	k	67/70 (96%)	51 (76%)	12 (18%)	4 (6%)	1	10
37	l	48/51 (94%)	38 (79%)	7 (15%)	3 (6%)	1	8
38	m	50/52 (96%)	42 (84%)	8 (16%)	0	100	100
39	n	23/25 (92%)	17 (74%)	5 (22%)	1 (4%)	2	16
40	o	102/106 (96%)	94 (92%)	6 (6%)	2 (2%)	6	31
41	p	89/92 (97%)	74 (83%)	11 (12%)	4 (4%)	2	15
42	r	122/137 (89%)	95 (78%)	14 (12%)	13 (11%)	0	2
43	s	194/303 (64%)	163 (84%)	27 (14%)	4 (2%)	5	31
44	t	151/195 (77%)	126 (83%)	22 (15%)	3 (2%)	6	31
48	K	204/217 (94%)	143 (70%)	51 (25%)	10 (5%)	1	13
51	BB	215/295 (73%)	193 (90%)	19 (9%)	3 (1%)	9	39
52	CC	211/264 (80%)	174 (82%)	33 (16%)	4 (2%)	6	33
53	DD	219/255 (86%)	185 (84%)	30 (14%)	4 (2%)	6	34
54	EE	226/281 (80%)	187 (83%)	36 (16%)	3 (1%)	9	40
55	FF	260/263 (99%)	212 (82%)	37 (14%)	11 (4%)	2	16
56	GG	181/204 (89%)	153 (84%)	19 (10%)	9 (5%)	1	13
57	HH	235/249 (94%)	197 (84%)	32 (14%)	6 (3%)	4	26
58	II	181/194 (93%)	147 (81%)	22 (12%)	12 (7%)	1	7
59	JJ	204/208 (98%)	173 (85%)	23 (11%)	8 (4%)	2	18
60	KK	183/194 (94%)	155 (85%)	23 (13%)	5 (3%)	4	25
61	LL	94/149 (63%)	84 (89%)	9 (10%)	1 (1%)	11	43
62	MM	139/158 (88%)	120 (86%)	16 (12%)	3 (2%)	5	29
63	NN	115/132 (87%)	91 (79%)	20 (17%)	4 (4%)	3	20
64	OO	147/151 (97%)	118 (80%)	22 (15%)	7 (5%)	2	14
65	PP	134/151 (89%)	116 (87%)	17 (13%)	1 (1%)	18	52
66	QQ	113/145 (78%)	83 (74%)	26 (23%)	4 (4%)	3	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	RR	140/172 (81%)	123 (88%)	16 (11%)	1 (1%)	18	52
68	SS	130/135 (96%)	114 (88%)	15 (12%)	1 (1%)	16	50
69	TT	142/152 (93%)	125 (88%)	14 (10%)	3 (2%)	5	31
70	UU	139/145 (96%)	120 (86%)	17 (12%)	2 (1%)	9	39
71	VV	98/119 (82%)	82 (84%)	14 (14%)	2 (2%)	6	31
72	WW	81/83 (98%)	71 (88%)	6 (7%)	4 (5%)	1	13
73	XX	127/130 (98%)	107 (84%)	17 (13%)	3 (2%)	4	28
74	YY	139/143 (97%)	112 (81%)	21 (15%)	6 (4%)	2	16
75	ZZ	122/134 (91%)	103 (84%)	17 (14%)	2 (2%)	7	36
76	aa	73/125 (58%)	65 (89%)	7 (10%)	1 (1%)	9	39
77	bb	99/115 (86%)	77 (78%)	16 (16%)	6 (6%)	1	9
78	cc	81/84 (96%)	66 (82%)	13 (16%)	2 (2%)	4	27
79	dd	60/69 (87%)	50 (83%)	9 (15%)	1 (2%)	7	35
80	ee	53/56 (95%)	33 (62%)	18 (34%)	2 (4%)	2	18
81	ff	55/133 (41%)	44 (80%)	9 (16%)	2 (4%)	2	19
82	gg	66/156 (42%)	49 (74%)	16 (24%)	1 (2%)	8	37
83	hh	310/317 (98%)	237 (76%)	69 (22%)	4 (1%)	9	40
84	jj	414/437 (95%)	344 (83%)	65 (16%)	5 (1%)	10	42
All	All	12114/13834 (88%)	10082 (83%)	1668 (14%)	364 (3%)	5	23

All (364) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	104	VAL
1	A	196	TRP
2	B	8	ALA
2	B	9	PRO
2	B	135	LYS
2	B	259	PRO
2	B	260	ALA
2	B	286	LYS
2	B	342	LYS
3	C	90	GLY
3	C	126	SER
3	C	150	LEU
4	D	44	TYR

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Mol	Chain	Res	Type
4	D	155	THR
5	E	186	ARG
5	E	194	GLN
6	F	136	GLU
6	F	137	PRO
6	F	179	GLY
8	H	128	MET
8	H	139	ALA
9	I	12	CYS
11	L	47	ALA
11	L	63	THR
12	M	19	PRO
15	P	114	ILE
16	Q	55	ARG
16	Q	148	VAL
16	Q	177	ALA
17	R	37	SER
19	T	79	GLN
19	T	80	VAL
22	W	47	ARG
23	X	94	ASN
23	X	118	ASP
25	Z	90	PRO
25	Z	100	VAL
26	a	114	LYS
27	b	7	HIS
29	d	74	ALA
30	e	42	ASP
30	e	43	ASN
31	f	107	PRO
32	g	16	ALA
32	g	69	LYS
33	h	94	ARG
35	j	25	LYS
36	k	30	ASP
36	k	62	PRO
42	r	11	ARG
42	r	13	CYS
42	r	20	ARG
42	r	69	GLY
42	r	121	GLN
43	s	46	SER

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Mol	Chain	Res	Type
48	K	95	LYS
48	K	201	VAL
51	BB	44	ASP
52	CC	190	PRO
53	DD	134	ASN
53	DD	174	ILE
55	FF	79	ASP
55	FF	144	ALA
55	FF	240	ARG
56	GG	55	ARG
56	GG	80	GLY
58	II	13	GLY
58	II	88	SER
58	II	107	LYS
58	II	119	SER
58	II	122	LEU
58	II	135	PHE
60	KK	19	PRO
62	MM	57	ASP
63	NN	45	ARG
64	OO	12	SER
72	WW	31	SER
72	WW	74	LYS
73	XX	28	ARG
74	YY	5	ARG
74	YY	10	ALA
74	YY	62	PRO
74	YY	65	ALA
74	YY	86	PRO
81	ff	106	LYS
81	ff	107	ARG
82	gg	89	LYS
83	hh	187	ASN
84	jj	314	MET
1	A	143	THR
1	A	234	LYS
1	A	241	ARG
2	B	228	TYR
2	B	264	PHE
2	B	304	SER
2	B	309	LEU
2	B	329	ASP

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Mol	Chain	Res	Type
3	C	194	GLY
3	C	288	ASP
4	D	222	GLN
6	F	99	GLY
7	G	239	GLY
8	H	40	HIS
8	H	52	LYS
8	H	61	TRP
8	H	85	THR
8	H	98	HIS
9	I	16	PRO
10	J	141	ILE
10	J	143	ASP
11	L	4	SER
11	L	95	GLY
13	N	57	GLN
13	N	184	ILE
13	N	201	HIS
14	O	20	ALA
16	Q	75	ARG
16	Q	159	PRO
17	R	100	ARG
18	S	166	ARG
20	U	67	LYS
22	W	15	PRO
23	X	119	ILE
29	d	58	GLY
32	g	60	ARG
32	g	76	ARG
33	h	47	ILE
35	j	77	GLY
37	l	19	GLN
37	l	20	ASN
37	l	31	THR
39	n	23	ARG
42	r	33	LYS
42	r	44	ILE
42	r	55	ALA
42	r	107	ARG
44	t	67	ARG
48	K	14	VAL
48	K	16	GLU

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Mol	Chain	Res	Type
48	K	199	GLN
53	DD	77	SER
55	FF	59	ASP
55	FF	132	GLY
56	GG	20	PHE
56	GG	41	VAL
56	GG	79	HIS
57	HH	68	LEU
57	HH	134	GLY
58	II	48	ALA
58	II	54	GLY
58	II	75	ILE
59	JJ	48	VAL
59	JJ	56	ARG
59	JJ	71	CYS
59	JJ	140	LYS
60	KK	146	SER
61	LL	39	ASN
62	MM	151	THR
64	OO	8	GLY
64	OO	26	LEU
64	OO	59	GLY
64	OO	103	GLU
64	OO	108	ASP
66	QQ	70	MET
66	QQ	104	GLN
70	UU	95	GLY
70	UU	111	LYS
76	aa	104	ARG
77	bb	26	CYS
77	bb	94	ASP
79	dd	49	PRO
80	ee	7	TYR
83	hh	161	SER
83	hh	224	GLY
84	jj	217	ASP
1	A	34	PHE
1	A	197	PRO
2	B	236	HIS
2	B	269	ALA
2	B	348	ARG
2	B	376	HIS

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Mol	Chain	Res	Type
3	C	18	SER
8	H	108	ASN
12	M	9	VAL
12	M	53	LYS
13	N	100	SER
14	O	70	PRO
16	Q	157	GLY
16	Q	160	HIS
18	S	161	ARG
18	S	165	PRO
19	T	60	LYS
19	T	81	LYS
20	U	45	GLU
21	V	92	ASP
27	b	36	ASP
27	b	37	PRO
29	d	96	GLU
29	d	116	ASN
30	e	125	PRO
31	f	37	ASP
31	f	60	PRO
32	g	50	PRO
35	j	12	ARG
35	j	26	ALA
36	k	40	ARG
41	p	7	LYS
42	r	68	SER
42	r	120	SER
43	s	34	ASN
44	t	94	LYS
48	K	43	PRO
48	K	83	PRO
48	K	193	LEU
52	CC	123	ALA
52	CC	202	GLN
54	EE	32	ASP
55	FF	223	SER
56	GG	16	ASP
57	HH	122	PRO
57	HH	198	ARG
65	PP	24	GLY
66	QQ	49	LEU

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Mol	Chain	Res	Type
71	VV	105	SER
72	WW	30	ALA
72	WW	73	ALA
73	XX	7	LEU
75	ZZ	64	PHE
77	bb	35	ALA
83	hh	13	GLY
1	A	31	ALA
2	B	198	ARG
3	C	65	GLU
3	C	75	ARG
3	C	141	GLY
4	D	46	THR
4	D	170	GLY
5	E	43	LYS
7	G	215	ASP
8	H	41	ILE
9	I	47	PRO
9	I	144	ASN
10	J	103	GLY
10	J	146	ARG
11	L	28	GLN
12	M	89	THR
15	P	21	ASN
15	P	36	ILE
17	R	35	ALA
17	R	84	THR
17	R	138	LEU
17	R	141	HIS
18	S	155	PRO
19	T	29	THR
21	V	22	VAL
21	V	74	LYS
21	V	75	LYS
22	W	19	ARG
22	W	27	LYS
23	X	42	THR
27	b	29	TYR
32	g	3	GLN
35	j	21	ARG
40	o	24	THR
41	p	9	GLY

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Mol	Chain	Res	Type
42	r	119	ARG
48	K	162	VAL
51	BB	137	ALA
54	EE	112	GLY
55	FF	155	LYS
55	FF	241	GLY
57	HH	135	PRO
59	JJ	92	ARG
59	JJ	123	ARG
59	JJ	143	LYS
60	KK	17	ARG
60	KK	41	ARG
66	QQ	18	ARG
67	RR	135	PRO
69	TT	100	ALA
71	VV	70	CYS
74	YY	92	ASN
77	bb	47	ALA
78	cc	59	CYS
80	ee	43	PHE
2	B	314	ILE
2	B	340	THR
3	C	4	ALA
3	C	6	PRO
3	C	265	GLY
5	E	93	ALA
6	F	230	GLY
9	I	117	GLY
22	W	11	TYR
24	Y	83	GLU
25	Z	7	PRO
25	Z	49	TYR
32	g	59	VAL
35	j	78	PHE
41	p	18	TYR
42	r	56	ASP
43	s	80	PRO
54	EE	93	THR
56	GG	43	GLU
57	HH	8	PRO
59	JJ	41	ARG
60	KK	147	PHE

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Mol	Chain	Res	Type
63	NN	59	PRO
63	NN	80	ASP
63	NN	95	ASP
69	TT	49	ASP
69	TT	137	LYS
77	bb	51	ARG
77	bb	61	ALA
78	cc	81	ARG
84	jj	118	LYS
84	jj	162	GLN
8	H	13	PRO
9	I	99	ILE
19	T	61	THR
20	U	28	PRO
22	W	8	PHE
24	Y	101	PRO
26	a	76	ASP
36	k	59	SER
52	CC	64	GLY
55	FF	17	HIS
55	FF	73	ASP
55	FF	231	GLY
56	GG	83	ASN
58	II	115	LYS
73	XX	95	PRO
84	jj	89	PRO
13	N	60	VAL
15	P	65	GLY
18	S	164	LYS
29	d	64	ILE
41	p	54	ILE
48	K	58	THR
51	BB	101	GLY
58	II	22	GLY
64	OO	79	GLY
15	P	7	ASP
15	P	117	ILE
30	e	41	ILE
30	e	59	GLY
58	II	8	ILE
75	ZZ	59	GLY
19	T	6	GLY

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Mol	Chain	Res	Type
24	Y	22	PRO
40	o	95	GLY
43	s	114	GLY
68	SS	69	ILE
1	A	230	PRO
5	E	188	PRO
5	E	209	VAL
6	F	229	GLY
8	H	4	ILE
12	M	25	VAL
18	S	158	VAL
56	GG	21	GLY
62	MM	150	GLY
44	t	36	GLY
53	DD	130	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	172/199 (86%)	146 (85%)	26 (15%)	3	14
2	B	342/348 (98%)	287 (84%)	55 (16%)	2	13
3	C	302/323 (94%)	267 (88%)	35 (12%)	5	24
4	D	247/250 (99%)	221 (90%)	26 (10%)	6	28
5	E	190/251 (76%)	170 (90%)	20 (10%)	6	28
6	F	196/218 (90%)	177 (90%)	19 (10%)	8	32
7	G	200/208 (96%)	179 (90%)	21 (10%)	6	28
8	H	169/171 (99%)	154 (91%)	15 (9%)	9	34
9	I	175/181 (97%)	147 (84%)	28 (16%)	2	13
10	J	143/149 (96%)	132 (92%)	11 (8%)	12	41
11	L	175/176 (99%)	158 (90%)	17 (10%)	8	32
12	M	116/151 (77%)	96 (83%)	20 (17%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	N	171/172 (99%)	148 (86%)	23 (14%)	4	19
14	O	170/171 (99%)	141 (83%)	29 (17%)	2	11
15	P	134/163 (82%)	114 (85%)	20 (15%)	3	15
16	Q	164/165 (99%)	140 (85%)	24 (15%)	3	16
17	R	159/160 (99%)	135 (85%)	24 (15%)	3	14
18	S	157/157 (100%)	138 (88%)	19 (12%)	5	22
19	T	139/140 (99%)	124 (89%)	15 (11%)	6	27
20	U	89/114 (78%)	85 (96%)	4 (4%)	24	58
21	V	100/107 (94%)	81 (81%)	19 (19%)	1	9
22	W	86/126 (68%)	77 (90%)	9 (10%)	6	28
23	X	106/134 (79%)	91 (86%)	15 (14%)	3	17
24	Y	124/135 (92%)	98 (79%)	26 (21%)	1	6
25	Z	117/118 (99%)	101 (86%)	16 (14%)	3	18
26	a	119/120 (99%)	109 (92%)	10 (8%)	10	38
27	b	84/172 (49%)	78 (93%)	6 (7%)	13	44
28	c	84/98 (86%)	71 (84%)	13 (16%)	2	14
29	d	98/110 (89%)	91 (93%)	7 (7%)	13	44
30	e	114/121 (94%)	98 (86%)	16 (14%)	3	17
31	f	88/89 (99%)	72 (82%)	16 (18%)	2	9
32	g	98/106 (92%)	85 (87%)	13 (13%)	4	19
33	h	109/110 (99%)	98 (90%)	11 (10%)	7	30
34	i	86/89 (97%)	78 (91%)	8 (9%)	8	33
35	j	73/80 (91%)	65 (89%)	8 (11%)	6	26
36	k	64/65 (98%)	57 (89%)	7 (11%)	6	26
37	l	47/48 (98%)	38 (81%)	9 (19%)	1	9
38	m	48/48 (100%)	38 (79%)	10 (21%)	1	7
39	n	24/24 (100%)	19 (79%)	5 (21%)	1	7
40	o	92/94 (98%)	79 (86%)	13 (14%)	3	17
41	p	74/75 (99%)	61 (82%)	13 (18%)	2	10
42	r	108/121 (89%)	94 (87%)	14 (13%)	4	20
43	s	164/258 (64%)	160 (98%)	4 (2%)	43	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	t	126/163 (77%)	120 (95%)	6 (5%)	23	56
48	K	190/196 (97%)	171 (90%)	19 (10%)	7	30
51	BB	180/246 (73%)	168 (93%)	12 (7%)	15	47
52	CC	194/231 (84%)	178 (92%)	16 (8%)	10	39
53	DD	187/206 (91%)	163 (87%)	24 (13%)	4	20
54	EE	190/232 (82%)	166 (87%)	24 (13%)	4	21
55	FF	224/225 (100%)	193 (86%)	31 (14%)	3	18
56	GG	158/170 (93%)	144 (91%)	14 (9%)	9	34
57	HH	207/218 (95%)	188 (91%)	19 (9%)	8	33
58	II	165/174 (95%)	139 (84%)	26 (16%)	2	13
59	JJ	178/180 (99%)	152 (85%)	26 (15%)	3	16
60	KK	161/168 (96%)	148 (92%)	13 (8%)	11	39
61	LL	87/125 (70%)	80 (92%)	7 (8%)	11	40
62	MM	130/142 (92%)	113 (87%)	17 (13%)	4	19
63	NN	99/108 (92%)	95 (96%)	4 (4%)	28	61
64	OO	130/131 (99%)	112 (86%)	18 (14%)	3	18
65	PP	106/119 (89%)	92 (87%)	14 (13%)	4	19
66	QQ	105/130 (81%)	95 (90%)	10 (10%)	8	32
67	RR	117/140 (84%)	109 (93%)	8 (7%)	14	46
68	SS	119/121 (98%)	106 (89%)	13 (11%)	6	26
69	TT	125/132 (95%)	118 (94%)	7 (6%)	19	52
70	UU	111/116 (96%)	105 (95%)	6 (5%)	20	53
71	VV	92/107 (86%)	80 (87%)	12 (13%)	4	20
72	WW	67/67 (100%)	61 (91%)	6 (9%)	9	34
73	XX	112/113 (99%)	98 (88%)	14 (12%)	4	21
74	YY	113/114 (99%)	96 (85%)	17 (15%)	3	15
75	ZZ	107/115 (93%)	95 (89%)	12 (11%)	6	25
76	aa	66/103 (64%)	64 (97%)	2 (3%)	36	66
77	bb	88/98 (90%)	80 (91%)	8 (9%)	9	34
78	cc	75/76 (99%)	67 (89%)	8 (11%)	6	27
79	dd	55/62 (89%)	53 (96%)	2 (4%)	31	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	ee	48/49 (98%)	43 (90%)	5 (10%)	7	28
81	ff	47/106 (44%)	42 (89%)	5 (11%)	6	27
82	gg	61/140 (44%)	54 (88%)	7 (12%)	5	24
83	hh	272/275 (99%)	244 (90%)	28 (10%)	7	28
84	jj	358/376 (95%)	323 (90%)	35 (10%)	7	31
All	All	10567/11789 (90%)	9353 (88%)	1214 (12%)	8	24

All (1214) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	20	VAL
1	A	29	LEU
1	A	32	VAL
1	A	40	TYR
1	A	44	ILE
1	A	70	LYS
1	A	73	THR
1	A	86	GLN
1	A	96	LEU
1	A	109	GLU
1	A	114	CYS
1	A	115	CYS
1	A	125	LYS
1	A	128	ARG
1	A	142	GLU
1	A	158	ILE
1	A	175	ILE
1	A	179	ILE
1	A	184	ARG
1	A	193	ARG
1	A	206	PRO
1	A	207	VAL
1	A	233	ARG
1	A	237	LEU
1	A	242	ARG
2	B	4	ARG
2	B	5	LYS
2	B	14	LEU
2	B	36	ASP

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Mol	Chain	Res	Type
2	B	53	MET
2	B	56	ILE
2	B	65	SER
2	B	67	VAL
2	B	73	VAL
2	B	74	GLU
2	B	77	THR
2	B	78	ILE
2	B	94	GLU
2	B	99	LEU
2	B	104	THR
2	B	114	CYS
2	B	115	LYS
2	B	124	LYS
2	B	126	LYS
2	B	138	GLN
2	B	154	LYS
2	B	158	GLN
2	B	160	ILE
2	B	162	VAL
2	B	168	MET
2	B	173	LEU
2	B	180	LEU
2	B	181	MET
2	B	184	GLN
2	B	207	VAL
2	B	223	THR
2	B	234	ARG
2	B	244	THR
2	B	246	ARG
2	B	254	ILE
2	B	258	HIS
2	B	262	VAL
2	B	266	VAL
2	B	286	LYS
2	B	298	LEU
2	B	308	ASP
2	B	309	LEU
2	B	310	SER
2	B	322	HIS
2	B	337	VAL
2	B	340	THR

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Mol	Chain	Res	Type
2	B	344	VAL
2	B	349	LYS
2	B	351	LEU
2	B	352	LEU
2	B	354	GLN
2	B	369	ASP
2	B	376	HIS
2	B	381	THR
2	B	386	LYS
3	C	7	LEU
3	C	35	ASP
3	C	42	THR
3	C	63	SER
3	C	71	ARG
3	C	73	VAL
3	C	85	HIS
3	C	100	ARG
3	C	118	THR
3	C	121	ARG
3	C	125	CYS
3	C	147	VAL
3	C	180	ILE
3	C	188	ARG
3	C	195	LYS
3	C	202	ILE
3	C	208	CYS
3	C	213	GLU
3	C	228	THR
3	C	230	LEU
3	C	234	LYS
3	C	246	VAL
3	C	248	ARG
3	C	260	LEU
3	C	261	ASP
3	C	262	ASP
3	C	267	TRP
3	C	284	MET
3	C	289	LEU
3	C	297	GLU
3	C	307	LYS
3	C	312	ARG
3	C	348	LYS

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Mol	Chain	Res	Type
3	C	351	VAL
3	C	353	ARG
4	D	7	VAL
4	D	18	VAL
4	D	23	ARG
4	D	34	LYS
4	D	36	LEU
4	D	43	LYS
4	D	45	ASN
4	D	59	ASP
4	D	93	THR
4	D	104	LEU
4	D	120	GLU
4	D	136	ASP
4	D	138	GLN
4	D	143	THR
4	D	146	LEU
4	D	152	ARG
4	D	163	LEU
4	D	189	GLU
4	D	191	ASN
4	D	193	GLU
4	D	206	ASP
4	D	224	SER
4	D	225	GLN
4	D	234	ASP
4	D	238	GLU
4	D	277	LYS
5	E	52	LEU
5	E	66	SER
5	E	112	LEU
5	E	117	ARG
5	E	123	ASP
5	E	140	VAL
5	E	143	LEU
5	E	144	ARG
5	E	164	ARG
5	E	165	VAL
5	E	178	VAL
5	E	182	LEU
5	E	194	GLN
5	E	202	THR

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Mol	Chain	Res	Type
5	E	214	HIS
5	E	219	TYR
5	E	261	LEU
5	E	281	THR
5	E	289	LEU
5	E	290	VAL
6	F	41	LEU
6	F	85	GLU
6	F	88	LEU
6	F	97	ILE
6	F	115	GLN
6	F	120	THR
6	F	122	VAL
6	F	136	GLU
6	F	148	SER
6	F	151	GLU
6	F	188	ASP
6	F	189	LEU
6	F	198	LYS
6	F	205	ASN
6	F	214	SER
6	F	228	GLU
6	F	237	ASP
6	F	242	LEU
6	F	245	ARG
7	G	96	GLN
7	G	116	LEU
7	G	122	ILE
7	G	128	LYS
7	G	143	GLN
7	G	159	THR
7	G	198	THR
7	G	223	LEU
7	G	226	LEU
7	G	242	ARG
7	G	249	ARG
7	G	251	THR
7	G	252	CYS
7	G	263	GLU
7	G	268	LEU
7	G	273	GLU
7	G	281	ASP

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Mol	Chain	Res	Type
7	G	284	ASP
7	G	285	GLU
7	G	295	LEU
7	G	312	LYS
8	H	1	MET
8	H	3	THR
8	H	12	ILE
8	H	14	GLU
8	H	18	ILE
8	H	20	LEU
8	H	41	ILE
8	H	47	LEU
8	H	65	LYS
8	H	89	ARG
8	H	106	GLN
8	H	117	PHE
8	H	141	LYS
8	H	177	ASP
8	H	186	THR
9	I	12	CYS
9	I	13	LYS
9	I	15	LYS
9	I	36	LEU
9	I	43	VAL
9	I	52	MET
9	I	60	LEU
9	I	61	SER
9	I	71	CYS
9	I	76	MET
9	I	77	VAL
9	I	83	ASP
9	I	88	ARG
9	I	97	ILE
9	I	99	ILE
9	I	101	LYS
9	I	121	LYS
9	I	126	VAL
9	I	129	VAL
9	I	131	ILE
9	I	138	ILE
9	I	142	LEU
9	I	144	ASN

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Mol	Chain	Res	Type
9	I	163	GLN
9	I	167	ILE
9	I	169	LYS
9	I	174	THR
9	I	180	GLU
10	J	16	ARG
10	J	51	SER
10	J	52	LYS
10	J	60	PHE
10	J	66	GLU
10	J	90	ARG
10	J	101	ASP
10	J	102	THR
10	J	128	LEU
10	J	168	GLN
10	J	175	LEU
11	L	4	SER
11	L	8	MET
11	L	9	ILE
11	L	10	LEU
11	L	20	ARG
11	L	27	ASN
11	L	59	VAL
11	L	74	ARG
11	L	94	ILE
11	L	101	ARG
11	L	107	THR
11	L	130	LYS
11	L	150	LEU
11	L	154	VAL
11	L	159	ASN
11	L	172	GLU
11	L	206	ASP
12	M	8	GLU
12	M	11	ARG
12	M	25	VAL
12	M	29	ASP
12	M	37	LEU
12	M	54	CYS
12	M	62	LEU
12	M	85	LYS
12	M	89	THR

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Mol	Chain	Res	Type
12	M	90	ARG
12	M	93	LYS
12	M	95	ILE
12	M	96	GLU
12	M	104	MET
12	M	105	THR
12	M	113	MET
12	M	116	LYS
12	M	124	LYS
12	M	125	ASN
12	M	132	ARG
13	N	25	VAL
13	N	29	GLN
13	N	43	THR
13	N	49	ARG
13	N	60	VAL
13	N	61	ILE
13	N	64	ILE
13	N	65	ARG
13	N	75	VAL
13	N	77	LYS
13	N	89	VAL
13	N	92	LEU
13	N	104	GLU
13	N	126	THR
13	N	134	LEU
13	N	143	ARG
13	N	145	ASN
13	N	151	ILE
13	N	174	LEU
13	N	178	HIS
13	N	182	HIS
13	N	198	LEU
13	N	204	ARG
14	O	7	LEU
14	O	16	LEU
14	O	34	VAL
14	O	36	VAL
14	O	39	GLU
14	O	42	ASN
14	O	43	ILE
14	O	52	LEU

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Mol	Chain	Res	Type
14	O	53	LYS
14	O	55	LEU
14	O	61	ARG
14	O	68	ARG
14	O	83	THR
14	O	94	ARG
14	O	96	GLN
14	O	113	ASP
14	O	117	ARG
14	O	118	MET
14	O	141	LEU
14	O	148	LYS
14	O	153	THR
14	O	155	THR
14	O	159	LYS
14	O	163	LYS
14	O	173	GLN
14	O	174	LEU
14	O	183	LYS
14	O	185	VAL
14	O	202	LEU
15	P	10	ASN
15	P	14	SER
15	P	22	LEU
15	P	24	VAL
15	P	31	GLU
15	P	34	GLN
15	P	51	VAL
15	P	62	ARG
15	P	79	THR
15	P	92	LEU
15	P	93	HIS
15	P	95	LEU
15	P	103	GLU
15	P	104	LEU
15	P	119	VAL
15	P	120	ASN
15	P	129	THR
15	P	149	ILE
15	P	150	LEU
15	P	154	GLU
16	Q	5	ILE

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Mol	Chain	Res	Type
16	Q	13	VAL
16	Q	17	GLU
16	Q	22	ASP
16	Q	23	ILE
16	Q	28	LEU
16	Q	29	VAL
16	Q	38	ARG
16	Q	54	SER
16	Q	61	LEU
16	Q	72	LEU
16	Q	77	ASN
16	Q	78	LYS
16	Q	91	ARG
16	Q	104	ARG
16	Q	119	LYS
16	Q	126	LEU
16	Q	138	LEU
16	Q	150	ARG
16	Q	158	THR
16	Q	161	SER
16	Q	168	ARG
16	Q	170	LYS
16	Q	172	ARG
17	R	5	ARG
17	R	10	LEU
17	R	13	SER
17	R	32	ILE
17	R	39	GLN
17	R	49	LEU
17	R	50	ILE
17	R	60	ARG
17	R	81	ARG
17	R	82	LYS
17	R	84	THR
17	R	89	MET
17	R	99	MET
17	R	105	LEU
17	R	117	ARG
17	R	123	LEU
17	R	127	VAL
17	R	137	ILE
17	R	146	LYS

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Mol	Chain	Res	Type
17	R	154	LEU
17	R	155	LEU
17	R	160	GLU
17	R	164	SER
17	R	178	GLN
18	S	2	LYS
18	S	7	LEU
18	S	16	CYS
18	S	57	SER
18	S	82	LEU
18	S	92	ASN
18	S	93	MET
18	S	101	THR
18	S	102	THR
18	S	109	CYS
18	S	112	ASP
18	S	131	GLU
18	S	132	ILE
18	S	142	VAL
18	S	159	LEU
18	S	161	ARG
18	S	164	LYS
18	S	168	THR
18	S	175	PHE
19	T	3	ASN
19	T	5	LYS
19	T	31	MET
19	T	41	ASP
19	T	50	LYS
19	T	67	VAL
19	T	74	ILE
19	T	76	VAL
19	T	78	LYS
19	T	80	VAL
19	T	96	ILE
19	T	120	LYS
19	T	122	LYS
19	T	136	ARG
19	T	142	ARG
20	U	63	LEU
20	U	83	LEU
20	U	87	THR

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Mol	Chain	Res	Type
20	U	101	ARG
21	V	15	ARG
21	V	18	LEU
21	V	22	VAL
21	V	25	VAL
21	V	26	ILE
21	V	28	CYS
21	V	41	SER
21	V	46	LYS
21	V	49	LEU
21	V	64	THR
21	V	66	LYS
21	V	69	LYS
21	V	77	HIS
21	V	82	ILE
21	V	94	VAL
21	V	106	VAL
21	V	108	ASN
21	V	123	LYS
21	V	124	GLU
22	W	2	LYS
22	W	15	PRO
22	W	23	ARG
22	W	25	ASP
22	W	32	LEU
22	W	41	LEU
22	W	42	SER
22	W	57	ARG
22	W	86	SER
23	X	39	LYS
23	X	45	THR
23	X	52	LEU
23	X	53	ARG
23	X	57	GLN
23	X	81	LEU
23	X	91	GLU
23	X	95	THR
23	X	101	ASP
23	X	119	ILE
23	X	123	LYS
23	X	127	LEU
23	X	131	ASP

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Mol	Chain	Res	Type
23	X	133	GLU
23	X	156	ILE
24	Y	8	THR
24	Y	11	ARG
24	Y	14	ASN
24	Y	28	LYS
24	Y	31	SER
24	Y	34	LEU
24	Y	37	GLU
24	Y	40	GLN
24	Y	54	GLU
24	Y	55	VAL
24	Y	58	VAL
24	Y	63	LYS
24	Y	71	VAL
24	Y	76	LYS
24	Y	89	LYS
24	Y	95	VAL
24	Y	97	VAL
24	Y	102	SER
24	Y	104	VAL
24	Y	105	VAL
24	Y	107	THR
24	Y	110	LYS
24	Y	112	ASP
24	Y	126	ARG
24	Y	130	LYS
24	Y	131	GLU
25	Z	3	LYS
25	Z	14	LEU
25	Z	33	THR
25	Z	35	ASP
25	Z	46	ILE
25	Z	53	VAL
25	Z	62	ILE
25	Z	64	LYS
25	Z	67	LYS
25	Z	83	THR
25	Z	94	THR
25	Z	99	ASP
25	Z	111	ARG
25	Z	124	THR

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Mol	Chain	Res	Type
25	Z	126	LYS
25	Z	134	LEU
26	a	4	ARG
26	a	8	THR
26	a	27	LYS
26	a	29	PRO
26	a	44	ASN
26	a	81	LEU
26	a	82	VAL
26	a	120	GLN
26	a	122	VAL
26	a	132	ARG
27	b	23	LYS
27	b	27	GLN
27	b	31	SER
27	b	50	ASN
27	b	55	LYS
27	b	75	LEU
28	c	18	LEU
28	c	36	LYS
28	c	48	LEU
28	c	52	CYS
28	c	55	LEU
28	c	56	ARG
28	c	78	ASN
28	c	81	LEU
28	c	83	THR
28	c	89	TYR
28	c	91	VAL
28	c	92	CYS
28	c	94	LEU
29	d	36	VAL
29	d	48	GLU
29	d	84	ILE
29	d	109	VAL
29	d	115	LYS
29	d	117	LEU
29	d	119	THR
30	e	13	VAL
30	e	18	LYS
30	e	41	ILE
30	e	47	ARG

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Mol	Chain	Res	Type
30	e	52	GLN
30	e	54	LEU
30	e	63	ASN
30	e	70	LEU
30	e	86	GLU
30	e	89	LEU
30	e	94	SER
30	e	102	ASN
30	e	109	LYS
30	e	122	VAL
30	e	123	THR
30	e	129	LEU
31	f	7	CYS
31	f	10	ILE
31	f	16	ARG
31	f	20	ASN
31	f	24	HIS
31	f	28	LEU
31	f	40	GLU
31	f	45	LYS
31	f	52	LYS
31	f	56	ASN
31	f	68	ARG
31	f	76	ARG
31	f	84	VAL
31	f	97	ILE
31	f	100	ARG
31	f	103	VAL
32	g	11	LEU
32	g	24	ARG
32	g	25	THR
32	g	29	ARG
32	g	33	LEU
32	g	46	CYS
32	g	54	ARG
32	g	59	VAL
32	g	61	PRO
32	g	68	SER
32	g	74	VAL
32	g	98	GLU
32	g	114	GLN
33	h	4	ILE

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Mol	Chain	Res	Type
33	h	13	LYS
33	h	15	GLU
33	h	22	ASP
33	h	27	GLU
33	h	28	LEU
33	h	77	LYS
33	h	78	TYR
33	h	88	THR
33	h	89	ARG
33	h	96	ASN
34	i	12	ASN
34	i	29	ARG
34	i	44	ILE
34	i	48	CYS
34	i	59	GLU
34	i	60	LEU
34	i	63	VAL
34	i	89	GLU
35	j	2	THR
35	j	12	ARG
35	j	15	THR
35	j	17	THR
35	j	20	ARG
35	j	45	ARG
35	j	55	ARG
35	j	58	THR
36	k	6	GLU
36	k	7	GLU
36	k	19	ASP
36	k	27	LYS
36	k	31	ASN
36	k	60	LEU
36	k	69	LEU
37	l	8	ARG
37	l	9	ILE
37	l	11	ARG
37	l	27	ILE
37	l	34	LYS
37	l	36	ARG
37	l	38	ASN
37	l	41	ARG
37	l	51	LEU

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Mol	Chain	Res	Type
38	m	53	GLU
38	m	55	SER
38	m	57	ARG
38	m	72	LYS
38	m	77	LEU
38	m	80	ARG
38	m	82	VAL
38	m	92	THR
38	m	96	ARG
38	m	102	LYS
39	n	9	ARG
39	n	13	LEU
39	n	16	LYS
39	n	19	LYS
39	n	20	MET
40	o	32	SER
40	o	33	LEU
40	o	45	GLN
40	o	59	LYS
40	o	62	THR
40	o	63	THR
40	o	64	LYS
40	o	71	GLU
40	o	72	CYS
40	o	83	LEU
40	o	88	CYS
40	o	96	ASP
40	o	105	GLN
41	p	4	ARG
41	p	7	LYS
41	p	28	LYS
41	p	29	ILE
41	p	33	GLN
41	p	47	MET
41	p	50	ARG
41	p	63	THR
41	p	73	THR
41	p	78	THR
41	p	79	VAL
41	p	85	ARG
41	p	87	LYS
42	r	4	HIS

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Mol	Chain	Res	Type
42	r	18	ILE
42	r	24	THR
42	r	32	LEU
42	r	37	SER
42	r	39	ARG
42	r	49	VAL
42	r	70	GLN
42	r	78	VAL
42	r	85	ASN
42	r	103	HIS
42	r	106	LEU
42	r	118	LEU
42	r	121	GLN
43	s	33	ASP
43	s	94	ASP
43	s	178	LEU
43	s	187	LEU
44	t	17	CYS
44	t	37	LEU
44	t	98	ILE
44	t	125	LEU
44	t	141	CYS
44	t	156	ASN
48	K	15	ARG
48	K	25	ARG
48	K	28	PHE
48	K	29	LEU
48	K	30	GLU
48	K	85	MET
48	K	93	LEU
48	K	111	LEU
48	K	118	LYS
48	K	130	LYS
48	K	134	PHE
48	K	144	MET
48	K	156	LYS
48	K	162	VAL
48	K	164	CYS
48	K	193	LEU
48	K	194	LEU
48	K	206	ILE
48	K	214	GLN

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Mol	Chain	Res	Type
51	BB	9	GLN
51	BB	11	LYS
51	BB	50	ASN
51	BB	59	LEU
51	BB	107	THR
51	BB	109	THR
51	BB	123	VAL
51	BB	136	GLU
51	BB	141	ASN
51	BB	142	LEU
51	BB	158	ASP
51	BB	213	GLU
52	CC	47	THR
52	CC	63	LYS
52	CC	68	GLU
52	CC	75	GLN
52	CC	105	LEU
52	CC	107	ARG
52	CC	125	VAL
52	CC	161	VAL
52	CC	173	THR
52	CC	175	GLU
52	CC	180	ASP
52	CC	181	LEU
52	CC	196	ASP
52	CC	212	VAL
52	CC	213	ARG
52	CC	225	LEU
53	DD	78	LEU
53	DD	85	SER
53	DD	107	LEU
53	DD	116	THR
53	DD	117	ARG
53	DD	121	ARG
53	DD	123	ARG
53	DD	139	LEU
53	DD	157	LEU
53	DD	160	LEU
53	DD	162	ILE
53	DD	172	ASN
53	DD	192	LEU
53	DD	194	ARG

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Mol	Chain	Res	Type
53	DD	206	SER
53	DD	213	LEU
53	DD	225	SER
53	DD	227	ARG
53	DD	236	PHE
53	DD	245	SER
53	DD	254	ASP
53	DD	255	LEU
53	DD	259	THR
53	DD	277	HIS
54	EE	23	GLU
54	EE	28	GLU
54	EE	39	VAL
54	EE	93	THR
54	EE	94	ARG
54	EE	103	GLU
54	EE	106	ARG
54	EE	117	ARG
54	EE	134	CYS
54	EE	139	SER
54	EE	142	LEU
54	EE	145	GLN
54	EE	146	ARG
54	EE	153	VAL
54	EE	154	ASP
54	EE	162	ASP
54	EE	167	TYR
54	EE	168	VAL
54	EE	169	ASP
54	EE	175	VAL
54	EE	177	LEU
54	EE	178	ARG
54	EE	208	VAL
54	EE	224	SER
55	FF	6	LYS
55	FF	24	THR
55	FF	38	LEU
55	FF	39	ARG
55	FF	59	ASP
55	FF	67	GLN
55	FF	77	ARG
55	FF	101	LEU

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Mol	Chain	Res	Type
55	FF	123	LEU
55	FF	129	ILE
55	FF	139	LEU
55	FF	140	VAL
55	FF	151	ASP
55	FF	158	ASP
55	FF	159	THR
55	FF	160	ILE
55	FF	162	ILE
55	FF	169	ILE
55	FF	173	ILE
55	FF	174	LYS
55	FF	176	ASP
55	FF	179	ASN
55	FF	199	GLU
55	FF	200	ARG
55	FF	211	LYS
55	FF	220	THR
55	FF	233	LYS
55	FF	238	LEU
55	FF	245	ARG
55	FF	253	ASP
55	FF	260	GLN
56	GG	25	THR
56	GG	29	GLN
56	GG	63	LYS
56	GG	66	CYS
56	GG	83	ASN
56	GG	88	MET
56	GG	107	ASN
56	GG	135	ARG
56	GG	137	GLN
56	GG	140	ASP
56	GG	144	LEU
56	GG	155	CYS
56	GG	172	CYS
56	GG	173	LEU
57	HH	6	SER
57	HH	12	CYS
57	HH	19	ASP
57	HH	41	LEU
57	HH	43	GLU

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Mol	Chain	Res	Type
57	HH	63	MET
57	HH	67	VAL
57	HH	73	VAL
57	HH	96	SER
57	HH	107	SER
57	HH	108	VAL
57	HH	133	LEU
57	HH	139	SER
57	HH	141	ILE
57	HH	160	LYS
57	HH	167	LYS
57	HH	177	GLN
57	HH	183	ARG
57	HH	213	LEU
58	II	17	ASP
58	II	24	SER
58	II	33	ASN
58	II	36	LEU
58	II	40	LEU
58	II	50	GLU
58	II	51	ILE
58	II	64	VAL
58	II	69	LEU
58	II	76	GLN
58	II	82	GLU
58	II	95	ILE
58	II	98	ARG
58	II	100	ILE
58	II	101	LEU
58	II	105	THR
58	II	106	ARG
58	II	116	ARG
58	II	122	LEU
58	II	134	VAL
58	II	149	ASP
58	II	166	VAL
58	II	171	GLU
58	II	179	LYS
58	II	186	ASN
58	II	191	GLU
59	JJ	7	ASN
59	JJ	18	ARG

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Mol	Chain	Res	Type
59	JJ	21	TYR
59	JJ	29	LEU
59	JJ	35	ASN
59	JJ	36	THR
59	JJ	47	ARG
59	JJ	60	LEU
59	JJ	73	THR
59	JJ	76	THR
59	JJ	82	VAL
59	JJ	88	ASN
59	JJ	121	LEU
59	JJ	130	THR
59	JJ	132	GLU
59	JJ	139	LYS
59	JJ	142	SER
59	JJ	158	ILE
59	JJ	160	SER
59	JJ	161	LEU
59	JJ	163	GLU
59	JJ	168	GLN
59	JJ	188	TYR
59	JJ	191	GLU
59	JJ	193	LYS
59	JJ	203	LYS
60	KK	12	THR
60	KK	27	GLN
60	KK	38	ARG
60	KK	42	GLU
60	KK	69	ARG
60	KK	83	ARG
60	KK	84	ILE
60	KK	88	ASP
60	KK	89	GLU
60	KK	97	ILE
60	KK	106	LEU
60	KK	119	LEU
60	KK	131	ARG
61	LL	2	LEU
61	LL	6	LYS
61	LL	20	VAL
61	LL	35	LEU
61	LL	43	LEU

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Mol	Chain	Res	Type
61	LL	72	THR
61	LL	81	ASP
62	MM	7	GLU
62	MM	8	ARG
62	MM	11	GLN
62	MM	37	TYR
62	MM	42	LEU
62	MM	56	ILE
62	MM	69	ARG
62	MM	82	MET
62	MM	85	THR
62	MM	114	SER
62	MM	121	GLN
62	MM	122	ILE
62	MM	126	VAL
62	MM	132	ARG
62	MM	134	LEU
62	MM	141	ASN
62	MM	146	THR
63	NN	14	VAL
63	NN	15	ASN
63	NN	22	LEU
63	NN	55	ASN
64	OO	9	LYS
64	OO	11	LEU
64	OO	12	SER
64	OO	14	SER
64	OO	27	LYS
64	OO	28	LEU
64	OO	42	LYS
64	OO	43	LYS
64	OO	55	ARG
64	OO	60	VAL
64	OO	62	GLN
64	OO	70	LYS
64	OO	83	ASP
64	OO	84	LEU
64	OO	96	VAL
64	OO	125	LEU
64	OO	140	LYS
64	OO	149	LEU
65	PP	25	GLU

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Mol	Chain	Res	Type
65	PP	50	LYS
65	PP	85	CYS
65	PP	91	THR
65	PP	107	THR
65	PP	128	ARG
65	PP	130	GLU
65	PP	137	SER
65	PP	138	ASP
65	PP	140	THR
65	PP	146	ARG
65	PP	147	ARG
65	PP	150	ARG
65	PP	151	LEU
66	QQ	15	PHE
66	QQ	29	SER
66	QQ	37	TYR
66	QQ	41	GLN
66	QQ	45	LEU
66	QQ	56	LEU
66	QQ	60	LEU
66	QQ	64	LYS
66	QQ	74	GLU
66	QQ	84	ILE
67	RR	31	LEU
67	RR	41	MET
67	RR	42	ILE
67	RR	72	VAL
67	RR	121	VAL
67	RR	123	ASP
67	RR	127	CYS
67	RR	146	ARG
68	SS	5	ARG
68	SS	7	LYS
68	SS	8	THR
68	SS	16	ILE
68	SS	30	THR
68	SS	37	GLU
68	SS	38	ILE
68	SS	44	LYS
68	SS	69	ILE
68	SS	70	SER
68	SS	81	ARG

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Mol	Chain	Res	Type
68	SS	101	ASP
68	SS	127	ASN
69	TT	71	MET
69	TT	83	PHE
69	TT	85	ASN
69	TT	99	LEU
69	TT	111	LEU
69	TT	132	ARG
69	TT	136	THR
70	UU	10	ASN
70	UU	28	LEU
70	UU	67	ARG
70	UU	87	VAL
70	UU	90	SER
70	UU	116	ASP
71	VV	26	SER
71	VV	48	LEU
71	VV	61	LEU
71	VV	65	THR
71	VV	72	GLU
71	VV	74	SER
71	VV	75	LYS
71	VV	84	ILE
71	VV	88	LEU
71	VV	106	ILE
71	VV	111	GLU
71	VV	115	THR
72	WW	10	ASP
72	WW	11	LEU
72	WW	42	VAL
72	WW	50	PHE
72	WW	70	LEU
72	WW	82	ASN
73	XX	2	VAL
73	XX	7	LEU
73	XX	14	ILE
73	XX	30	CYS
73	XX	65	LEU
73	XX	72	CYS
73	XX	83	LEU
73	XX	84	LYS
73	XX	91	ASN

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Mol	Chain	Res	Type
73	XX	93	LEU
73	XX	102	ILE
73	XX	103	VAL
73	XX	111	MET
73	XX	114	GLU
74	YY	4	CYS
74	YY	5	ARG
74	YY	7	LEU
74	YY	19	ASP
74	YY	20	GLN
74	YY	36	LEU
74	YY	52	LEU
74	YY	53	GLU
74	YY	58	GLU
74	YY	64	SER
74	YY	67	ARG
74	YY	70	VAL
74	YY	81	ILE
74	YY	115	ILE
74	YY	123	VAL
74	YY	130	LEU
74	YY	139	GLU
75	ZZ	5	VAL
75	ZZ	17	LEU
75	ZZ	20	ARG
75	ZZ	35	VAL
75	ZZ	44	LEU
75	ZZ	49	LYS
75	ZZ	68	LYS
75	ZZ	70	THR
75	ZZ	78	SER
75	ZZ	79	LEU
75	ZZ	101	LYS
75	ZZ	120	THR
76	aa	42	ASP
76	aa	69	THR
77	bb	24	THR
77	bb	29	CYS
77	bb	32	LYS
77	bb	41	ILE
77	bb	43	ASN
77	bb	46	GLU

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Mol	Chain	Res	Type
77	bb	88	SER
77	bb	102	ARG
78	cc	13	GLU
78	cc	26	GLN
78	cc	27	SER
78	cc	52	THR
78	cc	61	THR
78	cc	63	LEU
78	cc	67	THR
78	cc	77	CYS
79	dd	55	VAL
79	dd	66	ARG
80	ee	14	PHE
80	ee	26	ASN
80	ee	27	ARG
80	ee	30	LEU
80	ee	48	LYS
81	ff	95	GLN
81	ff	99	LYS
81	ff	100	LYS
81	ff	109	MET
81	ff	124	LYS
82	gg	83	LYS
82	gg	85	TYR
82	gg	86	THR
82	gg	91	ASN
82	gg	96	LYS
82	gg	97	LYS
82	gg	110	GLU
83	hh	15	ASN
83	hh	36	ARG
83	hh	37	ASP
83	hh	59	LEU
83	hh	64	HIS
83	hh	79	LEU
83	hh	87	LEU
83	hh	126	ASP
83	hh	129	ILE
83	hh	142	VAL
83	hh	144	ASP
83	hh	145	GLU
83	hh	149	GLU

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Mol	Chain	Res	Type
83	hh	152	SER
83	hh	153	CYS
83	hh	166	VAL
83	hh	184	LEU
83	hh	187	ASN
83	hh	191	HIS
83	hh	192	THR
83	hh	195	LEU
83	hh	196	ASN
83	hh	197	THR
83	hh	207	CYS
83	hh	212	LYS
83	hh	273	GLU
83	hh	287	THR
83	hh	289	LEU
84	jj	32	THR
84	jj	33	SER
84	jj	37	LEU
84	jj	51	MET
84	jj	63	LYS
84	jj	65	ARG
84	jj	76	THR
84	jj	101	VAL
84	jj	108	LYS
84	jj	124	LEU
84	jj	128	ASP
84	jj	157	LEU
84	jj	162	GLN
84	jj	188	LEU
84	jj	189	ARG
84	jj	202	VAL
84	jj	214	ILE
84	jj	217	ASP
84	jj	224	LEU
84	jj	232	PHE
84	jj	233	LYS
84	jj	245	ARG
84	jj	255	ASP
84	jj	256	ILE
84	jj	257	SER
84	jj	270	LEU
84	jj	280	PHE

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Mol	Chain	Res	Type
84	jj	292	ASP
84	jj	340	GLU
84	jj	347	THR
84	jj	352	LYS
84	jj	366	HIS
84	jj	368	LEU
84	jj	393	THR
84	jj	420	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (226) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	ASN
1	A	205	ASN
2	B	42	HIS
2	B	138	GLN
2	B	165	HIS
2	B	179	HIS
2	B	203	GLN
2	B	258	HIS
2	B	271	GLN
3	C	41	HIS
3	C	61	GLN
3	C	329	ASN
3	C	338	ASN
4	D	42	ASN
4	D	45	ASN
4	D	122	GLN
4	D	222	GLN
4	D	250	ASN
5	E	185	ASN
5	E	259	GLN
6	F	55	HIS
6	F	57	HIS
6	F	98	ASN
6	F	205	ASN
6	F	238	GLN
7	G	206	GLN
7	G	259	GLN
7	G	293	ASN
8	H	78	GLN
8	H	106	GLN

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Mol	Chain	Res	Type
8	H	116	ASN
8	H	156	ASN
9	I	51	HIS
9	I	59	GLN
9	I	100	ASN
9	I	163	GLN
10	J	10	ASN
10	J	112	HIS
10	J	155	HIS
11	L	19	GLN
11	L	67	HIS
11	L	159	ASN
12	M	48	GLN
12	M	125	ASN
13	N	8	GLN
13	N	91	GLN
13	N	99	GLN
13	N	145	ASN
13	N	178	HIS
13	N	199	GLN
14	O	5	GLN
14	O	96	GLN
14	O	167	HIS
14	O	173	GLN
15	P	34	GLN
15	P	80	GLN
15	P	120	ASN
16	Q	57	ASN
16	Q	125	GLN
17	R	36	ASN
17	R	39	GLN
17	R	40	GLN
17	R	178	GLN
18	S	146	HIS
19	T	3	ASN
19	T	49	GLN
19	T	77	ASN
19	T	79	GLN
19	T	90	ASN
19	T	127	GLN
21	V	36	ASN
21	V	107	ASN

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Mol	Chain	Res	Type
21	V	108	ASN
22	W	50	ASN
23	X	73	HIS
23	X	94	ASN
23	X	107	HIS
23	X	111	GLN
23	X	125	ASN
24	Y	14	ASN
24	Y	65	GLN
24	Y	96	HIS
24	Y	127	GLN
25	Z	79	HIS
25	Z	97	ASN
25	Z	127	ASN
26	a	25	HIS
26	a	28	HIS
26	a	85	GLN
26	a	93	ASN
26	a	120	GLN
27	b	12	GLN
27	b	50	ASN
29	d	18	ASN
29	d	69	ASN
29	d	79	ASN
29	d	93	ASN
29	d	116	ASN
29	d	118	GLN
31	f	24	HIS
31	f	56	ASN
31	f	80	ASN
32	g	100	GLN
32	g	112	GLN
32	g	114	GLN
33	h	96	ASN
33	h	98	HIS
34	i	20	ASN
35	j	30	GLN
36	k	28	ASN
36	k	31	ASN
37	l	4	HIS
37	l	33	ASN
37	l	38	ASN

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Mol	Chain	Res	Type
38	m	61	GLN
38	m	83	ASN
38	m	91	HIS
40	o	19	GLN
40	o	51	GLN
40	o	76	ASN
40	o	102	GLN
41	p	33	GLN
41	p	56	HIS
41	p	72	ASN
42	r	12	ASN
42	r	41	ASN
42	r	45	HIS
42	r	70	GLN
43	s	39	GLN
43	s	139	GLN
43	s	176	ASN
43	s	191	GLN
44	t	95	GLN
48	K	35	GLN
48	K	158	GLN
48	K	182	ASN
48	K	184	HIS
48	K	200	ASN
48	K	214	GLN
51	BB	24	HIS
52	CC	75	GLN
52	CC	124	HIS
52	CC	163	GLN
52	CC	202	GLN
53	DD	267	GLN
53	DD	272	HIS
54	EE	101	GLN
54	EE	145	GLN
54	EE	159	HIS
55	FF	50	ASN
55	FF	67	GLN
55	FF	179	ASN
55	FF	224	ASN
56	GG	36	GLN
56	GG	83	ASN
56	GG	101	HIS

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Mol	Chain	Res	Type
56	GG	114	ASN
56	GG	118	ASN
56	GG	179	ASN
57	HH	65	GLN
57	HH	110	ASN
57	HH	177	GLN
57	HH	202	ASN
58	II	25	GLN
58	II	97	GLN
58	II	157	HIS
58	II	163	GLN
59	JJ	7	ASN
59	JJ	35	ASN
59	JJ	84	ASN
59	JJ	111	GLN
59	JJ	138	ASN
59	JJ	181	GLN
60	KK	27	GLN
60	KK	75	ASN
60	KK	111	GLN
60	KK	113	GLN
61	LL	7	ASN
61	LL	32	HIS
62	MM	18	GLN
62	MM	19	ASN
63	NN	15	ASN
63	NN	19	GLN
63	NN	55	ASN
64	OO	5	HIS
64	OO	62	GLN
64	OO	138	ASN
65	PP	83	GLN
66	QQ	98	ASN
66	QQ	103	ASN
67	RR	29	ASN
67	RR	48	GLN
67	RR	86	GLN
68	SS	31	ASN
69	TT	11	HIS
69	TT	72	GLN
69	TT	76	GLN
69	TT	97	GLN

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Mol	Chain	Res	Type
69	TT	135	HIS
70	UU	10	ASN
70	UU	85	ASN
72	WW	21	ASN
72	WW	35	ASN
72	WW	47	ASN
73	XX	16	ASN
73	XX	82	GLN
73	XX	113	HIS
74	YY	77	ASN
74	YY	97	ASN
75	ZZ	85	ASN
77	bb	7	ASN
78	cc	49	HIS
78	cc	83	GLN
79	dd	29	GLN
81	ff	88	GLN
81	ff	131	ASN
82	gg	93	HIS
82	gg	139	HIS
83	hh	133	ASN
83	hh	222	ASN
83	hh	305	ASN
84	jj	67	ASN
84	jj	80	GLN
84	jj	200	ASN
84	jj	238	GLN
84	jj	380	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	5	3565/3594 (99%)	1667 (46%)	283 (7%)
46	7	118/119 (99%)	40 (33%)	5 (4%)
47	8	149/151 (98%)	63 (42%)	5 (3%)
49	2	1683/1697 (99%)	727 (43%)	107 (6%)
50	3	86/87 (98%)	44 (51%)	5 (5%)
85	4	193/194 (99%)	123 (63%)	28 (14%)
All	All	5794/5842 (99%)	2664 (45%)	433 (7%)

All (2664) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	5	6	C
45	5	9	C
45	5	10	A
45	5	12	A
45	5	13	U
45	5	14	C
45	5	16	G
45	5	18	C
45	5	19	G
45	5	22	G
45	5	25	A
45	5	26	C
45	5	28	C
45	5	35	U
45	5	37	U
45	5	38	A
45	5	39	A
45	5	42	A
45	5	44	A
45	5	48	G
45	5	49	U
45	5	56	A
45	5	58	G
45	5	59	A
45	5	64	A
45	5	65	A
45	5	66	A
45	5	68	U
45	5	70	A
45	5	72	C
45	5	73	A
45	5	74	G
45	5	77	U
45	5	84	A
45	5	88	A
45	5	91	G
45	5	93	G
45	5	94	A
45	5	95	G
45	5	96	U
45	5	97	G
45	5	101	A
45	5	109	G

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Mol	Chain	Res	Type
45	5	118	C
45	5	119	G
45	5	120	A
45	5	121	A
45	5	123	C
45	5	131	C
45	5	133	C
45	5	134	G
45	5	135	G
45	5	136	C
45	5	137	G
45	5	139	G
45	5	142	G
45	5	143	C
45	5	144	G
45	5	145	G
45	5	150	U
45	5	155	C
45	5	158	A
45	5	159	C
45	5	160	G
45	5	166	C
45	5	169	A
45	5	172	C
45	5	173	C
45	5	174	C
45	5	177	G
45	5	178	C
45	5	179	G
45	5	180	C
45	5	181	C
45	5	182	G
45	5	190	G
45	5	191	G
45	5	192	G
45	5	196	C
45	5	197	A
45	5	200	U
45	5	201	C
45	5	202	C
45	5	203	U
45	5	205	C

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Mol	Chain	Res	Type
45	5	209	U
45	5	210	C
45	5	211	G
45	5	216	C
45	5	218	A
45	5	219	G
45	5	220	C
45	5	223	G
45	5	224	U
45	5	225	G
45	5	231	U
45	5	232	G
45	5	233	U
45	5	234	G
45	5	235	A
45	5	236	G
45	5	241	G
45	5	244	G
45	5	246	G
45	5	248	C
45	5	252	C
45	5	254	G
45	5	255	C
45	5	256	G
45	5	257	C
45	5	258	G
45	5	259	C
45	5	260	C
45	5	261	G
45	5	262	G
45	5	263	G
45	5	264	C
45	5	265	C
45	5	266	C
45	5	267	G
45	5	268	G
45	5	270	U
45	5	271	C
45	5	276	C
45	5	278	G
45	5	280	G
45	5	282	C

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Mol	Chain	Res	Type
45	5	284	G
45	5	289	C
45	5	294	G
45	5	295	A
45	5	296	A
45	5	297	U
45	5	299	C
45	5	303	C
45	5	305	A
45	5	306	A
45	5	312	G
45	5	315	G
45	5	316	U
45	5	327	U
45	5	333	U
45	5	334	A
45	5	337	U
45	5	340	C
45	5	342	G
45	5	344	A
45	5	345	C
45	5	348	G
45	5	349	A
45	5	350	C
45	5	352	G
45	5	354	U
45	5	355	A
45	5	357	U
45	5	358	C
45	5	361	C
45	5	363	A
45	5	364	G
45	5	366	A
45	5	378	A
45	5	379	G
45	5	384	A
45	5	385	A
45	5	386	A
45	5	387	G
45	5	389	A
45	5	396	A
45	5	397	G

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Mol	Chain	Res	Type
45	5	399	G
45	5	404	U
45	5	408	A
45	5	409	G
45	5	410	A
45	5	412	G
45	5	413	G
45	5	414	C
45	5	415	G
45	5	417	G
45	5	418	A
45	5	422	C
45	5	423	G
45	5	425	U
45	5	429	A
45	5	431	G
45	5	432	U
45	5	436	C
45	5	437	G
45	5	446	C
45	5	448	G
45	5	449	C
45	5	450	G
45	5	452	A
45	5	453	G
45	5	454	U
45	5	455	C
45	5	456	C
45	5	463	A
45	5	464	G
45	5	465	G
45	5	466	A
45	5	467	U
45	5	468	U
45	5	469	C
45	5	470	A
45	5	477	C
45	5	478	G
45	5	479	G
45	5	480	C
45	5	481	G
45	5	482	G

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Mol	Chain	Res	Type
45	5	484	U
45	5	485	C
45	5	487	G
45	5	488	G
45	5	490	C
45	5	492	U
45	5	493	G
45	5	494	C
45	5	495	C
45	5	496	G
45	5	497	G
45	5	498	C
45	5	499	G
45	5	500	G
45	5	505	G
45	5	506	C
45	5	507	G
45	5	508	G
45	5	510	U
45	5	516	C
45	5	518	G
45	5	519	C
45	5	521	C
45	5	522	C
45	5	639	U
45	5	640	C
45	5	643	C
45	5	645	G
45	5	647	G
45	5	650	C
45	5	651	C
45	5	653	C
45	5	654	C
45	5	657	C
45	5	658	C
45	5	659	G
45	5	660	G
45	5	666	G
45	5	667	A
45	5	668	C
45	5	669	C
45	5	672	C

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Mol	Chain	Res	Type
45	5	673	C
45	5	675	C
45	5	677	G
45	5	678	C
45	5	679	C
45	5	684	G
45	5	685	C
45	5	686	A
45	5	688	U
45	5	690	C
45	5	694	C
45	5	695	G
45	5	696	C
45	5	697	G
45	5	700	G
45	5	701	G
45	5	703	G
45	5	704	C
45	5	705	G
45	5	706	C
45	5	714	G
45	5	719	C
45	5	723	A
45	5	730	G
45	5	731	G
45	5	733	A
45	5	734	G
45	5	737	C
45	5	740	G
45	5	747	A
45	5	749	G
45	5	753	C
45	5	754	C
45	5	756	G
45	5	757	G
45	5	758	G
45	5	760	G
45	5	905	C
45	5	907	C
45	5	908	G
45	5	910	G
45	5	913	U

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Mol	Chain	Res	Type
45	5	914	U
45	5	915	A
45	5	916	C
45	5	917	A
45	5	918	G
45	5	920	C
45	5	921	C
45	5	922(A)	G
45	5	922(B)	C
45	5	923	C
45	5	924	C
45	5	925	C
45	5	926	G
45	5	930	G
45	5	931	C
45	5	932	A
45	5	933	G
45	5	934	C
45	5	935	A
45	5	935(A)	G
45	5	936	C
45	5	943	A
45	5	944	A
45	5	945	U
45	5	954	C
45	5	955	G
45	5	956	A
45	5	957	G
45	5	959	G
45	5	960	A
45	5	961	G
45	5	963	G
45	5	966	A
45	5	967	C
45	5	968	C
45	5	969	C
45	5	970	G
45	5	973	G
45	5	974	C
45	5	978	G
45	5	979	C
45	5	983	C

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Mol	Chain	Res	Type
45	5	984	C
45	5	990	C
45	5	1070	G
45	5	1072	C
45	5	1073	G
45	5	1074	G
45	5	1075	G
45	5	1076	C
45	5	1078	A
45	5	1079	C
45	5	1081	C
45	5	1083	U
45	5	1084	C
45	5	1089	G
45	5	1094	G
45	5	1095	A
45	5	1096	C
45	5	1098	G
45	5	1176	C
45	5	1177	U
45	5	1178	G
45	5	1179	U
45	5	1186	U
45	5	1189	G
45	5	1190	C
45	5	1192	C
45	5	1193	C
45	5	1194	G
45	5	1195	G
45	5	1196	G
45	5	1198	G
45	5	1209	U
45	5	1211	G
45	5	1212	G
45	5	1214	C
45	5	1215	C
45	5	1216	C
45	5	1234	G
45	5	1235	G
45	5	1236	C
45	5	1237	C
45	5	1238	A

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Mol	Chain	Res	Type
45	5	1239	C
45	5	1245	C
45	5	1246	G
45	5	1251	C
45	5	1252	C
45	5	1272	C
45	5	1273	G
45	5	1275	G
45	5	1276	C
45	5	1279	A
45	5	1280	C
45	5	1281	G
45	5	1283	G
45	5	1284	G
45	5	1287	G
45	5	1288	G
45	5	1292	C
45	5	1293	G
45	5	1294	A
45	5	1295	U
45	5	1296	G
45	5	1301	C
45	5	1303	A
45	5	1304	C
45	5	1306	C
45	5	1309	C
45	5	1311	G
45	5	1312	A
45	5	1315	C
45	5	1316	G
45	5	1321	G
45	5	1322	A
45	5	1323	A
45	5	1324	A
45	5	1325	C
45	5	1326	A
45	5	1327	C
45	5	1328	G
45	5	1333	A
45	5	1335	G
45	5	1336	G
45	5	1337	A

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Mol	Chain	Res	Type
45	5	1339	U
45	5	1349	G
45	5	1353	G
45	5	1354	A
45	5	1358	G
45	5	1359	G
45	5	1360	G
45	5	1363	C
45	5	1370	G
45	5	1371	A
45	5	1373	A
45	5	1374	G
45	5	1376	C
45	5	1377	G
45	5	1378	C
45	5	1379	C
45	5	1380	G
45	5	1381	U
45	5	1387	A
45	5	1388	A
45	5	1390	G
45	5	1391	A
45	5	1392	A
45	5	1394	G
45	5	1395	U
45	5	1397	A
45	5	1398	A
45	5	1400	G
45	5	1401	C
45	5	1402	C
45	5	1404	G
45	5	1405	C
45	5	1411(C)	C
45	5	1412	G
45	5	1413	C
45	5	1414	C
45	5	1415	G
45	5	1418	C
45	5	1420	A
45	5	1421	G
45	5	1422	G
45	5	1425	G

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Mol	Chain	Res	Type
45	5	1433	A
45	5	1435	G
45	5	1436	C
45	5	1438	U
45	5	1440	U
45	5	1442	C
45	5	1443	A
45	5	1445	U
45	5	1446	C
45	5	1447	C
45	5	1448	G
45	5	1453	G
45	5	1456	C
45	5	1457	G
45	5	1458	C
45	5	1460	C
45	5	1461	C
45	5	1469	C
45	5	1470	G
45	5	1471	U
45	5	1474	C
45	5	1475	G
45	5	1476	C
45	5	1477	C
45	5	1478	C
45	5	1480	C
45	5	1481	C
45	5	1483	C
45	5	1484	G
45	5	1487	G
45	5	1489	G
45	5	1491	A
45	5	1492	G
45	5	1495	G
45	5	1497	A
45	5	1498	G
45	5	1501	C
45	5	1502	G
45	5	1503	A
45	5	1504	G
45	5	1511	U
45	5	1513	U

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Mol	Chain	Res	Type
45	5	1514	U
45	5	1515	A
45	5	1516	G
45	5	1518	A
45	5	1519	C
45	5	1521	C
45	5	1522	G
45	5	1523	A
45	5	1528	U
45	5	1531	U
45	5	1532	G
45	5	1534	A
45	5	1535	C
45	5	1536	U
45	5	1538	U
45	5	1539	G
45	5	1543	G
45	5	1547	A
45	5	1548	G
45	5	1556	C
45	5	1558	A
45	5	1559	G
45	5	1560	A
45	5	1562	G
45	5	1565	A
45	5	1566	C
45	5	1578	U
45	5	1579	C
45	5	1584	G
45	5	1586	G
45	5	1588	U
45	5	1589	C
45	5	1591	U
45	5	1592	G
45	5	1593	A
45	5	1594	C
45	5	1596	U
45	5	1598	C
45	5	1601	A
45	5	1602	U
45	5	1603	C
45	5	1609	U

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Mol	Chain	Res	Type
45	5	1611	C
45	5	1612	G
45	5	1613	A
45	5	1614	C
45	5	1615	C
45	5	1616	U
45	5	1618	G
45	5	1624	G
45	5	1625	G
45	5	1628	C
45	5	1631	A
45	5	1632	A
45	5	1633	G
45	5	1634	A
45	5	1637	A
45	5	1640	C
45	5	1641	G
45	5	1642	A
45	5	1651	G
45	5	1653	A
45	5	1654	G
45	5	1656	U
45	5	1658	G
45	5	1661	C
45	5	1666	C
45	5	1675	C
45	5	1676	C
45	5	1677	U
45	5	1678	C
45	5	1679	A
45	5	1680	G
45	5	1684	A
45	5	1685	G
45	5	1688	G
45	5	1689	G
45	5	1691	G
45	5	1692	C
45	5	1693	U
45	5	1694	C
45	5	1695	U
45	5	1696	C
45	5	1721	G

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Mol	Chain	Res	Type
45	5	1722	C
45	5	1727	U
45	5	1728	U
45	5	1730	U
45	5	1731	C
45	5	1734	G
45	5	1735	U
45	5	1740	C
45	5	1741	G
45	5	1742	A
45	5	1743	A
45	5	1744	U
45	5	1746	A
45	5	1748	U
45	5	1750	G
45	5	1754	U
45	5	1756	U
45	5	1761	G
45	5	1762	C
45	5	1763	C
45	5	1764	G
45	5	1765	A
45	5	1766	A
45	5	1768	C
45	5	1772	C
45	5	1773	U
45	5	1774	C
45	5	1775	A
45	5	1776	A
45	5	1778	C
45	5	1782	U
45	5	1785	C
45	5	1787	A
45	5	1795	A
45	5	1802	A
45	5	1803	G
45	5	1804	A
45	5	1805	A
45	5	1806	G
45	5	1820	U
45	5	1821	G
45	5	1825	A

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Mol	Chain	Res	Type
45	5	1826	G
45	5	1828	C
45	5	1831	G
45	5	1832	C
45	5	1833	G
45	5	1834	U
45	5	1835	G
45	5	1836	G
45	5	1837	A
45	5	1842	G
45	5	1843	A
45	5	1845	U
45	5	1850	A
45	5	1851	G
45	5	1854	G
45	5	1855	G
45	5	1856	C
45	5	1858	A
45	5	1869	G
45	5	1871	A
45	5	1874	A
45	5	1875	C
45	5	1880	G
45	5	1881	C
45	5	1882	U
45	5	1883	G
45	5	1884	C
45	5	1889	U
45	5	1890	G
45	5	1891	A
45	5	1892	A
45	5	1893	C
45	5	1896	A
45	5	1897	A
45	5	1899	G
45	5	1902	G
45	5	1903	G
45	5	1912	G
45	5	1913	C
45	5	1914	C
45	5	1916	G
45	5	1918	U

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Mol	Chain	Res	Type
45	5	1920	C
45	5	1921	C
45	5	1922	G
45	5	1929	A
45	5	1931	C
45	5	1932	A
45	5	1933	G
45	5	1936	C
45	5	1937	C
45	5	1941	A
45	5	1942	A
45	5	1943	A
45	5	1948	G
45	5	1957	U
45	5	1960	A
45	5	1961	G
45	5	1962	A
45	5	1963	C
45	5	1965	G
45	5	1966	C
45	5	1970	A
45	5	1971	U
45	5	1972	G
45	5	1973	G
45	5	1974	U
45	5	1976	G
45	5	1977	C
45	5	1978	C
45	5	1979	A
45	5	1980	U
45	5	1982	G
45	5	1983	A
45	5	1984	A
45	5	1985	G
45	5	1986	U
45	5	1987	C
45	5	1988	G
45	5	1990	A
45	5	1991	A
45	5	1992	U
45	5	1993	C
45	5	1994	C

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Mol	Chain	Res	Type
45	5	1996	C
45	5	1997	U
45	5	2001	G
45	5	2002	A
45	5	2003	G
45	5	2004	U
45	5	2005	G
45	5	2011	C
45	5	2014	C
45	5	2015	U
45	5	2017	A
45	5	2018	C
45	5	2023	C
45	5	2024	G
45	5	2025	A
45	5	2026	A
45	5	2028	C
45	5	2029	A
45	5	2031	C
45	5	2033	A
45	5	2035	C
45	5	2036	C
45	5	2041	A
45	5	2043	A
45	5	2047	A
45	5	2048	U
45	5	2049	G
45	5	2052	G
45	5	2054	U
45	5	2055	G
45	5	2056	G
45	5	2063	G
45	5	2069	A
45	5	2074	C
45	5	2076	G
45	5	2079	G
45	5	2084	U
45	5	2085	G
45	5	2086	G
45	5	2088	A
45	5	2089	G
45	5	2090	U

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Mol	Chain	Res	Type
45	5	2091	C
45	5	2092	G
45	5	2093	G
45	5	2094	C
45	5	2095	A
45	5	2096	G
45	5	2097	A
45	5	2098	G
45	5	2099	C
45	5	2100	G
45	5	2101	A
45	5	2102	G
45	5	2104	A
45	5	2105	A
45	5	2107	A
45	5	2108	G
45	5	2109	A
45	5	2259	G
45	5	2260	C
45	5	2261	G
45	5	2263	A
45	5	2264	C
45	5	2265	G
45	5	2266	C
45	5	2267	U
45	5	2268	A
45	5	2271	C
45	5	2277	C
45	5	2279	A
45	5	2280	G
45	5	2284	G
45	5	2289	C
45	5	2291	G
45	5	2296	G
45	5	2297	G
45	5	2298	U
45	5	2300	A
45	5	2301	G
45	5	2302	C
45	5	2303	C
45	5	2306	G
45	5	2307	A

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Mol	Chain	Res	Type
45	5	2313	A
45	5	2314	G
45	5	2318	G
45	5	2319	C
45	5	2325	C
45	5	2328	G
45	5	2329	U
45	5	2331	G
45	5	2333	G
45	5	2336	G
45	5	2337	C
45	5	2340	C
45	5	2346	C
45	5	2348	G
45	5	2349	A
45	5	2350	U
45	5	2351	C
45	5	2352	U
45	5	2353	U
45	5	2364	G
45	5	2365	C
45	5	2366	A
45	5	2367	A
45	5	2369	U
45	5	2373	C
45	5	2374	A
45	5	2376	A
45	5	2377	C
45	5	2380	G
45	5	2381	A
45	5	2382	A
45	5	2384	U
45	5	2385	U
45	5	2387	G
45	5	2395	A
45	5	2398	U
45	5	2399	G
45	5	2408	U
45	5	2409	U
45	5	2412	A
45	5	2413	U
45	5	2414	G

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Mol	Chain	Res	Type
45	5	2415	U
45	5	2417	A
45	5	2418	A
45	5	2422	C
45	5	2423	A
45	5	2424	G
45	5	2425	U
45	5	2426	U
45	5	2432	U
45	5	2437	C
45	5	2438	A
45	5	2439	G
45	5	2441	C
45	5	2444	U
45	5	2445	C
45	5	2447	U
45	5	2450	G
45	5	2456	G
45	5	2466	G
45	5	2467	U
45	5	2468	U
45	5	2469	C
45	5	2470	C
45	5	2471	G
45	5	2473	A
45	5	2475	G
45	5	2476	G
45	5	2477	A
45	5	2482	C
45	5	2484	A
45	5	2488	C
45	5	2489	C
45	5	2490	U
45	5	2491	C
45	5	2492	C
45	5	2494	U
45	5	2495	U
45	5	2496	G
45	5	2501	C
45	5	2503	G
45	5	2504	C
45	5	2505	C

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Mol	Chain	Res	Type
45	5	2506	G
45	5	2509	C
45	5	2510	G
45	5	2511	A
45	5	2512	A
45	5	2513	A
45	5	2514	G
45	5	2515	G
45	5	2517	A
45	5	2521	G
45	5	2525	U
45	5	2530	U
45	5	2531	C
45	5	2532	C
45	5	2533	C
45	5	2536	A
45	5	2539	C
45	5	2540	C
45	5	2544	G
45	5	2545	U
45	5	2546	G
45	5	2547	G
45	5	2548	C
45	5	2551	A
45	5	2552	G
45	5	2553	A
45	5	2554	U
45	5	2555	G
45	5	2558	C
45	5	2560	C
45	5	2561	C
45	5	2565	A
45	5	2566	G
45	5	2569	G
45	5	2570	U
45	5	2571	C
45	5	2575	U
45	5	2576	G
45	5	2578	G
45	5	2582	A
45	5	2583	C
45	5	2585	C

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Mol	Chain	Res	Type
45	5	2586	G
45	5	2587	A
45	5	2588	C
45	5	2589	C
45	5	2590	G
45	5	2593	C
45	5	2596	G
45	5	2597	G
45	5	2598	A
45	5	2599	G
45	5	2600	A
45	5	2601	A
45	5	2602	G
45	5	2611	A
45	5	2615	C
45	5	2618	G
45	5	2625	U
45	5	2626	U
45	5	2627	C
45	5	2631	U
45	5	2633	U
45	5	2634	C
45	5	2638	G
45	5	2639	U
45	5	2640	G
45	5	2641	A
45	5	2646	C
45	5	2648	G
45	5	2651	C
45	5	2656	U
45	5	2658	G
45	5	2659	A
45	5	2661	U
45	5	2662	G
45	5	2669	C
45	5	2671	C
45	5	2673	G
45	5	2684	C
45	5	2686	G
45	5	2687	U
45	5	2688	G
45	5	2690	C

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Mol	Chain	Res	Type
45	5	2693	G
45	5	2694	G
45	5	2696	A
45	5	2697	A
45	5	2703	G
45	5	2706	G
45	5	2707	U
45	5	2708	U
45	5	2709	C
45	5	2710	C
45	5	2711	G
45	5	2712	G
45	5	2714	G
45	5	2715	G
45	5	2716	C
45	5	2721	G
45	5	2726	G
45	5	2730	U
45	5	2732	G
45	5	2735	G
45	5	2740	U
45	5	2741	U
45	5	2743	A
45	5	2744	A
45	5	2746	A
45	5	2749	C
45	5	2751	G
45	5	2756	G
45	5	2758	G
45	5	2760	G
45	5	2761	U
45	5	2762	G
45	5	2763	U
45	5	2764	A
45	5	2768	C
45	5	2769	U
45	5	2770	C
45	5	2775	C
45	5	2777	G
45	5	2782	U
45	5	2787	A
45	5	2788	U

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Mol	Chain	Res	Type
45	5	2789	A
45	5	2790	U
45	5	2791	C
45	5	2793	G
45	5	2794	C
45	5	2795	A
45	5	2796	G
45	5	2798	A
45	5	2799	G
45	5	2800	G
45	5	2806	A
45	5	2807	A
45	5	2808	G
45	5	2811	G
45	5	2812	A
45	5	2813	A
45	5	2814	C
45	5	2815	A
45	5	2817	C
45	5	2825	A
45	5	2826	U
45	5	2827	G
45	5	2828	U
45	5	2832	A
45	5	2833	A
45	5	2834	C
45	5	2835	A
45	5	2838	G
45	5	2839	U
45	5	2840	A
45	5	2841	G
45	5	2842	G
45	5	2844	A
45	5	2849	A
45	5	2850	A
45	5	2855	G
45	5	2857	A
45	5	2862	G
45	5	2863	G
45	5	2867	C
45	5	2871	A
45	5	2873	U

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Mol	Chain	Res	Type
45	5	2874	U
45	5	2875	C
45	5	2876	G
45	5	2878	G
45	5	2883	G
45	5	2884	G
45	5	2885	A
45	5	2887	U
45	5	2888	G
45	5	2891	U
45	5	2900	U
45	5	3598	C
45	5	3600	G
45	5	3602	C
45	5	3604	A
45	5	3606	U
45	5	3607	U
45	5	3615	G
45	5	3616	U
45	5	3621	A
45	5	3625	G
45	5	3626	G
45	5	3629	A
45	5	3632	C
45	5	3633	C
45	5	3635	A
45	5	3637	U
45	5	3641	U
45	5	3642	A
45	5	3643	A
45	5	3644	U
45	5	3647	A
45	5	3648	A
45	5	3649	A
45	5	3659	G
45	5	3662	A
45	5	3669	G
45	5	3671	G
45	5	3672	G
45	5	3673	C
45	5	3674	G
45	5	3675	G

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Mol	Chain	Res	Type
45	5	3680	U
45	5	3683	C
45	5	3684	G
45	5	3685	C
45	5	3689	G
45	5	3690	U
45	5	3691	G
45	5	3692	A
45	5	3696	C
45	5	3698	G
45	5	3699	C
45	5	3700	C
45	5	3702	A
45	5	3711	A
45	5	3712	A
45	5	3713	U
45	5	3715	U
45	5	3718	A
45	5	3720	G
45	5	3724	A
45	5	3727	A
45	5	3728	A
45	5	3729	U
45	5	3730	U
45	5	3731	C
45	5	3733	A
45	5	3734	U
45	5	3742	G
45	5	3745	U
45	5	3748	A
45	5	3749	C
45	5	3750	G
45	5	3752	C
45	5	3753	G
45	5	3756	A
45	5	3760	A
45	5	3762	U
45	5	3765	G
45	5	3769	C
45	5	3771	C
45	5	3773	U
45	5	3776	G

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Mol	Chain	Res	Type
45	5	3777	G
45	5	3780	G
45	5	3781	C
45	5	3783	A
45	5	3784	A
45	5	3785	A
45	5	3786	U
45	5	3788	C
45	5	3789	C
45	5	3791	C
45	5	3792	G
45	5	3793	U
45	5	3794	C
45	5	3795	A
45	5	3797	C
45	5	3801	U
45	5	3807	A
45	5	3808	C
45	5	3809	G
45	5	3810	C
45	5	3811	G
45	5	3812	C
45	5	3814	U
45	5	3817	A
45	5	3818	U
45	5	3819	G
45	5	3828	A
45	5	3835	C
45	5	3838	U
45	5	3839	G
45	5	3840	U
45	5	3843	C
45	5	3844	U
45	5	3847	C
45	5	3858	C
45	5	3861	A
45	5	3865	A
45	5	3867	A
45	5	3873	G
45	5	3876	A
45	5	3877	A
45	5	3878	C

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Mol	Chain	Res	Type
45	5	3879	G
45	5	3880	G
45	5	3882	C
45	5	3890	A
45	5	3894	A
45	5	3898	G
45	5	3900	G
45	5	3901	A
45	5	3902	A
45	5	3904	G
45	5	3905	A
45	5	3906	A
45	5	3907	G
45	5	3908	A
45	5	3914	U
45	5	3915	U
45	5	3916	G
45	5	3917	A
45	5	3919	C
45	5	3921	U
45	5	3923	A
45	5	3925	U
45	5	3926	C
45	5	3930	U
45	5	3936	A
45	5	3938	G
45	5	3939	G
45	5	3941	G
45	5	3942	A
45	5	3943	A
45	5	3949	A
45	5	3951	G
45	5	3952	A
45	5	3953	G
45	5	3955	G
45	5	3956	G
45	5	3958	G
45	5	3961	G
45	5	3964	U
45	5	3965	A
45	5	3966	A
45	5	3968	U

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Mol	Chain	Res	Type
45	5	3969	G
45	5	3970	G
45	5	3971	G
45	5	3972	A
45	5	3975	C
45	5	3976	C
45	5	3977	C
45	5	4035	G
45	5	4039	G
45	5	4041	C
45	5	4045	G
45	5	4048	A
45	5	4049	U
45	5	4050	A
45	5	4051	C
45	5	4052	C
45	5	4053	A
45	5	4054	C
45	5	4055	U
45	5	4056	A
45	5	4057	C
45	5	4062	A
45	5	4064	C
45	5	4065	G
45	5	4066	U
45	5	4067	U
45	5	4068	U
45	5	4069	U
45	5	4070	U
45	5	4072	C
45	5	4075	U
45	5	4076	G
45	5	4077	A
45	5	4079	C
45	5	4084	G
45	5	4085	A
45	5	4086	G
45	5	4087	G
45	5	4088	C
45	5	4091	G
45	5	4092	G
45	5	4095	G

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Mol	Chain	Res	Type
45	5	4096	C
45	5	4097	G
45	5	4099	G
45	5	4100	C
45	5	4109	G
45	5	4110	C
45	5	4113	U
45	5	4114	C
45	5	4115	G
45	5	4116	C
45	5	4117	U
45	5	4118	U
45	5	4119	C
45	5	4120	U
45	5	4121	G
45	5	4122	G
45	5	4123	C
45	5	4124	G
45	5	4127	A
45	5	4128	A
45	5	4129	G
45	5	4132	C
45	5	4133	C
45	5	4134	C
45	5	4135	G
45	5	4136	G
45	5	4137	C
45	5	4147	G
45	5	4148	C
45	5	4152	G
45	5	4157	A
45	5	4158	C
45	5	4159	C
45	5	4162	C
45	5	4163	U
45	5	4164	C
45	5	4166	G
45	5	4167	G
45	5	4168	G
45	5	4171	C
45	5	4176	C
45	5	4183	G

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Mol	Chain	Res	Type
45	5	4184	G
45	5	4187	G
45	5	4189	U
45	5	4191	G
45	5	4194	U
45	5	4196	G
45	5	4200	G
45	5	4201	G
45	5	4202	U
45	5	4203	A
45	5	4205	A
45	5	4207	C
45	5	4214	A
45	5	4217	G
45	5	4219	A
45	5	4221	C
45	5	4222	G
45	5	4224	A
45	5	4229	U
45	5	4230	C
45	5	4231	C
45	5	4233	A
45	5	4234	A
45	5	4242	U
45	5	4243	C
45	5	4250	G
45	5	4251	A
45	5	4252	C
45	5	4254	G
45	5	4256	A
45	5	4257	A
45	5	4258	C
45	5	4260	U
45	5	4264	G
45	5	4265	U
45	5	4266	G
45	5	4267	G
45	5	4268	A
45	5	4269	G
45	5	4271	A
45	5	4272	G
45	5	4273	A

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Mol	Chain	Res	Type
45	5	4276	G
45	5	4278	C
45	5	4281	A
45	5	4283	G
45	5	4288	C
45	5	4291	G
45	5	4293	U
45	5	4294	C
45	5	4296	U
45	5	4298	A
45	5	4303	C
45	5	4304	A
45	5	4305	G
45	5	4306	U
45	5	4313	A
45	5	4318	C
45	5	4324	A
45	5	4326	G
45	5	4329	G
45	5	4330	G
45	5	4331	G
45	5	4336	A
45	5	4337	C
45	5	4339	A
45	5	4340	U
45	5	4343	U
45	5	4344	U
45	5	4346	U
45	5	4348	A
45	5	4349	C
45	5	4354	U
45	5	4355	G
45	5	4359	U
45	5	4362	A
45	5	4365	C
45	5	4369	A
45	5	4373	G
45	5	4374	U
45	5	4375	C
45	5	4376	A
45	5	4377	G
45	5	4378	A

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Mol	Chain	Res	Type
45	5	4380	A
45	5	4381	A
45	5	4382	G
45	5	4383	U
45	5	4387	C
45	5	4389	C
45	5	4393	G
45	5	4394	A
45	5	4398	C
45	5	4400	G
45	5	4401	G
45	5	4404	U
45	5	4405	G
45	5	4406	U
45	5	4410	G
45	5	4414	A
45	5	4415	A
45	5	4418	G
45	5	4419	U
45	5	4421	C
45	5	4422	A
45	5	4424	A
45	5	4426	C
45	5	4428	A
45	5	4430	G
45	5	4431	U
45	5	4433	G
45	5	4437	U
45	5	4439	U
45	5	4440	G
45	5	4442	U
45	5	4443	C
45	5	4444	C
45	5	4446	U
45	5	4447	C
45	5	4448	G
45	5	4449	A
45	5	4450	U
45	5	4452	U
45	5	4454	G
45	5	4455	G
45	5	4456	C

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Mol	Chain	Res	Type
45	5	4457	U
45	5	4459	U
45	5	4460	U
45	5	4461	C
45	5	4462	C
45	5	4463	U
45	5	4464	A
45	5	4465	U
45	5	4467	A
45	5	4469	U
45	5	4470	G
45	5	4471	U
45	5	4472	G
45	5	4475	G
45	5	4476	C
45	5	4477	A
45	5	4478	G
45	5	4480	A
45	5	4481	U
45	5	4482	U
45	5	4488	A
45	5	4489	G
45	5	4490	C
45	5	4500	U
45	5	4502	C
45	5	4504	C
45	5	4509	U
45	5	4510	A
45	5	4511	A
45	5	4512	U
45	5	4513	A
45	5	4515	G
45	5	4516	G
45	5	4517	A
45	5	4518	A
45	5	4519	C
45	5	4520	G
45	5	4521	U
45	5	4522	G
45	5	4527	G
45	5	4528	G
45	5	4529	G

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Mol	Chain	Res	Type
45	5	4530	U
45	5	4531	U
45	5	4534	G
45	5	4535	A
45	5	4536	C
45	5	4537	C
45	5	4538	G
45	5	4539	U
45	5	4543	G
45	5	4547	C
45	5	4548	A
45	5	4549	G
45	5	4551	U
45	5	4555	U
45	5	4556	U
45	5	4563	U
45	5	4570	G
45	5	4573	G
45	5	4575	G
45	5	4579	U
45	5	4581	G
45	5	4584	A
45	5	4588	U
45	5	4590	A
45	5	4599	A
45	5	4605	A
45	5	4606	G
45	5	4607	A
45	5	4614	G
45	5	4615	C
45	5	4617	G
45	5	4621	C
45	5	4632	U
45	5	4633	G
45	5	4634	U
45	5	4635	A
45	5	4636	U
45	5	4637	G
45	5	4638	U
45	5	4646	U
45	5	4649	G
45	5	4650	G

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Mol	Chain	Res	Type
45	5	4654	C
45	5	4657	U
45	5	4658	G
45	5	4662	C
45	5	4663	G
45	5	4665	A
45	5	4670	C
45	5	4672	A
45	5	4673	U
45	5	4675	U
45	5	4677	U
45	5	4680	G
45	5	4684	A
45	5	4688	C
45	5	4689	U
45	5	4693	C
45	5	4694	G
45	5	4695	C
45	5	4696	C
45	5	4700	A
45	5	4702	G
45	5	4703	U
45	5	4708	A
45	5	4709	U
45	5	4712	C
45	5	4713	G
45	5	4714	C
45	5	4715	C
45	5	4717	A
45	5	4720	C
45	5	4721	G
45	5	4724	A
45	5	4726	G
45	5	4728	U
45	5	4729	A
45	5	4736	C
45	5	4738	C
45	5	4740	G
45	5	4748	U
45	5	4750	G
45	5	4751	G
45	5	4752	U

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Mol	Chain	Res	Type
45	5	4753	U
45	5	4754	G
45	5	4757	C
45	5	4758	U
45	5	4759	C
45	5	4760	G
45	5	4761	G
45	5	4765	G
45	5	4771	C
45	5	4772	C
45	5	4775	C
45	5	4862	G
45	5	4863	G
45	5	4865	C
45	5	4869	U
45	5	4870	G
45	5	4871	C
45	5	4872	G
45	5	4873	G
45	5	4874	A
45	5	4875	G
45	5	4876	A
45	5	4877	G
45	5	4882	U
45	5	4883	C
45	5	4885	U
45	5	4892	A
45	5	4894	A
45	5	4895	C
45	5	4896	G
45	5	4903	G
45	5	4904	G
45	5	4905	C
45	5	4909	A
45	5	4912	G
45	5	4913	G
45	5	4914	G
45	5	4915	G
45	5	4917	C
45	5	4918	C
45	5	4920	C
45	5	4921	C

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Mol	Chain	Res	Type
45	5	4922	C
45	5	4923	U
45	5	4924	C
45	5	4926	C
45	5	4929	C
45	5	4930	C
45	5	4932	U
45	5	4933	C
45	5	4937	C
45	5	4938	A
45	5	4940	C
45	5	4941	G
45	5	4942	C
45	5	4944	C
45	5	4945	G
45	5	4948	C
45	5	4949	G
45	5	4950	U
45	5	4951	G
45	5	4954	G
45	5	4956	A
45	5	4958	C
45	5	4959	U
45	5	4960	G
45	5	4963	G
45	5	4964	C
45	5	4965	U
45	5	4966	A
45	5	4967	A
45	5	4968	A
45	5	4973	U
45	5	4974	C
45	5	4976	U
45	5	4977	A
45	5	4978	G
45	5	4979	A
45	5	4982	A
45	5	4987	C
45	5	4988	U
45	5	4989	U
45	5	4990	C
45	5	4993	G

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Mol	Chain	Res	Type
45	5	4999	G
45	5	5003	U
45	5	5006	U
45	5	5007	A
45	5	5016	A
45	5	5017	G
45	5	5018	C
45	5	5021	C
45	5	5029	C
45	5	5030	U
45	5	5033	G
45	5	5035	U
45	5	5036	C
45	5	5037	U
45	5	5038	A
45	5	5040	U
45	5	5041	G
45	5	5042	A
45	5	5050	C
45	5	5053	U
45	5	5054	C
45	5	5056	A
45	5	5057	C
45	5	5058	A
45	5	5061	A
45	5	5062	G
45	5	5064	G
45	5	5066	U
46	7	5	A
46	7	7	G
46	7	10	C
46	7	13	A
46	7	15	C
46	7	17	C
46	7	22	A
46	7	23	A
46	7	28	C
46	7	30	C
46	7	34	C
46	7	36	C
46	7	37	G
46	7	40	U

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Mol	Chain	Res	Type
46	7	41	G
46	7	42	A
46	7	44	C
46	7	51	G
46	7	52	C
46	7	53	U
46	7	54	A
46	7	57	C
46	7	64	G
46	7	66	G
46	7	69	U
46	7	78	C
46	7	82	G
46	7	83	A
46	7	93	G
46	7	94	C
46	7	97	G
46	7	98	G
46	7	99	G
46	7	100	A
46	7	101	A
46	7	110	G
46	7	113	G
46	7	116	G
46	7	117	G
46	7	119	U
47	8	2	G
47	8	3	A
47	8	10	G
47	8	15	G
47	8	17	A
47	8	26	C
47	8	28	C
47	8	32	C
47	8	33	G
47	8	34	U
47	8	35	C
47	8	36	G
47	8	37	A
47	8	38	U
47	8	43	A
47	8	46	G

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Mol	Chain	Res	Type
47	8	48	A
47	8	49	G
47	8	50	C
47	8	51	U
47	8	52	A
47	8	53	G
47	8	55	U
47	8	58	G
47	8	59	A
47	8	62	A
47	8	63	U
47	8	64	U
47	8	70	G
47	8	71	A
47	8	76	C
47	8	79	G
47	8	86	U
47	8	88	A
47	8	90	C
47	8	95	A
47	8	97	A
47	8	98	C
47	8	100	U
47	8	103	A
47	8	104	A
47	8	105	C
47	8	108	A
47	8	110	U
47	8	111	U
47	8	113	C
47	8	114	G
47	8	115	G
47	8	120	G
47	8	122	G
47	8	123	U
47	8	124	U
47	8	125	C
47	8	126	C
47	8	127	U
47	8	129	C
47	8	130	C
47	8	131	G

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Mol	Chain	Res	Type
47	8	137	A
47	8	138	C
47	8	147	G
47	8	153	C
47	8	156	U
49	2	2	A
49	2	3	C
49	2	4	C
49	2	5	U
49	2	6	G
49	2	7	G
49	2	10	G
49	2	11	A
49	2	15	U
49	2	17	C
49	2	22	A
49	2	25	A
49	2	31	U
49	2	33	G
49	2	37	C
49	2	41	G
49	2	42	A
49	2	46	A
49	2	48	C
49	2	56	G
49	2	58	C
49	2	60	A
49	2	62	G
49	2	64	A
49	2	65	C
49	2	66	G
49	2	67	C
49	2	68	A
49	2	69	C
49	2	70	G
49	2	71	G
49	2	72	C
49	2	73	C
49	2	74	G
49	2	75	G
49	2	77	A
49	2	78	C

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Mol	Chain	Res	Type
49	2	79	A
49	2	80	G
49	2	91	A
49	2	95	G
49	2	97	U
49	2	99	A
49	2	100	U
49	2	101	U
49	2	103	A
49	2	105	U
49	2	108	G
49	2	110	U
49	2	111	A
49	2	113	G
49	2	115	U
49	2	116	U
49	2	119	U
49	2	123	G
49	2	126	G
49	2	127	C
49	2	130	G
49	2	142	C
49	2	143	U
49	2	144	U
49	2	147	A
49	2	148	U
49	2	149	A
49	2	154	U
49	2	159	A
49	2	161	U
49	2	162	C
49	2	163	U
49	2	169	U
49	2	170	A
49	2	173	A
49	2	178	C
49	2	180	G
49	2	181	A
49	2	182	C
49	2	183	G
49	2	184	G
49	2	187	G

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Mol	Chain	Res	Type
49	2	188	C
49	2	190	G
49	2	192	C
49	2	198	U
49	2	200	G
49	2	201	C
49	2	203	G
49	2	209	A
49	2	210	U
49	2	211	G
49	2	221	A
49	2	222	U
49	2	224	A
49	2	302	A
49	2	306	C
49	2	307	G
49	2	308	G
49	2	309	G
49	2	310	C
49	2	312	G
49	2	313	A
49	2	314	U
49	2	317	C
49	2	318	A
49	2	319	C
49	2	320	G
49	2	321	C
49	2	322	C
49	2	330	G
49	2	331	C
49	2	332	G
49	2	333	G
49	2	336	A
49	2	338	G
49	2	343	A
49	2	347	G
49	2	349	A
49	2	351	G
49	2	352	U
49	2	354	U
49	2	358	C
49	2	362	C

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Mol	Chain	Res	Type
49	2	363	A
49	2	364	A
49	2	366	U
49	2	367	U
49	2	368	U
49	2	369	C
49	2	370	G
49	2	371	A
49	2	372	U
49	2	374	G
49	2	379	C
49	2	382	C
49	2	384	U
49	2	385	G
49	2	386	C
49	2	389	A
49	2	390	C
49	2	395	G
49	2	397	G
49	2	398	A
49	2	400	C
49	2	404	G
49	2	407	G
49	2	408	A
49	2	409	C
49	2	410	G
49	2	413	G
49	2	416	U
49	2	417	C
49	2	418	A
49	2	419	G
49	2	426	A
49	2	428	U
49	2	429	C
49	2	432	G
49	2	435	A
49	2	436	G
49	2	444	G
49	2	447	A
49	2	448	A
49	2	449	A
49	2	450	C

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Mol	Chain	Res	Type
49	2	452	G
49	2	460	A
49	2	461	U
49	2	462	C
49	2	465	A
49	2	466	G
49	2	469	A
49	2	470	G
49	2	471	G
49	2	472	C
49	2	473	A
49	2	474	G
49	2	485	A
49	2	486	A
49	2	487	U
49	2	490	C
49	2	491	C
49	2	492	C
49	2	493	A
49	2	496	C
49	2	497	C
49	2	500	A
49	2	501	C
49	2	502	C
49	2	503	C
49	2	507	G
49	2	509	G
49	2	512	A
49	2	517	C
49	2	518	G
49	2	521	A
49	2	525	A
49	2	527	C
49	2	530	U
49	2	531	A
49	2	532	C
49	2	533	A
49	2	534	G
49	2	535	G
49	2	536	A
49	2	537	C
49	2	539	C

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Mol	Chain	Res	Type
49	2	542	U
49	2	543	C
49	2	544	G
49	2	547	G
49	2	548	C
49	2	549	C
49	2	550	C
49	2	551	U
49	2	554	A
49	2	555	A
49	2	556	U
49	2	559	G
49	2	561	A
49	2	562	U
49	2	565	G
49	2	567	C
49	2	568	C
49	2	569	A
49	2	570	C
49	2	574	A
49	2	575	A
49	2	583	A
49	2	587	A
49	2	588	G
49	2	589	G
49	2	590	A
49	2	591	U
49	2	593	C
49	2	594	A
49	2	600	G
49	2	602	G
49	2	604	A
49	2	605	A
49	2	606	G
49	2	607	U
49	2	608	C
49	2	614	C
49	2	618	C
49	2	620	G
49	2	621	C
49	2	623	G
49	2	627	U

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Mol	Chain	Res	Type
49	2	628	A
49	2	629	A
49	2	631	U
49	2	634	A
49	2	635	G
49	2	636	C
49	2	637	U
49	2	640	A
49	2	641	A
49	2	643	A
49	2	644	G
49	2	646	G
49	2	656	G
49	2	657	U
49	2	658	U
49	2	659	G
49	2	660	C
49	2	661	U
49	2	663	C
49	2	664	A
49	2	666	U
49	2	667	U
49	2	668	A
49	2	669	A
49	2	671	A
49	2	672	A
49	2	673	G
49	2	676	C
49	2	679	A
49	2	684	G
49	2	689	U
49	2	693	A
49	2	696	G
49	2	733	C
49	2	734	C
49	2	736	C
49	2	743	U
49	2	744	G
49	2	751	G
49	2	752	G
49	2	753	C
49	2	754	G

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Mol	Chain	Res	Type
49	2	755	C
49	2	756	C
49	2	791	C
49	2	795	A
49	2	796	G
49	2	805	U
49	2	806	U
49	2	808	A
49	2	809	A
49	2	811	A
49	2	812	A
49	2	815	U
49	2	819	G
49	2	821	G
49	2	822	U
49	2	823	U
49	2	827	A
49	2	828	G
49	2	829	C
49	2	830	A
49	2	832	G
49	2	844	U
49	2	846	G
49	2	847	A
49	2	848	U
49	2	853	C
49	2	856	C
49	2	858	A
49	2	859	G
49	2	860	G
49	2	862	A
49	2	863	U
49	2	864	A
49	2	866	U
49	2	869	A
49	2	870	A
49	2	871	U
49	2	872	A
49	2	873	G
49	2	874	G
49	2	877	C
49	2	878	G

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Mol	Chain	Res	Type
49	2	879	C
49	2	884	C
49	2	885	U
49	2	886	A
49	2	887	U
49	2	888	U
49	2	890	U
49	2	891	G
49	2	892	U
49	2	895	G
49	2	897	U
49	2	898	U
49	2	899	U
49	2	900	C
49	2	905	C
49	2	908	A
49	2	910	G
49	2	913	A
49	2	914	U
49	2	916	A
49	2	919	A
49	2	920	A
49	2	921	G
49	2	922	A
49	2	926	A
49	2	933	G
49	2	934	G
49	2	938	A
49	2	940	U
49	2	943	U
49	2	944	A
49	2	947	G
49	2	948	C
49	2	950	C
49	2	954	U
49	2	955	A
49	2	956	G
49	2	962	A
49	2	966	U
49	2	971	G
49	2	972	A
49	2	973	C

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Mol	Chain	Res	Type
49	2	974	C
49	2	977	C
49	2	978	G
49	2	981	A
49	2	982	G
49	2	990	A
49	2	991	G
49	2	992	A
49	2	997	A
49	2	999	G
49	2	1002	U
49	2	1003	U
49	2	1008	A
49	2	1009	A
49	2	1016	U
49	2	1017	U
49	2	1020	A
49	2	1023	A
49	2	1026	C
49	2	1033	G
49	2	1034	A
49	2	1040	G
49	2	1041	G
49	2	1044	G
49	2	1047	C
49	2	1050	A
49	2	1051	G
49	2	1060	A
49	2	1062	A
49	2	1068	G
49	2	1070	A
49	2	1074	C
49	2	1082	A
49	2	1083	A
49	2	1084	A
49	2	1085	C
49	2	1086	G
49	2	1097	G
49	2	1099	G
49	2	1100	A
49	2	1105	G
49	2	1108	G

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Mol	Chain	Res	Type
49	2	1115	U
49	2	1116	C
49	2	1117	C
49	2	1118	C
49	2	1119	A
49	2	1121	G
49	2	1122	A
49	2	1123	C
49	2	1125	C
49	2	1134	G
49	2	1135	C
49	2	1138	C
49	2	1139	C
49	2	1140	G
49	2	1141	G
49	2	1144	A
49	2	1149	A
49	2	1150	A
49	2	1153	C
49	2	1154	U
49	2	1155	U
49	2	1157	G
49	2	1160	U
49	2	1162	C
49	2	1165	G
49	2	1166	G
49	2	1168	G
49	2	1191	C
49	2	1193	U
49	2	1194	A
49	2	1195	A
49	2	1200	A
49	2	1202	U
49	2	1203	G
49	2	1205	C
49	2	1207	G
49	2	1211	G
49	2	1215	C
49	2	1216	C
49	2	1221	G
49	2	1224	G
49	2	1233	G

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Mol	Chain	Res	Type
49	2	1234	C
49	2	1235	G
49	2	1236	G
49	2	1242	U
49	2	1251	A
49	2	1253	A
49	2	1254	C
49	2	1256	G
49	2	1257	G
49	2	1259	A
49	2	1260	A
49	2	1261	C
49	2	1262	C
49	2	1264	C
49	2	1266	C
49	2	1268	C
49	2	1272	C
49	2	1274	G
49	2	1275	G
49	2	1282	A
49	2	1284	A
49	2	1285	G
49	2	1286	G
49	2	1287	A
49	2	1290	G
49	2	1291	A
49	2	1292	C
49	2	1294	G
49	2	1296	U
49	2	1299	A
49	2	1301	A
49	2	1302	G
49	2	1304	U
49	2	1308	U
49	2	1314	U
49	2	1315	U
49	2	1318	G
49	2	1319	U
49	2	1323	U
49	2	1326	U
49	2	1327	G
49	2	1328	G

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Mol	Chain	Res	Type
49	2	1332	A
49	2	1333	U
49	2	1334	G
49	2	1337	C
49	2	1342	U
49	2	1344	A
49	2	1347	U
49	2	1348	G
49	2	1354	G
49	2	1356	G
49	2	1364	U
49	2	1365	G
49	2	1366	G
49	2	1371	U
49	2	1372	U
49	2	1374	C
49	2	1376	A
49	2	1378	A
49	2	1386	A
49	2	1387	G
49	2	1396	A
49	2	1397	U
49	2	1402	A
49	2	1403	C
49	2	1404	U
49	2	1405	A
49	2	1408	U
49	2	1410	C
49	2	1411	G
49	2	1412	C
49	2	1417	C
49	2	1426	U
49	2	1428	G
49	2	1429	G
49	2	1430	C
49	2	1444	U
49	2	1447	G
49	2	1453	C
49	2	1454	A
49	2	1455	A
49	2	1456	G
49	2	1457	U

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Mol	Chain	Res	Type
49	2	1462	U
49	2	1463	U
49	2	1464	C
49	2	1465	A
49	2	1466	G
49	2	1468	C
49	2	1470	C
49	2	1471	C
49	2	1475	G
49	2	1476	A
49	2	1477	U
49	2	1478	U
49	2	1479	G
49	2	1480	A
49	2	1483	A
49	2	1484	A
49	2	1487	A
49	2	1489	A
49	2	1490	G
49	2	1493	C
49	2	1494	U
49	2	1495	G
49	2	1496	U
49	2	1497	G
49	2	1498	A
49	2	1500	G
49	2	1505	U
49	2	1507	G
49	2	1508	A
49	2	1509	U
49	2	1510	G
49	2	1516	G
49	2	1520	G
49	2	1521	C
49	2	1527	C
49	2	1530	U
49	2	1531	A
49	2	1532	C
49	2	1533	A
49	2	1536	G
49	2	1542	C
49	2	1543	U

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Mol	Chain	Res	Type
49	2	1547	C
49	2	1548	G
49	2	1552	G
49	2	1553	C
49	2	1554	C
49	2	1555	U
49	2	1556	A
49	2	1558	C
49	2	1560	U
49	2	1561	A
49	2	1566	G
49	2	1568	C
49	2	1572	C
49	2	1574	C
49	2	1575	G
49	2	1577	G
49	2	1578	U
49	2	1579	A
49	2	1580	A
49	2	1581	C
49	2	1582	C
49	2	1585	U
49	2	1587	G
49	2	1588	A
49	2	1590	C
49	2	1591	C
49	2	1592	C
49	2	1596	U
49	2	1597	C
49	2	1598	G
49	2	1599	U
49	2	1600	G
49	2	1601	A
49	2	1602	U
49	2	1603	G
49	2	1604	G
49	2	1606	G
49	2	1607	A
49	2	1620	A
49	2	1621	U
49	2	1622	U
49	2	1623	A

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Mol	Chain	Res	Type
49	2	1625	U
49	2	1629	C
49	2	1632	G
49	2	1633	A
49	2	1635	C
49	2	1637	A
49	2	1638	G
49	2	1639	G
49	2	1641	A
49	2	1646	C
49	2	1647	A
49	2	1648	G
49	2	1654	G
49	2	1656	G
49	2	1660	C
49	2	1664	A
49	2	1665	G
49	2	1668	U
49	2	1671	G
49	2	1677	U
49	2	1680	G
49	2	1683	C
49	2	1692	U
49	2	1693	G
49	2	1697	A
49	2	1698	C
49	2	1699	A
49	2	1701	C
49	2	1702	G
49	2	1703	C
49	2	1706	G
49	2	1707	U
49	2	1710	C
49	2	1711	U
49	2	1713	C
49	2	1717	C
49	2	1720	U
49	2	1721	U
49	2	1722	G
49	2	1725	U
49	2	1726	G
49	2	1727	G

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Mol	Chain	Res	Type
49	2	1730	U
49	2	1731	A
49	2	1735	A
49	2	1736	G
49	2	1742	C
49	2	1746	U
49	2	1750	C
49	2	1752	C
49	2	1753	C
49	2	1756	C
49	2	1757	G
49	2	1758	G
49	2	1760	G
49	2	1761	U
49	2	1772	C
49	2	1774	C
49	2	1775	U
49	2	1778	C
49	2	1783	C
49	2	1784	G
49	2	1785	C
49	2	1792	G
49	2	1797	U
49	2	1800	A
49	2	1801	A
49	2	1803	U
49	2	1805	G
49	2	1811	C
49	2	1812	U
49	2	1815	A
49	2	1818	A
49	2	1819	A
49	2	1820	G
49	2	1824	A
49	2	1825	A
49	2	1826	G
49	2	1827	U
49	2	1829	G
49	2	1830	U
49	2	1831	A
49	2	1834	A
49	2	1835	A

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Mol	Chain	Res	Type
49	2	1836	G
49	2	1837	G
49	2	1838	U
49	2	1839	U
49	2	1845	A
49	2	1847	G
49	2	1849	G
49	2	1850	A
49	2	1851	A
49	2	1852	C
49	2	1853	C
49	2	1861	G
49	2	1863	A
49	2	1864	U
49	2	1865	C
49	2	1866	A
49	2	1867	U
49	2	1869	A
50	3	2	C
50	3	5	A
50	3	8	U
50	3	9	G
50	3	10	G
50	3	14	A
50	3	16	U
50	3	17	U
50	3	18	G
50	3	19	G
50	3	20	U
50	3	21	A
50	3	22	G
50	3	23	A
50	3	24	C
50	3	28	C
50	3	38	G
50	3	41	G
50	3	43	A
50	3	44	G
50	3	46	G
50	3	47	C
50	3	48	C
50	3	52	U

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Mol	Chain	Res	Type
50	3	53	A
50	3	54	G
50	3	56	G
50	3	59	U
50	3	62	G
50	3	63	G
50	3	64	G
50	3	70	G
50	3	71	U
50	3	72	C
50	3	73	C
50	3	74	C
50	3	76	U
50	3	78	C
50	3	79	U
50	3	80	C
50	3	84	A
50	3	85	C
50	3	86	C
50	3	87	A
85	4	6031	A
85	4	6032	A
85	4	6033	A
85	4	6034	A
85	4	6036	G
85	4	6037	U
85	4	6038	G
85	4	6039	A
85	4	6040	U
85	4	6041	C
85	4	6042	U
85	4	6043	U
85	4	6044	G
85	4	6045	C
85	4	6046	U
85	4	6048	G
85	4	6051	A
85	4	6053	U
85	4	6054	A
85	4	6055	C
85	4	6057	A
85	4	6059	U

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Mol	Chain	Res	Type
85	4	6061	U
85	4	6062	G
85	4	6064	G
85	4	6065	A
85	4	6068	U
85	4	6069	U
85	4	6070	A
85	4	6071	A
85	4	6072	U
85	4	6073	A
85	4	6074	A
85	4	6075	A
85	4	6080	A
85	4	6083	U
85	4	6085	G
85	4	6087	G
85	4	6088	C
85	4	6089	U
85	4	6090	A
85	4	6091	U
85	4	6092	U
85	4	6093	U
85	4	6095	U
85	4	6096	G
85	4	6097	U
85	4	6099	U
85	4	6101	U
85	4	6102	A
85	4	6106	U
85	4	6107	A
85	4	6109	C
85	4	6112	U
85	4	6113	U
85	4	6114	U
85	4	6116	G
85	4	6117	C
85	4	6118	U
85	4	6119	U
85	4	6121	A
85	4	6122	C
85	4	6123	G
85	4	6124	U

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Mol	Chain	Res	Type
85	4	6125	U
85	4	6126	C
85	4	6128	A
85	4	6131	A
85	4	6134	C
85	4	6136	U
85	4	6137	A
85	4	6138	G
85	4	6140	G
85	4	6141	G
85	4	6142	C
85	4	6144	G
85	4	6150	C
85	4	6151	A
85	4	6155	U
85	4	6156	C
85	4	6158	A
85	4	6163	G
85	4	6165	C
85	4	6166	C
85	4	6167	U
85	4	6168	C
85	4	6171	U
85	4	6172	G
85	4	6173	C
85	4	6174	G
85	4	6175	G
85	4	6176	U
85	4	6177	U
85	4	6178	U
85	4	6179	U
85	4	6180	U
85	4	6181	C
85	4	6182	A
85	4	6196	A
85	4	6197	A
85	4	6198	A
85	4	6199	A
85	4	6200	A
85	4	6201	C
85	4	6202	C
85	4	6203	U

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Mol	Chain	Res	Type
85	4	6204	A
85	4	6205	A
85	4	6206	G
85	4	6207	A
85	4	6208	A
85	4	6209	A
85	4	6211	U
85	4	6212	U
85	4	6213	A
85	4	6214	C
85	4	6215	C
85	4	6216	U
85	4	6217	C
85	4	6219	C
85	4	6220	U
85	4	6222	G
85	4	6223	U

All (433) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	5	12	A
45	5	13	U
45	5	42	A
45	5	47	A
45	5	48	G
45	5	58	G
45	5	72	C
45	5	119	G
45	5	134	G
45	5	135	G
45	5	159	C
45	5	189	G
45	5	200	U
45	5	207	G
45	5	209	U
45	5	210	C
45	5	217	C
45	5	219	G
45	5	233	U
45	5	235	A
45	5	245	C

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Mol	Chain	Res	Type
45	5	253	G
45	5	258	G
45	5	261	G
45	5	265	C
45	5	275	C
45	5	280	G
45	5	296	A
45	5	349	A
45	5	352	G
45	5	354	U
45	5	361	C
45	5	385	A
45	5	408	A
45	5	417	G
45	5	426	A
45	5	427	A
45	5	428	G
45	5	438	G
45	5	449	C
45	5	453	G
45	5	455	C
45	5	465	G
45	5	467	U
45	5	492	U
45	5	497	G
45	5	504	G
45	5	667	A
45	5	686	A
45	5	757	G
45	5	916	C
45	5	921	C
45	5	924	C
45	5	925	C
45	5	930	G
45	5	956	A
45	5	972	C
45	5	978	G
45	5	1072	C
45	5	1211	G
45	5	1215	C
45	5	1237	C
45	5	1238	A

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Mol	Chain	Res	Type
45	5	1271	G
45	5	1283	G
45	5	1286	C
45	5	1291	G
45	5	1294	A
45	5	1295	U
45	5	1314	C
45	5	1322	A
45	5	1358	G
45	5	1370	G
45	5	1380	G
45	5	1381	U
45	5	1386	C
45	5	1390	G
45	5	1437	C
45	5	1445	U
45	5	1455	G
45	5	1480	C
45	5	1484	G
45	5	1497	A
45	5	1502	G
45	5	1503	A
45	5	1517	G
45	5	1518	A
45	5	1521	C
45	5	1533	A
45	5	1558	A
45	5	1578	U
45	5	1601	A
45	5	1613	A
45	5	1632	A
45	5	1676	C
45	5	1678	C
45	5	1693	U
45	5	1740	C
45	5	1753	G
45	5	1768	C
45	5	1773	U
45	5	1779	U
45	5	1805	A
45	5	1833	G
45	5	1834	U

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Mol	Chain	Res	Type
45	5	1835	G
45	5	1854	G
45	5	1881	C
45	5	1883	G
45	5	1892	A
45	5	1913	C
45	5	1917	A
45	5	1947	U
45	5	1979	A
45	5	1986	U
45	5	2002	A
45	5	2003	G
45	5	2024	G
45	5	2046	G
45	5	2052	G
45	5	2055	G
45	5	2084	U
45	5	2089	G
45	5	2090	U
45	5	2091	C
45	5	2092	G
45	5	2093	G
45	5	2259	G
45	5	2260	C
45	5	2266	C
45	5	2279	A
45	5	2290	C
45	5	2310	C
45	5	2348	G
45	5	2361	G
45	5	2381	A
45	5	2398	U
45	5	2408	U
45	5	2425	U
45	5	2428	A
45	5	2437	C
45	5	2467	U
45	5	2468	U
45	5	2502	A
45	5	2503	G
45	5	2509	C
45	5	2530	U

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Mol	Chain	Res	Type
45	5	2531	C
45	5	2551	A
45	5	2575	U
45	5	2587	A
45	5	2597	G
45	5	2600	A
45	5	2656	U
45	5	2661	U
45	5	2695	A
45	5	2705	G
45	5	2710	C
45	5	2717	G
45	5	2760	G
45	5	2761	U
45	5	2763	U
45	5	2769	U
45	5	2782	U
45	5	2787	A
45	5	2788	U
45	5	2790	U
45	5	2794	C
45	5	2795	A
45	5	2806	A
45	5	2817	C
45	5	2826	U
45	5	2833	A
45	5	2849	A
45	5	2875	C
45	5	2887	U
45	5	3603	G
45	5	3606	U
45	5	3634	G
45	5	3642	A
45	5	3644	U
45	5	3647	A
45	5	3648	A
45	5	3673	C
45	5	3682	A
45	5	3689	G
45	5	3711	A
45	5	3784	A
45	5	3809	G

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Mol	Chain	Res	Type
45	5	3810	C
45	5	3811	G
45	5	3817	A
45	5	3843	C
45	5	3876	A
45	5	3878	C
45	5	3904	G
45	5	3907	G
45	5	3913	G
45	5	3938	G
45	5	3970	G
45	5	3976	C
45	5	4054	C
45	5	4070	U
45	5	4075	U
45	5	4076	G
45	5	4115	G
45	5	4119	C
45	5	4120	U
45	5	4146	G
45	5	4166	G
45	5	4170	A
45	5	4183	G
45	5	4221	C
45	5	4232	U
45	5	4253	A
45	5	4254	G
45	5	4257	A
45	5	4266	G
45	5	4269	G
45	5	4287	G
45	5	4305	G
45	5	4354	U
45	5	4374	U
45	5	4376	A
45	5	4378	A
45	5	4380	A
45	5	4393	G
45	5	4404	U
45	5	4414	A
45	5	4436	U
45	5	4443	C

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Mol	Chain	Res	Type
45	5	4447	C
45	5	4448	G
45	5	4449	A
45	5	4456	C
45	5	4459	U
45	5	4461	C
45	5	4462	C
45	5	4463	U
45	5	4464	A
45	5	4469	U
45	5	4475	G
45	5	4488	A
45	5	4497	U
45	5	4512	U
45	5	4516	G
45	5	4517	A
45	5	4520	G
45	5	4521	U
45	5	4527	G
45	5	4528	G
45	5	4555	U
45	5	4626	A
45	5	4630	G
45	5	4633	G
45	5	4635	A
45	5	4649	G
45	5	4693	C
45	5	4694	G
45	5	4699	U
45	5	4719	G
45	5	4771	C
45	5	4862	G
45	5	4870	G
45	5	4872	G
45	5	4882	U
45	5	4895	C
45	5	4904	G
45	5	4921	C
45	5	4925	U
45	5	4927	G
45	5	4936	G
45	5	4937	C

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Mol	Chain	Res	Type
45	5	4942	C
45	5	4944	C
45	5	4947	U
45	5	4949	G
45	5	4965	U
45	5	4975	G
45	5	4976	U
45	5	5006	U
45	5	5016	A
45	5	5040	U
46	7	13	A
46	7	32	A
46	7	52	C
46	7	89	G
46	7	109	U
47	8	37	A
47	8	48	A
47	8	51	U
47	8	110	U
47	8	124	U
49	2	1	U
49	2	6	G
49	2	24	C
49	2	41	G
49	2	45	A
49	2	55	U
49	2	70	G
49	2	110	U
49	2	115	U
49	2	126	G
49	2	160	U
49	2	161	U
49	2	182	C
49	2	183	G
49	2	294	U
49	2	305	U
49	2	308	G
49	2	312	G
49	2	313	A
49	2	317	C
49	2	363	A
49	2	400	C

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Mol	Chain	Res	Type
49	2	407	G
49	2	417	C
49	2	428	U
49	2	449	A
49	2	464	A
49	2	465	A
49	2	471	G
49	2	476	A
49	2	500	A
49	2	516	A
49	2	532	C
49	2	550	C
49	2	553	U
49	2	561	A
49	2	589	G
49	2	627	U
49	2	643	A
49	2	656	G
49	2	658	U
49	2	659	G
49	2	688	U
49	2	733	C
49	2	752	G
49	2	808	A
49	2	809	A
49	2	818	A
49	2	821	G
49	2	822	U
49	2	869	A
49	2	870	A
49	2	873	G
49	2	887	U
49	2	891	G
49	2	955	A
49	2	971	G
49	2	1002	U
49	2	1016	U
49	2	1027	A
49	2	1085	C
49	2	1091	C
49	2	1117	C
49	2	1137	U

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Mol	Chain	Res	Type
49	2	1153	C
49	2	1165	G
49	2	1217	A
49	2	1228	A
49	2	1253	A
49	2	1260	A
49	2	1286	G
49	2	1326	U
49	2	1342	U
49	2	1343	U
49	2	1395	C
49	2	1404	U
49	2	1454	A
49	2	1476	A
49	2	1477	U
49	2	1489	A
49	2	1493	C
49	2	1497	G
49	2	1508	A
49	2	1527	C
49	2	1606	G
49	2	1620	A
49	2	1621	U
49	2	1623	A
49	2	1630	A
49	2	1632	G
49	2	1637	A
49	2	1679	A
49	2	1697	A
49	2	1698	C
49	2	1701	C
49	2	1721	U
49	2	1783	C
49	2	1805	G
49	2	1820	G
49	2	1825	A
49	2	1830	U
49	2	1834	A
49	2	1835	A
49	2	1836	G
49	2	1837	G
49	2	1866	A

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Mol	Chain	Res	Type
49	2	1868	U
50	3	16	U
50	3	18	G
50	3	19	G
50	3	58	U
50	3	85	C
85	4	6032	A
85	4	6045	C
85	4	6053	U
85	4	6054	A
85	4	6072	U
85	4	6073	A
85	4	6074	A
85	4	6098	A
85	4	6106	U
85	4	6149	A
85	4	6150	C
85	4	6151	A
85	4	6174	G
85	4	6177	U
85	4	6178	U
85	4	6179	U
85	4	6180	U
85	4	6196	A
85	4	6199	A
85	4	6200	A
85	4	6201	C
85	4	6202	C
85	4	6203	U
85	4	6208	A
85	4	6212	U
85	4	6213	A
85	4	6215	C
85	4	6219	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	5	36
49	2	18
48	K	3
47	8	1
50	3	1
83	hh	1
3	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	42.98
1	5	1252:C	O3'	1271:G	P	33.33
1	5	1219:G	O3'	1233:G	P	21.96
1	2	697:G	O3'	729:C	P	20.32
1	5	1696:C	O3'	1720:C	P	19.72
1	2	834:C	O3'	841:G	P	19.68
1	2	130:G	O3'	141:A	P	19.30
1	5	4138:C	O3'	4146:G	P	18.68
1	5	3977:C	O3'	4034:G	P	18.51
1	2	323:C	O3'	329:G	P	17.86
1	5	5022:U	O3'	5028:G	P	17.72
1	5	523:C	O3'	638:G	P	17.19
1	5	1405:C	O3'	1411(A):G	P	17.18
1	2	1417:C	O3'	1423:C	P	16.83

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	4101:C	O3'	4107:G	P	16.60
1	2	756:C	O3'	788:G	P	16.59
1	5	990:C	O3'	1064:G	P	16.03
1	5	2901:G	O3'	3597:G	P	15.30
1	8	79:G	O3'	85:U	P	14.66
1	5	4777:C	O3'	4859:C	P	14.49
1	5	1364:U	O3'	1368:A	P	13.87
1	2	1761:U	O3'	1771:G	P	13.36
1	5	1100:U	O3'	1168:G	P	13.02
1	5	760:G	O3'	904:C	P	12.32
1	5	182:G	O3'	189:G	P	11.66
1	5	1180:C	O3'	1183:C	P	11.42
1	5	4729:A	O3'	4735:G	P	10.94
1	5	971(A):G	O3'	972:C	P	10.40
1	5	4045:G	O3'	4047:A	P	9.82
1	5	737:C	O3'	738(A):C	P	9.26
1	5	4740:G	O3'	4743:G	P	8.92
1	2	225:G	O3'	287:U	P	8.62
1	5	970:G	O3'	971:U	P	8.42
1	2	745:C	O3'	749:U	P	8.30
1	3	57:C	O3'	58:U	P	7.78
1	5	512:U	O3'	515:C	P	7.39
1	hh	2:THR	C	3:GLU	N	6.79
1	5	500:G	O3'	504:G	P	6.45
1	K	194:LEU	C	195:LYS	N	6.36
1	2	322:C	O3'	323:C	P	6.30
1	5	1957:U	O3'	1958:A	P	6.14
1	5	4899:G	O3'	4902:C	P	5.83
1	5	738(A):C	O3'	739:G	P	5.23
1	K	9:THR	C	10:LEU	N	5.09
1	2	903:A	O3'	904:A	P	4.97
1	5	971:U	O3'	971(A):G	P	4.58
1	K	172:VAL	C	173:LYS	N	4.43
1	2	304:C	O3'	305:U	P	4.19
1	2	1432:U	O3'	1438:A	P	4.18
1	5	1239:C	O3'	1244:G	P	4.17
1	2	689:U	O3'	690:G	P	3.92
1	2	798:G	O3'	799:U	P	3.90
1	5	751:G	O3'	752:G	P	3.80
1	5	170:C	O3'	171:U	P	3.64
1	5	1438:U	O3'	1440:U	P	3.38
1	5	267:G	O3'	268:G	P	3.24

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	132:ALA	C	133:LEU	N	3.18
1	5	5020:G	O3'	5021:C	P	3.14
1	2	736:C	O3'	743:U	P	3.12
1	2	886:A	O3'	887:U	P	3.07
1	2	902:G	O3'	903:A	P	3.07

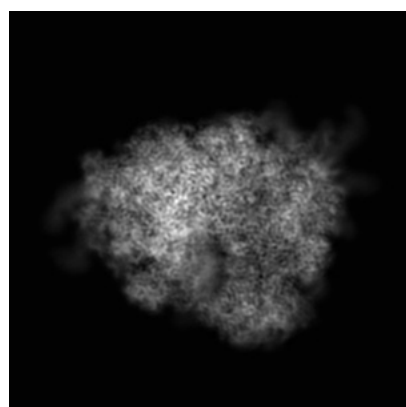
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7834. These allow visual inspection of the internal detail of the map and identification of artifacts.

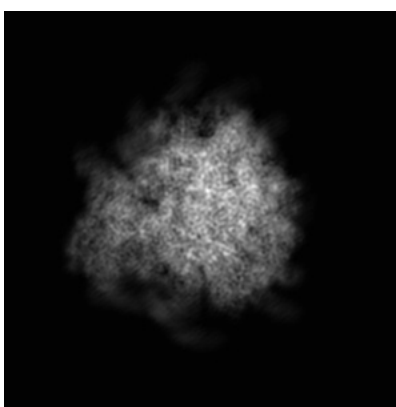
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

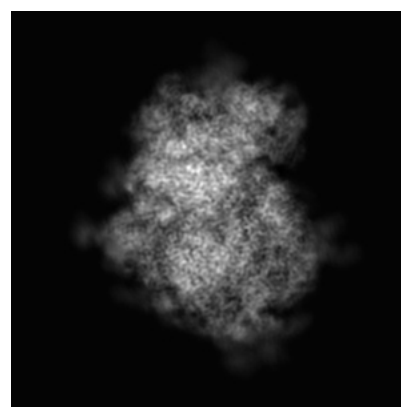
6.1.1 Primary map



X



Y

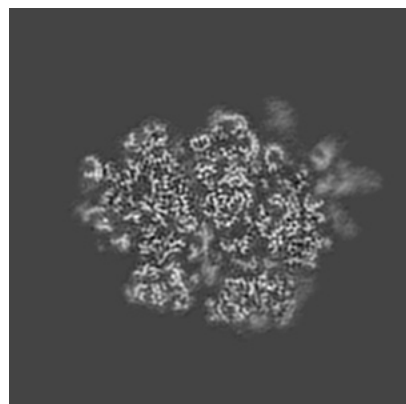


Z

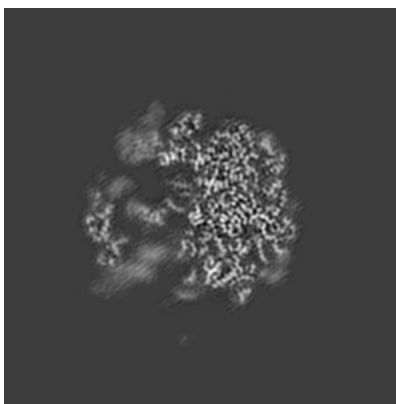
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

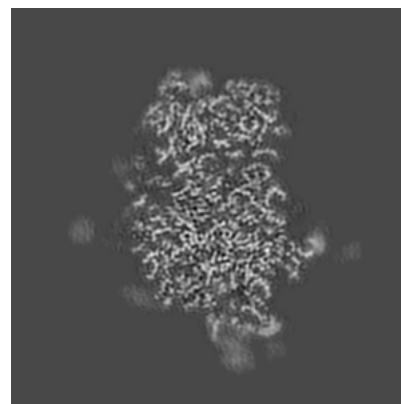
6.2.1 Primary map



X Index: 200



Y Index: 200

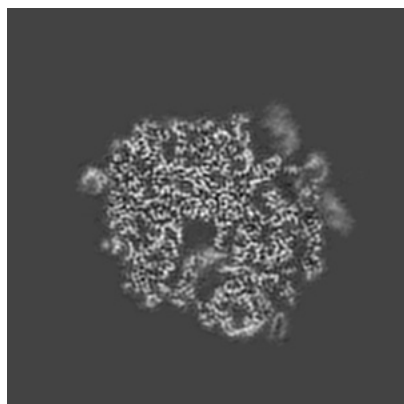


Z Index: 200

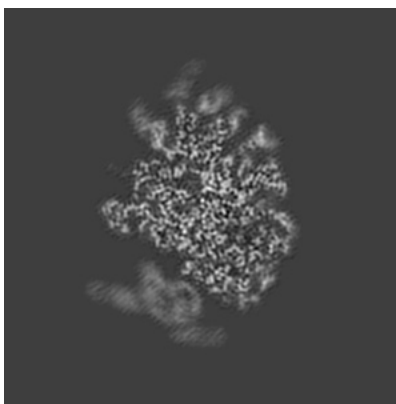
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

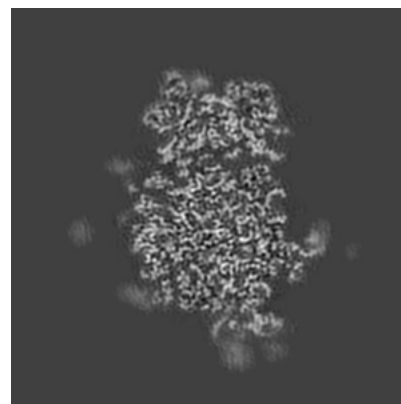
6.3.1 Primary map



X Index: 186



Y Index: 166

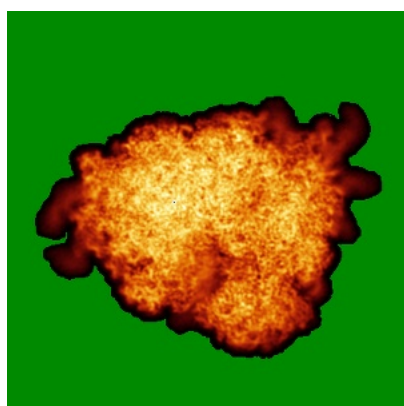


Z Index: 203

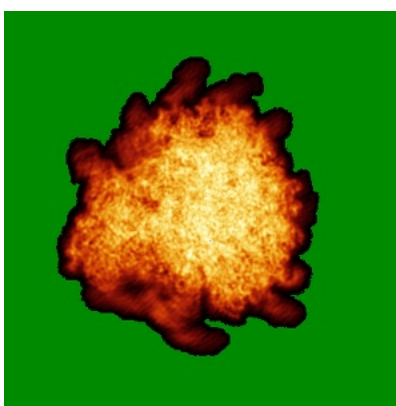
The images above show the largest variance slices of the map in three orthogonal directions.

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

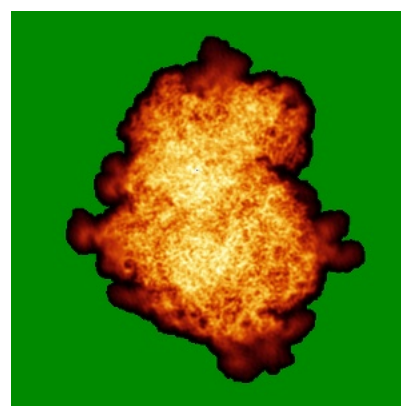
6.4.1 Primary map



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

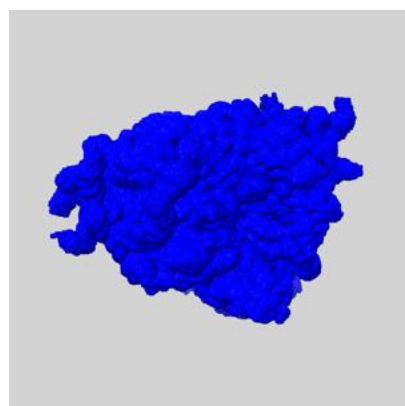
6.6 Mask visualisation [i](#)

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

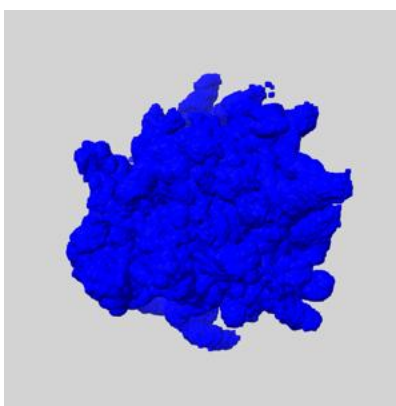
A mask typically either:

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

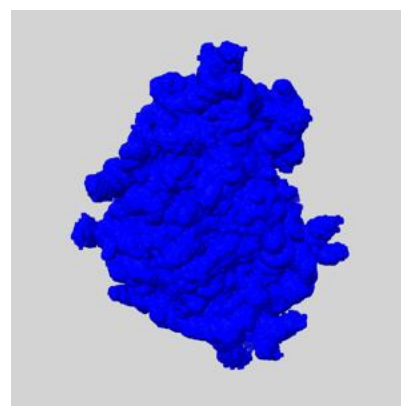
6.6.1 emd_7834_msk_1.map [i](#)



X



Y

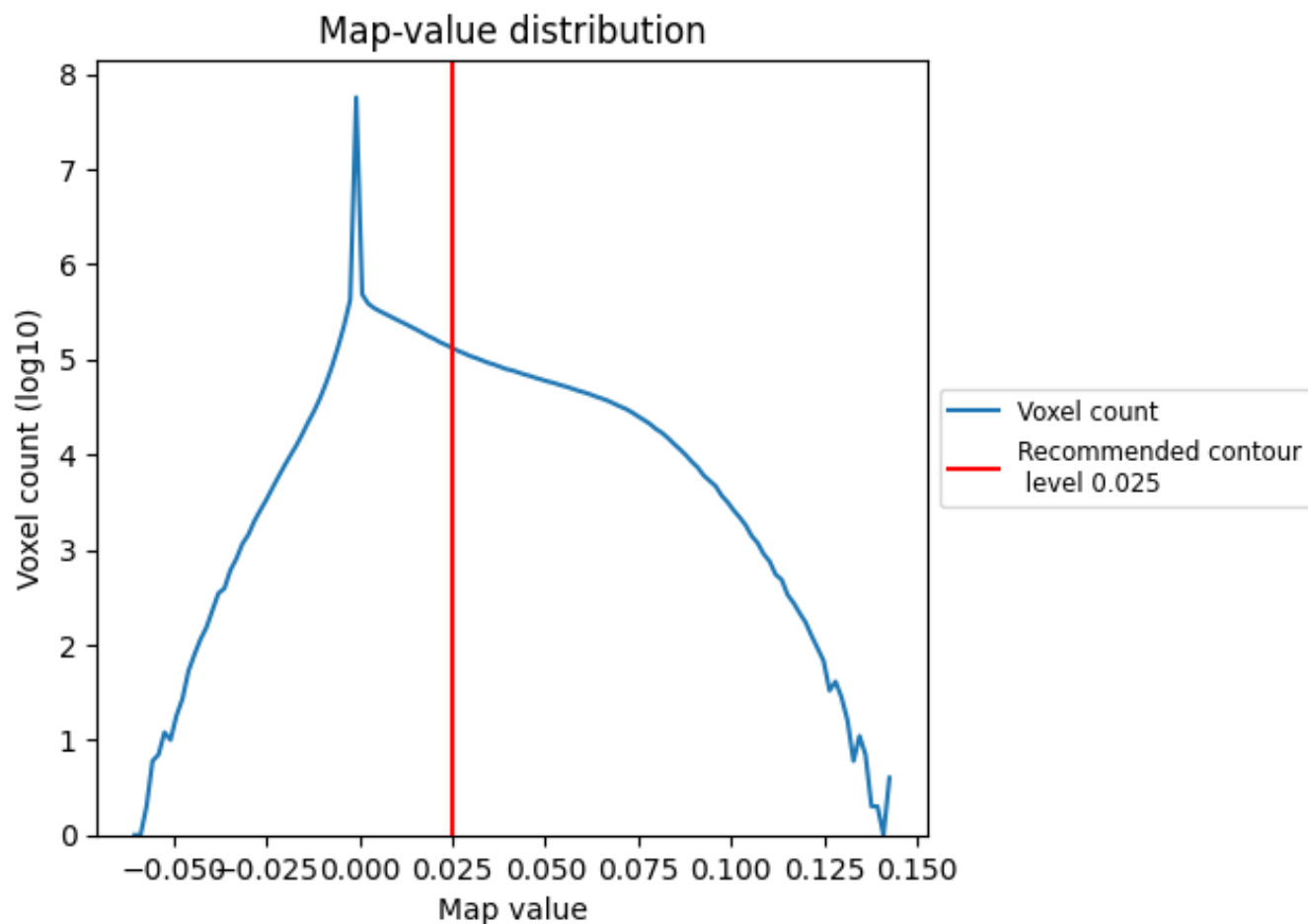


Z

7 Map analysis [i](#)

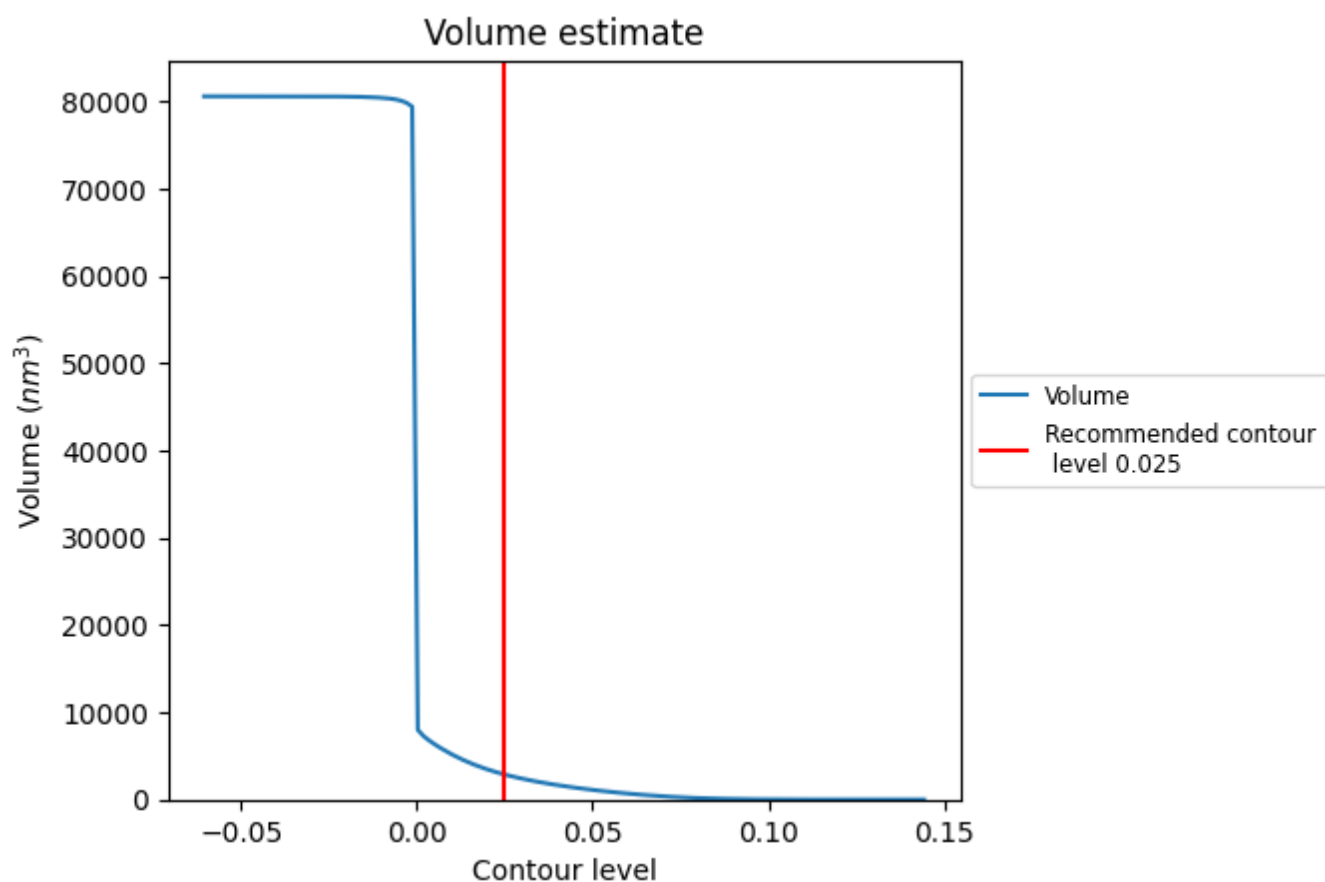
This section contains the results of statistical analysis of the map.

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.

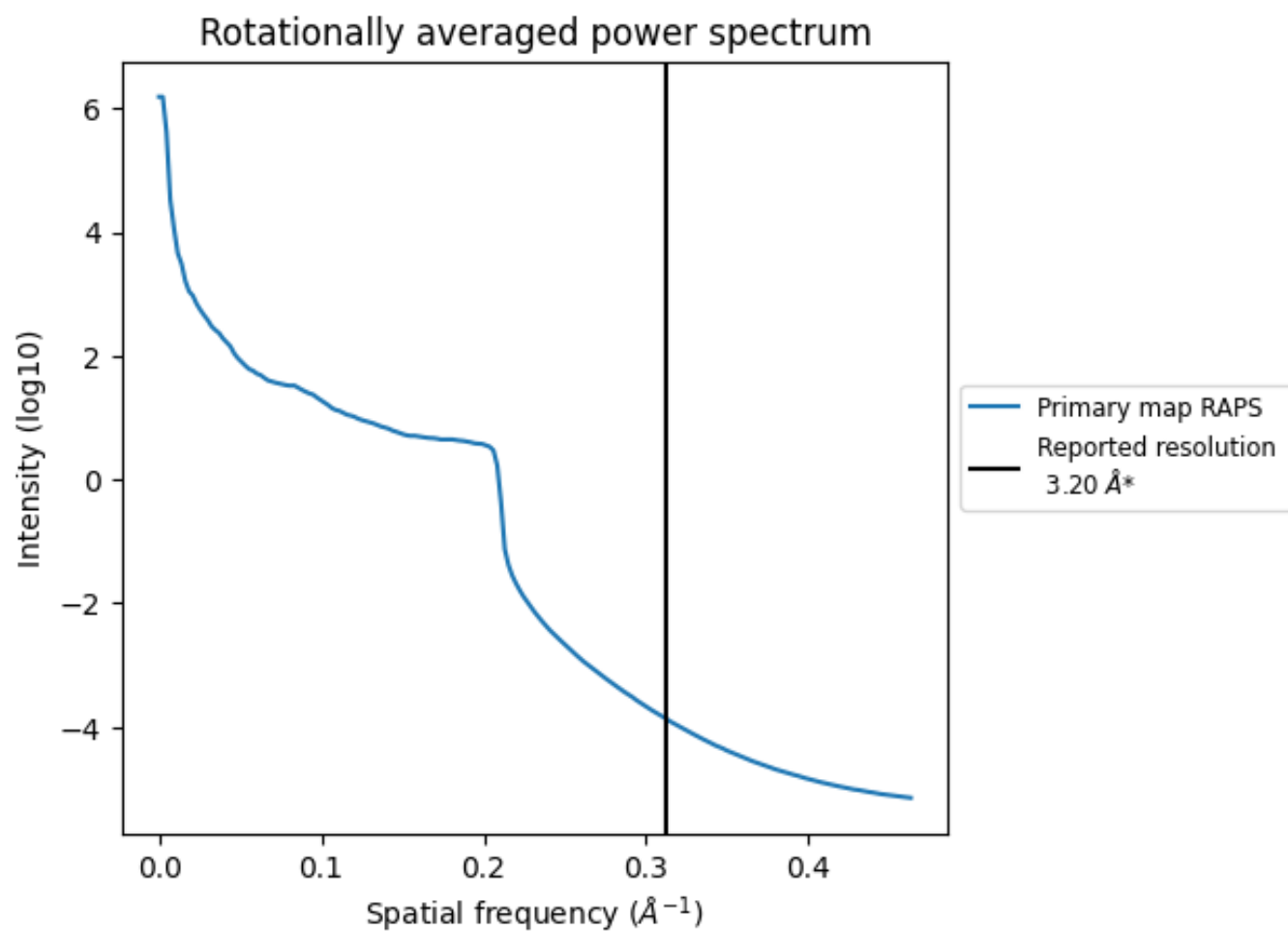
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2873 nm³; this corresponds to an approximate mass of 2595 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 ⓘ

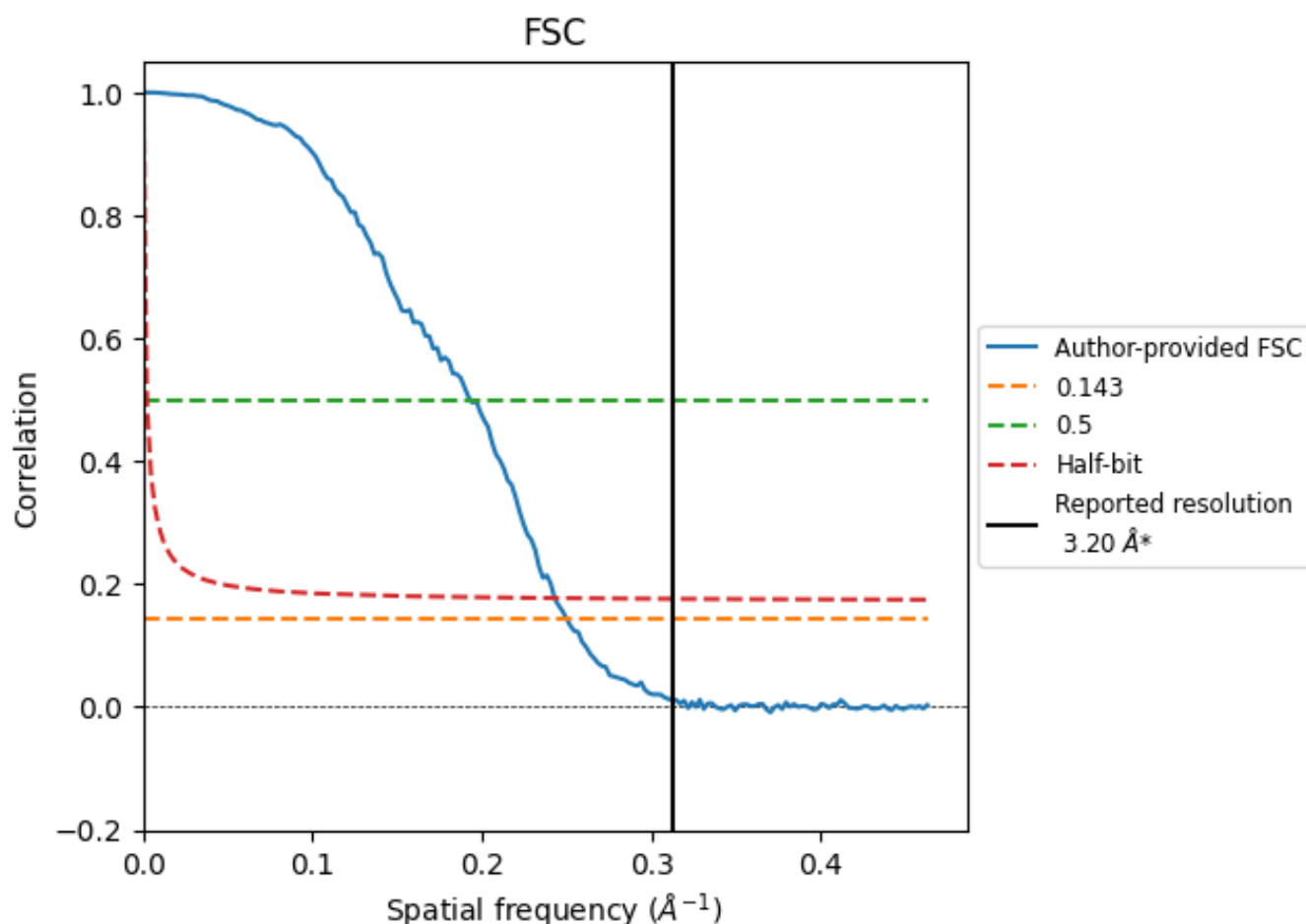


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

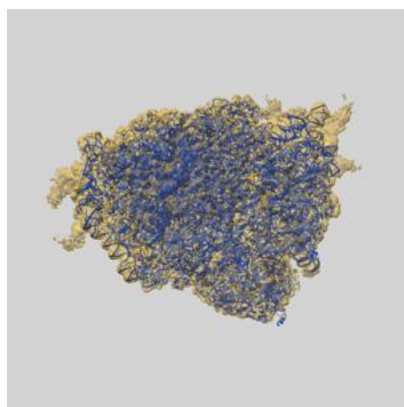
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	4.00	5.17	4.12
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.2 by more than 10 %

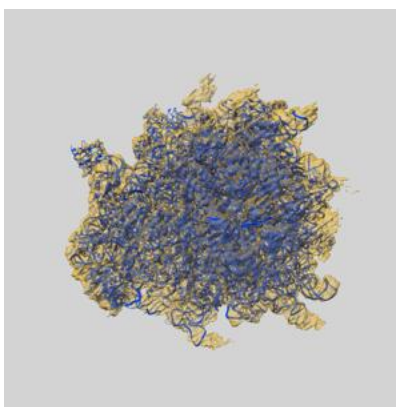
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7834 and PDB model 6D90. Per-residue inclusion information can be found in [section 3](#) on [page 24](#).

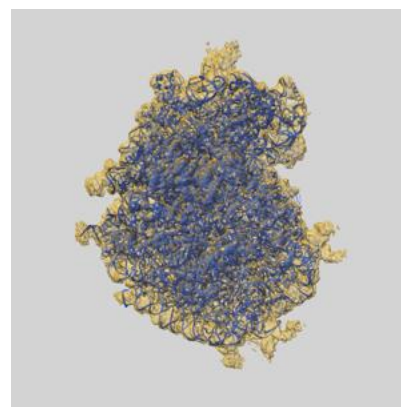
9.1 Map-model overlay [i](#)



X



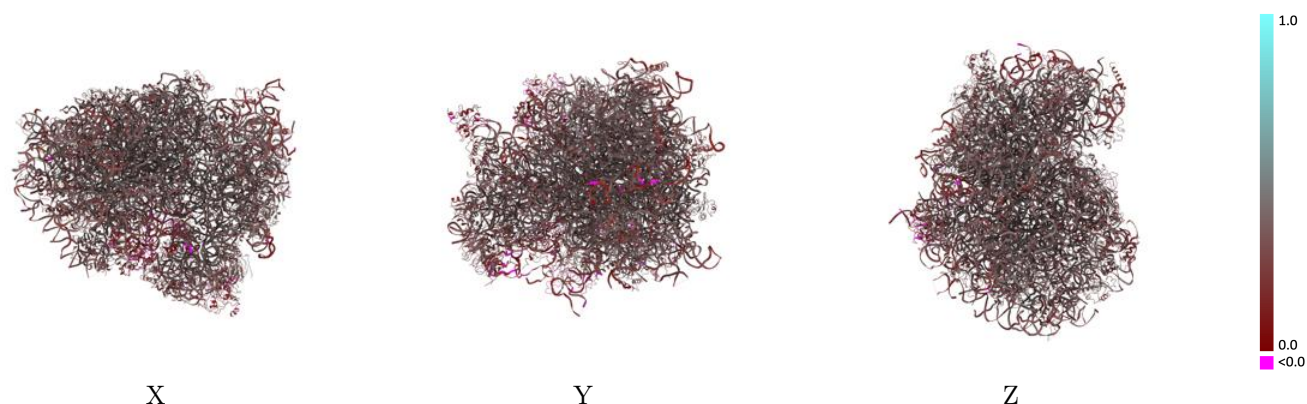
Y



Z

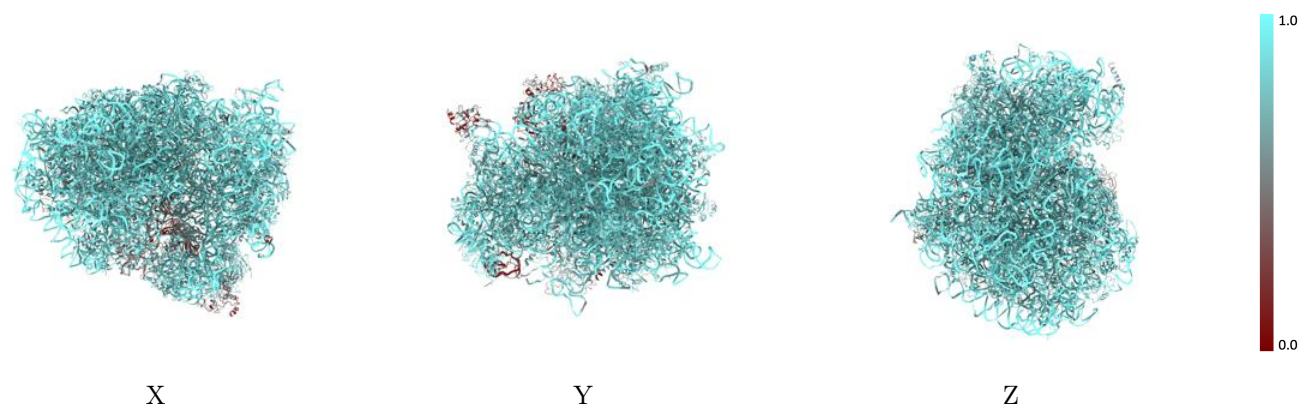
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



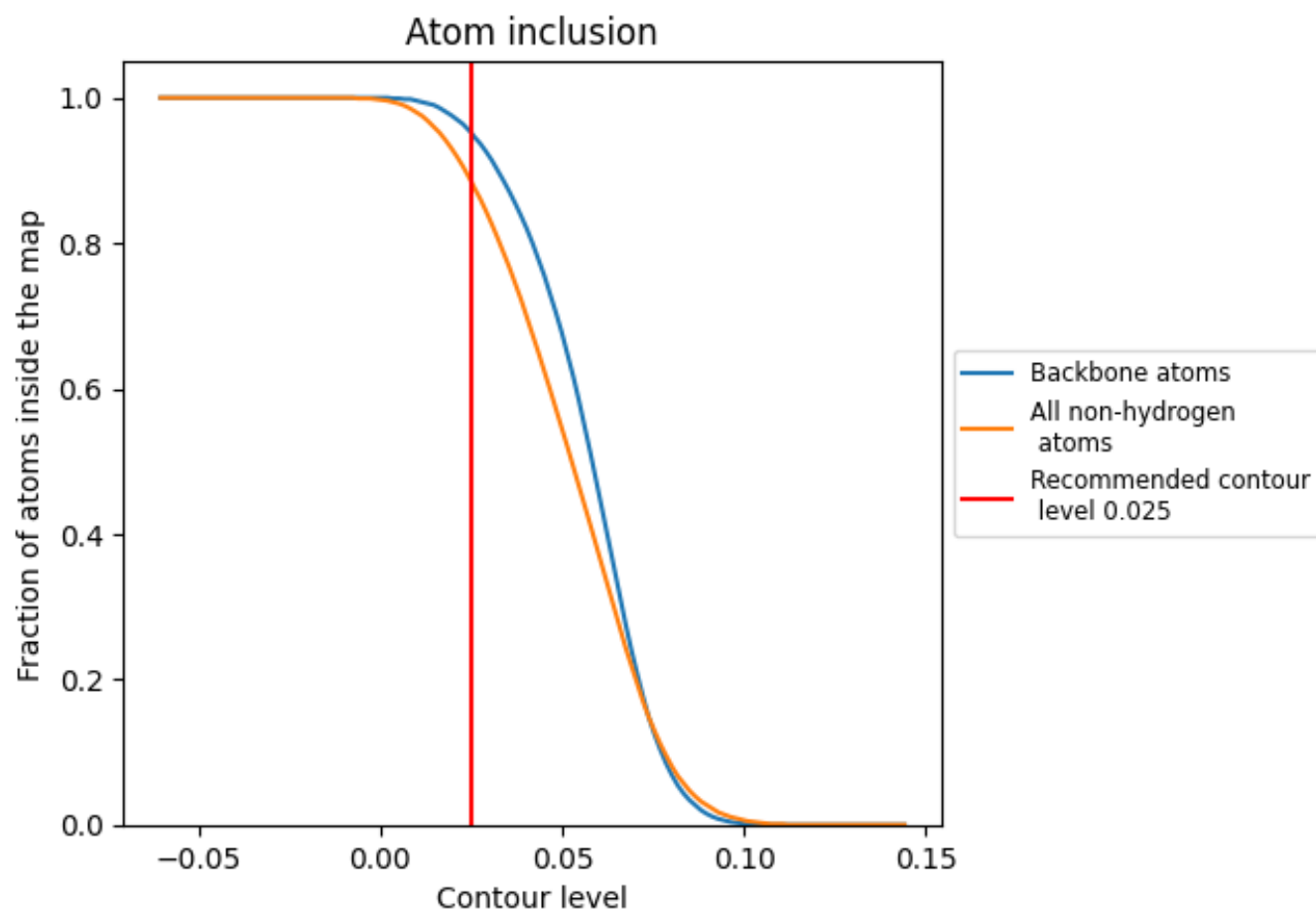
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 88% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8850	 0.3350
2	 0.9740	 0.3550
3	 0.8810	 0.2840
4	 0.5240	 0.1010
5	 0.9720	 0.3540
7	 0.9890	 0.3620
8	 0.9790	 0.3650
A	 0.8190	 0.3560
B	 0.8410	 0.3650
BB	 0.8110	 0.3080
C	 0.8330	 0.3510
CC	 0.8180	 0.3290
D	 0.8500	 0.3110
DD	 0.8350	 0.3540
E	 0.8510	 0.3350
EE	 0.7970	 0.3320
F	 0.8200	 0.3260
FF	 0.8330	 0.3570
G	 0.8020	 0.3200
GG	 0.7860	 0.3000
H	 0.8380	 0.3550
HH	 0.8230	 0.3130
I	 0.8380	 0.3560
II	 0.8120	 0.3140
J	 0.8070	 0.3190
JJ	 0.8180	 0.3150
K	 0.5930	 0.1140
KK	 0.8290	 0.3310
L	 0.8050	 0.3170
LL	 0.7990	 0.2930
M	 0.8430	 0.3310
MM	 0.8250	 0.3550
N	 0.8500	 0.3550
NN	 0.2660	 0.1780
O	 0.8340	 0.3410



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Chain	Atom inclusion	Q-score
OO	 0.8190	 0.3350
P	 0.8570	 0.3600
PP	 0.8230	 0.3220
Q	 0.8140	 0.3430
QQ	 0.8020	 0.2750
R	 0.8490	 0.3310
RR	 0.8080	 0.2890
S	 0.8450	 0.3550
SS	 0.7650	 0.2940
T	 0.8090	 0.3400
TT	 0.8090	 0.2920
U	 0.8370	 0.3430
UU	 0.8150	 0.2870
V	 0.8210	 0.3610
VV	 0.7750	 0.3300
W	 0.8090	 0.3160
WW	 0.8420	 0.3360
X	 0.8400	 0.3650
XX	 0.8130	 0.3540
Y	 0.8530	 0.3350
YY	 0.8360	 0.3630
Z	 0.8500	 0.3420
ZZ	 0.8510	 0.3390
a	 0.8440	 0.3560
aa	 0.7700	 0.2770
b	 0.7580	 0.2620
bb	 0.8250	 0.3310
c	 0.8250	 0.3320
cc	 0.8190	 0.3460
d	 0.8540	 0.3660
dd	 0.7910	 0.3360
e	 0.8650	 0.3750
ee	 0.8550	 0.3150
f	 0.8610	 0.3680
ff	 0.7390	 0.3160
g	 0.8420	 0.3610
gg	 0.5060	 0.2330
h	 0.8130	 0.3180
hh	 0.8390	 0.3060
i	 0.8320	 0.3300
j	 0.8850	 0.3610
jj	 0.4230	 0.2610

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Chain	Atom inclusion	Q-score
k	 0.8170	 0.3430
l	 0.8340	 0.3440
m	 0.8550	 0.3530
n	 0.8390	 0.3350
o	 0.8170	 0.3380
p	 0.8180	 0.3440
r	 0.8750	 0.3710
s	 0.3510	 0.1620
t	 0.5390	 0.1760