



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:24 PM UTC

PDB ID : 8BIP / pdb_00008bip
EMDB ID : EMD-16086
Title : Structure of a yeast 80S ribosome-bound N-Acetyltransferase B complex
Authors : Knorr, A.G.; Mackens-Kiani, T.; Musial, J.; Berninghausen, O.; Becker, T.;
Beatrix, B.; Beckmann, R.
Deposited on : 2022-11-02
Resolution : 3.10 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:

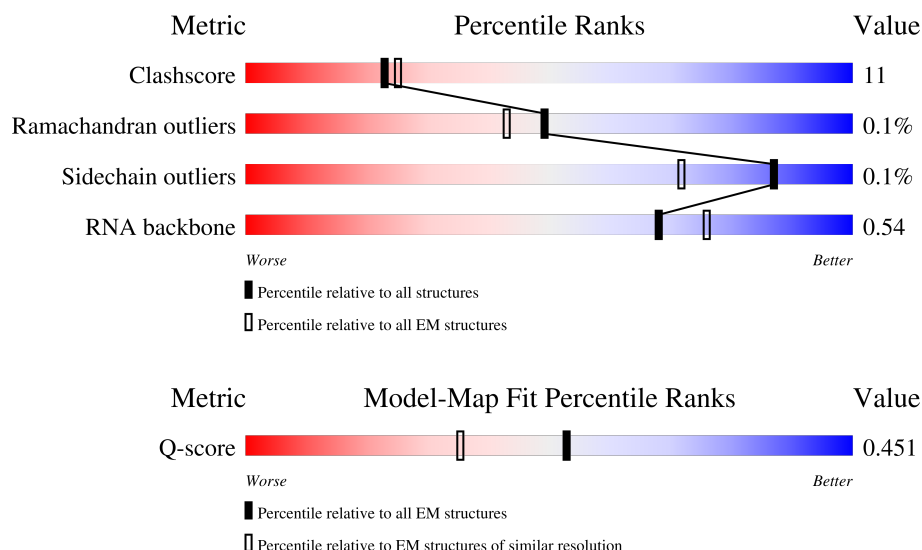
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 Å.

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



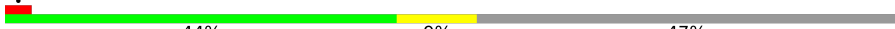
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	C4	121	
2	C3	158	
3	LA	251	

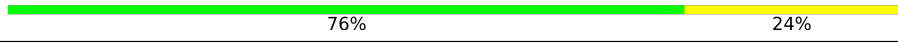
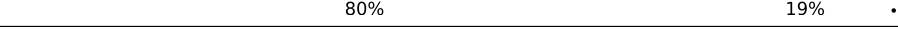
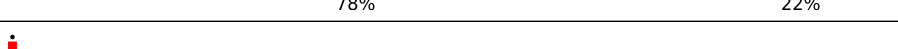
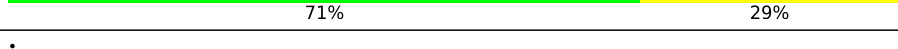
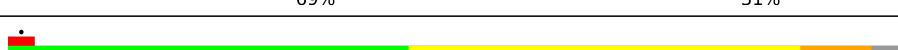
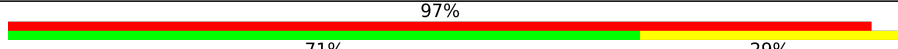
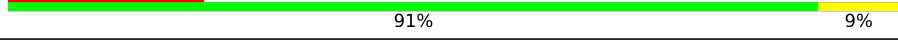
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Mol	Chain	Length	Quality of chain
4	LB	386	
5	LC	361	
6	LD	294	
7	LE	175	
8	LF	222	
9	LG	233	
10	LH	191	
11	LI	218	
12	LJ	169	
13	LL	193	
14	LM	136	
15	LN	203	
16	LO	197	
17	LP	183	
18	LQ	185	
19	LR	188	
20	LS	171	
21	LT	159	
22	LU	100	
23	LV	136	
24	LW	126	
25	LX	121	
26	LY	125	
27	LZ	135	
28	La	148	

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Mol	Chain	Length	Quality of chain
29	Lb	58	
30	Lc	96	
31	Ld	109	
32	Le	127	
33	Lf	106	
34	Lg	112	
35	Lh	119	
36	Li	99	
37	Lj	85	
38	Lk	77	
39	Ll	50	
40	Lm	52	
41	Ln	25	
42	Lo	103	
43	Lp	91	
44	1	3395	
45	A	195	
46	B	796	
47	8	23	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 134392 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 7 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	132	ALA	THR	conflict	UNP P05739
LE	146	ILE	LEU	conflict	UNP P05739
LE	173	MET	LEU	conflict	UNP P05739

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LG	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 12 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	LL	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LO	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	LP	183	Total	C	N	O	0	0
			1416	879	284	253		

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	LR	171	Total	C	N	O	0	0
			1378	850	294	234		

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LS	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LU	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LV	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LW	67	Total	C	N	O	S	0	0
			538	345	106	86	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	104	GLN	ASN	conflict	UNP P04449
LW	109	GLN	LEU	conflict	UNP P04449
LW	112	ASP	ASN	conflict	UNP P04449
LW	119	ALA	GLU	conflict	UNP P04449

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LX	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	LY	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	LZ	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	Lb	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ld	109	Total	C	N	O	S	0	0
			880	559	168	152	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lh	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	Lk	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ll	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 40 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 41 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 42 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 43 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 44 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	3301	Total	C	N	O	P	0	0
			70586	31525	12690	23070	3301		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 1262303
1	1962	A	G	conflict	GB 1262303

- Molecule 45 is a protein called N-terminal acetyltransferase B complex catalytic subunit NAT3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A	195	Total	C	N	O	S	0	0
			1612	1030	273	297	12		

- Molecule 46 is a protein called N-terminal acetyltransferase B complex subunit MDM20.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	B	796	Total	C	N	O	S	0	0
			6536	4195	1080	1231	30		

- Molecule 47 is a protein called Nascent peptide chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	8	23	Total	C	N	O	0	0
			115	69	23	23		

- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	C4	1	Total	Mg	0
			1	1	
48	C3	1	Total	Mg	0
			1	1	
48	LA	2	Total	Mg	0
			2	2	
48	LB	1	Total	Mg	0
			1	1	
48	LN	1	Total	Mg	0
			1	1	
48	LP	1	Total	Mg	0
			1	1	
48	LR	1	Total	Mg	0
			1	1	
48	LV	1	Total	Mg	0
			1	1	
48	Le	1	Total	Mg	0
			1	1	
48	1	196	Total	Mg	0
			196	196	

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	Lg	1	Total	Zn	0
			1	1	
49	Lj	1	Total	Zn	0
			1	1	
49	Lm	1	Total	Zn	0
			1	1	

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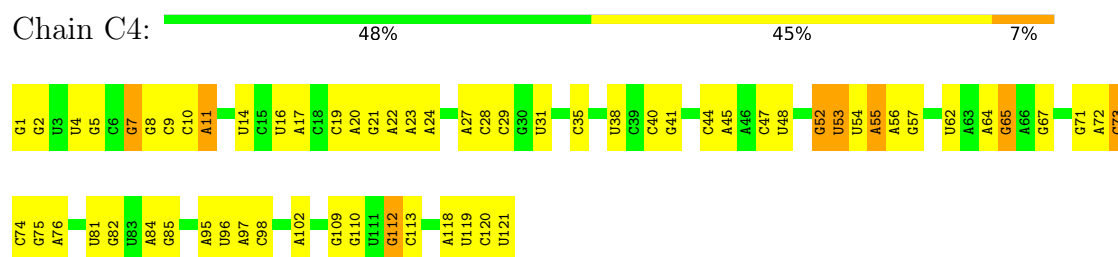
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Mol	Chain	Residues	Atoms		AltConf
49	Lo	1	Total 1	Zn 1	0
49	Lp	1	Total 1	Zn 1	0

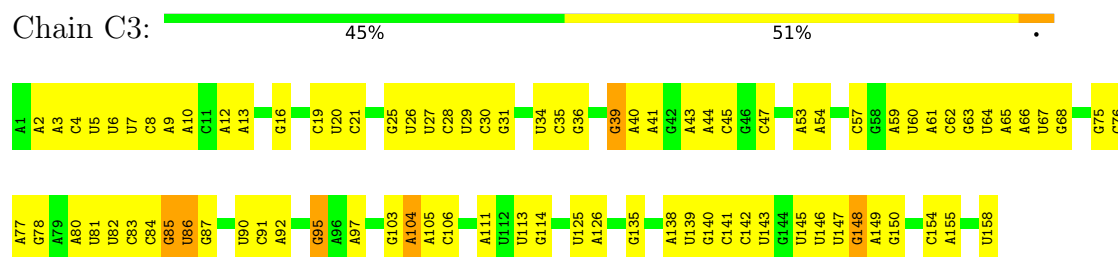
3 Residue-property plots

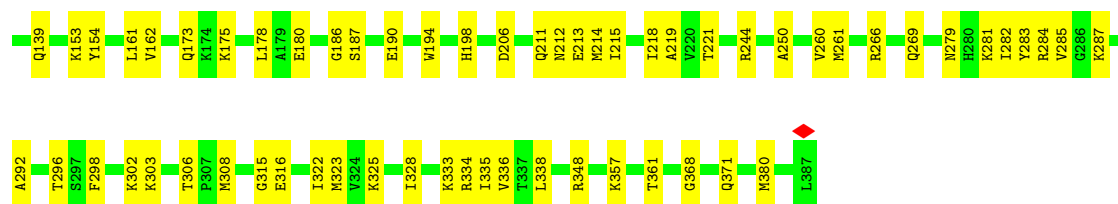
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 5S rRNA



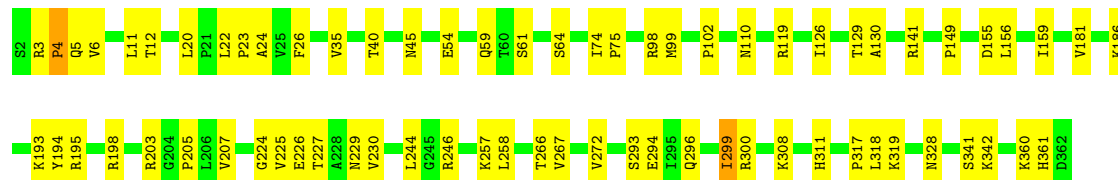
• Molecule 2: 5.8S rRNA





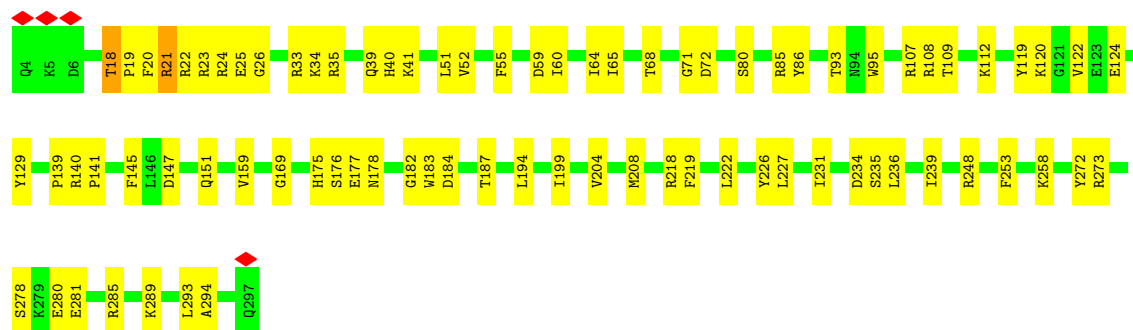
• Molecule 5: 60S ribosomal protein L4-A

Chain LC: 81% 19%



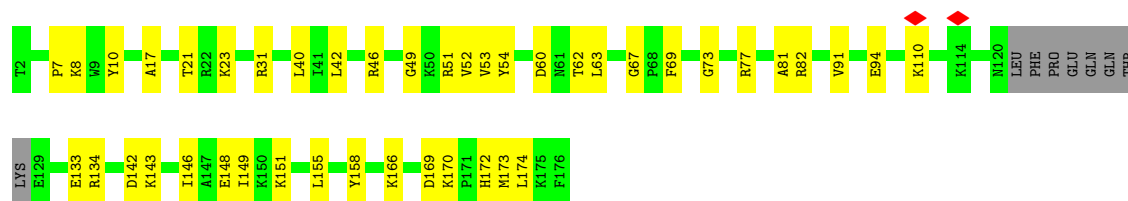
• Molecule 6: 60S ribosomal protein L5

Chain LD: 72% 27%



• Molecule 7: 60S ribosomal protein L6-B

Chain LE: 71% 25% 5%



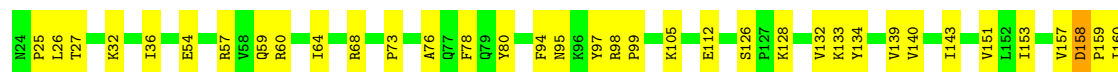
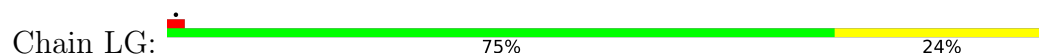
• Molecule 8: 60S ribosomal protein L7-A

Chain LF: 73% 27%

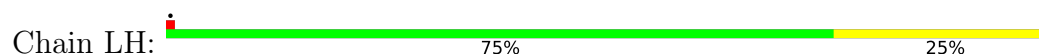




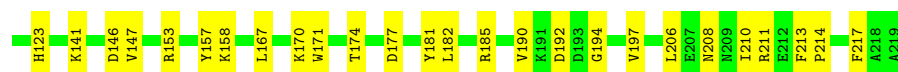
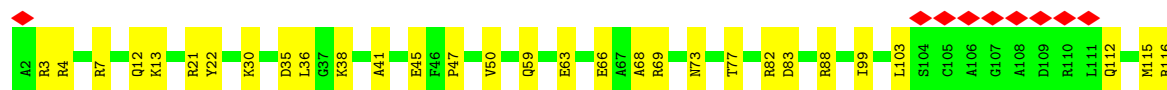
- Molecule 9: 60S ribosomal protein L8-A



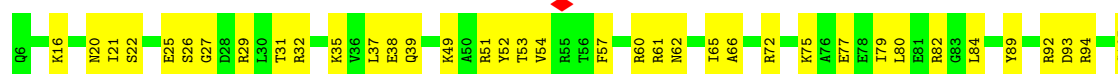
- Molecule 10: 60S ribosomal protein L9-A



- Molecule 11: 60S ribosomal protein L10

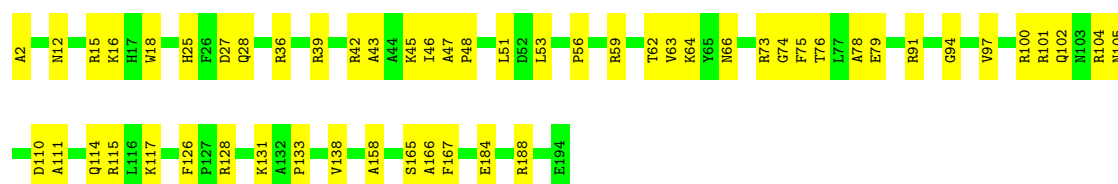


- Molecule 12: 60S ribosomal protein L11-B

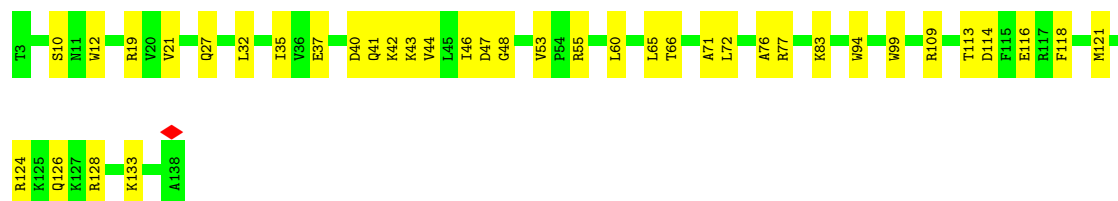
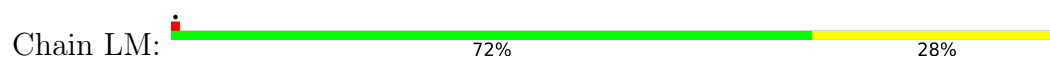


- Molecule 13: 60S ribosomal protein L13-A

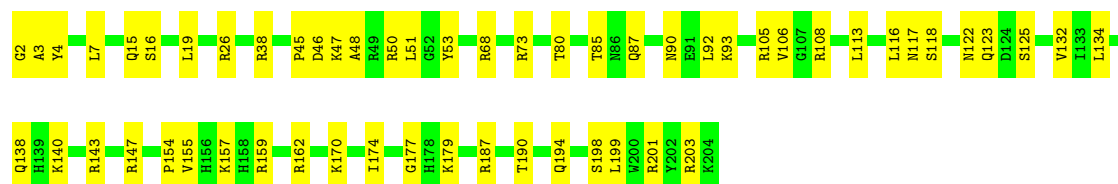




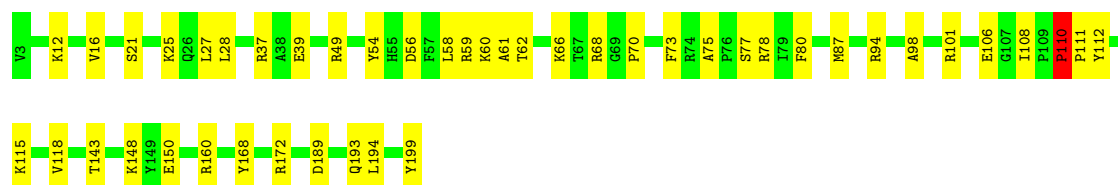
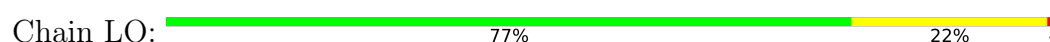
- Molecule 14: 60S ribosomal protein L14-A



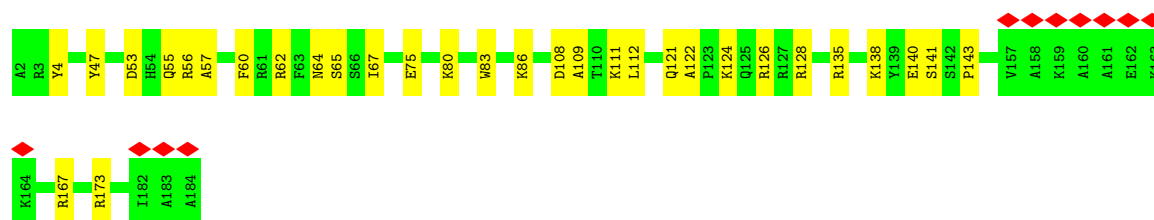
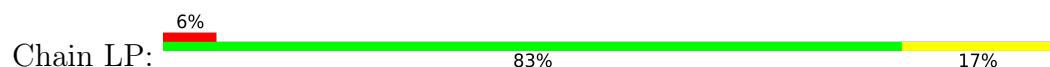
- Molecule 15: 60S ribosomal protein L15-A



- Molecule 16: 60S ribosomal protein L16-A

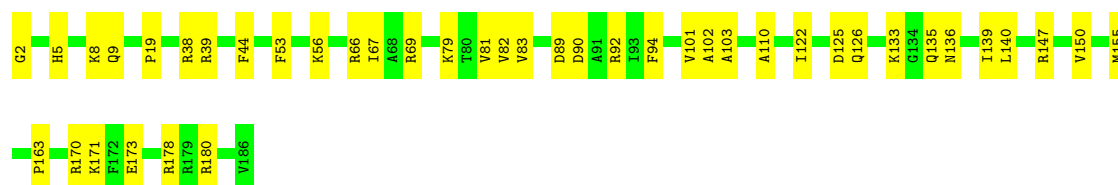


- Molecule 17: 60S ribosomal protein L17-A



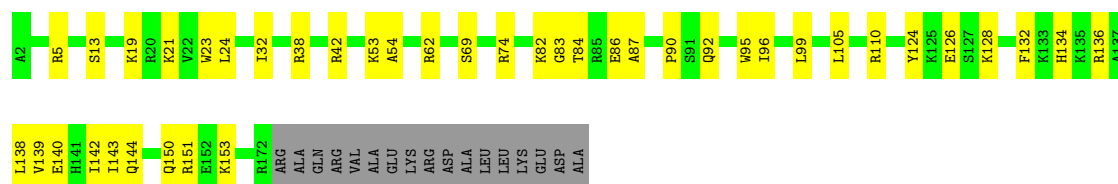
- Molecule 18: 60S ribosomal protein L18-A

Chain LQ:  77% 23%



- Molecule 19: 60S ribosomal protein L19-A

Chain LR:  69% 22% 9%



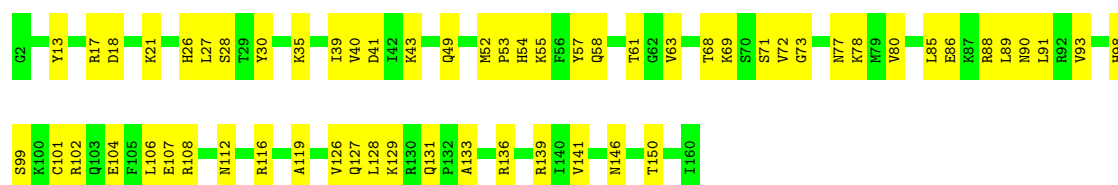
- Molecule 20: 60S ribosomal protein L20-A

Chain LS:  71% 29%



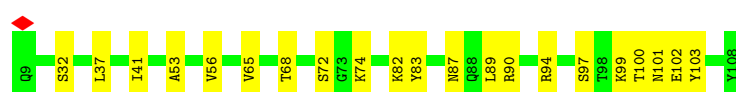
- Molecule 21: 60S ribosomal protein L21-A

Chain LT:  63% 37%



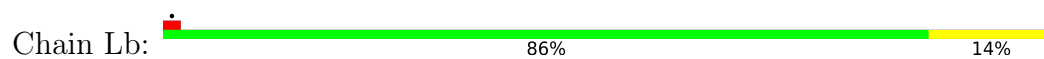
- Molecule 22: 60S ribosomal protein L22-A

Chain LU:  79% 21%

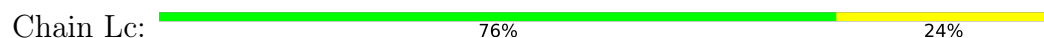


- Molecule 23: 60S ribosomal protein L23-A

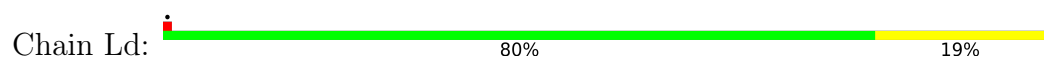
Chain LV:  77% 23%



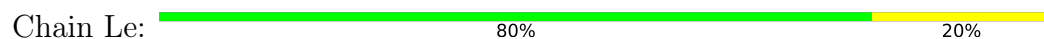
- Molecule 30: 60S ribosomal protein L30



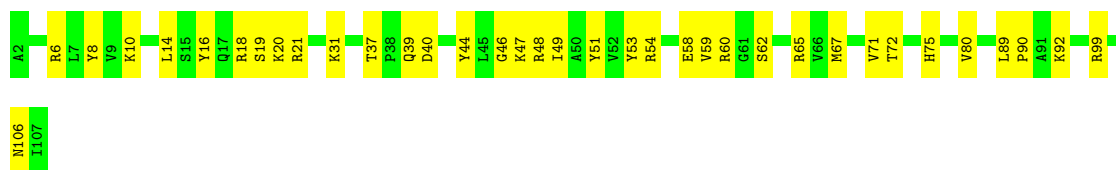
- Molecule 31: 60S ribosomal protein L31-A



- Molecule 32: 60S ribosomal protein L32



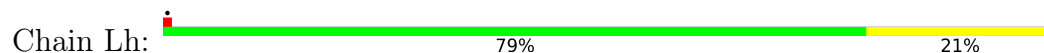
- Molecule 33: 60S ribosomal protein L33-A



- Molecule 34: 60S ribosomal protein L34-A

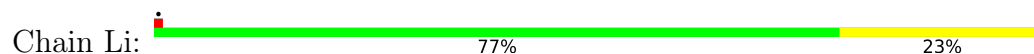


- Molecule 35: 60S ribosomal protein L35-A

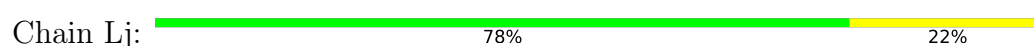




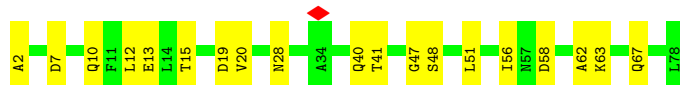
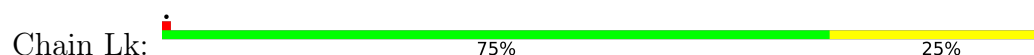
- Molecule 36: 60S ribosomal protein L36-A



- Molecule 37: 60S ribosomal protein L37-A



- Molecule 38: 60S ribosomal protein L38



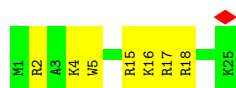
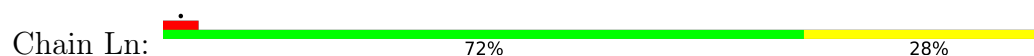
- Molecule 39: 60S ribosomal protein L39



- Molecule 40: 60S ribosomal protein L40-A



- Molecule 41: 60S ribosomal protein L41-A



- Molecule 42: 60S ribosomal protein L42-A

V2	K6	K15	R18	V25	A30	S34	Q38	R41	R42	K46	Q47	Q53	K61	A62	K63	T64	T65	V68	V69	L70	R71	L72	E73	C77	K78	T79	R80	T84	R87	F91	G94	Q99	Q102	A103	I104
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Chain Lp: 69% 31%

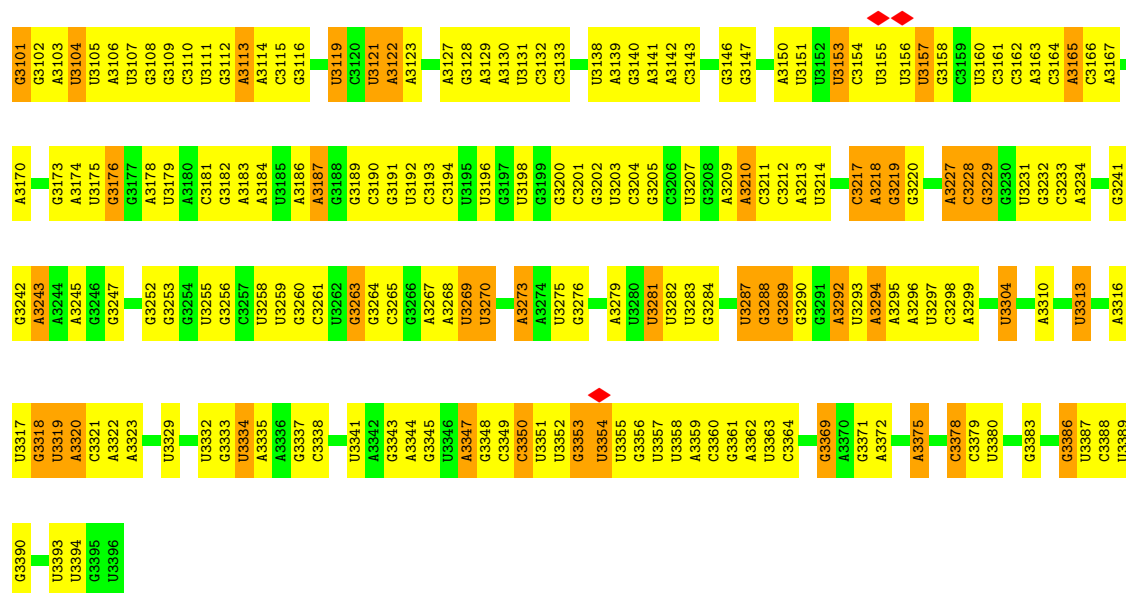
A2	K3	R4	V16	R17	Y18	L29	D38	C39	C42	K45	T46	V47	K48	R49	W55	T56	C57	S58	C59	S60	K61	A62	T63	V64	A68	Y69	T73	V79	T83	R84	R85	E88	E91	A92
----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain 1: 45% 44% 8% .

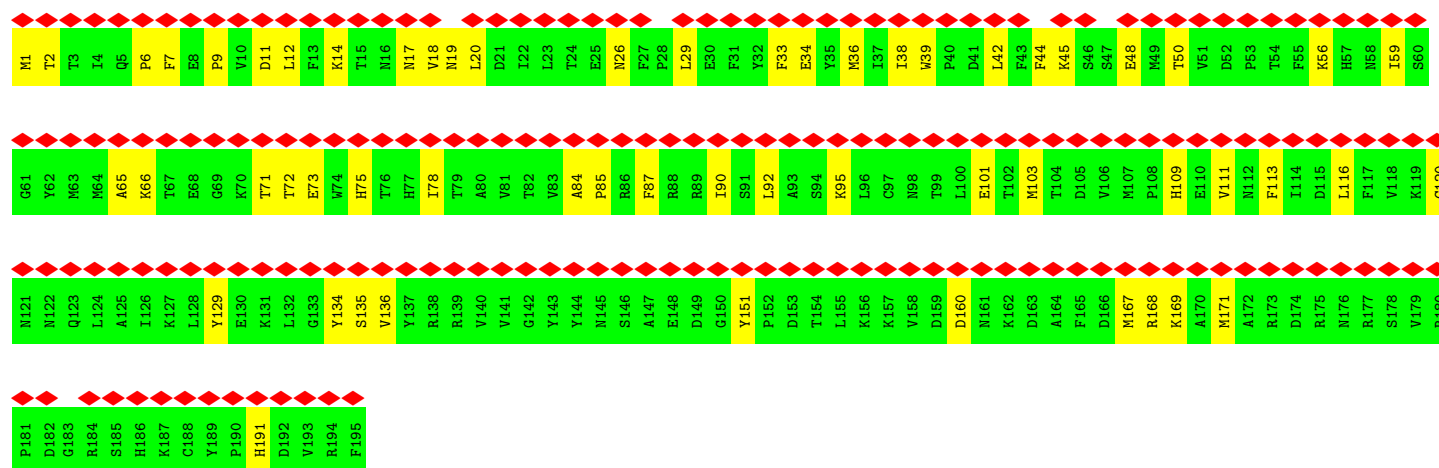
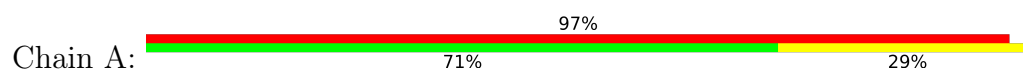
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A630	C702	A551	C	A324	U252	C179	U3
U631	G703	G552	G	A423	A253	C180	A99
G632	U704	A553	C	G424	A254	U181	C7
C633	A705	A554	A486	G425	A255		C8
C634	U706	U555	U487	U329	G256		U9
	G707	U556	U488	G426		U184	
C637	U708	A557	U488	C427	U257	C185	G104
G638	A709	U558	U488	A428	G337	U186	C105
G639	A710	A559	C490	U429	C338	A107	A13
U640	G711	C560	A491	U430	C339	U187	A106
C641	U712	C561	C492	U431	C260		A108
	G713	C562	U493	G432	C340	U190	A109
A646	A714	U563	G494	A343	G341	U191	U19
A647	U715	U563	U434	A342			A20
U648	A716	C564	C495	C346	A265	U194	C11
A649	C717	G567	C497	G347	G267	U195	U112
C650	U718	G568	A498	A348	G196		C113
U651	A720	G575	A501	G349	A199		G24
			U502	C350	C200		U25
C655		G579	C503	A351	G202		A26
A656	G725		A504	G353	G202		C29
A657	C727	G583	G505		U207		A40
G658	U728	U506	U444	G358	C208		A43
G659	C729	U507	G445	U278	A209		U44
A660	U730	U508	U446	U280	U210		C47
G661	C731	U509	U447	A361	G211		A48
U662	G732		U448	A366	G212		A49
C663		G514	U449	A367	A213		U50
U664	G742	C515	G450	G368	G214		A51
A665	A744	G516	U451	U286	G215		A52
G667	C745	G517	G	C287	G216		
G668	U746	G518	C	C288	U134		C
C596	A747	A519	C	A375	C135		G59
G597	U748	U520	U	G376	G218		A60
A598	C749	A521	C	A389	A219		A61
U598		A522	U	U292	G220		A62
G600	G752	U523	C	U393	A221		
U601	C753	U524	U	C293	A222		A65
A602	U754	U528	C	G394	U223		A67
	A755	A529	C	A295	C224		C68
A608	U681	G530	C	G397	U228		
G609	C757	U531	U	A398	G229		G75
G610	U758	A532	U	A399	U230		G76
A611	U759	G535	G	G400	G301		A77
U612	G760	U536	U	U401	U302		U78
C613	A761	A537	C	C403			U79
		U615	G	G406	G239		G80
A690	U762	U616	U	A306	U240		C81
A691	C763	G617	G	A307	G241		C82
A692	U764	C618	A	A308	C242		
A693		A619	G	U411	G243		G86
C694	G767	U620	G	U412	C244		
C695	C768	A621	G	U413	G245		U169
C696	U769	U545	G	U414	U246		G170
A697	C770	C546	G	G415	C315		G171
U698		G547	A	A416	C247		G172
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							A96



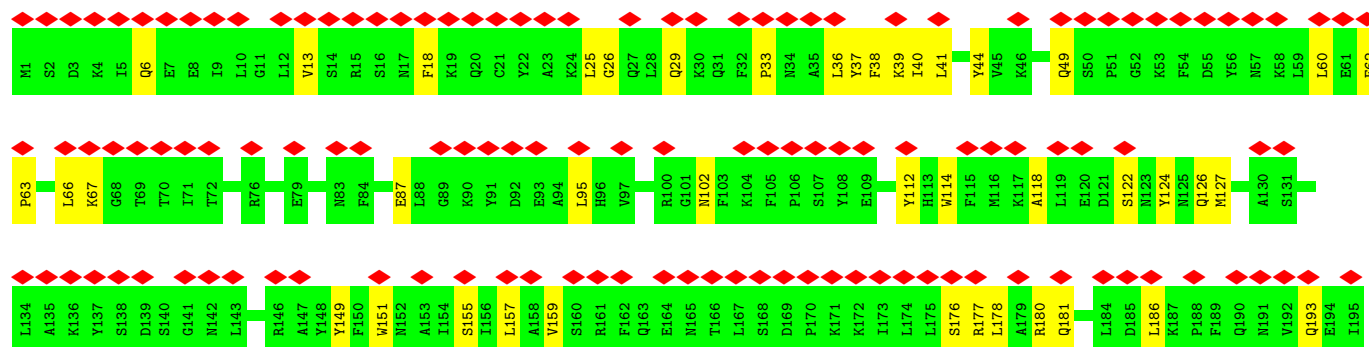
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G3030	G2950	A2758	A2678	U2587	G2513	U	G2302	G2206	C2118	U2057	G1993
G3031	U2955	U2759	A2679	U2588	U2514	U	G2303	U2209	A2119	G2058	U1994
A3032	G2956	C2765	A2680	A2593	A2515	U	G2304	G2210	G2120	A1995	A1996
U3037	C2960	U2766	C2682	U2597	G2522	U	G2305	A2213	G2121	U2059	U1997
U3038	U2961	U2767	U2683	G2598	A2523	G	G2306	A2214	U2129	A	G
C3039	U2962	U2768	C2684	G2598	A2524	A	G2307	A2215	U2130	G	U
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G3046	G2964	U2772	A2687	G2603	G2527	U	A2310	U2217	C2132	C	C1999
A3047	A2967	C2773	U2688	G2606	U2531	A	G2395	G2218	U2133	U	U2000
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G3051	G2972	U2775	A2690	G2607	G2534	U	A2397	A2220	A2138	U	G2002
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G3070	A2982	A2803	U2702	G2622	U2547	C	A2413	A2235	A2158	U2081	C2013
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U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2070	U2146	U2079
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2071	U2147	U2080
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2072	U2148	U2081
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2073	U2149	U2082
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2074	U2150	U2083
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2075	U2151	U2084
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2076	U2152	U2085
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2077	U2153	U2086
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2078	U2154	U2087
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2079	U2155	U2088
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2080	U2156	U2089
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2081	U2157	U2090
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2082	U2158	U2091
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2083	U2159	U2092
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2084	U2160	U2093
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2085	U2161	U2094
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2086	U2162	U2095
U3099	U3022	U2837	U2750	U2581	G2581	U	U2446	G2284	U2087	U2163	

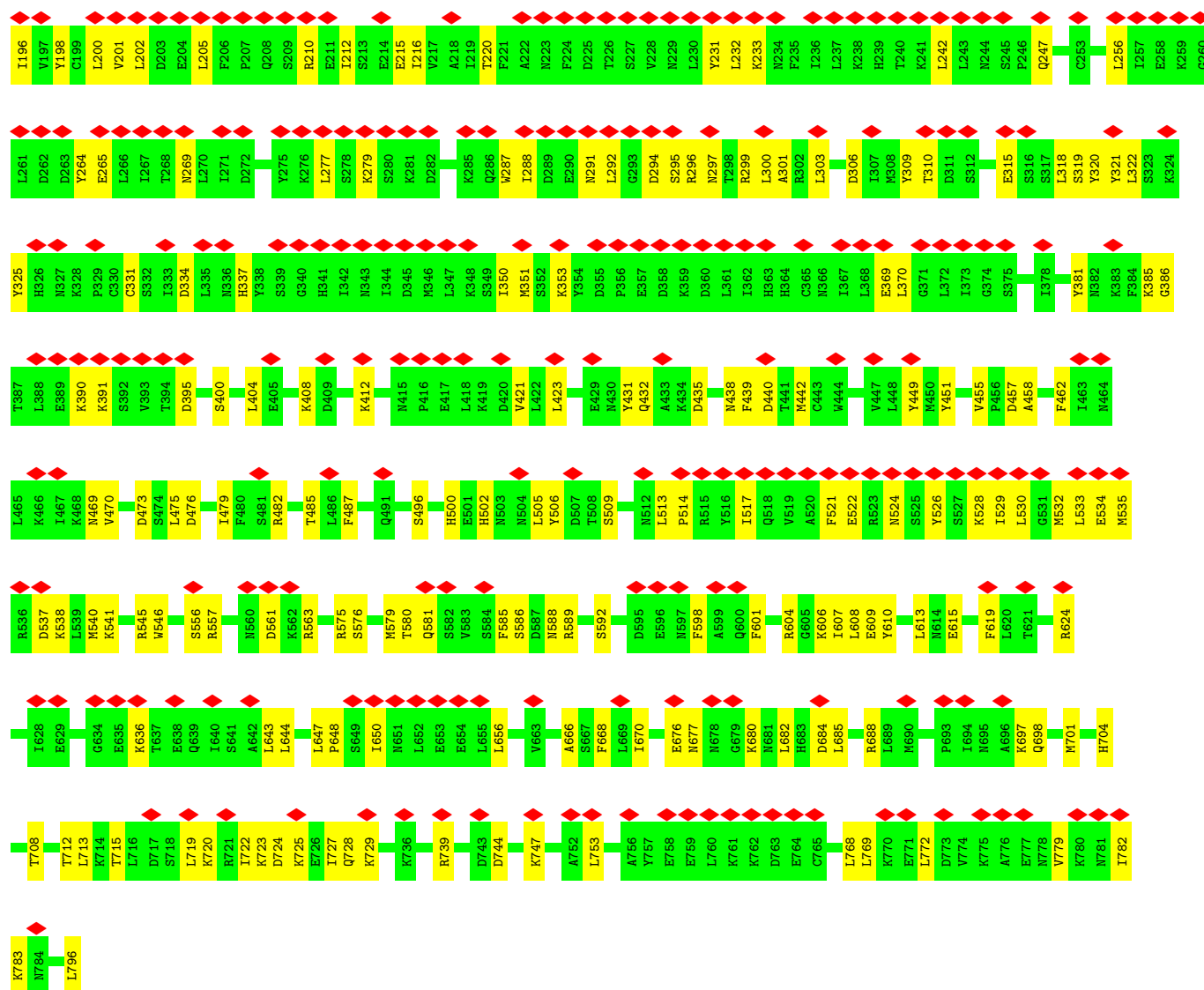


• Molecule 45: N-terminal acetyltransferase B complex catalytic subunit NAT3

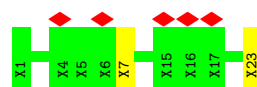
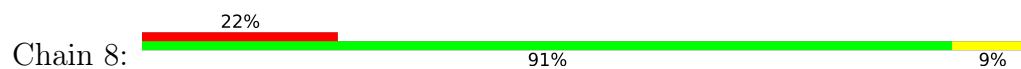


• Molecule 46: N-terminal acetyltransferase B complex subunit MDM2





• Molecule 47: Nascent peptide chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45530	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.563	Depositor
Minimum map value	-0.645	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.093	Depositor
Recommended contour level	0.215	Depositor
Map size (Å)	417.99997, 417.99997, 417.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	C4	0.16	0/2883	0.22	0/4491
2	C3	0.18	0/3746	0.26	0/5832
3	LA	0.19	0/1933	0.35	0/2598
4	LB	0.17	0/3146	0.31	0/4228
5	LC	0.18	0/2800	0.39	1/3790 (0.0%)
6	LD	0.18	0/2400	0.45	3/3239 (0.1%)
7	LE	0.15	0/1327	0.31	0/1790
8	LF	0.17	0/1821	0.30	0/2451
9	LG	0.16	0/1836	0.35	0/2481
10	LH	0.16	0/1529	0.35	0/2060
11	LI	0.16	0/1801	0.29	0/2416
12	LJ	0.16	0/1371	0.43	0/1838
13	LL	0.16	0/1568	0.36	0/2106
14	LM	0.16	0/1068	0.34	0/1438
15	LN	0.17	0/1757	0.31	0/2354
16	LO	0.17	0/1585	0.29	0/2128
17	LP	0.16	0/1439	0.28	0/1938
18	LQ	0.15	0/1465	0.26	0/1965
19	LR	0.16	0/1395	0.30	0/1861
20	LS	0.18	0/1473	0.37	0/1980
21	LT	0.18	0/1300	0.37	0/1743
22	LU	0.15	0/812	0.36	0/1099
23	LV	0.17	0/1018	0.36	0/1369
24	LW	0.17	0/550	0.30	0/731
25	LX	0.17	0/979	0.27	0/1321
26	LY	0.17	0/995	0.32	0/1329
27	LZ	0.16	0/1118	0.38	0/1497
28	La	0.17	0/1204	0.34	0/1612
29	Lb	0.16	0/473	0.38	0/629
30	Lc	0.16	0/745	0.30	0/1001
31	Ld	0.20	0/894	0.33	0/1200
32	Le	0.16	0/1038	0.29	0/1390

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lf	0.18	0/868	0.32	0/1168
34	Lg	0.17	0/890	0.33	0/1189
35	Lh	0.15	0/978	0.31	0/1301
36	Li	0.15	0/772	0.34	0/1026
37	Lj	0.17	0/685	0.29	0/908
38	Lk	0.16	0/618	0.32	0/826
39	Ll	0.20	0/443	0.38	0/588
40	Lm	0.17	0/423	0.41	0/562
41	Ln	0.13	0/230	0.32	0/296
42	Lo	0.16	0/836	0.37	0/1104
43	Lp	0.18	0/701	0.37	0/934
44	1	0.17	0/79000	0.27	0/123166
45	A	0.13	0/1654	0.32	0/2237
46	B	0.10	0/6665	0.29	0/8979
All	All	0.17	0/144232	0.29	4/212189 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	LG	0	2
16	LO	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	LC	294	GLU	N-CA-C	-10.71	98.88	112.90
6	LD	18	THR	CA-C-N	10.06	129.87	120.21
6	LD	18	THR	C-N-CA	10.06	129.87	120.21
6	LD	26	GLY	N-CA-C	-5.21	105.03	114.46

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	LG	158	ASP	Peptide
9	LG	76	ALA	Peptide

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Mol	Chain	Res	Type	Group
16	LO	110[A]	PRO	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	C4	2579	0	1304	64	0
2	C3	3353	0	1695	74	0
3	LA	1899	0	1956	51	0
4	LB	3075	0	3142	74	0
5	LC	2748	0	2859	74	0
6	LD	2351	0	2294	75	0
7	LE	1305	0	1373	35	0
8	LF	1784	0	1862	46	0
9	LG	1804	0	1877	42	0
10	LH	1508	0	1572	35	0
11	LI	1764	0	1804	39	0
12	LJ	1350	0	1381	50	0
13	LL	1543	0	1608	48	0
14	LM	1053	0	1149	31	0
15	LN	1720	0	1779	48	0
16	LO	1555	0	1659	34	0
17	LP	1416	0	1433	25	0
18	LQ	1441	0	1543	44	0
19	LR	1378	0	1462	34	0
20	LS	1437	0	1475	38	0
21	LT	1276	0	1323	51	0
22	LU	796	0	812	15	0
23	LV	1003	0	1048	21	0
24	LW	538	0	550	8	0
25	LX	964	0	1025	19	0
26	LY	984	0	1075	19	0
27	LZ	1092	0	1155	31	0
28	La	1173	0	1215	32	0
29	Lb	462	0	491	9	0
30	Lc	737	0	792	16	0
31	Ld	880	0	923	26	0
32	Le	1017	0	1081	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	Lf	850	0	880	27	0
34	Lg	880	0	943	28	0
35	Lh	969	0	1078	24	0
36	Li	766	0	844	17	0
37	Lj	670	0	673	17	0
38	Lk	612	0	682	13	0
39	Ll	436	0	475	21	0
40	Lm	417	0	455	13	0
41	Ln	229	0	273	6	0
42	Lo	824	0	888	25	0
43	Lp	694	0	735	24	0
44	1	70586	0	35467	1382	0
45	A	1612	0	1577	49	0
46	B	6536	0	6588	166	0
47	8	115	0	26	5	0
48	1	196	0	0	0	0
48	C3	1	0	0	0	0
48	C4	1	0	0	0	0
48	LA	2	0	0	0	0
48	LB	1	0	0	0	0
48	LN	1	0	0	0	0
48	LP	1	0	0	0	0
48	LR	1	0	0	0	0
48	LV	1	0	0	0	0
48	Le	1	0	0	0	0
49	Lg	1	0	0	0	0
49	Lj	1	0	0	0	0
49	Lm	1	0	0	0	0
49	Lo	1	0	0	0	0
49	Lp	1	0	0	0	0
All	All	134392	0	98301	2557	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 11.

All (2557) 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)
5:LC:299:ILE:HD12	18:LQ:39:ARG:O	1.24	1.30
44:1:2875:U:O4	47:8:23:UNK:C	1.79	1.28
5:LC:299:ILE:CD1	18:LQ:39:ARG:O	1.83	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Ld:7:VAL:HG22	31:Ld:77:ARG:O	1.41	1.21
44:1:1257:C:H42	44:1:1261:G:N2	1.45	1.14
5:LC:299:ILE:HD11	18:LQ:39:ARG:HB3	1.19	1.13
44:1:1257:C:N4	44:1:1261:G:H22	1.49	1.09
44:1:2875:U:O4	47:8:23:UNK:CA	2.03	1.07
5:LC:299:ILE:HD11	18:LQ:39:ARG:CB	1.86	1.06
44:1:1237:G:H1	44:1:1251:A:N6	1.56	1.02
5:LC:299:ILE:CD1	18:LQ:39:ARG:HB3	1.89	1.02
44:1:2875:U:O4	47:8:23:UNK:HA	1.59	1.00
4:LB:214:MET:HE1	4:LB:279:ASN:HA	1.47	0.96
44:1:2007:G:H1	44:1:2014:U:H3	1.13	0.94
44:1:2437:G:H1	44:1:2510:U:H3	0.99	0.92
31:Ld:10:ARG:HH12	44:1:3386:G:H4'	1.33	0.91
44:1:3192:U:H3	44:1:3200:G:H1	1.19	0.91
44:1:1985:G:O6	44:1:2036:U:N3	2.04	0.90
44:1:549:U:C4	44:1:550:A:N6	2.40	0.89
37:Lj:2:GLY:N	44:1:2138:A:HO2'	1.70	0.88
46:B:606:LYS:HA	46:B:609:GLU:HG2	1.55	0.88
44:1:542:G:N1	44:1:550:A:C6	2.41	0.87
34:Lg:46:ASP:HB2	34:Lg:84:CYS:SG	2.13	0.87
44:1:170:G:H1	44:1:248:U:H3	1.20	0.85
44:1:2442:G:H1	44:1:2505:U:H3	0.86	0.85
44:1:1352:A:H4'	44:1:1353:U:H5'	1.57	0.84
44:1:1019:G:H1	44:1:1033:U:H3	1.25	0.84
44:1:541:U:O4	44:1:542:G:O6	1.96	0.84
44:1:1237:G:H1	44:1:1251:A:H61	1.09	0.83
44:1:1564:U:H3	44:1:1575:A:H61	1.23	0.82
1:C4:10:C:C5	6:LD:20:PHE:HD1	1.97	0.82
40:Lm:80:PRO:HA	40:Lm:83:LYS:HG3	1.61	0.82
12:LJ:65:ILE:HD11	44:1:2681:U:H5'	1.61	0.82
26:LY:55:GLU:HB2	26:LY:108:LYS:HB3	1.62	0.82
3:LA:21:ARG:HD3	44:1:824:C:H5''	1.63	0.81
44:1:443:G:N2	44:1:492:C:O2	2.13	0.80
10:LH:9:GLN:HE22	10:LH:52:LEU:HD21	1.47	0.80
31:Ld:10:ARG:HH12	44:1:3386:G:C4'	1.95	0.80
44:1:1237:G:N1	44:1:1251:A:N6	2.21	0.80
44:1:1071:U:H3	44:1:1087:G:H1	1.28	0.80
34:Lg:46:ASP:CB	34:Lg:84:CYS:SG	2.70	0.80
12:LJ:52:TYR:HA	12:LJ:61:ARG:HG2	1.64	0.79
44:1:2427:U:H3	44:1:2602:G:H1	1.27	0.79
18:LQ:170:ARG:HD2	28:La:57:GLY:HA3	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lg:74:ARG:NH2	44:1:1639:C:OP2	2.14	0.79
13:LL:76:THR:OG1	13:LL:101:ARG:NH1	2.16	0.78
44:1:1955:U:O4	44:1:1956:A:N6	2.15	0.78
3:LA:177:LYS:HB2	43:Lp:69:TYR:HE2	1.49	0.78
13:LL:36:ARG:NH2	44:1:687:U:OP2	2.17	0.77
44:1:443:G:N1	44:1:492:C:N3	2.32	0.77
21:LT:102:ARG:HH21	44:1:1061:A:H4'	1.49	0.77
46:B:95:LEU:HB3	46:B:126:GLN:HE21	1.48	0.77
44:1:1805:C:H2'	44:1:1806:A:H8	1.50	0.76
23:LV:10:LYS:NZ	23:LV:56:ASP:OD1	2.18	0.76
38:Lk:63:LYS:O	38:Lk:67:GLN:NE2	2.19	0.76
1:C4:10:C:O2	6:LD:20:PHE:O	2.04	0.76
31:Ld:10:ARG:HH12	44:1:3386:G:C5'	1.98	0.76
5:LC:299:ILE:CD1	18:LQ:39:ARG:C	2.58	0.75
31:Ld:5:LYS:N	31:Ld:5:LYS:HD2	2.00	0.75
44:1:2442:G:N2	44:1:2505:U:O2	2.17	0.75
28:La:6:THR:HG22	28:La:8:THR:H	1.53	0.74
44:1:3042:U:OP2	44:1:3092:C:N4	2.21	0.74
15:LN:106:VAL:HG11	15:LN:132:VAL:HG21	1.70	0.74
44:1:1257:C:H42	44:1:1261:G:H22	0.78	0.74
44:1:2369:G:H2'	44:1:2370:G:C8	2.22	0.74
46:B:482:ARG:HH22	46:B:610:TYR:HB2	1.50	0.74
5:LC:293:SER:HA	5:LC:296:GLN:CG	2.17	0.73
10:LH:57:VAL:HG23	10:LH:68:LEU:HD12	1.71	0.73
25:LX:72:ALA:HB1	25:LX:83:VAL:HG21	1.71	0.73
44:1:524:U:O4	44:1:568:G:N1	2.20	0.73
43:Lp:39:CYS:CB	43:Lp:42:CYS:SG	2.73	0.73
2:C3:45:C:H4'	39:LI:11:GLN:HE21	1.54	0.73
44:1:1562:C:H2'	44:1:1563:C:C6	2.25	0.72
44:1:1569:U:H5'	44:1:1570:U:H5''	1.72	0.72
44:1:2255:A:H5'	44:1:2261:G:H22	1.53	0.72
5:LC:293:SER:HA	5:LC:296:GLN:HG2	1.72	0.72
5:LC:299:ILE:HD11	18:LQ:39:ARG:O	1.87	0.71
11:LI:116:ARG:HH22	44:1:2622:C:H42	1.37	0.71
23:LV:81:GLN:O	23:LV:98:ASN:ND2	2.23	0.71
44:1:655:C:H2'	44:1:656:A:H8	1.54	0.71
20:LS:8:GLN:HB2	20:LS:64:ILE:HD11	1.72	0.71
44:1:1985:G:H4'	44:1:1985:G:OP1	1.89	0.71
43:Lp:38:ASP:OD1	43:Lp:45:LYS:NZ	2.17	0.71
11:LI:208:ASN:HA	11:LI:211:ARG:HE	1.55	0.71
44:1:2960:C:H2'	44:1:2961:G:H8	1.56	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C3:114:G:HO2'	44:1:1530:U:HO2'	1.32	0.71
5:LC:361:HIS:O	20:LS:28:ARG:NH1	2.24	0.71
12:LJ:51:ARG:NH2	44:1:2681:U:OP2	2.24	0.71
34:Lg:41:ARG:HG2	34:Lg:56:THR:HG21	1.73	0.71
44:1:297:G:OP2	44:1:297:G:N2	2.22	0.71
43:Lp:4:ARG:NH1	44:1:837:A:OP2	2.23	0.71
44:1:1378:U:H2'	44:1:1379:G:H8	1.56	0.71
44:1:2964:G:N2	44:1:2967:A:OP2	2.21	0.71
7:LE:77:ARG:NH2	44:1:3273:A:OP2	2.22	0.70
9:LG:153:ILE:HD11	9:LG:166:LEU:HD22	1.72	0.70
1:C4:10:C:C5	6:LD:20:PHE:CD1	2.79	0.70
12:LJ:49:LYS:HB3	12:LJ:62:ASN:HA	1.73	0.70
44:1:664:U:H2'	44:1:665:A:C8	2.26	0.70
44:1:2357:A:H2'	44:1:2358:A:H8	1.56	0.70
27:LZ:88:ASP:OD1	27:LZ:121:ARG:NH2	2.24	0.70
24:LW:6:ASP:OD1	24:LW:9:SER:N	2.24	0.70
44:1:700:C:H2'	44:1:701:G:H8	1.57	0.70
22:LU:90:ARG:NH1	44:1:1682:U:O4	2.25	0.70
46:B:561:ASP:O	46:B:563:ARG:NH1	2.25	0.70
5:LC:299:ILE:HD11	18:LQ:39:ARG:C	2.17	0.70
44:1:411:U:H2'	44:1:412:G:H8	1.57	0.69
44:1:542:G:H1	44:1:549:U:H3	1.38	0.69
44:1:1240:A:H61	44:1:1244:A:H5''	1.55	0.69
12:LJ:32:ARG:HH21	12:LJ:121:GLY:HA3	1.56	0.69
31:Ld:75:ILE:HG12	31:Ld:93:VAL:HG22	1.75	0.69
44:1:2305:G:N2	44:1:2305:G:OP2	2.24	0.69
46:B:720:LYS:O	46:B:723:LYS:NZ	2.25	0.69
15:LN:2:GLY:N	44:1:117:U:OP2	2.26	0.69
18:LQ:81:VAL:HB	18:LQ:101:VAL:HG12	1.74	0.69
44:1:1958:U:O2	44:1:2083:G:O6	2.09	0.69
30:Lc:9:SER:O	30:Lc:13:LYS:NZ	2.22	0.69
20:LS:12:ARG:NH1	20:LS:57:GLU:OE2	2.26	0.69
33:Lf:49:ILE:HD11	33:Lf:71:VAL:HG13	1.74	0.69
44:1:518:G:N2	44:1:518:G:OP2	2.26	0.69
1:C4:14:U:H5''	6:LD:24:ARG:HH11	1.58	0.68
18:LQ:69:ARG:HH22	44:1:720:A:H3'	1.58	0.68
42:Lo:38:GLN:OE1	42:Lo:41:ARG:NH2	2.26	0.68
5:LC:110:ASN:HD22	15:LN:201:ARG:HB3	1.57	0.68
18:LQ:180:ARG:NH1	44:1:2720:G:OP2	2.27	0.68
27:LZ:27:LYS:HB3	27:LZ:42:LEU:HD12	1.74	0.68
25:LX:63:ILE:HD11	25:LX:102:LEU:HD12	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:2772:C:H4'	44:1:2773:C:H5'	1.75	0.68
44:1:3153:U:OP2	44:1:3293:U:O2'	2.09	0.68
39:Ll:27:ILE:HG23	39:Ll:30:ARG:HH12	1.57	0.68
44:1:1838:G:H5''	44:1:1839:A:H5'	1.74	0.68
44:1:1237:G:N2	44:1:1251:A:N1	2.39	0.68
44:1:2221:G:N2	44:1:2224:A:OP2	2.25	0.68
3:LA:95:SER:O	3:LA:100:ASN:ND2	2.25	0.68
31:Ld:55:LEU:HB2	31:Ld:95:PRO:HD3	1.75	0.68
44:1:2514:U:OP2	44:1:2586:G:N2	2.27	0.68
3:LA:37:ARG:NH1	44:1:2526:C:OP1	2.25	0.67
44:1:584:G:H2'	44:1:585:A:H8	1.59	0.67
1:C4:14:U:H5''	6:LD:24:ARG:NH1	2.10	0.67
35:Lh:34:GLN:HB3	35:Lh:38:ARG:HH21	1.58	0.67
4:LB:19:ARG:NH2	44:1:3045:G:OP1	2.27	0.67
16:LO:56[A]:ASP:OD1	16:LO:60[A]:LYS:NZ	2.27	0.67
1:C4:28:C:OP1	12:LJ:137:ARG:NH1	2.26	0.67
44:1:282:G:O2'	44:1:283:G:OP2	2.12	0.67
11:LI:3:ARG:NH2	44:1:2854:U:OP2	2.27	0.67
44:1:1280:C:H2'	44:1:1281:G:H8	1.59	0.67
44:1:2986:U:H2'	44:1:2987:A:H8	1.59	0.67
45:A:6:PRO:O	45:A:45:LYS:NZ	2.26	0.67
3:LA:54:ARG:NH2	44:1:2176:U:OP1	2.27	0.67
3:LA:145:LYS:HZ2	3:LA:157:VAL:HG12	1.60	0.67
17:LP:108:ASP:OD2	17:LP:111:LYS:NZ	2.24	0.67
10:LH:113:GLU:OE2	10:LH:115:ARG:NE	2.22	0.67
12:LJ:20:ASN:ND2	44:1:2681:U:O2	2.28	0.67
12:LJ:22:SER:OG	44:1:2675:C:N4	2.27	0.67
40:Lm:103:LEU:HD21	40:Lm:110:CYS:HA	1.76	0.67
4:LB:279:ASN:ND2	44:1:3098:G:OP1	2.27	0.67
16:LO:21[A]:SER:OG	44:1:1181:U:O4	2.12	0.67
46:B:350:ILE:HA	46:B:353:LYS:HD2	1.76	0.67
9:LG:249:ARG:HH12	44:1:2512:C:H5''	1.59	0.67
2:C3:67:U:H5''	37:Lj:85:LYS:HG2	1.77	0.66
9:LG:158:ASP:OD1	9:LG:159:PRO:HD3	1.95	0.66
31:Ld:4:LEU:CB	46:B:720:LYS:HE2	2.23	0.66
44:1:1119:C:H2'	44:1:1120:A:H8	1.60	0.66
44:1:170:G:N2	44:1:248:U:O2	2.27	0.66
28:La:102:ILE:HB	28:La:125:VAL:HG12	1.76	0.66
1:C4:45:A:OP1	6:LD:151:GLN:NE2	2.26	0.66
44:1:358:G:N2	44:1:361:A:OP2	2.28	0.66
44:1:1257:C:N3	44:1:1261:G:N1	2.40	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LJ:132:ASN:HA	12:LJ:154:THR:HG21	1.78	0.66
31:Ld:10:ARG:NH1	44:1:3386:G:H4'	2.08	0.66
1:C4:10:C:C4	6:LD:20:PHE:HD1	2.14	0.66
45:A:73:GLU:O	45:A:75:HIS:ND1	2.26	0.66
15:LN:113:LEU:HB2	15:LN:134:LEU:HD12	1.78	0.66
44:1:549:U:O4	44:1:550:A:N6	2.28	0.66
44:1:2960:C:H2'	44:1:2961:G:C8	2.31	0.66
46:B:287:TRP:O	46:B:291:ASN:ND2	2.27	0.66
1:C4:14:U:C5'	6:LD:24:ARG:NH1	2.59	0.66
44:1:2568:C:O2'	44:1:2569:A:O4'	2.13	0.66
44:1:3358:U:H2'	44:1:3359:A:H8	1.61	0.66
5:LC:156:LEU:HD12	5:LC:159:ILE:HD12	1.78	0.66
31:Ld:5:LYS:HD2	31:Ld:5:LYS:H	1.61	0.66
40:Lm:100:TYR:O	44:1:2895:G:O2'	2.14	0.66
44:1:1302:A:N7	44:1:2857:C:O2'	2.29	0.66
44:1:1563:C:H2'	44:1:1564:U:H6	1.58	0.66
44:1:541:U:C4	44:1:542:G:O6	2.48	0.65
20:LS:137:ARG:NH2	44:1:1214:U:OP2	2.30	0.65
10:LH:156:GLN:OE1	44:1:3109:G:N2	2.30	0.65
44:1:3016:A:H2'	44:1:3017:A:H8	1.60	0.65
12:LJ:53:THR:HG22	12:LJ:60:ARG:HA	1.79	0.65
44:1:1777:U:H2'	44:1:1778:G:C8	2.31	0.65
33:Lf:51:TYR:HB3	33:Lf:67:MET:HB2	1.79	0.65
44:1:544:C:O2	44:1:548:G:N2	2.29	0.65
46:B:540:MET:O	46:B:546:TRP:NE1	2.30	0.65
14:LM:48:GLY:HA3	14:LM:53:VAL:HB	1.77	0.65
39:Ll:13:MET:HE1	44:1:1493:G:C8	2.31	0.65
41:Ln:2:ARG:HE	41:Ln:4:LYS:HD3	1.61	0.65
44:1:627:U:H2'	44:1:628:A:H8	1.61	0.65
15:LN:2:GLY:N	44:1:116:A:OP2	2.30	0.65
45:A:92:LEU:HD13	45:A:95:LYS:HD2	1.77	0.65
3:LA:117:GLU:HG2	3:LA:124:GLY:H	1.62	0.65
3:LA:177:LYS:HB2	43:Lp:69:TYR:CE2	2.32	0.65
4:LB:306:THR:HG21	4:LB:316:GLU:HG3	1.79	0.65
10:LH:90:MET:HE3	10:LH:179:ILE:HG22	1.78	0.65
38:Lk:2:ALA:N	38:Lk:51:LEU:O	2.30	0.65
44:1:1280:C:H2'	44:1:1281:G:C8	2.31	0.65
44:1:1974:A:N6	44:1:2049:A:O4'	2.30	0.65
4:LB:348:ARG:HE	44:1:3037:U:H5''	1.62	0.64
15:LN:201:ARG:NH2	44:1:692:A:OP1	2.28	0.64
27:LZ:17:ARG:NH2	27:LZ:18:TYR:OH	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LB:187:SER:O	4:LB:190:GLU:N	2.24	0.64
6:LD:122:VAL:O	6:LD:248:ARG:NH2	2.30	0.64
9:LG:140:VAL:HG21	15:LN:3:ALA:HB2	1.78	0.64
10:LH:90:MET:HB3	10:LH:144:ILE:HG13	1.79	0.64
12:LJ:25:GLU:HG2	12:LJ:29:ARG:HH22	1.61	0.64
19:LR:13:SER:OG	19:LR:38:ARG:NH2	2.30	0.64
18:LQ:56:LYS:NZ	44:1:674:G:O6	2.30	0.64
44:1:2160:G:H2'	44:1:2161:G:H8	1.62	0.64
18:LQ:89:ASP:OD1	18:LQ:90:ASP:N	2.30	0.64
44:1:2437:G:N2	44:1:2510:U:O2	2.26	0.64
44:1:3204:C:H2'	44:1:3205:G:C8	2.33	0.64
13:LL:76:THR:O	13:LL:79:GLU:N	2.29	0.64
42:Lo:69:VAL:HG22	42:Lo:84:THR:HG22	1.79	0.64
44:1:1986:U:H3	44:1:2035:G:H1	1.45	0.64
44:1:2185:G:O2'	44:1:2314:U:OP2	2.13	0.64
44:1:1157:G:O2'	44:1:1169:A:N3	2.30	0.64
44:1:874:U:N3	44:1:2978:U:OP1	2.28	0.64
15:LN:90:ASN:ND2	44:1:2424:A:OP1	2.31	0.64
34:Lg:11:ASN:O	34:Lg:18:ASN:ND2	2.29	0.64
23:LV:104:ASN:OD1	23:LV:108:GLU:N	2.31	0.64
33:Lf:16:TYR:OH	33:Lf:89:LEU:O	2.14	0.64
44:1:1959:G:O6	44:1:2082:U:O2	2.14	0.64
8:LF:30:ARG:NH1	44:1:595:G:OP2	2.31	0.64
44:1:2842:U:OP1	44:1:2844:C:N4	2.28	0.64
44:1:1253:U:N3	44:1:1264:G:OP1	2.31	0.63
44:1:1661:G:H2'	44:1:1662:G:C8	2.34	0.63
1:C4:7:G:OP1	6:LD:33:ARG:NH1	2.31	0.63
44:1:638:C:N4	44:1:639:G:O6	2.32	0.63
1:C4:4:U:H2'	1:C4:5:G:H8	1.62	0.63
1:C4:10:C:N3	6:LD:20:PHE:HB3	2.12	0.63
2:C3:25:G:N7	26:LY:13:ARG:NH1	2.43	0.63
33:Lf:10:LYS:NZ	44:1:3175:U:OP1	2.26	0.63
44:1:3281:U:H2'	44:1:3282:U:C6	2.33	0.63
4:LB:57:VAL:HG22	4:LB:73:VAL:HG22	1.79	0.63
44:1:928:C:H2'	44:1:929:A:H8	1.64	0.63
44:1:3233:C:H2'	44:1:3234:A:C8	2.33	0.63
17:LP:62:ARG:NH1	44:1:412:G:OP1	2.31	0.63
39:Ll:27:ILE:O	39:Ll:33:ASN:ND2	2.31	0.63
44:1:1896:A:H61	44:1:2339:C:H42	1.44	0.63
45:A:151:TYR:OH	45:A:191:HIS:ND1	2.24	0.63
28:La:44:ASN:ND2	44:1:966:U:OP1	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:1497:C:H2'	44:1:1498:A:H8	1.62	0.63
46:B:66:LEU:HD12	46:B:67:LYS:HG3	1.79	0.63
46:B:476:ASP:OD2	46:B:502:HIS:ND1	2.31	0.63
2:C3:66:A:OP1	35:Lh:10:ARG:NH2	2.32	0.63
7:LE:46:ARG:NH2	44:1:3268:A:OP1	2.31	0.63
28:La:58:MET:HE1	44:1:2775:U:H1'	1.79	0.63
44:1:928:C:H2'	44:1:929:A:C8	2.34	0.63
16:LO:75[A]:ALA:HB3	16:LO:78[A]:ARG:HG2	1.79	0.63
16:LO:189[A]:ASP:OD1	16:LO:193[A]:GLN:NE2	2.32	0.63
33:Lf:60:ARG:NH2	44:1:622:A:O4'	2.32	0.63
44:1:3295:A:H2'	44:1:3296:A:H8	1.63	0.63
4:LB:368:GLY:O	24:LW:17:ARG:NH2	2.31	0.63
21:LT:116:ARG:NH2	44:1:1096:U:OP2	2.27	0.63
44:1:2137:U:OP2	44:1:2142:A:N6	2.26	0.63
6:LD:85:ARG:NH2	6:LD:86:TYR:OH	2.32	0.62
37:Lj:12:HIS:O	44:1:1490:A:O2'	2.17	0.62
44:1:1266:G:N2	44:1:1276:U:H1'	2.14	0.62
12:LJ:38:GLU:OE2	12:LJ:39:GLN:NE2	2.32	0.62
44:1:1786:G:H2'	44:1:1787:A:C8	2.34	0.62
3:LA:69:TYR:OH	44:1:2557:A:OP1	2.13	0.62
44:1:1940:G:H21	44:1:3362:A:H8	1.47	0.62
46:B:455:VAL:HG21	46:B:487:PHE:HB2	1.81	0.62
46:B:576:SER:HA	46:B:579:MET:HE2	1.81	0.62
27:LZ:22:LYS:H	27:LZ:49:TYR:HH	1.47	0.62
44:1:1421:G:H2'	44:1:1422:G:H8	1.64	0.62
44:1:1717:U:H2'	44:1:1718:G:C8	2.35	0.62
18:LQ:69:ARG:HD2	44:1:784:A:H8	1.62	0.62
20:LS:65:ASN:O	44:1:519:A:N6	2.29	0.62
34:Lg:46:ASP:HB3	34:Lg:84:CYS:SG	2.40	0.62
44:1:1348:U:O2	44:1:1349:G:N2	2.31	0.62
46:B:33:PRO:O	46:B:39:LYS:NZ	2.31	0.62
3:LA:36:GLU:OE1	3:LA:163:ARG:NH1	2.32	0.62
21:LT:88:ARG:HB2	44:1:2722:U:H4'	1.82	0.62
34:Lg:8:ARG:HB2	34:Lg:34:HIS:HE1	1.64	0.62
44:1:1621:A:H2'	44:1:1622:U:C6	2.35	0.62
44:1:1985:G:O6	44:1:2036:U:C4	2.52	0.62
22:LU:74:LYS:NZ	44:1:1678:G:O6	2.32	0.62
42:Lo:30:ALA:O	44:1:2767:U:O2'	2.14	0.62
44:1:1799:A:H2'	44:1:1800:A:H8	1.65	0.62
44:1:612:U:H2'	44:1:613:G:H8	1.65	0.62
44:1:1635:G:N2	44:1:1638:A:OP2	2.26	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:A:101:GLU:HG3	45:A:171:MET:HE1	1.81	0.62
43:Lp:4:ARG:NH2	44:1:838:G:O6	2.32	0.62
44:1:760:G:O2'	44:1:770:G:N2	2.31	0.62
44:1:2882:U:H2'	44:1:2883:U:C6	2.35	0.62
4:LB:211:GLN:NE2	4:LB:283:TYR:O	2.29	0.62
5:LC:193:LYS:HA	5:LC:198:ARG:HA	1.82	0.62
44:1:1015:U:O4	44:1:1035:G:N1	2.18	0.62
1:C4:10:C:C4	6:LD:20:PHE:CD1	2.87	0.61
1:C4:62:U:O2'	6:LD:285:ARG:NH2	2.32	0.61
3:LA:112:ILE:HG13	43:Lp:79:VAL:HG22	1.80	0.61
14:LM:109:ARG:NH1	44:1:3210:A:OP1	2.30	0.61
19:LR:105:LEU:HD23	19:LR:138:LEU:HD23	1.82	0.61
19:LR:140:GLU:OE2	19:LR:144:GLN:NE2	2.33	0.61
26:LY:103:LYS:NZ	44:1:217:U:O2	2.21	0.61
44:1:1152:G:N2	44:1:1152:G:OP2	2.32	0.61
1:C4:44:C:OP2	12:LJ:137:ARG:NH2	2.33	0.61
9:LG:240:ASN:OD1	44:1:2584:G:O2'	2.16	0.61
24:LW:22:VAL:HG22	24:LW:28:ILE:HG22	1.81	0.61
44:1:1084:A:H2'	44:1:1085:A:C8	2.35	0.61
44:1:2051:G:N2	44:1:2052:G:N7	2.47	0.61
44:1:2129:U:H2'	44:1:2130:G:C8	2.35	0.61
44:1:2366:C:H2'	44:1:2367:A:H8	1.65	0.61
3:LA:145:LYS:NZ	3:LA:157:VAL:HG12	2.16	0.61
13:LL:15:ARG:HE	44:1:798:G:H4'	1.65	0.61
44:1:2697:A:H2'	44:1:2698:G:C8	2.36	0.61
45:A:19:ASN:HB3	45:A:26:ASN:HD21	1.65	0.61
6:LD:107:ARG:NH1	6:LD:169:GLY:O	2.34	0.61
14:LM:133:LYS:NZ	44:1:3227:A:O2'	2.32	0.61
19:LR:38:ARG:NH1	44:1:1603:A:OP1	2.33	0.61
26:LY:12:ARG:NH1	44:1:215:G:OP1	2.33	0.61
44:1:591:G:N2	44:1:612:U:OP1	2.30	0.61
44:1:649:A:OP2	44:1:2868:U:O2'	2.17	0.61
8:LF:121:LYS:HB2	21:LT:133:ALA:HB3	1.82	0.61
44:1:2745:G:N2	44:1:2748:A:OP2	2.31	0.61
5:LC:193:LYS:NZ	44:1:1420:C:OP2	2.33	0.61
17:LP:64:ASN:O	17:LP:80:LYS:NZ	2.27	0.61
44:1:1178:G:N3	44:1:1328:C:O2'	2.33	0.61
45:A:134:TYR:HB3	45:A:167:MET:HE2	1.82	0.61
46:B:279:LYS:O	46:B:309:TYR:OH	2.18	0.61
21:LT:43:LYS:HA	21:LT:58:GLN:HE22	1.65	0.61
44:1:627:U:H2'	44:1:628:A:C8	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:2129:U:H2'	44:1:2130:G:H8	1.66	0.61
44:1:2344:U:H2'	44:1:2345:A:H8	1.66	0.61
5:LC:74:ILE:HD12	5:LC:75:PRO:HD2	1.83	0.61
22:LU:94:ARG:NH1	44:1:1679:A:OP1	2.34	0.61
44:1:542:G:C6	44:1:550:A:C6	2.89	0.61
44:1:1976:G:H22	44:1:2047:A:H1'	1.66	0.61
44:1:2429:G:H2'	44:1:2430:A:H8	1.64	0.61
44:1:3121:U:H1'	44:1:3122:A:H5''	1.83	0.61
45:A:1:MET:N	46:B:334:ASP:OD1	2.34	0.61
45:A:134:TYR:HB3	45:A:167:MET:CE	2.31	0.61
4:LB:136:LYS:O	4:LB:139:GLN:NE2	2.34	0.61
8:LF:121:LYS:NZ	8:LF:125:GLU:OE2	2.34	0.61
28:La:39:HIS:O	28:La:42:ARG:N	2.34	0.61
42:Lo:46:LYS:NZ	44:1:92:G:O5'	2.33	0.61
29:Lb:25:LYS:NZ	44:1:1106:G:O2'	2.33	0.61
12:LJ:82:ARG:HB3	12:LJ:112:LEU:HD13	1.82	0.60
14:LM:55:ARG:NH2	14:LM:76:ALA:O	2.34	0.60
15:LN:159:ARG:NH2	44:1:321:C:OP1	2.34	0.60
29:Lb:22:LYS:HA	29:Lb:22:LYS:HE3	1.83	0.60
44:1:1959:G:O6	44:1:2082:U:C2	2.54	0.60
3:LA:50:HIS:NE2	44:1:1795:U:OP2	2.23	0.60
5:LC:22:LEU:HD22	5:LC:26:PHE:HD2	1.64	0.60
8:LF:234:GLU:O	8:LF:237:ASN:ND2	2.34	0.60
9:LG:126:SER:OG	44:1:120:G:N2	2.34	0.60
5:LC:54:GLU:OE2	44:1:329:U:N3	2.33	0.60
11:LI:103:LEU:O	11:LI:112:GLN:NE2	2.34	0.60
11:LI:153:ARG:NH1	11:LI:157:TYR:OH	2.34	0.60
4:LB:28:ARG:NH2	44:1:3140:G:N7	2.50	0.60
26:LY:74:TYR:HD2	26:LY:77:LYS:HB2	1.65	0.60
28:La:117:ARG:NH2	44:1:718:G:OP1	2.33	0.60
31:Ld:10:ARG:HH12	44:1:3386:G:H5'	1.67	0.60
46:B:412:LYS:O	46:B:604:ARG:NH2	2.28	0.60
4:LB:59:ASP:HB2	4:LB:357:LYS:HE2	1.83	0.60
27:LZ:54:THR:HG23	27:LZ:56:LYS:H	1.67	0.60
44:1:671:U:H2'	44:1:672:A:H8	1.66	0.60
1:C4:2:G:H5'	6:LD:273:ARG:HD3	1.83	0.60
7:LE:60:ASP:OD1	7:LE:62:THR:OG1	2.20	0.60
18:LQ:66:ARG:NH1	44:1:785:G:OP2	2.34	0.60
32:Le:99:ASN:O	44:1:1388:U:O2'	2.18	0.60
38:Lk:20:VAL:HG12	38:Lk:47:GLY:HA2	1.83	0.60
44:1:2697:A:H2'	44:1:2698:G:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C4:112:G:H2'	1:C4:113:C:C6	2.36	0.60
6:LD:25:GLU:OE1	6:LD:25:GLU:HA	2.01	0.60
15:LN:4:TYR:OH	44:1:148:G:OP2	2.17	0.60
16:LO:27[A]:LEU:O	16:LO:101[A]:ARG:NH1	2.35	0.60
16:LO:115[A]:LYS:HD2	44:1:3178:A:H2'	1.84	0.60
44:1:655:C:H2'	44:1:656:A:C8	2.34	0.60
44:1:1203:A:H2'	44:1:1204:A:H8	1.66	0.60
44:1:1244:A:O2'	44:1:1247:U:OP1	2.15	0.60
44:1:3163:A:N6	44:1:3288:G:O6	2.34	0.60
44:1:2727:A:OP2	44:1:2728:G:N2	2.34	0.60
44:1:2883:U:H2'	44:1:2884:C:H6	1.66	0.60
3:LA:52:SER:HB3	3:LA:191:LEU:HD23	1.84	0.60
9:LG:95:ASN:OD1	9:LG:98:ARG:NH2	2.34	0.60
9:LG:97:TYR:HE2	9:LG:203:VAL:HG23	1.67	0.60
16:LO:110[A]:PRO:O	16:LO:112[A]:TYR:N	2.34	0.60
18:LQ:92:ARG:HG2	28:La:76:ASP:HB2	1.83	0.60
44:1:1178:G:N2	44:1:1329:U:O4'	2.35	0.60
45:A:2:THR:OG1	46:B:296:ARG:NH1	2.35	0.60
1:C4:8:G:O6	6:LD:21:ARG:NH2	2.35	0.60
4:LB:86:VAL:HA	4:LB:162:VAL:HG12	1.82	0.60
6:LD:41:LYS:HD2	21:LT:93:VAL:HG11	1.83	0.60
6:LD:226:TYR:HA	6:LD:231:ILE:HD13	1.84	0.60
8:LF:67:ARG:NH2	44:1:517:G:OP1	2.34	0.60
44:1:1959:G:C6	44:1:2082:U:O2	2.55	0.60
44:1:1973:G:N2	44:1:2050:C:O2'	2.35	0.60
44:1:3189:G:H1	44:1:3203:U:H3	1.50	0.60
3:LA:65:ASP:OD2	3:LA:68:LYS:N	2.34	0.59
18:LQ:38:ARG:NH2	44:1:1348:U:OP2	2.35	0.59
44:1:242:C:HO2'	44:1:243:G:H8	1.49	0.59
44:1:1553:U:H4'	44:1:1554:U:H5'	1.83	0.59
44:1:1814:A:H4'	44:1:1815:U:H5'	1.84	0.59
45:A:135:SER:N	45:A:168:ARG:O	2.29	0.59
46:B:589:ARG:NH2	46:B:613:LEU:O	2.34	0.59
1:C4:84:A:H2'	1:C4:85:G:C8	2.37	0.59
16:LO:25[A]:LYS:NZ	44:1:1178:G:OP2	2.29	0.59
27:LZ:57:HIS:HB3	27:LZ:61:LYS:HB2	1.84	0.59
44:1:656:A:H2'	44:1:657:A:C8	2.37	0.59
44:1:1277:C:O2'	44:1:1278:A:O5'	2.20	0.59
19:LR:126:GLU:HG3	19:LR:132:PHE:HE2	1.67	0.59
43:Lp:29:LEU:HD12	43:Lp:69:TYR:HD2	1.66	0.59
44:1:348:A:N3	44:1:352:A:O2'	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:415:G:H2'	44:1:416:A:H8	1.66	0.59
44:1:493:U:H3'	44:1:494:G:H8	1.65	0.59
44:1:1563:C:H2'	44:1:1564:U:C6	2.37	0.59
3:LA:183:GLY:HA2	44:1:896:A:H5'	1.84	0.59
10:LH:184:LYS:NZ	44:1:3111:U:OP1	2.33	0.59
14:LM:83:LYS:NZ	44:1:560:G:OP1	2.34	0.59
31:Ld:13:THR:OG1	31:Ld:72:ARG:NH1	2.34	0.59
44:1:3295:A:H2'	44:1:3296:A:C8	2.37	0.59
46:B:537:ASP:HA	46:B:540:MET:HE3	1.83	0.59
13:LL:100:ARG:NH1	44:1:76:G:O2'	2.29	0.59
32:Le:18:LYS:NZ	32:Le:30:GLU:OE1	2.36	0.59
33:Lf:21:ARG:O	44:1:633:C:O2'	2.19	0.59
44:1:346:C:N4	44:1:349:A:OP2	2.31	0.59
45:A:11:ASP:HA	45:A:14:LYS:HE2	1.85	0.59
2:C3:75:G:OP2	26:LY:74:TYR:OH	2.19	0.59
30:Lc:43:ILE:HB	30:Lc:90:VAL:HG22	1.84	0.59
40:Lm:114:LYS:O	44:1:1299:U:O2'	2.21	0.59
44:1:3182:G:H2'	44:1:3183:A:C8	2.38	0.59
44:1:3231:U:H2'	44:1:3232:G:H8	1.68	0.59
4:LB:219:ALA:HB2	4:LB:336:VAL:HG23	1.85	0.59
44:1:501:A:H2'	44:1:502:U:C6	2.37	0.59
44:1:656:A:H2'	44:1:657:A:H8	1.66	0.59
44:1:1336:U:H2'	44:1:1337:A:H8	1.66	0.59
44:1:3016:A:H2'	44:1:3017:A:C8	2.37	0.59
44:1:3165:A:H2'	44:1:3166:C:C6	2.37	0.59
5:LC:226:GLU:OE2	5:LC:246:ARG:NH1	2.35	0.59
26:LY:86:THR:HG22	26:LY:96:PRO:HA	1.85	0.59
32:Le:98:HIS:O	32:Le:125:ARG:NH1	2.36	0.59
44:1:542:G:O6	44:1:550:A:N6	2.36	0.59
44:1:2218:G:H2'	44:1:2219:A:H8	1.66	0.59
39:Ll:10:LYS:O	39:Ll:13:MET:HB2	2.02	0.59
44:1:664:U:H2'	44:1:665:A:H8	1.68	0.59
44:1:1229:G:H2'	44:1:1230:G:C8	2.38	0.59
44:1:3166:C:H2'	44:1:3167:A:H8	1.67	0.59
34:Lg:87:GLU:OE1	34:Lg:91:ARG:NH1	2.35	0.58
38:Lk:12:LEU:O	38:Lk:15:THR:OG1	2.20	0.58
44:1:1003:A:N1	44:1:1049:C:O2'	2.35	0.58
44:1:1244:A:N6	44:1:1271:A:OP1	2.36	0.58
44:1:2085:U:H2'	44:1:2086:A:C8	2.38	0.58
6:LD:278:SER:OG	6:LD:280:GLU:OE1	2.20	0.58
45:A:19:ASN:ND2	45:A:26:ASN:OD1	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:769:LEU:HD23	46:B:772:LEU:HD12	1.83	0.58
44:1:3267:A:OP1	44:1:3268:A:N6	2.36	0.58
11:LI:4:ARG:NH1	44:1:1128:U:OP1	2.32	0.58
21:LT:49:GLN:HA	21:LT:52:MET:HE2	1.86	0.58
44:1:835:G:O2'	44:1:857:G:N2	2.33	0.58
16:LO:61[A]:ALA:HA	16:LO:70[A]:PRO:HD2	1.85	0.58
44:1:3322:A:H2'	44:1:3323:A:C8	2.39	0.58
46:B:423:LEU:HD11	46:B:768:LEU:HD11	1.86	0.58
2:C3:9:A:H2'	2:C3:10:A:C8	2.38	0.58
16:LO:68[A]:ARG:NH1	44:1:2988:C:OP1	2.36	0.58
19:LR:5:ARG:NH1	44:1:1471:U:OP1	2.37	0.58
35:Lh:27:GLU:HA	35:Lh:30:GLU:HG2	1.86	0.58
44:1:26:A:N3	44:1:328:U:O2'	2.34	0.58
44:1:417:A:H2'	44:1:418:A:C8	2.38	0.58
13:LL:16:LYS:HG2	44:1:47:C:H5''	1.84	0.58
3:LA:220:GLY:O	44:1:2245:C:O2'	2.21	0.58
8:LF:88:ARG:NH2	8:LF:91:GLY:O	2.33	0.58
13:LL:43:ALA:HB2	13:LL:51:LEU:HD11	1.86	0.58
24:LW:4:GLU:HB2	24:LW:13:ILE:HB	1.84	0.58
33:Lf:19:SER:OG	44:1:1330:A:OP1	2.18	0.58
44:1:2429:G:H2'	44:1:2430:A:C8	2.39	0.58
45:A:134:TYR:CG	45:A:169:LYS:HB2	2.39	0.58
11:LI:38:LYS:HD2	11:LI:83:ASP:HB2	1.85	0.58
23:LV:30:GLY:HA3	23:LV:66:LYS:HE2	1.84	0.58
33:Lf:59:VAL:HG13	33:Lf:60:ARG:H	1.69	0.58
44:1:567:G:H2'	44:1:568:G:C8	2.39	0.58
44:1:1460:A:H2'	44:1:1461:A:H8	1.69	0.58
3:LA:204:MET:HE2	44:1:914:A:N1	2.19	0.58
6:LD:178:ASN:HA	6:LD:183:TRP:CD2	2.38	0.58
27:LZ:17:ARG:NH1	44:1:1634:G:N7	2.51	0.58
44:1:2351:U:H2'	44:1:2352:A:H8	1.68	0.57
46:B:193:GLN:HA	46:B:196:ILE:HD12	1.86	0.57
5:LC:311:HIS:O	5:LC:311:HIS:ND1	2.36	0.57
44:1:531:G:H2'	44:1:532:A:C8	2.38	0.57
44:1:1390:A:N6	44:1:1418:A:O2'	2.37	0.57
44:1:1404:G:N2	44:1:1407:A:OP2	2.33	0.57
44:1:1807:G:O2'	44:1:2559:U:O4	2.22	0.57
10:LH:26:LYS:HA	10:LH:35:THR:HG22	1.86	0.57
19:LR:110:ARG:NH1	44:1:1719:G:OP1	2.37	0.57
44:1:1966:U:O2	44:1:2057:G:N2	2.37	0.57
45:A:36:MET:HB2	46:B:528:LYS:HG3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LR:62:ARG:HH22	44:1:3067:C:H3'	1.68	0.57
44:1:2116:G:OP1	44:1:2118:C:N4	2.37	0.57
44:1:2357:A:H2'	44:1:2358:A:C8	2.39	0.57
44:1:2883:U:H2'	44:1:2884:C:C6	2.39	0.57
2:C3:142:C:H2'	2:C3:143:U:C6	2.39	0.57
20:LS:75:PHE:HA	20:LS:128:GLU:HA	1.87	0.57
23:LV:63:LYS:O	23:LV:70:ARG:NH1	2.36	0.57
44:1:2447:A:N1	44:1:2500:A:N6	2.52	0.57
46:B:496:SER:O	46:B:500:HIS:ND1	2.36	0.57
20:LS:166:LYS:NZ	20:LS:167:ARG:O	2.37	0.57
44:1:1279:C:H2'	44:1:1280:C:C6	2.39	0.57
44:1:3252:G:H2'	44:1:3253:G:C8	2.39	0.57
15:LN:147:ARG:NE	44:1:113:C:OP1	2.38	0.57
27:LZ:22:LYS:N	27:LZ:49:TYR:OH	2.32	0.57
28:La:59:ARG:NH1	44:1:283:G:O2'	2.31	0.57
44:1:563:U:H2'	44:1:564:G:H8	1.68	0.57
44:1:1776:G:H2'	44:1:1777:U:C6	2.40	0.57
44:1:2046:U:H2'	44:1:2047:A:N3	2.19	0.57
44:1:2413:A:H2'	44:1:2414:G:H8	1.69	0.57
44:1:2945:G:O2'	44:1:2948:C:OP2	2.19	0.57
46:B:44:TYR:OH	46:B:87:GLU:OE1	2.17	0.57
34:Lg:6:THR:HG22	44:1:1486:G:H21	1.70	0.57
42:Lo:61:LYS:NZ	42:Lo:63:LYS:O	2.37	0.57
46:B:294:ASP:OD2	46:B:299:ARG:NH2	2.37	0.57
17:LP:60:PHE:HB3	17:LP:64:ASN:HB3	1.87	0.57
24:LW:16:GLY:O	44:1:3050:U:O2'	2.23	0.57
44:1:631:U:H2'	44:1:632:G:H8	1.69	0.57
7:LE:52:VAL:HG23	7:LE:67:GLY:HA2	1.87	0.56
8:LF:106:LEU:HD21	8:LF:126:LEU:HD23	1.86	0.56
44:1:1132:C:H2'	44:1:1133:A:H8	1.70	0.56
44:1:1203:A:H2'	44:1:1204:A:C8	2.40	0.56
44:1:1261:G:O2'	44:1:1278:A:N1	2.30	0.56
2:C3:103:G:OP2	2:C3:105:A:O2'	2.22	0.56
12:LJ:31:THR:HG22	12:LJ:35:LYS:HZ3	1.69	0.56
17:LP:138:LYS:NZ	17:LP:140:GLU:OE2	2.29	0.56
18:LQ:125:ASP:OD1	18:LQ:126:GLN:N	2.37	0.56
30:Lc:74:ASN:HB3	30:Lc:86:ARG:HB2	1.86	0.56
39:Ll:37:TYR:O	44:1:351:A:N6	2.35	0.56
44:1:243:G:H2'	44:1:244:G:H8	1.70	0.56
44:1:1014:U:H3	44:1:1036:A:H61	1.51	0.56
44:1:1657:C:N4	44:1:1798:A:OP2	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:2103:U:H2'	44:1:2104:A:H8	1.69	0.56
44:1:2222:A:H2'	44:1:2223:A:C8	2.41	0.56
44:1:2611:U:H2'	44:1:2612:U:C6	2.40	0.56
44:1:2768:U:H2'	44:1:2769:A:H8	1.69	0.56
44:1:3344:A:N6	44:1:3361:G:O2'	2.37	0.56
45:A:7:PHE:HD2	45:A:45:LYS:HB3	1.69	0.56
20:LS:81:TYR:CE1	20:LS:90:MET:HE3	2.41	0.56
44:1:1194:G:H2'	44:1:1195:A:C8	2.39	0.56
44:1:1569:U:H5''	44:1:1570:U:C6	2.41	0.56
6:LD:184:ASP:OD2	6:LD:187:THR:OG1	2.20	0.56
44:1:1717:U:H2'	44:1:1718:G:H8	1.70	0.56
44:1:2344:U:H2'	44:1:2345:A:C8	2.40	0.56
44:1:2930:A:H2'	44:1:2931:C:C6	2.41	0.56
44:1:3203:U:H2'	44:1:3204:C:C6	2.40	0.56
1:C4:4:U:H2'	1:C4:5:G:C8	2.40	0.56
4:LB:266:ARG:NH2	44:1:2392:C:O2'	2.39	0.56
13:LL:131:LYS:NZ	13:LL:133:PRO:HB3	2.20	0.56
44:1:1581:C:C4	44:1:1582:C:H1'	2.41	0.56
4:LB:29:VAL:HG22	4:LB:218:ILE:HD13	1.87	0.56
14:LM:12:TRP:HB2	20:LS:172:TYR:C	2.31	0.56
44:1:3318:G:O2'	44:1:3320:A:OP2	2.24	0.56
2:C3:9:A:H2'	2:C3:10:A:H8	1.71	0.56
2:C3:143:U:OP1	15:LN:38:ARG:NH2	2.32	0.56
4:LB:47:LEU:HD12	4:LB:335:ILE:HD11	1.87	0.56
8:LF:62:ILE:HD11	8:LF:78:GLU:OE1	2.05	0.56
8:LF:94:LYS:NZ	44:1:1156:C:OP2	2.38	0.56
14:LM:37:GLU:HG2	20:LS:72:VAL:HG21	1.87	0.56
44:1:806:A:N3	44:1:2812:C:O2'	2.39	0.56
44:1:900:G:H1'	44:1:1589:A:N6	2.21	0.56
44:1:2579:G:H3'	44:1:2580:A:H8	1.69	0.56
44:1:2683:U:H2'	44:1:2684:C:H6	1.71	0.56
3:LA:40:TYR:HA	3:LA:91:GLY:HA3	1.88	0.56
5:LC:293:SER:HA	5:LC:296:GLN:CB	2.35	0.56
8:LF:88:ARG:HA	8:LF:134:VAL:HG12	1.88	0.56
11:LI:170:LYS:HA	11:LI:177:ASP:HA	1.88	0.56
18:LQ:67:ILE:HD12	18:LQ:81:VAL:HG11	1.88	0.56
42:Lo:42:ARG:NH1	44:1:91:G:OP2	2.39	0.56
43:Lp:46:THR:OG1	43:Lp:57:CYS:SG	2.64	0.56
44:1:490:C:H2'	44:1:492:C:H41	1.70	0.56
6:LD:34:LYS:HA	21:LT:27:LEU:HD11	1.86	0.56
25:LX:63:ILE:HG22	25:LX:86:VAL:HG12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:681:U:O2	44:1:696:C:N4	2.32	0.56
44:1:1621:A:H2'	44:1:1622:U:H6	1.71	0.56
44:1:2154:U:H2'	44:1:2155:G:H8	1.71	0.56
44:1:3164:C:O2'	44:1:3165:A:H8	1.88	0.56
4:LB:37:ARG:HG3	4:LB:186:GLY:HA2	1.88	0.55
7:LE:8:LYS:HZ2	44:1:1354:G:H5'	1.71	0.55
14:LM:19:ARG:HG2	14:LM:65:LEU:HD22	1.88	0.55
17:LP:173:ARG:NH2	44:1:618:C:OP1	2.39	0.55
27:LZ:71:PHE:HA	27:LZ:111:LYS:HE2	1.87	0.55
27:LZ:81:LEU:HD11	34:Lg:90:ILE:HG12	1.88	0.55
32:Le:47:ARG:NH1	44:1:634:C:O2'	2.39	0.55
46:B:514:PRO:HA	46:B:517:ILE:HD12	1.87	0.55
46:B:698:GLN:HB3	46:B:701:MET:HB2	1.89	0.55
16:LO:148[A]:LYS:NZ	44:1:3006:A:OP2	2.35	0.55
21:LT:80:VAL:HB	21:LT:85:LEU:HD23	1.88	0.55
38:Lk:28:ASN:HB2	38:Lk:40:GLN:HB3	1.86	0.55
44:1:158:G:H2'	44:1:159:A:H8	1.70	0.55
44:1:449:U:O2'	44:1:450:G:N2	2.40	0.55
44:1:768:C:N4	44:1:769:G:O6	2.40	0.55
44:1:966:U:H2'	44:1:967:A:C8	2.42	0.55
46:B:124:TYR:HA	46:B:127:MET:HE2	1.87	0.55
5:LC:296:GLN:HA	5:LC:296:GLN:NE2	2.22	0.55
44:1:1110:U:H2'	44:1:1111:U:C6	2.42	0.55
44:1:2676:A:H5'	44:1:2677:G:C8	2.41	0.55
44:1:2875:U:C4	47:8:23:UNK:HA	2.40	0.55
1:C4:1:G:O3'	6:LD:273:ARG:NH1	2.38	0.55
4:LB:20:LYS:NZ	4:LB:21:ARG:O	2.39	0.55
17:LP:122:ALA:HB3	17:LP:143:PRO:HB2	1.88	0.55
44:1:1909:A:H2'	44:1:1910:A:C8	2.41	0.55
2:C3:150:G:H21	9:LG:59:GLN:HE22	1.54	0.55
4:LB:221:THR:O	4:LB:334:ARG:NH1	2.40	0.55
8:LF:44:ILE:HD12	8:LF:180:SER:HB3	1.89	0.55
19:LR:150:GLN:HA	19:LR:153:LYS:NZ	2.21	0.55
44:1:1778:G:O2'	44:1:1780:G:OP2	2.25	0.55
45:A:6:PRO:HB3	46:B:231:TYR:HE1	1.72	0.55
1:C4:119:U:O5'	6:LD:258:LYS:NZ	2.39	0.55
14:LM:47:ASP:HB2	14:LM:55:ARG:HG3	1.89	0.55
29:Lb:19:ASN:ND2	44:1:969:C:OP1	2.35	0.55
44:1:307:A:H2'	44:1:308:A:C8	2.41	0.55
44:1:2656:A:C8	44:1:2658:G:C8	2.95	0.55
46:B:557:ARG:NH1	46:B:715:THR:OG1	2.33	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LB:282:ILE:HD13	4:LB:322:ILE:HG23	1.88	0.55
5:LC:3:ARG:HB3	5:LC:22:LEU:HB2	1.88	0.55
5:LC:293:SER:HA	5:LC:296:GLN:HB2	1.88	0.55
8:LF:80:GLN:OE1	21:LT:136:ARG:N	2.32	0.55
44:1:1622:U:H2'	44:1:1623:G:H8	1.72	0.55
44:1:3334:U:H4'	44:1:3335:A:H5'	1.88	0.55
44:1:3358:U:H2'	44:1:3359:A:C8	2.42	0.55
12:LJ:53:THR:HG23	12:LJ:61:ARG:HG3	1.87	0.55
12:LJ:150:ASN:HA	12:LJ:153:LYS:HD2	1.89	0.55
15:LN:46:ASP:OD1	15:LN:47:LYS:N	2.38	0.55
4:LB:206:ASP:OD2	4:LB:287:LYS:NZ	2.28	0.55
5:LC:296:GLN:HA	5:LC:296:GLN:HE21	1.72	0.55
29:Lb:33:LYS:NZ	44:1:2721:A:O3'	2.31	0.55
44:1:428:A:H2'	44:1:429:U:C6	2.42	0.55
44:1:1615:C:H2'	44:1:1616:U:C6	2.42	0.55
5:LC:11:LEU:HD21	5:LC:156:LEU:HB2	1.88	0.55
11:LI:192:ASP:HA	11:LI:197:VAL:HA	1.89	0.55
13:LL:75:PHE:H	13:LL:97:VAL:HA	1.72	0.55
19:LR:150:GLN:NE2	19:LR:151:ARG:HG3	2.22	0.55
26:LY:51:ARG:HG2	26:LY:52:ARG:H	1.70	0.55
33:Lf:37:THR:OG1	33:Lf:39:GLN:OE1	2.24	0.55
39:LI:23:LEU:HD12	39:LI:24:PRO:HD2	1.87	0.55
44:1:411:U:H2'	44:1:412:G:C8	2.41	0.55
44:1:1883:A:H2'	44:1:1884:A:H8	1.72	0.55
44:1:2193:U:H5'	44:1:2194:G:H5'	1.89	0.55
1:C4:19:C:H2'	1:C4:20:A:H8	1.71	0.54
8:LF:142:SER:O	8:LF:146:GLN:HG2	2.06	0.54
12:LJ:32:ARG:NH2	12:LJ:121:GLY:HA3	2.22	0.54
14:LM:35:ILE:HA	14:LM:46:ILE:HG22	1.90	0.54
28:La:114:GLY:O	28:La:137:LYS:NZ	2.36	0.54
34:Lg:79:SER:OG	34:Lg:80:ARG:NH1	2.39	0.54
44:1:2086:A:O2'	44:1:2087:C:OP1	2.24	0.54
44:1:3298:C:C2	44:1:3299:A:C8	2.95	0.54
46:B:95:LEU:HD13	46:B:126:GLN:HG3	1.90	0.54
2:C3:67:U:H2'	2:C3:68:G:H8	1.73	0.54
17:LP:56:ARG:NH2	17:LP:75:GLU:OE2	2.40	0.54
28:La:76:ASP:N	28:La:76:ASP:OD1	2.40	0.54
34:Lg:46:ASP:OD2	34:Lg:88:ARG:NH2	2.40	0.54
44:1:200:C:H41	44:1:217:U:H2'	1.71	0.54
46:B:585:PHE:HD2	46:B:615:GLU:HG3	1.72	0.54
15:LN:179:LYS:O	44:1:286:U:O2'	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Lc:55:GLU:HB3	34:Lg:94:LEU:HD11	1.90	0.54
44:1:1447:G:O2'	44:1:2355:G:O6	2.26	0.54
44:1:1596:C:H2'	44:1:1597:C:C6	2.42	0.54
44:1:2090:U:H2'	44:1:2091:U:C6	2.43	0.54
44:1:3183:A:H2'	44:1:3184:A:C8	2.43	0.54
44:1:3228:C:H4'	44:1:3229:G:O5'	2.07	0.54
45:A:90:ILE:HG13	45:A:92:LEU:HD23	1.89	0.54
46:B:517:ILE:HA	46:B:532:MET:HE1	1.89	0.54
4:LB:315:GLY:HA2	44:1:3379:C:H4'	1.89	0.54
6:LD:139:PRO:O	44:1:1079:A:O2'	2.20	0.54
8:LF:48:ASN:ND2	8:LF:182:ASP:OD2	2.39	0.54
20:LS:24:LEU:HD11	21:LT:141:VAL:HG11	1.89	0.54
31:Ld:7:VAL:HG22	31:Ld:77:ARG:C	2.27	0.54
32:Le:34:LYS:NZ	32:Le:52:GLN:OE1	2.40	0.54
44:1:414:U:H2'	44:1:415:G:H8	1.73	0.54
44:1:440:A:N7	44:1:441:U:O2'	2.38	0.54
44:1:542:G:C6	44:1:550:A:N1	2.76	0.54
44:1:1799:A:H2'	44:1:1800:A:C8	2.42	0.54
44:1:2106:A:H2'	44:1:2107:A:C8	2.43	0.54
46:B:202:LEU:HB3	46:B:212:ILE:HG23	1.90	0.54
46:B:644:LEU:HD12	46:B:647:LEU:HD12	1.89	0.54
44:1:494:G:H1	44:1:619:A:H2	1.55	0.54
2:C3:26:U:H3	44:1:337:G:H1	1.53	0.54
9:LG:160:ILE:O	9:LG:164:VAL:HG13	2.08	0.54
10:LH:36:LYS:HG2	10:LH:78:MET:CE	2.37	0.54
15:LN:143:ARG:HB3	35:Lh:96:GLU:OE2	2.08	0.54
44:1:129:U:H2'	44:1:130:A:C8	2.43	0.54
44:1:1798:A:H2'	44:1:1799:A:C8	2.42	0.54
44:1:1956:A:H2'	44:1:1957:G:C8	2.42	0.54
44:1:2103:U:H2'	44:1:2104:A:C8	2.42	0.54
1:C4:21:G:H4'	6:LD:272:TYR:OH	2.08	0.54
4:LB:95:THR:OG1	4:LB:98:GLY:O	2.22	0.54
6:LD:95:TRP:HZ3	6:LD:199:ILE:HD13	1.72	0.54
12:LJ:26:SER:OG	12:LJ:27:GLY:N	2.41	0.54
17:LP:128:ARG:HH22	47:8:7:UNK:CB	2.21	0.54
46:B:149:TYR:HB2	46:B:186:LEU:HD11	1.89	0.54
46:B:299:ARG:NH1	46:B:320:TYR:O	2.40	0.54
4:LB:95:THR:HG22	44:1:3243:A:H4'	1.90	0.54
9:LG:78:PHE:C	9:LG:80:TYR:H	2.16	0.54
14:LM:40:ASP:OD1	14:LM:41:GLN:N	2.34	0.54
35:Lh:30:GLU:HA	35:Lh:33:VAL:HG12	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Lp:17:ARG:HG3	43:Lp:18:TYR:CE2	2.43	0.54
44:1:2933:A:C2	44:1:3014:U:H4'	2.43	0.54
5:LC:45:ASN:ND2	44:1:693:A:OP1	2.40	0.54
44:1:3348:G:H1	44:1:3357:U:H3	1.56	0.54
46:B:719:LEU:HD22	46:B:722:ILE:HG12	1.90	0.54
5:LC:126:ILE:O	5:LC:129:THR:OG1	2.21	0.54
6:LD:35:ARG:HG2	44:1:2749:G:O2'	2.08	0.54
7:LE:52:VAL:HG22	7:LE:53:VAL:H	1.73	0.54
12:LJ:115:LYS:HD2	12:LJ:116:TYR:N	2.22	0.54
36:Li:36:ARG:NH1	44:1:265:A:O2'	2.40	0.54
40:Lm:87:SER:HB2	40:Lm:91:CYS:HB3	1.88	0.54
44:1:1039:U:H2'	44:1:1040:A:C8	2.42	0.54
44:1:1362:G:H2'	44:1:1363:A:C8	2.43	0.54
44:1:1920:U:O2'	44:1:1932:A:N7	2.38	0.54
44:1:2615:G:H2'	44:1:2616:C:C6	2.43	0.54
46:B:586:SER:OG	46:B:588:ASN:OD1	2.22	0.54
4:LB:266:ARG:HH21	44:1:2392:C:H1'	1.72	0.53
44:1:259:C:N4	44:1:260:C:N4	2.56	0.53
44:1:1279:C:H2'	44:1:1280:C:H6	1.73	0.53
44:1:3317:U:H6	46:B:729:LYS:HZ3	1.56	0.53
2:C3:30:C:H2'	2:C3:31:G:H8	1.72	0.53
5:LC:266:THR:HG23	5:LC:267:VAL:HG13	1.90	0.53
13:LL:56:PRO:HG3	13:LL:74:GLY:O	2.08	0.53
14:LM:10:SER:HB3	14:LM:12:TRP:HZ3	1.72	0.53
17:LP:4:TYR:OH	44:1:389:A:OP1	2.20	0.53
39:Li:28:ARG:HH21	39:Li:36:ARG:HH12	1.57	0.53
44:1:595:G:H1	44:1:609:G:H5''	1.73	0.53
44:1:1119:C:H2'	44:1:1120:A:C8	2.41	0.53
44:1:2618:G:O2'	44:1:2865:U:OP1	2.23	0.53
44:1:3006:A:H2'	44:1:3007:U:O4'	2.08	0.53
45:A:95:LYS:HZ1	46:B:295:SER:HB2	1.72	0.53
6:LD:294:ALA:HB1	11:LI:217:PHE:HB3	1.90	0.53
18:LQ:19:PRO:HB3	18:LQ:53:PHE:HA	1.89	0.53
18:LQ:133:LYS:HB2	18:LQ:135:GLN:OE1	2.08	0.53
44:1:708:G:N2	44:1:711:A:OP2	2.39	0.53
11:LI:21:ARG:NH2	11:LI:22:TYR:OH	2.40	0.53
11:LI:47:PRO:HD2	11:LI:141:LYS:HA	1.91	0.53
18:LQ:38:ARG:NE	44:1:1347:U:OP2	2.35	0.53
44:1:661:G:OP2	44:1:661:G:N2	2.30	0.53
44:1:1619:A:H2	44:1:1826:C:C2	2.26	0.53
2:C3:114:G:OP1	44:1:1831:U:O2'	2.20	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:616:G:H2'	44:1:617:G:C8	2.44	0.53
44:1:1564:U:C2	44:1:1565:G:C8	2.96	0.53
44:1:1597:C:H2'	44:1:1598:G:C8	2.44	0.53
44:1:2004:U:O2	44:1:2017:G:N2	2.41	0.53
46:B:196:ILE:HD13	46:B:231:TYR:HD2	1.72	0.53
5:LC:119:ARG:NH2	44:1:696:C:OP2	2.37	0.53
20:LS:154:HIS:ND1	44:1:3186:A:OP1	2.39	0.53
40:Lm:104:PRO:HG2	44:1:3119:U:H4'	1.91	0.53
44:1:196:G:N1	44:1:199:A:OP2	2.41	0.53
44:1:221:A:O2'	44:1:223:U:OP2	2.23	0.53
44:1:1340:G:H2'	44:1:1341:U:C6	2.44	0.53
44:1:3116:G:OP1	44:1:3116:G:N2	2.40	0.53
8:LF:206:LYS:NZ	44:1:1334:U:OP1	2.36	0.53
33:Lf:14:LEU:HD11	33:Lf:31:LYS:HB2	1.91	0.53
4:LB:130:PHE:O	4:LB:134:SER:OG	2.26	0.53
44:1:631:U:H2'	44:1:632:G:C8	2.43	0.53
44:1:1109:U:H2'	44:1:1110:U:C6	2.43	0.53
44:1:1355:A:H4'	44:1:1356:U:O5'	2.09	0.53
44:1:2985:C:H2'	44:1:2986:U:C6	2.44	0.53
44:1:3138:U:H2'	44:1:3139:A:H8	1.72	0.53
44:1:3201:C:H2'	44:1:3202:G:H8	1.74	0.53
3:LA:201:GLY:O	3:LA:204:MET:HB2	2.09	0.53
5:LC:207:VAL:HB	5:LC:227:THR:HG22	1.89	0.53
44:1:1108:U:H2'	44:1:1109:U:C6	2.44	0.53
44:1:2684:C:H2'	44:1:2685:C:H6	1.74	0.53
44:1:3258:U:O2'	44:1:3260:G:OP1	2.24	0.53
45:A:17:ASN:ND2	45:A:59:ILE:O	2.42	0.53
1:C4:71:G:H2'	1:C4:72:A:C8	2.44	0.53
33:Lf:59:VAL:HG13	33:Lf:60:ARG:N	2.23	0.53
44:1:269:G:H22	44:1:294:U:H2'	1.74	0.53
44:1:415:G:H2'	44:1:416:A:C8	2.43	0.53
44:1:1460:A:H2'	44:1:1461:A:C8	2.44	0.53
44:1:3107:U:H2'	44:1:3108:G:C8	2.44	0.53
6:LD:129:TYR:OH	6:LD:175:HIS:O	2.22	0.52
44:1:259:C:C4	44:1:260:C:N4	2.78	0.52
44:1:551:A:O2'	44:1:552:G:H8	1.92	0.52
44:1:1222:G:N2	44:1:1285:G:O2'	2.35	0.52
44:1:1662:G:H22	44:1:1787:A:H2	1.57	0.52
44:1:2040:U:H2'	44:1:2041:U:C6	2.43	0.52
44:1:3232:G:C6	44:1:3256:G:C6	2.97	0.52
1:C4:64:A:H5'	1:C4:65:G:H5''	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C3:149:A:H2'	2:C3:150:G:C8	2.44	0.52
9:LG:105:LYS:NZ	44:1:123:A:OP1	2.31	0.52
9:LG:143:ILE:HD11	9:LG:151:VAL:HG11	1.91	0.52
13:LL:25:HIS:HE2	15:LN:198:SER:HG	1.56	0.52
44:1:794:U:H2'	44:1:795:G:H8	1.75	0.52
44:1:1189:C:H42	44:1:1315:U:HO2'	1.55	0.52
44:1:1493:G:N2	44:1:1493:G:OP2	2.42	0.52
44:1:1571:A:H2'	44:1:1572:U:O4'	2.08	0.52
44:1:2426:U:H3	44:1:2603:G:H1	1.55	0.52
44:1:2430:A:H2'	44:1:2431:C:C6	2.45	0.52
44:1:2615:G:H2'	44:1:2616:C:H6	1.74	0.52
44:1:2812:C:H2'	44:1:2813:A:H8	1.74	0.52
46:B:202:LEU:HB2	46:B:216:ILE:HD11	1.91	0.52
2:C3:139:U:H2'	2:C3:140:G:H8	1.75	0.52
8:LF:165:ASP:OD1	8:LF:166:ASN:N	2.42	0.52
13:LL:45:LYS:HG3	13:LL:46:ILE:HG23	1.91	0.52
44:1:1240:A:N1	44:1:1244:A:H8	2.07	0.52
44:1:2747:A:H2'	44:1:2748:A:C8	2.45	0.52
2:C3:40:A:OP2	2:C3:103:G:N1	2.38	0.52
14:LM:124:ARG:NH2	44:1:3212:C:OP2	2.36	0.52
16:LO:194[A]:LEU:O	16:LO:199[A]:TYR:N	2.37	0.52
24:LW:45:ASN:HB3	24:LW:48:ARG:HG2	1.90	0.52
44:1:1616:U:H2'	44:1:1617:G:H8	1.74	0.52
44:1:1963:G:H2'	44:1:1964:C:H4'	1.91	0.52
44:1:3348:G:H2'	44:1:3349:C:C6	2.44	0.52
46:B:462:PHE:CZ	46:B:479:ILE:HB	2.44	0.52
1:C4:52:G:O2'	1:C4:53:U:OP1	2.26	0.52
2:C3:145:U:H2'	2:C3:146:U:C6	2.44	0.52
5:LC:360:LYS:NZ	44:1:519:A:N7	2.58	0.52
6:LD:60:ILE:HD11	6:LD:93:THR:HA	1.90	0.52
28:La:84:GLU:OE2	28:La:87:ARG:NH1	2.42	0.52
39:Ll:28:ARG:NH2	39:Ll:36:ARG:HH12	2.08	0.52
44:1:707:U:OP1	44:1:780:A:O2'	2.21	0.52
44:1:3110:C:H2'	44:1:3111:U:C6	2.45	0.52
46:B:457:ASP:OD1	46:B:458:ALA:N	2.42	0.52
46:B:724:ASP:HB2	46:B:727:ILE:HG12	1.91	0.52
5:LC:35:VAL:HG21	5:LC:244:LEU:HD21	1.90	0.52
8:LF:210:PRO:O	44:1:1167:U:O2'	2.25	0.52
10:LH:62:ARG:NH1	44:1:1210:U:OP1	2.43	0.52
44:1:760:G:N2	44:1:770:G:N3	2.58	0.52
44:1:3182:G:H2'	44:1:3183:A:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:157:LEU:HD21	46:B:201:VAL:HA	1.91	0.52
4:LB:212:ASN:O	4:LB:281:LYS:NZ	2.42	0.52
4:LB:250:ALA:HB1	44:1:2947:G:N3	2.24	0.52
4:LB:361:THR:H	4:LB:371:GLN:NE2	2.08	0.52
14:LM:113:THR:HG22	14:LM:116:GLU:CD	2.35	0.52
21:LT:18:ASP:HB2	21:LT:21:LYS:HB2	1.92	0.52
27:LZ:109:GLU:HA	27:LZ:112:LYS:HB2	1.90	0.52
40:Lm:97:ARG:NH1	40:Lm:121:LEU:O	2.43	0.52
44:1:640:U:H2'	44:1:641:C:C6	2.45	0.52
44:1:1733:G:H2'	44:1:1734:G:H8	1.75	0.52
44:1:3166:C:H2'	44:1:3167:A:C8	2.45	0.52
46:B:684:ASP:HB3	46:B:688:ARG:HH12	1.75	0.52
4:LB:250:ALA:HB3	44:1:2880:U:O2	2.10	0.52
8:LF:67:ARG:NH1	44:1:518:G:OP1	2.43	0.52
11:LI:66:GLU:OE1	11:LI:69:ARG:NH2	2.43	0.52
11:LI:190:VAL:HG13	11:LI:197:VAL:HG21	1.92	0.52
21:LT:41:ASP:HA	21:LT:61:THR:HA	1.91	0.52
27:LZ:54:THR:HG22	27:LZ:57:HIS:CE1	2.44	0.52
29:Lb:40:ARG:HH11	29:Lb:40:ARG:HG3	1.75	0.52
34:Lg:8:ARG:HB2	34:Lg:34:HIS:CE1	2.45	0.52
44:1:1229:G:H2'	44:1:1230:G:H8	1.75	0.52
44:1:1290:A:H2'	44:1:1291:A:C8	2.44	0.52
44:1:2102:U:H2'	44:1:2103:U:C6	2.45	0.52
44:1:3322:A:H2'	44:1:3323:A:H8	1.73	0.52
3:LA:84:THR:HG22	43:Lp:63:THR:H	1.75	0.52
5:LC:317:PRO:O	5:LC:318:LEU:HB2	2.10	0.52
10:LH:91:ARG:HD2	10:LH:143:GLU:HB3	1.92	0.52
44:1:1616:U:H2'	44:1:1617:G:C8	2.45	0.52
44:1:1713:G:O2'	44:1:1730:G:N2	2.42	0.52
44:1:2107:A:H2	44:1:3344:A:H8	1.56	0.52
44:1:2250:G:O6	44:1:2267:C:N4	2.42	0.52
3:LA:178:PRO:HB2	3:LA:180:LEU:HD12	1.91	0.52
6:LD:234:ASP:OD1	6:LD:235:SER:N	2.42	0.52
15:LN:190:THR:O	15:LN:194:GLN:HG3	2.10	0.52
16:LO:25[A]:LYS:NZ	44:1:1176:C:OP1	2.36	0.52
20:LS:90:MET:HE1	20:LS:114:HIS:CD2	2.45	0.52
30:Lc:40:LYS:NZ	30:Lc:93:LEU:O	2.43	0.52
44:1:1225:A:H3'	44:1:1226:G:H8	1.75	0.52
1:C4:14:U:H5'	6:LD:24:ARG:NH1	2.24	0.51
14:LM:77:ARG:NH2	44:1:524:U:OP1	2.38	0.51
41:Ln:16:LYS:HZ2	41:Ln:17:ARG:HH11	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:299:ARG:HG2	46:B:320:TYR:CE2	2.45	0.51
2:C3:95:G:O2'	37:Lj:81:GLY:O	2.25	0.51
5:LC:98:ARG:NH2	44:1:804:C:OP1	2.42	0.51
10:LH:8:GLN:OE1	10:LH:69:ARG:HD3	2.11	0.51
16:LO:59[A]:ARG:NH2	44:1:1307:G:OP1	2.43	0.51
32:Le:47:ARG:HH12	44:1:634:C:H4'	1.75	0.51
42:Lo:80:ARG:HD3	44:1:2769:A:H5''	1.92	0.51
44:1:207:U:H2'	44:1:208:C:H6	1.75	0.51
44:1:632:G:H2'	44:1:633:C:C6	2.46	0.51
44:1:2446:U:O2'	44:1:2447:A:OP1	2.21	0.51
46:B:288:ILE:HG23	46:B:292:LEU:HD12	1.92	0.51
31:Ld:5:LYS:N	46:B:720:LYS:HE3	2.25	0.51
44:1:629:U:H2'	44:1:630:A:C8	2.45	0.51
44:1:1945:A:H2'	44:1:1946:A:C8	2.46	0.51
45:A:71:THR:OG1	45:A:72:THR:N	2.44	0.51
1:C4:19:C:H2'	1:C4:20:A:C8	2.46	0.51
2:C3:146:U:H2'	2:C3:147:U:C6	2.46	0.51
4:LB:215:ILE:HD12	4:LB:338:LEU:HD12	1.92	0.51
4:LB:250:ALA:HB1	44:1:2947:G:C2	2.46	0.51
20:LS:66:GLU:OE2	20:LS:99:ARG:N	2.39	0.51
26:LY:81:GLN:OE1	26:LY:96:PRO:HB2	2.10	0.51
44:1:1597:C:H5'	44:1:1696:A:H1'	1.91	0.51
44:1:1666:G:H2'	44:1:1667:A:H8	1.76	0.51
8:LF:116:PHE:O	8:LF:199:ASN:ND2	2.43	0.51
20:LS:26:ARG:NH1	21:LT:150:THR:OG1	2.44	0.51
42:Lo:73:GLU:OE1	42:Lo:80:ARG:HB3	2.09	0.51
43:Lp:17:ARG:HG3	43:Lp:18:TYR:CD2	2.45	0.51
44:1:787:G:H2'	44:1:788:C:H6	1.74	0.51
44:1:987:U:H2'	44:1:988:U:C6	2.45	0.51
44:1:2708:C:H2'	44:1:2709:C:H6	1.75	0.51
44:1:3371:G:H2'	44:1:3372:A:H8	1.76	0.51
1:C4:71:G:H2'	1:C4:72:A:H8	1.75	0.51
4:LB:76:VAL:HG12	4:LB:325:LYS:HA	1.92	0.51
5:LC:61:SER:OG	44:1:929:A:OP1	2.22	0.51
11:LI:146:ASP:OD1	11:LI:147:VAL:N	2.44	0.51
16:LO:87[A]:MET:SD	44:1:1174:G:N2	2.84	0.51
22:LU:87:ASN:HB2	22:LU:89:LEU:HD23	1.92	0.51
27:LZ:95:VAL:O	27:LZ:100:THR:OG1	2.25	0.51
44:1:1525:G:H5'	44:1:1830:G:OP2	2.11	0.51
44:1:1696:A:H2'	44:1:1697:A:C8	2.46	0.51
46:B:369:GLU:OE2	46:B:370:LEU:HG	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LC:99:MET:SD	5:LC:102:PRO:HA	2.51	0.51
8:LF:138:TYR:HE2	8:LF:233:GLU:HB2	1.76	0.51
11:LI:13:LYS:NZ	44:1:1129:A:OP1	2.40	0.51
15:LN:170:LYS:NZ	44:1:288:C:OP1	2.37	0.51
21:LT:99:SER:OG	21:LT:101:CYS:SG	2.64	0.51
25:LX:111:ASN:HB2	25:LX:123:TYR:HB2	1.92	0.51
32:Le:23:ASP:OD2	44:1:424:G:O2'	2.28	0.51
44:1:248:U:H3'	44:1:249:U:H5''	1.92	0.51
44:1:296:A:H2'	44:1:297:G:C4	2.45	0.51
44:1:1290:A:H2'	44:1:1291:A:H8	1.75	0.51
44:1:2007:G:N2	44:1:2014:U:O2	2.32	0.51
44:1:2102:U:H2'	44:1:2103:U:H6	1.75	0.51
44:1:2218:G:H2'	44:1:2219:A:C8	2.45	0.51
44:1:3319:U:O2'	44:1:3320:A:OP1	2.27	0.51
8:LF:24:GLU:OE1	8:LF:27:ALA:N	2.40	0.51
13:LL:12:ASN:ND2	44:1:797:U:O2	2.44	0.51
15:LN:85:THR:OG1	44:1:44:U:OP1	2.23	0.51
22:LU:32:SER:HG	22:LU:83:TYR:HH	1.58	0.51
23:LV:94:TYR:OH	24:LW:41:LYS:NZ	2.31	0.51
33:Lf:72:THR:HG22	44:1:585:A:H4'	1.92	0.51
44:1:746:A:H2'	44:1:747:A:H8	1.75	0.51
44:1:1597:C:H2'	44:1:1598:G:H8	1.75	0.51
44:1:1896:A:H61	44:1:2339:C:N4	2.09	0.51
44:1:3184:A:N3	44:1:3187:A:O2'	2.36	0.51
45:A:18:VAL:HG22	45:A:84:ALA:HB2	1.91	0.51
10:LH:73:SER:OG	44:1:3113:A:OP1	2.27	0.51
18:LQ:5:HIS:ND1	18:LQ:9:GLN:OE1	2.43	0.51
23:LV:34:LEU:HD21	23:LV:102:ILE:HD11	1.93	0.51
33:Lf:37:THR:HG23	33:Lf:40:ASP:H	1.75	0.51
44:1:275:U:H2'	44:1:276:U:C6	2.46	0.51
44:1:952:A:H4'	44:1:968:G:H21	1.76	0.51
44:1:1234:G:H1	44:1:1254:C:H42	1.59	0.51
44:1:2829:U:C2	44:1:2830:G:C8	2.98	0.51
44:1:2843:U:OP2	44:1:2844:C:N4	2.39	0.51
44:1:3231:U:H2'	44:1:3232:G:C8	2.45	0.51
46:B:306:ASP:O	46:B:310:THR:OG1	2.28	0.51
3:LA:242:ARG:NH2	3:LA:243:THR:O	2.44	0.51
4:LB:77:THR:HG21	4:LB:328:ILE:HG12	1.93	0.51
10:LH:173:ARG:NH1	40:Lm:125:LYS:O	2.44	0.51
23:LV:57:MET:HE3	23:LV:126:TRP:CH2	2.45	0.51
39:LI:13:MET:SD	44:1:1493:G:O2'	2.67	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Lp:68:ALA:C	43:Lp:69:TYR:HD1	2.19	0.51
44:1:394:G:N1	44:1:397:A:OP2	2.43	0.51
44:1:542:G:N2	44:1:549:U:O2	2.44	0.51
44:1:760:G:N2	44:1:770:G:O2'	2.44	0.51
44:1:911:C:H2'	44:1:912:G:C8	2.46	0.51
44:1:2057:G:N2	44:1:2058:G:O6	2.39	0.51
44:1:2961:G:H2'	44:1:2962:U:C6	2.46	0.51
44:1:3190:C:H2'	44:1:3191:G:H8	1.77	0.51
45:A:136:VAL:HG22	45:A:167:MET:SD	2.50	0.51
46:B:265:GLU:O	46:B:269:ASN:ND2	2.42	0.51
46:B:753:LEU:HD21	46:B:782:ILE:HD11	1.92	0.51
2:C3:8:C:H2'	2:C3:9:A:C8	2.46	0.50
17:LP:67:ILE:HD11	17:LP:80:LYS:HB3	1.93	0.50
22:LU:72:SER:OG	44:1:1675:G:OP1	2.28	0.50
22:LU:97:SER:HA	22:LU:103:TYR:HA	1.94	0.50
23:LV:23:MET:O	23:LV:34:LEU:N	2.42	0.50
35:Lh:79:ASP:N	35:Lh:79:ASP:OD1	2.44	0.50
44:1:945:C:H2'	44:1:946:U:C6	2.47	0.50
44:1:1188:U:OP1	44:1:1210:U:O2'	2.21	0.50
44:1:1590:G:C2	44:1:1591:G:C8	2.99	0.50
44:1:2295:A:N3	44:1:2929:C:O2'	2.37	0.50
46:B:739:ARG:NH2	46:B:796:LEU:OXT	2.44	0.50
6:LD:23:ARG:HD2	6:LD:23:ARG:O	2.11	0.50
11:LI:7:ARG:NH2	44:1:2828:G:OP2	2.45	0.50
15:LN:68:ARG:NH2	44:1:292:U:OP2	2.33	0.50
18:LQ:67:ILE:HD13	18:LQ:140:LEU:HD12	1.94	0.50
44:1:616:G:H2'	44:1:617:G:H8	1.75	0.50
44:1:671:U:H2'	44:1:672:A:C8	2.44	0.50
44:1:748:U:H2'	44:1:749:C:C6	2.46	0.50
44:1:1624:G:O2'	44:1:1643:A:N1	2.44	0.50
44:1:2837:A:H2'	44:1:2845:A:N1	2.26	0.50
44:1:3349:C:H2'	44:1:3350:C:C6	2.46	0.50
46:B:624:ARG:HB2	46:B:668:PHE:CE1	2.46	0.50
2:C3:4:C:H2'	2:C3:5:U:C6	2.47	0.50
2:C3:141:C:H2'	2:C3:142:C:H6	1.75	0.50
40:Lm:79:GLU:O	40:Lm:81:SER:N	2.45	0.50
46:B:36:LEU:HA	46:B:39:LYS:HD3	1.92	0.50
2:C3:28:C:O2'	44:1:691:A:N1	2.42	0.50
7:LE:173:MET:HE1	44:1:3209:A:H2	1.74	0.50
13:LL:131:LYS:HZ2	13:LL:133:PRO:HB3	1.74	0.50
44:1:8:C:H2'	44:1:9:U:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:543:C:O2'	44:1:544:C:O4'	2.23	0.50
44:1:999:G:H2'	44:1:1000:C:C6	2.47	0.50
44:1:2047:A:H2'	44:1:2048:G:H4'	1.92	0.50
44:1:3107:U:H2'	44:1:3108:G:H8	1.76	0.50
4:LB:308:MET:HE2	44:1:3329:U:H5''	1.94	0.50
5:LC:193:LYS:HZ3	44:1:1419:A:H5''	1.75	0.50
27:LZ:41:ALA:HB2	27:LZ:77:TYR:HE1	1.75	0.50
39:Ll:36:ARG:HA	39:Ll:36:ARG:HH11	1.77	0.50
44:1:1357:G:H2'	44:1:1358:C:C6	2.47	0.50
44:1:1650:G:H2'	44:1:1651:U:C6	2.46	0.50
44:1:2955:U:OP2	44:1:2977:G:N1	2.44	0.50
46:B:449:TYR:HB2	46:B:458:ALA:HB2	1.94	0.50
46:B:722:ILE:O	46:B:728:GLN:NE2	2.43	0.50
3:LA:101:VAL:O	3:LA:101:VAL:HG12	2.11	0.50
6:LD:68:THR:OG1	6:LD:71:GLY:O	2.20	0.50
7:LE:54:TYR:CE1	7:LE:63:LEU:HB3	2.47	0.50
19:LR:124:TYR:OH	44:1:1721:U:OP2	2.25	0.50
20:LS:5:LYS:NZ	20:LS:32:SER:O	2.45	0.50
30:Lc:52:ARG:NH1	44:1:1729:A:O4'	2.30	0.50
36:Li:84:LYS:O	36:Li:87:VAL:HG22	2.11	0.50
44:1:1447:G:N2	44:1:2356:A:OP2	2.39	0.50
44:1:1973:G:C2	44:1:2048:G:H2'	2.47	0.50
44:1:2225:U:H2'	44:1:2226:U:C6	2.47	0.50
6:LD:140:ARG:O	44:1:1079:A:H4'	2.11	0.50
7:LE:158:TYR:OH	14:LM:114:ASP:OD2	2.21	0.50
11:LI:30:LYS:NZ	44:1:2853:A:OP1	2.38	0.50
17:LP:138:LYS:HZ2	44:1:2356:A:H5'	1.77	0.50
19:LR:138:LEU:O	19:LR:142:ILE:HD12	2.12	0.50
21:LT:54:HIS:CE1	21:LT:55:LYS:HG2	2.47	0.50
23:LV:15:LEU:HD13	23:LV:51:ALA:HB3	1.93	0.50
27:LZ:135:ARG:HH11	27:LZ:135:ARG:HG3	1.77	0.50
44:1:1362:G:H2'	44:1:1363:A:H8	1.77	0.50
46:B:6:GLN:OE1	46:B:37:TYR:OH	2.29	0.50
1:C4:31:U:O3'	6:LD:218:ARG:NH2	2.45	0.50
1:C4:47:C:OP1	6:LD:95:TRP:N	2.45	0.50
5:LC:299:ILE:HD12	5:LC:300:ARG:H	1.77	0.50
7:LE:31:ARG:NH2	7:LE:81:ALA:O	2.45	0.50
10:LH:124:ARG:NH1	10:LH:164:ILE:O	2.34	0.50
23:LV:28:ASN:ND2	23:LV:112:SER:OG	2.28	0.50
27:LZ:23:VAL:HG12	27:LZ:45:GLY:HA3	1.94	0.50
28:La:4:ARG:NH2	44:1:1427:U:OP2	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:20:A:H2'	44:1:21:G:C8	2.47	0.50
44:1:1416:C:H2'	44:1:1417:G:C4	2.47	0.50
44:1:1667:A:H2'	44:1:1668:G:C8	2.47	0.50
44:1:1982:G:N2	44:1:2040:U:H3	2.09	0.50
44:1:2837:A:P	44:1:2845:A:H61	2.34	0.50
44:1:3021:A:H61	44:1:3032:A:H3'	1.77	0.50
44:1:3089:C:H2'	44:1:3090:U:O4'	2.11	0.50
4:LB:36:ASP:HB3	4:LB:39:LYS:NZ	2.27	0.50
4:LB:296:THR:OG1	4:LB:357:LYS:O	2.30	0.50
9:LG:112:GLU:OE2	9:LG:126:SER:HB3	2.11	0.50
13:LL:104:ARG:NH2	44:1:75:G:OP2	2.44	0.50
19:LR:92:GLN:O	19:LR:96:ILE:HG12	2.11	0.50
44:1:1064:A:H4'	44:1:1065:A:O5'	2.11	0.50
44:1:1619:A:H2'	44:1:1620:U:O4'	2.12	0.50
44:1:3317:U:H1'	46:B:729:LYS:NZ	2.27	0.50
2:C3:39:G:H1'	2:C3:104:A:N6	2.27	0.49
4:LB:292:ALA:HB2	4:LB:302:LYS:HA	1.94	0.49
6:LD:34:LYS:HE2	21:LT:30:TYR:CE2	2.47	0.49
9:LG:139:VAL:HG21	9:LG:197:VAL:HG21	1.93	0.49
15:LN:51:LEU:HD13	15:LN:117:ASN:HD22	1.76	0.49
19:LR:42:ARG:NH2	44:1:1601:U:OP1	2.45	0.49
20:LS:77:VAL:HG12	20:LS:126:VAL:HG22	1.93	0.49
23:LV:65:GLY:O	23:LV:70:ARG:NH2	2.45	0.49
44:1:1046:A:H2'	44:1:1049:C:C5	2.47	0.49
44:1:2087:C:H2'	44:1:2088:A:H2'	1.93	0.49
44:1:2095:G:H2'	44:1:2096:A:H8	1.76	0.49
45:A:29:LEU:HD23	46:B:509:SER:HB3	1.93	0.49
46:B:178:LEU:HD12	46:B:181:GLN:HE21	1.76	0.49
46:B:636:LYS:NZ	46:B:676:GLU:OE1	2.38	0.49
4:LB:76:VAL:HG21	4:LB:323:MET:HE3	1.93	0.49
30:Lc:32:LYS:O	30:Lc:36:GLN:HG3	2.13	0.49
34:Lg:37:LYS:NZ	44:1:1656:A:OP2	2.45	0.49
43:Lp:39:CYS:HB3	43:Lp:42:CYS:SG	2.50	0.49
44:1:2440:G:H2'	44:1:2441:A:C8	2.47	0.49
44:1:3343:G:O2'	44:1:3362:A:N6	2.45	0.49
46:B:233:LYS:HG3	46:B:256:LEU:HD13	1.94	0.49
5:LC:194:TYR:HE2	44:1:341:G:C6	2.29	0.49
44:1:443:G:O6	44:1:492:C:N4	2.45	0.49
44:1:787:G:H2'	44:1:788:C:C6	2.47	0.49
44:1:2223:A:H2'	44:1:2224:A:C8	2.47	0.49
44:1:2291:A:H2'	44:1:2292:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:3375:A:O2'	44:1:3378:C:OP2	2.29	0.49
1:C4:96:U:OP1	20:LS:43:TYR:OH	2.22	0.49
4:LB:161:LEU:HB3	4:LB:178:LEU:HD11	1.94	0.49
5:LC:205:PRO:HD2	5:LC:225:VAL:HG22	1.94	0.49
13:LL:138:VAL:HG22	35:Lh:118:ILE:HG23	1.94	0.49
16:LO:16[A]:VAL:HG23	16:LO:80[A]:PHE:HD1	1.77	0.49
16:LO:54[A]:TYR:OH	16:LO:73[A]:PHE:O	2.31	0.49
16:LO:118[A]:VAL:HG21	20:LS:163:PHE:HB3	1.95	0.49
19:LR:150:GLN:HE22	19:LR:151:ARG:HG3	1.77	0.49
36:Li:58:ILE:HG23	36:Li:94:ILE:HD11	1.93	0.49
44:1:612:U:H2'	44:1:613:G:C8	2.47	0.49
44:1:710:A:H2'	44:1:711:A:C8	2.47	0.49
44:1:952:A:H4'	44:1:968:G:N2	2.27	0.49
44:1:1477:A:OP1	44:1:3075:G:O2'	2.26	0.49
44:1:3337:G:H2'	44:1:3338:C:C6	2.47	0.49
45:A:33:PHE:HA	45:A:36:MET:HE2	1.95	0.49
5:LC:299:ILE:HD11	18:LQ:39:ARG:CA	2.43	0.49
5:LC:300:ARG:O	18:LQ:39:ARG:NH1	2.45	0.49
5:LC:341:SER:OG	44:1:514:G:N3	2.44	0.49
8:LF:233:GLU:HG2	20:LS:35:VAL:HG22	1.95	0.49
11:LI:182:LEU:HD23	11:LI:185:ARG:HD3	1.94	0.49
15:LN:125:SER:HB3	44:1:2433:U:H1'	1.94	0.49
21:LT:13:TYR:OH	44:1:1050:U:OP2	2.20	0.49
25:LX:138:ARG:HG2	25:LX:138:ARG:HH11	1.77	0.49
44:1:1378:U:H2'	44:1:1379:G:C8	2.44	0.49
44:1:1659:U:H2'	44:1:1660:C:C6	2.47	0.49
1:C4:7:G:H5''	6:LD:22:ARG:HD3	1.94	0.49
1:C4:73:C:H1'	20:LS:13:ARG:HH22	1.77	0.49
6:LD:107:ARG:NH1	6:LD:120:LYS:O	2.45	0.49
8:LF:180:SER:N	8:LF:183:ASP:OD2	2.43	0.49
12:LJ:31:THR:HG22	12:LJ:35:LYS:NZ	2.28	0.49
16:LO:62[A]:THR:O	16:LO:66[A]:LYS:NZ	2.43	0.49
16:LO:143[A]:THR:HG21	16:LO:150[A]:GLU:OE1	2.13	0.49
19:LR:139:VAL:O	19:LR:143:ILE:HG12	2.13	0.49
29:Lb:18:ARG:HG2	29:Lb:18:ARG:HH11	1.77	0.49
44:1:65:A:H1'	44:1:77:A:H1'	1.93	0.49
44:1:759:U:H2'	44:1:760:G:O4'	2.13	0.49
44:1:1103:A:O2'	44:1:1104:G:H5'	2.12	0.49
44:1:1960:A:H2'	44:1:1961:G:H4'	1.94	0.49
44:1:2881:C:H2'	44:1:2882:U:C6	2.47	0.49
46:B:473:ASP:OD1	46:B:506:TYR:OH	2.16	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LB:7:GLU:HG2	44:1:2915:U:C5	2.47	0.49
4:LB:180:GLU:OE2	44:1:3002:C:O2'	2.20	0.49
4:LB:244:ARG:NH1	44:1:2981:U:OP2	2.42	0.49
4:LB:303:LYS:NZ	4:LB:371:GLN:OE1	2.44	0.49
6:LD:40:HIS:CE1	21:LT:69:LYS:HA	2.47	0.49
13:LL:16:LYS:NZ	44:1:49:A:OP1	2.38	0.49
21:LT:88:ARG:HH11	21:LT:88:ARG:HG3	1.77	0.49
27:LZ:28:PRO:O	27:LZ:29:HIS:ND1	2.45	0.49
32:Le:89:THR:HG22	32:Le:117:ILE:HD13	1.94	0.49
44:1:254:A:H2'	44:1:255:A:H8	1.77	0.49
44:1:432:G:H2'	44:1:433:A:H8	1.78	0.49
44:1:528:U:H2'	44:1:529:A:C8	2.47	0.49
44:1:584:G:H2'	44:1:585:A:C8	2.44	0.49
44:1:1977:C:N3	44:1:2046:U:O2'	2.40	0.49
44:1:3094:A:H2'	44:1:3095:U:C6	2.47	0.49
2:C3:39:G:H1'	2:C3:104:A:H61	1.78	0.49
3:LA:149:ARG:NH1	3:LA:153:GLY:O	2.46	0.49
4:LB:173:GLN:HG3	4:LB:175:LYS:H	1.77	0.49
44:1:1097:G:H4'	44:1:1098:A:O5'	2.13	0.49
44:1:2696:A:N7	44:1:2758:A:N6	2.60	0.49
44:1:3007:U:O4	44:1:3008:A:N6	2.46	0.49
45:A:9:PRO:HG3	45:A:36:MET:SD	2.53	0.49
46:B:299:ARG:HD2	46:B:325:TYR:HE2	1.77	0.49
1:C4:27:A:H2'	1:C4:28:C:C6	2.47	0.49
7:LE:7:PRO:HG2	7:LE:10:TYR:CZ	2.48	0.49
22:LU:56:VAL:HG22	22:LU:65:VAL:HG22	1.94	0.49
25:LX:125:ARG:NH1	44:1:1609:C:OP1	2.45	0.49
41:Ln:16:LYS:NZ	41:Ln:17:ARG:HH11	2.09	0.49
44:1:138:U:H2'	44:1:139:G:H8	1.78	0.49
44:1:242:C:O2'	44:1:243:G:H8	1.96	0.49
44:1:651:G:O2'	44:1:1435:A:OP1	2.31	0.49
44:1:3201:C:H2'	44:1:3202:G:C8	2.47	0.49
46:B:391:LYS:NZ	46:B:395:ASP:O	2.38	0.49
1:C4:40:C:O2	12:LJ:72:ARG:NE	2.27	0.49
1:C4:109:G:H2'	1:C4:110:G:H8	1.78	0.49
25:LX:57:LEU:HG	25:LX:62:VAL:HG12	1.94	0.49
30:Lc:49:PRO:HD3	44:1:1729:A:C6	2.48	0.49
32:Le:86:THR:HG22	32:Le:115:LEU:HD23	1.94	0.49
44:1:1472:U:H2'	44:1:1473:G:H8	1.78	0.49
44:1:1985:G:O6	44:1:2036:U:O4	2.30	0.49
44:1:2107:A:H2	44:1:3344:A:C8	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:112:TYR:OH	46:B:522:GLU:OE2	2.25	0.49
1:C4:23:A:H2'	1:C4:24:A:C8	2.47	0.48
2:C3:26:U:H2'	2:C3:27:U:C6	2.48	0.48
5:LC:317:PRO:C	5:LC:319:LYS:H	2.21	0.48
6:LD:236:LEU:HD12	6:LD:239:ILE:HD11	1.95	0.48
9:LG:54:GLU:HG3	9:LG:57:ARG:HH21	1.78	0.48
13:LL:158:ALA:HA	28:La:97:GLU:HA	1.95	0.48
21:LT:17:ARG:HG2	44:1:2700:G:H5''	1.94	0.48
35:Lh:83:LYS:O	37:Lj:73:ARG:NH2	2.43	0.48
42:Lo:72:LEU:O	42:Lo:80:ARG:HA	2.13	0.48
44:1:19:U:H2'	44:1:20:A:C8	2.48	0.48
44:1:1351:U:O2'	44:1:1352:A:H5'	2.13	0.48
44:1:1488:G:H5''	44:1:1838:G:O6	2.13	0.48
44:1:1560:G:N1	44:1:1580:A:N1	2.62	0.48
44:1:1622:U:H2'	44:1:1623:G:C8	2.48	0.48
44:1:1996:C:H2'	44:1:1997:U:C6	2.48	0.48
44:1:2495:C:H2'	44:1:2496:C:C6	2.48	0.48
7:LE:94:GLU:H	7:LE:94:GLU:CD	2.22	0.48
10:LH:10:ILE:HD11	10:LH:72:LYS:HA	1.95	0.48
13:LL:110:ASP:OD1	13:LL:110:ASP:N	2.45	0.48
19:LR:69:SER:HB3	19:LR:74:ARG:HB2	1.96	0.48
20:LS:92:LYS:HE3	20:LS:110:MET:HE1	1.95	0.48
31:Ld:10:ARG:NH1	44:1:3386:G:C5'	2.71	0.48
33:Lf:20:LYS:HG3	44:1:1178:G:O6	2.13	0.48
44:1:2213:A:H2'	44:1:2214:A:H8	1.78	0.48
44:1:2437:G:O6	44:1:2510:U:O4	2.31	0.48
44:1:2632:G:O6	44:1:2647:A:N6	2.47	0.48
44:1:3069:G:C2	44:1:3070:A:C8	3.01	0.48
44:1:3092:C:O2'	44:1:3094:A:OP2	2.23	0.48
46:B:38:PHE:HD1	46:B:41:LEU:HD12	1.78	0.48
46:B:400:SER:HB3	46:B:438:ASN:HD21	1.77	0.48
1:C4:38:U:N3	1:C4:41:G:OP2	2.44	0.48
15:LN:93:LYS:O	44:1:289:A:O2'	2.29	0.48
34:Lg:37:LYS:NZ	44:1:1591:G:H5''	2.28	0.48
42:Lo:65:THR:HG23	42:Lo:87:ARG:HH11	1.79	0.48
44:1:1246:G:O2'	44:1:1247:U:O4'	2.23	0.48
2:C3:4:C:H2'	2:C3:5:U:H6	1.78	0.48
2:C3:8:C:H2'	2:C3:9:A:H8	1.79	0.48
5:LC:229:ASN:OD1	5:LC:230:VAL:N	2.47	0.48
15:LN:68:ARG:NE	44:1:291:C:OP1	2.34	0.48
26:LY:53:ASP:O	26:LY:110:HIS:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Le:3:SER:HB2	32:Le:71:HIS:CE1	2.48	0.48
44:1:2376:G:H2'	44:1:2377:G:C8	2.49	0.48
44:1:2916:U:H2'	44:1:2917:G:H8	1.79	0.48
3:LA:70:ARG:HG2	44:1:1650:G:H5''	1.96	0.48
13:LL:73:ARG:NH2	44:1:110:G:OP2	2.47	0.48
27:LZ:125:GLY:C	27:LZ:128:GLN:HE22	2.22	0.48
31:Ld:4:LEU:HA	46:B:720:LYS:CE	2.44	0.48
44:1:2696:A:H2'	44:1:2697:A:C8	2.48	0.48
44:1:3065:G:H2'	44:1:3066:U:C6	2.48	0.48
1:C4:119:U:H2'	1:C4:120:C:C6	2.49	0.48
3:LA:135:ILE:HB	3:LA:149:ARG:HB3	1.95	0.48
8:LF:23:ALA:HB1	8:LF:25:GLN:HE22	1.79	0.48
8:LF:81:HIS:HB2	8:LF:138:TYR:CD1	2.49	0.48
13:LL:114:GLN:O	13:LL:117:LYS:HG2	2.12	0.48
14:LM:71:ALA:O	14:LM:72:LEU:HD23	2.14	0.48
14:LM:118:PHE:O	14:LM:121:MET:HB3	2.14	0.48
14:LM:126:GLN:NE2	44:1:3261:C:OP1	2.37	0.48
15:LN:155:VAL:O	15:LN:162:ARG:NH2	2.44	0.48
25:LX:121:LYS:NZ	44:1:1522:U:OP2	2.46	0.48
34:Lg:15:THR:HG22	34:Lg:18:ASN:HB2	1.94	0.48
44:1:662:U:H2'	44:1:663:C:C6	2.48	0.48
44:1:1029:G:H2'	44:1:1030:A:H8	1.77	0.48
44:1:1783:U:H2'	44:1:1784:G:C8	2.49	0.48
44:1:2266:U:H2'	44:1:2267:C:C6	2.48	0.48
7:LE:172:HIS:CD2	7:LE:173:MET:HG3	2.49	0.48
8:LF:210:PRO:HD3	8:LF:243:MET:SD	2.54	0.48
11:LI:4:ARG:NH2	44:1:2828:G:O2'	2.47	0.48
14:LM:32:LEU:HD21	14:LM:94:TRP:CG	2.48	0.48
19:LR:126:GLU:HG3	19:LR:132:PHE:CE2	2.48	0.48
20:LS:108:GLN:NE2	44:1:1322:U:O2	2.45	0.48
21:LT:127:GLN:HG2	44:1:1095:U:H3	1.78	0.48
44:1:1339:C:H2'	44:1:1340:G:C8	2.49	0.48
44:1:1480:G:O2'	44:1:1871:U:O4	2.26	0.48
44:1:2106:A:H2'	44:1:2107:A:H8	1.79	0.48
44:1:2684:C:H2'	44:1:2685:C:C6	2.48	0.48
44:1:2708:C:H2'	44:1:2709:C:C6	2.49	0.48
44:1:3150:A:H2'	44:1:3151:U:O4'	2.13	0.48
46:B:62:GLU:HG3	46:B:63:PRO:HD3	1.95	0.48
12:LJ:82:ARG:HE	12:LJ:112:LEU:HB3	1.79	0.48
15:LN:7:LEU:HD21	15:LN:45:PRO:HD2	1.95	0.48
44:1:243:G:H2'	44:1:244:G:C8	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:1335:C:H2'	44:1:1336:U:H6	1.79	0.48
44:1:2219:A:H2'	44:1:2220:A:H8	1.79	0.48
44:1:2407:C:H2'	44:1:2408:U:H6	1.78	0.48
46:B:585:PHE:N	46:B:615:GLU:OE2	2.47	0.48
5:LC:40:THR:HG23	44:1:1426:C:H4'	1.96	0.48
13:LL:15:ARG:HH12	44:1:96:G:C5'	2.27	0.48
14:LM:128:ARG:HH11	44:1:3213:A:P	2.37	0.48
44:1:436:A:H2'	44:1:437:G:C8	2.49	0.48
44:1:871:U:H2'	44:1:872:U:C6	2.49	0.48
44:1:1562:C:O2'	44:1:1563:C:O5'	2.29	0.48
44:1:3013:U:H2'	44:1:3014:U:C6	2.49	0.48
44:1:3332:U:H2'	44:1:3333:G:O4'	2.14	0.48
45:A:12:LEU:HB3	46:B:470:VAL:HG11	1.95	0.48
45:A:95:LYS:NZ	46:B:295:SER:HB2	2.28	0.48
46:B:220:THR:HG22	46:B:232:LEU:HD22	1.96	0.48
5:LC:141:ARG:HH21	44:1:1386:A:H5''	1.78	0.48
16:LO:37[A]:ARG:HG3	16:LO:108[A]:ILE:HG13	1.96	0.48
18:LQ:19:PRO:HD3	18:LQ:53:PHE:CD1	2.49	0.48
20:LS:42:TRP:O	20:LS:46:GLN:HG2	2.14	0.48
27:LZ:15:ARG:HG2	44:1:1637:A:H4'	1.95	0.48
27:LZ:136:PHE:O	44:1:2555:G:O2'	2.31	0.48
33:Lf:106:ASN:O	33:Lf:106:ASN:ND2	2.45	0.48
36:Li:56:ARG:NH1	44:1:2505:U:OP1	2.47	0.48
39:Ll:16:ALA:HB1	39:Ll:42:ARG:NH2	2.29	0.48
44:1:1623:G:C4	44:1:1624:G:C8	3.02	0.48
44:1:2812:C:H2'	44:1:2813:A:C8	2.49	0.48
44:1:3263:G:C2	44:1:3264:G:C8	3.02	0.48
12:LJ:82:ARG:HE	12:LJ:112:LEU:HD13	1.79	0.47
28:La:37:GLY:HA3	28:La:53:PHE:HZ	1.79	0.47
30:Lc:57:GLU:O	30:Lc:61:MET:N	2.35	0.47
44:1:887:G:H2'	44:1:888:A:C8	2.48	0.47
44:1:1189:C:N4	44:1:1315:U:O2'	2.36	0.47
44:1:1341:U:H2'	44:1:1342:C:C6	2.49	0.47
44:1:2091:U:H2'	44:1:2092:A:C8	2.49	0.47
44:1:3333:G:N2	44:1:3369:G:O2'	2.48	0.47
46:B:18:PHE:CD2	46:B:49:GLN:HG2	2.49	0.47
1:C4:16:U:H2'	1:C4:17:A:C8	2.49	0.47
8:LF:98:LYS:HB3	8:LF:99:PRO:HD3	1.96	0.47
9:LG:134:TYR:CG	9:LG:190:VAL:HG11	2.49	0.47
9:LG:242:ALA:N	44:1:2586:G:O6	2.47	0.47
12:LJ:21:ILE:HD13	12:LJ:37:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LJ:93:ASP:OD1	12:LJ:171:VAL:HB	2.15	0.47
12:LJ:141:ARG:O	12:LJ:145:LYS:NZ	2.33	0.47
15:LN:15:GLN:HB3	36:Li:52:PRO:HD2	1.95	0.47
44:1:129:U:H2'	44:1:130:A:H8	1.77	0.47
44:1:542:G:O6	44:1:549:U:O4	2.32	0.47
44:1:970:A:H2'	44:1:971:G:C8	2.49	0.47
44:1:1277:C:HO2'	44:1:1278:A:P	2.36	0.47
44:1:1667:A:H2'	44:1:1668:G:H8	1.79	0.47
44:1:3066:U:H2'	44:1:3067:C:C6	2.49	0.47
4:LB:244:ARG:NH2	44:1:2948:C:OP1	2.32	0.47
4:LB:292:ALA:HB2	4:LB:302:LYS:HD3	1.96	0.47
9:LG:25:PRO:HG2	9:LG:26:LEU:HD12	1.96	0.47
12:LJ:125:MET:HE2	12:LJ:125:MET:HA	1.96	0.47
13:LL:12:ASN:ND2	44:1:665:A:H2	2.13	0.47
18:LQ:147:ARG:HB2	18:LQ:150:VAL:HG23	1.96	0.47
31:Ld:7:VAL:CG2	31:Ld:78:LYS:HA	2.44	0.47
33:Lf:54:ARG:HD3	44:1:3279:A:N6	2.29	0.47
42:Lo:25:VAL:HG22	42:Lo:70:LEU:HD12	1.96	0.47
44:1:105:C:H2'	44:1:106:A:H8	1.79	0.47
44:1:136:G:H2'	44:1:137:G:H8	1.80	0.47
44:1:213:A:N6	44:1:228:U:O4'	2.47	0.47
44:1:585:A:H2'	44:1:586:C:C6	2.49	0.47
44:1:1072:G:H2'	44:1:1073:U:C6	2.49	0.47
44:1:1289:G:H2'	44:1:1290:A:H8	1.78	0.47
44:1:1650:G:H2'	44:1:1651:U:H6	1.80	0.47
44:1:2992:U:OP1	44:1:3310:A:O2'	2.26	0.47
44:1:3113:A:H2'	44:1:3114:A:O4'	2.13	0.47
46:B:408:LYS:O	46:B:412:LYS:HG2	2.14	0.47
46:B:768:LEU:O	46:B:772:LEU:N	2.44	0.47
7:LE:148:GLU:HA	7:LE:151:LYS:HE2	1.95	0.47
14:LM:124:ARG:NH2	44:1:3213:A:H62	2.13	0.47
21:LT:90:ASN:HD22	44:1:2736:A:H1'	1.78	0.47
21:LT:112:ASN:ND2	44:1:1063:G:O6	2.47	0.47
42:Lo:15:LYS:HA	42:Lo:18:ARG:HH12	1.78	0.47
44:1:207:U:H2'	44:1:208:C:C6	2.49	0.47
44:1:276:U:H2'	44:1:277:G:C8	2.49	0.47
44:1:290:G:H2'	44:1:291:C:C6	2.50	0.47
44:1:1219:C:H4'	44:1:1223:A:H5'	1.96	0.47
44:1:1646:G:H1'	44:1:1809:A:N6	2.29	0.47
44:1:1786:G:H2'	44:1:1787:A:H8	1.78	0.47
44:1:2709:C:H2'	44:1:2710:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:201:VAL:O	46:B:205:LEU:HB2	2.15	0.47
46:B:541:LYS:HA	46:B:546:TRP:HE1	1.79	0.47
5:LC:318:LEU:HD21	8:LF:146:GLN:OE1	2.15	0.47
8:LF:40:LYS:NZ	8:LF:170:GLU:OE2	2.47	0.47
9:LG:27:THR:HB	44:1:2563:G:H5''	1.96	0.47
22:LU:37:LEU:O	22:LU:41:ILE:HG12	2.14	0.47
34:Lg:67:LYS:N	44:1:1821:U:O2'	2.42	0.47
35:Lh:93:THR:OG1	44:1:135:C:O2	2.30	0.47
44:1:443:G:N2	44:1:492:C:C2	2.83	0.47
44:1:1340:G:H2'	44:1:1341:U:H6	1.79	0.47
44:1:2509:U:H2'	44:1:2510:U:C6	2.49	0.47
44:1:2618:G:C8	44:1:2865:U:H5''	2.49	0.47
44:1:2685:C:H2'	44:1:2686:A:H8	1.80	0.47
46:B:25:LEU:O	46:B:29:GLN:N	2.42	0.47
1:C4:74:C:H2'	1:C4:75:G:C8	2.50	0.47
3:LA:182:ALA:HB1	3:LA:196:TRP:HH2	1.80	0.47
3:LA:193:ARG:NH2	44:1:2174:G:OP2	2.34	0.47
7:LE:42:LEU:O	7:LE:49:GLY:N	2.32	0.47
11:LI:99:ILE:HB	11:LI:123:HIS:CD2	2.50	0.47
13:LL:59:ARG:HD2	13:LL:66:ASN:O	2.14	0.47
19:LR:82:LYS:O	44:1:1914:G:O2'	2.27	0.47
23:LV:90:GLY:O	24:LW:16:GLY:HA2	2.13	0.47
25:LX:105:VAL:HG13	25:LX:130:TYR:CD2	2.50	0.47
27:LZ:84:ARG:HH11	27:LZ:84:ARG:HG3	1.79	0.47
28:La:96:LYS:C	28:La:98:THR:H	2.21	0.47
44:1:158:G:H2'	44:1:159:A:C8	2.50	0.47
44:1:164:A:N1	44:1:258:G:C6	2.83	0.47
44:1:254:A:H2'	44:1:255:A:C8	2.49	0.47
44:1:594:U:P	44:1:609:G:H1	2.37	0.47
44:1:1615:C:H2'	44:1:1616:U:H6	1.77	0.47
44:1:1794:G:O2'	44:1:1796:G:N2	2.47	0.47
44:1:2423:U:H2'	44:1:2424:A:C8	2.49	0.47
44:1:2495:C:O2'	44:1:2496:C:OP1	2.30	0.47
46:B:526:TYR:HA	46:B:529:ILE:HD12	1.96	0.47
1:C4:112:G:H2'	1:C4:113:C:H6	1.80	0.47
5:LC:193:LYS:NZ	44:1:1419:A:H5''	2.29	0.47
6:LD:52:VAL:HG11	6:LD:65:ILE:HD12	1.97	0.47
6:LD:182:GLY:HA2	6:LD:194:LEU:HD23	1.96	0.47
7:LE:142:ASP:OD1	7:LE:143:LYS:N	2.47	0.47
12:LJ:25:GLU:HG2	12:LJ:29:ARG:NH2	2.30	0.47
16:LO:27[A]:LEU:HD12	16:LO:98[A]:ALA:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LU:99:LYS:HG3	22:LU:102:GLU:OE1	2.14	0.47
32:Le:96:ILE:HG21	32:Le:105:ARG:HG2	1.96	0.47
36:Li:53:TYR:CE1	44:1:294:U:H5''	2.50	0.47
44:1:86:G:O2'	44:1:98:G:O6	2.33	0.47
44:1:91:G:N2	44:1:95:A:OP2	2.45	0.47
44:1:170:G:O6	44:1:248:U:O4	2.33	0.47
44:1:324:A:H2'	44:1:325:A:C8	2.50	0.47
44:1:1128:U:H2'	44:1:1129:A:O4'	2.15	0.47
44:1:1413:G:H2'	44:1:1414:G:H8	1.79	0.47
44:1:1462:A:H2'	44:1:1463:U:C6	2.50	0.47
44:1:1529:A:OP2	44:1:1592:G:N2	2.48	0.47
44:1:1661:G:H2'	44:1:1662:G:H8	1.77	0.47
44:1:1709:C:H2'	44:1:1710:C:H6	1.79	0.47
44:1:1797:A:H2'	44:1:1798:A:C8	2.50	0.47
44:1:3356:G:H2'	44:1:3357:U:C6	2.50	0.47
46:B:297:ASN:O	46:B:301:ALA:N	2.46	0.47
2:C3:142:C:H2'	2:C3:143:U:H6	1.78	0.47
3:LA:80:GLU:OE1	43:Lp:73:THR:HG22	2.14	0.47
6:LD:25:GLU:O	12:LJ:144:CYS:HA	2.14	0.47
8:LF:186:HIS:O	8:LF:190:THR:OG1	2.27	0.47
13:LL:165:SER:O	13:LL:167:PHE:N	2.48	0.47
20:LS:6:GLU:OE2	20:LS:28:ARG:NH2	2.44	0.47
27:LZ:106:GLN:HA	27:LZ:109:GLU:OE2	2.15	0.47
33:Lf:6:ARG:NH1	33:Lf:8:TYR:O	2.42	0.47
44:1:261:U:H2'	44:1:262:U:C6	2.50	0.47
44:1:503:C:H2'	44:1:504:A:H8	1.79	0.47
44:1:1254:C:H41	44:1:1263:A:H5''	1.79	0.47
44:1:1709:C:H2'	44:1:1710:C:C6	2.50	0.47
44:1:2412:G:H2'	44:1:2413:A:C8	2.49	0.47
44:1:2536:A:H2'	44:1:2537:U:N3	2.29	0.47
44:1:3138:U:H2'	44:1:3139:A:C8	2.50	0.47
5:LC:130:ALA:HB2	5:LC:149:PRO:HG3	1.96	0.47
9:LG:161:GLU:CD	15:LN:26:ARG:HH22	2.23	0.47
21:LT:119:ALA:HB3	21:LT:126:VAL:HG12	1.95	0.47
23:LV:106:LYS:HD2	23:LV:106:LYS:O	2.15	0.47
44:1:966:U:H2'	44:1:967:A:H8	1.79	0.47
44:1:2223:A:OP2	44:1:2223:A:H8	1.97	0.47
44:1:2835:U:H2'	44:1:2836:C:O2	2.15	0.47
45:A:120:CYS:HB2	45:A:160:ASP:HA	1.97	0.47
46:B:524:ASN:HA	46:B:526:TYR:CE1	2.50	0.47
7:LE:143:LYS:HA	7:LE:146:ILE:HG12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LP:109:ALA:HA	17:LP:112:LEU:HD13	1.97	0.47
18:LQ:89:ASP:HB2	18:LQ:110:ALA:N	2.30	0.47
20:LS:161:LYS:NZ	44:1:3209:A:OP2	2.48	0.47
28:La:34:MET:HB2	44:1:96:G:P	2.55	0.47
36:Li:76:ARG:O	44:1:293:C:O2'	2.28	0.47
44:1:1783:U:H2'	44:1:1784:G:H8	1.80	0.47
44:1:2089:A:H2'	44:1:2090:U:C6	2.49	0.47
44:1:3052:G:H2'	44:1:3053:G:H8	1.80	0.47
44:1:3218:A:H5''	44:1:3219:G:C8	2.50	0.47
2:C3:13:A:O2'	17:LP:121:GLN:O	2.34	0.46
5:LC:186:LYS:NZ	44:1:1389:G:O6	2.44	0.46
6:LD:289:LYS:HG3	6:LD:293:LEU:HD13	1.98	0.46
9:LG:94:PHE:HB3	9:LG:189:LEU:HD21	1.96	0.46
10:LH:104:VAL:O	10:LH:111:PHE:N	2.48	0.46
12:LJ:29:ARG:HA	12:LJ:32:ARG:HD3	1.96	0.46
15:LN:174:ILE:HG13	15:LN:174:ILE:O	2.15	0.46
44:1:498:A:O2'	44:1:3273:A:N1	2.46	0.46
44:1:1351:U:O2'	44:1:1352:A:N3	2.48	0.46
44:1:1381:A:H2'	44:1:1382:G:H8	1.80	0.46
44:1:2328:U:H2'	44:1:2329:C:H6	1.81	0.46
44:1:2837:A:H2'	44:1:2845:A:C6	2.50	0.46
44:1:3217:C:C5	44:1:3220:G:H1'	2.49	0.46
44:1:3360:C:H2'	44:1:3361:G:O4'	2.15	0.46
44:1:3393:U:H2'	44:1:3394:U:C6	2.51	0.46
1:C4:9:C:OP1	21:LT:26:HIS:HB2	2.15	0.46
4:LB:298:PHE:CD2	4:LB:357:LYS:HG2	2.51	0.46
7:LE:91:VAL:HG13	7:LE:148:GLU:OE1	2.15	0.46
15:LN:118:SER:HB3	15:LN:132:VAL:HG12	1.96	0.46
44:1:507:U:H2'	44:1:508:U:C6	2.50	0.46
44:1:673:U:H2'	44:1:674:G:C8	2.50	0.46
44:1:860:G:O2'	44:1:895:A:H4'	2.15	0.46
44:1:1237:G:C8	44:1:1263:A:H1'	2.51	0.46
44:1:1785:U:H2'	44:1:1786:G:H8	1.80	0.46
44:1:2213:A:H2'	44:1:2214:A:C8	2.51	0.46
44:1:2219:A:H2'	44:1:2220:A:C8	2.50	0.46
44:1:2534:G:H2'	44:1:2535:A:C8	2.50	0.46
44:1:3151:U:H4'	44:1:3294:A:H1'	1.96	0.46
2:C3:76:C:H2'	2:C3:77:A:C8	2.50	0.46
2:C3:142:C:OP1	15:LN:38:ARG:NH1	2.48	0.46
9:LG:241:LYS:NZ	44:1:2588:U:OP1	2.44	0.46
13:LL:2:ALA:HB3	28:La:41:HIS:CE1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LM:44:VAL:HG13	14:LM:60:LEU:HD21	1.98	0.46
35:Lh:101:THR:HG23	35:Lh:104:GLN:H	1.80	0.46
38:Lk:19:ASP:OD1	38:Lk:20:VAL:N	2.48	0.46
44:1:542:G:C6	44:1:550:A:N6	2.83	0.46
44:1:552:G:H2'	44:1:553:U:C6	2.49	0.46
44:1:1646:G:H1'	44:1:1809:A:H61	1.80	0.46
44:1:1982:G:H2'	44:1:1983:G:C8	2.50	0.46
44:1:2767:U:H2'	44:1:2768:U:H6	1.80	0.46
44:1:2858:U:H2'	44:1:2859:U:C6	2.50	0.46
46:B:575:ARG:O	46:B:579:MET:HG2	2.15	0.46
46:B:685:LEU:HD23	46:B:688:ARG:HH21	1.81	0.46
1:C4:7:G:O2'	6:LD:72:ASP:OD1	2.31	0.46
4:LB:260:VAL:HG11	4:LB:266:ARG:NH1	2.31	0.46
4:LB:284:ARG:HB3	4:LB:323:MET:SD	2.54	0.46
11:LI:41:ALA:HB1	11:LI:45:GLU:OE2	2.15	0.46
13:LL:48:PRO:HG2	35:Lh:115:LYS:HD3	1.97	0.46
14:LM:21:VAL:HG12	14:LM:65:LEU:HD23	1.97	0.46
38:Lk:51:LEU:N	44:1:1613:A:OP1	2.46	0.46
44:1:493:U:H3'	44:1:494:G:C8	2.49	0.46
44:1:659:G:H2'	44:1:1432:C:H42	1.80	0.46
44:1:715:A:N1	44:1:781:G:O2'	2.45	0.46
44:1:1253:U:H5'	44:1:1263:A:H2	1.80	0.46
44:1:2356:A:H61	44:1:2983:C:H5	1.62	0.46
44:1:2440:G:H2'	44:1:2441:A:H8	1.80	0.46
46:B:26:GLY:HA2	46:B:29:GLN:HB2	1.98	0.46
46:B:315:GLU:OE2	46:B:319:SER:OG	2.26	0.46
1:C4:53:U:O2'	1:C4:55:A:N7	2.43	0.46
2:C3:145:U:H2'	2:C3:146:U:H6	1.79	0.46
3:LA:125:ALA:HB1	44:1:2177:G:C6	2.51	0.46
7:LE:166:LYS:N	7:LE:169:ASP:OD2	2.40	0.46
7:LE:170:LYS:HB3	7:LE:172:HIS:CE1	2.50	0.46
12:LJ:84:LEU:HB3	12:LJ:89:TYR:CD1	2.50	0.46
12:LJ:105:GLY:O	12:LJ:106:ILE:HD13	2.15	0.46
18:LQ:94:PHE:CE2	28:La:119:PRO:HD3	2.50	0.46
21:LT:78:LYS:NZ	44:1:2724:U:OP1	2.45	0.46
23:LV:65:GLY:H	23:LV:70:ARG:HH22	1.63	0.46
34:Lg:56:THR:O	34:Lg:57:LEU:HD23	2.15	0.46
44:1:863:C:H2'	44:1:864:G:O4'	2.16	0.46
44:1:1596:C:H2'	44:1:1597:C:H6	1.80	0.46
44:1:1791:C:H2'	44:1:1792:C:C6	2.50	0.46
44:1:2767:U:H2'	44:1:2768:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:3026:G:N2	44:1:3029:A:OP2	2.43	0.46
44:1:3051:U:C2	44:1:3052:G:C8	3.03	0.46
44:1:3218:A:H5'	44:1:3219:G:C5	2.51	0.46
44:1:3379:C:H2'	44:1:3380:U:C6	2.51	0.46
2:C3:103:G:P	2:C3:105:A:HO2'	2.39	0.46
6:LD:218:ARG:O	6:LD:222:LEU:HD23	2.15	0.46
33:Lf:53:TYR:CZ	33:Lf:65:ARG:HB2	2.50	0.46
39:Ll:36:ARG:HA	39:Ll:36:ARG:NH1	2.30	0.46
44:1:1785:U:H2'	44:1:1786:G:C8	2.50	0.46
44:1:3096:C:H2'	44:1:3097:C:C6	2.51	0.46
46:B:18:PHE:HB3	46:B:49:GLN:HE21	1.80	0.46
46:B:607:ILE:HG23	46:B:608:LEU:HD23	1.98	0.46
46:B:677:ASN:HB3	46:B:680:LYS:NZ	2.29	0.46
46:B:712:THR:HG23	46:B:713:LEU:HD22	1.97	0.46
4:LB:153:LYS:NZ	44:1:3241:G:OP2	2.41	0.46
5:LC:195:ARG:NH1	44:1:340:C:OP2	2.34	0.46
30:Lc:17:VAL:HG11	30:Lc:92:ILE:HD12	1.97	0.46
38:Lk:56:ILE:HG22	38:Lk:58:ASP:H	1.81	0.46
39:Ll:30:ARG:HG3	39:Ll:30:ARG:HH11	1.80	0.46
44:1:194:U:H2'	44:1:195:U:C6	2.51	0.46
44:1:1277:C:C2	44:1:1278:A:C8	3.04	0.46
44:1:2933:A:N1	44:1:3014:U:H4'	2.31	0.46
44:1:3371:G:H2'	44:1:3372:A:C8	2.50	0.46
46:B:37:TYR:HA	46:B:40:ILE:HD12	1.97	0.46
5:LC:6:VAL:N	5:LC:20:LEU:O	2.49	0.46
6:LD:52:VAL:HA	6:LD:147:ASP:HB3	1.97	0.46
12:LJ:112:LEU:O	12:LJ:114:ILE:HD12	2.16	0.46
16:LO:77[A]:SER:N	16:LO:106[A]:GLU:OE2	2.36	0.46
20:LS:22:PRO:O	21:LT:146:ASN:ND2	2.25	0.46
21:LT:108:ARG:O	21:LT:112:ASN:N	2.48	0.46
35:Lh:93:THR:HG22	35:Lh:96:GLU:OE1	2.15	0.46
44:1:663:C:H2'	44:1:664:U:C6	2.50	0.46
44:1:1596:C:O2'	44:1:1696:A:N3	2.42	0.46
44:1:1666:G:H2'	44:1:1667:A:C8	2.51	0.46
44:1:2160:G:H2'	44:1:2161:G:C8	2.48	0.46
44:1:2534:G:H2'	44:1:2535:A:H8	1.80	0.46
44:1:3082:C:H2'	44:1:3083:G:H8	1.80	0.46
46:B:124:TYR:CZ	46:B:533:LEU:HD11	2.51	0.46
2:C3:85:G:H4'	2:C3:86:U:OP1	2.16	0.46
4:LB:45:SER:OG	4:LB:46:PHE:N	2.48	0.46
4:LB:380:MET:O	44:1:3369:G:N1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LI:83:ASP:OD1	11:LI:83:ASP:N	2.49	0.46
19:LR:83:GLY:N	44:1:1864:A:OP1	2.37	0.46
28:La:36:GLY:HA2	28:La:39:HIS:HB2	1.97	0.46
44:1:80:G:H2'	44:1:81:C:H6	1.80	0.46
44:1:274:G:H2'	44:1:275:U:C6	2.51	0.46
44:1:952:A:C2	44:1:1114:U:H4'	2.50	0.46
44:1:2366:C:H2'	44:1:2367:A:C8	2.48	0.46
44:1:2655:U:H1'	44:1:2656:A:C2	2.51	0.46
44:1:2961:G:H2'	44:1:2962:U:H6	1.81	0.46
45:A:78:ILE:HB	45:A:116:LEU:HB3	1.98	0.46
6:LD:140:ARG:NH2	44:1:1079:A:OP2	2.49	0.46
32:Le:13:HIS:HB2	32:Le:57:TYR:HD2	1.81	0.46
40:Lm:96:CYS:HA	40:Lm:121:LEU:HD23	1.98	0.46
44:1:843:A:H2'	44:1:844:G:H8	1.82	0.46
44:1:900:G:H1'	44:1:1589:A:H61	1.80	0.46
44:1:1646:G:O2'	44:1:1808:G:N2	2.47	0.46
44:1:1660:C:H2'	44:1:1661:G:H8	1.81	0.46
44:1:2406:C:H2'	44:1:2407:C:C6	2.50	0.46
44:1:2972:G:H2'	44:1:2973:G:H8	1.81	0.46
44:1:3296:A:H2'	44:1:3297:U:H6	1.81	0.46
44:1:3317:U:H1'	46:B:729:LYS:HZ3	1.80	0.46
45:A:75:HIS:HA	45:A:111:VAL:HB	1.98	0.46
3:LA:119:LYS:NZ	44:1:2159:U:OP2	2.48	0.45
4:LB:261:MET:HE3	4:LB:261:MET:HB3	1.84	0.45
11:LI:12:GLN:HG2	11:LI:59:GLN:HG2	1.97	0.45
12:LJ:22:SER:HG	44:1:2675:C:N4	2.14	0.45
13:LL:39:ARG:NH1	44:1:107:A:OP1	2.41	0.45
19:LR:86:GLU:HG2	19:LR:90:PRO:HA	1.98	0.45
28:La:125:VAL:HG23	28:La:145:VAL:HG12	1.98	0.45
35:Lh:92:LEU:HD22	35:Lh:96:GLU:HG3	1.99	0.45
44:1:51:A:C4	44:1:52:A:C8	3.05	0.45
44:1:508:U:H3	44:1:583:G:H1	1.62	0.45
44:1:1339:C:H2'	44:1:1340:G:H8	1.81	0.45
44:1:2180:G:H2'	44:1:2181:C:C6	2.51	0.45
44:1:3072:C:H2'	44:1:3073:A:O4'	2.15	0.45
44:1:3160:U:H2'	44:1:3161:C:C6	2.50	0.45
46:B:210:ARG:NH1	46:B:242:LEU:O	2.49	0.45
46:B:351:MET:HE2	46:B:351:MET:HA	1.97	0.45
2:C3:141:C:H2'	2:C3:142:C:C6	2.51	0.45
9:LG:32:LYS:NZ	44:1:2561:A:O4'	2.49	0.45
18:LQ:79:LYS:HA	18:LQ:136:ASN:OD1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LZ:99:GLU:H	27:LZ:99:GLU:CD	2.25	0.45
33:Lf:18:ARG:NH2	33:Lf:20:LYS:O	2.50	0.45
44:1:728:G:H2'	44:1:729:C:H6	1.82	0.45
44:1:792:G:H2'	44:1:793:C:C6	2.51	0.45
44:1:1255:C:H2'	44:1:1256:G:H8	1.80	0.45
44:1:1277:C:O2'	44:1:1278:A:H8	1.99	0.45
44:1:1624:G:C4	44:1:1625:A:C8	3.04	0.45
44:1:2046:U:H2'	44:1:2047:A:C4	2.50	0.45
44:1:3000:A:H2'	44:1:3001:C:C6	2.51	0.45
44:1:3357:U:H2'	44:1:3358:U:C6	2.51	0.45
45:A:50:THR:HA	46:B:337:HIS:CD2	2.52	0.45
9:LG:178:ALA:HB2	9:LG:218:ILE:HG21	1.98	0.45
12:LJ:32:ARG:HG3	12:LJ:123:PHE:HE2	1.81	0.45
26:LY:88:GLU:HA	26:LY:88:GLU:OE2	2.16	0.45
37:Lj:27:PHE:HA	37:Lj:34:CYS:HA	1.99	0.45
44:1:179:C:H2'	44:1:180:C:H6	1.78	0.45
44:1:768:C:H2'	44:1:769:G:H8	1.80	0.45
44:1:1047:A:N3	44:1:2633:U:O2'	2.50	0.45
44:1:1899:G:O2'	44:1:2334:U:O4	2.29	0.45
44:1:2260:U:H2'	44:1:2261:G:O4'	2.16	0.45
44:1:3193:C:H2'	44:1:3194:C:C6	2.51	0.45
1:C4:97:A:H2'	1:C4:98:C:C6	2.52	0.45
4:LB:333:LYS:O	44:1:3304:U:N3	2.49	0.45
11:LI:36:LEU:HB3	11:LI:73:ASN:ND2	2.31	0.45
13:LL:126:PHE:HD2	35:Lh:115:LYS:HD2	1.81	0.45
13:LL:128:ARG:NH1	44:1:169:U:H4'	2.32	0.45
15:LN:199:LEU:HD23	15:LN:203:ARG:CZ	2.47	0.45
25:LX:50:ALA:HB1	35:Lh:66:VAL:HG11	1.99	0.45
31:Ld:10:ARG:NH1	44:1:3386:G:H5'	2.32	0.45
34:Lg:44:CYS:HA	34:Lg:51:LEU:HD23	1.97	0.45
44:1:2496:C:H2'	44:1:2497:U:C6	2.51	0.45
44:1:3122:A:C2	44:1:3123:A:C8	3.05	0.45
45:A:1:MET:SD	46:B:300:LEU:HD13	2.57	0.45
46:B:648:PRO:HB2	46:B:650:ILE:HG12	1.98	0.45
2:C3:139:U:H2'	2:C3:140:G:C8	2.52	0.45
3:LA:7:ASN:OD1	3:LA:8:GLN:N	2.50	0.45
5:LC:308:LYS:NZ	44:1:609:G:O6	2.45	0.45
13:LL:114:GLN:HB2	13:LL:117:LYS:NZ	2.31	0.45
20:LS:81:TYR:CE1	20:LS:88:HIS:HB2	2.51	0.45
21:LT:102:ARG:HD2	21:LT:106:LEU:HD21	1.97	0.45
44:1:245:U:H2'	44:1:246:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:649:A:H2'	44:1:650:C:C6	2.52	0.45
44:1:972:A:H2'	44:1:973:A:C8	2.52	0.45
44:1:1019:G:N2	44:1:1033:U:O2	2.39	0.45
44:1:1307:G:O2'	44:1:1308:A:OP2	2.31	0.45
44:1:3387:U:H2'	44:1:3388:C:C6	2.52	0.45
46:B:506:TYR:CD1	46:B:545:ARG:HG3	2.52	0.45
46:B:538:LYS:HE2	46:B:586:SER:OG	2.16	0.45
46:B:725:LYS:O	46:B:729:LYS:HG2	2.17	0.45
2:C3:57:C:OP2	37:Lj:68:LYS:NZ	2.48	0.45
3:LA:241:ARG:NH1	44:1:2155:G:OP1	2.43	0.45
5:LC:342:LYS:O	44:1:515:C:O2'	2.25	0.45
8:LF:206:LYS:HB3	44:1:1334:U:H5''	1.98	0.45
9:LG:73:PRO:HD3	9:LG:233:TRP:CD2	2.52	0.45
10:LH:22:SER:O	10:LH:23:ARG:HD3	2.17	0.45
11:LI:116:ARG:HH22	44:1:2622:C:N4	2.10	0.45
13:LL:111:ALA:O	13:LL:115:ARG:HB2	2.16	0.45
21:LT:53:PRO:HB3	21:LT:91:LEU:HD21	1.97	0.45
26:LY:3:LYS:HE3	26:LY:8:VAL:O	2.17	0.45
44:1:201:A:H2'	44:1:202:G:H8	1.81	0.45
44:1:495:G:H2'	44:1:496:C:C6	2.52	0.45
44:1:1246:G:O2'	44:1:1247:U:O5'	2.34	0.45
44:1:1320:C:H2'	44:1:1321:G:H8	1.81	0.45
44:1:1357:G:H2'	44:1:1358:C:H6	1.81	0.45
44:1:1497:C:H2'	44:1:1498:A:C8	2.47	0.45
44:1:1744:G:H2'	44:1:1745:C:H6	1.82	0.45
44:1:2284:C:N4	44:1:2308:C:O4'	2.49	0.45
46:B:779:VAL:O	46:B:783:LYS:HG2	2.16	0.45
3:LA:203:ALA:O	44:1:914:A:O2'	2.34	0.45
5:LC:4:PRO:O	5:LC:5:GLN:HG2	2.16	0.45
11:LI:50:VAL:HG12	11:LI:167:LEU:HD23	1.99	0.45
15:LN:50:ARG:NH2	44:1:267:G:O3'	2.49	0.45
18:LQ:89:ASP:HB3	44:1:677:A:OP1	2.17	0.45
19:LR:53:LYS:HG3	19:LR:54:ALA:N	2.32	0.45
20:LS:2:ALA:HA	44:1:1324:U:H5'	1.98	0.45
26:LY:56:VAL:CG1	26:LY:104:LEU:HG	2.46	0.45
35:Lh:47:VAL:O	35:Lh:51:ILE:HG13	2.17	0.45
39:Ll:28:ARG:HA	39:Ll:28:ARG:HD2	1.83	0.45
44:1:544:C:H2'	44:1:547:G:H1	1.81	0.45
44:1:562:C:H2'	44:1:563:U:C6	2.51	0.45
44:1:786:A:O3'	44:1:787:G:H8	2.00	0.45
44:1:987:U:H2'	44:1:988:U:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:1143:A:H5'	44:1:1368:U:H1'	1.98	0.45
44:1:1532:C:H2'	44:1:1533:U:C6	2.51	0.45
44:1:2096:A:H2'	44:1:2097:U:C6	2.51	0.45
44:1:2148:U:H2'	44:1:2149:A:C8	2.52	0.45
44:1:2876:C:H2'	44:1:2877:G:O4'	2.17	0.45
46:B:176:SER:HA	46:B:205:LEU:HD13	1.98	0.45
6:LD:64:ILE:HG13	6:LD:109:THR:HG21	1.98	0.45
13:LL:105:ASN:C	36:Li:20:MET:HE1	2.41	0.45
15:LN:93:LYS:HE3	44:1:276:U:O2	2.17	0.45
16:LO:168[A]:TYR:OH	44:1:3190:C:OP1	2.23	0.45
27:LZ:90:GLU:OE1	27:LZ:90:GLU:N	2.50	0.45
35:Lh:47:VAL:O	35:Lh:50:SER:OG	2.29	0.45
44:1:210:U:C2	44:1:230:U:H4'	2.51	0.45
44:1:791:A:H2'	44:1:792:G:H8	1.82	0.45
44:1:1506:A:H1'	44:1:1848:G:O6	2.17	0.45
44:1:1544:G:O2'	44:1:2167:A:H1'	2.16	0.45
44:1:1718:G:H2'	44:1:1719:G:H8	1.82	0.45
44:1:1895:A:N6	44:1:2335:G:O2'	2.49	0.45
44:1:2611:U:H2'	44:1:2612:U:H6	1.79	0.45
44:1:3101:G:H2'	44:1:3102:G:C8	2.52	0.45
7:LE:17:ALA:O	44:1:591:G:O2'	2.32	0.45
17:LP:126:ARG:HA	17:LP:140:GLU:HB3	1.99	0.45
18:LQ:122:ILE:HG23	18:LQ:126:GLN:HB2	1.99	0.45
21:LT:35:LYS:HE3	44:1:1084:A:H5''	1.98	0.45
27:LZ:89:VAL:HG12	27:LZ:92:PHE:CZ	2.52	0.45
44:1:100:A:H3'	44:1:101:G:H21	1.82	0.45
44:1:374:A:O2'	44:1:376:G:H5'	2.17	0.45
44:1:432:G:H2'	44:1:433:A:C8	2.51	0.45
44:1:748:U:H2'	44:1:749:C:H6	1.81	0.45
44:1:761:A:N6	44:1:769:G:H21	2.15	0.45
44:1:1047:A:H2'	44:1:1048:A:C8	2.51	0.45
44:1:1222:G:C2	44:1:1285:G:C4	3.05	0.45
44:1:1373:A:H2'	44:1:1374:G:C8	2.52	0.45
44:1:1895:A:O2'	44:1:3053:G:H4'	2.17	0.45
45:A:85:PRO:HG2	46:B:439:PHE:HZ	1.81	0.45
45:A:129:TYR:O	45:A:134:TYR:HB2	2.17	0.45
2:C3:138:A:H2'	2:C3:139:U:H6	1.82	0.45
3:LA:147:ARG:HG2	3:LA:157:VAL:HG22	1.98	0.45
4:LB:60:LEU:HD21	4:LB:62:ARG:HB2	1.99	0.45
9:LG:68:ARG:NH1	9:LG:237:ILE:O	2.50	0.45
9:LG:241:LYS:HB2	44:1:2586:G:C5	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LN:116:LEU:HD23	15:LN:117:ASN:OD1	2.16	0.45
18:LQ:173:GLU:OE2	28:La:49:HIS:ND1	2.46	0.45
21:LT:88:ARG:O	44:1:2722:U:O2'	2.33	0.45
37:Lj:3:LYS:HB3	44:1:2138:A:C4	2.52	0.45
44:1:307:A:H2'	44:1:308:A:H8	1.80	0.45
44:1:673:U:H2'	44:1:674:G:H8	1.82	0.45
44:1:697:A:H2'	44:1:698:U:C6	2.52	0.45
44:1:899:U:H2'	44:1:900:G:H8	1.82	0.45
44:1:1573:G:H2'	44:1:1574:C:O4'	2.17	0.45
44:1:2154:U:H2'	44:1:2155:G:C8	2.51	0.45
44:1:3121:U:H4'	44:1:3122:A:OP1	2.17	0.45
44:1:3127:A:H2'	44:1:3128:G:O4'	2.16	0.45
46:B:580:THR:O	46:B:581:GLN:NE2	2.50	0.45
1:C4:118:A:H2'	1:C4:119:U:C6	2.52	0.44
4:LB:66:LYS:NZ	23:LV:9:THR:OG1	2.50	0.44
12:LJ:150:ASN:OD1	12:LJ:151:SER:N	2.50	0.44
13:LL:166:ALA:HB3	28:La:135:GLU:OE2	2.16	0.44
15:LN:108:ARG:NH2	44:1:1547:G:OP1	2.49	0.44
37:Lj:67:LEU:O	37:Lj:70:VAL:HG12	2.17	0.44
44:1:259:C:N4	44:1:260:C:H41	2.15	0.44
44:1:291:C:H2'	44:1:292:U:H6	1.82	0.44
44:1:1120:A:H2'	44:1:1121:U:C6	2.52	0.44
44:1:1132:C:H2'	44:1:1133:A:C8	2.51	0.44
44:1:1174:G:H2'	44:1:1175:C:C6	2.52	0.44
44:1:2412:G:H2'	44:1:2413:A:H8	1.82	0.44
46:B:381:TYR:O	46:B:385:LYS:N	2.50	0.44
46:B:619:PHE:HZ	46:B:643:LEU:HD22	1.82	0.44
46:B:666:ALA:O	46:B:670:ILE:HG12	2.17	0.44
3:LA:117:GLU:HG2	3:LA:124:GLY:N	2.32	0.44
7:LE:149:ILE:HG23	7:LE:155:LEU:HD22	1.98	0.44
12:LJ:106:ILE:O	12:LJ:125:MET:N	2.46	0.44
18:LQ:170:ARG:O	18:LQ:171:LYS:HG2	2.16	0.44
21:LT:127:GLN:HG2	44:1:1095:U:N3	2.32	0.44
21:LT:129:LYS:HA	44:1:1098:A:OP2	2.17	0.44
44:1:301:G:H2'	44:1:302:U:C6	2.52	0.44
44:1:508:U:H2'	44:1:509:U:C6	2.52	0.44
44:1:542:G:C4	44:1:543:C:N3	2.85	0.44
44:1:702:C:C2	44:1:703:G:C8	3.06	0.44
44:1:717:C:H2'	44:1:718:G:O4'	2.18	0.44
44:1:967:A:C4	44:1:968:G:C8	3.05	0.44
44:1:993:G:N3	44:1:2637:A:H2'	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:1444:G:H2'	44:1:1445:U:O4'	2.16	0.44
44:1:1757:A:H2'	44:1:1758:G:C8	2.51	0.44
44:1:1976:G:N2	44:1:2047:A:O2'	2.50	0.44
44:1:2446:U:HO2'	44:1:2447:A:P	2.40	0.44
2:C3:2:A:C4	2:C3:3:A:C8	3.05	0.44
4:LB:94:GLU:OE1	4:LB:94:GLU:N	2.50	0.44
6:LD:41:LYS:HB2	21:LT:68:THR:O	2.17	0.44
6:LD:140:ARG:NH2	44:1:1078:U:H3'	2.32	0.44
10:LH:36:LYS:HG2	10:LH:78:MET:HE1	1.99	0.44
14:LM:121:MET:HE3	44:1:3214:U:O2	2.17	0.44
19:LR:84:THR:HG23	19:LR:87:ALA:H	1.83	0.44
20:LS:96:ASP:CG	20:LS:97:VAL:H	2.26	0.44
26:LY:74:TYR:CD2	26:LY:77:LYS:HB2	2.51	0.44
34:Lg:19:LYS:HA	34:Lg:19:LYS:HD2	1.86	0.44
44:1:1534:A:H2'	44:1:1535:A:C8	2.52	0.44
44:1:1921:A:H2'	44:1:1922:A:C8	2.52	0.44
44:1:2984:C:H2'	44:1:2985:C:C6	2.52	0.44
46:B:670:ILE:HD13	46:B:685:LEU:HB3	1.99	0.44
5:LC:155:ASP:OD1	5:LC:155:ASP:N	2.50	0.44
10:LH:6:THR:HG21	10:LH:65:VAL:HG13	1.99	0.44
16:LO:39[A]:GLU:CD	16:LO:39[A]:GLU:H	2.25	0.44
18:LQ:178:ARG:HA	18:LQ:178:ARG:HD2	1.74	0.44
28:La:13:GLY:HA2	44:1:943:U:H3'	2.00	0.44
31:Ld:5:LYS:H	46:B:720:LYS:HE3	1.80	0.44
31:Ld:10:ARG:NH1	44:1:3386:G:OP1	2.50	0.44
44:1:274:G:H2'	44:1:275:U:H6	1.83	0.44
44:1:395:A:H8	44:1:395:A:O5'	2.01	0.44
44:1:542:G:H1	44:1:550:A:N6	2.13	0.44
44:1:1363:A:H2'	44:1:1364:C:C6	2.53	0.44
44:1:2043:U:O4	44:1:2045:G:N2	2.34	0.44
44:1:3006:A:C2	44:1:3141:A:C4	3.06	0.44
45:A:103:MET:HE2	45:A:109:HIS:CE1	2.52	0.44
10:LH:62:ARG:NH2	44:1:3115:C:OP1	2.51	0.44
10:LH:155:SER:OG	44:1:3110:C:O3'	2.35	0.44
16:LO:60[A]:LYS:HE3	44:1:1307:G:H5''	1.99	0.44
20:LS:19:VAL:O	20:LS:19:VAL:HG13	2.17	0.44
27:LZ:23:VAL:HB	27:LZ:43:VAL:HB	2.00	0.44
28:La:75:LEU:HG	28:La:114:GLY:HA2	1.99	0.44
37:Lj:55:ARG:NH1	44:1:353:G:O6	2.51	0.44
38:Lk:7:ASP:OD2	38:Lk:10:GLN:N	2.48	0.44
44:1:646:A:H2'	44:1:647:A:O4'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:712:G:H2'	44:1:713:U:C6	2.53	0.44
44:1:2579:G:OP2	44:1:2580:A:O2'	2.31	0.44
44:1:3081:C:H2'	44:1:3082:C:H6	1.83	0.44
2:C3:36:G:OP1	37:Lj:66:TYR:OH	2.31	0.44
4:LB:34:LYS:HE2	4:LB:34:LYS:HB2	1.81	0.44
9:LG:99:PRO:HG2	9:LG:190:VAL:HG13	1.99	0.44
11:LI:3:ARG:NH1	11:LI:63:GLU:OE2	2.50	0.44
11:LI:171:TRP:O	11:LI:174:THR:OG1	2.29	0.44
12:LJ:21:ILE:CD1	12:LJ:37:LEU:HD21	2.47	0.44
14:LM:19:ARG:HB3	14:LM:35:ILE:HD12	2.00	0.44
15:LN:187:ARG:HD3	44:1:49:A:N7	2.33	0.44
20:LS:13:ARG:O	20:LS:22:PRO:HG2	2.18	0.44
44:1:127:G:H2'	44:1:128:G:H8	1.82	0.44
44:1:3051:U:H2'	44:1:3052:G:H8	1.82	0.44
44:1:3190:C:H2'	44:1:3191:G:C8	2.51	0.44
44:1:3294:A:H2'	44:1:3295:A:O4'	2.18	0.44
44:1:3320:A:H2'	44:1:3321:C:C6	2.53	0.44
44:1:3347:A:H2'	44:1:3348:G:H8	1.82	0.44
46:B:534:GLU:O	46:B:538:LYS:HG2	2.17	0.44
1:C4:11:A:N1	1:C4:67:G:O2'	2.43	0.44
4:LB:102:LEU:HD23	4:LB:102:LEU:H	1.83	0.44
6:LD:39:GLN:OE1	6:LD:40:HIS:N	2.51	0.44
6:LD:281:GLU:OE1	6:LD:281:GLU:N	2.49	0.44
12:LJ:94:ARG:HG2	44:1:2673:A:OP1	2.18	0.44
15:LN:105:ARG:HG2	15:LN:108:ARG:HH22	1.82	0.44
17:LP:167:ARG:NH2	44:1:620:U:OP1	2.50	0.44
30:Lc:13:LYS:HB3	30:Lc:100:ILE:CG2	2.47	0.44
35:Lh:31:LEU:HB3	35:Lh:44:ILE:HG22	1.99	0.44
44:1:79:U:N3	44:1:80:G:N7	2.66	0.44
44:1:296:A:H2'	44:1:297:G:N3	2.32	0.44
44:1:929:A:H2'	44:1:930:U:C6	2.53	0.44
44:1:2578:U:H2'	44:1:2579:G:O4'	2.17	0.44
44:1:2683:U:H2'	44:1:2684:C:C6	2.50	0.44
45:A:39:TRP:CZ3	45:A:66:LYS:HB2	2.53	0.44
2:C3:60:U:OP1	25:LX:54:TYR:OH	2.27	0.44
5:LC:22:LEU:HD22	5:LC:26:PHE:CD2	2.50	0.44
9:LG:241:LYS:O	9:LG:245:LYS:HD3	2.18	0.44
12:LJ:16:LYS:HB3	12:LJ:72:ARG:NH1	2.32	0.44
12:LJ:32:ARG:HG3	12:LJ:123:PHE:CE2	2.53	0.44
12:LJ:77:GLU:HA	12:LJ:80:LEU:HB3	2.00	0.44
26:LY:70:ILE:HD13	26:LY:82:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:209:A:H4'	44:1:211:A:C8	2.52	0.44
44:1:255:A:H2'	44:1:256:G:C8	2.53	0.44
44:1:412:G:H2'	44:1:413:U:C6	2.53	0.44
44:1:428:A:H2'	44:1:429:U:H6	1.82	0.44
44:1:1237:G:C6	44:1:1251:A:N6	2.81	0.44
44:1:1764:U:H3'	44:1:1765:U:H4'	2.00	0.44
44:1:2133:U:O4	44:1:2147:A:H2	2.00	0.44
44:1:2416:U:H2'	44:1:2417:U:C6	2.53	0.44
44:1:2677:G:N2	44:1:2679:A:H2	2.16	0.44
44:1:3101:G:H2'	44:1:3102:G:H8	1.82	0.44
44:1:3218:A:H4'	44:1:3219:G:O5'	2.18	0.44
45:A:42:LEU:HD13	45:A:65:ALA:HB3	2.00	0.44
2:C3:43:A:H2'	2:C3:44:A:H8	1.82	0.44
7:LE:77:ARG:HH11	7:LE:77:ARG:HG2	1.83	0.44
17:LP:83:TRP:O	44:1:2352:A:H5''	2.18	0.44
21:LT:131:GLN:OE1	21:LT:131:GLN:HA	2.18	0.44
42:Lo:34:SER:OG	44:1:2767:U:OP1	2.33	0.44
44:1:945:C:H2'	44:1:946:U:H6	1.81	0.44
44:1:1956:A:N1	44:1:2086:A:N6	2.66	0.44
44:1:3017:A:H2'	44:1:3018:C:H6	1.83	0.44
3:LA:204:MET:SD	3:LA:209:HIS:HB2	2.57	0.43
5:LC:11:LEU:HD12	5:LC:155:ASP:OD2	2.18	0.43
5:LC:181:VAL:HG11	5:LC:224:GLY:HA3	2.00	0.43
6:LD:129:TYR:CG	6:LD:177:GLU:HB3	2.53	0.43
17:LP:47:TYR:OH	17:LP:57:ALA:O	2.33	0.43
23:LV:47:ASN:ND2	44:1:2880:U:OP1	2.49	0.43
30:Lc:22:LYS:HG3	30:Lc:93:LEU:HB2	1.99	0.43
36:Li:70:ARG:HD3	36:Li:84:LYS:HG2	2.00	0.43
42:Lo:99:GLN:OE1	42:Lo:99:GLN:N	2.51	0.43
44:1:598:A:H2'	44:1:599:C:C6	2.53	0.43
44:1:1072:G:H2'	44:1:1073:U:H6	1.83	0.43
44:1:1239:C:H2'	44:1:1240:A:H8	1.83	0.43
44:1:2112:U:H4'	44:1:2113:A:H5'	1.99	0.43
44:1:2406:C:H2'	44:1:2407:C:H6	1.82	0.43
44:1:2526:C:H2'	44:1:2527:G:H8	1.83	0.43
46:B:13:VAL:HG13	46:B:18:PHE:HE1	1.83	0.43
2:C3:21:C:OP1	5:LC:193:LYS:NZ	2.42	0.43
4:LB:7:GLU:HG2	44:1:2915:U:H5	1.81	0.43
4:LB:21:ARG:HG2	4:LB:269:GLN:NE2	2.33	0.43
4:LB:221:THR:OG1	44:1:3047:U:OP1	2.35	0.43
8:LF:197:GLN:OE1	8:LF:197:GLN:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LG:60:ARG:O	9:LG:64:ILE:HG12	2.18	0.43
10:LH:9:GLN:NE2	10:LH:52:LEU:HD11	2.33	0.43
10:LH:59:ASN:HB2	14:LM:41:GLN:HE21	1.82	0.43
16:LO:49[A]:ARG:HH12	44:1:1190:A:H2'	1.83	0.43
19:LR:19:LYS:NZ	44:1:1876:U:OP1	2.51	0.43
34:Lg:44:CYS:SG	34:Lg:81:CYS:N	2.81	0.43
39:Ll:2:ALA:N	44:1:1492:G:N7	2.67	0.43
44:1:255:A:H2'	44:1:256:G:H8	1.83	0.43
44:1:342:A:C4	44:1:368:G:N7	2.86	0.43
44:1:1176:C:H2'	44:1:1177:G:N2	2.33	0.43
44:1:2806:U:H2'	44:1:2807:U:C6	2.53	0.43
44:1:3038:U:H2'	44:1:3039:C:O4'	2.17	0.43
44:1:3132:C:H2'	44:1:3133:C:C6	2.53	0.43
46:B:155:SER:O	46:B:159:VAL:HG23	2.18	0.43
46:B:180:ARG:NH2	46:B:215:GLU:OE1	2.51	0.43
1:C4:16:U:H2'	1:C4:17:A:H8	1.82	0.43
8:LF:156:ILE:HD13	8:LF:161:VAL:HB	1.99	0.43
12:LJ:75:LYS:O	12:LJ:79:ILE:HG13	2.18	0.43
21:LT:71:SER:OG	21:LT:72:VAL:N	2.51	0.43
26:LY:32:SER:HA	26:LY:49:PRO:HA	2.01	0.43
33:Lf:58:GLU:OE2	33:Lf:62:SER:N	2.50	0.43
42:Lo:15:LYS:HA	42:Lo:18:ARG:NH1	2.33	0.43
44:1:155:G:N1	44:1:265:A:OP2	2.37	0.43
44:1:170:G:N1	44:1:248:U:N3	2.42	0.43
44:1:339:C:OP1	44:1:1380:G:O2'	2.33	0.43
44:1:1049:C:H2'	44:1:1050:U:C6	2.53	0.43
44:1:1397:C:N4	44:1:1414:G:O6	2.52	0.43
44:1:1472:U:H2'	44:1:1473:G:C8	2.53	0.43
44:1:1561:G:O2'	44:1:1562:C:H5'	2.17	0.43
44:1:1788:C:C2	44:1:1789:G:C8	3.06	0.43
46:B:431:TYR:O	46:B:435:ASP:N	2.50	0.43
46:B:708:THR:O	46:B:712:THR:HG22	2.18	0.43
3:LA:128:ARG:HE	3:LA:128:ARG:HB3	1.64	0.43
4:LB:173:GLN:OE1	44:1:3313:U:H4'	2.18	0.43
6:LD:204:VAL:O	6:LD:208:MET:HG2	2.19	0.43
13:LL:62:THR:O	13:LL:64:LYS:N	2.51	0.43
20:LS:10:ILE:O	20:LS:59:VAL:HG22	2.18	0.43
35:Lh:83:LYS:O	35:Lh:83:LYS:HG3	2.18	0.43
39:Ll:15:LYS:O	39:Ll:19:GLN:HG2	2.18	0.43
44:1:180:C:H2'	44:1:181:U:H6	1.84	0.43
44:1:985:U:H2'	44:1:986:U:H6	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:1177:G:N2	44:1:1177:G:OP1	2.27	0.43
44:1:1525:G:H2'	44:1:1525:G:N3	2.34	0.43
44:1:2662:G:H2'	44:1:2663:G:H8	1.83	0.43
44:1:2975:U:H2'	44:1:2976:A:C8	2.53	0.43
2:C3:67:U:H2'	2:C3:68:G:C8	2.53	0.43
5:LC:22:LEU:HA	5:LC:23:PRO:HD3	1.89	0.43
5:LC:64:SER:HA	5:LC:75:PRO:HA	2.01	0.43
19:LR:42:ARG:HH22	44:1:1601:U:P	2.41	0.43
33:Lf:75:HIS:N	33:Lf:80:VAL:O	2.51	0.43
38:Lk:63:LYS:HZ1	44:1:1975:C:H4'	1.83	0.43
44:1:543:C:O2'	44:1:544:C:O5'	2.37	0.43
44:1:553:U:H2'	44:1:554:A:O4'	2.18	0.43
44:1:788:C:C2	44:1:789:A:C8	3.06	0.43
44:1:1120:A:H2'	44:1:1121:U:H6	1.83	0.43
44:1:1836:C:H2'	44:1:1837:U:C6	2.53	0.43
44:1:2864:A:H2'	44:1:2865:U:C6	2.53	0.43
44:1:2889:C:H2'	44:1:2890:A:H8	1.84	0.43
44:1:3353:G:H3'	44:1:3354:U:O4'	2.19	0.43
46:B:768:LEU:O	46:B:772:LEU:HG	2.18	0.43
1:C4:35:C:O2	1:C4:45:A:O2'	2.36	0.43
2:C3:27:U:H2'	2:C3:28:C:H6	1.83	0.43
3:LA:147:ARG:HG2	3:LA:157:VAL:HG13	2.01	0.43
9:LG:99:PRO:HD3	9:LG:132:VAL:HG12	2.00	0.43
11:LI:115:MET:HE3	11:LI:115:MET:HB3	1.77	0.43
11:LI:158:LYS:NZ	44:1:2852:C:N3	2.57	0.43
15:LN:154:PRO:O	15:LN:157:LYS:HG3	2.18	0.43
32:Le:42:VAL:O	32:Le:52:GLN:NE2	2.52	0.43
33:Lf:20:LYS:NZ	44:1:1177:G:N7	2.67	0.43
44:1:176:G:C2	44:1:243:G:C5	3.06	0.43
44:1:506:U:H2'	44:1:507:U:O4'	2.18	0.43
44:1:725:G:O6	44:1:746:A:N6	2.51	0.43
44:1:2582:C:H2'	44:1:2583:C:H6	1.84	0.43
44:1:2681:U:H2'	44:1:2682:C:H6	1.84	0.43
44:1:3269:U:H4'	44:1:3270:U:O5'	2.19	0.43
8:LF:173:LEU:HB3	8:LF:178:ILE:HB	2.00	0.43
9:LG:128:LYS:NZ	9:LG:202:GLU:OE1	2.35	0.43
43:Lp:88:GLU:HA	43:Lp:91:GLU:HG3	2.00	0.43
44:1:61:A:C4	44:1:62:A:C8	3.07	0.43
44:1:393:U:H2'	44:1:394:G:O4'	2.19	0.43
44:1:434:U:H2'	44:1:435:C:C6	2.54	0.43
44:1:596:C:N3	44:1:608:A:O2'	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:992:A:O2'	44:1:993:G:H5'	2.18	0.43
44:1:998:A:H2'	44:1:999:G:C8	2.54	0.43
44:1:1478:C:H2'	44:1:1479:U:C6	2.53	0.43
44:1:2045:G:H2'	44:1:2046:U:C6	2.53	0.43
44:1:2495:C:HO2'	44:1:2496:C:P	2.41	0.43
44:1:2542:U:O2'	44:1:2543:U:H5''	2.18	0.43
44:1:2651:G:H5''	44:1:2652:U:O4'	2.18	0.43
44:1:3157:U:H4'	44:1:3158:G:H5'	2.01	0.43
45:A:103:MET:O	45:A:103:MET:HE3	2.18	0.43
1:C4:47:C:H2'	1:C4:48:U:C6	2.54	0.43
1:C4:73:C:N4	20:LS:19:VAL:HG11	2.33	0.43
7:LE:21:THR:HG22	7:LE:23:LYS:H	1.83	0.43
10:LH:19:SER:HB3	10:LH:26:LYS:HB3	2.01	0.43
13:LL:184:GLU:O	13:LL:188:ARG:HG2	2.18	0.43
15:LN:122:ASN:OD1	15:LN:123:GLN:N	2.45	0.43
21:LT:136:ARG:HB3	21:LT:139:ARG:HH21	1.84	0.43
34:Lg:104:VAL:HA	34:Lg:107:GLU:OE2	2.18	0.43
41:Ln:2:ARG:HB3	41:Ln:5:TRP:CD1	2.53	0.43
42:Lo:80:ARG:CD	44:1:2769:A:H5''	2.49	0.43
44:1:542:G:N1	44:1:550:A:N1	2.66	0.43
44:1:1275:C:H2'	44:1:1276:U:O4'	2.19	0.43
44:1:1757:A:H2'	44:1:1758:G:H8	1.84	0.43
44:1:1798:A:H2'	44:1:1799:A:H8	1.81	0.43
44:1:2427:U:H2'	44:1:2428:U:C6	2.54	0.43
46:B:739:ARG:N	46:B:739:ARG:HD2	2.34	0.43
1:C4:118:A:H5''	6:LD:253:PHE:HZ	1.84	0.43
2:C3:5:U:H2'	2:C3:6:U:C6	2.54	0.43
6:LD:60:ILE:HB	6:LD:80:SER:HB3	2.00	0.43
8:LF:176:TYR:HB3	8:LF:194:HIS:CG	2.54	0.43
10:LH:89:LYS:HG2	10:LH:145:VAL:HG22	2.01	0.43
11:LI:213:PHE:N	11:LI:214:PRO:HD3	2.34	0.43
32:Le:87:MET:HE3	32:Le:87:MET:HA	2.00	0.43
36:Li:98:ARG:HG3	36:Li:99:ARG:HH22	1.83	0.43
37:Lj:21:ARG:NH2	37:Lj:41:ALA:O	2.37	0.43
40:Lm:110:CYS:SG	40:Lm:112:LYS:HG2	2.58	0.43
44:1:429:U:H2'	44:1:430:U:H6	1.82	0.43
44:1:1881:A:H2'	44:1:1882:G:H8	1.84	0.43
44:1:2049:A:N6	44:1:2051:G:H1'	2.34	0.43
44:1:3015:G:H2'	44:1:3016:A:H8	1.83	0.43
45:A:20:LEU:HD11	46:B:475:LEU:HD11	2.01	0.43
45:A:113:PHE:HB2	45:A:169:LYS:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:701:MET:HA	46:B:704:HIS:HB3	2.01	0.43
2:C3:16:G:N2	44:1:406:G:H1'	2.34	0.43
5:LC:3:ARG:NH1	5:LC:24:ALA:HA	2.34	0.43
13:LL:76:THR:O	13:LL:78:ALA:N	2.52	0.43
19:LR:128:LYS:NZ	44:1:1724:U:OP1	2.39	0.43
44:1:100:A:H2'	44:1:101:G:N3	2.34	0.43
44:1:1252:A:H2'	44:1:1253:U:C6	2.54	0.43
44:1:2038:C:H2'	44:1:2039:C:C6	2.54	0.43
44:1:2740:A:H2'	44:1:2741:C:C6	2.53	0.43
44:1:2805:G:H2'	44:1:2806:U:C6	2.54	0.43
44:1:3292:A:H2'	44:1:3293:U:C6	2.54	0.43
2:C3:28:C:H2'	2:C3:29:U:H6	1.84	0.42
3:LA:94:ALA:O	3:LA:102:LEU:HD11	2.19	0.42
6:LD:108:ARG:HG2	6:LD:112:LYS:HZ1	1.84	0.42
8:LF:40:LYS:O	8:LF:44:ILE:HG12	2.19	0.42
9:LG:173:MET:HE3	36:LI:39:PHE:HZ	1.84	0.42
11:LI:68:ALA:HB2	11:LI:158:LYS:HB2	2.01	0.42
11:LI:194:GLY:HA3	44:1:1011:A:H5'	2.01	0.42
21:LT:73:GLY:HA2	21:LT:89:LEU:O	2.19	0.42
29:Lb:27:TYR:CD2	44:1:747:A:H4'	2.53	0.42
30:Lc:22:LYS:HG2	30:Lc:94:GLU:HB3	2.00	0.42
31:Ld:17:HIS:HB2	31:Ld:69:TYR:HB3	2.01	0.42
44:1:7:C:H2'	44:1:8:C:C6	2.54	0.42
44:1:567:G:H2'	44:1:568:G:H8	1.80	0.42
44:1:727:G:OP2	44:1:742:G:N2	2.52	0.42
44:1:998:A:H2'	44:1:999:G:H8	1.84	0.42
44:1:1194:G:H8	44:1:1194:G:O5'	2.02	0.42
44:1:1299:U:H2'	44:1:1300:G:O4'	2.18	0.42
44:1:1363:A:H2'	44:1:1364:C:H6	1.84	0.42
44:1:1743:G:C2	44:1:1744:G:C8	3.07	0.42
44:1:1809:A:H2'	44:1:1810:A:O4'	2.19	0.42
44:1:2430:A:H2'	44:1:2431:C:H6	1.82	0.42
44:1:2700:G:H2'	44:1:2701:U:C6	2.53	0.42
44:1:2723:U:H2'	44:1:2724:U:C6	2.54	0.42
44:1:3105:U:H2'	44:1:3106:A:H8	1.84	0.42
46:B:315:GLU:HG2	46:B:350:ILE:HD11	2.00	0.42
46:B:421:VAL:HG21	46:B:451:TYR:HE2	1.82	0.42
3:LA:68:LYS:HD3	3:LA:70:ARG:HE	1.84	0.42
6:LD:18:THR:HA	6:LD:19:PRO:HD3	1.77	0.42
8:LF:132:PRO:HA	8:LF:229:PHE:CD1	2.53	0.42
8:LF:138:TYR:CE2	8:LF:233:GLU:HB2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LJ:21:ILE:HD11	12:LJ:125:MET:HE1	2.01	0.42
23:LV:81:GLN:NE2	23:LV:83:LYS:O	2.48	0.42
28:La:74:ASN:HA	28:La:113:LEU:O	2.19	0.42
30:Lc:10:ILE:HA	30:Lc:13:LYS:HE2	2.01	0.42
33:Lf:48:ARG:HH11	33:Lf:48:ARG:HG3	1.83	0.42
41:Ln:15:ARG:HD3	41:Ln:18:ARG:NH2	2.34	0.42
43:Lp:84:ARG:HH22	43:Lp:85:ARG:HG3	1.84	0.42
44:1:312:C:H2'	44:1:313:A:C8	2.54	0.42
44:1:1333:C:H2'	44:1:1334:U:C6	2.54	0.42
44:1:1359:C:H2'	44:1:1360:C:H6	1.84	0.42
44:1:1478:C:H2'	44:1:1479:U:H6	1.84	0.42
44:1:2086:A:O2'	44:1:2087:C:H5'	2.19	0.42
44:1:2215:A:C4	44:1:2216:G:C8	3.08	0.42
44:1:2660:G:OP1	44:1:2750:U:O2'	2.37	0.42
44:1:2689:A:N3	44:1:2689:A:H2'	2.34	0.42
44:1:3017:A:H2'	44:1:3018:C:C6	2.54	0.42
45:A:1:MET:HG2	46:B:264:TYR:CZ	2.54	0.42
46:B:432:GLN:CD	46:B:442:MET:HB2	2.43	0.42
2:C3:29:U:H5''	13:LL:27:ASP:HB3	2.00	0.42
2:C3:77:A:H2'	2:C3:78:G:O4'	2.19	0.42
3:LA:137:ILE:HD11	3:LA:149:ARG:HB2	2.00	0.42
6:LD:119:TYR:CD2	6:LD:141:PRO:HB3	2.54	0.42
9:LG:68:ARG:NE	44:1:2514:U:OP1	2.52	0.42
13:LL:102:GLN:HE21	36:Li:25:LYS:HD3	1.84	0.42
20:LS:76:GLY:N	20:LS:127:ALA:O	2.36	0.42
22:LU:100:THR:HA	44:1:1677:G:OP1	2.19	0.42
26:LY:23:PRO:O	26:LY:27:ARG:HG3	2.19	0.42
27:LZ:84:ARG:HG3	27:LZ:84:ARG:NH1	2.34	0.42
30:Lc:11:ASN:OD1	30:Lc:12:GLN:N	2.52	0.42
35:Lh:93:THR:OG1	44:1:135:C:H1'	2.18	0.42
39:Ll:10:LYS:HA	39:Ll:13:MET:HG3	2.02	0.42
44:1:184:U:H2'	44:1:185:C:C6	2.54	0.42
44:1:731:U:H2'	44:1:732:C:C6	2.54	0.42
44:1:798:G:H2'	44:1:799:G:O4'	2.19	0.42
44:1:970:A:H2'	44:1:971:G:H8	1.84	0.42
44:1:1261:G:H3'	44:1:1261:G:N3	2.34	0.42
44:1:1590:G:O2'	44:1:1797:A:N6	2.52	0.42
44:1:2205:U:H5'	44:1:2206:G:OP2	2.19	0.42
44:1:2724:U:OP2	44:1:2726:C:N4	2.52	0.42
44:1:2998:U:H2'	44:1:2999:U:C6	2.54	0.42
44:1:3064:U:H2'	44:1:3065:G:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:3163:A:N6	44:1:3288:G:C6	2.87	0.42
45:A:26:ASN:O	46:B:469:ASN:ND2	2.52	0.42
46:B:322:LEU:HD13	46:B:351:MET:HE3	2.02	0.42
2:C3:6:U:H2'	2:C3:7:U:C6	2.54	0.42
2:C3:75:G:H2'	2:C3:76:C:C6	2.54	0.42
4:LB:35:ASP:OD2	4:LB:37:ARG:NH1	2.52	0.42
13:LL:47:ALA:HB3	13:LL:48:PRO:HD3	2.01	0.42
15:LN:73:ARG:HE	15:LN:92:LEU:HD11	1.83	0.42
17:LP:86:LYS:NZ	44:1:2354:C:OP1	2.48	0.42
18:LQ:82:VAL:HB	18:LQ:139:ILE:HG13	2.01	0.42
21:LT:39:ILE:HD13	21:LT:63:VAL:HG22	2.01	0.42
21:LT:69:LYS:HB3	44:1:2737:C:OP1	2.19	0.42
23:LV:44:SER:OG	44:1:2935:U:O4	2.35	0.42
40:Lm:88:LYS:HA	40:Lm:92:ASP:HB2	2.01	0.42
43:Lp:16:VAL:HG12	44:1:1927:G:C8	2.54	0.42
44:1:297:G:H8	44:1:299:G:H1'	1.84	0.42
44:1:1214:U:H2'	44:1:1215:U:C6	2.54	0.42
44:1:1443:G:H2'	44:1:1444:G:C8	2.54	0.42
44:1:1660:C:H2'	44:1:1661:G:C8	2.54	0.42
44:1:1921:A:H2'	44:1:1922:A:H8	1.83	0.42
44:1:1973:G:O3'	44:1:1974:A:H8	2.02	0.42
44:1:1982:G:H2'	44:1:1983:G:H8	1.84	0.42
44:1:2232:A:H2'	44:1:2233:A:C8	2.53	0.42
44:1:2291:A:C6	44:1:2302:G:C6	3.07	0.42
44:1:2571:U:H4'	44:1:2572:C:H5'	2.01	0.42
44:1:2974:U:H2'	44:1:2975:U:C6	2.54	0.42
44:1:3163:A:H2'	44:1:3164:C:C6	2.54	0.42
44:1:3232:G:H2'	44:1:3233:C:C6	2.54	0.42
46:B:60:LEU:C	46:B:63:PRO:HD2	2.45	0.42
46:B:529:ILE:O	46:B:533:LEU:N	2.49	0.42
1:C4:10:C:C6	6:LD:20:PHE:HD1	2.34	0.42
6:LD:51:LEU:N	6:LD:145:PHE:O	2.35	0.42
9:LG:219:ASP:HB2	9:LG:223:ALA:HB3	2.01	0.42
15:LN:143:ARG:HE	35:Lh:92:LEU:HD23	1.83	0.42
16:LO:12[A]:LYS:NZ	44:1:3184:A:OP2	2.28	0.42
18:LQ:102:ALA:HA	18:LQ:122:ILE:O	2.20	0.42
28:La:7:LYS:NZ	44:1:1372:C:OP2	2.52	0.42
31:Ld:11:GLU:HG2	31:Ld:74:ARG:HG3	2.00	0.42
43:Lp:49:ARG:HB2	43:Lp:55:TRP:CZ3	2.53	0.42
44:1:128:G:H2'	44:1:129:U:C6	2.55	0.42
44:1:589:A:N6	44:1:610:G:H1'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:907:G:C5	44:1:926:A:C8	3.08	0.42
44:1:1085:A:H2'	44:1:1086:C:C6	2.54	0.42
44:1:1940:G:H2'	44:1:1941:C:C6	2.55	0.42
44:1:1957:G:H2'	44:1:1958:U:O4'	2.20	0.42
44:1:2827:U:O2'	44:1:2829:U:O4	2.36	0.42
44:1:3210:A:C4	44:1:3211:C:C5	3.08	0.42
44:1:3232:G:H2'	44:1:3233:C:H6	1.84	0.42
3:LA:221:LYS:HB2	3:LA:221:LYS:HE3	1.78	0.42
4:LB:123:TYR:CE1	4:LB:124:LYS:HG2	2.54	0.42
5:LC:299:ILE:HD12	5:LC:299:ILE:HA	1.79	0.42
7:LE:40:LEU:HD11	7:LE:54:TYR:HB2	2.02	0.42
21:LT:86:GLU:OE1	21:LT:88:ARG:NE	2.52	0.42
36:Li:71:LYS:NZ	44:1:2223:A:OP1	2.52	0.42
42:Lo:47:GLN:OE1	42:Lo:53:GLN:NE2	2.53	0.42
44:1:82:C:N3	44:1:104:G:N1	2.67	0.42
44:1:1913:A:N3	44:1:2120:A:H2'	2.34	0.42
44:1:2722:U:H2'	44:1:2723:U:H6	1.85	0.42
44:1:3023:U:H2'	44:1:3024:A:H8	1.85	0.42
44:1:3111:U:H2'	44:1:3112:G:O4'	2.20	0.42
9:LG:97:TYR:CE2	9:LG:203:VAL:HG23	2.49	0.42
26:LY:100:HIS:CD2	44:1:217:U:H4'	2.54	0.42
32:Le:50:ILE:HG22	44:1:426:G:H5'	2.02	0.42
44:1:552:G:H2'	44:1:553:U:H6	1.84	0.42
44:1:792:G:H2'	44:1:793:C:H6	1.85	0.42
44:1:1134:G:O2'	44:1:2642:A:N3	2.37	0.42
44:1:1370:G:H2'	44:1:1371:G:H8	1.84	0.42
44:1:1470:U:H2'	44:1:1471:U:C6	2.55	0.42
44:1:1896:A:N6	44:1:2339:C:H42	2.15	0.42
44:1:2279:A:N7	44:1:2288:G:C8	2.87	0.42
44:1:2315:G:C2	44:1:2316:G:N7	2.87	0.42
44:1:2662:G:H2'	44:1:2663:G:C8	2.54	0.42
2:C3:19:C:H2'	2:C3:20:U:C6	2.55	0.42
2:C3:26:U:H2'	2:C3:27:U:H6	1.83	0.42
2:C3:43:A:H2'	2:C3:44:A:C8	2.55	0.42
2:C3:64:U:C2	2:C3:65:A:C8	3.08	0.42
2:C3:140:G:C6	44:1:20:A:C6	3.08	0.42
6:LD:176:SER:HB2	44:1:2746:A:H4'	2.00	0.42
20:LS:7:TYR:HD2	20:LS:37:ALA:HB2	1.85	0.42
21:LT:57:TYR:CE2	21:LT:89:LEU:HD21	2.54	0.42
21:LT:112:ASN:OD1	21:LT:128:LEU:HD23	2.20	0.42
22:LU:97:SER:HB2	22:LU:103:TYR:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LX:90:ALA:O	25:LX:120:LYS:NZ	2.51	0.42
29:Lb:35:VAL:CG1	29:Lb:40:ARG:HD3	2.50	0.42
31:Ld:4:LEU:CB	46:B:720:LYS:CE	2.94	0.42
31:Ld:110:GLU:OE1	31:Ld:110:GLU:N	2.53	0.42
32:Le:78:ASN:C	32:Le:108:ILE:HD11	2.44	0.42
39:Ll:11:GLN:OE1	39:Ll:11:GLN:HA	2.20	0.42
44:1:276:U:H2'	44:1:277:G:H8	1.82	0.42
44:1:613:G:H2'	44:1:614:C:C6	2.54	0.42
44:1:1231:A:H5''	44:1:1232:C:H5'	2.02	0.42
44:1:1335:C:C2	44:1:1336:U:C5	3.08	0.42
44:1:2413:A:H2'	44:1:2414:G:C8	2.54	0.42
46:B:247:GLN:HA	46:B:277:LEU:HD11	2.02	0.42
46:B:303:LEU:HD11	46:B:318:LEU:HA	2.02	0.42
5:LC:203:ARG:HD2	44:1:1383:G:H5''	2.01	0.42
8:LF:100:ARG:O	8:LF:104:GLN:HG3	2.20	0.42
9:LG:139:VAL:O	9:LG:143:ILE:HD12	2.20	0.42
10:LH:22:SER:HB2	44:1:3187:A:OP1	2.19	0.42
10:LH:41:ILE:HD13	10:LH:71:VAL:HG21	2.02	0.42
13:LL:100:ARG:NH1	44:1:77:A:H5'	2.35	0.42
19:LR:21:LYS:O	19:LR:53:LYS:HB2	2.20	0.42
33:Lf:44:TYR:O	33:Lf:47:LYS:HG2	2.20	0.42
40:Lm:100:TYR:OH	44:1:2848:G:OP1	2.33	0.42
44:1:1260:A:H1'	44:1:1280:C:H1'	2.01	0.42
44:1:1618:G:C2	44:1:1619:A:C2	3.08	0.42
44:1:1631:C:H5''	44:1:1632:A:H5''	2.02	0.42
44:1:2379:U:H2'	44:1:2380:U:C6	2.55	0.42
44:1:2416:U:H2'	44:1:2417:U:H6	1.85	0.42
44:1:2709:C:C2	44:1:2710:C:C5	3.07	0.42
44:1:2736:A:H2'	44:1:2737:C:O4'	2.20	0.42
44:1:2831:G:H2'	44:1:2832:C:C6	2.54	0.42
44:1:3176:G:O6	44:1:3213:A:H2	2.03	0.42
46:B:157:LEU:HD13	46:B:530:LEU:HD11	2.01	0.42
46:B:656:LEU:HD13	46:B:668:PHE:HB3	2.01	0.42
2:C3:41:A:HO2'	37:Lj:59:THR:HG1	1.59	0.42
4:LB:211:GLN:OE1	4:LB:285:VAL:N	2.49	0.42
4:LB:213:GLU:O	4:LB:282:ILE:HG22	2.19	0.42
5:LC:59:GLN:OE1	37:Lj:55:ARG:NH2	2.51	0.42
5:LC:272:VAL:HG22	44:1:696:C:OP1	2.20	0.42
9:LG:36:ILE:H	9:LG:36:ILE:HD12	1.84	0.42
11:LI:35:ASP:OD1	11:LI:88:ARG:HG3	2.19	0.42
14:LM:66:THR:HG22	14:LM:99:TRP:CZ3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LT:40:VAL:HG12	21:LT:98:HIS:HA	2.01	0.42
37:Lj:5:THR:OG1	44:1:884:A:OP1	2.36	0.42
42:Lo:63:LYS:HD3	42:Lo:87:ARG:NH2	2.35	0.42
42:Lo:68:VAL:HG21	42:Lo:91:PHE:CE2	2.55	0.42
44:1:170:G:H2'	44:1:171:G:C8	2.55	0.42
44:1:433:A:H2'	44:1:434:U:C6	2.55	0.42
44:1:727:G:H2'	44:1:728:G:O4'	2.20	0.42
44:1:843:A:H2'	44:1:844:G:C8	2.55	0.42
44:1:1190:A:H2'	44:1:1190:A:N3	2.35	0.42
44:1:1244:A:N1	44:1:1271:A:H5'	2.35	0.42
44:1:1534:A:OP2	44:1:1586:G:N1	2.36	0.42
44:1:1679:A:H2'	44:1:1680:G:H8	1.85	0.42
44:1:2248:C:O2'	44:1:2272:G:H1'	2.20	0.42
44:1:2396:G:OP1	44:1:2397:A:O2'	2.22	0.42
44:1:3102:G:H2'	44:1:3103:A:C8	2.55	0.42
44:1:3211:C:H2'	44:1:3212:C:C6	2.55	0.42
44:1:3297:U:H2'	44:1:3298:C:H6	1.85	0.42
46:B:95:LEU:HD11	46:B:118:ALA:HA	2.02	0.42
46:B:400:SER:HB3	46:B:438:ASN:ND2	2.34	0.42
2:C3:53:A:C4	2:C3:54:A:C8	3.08	0.41
3:LA:70:ARG:NH2	44:1:2522:G:O6	2.53	0.41
7:LE:73:GLY:O	44:1:3267:A:O2'	2.34	0.41
10:LH:48:VAL:HG21	10:LH:54:LYS:HE2	2.00	0.41
11:LI:73:ASN:O	11:LI:77:THR:HG23	2.20	0.41
15:LN:140:LYS:HG3	44:1:127:G:OP1	2.20	0.41
17:LP:53:ASP:OD1	17:LP:55:GLN:HG2	2.18	0.41
19:LR:23:TRP:CD1	44:1:1473:G:H5''	2.55	0.41
20:LS:88:HIS:NE2	44:1:1293:U:O2'	2.53	0.41
21:LT:26:HIS:ND1	21:LT:28:SER:OG	2.53	0.41
21:LT:104:GLU:HA	21:LT:107:GLU:HG3	2.02	0.41
25:LX:105:VAL:HG11	25:LX:126:LEU:HD13	2.02	0.41
28:La:94:ALA:HB2	28:La:121:VAL:HG22	2.02	0.41
44:1:66:A:N6	44:1:76:G:H1'	2.35	0.41
44:1:421:G:O6	44:1:2383:C:O2'	2.28	0.41
44:1:716:A:OP1	44:1:752:C:O2'	2.38	0.41
44:1:822:G:H2'	44:1:823:C:H6	1.85	0.41
44:1:955:U:H2'	44:1:956:U:C6	2.55	0.41
44:1:972:A:H2'	44:1:973:A:H8	1.85	0.41
44:1:1029:G:C2	44:1:1030:A:N7	2.88	0.41
44:1:1361:U:H2'	44:1:1362:G:C8	2.55	0.41
44:1:1523:U:OP2	44:1:1604:G:O2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:2619:G:C8	44:1:2819:A:H4'	2.55	0.41
44:1:3287:U:H3'	44:1:3288:G:C8	2.55	0.41
4:LB:106:TRP:HB2	4:LB:133:TYR:CE1	2.56	0.41
4:LB:153:LYS:HD3	4:LB:154:TYR:CZ	2.55	0.41
7:LE:169:ASP:HB2	7:LE:174:LEU:HD11	2.02	0.41
8:LF:221:LYS:O	8:LF:227:GLY:HA3	2.20	0.41
15:LN:80:THR:HG21	15:LN:87:GLN:HA	2.01	0.41
16:LO:54[A]:TYR:CE1	16:LO:58[A]:LEU:HD21	2.55	0.41
17:LP:138:LYS:NZ	44:1:2356:A:H5'	2.35	0.41
19:LR:24:LEU:HD23	19:LR:32:ILE:HG21	2.01	0.41
22:LU:101:ASN:HA	22:LU:103:TYR:CE1	2.55	0.41
25:LX:138:ARG:HG2	25:LX:138:ARG:NH1	2.34	0.41
26:LY:115:ARG:O	26:LY:119:ILE:HG12	2.21	0.41
32:Le:126:LEU:HD23	32:Le:126:LEU:HA	1.90	0.41
34:Lg:96:GLU:OE2	44:1:2555:G:N1	2.37	0.41
36:Li:67:LYS:O	36:Li:71:LYS:HG2	2.20	0.41
42:Lo:71:ARG:HD3	42:Lo:80:ARG:HB2	2.02	0.41
44:1:7:C:H2'	44:1:8:C:H6	1.85	0.41
44:1:24:G:H2'	44:1:25:U:O4'	2.19	0.41
44:1:129:U:H3	44:1:139:G:H1	1.67	0.41
44:1:757:C:H2'	44:1:758:C:O4'	2.20	0.41
44:1:1105:A:H2'	44:1:1106:G:C8	2.55	0.41
44:1:2193:U:O2'	44:1:2313:A:OP2	2.22	0.41
44:1:2824:G:H2'	44:1:2825:C:H6	1.85	0.41
44:1:3084:C:H2'	44:1:3085:G:O4'	2.19	0.41
44:1:3234:A:H61	44:1:3253:G:H1	1.67	0.41
44:1:3283:U:H2'	44:1:3284:G:C8	2.55	0.41
46:B:198:TYR:CZ	46:B:202:LEU:HD11	2.55	0.41
46:B:485:THR:HB	46:B:704:HIS:HA	2.02	0.41
46:B:682:LEU:HA	46:B:685:LEU:HB2	2.02	0.41
7:LE:46:ARG:HD2	44:1:3270:U:C4	2.55	0.41
8:LF:67:ARG:HD3	44:1:520:U:O4	2.19	0.41
10:LH:161:LEU:O	10:LH:164:ILE:HG22	2.20	0.41
11:LI:206:LEU:O	11:LI:210:ILE:HG12	2.20	0.41
18:LQ:155:MET:HE2	18:LQ:163:PRO:HB3	2.02	0.41
22:LU:82:LYS:HE3	22:LU:82:LYS:HB3	1.84	0.41
25:LX:125:ARG:HH22	44:1:1610:G:P	2.43	0.41
32:Le:98:HIS:ND1	44:1:1411:C:OP1	2.53	0.41
34:Lg:36:LYS:NZ	44:1:1595:U:OP2	2.39	0.41
39:Ll:12:LYS:HA	39:Ll:12:LYS:HD2	1.94	0.41
42:Lo:6:LYS:HD3	42:Lo:94:GLY:HA3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:66:A:H61	44:1:76:G:H1'	1.85	0.41
44:1:208:C:H2'	44:1:209:A:O4'	2.20	0.41
44:1:601:U:H2'	44:1:602:A:C8	2.56	0.41
44:1:726:G:H21	44:1:744:A:H62	1.69	0.41
44:1:1659:U:H2'	44:1:1660:C:H6	1.83	0.41
44:1:1781:C:H2'	44:1:1782:U:C6	2.54	0.41
44:1:1789:G:C2	44:1:1790:G:C8	3.08	0.41
44:1:2389:C:H2'	44:1:2390:A:H8	1.84	0.41
44:1:2536:A:H2'	44:1:2537:U:C2	2.56	0.41
44:1:2565:U:H2'	44:1:2566:C:C6	2.56	0.41
44:1:2597:U:H2'	44:1:2598:G:H8	1.84	0.41
44:1:2986:U:C2	44:1:2987:A:C8	3.08	0.41
46:B:386:GLY:O	46:B:390:LYS:HE3	2.20	0.41
5:LC:257:LYS:HE2	5:LC:257:LYS:HB3	1.84	0.41
15:LN:16:SER:OG	15:LN:19:LEU:HD23	2.20	0.41
15:LN:177:GLY:HA2	44:1:68:C:O3'	2.20	0.41
18:LQ:83:VAL:O	18:LQ:103:ALA:HA	2.21	0.41
27:LZ:83:THR:HG22	34:Lg:93:PHE:CZ	2.56	0.41
36:Li:88:GLU:HA	36:Li:91:ASN:HB2	2.01	0.41
44:1:138:U:H2'	44:1:139:G:C8	2.56	0.41
44:1:279:U:H2'	44:1:280:U:C6	2.56	0.41
44:1:416:A:H2'	44:1:417:A:C8	2.55	0.41
44:1:536:U:C2	44:1:537:A:C8	3.09	0.41
44:1:788:C:H2'	44:1:789:A:H8	1.86	0.41
44:1:949:C:H2'	44:1:950:G:O4'	2.19	0.41
44:1:1154:A:H5''	44:1:1155:C:H5	1.86	0.41
44:1:1498:A:H2'	44:1:1499:C:C6	2.55	0.41
44:1:1948:G:C2	44:1:2099:A:C2	3.08	0.41
44:1:2249:G:O2'	44:1:2250:G:OP1	2.34	0.41
44:1:2707:C:H2'	44:1:2708:C:C6	2.56	0.41
44:1:2930:A:H2'	44:1:2931:C:H6	1.85	0.41
44:1:3104:U:H5''	44:1:3128:G:O6	2.21	0.41
45:A:7:PHE:H	45:A:44:PHE:HA	1.85	0.41
46:B:469:ASN:HA	46:B:505:LEU:HD11	2.03	0.41
46:B:513:LEU:HD22	46:B:535:MET:HE1	2.02	0.41
46:B:589:ARG:NH1	46:B:613:LEU:HB3	2.34	0.41
5:LC:141:ARG:NH2	44:1:1386:A:H5''	2.35	0.41
8:LF:29:GLU:OE1	8:LF:29:GLU:N	2.51	0.41
21:LT:90:ASN:ND2	44:1:2736:A:H1'	2.36	0.41
37:Lj:39:TYR:CG	37:Lj:40:PRO:HA	2.56	0.41
38:Lk:41:THR:HG21	38:Lk:62:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:122:A:C2	44:1:149:U:C2	3.08	0.41
44:1:259:C:H2'	44:1:260:C:C6	2.55	0.41
44:1:1306:G:O6	44:1:2366:C:O2'	2.36	0.41
44:1:1361:U:H2'	44:1:1362:G:H8	1.85	0.41
44:1:2499:U:H2'	44:1:2500:A:C8	2.56	0.41
44:1:2582:C:H2'	44:1:2583:C:C6	2.55	0.41
44:1:2661:G:H2'	44:1:2662:G:H8	1.85	0.41
44:1:2666:C:OP2	44:1:2687:G:N1	2.52	0.41
44:1:2708:C:C2	44:1:2709:C:C5	3.08	0.41
44:1:2978:U:O2'	44:1:2979:U:H5'	2.20	0.41
44:1:3183:A:H2'	44:1:3184:A:H8	1.83	0.41
46:B:177:ARG:HH22	46:B:180:ARG:HD3	1.85	0.41
46:B:412:LYS:HA	46:B:412:LYS:HD2	1.88	0.41
46:B:744:ASP:HA	46:B:747:LYS:NZ	2.35	0.41
1:C4:1:G:H4'	6:LD:273:ARG:NH2	2.36	0.41
1:C4:52:G:O2'	1:C4:53:U:P	2.79	0.41
4:LB:100:ARG:HD2	44:1:3146:G:H4'	2.03	0.41
8:LF:24:GLU:OE1	8:LF:26:VAL:N	2.48	0.41
9:LG:133:LYS:N	9:LG:199:ALA:O	2.47	0.41
10:LH:139:ASN:OD1	10:LH:140:VAL:HG23	2.20	0.41
11:LI:181:TYR:CZ	11:LI:185:ARG:HD2	2.56	0.41
16:LO:108[A]:ILE:HD12	16:LO:160[A]:ARG:CZ	2.50	0.41
18:LQ:44:PHE:CD1	18:LQ:139:ILE:HD11	2.56	0.41
19:LR:128:LYS:HZ1	44:1:1724:U:P	2.42	0.41
27:LZ:120:GLU:HA	27:LZ:120:GLU:OE2	2.21	0.41
28:La:26:ARG:HA	28:La:26:ARG:HD3	1.81	0.41
28:La:75:LEU:HD23	28:La:75:LEU:HA	1.86	0.41
34:Lg:98:GLN:HA	34:Lg:98:GLN:OE1	2.20	0.41
38:Lk:12:LEU:HD12	38:Lk:13:GLU:N	2.35	0.41
38:Lk:48:SER:HB3	44:1:1825:G:OP1	2.21	0.41
44:1:632:G:H2'	44:1:633:C:H6	1.84	0.41
44:1:668:G:H2'	44:1:669:U:H6	1.85	0.41
44:1:840:C:H2'	44:1:841:A:H8	1.85	0.41
44:1:903:U:H2'	44:1:904:A:H8	1.84	0.41
44:1:1387:G:H1'	44:1:1421:G:N2	2.35	0.41
44:1:1801:U:H2'	44:1:1802:C:C6	2.56	0.41
44:1:2677:G:N3	44:1:2677:G:H2'	2.35	0.41
44:1:2866:U:O2	44:1:2867:C:N4	2.54	0.41
44:1:2915:U:H5''	44:1:2916:U:H5'	2.02	0.41
44:1:3146:G:H2'	44:1:3147:G:C8	2.55	0.41
44:1:3252:G:H2'	44:1:3253:G:H8	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C3:154:C:H2'	2:C3:155:A:C8	2.55	0.41
3:LA:182:ALA:O	3:LA:186:PHE:N	2.43	0.41
3:LA:244:GLY:HA3	44:1:2242:A:H5''	2.03	0.41
14:LM:42:LYS:NZ	14:LM:43:LYS:HD2	2.36	0.41
15:LN:48:ALA:C	15:LN:53:TYR:HB3	2.46	0.41
22:LU:53:ALA:O	22:LU:68:THR:HG22	2.21	0.41
43:Lp:59:CYS:C	43:Lp:61:LYS:H	2.29	0.41
44:1:874:U:H5''	44:1:2950:G:OP1	2.21	0.41
44:1:1862:U:H2'	44:1:1863:G:O4'	2.20	0.41
44:1:2369:G:H2'	44:1:2370:G:H8	1.80	0.41
44:1:3021:A:N1	44:1:3032:A:H5''	2.36	0.41
44:1:3191:G:C6	44:1:3202:G:C6	3.09	0.41
44:1:3353:G:C6	44:1:3356:G:C6	3.09	0.41
44:1:3353:G:O2'	44:1:3356:G:OP2	2.39	0.41
44:1:3363:U:H2'	44:1:3364:C:H6	1.85	0.41
46:B:151:TRP:CZ2	46:B:521:PHE:HB3	2.56	0.41
1:C4:95:A:H2'	1:C4:96:U:O4'	2.20	0.41
2:C3:154:C:H5''	9:LG:181:LYS:HE2	2.02	0.41
3:LA:33:ASP:O	3:LA:37:ARG:HG2	2.21	0.41
4:LB:194:TRP:O	4:LB:198:HIS:ND1	2.49	0.41
6:LD:59:ASP:OD1	6:LD:80:SER:OG	2.36	0.41
7:LE:174:LEU:HD23	7:LE:174:LEU:HA	1.90	0.41
10:LH:90:MET:HB3	10:LH:144:ILE:CG1	2.46	0.41
12:LJ:54:VAL:HG21	12:LJ:57:PHE:CD2	2.56	0.41
12:LJ:65:ILE:HG13	12:LJ:66:ALA:N	2.34	0.41
17:LP:65:SER:HB2	44:1:1446:A:H5''	2.03	0.41
21:LT:54:HIS:CD2	44:1:2724:U:H4'	2.56	0.41
23:LV:33:ASN:OD1	23:LV:64:LYS:N	2.53	0.41
27:LZ:99:GLU:O	27:LZ:106:GLN:NE2	2.53	0.41
41:Ln:16:LYS:NZ	41:Ln:17:ARG:NH1	2.69	0.41
44:1:195:U:H2'	44:1:196:G:O4'	2.21	0.41
44:1:314:U:H2'	44:1:315:C:C6	2.56	0.41
44:1:1278:A:C8	44:1:1279:C:C5	3.09	0.41
44:1:1733:G:H2'	44:1:1734:G:C8	2.56	0.41
44:1:2975:U:H2'	44:1:2976:A:H8	1.86	0.41
44:1:3102:G:H2'	44:1:3103:A:H8	1.86	0.41
1:C4:22:A:C8	6:LD:272:TYR:CE2	3.08	0.41
2:C3:91:C:H2'	2:C3:92:A:C8	2.55	0.41
2:C3:135:G:P	25:LX:56:ARG:HH22	2.44	0.41
3:LA:57:PRO:HG2	3:LA:78:ALA:HB3	2.03	0.41
6:LD:177:GLU:OE1	6:LD:177:GLU:N	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LD:219:PHE:HE2	6:LD:227:LEU:HD21	1.86	0.41
7:LE:51:ARG:HD3	7:LE:158:TYR:CE2	2.55	0.41
7:LE:82:ARG:HD2	7:LE:82:ARG:HA	1.69	0.41
8:LF:150:LYS:HD3	8:LF:244:ASN:HD21	1.85	0.41
13:LL:42:ARG:O	13:LL:46:ILE:HG12	2.21	0.41
13:LL:53:LEU:HD22	13:LL:94:GLY:HA2	2.03	0.41
14:LM:47:ASP:OD1	14:LM:48:GLY:N	2.54	0.41
16:LO:49[A]:ARG:HH22	44:1:1193:A:H8	1.69	0.41
18:LQ:2:GLY:N	44:1:1159:A:OP1	2.54	0.41
19:LR:134:HIS:CE1	19:LR:136:ARG:HB3	2.56	0.41
28:La:78:LEU:HD12	28:La:81:LEU:HD12	2.03	0.41
31:Ld:27:LYS:C	31:Ld:30:PRO:HD2	2.45	0.41
34:Lg:103:LYS:HE3	34:Lg:103:LYS:HB3	1.90	0.41
35:Lh:74:LYS:HE2	35:Lh:75:TYR:CZ	2.56	0.41
36:Li:9:ILE:HG22	36:Li:10:GLY:N	2.36	0.41
42:Lo:77:CYS:SG	42:Lo:79:THR:OG1	2.77	0.41
43:Lp:48:LYS:HB3	43:Lp:48:LYS:HE3	1.80	0.41
44:1:180:C:H2'	44:1:181:U:C6	2.55	0.41
44:1:224:C:H2'	44:1:225:C:C6	2.56	0.41
44:1:287:G:H2'	44:1:288:C:C6	2.56	0.41
44:1:291:C:H2'	44:1:292:U:C6	2.55	0.41
44:1:301:G:H2'	44:1:302:U:H6	1.85	0.41
44:1:503:C:H2'	44:1:504:A:C8	2.56	0.41
44:1:507:U:H2'	44:1:508:U:H6	1.84	0.41
44:1:540:U:H2'	44:1:541:U:C6	2.56	0.41
44:1:821:U:H2'	44:1:822:G:H8	1.85	0.41
44:1:1117:G:C6	44:1:1142:G:N2	2.89	0.41
44:1:1176:C:OP2	44:1:1177:G:O2'	2.28	0.41
44:1:1643:A:H2'	44:1:1644:C:C2	2.56	0.41
44:1:1746:U:C2	44:1:1747:G:C8	3.08	0.41
44:1:1804:A:H2'	44:1:1805:C:C6	2.56	0.41
44:1:1827:C:H2'	44:1:1828:A:C8	2.56	0.41
44:1:1828:A:H2'	44:1:1829:G:C8	2.56	0.41
44:1:1978:A:H2'	44:1:1979:G:C8	2.55	0.41
44:1:2041:U:H2'	44:1:2042:G:O4'	2.21	0.41
44:1:2095:G:H2'	44:1:2096:A:C8	2.56	0.41
44:1:2249:G:HO2'	44:1:2250:G:P	2.44	0.41
44:1:2504:U:H2'	44:1:2505:U:H6	1.86	0.41
44:1:2765:C:H2'	44:1:2766:U:H6	1.86	0.41
44:1:3255:U:H2'	44:1:3256:G:C8	2.56	0.41
44:1:3264:G:H2'	44:1:3265:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:3289:G:H2'	44:1:3290:G:H8	1.86	0.41
45:A:48:GLU:HG3	45:A:87:PHE:CZ	2.56	0.41
45:A:56:LYS:HD3	46:B:592:SER:HB2	2.02	0.41
46:B:102:ASN:HD22	46:B:114:TRP:HE3	1.68	0.41
46:B:598:PHE:HA	46:B:601:PHE:HB3	2.02	0.41
1:C4:81:U:H2'	1:C4:82:G:H8	1.85	0.41
3:LA:83:HIS:HA	43:Lp:64:VAL:HA	2.03	0.41
4:LB:53:MET:HE2	4:LB:53:MET:HB3	1.94	0.41
7:LE:69:PHE:CE1	44:1:3267:A:H2'	2.56	0.41
7:LE:110:LYS:H	7:LE:110:LYS:HG3	1.63	0.41
10:LH:87:LYS:HD3	10:LH:89:LYS:HE3	2.03	0.41
16:LO:168[A]:TYR:OH	16:LO:172[A]:ARG:HD3	2.21	0.41
30:Lc:9:SER:O	30:Lc:12:GLN:NE2	2.54	0.41
32:Le:36:LYS:NZ	44:1:945:C:OP1	2.55	0.41
33:Lf:90:PRO:C	33:Lf:92:LYS:H	2.28	0.41
35:Lh:5:LYS:HB2	35:Lh:8:GLU:OE1	2.21	0.41
35:Lh:118:ILE:HG23	35:Lh:118:ILE:O	2.21	0.41
42:Lo:99:GLN:HG2	42:Lo:102:GLN:OE1	2.20	0.41
44:1:29:C:H4'	44:1:62:A:H4'	2.03	0.41
44:1:1560:G:H2'	44:1:1561:G:C8	2.55	0.41
44:1:2318:U:H2'	44:1:2319:U:O4'	2.21	0.41
44:1:2831:G:H2'	44:1:2832:C:H6	1.85	0.41
44:1:2889:C:H2'	44:1:2890:A:C8	2.56	0.41
44:1:3162:C:H2'	44:1:3163:A:C8	2.57	0.41
44:1:3165:A:H2'	44:1:3166:C:H6	1.83	0.41
45:A:167:MET:HE3	45:A:168:ARG:N	2.36	0.41
46:B:556:SER:HB3	46:B:561:ASP:HB2	2.03	0.41
2:C3:28:C:H2'	2:C3:29:U:C6	2.57	0.40
2:C3:66:A:H2'	2:C3:67:U:C6	2.57	0.40
2:C3:148:G:H2'	2:C3:149:A:C8	2.55	0.40
5:LC:328:ASN:OD1	8:LF:48:ASN:ND2	2.54	0.40
6:LD:55:PHE:HE2	6:LD:159:VAL:HA	1.86	0.40
7:LE:149:ILE:H	7:LE:149:ILE:HD12	1.86	0.40
9:LG:157:VAL:HG13	44:1:147:U:C4	2.57	0.40
13:LL:91:ARG:NH1	44:1:110:G:H5'	2.36	0.40
21:LT:88:ARG:NH1	29:Lb:33:LYS:O	2.53	0.40
31:Ld:41:LYS:HG2	31:Ld:47:ASP:HA	2.02	0.40
43:Lp:79:VAL:O	43:Lp:83:ILE:HG12	2.21	0.40
44:1:179:C:H2'	44:1:180:C:C6	2.55	0.40
44:1:2202:C:H2'	44:1:2203:U:C6	2.56	0.40
44:1:2510:U:H2'	44:1:2511:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:3212:C:C4	44:1:3213:A:C2	3.09	0.40
44:1:3362:A:H2'	44:1:3363:U:O4'	2.21	0.40
46:B:404:LEU:HD11	46:B:440:ASP:HB3	2.02	0.40
1:C4:29:C:OP2	12:LJ:137:ARG:HD2	2.20	0.40
2:C3:41:A:O2'	37:Lj:59:THR:OG1	2.29	0.40
5:LC:119:ARG:NE	44:1:695:C:OP1	2.36	0.40
7:LE:133:GLU:HG2	7:LE:134:ARG:N	2.36	0.40
10:LH:46:THR:HB	10:LH:54:LYS:HB2	2.03	0.40
13:LL:28:GLN:NE2	44:1:684:G:OP2	2.37	0.40
13:LL:111:ALA:HA	13:LL:114:GLN:HG3	2.03	0.40
16:LO:28[A]:LEU:HD12	16:LO:94[A]:ARG:NH2	2.36	0.40
19:LR:74:ARG:NE	44:1:1942:U:OP2	2.31	0.40
25:LX:105:VAL:HG12	25:LX:126:LEU:HD22	2.02	0.40
33:Lf:8:TYR:CE1	33:Lf:99:ARG:HG2	2.56	0.40
42:Lo:15:LYS:HB3	42:Lo:15:LYS:HE2	1.88	0.40
42:Lo:68:VAL:HG21	42:Lo:91:PHE:CD2	2.56	0.40
44:1:366:A:H2'	44:1:367:A:O4'	2.21	0.40
44:1:448:U:H2'	44:1:449:U:C6	2.56	0.40
44:1:542:G:N1	44:1:549:U:N3	2.45	0.40
44:1:776:U:H5	44:1:2719:U:O2	2.03	0.40
44:1:824:C:O2'	44:1:1534:A:N3	2.52	0.40
44:1:1018:G:H8	44:1:1018:G:OP2	2.04	0.40
44:1:1246:G:O4'	44:1:1264:G:H5''	2.21	0.40
44:1:1322:U:H2'	44:1:1323:G:H8	1.85	0.40
44:1:2146:C:H2'	44:1:2147:A:H8	1.85	0.40
44:1:2331:C:H2'	44:1:2332:A:C8	2.57	0.40
44:1:2428:U:H2'	44:1:2429:G:H8	1.85	0.40
44:1:2526:C:H2'	44:1:2527:G:C8	2.56	0.40
44:1:2685:C:H2'	44:1:2686:A:C8	2.57	0.40
44:1:2707:C:C2	44:1:2708:C:C5	3.08	0.40
44:1:3182:G:C6	44:1:3183:A:C6	3.09	0.40
46:B:122:SER:HB2	46:B:580:THR:HG22	2.03	0.40
46:B:200:LEU:HD13	46:B:530:LEU:HD12	2.03	0.40
1:C4:56:A:C4	1:C4:57:G:C8	3.10	0.40
6:LD:124:GLU:CD	6:LD:124:GLU:H	2.29	0.40
11:LI:82:ARG:NH2	11:LI:83:ASP:HB3	2.36	0.40
13:LL:18:TRP:NE1	44:1:799:G:O2'	2.52	0.40
14:LM:121:MET:HE3	44:1:3214:U:C2	2.56	0.40
17:LP:124:LYS:HD2	17:LP:141:SER:O	2.21	0.40
17:LP:135:ARG:NH2	44:1:879:U:O2'	2.53	0.40
27:LZ:111:LYS:HA	27:LZ:114:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Lf:46:GLY:H	33:Lf:71:VAL:HG23	1.86	0.40
43:Lp:46:THR:HB	43:Lp:58:SER:OG	2.22	0.40
44:1:713:U:O2'	44:1:754:G:OP1	2.37	0.40
44:1:1958:U:C2	44:1:2083:G:O6	2.73	0.40
44:1:2279:A:C2	44:1:2283:G:C6	3.10	0.40
44:1:2671:A:H2'	44:1:2672:G:O4'	2.22	0.40
45:A:34:GLU:O	45:A:38:ILE:HG22	2.21	0.40
46:B:435:ASP:CG	46:B:438:ASN:HB2	2.46	0.40
1:C4:81:U:H2'	1:C4:82:G:C8	2.57	0.40
2:C3:12:A:C6	2:C3:13:A:N7	2.90	0.40
2:C3:47:C:H1'	2:C3:61:A:H2'	2.03	0.40
3:LA:143:GLU:O	3:LA:144:ASN:C	2.64	0.40
13:LL:165:SER:C	13:LL:167:PHE:H	2.29	0.40
18:LQ:8:LYS:NZ	44:1:971:G:OP1	2.37	0.40
19:LR:95:TRP:NE1	44:1:855:U:H4'	2.37	0.40
23:LV:80:ARG:HB2	23:LV:99:ALA:HB3	2.04	0.40
25:LX:57:LEU:HD12	25:LX:57:LEU:HA	1.84	0.40
36:Li:60:LEU:HD12	36:Li:72:VAL:HG21	2.04	0.40
44:1:275:U:H2'	44:1:276:U:H6	1.84	0.40
44:1:516:A:C6	44:1:575:G:C6	3.10	0.40
44:1:1461:A:H2'	44:1:1462:A:H8	1.87	0.40
44:1:1637:A:H2'	44:1:1638:A:C8	2.57	0.40
44:1:1935:G:H2'	44:1:1936:A:H8	1.87	0.40
44:1:2200:U:C2	44:1:2201:G:C8	3.09	0.40
44:1:2258:U:C2	44:1:2259:A:C8	3.10	0.40
44:1:2328:U:H2'	44:1:2329:C:C6	2.56	0.40
44:1:2585:G:N3	44:1:2585:G:H2'	2.35	0.40
44:1:2999:U:H2'	44:1:3000:A:C8	2.57	0.40
46:B:697:LYS:HA	46:B:697:LYS:HD3	2.00	0.40
46:B:698:GLN:O	46:B:701:MET:HE2	2.21	0.40
2:C3:45:C:C4'	39:Li:11:GLN:HE21	2.30	0.40
5:LC:258:LEU:HA	5:LC:258:LEU:HD12	1.86	0.40
8:LF:165:ASP:OD1	8:LF:165:ASP:C	2.65	0.40
10:LH:20:ILE:HG12	10:LH:25:VAL:HG13	2.03	0.40
12:LJ:32:ARG:HA	12:LJ:35:LYS:HE2	2.03	0.40
12:LJ:92:ARG:HD2	12:LJ:172:LEU:HG	2.03	0.40
15:LN:138:GLN:NE2	44:1:19:U:H4'	2.37	0.40
16:LO:49[A]:ARG:NH1	44:1:1190:A:H2'	2.37	0.40
17:LP:86:LYS:HB2	44:1:2353:G:H5''	2.04	0.40
19:LR:99:LEU:HD23	19:LR:99:LEU:HA	1.85	0.40
20:LS:132:THR:C	20:LS:134:ASP:H	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LX:73:MET:HA	25:LX:73:MET:HE3	2.03	0.40
28:La:28:HIS:CD2	28:La:32:ARG:HG2	2.56	0.40
44:1:260:C:H2'	44:1:261:U:C6	2.56	0.40
44:1:529:A:H2'	44:1:530:G:C8	2.56	0.40
44:1:756:U:H2'	44:1:757:C:H6	1.87	0.40
44:1:1462:A:H2'	44:1:1463:U:H6	1.86	0.40
44:1:1866:C:H5'	44:1:1867:A:OP2	2.20	0.40
44:1:1954:G:H2'	44:1:1955:U:C6	2.56	0.40
44:1:2302:G:C6	44:1:2303:A:N7	2.89	0.40
45:A:1:MET:HG2	46:B:264:TYR:CE1	2.57	0.40
46:B:321:TYR:OH	46:B:331:CYS:HA	2.22	0.40
46:B:598:PHE:CZ	46:B:608:LEU:HG	2.57	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	
3	LA	249/251 (99%)	232 (93%)	17 (7%)	0	100	100
4	LB	384/386 (100%)	357 (93%)	27 (7%)	0	100	100
5	LC	359/361 (99%)	334 (93%)	24 (7%)	1 (0%)	36	67
6	LD	292/294 (99%)	279 (96%)	12 (4%)	1 (0%)	36	67
7	LE	163/175 (93%)	154 (94%)	9 (6%)	0	100	100
8	LF	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
9	LG	231/233 (99%)	220 (95%)	11 (5%)	0	100	100
10	LH	189/191 (99%)	178 (94%)	11 (6%)	0	100	100
11	LI	216/218 (99%)	209 (97%)	7 (3%)	0	100	100
12	LJ	167/169 (99%)	152 (91%)	15 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	LL	191/193 (99%)	175 (92%)	15 (8%)	1 (0%)	24	57
14	LM	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
15	LN	201/203 (99%)	188 (94%)	13 (6%)	0	100	100
16	LO	195/197 (99%)	188 (96%)	5 (3%)	2 (1%)	12	41
17	LP	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
18	LQ	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
19	LR	169/188 (90%)	164 (97%)	5 (3%)	0	100	100
20	LS	169/171 (99%)	160 (95%)	9 (5%)	0	100	100
21	LT	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
22	LU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
23	LV	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
24	LW	65/126 (52%)	63 (97%)	2 (3%)	0	100	100
25	LX	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
26	LY	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
27	LZ	133/135 (98%)	122 (92%)	11 (8%)	0	100	100
28	La	146/148 (99%)	130 (89%)	16 (11%)	0	100	100
29	Lb	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
30	Lc	94/96 (98%)	94 (100%)	0	0	100	100
31	Ld	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
32	Le	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
33	Lf	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
34	Lg	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
35	Lh	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
36	Li	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
37	Lj	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
38	Lk	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
39	Ll	48/50 (96%)	48 (100%)	0	0	100	100
40	Lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
41	Ln	23/25 (92%)	23 (100%)	0	0	100	100
42	Lo	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
43	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	A	193/195 (99%)	189 (98%)	4 (2%)	0	100	100
46	B	794/796 (100%)	784 (99%)	10 (1%)	0	100	100
All	All	7134/7306 (98%)	6797 (95%)	332 (5%)	5 (0%)	49	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	LD	21	ARG
16	LO	111[A]	PRO
13	LL	63	VAL
16	LO	110[A]	PRO
5	LC	4	PRO

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	
3	LA	190/193 (98%)	190 (100%)	0	100	100
4	LB	319/322 (99%)	319 (100%)	0	100	100
5	LC	288/288 (100%)	286 (99%)	2 (1%)	76	82
6	LD	241/243 (99%)	241 (100%)	0	100	100
7	LE	138/153 (90%)	138 (100%)	0	100	100
8	LF	186/186 (100%)	186 (100%)	0	100	100
9	LG	187/191 (98%)	187 (100%)	0	100	100
10	LH	168/171 (98%)	168 (100%)	0	100	100
11	LI	185/185 (100%)	185 (100%)	0	100	100
12	LJ	146/147 (99%)	146 (100%)	0	100	100
13	LL	154/154 (100%)	154 (100%)	0	100	100
14	LM	107/107 (100%)	106 (99%)	1 (1%)	70	80
15	LN	175/175 (100%)	175 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	LO	160/160 (100%)	160 (100%)	0	100	100
17	LP	138/145 (95%)	138 (100%)	0	100	100
18	LQ	150/150 (100%)	150 (100%)	0	100	100
19	LR	139/153 (91%)	139 (100%)	0	100	100
20	LS	155/155 (100%)	155 (100%)	0	100	100
21	LT	136/136 (100%)	135 (99%)	1 (1%)	76	82
22	LU	87/87 (100%)	87 (100%)	0	100	100
23	LV	104/104 (100%)	104 (100%)	0	100	100
24	LW	54/107 (50%)	54 (100%)	0	100	100
25	LX	104/105 (99%)	104 (100%)	0	100	100
26	LY	108/108 (100%)	108 (100%)	0	100	100
27	LZ	115/115 (100%)	115 (100%)	0	100	100
28	La	118/118 (100%)	118 (100%)	0	100	100
29	Lb	46/46 (100%)	46 (100%)	0	100	100
30	Lc	81/81 (100%)	81 (100%)	0	100	100
31	Ld	93/96 (97%)	91 (98%)	2 (2%)	45	71
32	Le	108/109 (99%)	108 (100%)	0	100	100
33	Lf	90/90 (100%)	90 (100%)	0	100	100
34	Lg	95/95 (100%)	94 (99%)	1 (1%)	65	78
35	Lh	104/104 (100%)	104 (100%)	0	100	100
36	Li	80/81 (99%)	80 (100%)	0	100	100
37	Lj	69/69 (100%)	69 (100%)	0	100	100
38	Lk	68/68 (100%)	68 (100%)	0	100	100
39	Ll	45/45 (100%)	45 (100%)	0	100	100
40	Lm	47/47 (100%)	47 (100%)	0	100	100
41	Ln	22/23 (96%)	22 (100%)	0	100	100
42	Lo	87/88 (99%)	87 (100%)	0	100	100
43	Lp	71/71 (100%)	71 (100%)	0	100	100
45	A	180/180 (100%)	180 (100%)	0	100	100
46	B	743/743 (100%)	743 (100%)	0	100	100
All	All	6081/6194 (98%)	6074 (100%)	7 (0%)	87	90

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	LC	12	THR
5	LC	299	ILE
14	LM	27	GLN
21	LT	77	ASN
31	Ld	7	VAL
31	Ld	8	VAL
34	Lg	84	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
3	LA	83	HIS
4	LB	121	ASN
5	LC	58	HIS
7	LE	28	GLN
8	LF	48	ASN
9	LG	59	GLN
11	LI	73	ASN
11	LI	163	GLN
11	LI	209	ASN
13	LL	12	ASN
13	LL	103	ASN
15	LN	182	ASN
17	LP	28	ASN
17	LP	50	GLN
17	LP	121	GLN
17	LP	137	ASN
18	LQ	158	HIS
19	LR	150	GLN
20	LS	62	ASN
20	LS	122	HIS
22	LU	49	ASN
23	LV	98	ASN
26	LY	4	GLN
27	LZ	57	HIS
27	LZ	127	ASN
27	LZ	128	GLN
28	La	62	HIS
28	La	64	GLN
28	La	67	HIS
30	Lc	75	ASN

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Mol	Chain	Res	Type
32	Le	71	HIS
34	Lg	34	HIS
38	Lk	10	GLN
39	Ll	11	GLN
40	Lm	109	ASN
42	Lo	47	GLN
42	Lo	53	GLN
42	Lo	90	HIS
45	A	123	GLN
45	A	145	ASN
46	B	49	GLN
46	B	163	GLN
46	B	379	ASN
46	B	430	ASN
46	B	464	ASN
46	B	512	ASN
46	B	657	ASN
46	B	681	ASN
46	B	699	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C4	120/121 (99%)	11 (9%)	1 (0%)
2	C3	157/158 (99%)	25 (15%)	1 (0%)
44	1	3297/3395 (97%)	579 (17%)	34 (1%)
All	All	3574/3674 (97%)	615 (17%)	36 (1%)

All (615) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C4	7	G
1	C4	11	A
1	C4	53	U
1	C4	54	U
1	C4	55	A
1	C4	65	G
1	C4	73	C
1	C4	76	A
1	C4	102	A
1	C4	112	G

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Mol	Chain	Res	Type
1	C4	121	U
2	C3	34	U
2	C3	35	C
2	C3	39	G
2	C3	59	A
2	C3	62	C
2	C3	63	G
2	C3	80	A
2	C3	81	U
2	C3	82	U
2	C3	83	C
2	C3	84	C
2	C3	85	G
2	C3	86	U
2	C3	87	G
2	C3	90	U
2	C3	95	G
2	C3	97	A
2	C3	104	A
2	C3	106	C
2	C3	111	A
2	C3	113	U
2	C3	125	U
2	C3	126	A
2	C3	148	G
2	C3	158	U
44	1	13	A
44	1	14	U
44	1	18	G
44	1	26	A
44	1	40	A
44	1	43	A
44	1	49	A
44	1	59	G
44	1	60	A
44	1	65	A
44	1	66	A
44	1	77	A
44	1	92	G
44	1	99	A
44	1	109	A
44	1	110	G

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Mol	Chain	Res	Type
44	1	111	C
44	1	113	C
44	1	116	A
44	1	117	U
44	1	118	U
44	1	120	G
44	1	121	A
44	1	122	A
44	1	133	U
44	1	134	U
44	1	135	C
44	1	136	G
44	1	150	A
44	1	156	G
44	1	157	A
44	1	165	A
44	1	166	C
44	1	173	G
44	1	187	A
44	1	190	U
44	1	191	U
44	1	200	C
44	1	210	U
44	1	213	A
44	1	218	G
44	1	219	A
44	1	221	A
44	1	234	G
44	1	240	U
44	1	241	G
44	1	243	G
44	1	245	U
44	1	251	G
44	1	252	U
44	1	269	G
44	1	283	G
44	1	286	U
44	1	295	A
44	1	305	U
44	1	323	A
44	1	329	U
44	1	339	C

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Mol	Chain	Res	Type
44	1	350	C
44	1	351	A
44	1	376	G
44	1	398	A
44	1	399	A
44	1	401	U
44	1	402	A
44	1	403	C
44	1	421	G
44	1	422	A
44	1	439	C
44	1	440	A
44	1	441	U
44	1	442	G
44	1	445	G
44	1	446	U
44	1	447	U
44	1	448	U
44	1	450	G
44	1	451	U
44	1	487	U
44	1	488	U
44	1	489	U
44	1	491	A
44	1	494	G
44	1	503	C
44	1	521	A
44	1	523	A
44	1	535	G
44	1	536	U
44	1	543	C
44	1	544	C
44	1	546	C
44	1	547	G
44	1	552	G
44	1	555	U
44	1	557	A
44	1	559	A
44	1	579	G
44	1	609	G
44	1	611	A
44	1	620	U

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Mol	Chain	Res	Type
44	1	621	A
44	1	637	C
44	1	638	C
44	1	649	A
44	1	667	C
44	1	677	A
44	1	681	U
44	1	690	A
44	1	691	A
44	1	705	A
44	1	712	G
44	1	716	A
44	1	719	U
44	1	720	A
44	1	727	G
44	1	764	U
44	1	767	U
44	1	776	U
44	1	777	U
44	1	780	A
44	1	781	G
44	1	785	G
44	1	786	A
44	1	806	A
44	1	817	A
44	1	830	A
44	1	846	A
44	1	847	A
44	1	849	C
44	1	857	G
44	1	861	C
44	1	865	U
44	1	874	U
44	1	879	U
44	1	896	A
44	1	907	G
44	1	908	G
44	1	914	A
44	1	916	G
44	1	917	A
44	1	921	A
44	1	923	C

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Mol	Chain	Res	Type
44	1	937	G
44	1	944	C
44	1	953	G
44	1	959	C
44	1	960	U
44	1	974	G
44	1	979	U
44	1	980	A
44	1	1002	A
44	1	1010	G
44	1	1015	U
44	1	1016	C
44	1	1018	G
44	1	1020	G
44	1	1021	G
44	1	1024	G
44	1	1032	C
44	1	1035	G
44	1	1036	A
44	1	1047	A
44	1	1049	C
44	1	1063	G
44	1	1064	A
44	1	1065	A
44	1	1072	G
44	1	1080	A
44	1	1081	U
44	1	1093	A
44	1	1094	U
44	1	1095	U
44	1	1097	G
44	1	1098	A
44	1	1103	A
44	1	1104	G
44	1	1117	G
44	1	1131	G
44	1	1144	U
44	1	1153	A
44	1	1159	A
44	1	1178	G
44	1	1180	A
44	1	1181	U

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Mol	Chain	Res	Type
44	1	1190	A
44	1	1192	C
44	1	1193	A
44	1	1196	C
44	1	1201	C
44	1	1208	U
44	1	1217	A
44	1	1222	G
44	1	1227	C
44	1	1232	C
44	1	1235	U
44	1	1236	G
44	1	1238	C
44	1	1241	U
44	1	1245	A
44	1	1246	G
44	1	1253	U
44	1	1258	U
44	1	1262	G
44	1	1263	A
44	1	1264	G
44	1	1266	G
44	1	1269	U
44	1	1270	A
44	1	1271	A
44	1	1274	A
44	1	1278	A
44	1	1279	C
44	1	1285	G
44	1	1287	A
44	1	1307	G
44	1	1308	A
44	1	1309	U
44	1	1315	U
44	1	1330	A
44	1	1348	U
44	1	1349	G
44	1	1351	U
44	1	1352	A
44	1	1353	U
44	1	1354	G
44	1	1355	A

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Mol	Chain	Res	Type
44	1	1356	U
44	1	1357	G
44	1	1386	A
44	1	1399	A
44	1	1400	G
44	1	1417	G
44	1	1419	A
44	1	1434	G
44	1	1437	C
44	1	1446	A
44	1	1450	G
44	1	1481	A
44	1	1483	G
44	1	1487	G
44	1	1495	U
44	1	1508	C
44	1	1523	U
44	1	1556	C
44	1	1557	A
44	1	1560	G
44	1	1562	C
44	1	1563	C
44	1	1566	A
44	1	1567	U
44	1	1568	U
44	1	1569	U
44	1	1572	U
44	1	1573	G
44	1	1575	A
44	1	1576	G
44	1	1580	A
44	1	1581	C
44	1	1582	C
44	1	1583	A
44	1	1587	A
44	1	1588	A
44	1	1589	A
44	1	1605	A
44	1	1607	U
44	1	1619	A
44	1	1620	U
44	1	1621	A

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Mol	Chain	Res	Type
44	1	1629	U
44	1	1639	C
44	1	1642	A
44	1	1643	A
44	1	1645	U
44	1	1657	C
44	1	1683	A
44	1	1688	U
44	1	1717	U
44	1	1724	U
44	1	1725	C
44	1	1736	G
44	1	1741	A
44	1	1750	A
44	1	1751	G
44	1	1761	C
44	1	1765	U
44	1	1766	G
44	1	1770	G
44	1	1775	G
44	1	1780	G
44	1	1788	C
44	1	1797	A
44	1	1808	G
44	1	1814	A
44	1	1816	A
44	1	1817	G
44	1	1819	U
44	1	1820	U
44	1	1821	U
44	1	1835	A
44	1	1839	A
44	1	1840	U
44	1	1841	A
44	1	1842	A
44	1	1846	C
44	1	1849	C
44	1	1850	A
44	1	1866	C
44	1	1867	A
44	1	1878	G
44	1	1880	U

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Mol	Chain	Res	Type
44	1	1893	A
44	1	1906	G
44	1	1952	G
44	1	1953	G
44	1	1954	G
44	1	1955	U
44	1	1958	U
44	1	1960	A
44	1	1961	G
44	1	1962	A
44	1	1963	G
44	1	1964	C
44	1	1972	A
44	1	1973	G
44	1	1976	G
44	1	1981	G
44	1	1984	C
44	1	1985	G
44	1	1988	C
44	1	1994	G
44	1	2001	U
44	1	2006	G
44	1	2010	U
44	1	2013	C
44	1	2017	G
44	1	2020	A
44	1	2022	G
44	1	2025	G
44	1	2035	G
44	1	2039	C
44	1	2044	U
44	1	2045	G
44	1	2047	A
44	1	2048	G
44	1	2049	A
44	1	2050	C
44	1	2059	U
44	1	2081	U
44	1	2082	U
44	1	2087	C
44	1	2088	A
44	1	2093	A

Continued on next page...

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Mol	Chain	Res	Type
44	1	2101	C
44	1	2102	U
44	1	2107	A
44	1	2111	G
44	1	2112	U
44	1	2113	A
44	1	2114	C
44	1	2121	G
44	1	2122	G
44	1	2131	A
44	1	2144	A
44	1	2158	A
44	1	2169	G
44	1	2170	U
44	1	2171	G
44	1	2188	A
44	1	2192	C
44	1	2193	U
44	1	2194	G
44	1	2206	G
44	1	2209	U
44	1	2210	G
44	1	2222	A
44	1	2223	A
44	1	2244	A
44	1	2249	G
44	1	2250	G
44	1	2255	A
44	1	2256	A
44	1	2270	A
44	1	2272	G
44	1	2273	G
44	1	2281	A
44	1	2282	U
44	1	2288	G
44	1	2307	G
44	1	2310	U
44	1	2313	A
44	1	2314	U
44	1	2315	G
44	1	2336	U
44	1	2373	A

Continued on next page...

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Mol	Chain	Res	Type
44	1	2374	C
44	1	2375	G
44	1	2385	G
44	1	2388	U
44	1	2393	G
44	1	2394	G
44	1	2397	A
44	1	2402	A
44	1	2403	G
44	1	2404	A
44	1	2411	U
44	1	2435	G
44	1	2437	G
44	1	2438	A
44	1	2439	A
44	1	2445	A
44	1	2446	U
44	1	2447	A
44	1	2452	G
44	1	2496	C
44	1	2498	U
44	1	2501	U
44	1	2502	A
44	1	2506	U
44	1	2507	C
44	1	2508	U
44	1	2514	U
44	1	2515	A
44	1	2522	G
44	1	2524	A
44	1	2525	G
44	1	2531	C
44	1	2537	U
44	1	2538	U
44	1	2539	C
44	1	2540	A
44	1	2541	U
44	1	2542	U
44	1	2544	U
44	1	2547	A
44	1	2548	C
44	1	2549	G

Continued on next page...

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Mol	Chain	Res	Type
44	1	2552	C
44	1	2561	A
44	1	2569	A
44	1	2570	U
44	1	2571	U
44	1	2572	C
44	1	2573	G
44	1	2585	G
44	1	2593	A
44	1	2606	G
44	1	2607	G
44	1	2614	G
44	1	2635	A
44	1	2638	C
44	1	2652	U
44	1	2656	A
44	1	2672	G
44	1	2674	A
44	1	2677	G
44	1	2689	A
44	1	2691	A
44	1	2694	A
44	1	2696	A
44	1	2704	A
44	1	2719	U
44	1	2728	G
44	1	2729	U
44	1	2737	C
44	1	2752	U
44	1	2753	G
44	1	2755	C
44	1	2772	C
44	1	2773	C
44	1	2777	G
44	1	2778	G
44	1	2788	C
44	1	2796	G
44	1	2800	G
44	1	2801	A
44	1	2803	A
44	1	2810	C
44	1	2816	G

Continued on next page...

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Mol	Chain	Res	Type
44	1	2817	A
44	1	2821	C
44	1	2842	U
44	1	2844	C
44	1	2845	A
44	1	2867	C
44	1	2871	G
44	1	2872	A
44	1	2873	U
44	1	2875	U
44	1	2887	A
44	1	2889	C
44	1	2911	A
44	1	2915	U
44	1	2923	U
44	1	2935	U
44	1	2936	A
44	1	2947	G
44	1	2971	A
44	1	2983	C
44	1	2992	U
44	1	2996	U
44	1	2997	G
44	1	3012	A
44	1	3030	G
44	1	3059	G
44	1	3074	G
44	1	3078	U
44	1	3086	A
44	1	3092	C
44	1	3093	C
44	1	3101	G
44	1	3104	U
44	1	3113	A
44	1	3119	U
44	1	3122	A
44	1	3129	A
44	1	3130	A
44	1	3131	U
44	1	3142	A
44	1	3143	C
44	1	3153	U

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Mol	Chain	Res	Type
44	1	3154	C
44	1	3155	U
44	1	3156	U
44	1	3157	U
44	1	3165	A
44	1	3170	A
44	1	3173	G
44	1	3174	A
44	1	3176	G
44	1	3179	U
44	1	3181	C
44	1	3187	A
44	1	3196	U
44	1	3198	U
44	1	3207	U
44	1	3210	A
44	1	3217	C
44	1	3218	A
44	1	3219	G
44	1	3227	A
44	1	3229	G
44	1	3242	G
44	1	3243	A
44	1	3245	A
44	1	3247	G
44	1	3259	U
44	1	3263	G
44	1	3269	U
44	1	3270	U
44	1	3273	A
44	1	3276	G
44	1	3281	U
44	1	3287	U
44	1	3288	G
44	1	3289	G
44	1	3292	A
44	1	3294	A
44	1	3304	U
44	1	3313	U
44	1	3316	A
44	1	3318	G
44	1	3319	U

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Mol	Chain	Res	Type
44	1	3320	A
44	1	3334	U
44	1	3341	U
44	1	3345	G
44	1	3347	A
44	1	3351	U
44	1	3352	U
44	1	3353	G
44	1	3354	U
44	1	3355	U
44	1	3369	G
44	1	3375	A
44	1	3378	C
44	1	3383	G
44	1	3386	G
44	1	3389	U
44	1	3390	G

All (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C4	52	G
2	C3	85	G
44	1	13	A
44	1	239	G
44	1	282	G
44	1	637	C
44	1	715	A
44	1	763	G
44	1	916	G
44	1	1064	A
44	1	1097	G
44	1	1307	G
44	1	1355	A
44	1	1562	C
44	1	1568	U
44	1	1815	U
44	1	1820	U
44	1	1959	G
44	1	1983	G
44	1	2086	A
44	1	2101	C

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Mol	Chain	Res	Type
44	1	2112	U
44	1	2249	G
44	1	2446	U
44	1	2495	C
44	1	2537	U
44	1	2541	U
44	1	2547	A
44	1	3121	U
44	1	3218	A
44	1	3228	C
44	1	3269	U
44	1	3275	U
44	1	3319	U
44	1	3350	C
44	1	3351	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 211 ligands modelled in this entry, 211 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

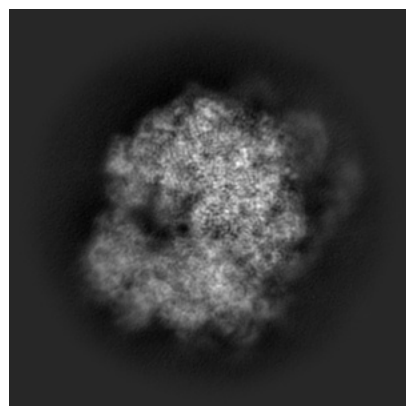
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16086. These allow visual inspection of the internal detail of the map and identification of artifacts.

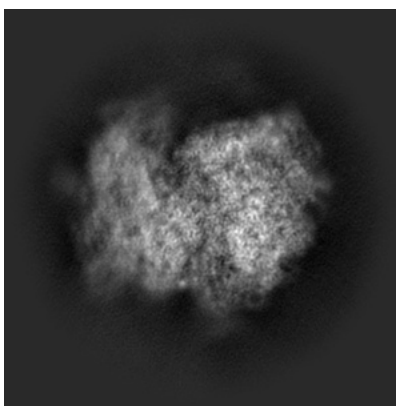
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

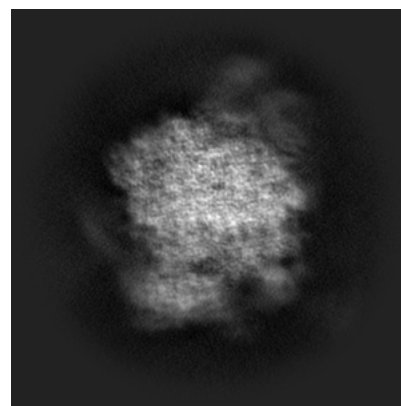
6.1.1 Primary map



X

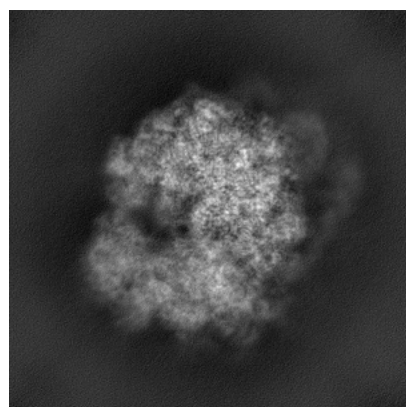


Y

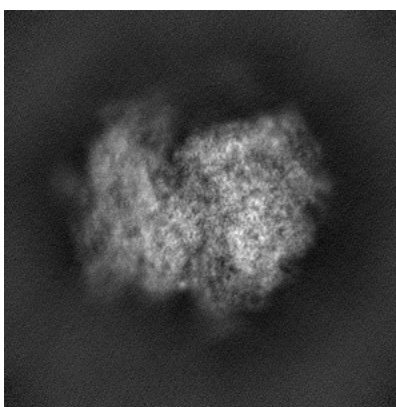


Z

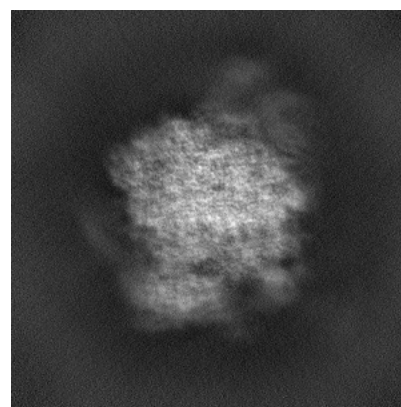
6.1.2 Raw map



X



Y

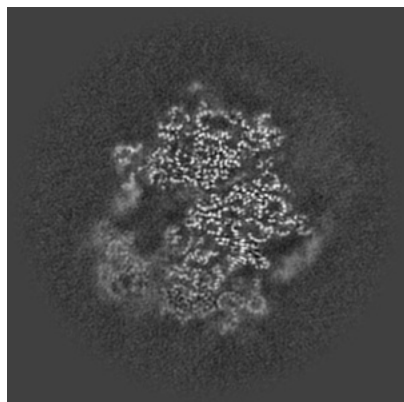


Z

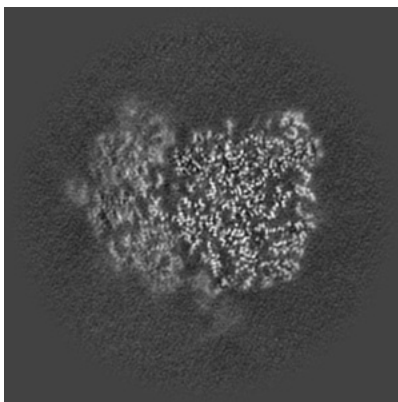
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

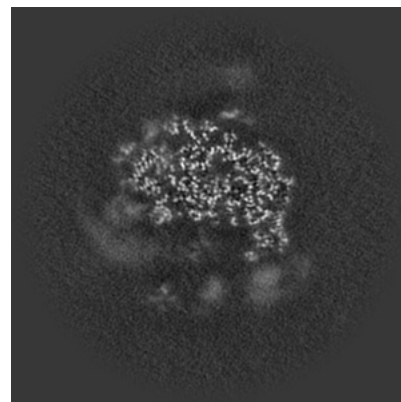
6.2.1 Primary map



X Index: 200

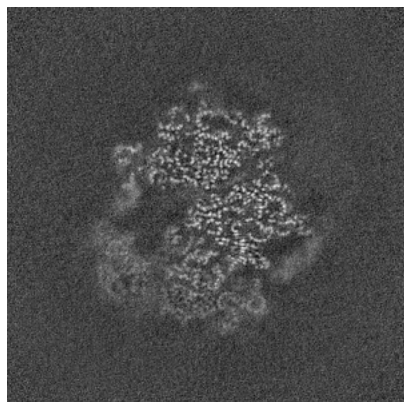


Y Index: 200

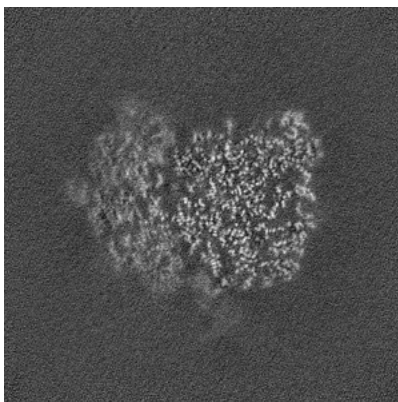


Z Index: 200

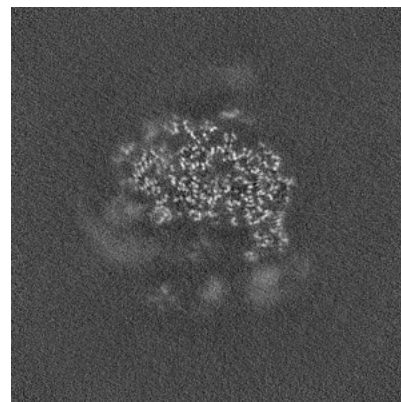
6.2.2 Raw map



X Index: 200



Y Index: 200

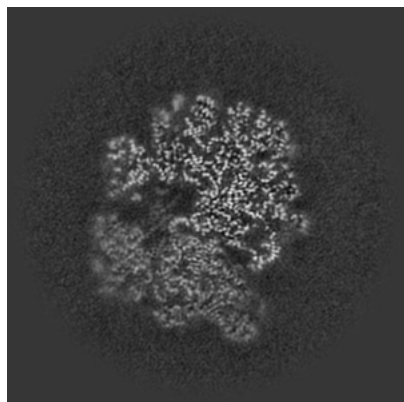


Z Index: 200

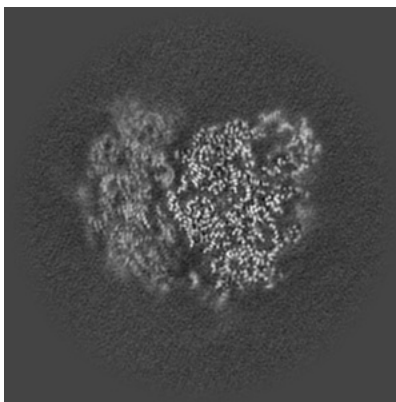
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

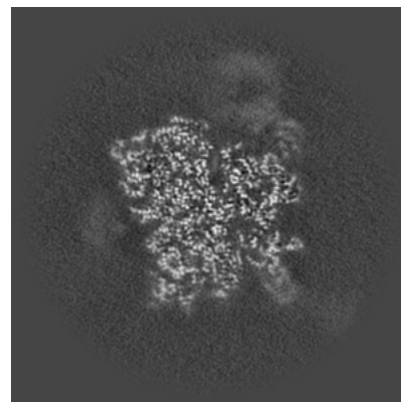
6.3.1 Primary map



X Index: 182

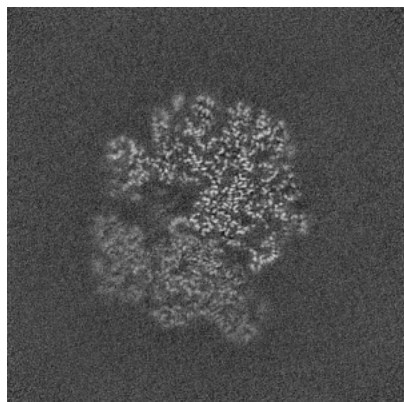


Y Index: 210

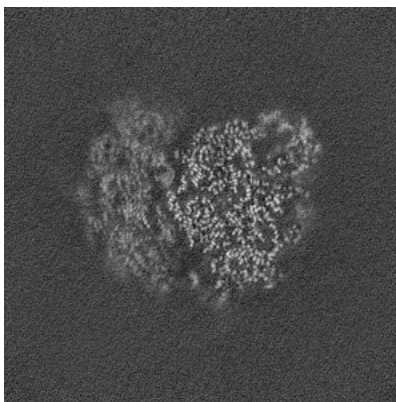


Z Index: 235

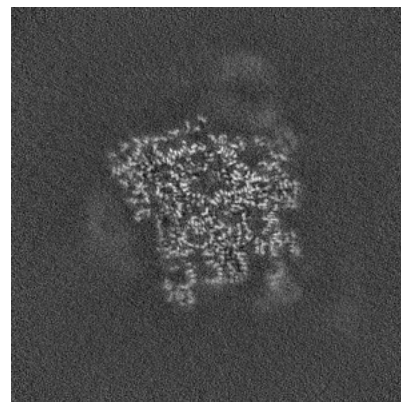
6.3.2 Raw map



X Index: 183



Y Index: 210

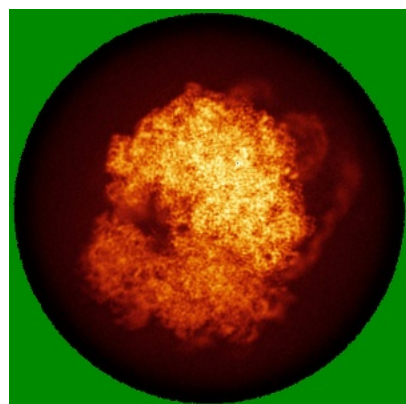


Z Index: 226

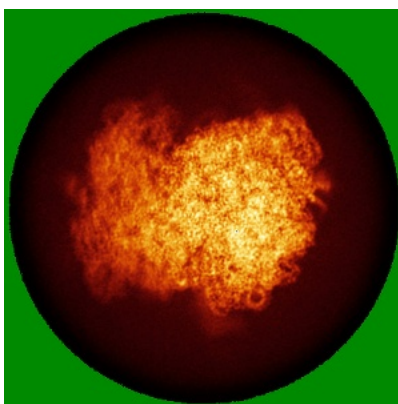
The images above show the largest variance slices of the map in three orthogonal directions.

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

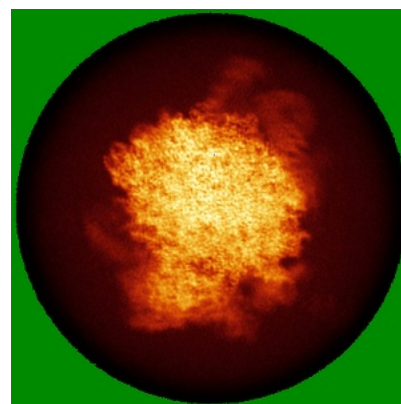
6.4.1 Primary map



X

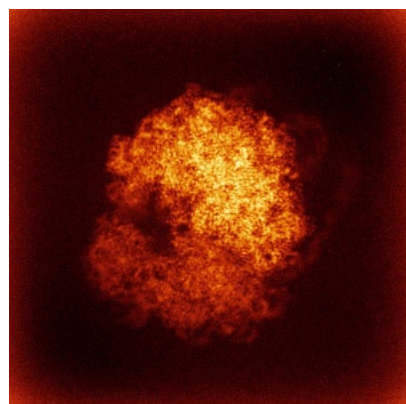


Y

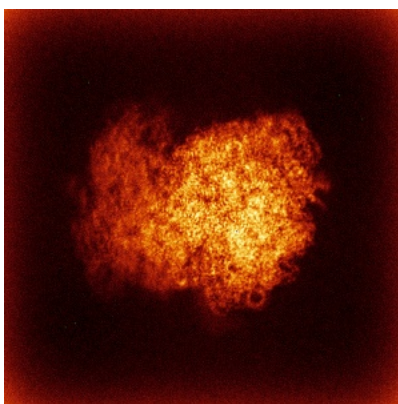


Z

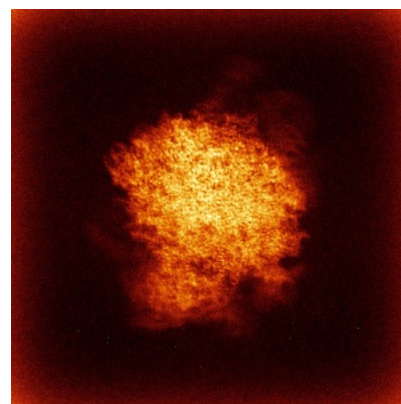
6.4.2 Raw map



X



Y

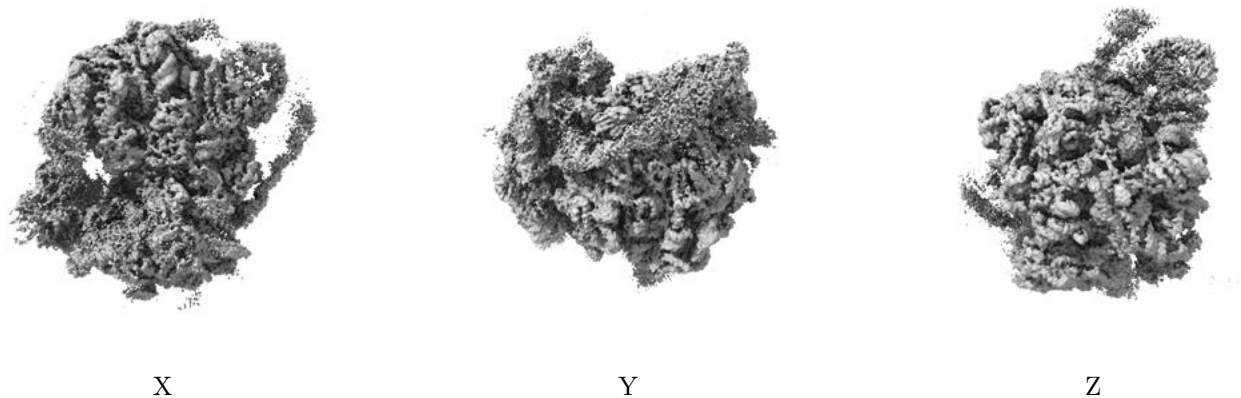


Z

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

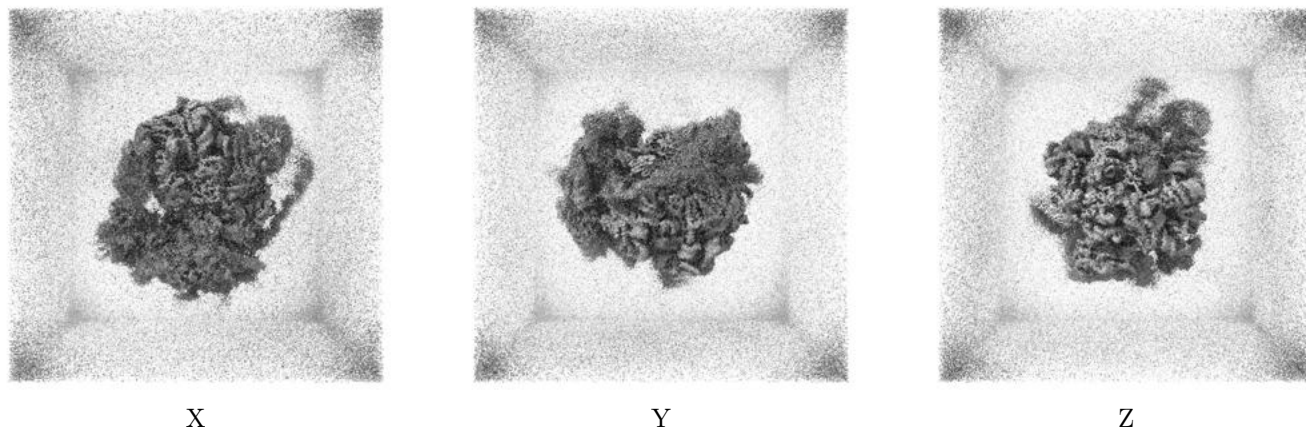
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.215. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

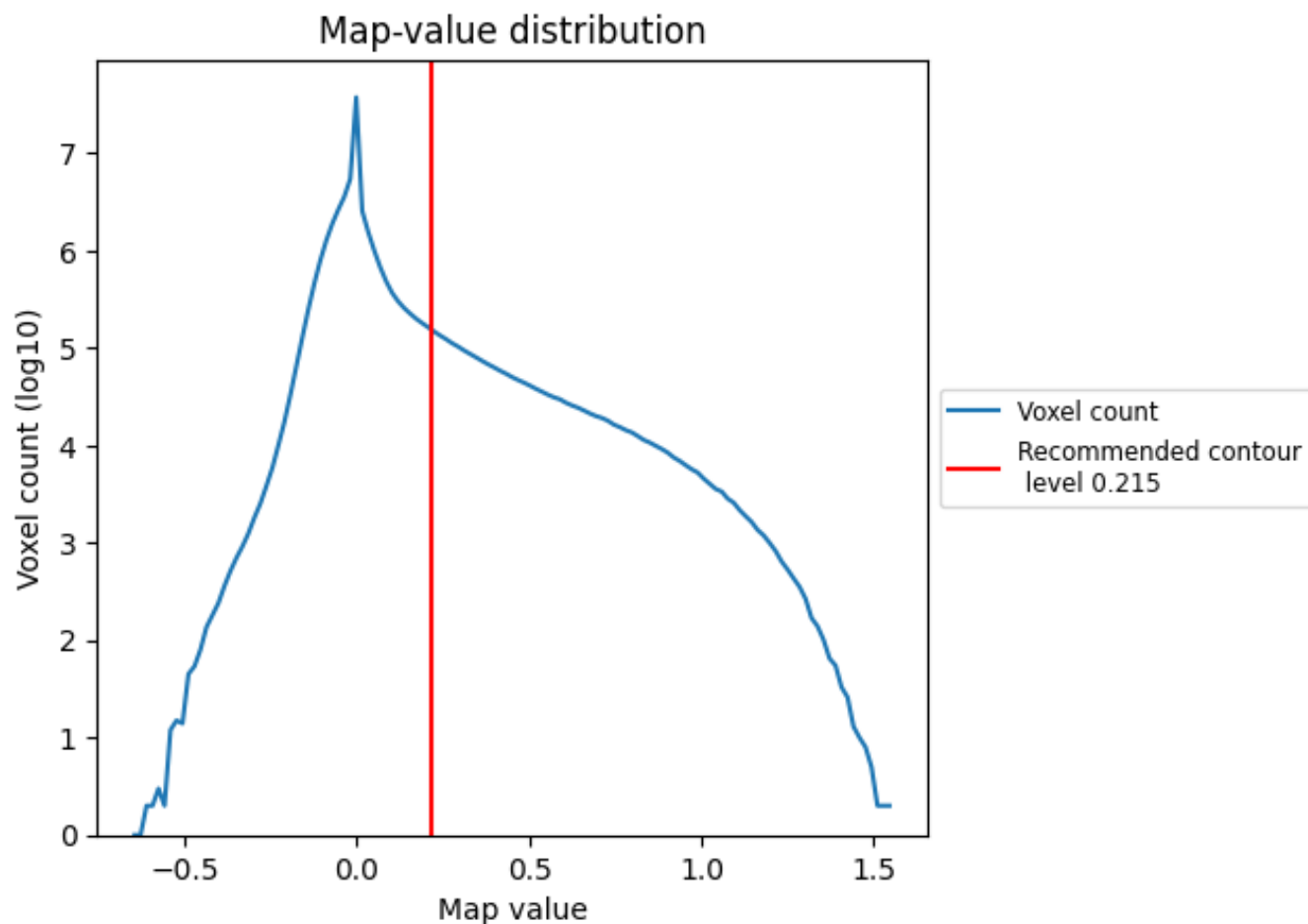
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

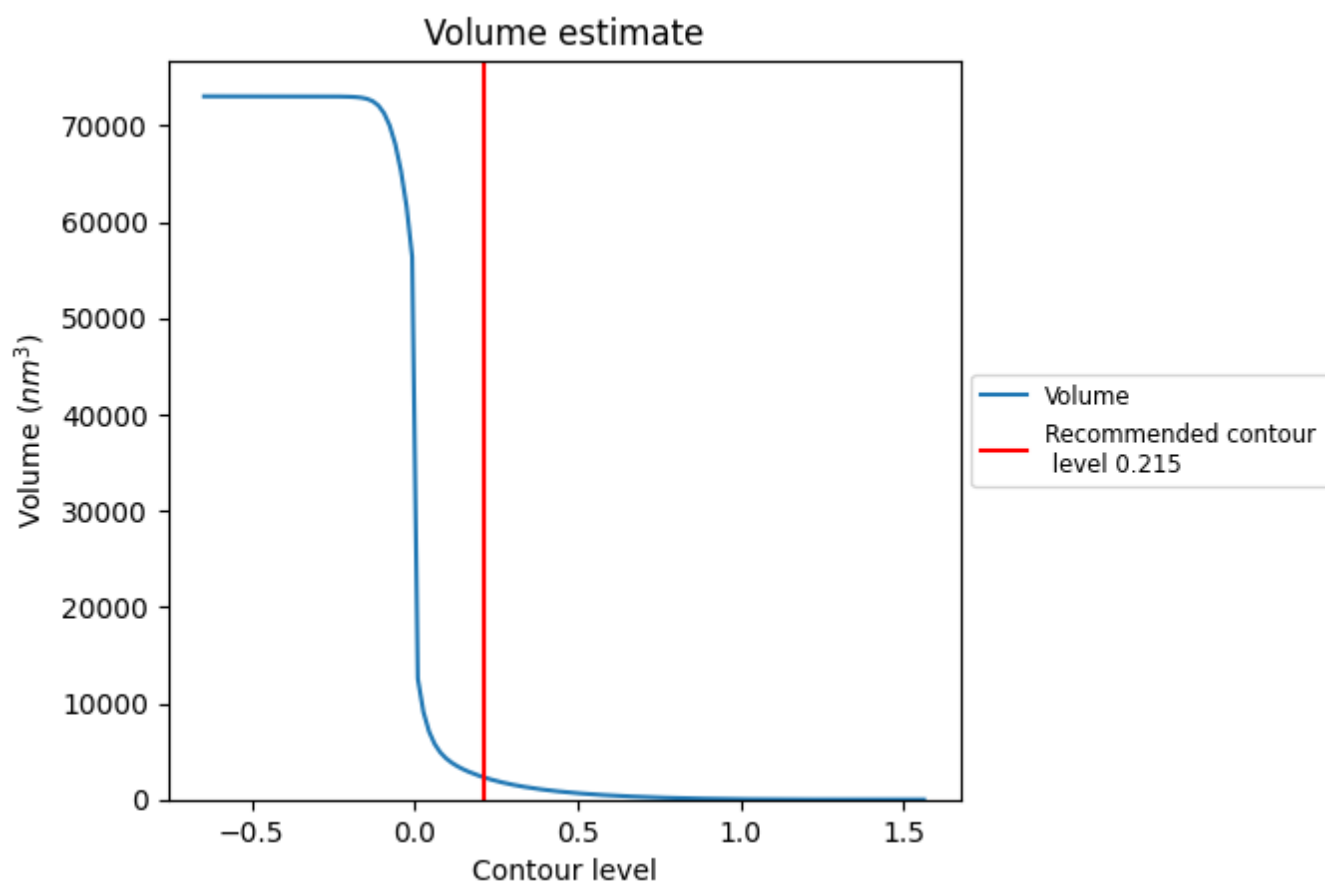
This section contains the results of statistical analysis of the map.

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.

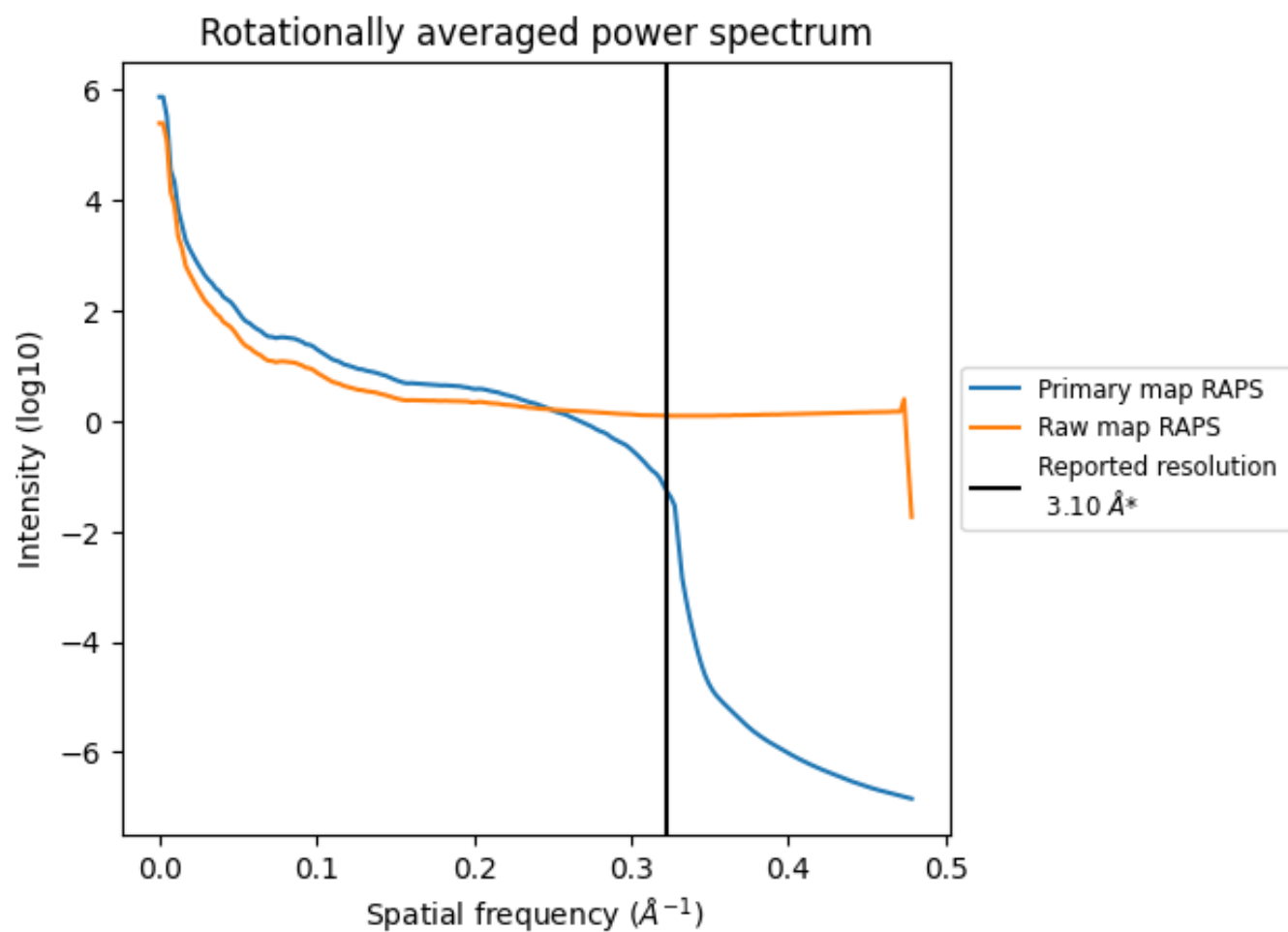
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2283 nm³; this corresponds to an approximate mass of 2062 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

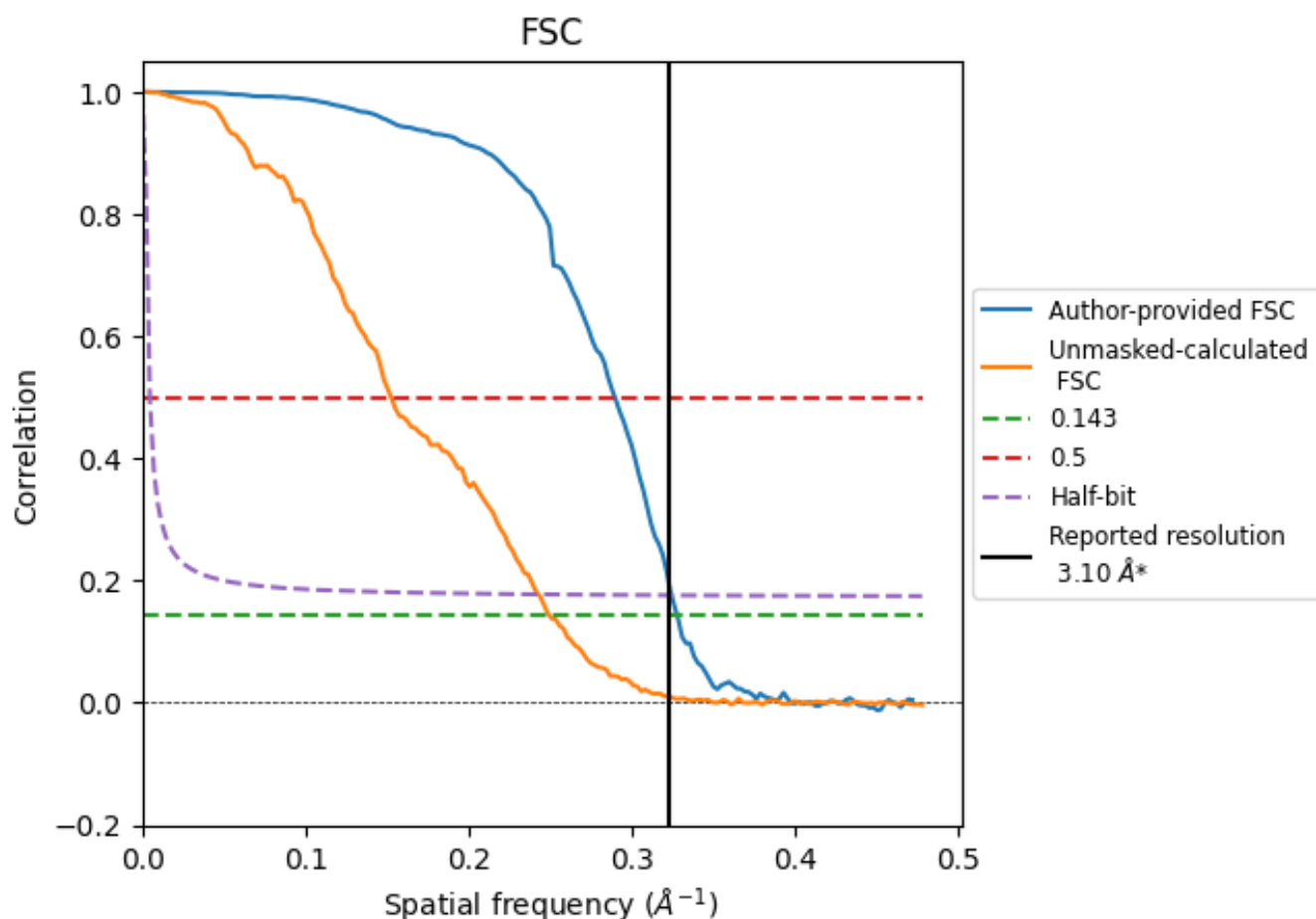


*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

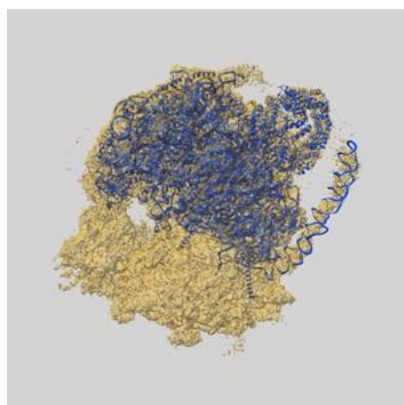
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.05	3.45	3.08
Unmasked-calculated*	4.00	6.55	4.11

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.1 by more than 10 %

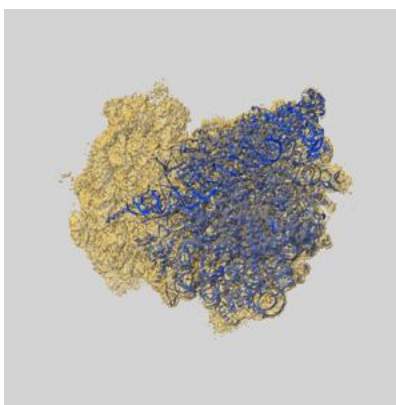
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16086 and PDB model 8BIP. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

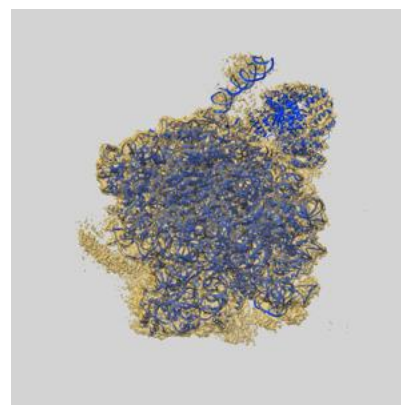
9.1 Map-model overlay [i](#)



X



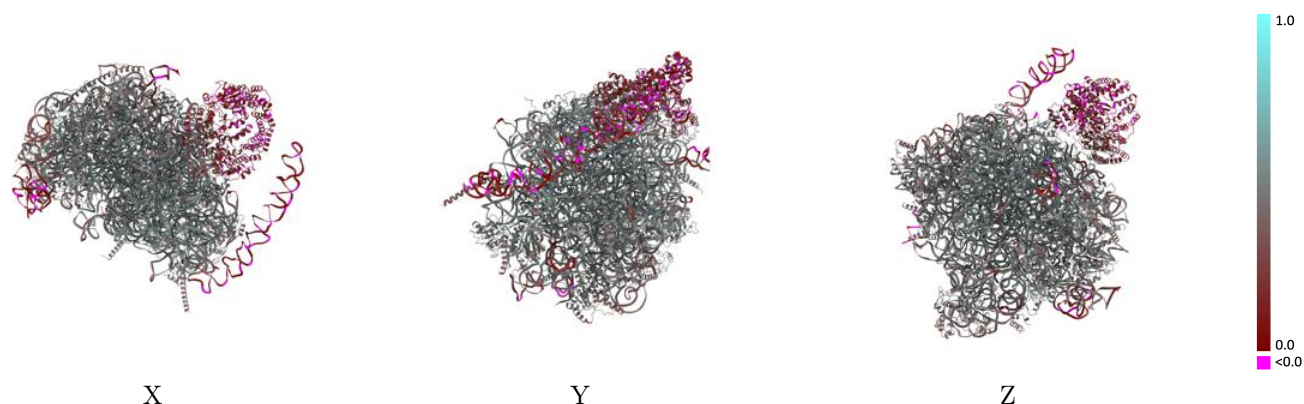
Y



Z

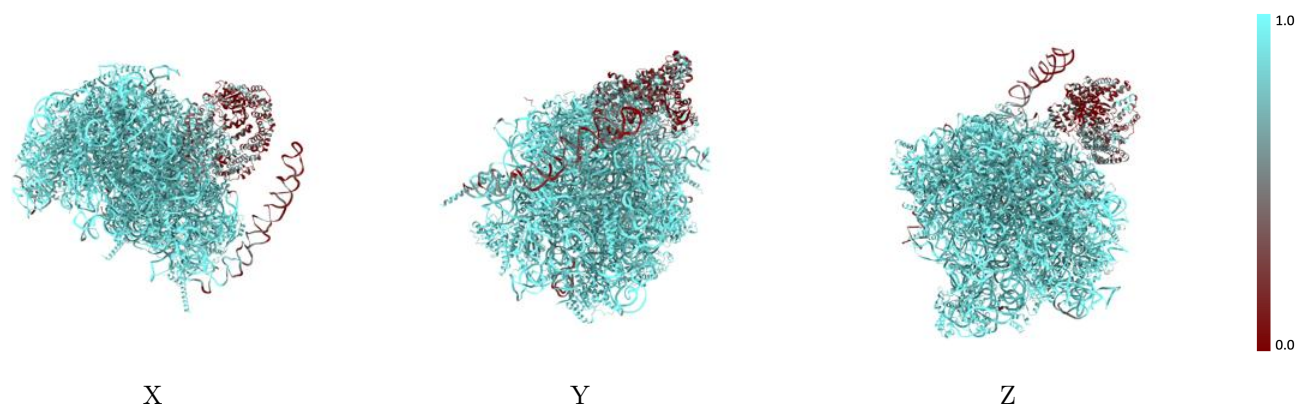
The images above show the 3D surface view of the map at the recommended contour level 0.215 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



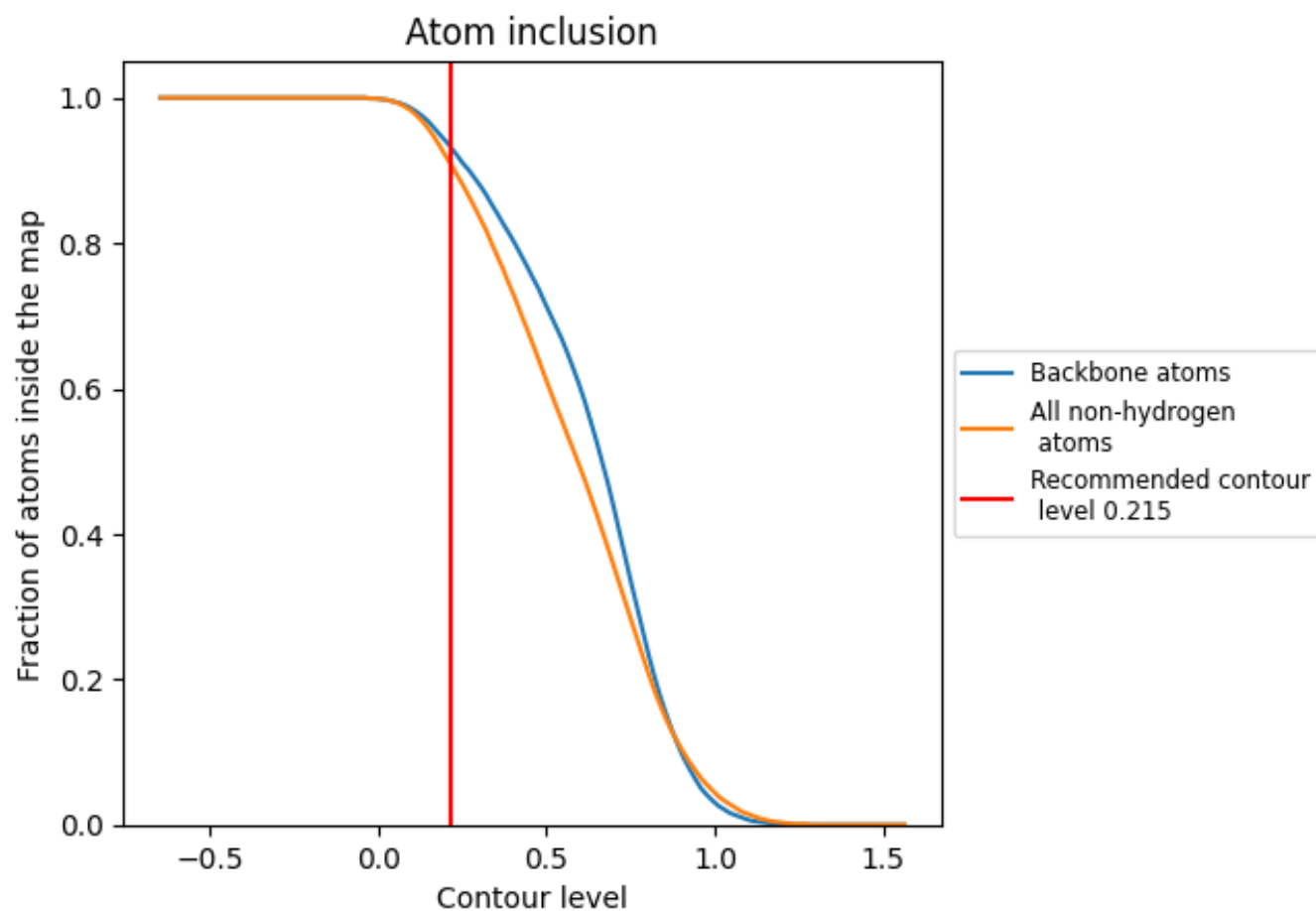
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.215).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% 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 (0.215) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.4510
1	 0.9540	 0.4550
8	 0.7220	 0.4130
A	 0.0550	 0.0950
B	 0.4360	 0.1860
C3	 0.9930	 0.4860
C4	 0.9980	 0.4740
LA	 0.9140	 0.5230
LB	 0.9420	 0.5050
LC	 0.9430	 0.5040
LD	 0.9270	 0.4260
LE	 0.9280	 0.4510
LF	 0.9450	 0.4930
LG	 0.9090	 0.4540
LH	 0.9280	 0.4700
LI	 0.9030	 0.4810
LJ	 0.8540	 0.4040
LL	 0.9380	 0.4750
LM	 0.9240	 0.4630
LN	 0.9430	 0.5170
LO	 0.9390	 0.4950
LP	 0.9040	 0.5080
LQ	 0.9530	 0.5080
LR	 0.9110	 0.4920
LS	 0.9250	 0.5000
LT	 0.9260	 0.5040
LU	 0.9010	 0.4630
LV	 0.8790	 0.5090
LW	 0.8850	 0.4970
LX	 0.9040	 0.5050
LY	 0.9440	 0.5030
LZ	 0.9390	 0.4740
La	 0.9540	 0.5110
Lb	 0.9140	 0.4700
Lc	 0.9320	 0.4800



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Chain	Atom inclusion	Q-score
Ld	 0.9170	 0.5130
Le	 0.9300	 0.5220
Lf	 0.9390	 0.5150
Lg	 0.9300	 0.5130
Lh	 0.9400	 0.4760
Li	 0.8920	 0.4520
Lj	 0.9740	 0.5340
Lk	 0.9130	 0.4740
Ll	 0.9420	 0.5140
Lm	 0.9080	 0.4920
Ln	 0.8410	 0.4580
Lo	 0.9340	 0.4970
Lp	 0.9060	 0.5050