



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 04:00 AM UTC

PDB ID : 7JT2 / pdb_00007jt2
EMDB ID : EMD-22469
Title : 70S ribosome stalled on long mRNA with ArfB bound in the A site
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2020-08-16
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

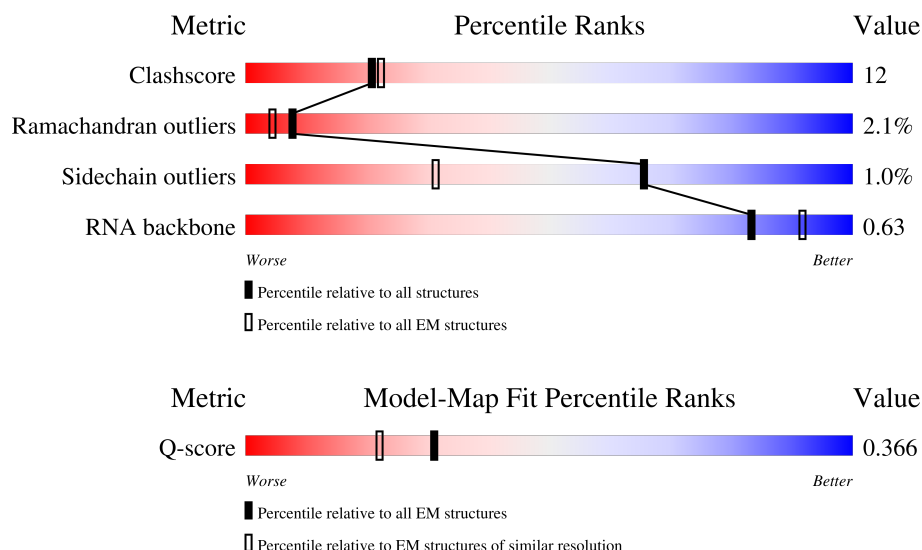
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

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



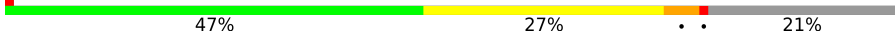
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	

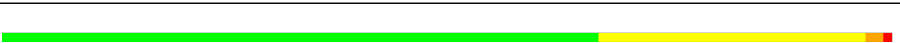
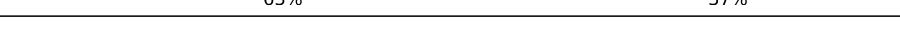
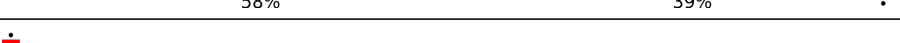
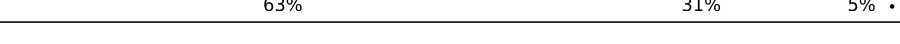
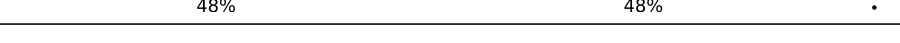
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	165	
8	j	142	
9	k	122	
10	l	143	
11	m	136	
12	n	120	
13	o	116	
14	p	114	
15	q	117	
16	r	103	
17	s	110	
18	t	93	
19	u	102	
20	v	94	
21	w	75	
22	x	77	
23	y	63	
24	z	58	
25	B	56	
26	C	50	
27	D	46	
28	E	64	

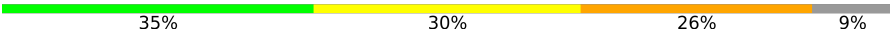
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Mol	Chain	Length	Quality of chain
29	F	38	
30	G	225	
31	H	206	
32	I	205	
33	J	157	
34	K	100	
35	L	151	
36	M	129	
37	N	127	
38	O	98	
39	P	116	
40	Q	123	
41	R	114	
42	S	100	
43	T	88	
44	U	82	
45	V	80	
46	W	65	
47	X	79	
48	Y	85	
49	Z	65	
50	3	1539	
51	1	2903	
52	2	120	
53	5	77	

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Mol	Chain	Length	Quality of chain
54	4	23	 35% 30% 26% 9%
55	8	132	 49% 39% 10% •

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 145984 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

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

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L13.

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

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 10 is a protein called 50S ribosomal protein L15.

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

- Molecule 11 is a protein called 50S ribosomal protein L16.

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

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 13 is a protein called 50S ribosomal protein L18.

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

- Molecule 14 is a protein called 50S ribosomal protein L19.

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

- Molecule 15 is a protein called 50S ribosomal protein L20.

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

- Molecule 16 is a protein called 50S ribosomal protein L21.

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

- Molecule 17 is a protein called 50S ribosomal protein L22.

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

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	u	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 20 is a protein called 50S ribosomal protein L25.

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

- Molecule 21 is a protein called 50S ribosomal protein L27.

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

- Molecule 22 is a protein called 50S ribosomal protein L28.

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

- Molecule 23 is a protein called 50S ribosomal protein L29.

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

- Molecule 24 is a protein called 50S ribosomal protein L30.

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

- Molecule 25 is a protein called 50S ribosomal protein L32.

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

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 27 is a protein called 50S ribosomal protein L34.

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

- Molecule 28 is a protein called 50S ribosomal protein L35.

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

- Molecule 29 is a protein called 50S ribosomal protein L36.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 31 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 32 is a protein called 30S ribosomal protein S4.

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

- Molecule 33 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 34 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 35 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 36 is a protein called 30S ribosomal protein S8.

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

- Molecule 37 is a protein called 30S ribosomal protein S9.

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

- Molecule 38 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 39 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 40 is a protein called 30S ribosomal protein S12.

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

- Molecule 41 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 42 is a protein called 30S ribosomal protein S14.

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

- Molecule 43 is a protein called 30S ribosomal protein S15.

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

- Molecule 44 is a protein called 30S ribosomal protein S16.

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

- Molecule 45 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 46 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 47 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 48 is a protein called 30S ribosomal protein S20.

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

- Molecule 49 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 50 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	1539	Total	C	N	O	P	0	0
			33012	14725	6053	10696	1538		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	1490	C	U	conflict	GB 1789840096

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62315	27801	11468	20144	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 53 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	21	Total 461	C 207	N 96	O 137	P 21	0	0

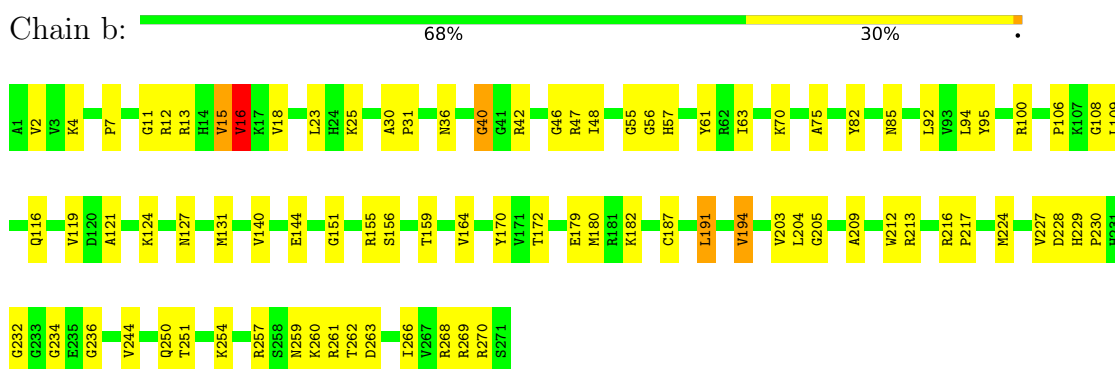
- Molecule 55 is a protein called Peptidyl-tRNA hydrolase ArfB.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	132	Total 1031	C 638	N 204	O 187	S 2	0	0

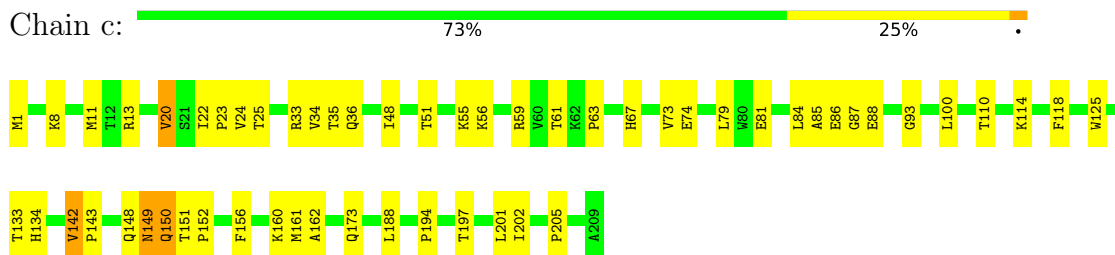
3 Residue-property plots

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.

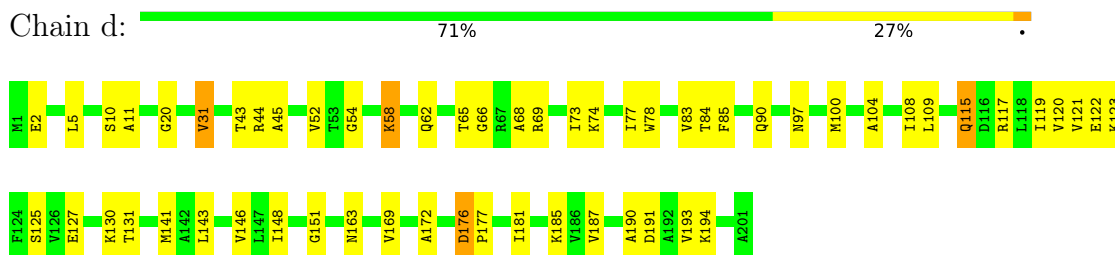
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

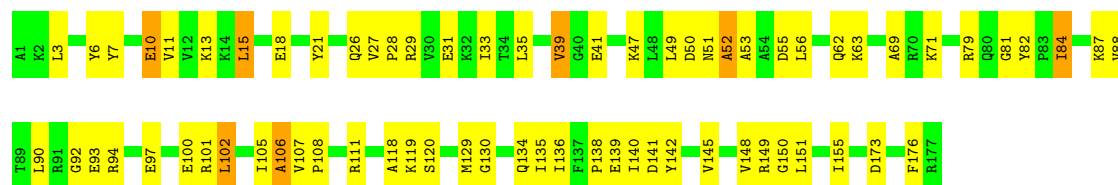


- Molecule 3: 50S ribosomal protein L4



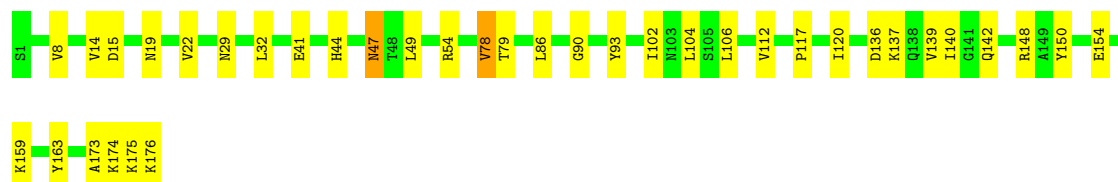
- Molecule 4: 50S ribosomal protein L5





• Molecule 5: 50S ribosomal protein L6

Chain f: 79% 20% .



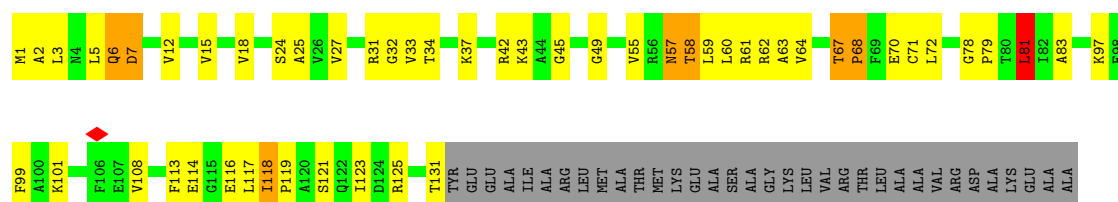
• Molecule 6: 50S ribosomal protein L9

Chain g: 70% 29% .



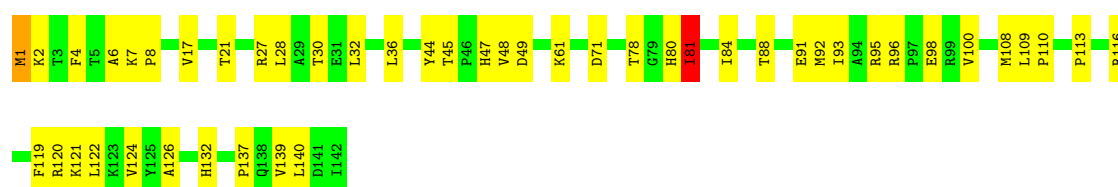
• Molecule 7: 50S ribosomal protein L10

Chain h: 47% 27% . . 21%



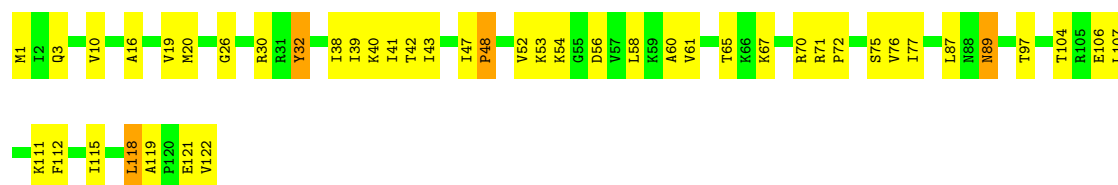
• Molecule 8: 50S ribosomal protein L13

Chain j: 67% 32% . .



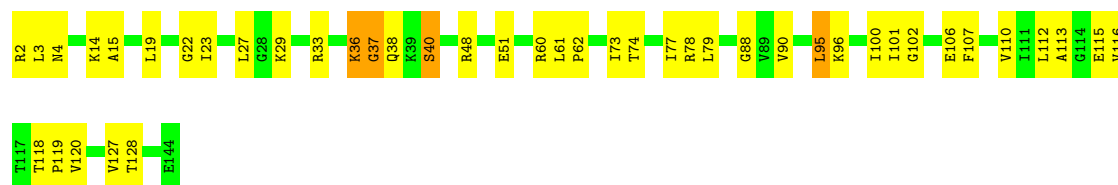
• Molecule 9: 50S ribosomal protein L14

Chain k:  63% 34% .



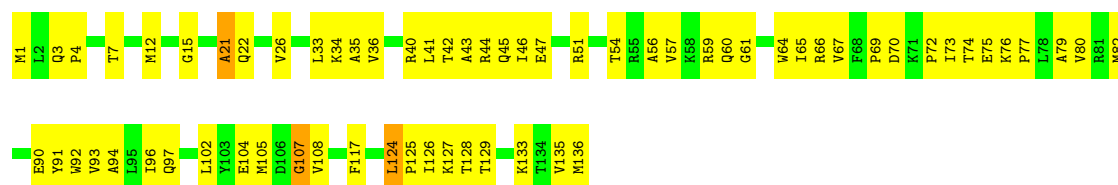
- Molecule 10: 50S ribosomal protein L15

Chain l:  69% 28% .



- Molecule 11: 50S ribosomal protein L16

Chain m:  52% 46% .



- Molecule 12: 50S ribosomal protein L17

Chain n:  66% 34% .



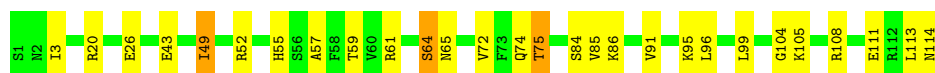
- Molecule 13: 50S ribosomal protein L18

Chain o:  73% 24% .



- Molecule 14: 50S ribosomal protein L19

Chain p:  75% 22% .



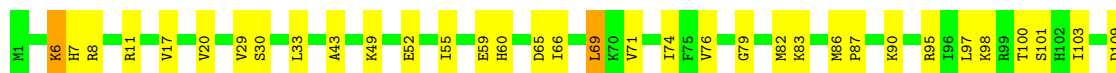
- Molecule 15: 50S ribosomal protein L20



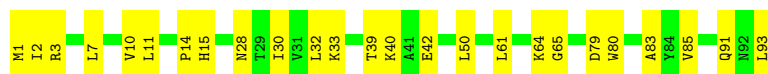
- Molecule 16: 50S ribosomal protein L21



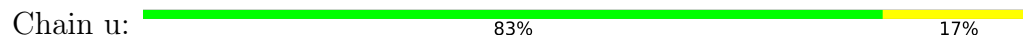
- Molecule 17: 50S ribosomal protein L22



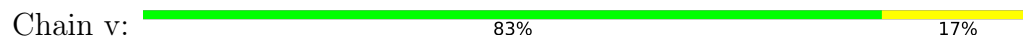
- Molecule 18: 50S ribosomal protein L23



- Molecule 19: 50S ribosomal protein L24



- Molecule 20: 50S ribosomal protein L25





- Molecule 21: 50S ribosomal protein L27

Chain w: 85% 13%



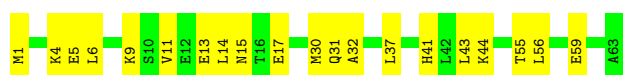
- Molecule 22: 50S ribosomal protein L28

Chain x: 74% 26%



- Molecule 23: 50S ribosomal protein L29

Chain y: 68% 32%



- Molecule 24: 50S ribosomal protein L30

Chain z: 83% 17%



- Molecule 25: 50S ribosomal protein L32

Chain B: 64% 34%



- Molecule 26: 50S ribosomal protein L33

Chain C: 84% 16%



- Molecule 27: 50S ribosomal protein L34

Chain D: 74% 24%



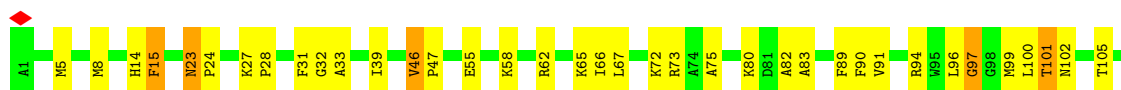
- Molecule 28: 50S ribosomal protein L35



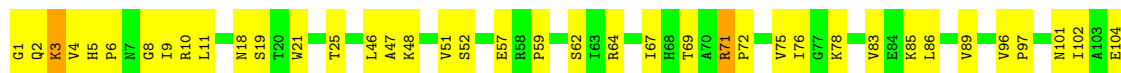
- Molecule 29: 50S ribosomal protein L36



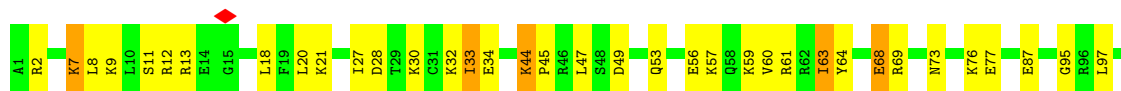
- Molecule 30: 30S ribosomal protein S2



- Molecule 31: 30S ribosomal protein S3



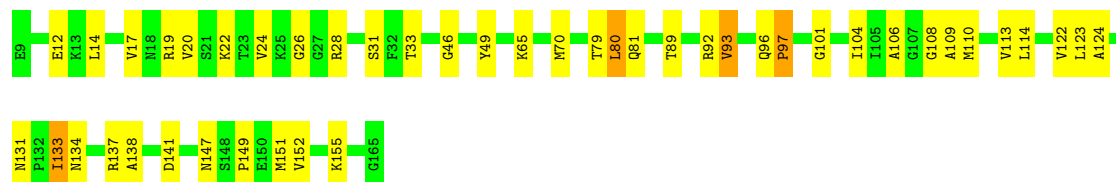
- Molecule 32: 30S ribosomal protein S4





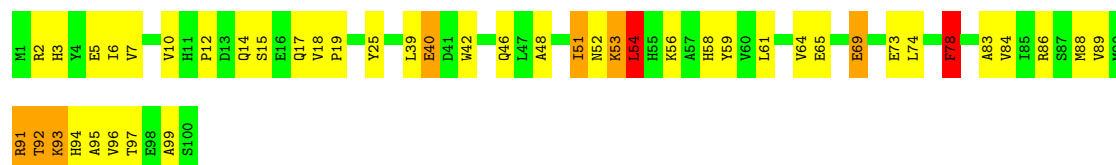
- Molecule 33: 30S ribosomal protein S5

Chain J: 71% 26% .



- Molecule 34: 30S ribosomal protein S6

Chain K: 55% 36% 7% .



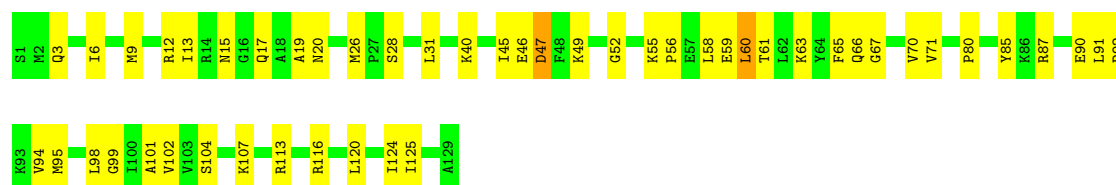
- Molecule 35: 30S ribosomal protein S7

Chain L: 79% 19% .



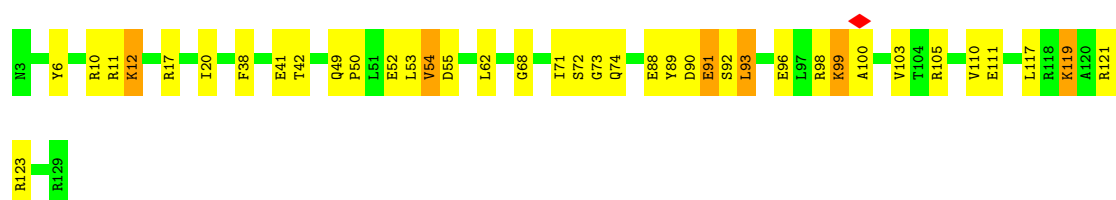
- Molecule 36: 30S ribosomal protein S8

Chain M: 62% 36% .



- Molecule 37: 30S ribosomal protein S9

Chain N: 69% 27% 5% .



- Molecule 38: 30S ribosomal protein S10

Chain O:  66% 29% ..



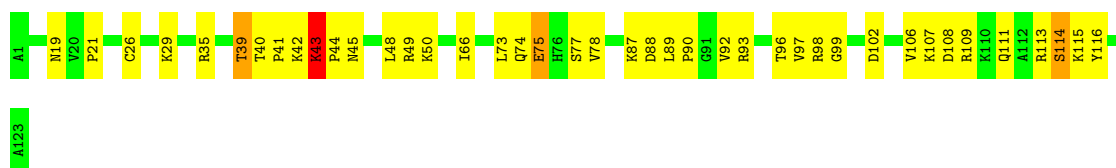
- Molecule 39: 30S ribosomal protein S11

Chain P:  72% 23% 5%



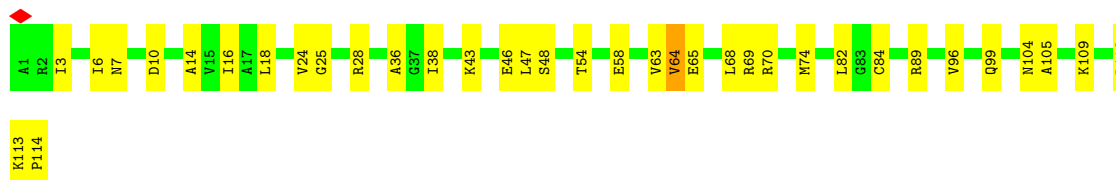
- Molecule 40: 30S ribosomal protein S12

Chain Q:  67% 30% ..



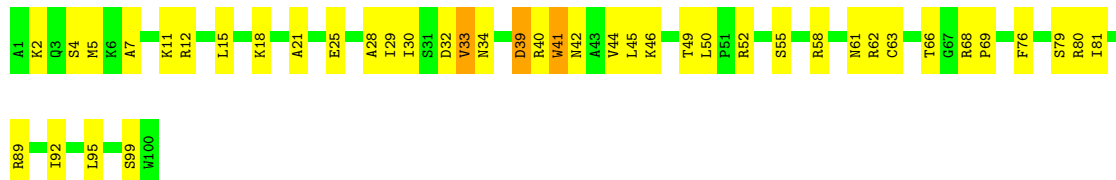
- Molecule 41: 30S ribosomal protein S13

Chain R:  68% 31% .



- Molecule 42: 30S ribosomal protein S14

Chain S:  58% 39% .



- Molecule 43: 30S ribosomal protein S15

Chain T:  70% 27% .



- Molecule 44: 30S ribosomal protein S16



- Molecule 45: 30S ribosomal protein S17



- Molecule 46: 30S ribosomal protein S18



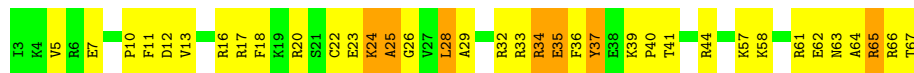
- Molecule 47: 30S ribosomal protein S19



- Molecule 48: 30S ribosomal protein S20



- Molecule 49: 30S ribosomal protein S21



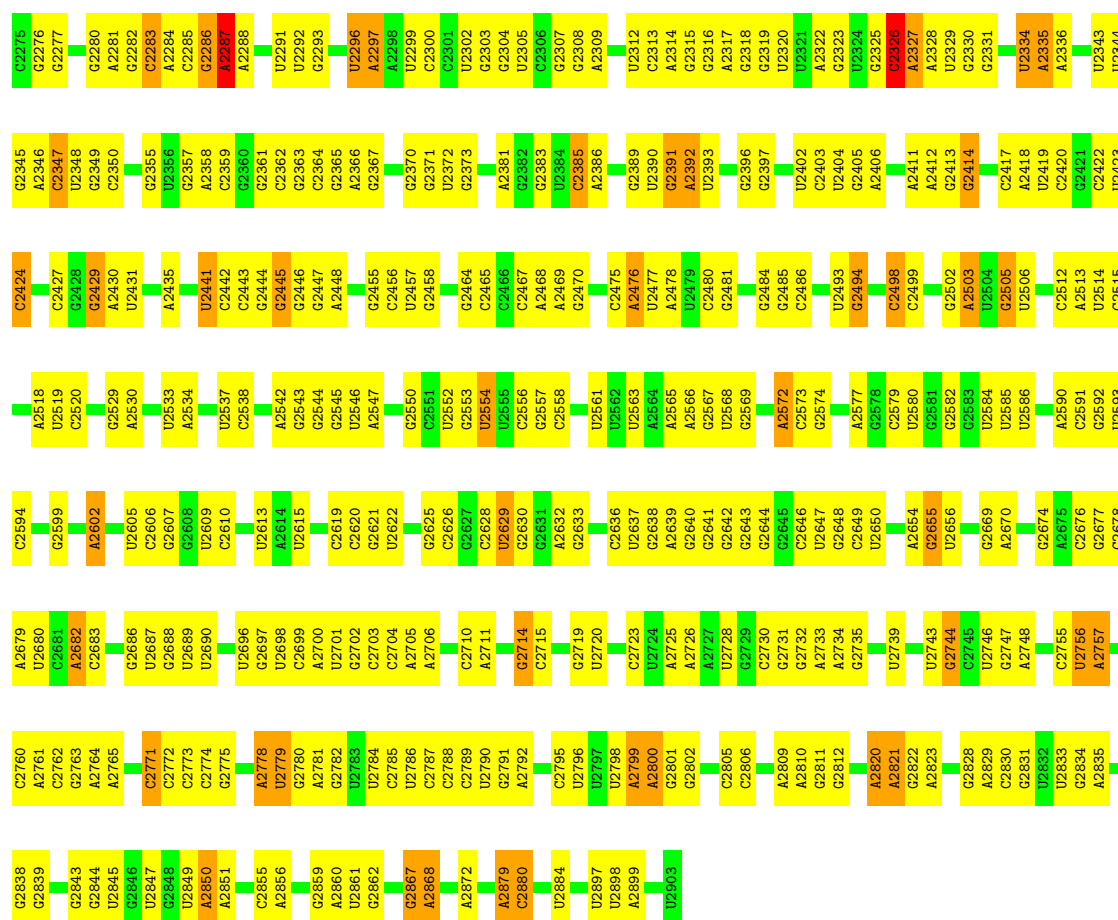
- Molecule 50: 16S ribosomal RNA



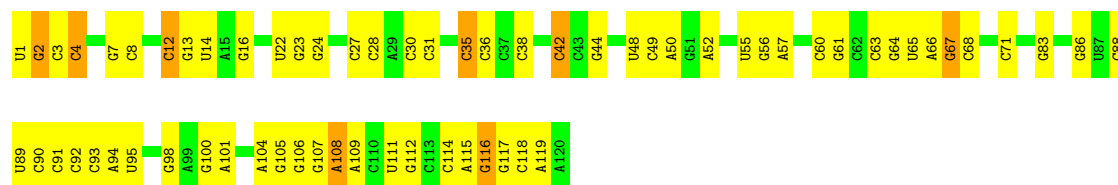
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G1255	G1178	A1102	U1007	G833	U740	U662	G557		C372	C285	C194	C95	G9
A1257	G1182	G1104	A1014	U837	G741	A663	A559	A456	A373	C286	A196	G100	A10
G1258	U1183	G1015	A915	C838	G742	A664	A560	A457	G376	G289	G201	G100	G11
G1259	G1184	A1016	U916	C839	A743	A665	U561		G377		G202	A109	
G1260	G1185	U1017	G917		A745		C564	U463	U387	G297	G203	A109	A16
A1261	G1186	G1018	A918	U842	A746		U565	U469	U388	U304	G204	G110	U17
	U1264	A1111	A919	U843	A747	A673	C566	C469	U389	G305	A205	G111	C18
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		C1114	G833	G847	A750	U680	A572	U479	C393	G211	G211	U114	G21
		U1115	C934	G848	A751	C879	A573	U480	A393	G212	G212	G115	G22
		U1116	A935	G849	A752	U680	A574		G394	U308	U308	G116	
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		G1124	G839	G854	A757	U685	A579	U487	G402	C313	C217	G122	G31
		G1127	G840	U855	A758	U686	A580	U488	C403	C314	G220	U123	A32
		C1128	C856	U856	A759	U687	A581	U489	C404	C315	C221	U124	G35
		C1129	C857	U857	A760	U688	A582	U490	C405	C316	C222	G128	C36
		A1130	C858	U858	A761	U689	A583	U491	C406	G319	C223	U129	U37
		U1205	C859	U859	A762	U690	A584	U492	C407	A320	U224	A130	G38
G1206	G1206	A1044	C860	U860	A763	U691	A585	U493	C408	A321	C225	G129	G39
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		A1046	G862	U862	A765	U693	A587	U495	C410	U323	G227	G144	G41
		U1052	A865	U863	A766	U694	A588	U496	C411	A325	G228	G145	G42
		G1053	C866	U864	A767	U695	A589	U497	C412	A326	G229	G146	
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		U1062	G868	U866	A769	U697	A591	U499	C414	C328	A236	A151	C48
		U1063	C869	U867	A770	U698	A592	U500	C415	A329	A237	A152	U49
		G1064	U870	U871	A771	U699	A593	U501	C416	G332	U243	A153	A50
		U1065	U872	U873	A772	U700	A594	U502	C417	U335	U244	G159	A51
		C1066	A878	U874	A773	U701	A595	U503	C418	C336	U245	A162	C54
		U1067	U875	U876	A774	U702	A596	U504	C419	A337	G247	A163	A55
		C1068	U877	U878	A775	U703	A597	U505	C420	U340	A250	C163	U56
		A1069	U879	U880	A776	U704	A598	U506	C421	C341	G251	G166	G57
		G1070	U881	U882	A777	U705	A599	U507	C422	G342	U252	A167	C58
		U1071	U883	U884	A778	U706	A600	U508	C423	C343	U253	A168	A59
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		U1074	U889	U889	A781	U709	U603	U511	C426	G346	U255	C178	G68
		U1075	U890	U890	A782	U710	U604	U512	C427	A347	U256	A179	G69
		C1076	U891	U891	A783	U711	U605	U513	C428	G348	G257	G180	A74
		A1077	U892	U892	A784	U712	U606	U514	C429	C352	U258	A181	G75
		G1078	U893	U893	A785	U713	U607	U515	C430	A353	G259	A182	G76
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		A1081	U896	U896	A788	U716	U610	U518		C356	U262	U185	G82
		G1082	U897	U897	A789	U717	U611	U519		U358	G263	G186	G83
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		G1085	U900	U900	A792	U720	U614	U522		U363	G266	U189	U85
		U1086	U901	U901	A793	U721	U615	U523		A279	G267	A190	G86
		U1087	U902	U902	A794	U722	U616	U524		C280	C268	G191	C87
		G1088	U903	U903	A795	U723	U617	U525					
		A1089	U904	U904	A796	U724	U618	U526					
		U1089	U905	U905	A797	U725	U619	U527					
		G1090	U906	U906	A798	U726	U620	U528					
		U1091	U907	U907	A799	U727	U621	U529					
		C1092	U908	U908	A800	U728	U622	U530					
		G1093	U909	U909	A801	U729	U623	U531					
		U1094	U910	U910	A802	U730	U624	U532					
		U1095	U911	U911	A803	U731	U625	U533					
		C1096	U912	U912	A804	U732	U626	U534					
		U1097	U913	U913	A805	U733	U627	U535					
		C1098	U914	U914	A806	U734	U628	U536					
		G1099	U915	U915	A807	U735	U629	U537					
		U1252	U916	U916	A808	U736	U630	U538					
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		G1277	U940	U940	A832	U760	U654	U562					
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		G1279	U942	U942	A834	U762	U656	U564					
		A1280	U943	U943	A835	U763	U657	U565					
		G1281	U944	U944	A836	U764	U658	U566					
		A1282	U945	U945	A837	U765	U659	U567					
		G1283	U946	U946	A838	U766	U660	U568					
		A1284	U947	U947	A839	U767	U661	U569					
		G1285	U948	U948	A840	U768	U662	U570					
		A1286	U949	U949	A841	U769	U663	U571					
		G1287	U950	U950	A842	U770	U664	U572					
		A1288	U951	U951	A843	U771	U665	U573					
		G1289	U952	U952	A844	U772	U666	U574					
		A1290	U953	U953	A845	U773	U667	U575					
		G1291	U954	U954	A846	U774	U668	U576					
		A1292	U955	U955	A847	U775	U669	U577					
		G1293	U956	U956	A848	U776	U670	U578					
		A1294	U957	U957	A849	U777	U671	U579					
		G1295	U958	U958	A850	U778	U672	U580					
		A1296	U959	U959	A851	U779	U673	U581					
		G1297	U960	U960	A852	U780	U674	U582					
		A1298	U961	U961	A853	U781	U675	U583					
		G1299	U962	U962	A854	U782	U676	U584					
		A1300	U963	U963	A855	U783	U677	U585					
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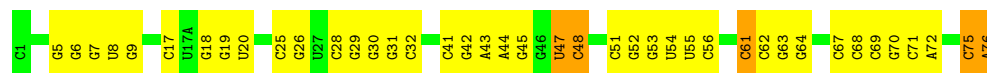
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C2207	C2207	C2066	C2066	A1981	C2066	A1981	A1889	A1803	U1736	A1640	G1543	U1458	A1365	G1284	G1185	A1111	A1027
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C2210	C2210	C2068	C2068	G1983	C2068	G1983	G1891	A1808	G1739	C1646	C1550	U1461	A1368	A1287	U1188	C1118	C1045
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C2212	C2212	A2071	A2071	U1991	A2071	U1991	A1900	A1810	C1741	U1648	A1552	U1463	G1370	G1289	U1190	G1123	A1046
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U2214	U2214	C2073	C2073	U1993	C2073	U1993	A1902	U1812	G1743	A1652	G1555	U1465	G1372	G1291	U1192	G1125	C1053
C2215	C2215	U2075	U2075	C1905	U2075	C1905	G1904	G1813	G1744	G1653	C1558	U1466	U1378	G1300	U1203	G1126	A1054
G2216	G2216	C2078	C2078	U1994	C2078	U1994	G1905	A1814	A1745	A1654	C1559	U1467	U1379	A1301	G1206	A1126	G1055
U2217	U2217	U2079	U2079	G1995	U2079	G1995	G1906	A1815	U1746	A1655	U1559	U1470	U1380	A1302	U1207	A1127	G1056
C2218	C2218	A2080	A2080	C1997	A2080	C1997	G1907	A1816	U1747	U1656	G1560	U1471	U1381	G1303	U1208	G1128	G1057
G2219	G2219	C1997	C1997	U1998	C1997	U1998	G1908	G1817	G1748	C1658	C1561	U1472	U1382	G1304	U1209	U1132	U1058
U2220	U2220	U2080	U2080	G1998	U2080	G1998	G1909	U1818	G1749	G1659	U1562	U1473	U1383	A1304	G1210	U1133	U1059
C2221	C2221	C2086	C2086	U2011	C2086	U2011	G1910	U1819	G1750	G1660	U1563	U1474	U1384	G1305	G1211	C1135	U1060
G2222	G2222	G2087	G2087	G1911	G2087	G1911	G1911	A1821	G1751	G1661	U1564	U1475	U1385	G1306	G1212	G1136	U1061
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C2227	C2227	U2093	U2093	A1916	U2093	A1916	G1916	U1826	G1756	A1669	C1569	U1480	U1390	G1311	G1220	U1142	U1066
G2228	G2228	A2097	A2097	A1917	A2097	A1917	G1917	U1827	A1757	A1672	U1570	U1481	U1391	G1312	G1221	A1143	A1067
U2229	U2229	C2096	C2096	A1918	C2096	A1918	G1918	G1828	U1758	G1673	A1571	U1482	U1392	G1313	U1222	G1149	A1068
C2230	C2230	A2098	A2098	A1919	A2098	A1919	G1919	A1829	G1759	G1674	A1572	U1483	U1393	G1314	G1223	G1150	A1069
U2231	U2231	C2097	C2097	C1920	C2097	C1920	G1920	U1830	A1762	G1681	U1573	U1484	U1394	G1315	G1224	A1151	A1070
C2232	C2232	U2098	U2098	G1921	U2098	G1921	G1921	U1831	G1763	G1682	U1574	U1485	U1395	G1316	G1225	G1151	G1071
G2233	G2233	A2100	A2100	A1922	A2100	A1922	G1922	U1832	C1764	U1683	U1575	U1486	U1396	G1317	U1226	C1152	A1072
U2234	U2234	C2100	C2100	A1923	C2100	A1923	G1923	G1833	U1765	U1684	U1576	U1487	U1397	G1318	G1227	G1152	A1073
C2235	C2235	A2101	A2101	A1924	A2101	A1924	G1924	U1834	U1766	G1685	U1577	U1488	U1398	G1319	U1228	G1153	G1074
U2236	U2236	G2102	G2102	A1925	G2102	A1925	G1925	U1835	G1767	C1686	U1578	U1489	U1399	G1320	G1229	A1155	C1075
C2237	C2237	C2103	C2103	A1926	C2103	A1926	G1926	U1836	U1768	U1686	U1579	U1490	U1400	G1321	U1230	A1156	A1077
G2238	G2238	A2104	A2104	A1927	A2104	A1927	G1927	U1837	C1769	U1687	U1580	U1491	U1401	G1322	G1231	G1160	U1078
U2239	U2239	U2105	U2105	A1928	U2105	A1928	G1928	U1838	U1770	A1690	U1581	U1492	U1402	G1323	U1232	G1161	A1080
C2240	C2240	C2106	C2106	A1929	C2106	A1929	G1929	U1839	G1771	C1691	U1582	U1493	U1403	G1324	G1233	G1162	U1083
U2241	U2241	A2107	A2107	A1930	A2107	A1930	G1930	U1840	U1772	U1692	U1583	U1494	U1404	G1325	U1234	C1163	A1084
C2242	C2242	G2110	G2110	A1931	G2110	A1931	G1931	U1841	C1773	U1693	U1584	U1495	U1405	G1326	U1235	G1164	A1085
U2243	U2243	U2111	U2111	A1932	U2111	A1932	G1932	U1842	U1774	U1694	U1585	U1496	U1406	G1327	U1236	G1165	A1086
C2244	C2244	A2112	A2112	A1933	A2112	A1933	G1933	U1843	U1775	C1695	U1586	U1497	U1407	G1328	U1237	G1166	A1087
G2245	G2245	C2113	C2113	A1934	C2113	A1934	G1934	U1844	U1776	U1696	U1587	U1498	U1408	G1329	U1238	G1167	A1088
U2246	U2246	U2114	U2114	A1935	U2114	A1935	G1935	U1845	U1777	U1697	U1588	U1499	U1409	G1330	U1239	G1168	A1089
C2247	C2247	A2115	A2115	A1936	A2115	A1936	G1936	U1846	U1778	U1698	U1589	U1500	U1410	G1331	U1240	G1169	A1090
U2248	U2248	C2116	C2116	A1937	C2116	A1937	G1937	U1847	G1779	U1699	U1590	U1501	U1411	G1332	U1241	G1170	A1091
C2249	C2249	U2117	U2117	A1938	U2117	A1938	G1938	U1848	U1780	U1700	U1591	U1502	U1412	G1333	U1242	G1171	C1092
U2250	U2250	A2118	A2118	A1939	A2118	A1939	G1939	U1849	U1781	U1701	U1592	U1503	U1413	G1334	U1243	G1172	U1093
G2251	G2251	C2119	C2119	A1940	C2119	A1940	G1940	U1850	U1782	U1702	U1593	U1504	U1414	G1335	U1244	C1163	
U2252	U2252	U2119	U2119	A1941	U2119	A1941	G1941	U1851	U1783	U1703	U1594	U1505	U1415	G1336	U1245	C1164	
C2253	C2253	A2120	A2120	A1942	A2120	A1942	G1942	U1852	U1784	U1704	U1595	U1506	U1416	G1337	U1246	C1165	
U2254	U2254	C2120	C2120	A1943	C2120	A1943	G1943	U1853	U1785	U1705	U1596	U1507	U1417	G1338	U1247	G1166	
C2255	C2255	U2121	U2121	A1944	U2121	A1944	G1944	U1854	U1786	U1706	U1597	U1508	U1418	G1339	U1248	G1167	
U2256	U2256	A2121	A2121	A1945	A2121	A1945	G1945	U1855	U1787	U1707	U1598	U1509	U1419	G1340	U1249	G1168	
C2257	C2257	C2122	C2122	A1946	C2122	A1946	G1946	U1856	U1788	U1708	U1599	U1510	U1420	G1341	U1250	G1169	
U2258	U2258	U2122	U2122	A1947	U2122	A1947	G1947	U1857	U1789	U1709	U1600	U1511	U1421	G1342	U1251	C1170	
C2259	C2259	A2122	A2122	A1948	A2122	A1948	G1948	U1858	U1790	U1710	U1601	U1512	U1422	G1343	U1252	G1171	
U2260	U2260	C2123	C2123	A1949	C2123	A1949	G1949	U1859	U1791	U1711	U1602	U1513	U1423	G1344	U1253	G1172	
C2261	C2261	U2123	U2123	A1950	U2123	A1950	G1950	U1860	U1792	U1712	U1603	U1514	U1424	G1345	U1254	A1268	
U2262	U2262	A2123	A2123	A1951	A2123	A1951	G1951	U1861	U1793	U1713	U1604	U1515	U1425	G1346	U1255	U1173	
C2263	C2263	C2124	C2124	A1952	C2124	A1952	G1952	U1862	U1794	U1714	U1605	U1516	U1426	G1347	U1256		
U2264	U2264	U2124	U2124	A1953	U2124	A1953	G1953	U1863	U1795	U1715	U1606	U1517	U1427	G1348	U1257		
C2265	C2265	A2124	A2124	A1954	A2124	A1954	G1954	U1864	U1796	U1716	U1607	U1518	U1428	G1349	U1258		
U2266	U2266	C2125	C2125	A1955	C2125	A1955	G1955	U1865	U1797	U1717	U1608	U1519	U1429	G1350	U1259		
C2267	C2267	U2125	U2125	A1956	U2125	A1956	G1956	U1866	U1798	U1718	U1609	U1520	U1430	G1351	U1260		
U2268	U2268	A2125	A2125	A1957	A2125	A1957	G1957	U									



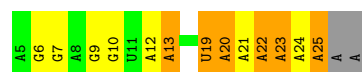
• Molecule 52: 5S ribosomal RNA



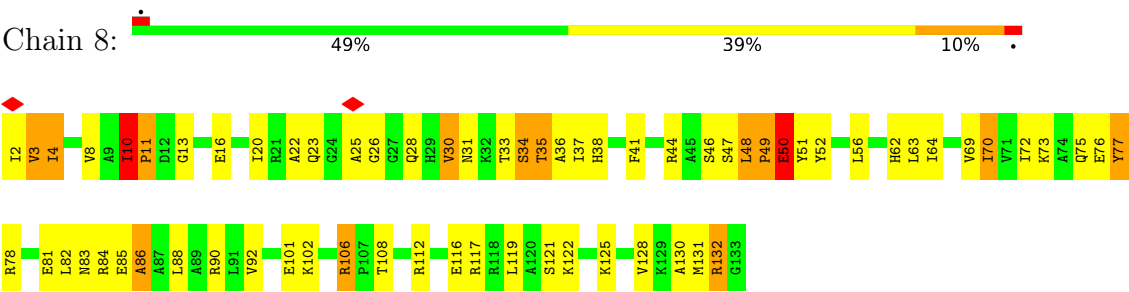
• Molecule 53: tRNA^{fMet}



• Molecule 54: mRNA



● Molecule 55: Peptidyl-tRNA hydrolase ArfB



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8184	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.966	Depositor
Minimum map value	-5.215	Depositor
Average map value	0.097	Depositor
Map value standard deviation	0.602	Depositor
Recommended contour level	0.43	Depositor
Map size ($\text{\AA}$)	375.12003, 375.12003, 375.12003	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.042, 1.042, 1.042	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	b	0.35	0/2122	0.94	9/2852 (0.3%)
2	c	0.35	0/1586	0.89	3/2134 (0.1%)
3	d	0.32	0/1571	0.93	7/2113 (0.3%)
4	e	0.36	0/1435	1.03	11/1926 (0.6%)
5	f	0.35	0/1343	0.86	1/1816 (0.1%)
6	g	0.36	0/1122	1.04	7/1515 (0.5%)
7	h	0.40	0/1001	1.10	8/1350 (0.6%)
8	j	0.35	0/1152	0.97	7/1551 (0.5%)
9	k	0.37	0/948	1.02	3/1268 (0.2%)
10	l	0.35	0/1054	0.99	6/1403 (0.4%)
11	m	0.35	0/1093	0.97	10/1460 (0.7%)
12	n	0.35	0/974	0.90	4/1301 (0.3%)
13	o	0.31	0/902	0.88	3/1209 (0.2%)
14	p	0.34	0/929	0.83	1/1242 (0.1%)
15	q	0.33	0/960	0.94	4/1278 (0.3%)
16	r	0.34	0/829	0.93	4/1107 (0.4%)
17	s	0.35	0/864	0.95	2/1156 (0.2%)
18	t	0.32	0/745	0.88	2/994 (0.2%)
19	u	0.33	0/788	0.92	3/1051 (0.3%)
20	v	0.32	0/766	0.98	2/1025 (0.2%)
21	w	0.32	0/582	0.89	2/769 (0.3%)
22	x	0.32	0/635	0.84	1/848 (0.1%)
23	y	0.30	0/510	0.89	1/677 (0.1%)
24	z	0.34	0/453	0.89	1/605 (0.2%)
25	B	0.35	0/450	0.85	1/599 (0.2%)
26	C	0.34	0/417	0.79	0/554
27	D	0.39	0/380	0.96	2/498 (0.4%)
28	E	0.33	0/513	0.86	0/676
29	F	0.34	0/303	0.95	1/397 (0.3%)
30	G	0.34	0/1788	0.96	8/2408 (0.3%)
31	H	0.34	0/1652	0.96	9/2225 (0.4%)
32	I	0.35	0/1665	1.07	12/2227 (0.5%)
33	J	0.33	0/1170	0.96	4/1573 (0.3%)
34	K	0.36	0/836	1.05	5/1128 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	L	0.34	0/1196	0.95	1/1602 (0.1%)
36	M	0.33	0/989	0.94	2/1326 (0.2%)
37	N	0.36	0/1034	1.00	7/1375 (0.5%)
38	O	0.37	0/797	1.01	5/1077 (0.5%)
39	P	0.35	0/886	1.01	6/1195 (0.5%)
40	Q	0.33	0/969	0.98	4/1300 (0.3%)
41	R	0.36	0/893	0.88	2/1193 (0.2%)
42	S	0.33	0/817	1.00	5/1088 (0.5%)
43	T	0.31	0/722	1.03	6/964 (0.6%)
44	U	0.36	0/659	0.89	1/884 (0.1%)
45	V	0.37	0/658	0.89	2/881 (0.2%)
46	W	0.38	0/545	1.05	4/731 (0.5%)
47	X	0.38	0/653	0.95	3/877 (0.3%)
48	Y	0.31	0/671	1.01	4/888 (0.5%)
49	Z	0.36	0/551	1.08	5/728 (0.7%)
50	3	0.43	0/36963	0.49	4/57662 (0.0%)
51	1	0.44	0/69794	0.50	7/108883 (0.0%)
52	2	0.44	0/2872	0.49	0/4479
53	5	0.43	0/1832	0.48	0/2855
54	4	0.50	0/520	0.66	0/810
55	8	0.37	0/1043	1.22	17/1399 (1.2%)
All	All	0.41	0/158602	0.65	229/237132 (0.1%)

There are no bond length outliers.

All (229) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	8	106	ARG	N-CA-C	-9.76	98.90	110.13
31	H	204	GLY	N-CA-C	9.37	124.22	112.14
3	d	73	ILE	N-CA-C	-8.87	104.05	112.83
4	e	106	ALA	N-CA-C	8.37	120.03	111.07
55	8	47	SER	N-CA-C	8.37	122.85	112.47
42	S	39	ASP	N-CA-C	-8.20	103.06	113.23
15	q	85	ALA	N-CA-C	-8.17	103.33	113.38
8	j	71	ASP	N-CA-C	7.97	121.81	112.72
49	Z	12	ASP	N-CA-C	7.97	122.38	111.54
1	b	213	ARG	N-CA-C	-7.97	103.35	113.23
42	S	41	TRP	N-CA-C	-7.95	102.69	111.36
43	T	43	ALA	N-CA-C	-7.86	102.70	111.82
11	m	107	GLY	N-CA-C	-7.85	103.94	115.63
32	I	7	LYS	N-CA-C	7.82	122.08	112.54
36	M	67	GLY	N-CA-C	-7.63	103.14	113.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	G	23	ASN	CA-C-N	7.58	128.26	119.47
30	G	23	ASN	C-N-CA	7.58	128.26	119.47
38	O	28	THR	N-CA-C	-7.55	103.06	111.82
48	Y	6	ALA	N-CA-C	-7.53	103.17	112.88
4	e	149	ARG	N-CA-C	7.48	121.51	110.30
33	J	101	GLY	N-CA-C	-7.47	104.01	115.66
44	U	62	GLY	N-CA-C	-7.42	105.45	114.66
46	W	69	TYR	N-CA-C	-7.39	102.38	111.40
32	I	146	GLU	N-CA-C	7.27	118.85	111.07
38	O	77	VAL	N-CA-C	7.21	117.31	110.53
6	g	44	ILE	N-CA-C	-7.10	103.86	110.53
43	T	60	SER	N-CA-C	-7.09	103.30	112.23
7	h	118	ILE	N-CA-C	7.07	124.15	108.88
7	h	125	ARG	N-CA-C	7.05	120.22	110.35
1	b	70	LYS	N-CA-C	-7.03	101.06	110.55
6	g	27	ARG	N-CA-C	7.02	119.01	111.36
45	V	68	LYS	N-CA-C	-6.96	103.75	111.82
1	b	15	VAL	N-CA-C	6.95	118.87	108.23
49	Z	18	PHE	N-CA-C	-6.93	103.50	112.23
49	Z	13	VAL	N-CA-C	-6.92	98.49	108.53
46	W	66	LEU	N-CA-C	-6.87	103.90	112.90
47	X	32	THR	N-CA-C	6.83	117.29	108.34
4	e	139	GLU	N-CA-C	6.78	118.75	111.36
3	d	115	GLN	N-CA-C	-6.78	104.14	112.88
55	8	46	SER	N-CA-C	6.77	120.35	107.75
9	k	111	LYS	N-CA-C	-6.77	103.70	112.23
10	l	95	LEU	N-CA-C	-6.74	104.54	112.89
42	S	49	THR	N-CA-C	-6.71	104.03	111.82
36	M	46	GLU	N-CA-C	6.71	120.45	110.52
32	I	102	TYR	N-CA-C	-6.67	103.82	112.23
41	R	69	ARG	N-CA-C	-6.65	104.11	111.36
32	I	132	ALA	N-CA-C	6.61	120.45	112.38
51	1	2326	C	C2'-C3'-O3'	6.58	123.57	113.70
39	P	75	GLU	N-CA-C	-6.54	104.23	111.36
30	G	99	MET	N-CA-C	-6.49	103.71	111.69
43	T	52	ARG	N-CA-C	-6.46	104.32	111.82
39	P	55	ARG	N-CA-C	-6.46	105.41	113.28
1	b	40	GLY	N-CA-C	-6.44	105.17	115.08
19	u	6	ARG	N-CA-C	6.41	118.27	111.28
29	F	5	ALA	N-CA-C	-6.34	103.87	113.89
55	8	48	LEU	CA-C-N	6.34	127.77	119.84
55	8	48	LEU	C-N-CA	6.34	127.77	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	g	76	GLU	N-CA-C	6.33	120.15	111.54
6	g	88	GLY	N-CA-C	6.33	124.09	115.30
32	I	68	GLU	N-CA-C	6.32	118.17	111.28
37	N	93	LEU	N-CA-C	-6.32	104.49	111.82
16	r	26	ASP	N-CA-C	6.31	119.42	109.96
6	g	9	VAL	N-CA-C	6.28	122.40	109.34
32	I	63	ILE	N-CA-C	-6.28	107.01	113.10
10	l	60	ARG	N-CA-C	-6.24	106.20	113.88
30	G	177	ASN	N-CA-C	-6.23	104.59	111.82
37	N	91	GLU	N-CA-C	6.23	124.07	110.80
7	h	43	LYS	N-CA-C	-6.22	104.60	111.82
1	b	12	ARG	N-CA-C	-6.21	104.29	113.61
2	c	100	LEU	N-CA-C	-6.21	104.59	111.36
42	S	21	ALA	N-CA-C	-6.21	104.77	112.90
16	r	50	GLY	N-CA-C	-6.20	98.49	113.18
16	r	54	VAL	N-CA-C	6.18	122.20	109.34
7	h	6	GLN	N-CA-C	-6.17	104.45	112.23
24	z	13	ILE	N-CA-C	-6.17	106.74	111.62
12	n	68	ALA	N-CA-C	-6.17	104.56	111.28
27	D	5	PHE	N-CA-C	6.12	117.98	107.28
10	l	40	SER	N-CA-C	-6.10	104.34	112.94
11	m	125	PRO	N-CA-C	6.08	121.50	114.20
23	y	15	ASN	N-CA-C	-6.08	104.73	111.36
30	G	118	THR	N-CA-C	-6.05	105.72	113.23
7	h	57	ASN	N-CA-C	-6.05	101.25	109.54
11	m	66	ARG	N-CA-C	6.03	117.52	111.07
51	1	1178	C	N1-C1'-C2'	6.02	121.03	112.00
10	l	37	GLY	N-CA-C	-5.99	104.54	112.81
46	W	17	VAL	N-CA-C	5.95	121.72	109.34
55	8	10	ILE	CA-C-N	5.95	125.89	119.76
55	8	10	ILE	C-N-CA	5.95	125.89	119.76
4	e	150	GLY	N-CA-C	-5.93	104.62	112.81
40	Q	43	LYS	N-CA-C	5.92	122.90	109.81
7	h	2	ALA	N-CA-C	-5.92	107.29	114.75
10	l	96	LYS	N-CA-C	-5.91	104.78	112.23
1	b	11	GLY	N-CA-C	-5.91	106.88	114.85
7	h	7	ASP	N-CA-C	-5.89	104.81	112.23
51	1	1020	A	C2'-C3'-O3'	5.88	118.33	109.50
55	8	128	VAL	N-CA-C	5.88	112.50	106.21
55	8	92	VAL	N-CA-C	5.79	116.53	110.62
25	B	53	VAL	N-CA-C	5.77	121.35	109.34
48	Y	8	LYS	N-CA-C	-5.77	105.13	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	8	4	ILE	N-CA-C	5.75	121.31	109.34
12	n	50	PRO	N-CA-C	-5.75	106.03	113.57
32	I	33	ILE	N-CA-C	5.73	116.68	110.21
11	m	67	VAL	N-CA-C	5.72	117.84	108.97
39	P	97	ARG	N-CA-C	-5.72	105.13	111.36
31	H	67	ILE	N-CA-C	5.71	116.08	107.80
4	e	10	GLU	N-CA-C	5.71	117.99	111.02
30	G	135	MET	N-CA-C	-5.71	105.04	112.23
11	m	56	ALA	N-CA-C	5.70	117.58	111.36
40	Q	114	SER	N-CA-C	-5.70	104.98	111.14
22	x	6	VAL	N-CA-C	5.69	120.01	112.04
5	f	15	ASP	N-CA-C	5.68	118.24	110.24
15	q	40	LYS	N-CA-C	-5.67	105.08	112.23
4	e	84	ILE	N-CA-C	5.67	116.32	110.82
48	Y	15	LYS	N-CA-C	-5.64	105.65	112.54
7	h	108	VAL	N-CA-C	-5.64	105.34	113.07
33	J	141	ASP	N-CA-C	-5.63	105.23	111.36
49	Z	11	PHE	N-CA-C	5.63	117.58	108.41
37	N	54	VAL	N-CA-C	5.62	115.70	110.42
38	O	42	LEU	CA-C-N	5.61	126.85	119.84
38	O	42	LEU	C-N-CA	5.61	126.85	119.84
40	Q	73	LEU	N-CA-C	5.61	118.87	109.95
48	Y	28	ARG	N-CA-C	5.60	117.83	111.11
33	J	133	ILE	N-CA-C	5.59	115.79	110.53
51	1	2287	A	N9-C1'-C2'	5.59	120.39	112.00
32	I	155	LYS	N-CA-C	-5.58	104.59	111.40
32	I	44	LYS	N-CA-C	5.57	117.70	109.62
8	j	119	PHE	N-CA-C	-5.56	105.22	112.23
49	Z	28	LEU	N-CA-C	-5.55	104.87	111.69
19	u	75	ALA	N-CA-C	-5.54	104.75	112.45
37	N	96	GLU	N-CA-C	-5.54	106.02	112.89
15	q	102	LYS	N-CA-C	5.54	117.32	111.28
47	X	15	LEU	N-CA-C	5.53	117.31	111.28
55	8	3	VAL	N-CA-C	-5.53	97.83	109.34
11	m	21	ALA	N-CA-C	5.53	117.46	110.33
39	P	117	HIS	N-CA-C	-5.52	103.98	111.55
43	T	68	TYR	N-CA-C	-5.52	105.34	111.36
33	J	138	ALA	N-CA-C	5.52	117.38	111.36
11	m	124	LEU	CA-C-N	5.50	126.23	120.12
11	m	124	LEU	C-N-CA	5.50	126.23	120.12
21	w	69	GLY	CA-C-N	5.50	125.16	119.05
21	w	69	GLY	C-N-CA	5.50	125.16	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	H	129	PHE	N-CA-C	5.47	117.24	111.28
8	j	92	MET	N-CA-C	-5.46	105.36	112.23
11	m	59	ARG	N-CA-C	5.46	119.22	112.24
45	V	55	GLY	N-CA-C	5.44	126.07	113.18
32	I	97	LEU	N-CA-C	5.43	116.88	111.07
51	l	1930	G	N9-C1'-C2'	5.43	120.15	112.00
46	W	62	ARG	N-CA-C	-5.43	106.16	112.89
12	n	116	VAL	N-CA-C	5.42	119.65	112.76
6	g	98	ASP	N-CA-C	5.42	117.19	111.28
4	e	51	ASN	N-CA-C	-5.42	106.17	112.89
17	s	69	LEU	N-CA-C	5.41	118.29	110.28
34	K	73	GLU	N-CA-C	-5.41	106.19	112.89
31	H	71	ARG	CA-C-N	5.38	125.03	119.05
31	H	71	ARG	C-N-CA	5.38	125.03	119.05
20	v	40	ILE	N-CA-C	5.38	116.32	108.53
30	G	111	LYS	N-CA-C	-5.37	105.51	111.36
34	K	69	GLU	N-CA-C	5.36	120.21	111.37
18	t	10	VAL	N-CA-C	5.36	120.48	109.34
42	S	50	LEU	N-CA-C	-5.36	103.29	109.93
14	p	75	THR	N-CA-C	5.34	122.17	110.80
2	c	156	PHE	N-CA-C	5.33	117.60	110.35
55	8	30	VAL	N-CA-C	5.33	117.75	111.09
39	P	116	PRO	N-CA-C	-5.30	102.91	111.77
50	3	1190	G	C2'-C3'-O3'	5.29	117.44	109.50
1	b	16	VAL	N-CA-C	-5.29	99.33	106.85
55	8	82	LEU	N-CA-C	-5.29	105.57	112.23
32	I	32	LYS	N-CA-C	-5.28	103.95	111.24
9	k	119	ALA	N-CA-C	-5.28	103.39	109.93
55	8	86	ALA	N-CA-C	-5.27	105.70	111.82
47	X	71	GLY	N-CA-C	-5.26	108.13	114.66
37	N	103	VAL	N-CA-C	-5.26	105.66	113.39
41	R	36	ALA	N-CA-C	-5.26	106.37	112.89
3	d	176	ASP	CA-C-N	5.25	125.06	119.28
3	d	176	ASP	C-N-CA	5.25	125.06	119.28
4	e	52	ALA	N-CA-C	-5.25	106.38	112.89
32	I	114	ARG	N-CA-C	-5.24	105.48	111.14
51	l	2173	A	N9-C1'-C2'	5.24	119.85	112.00
4	e	53	ALA	N-CA-C	-5.22	106.42	112.89
13	o	86	GLY	N-CA-C	5.22	121.29	115.08
17	s	6	LYS	N-CA-C	5.22	116.83	110.41
31	H	85	LYS	N-CA-C	-5.22	105.66	112.23
43	T	26	VAL	N-CA-C	5.21	115.42	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	496	A	N9-C1'-C2'	5.21	119.81	112.00
34	K	78	PHE	N-CA-C	-5.21	106.26	113.18
30	G	62	ARG	N-CA-C	-5.20	106.52	112.92
15	q	32	ARG	N-CA-C	5.20	117.62	111.33
3	d	31	VAL	N-CA-C	5.18	115.96	110.72
27	D	45	SER	N-CA-C	-5.18	106.09	112.72
55	8	38	HIS	N-CA-C	5.18	117.17	108.73
40	Q	99	GLY	N-CA-C	-5.18	105.09	114.46
8	j	44	TYR	N-CA-C	5.17	117.72	109.96
4	e	15	LEU	N-CA-C	5.17	119.21	113.01
1	b	191	LEU	N-CA-C	5.16	116.99	110.33
16	r	53	PHE	N-CA-C	-5.16	104.18	111.56
34	K	83	ALA	N-CA-C	-5.16	106.14	112.90
20	v	45	ASP	N-CA-C	5.16	117.57	111.33
50	3	1300	G	N9-C1'-C2'	5.16	119.73	112.00
3	d	58	LYS	CA-C-N	5.15	126.28	119.84
3	d	58	LYS	C-N-CA	5.15	126.28	119.84
31	H	5	HIS	CA-C-N	5.15	126.28	119.84
31	H	5	HIS	C-N-CA	5.15	126.28	119.84
19	u	28	LEU	N-CA-C	5.13	116.55	110.19
8	j	96	ARG	CA-C-N	5.11	124.90	119.28
8	j	96	ARG	C-N-CA	5.11	124.90	119.28
55	8	13	GLY	N-CA-C	-5.10	107.94	114.37
38	O	100	ILE	N-CA-C	5.09	115.64	108.36
8	j	139	VAL	N-CA-C	5.09	113.93	106.55
39	P	67	GLU	N-CA-C	-5.09	105.81	111.36
12	n	67	PHE	N-CA-C	-5.09	107.62	113.88
37	N	42	THR	N-CA-C	5.08	117.46	110.35
2	c	150	GLN	N-CA-C	5.08	117.20	111.11
55	8	11	PRO	N-CA-C	5.07	119.04	111.14
34	K	39	LEU	N-CA-C	-5.06	105.14	113.50
10	l	115	GLU	N-CA-C	5.06	118.31	111.17
50	3	1347	G	N9-C1'-C2'	5.06	119.59	112.00
37	N	119	LYS	N-CA-C	5.05	115.65	107.32
18	t	83	ALA	N-CA-C	5.04	116.63	108.26
13	o	41	ALA	CA-C-N	5.04	124.76	119.82
13	o	41	ALA	C-N-CA	5.04	124.76	119.82
4	e	151	LEU	N-CA-C	5.04	114.80	108.45
1	b	194	VAL	N-CA-C	5.03	116.50	109.80
43	T	74	VAL	N-CA-C	5.03	115.80	110.72
35	L	42	VAL	N-CA-C	5.02	117.33	111.05
31	H	3	LYS	N-CA-C	5.02	116.58	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	g	97	ARG	N-CA-C	5.01	116.60	111.03
9	k	38	ILE	N-CA-C	5.01	116.05	109.58
51	l	1818	U	N1-C1'-C2'	5.01	119.51	112.00
11	m	74	THR	N-CA-C	5.00	117.76	109.85

There are no chirality outliers.

There are no planarity outliers.

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	b	2083	0	2157	72	0
2	c	1565	0	1616	42	0
3	d	1552	0	1619	42	0
4	e	1411	0	1447	45	0
5	f	1323	0	1374	22	0
6	g	1111	0	1148	23	0
7	h	988	0	1025	37	0
8	j	1129	0	1162	39	0
9	k	939	0	1012	37	0
10	l	1045	0	1117	36	0
11	m	1074	0	1157	43	0
12	n	961	0	1000	27	0
13	o	892	0	923	26	0
14	p	917	0	965	24	0
15	q	947	0	1022	36	0
16	r	816	0	839	25	0
17	s	857	0	922	23	0
18	t	739	0	807	20	0
19	u	780	0	834	8	0
20	v	753	0	780	12	0
21	w	575	0	592	14	0
22	x	625	0	655	20	0
23	y	509	0	543	14	0
24	z	449	0	491	6	0
25	B	444	0	461	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	C	410	0	440	4	0
27	D	377	0	418	9	0
28	E	504	0	574	16	0
29	F	302	0	343	11	0
30	G	1757	0	1787	42	0
31	H	1625	0	1699	41	0
32	I	1643	0	1710	64	0
33	J	1157	0	1199	35	0
34	K	818	0	808	35	0
35	L	1182	0	1240	22	0
36	M	979	0	1034	37	0
37	N	1022	0	1070	36	0
38	O	787	0	828	21	0
39	P	870	0	878	24	0
40	Q	955	0	1019	29	0
41	R	884	0	944	23	0
42	S	805	0	847	37	0
43	T	714	0	737	13	0
44	U	649	0	666	23	0
45	V	649	0	691	27	0
46	W	536	0	552	15	0
47	X	638	0	665	31	0
48	Y	665	0	714	13	0
49	Z	545	0	579	30	0
50	3	33012	0	16619	652	0
51	1	62315	0	31346	1173	0
52	2	2568	0	1303	58	0
53	5	1640	0	837	31	0
54	4	461	0	229	11	0
55	8	1031	0	1087	57	0
All	All	145984	0	98531	2942	0

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

All (2942) 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)
33:J:110:MET:HE1	50:3:9:G:H5'	1.34	1.10
21:w:39:THR:H	51:1:2331:G:H4'	1.19	1.06
20:v:9:ARG:HG2	20:v:41:GLU:HG3	1.37	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:45:G:H5''	51:1:46:G:H5'	1.30	1.05
2:c:173:GLN:HE21	51:1:2731:G:H4'	1.20	1.03
51:1:1304:A:H2'	51:1:1305:C:H5''	1.37	1.03
51:1:1906:G:H2'	51:1:1907:G:H5''	1.42	1.01
51:1:898:C:H2'	51:1:899:A:H5'	1.43	1.00
16:r:6:GLN:HG3	16:r:11:GLN:HE22	1.26	0.99
51:1:1300:G:H4'	51:1:1301:A:H5''	1.40	0.98
11:m:64:TRP:HE1	51:1:873:C:H4'	1.24	0.98
51:1:1869:G:H3'	51:1:1870:C:C5'	1.95	0.97
50:3:813:U:H2'	50:3:814:A:H5''	1.45	0.95
35:L:6:ILE:H	35:L:6:ILE:HD12	1.29	0.94
43:T:88:ARG:H	43:T:88:ARG:HD3	1.33	0.94
51:1:1062:G:H1	51:1:1076:C:H42	1.17	0.93
2:c:142:VAL:HG22	2:c:143:PRO:HD2	1.49	0.92
51:1:1869:G:H3'	51:1:1870:C:H5''	1.53	0.91
22:x:60:LYS:HZ2	51:1:372:G:H5''	1.35	0.91
51:1:2573:C:H5''	51:1:2574:G:H5''	1.52	0.89
3:d:84:THR:HG21	51:1:586:A:H5'	1.54	0.89
2:c:148:GLN:O	51:1:2052:A:H4'	1.71	0.88
51:1:2114:A:H61	51:1:2117:A:H62	1.21	0.88
2:c:1:MET:HB2	2:c:205:PRO:HG2	1.55	0.87
51:1:1173:U:H2'	51:1:1174:U:H4'	1.57	0.87
11:m:12:MET:HA	51:1:910:A:H62	1.35	0.87
52:2:3:C:H2'	52:2:4:C:H5''	1.57	0.87
13:o:12:THR:HG23	51:1:2334:U:H4'	1.54	0.86
34:K:53:LYS:HD3	34:K:54:LEU:H	1.41	0.86
50:3:327:A:O2'	50:3:328:C:H4'	1.75	0.86
35:L:71:THR:HG23	35:L:72:VAL:HG23	1.57	0.86
50:3:842:U:H3'	50:3:843:U:H5''	1.57	0.86
4:e:10:GLU:HA	4:e:13:LYS:HE2	1.58	0.85
32:I:131:ILE:HG23	50:3:403:C:H5'	1.55	0.85
51:1:1069:A:H4'	51:1:1096:A:H4'	1.59	0.85
51:1:1020:A:H1'	51:1:1021:A:OP2	1.75	0.85
4:e:135:ILE:HD12	4:e:140:ILE:HG23	1.58	0.84
50:3:1474:U:H2'	50:3:1475:G:H5''	1.57	0.84
2:c:151:THR:HB	2:c:152:PRO:HD3	1.57	0.84
51:1:1179:G:H2'	51:1:1180:U:H4'	1.58	0.84
51:1:1304:A:C2'	51:1:1305:C:H5''	2.08	0.84
51:1:2800:A:H3'	51:1:2801:G:H5'	1.57	0.84
55:8:121:SER:O	55:8:125:LYS:HG2	1.78	0.84
51:1:2413:G:H2'	51:1:2414:G:H5''	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:484:G:H4'	50:3:485:U:H5''	1.61	0.83
51:1:784:G:H5'	51:1:785:G:OP1	1.79	0.83
1:b:15:VAL:HG22	1:b:205:GLY:HA3	1.60	0.82
51:1:1177:G:H2'	51:1:1178:C:H4'	1.58	0.82
19:u:42:LYS:HD2	19:u:57:ILE:HD12	1.60	0.81
51:1:1807:G:H2'	51:1:1808:A:H5'	1.62	0.81
7:h:34:THR:HG23	51:1:1055:G:O2'	1.80	0.81
45:V:61:ARG:HD2	45:V:75:VAL:HG22	1.63	0.80
3:d:52:VAL:HG23	3:d:74:LYS:HD2	1.61	0.80
51:1:1906:G:C2'	51:1:1907:G:H5''	2.10	0.80
51:1:2129:C:H2'	51:1:2130:U:H5'	1.62	0.80
51:1:2104:C:H42	51:1:2185:U:H3	1.29	0.80
51:1:1100:C:H2'	51:1:1101:U:H4'	1.63	0.80
6:g:43:ASN:HA	6:g:46:PHE:HB2	1.63	0.79
51:1:1300:G:C4'	51:1:1301:A:H5''	2.12	0.79
51:1:2134:A:H1'	51:1:2158:A:H4'	1.65	0.79
51:1:2493:U:H3'	51:1:2494:G:H5''	1.64	0.79
4:e:102:LEU:HA	4:e:106:ALA:HB3	1.64	0.79
6:g:96:THR:HG23	6:g:97:ARG:H	1.47	0.78
38:O:51:VAL:HG23	42:S:80:ARG:HB2	1.65	0.78
22:x:63:ILE:H	22:x:63:ILE:HD12	1.48	0.78
45:V:16:MET:SD	50:3:276:G:H5'	2.24	0.78
51:1:2286:G:H5''	51:1:2287:A:OP1	1.84	0.78
29:F:12:ARG:HH11	51:1:1091:G:H4'	1.47	0.78
50:3:1052:U:H2'	50:3:1200:C:H41	1.47	0.77
51:1:704:G:H2'	51:1:726:G:H22	1.49	0.76
9:k:47:ILE:HG12	9:k:48:PRO:HD2	1.67	0.76
22:x:60:LYS:NZ	51:1:372:G:H5''	2.00	0.76
33:J:110:MET:HE1	50:3:9:G:C5'	2.13	0.76
51:1:1060:U:H4'	51:1:1061:U:H5'	1.68	0.76
40:Q:49:ARG:HH22	50:3:522:C:H41	1.35	0.75
26:C:32:LYS:HB3	26:C:50:GLU:HG2	1.69	0.75
51:1:1936:A:H2	51:1:1943:U:H3	1.35	0.75
49:Z:33:ARG:O	49:Z:34:ARG:HB2	1.87	0.75
50:3:181:A:H62	50:3:194:C:H2'	1.52	0.74
50:3:1237:C:H4'	50:3:1334:G:H21	1.52	0.74
51:1:322:A:H5'	51:1:340:A:H1'	1.68	0.74
38:O:27:GLU:O	38:O:30:LYS:HG2	1.87	0.74
31:H:57:GLU:HG3	31:H:59:PRO:HD3	1.68	0.74
34:K:86:ARG:HH12	50:3:673:A:H4'	1.51	0.74
2:c:173:GLN:NE2	51:1:2731:G:H4'	2.00	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:F:11:CYS:HG	29:F:14:CYS:HG	1.36	0.74
50:3:1413:A:H2	50:3:1487:G:H22	1.36	0.74
34:K:14:GLN:HA	34:K:17:GLN:HE21	1.53	0.73
50:3:82:G:H3'	50:3:83:C:H5'	1.70	0.73
32:I:44:LYS:HD2	32:I:45:PRO:HD2	1.69	0.73
50:3:1030:U:H2'	50:3:1031:C:H5'	1.70	0.73
31:H:156:LEU:HD13	31:H:195:ILE:HD13	1.69	0.73
16:r:27:ILE:HG13	16:r:28:ALA:H	1.53	0.73
51:1:898:C:C2'	51:1:899:A:H5'	2.17	0.73
32:I:68:GLU:HG3	50:3:545:C:H5''	1.71	0.73
50:3:813:U:C2'	50:3:814:A:H5''	2.17	0.73
51:1:467:G:O2'	51:1:468:G:H5'	1.89	0.73
51:1:948:C:H2'	51:1:949:G:H8	1.52	0.73
51:1:2296:U:H5''	51:1:2297:A:OP1	1.88	0.73
51:1:2682:A:H61	51:1:2728:U:H1'	1.53	0.73
4:e:105:ILE:HG21	4:e:138:PRO:HG3	1.71	0.73
9:k:121:GLU:HG3	9:k:122:VAL:HG23	1.70	0.73
51:1:1086:A:H1'	51:1:1103:A:H61	1.55	0.72
50:3:145:G:H2'	50:3:146:G:C4'	2.19	0.72
51:1:1060:U:H1'	51:1:1062:G:H5'	1.70	0.72
36:M:28:SER:HB3	36:M:58:LEU:HB2	1.72	0.72
50:3:225:C:H2'	50:3:226:G:H5''	1.72	0.72
40:Q:49:ARG:NH2	50:3:522:C:H41	1.86	0.72
45:V:25:GLU:HG2	45:V:40:THR:HG22	1.70	0.72
39:P:30:ILE:HG23	39:P:45:THR:HG22	1.72	0.72
16:r:5:PHE:HB3	16:r:59:ILE:HD12	1.71	0.72
51:1:2345:G:N3	51:1:2381:A:H2'	2.05	0.72
13:o:39:VAL:HG13	13:o:48:LEU:HB2	1.72	0.71
17:s:69:LEU:HD23	17:s:109:ASP:HB3	1.71	0.71
11:m:64:TRP:NE1	51:1:873:C:H4'	2.03	0.71
51:1:11:C:H2'	51:1:12:U:H5''	1.70	0.71
51:1:1213:A:N6	51:1:1236:G:H1'	2.04	0.71
50:3:483:C:H2'	50:3:484:G:C8	2.25	0.71
51:1:1100:C:H3'	51:1:1101:U:H5''	1.72	0.71
51:1:1268:A:H2'	51:1:1269:A:O4'	1.90	0.71
51:1:2287:A:O2'	51:1:2288:A:H2'	1.91	0.71
2:c:20:VAL:HG13	9:k:72:PRO:HB2	1.72	0.71
30:G:23:ASN:HD22	30:G:191:ASP:HB2	1.56	0.71
29:F:36:ARG:HG2	29:F:37:GLN:H	1.56	0.71
10:l:23:ILE:HG13	16:r:82:HIS:CE1	2.26	0.71
34:K:92:THR:O	34:K:93:LYS:HB2	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:w:70:PRO:HG3	52:2:12:C:H42	1.54	0.70
51:1:548:G:H2'	51:1:549:G:H4'	1.73	0.70
9:k:104:THR:HG22	9:k:106:GLU:H	1.56	0.70
51:1:886:A:H4'	51:1:890:C:H41	1.54	0.70
51:1:1728:C:H2'	51:1:1729:U:H5''	1.73	0.70
30:G:5:MET:HA	30:G:8:MET:HE2	1.72	0.70
51:1:511:U:H2'	51:1:512:G:H5'	1.71	0.70
4:e:87:LYS:HD3	51:1:2313:C:H5''	1.72	0.70
32:I:56:GLU:HA	32:I:59:LYS:HE3	1.71	0.70
35:L:28:ILE:HG22	35:L:104:VAL:HG21	1.72	0.70
51:1:1956:U:H2'	51:1:1957:C:H5'	1.72	0.70
32:I:56:GLU:O	32:I:59:LYS:HG2	1.92	0.70
51:1:2413:G:C2'	51:1:2414:G:H5''	2.22	0.70
39:P:118:ASN:HB2	50:3:718:A:H5'	1.72	0.69
51:1:1701:A:H2'	51:1:1702:G:H5'	1.74	0.69
14:p:3:ILE:H	14:p:3:ILE:HD12	1.56	0.69
42:S:68:ARG:HD3	50:3:1202:U:H4'	1.73	0.69
3:d:181:ILE:HD12	10:l:3:LEU:HD13	1.74	0.69
4:e:71:LYS:HE3	51:1:2299:U:OP1	1.93	0.69
7:h:1:MET:HE2	7:h:7:ASP:HA	1.75	0.69
51:1:2286:G:H4'	51:1:2287:A:O4'	1.91	0.69
7:h:33:VAL:HA	51:1:1055:G:H4'	1.74	0.69
32:I:18:LEU:HD23	32:I:18:LEU:H	1.56	0.69
8:j:30:THR:HG21	51:1:1005:C:O2'	1.93	0.69
50:3:513:C:H2'	50:3:514:C:C6	2.27	0.69
42:S:52:ARG:HH11	50:3:1317:C:H42	1.40	0.69
51:1:672:C:O2'	51:1:673:C:H5'	1.91	0.69
10:l:33:ARG:HD2	51:1:587:C:H42	1.57	0.69
29:F:12:ARG:NH1	51:1:1091:G:H4'	2.08	0.69
37:N:11:ARG:HG2	37:N:12:LYS:HG2	1.75	0.69
13:o:3:LYS:HG2	13:o:7:ARG:HH21	1.57	0.69
40:Q:43:LYS:HB3	40:Q:44:PRO:HD3	1.75	0.69
41:R:43:LYS:HB2	41:R:46:GLU:HG2	1.75	0.69
30:G:114:LYS:HA	30:G:117:GLU:HG2	1.76	0.68
51:1:2514:U:H2'	51:1:2515:C:C6	2.27	0.68
3:d:77:ILE:HG23	3:d:78:TRP:HD1	1.58	0.68
53:5:62:C:H2'	53:5:63:G:C8	2.28	0.68
50:3:1256:A:H4'	50:3:1258:G:N9	2.09	0.68
51:1:1802:A:H2'	51:1:1803:A:C8	2.29	0.68
13:o:51:ALA:HB3	13:o:78:VAL:HG12	1.76	0.68
6:g:21:VAL:HG22	6:g:22:LYS:H	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:736:C:H2'	50:3:737:C:C6	2.28	0.68
51:1:2345:G:H5'	51:1:2347:C:H5'	1.73	0.68
51:1:2573:C:N4	55:8:33:THR:HA	2.08	0.68
32:I:53:GLN:HG2	32:I:198:LEU:HD22	1.75	0.68
34:K:86:ARG:NH1	50:3:673:A:H4'	2.08	0.68
3:d:119:ILE:HG12	3:d:185:LYS:HD2	1.76	0.68
51:1:139:U:H5'	51:1:140:C:O4'	1.93	0.68
28:E:32:LEU:HA	28:E:35:LYS:HD2	1.76	0.68
32:I:120:LYS:HG2	32:I:130:ASN:HB2	1.76	0.68
40:Q:39:THR:HG22	40:Q:40:THR:H	1.59	0.68
3:d:163:ASN:HB2	51:1:322:A:OP2	1.94	0.67
50:3:405:U:H3'	50:3:406:G:H5'	1.75	0.67
1:b:23:LEU:HD13	1:b:82:TYR:HB2	1.76	0.67
51:1:917:A:H5''	51:1:2268:A:H61	1.59	0.67
43:T:2:LEU:HB2	43:T:34:GLN:HE22	1.59	0.67
33:J:20:VAL:HG23	33:J:31:SER:HB2	1.75	0.67
51:1:473:G:O2'	51:1:474:G:H5'	1.95	0.67
51:1:528:A:N1	51:1:2042:A:H2'	2.10	0.67
51:1:1179:G:C2'	51:1:1180:U:H4'	2.25	0.67
41:R:109:LYS:HD2	50:3:1227:A:OP2	1.94	0.67
50:3:49:U:H3	50:3:362:G:H1'	1.59	0.67
50:3:1379:G:O2'	50:3:1380:U:H5'	1.94	0.67
51:1:1625:C:H2'	51:1:1626:A:O4'	1.95	0.67
51:1:1725:U:H3	51:1:1735:A:H61	1.41	0.67
36:M:107:LYS:HZ2	36:M:120:LEU:HD13	1.60	0.67
4:e:142:TYR:HA	4:e:145:VAL:HG23	1.76	0.67
7:h:32:GLY:O	51:1:1055:G:H5'	1.95	0.67
27:D:14:ARG:HD2	51:1:771:G:OP1	1.93	0.67
46:W:13:THR:HG23	46:W:17:VAL:HA	1.76	0.67
50:3:1218:C:H2'	50:3:1219:A:C8	2.30	0.67
50:3:1474:U:C2'	50:3:1475:G:H5''	2.25	0.67
51:1:2248:C:H2'	51:1:2249:U:H5'	1.77	0.67
39:P:43:TRP:HE1	50:3:686:U:H4'	1.60	0.66
50:3:145:G:H2'	50:3:146:G:H4'	1.77	0.66
3:d:148:ILE:HB	3:d:169:VAL:HG22	1.77	0.66
10:l:48:ARG:HD2	28:E:59:ALA:O	1.95	0.66
51:1:2123:G:H5''	51:1:2170:A:H5'	1.77	0.66
1:b:155:ARG:NH2	51:1:1818:U:H5	1.94	0.66
11:m:42:THR:OG1	11:m:45:GLN:HG3	1.95	0.66
50:3:842:U:H3'	50:3:843:U:C5'	2.24	0.66
54:4:19:U:H4'	54:4:20:A:N7	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:N:17:ARG:HH22	50:3:1129:C:C5'	2.09	0.66
51:1:639:U:H2'	51:1:640:C:C6	2.31	0.66
14:p:26:GLU:HG2	14:p:86:LYS:HE2	1.77	0.66
1:b:46:GLY:HA3	51:1:773:U:H5'	1.77	0.66
9:k:65:THR:HG22	9:k:67:LYS:H	1.61	0.66
22:x:17:ARG:HD3	22:x:23:ALA:HB2	1.78	0.66
50:3:1346:A:O2'	50:3:1347:G:H4'	1.95	0.66
50:3:1170:A:H2'	50:3:1171:A:O4'	1.96	0.66
51:1:20:C:H2'	51:1:21:A:H8	1.60	0.66
51:1:741:U:H2'	51:1:742:A:H8	1.61	0.66
51:1:1981:A:H5''	51:1:1982:U:OP2	1.95	0.66
42:S:42:ASN:O	42:S:46:LYS:HG3	1.96	0.65
51:1:2419:U:H2'	51:1:2420:C:C6	2.31	0.65
51:1:215:G:H4'	51:1:216:A:H4'	1.79	0.65
51:1:2585:U:H4'	51:1:2586:U:H5'	1.77	0.65
15:q:50:ARG:HD3	51:1:1156:A:C8	2.30	0.65
50:3:1516:G:H2'	50:3:1518:A:OP2	1.95	0.65
51:1:833:A:H2'	51:1:834:G:C8	2.32	0.65
5:f:29:ASN:HB2	5:f:78:VAL:HA	1.78	0.65
36:M:124:ILE:H	36:M:124:ILE:HD12	1.61	0.65
50:3:392:C:H2'	50:3:393:A:C8	2.32	0.65
51:1:543:G:H8	51:1:543:G:H5'	1.61	0.65
51:1:1971:U:H5'	51:1:1972:G:H5''	1.78	0.65
51:1:2265:U:H3'	51:1:2266:A:H5''	1.78	0.65
52:2:35:C:H2'	52:2:36:C:H5'	1.77	0.65
2:c:61:THR:OG1	2:c:63:PRO:HD2	1.97	0.65
5:f:173:ALA:HB3	5:f:176:LYS:O	1.96	0.65
50:3:392:C:H2'	50:3:393:A:H8	1.60	0.65
50:3:413:G:H5'	50:3:414:A:H5'	1.79	0.65
50:3:784:A:H2'	50:3:785:G:H8	1.61	0.65
12:n:8:ARG:HB2	12:n:43:GLU:OE2	1.97	0.65
40:Q:98:ARG:HB2	40:Q:116:TYR:HA	1.78	0.65
47:X:66:VAL:HG13	47:X:67:GLY:H	1.62	0.65
9:k:71:ARG:HD3	9:k:72:PRO:HD2	1.78	0.65
45:V:5:ARG:NH2	50:3:128:G:H5'	2.12	0.65
45:V:12:VAL:HB	45:V:21:VAL:HG13	1.77	0.65
50:3:1497:G:O2'	50:3:1498:U:H5'	1.97	0.65
51:1:1437:C:H2'	51:1:1438:U:C6	2.32	0.65
42:S:52:ARG:HG2	42:S:58:ARG:HH12	1.62	0.65
51:1:948:C:H2'	51:1:949:G:C8	2.32	0.65
28:E:61:LEU:HD12	28:E:61:LEU:O	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:I:63:ILE:HG13	32:I:64:TYR:HD2	1.63	0.64
51:1:1779:U:H5	51:1:1784:A:N7	1.95	0.64
52:2:3:C:C2'	52:2:4:C:H5''	2.25	0.64
20:v:75:GLN:HB2	20:v:92:VAL:HG23	1.79	0.64
42:S:52:ARG:HG2	42:S:58:ARG:NH1	2.12	0.64
51:1:2297:A:H62	51:1:2319:G:H1'	1.60	0.64
51:1:2315:G:H2'	51:1:2316:G:H8	1.63	0.64
3:d:108:ILE:HG23	3:d:109:LEU:HD12	1.79	0.64
15:q:10:ARG:HH22	51:1:29:U:H1'	1.62	0.64
49:Z:26:GLY:HA2	54:4:9:G:C5'	2.28	0.64
50:3:452:A:H61	50:3:480:U:H3	1.44	0.64
51:1:741:U:H2'	51:1:742:A:C8	2.32	0.64
51:1:807:U:H2'	51:1:808:G:H8	1.62	0.64
51:1:1357:C:H2'	51:1:1358:G:O4'	1.97	0.64
2:c:13:ARG:HG2	14:p:55:HIS:CE1	2.33	0.64
51:1:2834:G:O2'	51:1:2835:A:H5'	1.97	0.64
50:3:1412:C:H2'	50:3:1413:A:C8	2.33	0.64
55:8:64:ILE:HA	55:8:70:ILE:HA	1.79	0.64
51:1:2145:C:H3'	51:1:2146:C:H5'	1.80	0.64
15:q:17:LEU:HA	15:q:20:ALA:HB3	1.80	0.64
51:1:1062:G:H2'	51:1:1063:G:C8	2.33	0.64
51:1:2267:A:H5''	51:1:2268:A:H5'	1.79	0.64
51:1:2281:A:O2'	51:1:2282:G:H5'	1.97	0.64
55:8:49:PRO:O	55:8:51:TYR:N	2.30	0.64
11:m:4:PRO:HB2	11:m:7:THR:HG22	1.79	0.64
21:w:70:PRO:HG3	52:2:12:C:N4	2.13	0.64
51:1:189:G:H2'	51:1:205:G:H22	1.63	0.64
51:1:1914:C:O2'	51:1:1915:U:H5'	1.96	0.64
9:k:32:TYR:OH	51:1:2726:A:H4'	1.98	0.63
12:n:36:THR:HG22	12:n:37:THR:H	1.63	0.63
50:3:1199:U:H2'	50:3:1200:C:H5'	1.80	0.63
51:1:1796:U:H2'	51:1:1797:G:C8	2.32	0.63
51:1:2106:U:O2'	51:1:2107:G:H5'	1.97	0.63
51:1:2159:G:O2'	51:1:2160:C:H5'	1.98	0.63
50:3:844:G:H2'	50:3:846:G:H1'	1.78	0.63
55:8:56:LEU:HD21	55:8:70:ILE:HD11	1.80	0.63
50:3:29:U:O2'	50:3:30:U:H5'	1.99	0.63
51:1:1111:A:O2'	51:1:1112:G:H4'	1.98	0.63
31:H:185:THR:HG22	31:H:198:LYS:HG2	1.80	0.63
49:Z:7:GLU:HB3	49:Z:10:PRO:HG2	1.81	0.63
50:3:373:A:H61	50:3:391:G:H1'	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:r:6:GLN:HG3	16:r:11:GLN:NE2	2.08	0.63
7:h:67:THR:H	7:h:68:PRO:HD2	1.64	0.63
11:m:76:LYS:HD2	51:1:956:G:H5''	1.78	0.63
11:m:45:GLN:HE21	51:1:2485:G:H5''	1.63	0.63
34:K:52:ASN:O	34:K:53:LYS:HB2	1.98	0.63
51:1:1790:C:H2'	51:1:1791:A:C5	2.34	0.63
51:1:2679:A:O2'	51:1:2680:U:H5'	1.99	0.63
4:e:63:LYS:O	52:2:42:C:H1'	1.98	0.63
39:P:19:VAL:HG12	39:P:82:GLU:HB3	1.81	0.62
50:3:955:U:H3	50:3:1225:A:H61	1.46	0.62
50:3:1137:C:H5'	50:3:1138:G:H5'	1.80	0.62
36:M:102:VAL:HG13	36:M:125:ILE:HB	1.82	0.62
50:3:664:G:H22	50:3:741:G:H1	1.46	0.62
50:3:1088:G:H21	50:3:1167:A:H61	1.45	0.62
50:3:848:C:H2'	50:3:849:G:O4'	1.98	0.62
51:1:654:A:H3'	51:1:654:A:N3	2.14	0.62
2:c:13:ARG:HG2	14:p:55:HIS:HE1	1.63	0.62
51:1:2396:G:H2'	51:1:2397:G:H8	1.63	0.62
52:2:86:G:C6	52:2:88:C:H1'	2.34	0.62
45:V:16:MET:HB3	45:V:19:SER:HB2	1.80	0.62
50:3:665:A:O4'	50:3:733:G:H1'	1.99	0.62
50:3:1135:U:H2'	50:3:1137:C:OP2	1.99	0.62
51:1:2209:G:H3'	51:1:2210:U:H5''	1.81	0.62
52:2:3:C:H42	52:2:117:G:H1	1.48	0.62
53:5:69:C:H2'	53:5:70:G:C8	2.35	0.62
32:I:152:SER:OG	50:3:436:C:H4'	1.99	0.62
50:3:784:A:H2'	50:3:785:G:C8	2.33	0.62
51:1:481:G:H1'	51:1:506:G:N2	2.15	0.62
51:1:1394:U:H4'	51:1:1603:A:H4'	1.80	0.62
51:1:2638:G:H1'	51:1:2778:A:H61	1.65	0.62
39:P:88:PRO:HG2	39:P:89:GLY:H	1.64	0.62
51:1:1178:C:O2	51:1:1178:C:H2'	1.98	0.62
51:1:2784:U:H2'	51:1:2785:C:C6	2.35	0.62
47:X:77:ARG:HD2	50:3:1225:A:O2'	2.00	0.62
51:1:1141:U:H4'	51:1:1142:A:O4'	2.00	0.62
21:w:74:LYS:HE3	51:1:858:G:OP1	1.99	0.62
30:G:115:ASP:O	30:G:118:THR:HG22	2.00	0.62
51:1:2023:C:H2'	51:1:2024:G:H8	1.64	0.62
55:8:77:TYR:HB2	55:8:83:ASN:OD1	2.00	0.62
33:J:81:GLN:HE22	33:J:149:PRO:HB3	1.64	0.62
34:K:64:VAL:HG22	34:K:65:GLU:N	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:U:71:VAL:O	44:U:75:ILE:HG13	2.00	0.62
51:1:742:A:H2'	51:1:743:A:C8	2.35	0.62
51:1:1316:U:H2'	51:1:1317:G:C8	2.34	0.62
10:l:101:ILE:HG13	10:l:102:GLY:H	1.65	0.61
25:B:28:SER:HB3	25:B:39:ARG:HD2	1.81	0.61
36:M:52:GLY:HA3	36:M:56:PRO:HA	1.81	0.61
49:Z:26:GLY:HA2	54:4:9:G:H5''	1.81	0.61
50:3:478:A:H2'	50:3:479:U:H4'	1.82	0.61
51:1:2156:G:H2'	51:1:2157:G:H5'	1.81	0.61
32:I:151:GLN:CD	50:3:437:U:H4'	2.25	0.61
50:3:279:A:H5'	50:3:281:G:H5'	1.80	0.61
50:3:484:G:H4'	50:3:485:U:C5'	2.29	0.61
51:1:20:C:H2'	51:1:21:A:C8	2.34	0.61
51:1:546:U:H2'	51:1:547:A:H4'	1.82	0.61
51:1:1251:C:O2'	51:1:1252:G:H3'	1.99	0.61
51:1:2606:C:H2'	51:1:2607:G:H8	1.64	0.61
16:r:41:ILE:HG23	16:r:47:VAL:HB	1.81	0.61
36:M:63:LYS:HB3	36:M:70:VAL:HG21	1.83	0.61
42:S:52:ARG:HD2	50:3:1219:A:OP1	2.00	0.61
44:U:2:VAL:HG23	44:U:65:ALA:HA	1.83	0.61
9:k:76:VAL:H	14:p:72:VAL:HG22	1.66	0.61
51:1:1509:A:H2'	51:1:1510:G:C8	2.35	0.61
51:1:1690:A:H2'	51:1:1691:C:O4'	1.99	0.61
50:3:1253:G:H2'	50:3:1254:A:C8	2.35	0.61
55:8:62:HIS:O	55:8:63:LEU:HB2	2.01	0.61
1:b:116:GLN:HE21	1:b:121:ALA:HA	1.65	0.61
12:n:63:ARG:CZ	51:1:1454:C:H5'	2.30	0.61
20:v:9:ARG:CG	20:v:41:GLU:HG3	2.23	0.61
34:K:46:GLN:HA	34:K:56:LYS:HA	1.82	0.61
40:Q:26:CYS:HB2	40:Q:29:LYS:HE2	1.82	0.61
51:1:858:G:H21	51:1:2268:A:H2'	1.66	0.61
51:1:873:C:H2'	51:1:874:G:H8	1.66	0.61
51:1:1565:C:O2'	51:1:1566:A:H2'	2.00	0.61
51:1:2646:C:H2'	51:1:2647:U:O4'	2.01	0.61
2:c:114:LYS:HD3	51:1:2723:C:OP1	2.01	0.61
5:f:174:LYS:HG3	5:f:175:LYS:HG2	1.82	0.61
50:3:252:U:O2	50:3:252:U:H2'	2.00	0.61
50:3:1084:G:H5'	50:3:1102:A:OP2	2.01	0.61
50:3:1305:G:N2	50:3:1331:G:H2'	2.16	0.61
51:1:161:A:H3'	51:1:162:U:H5''	1.83	0.61
51:1:594:U:H2'	51:1:595:C:C6	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:704:G:H2'	51:1:726:G:N2	2.15	0.61
33:J:131:ASN:ND2	33:J:134:ASN:H	1.98	0.61
20:v:9:ARG:HG2	20:v:41:GLU:CG	2.23	0.60
27:D:12:ARG:HD2	51:1:686:U:O4	2.01	0.60
32:I:60:VAL:HG22	32:I:194:ILE:HD13	1.81	0.60
50:3:254:G:O2'	50:3:255:G:H5'	2.01	0.60
51:1:2070:A:H2'	51:1:2071:A:C8	2.36	0.60
51:1:2248:C:C2'	51:1:2249:U:H5'	2.31	0.60
51:1:2413:G:C3'	51:1:2414:G:H5''	2.31	0.60
51:1:2798:U:H4'	51:1:2799:A:C5	2.36	0.60
11:m:73:ILE:HD11	11:m:91:TYR:CE2	2.36	0.60
50:3:1296:C:H4'	50:3:1302:C:H42	1.64	0.60
50:3:1515:G:H1	50:3:1520:C:H42	1.49	0.60
51:1:685:A:H5''	51:1:788:A:H62	1.65	0.60
7:h:67:THR:N	7:h:68:PRO:HD2	2.17	0.60
48:Y:8:LYS:O	48:Y:12:GLN:HG3	2.01	0.60
50:3:179:A:H61	50:3:196:A:H62	1.47	0.60
50:3:440:C:H3'	50:3:441:A:H5''	1.83	0.60
51:1:833:A:H2'	51:1:834:G:H8	1.66	0.60
15:q:5:ARG:NH1	51:1:585:G:N7	2.50	0.60
50:3:1522:U:H2'	50:3:1523:G:H8	1.66	0.60
51:1:1434:A:H2'	51:1:1435:G:C8	2.36	0.60
51:1:2585:U:H3	55:8:28:GLN:HE22	1.47	0.60
22:x:7:THR:HG23	22:x:9:LYS:HG3	1.82	0.60
25:B:2:VAL:HG22	25:B:3:GLN:H	1.66	0.60
50:3:211:G:H2'	50:3:212:G:H5'	1.84	0.60
50:3:572:A:H5''	50:3:917:G:H4'	1.83	0.60
51:1:760:G:H2'	51:1:761:A:O4'	2.02	0.60
51:1:2150:C:H2'	51:1:2151:U:O4'	2.00	0.60
51:1:2493:U:C3'	51:1:2494:G:H5''	2.31	0.60
1:b:156:SER:HB2	51:1:1818:U:H5'	1.84	0.60
11:m:45:GLN:NE2	51:1:2485:G:H5''	2.17	0.60
32:I:187:ARG:HD2	32:I:190:LEU:HD12	1.83	0.60
51:1:2795:C:H2'	51:1:2796:U:O4'	2.02	0.60
1:b:156:SER:O	1:b:194:VAL:HG21	2.02	0.60
24:z:35:VAL:HG22	24:z:37:ARG:HH12	1.66	0.60
51:1:742:A:H2'	51:1:743:A:H8	1.67	0.60
51:1:1273:U:H5''	51:1:1646:C:N4	2.17	0.60
4:e:106:ALA:HA	4:e:136:ILE:HG22	1.84	0.59
33:J:79:THR:O	33:J:80:LEU:HB2	2.01	0.59
40:Q:107:LYS:HG3	40:Q:108:ASP:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:1251:A:O2'	50:3:1370:G:H5'	2.02	0.59
9:k:3:GLN:NE2	9:k:32:TYR:HB3	2.17	0.59
10:l:95:LEU:HD22	10:l:100:ILE:HD11	1.83	0.59
30:G:66:ILE:N	30:G:66:ILE:HD12	2.16	0.59
30:G:142:LYS:HA	30:G:145:ASN:HD21	1.67	0.59
41:R:16:ILE:HG21	50:3:1302:C:O4'	2.02	0.59
51:1:2533:U:H2'	51:1:2534:A:O4'	2.02	0.59
8:j:132:HIS:NE2	51:1:7:G:H5'	2.17	0.59
32:I:30:LYS:HB3	50:3:411:A:C8	2.36	0.59
36:M:80:PRO:HG2	50:3:878:A:C5'	2.33	0.59
40:Q:48:LEU:HB2	50:3:520:A:OP1	2.02	0.59
40:Q:77:SER:OG	40:Q:102:ASP:HB3	2.02	0.59
51:1:2065:C:H2'	51:1:2066:C:C6	2.37	0.59
51:1:2573:C:H5''	51:1:2574:G:C5'	2.31	0.59
55:8:20:ILE:C	55:8:35:THR:HG22	2.27	0.59
40:Q:41:PRO:HB3	40:Q:88:ASP:HB3	1.83	0.59
50:3:950:U:H2'	50:3:951:G:H8	1.68	0.59
51:1:644:A:H2'	51:1:645:C:C4'	2.33	0.59
51:1:1052:C:H2'	51:1:1053:C:C6	2.37	0.59
51:1:2243:U:H2'	51:1:2244:U:C6	2.37	0.59
53:5:69:C:H2'	53:5:70:G:H8	1.68	0.59
10:l:79:LEU:HD12	10:l:116:VAL:HG21	1.83	0.59
15:q:90:ASP:HB3	51:1:997:G:H5'	1.85	0.59
51:1:2128:G:H1	51:1:2173:A:H2	1.50	0.59
38:O:40:ILE:H	38:O:40:ILE:HD12	1.67	0.59
50:3:75:G:H2'	50:3:76:G:H5'	1.84	0.59
51:1:445:C:O2'	51:1:446:G:H5'	2.01	0.59
51:1:1775:U:H2'	51:1:1776:G:H5'	1.84	0.59
51:1:2655:G:O2'	51:1:2656:U:H5	1.86	0.59
50:3:225:C:C2'	50:3:226:G:H5''	2.32	0.59
50:3:225:C:C3'	50:3:226:G:H5''	2.33	0.59
50:3:1305:G:H22	50:3:1331:G:H2'	1.67	0.59
51:1:1316:U:H2'	51:1:1317:G:H8	1.68	0.59
51:1:2590:A:H2'	51:1:2591:C:C6	2.38	0.59
16:r:91:GLN:HE22	51:1:1162:G:H21	1.49	0.59
51:1:962:G:H21	51:1:2250:G:H22	1.51	0.59
51:1:1695:G:H3'	51:1:1695:G:N3	2.18	0.59
41:R:64:VAL:HG12	41:R:65:GLU:H	1.67	0.59
51:1:538:A:H2'	51:1:539:G:O4'	2.03	0.59
51:1:1177:G:C5	51:1:1178:C:H1'	2.38	0.59
51:1:1773:A:H2'	51:1:1774:C:H5'	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2529:G:H5''	51:1:2530:A:H5''	1.85	0.59
51:1:2563:U:H2'	51:1:2565:A:OP2	2.02	0.59
1:b:234:GLY:N	51:1:2599:G:OP2	2.28	0.58
5:f:106:LEU:HD11	5:f:150:TYR:HB3	1.85	0.58
17:s:8:ARG:HD3	51:1:494:G:OP1	2.03	0.58
50:3:1517:G:O2'	50:3:1518:A:H5'	2.03	0.58
51:1:532:A:H2'	51:1:532:A:N3	2.17	0.58
51:1:745:G:O2'	51:1:748:G:H1'	2.03	0.58
51:1:225:C:H2'	51:1:226:A:O4'	2.03	0.58
51:1:310:A:O2'	51:1:311:A:H5''	2.02	0.58
51:1:828:U:H4'	51:1:831:G:N1	2.18	0.58
51:1:1063:G:H1	51:1:1075:C:H42	1.51	0.58
51:1:1065:U:H3'	51:1:1066:U:H5''	1.84	0.58
55:8:28:GLN:HA	55:8:31:ASN:HD21	1.67	0.58
11:m:64:TRP:HE1	51:1:873:C:C4'	2.07	0.58
33:J:133:ILE:H	33:J:133:ILE:HD12	1.67	0.58
47:X:54:ARG:HH22	47:X:78:THR:HG21	1.69	0.58
50:3:1052:U:H2'	50:3:1200:C:N4	2.16	0.58
50:3:1369:C:H2'	50:3:1370:G:C8	2.38	0.58
51:1:813:U:H2'	51:1:814:C:C6	2.38	0.58
51:1:1701:A:C2'	51:1:1702:G:H5'	2.33	0.58
34:K:53:LYS:CD	34:K:54:LEU:H	2.13	0.58
50:3:440:C:H2'	50:3:441:A:C4'	2.32	0.58
51:1:644:A:H61	51:1:2349:G:H21	1.51	0.58
51:1:2166:U:H2'	51:1:2167:U:H5'	1.85	0.58
7:h:68:PRO:HA	7:h:72:LEU:HG	1.84	0.58
19:u:35:VAL:HG13	19:u:38:ILE:HB	1.84	0.58
50:3:440:C:C3'	50:3:441:A:H5''	2.33	0.58
1:b:229:HIS:CG	1:b:230:PRO:HD2	2.39	0.58
9:k:3:GLN:HE21	9:k:32:TYR:HB3	1.69	0.58
10:l:4:ASN:O	51:1:1243:C:H1'	2.03	0.58
32:I:161:ALA:O	32:I:164:ARG:HG2	2.04	0.58
51:1:847:U:O2	51:1:847:U:H2'	2.04	0.58
51:1:2233:U:H2'	51:1:2234:G:H8	1.67	0.58
55:8:2:ILE:N	55:8:11:PRO:HA	2.18	0.58
12:n:72:ASP:O	12:n:75:ILE:HG22	2.02	0.58
50:3:304:U:O2'	50:3:305:G:H5'	2.03	0.58
50:3:1137:C:H4'	50:3:1138:G:N2	2.17	0.58
51:1:227:A:O2'	51:1:228:C:H4'	2.03	0.58
51:1:1727:C:O2'	51:1:1728:C:H5'	2.04	0.58
8:j:81:ILE:HG21	51:1:2514:U:H4'	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1911:U:H2'	51:1:1918:A:N1	2.19	0.58
1:b:4:LYS:HA	1:b:16:VAL:HA	1.85	0.58
40:Q:78:VAL:O	40:Q:102:ASP:HB2	2.04	0.58
48:Y:35:TYR:HA	48:Y:38:ILE:HG22	1.86	0.58
49:Z:29:ALA:HA	49:Z:32:ARG:CD	2.33	0.58
3:d:117:ARG:HH12	10:l:2:ARG:HG2	1.69	0.58
6:g:54:LEU:HD12	6:g:55:GLU:N	2.18	0.58
49:Z:20:ARG:HA	49:Z:24:LYS:HD3	1.86	0.58
50:3:1113:C:H42	50:3:1187:G:H1	1.51	0.58
50:3:1513:A:H2'	50:3:1514:G:C8	2.38	0.58
51:1:799:G:H5''	51:1:800:A:H2'	1.86	0.58
37:N:111:GLU:OE1	50:3:1186:G:H4'	2.03	0.57
38:O:57:VAL:HG12	38:O:58:ASN:H	1.68	0.57
41:R:82:LEU:HD23	41:R:84:CYS:SG	2.44	0.57
50:3:1299:A:H2'	50:3:1300:G:H4'	1.86	0.57
51:1:965:C:H2'	51:1:966:G:H8	1.67	0.57
51:1:2602:A:N7	55:8:30:VAL:HB	2.19	0.57
1:b:119:VAL:HG21	6:g:91:PHE:HB3	1.86	0.57
38:O:42:LEU:HG	38:O:73:LEU:HD23	1.86	0.57
50:3:662:U:H2'	50:3:663:A:C8	2.39	0.57
51:1:296:U:H2'	51:1:297:G:C8	2.39	0.57
8:j:4:PHE:HB3	15:q:63:ARG:HH12	1.68	0.57
11:m:69:PRO:HA	11:m:94:ALA:HB2	1.86	0.57
12:n:3:HIS:CD2	51:1:2820:A:H4'	2.39	0.57
44:U:4:ILE:HB	44:U:67:ILE:HA	1.86	0.57
50:3:1517:G:C2'	50:3:1518:A:H5'	2.35	0.57
50:3:1522:U:H2'	50:3:1523:G:C8	2.39	0.57
51:1:1252:G:O2'	51:1:1253:A:H5''	2.04	0.57
55:8:119:LEU:O	55:8:122:LYS:HG2	2.04	0.57
8:j:78:THR:HG23	8:j:80:HIS:H	1.68	0.57
12:n:26:GLY:HA2	12:n:75:ILE:HD12	1.87	0.57
22:x:9:LYS:NZ	51:1:397:U:OP2	2.30	0.57
42:S:68:ARG:HD2	42:S:69:PRO:HD2	1.86	0.57
50:3:56:U:H2'	50:3:57:G:C8	2.40	0.57
51:1:184:C:H2'	51:1:185:G:H8	1.69	0.57
51:1:1300:G:H4'	51:1:1301:A:C5'	2.23	0.57
51:1:2391:G:H4'	51:1:2392:A:OP1	2.05	0.57
51:1:2676:C:H2'	51:1:2677:G:H8	1.69	0.57
39:P:43:TRP:NE1	50:3:686:U:H4'	2.18	0.57
50:3:1227:A:H2'	50:3:1228:C:H5'	1.87	0.57
51:1:1172:C:H2'	51:1:1173:U:H5''	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1874:C:H2'	51:1:1875:G:O4'	2.04	0.57
1:b:216:ARG:HB3	1:b:217:PRO:HD2	1.86	0.57
23:y:9:LYS:O	23:y:13:GLU:HG2	2.05	0.57
36:M:3:GLN:HE21	50:3:755:G:H21	1.53	0.57
37:N:71:ILE:HG23	37:N:72:SER:H	1.69	0.57
50:3:1330:U:H2'	50:3:1331:G:O4'	2.05	0.57
51:1:141:G:H2'	51:1:142:A:H5'	1.86	0.57
51:1:1023:U:O2'	51:1:1122:G:H5'	2.05	0.57
51:1:1476:U:H3	51:1:1515:A:H62	1.51	0.57
51:1:2327:A:H2'	51:1:2328:A:C8	2.39	0.57
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.86	0.57
33:J:131:ASN:HD22	33:J:134:ASN:HB2	1.69	0.57
43:T:56:LEU:HA	43:T:59:VAL:HG12	1.87	0.57
45:V:5:ARG:NH2	50:3:128:G:C5'	2.68	0.57
50:3:272:C:H2'	50:3:273:U:C6	2.39	0.57
50:3:422:C:H4'	50:3:423:G:C2	2.39	0.57
51:1:1412:U:H2'	51:1:1413:A:C8	2.40	0.57
7:h:45:GLY:HA2	7:h:49:GLY:HA2	1.86	0.57
36:M:12:ARG:NH2	50:3:826:C:H5'	2.20	0.57
45:V:30:HIS:HD2	45:V:33:TYR:H	1.51	0.57
50:3:56:U:H2'	50:3:57:G:H8	1.69	0.57
50:3:889:A:H5'	50:3:891:U:H1'	1.86	0.57
51:1:184:C:H2'	51:1:185:G:C8	2.40	0.57
51:1:1319:C:O2'	51:1:1320:C:H5'	2.04	0.57
51:1:2148:G:H2'	51:1:2149:U:C6	2.40	0.57
51:1:2348:U:O2'	51:1:2349:G:H5'	2.04	0.57
52:2:63:C:H2'	52:2:64:G:H8	1.70	0.57
50:3:352:C:H4'	50:3:354:G:OP1	2.04	0.57
51:1:1304:A:C3'	51:1:1305:C:H5''	2.34	0.57
51:1:1409:U:H2'	51:1:1410:G:C8	2.40	0.57
30:G:83:ALA:HB3	30:G:90:PHE:CD2	2.40	0.57
36:M:15:ASN:O	36:M:19:ALA:HB3	2.05	0.57
51:1:935:C:H2'	51:1:936:A:H8	1.69	0.57
51:1:1990:C:H2'	51:1:1991:U:O4'	2.05	0.57
22:x:4:CYS:HB3	22:x:9:LYS:H	1.70	0.56
43:T:45:HIS:O	43:T:47:LYS:N	2.38	0.56
44:U:6:LEU:HG	44:U:17:TYR:HB3	1.86	0.56
50:3:709:U:H2'	50:3:710:G:C8	2.40	0.56
51:1:767:U:H2'	51:1:768:G:H8	1.68	0.56
51:1:1065:U:H3'	51:1:1066:U:C5'	2.34	0.56
51:1:1103:A:H3'	51:1:1104:C:H6	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1173:U:C2'	51:1:1174:U:H4'	2.32	0.56
51:1:1728:C:C2'	51:1:1729:U:H5''	2.34	0.56
51:1:2756:U:H4'	51:1:2757:A:OP1	2.03	0.56
54:4:6:G:H2'	54:4:7:G:O4'	2.04	0.56
8:j:27:ARG:HH22	51:1:1142:A:H4'	1.70	0.56
15:q:106:THR:O	15:q:109:VAL:HG12	2.05	0.56
30:G:83:ALA:HB3	30:G:90:PHE:HD2	1.69	0.56
35:L:101:ARG:HE	50:3:939:G:H4'	1.70	0.56
42:S:4:SER:HA	50:3:994:A:C2	2.40	0.56
50:3:257:G:H2'	50:3:258:G:H8	1.70	0.56
50:3:865:A:H5'	50:3:1078:U:O4	2.05	0.56
51:1:1378:A:H1'	51:1:1379:U:C5	2.40	0.56
51:1:1736:U:O2'	51:1:1737:G:H5'	2.06	0.56
51:1:2573:C:H41	55:8:33:THR:HA	1.69	0.56
53:5:51:C:H2'	53:5:52:G:C8	2.40	0.56
55:8:35:THR:O	55:8:37:ILE:HG12	2.05	0.56
8:j:27:ARG:HD3	51:1:1143:A:H62	1.69	0.56
17:s:11:ARG:HA	17:s:100:THR:HG22	1.87	0.56
44:U:20:VAL:HG23	44:U:35:ARG:HA	1.87	0.56
50:3:813:U:H2'	50:3:814:A:C5'	2.28	0.56
51:1:1336:A:H2'	51:1:1337:G:H8	1.70	0.56
51:1:2096:C:H42	51:1:2193:G:H1	1.53	0.56
14:p:52:ARG:HH22	51:1:2720:U:H5''	1.70	0.56
19:u:46:LYS:HD2	19:u:47:PRO:HD2	1.86	0.56
23:y:55:THR:O	23:y:59:GLU:HG2	2.05	0.56
47:X:32:THR:OG1	47:X:33:TRP:N	2.39	0.56
50:3:20:U:H2'	50:3:21:G:O4'	2.05	0.56
50:3:868:C:H2'	50:3:869:G:O4'	2.06	0.56
51:1:64:A:H2'	51:1:65:U:C6	2.40	0.56
51:1:873:C:H2'	51:1:874:G:C8	2.40	0.56
9:k:112:PHE:HB3	9:k:115:ILE:HD12	1.87	0.56
15:q:54:ARG:HD3	51:1:1155:A:H5''	1.87	0.56
32:I:2:ARG:HH22	50:3:407:U:H5'	1.70	0.56
50:3:146:G:H2'	50:3:147:G:C8	2.40	0.56
50:3:235:C:H2'	50:3:236:A:C8	2.41	0.56
51:1:2315:G:H2'	51:1:2316:G:C8	2.41	0.56
51:1:2710:C:H2'	51:1:2711:A:C8	2.40	0.56
54:4:6:G:C2'	54:4:7:G:H5'	2.35	0.56
1:b:57:HIS:ND1	51:1:1567:G:H5'	2.21	0.56
4:e:39:VAL:HG12	4:e:41:GLU:H	1.70	0.56
4:e:79:ARG:HD2	53:5:56:C:H1'	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Z:67:THR:OG1	50:3:1088:G:H4'	2.05	0.56
51:1:1775:U:C2'	51:1:1776:G:H5'	2.34	0.56
51:1:1885:A:H2'	51:1:1886:U:H5'	1.87	0.56
25:B:14:MET:HE2	51:1:2045:C:H5''	1.88	0.56
28:E:55:GLY:O	28:E:58:ILE:HG22	2.05	0.56
50:3:143:A:H2	50:3:220:G:H1	1.52	0.56
50:3:769:G:H4'	50:3:1513:A:H4'	1.88	0.56
50:3:1314:C:H2'	50:3:1315:U:C6	2.41	0.56
51:1:1827:U:O2'	51:1:1828:G:H5'	2.06	0.56
51:1:2413:G:H2'	51:1:2414:G:C5'	2.31	0.56
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.87	0.56
3:d:190:ALA:O	3:d:193:VAL:HG12	2.06	0.56
10:l:101:ILE:HG13	10:l:102:GLY:N	2.21	0.56
31:H:2:GLN:HB2	50:3:1190:G:O2'	2.05	0.56
50:3:621:A:H2'	50:3:622:A:C8	2.39	0.56
50:3:695:A:H2'	50:3:696:A:C8	2.41	0.56
53:5:6:G:O2'	53:5:7:G:H5'	2.06	0.56
50:3:66:A:H5'	50:3:173:U:O4	2.06	0.56
50:3:560:A:H5'	50:3:566:G:N2	2.21	0.56
51:1:18:U:H2'	51:1:19:A:C8	2.41	0.56
51:1:2224:G:H4'	51:1:2226:C:C2	2.40	0.56
55:8:44:ARG:HB3	55:8:56:LEU:HD23	1.88	0.56
1:b:7:PRO:HG3	51:1:1694:C:OP1	2.05	0.56
2:c:142:VAL:CG2	2:c:143:PRO:HD2	2.30	0.56
33:J:114:LEU:HD13	33:J:122:VAL:HG21	1.87	0.56
41:R:70:ARG:O	41:R:74:MET:HG3	2.06	0.56
51:1:1919:A:H2'	51:1:1920:C:H5'	1.88	0.56
3:d:77:ILE:HG23	3:d:78:TRP:CD1	2.39	0.55
7:h:58:THR:HA	7:h:63:ALA:HB2	1.88	0.55
17:s:79:GLY:H	17:s:101:SER:HA	1.71	0.55
18:t:1:MET:HE1	51:1:138:U:N3	2.21	0.55
23:y:6:LEU:HA	23:y:56:LEU:HD11	1.88	0.55
27:D:12:ARG:HH11	27:D:44:VAL:HG11	1.70	0.55
37:N:68:GLY:HA2	50:3:1250:A:H4'	1.88	0.55
50:3:678:U:H2'	50:3:679:C:C6	2.41	0.55
50:3:687:A:N3	50:3:688:G:H1'	2.21	0.55
50:3:1515:G:H2'	50:3:1516:G:C8	2.41	0.55
51:1:305:C:H42	51:1:312:G:H1	1.53	0.55
51:1:974:G:H1'	51:1:975:A:C8	2.41	0.55
51:1:1683:U:H2'	51:1:1684:G:C8	2.41	0.55
51:1:2196:C:O2'	51:1:2197:U:H5'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2556:C:H2'	51:1:2557:G:O4'	2.06	0.55
7:h:27:VAL:HB	7:h:83:ALA:HB3	1.88	0.55
50:3:438:U:O4	50:3:493:A:H2'	2.06	0.55
50:3:1237:C:H4'	50:3:1334:G:N2	2.19	0.55
50:3:1356:G:H2'	50:3:1357:A:C8	2.41	0.55
51:1:296:U:H2'	51:1:297:G:H8	1.71	0.55
51:1:2669:G:H2'	51:1:2670:A:H8	1.70	0.55
50:3:16:A:O2'	50:3:17:U:H5'	2.07	0.55
50:3:256:U:H2'	50:3:257:G:C8	2.42	0.55
50:3:1346:A:H2'	50:3:1346:A:N3	2.21	0.55
51:1:437:U:H2'	51:1:438:G:C8	2.41	0.55
51:1:940:G:H2'	51:1:941:A:O4'	2.06	0.55
51:1:1139:G:O2'	51:1:1140:C:H5'	2.07	0.55
7:h:12:VAL:HA	7:h:15:VAL:HG22	1.88	0.55
34:K:5:GLU:OE2	34:K:5:GLU:N	2.40	0.55
50:3:451:A:H4'	50:3:452:A:O4'	2.05	0.55
50:3:837:U:H2'	50:3:838:G:C8	2.41	0.55
51:1:340:A:H2'	51:1:341:C:O4'	2.06	0.55
51:1:1773:A:C2'	51:1:1774:C:H5'	2.37	0.55
51:1:1810:A:H2'	51:1:1811:G:H5'	1.88	0.55
51:1:2183:A:H2'	51:1:2184:A:C8	2.40	0.55
55:8:49:PRO:HB2	55:8:52:TYR:HD2	1.71	0.55
18:t:1:MET:HE3	18:t:3:ARG:HB2	1.87	0.55
20:v:14:LYS:HB2	52:2:98:G:H1	1.71	0.55
42:S:39:ASP:HA	42:S:42:ASN:HD22	1.71	0.55
50:3:437:U:O2'	50:3:438:U:H5'	2.06	0.55
51:1:1351:C:H2'	51:1:1352:U:C6	2.42	0.55
51:1:1909:C:H2'	51:1:1910:G:H8	1.71	0.55
51:1:2698:U:H2'	51:1:2699:C:C6	2.42	0.55
12:n:44:LEU:HD23	12:n:113:ILE:HD13	1.89	0.55
37:N:49:GLN:O	37:N:52:GLU:HG3	2.06	0.55
46:W:20:ILE:H	46:W:53:GLN:HE22	1.54	0.55
50:3:730:G:H2'	50:3:731:G:H5'	1.88	0.55
51:1:546:U:H2'	51:1:547:A:C4'	2.36	0.55
51:1:1173:U:H1'	51:1:1177:G:O6	2.07	0.55
55:8:33:THR:O	55:8:35:THR:N	2.39	0.55
1:b:2:VAL:HG12	1:b:18:VAL:HG22	1.88	0.55
2:c:150:GLN:HB2	51:1:2572:A:N7	2.22	0.55
6:g:129:GLU:HB3	6:g:143:ILE:HD12	1.88	0.55
34:K:64:VAL:HG22	34:K:65:GLU:H	1.71	0.55
35:L:23:ALA:O	35:L:26:VAL:HG12	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:V:5:ARG:HH22	50:3:128:G:H5''	1.72	0.55
51:1:580:U:H2'	51:1:581:C:C6	2.42	0.55
51:1:1900:A:H1'	51:1:1970:A:H2'	1.87	0.55
51:1:2843:G:O2'	51:1:2844:G:H5'	2.06	0.55
2:c:133:THR:HG23	2:c:134:HIS:HD2	1.72	0.55
8:j:109:LEU:HD23	8:j:110:PRO:N	2.22	0.55
35:L:101:ARG:NH2	50:3:1376:U:H5'	2.22	0.55
37:N:54:VAL:HG13	37:N:55:ASP:H	1.71	0.55
51:1:581:C:H2'	51:1:582:A:C8	2.42	0.55
51:1:925:A:H2'	51:1:926:G:H8	1.71	0.55
51:1:1956:U:C2'	51:1:1957:C:H5'	2.36	0.55
51:1:2747:G:O6	51:1:2755:C:H5''	2.07	0.55
12:n:24:MET:HE3	12:n:36:THR:HG21	1.88	0.55
29:F:1:MET:HB2	29:F:34:LYS:O	2.07	0.55
33:J:109:ALA:O	33:J:113:VAL:HG23	2.07	0.55
35:L:73:GLU:OE1	35:L:140:VAL:HG13	2.07	0.55
35:L:136:LYS:O	35:L:140:VAL:HG23	2.07	0.55
50:3:162:A:H2'	50:3:163:C:O4'	2.07	0.55
51:1:310:A:C2'	51:1:311:A:H5''	2.37	0.55
51:1:414:C:H2'	51:1:415:A:C8	2.42	0.55
51:1:1709:U:O2'	51:1:2859:G:H1'	2.05	0.55
51:1:1736:U:H2'	51:1:1737:G:O4'	2.06	0.55
51:1:1739:A:H2'	51:1:1740:G:O4'	2.07	0.55
51:1:2187:U:H2'	51:1:2188:U:C6	2.41	0.55
51:1:2422:C:H2'	51:1:2424:C:C6	2.41	0.55
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.89	0.55
15:q:90:ASP:CB	51:1:997:G:H5'	2.37	0.55
41:R:54:THR:O	41:R:58:GLU:HG2	2.07	0.55
50:3:82:G:H3'	50:3:83:C:C5'	2.35	0.55
50:3:1446:A:O2'	50:3:1447:A:H5'	2.07	0.55
51:1:2283:C:H2'	51:1:2284:A:O4'	2.07	0.55
51:1:2636:C:H2'	51:1:2637:U:H6	1.72	0.55
39:P:52:ARG:HD2	39:P:52:ARG:N	2.22	0.54
47:X:9:PHE:CD2	50:3:1318:A:H4'	2.42	0.54
49:Z:58:LYS:HA	49:Z:61:ARG:HG3	1.89	0.54
50:3:1197:A:H2'	50:3:1198:G:H5''	1.89	0.54
51:1:1213:A:H62	51:1:1236:G:H1'	1.70	0.54
51:1:2498:C:O2'	51:1:2499:C:H5'	2.06	0.54
14:p:26:GLU:HA	14:p:43:GLU:HA	1.90	0.54
47:X:45:GLY:H	47:X:61:VAL:HG23	1.72	0.54
48:Y:35:TYR:O	48:Y:39:GLU:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Z:16:ARG:HG3	49:Z:17:ARG:NH2	2.23	0.54
50:3:663:A:H2'	50:3:664:G:C8	2.42	0.54
50:3:1342:C:H2'	50:3:1343:G:C8	2.43	0.54
50:3:1342:C:H2'	50:3:1343:G:H8	1.72	0.54
51:1:1539:U:H2'	51:1:1540:G:C8	2.42	0.54
51:1:2860:A:H2'	51:1:2861:U:H5'	1.88	0.54
53:5:75:C:OP2	55:8:78:ARG:NH2	2.40	0.54
55:8:64:ILE:HG22	55:8:70:ILE:HG12	1.89	0.54
3:d:146:VAL:HG12	3:d:185:LYS:HB3	1.88	0.54
11:m:34:LYS:HB3	11:m:129:THR:HG23	1.88	0.54
50:3:415:A:H61	50:3:428:G:H1	1.54	0.54
50:3:1163:A:H2'	50:3:1164:G:C8	2.41	0.54
51:1:662:G:O2'	51:1:663:G:H5'	2.07	0.54
51:1:897:C:N4	51:1:898:C:H41	2.05	0.54
51:1:2213:U:H2'	51:1:2214:C:H5'	1.89	0.54
22:x:67:LEU:HB3	22:x:71:ARG:HH21	1.72	0.54
34:K:96:VAL:HG22	34:K:97:THR:N	2.22	0.54
50:3:1044:A:C5	50:3:1045:C:H1'	2.42	0.54
51:1:286:U:H2'	51:1:287:G:C8	2.42	0.54
7:h:81:LEU:H	51:1:1107:G:H4'	1.73	0.54
11:m:36:VAL:HG13	11:m:127:LYS:HB3	1.90	0.54
25:B:52:LYS:O	25:B:54:ILE:N	2.41	0.54
36:M:80:PRO:HG2	50:3:878:A:H5'	1.89	0.54
39:P:43:TRP:HE1	50:3:686:U:C4'	2.19	0.54
41:R:24:VAL:HA	50:3:1329:A:H5''	1.90	0.54
50:3:1071:C:H2'	50:3:1072:G:C8	2.43	0.54
51:1:69:C:O2'	51:1:70:G:H5'	2.07	0.54
51:1:703:U:H2'	51:1:704:G:O4'	2.08	0.54
51:1:996:A:H2'	51:1:997:G:H8	1.73	0.54
51:1:2136:G:H2'	51:1:2136:G:N3	2.23	0.54
1:b:56:GLY:HA2	1:b:212:TRP:HA	1.89	0.54
7:h:3:LEU:HG	7:h:5:LEU:H	1.72	0.54
9:k:19:VAL:HG22	9:k:43:ILE:HA	1.89	0.54
9:k:77:ILE:HD12	9:k:77:ILE:N	2.23	0.54
10:l:90:VAL:HG23	10:l:95:LEU:HD21	1.90	0.54
37:N:54:VAL:HG13	37:N:55:ASP:OD1	2.06	0.54
51:1:704:G:H1'	51:1:727:A:N6	2.23	0.54
51:1:1594:U:H2'	51:1:1595:C:C6	2.42	0.54
52:2:56:G:H4'	52:2:57:A:C8	2.42	0.54
8:j:81:ILE:H	8:j:81:ILE:HD12	1.73	0.54
11:m:41:LEU:HD12	11:m:96:ILE:HD11	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:x:4:CYS:SG	22:x:7:THR:HG22	2.48	0.54
45:V:48:GLU:HB2	45:V:51:GLU:OE2	2.06	0.54
49:Z:57:LYS:O	49:Z:61:ARG:HG3	2.08	0.54
50:3:414:A:N3	50:3:414:A:H2'	2.23	0.54
50:3:1395:C:H5''	50:3:1402:C:H4'	1.89	0.54
51:1:767:U:H2'	51:1:768:G:C8	2.42	0.54
51:1:927:A:H2'	51:1:928:A:C8	2.43	0.54
51:1:1161:C:H2'	51:1:1162:G:C8	2.43	0.54
51:1:1936:A:H3'	51:1:1937:A:H5'	1.89	0.54
51:1:2101:A:H2'	51:1:2102:G:C8	2.43	0.54
55:8:28:GLN:HA	55:8:31:ASN:ND2	2.22	0.54
17:s:90:LYS:HA	51:1:751:A:O4'	2.07	0.54
47:X:50:VAL:HG22	47:X:51:HIS:H	1.73	0.54
48:Y:48:LYS:O	48:Y:52:GLU:HG2	2.07	0.54
50:3:1119:C:H2'	50:3:1120:C:C6	2.42	0.54
3:d:119:ILE:HB	3:d:187:VAL:HG12	1.89	0.54
28:E:20:GLY:HA2	28:E:54:LEU:HD11	1.90	0.54
42:S:76:PHE:HE1	42:S:95:LEU:HD21	1.73	0.54
50:3:575:G:O2'	50:3:821:G:H5'	2.08	0.54
51:1:255:A:H2'	51:1:256:A:O4'	2.08	0.54
51:1:1164:C:H2'	51:1:1165:A:C8	2.43	0.54
51:1:2143:C:H2'	51:1:2144:G:O4'	2.08	0.54
51:1:2328:A:H2'	51:1:2329:U:C6	2.43	0.54
52:2:106:G:H2'	52:2:107:G:O4'	2.07	0.54
4:e:84:ILE:HD13	51:1:2312:U:H5'	1.89	0.54
6:g:54:LEU:O	6:g:58:LEU:HG	2.08	0.54
7:h:31:ARG:HG3	51:1:1054:A:H4'	1.90	0.54
9:k:43:ILE:HG12	9:k:52:VAL:HG21	1.90	0.54
12:n:6:SER:HB2	12:n:46:ARG:HH22	1.73	0.54
36:M:85:TYR:CD2	50:3:598:U:H4'	2.43	0.54
41:R:84:CYS:HB2	47:X:72:GLU:HG3	1.89	0.54
51:1:878:A:H2'	51:1:879:G:O4'	2.08	0.54
51:1:1103:A:H3'	51:1:1104:C:C6	2.43	0.54
51:1:2098:U:H2'	51:1:2099:U:O4'	2.08	0.54
51:1:2605:U:H2'	51:1:2606:C:C6	2.42	0.54
5:f:120:ILE:HD11	5:f:139:VAL:HG13	1.89	0.53
16:r:74:ILE:HB	16:r:87:GLN:HB3	1.90	0.53
22:x:13:THR:HG22	22:x:27:ARG:HG2	1.89	0.53
33:J:28:ARG:HH21	50:3:1396:A:H1'	1.72	0.53
50:3:631:C:H3'	50:3:632:U:H5'	1.90	0.53
50:3:929:G:OP1	50:3:1534:A:H1'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:226:A:H2'	51:1:227:A:O4'	2.08	0.53
51:1:2602:A:C2	55:8:78:ARG:HA	2.43	0.53
51:1:2849:U:H4'	51:1:2868:A:C2	2.43	0.53
30:G:127:LYS:HG3	30:G:128:LEU:HG	1.91	0.53
30:G:160:LEU:HD23	30:G:180:ILE:HG21	1.89	0.53
31:H:1:GLY:HA2	50:3:1060:U:C5	2.42	0.53
41:R:24:VAL:HG23	41:R:28:ARG:HB3	1.90	0.53
50:3:1306:A:N6	50:3:1331:G:H1'	2.24	0.53
50:3:1512:U:H2'	50:3:1513:A:C8	2.44	0.53
51:1:672:C:C2'	51:1:673:C:H5'	2.38	0.53
51:1:1092:C:H2'	51:1:1093:G:O4'	2.08	0.53
51:1:2404:U:H2'	51:1:2405:G:O4'	2.08	0.53
51:1:2584:U:H5''	55:8:25:ALA:HA	1.90	0.53
51:1:2606:C:H2'	51:1:2607:G:C8	2.42	0.53
51:1:2682:A:O2'	51:1:2683:C:H5'	2.08	0.53
53:5:62:C:H2'	53:5:63:G:H8	1.73	0.53
13:o:33:ARG:O	13:o:34:HIS:HB2	2.09	0.53
19:u:42:LYS:HE3	51:1:499:U:H5'	1.91	0.53
31:H:149:LYS:HE2	31:H:151:GLU:OE2	2.08	0.53
50:3:715:A:H2'	50:3:716:A:C8	2.43	0.53
50:3:869:G:H4'	50:3:872:A:C8	2.43	0.53
51:1:32:C:H2'	51:1:33:C:C6	2.43	0.53
51:1:1623:G:O2'	51:1:1624:U:H5'	2.08	0.53
51:1:2093:G:N7	51:1:2225:A:H2'	2.24	0.53
51:1:2372:U:H2'	51:1:2373:G:H8	1.73	0.53
11:m:124:LEU:HD11	11:m:128:THR:HG22	1.89	0.53
35:L:104:VAL:O	35:L:108:ARG:HG2	2.08	0.53
37:N:17:ARG:HH22	50:3:1129:C:H5'	1.72	0.53
42:S:12:ARG:HH12	42:S:55:SER:H	1.56	0.53
50:3:767:A:H2'	50:3:768:A:C8	2.43	0.53
50:3:860:A:H2'	50:3:861:G:O4'	2.08	0.53
50:3:1513:A:H2'	50:3:1514:G:H8	1.73	0.53
51:1:48:G:O3'	51:1:51:G:H5'	2.07	0.53
51:1:181:A:H2'	51:1:182:A:C8	2.43	0.53
51:1:1417:C:H2'	51:1:1418:G:O4'	2.08	0.53
31:H:72:PRO:HD3	31:H:104:GLU:OE1	2.08	0.53
40:Q:42:LYS:HD2	40:Q:90:PRO:HG3	1.91	0.53
50:3:425:G:O2'	50:3:426:U:H5'	2.09	0.53
50:3:950:U:H2'	50:3:951:G:C8	2.44	0.53
51:1:189:G:H2'	51:1:205:G:N2	2.23	0.53
51:1:2590:A:H2'	51:1:2591:C:H6	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:8:VAL:HG22	55:8:10:ILE:H	1.74	0.53
3:d:115:GLN:O	3:d:117:ARG:HG3	2.09	0.53
9:k:30:ARG:HD2	51:1:2674:G:H4'	1.90	0.53
42:S:41:TRP:O	42:S:44:VAL:HG22	2.08	0.53
49:Z:35:GLU:C	49:Z:37:TYR:H	2.15	0.53
50:3:411:A:N3	50:3:413:G:H1'	2.24	0.53
50:3:887:G:H2'	50:3:888:G:H5'	1.89	0.53
50:3:918:A:H2'	50:3:919:A:C8	2.44	0.53
50:3:1045:C:H2'	50:3:1046:A:H5'	1.91	0.53
51:1:275:C:H2'	51:1:276:U:H4'	1.90	0.53
51:1:2011:U:H2'	51:1:2012:G:O4'	2.08	0.53
4:e:102:LEU:HD13	4:e:106:ALA:HB3	1.89	0.53
5:f:174:LYS:HE3	51:1:2529:G:H4'	1.89	0.53
37:N:52:GLU:OE2	37:N:53:LEU:HB2	2.08	0.53
39:P:44:ALA:HB3	39:P:69:CYS:SG	2.49	0.53
50:3:463:U:H3	50:3:469:C:H42	1.57	0.53
50:3:1128:C:O2'	50:3:1129:C:H5'	2.09	0.53
50:3:1211:U:H4'	50:3:1213:A:N3	2.24	0.53
51:1:935:C:H2'	51:1:936:A:C8	2.44	0.53
51:1:2730:C:H2'	51:1:2731:G:C8	2.44	0.53
9:k:58:LEU:HA	9:k:89:ASN:ND2	2.24	0.53
38:O:59:LYS:HD3	50:3:973:G:OP1	2.08	0.53
40:Q:66:ILE:HD13	40:Q:96:THR:HG21	1.90	0.53
50:3:1352:C:H2'	50:3:1353:G:C8	2.44	0.53
51:1:128:C:H2'	51:1:129:C:C6	2.44	0.53
51:1:925:A:H2'	51:1:926:G:C8	2.44	0.53
51:1:2553:G:H3'	51:1:2554:U:H5''	1.91	0.53
1:b:257:ARG:NH1	51:1:1799:G:OP1	2.36	0.53
12:n:90:ARG:NH1	51:1:2880:C:O2'	2.39	0.53
47:X:66:VAL:HG13	47:X:67:GLY:N	2.24	0.53
50:3:146:G:H2'	50:3:147:G:H8	1.73	0.53
50:3:505:G:H2'	50:3:506:G:C8	2.43	0.53
50:3:1157:A:N6	50:3:1178:G:H1'	2.23	0.53
50:3:1293:C:H2'	50:3:1294:G:C8	2.44	0.53
50:3:1435:G:H2'	50:3:1436:U:C6	2.44	0.53
50:3:1526:G:H2'	50:3:1527:U:C6	2.44	0.53
51:1:327:G:O2'	51:1:328:U:H5'	2.09	0.53
51:1:1336:A:H2'	51:1:1337:G:C8	2.43	0.53
51:1:1443:U:H2'	51:1:1444:G:H8	1.73	0.53
51:1:2446:G:H2'	51:1:2447:G:H5''	1.90	0.53
51:1:2593:U:H2'	51:1:2594:C:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2655:G:HO2'	51:1:2656:U:H5	1.57	0.53
1:b:227:VAL:HG11	51:1:784:G:C2	2.44	0.53
11:m:72:PRO:HD3	11:m:92:TRP:CZ3	2.44	0.53
17:s:30:SER:O	17:s:33:LEU:HG	2.08	0.53
50:3:673:A:H2'	50:3:674:G:C8	2.44	0.53
50:3:1188:A:H2'	50:3:1189:U:H5'	1.90	0.53
50:3:1256:A:H5'	50:3:1258:G:H1'	1.92	0.53
51:1:1278:C:H2'	51:1:1279:G:C8	2.44	0.53
51:1:2194:U:H2'	51:1:2195:U:C6	2.43	0.53
52:2:56:G:H4'	52:2:57:A:H8	1.74	0.53
53:5:44:A:H2'	53:5:45:G:O4'	2.09	0.53
16:r:88:GLY:O	51:1:1224:U:H4'	2.08	0.52
30:G:192:PRO:HG2	30:G:193:ASP:H	1.74	0.52
50:3:204:G:H2'	50:3:205:A:H8	1.74	0.52
50:3:540:G:H2'	50:3:541:G:H8	1.73	0.52
50:3:1173:U:H2'	50:3:1174:G:C8	2.44	0.52
51:1:1161:C:H2'	51:1:1162:G:H8	1.74	0.52
51:1:1179:G:C3'	51:1:1180:U:H4'	2.39	0.52
51:1:1182:G:H2'	51:1:1183:U:O4'	2.10	0.52
51:1:2047:C:O2'	51:1:2048:G:H5'	2.09	0.52
51:1:2467:C:H2'	51:1:2468:A:O4'	2.10	0.52
53:5:5:G:H2'	53:5:6:G:H8	1.74	0.52
1:b:16:VAL:H	1:b:203:VAL:HG22	1.73	0.52
13:o:24:THR:HG23	13:o:90:VAL:HG12	1.92	0.52
50:3:731:G:O2'	50:3:732:C:H5'	2.09	0.52
50:3:1488:G:H2'	50:3:1489:G:H8	1.75	0.52
51:1:162:U:O2'	51:1:163:C:H5'	2.09	0.52
51:1:395:U:H2'	51:1:396:G:C8	2.44	0.52
51:1:419:U:H2'	51:1:420:C:C6	2.44	0.52
51:1:1443:U:H2'	51:1:1444:G:C8	2.43	0.52
51:1:1681:G:N3	51:1:1762:A:H2'	2.23	0.52
51:1:2322:A:H2'	51:1:2323:G:O4'	2.09	0.52
55:8:49:PRO:HB2	55:8:52:TYR:CD2	2.44	0.52
22:x:16:ASN:HB3	22:x:24:THR:CG2	2.39	0.52
28:E:31:ILE:HG23	28:E:31:ILE:O	2.09	0.52
30:G:14:HIS:O	30:G:15:PHE:O	2.26	0.52
37:N:105:ARG:O	37:N:105:ARG:HD3	2.07	0.52
38:O:10:LEU:HG	38:O:18:ILE:HD11	1.92	0.52
50:3:539:A:H2'	50:3:540:G:C8	2.44	0.52
50:3:692:U:H2'	50:3:694:A:OP2	2.08	0.52
51:1:593:U:H2'	51:1:594:U:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:t:3:ARG:O	18:t:7:LEU:HD13	2.09	0.52
34:K:2:ARG:HD3	34:K:91:ARG:HH22	1.74	0.52
35:L:6:ILE:H	35:L:6:ILE:CD1	2.04	0.52
37:N:121:ARG:HG3	50:3:1348:U:H4'	1.92	0.52
45:V:5:ARG:HH22	50:3:128:G:C5'	2.22	0.52
51:1:611:C:H2'	51:1:612:G:O4'	2.08	0.52
51:1:1219:U:H2'	51:1:1220:G:C8	2.45	0.52
51:1:1468:U:H2'	51:1:1522:A:N6	2.25	0.52
51:1:1997:C:O2'	51:1:1998:A:H5'	2.10	0.52
13:o:31:THR:HG22	13:o:32:PRO:HD2	1.91	0.52
15:q:3:VAL:HG11	51:1:1249:U:H4'	1.92	0.52
34:K:48:ALA:HB1	46:W:68:PRO:HG3	1.91	0.52
35:L:69:ARG:HE	35:L:95:ARG:HG2	1.74	0.52
36:M:55:LYS:HE2	50:3:652:U:O2'	2.08	0.52
46:W:62:ARG:NH1	50:3:718:A:N6	2.57	0.52
50:3:887:G:C2'	50:3:888:G:H5'	2.39	0.52
51:1:1779:U:C5	51:1:1784:A:N7	2.78	0.52
51:1:2553:G:O6	55:8:23:GLN:HG3	2.10	0.52
51:1:2629:U:O2'	51:1:2630:G:H5''	2.10	0.52
29:F:4:ARG:NH2	51:1:2477:U:O2	2.42	0.52
31:H:21:TRP:HA	38:O:95:GLY:HA2	1.92	0.52
50:3:955:U:H1'	50:3:1227:A:H61	1.74	0.52
50:3:1396:A:H4'	50:3:1397:C:H5''	1.91	0.52
51:1:2103:C:H2'	51:1:2104:C:C5	2.45	0.52
51:1:2299:U:H2'	51:1:2300:C:O4'	2.10	0.52
51:1:2396:G:H2'	51:1:2397:G:C8	2.45	0.52
52:2:66:A:H5''	52:2:67:G:OP1	2.10	0.52
1:b:159:THR:H	1:b:194:VAL:CG2	2.21	0.52
4:e:79:ARG:NH2	53:5:56:C:C2	2.77	0.52
7:h:25:ALA:HB1	7:h:99:PHE:CE2	2.44	0.52
8:j:108:MET:HG2	51:1:1006:C:H1'	1.92	0.52
14:p:3:ILE:HD12	14:p:3:ILE:N	2.25	0.52
15:q:23:TYR:CE1	51:1:533:G:H5'	2.45	0.52
16:r:27:ILE:HG13	16:r:28:ALA:N	2.23	0.52
21:w:39:THR:HG21	51:1:2336:A:H61	1.73	0.52
25:B:10:SER:O	25:B:14:MET:HG3	2.10	0.52
51:1:1071:G:H1'	51:1:1089:A:C5	2.45	0.52
51:1:1073:A:H2'	51:1:1074:G:O4'	2.10	0.52
51:1:1997:C:H2'	51:1:1998:A:H8	1.75	0.52
51:1:2059:A:N6	51:1:2503:A:H2'	2.24	0.52
51:1:2282:G:H4'	51:1:2389:G:O2'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:11:MET:HG2	2:c:25:THR:OG1	2.10	0.52
3:d:2:GLU:HB3	3:d:11:ALA:HB1	1.92	0.52
5:f:32:LEU:HD13	5:f:78:VAL:HG22	1.90	0.52
6:g:94:ILE:O	6:g:121:VAL:HG22	2.10	0.52
8:j:113:PRO:HD2	51:1:558:U:OP1	2.10	0.52
23:y:6:LEU:HD23	23:y:6:LEU:O	2.09	0.52
38:O:10:LEU:HD11	38:O:22:THR:HB	1.92	0.52
49:Z:16:ARG:HG3	49:Z:17:ARG:HH22	1.74	0.52
50:3:513:C:H2'	50:3:514:C:H6	1.72	0.52
50:3:884:U:H4'	50:3:885:G:H5''	1.91	0.52
51:1:1982:U:H2'	51:1:1983:G:H8	1.75	0.52
51:1:2861:U:H2'	51:1:2862:G:H8	1.75	0.52
52:2:60:C:H2'	52:2:61:G:H8	1.75	0.52
36:M:26:MET:HE3	36:M:60:LEU:HD11	1.92	0.52
42:S:62:ARG:NH2	50:3:981:U:O3'	2.42	0.52
47:X:30:LEU:H	47:X:48:ILE:HA	1.75	0.52
50:3:1238:A:H2'	50:3:1239:A:H5'	1.92	0.52
50:3:1376:U:H2'	50:3:1377:A:C8	2.45	0.52
51:1:46:G:H2'	51:1:47:C:C6	2.45	0.52
1:b:40:GLY:O	1:b:42:ARG:NH1	2.43	0.52
2:c:55:LYS:HG2	2:c:56:LYS:N	2.25	0.52
3:d:141:MET:HG3	3:d:143:LEU:HG	1.92	0.52
50:3:145:G:H3'	50:3:146:G:H5''	1.90	0.52
50:3:257:G:H2'	50:3:258:G:C8	2.45	0.52
50:3:1028:C:N4	50:3:1033:G:H22	2.08	0.52
51:1:1906:G:C3'	51:1:1907:G:H5''	2.39	0.52
51:1:1979:U:O2'	51:1:1980:G:H5'	2.10	0.52
51:1:2389:G:H5''	51:1:2390:U:O4'	2.09	0.52
2:c:24:VAL:HG11	2:c:188:LEU:HG	1.92	0.51
4:e:69:ALA:H	4:e:82:TYR:H	1.58	0.51
10:l:88:GLY:O	10:l:120:VAL:HG23	2.10	0.51
13:o:103:VAL:HA	13:o:106:LEU:HD12	1.92	0.51
16:r:35:PHE:HB2	16:r:59:ILE:HB	1.91	0.51
49:Z:23:GLU:O	49:Z:25:ALA:N	2.37	0.51
50:3:885:G:H2'	50:3:886:G:H8	1.75	0.51
50:3:1309:G:H2'	50:3:1310:G:C8	2.46	0.51
51:1:1589:U:H2'	51:1:1590:A:C8	2.45	0.51
51:1:2210:U:H6	51:1:2210:U:OP1	1.93	0.51
51:1:2291:U:H2'	51:1:2292:U:C6	2.46	0.51
10:l:73:ILE:HG22	10:l:106:GLU:H	1.76	0.51
15:q:48:ASP:HA	15:q:51:GLN:HB2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:34:ARG:NH2	51:1:467:G:OP2	2.41	0.51
31:H:2:GLN:HG3	31:H:3:LYS:HD2	1.93	0.51
36:M:91:LEU:HD23	36:M:116:ARG:HG3	1.91	0.51
43:T:10:ILE:O	43:T:13:GLU:HG2	2.09	0.51
50:3:54:C:H2'	50:3:352:C:H41	1.75	0.51
50:3:243:A:H4'	50:3:244:U:H3'	1.92	0.51
51:1:1164:C:H2'	51:1:1165:A:H8	1.75	0.51
51:1:1168:G:H1	51:1:1181:U:H3	1.58	0.51
51:1:1909:C:H2'	51:1:1910:G:C8	2.46	0.51
51:1:1917:U:C2'	51:1:1918:A:H5'	2.39	0.51
51:1:2303:G:H2'	51:1:2304:G:H8	1.75	0.51
8:j:27:ARG:HD2	51:1:1012:U:H3	1.75	0.51
9:k:47:ILE:CG1	9:k:48:PRO:HD2	2.38	0.51
34:K:42:TRP:HE1	34:K:61:LEU:HB2	1.76	0.51
50:3:67:C:H2'	50:3:68:G:C8	2.46	0.51
50:3:428:G:H8	50:3:428:G:OP1	1.93	0.51
51:1:145:C:H2'	51:1:146:A:C8	2.46	0.51
51:1:755:U:H2'	51:1:756:A:C8	2.45	0.51
51:1:2772:C:H2'	51:1:2773:C:C6	2.45	0.51
51:1:2786:U:H2'	51:1:2787:C:H6	1.73	0.51
51:1:2834:G:H2'	51:1:2879:A:H61	1.74	0.51
11:m:33:LEU:HD22	11:m:102:LEU:HD13	1.92	0.51
25:B:2:VAL:HG22	25:B:3:GLN:N	2.26	0.51
34:K:3:HIS:CD2	34:K:95:ALA:H	2.28	0.51
42:S:33:VAL:CG2	50:3:1272:G:H5'	2.40	0.51
50:3:810:C:H2'	50:3:811:C:O4'	2.10	0.51
50:3:993:G:N3	50:3:993:G:H2'	2.26	0.51
50:3:1138:G:H3'	50:3:1138:G:N3	2.25	0.51
51:1:95:A:H2'	51:1:96:C:H5''	1.93	0.51
51:1:1592:C:H2'	51:1:1593:A:C8	2.46	0.51
8:j:109:LEU:HD23	8:j:110:PRO:HD2	1.93	0.51
14:p:105:LYS:O	14:p:108:ARG:HG2	2.10	0.51
25:B:2:VAL:HG21	51:1:2016:U:H1'	1.93	0.51
30:G:46:VAL:HG23	30:G:47:PRO:HD3	1.92	0.51
34:K:53:LYS:HB3	34:K:54:LEU:HD23	1.91	0.51
51:1:1335:C:H2'	51:1:1336:A:C8	2.46	0.51
53:5:6:G:C2'	53:5:7:G:H5'	2.40	0.51
55:8:86:ALA:O	55:8:90:ARG:HG3	2.10	0.51
5:f:41:GLU:HG3	5:f:54:ARG:HH21	1.76	0.51
6:g:96:THR:HG23	6:g:97:ARG:N	2.22	0.51
50:3:251:G:H4'	50:3:252:U:O5'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:1086:U:H3	50:3:1099:G:H22	1.58	0.51
50:3:1119:C:H2'	50:3:1120:C:H6	1.74	0.51
51:1:861:A:H2'	51:1:862:G:O4'	2.11	0.51
51:1:1758:U:C5	51:1:2696:U:H5'	2.46	0.51
51:1:2066:C:O2'	51:1:2067:G:H5'	2.10	0.51
51:1:2786:U:H2'	51:1:2787:C:C6	2.46	0.51
53:5:18:G:H1	53:5:55:U:H1'	1.76	0.51
1:b:92:LEU:HD11	1:b:100:ARG:HB3	1.93	0.51
1:b:204:LEU:HB3	1:b:209:ALA:HB3	1.92	0.51
2:c:55:LYS:HG2	2:c:56:LYS:H	1.76	0.51
12:n:63:ARG:NH2	51:1:1454:C:H5'	2.25	0.51
21:w:67:VAL:HB	21:w:74:LYS:HD3	1.92	0.51
32:l:8:LEU:HD23	32:l:18:LEU:HD11	1.93	0.51
34:k:15:SER:O	34:k:18:VAL:HG23	2.10	0.51
39:p:19:VAL:HG23	39:p:34:THR:HG23	1.92	0.51
50:3:80:A:H62	50:3:86:G:H21	1.59	0.51
50:3:1255:G:H2'	50:3:1279:G:H1	1.75	0.51
51:1:519:U:H2'	51:1:520:G:C8	2.46	0.51
51:1:786:C:O2'	51:1:787:C:H5'	2.11	0.51
4:e:97:GLU:O	4:e:101:ARG:HG2	2.11	0.51
5:f:136:ASP:HB2	5:f:139:VAL:HG12	1.92	0.51
16:r:91:GLN:HE21	51:1:993:G:H1'	1.75	0.51
18:t:39:THR:HG22	18:t:42:GLU:HB2	1.93	0.51
50:3:781:A:OP1	50:3:1523:G:H5'	2.10	0.51
50:3:1202:U:H2'	50:3:1203:C:O4'	2.10	0.51
50:3:1228:C:H2'	50:3:1229:A:H8	1.75	0.51
51:1:1410:G:H2'	51:1:1411:U:C6	2.44	0.51
51:1:1815:A:H8	51:1:1815:A:OP1	1.94	0.51
51:1:2302:U:H2'	51:1:2303:G:C8	2.46	0.51
51:1:2760:C:O2'	51:1:2761:A:H5'	2.10	0.51
6:g:116:ARG:HB2	6:g:131:SER:OG	2.11	0.51
10:l:3:LEU:HD23	51:1:1203:U:H5'	1.91	0.51
13:o:33:ARG:HG3	52:2:52:A:H62	1.76	0.51
15:q:36:GLN:NE2	51:1:1252:G:H22	2.09	0.51
21:w:12:SER:HB2	51:1:2262:U:H5	1.76	0.51
32:l:27:ILE:HG13	32:l:28:ASP:H	1.75	0.51
50:3:1323:G:H2'	50:3:1324:A:C8	2.46	0.51
51:1:2039:U:H2'	51:1:2040:G:C8	2.44	0.51
51:1:2207:C:H2'	51:1:2208:C:C6	2.46	0.51
4:e:39:VAL:HG21	4:e:49:LEU:HD13	1.93	0.51
22:x:68:ALA:O	22:x:71:ARG:HG2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Q:89:LEU:C	40:Q:89:LEU:HD23	2.36	0.51
50:3:1230:C:H5'	53:5:30:G:H5''	1.93	0.51
51:1:2529:G:H5''	51:1:2530:A:C5'	2.41	0.51
52:2:35:C:C2'	52:2:36:C:H5'	2.41	0.51
53:5:41:C:H2'	53:5:42:G:C8	2.45	0.51
54:4:9:G:H2'	54:4:10:G:O4'	2.10	0.51
55:8:63:LEU:HD22	55:8:72:ILE:HA	1.93	0.51
10:l:3:LEU:HD23	51:1:1203:U:C4'	2.40	0.50
10:l:62:PRO:HA	51:1:2393:U:O3'	2.11	0.50
13:o:100:HIS:CE1	52:2:38:C:H4'	2.47	0.50
28:E:44:ARG:N	28:E:45:PRO:HD2	2.25	0.50
38:O:37:ARG:HG3	50:3:1124:G:H5''	1.93	0.50
50:3:402:G:H2'	50:3:403:C:C6	2.46	0.50
50:3:1296:C:H4'	50:3:1302:C:N4	2.26	0.50
51:1:399:U:OP1	51:1:2090:A:H5''	2.10	0.50
51:1:871:U:H2'	51:1:872:U:C6	2.46	0.50
51:1:1138:G:H2'	51:1:1139:G:O4'	2.10	0.50
51:1:1326:U:H2'	51:1:1327:A:H8	1.75	0.50
51:1:1344:U:H3'	51:1:1345:C:H5'	1.92	0.50
51:1:1935:G:H1'	51:1:1964:G:N2	2.26	0.50
55:8:20:ILE:HD12	55:8:20:ILE:N	2.26	0.50
11:m:124:LEU:HD12	11:m:126:ILE:H	1.76	0.50
29:F:11:CYS:SG	29:F:14:CYS:N	2.84	0.50
50:3:284:C:H2'	50:3:285:C:C6	2.46	0.50
50:3:751:U:H2'	50:3:752:G:H5'	1.92	0.50
51:1:1310:G:H3'	51:1:1311:G:C8	2.45	0.50
51:1:2625:G:H2'	51:1:2626:C:O4'	2.11	0.50
51:1:2714:G:O2'	51:1:2715:C:H5'	2.12	0.50
51:1:2898:U:H2'	51:1:2899:A:H8	1.76	0.50
55:8:73:LYS:O	55:8:90:ARG:NH1	2.45	0.50
16:r:68:ARG:HA	16:r:92:TRP:HA	1.93	0.50
34:K:40:GLU:HG2	34:K:99:ALA:HA	1.92	0.50
36:M:17:GLN:HE21	36:M:71:VAL:HG12	1.76	0.50
50:3:308:C:H2'	50:3:309:A:C8	2.46	0.50
51:1:845:A:C5	51:1:847:U:H1'	2.46	0.50
51:1:1458:U:H4'	51:1:1459:G:C4	2.46	0.50
51:1:1827:U:C2'	51:1:1828:G:H5'	2.41	0.50
51:1:2048:G:H2'	51:1:2049:G:O4'	2.12	0.50
51:1:2285:C:O2'	51:1:2287:A:H1'	2.11	0.50
51:1:2821:A:H2'	51:1:2822:G:O4'	2.11	0.50
2:c:148:GLN:HE21	51:1:2574:G:H21	1.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:E:32:LEU:N	28:E:32:LEU:HD12	2.27	0.50
37:N:90:ASP:O	37:N:92:SER:N	2.35	0.50
44:U:20:VAL:HG22	44:U:21:VAL:N	2.26	0.50
50:3:204:G:H2'	50:3:205:A:C8	2.47	0.50
50:3:419:C:C2'	50:3:420:U:H5'	2.41	0.50
50:3:724:G:H2'	50:3:725:G:C8	2.46	0.50
50:3:846:G:H2'	50:3:846:G:N3	2.26	0.50
51:1:851:C:H2'	51:1:852:U:C6	2.47	0.50
51:1:1091:G:H2'	51:1:1092:C:C6	2.45	0.50
51:1:1356:G:H2'	51:1:1357:C:C6	2.46	0.50
52:2:3:C:C3'	52:2:4:C:H5''	2.41	0.50
4:e:129:MET:SD	4:e:130:GLY:N	2.85	0.50
9:k:43:ILE:HD12	9:k:43:ILE:N	2.26	0.50
18:t:11:LEU:HD22	18:t:32:LEU:HD11	1.94	0.50
35:L:10:LYS:HD3	35:L:11:ILE:N	2.26	0.50
50:3:68:G:H2'	50:3:69:G:O4'	2.10	0.50
50:3:578:C:H2'	50:3:579:A:C8	2.47	0.50
51:1:1075:C:H5'	51:1:1076:C:C5	2.46	0.50
51:1:2029:G:O6	51:1:2032:G:H5''	2.11	0.50
51:1:2699:C:H2'	51:1:2700:A:C8	2.46	0.50
52:2:48:U:H2'	52:2:49:C:C6	2.46	0.50
55:8:16:GLU:HB2	55:8:41:PHE:HB2	1.94	0.50
1:b:94:LEU:HD13	1:b:100:ARG:HD3	1.94	0.50
47:X:12:LEU:HD12	47:X:13:HIS:N	2.27	0.50
50:3:193:C:O2'	50:3:194:C:H5'	2.10	0.50
50:3:253:A:H2'	50:3:254:G:C8	2.46	0.50
51:1:722:A:H2'	51:1:723:C:C6	2.46	0.50
51:1:881:G:H2'	51:1:882:G:H8	1.75	0.50
51:1:1468:U:H2'	51:1:1522:A:H61	1.76	0.50
51:1:2643:G:H2'	51:1:2644:G:O4'	2.12	0.50
51:1:2703:C:H2'	51:1:2704:C:C6	2.47	0.50
4:e:107:VAL:CG1	4:e:108:PRO:HD3	2.41	0.50
11:m:79:ALA:HA	51:1:2494:G:O2'	2.12	0.50
31:H:182:ASP:HB3	31:H:201:ILE:HB	1.93	0.50
51:1:2102:G:H2'	51:1:2103:C:O4'	2.11	0.50
51:1:2475:C:H2'	51:1:2476:A:H5'	1.94	0.50
51:1:2743:U:H2'	51:1:2744:G:O4'	2.10	0.50
52:2:117:G:C2'	52:2:118:C:H5'	2.41	0.50
52:2:118:C:H2'	52:2:119:A:C8	2.47	0.50
1:b:25:LYS:HA	51:1:1567:G:H22	1.77	0.50
2:c:118:PHE:HB2	51:1:2823:A:OP1	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:m:64:TRP:HB2	11:m:104:GLU:HB2	1.93	0.50
15:q:70:GLN:HE22	15:q:102:LYS:HE3	1.77	0.50
15:q:91:ARG:CD	15:q:91:ARG:H	2.24	0.50
33:J:96:GLN:HB3	33:J:123:LEU:HD12	1.94	0.50
37:N:38:PHE:HD2	37:N:41:GLU:HG2	1.77	0.50
41:R:99:GLN:NE2	50:3:1307:U:OP1	2.45	0.50
50:3:144:G:H2'	50:3:145:G:C8	2.46	0.50
50:3:308:C:H2'	50:3:309:A:H8	1.77	0.50
50:3:604:G:H2'	50:3:605:U:O4'	2.12	0.50
50:3:953:G:H2'	50:3:954:G:O4'	2.12	0.50
51:1:27:G:N2	51:1:512:G:H1'	2.27	0.50
51:1:239:C:H2'	51:1:240:C:O4'	2.11	0.50
51:1:562:U:O4'	51:1:2036:C:H5'	2.12	0.50
51:1:1352:U:O2'	51:1:1353:A:H5'	2.12	0.50
51:1:1355:G:O2'	51:1:1356:G:H5'	2.11	0.50
51:1:2023:C:H2'	51:1:2024:G:C8	2.45	0.50
51:1:2123:G:H22	51:1:2176:A:N6	2.09	0.50
51:1:2149:U:H2'	51:1:2150:C:O4'	2.11	0.50
52:2:2:G:H2'	52:2:3:C:O4'	2.12	0.50
3:d:191:ASP:HA	3:d:194:LYS:HE3	1.94	0.50
4:e:84:ILE:HG21	51:1:2312:U:H5'	1.94	0.50
10:l:74:THR:HG22	10:l:107:PHE:HB2	1.94	0.50
14:p:104:GLY:HA3	50:3:1432:G:OP1	2.12	0.50
18:t:1:MET:HE1	51:1:138:U:H3	1.75	0.50
37:N:17:ARG:HH12	50:3:1129:C:H4'	1.77	0.50
39:P:15:VAL:HG22	39:P:76:TYR:HB3	1.94	0.50
50:3:116:A:H2'	50:3:117:G:O4'	2.12	0.50
50:3:847:G:O2'	50:3:848:C:H5'	2.11	0.50
51:1:363:G:H2'	51:1:364:C:C6	2.47	0.50
51:1:1183:U:H2'	51:1:1184:U:C6	2.47	0.50
51:1:1917:U:O2'	51:1:1918:A:H5'	2.11	0.50
51:1:2326:C:H6	51:1:2326:C:H5''	1.77	0.50
22:x:18:SER:HB2	51:1:2080:A:H5'	1.94	0.49
23:y:11:VAL:HA	23:y:14:LEU:HB2	1.94	0.49
42:S:52:ARG:HH11	50:3:1317:C:N4	2.07	0.49
50:3:1256:A:H4'	50:3:1258:G:C4	2.47	0.49
51:1:581:C:H2'	51:1:582:A:H8	1.76	0.49
55:8:2:ILE:HG23	55:8:2:ILE:O	2.11	0.49
7:h:114:GLU:HA	7:h:123:ILE:HA	1.94	0.49
30:G:111:LYS:HA	30:G:114:LYS:HZ2	1.76	0.49
50:3:59:A:H5''	50:3:387:U:H5''	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:129:A:H1'	50:3:130:A:C8	2.47	0.49
50:3:1026:G:H1	50:3:1035:A:H61	1.61	0.49
50:3:1497:G:C2'	50:3:1498:U:H5'	2.42	0.49
51:1:481:G:H1'	51:1:506:G:H21	1.78	0.49
51:1:706:A:H2'	51:1:707:G:O4'	2.12	0.49
51:1:917:A:H5''	51:1:2268:A:N6	2.26	0.49
51:1:1102:C:H2'	51:1:1103:A:O4'	2.12	0.49
51:1:1278:C:H2'	51:1:1279:G:H8	1.77	0.49
51:1:1947:C:O2'	51:1:1948:G:H5'	2.12	0.49
51:1:2455:G:H2'	51:1:2456:C:C6	2.47	0.49
52:2:30:C:H2'	52:2:31:C:O4'	2.12	0.49
52:2:104:A:H2'	52:2:105:G:O4'	2.12	0.49
2:c:149:ASN:HB3	51:1:2572:A:OP2	2.12	0.49
8:j:93:ILE:HD13	8:j:100:VAL:HG21	1.94	0.49
13:o:33:ARG:O	13:o:34:HIS:CB	2.60	0.49
31:H:62:SER:CB	31:H:97:PRO:HG2	2.42	0.49
44:U:5:ARG:NH2	50:3:376:G:O2'	2.46	0.49
47:X:36:ARG:NH2	50:3:1220:G:OP1	2.46	0.49
50:3:74:A:H2'	50:3:75:G:C8	2.47	0.49
50:3:441:A:H3'	50:3:442:G:H8	1.77	0.49
50:3:540:G:H2'	50:3:541:G:C8	2.47	0.49
50:3:1412:C:H2'	50:3:1413:A:H8	1.76	0.49
51:1:565:C:H4'	51:1:1253:A:C6	2.48	0.49
51:1:1083:U:H2'	51:1:1085:A:OP2	2.12	0.49
51:1:1609:A:H1'	51:1:1616:A:C1'	2.42	0.49
51:1:1904:G:O2'	51:1:1905:C:H5'	2.11	0.49
51:1:2155:U:H2'	51:1:2156:G:H5'	1.94	0.49
51:1:2262:U:H2'	51:1:2263:C:C6	2.47	0.49
1:b:16:VAL:CG2	1:b:203:VAL:HG22	2.43	0.49
7:h:61:ARG:NE	51:1:1046:A:O5'	2.46	0.49
11:m:40:ARG:HB3	11:m:93:VAL:HG11	1.94	0.49
15:q:91:ARG:N	15:q:91:ARG:HD2	2.27	0.49
31:H:96:VAL:HB	31:H:97:PRO:HD2	1.93	0.49
50:3:403:C:O2'	50:3:404:G:H5'	2.12	0.49
51:1:414:C:H2'	51:1:415:A:H8	1.77	0.49
51:1:565:C:H4'	51:1:1253:A:N6	2.28	0.49
51:1:669:G:H2'	51:1:669:G:N3	2.27	0.49
51:1:1149:G:H2'	51:1:1150:C:C6	2.47	0.49
51:1:2233:U:H2'	51:1:2234:G:C8	2.46	0.49
51:1:2800:A:H3'	51:1:2801:G:C5'	2.36	0.49
1:b:259:ASN:HD22	1:b:262:THR:HG22	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:14:VAL:HG21	5:f:79:THR:HG22	1.94	0.49
11:m:57:VAL:HG12	11:m:60:GLN:HB2	1.95	0.49
14:p:61:ARG:NH2	14:p:99:LEU:O	2.46	0.49
28:E:16:THR:OG1	28:E:17:GLY:N	2.43	0.49
32:I:195:ASN:HB3	32:I:197:HIS:ND1	2.27	0.49
37:N:10:ARG:NH2	50:3:1119:C:OP2	2.46	0.49
38:O:10:LEU:HD23	38:O:10:LEU:H	1.77	0.49
50:3:114:U:O2'	50:3:115:G:H5'	2.12	0.49
50:3:1205:U:H2'	50:3:1206:G:H8	1.77	0.49
51:1:554:U:H2'	51:1:555:G:O4'	2.12	0.49
51:1:560:C:H2'	51:1:561:G:O4'	2.13	0.49
51:1:603:A:N6	51:1:655:A:H5'	2.28	0.49
51:1:1100:C:H2'	51:1:1101:U:C4'	2.37	0.49
51:1:1209:U:H2'	51:1:1210:G:H21	1.77	0.49
51:1:2898:U:H2'	51:1:2899:A:C8	2.47	0.49
54:4:12:A:O2'	54:4:13:A:N7	2.45	0.49
11:m:133:LYS:C	11:m:133:LYS:HD3	2.38	0.49
44:U:80:LYS:N	44:U:80:LYS:HD3	2.27	0.49
47:X:50:VAL:HG22	47:X:51:HIS:N	2.27	0.49
50:3:538:G:H2'	50:3:539:A:H8	1.78	0.49
50:3:543:U:H2'	50:3:544:G:H8	1.78	0.49
50:3:684:U:H2'	50:3:685:G:O4'	2.12	0.49
51:1:242:G:N2	51:1:254:G:H2'	2.27	0.49
51:1:322:A:H5'	51:1:340:A:C1'	2.40	0.49
51:1:749:A:H4'	51:1:1271:G:N3	2.27	0.49
51:1:1515:A:H3'	51:1:1516:G:H8	1.78	0.49
51:1:2307:G:H5'	51:1:2308:G:N3	2.28	0.49
51:1:2772:C:H2'	51:1:2773:C:H6	1.78	0.49
2:c:194:PRO:HA	51:1:2680:U:C5'	2.42	0.49
17:s:71:VAL:HG21	17:s:74:ILE:HD11	1.94	0.49
30:G:32:GLY:HA2	30:G:39:ILE:CD1	2.42	0.49
32:I:110:ARG:O	32:I:114:ARG:HG2	2.13	0.49
37:N:74:GLN:NE2	50:3:1249:C:H4'	2.27	0.49
38:O:10:LEU:HD23	38:O:72:ARG:O	2.13	0.49
40:Q:19:ASN:O	40:Q:21:PRO:HD3	2.12	0.49
50:3:250:A:O4'	50:3:252:U:H1'	2.13	0.49
50:3:674:G:H2'	50:3:675:A:C8	2.48	0.49
50:3:865:A:H2'	50:3:866:C:C6	2.48	0.49
51:1:2113:U:H2'	51:1:2119:A:N6	2.28	0.49
2:c:51:THR:HB	2:c:79:LEU:HD23	1.94	0.49
19:u:5:ARG:N	19:u:8:ASP:OD2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S:58:ARG:HH21	50:3:980:C:H4'	1.77	0.49
49:Z:64:ALA:C	49:Z:66:ARG:H	2.20	0.49
50:3:1260:G:H4'	50:3:1283:U:O2'	2.12	0.49
51:1:1277:G:O2'	51:1:1278:C:H5'	2.13	0.49
51:1:1360:G:H2'	51:1:1361:G:H5'	1.94	0.49
51:1:2052:A:H2'	51:1:2053:G:H8	1.77	0.49
51:1:2628:C:H3'	51:1:2629:U:H5'	1.95	0.49
52:2:22:U:H2'	52:2:23:G:C8	2.48	0.49
3:d:130:LYS:HD3	51:1:321:U:OP2	2.12	0.49
30:G:32:GLY:O	30:G:33:ALA:HB3	2.13	0.49
30:G:105:THR:HG21	50:3:1073:U:H1'	1.94	0.49
31:H:9:ILE:HG23	31:H:10:ARG:HG3	1.95	0.49
42:S:39:ASP:HA	42:S:42:ASN:ND2	2.27	0.49
50:3:129:A:O2'	50:3:130:A:H5''	2.13	0.49
50:3:837:U:H2'	50:3:838:G:H8	1.76	0.49
51:1:95:A:C3'	51:1:96:C:H5''	2.43	0.49
51:1:534:U:H2'	51:1:535:G:H8	1.78	0.49
51:1:1295:C:H2'	51:1:1296:G:C8	2.48	0.49
51:1:1654:A:O2'	51:1:1655:A:H5'	2.13	0.49
51:1:2805:C:H2'	51:1:2806:C:C6	2.48	0.49
55:8:37:ILE:HD12	55:8:75:GLN:HA	1.94	0.49
1:b:244:VAL:HG12	1:b:250:GLN:HA	1.95	0.49
11:m:35:ALA:HB2	11:m:102:LEU:HD11	1.93	0.49
11:m:135:VAL:O	11:m:136:MET:HB2	2.13	0.49
36:M:31:LEU:HD22	50:3:643:C:H5''	1.94	0.49
50:3:1514:G:H2'	50:3:1515:G:C8	2.48	0.49
51:1:74:A:H4'	51:1:75:G:O5'	2.12	0.49
51:1:1652:A:H2'	51:1:1653:G:O4'	2.12	0.49
51:1:1812:U:H2'	51:1:1813:G:C8	2.48	0.49
51:1:1842:G:H2'	51:1:1843:C:C6	2.48	0.49
51:1:1882:U:O2'	51:1:1883:U:H5'	2.13	0.49
51:1:2070:A:H2'	51:1:2071:A:H8	1.77	0.49
51:1:2861:U:H2'	51:1:2862:G:C8	2.48	0.49
3:d:58:LYS:HE2	3:d:62:GLN:HB2	1.94	0.48
9:k:1:MET:HG2	9:k:3:GLN:HE22	1.78	0.48
14:p:59:THR:HG22	14:p:72:VAL:HG12	1.94	0.48
17:s:7:HIS:HB3	17:s:103:ILE:HB	1.95	0.48
22:x:60:LYS:NZ	51:1:371:A:O2'	2.41	0.48
26:C:8:ILE:HD11	26:C:33:LEU:HD12	1.93	0.48
50:3:58:C:O2'	50:3:59:A:H5'	2.12	0.48
50:3:838:G:H2'	50:3:839:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:1256:A:H4'	50:3:1258:G:C8	2.47	0.48
51:1:455:C:O2	51:1:472:A:H2'	2.13	0.48
51:1:691:C:O2'	51:1:692:C:H5'	2.12	0.48
51:1:740:C:H5''	51:1:1784:A:OP1	2.13	0.48
51:1:877:A:H2'	51:1:878:A:C8	2.48	0.48
55:8:23:GLN:HB3	55:8:75:GLN:NE2	2.26	0.48
3:d:90:GLN:NE2	51:1:590:A:OP1	2.46	0.48
8:j:109:LEU:HD23	8:j:110:PRO:CD	2.43	0.48
20:v:82:TYR:CE2	20:v:83:LYS:HG3	2.49	0.48
32:l:164:ARG:HG3	32:l:166:LYS:HD3	1.95	0.48
33:j:108:GLY:O	33:j:109:ALA:HB3	2.13	0.48
42:s:42:ASN:HA	42:s:45:LEU:HD12	1.95	0.48
50:3:724:G:H2'	50:3:725:G:H8	1.77	0.48
50:3:981:U:H2'	50:3:982:U:C5	2.48	0.48
51:1:215:G:C4'	51:1:216:A:H4'	2.41	0.48
51:1:677:A:O2'	51:1:2071:A:H5'	2.12	0.48
51:1:694:U:H3	51:1:768:G:H1	1.59	0.48
51:1:704:G:H1'	51:1:727:A:H61	1.78	0.48
51:1:1549:A:H2'	51:1:1550:C:O4'	2.13	0.48
51:1:2572:A:OP1	51:1:2574:G:H4'	2.13	0.48
51:1:2796:U:H2'	51:1:2798:U:OP2	2.12	0.48
1:b:36:ASN:ND2	1:b:61:TYR:HB2	2.27	0.48
4:e:107:VAL:HG12	4:e:108:PRO:HD3	1.95	0.48
9:k:107:LEU:HD23	9:k:107:LEU:O	2.13	0.48
10:l:14:LYS:O	10:l:15:ALA:HB3	2.13	0.48
30:g:129:THR:HG23	30:g:132:GLU:H	1.78	0.48
35:l:10:LYS:NZ	35:l:12:LEU:HD13	2.27	0.48
47:x:39:ILE:HD12	47:x:43:MET:HE3	1.94	0.48
51:1:202:U:H2'	51:1:203:A:O4'	2.13	0.48
51:1:1111:A:C2'	51:1:1112:G:H4'	2.43	0.48
51:1:1744:A:H3'	51:1:1745:A:H8	1.77	0.48
51:1:2216:G:H2'	51:1:2217:G:H8	1.77	0.48
51:1:2238:G:H2'	51:1:2238:G:N3	2.28	0.48
51:1:2391:G:H2'	51:1:2424:C:N4	2.29	0.48
51:1:2743:U:H3'	51:1:2744:G:H5''	1.94	0.48
1:b:94:LEU:HD13	1:b:100:ARG:HE	1.78	0.48
6:g:129:GLU:HG3	6:g:141:LYS:HD2	1.94	0.48
8:j:17:VAL:HG23	8:j:137:PRO:HB2	1.94	0.48
18:t:28:ASN:HD22	18:t:91:GLN:HB3	1.79	0.48
30:g:80:LYS:HG3	30:g:90:PHE:CE1	2.48	0.48
38:o:5:ARG:NH1	38:o:77:VAL:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:189:A:H2'	50:3:190:A:O4'	2.13	0.48
50:3:440:C:H2'	50:3:441:A:H5''	1.94	0.48
50:3:560:A:H4'	50:3:561:U:H5'	1.96	0.48
50:3:1309:G:H2'	50:3:1310:G:H8	1.78	0.48
51:1:983:A:C6	51:1:984:A:C2	3.01	0.48
51:1:1807:G:C2'	51:1:1808:A:H5'	2.39	0.48
51:1:1858:A:C2	51:1:1859:U:H1'	2.48	0.48
51:1:2412:A:H2'	51:1:2413:G:O4'	2.13	0.48
51:1:2543:G:H2'	51:1:2544:G:C8	2.48	0.48
2:c:35:THR:HG22	2:c:73:VAL:HG21	1.95	0.48
7:h:33:VAL:O	7:h:37:LYS:HG2	2.13	0.48
10:l:22:GLY:H	51:1:811:U:H2'	1.78	0.48
11:m:22:GLN:HG3	51:1:907:G:H5'	1.95	0.48
31:H:151:GLU:HG3	31:H:166:TRP:HA	1.95	0.48
32:I:57:LYS:HE2	32:I:202:LEU:HB2	1.94	0.48
37:N:117:LEU:HD22	37:N:123:ARG:HG2	1.95	0.48
47:X:4:LEU:HD23	47:X:6:LYS:N	2.28	0.48
50:3:538:G:H2'	50:3:539:A:C8	2.48	0.48
50:3:858:G:O6	50:3:869:G:H3'	2.14	0.48
50:3:1033:G:H2'	50:3:1034:G:H5'	1.95	0.48
51:1:1127:A:H2'	51:1:1128:G:H5''	1.96	0.48
51:1:1558:C:H4'	51:1:1560:G:OP2	2.14	0.48
51:1:1601:G:O2'	51:1:1602:U:H5'	2.13	0.48
51:1:1786:A:H1'	51:1:1938:A:N6	2.28	0.48
51:1:1810:A:C2'	51:1:1811:G:H5'	2.42	0.48
51:1:1846:G:H2'	51:1:1847:A:O4'	2.13	0.48
51:1:2362:C:H2'	51:1:2363:G:H8	1.78	0.48
51:1:2469:A:H2'	51:1:2470:G:H5'	1.96	0.48
51:1:2585:U:H4'	51:1:2586:U:C5'	2.43	0.48
51:1:2636:C:H2'	51:1:2637:U:C6	2.48	0.48
52:2:60:C:H2'	52:2:61:G:C8	2.48	0.48
1:b:55:GLY:H	51:1:692:C:P	2.37	0.48
5:f:148:ARG:HD2	5:f:163:TYR:CE1	2.49	0.48
13:o:13:ARG:HB2	51:1:2335:A:OP1	2.13	0.48
14:p:26:GLU:OE2	14:p:84:SER:OG	2.32	0.48
24:z:36:GLU:O	24:z:37:ARG:NH1	2.43	0.48
32:I:7:LYS:HB2	32:I:20:LEU:CD2	2.44	0.48
34:K:91:ARG:HG3	34:K:92:THR:H	1.78	0.48
50:3:245:U:O2'	50:3:246:A:H5'	2.13	0.48
51:1:1172:C:C3'	51:1:1173:U:H5''	2.43	0.48
51:1:1287:A:C2'	51:1:1288:G:H5'	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1506:U:H2'	51:1:1507:C:C6	2.48	0.48
51:1:1749:A:H2'	51:1:1750:G:C8	2.48	0.48
51:1:1794:A:H2'	51:1:1795:C:C6	2.49	0.48
51:1:2417:C:H2'	51:1:2418:A:H8	1.78	0.48
52:2:65:U:H3'	52:2:108:A:N6	2.28	0.48
2:c:59:ARG:HH11	51:1:2830:C:H3'	1.79	0.48
4:e:92:GLY:O	4:e:94:ARG:N	2.41	0.48
6:g:70:GLU:HB2	6:g:134:VAL:HG21	1.94	0.48
18:t:65:GLY:H	18:t:79:ASP:CG	2.21	0.48
30:G:118:THR:O	30:G:121:GLN:HG2	2.13	0.48
36:M:80:PRO:HG2	50:3:878:A:H5''	1.94	0.48
41:R:89:ARG:HG3	41:R:96:VAL:HA	1.96	0.48
43:T:22:GLY:O	50:3:751:U:H1'	2.14	0.48
44:U:19:VAL:HG13	44:U:36:VAL:HB	1.96	0.48
50:3:210:C:H5'	50:3:211:G:C2	2.48	0.48
50:3:584:G:H2'	50:3:585:G:H8	1.78	0.48
50:3:1014:A:N3	50:3:1219:A:H1'	2.27	0.48
51:1:2110:G:H5'	51:1:2145:C:N4	2.29	0.48
51:1:2123:G:H22	51:1:2176:A:H61	1.62	0.48
51:1:2897:U:H2'	51:1:2898:U:C6	2.49	0.48
1:b:75:ALA:HB2	1:b:95:TYR:CD1	2.48	0.48
2:c:33:ARG:NH2	2:c:74:GLU:HB2	2.29	0.48
2:c:133:THR:HG23	2:c:134:HIS:CD2	2.49	0.48
8:j:36:LEU:HD11	8:j:122:LEU:HD13	1.95	0.48
15:q:5:ARG:HD2	51:1:1250:G:H5''	1.94	0.48
33:J:89:THR:O	33:J:134:ASN:ND2	2.47	0.48
42:S:11:LYS:O	42:S:15:LEU:HD13	2.13	0.48
45:V:39:ARG:HD2	50:3:280:C:O2'	2.14	0.48
50:3:745:G:H5'	50:3:851:G:H21	1.79	0.48
50:3:1060:U:H2'	50:3:1061:G:H8	1.78	0.48
50:3:1306:A:H62	50:3:1331:G:H1'	1.78	0.48
51:1:1842:G:H2'	51:1:1843:C:H6	1.79	0.48
52:2:91:C:H2'	52:2:92:C:H6	1.79	0.48
13:o:68:LYS:HZ1	13:o:101:GLY:HA2	1.79	0.48
25:B:49:ARG:HG3	51:1:2884:U:C6	2.48	0.48
30:G:82:ALA:HB2	30:G:213:LEU:HD21	1.95	0.48
37:N:89:TYR:CD2	37:N:93:LEU:HB3	2.49	0.48
41:R:3:ILE:HG23	41:R:7:ASN:HD22	1.79	0.48
44:U:14:ARG:HD2	44:U:14:ARG:O	2.14	0.48
49:Z:5:VAL:HG22	49:Z:7:GLU:HG2	1.96	0.48
49:Z:35:GLU:O	49:Z:37:TYR:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:681:A:H2'	50:3:682:G:C8	2.49	0.48
50:3:1316:G:H2'	50:3:1317:C:H5'	1.95	0.48
51:1:7:G:H2'	51:1:8:C:C6	2.48	0.48
51:1:856:G:H2'	51:1:857:G:C8	2.49	0.48
51:1:1447:C:H2'	51:1:1448:G:H8	1.79	0.48
51:1:2859:G:H2'	51:1:2860:A:C8	2.48	0.48
8:j:47:HIS:ND1	8:j:48:VAL:HG23	2.28	0.48
15:q:30:VAL:CG2	15:q:33:VAL:HG12	2.43	0.48
20:v:9:ARG:HD3	20:v:39:ALA:HB1	1.94	0.48
21:w:39:THR:N	51:1:2331:G:H4'	2.04	0.48
42:S:7:ALA:HB1	50:3:995:C:H5'	1.95	0.48
50:3:419:C:O2'	50:3:420:U:H5'	2.14	0.48
51:1:4:U:H2'	51:1:5:A:C8	2.48	0.48
51:1:1343:G:N3	51:1:1343:G:H2'	2.28	0.48
51:1:1837:C:H2'	51:1:1899:A:H61	1.79	0.48
51:1:2241:A:H2'	51:1:2242:G:C8	2.49	0.48
51:1:2636:C:O2'	51:1:2637:U:H5'	2.14	0.48
2:c:85:ALA:HB3	2:c:88:GLU:OE1	2.14	0.47
3:d:31:VAL:HG21	3:d:104:ALA:HB2	1.96	0.47
10:l:23:ILE:HG13	16:r:82:HIS:NE2	2.29	0.47
10:l:79:LEU:HD23	10:l:112:LEU:HA	1.96	0.47
15:q:47:ARG:HG3	51:1:1156:A:N6	2.29	0.47
15:q:82:LEU:CD2	15:q:87:VAL:HB	2.44	0.47
23:y:44:LYS:HE3	51:1:61:C:OP1	2.13	0.47
25:B:8:THR:OG1	25:B:9:ARG:N	2.47	0.47
30:G:32:GLY:HA2	30:G:39:ILE:HD12	1.95	0.47
32:I:73:ASN:O	32:I:77:GLU:HG3	2.14	0.47
37:N:38:PHE:HB2	37:N:41:GLU:OE2	2.14	0.47
50:3:603:U:H2'	50:3:604:G:H8	1.78	0.47
50:3:622:A:H2'	50:3:623:C:H5'	1.96	0.47
50:3:1327:C:H2'	50:3:1328:C:C6	2.48	0.47
51:1:139:U:H5'	51:1:140:C:C4'	2.43	0.47
51:1:351:C:O2'	51:1:352:A:H5'	2.13	0.47
51:1:1052:C:H2'	51:1:1053:C:H6	1.78	0.47
51:1:1766:G:O2'	51:1:1767:G:H5'	2.13	0.47
1:b:13:ARG:NH2	51:1:1693:U:O2	2.39	0.47
2:c:151:THR:HB	2:c:152:PRO:CD	2.39	0.47
24:z:44:ARG:HD3	24:z:47:ILE:HD12	1.97	0.47
32:I:95:GLY:HA2	32:I:136:VAL:HG22	1.96	0.47
35:L:74:VAL:HB	35:L:85:GLN:HB3	1.96	0.47
38:O:17:LEU:O	38:O:20:GLN:NE2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:440:C:H2'	50:3:441:A:C5'	2.44	0.47
51:1:1055:G:H1	51:1:1104:C:H42	1.60	0.47
51:1:1170:C:H2'	51:1:1171:G:C8	2.49	0.47
51:1:1219:U:H2'	51:1:1220:G:H8	1.79	0.47
51:1:1287:A:H2'	51:1:1288:G:H5'	1.96	0.47
53:5:47:U:H3'	53:5:48:C:H5''	1.96	0.47
1:b:75:ALA:HB2	1:b:95:TYR:CE1	2.49	0.47
7:h:67:THR:HG23	7:h:68:PRO:HD3	1.96	0.47
12:n:2:ARG:HA	12:n:5:LYS:HD2	1.96	0.47
25:B:1:ALA:HA	51:1:2577:A:H2	1.79	0.47
30:G:100:LEU:O	30:G:102:ASN:N	2.47	0.47
31:H:72:PRO:HD3	31:H:104:GLU:CD	2.40	0.47
33:J:28:ARG:NH2	50:3:1396:A:O3'	2.48	0.47
33:J:151:MET:SD	33:J:155:LYS:NZ	2.87	0.47
43:T:17:ASP:HB2	43:T:20:ASP:HB2	1.96	0.47
50:3:37:U:H2'	50:3:38:G:O4'	2.14	0.47
50:3:396:C:C3'	50:3:397:A:H5''	2.44	0.47
51:1:473:G:C2'	51:1:474:G:H5'	2.44	0.47
51:1:2156:G:C2'	51:1:2157:G:H5'	2.44	0.47
51:1:2579:C:O2'	51:1:2580:U:H5'	2.14	0.47
51:1:2743:U:C3'	51:1:2744:G:H5''	2.44	0.47
53:5:17:C:H4'	53:5:61:C:OP1	2.14	0.47
4:e:134:GLN:HE22	4:e:145:VAL:HG13	1.79	0.47
8:j:1:MET:SD	8:j:1:MET:N	2.86	0.47
19:u:5:ARG:HB2	19:u:93:ARG:NH2	2.30	0.47
32:I:33:ILE:HG12	32:I:34:GLU:HG3	1.96	0.47
44:U:3:THR:HG23	44:U:66:THR:HG23	1.97	0.47
50:3:41:G:H2'	50:3:42:G:H8	1.79	0.47
50:3:297:G:H4'	50:3:557:G:H4'	1.96	0.47
50:3:319:G:O2'	50:3:320:A:H5'	2.15	0.47
50:3:376:G:O2'	50:3:377:G:H5'	2.15	0.47
50:3:555:U:H2'	50:3:556:C:C6	2.49	0.47
50:3:767:A:H2'	50:3:768:A:H8	1.80	0.47
50:3:1243:C:H2'	50:3:1244:G:H8	1.80	0.47
50:3:1429:A:H2'	50:3:1430:A:H8	1.77	0.47
51:1:207:A:H2'	51:1:208:C:O4'	2.14	0.47
51:1:441:U:H2'	51:1:442:G:C8	2.49	0.47
51:1:779:U:H2'	51:1:780:G:C8	2.49	0.47
51:1:1177:G:C2'	51:1:1178:C:H4'	2.37	0.47
51:1:1571:A:H2'	51:1:1572:A:C8	2.49	0.47
51:1:2200:C:O2'	51:1:2201:G:H5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2276:G:O2'	51:1:2277:G:H5'	2.13	0.47
52:2:111:U:H2'	52:2:112:G:H8	1.78	0.47
1:b:269:ARG:HG2	1:b:270:ARG:H	1.80	0.47
10:l:110:VAL:HB	10:l:127:VAL:HG12	1.96	0.47
28:E:32:LEU:HB3	28:E:40:LYS:HD3	1.95	0.47
36:M:40:LYS:HZ2	36:M:47:ASP:H	1.62	0.47
37:N:98:ARG:O	37:N:100:ALA:N	2.38	0.47
38:O:6:ILE:HD12	38:O:6:ILE:N	2.29	0.47
47:X:76:THR:HG23	47:X:77:ARG:HG3	1.97	0.47
48:Y:79:THR:O	48:Y:82:ILE:HG22	2.13	0.47
50:3:843:U:H5'	50:3:844:G:C8	2.49	0.47
50:3:1527:U:H2'	50:3:1528:U:C6	2.49	0.47
51:1:288:U:H2'	51:1:289:G:H8	1.80	0.47
51:1:886:A:H3'	51:1:887:U:H4'	1.95	0.47
51:1:1000:A:H2'	51:1:1001:A:C8	2.48	0.47
51:1:1447:C:H2'	51:1:1448:G:C8	2.50	0.47
51:1:1508:A:H2'	51:1:1509:A:O4'	2.14	0.47
51:1:1769:U:H2'	51:1:1770:G:H8	1.80	0.47
51:1:1773:A:N7	51:1:1829:A:H1'	2.28	0.47
51:1:2088:A:H2'	51:1:2089:C:C6	2.48	0.47
2:c:81:GLU:CD	51:1:2636:C:H4'	2.40	0.47
9:k:26:GLY:HA3	9:k:30:ARG:NH1	2.30	0.47
32:I:131:ILE:HD13	50:3:620:C:C2	2.49	0.47
32:I:163:GLN:O	32:I:163:GLN:HG2	2.14	0.47
44:U:18:GLN:HA	44:U:38:PHE:HA	1.96	0.47
45:V:61:ARG:CD	45:V:75:VAL:HG22	2.40	0.47
47:X:38:THR:OG1	47:X:39:ILE:N	2.48	0.47
50:3:75:G:C2'	50:3:76:G:H5'	2.45	0.47
50:3:891:U:O2'	50:3:892:A:H5'	2.14	0.47
50:3:961:U:O5'	50:3:961:U:H6	1.97	0.47
50:3:1114:C:H2'	50:3:1115:U:C6	2.50	0.47
51:1:1159:U:O2'	51:1:1160:G:H5'	2.15	0.47
51:1:1404:C:O2'	51:1:1405:U:H5'	2.15	0.47
51:1:1946:U:H2'	51:1:1947:C:C6	2.48	0.47
51:1:2385:C:H2'	51:1:2386:A:C8	2.49	0.47
1:b:94:LEU:HD13	1:b:100:ARG:NE	2.29	0.47
3:d:5:LEU:HG	3:d:120:VAL:O	2.14	0.47
3:d:68:ALA:HA	51:1:1255:U:C6	2.50	0.47
4:e:47:LYS:O	4:e:50:ASP:OD1	2.32	0.47
4:e:62:GLN:HE21	4:e:88:VAL:HG13	1.80	0.47
4:e:90:LEU:HD11	4:e:94:ARG:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:21:VAL:HG22	6:g:22:LYS:N	2.27	0.47
10:l:22:GLY:H	51:1:811:U:C2'	2.28	0.47
15:q:36:GLN:NE2	51:1:1252:G:H1	2.13	0.47
15:q:57:ARG:NH2	15:q:91:ARG:HH12	2.11	0.47
16:r:63:VAL:HG12	16:r:96:VAL:HG12	1.97	0.47
32:I:13:ARG:CZ	50:3:543:U:H5''	2.45	0.47
32:I:28:ASP:HB2	32:I:33:ILE:HG22	1.97	0.47
36:M:3:GLN:HE21	50:3:755:G:N2	2.12	0.47
36:M:9:MET:O	36:M:13:ILE:HG13	2.14	0.47
36:M:60:LEU:N	36:M:60:LEU:HD23	2.29	0.47
36:M:65:PHE:CD2	36:M:66:GLN:HG2	2.50	0.47
36:M:91:LEU:HD12	36:M:92:PRO:HD2	1.97	0.47
40:Q:26:CYS:CB	40:Q:29:LYS:HE2	2.45	0.47
40:Q:92:VAL:C	40:Q:93:ARG:HD3	2.40	0.47
42:S:18:LYS:HD3	50:3:1007:U:OP1	2.15	0.47
50:3:635:A:H2'	50:3:636:U:C6	2.49	0.47
50:3:1211:U:H4'	50:3:1213:A:C4	2.49	0.47
50:3:1485:U:O2'	50:3:1486:G:H5'	2.14	0.47
50:3:1486:G:H2'	50:3:1487:G:C8	2.50	0.47
51:1:95:A:H3'	51:1:96:C:H5''	1.95	0.47
51:1:257:C:H2'	51:1:258:G:O4'	2.15	0.47
51:1:259:G:O2'	51:1:260:G:H5'	2.14	0.47
51:1:502:A:H2'	51:1:503:A:H5'	1.97	0.47
51:1:962:G:O2'	51:1:963:U:H5'	2.15	0.47
51:1:1020:A:C1'	51:1:1021:A:OP2	2.55	0.47
51:1:1074:G:H2'	51:1:1075:C:H5''	1.96	0.47
51:1:1672:A:C2	51:1:2582:G:H5'	2.50	0.47
51:1:1856:U:H2'	51:1:1857:G:O4'	2.15	0.47
51:1:1890:A:H2'	51:1:1891:G:O4'	2.15	0.47
51:1:2443:C:H2'	51:1:2444:G:C8	2.49	0.47
51:1:2592:G:H2'	51:1:2593:U:O4'	2.15	0.47
53:5:53:G:H2'	53:5:54:U:C6	2.49	0.47
54:4:6:G:O2'	54:4:7:G:H5'	2.15	0.47
3:d:77:ILE:HD11	51:1:1256:G:H1'	1.96	0.47
13:o:94:ARG:NH2	51:1:2293:G:H5''	2.30	0.47
39:P:124:LYS:HE2	50:3:1524:C:OP2	2.14	0.47
40:Q:106:VAL:HB	40:Q:109:ARG:HD2	1.97	0.47
42:S:66:THR:HG22	50:3:1203:C:H4'	1.97	0.47
48:Y:59:ARG:NH1	50:3:177:G:OP1	2.48	0.47
50:3:246:A:N3	50:3:247:G:H1'	2.29	0.47
50:3:502:A:H2'	50:3:503:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:1245:C:H2'	50:3:1246:A:C8	2.50	0.47
50:3:1293:C:H2'	50:3:1294:G:H8	1.80	0.47
51:1:548:G:H3'	51:1:549:G:H5''	1.97	0.47
51:1:686:U:H3'	51:1:687:C:H5'	1.96	0.47
51:1:1026:G:H2'	51:1:1027:A:H8	1.80	0.47
51:1:2224:G:H4'	51:1:2226:C:N3	2.30	0.47
17:s:71:VAL:HG13	17:s:71:VAL:O	2.14	0.47
24:z:52:PHE:CD2	52:2:83:G:H4'	2.50	0.47
32:I:9:LYS:HG2	32:I:12:ARG:HH21	1.80	0.47
36:M:95:MET:HB3	36:M:98:LEU:HG	1.96	0.47
37:N:122:ARG:NH1	37:N:123:ARG:O	2.47	0.47
49:Z:26:GLY:HA2	54:4:9:G:H5'	1.95	0.47
49:Z:29:ALA:HA	49:Z:32:ARG:HD2	1.96	0.47
50:3:977:A:H3'	50:3:977:A:N3	2.29	0.47
50:3:1228:C:H2'	50:3:1229:A:C8	2.50	0.47
51:1:804:A:H2'	51:1:806:C:C4	2.50	0.47
51:1:1063:G:H22	51:1:1075:C:N4	2.11	0.47
51:1:1103:A:H2'	51:1:1103:A:N3	2.30	0.47
51:1:2619:C:H2'	51:1:2620:C:C6	2.49	0.47
51:1:2686:G:H2'	51:1:2687:U:O4'	2.15	0.47
55:8:3:VAL:HG12	55:8:10:ILE:O	2.15	0.47
5:f:8:VAL:HB	5:f:49:LEU:HB2	1.97	0.47
10:l:118:THR:HA	10:l:119:PRO:HD3	1.80	0.47
13:o:31:THR:HG21	52:2:28:C:OP1	2.14	0.47
17:s:79:GLY:HA2	51:1:25:U:H5'	1.95	0.47
25:B:16:ARG:HA	25:B:19:ASP:HB2	1.96	0.47
30:G:145:ASN:OD1	30:G:146:SER:N	2.48	0.47
32:I:87:GLU:N	32:I:87:GLU:OE2	2.47	0.47
47:X:4:LEU:HD22	47:X:7:GLY:O	2.15	0.47
50:3:123:U:H5''	50:3:311:C:O2'	2.15	0.47
50:3:407:U:H2'	50:3:408:A:H8	1.80	0.47
50:3:738:C:H2'	50:3:739:C:C6	2.49	0.47
50:3:1218:C:H2'	50:3:1219:A:H8	1.79	0.47
50:3:1245:C:H2'	50:3:1246:A:H8	1.79	0.47
51:1:1087:G:H5''	51:1:1088:A:OP2	2.15	0.47
51:1:1432:G:H2'	51:1:1433:A:C8	2.50	0.47
51:1:1911:U:H2'	51:1:1918:A:C2	2.50	0.47
51:1:2405:G:H2'	51:1:2411:A:H62	1.80	0.47
52:2:55:U:O2'	52:2:56:G:H5'	2.15	0.47
53:5:76:A:H5''	55:8:26:GLY:O	2.15	0.47
3:d:69:ARG:HD3	51:1:674:G:H1'	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:24:SER:HG	7:h:116:GLU:H	1.60	0.46
8:j:78:THR:HG21	51:1:2642:G:OP1	2.15	0.46
8:j:84:ILE:HG23	8:j:84:ILE:O	2.15	0.46
23:y:31:GLN:HG2	23:y:37:LEU:HB2	1.97	0.46
28:E:62:PRO:HG2	28:E:63:TYR:H	1.80	0.46
31:H:122:GLN:OE1	31:H:125:ARG:NH2	2.48	0.46
32:I:154:VAL:HA	32:I:157:ALA:HB3	1.97	0.46
50:3:90:C:H2'	50:3:91:U:C6	2.50	0.46
50:3:1186:G:O2'	50:3:1187:G:H5'	2.14	0.46
51:1:807:U:H2'	51:1:808:G:C8	2.47	0.46
51:1:1609:A:H1'	51:1:1616:A:O4'	2.15	0.46
51:1:2362:C:H2'	51:1:2363:G:C8	2.50	0.46
51:1:2464:G:H2'	51:1:2465:C:C6	2.49	0.46
53:5:71:C:H2'	53:5:72:A:C8	2.50	0.46
55:8:121:SER:HA	55:8:125:LYS:HE2	1.97	0.46
1:b:36:ASN:HD21	1:b:61:TYR:HB2	1.80	0.46
1:b:57:HIS:CE1	51:1:1567:G:H5'	2.50	0.46
1:b:144:GLU:HA	1:b:151:GLY:HA2	1.97	0.46
6:g:99:ILE:O	6:g:103:VAL:HG23	2.16	0.46
9:k:19:VAL:HG11	9:k:41:ILE:HD12	1.97	0.46
9:k:58:LEU:HA	9:k:89:ASN:HD22	1.80	0.46
20:v:14:LYS:HB2	52:2:98:G:N1	2.30	0.46
22:x:13:THR:OG1	51:1:188:G:H5'	2.15	0.46
36:M:113:ARG:HA	36:M:116:ARG:HH21	1.80	0.46
41:R:113:LYS:HB3	41:R:114:PRO:HD3	1.96	0.46
50:3:220:G:O2'	50:3:221:C:H5'	2.15	0.46
50:3:335:C:H2'	50:3:336:A:C8	2.51	0.46
50:3:436:C:H2'	50:3:437:U:C6	2.50	0.46
50:3:477:C:H2'	50:3:478:A:C8	2.50	0.46
50:3:1368:A:O2'	50:3:1369:C:H5'	2.16	0.46
51:1:45:G:C5'	51:1:46:G:H5'	2.23	0.46
51:1:2485:G:O2'	51:1:2486:C:H5'	2.16	0.46
51:1:2734:A:H2'	51:1:2735:G:O4'	2.15	0.46
52:2:14:U:H5'	52:2:71:C:O4'	2.16	0.46
2:c:161:MET:HG2	2:c:162:ALA:H	1.80	0.46
7:h:55:VAL:HG22	51:1:1084:A:OP1	2.15	0.46
10:l:33:ARG:CD	51:1:587:C:H42	2.27	0.46
13:o:93:ASP:OD2	13:o:95:SER:HB3	2.15	0.46
16:r:49:ILE:HG22	16:r:54:VAL:HG22	1.96	0.46
36:M:6:ILE:HA	36:M:9:MET:HE2	1.97	0.46
41:R:47:LEU:HD23	41:R:48:SER:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:W:48:ALA:O	46:W:52:ARG:HG2	2.16	0.46
50:3:938:A:H1'	50:3:1376:U:O2'	2.15	0.46
50:3:1340:A:O2'	50:3:1341:U:H5'	2.15	0.46
51:1:6:A:H2'	51:1:7:G:C8	2.50	0.46
51:1:537:G:H22	51:1:555:G:H2'	1.80	0.46
51:1:2703:C:H2'	51:1:2704:C:H6	1.80	0.46
10:l:51:GLU:N	10:l:51:GLU:OE1	2.48	0.46
12:n:69:ARG:O	12:n:70:THR:OG1	2.32	0.46
13:o:34:HIS:CE1	52:2:27:C:H5''	2.49	0.46
31:H:62:SER:HB2	31:H:97:PRO:HG2	1.97	0.46
32:I:7:LYS:HB2	32:I:20:LEU:HG	1.97	0.46
34:K:92:THR:OG1	34:K:93:LYS:N	2.31	0.46
41:R:25:GLY:H	50:3:1329:A:H5''	1.81	0.46
42:S:29:ILE:HG23	42:S:30:ILE:HG23	1.98	0.46
45:V:30:HIS:HB2	45:V:37:ILE:HD11	1.97	0.46
45:V:33:TYR:HE1	50:3:564:C:H5'	1.80	0.46
46:W:41:SER:HA	46:W:44:THR:HG22	1.97	0.46
49:Z:28:LEU:O	49:Z:32:ARG:HG3	2.15	0.46
50:3:113:G:H1'	50:3:354:G:H5''	1.97	0.46
50:3:1515:G:H2'	50:3:1516:G:H8	1.81	0.46
51:1:2026:U:H2'	51:1:2027:G:C8	2.50	0.46
51:1:2040:G:O2'	51:1:2041:U:H5'	2.16	0.46
52:2:1:U:H3	52:2:119:A:H61	1.64	0.46
1:b:228:ASP:CG	51:1:780:G:H1	2.22	0.46
7:h:119:PRO:HG2	7:h:121:SER:H	1.80	0.46
8:j:120:ARG:HD3	51:1:2780:G:OP2	2.16	0.46
17:s:55:ILE:HG21	17:s:66:ILE:HD12	1.98	0.46
31:H:19:SER:HB2	31:H:21:TRP:HE1	1.80	0.46
32:I:109:THR:HG23	32:I:112:GLU:HB3	1.97	0.46
45:V:20:ILE:HG12	45:V:47:ASP:OD2	2.16	0.46
50:3:1195:C:H2'	50:3:1197:A:O4'	2.16	0.46
50:3:1390:U:H2'	50:3:1391:U:C6	2.50	0.46
51:1:576:U:H2'	51:1:577:G:H8	1.79	0.46
51:1:1502:A:H2'	51:1:1503:A:O4'	2.14	0.46
51:1:2676:C:H2'	51:1:2677:G:C8	2.51	0.46
51:1:2828:G:H2'	51:1:2829:A:H8	1.80	0.46
1:b:269:ARG:HG2	1:b:270:ARG:N	2.31	0.46
4:e:29:ARG:HH12	4:e:31:GLU:HA	1.80	0.46
32:I:73:ASN:HA	32:I:76:LYS:HE3	1.98	0.46
34:K:42:TRP:CH2	46:W:23:LYS:HB2	2.51	0.46
35:L:2:ARG:HB2	50:3:933:G:OP2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:224:U:H2'	50:3:225:C:C6	2.51	0.46
51:1:15:G:O2'	51:1:16:C:H5'	2.15	0.46
51:1:660:C:H2'	51:1:661:A:C8	2.50	0.46
51:1:894:U:H2'	51:1:895:U:O4'	2.15	0.46
1:b:140:VAL:HG12	1:b:191:LEU:HA	1.97	0.46
1:b:261:ARG:HB3	51:1:2227:A:O2'	2.16	0.46
7:h:70:GLU:O	7:h:71:CYS:SG	2.74	0.46
8:j:81:ILE:HD12	8:j:81:ILE:N	2.31	0.46
14:p:64:SER:OG	14:p:65:ASN:N	2.47	0.46
31:H:18:ASN:ND2	42:S:89:ARG:O	2.49	0.46
43:T:44:GLU:C	43:T:46:LYS:H	2.24	0.46
48:Y:27:MET:HE1	48:Y:57:VAL:HA	1.97	0.46
50:3:410:G:H2'	50:3:429:U:C4	2.51	0.46
50:3:976:G:H2'	50:3:1362:A:N1	2.30	0.46
50:3:1028:C:H3'	50:3:1029:U:C5'	2.46	0.46
50:3:1488:G:O2'	50:3:1489:G:H5'	2.16	0.46
51:1:481:G:N1	51:1:507:A:H1'	2.30	0.46
51:1:1059:G:H2'	51:1:1060:U:C5	2.51	0.46
51:1:1314:C:H42	51:1:1338:G:H1	1.63	0.46
51:1:1932:A:H2'	51:1:1933:G:O4'	2.15	0.46
8:j:88:THR:OG1	8:j:91:GLU:HG2	2.16	0.46
13:o:30:ARG:HH22	52:2:48:U:P	2.39	0.46
14:p:91:VAL:HG21	14:p:96:LEU:HD21	1.98	0.46
15:q:27:ARG:NH2	51:1:532:A:H3'	2.31	0.46
15:q:91:ARG:CD	15:q:91:ARG:N	2.79	0.46
17:s:49:LYS:O	17:s:52:GLU:HG3	2.15	0.46
39:P:80:ASN:OD1	39:P:80:ASN:N	2.49	0.46
43:T:74:VAL:O	43:T:77:TYR:HB3	2.16	0.46
44:U:57:ILE:O	44:U:61:VAL:HG22	2.15	0.46
50:3:187:G:H2'	50:3:189:A:OP2	2.16	0.46
50:3:335:C:H2'	50:3:336:A:H8	1.81	0.46
50:3:1002:G:H2'	50:3:1003:G:C8	2.51	0.46
51:1:1273:U:H5''	51:1:1646:C:H41	1.80	0.46
51:1:2078:C:H2'	51:1:2079:U:C6	2.51	0.46
51:1:2838:G:H2'	51:1:2839:G:C8	2.50	0.46
22:x:60:LYS:HZ2	51:1:372:G:C5'	2.18	0.46
30:G:151:LYS:HD2	30:G:152:ASP:OD2	2.15	0.46
31:H:179:ALA:HB1	31:H:202:PHE:HE1	1.81	0.46
34:K:10:VAL:HG22	34:K:58:HIS:HB3	1.98	0.46
47:X:40:PHE:H	47:X:43:MET:HE2	1.81	0.46
50:3:151:A:H2'	50:3:152:A:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:410:G:H2'	50:3:429:U:O4	2.16	0.46
50:3:415:A:N6	50:3:428:G:H1	2.14	0.46
50:3:478:A:H2'	50:3:479:U:C4'	2.45	0.46
50:3:1164:G:H2'	50:3:1165:U:C6	2.51	0.46
51:1:279:A:H2'	51:1:280:U:O4'	2.16	0.46
51:1:598:U:H2'	51:1:599:A:C8	2.51	0.46
51:1:1239:G:H2'	51:1:1240:U:O4'	2.14	0.46
51:1:1368:G:H2'	51:1:1369:G:H8	1.81	0.46
51:1:1742:U:H2'	51:1:1743:G:O4'	2.16	0.46
51:1:1827:U:H2'	51:1:1828:G:O4'	2.15	0.46
51:1:2427:C:H5''	51:1:2429:G:H5'	1.97	0.46
53:5:8:U:H4'	53:5:48:C:H4'	1.97	0.46
2:c:148:GLN:HE21	51:1:2574:G:N2	2.14	0.46
5:f:19:ASN:O	5:f:22:VAL:HG12	2.16	0.46
7:h:67:THR:H	7:h:68:PRO:CD	2.28	0.46
9:k:41:ILE:HD13	9:k:60:ALA:HB2	1.98	0.46
12:n:54:LEU:HD21	12:n:65:LEU:HB3	1.97	0.46
12:n:57:THR:HG23	12:n:62:ASN:HD21	1.80	0.46
14:p:111:GLU:HB2	14:p:113:LEU:HG	1.98	0.46
23:y:1:MET:O	23:y:5:GLU:HG3	2.16	0.46
24:z:8:GLN:HG3	24:z:53:MET:HE1	1.96	0.46
35:L:41:ILE:HD13	35:L:115:MET:HG2	1.97	0.46
50:3:285:C:H2'	50:3:286:C:C6	2.51	0.46
50:3:570:G:H5'	50:3:820:U:O4'	2.16	0.46
50:3:700:G:O2'	50:3:701:U:H5''	2.16	0.46
50:3:1476:A:H2'	50:3:1477:U:C6	2.51	0.46
50:3:1506:U:O2'	50:3:1507:A:H5'	2.15	0.46
51:1:139:U:H3'	51:1:140:C:H5'	1.98	0.46
51:1:254:G:C2'	51:1:255:A:H5''	2.44	0.46
51:1:609:A:H2'	51:1:610:C:O4'	2.17	0.46
51:1:1186:G:H2'	51:1:1187:G:O4'	2.16	0.46
51:1:1370:C:H2'	51:1:1371:G:O4'	2.15	0.46
51:1:1601:G:C2'	51:1:1602:U:H5'	2.46	0.46
51:1:2346:A:H3'	51:1:2347:C:C5'	2.46	0.46
52:2:49:C:H2'	52:2:50:A:H8	1.80	0.46
5:f:142:GLN:HE22	51:1:2744:G:H21	1.63	0.45
15:q:27:ARG:NH2	51:1:532:A:H5'	2.31	0.45
33:J:92:ARG:O	33:J:93:VAL:C	2.59	0.45
50:3:110:C:H2'	50:3:111:G:O4'	2.16	0.45
50:3:323:U:H2'	50:3:324:G:O4'	2.17	0.45
50:3:857:C:H2'	50:3:858:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:621:A:H2'	51:1:622:G:O4'	2.16	0.45
51:1:624:C:O2'	51:1:657:U:H5''	2.16	0.45
51:1:854:C:O2'	51:1:855:G:H5'	2.17	0.45
51:1:879:G:H1	51:1:898:C:H42	1.63	0.45
51:1:1077:A:H2'	51:1:1078:U:O4'	2.16	0.45
51:1:1592:C:H2'	51:1:1593:A:H8	1.80	0.45
51:1:2345:G:C5'	51:1:2347:C:H5'	2.45	0.45
1:b:46:GLY:HA3	51:1:773:U:C5'	2.44	0.45
1:b:229:HIS:ND1	1:b:230:PRO:HD2	2.31	0.45
5:f:137:LYS:HA	5:f:140:ILE:HG22	1.97	0.45
12:n:36:THR:HG23	51:1:1278:C:OP1	2.17	0.45
25:B:47:TYR:CE1	25:B:52:LYS:HD3	2.50	0.45
30:G:27:LYS:HB2	30:G:28:PRO:HD3	1.98	0.45
33:J:147:ASN:HD22	33:J:152:VAL:HG11	1.80	0.45
47:X:18:VAL:HG11	47:X:43:MET:HG2	1.99	0.45
48:Y:3:ILE:O	48:Y:3:ILE:HG13	2.16	0.45
50:3:178:C:O2'	50:3:179:A:H5'	2.16	0.45
50:3:417:G:O2'	50:3:418:C:H5'	2.15	0.45
50:3:721:G:H4'	50:3:722:G:O4'	2.17	0.45
50:3:885:G:H2'	50:3:886:G:C8	2.49	0.45
50:3:1116:U:O2'	50:3:1117:A:H5'	2.16	0.45
50:3:1318:A:H2'	50:3:1319:A:H5'	1.98	0.45
50:3:1376:U:H2'	50:3:1377:A:H8	1.81	0.45
50:3:1391:U:H2'	50:3:1392:G:C8	2.51	0.45
51:1:30:G:H2'	51:1:31:C:C6	2.51	0.45
51:1:845:A:N3	51:1:845:A:H3'	2.30	0.45
51:1:1645:G:H5''	51:1:1646:C:H5'	1.97	0.45
51:1:1823:G:O2'	51:1:1824:G:H5'	2.17	0.45
51:1:2303:G:H2'	51:1:2304:G:C8	2.51	0.45
9:k:1:MET:HG3	9:k:32:TYR:CG	2.51	0.45
23:y:41:HIS:CG	51:1:96:C:H4'	2.51	0.45
30:G:142:LYS:HA	30:G:145:ASN:ND2	2.32	0.45
33:J:28:ARG:NH2	50:3:1396:A:H1'	2.31	0.45
36:M:124:ILE:HD12	36:M:124:ILE:N	2.30	0.45
37:N:6:TYR:CZ	50:3:1147:C:H4'	2.51	0.45
37:N:73:GLY:N	50:3:1372:U:OP1	2.47	0.45
40:Q:114:SER:N	50:3:502:A:OP1	2.47	0.45
42:S:32:ASP:O	42:S:40:ARG:NH2	2.49	0.45
42:S:52:ARG:NH1	50:3:1317:C:H42	2.12	0.45
50:3:279:A:C5'	50:3:281:G:H5'	2.44	0.45
50:3:328:C:H5'	50:3:329:A:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:358:U:H2'	50:3:359:G:C8	2.51	0.45
51:1:1153:C:H2'	51:1:1154:G:O4'	2.17	0.45
51:1:1542:U:H2'	51:1:1543:G:O4'	2.16	0.45
51:1:2024:G:OP2	51:1:2034:U:H4'	2.15	0.45
51:1:2638:G:H1'	51:1:2778:A:N6	2.29	0.45
55:8:112:ARG:HG2	55:8:116:GLU:HB2	1.97	0.45
3:d:148:ILE:HD13	3:d:187:VAL:CG2	2.46	0.45
7:h:117:LEU:HG	7:h:118:ILE:HG12	1.98	0.45
9:k:71:ARG:HB3	9:k:75:SER:HB3	1.99	0.45
9:k:97:THR:O	9:k:118:LEU:HD22	2.16	0.45
30:G:23:ASN:HA	30:G:24:PRO:HD3	1.72	0.45
44:U:19:VAL:CG1	44:U:37:GLY:H	2.29	0.45
50:3:112:G:H21	50:3:354:G:H5'	1.80	0.45
50:3:246:A:O3'	50:3:247:G:H4'	2.17	0.45
50:3:896:C:H2'	50:3:897:C:C6	2.52	0.45
50:3:1025:U:H5''	50:3:1026:G:H5'	1.98	0.45
51:1:35:G:H2'	51:1:36:G:O4'	2.16	0.45
51:1:155:A:H2'	51:1:156:A:C8	2.51	0.45
51:1:515:A:H1'	51:1:581:C:H1'	1.98	0.45
52:2:100:G:H2'	52:2:101:A:O4'	2.17	0.45
11:m:73:ILE:HD11	11:m:91:TYR:CZ	2.52	0.45
12:n:20:MET:HE3	51:1:1277:G:H4'	1.98	0.45
15:q:82:LEU:HD21	15:q:87:VAL:HB	1.97	0.45
21:w:20:LYS:HD3	51:1:2355:G:H4'	1.98	0.45
35:L:14:ASP:H	35:L:19:SER:H	1.64	0.45
36:M:40:LYS:NZ	36:M:47:ASP:H	2.15	0.45
45:V:6:THR:HG22	45:V:7:LEU:H	1.80	0.45
50:3:10:A:H2'	50:3:11:G:H8	1.82	0.45
50:3:599:C:H2'	50:3:600:A:H8	1.80	0.45
50:3:855:U:H2'	50:3:856:C:C6	2.52	0.45
50:3:1162:C:H2'	50:3:1163:A:C8	2.52	0.45
51:1:195:A:H2'	51:1:198:C:N4	2.31	0.45
51:1:248:G:O5'	51:1:249:C:H5'	2.16	0.45
51:1:575:A:O2'	51:1:576:U:H5'	2.16	0.45
51:1:929:U:H2'	51:1:930:G:C8	2.51	0.45
51:1:2850:A:H2'	51:1:2851:A:O4'	2.17	0.45
4:e:7:TYR:CE1	4:e:11:VAL:HG21	2.51	0.45
4:e:52:ALA:O	4:e:55:ASP:HB2	2.17	0.45
51:1:62:U:H2'	51:1:63:A:C8	2.52	0.45
51:1:331:C:O2'	51:1:332:A:H5'	2.16	0.45
51:1:364:C:H2'	51:1:365:U:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1111:A:H2'	51:1:1112:G:H4'	1.99	0.45
51:1:1283:G:H1'	51:1:1329:U:O2	2.16	0.45
51:1:1440:U:H2'	51:1:1441:G:C8	2.52	0.45
51:1:2103:C:H2'	51:1:2104:C:C6	2.52	0.45
51:1:2128:G:H2'	51:1:2129:C:O4'	2.16	0.45
51:1:2236:U:H2'	51:1:2237:G:O4'	2.17	0.45
51:1:2444:G:H2'	51:1:2445:G:O4'	2.17	0.45
51:1:2705:A:H2'	51:1:2706:A:O4'	2.17	0.45
1:b:116:GLN:HG3	1:b:121:ALA:HB1	1.98	0.45
1:b:244:VAL:HA	1:b:251:THR:HG22	1.99	0.45
10:l:19:LEU:HD23	10:l:27:LEU:HB3	1.99	0.45
15:q:36:GLN:HE21	51:1:1252:G:H1	1.63	0.45
31:H:176:THR:HG22	50:3:1111:A:N1	2.32	0.45
39:P:58:THR:OG1	39:P:59:PRO:HD2	2.17	0.45
39:P:126:ARG:HB2	49:Z:33:ARG:HD2	1.99	0.45
50:3:829:G:O2'	50:3:830:G:H5'	2.17	0.45
51:1:445:C:C2'	51:1:446:G:H5'	2.47	0.45
51:1:826:U:H5''	51:1:2429:G:P	2.57	0.45
51:1:1304:A:H2'	51:1:1305:C:C5'	2.28	0.45
51:1:1564:C:H2'	51:1:1565:C:O4'	2.16	0.45
52:2:63:C:H2'	52:2:64:G:C8	2.51	0.45
52:2:114:C:H2'	52:2:115:A:H8	1.82	0.45
16:r:28:ALA:HB3	16:r:31:GLU:OE1	2.17	0.45
17:s:97:LEU:HD23	17:s:97:LEU:H	1.82	0.45
50:3:225:C:H3'	50:3:226:G:H5''	1.98	0.45
50:3:952:U:O2'	50:3:953:G:H5'	2.16	0.45
50:3:1028:C:H42	50:3:1033:G:H22	1.64	0.45
50:3:1162:C:H2'	50:3:1163:A:H8	1.82	0.45
50:3:1496:C:H2'	50:3:1497:G:O4'	2.17	0.45
51:1:859:G:C2'	51:1:860:U:OP2	2.65	0.45
51:1:1860:G:H2'	51:1:1861:G:C8	2.52	0.45
51:1:1995:U:H2'	51:1:1996:C:C5	2.51	0.45
51:1:2028:U:H2'	51:1:2029:G:O4'	2.17	0.45
51:1:2112:G:H2'	51:1:2112:G:N3	2.32	0.45
51:1:2240:U:O2'	51:1:2241:A:H5'	2.17	0.45
51:1:2372:U:H2'	51:1:2373:G:C8	2.52	0.45
51:1:2512:C:H2'	51:1:2513:A:O4'	2.17	0.45
51:1:2701:U:H3'	51:1:2702:G:H5''	1.98	0.45
52:2:65:U:H3'	52:2:108:A:H61	1.81	0.45
1:b:16:VAL:HG22	1:b:203:VAL:HG22	1.98	0.45
4:e:21:TYR:HB3	4:e:26:GLN:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:69:ALA:HB3	4:e:81:GLY:H	1.82	0.45
11:m:61:GLY:HA2	11:m:107:GLY:HA3	1.98	0.45
33:J:80:LEU:HB3	33:J:97:PRO:HB3	1.99	0.45
34:K:69:GLU:CD	34:K:69:GLU:H	2.25	0.45
37:N:98:ARG:O	37:N:99:LYS:HG3	2.15	0.45
44:U:20:VAL:HG22	44:U:21:VAL:H	1.82	0.45
50:3:420:U:H2'	50:3:422:C:O4'	2.17	0.45
50:3:505:G:H2'	50:3:506:G:H8	1.80	0.45
51:1:195:A:H2'	51:1:198:C:H41	1.81	0.45
51:1:660:C:H2'	51:1:661:A:H8	1.81	0.45
53:5:5:G:H2'	53:5:6:G:C8	2.51	0.45
9:k:19:VAL:CG1	9:k:41:ILE:HB	2.47	0.45
14:p:105:LYS:N	50:3:1432:G:OP1	2.43	0.45
17:s:17:VAL:HB	17:s:76:VAL:HG11	1.99	0.45
30:G:39:ILE:HD12	30:G:39:ILE:N	2.32	0.45
32:I:147:LYS:NZ	50:3:490:C:H5''	2.31	0.45
43:T:31:LEU:HD22	43:T:58:MET:HB2	1.98	0.45
45:V:32:ILE:HD12	45:V:32:ILE:N	2.32	0.45
45:V:42:LYS:C	45:V:43:LEU:HD12	2.42	0.45
50:3:440:C:C2'	50:3:441:A:H5''	2.47	0.45
50:3:456:A:H2'	50:3:457:G:H8	1.81	0.45
50:3:730:G:C2'	50:3:731:G:H5'	2.47	0.45
50:3:1096:C:H2'	50:3:1097:C:C6	2.51	0.45
50:3:1227:A:C2'	50:3:1228:C:H5'	2.47	0.45
51:1:222:A:N1	51:1:233:A:H5''	2.32	0.45
51:1:1611:C:H6	51:1:1611:C:H5'	1.82	0.45
51:1:2789:C:H2'	51:1:2790:U:H5'	1.99	0.45
53:5:28:C:H2'	53:5:29:G:H8	1.82	0.45
6:g:3:VAL:HG22	6:g:4:ILE:N	2.31	0.44
7:h:67:THR:N	7:h:68:PRO:CD	2.79	0.44
8:j:28:LEU:HD23	8:j:28:LEU:C	2.42	0.44
12:n:15:SER:OG	51:1:2710:C:OP1	2.34	0.44
13:o:15:ARG:HH21	13:o:95:SER:HB2	1.82	0.44
18:t:15:HIS:H	18:t:32:LEU:HA	1.81	0.44
18:t:33:LYS:HE3	18:t:80:TRP:CG	2.52	0.44
21:w:20:LYS:HE3	51:1:2355:G:O2'	2.17	0.44
27:D:8:SER:O	27:D:12:ARG:HG2	2.17	0.44
29:F:11:CYS:HB3	29:F:33:HIS:CE1	2.52	0.44
32:I:49:ASP:OD1	32:I:53:GLN:NE2	2.50	0.44
33:J:17:VAL:HA	33:J:33:THR:O	2.18	0.44
40:Q:107:LYS:HG3	40:Q:108:ASP:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:V:64:ARG:O	45:V:66:LEU:HG	2.17	0.44
46:W:13:THR:HG23	46:W:18:GLN:H	1.81	0.44
50:3:985:C:H2'	50:3:986:U:C6	2.52	0.44
50:3:1198:G:H2'	50:3:1199:U:C6	2.52	0.44
50:3:1204:A:O2'	50:3:1205:U:H5'	2.18	0.44
50:3:1534:A:H5'	50:3:1535:C:OP1	2.17	0.44
51:1:164:C:H2'	51:1:165:A:H5'	1.99	0.44
51:1:880:G:H2'	51:1:881:G:O4'	2.16	0.44
51:1:2773:C:H2'	51:1:2774:C:H6	1.81	0.44
52:2:7:G:O2'	52:2:8:C:H5'	2.18	0.44
52:2:111:U:H2'	52:2:112:G:C8	2.51	0.44
55:8:3:VAL:CG1	55:8:10:ILE:HG23	2.47	0.44
9:k:53:LYS:N	9:k:56:ASP:OD2	2.46	0.44
11:m:44:ARG:HB3	51:1:2484:G:OP1	2.17	0.44
14:p:20:ARG:HG2	51:1:2867:G:O6	2.17	0.44
17:s:59:GLU:OE2	17:s:60:HIS:HB2	2.18	0.44
18:t:61:LEU:HB3	51:1:1341:G:H4'	1.99	0.44
31:H:1:GLY:HA2	50:3:1060:U:C4	2.51	0.44
32:I:189:ASP:OD2	32:I:189:ASP:N	2.49	0.44
39:P:113:THR:HB	39:P:115:ILE:HG12	2.00	0.44
40:Q:107:LYS:CG	40:Q:108:ASP:H	2.30	0.44
50:3:829:G:H2'	50:3:830:G:H8	1.83	0.44
50:3:912:C:O2'	50:3:913:A:H5'	2.17	0.44
51:1:1022:G:N2	51:1:1142:A:H2	2.14	0.44
51:1:1300:G:C3'	51:1:1301:A:H5'	2.48	0.44
51:1:1310:G:H3'	51:1:1311:G:H8	1.83	0.44
51:1:1661:G:O2'	51:1:1662:U:H5'	2.17	0.44
51:1:2732:G:C3'	51:1:2733:A:H5'	2.48	0.44
53:5:28:C:H2'	53:5:29:G:C8	2.52	0.44
55:8:76:GLU:O	55:8:77:TYR:CG	2.71	0.44
1:b:269:ARG:HG2	1:b:269:ARG:HH11	1.82	0.44
2:c:48:ILE:HG23	2:c:84:LEU:HD21	1.99	0.44
4:e:111:ARG:HH21	41:R:6:ILE:HD12	1.82	0.44
5:f:175:LYS:HG3	5:f:176:LYS:HG2	1.98	0.44
6:g:90:LEU:HD12	6:g:90:LEU:N	2.32	0.44
11:m:1:MET:SD	11:m:3:GLN:NE2	2.91	0.44
15:q:60:TRP:CZ2	15:q:92:LYS:HG3	2.52	0.44
18:t:3:ARG:HD3	51:1:143:C:O2'	2.18	0.44
30:G:100:LEU:C	30:G:102:ASN:H	2.24	0.44
30:G:101:THR:O	50:3:1074:G:H4'	2.16	0.44
44:U:19:VAL:HG12	44:U:37:GLY:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Z:44:ARG:NH1	50:3:723:U:H5'	2.33	0.44
50:3:519:C:N4	50:3:520:A:C6	2.86	0.44
50:3:986:U:H2'	50:3:987:G:O4'	2.17	0.44
50:3:1014:A:H2'	50:3:1015:G:O4'	2.17	0.44
50:3:1104:G:O2'	50:3:1105:A:H5'	2.17	0.44
51:1:1229:C:H2'	51:1:1230:A:C8	2.52	0.44
51:1:1409:U:H2'	51:1:1410:G:H8	1.80	0.44
51:1:1810:A:H2'	51:1:1811:G:C5'	2.47	0.44
51:1:1837:C:H2'	51:1:1899:A:N6	2.32	0.44
52:2:3:C:H3'	52:2:4:C:C5'	2.47	0.44
53:5:41:C:H2'	53:5:42:G:H8	1.81	0.44
32:I:57:LYS:HD3	32:I:61:ARG:HH12	1.82	0.44
33:J:65:LYS:NZ	50:3:1075:U:OP2	2.50	0.44
34:K:78:PHE:HD1	34:K:84:VAL:HG11	1.82	0.44
39:P:52:ARG:HD2	39:P:52:ARG:H	1.80	0.44
50:3:416:G:H2'	50:3:417:G:C8	2.52	0.44
51:1:141:G:H3'	51:1:142:A:O4'	2.17	0.44
51:1:831:G:C2'	51:1:832:U:H5'	2.48	0.44
51:1:1062:G:H1	51:1:1076:C:N4	1.99	0.44
51:1:2602:A:N6	55:8:34:SER:OG	2.51	0.44
9:k:48:PRO:HB3	50:3:1422:G:H5'	2.00	0.44
15:q:2:ARG:HH22	51:1:446:G:C5'	2.29	0.44
15:q:39:ILE:HD12	15:q:39:ILE:HA	1.92	0.44
31:H:171:ARG:HB3	50:3:1106:G:H5''	1.98	0.44
42:S:2:LYS:HG2	42:S:5:MET:H	1.83	0.44
45:V:15:LYS:HG3	50:3:275:G:H5'	1.99	0.44
45:V:29:LYS:HB3	45:V:36:PHE:CE1	2.53	0.44
47:X:4:LEU:HD23	47:X:6:LYS:H	1.81	0.44
51:1:1528:A:H2'	51:1:1529:G:H5'	2.00	0.44
51:1:1775:U:H2'	51:1:1776:G:C5'	2.47	0.44
51:1:2142:A:H2'	51:1:2143:C:O4'	2.16	0.44
51:1:2216:G:H2'	51:1:2217:G:C8	2.52	0.44
51:1:2678:C:H2'	51:1:2679:A:H8	1.82	0.44
51:1:2855:C:H2'	51:1:2856:A:H8	1.82	0.44
1:b:131:MET:HE2	1:b:187:CYS:HB2	1.98	0.44
6:g:6:LEU:HD11	6:g:37:VAL:HG13	1.97	0.44
14:p:57:ALA:HB2	14:p:74:GLN:HE22	1.81	0.44
16:r:22:LEU:HD12	16:r:23:GLU:O	2.18	0.44
17:s:86:MET:HA	17:s:87:PRO:HD3	1.84	0.44
25:B:3:GLN:HA	51:1:2615:U:C2	2.52	0.44
31:H:116:ALA:O	31:H:119:ILE:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:K:51:ILE:O	34:K:52:ASN:CG	2.60	0.44
38:O:23:ALA:O	38:O:26:VAL:HG12	2.17	0.44
50:3:191:G:H2'	50:3:192:A:C8	2.52	0.44
50:3:201:G:H2'	50:3:202:G:H8	1.83	0.44
50:3:678:U:H2'	50:3:679:C:H6	1.81	0.44
50:3:1128:C:H2'	50:3:1129:C:C6	2.53	0.44
50:3:1211:U:H5'	50:3:1213:A:H1'	2.00	0.44
50:3:1316:G:N2	50:3:1318:A:H3'	2.33	0.44
50:3:1431:A:H2	50:3:1469:C:N4	2.16	0.44
50:3:1511:G:O2'	50:3:1512:U:H5'	2.18	0.44
50:3:1517:G:H2'	50:3:1518:A:H5'	1.99	0.44
51:1:162:U:C2'	51:1:163:C:H5'	2.47	0.44
51:1:310:A:H2'	51:1:311:A:H5''	1.98	0.44
51:1:362:A:H5''	51:1:363:G:N7	2.32	0.44
51:1:399:U:H2'	51:1:400:G:O4'	2.17	0.44
51:1:413:C:H2'	51:1:414:C:C6	2.52	0.44
51:1:679:C:H2'	51:1:680:C:C6	2.52	0.44
51:1:766:U:H2'	51:1:767:U:C6	2.52	0.44
51:1:1285:A:H2'	51:1:1286:A:H5'	1.99	0.44
51:1:1757:A:O5'	51:1:1757:A:H8	2.01	0.44
51:1:1866:A:H2'	51:1:1867:G:H5'	1.99	0.44
51:1:2345:G:H5'	51:1:2347:C:O4'	2.17	0.44
51:1:2762:C:H2'	51:1:2763:G:O4'	2.18	0.44
8:j:116:ARG:NH2	51:1:529:A:OP2	2.48	0.44
10:l:36:LYS:HE2	51:1:568:U:OP1	2.18	0.44
11:m:51:ARG:HA	11:m:54:THR:HG22	2.00	0.44
17:s:83:LYS:HG2	17:s:95:ARG:HH12	1.82	0.44
18:t:14:PRO:HD3	23:y:30:MET:HE2	1.99	0.44
20:v:80:HIS:HB3	20:v:83:LYS:O	2.18	0.44
23:y:1:MET:HA	23:y:4:LYS:HB3	2.00	0.44
25:B:38:LEU:HB3	25:B:41:HIS:HB2	2.00	0.44
27:D:34:ARG:HG3	27:D:42:LEU:HD12	2.00	0.44
32:I:152:SER:HA	32:I:155:LYS:NZ	2.33	0.44
50:3:603:U:H2'	50:3:604:G:C8	2.53	0.44
50:3:1176:A:H2'	50:3:1177:G:O4'	2.18	0.44
50:3:1197:A:H2'	50:3:1198:G:C5'	2.47	0.44
51:1:211:C:H2'	51:1:212:G:C8	2.52	0.44
51:1:633:A:H2'	51:1:634:C:O4'	2.18	0.44
51:1:1639:C:O2'	51:1:1640:A:H5'	2.18	0.44
51:1:1709:U:H2'	51:1:1710:G:C8	2.52	0.44
1:b:155:ARG:NH2	51:1:1818:U:C5	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:170:TYR:CD1	1:b:182:LYS:HG2	2.53	0.44
1:b:224:MET:O	1:b:232:GLY:HA3	2.17	0.44
13:o:75:GLY:O	13:o:78:VAL:HG22	2.18	0.44
18:t:2:ILE:HD11	51:1:144:A:H4'	1.99	0.44
30:G:160:LEU:HB2	30:G:182:VAL:HG12	2.00	0.44
34:K:7:VAL:CG1	34:K:88:MET:HG2	2.48	0.44
36:M:87:ARG:H	36:M:90:GLU:CG	2.31	0.44
36:M:94:VAL:HG21	36:M:101:ALA:HB2	2.00	0.44
48:Y:19:HIS:HB2	48:Y:23:ARG:NH1	2.32	0.44
50:3:859:G:H2'	50:3:860:A:C8	2.53	0.44
50:3:1391:U:H2'	50:3:1392:G:H8	1.83	0.44
50:3:1463:U:H2'	50:3:1464:U:C6	2.53	0.44
51:1:751:A:C5	51:1:789:A:C6	3.05	0.44
51:1:1001:A:H2'	51:1:1002:G:O4'	2.18	0.44
51:1:1504:A:H2'	51:1:1505:A:C8	2.53	0.44
51:1:2128:G:H22	51:1:2173:A:H2	1.66	0.44
7:h:33:VAL:HG12	7:h:34:THR:N	2.33	0.44
12:n:36:THR:HG22	12:n:37:THR:N	2.30	0.44
12:n:47:VAL:HG23	12:n:48:VAL:HG13	2.00	0.44
15:q:32:ARG:HG3	51:1:581:C:OP1	2.18	0.44
15:q:91:ARG:NH2	51:1:1153:C:OP1	2.51	0.44
47:X:35:ARG:HB3	47:X:71:GLY:HA3	2.00	0.44
50:3:37:U:O2'	50:3:38:G:H5'	2.18	0.44
50:3:195:A:H2'	50:3:196:A:C8	2.52	0.44
50:3:763:G:H2'	50:3:764:C:C6	2.53	0.44
51:1:968:C:H2'	51:1:969:G:C8	2.53	0.44
51:1:1594:U:H2'	51:1:1595:C:H6	1.82	0.44
51:1:1997:C:H2'	51:1:1998:A:C8	2.53	0.44
51:1:2314:A:H2'	51:1:2315:G:C8	2.53	0.44
51:1:2843:G:C2'	51:1:2844:G:H5'	2.48	0.44
1:b:263:ASP:O	1:b:266:ILE:HG22	2.18	0.43
2:c:194:PRO:HA	51:1:2680:U:H5''	1.99	0.43
3:d:123:LYS:HD3	3:d:125:SER:HB3	1.99	0.43
9:k:60:ALA:HA	9:k:87:LEU:HG	2.00	0.43
30:G:170:ILE:O	30:G:174:GLU:HG2	2.17	0.43
31:H:46:LEU:O	31:H:48:LYS:N	2.44	0.43
31:H:189:HIS:NE2	50:3:1205:U:H4'	2.33	0.43
49:Z:23:GLU:OE2	49:Z:28:LEU:HB2	2.17	0.43
50:3:751:U:C2'	50:3:752:G:H5'	2.48	0.43
50:3:882:C:O2'	50:3:883:C:H5'	2.18	0.43
50:3:1488:G:H2'	50:3:1489:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:745:G:H2'	51:1:746:U:H5'	2.00	0.43
51:1:1470:A:H61	51:1:1521:G:H1'	1.83	0.43
51:1:1635:A:H2'	51:1:1636:U:O4'	2.18	0.43
51:1:1794:A:H2'	51:1:1795:C:H6	1.82	0.43
51:1:2366:A:H2'	51:1:2367:G:O4'	2.18	0.43
52:2:1:U:H2'	52:2:2:G:H5'	2.00	0.43
12:n:32:GLU:OE1	12:n:115:LEU:HD12	2.18	0.43
17:s:82:MET:HB2	17:s:98:LYS:HB2	2.01	0.43
32:I:169:TRP:CG	32:I:185:PRO:HG3	2.53	0.43
44:U:8:ARG:H	44:U:28:ARG:HD3	1.83	0.43
44:U:31:ARG:HB2	50:3:310:G:H5''	2.00	0.43
45:V:37:ILE:H	45:V:37:ILE:HD12	1.83	0.43
50:3:9:G:H2'	50:3:10:A:H8	1.83	0.43
50:3:1369:C:H2'	50:3:1370:G:H8	1.83	0.43
51:1:1501:G:O2'	51:1:1502:A:H5'	2.18	0.43
51:1:1554:U:H3'	51:1:1555:G:H5'	2.00	0.43
51:1:1860:G:H2'	51:1:1861:G:H8	1.83	0.43
51:1:2637:U:H2'	51:1:2638:G:O4'	2.18	0.43
51:1:2638:G:H22	51:1:2775:G:H2'	1.83	0.43
51:1:2678:C:H2'	51:1:2679:A:C8	2.54	0.43
55:8:101:GLU:HB3	55:8:102:LYS:H	1.72	0.43
5:f:104:LEU:HD23	5:f:112:VAL:O	2.18	0.43
18:t:93:LEU:HD23	18:t:93:LEU:C	2.44	0.43
20:v:83:LYS:HA	20:v:84:PRO:HD3	1.84	0.43
28:E:2:LYS:NZ	51:1:242:G:OP2	2.52	0.43
32:I:184:LYS:HA	32:I:185:PRO:HD3	1.83	0.43
36:M:94:VAL:HB	36:M:99:GLY:O	2.18	0.43
38:O:7:ARG:HG2	38:O:75:ASP:OD1	2.18	0.43
38:O:43:PRO:HA	50:3:1151:A:H5'	1.99	0.43
43:T:1:SER:OG	43:T:2:LEU:N	2.51	0.43
44:U:36:VAL:HG11	44:U:57:ILE:HG13	2.00	0.43
50:3:59:A:H1'	50:3:354:G:N2	2.34	0.43
50:3:1411:C:H2'	50:3:1412:C:C6	2.53	0.43
51:1:222:A:C2	51:1:233:A:H5''	2.53	0.43
51:1:576:U:H2'	51:1:577:G:C8	2.52	0.43
51:1:867:C:O2	51:1:913:U:H4'	2.18	0.43
51:1:910:A:H2'	51:1:911:A:C8	2.53	0.43
51:1:1172:C:C2'	51:1:1173:U:H5''	2.47	0.43
51:1:1536:C:H4'	51:1:1537:G:C2	2.53	0.43
51:1:1833:C:O2'	51:1:1834:U:H5'	2.19	0.43
51:1:2220:U:O2'	51:1:2221:G:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:48:LEU:O	55:8:50:GLU:N	2.51	0.43
55:8:62:HIS:CD2	55:8:63:LEU:HG	2.53	0.43
1:b:47:ARG:HD3	51:1:778:G:H5''	1.99	0.43
4:e:15:LEU:HD13	4:e:18:GLU:HB2	2.00	0.43
4:e:35:LEU:HD23	4:e:56:LEU:HD22	1.99	0.43
8:j:21:THR:HG23	8:j:61:LYS:HE2	2.00	0.43
14:p:3:ILE:H	14:p:3:ILE:CD1	2.27	0.43
22:x:36:ARG:HG2	51:1:2200:C:OP1	2.18	0.43
32:I:11:SER:HB2	32:I:18:LEU:HD13	2.00	0.43
32:I:57:LYS:HG3	32:I:199:ILE:HG23	2.00	0.43
32:I:137:SER:N	32:I:140:ASP:OD2	2.51	0.43
33:J:131:ASN:HD21	33:J:133:ILE:HB	1.83	0.43
34:K:7:VAL:HG13	34:K:7:VAL:O	2.18	0.43
37:N:88:GLU:H	37:N:88:GLU:HG2	1.57	0.43
49:Z:17:ARG:HE	49:Z:20:ARG:HG3	1.84	0.43
50:3:408:A:H2'	50:3:409:U:O4'	2.19	0.43
50:3:887:G:H2'	50:3:888:G:C5'	2.49	0.43
51:1:36:G:O2'	51:1:37:C:H5'	2.18	0.43
51:1:167:A:C2'	51:1:168:G:H5'	2.48	0.43
51:1:2052:A:H2'	51:1:2053:G:C8	2.53	0.43
51:1:2469:A:C2'	51:1:2470:G:H5'	2.48	0.43
51:1:2687:U:H2'	51:1:2688:G:O4'	2.18	0.43
53:5:63:G:H2'	53:5:64:G:H8	1.83	0.43
1:b:257:ARG:HH22	1:b:262:THR:HG23	1.84	0.43
9:k:10:VAL:HG21	9:k:16:ALA:HB3	2.00	0.43
18:t:30:ILE:HG23	18:t:85:VAL:HB	2.00	0.43
22:x:31:ASN:ND2	51:1:2230:G:N3	2.67	0.43
31:H:69:THR:HG21	31:H:75:VAL:HG21	1.99	0.43
32:I:30:LYS:HD2	50:3:411:A:H2'	1.99	0.43
32:I:195:ASN:HB3	32:I:197:HIS:CE1	2.54	0.43
36:M:49:LYS:N	36:M:59:GLU:O	2.50	0.43
50:3:955:U:C1'	50:3:1227:A:H61	2.32	0.43
51:1:230:G:O2'	51:1:231:A:H5'	2.18	0.43
51:1:290:U:H2'	51:1:291:G:H8	1.84	0.43
51:1:649:G:H2'	51:1:650:C:O4'	2.19	0.43
51:1:864:G:O2'	51:1:865:C:H5'	2.18	0.43
51:1:1387:A:H2'	51:1:1388:G:C8	2.53	0.43
51:1:1441:G:H2'	51:1:1442:U:C6	2.53	0.43
51:1:1505:A:H2'	51:1:1506:U:O4'	2.17	0.43
51:1:1709:U:H2'	51:1:1710:G:H8	1.82	0.43
51:1:1744:A:H3'	51:1:1745:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2179:C:H2'	51:1:2180:U:C5	2.54	0.43
51:1:2591:C:H2'	51:1:2592:G:C8	2.53	0.43
53:5:71:C:H2'	53:5:72:A:H8	1.83	0.43
1:b:164:VAL:HB	1:b:172:THR:HB	2.01	0.43
5:f:44:HIS:NE2	5:f:47:ASN:HA	2.33	0.43
31:H:189:HIS:CD2	50:3:1205:U:H4'	2.54	0.43
50:3:10:A:H2'	50:3:11:G:C8	2.54	0.43
50:3:188:C:H2'	50:3:189:A:O4'	2.19	0.43
50:3:415:A:H2'	50:3:416:G:C8	2.53	0.43
50:3:502:A:H61	50:3:543:U:H3	1.67	0.43
51:1:168:G:O2'	51:1:169:G:H5'	2.18	0.43
51:1:1335:C:H2'	51:1:1336:A:H8	1.84	0.43
51:1:1366:A:H2'	51:1:1367:A:O4'	2.17	0.43
51:1:1383:A:H2	51:1:1406:U:H1'	1.83	0.43
51:1:1685:C:H2'	51:1:1686:C:C6	2.53	0.43
51:1:2385:C:H2'	51:1:2386:A:H8	1.84	0.43
51:1:2468:A:H2'	51:1:2481:G:H22	1.84	0.43
2:c:22:ILE:HA	2:c:23:PRO:HD3	1.84	0.43
2:c:110:THR:HG23	2:c:202:ILE:HB	2.01	0.43
5:f:154:GLU:CD	5:f:159:LYS:HB2	2.43	0.43
18:t:64:LYS:NZ	51:1:1601:G:OP1	2.52	0.43
48:Y:67:HIS:O	48:Y:68:LYS:HB3	2.19	0.43
50:3:116:A:O2'	50:3:117:G:H5'	2.19	0.43
50:3:1004:A:H2'	50:3:1005:A:O4'	2.19	0.43
50:3:1015:G:O2'	50:3:1016:A:H5'	2.17	0.43
50:3:1157:A:H4'	50:3:1158:C:O5'	2.18	0.43
50:3:1225:A:H5'	50:3:1226:C:OP2	2.19	0.43
50:3:1333:A:H3'	50:3:1334:G:H8	1.84	0.43
51:1:1481:U:H2'	51:1:1482:G:H4'	1.99	0.43
51:1:2265:U:H3'	51:1:2266:A:C5'	2.46	0.43
51:1:2431:U:O5'	51:1:2431:U:H6	2.02	0.43
51:1:2537:U:H2'	51:1:2538:C:C6	2.54	0.43
51:1:2639:A:H2'	51:1:2640:G:O4'	2.19	0.43
52:2:117:G:O2'	52:2:118:C:H5'	2.19	0.43
55:8:69:VAL:O	55:8:70:ILE:C	2.61	0.43
55:8:119:LEU:HA	55:8:122:LYS:HE3	2.00	0.43
4:e:120:SER:HB2	51:1:2304:G:H5'	2.00	0.43
12:n:100:CYS:HB2	12:n:112:TYR:HD2	1.83	0.43
17:s:29:VAL:HG21	17:s:69:LEU:HB2	2.01	0.43
31:H:145:ALA:HB3	31:H:148:ILE:HD11	1.99	0.43
33:J:108:GLY:H	50:3:9:G:H4'	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:N:110:VAL:HG23	50:3:1348:U:OP2	2.19	0.43
38:O:8:ILE:HD12	38:O:100:ILE:HD12	2.01	0.43
41:R:14:ALA:O	41:R:18:LEU:HG	2.18	0.43
41:R:38:ILE:HD12	41:R:38:ILE:N	2.33	0.43
49:Z:33:ARG:HH11	49:Z:33:ARG:HG3	1.83	0.43
50:3:775:G:H2'	50:3:776:G:C8	2.54	0.43
50:3:880:C:O2'	50:3:881:G:H5'	2.19	0.43
50:3:1098:C:H2'	50:3:1099:G:C8	2.54	0.43
50:3:1202:U:C2'	50:3:1203:C:H5'	2.49	0.43
50:3:1424:U:H2'	50:3:1425:U:O4'	2.18	0.43
51:1:1152:C:O2'	51:1:1153:C:H5'	2.19	0.43
51:1:1871:A:P	51:1:1871:A:H8	2.42	0.43
51:1:2746:U:H2'	51:1:2747:G:O4'	2.19	0.43
52:2:66:A:H4'	52:2:67:G:C8	2.54	0.43
4:e:100:GLU:OE1	4:e:101:ARG:NH2	2.51	0.43
11:m:43:ALA:O	11:m:46:ILE:HG22	2.18	0.43
18:t:50:LEU:HD12	18:t:50:LEU:N	2.34	0.43
22:x:48:LEU:HB3	22:x:50:VAL:HG13	1.99	0.43
31:H:52:SER:HA	31:H:113:LYS:HG2	2.00	0.43
31:H:62:SER:HA	31:H:96:VAL:HB	2.00	0.43
32:I:9:LYS:HD2	50:3:428:G:H5''	2.01	0.43
32:I:161:ALA:O	32:I:164:ARG:NH1	2.51	0.43
33:J:137:ARG:NH1	50:3:1078:U:H4'	2.34	0.43
40:Q:50:LYS:O	40:Q:66:ILE:HB	2.19	0.43
50:3:128:G:H2'	50:3:129:A:C8	2.54	0.43
50:3:346:G:H2'	50:3:347:G:O4'	2.19	0.43
50:3:349:A:O2'	50:3:350:G:H5'	2.18	0.43
50:3:446:G:C2	50:3:447:G:H1'	2.54	0.43
50:3:446:G:H2'	50:3:447:G:O4'	2.19	0.43
50:3:578:C:H2'	50:3:579:A:H8	1.84	0.43
51:1:68:G:H2'	51:1:69:C:O4'	2.18	0.43
51:1:1507:C:H2'	51:1:1508:A:O4'	2.19	0.43
51:1:1583:A:H4'	51:1:1585:C:C4	2.54	0.43
51:1:1769:U:H2'	51:1:1770:G:C8	2.54	0.43
51:1:2214:C:O5'	51:1:2214:C:H6	2.01	0.43
51:1:2372:U:O2'	51:1:2373:G:H5'	2.19	0.43
51:1:2457:U:O2'	51:1:2458:G:H5'	2.19	0.43
51:1:2785:C:H2'	51:1:2786:U:C6	2.54	0.43
51:1:2810:A:H2'	51:1:2811:G:O4'	2.19	0.43
55:8:23:GLN:HE21	55:8:75:GLN:HE22	1.67	0.43
55:8:81:GLU:HA	55:8:84:ARG:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:k:20:MET:O	9:k:42:THR:HG22	2.19	0.43
10:l:61:LEU:O	28:E:12:ARG:NE	2.50	0.43
11:m:36:VAL:HG23	20:v:82:TYR:HB2	2.01	0.43
12:n:31:HIS:O	12:n:32:GLU:HB2	2.19	0.43
13:o:33:ARG:NE	52:2:52:A:C5	2.87	0.43
17:s:49:LYS:NZ	51:1:489:G:N7	2.67	0.43
31:H:8:GLY:HA2	31:H:11:LEU:HD13	2.00	0.43
31:H:71:ARG:HD2	31:H:72:PRO:HD2	2.01	0.43
32:I:119:HIS:CD2	50:3:438:U:H4'	2.53	0.43
39:P:28:ASN:OD1	39:P:30:ILE:HG13	2.19	0.43
47:X:44:ILE:HD13	47:X:63:ASP:OD1	2.19	0.43
50:3:543:U:H2'	50:3:544:G:C8	2.54	0.43
50:3:750:C:H2'	50:3:751:U:C6	2.54	0.43
50:3:865:A:H5'	50:3:1078:U:C4	2.54	0.43
50:3:879:C:H2'	50:3:880:C:C6	2.54	0.43
50:3:1045:C:C2'	50:3:1046:A:H5'	2.49	0.43
50:3:1130:A:H61	50:3:1144:G:H1'	1.84	0.43
50:3:1469:C:H2'	50:3:1470:U:H5'	2.01	0.43
51:1:520:G:H2'	51:1:521:U:C6	2.54	0.43
51:1:572:A:H5''	51:1:573:U:OP2	2.19	0.43
51:1:1101:U:H2'	51:1:1102:C:C6	2.53	0.43
51:1:1440:U:H2'	51:1:1441:G:H8	1.84	0.43
51:1:2317:A:H2'	51:1:2318:G:O4'	2.18	0.43
51:1:2370:G:H2'	51:1:2371:G:C8	2.54	0.43
3:d:83:VAL:HG12	3:d:85:PHE:H	1.84	0.42
7:h:64:VAL:O	7:h:68:PRO:HD3	2.19	0.42
23:y:14:LEU:HA	23:y:17:GLU:HB3	2.01	0.42
29:F:16:ILE:H	29:F:16:ILE:HD12	1.84	0.42
31:H:78:LYS:O	31:H:78:LYS:HD3	2.18	0.42
32:I:7:LYS:HD2	32:I:21:LYS:HD2	2.01	0.42
34:K:18:VAL:HB	34:K:19:PRO:HD3	2.01	0.42
39:P:118:ASN:HD22	39:P:118:ASN:HA	1.61	0.42
41:R:63:VAL:HG12	41:R:68:LEU:HG	2.00	0.42
42:S:80:ARG:HG3	42:S:81:ILE:N	2.34	0.42
50:3:216:U:H2'	50:3:217:C:C6	2.53	0.42
50:3:1511:G:H2'	50:3:1512:U:O4'	2.19	0.42
51:1:158:U:O2'	51:1:159:G:H5'	2.19	0.42
51:1:571:U:O2	51:1:573:U:H2'	2.18	0.42
51:1:1710:G:O2'	51:1:1711:A:H5'	2.19	0.42
51:1:1866:A:H2'	51:1:1867:G:O4'	2.18	0.42
51:1:2799:A:H2'	51:1:2800:A:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:259:ASN:O	1:b:260:LYS:HB2	2.20	0.42
10:l:51:GLU:HB2	51:1:833:A:H1'	2.00	0.42
10:l:128:THR:HG21	51:1:636:G:H3'	2.01	0.42
12:n:96:ARG:HH22	25:B:51:ARG:HH11	1.67	0.42
16:r:68:ARG:NH2	51:1:1223:G:OP1	2.53	0.42
28:E:4:LYS:NZ	51:1:253:C:OP2	2.45	0.42
32:I:87:GLU:HG3	32:I:187:ARG:HH11	1.83	0.42
33:J:12:GLU:H	33:J:12:GLU:HG2	1.67	0.42
33:J:24:VAL:HG23	33:J:26:GLY:H	1.84	0.42
37:N:20:ILE:HG22	37:N:62:LEU:HD22	2.01	0.42
42:S:52:ARG:NH1	50:3:1317:C:N4	2.68	0.42
49:Z:41:THR:O	49:Z:44:ARG:HG3	2.18	0.42
50:3:750:C:H2'	50:3:751:U:H6	1.84	0.42
50:3:982:U:H4'	50:3:983:A:O5'	2.18	0.42
50:3:1017:U:H2'	50:3:1018:G:C8	2.54	0.42
50:3:1106:G:O2'	50:3:1107:C:H5'	2.18	0.42
51:1:96:C:H2'	51:1:97:C:C6	2.54	0.42
51:1:519:U:H2'	51:1:520:G:H8	1.84	0.42
51:1:522:A:H2'	51:1:523:C:C6	2.53	0.42
51:1:1181:U:H2'	51:1:1182:G:C8	2.54	0.42
51:1:1339:G:H2'	51:1:1340:U:O2	2.19	0.42
51:1:1339:G:H21	51:1:1603:A:H1'	1.84	0.42
51:1:1563:U:O2'	51:1:1564:C:H5'	2.19	0.42
51:1:1795:C:H2'	51:1:1796:U:O4'	2.18	0.42
51:1:1956:U:H2'	51:1:1957:C:C5'	2.44	0.42
51:1:2037:A:H2'	51:1:2038:G:C8	2.55	0.42
51:1:2098:U:O2'	51:1:2099:U:H5'	2.18	0.42
51:1:2148:G:H2'	51:1:2149:U:C5	2.54	0.42
51:1:2185:U:H2'	51:1:2186:G:C8	2.53	0.42
51:1:2273:A:H2'	51:1:2274:A:C8	2.54	0.42
51:1:2642:G:O2'	51:1:2643:G:H5'	2.19	0.42
2:c:8:LYS:HB2	2:c:201:LEU:HD11	2.02	0.42
2:c:36:GLN:HB2	2:c:67:HIS:HE1	1.84	0.42
3:d:131:THR:HG21	51:1:320:A:H2'	2.00	0.42
4:e:10:GLU:O	4:e:13:LYS:HG2	2.20	0.42
7:h:57:ASN:CG	7:h:62:ARG:HD3	2.44	0.42
11:m:46:ILE:HD12	11:m:46:ILE:HA	1.93	0.42
14:p:85:VAL:HG22	14:p:86:LYS:N	2.35	0.42
40:Q:19:ASN:C	40:Q:21:PRO:HD3	2.44	0.42
40:Q:115:LYS:O	40:Q:116:TYR:HB2	2.19	0.42
42:S:63:CYS:HB2	42:S:79:SER:OG	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:V:30:HIS:CD2	45:V:33:TYR:H	2.35	0.42
46:W:31:TYR:O	46:W:39:VAL:HG22	2.19	0.42
50:3:17:U:H2'	50:3:18:C:C6	2.55	0.42
50:3:314:C:O2'	50:3:315:A:H5'	2.19	0.42
50:3:784:A:H4'	51:1:1837:C:OP1	2.18	0.42
50:3:1039:G:H2'	50:3:1040:U:C6	2.53	0.42
50:3:1127:G:H5'	50:3:1280:A:O2'	2.20	0.42
51:1:78:U:H2'	51:1:79:C:C6	2.55	0.42
51:1:371:A:H61	51:1:401:A:H3'	1.84	0.42
51:1:724:U:O2'	51:1:725:G:H5'	2.19	0.42
51:1:864:G:H21	51:1:866:A:H62	1.68	0.42
51:1:1103:A:H2'	51:1:1104:C:OP1	2.20	0.42
51:1:2186:G:H2'	51:1:2187:U:O4'	2.20	0.42
51:1:2364:C:H2'	51:1:2365:G:O4'	2.18	0.42
53:5:31:G:H2'	53:5:32:C:C6	2.54	0.42
54:4:22:A:O2'	54:4:23:A:O4'	2.37	0.42
1:b:254:LYS:O	51:1:1797:G:H4'	2.20	0.42
32:I:13:ARG:NE	50:3:543:U:H5''	2.34	0.42
36:M:107:LYS:NZ	36:M:120:LEU:HD22	2.35	0.42
37:N:119:LYS:HE3	50:3:1351:U:O4	2.19	0.42
41:R:10:ASP:OD2	41:R:10:ASP:N	2.52	0.42
44:U:25:ARG:HE	50:3:230:G:H4'	1.84	0.42
44:U:26:ASN:ND2	44:U:31:ARG:HB3	2.34	0.42
45:V:32:ILE:HD12	45:V:32:ILE:H	1.84	0.42
47:X:3:SER:OG	47:X:4:LEU:N	2.53	0.42
50:3:710:G:O2'	50:3:711:G:H5'	2.20	0.42
50:3:1308:U:H2'	50:3:1309:G:C8	2.54	0.42
51:1:226:A:H2'	51:1:227:A:C8	2.54	0.42
51:1:729:G:H4'	51:1:763:G:H5'	2.00	0.42
51:1:1341:G:C2	51:1:1398:C:H4'	2.54	0.42
51:1:2552:U:C6	51:1:2554:U:H5'	2.54	0.42
1:b:124:LYS:HG3	1:b:127:ASN:OD1	2.20	0.42
2:c:194:PRO:HA	51:1:2680:U:H5'	2.02	0.42
3:d:5:LEU:HA	3:d:120:VAL:HG23	2.00	0.42
10:l:77:ILE:HD11	10:l:101:ILE:HG23	2.02	0.42
11:m:105:MET:HE3	11:m:108:VAL:HG21	2.01	0.42
13:o:40:ILE:HD13	52:2:8:C:O2'	2.20	0.42
16:r:21:ARG:HG3	16:r:93:PHE:HD2	1.83	0.42
16:r:80:ARG:NH1	16:r:80:ARG:HB2	2.34	0.42
29:F:16:ILE:HD12	29:F:16:ILE:N	2.35	0.42
50:3:159:G:N2	50:3:163:C:N4	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:252:U:O2	50:3:252:U:C2'	2.67	0.42
50:3:696:A:H2'	50:3:697:U:H6	1.85	0.42
50:3:911:U:H2'	50:3:912:C:C6	2.55	0.42
50:3:1086:U:O5'	50:3:1086:U:H6	2.03	0.42
50:3:1188:A:C2'	50:3:1189:U:H5'	2.49	0.42
50:3:1530:G:H2'	50:3:1531:A:H8	1.85	0.42
51:1:217:A:H2'	51:1:218:A:O4'	2.19	0.42
51:1:494:G:O2'	51:1:495:G:H5'	2.19	0.42
51:1:756:A:H2'	51:1:757:G:O4'	2.19	0.42
51:1:1028:A:N6	51:1:1125:G:H2'	2.34	0.42
51:1:1079:C:H2'	51:1:1080:A:C8	2.54	0.42
51:1:1562:U:H2'	51:1:1563:U:O4'	2.19	0.42
51:1:1658:C:H2'	51:1:1659:G:C8	2.55	0.42
52:2:93:C:H2'	52:2:94:A:H8	1.84	0.42
53:5:25:C:O2'	53:5:26:G:H5'	2.19	0.42
1:b:269:ARG:NH2	51:1:1798:U:OP2	2.49	0.42
3:d:43:THR:HB	51:1:38:A:N3	2.34	0.42
11:m:75:GLU:HB2	11:m:90:GLU:HG3	2.01	0.42
17:s:6:LYS:HG3	51:1:494:G:H4'	2.01	0.42
22:x:16:ASN:HB3	22:x:24:THR:HG23	2.00	0.42
33:J:19:ARG:NE	55:8:131:MET:SD	2.92	0.42
41:R:104:ASN:HB3	41:R:105:ALA:H	1.74	0.42
50:3:754:C:H3'	50:3:754:C:O2	2.20	0.42
50:3:823:C:H2'	50:3:824:G:C8	2.54	0.42
50:3:1140:C:H2'	50:3:1141:C:C6	2.54	0.42
51:1:18:U:H2'	51:1:19:A:H8	1.82	0.42
51:1:466:A:H2'	51:1:467:G:H5'	2.00	0.42
51:1:828:U:H2'	51:1:829:A:C8	2.55	0.42
51:1:1246:A:H2'	51:1:1247:A:O4'	2.18	0.42
51:1:1479:G:O2'	51:1:1480:C:H5'	2.19	0.42
51:1:1777:U:O2'	51:1:1778:U:H5'	2.20	0.42
51:1:1990:C:H2'	51:1:1991:U:C1'	2.49	0.42
51:1:2441:U:O2'	51:1:2442:C:H5'	2.19	0.42
52:2:94:A:H2'	52:2:95:U:O4'	2.19	0.42
1:b:61:TYR:HA	1:b:85:ASN:OD1	2.19	0.42
4:e:50:ASP:OD1	4:e:50:ASP:N	2.52	0.42
27:D:22:MET:O	27:D:28:ARG:NH1	2.52	0.42
30:G:143:LEU:O	30:G:147:LEU:HB3	2.19	0.42
34:K:12:PRO:HA	34:K:15:SER:HB3	2.01	0.42
36:M:45:ILE:HD11	36:M:60:LEU:HB2	2.01	0.42
42:S:25:GLU:HA	42:S:28:ALA:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:X:36:ARG:HB2	50:3:1318:A:O2'	2.19	0.42
50:3:819:A:H5'	50:3:820:U:C5	2.54	0.42
50:3:1325:C:O2'	50:3:1326:U:H5'	2.20	0.42
50:3:1401:G:C2'	50:3:1402:C:H5'	2.50	0.42
51:1:241:A:O3'	51:1:242:G:H4'	2.20	0.42
51:1:394:C:H2'	51:1:395:U:O4'	2.19	0.42
51:1:633:A:H1'	51:1:2403:C:H4'	2.02	0.42
51:1:814:C:H2'	51:1:815:C:C6	2.54	0.42
51:1:1198:U:H2'	51:1:1199:U:C6	2.54	0.42
51:1:1275:A:N6	51:1:1296:G:H4'	2.34	0.42
51:1:1437:C:H2'	51:1:1438:U:H6	1.82	0.42
51:1:1857:G:H1'	51:1:1885:A:N6	2.34	0.42
51:1:2040:G:H2'	51:1:2041:U:O4'	2.20	0.42
52:2:115:A:H2'	52:2:116:G:C8	2.54	0.42
55:8:10:ILE:HA	55:8:11:PRO:HD2	1.88	0.42
2:c:125:TRP:CG	2:c:160:LYS:HB3	2.55	0.42
4:e:47:LYS:HA	4:e:47:LYS:HD3	1.89	0.42
6:g:43:ASN:HA	6:g:43:ASN:HD22	1.67	0.42
7:h:12:VAL:O	7:h:15:VAL:HG22	2.19	0.42
9:k:40:LYS:NZ	51:1:2561:U:O3'	2.47	0.42
20:v:76:ASP:OD1	20:v:77:VAL:N	2.53	0.42
26:C:36:LYS:HG3	26:C:46:VAL:O	2.19	0.42
30:G:72:LYS:HB2	30:G:75:ALA:HB3	2.01	0.42
32:I:2:ARG:NH2	50:3:407:U:H5'	2.32	0.42
40:Q:113:ARG:HE	50:3:501:C:P	2.42	0.42
46:W:54:LEU:O	46:W:58:ILE:HG12	2.19	0.42
49:Z:22:CYS:SG	49:Z:23:GLU:N	2.93	0.42
50:3:748:G:H2'	50:3:749:A:H8	1.84	0.42
50:3:1225:A:H2'	50:3:1225:A:N3	2.35	0.42
50:3:1429:A:H2'	50:3:1430:A:C8	2.55	0.42
51:1:598:U:H2'	51:1:599:A:H8	1.85	0.42
51:1:825:A:O2'	51:1:826:U:H5'	2.20	0.42
51:1:831:G:H2'	51:1:832:U:H5'	2.02	0.42
51:1:1117:C:O2'	51:1:1118:C:H5'	2.20	0.42
51:1:2033:A:H1'	51:1:2035:G:OP2	2.20	0.42
52:2:16:G:H1	52:2:68:C:H42	1.67	0.42
52:2:117:G:H2'	52:2:118:C:H5'	2.02	0.42
9:k:71:ARG:HD3	9:k:71:ARG:HA	1.95	0.42
30:G:96:LEU:O	30:G:97:GLY:C	2.63	0.42
31:H:4:VAL:O	31:H:6:PRO:HD3	2.19	0.42
32:I:7:LYS:O	32:I:20:LEU:HD23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:X:35:ARG:HA	47:X:70:LEU:HD12	2.01	0.42
50:3:9:G:O2'	50:3:10:A:H5'	2.20	0.42
50:3:222:C:H2'	50:3:223:A:C8	2.54	0.42
50:3:592:G:H2'	50:3:593:U:O4'	2.18	0.42
50:3:742:G:O2'	50:3:743:A:H5'	2.20	0.42
50:3:746:A:H4'	50:3:837:U:O2'	2.20	0.42
51:1:277:G:H3'	51:1:277:G:N3	2.35	0.42
51:1:832:U:H2'	51:1:833:A:C8	2.55	0.42
51:1:979:A:H2'	51:1:982:C:H42	1.84	0.42
51:1:2519:U:C6	51:1:2542:A:N6	2.88	0.42
3:d:151:GLY:HA2	3:d:172:ALA:HB2	2.02	0.42
7:h:59:LEU:HG	7:h:60:LEU:HD23	2.02	0.42
8:j:2:LYS:HE3	51:1:995:C:N4	2.35	0.42
8:j:6:ALA:H	8:j:45:THR:HG21	1.85	0.42
8:j:109:LEU:CD2	8:j:110:PRO:HD2	2.49	0.42
23:y:32:ALA:HB2	23:y:37:LEU:HD23	2.02	0.42
32:l:69:ARG:NH1	50:3:402:G:OP2	2.53	0.42
33:J:104:ILE:H	33:J:104:ILE:HD12	1.85	0.42
37:N:17:ARG:HD3	50:3:1147:C:O2'	2.20	0.42
46:W:49:LYS:NZ	50:3:663:A:H5'	2.35	0.42
47:X:10:ILE:HG12	47:X:37:SER:HB3	2.02	0.42
50:3:580:C:H2'	50:3:581:G:O4'	2.20	0.42
50:3:945:G:N3	50:3:945:G:H2'	2.35	0.42
50:3:1185:G:H2'	50:3:1186:G:C8	2.55	0.42
50:3:1264:U:H3	50:3:1271:A:H61	1.68	0.42
50:3:1280:A:O2'	50:3:1281:C:H5'	2.20	0.42
50:3:1384:C:H2'	50:3:1385:G:H8	1.85	0.42
50:3:1420:U:H2'	50:3:1421:G:C8	2.55	0.42
51:1:842:U:H2'	51:1:843:G:C8	2.55	0.42
51:1:1188:U:O2'	51:1:1189:A:H5'	2.20	0.42
51:1:1469:A:H2'	51:1:1470:A:C8	2.55	0.42
51:1:2114:A:N7	51:1:2115:G:H1'	2.35	0.42
51:1:2484:G:O2'	51:1:2485:G:H5'	2.19	0.42
51:1:2771:C:H2'	51:1:2772:C:C6	2.55	0.42
1:b:209:ALA:HA	1:b:212:TRP:CE2	2.55	0.41
3:d:45:ALA:CB	51:1:38:A:H4'	2.50	0.41
7:h:1:MET:HE3	7:h:6:GLN:HG3	2.02	0.41
10:l:38:GLN:HG2	51:1:805:G:H5''	2.02	0.41
31:H:59:PRO:O	31:H:62:SER:OG	2.36	0.41
35:L:39:GLU:O	35:L:42:VAL:HG22	2.19	0.41
36:M:45:ILE:HG13	36:M:61:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:N:74:GLN:HE22	50:3:1249:C:H4'	1.84	0.41
44:U:25:ARG:NH2	50:3:230:G:O4'	2.52	0.41
45:V:14:ASP:O	45:V:16:MET:N	2.53	0.41
50:3:1444:U:H2'	50:3:1445:U:C6	2.55	0.41
50:3:1499:A:O2'	50:3:1500:A:H5'	2.20	0.41
51:1:397:U:O5'	51:1:397:U:H6	2.03	0.41
51:1:588:U:H2'	51:1:589:U:C6	2.54	0.41
51:1:965:C:H2'	51:1:966:G:C8	2.51	0.41
51:1:969:G:H2'	51:1:970:U:C6	2.54	0.41
51:1:1061:U:H4'	51:1:1070:A:O4'	2.20	0.41
51:1:1435:G:O2'	51:1:1436:G:H5'	2.20	0.41
51:1:2621:G:H2'	51:1:2622:U:O4'	2.20	0.41
53:5:42:G:H2'	53:5:43:A:H8	1.85	0.41
2:c:197:THR:O	51:1:2820:A:N6	2.53	0.41
3:d:65:THR:OG1	3:d:66:GLY:N	2.51	0.41
5:f:102:ILE:HG22	5:f:104:LEU:HD22	2.02	0.41
11:m:65:ILE:N	11:m:65:ILE:HD12	2.35	0.41
28:E:44:ARG:N	28:E:45:PRO:CD	2.83	0.41
35:L:101:ARG:O	35:L:105:GLU:HG3	2.20	0.41
47:X:36:ARG:HD3	50:3:1318:A:H1'	2.02	0.41
50:3:109:A:C6	50:3:326:G:C6	3.08	0.41
50:3:537:G:H2'	50:3:538:G:C8	2.55	0.41
50:3:832:G:O2'	50:3:833:G:H5'	2.20	0.41
50:3:1014:A:C2	50:3:1219:A:H1'	2.55	0.41
50:3:1202:U:H2'	50:3:1203:C:H5'	2.02	0.41
51:1:1172:C:H3'	51:1:1173:U:H5''	2.02	0.41
51:1:1442:U:H2'	51:1:1443:U:C6	2.55	0.41
51:1:1937:A:O2'	51:1:1938:A:H3'	2.20	0.41
51:1:2086:U:H2'	51:1:2087:G:C8	2.55	0.41
51:1:2505:G:N2	51:1:2506:U:O4	2.50	0.41
3:d:84:THR:CG2	51:1:586:A:H5'	2.37	0.41
7:h:33:VAL:HA	51:1:1055:G:C5'	2.51	0.41
8:j:7:LYS:HA	8:j:8:PRO:HD3	1.89	0.41
10:l:78:ARG:HB3	10:l:113:ALA:HB2	2.03	0.41
11:m:41:LEU:CD1	11:m:96:ILE:HD11	2.50	0.41
30:G:31:PHE:O	30:G:39:ILE:HB	2.20	0.41
30:G:67:LEU:HD11	30:G:91:VAL:HG23	2.03	0.41
31:H:76:ILE:HG22	31:H:83:VAL:HG21	2.02	0.41
33:J:46:GLY:HA3	33:J:70:MET:HE2	2.02	0.41
34:K:6:ILE:HD13	34:K:89:VAL:HG22	2.01	0.41
37:N:17:ARG:HH22	50:3:1129:C:H5''	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Q:40:THR:HA	40:Q:41:PRO:HD3	1.83	0.41
50:3:593:U:H2'	50:3:594:U:C6	2.56	0.41
50:3:626:G:H2'	50:3:627:G:C8	2.56	0.41
50:3:665:A:N3	50:3:732:C:H2'	2.36	0.41
51:1:38:A:H2'	51:1:39:G:O4'	2.20	0.41
51:1:139:U:C5'	51:1:140:C:H5'	2.50	0.41
51:1:580:U:H2'	51:1:581:C:H6	1.84	0.41
51:1:1387:A:H5'	51:1:1469:A:H1'	2.02	0.41
51:1:1476:U:O2'	51:1:1477:A:H5'	2.21	0.41
51:1:1741:C:O2'	51:1:1742:U:H5'	2.19	0.41
51:1:1780:A:H3'	51:1:1781:U:H2'	2.01	0.41
51:1:2087:G:H2'	51:1:2088:A:H8	1.84	0.41
51:1:2329:U:H2'	51:1:2330:G:C8	2.55	0.41
51:1:2830:C:O2'	51:1:2831:G:H5'	2.20	0.41
1:b:48:ILE:HG13	51:1:779:U:OP1	2.19	0.41
1:b:94:LEU:HD13	1:b:100:ARG:CD	2.50	0.41
7:h:101:LYS:C	7:h:101:LYS:HD3	2.45	0.41
10:l:3:LEU:HD23	51:1:1203:U:C5'	2.50	0.41
11:m:33:LEU:HB2	11:m:117:PHE:CE1	2.56	0.41
21:w:17:LEU:HD11	21:w:37:ARG:NH2	2.36	0.41
24:z:35:VAL:HG22	24:z:37:ARG:NH1	2.35	0.41
32:I:147:LYS:HZ2	50:3:490:C:H5''	1.86	0.41
38:O:15:HIS:ND1	38:O:16:ARG:HG2	2.35	0.41
39:P:24:ALA:HB1	39:P:89:GLY:HA3	2.03	0.41
42:S:29:ILE:O	42:S:34:ASN:ND2	2.53	0.41
43:T:88:ARG:HD3	43:T:88:ARG:N	2.16	0.41
51:1:167:A:H2'	51:1:168:G:O4'	2.20	0.41
51:1:644:A:H2'	51:1:645:C:O4'	2.20	0.41
51:1:987:C:H2'	51:1:988:A:O4'	2.21	0.41
51:1:1127:A:C2'	51:1:1128:G:H5''	2.50	0.41
51:1:1435:G:H2'	51:1:1436:G:H8	1.84	0.41
51:1:1842:G:H2'	51:1:1843:C:O4'	2.20	0.41
51:1:2169:A:H2'	51:1:2170:A:O4'	2.21	0.41
51:1:2557:G:H2'	51:1:2558:C:C6	2.55	0.41
51:1:2632:A:O2'	51:1:2633:G:H5'	2.21	0.41
51:1:2697:G:H2'	51:1:2698:U:O4'	2.20	0.41
51:1:2849:U:H4'	51:1:2850:A:H5'	2.03	0.41
51:1:2855:C:H2'	51:1:2856:A:C8	2.55	0.41
4:e:118:ALA:C	4:e:119:LYS:HD2	2.45	0.41
16:r:10:LYS:HG2	51:1:996:A:O4'	2.20	0.41
21:w:39:THR:HG21	51:1:2336:A:N6	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:17:SER:OG	51:1:15:G:H4'	2.20	0.41
28:E:30:HIS:O	28:E:31:ILE:C	2.63	0.41
29:F:8:LYS:H	29:F:35:GLN:HE22	1.67	0.41
33:J:22:LYS:HD3	50:3:1081:A:H5'	2.01	0.41
33:J:104:ILE:HD12	33:J:104:ILE:N	2.35	0.41
37:N:98:ARG:NH2	50:3:1177:G:OP2	2.53	0.41
46:W:13:THR:HB	46:W:50:TYR:HE1	1.86	0.41
50:3:605:U:H2'	50:3:606:G:C8	2.55	0.41
51:1:167:A:H2'	51:1:168:G:H5'	2.02	0.41
51:1:419:U:H2'	51:1:420:C:H6	1.85	0.41
51:1:467:G:C2'	51:1:468:G:H5'	2.49	0.41
51:1:809:G:O2'	51:1:810:U:H5'	2.20	0.41
51:1:1026:G:H2'	51:1:1027:A:C8	2.55	0.41
51:1:1669:A:H5''	51:1:2550:G:OP1	2.20	0.41
55:8:77:TYR:HB2	55:8:83:ASN:CG	2.45	0.41
1:b:156:SER:HB3	1:b:159:THR:HG21	2.02	0.41
3:d:68:ALA:HA	51:1:1255:U:C5	2.55	0.41
3:d:176:ASP:HA	3:d:177:PRO:HD3	1.83	0.41
4:e:27:VAL:HA	4:e:28:PRO:HD3	1.92	0.41
8:j:49:ASP:OD2	8:j:121:LYS:HE2	2.20	0.41
8:j:95:ARG:HA	8:j:95:ARG:HD2	1.77	0.41
11:m:1:MET:HA	11:m:47:GLU:HG3	2.03	0.41
11:m:82:MET:HE2	51:1:960:A:H61	1.85	0.41
14:p:105:LYS:HE3	14:p:105:LYS:HB3	1.82	0.41
18:t:40:LYS:HD2	51:1:1598:A:H5''	2.02	0.41
30:G:94:ARG:NH1	50:3:1100:C:H5	2.18	0.41
34:K:7:VAL:HG12	34:K:88:MET:HG2	2.01	0.41
34:K:42:TRP:HB2	34:K:59:TYR:HB2	2.03	0.41
35:L:56:SER:OG	35:L:59:GLU:HB2	2.20	0.41
39:P:126:ARG:HH22	50:3:693:G:P	2.44	0.41
43:T:50:HIS:O	43:T:53:ARG:HB3	2.20	0.41
48:Y:4:LYS:HG3	50:3:332:G:P	2.60	0.41
49:Z:33:ARG:O	49:Z:33:ARG:HG3	2.20	0.41
50:3:350:G:H2'	50:3:351:G:C8	2.55	0.41
50:3:1144:G:O2'	50:3:1145:A:H5'	2.20	0.41
50:3:1514:G:H2'	50:3:1515:G:H8	1.84	0.41
51:1:11:C:C2'	51:1:12:U:H5''	2.47	0.41
51:1:95:A:C2'	51:1:96:C:H5''	2.50	0.41
51:1:479:A:H1'	51:1:481:G:H5''	2.02	0.41
51:1:566:U:O2'	51:1:567:U:H5'	2.20	0.41
51:1:2159:G:C2'	51:1:2160:C:H5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:48:LEU:HA	55:8:49:PRO:HD3	1.88	0.41
4:e:15:LEU:HA	4:e:18:GLU:HB2	2.02	0.41
4:e:35:LEU:HB2	4:e:88:VAL:HB	2.02	0.41
7:h:42:ARG:NE	7:h:42:ARG:HA	2.36	0.41
9:k:39:ILE:O	9:k:39:ILE:HG13	2.19	0.41
18:t:64:LYS:HA	18:t:79:ASP:OD2	2.21	0.41
34:K:51:ILE:C	34:K:53:LYS:H	2.29	0.41
40:Q:43:LYS:HB3	40:Q:44:PRO:CD	2.47	0.41
40:Q:45:ASN:HA	55:8:117:ARG:HH11	1.85	0.41
44:U:5:ARG:NE	50:3:376:G:O3'	2.53	0.41
46:W:13:THR:O	46:W:15:GLU:N	2.54	0.41
49:Z:37:TYR:HB3	50:3:1526:G:OP2	2.20	0.41
50:3:1234:C:H1'	50:3:1364:U:O2	2.20	0.41
51:1:95:A:H2'	51:1:96:C:C5'	2.49	0.41
51:1:126:A:C6	51:1:127:A:N1	2.88	0.41
51:1:582:A:H2'	51:1:583:G:H8	1.86	0.41
51:1:1075:C:H5'	51:1:1076:C:H5	1.84	0.41
51:1:1431:A:O2'	51:1:1432:G:H5'	2.21	0.41
51:1:1512:C:O2'	51:1:1513:U:H5'	2.20	0.41
51:1:1758:U:H5	51:1:2696:U:H5'	1.84	0.41
51:1:1821:A:H2'	51:1:1822:C:C6	2.56	0.41
51:1:1914:C:P	55:8:106:ARG:NH1	2.94	0.41
51:1:2480:C:H2'	51:1:2481:G:O4'	2.20	0.41
51:1:2553:G:C3'	51:1:2554:U:H5''	2.51	0.41
51:1:2641:G:O2'	51:1:2642:G:H5'	2.21	0.41
54:4:25:A:H5''	55:8:108:THR:HG22	2.03	0.41
55:8:85:GLU:HA	55:8:88:LEU:HB2	2.02	0.41
1:b:180:MET:HE2	1:b:268:ARG:HE	1.86	0.41
2:c:34:VAL:HG13	2:c:93:GLY:H	1.85	0.41
5:f:86:LEU:HD12	5:f:86:LEU:N	2.36	0.41
7:h:61:ARG:HD2	7:h:61:ARG:HA	1.92	0.41
8:j:8:PRO:HG3	8:j:48:VAL:HG13	2.02	0.41
8:j:28:LEU:O	8:j:32:LEU:HD13	2.21	0.41
8:j:120:ARG:HD3	51:1:2780:G:H5'	2.03	0.41
10:l:37:GLY:N	10:l:40:SER:OG	2.49	0.41
13:o:31:THR:CG2	13:o:32:PRO:HD2	2.50	0.41
17:s:20:VAL:HG21	17:s:43:ALA:HB3	2.03	0.41
21:w:69:GLY:HA2	21:w:70:PRO:HD3	1.91	0.41
30:G:55:GLU:HA	30:G:58:LYS:NZ	2.36	0.41
36:M:104:SER:O	50:3:642:A:H2	2.03	0.41
47:X:57:VAL:HA	47:X:58:PRO:HD3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:35:G:H2'	50:3:36:C:C6	2.56	0.41
50:3:253:A:N6	50:3:274:A:C6	2.89	0.41
50:3:355:C:O2'	50:3:388:G:H1'	2.21	0.41
50:3:414:A:H62	50:3:430:A:H61	1.68	0.41
50:3:438:U:H3'	50:3:493:A:N6	2.36	0.41
50:3:1171:A:H2'	50:3:1172:C:C6	2.55	0.41
51:1:629:G:H5''	51:1:650:C:O2'	2.21	0.41
51:1:737:C:H2'	51:1:738:G:O4'	2.21	0.41
51:1:1167:C:H2'	51:1:1168:G:C8	2.56	0.41
51:1:1326:U:H2'	51:1:1327:A:C8	2.55	0.41
51:1:1423:G:H2'	51:1:1424:G:H8	1.86	0.41
51:1:1430:G:H2'	51:1:1431:A:C8	2.55	0.41
51:1:1583:A:H4'	51:1:1585:C:N4	2.36	0.41
51:1:1753:G:N2	51:1:1755:A:H3'	2.36	0.41
51:1:2114:A:H5''	51:1:2119:A:N6	2.35	0.41
51:1:2788:C:H2'	51:1:2789:C:C6	2.56	0.41
55:8:132:ARG:O	55:8:132:ARG:HG2	2.21	0.41
3:d:97:ASN:HB2	3:d:100:MET:HG3	2.03	0.41
6:g:117:LEU:HA	6:g:118:PRO:HD3	1.84	0.41
7:h:97:LYS:NZ	7:h:131:THR:HG21	2.36	0.41
8:j:98:GLU:HB2	8:j:124:VAL:HG13	2.03	0.41
11:m:21:ALA:HB2	11:m:97:GLN:O	2.20	0.41
12:n:2:ARG:HD2	51:1:2822:G:O6	2.21	0.41
13:o:32:PRO:CB	52:2:52:A:H61	2.34	0.41
13:o:98:GLN:HG3	13:o:100:HIS:HB2	2.02	0.41
15:q:32:ARG:NH2	51:1:578:G:O2'	2.54	0.41
16:r:97:LYS:HZ2	16:r:97:LYS:HG3	1.74	0.41
30:G:65:LYS:HD2	30:G:89:PHE:HE2	1.85	0.41
30:G:137:THR:O	30:G:141:GLU:HG2	2.20	0.41
31:H:86:LEU:HA	31:H:89:VAL:HG12	2.01	0.41
32:I:53:GLN:CB	32:I:202:LEU:HD11	2.51	0.41
37:N:49:GLN:N	37:N:50:PRO:HD2	2.36	0.41
37:N:71:ILE:HG23	37:N:72:SER:N	2.35	0.41
42:S:62:ARG:NH1	42:S:69:PRO:HB3	2.36	0.41
42:S:99:SER:OG	50:3:1187:G:N3	2.54	0.41
47:X:49:ALA:HA	47:X:58:PRO:HA	2.03	0.41
48:Y:41:GLY:HA2	48:Y:85:LEU:HD11	2.02	0.41
49:Z:39:LYS:HB3	49:Z:40:PRO:HD3	2.02	0.41
50:3:47:C:H5'	50:3:365:U:C2	2.56	0.41
50:3:358:U:H2'	50:3:359:G:H8	1.84	0.41
50:3:572:A:C5'	50:3:917:G:H4'	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:3:778:G:H2'	50:3:779:C:O4'	2.21	0.41
50:3:893:C:H2'	50:3:894:G:C8	2.56	0.41
50:3:1071:C:H2'	50:3:1072:G:H8	1.84	0.41
50:3:1167:A:N3	50:3:1167:A:H2'	2.36	0.41
50:3:1198:G:H8	50:3:1198:G:H5'	1.85	0.41
50:3:1238:A:C8	50:3:1303:C:H1'	2.56	0.41
50:3:1346:A:C2'	50:3:1347:G:H4'	2.51	0.41
50:3:1528:U:H4'	50:3:1529:G:H21	1.85	0.41
51:1:173:A:H2'	51:1:174:U:C6	2.56	0.41
51:1:186:G:H2'	51:1:187:G:H8	1.84	0.41
51:1:527:C:C4	51:1:2779:U:H2'	2.55	0.41
51:1:816:C:H2'	51:1:817:C:C6	2.56	0.41
51:1:816:C:H2'	51:1:817:C:H6	1.85	0.41
51:1:1023:U:H4'	51:1:1123:C:OP1	2.21	0.41
51:1:1150:C:H2'	51:1:1151:A:O4'	2.21	0.41
51:1:1749:A:H2'	51:1:1750:G:H8	1.85	0.41
51:1:2087:G:H2'	51:1:2088:A:C8	2.55	0.41
51:1:2326:C:O2'	51:1:2327:A:OP1	2.29	0.41
51:1:2413:G:H3'	51:1:2414:G:H5''	2.02	0.41
51:1:2648:G:H2'	51:1:2649:C:O4'	2.21	0.41
51:1:2844:G:H2'	51:1:2845:U:C6	2.56	0.41
3:d:54:GLY:HA3	3:d:74:LYS:HD3	2.02	0.41
3:d:121:VAL:HG22	3:d:122:GLU:H	1.86	0.41
4:e:3:LEU:HA	4:e:6:TYR:HB3	2.03	0.41
5:f:90:GLY:HA3	5:f:93:TYR:CD2	2.56	0.41
16:r:60:LYS:HB2	16:r:100:GLY:HA3	2.03	0.41
39:P:125:LYS:O	39:P:126:ARG:HB2	2.21	0.41
42:S:5:MET:HE2	42:S:62:ARG:CZ	2.51	0.41
50:3:915:A:H2'	50:3:916:U:H5'	2.03	0.41
50:3:1098:C:H2'	50:3:1099:G:H8	1.85	0.41
51:1:616:A:H2'	51:1:617:G:O4'	2.21	0.41
51:1:942:G:H2'	51:1:943:A:O4'	2.21	0.41
51:1:2112:G:H5''	51:1:2113:U:C5	2.56	0.41
51:1:2358:A:H2'	51:1:2359:C:O4'	2.21	0.41
51:1:2361:G:O2'	51:1:2362:C:H5'	2.21	0.41
51:1:2649:C:H2'	51:1:2650:U:C6	2.56	0.41
1:b:204:LEU:HB3	1:b:209:ALA:CB	2.50	0.40
3:d:5:LEU:HB2	3:d:10:SER:H	1.86	0.40
4:e:33:ILE:HG22	4:e:155:ILE:HD12	2.01	0.40
6:g:79:THR:C	6:g:80:ILE:HD12	2.46	0.40
11:m:77:PRO:O	11:m:80:VAL:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:n:24:MET:HE1	12:n:40:LYS:HB3	2.02	0.40
13:o:35:ILE:HD11	13:o:102:ARG:HD2	2.03	0.40
17:s:52:GLU:OE2	51:1:488:G:H5'	2.21	0.40
27:D:21:ARG:NH1	51:1:466:A:H5'	2.36	0.40
39:P:31:VAL:O	39:P:31:VAL:HG13	2.20	0.40
46:W:13:THR:O	46:W:16:GLY:N	2.53	0.40
49:Z:63:ASN:HD22	49:Z:65:ARG:HG3	1.85	0.40
50:3:320:A:H2'	50:3:321:A:O4'	2.21	0.40
50:3:1306:A:N6	50:3:1331:G:O2'	2.55	0.40
50:3:1329:A:O2'	50:3:1330:U:H5'	2.21	0.40
50:3:1484:C:H2'	50:3:1485:U:O4'	2.21	0.40
51:1:288:U:H2'	51:1:289:G:C8	2.56	0.40
51:1:705:A:C2	51:1:727:A:H1'	2.56	0.40
51:1:823:C:H2'	51:1:824:U:O4'	2.22	0.40
51:1:1210:G:O5'	51:1:1212:G:H5'	2.21	0.40
51:1:1464:G:H2'	51:1:1465:G:C8	2.56	0.40
51:1:1512:C:H2'	51:1:1513:U:O4'	2.21	0.40
51:1:1682:G:H2'	51:1:1683:U:C6	2.56	0.40
51:1:1795:C:C4	51:1:1796:U:C4	3.09	0.40
51:1:2104:C:H2'	51:1:2105:U:C6	2.56	0.40
51:1:2568:U:H2'	51:1:2569:G:O4'	2.21	0.40
51:1:2719:G:H5'	51:1:2847:U:OP1	2.21	0.40
51:1:2781:A:H5''	51:1:2782:G:H5'	2.03	0.40
6:g:29:PHE:HB2	51:1:2198:A:C2	2.56	0.40
12:n:31:HIS:C	12:n:33:ILE:H	2.29	0.40
19:u:73:ASN:O	19:u:74:ALA:HB3	2.22	0.40
27:D:9:VAL:HG12	51:1:1309:G:OP1	2.22	0.40
32:I:8:LEU:HD12	50:3:429:U:H5'	2.03	0.40
33:J:14:LEU:C	33:J:14:LEU:HD23	2.46	0.40
33:J:106:ALA:HB2	33:J:124:ALA:HB3	2.02	0.40
35:L:113:LYS:HB2	50:3:1297:G:H21	1.85	0.40
46:W:12:PHE:O	46:W:13:THR:C	2.63	0.40
50:3:166:U:H2'	50:3:167:A:C8	2.55	0.40
50:3:854:U:H2'	50:3:855:U:C6	2.56	0.40
51:1:441:U:O2'	51:1:442:G:H5'	2.21	0.40
51:1:1712:U:H2'	51:1:1713:A:C8	2.57	0.40
51:1:1866:A:C2'	51:1:1867:G:H5'	2.51	0.40
51:1:2654:A:O3'	51:1:2655:G:H4'	2.21	0.40
51:1:2811:G:O2'	51:1:2812:G:H5'	2.21	0.40
52:2:4:C:H5'	52:2:4:C:H6	1.86	0.40
53:5:67:C:H2'	53:5:68:C:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:224:MET:HE2	51:1:782:A:C6	2.55	0.40
14:p:49:ILE:H	14:p:95:LYS:NZ	2.19	0.40
14:p:114:ASN:HD22	14:p:114:ASN:HA	1.72	0.40
15:q:67:ALA:O	15:q:70:GLN:HG2	2.21	0.40
19:u:90:LYS:HE2	19:u:90:LYS:HB2	1.94	0.40
21:w:10:ARG:NH1	51:1:2280:G:N7	2.70	0.40
31:H:64:ARG:HE	31:H:101:ASN:ND2	2.19	0.40
35:L:101:ARG:NE	50:3:939:G:H4'	2.34	0.40
37:N:54:VAL:HG13	37:N:55:ASP:N	2.35	0.40
47:X:14:LEU:O	47:X:18:VAL:HG23	2.21	0.40
50:3:819:A:H5'	50:3:820:U:H5	1.85	0.40
50:3:871:U:H5''	50:3:872:A:OP2	2.21	0.40
51:1:420:C:H2'	51:1:421:C:C6	2.56	0.40
51:1:523:C:O2'	51:1:524:G:H5'	2.21	0.40
51:1:1063:G:N2	51:1:1075:C:H42	2.20	0.40
51:1:1796:U:H2'	51:1:1797:G:H8	1.81	0.40
51:1:1887:C:H2'	51:1:1888:G:O4'	2.21	0.40
3:d:44:ARG:NH1	51:1:1248:G:OP1	2.35	0.40
6:g:15:LEU:HD23	6:g:15:LEU:C	2.46	0.40
8:j:113:PRO:HG3	51:1:529:A:OP2	2.21	0.40
9:k:70:ARG:NH2	51:1:2683:C:O2	2.55	0.40
15:q:51:GLN:HB3	15:q:55:GLN:HE21	1.86	0.40
15:q:102:LYS:HD2	15:q:102:LYS:HA	1.93	0.40
16:r:79:ARG:HH22	51:1:563:A:P	2.44	0.40
23:y:43:LEU:HD22	51:1:61:C:H5''	2.03	0.40
31:H:75:VAL:HG11	31:H:102:ILE:HG21	2.03	0.40
32:I:122:ILE:HD12	32:I:122:ILE:HA	1.97	0.40
34:K:25:TYR:CD1	34:K:74:LEU:HD11	2.56	0.40
38:O:78:GLU:HG2	38:O:80:THR:HG23	2.02	0.40
39:P:53:GLY:O	39:P:55:ARG:N	2.44	0.40
41:R:112:ARG:N	41:R:112:ARG:HD3	2.37	0.40
42:S:92:ILE:HB	42:S:95:LEU:HD22	2.04	0.40
45:V:38:LYS:O	45:V:38:LYS:HD2	2.21	0.40
50:3:340:U:H2'	50:3:341:C:C6	2.57	0.40
50:3:800:G:H2'	50:3:801:U:C5	2.56	0.40
50:3:1431:A:H2'	50:3:1432:G:O4'	2.21	0.40
51:1:236:C:H2'	51:1:237:C:C6	2.56	0.40
51:1:270:A:C2	51:1:369:U:H4'	2.56	0.40
51:1:327:G:H2'	51:1:328:U:O4'	2.22	0.40
51:1:686:U:H3'	51:1:687:C:C5'	2.51	0.40
51:1:1125:G:H3'	51:1:1126:A:H2'	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1526:C:H2'	51:1:1527:G:O4'	2.22	0.40
51:1:1551:A:H2'	51:1:1552:A:O4'	2.22	0.40
51:1:2075:U:H2'	51:1:2238:G:N2	2.36	0.40
51:1:2343:U:O2'	51:1:2344:U:H5'	2.21	0.40
51:1:2545:G:C2'	51:1:2546:U:H5'	2.51	0.40
51:1:2732:G:H3'	51:1:2733:A:C5'	2.52	0.40
1:b:209:ALA:HA	1:b:212:TRP:NE1	2.36	0.40
8:j:140:LEU:HD12	8:j:140:LEU:C	2.47	0.40
26:C:41:VAL:HG23	26:C:42:VAL:HG13	2.03	0.40
31:H:110:LEU:HD22	31:H:145:ALA:HB2	2.03	0.40
32:I:30:LYS:HB3	50:3:411:A:N7	2.36	0.40
32:I:145:ARG:HH21	32:I:148:ALA:HB2	1.87	0.40
32:I:151:GLN:O	32:I:152:SER:OG	2.33	0.40
33:J:79:THR:OG1	33:J:80:LEU:N	2.54	0.40
40:Q:74:GLN:HE21	40:Q:75:GLU:HB2	1.86	0.40
48:Y:68:LYS:HE3	50:3:185:U:H4'	2.04	0.40
50:3:696:A:H2'	50:3:697:U:C6	2.56	0.40
50:3:768:A:OP1	50:3:804:U:H4'	2.22	0.40
50:3:936:C:H2'	50:3:937:A:C8	2.56	0.40
50:3:1062:U:H2'	50:3:1063:C:C6	2.57	0.40
50:3:1171:A:O2'	50:3:1172:C:H5'	2.21	0.40
50:3:1434:A:H2'	50:3:1435:G:O4'	2.22	0.40
51:1:227:A:C2'	51:1:228:C:H4'	2.52	0.40
51:1:1057:A:H2'	51:1:1057:A:N3	2.36	0.40
51:1:1367:A:H2'	51:1:1368:G:H5'	2.04	0.40
51:1:1746:A:H2'	51:1:1747:U:C6	2.55	0.40
51:1:1747:U:H2'	51:1:1748:C:C6	2.56	0.40
51:1:2801:G:H2'	51:1:2802:G:C8	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	236 (88%)	29 (11%)	4 (2%)	8	37
2	c	207/209 (99%)	180 (87%)	23 (11%)	4 (2%)	6	33
3	d	199/201 (99%)	181 (91%)	16 (8%)	2 (1%)	12	44
4	e	175/177 (99%)	155 (89%)	15 (9%)	5 (3%)	3	26
5	f	174/176 (99%)	161 (92%)	11 (6%)	2 (1%)	11	43
6	g	147/149 (99%)	123 (84%)	20 (14%)	4 (3%)	4	27
7	h	129/165 (78%)	99 (77%)	24 (19%)	6 (5%)	2	17
8	j	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	9	38
9	k	120/122 (98%)	103 (86%)	13 (11%)	4 (3%)	3	23
10	l	141/143 (99%)	119 (84%)	20 (14%)	2 (1%)	9	38
11	m	134/136 (98%)	125 (93%)	7 (5%)	2 (2%)	8	37
12	n	118/120 (98%)	95 (80%)	21 (18%)	2 (2%)	7	35
13	o	114/116 (98%)	104 (91%)	8 (7%)	2 (2%)	6	34
14	p	112/114 (98%)	101 (90%)	9 (8%)	2 (2%)	6	34
15	q	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
16	r	101/103 (98%)	83 (82%)	17 (17%)	1 (1%)	12	44
17	s	108/110 (98%)	93 (86%)	14 (13%)	1 (1%)	14	47
18	t	91/93 (98%)	80 (88%)	11 (12%)	0	100	100
19	u	100/102 (98%)	86 (86%)	13 (13%)	1 (1%)	12	44
20	v	92/94 (98%)	83 (90%)	9 (10%)	0	100	100
21	w	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
22	x	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
23	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
24	z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
25	B	54/56 (96%)	49 (91%)	4 (7%)	1 (2%)	6	33
26	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
27	D	44/46 (96%)	39 (89%)	4 (9%)	1 (2%)	5	30
28	E	62/64 (97%)	49 (79%)	10 (16%)	3 (5%)	2	16
29	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	26
30	G	223/225 (99%)	192 (86%)	26 (12%)	5 (2%)	5	30
31	H	204/206 (99%)	188 (92%)	14 (7%)	2 (1%)	12	44
32	I	203/205 (99%)	173 (85%)	29 (14%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	J	155/157 (99%)	122 (79%)	29 (19%)	4 (3%)	4	27
34	K	98/100 (98%)	77 (79%)	15 (15%)	6 (6%)	1	12
35	L	149/151 (99%)	133 (89%)	15 (10%)	1 (1%)	18	51
36	M	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	36
37	N	125/127 (98%)	101 (81%)	21 (17%)	3 (2%)	4	29
38	O	96/98 (98%)	78 (81%)	16 (17%)	2 (2%)	5	31
39	P	114/116 (98%)	86 (75%)	23 (20%)	5 (4%)	2	17
40	Q	121/123 (98%)	98 (81%)	20 (16%)	3 (2%)	4	28
41	R	112/114 (98%)	96 (86%)	16 (14%)	0	100	100
42	S	98/100 (98%)	87 (89%)	9 (9%)	2 (2%)	6	32
43	T	86/88 (98%)	78 (91%)	7 (8%)	1 (1%)	10	41
44	U	80/82 (98%)	70 (88%)	9 (11%)	1 (1%)	9	39
45	V	78/80 (98%)	63 (81%)	10 (13%)	5 (6%)	1	11
46	W	63/65 (97%)	56 (89%)	3 (5%)	4 (6%)	1	12
47	X	77/79 (98%)	66 (86%)	10 (13%)	1 (1%)	9	39
48	Y	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	10	41
49	Z	63/65 (97%)	48 (76%)	8 (13%)	7 (11%)	0	5
55	8	130/132 (98%)	99 (76%)	20 (15%)	11 (8%)	0	7
All	All	5780/5914 (98%)	5000 (86%)	661 (11%)	119 (2%)	8	31

All (119) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	e	173	ASP
5	f	47	ASN
5	f	117	PRO
6	g	9	VAL
7	h	81	LEU
8	j	81	ILE
11	m	70	ASP
13	o	34	HIS
14	p	75	THR
16	r	54	VAL
25	B	53	VAL
28	E	31	ILE
29	F	37	GLN

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Mol	Chain	Res	Type
30	G	15	PHE
33	J	93	VAL
34	K	53	LYS
34	K	54	LEU
34	K	93	LYS
37	N	91	GLU
37	N	99	LYS
39	P	125	LYS
43	T	46	LYS
44	U	79	ASN
45	V	15	LYS
46	W	14	ALA
46	W	17	VAL
55	8	4	ILE
55	8	36	ALA
55	8	49	PRO
55	8	50	GLU
55	8	70	ILE
55	8	130	ALA
55	8	132	ARG
1	b	179	GLU
2	c	86	GLU
4	e	93	GLU
6	g	49	ALA
7	h	78	GLY
9	k	32	TYR
9	k	54	LYS
11	m	15	GLY
12	n	71	ARG
17	s	65	ASP
30	G	97	GLY
30	G	101	THR
32	I	47	LEU
33	J	80	LEU
34	K	40	GLU
36	M	20	ASN
39	P	54	SER
39	P	89	GLY
45	V	17	GLU
45	V	55	GLY
46	W	13	THR
49	Z	24	LYS

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Mol	Chain	Res	Type
49	Z	34	ARG
49	Z	36	PHE
55	8	34	SER
55	8	77	TYR
2	c	149	ASN
6	g	10	ALA
6	g	113	SER
7	h	113	PHE
9	k	89	ASN
13	o	12	THR
28	E	17	GLY
30	G	192	PRO
31	H	47	ALA
34	K	92	THR
34	K	94	HIS
36	M	47	ASP
38	O	34	ALA
40	Q	35	ARG
48	Y	5	SER
55	8	22	ALA
2	c	20	VAL
3	d	20	GLY
3	d	127	GLU
10	l	29	LYS
10	l	36	LYS
33	J	49	TYR
40	Q	43	LYS
46	W	12	PHE
49	Z	25	ALA
49	Z	35	GLU
49	Z	37	TYR
1	b	108	GLY
4	e	176	PHE
7	h	68	PRO
8	j	126	ALA
12	n	106	ASP
14	p	64	SER
19	u	88	ASP
28	E	16	THR
30	G	73	ARG
31	H	25	THR
33	J	97	PRO

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Mol	Chain	Res	Type
35	L	18	GLY
37	N	12	LYS
38	O	42	LEU
39	P	88	PRO
42	S	61	ASN
45	V	49	ASN
45	V	70	LYS
47	X	34	SER
1	b	236	GLY
4	e	39	VAL
7	h	79	PRO
27	D	42	LEU
39	P	52	ARG
40	Q	87	LYS
42	S	33	VAL
49	Z	65	ARG
1	b	63	ILE
2	c	87	GLY
7	h	67	THR
9	k	48	PRO
4	e	148	VAL
55	8	10	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	215 (100%)	1 (0%)	81	80
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	146 (99%)	2 (1%)	59	71
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	78
6	g	114/114 (100%)	112 (98%)	2 (2%)	51	69
7	h	100/123 (81%)	97 (97%)	3 (3%)	36	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	j	116/116 (100%)	114 (98%)	2 (2%)	53	70
9	k	103/103 (100%)	101 (98%)	2 (2%)	50	68
10	l	102/102 (100%)	102 (100%)	0	100	100
11	m	109/109 (100%)	108 (99%)	1 (1%)	70	76
12	n	100/100 (100%)	100 (100%)	0	100	100
13	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
14	p	99/99 (100%)	98 (99%)	1 (1%)	68	75
15	q	89/89 (100%)	89 (100%)	0	100	100
16	r	84/84 (100%)	84 (100%)	0	100	100
17	s	93/93 (100%)	93 (100%)	0	100	100
18	t	80/80 (100%)	80 (100%)	0	100	100
19	u	83/83 (100%)	82 (99%)	1 (1%)	63	73
20	v	78/78 (100%)	76 (97%)	2 (3%)	40	62
21	w	57/57 (100%)	56 (98%)	1 (2%)	51	69
22	x	67/67 (100%)	67 (100%)	0	100	100
23	y	55/55 (100%)	55 (100%)	0	100	100
24	z	48/48 (100%)	47 (98%)	1 (2%)	47	66
25	B	47/47 (100%)	46 (98%)	1 (2%)	47	66
26	C	45/45 (100%)	45 (100%)	0	100	100
27	D	38/38 (100%)	38 (100%)	0	100	100
28	E	51/51 (100%)	51 (100%)	0	100	100
29	F	34/34 (100%)	33 (97%)	1 (3%)	37	60
30	G	186/186 (100%)	185 (100%)	1 (0%)	81	80
31	H	170/170 (100%)	168 (99%)	2 (1%)	63	73
32	I	172/172 (100%)	172 (100%)	0	100	100
33	J	119/119 (100%)	119 (100%)	0	100	100
34	K	87/87 (100%)	83 (95%)	4 (5%)	24	50
35	L	124/124 (100%)	122 (98%)	2 (2%)	55	70
36	M	104/104 (100%)	103 (99%)	1 (1%)	68	75
37	N	105/105 (100%)	105 (100%)	0	100	100
38	O	86/86 (100%)	84 (98%)	2 (2%)	44	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	P	89/89 (100%)	88 (99%)	1 (1%)	65	74
40	Q	103/103 (100%)	99 (96%)	4 (4%)	28	54
41	R	92/92 (100%)	91 (99%)	1 (1%)	65	74
42	S	83/83 (100%)	83 (100%)	0	100	100
43	T	76/76 (100%)	76 (100%)	0	100	100
44	U	65/65 (100%)	65 (100%)	0	100	100
45	V	74/74 (100%)	73 (99%)	1 (1%)	59	71
46	W	56/56 (100%)	56 (100%)	0	100	100
47	X	70/70 (100%)	69 (99%)	1 (1%)	59	71
48	Y	65/65 (100%)	65 (100%)	0	100	100
49	Z	55/55 (100%)	54 (98%)	1 (2%)	51	69
55	8	108/108 (100%)	106 (98%)	2 (2%)	50	68
All	All	4797/4820 (100%)	4750 (99%)	47 (1%)	65	75

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	16	VAL
2	c	142	VAL
4	e	102	LEU
4	e	141	ASP
5	f	78	VAL
6	g	45	GLU
6	g	108	VAL
7	h	18	VAL
7	h	58	THR
7	h	81	LEU
8	j	1	MET
8	j	81	ILE
9	k	61	VAL
9	k	118	LEU
11	m	26	VAL
13	o	32	PRO
14	p	49	ILE
19	u	27	VAL
20	v	65	VAL
20	v	72	VAL
21	w	66	GLU

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Mol	Chain	Res	Type
24	z	26	LEU
25	B	53	VAL
29	F	16	ILE
30	G	46	VAL
31	H	51	VAL
31	H	122	GLN
34	K	51	ILE
34	K	54	LEU
34	K	78	PHE
34	K	91	ARG
35	L	6	ILE
35	L	14	ASP
36	M	60	LEU
38	O	51	VAL
38	O	57	VAL
39	P	118	ASN
40	Q	39	THR
40	Q	75	GLU
40	Q	97	VAL
40	Q	111	GLN
41	R	64	VAL
45	V	6	THR
47	X	70	LEU
49	Z	62	GLU
55	8	35	THR
55	8	50	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	36	ASN
1	b	45	ASN
1	b	52	HIS
1	b	69	ASN
1	b	89	ASN
1	b	116	GLN
1	b	199	HIS
1	b	250	GLN
2	c	32	ASN
2	c	36	GLN
2	c	42	ASN
2	c	67	HIS

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Mol	Chain	Res	Type
2	c	134	HIS
2	c	148	GLN
2	c	173	GLN
2	c	185	ASN
3	d	24	ASN
3	d	97	ASN
3	d	165	HIS
3	d	195	GLN
4	e	20	ASN
4	e	36	ASN
4	e	126	ASN
5	f	19	ASN
5	f	21	GLN
5	f	29	ASN
5	f	142	GLN
6	g	43	ASN
8	j	58	ASN
8	j	131	ASN
8	j	135	GLN
9	k	3	GLN
9	k	5	GLN
9	k	88	ASN
10	l	54	GLN
11	m	22	GLN
12	n	23	ASN
12	n	62	ASN
13	o	34	HIS
14	p	9	GLN
14	p	74	GLN
14	p	114	ASN
15	q	36	GLN
15	q	51	GLN
15	q	65	ASN
15	q	70	GLN
15	q	71	ASN
16	r	11	GLN
16	r	12	HIS
16	r	66	HIS
16	r	82	HIS
16	r	91	GLN
18	t	28	ASN
18	t	59	ASN

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Mol	Chain	Res	Type
19	u	68	ASN
19	u	73	ASN
20	v	5	ASN
20	v	44	HIS
20	v	49	ASN
20	v	80	HIS
23	y	25	GLN
24	z	33	HIS
25	B	5	ASN
26	C	18	HIS
26	C	25	ASN
27	D	6	GLN
27	D	29	GLN
28	E	30	HIS
28	E	42	HIS
29	F	35	GLN
29	F	37	GLN
30	G	23	ASN
30	G	57	ASN
30	G	88	GLN
30	G	119	GLN
30	G	167	HIS
30	G	169	HIS
30	G	177	ASN
30	G	202	ASN
31	H	68	HIS
32	I	53	GLN
32	I	119	HIS
32	I	139	ASN
32	I	163	GLN
33	J	11	GLN
33	J	18	ASN
33	J	60	GLN
33	J	81	GLN
33	J	120	HIS
33	J	131	ASN
34	K	17	GLN
35	L	27	ASN
35	L	85	GLN
35	L	141	HIS
36	M	3	GLN
36	M	17	GLN

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Mol	Chain	Res	Type
37	N	30	ASN
37	N	49	GLN
37	N	74	GLN
37	N	80	HIS
38	O	56	HIS
38	O	99	GLN
39	P	14	GLN
39	P	63	GLN
40	Q	5	GLN
40	Q	74	GLN
41	R	7	ASN
42	S	42	ASN
42	S	61	ASN
42	S	65	GLN
42	S	70	HIS
43	T	34	GLN
43	T	36	ASN
43	T	79	GLN
44	U	9	HIS
44	U	18	GLN
44	U	40	ASN
44	U	63	GLN
45	V	46	HIS
46	W	73	HIS
48	Y	60	GLN
55	8	23	GLN
55	8	75	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	1538/1539 (99%)	157 (10%)	2 (0%)
51	1	2902/2903 (99%)	365 (12%)	9 (0%)
52	2	119/120 (99%)	14 (11%)	0
53	5	76/77 (98%)	8 (10%)	0
54	4	20/23 (86%)	6 (30%)	2 (10%)
All	All	4655/4662 (99%)	550 (11%)	13 (0%)

All (550) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	6	G
50	3	9	G
50	3	22	G
50	3	31	G
50	3	32	A
50	3	39	G
50	3	48	C
50	3	51	A
50	3	75	G
50	3	82	G
50	3	83	C
50	3	84	U
50	3	87	C
50	3	95	C
50	3	100	G
50	3	121	U
50	3	130	A
50	3	144	G
50	3	146	G
50	3	183	C
50	3	209	U
50	3	210	C
50	3	226	G
50	3	247	G
50	3	251	G
50	3	253	A
50	3	266	G
50	3	267	C
50	3	279	A
50	3	280	C
50	3	281	G
50	3	289	G
50	3	316	C
50	3	345	C
50	3	352	C
50	3	367	U
50	3	372	C
50	3	412	A
50	3	421	U
50	3	422	C
50	3	430	A
50	3	441	A
50	3	448	A

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Mol	Chain	Res	Type
50	3	480	U
50	3	485	U
50	3	486	U
50	3	497	G
50	3	509	A
50	3	518	C
50	3	533	A
50	3	547	A
50	3	559	A
50	3	561	U
50	3	564	C
50	3	572	A
50	3	573	A
50	3	575	G
50	3	576	C
50	3	577	G
50	3	596	A
50	3	633	G
50	3	642	A
50	3	665	A
50	3	687	A
50	3	702	A
50	3	703	G
50	3	713	G
50	3	724	G
50	3	755	G
50	3	777	A
50	3	814	A
50	3	817	C
50	3	818	G
50	3	819	A
50	3	821	G
50	3	842	U
50	3	843	U
50	3	844	G
50	3	845	A
50	3	846	G
50	3	847	G
50	3	902	G
50	3	934	C
50	3	935	A
50	3	938	A

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Mol	Chain	Res	Type
50	3	960	U
50	3	961	U
50	3	966	G
50	3	969	A
50	3	975	A
50	3	976	G
50	3	977	A
50	3	992	U
50	3	993	G
50	3	994	A
50	3	1004	A
50	3	1029	U
50	3	1030	U
50	3	1031	C
50	3	1032	G
50	3	1033	G
50	3	1034	G
50	3	1053	G
50	3	1054	C
50	3	1094	G
50	3	1101	A
50	3	1137	C
50	3	1138	G
50	3	1139	G
50	3	1140	C
50	3	1146	A
50	3	1159	U
50	3	1168	U
50	3	1182	G
50	3	1184	G
50	3	1191	A
50	3	1196	A
50	3	1198	G
50	3	1201	A
50	3	1225	A
50	3	1227	A
50	3	1238	A
50	3	1241	G
50	3	1256	A
50	3	1258	G
50	3	1261	A
50	3	1275	A

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Mol	Chain	Res	Type
50	3	1278	G
50	3	1280	A
50	3	1287	A
50	3	1299	A
50	3	1300	G
50	3	1317	C
50	3	1336	C
50	3	1346	A
50	3	1347	G
50	3	1363	A
50	3	1378	C
50	3	1381	U
50	3	1394	A
50	3	1395	C
50	3	1429	A
50	3	1446	A
50	3	1448	C
50	3	1452	C
50	3	1475	G
50	3	1492	A
50	3	1493	A
50	3	1494	G
50	3	1503	A
50	3	1506	U
50	3	1517	G
50	3	1520	C
50	3	1529	G
50	3	1530	G
50	3	1533	C
50	3	1535	C
51	1	10	A
51	1	12	U
51	1	35	G
51	1	50	U
51	1	51	G
51	1	71	A
51	1	74	A
51	1	75	G
51	1	96	C
51	1	119	A
51	1	120	U
51	1	137	U

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Mol	Chain	Res	Type
51	1	139	U
51	1	141	G
51	1	142	A
51	1	162	U
51	1	163	C
51	1	181	A
51	1	196	A
51	1	216	A
51	1	219	A
51	1	221	A
51	1	222	A
51	1	228	C
51	1	229	C
51	1	233	A
51	1	248	G
51	1	249	C
51	1	255	A
51	1	266	G
51	1	276	U
51	1	278	A
51	1	294	A
51	1	301	G
51	1	311	A
51	1	312	G
51	1	323	C
51	1	324	A
51	1	329	G
51	1	330	A
51	1	362	A
51	1	363	G
51	1	371	A
51	1	372	G
51	1	386	G
51	1	387	U
51	1	404	A
51	1	405	U
51	1	406	G
51	1	411	G
51	1	424	G
51	1	481	G
51	1	491	G
51	1	504	A

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Mol	Chain	Res	Type
51	1	505	A
51	1	529	A
51	1	530	G
51	1	531	C
51	1	532	A
51	1	543	G
51	1	548	G
51	1	549	G
51	1	563	A
51	1	572	A
51	1	573	U
51	1	575	A
51	1	588	U
51	1	603	A
51	1	615	U
51	1	627	A
51	1	637	A
51	1	646	U
51	1	654	A
51	1	686	U
51	1	687	C
51	1	730	A
51	1	747	C
51	1	752	A
51	1	757	G
51	1	764	A
51	1	774	G
51	1	776	G
51	1	782	A
51	1	784	G
51	1	785	G
51	1	805	G
51	1	812	C
51	1	819	A
51	1	827	U
51	1	828	U
51	1	830	G
51	1	845	A
51	1	846	U
51	1	847	U
51	1	858	G
51	1	860	U

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Mol	Chain	Res	Type
51	1	878	A
51	1	887	U
51	1	896	A
51	1	910	A
51	1	914	G
51	1	915	C
51	1	932	U
51	1	941	A
51	1	945	A
51	1	946	C
51	1	959	A
51	1	961	C
51	1	974	G
51	1	975	A
51	1	983	A
51	1	985	C
51	1	995	C
51	1	996	A
51	1	1012	U
51	1	1013	C
51	1	1021	A
51	1	1022	G
51	1	1033	U
51	1	1045	C
51	1	1046	A
51	1	1062	G
51	1	1065	U
51	1	1066	U
51	1	1068	G
51	1	1070	A
51	1	1071	G
51	1	1075	C
51	1	1084	A
51	1	1088	A
51	1	1101	U
51	1	1104	C
51	1	1111	A
51	1	1126	A
51	1	1132	U
51	1	1135	C
51	1	1151	A
51	1	1172	C

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Mol	Chain	Res	Type
51	1	1173	U
51	1	1174	U
51	1	1176	U
51	1	1178	C
51	1	1179	G
51	1	1180	U
51	1	1206	G
51	1	1211	C
51	1	1212	G
51	1	1247	A
51	1	1248	G
51	1	1251	C
51	1	1253	A
51	1	1256	G
51	1	1271	G
51	1	1272	A
51	1	1301	A
51	1	1302	A
51	1	1305	C
51	1	1321	A
51	1	1329	U
51	1	1332	G
51	1	1345	C
51	1	1365	A
51	1	1378	A
51	1	1379	U
51	1	1383	A
51	1	1398	C
51	1	1416	G
51	1	1419	A
51	1	1420	A
51	1	1454	C
51	1	1461	C
51	1	1482	G
51	1	1490	A
51	1	1497	U
51	1	1515	A
51	1	1524	G
51	1	1535	A
51	1	1536	C
51	1	1555	G
51	1	1559	U

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Mol	Chain	Res	Type
51	1	1560	G
51	1	1569	A
51	1	1607	C
51	1	1608	A
51	1	1611	C
51	1	1616	A
51	1	1647	U
51	1	1648	U
51	1	1654	A
51	1	1674	G
51	1	1698	A
51	1	1703	G
51	1	1713	A
51	1	1715	G
51	1	1729	U
51	1	1730	C
51	1	1738	G
51	1	1758	U
51	1	1764	C
51	1	1773	A
51	1	1782	U
51	1	1791	A
51	1	1800	C
51	1	1801	A
51	1	1802	A
51	1	1808	A
51	1	1816	C
51	1	1829	A
51	1	1870	C
51	1	1871	A
51	1	1901	A
51	1	1906	G
51	1	1907	G
51	1	1913	A
51	1	1914	C
51	1	1929	G
51	1	1930	G
51	1	1937	A
51	1	1938	A
51	1	1944	U
51	1	1955	U
51	1	1962	C

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Mol	Chain	Res	Type
51	1	1964	G
51	1	1966	A
51	1	1967	C
51	1	1970	A
51	1	1971	U
51	1	1972	G
51	1	1982	U
51	1	1991	U
51	1	1993	U
51	1	1997	C
51	1	2022	U
51	1	2023	C
51	1	2030	A
51	1	2031	A
51	1	2036	C
51	1	2043	C
51	1	2046	G
51	1	2055	C
51	1	2056	G
51	1	2060	A
51	1	2061	G
51	1	2062	A
51	1	2069	G
51	1	2072	C
51	1	2093	G
51	1	2096	C
51	1	2111	U
51	1	2112	G
51	1	2113	U
51	1	2114	A
51	1	2118	U
51	1	2119	A
51	1	2126	A
51	1	2130	U
51	1	2131	U
51	1	2132	U
51	1	2133	G
51	1	2135	A
51	1	2136	G
51	1	2140	G
51	1	2145	C
51	1	2147	A

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Mol	Chain	Res	Type
51	1	2154	A
51	1	2158	A
51	1	2159	G
51	1	2161	C
51	1	2165	C
51	1	2166	U
51	1	2167	U
51	1	2168	G
51	1	2169	A
51	1	2171	A
51	1	2172	U
51	1	2173	A
51	1	2174	C
51	1	2175	C
51	1	2180	U
51	1	2198	A
51	1	2199	A
51	1	2203	U
51	1	2204	G
51	1	2210	U
51	1	2213	U
51	1	2225	A
51	1	2238	G
51	1	2239	G
51	1	2259	U
51	1	2266	A
51	1	2283	C
51	1	2287	A
51	1	2297	A
51	1	2305	U
51	1	2309	A
51	1	2320	U
51	1	2325	G
51	1	2327	A
51	1	2334	U
51	1	2335	A
51	1	2347	C
51	1	2350	C
51	1	2357	G
51	1	2383	G
51	1	2385	C
51	1	2392	A

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Mol	Chain	Res	Type
51	1	2402	U
51	1	2406	A
51	1	2414	G
51	1	2423	U
51	1	2424	C
51	1	2429	G
51	1	2430	A
51	1	2435	A
51	1	2441	U
51	1	2445	G
51	1	2448	A
51	1	2476	A
51	1	2478	A
51	1	2494	G
51	1	2498	C
51	1	2502	G
51	1	2503	A
51	1	2505	G
51	1	2518	A
51	1	2520	C
51	1	2547	A
51	1	2554	U
51	1	2566	A
51	1	2567	G
51	1	2572	A
51	1	2602	A
51	1	2609	U
51	1	2610	C
51	1	2613	U
51	1	2629	U
51	1	2655	G
51	1	2682	A
51	1	2689	U
51	1	2690	U
51	1	2714	G
51	1	2725	A
51	1	2739	U
51	1	2744	G
51	1	2748	A
51	1	2757	A
51	1	2764	A
51	1	2765	A

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Mol	Chain	Res	Type
51	1	2771	C
51	1	2778	A
51	1	2779	U
51	1	2791	G
51	1	2792	A
51	1	2799	A
51	1	2800	A
51	1	2809	A
51	1	2820	A
51	1	2821	A
51	1	2833	U
51	1	2850	A
51	1	2867	G
51	1	2868	A
51	1	2872	A
51	1	2879	A
51	1	2880	C
52	2	2	G
52	2	4	C
52	2	12	C
52	2	13	G
52	2	24	G
52	2	35	C
52	2	42	C
52	2	44	G
52	2	67	G
52	2	89	U
52	2	90	C
52	2	108	A
52	2	109	A
52	2	116	G
53	5	9	G
53	5	19	G
53	5	20	U
53	5	47	U
53	5	48	C
53	5	61	C
53	5	75	C
53	5	76	A
54	4	13	A
54	4	19	U
54	4	20	A

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Mol	Chain	Res	Type
54	4	21	A
54	4	23	A
54	4	25	A

All (13) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	429	U
50	3	1190	G
51	1	784	G
51	1	827	U
51	1	859	G
51	1	1020	A
51	1	2286	G
51	1	2296	U
51	1	2326	C
51	1	2391	G
51	1	2756	U
54	4	22	A
54	4	24	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

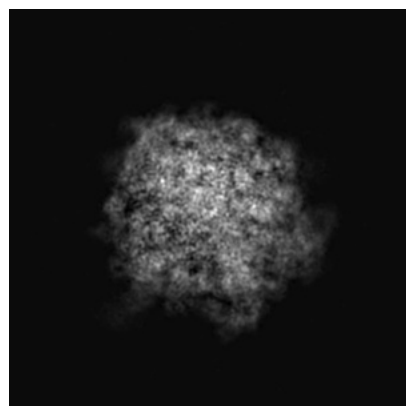
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22469. These allow visual inspection of the internal detail of the map and identification of artifacts.

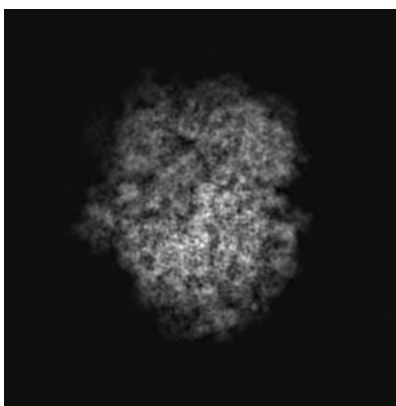
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

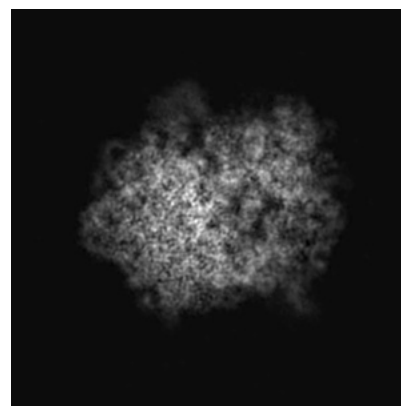
6.1.1 Primary map



X

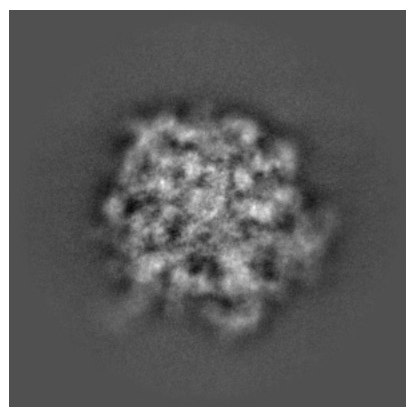


Y

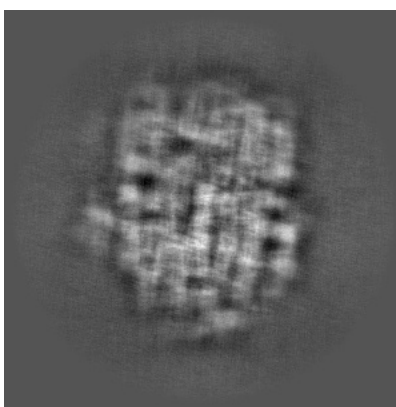


Z

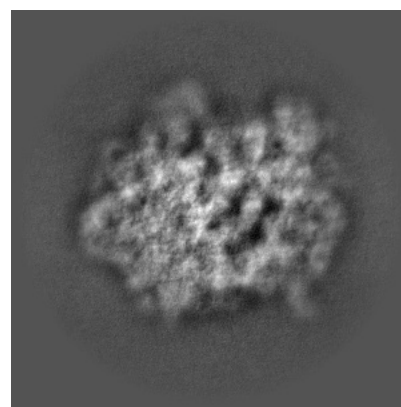
6.1.2 Raw map



X



Y

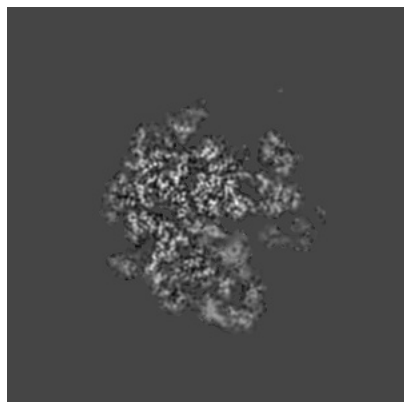


Z

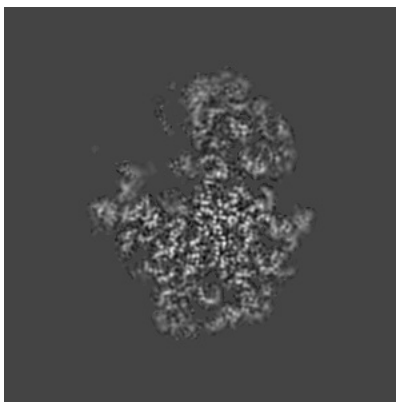
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

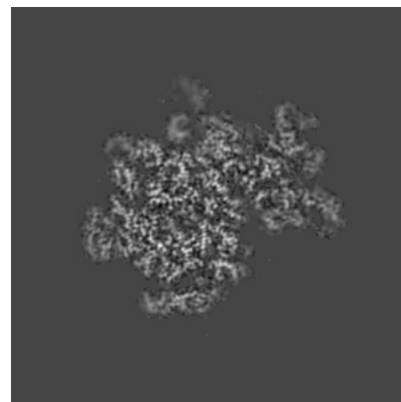
6.2.1 Primary map



X Index: 180

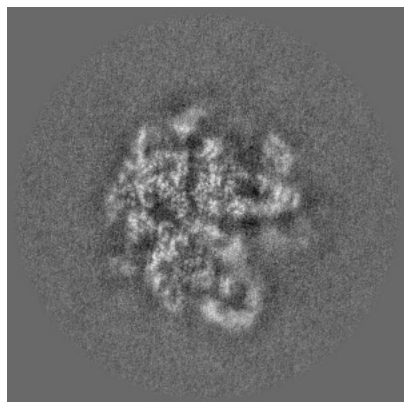


Y Index: 180

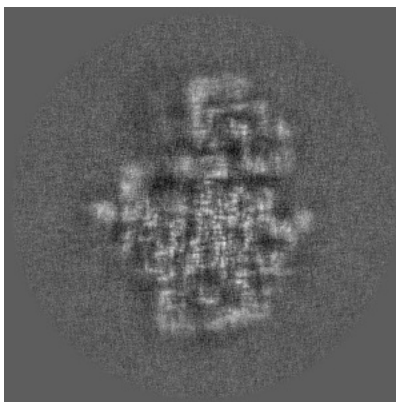


Z Index: 180

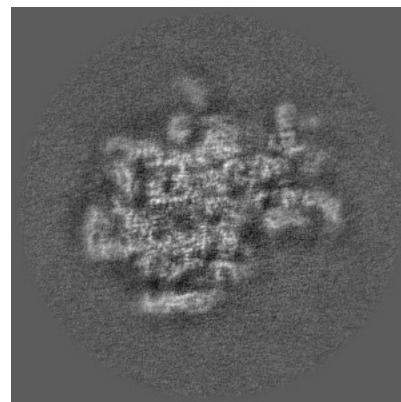
6.2.2 Raw map



X Index: 180



Y Index: 180

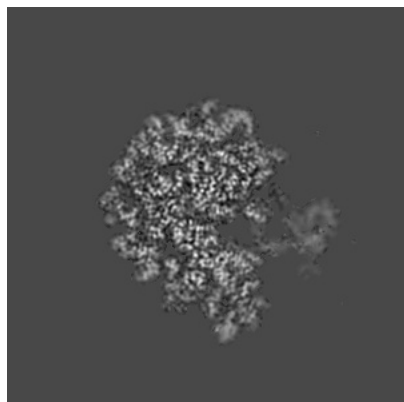


Z Index: 180

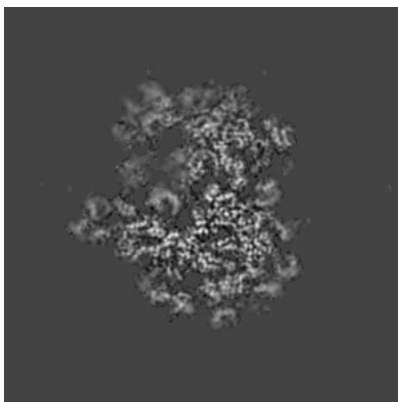
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

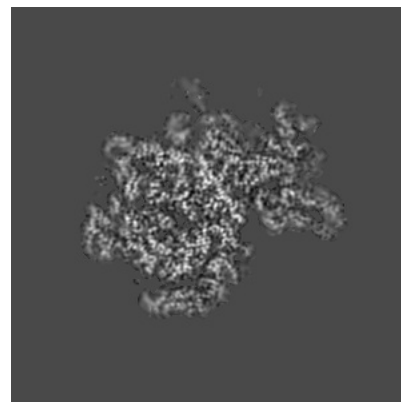
6.3.1 Primary map



X Index: 163

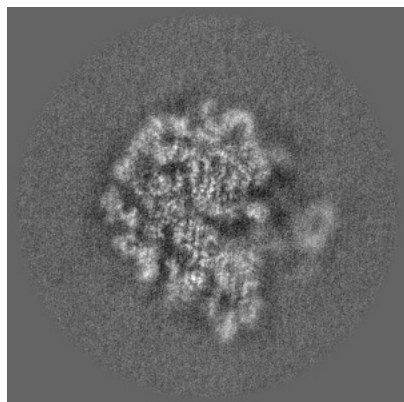


Y Index: 192

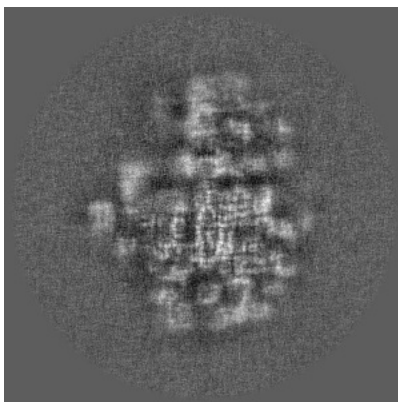


Z Index: 182

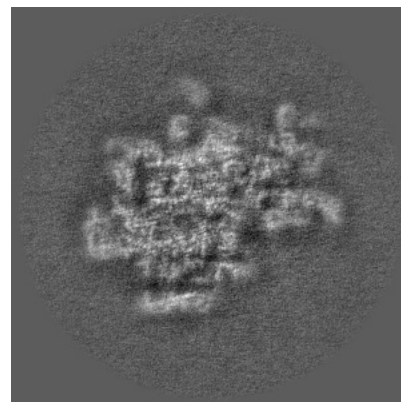
6.3.2 Raw map



X Index: 163



Y Index: 183

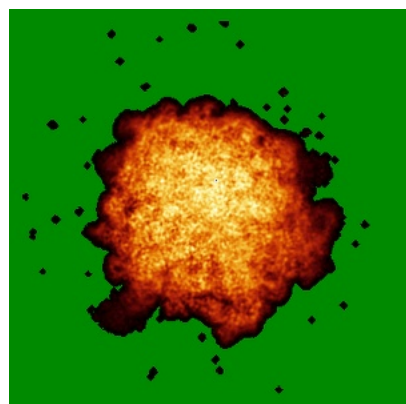


Z Index: 179

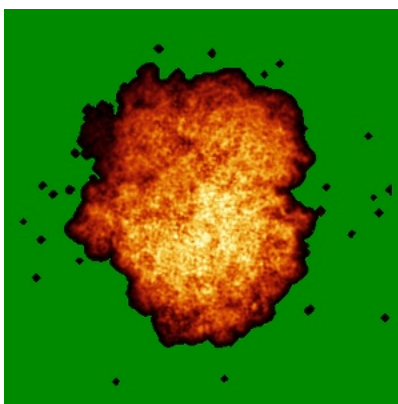
The images above show the largest variance slices of the map in three orthogonal directions.

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

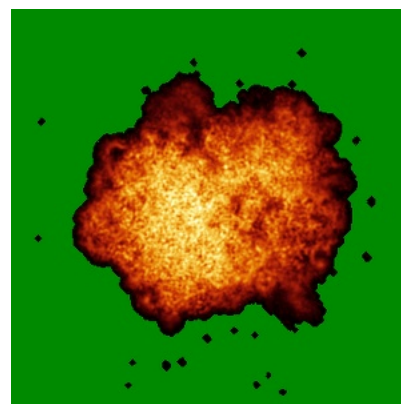
6.4.1 Primary map



X

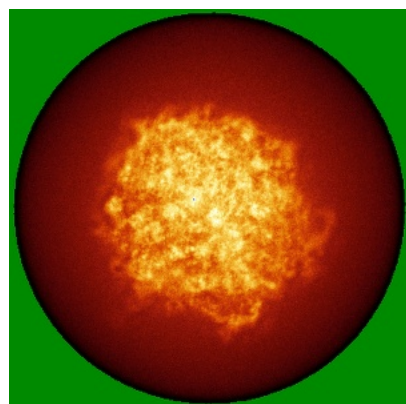


Y

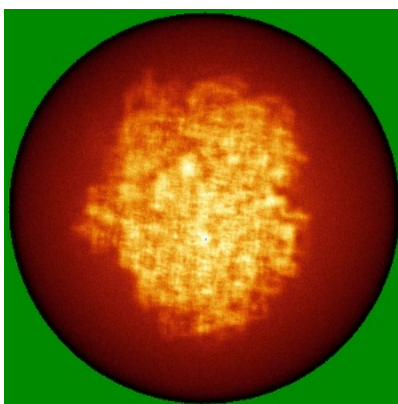


Z

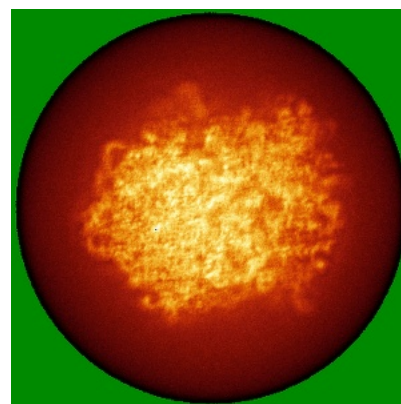
6.4.2 Raw map



X



Y

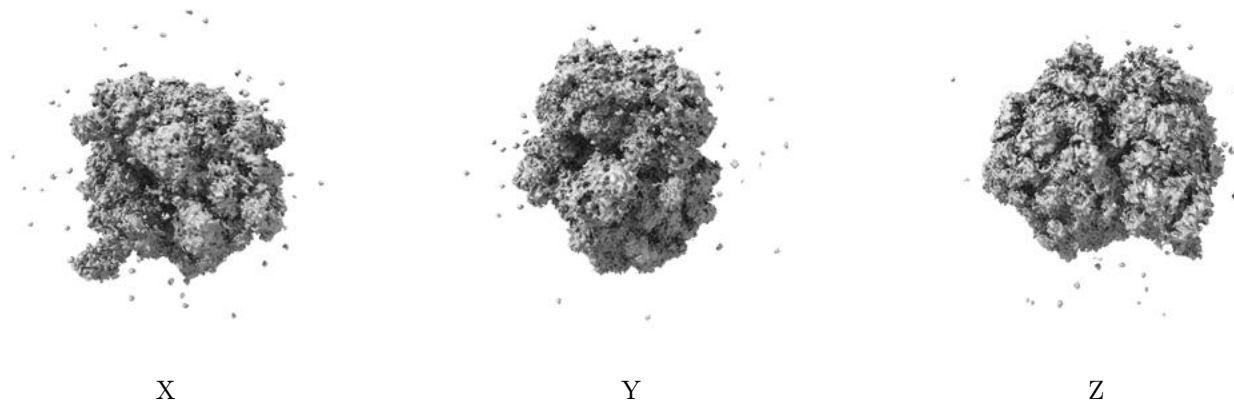


Z

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.

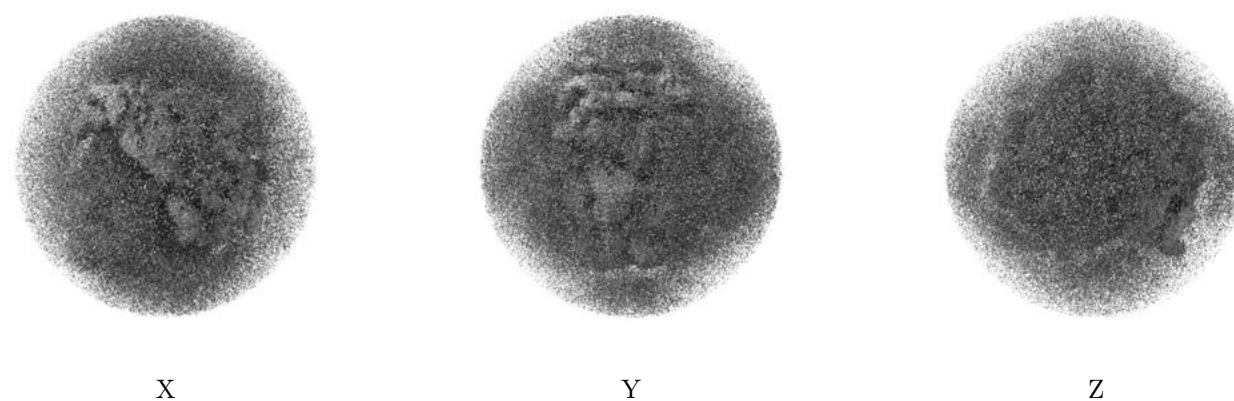
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.43. 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.

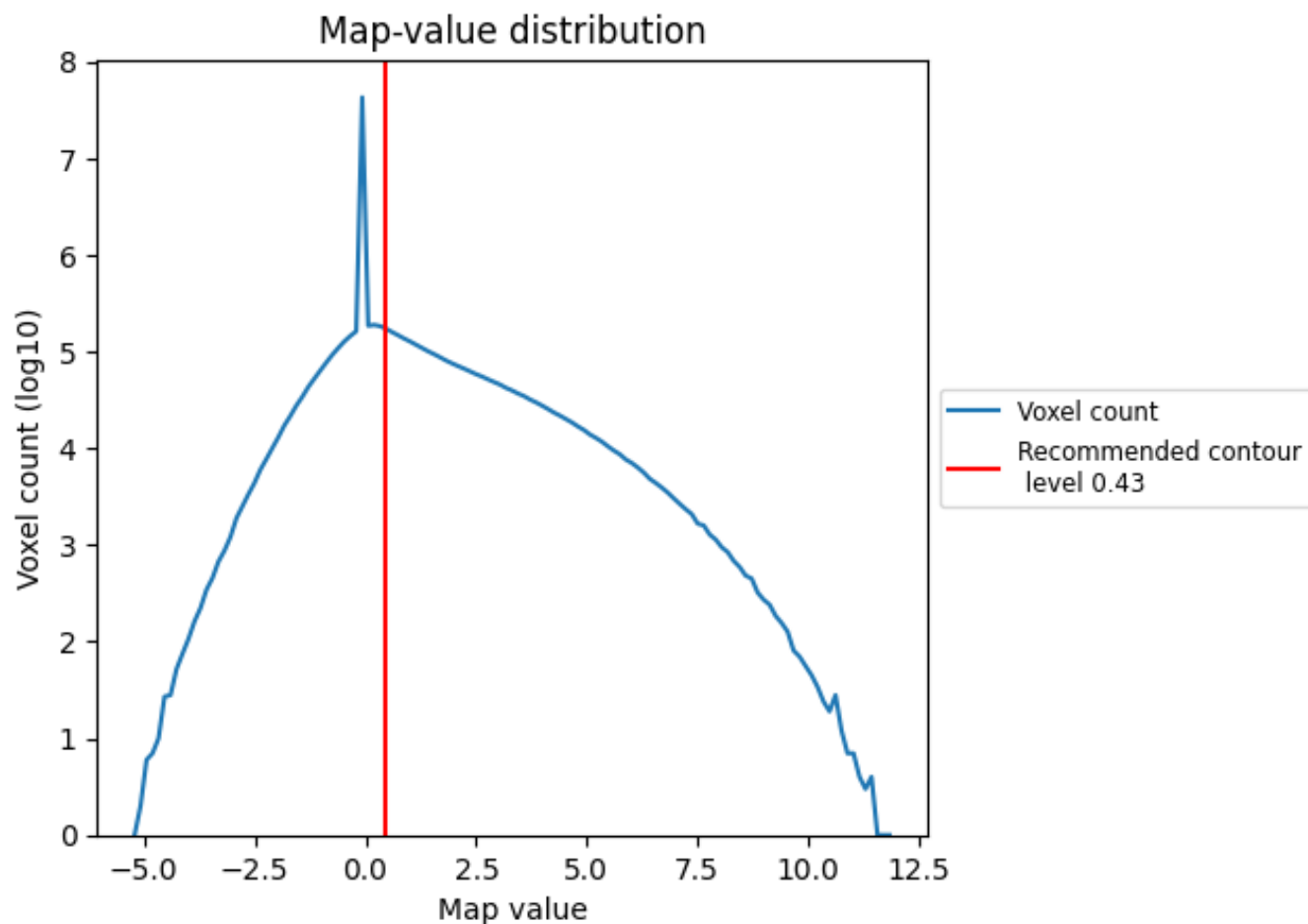
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

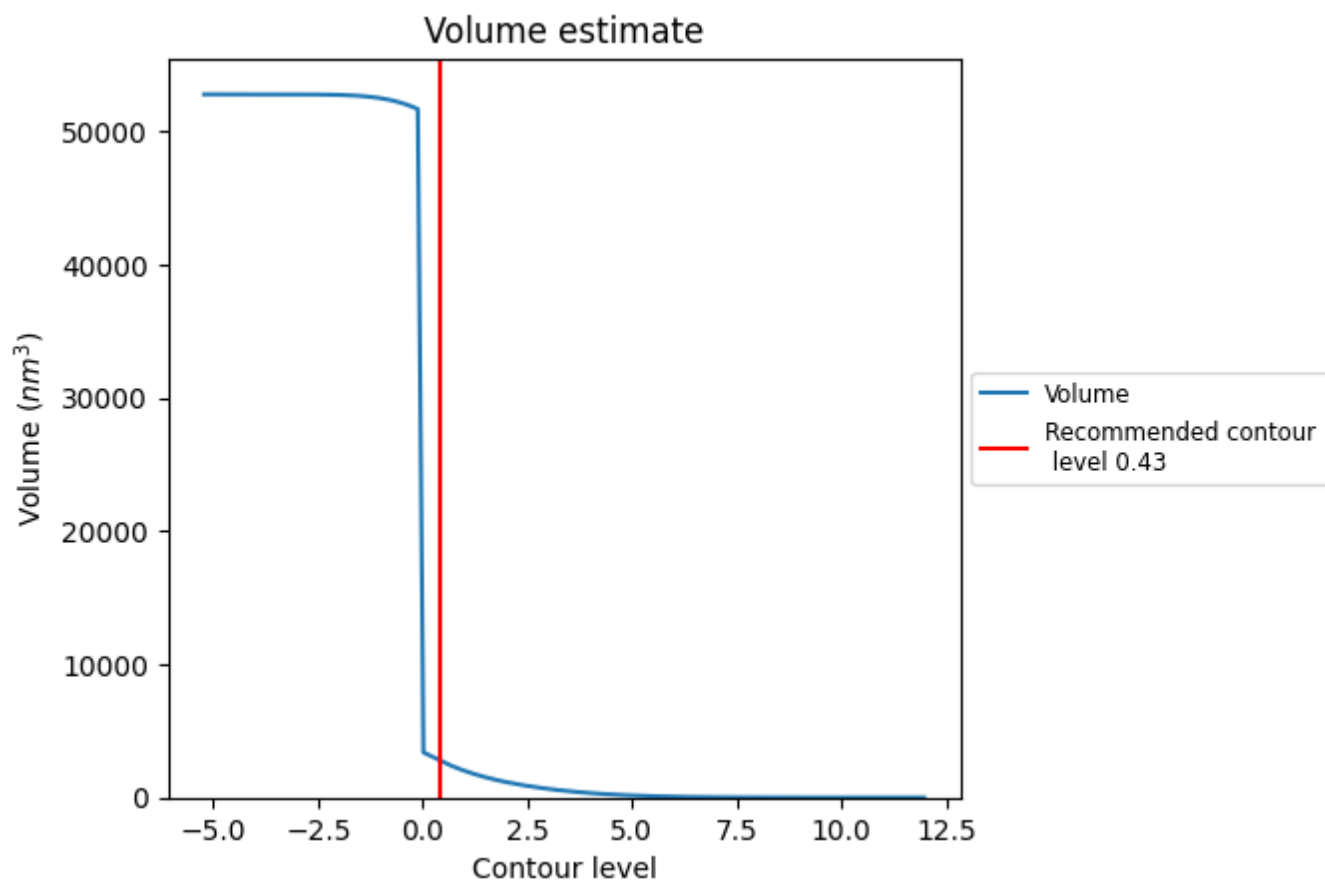
This section contains the results of statistical analysis of the map.

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.

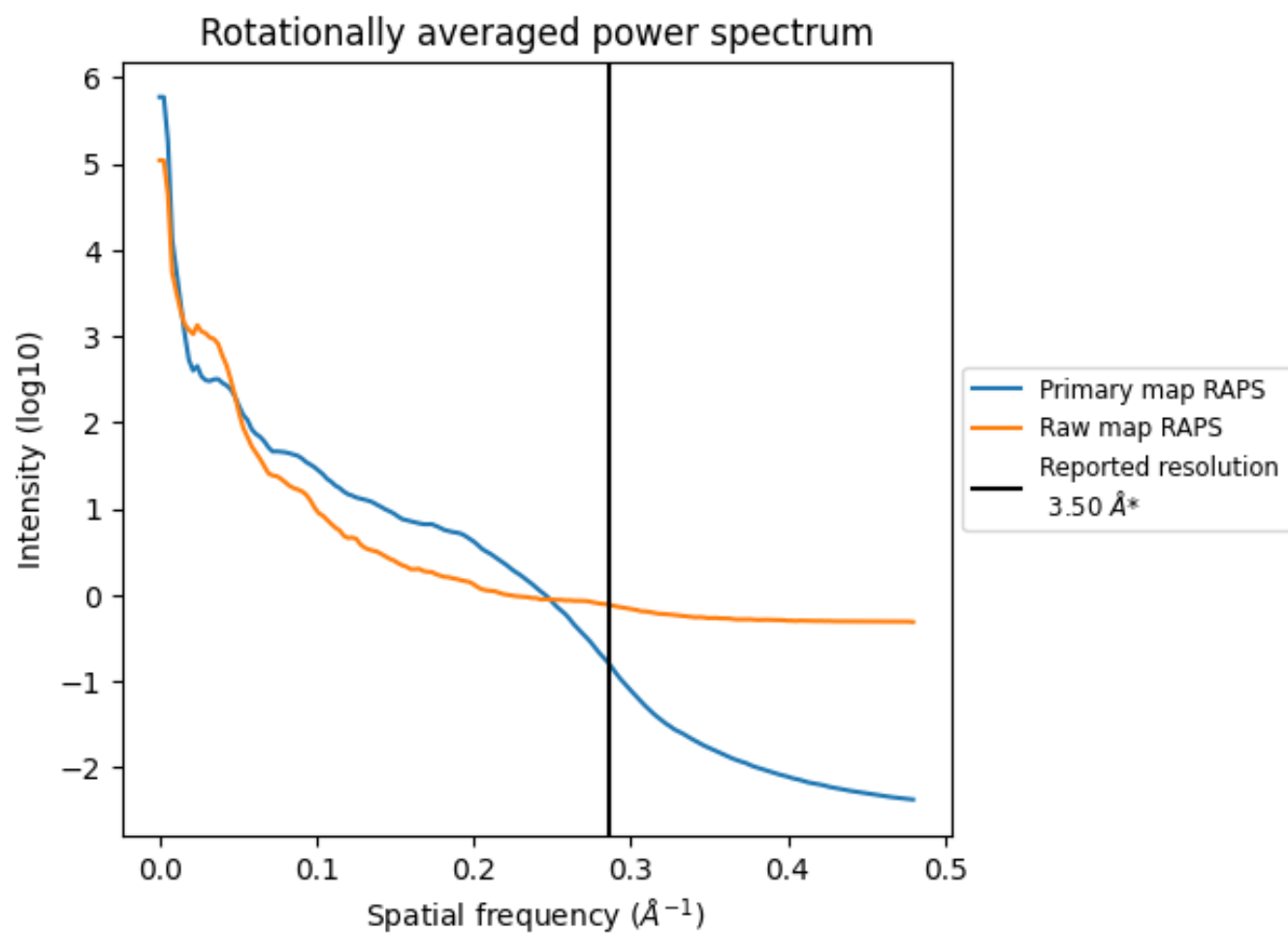
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2750 nm³; this corresponds to an approximate mass of 2484 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 ⓘ

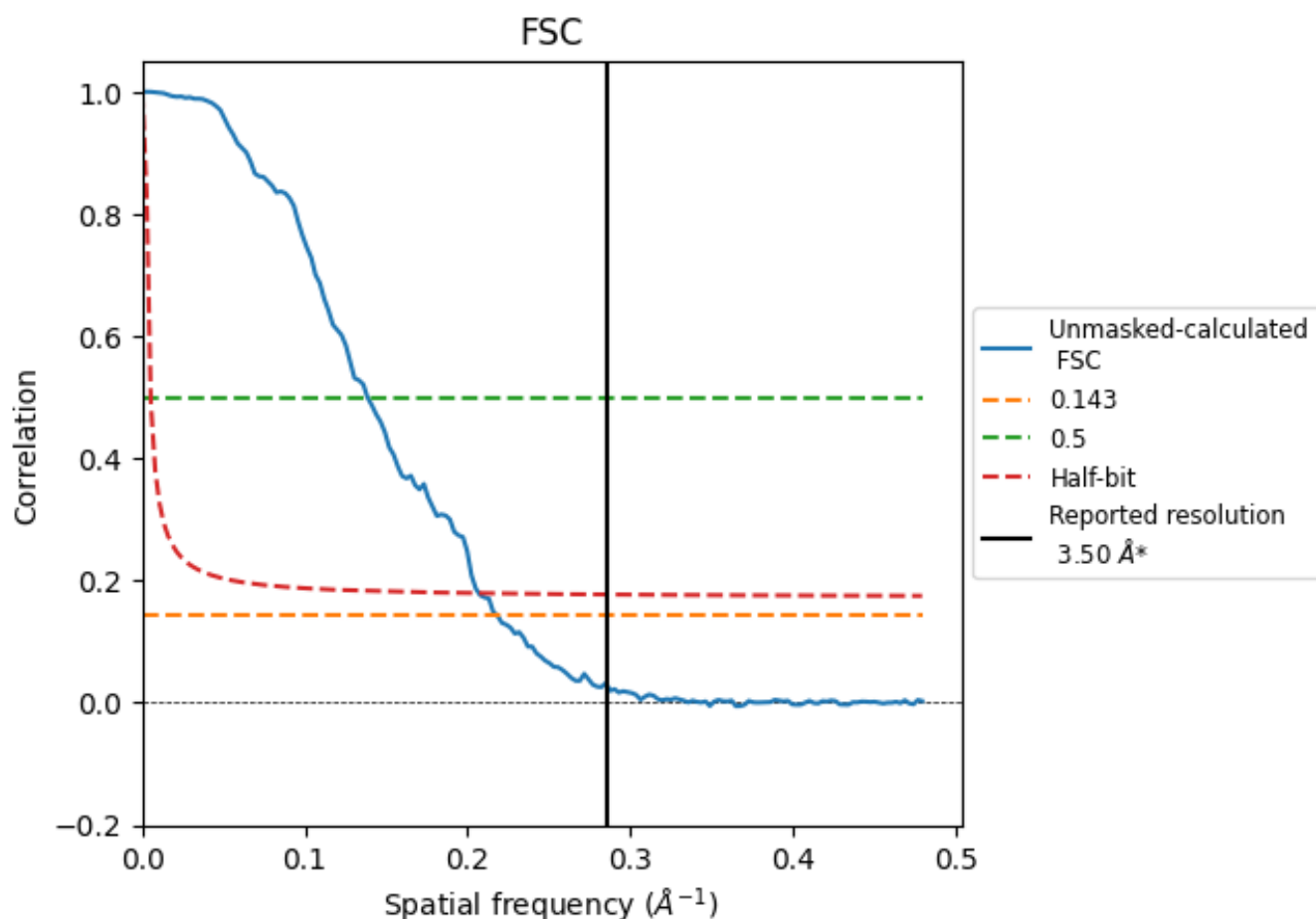


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

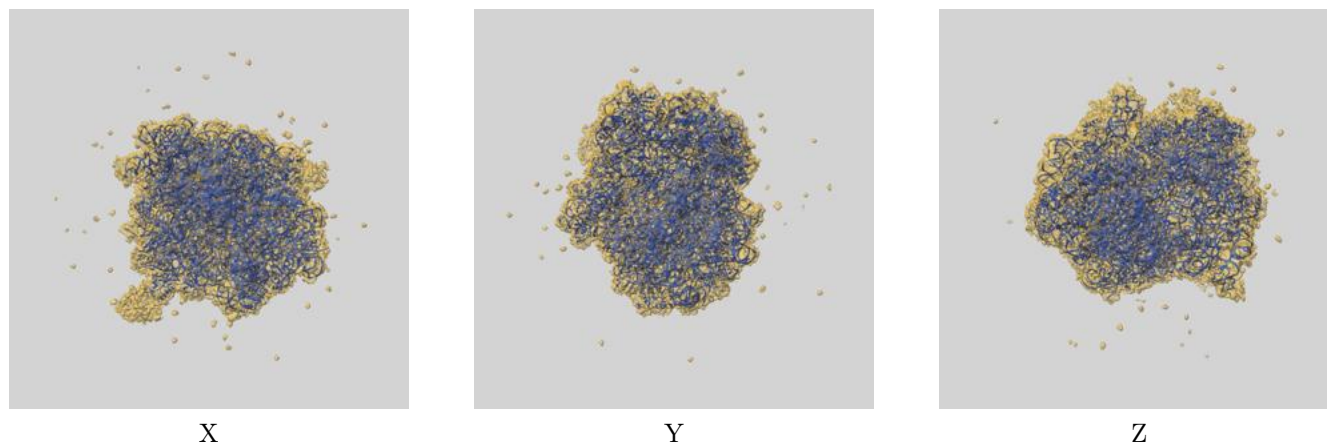
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.58	7.22	4.83

*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 4.58 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

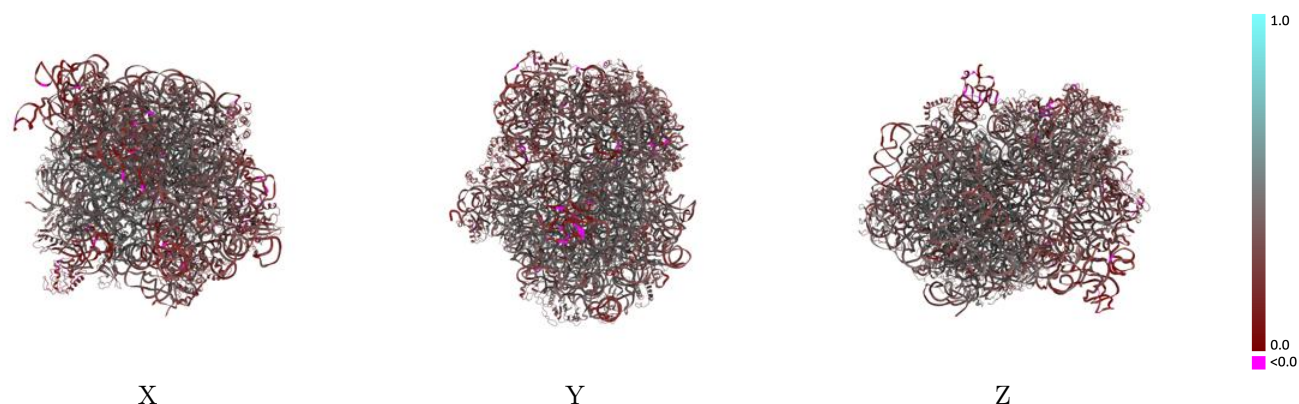
This section contains information regarding the fit between EMDB map EMD-22469 and PDB model 7JT2. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



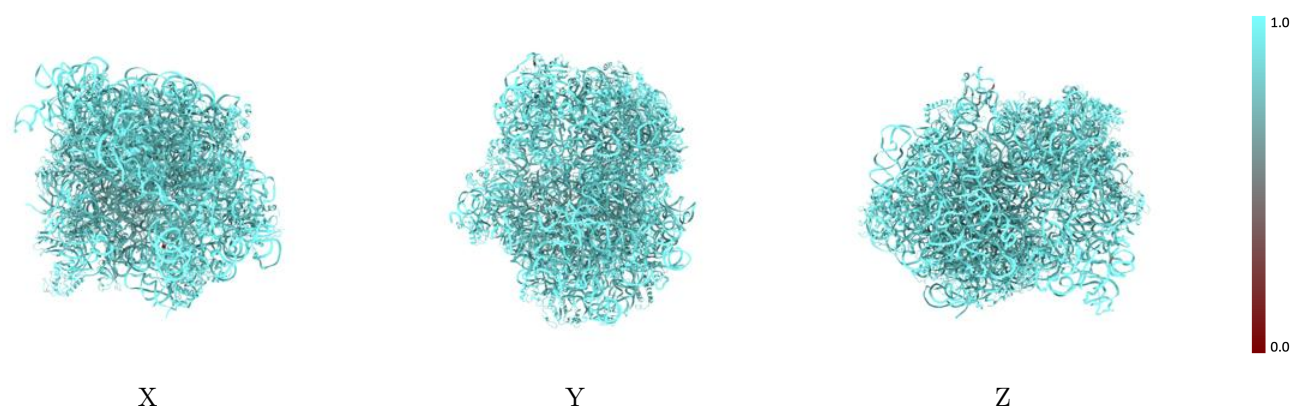
The images above show the 3D surface view of the map at the recommended contour level 0.43 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



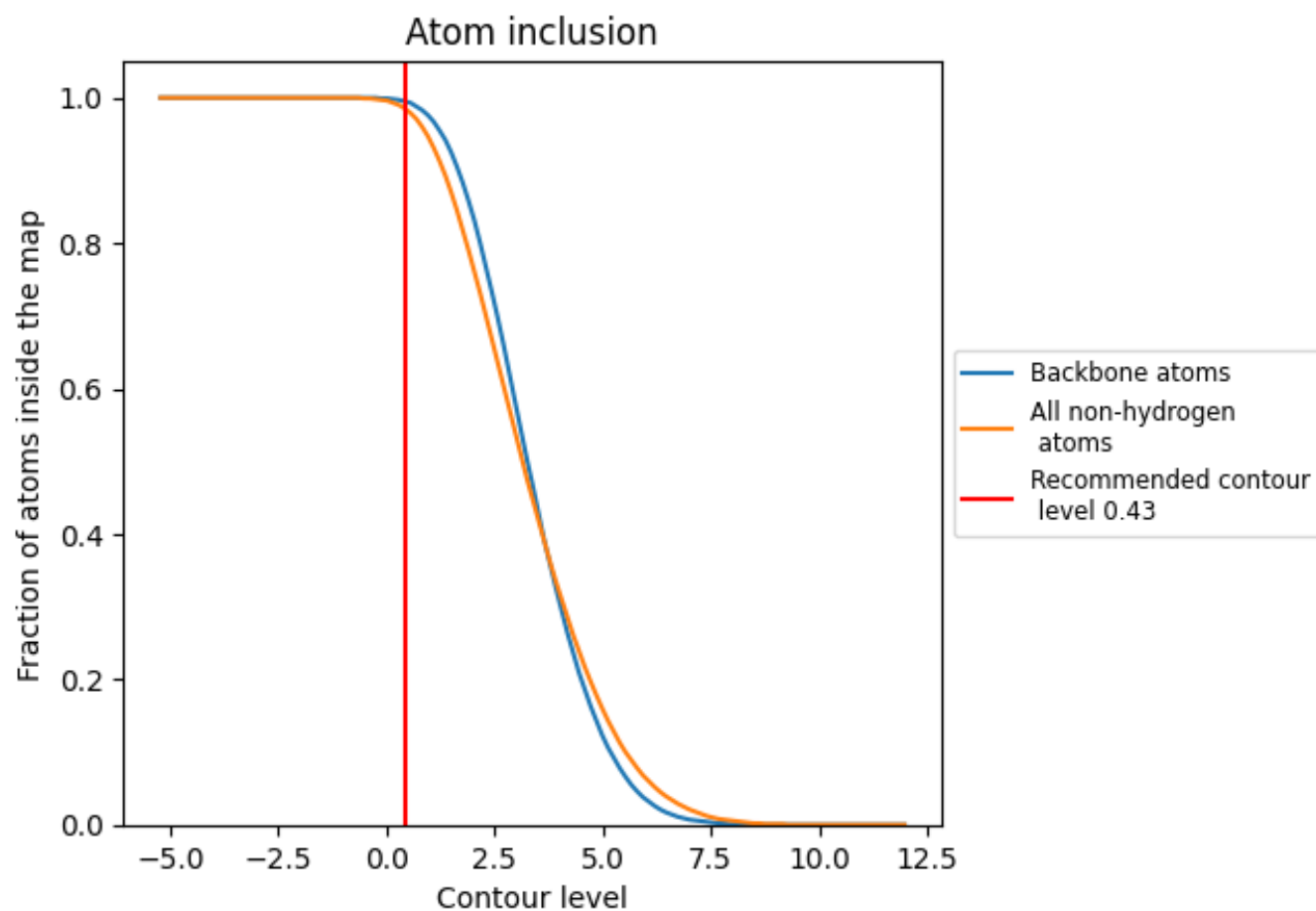
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.43).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.43) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9850	 0.3660
1	 0.9930	 0.3880
2	 0.9950	 0.3270
3	 0.9910	 0.3380
4	 0.9720	 0.2130
5	 0.9870	 0.2890
8	 0.9400	 0.3190
B	 0.9700	 0.4110
C	 0.9750	 0.3730
D	 0.9750	 0.4490
E	 0.9780	 0.4270
F	 0.9760	 0.4220
G	 0.9620	 0.3140
H	 0.9680	 0.3520
I	 0.9470	 0.2780
J	 0.9740	 0.3840
K	 0.9760	 0.3470
L	 0.9750	 0.3080
M	 0.9650	 0.3540
N	 0.9610	 0.3130
O	 0.9210	 0.3180
P	 0.9800	 0.3610
Q	 0.9740	 0.3570
R	 0.9670	 0.3140
S	 0.9420	 0.3180
T	 0.9780	 0.3580
U	 0.9510	 0.3430
V	 0.9870	 0.3610
W	 0.9630	 0.3730
X	 0.9870	 0.2990
Y	 0.9540	 0.2790
Z	 0.9300	 0.3250
b	 0.9780	 0.4510
c	 0.9730	 0.4310
d	 0.9770	 0.3940



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Chain	Atom inclusion	Q-score
e	 0.9810	 0.3000
f	 0.9880	 0.3550
g	 0.9830	 0.3060
h	 0.9380	 0.1850
j	 0.9740	 0.4160
k	 0.9800	 0.4170
l	 0.9650	 0.3970
m	 0.9700	 0.4190
n	 0.9630	 0.4180
o	 0.9660	 0.3400
p	 0.9850	 0.4160
q	 0.9750	 0.4230
r	 0.9700	 0.3960
s	 0.9740	 0.4190
t	 0.9680	 0.4020
u	 0.9870	 0.3720
v	 0.9780	 0.3910
w	 0.9710	 0.4300
x	 0.9930	 0.4340
y	 0.9700	 0.3330
z	 0.9860	 0.4030