



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 06:17 PM UTC

PDB ID : 6GQV / pdb_00006gqv
EMDB ID : EMD-0049
Title : Cryo-EM reconstruction of yeast 80S ribosome in complex with mRNA, tRNA and eEF2 (GMPPCP)
Authors : Pellegrino, S.; Yusupov, M.; Yusupova, G.; Hashem, Y.
Deposited on : 2018-06-08
Resolution : 4.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

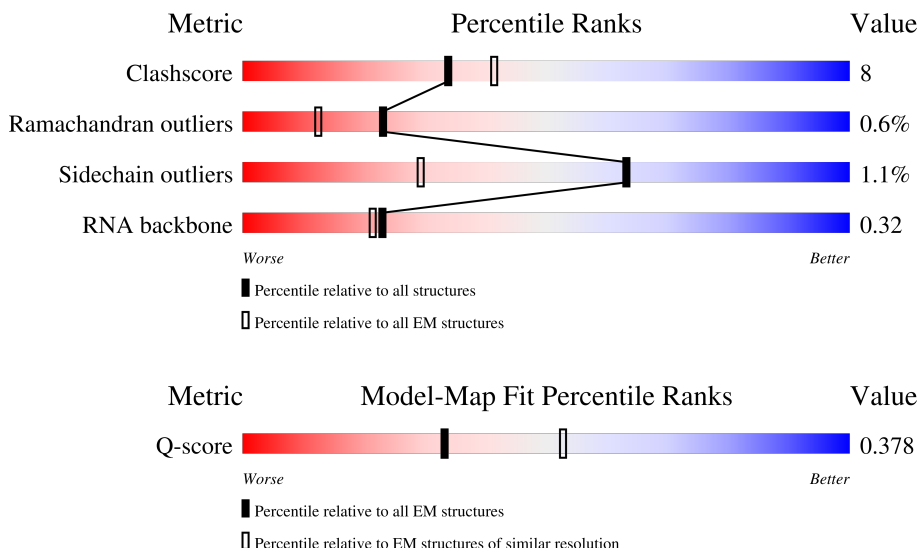
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	7587 (3.50 - 4.50)

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	1	3396	
2	3	121	
3	4	158	

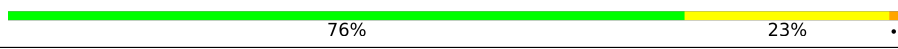
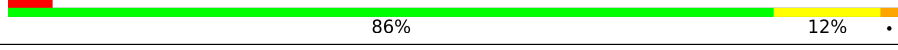
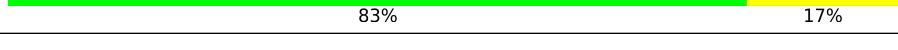
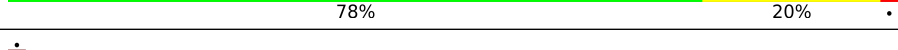
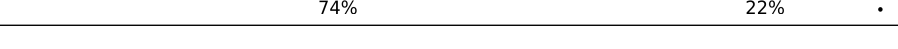
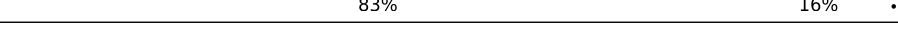
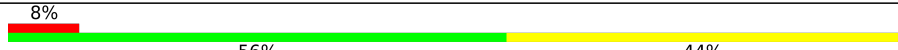
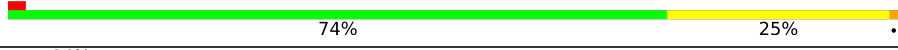
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Mol	Chain	Length	Quality of chain
4	P0	189	
5	P2	94	
6	A	252	
7	B	386	
8	C	361	
9	D	296	
10	E	175	
11	F	222	
12	G	233	
13	H	191	
14	I	220	
15	J	169	
16	L	193	
17	M	136	
18	N	203	
19	O	197	
20	P	183	
21	Q	185	
22	R	188	
23	S	172	
24	T	159	
25	U	100	
26	V	136	
27	W	62	
28	X	121	

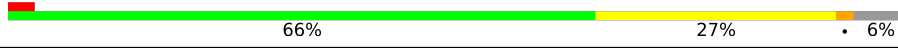
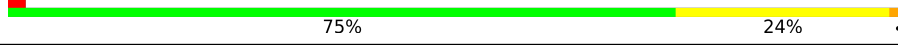
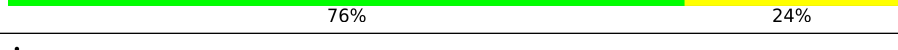
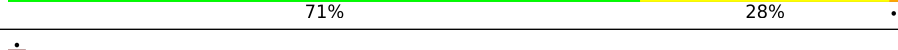
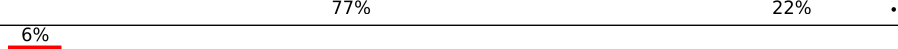
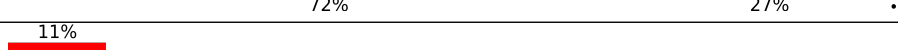
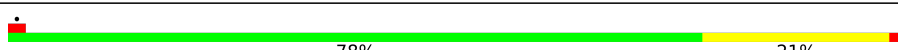
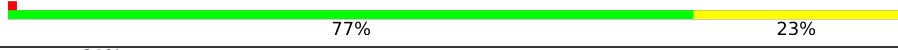
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Mol	Chain	Length	Quality of chain
29	Y	126	
30	Z	135	
31	a	148	
32	b	58	
33	c	97	
34	d	109	
35	e	127	
36	f	106	
37	g	112	
38	h	119	
39	i	99	
40	j	87	
41	k	77	
42	l	50	
43	m	52	
44	n	25	
45	o	105	
46	p	91	
47	2	1797	
48	q	206	
49	r	214	
50	s	217	
51	t	223	
52	u	260	
53	v	206	

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Mol	Chain	Length	Quality of chain
54	w	223	
55	x	184	
56	y	199	
57	z	185	
58	AA	105	
59	AB	153	
60	AC	124	
61	AD	150	
62	AE	127	
63	AF	124	
64	AG	141	
65	AH	125	
66	AI	145	
67	AJ	143	
68	AK	107	
69	AL	87	
70	AM	129	
71	AN	144	
72	AO	134	
73	AP	70	
74	AQ	97	
75	AR	81	
76	AS	63	
77	AT	53	
78	AU	60	

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Mol	Chain	Length	Quality of chain
79	AV	318	
80	AW	37	
81	AX	837	
82	AY	76	
83	AZ	7	
84	BA	204	

2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 212058 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3223	Total	C	N	O	P	0	0
			68931	30790	12416	22502	3223		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P0	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 5 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P2	94	Total	C	N	O	S	0	0
			723	448	138	135	2		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 7 is a protein called 60S ribosomal protein L3.

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

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 14 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	211	Total	C	N	O	S	0	0
			1705	1083	322	294	6		

- Molecule 15 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	183	Total	C	N	O	S	0	0
			1420	882	281	257			

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	136	Total	C	N	O	S	0	0
			997	625	186	179	7		

- Molecule 27 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	62	Total	C	N	O	S	0	0
			513	330	101	81	1		

- Molecule 28 is a protein called 60S ribosomal protein L25.

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

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L28.

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

- Molecule 32 is a protein called 60S ribosomal protein L29.

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

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 41 is a protein called 60S ribosomal protein L38.

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

- Molecule 42 is a protein called 60S ribosomal protein L39.

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

- Molecule 43 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 44 is a protein called 60S ribosomal protein L41-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 45 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	1776	Total	C	N	O	P	0	0
			37845	16918	6702	12449	1776		

- Molecule 48 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 49 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 50 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 51 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 52 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 53 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 54 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	223	Total	C	N	O	S	0	0
			1790	1123	346	318	3		

- Molecule 55 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	x	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 56 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	y	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 57 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	z	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 58 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AA	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 59 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AB	153	Total	C	N	O	S	0	0
			1220	780	231	206	3		

- Molecule 60 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AC	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 61 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AD	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 62 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AE	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 63 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AF	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 64 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AG	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 65 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AH	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 66 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AI	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 67 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AJ	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 68 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AK	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 69 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AL	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 70 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AM	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 71 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AN	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 72 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AO	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 73 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AP	70	Total	C	N	O		0	0
			563	360	104	99			

- Molecule 74 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AQ	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 75 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AR	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 76 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AS	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 77 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AT	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 78 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AU	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AV	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AW	37	Total	C	N	O	S	0	0
			287	177	57	49	4		

- Molecule 81 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AX	837	Total	C	N	O	S	0	0
			6523	4143	1120	1231	29		

- Molecule 82 is a RNA chain called Transfer RNA - Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	AY	76	Total	C	N	O	P	0	0
			1626	725	293	532	76		

- Molecule 83 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	AZ	7	Total	C	N	O	P	0	0
			144	65	21	51	7		

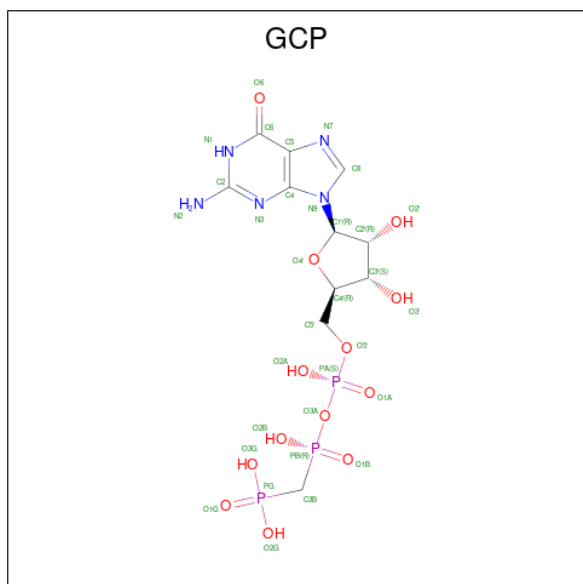
- Molecule 84 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BA	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	j	1	Total	Zn	0
			1	1	
85	m	1	Total	Zn	0
			1	1	
85	o	1	Total	Zn	0
			1	1	
85	p	1	Total	Zn	0
			1	1	
85	AQ	1	Total	Zn	0
			1	1	
85	AR	1	Total	Zn	0
			1	1	
85	AT	1	Total	Zn	0
			1	1	
85	AW	1	Total	Zn	0
			1	1	

- Molecule 86 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

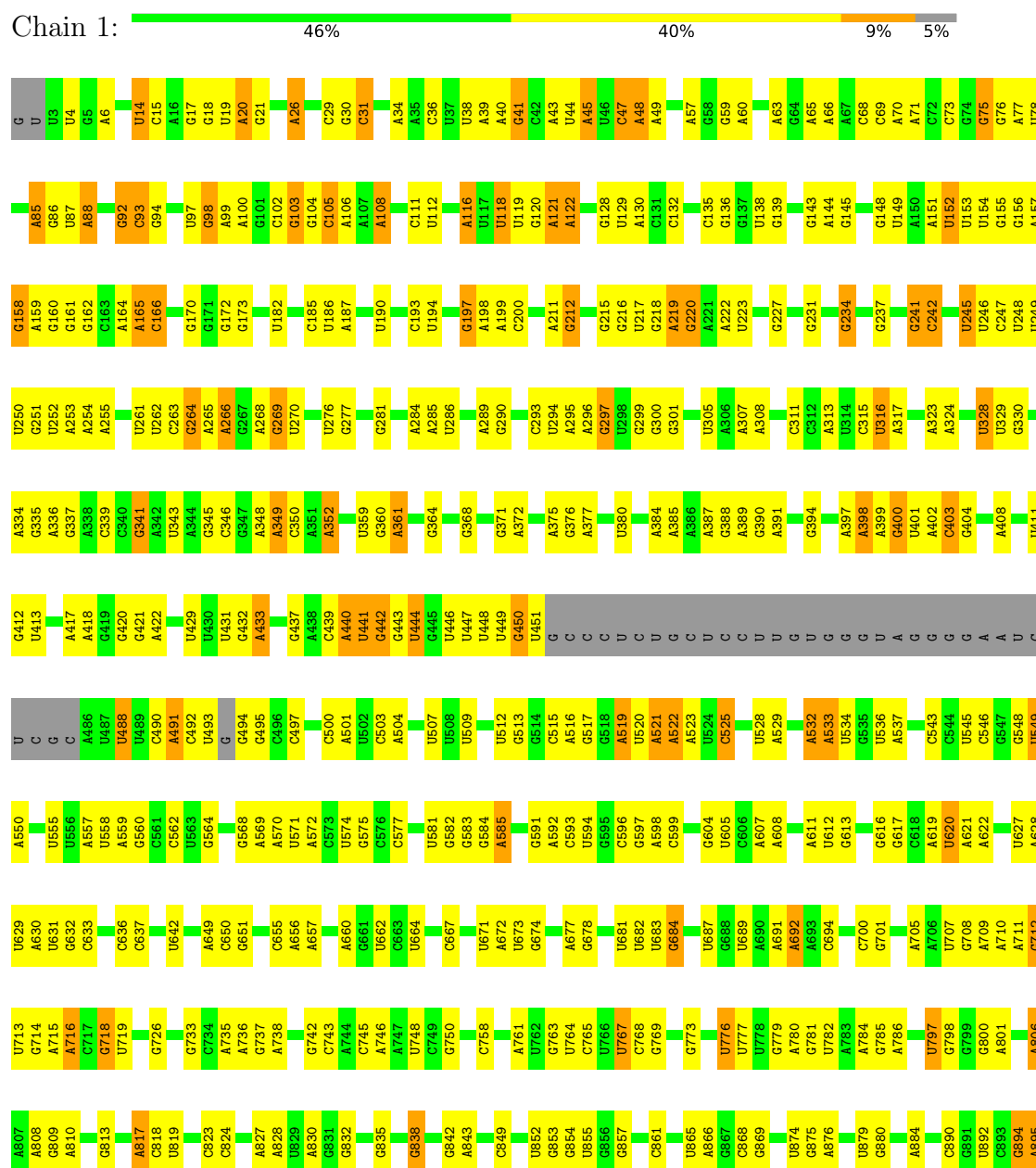


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
86	AX	1	32	11	5	13	3	0

3 Residue-property plots

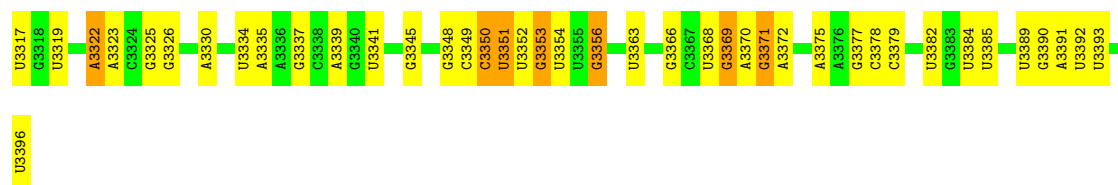
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S ribosomal RNA



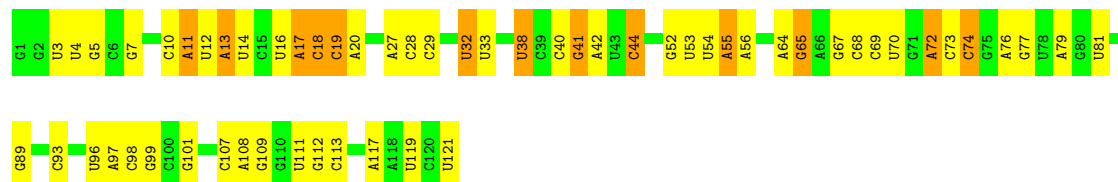






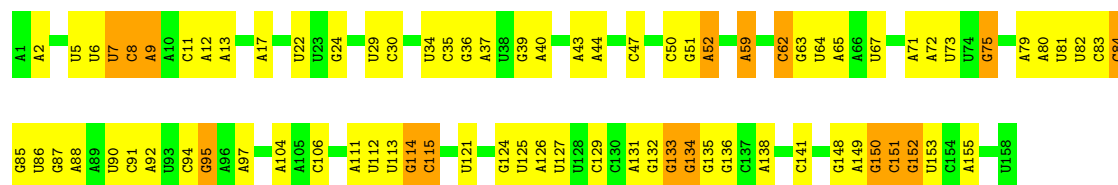
• Molecule 2: 5S ribosomal RNA

Chain 3: 52% 37% 11%



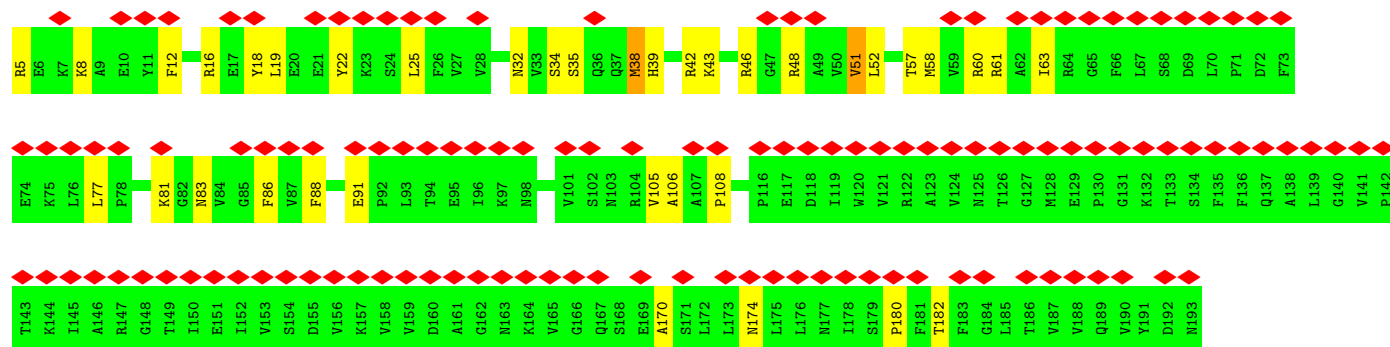
• Molecule 3: 5.8S ribosomal RNA

Chain 4: 49% 41% 10%



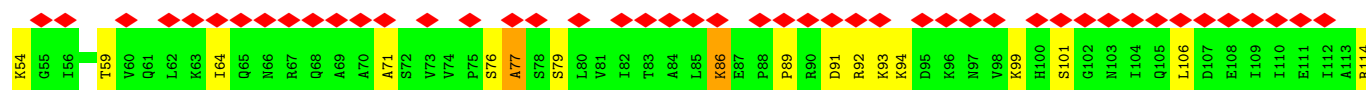
• Molecule 4: 60S acidic ribosomal protein P0

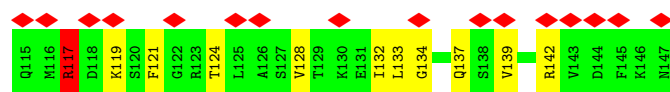
Chain P0: 67% 80% 19%



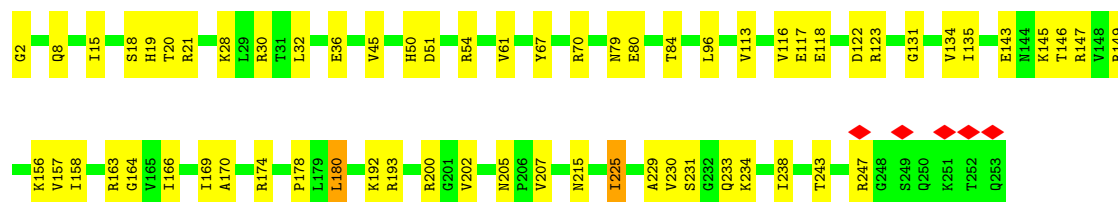
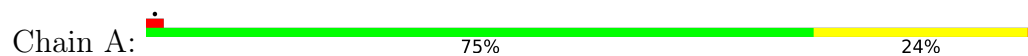
• Molecule 5: 60S ribosomal protein L12-A

Chain P2: 66% 70% 27%

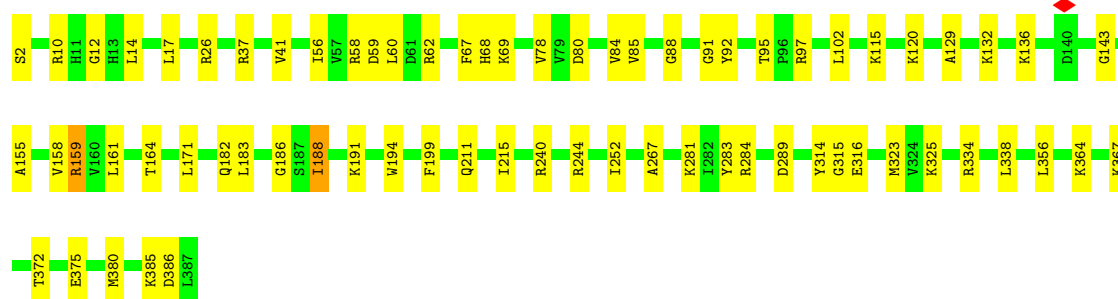
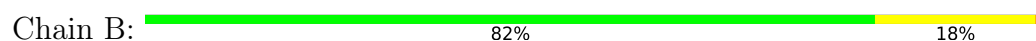




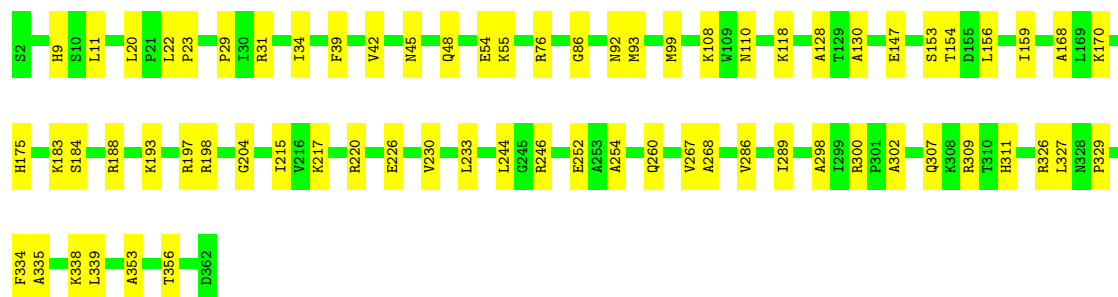
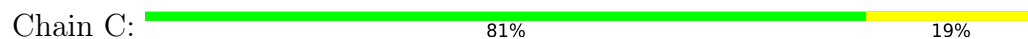
• Molecule 6: 60S ribosomal protein L2-A



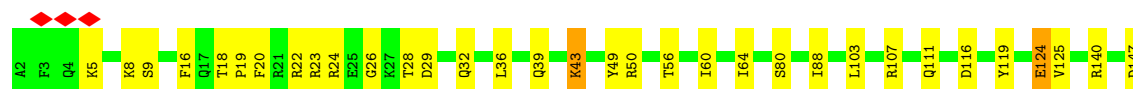
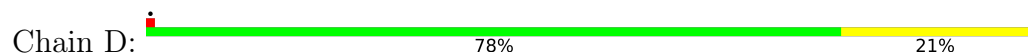
• Molecule 7: 60S ribosomal protein L3

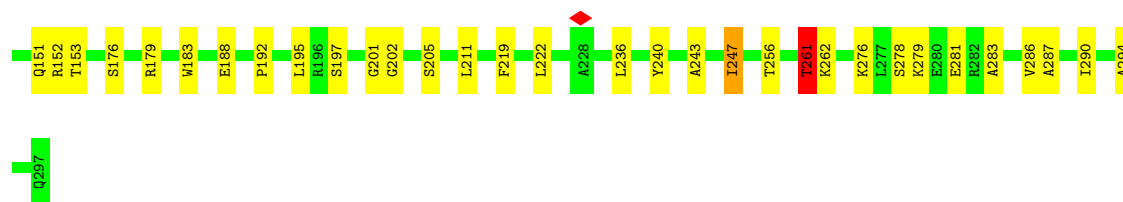


• Molecule 8: 60S ribosomal protein L4-A

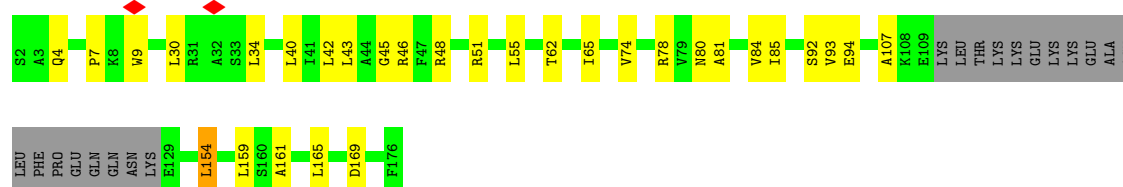


• Molecule 9: 60S ribosomal protein L5

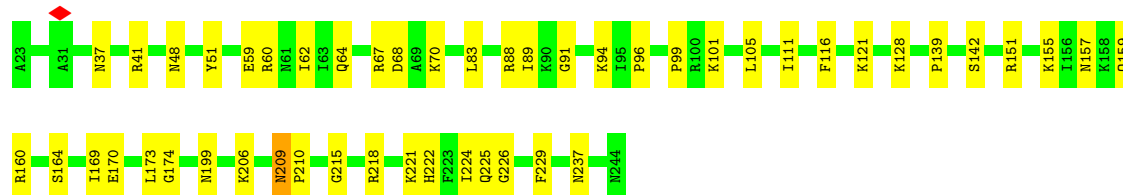
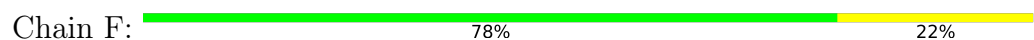




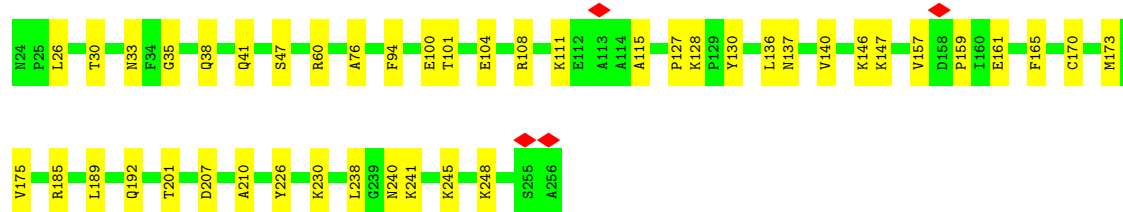
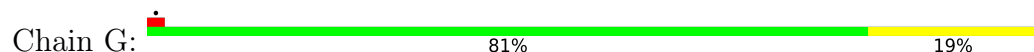
• Molecule 10: 60S ribosomal protein L6-A



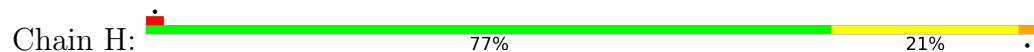
• Molecule 11: 60S ribosomal protein L7-A



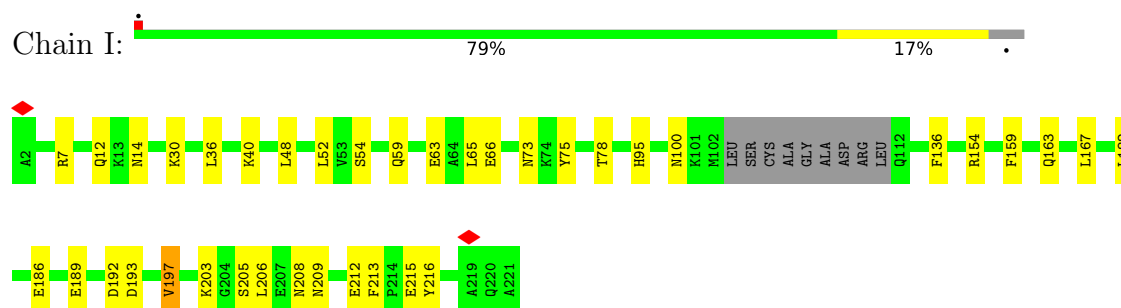
• Molecule 12: 60S ribosomal protein L8-A



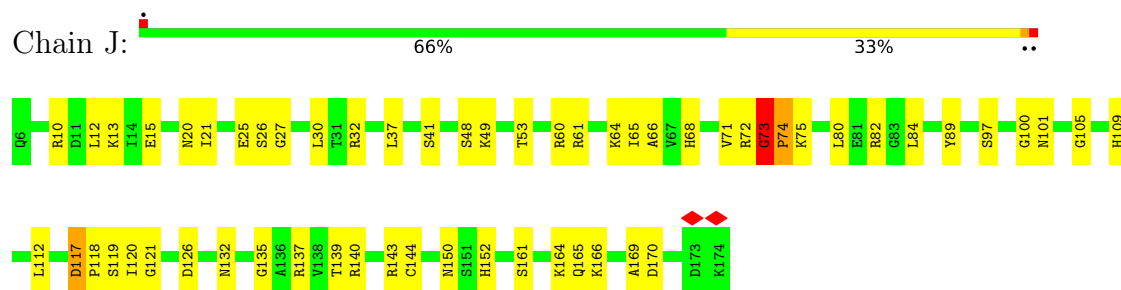
• Molecule 13: 60S ribosomal protein L9-A



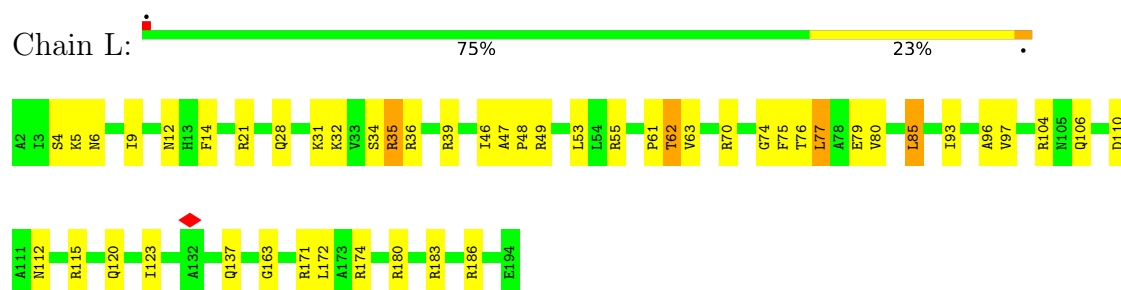
- Molecule 14: 60S ribosomal protein L10



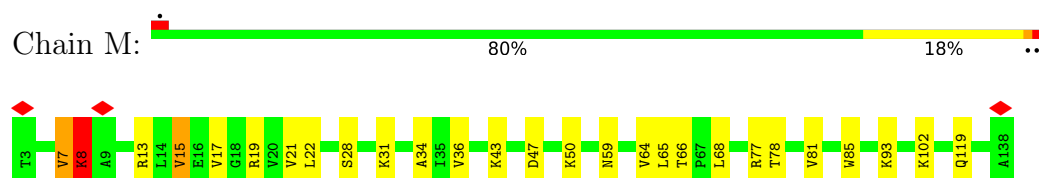
- Molecule 15: 60S ribosomal protein L11-B



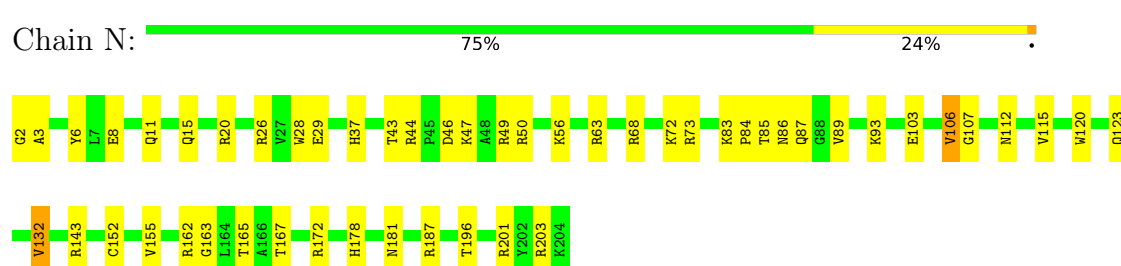
- Molecule 16: 60S ribosomal protein L13-A



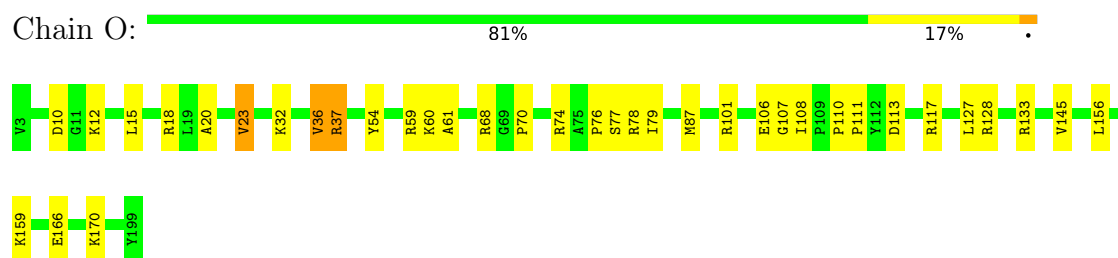
- Molecule 17: 60S ribosomal protein L14-A



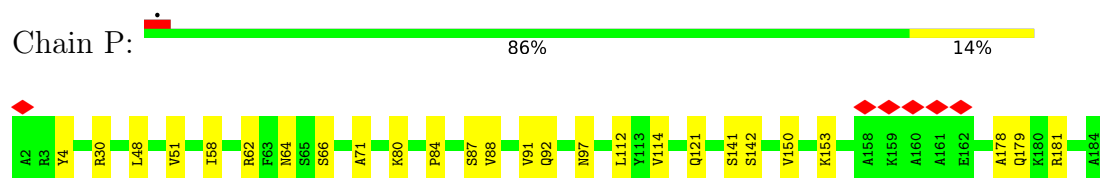
- Molecule 18: 60S ribosomal protein L15-A



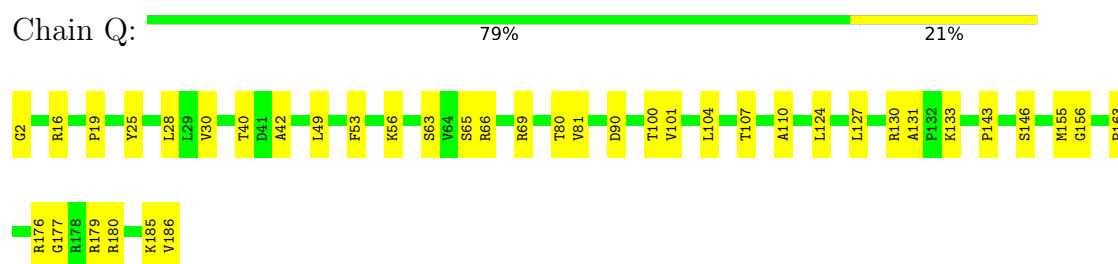
- Molecule 19: 60S ribosomal protein L16-A



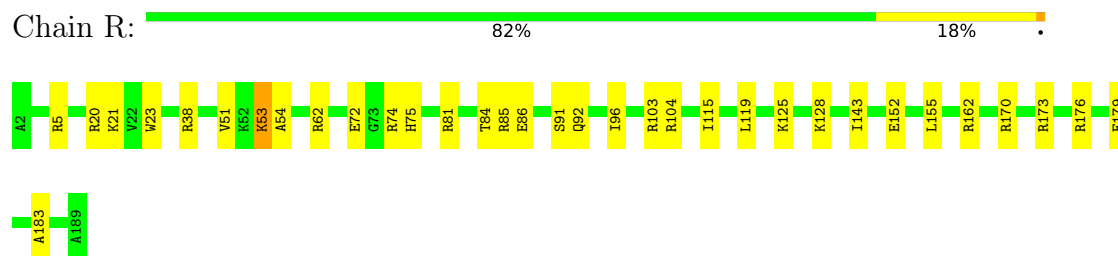
- Molecule 20: 60S ribosomal protein L17-A



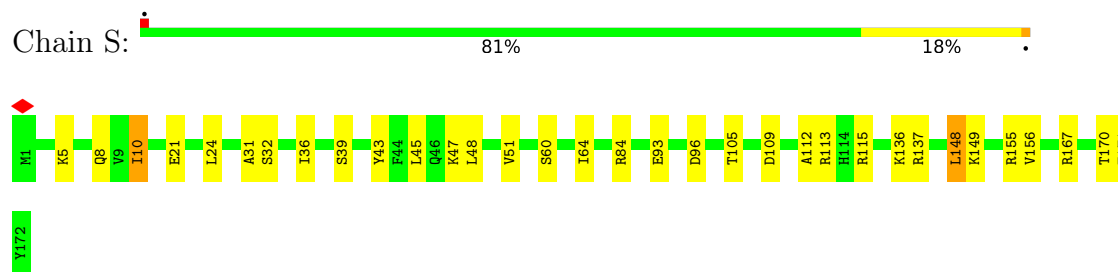
- Molecule 21: 60S ribosomal protein L18-A



- Molecule 22: 60S ribosomal protein L19-A



- Molecule 23: 60S ribosomal protein L20-A



- Molecule 24: 60S ribosomal protein L21-A

Chain T:  83% 17%



- Molecule 25: 60S ribosomal protein L22-A

Chain U:  88% 12%



- Molecule 26: 60S ribosomal protein L23-A

Chain V:  81% 18%



- Molecule 27: 60S ribosomal protein L24-A

Chain W:  82% 18%



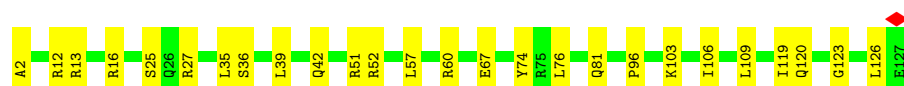
- Molecule 28: 60S ribosomal protein L25

Chain X:  83% 17%



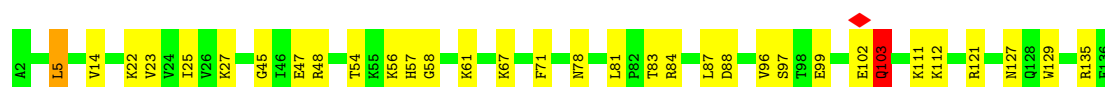
- Molecule 29: 60S ribosomal protein L26-A

Chain Y:  79% 21%

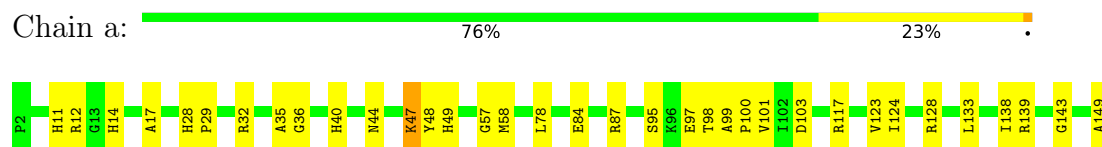


- Molecule 30: 60S ribosomal protein L27-A

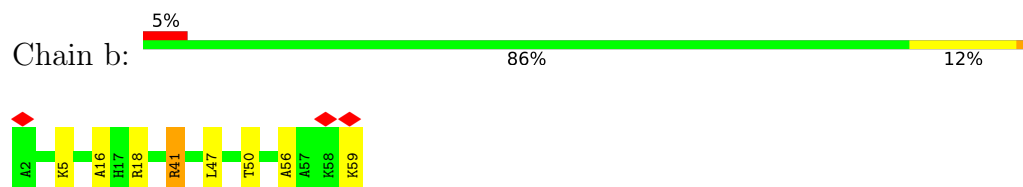
Chain Z:  76% 23%



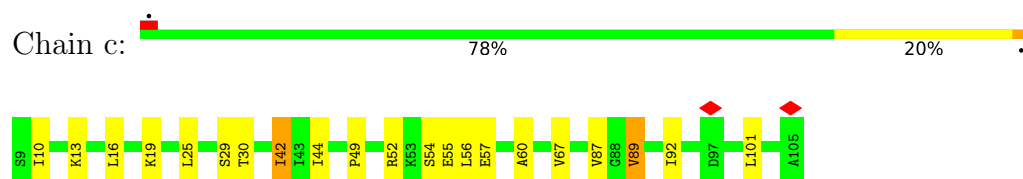
- Molecule 31: 60S ribosomal protein L28



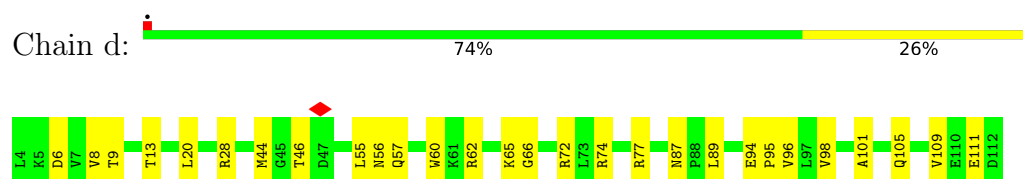
- Molecule 32: 60S ribosomal protein L29



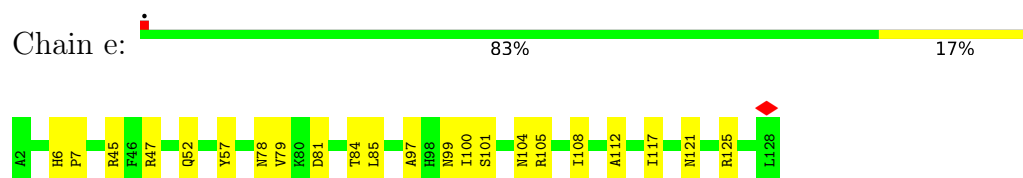
- Molecule 33: 60S ribosomal protein L30



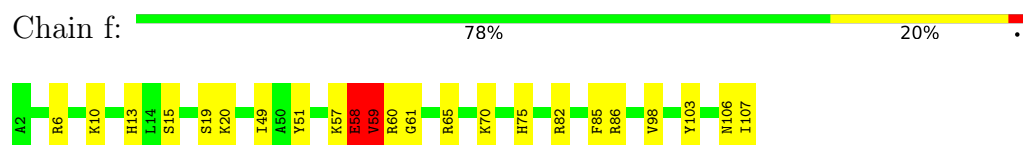
- Molecule 34: 60S ribosomal protein L31-A



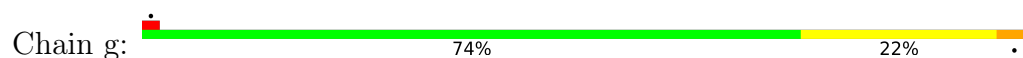
- Molecule 35: 60S ribosomal protein L32



- Molecule 36: 60S ribosomal protein L33-A

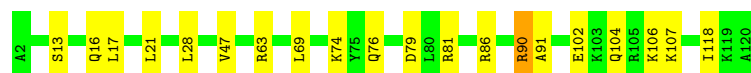
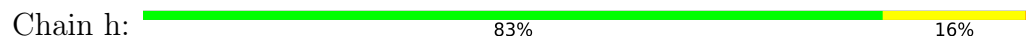


- Molecule 37: 60S ribosomal protein L34-A





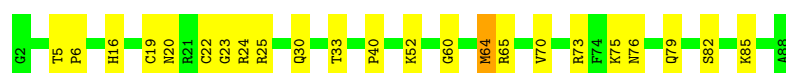
- Molecule 38: 60S ribosomal protein L35-A



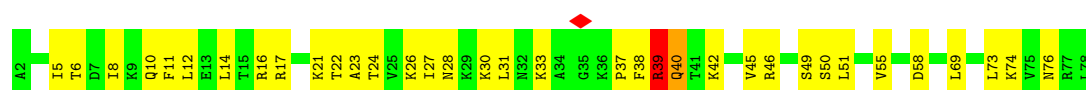
- Molecule 39: 60S ribosomal protein L36-A



- Molecule 40: 60S ribosomal protein L37-A



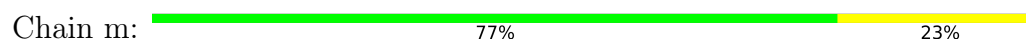
- Molecule 41: 60S ribosomal protein L38



- Molecule 42: 60S ribosomal protein L39

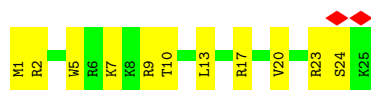


- Molecule 43: Ubiquitin-60S ribosomal protein L40

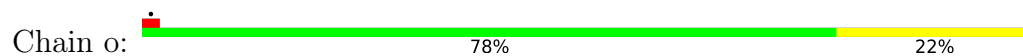


- Molecule 44: 60S ribosomal protein L41-B

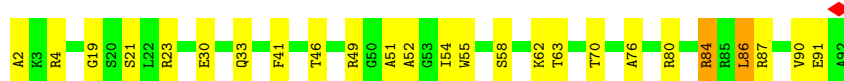




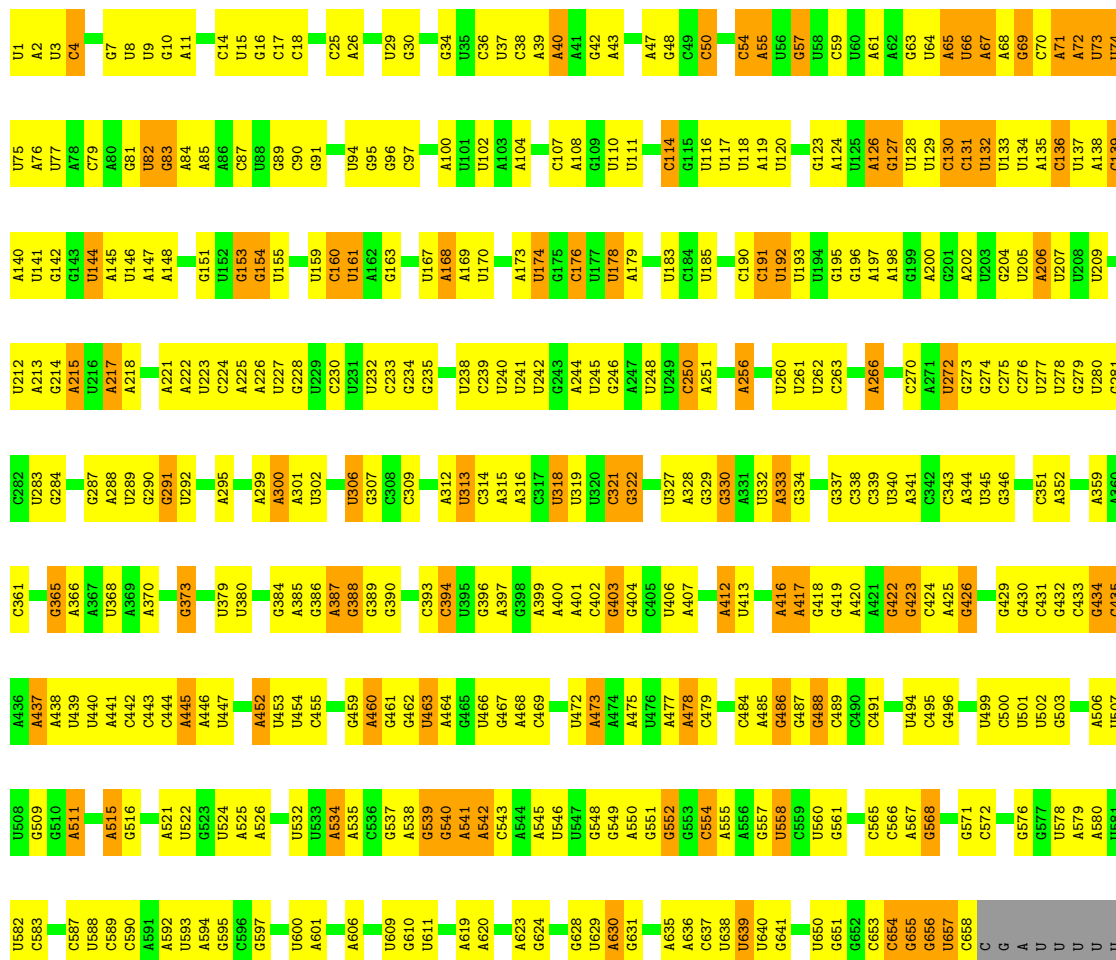
- Molecule 45: 60S ribosomal protein L42-A



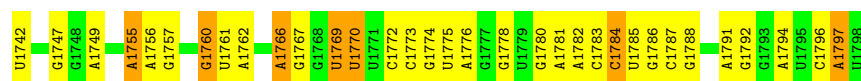
- Molecule 46: 60S ribosomal protein L43-A



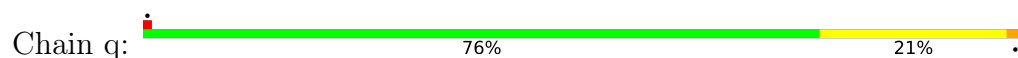
- Molecule 47: 18S ribosomal RNA



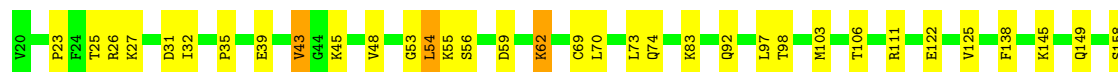
G1670	A1593	G1454	A1391	G1328	U1253	U1191	C1123	U1025	G948	U882	U813	A734	C
G1671	G1594	G1455	U1392	A1329	U1254	C1192	C1123	A1030	G949	C853	A814	C735	G
G1672	U1595	C1456	G1393	C1332	G1255	A1193	A1124	A1031	C950	A884	G815	C736	U
G1673	C1596	C1457	G1394	C1333	A1256	A1194	A1125	G1032	A951	G885	G816	A737	G
G1674	A1597	G1458	U1395	G1334	U1257	C1195	A1126	A952	A952	U886	A817	G738	U
G1675	U1598	C1459	U1396	U1335	U1258	A1196	A1132	A1036	G953	C818	G818	G739	A
U1676	C1597	A1460	U1397	U1336	U1259	C1199	A1133	A1037	G954	C819	A740	C740	C
C1677	U1528	C1461	U1398	A1337	U1260	G1199	C1134	A1039	G957	U820	C741	U742	U
A1678	U1529	C1465	C1399	A1337	G1261	G1200	C1135	A1039	C957	A891	U743	G876	G876
G1679	U1530	G1466	A1400	C1338	U1262	G1201	U1136	G1040	U958	C890	C744	G877	G877
G1680	C1531	C1467	A1401	C1339	G1263	A1202	U1137	G1041	U959	G895	U745	A878	A878
C1681	U1532	U1468	G1402	U1340	G1264	A1203	A1138	G1042	U960	U896	U746	U679	U679
U1682	C1533	C1469	C1403	A1341	G1265	A1204	A1139	A1043	U961	C897	U749	U680	U680
U1683	G1534	A1469	C1404	C1342	U1266	C1205	G1140	C1045	C962	A888	U750	U681	U681
G1684	U1535	C1470	G1405	U1343	G1267	U1206	G1046	G1046	A963	G899	A752	A753	C
C1685	C1537	A1471	A1406	A1344	U1268	C1207	U964	G1047	U964	A900	C886	C887	C886
U1688	G1537	C1472	U1407	A1345	U1269	A1208	U965	G901	U965	G901	A757	A757	G887
U1689	U1538	U1473	G1408	A1346	G1270	C1209	A1147	U1052	A966	G902	U758	C892	C892
A1690	C1539	G1474	A1409	U1347	G1271	A1210	C1148	G1053	A967	U903	U759	U893	U893
C1691	G1540	A1475	A1410	A1348	U1272	A1211	G1149	U066	U968	G904	A760	U694	U694
C1615	U1541	C1476	A1411	G1349	U1273	G1212	G1150	U1056	C969	A905	G761	U695	U695
G1616	G1542	C1481	G1412	U1350	C1274	G1213	A1151	U	A970	A907	G765	C696	C696
U1617	A1543	C1482	U1413	G1351	U1275	A1214	A1152	U	A971	U908	U766	C697	C697
C1618	U1544	A1483	U1414	G1352	U1276	C1215	G1153	U	G976	U909	U767	U698	U698
C1619	A1545	C1484	U1415	U1353	G1277	G1216	G1154	U	G976	U909	U768	U699	U699
C1620	U1545	G1484	G1416	G1354	G1278	A1217	G1155	A	G976	C910	C768	C700	C700
C1623	U1552	C1485	C1485	C1355	C1284	G1218	C1156	A1062	G980	U911	G772	U701	U701
C1624	G1553	U1486	G1419	U1356	U1285	A1219	A1157	U1070	U981	U912	C773	G702	G702
U1628	U1554	A1487	A1420	A1357	U1286	C1220	C1158	C1071	G986	G913	A774	G703	G703
A1631	A1555	C1488	A1421	C1360	U1287	A1221	C1159	U1071	G987	G914	G775	C704	C704
C1632	U1556	U1489	A1422	U1361	G1288	G1222	A1160	G1074	C990	U916	C776	U705	U705
C1633	U1557	C1490	A1425	U1362	U1289	A1223	C1161	U1080	C991	U917	C777	A706	A706
C1634	U1558	U1491	C1426	U1363	U1290	G1225	C1162	C1075	G992	U918	C778	A707	A707
C1635	C1559	A1492	G1427	G1364	U1291	A1226	G1163	A1076	C993	U919	C779	C708	C708
C1636	U1560	C1493	G1428	U1365	U1292	A1227	G1164	U1081	A993	U920	U780	C709	C709
C1637	U1561	U1495	G1429	U1366	C1293	G1228	G1165	U1082	A1001	U921	U781	U710	U710
C1638	G1562	U1496	U1430	C1367	G1297	G1229	G1167	C1082	G1002	G922	U782	U711	U711
C1639	C1563	U1497	C1431	G1368	U1298	A1230	U1168	G1083	A1003	A923	C783	G712	G712
G1642	U1564	G1498	U1432	U1369	G1299	U1231	G1169	U1084	U1004	U924	C784	A713	A713
A1707	U1565	G1499	G1433	U1370	A1300	U1232	G1170	A1087	U1005	G925	U785	G714	G714
U1708	U1566	G1502	G1434	U1371	U1301	G1233	A1171	A1088	A1006	A926	C786	U715	U715
C1709	U1567	A1503	U1435	C1372	C1306	A1234	G1172	A1091	C1010	U927	A788	C716	C716
U1710	C1568	G1504	U1436	C1373	C1309	G1235	C1173	A1092	G1011	U928	A789	C717	C717
C1711	U1569	A1505	G1438	C1374	U1310	A1236	C1174	U1097	U1012	A929	A793	U718	U718
U1712	U1570	G1506	C1439	C1375	U1311	G1237	U1175	A1098	A1013	C931	U794	U719	U719
G1713	U1571	U1507	C1440	C1376	U1312	A1238	G1178	G1014	U1014	U932	U795	G720	G720
A1714	U1572	U1508	C1441	C1377	U1313	U1239	C1180	U1099	U1015	U933	A796	U721	U721
C1715	G1572	U1509	U1442	C1378	A1314	G1241	G1179	G1100	C1016	C934	C797	G722	G722
G1716	A1573	U1510	A1443	U1380	U1315	A1242	U1181	G1108	A1020	U935	C798	G723	G723
G1717	U1574	G1512	A1444	U1381	G1316	G1243	U1182	G1109	C1021	G936	U800	C724	C724
G1720	C1575	G1513	U1445	A1382	G1317	A1244	A1183	G1110	C1022	U937	G801	U725	U725
G1721	U1576	U1514	C1447	G1383	U1318	G1245	A1184	A1023	A1023	G872	A806	C726	C726
G1722	A1577	A1515	G1448	G1385	U1319	C1246	U1185	U1024	A941	U873	U727	U727	U727
A1730	U1578	A1516	U1449	G1387	A1321	U1249	U1187	A1025	A1025	G877	U728	U728	U728
U1731	G1582	U1517	U1450	A1388	A1326	U1250	G1188	A1026	A1026	G877	U729	U729	U729
A1732	U1583	C1518	U1451	U1389	A1326	U1251	A1189	A1027	A1027	G877	U730	U730	U730
G1733	G1584	U1519	U1452	U1390	C1327	C1252	C1190	G1118	C1028	U947	A812	C732	C732
U1734	U1585	U1520	G1453	U1390	C1327	C1252	C1190	G1118	C1028	U947	A812	C732	C732
U1735	A1587	U1520	G1453	U1390	C1327	C1252	C1190	G1118	C1028	U947	A812	C732	C732
C1736	G1588	U1520	G1453	U1390	C1327	C1252	C1190	G1118	C1028	U947	A812	C732	C732
U1737	U1589	U1520	G1453	U1390	C1327	C1252	C1190	G1118	C1028	U947	A812	C732	C732
U1738	A1592	U1520	G1453	U1390	C1327	C1252	C1190	G1118	C1028	U947	A812	C732	C732



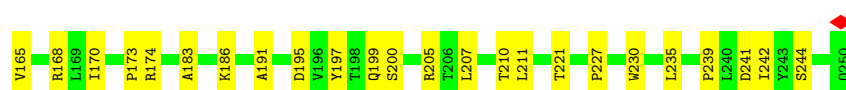
• Molecule 48: 40S ribosomal protein S0-A



• Molecule 49: 40S ribosomal protein S1-A



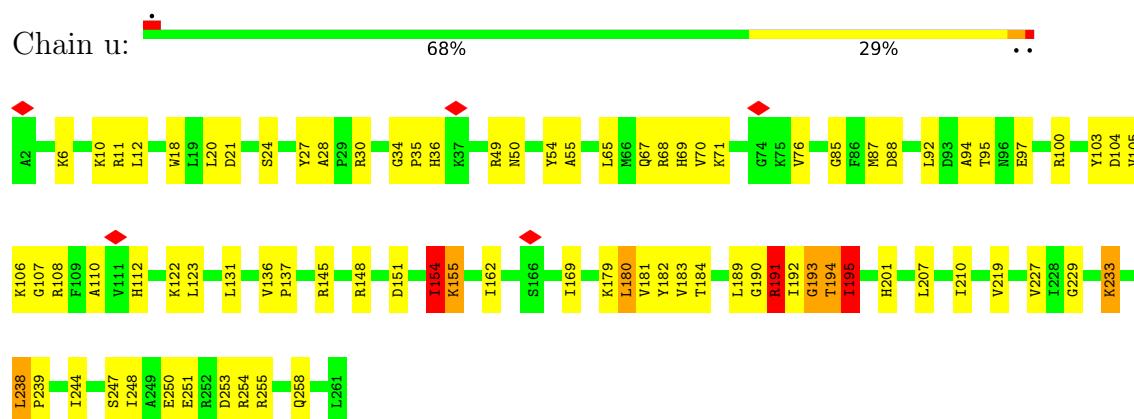
• Molecule 50: 40S ribosomal protein S2



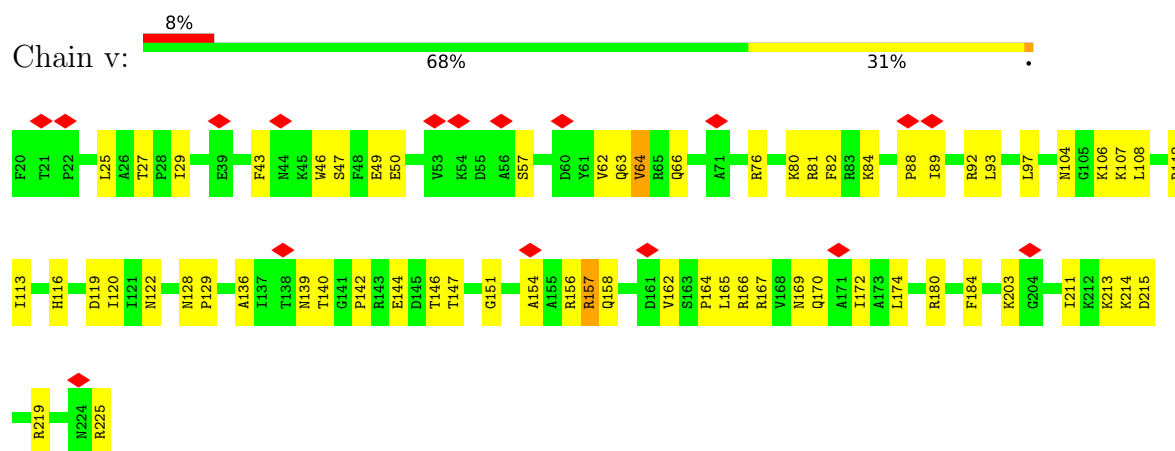
• Molecule 51: 40S ribosomal protein S3



- Molecule 52: 40S ribosomal protein S4-A



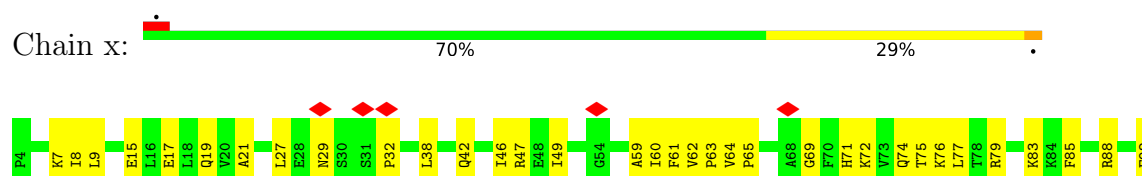
- Molecule 53: 40S ribosomal protein S5

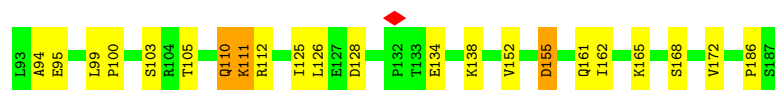


- Molecule 54: 40S ribosomal protein S6-A

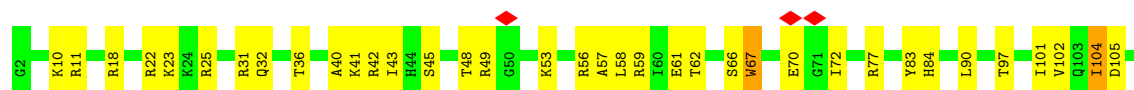


- Molecule 55: 40S ribosomal protein S7-A

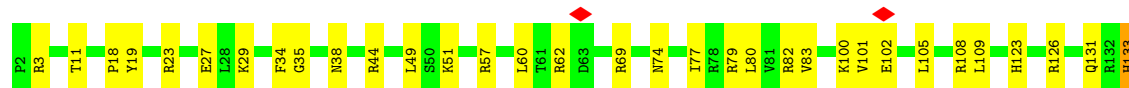
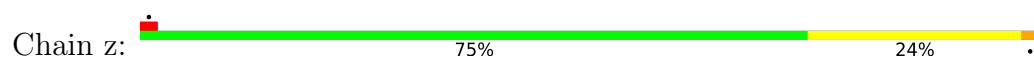




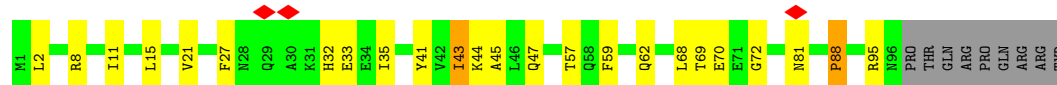
- Molecule 56: 40S ribosomal protein S8-A



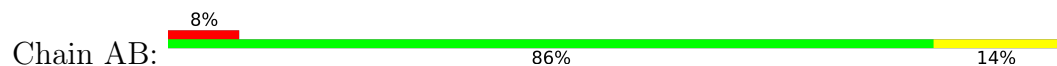
- Molecule 57: 40S ribosomal protein S9-A



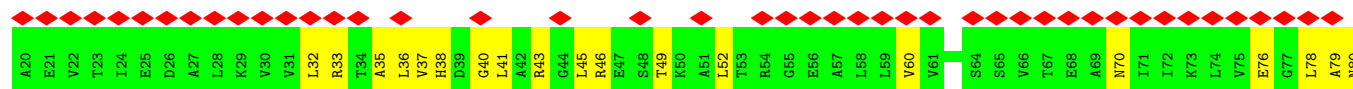
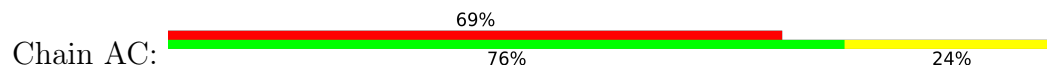
- Molecule 58: 40S ribosomal protein S10-A

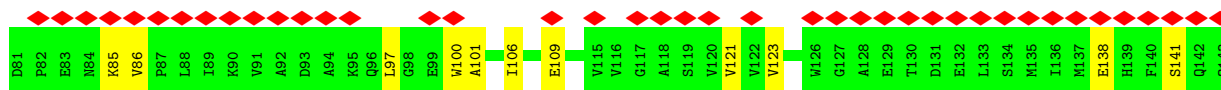


- Molecule 59: 40S ribosomal protein S11-A



- Molecule 60: 40S ribosomal protein S12

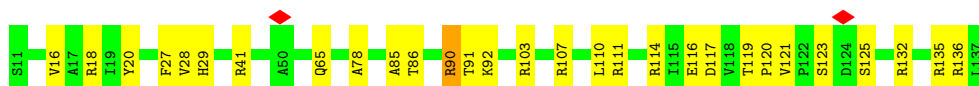
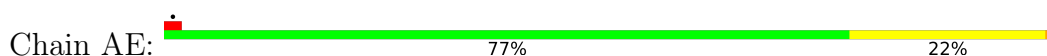




- Molecule 61: 40S ribosomal protein S13



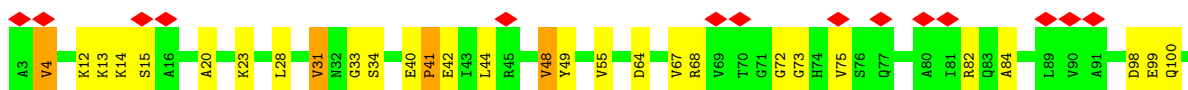
- Molecule 62: 40S ribosomal protein S14-B



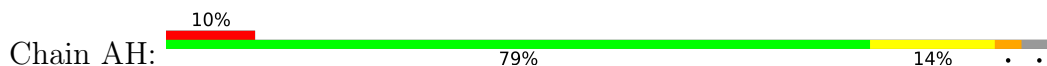
- Molecule 63: 40S ribosomal protein S15

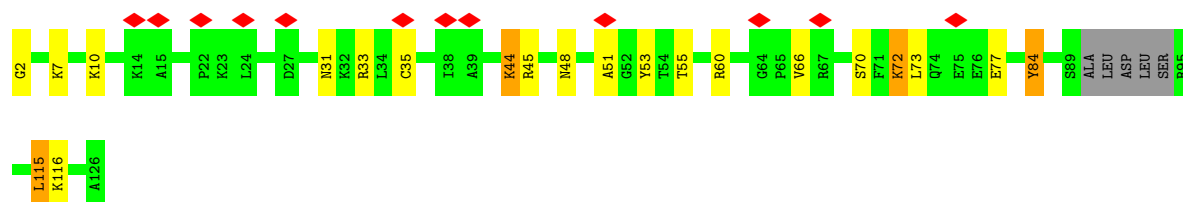


- Molecule 64: 40S ribosomal protein S16-A

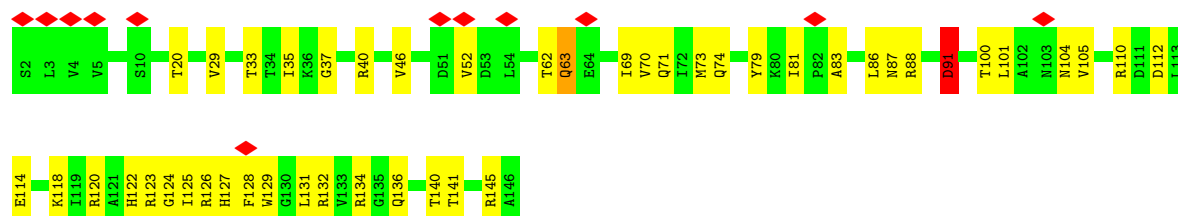


- Molecule 65: 40S ribosomal protein S17-B

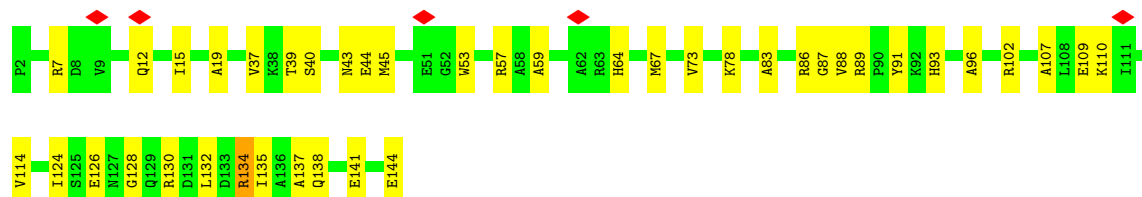




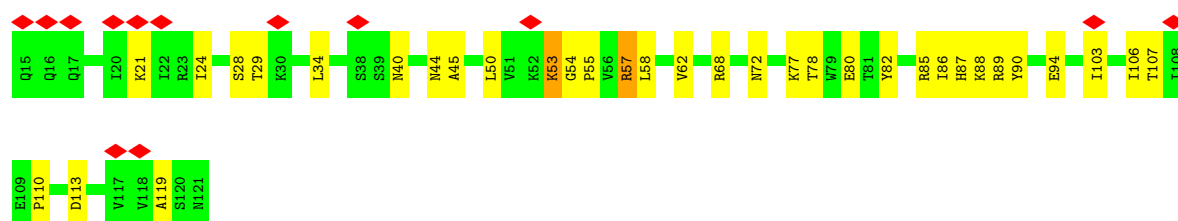
- Molecule 66: 40S ribosomal protein S18-A



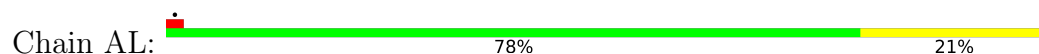
- Molecule 67: 40S ribosomal protein S19-A



- Molecule 68: 40S ribosomal protein S20



- Molecule 69: 40S ribosomal protein S21-A



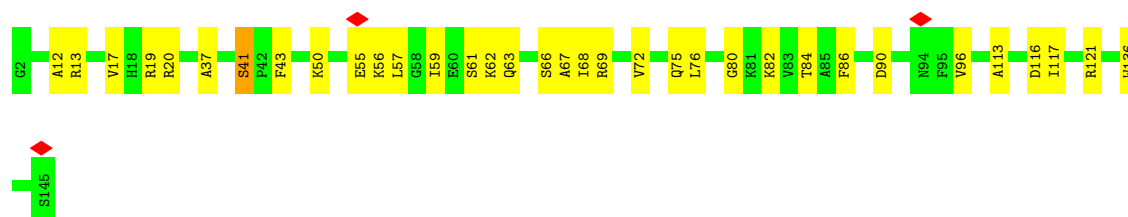
- Molecule 70: 40S ribosomal protein S22-A

Chain AM:  80% 20%



- Molecule 71: 40S ribosomal protein S23-A

Chain AN:  76% 23%



- Molecule 72: 40S ribosomal protein S24-A

Chain AO:  74% 26%



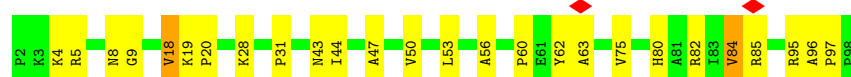
- Molecule 73: 40S ribosomal protein S25-A

Chain AP:  23% 63% 37%



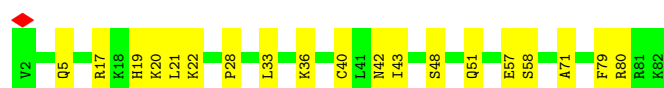
- Molecule 74: 40S ribosomal protein S26-B

Chain AQ:  73% 25%



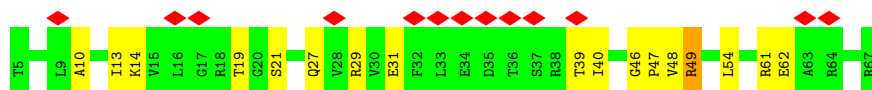
- Molecule 75: 40S ribosomal protein S27-A

Chain AR:  77% 23%

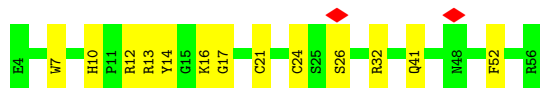
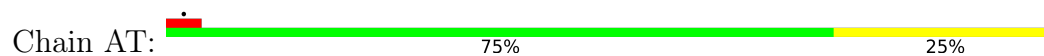


- Molecule 76: 40S ribosomal protein S28-A

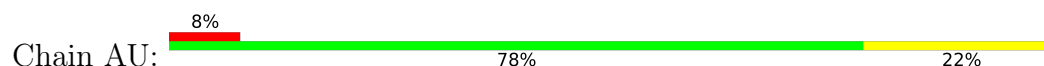
Chain AS:  21% 73% 25%



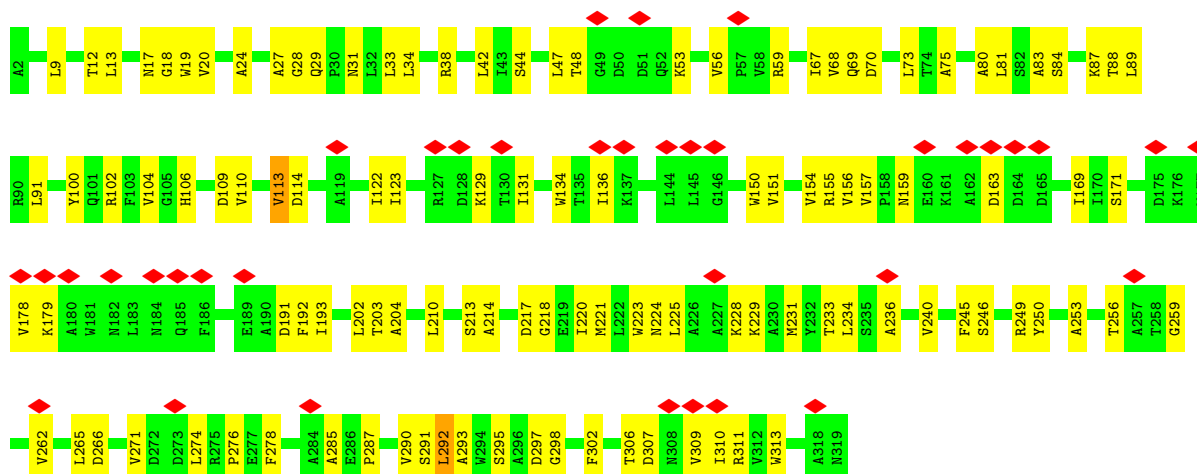
- Molecule 77: 40S ribosomal protein S29-A



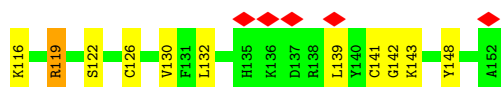
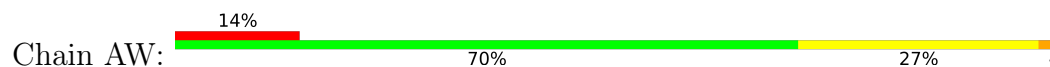
- Molecule 78: 40S ribosomal protein S30-A



- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

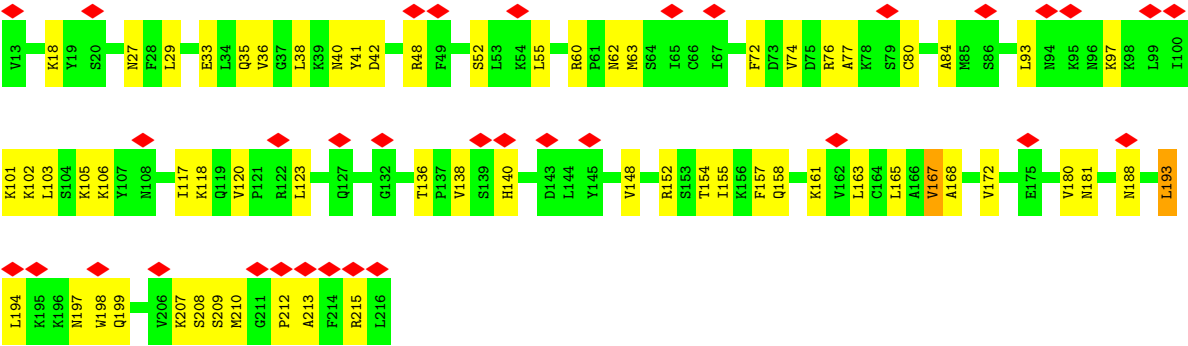


- Molecule 80: Ubiquitin-40S ribosomal protein S31



- Molecule 81: Elongation factor 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	86500	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.306	Depositor
Minimum map value	-0.179	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.033	Depositor
Map size ($\text{\AA}$)	396.0, 396.0, 396.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	1	0.32	0/77157	0.49	2/120295 (0.0%)
2	3	0.29	0/2883	0.48	0/4491
3	4	0.33	0/3746	0.51	0/5832
4	P0	0.32	1/1498 (0.1%)	0.71	0/2025
5	P2	0.33	0/728	1.05	3/975 (0.3%)
6	A	0.39	0/1948	0.77	2/2617 (0.1%)
7	B	0.34	0/3146	0.71	2/4228 (0.0%)
8	C	0.34	0/2800	0.77	1/3790 (0.0%)
9	D	0.28	0/2425	0.71	4/3271 (0.1%)
10	E	0.28	0/1260	0.74	2/1694 (0.1%)
11	F	0.34	0/1821	0.76	0/2451
12	G	0.29	0/1836	0.71	0/2481
13	H	0.33	0/1539	0.79	3/2073 (0.1%)
14	I	0.31	0/1741	0.72	2/2335 (0.1%)
15	J	0.30	0/1374	0.90	2/1842 (0.1%)
16	L	0.33	0/1568	0.79	2/2106 (0.1%)
17	M	0.28	0/1068	0.69	1/1438 (0.1%)
18	N	0.37	0/1757	0.72	0/2354
19	O	0.35	0/1585	0.73	0/2128
20	P	0.31	0/1443	0.69	1/1944 (0.1%)
21	Q	0.33	0/1465	0.73	0/1965
22	R	0.29	0/1538	0.70	1/2050 (0.0%)
23	S	0.33	0/1481	0.71	0/1990
24	T	0.34	0/1300	0.70	2/1743 (0.1%)
25	U	0.27	0/812	0.68	0/1099
26	V	0.36	0/1012	0.76	0/1362
27	W	0.29	0/525	0.69	0/696
28	X	0.26	0/979	0.57	0/1321
29	Y	0.29	0/1004	0.66	0/1341
30	Z	0.34	0/1118	0.71	1/1497 (0.1%)
31	a	0.34	0/1204	0.78	3/1612 (0.2%)
32	b	0.31	0/473	0.67	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.25	0/751	0.59	0/1008
34	d	0.35	0/897	0.70	0/1205
35	e	0.33	0/1041	0.71	0/1394
36	f	0.35	0/868	0.77	3/1168 (0.3%)
37	g	0.31	0/890	0.81	1/1189 (0.1%)
38	h	0.29	0/978	0.77	1/1301 (0.1%)
39	i	0.33	0/778	0.79	0/1034
40	j	0.34	0/696	0.83	0/923
41	k	0.32	0/618	0.86	2/826 (0.2%)
42	l	0.35	0/443	0.98	2/588 (0.3%)
43	m	0.30	0/423	0.69	0/562
44	n	0.31	0/234	0.80	0/300
45	o	0.33	0/860	0.83	2/1136 (0.2%)
46	p	0.39	0/701	0.76	0/934
47	2	0.28	0/42328	0.52	5/65955 (0.0%)
48	q	0.29	0/1617	0.77	3/2215 (0.1%)
49	r	0.31	0/1735	0.88	7/2335 (0.3%)
50	s	0.28	0/1665	0.71	2/2263 (0.1%)
51	t	0.26	0/1759	0.68	0/2368
52	u	0.29	0/2109	0.87	9/2839 (0.3%)
53	v	0.29	0/1629	0.83	4/2202 (0.2%)
54	w	0.33	0/1814	0.96	4/2425 (0.2%)
55	x	0.28	0/1506	0.82	0/2028
56	y	0.29	0/1514	0.81	4/2021 (0.2%)
57	z	0.29	0/1519	0.79	0/2035
58	AA	0.29	0/789	0.82	1/1067 (0.1%)
59	AB	0.31	0/1247	0.69	0/1681
60	AC	0.24	0/898	0.70	0/1220
61	AD	0.30	0/1215	0.85	2/1638 (0.1%)
62	AE	0.31	0/901	0.75	0/1217
63	AF	0.30	0/998	0.84	0/1341
64	AG	0.29	0/1125	0.80	5/1510 (0.3%)
65	AH	0.27	0/935	0.75	0/1254
66	AI	0.27	0/1211	0.72	0/1628
67	AJ	0.26	0/1130	0.69	0/1517
68	AK	0.30	0/865	0.92	2/1169 (0.2%)
69	AL	0.35	0/693	0.92	1/935 (0.1%)
70	AM	0.28	0/1038	0.65	0/1395
71	AN	0.33	0/1139	0.79	0/1518
72	AO	0.27	0/1087	0.65	0/1449
73	AP	0.33	0/571	0.84	0/768
74	AQ	0.33	0/782	0.93	2/1047 (0.2%)
75	AR	0.25	0/620	0.83	1/838 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AS	0.27	0/499	0.76	0/670
77	AT	0.28	0/452	0.75	0/600
78	AU	0.27	0/483	0.79	0/643
79	AV	0.25	0/2490	0.67	0/3389
80	AW	0.23	0/292	0.70	0/390
81	AX	0.32	0/6626	0.87	8/8970 (0.1%)
82	AY	0.25	0/1818	0.55	2/2831 (0.1%)
83	AZ	0.50	0/159	1.60	4/244 (1.6%)
84	BA	0.30	0/1634	0.83	1/2195 (0.0%)
All	All	0.31	1/227304 (0.0%)	0.63	112/333053 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	P0	0	2
5	P2	0	1
7	B	0	1
8	C	0	1
9	D	0	4
10	E	0	2
11	F	0	2
12	G	0	3
14	I	0	3
15	J	0	6
16	L	0	2
17	M	0	2
18	N	0	1
19	O	0	3
22	R	0	1
23	S	0	2
30	Z	0	1
31	a	0	2
32	b	0	1
34	d	0	1
36	f	0	2
37	g	0	4
38	h	0	2
39	i	0	3
40	j	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
41	k	0	2
45	o	0	2
46	p	0	1
48	q	0	2
49	r	0	3
50	s	0	1
51	t	0	4
52	u	0	7
53	v	0	4
54	w	0	6
55	x	0	3
56	y	0	1
57	z	0	3
58	AA	0	2
59	AB	0	1
61	AD	0	2
62	AE	0	3
63	AF	0	2
64	AG	0	4
65	AH	0	1
66	AI	0	1
67	AJ	0	1
68	AK	0	2
69	AL	0	2
71	AN	0	2
73	AP	0	1
74	AQ	0	3
75	AR	0	1
76	AS	0	1
78	AU	0	1
80	AW	0	1
81	AX	0	15
84	BA	0	3
All	All	0	143

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P0	77	LEU	C-N	6.31	1.38	1.33

All (112) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	AK	57	ARG	CA-C-N	14.83	141.55	120.49
68	AK	57	ARG	C-N-CA	14.83	141.55	120.49
83	AZ	48	U	C1'-C2'-O2'	-14.36	86.86	108.40
83	AZ	48	U	C2'-C3'-O3'	-13.04	94.13	113.70
84	BA	117	ILE	N-CA-C	-10.36	103.87	113.71
5	P2	117	ARG	N-CA-C	10.33	128.75	107.37
5	P2	86	LYS	CA-C-N	9.68	134.24	120.49
5	P2	86	LYS	C-N-CA	9.68	134.24	120.49
83	AZ	48	U	C3'-C2'-O2'	9.42	124.83	110.70
82	AY	45	G	OP1-P-O3'	-9.12	80.64	108.00
15	J	73	GLY	CA-C-N	8.31	130.23	119.84
15	J	73	GLY	C-N-CA	8.31	130.23	119.84
17	M	15	VAL	N-CA-C	8.00	114.77	106.21
64	AG	48	VAL	N-CA-C	-7.89	103.56	111.77
6	A	202	VAL	N-CA-C	-7.86	105.05	112.83
81	AX	247	ASP	CA-C-N	7.64	135.46	121.70
81	AX	247	ASP	C-N-CA	7.64	135.46	121.70
31	a	47	LYS	CA-C-N	7.62	136.10	121.54
31	a	47	LYS	C-N-CA	7.62	136.10	121.54
41	k	39	ARG	CA-C-N	7.42	135.71	121.54
41	k	39	ARG	C-N-CA	7.42	135.71	121.54
10	E	9	TRP	CA-C-N	-7.26	112.87	122.74
10	E	9	TRP	C-N-CA	-7.26	112.87	122.74
53	v	49	GLU	CA-C-N	7.23	135.35	121.54
53	v	49	GLU	C-N-CA	7.23	135.35	121.54
42	l	27	ILE	CA-C-N	7.02	134.95	121.54
42	l	27	ILE	C-N-CA	7.02	134.95	121.54
49	r	178	GLY	N-CA-C	-6.98	100.41	110.60
13	H	151	VAL	N-CA-C	-6.93	106.47	113.47
56	y	119	GLN	CA-C-N	6.74	133.83	121.70
56	y	119	GLN	C-N-CA	6.74	133.83	121.70
54	w	90	GLY	CA-C-N	6.58	133.54	121.70
54	w	90	GLY	C-N-CA	6.58	133.54	121.70
52	u	154	ILE	CA-C-N	6.56	134.07	121.54
52	u	154	ILE	C-N-CA	6.56	134.07	121.54
58	AA	88	PRO	N-CA-CB	6.47	110.05	103.25
54	w	91	GLU	CA-CB-CG	6.46	127.02	114.10
6	A	15	ILE	N-CA-C	-6.45	107.01	113.20
82	AY	45	G	OP2-P-O3'	-6.35	88.95	108.00
22	R	53	LYS	CA-CB-CG	6.24	126.58	114.10
56	y	67	TRP	CA-C-N	6.22	132.90	121.70
56	y	67	TRP	C-N-CA	6.22	132.90	121.70
14	I	193	ASP	CA-C-N	6.03	126.78	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	I	193	ASP	C-N-CA	6.03	126.78	120.03
7	B	211	GLN	CA-C-N	6.00	130.90	122.08
7	B	211	GLN	C-N-CA	6.00	130.90	122.08
36	f	58	GLU	CA-C-N	5.98	132.73	121.97
36	f	58	GLU	C-N-CA	5.98	132.73	121.97
37	g	81	CYS	CA-CB-SG	5.94	128.06	114.40
52	u	191	ARG	CA-C-N	5.85	132.50	121.97
52	u	191	ARG	C-N-CA	5.85	132.50	121.97
81	AX	149	GLU	CA-C-N	5.78	132.10	121.70
81	AX	149	GLU	C-N-CA	5.78	132.10	121.70
49	r	54	LEU	CA-C-N	5.75	132.52	121.54
49	r	54	LEU	C-N-CA	5.75	132.52	121.54
49	r	177	GLN	CA-CB-CG	5.74	125.58	114.10
13	H	168	ARG	CA-C-N	5.70	136.53	126.45
13	H	168	ARG	C-N-CA	5.70	136.53	126.45
24	T	18	ASP	CA-C-N	5.63	129.71	121.31
24	T	18	ASP	C-N-CA	5.63	129.71	121.31
45	o	6	LYS	CA-C-N	5.62	132.27	121.54
45	o	6	LYS	C-N-CA	5.62	132.27	121.54
1	1	3156	U	P-O3'-C3'	5.56	128.53	120.20
36	f	59	VAL	N-CA-C	-5.55	97.80	109.34
49	r	206	PRO	CA-C-N	5.51	132.07	121.54
49	r	206	PRO	C-N-CA	5.51	132.07	121.54
83	AZ	48	U	C4'-C3'-O3'	-5.50	104.75	113.00
47	2	706	A	P-O3'-C3'	5.49	128.43	120.20
47	2	1755	A	P-O3'-C3'	5.46	128.39	120.20
52	u	94	ALA	CA-C-N	5.45	131.95	121.54
52	u	94	ALA	C-N-CA	5.45	131.95	121.54
81	AX	55	ARG	N-CA-CB	-5.45	107.96	114.17
31	a	47	LYS	CA-CB-CG	5.41	124.92	114.10
1	1	2541	U	P-O3'-C3'	5.39	128.28	120.20
61	AD	137	PRO	CA-C-N	5.39	135.98	126.45
61	AD	137	PRO	C-N-CA	5.39	135.98	126.45
52	u	193	GLY	CA-C-N	5.38	131.81	121.54
52	u	193	GLY	C-N-CA	5.38	131.81	121.54
53	v	184	PHE	CA-C-N	5.38	131.81	121.54
53	v	184	PHE	C-N-CA	5.38	131.81	121.54
30	Z	103	GLN	CA-CB-CG	5.37	124.84	114.10
54	w	93	LYS	N-CA-C	-5.29	99.53	110.80
81	AX	61	LYS	CA-C-N	5.28	135.51	126.32
81	AX	61	LYS	C-N-CA	5.28	135.51	126.32
64	AG	31	VAL	CA-C-N	5.28	131.62	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AG	31	VAL	C-N-CA	5.28	131.62	121.54
75	AR	21	LEU	CA-CB-CG	5.25	134.66	116.30
9	D	124	GLU	CA-C-N	5.24	131.41	121.97
9	D	124	GLU	C-N-CA	5.24	131.41	121.97
74	AQ	60	PRO	CA-C-N	5.23	131.53	121.54
74	AQ	60	PRO	C-N-CA	5.23	131.53	121.54
9	D	261	THR	CA-C-N	5.21	131.49	121.54
9	D	261	THR	C-N-CA	5.21	131.49	121.54
48	q	113	ARG	N-CA-C	5.19	121.85	110.80
81	AX	580	PRO	N-CA-C	5.18	119.70	111.26
47	2	1491	U	P-O3'-C3'	5.16	127.95	120.20
16	L	62	THR	CA-C-N	5.12	131.19	121.97
16	L	62	THR	C-N-CA	5.12	131.19	121.97
8	C	215	ILE	N-CA-C	-5.12	107.82	112.12
64	AG	41	PRO	CA-C-N	5.11	131.30	121.54
64	AG	41	PRO	C-N-CA	5.11	131.30	121.54
38	h	91	ALA	N-CA-C	5.11	116.89	110.91
48	q	38	PHE	CA-C-N	5.10	130.06	122.82
48	q	38	PHE	C-N-CA	5.10	130.06	122.82
49	r	54	LEU	CA-CB-CG	5.09	134.12	116.30
69	AL	10	GLU	CA-CB-CG	5.07	124.23	114.10
52	u	195	ILE	N-CA-C	-5.06	98.81	109.34
47	2	217	A	P-O3'-C3'	5.06	127.78	120.20
20	P	179	GLN	N-CA-C	-5.03	107.14	113.28
47	2	144	U	P-O3'-C3'	5.03	127.74	120.20
50	s	95	ARG	CA-C-N	5.02	129.54	122.46
50	s	95	ARG	C-N-CA	5.02	129.54	122.46

There are no chirality outliers.

All (143) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
58	AA	57	THR	Peptide
58	AA	59	PHE	Peptide
59	AB	6	THR	Peptide
61	AD	104	ARG	Peptide
61	AD	60	VAL	Peptide
62	AE	123	SER	Peptide
62	AE	90	ARG	Peptide
62	AE	91	THR	Peptide
63	AF	16	SER	Peptide
63	AF	47	ARG	Peptide

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Mol	Chain	Res	Type	Group
64	AG	33	GLY	Peptide
64	AG	4	VAL	Peptide
64	AG	40	GLU	Peptide
64	AG	49	TYR	Peptide
65	AH	84	TYR	Peptide
66	AI	91	ASP	Peptide
67	AJ	134	ARG	Peptide
68	AK	119	ALA	Peptide
68	AK	53	LYS	Peptide
69	AL	51	VAL	Peptide
69	AL	52	THR	Peptide
71	AN	113	ALA	Peptide
71	AN	41	SER	Peptide
73	AP	54	VAL	Peptide
74	AQ	43	ASN	Peptide
74	AQ	63	ALA	Peptide
74	AQ	9	GLY	Peptide
75	AR	80	ARG	Peptide
76	AS	49	ARG	Peptide
78	AU	3	LYS	Peptide
80	AW	119	ARG	Peptide
81	AX	144	ARG	Peptide
81	AX	247	ASP	Peptide
81	AX	251	ASN	Peptide
81	AX	273	PHE	Peptide
81	AX	305	ILE	Peptide
81	AX	394	PHE	Peptide
81	AX	482	LYS	Peptide
81	AX	487	PRO	Peptide
81	AX	579	SER	Peptide
81	AX	583	HIS	Peptide
81	AX	587	TYR	Peptide
81	AX	608	PRO	Peptide
81	AX	721	ASP	Peptide
81	AX	764	PRO	Peptide
81	AX	829	LYS	Peptide
7	B	159	ARG	Peptide
84	BA	120	VAL	Peptide
84	BA	136	THR	Peptide
84	BA	72	PHE	Peptide
8	C	93	MET	Peptide
9	D	124	GLU	Peptide

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Mol	Chain	Res	Type	Group
9	D	19	PRO	Peptide
9	D	281	GLU	Peptide
9	D	43	LYS	Peptide
10	E	4	GLN	Peptide
10	E	7	PRO	Peptide
11	F	157	ASN	Peptide
11	F	215	GLY	Peptide
12	G	192	GLN	Peptide
12	G	30	THR	Peptide
12	G	76	ALA	Peptide
14	I	197	VAL	Peptide
14	I	215	GLU	Peptide
14	I	65	LEU	Peptide
15	J	10	ARG	Peptide
15	J	117	ASP	Peptide
15	J	165	GLN	Peptide
15	J	170	ASP	Peptide
15	J	73	GLY	Peptide
15	J	74	PRO	Peptide
16	L	47	ALA	Peptide
16	L	76	THR	Peptide
17	M	7	VAL	Peptide
17	M	8	LYS	Peptide
18	N	46	ASP	Peptide
19	O	110	PRO	Peptide
19	O	36	VAL	Peptide
19	O	78	ARG	Peptide
4	P0	16	ARG	Peptide
4	P0	38	MET	Peptide
5	P2	77	ALA	Peptide
22	R	54	ALA	Peptide
23	S	148	LEU	Peptide
23	S	149	LYS	Peptide
30	Z	102	GLU	Peptide
31	a	14	HIS	Peptide
31	a	57	GLY	Peptide
32	b	41	ARG	Peptide
34	d	87	ASN	Peptide
36	f	58	GLU	Peptide
36	f	59	VAL	Peptide
37	g	65	VAL	Peptide
37	g	66	SER	Peptide

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Mol	Chain	Res	Type	Group
37	g	80	ARG	Peptide
37	g	82	ALA	Peptide
38	h	69	LEU	Peptide
38	h	90	ARG	Peptide
39	i	26	ILE	Peptide
39	i	52	PRO	Peptide
39	i	97	SER	Peptide
40	j	5	THR	Peptide
40	j	64	MET	Peptide
40	j	82	SER	Peptide
41	k	38	PHE	Peptide
41	k	39	ARG	Peptide
45	o	33	ALA	Peptide
45	o	7	THR	Peptide
46	p	84	ARG	Peptide
48	q	111	ILE	Peptide
48	q	112	THR	Peptide
49	r	177	GLN	Peptide
49	r	206	PRO	Peptide
49	r	54	LEU	Peptide
50	s	39	THR	Peptide
51	t	202	LEU	Peptide
51	t	219	ALA	Peptide
51	t	220	PRO	Peptide
51	t	221	SER	Peptide
52	u	110	ALA	Peptide
52	u	154	ILE	Peptide
52	u	191	ARG	Peptide
52	u	194	THR	Peptide
52	u	195	ILE	Peptide
52	u	201	HIS	Peptide
52	u	233	LYS	Peptide
53	v	128	ASN	Peptide
53	v	157	ARG	Peptide
53	v	57	SER	Peptide
53	v	64	VAL	Peptide
54	w	100	ALA	Peptide
54	w	148	SER	Peptide
54	w	153	VAL	Peptide
54	w	67	VAL	Peptide
54	w	9	VAL	Peptide
54	w	92	ARG	Peptide

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Mol	Chain	Res	Type	Group
55	x	110	GLN	Peptide
55	x	155	ASP	Peptide
55	x	64	VAL	Peptide
56	y	23	LYS	Peptide
57	z	133	HIS	Peptide
57	z	163	PRO	Peptide
57	z	171	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68931	0	34637	715	0
2	3	2579	0	1304	40	0
3	4	3353	0	1695	39	0
4	P0	1473	0	1514	34	0
5	P2	723	0	774	20	0
6	A	1914	0	1981	49	0
7	B	3075	0	3142	49	0
8	C	2748	0	2859	46	0
9	D	2375	0	2325	38	0
10	E	1239	0	1326	20	0
11	F	1784	0	1862	39	0
12	G	1804	0	1877	26	0
13	H	1518	0	1587	31	0
14	I	1705	0	1736	23	0
15	J	1353	0	1383	38	0
16	L	1543	0	1608	38	0
17	M	1053	0	1149	20	0
18	N	1720	0	1779	46	0
19	O	1555	0	1659	23	0
20	P	1420	0	1437	16	0
21	Q	1441	0	1543	30	0
22	R	1521	0	1617	27	0
23	S	1445	0	1487	23	0
24	T	1276	0	1323	19	0
25	U	796	0	812	6	0
26	V	997	0	1037	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	W	513	0	540	7	0
28	X	964	0	1025	15	0
29	Y	993	0	1081	22	0
30	Z	1092	0	1155	22	0
31	a	1173	0	1215	25	0
32	b	462	0	491	9	0
33	c	743	0	797	12	0
34	d	883	0	918	19	0
35	e	1020	0	1090	16	0
36	f	850	0	880	15	0
37	g	880	0	941	20	0
38	h	969	0	1078	10	0
39	i	771	0	849	19	0
40	j	681	0	683	15	0
41	k	612	0	682	23	0
42	l	436	0	475	8	0
43	m	417	0	455	9	0
44	n	233	0	284	9	0
45	o	847	0	916	12	0
46	p	694	0	736	18	0
47	2	37845	0	19040	604	0
48	q	1577	0	1567	29	0
49	r	1709	0	1784	32	0
50	s	1635	0	1723	39	0
51	t	1734	0	1817	45	0
52	u	2068	0	2154	54	0
53	v	1609	0	1675	42	0
54	w	1790	0	1881	63	0
55	x	1481	0	1572	35	0
56	y	1489	0	1525	47	0
57	z	1494	0	1573	34	0
58	AA	772	0	727	20	0
59	AB	1220	0	1281	15	0
60	AC	890	0	887	20	0
61	AD	1192	0	1255	24	0
62	AE	891	0	883	21	0
63	AF	977	0	1002	26	0
64	AG	1105	0	1166	30	0
65	AH	926	0	930	21	0
66	AI	1192	0	1222	30	0
67	AJ	1112	0	1124	28	0
68	AK	855	0	917	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	AL	684	0	672	15	0
70	AM	1021	0	1060	19	0
71	AN	1121	0	1196	24	0
72	AO	1073	0	1132	29	0
73	AP	563	0	603	17	0
74	AQ	769	0	815	20	0
75	AR	610	0	633	12	0
76	AS	497	0	535	13	0
77	AT	442	0	430	13	0
78	AU	475	0	525	11	0
79	AV	2437	0	2386	74	0
80	AW	287	0	285	8	0
81	AX	6523	0	6581	161	0
82	AY	1626	0	820	16	0
83	AZ	144	0	74	5	0
84	BA	1609	0	1701	40	0
85	AQ	1	0	0	0	0
85	AR	1	0	0	0	0
85	AT	1	0	0	0	0
85	AW	1	0	0	0	0
85	j	1	0	0	0	0
85	m	1	0	0	0	0
85	o	1	0	0	0	0
85	p	1	0	0	0	0
86	AX	32	0	14	3	0
All	All	212058	0	158911	2901	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 8.

All (2901) 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)
81:AX:699:DDE:HAC2	83:AZ:49:U:O2'	1.45	1.13
1:1:3231:U:H3	1:1:3256:G:H1	1.05	1.04
47:2:142:G:H5''	54:w:142:ARG:HH22	1.20	1.01
47:2:142:G:N1	47:2:173:A:H2	1.59	1.00
1:1:88:A:H62	1:1:98:G:N2	1.58	0.99
47:2:699:U:H3	47:2:739:G:H1	1.02	0.96
47:2:1663:G:H1	47:2:1738:U:H3	1.05	0.96
65:AH:44:LYS:HE3	65:AH:48:ASN:ND2	1.80	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1538:G:H21	1:1:1583:A:N6	1.63	0.95
47:2:1499:G:H1	47:2:1508:U:H3	0.96	0.94
81:AX:713:THR:O	81:AX:717:PHE:HB3	1.66	0.94
1:1:1626:U:H3	1:1:1817:G:H1	1.16	0.94
47:2:40:A:H62	47:2:467:G:H21	1.10	0.94
47:2:629:U:H3	47:2:970:A:H62	1.12	0.94
47:2:273:G:H1	47:2:283:U:H3	1.09	0.93
1:1:1538:G:H21	1:1:1583:A:H62	0.93	0.93
1:1:1538:G:N2	1:1:1583:A:H62	1.66	0.93
1:1:88:A:N6	1:1:98:G:H21	1.67	0.93
1:1:509:U:H3	1:1:582:G:H1	1.06	0.92
47:2:515:A:H62	47:2:537:G:H21	1.11	0.91
47:2:214:G:H21	47:2:251:A:H62	1.14	0.91
81:AX:225:PHE:O	81:AX:229:TYR:HB2	1.71	0.90
2:3:79:A:H62	2:3:101:G:H21	1.13	0.90
81:AX:78:TYR:HA	81:AX:98:PHE:O	1.70	0.90
1:1:88:A:H62	1:1:98:G:H21	0.93	0.90
1:1:172:G:H1	1:1:246:U:H3	1.18	0.90
81:AX:663:VAL:O	81:AX:667:PHE:HB2	1.74	0.88
81:AX:699:DDE:CAC	83:AZ:49:U:O2'	2.21	0.87
47:2:1588:G:H1	47:2:1608:U:H3	0.88	0.87
47:2:1387:G:H21	47:2:1410:A:H2	1.22	0.85
47:2:142:G:H5''	54:w:142:ARG:NH2	1.92	0.83
1:1:528:U:H3	1:1:564:G:H1	1.24	0.83
47:2:96:G:H1	47:2:387:A:N6	1.78	0.81
47:2:174:U:H3	47:2:266:A:H62	1.28	0.81
2:3:79:A:H62	2:3:101:G:N2	1.76	0.81
81:AX:364:ALA:O	81:AX:368:ALA:HB3	1.80	0.80
81:AX:348:ALA:O	81:AX:352:ARG:HB3	1.80	0.80
47:2:1665:U:H3	47:2:1736:G:H1	1.29	0.80
1:1:182:U:H3	1:1:234:G:H1	1.30	0.79
1:1:507:U:H3	1:1:584:G:H1	1.29	0.79
47:2:126:A:H62	47:2:291:G:H21	1.30	0.79
47:2:515:A:H62	47:2:537:G:N2	1.81	0.79
47:2:1354:G:O6	47:2:1369:U:C2	2.36	0.79
47:2:142:G:N1	47:2:173:A:C2	2.40	0.78
47:2:715:U:H3	47:2:723:G:H1	1.31	0.78
47:2:976:G:H1	47:2:1023:A:HO2'	1.30	0.77
47:2:515:A:N6	47:2:537:G:H21	1.83	0.77
47:2:752:A:H2	47:2:797:G:H1	1.32	0.77
47:2:214:G:N2	47:2:251:A:H62	1.82	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P0:60:ARG:HH11	4:P0:63:ILE:HG21	1.51	0.76
81:AX:74:ALA:HA	81:AX:102:LEU:O	1.86	0.76
47:2:223:U:H3	47:2:838:G:H1	1.34	0.75
47:2:40:A:H62	47:2:467:G:N2	1.83	0.75
47:2:991:G:H21	47:2:1013:A:H62	1.34	0.75
47:2:1379:C:H4'	64:AG:12:LYS:HZ1	1.51	0.75
1:1:1258:U:H4'	4:P0:42:ARG:HH11	1.50	0.74
47:2:695:U:OP2	47:2:695:U:H2'	1.87	0.74
1:1:1195:A:H61	1:1:1313:G:H1	1.36	0.74
81:AX:405:VAL:O	81:AX:447:ASP:HA	1.86	0.74
47:2:898:A:N6	47:2:914:G:C2	2.56	0.74
47:2:1638:G:H5''	47:2:1638:G:H8	1.53	0.74
47:2:1170:G:H1	47:2:1469:A:H2	1.35	0.74
65:AH:44:LYS:HE3	65:AH:48:ASN:HD21	1.52	0.73
47:2:1387:G:N2	47:2:1410:A:C2	2.53	0.73
48:q:70:PRO:HB2	48:q:94:GLY:H	1.54	0.73
66:AI:140:THR:HG22	66:AI:141:THR:HG23	1.71	0.72
81:AX:564:ARG:O	81:AX:725:GLN:HB3	1.88	0.72
47:2:96:G:H1	47:2:387:A:H61	1.34	0.72
47:2:1410:A:H5''	64:AG:118:ILE:HG13	1.72	0.71
1:1:1360:C:H1'	8:C:307:GLN:HE21	1.56	0.71
47:2:1216:C:O2	47:2:1446:A:N6	2.24	0.70
47:2:780:A:N7	72:AO:10:ARG:NH1	2.38	0.70
16:L:21:ARG:HB3	18:N:196:THR:HG22	1.73	0.70
81:AX:589:LYS:O	81:AX:687:ASN:HB2	1.90	0.70
23:S:32:SER:H	23:S:36:ILE:HD11	1.56	0.70
47:2:241:U:H5''	54:w:219:ARG:HH22	1.55	0.70
47:2:1182:U:C4	47:2:1185:U:OP2	2.45	0.70
47:2:1502:G:H21	47:2:1505:A:H62	1.39	0.70
79:AV:114:ASP:HB2	79:AV:123:ILE:HG23	1.74	0.69
2:3:79:A:N6	2:3:101:G:H21	1.89	0.69
47:2:1387:G:N2	47:2:1410:A:H2	1.91	0.69
52:u:162:ILE:HG22	52:u:169:ILE:HG22	1.75	0.69
69:AL:33:GLN:HE21	69:AL:52:THR:HG23	1.56	0.69
15:J:53:THR:HG23	15:J:61:ARG:HG2	1.75	0.69
47:2:895:G:C2	47:2:918:U:O2	2.46	0.68
48:q:140:ASN:HD22	50:s:62:PRO:HD3	1.57	0.68
52:u:136:VAL:HG21	52:u:148:ARG:HE	1.58	0.68
1:1:687:U:OP2	16:L:36:ARG:NH2	2.25	0.68
47:2:1183:A:O2'	47:2:1184:A:H5'	1.94	0.68
11:F:91:GLY:HA2	11:F:111:ILE:HD11	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:R:23:TRP:HB2	22:R:53:LYS:HD2	1.75	0.68
36:f:6:ARG:HH12	36:f:10:LYS:HG3	1.58	0.68
47:2:1186:U:N3	47:2:1208:A:C6	2.62	0.68
55:x:125:ILE:HA	55:x:128:ASP:HB3	1.75	0.68
1:1:3229:G:H1	1:1:3258:U:H3	1.42	0.68
76:AS:40:ILE:HG12	76:AS:61:ARG:H	1.58	0.68
41:k:69:LEU:HD21	41:k:73:LEU:HD11	1.76	0.68
47:2:1216:C:N3	47:2:1446:A:N7	2.42	0.67
47:2:1488:G:H3'	47:2:1515:A:H61	1.58	0.67
1:1:951:A:H8	1:1:1113:G:H21	1.41	0.67
60:AC:35:ALA:HB3	60:AC:41:LEU:HG	1.76	0.67
59:AB:2:SER:HB2	59:AB:81:HIS:HB3	1.77	0.67
1:1:3222:U:H3	1:1:3263:G:H1	1.42	0.67
8:C:329:PRO:HB3	11:F:41:ARG:HH21	1.59	0.67
79:AV:9:LEU:HD11	79:AV:311:ARG:HB3	1.76	0.67
79:AV:31:ASN:HB3	79:AV:47:LEU:H	1.60	0.67
82:AY:34:G:H1	83:AZ:48:U:H3	1.41	0.66
15:J:27:GLY:H	15:J:30:LEU:HD23	1.61	0.66
34:d:6:ASP:O	34:d:77:ARG:NH2	2.28	0.66
1:1:543:C:N4	1:1:549:U:H3	1.94	0.66
47:2:898:A:N6	47:2:914:G:N2	2.43	0.66
47:2:993:A:H62	47:2:1011:G:H21	1.42	0.66
47:2:1158:C:OP2	47:2:1161:C:N4	2.29	0.66
9:D:49:TYR:HB3	9:D:64:ILE:HD11	1.77	0.66
6:A:247:ARG:NH2	47:2:993:A:N1	2.44	0.66
34:d:44:MET:HG3	34:d:77:ARG:HH11	1.60	0.66
48:q:33:GLN:HE21	48:q:153:SER:HB2	1.60	0.66
66:AI:88:ARG:NH2	66:AI:91:ASP:OD1	2.29	0.66
47:2:993:A:H62	47:2:1011:G:N2	1.94	0.65
47:2:1170:G:O6	47:2:1469:A:N1	2.28	0.65
62:AE:111:ARG:HA	74:AQ:56:ALA:HB1	1.78	0.65
14:I:12:GLN:HB2	14:I:59:GLN:HE22	1.61	0.65
30:Z:22:LYS:NZ	30:Z:129:TRP:O	2.29	0.65
1:1:1126:G:OP2	14:I:14:ASN:ND2	2.30	0.65
1:1:3158:G:O6	1:1:3292:A:N1	2.29	0.65
1:1:3160:U:H3	1:1:3290:G:H1	1.42	0.65
47:2:151:G:N3	54:w:13:GLN:NE2	2.45	0.65
51:t:66:ILE:HG13	51:t:86:LEU:HD22	1.79	0.65
84:BA:138:VAL:HG22	84:BA:140:HIS:H	1.62	0.65
1:1:2491:A:H1'	84:BA:207:LYS:HB3	1.78	0.65
47:2:1022:C:O2'	47:2:1125:A:N6	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:x:76:LYS:HA	55:x:79:ARG:HG2	1.77	0.65
1:1:103:G:OP1	16:L:70:ARG:NH1	2.29	0.65
63:AF:91:GLY:H	63:AF:107:ILE:HB	1.62	0.65
1:1:2554:A:N7	46:p:62:LYS:NZ	2.44	0.65
11:F:83:LEU:HD11	11:F:116:PHE:HB3	1.78	0.65
19:O:32:LYS:HG2	19:O:101:ARG:HB2	1.79	0.65
47:2:1797:A:N1	74:AQ:82:ARG:NH1	2.45	0.65
54:w:70:PRO:HG3	54:w:101:ILE:HD13	1.78	0.65
80:AW:126:CYS:SG	80:AW:143:LYS:NZ	2.70	0.65
7:B:78:VAL:HG12	7:B:323:MET:HE1	1.78	0.64
47:2:1157:A:N7	47:2:1618:C:N4	2.45	0.64
47:2:752:A:N1	47:2:797:G:O6	2.30	0.64
62:AE:20:TYR:HB3	62:AE:27:PHE:HB2	1.79	0.64
3:4:67:U:H5'	40:j:85:LYS:HB3	1.79	0.64
4:P0:25:LEU:HD11	4:P0:86:PHE:HB2	1.79	0.64
51:t:98:ALA:HA	51:t:188:ILE:HD12	1.78	0.64
72:AO:132:ARG:HA	72:AO:135:ASP:HB3	1.79	0.64
84:BA:84:ALA:HB2	84:BA:148:VAL:HG21	1.79	0.64
1:1:1693:C:HO2'	1:1:1772:U:HO2'	1.45	0.64
47:2:1182:U:C5	47:2:1185:U:OP2	2.50	0.64
47:2:1387:G:OP1	65:AH:33:ARG:NH2	2.31	0.64
65:AH:44:LYS:CE	65:AH:48:ASN:ND2	2.58	0.64
81:AX:520:THR:HG22	81:AX:530:VAL:HG23	1.78	0.64
54:w:90:GLY:H	54:w:91:GLU:HG3	1.63	0.64
81:AX:320:LEU:HA	81:AX:323:VAL:HG12	1.79	0.64
19:O:10:ASP:OD2	23:S:167:ARG:NH2	2.31	0.64
1:1:523:A:H61	1:1:571:U:H3	1.43	0.64
12:G:157:VAL:HG13	12:G:159:PRO:HD2	1.79	0.64
47:2:1170:G:N1	47:2:1469:A:C2	2.65	0.64
47:2:1335:U:H3	47:2:1416:G:H1	1.45	0.64
57:z:23:ARG:NH1	57:z:27:GLU:OE2	2.29	0.64
34:d:72:ARG:NH2	34:d:105:GLN:O	2.31	0.64
77:AT:10:HIS:HD2	77:AT:12:ARG:HB3	1.63	0.64
84:BA:41:TYR:H	84:BA:199:GLN:HE22	1.46	0.64
1:1:1913:A:HO2'	1:1:2120:A:HO2'	1.46	0.64
43:m:103:LEU:HD11	43:m:110:CYS:HA	1.79	0.64
47:2:214:G:H21	47:2:251:A:N6	1.93	0.64
55:x:161:GLN:HG3	55:x:162:ILE:HD12	1.79	0.64
66:AI:134:ARG:HB2	66:AI:136:GLN:HE22	1.62	0.64
67:AJ:83:ALA:HB1	67:AJ:91:TYR:HB3	1.80	0.64
1:1:1195:A:N6	1:1:1313:G:H1	1.95	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:Q:80:THR:HG21	21:Q:130:ARG:HH12	1.63	0.63
1:1:1315:U:OP1	19:O:128:ARG:NH1	2.31	0.63
63:AF:124:THR:HG23	63:AF:127:ARG:HE	1.63	0.63
2:3:97:A:HO2'	11:F:222:HIS:HD1	1.46	0.63
6:A:229:ALA:HB1	6:A:233:GLN:HE21	1.61	0.63
41:k:46:ARG:NH2	41:k:50:SER:O	2.32	0.63
1:1:2939:G:OP2	7:B:2:SER:N	2.31	0.63
1:1:3174:A:N6	1:1:3279:A:N3	2.46	0.63
16:L:61:PRO:HB2	16:L:62:THR:HG23	1.80	0.63
47:2:654:C:N4	47:2:656:G:N7	2.46	0.63
47:2:1184:A:N6	63:AF:122:THR:O	2.30	0.63
81:AX:59:THR:HB	81:AX:440:ARG:HG3	1.79	0.63
81:AX:172:GLU:HG2	81:AX:271:ARG:HH21	1.63	0.63
1:1:92:G:OP1	45:o:46:LYS:NZ	2.31	0.63
1:1:3188:G:OP2	17:M:8:LYS:NZ	2.31	0.63
14:I:30:LYS:HE3	14:I:63:GLU:HG2	1.80	0.63
57:z:171:ARG:HD3	57:z:174:ARG:HE	1.63	0.63
1:1:853:G:N7	46:p:2:ALA:N	2.47	0.63
40:j:19:CYS:SG	40:j:20:ASN:N	2.72	0.63
47:2:895:G:N1	47:2:918:U:N3	2.46	0.63
47:2:1174:C:H42	47:2:1465:C:H42	1.47	0.63
1:1:2584:G:O2'	12:G:240:ASN:ND2	2.32	0.63
47:2:486:G:N2	47:2:501:U:O2	2.31	0.62
50:s:152:HIS:ND1	50:s:195:ASP:OD2	2.30	0.62
60:AC:52:LEU:HD22	60:AC:78:LEU:HD11	1.80	0.62
1:1:1568:U:H5'	1:1:1569:U:H5'	1.80	0.62
6:A:51:ASP:OD2	6:A:54:ARG:NH1	2.31	0.62
1:1:361:A:OP2	40:j:24:ARG:NH1	2.26	0.62
41:k:6:THR:OG1	41:k:10:GLN:NE2	2.32	0.62
50:s:38:VAL:HG13	50:s:39:THR:HG23	1.81	0.62
51:t:98:ALA:HB2	51:t:169:ASP:HB3	1.79	0.62
84:BA:35:GLN:NE2	84:BA:63:MET:O	2.32	0.62
50:s:142:GLY:H	50:s:154:LEU:HA	1.63	0.62
53:v:81:ARG:HA	53:v:84:LYS:HE3	1.82	0.62
1:1:1147:G:OP1	35:e:47:ARG:NH1	2.32	0.62
30:Z:71:PHE:HA	30:Z:111:LYS:HE3	1.80	0.62
2:3:44:C:OP2	15:J:137:ARG:NH2	2.32	0.62
37:g:81:CYS:H	37:g:84:CYS:HB2	1.65	0.62
38:h:102:GLU:OE1	38:h:106:LYS:NZ	2.30	0.62
44:n:5:TRP:HE1	47:2:1784:C:H41	1.47	0.62
47:2:542:A:N1	78:AU:28:LYS:NZ	2.43	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:y:157:GLU:HA	56:y:160:PHE:HD2	1.64	0.62
69:AL:39:VAL:HB	69:AL:43:GLY:HA2	1.80	0.62
1:1:824:C:H5''	6:A:21:ARG:HG2	1.82	0.62
1:1:1245:A:N6	1:1:1271:A:N3	2.46	0.62
55:x:85:PHE:O	55:x:88:ARG:NH1	2.32	0.62
84:BA:74:VAL:HG12	84:BA:76:ARG:H	1.64	0.62
1:1:2981:U:OP2	7:B:244:ARG:NH2	2.33	0.62
1:1:1255:C:H2'	1:1:1256:G:H8	1.65	0.62
1:1:1639:C:OP2	37:g:74:ARG:NH2	2.33	0.62
6:A:45:VAL:HG12	6:A:61:VAL:HG12	1.82	0.62
34:d:74:ARG:NH1	34:d:94:GLU:OE1	2.33	0.62
47:2:1383:G:OP1	68:AK:89:ARG:NH1	2.32	0.62
4:P0:8:LYS:O	4:P0:12:PHE:HB2	1.99	0.62
30:Z:54:THR:HG23	30:Z:56:LYS:H	1.65	0.62
34:d:109:VAL:HG13	34:d:111:GLU:H	1.63	0.62
67:AJ:126:GLU:OE1	67:AJ:130:ARG:NH1	2.33	0.62
1:1:3003:G:OP2	7:B:26:ARG:NH2	2.33	0.61
11:F:222:HIS:H	11:F:225:GLN:HE21	1.48	0.61
47:2:127:G:H5''	54:w:194:LYS:HD2	1.82	0.61
1:1:1119:C:H2'	1:1:1120:A:H8	1.65	0.61
16:L:48:PRO:HB3	16:L:137:GLN:HB3	1.82	0.61
18:N:106:VAL:HG11	18:N:132:VAL:HG21	1.81	0.61
47:2:1297:G:N2	47:2:1300:A:OP2	2.32	0.61
1:1:509:U:O2	1:1:582:G:N2	2.29	0.61
51:t:114:ALA:HB1	51:t:116:ARG:HH11	1.65	0.61
47:2:886:U:H2'	47:2:887:A:H8	1.65	0.61
53:v:142:PRO:HD2	53:v:167:ARG:HG2	1.83	0.61
64:AG:48:VAL:O	64:AG:82:ARG:NH1	2.33	0.61
1:1:1949:G:OP1	22:R:104:ARG:NH1	2.33	0.61
16:L:4:SER:O	31:a:44:ASN:ND2	2.34	0.61
57:z:18:PRO:O	57:z:23:ARG:NH2	2.34	0.61
1:1:597:G:OP1	11:F:41:ARG:NH1	2.32	0.61
1:1:1761:C:N3	1:1:1765:U:O4	2.33	0.61
29:Y:12:ARG:HH21	29:Y:16:ARG:HH22	1.49	0.61
47:2:343:C:H2'	47:2:344:A:H8	1.66	0.61
50:s:89:GLN:HA	50:s:93:GLY:HA2	1.81	0.61
1:1:936:A:OP1	31:a:32:ARG:NH2	2.33	0.61
47:2:628:G:N1	47:2:970:A:OP2	2.32	0.61
47:2:1186:U:C4	47:2:1208:A:N1	2.68	0.61
67:AJ:40:SER:HB3	67:AJ:43:ASN:HB2	1.83	0.61
47:2:576:G:H22	71:AN:67:ALA:HB2	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1456:C:O5'	47:2:1457:C:H5''	2.01	0.61
13:H:47:LYS:HD2	13:H:50:ASN:H	1.66	0.60
47:2:1471:A:N7	47:2:1538:U:O2	2.33	0.60
62:AE:103:ARG:NH1	74:AQ:47:ALA:O	2.34	0.60
68:AK:106:ILE:HG23	68:AK:107:THR:HG23	1.83	0.60
1:1:2969:A:N7	6:A:215:ASN:ND2	2.48	0.60
47:2:306:U:OP2	59:AB:88:ARG:NH1	2.33	0.60
47:2:1021:C:O2'	47:2:1124:A:N6	2.34	0.60
1:1:1231:A:N6	1:1:1277:C:OP2	2.31	0.60
7:B:188:ILE:HA	7:B:191:LYS:HG2	1.83	0.60
47:2:1202:A:H62	47:2:1456:C:H2'	1.67	0.60
52:u:255:ARG:HA	52:u:258:GLN:HG2	1.81	0.60
81:AX:91:GLN:HE22	81:AX:344:SER:H	1.48	0.60
1:1:2812:C:H2'	1:1:2813:A:H8	1.65	0.60
13:H:91:ARG:NH2	13:H:143:GLU:OE2	2.34	0.60
47:2:1163:A:N3	47:2:1613:U:O2'	2.30	0.60
58:AA:8:ARG:NH2	58:AA:41:TYR:O	2.34	0.60
68:AK:103:ILE:HA	68:AK:106:ILE:HG22	1.83	0.60
1:1:1015:U:N3	1:1:1035:G:N1	2.47	0.60
46:p:84:ARG:NH2	47:2:882:U:OP1	2.35	0.60
47:2:462:G:H5'	57:z:3:ARG:HH21	1.66	0.60
47:2:900:A:H3'	47:2:901:G:H21	1.67	0.60
47:2:1544:U:H4'	66:AI:145:ARG:HH22	1.66	0.60
54:w:186:ARG:O	54:w:190:GLN:NE2	2.35	0.60
1:1:173:G:O6	1:1:245:U:O2	2.20	0.60
1:1:1015:U:O2	1:1:1035:G:O6	2.20	0.60
1:1:3192:U:O2	1:1:3200:G:N2	2.33	0.60
6:A:30:ARG:NH1	6:A:36:GLU:OE2	2.34	0.60
8:C:39:PHE:HA	8:C:42:VAL:HG12	1.83	0.60
18:N:163:GLY:O	18:N:172:ARG:NH1	2.33	0.60
49:r:190:PRO:HG2	49:r:192:VAL:HG23	1.83	0.60
72:AO:20:ARG:HD2	72:AO:74:LEU:HD11	1.83	0.60
1:1:1389:G:H5''	35:e:101:SER:HB3	1.83	0.60
47:2:55:A:H3'	47:2:403:G:H22	1.67	0.60
47:2:126:A:OP2	54:w:201:GLN:NE2	2.35	0.60
47:2:273:G:N2	47:2:283:U:O2	2.31	0.60
79:AV:202:LEU:HD13	79:AV:213:SER:HB3	1.84	0.60
1:1:3008:A:OP2	19:O:74:ARG:NH1	2.30	0.60
1:1:3304:U:O3'	7:B:334:ARG:NH2	2.35	0.60
51:t:64:ARG:HD3	58:AA:70:GLU:HG3	1.84	0.60
64:AG:106:LYS:HG3	64:AG:109:PHE:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:364:G:OP2	40:j:52:LYS:NZ	2.34	0.60
2:3:97:A:O2'	11:F:222:HIS:ND1	2.34	0.60
22:R:86:GLU:HG2	22:R:91:SER:H	1.67	0.60
47:2:1221:A:H62	47:2:1263:G:H21	1.49	0.60
55:x:8:ILE:HA	55:x:42:GLN:HG3	1.83	0.60
1:1:1420:C:OP2	8:C:193:LYS:NZ	2.32	0.59
5:P2:94:LYS:NZ	5:P2:101:SER:O	2.35	0.59
11:F:151:ARG:NH2	11:F:206:LYS:O	2.35	0.59
49:r:59:ASP:O	49:r:62:LYS:NZ	2.35	0.59
71:AN:75:GLN:HE21	71:AN:80:GLY:HA2	1.67	0.59
1:1:2703:A:N6	9:D:28:THR:O	2.35	0.59
46:p:49:ARG:HH21	46:p:52:ALA:HA	1.67	0.59
52:u:180:LEU:HA	52:u:194:THR:HA	1.83	0.59
81:AX:382:VAL:HG21	81:AX:396:ALA:HB1	1.84	0.59
47:2:1204:A:OP1	47:2:1206:U:N3	2.31	0.59
81:AX:54:ALA:O	81:AX:440:ARG:NH2	2.34	0.59
1:1:1807:G:OP1	30:Z:135:ARG:NH1	2.35	0.59
1:1:2268:U:H2'	1:1:2269:U:H2'	1.84	0.59
1:1:3158:G:H1	1:1:3292:A:H2	1.45	0.59
16:L:80:VAL:HG22	16:L:85:LEU:HB3	1.84	0.59
18:N:103:GLU:HA	18:N:106:VAL:HG12	1.82	0.59
43:m:97:ARG:HD2	43:m:120:GLN:HB3	1.83	0.59
47:2:993:A:N6	47:2:1011:G:H21	2.00	0.59
47:2:1329:A:N1	65:AH:7:LYS:NZ	2.50	0.59
47:2:1412:G:OP1	53:v:76:ARG:NH2	2.35	0.59
47:2:1519:U:H3'	47:2:1520:U:H2'	1.84	0.59
47:2:1594:G:OP2	47:2:1596:C:N4	2.32	0.59
54:w:33:GLY:HA2	54:w:51:LYS:HB2	1.83	0.59
59:AB:7:VAL:HG11	59:AB:53:TYR:HA	1.84	0.59
75:AR:33:LEU:HD21	75:AR:79:PHE:HB2	1.84	0.59
81:AX:417:ASN:HA	81:AX:477:ASN:HD22	1.67	0.59
1:1:31:C:OP2	18:N:187:ARG:NH2	2.35	0.59
1:1:1071:U:H3	1:1:1087:G:H1	1.50	0.59
1:1:2435:G:OP2	18:N:20:ARG:NH1	2.36	0.59
1:1:3369:G:N2	7:B:380:MET:O	2.36	0.59
3:4:141:C:O2	18:N:112:ASN:ND2	2.35	0.59
47:2:1466:G:OP2	64:AG:139:GLN:NE2	2.35	0.59
81:AX:434:VAL:HG13	81:AX:445:ILE:HG13	1.84	0.59
84:BA:193:LEU:HD13	84:BA:194:LEU:H	1.67	0.59
1:1:2516:U:O2'	1:1:2595:A:N6	2.36	0.59
47:2:418:G:O2'	54:w:59:GLN:NE2	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:u:184:THR:HA	52:u:189:LEU:HB2	1.85	0.59
5:P2:119:LYS:HE3	5:P2:128:VAL:HG11	1.85	0.59
60:AC:97:LEU:HA	60:AC:100:TRP:HB3	1.85	0.59
84:BA:40:ASN:OD1	84:BA:199:GLN:NE2	2.36	0.59
1:1:2137:U:OP2	1:1:2142:A:N6	2.33	0.59
1:1:2157:G:N2	1:1:2177:G:O2'	2.36	0.59
1:1:3268:A:OP1	10:E:46:ARG:NH2	2.35	0.59
18:N:155:VAL:O	18:N:162:ARG:NH2	2.36	0.59
47:2:284:G:O6	54:w:188:ARG:NH1	2.36	0.59
47:2:1456:C:OP2	47:2:1457:C:H3'	2.02	0.59
52:u:18:TRP:O	52:u:50:ASN:ND2	2.36	0.59
82:AY:4:G:N2	82:AY:69:U:O2	2.35	0.59
1:1:69:C:H5''	18:N:178:HIS:HB3	1.85	0.59
1:1:2449:A:N6	1:1:2497:U:OP2	2.36	0.59
5:P2:99:LYS:HZ2	5:P2:139:VAL:HG11	1.68	0.59
30:Z:88:ASP:O	30:Z:121:ARG:NH2	2.34	0.59
1:1:1117:G:O6	1:1:1142:G:N2	2.36	0.59
3:4:37:A:OP2	38:h:86:ARG:NH1	2.36	0.59
5:P2:114:ARG:HG3	5:P2:119:LYS:HZ3	1.68	0.59
52:u:193:GLY:HA3	52:u:210:ILE:HG23	1.84	0.59
81:AX:305:ILE:HD13	81:AX:307:LEU:HD13	1.85	0.59
1:1:2762:A:O2'	21:Q:176:ARG:NH1	2.36	0.58
2:3:99:G:O2'	11:F:128:LYS:NZ	2.36	0.58
3:4:24:G:OP2	29:Y:13:ARG:NH2	2.35	0.58
13:H:18:VAL:HG23	13:H:27:VAL:HG12	1.85	0.58
47:2:333:A:OP1	56:y:48:THR:OG1	2.20	0.58
47:2:399:A:OP1	56:y:49:ARG:NH1	2.36	0.58
47:2:817:A:O4'	55:x:110:GLN:NE2	2.36	0.58
47:2:895:G:N2	47:2:918:U:O2	2.36	0.58
48:q:140:ASN:ND2	50:s:60:SER:O	2.36	0.58
1:1:671:U:H2'	1:1:672:A:H8	1.68	0.58
1:1:700:C:H2'	1:1:701:G:H8	1.67	0.58
1:1:3379:C:H4'	7:B:315:GLY:HA2	1.84	0.58
1:1:1471:U:OP1	22:R:5:ARG:NH2	2.36	0.58
1:1:3070:A:OP1	22:R:62:ARG:NH2	2.36	0.58
1:1:3234:A:H2	1:1:3253:G:H1	1.50	0.58
19:O:20:ALA:HA	19:O:23:VAL:HG12	1.84	0.58
81:AX:186:ASN:HD21	81:AX:201:GLN:HG3	1.68	0.58
1:1:431:U:OP1	36:f:65:ARG:NH1	2.37	0.58
1:1:1825:G:OP1	41:k:17:ARG:NH2	2.34	0.58
6:A:8:GLN:NE2	6:A:231:SER:OG	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:H:166:ARG:O	13:H:168:ARG:NH2	2.35	0.58
47:2:912:U:O2	47:2:914:G:N1	2.35	0.58
51:t:169:ASP:OD1	51:t:190:ARG:NH1	2.36	0.58
1:1:1431:G:OP2	31:a:12:ARG:NH1	2.34	0.58
22:R:92:GLN:HE21	22:R:96:ILE:HD11	1.69	0.58
23:S:8:GLN:HB3	23:S:64:ILE:HD11	1.85	0.58
41:k:28:ASN:HB2	41:k:40:GLN:HG2	1.85	0.58
47:2:385:A:OP1	56:y:22:ARG:NH2	2.36	0.58
50:s:195:ASP:N	50:s:195:ASP:OD1	2.33	0.58
57:z:161:THR:HA	57:z:167:ALA:HB3	1.86	0.58
1:1:14:U:H1'	28:X:42:ARG:HH11	1.69	0.58
21:Q:66:ARG:HH12	21:Q:143:PRO:HD3	1.69	0.58
29:Y:39:LEU:HG	29:Y:42:GLN:HE21	1.67	0.58
47:2:560:U:H2'	47:2:561:G:H8	1.69	0.58
47:2:1214:U:H1'	77:AT:7:TRP:HE1	1.69	0.58
1:1:1825:G:OP2	41:k:49:SER:OG	2.22	0.58
2:3:18:C:OP2	15:J:150:ASN:ND2	2.37	0.58
47:2:123:G:H4'	52:u:145:ARG:HG3	1.85	0.58
47:2:435:C:OP2	71:AN:50:LYS:NZ	2.36	0.58
47:2:1345:A:O2'	47:2:1348:A:N6	2.36	0.58
47:2:1429:G:O2'	68:AK:72:ASN:ND2	2.37	0.58
49:r:158:SER:O	49:r:162:ARG:NH1	2.35	0.58
59:AB:68:GLY:HA3	59:AB:127:GLN:HE21	1.68	0.58
1:1:432:G:H1	1:1:627:U:H3	1.52	0.58
1:1:900:G:N3	1:1:1589:A:N6	2.52	0.58
1:1:1213:G:H5''	23:S:137:ARG:HH21	1.69	0.58
1:1:3172:A:O2'	19:O:101:ARG:NH2	2.37	0.58
12:G:226:TYR:O	12:G:230:LYS:NZ	2.36	0.58
28:X:90:ALA:O	28:X:120:LYS:NZ	2.37	0.58
34:d:8:VAL:HG22	34:d:77:ARG:HH22	1.69	0.58
47:2:1502:G:N7	67:AJ:102:ARG:NH2	2.50	0.58
47:2:1666:U:H3	47:2:1735:U:H3	1.50	0.58
65:AH:44:LYS:CE	65:AH:48:ASN:HD22	2.17	0.58
1:1:155:G:N2	1:1:264:G:O2'	2.35	0.58
1:1:1221:A:C5	4:P0:8:LYS:NZ	2.63	0.58
47:2:91:G:OP1	47:2:397:A:N6	2.35	0.58
47:2:749:U:O3'	70:AM:120:HIS:NE2	2.36	0.58
53:v:62:VAL:HG12	53:v:64:VAL:H	1.68	0.58
56:y:42:ARG:HD3	56:y:59:ARG:HD2	1.85	0.58
68:AK:40:ASN:O	68:AK:44:ASN:ND2	2.36	0.58
81:AX:81:MET:N	81:AX:81:MET:SD	2.77	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:AX:301:GLU:HA	81:AX:305:ILE:H	1.69	0.58
1:1:1616:U:H2'	1:1:1617:G:H8	1.68	0.58
1:1:1916:U:O3'	22:R:85:ARG:NH2	2.36	0.58
1:1:2772:C:H4'	1:1:2773:C:H5'	1.86	0.58
8:C:76:ARG:NH1	8:C:86:GLY:O	2.35	0.58
34:d:98:VAL:HG11	34:d:101:ALA:HB2	1.85	0.58
47:2:318:U:O3'	56:y:11:ARG:NH1	2.36	0.58
47:2:638:U:O2'	55:x:112:ARG:NH1	2.37	0.58
64:AG:20:ALA:HB2	64:AG:84:ALA:HB1	1.85	0.58
66:AI:83:ALA:HA	66:AI:86:LEU:HD23	1.85	0.58
84:BA:103:LEU:HB2	84:BA:106:LYS:HD2	1.86	0.58
1:1:217:U:O2	29:Y:103:LYS:NZ	2.37	0.57
1:1:2216:G:H1	1:1:2229:A:H61	1.51	0.57
29:Y:35:LEU:HD21	29:Y:39:LEU:HD22	1.86	0.57
40:j:22:CYS:SG	40:j:23:GLY:N	2.77	0.57
45:o:74:CYS:SG	45:o:75:VAL:N	2.76	0.57
47:2:1109:G:H1	47:2:1136:U:H3	1.50	0.57
1:1:3187:A:H5''	17:M:8:LYS:HE2	1.85	0.57
3:4:95:G:OP1	40:j:76:ASN:ND2	2.31	0.57
34:d:9:THR:HG23	34:d:109:VAL:HG11	1.86	0.57
37:g:44:CYS:SG	37:g:45:GLY:N	2.77	0.57
44:n:17:ARG:NH1	47:2:1749:A:O2'	2.36	0.57
47:2:639:U:H3	55:x:100:PRO:HA	1.69	0.57
47:2:867:G:H5'	61:AD:4:MET:HE1	1.86	0.57
68:AK:58:LEU:O	68:AK:89:ARG:NH2	2.37	0.57
81:AX:489:VAL:O	81:AX:531:ALA:HA	2.05	0.57
81:AX:633:ILE:HG13	81:AX:646:VAL:HG22	1.86	0.57
1:1:3123:A:HO2'	13:H:40:HIS:HD1	1.51	0.57
41:k:22:THR:HA	41:k:74:LYS:HB2	1.86	0.57
47:2:868:G:OP1	61:AD:121:ARG:NH1	2.37	0.57
47:2:1588:G:N2	47:2:1608:U:O2	2.29	0.57
49:r:145:LYS:HG2	49:r:149:GLN:HG3	1.86	0.57
1:1:616:G:H2'	1:1:617:G:H8	1.70	0.57
1:1:726:G:N1	1:1:743:C:OP2	2.33	0.57
1:1:1386:A:HO2'	8:C:184:SER:HG	1.49	0.57
1:1:2093:A:H5''	22:R:143:ILE:HD13	1.87	0.57
1:1:2608:G:OP1	6:A:2:GLY:N	2.37	0.57
1:1:2898:G:OP2	13:H:173:ARG:NH2	2.37	0.57
1:1:3028:G:N2	81:AX:535:GLU:OE2	2.37	0.57
16:L:106:GLN:HE21	39:i:18:THR:HG23	1.70	0.57
47:2:1152:A:OP1	74:AQ:85:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1396:U:O2	47:2:1402:G:O6	2.21	0.57
47:2:1474:G:OP1	53:v:106:LYS:NZ	2.38	0.57
47:2:1529:C:O2	67:AJ:12:GLN:NE2	2.38	0.57
49:r:162:ARG:HA	49:r:165:ARG:HG2	1.87	0.57
53:v:146:THR:HB	53:v:157:ARG:HB2	1.87	0.57
56:y:40:ALA:HA	56:y:61:GLU:HB2	1.87	0.57
60:AC:79:ALA:HA	60:AC:86:VAL:HG12	1.86	0.57
63:AF:103:ASN:ND2	63:AF:119:PHE:O	2.38	0.57
73:AP:68:ARG:HB2	73:AP:70:LYS:HB2	1.86	0.57
81:AX:574:THR:HA	81:AX:589:LYS:HE3	1.85	0.57
1:1:1307:G:OP1	19:O:59:ARG:NH1	2.35	0.57
3:4:5:U:OP2	20:P:62:ARG:NH1	2.38	0.57
47:2:57:G:OP1	72:AO:112:LYS:NZ	2.38	0.57
47:2:1350:U:O4	47:2:1376:C:N3	2.38	0.57
70:AM:11:LEU:HD12	70:AM:74:VAL:HB	1.85	0.57
79:AV:122:ILE:HB	79:AV:134:TRP:HB2	1.86	0.57
81:AX:10:ARG:NH2	81:AX:447:ASP:O	2.37	0.57
81:AX:584:ASN:ND2	81:AX:704:GLN:OE1	2.38	0.57
1:1:336:A:O2'	8:C:48:GLN:NE2	2.35	0.57
1:1:1062:A:H5''	1:1:1063:G:H5'	1.87	0.57
1:1:1910:A:N3	1:1:2333:C:O2'	2.35	0.57
1:1:2146:C:OP1	6:A:200:ARG:NH1	2.38	0.57
1:1:2450:G:H22	1:1:2495:C:H42	1.52	0.57
21:Q:40:THR:HG23	21:Q:42:ALA:H	1.70	0.57
67:AJ:128:GLY:HA2	67:AJ:132:LEU:HB2	1.87	0.57
79:AV:156:VAL:HG22	79:AV:169:ILE:HG22	1.87	0.57
79:AV:287:PRO:HG3	79:AV:307:ASP:HB3	1.86	0.57
49:r:53:GLY:HA2	49:r:56:SER:HB2	1.85	0.57
56:y:41:LYS:N	56:y:59:ARG:O	2.37	0.57
58:AA:62:GLN:HE22	77:AT:24:CYS:HA	1.69	0.57
70:AM:24:GLN:HE22	75:AR:5:GLN:H	1.51	0.57
1:1:2117:A:HO2'	1:1:3080:G:HO2'	1.51	0.57
1:1:3151:U:OP1	7:B:132:LYS:NZ	2.37	0.57
52:u:151:ASP:HB3	52:u:154:ILE:HD11	1.87	0.57
56:y:57:ALA:HB2	56:y:177:GLY:HA2	1.86	0.57
59:AB:33:ARG:NH1	59:AB:53:TYR:O	2.32	0.57
80:AW:141:CYS:SG	80:AW:142:GLY:N	2.77	0.57
81:AX:120:ARG:O	81:AX:352:ARG:NH2	2.35	0.57
81:AX:682:ARG:NH1	81:AX:803:THR:OG1	2.38	0.57
81:AX:721:ASP:HA	81:AX:809:LEU:HD23	1.86	0.57
1:1:1633:C:N3	1:1:1641:U:O4	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2790:A:OP1	21:Q:180:ARG:NH1	2.38	0.57
8:C:286:VAL:HG21	21:Q:28:LEU:HD21	1.85	0.57
46:p:46:THR:HG22	46:p:58:SER:HB2	1.87	0.57
47:2:222:A:H62	47:2:833:U:H3	1.50	0.57
47:2:593:U:H3'	57:z:38:ASN:HD22	1.69	0.57
52:u:10:LYS:HA	52:u:28:ALA:H	1.70	0.57
61:AD:13:SER:O	75:AR:20:LYS:NZ	2.35	0.57
79:AV:302:PHE:HA	79:AV:313:TRP:H	1.68	0.57
81:AX:150:ARG:HB3	81:AX:197:LEU:HD11	1.86	0.57
84:BA:60:ARG:HH21	84:BA:180:VAL:HG21	1.69	0.57
1:1:1246:G:H21	1:1:1264:G:H22	1.51	0.56
1:1:2685:C:H2'	1:1:2686:A:H8	1.70	0.56
34:d:13:THR:HG23	34:d:72:ARG:HH21	1.70	0.56
47:2:94:U:H4'	52:u:6:LYS:HA	1.87	0.56
47:2:1221:A:H62	47:2:1263:G:N2	2.01	0.56
47:2:1311:U:H4'	65:AH:2:GLY:HA2	1.87	0.56
47:2:1343:U:O2	68:AK:57:ARG:NH1	2.38	0.56
1:1:170:G:O6	1:1:248:U:O2	2.23	0.56
1:1:533:A:N7	1:1:555:U:C2	2.73	0.56
1:1:1259:A:H62	4:P0:38:MET:HE2	1.69	0.56
1:1:2948:C:OP1	7:B:244:ARG:NH1	2.37	0.56
1:1:3225:C:H2'	1:1:3226:A:H8	1.70	0.56
27:W:52:THR:HG23	27:W:55:PHE:H	1.68	0.56
39:i:59:ASP:OD1	39:i:62:ARG:NH2	2.38	0.56
73:AP:72:GLY:O	73:AP:76:ALA:N	2.38	0.56
1:1:216:G:OP1	29:Y:16:ARG:NH2	2.37	0.56
1:1:444:U:O4	1:1:492:C:N3	2.38	0.56
1:1:2180:G:OP1	6:A:174:ARG:NH2	2.35	0.56
1:1:3244:A:OP1	7:B:97:ARG:NH2	2.38	0.56
4:P0:18:TYR:HE2	4:P0:52:LEU:HD11	1.70	0.56
6:A:178:PRO:HB2	6:A:180:LEU:HB2	1.87	0.56
28:X:88:MET:N	28:X:88:MET:SD	2.75	0.56
30:Z:27:LYS:NZ	30:Z:97:SER:OG	2.37	0.56
35:e:100:ILE:HB	35:e:105:ARG:HH21	1.70	0.56
47:2:70:C:H2'	47:2:71:A:H4'	1.86	0.56
47:2:699:U:O2	47:2:739:G:N2	2.31	0.56
47:2:898:A:H62	47:2:914:G:N2	2.01	0.56
47:2:1135:U:OP2	71:AN:121:ARG:NH2	2.37	0.56
47:2:1552:U:OP2	63:AF:43:ARG:NH2	2.37	0.56
49:r:69:CYS:SG	49:r:70:LEU:N	2.77	0.56
49:r:70:LEU:HA	49:r:73:LEU:HG	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:t:11:LEU:HD11	68:AK:86:ILE:HG12	1.86	0.56
59:AB:101:GLU:OE2	71:AN:13:ARG:NE	2.37	0.56
67:AJ:135:ILE:HA	67:AJ:138:GLN:HB3	1.86	0.56
79:AV:278:PHE:HB3	79:AV:287:PRO:HD2	1.87	0.56
81:AX:153:PRO:HD2	81:AX:200:VAL:HG11	1.87	0.56
1:1:655:C:H2'	1:1:656:A:H8	1.70	0.56
1:1:950:G:N1	1:1:1368:U:OP2	2.33	0.56
18:N:68:ARG:HH22	18:N:123:GLN:HE21	1.54	0.56
47:2:1219:A:OP1	58:AA:44:LYS:NZ	2.30	0.56
48:q:21:ASN:HD21	48:q:24:LEU:HD23	1.70	0.56
54:w:138:ALA:HB2	54:w:175:ILE:HD13	1.87	0.56
70:AM:103:ILE:HA	70:AM:112:ASP:HA	1.87	0.56
81:AX:128:VAL:HG12	81:AX:156:VAL:HG13	1.87	0.56
1:1:118:U:N3	1:1:122:A:OP2	2.34	0.56
1:1:684:G:OP1	16:L:35:ARG:NH2	2.38	0.56
6:A:50:HIS:ND1	6:A:51:ASP:O	2.38	0.56
28:X:108:LEU:HB3	28:X:127:THR:HG22	1.87	0.56
47:2:222:A:N7	47:2:833:U:O2	2.38	0.56
47:2:1496:U:O2	47:2:1512:G:C6	2.58	0.56
48:q:122:ILE:HD13	48:q:174:TRP:HE1	1.71	0.56
80:AW:116:LYS:HE3	80:AW:119:ARG:HE	1.70	0.56
13:H:129:ARG:NH2	13:H:152:GLU:O	2.39	0.56
31:a:100:PRO:HD2	31:a:123:VAL:HG12	1.87	0.56
34:d:74:ARG:HH21	34:d:109:VAL:HG21	1.71	0.56
47:2:1335:U:O4	47:2:1416:G:O6	2.24	0.56
47:2:1388:A:H8	47:2:1388:A:OP1	1.88	0.56
54:w:31:ARG:HG3	54:w:34:GLN:HE22	1.70	0.56
56:y:43:ILE:HG22	56:y:57:ALA:HA	1.87	0.56
66:AI:46:VAL:HG11	66:AI:73:MET:HB3	1.88	0.56
67:AJ:141:GLU:HA	67:AJ:144:GLU:HG2	1.88	0.56
81:AX:283:ARG:HH12	81:AX:299:LEU:HD21	1.71	0.56
1:1:388:G:H1'	20:P:97:ASN:HD21	1.69	0.56
8:C:334:PHE:HA	8:C:339:LEU:HD12	1.88	0.56
13:H:20:ILE:HD11	17:M:7:VAL:HG13	1.87	0.56
47:2:434:G:N2	47:2:437:A:OP2	2.36	0.56
47:2:655:G:N1	47:2:679:U:N3	2.54	0.56
47:2:1132:A:H2'	47:2:1133:A:H8	1.71	0.56
47:2:1682:U:O4	47:2:1720:G:N2	2.39	0.56
1:1:3000:A:O3'	7:B:120:LYS:NZ	2.39	0.56
12:G:100:GLU:OE2	12:G:108:ARG:NH1	2.39	0.56
47:2:127:G:O6	54:w:199:GLN:NE2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1482:C:OP2	47:2:1521:G:N1	2.38	0.56
47:2:1553:G:N1	47:2:1556:A:OP2	2.39	0.56
61:AD:17:PRO:HG3	75:AR:28:PRO:HG3	1.88	0.56
65:AH:60:ARG:HH12	65:AH:66:VAL:HG11	1.69	0.56
79:AV:38:ARG:HA	79:AV:67:ILE:HG12	1.86	0.56
79:AV:245:PHE:HE1	79:AV:250:TYR:HA	1.70	0.56
83:AZ:49:U:O2	83:AZ:49:U:H2'	2.06	0.56
1:1:2522:G:O6	6:A:70:ARG:NH2	2.38	0.56
1:1:3023:U:O3'	81:AX:162:ARG:NH1	2.39	0.56
22:R:115:ILE:HD11	22:R:119:LEU:HD23	1.87	0.56
23:S:109:ASP:OD1	23:S:113:ARG:NH1	2.39	0.56
35:e:79:VAL:HG21	35:e:104:ASN:HB2	1.88	0.56
47:2:396:G:H22	47:2:399:A:H5''	1.71	0.56
47:2:871:G:H2'	47:2:872:G:C8	2.40	0.56
50:s:239:PRO:HA	50:s:242:ILE:HG22	1.86	0.56
56:y:114:GLU:HA	56:y:118:GLY:H	1.71	0.56
60:AC:35:ALA:HB1	60:AC:40:GLY:H	1.70	0.56
74:AQ:4:LYS:HG3	74:AQ:5:ARG:HD3	1.86	0.56
81:AX:412:ARG:NH2	81:AX:472:SER:O	2.39	0.56
81:AX:510:ARG:HH22	81:AX:549:HIS:HA	1.71	0.56
1:1:34:A:OP1	18:N:86:ASN:ND2	2.39	0.56
1:1:36:C:OP2	18:N:83:LYS:NZ	2.38	0.56
1:1:1834:U:OP1	42:l:5:LYS:NZ	2.39	0.56
19:O:113:ASP:O	19:O:117:ARG:NH1	2.39	0.56
47:2:1265:G:O6	47:2:1444:A:C6	2.58	0.56
1:1:172:G:N2	1:1:246:U:O2	2.34	0.55
1:1:1836:C:H41	42:l:3:ALA:HB2	1.70	0.55
1:1:3150:A:O2'	1:1:3294:A:O2'	2.25	0.55
6:A:117:GLU:HB2	6:A:122:ASP:HB2	1.88	0.55
9:D:261:THR:OG1	9:D:262:LYS:N	2.39	0.55
41:k:14:LEU:HD13	41:k:45:VAL:HG21	1.87	0.55
47:2:1342:C:O2'	79:AV:102:ARG:NH2	2.37	0.55
66:AI:70:VAL:HG12	66:AI:74:GLN:HE22	1.71	0.55
81:AX:380:LEU:O	81:AX:468:THR:HA	2.06	0.55
1:1:953:G:N2	1:1:1115:G:OP1	2.39	0.55
1:1:1729:A:N6	46:p:41:PHE:O	2.39	0.55
1:1:2154:U:O2'	6:A:238:ILE:O	2.24	0.55
5:P2:76:SER:O	5:P2:117:ARG:HB3	2.06	0.55
22:R:176:ARG:NH2	47:2:853:G:OP2	2.39	0.55
47:2:1266:U:H1'	47:2:1443:U:H3	1.71	0.55
58:AA:11:ILE:HD12	58:AA:35:ILE:HG23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:AX:777:SER:HA	81:AX:780:PHE:HB2	1.88	0.55
1:1:2177:G:N1	6:A:118:GLU:OE2	2.39	0.55
39:i:56:ARG:HE	39:i:76:ARG:HH12	1.54	0.55
47:2:609:U:O2'	71:AN:19:ARG:NH2	2.39	0.55
47:2:628:G:H21	47:2:971:A:H62	1.53	0.55
47:2:1514:U:O2'	51:t:4:LEU:O	2.21	0.55
53:v:225:ARG:NH1	76:AS:62:GLU:O	2.39	0.55
74:AQ:50:VAL:HA	74:AQ:53:LEU:HB3	1.88	0.55
1:1:129:U:H3	1:1:139:G:H1	1.53	0.55
1:1:1316:C:OP2	19:O:133:ARG:NH1	2.39	0.55
1:1:1360:C:OP1	8:C:309:ARG:NH2	2.39	0.55
4:P0:60:ARG:HH12	4:P0:63:ILE:HD13	1.72	0.55
47:2:195:G:O6	56:y:141:ARG:NH2	2.39	0.55
62:AE:86:THR:HB	62:AE:90:ARG:HG3	1.87	0.55
71:AN:57:LEU:HA	78:AU:4:VAL:HG12	1.86	0.55
81:AX:545:LEU:HD12	81:AX:554:LEU:HD11	1.88	0.55
82:AY:9:A:H62	82:AY:23:A:H62	1.54	0.55
1:1:533:A:N7	1:1:555:U:N3	2.54	0.55
1:1:1355:A:H4'	1:1:1356:U:H5''	1.88	0.55
1:1:2922:G:N2	1:1:2952:G:O2'	2.40	0.55
1:1:3186:A:H61	13:H:58:HIS:H	1.53	0.55
21:Q:16:ARG:NH1	21:Q:53:PHE:O	2.39	0.55
50:s:49:LYS:NZ	50:s:55:GLU:OE2	2.40	0.55
67:AJ:44:GLU:HG2	67:AJ:45:MET:HG2	1.88	0.55
73:AP:42:LEU:HA	73:AP:71:ILE:HD13	1.87	0.55
1:1:269:G:OP1	18:N:47:LYS:NZ	2.31	0.55
1:1:1295:G:OP2	23:S:84:ARG:NH1	2.40	0.55
1:1:2158:A:OP2	6:A:156:LYS:NZ	2.30	0.55
6:A:225:ILE:HD11	6:A:238:ILE:HG22	1.89	0.55
15:J:109:HIS:HA	15:J:112:LEU:HD23	1.89	0.55
33:c:54:SER:HA	33:c:57:GLU:HG2	1.88	0.55
47:2:1433:G:N2	77:AT:41:GLN:O	2.39	0.55
54:w:57:ASP:OD2	54:w:98:ARG:NH2	2.39	0.55
63:AF:93:VAL:HG22	63:AF:106:GLU:HA	1.87	0.55
1:1:597:G:OP2	11:F:37:ASN:ND2	2.39	0.55
29:Y:120:GLN:HB3	29:Y:126:LEU:HD12	1.88	0.55
47:2:521:A:N3	72:AO:34:ASN:ND2	2.55	0.55
47:2:1596:C:H5''	77:AT:32:ARG:HH21	1.72	0.55
52:u:180:LEU:N	52:u:229:GLY:O	2.36	0.55
75:AR:40:CYS:SG	75:AR:58:SER:OG	2.64	0.55
1:1:212:G:OP2	29:Y:2:ALA:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1336:U:H2'	1:1:1337:A:H8	1.70	0.55
10:E:42:LEU:HA	10:E:84:VAL:HG12	1.89	0.55
41:k:23:ALA:HB3	41:k:73:LEU:HD13	1.88	0.55
47:2:1199:G:OP2	77:AT:41:GLN:NE2	2.40	0.55
1:1:3158:G:C6	1:1:3292:A:N1	2.75	0.55
37:g:39:ALA:HB2	37:g:58:ARG:HD2	1.89	0.55
47:2:1670:G:H21	47:2:1731:A:H62	1.53	0.55
74:AQ:5:ARG:NH2	74:AQ:8:ASN:O	2.39	0.55
79:AV:28:GLY:N	79:AV:75:ALA:O	2.39	0.55
1:1:1877:U:O2'	1:1:1878:G:N2	2.40	0.55
3:4:83:C:O2	29:Y:51:ARG:NH2	2.39	0.55
5:P2:94:LYS:HZ1	5:P2:139:VAL:HB	1.71	0.55
13:H:102:ASN:HD21	13:H:115:ARG:HH12	1.53	0.55
26:V:14:SER:O	26:V:81:GLN:NE2	2.39	0.55
47:2:1591:C:H2'	47:2:1592:A:H8	1.71	0.55
47:2:1785:U:H2'	47:2:1786:G:H8	1.72	0.55
51:t:138:VAL:HG12	51:t:184:ILE:HG23	1.89	0.55
52:u:54:TYR:O	72:AO:20:ARG:NH1	2.40	0.55
56:y:171:SER:HB3	56:y:180:ASP:H	1.71	0.55
81:AX:397:PHE:HA	81:AX:455:GLY:HA2	1.88	0.55
1:1:1117:G:H5'	32:b:5:LYS:HE3	1.89	0.54
1:1:3003:G:O2'	7:B:92:TYR:OH	2.25	0.54
8:C:204:GLY:O	8:C:246:ARG:NH2	2.38	0.54
47:2:34:G:O2'	47:2:515:A:O2'	2.25	0.54
57:z:173:ALA:HA	57:z:176:ASN:HB2	1.89	0.54
62:AE:65:GLN:O	62:AE:107:ARG:NH1	2.40	0.54
81:AX:396:ALA:HB2	81:AX:459:ILE:HD11	1.88	0.54
1:1:899:U:H2'	1:1:900:G:H8	1.72	0.54
8:C:29:PRO:HB3	21:Q:25:TYR:HE2	1.72	0.54
20:P:141:SER:OG	20:P:142:SER:N	2.39	0.54
24:T:17:ARG:NH1	24:T:45:ASN:OD1	2.40	0.54
47:2:1289:U:H5'	50:s:91:ARG:HH22	1.72	0.54
47:2:1638:G:C5'	47:2:1638:G:C8	2.90	0.54
50:s:235:LEU:HB3	69:AL:52:THR:HG21	1.90	0.54
81:AX:129:VAL:HB	81:AX:157:ILE:HG22	1.89	0.54
1:1:2163:C:OP2	6:A:234:LYS:NZ	2.41	0.54
2:3:11:A:N6	9:D:16:PHE:O	2.40	0.54
10:E:51:ARG:NH1	10:E:161:ALA:O	2.40	0.54
47:2:1638:G:H8	47:2:1638:G:C5'	2.19	0.54
58:AA:27:PHE:O	77:AT:12:ARG:NH2	2.40	0.54
58:AA:68:LEU:HD12	58:AA:72:GLY:HA3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:182:U:O2	1:1:234:G:N2	2.34	0.54
1:1:631:U:H2'	1:1:632:G:H8	1.72	0.54
1:1:2303:A:OP1	44:n:23:ARG:NH2	2.41	0.54
8:C:45:ASN:HA	8:C:110:ASN:HD22	1.71	0.54
37:g:38:LEU:O	37:g:58:ARG:NH1	2.40	0.54
45:o:37:ALA:O	45:o:41:ARG:NE	2.39	0.54
47:2:1387:G:N7	65:AH:44:LYS:NZ	2.55	0.54
47:2:1489:U:OP1	51:t:9:ARG:NH1	2.39	0.54
47:2:1714:A:H2'	47:2:1715:G:H8	1.72	0.54
52:u:106:LYS:HD2	52:u:108:ARG:HH12	1.73	0.54
57:z:163:PRO:HA	57:z:166:GLY:H	1.73	0.54
69:AL:33:GLN:NE2	69:AL:35:ASN:OD1	2.35	0.54
81:AX:265:GLU:OE2	81:AX:267:LYS:NZ	2.40	0.54
1:1:49:A:O2'	18:N:187:ARG:NH1	2.41	0.54
1:1:1152:G:N2	1:1:1152:G:OP2	2.40	0.54
47:2:1636:C:H4'	47:2:1637:C:H5''	1.89	0.54
52:u:131:LEU:HA	52:u:137:PRO:HA	1.88	0.54
79:AV:109:ASP:OD1	79:AV:109:ASP:N	2.41	0.54
81:AX:55:ARG:NH1	86:AX:901:GCP:O1G	2.41	0.54
1:1:197:G:H21	1:1:218:G:H21	1.56	0.54
1:1:708:G:N2	1:1:711:A:OP2	2.41	0.54
1:1:1613:A:OP2	41:k:46:ARG:NH2	2.36	0.54
1:1:2831:G:N2	1:1:2858:U:O2	2.40	0.54
47:2:50:C:OP1	47:2:423:G:N2	2.41	0.54
47:2:110:U:OP1	47:2:753:A:O2'	2.26	0.54
47:2:772:G:N2	47:2:774:A:O2'	2.40	0.54
47:2:1239:U:O2	47:2:1246:C:N4	2.40	0.54
53:v:139:ASN:ND2	53:v:203:LYS:O	2.41	0.54
53:v:154:ALA:O	53:v:156:ARG:NH1	2.39	0.54
81:AX:416:PRO:O	81:AX:477:ASN:ND2	2.41	0.54
1:1:1834:U:OP2	42:l:10:LYS:NZ	2.37	0.54
1:1:2494:A:OP1	84:BA:161:LYS:NZ	2.34	0.54
1:1:2775:U:O2'	1:1:2777:G:N2	2.39	0.54
4:P0:60:ARG:NH1	4:P0:63:ILE:HG21	2.21	0.54
5:P2:94:LYS:HE3	5:P2:99:LYS:HG3	1.90	0.54
6:A:247:ARG:NH1	47:2:1012:U:O4'	2.41	0.54
16:L:163:GLY:HA2	31:a:139:ARG:HH22	1.73	0.54
47:2:715:U:O2	47:2:723:G:N2	2.36	0.54
58:AA:15:LEU:HD13	58:AA:21:VAL:HG23	1.89	0.54
79:AV:122:ILE:O	79:AV:134:TRP:N	2.38	0.54
81:AX:488:VAL:HG13	81:AX:489:VAL:HG13	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2270:A:H2'	1:1:2271:A:C8	2.43	0.54
1:1:2447:A:N6	1:1:2501:U:O2	2.40	0.54
1:1:2838:A:OP1	14:I:154:ARG:NH1	2.41	0.54
7:B:284:ARG:H	7:B:323:MET:HB2	1.73	0.54
29:Y:81:GLN:HE21	29:Y:96:PRO:HB2	1.73	0.54
47:2:478:A:N6	47:2:539:G:O6	2.40	0.54
47:2:526:A:OP1	72:AO:93:ARG:NH2	2.41	0.54
47:2:629:U:O4	47:2:970:A:N7	2.41	0.54
57:z:74:ASN:HA	57:z:77:ILE:HG22	1.89	0.54
66:AI:81:ILE:HG22	66:AI:83:ALA:H	1.72	0.54
1:1:121:A:N6	12:G:127:PRO:O	2.40	0.54
1:1:1365:G:OP1	21:Q:2:GLY:N	2.41	0.54
1:1:2895:G:OP1	13:H:166:ARG:NH2	2.41	0.54
8:C:54:GLU:HG3	8:C:55:LYS:HG2	1.90	0.54
23:S:105:THR:O	23:S:109:ASP:N	2.41	0.54
30:Z:14:VAL:HG13	37:g:89:ILE:HD11	1.90	0.54
47:2:589:C:H5'	78:AU:42:ARG:HH22	1.72	0.54
47:2:1482:C:O2'	64:AG:72:GLY:O	2.26	0.54
47:2:1514:U:H1'	51:t:6:SER:HB2	1.89	0.54
79:AV:217:ASP:O	79:AV:236:ALA:N	2.39	0.54
81:AX:283:ARG:O	81:AX:287:ALA:HB3	2.07	0.54
1:1:296:A:H3'	1:1:297:G:H21	1.72	0.54
1:1:1863:G:N1	1:1:1866:C:OP2	2.41	0.54
1:1:2473:C:OP2	1:1:2474:G:N1	2.41	0.54
47:2:72:A:O2'	47:2:73:U:O4'	2.23	0.54
47:2:1152:A:H4'	74:AQ:85:ARG:HD3	1.90	0.54
50:s:158:THR:HG21	50:s:221:THR:HG22	1.88	0.54
57:z:102:GLU:HA	57:z:105:LEU:HB2	1.89	0.54
66:AI:123:ARG:O	66:AI:127:HIS:ND1	2.32	0.54
79:AV:81:LEU:HD13	79:AV:89:LEU:HB3	1.90	0.54
1:1:1228:C:N4	1:1:1282:G:O6	2.41	0.53
8:C:335:ALA:HA	8:C:338:LYS:HA	1.90	0.53
9:D:36:LEU:HD23	9:D:50:ARG:HD2	1.89	0.53
15:J:15:GLU:OE1	15:J:132:ASN:ND2	2.41	0.53
30:Z:99:GLU:O	30:Z:103:GLN:NE2	2.41	0.53
49:r:189:ILE:HG23	49:r:190:PRO:HD3	1.88	0.53
67:AJ:107:ALA:O	67:AJ:110:LYS:NZ	2.38	0.53
73:AP:38:HIS:NE2	73:AP:66:VAL:O	2.42	0.53
79:AV:29:GLN:HE22	79:AV:31:ASN:HB2	1.72	0.53
81:AX:723:LYS:HD2	81:AX:805:GLY:HA2	1.89	0.53
1:1:3273:A:H5'	10:E:45:GLY:HA2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:38:U:N3	2:3:41:G:OP2	2.42	0.53
10:E:43:LEU:HD21	10:E:85:ILE:HD12	1.90	0.53
47:2:160:C:OP1	54:w:85:ARG:NH2	2.41	0.53
47:2:346:G:O2'	59:AB:80:MET:SD	2.63	0.53
47:2:1797:A:H4'	74:AQ:95:ARG:HG3	1.89	0.53
48:q:33:GLN:NE2	69:AL:63:GLY:O	2.40	0.53
81:AX:310:ASP:OD2	81:AX:310:ASP:N	2.27	0.53
1:1:2812:C:H2'	1:1:2813:A:C8	2.43	0.53
1:1:3392:U:H2'	1:1:3393:U:H6	1.73	0.53
2:3:98:C:OP1	23:S:39:SER:OG	2.26	0.53
7:B:60:LEU:HD13	7:B:62:ARG:HG2	1.89	0.53
11:F:37:ASN:O	11:F:41:ARG:N	2.41	0.53
47:2:752:A:C2	47:2:797:G:N1	2.75	0.53
47:2:1638:G:H5''	47:2:1638:G:C8	2.40	0.53
47:2:1677:C:OP1	56:y:42:ARG:NH2	2.41	0.53
48:q:148:ASP:OD1	48:q:148:ASP:N	2.41	0.53
51:t:109:LEU:HD13	51:t:175:VAL:HG21	1.90	0.53
67:AJ:86:ARG:HG2	67:AJ:89:ARG:HH21	1.72	0.53
1:1:1011:A:OP1	14:I:40:LYS:NZ	2.42	0.53
1:1:1184:A:H5''	17:M:59:ASN:HD22	1.74	0.53
1:1:1305:U:OP2	1:1:2939:G:N2	2.42	0.53
34:d:20:LEU:HD21	34:d:28:ARG:HB3	1.90	0.53
38:h:63:ARG:NH2	38:h:79:ASP:O	2.41	0.53
47:2:899:G:H2'	47:2:900:A:H8	1.73	0.53
47:2:1354:G:O6	47:2:1369:U:O2	2.25	0.53
47:2:1483:A:N3	47:2:1607:G:O2'	2.35	0.53
48:q:122:ILE:HA	48:q:144:ILE:HG22	1.90	0.53
1:1:1257:C:H4'	4:P0:43:LYS:HA	1.90	0.53
1:1:1907:C:O2	7:B:240:ARG:NH2	2.37	0.53
33:c:30:THR:HG21	33:c:89:VAL:HG22	1.90	0.53
41:k:27:ILE:HD11	41:k:39:ARG:HD3	1.89	0.53
47:2:1350:U:O4	47:2:1376:C:C4	2.62	0.53
47:2:1466:G:OP1	64:AG:132:LYS:NZ	2.42	0.53
53:v:93:LEU:HD23	53:v:172:ILE:HG23	1.90	0.53
61:AD:101:HIS:HA	61:AD:104:ARG:HE	1.72	0.53
1:1:517:G:H5'	11:F:60:ARG:HH22	1.73	0.53
1:1:596:C:O2	8:C:326:ARG:NH2	2.42	0.53
1:1:937:G:OP2	1:1:938:C:N4	2.37	0.53
1:1:1228:C:O2'	4:P0:32:ASN:ND2	2.41	0.53
1:1:2722:U:H4'	24:T:88:ARG:HB2	1.89	0.53
35:e:78:ASN:O	35:e:81:ASP:N	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:155:U:O4	72:AO:132:ARG:NH1	2.42	0.53
47:2:1172:G:HO2'	47:2:1543:A:HO2'	1.52	0.53
47:2:1476:C:H1'	47:2:1539:G:H21	1.73	0.53
47:2:1673:G:OP1	54:w:94:ARG:NH2	2.42	0.53
53:v:112:ARG:HH22	73:AP:95:HIS:HB3	1.73	0.53
84:BA:27:ASN:HD22	84:BA:212:PRO:HD2	1.74	0.53
1:1:1483:G:OP2	1:1:1858:A:N6	2.41	0.53
8:C:170:LYS:HE3	8:C:175:HIS:HA	1.91	0.53
10:E:40:LEU:HD12	10:E:84:VAL:HB	1.89	0.53
10:E:62:THR:OG1	10:E:78:ARG:NH1	2.42	0.53
47:2:7:G:N7	50:s:205:ARG:NH2	2.57	0.53
47:2:307:G:H5''	59:AB:103:ARG:HH21	1.74	0.53
47:2:1635:A:H61	50:s:92:ALA:HA	1.73	0.53
75:AR:36:LYS:HB3	75:AR:43:ILE:HG13	1.89	0.53
81:AX:60:ARG:NH1	81:AX:61:LYS:O	2.42	0.53
81:AX:247:ASP:OD1	81:AX:247:ASP:N	2.30	0.53
1:1:2165:G:N2	1:1:2168:A:OP2	2.41	0.53
1:1:2493:U:OP1	84:BA:41:TYR:OH	2.26	0.53
1:1:3206:C:OP2	17:M:102:LYS:NZ	2.42	0.53
7:B:159:ARG:HB2	7:B:183:LEU:H	1.74	0.53
19:O:54:TYR:HE2	19:O:145:VAL:HG11	1.73	0.53
19:O:61:ALA:HA	19:O:70:PRO:HD2	1.91	0.53
21:Q:30:VAL:HG23	21:Q:49:LEU:HD21	1.91	0.53
47:2:692:C:OP1	47:2:697:C:N4	2.42	0.53
47:2:1389:C:O2'	65:AH:48:ASN:O	2.21	0.53
54:w:67:VAL:HG12	54:w:69:LEU:H	1.74	0.53
1:1:2389:C:H5''	20:P:66:SER:HA	1.90	0.53
1:1:2916:U:H2'	1:1:2917:G:H8	1.73	0.53
1:1:3186:A:OP2	23:S:170:THR:OG1	2.26	0.53
1:1:3231:U:O4	1:1:3256:G:O6	2.27	0.53
3:4:8:C:H2'	3:4:9:A:C8	2.44	0.53
15:J:48:SER:HB3	15:J:66:ALA:HB3	1.90	0.53
47:2:686:C:O3'	70:AM:118:ARG:NH2	2.41	0.53
47:2:752:A:H2	47:2:797:G:N1	2.05	0.53
47:2:826:U:H3	47:2:846:G:H1	1.56	0.53
51:t:126:VAL:O	51:t:131:ALA:N	2.42	0.53
79:AV:19:TRP:HB2	79:AV:290:VAL:HG21	1.91	0.53
1:1:1237:G:N7	1:1:1263:A:O2'	2.39	0.53
18:N:143:ARG:NH1	18:N:152:CYS:SG	2.81	0.53
47:2:703:G:N2	47:2:736:C:O2	2.42	0.53
56:y:167:ALA:HA	56:y:183:ILE:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:AX:54:ALA:HB1	81:AX:440:ARG:HH22	1.74	0.53
1:1:439:C:O2	1:1:619:A:O2'	2.27	0.52
1:1:2685:C:H2'	1:1:2686:A:C8	2.44	0.52
6:A:131:GLY:H	6:A:169:ILE:HB	1.73	0.52
34:d:62:ARG:NH1	34:d:66:GLY:O	2.43	0.52
47:2:991:G:N2	47:2:1013:A:H62	2.04	0.52
50:s:95:ARG:O	50:s:97:ARG:NH1	2.42	0.52
52:u:11:ARG:NH2	52:u:24:SER:OG	2.42	0.52
53:v:82:PHE:O	76:AS:49:ARG:NH1	2.43	0.52
54:w:4:ASN:HA	54:w:15:THR:HA	1.90	0.52
81:AX:485:VAL:HG21	81:AX:793:PHE:HD1	1.73	0.52
1:1:835:G:O2'	1:1:857:G:N2	2.39	0.52
1:1:1750:A:O5'	41:k:26:LYS:NZ	2.39	0.52
1:1:1940:G:OP1	22:R:75:HIS:ND1	2.42	0.52
8:C:326:ARG:HG3	8:C:327:LEU:HD12	1.91	0.52
18:N:8:GLU:OE1	18:N:50:ARG:NH2	2.40	0.52
23:S:21:GLU:OE2	24:T:146:ASN:ND2	2.42	0.52
31:a:11:HIS:ND1	31:a:17:ALA:O	2.42	0.52
47:2:196:G:O6	56:y:141:ARG:NH2	2.42	0.52
54:w:57:ASP:HB3	54:w:98:ARG:HH12	1.73	0.52
1:1:577:C:OP1	11:F:142:SER:OG	2.23	0.52
1:1:2456:A:OP2	1:1:2460:U:N3	2.43	0.52
1:1:2669:G:H2'	1:1:2670:G:H8	1.74	0.52
1:1:3309:G:H5''	20:P:71:ALA:HB2	1.90	0.52
4:P0:48:ARG:NH2	4:P0:91:GLU:OE1	2.42	0.52
28:X:80:ASN:HD21	28:X:131:ASP:HA	1.74	0.52
47:2:1219:A:O2'	58:AA:47:GLN:O	2.27	0.52
47:2:1672:G:H2'	47:2:1673:G:C8	2.45	0.52
49:r:32:ILE:HG23	49:r:43:VAL:HG13	1.91	0.52
51:t:106:LYS:NZ	51:t:174:HIS:O	2.41	0.52
52:u:250:GLU:HA	52:u:253:ASP:HB2	1.92	0.52
56:y:36:THR:HA	56:y:58:LEU:HG	1.90	0.52
57:z:29:LYS:NZ	78:AU:40:TYR:O	2.40	0.52
79:AV:246:SER:OG	79:AV:297:ASP:O	2.27	0.52
1:1:341:G:O2'	3:4:22:U:O4	2.27	0.52
9:D:290:ILE:O	9:D:294:ALA:N	2.38	0.52
33:c:25:LEU:O	33:c:29:SER:OG	2.24	0.52
47:2:1544:U:H5''	66:AI:132:ARG:HH12	1.74	0.52
49:r:23:PRO:HA	49:r:26:ARG:HH21	1.74	0.52
50:s:139:ILE:HD13	50:s:191:ALA:HB1	1.91	0.52
52:u:105:VAL:HG23	52:u:106:LYS:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:AC:32:LEU:HD22	60:AC:121:VAL:HG22	1.92	0.52
72:AO:57:VAL:HA	72:AO:73:GLY:HA2	1.90	0.52
81:AX:88:GLU:OE2	81:AX:237:LYS:NZ	2.39	0.52
81:AX:387:PRO:HA	81:AX:394:PHE:HB2	1.91	0.52
1:1:1530:U:O2'	3:4:115:C:OP1	2.28	0.52
1:1:2413:A:H2'	1:1:2414:G:H8	1.75	0.52
1:1:2720:G:H1	1:1:2736:A:H61	1.58	0.52
7:B:14:LEU:HA	7:B:17:LEU:HD13	1.92	0.52
47:2:654:C:H3'	47:2:655:G:H4'	1.92	0.52
47:2:938:G:N2	47:2:941:A:OP2	2.42	0.52
47:2:1255:G:N7	60:AC:46:ARG:NH1	2.58	0.52
49:r:83:LYS:HE2	49:r:106:THR:HG22	1.91	0.52
57:z:171:ARG:HE	57:z:174:ARG:HB3	1.75	0.52
63:AF:83:MET:HB3	63:AF:116:LEU:HD13	1.91	0.52
70:AM:23:ARG:NH2	70:AM:66:ASN:O	2.43	0.52
75:AR:42:ASN:ND2	75:AR:57:GLU:OE2	2.42	0.52
1:1:1071:U:O2	1:1:1087:G:N2	2.36	0.52
41:k:5:ILE:HD11	41:k:11:PHE:HD1	1.74	0.52
41:k:12:LEU:O	41:k:16:ARG:NH1	2.42	0.52
47:2:788:A:OP2	52:u:108:ARG:NH1	2.43	0.52
47:2:947:U:H2'	47:2:948:G:H8	1.75	0.52
53:v:174:LEU:HD11	53:v:213:LYS:HB3	1.92	0.52
1:1:359:U:O2'	40:j:16:HIS:ND1	2.43	0.52
39:i:97:SER:O	39:i:99:ARG:N	2.43	0.52
47:2:761:G:OP2	57:z:51:LYS:NZ	2.43	0.52
47:2:821:U:O2	47:2:852:C:N3	2.43	0.52
47:2:886:U:O2'	62:AE:121:VAL:O	2.27	0.52
47:2:1206:U:O2'	77:AT:16:LYS:NZ	2.42	0.52
1:1:1278:A:OP2	1:1:1279:C:N4	2.38	0.52
9:D:107:ARG:NH1	9:D:116:ASP:OD1	2.42	0.52
31:a:101:VAL:HG22	31:a:124:ILE:HD11	1.92	0.52
47:2:442:C:OP1	72:AO:106:GLN:NE2	2.40	0.52
47:2:473:A:OP1	57:z:44:ARG:NH1	2.42	0.52
47:2:843:U:H2'	47:2:844:A:H8	1.74	0.52
47:2:1693:A:H2	47:2:1709:C:H42	1.58	0.52
57:z:62:ARG:O	57:z:69:ARG:NH1	2.42	0.52
62:AE:29:HIS:HB3	62:AE:41:ARG:HA	1.92	0.52
66:AI:87:ASN:ND2	66:AI:100:THR:OG1	2.43	0.52
81:AX:283:ARG:O	81:AX:287:ALA:CB	2.58	0.52
1:1:2525:G:N7	6:A:67:TYR:OH	2.40	0.52
1:1:2703:A:OP2	9:D:23:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:13:A:H5'	2:3:14:U:H5	1.74	0.52
19:O:15:LEU:HB2	19:O:18:ARG:HB3	1.92	0.52
47:2:205:U:H2'	47:2:206:A:H8	1.75	0.52
47:2:821:U:H3	47:2:852:C:N4	2.07	0.52
47:2:1469:A:HO2'	47:2:1540:G:H21	1.55	0.52
50:s:170:ILE:HG23	50:s:197:TYR:HB2	1.92	0.52
52:u:251:GLU:HA	52:u:254:ARG:HG2	1.92	0.52
71:AN:69:ARG:HB3	71:AN:86:PHE:HE1	1.75	0.52
1:1:93:C:OP2	45:o:55:LYS:NZ	2.43	0.52
1:1:1591:G:OP1	37:g:37:LYS:NZ	2.39	0.52
8:C:9:HIS:NE2	8:C:147:GLU:OE2	2.43	0.52
10:E:92:SER:OG	10:E:94:GLU:OE1	2.28	0.52
26:V:2:SER:N	26:V:40:LYS:O	2.43	0.52
47:2:816:G:O6	47:2:855:A:N1	2.43	0.52
47:2:1382:A:H4'	68:AK:89:ARG:HH12	1.74	0.52
48:q:27:ARG:O	48:q:30:GLN:NE2	2.42	0.52
63:AF:121:ILE:HD12	66:AI:126:ARG:HH22	1.75	0.52
1:1:852:U:H2'	1:1:853:G:H8	1.74	0.51
1:1:1568:U:O2'	1:1:1571:A:N1	2.43	0.51
1:1:2458:A:N6	1:1:2487:U:O2	2.40	0.51
11:F:116:PHE:O	11:F:199:ASN:ND2	2.42	0.51
13:H:23:ARG:HD3	13:H:39:LYS:HA	1.92	0.51
18:N:3:ALA:HA	18:N:6:TYR:HD2	1.74	0.51
27:W:6:ASP:OD2	27:W:9:SER:N	2.41	0.51
35:e:79:VAL:HG13	35:e:108:ILE:HG23	1.92	0.51
47:2:215:A:H62	47:2:242:U:H2'	1.75	0.51
47:2:1344:A:H4'	68:AK:55:PRO:HD2	1.91	0.51
48:q:64:ILE:HD11	48:q:181:VAL:HG11	1.91	0.51
52:u:95:THR:HG21	72:AO:16:PRO:HG2	1.91	0.51
54:w:24:ILE:HD12	54:w:25:ARG:HE	1.74	0.51
79:AV:256:THR:OG1	79:AV:259:GLY:N	2.42	0.51
81:AX:258:THR:HG23	81:AX:260:LYS:H	1.75	0.51
1:1:809:G:N1	1:1:932:U:O4	2.43	0.51
1:1:1221:A:N7	4:P0:8:LYS:NZ	2.57	0.51
1:1:3379:C:O2'	7:B:316:GLU:OE2	2.29	0.51
3:4:150:G:O2'	3:4:152:G:OP1	2.27	0.51
33:c:44:ILE:HD11	33:c:56:LEU:HD11	1.91	0.51
47:2:1596:C:O2	77:AT:32:ARG:NH2	2.43	0.51
66:AI:110:ARG:O	66:AI:114:GLU:N	2.40	0.51
1:1:797:U:H2'	1:1:798:G:H8	1.75	0.51
1:1:3234:A:N1	1:1:3253:G:O6	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:53:THR:HA	15:J:60:ARG:HA	1.92	0.51
40:j:25:ARG:NH1	42:l:50:ASN:OD1	2.43	0.51
47:2:537:G:OP2	57:z:175:ARG:NH1	2.44	0.51
49:r:170:GLU:HB3	49:r:174:LYS:HE3	1.91	0.51
53:v:164:PRO:HD2	76:AS:48:VAL:HG22	1.92	0.51
55:x:75:THR:OG1	55:x:79:ARG:NH2	2.40	0.51
65:AH:44:LYS:HE3	65:AH:48:ASN:HD22	1.65	0.51
73:AP:95:HIS:NE2	73:AP:98:GLN:O	2.43	0.51
84:BA:42:ASP:OD2	84:BA:188:ASN:ND2	2.41	0.51
1:1:63:A:N3	1:1:78:U:O2'	2.38	0.51
1:1:444:U:N3	1:1:492:C:O2	2.44	0.51
1:1:1095:U:O2	24:T:129:LYS:N	2.42	0.51
1:1:2682:C:O4'	15:J:20:ASN:ND2	2.42	0.51
3:4:47:C:O2'	3:4:62:C:OP2	2.29	0.51
8:C:226:GLU:OE1	8:C:246:ARG:NH2	2.40	0.51
13:H:31:ARG:HH12	13:H:187:ILE:HG21	1.75	0.51
24:T:82:ASN:HD21	32:b:16:ALA:HA	1.75	0.51
37:g:96:GLU:HG3	37:g:99:LYS:HD3	1.92	0.51
47:2:146:U:N3	47:2:168:A:C8	2.72	0.51
47:2:1278:G:OP1	51:t:185:LYS:NZ	2.37	0.51
47:2:1408:G:O2'	79:AV:17:ASN:ND2	2.43	0.51
47:2:1470:C:O2	47:2:1572:G:O2'	2.24	0.51
52:u:103:TYR:O	52:u:182:TYR:OH	2.28	0.51
81:AX:544:ASP:O	81:AX:549:HIS:ND1	2.43	0.51
1:1:68:C:OP2	1:1:301:G:N2	2.43	0.51
1:1:612:U:H2'	1:1:613:G:H8	1.75	0.51
1:1:1530:U:O2'	3:4:114:G:O2'	2.25	0.51
1:1:1814:A:H5''	1:1:1816:A:H1'	1.92	0.51
7:B:372:THR:HG23	7:B:375:GLU:HB2	1.92	0.51
31:a:84:GLU:OE1	31:a:87:ARG:NH1	2.41	0.51
47:2:250:C:H2'	47:2:251:A:H8	1.76	0.51
47:2:576:G:N1	71:AN:66:SER:OG	2.43	0.51
47:2:849:C:H2'	47:2:850:A:C8	2.46	0.51
56:y:84:HIS:NE2	56:y:97:THR:OG1	2.43	0.51
59:AB:85:VAL:HA	59:AB:108:PRO:HA	1.93	0.51
79:AV:249:ARG:NH1	79:AV:297:ASP:O	2.44	0.51
1:1:1488:G:H2'	1:1:1489:A:H8	1.76	0.51
3:4:133:G:H2'	3:4:134:G:C8	2.46	0.51
16:L:120:GLN:HA	16:L:123:ILE:HG12	1.92	0.51
36:f:13:HIS:NE2	36:f:15:SER:O	2.43	0.51
47:2:1544:U:H5''	66:AI:132:ARG:HH22	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:w:20:ASP:HB3	54:w:23:ARG:HB2	1.93	0.51
55:x:71:HIS:HA	55:x:74:GLN:HG2	1.91	0.51
59:AB:63:LEU:O	59:AB:129:ARG:NH2	2.43	0.51
65:AH:31:ASN:O	65:AH:35:CYS:N	2.44	0.51
66:AI:20:THR:HG21	66:AI:35:ILE:HA	1.93	0.51
66:AI:62:THR:OG1	66:AI:63:GLN:N	2.43	0.51
70:AM:55:ASP:OD2	70:AM:57:ARG:NH1	2.43	0.51
72:AO:57:VAL:O	72:AO:94:TYR:OH	2.29	0.51
1:1:985:U:O4'	11:F:101:LYS:NZ	2.42	0.51
1:1:1881:A:H2'	1:1:1882:G:H8	1.76	0.51
1:1:3309:G:OP2	1:1:3309:G:N2	2.41	0.51
5:P2:91:ASP:OD2	5:P2:92:ARG:NH2	2.44	0.51
9:D:5:LYS:NZ	9:D:9:SER:OG	2.44	0.51
47:2:65:A:H2	47:2:84:A:H62	1.58	0.51
47:2:1001:A:OP1	82:AY:38:A:O2'	2.27	0.51
47:2:1278:G:H5''	51:t:185:LYS:HD3	1.92	0.51
47:2:1486:G:O6	47:2:1520:U:O4	2.28	0.51
52:u:11:ARG:NH1	52:u:21:ASP:OD1	2.42	0.51
55:x:79:ARG:O	55:x:83:LYS:NZ	2.41	0.51
55:x:134:GLU:OE2	55:x:155:ASP:N	2.44	0.51
1:1:894:G:H4'	1:1:895:A:H5'	1.93	0.51
1:1:2661:G:H2'	1:1:2662:G:H8	1.76	0.51
2:3:28:C:H4'	15:J:135:GLY:HA2	1.93	0.51
6:A:96:LEU:HD11	46:p:86:LEU:HD12	1.92	0.51
35:e:97:ALA:HB3	35:e:100:ILE:HG13	1.91	0.51
47:2:821:U:H3	47:2:852:C:H42	1.58	0.51
47:2:1165:G:H5'	47:2:1612:U:H1'	1.93	0.51
53:v:147:THR:OG1	53:v:158:GLN:O	2.29	0.51
79:AV:18:GLY:HA2	79:AV:306:THR:HG23	1.92	0.51
1:1:158:G:H2'	1:1:159:A:H8	1.76	0.51
1:1:536:U:H2'	1:1:537:A:H8	1.75	0.51
1:1:712:G:O3'	16:L:174:ARG:NH1	2.42	0.51
1:1:1923:C:H42	1:1:1929:G:H22	1.59	0.51
1:1:2461:A:O2'	1:1:2484:A:N6	2.40	0.51
1:1:2700:G:H5''	24:T:17:ARG:HG2	1.93	0.51
1:1:3322:A:H2'	1:1:3323:A:C8	2.46	0.51
12:G:170:CYS:HB2	12:G:175:VAL:HG23	1.93	0.51
13:H:134:ILE:HB	13:H:144:ILE:HD11	1.93	0.51
16:L:31:LYS:HD3	16:L:34:SER:HB2	1.93	0.51
47:2:936:G:OP1	47:2:1074:G:N2	2.34	0.51
47:2:1041:G:H2'	47:2:1042:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:t:65:ARG:NH2	51:t:68:GLU:OE2	2.44	0.51
51:t:221:SER:HB3	79:AV:193:ILE:HG22	1.92	0.51
55:x:155:ASP:HA	55:x:186:PRO:HD2	1.92	0.51
73:AP:65:LEU:HB3	73:AP:70:LYS:HD3	1.93	0.51
79:AV:287:PRO:HG2	79:AV:311:ARG:HH12	1.76	0.51
84:BA:208:SER:OG	84:BA:209:SER:N	2.44	0.51
1:1:543:C:N4	1:1:549:U:N3	2.52	0.51
1:1:1168:U:H2'	1:1:1169:A:H8	1.76	0.51
1:1:2292:U:O2'	47:2:1656:U:O2'	2.25	0.51
1:1:2463:G:OP1	1:1:2485:A:N6	2.44	0.51
3:4:52:A:OP1	42:l:21:ARG:NH1	2.41	0.51
4:P0:108:PRO:HB2	4:P0:174:ASN:HD22	1.75	0.51
12:G:161:GLU:OE1	18:N:11:GLN:NE2	2.32	0.51
24:T:45:ASN:HD22	24:T:94:GLU:HG3	1.75	0.51
29:Y:35:LEU:HD22	29:Y:36:SER:H	1.75	0.51
47:2:1186:U:C4	47:2:1208:A:C6	2.98	0.51
47:2:1409:G:N2	47:2:1412:G:OP2	2.39	0.51
49:r:145:LYS:HE2	49:r:149:GLN:HB2	1.92	0.51
52:u:68:ARG:HA	52:u:76:VAL:HG11	1.93	0.51
65:AH:115:LEU:HD13	65:AH:116:LYS:H	1.76	0.51
71:AN:68:ILE:HD13	78:AU:6:GLY:HA2	1.92	0.51
79:AV:81:LEU:HB2	79:AV:113:VAL:HG21	1.92	0.51
79:AV:179:LYS:HG2	79:AV:191:ASP:HA	1.93	0.51
79:AV:221:MET:SD	79:AV:233:THR:OG1	2.69	0.51
81:AX:333:ALA:O	81:AX:337:MET:HB2	2.11	0.51
84:BA:36:VAL:HG22	84:BA:208:SER:HB3	1.93	0.51
1:1:497:C:O3'	36:f:86:ARG:NH2	2.43	0.50
1:1:3351:U:H5	1:1:3353:G:H21	1.59	0.50
7:B:159:ARG:HB2	7:B:182:GLN:HA	1.93	0.50
11:F:139:PRO:HA	11:F:237:ASN:HD21	1.74	0.50
11:F:170:GLU:HA	11:F:174:GLY:HA3	1.92	0.50
12:G:140:VAL:HG11	18:N:3:ALA:HB2	1.92	0.50
47:2:406:U:H2'	47:2:407:A:H8	1.75	0.50
47:2:1252:C:O2'	80:AW:141:CYS:O	2.28	0.50
56:y:83:TYR:HB3	56:y:101:ILE:HD12	1.93	0.50
79:AV:225:LEU:O	79:AV:228:LYS:NZ	2.37	0.50
82:AY:28:C:H2'	82:AY:29:A:H8	1.76	0.50
1:1:491:A:N6	1:1:492:C:O2	2.44	0.50
1:1:1674:G:OP1	25:U:70:LYS:NZ	2.42	0.50
1:1:2518:C:H2'	1:1:2519:A:H8	1.75	0.50
1:1:2618:G:OP1	1:1:2644:C:O2'	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3271:G:N2	10:E:107:ALA:O	2.43	0.50
1:1:3322:A:H2'	1:1:3323:A:H8	1.76	0.50
47:2:126:A:H62	47:2:291:G:N2	2.03	0.50
49:r:92:GLN:OE1	49:r:97:LEU:N	2.44	0.50
53:v:144:GLU:HA	53:v:162:VAL:HB	1.92	0.50
55:x:8:ILE:HG23	55:x:42:GLN:HA	1.92	0.50
74:AQ:20:PRO:HA	74:AQ:31:PRO:HA	1.93	0.50
1:1:85:A:N6	1:1:100:A:OP2	2.41	0.50
1:1:969:C:O3'	32:b:18:ARG:NH1	2.45	0.50
1:1:1260:A:O2'	1:1:1261:G:O4'	2.24	0.50
1:1:3276:G:OP1	10:E:48:ARG:NH2	2.44	0.50
19:O:77:SER:N	19:O:106:GLU:OE2	2.45	0.50
26:V:70:ARG:HG3	26:V:71:LYS:HG2	1.92	0.50
28:X:105:VAL:HG13	28:X:126:LEU:HD11	1.93	0.50
47:2:443:C:O2'	47:2:445:A:N7	2.42	0.50
47:2:966:A:H2'	47:2:967:A:H8	1.76	0.50
47:2:1178:G:H3'	47:2:1179:G:H8	1.76	0.50
49:r:179:SER:HB3	49:r:184:LEU:HB2	1.92	0.50
51:t:99:VAL:HG12	51:t:173:ARG:HH21	1.76	0.50
54:w:51:LYS:HG3	54:w:112:VAL:HG13	1.93	0.50
59:AB:133:LYS:O	59:AB:136:ARG:NH1	2.44	0.50
69:AL:38:LYS:N	69:AL:49:GLU:OE1	2.44	0.50
1:1:2469:G:N1	1:1:2477:G:O2'	2.43	0.50
1:1:2794:G:N2	82:AY:76:A:O2'	2.45	0.50
1:1:2960:C:H2'	1:1:2961:G:C8	2.46	0.50
9:D:103:LEU:HB3	9:D:247:ILE:HG21	1.92	0.50
47:2:256:A:O2'	56:y:72:ILE:O	2.23	0.50
47:2:895:G:N1	47:2:918:U:C2	2.79	0.50
47:2:1524:A:H5'	67:AJ:78:LYS:HG2	1.93	0.50
81:AX:186:ASN:HA	81:AX:189:VAL:HG12	1.92	0.50
1:1:655:C:H2'	1:1:656:A:C8	2.46	0.50
1:1:1897:G:O2'	26:V:16:GLY:O	2.25	0.50
1:1:2473:C:H5''	1:1:2474:G:C2	2.46	0.50
1:1:3190:C:H2'	1:1:3191:G:H8	1.76	0.50
16:L:9:ILE:HG12	31:a:49:HIS:CE1	2.47	0.50
35:e:6:HIS:ND1	35:e:7:PRO:O	2.43	0.50
47:2:195:G:H2'	47:2:196:G:H8	1.77	0.50
47:2:767:U:OP2	72:AO:63:GLN:NE2	2.41	0.50
47:2:1584:G:N2	47:2:1611:A:OP2	2.38	0.50
51:t:65:ARG:HH12	58:AA:69:THR:HG22	1.76	0.50
61:AD:119:GLU:O	61:AD:123:HIS:ND1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AG:120:ASP:OD2	64:AG:123:ARG:NH1	2.45	0.50
68:AK:28:SER:HB3	68:AK:34:LEU:HB2	1.91	0.50
69:AL:15:ARG:HE	69:AL:24:ILE:HG13	1.76	0.50
77:AT:21:CYS:HB3	77:AT:26:SER:HB2	1.93	0.50
79:AV:69:GLN:H	79:AV:84:SER:HA	1.75	0.50
79:AV:262:VAL:HG13	79:AV:271:VAL:HB	1.93	0.50
81:AX:214:GLY:N	86:AX:901:GCP:O6	2.38	0.50
1:1:786:A:OP2	21:Q:146:SER:OG	2.30	0.50
18:N:103:GLU:O	18:N:107:GLY:N	2.38	0.50
20:P:88:VAL:HA	20:P:91:VAL:HG22	1.94	0.50
43:m:98:LYS:HD2	43:m:118:THR:HG21	1.94	0.50
47:2:1471:A:H2	47:2:1474:G:H21	1.60	0.50
47:2:1511:U:H2'	47:2:1512:G:C8	2.47	0.50
51:t:164:VAL:HG12	51:t:168:ILE:HD13	1.92	0.50
58:AA:15:LEU:HD21	58:AA:68:LEU:HD22	1.93	0.50
1:1:616:G:H2'	1:1:617:G:C8	2.46	0.50
1:1:1542:G:H2'	1:1:1543:G:H8	1.77	0.50
1:1:2565:U:H3	1:1:2576:G:H1	1.59	0.50
1:1:2722:U:O2'	24:T:88:ARG:O	2.27	0.50
6:A:147:ARG:HG2	6:A:157:VAL:HG12	1.94	0.50
7:B:215:ILE:HD12	7:B:338:LEU:HD12	1.94	0.50
9:D:153:THR:O	9:D:179:ARG:NH2	2.44	0.50
30:Z:5:LEU:HD11	30:Z:25:ILE:HD13	1.94	0.50
34:d:55:LEU:HD23	34:d:95:PRO:HG3	1.94	0.50
47:2:290:G:H2'	47:2:291:G:H8	1.75	0.50
52:u:179:LYS:O	52:u:194:THR:OG1	2.23	0.50
52:u:184:THR:HG23	52:u:189:LEU:HD13	1.93	0.50
55:x:99:LEU:HD21	55:x:112:ARG:HG3	1.92	0.50
55:x:138:LYS:HB3	70:AM:54:ASP:HB3	1.92	0.50
79:AV:253:ALA:HA	79:AV:262:VAL:HA	1.92	0.50
1:1:105:C:H2'	1:1:106:A:C8	2.46	0.50
1:1:149:U:O3'	18:N:56:LYS:NZ	2.44	0.50
1:1:1167:U:O2'	11:F:210:PRO:O	2.28	0.50
1:1:1663:C:H2'	1:1:1664:G:H8	1.75	0.50
1:1:2464:U:OP1	84:BA:158:GLN:NE2	2.31	0.50
6:A:30:ARG:HB3	6:A:163:ARG:HH22	1.77	0.50
7:B:58:ARG:NH1	7:B:283:TYR:OH	2.43	0.50
11:F:64:GLN:O	11:F:68:ASP:N	2.45	0.50
14:I:192:ASP:HA	14:I:197:VAL:HG12	1.92	0.50
15:J:89:TYR:HB3	15:J:169:ALA:HA	1.94	0.50
29:Y:35:LEU:HD23	29:Y:106:ILE:HG13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:j:33:THR:HG22	40:j:40:PRO:HD2	1.94	0.50
47:2:992:A:O2'	47:2:1785:U:O2	2.28	0.50
47:2:1056:U:O2	47:2:1062:A:N6	2.44	0.50
47:2:1276:U:H2'	47:2:1277:G:H8	1.76	0.50
52:u:65:LEU:HD23	52:u:70:VAL:HG23	1.93	0.50
55:x:27:LEU:HA	55:x:32:PRO:HG2	1.93	0.50
72:AO:29:HIS:ND1	72:AO:32:ARG:O	2.43	0.50
81:AX:55:ARG:NH1	81:AX:69:THR:OG1	2.45	0.50
8:C:11:LEU:HD12	8:C:168:ALA:HB1	1.94	0.50
12:G:207:ASP:HB3	12:G:210:ALA:HB3	1.93	0.50
18:N:26:ARG:HH22	18:N:43:THR:HB	1.76	0.50
41:k:21:LYS:HD3	41:k:46:ARG:HG2	1.94	0.50
47:2:541:A:O2'	47:2:542:A:N3	2.41	0.50
47:2:866:G:OP1	61:AD:3:ARG:NH1	2.44	0.50
48:q:112:THR:O	48:q:114:SER:N	2.45	0.50
49:r:188:LEU:HD21	49:r:212:VAL:HG11	1.93	0.50
54:w:71:THR:HG22	54:w:72:ARG:HD3	1.94	0.50
61:AD:16:ILE:HD12	61:AD:17:PRO:HD2	1.94	0.50
63:AF:43:ARG:HE	63:AF:47:ARG:HD2	1.76	0.50
81:AX:30:HIS:N	86:AX:901:GCP:O2B	2.40	0.50
81:AX:295:GLU:O	81:AX:299:LEU:CB	2.60	0.50
1:1:903:U:H2'	1:1:904:A:H8	1.76	0.49
1:1:1343:A:H2'	1:1:1344:G:H8	1.77	0.49
5:P2:86:LYS:HD3	5:P2:106:LEU:HD21	1.93	0.49
11:F:59:GLU:HA	11:F:62:ILE:HG22	1.93	0.49
47:2:191:C:N4	47:2:195:G:O6	2.45	0.49
47:2:1591:C:H2'	47:2:1592:A:C8	2.47	0.49
66:AI:118:LYS:O	66:AI:120:ARG:NH2	2.45	0.49
81:AX:22:MET:HE1	81:AX:338:ILE:HB	1.94	0.49
84:BA:38:LEU:HG	84:BA:165:LEU:HG	1.93	0.49
84:BA:207:LYS:HB2	84:BA:213:ALA:HB2	1.94	0.49
1:1:400:G:H4'	1:1:400:G:OP1	2.10	0.49
1:1:1102:A:OP1	11:F:155:LYS:NZ	2.45	0.49
1:1:1195:A:H1'	1:1:1319:G:H4'	1.94	0.49
47:2:1345:A:H4'	68:AK:53:LYS:HB3	1.93	0.49
70:AM:17:ALA:O	70:AM:21:GLY:N	2.45	0.49
79:AV:70:ASP:O	79:AV:83:ALA:N	2.45	0.49
79:AV:88:THR:HA	79:AV:104:VAL:HA	1.92	0.49
81:AX:117:ALA:O	81:AX:121:VAL:N	2.36	0.49
7:B:80:ASP:OD2	7:B:314:TYR:OH	2.30	0.49
8:C:170:LYS:O	8:C:175:HIS:NE2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:H:27:VAL:HG21	13:H:78:MET:HB3	1.94	0.49
45:o:38:GLN:HE22	45:o:42:ARG:HE	1.61	0.49
46:p:90:VAL:HG13	46:p:91:GLU:HG2	1.93	0.49
47:2:69:G:O6	47:2:82:U:O2	2.31	0.49
47:2:486:G:O6	47:2:501:U:O4	2.30	0.49
47:2:540:G:OP1	47:2:541:A:N6	2.45	0.49
47:2:1166:A:H5'	53:v:104:ASN:HD22	1.77	0.49
53:v:108:LEU:HD12	64:AG:44:LEU:HD11	1.94	0.49
70:AM:31:SER:OG	70:AM:32:LYS:N	2.46	0.49
79:AV:34:LEU:HA	79:AV:44:SER:HA	1.94	0.49
81:AX:743:ILE:HA	81:AX:746:VAL:HG12	1.95	0.49
84:BA:167:VAL:HB	84:BA:181:ASN:HD21	1.77	0.49
1:1:276:U:O2	18:N:93:LYS:NZ	2.41	0.49
1:1:995:U:H2'	1:1:996:A:H8	1.77	0.49
1:1:1497:C:H2'	1:1:1498:A:H8	1.78	0.49
1:1:2703:A:H5''	1:1:2704:A:H5'	1.94	0.49
9:D:29:ASP:OD2	9:D:32:GLN:N	2.44	0.49
11:F:48:ASN:HA	11:F:51:TYR:HB2	1.94	0.49
31:a:28:HIS:CE1	31:a:32:ARG:HH21	2.31	0.49
45:o:46:LYS:HG2	45:o:54:THR:HG21	1.94	0.49
47:2:524:U:O4	72:AO:93:ARG:NH1	2.36	0.49
47:2:629:U:OP2	47:2:969:C:N4	2.46	0.49
47:2:1183:A:N6	63:AF:122:THR:O	2.46	0.49
47:2:1199:G:N2	47:2:1594:G:O2'	2.45	0.49
81:AX:818:ILE:HA	81:AX:821:ALA:HB3	1.95	0.49
1:1:21:G:OP2	3:4:36:G:N2	2.30	0.49
1:1:1255:C:H2'	1:1:1256:G:C8	2.45	0.49
1:1:1629:U:H5'	30:Z:112:LYS:HE2	1.93	0.49
1:1:2477:G:OP2	1:1:2481:G:N2	2.45	0.49
2:3:12:U:OP2	2:3:68:C:O2'	2.30	0.49
7:B:385:LYS:NZ	7:B:386:ASP:O	2.46	0.49
12:G:241:LYS:O	12:G:245:LYS:NZ	2.37	0.49
47:2:655:G:N1	47:2:679:U:C4	2.81	0.49
47:2:1169:G:N2	47:2:1575:G:N7	2.61	0.49
47:2:1272:U:O2	47:2:1438:G:O6	2.30	0.49
47:2:1605:G:H5''	64:AG:127:LYS:HB3	1.93	0.49
68:AK:58:LEU:HD21	68:AK:88:LYS:HE2	1.94	0.49
72:AO:102:LYS:HD3	72:AO:108:ARG:HH22	1.78	0.49
79:AV:292:LEU:HD13	79:AV:293:ALA:H	1.78	0.49
81:AX:728:VAL:HA	81:AX:773:PRO:HA	1.94	0.49
83:AZ:45:A:H4'	83:AZ:46:U:H5'	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1194:G:H2'	1:1:1195:A:C8	2.47	0.49
1:1:2196:C:H2'	1:1:2242:A:H61	1.78	0.49
5:P2:106:LEU:H	5:P2:142:ARG:HG2	1.77	0.49
6:A:205:ASN:OD1	6:A:205:ASN:N	2.45	0.49
47:2:130:C:O2'	47:2:136:C:O2	2.31	0.49
47:2:1568:C:O2'	66:AI:40:ARG:NH1	2.38	0.49
56:y:102:VAL:O	56:y:167:ALA:N	2.45	0.49
61:AD:19:SER:OG	61:AD:21:ASN:O	2.29	0.49
81:AX:662:SER:O	81:AX:666:ALA:CB	2.60	0.49
1:1:1261:G:H1'	1:1:1278:A:H61	1.78	0.49
1:1:1869:C:O3'	1:1:3077:A:O2'	2.30	0.49
1:1:2953:U:H2'	1:1:2954:U:H2'	1.94	0.49
7:B:37:ARG:HD2	7:B:186:GLY:HA2	1.94	0.49
13:H:22:SER:HA	17:M:8:LYS:HD2	1.94	0.49
47:2:630:A:H3'	47:2:631:G:H8	1.77	0.49
73:AP:41:ILE:HA	73:AP:75:LEU:HD23	1.94	0.49
75:AR:48:SER:O	75:AR:71:ALA:N	2.46	0.49
76:AS:19:THR:OG1	76:AS:27:GLN:NE2	2.45	0.49
1:1:673:U:H2'	1:1:674:G:H8	1.77	0.49
2:3:3:U:H2'	2:3:4:U:H6	1.77	0.49
9:D:211:LEU:HB3	9:D:219:PHE:HB2	1.95	0.49
17:M:68:LEU:HD21	17:M:93:LYS:HD2	1.94	0.49
47:2:459:G:OP2	72:AO:105:ARG:NH2	2.44	0.49
47:2:1350:U:C4	47:2:1376:C:N3	2.80	0.49
47:2:1770:U:H5	74:AQ:28:LYS:HE2	1.77	0.49
50:s:168:ARG:HB3	50:s:199:GLN:HB2	1.95	0.49
73:AP:59:TYR:HB3	73:AP:64:VAL:HG11	1.95	0.49
84:BA:52:SER:H	84:BA:157:PHE:HB2	1.76	0.49
1:1:1576:G:O2'	1:1:2560:C:N4	2.45	0.49
1:1:3118:C:O3'	43:m:106:ARG:NH1	2.46	0.49
18:N:84:PRO:HA	18:N:87:GLN:HB2	1.95	0.49
20:P:64:ASN:HB2	20:P:80:LYS:HD2	1.94	0.49
47:2:114:C:O2'	59:AB:65:SER:OG	2.30	0.49
47:2:463:U:O2'	47:2:526:A:N6	2.46	0.49
47:2:1413:U:OP1	53:v:80:LYS:NZ	2.42	0.49
81:AX:460:ASP:OD1	81:AX:460:ASP:N	2.45	0.49
82:AY:25:C:H2'	82:AY:26:G:H8	1.77	0.49
1:1:432:G:OP1	36:f:57:LYS:NZ	2.46	0.49
1:1:1079:A:O2'	9:D:140:ARG:O	2.28	0.49
1:1:2692:A:O2'	1:1:2707:C:OP1	2.31	0.49
1:1:2786:G:N2	31:a:58:MET:SD	2.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3192:U:H3	1:1:3200:G:H1	1.60	0.49
1:1:3353:G:O2'	1:1:3356:G:O4'	2.31	0.49
5:P2:54:LYS:HB2	5:P2:79:SER:HB2	1.95	0.49
14:I:48:LEU:HD11	14:I:167:LEU:HD11	1.94	0.49
16:L:77:LEU:HA	16:L:80:VAL:HG12	1.95	0.49
20:P:51:VAL:HG11	20:P:58:ILE:HG13	1.94	0.49
47:2:394:C:OP1	54:w:92:ARG:NH1	2.45	0.49
47:2:797:G:O3'	59:AB:69:LYS:NZ	2.45	0.49
47:2:822:U:H2'	47:2:823:G:C8	2.48	0.49
47:2:1499:G:O6	47:2:1508:U:O4	2.31	0.49
51:t:18:TYR:O	51:t:22:ASN:ND2	2.45	0.49
51:t:63:GLY:O	51:t:67:ASN:ND2	2.46	0.49
1:1:1561:G:O6	28:X:33:ARG:NH1	2.46	0.48
1:1:1799:A:H2'	1:1:1800:A:H8	1.78	0.48
1:1:2185:G:O2'	1:1:2314:U:OP2	2.31	0.48
1:1:2393:G:H4'	7:B:252:ILE:HG13	1.94	0.48
1:1:3123:A:O2'	13:H:40:HIS:ND1	2.44	0.48
47:2:555:A:N3	47:2:590:C:O2'	2.39	0.48
47:2:1391:A:N6	47:2:1412:G:O2'	2.45	0.48
52:u:100:ARG:HB3	52:u:112:HIS:HD2	1.77	0.48
57:z:49:LEU:HD21	57:z:100:LYS:HD2	1.94	0.48
63:AF:20:VAL:HG13	63:AF:25:LEU:HD23	1.95	0.48
73:AP:45:GLU:HG3	73:AP:46:LYS:HG2	1.94	0.48
76:AS:10:ALA:O	76:AS:54:LEU:N	2.46	0.48
1:1:3003:G:HO2'	7:B:92:TYR:HH	1.55	0.48
3:4:134:G:H2'	3:4:135:G:H8	1.78	0.48
11:F:64:GLN:HA	11:F:67:ARG:HB2	1.94	0.48
14:I:52:LEU:HD12	14:I:136:PHE:HD2	1.79	0.48
17:M:21:VAL:HG12	17:M:65:LEU:HB3	1.95	0.48
26:V:93:LEU:HB3	27:W:20:LEU:HG	1.95	0.48
47:2:146:U:C2	47:2:168:A:N7	2.81	0.48
55:x:27:LEU:HD12	55:x:38:LEU:HB3	1.94	0.48
81:AX:510:ARG:O	81:AX:514:SER:OG	2.29	0.48
84:BA:33:GLU:HB2	84:BA:63:MET:HG3	1.94	0.48
1:1:784:A:O2'	21:Q:65:SER:OG	2.30	0.48
1:1:1949:G:O6	1:1:2097:U:O2	2.31	0.48
1:1:2883:U:OP1	7:B:10:ARG:NH1	2.46	0.48
14:I:182:LEU:O	14:I:186:GLU:N	2.41	0.48
18:N:37:HIS:CE1	18:N:63:ARG:HD2	2.49	0.48
36:f:75:HIS:HD2	36:f:82:ARG:HD2	1.79	0.48
42:l:9:ILE:HG22	42:l:13:MET:HE3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:461:G:O3'	57:z:3:ARG:NH2	2.45	0.48
47:2:950:C:O2'	61:AD:101:HIS:ND1	2.45	0.48
51:t:167:PHE:O	51:t:190:ARG:N	2.46	0.48
60:AC:33:ARG:HH11	60:AC:36:LEU:HD11	1.78	0.48
68:AK:21:LYS:HA	68:AK:94:GLU:HG2	1.95	0.48
81:AX:179:ALA:O	81:AX:183:GLU:HB2	2.13	0.48
81:AX:669:TRP:HE3	81:AX:710:ARG:HH12	1.61	0.48
1:1:128:G:OP2	38:h:74:LYS:NZ	2.46	0.48
1:1:289:A:H2'	1:1:290:G:H8	1.77	0.48
1:1:1064:A:H61	1:1:1092:C:H2'	1.79	0.48
1:1:2117:A:N6	1:1:3064:U:O2'	2.46	0.48
13:H:73:SER:O	13:H:77:ASN:ND2	2.47	0.48
41:k:31:LEU:HA	41:k:37:PRO:HA	1.95	0.48
47:2:167:U:H1'	54:w:133:LEU:HD23	1.95	0.48
79:AV:20:VAL:O	79:AV:291:SER:OG	2.31	0.48
81:AX:30:HIS:HD2	81:AX:128:VAL:HG23	1.78	0.48
81:AX:407:SER:HB2	81:AX:433:ARG:HA	1.95	0.48
81:AX:508:LEU:HA	81:AX:511:LEU:HB2	1.95	0.48
1:1:583:G:O3'	36:f:106:ASN:ND2	2.47	0.48
1:1:1677:G:H1	1:1:1691:U:H3	1.61	0.48
9:D:201:GLY:HA3	9:D:240:TYR:HE2	1.78	0.48
14:I:75:TYR:O	14:I:78:THR:OG1	2.32	0.48
31:a:138:ILE:O	31:a:143:GLY:N	2.47	0.48
39:i:56:ARG:HH21	39:i:76:ARG:HH22	1.62	0.48
47:2:161:U:OP2	54:w:85:ARG:NH2	2.32	0.48
47:2:588:U:O2'	78:AU:57:ASN:ND2	2.42	0.48
72:AO:63:GLN:HB3	72:AO:68:LYS:HD3	1.95	0.48
73:AP:62:VAL:HG23	73:AP:77:ARG:HH11	1.78	0.48
1:1:30:G:OP1	18:N:172:ARG:NE	2.43	0.48
1:1:674:G:O6	21:Q:56:LYS:NZ	2.46	0.48
1:1:768:C:N4	1:1:769:G:O6	2.47	0.48
1:1:1019:G:N2	1:1:1034:U:O2'	2.32	0.48
1:1:2211:U:OP1	82:AY:3:G:O2'	2.32	0.48
1:1:3069:G:H2'	1:1:3070:A:H8	1.78	0.48
11:F:221:LYS:NZ	11:F:226:GLY:O	2.47	0.48
16:L:32:LYS:HA	16:L:35:ARG:HE	1.78	0.48
16:L:112:ASN:HA	16:L:115:ARG:HB3	1.94	0.48
21:Q:63:SER:OG	21:Q:90:ASP:OD2	2.30	0.48
35:e:84:THR:HG23	35:e:85:LEU:HG	1.95	0.48
47:2:368:U:O2	47:2:373:G:O6	2.32	0.48
47:2:412:A:H1'	47:2:422:G:H22	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1163:A:H1'	47:2:1614:A:H5'	1.93	0.48
48:q:129:ASP:HB3	48:q:132:ALA:HB3	1.96	0.48
51:t:202:LEU:O	51:t:204:ASP:N	2.44	0.48
54:w:33:GLY:N	54:w:52:ILE:O	2.46	0.48
54:w:90:GLY:N	54:w:91:GLU:HG3	2.27	0.48
1:1:733:G:O2'	1:1:735:A:N7	2.41	0.48
1:1:838:G:O6	1:1:855:U:O2	2.31	0.48
1:1:1257:C:H5''	4:P0:46:ARG:HD2	1.95	0.48
9:D:111:GLN:HA	9:D:116:ASP:HB2	1.95	0.48
14:I:36:LEU:HD11	14:I:73:ASN:HD22	1.79	0.48
15:J:161:SER:O	15:J:164:LYS:NZ	2.43	0.48
17:M:34:ALA:HB2	17:M:85:TRP:HZ3	1.79	0.48
19:O:127:LEU:HB2	23:S:156:VAL:HG12	1.96	0.48
47:2:64:U:HO2'	47:2:168:A:HO2'	1.59	0.48
47:2:884:A:H2'	47:2:885:G:H8	1.77	0.48
47:2:1170:G:C6	47:2:1469:A:N1	2.82	0.48
47:2:1255:G:H21	47:2:1256:A:N6	2.12	0.48
47:2:1268:G:N2	47:2:1447:C:O2	2.46	0.48
47:2:1336:A:H1'	64:AG:123:ARG:HB3	1.96	0.48
50:s:157:LYS:HD3	50:s:170:ILE:HD12	1.96	0.48
52:u:49:ARG:HB3	52:u:55:ALA:HB3	1.96	0.48
57:z:79:ARG:HA	57:z:82:ARG:HB2	1.95	0.48
61:AD:88:LEU:HD22	61:AD:129:TYR:HE2	1.77	0.48
68:AK:45:ALA:HA	68:AK:50:LEU:HD13	1.95	0.48
80:AW:130:VAL:HB	80:AW:142:GLY:HA3	1.95	0.48
1:1:70:A:N6	1:1:71:A:N1	2.61	0.48
1:1:1086:C:H1'	32:b:47:LEU:HD21	1.94	0.48
8:C:217:LYS:HA	8:C:220:ARG:HB2	1.95	0.48
33:c:10:ILE:HG22	33:c:13:LYS:HD2	1.96	0.48
47:2:142:G:H1	47:2:173:A:H2	0.77	0.48
47:2:197:A:H2'	47:2:198:A:H8	1.78	0.48
47:2:1192:C:H3'	47:2:1193:A:H2'	1.95	0.48
47:2:1316:G:H4'	65:AH:10:LYS:HE3	1.94	0.48
49:r:25:THR:HG23	49:r:26:ARG:HD3	1.95	0.48
53:v:215:ASP:O	53:v:219:ARG:N	2.47	0.48
54:w:122:GLU:HA	54:w:126:ASP:HB3	1.96	0.48
57:z:131:GLN:O	57:z:133:HIS:ND1	2.46	0.48
67:AJ:64:HIS:ND1	67:AJ:67:MET:SD	2.75	0.48
68:AK:78:THR:OG1	68:AK:80:GLU:OE2	2.31	0.48
73:AP:90:LYS:HD3	73:AP:91:PRO:HD2	1.95	0.48
81:AX:399:ARG:HA	81:AX:453:ILE:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:784:A:H2'	21:Q:69:ARG:HE	1.79	0.48
6:A:80:GLU:HA	6:A:170:ALA:HB2	1.96	0.48
50:s:156:THR:HB	70:AM:95:PRO:HB3	1.96	0.48
63:AF:87:PRO:HD3	63:AF:112:LEU:HD21	1.96	0.48
64:AG:100:GLN:HG3	79:AV:56:VAL:HG12	1.94	0.48
79:AV:27:ALA:H	79:AV:75:ALA:HA	1.79	0.48
1:1:75:G:H3'	1:1:76:G:H8	1.77	0.48
1:1:2629:U:O4	24:T:2:GLY:N	2.46	0.48
9:D:278:SER:OG	9:D:279:LYS:N	2.45	0.48
12:G:146:LYS:NZ	12:G:173:MET:O	2.34	0.48
16:L:6:ASN:HD21	21:Q:155:MET:HG3	1.78	0.48
19:O:37:ARG:HG2	19:O:107:GLY:HA2	1.96	0.48
29:Y:27:ARG:NH2	29:Y:76:LEU:O	2.46	0.48
37:g:76:TYR:HE2	37:g:80:ARG:HD2	1.79	0.48
46:p:84:ARG:HB3	46:p:87:ARG:HH21	1.77	0.48
47:2:593:U:O5'	57:z:38:ASN:ND2	2.46	0.48
47:2:898:A:N6	47:2:912:U:O4'	2.46	0.48
47:2:1335:U:C4	47:2:1416:G:O6	2.67	0.48
52:u:67:GLN:HB2	52:u:69:HIS:CD2	2.49	0.48
52:u:181:VAL:HG22	52:u:227:VAL:HG12	1.95	0.48
71:AN:75:GLN:NE2	71:AN:76:LEU:O	2.47	0.48
76:AS:29:ARG:NH2	76:AS:40:ILE:O	2.47	0.48
79:AV:295:SER:H	79:AV:298:GLY:HA2	1.79	0.48
81:AX:567:VAL:HG13	81:AX:592:PRO:HG3	1.95	0.48
1:1:266:A:N6	39:i:26:ILE:O	2.40	0.47
1:1:838:G:O6	46:p:4:ARG:NH2	2.47	0.47
1:1:3152:U:H5''	1:1:3293:U:H1'	1.95	0.47
6:A:225:ILE:HD13	6:A:234:LYS:HG2	1.96	0.47
7:B:102:LEU:HD12	7:B:155:ALA:HB2	1.96	0.47
16:L:46:ILE:HD12	16:L:49:ARG:HB2	1.95	0.47
19:O:166:GLU:O	19:O:170:LYS:NZ	2.42	0.47
25:U:41:ILE:HD13	25:U:54:VAL:HG21	1.95	0.47
46:p:51:ALA:HB3	46:p:54:ILE:HD12	1.95	0.47
47:2:1469:A:O2'	47:2:1540:G:N2	2.32	0.47
63:AF:37:ALA:O	63:AF:42:ARG:NH1	2.47	0.47
79:AV:91:LEU:HB3	79:AV:100:TYR:HB2	1.96	0.47
81:AX:365:ASN:HA	81:AX:369:ILE:HB	1.96	0.47
1:1:417:A:H2'	1:1:418:A:C8	2.49	0.47
1:1:450:G:N1	1:1:488:U:O5'	2.43	0.47
1:1:974:G:OP1	21:Q:16:ARG:NE	2.37	0.47
1:1:980:A:N6	1:1:1105:A:O2'	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1348:U:O2	1:1:1349:G:N2	2.47	0.47
1:1:1649:U:H2'	1:1:1650:G:H8	1.78	0.47
1:1:1670:C:O2'	1:1:1860:G:OP1	2.29	0.47
1:1:2895:G:O2'	43:m:100:TYR:O	2.32	0.47
1:1:3314:A:H2'	1:1:3315:G:C8	2.49	0.47
4:P0:60:ARG:NH1	4:P0:63:ILE:HD13	2.29	0.47
4:P0:105:VAL:HG11	4:P0:180:PRO:HA	1.96	0.47
8:C:31:ARG:HB2	8:C:34:ILE:HG22	1.96	0.47
47:2:126:A:N1	47:2:263:C:O2'	2.40	0.47
47:2:1545:A:N7	66:AI:134:ARG:NH2	2.62	0.47
57:z:35:GLY:HA3	57:z:123:HIS:NE2	2.29	0.47
69:AL:49:GLU:HB3	69:AL:50:TYR:H	1.56	0.47
72:AO:44:LEU:HD12	72:AO:55:VAL:HG11	1.96	0.47
1:1:116:A:OP1	18:N:2:GLY:N	2.48	0.47
1:1:411:U:H2'	1:1:412:G:H8	1.79	0.47
1:1:979:U:O2'	1:1:980:A:O4'	2.28	0.47
1:1:1155:C:O2'	1:1:1197:A:N1	2.43	0.47
1:1:1411:C:O2'	35:e:121:ASN:ND2	2.45	0.47
1:1:2250:G:O6	1:1:2266:U:O2	2.31	0.47
5:P2:133:LEU:HD23	5:P2:134:GLY:H	1.79	0.47
47:2:1253:U:H4'	80:AW:143:LYS:HD3	1.95	0.47
47:2:1350:U:N3	47:2:1376:C:C2	2.82	0.47
49:r:164:ILE:HD11	49:r:207:LEU:HD11	1.97	0.47
61:AD:147:SER:HA	61:AD:150:VAL:HG12	1.97	0.47
79:AV:210:LEU:HD22	79:AV:265:LEU:HD12	1.96	0.47
82:AY:61:C:H2'	82:AY:62:A:H8	1.79	0.47
1:1:281:G:O6	18:N:181:ASN:ND2	2.47	0.47
1:1:713:U:H5''	16:L:171:ARG:HH12	1.78	0.47
1:1:718:G:OP1	31:a:117:ARG:NH2	2.46	0.47
1:1:817:A:OP1	40:j:30:GLN:NE2	2.40	0.47
1:1:2173:U:O3'	6:A:193:ARG:NH2	2.38	0.47
1:1:3175:U:OP1	36:f:10:LYS:NZ	2.35	0.47
1:1:3186:A:O2'	13:H:23:ARG:NH1	2.47	0.47
1:1:3325:G:H2'	1:1:3326:G:H8	1.80	0.47
1:1:3334:U:H4'	1:1:3335:A:H5'	1.94	0.47
9:D:183:TRP:HZ2	9:D:188:GLU:HG3	1.79	0.47
20:P:84:PRO:HB2	20:P:87:SER:HB3	1.96	0.47
47:2:895:G:O3'	49:r:27:LYS:NZ	2.47	0.47
47:2:1483:A:OP1	47:2:1521:G:N2	2.40	0.47
49:r:122:GLU:O	49:r:165:ARG:NH1	2.47	0.47
53:v:92:ARG:NH2	53:v:169:ASN:OD1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AG:23:LYS:O	64:AG:64:ASP:N	2.48	0.47
81:AX:187:VAL:O	81:AX:191:THR:OG1	2.28	0.47
81:AX:279:ASP:HA	81:AX:282:PHE:HB2	1.97	0.47
1:1:219:A:O2'	1:1:220:G:N2	2.36	0.47
1:1:315:C:H5	39:i:28:TYR:HE1	1.61	0.47
1:1:1105:A:H2'	1:1:1106:G:C8	2.48	0.47
1:1:1390:A:H4'	1:1:1391:C:H5''	1.95	0.47
1:1:1862:U:O2	1:1:1868:G:O6	2.31	0.47
1:1:1921:A:N1	1:1:1922:A:N6	2.63	0.47
4:P0:8:LYS:HB2	4:P0:12:PHE:CE2	2.49	0.47
9:D:192:PRO:HA	9:D:195:LEU:HB3	1.96	0.47
9:D:197:SER:O	9:D:202:GLY:N	2.46	0.47
37:g:44:CYS:SG	37:g:47:CYS:N	2.73	0.47
47:2:558:U:H3	51:t:143:ARG:HH22	1.62	0.47
47:2:966:A:H2'	47:2:967:A:C8	2.49	0.47
47:2:1266:U:N3	47:2:1442:U:O4	2.47	0.47
50:s:148:LEU:HA	69:AL:4:ASP:HB2	1.96	0.47
71:AN:37:ALA:O	71:AN:41:SER:OG	2.32	0.47
79:AV:131:ILE:HG12	79:AV:151:VAL:HG11	1.96	0.47
81:AX:348:ALA:O	81:AX:352:ARG:CB	2.57	0.47
81:AX:542:LEU:HD13	81:AX:556:ILE:HD12	1.95	0.47
1:1:1064:A:N6	1:1:1096:U:O4	2.48	0.47
1:1:1325:U:H2'	1:1:1326:A:H8	1.80	0.47
1:1:1603:A:OP1	22:R:38:ARG:NH2	2.42	0.47
1:1:2344:U:H2'	1:1:2345:A:H8	1.79	0.47
2:3:28:C:H1'	2:3:55:A:H61	1.80	0.47
3:4:8:C:H2'	3:4:9:A:H8	1.79	0.47
3:4:94:C:H5''	40:j:76:ASN:HD21	1.78	0.47
4:P0:19:LEU:HG	4:P0:88:PHE:HZ	1.80	0.47
4:P0:170:ALA:O	4:P0:174:ASN:N	2.40	0.47
13:H:90:MET:HB3	13:H:144:ILE:HG23	1.95	0.47
44:n:7:LYS:HA	44:n:10:THR:HG22	1.97	0.47
47:2:222:A:N6	47:2:833:U:H3	2.11	0.47
47:2:1319:A:H3'	48:q:101:ARG:HH12	1.80	0.47
55:x:126:LEU:HD11	55:x:152:VAL:HG21	1.97	0.47
81:AX:30:HIS:CD2	81:AX:128:VAL:HG23	2.49	0.47
1:1:1277:C:H2'	1:1:1278:A:H8	1.79	0.47
1:1:1282:G:O4'	4:P0:83:ASN:ND2	2.48	0.47
1:1:2335:G:N2	1:1:2339:C:O2	2.47	0.47
1:1:2357:A:H2'	1:1:2358:A:C8	2.50	0.47
1:1:2828:G:OP1	14:I:7:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P0:58:MET:HA	4:P0:61:ARG:HD3	1.97	0.47
6:A:116:VAL:HG12	6:A:164:GLY:HA3	1.96	0.47
13:H:98:PRO:HD3	81:AX:167:LEU:HD13	1.95	0.47
14:I:54:SER:HA	14:I:163:GLN:HB2	1.97	0.47
15:J:26:SER:HB3	15:J:30:LEU:HB3	1.96	0.47
15:J:117:ASP:O	15:J:119:SER:N	2.48	0.47
21:Q:155:MET:HE1	21:Q:163:PRO:HG3	1.96	0.47
25:U:94:ARG:HB2	25:U:106:ALA:HB3	1.96	0.47
47:2:67:A:N6	47:2:83:G:O2'	2.47	0.47
47:2:89:G:H21	47:2:452:A:H5'	1.80	0.47
47:2:155:U:H4'	54:w:58:LYS:HD2	1.97	0.47
47:2:1352:G:O6	47:2:1373:C:N4	2.48	0.47
47:2:1387:G:H1'	47:2:1410:A:H61	1.78	0.47
47:2:1689:A:H61	47:2:1712:A:H2'	1.79	0.47
51:t:132:LYS:O	51:t:156:PHE:N	2.46	0.47
53:v:89:ILE:HA	53:v:92:ARG:HB2	1.96	0.47
53:v:136:ALA:O	53:v:140:THR:OG1	2.33	0.47
56:y:114:GLU:HG2	56:y:119:GLN:H	1.79	0.47
60:AC:32:LEU:HD13	60:AC:121:VAL:HG13	1.97	0.47
61:AD:23:PRO:HB2	61:AD:25:TRP:CD1	2.50	0.47
61:AD:30:SER:OG	61:AD:66:ILE:O	2.24	0.47
62:AE:16:VAL:HG12	62:AE:18:ARG:HB2	1.97	0.47
79:AV:73:LEU:HA	79:AV:80:ALA:HB2	1.96	0.47
79:AV:122:ILE:HD11	79:AV:136:ILE:HD13	1.97	0.47
79:AV:214:ALA:HB1	79:AV:218:GLY:HA2	1.96	0.47
81:AX:307:LEU:HD11	81:AX:323:VAL:HG23	1.96	0.47
82:AY:60:C:H5''	82:AY:61:C:H5	1.80	0.47
1:1:440:A:H8	1:1:441:U:H4'	1.79	0.47
1:1:520:U:OP2	11:F:70:LYS:NZ	2.44	0.47
1:1:798:G:O2'	16:L:14:PHE:O	2.32	0.47
1:1:2450:G:O6	1:1:2496:C:O2'	2.33	0.47
1:1:2960:C:H2'	1:1:2961:G:H8	1.78	0.47
8:C:260:GLN:HE22	8:C:267:VAL:HG11	1.80	0.47
15:J:37:LEU:O	15:J:41:SER:OG	2.30	0.47
44:n:5:TRP:NE1	47:2:1784:C:H41	2.11	0.47
47:2:776:G:O6	72:AO:11:LYS:NZ	2.37	0.47
47:2:861:U:O2'	70:AM:56:HIS:O	2.31	0.47
54:w:49:VAL:HB	54:w:114:VAL:HB	1.97	0.47
61:AD:145:THR:HG22	61:AD:148:ALA:HB3	1.97	0.47
72:AO:103:ALA:HB1	72:AO:107:GLN:HG2	1.96	0.47
1:1:149:U:OP2	18:N:49:ARG:NH2	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:151:A:H5''	1:1:152:U:H5	1.79	0.47
1:1:1238:C:H4'	5:P2:137:GLN:HE21	1.80	0.47
1:1:2779:A:O2'	16:L:180:ARG:NH2	2.48	0.47
1:1:2883:U:H3	1:1:2939:G:H1	1.62	0.47
1:1:3153:U:H4'	1:1:3154:C:H3'	1.95	0.47
2:3:56:A:H4'	15:J:152:HIS:HB2	1.96	0.47
8:C:298:ALA:HB1	21:Q:133:LYS:HE3	1.96	0.47
16:L:53:LEU:HD13	16:L:96:ALA:HB2	1.97	0.47
21:Q:177:GLY:O	21:Q:186:VAL:N	2.48	0.47
44:n:2:ARG:NH1	47:2:1772:C:OP2	2.48	0.47
47:2:1045:C:H2'	47:2:1046:G:H8	1.79	0.47
47:2:1097:U:O3'	50:s:168:ARG:NH2	2.47	0.47
55:x:7:LYS:O	55:x:42:GLN:NE2	2.48	0.47
56:y:104:ILE:HD12	56:y:105:ASP:H	1.78	0.47
79:AV:155:ARG:HD3	79:AV:203:THR:HA	1.97	0.47
81:AX:564:ARG:O	81:AX:725:GLN:CB	2.60	0.47
81:AX:601:ILE:HG22	81:AX:606:ILE:HD11	1.97	0.47
1:1:38:U:H2'	1:1:39:A:H8	1.79	0.47
1:1:159:A:H2'	1:1:160:G:H8	1.80	0.47
1:1:562:C:OP2	17:M:77:ARG:NE	2.48	0.47
1:1:692:A:OP1	18:N:201:ARG:NH2	2.48	0.47
1:1:1307:G:O4'	19:O:60:LYS:NZ	2.48	0.47
1:1:1310:G:H2'	1:1:1311:G:C8	2.50	0.47
1:1:2471:U:O2	1:1:2475:G:C6	2.68	0.47
1:1:3158:G:N1	1:1:3292:A:C2	2.75	0.47
3:4:59:A:O2'	28:X:61:LYS:NZ	2.33	0.47
3:4:83:C:H4'	3:4:84:C:H5''	1.96	0.47
6:A:247:ARG:NH2	47:2:1011:G:O2'	2.47	0.47
12:G:35:GLY:O	12:G:41:GLN:NE2	2.47	0.47
23:S:10:ILE:HD11	23:S:60:SER:HB3	1.97	0.47
47:2:560:U:H2'	47:2:561:G:C8	2.50	0.47
47:2:932:U:H4'	47:2:933:A:H5''	1.96	0.47
48:q:182:LEU:HB3	48:q:188:LEU:HB3	1.97	0.47
57:z:19:TYR:HA	57:z:23:ARG:HH21	1.80	0.47
81:AX:5:THR:O	81:AX:8:GLN:N	2.48	0.47
1:1:3243:A:H4'	7:B:95:THR:HG22	1.96	0.46
5:P2:64:ILE:H	5:P2:71:ALA:HB3	1.80	0.46
45:o:76:LYS:NZ	45:o:77:CYS:SG	2.87	0.46
48:q:41:ARG:HB2	48:q:47:VAL:HG23	1.97	0.46
48:q:41:ARG:HD2	48:q:42:PRO:HD2	1.97	0.46
48:q:84:ARG:NH1	65:AH:84:TYR:OH	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:t:78:LYS:NZ	58:AA:33:GLU:O	2.47	0.46
81:AX:588:LEU:HD11	81:AX:686:VAL:HB	1.98	0.46
81:AX:663:VAL:HA	81:AX:666:ALA:HB3	1.98	0.46
1:1:199:A:H5''	29:Y:60:ARG:HD2	1.96	0.46
1:1:1257:C:P	4:P0:46:ARG:HH11	2.37	0.46
1:1:2340:U:H2'	1:1:2341:A:C8	2.50	0.46
1:1:2471:U:O2	1:1:2475:G:O6	2.33	0.46
1:1:2945:G:O2'	1:1:2948:C:OP2	2.26	0.46
1:1:3052:G:H2'	1:1:3053:G:H8	1.80	0.46
1:1:3283:U:H2'	1:1:3284:G:H8	1.79	0.46
10:E:165:LEU:HD12	10:E:169:ASP:HB3	1.97	0.46
15:J:26:SER:OG	15:J:64:LYS:O	2.33	0.46
15:J:105:GLY:HA2	15:J:126:ASP:HA	1.98	0.46
17:M:13:ARG:HB3	17:M:19:ARG:HH12	1.80	0.46
27:W:47:ARG:HH21	27:W:58:HIS:HB3	1.80	0.46
47:2:29:U:H2'	47:2:30:G:H8	1.80	0.46
47:2:445:A:H2'	47:2:446:A:H8	1.81	0.46
47:2:887:A:H5''	62:AE:120:PRO:HB2	1.97	0.46
50:s:153:SER:OG	50:s:154:LEU:N	2.48	0.46
52:u:36:HIS:CE1	52:u:85:GLY:HA2	2.50	0.46
55:x:46:ILE:HD12	55:x:60:ILE:HG12	1.96	0.46
1:1:431:U:H2'	1:1:432:G:H8	1.80	0.46
1:1:2492:C:O2'	1:1:2493:U:O4'	2.33	0.46
1:1:2515:A:N6	1:1:2592:G:O2'	2.45	0.46
4:P0:5:ARG:HG2	4:P0:8:LYS:HE3	1.96	0.46
6:A:28:LYS:HB3	6:A:123:ARG:HB3	1.98	0.46
21:Q:81:VAL:HG13	21:Q:101:VAL:HG23	1.97	0.46
45:o:44:ASP:HA	45:o:47:GLN:HG3	1.97	0.46
47:2:953:G:H2'	47:2:954:G:C8	2.51	0.46
47:2:1344:A:O2'	68:AK:55:PRO:O	2.30	0.46
47:2:1588:G:O6	47:2:1608:U:O4	2.33	0.46
51:t:215:GLU:HB2	51:t:218:LEU:HD11	1.98	0.46
56:y:153:GLU:OE1	56:y:156:VAL:N	2.49	0.46
58:AA:32:HIS:HD2	58:AA:35:ILE:HB	1.80	0.46
1:1:1616:U:H2'	1:1:1617:G:C8	2.50	0.46
1:1:1660:C:H2'	1:1:1661:G:H8	1.80	0.46
1:1:1949:G:H5''	22:R:104:ARG:HH22	1.81	0.46
1:1:2181:C:OP1	6:A:192:LYS:NZ	2.45	0.46
1:1:2662:G:H2'	1:1:2663:G:H8	1.80	0.46
1:1:3023:U:H2'	1:1:3024:A:H8	1.80	0.46
1:1:3108:G:OP2	1:1:3120:C:N4	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3141:A:H3'	1:1:3142:A:H4'	1.97	0.46
3:4:91:C:H1'	29:Y:25:SER:HB3	1.96	0.46
15:J:97:SER:HG	15:J:101:ASN:H	1.61	0.46
21:Q:104:LEU:HB3	21:Q:124:LEU:HD23	1.97	0.46
26:V:21:ALA:HB3	26:V:36:ILE:HD12	1.97	0.46
47:2:322:G:O2'	56:y:10:LYS:NZ	2.49	0.46
47:2:1165:G:O2'	47:2:1166:A:O5'	2.29	0.46
47:2:1436:A:OP2	51:t:27:ARG:NH2	2.48	0.46
66:AI:124:GLY:O	66:AI:128:PHE:N	2.47	0.46
70:AM:30:SER:HB3	70:AM:61:ILE:HG12	1.97	0.46
79:AV:192:PHE:HZ	79:AV:228:LYS:HE3	1.81	0.46
81:AX:295:GLU:O	81:AX:299:LEU:HB3	2.16	0.46
81:AX:379:MET:HA	81:AX:469:LEU:O	2.16	0.46
84:BA:55:LEU:HG	84:BA:155:ILE:HG22	1.97	0.46
1:1:1447:G:O2'	1:1:2355:G:O6	2.32	0.46
1:1:1477:A:OP1	1:1:3075:G:O2'	2.34	0.46
1:1:1739:U:H3'	1:1:1740:U:H6	1.80	0.46
1:1:2154:U:H2'	1:1:2155:G:H8	1.81	0.46
1:1:2424:A:H61	6:A:230:VAL:HG11	1.80	0.46
8:C:92:ASN:N	8:C:92:ASN:OD1	2.47	0.46
13:H:91:ARG:HH11	43:m:82:LEU:HD11	1.80	0.46
22:R:170:ARG:HE	22:R:173:ARG:HG2	1.80	0.46
37:g:41:ARG:HG3	37:g:56:THR:HG22	1.97	0.46
47:2:174:U:O4	47:2:266:A:N7	2.49	0.46
47:2:340:U:H2'	47:2:341:A:C8	2.51	0.46
47:2:478:A:OP1	78:AU:33:ARG:NH1	2.46	0.46
47:2:698:U:H2'	47:2:699:U:C6	2.51	0.46
47:2:775:G:O6	47:2:785:U:O2	2.34	0.46
47:2:1714:A:H2'	47:2:1715:G:C8	2.49	0.46
47:2:1733:C:H2'	47:2:1734:U:H6	1.80	0.46
54:w:193:LEU:O	54:w:197:ASN:N	2.40	0.46
1:1:916:G:C6	6:A:207:VAL:HG21	2.51	0.46
1:1:1233:G:H5'	4:P0:39:HIS:CE1	2.51	0.46
1:1:1539:A:N7	1:1:1553:U:C2	2.84	0.46
1:1:3165:A:H61	1:1:3285:C:H42	1.64	0.46
1:1:3308:C:H3'	1:1:3309:G:H21	1.80	0.46
6:A:135:ILE:HB	6:A:149:ARG:HB3	1.98	0.46
28:X:57:LEU:HD11	28:X:89:LYS:HG3	1.97	0.46
42:l:43:ASN:HD22	42:l:44:TRP:H	1.64	0.46
47:2:890:C:H2'	47:2:891:A:H8	1.80	0.46
47:2:1164:G:HO2'	47:2:1612:U:HO2'	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:u:10:LYS:HA	52:u:27:TYR:HA	1.98	0.46
53:v:166:ARG:HE	53:v:170:GLN:HB2	1.80	0.46
63:AF:66:ALA:HB3	63:AF:74:ALA:HB2	1.97	0.46
65:AH:51:ALA:O	65:AH:55:THR:N	2.44	0.46
79:AV:68:VAL:HG13	79:AV:84:SER:HB2	1.97	0.46
1:1:733:G:N2	1:1:736:A:OP2	2.48	0.46
1:1:1660:C:H2'	1:1:1661:G:C8	2.50	0.46
10:E:62:THR:HG21	10:E:78:ARG:HD3	1.97	0.46
15:J:21:ILE:HD13	15:J:37:LEU:HD11	1.97	0.46
15:J:126:ASP:N	15:J:126:ASP:OD1	2.49	0.46
15:J:143:ARG:NH1	15:J:144:CYS:SG	2.88	0.46
40:j:70:VAL:HA	40:j:73:ARG:HB3	1.98	0.46
41:k:24:THR:HG22	41:k:76:ASN:HB3	1.97	0.46
47:2:636:A:O3'	70:AM:31:SER:OG	2.32	0.46
47:2:1046:G:H2'	47:2:1047:G:H8	1.80	0.46
47:2:1379:C:O2	64:AG:68:ARG:NH2	2.49	0.46
48:q:74:VAL:HG13	48:q:118:PRO:HB3	1.98	0.46
51:t:94:ARG:O	51:t:101:GLN:NE2	2.43	0.46
54:w:4:ASN:HB3	54:w:110:ALA:HA	1.97	0.46
1:1:300:G:H2'	1:1:301:G:H8	1.80	0.46
1:1:1149:G:H21	1:1:1199:C:N4	2.14	0.46
2:3:81:U:H3	2:3:99:G:H1	1.63	0.46
26:V:17:LEU:HD21	26:V:23:MET:HE1	1.97	0.46
30:Z:78:ASN:OD1	30:Z:78:ASN:N	2.44	0.46
47:2:738:G:H2'	47:2:739:G:H8	1.79	0.46
47:2:866:G:H2'	47:2:867:G:H8	1.80	0.46
47:2:1278:G:O6	47:2:1430:U:C4	2.69	0.46
64:AG:143:ARG:NH1	82:AY:35:A:OP1	2.49	0.46
67:AJ:132:LEU:HA	67:AJ:135:ILE:HG13	1.98	0.46
67:AJ:134:ARG:HA	67:AJ:137:ALA:HB3	1.96	0.46
84:BA:40:ASN:HB3	84:BA:163:LEU:HG	1.97	0.46
84:BA:60:ARG:HH22	84:BA:168:ALA:HB2	1.80	0.46
1:1:515:C:H2'	1:1:516:A:H8	1.80	0.46
1:1:1640:G:C6	1:1:1641:U:O4	2.69	0.46
1:1:1899:G:H21	1:1:2337:C:H42	1.63	0.46
1:1:2661:G:H2'	1:1:2662:G:C8	2.50	0.46
1:1:3121:U:H1'	1:1:3122:A:H5''	1.98	0.46
7:B:281:LYS:HB3	7:B:325:LYS:HB2	1.98	0.46
15:J:97:SER:OG	15:J:100:GLY:N	2.47	0.46
26:V:56:ASP:OD1	26:V:56:ASP:N	2.49	0.46
35:e:100:ILE:O	35:e:125:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:4:C:OP2	50:s:200:SER:OG	2.28	0.46
47:2:54:C:OP1	72:AO:113:ASN:ND2	2.47	0.46
47:2:657:U:O2'	47:2:677:G:N1	2.37	0.46
47:2:1213:G:N2	47:2:1450:U:O2	2.49	0.46
47:2:1332:C:H5''	65:AH:45:ARG:HH12	1.79	0.46
47:2:1473:U:H3	53:v:97:LEU:HD11	1.80	0.46
56:y:97:THR:HA	56:y:173:PRO:HG2	1.97	0.46
56:y:152:ILE:HG13	56:y:153:GLU:H	1.80	0.46
74:AQ:5:ARG:HB2	74:AQ:8:ASN:HA	1.96	0.46
1:1:19:U:H2'	1:1:20:A:C8	2.50	0.46
1:1:69:C:OP1	18:N:178:HIS:ND1	2.30	0.46
1:1:532:A:H61	1:1:560:G:H1	1.64	0.46
1:1:3190:C:H2'	1:1:3191:G:C8	2.51	0.46
1:1:3196:U:OP2	1:1:3197:G:N2	2.49	0.46
6:A:143:GLU:O	6:A:145:LYS:N	2.49	0.46
21:Q:127:LEU:O	21:Q:131:ALA:N	2.41	0.46
30:Z:87:LEU:HD13	30:Z:127:ASN:HD21	1.81	0.46
33:c:25:LEU:HD12	33:c:87:VAL:HG21	1.97	0.46
38:h:76:GLN:O	38:h:81:ARG:NH2	2.49	0.46
47:2:313:U:O4'	47:2:1118:G:N2	2.49	0.46
47:2:340:U:H2'	47:2:341:A:H8	1.81	0.46
47:2:554:C:N4	47:2:571:G:O6	2.49	0.46
47:2:1613:U:H2'	47:2:1614:A:H8	1.81	0.46
65:AH:73:LEU:O	65:AH:77:GLU:N	2.39	0.46
1:1:143:G:H2'	1:1:144:A:H8	1.80	0.45
1:1:316:U:O2'	39:i:30:LYS:NZ	2.41	0.45
1:1:400:G:OP1	1:1:403:C:O2'	2.34	0.45
1:1:568:G:H2'	1:1:569:A:C8	2.51	0.45
1:1:2175:U:O4	6:A:20:THR:OG1	2.34	0.45
1:1:2213:A:H2'	1:1:2214:A:H8	1.80	0.45
1:1:2467:G:N2	1:1:2487:U:OP2	2.48	0.45
17:M:15:VAL:HA	17:M:19:ARG:HG3	1.98	0.45
34:d:46:THR:OG1	34:d:89:LEU:O	2.31	0.45
47:2:716:C:H5	47:2:723:G:H21	1.65	0.45
47:2:843:U:H2'	47:2:844:A:C8	2.50	0.45
47:2:1182:U:H5'	63:AF:124:THR:HG21	1.99	0.45
47:2:1642:G:N3	47:2:1781:A:O2'	2.49	0.45
54:w:29:ASP:HA	54:w:101:ILE:HG13	1.98	0.45
57:z:108:ARG:HH21	57:z:144:PRO:HB2	1.82	0.45
81:AX:571:SER:HB3	81:AX:589:LYS:HD2	1.97	0.45
81:AX:581:ASN:O	81:AX:582:LYS:HB3	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:345:G:N1	1:1:349:A:OP2	2.38	0.45
1:1:683:U:OP2	16:L:28:GLN:NE2	2.47	0.45
1:1:737:G:H2'	1:1:738:A:H8	1.81	0.45
1:1:2217:U:H2'	1:1:2218:G:H8	1.80	0.45
1:1:2486:A:N7	84:BA:101:LYS:NZ	2.64	0.45
1:1:2769:A:H5''	45:o:80:ARG:HD3	1.97	0.45
1:1:3237:U:H1'	1:1:3251:U:H1'	1.97	0.45
10:E:30:LEU:HD13	10:E:34:LEU:HD12	1.97	0.45
13:H:115:ARG:HE	13:H:123:ILE:HD12	1.81	0.45
16:L:35:ARG:O	16:L:39:ARG:NE	2.50	0.45
27:W:13:ILE:HG22	27:W:32:GLN:HG2	1.99	0.45
28:X:132:ALA:O	28:X:136:ALA:N	2.46	0.45
31:a:99:ALA:HB1	31:a:123:VAL:HA	1.98	0.45
37:g:99:LYS:O	37:g:103:LYS:NZ	2.48	0.45
47:2:384:G:O3'	56:y:22:ARG:NH1	2.47	0.45
47:2:650:U:H2'	47:2:651:G:H8	1.81	0.45
49:r:35:PRO:HD3	49:r:98:THR:HG23	1.99	0.45
49:r:39:GLU:HB3	49:r:74:GLN:HA	1.98	0.45
54:w:187:LYS:HE3	54:w:191:ARG:HE	1.80	0.45
55:x:9:LEU:HD11	55:x:21:ALA:HB2	1.97	0.45
69:AL:15:ARG:HH12	69:AL:33:GLN:HB2	1.81	0.45
79:AV:12:THR:HG23	79:AV:309:VAL:HG13	1.97	0.45
81:AX:288:ILE:HD11	81:AX:319:LEU:HD21	1.98	0.45
81:AX:472:SER:OG	81:AX:473:GLU:N	2.50	0.45
82:AY:54:U:O2'	84:BA:48:ARG:NH2	2.50	0.45
1:1:597:G:H4'	11:F:41:ARG:HH12	1.81	0.45
1:1:631:U:H2'	1:1:632:G:C8	2.51	0.45
1:1:673:U:H2'	1:1:674:G:C8	2.51	0.45
1:1:684:G:H5''	16:L:35:ARG:HH22	1.82	0.45
1:1:993:G:N2	1:1:1056:U:O4	2.43	0.45
1:1:1630:U:H5'	30:Z:67:LYS:HE2	1.98	0.45
3:4:43:A:H2'	3:4:44:A:H8	1.81	0.45
7:B:136:LYS:HB3	7:B:143:GLY:HA3	1.98	0.45
17:M:28:SER:O	17:M:31:LYS:NZ	2.43	0.45
18:N:15:GLN:HG2	39:i:51:SER:HB2	1.99	0.45
47:2:139:C:N3	47:2:176:C:N4	2.61	0.45
47:2:223:U:O2	47:2:838:G:N2	2.40	0.45
47:2:1504:G:N3	47:2:1563:C:O2'	2.49	0.45
47:2:1552:U:O2'	47:2:1597:A:N3	2.41	0.45
56:y:10:LYS:O	56:y:18:ARG:NH2	2.42	0.45
56:y:84:HIS:HB2	56:y:90:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:AN:41:SER:O	71:AN:43:PHE:N	2.47	0.45
77:AT:13:ARG:HD3	77:AT:14:TYR:HB3	1.99	0.45
1:1:1084:A:H2'	1:1:1085:A:C8	2.51	0.45
1:1:1476:G:O6	1:1:1877:U:O4	2.33	0.45
1:1:2528:G:OP1	12:G:248:LYS:NZ	2.45	0.45
1:1:2793:G:H3'	82:AY:76:A:H62	1.81	0.45
1:1:3005:A:N1	1:1:3140:G:O2'	2.46	0.45
8:C:188:ARG:NH1	8:C:197:ARG:HB3	2.32	0.45
9:D:60:ILE:H	9:D:80:SER:HB3	1.81	0.45
24:T:79:MET:HG2	24:T:84:TYR:CE1	2.52	0.45
47:2:568:G:N7	71:AN:69:ARG:NH1	2.64	0.45
47:2:789:A:O2'	52:u:106:LYS:NZ	2.46	0.45
47:2:1609:U:H5''	64:AG:75:VAL:HG23	1.98	0.45
50:s:165:VAL:HG21	50:s:210:THR:HG22	1.98	0.45
51:t:78:LYS:HZ2	58:AA:33:GLU:HB2	1.80	0.45
52:u:191:ARG:NE	52:u:244:ILE:O	2.44	0.45
59:AB:101:GLU:HB2	71:AN:12:ALA:HB3	1.98	0.45
60:AC:76:GLU:O	60:AC:80:ASN:N	2.49	0.45
64:AG:4:VAL:HG22	64:AG:23:LYS:HB2	1.98	0.45
76:AS:46:GLY:HA3	76:AS:47:PRO:HD3	1.71	0.45
79:AV:157:VAL:HG22	79:AV:204:ALA:HB3	1.98	0.45
80:AW:122:SER:O	80:AW:148:TYR:OH	2.34	0.45
81:AX:6:VAL:HA	81:AX:7:ASP:HA	1.59	0.45
1:1:612:U:H2'	1:1:613:G:C8	2.51	0.45
1:1:1306:G:N2	1:1:1307:G:N7	2.65	0.45
1:1:1381:A:H2'	1:1:1382:G:H8	1.80	0.45
2:3:64:A:H5'	2:3:65:G:H5''	1.98	0.45
11:F:96:PRO:HB2	11:F:99:PRO:HD2	1.97	0.45
25:U:42:LYS:NZ	25:U:45:GLY:O	2.41	0.45
26:V:128:ARG:NH1	26:V:132:ASN:OD1	2.50	0.45
37:g:72:VAL:HG13	37:g:74:ARG:H	1.81	0.45
40:j:76:ASN:HB3	40:j:79:GLN:HE22	1.82	0.45
47:2:694:U:O2'	47:2:695:U:H5'	2.16	0.45
47:2:713:A:H2'	47:2:714:G:C8	2.51	0.45
47:2:731:C:OP1	47:2:732:G:N2	2.49	0.45
62:AE:78:ALA:HA	62:AE:111:ARG:HB2	1.99	0.45
71:AN:17:VAL:HG23	71:AN:20:ARG:HH12	1.81	0.45
80:AW:132:LEU:HB3	80:AW:139:LEU:HD23	1.98	0.45
81:AX:627:VAL:O	81:AX:631:ARG:NH1	2.50	0.45
84:BA:29:LEU:HB2	84:BA:210:MET:HE1	1.99	0.45
1:1:334:A:H2'	1:1:335:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:389:A:OP1	20:P:4:TYR:OH	2.32	0.45
1:1:584:G:H2'	1:1:585:A:H8	1.81	0.45
1:1:708:G:O2'	1:1:710:A:N7	2.41	0.45
1:1:1073:U:H1'	32:b:50:THR:HB	1.98	0.45
1:1:1295:G:O2'	23:S:115:ARG:NH1	2.50	0.45
1:1:1388:U:O2'	35:e:99:ASN:O	2.29	0.45
1:1:1475:A:H4'	34:d:57:GLN:HG3	1.99	0.45
1:1:2218:G:H2'	1:1:2219:A:H8	1.82	0.45
1:1:2515:A:H5''	18:N:28:TRP:CD1	2.51	0.45
2:3:96:U:H2'	2:3:97:A:H8	1.81	0.45
3:4:64:U:H2'	3:4:65:A:H8	1.81	0.45
3:4:151:C:O2'	3:4:153:U:OP2	2.33	0.45
12:G:101:THR:OG1	12:G:104:GLU:OE1	2.26	0.45
12:G:128:LYS:NZ	12:G:130:TYR:OH	2.50	0.45
15:J:32:ARG:HD2	15:J:121:GLY:HA3	1.99	0.45
26:V:23:MET:HB3	26:V:34:LEU:HB2	1.99	0.45
33:c:92:ILE:HD11	33:c:101:LEU:HD21	1.99	0.45
34:d:72:ARG:HG3	34:d:96:VAL:HG21	1.98	0.45
44:n:10:THR:HA	44:n:13:LEU:HD22	1.99	0.45
47:2:29:U:H2'	47:2:30:G:C8	2.52	0.45
47:2:416:A:O2'	47:2:418:G:N7	2.50	0.45
47:2:896:U:O2	62:AE:41:ARG:NH1	2.50	0.45
47:2:1797:A:O2'	74:AQ:95:ARG:O	2.33	0.45
50:s:183:ALA:HB1	50:s:211:LEU:HD11	1.97	0.45
58:AA:43:ILE:HG23	58:AA:47:GLN:HE22	1.81	0.45
61:AD:70:LYS:HG3	61:AD:73:ARG:HH21	1.81	0.45
66:AI:62:THR:OG1	66:AI:63:GLN:OE1	2.34	0.45
74:AQ:84:VAL:HG13	74:AQ:85:ARG:H	1.81	0.45
81:AX:27:HIS:CD2	81:AX:28:VAL:HG22	2.52	0.45
81:AX:308:LYS:O	81:AX:311:GLU:HB2	2.17	0.45
81:AX:538:LEU:HD12	81:AX:539:GLU:HG2	1.99	0.45
1:1:47:C:H3'	1:1:48:A:H8	1.81	0.45
1:1:316:U:H5	39:i:27:SER:HB2	1.82	0.45
1:1:694:C:OP2	8:C:118:LYS:NZ	2.41	0.45
1:1:2155:G:H2'	1:1:2156:C:C6	2.52	0.45
1:1:2986:U:H2'	1:1:2987:A:H8	1.81	0.45
1:1:3008:A:H2'	1:1:3009:G:H8	1.82	0.45
2:3:16:U:H2'	2:3:17:A:C8	2.52	0.45
2:3:108:A:H2'	2:3:109:G:H8	1.82	0.45
8:C:22:LEU:HA	8:C:23:PRO:HD3	1.82	0.45
16:L:75:PHE:HE1	16:L:112:ASN:HB2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:T:54:HIS:CE1	24:T:55:LYS:HG2	2.52	0.45
33:c:16:LEU:HB2	33:c:19:LYS:HE3	1.99	0.45
47:2:107:C:H2'	47:2:108:A:H8	1.81	0.45
47:2:300:A:H2'	47:2:301:A:H8	1.82	0.45
49:r:103:MET:HE2	49:r:188:LEU:HD11	1.98	0.45
55:x:60:ILE:H	55:x:92:PHE:HB2	1.82	0.45
56:y:45:SER:HB3	56:y:53:LYS:HD2	1.98	0.45
56:y:154:SER:O	56:y:158:SER:N	2.47	0.45
57:z:182:GLU:HA	57:z:186:GLU:HA	1.98	0.45
63:AF:15:HIS:CE1	63:AF:22:LEU:HB3	2.51	0.45
79:AV:87:LYS:HB3	79:AV:106:HIS:H	1.82	0.45
82:AY:28:C:H2'	82:AY:29:A:C8	2.52	0.45
1:1:1112:A:OP1	16:L:5:LYS:NZ	2.40	0.45
2:3:19:C:H2'	2:3:20:A:H8	1.81	0.45
2:3:64:A:H62	14:I:209:ASN:HD21	1.63	0.45
12:G:165:PHE:HZ	18:N:3:ALA:HB1	1.80	0.45
18:N:73:ARG:HG2	18:N:89:VAL:HG23	1.98	0.45
19:O:36:VAL:HB	19:O:108:ILE:HG13	1.98	0.45
29:Y:51:ARG:HG2	29:Y:52:ARG:H	1.82	0.45
38:h:13:SER:H	38:h:16:GLN:NE2	2.15	0.45
47:2:96:G:N2	47:2:387:A:N1	2.61	0.45
47:2:126:A:N6	47:2:291:G:H21	2.07	0.45
47:2:388:G:OP1	47:2:423:G:O2'	2.32	0.45
47:2:628:G:N2	47:2:971:A:H62	2.14	0.45
47:2:890:C:H2'	47:2:891:A:C8	2.51	0.45
51:t:95:GLY:HA3	51:t:126:VAL:HB	1.99	0.45
52:u:195:ILE:HD12	52:u:195:ILE:HA	1.88	0.45
61:AD:52:VAL:HG23	61:AD:55:ARG:HH21	1.82	0.45
64:AG:98:ASP:OD1	79:AV:59:ARG:NH1	2.49	0.45
72:AO:21:LYS:HB3	72:AO:75:VAL:HG13	1.99	0.45
1:1:981:U:H2'	1:1:982:C:C6	2.51	0.45
1:1:1724:U:O4	22:R:125:LYS:NZ	2.50	0.45
1:1:2488:A:C5	1:1:2489:C:H1'	2.52	0.45
2:3:38:U:O2'	2:3:42:A:N6	2.46	0.45
18:N:26:ARG:NH2	18:N:43:THR:HB	2.32	0.45
30:Z:47:GLU:HG2	30:Z:71:PHE:HB3	1.98	0.45
39:i:87:VAL:O	39:i:91:ASN:N	2.43	0.45
45:o:8:ARG:HA	45:o:8:ARG:HD2	1.82	0.45
47:2:487:G:H2'	47:2:488:G:H5''	1.98	0.45
49:r:103:MET:HB3	49:r:215:VAL:HG12	1.99	0.45
51:t:40:ARG:HD2	68:AK:110:PRO:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:t:126:VAL:HG13	51:t:131:ALA:HB2	1.98	0.45
52:u:250:GLU:O	52:u:254:ARG:N	2.45	0.45
79:AV:24:ALA:HB3	79:AV:33:LEU:HD22	1.99	0.45
79:AV:231:MET:HE1	79:AV:266:ASP:HA	1.98	0.45
81:AX:395:TYR:CG	81:AX:457:VAL:HG12	2.51	0.45
1:1:289:A:H2'	1:1:290:G:C8	2.52	0.45
1:1:2462:A:N1	1:1:2494:A:O2'	2.43	0.45
1:1:3049:A:O2'	7:B:364:LYS:NZ	2.50	0.45
11:F:121:LYS:HD3	24:T:133:ALA:HB3	1.99	0.45
23:S:5:LYS:N	23:S:31:ALA:O	2.49	0.45
31:a:95:SER:OG	31:a:97:GLU:O	2.33	0.45
47:2:868:G:H1	47:2:960:U:H3	1.64	0.45
50:s:102:VAL:O	50:s:114:GLY:N	2.49	0.45
50:s:241:ASP:HA	50:s:244:SER:HB2	1.98	0.45
51:t:124:ARG:HA	51:t:127:MET:HB2	1.98	0.45
51:t:204:ASP:OD1	51:t:205:ALA:N	2.49	0.45
55:x:15:GLU:O	55:x:19:GLN:N	2.48	0.45
63:AF:118:GLU:O	66:AI:122:HIS:N	2.45	0.45
66:AI:101:LEU:HB2	66:AI:104:ASN:HB3	1.98	0.45
75:AR:19:HIS:HB3	75:AR:22:LYS:HG2	1.99	0.45
79:AV:224:ASN:HB3	79:AV:228:LYS:H	1.82	0.45
81:AX:711:ARG:O	81:AX:715:ALA:HB3	2.17	0.45
2:3:42:A:O4'	15:J:72:ARG:NH1	2.42	0.44
47:2:16:G:H21	47:2:1138:A:H62	1.64	0.44
47:2:460:A:H3'	47:2:461:G:H8	1.82	0.44
48:q:88:LYS:HB3	48:q:202:TYR:HE1	1.83	0.44
49:r:197:ILE:HG21	49:r:210:ILE:HD13	1.98	0.44
50:s:45:VAL:HG11	50:s:68:ILE:HG12	1.99	0.44
79:AV:87:LYS:HA	79:AV:110:VAL:HG22	1.99	0.44
1:1:806:A:N3	1:1:2812:C:O2'	2.47	0.44
1:1:2290:C:H2'	1:1:2291:A:C8	2.51	0.44
8:C:128:ALA:HB1	8:C:244:LEU:HB3	1.99	0.44
8:C:286:VAL:HA	8:C:289:ILE:HG22	1.99	0.44
47:2:10:G:H1	47:2:1144:U:H3	1.64	0.44
47:2:472:U:H5''	57:z:11:THR:HG22	2.00	0.44
47:2:905:A:N6	47:2:906:A:N1	2.64	0.44
47:2:1170:G:N1	47:2:1469:A:H2	2.08	0.44
47:2:1542:G:H3'	67:AJ:87:GLY:HA2	1.98	0.44
47:2:1662:G:H2'	47:2:1663:G:H8	1.82	0.44
54:w:57:ASP:OD1	54:w:61:PHE:N	2.49	0.44
55:x:69:GLY:HA2	55:x:72:LYS:HE2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AG:31:VAL:HB	64:AG:34:SER:HB3	1.98	0.44
81:AX:636:PHE:HB3	81:AX:645:LEU:HD13	1.98	0.44
1:1:348:A:N3	1:1:352:A:O2'	2.45	0.44
1:1:682:U:O2'	16:L:28:GLN:NE2	2.50	0.44
1:1:1234:G:H21	5:P2:132:ILE:HA	1.82	0.44
1:1:2898:G:N7	43:m:125:LYS:NZ	2.66	0.44
15:J:139:THR:HG23	15:J:140:ARG:HE	1.82	0.44
34:d:44:MET:SD	34:d:44:MET:N	2.90	0.44
44:n:20:VAL:O	44:n:24:SER:OG	2.27	0.44
47:2:1333:C:H2'	47:2:1334:U:H6	1.82	0.44
51:t:159:HIS:HA	51:t:160:SER:HA	1.89	0.44
58:AA:8:ARG:HE	58:AA:45:ALA:HB3	1.83	0.44
61:AD:92:ILE:HG22	61:AD:122:ILE:HD12	1.99	0.44
76:AS:13:ILE:HG22	76:AS:14:LYS:HG2	1.99	0.44
1:1:34:A:H5'	18:N:86:ASN:HD21	1.82	0.44
1:1:908:G:N2	1:1:2609:A:OP1	2.50	0.44
1:1:1497:C:H2'	1:1:1498:A:C8	2.53	0.44
1:1:1596:C:OP2	1:1:1606:U:N3	2.43	0.44
1:1:1748:G:OP2	41:k:42:LYS:NZ	2.41	0.44
1:1:3349:C:OP2	1:1:3350:C:N4	2.50	0.44
3:4:13:A:O2'	20:P:121:GLN:O	2.34	0.44
30:Z:54:THR:HG22	30:Z:57:HIS:CE1	2.52	0.44
41:k:8:ILE:HA	41:k:11:PHE:HB3	1.98	0.44
47:2:153:G:H2'	47:2:154:G:C8	2.52	0.44
47:2:1257:U:H2'	58:AA:2:LEU:HD12	1.98	0.44
47:2:1404:C:H2'	47:2:1405:G:C8	2.53	0.44
52:u:88:ASP:HA	52:u:122:LYS:HE3	1.99	0.44
71:AN:72:VAL:O	71:AN:84:THR:OG1	2.26	0.44
79:AV:129:LYS:HA	79:AV:151:VAL:HG23	1.99	0.44
79:AV:274:LEU:HD12	79:AV:276:PRO:HD3	2.00	0.44
81:AX:295:GLU:HB2	81:AX:299:LEU:HB2	2.00	0.44
81:AX:568:GLU:HG2	81:AX:569:SER:H	1.83	0.44
1:1:1649:U:H2'	1:1:1650:G:C8	2.53	0.44
6:A:32:LEU:HD13	6:A:163:ARG:HD3	2.00	0.44
8:C:159:ILE:HD12	8:C:159:ILE:HA	1.86	0.44
11:F:89:ILE:HD11	11:F:229:PHE:HB3	1.98	0.44
12:G:33:ASN:ND2	12:G:38:GLN:HE21	2.16	0.44
46:p:19:GLY:O	46:p:23:ARG:NE	2.50	0.44
47:2:1617:U:O2'	76:AS:21:SER:O	2.33	0.44
63:AF:96:ILE:HD12	63:AF:119:PHE:HB2	2.00	0.44
72:AO:15:ASN:HD22	72:AO:20:ARG:HE	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:AO:41:ARG:NH1	72:AO:53:ASP:OD1	2.50	0.44
84:BA:60:ARG:HH12	84:BA:172:VAL:HG21	1.83	0.44
84:BA:77:ALA:HA	84:BA:80:CYS:HB2	1.99	0.44
1:1:2682:C:H5''	15:J:68:HIS:CE1	2.52	0.44
8:C:230:VAL:HG11	8:C:254:ALA:HB1	1.99	0.44
12:G:240:ASN:OD1	12:G:240:ASN:N	2.51	0.44
32:b:56:ALA:HA	32:b:59:LYS:HE3	2.00	0.44
47:2:178:U:N3	54:w:191:ARG:O	2.39	0.44
47:2:600:U:H2'	47:2:601:A:C8	2.53	0.44
47:2:1388:A:OP1	47:2:1388:A:C8	2.70	0.44
48:q:62:ARG:NH1	69:AL:39:VAL:HG22	2.33	0.44
52:u:18:TRP:HB3	52:u:20:LEU:HD13	1.99	0.44
1:1:884:A:OP2	1:1:2139:A:N6	2.51	0.44
1:1:1321:G:H21	23:S:112:ALA:HB2	1.83	0.44
1:1:2338:C:H3'	1:1:2339:C:H2'	1.99	0.44
1:1:3185:U:HO2'	23:S:170:THR:HG1	1.63	0.44
2:3:13:A:OP2	2:3:67:G:N2	2.46	0.44
4:P0:22:TYR:CG	4:P0:88:PHE:HB3	2.52	0.44
9:D:88:ILE:HD11	9:D:243:ALA:HB2	2.00	0.44
15:J:48:SER:OG	15:J:49:LYS:N	2.49	0.44
19:O:37:ARG:HG3	19:O:108:ILE:HD12	2.00	0.44
29:Y:106:ILE:HD12	29:Y:109:LEU:HD21	1.99	0.44
35:e:112:ALA:HB1	35:e:117:ILE:HB	2.00	0.44
47:2:1148:C:H2'	47:2:1149:G:C8	2.53	0.44
48:q:22:THR:HG21	48:q:172:LEU:HD11	2.00	0.44
52:u:11:ARG:NH1	52:u:21:ASP:O	2.51	0.44
56:y:62:THR:HA	56:y:77:ARG:HA	2.00	0.44
61:AD:41:ALA:HA	61:AD:45:LEU:HD22	1.99	0.44
62:AE:86:THR:OG1	62:AE:92:LYS:N	2.51	0.44
66:AI:52:VAL:HG21	66:AI:69:ILE:HD11	1.98	0.44
79:AV:129:LYS:HB3	79:AV:150:TRP:HD1	1.83	0.44
81:AX:285:PHE:HA	81:AX:288:ILE:HG22	1.99	0.44
1:1:158:G:H2'	1:1:159:A:C8	2.53	0.44
1:1:521:A:N6	1:1:572:A:N3	2.65	0.44
1:1:700:C:H2'	1:1:701:G:C8	2.52	0.44
1:1:1722:U:OP2	22:R:103:ARG:NH1	2.50	0.44
1:1:1900:A:H61	1:1:1908:A:H61	1.66	0.44
1:1:1915:A:H5'	22:R:84:THR:HG22	2.00	0.44
1:1:2789:U:OP1	21:Q:179:ARG:NH1	2.51	0.44
2:3:40:C:O2	15:J:72:ARG:NH2	2.51	0.44
3:4:131:A:H2'	3:4:132:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:84:THR:HG1	46:p:63:THR:HG1	1.66	0.44
7:B:88:GLY:HA2	7:B:199:PHE:HE1	1.82	0.44
12:G:47:SER:HB3	28:X:27:ARG:H	1.82	0.44
12:G:94:PHE:HB2	12:G:189:LEU:HD11	2.00	0.44
13:H:129:ARG:HH22	13:H:156:GLN:HB3	1.82	0.44
14:I:208:ASN:O	14:I:212:GLU:N	2.48	0.44
17:M:17:VAL:HG13	17:M:36:VAL:HA	2.00	0.44
22:R:179:GLU:O	22:R:183:ALA:N	2.37	0.44
47:2:472:U:H2'	47:2:473:A:H8	1.82	0.44
47:2:884:A:H2'	47:2:885:G:C8	2.53	0.44
47:2:1241:G:O6	47:2:1451:C:O2'	2.28	0.44
56:y:67:TRP:HZ3	56:y:70:GLU:HB3	1.83	0.44
56:y:142:LYS:O	56:y:146:ARG:NE	2.38	0.44
68:AK:58:LEU:HD22	68:AK:90:TYR:H	1.83	0.44
76:AS:31:GLU:HB3	76:AS:39:THR:HB	2.00	0.44
1:1:768:C:H2'	1:1:769:G:H8	1.82	0.44
1:1:916:G:O4'	6:A:205:ASN:ND2	2.51	0.44
1:1:1039:U:H2'	1:1:1040:A:C8	2.53	0.44
1:1:2213:A:H2'	1:1:2214:A:C8	2.53	0.44
1:1:2746:A:H4'	9:D:176:SER:HB2	1.98	0.44
1:1:3287:U:H2'	1:1:3288:G:H8	1.82	0.44
5:P2:114:ARG:NH2	5:P2:124:THR:O	2.51	0.44
7:B:115:LYS:HE3	7:B:129:ALA:HB3	2.00	0.44
8:C:153:SER:OG	8:C:154:THR:N	2.50	0.44
8:C:193:LYS:HE3	8:C:193:LYS:HB2	1.78	0.44
14:I:159:PHE:HB2	14:I:163:GLN:HE22	1.83	0.44
17:M:22:LEU:HB3	17:M:64:VAL:HG23	1.99	0.44
20:P:178:ALA:HB2	20:P:181:ARG:HH11	1.82	0.44
47:2:551:G:H2'	47:2:552:G:H8	1.82	0.44
47:2:713:A:H2'	47:2:714:G:H8	1.83	0.44
47:2:1173:C:H2'	47:2:1174:C:H6	1.83	0.44
47:2:1623:C:H2'	47:2:1624:C:C6	2.52	0.44
49:r:138:PHE:HD2	49:r:214:LYS:HB3	1.83	0.44
61:AD:46:THR:HA	61:AD:47:PRO:HD3	1.89	0.44
62:AE:117:ASP:HB2	62:AE:119:THR:HG23	2.00	0.44
66:AI:88:ARG:NH2	66:AI:112:ASP:OD2	2.50	0.44
81:AX:369:ILE:HG23	81:AX:402:ALA:HB2	1.99	0.44
81:AX:495:VAL:HG21	81:AX:503:LYS:HE2	2.00	0.44
81:AX:816:GLY:HA2	81:AX:819:VAL:HG12	1.98	0.44
3:4:43:A:H2'	3:4:44:A:C8	2.53	0.43
9:D:22:ARG:O	9:D:26:GLY:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:Q:80:THR:OG1	21:Q:100:THR:O	2.33	0.43
26:V:101:VAL:HG11	26:V:114:ILE:HD12	1.99	0.43
27:W:28:ILE:H	27:W:28:ILE:HG13	1.60	0.43
36:f:19:SER:OG	36:f:20:LYS:N	2.50	0.43
47:2:327:U:H2'	47:2:328:A:C8	2.53	0.43
47:2:820:U:O4	47:2:854:U:O2'	2.26	0.43
51:t:15:GLY:HA2	51:t:19:ALA:H	1.82	0.43
54:w:77:LEU:HB2	54:w:84:TYR:HE2	1.83	0.43
55:x:47:ARG:HB3	55:x:59:ALA:HB3	2.00	0.43
55:x:49:ILE:HD11	55:x:172:VAL:HA	1.99	0.43
55:x:74:GLN:HA	55:x:77:LEU:HD13	1.99	0.43
56:y:61:GLU:OE1	56:y:62:THR:OG1	2.34	0.43
57:z:100:LYS:HG3	57:z:101:VAL:H	1.82	0.43
60:AC:60:VAL:O	60:AC:85:LYS:NZ	2.46	0.43
68:AK:62:VAL:HA	68:AK:85:ARG:HH21	1.82	0.43
73:AP:77:ARG:HA	73:AP:80:LEU:HB2	2.00	0.43
81:AX:226:ALA:HB1	81:AX:237:LYS:HG2	1.98	0.43
81:AX:468:THR:O	81:AX:470:THR:OG1	2.35	0.43
1:1:2218:G:H2'	1:1:2219:A:C8	2.54	0.43
1:1:2989:U:O2'	7:B:267:ALA:O	2.25	0.43
1:1:3181:C:H2'	1:1:3182:G:C8	2.53	0.43
3:4:75:G:OP2	29:Y:74:TYR:OH	2.33	0.43
7:B:56:ILE:HD11	7:B:356:LEU:HD22	2.00	0.43
7:B:171:LEU:HD23	7:B:314:TYR:HE1	1.83	0.43
8:C:20:LEU:HD21	8:C:252:GLU:HG3	1.99	0.43
10:E:80:ASN:HD22	10:E:81:ALA:H	1.67	0.43
13:H:103:ILE:HD12	13:H:134:ILE:HD11	2.00	0.43
16:L:12:ASN:OD1	16:L:12:ASN:N	2.49	0.43
22:R:176:ARG:H	22:R:176:ARG:HD3	1.82	0.43
23:S:45:LEU:HD13	23:S:51:VAL:HB	2.01	0.43
26:V:80:ARG:NH1	26:V:117:PRO:O	2.42	0.43
27:W:22:VAL:HG22	27:W:28:ILE:HG22	1.99	0.43
29:Y:119:ILE:O	29:Y:123:GLY:N	2.51	0.43
41:k:46:ARG:HH21	41:k:51:LEU:HD13	1.82	0.43
47:2:877:G:H22	47:2:951:A:H2	1.66	0.43
47:2:991:G:H21	47:2:1013:A:N6	2.11	0.43
47:2:1775:U:H2'	47:2:1776:A:C8	2.53	0.43
50:s:186:LYS:HE2	50:s:186:LYS:HB3	1.81	0.43
52:u:71:LYS:HG2	52:u:76:VAL:HG22	1.99	0.43
54:w:102:VAL:HG13	54:w:106:LEU:HG	2.00	0.43
55:x:165:LYS:O	55:x:168:SER:OG	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:y:42:ARG:HH11	56:y:59:ARG:HD2	1.83	0.43
81:AX:432:GLN:HE21	81:AX:457:VAL:HG21	1.82	0.43
1:1:39:A:H5''	31:a:35:ALA:HB2	2.00	0.43
1:1:241:G:N2	1:1:242:C:O4'	2.51	0.43
1:1:716:A:C6	31:a:117:ARG:HD2	2.54	0.43
1:1:767:U:H4'	16:L:186:ARG:HH22	1.84	0.43
1:1:1244:A:OP1	1:1:1245:A:N6	2.45	0.43
1:1:2988:C:OP1	19:O:68:ARG:NH2	2.40	0.43
1:1:3060:C:H2'	1:1:3061:G:H8	1.83	0.43
1:1:3086:A:H5''	7:B:367:LYS:HG3	2.00	0.43
1:1:3162:C:H2'	1:1:3163:A:C8	2.53	0.43
7:B:68:HIS:CD2	7:B:69:LYS:HG2	2.53	0.43
7:B:289:ASP:N	7:B:289:ASP:OD1	2.47	0.43
12:G:137:ASN:HA	12:G:140:VAL:HG12	2.00	0.43
13:H:77:ASN:O	13:H:81:GLY:N	2.41	0.43
15:J:82:ARG:NH2	15:J:112:LEU:O	2.52	0.43
17:M:43:LYS:NZ	23:S:96:ASP:OD1	2.35	0.43
47:2:365:G:H5'	47:2:757:A:H61	1.83	0.43
47:2:655:G:O6	47:2:679:U:O4	2.36	0.43
47:2:883:C:H2'	47:2:884:A:C8	2.53	0.43
47:2:1454:G:H4'	63:AF:122:THR:HG21	2.00	0.43
52:u:6:LYS:O	52:u:30:ARG:NH1	2.46	0.43
52:u:183:VAL:HG13	52:u:190:GLY:H	1.83	0.43
53:v:151:GLY:HA3	53:v:156:ARG:HG2	2.00	0.43
57:z:134:ILE:HG22	57:z:158:PHE:HA	1.99	0.43
66:AI:125:ILE:HA	66:AI:128:PHE:HB3	2.00	0.43
71:AN:90:ASP:HB3	71:AN:136:TRP:HE1	1.83	0.43
78:AU:7:SER:O	78:AU:10:ARG:N	2.47	0.43
81:AX:55:ARG:NH1	81:AX:69:THR:HG1	2.16	0.43
1:1:215:G:OP2	8:C:198:ARG:NH1	2.51	0.43
1:1:307:A:H2'	1:1:308:A:C8	2.54	0.43
1:1:543:C:N4	1:1:549:U:C4	2.84	0.43
1:1:842:G:H2'	1:1:843:A:H8	1.81	0.43
1:1:1597:C:OP1	37:g:8:ARG:NH1	2.46	0.43
1:1:3201:C:H2'	1:1:3202:G:C8	2.53	0.43
9:D:5:LYS:HD2	9:D:5:LYS:HA	1.86	0.43
18:N:72:LYS:HD2	18:N:89:VAL:HG22	1.99	0.43
24:T:53:PRO:HB3	24:T:91:LEU:HD11	2.00	0.43
25:U:97:SER:OG	25:U:99:LYS:O	2.35	0.43
47:2:97:C:H1'	47:2:426:G:H5'	2.00	0.43
47:2:780:A:C8	72:AO:8:ARG:HD3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1045:C:H2'	47:2:1046:G:C8	2.54	0.43
47:2:1215:C:N4	47:2:1449:U:O2	2.48	0.43
52:u:238:LEU:HD22	52:u:239:PRO:HD2	1.99	0.43
57:z:34:PHE:HZ	57:z:102:GLU:HG2	1.83	0.43
58:AA:81:ASN:HB2	60:AC:37:VAL:HG11	2.01	0.43
70:AM:41:MET:HE2	70:AM:46:TYR:HD2	1.83	0.43
81:AX:662:SER:O	81:AX:666:ALA:HB2	2.18	0.43
84:BA:38:LEU:HD12	84:BA:163:LEU:HB3	1.99	0.43
1:1:1783:U:H2'	1:1:1784:G:C8	2.53	0.43
1:1:3008:A:H2'	1:1:3009:G:C8	2.53	0.43
3:4:29:U:H2'	3:4:30:C:H6	1.84	0.43
8:C:311:HIS:CE1	11:F:164:SER:HG	2.36	0.43
15:J:109:HIS:HE1	15:J:120:ILE:HD12	1.84	0.43
26:V:23:MET:HE2	26:V:36:ILE:HD11	2.00	0.43
30:Z:83:THR:OG1	30:Z:84:ARG:N	2.48	0.43
33:c:49:PRO:HG2	33:c:52:ARG:HG2	2.01	0.43
39:i:51:SER:O	39:i:53:TYR:N	2.46	0.43
47:2:321:C:N4	47:2:1667:A:OP2	2.51	0.43
47:2:332:U:OP1	56:y:31:ARG:NH1	2.46	0.43
47:2:844:A:H2'	47:2:845:G:C8	2.53	0.43
47:2:927:C:O2	62:AE:125:SER:OG	2.33	0.43
47:2:1205:C:O2	77:AT:17:GLY:N	2.50	0.43
47:2:1217:A:OP2	58:AA:44:LYS:NZ	2.41	0.43
47:2:1255:G:C8	60:AC:46:ARG:HG3	2.53	0.43
47:2:1684:U:O2	47:2:1717:G:O6	2.36	0.43
53:v:43:PHE:HB3	53:v:46:TRP:HB2	2.00	0.43
60:AC:41:LEU:HD22	60:AC:123:VAL:HA	1.99	0.43
63:AF:94:VAL:HG13	63:AF:96:ILE:HD11	1.99	0.43
1:1:26:A:N3	1:1:328:U:O2'	2.46	0.43
1:1:525:C:O2	1:1:568:G:N2	2.43	0.43
1:1:2609:A:H2'	1:1:2610:G:H8	1.84	0.43
1:1:2662:G:H2'	1:1:2663:G:C8	2.52	0.43
1:1:3068:U:OP2	22:R:62:ARG:NH1	2.51	0.43
9:D:205:SER:HB3	9:D:236:LEU:HD13	2.00	0.43
21:Q:185:LYS:HE2	21:Q:185:LYS:HB3	1.92	0.43
24:T:103:GLN:HA	24:T:106:LEU:HB2	1.99	0.43
47:2:1147:A:H2'	47:2:1148:C:H6	1.84	0.43
47:2:1529:C:H1'	67:AJ:12:GLN:HE22	1.84	0.43
47:2:1788:G:N7	62:AE:132:ARG:NH1	2.56	0.43
49:r:125:VAL:HG11	49:r:173:THR:HG22	2.00	0.43
50:s:37:PRO:O	50:s:43:ARG:NE	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:AQ:18:VAL:HG13	74:AQ:19:LYS:H	1.83	0.43
81:AX:380:LEU:HG	81:AX:469:LEU:HB2	1.99	0.43
84:BA:36:VAL:H	84:BA:62:ASN:HD21	1.67	0.43
84:BA:55:LEU:HD21	84:BA:154:THR:HA	1.99	0.43
1:1:1090:G:H2'	1:1:1091:A:C8	2.53	0.43
1:1:1150:A:N6	1:1:2369:G:O2'	2.52	0.43
1:1:1392:G:O2'	1:1:1417:G:N1	2.49	0.43
1:1:1661:G:H2'	1:1:1662:G:C8	2.53	0.43
2:3:32:U:H1'	2:3:33:U:H5	1.83	0.43
2:3:111:U:OP2	9:D:276:LYS:NZ	2.43	0.43
11:F:121:LYS:HZ3	24:T:132:PRO:HA	1.83	0.43
12:G:111:LYS:HA	12:G:115:ALA:HB3	2.00	0.43
24:T:101:CYS:SG	24:T:102:ARG:N	2.92	0.43
47:2:131:C:H5'	47:2:132:U:H3'	2.01	0.43
47:2:845:G:H2'	47:2:846:G:H8	1.83	0.43
47:2:863:A:H4'	70:AM:57:ARG:HD3	1.99	0.43
47:2:929:A:N1	49:r:111:ARG:NH2	2.64	0.43
47:2:1665:U:O2	47:2:1736:G:N2	2.38	0.43
48:q:102:PHE:HD2	48:q:104:PRO:HA	1.83	0.43
54:w:188:ARG:O	54:w:192:ALA:N	2.51	0.43
67:AJ:37:VAL:HG12	67:AJ:39:THR:H	1.83	0.43
81:AX:724:ILE:H	81:AX:724:ILE:HG13	1.65	0.43
1:1:1347:U:OP1	8:C:300:ARG:NH1	2.52	0.43
11:F:169:ILE:O	11:F:174:GLY:N	2.52	0.43
13:H:12:VAL:N	13:H:51:GLN:O	2.50	0.43
13:H:150:SER:OG	13:H:151:VAL:N	2.52	0.43
14:I:189:GLU:HA	14:I:213:PHE:CZ	2.54	0.43
22:R:152:GLU:HA	22:R:155:LEU:HD23	2.00	0.43
47:2:319:U:H5'	56:y:11:ARG:HH12	1.84	0.43
47:2:540:G:N2	47:2:542:A:N7	2.65	0.43
47:2:1593:A:H2'	47:2:1594:G:H8	1.83	0.43
54:w:3:LEU:O	54:w:16:PHE:N	2.46	0.43
54:w:36:VAL:HB	54:w:50:PHE:HB2	1.99	0.43
61:AD:91:LEU:HD21	61:AD:121:ARG:HG2	2.01	0.43
1:1:1008:U:H2'	1:1:1009:A:C8	2.54	0.43
1:1:3005:A:O2'	1:1:3140:G:N2	2.51	0.43
3:4:150:G:OP1	28:X:27:ARG:NH2	2.44	0.43
4:P0:34:SER:OG	4:P0:35:SER:N	2.52	0.43
23:S:93:GLU:OE2	23:S:136:LYS:N	2.48	0.43
47:2:195:G:H2'	47:2:196:G:C8	2.54	0.43
47:2:1256:A:H3'	60:AC:43:ARG:HH21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:v:47:SER:H	53:v:129:PRO:HD2	1.84	0.43
61:AD:108:ASP:HB3	61:AD:111:ALA:HB3	2.01	0.43
62:AE:116:GLU:HG2	74:AQ:44:ILE:HG21	2.01	0.43
64:AG:140:LYS:HE2	64:AG:140:LYS:HB2	1.84	0.43
65:AH:10:LYS:HG2	65:AH:53:TYR:CE1	2.54	0.43
66:AI:129:TRP:HB3	66:AI:131:LEU:HD13	2.00	0.43
71:AN:59:ILE:HD11	71:AN:117:ILE:HG23	2.00	0.43
79:AV:13:LEU:O	79:AV:310:ILE:N	2.52	0.43
81:AX:20:ARG:HH21	81:AX:338:ILE:HG13	1.83	0.43
81:AX:510:ARG:HH12	81:AX:549:HIS:CG	2.36	0.43
84:BA:41:TYR:OH	84:BA:215:ARG:NH2	2.52	0.43
84:BA:105:LYS:HE3	84:BA:152:ARG:HB3	2.00	0.43
1:1:835:G:HO2'	1:1:857:G:H22	1.66	0.43
1:1:2440:G:H2'	1:1:2441:A:H8	1.83	0.43
2:3:27:A:OP2	9:D:56:THR:OG1	2.37	0.43
2:3:97:A:H5''	11:F:224:ILE:HD11	2.01	0.43
3:4:152:G:OP1	12:G:60:ARG:NE	2.48	0.43
8:C:108:LYS:HA	18:N:203:ARG:HH21	1.84	0.43
22:R:23:TRP:HB3	22:R:51:VAL:HG12	2.00	0.43
37:g:93:PHE:HD2	37:g:94:LEU:HD12	1.84	0.43
47:2:1002:G:N2	47:2:1760:G:O3'	2.48	0.43
48:q:65:ALA:HA	48:q:185:ARG:HH21	1.83	0.43
72:AO:87:PRO:HB2	72:AO:90:ARG:HB2	1.99	0.43
79:AV:154:VAL:HA	79:AV:171:SER:HA	2.01	0.43
81:AX:732:GLU:HB2	81:AX:795:GLN:HB2	2.01	0.43
1:1:170:G:C6	1:1:248:U:O2	2.71	0.42
1:1:300:G:H2'	1:1:301:G:C8	2.54	0.42
1:1:398:A:O2'	1:1:1416:C:OP2	2.37	0.42
1:1:1589:A:OP2	37:g:11:ASN:ND2	2.53	0.42
1:1:2687:G:H5'	9:D:8:LYS:HE2	2.01	0.42
7:B:41:VAL:HG11	7:B:194:TRP:CG	2.54	0.42
7:B:91:GLY:HA2	7:B:158:VAL:HA	2.01	0.42
16:L:104:ARG:HA	39:i:20:MET:HB3	2.00	0.42
16:L:183:ARG:HA	16:L:186:ARG:HG2	2.01	0.42
47:2:107:C:H2'	47:2:108:A:C8	2.54	0.42
47:2:848:C:H2'	47:2:849:C:C6	2.54	0.42
47:2:1557:U:OP2	47:2:1559:A:O2'	2.36	0.42
48:q:25:GLY:O	48:q:165:ARG:NH2	2.42	0.42
54:w:52:ILE:HD11	54:w:109:LEU:HB3	2.01	0.42
69:AL:58:TYR:OH	69:AL:62:ARG:NE	2.49	0.42
1:1:297:G:OP2	1:1:297:G:N2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1630:U:H3'	30:Z:67:LYS:HE2	2.00	0.42
1:1:1803:C:H2'	1:1:1804:A:H8	1.84	0.42
1:1:2479:C:H4'	84:BA:102:LYS:HE3	2.01	0.42
2:3:107:C:OP1	14:I:203:LYS:NZ	2.52	0.42
3:4:94:C:OP1	40:j:75:LYS:NZ	2.38	0.42
7:B:59:ASP:OD1	7:B:59:ASP:N	2.50	0.42
11:F:88:ARG:NH2	11:F:91:GLY:O	2.52	0.42
12:G:147:LYS:O	12:G:201:THR:OG1	2.28	0.42
17:M:78:THR:HA	17:M:81:VAL:HG12	2.00	0.42
22:R:20:ARG:HG3	22:R:21:LYS:HG3	2.01	0.42
39:i:54:GLU:HB2	39:i:90:MET:HE1	2.01	0.42
47:2:212:U:H2'	47:2:213:A:C8	2.54	0.42
47:2:406:U:H2'	47:2:407:A:C8	2.52	0.42
47:2:1560:U:O2	47:2:1598:U:O2'	2.30	0.42
47:2:1613:U:H2'	47:2:1614:A:C8	2.54	0.42
47:2:1666:U:H2'	47:2:1667:A:C8	2.54	0.42
54:w:36:VAL:N	54:w:50:PHE:O	2.49	0.42
54:w:101:ILE:H	54:w:101:ILE:HD12	1.85	0.42
57:z:80:LEU:HA	57:z:83:VAL:HG22	2.01	0.42
64:AG:99:GLU:O	64:AG:103:ASN:N	2.41	0.42
67:AJ:53:TRP:O	67:AJ:57:ARG:NH1	2.51	0.42
81:AX:145:GLN:HA	81:AX:146:ALA:HA	1.56	0.42
1:1:951:A:OP2	1:1:1367:G:N2	2.36	0.42
1:1:1021:G:H21	1:1:1033:U:H3	1.67	0.42
1:1:1347:U:OP2	8:C:300:ARG:NH2	2.51	0.42
1:1:2323:G:O2'	1:1:2325:G:OP2	2.23	0.42
1:1:3021:A:N6	1:1:3033:A:OP2	2.50	0.42
1:1:3076:C:OP2	34:d:65:LYS:NZ	2.52	0.42
41:k:58:ASP:OD1	41:k:58:ASP:N	2.43	0.42
47:2:699:U:O4	47:2:739:G:O6	2.37	0.42
47:2:1099:U:OP1	70:AM:71:LYS:NZ	2.52	0.42
47:2:1385:G:H2'	47:2:1386:G:H8	1.84	0.42
47:2:1397:U:O2'	47:2:1401:A:N6	2.52	0.42
47:2:1773:C:H2'	47:2:1774:G:H8	1.85	0.42
54:w:137:ARG:HH11	54:w:177:ARG:NH1	2.18	0.42
60:AC:45:LEU:O	60:AC:49:THR:OG1	2.36	0.42
66:AI:37:GLY:HA3	66:AI:105:VAL:HG11	2.00	0.42
71:AN:82:LYS:HA	71:AN:82:LYS:HD2	1.82	0.42
81:AX:41:GLN:HB3	81:AX:46:ILE:HD13	2.01	0.42
81:AX:696:ASP:HB2	81:AX:700:ARG:HB3	2.00	0.42
81:AX:726:GLU:HA	81:AX:727:PRO:HD3	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:809:G:H2'	1:1:810:A:H8	1.85	0.42
1:1:1524:A:O2'	1:1:1526:U:OP2	2.24	0.42
1:1:2451:G:H21	1:1:2452:G:H1'	1.84	0.42
1:1:3162:C:H2'	1:1:3163:A:H8	1.84	0.42
3:4:6:U:H2'	3:4:7:U:H6	1.85	0.42
14:I:100:ASN:OD1	14:I:100:ASN:N	2.52	0.42
21:Q:155:MET:HE3	21:Q:155:MET:HB3	1.85	0.42
22:R:72:GLU:O	22:R:74:ARG:NH1	2.46	0.42
26:V:69:LEU:H	26:V:69:LEU:HG	1.69	0.42
38:h:104:GLN:HA	38:h:107:LYS:HB3	2.00	0.42
47:2:1070:C:H5'	75:AR:17:ARG:HH22	1.84	0.42
47:2:1157:A:H3'	47:2:1160:A:H62	1.84	0.42
47:2:1524:A:O2'	67:AJ:93:HIS:ND1	2.38	0.42
50:s:52:THR:OG1	50:s:54:GLU:OE1	2.33	0.42
54:w:212:LEU:HA	54:w:215:ARG:HB3	2.00	0.42
55:x:103:SER:OG	55:x:105:THR:OG1	2.38	0.42
57:z:57:ARG:HA	57:z:60:LEU:HB3	2.00	0.42
57:z:126:ARG:HE	78:AU:33:ARG:HE	1.66	0.42
64:AG:128:LYS:HB2	64:AG:137:ARG:NH2	2.34	0.42
69:AL:19:ALA:O	69:AL:71:ARG:NH1	2.51	0.42
81:AX:709:MET:HA	81:AX:712:ALA:HB3	2.00	0.42
81:AX:832:VAL:HA	81:AX:833:PRO:HD3	1.87	0.42
1:1:413:U:OP1	20:P:30:ARG:NH2	2.53	0.42
1:1:989:A:H2'	1:1:990:U:O4'	2.19	0.42
1:1:1363:A:OP1	11:F:160:ARG:NH1	2.49	0.42
1:1:1592:G:OP1	37:g:58:ARG:NH2	2.40	0.42
1:1:2445:A:H1'	1:1:2504:U:H3	1.85	0.42
1:1:3201:C:H2'	1:1:3202:G:H8	1.85	0.42
3:4:155:A:O2'	12:G:185:ARG:NH2	2.43	0.42
14:I:12:GLN:HE22	14:I:95:HIS:CE1	2.38	0.42
31:a:36:GLY:HA3	31:a:40:HIS:CE1	2.55	0.42
39:i:58:ILE:HG22	39:i:62:ARG:HH21	1.84	0.42
47:2:163:G:H4'	54:w:53:SER:HB2	2.01	0.42
47:2:290:G:H2'	47:2:291:G:C8	2.53	0.42
52:u:104:ASP:OD1	52:u:108:ARG:N	2.52	0.42
54:w:77:LEU:HD12	54:w:81:VAL:HG21	2.02	0.42
81:AX:280:PRO:O	81:AX:284:LEU:HB2	2.19	0.42
81:AX:597:VAL:HA	81:AX:600:ALA:HB3	2.01	0.42
1:1:715:A:H5''	31:a:133:LEU:HD23	2.02	0.42
1:1:776:U:H4'	32:b:41:ARG:HH12	1.83	0.42
1:1:1090:G:H2'	1:1:1091:A:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1233:G:H21	5:P2:121:PHE:HZ	1.66	0.42
1:1:1257:C:OP1	4:P0:46:ARG:NH1	2.53	0.42
1:1:1405:U:H1'	35:e:57:TYR:HB2	2.02	0.42
2:3:119:U:OP1	9:D:256:THR:OG1	2.32	0.42
6:A:50:HIS:HD2	46:p:52:ALA:H	1.66	0.42
7:B:67:PHE:HD2	26:V:88:ARG:HD2	1.84	0.42
14:I:205:SER:OG	14:I:206:LEU:N	2.52	0.42
15:J:73:GLY:O	15:J:75:LYS:N	2.46	0.42
35:e:108:ILE:H	35:e:108:ILE:HG13	1.72	0.42
39:i:5:THR:HG21	39:i:11:LEU:HB3	2.01	0.42
47:2:272:U:O2'	47:2:273:G:O4'	2.38	0.42
47:2:484:C:H2'	47:2:485:A:C8	2.54	0.42
47:2:534:A:H3'	47:2:535:A:H8	1.85	0.42
47:2:957:G:H21	75:AR:51:GLN:HE22	1.66	0.42
47:2:1278:G:H4'	51:t:172:THR:HG21	2.02	0.42
47:2:1453:G:O3'	63:AF:81:ARG:NH2	2.52	0.42
54:w:103:GLY:H	54:w:106:LEU:HD23	1.85	0.42
56:y:56:ARG:HH11	56:y:58:LEU:HD13	1.85	0.42
79:AV:34:LEU:HD11	79:AV:42:LEU:HB3	2.01	0.42
79:AV:220:ILE:HD12	79:AV:234:LEU:HD13	2.01	0.42
81:AX:643:PRO:HG2	81:AX:682:ARG:HA	2.02	0.42
1:1:441:U:H5''	1:1:442:G:C8	2.54	0.42
13:H:1:MET:HE3	13:H:3:TYR:HD1	1.85	0.42
15:J:48:SER:N	15:J:66:ALA:O	2.53	0.42
33:c:42:ILE:HD11	33:c:67:VAL:HG22	2.02	0.42
47:2:502:U:H2'	47:2:503:G:C8	2.55	0.42
47:2:650:U:H2'	47:2:651:G:C8	2.54	0.42
47:2:730:G:H21	47:2:732:G:N2	2.18	0.42
47:2:793:A:H5'	47:2:794:U:H5'	2.00	0.42
47:2:1727:G:N2	56:y:32:GLN:OE1	2.53	0.42
53:v:164:PRO:HD3	76:AS:54:LEU:HD13	2.02	0.42
53:v:165:LEU:HD23	76:AS:47:PRO:HB2	2.01	0.42
67:AJ:109:GLU:HA	67:AJ:114:VAL:HB	2.01	0.42
72:AO:102:LYS:HB2	72:AO:108:ARG:NH2	2.35	0.42
79:AV:240:VAL:HA	79:AV:256:THR:HG22	2.01	0.42
81:AX:300:LEU:O	81:AX:305:ILE:N	2.53	0.42
81:AX:506:GLU:HA	81:AX:509:LYS:HB2	2.01	0.42
82:AY:14:A:H2'	82:AY:15:G:C8	2.55	0.42
1:1:585:A:OP1	36:f:70:LYS:NZ	2.40	0.42
1:1:1225:A:H3'	1:1:1226:G:H8	1.84	0.42
1:1:1231:A:O2'	1:1:1278:A:N6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1542:G:H2'	1:1:1543:G:C8	2.53	0.42
1:1:2697:A:H2'	1:1:2698:G:H8	1.84	0.42
1:1:3051:U:H1'	26:V:92:PHE:CE2	2.55	0.42
1:1:3107:U:OP1	43:m:114:LYS:NZ	2.34	0.42
2:3:19:C:H2'	2:3:20:A:C8	2.55	0.42
9:D:283:ALA:HA	9:D:286:VAL:HG12	2.02	0.42
10:E:51:ARG:HG2	10:E:159:LEU:HD13	2.01	0.42
15:J:13:LYS:HA	15:J:13:LYS:HD2	1.89	0.42
24:T:112:ASN:O	24:T:116:ARG:N	2.52	0.42
35:e:45:ARG:HD3	35:e:52:GLN:HE22	1.85	0.42
47:2:146:U:O2	47:2:168:A:N7	2.53	0.42
47:2:511:A:OP2	57:z:176:ASN:ND2	2.53	0.42
47:2:696:C:O2	47:2:696:C:H2'	2.19	0.42
47:2:1366:U:H4'	67:AJ:7:ARG:HD3	2.01	0.42
47:2:1614:A:OP2	47:2:1615:C:N4	2.40	0.42
47:2:1733:C:H2'	47:2:1734:U:C6	2.55	0.42
50:s:227:PRO:HA	50:s:230:TRP:CD2	2.55	0.42
52:u:180:LEU:HD23	52:u:233:LYS:HB3	2.02	0.42
54:w:47:GLY:HA3	54:w:117:GLY:HA2	2.02	0.42
54:w:142:ARG:HE	54:w:149:LYS:HD2	1.85	0.42
62:AE:114:ARG:HG3	74:AQ:62:TYR:CZ	2.55	0.42
64:AG:15:SER:HB2	64:AG:73:GLY:H	1.85	0.42
64:AG:55:VAL:HG23	64:AG:107:LYS:HB2	2.01	0.42
70:AM:37:PHE:HE1	70:AM:103:ILE:HG12	1.85	0.42
81:AX:643:PRO:HB2	81:AX:683:SER:H	1.83	0.42
1:1:528:U:H2'	1:1:529:A:C8	2.55	0.42
1:1:1054:A:H5''	1:1:2637:A:H61	1.83	0.42
1:1:3291:G:H2'	1:1:3292:A:C8	2.54	0.42
1:1:3294:A:H2'	1:1:3295:A:O4'	2.20	0.42
3:4:11:C:H2'	3:4:12:A:H8	1.84	0.42
10:E:154:LEU:HD12	17:M:119:GLN:HG2	2.01	0.42
19:O:87:MET:N	19:O:87:MET:SD	2.92	0.42
31:a:149:ALA:HA	39:i:8:ALA:HB2	2.02	0.42
32:b:18:ARG:HH11	32:b:18:ARG:HD2	1.73	0.42
33:c:55:GLU:HA	37:g:94:LEU:HD21	2.02	0.42
39:i:58:ILE:HD13	39:i:58:ILE:HA	1.92	0.42
46:p:55:TRP:NE1	46:p:70:THR:O	2.53	0.42
46:p:76:ALA:HB1	46:p:80:ARG:HH12	1.85	0.42
47:2:17:C:H2'	47:2:18:C:C6	2.55	0.42
47:2:127:G:H21	47:2:178:U:H2'	1.85	0.42
47:2:698:U:H2'	47:2:699:U:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:1191:U:O2'	47:2:1193:A:O2'	2.31	0.42
47:2:1482:C:N3	47:2:1526:A:N6	2.67	0.42
53:v:63:GLN:O	53:v:66:GLN:N	2.53	0.42
60:AC:97:LEU:HG	60:AC:101:ALA:HB2	2.02	0.42
71:AN:61:SER:OG	71:AN:62:LYS:N	2.47	0.42
79:AV:48:THR:OG1	79:AV:53:LYS:O	2.29	0.42
81:AX:12:LEU:HB3	81:AX:15:LYS:NZ	2.35	0.42
81:AX:278:LEU:HB2	81:AX:281:ILE:HG22	2.01	0.42
1:1:20:A:H2'	1:1:21:G:C8	2.55	0.42
1:1:108:A:N7	16:L:55:ARG:NH2	2.68	0.42
1:1:261:U:H2'	1:1:262:U:C6	2.55	0.42
1:1:1914:G:N2	22:R:81:ARG:O	2.41	0.42
1:1:3371:G:H2'	1:1:3372:A:H8	1.84	0.42
3:4:91:C:H2'	3:4:92:A:H8	1.85	0.42
9:D:151:GLN:NE2	9:D:152:ARG:O	2.53	0.42
10:E:43:LEU:HG	36:f:103:TYR:HB3	2.00	0.42
20:P:112:LEU:HD12	20:P:150:VAL:HB	2.01	0.42
30:Z:23:VAL:HG23	30:Z:45:GLY:HA3	2.02	0.42
31:a:97:GLU:OE1	31:a:98:THR:OG1	2.34	0.42
47:2:1172:G:H21	67:AJ:88:VAL:HG11	1.85	0.42
47:2:1264:G:N2	47:2:1265:G:N3	2.67	0.42
53:v:63:GLN:HB2	53:v:88:PRO:HA	2.01	0.42
53:v:119:ASP:HA	53:v:122:ASN:HB3	2.02	0.42
54:w:28:PHE:HB2	54:w:101:ILE:HG23	2.01	0.42
79:AV:102:ARG:HG3	79:AV:104:VAL:HG13	2.00	0.42
1:1:165:A:H2'	1:1:166:C:C6	2.54	0.41
1:1:408:A:N3	1:1:655:C:O2'	2.48	0.41
1:1:417:A:H2'	1:1:418:A:H8	1.84	0.41
1:1:1343:A:H2'	1:1:1344:G:C8	2.54	0.41
1:1:2553:U:C4	37:g:95:ILE:HG12	2.54	0.41
4:P0:43:LYS:HD3	5:P2:121:PHE:HD1	1.85	0.41
4:P0:57:THR:HG22	4:P0:60:ARG:HB2	2.02	0.41
10:E:55:LEU:HA	10:E:93:VAL:HG11	2.01	0.41
24:T:17:ARG:HD2	24:T:17:ARG:HA	1.88	0.41
34:d:56:ASN:HD22	34:d:60:TRP:HZ3	1.68	0.41
38:h:28:LEU:HD12	38:h:47:VAL:HG13	2.01	0.41
47:2:485:A:H2'	47:2:486:G:C8	2.55	0.41
47:2:1187:U:H2'	47:2:1188:G:C8	2.54	0.41
47:2:1338:C:H1'	47:2:1410:A:C4	2.54	0.41
47:2:1353:U:N3	47:2:1367:G:O6	2.50	0.41
54:w:126:ASP:OD1	54:w:126:ASP:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:y:84:HIS:HE2	56:y:97:THR:HG1	1.65	0.41
56:y:104:ILE:H	56:y:104:ILE:HG13	1.62	0.41
64:AG:20:ALA:HA	64:AG:67:VAL:HG22	2.03	0.41
68:AK:54:GLY:HA3	68:AK:55:PRO:HD3	1.92	0.41
68:AK:82:TYR:HB3	77:AT:52:PHE:HB3	2.01	0.41
79:AV:159:ASN:HD22	79:AV:163:ASP:HA	1.83	0.41
81:AX:21:ASN:HD22	81:AX:453:ILE:HD11	1.85	0.41
81:AX:320:LEU:O	81:AX:324:MET:HG3	2.20	0.41
81:AX:589:LYS:O	81:AX:687:ASN:CB	2.64	0.41
84:BA:97:LYS:HA	84:BA:123:LEU:HD13	2.00	0.41
1:1:394:G:H22	1:1:397:A:H5'	1.85	0.41
1:1:519:A:C8	1:1:522:A:H5'	2.55	0.41
1:1:852:U:H2'	1:1:853:G:C8	2.54	0.41
1:1:2105:G:H2'	1:1:2106:A:H8	1.85	0.41
1:1:2609:A:H2'	1:1:2610:G:C8	2.55	0.41
8:C:353:ALA:O	8:C:356:THR:OG1	2.30	0.41
44:n:1:MET:HE2	44:n:9:ARG:HH22	1.85	0.41
45:o:34:SER:OG	45:o:35:LEU:O	2.28	0.41
47:2:147:A:H2'	47:2:148:A:H8	1.85	0.41
47:2:918:U:H2'	47:2:919:A:H8	1.85	0.41
47:2:1211:A:H4'	63:AF:100:LYS:HE3	2.02	0.41
47:2:1300:A:H4'	50:s:86:VAL:HG11	2.02	0.41
47:2:1486:G:O6	47:2:1520:U:C4	2.73	0.41
49:r:161:ILE:HA	49:r:164:ILE:HG22	2.02	0.41
51:t:219:ALA:HA	51:t:220:PRO:HD3	1.93	0.41
52:u:155:LYS:HA	52:u:155:LYS:HD2	1.85	0.41
52:u:207:LEU:HD12	52:u:219:VAL:HG12	2.02	0.41
54:w:74:LYS:HA	54:w:96:SER:HA	2.02	0.41
56:y:67:TRP:CZ3	56:y:70:GLU:HB3	2.55	0.41
56:y:121:LEU:HA	56:y:122:GLY:HA2	1.79	0.41
62:AE:85:ALA:H	62:AE:119:THR:HG22	1.85	0.41
64:AG:13:LYS:HG2	64:AG:14:LYS:H	1.84	0.41
66:AI:29:VAL:O	66:AI:33:THR:OG1	2.34	0.41
81:AX:510:ARG:HA	81:AX:513:LYS:HG2	2.02	0.41
1:1:737:G:H2'	1:1:738:A:C8	2.55	0.41
1:1:1119:C:H2'	1:1:1120:A:C8	2.49	0.41
1:1:1679:A:H2'	1:1:1680:G:H8	1.85	0.41
1:1:3011:A:N6	7:B:12:GLY:O	2.53	0.41
1:1:3101:G:H2'	1:1:3102:G:C8	2.55	0.41
4:P0:106:ALA:HB3	4:P0:182:THR:HG21	2.02	0.41
13:H:8:GLN:HG2	13:H:72:LYS:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:N:26:ARG:HA	18:N:29:GLU:HG2	2.01	0.41
21:Q:19:PRO:HD3	21:Q:53:PHE:CE1	2.55	0.41
36:f:59:VAL:O	36:f:61:GLY:N	2.53	0.41
40:j:60:GLY:HA2	40:j:64:MET:HG3	2.02	0.41
45:o:67:LYS:HA	45:o:87:ARG:HA	2.02	0.41
47:2:702:G:O6	47:2:737:A:N6	2.53	0.41
47:2:1123:C:H2'	47:2:1124:A:C4	2.55	0.41
47:2:1386:G:C2'	47:2:1387:G:H5'	2.50	0.41
50:s:147:ASN:O	69:AL:4:ASP:N	2.53	0.41
54:w:64:LYS:HE3	54:w:81:VAL:HG13	2.02	0.41
81:AX:669:TRP:HA	81:AX:670:ALA:HA	1.72	0.41
84:BA:123:LEU:HD23	84:BA:123:LEU:H	1.85	0.41
1:1:41:G:N2	1:1:2803:A:H62	2.18	0.41
1:1:650:C:H2'	1:1:651:G:C8	2.55	0.41
1:1:745:C:H2'	1:1:746:A:C8	2.55	0.41
1:1:1563:C:H3'	1:1:1564:U:H4'	2.02	0.41
1:1:1632:A:OP1	30:Z:48:ARG:NH1	2.53	0.41
1:1:1717:U:H2'	1:1:1718:G:C8	2.56	0.41
5:P2:59:THR:HB	5:P2:77:ALA:HB3	2.03	0.41
6:A:117:GLU:OE1	6:A:123:ARG:N	2.47	0.41
42:l:30:ARG:HB2	42:l:33:ASN:HB2	2.03	0.41
47:2:130:C:H4'	47:2:176:C:H5''	2.02	0.41
47:2:902:G:N2	47:2:907:A:OP2	2.53	0.41
47:2:961:U:H2'	47:2:962:C:C6	2.56	0.41
47:2:1147:A:H2'	47:2:1148:C:C6	2.56	0.41
47:2:1228:G:N3	60:AC:70:ASN:ND2	2.69	0.41
47:2:1694:A:O2'	47:2:1707:A:N3	2.54	0.41
47:2:1766:A:N1	74:AQ:80:HIS:NE2	2.65	0.41
48:q:48:ILE:H	48:q:48:ILE:HG13	1.71	0.41
51:t:218:LEU:HD13	79:AV:193:ILE:HG12	2.02	0.41
53:v:27:THR:HG21	64:AG:28:LEU:HA	2.01	0.41
55:x:111:LYS:HG3	55:x:112:ARG:H	1.85	0.41
79:AV:223:TRP:O	79:AV:229:LYS:NZ	2.44	0.41
81:AX:437:MET:N	81:AX:437:MET:SD	2.93	0.41
81:AX:459:ILE:HD13	81:AX:463:LEU:HD12	2.02	0.41
84:BA:93:LEU:O	84:BA:118:LYS:NZ	2.49	0.41
1:1:500:C:H2'	1:1:501:A:H8	1.86	0.41
1:1:629:U:H2'	1:1:630:A:C8	2.55	0.41
1:1:928:C:H2'	1:1:929:A:C8	2.55	0.41
1:1:1156:C:OP2	11:F:94:LYS:NZ	2.40	0.41
1:1:2225:U:H2'	1:1:2226:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2344:U:H2'	1:1:2345:A:C8	2.54	0.41
1:1:3064:U:H2'	1:1:3065:G:C8	2.56	0.41
2:3:3:U:H2'	2:3:4:U:C6	2.54	0.41
2:3:72:A:O2'	2:3:74:C:OP1	2.35	0.41
3:4:7:U:H2'	3:4:8:C:H6	1.86	0.41
13:H:31:ARG:NH2	13:H:83:THR:O	2.49	0.41
17:M:19:ARG:NH1	17:M:66:THR:O	2.36	0.41
20:P:48:LEU:HD23	20:P:92:GLN:HB3	2.02	0.41
29:Y:57:LEU:HB2	29:Y:67:GLU:HG2	2.02	0.41
47:2:66:U:C4	54:w:173:PRO:HG3	2.55	0.41
47:2:1026:A:N6	47:2:1772:C:O2'	2.54	0.41
47:2:1081:A:H4'	47:2:1082:C:N3	2.36	0.41
47:2:1195:C:N4	64:AG:142:TYR:O	2.53	0.41
47:2:1199:G:O6	68:AK:68:ARG:N	2.49	0.41
47:2:1393:C:H2'	47:2:1394:G:C8	2.55	0.41
47:2:1773:C:H2'	47:2:1774:G:C8	2.56	0.41
55:x:61:PHE:HB3	55:x:95:GLU:HB2	2.02	0.41
81:AX:169:VAL:HG11	81:AX:174:LEU:HD13	2.02	0.41
81:AX:612:PHE:O	81:AX:616:ALA:HB2	2.21	0.41
1:1:1066:G:H2'	1:1:1067:U:C6	2.56	0.41
1:1:1281:G:N2	4:P0:83:ASN:OD1	2.53	0.41
1:1:1565:G:N2	1:1:1566:A:O4'	2.54	0.41
1:1:1941:C:H2'	1:1:1942:U:C6	2.56	0.41
10:E:43:LEU:HD23	10:E:84:VAL:HA	2.02	0.41
41:k:42:LYS:HG2	41:k:55:VAL:HG22	2.02	0.41
47:2:250:C:H2'	47:2:251:A:C8	2.56	0.41
47:2:329:G:H2'	47:2:330:G:C8	2.54	0.41
47:2:1157:A:H3'	47:2:1160:A:N6	2.36	0.41
47:2:1187:U:H2'	47:2:1188:G:H8	1.86	0.41
47:2:1393:C:H4'	79:AV:285:ALA:HB2	2.01	0.41
47:2:1512:G:H2'	47:2:1513:G:H8	1.85	0.41
47:2:1610:G:H4'	53:v:107:LYS:HD2	2.02	0.41
48:q:195:TRP:CE2	48:q:197:ILE:HD13	2.55	0.41
63:AF:87:PRO:HG3	63:AF:112:LEU:HD11	2.03	0.41
67:AJ:15:ILE:HG23	67:AJ:59:ALA:HB3	2.02	0.41
73:AP:65:LEU:HD13	73:AP:70:LYS:HE3	2.01	0.41
81:AX:212:GLY:HA3	81:AX:219:ALA:HA	2.02	0.41
81:AX:348:ALA:HA	81:AX:351:TYR:CZ	2.56	0.41
1:1:827:A:H2'	1:1:828:A:H8	1.86	0.41
1:1:1254:C:H5	1:1:1263:A:H5''	1.85	0.41
1:1:1336:U:H2'	1:1:1337:A:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1429:G:C4	8:C:99:MET:HE3	2.56	0.41
1:1:1560:G:O6	28:X:33:ARG:NH1	2.54	0.41
2:3:28:C:OP1	15:J:137:ARG:NH1	2.49	0.41
6:A:113:VAL:HG23	6:A:134:VAL:HG23	2.03	0.41
6:A:146:THR:N	6:A:158:ILE:O	2.48	0.41
11:F:209:ASN:HD22	11:F:209:ASN:HA	1.50	0.41
16:L:106:GLN:O	16:L:110:ASP:N	2.51	0.41
17:M:47:ASP:HB3	17:M:81:VAL:HG11	2.02	0.41
21:Q:107:THR:HB	21:Q:110:ALA:HB2	2.02	0.41
29:Y:12:ARG:HH21	29:Y:16:ARG:NH2	2.18	0.41
47:2:73:U:O2'	47:2:74:U:O4'	2.30	0.41
47:2:686:C:O2'	70:AM:118:ARG:NH2	2.53	0.41
47:2:1181:U:O2'	63:AF:127:ARG:NH1	2.53	0.41
47:2:1498:G:H5'	67:AJ:73:VAL:HG12	2.03	0.41
49:r:31:ASP:HA	49:r:45:LYS:HB2	2.03	0.41
50:s:157:LYS:HD2	50:s:168:ARG:HH11	1.85	0.41
81:AX:708:THR:O	81:AX:712:ALA:CB	2.69	0.41
1:1:2166:A:H2'	1:1:2167:A:C8	2.55	0.41
1:1:2412:G:H2'	1:1:2413:A:H8	1.86	0.41
1:1:2467:G:O2'	1:1:2478:C:O2'	2.37	0.41
1:1:3101:G:H2'	1:1:3102:G:H8	1.86	0.41
10:E:85:ILE:HG12	36:f:107:ILE:HD12	2.02	0.41
38:h:17:LEU:O	38:h:21:LEU:N	2.53	0.41
47:2:66:U:H5'	54:w:173:PRO:HA	2.03	0.41
47:2:549:G:H2'	47:2:550:A:H8	1.85	0.41
47:2:1041:G:H2'	47:2:1042:G:H8	1.86	0.41
47:2:1232:U:H2'	47:2:1233:G:C8	2.56	0.41
47:2:1356:U:O2'	47:2:1357:A:N7	2.46	0.41
47:2:1612:U:OP1	53:v:92:ARG:NH1	2.53	0.41
48:q:184:LEU:HD11	69:AL:39:VAL:HG21	2.02	0.41
50:s:152:HIS:CG	50:s:174:ARG:HB3	2.56	0.41
52:u:92:LEU:HG	52:u:97:GLU:HG2	2.02	0.41
52:u:107:GLY:HA2	52:u:189:LEU:HD11	2.02	0.41
53:v:25:LEU:HD21	53:v:29:ILE:HB	2.03	0.41
54:w:63:MET:HA	54:w:98:ARG:O	2.20	0.41
54:w:184:LEU:HA	54:w:187:LYS:HB3	2.02	0.41
55:x:62:VAL:H	55:x:94:ALA:HA	1.86	0.41
56:y:66:SER:OG	56:y:67:TRP:N	2.54	0.41
68:AK:113:ASP:OD1	68:AK:113:ASP:N	2.50	0.41
81:AX:15:LYS:O	81:AX:19:VAL:N	2.54	0.41
81:AX:288:ILE:O	81:AX:317:LYS:NZ	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:86:G:N2	1:1:87:U:O4	2.52	0.41
1:1:620:U:O2'	1:1:622:A:N7	2.42	0.41
1:1:1621:A:H2'	1:1:1622:U:H6	1.85	0.41
1:1:1638:A:N3	1:1:1709:C:H1'	2.36	0.41
1:1:1696:A:OP2	1:1:1749:A:N6	2.54	0.41
1:1:1706:C:N4	1:1:1738:C:H42	2.19	0.41
1:1:1757:A:H2'	1:1:1758:G:C8	2.56	0.41
1:1:1760:A:H62	1:1:1766:G:H1'	1.86	0.41
1:1:1946:A:H2'	1:1:1947:G:C8	2.56	0.41
1:1:2441:A:H2'	1:1:2442:G:C8	2.55	0.41
1:1:2457:G:H3'	1:1:2458:A:H2'	2.02	0.41
1:1:2555:G:C2	37:g:92:ALA:HA	2.56	0.41
1:1:2711:C:O2'	1:1:2744:U:OP1	2.39	0.41
1:1:2933:A:C2	1:1:3014:U:H4'	2.56	0.41
1:1:3107:U:H2'	1:1:3108:G:C8	2.55	0.41
1:1:3185:U:O2'	23:S:170:THR:OG1	2.34	0.41
1:1:3203:U:H2'	1:1:3204:C:C6	2.56	0.41
4:P0:42:ARG:CZ	4:P0:51:VAL:HG13	2.51	0.41
8:C:34:ILE:HA	8:C:34:ILE:HD12	1.88	0.41
16:L:74:GLY:HA3	16:L:97:VAL:HA	2.03	0.41
18:N:44:ARG:NH2	18:N:120:TRP:O	2.52	0.41
21:Q:155:MET:HE3	21:Q:156:GLY:H	1.86	0.41
26:V:77:ILE:HD11	26:V:126:TRP:CD1	2.56	0.41
28:X:93:TYR:O	28:X:97:LYS:N	2.51	0.41
30:Z:58:GLY:H	30:Z:61:LYS:HE3	1.86	0.41
36:f:49:ILE:HG21	36:f:85:PHE:CE1	2.56	0.41
38:h:90:ARG:HA	38:h:90:ARG:HD3	1.92	0.41
46:p:30:GLU:HA	46:p:33:GLN:HB3	2.03	0.41
47:2:191:C:C2	47:2:192:U:H1'	2.56	0.41
47:2:385:A:H2'	47:2:386:G:C8	2.56	0.41
47:2:386:G:P	56:y:25:ARG:HH22	2.43	0.41
47:2:821:U:H2'	47:2:822:U:C6	2.55	0.41
47:2:897:C:O2	62:AE:41:ARG:NH2	2.54	0.41
47:2:1040:G:H2'	47:2:1041:G:C8	2.56	0.41
47:2:1528:U:O2'	64:AG:42:GLU:OE1	2.29	0.41
47:2:1534:G:H4'	47:2:1536:G:H22	1.86	0.41
48:q:31:VAL:HG21	48:q:152:PRO:HA	2.03	0.41
49:r:205:PHE:HD2	49:r:207:LEU:HD23	1.86	0.41
51:t:210:GLU:HA	51:t:211:PRO:HD3	1.88	0.41
53:v:120:ILE:HG12	73:AP:100:ILE:HD12	2.03	0.41
57:z:29:LYS:HZ2	78:AU:44:PHE:H	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:AD:104:ARG:O	61:AD:106:ARG:N	2.54	0.41
63:AF:89:MET:HB2	63:AF:92:SER:HB3	2.03	0.41
67:AJ:124:ILE:HD12	67:AJ:124:ILE:HA	1.96	0.41
71:AN:55:GLU:HG3	71:AN:56:LYS:H	1.86	0.41
74:AQ:96:ALA:HA	74:AQ:97:PRO:HD3	1.91	0.41
79:AV:73:LEU:HD13	79:AV:80:ALA:HB2	2.02	0.41
81:AX:149:GLU:H	81:AX:150:ARG:HA	1.86	0.41
81:AX:579:SER:H	81:AX:585:ARG:HH12	1.69	0.41
81:AX:733:ILE:HG22	81:AX:794:PRO:HB3	2.01	0.41
82:AY:9:A:O3'	82:AY:45:G:O2'	2.34	0.41
1:1:1321:G:N2	23:S:112:ALA:HB2	2.36	0.41
1:1:2882:U:H2'	1:1:2883:U:C6	2.56	0.41
1:1:3157:U:H1'	1:1:3158:G:C8	2.56	0.41
5:P2:89:PRO:O	5:P2:93:LYS:NZ	2.49	0.41
9:D:107:ARG:NH2	9:D:119:TYR:O	2.51	0.41
9:D:222:LEU:HA	9:D:222:LEU:HD13	1.88	0.41
20:P:153:LYS:H	20:P:153:LYS:HD2	1.86	0.41
23:S:155:ARG:NH1	23:S:171:PHE:O	2.54	0.41
30:Z:5:LEU:HD22	30:Z:5:LEU:HA	1.90	0.41
33:c:57:GLU:HA	33:c:60:ALA:HB3	2.03	0.41
41:k:30:LYS:N	41:k:39:ARG:O	2.54	0.41
47:2:898:A:C6	47:2:914:G:N2	2.89	0.41
47:2:1267:G:O2'	47:2:1448:G:O2'	2.28	0.41
47:2:1299:G:H2'	47:2:1300:A:C8	2.56	0.41
53:v:113:ILE:HA	53:v:116:HIS:HB2	2.03	0.41
53:v:211:ILE:HD13	53:v:214:LYS:HD3	2.02	0.41
54:w:1:MET:HA	54:w:109:LEU:HD23	2.03	0.41
60:AC:37:VAL:HG12	60:AC:38:HIS:CD2	2.56	0.41
73:AP:50:ILE:H	73:AP:50:ILE:HG13	1.66	0.41
73:AP:77:ARG:HG2	73:AP:80:LEU:HD12	2.03	0.41
81:AX:221:THR:H	81:AX:224:GLN:HE22	1.69	0.41
81:AX:486:SER:OG	81:AX:533:THR:O	2.38	0.41
81:AX:586:ILE:HD11	81:AX:688:ILE:HB	2.02	0.41
1:1:254:A:H2'	1:1:255:A:H8	1.87	0.40
1:1:735:A:H2'	1:1:736:A:H8	1.87	0.40
1:1:1268:G:OP1	43:m:126:LYS:NZ	2.48	0.40
15:J:25:GLU:HA	15:J:65:ILE:HG22	2.03	0.40
24:T:142:SER:OG	24:T:143:THR:N	2.55	0.40
30:Z:27:LYS:NZ	30:Z:96:VAL:O	2.42	0.40
47:2:329:G:H2'	47:2:330:G:H8	1.86	0.40
47:2:549:G:H2'	47:2:550:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:587:C:OP1	78:AU:23:LYS:NZ	2.41	0.40
47:2:641:G:O6	47:2:693:U:O2	2.38	0.40
47:2:822:U:H2'	47:2:823:G:H8	1.85	0.40
47:2:958:U:OP2	75:AR:20:LYS:NZ	2.51	0.40
47:2:1410:A:H2'	47:2:1411:A:C8	2.56	0.40
47:2:1484:G:O2'	47:2:1606:C:O3'	2.37	0.40
52:u:87:MET:SD	52:u:123:LEU:N	2.83	0.40
52:u:181:VAL:HA	52:u:227:VAL:HA	2.02	0.40
53:v:211:ILE:HA	53:v:214:LYS:HB2	2.04	0.40
84:BA:118:LYS:HE3	84:BA:118:LYS:HB3	1.72	0.40
1:1:29:C:O2'	18:N:162:ARG:O	2.39	0.40
1:1:170:G:H1'	1:1:250:U:H3	1.86	0.40
1:1:598:A:H2'	1:1:599:C:C6	2.56	0.40
1:1:1171:G:OP2	11:F:218:ARG:NH1	2.54	0.40
1:1:1723:A:OP1	22:R:128:LYS:NZ	2.54	0.40
1:1:2681:U:H4'	15:J:66:ALA:HB2	2.02	0.40
2:3:5:G:OP1	15:J:143:ARG:NH2	2.54	0.40
3:4:71:A:OP2	29:Y:51:ARG:NH1	2.54	0.40
6:A:18:SER:OG	6:A:19:HIS:N	2.54	0.40
12:G:136:LEU:HD21	18:N:3:ALA:HB3	2.04	0.40
14:I:30:LYS:NZ	14:I:66:GLU:HB3	2.36	0.40
14:I:213:PHE:CE2	14:I:216:TYR:HB2	2.56	0.40
19:O:156:LEU:HD12	19:O:159:LYS:HE2	2.03	0.40
23:S:43:TYR:O	23:S:47:LYS:NZ	2.49	0.40
47:2:924:A:H2'	47:2:925:G:C8	2.56	0.40
47:2:1087:A:H2'	47:2:1088:A:C8	2.56	0.40
52:u:34:GLY:HA2	52:u:35:PRO:HD3	1.94	0.40
68:AK:77:LYS:HB3	68:AK:77:LYS:HE3	1.90	0.40
72:AO:113:ASN:OD1	72:AO:114:ARG:N	2.53	0.40
1:1:75:G:H1'	16:L:61:PRO:HG3	2.04	0.40
1:1:776:U:H4'	32:b:41:ARG:NH1	2.37	0.40
1:1:2174:G:P	6:A:193:ARG:HH22	2.43	0.40
1:1:2565:U:H2'	1:1:2566:C:C6	2.56	0.40
1:1:3204:C:H2'	1:1:3205:G:C8	2.56	0.40
7:B:84:VAL:HG12	7:B:164:THR:HA	2.03	0.40
9:D:50:ARG:NH1	9:D:147:ASP:OD2	2.54	0.40
16:L:79:GLU:OE2	16:L:112:ASN:ND2	2.55	0.40
22:R:162:ARG:HH12	47:2:849:C:H5''	1.85	0.40
31:a:28:HIS:HA	31:a:29:PRO:HD3	1.82	0.40
31:a:32:ARG:HH11	31:a:32:ARG:HD2	1.74	0.40
36:f:51:TYR:HD1	36:f:98:VAL:HG22	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2:486:G:N1	47:2:501:U:N3	2.39	0.40
47:2:813:U:C4	59:AB:153:PHE:HB3	2.57	0.40
47:2:953:G:H2'	47:2:954:G:H8	1.87	0.40
47:2:1222:C:H2'	47:2:1223:A:H8	1.86	0.40
47:2:1310:U:H2'	47:2:1311:U:C6	2.56	0.40
47:2:1388:A:H5''	65:AH:44:LYS:NZ	2.36	0.40
47:2:1617:U:O2'	47:2:1618:C:O4'	2.39	0.40
47:2:1769:U:O2	62:AE:136:ARG:NH1	2.52	0.40
50:s:157:LYS:HD2	50:s:168:ARG:NH1	2.37	0.40
55:x:9:LEU:HD22	55:x:17:GLU:HB3	2.03	0.40
60:AC:138:GLU:OE1	60:AC:141:SER:OG	2.39	0.40
67:AJ:19:ALA:HB2	67:AJ:59:ALA:HB3	2.03	0.40
67:AJ:40:SER:HA	67:AJ:96:ALA:HA	2.04	0.40
68:AK:29:THR:O	68:AK:87:HIS:ND1	2.40	0.40
79:AV:178:VAL:HB	79:AV:192:PHE:HB2	2.03	0.40
1:1:45:A:OP2	18:N:85:THR:OG1	2.34	0.40
1:1:293:C:O2'	39:i:76:ARG:O	2.26	0.40
1:1:707:U:H2'	1:1:708:G:C8	2.57	0.40
1:1:768:C:H2'	1:1:769:G:C8	2.57	0.40
1:1:2722:U:H2'	1:1:2723:U:H6	1.86	0.40
1:1:2889:C:H2'	1:1:2890:A:H8	1.86	0.40
1:1:3252:G:H2'	1:1:3253:G:H8	1.85	0.40
6:A:79:ASN:ND2	6:A:166:ILE:O	2.54	0.40
9:D:18:THR:HB	9:D:24:ARG:HD3	2.02	0.40
9:D:39:GLN:HE21	9:D:43:LYS:HG3	1.85	0.40
18:N:165:THR:OG1	18:N:167:THR:OG1	2.32	0.40
31:a:103:ASP:OD1	31:a:103:ASP:N	2.55	0.40
47:2:416:A:H3'	47:2:417:A:C8	2.56	0.40
47:2:1268:G:O2'	47:2:1270:G:OP1	2.32	0.40
51:t:62:ASN:HD21	58:AA:95:ARG:HA	1.85	0.40
51:t:109:LEU:H	51:t:109:LEU:HG	1.67	0.40
55:x:62:VAL:HA	55:x:63:PRO:HD3	1.93	0.40
65:AH:66:VAL:O	65:AH:70:SER:OG	2.34	0.40
71:AN:75:GLN:HB2	71:AN:82:LYS:HZ3	1.86	0.40
1:1:268:A:H5''	18:N:47:LYS:HE3	2.02	0.40
1:1:432:G:H2'	1:1:433:A:C8	2.56	0.40
1:1:707:U:OP1	1:1:779:G:O2'	2.38	0.40
1:1:928:C:H2'	1:1:929:A:H8	1.86	0.40
1:1:999:G:H2'	1:1:1000:C:C6	2.56	0.40
1:1:1258:U:O3'	4:P0:42:ARG:NH1	2.54	0.40
1:1:1347:U:H5''	8:C:302:ALA:HB1	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1476:G:H1	1:1:1877:U:H3	1.69	0.40
1:1:1622:U:H2'	1:1:1623:G:H8	1.86	0.40
1:1:1713:G:N2	1:1:1731:A:OP2	2.51	0.40
1:1:1723:A:N1	1:1:1788:C:O2'	2.48	0.40
1:1:2189:U:O3'	46:p:21:SER:OG	2.36	0.40
1:1:3305:A:P	7:B:334:ARG:HH22	2.44	0.40
2:3:98:C:H5'	11:F:222:HIS:HE1	1.87	0.40
9:D:287:ALA:HA	9:D:290:ILE:HG12	2.04	0.40
19:O:76:PRO:HA	19:O:79:ILE:HG22	2.03	0.40
25:U:50:LEU:HD11	25:U:54:VAL:H	1.86	0.40
26:V:87:ARG:NH1	26:V:93:LEU:HD21	2.37	0.40
28:X:115:ARG:N	28:X:119:THR:O	2.48	0.40
31:a:128:ARG:NE	31:a:149:ALA:O	2.54	0.40
47:2:986:G:H2'	47:2:987:G:O4'	2.21	0.40
47:2:1593:A:H2'	47:2:1594:G:C8	2.57	0.40
50:s:144:TRP:CE2	50:s:173:PRO:HD3	2.56	0.40
52:u:247:SER:OG	52:u:248:ILE:N	2.55	0.40
53:v:97:LEU:HB2	53:v:180:ARG:NH1	2.37	0.40
61:AD:143:SER:HA	61:AD:146:ALA:HB2	2.03	0.40
62:AE:114:ARG:HG3	74:AQ:62:TYR:CE2	2.56	0.40
63:AF:121:ILE:HG22	63:AF:123:TYR:H	1.86	0.40
66:AI:71:GLN:NE2	66:AI:79:TYR:OH	2.48	0.40
71:AN:116:ASP:OD1	71:AN:116:ASP:N	2.53	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	
4	P0	187/189 (99%)	145 (78%)	42 (22%)	0	100	100
5	P2	92/94 (98%)	64 (70%)	28 (30%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	250/252 (99%)	217 (87%)	33 (13%)	0	100	100
7	B	384/386 (100%)	335 (87%)	48 (12%)	1 (0%)	36	70
8	C	359/361 (99%)	305 (85%)	52 (14%)	2 (1%)	21	57
9	D	294/296 (99%)	248 (84%)	43 (15%)	3 (1%)	12	45
10	E	152/175 (87%)	137 (90%)	15 (10%)	0	100	100
11	F	220/222 (99%)	194 (88%)	25 (11%)	1 (0%)	24	60
12	G	231/233 (99%)	204 (88%)	27 (12%)	0	100	100
13	H	189/191 (99%)	168 (89%)	20 (11%)	1 (0%)	24	60
14	I	207/220 (94%)	178 (86%)	29 (14%)	0	100	100
15	J	167/169 (99%)	130 (78%)	34 (20%)	3 (2%)	6	34
16	L	191/193 (99%)	166 (87%)	23 (12%)	2 (1%)	12	45
17	M	134/136 (98%)	121 (90%)	12 (9%)	1 (1%)	18	54
18	N	201/203 (99%)	172 (86%)	29 (14%)	0	100	100
19	O	195/197 (99%)	171 (88%)	21 (11%)	3 (2%)	8	38
20	P	181/183 (99%)	161 (89%)	20 (11%)	0	100	100
21	Q	183/185 (99%)	165 (90%)	18 (10%)	0	100	100
22	R	186/188 (99%)	170 (91%)	16 (9%)	0	100	100
23	S	170/172 (99%)	151 (89%)	19 (11%)	0	100	100
24	T	157/159 (99%)	146 (93%)	11 (7%)	0	100	100
25	U	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
26	V	134/136 (98%)	120 (90%)	14 (10%)	0	100	100
27	W	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
28	X	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
29	Y	124/126 (98%)	115 (93%)	9 (7%)	0	100	100
30	Z	133/135 (98%)	115 (86%)	17 (13%)	1 (1%)	16	52
31	a	146/148 (99%)	118 (81%)	25 (17%)	3 (2%)	5	32
32	b	56/58 (97%)	46 (82%)	10 (18%)	0	100	100
33	c	95/97 (98%)	90 (95%)	5 (5%)	0	100	100
34	d	107/109 (98%)	95 (89%)	12 (11%)	0	100	100
35	e	125/127 (98%)	103 (82%)	22 (18%)	0	100	100
36	f	104/106 (98%)	90 (86%)	11 (11%)	3 (3%)	3	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	g	110/112 (98%)	98 (89%)	10 (9%)	2 (2%)	6	34
38	h	117/119 (98%)	100 (86%)	17 (14%)	0	100	100
39	i	97/99 (98%)	75 (77%)	21 (22%)	1 (1%)	12	45
40	j	85/87 (98%)	67 (79%)	16 (19%)	2 (2%)	4	30
41	k	75/77 (97%)	54 (72%)	19 (25%)	2 (3%)	4	28
42	l	48/50 (96%)	36 (75%)	11 (23%)	1 (2%)	5	32
43	m	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
44	n	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
45	o	103/105 (98%)	78 (76%)	25 (24%)	0	100	100
46	p	89/91 (98%)	78 (88%)	11 (12%)	0	100	100
48	q	204/206 (99%)	162 (79%)	39 (19%)	3 (2%)	8	38
49	r	212/214 (99%)	167 (79%)	41 (19%)	4 (2%)	6	34
50	s	215/217 (99%)	187 (87%)	27 (13%)	1 (0%)	24	60
51	t	221/223 (99%)	182 (82%)	37 (17%)	2 (1%)	14	48
52	u	258/260 (99%)	195 (76%)	61 (24%)	2 (1%)	16	52
53	v	204/206 (99%)	162 (79%)	41 (20%)	1 (0%)	24	60
54	w	221/223 (99%)	167 (76%)	47 (21%)	7 (3%)	3	25
55	x	182/184 (99%)	145 (80%)	34 (19%)	3 (2%)	7	37
56	y	184/199 (92%)	148 (80%)	36 (20%)	0	100	100
57	z	183/185 (99%)	147 (80%)	36 (20%)	0	100	100
58	AA	94/105 (90%)	76 (81%)	17 (18%)	1 (1%)	11	44
59	AB	151/153 (99%)	131 (87%)	18 (12%)	2 (1%)	9	41
60	AC	122/124 (98%)	93 (76%)	27 (22%)	2 (2%)	7	37
61	AD	148/150 (99%)	118 (80%)	27 (18%)	3 (2%)	6	33
62	AE	125/127 (98%)	104 (83%)	21 (17%)	0	100	100
63	AF	122/124 (98%)	89 (73%)	33 (27%)	0	100	100
64	AG	139/141 (99%)	111 (80%)	27 (19%)	1 (1%)	18	54
65	AH	116/125 (93%)	98 (84%)	17 (15%)	1 (1%)	14	48
66	AI	143/145 (99%)	117 (82%)	24 (17%)	2 (1%)	9	39
67	AJ	141/143 (99%)	126 (89%)	15 (11%)	0	100	100
68	AK	105/107 (98%)	90 (86%)	15 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	AL	85/87 (98%)	64 (75%)	19 (22%)	2 (2%)	4	30
70	AM	127/129 (98%)	115 (91%)	11 (9%)	1 (1%)	16	52
71	AN	142/144 (99%)	108 (76%)	34 (24%)	0	100	100
72	AO	132/134 (98%)	115 (87%)	17 (13%)	0	100	100
73	AP	68/70 (97%)	52 (76%)	15 (22%)	1 (2%)	8	38
74	AQ	95/97 (98%)	70 (74%)	25 (26%)	0	100	100
75	AR	79/81 (98%)	58 (73%)	21 (27%)	0	100	100
76	AS	61/63 (97%)	49 (80%)	12 (20%)	0	100	100
77	AT	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
78	AU	58/60 (97%)	42 (72%)	16 (28%)	0	100	100
79	AV	316/318 (99%)	252 (80%)	64 (20%)	0	100	100
80	AW	35/37 (95%)	21 (60%)	14 (40%)	0	100	100
81	AX	834/837 (100%)	676 (81%)	155 (19%)	3 (0%)	30	65
84	BA	202/204 (99%)	153 (76%)	47 (23%)	2 (1%)	12	45
All	All	12203/12421 (98%)	10189 (84%)	1938 (16%)	76 (1%)	23	57

All (76) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	i	98	ARG
40	j	65	ARG
42	l	30	ARG
48	q	113	ARG
54	w	68	LEU
54	w	93	LYS
61	AD	105	ASN
64	AG	41	PRO
16	L	63	VAL
16	L	77	LEU
17	M	8	LYS
31	a	78	LEU
36	f	58	GLU
36	f	60	ARG
49	r	55	LYS
49	r	62	LYS
50	s	40	LYS
52	u	195	ILE

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Mol	Chain	Res	Type
54	w	92	ARG
55	x	111	LYS
60	AC	109	GLU
8	C	130	ALA
11	F	159	GLN
15	J	74	PRO
15	J	166	LYS
19	O	111	PRO
31	a	47	LYS
41	k	40	GLN
49	r	206	PRO
49	r	207	LEU
51	t	220	PRO
53	v	50	GLU
54	w	10	ASN
54	w	100	ALA
55	x	29	ASN
55	x	65	PRO
81	AX	698	ILE
9	D	20	PHE
9	D	261	THR
19	O	12	LYS
31	a	48	TYR
48	q	112	THR
52	u	155	LYS
59	AB	56	LYS
66	AI	91	ASP
69	AL	52	THR
69	AL	81	ASN
84	BA	197	ASN
8	C	268	ALA
13	H	50	ASN
37	g	66	SER
37	g	67	LYS
41	k	33	LYS
48	q	114	SER
61	AD	139	TRP
65	AH	72	LYS
66	AI	63	GLN
19	O	37	ARG
54	w	101	ILE
61	AD	85	PRO

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Mol	Chain	Res	Type
73	AP	97	LYS
84	BA	198	TRP
9	D	125	VAL
51	t	203	PRO
59	AB	7	VAL
40	j	6	PRO
81	AX	252	PRO
36	f	59	VAL
81	AX	741	GLY
15	J	118	PRO
30	Z	103	GLN
54	w	85	ARG
70	AM	67	GLY
7	B	188	ILE
58	AA	88	PRO
60	AC	106	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	
4	P0	160/160 (100%)	158 (99%)	2 (1%)	61	72
5	P2	81/81 (100%)	80 (99%)	1 (1%)	63	73
6	A	193/194 (100%)	190 (98%)	3 (2%)	55	70
7	B	321/322 (100%)	319 (99%)	2 (1%)	78	81
8	C	288/288 (100%)	285 (99%)	3 (1%)	68	76
9	D	244/244 (100%)	243 (100%)	1 (0%)	84	84
10	E	134/152 (88%)	131 (98%)	3 (2%)	45	65
11	F	186/186 (100%)	183 (98%)	3 (2%)	55	70
12	G	187/191 (98%)	185 (99%)	2 (1%)	65	74
13	H	171/171 (100%)	169 (99%)	2 (1%)	63	73
14	I	177/186 (95%)	177 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	J	147/147 (100%)	143 (97%)	4 (3%)	39	60
16	L	154/154 (100%)	150 (97%)	4 (3%)	40	61
17	M	107/107 (100%)	106 (99%)	1 (1%)	70	76
18	N	175/175 (100%)	172 (98%)	3 (2%)	53	68
19	O	160/160 (100%)	159 (99%)	1 (1%)	78	81
20	P	140/145 (97%)	139 (99%)	1 (1%)	76	79
21	Q	150/150 (100%)	150 (100%)	0	100	100
22	R	153/153 (100%)	153 (100%)	0	100	100
23	S	156/156 (100%)	152 (97%)	4 (3%)	40	61
24	T	136/136 (100%)	134 (98%)	2 (2%)	57	70
25	U	87/87 (100%)	85 (98%)	2 (2%)	44	64
26	V	103/104 (99%)	102 (99%)	1 (1%)	68	76
27	W	54/54 (100%)	54 (100%)	0	100	100
28	X	104/105 (99%)	104 (100%)	0	100	100
29	Y	109/109 (100%)	109 (100%)	0	100	100
30	Z	115/115 (100%)	113 (98%)	2 (2%)	53	68
31	a	118/118 (100%)	118 (100%)	0	100	100
32	b	46/46 (100%)	46 (100%)	0	100	100
33	c	81/81 (100%)	79 (98%)	2 (2%)	42	62
34	d	94/96 (98%)	94 (100%)	0	100	100
35	e	109/109 (100%)	109 (100%)	0	100	100
36	f	90/90 (100%)	90 (100%)	0	100	100
37	g	95/95 (100%)	94 (99%)	1 (1%)	65	74
38	h	104/104 (100%)	103 (99%)	1 (1%)	68	76
39	i	81/81 (100%)	79 (98%)	2 (2%)	42	62
40	j	70/70 (100%)	70 (100%)	0	100	100
41	k	68/68 (100%)	68 (100%)	0	100	100
42	l	45/45 (100%)	45 (100%)	0	100	100
43	m	47/47 (100%)	47 (100%)	0	100	100
44	n	23/23 (100%)	23 (100%)	0	100	100
45	o	90/90 (100%)	89 (99%)	1 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	p	71/71 (100%)	70 (99%)	1 (1%)	59	71
48	q	164/173 (95%)	161 (98%)	3 (2%)	51	68
49	r	191/191 (100%)	186 (97%)	5 (3%)	40	61
50	s	176/176 (100%)	175 (99%)	1 (1%)	78	81
51	t	182/182 (100%)	179 (98%)	3 (2%)	55	70
52	u	221/221 (100%)	217 (98%)	4 (2%)	51	68
53	v	173/173 (100%)	173 (100%)	0	100	100
54	w	189/191 (99%)	186 (98%)	3 (2%)	55	70
55	x	165/165 (100%)	165 (100%)	0	100	100
56	y	150/160 (94%)	149 (99%)	1 (1%)	76	79
57	z	158/158 (100%)	157 (99%)	1 (1%)	78	81
58	AA	77/98 (79%)	76 (99%)	1 (1%)	61	72
59	AB	133/134 (99%)	133 (100%)	0	100	100
60	AC	88/100 (88%)	88 (100%)	0	100	100
61	AD	127/127 (100%)	124 (98%)	3 (2%)	43	63
62	AE	81/96 (84%)	78 (96%)	3 (4%)	30	52
63	AF	101/104 (97%)	99 (98%)	2 (2%)	48	66
64	AG	117/117 (100%)	117 (100%)	0	100	100
65	AH	94/113 (83%)	91 (97%)	3 (3%)	34	56
66	AI	128/128 (100%)	128 (100%)	0	100	100
67	AJ	115/115 (100%)	115 (100%)	0	100	100
68	AK	100/100 (100%)	99 (99%)	1 (1%)	68	76
69	AL	74/74 (100%)	74 (100%)	0	100	100
70	AM	110/110 (100%)	109 (99%)	1 (1%)	70	76
71	AN	119/119 (100%)	117 (98%)	2 (2%)	53	68
72	AO	112/112 (100%)	112 (100%)	0	100	100
73	AP	61/61 (100%)	61 (100%)	0	100	100
74	AQ	83/83 (100%)	80 (96%)	3 (4%)	31	53
75	AR	70/70 (100%)	70 (100%)	0	100	100
76	AS	56/56 (100%)	56 (100%)	0	100	100
77	AT	47/47 (100%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	AU	51/51 (100%)	50 (98%)	1 (2%)	48	66
79	AV	259/261 (99%)	257 (99%)	2 (1%)	73	77
80	AW	31/31 (100%)	31 (100%)	0	100	100
81	AX	708/709 (100%)	694 (98%)	14 (2%)	48	66
84	BA	185/185 (100%)	182 (98%)	3 (2%)	55	70
All	All	10320/10457 (99%)	10205 (99%)	115 (1%)	63	74

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	P0	51	VAL
4	P0	81	LYS
5	P2	117	ARG
6	A	180	LEU
6	A	225	ILE
6	A	243	THR
7	B	85	VAL
7	B	161	LEU
8	C	156	LEU
8	C	183	LYS
8	C	233	LEU
9	D	247	ILE
10	E	65	ILE
10	E	74	VAL
10	E	154	LEU
11	F	105	LEU
11	F	173	LEU
11	F	209	ASN
12	G	26	LEU
12	G	238	LEU
13	H	38	LEU
13	H	48	VAL
15	J	12	LEU
15	J	71	VAL
15	J	80	LEU
15	J	84	LEU
16	L	35	ARG
16	L	85	LEU
16	L	93	ILE
16	L	172	LEU

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Mol	Chain	Res	Type
17	M	50	LYS
18	N	106	VAL
18	N	115	VAL
18	N	132	VAL
19	O	23	VAL
20	P	114	VAL
23	S	10	ILE
23	S	24	LEU
23	S	48	LEU
23	S	148	LEU
24	T	80	VAL
24	T	89	LEU
25	U	56	VAL
25	U	84	LEU
26	V	69	LEU
30	Z	5	LEU
30	Z	81	LEU
33	c	42	ILE
33	c	89	VAL
37	g	47	CYS
38	h	118	ILE
39	i	43	LEU
39	i	60	LEU
45	o	15	LYS
46	p	86	LEU
48	q	48	ILE
48	q	67	ILE
48	q	188	LEU
49	r	43	VAL
49	r	48	VAL
49	r	161	ILE
49	r	176	VAL
49	r	188	LEU
50	s	207	LEU
51	t	4	LEU
51	t	21	LEU
51	t	109	LEU
52	u	12	LEU
52	u	180	LEU
52	u	192	ILE
52	u	238	LEU
54	w	18	ILE

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Mol	Chain	Res	Type
54	w	71	THR
54	w	167	LYS
56	y	104	ILE
57	z	109	LEU
58	AA	43	ILE
61	AD	16	ILE
61	AD	33	VAL
61	AD	104	ARG
62	AE	28	VAL
62	AE	110	LEU
62	AE	135	ARG
63	AF	36	LEU
63	AF	126	VAL
65	AH	44	LYS
65	AH	72	LYS
65	AH	115	LEU
68	AK	24	ILE
70	AM	63	VAL
71	AN	63	GLN
71	AN	96	VAL
74	AQ	18	VAL
74	AQ	75	VAL
74	AQ	84	VAL
78	AU	8	LEU
79	AV	113	VAL
79	AV	292	LEU
81	AX	119	LEU
81	AX	156	VAL
81	AX	244	LEU
81	AX	247	ASP
81	AX	306	VAL
81	AX	310	ASP
81	AX	328	LEU
81	AX	465	LYS
81	AX	538	LEU
81	AX	545	LEU
81	AX	632	LYS
81	AX	646	VAL
81	AX	647	ILE
81	AX	693	LEU
84	BA	18	LYS
84	BA	167	VAL

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Mol	Chain	Res	Type
84	BA	193	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (196) such sidechains are listed below:

Mol	Chain	Res	Type
4	P0	32	ASN
4	P0	39	HIS
4	P0	174	ASN
4	P0	189	GLN
5	P2	66	ASN
5	P2	137	GLN
6	A	8	GLN
6	A	38	HIS
6	A	86	GLN
6	A	139	HIS
6	A	194	ASN
6	A	233	GLN
7	B	68	HIS
7	B	173	GLN
7	B	177	HIS
7	B	243	HIS
8	C	5	GLN
8	C	18	ASN
8	C	48	GLN
8	C	59	GLN
8	C	201	GLN
8	C	221	ASN
8	C	260	GLN
8	C	307	GLN
9	D	39	GLN
9	D	63	GLN
9	D	90	HIS
9	D	264	GLN
10	E	80	ASN
11	F	104	GLN
11	F	172	ASN
11	F	209	ASN
11	F	225	GLN
11	F	231	ASN
11	F	237	ASN
12	G	33	ASN
12	G	191	ASN

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Mol	Chain	Res	Type
12	G	240	ASN
13	H	116	ASN
14	I	14	ASN
14	I	51	HIS
14	I	59	GLN
14	I	95	HIS
15	J	39	GLN
15	J	43	GLN
15	J	109	HIS
16	L	6	ASN
16	L	28	GLN
16	L	37	ASN
16	L	102	GLN
16	L	103	ASN
17	M	27	GLN
18	N	37	HIS
18	N	86	ASN
18	N	123	GLN
18	N	138	GLN
18	N	139	HIS
19	O	42	ASN
19	O	72	HIS
20	P	34	GLN
20	P	50	GLN
20	P	97	ASN
21	Q	45	ASN
21	Q	78	ASN
22	R	34	GLN
22	R	36	ASN
22	R	39	ASN
22	R	92	GLN
22	R	134	HIS
22	R	156	ASN
22	R	166	ASN
24	T	49	GLN
24	T	54	HIS
24	T	82	ASN
24	T	95	HIS
24	T	134	GLN
28	X	80	ASN
29	Y	42	GLN
29	Y	81	GLN

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Mol	Chain	Res	Type
30	Z	29	HIS
30	Z	36	HIS
30	Z	106	GLN
30	Z	122	HIS
30	Z	128	GLN
31	a	28	HIS
31	a	39	HIS
31	a	40	HIS
31	a	49	HIS
32	b	19	ASN
33	c	75	ASN
35	e	13	HIS
35	e	20	HIS
35	e	35	GLN
35	e	88	HIS
36	f	75	HIS
38	h	59	ASN
38	h	113	GLN
39	i	12	ASN
39	i	91	ASN
41	k	10	GLN
42	l	43	ASN
43	m	117	HIS
43	m	119	ASN
45	o	38	GLN
45	o	53	GLN
45	o	59	HIS
45	o	82	GLN
48	q	21	ASN
48	q	28	ASN
48	q	33	GLN
48	q	69	ASN
48	q	140	ASN
48	q	163	ASN
49	r	95	ASN
49	r	149	GLN
49	r	153	HIS
49	r	160	HIS
49	r	177	GLN
49	r	199	ASN
49	r	211	HIS
51	t	174	HIS

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Mol	Chain	Res	Type
52	u	17	HIS
52	u	69	HIS
52	u	130	GLN
52	u	231	GLN
53	v	63	GLN
53	v	79	ASN
53	v	95	ASN
53	v	103	ASN
53	v	122	ASN
53	v	128	ASN
53	v	224	ASN
54	w	4	ASN
54	w	59	GLN
54	w	176	GLN
54	w	190	GLN
55	x	42	GLN
55	x	108	GLN
55	x	180	GLN
57	z	38	ASN
57	z	112	GLN
57	z	139	GLN
57	z	155	HIS
57	z	176	ASN
58	AA	9	ASN
58	AA	12	HIS
58	AA	29	GLN
58	AA	39	ASN
58	AA	62	GLN
58	AA	81	ASN
59	AB	14	GLN
59	AB	92	HIS
59	AB	127	GLN
60	AC	96	GLN
61	AD	21	ASN
61	AD	36	GLN
61	AD	58	HIS
64	AG	32	ASN
66	AI	71	GLN
66	AI	136	GLN
67	AJ	16	ASN
67	AJ	23	GLN
67	AJ	77	ASN

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Mol	Chain	Res	Type
69	AL	81	ASN
70	AM	15	ASN
70	AM	42	GLN
70	AM	64	GLN
70	AM	113	HIS
71	AN	27	ASN
71	AN	63	GLN
71	AN	75	GLN
74	AQ	72	HIS
75	AR	19	HIS
75	AR	26	GLN
75	AR	51	GLN
77	AT	41	GLN
78	AU	57	ASN
79	AV	17	ASN
79	AV	101	GLN
79	AV	248	ASN
81	AX	101	ASN
81	AX	108	HIS
81	AX	186	ASN
81	AX	201	GLN
81	AX	224	GLN
81	AX	432	GLN
81	AX	452	ASN
81	AX	528	HIS
81	AX	573	GLN
81	AX	734	GLN
81	AX	759	GLN
84	BA	62	ASN
84	BA	141	ASN
84	BA	181	ASN
84	BA	197	ASN
84	BA	199	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3220/3396 (94%)	1076 (33%)	33 (1%)
2	3	120/121 (99%)	28 (23%)	3 (2%)
3	4	157/158 (99%)	48 (30%)	5 (3%)
47	2	1774/1797 (98%)	779 (43%)	38 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
82	AY	75/76 (98%)	29 (38%)	0
83	AZ	6/7 (85%)	5 (83%)	2 (33%)
All	All	5352/5555 (96%)	1965 (36%)	81 (1%)

All (1965) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	U
1	1	6	A
1	1	14	U
1	1	15	C
1	1	17	G
1	1	18	G
1	1	20	A
1	1	26	A
1	1	31	C
1	1	40	A
1	1	41	G
1	1	43	A
1	1	44	U
1	1	45	A
1	1	47	C
1	1	48	A
1	1	57	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	73	C
1	1	75	G
1	1	77	A
1	1	85	A
1	1	88	A
1	1	92	G
1	1	93	C
1	1	94	G
1	1	98	G
1	1	99	A
1	1	102	C
1	1	103	G
1	1	104	G
1	1	105	C

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Mol	Chain	Res	Type
1	1	108	A
1	1	111	C
1	1	112	U
1	1	116	A
1	1	118	U
1	1	119	U
1	1	121	A
1	1	122	A
1	1	130	A
1	1	132	C
1	1	135	C
1	1	136	G
1	1	138	U
1	1	145	G
1	1	148	G
1	1	152	U
1	1	153	U
1	1	154	U
1	1	156	G
1	1	157	A
1	1	158	G
1	1	161	G
1	1	162	G
1	1	164	A
1	1	165	A
1	1	166	C
1	1	185	C
1	1	186	U
1	1	187	A
1	1	190	U
1	1	193	C
1	1	194	U
1	1	197	G
1	1	198	A
1	1	200	C
1	1	211	A
1	1	212	G
1	1	219	A
1	1	220	G
1	1	222	A
1	1	223	U
1	1	227	G

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Mol	Chain	Res	Type
1	1	231	G
1	1	234	G
1	1	237	G
1	1	241	G
1	1	242	C
1	1	245	U
1	1	247	C
1	1	249	U
1	1	251	G
1	1	252	U
1	1	253	A
1	1	263	C
1	1	264	G
1	1	265	A
1	1	266	A
1	1	269	G
1	1	270	U
1	1	277	G
1	1	284	A
1	1	285	A
1	1	286	U
1	1	294	U
1	1	295	A
1	1	297	G
1	1	299	G
1	1	305	U
1	1	311	C
1	1	313	A
1	1	316	U
1	1	317	A
1	1	324	A
1	1	328	U
1	1	329	U
1	1	330	G
1	1	337	G
1	1	339	C
1	1	341	G
1	1	343	U
1	1	346	C
1	1	349	A
1	1	350	C
1	1	352	A

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Mol	Chain	Res	Type
1	1	361	A
1	1	368	G
1	1	371	G
1	1	372	A
1	1	375	A
1	1	376	G
1	1	377	A
1	1	380	U
1	1	384	A
1	1	385	A
1	1	387	A
1	1	390	G
1	1	391	A
1	1	398	A
1	1	399	A
1	1	400	G
1	1	401	U
1	1	402	A
1	1	403	C
1	1	404	G
1	1	420	G
1	1	421	G
1	1	422	A
1	1	429	U
1	1	433	A
1	1	437	G
1	1	440	A
1	1	441	U
1	1	442	G
1	1	443	G
1	1	444	U
1	1	446	U
1	1	447	U
1	1	448	U
1	1	449	U
1	1	450	G
1	1	451	U
1	1	488	U
1	1	490	C
1	1	491	A
1	1	493	U
1	1	494	G

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Mol	Chain	Res	Type
1	1	495	G
1	1	503	C
1	1	504	A
1	1	512	U
1	1	513	G
1	1	519	A
1	1	521	A
1	1	522	A
1	1	525	C
1	1	532	A
1	1	533	A
1	1	534	U
1	1	545	U
1	1	546	C
1	1	548	G
1	1	549	U
1	1	550	A
1	1	557	A
1	1	558	U
1	1	559	A
1	1	570	A
1	1	574	U
1	1	575	G
1	1	581	U
1	1	585	A
1	1	591	G
1	1	592	A
1	1	593	C
1	1	594	U
1	1	604	G
1	1	605	U
1	1	607	A
1	1	608	A
1	1	611	A
1	1	620	U
1	1	621	A
1	1	628	A
1	1	633	C
1	1	636	C
1	1	637	C
1	1	642	U
1	1	649	A

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Mol	Chain	Res	Type
1	1	657	A
1	1	660	A
1	1	662	U
1	1	664	U
1	1	667	C
1	1	677	A
1	1	678	G
1	1	681	U
1	1	684	G
1	1	689	U
1	1	691	A
1	1	692	A
1	1	705	A
1	1	709	A
1	1	712	G
1	1	714	G
1	1	716	A
1	1	718	G
1	1	719	U
1	1	742	G
1	1	748	U
1	1	750	G
1	1	758	C
1	1	761	A
1	1	763	G
1	1	764	U
1	1	765	C
1	1	767	U
1	1	773	G
1	1	776	U
1	1	777	U
1	1	780	A
1	1	781	G
1	1	782	U
1	1	785	G
1	1	797	U
1	1	800	G
1	1	801	A
1	1	806	A
1	1	808	A
1	1	813	G
1	1	817	A

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Mol	Chain	Res	Type
1	1	818	C
1	1	819	U
1	1	823	C
1	1	830	A
1	1	832	G
1	1	838	G
1	1	849	C
1	1	854	G
1	1	861	C
1	1	865	U
1	1	866	A
1	1	868	C
1	1	869	G
1	1	874	U
1	1	875	G
1	1	876	A
1	1	879	U
1	1	880	G
1	1	890	C
1	1	892	U
1	1	894	G
1	1	895	A
1	1	896	A
1	1	907	G
1	1	908	G
1	1	909	G
1	1	911	C
1	1	914	A
1	1	915	A
1	1	916	G
1	1	917	A
1	1	922	U
1	1	923	C
1	1	924	G
1	1	933	A
1	1	937	G
1	1	941	G
1	1	943	U
1	1	944	C
1	1	951	A
1	1	959	C
1	1	960	U

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Mol	Chain	Res	Type
1	1	962	A
1	1	963	G
1	1	964	G
1	1	971	G
1	1	974	G
1	1	977	C
1	1	979	U
1	1	980	A
1	1	981	U
1	1	983	A
1	1	984	G
1	1	985	U
1	1	990	U
1	1	991	G
1	1	994	G
1	1	1002	A
1	1	1006	A
1	1	1008	U
1	1	1009	A
1	1	1013	G
1	1	1014	U
1	1	1015	U
1	1	1016	C
1	1	1017	C
1	1	1019	G
1	1	1020	G
1	1	1021	G
1	1	1022	U
1	1	1024	G
1	1	1028	U
1	1	1029	G
1	1	1030	A
1	1	1031	C
1	1	1032	C
1	1	1033	U
1	1	1034	U
1	1	1035	G
1	1	1036	A
1	1	1037	C
1	1	1038	C
1	1	1042	U
1	1	1043	C

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Mol	Chain	Res	Type
1	1	1047	A
1	1	1051	U
1	1	1059	G
1	1	1061	A
1	1	1064	A
1	1	1066	G
1	1	1068	C
1	1	1072	G
1	1	1080	A
1	1	1081	U
1	1	1083	G
1	1	1085	A
1	1	1088	U
1	1	1089	G
1	1	1093	A
1	1	1094	U
1	1	1095	U
1	1	1096	U
1	1	1097	G
1	1	1098	A
1	1	1100	U
1	1	1103	A
1	1	1111	U
1	1	1117	G
1	1	1127	G
1	1	1129	A
1	1	1131	G
1	1	1136	A
1	1	1137	C
1	1	1143	A
1	1	1144	U
1	1	1151	U
1	1	1154	A
1	1	1155	C
1	1	1158	A
1	1	1159	A
1	1	1171	G
1	1	1172	G
1	1	1174	G
1	1	1177	G
1	1	1178	G
1	1	1180	A

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Mol	Chain	Res	Type
1	1	1181	U
1	1	1182	A
1	1	1186	G
1	1	1190	A
1	1	1191	U
1	1	1193	A
1	1	1196	C
1	1	1197	A
1	1	1198	C
1	1	1199	C
1	1	1200	A
1	1	1201	C
1	1	1203	A
1	1	1206	G
1	1	1209	G
1	1	1210	U
1	1	1212	A
1	1	1215	U
1	1	1217	A
1	1	1218	U
1	1	1219	C
1	1	1220	U
1	1	1222	G
1	1	1224	C
1	1	1225	A
1	1	1229	G
1	1	1233	G
1	1	1235	U
1	1	1236	G
1	1	1239	C
1	1	1240	A
1	1	1241	U
1	1	1244	A
1	1	1245	A
1	1	1246	G
1	1	1248	C
1	1	1249	G
1	1	1252	A
1	1	1253	U
1	1	1254	C
1	1	1257	C
1	1	1258	U

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Mol	Chain	Res	Type
1	1	1260	A
1	1	1262	G
1	1	1263	A
1	1	1264	G
1	1	1267	U
1	1	1271	A
1	1	1272	C
1	1	1275	C
1	1	1280	C
1	1	1281	G
1	1	1282	G
1	1	1283	C
1	1	1284	C
1	1	1286	A
1	1	1287	A
1	1	1291	A
1	1	1292	C
1	1	1295	G
1	1	1301	A
1	1	1302	A
1	1	1303	A
1	1	1305	U
1	1	1307	G
1	1	1308	A
1	1	1309	U
1	1	1313	G
1	1	1316	C
1	1	1318	A
1	1	1319	G
1	1	1321	G
1	1	1325	U
1	1	1331	U
1	1	1332	A
1	1	1337	A
1	1	1338	C
1	1	1340	G
1	1	1341	U
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1351	U
1	1	1352	A

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Mol	Chain	Res	Type
1	1	1354	G
1	1	1355	A
1	1	1356	U
1	1	1357	G
1	1	1362	G
1	1	1364	C
1	1	1370	G
1	1	1374	G
1	1	1375	G
1	1	1386	A
1	1	1390	A
1	1	1391	C
1	1	1392	G
1	1	1394	A
1	1	1397	C
1	1	1399	A
1	1	1400	G
1	1	1406	A
1	1	1411	C
1	1	1416	C
1	1	1418	A
1	1	1419	A
1	1	1425	U
1	1	1434	G
1	1	1437	C
1	1	1441	G
1	1	1442	U
1	1	1446	A
1	1	1450	G
1	1	1452	A
1	1	1455	U
1	1	1456	A
1	1	1460	A
1	1	1466	G
1	1	1469	C
1	1	1470	U
1	1	1482	A
1	1	1483	G
1	1	1484	U
1	1	1485	G
1	1	1490	A
1	1	1491	A

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Mol	Chain	Res	Type
1	1	1496	C
1	1	1502	C
1	1	1507	G
1	1	1508	C
1	1	1511	U
1	1	1512	U
1	1	1523	U
1	1	1526	U
1	1	1533	U
1	1	1536	G
1	1	1546	A
1	1	1551	C
1	1	1554	U
1	1	1556	C
1	1	1557	A
1	1	1558	A
1	1	1559	A
1	1	1560	G
1	1	1562	C
1	1	1564	U
1	1	1565	G
1	1	1568	U
1	1	1569	U
1	1	1570	U
1	1	1571	A
1	1	1572	U
1	1	1574	C
1	1	1576	G
1	1	1579	C
1	1	1580	A
1	1	1581	C
1	1	1583	A
1	1	1584	U
1	1	1587	A
1	1	1588	A
1	1	1589	A
1	1	1593	A
1	1	1596	C
1	1	1605	A
1	1	1606	U
1	1	1607	U
1	1	1613	A

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Mol	Chain	Res	Type
1	1	1621	A
1	1	1629	U
1	1	1632	A
1	1	1633	C
1	1	1642	A
1	1	1643	A
1	1	1645	U
1	1	1647	A
1	1	1654	A
1	1	1656	A
1	1	1657	C
1	1	1666	G
1	1	1671	C
1	1	1678	G
1	1	1680	G
1	1	1683	A
1	1	1702	U
1	1	1703	U
1	1	1711	C
1	1	1713	G
1	1	1715	A
1	1	1717	U
1	1	1718	G
1	1	1724	U
1	1	1728	G
1	1	1730	G
1	1	1735	G
1	1	1736	G
1	1	1738	C
1	1	1739	U
1	1	1740	U
1	1	1748	G
1	1	1749	A
1	1	1750	A
1	1	1751	G
1	1	1752	A
1	1	1754	G
1	1	1756	C
1	1	1760	A
1	1	1761	C
1	1	1764	U
1	1	1765	U

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Mol	Chain	Res	Type
1	1	1767	C
1	1	1770	G
1	1	1773	C
1	1	1775	G
1	1	1776	G
1	1	1777	U
1	1	1779	C
1	1	1780	G
1	1	1784	G
1	1	1788	C
1	1	1793	C
1	1	1795	U
1	1	1797	A
1	1	1813	A
1	1	1815	U
1	1	1816	A
1	1	1820	U
1	1	1821	U
1	1	1824	U
1	1	1838	G
1	1	1840	U
1	1	1841	A
1	1	1842	A
1	1	1846	C
1	1	1847	A
1	1	1850	A
1	1	1851	G
1	1	1855	U
1	1	1863	G
1	1	1864	A
1	1	1866	C
1	1	1868	G
1	1	1877	U
1	1	1878	G
1	1	1879	A
1	1	1880	U
1	1	1885	U
1	1	1886	A
1	1	1892	G
1	1	1895	A
1	1	1896	A
1	1	1900	A

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Mol	Chain	Res	Type
1	1	1905	G
1	1	1906	G
1	1	1912	U
1	1	1916	U
1	1	1920	U
1	1	1922	A
1	1	1926	C
1	1	1930	A
1	1	1931	U
1	1	1932	A
1	1	1933	A
1	1	1934	G
1	1	1935	G
1	1	1948	G
1	1	1953	G
1	1	1954	G
1	1	1955	U
1	1	2095	G
1	1	2099	A
1	1	2100	A
1	1	2101	C
1	1	2102	U
1	1	2107	A
1	1	2110	G
1	1	2111	G
1	1	2112	U
1	1	2114	C
1	1	2115	G
1	1	2116	G
1	1	2117	A
1	1	2122	G
1	1	2123	G
1	1	2131	A
1	1	2138	A
1	1	2139	A
1	1	2140	U
1	1	2142	A
1	1	2145	A
1	1	2148	U
1	1	2158	A
1	1	2159	U
1	1	2166	A

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Mol	Chain	Res	Type
1	1	2169	G
1	1	2170	U
1	1	2175	U
1	1	2176	U
1	1	2180	G
1	1	2182	A
1	1	2184	U
1	1	2188	A
1	1	2192	C
1	1	2194	G
1	1	2205	U
1	1	2207	A
1	1	2209	U
1	1	2210	G
1	1	2213	A
1	1	2215	A
1	1	2221	G
1	1	2222	A
1	1	2223	A
1	1	2225	U
1	1	2231	C
1	1	2243	A
1	1	2246	G
1	1	2249	G
1	1	2256	A
1	1	2257	C
1	1	2265	C
1	1	2269	U
1	1	2270	A
1	1	2271	A
1	1	2273	G
1	1	2274	U
1	1	2281	A
1	1	2282	U
1	1	2283	G
1	1	2284	C
1	1	2285	C
1	1	2286	U
1	1	2287	C
1	1	2298	U
1	1	2299	A
1	1	2301	U

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Mol	Chain	Res	Type
1	1	2304	C
1	1	2305	G
1	1	2306	C
1	1	2307	G
1	1	2308	C
1	1	2309	A
1	1	2310	U
1	1	2313	A
1	1	2315	G
1	1	2318	U
1	1	2324	A
1	1	2334	U
1	1	2335	G
1	1	2336	U
1	1	2339	C
1	1	2347	U
1	1	2350	C
1	1	2352	A
1	1	2359	C
1	1	2372	A
1	1	2374	C
1	1	2375	G
1	1	2386	A
1	1	2391	G
1	1	2393	G
1	1	2397	A
1	1	2398	A
1	1	2401	A
1	1	2402	A
1	1	2403	G
1	1	2404	A
1	1	2410	U
1	1	2411	U
1	1	2418	G
1	1	2419	A
1	1	2435	G
1	1	2446	U
1	1	2448	G
1	1	2452	G
1	1	2453	U
1	1	2455	U
1	1	2456	A

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Mol	Chain	Res	Type
1	1	2458	A
1	1	2459	A
1	1	2460	U
1	1	2461	A
1	1	2462	A
1	1	2463	G
1	1	2467	G
1	1	2468	A
1	1	2474	G
1	1	2475	G
1	1	2476	C
1	1	2477	G
1	1	2478	C
1	1	2479	C
1	1	2482	U
1	1	2486	A
1	1	2487	U
1	1	2488	A
1	1	2489	C
1	1	2490	C
1	1	2491	A
1	1	2492	C
1	1	2494	A
1	1	2496	C
1	1	2497	U
1	1	2498	U
1	1	2499	U
1	1	2502	A
1	1	2505	U
1	1	2506	U
1	1	2507	C
1	1	2508	U
1	1	2509	U
1	1	2510	U
1	1	2512	C
1	1	2514	U
1	1	2522	G
1	1	2523	A
1	1	2529	A
1	1	2530	G
1	1	2532	U
1	1	2536	A

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Mol	Chain	Res	Type
1	1	2537	U
1	1	2538	U
1	1	2539	C
1	1	2540	A
1	1	2541	U
1	1	2542	U
1	1	2543	U
1	1	2544	U
1	1	2547	A
1	1	2548	C
1	1	2549	G
1	1	2550	U
1	1	2552	C
1	1	2553	U
1	1	2555	G
1	1	2557	A
1	1	2558	U
1	1	2559	U
1	1	2560	C
1	1	2561	A
1	1	2566	C
1	1	2569	A
1	1	2570	U
1	1	2571	U
1	1	2572	C
1	1	2575	G
1	1	2585	G
1	1	2587	U
1	1	2588	U
1	1	2589	G
1	1	2590	A
1	1	2593	A
1	1	2602	G
1	1	2606	G
1	1	2607	G
1	1	2608	G
1	1	2612	U
1	1	2614	G
1	1	2615	G
1	1	2620	G
1	1	2626	A
1	1	2635	A

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Mol	Chain	Res	Type
1	1	2652	U
1	1	2656	A
1	1	2657	A
1	1	2663	G
1	1	2668	U
1	1	2672	G
1	1	2674	A
1	1	2676	A
1	1	2677	G
1	1	2678	A
1	1	2681	U
1	1	2684	C
1	1	2688	U
1	1	2689	A
1	1	2690	G
1	1	2691	A
1	1	2693	C
1	1	2696	A
1	1	2704	A
1	1	2705	A
1	1	2707	C
1	1	2714	G
1	1	2719	U
1	1	2728	G
1	1	2729	U
1	1	2731	U
1	1	2732	G
1	1	2737	C
1	1	2740	A
1	1	2743	A
1	1	2746	A
1	1	2749	G
1	1	2753	G
1	1	2762	A
1	1	2771	U
1	1	2772	C
1	1	2773	C
1	1	2776	C
1	1	2777	G
1	1	2778	G
1	1	2779	A
1	1	2780	A

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Mol	Chain	Res	Type
1	1	2781	U
1	1	2787	G
1	1	2791	G
1	1	2794	G
1	1	2795	U
1	1	2796	G
1	1	2798	C
1	1	2799	A
1	1	2800	G
1	1	2801	A
1	1	2803	A
1	1	2808	A
1	1	2810	C
1	1	2816	G
1	1	2817	A
1	1	2819	A
1	1	2821	C
1	1	2827	U
1	1	2830	G
1	1	2831	G
1	1	2834	G
1	1	2843	U
1	1	2844	C
1	1	2845	A
1	1	2847	A
1	1	2850	G
1	1	2856	G
1	1	2857	C
1	1	2860	U
1	1	2861	U
1	1	2863	G
1	1	2867	C
1	1	2869	U
1	1	2870	C
1	1	2871	G
1	1	2872	A
1	1	2873	U
1	1	2886	U
1	1	2887	A
1	1	2888	U
1	1	2889	C
1	1	2899	C

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Mol	Chain	Res	Type
1	1	2900	A
1	1	2903	A
1	1	2904	U
1	1	2907	G
1	1	2911	A
1	1	2914	G
1	1	2918	G
1	1	2922	G
1	1	2923	U
1	1	2925	C
1	1	2930	A
1	1	2935	U
1	1	2936	A
1	1	2938	G
1	1	2941	A
1	1	2942	C
1	1	2947	G
1	1	2952	G
1	1	2953	U
1	1	2954	U
1	1	2955	U
1	1	2971	A
1	1	2982	A
1	1	2983	C
1	1	2984	C
1	1	2990	G
1	1	2995	A
1	1	2996	U
1	1	2997	G
1	1	3003	G
1	1	3011	A
1	1	3012	A
1	1	3021	A
1	1	3023	U
1	1	3032	A
1	1	3033	A
1	1	3036	G
1	1	3046	A
1	1	3049	A
1	1	3055	U
1	1	3058	U
1	1	3070	A

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Mol	Chain	Res	Type
1	1	3077	A
1	1	3079	U
1	1	3080	G
1	1	3086	A
1	1	3090	U
1	1	3092	C
1	1	3101	G
1	1	3104	U
1	1	3106	A
1	1	3117	C
1	1	3118	C
1	1	3122	A
1	1	3125	U
1	1	3127	A
1	1	3128	G
1	1	3131	U
1	1	3136	G
1	1	3142	A
1	1	3143	C
1	1	3151	U
1	1	3153	U
1	1	3154	C
1	1	3155	U
1	1	3156	U
1	1	3157	U
1	1	3158	G
1	1	3160	U
1	1	3164	C
1	1	3167	A
1	1	3168	A
1	1	3169	U
1	1	3170	A
1	1	3172	A
1	1	3173	G
1	1	3175	U
1	1	3176	G
1	1	3177	G
1	1	3179	U
1	1	3181	C
1	1	3182	G
1	1	3184	A
1	1	3185	U

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Mol	Chain	Res	Type
1	1	3186	A
1	1	3187	A
1	1	3188	G
1	1	3194	C
1	1	3195	U
1	1	3196	U
1	1	3202	G
1	1	3206	C
1	1	3207	U
1	1	3210	A
1	1	3213	A
1	1	3214	U
1	1	3215	A
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3222	U
1	1	3223	A
1	1	3224	G
1	1	3227	A
1	1	3228	C
1	1	3236	U
1	1	3237	U
1	1	3239	G
1	1	3240	C
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3253	G
1	1	3260	G
1	1	3263	G
1	1	3269	U
1	1	3270	U
1	1	3271	G
1	1	3273	A
1	1	3276	G
1	1	3278	C
1	1	3281	U
1	1	3285	C
1	1	3289	G
1	1	3290	G
1	1	3294	A

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Mol	Chain	Res	Type
1	1	3304	U
1	1	3306	U
1	1	3317	U
1	1	3319	U
1	1	3322	A
1	1	3330	A
1	1	3337	G
1	1	3339	A
1	1	3341	U
1	1	3345	G
1	1	3348	G
1	1	3350	C
1	1	3351	U
1	1	3352	U
1	1	3353	G
1	1	3354	U
1	1	3356	G
1	1	3363	U
1	1	3366	G
1	1	3368	U
1	1	3369	G
1	1	3370	A
1	1	3371	G
1	1	3375	A
1	1	3377	G
1	1	3378	C
1	1	3382	U
1	1	3384	U
1	1	3385	U
1	1	3389	U
1	1	3390	G
1	1	3391	A
1	1	3396	U
2	3	7	G
2	3	10	C
2	3	11	A
2	3	13	A
2	3	17	A
2	3	19	C
2	3	29	C
2	3	32	U
2	3	38	U

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Mol	Chain	Res	Type
2	3	41	G
2	3	44	C
2	3	52	G
2	3	53	U
2	3	54	U
2	3	55	A
2	3	65	G
2	3	69	C
2	3	70	U
2	3	73	C
2	3	74	C
2	3	76	A
2	3	77	G
2	3	89	G
2	3	93	C
2	3	112	G
2	3	113	C
2	3	117	A
2	3	121	U
3	4	2	A
3	4	8	C
3	4	9	A
3	4	17	A
3	4	34	U
3	4	35	C
3	4	39	G
3	4	40	A
3	4	50	C
3	4	51	G
3	4	52	A
3	4	59	A
3	4	62	C
3	4	63	G
3	4	73	U
3	4	75	G
3	4	79	A
3	4	80	A
3	4	81	U
3	4	82	U
3	4	84	C
3	4	85	G
3	4	86	U

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Mol	Chain	Res	Type
3	4	87	G
3	4	88	A
3	4	90	U
3	4	95	G
3	4	97	A
3	4	104	A
3	4	106	C
3	4	111	A
3	4	112	U
3	4	113	U
3	4	115	C
3	4	121	U
3	4	124	G
3	4	125	U
3	4	126	A
3	4	127	U
3	4	129	C
3	4	134	G
3	4	136	G
3	4	138	A
3	4	148	G
3	4	149	A
3	4	150	G
3	4	151	C
3	4	152	G
47	2	2	A
47	2	3	U
47	2	4	C
47	2	8	U
47	2	9	U
47	2	11	A
47	2	14	C
47	2	15	U
47	2	25	C
47	2	26	A
47	2	37	U
47	2	38	C
47	2	39	A
47	2	40	A
47	2	42	G
47	2	43	A
47	2	47	A

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Mol	Chain	Res	Type
47	2	48	G
47	2	50	C
47	2	54	C
47	2	55	A
47	2	57	G
47	2	59	C
47	2	61	A
47	2	63	G
47	2	65	A
47	2	66	U
47	2	67	A
47	2	68	A
47	2	69	G
47	2	71	A
47	2	72	A
47	2	73	U
47	2	74	U
47	2	75	U
47	2	76	A
47	2	77	U
47	2	79	C
47	2	81	G
47	2	82	U
47	2	83	G
47	2	85	A
47	2	87	C
47	2	90	C
47	2	95	G
47	2	100	A
47	2	102	U
47	2	104	A
47	2	111	U
47	2	114	C
47	2	116	U
47	2	117	U
47	2	118	U
47	2	119	A
47	2	120	U
47	2	124	A
47	2	126	A
47	2	127	G
47	2	128	U

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Mol	Chain	Res	Type
47	2	129	U
47	2	130	C
47	2	131	C
47	2	132	U
47	2	133	U
47	2	134	U
47	2	135	A
47	2	136	C
47	2	137	U
47	2	138	A
47	2	139	C
47	2	140	A
47	2	141	U
47	2	145	A
47	2	153	G
47	2	154	G
47	2	159	U
47	2	160	C
47	2	161	U
47	2	168	A
47	2	169	A
47	2	170	U
47	2	174	U
47	2	176	C
47	2	178	U
47	2	179	A
47	2	183	U
47	2	185	U
47	2	190	C
47	2	191	C
47	2	192	U
47	2	193	U
47	2	200	A
47	2	202	A
47	2	204	G
47	2	207	U
47	2	209	U
47	2	215	A
47	2	217	A
47	2	218	A
47	2	221	A
47	2	224	C

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Mol	Chain	Res	Type
47	2	225	A
47	2	226	A
47	2	227	U
47	2	228	G
47	2	230	C
47	2	232	U
47	2	233	C
47	2	234	G
47	2	235	G
47	2	238	U
47	2	239	C
47	2	240	U
47	2	244	A
47	2	245	U
47	2	246	G
47	2	248	U
47	2	250	C
47	2	256	A
47	2	260	U
47	2	261	U
47	2	262	U
47	2	266	A
47	2	270	C
47	2	272	U
47	2	274	G
47	2	275	C
47	2	276	C
47	2	277	U
47	2	278	U
47	2	279	G
47	2	280	U
47	2	281	G
47	2	287	G
47	2	288	A
47	2	289	U
47	2	291	G
47	2	292	U
47	2	295	A
47	2	299	A
47	2	300	A
47	2	302	U
47	2	306	U

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Mol	Chain	Res	Type
47	2	309	C
47	2	312	A
47	2	313	U
47	2	314	C
47	2	315	A
47	2	316	A
47	2	318	U
47	2	321	C
47	2	322	G
47	2	330	G
47	2	333	A
47	2	334	G
47	2	337	G
47	2	338	C
47	2	339	C
47	2	345	U
47	2	351	C
47	2	352	A
47	2	359	A
47	2	361	C
47	2	365	G
47	2	366	A
47	2	370	A
47	2	373	G
47	2	379	U
47	2	380	U
47	2	388	G
47	2	389	G
47	2	390	G
47	2	393	C
47	2	394	C
47	2	400	A
47	2	401	A
47	2	402	C
47	2	404	G
47	2	412	A
47	2	413	U
47	2	416	A
47	2	417	A
47	2	419	G
47	2	420	A
47	2	422	G

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Mol	Chain	Res	Type
47	2	423	G
47	2	424	C
47	2	425	A
47	2	426	G
47	2	429	G
47	2	430	G
47	2	432	G
47	2	433	C
47	2	434	G
47	2	435	C
47	2	437	A
47	2	438	A
47	2	439	U
47	2	440	U
47	2	441	A
47	2	444	C
47	2	445	A
47	2	447	U
47	2	452	A
47	2	453	U
47	2	454	U
47	2	455	C
47	2	460	A
47	2	463	U
47	2	464	A
47	2	466	U
47	2	468	A
47	2	469	C
47	2	473	A
47	2	475	A
47	2	477	A
47	2	478	A
47	2	479	C
47	2	486	G
47	2	488	G
47	2	489	C
47	2	491	C
47	2	494	U
47	2	495	C
47	2	496	G
47	2	499	U
47	2	500	C

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Mol	Chain	Res	Type
47	2	506	A
47	2	507	U
47	2	509	G
47	2	511	A
47	2	515	A
47	2	516	G
47	2	522	U
47	2	525	A
47	2	532	U
47	2	534	A
47	2	538	A
47	2	539	G
47	2	540	G
47	2	541	A
47	2	542	A
47	2	543	C
47	2	545	A
47	2	546	U
47	2	548	G
47	2	552	G
47	2	554	C
47	2	557	G
47	2	558	U
47	2	565	C
47	2	566	C
47	2	567	A
47	2	568	G
47	2	572	C
47	2	578	U
47	2	579	A
47	2	580	A
47	2	582	U
47	2	583	C
47	2	592	A
47	2	594	A
47	2	595	G
47	2	597	G
47	2	606	A
47	2	610	G
47	2	611	U
47	2	619	A
47	2	620	A

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Mol	Chain	Res	Type
47	2	623	A
47	2	624	G
47	2	630	A
47	2	635	A
47	2	637	C
47	2	639	U
47	2	640	U
47	2	653	C
47	2	654	C
47	2	655	G
47	2	656	G
47	2	657	U
47	2	658	C
47	2	677	G
47	2	679	U
47	2	680	U
47	2	681	U
47	2	686	C
47	2	687	G
47	2	692	C
47	2	693	U
47	2	695	U
47	2	696	C
47	2	697	C
47	2	698	U
47	2	699	U
47	2	700	C
47	2	702	G
47	2	705	U
47	2	706	A
47	2	707	A
47	2	709	C
47	2	710	U
47	2	711	U
47	2	712	G
47	2	713	A
47	2	715	U
47	2	718	U
47	2	719	U
47	2	720	G
47	2	721	U
47	2	722	G

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Mol	Chain	Res	Type
47	2	723	G
47	2	725	U
47	2	727	U
47	2	728	U
47	2	729	G
47	2	731	C
47	2	732	G
47	2	733	A
47	2	734	A
47	2	735	C
47	2	738	G
47	2	741	C
47	2	742	U
47	2	743	U
47	2	744	U
47	2	757	A
47	2	760	A
47	2	765	G
47	2	766	U
47	2	767	U
47	2	768	C
47	2	775	G
47	2	777	C
47	2	778	G
47	2	779	U
47	2	780	A
47	2	781	U
47	2	783	G
47	2	784	C
47	2	789	A
47	2	793	A
47	2	794	U
47	2	795	U
47	2	799	A
47	2	801	G
47	2	806	A
47	2	810	G
47	2	811	A
47	2	812	A
47	2	813	U
47	2	814	A
47	2	816	G

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Mol	Chain	Res	Type
47	2	817	A
47	2	819	G
47	2	820	U
47	2	821	U
47	2	824	G
47	2	826	U
47	2	827	C
47	2	831	U
47	2	833	U
47	2	834	G
47	2	836	U
47	2	839	U
47	2	841	U
47	2	842	C
47	2	843	U
47	2	845	G
47	2	853	G
47	2	859	A
47	2	860	U
47	2	863	A
47	2	864	U
47	2	873	U
47	2	881	A
47	2	895	G
47	2	898	A
47	2	903	U
47	2	904	G
47	2	905	A
47	2	906	A
47	2	909	U
47	2	911	U
47	2	913	G
47	2	916	U
47	2	919	A
47	2	921	U
47	2	922	G
47	2	923	A
47	2	924	A
47	2	928	U
47	2	931	C
47	2	932	U
47	2	933	A

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Mol	Chain	Res	Type
47	2	934	C
47	2	935	U
47	2	944	A
47	2	951	A
47	2	960	U
47	2	964	U
47	2	966	A
47	2	980	G
47	2	981	U
47	2	986	G
47	2	990	C
47	2	992	A
47	2	993	A
47	2	1003	A
47	2	1004	U
47	2	1005	A
47	2	1010	C
47	2	1011	G
47	2	1014	G
47	2	1016	C
47	2	1020	A
47	2	1021	C
47	2	1022	C
47	2	1023	A
47	2	1025	A
47	2	1026	A
47	2	1027	A
47	2	1028	C
47	2	1030	A
47	2	1031	U
47	2	1032	G
47	2	1036	A
47	2	1040	G
47	2	1043	A
47	2	1052	U
47	2	1053	G
47	2	1056	U
47	2	1071	U
47	2	1076	A
47	2	1080	U
47	2	1082	C
47	2	1083	G

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Mol	Chain	Res	Type
47	2	1091	A
47	2	1092	A
47	2	1097	U
47	2	1098	U
47	2	1099	U
47	2	1100	G
47	2	1108	G
47	2	1109	G
47	2	1110	G
47	2	1113	A
47	2	1117	U
47	2	1118	G
47	2	1125	A
47	2	1137	A
47	2	1138	A
47	2	1139	A
47	2	1140	G
47	2	1147	A
47	2	1149	G
47	2	1150	G
47	2	1153	G
47	2	1154	G
47	2	1155	G
47	2	1157	A
47	2	1158	C
47	2	1159	C
47	2	1160	A
47	2	1162	C
47	2	1163	A
47	2	1164	G
47	2	1165	G
47	2	1166	A
47	2	1167	G
47	2	1168	U
47	2	1170	G
47	2	1171	A
47	2	1172	G
47	2	1174	C
47	2	1175	U
47	2	1179	G
47	2	1182	U
47	2	1183	A

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Mol	Chain	Res	Type
47	2	1184	A
47	2	1185	U
47	2	1186	U
47	2	1189	A
47	2	1190	C
47	2	1192	C
47	2	1193	A
47	2	1194	A
47	2	1196	A
47	2	1199	G
47	2	1200	G
47	2	1201	G
47	2	1202	A
47	2	1203	A
47	2	1205	C
47	2	1207	C
47	2	1208	A
47	2	1209	C
47	2	1214	U
47	2	1216	C
47	2	1217	A
47	2	1219	A
47	2	1220	C
47	2	1222	C
47	2	1223	A
47	2	1225	U
47	2	1226	A
47	2	1227	A
47	2	1228	G
47	2	1229	G
47	2	1230	A
47	2	1231	U
47	2	1232	U
47	2	1233	G
47	2	1234	A
47	2	1236	A
47	2	1237	G
47	2	1238	A
47	2	1239	U
47	2	1240	U
47	2	1241	G
47	2	1242	A

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Mol	Chain	Res	Type
47	2	1243	G
47	2	1244	A
47	2	1245	G
47	2	1249	U
47	2	1250	U
47	2	1251	U
47	2	1252	C
47	2	1253	U
47	2	1255	G
47	2	1256	A
47	2	1258	U
47	2	1259	U
47	2	1260	U
47	2	1262	U
47	2	1263	G
47	2	1264	G
47	2	1266	U
47	2	1267	G
47	2	1270	G
47	2	1271	G
47	2	1273	G
47	2	1274	C
47	2	1275	A
47	2	1276	U
47	2	1284	C
47	2	1285	U
47	2	1286	U
47	2	1287	A
47	2	1290	U
47	2	1293	U
47	2	1301	U
47	2	1306	C
47	2	1309	C
47	2	1312	A
47	2	1313	A
47	2	1314	U
47	2	1315	U
47	2	1320	U
47	2	1321	A
47	2	1326	A
47	2	1327	C
47	2	1328	G

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Mol	Chain	Res	Type
47	2	1333	C
47	2	1335	U
47	2	1336	A
47	2	1339	C
47	2	1340	U
47	2	1341	A
47	2	1343	U
47	2	1344	A
47	2	1345	A
47	2	1346	A
47	2	1347	U
47	2	1348	A
47	2	1352	G
47	2	1353	U
47	2	1354	G
47	2	1355	C
47	2	1356	U
47	2	1360	A
47	2	1362	U
47	2	1363	U
47	2	1364	G
47	2	1367	G
47	2	1370	U
47	2	1371	A
47	2	1372	U
47	2	1374	C
47	2	1380	U
47	2	1381	U
47	2	1382	A
47	2	1383	G
47	2	1384	A
47	2	1385	G
47	2	1386	G
47	2	1387	G
47	2	1388	A
47	2	1390	U
47	2	1391	A
47	2	1394	G
47	2	1395	G
47	2	1396	U
47	2	1398	U
47	2	1399	C

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Mol	Chain	Res	Type
47	2	1400	A
47	2	1402	G
47	2	1406	A
47	2	1408	G
47	2	1409	G
47	2	1412	G
47	2	1413	U
47	2	1414	U
47	2	1415	U
47	2	1416	G
47	2	1419	G
47	2	1421	A
47	2	1425	A
47	2	1427	A
47	2	1428	G
47	2	1429	G
47	2	1432	U
47	2	1433	G
47	2	1434	U
47	2	1436	A
47	2	1439	C
47	2	1440	C
47	2	1443	U
47	2	1444	A
47	2	1445	G
47	2	1446	A
47	2	1447	C
47	2	1448	G
47	2	1449	U
47	2	1450	U
47	2	1451	C
47	2	1454	G
47	2	1455	G
47	2	1456	C
47	2	1457	C
47	2	1458	G
47	2	1459	C
47	2	1460	A
47	2	1461	C
47	2	1466	G
47	2	1468	U
47	2	1471	A

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Mol	Chain	Res	Type
47	2	1472	C
47	2	1473	U
47	2	1474	G
47	2	1482	C
47	2	1486	G
47	2	1487	A
47	2	1489	U
47	2	1490	C
47	2	1491	U
47	2	1492	A
47	2	1493	A
47	2	1506	G
47	2	1508	U
47	2	1509	C
47	2	1511	U
47	2	1515	A
47	2	1516	A
47	2	1517	U
47	2	1518	C
47	2	1523	G
47	2	1524	A
47	2	1525	A
47	2	1529	C
47	2	1531	G
47	2	1532	U
47	2	1534	G
47	2	1535	U
47	2	1536	G
47	2	1537	C
47	2	1538	U
47	2	1539	G
47	2	1540	G
47	2	1542	G
47	2	1554	U
47	2	1555	A
47	2	1557	U
47	2	1559	A
47	2	1560	U
47	2	1562	G
47	2	1565	C
47	2	1567	U
47	2	1572	G

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Mol	Chain	Res	Type
47	2	1573	A
47	2	1574	G
47	2	1575	G
47	2	1576	A
47	2	1577	A
47	2	1582	U
47	2	1583	A
47	2	1584	G
47	2	1587	A
47	2	1591	C
47	2	1601	G
47	2	1604	U
47	2	1605	G
47	2	1607	G
47	2	1608	U
47	2	1611	A
47	2	1616	G
47	2	1618	C
47	2	1619	C
47	2	1620	C
47	2	1624	C
47	2	1628	U
47	2	1631	A
47	2	1633	A
47	2	1634	C
47	2	1635	A
47	2	1636	C
47	2	1638	G
47	2	1639	C
47	2	1646	C
47	2	1651	A
47	2	1654	G
47	2	1656	U
47	2	1657	U
47	2	1658	G
47	2	1664	C
47	2	1665	U
47	2	1666	U
47	2	1675	C
47	2	1678	A
47	2	1680	G
47	2	1681	A

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Mol	Chain	Res	Type
47	2	1682	U
47	2	1684	U
47	2	1685	G
47	2	1688	U
47	2	1689	A
47	2	1693	A
47	2	1694	A
47	2	1697	G
47	2	1699	G
47	2	1700	C
47	2	1701	A
47	2	1702	A
47	2	1703	C
47	2	1704	U
47	2	1708	U
47	2	1709	C
47	2	1711	C
47	2	1712	A
47	2	1713	G
47	2	1714	A
47	2	1715	G
47	2	1717	G
47	2	1730	A
47	2	1731	A
47	2	1738	U
47	2	1742	U
47	2	1747	G
47	2	1755	A
47	2	1756	A
47	2	1757	G
47	2	1760	G
47	2	1761	U
47	2	1762	A
47	2	1766	A
47	2	1767	G
47	2	1769	U
47	2	1770	U
47	2	1778	G
47	2	1780	G
47	2	1782	A
47	2	1783	C
47	2	1784	C

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Mol	Chain	Res	Type
47	2	1787	C
47	2	1791	A
47	2	1792	G
47	2	1794	A
47	2	1796	C
47	2	1797	A
82	AY	8	U
82	AY	10	G
82	AY	11	C
82	AY	15	G
82	AY	18	G
82	AY	19	G
82	AY	20	G
82	AY	23	A
82	AY	25	C
82	AY	33	U
82	AY	38	A
82	AY	45	G
82	AY	46	G
82	AY	47	U
82	AY	48	C
82	AY	49	C
82	AY	50	U
82	AY	51	G
82	AY	55	U
82	AY	57	G
82	AY	58	A
82	AY	59	U
82	AY	60	C
82	AY	61	C
82	AY	66	A
82	AY	68	U
82	AY	71	G
82	AY	74	C
82	AY	76	A
83	AZ	44	A
83	AZ	45	A
83	AZ	46	U
83	AZ	48	U
83	AZ	49	U

All (81) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	97	U
1	1	120	G
1	1	165	A
1	1	197	G
1	1	264	G
1	1	323	A
1	1	360	G
1	1	443	G
1	1	490	C
1	1	1015	U
1	1	1028	U
1	1	1079	A
1	1	1084	A
1	1	1128	U
1	1	1136	A
1	1	1197	A
1	1	1232	C
1	1	1405	U
1	1	1415	U
1	1	1620	U
1	1	1837	U
1	1	2270	A
1	1	2306	C
1	1	2541	U
1	1	2587	U
1	1	2614	G
1	1	2706	G
1	1	2981	U
1	1	3105	U
1	1	3121	U
1	1	3156	U
1	1	3193	C
1	1	3218	A
2	3	18	C
2	3	52	G
2	3	72	A
3	4	7	U
3	4	39	G
3	4	72	A
3	4	114	G
3	4	133	G
47	2	1	U
47	2	36	C

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Mol	Chain	Res	Type
47	2	118	U
47	2	132	U
47	2	144	U
47	2	206	A
47	2	217	A
47	2	333	A
47	2	387	A
47	2	388	G
47	2	393	C
47	2	403	G
47	2	431	C
47	2	541	A
47	2	697	C
47	2	698	U
47	2	706	A
47	2	728	U
47	2	740	A
47	2	767	U
47	2	1002	G
47	2	1039	A
47	2	1116	A
47	2	1138	A
47	2	1181	U
47	2	1273	G
47	2	1347	U
47	2	1399	C
47	2	1444	A
47	2	1455	G
47	2	1481	C
47	2	1491	U
47	2	1632	C
47	2	1638	G
47	2	1680	G
47	2	1684	U
47	2	1707	A
47	2	1755	A
83	AZ	44	A
83	AZ	48	U

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	DDE	AX	699	81	18,20,21	2.04	6 (33%)	17,28,30	1.31	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	DDE	AX	699	81	-	6/20/21/23	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	AX	699	DDE	CBI-NAD	5.97	1.46	1.32
81	AX	699	DDE	CAT-CE1	2.96	1.54	1.49
81	AX	699	DDE	CG-ND1	-2.80	1.33	1.38
81	AX	699	DDE	OAG-CBI	-2.35	1.19	1.23
81	AX	699	DDE	CBW-NCB	-2.16	1.49	1.54
81	AX	699	DDE	CB-CG	2.13	1.55	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	AX	699	DDE	OAG-CBI-NAD	-2.89	117.94	123.04
81	AX	699	DDE	CAC-NCB-CAB	2.75	118.43	107.99

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	AX	699	DDE	N-CA-CB-CG
81	AX	699	DDE	C-CA-CB-CG
81	AX	699	DDE	CAT-CAU-CBW-CBI

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Mol	Chain	Res	Type	Atoms
81	AX	699	DDE	OAG-CBI-CBW-CAU
81	AX	699	DDE	NAD-CBI-CBW-CAU
81	AX	699	DDE	CAU-CAT-CE1-NE2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	AX	699	DDE	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 8 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
86	GCP	AX	901	-	32,34,34	0.72	2 (6%)	49,54,54	0.96	3 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	GCP	AX	901	-	-	5/19/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	AX	901	GCP	PG-O1G	2.28	1.54	1.50
86	AX	901	GCP	PG-O3G	-2.18	1.50	1.55

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	AX	901	GCP	O1B-PB-C3B	4.09	119.81	109.05
86	AX	901	GCP	O1G-PG-C3B	-2.73	105.42	111.37
86	AX	901	GCP	O3G-PG-C3B	2.51	112.48	106.40

There are no chirality outliers.

All (5) torsion outliers are listed below:

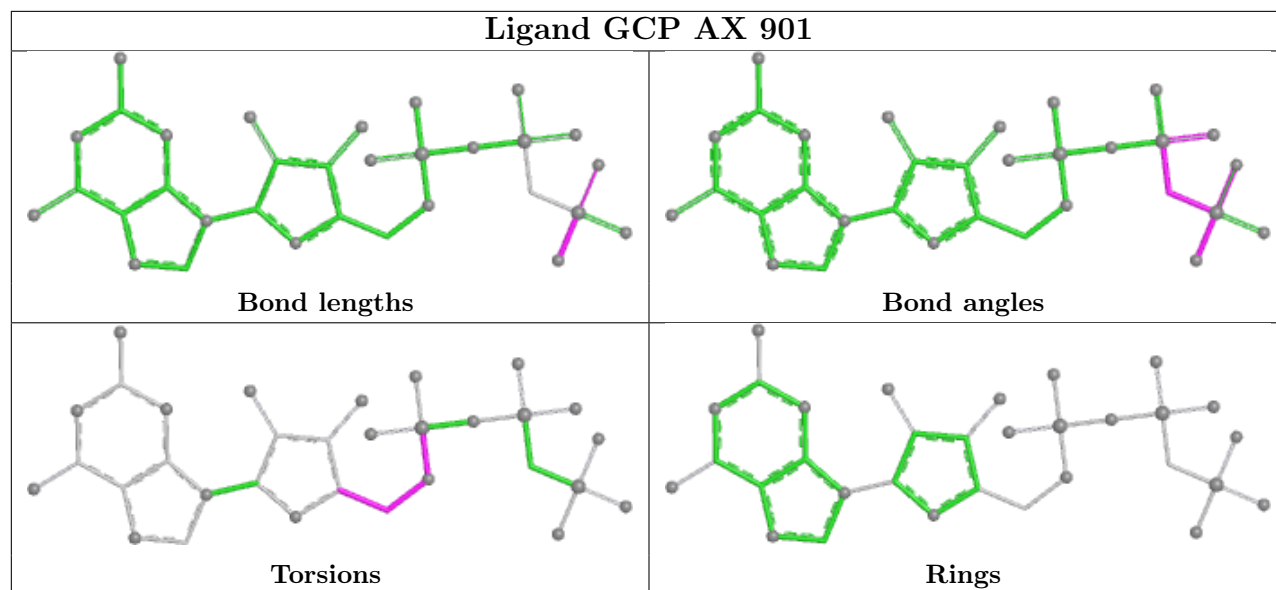
Mol	Chain	Res	Type	Atoms
86	AX	901	GCP	C5'-O5'-PA-O3A
86	AX	901	GCP	C5'-O5'-PA-O1A
86	AX	901	GCP	C5'-O5'-PA-O2A
86	AX	901	GCP	C4'-C5'-O5'-PA
86	AX	901	GCP	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	AX	901	GCP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

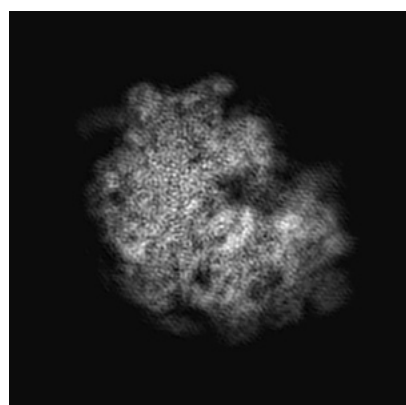
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0049. These allow visual inspection of the internal detail of the map and identification of artifacts.

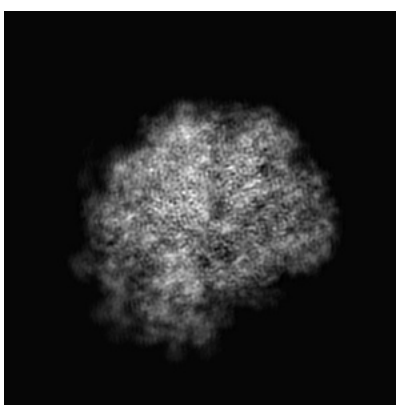
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

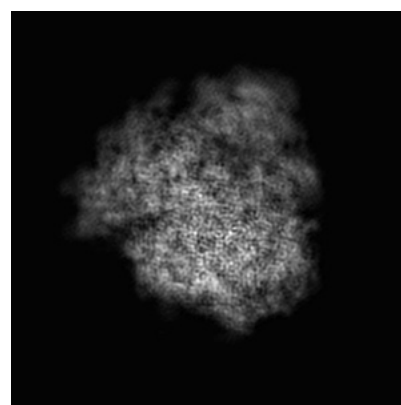
6.1.1 Primary map



X



Y

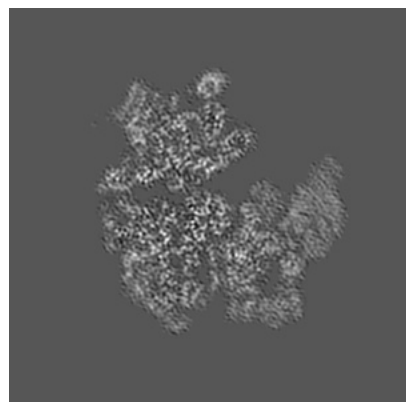


Z

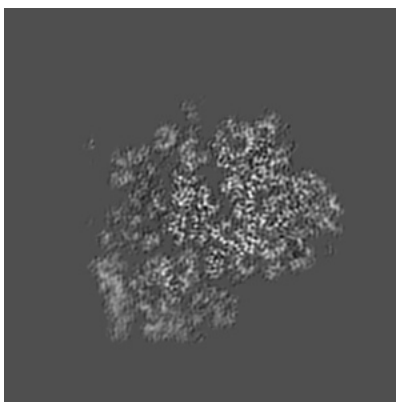
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

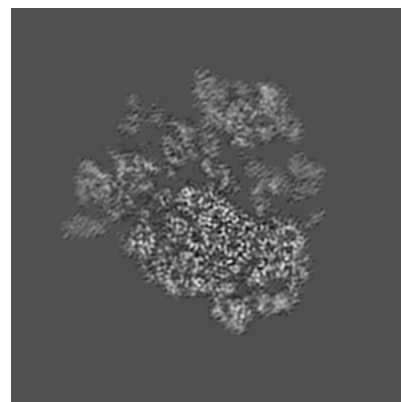
6.2.1 Primary map



X Index: 180



Y Index: 180

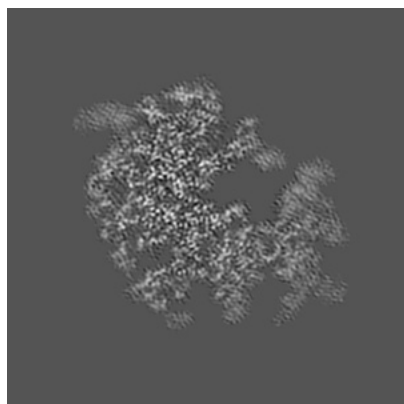


Z Index: 180

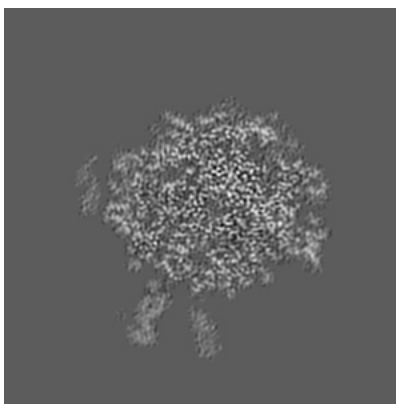
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

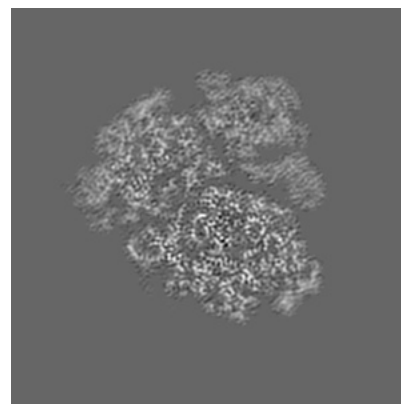
6.3.1 Primary map



X Index: 194



Y Index: 158

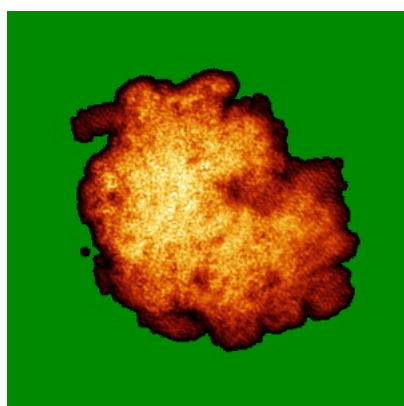


Z Index: 166

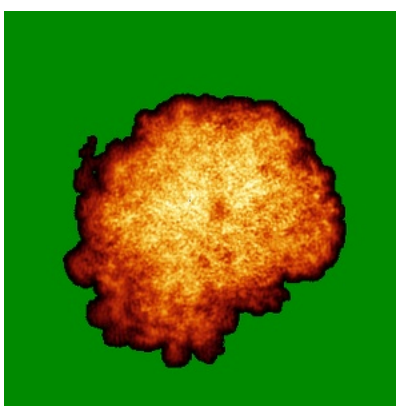
The images above show the largest variance slices of the map in three orthogonal directions.

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

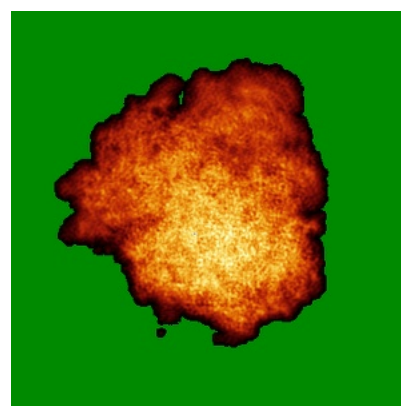
6.4.1 Primary map



X



Y

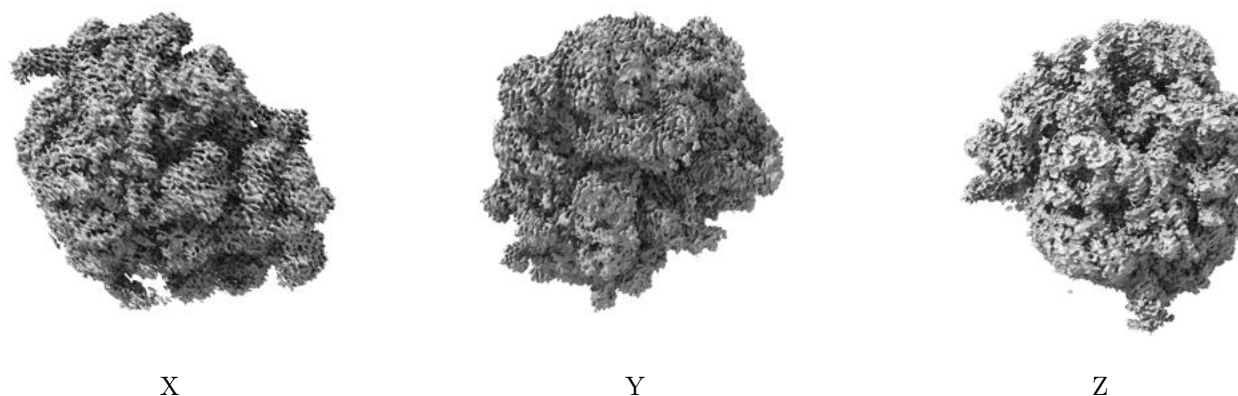


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.033. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

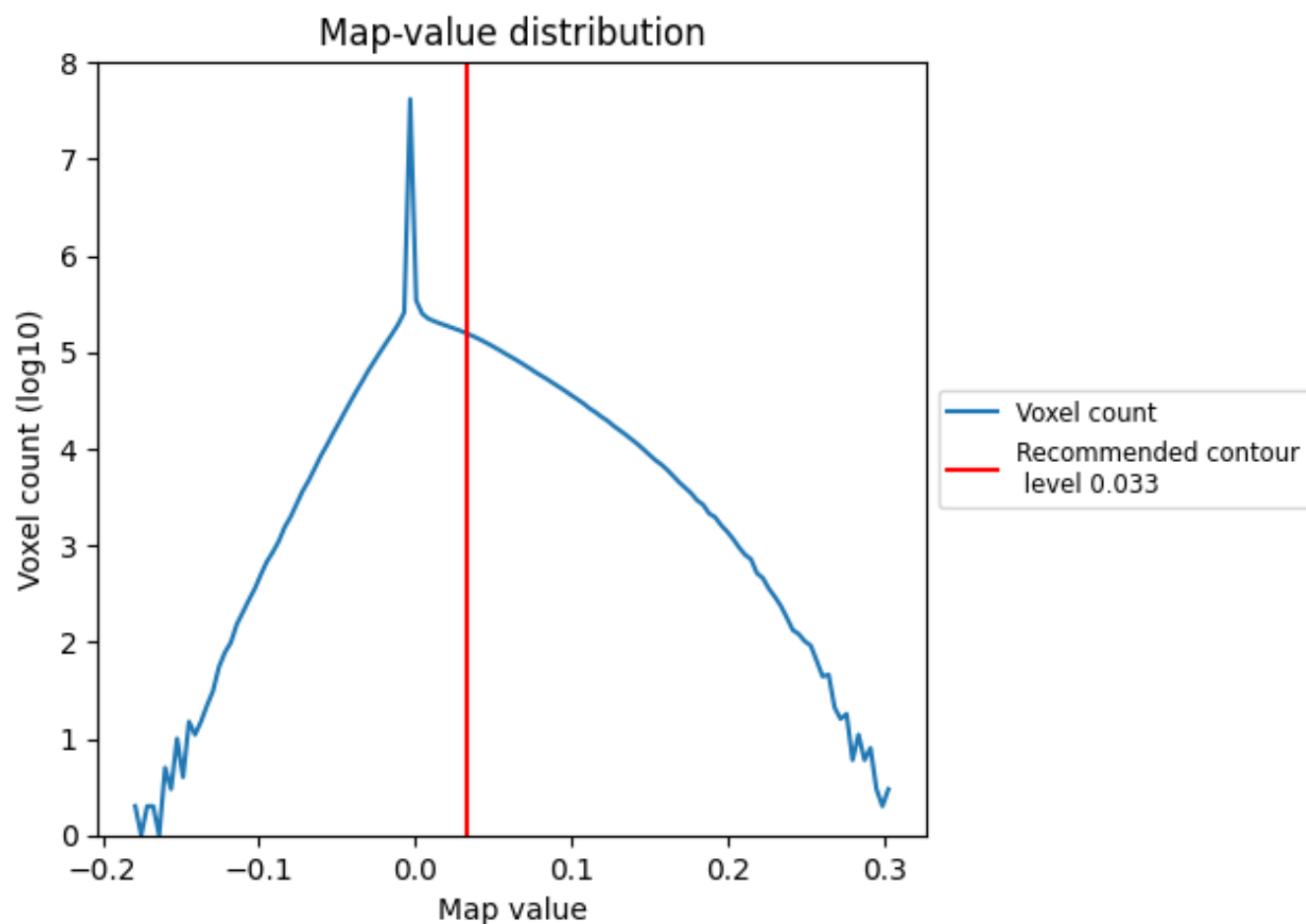
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

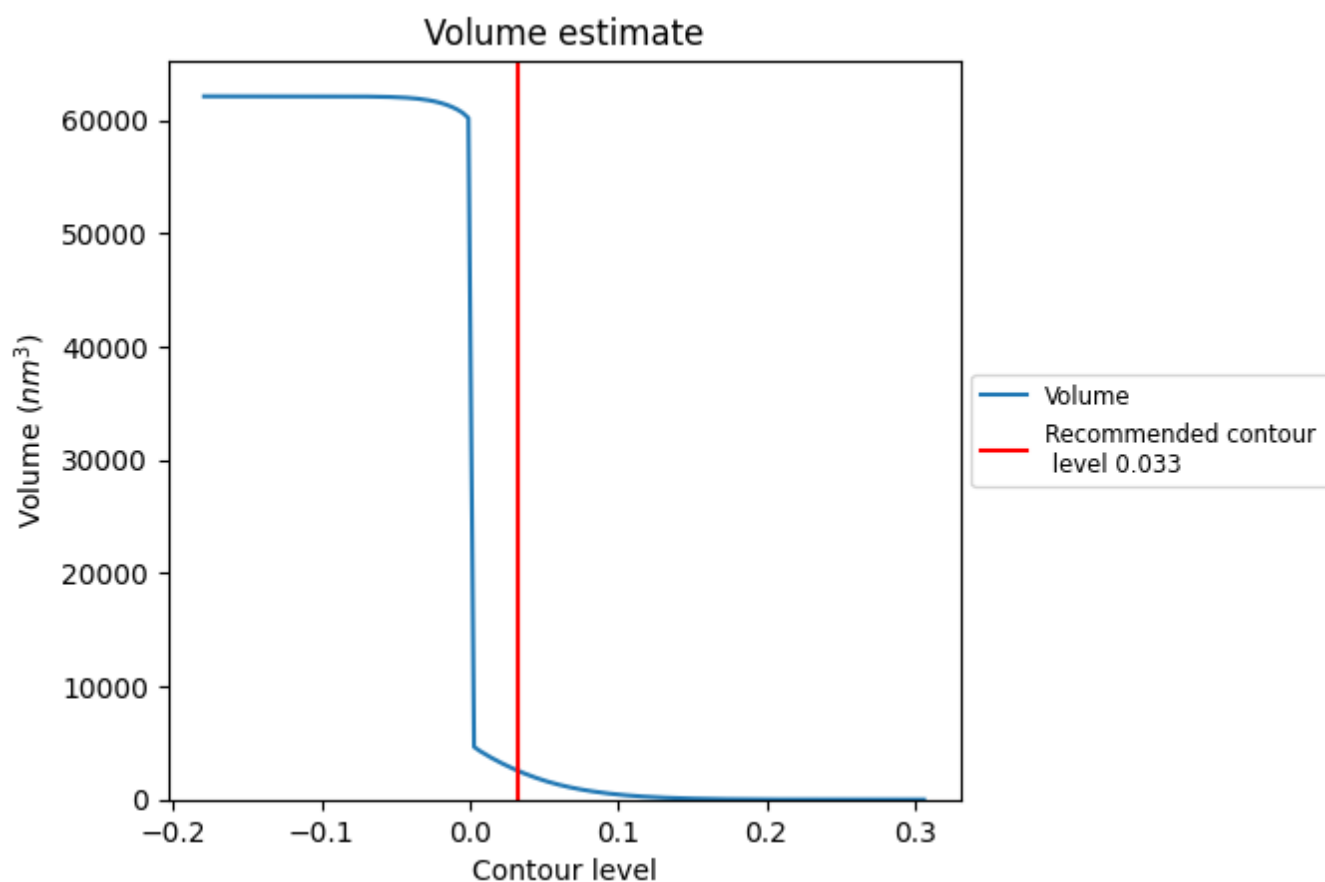
This section contains the results of statistical analysis of the map.

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.

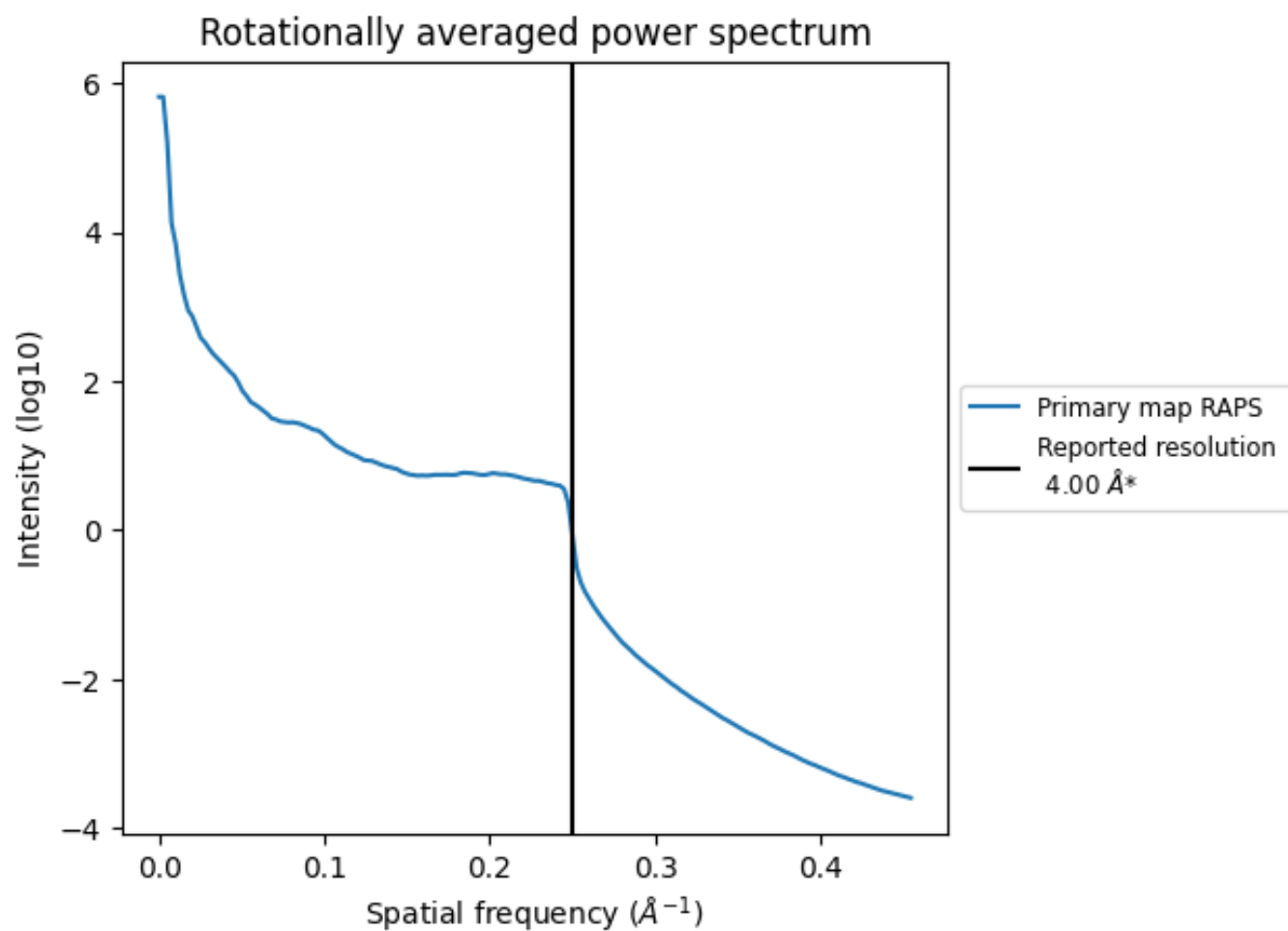
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2513 nm³; this corresponds to an approximate mass of 2270 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 0.250 Å⁻¹

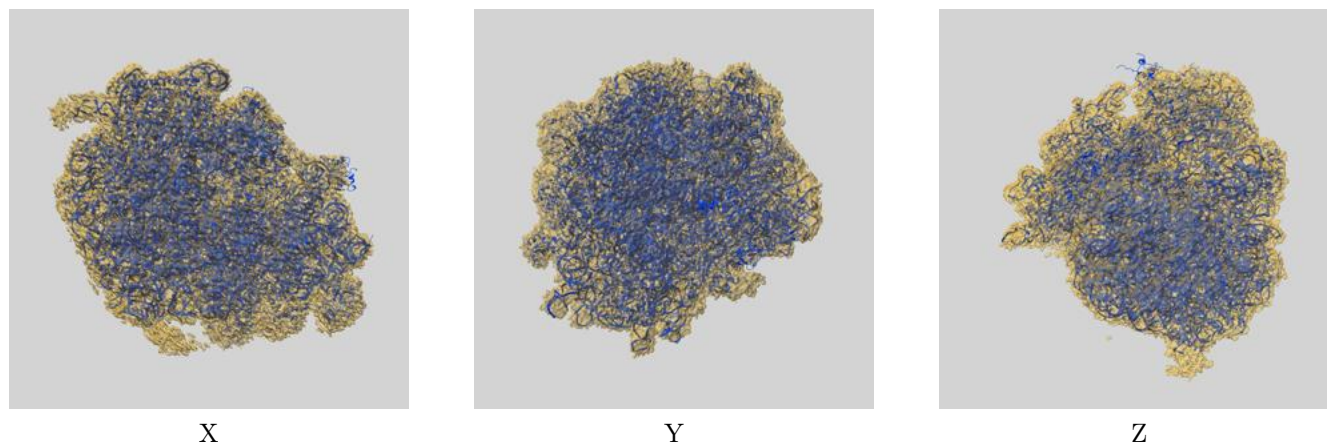
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

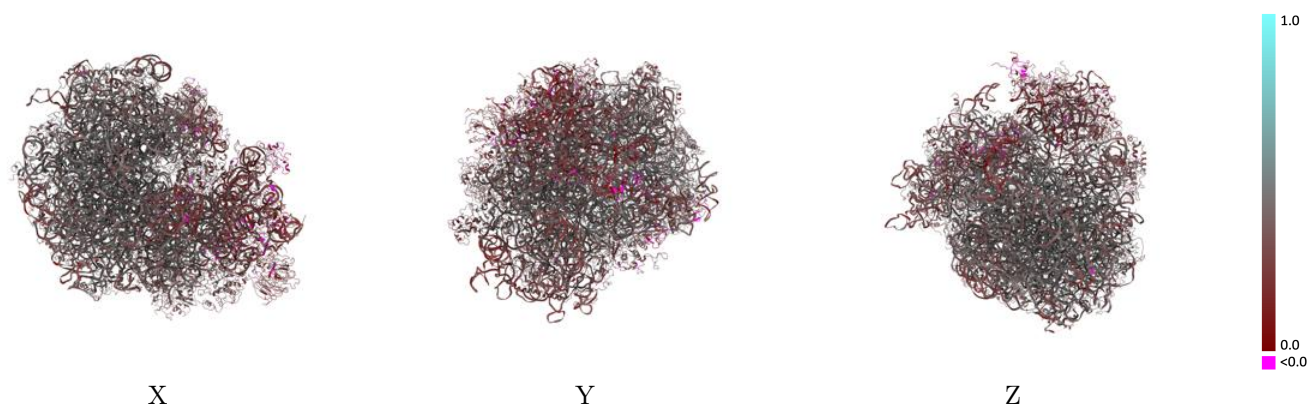
This section contains information regarding the fit between EMDB map EMD-0049 and PDB model 6GQV. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



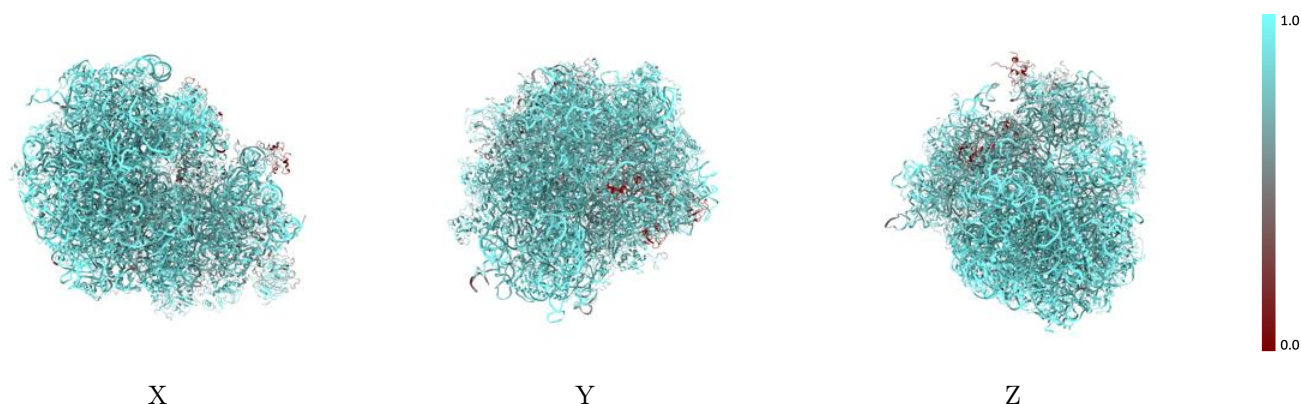
The images above show the 3D surface view of the map at the recommended contour level 0.033 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



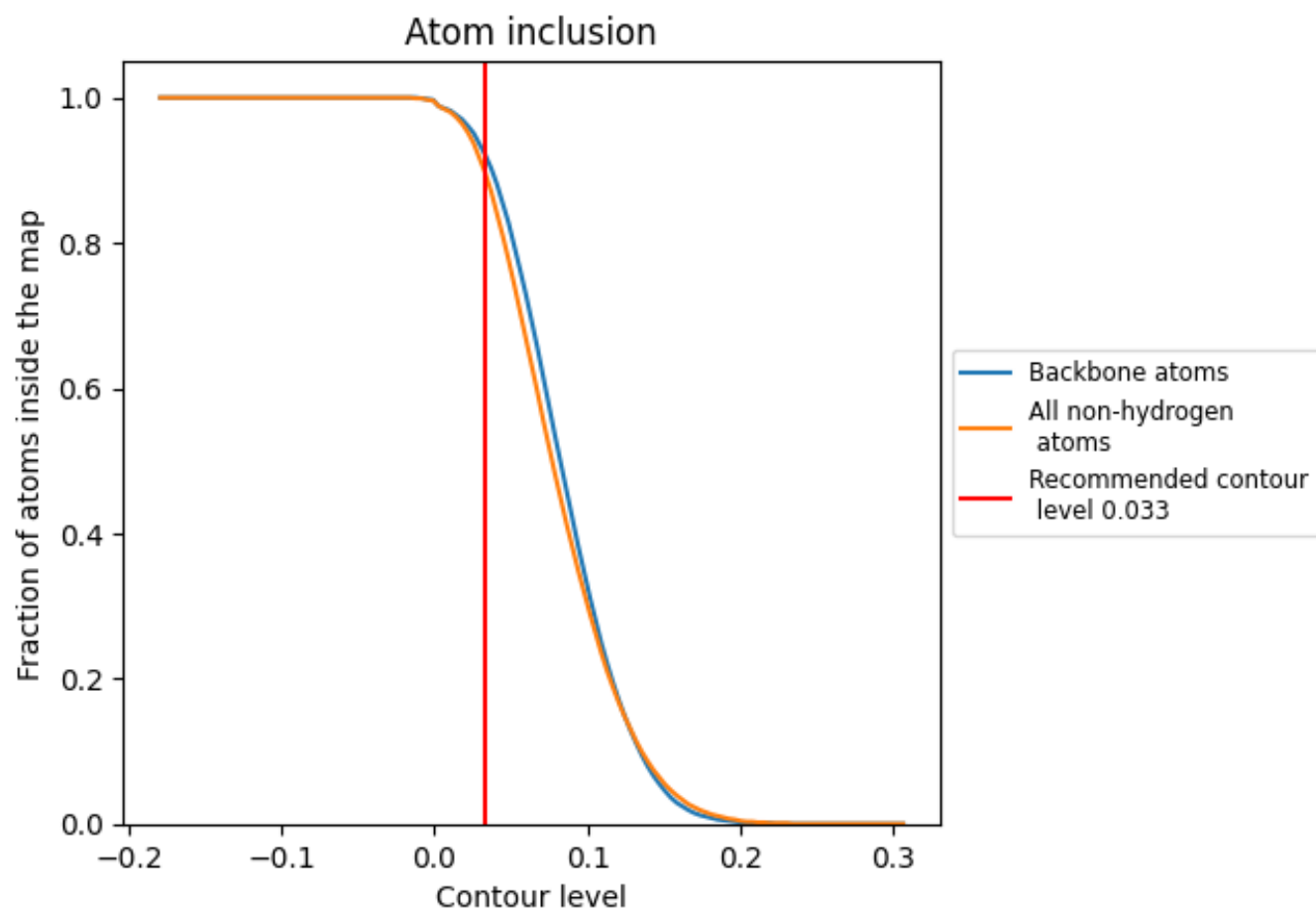
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.033).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.033) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8970	 0.3780
1	 0.9620	 0.4060
2	 0.9300	 0.3390
3	 0.9810	 0.3960
4	 0.9710	 0.4200
A	 0.8630	 0.4620
AA	 0.8670	 0.2720
AB	 0.7910	 0.3950
AC	 0.2450	 0.1250
AD	 0.8670	 0.3920
AE	 0.8890	 0.3890
AF	 0.8080	 0.2840
AG	 0.7620	 0.2500
AH	 0.7470	 0.2820
AI	 0.7790	 0.2900
AJ	 0.8080	 0.2680
AK	 0.6880	 0.2810
AL	 0.8280	 0.3480
AM	 0.8550	 0.4190
AN	 0.8110	 0.4140
AO	 0.8750	 0.3220
AP	 0.6250	 0.2320
AQ	 0.8550	 0.3750
AR	 0.8740	 0.3780
AS	 0.6370	 0.2470
AT	 0.8700	 0.3180
AU	 0.8100	 0.3710
AV	 0.7500	 0.2590
AW	 0.6640	 0.2630
AX	 0.7640	 0.3440
AY	 0.8380	 0.2940
AZ	 0.4440	 0.3240
B	 0.9000	 0.4470
BA	 0.6630	 0.2530
C	 0.9280	 0.4430



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Chain	Atom inclusion	Q-score
D	 0.9010	 0.3750
E	 0.9090	 0.4020
F	 0.9020	 0.4280
G	 0.9020	 0.4100
H	 0.8780	 0.4080
I	 0.8960	 0.4300
J	 0.8660	 0.3700
L	 0.9230	 0.4270
M	 0.9100	 0.4030
N	 0.9070	 0.4580
O	 0.9000	 0.4250
P	 0.8980	 0.4500
P0	 0.2760	 0.1750
P2	 0.3050	 0.1930
Q	 0.9150	 0.4480
R	 0.9010	 0.4200
S	 0.9070	 0.4280
T	 0.8930	 0.4360
U	 0.8980	 0.3800
V	 0.8320	 0.4470
W	 0.8490	 0.4290
X	 0.8920	 0.4150
Y	 0.9170	 0.4220
Z	 0.9050	 0.4140
a	 0.9260	 0.4490
b	 0.8920	 0.4260
c	 0.8960	 0.4210
d	 0.8820	 0.4400
e	 0.8930	 0.4460
f	 0.9000	 0.4490
g	 0.8810	 0.4480
h	 0.8910	 0.4170
i	 0.9060	 0.4080
j	 0.9280	 0.4760
k	 0.8610	 0.3850
l	 0.8840	 0.4430
m	 0.8940	 0.4490
n	 0.7880	 0.4600
o	 0.8770	 0.4430
p	 0.8480	 0.4440
q	 0.8610	 0.3510
r	 0.8990	 0.3770

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Chain	Atom inclusion	Q-score
s	 0.8630	 0.4010
t	 0.7250	 0.2790
u	 0.8770	 0.3550
v	 0.7480	 0.2720
w	 0.8770	 0.3310
x	 0.8420	 0.3220
y	 0.8420	 0.3460
z	 0.8880	 0.3620