



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2024 – 10:15 PM EDT

PDB ID : 4V89  
Title : Crystal Structure of Release Factor RF3 Trapped in the GTP State on a Rotated Conformation of the Ribosome (without viomycin)  
Authors : Zhou, J.; Lancaster, L.; Trakhanov, S.; Noller, H.F.  
Deposited on : 2011-11-17  
Resolution : 3.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

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>.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

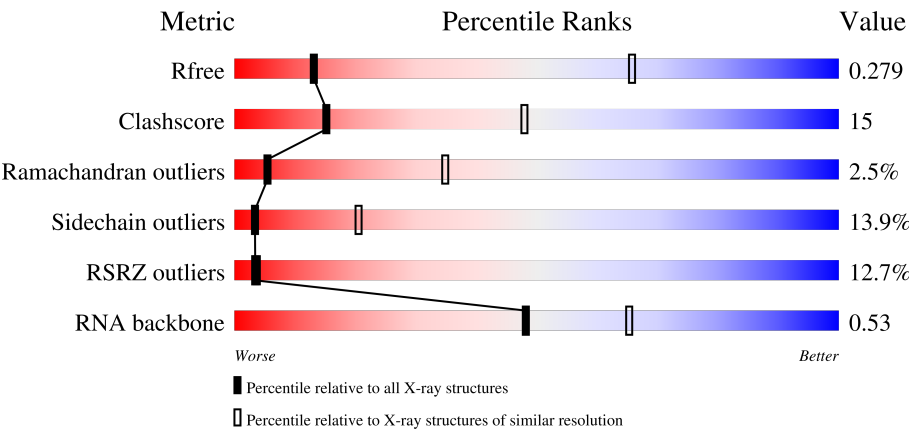
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	130704	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)
RNA backbone	3102	1027 (4.40-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1533	<div><div>3%</div><div>50%39%10%</div></div>
2	AB	241	<div><div>32%</div><div>45%37%9%10%</div></div>
3	AC	233	<div><div>9%</div><div>48%33%8%12%</div></div>
4	AD	206	<div><div>10%</div><div>49%44%7%</div></div>

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Mol	Chain	Length	Quality of chain
5	AE	167	
6	AF	135	
7	AG	179	
8	AH	130	
9	AI	130	
10	AJ	103	
11	AK	129	
12	AL	124	
13	AM	118	
14	AN	101	
15	AO	89	
16	AP	82	
17	AQ	84	
18	AR	75	
19	AS	92	
20	AT	87	
21	AU	71	
22	AV	27	
23	AW	534	
24	B0	85	
25	B1	78	
26	B2	63	
27	B3	59	
28	B4	57	
29	B5	55	

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Mol	Chain	Length	Quality of chain
30	B6	46	
31	B7	65	
32	B8	38	
33	BA	2903	
34	BB	118	
35	BC	273	
36	BD	209	
37	BE	201	
38	BF	179	
39	BG	177	
40	BH	165	
41	BI	142	
42	BJ	121	
42	BK	121	
42	BL	121	
42	BM	121	
43	BN	142	
44	BO	123	
45	BP	144	
46	BQ	136	
47	BR	127	
48	BS	117	
49	BT	115	
50	BU	118	
51	BV	103	

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Mol	Chain	Length	Quality of chain
52	BW	110	<div><div></div><div>3%</div><div>63%</div><div>29%</div><div>8%</div></div>
53	BX	100	<div><div></div><div>12%</div><div>39%</div><div>47%</div><div>6%</div><div>7%</div></div>
54	BY	104	<div><div></div><div>15%</div><div>62%</div><div>30%</div><div>6%</div></div>
55	BZ	94	<div><div></div><div>6%</div><div>68%</div><div>30%</div><div></div></div>

## 2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146665 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1532	Total	C	N	O	P	0	0	0
			32873	14661	6031	10649	1532			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	218	Total	C	N	O	S	0	0	0
			1704	1081	305	311	7			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1624	1028	305	288	3			

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0	0
			1105	687	211	201	6			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			817	515	148	148	6			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	151	Total	C	N	O	S	0	0	0
			1181	735	227	215	4			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0	0
			786	493	150	142	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	114	Total	C	N	O	S	0	0	0
			883	546	178	156	3			

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0	0
			714	439	144	130	1			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			649	406	128	114	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	80	Total	C	N	O	S	0	0	0
			648	411	121	113	3			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	55	Total	C	N	O	0	0	0
			455	288	86	81			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	79	Total	C	N	O	S	0	0	0
			637	408	120	107	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 21 is a protein called 30S ribosomal protein S21.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AU	51	Total	C	N	O	S	0	0	0
			425	265	86	73	1			

- Molecule 22 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	6	Total	C	N	O	P	0	0	0
			129	58	24	41	6			

- Molecule 23 is a protein called Peptide chain release factor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AW	525	Total	C	N	O	S	0	0	0
			4144	2617	722	783	22			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AW	530	HIS	-	EXPRESSION TAG	UNP P0A7I4
AW	531	HIS	-	EXPRESSION TAG	UNP P0A7I4
AW	532	HIS	-	EXPRESSION TAG	UNP P0A7I4
AW	533	HIS	-	EXPRESSION TAG	UNP P0A7I4
AW	534	HIS	-	EXPRESSION TAG	UNP P0A7I4

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	B0	79	Total	C	N	O	S	0	0	0
			596	367	120	108	1			

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	B1	77	Total	C	N	O	S	0	0	0
			625	388	129	106	2			

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	B2	63	Total	C	N	O	S	0	0	0
			509	313	99	95	2			

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	B3	58	Total	C	N	O	S	0	0	0
			449	281	87	79	2			

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	B4	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
29	B5	50	Total	C	N	O	0	0	0
			409	263	75	71			

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	B6	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	B7	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	B8	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			

- Molecule 33 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BA	2853	Total	C	N	O	P	0	0	0
			61252	27324	11274	19801	2853			

- Molecule 34 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BB	118	Total	C	N	O	P	0	0	0
			2529	1126	464	821	118			

- Molecule 35 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BC	271	Total	C	N	O	S	0	0	0
			2082	1288	423	364	7			

- Molecule 36 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BD	209	Total	C	N	O	S	0	0	0
			1565	979	288	294	4			

- Molecule 37 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BE	201	Total	C	N	O	S	0	0	0
			1552	974	283	290	5			

- Molecule 38 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BF	177	Total	C	N	O	S	0	0	0
			1410	899	249	256	6			

- Molecule 39 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BG	176	Total	C	N	O	S	0	0	0
			1323	832	243	246	2			

- Molecule 40 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BH	163	Total	C	N	O	S	0	0	0
			1230	775	219	229	7			

- Molecule 41 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BI	141	Total	C	N	O	S	0	0	0
			1032	651	179	196	6			

- Molecule 42 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BJ	30	Total	C	N	O	S	0	0	0
			227	144	33	47	3			
42	BK	30	Total	C	N	O	S	0	0	0
			227	144	33	47	3			
42	BL	30	Total	C	N	O	S	0	0	0
			227	144	33	47	3			
42	BM	30	Total	C	N	O	S	0	0	0
			227	144	33	47	3			

- Molecule 43 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BN	142	Total	C	N	O	S	0	0	0
			1129	714	212	199	4			

- Molecule 44 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BO	122	Total	C	N	O	S	0	0	0
			938	587	180	165	6			

- Molecule 45 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BP	143	Total	C	N	O	S	0	0	0
			1045	649	206	189	1			

- Molecule 46 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BQ	136	Total	C	N	O	S	0	0	0
			1074	686	205	177	6			

- Molecule 47 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	BR	120	Total	C	N	O	S	0	0	0
			960	593	196	166	5			

- Molecule 48 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	BS	116	Total	C	N	O		0	0	0
			892	552	178	162				

- Molecule 49 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	BT	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	BU	117	Total	C	N	O		0	0	0
			947	604	192	151				

- Molecule 51 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	BV	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			

- Molecule 52 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	BW	110	Total	C	N	O	S	0	0	0
			857	532	166	156	3			

- Molecule 53 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	BX	93	Total	C	N	O	S	0	0	0
			738	466	139	131	2			

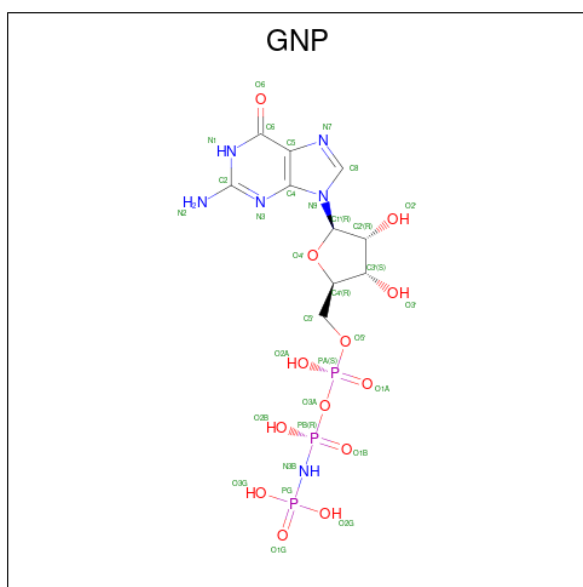
- Molecule 54 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
54	BY	102	Total	C	N	O	0	0	0
			779	492	146	141			

- Molecule 55 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	BZ	94	Total	C	N	O	S	0	0	0
			753	479	137	134	3			

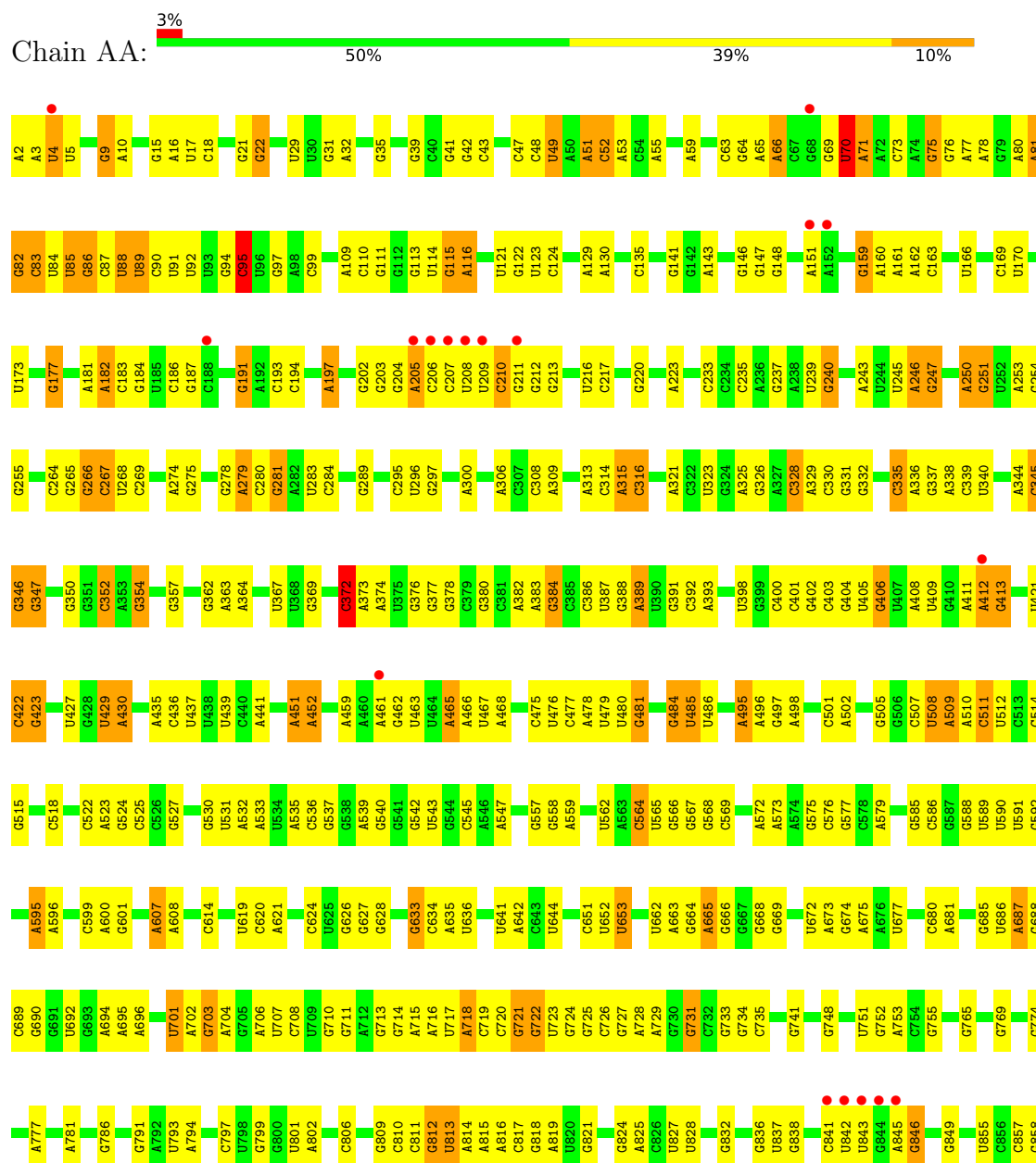
- Molecule 56 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula:  $C_{10}H_{17}N_6O_{13}P_3$ ).

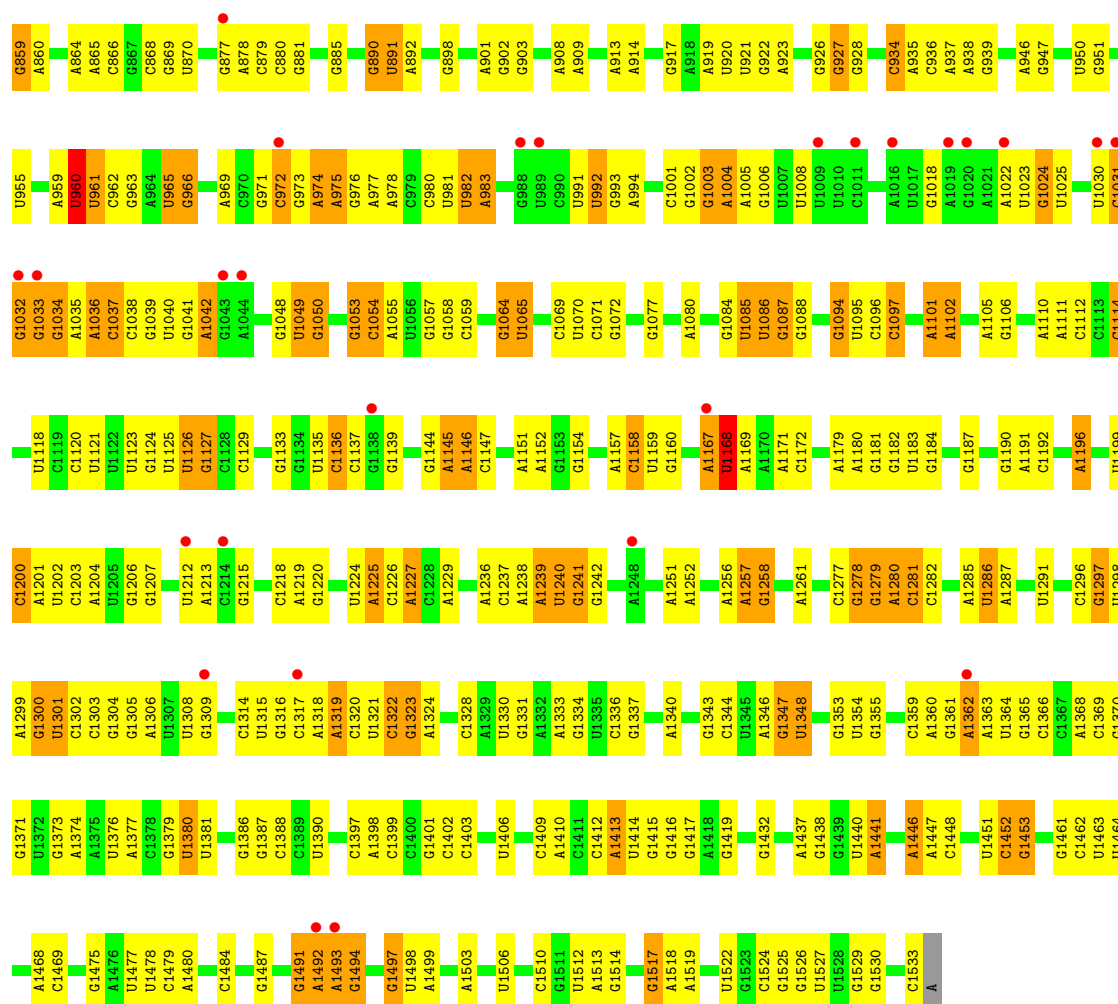


### 3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

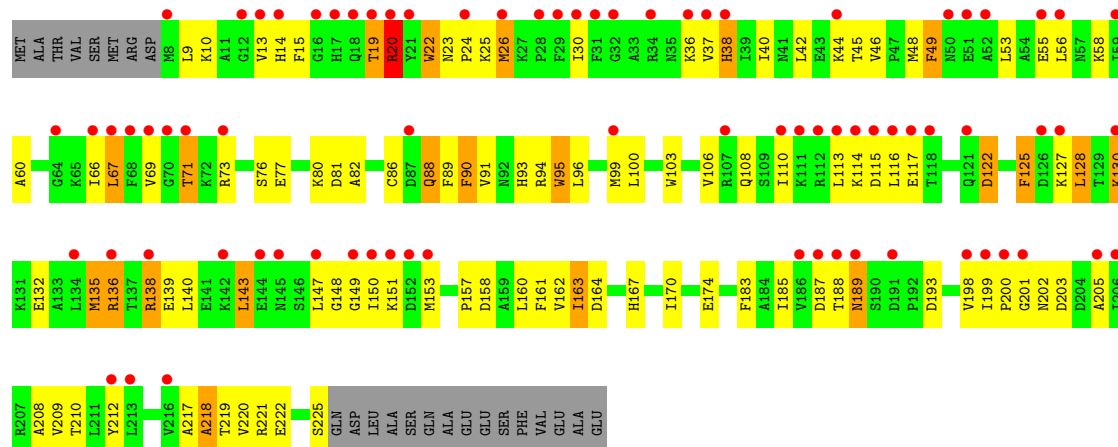
#### • Molecule 1: 16S rRNA





### • Molecule 2: 30S ribosomal protein S2

Chain AB: 32% 45% 37% 9% 10%

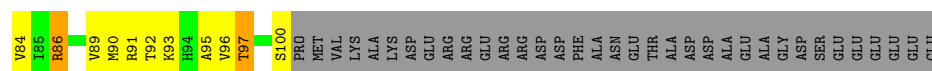


### • Molecule 3: 30S ribosomal protein S3

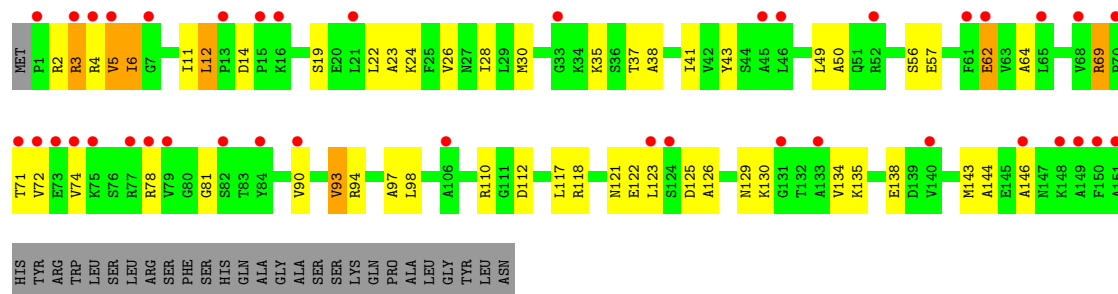
Chain AC: 9% 48% 33% 8% 12%



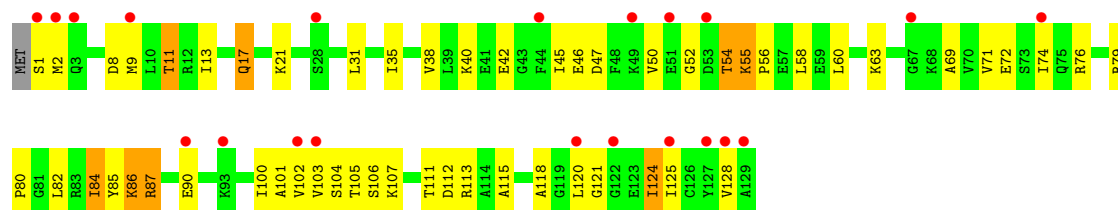




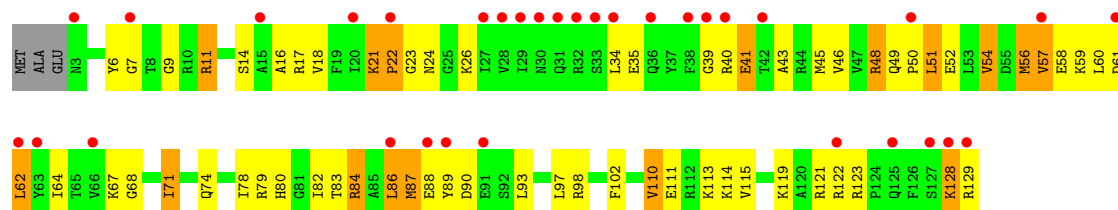
• Molecule 7: 30S ribosomal protein S7



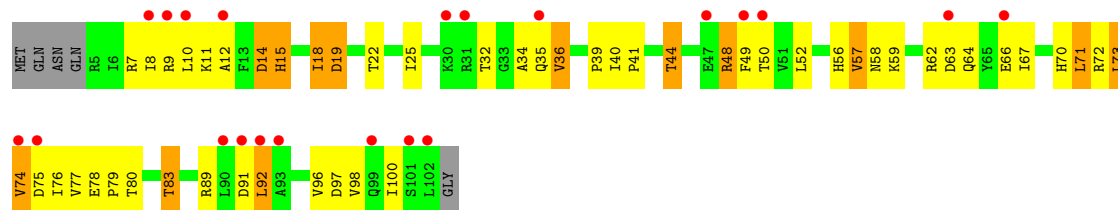
• Molecule 8: 30S ribosomal protein S8



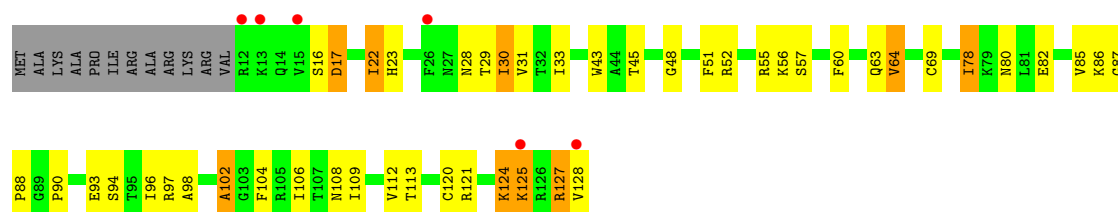
• Molecule 9: 30S ribosomal protein S9



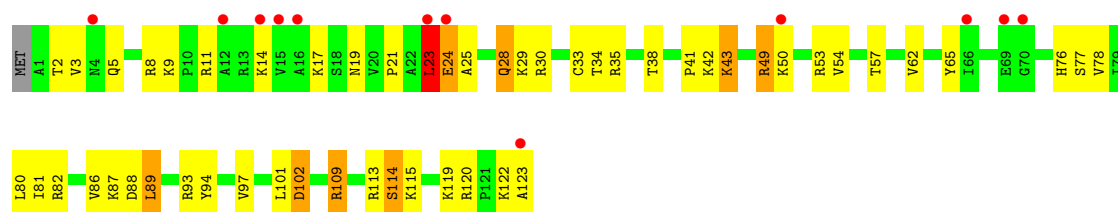
• Molecule 10: 30S ribosomal protein S10



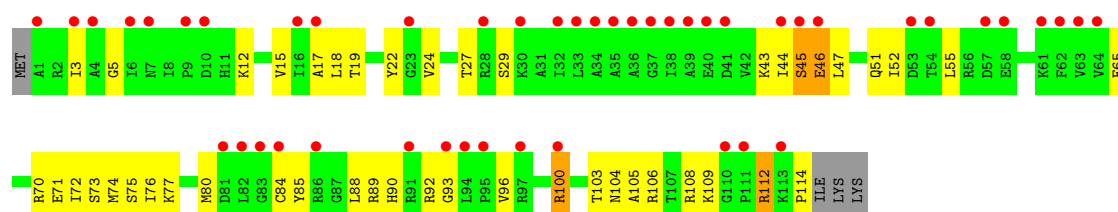
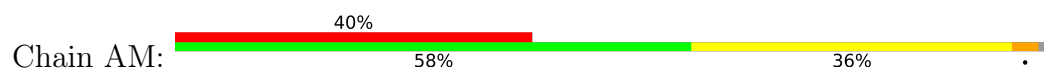
• Molecule 11: 30S ribosomal protein S11



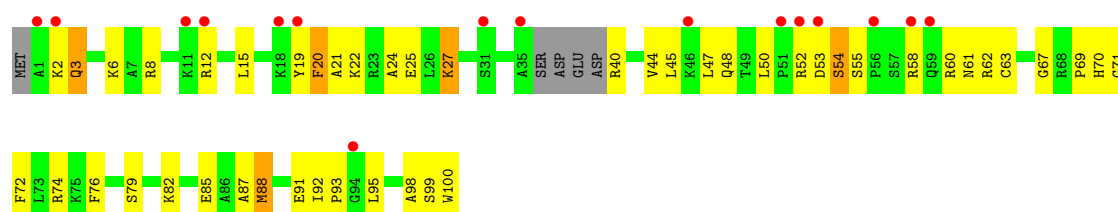
• Molecule 12: 30S ribosomal protein S12



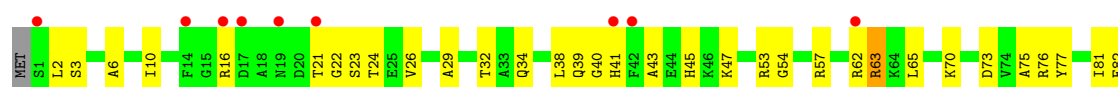
• Molecule 13: 30S ribosomal protein S13

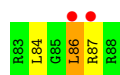


• Molecule 14: 30S ribosomal protein S14

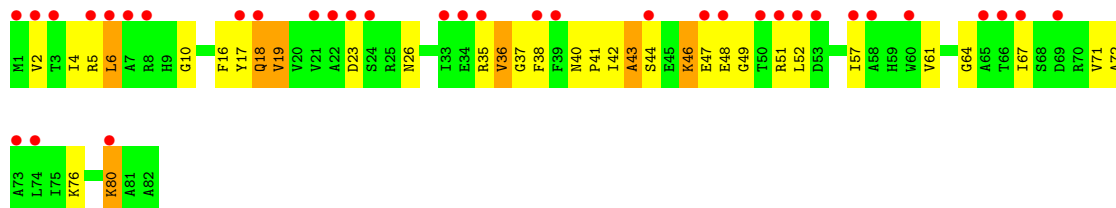
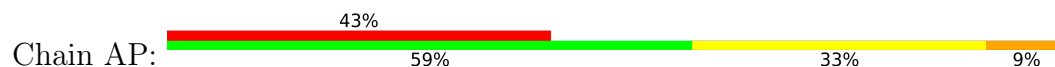


• Molecule 15: 30S ribosomal protein S15

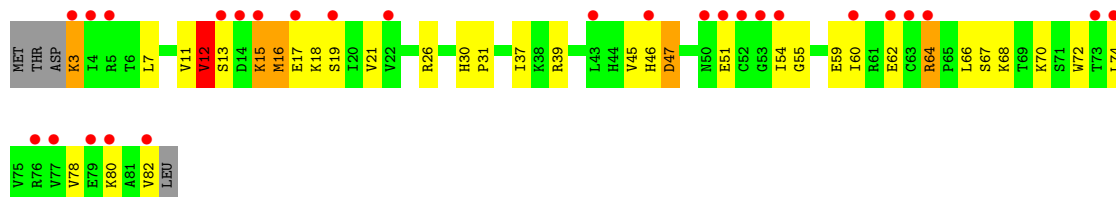




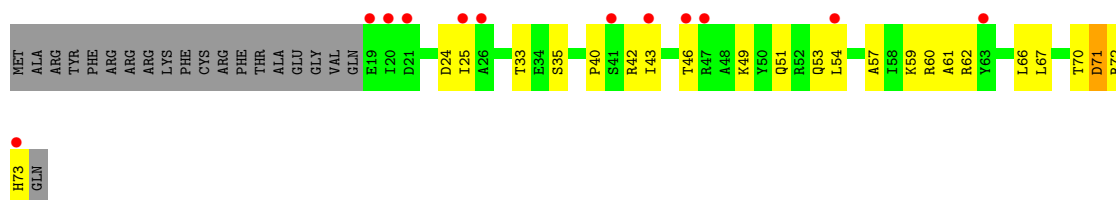
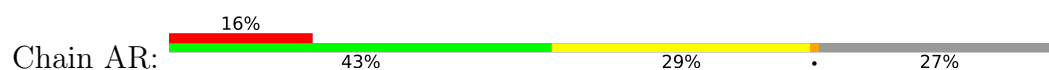
- Molecule 16: 30S ribosomal protein S16



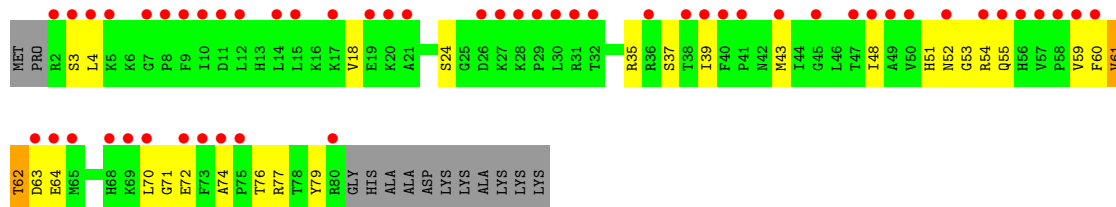
- Molecule 17: 30S ribosomal protein S17



- Molecule 18: 30S ribosomal protein S18



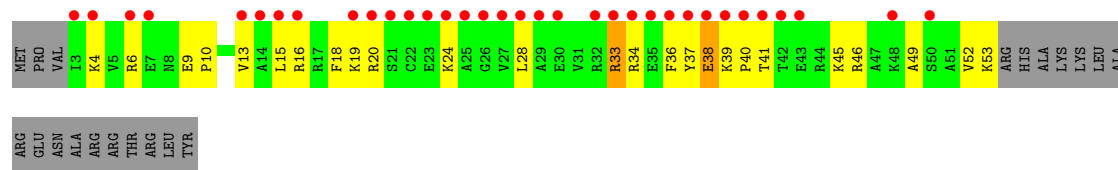
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20



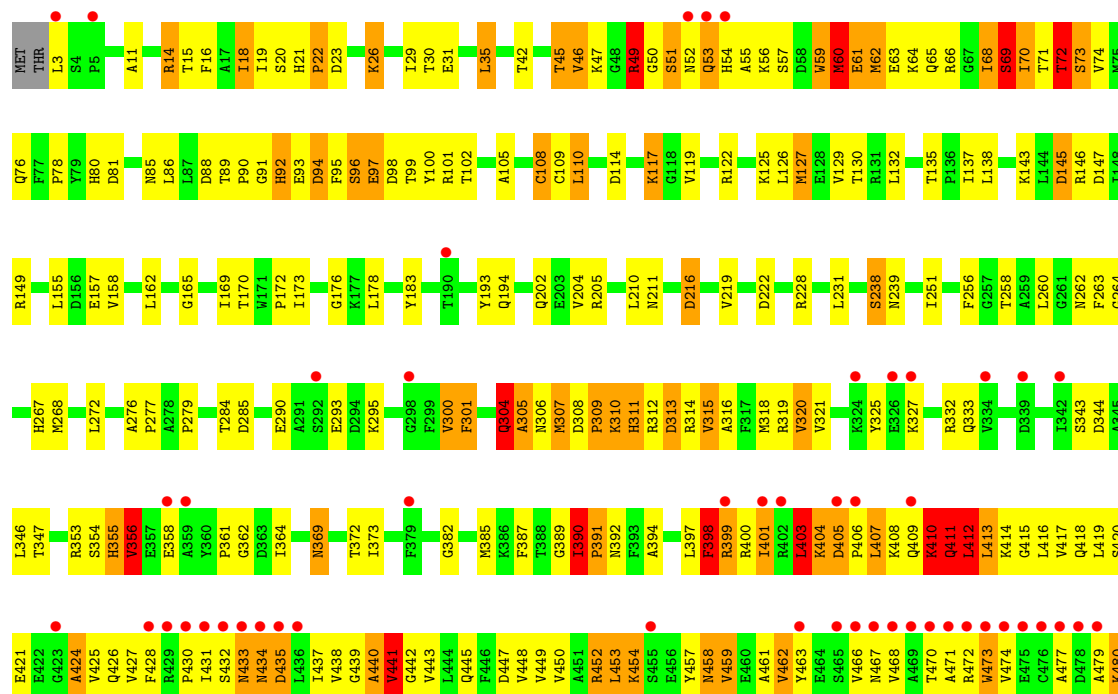
- Molecule 21: 30S ribosomal protein S21

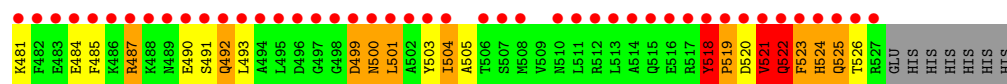


- Molecule 22: messenger RNA

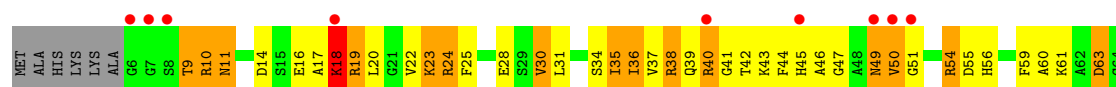


- Molecule 23: Peptide chain release factor 3

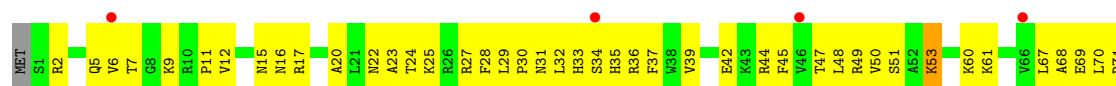
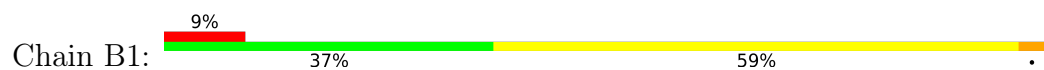




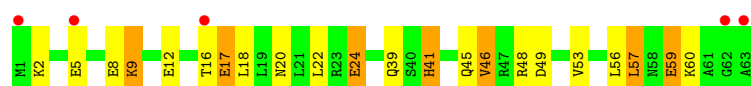
• Molecule 24: 50S ribosomal protein L27



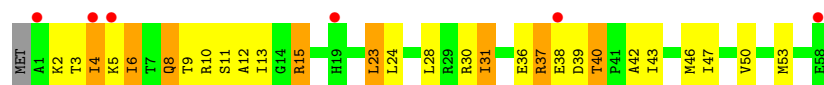
• Molecule 25: 50S ribosomal protein L28



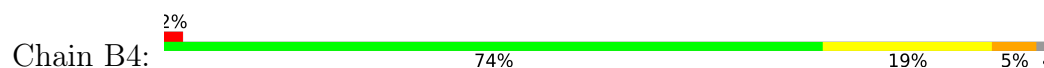
• Molecule 26: 50S ribosomal protein L29



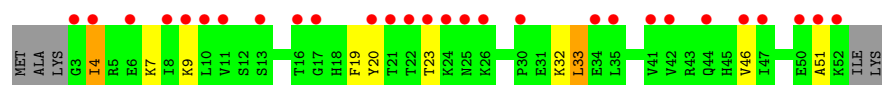
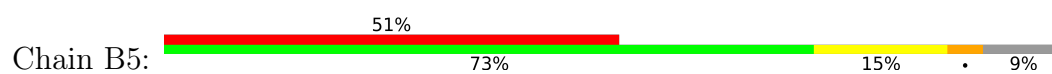
• Molecule 27: 50S ribosomal protein L30



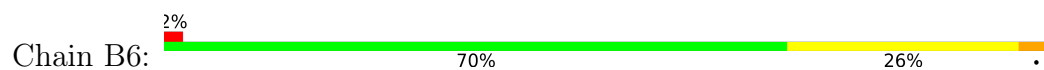
• Molecule 28: 50S ribosomal protein L32



• Molecule 29: 50S ribosomal protein L33



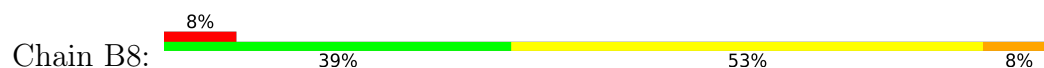
- Molecule 30: 50S ribosomal protein L34



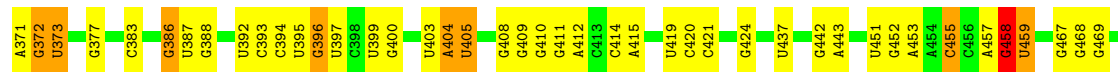
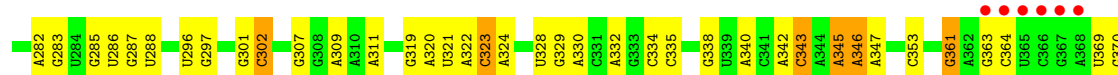
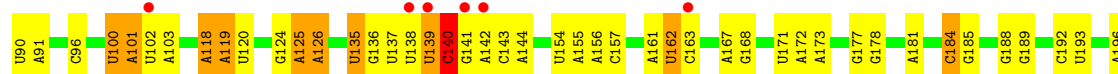
- Molecule 31: 50S ribosomal protein L35

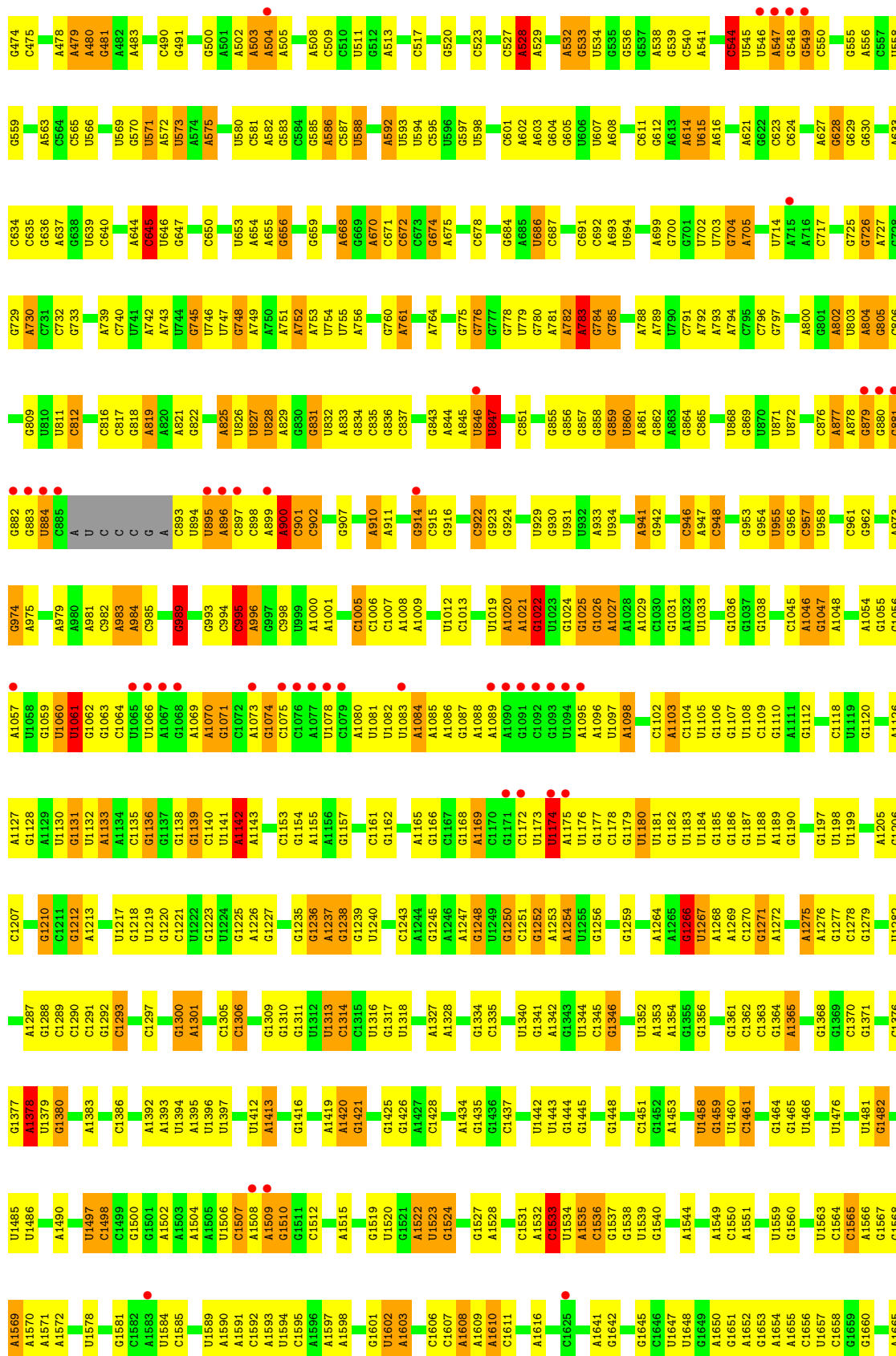


- Molecule 32: 50S ribosomal protein L36



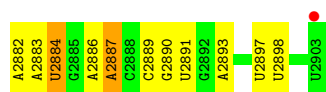
- Molecule 33: 23S rRNA





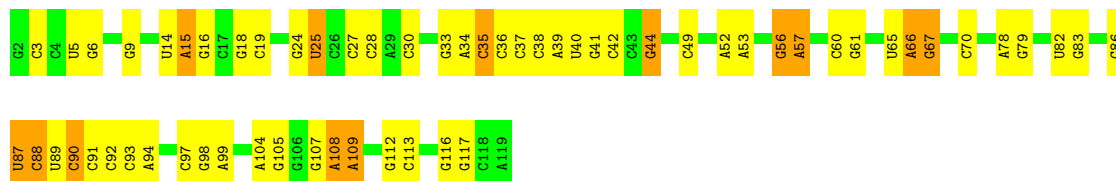


C2794	U2698	G2595	A2497	C2403	A2328	U2249	A	G	G1935	U1758	G1666
C2795	C2704	U2596	C2496	U2404	U2329	G2250	C	A	A1936	A1759	G1667
U2798	G2502	G2597	G2502	G2405	G2330	U2258	A	U	A1937	C1764	A1668
A2800	A2503	A2598	U2504	A2406	G2331	U2259	G	A	A1847	C1765	A1669
G2801	U2504	G2603	G2505	A2407	C2332	U2260	U	G	A1848	U1671	U1670
G2802	G2714	G2603	U2506	G2415	U2334	C2261	U	U	G1850	G1674	U1671
G2803	G2719	U2609	U2506	C2416	A2335	U2262	G	G	U1851	G1675	G1674
U2804	U2720	C2612	A2518	A2417	A2336	C2263	G	G	A1852	A1676	A1677
C2805	A2721	U2619	U2418	A2418	G2337	C2264	A	G	A1853	U1775	A1677
C2806	G2722	U2613	U2419	A2419	C2338	C2265	G	G	G1857	C1774	U1677
G2809	C2723	C2420	C2520	C2420	C2339	A2267	G	G	A1858	U1782	U1688
A2810	A2726	U2615	C2527	U2423	A2340	A2268	G	G	A1866	A1783	U1688
G2811	A2727	U2616	U2528	C2424	C2341	G2269	C	U	A1866	U1784	U1688
G2812	A2727	U2617	G2529	A2425	C2342	U2272	U	U	A1866	A1785	U1688
G2813	U2728	G2632	A2532	A2426	G2346	A2273	U	U	A1869	A1786	G1695
G2814	G2729	G2632	G2532	A2427	C2347	A2274	U	U	G1870	A1787	A1705
A2814	C2730	G2621	C2540	G2428	C2347	C2275	A	A	A1871	C1788	A1705
C2815	G2733	G2627	A2541	G2429	U2348	G2276	U	U	A1872	C1789	G1706
G2818	A2733	C2628	A2541	A2430	C2349	G2277	U	U	G1873	C1790	C1706
G2819	A2734	U2629	G2544	A2433	C2350	A2278	U	U	A1874	A1791	C1708
A2820	G2735	G2630	G2544	A2434	G2351	C2283	U	U	A1875	G1792	U1709
A2821	A2736	G2631	A2547	A2435	A2352	G2284	U	U	G1884	C1793	G1710
G2822	G2737	A2632	U2548	A2435	C2353	G2285	U	U	A1889	A1794	U1714
A2823	A2740	C2636	G2549	U2441	C2354	A2286	U	U	A1889	C1795	U1714
C2824	A2741	U2637	G2550	C2442	G2355	A2287	U	U	A1894	U1796	G1715
G2825	G2742	G2638	C2551	G2443	C2356	G2288	U	U	C1894	U1797	G1715
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G2834	G2744	G2640	G2553	G2445	C2358	G2290	U	U	C1895	U1799	A1717
G2838	G2747	C2646	U2554	A2448	C2359	U2291	U	U	C1902	G1800	A1722
C2839	A2748	U2647	U2555	A2449	C2360	U2292	U	U	G1903	A1801	G1723
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G2842	A2757	U2656	U2561	A2459	C2363	G2295	U	U	G1906	A1808	C1727
U2845	G2758	A2657	A2566	C2466	G2364	A2297	U	U	C1909	U1812	G1728
G2846	G2759	C2658	G2567	C2467	C2365	A2298	U	U	G1910	G1813	U1729
G2848	C2762	G2659	U2570	A2468	G2375	G2302	U	U	U1911	C1730	C1730
U2849	G2765	U2662	U2571	A2470	A2376	G2303	U	U	A1912	C1816	G1732
G2857	A2766	G2663	A2572	A2471	A2377	G2304	U	U	G1913	U1817	G1733
A2860	U2769	C2677	C2573	C2472	A2378	G2305	U	U	C1914	G1734	G1734
G2861	G2778	G2678	C2574	C2473	A2379	G2306	U	U	U1915	A1819	A1735
A2862	A2778	A2679	A2577	U2477	C2386	G2307	U	U	C1922	C1822	U1736
A2863	U2784	U2680	G2576	A2478	G2382	G2308	U	U	A1918	U1827	G1738
G2864	C2785	C2683	C2579	G2481	G2383	A2309	U	U	A1919	U1828	U1742
G2865	G2786	U2684	U2580	G2485	U2384	G2310	U	U	C1920	A1829	A1744
G2866	U2870	U2689	U2584	G2485	C2394	U2321	U	U	C1921	C1833	A1746
G2867	A2871	U2690	U2585	G2485	C2395	A2322	U	U	U2022	U1926	U1746
G2868	A2872	C2691	U2586	U2489	C2396	G2323	U	U	C2023	A1927	A1746
G2869	A2873	G2692	U2586	G2490	U2397	U2324	U	U	A1928	G1835	G1748
A2879	U2790	U2693	C2591	U2491	U2398	U2325	U	U	G1836	C1836	A1749
C2880	A2792	G2693	C2591	C2496	G2399	C2326	U	U	C1837	G1750	G1750
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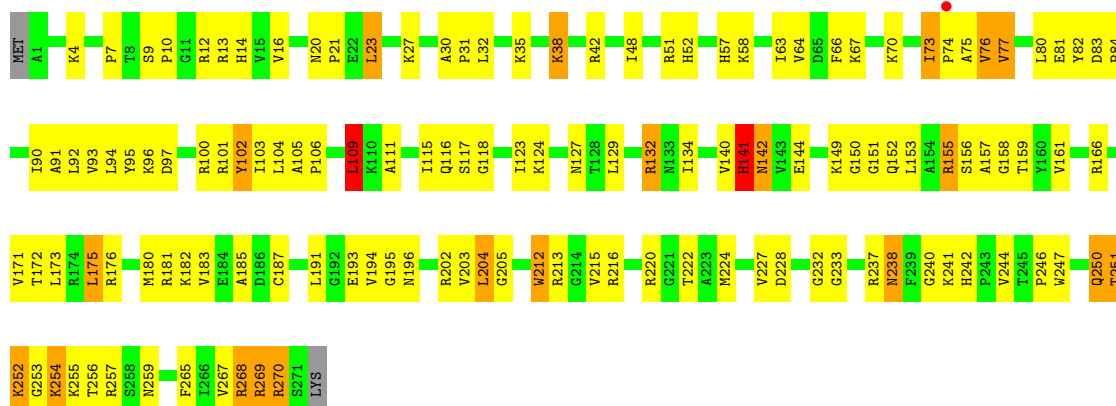
• Molecule 34: 5S rRNA

Chain BB: 48% 41% 11%



• Molecule 35: 50S ribosomal protein L2

Chain BC: 50% 41% 7% ..



• Molecule 36: 50S ribosomal protein L3

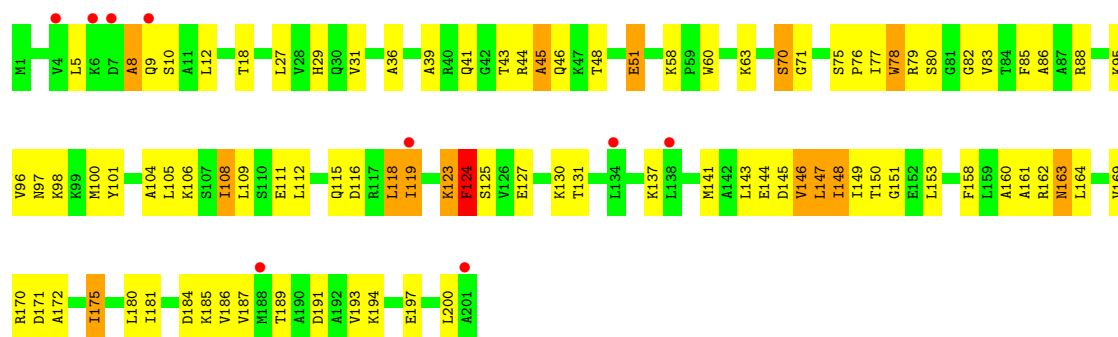
Chain BD: 46% 46% 8%



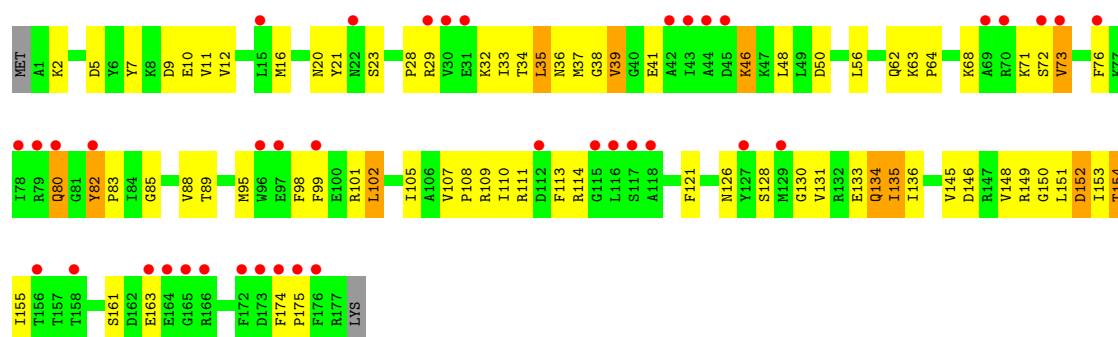
• Molecule 37: 50S ribosomal protein L4

Chain BE: 4% 54% 38% 7%

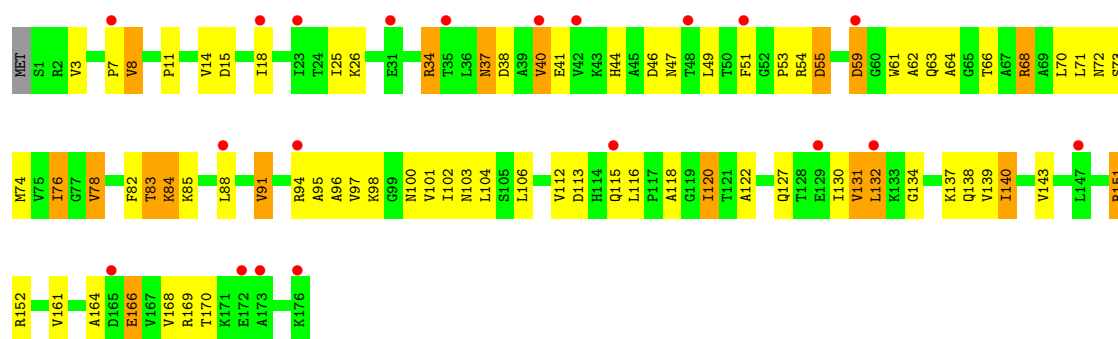




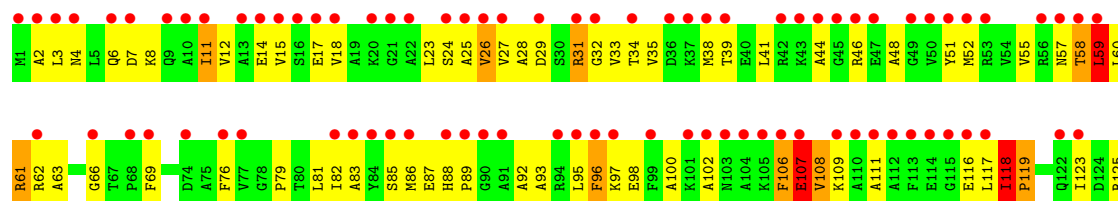
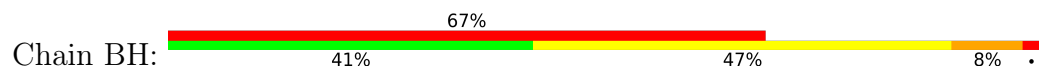
• Molecule 38: 50S ribosomal protein L5

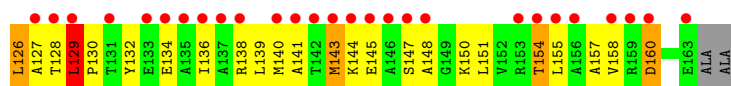


• Molecule 39: 50S ribosomal protein L6

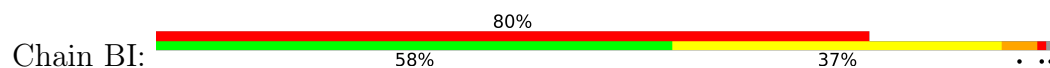


• Molecule 40: 50S ribosomal protein L10

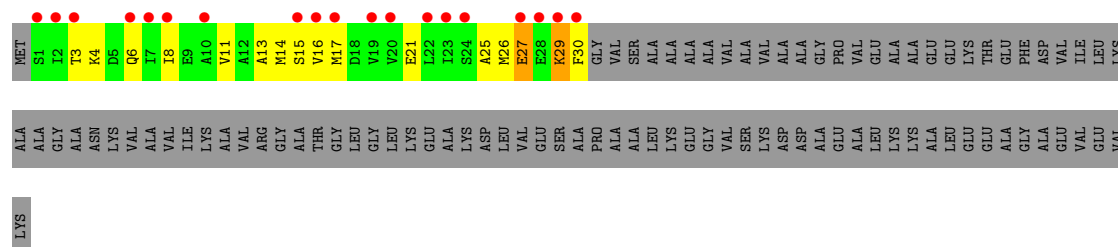




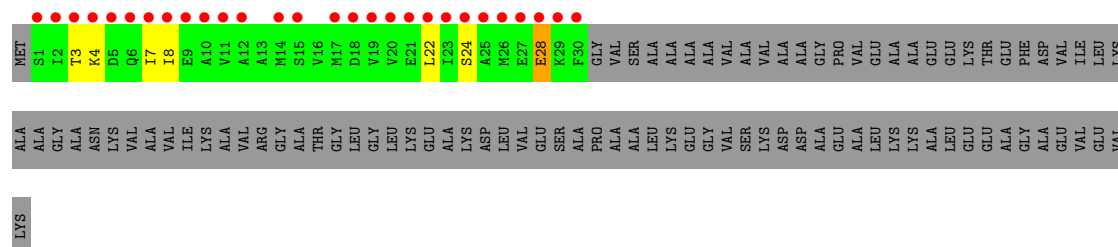
- Molecule 41: 50S ribosomal protein L11



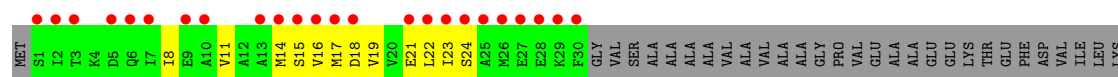
- Molecule 42: 50S ribosomal protein L7/L12

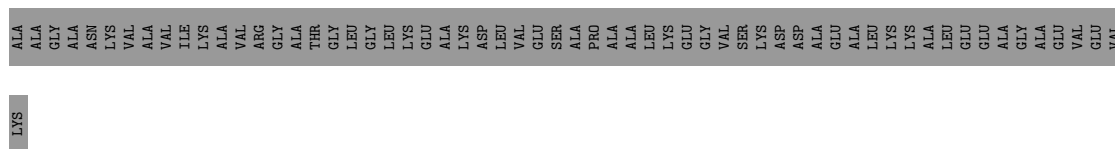


- Molecule 42: 50S ribosomal protein L7/L12

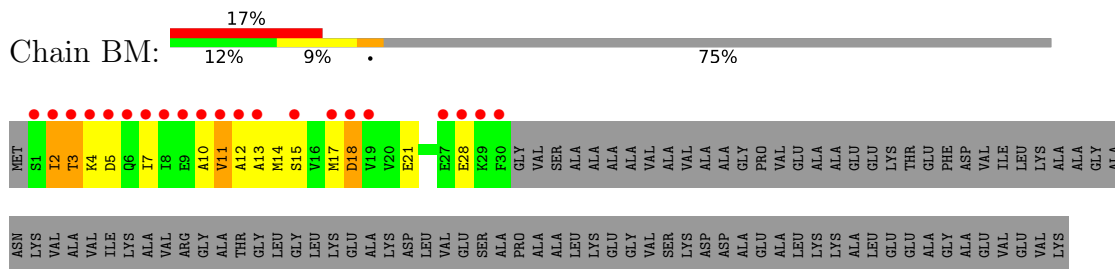


- Molecule 42: 50S ribosomal protein L7/L12

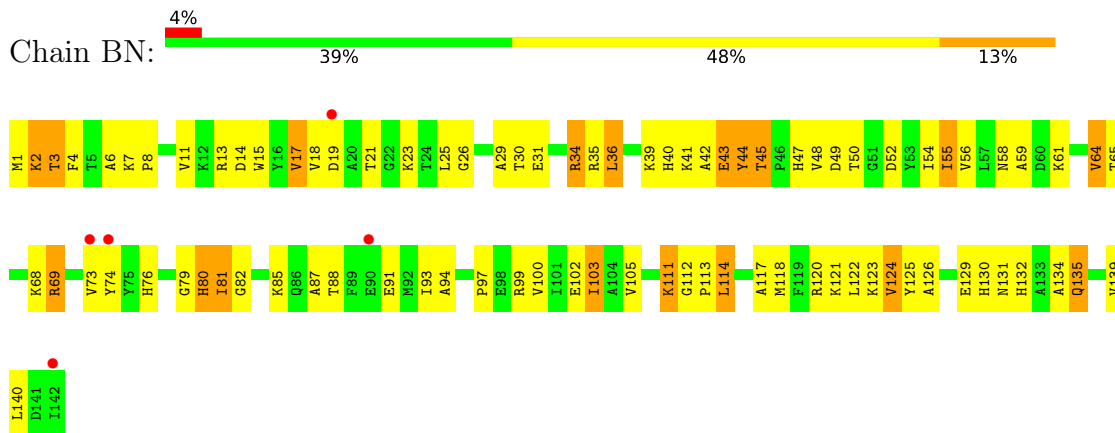




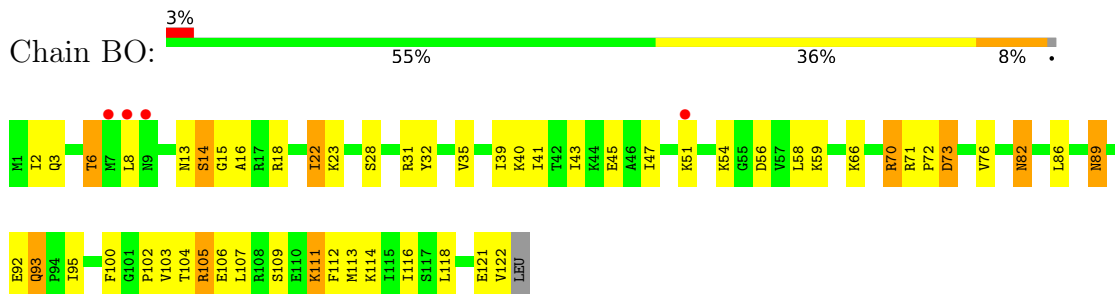
- Molecule 42: 50S ribosomal protein L7/L12



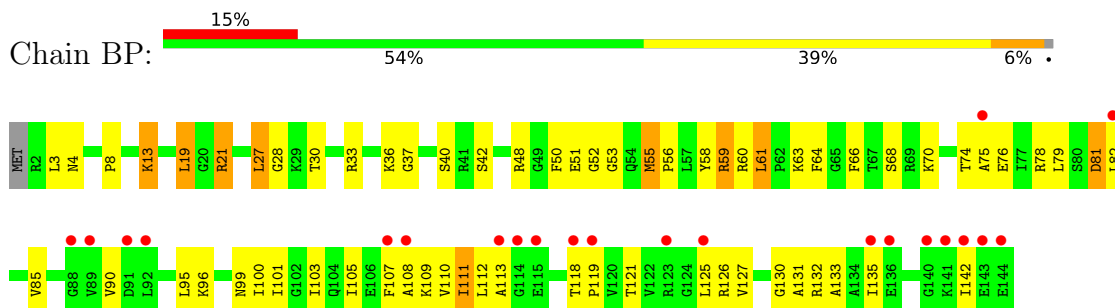
- Molecule 43: 50S ribosomal protein L13



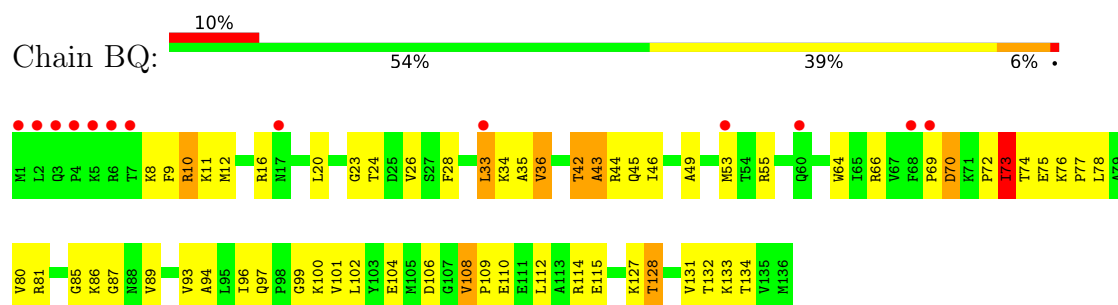
- Molecule 44: 50S ribosomal protein L14



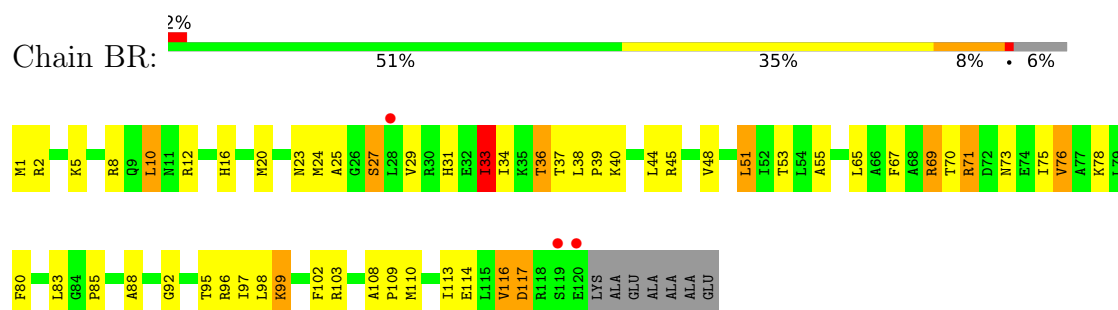
- Molecule 45: 50S ribosomal protein L15



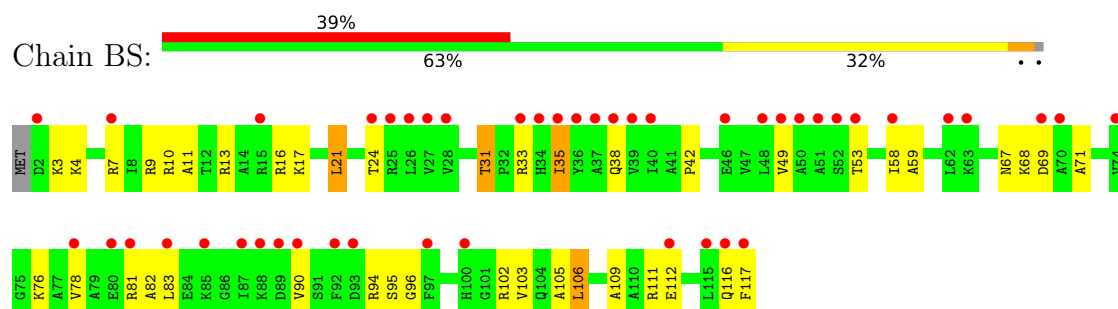
- Molecule 46: 50S ribosomal protein L16



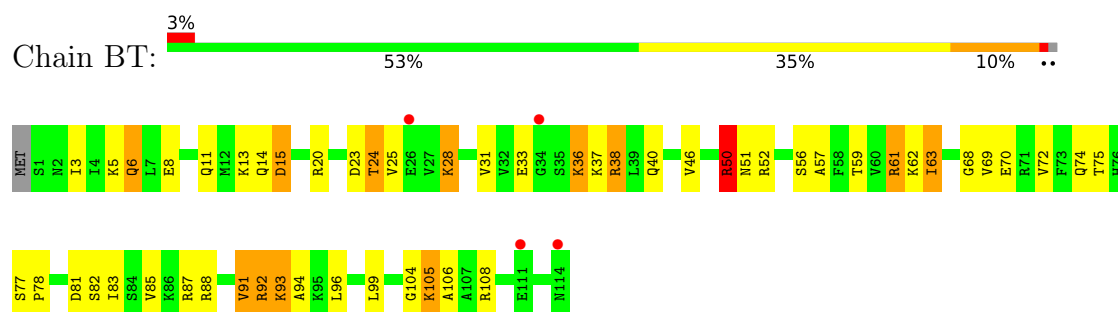
- Molecule 47: 50S ribosomal protein L17



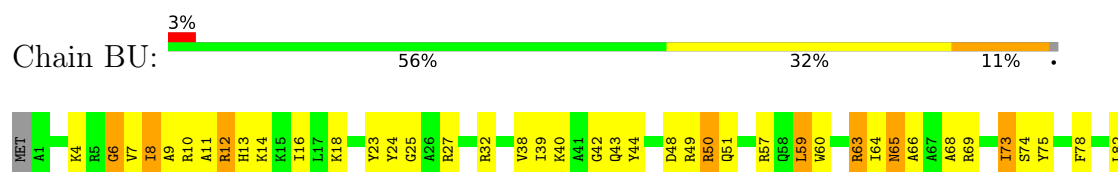
- Molecule 48: 50S ribosomal protein L18

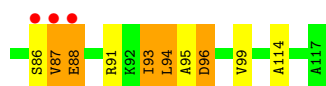


- Molecule 49: 50S ribosomal protein L19

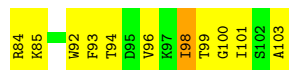
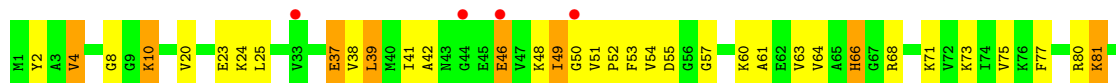


- Molecule 50: 50S ribosomal protein L20

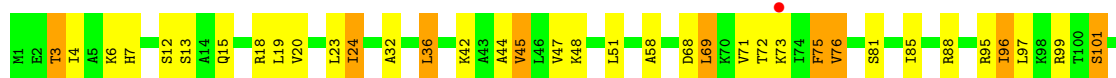




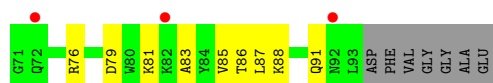
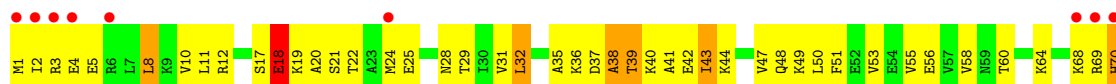
- Molecule 51: 50S ribosomal protein L21



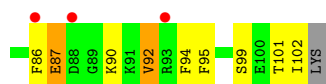
- Molecule 52: 50S ribosomal protein L22



- Molecule 53: 50S ribosomal protein L23

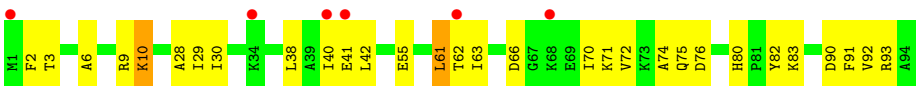


- Molecule 54: 50S ribosomal protein L24



- Molecule 55: 50S ribosomal protein L25







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	258.00Å 312.00Å 333.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.70 59.67 – 3.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.70) 98.1 (59.67-3.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.52 (at 3.49Å)	Xtriage
Refinement program	PHENIX, CNS 1.2	Depositor
R, $R_{free}$	0.240 , 0.290 0.233 , 0.279	Depositor DCC
$R_{free}$ test set	16644 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	83.9	Xtriage
Anisotropy	0.485	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 93.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	146665	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.60% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	AA	0.41	0/36809	0.84	55/57423 (0.1%)
2	AB	0.32	0/1735	0.65	0/2338
3	AC	0.35	0/1651	0.57	0/2225
4	AD	0.35	0/1665	0.58	0/2227
5	AE	0.38	0/1118	0.69	0/1504
6	AF	0.36	0/835	0.60	0/1128
7	AG	0.29	0/1195	0.52	0/1602
8	AH	0.31	0/989	0.53	0/1326
9	AI	0.32	0/1034	0.61	0/1375
10	AJ	0.33	0/796	0.59	0/1077
11	AK	0.35	0/893	0.61	0/1205
12	AL	0.36	0/969	0.70	1/1300 (0.1%)
13	AM	0.29	0/892	0.58	0/1193
14	AN	0.31	0/785	0.66	0/1043
15	AO	0.34	0/722	0.60	0/964
16	AP	0.35	0/659	0.61	0/884
17	AQ	0.36	0/657	0.66	0/881
18	AR	0.41	0/462	0.61	0/621
19	AS	0.28	0/652	0.49	0/877
20	AT	0.41	0/671	0.68	0/888
21	AU	0.34	0/430	0.69	0/570
22	AV	0.45	0/144	0.93	0/222
23	AW	0.48	4/4221 (0.1%)	0.72	4/5702 (0.1%)
24	B0	0.48	0/603	0.82	0/797
25	B1	0.37	0/635	0.69	0/848
26	B2	0.41	0/510	0.75	1/677 (0.1%)
27	B3	0.39	0/453	0.68	0/605
28	B4	0.41	0/450	0.66	0/599
29	B5	0.40	0/416	0.55	0/554
30	B6	0.43	0/380	0.67	0/498
31	B7	0.39	0/513	0.70	1/676 (0.1%)
32	B8	0.36	0/303	0.64	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	BA	0.50	3/68601 (0.0%)	0.94	135/107017 (0.1%)
34	BB	0.41	0/2828	0.83	0/4410
35	BC	0.43	0/2121	0.76	1/2852 (0.0%)
36	BD	0.49	0/1586	0.80	0/2134
37	BE	0.40	0/1571	0.72	1/2113 (0.0%)
38	BF	0.33	0/1434	0.55	0/1926
39	BG	0.40	0/1343	0.65	0/1816
40	BH	0.36	0/1244	0.74	2/1675 (0.1%)
41	BI	0.29	0/1046	0.60	0/1410
42	BJ	0.35	0/227	0.65	0/304
42	BK	0.31	0/227	0.51	0/304
42	BL	0.30	0/227	0.51	0/304
42	BM	0.36	0/227	0.58	0/304
43	BN	0.49	0/1152	0.78	0/1551
44	BO	0.44	0/947	0.71	0/1268
45	BP	0.40	0/1054	0.77	1/1403 (0.1%)
46	BQ	0.39	0/1093	0.63	0/1460
47	BR	0.45	0/973	0.75	1/1301 (0.1%)
48	BS	0.34	0/902	0.57	0/1209
49	BT	0.46	0/929	0.75	0/1242
50	BU	0.54	0/960	0.73	0/1278
51	BV	0.37	0/829	0.71	0/1107
52	BW	0.48	0/864	0.77	0/1156
53	BX	0.45	0/744	0.78	0/994
54	BY	0.40	0/787	0.73	0/1051
55	BZ	0.35	0/766	0.59	0/1025
All	All	0.44	7/158929 (0.0%)	0.84	203/236840 (0.1%)

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
2	AB	0	3
3	AC	0	1
5	AE	0	2
6	AF	0	1
11	AK	0	1
13	AM	0	1
14	AN	0	2
23	AW	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	B0	0	1
37	BE	0	1
39	BG	0	1
40	BH	0	3
41	BI	0	2
43	BN	0	1
45	BP	0	1
47	BR	0	1
50	BU	0	1
53	BX	0	1
54	BY	0	1
All	All	0	28

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	BA	1914	C	O3'-P	-15.87	1.42	1.61
23	AW	22	PRO	C-N	9.22	1.55	1.34
33	BA	2104	C	O3'-P	-8.83	1.50	1.61
23	AW	72	THR	C-O	5.98	1.34	1.23
23	AW	73	SER	CB-OG	5.42	1.49	1.42
23	AW	65	GLN	C-N	-5.15	1.22	1.34
33	BA	1142	A	N9-C4	-5.04	1.34	1.37

All (203) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BA	1914	C	OP2-P-O3'	13.60	135.11	105.20
33	BA	1914	C	P-O3'-C3'	-12.52	104.68	119.70
33	BA	140	C	C2-N1-C1'	9.97	129.77	118.80
33	BA	645	C	C2-N1-C1'	9.86	129.65	118.80
35	BC	109	LEU	CA-CB-CG	9.67	137.53	115.30
1	AA	1126	U	C2-N1-C1'	9.36	128.93	117.70
1	AA	1168	U	C2-N1-C1'	8.90	128.38	117.70
33	BA	1061	U	C2-N1-C1'	8.81	128.28	117.70
1	AA	328	C	N1-C2-O2	8.70	124.12	118.90
33	BA	1297	C	C6-N1-C2	-8.60	116.86	120.30
33	BA	1174	U	C2-N1-C1'	8.47	127.87	117.70
33	BA	645	C	N1-C2-O2	8.47	123.98	118.90
33	BA	140	C	N1-C2-O2	8.41	123.95	118.90
1	AA	1136	C	C2-N1-C1'	8.20	127.81	118.80
33	BA	1914	C	OP1-P-O3'	-8.15	87.26	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BA	645	C	C6-N1-C1'	-8.09	111.09	120.80
33	BA	989	G	N3-C4-C5	-7.85	124.67	128.60
33	BA	1313	U	C2-N1-C1'	7.76	127.01	117.70
33	BA	1913	A	N1-C6-N6	7.71	123.23	118.60
33	BA	804	A	C8-N9-C4	7.59	108.84	105.80
1	AA	1136	C	N1-C2-O2	7.56	123.44	118.90
33	BA	2612	C	C6-N1-C2	7.54	123.32	120.30
1	AA	328	C	C2-N1-C1'	7.50	127.05	118.80
33	BA	1174	U	N1-C2-O2	7.48	128.04	122.80
33	BA	1602	U	C5-C4-O4	7.48	130.39	125.90
12	AL	23	LEU	CA-CB-CG	7.47	132.49	115.30
33	BA	1251	C	C6-N1-C2	-7.16	117.44	120.30
33	BA	1061	U	N1-C2-O2	7.03	127.72	122.80
1	AA	1126	U	N1-C2-O2	7.00	127.70	122.80
33	BA	2541	A	C8-N9-C4	6.95	108.58	105.80
1	AA	85	U	C2-N1-C1'	6.95	126.04	117.70
1	AA	1126	U	C6-N1-C1'	-6.93	111.50	121.20
33	BA	140	C	C6-N1-C1'	-6.92	112.49	120.80
33	BA	1314	C	C6-N1-C2	-6.87	117.55	120.30
33	BA	457	A	C8-N9-C4	6.81	108.53	105.80
33	BA	1837	C	C6-N1-C2	6.80	123.02	120.30
33	BA	1314	C	C2-N1-C1'	6.72	126.19	118.80
33	BA	1174	U	N3-C2-O2	-6.61	117.58	122.20
33	BA	1914	C	O3'-P-O5'	-6.48	91.69	104.00
1	AA	335	C	C6-N1-C2	-6.46	117.72	120.30
33	BA	900	A	N7-C8-N9	6.46	117.03	113.80
33	BA	458	G	C4-N9-C1'	-6.44	118.12	126.50
33	BA	1254	A	C8-N9-C4	-6.43	103.23	105.80
33	BA	140	C	C6-N1-C2	-6.41	117.74	120.30
1	AA	372	C	C6-N1-C2	6.40	122.86	120.30
33	BA	674	G	C8-N9-C4	6.39	108.96	106.40
33	BA	1061	U	N3-C2-O2	-6.34	117.76	122.20
33	BA	748	G	C4-N9-C1'	-6.29	118.33	126.50
1	AA	31	G	N3-C4-C5	-6.27	125.47	128.60
33	BA	2544	G	N1-C6-O6	6.24	123.65	119.90
33	BA	955	U	C6-N1-C2	-6.24	117.26	121.00
33	BA	140	C	N3-C2-O2	-6.23	117.54	121.90
1	AA	614	C	C6-N1-C2	-6.21	117.81	120.30
33	BA	1934	C	C2-N1-C1'	-6.21	111.97	118.80
1	AA	1168	U	N1-C2-O2	6.21	127.15	122.80
33	BA	989	G	N3-C4-N9	6.17	129.70	126.00
33	BA	458	G	C8-N9-C4	6.14	108.86	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BA	1934	C	C6-N1-C2	6.11	122.74	120.30
23	AW	26	LYS	O-C-N	6.09	132.45	122.70
1	AA	328	C	C6-N1-C1'	-6.07	113.52	120.80
1	AA	328	C	N3-C2-O2	-6.06	117.66	121.90
1	AA	1097	C	C6-N1-C2	-6.05	117.88	120.30
1	AA	569	C	C6-N1-C2	-6.04	117.89	120.30
1	AA	70	U	C2-N1-C1'	6.02	124.93	117.70
33	BA	776	G	C4-N9-C1'	6.02	134.32	126.50
1	AA	1136	C	C6-N1-C1'	-6.01	113.58	120.80
33	BA	1266	G	C4-N9-C1'	-6.01	118.69	126.50
1	AA	1112	C	C6-N1-C2	-6.00	117.90	120.30
26	B2	22	LEU	CA-CB-CG	5.97	129.04	115.30
33	BA	1936	A	N1-C2-N3	5.97	132.29	129.30
33	BA	529	A	N9-C4-C5	5.96	108.19	105.80
33	BA	745	G	C8-N9-C4	-5.96	104.02	106.40
33	BA	1210	G	C8-N9-C4	-5.96	104.02	106.40
33	BA	1616	A	C8-N9-C4	-5.95	103.42	105.80
33	BA	2612	C	C5-C6-N1	-5.93	118.03	121.00
33	BA	517	C	C6-N1-C2	5.92	122.67	120.30
1	AA	1416	G	C8-N9-C4	5.89	108.76	106.40
33	BA	140	C	C5-C6-N1	5.89	123.94	121.00
23	AW	522	GLN	C-N-CA	5.87	136.38	121.70
33	BA	900	A	C8-N9-C4	-5.87	103.45	105.80
33	BA	1913	A	N9-C4-C5	-5.87	103.45	105.80
1	AA	1168	U	C6-N1-C1'	-5.87	112.99	121.20
1	AA	934	C	C6-N1-C2	-5.85	117.96	120.30
33	BA	1706	C	C6-N1-C2	5.84	122.64	120.30
33	BA	528	A	C2-N3-C4	-5.84	107.68	110.60
1	AA	1158	C	C6-N1-C2	-5.83	117.97	120.30
47	BR	33	ILE	CB-CA-C	-5.82	99.97	111.60
33	BA	1061	U	C5-C6-N1	5.80	125.60	122.70
33	BA	783	A	N1-C6-N6	5.79	122.07	118.60
33	BA	1533	C	N1-C2-O2	5.78	122.37	118.90
33	BA	989	G	C4-N9-C1'	5.76	133.99	126.50
1	AA	64	G	C8-N9-C4	5.75	108.70	106.40
33	BA	672	C	C6-N1-C2	-5.74	118.00	120.30
33	BA	28	A	N7-C8-N9	5.74	116.67	113.80
33	BA	1266	G	C8-N9-C1'	5.74	134.46	127.00
33	BA	2353	G	C2-N3-C4	5.72	114.76	111.90
33	BA	1828	G	C5-C6-O6	5.72	132.03	128.60
33	BA	2433	A	N9-C4-C5	-5.71	103.52	105.80
33	BA	1930	G	C4-N9-C1'	-5.70	119.09	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BA	1254	A	N9-C4-C5	5.70	108.08	105.80
33	BA	1983	G	N3-C4-C5	5.69	131.44	128.60
1	AA	95	C	N1-C2-O2	5.64	122.29	118.90
1	AA	1168	U	C5-C6-N1	5.64	125.52	122.70
33	BA	1305	C	C2-N1-C1'	5.63	125.00	118.80
33	BA	984	A	C2-N3-C4	-5.63	107.78	110.60
33	BA	1174	U	C6-N1-C1'	-5.62	113.33	121.20
33	BA	2627	G	C8-N9-C4	-5.62	104.15	106.40
33	BA	2433	A	C8-N9-C4	5.61	108.05	105.80
33	BA	1061	U	C6-N1-C1'	-5.61	113.35	121.20
1	AA	49	U	C6-N1-C2	5.61	124.36	121.00
33	BA	1611	C	C6-N1-C2	-5.58	118.07	120.30
33	BA	705	A	C8-N9-C4	-5.56	103.58	105.80
33	BA	748	G	C8-N9-C4	5.56	108.62	106.40
1	AA	135	C	C6-N1-C2	-5.55	118.08	120.30
1	AA	1158	C	C2-N1-C1'	5.55	124.90	118.80
1	AA	960	U	C2-N1-C1'	5.54	124.35	117.70
33	BA	922	C	C6-N1-C2	-5.54	118.08	120.30
1	AA	566	G	N3-C4-C5	-5.54	125.83	128.60
31	B7	56	LEU	CA-CB-CG	5.54	128.04	115.30
1	AA	1126	U	C5-C6-N1	5.53	125.47	122.70
33	BA	1911	U	O3'-P-O5'	-5.52	93.51	104.00
1	AA	31	G	N3-C4-N9	5.52	129.31	126.00
33	BA	791	C	C6-N1-C2	-5.51	118.09	120.30
33	BA	778	G	N1-C6-O6	5.50	123.20	119.90
33	BA	1660	G	C8-N9-C4	5.49	108.60	106.40
33	BA	776	G	N3-C4-C5	-5.49	125.86	128.60
1	AA	316	C	C6-N1-C2	-5.48	118.11	120.30
45	BP	112	LEU	CA-CB-CG	5.47	127.88	115.30
1	AA	88	U	C2-N1-C1'	5.46	124.26	117.70
1	AA	1136	C	N3-C2-O2	-5.45	118.08	121.90
33	BA	825	A	C8-N9-C4	-5.45	103.62	105.80
33	BA	184	C	C6-N1-C2	5.45	122.48	120.30
33	BA	776	G	C8-N9-C4	-5.45	104.22	106.40
1	AA	495	A	N9-C4-C5	5.44	107.98	105.80
33	BA	544	C	C6-N1-C2	-5.42	118.13	120.30
33	BA	2842	G	C8-N9-C4	5.42	108.57	106.40
33	BA	1293	C	N3-C4-C5	-5.41	119.73	121.90
33	BA	2359	C	C6-N1-C2	5.41	122.47	120.30
33	BA	802	A	C8-N9-C4	-5.41	103.64	105.80
33	BA	1254	A	N1-C6-N6	-5.40	115.36	118.60
33	BA	1533	C	C2-N1-C1'	5.40	124.74	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	85	U	N1-C2-O2	5.39	126.57	122.80
33	BA	529	A	C8-N9-C4	-5.36	103.66	105.80
1	AA	1114	C	C6-N1-C2	-5.36	118.16	120.30
1	AA	495	A	C8-N9-C4	-5.35	103.66	105.80
1	AA	1322	C	C2-N1-C1'	5.35	124.68	118.80
33	BA	1971	U	C6-N1-C2	-5.34	117.79	121.00
33	BA	571	U	C6-N1-C1'	5.34	128.68	121.20
33	BA	1378	A	P-O3'-C3'	5.33	126.10	119.70
1	AA	1168	U	N3-C2-O2	-5.32	118.48	122.20
33	BA	323	C	C2-N1-C1'	5.31	124.64	118.80
33	BA	302	C	C6-N1-C2	5.29	122.42	120.30
33	BA	1971	U	C5-C6-N1	5.28	125.34	122.70
33	BA	957	C	C6-N1-C2	-5.28	118.19	120.30
1	AA	701	U	N1-C2-O2	5.27	126.49	122.80
33	BA	474	G	C8-N9-C4	5.27	108.51	106.40
23	AW	69	SER	N-CA-C	5.27	125.23	111.00
33	BA	645	C	C5-C6-N1	5.26	123.63	121.00
33	BA	948	C	N3-C4-C5	5.25	124.00	121.90
33	BA	847	U	N1-C2-O2	5.23	126.46	122.80
33	BA	1022	G	N9-C4-C5	5.23	107.49	105.40
33	BA	32	C	C6-N1-C2	5.22	122.39	120.30
33	BA	778	G	C4-C5-N7	5.22	112.89	110.80
33	BA	2704	C	C6-N1-C2	-5.20	118.22	120.30
40	BH	129	LEU	CA-CB-CG	5.19	127.24	115.30
33	BA	995	C	P-O3'-C3'	5.19	125.92	119.70
33	BA	678	C	C6-N1-C2	5.18	122.37	120.30
1	AA	961	U	C6-N1-C2	-5.17	117.90	121.00
33	BA	20	C	C6-N1-C2	5.17	122.37	120.30
1	AA	525	C	C6-N1-C2	-5.16	118.23	120.30
40	BH	160	ASP	CB-CG-OD2	5.16	122.94	118.30
1	AA	88	U	N1-C2-O2	5.16	126.41	122.80
23	AW	26	LYS	CA-C-N	-5.15	105.86	117.20
33	BA	650	C	C6-N1-C2	-5.15	118.24	120.30
33	BA	571	U	C5-C4-O4	5.15	128.99	125.90
33	BA	745	G	N9-C4-C5	5.14	107.46	105.40
33	BA	2609	U	C6-N1-C2	-5.14	117.91	121.00
33	BA	1828	G	C4-C5-N7	-5.13	108.75	110.80
33	BA	74	A	C8-N9-C4	-5.13	103.75	105.80
33	BA	1190	G	C8-N9-C4	5.13	108.45	106.40
1	AA	95	C	N3-C2-O2	-5.13	118.31	121.90
37	BE	124	PHE	N-CA-C	-5.12	97.17	111.00
33	BA	1313	U	N1-C2-O2	5.11	126.38	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BA	1857	G	N3-C4-C5	-5.11	126.05	128.60
33	BA	811	U	C2-N1-C1'	-5.10	111.58	117.70
1	AA	85	U	C6-N1-C1'	-5.09	114.07	121.20
33	BA	124	G	C8-N9-C4	-5.09	104.36	106.40
33	BA	1313	U	N3-C2-O2	-5.09	118.64	122.20
1	AA	323	U	C6-N1-C2	-5.08	117.95	121.00
33	BA	847	U	C2-N1-C1'	5.08	123.79	117.70
33	BA	2868	A	C8-N9-C4	-5.08	103.77	105.80
1	AA	1158	C	N3-C2-O2	-5.08	118.35	121.90
33	BA	212	G	C8-N9-C4	5.07	108.43	106.40
33	BA	783	A	C4-C5-N7	5.07	113.24	110.70
33	BA	28	A	C8-N9-C4	-5.06	103.77	105.80
33	BA	421	C	C6-N1-C2	-5.06	118.28	120.30
33	BA	1995	U	C5-C6-N1	-5.06	120.17	122.70
1	AA	4	U	C2-N1-C1'	5.03	123.74	117.70
1	AA	386	C	C6-N1-C2	5.03	122.31	120.30
33	BA	592	A	C8-N9-C4	-5.03	103.79	105.80
33	BA	2819	G	C8-N9-C4	5.03	108.41	106.40
33	BA	1913	A	C8-N9-C4	5.03	107.81	105.80
1	AA	1286	U	C2-N1-C1'	5.02	123.72	117.70

There are no chirality outliers.

All (28) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	135	MET	Peptide
2	AB	20	ARG	Peptide
2	AB	218	ALA	Peptide
3	AC	153	SER	Peptide
5	AE	121	ASN	Peptide
5	AE	78	GLY	Peptide
6	AF	53	LYS	Peptide
11	AK	102	ALA	Peptide
13	AM	45	SER	Peptide
14	AN	48	GLN	Peptide
14	AN	50	LEU	Peptide
23	AW	410	LYS	Peptide
23	AW	411	GLN	Peptide
23	AW	74	VAL	Mainchain
24	B0	18	LYS	Peptide
37	BE	8	ALA	Peptide
39	BG	83	THR	Peptide

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Mol	Chain	Res	Type	Group
40	BH	106	PHE	Peptide
40	BH	118	ILE	Peptide
40	BH	129	LEU	Peptide
41	BI	30	GLN	Peptide
41	BI	83	ALA	Peptide
43	BN	43	GLU	Peptide
45	BP	28	GLY	Peptide
47	BR	116	VAL	Peptide
50	BU	6	GLY	Peptide
53	BX	39	THR	Peptide
54	BY	87	GLU	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32873	0	16542	561	1
2	AB	1704	0	1732	81	0
3	AC	1624	0	1699	67	4
4	AD	1643	0	1710	70	1
5	AE	1105	0	1148	46	0
6	AF	817	0	808	33	0
7	AG	1181	0	1240	34	0
8	AH	979	0	1034	35	0
9	AI	1022	0	1070	53	0
10	AJ	786	0	828	43	0
11	AK	877	0	887	37	0
12	AL	955	0	1019	63	0
13	AM	883	0	944	38	0
14	AN	774	0	827	41	0
15	AO	714	0	737	21	0
16	AP	649	0	666	23	0
17	AQ	648	0	691	26	0
18	AR	455	0	478	14	0
19	AS	637	0	665	17	1
20	AT	665	0	714	24	0
21	AU	425	0	449	22	0
22	AV	129	0	65	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	AW	4144	0	4127	307	0
24	B0	596	0	610	71	0
25	B1	625	0	655	36	0
26	B2	509	0	543	15	0
27	B3	449	0	491	21	0
28	B4	444	0	461	14	0
29	B5	409	0	440	6	0
30	B6	377	0	418	8	0
31	B7	504	0	574	16	0
32	B8	302	0	340	21	0
33	BA	61252	0	30808	1107	4
34	BB	2529	0	1281	45	0
35	BC	2082	0	2157	119	0
36	BD	1565	0	1616	102	0
37	BE	1552	0	1619	65	0
38	BF	1410	0	1447	62	0
39	BG	1323	0	1374	58	0
40	BH	1230	0	1282	91	0
41	BI	1032	0	1088	42	0
42	BJ	227	0	237	13	0
42	BK	227	0	237	5	0
42	BL	227	0	237	8	0
42	BM	227	0	237	14	0
43	BN	1129	0	1162	67	0
44	BO	938	0	1012	38	0
45	BP	1045	0	1117	49	0
46	BQ	1074	0	1157	46	0
47	BR	960	0	1000	41	0
48	BS	892	0	923	26	0
49	BT	917	0	965	44	0
50	BU	947	0	1022	55	0
51	BV	816	0	839	49	0
52	BW	857	0	922	24	0
53	BX	738	0	807	40	0
54	BY	779	0	834	26	0
55	BZ	753	0	780	19	1
56	AW	32	0	13	7	0
57	AW	1	0	0	0	0
All	All	146665	0	100785	3630	6

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 15.

All (3630) 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)
1:AA:497:G:OP2	23:AW:480:LYS:HE3	1.11	1.25
1:AA:497:G:OP2	23:AW:480:LYS:CE	1.83	1.25
12:AL:101:LEU:HG	23:AW:409:GLN:NE2	1.53	1.21
33:BA:974:G:C8	33:BA:989:G:C2	2.31	1.18
40:BH:25:ALA:HB3	40:BH:85:SER:OG	1.38	1.18
33:BA:1914:C:H2'	33:BA:1915:U:O4'	1.41	1.17
33:BA:2150:C:H2'	33:BA:2151:U:C5	1.82	1.14
33:BA:2149:U:O3'	33:BA:2150:C:H4'	1.36	1.13
23:AW:20:SER:OG	23:AW:26:LYS:CD	1.97	1.12
33:BA:2107:G:O6	33:BA:2183:A:C6	2.01	1.12
33:BA:2149:U:H5''	33:BA:2150:C:OP2	1.48	1.12
23:AW:146:ARG:NH1	33:BA:2657:A:OP2	1.84	1.11
23:AW:20:SER:OG	23:AW:26:LYS:HD2	1.51	1.09
12:AL:102:ASP:OD1	23:AW:407:LEU:HD11	1.54	1.08
23:AW:59:TRP:NE1	23:AW:69:SER:OG	1.87	1.06
12:AL:101:LEU:HG	23:AW:409:GLN:HE22	0.90	1.05
33:BA:974:G:N7	33:BA:989:G:C2	2.25	1.05
12:AL:123:ALA:O	23:AW:487:ARG:NH1	1.91	1.03
12:AL:30:ARG:NH1	23:AW:408:LYS:HG3	1.75	1.02
23:AW:145:ASP:OD2	56:AW:601:GNP:N2	1.92	1.02
11:AK:87:GLY:H	11:AK:113:THR:HG22	1.24	1.01
1:AA:1492:A:N1	33:BA:1913:A:C2	2.29	1.01
33:BA:974:G:C8	33:BA:989:G:N3	2.29	1.00
12:AL:101:LEU:CG	23:AW:409:GLN:HE22	1.74	0.99
33:BA:974:G:N7	33:BA:989:G:C4	2.30	0.99
12:AL:23:LEU:HG	12:AL:24:GLU:H	1.28	0.99
33:BA:2150:C:O2'	33:BA:2151:U:O5'	1.78	0.98
49:BT:50:ARG:HB3	49:BT:57:ALA:H	1.26	0.97
33:BA:2150:C:H2'	33:BA:2151:U:C6	1.99	0.97
49:BT:50:ARG:HD3	49:BT:56:SER:HB3	1.43	0.97
23:AW:411:GLN:H	23:AW:414:LYS:HB3	1.29	0.97
23:AW:61:GLU:HG3	23:AW:64:LYS:HE3	1.45	0.96
33:BA:974:G:N7	33:BA:989:G:N3	2.14	0.94
33:BA:1914:C:O2'	33:BA:1915:U:H5'	1.67	0.94
23:AW:70:ILE:HG23	23:AW:95:PHE:HZ	1.32	0.93
33:BA:2149:U:C5'	33:BA:2150:C:OP2	2.17	0.93
25:B1:31:ASN:OD1	25:B1:33:HIS:NE2	2.02	0.93
33:BA:1914:C:C2'	33:BA:1915:U:H5'	1.97	0.93
1:AA:497:G:P	23:AW:480:LYS:HE2	2.09	0.92
33:BA:995:C:O2'	33:BA:996:A:OP2	1.87	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:412:LEU:HB2	23:AW:459:VAL:HG11	1.52	0.92
33:BA:2149:U:C3'	33:BA:2150:C:H4'	1.99	0.92
33:BA:2597:G:H5'	35:BC:240:GLY:HA3	1.50	0.91
23:AW:23:ASP:OD2	23:AW:68:ILE:HD13	1.71	0.91
33:BA:161:A:H3'	33:BA:162:U:H5''	1.53	0.91
33:BA:2107:G:O6	33:BA:2183:A:C5	2.25	0.90
40:BH:11:ILE:HG21	40:BH:66:GLY:HA3	1.54	0.89
33:BA:45:G:H5''	33:BA:46:G:H5'	1.53	0.89
1:AA:690:G:O6	11:AK:52:ARG:NH2	2.05	0.89
12:AL:78:VAL:HG21	23:AW:407:LEU:HB2	1.51	0.89
23:AW:70:ILE:O	23:AW:95:PHE:HE2	1.56	0.89
42:BJ:14:MET:HB2	42:BM:12:ALA:HA	1.53	0.89
43:BN:43:GLU:O	43:BN:45:THR:N	2.05	0.88
8:AH:52:GLY:HA3	8:AH:56:PRO:HA	1.53	0.88
24:B0:19:ARG:HA	24:B0:34:SER:HA	1.56	0.88
49:BT:63:ILE:HA	49:BT:68:GLY:HA2	1.56	0.88
33:BA:1085:A:H61	40:BH:34:THR:HG22	1.40	0.87
33:BA:27:G:HO2'	33:BA:28:A:H8	0.93	0.87
1:AA:877:G:H21	8:AH:1:SER:HB2	1.37	0.87
39:BG:84:LYS:HG3	39:BG:131:VAL:HG23	1.54	0.87
43:BN:19:ASP:O	43:BN:23:LYS:NZ	2.07	0.86
23:AW:416:LEU:HB3	23:AW:427:VAL:HG11	1.55	0.86
24:B0:30:VAL:HG12	33:BA:2353:G:H1'	1.56	0.86
33:BA:1568:G:H4'	35:BC:58:LYS:HB3	1.54	0.86
45:BP:132:ARG:HG3	45:BP:142:ILE:HG13	1.57	0.86
1:AA:1492:A:H2'	1:AA:1493:A:H5''	1.57	0.85
33:BA:1073:A:H3'	33:BA:1074:G:H5''	1.56	0.85
23:AW:439:GLY:HA2	23:AW:440:ALA:HB2	1.56	0.85
33:BA:1060:U:H4'	33:BA:1061:U:H5'	1.58	0.85
1:AA:498:A:P	23:AW:480:LYS:NZ	2.50	0.85
1:AA:497:G:P	23:AW:480:LYS:CE	2.64	0.84
43:BN:3:THR:HG21	50:BU:60:TRP:HE1	1.42	0.84
33:BA:1715:G:N2	33:BA:1744:A:OP2	2.09	0.84
33:BA:1914:C:C2'	33:BA:1915:U:C5'	2.54	0.84
46:BQ:34:LYS:HE3	46:BQ:131:VAL:HG11	1.60	0.84
10:AJ:50:THR:HG22	10:AJ:64:GLN:HG2	1.60	0.83
33:BA:503:A:H5''	33:BA:504:A:H3'	1.60	0.83
40:BH:59:LEU:HD23	40:BH:62:ARG:HD2	1.60	0.83
40:BH:25:ALA:CB	40:BH:85:SER:OG	2.26	0.83
33:BA:71:A:O2'	33:BA:72:U:OP2	1.95	0.83
33:BA:1914:C:C5	33:BA:1915:U:C5	2.67	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BE:51:GLU:OE2	37:BE:88:ARG:NH1	2.11	0.83
1:AA:73:C:H42	1:AA:97:G:H1	1.27	0.82
23:AW:50:GLY:HA3	33:BA:2655:G:C8	2.14	0.82
36:BD:16:THR:OG1	36:BD:18:ASP:OD1	1.97	0.82
41:BI:3:LYS:HD3	41:BI:4:VAL:HG23	1.62	0.82
13:AM:12:LYS:HB2	13:AM:17:ALA:HB2	1.60	0.82
23:AW:101:ARG:HG2	23:AW:391:PRO:HD2	1.62	0.82
33:BA:1914:C:H2'	33:BA:1915:U:C5'	2.09	0.82
33:BA:2720:U:OP1	49:BT:52:ARG:NH2	2.11	0.82
13:AM:5:GLY:HA3	13:AM:65:GLU:HG3	1.61	0.81
51:BV:60:LYS:H	51:BV:100:GLY:HA3	1.46	0.81
33:BA:1566:A:H5'	35:BC:213:ARG:NH1	1.95	0.81
48:BS:67:ASN:O	48:BS:69:ASP:N	2.14	0.81
2:AB:135:MET:HG3	2:AB:138:ARG:HE	1.44	0.81
33:BA:1914:C:H2'	33:BA:1915:U:C4'	2.10	0.81
23:AW:20:SER:OG	23:AW:26:LYS:NZ	2.13	0.80
23:AW:70:ILE:HG23	23:AW:95:PHE:CZ	2.16	0.80
24:B0:54:ARG:NH2	33:BA:2384:U:OP2	2.15	0.80
33:BA:276:U:O2'	33:BA:278:A:N7	2.15	0.80
23:AW:70:ILE:HG22	23:AW:71:THR:N	1.95	0.80
40:BH:97:LYS:HD2	40:BH:130:PRO:HB3	1.63	0.80
33:BA:895:U:O2'	33:BA:896:A:P	2.38	0.80
23:AW:222:ASP:OD2	39:BG:94:ARG:HD2	1.81	0.80
10:AJ:52:LEU:HD23	10:AJ:62:ARG:HG3	1.64	0.79
23:AW:64:LYS:HE2	23:AW:71:THR:H	1.47	0.79
1:AA:41:G:H2'	1:AA:42:G:H8	1.48	0.79
23:AW:20:SER:HG	23:AW:26:LYS:HD2	1.43	0.79
53:BX:29:THR:HA	53:BX:86:THR:HA	1.65	0.79
1:AA:82:G:O6	1:AA:87:C:N4	2.16	0.79
1:AA:978:A:OP2	1:AA:1362:A:N6	2.17	0.78
2:AB:187:ASP:HB2	2:AB:203:ASP:HB3	1.64	0.78
33:BA:2050:C:H4'	36:BD:143:PRO:HG2	1.65	0.78
2:AB:103:TRP:HE1	2:AB:150:ILE:HD11	1.48	0.78
33:BA:242:G:N2	33:BA:255:A:OP2	2.15	0.78
50:BU:91:ARG:HH21	50:BU:93:ILE:HG12	1.48	0.78
23:AW:20:SER:OG	23:AW:26:LYS:CE	2.30	0.78
1:AA:1281:C:H5''	1:AA:1282:C:H5	1.47	0.78
33:BA:812:C:H4'	50:BU:12:ARG:HH12	1.49	0.78
36:BD:122:VAL:HA	36:BD:127:PHE:H	1.47	0.78
9:AI:50:PRO:HD3	9:AI:79:ARG:HG2	1.65	0.77
23:AW:238:SER:OG	23:AW:239:ASN:N	2.12	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:5:LYS:HG3	27:B3:36:GLU:HG2	1.65	0.77
1:AA:1366:C:O2'	10:AJ:62:ARG:NH2	2.18	0.77
33:BA:674:G:H5''	37:BE:71:GLY:H	1.49	0.77
7:AG:14:ASP:HB3	7:AG:19:SER:H	1.50	0.77
12:AL:30:ARG:HH11	23:AW:408:LYS:HG3	1.48	0.77
1:AA:498:A:P	23:AW:480:LYS:HZ1	2.08	0.77
23:AW:26:LYS:CE	23:AW:89:THR:O	2.32	0.77
36:BD:106:LYS:HB3	36:BD:206:ALA:HB3	1.65	0.77
5:AE:105:ILE:HG13	5:AE:123:LEU:HA	1.67	0.77
33:BA:1277:G:H5'	47:BR:20:MET:HE2	1.66	0.77
8:AH:1:SER:OG	8:AH:2:MET:N	2.18	0.77
38:BF:134:GLN:HG2	38:BF:135:ILE:H	1.50	0.77
1:AA:955:U:H3	1:AA:1225:A:H61	1.33	0.77
2:AB:218:ALA:HB1	2:AB:221:ARG:HH21	1.48	0.77
24:B0:45:HIS:HB2	24:B0:50:VAL:HG13	1.67	0.77
33:BA:2150:C:C2'	33:BA:2151:U:C5	2.67	0.77
12:AL:30:ARG:HH12	23:AW:408:LYS:CE	1.98	0.76
33:BA:1998:A:OP2	36:BD:141:ARG:NH2	2.19	0.76
33:BA:2303:G:N2	33:BA:2313:C:O2	2.17	0.76
33:BA:1565:C:O2'	33:BA:1566:A:H2'	1.85	0.76
4:AD:109:THR:HG23	4:AD:112:GLU:H	1.51	0.76
33:BA:2107:G:C6	33:BA:2183:A:C6	2.73	0.76
37:BE:5:LEU:HD12	37:BE:10:SER:HB3	1.67	0.76
3:AC:13:ILE:HD11	3:AC:177:LEU:HB3	1.65	0.76
23:AW:62:MET:HG2	23:AW:454:LYS:HG2	1.65	0.76
23:AW:355:HIS:HA	23:AW:356:VAL:HG23	1.68	0.76
24:B0:9:THR:OG1	24:B0:10:ARG:N	2.17	0.76
53:BX:32:LEU:H	53:BX:83:ALA:HB3	1.50	0.76
39:BG:164:ALA:H	39:BG:166:GLU:HG3	1.49	0.76
27:B3:2:LYS:HB3	27:B3:39:ASP:HB2	1.67	0.76
20:AT:4:LYS:HD3	20:AT:6:ALA:H	1.52	0.75
23:AW:26:LYS:NZ	23:AW:89:THR:O	2.18	0.75
23:AW:399:ARG:HH12	23:AW:448:VAL:HG11	1.52	0.75
33:BA:1056:G:O5'	33:BA:1056:G:H8	1.69	0.75
33:BA:2425:A:H4'	33:BA:2426:A:H5''	1.69	0.75
16:AP:48:GLU:HG3	16:AP:49:GLY:H	1.51	0.75
15:AO:63:ARG:HG2	15:AO:87:ARG:HH12	1.50	0.75
40:BH:2:ALA:HB3	40:BH:6:GLN:HB2	1.67	0.75
23:AW:70:ILE:O	23:AW:95:PHE:CE2	2.40	0.75
26:B2:57:LEU:HA	26:B2:60:LYS:HB3	1.68	0.75
14:AN:21:ALA:H	14:AN:24:ALA:HB3	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:522:GLN:HB2	23:AW:523:PHE:HB2	1.68	0.75
1:AA:619:U:H3	4:AD:130:ASN:HB3	1.51	0.74
33:BA:2273:A:H2'	33:BA:2274:A:C8	2.22	0.74
23:AW:59:TRP:CE2	23:AW:69:SER:OG	2.41	0.74
33:BA:558:U:H5''	43:BN:111:LYS:HE2	1.69	0.74
33:BA:962:G:H21	33:BA:2250:G:H1	1.33	0.74
33:BA:1248:G:OP2	37:BE:44:ARG:NH1	2.18	0.74
49:BT:50:ARG:HB3	49:BT:57:ALA:N	2.00	0.74
43:BN:26:GLY:HA2	43:BN:29:ALA:HB3	1.68	0.74
1:AA:498:A:OP1	23:AW:480:LYS:NZ	2.20	0.74
35:BC:67:LYS:HA	35:BC:150:GLY:HA2	1.69	0.74
6:AF:47:LEU:HD12	6:AF:55:HIS:HA	1.69	0.74
49:BT:96:LEU:HB3	49:BT:99:LEU:HD23	1.68	0.74
52:BW:18:ARG:HG3	52:BW:76:VAL:HG13	1.68	0.74
39:BG:41:GLU:OE2	39:BG:54:ARG:NH2	2.20	0.74
1:AA:1452:C:H4'	1:AA:1453:G:C2	2.23	0.74
35:BC:144:GLU:HA	35:BC:151:GLY:HA2	1.68	0.74
42:BM:2:ILE:HD13	42:BM:3:THR:H	1.51	0.74
23:AW:493:LEU:HD23	23:AW:503:TYR:HA	1.70	0.73
33:BA:2491:U:H5'	33:BA:2570:G:H5''	1.70	0.73
52:BW:69:LEU:HG	52:BW:107:VAL:HG22	1.70	0.73
24:B0:39:GLN:HG3	24:B0:42:THR:HB	1.70	0.73
2:AB:114:LYS:HA	2:AB:117:GLU:HG2	1.69	0.73
8:AH:86:LYS:HG3	8:AH:90:GLU:HB3	1.71	0.73
33:BA:704:G:H2'	33:BA:726:G:H22	1.53	0.73
33:BA:2532:G:N2	33:BA:2663:G:O2'	2.21	0.73
33:BA:1509:A:O2'	33:BA:1510:G:O5'	2.04	0.73
33:BA:1057:A:N6	33:BA:1087:G:OP2	2.22	0.73
33:BA:1064:C:N4	33:BA:1070:A:OP2	2.20	0.73
48:BS:106:LEU:HA	48:BS:109:ALA:HB3	1.69	0.73
33:BA:1481:U:H2'	33:BA:1482:G:H4'	1.71	0.72
23:AW:20:SER:OG	23:AW:26:LYS:CG	2.36	0.72
31:B7:24:LYS:HD2	45:BP:64:PHE:HB3	1.71	0.72
43:BN:31:GLU:HA	43:BN:34:ARG:HG2	1.69	0.72
45:BP:74:THR:HG22	45:BP:107:PHE:HB2	1.71	0.72
33:BA:2150:C:C2	33:BA:2151:U:C4	2.78	0.72
1:AA:677:U:H3	1:AA:713:G:H22	1.37	0.72
23:AW:260:LEU:HD21	33:BA:2655:G:H5'	1.72	0.72
23:AW:300:VAL:H	23:AW:318:MET:HG3	1.54	0.72
1:AA:429:U:H3'	4:AD:8:LEU:HD23	1.70	0.72
33:BA:2150:C:C2'	33:BA:2151:U:C6	2.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:40:ILE:HG21	2:AB:201:GLY:H	1.52	0.72
1:AA:651:C:N4	1:AA:753:A:OP2	2.18	0.72
35:BC:16:VAL:HB	35:BC:203:VAL:HG23	1.72	0.72
7:AG:110:ARG:NH1	7:AG:122:GLU:OE2	2.22	0.72
23:AW:76:GLN:HE21	23:AW:85:ASN:HD21	1.37	0.72
23:AW:312:ARG:O	23:AW:314:ARG:N	2.22	0.72
33:BA:1165:A:H2'	33:BA:1166:G:H8	1.55	0.72
33:BA:1693:U:O2'	35:BC:13:ARG:NH2	2.23	0.72
35:BC:124:LYS:HB3	35:BC:127:ASN:HD22	1.54	0.72
8:AH:103:VAL:HG12	8:AH:124:ILE:HG22	1.70	0.71
38:BF:35:LEU:HB3	38:BF:153:ILE:HG22	1.72	0.71
1:AA:205:A:OP1	1:AA:205:A:H4'	1.90	0.71
12:AL:30:ARG:HH12	23:AW:408:LYS:HE2	1.54	0.71
33:BA:27:G:O2'	33:BA:28:A:H8	1.70	0.71
45:BP:108:ALA:HB3	45:BP:125:LEU:HD22	1.72	0.71
23:AW:92:HIS:HB3	23:AW:95:PHE:HB3	1.71	0.71
2:AB:99:MET:HA	2:AB:106:VAL:HG21	1.72	0.71
33:BA:974:G:C8	33:BA:989:G:N2	2.59	0.71
33:BA:1056:G:H4'	40:BH:34:THR:HG21	1.73	0.71
37:BE:70:SER:O	37:BE:70:SER:OG	2.07	0.71
5:AE:79:THR:OG1	5:AE:80:LEU:N	2.23	0.71
9:AI:56:MET:SD	9:AI:57:VAL:N	2.57	0.71
23:AW:60:MET:SD	23:AW:61:GLU:N	2.64	0.71
24:B0:31:LEU:HD22	33:BA:2354:C:H4'	1.71	0.71
33:BA:1996:C:OP1	44:BO:31:ARG:NE	2.23	0.71
42:BM:3:THR:OG1	42:BM:4:LYS:N	2.22	0.71
33:BA:2150:C:C2	33:BA:2151:U:O4	2.43	0.71
34:BB:49:C:OP1	48:BS:102:ARG:HG2	1.91	0.71
1:AA:687:A:N6	1:AA:703:G:O2'	2.23	0.71
34:BB:15:A:H1'	34:BB:109:A:C8	2.26	0.71
1:AA:451:A:H4'	1:AA:452:A:O5'	1.90	0.71
24:B0:17:ALA:HB1	24:B0:36:ILE:HA	1.73	0.71
33:BA:1779:U:H5	33:BA:1784:A:N7	1.89	0.71
33:BA:2757:A:N1	39:BG:66:THR:HG21	2.05	0.71
39:BG:96:ALA:HB3	39:BG:103:ASN:HB3	1.72	0.71
1:AA:974:A:H4'	1:AA:975:A:H5'	1.72	0.70
1:AA:1241:G:H2'	1:AA:1242:G:H8	1.56	0.70
33:BA:1097:U:H1'	41:BI:8:VAL:HG12	1.72	0.70
33:BA:2047:C:O2'	33:BA:2823:A:N1	2.23	0.70
1:AA:511:C:O2	1:AA:540:G:N2	2.22	0.70
4:AD:117:VAL:HG13	4:AD:122:ILE:HD11	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:81:A:N7	1:AA:83:C:N4	2.38	0.70
33:BA:1000:A:H2'	33:BA:1001:A:C8	2.26	0.70
17:AQ:11:VAL:HB	17:AQ:55:GLY:H	1.57	0.70
33:BA:1812:U:H2'	33:BA:1813:G:C8	2.26	0.70
33:BA:2149:U:H2'	33:BA:2150:C:O2'	1.91	0.70
39:BG:61:TRP:O	39:BG:64:ALA:N	2.23	0.70
23:AW:500:ASN:HB2	23:AW:501:LEU:HG	1.74	0.70
1:AA:41:G:H2'	1:AA:42:G:C8	2.27	0.70
6:AF:3:HIS:H	6:AF:92:THR:HG23	1.57	0.70
33:BA:74:A:H4'	33:BA:75:G:O5'	1.92	0.70
1:AA:710:G:OP1	6:AF:53:LYS:NZ	2.22	0.69
4:AD:55:ARG:HA	4:AD:55:ARG:HH11	1.55	0.69
24:B0:18:LYS:HG2	33:BA:2269:G:O2'	1.92	0.69
33:BA:2845:U:O3'	49:BT:52:ARG:NH1	2.25	0.69
1:AA:1105:A:H2'	1:AA:1106:G:H8	1.55	0.69
14:AN:44:VAL:HG23	14:AN:45:LEU:H	1.57	0.69
12:AL:78:VAL:HG21	23:AW:407:LEU:CB	2.22	0.69
33:BA:2060:A:H3'	37:BE:63:LYS:HZ3	1.56	0.69
38:BF:128:SER:HA	38:BF:154:THR:HA	1.72	0.69
23:AW:138:LEU:HD11	23:AW:272:LEU:HD23	1.73	0.69
23:AW:399:ARG:HH22	23:AW:448:VAL:HG21	1.57	0.69
24:B0:39:GLN:O	33:BA:2331:G:O2'	2.07	0.69
1:AA:522:C:OP2	12:AL:65:TYR:OH	2.10	0.69
1:AA:1147:C:O2	9:AI:17:ARG:NH1	2.25	0.69
33:BA:1563:U:H2'	33:BA:1564:C:C6	2.27	0.69
37:BE:5:LEU:HB3	37:BE:8:ALA:HB3	1.74	0.69
37:BE:131:THR:HG22	37:BE:160:ALA:HA	1.75	0.69
38:BF:68:LYS:HA	38:BF:83:PRO:HA	1.74	0.69
1:AA:374:A:H5''	1:AA:452:A:C2	2.27	0.69
20:AT:38:ILE:HD11	20:AT:82:ILE:HG22	1.72	0.69
23:AW:59:TRP:CZ2	23:AW:69:SER:CB	2.75	0.69
32:B8:9:LYS:HG3	32:B8:16:ILE:HG13	1.74	0.69
33:BA:41:C:H2'	33:BA:42:A:O4'	1.93	0.69
33:BA:783:A:H8	33:BA:784:G:H4'	1.56	0.69
51:BV:49:ILE:HG13	51:BV:52:PRO:HA	1.73	0.69
1:AA:1441:A:H62	1:AA:1461:G:H21	1.39	0.69
5:AE:80:LEU:HD23	5:AE:122:VAL:HG11	1.74	0.69
12:AL:78:VAL:CG2	23:AW:407:LEU:HD12	2.23	0.69
12:AL:101:LEU:CG	23:AW:409:GLN:NE2	2.44	0.69
39:BG:34:ARG:HH11	39:BG:34:ARG:H	1.40	0.69
43:BN:6:ALA:HB3	43:BN:45:THR:HG21	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2304:G:H22	33:BA:2312:U:H3	1.39	0.69
33:BA:900:A:O2'	33:BA:901:C:OP1	2.10	0.69
54:BY:6:ARG:NH2	54:BY:25:LYS:O	2.26	0.69
33:BA:332:A:O2'	33:BA:334:C:OP2	2.11	0.68
33:BA:899:A:H2'	33:BA:900:A:H8	1.58	0.68
33:BA:947:A:HO2'	33:BA:984:A:H2	1.41	0.68
34:BB:5:U:H2'	34:BB:6:G:C8	2.28	0.68
1:AA:599:C:H5''	8:AH:87:ARG:HA	1.73	0.68
14:AN:8:ARG:HB3	14:AN:12:ARG:HH12	1.58	0.68
23:AW:26:LYS:HE2	23:AW:89:THR:O	1.92	0.68
39:BG:59:ASP:HB3	39:BG:63:GLN:HG3	1.74	0.68
33:BA:458:G:O2'	33:BA:459:U:OP2	2.10	0.68
33:BA:2598:A:H5''	35:BC:233:GLY:HA3	1.74	0.68
24:B0:28:GLU:HB3	24:B0:31:LEU:HD21	1.74	0.68
24:B0:39:GLN:C	24:B0:41:GLY:H	1.96	0.68
27:B3:8:GLN:HG3	27:B3:28:LEU:HB3	1.75	0.68
51:BV:24:LYS:HA	51:BV:94:THR:HG23	1.75	0.68
1:AA:380:G:N2	1:AA:383:A:OP2	2.27	0.68
1:AA:972:C:H1'	10:AJ:57:VAL:HG23	1.76	0.68
23:AW:47:LYS:HE2	23:AW:66:ARG:O	1.93	0.68
24:B0:23:LYS:HG2	33:BA:855:G:H21	1.57	0.68
33:BA:2104:C:H2'	33:BA:2105:U:O4'	1.94	0.68
4:AD:200:VAL:HG12	5:AE:102:THR:HG23	1.76	0.68
9:AI:6:TYR:HE2	9:AI:17:ARG:HB2	1.59	0.68
23:AW:399:ARG:NE	23:AW:445:GLN:OE1	2.20	0.68
33:BA:1266:G:O2'	33:BA:1267:U:OP2	2.11	0.68
43:BN:111:LYS:HD2	43:BN:112:GLY:H	1.58	0.68
23:AW:472:ARG:HG3	23:AW:504:ILE:H	1.59	0.68
33:BA:2726:A:O2'	33:BA:2727:A:O5'	2.10	0.68
33:BA:2147:A:H3'	33:BA:2148:G:H5'	1.76	0.68
1:AA:965:U:H5''	1:AA:966:G:OP1	1.95	0.67
34:BB:34:A:N6	34:BB:44:G:O2'	2.26	0.67
5:AE:11:GLN:HB3	5:AE:39:GLY:O	1.94	0.67
23:AW:18:ILE:HG12	23:AW:110:LEU:HD23	1.74	0.67
33:BA:877:A:H1'	33:BA:900:A:H61	1.59	0.67
52:BW:20:VAL:HG11	52:BW:44:ALA:HA	1.76	0.67
1:AA:1513:A:H2'	1:AA:1514:G:C8	2.29	0.67
12:AL:122:LYS:HE2	23:AW:491:SER:OG	1.94	0.67
23:AW:474:VAL:HG22	23:AW:501:LEU:HD12	1.75	0.67
39:BG:97:VAL:HG22	39:BG:102:ILE:HG12	1.75	0.67
5:AE:12:GLU:OE1	5:AE:67:ARG:NH1	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:BT:15:ASP:N	49:BT:15:ASP:OD1	2.28	0.67
4:AD:124:VAL:O	4:AD:126:GLY:N	2.26	0.67
33:BA:140:C:H5'	33:BA:141:G:H21	1.58	0.67
34:BB:56:G:H5'	38:BF:23:SER:HB2	1.74	0.67
35:BC:255:LYS:O	35:BC:257:ARG:N	2.28	0.67
39:BG:88:LEU:HD22	39:BG:161:VAL:HG22	1.77	0.67
50:BU:6:GLY:HA2	50:BU:9:ALA:H	1.60	0.67
50:BU:88:GLU:HG2	51:BV:49:ILE:HG12	1.75	0.67
10:AJ:80:THR:HG22	10:AJ:83:THR:H	1.59	0.67
23:AW:130:THR:HG21	23:AW:137:ILE:HD11	1.77	0.67
1:AA:94:G:H5''	1:AA:95:C:OP1	1.95	0.67
23:AW:307:MET:HG3	23:AW:308:ASP:HA	1.77	0.67
33:BA:2150:C:H2'	33:BA:2151:U:H5	1.56	0.67
1:AA:83:C:N3	1:AA:86:G:N2	2.42	0.67
1:AA:1088:G:H21	1:AA:1167:A:H62	1.43	0.67
1:AA:1512:U:H2'	1:AA:1513:A:H8	1.59	0.67
11:AK:124:LYS:HG2	21:AU:34:ARG:HG2	1.77	0.67
33:BA:1791:A:O2'	35:BC:205:GLY:HA2	1.95	0.67
1:AA:928:G:O2'	1:AA:1533:C:OP1	2.11	0.67
23:AW:108:CYS:SG	23:AW:109:CYS:N	2.68	0.67
1:AA:1492:A:H2'	1:AA:1493:A:C5'	2.24	0.66
33:BA:1654:A:H2'	33:BA:1655:A:H8	1.58	0.66
40:BH:88:HIS:HB2	40:BH:89:PRO:HD3	1.76	0.66
1:AA:812:G:O2'	1:AA:813:U:OP2	2.09	0.66
23:AW:472:ARG:HD2	23:AW:503:TYR:HB3	1.76	0.66
31:B7:53:ASP:HA	31:B7:56:LEU:HD23	1.77	0.66
33:BA:878:A:N6	33:BA:879:G:N3	2.43	0.66
24:B0:59:PHE:CZ	33:BA:2365:G:H4'	2.30	0.66
39:BG:95:ALA:HB2	39:BG:104:LEU:HD23	1.77	0.66
1:AA:1033:G:H2'	1:AA:1034:G:H5''	1.76	0.66
23:AW:210:LEU:O	23:AW:228:ARG:NH1	2.28	0.66
23:AW:403:LEU:HD12	23:AW:407:LEU:HD23	1.76	0.66
37:BE:46:GLN:O	37:BE:86:ALA:HB1	1.95	0.66
40:BH:31:ARG:HH12	40:BH:109:LYS:HE3	1.60	0.66
33:BA:1009:A:N3	33:BA:1153:C:O2'	2.25	0.66
23:AW:59:TRP:CZ2	23:AW:69:SER:HB3	2.30	0.66
23:AW:522:GLN:CB	23:AW:523:PHE:HB2	2.26	0.66
33:BA:1858:A:N6	33:BA:1884:G:O2'	2.29	0.66
11:AK:78:ILE:HB	11:AK:104:PHE:HE1	1.60	0.66
15:AO:24:THR:HG23	15:AO:65:LEU:HD12	1.78	0.66
19:AS:51:HIS:CD2	19:AS:53:GLY:H	2.13	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BB:5:U:OP1	34:BB:61:G:O2'	2.11	0.66
40:BH:26:VAL:HG13	40:BH:82:ILE:HD12	1.78	0.66
36:BD:73:VAL:HG23	36:BD:74:GLU:H	1.60	0.66
5:AE:148:SER:HB2	5:AE:151:MET:HB2	1.79	0.65
33:BA:1169:A:H61	33:BA:1180:U:H3	1.43	0.65
33:BA:1594:U:H2'	33:BA:1595:C:C6	2.31	0.65
46:BQ:110:GLU:OE2	46:BQ:114:ARG:NH2	2.30	0.65
1:AA:951:G:OP2	13:AM:100:ARG:NH2	2.29	0.65
23:AW:59:TRP:HZ2	23:AW:69:SER:HB3	1.61	0.65
33:BA:1818:U:OP2	35:BC:155:ARG:NH1	2.29	0.65
33:BA:1993:U:H4'	36:BD:133:THR:HG21	1.78	0.65
2:AB:89:PHE:HB3	2:AB:149:GLY:HA2	1.78	0.65
6:AF:36:ILE:HG22	6:AF:64:VAL:HG22	1.78	0.65
43:BN:111:LYS:CD	43:BN:112:GLY:H	2.08	0.65
50:BU:48:ASP:HA	50:BU:51:GLN:HB2	1.77	0.65
50:BU:63:ARG:NH1	50:BU:96:ASP:HA	2.11	0.65
33:BA:1818:U:H5''	35:BC:156:SER:HB2	1.79	0.65
8:AH:82:LEU:HD12	12:AL:3:VAL:HG11	1.77	0.65
11:AK:23:HIS:HB3	11:AK:30:ILE:HG23	1.78	0.65
23:AW:401:ILE:HD11	23:AW:438:VAL:HG21	1.78	0.65
33:BA:784:G:O2'	33:BA:785:G:H5''	1.97	0.65
1:AA:1280:A:OP1	10:AJ:9:ARG:NH1	2.30	0.65
1:AA:1406:U:O2	1:AA:1517:G:N2	2.29	0.65
17:AQ:47:ASP:OD2	17:AQ:47:ASP:N	2.30	0.65
50:BU:42:GLY:HA3	51:BV:75:VAL:HG21	1.77	0.65
14:AN:87:ALA:HB2	14:AN:92:ILE:HD12	1.78	0.65
23:AW:403:LEU:HG	23:AW:412:LEU:HG	1.77	0.65
35:BC:242:HIS:O	35:BC:244:VAL:HG13	1.97	0.65
54:BY:80:ASP:HB3	54:BY:95:PHE:HD2	1.62	0.65
23:AW:19:ILE:HB	23:AW:126:LEU:HD13	1.79	0.65
23:AW:445:GLN:O	23:AW:463:TYR:OH	2.11	0.65
35:BC:32:LEU:O	35:BC:63:ILE:HG12	1.97	0.65
12:AL:62:VAL:HG21	12:AL:94:TYR:HE2	1.60	0.64
23:AW:23:ASP:OD2	23:AW:68:ILE:CD1	2.44	0.64
24:B0:9:THR:HG23	24:B0:10:ARG:HH11	1.63	0.64
33:BA:1923:U:H2'	33:BA:1924:C:C6	2.32	0.64
1:AA:211:G:C2	1:AA:212:G:H1'	2.33	0.64
1:AA:1492:A:H5''	12:AL:43:LYS:HG3	1.79	0.64
8:AH:42:GLU:HG3	8:AH:100:ILE:HD13	1.77	0.64
12:AL:78:VAL:HG21	23:AW:407:LEU:HD12	1.79	0.64
33:BA:2557:G:H2'	33:BA:2558:C:C6	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BD:118:PHE:O	36:BD:120:GLY:N	2.29	0.64
49:BT:105:LYS:HA	49:BT:108:ARG:HD3	1.79	0.64
12:AL:62:VAL:HG21	12:AL:94:TYR:CE2	2.33	0.64
23:AW:158:VAL:HG13	23:AW:162:LEU:HD12	1.79	0.64
50:BU:91:ARG:NH1	51:BV:10:LYS:HB3	2.13	0.64
55:BZ:72:VAL:HG12	55:BZ:93:ARG:HA	1.78	0.64
1:AA:352:C:H4'	1:AA:354:G:OP1	1.98	0.64
1:AA:1054:C:H1'	1:AA:1196:A:C5	2.33	0.64
1:AA:1126:U:H1'	1:AA:1281:C:H1'	1.79	0.64
13:AM:44:ILE:HA	13:AM:47:LEU:HB2	1.79	0.64
33:BA:1889:A:N3	33:BA:2086:U:O2'	2.26	0.64
36:BD:118:PHE:HD2	36:BD:119:ALA:H	1.44	0.64
40:BH:52:MET:HG3	40:BH:95:LEU:HD11	1.80	0.64
43:BN:17:VAL:HG12	43:BN:139:VAL:HG23	1.80	0.64
23:AW:149:ARG:NH1	23:AW:157:GLU:OE1	2.31	0.64
25:B1:9:LYS:NZ	33:BA:396:G:OP2	2.30	0.64
33:BA:2149:U:H3'	33:BA:2150:C:C4'	2.28	0.64
35:BC:116:GLN:N	35:BC:127:ASN:OD1	2.25	0.64
41:BI:19:PRO:HB2	41:BI:22:PRO:HD2	1.78	0.64
53:BX:39:THR:HB	53:BX:41:ALA:H	1.63	0.64
1:AA:3:A:N1	1:AA:628:G:O2'	2.31	0.64
1:AA:920:U:H2'	1:AA:921:U:C6	2.32	0.64
6:AF:38:ARG:HG3	6:AF:39:LEU:N	2.12	0.64
33:BA:2052:A:H4'	36:BD:148:GLN:O	1.97	0.64
1:AA:204:G:H3'	1:AA:205:A:H5''	1.78	0.64
4:AD:160:LEU:H	4:AD:160:LEU:HD13	1.62	0.64
33:BA:528:A:N1	33:BA:2042:A:H2'	2.12	0.64
33:BA:2804:U:H2'	33:BA:2805:C:H6	1.63	0.64
33:BA:1007:C:OP1	43:BN:39:LYS:NZ	2.30	0.64
33:BA:1392:A:N7	53:BX:19:LYS:HD2	2.13	0.64
55:BZ:76:ASP:H	55:BZ:90:ASP:HB2	1.63	0.64
4:AD:10:LEU:HD22	4:AD:62:ARG:HG3	1.80	0.64
9:AI:50:PRO:HB3	9:AI:83:THR:HG23	1.79	0.64
52:BW:3:THR:OG1	52:BW:3:THR:O	2.12	0.64
2:AB:103:TRP:NE1	2:AB:150:ILE:HD11	2.13	0.63
9:AI:51:LEU:HA	9:AI:54:VAL:HG23	1.79	0.63
53:BX:5:GLU:HA	53:BX:8:LEU:HD23	1.78	0.63
1:AA:477:C:H2'	1:AA:478:A:C8	2.33	0.63
2:AB:69:VAL:HB	2:AB:162:VAL:HG12	1.79	0.63
14:AN:40:ARG:HH12	14:AN:44:VAL:HG21	1.62	0.63
23:AW:56:LYS:HB2	23:AW:57:SER:HA	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:135:U:H3	33:BA:144:A:H61	1.43	0.63
37:BE:148:ILE:HA	37:BE:187:VAL:HB	1.78	0.63
5:AE:46:GLY:HA3	5:AE:70:MET:HG2	1.79	0.63
18:AR:33:THR:HG23	18:AR:35:SER:H	1.63	0.63
33:BA:1183:U:H2'	33:BA:1184:U:C6	2.33	0.63
33:BA:1914:C:C2'	33:BA:1915:U:O4'	2.34	0.63
1:AA:212:G:H2'	1:AA:213:G:H8	1.63	0.63
1:AA:345:C:O2'	1:AA:346:G:O5'	2.15	0.63
6:AF:91:ARG:HG3	6:AF:92:THR:H	1.62	0.63
14:AN:55:SER:HB3	14:AN:58:ARG:HB2	1.80	0.63
37:BE:161:ALA:HA	37:BE:164:LEU:HB2	1.81	0.63
54:BY:27:VAL:HG23	54:BY:33:VAL:HG12	1.79	0.63
4:AD:106:PHE:HB3	4:AD:144:ILE:HD11	1.80	0.63
4:AD:124:VAL:C	4:AD:126:GLY:H	2.02	0.63
12:AL:30:ARG:NH1	23:AW:408:LYS:CG	2.59	0.63
17:AQ:11:VAL:HG12	17:AQ:13:SER:H	1.64	0.63
31:B7:5:THR:HG22	31:B7:62:PRO:HD2	1.81	0.63
33:BA:100:U:H4'	33:BA:101:A:O5'	1.98	0.63
33:BA:323:C:H6	33:BA:1205:A:N1	1.96	0.63
33:BA:2148:G:C6	33:BA:2149:U:O2	2.51	0.63
33:BA:2149:U:C3'	33:BA:2150:C:C4'	2.75	0.63
4:AD:61:ARG:HH21	4:AD:67:LEU:HD22	1.62	0.63
24:B0:38:ARG:HH21	33:BA:2262:U:H5''	1.63	0.63
33:BA:1904:G:O2'	33:BA:1928:A:N1	2.26	0.63
33:BA:2788:C:H2'	33:BA:2789:C:C6	2.33	0.63
1:AA:518:C:H2'	1:AA:530:G:C8	2.33	0.63
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.16	0.63
23:AW:21:HIS:HD2	23:AW:122:ARG:H	1.47	0.63
35:BC:134:ILE:O	35:BC:166:ARG:NH1	2.32	0.63
6:AF:89:VAL:HG22	6:AF:90:MET:H	1.64	0.63
23:AW:26:LYS:HG3	56:AW:601:GNP:O1B	1.99	0.63
2:AB:53:LEU:HD13	2:AB:56:LEU:HD12	1.80	0.63
10:AJ:40:ILE:HB	10:AJ:73:LEU:HB2	1.81	0.63
16:AP:6:LEU:HG	16:AP:17:TYR:HB3	1.81	0.63
30:B6:21:ARG:HG2	30:B6:31:LEU:HG	1.80	0.63
45:BP:76:GLU:HB2	45:BP:111:ILE:HD12	1.81	0.63
8:AH:104:SER:HB2	8:AH:125:ILE:HD11	1.79	0.62
10:AJ:12:ALA:HB2	10:AJ:96:VAL:HG13	1.81	0.62
33:BA:900:A:H2	33:BA:901:C:H5	1.46	0.62
33:BA:1812:U:H2'	33:BA:1813:G:H8	1.63	0.62
28:B4:9:ARG:HB2	28:B4:12:ARG:NH2	2.13	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BG:84:LYS:HB2	39:BG:132:LEU:H	1.64	0.62
23:AW:304:GLN:O	23:AW:306:ASN:N	2.32	0.62
28:B4:47:TYR:CE2	28:B4:52:LYS:HB2	2.33	0.62
33:BA:184:C:H2'	33:BA:185:G:H8	1.64	0.62
33:BA:1458:U:H4'	33:BA:1459:G:O5'	1.98	0.62
49:BT:105:LYS:HA	49:BT:108:ARG:HH21	1.62	0.62
5:AE:104:ILE:HG13	5:AE:111:ARG:HG3	1.80	0.62
40:BH:15:VAL:HA	40:BH:18:VAL:HG23	1.81	0.62
4:AD:197:HIS:O	4:AD:201:GLU:HB2	1.99	0.62
13:AM:106:ARG:HH12	13:AM:109:LYS:HD3	1.64	0.62
27:B3:8:GLN:O	27:B3:10:ARG:N	2.32	0.62
46:BQ:12:MET:HB2	46:BQ:72:PRO:HD2	1.81	0.62
52:BW:109:ASP:OD1	52:BW:110:ARG:N	2.32	0.62
1:AA:545:C:H5'	4:AD:68:GLU:HG3	1.81	0.62
1:AA:1347:G:O6	9:AI:11:ARG:NH2	2.33	0.62
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.35	0.62
1:AA:1512:U:H2'	1:AA:1513:A:C8	2.35	0.62
23:AW:80:HIS:ND1	23:AW:81:ASP:OD1	2.27	0.62
33:BA:974:G:N7	33:BA:989:G:C5	2.67	0.62
1:AA:412:A:H5'	1:AA:413:G:OP1	2.00	0.62
23:AW:59:TRP:NE1	23:AW:69:SER:CA	2.63	0.62
26:B2:2:LYS:HB2	33:BA:102:U:H3	1.64	0.62
41:BI:135:MET:N	41:BI:135:MET:SD	2.73	0.62
49:BT:5:LYS:HA	49:BT:8:GLU:HB2	1.82	0.62
6:AF:67:PRO:HG2	6:AF:70:VAL:HG22	1.80	0.62
23:AW:314:ARG:CZ	23:AW:421:GLU:HB2	2.29	0.62
36:BD:15:PHE:H	49:BT:11:GLN:HE22	1.47	0.62
38:BF:134:GLN:O	38:BF:136:ILE:N	2.31	0.62
42:BJ:27:GLU:HA	42:BJ:29:LYS:HG3	1.80	0.62
51:BV:49:ILE:HB	51:BV:51:VAL:O	2.00	0.62
38:BF:64:PRO:HA	38:BF:88:VAL:HG22	1.82	0.62
5:AE:100:GLU:HB3	5:AE:121:ASN:HA	1.81	0.62
5:AE:156:ARG:NH2	8:AH:113:ARG:HH12	1.98	0.62
11:AK:22:ILE:HD11	11:AK:85:VAL:HG22	1.82	0.62
33:BA:1181:U:H2'	33:BA:1182:G:C8	2.33	0.62
1:AA:87:C:H2'	1:AA:88:U:O4'	2.00	0.61
4:AD:43:ARG:O	4:AD:45:PRO:HD3	2.00	0.61
33:BA:1914:C:C5	33:BA:1915:U:C4	2.88	0.61
42:BM:14:MET:O	42:BM:17:MET:N	2.33	0.61
6:AF:6:ILE:HG12	6:AF:89:VAL:HG23	1.82	0.61
24:B0:43:LYS:HD2	24:B0:79:ILE:HD11	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2375:G:N2	33:BA:2378:A:OP2	2.30	0.61
35:BC:250:GLN:HG2	35:BC:254:LYS:HG3	1.82	0.61
1:AA:1300:G:O2'	1:AA:1301:U:O5'	2.16	0.61
28:B4:40:HIS:ND1	33:BA:2815:C:O2'	2.30	0.61
32:B8:7:VAL:O	32:B8:35:GLN:NE2	2.33	0.61
35:BC:83:ASP:HB2	35:BC:90:ILE:HD12	1.81	0.61
1:AA:430:A:OP2	4:AD:7:LYS:HG2	2.00	0.61
10:AJ:11:LYS:HG3	10:AJ:97:ASP:HB3	1.82	0.61
24:B0:49:ASN:HB2	24:B0:60:ALA:HA	1.82	0.61
28:B4:3:GLN:HA	33:BA:2615:U:C2	2.35	0.61
36:BD:107:VAL:HG13	36:BD:203:VAL:HG23	1.82	0.61
37:BE:149:ILE:HD12	37:BE:175:ILE:HB	1.82	0.61
43:BN:44:TYR:HB2	50:BU:63:ARG:HB3	1.81	0.61
50:BU:68:ALA:HB1	50:BU:73:ILE:HG23	1.81	0.61
33:BA:1105:U:H2'	33:BA:1106:G:H8	1.66	0.61
33:BA:1800:C:OP2	35:BC:181:ARG:NH1	2.33	0.61
33:BA:1894:C:H2'	33:BA:1895:C:H6	1.66	0.61
34:BB:66:A:H4'	34:BB:67:G:OP1	2.01	0.61
1:AA:1387:G:H2'	1:AA:1388:C:C6	2.35	0.61
11:AK:28:ASN:OD1	11:AK:29:THR:N	2.33	0.61
33:BA:38:A:O2'	37:BE:43:THR:HA	2.00	0.61
33:BA:879:G:N1	33:BA:880:G:O6	2.33	0.61
36:BD:105:LYS:HE3	36:BD:176:ASP:HB3	1.81	0.61
52:BW:12:SER:O	52:BW:101:SER:OG	2.19	0.61
1:AA:2:A:N6	1:AA:3:A:N1	2.49	0.61
1:AA:82:G:O4'	1:AA:89:U:O2'	2.19	0.61
1:AA:337:G:H2'	1:AA:338:A:C8	2.36	0.61
1:AA:596:A:H61	1:AA:644:U:H3	1.48	0.61
1:AA:1005:A:OP2	1:AA:1024:G:N2	2.33	0.61
1:AA:1492:A:N1	33:BA:1913:A:H2	1.98	0.61
26:B2:45:GLN:O	26:B2:46:VAL:HB	2.00	0.61
33:BA:503:A:H4'	33:BA:504:A:O5'	1.99	0.61
33:BA:1082:U:H5'	41:BI:118:GLY:HA2	1.82	0.61
42:BJ:13:ALA:O	42:BJ:17:MET:HB2	2.01	0.61
1:AA:509:A:N3	1:AA:543:U:O2'	2.32	0.61
1:AA:992:U:O2'	1:AA:993:G:N2	2.34	0.61
1:AA:1191:A:H5''	3:AC:3:LYS:HE3	1.82	0.61
1:AA:1527:U:OP2	21:AU:38:GLU:HG2	2.00	0.61
33:BA:172:A:H2'	33:BA:173:A:C8	2.36	0.61
33:BA:458:G:O2'	33:BA:459:U:P	2.59	0.61
33:BA:1019:U:H3	33:BA:1142:A:H62	1.49	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:591:U:H2'	1:AA:592:G:H8	1.65	0.61
1:AA:1492:A:C6	33:BA:1913:A:C2	2.88	0.61
2:AB:113:LEU:HD13	2:AB:143:LEU:HD12	1.83	0.61
15:AO:84:LEU:HB3	15:AO:86:LEU:HD22	1.83	0.61
33:BA:364:C:O5'	33:BA:364:C:H6	1.84	0.61
33:BA:580:U:H2'	33:BA:581:C:C6	2.36	0.61
44:BO:103:VAL:O	44:BO:122:VAL:HB	2.01	0.61
25:B1:67:LEU:HD13	25:B1:77:TYR:CE1	2.36	0.60
38:BF:7:TYR:OH	38:BF:29:ARG:HB3	2.01	0.60
51:BV:25:LEU:H	51:BV:94:THR:HG21	1.66	0.60
1:AA:1002:G:H1	1:AA:1038:C:H42	1.49	0.60
9:AI:56:MET:HB3	9:AI:60:LEU:HD23	1.82	0.60
33:BA:1069:A:O2'	33:BA:1070:A:H5''	2.00	0.60
33:BA:2150:C:N3	33:BA:2151:U:O4	2.34	0.60
41:BI:33:ASN:HB3	41:BI:36:GLU:HB2	1.83	0.60
7:AG:135:LYS:HD2	7:AG:138:GLU:HB2	1.83	0.60
8:AH:13:ILE:HD11	8:AH:60:LEU:HD12	1.83	0.60
20:AT:19:HIS:O	20:AT:22:SER:OG	2.16	0.60
36:BD:184:ARG:HB3	36:BD:186:LEU:HD13	1.83	0.60
1:AA:70:U:HO2'	1:AA:71:A:H8	1.49	0.60
1:AA:251:G:N1	1:AA:266:G:O6	2.34	0.60
4:AD:187:ARG:NH1	4:AD:190:LEU:O	2.34	0.60
6:AF:43:GLY:HA2	6:AF:58:HIS:CE1	2.37	0.60
23:AW:300:VAL:HG12	23:AW:301:PHE:H	1.66	0.60
26:B2:5:GLU:O	26:B2:8:GLU:HB2	2.00	0.60
33:BA:1894:C:H2'	33:BA:1895:C:C6	2.37	0.60
36:BD:157:LYS:HD2	43:BN:79:GLY:O	2.01	0.60
52:BW:42:LYS:O	52:BW:45:VAL:HG13	2.02	0.60
53:BX:38:ALA:HB1	53:BX:43:ILE:HG22	1.81	0.60
1:AA:1105:A:H2'	1:AA:1106:G:C8	2.35	0.60
19:AS:35:ARG:NH2	19:AS:71:GLY:O	2.34	0.60
33:BA:877:A:H1'	33:BA:900:A:N6	2.16	0.60
45:BP:110:VAL:HB	45:BP:127:VAL:HG23	1.84	0.60
1:AA:70:U:C5	1:AA:94:G:H2'	2.36	0.60
4:AD:53:GLN:HA	4:AD:198:LEU:HD22	1.82	0.60
38:BF:98:PHE:O	38:BF:102:LEU:HB2	2.01	0.60
1:AA:982:U:H4'	1:AA:983:A:O5'	2.01	0.60
3:AC:184:ASN:HD22	3:AC:185:THR:H	1.50	0.60
12:AL:49:ARG:HG2	12:AL:89:LEU:HD21	1.83	0.60
23:AW:59:TRP:CZ2	23:AW:69:SER:OG	2.55	0.60
23:AW:472:ARG:HH21	23:AW:505:ALA:HB2	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:639:U:H2'	33:BA:640:C:C6	2.37	0.60
33:BA:1914:C:C6	33:BA:1915:U:C5	2.89	0.60
35:BC:171:VAL:HG23	35:BC:185:ALA:HB2	1.84	0.60
38:BF:108:PRO:HA	38:BF:113:PHE:CD2	2.36	0.60
40:BH:11:ILE:CG2	40:BH:66:GLY:HA3	2.29	0.60
40:BH:138:ARG:HG2	42:BK:22:LEU:HD11	1.83	0.60
45:BP:79:LEU:H	45:BP:113:ALA:HB3	1.66	0.60
1:AA:422:C:O2'	1:AA:423:G:O5'	2.19	0.60
1:AA:642:A:N3	8:AH:104:SER:OG	2.28	0.60
1:AA:1218:C:H2'	1:AA:1219:A:C8	2.37	0.60
1:AA:1297:G:H5'	1:AA:1302:C:H42	1.67	0.60
23:AW:427:VAL:HG12	23:AW:438:VAL:HG22	1.83	0.60
33:BA:197:A:N6	33:BA:2430:A:H2'	2.16	0.60
48:BS:11:ALA:HB2	48:BS:96:GLY:N	2.17	0.60
1:AA:1004:A:H2'	1:AA:1005:A:O4'	2.02	0.60
14:AN:63:CYS:HB3	14:AN:67:GLY:H	1.65	0.60
23:AW:518:TYR:CD1	23:AW:519:PRO:HA	2.36	0.60
33:BA:215:G:H4'	33:BA:216:A:H4'	1.84	0.60
39:BG:44:HIS:HA	39:BG:49:LEU:HD23	1.83	0.60
1:AA:411:A:C5	1:AA:413:G:H1'	2.37	0.60
10:AJ:10:LEU:HB3	10:AJ:18:ILE:HD11	1.82	0.60
23:AW:35:LEU:HD11	23:AW:262:ASN:HD21	1.67	0.60
33:BA:859:G:O2'	33:BA:860:U:O5'	2.18	0.60
33:BA:923:G:H2'	33:BA:924:G:H8	1.65	0.60
33:BA:2233:U:H2'	33:BA:2234:G:C8	2.37	0.60
33:BA:2334:U:N3	48:BS:16:ARG:HG2	2.17	0.60
40:BH:29:ASP:H	40:BH:81:LEU:HD22	1.66	0.60
1:AA:369:G:OP2	1:AA:388:G:N2	2.27	0.59
1:AA:922:G:H4'	5:AE:24:VAL:HA	1.83	0.59
6:AF:47:LEU:HD13	6:AF:51:ILE:HG22	1.84	0.59
23:AW:53:GLN:O	23:AW:55:ALA:N	2.32	0.59
23:AW:63:GLU:HB2	23:AW:450:VAL:HG11	1.83	0.59
23:AW:522:GLN:HB2	23:AW:524:HIS:H	1.67	0.59
1:AA:73:C:H41	1:AA:94:G:H22	1.50	0.59
5:AE:88:HIS:CE1	5:AE:137:ARG:HD3	2.38	0.59
10:AJ:48:ARG:HG3	10:AJ:66:GLU:HB3	1.82	0.59
33:BA:782:A:H5'	33:BA:783:A:C2	2.36	0.59
33:BA:1378:A:O2'	33:BA:1380:G:OP2	2.20	0.59
33:BA:2149:U:H3'	33:BA:2150:C:H4'	1.84	0.59
1:AA:1147:C:H4'	9:AI:6:TYR:CE1	2.38	0.59
5:AE:91:SER:OG	5:AE:129:SER:O	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:6:ILE:HD11	6:AF:71:ILE:HD11	1.82	0.59
23:AW:147:ASP:HB3	39:BG:91:VAL:HG11	1.84	0.59
33:BA:118:A:N3	33:BA:178:G:H1'	2.17	0.59
33:BA:582:A:H2'	33:BA:583:G:C8	2.37	0.59
33:BA:1290:C:H2'	33:BA:1291:C:H6	1.67	0.59
33:BA:1442:U:H2'	33:BA:1443:U:C6	2.37	0.59
3:AC:10:ARG:HB3	3:AC:15:LYS:HB2	1.84	0.59
23:AW:59:TRP:NE1	23:AW:69:SER:HA	2.18	0.59
32:B8:11:CYS:SG	32:B8:33:HIS:ND1	2.71	0.59
32:B8:22:VAL:HG11	32:B8:36:ARG:HG2	1.84	0.59
33:BA:2105:U:C4	33:BA:2106:U:O4	2.55	0.59
23:AW:105:ALA:O	23:AW:319:ARG:NH1	2.32	0.59
33:BA:2149:U:O3'	33:BA:2150:C:C4'	2.30	0.59
1:AA:1152:A:H5'	10:AJ:15:HIS:CD2	2.38	0.59
5:AE:35:LEU:HD21	5:AE:136:VAL:HG11	1.83	0.59
5:AE:103:GLY:HA2	5:AE:121:ASN:HA	1.85	0.59
32:B8:16:ILE:HG12	32:B8:25:VAL:HG22	1.85	0.59
33:BA:2577:A:H5''	33:BA:2578:G:H5'	1.84	0.59
42:BJ:13:ALA:O	42:BJ:14:MET:HG2	2.02	0.59
49:BT:91:VAL:O	49:BT:92:ARG:HG2	2.02	0.59
49:BT:91:VAL:HG11	49:BT:96:LEU:HD21	1.85	0.59
3:AC:126:ARG:HH12	3:AC:192:TYR:HE2	1.49	0.59
3:AC:139:ASN:HA	3:AC:142:ARG:HB2	1.84	0.59
7:AG:14:ASP:OD2	7:AG:43:TYR:OH	2.15	0.59
7:AG:78:ARG:NH1	7:AG:81:GLY:O	2.35	0.59
24:B0:37:VAL:HG13	24:B0:55:ASP:O	2.01	0.59
24:B0:39:GLN:HG2	24:B0:40:ARG:N	2.18	0.59
30:B6:9:VAL:HG12	33:BA:1309:G:OP1	2.02	0.59
32:B8:15:LYS:HE3	32:B8:17:VAL:HG22	1.84	0.59
33:BA:136:G:H1	33:BA:143:C:H42	1.51	0.59
33:BA:395:U:O2'	33:BA:396:G:N7	2.34	0.59
33:BA:900:A:C2	33:BA:901:C:H5	2.21	0.59
33:BA:900:A:H3'	33:BA:902:C:H41	1.68	0.59
33:BA:910:A:N3	33:BA:2264:C:O2'	2.34	0.59
33:BA:2152:G:H2'	33:BA:2153:C:O4'	2.01	0.59
35:BC:124:LYS:HB3	35:BC:127:ASN:ND2	2.18	0.59
47:BR:69:ARG:O	47:BR:71:ARG:N	2.32	0.59
7:AG:62:GLU:OE1	7:AG:69:ARG:NH2	2.35	0.59
23:AW:56:LYS:H	23:AW:57:SER:HB3	1.68	0.59
24:B0:59:PHE:CE2	33:BA:2365:G:H4'	2.37	0.59
33:BA:538:A:H2'	33:BA:539:G:O4'	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BC:180:MET:HG3	35:BC:268:ARG:HB3	1.85	0.59
43:BN:132:HIS:O	43:BN:135:GLN:HG2	2.03	0.59
44:BO:18:ARG:H	44:BO:45:GLU:HB2	1.67	0.59
1:AA:250:A:H4'	1:AA:251:G:O5'	2.02	0.59
1:AA:402:G:C6	1:AA:403:C:C4	2.91	0.59
1:AA:1035:A:H2'	1:AA:1036:A:O4'	2.02	0.59
11:AK:94:SER:HA	11:AK:97:ARG:HG2	1.84	0.59
25:B1:69:GLU:O	25:B1:71:ARG:N	2.36	0.59
33:BA:1797:G:O3'	35:BC:255:LYS:HA	2.02	0.59
43:BN:44:TYR:HE2	50:BU:99:VAL:HG21	1.68	0.59
43:BN:100:VAL:O	43:BN:103:ILE:HD13	2.03	0.59
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.35	0.58
4:AD:86:GLY:HA3	4:AD:196:GLU:HB3	1.84	0.58
8:AH:87:ARG:O	8:AH:121:GLY:HA3	2.04	0.58
19:AS:3:SER:HB2	19:AS:4:LEU:HD12	1.84	0.58
23:AW:59:TRP:O	23:AW:64:LYS:HD2	2.03	0.58
23:AW:401:ILE:HG22	23:AW:461:ALA:HB1	1.84	0.58
24:B0:39:GLN:HG3	24:B0:42:THR:H	1.67	0.58
33:BA:668:A:H2'	33:BA:670:A:H62	1.68	0.58
33:BA:1059:G:N2	41:BI:127:SER:O	2.25	0.58
33:BA:1654:A:H2'	33:BA:1655:A:C8	2.39	0.58
45:BP:81:ASP:HB3	45:BP:100:ILE:HD12	1.85	0.58
54:BY:53:GLN:N	54:BY:53:GLN:OE1	2.36	0.58
3:AC:152:VAL:HG12	3:AC:197:VAL:HG13	1.84	0.58
23:AW:50:GLY:HA3	33:BA:2655:G:H8	1.68	0.58
23:AW:145:ASP:OD2	56:AW:601:GNP:C2	2.51	0.58
33:BA:1045:C:H5''	33:BA:1046:A:H5'	1.85	0.58
36:BD:68:PHE:CB	36:BD:73:VAL:HG12	2.33	0.58
38:BF:38:GLY:HA2	38:BF:85:GLY:HA3	1.85	0.58
42:BJ:3:THR:HG22	42:BJ:6:GLN:HB2	1.83	0.58
27:B3:12:ALA:HA	27:B3:15:ARG:HD3	1.86	0.58
33:BA:674:G:H5''	37:BE:71:GLY:N	2.18	0.58
33:BA:819:A:OP2	33:BA:1187:G:N2	2.23	0.58
37:BE:149:ILE:HD11	37:BE:172:ALA:HA	1.86	0.58
44:BO:111:LYS:H	44:BO:111:LYS:HE2	1.67	0.58
52:BW:72:THR:O	52:BW:73:LYS:HD2	2.02	0.58
53:BX:44:LYS:O	53:BX:48:GLN:HG2	2.03	0.58
16:AP:18:GLN:HE21	16:AP:35:ARG:HD2	1.69	0.58
32:B8:2:LYS:NZ	33:BA:2478:A:OP2	2.26	0.58
32:B8:36:ARG:HG2	32:B8:37:GLN:H	1.66	0.58
33:BA:27:G:H1'	33:BA:513:A:H62	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BE:158:PHE:HA	37:BE:169:VAL:HG21	1.85	0.58
1:AA:210:C:O2'	1:AA:211:G:N2	2.36	0.58
1:AA:383:A:C5	1:AA:384:G:H1'	2.38	0.58
1:AA:980:C:O3'	14:AN:12:ARG:NH2	2.37	0.58
33:BA:899:A:H2'	33:BA:900:A:C8	2.38	0.58
33:BA:1243:C:H1'	45:BP:4:ASN:O	2.03	0.58
43:BN:118:MET:HA	43:BN:121:LYS:HE2	1.86	0.58
1:AA:662:U:H2'	1:AA:663:A:C8	2.39	0.58
2:AB:40:ILE:HG12	2:AB:201:GLY:HA2	1.84	0.58
33:BA:2748:A:H1'	39:BG:66:THR:HG22	1.85	0.58
36:BD:13:ARG:HE	36:BD:21:SER:HG	1.48	0.58
1:AA:86:G:O2'	1:AA:87:C:O4'	2.18	0.58
33:BA:947:A:O2'	33:BA:984:A:H2	1.87	0.58
38:BF:10:GLU:C	38:BF:12:VAL:H	2.06	0.58
40:BH:57:ASN:C	40:BH:59:LEU:H	2.06	0.58
53:BX:39:THR:O	53:BX:40:LYS:HB2	2.04	0.58
1:AA:1054:C:H1'	1:AA:1196:A:N7	2.17	0.58
4:AD:25:ARG:NH1	4:AD:30:LYS:HE3	2.19	0.58
5:AE:87:VAL:HG12	5:AE:92:ARG:HA	1.86	0.58
23:AW:59:TRP:CE3	23:AW:59:TRP:HA	2.39	0.58
33:BA:1844:C:H5'	35:BC:253:GLY:O	2.04	0.58
53:BX:76:ARG:NH2	53:BX:79:ASP:OD1	2.37	0.58
1:AA:1171:A:H2'	1:AA:1172:C:C6	2.39	0.58
1:AA:1491:G:C2'	1:AA:1492:A:OP2	2.52	0.58
13:AM:43:LYS:C	13:AM:45:SER:H	2.06	0.58
33:BA:993:G:OP1	50:BU:49:ARG:NE	2.31	0.58
33:BA:1666:G:H4'	44:BO:6:THR:HG23	1.86	0.58
44:BO:2:ILE:O	44:BO:3:GLN:HG2	2.03	0.58
1:AA:1101:A:H4'	1:AA:1102:A:O5'	2.04	0.58
14:AN:21:ALA:N	14:AN:24:ALA:HB3	2.19	0.58
21:AU:33:ARG:HD3	21:AU:34:ARG:H	1.67	0.58
23:AW:314:ARG:NH2	23:AW:418:GLN:HA	2.19	0.58
33:BA:2580:U:OP1	36:BD:137:SER:OG	2.20	0.58
33:BA:2680:U:OP1	36:BD:114:LYS:HG3	2.02	0.58
36:BD:121:THR:HB	36:BD:127:PHE:CD1	2.39	0.58
51:BV:49:ILE:HG22	51:BV:54:VAL:HG13	1.86	0.58
10:AJ:8:ILE:HB	10:AJ:74:VAL:HB	1.86	0.57
23:AW:448:VAL:HG13	23:AW:452:ARG:HH21	1.68	0.57
33:BA:171:U:H2'	33:BA:172:A:C8	2.39	0.57
33:BA:1217:U:OP2	50:BU:14:LYS:NZ	2.24	0.57
36:BD:91:THR:C	36:BD:93:GLY:H	2.06	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:63:ILE:HG23	4:AD:64:TYR:CD1	2.39	0.57
23:AW:68:ILE:HG23	23:AW:68:ILE:O	2.03	0.57
23:AW:97:GLU:O	23:AW:99:THR:N	2.37	0.57
23:AW:399:ARG:HG3	23:AW:438:VAL:O	2.05	0.57
33:BA:1425:G:H2'	33:BA:1426:G:C8	2.39	0.57
35:BC:13:ARG:HG2	35:BC:14:HIS:CD2	2.39	0.57
55:BZ:63:ILE:O	55:BZ:70:ILE:N	2.31	0.57
24:B0:41:GLY:HA2	24:B0:44:PHE:CE2	2.40	0.57
33:BA:90:U:H2'	33:BA:91:A:C8	2.39	0.57
36:BD:119:ALA:HB1	36:BD:123:LYS:HB3	1.86	0.57
50:BU:23:TYR:HB3	50:BU:27:ARG:HB3	1.86	0.57
3:AC:118:SER:O	3:AC:122:GLN:HG2	2.04	0.57
12:AL:23:LEU:HG	12:AL:24:GLU:N	2.09	0.57
33:BA:1442:U:H2'	33:BA:1443:U:H6	1.69	0.57
33:BA:1549:A:H2'	33:BA:1550:C:C6	2.39	0.57
33:BA:2107:G:C6	33:BA:2183:A:C5	2.91	0.57
47:BR:38:LEU:HB3	47:BR:39:PRO:HD3	1.87	0.57
51:BV:42:ALA:HA	51:BV:46:GLU:HB2	1.84	0.57
52:BW:24:ILE:HG23	52:BW:71:VAL:HG11	1.87	0.57
2:AB:22:TRP:CZ3	2:AB:24:PRO:HA	2.39	0.57
23:AW:70:ILE:O	23:AW:90:PRO:HB3	2.04	0.57
24:B0:23:LYS:NZ	33:BA:923:G:H21	2.03	0.57
24:B0:39:GLN:O	24:B0:41:GLY:N	2.34	0.57
25:B1:34:SER:HA	25:B1:48:LEU:O	2.05	0.57
33:BA:2146:C:H4'	33:BA:2147:A:OP1	2.02	0.57
40:BH:155:LEU:HD22	42:BL:22:LEU:HB3	1.87	0.57
40:BH:157:ALA:O	40:BH:160:ASP:N	2.37	0.57
44:BO:106:GLU:N	44:BO:106:GLU:OE1	2.37	0.57
47:BR:44:LEU:O	47:BR:48:VAL:HG23	2.05	0.57
1:AA:1203:C:H2'	1:AA:1204:A:H8	1.68	0.57
9:AI:18:VAL:HG22	9:AI:64:ILE:HG23	1.86	0.57
13:AM:47:LEU:HD23	13:AM:51:GLN:HB3	1.87	0.57
24:B0:37:VAL:HG12	24:B0:38:ARG:H	1.69	0.57
33:BA:244:A:C2	33:BA:245:G:H1'	2.39	0.57
33:BA:2548:U:O2	44:BO:23:LYS:NZ	2.36	0.57
37:BE:27:LEU:O	37:BE:31:VAL:HG23	2.04	0.57
1:AA:922:G:H2'	1:AA:923:A:C8	2.39	0.57
2:AB:73:ARG:HA	2:AB:76:SER:HB3	1.87	0.57
2:AB:164:ASP:HB2	2:AB:203:ASP:HB2	1.86	0.57
3:AC:56:ILE:HD12	3:AC:65:VAL:HG22	1.86	0.57
10:AJ:14:ASP:OD2	10:AJ:14:ASP:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AL:30:ARG:NH1	23:AW:408:LYS:HE2	2.18	0.57
23:AW:59:TRP:HZ2	23:AW:69:SER:CB	2.17	0.57
26:B2:48:ARG:CZ	33:BA:75:G:H4'	2.35	0.57
33:BA:31:C:O3'	33:BA:1238:G:H5'	2.05	0.57
33:BA:2726:A:HO2'	33:BA:2727:A:P	2.27	0.57
36:BD:32:ASN:HB3	36:BD:50:VAL:HG11	1.85	0.57
49:BT:50:ARG:HD2	49:BT:51:ASN:H	1.70	0.57
1:AA:765:G:H1	1:AA:812:G:H2'	1.70	0.57
1:AA:971:G:H5''	1:AA:972:C:H5''	1.87	0.57
1:AA:974:A:H8	1:AA:974:A:OP1	1.87	0.57
1:AA:983:A:H5'	14:AN:2:LYS:NZ	2.20	0.57
1:AA:1410:A:C6	1:AA:1491:G:O6	2.58	0.57
5:AE:149:PRO:HG2	5:AE:150:GLU:HG2	1.85	0.57
6:AF:40:GLU:OE1	6:AF:100:SER:OG	2.20	0.57
33:BA:1818:U:H3'	35:BC:155:ARG:HB2	1.87	0.57
40:BH:51:TYR:HB2	40:BH:89:PRO:HD2	1.85	0.57
44:BO:23:LYS:HB3	44:BO:40:LYS:HB3	1.86	0.57
1:AA:182:A:N1	1:AA:223:A:O2'	2.32	0.57
1:AA:501:C:H2'	1:AA:502:A:C8	2.40	0.57
2:AB:71:THR:HB	2:AB:167:HIS:HE1	1.69	0.57
37:BE:76:PRO:HA	37:BE:82:GLY:HA2	1.87	0.57
46:BQ:42:THR:O	46:BQ:44:ARG:N	2.37	0.57
48:BS:67:ASN:C	48:BS:69:ASP:H	2.07	0.57
1:AA:197:A:N1	1:AA:220:G:O2'	2.35	0.57
21:AU:36:PHE:HB3	21:AU:40:PRO:HD3	1.86	0.57
33:BA:962:G:N2	33:BA:2250:G:H1	2.02	0.57
33:BA:1497:U:H5''	33:BA:1498:C:OP2	2.05	0.57
38:BF:33:ILE:HD12	38:BF:155:ILE:HG13	1.87	0.57
46:BQ:66:ARG:HB2	46:BQ:101:VAL:O	2.05	0.57
46:BQ:72:PRO:O	46:BQ:89:VAL:HG13	2.05	0.57
1:AA:409:U:OP1	4:AD:23:GLY:HA3	2.04	0.56
21:AU:16:ARG:HD2	21:AU:19:LYS:HE2	1.86	0.56
24:B0:23:LYS:HD3	33:BA:855:G:N3	2.20	0.56
27:B3:8:GLN:HB3	27:B3:31:ILE:HA	1.86	0.56
38:BF:110:ILE:HG12	38:BF:136:ILE:HG21	1.87	0.56
44:BO:13:ASN:O	44:BO:15:GLY:N	2.38	0.56
46:BQ:23:GLY:O	46:BQ:101:VAL:HG12	2.04	0.56
53:BX:12:ARG:HG2	53:BX:35:ALA:H	1.69	0.56
1:AA:9:G:H5'	5:AE:107:GLY:HA3	1.87	0.56
1:AA:1363:A:O2'	1:AA:1365:G:N7	2.38	0.56
6:AF:62:MET:HG3	6:AF:64:VAL:HG23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:56:SER:OG	7:AG:57:GLU:N	2.37	0.56
33:BA:17:G:H2'	33:BA:18:U:C6	2.40	0.56
35:BC:95:TYR:HE1	35:BC:101:ARG:HD2	1.70	0.56
55:BZ:2:PHE:O	55:BZ:62:THR:OG1	2.22	0.56
1:AA:537:G:H5''	12:AL:109:ARG:NH1	2.19	0.56
1:AA:721:G:H4'	1:AA:722:G:O5'	2.05	0.56
1:AA:1088:G:H21	1:AA:1167:A:N6	2.02	0.56
4:AD:73:ASN:HA	4:AD:76:LYS:HE2	1.86	0.56
5:AE:110:MET:HG3	5:AE:139:THR:HG21	1.88	0.56
11:AK:63:GLN:HG3	11:AK:98:ALA:HB2	1.87	0.56
14:AN:8:ARG:HB3	14:AN:12:ARG:NH1	2.19	0.56
23:AW:64:LYS:CE	23:AW:71:THR:H	2.17	0.56
23:AW:394:ALA:HB2	23:AW:525:GLN:HG2	1.86	0.56
24:B0:63:ASP:OD1	24:B0:63:ASP:N	2.37	0.56
33:BA:197:A:H62	33:BA:2430:A:H2'	1.70	0.56
33:BA:878:A:C6	33:BA:879:G:H1'	2.41	0.56
33:BA:1212:G:O2'	33:BA:1236:G:N2	2.38	0.56
33:BA:1485:U:H2'	33:BA:1486:U:C6	2.41	0.56
36:BD:121:THR:O	36:BD:122:VAL:HB	2.04	0.56
36:BD:146:ILE:HD12	36:BD:155:VAL:HG21	1.86	0.56
37:BE:194:LYS:O	37:BE:197:GLU:HB3	2.05	0.56
48:BS:7:ARG:NH1	48:BS:95:SER:O	2.38	0.56
24:B0:30:VAL:CG1	33:BA:2353:G:H1'	2.32	0.56
33:BA:1935:G:H1'	33:BA:1964:G:N2	2.21	0.56
33:BA:2305:U:H5''	38:BF:130:GLY:HA3	1.87	0.56
1:AA:17:U:H2'	1:AA:18:C:C6	2.40	0.56
1:AA:666:G:OP2	1:AA:725:G:N2	2.33	0.56
4:AD:105:GLY:HA3	4:AD:161:ALA:HB1	1.88	0.56
11:AK:22:ILE:HG22	11:AK:31:VAL:HG22	1.86	0.56
23:AW:71:THR:HG22	23:AW:72:THR:H	1.70	0.56
35:BC:106:PRO:HG2	35:BC:109:LEU:H	1.70	0.56
1:AA:35:G:O2'	12:AL:114:SER:O	2.19	0.56
1:AA:82:G:N2	1:AA:88:U:HO2'	2.04	0.56
1:AA:202:G:H21	1:AA:466:A:H61	1.53	0.56
3:AC:142:ARG:HB3	3:AC:143:LEU:HD13	1.87	0.56
4:AD:149:LYS:NZ	4:AD:176:LYS:O	2.38	0.56
23:AW:108:CYS:HA	23:AW:135:THR:HG23	1.88	0.56
33:BA:704:G:H1'	33:BA:727:A:N6	2.20	0.56
33:BA:1819:A:H5''	35:BC:159:THR:HG21	1.87	0.56
33:BA:2377:A:O2'	48:BS:117:PHE:O	2.19	0.56
33:BA:974:G:O2'	33:BA:975:A:OP2	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1566:A:H5'	35:BC:213:ARG:HH12	1.68	0.56
47:BR:103:ARG:HB2	47:BR:110:MET:HE3	1.87	0.56
1:AA:412:A:H4'	1:AA:413:G:O5'	2.05	0.56
12:AL:43:LYS:HD3	12:AL:43:LYS:H	1.70	0.56
33:BA:372:G:O2'	33:BA:373:U:P	2.63	0.56
33:BA:864:G:C6	33:BA:865:C:N4	2.74	0.56
33:BA:1327:A:H2'	33:BA:1328:A:O4'	2.05	0.56
33:BA:1392:A:H61	53:BX:18:GLU:HG2	1.71	0.56
33:BA:1657:U:H2'	33:BA:1658:C:H6	1.70	0.56
33:BA:2209:G:C2	33:BA:2216:G:C2	2.92	0.56
33:BA:2345:G:H4'	33:BA:2346:A:H5''	1.87	0.56
33:BA:2804:U:H2'	33:BA:2805:C:C6	2.40	0.56
36:BD:108:ASP:HA	36:BD:173:GLN:HA	1.87	0.56
23:AW:428:PHE:HB2	23:AW:437:ILE:HB	1.87	0.56
23:AW:453:LEU:HD13	23:AW:458:ASN:HA	1.87	0.56
29:B5:20:TYR:HH	33:BA:2347:C:HO2'	1.49	0.56
38:BF:128:SER:OG	38:BF:154:THR:HB	2.06	0.56
12:AL:24:GLU:CD	12:AL:29:LYS:HZ1	2.10	0.56
23:AW:525:GLN:HE21	23:AW:525:GLN:N	2.04	0.56
33:BA:1029:A:OP1	46:BQ:127:LYS:NZ	2.27	0.56
33:BA:1792:G:O2'	33:BA:1830:C:OP1	2.23	0.56
33:BA:1914:C:C6	33:BA:1915:U:C6	2.93	0.56
1:AA:115:G:H4'	1:AA:116:A:O5'	2.06	0.55
9:AI:22:PRO:HA	9:AI:60:LEU:HA	1.88	0.55
33:BA:1084:A:C2	33:BA:1105:U:H1'	2.41	0.55
33:BA:2591:C:P	35:BC:237:ARG:HG3	2.46	0.55
33:BA:2794:C:H2'	33:BA:2795:C:C6	2.41	0.55
39:BG:11:PRO:O	39:BG:14:VAL:HG22	2.07	0.55
1:AA:376:G:H5''	16:AP:5:ARG:HB2	1.87	0.55
1:AA:408:A:OP1	4:AD:109:THR:HG21	2.07	0.55
1:AA:624:C:H4'	16:AP:10:GLY:O	2.07	0.55
1:AA:950:U:H2'	1:AA:951:G:C8	2.41	0.55
1:AA:972:C:OP2	10:AJ:59:LYS:HE3	2.05	0.55
2:AB:82:ALA:HB3	2:AB:217:ALA:HB1	1.88	0.55
6:AF:22:ILE:HD11	6:AF:60:VAL:HG11	1.89	0.55
23:AW:59:TRP:NE1	23:AW:69:SER:CB	2.69	0.55
29:B5:7:LYS:HA	29:B5:23:THR:HG22	1.88	0.55
35:BC:173:LEU:HD22	35:BC:183:VAL:HG21	1.88	0.55
40:BH:52:MET:HE1	40:BH:87:GLU:HG2	1.88	0.55
40:BH:93:ALA:HA	40:BH:129:LEU:O	2.05	0.55
42:BJ:21:GLU:HB3	42:BK:7:ILE:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.38	0.55
9:AI:24:ASN:HB2	9:AI:26:LYS:HE3	1.88	0.55
18:AR:70:THR:OG1	18:AR:71:ASP:N	2.38	0.55
23:AW:145:ASP:OD2	56:AW:601:GNP:N1	2.39	0.55
33:BA:1183:U:H2'	33:BA:1184:U:H6	1.71	0.55
53:BX:39:THR:HB	53:BX:42:GLU:H	1.71	0.55
2:AB:20:ARG:CZ	2:AB:20:ARG:HA	2.36	0.55
33:BA:1316:U:H2'	33:BA:1317:G:C8	2.41	0.55
33:BA:1794:A:H2'	33:BA:1795:C:C6	2.41	0.55
33:BA:2597:G:C5'	35:BC:240:GLY:HA3	2.30	0.55
35:BC:38:LYS:NZ	35:BC:57:HIS:O	2.29	0.55
37:BE:77:ILE:HG13	37:BE:78:TRP:HE3	1.71	0.55
3:AC:10:ARG:O	3:AC:13:ILE:N	2.29	0.55
33:BA:247:G:H4'	33:BA:386:G:C5	2.41	0.55
33:BA:645:C:N4	33:BA:2350:C:O2'	2.38	0.55
33:BA:659:G:H4'	37:BE:95:LYS:HB3	1.87	0.55
41:BI:27:LEU:HD21	41:BI:34:ILE:HG23	1.88	0.55
1:AA:1125:U:C4	1:AA:1127:G:C4	2.95	0.55
1:AA:1361:G:N2	1:AA:1362:A:N7	2.54	0.55
23:AW:399:ARG:CZ	23:AW:445:GLN:HB3	2.37	0.55
23:AW:472:ARG:HG3	23:AW:504:ILE:HA	1.89	0.55
33:BA:483:A:C8	54:BY:44:HIS:HD2	2.25	0.55
33:BA:779:U:OP1	35:BC:48:ILE:HD12	2.07	0.55
33:BA:1444:G:H2'	33:BA:1445:G:H8	1.71	0.55
33:BA:2311:A:H5'	33:BA:2312:U:OP2	2.06	0.55
33:BA:2485:G:H5''	46:BQ:45:GLN:HE21	1.71	0.55
36:BD:118:PHE:C	36:BD:120:GLY:H	2.09	0.55
53:BX:36:LYS:O	53:BX:81:LYS:HD2	2.07	0.55
1:AA:591:U:H2'	1:AA:592:G:C8	2.42	0.55
1:AA:714:G:H2'	1:AA:715:A:C8	2.41	0.55
1:AA:1437:A:H5''	20:AT:28:ARG:NH1	2.21	0.55
26:B2:41:HIS:CE1	33:BA:96:C:H4'	2.41	0.55
33:BA:634:C:H2'	33:BA:635:C:C6	2.42	0.55
33:BA:645:C:O2	33:BA:645:C:H2'	2.06	0.55
33:BA:2849:U:H4'	33:BA:2868:A:C2	2.41	0.55
38:BF:82:TYR:HD2	38:BF:83:PRO:HD2	1.72	0.55
44:BO:39:ILE:HG23	44:BO:41:ILE:HD13	1.89	0.55
25:B1:31:ASN:CG	25:B1:33:HIS:HE2	2.07	0.55
33:BA:167:A:H2'	33:BA:168:G:O4'	2.07	0.55
36:BD:184:ARG:NH1	49:BT:6:GLN:HE22	2.05	0.55
7:AG:12:LEU:H	7:AG:12:LEU:HD22	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AQ:45:VAL:HG11	17:AQ:60:ILE:HD12	1.88	0.55
33:BA:1757:A:H3'	33:BA:1758:U:C5'	2.37	0.55
2:AB:185:ILE:HA	2:AB:199:ILE:HB	1.89	0.55
4:AD:109:THR:OG1	4:AD:110:ARG:N	2.39	0.55
27:B3:46:MET:O	27:B3:50:VAL:HG22	2.07	0.55
31:B7:12:ARG:NH1	33:BA:250:G:OP2	2.37	0.55
33:BA:1420:A:H5'	33:BA:1421:G:OP2	2.07	0.55
33:BA:2147:A:H3'	33:BA:2148:G:C5'	2.37	0.55
43:BN:36:LEU:O	43:BN:121:LYS:NZ	2.37	0.55
55:BZ:9:ARG:HG2	55:BZ:41:GLU:HB3	1.89	0.55
1:AA:507:C:H3'	1:AA:508:U:H5''	1.88	0.54
23:AW:490:GLU:HA	23:AW:493:LEU:HD12	1.89	0.54
25:B1:73:ARG:HD2	25:B1:75:GLU:HG3	1.88	0.54
40:BH:23:LEU:HB2	40:BH:92:ALA:HB1	1.89	0.54
43:BN:14:ASP:O	43:BN:52:ASP:HB3	2.07	0.54
44:BO:105:ARG:HD3	44:BO:105:ARG:H	1.72	0.54
1:AA:501:C:H2'	1:AA:502:A:H8	1.72	0.54
3:AC:19:SER:HB2	3:AC:39:ARG:NH2	2.21	0.54
4:AD:63:ILE:HG23	4:AD:64:TYR:HD1	1.71	0.54
4:AD:123:MET:HB3	4:AD:128:VAL:HA	1.87	0.54
23:AW:432:SER:O	23:AW:434:ASN:N	2.34	0.54
23:AW:472:ARG:HA	23:AW:473:TRP:HB2	1.89	0.54
24:B0:47:GLY:HA3	24:B0:80:SER:HB3	1.88	0.54
33:BA:580:U:H2'	33:BA:581:C:H6	1.72	0.54
33:BA:704:G:H2'	33:BA:726:G:N2	2.20	0.54
33:BA:1444:G:H2'	33:BA:1445:G:C8	2.42	0.54
33:BA:1654:A:O2'	36:BD:118:PHE:CG	2.58	0.54
53:BX:29:THR:CA	53:BX:86:THR:HA	2.34	0.54
1:AA:441:A:H1'	1:AA:497:G:N2	2.22	0.54
2:AB:95:TRP:CZ2	2:AB:100:LEU:HD23	2.43	0.54
14:AN:98:ALA:HB1	14:AN:100:TRP:HZ3	1.72	0.54
23:AW:473:TRP:HA	23:AW:524:HIS:O	2.08	0.54
23:AW:479:ALA:O	23:AW:481:LYS:N	2.39	0.54
33:BA:572:A:H5''	33:BA:573:U:OP2	2.07	0.54
33:BA:1024:G:C8	33:BA:1025:G:H2'	2.41	0.54
33:BA:2149:U:H3'	33:BA:2150:C:O4'	2.07	0.54
33:BA:2857:G:N2	33:BA:2860:A:OP2	2.39	0.54
36:BD:40:LEU:H	36:BD:40:LEU:HD12	1.72	0.54
39:BG:83:THR:HA	39:BG:84:LYS:NZ	2.23	0.54
2:AB:71:THR:HG21	2:AB:94:ARG:HD3	1.88	0.54
12:AL:78:VAL:HB	23:AW:407:LEU:HD12	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AQ:46:HIS:HA	17:AQ:70:LYS:HE3	1.89	0.54
24:B0:16:GLU:HG3	33:BA:2356:U:H4'	1.89	0.54
33:BA:251:A:OP1	45:BP:58:TYR:OH	2.20	0.54
33:BA:2052:A:C8	36:BD:146:ILE:HD11	2.42	0.54
33:BA:2064:C:H2'	33:BA:2065:C:C6	2.43	0.54
36:BD:68:PHE:HB3	36:BD:73:VAL:HG12	1.90	0.54
44:BO:18:ARG:HB2	44:BO:45:GLU:HG2	1.90	0.54
55:BZ:80:HIS:HB3	55:BZ:83:LYS:O	2.08	0.54
3:AC:146:LYS:HB2	3:AC:202:PHE:CD2	2.43	0.54
33:BA:404:A:H1'	33:BA:405:U:OP2	2.08	0.54
33:BA:691:C:H4'	35:BC:42:ARG:HH12	1.72	0.54
33:BA:1236:G:O2'	33:BA:1237:A:H8	1.91	0.54
34:BB:112:G:H2'	34:BB:113:C:H6	1.72	0.54
50:BU:63:ARG:HH12	50:BU:96:ASP:HB2	1.71	0.54
1:AA:892:A:O2'	1:AA:1415:G:H4'	2.07	0.54
1:AA:1370:G:O5'	9:AI:110:VAL:HG21	2.08	0.54
7:AG:4:ARG:NH1	7:AG:5:VAL:O	2.41	0.54
14:AN:82:LYS:HE2	14:AN:82:LYS:HA	1.88	0.54
23:AW:439:GLY:HA2	23:AW:440:ALA:CB	2.33	0.54
33:BA:1187:G:HO2'	33:BA:1188:U:H6	1.55	0.54
33:BA:1506:U:H2'	33:BA:1507:C:C6	2.43	0.54
33:BA:1970:A:H5'	33:BA:1972:G:H1'	1.89	0.54
40:BH:17:GLU:HG2	40:BH:88:HIS:CE1	2.42	0.54
40:BH:25:ALA:HB3	40:BH:85:SER:HG	1.64	0.54
40:BH:57:ASN:C	40:BH:59:LEU:N	2.61	0.54
1:AA:404:G:H2'	1:AA:405:U:H6	1.72	0.54
3:AC:13:ILE:O	3:AC:15:LYS:N	2.40	0.54
23:AW:91:GLY:O	23:AW:92:HIS:HB2	2.08	0.54
33:BA:307:G:N2	33:BA:309:A:H3'	2.22	0.54
33:BA:611:C:H2'	33:BA:612:G:O4'	2.08	0.54
33:BA:923:G:H2'	33:BA:924:G:C8	2.42	0.54
34:BB:66:A:OP2	34:BB:108:A:N6	2.40	0.54
35:BC:76:VAL:HG22	35:BC:96:LYS:HZ2	1.71	0.54
36:BD:4:LEU:HD23	36:BD:29:VAL:HG11	1.89	0.54
38:BF:35:LEU:HA	38:BF:153:ILE:HA	1.90	0.54
40:BH:28:ALA:H	40:BH:111:ALA:HB2	1.70	0.54
40:BH:32:GLY:HA2	40:BH:108:VAL:HG22	1.89	0.54
47:BR:85:PRO:HA	47:BR:88:ALA:HB2	1.90	0.54
53:BX:43:ILE:HD11	53:BX:58:VAL:HG21	1.88	0.54
1:AA:235:C:H1'	17:AQ:62:GLU:OE2	2.08	0.54
1:AA:720:C:H5''	18:AR:40:PRO:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:143:SER:HB3	4:AD:178:GLU:HB2	1.90	0.54
5:AE:56:PRO:O	5:AE:59:ILE:HG13	2.07	0.54
12:AL:78:VAL:HG21	23:AW:407:LEU:CG	2.37	0.54
23:AW:15:THR:OG1	23:AW:362:GLY:O	2.13	0.54
33:BA:692:C:H2'	33:BA:693:A:C8	2.43	0.54
33:BA:1969:A:O2'	33:BA:1972:G:N3	2.34	0.54
36:BD:9:VAL:HG13	36:BD:26:VAL:O	2.07	0.54
37:BE:124:PHE:O	37:BE:125:SER:HB2	2.08	0.54
39:BG:120:ILE:HD11	39:BG:132:LEU:HD12	1.89	0.54
44:BO:104:THR:HB	44:BO:106:GLU:OE1	2.08	0.54
1:AA:514:C:H2'	1:AA:515:G:C8	2.42	0.54
1:AA:718:A:H62	18:AR:62:ARG:HH12	1.53	0.54
3:AC:183:TYR:HA	3:AC:199:VAL:O	2.08	0.54
19:AS:62:THR:HG22	19:AS:63:ASP:H	1.72	0.54
23:AW:20:SER:O	23:AW:122:ARG:NH1	2.41	0.54
23:AW:59:TRP:HE1	23:AW:69:SER:CB	2.16	0.54
24:B0:37:VAL:HG12	24:B0:38:ARG:N	2.23	0.54
33:BA:692:C:H2'	33:BA:693:A:H8	1.73	0.54
33:BA:846:U:O2'	33:BA:847:U:H5''	2.07	0.54
33:BA:1061:U:H6	41:BI:9:LYS:HG3	1.73	0.54
33:BA:1252:G:H1'	50:BU:32:ARG:HH22	1.71	0.54
33:BA:1270:C:H5''	33:BA:1271:G:H5'	1.89	0.54
36:BD:146:ILE:HA	36:BD:159:LYS:HE2	1.89	0.54
45:BP:96:LYS:HD3	45:BP:103:ILE:HA	1.90	0.54
48:BS:49:VAL:HG21	48:BS:82:ALA:HA	1.89	0.54
51:BV:10:LYS:NZ	51:BV:23:GLU:OE1	2.38	0.54
1:AA:369:G:N2	1:AA:393:A:H1'	2.23	0.54
1:AA:793:U:O4	1:AA:1517:G:H8	1.90	0.54
1:AA:1190:G:H5'	3:AC:175:HIS:NE2	2.23	0.54
9:AI:24:ASN:HA	9:AI:58:GLU:O	2.08	0.54
23:AW:129:VAL:O	23:AW:132:LEU:HB2	2.09	0.54
23:AW:310:LYS:O	23:AW:311:HIS:ND1	2.41	0.54
23:AW:347:THR:O	23:AW:354:SER:HB3	2.08	0.54
23:AW:472:ARG:HG3	23:AW:504:ILE:N	2.22	0.54
33:BA:140:C:O2	33:BA:140:C:H2'	2.07	0.54
33:BA:1656:C:H2'	33:BA:1657:U:H6	1.73	0.54
33:BA:2415:G:H4'	45:BP:66:PHE:HB2	1.89	0.54
35:BC:66:PHE:HB3	35:BC:150:GLY:O	2.08	0.54
47:BR:36:THR:OG1	47:BR:37:THR:N	2.40	0.54
50:BU:91:ARG:NH2	50:BU:93:ILE:HG12	2.20	0.54
1:AA:680:C:H2'	1:AA:681:A:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:148:ILE:HG13	3:AC:201:ILE:HG12	1.90	0.53
8:AH:40:LYS:HG3	8:AH:47:ASP:HA	1.90	0.53
33:BA:993:G:OP2	50:BU:50:ARG:NH2	2.41	0.53
38:BF:134:GLN:C	38:BF:136:ILE:H	2.10	0.53
47:BR:24:MET:HG2	47:BR:44:LEU:HD22	1.89	0.53
51:BV:2:TYR:H	51:BV:42:ALA:HB3	1.73	0.53
1:AA:129:A:O2'	1:AA:130:A:H8	1.91	0.53
14:AN:63:CYS:HB2	14:AN:79:SER:OG	2.07	0.53
16:AP:35:ARG:HH21	16:AP:51:ARG:HH12	1.56	0.53
31:B7:11:LYS:NZ	33:BA:247:G:O6	2.28	0.53
33:BA:215:G:C4'	33:BA:216:A:H4'	2.38	0.53
33:BA:630:G:N2	33:BA:633:A:OP2	2.37	0.53
33:BA:2276:G:OP2	46:BQ:85:GLY:N	2.40	0.53
33:BA:2322:A:H2'	33:BA:2323:G:O4'	2.08	0.53
41:BI:32:VAL:HG22	41:BI:66:PHE:CD2	2.44	0.53
51:BV:38:VAL:HG22	51:BV:54:VAL:HG22	1.90	0.53
1:AA:1241:G:H2'	1:AA:1242:G:C8	2.40	0.53
1:AA:1493:A:C2'	1:AA:1494:G:OP1	2.57	0.53
11:AK:108:ASN:HB3	21:AU:6:ARG:HG2	1.89	0.53
12:AL:30:ARG:HH11	23:AW:408:LYS:CG	2.19	0.53
20:AT:8:LYS:O	20:AT:12:GLN:HB2	2.08	0.53
20:AT:66:ILE:O	20:AT:70:LYS:HB3	2.08	0.53
23:AW:49:ARG:NH2	33:BA:2664:G:O6	2.41	0.53
31:B7:12:ARG:HD3	45:BP:61:LEU:O	2.08	0.53
31:B7:54:LEU:HG	31:B7:58:ILE:HD11	1.90	0.53
35:BC:251:THR:HG22	35:BC:252:LYS:H	1.73	0.53
1:AA:1386:G:H2'	1:AA:1387:G:H8	1.72	0.53
11:AK:93:GLU:O	11:AK:96:ILE:HG12	2.09	0.53
15:AO:6:ALA:O	15:AO:10:ILE:HG12	2.09	0.53
23:AW:26:LYS:O	23:AW:29:ILE:HG22	2.09	0.53
33:BA:324:A:N6	33:BA:338:G:O2'	2.39	0.53
33:BA:2046:G:H2'	33:BA:2047:C:H6	1.73	0.53
33:BA:2197:U:O2'	33:BA:2198:A:H2'	2.09	0.53
43:BN:93:ILE:O	43:BN:97:PRO:HG3	2.08	0.53
1:AA:908:A:H2'	1:AA:909:A:C8	2.44	0.53
6:AF:26:THR:HG22	6:AF:36:ILE:HG21	1.91	0.53
33:BA:1225:G:C2	33:BA:1226:A:C2	2.97	0.53
33:BA:2314:A:H2'	33:BA:2315:G:C8	2.43	0.53
33:BA:2847:U:H2'	33:BA:2848:G:O4'	2.09	0.53
36:BD:125:TRP:CG	36:BD:160:LYS:HB3	2.44	0.53
40:BH:144:LYS:HB2	40:BH:148:ALA:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BI:135:MET:HG2	41:BI:137:LEU:HG	1.91	0.53
43:BN:49:ASP:OD2	43:BN:121:LYS:NZ	2.32	0.53
44:BO:113:MET:O	44:BO:116:ILE:HG13	2.09	0.53
46:BQ:74:THR:HG21	46:BQ:86:LYS:HE3	1.89	0.53
42:BJ:15:SER:HB3	42:BM:11:VAL:HG12	1.90	0.53
45:BP:30:THR:O	45:BP:33:ARG:HG2	2.09	0.53
49:BT:33:GLU:HB2	49:BT:38:ARG:HH11	1.73	0.53
1:AA:1237:C:H3'	1:AA:1238:A:H5'	1.90	0.53
12:AL:34:THR:HG22	12:AL:35:ARG:HG2	1.89	0.53
18:AR:57:ALA:HA	18:AR:60:ARG:HD3	1.91	0.53
21:AU:33:ARG:HE	21:AU:34:ARG:HG3	1.74	0.53
23:AW:45:THR:N	23:AW:56:LYS:O	2.41	0.53
23:AW:522:GLN:HB2	23:AW:523:PHE:CB	2.37	0.53
31:B7:3:ILE:HD11	33:BA:592:A:N3	2.23	0.53
33:BA:1914:C:C4	33:BA:1915:U:C4	2.96	0.53
33:BA:2052:A:OP1	36:BD:145:SER:HA	2.08	0.53
33:BA:2060:A:H3'	37:BE:63:LYS:NZ	2.21	0.53
33:BA:2224:G:H4'	33:BA:2226:C:C2	2.43	0.53
35:BC:118:GLY:O	35:BC:129:LEU:HD23	2.09	0.53
49:BT:50:ARG:CD	49:BT:56:SER:HB3	2.29	0.53
50:BU:86:SER:HB2	51:BV:50:GLY:O	2.09	0.53
53:BX:83:ALA:HB1	53:BX:85:VAL:HG23	1.91	0.53
1:AA:373:A:H1'	1:AA:481:G:H1'	1.90	0.53
1:AA:1036:A:H2'	1:AA:1037:C:C4	2.44	0.53
9:AI:83:THR:HG21	9:AI:102:PHE:HB3	1.90	0.53
21:AU:52:VAL:HG13	21:AU:53:LYS:H	1.73	0.53
27:B3:9:THR:HB	27:B3:53:MET:O	2.09	0.53
27:B3:11:SER:OG	27:B3:13:ILE:HG12	2.09	0.53
33:BA:686:U:H2'	33:BA:788:A:N1	2.24	0.53
33:BA:1056:G:H4'	40:BH:34:THR:CG2	2.38	0.53
33:BA:1665:A:H5''	44:BO:66:LYS:HG3	1.90	0.53
33:BA:1918:A:O2'	33:BA:1920:C:N4	2.42	0.53
33:BA:2329:U:H2'	33:BA:2330:G:C8	2.43	0.53
39:BG:84:LYS:CB	39:BG:132:LEU:H	2.21	0.53
40:BH:44:ALA:HA	40:BH:48:ALA:HB3	1.91	0.53
51:BV:66:HIS:CD2	51:BV:66:HIS:H	2.26	0.53
1:AA:978:A:HO2'	1:AA:1322:C:H5	1.55	0.53
23:AW:300:VAL:O	23:AW:301:PHE:HB3	2.09	0.53
33:BA:118:A:C8	33:BA:119:A:N7	2.77	0.53
33:BA:475:C:C4	33:BA:481:G:O6	2.62	0.53
33:BA:1279:G:H4'	47:BR:31:HIS:CD2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:380:G:C2	1:AA:384:G:C6	2.97	0.53
1:AA:564:C:C4	1:AA:565:U:C4	2.97	0.53
3:AC:36:PHE:HA	3:AC:39:ARG:HD2	1.91	0.53
3:AC:179:ALA:HB1	3:AC:202:PHE:HE1	1.73	0.53
33:BA:544:C:H5'	33:BA:545:U:OP2	2.09	0.53
33:BA:859:G:O2'	33:BA:860:U:P	2.67	0.53
36:BD:106:LYS:HB3	36:BD:206:ALA:CB	2.37	0.53
36:BD:175:LEU:HD22	36:BD:190:LYS:O	2.09	0.53
38:BF:56:LEU:HD13	38:BF:88:VAL:HG23	1.90	0.53
1:AA:254:G:OP1	17:AQ:67:SER:OG	2.24	0.52
1:AA:514:C:H2'	1:AA:515:G:H8	1.74	0.52
1:AA:812:G:HO2'	1:AA:813:U:P	2.28	0.52
1:AA:816:A:OP1	1:AA:1526:G:O2'	2.21	0.52
1:AA:1123:U:O2'	10:AJ:39:PRO:O	2.26	0.52
23:AW:472:ARG:HG3	23:AW:504:ILE:CA	2.39	0.52
32:B8:4:ARG:HB2	33:BA:2466:C:OP1	2.09	0.52
34:BB:5:U:H2'	34:BB:6:G:H8	1.70	0.52
34:BB:56:G:H5''	34:BB:57:A:OP1	2.09	0.52
35:BC:159:THR:O	35:BC:194:VAL:HG12	2.08	0.52
40:BH:57:ASN:O	40:BH:59:LEU:N	2.42	0.52
47:BR:73:ASN:HA	47:BR:76:VAL:HG12	1.91	0.52
23:AW:408:LYS:HB3	23:AW:409:GLN:O	2.08	0.52
33:BA:394:C:H2'	33:BA:395:U:C6	2.44	0.52
33:BA:755:U:H2'	33:BA:756:A:C8	2.44	0.52
33:BA:1165:A:H2'	33:BA:1166:G:C8	2.40	0.52
33:BA:1290:C:H2'	33:BA:1291:C:C6	2.44	0.52
33:BA:1666:G:H1'	44:BO:3:GLN:OE1	2.09	0.52
33:BA:1936:A:C2	33:BA:1943:U:H5	2.27	0.52
35:BC:161:VAL:HG21	35:BC:175:LEU:HD12	1.90	0.52
36:BD:114:LYS:O	36:BD:114:LYS:HE3	2.08	0.52
54:BY:6:ARG:O	54:BY:24:VAL:HB	2.10	0.52
1:AA:1257:A:H4'	1:AA:1258:G:OP2	2.10	0.52
1:AA:1347:G:O2'	1:AA:1348:U:P	2.67	0.52
33:BA:1962:C:O2'	33:BA:1964:G:OP2	2.26	0.52
33:BA:2104:C:H42	33:BA:2185:U:H3	1.58	0.52
33:BA:2485:G:H5''	46:BQ:45:GLN:NE2	2.24	0.52
34:BB:24:G:O2'	34:BB:27:C:N4	2.42	0.52
37:BE:29:HIS:CE1	45:BP:8:PRO:HD3	2.45	0.52
44:BO:71:ARG:HB3	44:BO:72:PRO:HD2	1.90	0.52
48:BS:3:LYS:HG3	48:BS:4:LYS:H	1.75	0.52
49:BT:61:ARG:HG2	49:BT:70:GLU:HG2	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:404:G:H4'	1:AA:439:U:H3	1.75	0.52
1:AA:926:G:N2	22:AV:15:A:H4'	2.24	0.52
1:AA:1347:G:H22	1:AA:1374:A:P	2.32	0.52
33:BA:559:G:OP1	43:BN:111:LYS:HE3	2.10	0.52
33:BA:1022:G:H22	33:BA:1142:A:H2	1.51	0.52
33:BA:2325:G:C6	33:BA:2326:C:N4	2.77	0.52
38:BF:34:THR:HG22	38:BF:89:THR:HA	1.90	0.52
2:AB:125:PHE:N	2:AB:125:PHE:HD2	2.07	0.52
25:B1:16:ASN:HD22	33:BA:2081:U:H5''	1.75	0.52
33:BA:171:U:H2'	33:BA:172:A:H8	1.74	0.52
33:BA:1095:A:C2	41:BI:29:GLN:HB3	2.44	0.52
33:BA:1266:G:O2'	33:BA:2012:G:N1	2.38	0.52
1:AA:1227:A:O2'	13:AM:114:PRO:HG2	2.09	0.52
11:AK:57:SER:O	11:AK:90:PRO:HG3	2.09	0.52
33:BA:2013:A:H4'	52:BW:96:ILE:HG22	1.92	0.52
33:BA:2046:G:H2'	33:BA:2047:C:C6	2.45	0.52
33:BA:2848:G:H2'	33:BA:2867:G:N2	2.23	0.52
39:BG:106:LEU:HD13	39:BG:151:ARG:HB2	1.92	0.52
47:BR:48:VAL:HA	47:BR:51:LEU:HD22	1.91	0.52
4:AD:116:LEU:HB3	4:AD:121:ALA:HB3	1.92	0.52
6:AF:3:HIS:HB3	6:AF:95:ALA:HB2	1.92	0.52
10:AJ:12:ALA:HB3	10:AJ:18:ILE:HG12	1.92	0.52
23:AW:499:ASP:O	23:AW:500:ASN:HB3	2.10	0.52
24:B0:23:LYS:HE2	33:BA:923:G:N3	2.24	0.52
33:BA:974:G:C6	33:BA:989:G:C6	2.98	0.52
33:BA:1539:U:H2'	33:BA:1540:G:H8	1.75	0.52
33:BA:2683:C:O2	44:BO:70:ARG:NH2	2.33	0.52
37:BE:60:TRP:CZ2	37:BE:70:SER:HB3	2.44	0.52
39:BG:3:VAL:O	39:BG:68:ARG:HG3	2.10	0.52
39:BG:84:LYS:HB3	39:BG:132:LEU:O	2.10	0.52
40:BH:144:LYS:HD2	40:BH:148:ALA:HB2	1.91	0.52
51:BV:66:HIS:HB3	51:BV:94:THR:HG22	1.91	0.52
1:AA:77:A:H62	1:AA:90:C:N4	2.06	0.52
1:AA:109:A:C6	1:AA:326:G:C6	2.98	0.52
1:AA:1145:A:O2'	1:AA:1146:A:O5'	2.28	0.52
1:AA:1225:A:H2'	1:AA:1225:A:N3	2.23	0.52
3:AC:159:ALA:HB1	3:AC:161:ILE:HD13	1.92	0.52
4:AD:84:ASN:HB3	4:AD:87:GLU:HG2	1.92	0.52
7:AG:71:THR:HG22	7:AG:72:VAL:HG13	1.92	0.52
10:AJ:36:VAL:HG22	10:AJ:76:ILE:HG12	1.92	0.52
23:AW:521:VAL:HG22	23:AW:522:GLN:HG2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B1:7:THR:HG21	25:B1:53:LYS:HD3	1.91	0.52
33:BA:1060:U:O4'	33:BA:1062:G:H5'	2.09	0.52
34:BB:37:C:C5	34:BB:38:C:C4	2.98	0.52
34:BB:112:G:H2'	34:BB:113:C:C6	2.45	0.52
36:BD:25:THR:HG21	36:BD:193:VAL:HG22	1.92	0.52
50:BU:86:SER:O	51:BV:51:VAL:HA	2.09	0.52
1:AA:579:A:O2'	15:AO:53:ARG:NH1	2.42	0.52
10:AJ:7:ARG:HA	10:AJ:75:ASP:HA	1.91	0.52
25:B1:76:LYS:HG3	25:B1:77:TYR:H	1.75	0.52
26:B2:46:VAL:HA	26:B2:49:ASP:HB2	1.91	0.52
33:BA:483:A:C8	54:BY:44:HIS:CD2	2.97	0.52
33:BA:948:C:H1'	33:BA:984:A:O2'	2.10	0.52
33:BA:2788:C:O2'	33:BA:2809:A:N3	2.39	0.52
1:AA:664:G:H22	1:AA:741:G:H1	1.58	0.52
5:AE:22:LYS:HB3	5:AE:29:ILE:HG23	1.92	0.52
7:AG:24:LYS:O	7:AG:28:ILE:HG12	2.10	0.52
33:BA:270:A:N1	33:BA:369:U:O2'	2.34	0.52
33:BA:1141:U:H4'	33:BA:1142:A:O4'	2.10	0.52
33:BA:2105:U:C4	33:BA:2106:U:C4	2.98	0.52
33:BA:2339:C:H2'	33:BA:2340:A:C8	2.45	0.52
35:BC:244:VAL:HG12	35:BC:250:GLN:HA	1.92	0.52
38:BF:111:ARG:NH1	38:BF:133:GLU:OE2	2.43	0.52
40:BH:7:ASP:O	40:BH:11:ILE:HG12	2.09	0.52
40:BH:102:ALA:O	40:BH:107:GLU:HB2	2.09	0.52
40:BH:129:LEU:HB3	40:BH:132:TYR:CE1	2.44	0.52
42:BJ:26:MET:HE2	42:BJ:29:LYS:HD3	1.91	0.52
50:BU:60:TRP:O	50:BU:64:ILE:HG12	2.10	0.52
51:BV:4:VAL:HG23	51:BV:39:LEU:HG	1.92	0.52
1:AA:607:A:H2'	1:AA:608:A:H8	1.75	0.51
1:AA:955:U:H3	1:AA:1225:A:N6	2.07	0.51
1:AA:1126:U:O2	1:AA:1126:U:H2'	2.10	0.51
9:AI:9:GLY:N	9:AI:84:ARG:HH12	2.08	0.51
21:AU:33:ARG:NE	21:AU:34:ARG:HG3	2.25	0.51
23:AW:59:TRP:CD2	23:AW:64:LYS:HD3	2.45	0.51
23:AW:290:GLU:HB2	23:AW:293:GLU:HG3	1.92	0.51
23:AW:369:ASN:ND2	23:AW:373:ILE:H	2.08	0.51
33:BA:834:G:C6	33:BA:835:C:C4	2.98	0.51
33:BA:1172:C:C4	33:BA:1173:U:H1'	2.45	0.51
33:BA:1313:U:H2'	33:BA:1610:A:C2	2.45	0.51
33:BA:2898:U:O2'	43:BN:134:ALA:O	2.24	0.51
36:BD:47:ALA:HA	36:BD:84:LEU:HG	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:BV:20:VAL:HG22	51:BV:98:ILE:HD11	1.91	0.51
1:AA:1479:C:H2'	1:AA:1480:A:H8	1.76	0.51
10:AJ:10:LEU:HD11	10:AJ:98:VAL:HG12	1.92	0.51
12:AL:2:THR:HB	12:AL:5:GLN:HB2	1.92	0.51
16:AP:35:ARG:HH21	16:AP:51:ARG:NH1	2.07	0.51
23:AW:470:THR:HA	23:AW:471:ALA:HB3	1.91	0.51
25:B1:60:LYS:HE3	33:BA:372:G:N9	2.25	0.51
26:B2:49:ASP:O	26:B2:53:VAL:HG23	2.09	0.51
33:BA:404:A:H4'	33:BA:405:U:O5'	2.10	0.51
34:BB:65:U:H3'	34:BB:108:A:N6	2.26	0.51
35:BC:157:ALA:HB1	35:BC:196:ASN:HB3	1.92	0.51
36:BD:68:PHE:HB3	36:BD:73:VAL:HA	1.90	0.51
38:BF:134:GLN:OE1	38:BF:134:GLN:N	2.38	0.51
41:BI:63:ASP:OD1	41:BI:63:ASP:N	2.43	0.51
54:BY:94:PHE:HA	54:BY:101:THR:HA	1.92	0.51
1:AA:1096:C:H2'	1:AA:1097:C:C6	2.46	0.51
1:AA:1510:C:C2	1:AA:1526:G:N2	2.78	0.51
10:AJ:19:ASP:OD2	10:AJ:72:ARG:NH2	2.43	0.51
23:AW:173:ILE:HG21	23:AW:219:VAL:HG11	1.93	0.51
31:B7:22:LYS:HA	31:B7:47:ALA:O	2.10	0.51
1:AA:71:A:H61	1:AA:99:C:H1'	1.76	0.51
1:AA:114:U:H2'	1:AA:115:G:C8	2.45	0.51
15:AO:70:LYS:HA	15:AO:77:TYR:HB2	1.91	0.51
17:AQ:15:LYS:HZ1	17:AQ:17:GLU:HB2	1.75	0.51
24:B0:9:THR:HG23	24:B0:10:ARG:HD3	1.92	0.51
33:BA:320:A:H4'	33:BA:322:A:N7	2.26	0.51
33:BA:675:A:C4	33:BA:804:A:C2	2.99	0.51
33:BA:1026:G:H2'	33:BA:1027:A:C8	2.45	0.51
33:BA:1838:C:H4'	33:BA:1839:G:C8	2.46	0.51
33:BA:2233:U:H2'	33:BA:2234:G:H8	1.74	0.51
33:BA:2267:A:H5''	33:BA:2268:A:H5'	1.92	0.51
36:BD:176:ASP:OD2	36:BD:176:ASP:N	2.42	0.51
38:BF:37:MET:HG2	38:BF:151:LEU:HB3	1.91	0.51
43:BN:74:TYR:HB2	43:BN:87:ALA:O	2.10	0.51
1:AA:1192:C:OP2	3:AC:3:LYS:NZ	2.33	0.51
1:AA:1513:A:H2'	1:AA:1514:G:H8	1.74	0.51
2:AB:125:PHE:N	2:AB:125:PHE:CD2	2.78	0.51
12:AL:41:PRO:HA	12:AL:89:LEU:HD13	1.92	0.51
12:AL:78:VAL:CB	23:AW:407:LEU:HD12	2.40	0.51
13:AM:105:ALA:HB3	13:AM:109:LYS:HD2	1.93	0.51
23:AW:290:GLU:N	23:AW:293:GLU:OE2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:B5:7:LYS:HE3	31:B7:33:THR:HG21	1.93	0.51
36:BD:97:SER:OG	36:BD:98:VAL:N	2.43	0.51
1:AA:129:A:HO2'	1:AA:130:A:H8	1.57	0.51
1:AA:216:U:H2'	1:AA:217:C:C6	2.46	0.51
1:AA:1203:C:H2'	1:AA:1204:A:C8	2.45	0.51
12:AL:23:LEU:C	12:AL:25:ALA:H	2.13	0.51
16:AP:61:VAL:O	16:AP:64:GLY:N	2.42	0.51
28:B4:47:TYR:HA	28:B4:52:LYS:HA	1.93	0.51
33:BA:601:C:O2'	33:BA:605:G:OP1	2.23	0.51
33:BA:953:G:H5''	46:BQ:16:ARG:NH1	2.26	0.51
33:BA:1219:U:H2'	33:BA:1220:G:C8	2.45	0.51
33:BA:2747:G:O6	33:BA:2755:C:H5''	2.10	0.51
34:BB:66:A:H61	34:BB:107:G:H2'	1.75	0.51
35:BC:144:GLU:HB2	35:BC:187:CYS:HB3	1.91	0.51
39:BG:70:LEU:O	39:BG:74:MET:HG3	2.10	0.51
40:BH:138:ARG:HA	40:BH:141:ALA:HB3	1.93	0.51
50:BU:24:TYR:O	50:BU:27:ARG:HB2	2.10	0.51
55:BZ:61:LEU:HD11	55:BZ:74:ALA:HB2	1.93	0.51
1:AA:403:C:H2'	1:AA:404:G:H8	1.76	0.51
1:AA:976:G:OP1	14:AN:70:HIS:ND1	2.31	0.51
1:AA:1005:A:H2'	1:AA:1006:G:O4'	2.11	0.51
1:AA:1239:A:H1'	1:AA:1241:G:C4	2.45	0.51
1:AA:1314:C:N4	19:AS:3:SER:O	2.40	0.51
1:AA:1437:A:H2'	1:AA:1438:G:H8	1.76	0.51
3:AC:32:LEU:HD21	14:AN:92:ILE:HG12	1.92	0.51
4:AD:71:PHE:O	4:AD:74:TYR:HB2	2.11	0.51
25:B1:5:GLN:HG3	25:B1:49:ARG:O	2.10	0.51
33:BA:883:G:O3'	33:BA:896:A:N6	2.40	0.51
33:BA:900:A:HO2'	33:BA:901:C:P	2.30	0.51
33:BA:1993:U:H4'	36:BD:133:THR:CG2	2.40	0.51
38:BF:10:GLU:O	38:BF:12:VAL:N	2.31	0.51
40:BH:58:THR:C	40:BH:60:LEU:N	2.63	0.51
41:BI:72:THR:HG21	41:BI:112:LYS:HB3	1.92	0.51
50:BU:91:ARG:HH11	51:BV:10:LYS:HB3	1.76	0.51
55:BZ:72:VAL:HG21	55:BZ:91:PHE:HB3	1.92	0.51
3:AC:5:HIS:ND1	14:AN:88:MET:HB3	2.25	0.51
7:AG:30:MET:SD	7:AG:35:LYS:HB2	2.50	0.51
10:AJ:57:VAL:HG22	10:AJ:58:ASN:H	1.76	0.51
12:AL:34:THR:N	12:AL:53:ARG:O	2.43	0.51
23:AW:11:ALA:O	23:AW:14:ARG:NH2	2.43	0.51
23:AW:64:LYS:HG2	23:AW:70:ILE:HB	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:B4:39:ARG:HG3	33:BA:2884:U:O4	2.10	0.51
33:BA:629:G:N3	33:BA:639:U:O2'	2.42	0.51
33:BA:880:G:O6	33:BA:898:C:N3	2.44	0.51
33:BA:955:U:H5''	46:BQ:86:LYS:HD2	1.91	0.51
33:BA:2134:A:O2'	33:BA:2135:A:H8	1.93	0.51
34:BB:60:C:H2'	34:BB:61:G:H8	1.76	0.51
34:BB:87:U:H5'	34:BB:88:C:OP2	2.10	0.51
36:BD:136:ASN:OD1	36:BD:139:SER:HB2	2.10	0.51
43:BN:76:HIS:CE1	43:BN:85:LYS:HB2	2.45	0.51
1:AA:1354:U:H2'	1:AA:1355:G:C8	2.46	0.51
3:AC:6:PRO:HB3	3:AC:174:LEU:CD1	2.41	0.51
5:AE:153:ALA:HA	5:AE:156:ARG:HB2	1.92	0.51
21:AU:24:LYS:HA	21:AU:28:LEU:HD12	1.93	0.51
23:AW:437:ILE:HD12	23:AW:504:ILE:HD13	1.92	0.51
24:B0:71:LYS:HB3	24:B0:73:PRO:HD2	1.93	0.51
33:BA:587:C:H5'	37:BE:85:PHE:CE2	2.46	0.51
33:BA:832:U:H2'	33:BA:833:A:C8	2.46	0.51
33:BA:2470:G:OP1	46:BQ:55:ARG:NH1	2.44	0.51
36:BD:122:VAL:HA	36:BD:127:PHE:N	2.20	0.51
40:BH:23:LEU:HG	40:BH:24:SER:H	1.76	0.51
1:AA:1308:U:OP1	13:AM:96:VAL:N	2.33	0.51
8:AH:45:ILE:HD13	8:AH:60:LEU:HD22	1.92	0.51
24:B0:39:GLN:C	24:B0:41:GLY:N	2.64	0.51
33:BA:742:A:H2'	33:BA:743:A:C8	2.46	0.51
33:BA:1181:U:H2'	33:BA:1182:G:H8	1.75	0.51
33:BA:1705:A:N6	33:BA:1706:C:H42	2.09	0.51
33:BA:1906:G:C8	33:BA:1929:G:H2'	2.45	0.51
33:BA:1930:G:H22	33:BA:1969:A:P	2.34	0.51
33:BA:2728:U:H5'	44:BO:70:ARG:NH2	2.26	0.51
40:BH:136:ILE:HA	40:BH:139:LEU:HD12	1.93	0.51
1:AA:203:G:H1'	1:AA:465:A:H61	1.76	0.50
1:AA:1180:A:OP2	9:AI:98:ARG:NH2	2.40	0.50
2:AB:125:PHE:HD2	2:AB:125:PHE:H	1.59	0.50
11:AK:86:LYS:HB2	11:AK:112:VAL:HG23	1.94	0.50
11:AK:93:GLU:OE2	11:AK:97:ARG:NH2	2.44	0.50
24:B0:17:ALA:HA	24:B0:35:ILE:HG23	1.92	0.50
24:B0:23:LYS:HZ3	33:BA:923:G:H21	1.57	0.50
32:B8:10:LEU:HD12	32:B8:33:HIS:CD2	2.46	0.50
33:BA:884:U:O5'	33:BA:884:U:H6	1.93	0.50
33:BA:1056:G:O5'	33:BA:1056:G:C8	2.59	0.50
33:BA:1082:U:C5'	41:BI:118:GLY:HA2	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BB:40:U:N3	34:BB:44:G:OP2	2.42	0.50
34:BB:91:C:H2'	34:BB:92:C:C6	2.46	0.50
35:BC:166:ARG:HB3	35:BC:171:VAL:HG22	1.93	0.50
40:BH:144:LYS:HB3	40:BH:147:SER:OG	2.11	0.50
45:BP:130:GLY:O	45:BP:133:ALA:HB3	2.10	0.50
51:BV:39:LEU:HA	51:BV:49:ILE:HG21	1.93	0.50
54:BY:90:LYS:HB2	54:BY:92:VAL:HG23	1.93	0.50
1:AA:59:A:N6	1:AA:331:G:H1'	2.26	0.50
1:AA:362:G:N7	23:AW:408:LYS:NZ	2.59	0.50
1:AA:672:U:H2'	1:AA:673:A:C8	2.46	0.50
1:AA:692:U:H2'	1:AA:694:A:OP2	2.11	0.50
1:AA:818:G:O2'	1:AA:819:A:H5'	2.11	0.50
1:AA:908:A:H2'	1:AA:909:A:H8	1.76	0.50
1:AA:1048:G:O3'	1:AA:1049:U:H3'	2.12	0.50
14:AN:19:TYR:O	14:AN:22:LYS:HB3	2.12	0.50
33:BA:1657:U:H2'	33:BA:1658:C:C6	2.46	0.50
33:BA:2148:G:H2'	33:BA:2149:U:O5'	2.10	0.50
38:BF:41:GLU:HB2	38:BF:48:LEU:HD23	1.93	0.50
39:BG:120:ILE:HD13	39:BG:143:VAL:HG21	1.93	0.50
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.47	0.50
1:AA:1478:U:H2'	1:AA:1479:C:C6	2.47	0.50
5:AE:148:SER:CB	5:AE:151:MET:HB2	2.41	0.50
33:BA:479:A:H4'	33:BA:480:A:OP1	2.11	0.50
33:BA:864:G:O2'	33:BA:914:G:O6	2.29	0.50
33:BA:2073:C:H5''	35:BC:227:VAL:HG12	1.92	0.50
36:BD:8:LYS:NZ	36:BD:193:VAL:O	2.35	0.50
36:BD:172:VAL:HG12	36:BD:173:GLN:O	2.11	0.50
39:BG:94:ARG:HG3	39:BG:127:GLN:OE1	2.10	0.50
46:BQ:36:VAL:HG22	55:BZ:82:TYR:HB2	1.94	0.50
1:AA:364:A:OP1	23:AW:410:LYS:NZ	2.45	0.50
1:AA:857:C:H2'	1:AA:858:G:O4'	2.12	0.50
1:AA:1126:U:H1'	1:AA:1281:C:C1'	2.42	0.50
23:AW:64:LYS:HE2	23:AW:71:THR:N	2.21	0.50
33:BA:882:G:H2'	33:BA:883:G:C8	2.45	0.50
33:BA:974:G:C5	33:BA:989:G:C6	2.99	0.50
33:BA:1047:G:HO2'	33:BA:1048:A:H8	1.58	0.50
33:BA:1252:G:H1'	50:BU:32:ARG:NH2	2.26	0.50
33:BA:2394:C:H5''	45:BP:63:LYS:HE2	1.94	0.50
35:BC:183:VAL:HG12	35:BC:187:CYS:SG	2.52	0.50
38:BF:36:ASN:O	38:BF:151:LEU:HB2	2.11	0.50
39:BG:102:ILE:O	39:BG:113:ASP:HA	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:267:C:OP2	17:AQ:68:LYS:HD2	2.11	0.50
1:AA:376:G:H2'	1:AA:377:G:H8	1.76	0.50
2:AB:22:TRP:CG	2:AB:22:TRP:O	2.64	0.50
3:AC:69:THR:HG21	3:AC:75:VAL:HG21	1.92	0.50
11:AK:17:ASP:HB3	11:AK:80:ASN:OD1	2.12	0.50
12:AL:30:ARG:NH1	23:AW:408:LYS:CE	2.73	0.50
14:AN:52:ARG:HG3	14:AN:58:ARG:NH1	2.26	0.50
20:AT:77:ASN:O	20:AT:81:GLN:HG3	2.12	0.50
24:B0:40:ARG:H	24:B0:56:HIS:HB3	1.77	0.50
28:B4:47:TYR:CE1	28:B4:52:LYS:HD3	2.47	0.50
32:B8:29:ALA:O	39:BG:169:ARG:NH2	2.44	0.50
33:BA:974:G:C5	33:BA:989:G:C2	2.99	0.50
33:BA:1106:G:H5''	40:BH:59:LEU:CD1	2.41	0.50
33:BA:1796:U:H2'	33:BA:1797:G:C8	2.47	0.50
33:BA:2149:U:H3'	33:BA:2149:U:H6	1.76	0.50
41:BI:89:SER:HB3	41:BI:92:PRO:HG3	1.93	0.50
46:BQ:66:ARG:NH1	46:BQ:104:GLU:OE1	2.45	0.50
1:AA:689:C:OP1	11:AK:45:THR:OG1	2.27	0.50
1:AA:937:A:H1'	1:AA:1379:G:N2	2.26	0.50
1:AA:1258:G:OP2	1:AA:1258:G:H8	1.95	0.50
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.27	0.50
17:AQ:45:VAL:HG22	17:AQ:72:TRP:HB2	1.94	0.50
33:BA:941:A:H2'	33:BA:942:G:C8	2.47	0.50
33:BA:1269:A:H2'	33:BA:1270:C:C6	2.47	0.50
33:BA:1533:C:H42	33:BA:1538:G:H1	1.60	0.50
33:BA:2225:A:H4'	33:BA:2226:C:O5'	2.12	0.50
33:BA:2423:U:O2'	33:BA:2424:C:OP2	2.29	0.50
33:BA:2489:U:C4	33:BA:2490:G:C6	3.00	0.50
34:BB:93:C:H2'	34:BB:94:A:C8	2.47	0.50
44:BO:16:ALA:HB2	44:BO:86:LEU:HD11	1.94	0.50
47:BR:96:ARG:HH12	47:BR:116:VAL:HG21	1.77	0.50
49:BT:24:THR:HB	49:BT:87:ARG:HB3	1.93	0.50
50:BU:60:TRP:CE2	50:BU:93:ILE:HB	2.46	0.50
54:BY:24:VAL:HG22	54:BY:35:VAL:HG22	1.94	0.50
1:AA:42:G:C6	1:AA:43:C:C4	2.99	0.50
1:AA:926:G:H5''	1:AA:927:G:O5'	2.12	0.50
2:AB:163:ILE:HG13	2:AB:164:ASP:H	1.75	0.50
3:AC:59:PRO:HG2	3:AC:62:SER:HB3	1.92	0.50
3:AC:166:TRP:HE3	3:AC:166:TRP:H	1.58	0.50
13:AM:106:ARG:HH21	13:AM:112:ARG:HB3	1.76	0.50
14:AN:53:ASP:OD2	14:AN:58:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:333:GLN:NE2	23:AW:372:THR:O	2.35	0.50
33:BA:1061:U:O4	41:BI:11:GLN:NE2	2.45	0.50
33:BA:1902:C:C5	33:BA:1903:G:C8	2.99	0.50
43:BN:64:VAL:HG11	43:BN:69:ARG:H	1.77	0.50
46:BQ:69:PRO:HA	46:BQ:94:ALA:HB2	1.94	0.50
2:AB:150:ILE:O	2:AB:153:MET:N	2.42	0.50
4:AD:61:ARG:NH2	4:AD:67:LEU:HD22	2.26	0.50
13:AM:71:GLU:O	13:AM:74:MET:HB3	2.12	0.50
16:AP:4:ILE:O	16:AP:71:VAL:HG21	2.12	0.50
24:B0:40:ARG:HB3	33:BA:2336:A:H61	1.75	0.50
33:BA:623:C:H2'	33:BA:624:C:C6	2.47	0.50
33:BA:659:G:O5'	37:BE:95:LYS:HD3	2.11	0.50
33:BA:836:G:C5	33:BA:837:C:C4	3.00	0.50
33:BA:1567:G:H2'	35:BC:84:PRO:HG3	1.92	0.50
33:BA:1695:G:H1'	35:BC:7:PRO:O	2.12	0.50
33:BA:2740:A:H2'	33:BA:2741:A:C8	2.47	0.50
35:BC:149:LYS:HD3	35:BC:152:GLN:OE1	2.10	0.50
42:BM:13:ALA:O	42:BM:18:ASP:HB2	2.12	0.50
55:BZ:6:ALA:HB2	55:BZ:42:LEU:HD23	1.94	0.50
1:AA:265:G:H2'	1:AA:267:C:H5	1.77	0.50
3:AC:52:SER:OG	3:AC:53:ARG:N	2.45	0.50
8:AH:17:GLN:NE2	8:AH:71:VAL:H	2.09	0.50
16:AP:37:GLY:HA3	16:AP:52:LEU:HA	1.93	0.50
28:B4:40:HIS:CE1	33:BA:2815:C:HO2'	2.28	0.50
33:BA:1313:U:H5''	33:BA:1314:C:OP2	2.12	0.50
33:BA:2364:C:H2'	33:BA:2365:G:O4'	2.11	0.50
36:BD:110:THR:HA	36:BD:171:THR:HB	1.94	0.50
54:BY:86:PHE:CD1	54:BY:101:THR:HG21	2.47	0.50
1:AA:297:G:N2	1:AA:300:A:OP2	2.44	0.49
1:AA:710:G:H2'	1:AA:711:G:H8	1.77	0.49
1:AA:781:A:O2'	1:AA:1522:U:O2	2.29	0.49
1:AA:1493:A:O2'	1:AA:1494:G:OP1	2.30	0.49
2:AB:132:GLU:O	2:AB:136:ARG:HB2	2.12	0.49
13:AM:70:ARG:O	13:AM:74:MET:HB2	2.12	0.49
20:AT:67:HIS:HB3	20:AT:68:LYS:HZ2	1.77	0.49
24:B0:38:ARG:NH2	33:BA:2262:U:H5''	2.26	0.49
33:BA:78:U:H2'	33:BA:79:C:C6	2.46	0.49
33:BA:345:A:O2'	33:BA:346:A:N7	2.36	0.49
33:BA:1179:G:H3'	33:BA:1180:U:H4'	1.94	0.49
33:BA:1425:G:N1	33:BA:1426:G:C2	2.80	0.49
33:BA:1549:A:H2'	33:BA:1550:C:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BC:95:TYR:CE1	35:BC:101:ARG:HD2	2.47	0.49
1:AA:765:G:H22	1:AA:812:G:HO2'	1.60	0.49
1:AA:950:U:H2'	1:AA:951:G:H8	1.78	0.49
4:AD:12:ARG:HG2	4:AD:33:ILE:HD12	1.94	0.49
5:AE:80:LEU:HB3	5:AE:146:MET:HE1	1.93	0.49
16:AP:43:ALA:O	16:AP:46:LYS:HD2	2.12	0.49
20:AT:53:MET:O	20:AT:57:VAL:HG23	2.12	0.49
23:AW:407:LEU:HB3	23:AW:409:GLN:HG3	1.94	0.49
33:BA:1070:A:N7	33:BA:1096:A:O2'	2.41	0.49
33:BA:1197:G:H2'	33:BA:1198:U:C6	2.48	0.49
33:BA:1277:G:H5'	47:BR:20:MET:CE	2.40	0.49
33:BA:1539:U:H2'	33:BA:1540:G:C8	2.47	0.49
35:BC:77:VAL:HG13	35:BC:111:ALA:HA	1.94	0.49
38:BF:71:LYS:HD3	38:BF:80:GLN:HG3	1.92	0.49
48:BS:58:ILE:HD11	48:BS:81:ARG:NH2	2.28	0.49
51:BV:54:VAL:HG23	51:BV:57:GLY:HA3	1.95	0.49
52:BW:6:LYS:HB3	52:BW:104:THR:HG23	1.95	0.49
1:AA:243:A:C2	1:AA:246:A:C8	3.00	0.49
1:AA:728:A:H2'	1:AA:729:A:C8	2.48	0.49
1:AA:1053:G:O6	1:AA:1199:U:H2'	2.12	0.49
1:AA:1491:G:H2'	1:AA:1492:A:OP2	2.12	0.49
9:AI:74:GLN:O	9:AI:78:ILE:HG12	2.11	0.49
23:AW:314:ARG:NH1	23:AW:421:GLU:HB2	2.27	0.49
27:B3:40:THR:HG23	27:B3:43:ILE:HG23	1.95	0.49
33:BA:805:G:N2	33:BA:829:A:OP1	2.46	0.49
33:BA:895:U:O2'	33:BA:896:A:OP1	2.30	0.49
33:BA:974:G:C5	33:BA:989:G:N1	2.80	0.49
33:BA:1219:U:H2'	33:BA:1220:G:H8	1.78	0.49
33:BA:1857:G:N2	33:BA:1884:G:H2'	2.27	0.49
33:BA:2107:G:N7	33:BA:2183:A:N1	2.60	0.49
37:BE:97:ASN:HB2	37:BE:100:MET:HG3	1.95	0.49
37:BE:145:ASP:HB3	37:BE:184:ASP:HB2	1.94	0.49
39:BG:51:PHE:CD2	39:BG:68:ARG:HG2	2.47	0.49
40:BH:48:ALA:HA	40:BH:51:TYR:HE2	1.77	0.49
1:AA:345:C:H1'	1:AA:346:G:C2	2.47	0.49
1:AA:1299:A:H2'	1:AA:1301:U:H1'	1.94	0.49
9:AI:34:LEU:HG	9:AI:39:GLY:HA3	1.94	0.49
12:AL:28:GLN:HG3	12:AL:80:LEU:HD21	1.92	0.49
20:AT:43:LYS:HE2	20:AT:86:ALA:HB1	1.95	0.49
33:BA:533:G:C5	33:BA:534:U:C4	3.00	0.49
33:BA:614:A:O2'	33:BA:615:U:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:895:U:HO2'	33:BA:896:A:P	2.28	0.49
33:BA:1141:U:H2'	43:BN:65:THR:CG2	2.42	0.49
33:BA:1509:A:O2'	33:BA:1510:G:O4'	2.30	0.49
36:BD:114:LYS:NZ	36:BD:116:LYS:HE2	2.27	0.49
37:BE:127:GLU:H	37:BE:127:GLU:CD	2.15	0.49
44:BO:43:ILE:HG13	44:BO:56:ASP:HB2	1.93	0.49
50:BU:8:ILE:O	50:BU:11:ALA:HB3	2.13	0.49
55:BZ:62:THR:HA	55:BZ:71:LYS:HA	1.93	0.49
1:AA:404:G:H2'	1:AA:405:U:C6	2.48	0.49
2:AB:25:LYS:HE2	2:AB:193:ASP:HB2	1.95	0.49
3:AC:106:ARG:HD3	3:AC:106:ARG:H	1.78	0.49
23:AW:194:GLN:HB2	23:AW:205:ARG:HH12	1.76	0.49
33:BA:377:G:H1	33:BA:397:U:H3	1.59	0.49
33:BA:392:U:H2'	33:BA:393:C:H6	1.76	0.49
33:BA:528:A:C2	33:BA:2042:A:H2'	2.47	0.49
33:BA:588:U:H1'	37:BE:85:PHE:CG	2.48	0.49
33:BA:1026:G:H2'	33:BA:1027:A:H8	1.77	0.49
33:BA:1571:A:H2'	33:BA:1572:A:C8	2.47	0.49
33:BA:1757:A:H3'	33:BA:1758:U:H5'	1.94	0.49
33:BA:2180:U:H2'	33:BA:2181:U:C5	2.48	0.49
1:AA:247:G:C6	1:AA:278:G:C2	3.00	0.49
1:AA:642:A:N7	8:AH:106:SER:HA	2.28	0.49
1:AA:688:G:H5'	11:AK:48:GLY:HA2	1.95	0.49
1:AA:786:G:C2	1:AA:797:C:C2	3.01	0.49
1:AA:1236:A:H4'	1:AA:1304:G:H4'	1.95	0.49
2:AB:19:THR:HA	2:AB:37:VAL:HG23	1.95	0.49
3:AC:130:ARG:HA	3:AC:133:MET:HE2	1.93	0.49
23:AW:355:HIS:HA	23:AW:356:VAL:CG2	2.41	0.49
28:B4:2:VAL:HG23	33:BA:2015:A:C6	2.47	0.49
33:BA:228:C:H4'	33:BA:229:C:H5''	1.95	0.49
33:BA:827:U:H2'	33:BA:2068:U:C2	2.47	0.49
33:BA:1829:A:O2'	35:BC:14:HIS:CE1	2.66	0.49
33:BA:2182:U:C2'	33:BA:2183:A:OP1	2.61	0.49
33:BA:2561:U:O3'	44:BO:40:LYS:HE2	2.12	0.49
43:BN:45:THR:OG1	43:BN:48:VAL:HB	2.12	0.49
50:BU:73:ILE:HG13	50:BU:74:SER:N	2.27	0.49
51:BV:8:GLY:O	51:BV:10:LYS:HE3	2.12	0.49
51:BV:77:PHE:HD2	51:BV:84:ARG:HB3	1.78	0.49
1:AA:585:G:C6	1:AA:586:C:C4	3.00	0.49
1:AA:824:G:H2'	1:AA:825:A:H8	1.78	0.49
2:AB:30:ILE:HD11	2:AB:38:HIS:CG	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:17:TRP:CD1	14:AN:93:PRO:HA	2.48	0.49
8:AH:38:VAL:HG11	8:AH:102:VAL:HG22	1.95	0.49
12:AL:49:ARG:NH1	12:AL:88:ASP:OD1	2.44	0.49
23:AW:59:TRP:HA	23:AW:59:TRP:HE3	1.75	0.49
23:AW:72:THR:HG21	23:AW:102:THR:HG21	1.94	0.49
23:AW:211:ASN:HA	23:AW:228:ARG:NH1	2.28	0.49
23:AW:485:PHE:C	23:AW:487:ARG:H	2.16	0.49
25:B1:60:LYS:HE3	33:BA:372:G:C8	2.48	0.49
31:B7:39:ARG:HH11	33:BA:2362:C:H5''	1.77	0.49
32:B8:2:LYS:HB2	32:B8:35:GLN:HG2	1.95	0.49
32:B8:30:GLU:HG3	32:B8:32:LYS:H	1.76	0.49
33:BA:597:G:H2'	33:BA:598:U:C6	2.47	0.49
33:BA:760:G:H2'	33:BA:761:A:O4'	2.12	0.49
33:BA:994:C:O2	51:BV:10:LYS:HE2	2.13	0.49
33:BA:1024:G:P	33:BA:1025:G:H3'	2.52	0.49
33:BA:2150:C:O2'	33:BA:2151:U:P	2.70	0.49
33:BA:2272:U:O5'	33:BA:2272:U:H6	1.95	0.49
33:BA:2310:C:H2'	38:BF:76:PHE:CE1	2.48	0.49
33:BA:2838:G:H1'	47:BR:45:ARG:NH1	2.26	0.49
35:BC:92:LEU:HD13	35:BC:102:TYR:CE1	2.47	0.49
35:BC:106:PRO:HA	35:BC:141:HIS:NE2	2.27	0.49
41:BI:8:VAL:HG22	41:BI:58:ILE:HG13	1.94	0.49
45:BP:42:SER:O	45:BP:42:SER:OG	2.31	0.49
48:BS:24:THR:HG22	48:BS:42:PRO:HD3	1.93	0.49
51:BV:66:HIS:CG	51:BV:94:THR:HG22	2.47	0.49
13:AM:19:THR:HA	13:AM:24:VAL:HG23	1.94	0.49
23:AW:415:GLY:HA2	23:AW:457:TYR:CZ	2.48	0.49
24:B0:51:GLY:HA3	24:B0:59:PHE:CZ	2.48	0.49
33:BA:565:C:H2'	33:BA:566:U:O4'	2.12	0.49
33:BA:859:G:HO2'	33:BA:860:U:P	2.35	0.49
33:BA:1081:U:H4'	41:BI:123:ALA:HB1	1.94	0.49
33:BA:2082:A:H2'	33:BA:2083:G:O4'	2.13	0.49
36:BD:114:LYS:HZ2	36:BD:116:LYS:HE2	1.76	0.49
40:BH:100:ALA:HB2	40:BH:125:ARG:CZ	2.43	0.49
42:BM:3:THR:O	42:BM:7:ILE:HG12	2.13	0.49
1:AA:308:C:H2'	1:AA:309:A:H8	1.77	0.49
1:AA:1003:G:N2	1:AA:1005:A:H5'	2.28	0.49
1:AA:1239:A:H4'	1:AA:1240:U:C5'	2.43	0.49
1:AA:1437:A:H5''	20:AT:28:ARG:HH12	1.78	0.49
9:AI:23:GLY:H	9:AI:61:ASP:H	1.61	0.49
9:AI:59:LYS:HD2	9:AI:60:LEU:HD22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:408:LYS:HG2	23:AW:409:GLN:HB2	1.95	0.49
27:B3:43:ILE:O	27:B3:47:ILE:HG12	2.12	0.49
33:BA:1005:C:H2'	33:BA:1006:C:C6	2.48	0.49
33:BA:1565:C:HO2'	33:BA:1566:A:H2'	1.76	0.49
33:BA:2207:C:C2	33:BA:2218:G:C2	3.01	0.49
33:BA:2469:A:N6	33:BA:2481:G:O2'	2.46	0.49
38:BF:161:SER:OG	38:BF:163:GLU:HB3	2.12	0.49
53:BX:10:VAL:HG23	53:BX:11:LEU:HD23	1.93	0.49
1:AA:497:G:H2'	1:AA:498:A:C8	2.48	0.49
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.48	0.49
9:AI:21:LYS:O	9:AI:23:GLY:N	2.42	0.49
11:AK:33:ILE:HG12	11:AK:69:CYS:SG	2.53	0.49
17:AQ:64:ARG:H	17:AQ:64:ARG:HD3	1.77	0.49
23:AW:91:GLY:HA2	23:AW:122:ARG:NH1	2.28	0.49
33:BA:458:G:O2'	33:BA:469:G:N1	2.46	0.49
33:BA:582:A:OP1	50:BU:13:HIS:ND1	2.37	0.49
33:BA:2502:G:H5''	33:BA:2503:A:H5''	1.95	0.49
50:BU:65:ASN:ND2	50:BU:69:ARG:HD3	2.28	0.49
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.77	0.48
1:AA:1359:C:H5	14:AN:74:ARG:HH12	1.61	0.48
1:AA:1478:U:H2'	1:AA:1479:C:H6	1.78	0.48
3:AC:153:SER:CB	3:AC:164:THR:HG22	2.43	0.48
14:AN:15:LEU:O	14:AN:54:SER:OG	2.20	0.48
23:AW:94:ASP:HB3	23:AW:443:VAL:H	1.77	0.48
24:B0:23:LYS:HE3	24:B0:24:ARG:HG3	1.95	0.48
33:BA:558:U:H5'	43:BN:114:LEU:HD12	1.95	0.48
33:BA:616:A:H4'	37:BE:101:TYR:CE2	2.48	0.48
33:BA:1353:A:H2'	33:BA:1354:A:C8	2.48	0.48
34:BB:93:C:H2'	34:BB:94:A:H8	1.78	0.48
41:BI:7:TYR:HB3	41:BI:57:VAL:HG13	1.95	0.48
47:BR:2:ARG:HA	47:BR:5:LYS:HD2	1.93	0.48
51:BV:61:ALA:HB1	51:BV:98:ILE:H	1.78	0.48
51:BV:64:VAL:HG23	51:BV:96:VAL:HA	1.94	0.48
1:AA:392:C:H2'	1:AA:393:A:H8	1.78	0.48
1:AA:557:G:C6	1:AA:558:G:C6	3.01	0.48
1:AA:1071:C:H2'	1:AA:1072:G:H8	1.77	0.48
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.47	0.48
5:AE:80:LEU:HD12	5:AE:146:MET:SD	2.53	0.48
17:AQ:16:MET:HB2	17:AQ:19:SER:H	1.78	0.48
24:B0:23:LYS:HD2	24:B0:24:ARG:H	1.77	0.48
33:BA:37:C:O2'	37:BE:45:ALA:HA	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:372:G:O2'	33:BA:373:U:OP2	2.31	0.48
33:BA:745:G:H2'	33:BA:746:U:H5'	1.95	0.48
33:BA:983:A:C6	33:BA:984:A:C2	3.01	0.48
33:BA:1716:U:H2'	33:BA:1717:A:H8	1.78	0.48
33:BA:1926:U:O2	33:BA:1929:G:N1	2.46	0.48
38:BF:131:VAL:HG22	38:BF:151:LEU:H	1.78	0.48
40:BH:23:LEU:HD22	40:BH:92:ALA:O	2.13	0.48
45:BP:76:GLU:HB2	45:BP:111:ILE:CD1	2.43	0.48
47:BR:65:LEU:HD21	47:BR:69:ARG:NH1	2.27	0.48
48:BS:4:LYS:HD2	48:BS:7:ARG:HH21	1.77	0.48
50:BU:73:ILE:HG13	50:BU:74:SER:H	1.78	0.48
54:BY:86:PHE:CG	54:BY:101:THR:HG21	2.48	0.48
2:AB:44:LYS:O	2:AB:48:MET:HB2	2.13	0.48
5:AE:114:LEU:HD12	5:AE:114:LEU:HA	1.73	0.48
7:AG:134:VAL:O	7:AG:138:GLU:HG2	2.13	0.48
12:AL:30:ARG:HH12	23:AW:408:LYS:HG3	1.68	0.48
15:AO:77:TYR:OH	15:AO:87:ARG:HG2	2.13	0.48
23:AW:59:TRP:CE2	23:AW:69:SER:CB	2.96	0.48
24:B0:9:THR:HG23	24:B0:10:ARG:NH1	2.27	0.48
24:B0:23:LYS:HB3	33:BA:856:G:H1'	1.95	0.48
25:B1:27:ARG:NH2	33:BA:1365:A:O5'	2.40	0.48
33:BA:1154:G:OP2	50:BU:57:ARG:NH1	2.46	0.48
33:BA:1268:A:H2'	33:BA:1269:A:O4'	2.13	0.48
33:BA:1292:G:H2'	33:BA:1293:C:C6	2.48	0.48
33:BA:2334:U:H3	48:BS:16:ARG:HG2	1.78	0.48
34:BB:65:U:H3'	34:BB:108:A:H61	1.77	0.48
36:BD:33:ARG:NH2	36:BD:74:GLU:O	2.46	0.48
46:BQ:28:PHE:HB3	46:BQ:64:TRP:CE2	2.48	0.48
48:BS:67:ASN:N	48:BS:67:ASN:OD1	2.46	0.48
51:BV:81:LYS:HA	51:BV:81:LYS:HD3	1.57	0.48
1:AA:1031:C:H4'	1:AA:1032:G:C4	2.48	0.48
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.48	0.48
6:AF:50:PRO:HD3	18:AR:73:HIS:HB3	1.95	0.48
7:AG:93:VAL:HG23	7:AG:94:ARG:H	1.77	0.48
7:AG:94:ARG:CZ	7:AG:98:LEU:HD21	2.43	0.48
16:AP:80:LYS:HB2	16:AP:80:LYS:HZ2	1.78	0.48
23:AW:16:PHE:CZ	23:AW:276:ALA:HB1	2.48	0.48
23:AW:117:LYS:O	23:AW:149:ARG:NH2	2.46	0.48
23:AW:300:VAL:HG13	23:AW:316:ALA:HB1	1.96	0.48
23:AW:448:VAL:HG13	23:AW:452:ARG:NH2	2.28	0.48
23:AW:452:ARG:HA	23:AW:452:ARG:HD3	1.63	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:63:A:C2	33:BA:64:A:C5	3.01	0.48
33:BA:322:A:H3'	37:BE:163:ASN:HD21	1.79	0.48
33:BA:594:U:H2'	33:BA:595:C:C6	2.48	0.48
33:BA:828:U:H4'	33:BA:831:G:N1	2.29	0.48
33:BA:1306:C:H5''	33:BA:1606:C:N4	2.28	0.48
33:BA:1570:A:C6	33:BA:1571:A:C6	3.02	0.48
33:BA:2302:U:H2'	33:BA:2303:G:H8	1.77	0.48
33:BA:2881:U:H2'	33:BA:2882:A:C8	2.47	0.48
34:BB:35:C:H2'	34:BB:36:C:O4'	2.13	0.48
36:BD:21:SER:HB2	44:BO:73:ASP:HA	1.95	0.48
42:BJ:4:LYS:O	42:BJ:8:ILE:HG12	2.13	0.48
44:BO:13:ASN:OD1	44:BO:14:SER:N	2.42	0.48
44:BO:31:ARG:HB3	44:BO:32:TYR:CE1	2.49	0.48
1:AA:308:C:H2'	1:AA:309:A:C8	2.49	0.48
1:AA:938:A:C6	1:AA:939:G:C5	3.01	0.48
1:AA:1065:U:H5''	1:AA:1190:G:N2	2.29	0.48
2:AB:95:TRP:HZ2	2:AB:100:LEU:HD23	1.77	0.48
4:AD:64:TYR:CE2	4:AD:93:LEU:HB3	2.48	0.48
9:AI:9:GLY:H	9:AI:84:ARG:HH12	1.62	0.48
26:B2:56:LEU:HA	26:B2:59:GLU:HG2	1.95	0.48
33:BA:319:G:H2'	33:BA:320:A:O4'	2.14	0.48
33:BA:1392:A:C6	33:BA:1393:A:C6	3.01	0.48
33:BA:1522:A:H1'	33:BA:1524:G:C5	2.48	0.48
33:BA:2572:A:N7	36:BD:150:GLN:HB3	2.28	0.48
38:BF:128:SER:HA	38:BF:153:ILE:O	2.13	0.48
40:BH:23:LEU:HD13	40:BH:92:ALA:HB1	1.95	0.48
43:BN:21:THR:HG23	43:BN:61:LYS:HB3	1.95	0.48
45:BP:33:ARG:HE	45:BP:40:SER:HA	1.78	0.48
45:BP:75:ALA:HB2	45:BP:105:ILE:HG12	1.96	0.48
46:BQ:35:ALA:O	46:BQ:36:VAL:HB	2.14	0.48
1:AA:673:A:H4'	6:AF:86:ARG:HE	1.78	0.48
1:AA:1145:A:O2'	1:AA:1146:A:H8	1.97	0.48
3:AC:21:TRP:HB3	3:AC:58:ARG:H	1.79	0.48
6:AF:6:ILE:H	6:AF:62:MET:HB3	1.78	0.48
23:AW:50:GLY:HA3	33:BA:2655:G:N7	2.28	0.48
23:AW:279:PRO:HG3	23:AW:362:GLY:HA3	1.96	0.48
23:AW:500:ASN:HB2	23:AW:501:LEU:CG	2.42	0.48
25:B1:36:ARG:HG3	25:B1:47:THR:HB	1.94	0.48
26:B2:17:GLU:HB2	26:B2:53:VAL:HG11	1.96	0.48
27:B3:6:ILE:HG21	27:B3:47:ILE:HD12	1.96	0.48
33:BA:825:A:H2'	33:BA:826:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1774:C:O2	35:BC:10:PRO:HB2	2.12	0.48
33:BA:1838:C:H4'	33:BA:1839:G:H8	1.77	0.48
33:BA:2205:A:OP1	35:BC:67:LYS:NZ	2.46	0.48
35:BC:81:GLU:OE1	35:BC:102:TYR:OH	2.20	0.48
36:BD:149:ASN:OD1	36:BD:150:GLN:N	2.45	0.48
37:BE:105:LEU:HB2	37:BE:200:LEU:HD11	1.96	0.48
39:BG:62:ALA:O	39:BG:66:THR:HG23	2.13	0.48
1:AA:73:C:N4	1:AA:97:G:H1	2.04	0.48
1:AA:599:C:H2'	1:AA:600:A:C8	2.48	0.48
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.96	0.48
13:AM:44:ILE:HA	13:AM:47:LEU:CB	2.44	0.48
23:AW:71:THR:HG22	23:AW:72:THR:N	2.28	0.48
23:AW:145:ASP:CG	56:AW:601:GNP:HN1	2.17	0.48
23:AW:448:VAL:HG22	23:AW:452:ARG:HH21	1.79	0.48
24:B0:23:LYS:HG3	24:B0:24:ARG:O	2.13	0.48
25:B1:2:ARG:O	25:B1:11:PRO:HD3	2.13	0.48
33:BA:259:G:HO2'	33:BA:621:A:HO2'	1.62	0.48
33:BA:566:U:H5	51:BV:80:ARG:HG2	1.78	0.48
33:BA:586:A:N1	33:BA:809:G:O2'	2.37	0.48
33:BA:725:G:C6	33:BA:726:G:N1	2.82	0.48
33:BA:780:G:H2'	33:BA:782:A:N7	2.28	0.48
33:BA:1394:U:H4'	33:BA:1603:A:H4'	1.94	0.48
33:BA:1936:A:H2	33:BA:1943:U:C5	2.32	0.48
33:BA:1999:C:H5''	33:BA:2723:C:O2'	2.13	0.48
36:BD:186:LEU:HD11	49:BT:3:ILE:HG12	1.96	0.48
39:BG:73:SER:HA	39:BG:76:ILE:HG22	1.96	0.48
43:BN:88:THR:O	43:BN:91:GLU:N	2.47	0.48
43:BN:88:THR:HG22	43:BN:91:GLU:CD	2.33	0.48
55:BZ:28:ALA:N	55:BZ:40:ILE:O	2.46	0.48
1:AA:1227:A:OP2	13:AM:109:LYS:HE2	2.14	0.48
1:AA:1492:A:N6	33:BA:1913:A:C2	2.82	0.48
3:AC:13:ILE:C	3:AC:15:LYS:H	2.17	0.48
9:AI:6:TYR:CG	9:AI:7:GLY:N	2.82	0.48
21:AU:19:LYS:HB2	21:AU:20:ARG:HH11	1.78	0.48
23:AW:64:LYS:NZ	23:AW:71:THR:O	2.38	0.48
23:AW:419:LEU:HD12	23:AW:452:ARG:NH2	2.27	0.48
24:B0:43:LYS:HB3	24:B0:79:ILE:HD11	1.96	0.48
32:B8:16:ILE:HA	32:B8:24:ARG:O	2.13	0.48
33:BA:833:A:H2'	33:BA:834:G:C8	2.48	0.48
37:BE:36:ALA:O	37:BE:39:ALA:HB3	2.13	0.48
39:BG:46:ASP:OD1	39:BG:47:ASN:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BG:95:ALA:CB	39:BG:104:LEU:HD23	2.44	0.48
40:BH:23:LEU:HD21	40:BH:96:PHE:CD2	2.49	0.48
40:BH:60:LEU:O	40:BH:62:ARG:N	2.46	0.48
46:BQ:11:LYS:NZ	46:BQ:87:GLY:O	2.30	0.48
48:BS:4:LYS:CD	48:BS:7:ARG:HH21	2.26	0.48
1:AA:51:A:H4'	1:AA:52:C:O5'	2.13	0.48
1:AA:1380:U:C5	7:AG:2:ARG:HA	2.48	0.48
7:AG:3:ARG:HG3	7:AG:4:ARG:H	1.79	0.48
7:AG:129:ASN:C	7:AG:134:VAL:HG21	2.35	0.48
8:AH:79:ARG:HB2	8:AH:80:PRO:HD2	1.95	0.48
11:AK:88:PRO:HD3	21:AU:28:LEU:HD13	1.95	0.48
20:AT:43:LYS:HB3	20:AT:86:ALA:HB1	1.96	0.48
23:AW:96:SER:HA	23:AW:97:GLU:CB	2.43	0.48
26:B2:56:LEU:HA	26:B2:59:GLU:CG	2.44	0.48
33:BA:703:U:H2'	33:BA:704:G:O4'	2.14	0.48
33:BA:752:A:H62	33:BA:2609:U:H3	1.60	0.48
33:BA:1378:A:C4	33:BA:1380:G:N7	2.82	0.48
33:BA:2007:U:H2'	33:BA:2008:C:C6	2.49	0.48
33:BA:2220:U:H2'	33:BA:2221:G:C8	2.49	0.48
35:BC:20:ASN:O	35:BC:23:LEU:HB2	2.13	0.48
35:BC:180:MET:HG3	35:BC:268:ARG:HH11	1.79	0.48
38:BF:21:TYR:CE2	38:BF:28:PRO:HD3	2.49	0.48
40:BH:27:VAL:O	40:BH:83:ALA:N	2.40	0.48
42:BL:21:GLU:O	42:BL:24:SER:OG	2.22	0.48
53:BX:56:GLU:HA	53:BX:88:LYS:HE2	1.95	0.48
55:BZ:75:GLN:HB2	55:BZ:92:VAL:HG23	1.95	0.48
1:AA:239:U:H5''	1:AA:240:G:OP2	2.14	0.48
1:AA:1377:A:H2'	7:AG:6:ILE:HD11	1.96	0.48
2:AB:23:ASN:HB2	2:AB:189:ASN:O	2.13	0.48
2:AB:26:MET:HG2	2:AB:188:THR:HA	1.96	0.48
3:AC:153:SER:HB3	3:AC:164:THR:HG22	1.96	0.48
4:AD:61:ARG:HG2	4:AD:71:PHE:CD2	2.49	0.48
5:AE:156:ARG:HH22	8:AH:113:ARG:HH12	1.61	0.48
33:BA:301:G:P	54:BY:81:ARG:HH12	2.37	0.48
33:BA:1055:G:H4'	40:BH:33:VAL:HA	1.96	0.48
33:BA:1559:U:H4'	33:BA:1560:G:OP2	2.14	0.48
33:BA:1568:G:H4'	35:BC:58:LYS:CB	2.36	0.48
33:BA:1848:A:H2'	33:BA:1849:G:O4'	2.13	0.48
33:BA:1947:C:H2'	33:BA:1948:G:C8	2.49	0.48
33:BA:2294:G:H5''	48:BS:10:ARG:HD3	1.96	0.48
35:BC:224:MET:HB3	35:BC:228:ASP:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BD:108:ASP:N	36:BD:204:LYS:O	2.46	0.48
46:BQ:26:VAL:HA	46:BQ:104:GLU:OE1	2.13	0.48
1:AA:542:G:H2'	1:AA:543:U:H6	1.79	0.47
9:AI:83:THR:HG22	9:AI:97:LEU:HD21	1.96	0.47
14:AN:3:GLN:HA	14:AN:6:LYS:HE2	1.96	0.47
14:AN:20:PHE:HB2	14:AN:54:SER:OG	2.14	0.47
18:AR:40:PRO:HG2	18:AR:43:ILE:HG12	1.96	0.47
25:B1:68:ALA:O	25:B1:72:ALA:HB2	2.13	0.47
33:BA:342:A:H2'	33:BA:343:C:O4'	2.14	0.47
33:BA:587:C:OP2	45:BP:21:ARG:NH1	2.48	0.47
33:BA:686:U:H2'	33:BA:788:A:C2	2.49	0.47
33:BA:2416:C:N4	33:BA:2417:C:H41	2.12	0.47
33:BA:2444:G:OP2	37:BE:63:LYS:HD2	2.14	0.47
33:BA:2848:G:H2'	33:BA:2867:G:H22	1.79	0.47
34:BB:28:C:OP1	48:BS:31:THR:HG21	2.14	0.47
45:BP:55:MET:HG3	45:BP:59:ARG:HB2	1.96	0.47
45:BP:68:SER:C	45:BP:70:LYS:H	2.17	0.47
1:AA:497:G:H5''	23:AW:480:LYS:HE2	1.95	0.47
1:AA:707:U:H2'	1:AA:708:C:C6	2.48	0.47
1:AA:1463:U:H2'	1:AA:1464:U:C6	2.48	0.47
3:AC:63:ILE:HG12	3:AC:65:VAL:HG23	1.96	0.47
9:AI:49:GLN:N	9:AI:50:PRO:HD2	2.29	0.47
10:AJ:35:GLN:HG2	10:AJ:77:VAL:HB	1.96	0.47
12:AL:78:VAL:HG21	23:AW:407:LEU:CD1	2.42	0.47
33:BA:816:C:H2'	33:BA:817:C:H6	1.79	0.47
33:BA:881:G:H2'	33:BA:882:G:C8	2.49	0.47
33:BA:974:G:N7	33:BA:989:G:N1	2.61	0.47
33:BA:979:A:H2'	33:BA:982:C:H42	1.80	0.47
33:BA:2845:U:H5''	49:BT:51:ASN:O	2.14	0.47
35:BC:105:ALA:HA	35:BC:106:PRO:HD2	1.77	0.47
36:BD:125:TRP:CD2	36:BD:160:LYS:HB3	2.49	0.47
37:BE:48:THR:N	37:BE:51:GLU:HG3	2.29	0.47
37:BE:119:ILE:O	37:BE:119:ILE:HG12	2.15	0.47
40:BH:60:LEU:O	40:BH:63:ALA:N	2.48	0.47
43:BN:59:ALA:H	43:BN:126:ALA:HA	1.79	0.47
51:BV:25:LEU:H	51:BV:94:THR:CG2	2.27	0.47
53:BX:29:THR:HA	53:BX:86:THR:CA	2.42	0.47
1:AA:706:A:H4'	11:AK:30:ILE:HD12	1.94	0.47
1:AA:1302:C:OP1	13:AM:12:LYS:HE2	2.15	0.47
2:AB:60:ALA:HB2	2:AB:220:VAL:HG13	1.96	0.47
19:AS:35:ARG:NH2	19:AS:74:ALA:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B1:39:VAL:HG22	25:B1:44:ARG:O	2.14	0.47
33:BA:84:A:H4'	33:BA:85:G:O5'	2.13	0.47
33:BA:893:C:H2'	33:BA:894:U:O4'	2.14	0.47
33:BA:1022:G:C6	33:BA:1140:C:C4	3.02	0.47
33:BA:1103:A:H5'	33:BA:1104:C:OP2	2.14	0.47
33:BA:1300:G:H5''	33:BA:1301:A:H5'	1.96	0.47
33:BA:1731:G:O2'	33:BA:1732:C:H3'	2.15	0.47
33:BA:2889:C:H2'	33:BA:2890:G:O4'	2.14	0.47
40:BH:51:TYR:HB2	40:BH:89:PRO:HG2	1.96	0.47
41:BI:53:PRO:HD2	41:BI:77:VAL:HG21	1.96	0.47
47:BR:69:ARG:C	47:BR:71:ARG:H	2.16	0.47
48:BS:102:ARG:HA	48:BS:105:ALA:HB3	1.95	0.47
1:AA:666:G:H5'	1:AA:726:C:H1'	1.96	0.47
1:AA:774:G:N2	1:AA:806:C:C2	2.83	0.47
1:AA:1330:U:H4'	13:AM:22:TYR:CE1	2.49	0.47
3:AC:14:VAL:O	3:AC:15:LYS:HD2	2.15	0.47
14:AN:82:LYS:HE2	14:AN:85:GLU:HG3	1.96	0.47
17:AQ:55:GLY:HA3	17:AQ:82:VAL:HG11	1.96	0.47
33:BA:883:G:O2'	33:BA:896:A:N7	2.37	0.47
33:BA:996:A:H5'	50:BU:93:ILE:HG21	1.95	0.47
33:BA:1061:U:H1'	33:BA:1070:A:H1'	1.96	0.47
33:BA:1370:C:H2'	33:BA:1371:G:O4'	2.15	0.47
33:BA:1563:U:H2'	33:BA:1564:C:H6	1.76	0.47
33:BA:1799:G:OP2	35:BC:269:ARG:NH2	2.47	0.47
33:BA:2398:U:H2'	33:BA:2399:G:C8	2.50	0.47
43:BN:91:GLU:O	43:BN:94:ALA:HB3	2.13	0.47
50:BU:78:PHE:CZ	50:BU:82:LEU:HD11	2.49	0.47
51:BV:41:ILE:HD13	51:BV:103:ALA:HA	1.96	0.47
1:AA:147:G:H2'	1:AA:148:G:C8	2.49	0.47
2:AB:66:ILE:O	2:AB:160:LEU:HA	2.14	0.47
9:AI:9:GLY:HA2	9:AI:80:HIS:ND1	2.29	0.47
18:AR:61:ALA:HB3	18:AR:67:LEU:HD12	1.96	0.47
23:AW:20:SER:HB3	23:AW:26:LYS:HG2	1.97	0.47
33:BA:1071:G:H1'	33:BA:1089:A:N7	2.29	0.47
33:BA:1363:C:H2'	33:BA:1364:G:H8	1.79	0.47
33:BA:1531:C:H2'	33:BA:1532:A:C8	2.50	0.47
33:BA:1671:U:N3	33:BA:1674:G:OP2	2.38	0.47
33:BA:2691:C:C4	33:BA:2719:G:N2	2.83	0.47
33:BA:2867:G:O2'	33:BA:2868:A:H8	1.98	0.47
34:BB:116:G:H2'	34:BB:117:G:H8	1.78	0.47
35:BC:182:LYS:N	35:BC:265:PHE:O	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BD:60:VAL:HG23	36:BD:64:GLU:HB2	1.95	0.47
40:BH:11:ILE:HG23	40:BH:63:ALA:HA	1.96	0.47
46:BQ:64:TRP:CZ3	46:BQ:106:ASP:HB2	2.50	0.47
1:AA:204:G:H3'	1:AA:205:A:C5'	2.43	0.47
1:AA:478:A:H2'	1:AA:479:U:O4'	2.15	0.47
1:AA:652:U:HO2'	1:AA:653:U:P	2.38	0.47
1:AA:1291:U:H4'	9:AI:41:GLU:HG3	1.97	0.47
2:AB:162:VAL:HG23	2:AB:163:ILE:O	2.14	0.47
2:AB:209:VAL:HG23	2:AB:210:THR:H	1.79	0.47
13:AM:92:ARG:HG2	13:AM:92:ARG:HH11	1.80	0.47
23:AW:491:SER:N	23:AW:492:GLN:HB2	2.30	0.47
25:B1:17:ARG:HD2	25:B1:23:ALA:HA	1.95	0.47
33:BA:826:U:O2'	45:BP:53:GLY:HA3	2.15	0.47
33:BA:1106:G:H5''	40:BH:59:LEU:HD11	1.97	0.47
33:BA:1141:U:H6	43:BN:65:THR:HG22	1.79	0.47
36:BD:61:THR:OG1	36:BD:63:PRO:HD2	2.15	0.47
36:BD:91:THR:C	36:BD:93:GLY:N	2.67	0.47
45:BP:90:VAL:HG13	45:BP:95:LEU:HD21	1.96	0.47
47:BR:117:ASP:OD2	47:BR:117:ASP:N	2.47	0.47
1:AA:123:U:H2'	1:AA:124:C:H6	1.79	0.47
1:AA:484:G:H4'	1:AA:485:U:O5'	2.15	0.47
1:AA:1386:G:H2'	1:AA:1387:G:C8	2.49	0.47
9:AI:119:LYS:HG3	9:AI:122:ARG:HB3	1.97	0.47
10:AJ:91:ASP:OD2	10:AJ:92:LEU:N	2.47	0.47
15:AO:32:THR:HG23	15:AO:62:ARG:NH1	2.29	0.47
23:AW:127:MET:HG3	23:AW:162:LEU:HD22	1.96	0.47
23:AW:146:ARG:CZ	33:BA:2659:G:O6	2.63	0.47
23:AW:276:ALA:HA	23:AW:277:PRO:HD3	1.80	0.47
23:AW:307:MET:CG	23:AW:308:ASP:HA	2.44	0.47
24:B0:30:VAL:HG11	33:BA:2352:A:C6	2.50	0.47
29:B5:33:LEU:H	29:B5:51:ALA:HB3	1.80	0.47
31:B7:7:ARG:HD2	31:B7:7:ARG:HA	1.59	0.47
32:B8:9:LYS:HE2	32:B8:9:LYS:HB2	1.72	0.47
32:B8:36:ARG:HD3	33:BA:2742:G:OP1	2.14	0.47
33:BA:687:C:N3	33:BA:788:A:H5'	2.30	0.47
33:BA:882:G:C2	33:BA:895:U:O2	2.67	0.47
33:BA:900:A:O2'	33:BA:901:C:P	2.71	0.47
33:BA:1020:A:H4'	33:BA:1021:A:O5'	2.14	0.47
33:BA:1056:G:O2'	33:BA:1086:A:H8	1.98	0.47
33:BA:1550:C:H2'	33:BA:1551:A:H8	1.79	0.47
33:BA:1728:C:O2	33:BA:1731:G:N2	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1837:C:H4'	33:BA:1928:A:H4'	1.96	0.47
33:BA:2197:U:O2'	33:BA:2198:A:C8	2.66	0.47
33:BA:2310:C:H2'	38:BF:76:PHE:HE1	1.79	0.47
33:BA:2756:U:H1'	33:BA:2757:A:H5''	1.97	0.47
35:BC:103:ILE:HG22	35:BC:104:LEU:O	2.15	0.47
36:BD:149:ASN:O	36:BD:152:PRO:HD2	2.15	0.47
39:BG:122:ALA:HB2	39:BG:132:LEU:HB3	1.97	0.47
41:BI:100:ILE:HG22	41:BI:101:SER:H	1.79	0.47
43:BN:31:GLU:OE2	43:BN:35:ARG:NH1	2.46	0.47
45:BP:78:ARG:NH1	45:BP:113:ALA:HB1	2.28	0.47
47:BR:48:VAL:O	47:BR:51:LEU:N	2.47	0.47
53:BX:19:LYS:O	53:BX:20:ALA:C	2.53	0.47
53:BX:22:THR:O	53:BX:25:GLU:HB3	2.14	0.47
54:BY:6:ARG:HD2	54:BY:6:ARG:HA	1.54	0.47
1:AA:765:G:N2	1:AA:812:G:O2'	2.48	0.47
4:AD:29:THR:C	4:AD:31:CYS:H	2.18	0.47
23:AW:284:THR:HG21	23:AW:385:MET:SD	2.55	0.47
33:BA:878:A:N6	33:BA:900:A:H1'	2.29	0.47
33:BA:1334:G:C6	33:BA:1335:C:C4	3.03	0.47
33:BA:1799:G:H22	33:BA:1818:U:H2'	1.79	0.47
33:BA:2489:U:HO2'	33:BA:2491:U:H5	1.60	0.47
34:BB:60:C:H2'	34:BB:61:G:C8	2.50	0.47
50:BU:87:VAL:HB	51:BV:52:PRO:HD3	1.97	0.47
50:BU:91:ARG:HB3	50:BU:94:LEU:H	1.79	0.47
54:BY:60:LYS:HA	54:BY:60:LYS:HD2	1.68	0.47
1:AA:716:A:H2'	1:AA:717:U:O4'	2.14	0.47
1:AA:975:A:O2'	14:AN:71:GLY:HA2	2.15	0.47
1:AA:1347:G:O2'	1:AA:1348:U:OP2	2.33	0.47
7:AG:35:LYS:HA	7:AG:38:ALA:HB3	1.96	0.47
16:AP:57:ILE:O	16:AP:61:VAL:HG23	2.14	0.47
18:AR:40:PRO:HB2	18:AR:42:ARG:HG2	1.97	0.47
23:AW:172:PRO:HD3	23:AW:256:PHE:CG	2.50	0.47
23:AW:398:PHE:CG	23:AW:399:ARG:N	2.83	0.47
23:AW:401:ILE:HD11	23:AW:438:VAL:CG2	2.44	0.47
24:B0:10:ARG:O	24:B0:11:ASN:HB2	2.14	0.47
33:BA:1054:A:O3'	40:BH:31:ARG:HA	2.13	0.47
33:BA:1236:G:HO2'	33:BA:1237:A:H8	1.60	0.47
33:BA:1509:A:O2'	33:BA:1510:G:C8	2.65	0.47
33:BA:1710:G:C2	33:BA:1749:A:C2	3.03	0.47
33:BA:2314:A:H2'	33:BA:2315:G:H8	1.80	0.47
33:BA:2470:G:H2'	33:BA:2471:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2576:G:O2'	33:BA:2579:C:OP2	2.27	0.47
33:BA:2886:A:C2	33:BA:2887:A:H1'	2.50	0.47
35:BC:4:LYS:HG2	35:BC:16:VAL:HG22	1.97	0.47
36:BD:2:ILE:HG13	36:BD:100:LEU:HD21	1.97	0.47
38:BF:16:MET:O	38:BF:20:ASN:HA	2.15	0.47
39:BG:54:ARG:HD3	39:BG:55:ASP:N	2.29	0.47
1:AA:1152:A:H5'	10:AJ:15:HIS:HD2	1.79	0.47
4:AD:60:VAL:O	4:AD:63:ILE:HG22	2.14	0.47
12:AL:23:LEU:O	12:AL:25:ALA:N	2.47	0.47
15:AO:40:GLY:O	15:AO:43:ALA:HB3	2.15	0.47
27:B3:4:ILE:HG12	27:B3:5:LYS:N	2.29	0.47
33:BA:607:U:OP1	37:BE:98:LYS:HG3	2.15	0.47
33:BA:699:A:H2'	33:BA:700:G:O4'	2.15	0.47
33:BA:812:C:H5''	33:BA:1250:G:O2'	2.15	0.47
33:BA:1063:G:H2'	33:BA:1064:C:O4'	2.14	0.47
33:BA:1353:A:C8	33:BA:1378:A:N6	2.83	0.47
33:BA:2391:G:O6	33:BA:2425:A:H8	1.97	0.47
33:BA:2793:C:O2	33:BA:2803:G:N2	2.37	0.47
33:BA:2822:G:OP1	36:BD:164:GLN:NE2	2.44	0.47
36:BD:9:VAL:HG22	36:BD:26:VAL:HB	1.97	0.47
42:BJ:16:VAL:HG13	42:BM:11:VAL:HG11	1.97	0.47
43:BN:55:ILE:HD12	43:BN:132:HIS:HD2	1.79	0.47
47:BR:67:PHE:O	47:BR:71:ARG:HA	2.14	0.47
51:BV:61:ALA:HB2	51:BV:98:ILE:HA	1.96	0.47
1:AA:123:U:H2'	1:AA:124:C:C6	2.50	0.46
1:AA:878:A:H5''	8:AH:80:PRO:HG2	1.97	0.46
2:AB:80:LYS:HD3	2:AB:90:PHE:CE1	2.50	0.46
8:AH:101:ALA:HB3	8:AH:112:ASP:HB3	1.97	0.46
14:AN:61:ASN:HB3	14:AN:72:PHE:CE1	2.49	0.46
16:AP:19:VAL:HG13	16:AP:36:VAL:O	2.15	0.46
33:BA:1020:A:C2	33:BA:1141:U:C2	3.03	0.46
33:BA:2148:G:C2'	33:BA:2149:U:O5'	2.63	0.46
33:BA:2243:U:H2'	33:BA:2244:U:C6	2.51	0.46
33:BA:2250:G:H21	33:BA:2496:C:H5''	1.80	0.46
33:BA:2697:G:H2'	33:BA:2698:U:O4'	2.15	0.46
34:BB:104:A:H2'	34:BB:105:G:O4'	2.15	0.46
35:BC:70:LYS:HG3	35:BC:95:TYR:CE1	2.50	0.46
36:BD:47:ALA:HB2	36:BD:83:ARG:HA	1.96	0.46
36:BD:159:LYS:HD3	36:BD:160:LYS:N	2.30	0.46
40:BH:4:ASN:O	40:BH:8:LYS:HG3	2.15	0.46
46:BQ:46:ILE:O	46:BQ:49:ALA:HB3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:BT:31:VAL:HG11	49:BT:40:GLN:HB2	1.97	0.46
1:AA:82:G:N2	1:AA:88:U:O2'	2.49	0.46
1:AA:237:G:H5''	17:AQ:26:ARG:NH2	2.29	0.46
2:AB:110:ILE:HG12	2:AB:150:ILE:HG13	1.97	0.46
2:AB:163:ILE:HD12	2:AB:185:ILE:HG12	1.97	0.46
8:AH:31:LEU:O	8:AH:35:ILE:HG12	2.16	0.46
9:AI:6:TYR:CE2	9:AI:17:ARG:HB2	2.46	0.46
9:AI:56:MET:HB3	9:AI:60:LEU:CD2	2.46	0.46
16:AP:42:ILE:O	16:AP:44:SER:N	2.48	0.46
23:AW:50:GLY:CA	33:BA:2655:G:N7	2.78	0.46
23:AW:403:LEU:HD21	23:AW:459:VAL:HG12	1.97	0.46
33:BA:282:A:H2'	33:BA:283:G:C8	2.50	0.46
33:BA:414:C:H2'	33:BA:415:A:C8	2.51	0.46
33:BA:1131:G:N2	33:BA:2024:G:H21	2.14	0.46
33:BA:1570:A:H2'	33:BA:1571:A:C8	2.51	0.46
33:BA:1708:C:H2'	33:BA:1709:U:C6	2.49	0.46
33:BA:1914:C:C3'	33:BA:1915:U:C5'	2.91	0.46
33:BA:2071:A:H2'	33:BA:2072:C:C6	2.50	0.46
33:BA:2103:C:N4	33:BA:2185:U:O4	2.47	0.46
33:BA:2230:G:H2'	33:BA:2231:U:H6	1.80	0.46
33:BA:2825:G:H5''	33:BA:2825:G:N3	2.30	0.46
33:BA:2840:C:H2'	33:BA:2841:C:C6	2.50	0.46
49:BT:33:GLU:HB3	49:BT:36:LYS:O	2.15	0.46
49:BT:50:ARG:H	49:BT:50:ARG:HG3	1.44	0.46
50:BU:39:ILE:O	50:BU:43:GLN:HG3	2.14	0.46
1:AA:82:G:C8	1:AA:89:U:H1'	2.51	0.46
1:AA:160:A:H2'	1:AA:161:A:O4'	2.15	0.46
1:AA:279:A:H5''	1:AA:280:C:O5'	2.16	0.46
1:AA:890:G:O2'	1:AA:891:U:P	2.73	0.46
9:AI:87:MET:SD	9:AI:88:GLU:N	2.89	0.46
23:AW:300:VAL:HA	23:AW:318:MET:HA	1.98	0.46
33:BA:42:A:H61	33:BA:437:U:H3	1.64	0.46
33:BA:1045:C:H5'	33:BA:1047:G:O4'	2.16	0.46
33:BA:1153:C:H5'	50:BU:75:TYR:HE2	1.81	0.46
33:BA:1656:C:H2'	33:BA:1657:U:C6	2.50	0.46
33:BA:1853:A:N1	33:BA:2087:G:H1'	2.29	0.46
33:BA:2834:G:O3'	36:BD:56:LYS:NZ	2.47	0.46
36:BD:5:VAL:HG21	36:BD:80:TRP:CD2	2.50	0.46
36:BD:120:GLY:HA2	36:BD:162:ALA:CB	2.45	0.46
38:BF:130:GLY:HA2	38:BF:152:ASP:HA	1.97	0.46
43:BN:4:PHE:HD1	43:BN:44:TYR:CE2	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BP:109:LYS:HG2	45:BP:126:ARG:HB3	1.97	0.46
52:BW:97:LEU:H	52:BW:97:LEU:HD22	1.80	0.46
1:AA:346:G:N2	1:AA:347:G:C8	2.84	0.46
1:AA:1359:C:O2'	1:AA:1361:G:N7	2.48	0.46
4:AD:124:VAL:C	4:AD:126:GLY:N	2.69	0.46
5:AE:59:ILE:O	5:AE:62:ALA:HB3	2.15	0.46
6:AF:20:GLY:O	6:AF:24:ARG:HD3	2.16	0.46
15:AO:54:GLY:O	15:AO:57:ARG:HB3	2.15	0.46
15:AO:73:ASP:OD1	15:AO:75:ALA:HB3	2.15	0.46
21:AU:38:GLU:HG3	21:AU:41:THR:OG1	2.16	0.46
23:AW:147:ASP:HB3	39:BG:91:VAL:CG1	2.45	0.46
23:AW:315:VAL:HG11	23:AW:346:LEU:HD12	1.98	0.46
23:AW:449:VAL:HG23	23:AW:463:TYR:OH	2.15	0.46
23:AW:523:PHE:O	23:AW:525:GLN:NE2	2.49	0.46
24:B0:23:LYS:HD3	33:BA:855:G:H1'	1.97	0.46
33:BA:868:U:C4	33:BA:869:G:N7	2.84	0.46
33:BA:1080:A:H4'	41:BI:126:ARG:HB2	1.97	0.46
33:BA:1126:A:H4'	33:BA:1127:A:O5'	2.15	0.46
33:BA:1174:U:O2	33:BA:1174:U:H2'	2.14	0.46
33:BA:2335:A:OP1	48:BS:13:ARG:HD2	2.15	0.46
33:BA:2557:G:H2'	33:BA:2558:C:H6	1.81	0.46
33:BA:2677:G:H2'	33:BA:2678:C:H6	1.79	0.46
33:BA:2813:A:H2'	33:BA:2814:A:C8	2.50	0.46
35:BC:180:MET:HB2	35:BC:267:VAL:HB	1.96	0.46
36:BD:117:GLY:HA2	36:BD:164:GLN:NE2	2.30	0.46
39:BG:61:TRP:HA	39:BG:61:TRP:CE3	2.49	0.46
1:AA:337:G:H2'	1:AA:338:A:H8	1.80	0.46
1:AA:902:G:O2'	1:AA:903:G:H5'	2.16	0.46
1:AA:1302:C:H5''	1:AA:1303:C:OP2	2.15	0.46
2:AB:148:GLY:HA2	2:AB:151:LYS:HE2	1.98	0.46
3:AC:96:VAL:HB	3:AC:97:PRO:HD2	1.98	0.46
8:AH:74:ILE:HD13	8:AH:128:VAL:HG22	1.97	0.46
9:AI:111:GLU:OE2	9:AI:114:LYS:NZ	2.46	0.46
20:AT:27:MET:CE	20:AT:57:VAL:HG22	2.45	0.46
23:AW:22:PRO:HA	56:AW:601:GNP:O2G	2.15	0.46
23:AW:306:ASN:HD21	23:AW:313:ASP:HB2	1.80	0.46
23:AW:491:SER:HB2	23:AW:492:GLN:HB2	1.98	0.46
32:B8:9:LYS:H	32:B8:9:LYS:HD3	1.80	0.46
33:BA:829:A:N7	33:BA:2248:C:H5'	2.31	0.46
33:BA:1412:U:H2'	33:BA:1413:A:C8	2.51	0.46
33:BA:2578:G:N7	36:BD:145:SER:HB2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BC:70:LYS:NZ	35:BC:97:ASP:OD2	2.49	0.46
35:BC:180:MET:HB2	35:BC:268:ARG:H	1.80	0.46
35:BC:250:GLN:CD	35:BC:250:GLN:H	2.17	0.46
38:BF:71:LYS:HD3	38:BF:71:LYS:HA	1.81	0.46
43:BN:40:HIS:C	50:BU:66:ALA:HB1	2.36	0.46
45:BP:21:ARG:HD3	45:BP:21:ARG:HA	1.64	0.46
53:BX:17:SER:H	53:BX:21:SER:CB	2.28	0.46
1:AA:169:C:H2'	1:AA:170:U:H6	1.80	0.46
1:AA:975:A:N1	1:AA:1366:C:O2'	2.46	0.46
2:AB:222:GLU:OE1	2:AB:225:SER:HA	2.16	0.46
12:AL:78:VAL:HG12	12:AL:101:LEU:HD23	1.96	0.46
16:AP:38:PHE:CE2	16:AP:51:ARG:HB3	2.50	0.46
33:BA:995:C:O2'	33:BA:996:A:P	2.74	0.46
33:BA:1652:A:N7	33:BA:1653:G:C6	2.84	0.46
33:BA:1669:A:H5''	33:BA:2550:G:OP1	2.15	0.46
33:BA:1789:A:H2'	33:BA:1790:C:O4'	2.16	0.46
33:BA:1827:U:H2'	33:BA:1828:G:O4'	2.15	0.46
33:BA:2297:A:C2	33:BA:2298:A:C8	3.03	0.46
33:BA:2800:A:H3'	33:BA:2801:G:H5'	1.98	0.46
33:BA:2846:G:P	49:BT:52:ARG:HH12	2.39	0.46
33:BA:2849:U:OP1	49:BT:92:ARG:NH1	2.48	0.46
44:BO:59:LYS:HE2	44:BO:89:ASN:ND2	2.31	0.46
53:BX:28:ASN:HA	53:BX:91:GLN:HE22	1.81	0.46
1:AA:868:C:H2'	1:AA:869:G:O4'	2.15	0.46
1:AA:1058:G:H2'	1:AA:1059:C:O4'	2.16	0.46
3:AC:34:SER:O	3:AC:38:VAL:HG13	2.16	0.46
5:AE:131:ASN:O	5:AE:135:VAL:HG12	2.16	0.46
16:AP:10:GLY:HA3	16:AP:16:PHE:N	2.30	0.46
23:AW:30:THR:HG23	23:AW:86:LEU:HD21	1.97	0.46
25:B1:15:ASN:OD1	25:B1:25:LYS:HD3	2.15	0.46
33:BA:208:C:H2'	33:BA:209:C:C6	2.50	0.46
33:BA:639:U:H2'	33:BA:640:C:H6	1.78	0.46
33:BA:816:C:H2'	33:BA:817:C:C6	2.51	0.46
33:BA:954:G:C5	33:BA:955:U:C5	3.04	0.46
33:BA:1061:U:O2'	33:BA:1070:A:H4'	2.16	0.46
33:BA:1805:A:H5''	35:BC:247:TRP:CE2	2.51	0.46
33:BA:1947:C:H2'	33:BA:1948:G:H8	1.79	0.46
33:BA:2636:C:H2'	33:BA:2637:U:C6	2.51	0.46
36:BD:13:ARG:NE	36:BD:21:SER:OG	2.32	0.46
36:BD:172:VAL:HG23	36:BD:194:PRO:HD3	1.97	0.46
39:BG:25:ILE:HG22	39:BG:78:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BG:104:LEU:HB2	39:BG:112:VAL:CG2	2.45	0.46
42:BM:2:ILE:HD12	42:BM:5:ASP:HB2	1.97	0.46
43:BN:80:HIS:HB2	43:BN:81:ILE:HG22	1.98	0.46
43:BN:105:VAL:HG11	43:BN:122:LEU:CD2	2.45	0.46
46:BQ:33:LEU:CD2	46:BQ:128:THR:HB	2.46	0.46
46:BQ:53:MET:HE2	46:BQ:53:MET:HB2	1.59	0.46
51:BV:49:ILE:HD13	51:BV:49:ILE:H	1.81	0.46
1:AA:15:G:C6	1:AA:16:A:C5	3.03	0.46
1:AA:363:A:OP1	12:AL:29:LYS:HE2	2.16	0.46
1:AA:734:G:C2	1:AA:735:C:C2	3.03	0.46
1:AA:811:C:O2'	1:AA:901:A:N1	2.47	0.46
1:AA:981:U:O3'	14:AN:62:ARG:NH2	2.49	0.46
1:AA:1054:C:O2'	1:AA:1055:A:H5''	2.16	0.46
1:AA:1401:G:H2'	1:AA:1402:C:O4'	2.16	0.46
3:AC:13:ILE:HB	3:AC:14:VAL:HG23	1.97	0.46
19:AS:52:ASN:HB2	19:AS:76:THR:HA	1.98	0.46
25:B1:35:HIS:HB3	25:B1:37:PHE:CE2	2.51	0.46
33:BA:286:U:H2'	33:BA:287:G:C8	2.51	0.46
33:BA:452:G:C6	33:BA:453:A:C6	3.03	0.46
33:BA:1005:C:H2'	33:BA:1006:C:H6	1.80	0.46
36:BD:110:THR:HB	36:BD:202:ILE:HB	1.98	0.46
46:BQ:108:VAL:HG13	46:BQ:109:PRO:HD2	1.96	0.46
48:BS:53:THR:O	48:BS:59:ALA:HB2	2.16	0.46
49:BT:81:ASP:OD2	49:BT:82:SER:N	2.48	0.46
54:BY:48:VAL:O	54:BY:53:GLN:HB3	2.16	0.46
1:AA:991:U:H5''	1:AA:992:U:OP1	2.16	0.46
2:AB:14:HIS:O	2:AB:202:ASN:HB2	2.16	0.46
11:AK:16:SER:O	11:AK:78:ILE:HA	2.16	0.46
11:AK:87:GLY:N	11:AK:113:THR:HG22	2.09	0.46
24:B0:11:ASN:ND2	33:BA:2264:C:H41	2.14	0.46
25:B1:31:ASN:O	25:B1:51:SER:HA	2.15	0.46
33:BA:27:G:O2'	33:BA:28:A:O5'	2.33	0.46
33:BA:1205:A:H4'	33:BA:1206:G:OP2	2.16	0.46
33:BA:1534:U:H5'	33:BA:1535:A:OP1	2.15	0.46
33:BA:1936:A:C2	33:BA:1943:U:C5	3.03	0.46
33:BA:2840:C:H2'	33:BA:2841:C:H6	1.80	0.46
39:BG:137:LYS:O	39:BG:140:ILE:HG13	2.15	0.46
41:BI:32:VAL:HG22	41:BI:66:PHE:CG	2.51	0.46
46:BQ:33:LEU:HD22	46:BQ:128:THR:HB	1.98	0.46
1:AA:246:A:H4'	1:AA:247:G:OP1	2.15	0.46
1:AA:858:G:O2'	1:AA:859:G:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1110:A:H8	1:AA:1110:A:O5'	1.99	0.46
1:AA:1479:C:H2'	1:AA:1480:A:C8	2.51	0.46
3:AC:86:LEU:O	3:AC:90:VAL:HG23	2.15	0.46
3:AC:113:LYS:HD3	3:AC:184:ASN:CG	2.35	0.46
4:AD:23:GLY:HA2	4:AD:108:ALA:HB1	1.98	0.46
4:AD:58:GLN:O	4:AD:62:ARG:HG2	2.16	0.46
23:AW:94:ASP:HB3	23:AW:442:GLY:HA3	1.98	0.46
23:AW:169:ILE:HG22	23:AW:170:THR:HG23	1.97	0.46
33:BA:34:U:H4'	33:BA:35:G:OP2	2.14	0.46
33:BA:1059:G:H5''	33:BA:1060:U:H3'	1.98	0.46
33:BA:2417:C:C2	33:BA:2418:A:C8	3.04	0.46
36:BD:104:VAL:HG11	36:BD:205:PRO:HB3	1.98	0.46
37:BE:5:LEU:HD23	37:BE:5:LEU:HA	1.65	0.46
45:BP:95:LEU:HD23	45:BP:100:ILE:HD11	1.98	0.46
46:BQ:35:ALA:O	46:BQ:128:THR:HA	2.16	0.46
53:BX:11:LEU:HD11	53:BX:47:VAL:HG22	1.98	0.46
1:AA:635:A:H2'	1:AA:636:U:C6	2.51	0.45
1:AA:1281:C:H5''	1:AA:1282:C:C5	2.38	0.45
2:AB:10:LYS:HB2	2:AB:10:LYS:HE3	1.69	0.45
4:AD:7:LYS:HG3	4:AD:8:LEU:HD22	1.97	0.45
5:AE:12:GLU:HB3	5:AE:38:VAL:HG12	1.98	0.45
5:AE:106:ALA:HB2	5:AE:124:ALA:HB3	1.97	0.45
7:AG:23:ALA:O	7:AG:26:VAL:HG22	2.16	0.45
9:AI:90:ASP:OD2	9:AI:93:LEU:HG	2.16	0.45
22:AV:15:A:N3	22:AV:15:A:H2'	2.30	0.45
33:BA:265:A:H4'	33:BA:266:G:OP1	2.16	0.45
33:BA:2259:U:H2'	33:BA:2260:C:H6	1.81	0.45
33:BA:2305:U:C4	33:BA:2306:C:C4	3.04	0.45
33:BA:2758:A:H2'	33:BA:2759:G:H5'	1.98	0.45
33:BA:2784:U:H2'	33:BA:2785:C:C6	2.51	0.45
43:BN:19:ASP:OD2	43:BN:58:ASN:HB2	2.15	0.45
51:BV:49:ILE:HG12	51:BV:49:ILE:O	2.17	0.45
1:AA:148:G:O2'	1:AA:1446:A:N3	2.37	0.45
1:AA:719:C:N4	18:AR:59:LYS:HE2	2.31	0.45
3:AC:163:ARG:NH1	3:AC:165:GLU:OE2	2.49	0.45
5:AE:44:ARG:HG2	5:AE:72:ASN:OD1	2.17	0.45
5:AE:143:LEU:O	5:AE:146:MET:HB3	2.16	0.45
6:AF:38:ARG:HE	6:AF:97:THR:HA	1.82	0.45
7:AG:121:ASN:O	7:AG:125:ASP:HB2	2.15	0.45
9:AI:86:LEU:O	9:AI:93:LEU:HD11	2.15	0.45
23:AW:68:ILE:HD11	56:AW:601:GNP:H5'1	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1062:G:H2'	33:BA:1063:G:C8	2.51	0.45
33:BA:1070:A:C2	41:BI:9:LYS:HG2	2.52	0.45
33:BA:1139:G:O2'	33:BA:1143:A:N1	2.40	0.45
33:BA:1361:G:H2'	33:BA:1362:C:C6	2.51	0.45
33:BA:2137:U:O4	33:BA:2154:A:C6	2.69	0.45
33:BA:2154:A:C4	33:BA:2155:U:H1'	2.52	0.45
33:BA:2897:U:H2'	33:BA:2898:U:C6	2.51	0.45
37:BE:108:ILE:HG13	37:BE:181:ILE:HG12	1.98	0.45
38:BF:39:VAL:HG12	38:BF:85:GLY:HA2	1.98	0.45
39:BG:8:VAL:HB	39:BG:49:LEU:H	1.81	0.45
39:BG:71:LEU:HD13	39:BG:74:MET:SD	2.57	0.45
55:BZ:70:ILE:HD13	55:BZ:70:ILE:HA	1.83	0.45
1:AA:345:C:HO2'	1:AA:346:G:P	2.39	0.45
1:AA:908:A:C2	1:AA:909:A:C5	3.04	0.45
8:AH:79:ARG:HG3	8:AH:82:LEU:H	1.80	0.45
12:AL:102:ASP:OD1	23:AW:407:LEU:CD1	2.44	0.45
23:AW:310:LYS:HE2	23:AW:310:LYS:HB3	1.67	0.45
24:B0:22:VAL:O	24:B0:25:PHE:HD2	1.99	0.45
24:B0:28:GLU:O	24:B0:31:LEU:HG	2.16	0.45
26:B2:16:THR:O	26:B2:20:ASN:HB2	2.16	0.45
33:BA:1070:A:C2	33:BA:1097:U:H4'	2.52	0.45
33:BA:1082:U:O3'	40:BH:41:LEU:HD13	2.16	0.45
35:BC:158:GLY:H	35:BC:194:VAL:HG13	1.80	0.45
38:BF:2:LYS:O	38:BF:5:ASP:N	2.49	0.45
39:BG:38:ASP:N	39:BG:38:ASP:OD1	2.48	0.45
39:BG:100:ASN:O	39:BG:116:LEU:HB2	2.15	0.45
41:BI:64:ARG:HD2	41:BI:64:ARG:HA	1.64	0.45
53:BX:28:ASN:OD1	53:BX:29:THR:HG22	2.16	0.45
53:BX:50:LEU:H	53:BX:50:LEU:HD12	1.81	0.45
1:AA:403:C:H2'	1:AA:404:G:C8	2.51	0.45
1:AA:484:G:H4'	1:AA:485:U:C5'	2.46	0.45
1:AA:717:U:C4	1:AA:734:G:N7	2.84	0.45
1:AA:1144:G:N2	1:AA:1146:A:H62	2.15	0.45
1:AA:1300:G:O2'	1:AA:1301:U:P	2.74	0.45
1:AA:1410:A:N1	1:AA:1491:G:O6	2.50	0.45
2:AB:46:VAL:HA	2:AB:49:PHE:CE2	2.52	0.45
4:AD:61:ARG:HH21	4:AD:67:LEU:CD2	2.30	0.45
4:AD:137:SER:HB2	4:AD:140:ASP:OD1	2.17	0.45
8:AH:115:ALA:HA	8:AH:118:ALA:HB3	1.98	0.45
21:AU:36:PHE:HB3	21:AU:40:PRO:CD	2.46	0.45
23:AW:146:ARG:HH11	33:BA:2657:A:P	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:413:LEU:O	23:AW:417:VAL:N	2.32	0.45
24:B0:20:LEU:HD13	33:BA:2355:G:H4'	1.99	0.45
25:B1:17:ARG:NH1	33:BA:201:C:OP1	2.50	0.45
27:B3:42:ALA:O	33:BA:851:C:O2'	2.34	0.45
33:BA:523:C:H5''	33:BA:540:C:O2'	2.15	0.45
33:BA:547:A:N6	33:BA:549:G:H22	2.14	0.45
33:BA:675:A:OP1	37:BE:58:LYS:HE2	2.16	0.45
33:BA:784:G:C5	33:BA:792:A:C8	3.05	0.45
33:BA:843:G:H2'	33:BA:844:A:C8	2.52	0.45
33:BA:1476:U:H4'	33:BA:1732:C:O2'	2.16	0.45
33:BA:1569:A:N6	33:BA:1570:A:C6	2.84	0.45
33:BA:1590:A:H2'	33:BA:1591:A:C8	2.52	0.45
33:BA:1818:U:O4	35:BC:152:GLN:HG2	2.17	0.45
33:BA:1847:A:H2'	33:BA:1848:A:C8	2.52	0.45
33:BA:2228:G:H2'	33:BA:2229:U:C6	2.51	0.45
33:BA:2554:U:H2'	33:BA:2555:U:C6	2.52	0.45
33:BA:2741:A:H2'	33:BA:2742:G:O4'	2.16	0.45
35:BC:105:ALA:O	35:BC:195:GLY:N	2.40	0.45
37:BE:106:LYS:HG3	37:BE:200:LEU:HD12	1.99	0.45
41:BI:100:ILE:HD12	41:BI:105:LEU:HD11	1.98	0.45
49:BT:62:LYS:HB3	49:BT:69:VAL:HG13	1.97	0.45
50:BU:8:ILE:H	50:BU:8:ILE:HG12	1.52	0.45
53:BX:60:THR:HB	53:BX:81:LYS:HE2	1.98	0.45
1:AA:49:U:H3	1:AA:362:G:H1'	1.81	0.45
1:AA:81:A:H2	1:AA:88:U:H3	1.64	0.45
1:AA:335:C:H2'	1:AA:336:A:H8	1.81	0.45
1:AA:537:G:H5''	12:AL:109:ARG:HH12	1.82	0.45
1:AA:662:U:O2'	1:AA:836:G:O5'	2.35	0.45
1:AA:1086:U:H5'	1:AA:1087:G:OP2	2.17	0.45
1:AA:1151:A:H5''	10:AJ:44:THR:OG1	2.17	0.45
3:AC:41:TYR:OH	3:AC:89:VAL:HG21	2.17	0.45
7:AG:74:VAL:HG11	7:AG:143:MET:HG3	1.99	0.45
11:AK:28:ASN:HB2	11:AK:56:LYS:HE3	1.99	0.45
23:AW:314:ARG:NH1	23:AW:418:GLN:O	2.50	0.45
23:AW:430:PRO:HD2	23:AW:435:ASP:O	2.17	0.45
25:B1:20:ALA:HB3	25:B1:22:ASN:OD1	2.16	0.45
28:B4:45:ASP:O	28:B4:52:LYS:HE3	2.17	0.45
30:B6:1:MET:HE3	30:B6:2:LYS:H	1.82	0.45
33:BA:27:G:H1'	33:BA:513:A:N6	2.30	0.45
33:BA:784:G:C6	35:BC:227:VAL:HG11	2.52	0.45
33:BA:859:G:H2'	33:BA:916:G:H1	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1047:G:O2'	33:BA:1110:G:N2	2.50	0.45
33:BA:1131:G:O2'	33:BA:1133:A:N7	2.40	0.45
34:BB:82:U:H2'	34:BB:83:G:H8	1.82	0.45
35:BC:132:ARG:HD3	35:BC:132:ARG:HA	1.58	0.45
36:BD:28:GLU:HA	36:BD:185:ASN:O	2.17	0.45
39:BG:15:ASP:OD2	39:BG:26:LYS:N	2.49	0.45
40:BH:132:TYR:C	40:BH:134:GLU:H	2.20	0.45
45:BP:79:LEU:HD23	45:BP:79:LEU:HA	1.70	0.45
48:BS:35:ILE:HG21	48:BS:71:ALA:HA	1.97	0.45
50:BU:16:ILE:HG23	50:BU:38:VAL:HG21	1.99	0.45
1:AA:507:C:C3'	1:AA:508:U:H5''	2.47	0.45
1:AA:511:C:O2'	1:AA:512:U:O4'	2.35	0.45
1:AA:539:A:H2'	1:AA:540:G:C8	2.51	0.45
1:AA:919:A:O5'	1:AA:919:A:H8	1.98	0.45
1:AA:1085:U:H1'	1:AA:1094:G:C6	2.52	0.45
1:AA:1114:C:C2	1:AA:1187:G:C2	3.05	0.45
2:AB:95:TRP:HH2	2:AB:100:LEU:HB2	1.82	0.45
2:AB:147:LEU:HB3	2:AB:150:ILE:CG2	2.47	0.45
4:AD:202:LEU:O	4:AD:205:LYS:HE2	2.15	0.45
12:AL:42:LYS:HG3	12:AL:88:ASP:O	2.17	0.45
13:AM:73:SER:HA	13:AM:76:ILE:HD12	1.96	0.45
23:AW:308:ASP:CG	23:AW:309:PRO:HD2	2.37	0.45
23:AW:522:GLN:OE1	23:AW:524:HIS:ND1	2.48	0.45
33:BA:139:U:C5	53:BX:1:MET:HG2	2.52	0.45
33:BA:532:A:OP2	50:BU:40:LYS:HD3	2.16	0.45
33:BA:694:U:OP1	33:BA:1569:A:H1'	2.16	0.45
33:BA:1676:A:H2'	33:BA:1677:A:O4'	2.17	0.45
33:BA:1746:A:H2'	33:BA:1747:U:C6	2.52	0.45
33:BA:2230:G:C5	33:BA:2231:U:C5	3.05	0.45
44:BO:102:PRO:HB3	44:BO:121:GLU:HB3	1.99	0.45
1:AA:1343:G:O3'	9:AI:123:ARG:HB3	2.16	0.45
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.17	0.45
2:AB:170:ILE:O	2:AB:174:GLU:HB2	2.16	0.45
4:AD:6:PRO:HB2	4:AD:9:LYS:HB2	1.99	0.45
10:AJ:67:ILE:HG13	14:AN:95:LEU:HD13	1.99	0.45
12:AL:33:CYS:H	12:AL:54:VAL:HG13	1.82	0.45
13:AM:84:CYS:O	13:AM:88:LEU:HG	2.16	0.45
14:AN:60:ARG:O	14:AN:61:ASN:HB2	2.17	0.45
16:AP:23:ASP:HB3	16:AP:26:ASN:HD22	1.81	0.45
17:AQ:13:SER:HB3	17:AQ:16:MET:HE1	1.98	0.45
19:AS:18:VAL:HG11	19:AS:43:MET:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B1:29:LEU:HD23	33:BA:2231:U:OP1	2.16	0.45
33:BA:118:A:C8	33:BA:119:A:C8	3.05	0.45
33:BA:239:C:H2'	33:BA:240:C:O4'	2.17	0.45
33:BA:478:A:C6	33:BA:480:A:C6	3.05	0.45
33:BA:623:C:H2'	33:BA:624:C:H6	1.82	0.45
33:BA:781:A:OP1	35:BC:216:ARG:NH2	2.49	0.45
33:BA:1008:A:N6	33:BA:1136:G:C6	2.85	0.45
33:BA:1138:G:H2'	33:BA:1139:G:O4'	2.16	0.45
33:BA:1289:C:H2'	33:BA:1290:C:H6	1.81	0.45
33:BA:1709:U:C2	33:BA:1750:G:N2	2.85	0.45
40:BH:12:VAL:HG13	40:BH:69:PHE:HZ	1.81	0.45
42:BL:11:VAL:HG21	42:BM:28:GLU:OE1	2.16	0.45
43:BN:13:ARG:HD3	43:BN:13:ARG:HA	1.63	0.45
46:BQ:10:ARG:HH12	46:BQ:89:VAL:H	1.65	0.45
49:BT:59:THR:OG1	49:BT:72:VAL:HG12	2.16	0.45
55:BZ:29:ILE:HD12	55:BZ:38:LEU:O	2.17	0.45
1:AA:15:G:C2	1:AA:16:A:C4	3.05	0.45
1:AA:810:C:H2'	1:AA:811:C:O4'	2.17	0.45
1:AA:928:G:C2	1:AA:1390:U:O2	2.70	0.45
1:AA:1118:U:H1'	1:AA:1179:A:C4	2.52	0.45
3:AC:49:ALA:HB1	3:AC:75:VAL:HG22	1.99	0.45
9:AI:83:THR:HG21	9:AI:102:PHE:CB	2.47	0.45
23:AW:46:VAL:O	23:AW:49:ARG:HB2	2.17	0.45
23:AW:398:PHE:O	23:AW:399:ARG:HB2	2.17	0.45
25:B1:32:LEU:HD23	25:B1:49:ARG:HE	1.81	0.45
25:B1:61:LYS:NZ	33:BA:372:G:OP1	2.50	0.45
28:B4:28:SER:HB2	28:B4:37:HIS:NE2	2.31	0.45
32:B8:9:LYS:H	32:B8:9:LYS:CD	2.30	0.45
33:BA:321:U:H5''	37:BE:131:THR:HG23	1.99	0.45
33:BA:555:G:HO2'	33:BA:556:A:H8	1.65	0.45
33:BA:871:U:H2'	33:BA:872:U:C6	2.51	0.45
33:BA:1212:G:HO2'	33:BA:1213:A:P	2.38	0.45
33:BA:1509:A:O2'	33:BA:1510:G:H8	2.00	0.45
33:BA:1509:A:O2'	33:BA:1510:G:P	2.74	0.45
38:BF:146:ASP:HB2	38:BF:149:ARG:HH21	1.82	0.45
40:BH:117:LEU:O	40:BH:119:PRO:HD2	2.17	0.45
40:BH:126:LEU:HD13	40:BH:127:ALA:H	1.81	0.45
42:BL:15:SER:OG	42:BL:16:VAL:N	2.50	0.45
50:BU:65:ASN:HD21	50:BU:69:ARG:NH2	2.15	0.45
1:AA:268:U:H2'	1:AA:269:C:C6	2.51	0.45
1:AA:575:G:C6	1:AA:821:G:N7	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:681:A:C2	1:AA:710:G:C2	3.05	0.45
1:AA:801:U:H2'	1:AA:802:A:C8	2.52	0.45
1:AA:983:A:H5'	14:AN:2:LYS:HZ1	1.80	0.45
1:AA:1306:A:N6	1:AA:1331:G:H1'	2.31	0.45
1:AA:1461:G:H2'	1:AA:1462:C:C6	2.52	0.45
2:AB:130:LYS:HA	2:AB:130:LYS:NZ	2.30	0.45
7:AG:144:ALA:C	7:AG:146:ALA:H	2.21	0.45
8:AH:85:TYR:O	8:AH:86:LYS:HD2	2.17	0.45
27:B3:37:ARG:HH12	33:BA:929:U:H4'	1.82	0.45
33:BA:49:A:N6	33:BA:177:G:C4	2.85	0.45
33:BA:1006:C:C2	33:BA:1138:G:N2	2.85	0.45
33:BA:1097:U:C5	33:BA:1098:A:H1'	2.52	0.45
33:BA:1316:U:H2'	33:BA:1317:G:H8	1.79	0.45
33:BA:1589:U:H2'	33:BA:1590:A:C8	2.52	0.45
33:BA:2109:U:C4	33:BA:2181:U:O4	2.70	0.45
33:BA:2197:U:O2'	33:BA:2198:A:O5'	2.34	0.45
38:BF:33:ILE:HG12	38:BF:95:MET:HG3	1.99	0.45
40:BH:51:TYR:HB2	40:BH:89:PRO:CD	2.47	0.45
41:BI:123:ALA:HA	41:BI:126:ARG:NE	2.32	0.45
43:BN:36:LEU:HD21	43:BN:122:LEU:HB2	1.98	0.45
43:BN:42:ALA:O	43:BN:44:TYR:HB3	2.17	0.45
43:BN:81:ILE:HG12	43:BN:82:GLY:H	1.81	0.45
44:BO:73:ASP:O	49:BT:74:GLN:HG3	2.17	0.45
49:BT:20:ARG:HB3	49:BT:23:ASP:OD1	2.16	0.45
1:AA:340:U:C2	1:AA:350:G:N2	2.85	0.45
1:AA:695:A:H2'	1:AA:696:A:C8	2.51	0.45
1:AA:1053:G:N7	1:AA:1200:C:H5''	2.32	0.45
1:AA:1168:U:H5''	1:AA:1169:A:OP2	2.17	0.45
1:AA:1348:U:H4'	9:AI:121:ARG:HG3	1.99	0.45
2:AB:44:LYS:HD2	2:AB:44:LYS:HA	1.72	0.45
15:AO:29:ALA:HA	15:AO:84:LEU:HD21	1.98	0.45
16:AP:23:ASP:HB3	16:AP:26:ASN:ND2	2.32	0.45
17:AQ:66:LEU:HD23	17:AQ:66:LEU:HA	1.81	0.45
33:BA:38:A:N3	37:BE:43:THR:HB	2.32	0.45
33:BA:878:A:C6	33:BA:900:A:H1'	2.51	0.45
33:BA:1223:G:C6	33:BA:1227:G:C6	3.05	0.45
33:BA:1239:G:H2'	33:BA:1240:U:O4'	2.16	0.45
33:BA:1607:C:H5''	33:BA:1608:A:H5'	1.98	0.45
33:BA:1858:A:H8	33:BA:1858:A:OP2	2.00	0.45
33:BA:1923:U:H2'	33:BA:1924:C:H6	1.78	0.45
33:BA:2093:G:H1'	33:BA:2198:A:H2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2328:A:H2'	33:BA:2329:U:C6	2.52	0.45
33:BA:2662:A:H2'	33:BA:2663:G:O4'	2.17	0.45
33:BA:2755:C:O2'	33:BA:2756:U:H2'	2.17	0.45
36:BD:110:THR:N	36:BD:202:ILE:O	2.49	0.45
39:BG:37:ASN:HB3	39:BG:40:VAL:HG13	1.99	0.45
39:BG:130:ILE:HG22	39:BG:132:LEU:HD22	1.99	0.45
40:BH:32:GLY:HA2	40:BH:108:VAL:CG2	2.47	0.45
49:BT:57:ALA:HB2	49:BT:74:GLN:HA	1.98	0.45
1:AA:205:A:H3'	1:AA:206:C:C6	2.51	0.44
1:AA:253:A:H2'	1:AA:254:G:C8	2.51	0.44
1:AA:1321:U:C4	1:AA:1322:C:N4	2.85	0.44
2:AB:53:LEU:HA	2:AB:56:LEU:HB3	1.98	0.44
4:AD:169:TRP:HB2	4:AD:183:ARG:O	2.15	0.44
21:AU:39:LYS:N	21:AU:40:PRO:HD2	2.32	0.44
23:AW:125:LYS:O	23:AW:129:VAL:HG23	2.18	0.44
23:AW:145:ASP:O	23:AW:176:GLY:HA2	2.17	0.44
24:B0:17:ALA:O	24:B0:18:LYS:HB2	2.17	0.44
27:B3:23:LEU:HD12	27:B3:23:LEU:HA	1.86	0.44
31:B7:26:ALA:O	31:B7:43:LEU:HD13	2.17	0.44
33:BA:861:A:H2'	33:BA:862:G:O4'	2.17	0.44
33:BA:933:A:H5'	33:BA:934:U:OP2	2.16	0.44
33:BA:2094:A:C2	33:BA:2196:C:C2	3.04	0.44
33:BA:2308:G:H2'	33:BA:2310:C:H41	1.82	0.44
33:BA:2398:U:H2'	33:BA:2399:G:H8	1.81	0.44
33:BA:2880:C:H1'	47:BR:92:GLY:H	1.82	0.44
33:BA:2881:U:H2'	33:BA:2882:A:H8	1.82	0.44
35:BC:172:THR:HG22	35:BC:182:LYS:HG2	1.97	0.44
36:BD:27:ILE:HB	36:BD:187:LEU:HB3	1.99	0.44
37:BE:137:LYS:O	37:BE:141:MET:HG3	2.17	0.44
37:BE:147:LEU:HB3	37:BE:186:VAL:HG23	1.98	0.44
38:BF:133:GLU:H	38:BF:150:GLY:HA3	1.82	0.44
40:BH:136:ILE:HD12	40:BH:136:ILE:H	1.81	0.44
41:BI:20:SER:HB3	41:BI:21:PRO:HD3	1.99	0.44
41:BI:44:LYS:HA	41:BI:44:LYS:HD2	1.77	0.44
45:BP:51:GLU:OE1	45:BP:56:PRO:HA	2.17	0.44
50:BU:59:LEU:HD23	50:BU:59:LEU:HA	1.83	0.44
54:BY:94:PHE:HD1	54:BY:99:SER:HA	1.81	0.44
55:BZ:10:LYS:HD3	55:BZ:10:LYS:H	1.82	0.44
1:AA:243:A:N6	1:AA:281:G:O2'	2.49	0.44
1:AA:1071:C:H2'	1:AA:1072:G:C8	2.52	0.44
5:AE:15:ILE:HD12	5:AE:109:ALA:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:8:ASP:HA	8:AH:11:THR:HG22	1.98	0.44
8:AH:46:GLU:HA	8:AH:63:LYS:HD2	2.00	0.44
20:AT:78:LEU:HD23	20:AT:78:LEU:HA	1.54	0.44
23:AW:100:TYR:CE1	23:AW:129:VAL:HG21	2.52	0.44
23:AW:304:GLN:HG2	23:AW:305:ALA:N	2.31	0.44
33:BA:586:A:C2	33:BA:1254:A:C2	3.06	0.44
33:BA:1103:A:H5''	33:BA:1104:C:C5	2.52	0.44
33:BA:1177:G:H2'	33:BA:1178:C:O4'	2.16	0.44
33:BA:1275:A:H3'	33:BA:1645:G:O2'	2.16	0.44
33:BA:1568:G:C4'	35:BC:58:LYS:HB3	2.38	0.44
33:BA:1818:U:O2'	33:BA:1819:A:P	2.75	0.44
33:BA:2690:U:O2'	33:BA:2872:A:H1'	2.17	0.44
38:BF:63:LYS:HA	38:BF:64:PRO:HD3	1.81	0.44
38:BF:98:PHE:HA	38:BF:101:ARG:HG2	1.98	0.44
43:BN:55:ILE:HD11	43:BN:130:HIS:CG	2.53	0.44
44:BO:111:LYS:H	44:BO:111:LYS:CE	2.30	0.44
51:BV:71:LYS:HE3	51:BV:73:LYS:HE3	1.99	0.44
1:AA:130:A:O2'	1:AA:264:C:H5'	2.16	0.44
1:AA:1219:A:H2'	1:AA:1220:G:H8	1.82	0.44
1:AA:1277:C:O2'	1:AA:1279:G:H1'	2.17	0.44
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.53	0.44
9:AI:21:LYS:HE3	9:AI:21:LYS:HB3	1.72	0.44
17:AQ:12:VAL:O	17:AQ:13:SER:HB2	2.18	0.44
19:AS:39:ILE:HD13	19:AS:61:VAL:HG12	1.98	0.44
24:B0:44:PHE:O	24:B0:78:PHE:HA	2.17	0.44
25:B1:16:ASN:ND2	33:BA:2081:U:H5''	2.32	0.44
33:BA:125:A:H4'	33:BA:126:A:OP2	2.18	0.44
33:BA:511:U:H4'	33:BA:1235:G:H4'	1.98	0.44
33:BA:899:A:C2'	33:BA:900:A:H8	2.28	0.44
33:BA:2031:A:C6	33:BA:2498:C:H1'	2.52	0.44
33:BA:2197:U:C2'	33:BA:2198:A:H2'	2.47	0.44
33:BA:2561:U:H4'	44:BO:22:ILE:HD11	1.97	0.44
47:BR:8:ARG:HD2	47:BR:10:LEU:HD11	2.00	0.44
47:BR:8:ARG:O	47:BR:10:LEU:HD22	2.17	0.44
53:BX:69:ARG:HB3	53:BX:70:HIS:H	1.60	0.44
54:BY:42:LYS:HD3	54:BY:42:LYS:N	2.32	0.44
1:AA:376:G:C2	1:AA:389:A:C2	3.05	0.44
1:AA:1237:C:O2'	1:AA:1300:G:N2	2.40	0.44
1:AA:1300:G:HO2'	1:AA:1301:U:P	2.39	0.44
2:AB:40:ILE:HG21	2:AB:201:GLY:N	2.27	0.44
4:AD:151:GLN:H	4:AD:154:VAL:CG1	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:54:THR:HG23	8:AH:55:LYS:HD3	1.99	0.44
13:AM:93:GLY:HA2	13:AM:108:ARG:NH1	2.33	0.44
16:AP:40:ASN:HA	16:AP:41:PRO:HD2	1.88	0.44
24:B0:20:LEU:CD1	33:BA:2355:G:H4'	2.47	0.44
33:BA:271:G:H1'	33:BA:272:A:C8	2.52	0.44
33:BA:612:G:C2	33:BA:614:A:H1'	2.51	0.44
33:BA:2423:U:O2'	33:BA:2424:C:P	2.76	0.44
33:BA:2727:A:O2'	44:BO:70:ARG:NH2	2.50	0.44
35:BC:129:LEU:HD12	35:BC:191:LEU:HD21	2.00	0.44
35:BC:153:LEU:H	35:BC:153:LEU:HG	1.44	0.44
41:BI:30:GLN:HG2	41:BI:32:VAL:H	1.83	0.44
42:BL:17:MET:O	42:BL:21:GLU:HG3	2.17	0.44
53:BX:8:LEU:HA	53:BX:8:LEU:HD13	1.46	0.44
1:AA:479:U:O2'	1:AA:480:U:H5'	2.17	0.44
1:AA:595:A:C5	1:AA:641:U:C4	3.05	0.44
1:AA:664:G:H2'	1:AA:666:G:OP1	2.18	0.44
1:AA:685:G:H2'	1:AA:686:U:C6	2.53	0.44
1:AA:859:G:H2'	1:AA:860:A:C8	2.53	0.44
1:AA:923:A:OP1	5:AE:25:LYS:HG2	2.17	0.44
1:AA:962:C:H2'	1:AA:963:G:H8	1.83	0.44
2:AB:116:LEU:HD12	2:AB:140:LEU:HD11	1.99	0.44
3:AC:83:VAL:HG12	3:AC:100:ILE:HG21	1.99	0.44
19:AS:37:SER:O	19:AS:70:LEU:HG	2.17	0.44
23:AW:19:ILE:HA	23:AW:89:THR:OG1	2.18	0.44
33:BA:585:G:H5''	33:BA:586:A:OP1	2.17	0.44
33:BA:859:G:H2'	33:BA:916:G:N1	2.33	0.44
33:BA:1340:U:C5	33:BA:1603:A:C8	3.06	0.44
33:BA:1465:G:H2'	33:BA:1466:U:O4'	2.18	0.44
33:BA:1656:C:C2	33:BA:1657:U:C5	3.05	0.44
33:BA:2022:U:O2'	33:BA:2617:U:H5'	2.17	0.44
33:BA:2023:C:H4'	33:BA:2617:U:O3'	2.17	0.44
33:BA:2137:U:H6	33:BA:2137:U:O5'	2.01	0.44
35:BC:156:SER:O	35:BC:194:VAL:HG11	2.18	0.44
37:BE:75:SER:O	37:BE:78:TRP:HB2	2.17	0.44
38:BF:110:ILE:HD11	38:BF:136:ILE:HD13	1.99	0.44
40:BH:25:ALA:CA	40:BH:85:SER:HG	2.31	0.44
43:BN:114:LEU:HD23	43:BN:114:LEU:HA	1.80	0.44
46:BQ:10:ARG:NH1	46:BQ:89:VAL:H	2.15	0.44
1:AA:186:C:O4'	20:AT:75:LYS:HD2	2.18	0.44
1:AA:255:G:H4'	17:AQ:18:LYS:HD2	1.98	0.44
1:AA:567:G:H2'	1:AA:568:G:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:23:THR:HA	5:AE:28:ARG:HA	2.00	0.44
6:AF:9:MET:HA	6:AF:58:HIS:O	2.17	0.44
9:AI:16:ALA:CB	9:AI:78:ILE:HD13	2.48	0.44
10:AJ:11:LYS:HE2	10:AJ:71:LEU:HD21	1.99	0.44
13:AM:46:GLU:HG3	13:AM:46:GLU:O	2.17	0.44
14:AN:27:LYS:HE3	14:AN:27:LYS:HB2	1.91	0.44
23:AW:89:THR:HA	23:AW:90:PRO:HD2	1.59	0.44
23:AW:472:ARG:CD	23:AW:503:TYR:HB3	2.44	0.44
25:B1:39:VAL:HG21	25:B1:42:GLU:HB2	1.99	0.44
27:B3:40:THR:O	27:B3:43:ILE:HG13	2.18	0.44
33:BA:77:G:C6	33:BA:78:U:C4	3.06	0.44
33:BA:644:A:H61	33:BA:2349:G:H21	1.66	0.44
33:BA:1376:C:N4	33:BA:1377:G:C6	2.86	0.44
33:BA:1830:C:H6	33:BA:1830:C:O5'	2.01	0.44
33:BA:2182:U:H2'	33:BA:2183:A:OP1	2.17	0.44
33:BA:2621:G:P	36:BD:124:ARG:HH22	2.40	0.44
33:BA:2646:C:H2'	33:BA:2647:U:O4'	2.17	0.44
34:BB:116:G:H2'	34:BB:117:G:C8	2.51	0.44
35:BC:171:VAL:HG23	35:BC:185:ALA:CB	2.47	0.44
37:BE:123:LYS:HG3	37:BE:124:PHE:H	1.82	0.44
39:BG:168:VAL:O	39:BG:170:THR:HG23	2.18	0.44
40:BH:14:GLU:HA	40:BH:17:GLU:HG3	2.00	0.44
47:BR:20:MET:O	47:BR:23:ASN:HB2	2.18	0.44
48:BS:94:ARG:H	48:BS:94:ARG:HG3	1.50	0.44
1:AA:110:C:H2'	1:AA:111:G:O4'	2.17	0.44
1:AA:391:G:C6	1:AA:392:C:C4	3.06	0.44
1:AA:505:G:C6	1:AA:535:A:C2	3.05	0.44
1:AA:1111:A:N1	3:AC:176:THR:OG1	2.43	0.44
3:AC:155:ARG:HH11	3:AC:192:TYR:HB2	1.82	0.44
4:AD:8:LEU:O	4:AD:12:ARG:HG3	2.18	0.44
4:AD:84:ASN:O	4:AD:88:ASN:ND2	2.45	0.44
10:AJ:80:THR:HB	10:AJ:83:THR:CG2	2.47	0.44
11:AK:60:PHE:O	11:AK:64:VAL:HG13	2.17	0.44
23:AW:428:PHE:N	23:AW:437:ILE:O	2.46	0.44
23:AW:452:ARG:O	23:AW:459:VAL:HG23	2.16	0.44
23:AW:474:VAL:CG2	23:AW:501:LEU:H	2.31	0.44
33:BA:7:G:H4'	43:BN:15:TRP:CZ2	2.53	0.44
33:BA:1212:G:HO2'	33:BA:1236:G:N2	2.14	0.44
33:BA:1342:A:O2'	33:BA:1344:U:OP2	2.26	0.44
36:BD:68:PHE:HB2	36:BD:73:VAL:HG12	1.99	0.44
36:BD:106:LYS:H	36:BD:106:LYS:HD2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BE:18:THR:HG22	37:BE:106:LYS:HE3	2.00	0.44
40:BH:24:SER:HB2	40:BH:116:GLU:CD	2.38	0.44
41:BI:109:ALA:HA	41:BI:128:ILE:HD12	2.00	0.44
43:BN:4:PHE:N	43:BN:44:TYR:OH	2.51	0.44
1:AA:187:G:C2	1:AA:191:G:C6	3.06	0.44
1:AA:589:U:H2'	1:AA:590:U:C6	2.52	0.44
1:AA:607:A:H2'	1:AA:608:A:C8	2.52	0.44
1:AA:1219:A:H2'	1:AA:1220:G:C8	2.53	0.44
2:AB:82:ALA:O	2:AB:88:GLN:NE2	2.49	0.44
3:AC:19:SER:HB3	14:AN:91:GLU:O	2.17	0.44
24:B0:16:GLU:HB2	24:B0:17:ALA:H	1.34	0.44
33:BA:156:A:H2'	33:BA:157:C:C6	2.53	0.44
33:BA:800:A:H8	33:BA:800:A:OP1	2.00	0.44
33:BA:817:C:C2	33:BA:818:G:C8	3.06	0.44
33:BA:2572:A:OP1	33:BA:2574:G:H4'	2.18	0.44
33:BA:2591:C:OP1	35:BC:237:ARG:HG3	2.18	0.44
37:BE:153:LEU:HB2	37:BE:171:ASP:HB3	1.99	0.44
44:BO:70:ARG:HD3	44:BO:76:VAL:HG22	2.00	0.44
1:AA:29:U:H5'	1:AA:296:U:OP1	2.18	0.44
1:AA:69:G:H5'	1:AA:70:U:OP1	2.17	0.44
1:AA:727:G:C2	1:AA:731:G:C2	3.05	0.44
1:AA:728:A:C6	1:AA:729:A:C6	3.05	0.44
1:AA:946:A:H2'	1:AA:947:G:C8	2.53	0.44
6:AF:52:ASN:O	6:AF:53:LYS:HB2	2.18	0.44
9:AI:43:ALA:O	9:AI:46:VAL:HG22	2.18	0.44
17:AQ:3:LYS:HE3	17:AQ:3:LYS:HB3	1.81	0.44
23:AW:407:LEU:HD22	23:AW:409:GLN:HG3	2.00	0.44
23:AW:503:TYR:O	23:AW:504:ILE:HB	2.17	0.44
33:BA:42:A:N6	33:BA:437:U:H3	2.16	0.44
33:BA:247:G:H4'	33:BA:386:G:C6	2.53	0.44
33:BA:320:A:HO2'	33:BA:322:A:H8	1.65	0.44
33:BA:520:G:H5'	52:BW:73:LYS:NZ	2.33	0.44
33:BA:569:U:C4	33:BA:570:G:C6	3.05	0.44
33:BA:1019:U:O2'	33:BA:1021:A:N7	2.42	0.44
33:BA:1187:G:OP1	51:BV:85:LYS:NZ	2.51	0.44
33:BA:1527:G:N1	33:BA:1544:A:OP2	2.40	0.44
33:BA:2730:C:H4'	36:BD:174:SER:HB3	2.00	0.44
34:BB:33:G:H2'	34:BB:34:A:O4'	2.18	0.44
40:BH:26:VAL:HG22	40:BH:82:ILE:HG21	1.99	0.44
44:BO:8:LEU:HB2	44:BO:82:ASN:HB2	1.99	0.44
1:AA:9:G:H2'	1:AA:10:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:21:G:H2'	1:AA:22:G:C8	2.53	0.43
1:AA:77:A:N6	1:AA:91:U:O4	2.51	0.43
1:AA:673:A:H2'	1:AA:674:G:C8	2.53	0.43
4:AD:57:LYS:HG3	4:AD:58:GLN:N	2.32	0.43
7:AG:64:ALA:HB1	7:AG:126:ALA:HB3	2.00	0.43
18:AR:70:THR:OG1	18:AR:72:ARG:HG2	2.18	0.43
20:AT:67:HIS:HB3	20:AT:68:LYS:NZ	2.33	0.43
27:B3:24:LEU:HD21	33:BA:930:G:H1'	2.00	0.43
31:B7:29:ARG:HD2	33:BA:2394:C:OP2	2.18	0.43
33:BA:184:C:H2'	33:BA:185:G:C8	2.50	0.43
33:BA:671:C:H2'	33:BA:672:C:H6	1.83	0.43
39:BG:53:PRO:HB3	39:BG:61:TRP:H	1.83	0.43
39:BG:84:LYS:HB2	39:BG:85:LYS:H	1.62	0.43
41:BI:56:VAL:HG21	41:BI:68:PHE:HD2	1.82	0.43
42:BK:4:LYS:O	42:BK:8:ILE:HG12	2.17	0.43
46:BQ:43:ALA:O	46:BQ:46:ILE:HG12	2.18	0.43
47:BR:78:LYS:HG2	47:BR:83:LEU:HD13	2.00	0.43
55:BZ:76:ASP:N	55:BZ:90:ASP:HB2	2.33	0.43
1:AA:55:A:C6	23:AW:311:HIS:CE1	3.06	0.43
1:AA:484:G:H4'	1:AA:485:U:H5'	2.00	0.43
1:AA:634:C:H2'	1:AA:635:A:C8	2.52	0.43
1:AA:1031:C:O2'	1:AA:1032:G:N2	2.51	0.43
1:AA:1039:G:C6	1:AA:1040:U:C4	3.06	0.43
1:AA:1225:A:H1'	19:AS:77:ARG:HD2	2.00	0.43
2:AB:164:ASP:CB	2:AB:203:ASP:HB2	2.48	0.43
5:AE:33:THR:HG22	5:AE:51:LYS:HE2	1.99	0.43
5:AE:55:VAL:O	5:AE:59:ILE:HG23	2.18	0.43
5:AE:96:GLN:HA	5:AE:97:PRO:HD2	1.50	0.43
6:AF:48:ALA:HB2	18:AR:66:LEU:O	2.18	0.43
13:AM:85:TYR:O	13:AM:88:LEU:HB2	2.18	0.43
23:AW:307:MET:HE2	23:AW:309:PRO:HD3	2.00	0.43
23:AW:390:ILE:HA	23:AW:391:PRO:HD3	1.72	0.43
23:AW:410:LYS:HA	23:AW:414:LYS:H	1.84	0.43
23:AW:466:VAL:HG12	23:AW:468:VAL:HG23	2.00	0.43
30:B6:34:ARG:NH1	30:B6:39:ARG:HG2	2.33	0.43
33:BA:569:U:H2'	33:BA:570:G:O4'	2.17	0.43
33:BA:700:G:C6	33:BA:733:G:N2	2.86	0.43
33:BA:740:C:H5''	33:BA:1784:A:OP1	2.19	0.43
33:BA:1509:A:HO2'	33:BA:1510:G:H8	1.64	0.43
33:BA:2258:C:O2'	33:BA:2426:A:H4'	2.18	0.43
34:BB:24:G:H4'	34:BB:25:U:H5	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BF:62:GLN:HB3	38:BF:63:LYS:H	1.63	0.43
38:BF:101:ARG:O	38:BF:105:ILE:HG13	2.18	0.43
40:BH:18:VAL:HA	40:BH:86:MET:HE2	2.00	0.43
40:BH:35:VAL:O	40:BH:39:THR:HG23	2.17	0.43
40:BH:134:GLU:O	40:BH:136:ILE:N	2.51	0.43
48:BS:90:VAL:O	48:BS:117:PHE:HB3	2.18	0.43
1:AA:129:A:O2'	1:AA:130:A:C8	2.70	0.43
1:AA:335:C:H2'	1:AA:336:A:C8	2.54	0.43
1:AA:427:U:OP1	4:AD:12:ARG:NH2	2.51	0.43
1:AA:865:A:H2'	1:AA:866:C:C6	2.53	0.43
1:AA:972:C:O2'	10:AJ:57:VAL:HA	2.18	0.43
1:AA:1206:G:H2'	1:AA:1207:G:O4'	2.17	0.43
6:AF:92:THR:HG22	6:AF:93:LYS:N	2.33	0.43
7:AG:117:LEU:O	7:AG:121:ASN:ND2	2.49	0.43
11:AK:102:ALA:HB3	11:AK:104:PHE:H	1.83	0.43
11:AK:106:ILE:HG12	11:AK:109:ILE:HD11	2.01	0.43
20:AT:21:ALA:O	20:AT:25:SER:HB2	2.19	0.43
23:AW:420:SER:HB3	23:AW:426:GLN:OE1	2.18	0.43
23:AW:471:ALA:HA	23:AW:472:ARG:O	2.18	0.43
26:B2:9:LYS:O	26:B2:12:GLU:N	2.51	0.43
33:BA:1045:C:C5'	33:BA:1046:A:H5'	2.47	0.43
33:BA:1074:G:H4'	33:BA:1074:G:OP1	2.17	0.43
33:BA:1095:A:H2	41:BI:29:GLN:HB3	1.83	0.43
33:BA:2335:A:C6	33:BA:2337:G:H1'	2.53	0.43
33:BA:2505:G:O2'	33:BA:2506:U:H5'	2.17	0.43
35:BC:67:LYS:HG2	35:BC:150:GLY:HA2	2.00	0.43
38:BF:46:LYS:H	38:BF:46:LYS:HD2	1.83	0.43
43:BN:56:VAL:O	43:BN:124:VAL:O	2.35	0.43
45:BP:95:LEU:HD13	45:BP:101:ILE:HD11	2.00	0.43
50:BU:63:ARG:CZ	50:BU:96:ASP:HA	2.47	0.43
52:BW:32:ALA:O	52:BW:36:LEU:HB2	2.19	0.43
53:BX:86:THR:O	53:BX:87:LEU:HG	2.19	0.43
1:AA:325:A:N6	1:AA:326:G:C2	2.87	0.43
1:AA:497:G:OP1	23:AW:480:LYS:HE2	2.18	0.43
2:AB:139:GLU:O	2:AB:143:LEU:HG	2.18	0.43
3:AC:81:GLU:O	3:AC:84:GLU:HB3	2.18	0.43
3:AC:122:GLN:HB3	3:AC:127:VAL:CG2	2.48	0.43
5:AE:121:ASN:HD22	5:AE:121:ASN:N	2.16	0.43
12:AL:29:LYS:O	12:AL:80:LEU:HD12	2.18	0.43
20:AT:78:LEU:O	20:AT:82:ILE:HG23	2.17	0.43
23:AW:49:ARG:HB3	23:AW:50:GLY:H	1.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:319:ARG:HA	23:AW:364:ILE:HD13	1.98	0.43
33:BA:207:A:H2'	33:BA:208:C:O4'	2.19	0.43
33:BA:1036:G:C6	33:BA:1120:G:C5	3.06	0.43
33:BA:1287:A:H5'	47:BR:103:ARG:HD2	1.99	0.43
33:BA:2109:U:H2'	33:BA:2110:G:H5'	1.99	0.43
33:BA:2286:G:H5''	33:BA:2287:A:O5'	2.19	0.43
33:BA:2540:C:H2'	33:BA:2541:A:O4'	2.18	0.43
33:BA:2654:A:H8	33:BA:2654:A:OP1	2.02	0.43
33:BA:2867:G:O2'	33:BA:2868:A:P	2.77	0.43
34:BB:91:C:H2'	34:BB:92:C:H6	1.83	0.43
35:BC:32:LEU:HD23	35:BC:32:LEU:HA	1.70	0.43
36:BD:109:VAL:HA	36:BD:203:VAL:HA	2.00	0.43
38:BF:135:ILE:HD11	38:BF:145:VAL:HG11	2.00	0.43
42:BK:3:THR:O	42:BK:7:ILE:HG12	2.18	0.43
45:BP:118:THR:HA	45:BP:119:PRO:HD3	1.81	0.43
45:BP:131:ALA:O	45:BP:135:ILE:HG12	2.18	0.43
1:AA:177:G:OP2	20:AT:63:LYS:NZ	2.52	0.43
1:AA:382:A:H2'	1:AA:383:A:C8	2.54	0.43
1:AA:686:U:H1'	11:AK:43:TRP:CZ2	2.54	0.43
1:AA:908:A:C2	1:AA:909:A:C4	3.07	0.43
1:AA:1309:G:P	13:AM:90:HIS:HE2	2.41	0.43
9:AI:18:VAL:HG11	9:AI:82:ILE:HG12	2.01	0.43
10:AJ:10:LEU:CD1	10:AJ:98:VAL:HG12	2.48	0.43
12:AL:21:PRO:C	12:AL:23:LEU:H	2.21	0.43
24:B0:37:VAL:HG12	24:B0:38:ARG:HD3	2.00	0.43
33:BA:244:A:H2'	33:BA:245:G:O4'	2.19	0.43
33:BA:479:A:H4'	33:BA:480:A:H5'	1.99	0.43
33:BA:733:G:H8	33:BA:733:G:O5'	2.00	0.43
33:BA:947:A:H2'	33:BA:948:C:C6	2.53	0.43
33:BA:1219:U:OP2	50:BU:18:LYS:NZ	2.41	0.43
33:BA:1650:A:C2	33:BA:2008:C:N3	2.86	0.43
33:BA:1905:C:H4'	33:BA:1929:G:H8	1.83	0.43
33:BA:2677:G:H2'	33:BA:2678:C:C6	2.54	0.43
43:BN:64:VAL:HG13	43:BN:68:LYS:HB2	2.01	0.43
47:BR:96:ARG:HD3	47:BR:98:LEU:HD21	1.99	0.43
1:AA:295:C:C4	1:AA:296:U:C4	3.07	0.43
1:AA:400:C:O2'	1:AA:401:C:H5'	2.18	0.43
2:AB:9:LEU:HD12	2:AB:42:LEU:HD22	1.99	0.43
2:AB:45:THR:HG23	2:AB:200:PRO:HG2	2.00	0.43
9:AI:48:ARG:HH21	9:AI:52:GLU:HA	1.83	0.43
23:AW:216:ASP:OD2	23:AW:216:ASP:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:B0:76:ARG:O	24:B0:78:PHE:HD2	2.01	0.43
27:B3:15:ARG:HD2	27:B3:15:ARG:N	2.34	0.43
31:B7:22:LYS:HE2	33:BA:630:G:OP1	2.19	0.43
33:BA:307:G:H2'	33:BA:309:A:OP2	2.18	0.43
33:BA:836:G:N7	33:BA:837:C:N4	2.66	0.43
33:BA:1022:G:C5	33:BA:1140:C:C4	3.06	0.43
33:BA:1038:G:C2	33:BA:1118:C:C2	3.07	0.43
33:BA:1317:G:H2'	33:BA:1318:U:O4'	2.19	0.43
33:BA:1448:G:C2	33:BA:1464:G:C2	3.06	0.43
33:BA:1460:U:H5''	33:BA:1461:C:OP2	2.18	0.43
33:BA:1851:U:C4	33:BA:1852:U:C4	3.06	0.43
33:BA:2155:U:C4	33:BA:2156:G:C6	3.06	0.43
33:BA:2291:U:H2'	33:BA:2292:U:C6	2.54	0.43
33:BA:2404:U:H2'	33:BA:2405:G:O4'	2.19	0.43
34:BB:14:U:OP2	34:BB:70:C:O2'	2.36	0.43
37:BE:146:VAL:HA	37:BE:185:LYS:O	2.18	0.43
40:BH:28:ALA:CB	40:BH:111:ALA:HB2	2.49	0.43
45:BP:78:ARG:CZ	45:BP:113:ALA:HB1	2.48	0.43
49:BT:23:ASP:OD2	49:BT:88:ARG:HA	2.18	0.43
50:BU:64:ILE:HD11	50:BU:95:ALA:CB	2.48	0.43
50:BU:86:SER:HB3	51:BV:51:VAL:HG12	1.99	0.43
53:BX:39:THR:HB	53:BX:41:ALA:N	2.32	0.43
1:AA:49:U:O4	1:AA:362:G:N2	2.51	0.43
1:AA:380:G:N2	1:AA:384:G:C6	2.86	0.43
1:AA:751:U:H1'	15:AO:22:GLY:O	2.18	0.43
1:AA:936:C:H2'	1:AA:937:A:O4'	2.18	0.43
1:AA:1064:G:N2	1:AA:1190:G:O2'	2.52	0.43
13:AM:52:ILE:HD12	13:AM:55:LEU:HD12	2.00	0.43
23:AW:401:ILE:HD12	23:AW:416:LEU:HD11	2.00	0.43
26:B2:20:ASN:O	26:B2:24:GLU:HB2	2.18	0.43
33:BA:88:G:C2	33:BA:89:A:C8	3.06	0.43
33:BA:205:G:O2'	33:BA:206:U:OP2	2.36	0.43
33:BA:408:G:H1	33:BA:419:U:H3	1.66	0.43
33:BA:452:G:N2	33:BA:458:G:C4	2.86	0.43
33:BA:748:G:O6	33:BA:751:A:H5'	2.19	0.43
33:BA:826:U:H1'	45:BP:53:GLY:H	1.83	0.43
33:BA:1063:G:H1	33:BA:1075:C:H42	1.66	0.43
33:BA:1288:G:C4	33:BA:1327:A:C2	3.06	0.43
33:BA:1290:C:C2	33:BA:1291:C:C5	3.07	0.43
33:BA:2340:A:H2'	33:BA:2341:G:C8	2.54	0.43
33:BA:2433:A:H5''	33:BA:2434:A:OP1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2692:G:H2'	33:BA:2693:G:H8	1.84	0.43
35:BC:73:ILE:HA	35:BC:74:PRO:HD3	1.85	0.43
36:BD:91:THR:O	36:BD:93:GLY:N	2.51	0.43
36:BD:117:GLY:N	36:BD:165:MET:O	2.47	0.43
40:BH:33:VAL:HG12	40:BH:35:VAL:H	1.83	0.43
49:BT:93:LYS:HG3	49:BT:94:ALA:N	2.34	0.43
51:BV:37:GLU:HB2	51:BV:53:PHE:CE1	2.53	0.43
51:BV:66:HIS:HB3	51:BV:94:THR:HA	1.99	0.43
1:AA:866:C:C4'	1:AA:919:A:H5'	2.49	0.43
2:AB:161:PHE:HA	2:AB:183:PHE:O	2.19	0.43
3:AC:18:ASN:O	3:AC:55:VAL:HA	2.19	0.43
3:AC:183:TYR:HE1	3:AC:198:LYS:HB3	1.84	0.43
4:AD:89:LEU:HD22	4:AD:199:ILE:HD12	2.01	0.43
6:AF:45:ARG:HG2	6:AF:46:GLN:N	2.33	0.43
7:AG:71:THR:O	7:AG:90:VAL:HG12	2.18	0.43
9:AI:46:VAL:HA	9:AI:49:GLN:HG3	2.01	0.43
13:AM:92:ARG:NH1	19:AS:79:TYR:CZ	2.86	0.43
23:AW:114:ASP:HB3	23:AW:117:LYS:HB2	2.01	0.43
23:AW:411:GLN:N	23:AW:414:LYS:HB3	2.13	0.43
23:AW:434:ASN:HB3	23:AW:435:ASP:H	1.41	0.43
23:AW:472:ARG:CG	23:AW:504:ILE:H	2.28	0.43
24:B0:49:ASN:HA	24:B0:61:LYS:H	1.83	0.43
33:BA:242:G:N2	33:BA:254:G:H2'	2.34	0.43
33:BA:729:G:H2'	33:BA:1775:U:H1'	2.00	0.43
33:BA:751:A:H5''	33:BA:752:A:OP1	2.19	0.43
33:BA:1288:G:C8	33:BA:1327:A:C6	3.06	0.43
33:BA:1356:G:C2	33:BA:1376:C:O2	2.71	0.43
33:BA:1652:A:OP1	47:BR:8:ARG:HD3	2.18	0.43
33:BA:2330:G:C2	33:BA:2386:A:C2	3.07	0.43
33:BA:2379:G:H4'	48:BS:21:LEU:HD11	2.00	0.43
33:BA:2551:C:C4	33:BA:2552:U:C4	3.07	0.43
33:BA:2721:A:H2'	33:BA:2722:G:O4'	2.18	0.43
33:BA:2793:C:H2'	33:BA:2794:C:C6	2.54	0.43
33:BA:2805:C:H2'	33:BA:2806:C:O4'	2.19	0.43
34:BB:38:C:H2'	34:BB:39:A:C8	2.54	0.43
42:BM:14:MET:HG2	42:BM:17:MET:HG2	2.00	0.43
43:BN:11:VAL:HG11	43:BN:50:THR:HA	2.01	0.43
43:BN:64:VAL:HG11	43:BN:69:ARG:N	2.33	0.43
52:BW:24:ILE:HD12	52:BW:24:ILE:HA	1.73	0.43
1:AA:202:G:N2	1:AA:216:U:O2	2.52	0.43
1:AA:595:A:H61	1:AA:641:U:H2'	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:2:GLN:H	3:AC:2:GLN:CD	2.23	0.43
20:AT:53:MET:O	20:AT:56:ILE:HG22	2.18	0.43
23:AW:472:ARG:HA	23:AW:473:TRP:CB	2.46	0.43
27:B3:3:THR:HA	27:B3:37:ARG:O	2.19	0.43
33:BA:540:C:H2'	33:BA:541:A:H8	1.84	0.43
33:BA:558:U:OP1	43:BN:113:PRO:HD2	2.18	0.43
33:BA:781:A:O2'	33:BA:1788:C:O2	2.34	0.43
33:BA:1225:G:N1	33:BA:1226:A:N1	2.67	0.43
33:BA:1264:A:H2'	33:BA:2014:A:N6	2.33	0.43
33:BA:2092:U:H4'	33:BA:2093:G:O5'	2.18	0.43
33:BA:2547:A:H2'	33:BA:2548:U:C6	2.54	0.43
35:BC:80:LEU:HD11	35:BC:109:LEU:HB2	2.01	0.43
37:BE:118:LEU:HD23	37:BE:186:VAL:O	2.18	0.43
41:BI:112:LYS:HB3	41:BI:115:ASP:HB3	2.01	0.43
47:BR:55:ALA:HA	47:BR:80:PHE:CZ	2.54	0.43
47:BR:99:LYS:H	47:BR:99:LYS:HG3	1.62	0.43
52:BW:20:VAL:O	52:BW:23:LEU:HB2	2.18	0.43
1:AA:791:G:N2	1:AA:1497:G:O3'	2.50	0.43
2:AB:96:LEU:H	2:AB:99:MET:HE3	1.84	0.43
2:AB:127:LYS:HD2	2:AB:127:LYS:HA	1.72	0.43
4:AD:56:GLU:OE2	4:AD:194:ILE:HA	2.19	0.43
9:AI:46:VAL:O	9:AI:49:GLN:HB2	2.18	0.43
10:AJ:44:THR:HG23	10:AJ:70:HIS:HA	2.01	0.43
12:AL:113:ARG:NH2	12:AL:120:ARG:HG2	2.34	0.43
14:AN:12:ARG:HG2	14:AN:53:ASP:HB3	2.01	0.43
23:AW:428:PHE:HB3	23:AW:504:ILE:HD11	2.01	0.43
25:B1:28:PHE:HB3	33:BA:396:G:H1'	2.01	0.43
33:BA:587:C:N3	45:BP:33:ARG:NH2	2.67	0.43
33:BA:1652:A:C2	33:BA:2006:C:N3	2.87	0.43
33:BA:1798:U:C4	33:BA:1819:A:C2	3.07	0.43
33:BA:1927:A:H2'	33:BA:1928:A:C8	2.54	0.43
33:BA:2015:A:H3'	33:BA:2016:U:H6	1.84	0.43
35:BC:222:THR:HA	35:BC:232:GLY:HA2	2.00	0.43
37:BE:27:LEU:HG	37:BE:104:ALA:HB2	2.01	0.43
37:BE:111:GLU:OE1	37:BE:115:GLN:NE2	2.45	0.43
46:BQ:26:VAL:HG13	46:BQ:104:GLU:CD	2.39	0.43
1:AA:357:G:O2'	23:AW:311:HIS:CE1	2.72	0.42
1:AA:600:A:H2'	1:AA:601:G:C8	2.54	0.42
1:AA:1057:G:O3'	3:AC:196:GLY:HA3	2.19	0.42
5:AE:94:PHE:CZ	5:AE:96:GLN:HG2	2.54	0.42
6:AF:20:GLY:O	6:AF:23:GLU:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:22:ILE:HD13	11:AK:22:ILE:H	1.84	0.42
12:AL:33:CYS:HB3	12:AL:76:HIS:O	2.18	0.42
14:AN:62:ARG:HG2	14:AN:69:PRO:HB3	2.00	0.42
17:AQ:7:LEU:O	17:AQ:59:GLU:HA	2.19	0.42
23:AW:71:THR:CG2	23:AW:72:THR:H	2.31	0.42
23:AW:96:SER:HB3	23:AW:99:THR:H	1.84	0.42
23:AW:114:ASP:CG	23:AW:143:LYS:HD2	2.40	0.42
23:AW:490:GLU:HA	23:AW:493:LEU:HB2	2.00	0.42
33:BA:571:U:C4	33:BA:575:A:C5	3.08	0.42
33:BA:592:A:C6	33:BA:593:U:C4	3.06	0.42
33:BA:621:A:OP2	45:BP:99:ASN:ND2	2.52	0.42
33:BA:1046:A:N6	40:BH:8:LYS:HE2	2.34	0.42
33:BA:1104:C:H2'	33:BA:1105:U:C6	2.54	0.42
33:BA:1236:G:O2'	33:BA:1237:A:C8	2.70	0.42
33:BA:1641:A:H2'	33:BA:1642:G:O4'	2.18	0.42
33:BA:2221:G:H2'	33:BA:2222:C:C6	2.54	0.42
34:BB:88:C:O2'	34:BB:90:C:N4	2.51	0.42
34:BB:97:C:H2'	34:BB:98:G:O4'	2.18	0.42
35:BC:94:LEU:HB2	35:BC:100:ARG:HD3	2.01	0.42
36:BD:112:THR:O	36:BD:195:GLY:HA2	2.19	0.42
38:BF:21:TYR:HE2	38:BF:28:PRO:HD3	1.84	0.42
39:BG:74:MET:O	39:BG:78:VAL:HG22	2.19	0.42
43:BN:81:ILE:HG12	43:BN:82:GLY:N	2.34	0.42
45:BP:55:MET:HA	45:BP:56:PRO:HD3	1.79	0.42
1:AA:522:C:H41	12:AL:49:ARG:HH22	1.67	0.42
1:AA:1036:A:H2'	1:AA:1037:C:C5	2.54	0.42
1:AA:1477:U:H2'	1:AA:1478:U:C6	2.54	0.42
2:AB:205:ALA:HB3	2:AB:208:ALA:HB3	2.02	0.42
7:AG:22:LEU:O	7:AG:26:VAL:HG13	2.19	0.42
7:AG:94:ARG:O	7:AG:97:ALA:HB3	2.20	0.42
8:AH:84:ILE:HG22	8:AH:124:ILE:HD11	2.00	0.42
14:AN:53:ASP:HA	14:AN:58:ARG:HH11	1.84	0.42
17:AQ:30:HIS:HA	17:AQ:31:PRO:HD3	1.75	0.42
23:AW:20:SER:CB	23:AW:26:LYS:HG2	2.49	0.42
23:AW:405:ASP:O	23:AW:407:LEU:N	2.53	0.42
30:B6:34:ARG:HH12	30:B6:39:ARG:HG2	1.85	0.42
33:BA:189:G:H2'	33:BA:205:G:N2	2.34	0.42
33:BA:296:U:H2'	33:BA:297:G:C8	2.54	0.42
33:BA:1073:A:H3'	33:BA:1074:G:C5'	2.38	0.42
33:BA:1592:C:H2'	33:BA:1593:A:C8	2.54	0.42
33:BA:1722:A:H2'	33:BA:1723:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2846:G:OP1	49:BT:52:ARG:NH1	2.51	0.42
38:BF:10:GLU:C	38:BF:12:VAL:N	2.72	0.42
38:BF:174:PHE:HA	38:BF:175:PRO:HD3	1.82	0.42
40:BH:14:GLU:CD	40:BH:57:ASN:HD22	2.23	0.42
45:BP:36:LYS:HB3	45:BP:37:GLY:H	1.61	0.42
45:BP:127:VAL:HG11	45:BP:142:ILE:HG21	2.01	0.42
49:BT:24:THR:O	49:BT:24:THR:HG23	2.17	0.42
52:BW:12:SER:OG	52:BW:13:SER:N	2.52	0.42
52:BW:51:LEU:HA	52:BW:105:VAL:HG11	2.01	0.42
52:BW:75:PHE:N	52:BW:75:PHE:CD1	2.87	0.42
55:BZ:80:HIS:ND1	55:BZ:83:LYS:HB2	2.33	0.42
1:AA:113:G:C2	1:AA:315:A:C2	3.06	0.42
1:AA:475:C:H2'	1:AA:476:U:C6	2.54	0.42
1:AA:652:U:O4	1:AA:752:G:H2'	2.20	0.42
1:AA:837:U:H2'	1:AA:838:G:C8	2.54	0.42
1:AA:864:A:H2	1:AA:917:G:N3	2.17	0.42
1:AA:878:A:C5'	8:AH:80:PRO:HG2	2.48	0.42
1:AA:1125:U:OP2	1:AA:1145:A:N6	2.52	0.42
2:AB:67:LEU:HD21	2:AB:91:VAL:HG23	2.01	0.42
6:AF:6:ILE:HD12	6:AF:62:MET:HG2	2.01	0.42
9:AI:14:SER:OG	9:AI:68:GLY:O	2.30	0.42
11:AK:127:ARG:HB2	21:AU:33:ARG:HH22	1.84	0.42
14:AN:92:ILE:HA	14:AN:93:PRO:HD3	1.75	0.42
23:AW:72:THR:CG2	23:AW:88:ASP:H	2.32	0.42
23:AW:114:ASP:OD2	23:AW:143:LYS:NZ	2.45	0.42
25:B1:50:VAL:HG12	25:B1:51:SER:O	2.19	0.42
33:BA:372:G:H2'	33:BA:400:G:O6	2.18	0.42
33:BA:540:C:H2'	33:BA:541:A:C8	2.54	0.42
33:BA:883:G:C5	33:BA:884:U:C4	3.07	0.42
33:BA:956:G:P	46:BQ:86:LYS:HG3	2.59	0.42
33:BA:1199:U:H5'	50:BU:4:LYS:HG2	2.01	0.42
33:BA:1346:G:C2	33:BA:1601:G:C2	3.08	0.42
33:BA:1522:A:O2'	33:BA:1523:U:O5'	2.36	0.42
33:BA:2800:A:H3'	33:BA:2801:G:C5'	2.49	0.42
33:BA:2811:G:H2'	33:BA:2812:G:O4'	2.20	0.42
33:BA:2846:G:P	49:BT:52:ARG:NH1	2.92	0.42
35:BC:30:ALA:N	35:BC:31:PRO:HD2	2.34	0.42
43:BN:81:ILE:HG23	43:BN:82:GLY:H	1.84	0.42
44:BO:76:VAL:HB	49:BT:72:VAL:CG2	2.49	0.42
53:BX:51:PHE:O	53:BX:53:VAL:HG13	2.19	0.42
1:AA:59:A:H61	1:AA:331:G:H1'	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:88:U:O2	1:AA:88:U:H2'	2.19	0.42
1:AA:373:A:C1'	1:AA:481:G:H1'	2.49	0.42
1:AA:620:C:H2'	1:AA:621:A:O4'	2.18	0.42
1:AA:668:G:H2'	1:AA:669:G:H8	1.85	0.42
1:AA:797:C:OP1	11:AK:125:LYS:HG3	2.19	0.42
1:AA:1368:A:O2'	1:AA:1369:C:H5'	2.19	0.42
1:AA:1524:C:H2'	1:AA:1525:G:C8	2.54	0.42
2:AB:20:ARG:HA	2:AB:20:ARG:NH1	2.34	0.42
2:AB:153:MET:CE	2:AB:157:PRO:HG3	2.49	0.42
4:AD:145:ARG:O	4:AD:149:LYS:HG3	2.20	0.42
21:AU:46:ARG:HA	21:AU:49:ALA:HB3	2.02	0.42
23:AW:320:VAL:HG12	23:AW:361:PRO:HA	2.01	0.42
25:B1:2:ARG:HG3	33:BA:1364:G:OP1	2.19	0.42
30:B6:25:LYS:HE3	30:B6:25:LYS:HB2	1.87	0.42
33:BA:821:A:H5''	33:BA:822:G:O5'	2.19	0.42
33:BA:856:G:H2'	33:BA:857:G:C8	2.54	0.42
33:BA:1056:G:H5'	40:BH:34:THR:OG1	2.20	0.42
33:BA:1107:G:H2'	33:BA:1108:U:C6	2.54	0.42
33:BA:1153:C:H2'	33:BA:1154:G:O4'	2.19	0.42
33:BA:1550:C:H2'	33:BA:1551:A:C8	2.54	0.42
33:BA:1651:G:N2	33:BA:2007:U:C2	2.87	0.42
33:BA:1835:G:H1'	33:BA:1931:U:C2	2.53	0.42
33:BA:2428:G:H21	45:BP:60:ARG:HD3	1.85	0.42
35:BC:181:ARG:HG2	35:BC:182:LYS:N	2.34	0.42
37:BE:58:LYS:HA	37:BE:71:GLY:O	2.20	0.42
37:BE:58:LYS:HG3	37:BE:71:GLY:HA2	2.02	0.42
37:BE:119:ILE:HD13	37:BE:119:ILE:H	1.85	0.42
37:BE:151:GLY:HA3	37:BE:191:ASP:OD1	2.19	0.42
40:BH:35:VAL:HA	40:BH:38:MET:HB2	2.00	0.42
43:BN:49:ASP:CG	43:BN:121:LYS:HZ3	2.20	0.42
43:BN:117:ALA:HA	43:BN:120:ARG:NH2	2.34	0.42
1:AA:114:U:O2'	1:AA:115:G:H5'	2.20	0.42
1:AA:182:A:N7	1:AA:184:G:C5	2.88	0.42
3:AC:143:LEU:HD22	3:AC:143:LEU:H	1.84	0.42
6:AF:44:ARG:HG3	6:AF:58:HIS:ND1	2.35	0.42
11:AK:17:ASP:HA	11:AK:80:ASN:O	2.19	0.42
17:AQ:46:HIS:N	17:AQ:72:TRP:O	2.34	0.42
21:AU:36:PHE:O	21:AU:37:TYR:HB3	2.19	0.42
21:AU:38:GLU:O	21:AU:41:THR:OG1	2.26	0.42
33:BA:167:A:C2	33:BA:168:G:H1'	2.54	0.42
33:BA:210:C:H2'	33:BA:211:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:802:A:C5	33:BA:803:U:C4	3.06	0.42
33:BA:1250:G:OP2	45:BP:21:ARG:NH2	2.53	0.42
33:BA:1669:A:O3'	33:BA:2549:G:H5'	2.19	0.42
33:BA:1973:G:C6	33:BA:1974:C:C4	3.07	0.42
33:BA:2033:A:H4'	33:BA:2034:U:OP1	2.20	0.42
33:BA:2584:U:H2'	33:BA:2585:U:H5'	2.00	0.42
36:BD:22:ILE:HA	36:BD:23:PRO:HD3	1.91	0.42
37:BE:112:LEU:HD13	37:BE:186:VAL:HG11	2.02	0.42
39:BG:7:PRO:O	39:BG:68:ARG:NH1	2.50	0.42
40:BH:98:GLU:O	40:BH:102:ALA:HB2	2.20	0.42
47:BR:12:ARG:HE	47:BR:16:HIS:CE1	2.38	0.42
49:BT:28:LYS:N	49:BT:28:LYS:HE3	2.35	0.42
50:BU:24:TYR:CD1	50:BU:25:GLY:N	2.87	0.42
1:AA:70:U:C2	1:AA:94:G:C5	3.07	0.42
1:AA:110:C:C4	1:AA:111:G:C5	3.08	0.42
1:AA:148:G:H1'	1:AA:1447:A:H1'	2.02	0.42
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.34	0.42
15:AO:23:SER:HB3	15:AO:26:VAL:HG23	2.00	0.42
20:AT:8:LYS:HA	20:AT:11:ILE:HG22	2.01	0.42
23:AW:20:SER:N	23:AW:26:LYS:NZ	2.67	0.42
23:AW:419:LEU:HG	23:AW:452:ARG:HH12	1.84	0.42
23:AW:425:VAL:HB	23:AW:426:GLN:H	1.67	0.42
24:B0:17:ALA:HA	24:B0:35:ILE:CG2	2.49	0.42
24:B0:70:VAL:C	24:B0:71:LYS:HD2	2.39	0.42
33:BA:1054:A:O2'	40:BH:31:ARG:N	2.53	0.42
33:BA:1716:U:H2'	33:BA:1717:A:C8	2.54	0.42
33:BA:1837:C:H1'	33:BA:1928:A:H1'	2.02	0.42
33:BA:1960:A:C6	33:BA:1961:C:C4	3.08	0.42
33:BA:2376:A:H2'	33:BA:2377:A:O4'	2.19	0.42
33:BA:2790:U:H5'	33:BA:2893:A:N7	2.35	0.42
54:BY:95:PHE:O	54:BY:99:SER:HA	2.20	0.42
1:AA:80:A:C2	1:AA:81:A:H1'	2.54	0.42
1:AA:377:G:H2'	1:AA:378:G:C8	2.55	0.42
1:AA:1085:U:H1'	1:AA:1094:G:C5	2.55	0.42
1:AA:1191:A:OP1	3:AC:3:LYS:HD3	2.20	0.42
11:AK:30:ILE:HG12	11:AK:31:VAL:N	2.33	0.42
13:AM:106:ARG:HE	13:AM:112:ARG:HE	1.66	0.42
17:AQ:13:SER:HB3	17:AQ:16:MET:CE	2.50	0.42
23:AW:193:TYR:HA	23:AW:263:PHE:CE1	2.53	0.42
23:AW:314:ARG:HB2	23:AW:369:ASN:HB3	2.02	0.42
24:B0:68:PHE:CE1	24:B0:79:ILE:HD12	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:703:U:O2	33:BA:730:A:C2	2.72	0.42
33:BA:1182:G:H2'	33:BA:1183:U:O4'	2.20	0.42
33:BA:2107:G:C5	33:BA:2183:A:N1	2.88	0.42
33:BA:2678:C:H2'	33:BA:2679:A:O4'	2.19	0.42
35:BC:80:LEU:HD23	35:BC:91:ALA:HB2	2.01	0.42
35:BC:204:LEU:HB3	35:BC:205:GLY:H	1.57	0.42
49:BT:25:VAL:HA	49:BT:85:VAL:O	2.20	0.42
1:AA:405:U:O4	4:AD:1:ALA:N	2.52	0.42
1:AA:866:C:H4'	1:AA:919:A:H5'	2.02	0.42
1:AA:973:G:H3'	1:AA:974:A:H5''	2.01	0.42
1:AA:1157:A:H4'	1:AA:1158:C:O4'	2.19	0.42
1:AA:1229:A:OP2	13:AM:112:ARG:HD3	2.20	0.42
1:AA:1406:U:H1'	1:AA:1518:A:H4'	2.01	0.42
2:AB:135:MET:HA	2:AB:138:ARG:HG2	2.02	0.42
3:AC:148:ILE:HG12	3:AC:149:LYS:N	2.35	0.42
3:AC:179:ALA:HB1	3:AC:202:PHE:CE1	2.53	0.42
4:AD:2:ARG:CZ	4:AD:114:ARG:HD2	2.49	0.42
4:AD:169:TRP:CD2	4:AD:185:PRO:HB3	2.55	0.42
10:AJ:50:THR:HG22	10:AJ:64:GLN:CG	2.41	0.42
12:AL:119:LYS:NZ	23:AW:431:ILE:O	2.41	0.42
14:AN:52:ARG:HA	14:AN:52:ARG:HD3	1.70	0.42
23:AW:264:GLY:HA2	23:AW:267:HIS:CE1	2.54	0.42
33:BA:979:A:H2'	33:BA:982:C:N4	2.35	0.42
33:BA:1245:G:OP1	45:BP:13:LYS:HE3	2.19	0.42
33:BA:2638:G:H1'	33:BA:2778:A:H61	1.85	0.42
33:BA:2820:A:OP1	47:BR:2:ARG:NH2	2.53	0.42
35:BC:141:HIS:NE2	35:BC:194:VAL:HA	2.35	0.42
35:BC:152:GLN:O	35:BC:155:ARG:HG3	2.20	0.42
36:BD:89:GLU:HG3	36:BD:94:GLN:OE1	2.19	0.42
40:BH:95:LEU:HD13	40:BH:95:LEU:HA	1.92	0.42
44:BO:18:ARG:HB2	44:BO:45:GLU:CG	2.49	0.42
46:BQ:73:ILE:O	46:BQ:73:ILE:HG22	2.19	0.42
47:BR:33:ILE:HG23	47:BR:114:GLU:HB3	2.01	0.42
47:BR:108:ALA:O	47:BR:110:MET:HG2	2.19	0.42
48:BS:83:LEU:HD13	48:BS:83:LEU:HA	1.92	0.42
1:AA:339:C:H2'	1:AA:340:U:C6	2.54	0.42
1:AA:633:G:H2'	1:AA:634:C:C6	2.55	0.42
1:AA:689:C:OP2	11:AK:52:ARG:NH1	2.51	0.42
1:AA:1069:C:H4'	1:AA:1192:C:O2	2.20	0.42
2:AB:19:THR:HB	2:AB:37:VAL:HB	2.01	0.42
4:AD:131:ILE:HD13	4:AD:131:ILE:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:11:HIS:HA	6:AF:12:PRO:HD2	1.83	0.42
12:AL:38:THR:HG22	12:AL:50:LYS:HA	2.01	0.42
15:AO:41:HIS:CE1	15:AO:45:HIS:CD2	3.08	0.42
19:AS:48:ILE:H	19:AS:48:ILE:HG13	1.53	0.42
23:AW:22:PRO:HG3	23:AW:91:GLY:C	2.40	0.42
33:BA:78:U:H2'	33:BA:79:C:H6	1.85	0.42
33:BA:301:G:O5'	54:BY:81:ARG:NH1	2.53	0.42
33:BA:572:A:OP2	51:BV:80:ARG:NH2	2.53	0.42
33:BA:1278:C:H2'	33:BA:1279:G:C8	2.54	0.42
33:BA:1734:G:H2'	33:BA:1735:A:C8	2.55	0.42
38:BF:133:GLU:HA	38:BF:148:VAL:O	2.19	0.42
40:BH:24:SER:HB3	40:BH:86:MET:HE1	2.02	0.42
41:BI:50:LYS:HE2	41:BI:50:LYS:HB2	1.88	0.42
42:BL:8:ILE:HD13	42:BL:8:ILE:HA	1.92	0.42
42:BL:14:MET:HA	42:BL:14:MET:CE	2.50	0.42
42:BM:11:VAL:HG12	42:BM:11:VAL:O	2.20	0.42
44:BO:111:LYS:HG3	44:BO:112:PHE:CE2	2.54	0.42
46:BQ:8:LYS:HB3	46:BQ:9:PHE:CD2	2.54	0.42
50:BU:57:ARG:HA	50:BU:60:TRP:CE3	2.54	0.42
51:BV:61:ALA:HA	51:BV:99:THR:H	1.84	0.42
1:AA:436:C:H2'	1:AA:437:U:C6	2.55	0.42
1:AA:509:A:C6	1:AA:510:A:C6	3.08	0.42
1:AA:1256:A:N1	1:AA:1278:G:N2	2.68	0.42
1:AA:1417:G:N2	1:AA:1484:C:N4	2.67	0.42
3:AC:71:ARG:O	3:AC:75:VAL:HG23	2.20	0.42
4:AD:101:VAL:HG13	4:AD:106:PHE:HB2	2.01	0.42
23:AW:285:ASP:OD1	23:AW:285:ASP:N	2.53	0.42
25:B1:68:ALA:C	25:B1:69:GLU:O	2.57	0.42
28:B4:47:TYR:CD2	28:B4:52:LYS:HB2	2.55	0.42
29:B5:32:LYS:HA	29:B5:51:ALA:O	2.20	0.42
33:BA:37:C:H4'	33:BA:451:U:OP1	2.20	0.42
33:BA:483:A:O4'	54:BY:44:HIS:HB3	2.20	0.42
33:BA:1084:A:H5'	40:BH:55:VAL:HG13	2.01	0.42
33:BA:1789:A:OP1	35:BC:220:ARG:HD3	2.20	0.42
33:BA:1902:C:H4'	35:BC:241:LYS:O	2.20	0.42
33:BA:2134:A:O2'	33:BA:2135:A:C8	2.68	0.42
33:BA:2822:G:H2'	33:BA:2823:A:H5''	2.01	0.42
34:BB:18:G:C6	34:BB:19:C:C4	3.08	0.42
39:BG:82:PHE:N	39:BG:134:GLY:O	2.53	0.42
41:BI:15:GLY:HA2	41:BI:50:LYS:HB3	2.00	0.42
42:BL:19:VAL:O	42:BL:23:ILE:HB	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BN:44:TYR:CE2	50:BU:99:VAL:HG21	2.50	0.42
45:BP:95:LEU:HB2	45:BP:101:ILE:CD1	2.50	0.42
50:BU:64:ILE:HA	50:BU:64:ILE:HD13	1.76	0.42
51:BV:68:ARG:HD3	51:BV:92:TRP:CE2	2.54	0.42
53:BX:20:ALA:O	53:BX:24:MET:HB2	2.19	0.42
54:BY:47:PRO:HB3	54:BY:55:GLY:N	2.35	0.42
1:AA:406:G:N2	1:AA:437:U:C2	2.87	0.41
1:AA:674:G:H2'	1:AA:675:A:C8	2.54	0.41
1:AA:1023:U:H2'	1:AA:1024:G:C8	2.55	0.41
1:AA:1180:A:P	9:AI:98:ARG:HH22	2.43	0.41
2:AB:80:LYS:HB2	2:AB:90:PHE:CD1	2.54	0.41
2:AB:205:ALA:O	2:AB:209:VAL:HG22	2.20	0.41
5:AE:54:GLU:HB3	5:AE:56:PRO:HD2	2.02	0.41
8:AH:17:GLN:NE2	8:AH:69:ALA:HB1	2.35	0.41
12:AL:14:LYS:HE3	12:AL:14:LYS:HB2	1.88	0.41
23:AW:61:GLU:HB2	23:AW:64:LYS:HG3	2.02	0.41
23:AW:101:ARG:NH1	23:AW:392:ASN:OD1	2.53	0.41
23:AW:401:ILE:HA	23:AW:462:VAL:O	2.20	0.41
33:BA:200:U:H2'	33:BA:201:C:O4'	2.20	0.41
33:BA:253:C:H2'	33:BA:254:G:O4'	2.20	0.41
33:BA:536:G:H21	43:BN:47:HIS:CG	2.38	0.41
33:BA:1000:A:N6	33:BA:1155:A:C8	2.88	0.41
33:BA:1109:C:C4	33:BA:1110:G:C2	3.08	0.41
33:BA:1310:G:H3'	33:BA:1311:G:C8	2.55	0.41
33:BA:2273:A:H2'	33:BA:2274:A:H8	1.76	0.41
33:BA:2340:A:H2'	33:BA:2341:G:H8	1.85	0.41
33:BA:2527:C:H2'	33:BA:2528:U:O4'	2.19	0.41
33:BA:2595:G:O6	35:BC:238:ASN:ND2	2.53	0.41
33:BA:2840:C:H5''	47:BR:53:THR:OG1	2.20	0.41
34:BB:82:U:H2'	34:BB:83:G:C8	2.55	0.41
34:BB:86:G:N1	34:BB:88:C:H1'	2.35	0.41
36:BD:113:SER:O	36:BD:167:ASN:HA	2.20	0.41
38:BF:111:ARG:HD3	38:BF:111:ARG:HA	1.59	0.41
38:BF:121:PHE:HA	38:BF:126:ASN:O	2.20	0.41
43:BN:99:ARG:O	43:BN:102:GLU:HB2	2.19	0.41
51:BV:41:ILE:O	51:BV:46:GLU:HB2	2.19	0.41
2:AB:122:ASP:OD1	2:AB:122:ASP:N	2.53	0.41
10:AJ:41:PRO:HA	10:AJ:72:ARG:HH11	1.85	0.41
10:AJ:77:VAL:O	10:AJ:79:PRO:HD3	2.20	0.41
13:AM:72:ILE:O	13:AM:75:SER:OG	2.25	0.41
14:AN:20:PHE:C	14:AN:22:LYS:H	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AU:19:LYS:HB2	21:AU:20:ARG:NH1	2.34	0.41
24:B0:19:ARG:HH12	33:BA:922:C:H1'	1.86	0.41
30:B6:16:HIS:ND1	33:BA:684:G:OP1	2.50	0.41
30:B6:18:PHE:HA	30:B6:43:THR:HG21	2.01	0.41
33:BA:319:G:C6	33:BA:320:A:C5	3.08	0.41
33:BA:628:G:C6	33:BA:636:G:C2	3.08	0.41
33:BA:806:C:O2	33:BA:2444:G:O2'	2.38	0.41
33:BA:1566:A:C6	35:BC:212:TRP:CZ3	3.09	0.41
33:BA:2149:U:C4'	33:BA:2150:C:OP2	2.66	0.41
33:BA:2305:U:C5	38:BF:151:LEU:HA	2.55	0.41
33:BA:2472:G:H2'	33:BA:2475:C:H42	1.85	0.41
34:BB:56:G:H4'	34:BB:57:A:O5'	2.20	0.41
36:BD:48:ILE:HG23	36:BD:84:LEU:HD21	2.02	0.41
38:BF:72:SER:HB2	38:BF:80:GLN:HB2	2.01	0.41
40:BH:150:LYS:HA	40:BH:154:THR:OG1	2.20	0.41
47:BR:25:ALA:O	47:BR:29:VAL:HG23	2.20	0.41
49:BT:104:GLY:C	49:BT:106:ALA:H	2.23	0.41
52:BW:96:ILE:HG13	52:BW:96:ILE:O	2.19	0.41
1:AA:313:A:H2'	1:AA:314:C:C6	2.55	0.41
1:AA:827:U:C4	1:AA:870:U:C2	3.08	0.41
1:AA:1001:C:H2'	1:AA:1002:G:C8	2.54	0.41
1:AA:1005:A:O5'	1:AA:1005:A:H8	2.04	0.41
1:AA:1525:G:OP1	11:AK:121:ARG:NH2	2.52	0.41
2:AB:163:ILE:HD12	2:AB:163:ILE:HA	1.81	0.41
18:AR:49:LYS:HG2	18:AR:53:GLN:HE21	1.85	0.41
24:B0:24:ARG:HD3	24:B0:65:LYS:HE2	2.01	0.41
33:BA:2:G:H2'	33:BA:3:U:C6	2.56	0.41
33:BA:998:C:OP2	50:BU:57:ARG:NH2	2.50	0.41
33:BA:1392:A:N6	53:BX:18:GLU:HG2	2.34	0.41
33:BA:1651:G:C2	33:BA:2007:U:C2	3.08	0.41
33:BA:1735:A:H2'	33:BA:1736:U:O4'	2.20	0.41
33:BA:1839:G:C5	33:BA:1840:G:C8	3.09	0.41
35:BC:51:ARG:NH2	35:BC:246:PRO:HG2	2.34	0.41
35:BC:75:ALA:HB3	35:BC:115:ILE:HG22	2.01	0.41
36:BD:129:THR:HG23	36:BD:130:GLN:O	2.21	0.41
40:BH:24:SER:OG	40:BH:117:LEU:N	2.53	0.41
42:BM:18:ASP:O	42:BM:21:GLU:HB2	2.20	0.41
46:BQ:132:THR:HG22	46:BQ:133:LYS:N	2.35	0.41
53:BX:5:GLU:O	53:BX:8:LEU:HB2	2.20	0.41
55:BZ:30:ILE:HG12	55:BZ:91:PHE:HB2	2.01	0.41
1:AA:265:G:H5''	17:AQ:66:LEU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:983:A:O2'	1:AA:1050:G:OP1	2.29	0.41
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.21	0.41
10:AJ:19:ASP:HA	10:AJ:22:THR:HB	2.01	0.41
10:AJ:56:HIS:HD2	10:AJ:57:VAL:N	2.18	0.41
13:AM:84:CYS:HB2	19:AS:72:GLU:HB3	2.01	0.41
25:B1:30:PRO:HA	33:BA:396:G:O3'	2.20	0.41
26:B2:8:GLU:H	26:B2:60:LYS:NZ	2.19	0.41
33:BA:500:G:N2	33:BA:502:A:H3'	2.35	0.41
33:BA:739:A:H1'	33:BA:740:C:H5	1.84	0.41
33:BA:1522:A:O2'	33:BA:1523:U:P	2.78	0.41
33:BA:1708:C:H2'	33:BA:1709:U:H6	1.85	0.41
33:BA:1786:A:H1'	33:BA:1938:A:N6	2.35	0.41
33:BA:1872:A:H2'	33:BA:1873:G:O4'	2.20	0.41
33:BA:2151:U:N3	33:BA:2152:G:C5	2.88	0.41
33:BA:2230:G:H2'	33:BA:2231:U:C6	2.55	0.41
33:BA:2357:G:N2	33:BA:2360:G:OP2	2.46	0.41
35:BC:67:LYS:HG2	35:BC:150:GLY:CA	2.50	0.41
40:BH:58:THR:O	40:BH:60:LEU:HG	2.20	0.41
46:BQ:64:TRP:HB2	46:BQ:104:GLU:HB2	2.03	0.41
52:BW:3:THR:OG1	52:BW:58:ALA:HB2	2.21	0.41
1:AA:70:U:O2'	1:AA:71:A:H8	2.04	0.41
1:AA:1368:A:OP2	9:AI:113:LYS:NZ	2.37	0.41
3:AC:42:LEU:HD12	3:AC:42:LEU:HA	1.88	0.41
4:AD:3:TYR:O	4:AD:4:LEU:HB2	2.21	0.41
5:AE:104:ILE:HD12	5:AE:104:ILE:HA	1.84	0.41
5:AE:153:ALA:HA	5:AE:156:ARG:CB	2.50	0.41
11:AK:60:PHE:O	11:AK:63:GLN:HB3	2.20	0.41
16:AP:76:LYS:HZ3	16:AP:80:LYS:HB2	1.85	0.41
19:AS:48:ILE:HD12	19:AS:59:VAL:O	2.20	0.41
23:AW:165:GLY:HA3	23:AW:251:ILE:HG22	2.02	0.41
23:AW:172:PRO:HD3	23:AW:256:PHE:CD1	2.55	0.41
23:AW:183:TYR:CZ	23:AW:210:LEU:HD13	2.56	0.41
25:B1:32:LEU:HD23	25:B1:49:ARG:NE	2.35	0.41
33:BA:796:C:H2'	33:BA:797:G:C8	2.55	0.41
33:BA:2146:C:C4'	33:BA:2147:A:OP1	2.67	0.41
33:BA:2347:C:H4'	33:BA:2347:C:OP1	2.21	0.41
33:BA:2757:A:N3	33:BA:2757:A:H2'	2.36	0.41
35:BC:20:ASN:HA	35:BC:21:PRO:HD2	1.92	0.41
35:BC:265:PHE:N	35:BC:265:PHE:CD1	2.88	0.41
36:BD:5:VAL:HG22	36:BD:202:ILE:HD13	2.03	0.41
36:BD:35:THR:N	36:BD:49:GLN:O	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BE:193:VAL:O	37:BE:197:GLU:HB2	2.20	0.41
39:BG:8:VAL:HB	39:BG:49:LEU:HB2	2.03	0.41
46:BQ:20:LEU:HD13	46:BQ:20:LEU:HA	1.78	0.41
46:BQ:76:LYS:HA	46:BQ:77:PRO:HD3	1.90	0.41
52:BW:36:LEU:HD12	52:BW:36:LEU:HA	1.71	0.41
1:AA:75:G:H1	1:AA:95:C:H42	1.69	0.41
1:AA:665:A:C8	1:AA:725:G:C2	3.09	0.41
1:AA:812:G:O2'	1:AA:813:U:P	2.75	0.41
1:AA:1432:G:H1'	1:AA:1468:A:N6	2.35	0.41
1:AA:1479:C:C2	1:AA:1480:A:C8	3.09	0.41
3:AC:15:LYS:HE3	3:AC:180:ASP:OD1	2.20	0.41
3:AC:35:ASP:OD2	3:AC:39:ARG:NE	2.52	0.41
7:AG:110:ARG:HB3	7:AG:118:ARG:HB3	2.03	0.41
9:AI:62:LEU:HD12	9:AI:64:ILE:HD11	2.03	0.41
15:AO:63:ARG:HD3	15:AO:87:ARG:HH22	1.85	0.41
23:AW:325:TYR:OH	23:AW:327:LYS:HA	2.20	0.41
33:BA:784:G:N7	33:BA:792:A:N7	2.69	0.41
33:BA:974:G:N7	33:BA:989:G:C6	2.89	0.41
33:BA:1597:A:H5''	33:BA:1598:A:H5'	2.02	0.41
33:BA:2395:C:OP1	45:BP:63:LYS:NZ	2.51	0.41
33:BA:2708:G:H1'	47:BR:71:ARG:NH2	2.35	0.41
33:BA:2846:G:H1	33:BA:2870:C:H42	1.67	0.41
36:BD:5:VAL:HG21	36:BD:80:TRP:CE3	2.55	0.41
39:BG:15:ASP:OD2	39:BG:26:LYS:HG2	2.21	0.41
40:BH:143:MET:O	40:BH:148:ALA:HB3	2.20	0.41
42:BJ:27:GLU:HG2	42:BJ:29:LYS:HZ1	1.85	0.41
52:BW:44:ALA:O	52:BW:47:VAL:HG12	2.19	0.41
53:BX:39:THR:OG1	53:BX:42:GLU:HB2	2.20	0.41
1:AA:66:A:H4'	1:AA:173:U:C5	2.56	0.41
1:AA:523:A:H8	1:AA:523:A:O5'	2.03	0.41
1:AA:842:U:HO2'	1:AA:846:G:H1	1.68	0.41
1:AA:959:A:H5''	1:AA:960:U:OP2	2.21	0.41
2:AB:188:THR:O	2:AB:188:THR:OG1	2.30	0.41
18:AR:46:THR:HG23	18:AR:51:GLN:HB2	2.01	0.41
23:AW:45:THR:HB	23:AW:46:VAL:H	1.50	0.41
23:AW:119:VAL:HB	23:AW:157:GLU:HG2	2.03	0.41
29:B5:20:TYR:OH	33:BA:2347:C:O2'	2.27	0.41
32:B8:6:SER:HB2	33:BA:1031:G:H4'	2.03	0.41
33:BA:910:A:C6	33:BA:911:A:C6	3.08	0.41
33:BA:946:C:H2'	33:BA:947:A:H8	1.86	0.41
33:BA:981:A:H5''	33:BA:982:C:OP2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1500:G:O2'	35:BC:100:ARG:NH1	2.54	0.41
33:BA:1828:G:O6	35:BC:220:ARG:HD2	2.19	0.41
33:BA:2150:C:O2'	33:BA:2151:U:C6	2.72	0.41
33:BA:2443:C:H2'	33:BA:2444:G:C8	2.56	0.41
40:BH:139:LEU:HD21	42:BJ:25:ALA:HB3	2.03	0.41
41:BI:105:LEU:HA	41:BI:108:ILE:HB	2.02	0.41
46:BQ:108:VAL:HG13	46:BQ:112:LEU:HB3	2.02	0.41
1:AA:193:C:H2'	1:AA:194:C:H6	1.85	0.41
1:AA:668:G:C4	1:AA:669:G:C8	3.09	0.41
1:AA:937:A:H1'	1:AA:1379:G:H22	1.85	0.41
1:AA:1005:A:C2	1:AA:1006:G:H1'	2.56	0.41
2:AB:73:ARG:HA	2:AB:76:SER:CB	2.51	0.41
2:AB:89:PHE:HB3	2:AB:149:GLY:CA	2.48	0.41
2:AB:170:ILE:H	2:AB:170:ILE:HG13	1.67	0.41
4:AD:14:GLU:OE2	4:AD:55:ARG:NH1	2.53	0.41
4:AD:166:LYS:HA	4:AD:167:PRO:HD3	1.78	0.41
9:AI:59:LYS:NZ	9:AI:60:LEU:HD22	2.36	0.41
9:AI:128:LYS:HD2	9:AI:129:ARG:H	1.85	0.41
11:AK:78:ILE:H	11:AK:78:ILE:HG13	1.68	0.41
12:AL:115:LYS:H	12:AL:115:LYS:HG3	1.55	0.41
15:AO:2:LEU:HD12	15:AO:3:SER:H	1.86	0.41
15:AO:77:TYR:CZ	15:AO:81:ILE:HD13	2.55	0.41
23:AW:403:LEU:HA	23:AW:461:ALA:HA	2.02	0.41
23:AW:491:SER:CA	23:AW:492:GLN:HB2	2.51	0.41
33:BA:71:A:HO2'	33:BA:72:U:P	2.39	0.41
33:BA:467:G:H2'	33:BA:468:G:O4'	2.20	0.41
33:BA:602:A:C2	33:BA:656:G:C6	3.09	0.41
33:BA:749:A:H4'	33:BA:1271:G:N3	2.36	0.41
33:BA:780:G:H21	33:BA:783:A:H62	1.68	0.41
33:BA:819:A:H5'	33:BA:973:A:N1	2.36	0.41
33:BA:2292:U:H2'	33:BA:2293:G:C8	2.55	0.41
35:BC:52:HIS:HA	35:BC:216:ARG:HB2	2.03	0.41
38:BF:73:VAL:HG21	38:BF:76:PHE:HD1	1.85	0.41
39:BG:101:VAL:HG12	39:BG:115:GLN:HA	2.03	0.41
40:BH:143:MET:C	40:BH:145:GLU:H	2.24	0.41
1:AA:73:C:H41	1:AA:94:G:N2	2.17	0.41
1:AA:159:G:N2	1:AA:162:A:OP2	2.49	0.41
1:AA:283:U:C4	1:AA:284:C:C4	3.09	0.41
1:AA:383:A:C6	1:AA:384:G:H1'	2.56	0.41
1:AA:626:G:C6	1:AA:627:G:C5	3.09	0.41
1:AA:774:G:C2	1:AA:806:C:C2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:824:G:H2'	1:AA:825:A:C8	2.55	0.41
1:AA:890:G:C2'	1:AA:891:U:OP2	2.69	0.41
1:AA:1040:U:H2'	1:AA:1041:G:C8	2.56	0.41
1:AA:1168:U:O2	1:AA:1168:U:H2'	2.21	0.41
1:AA:1321:U:H5'	13:AM:85:TYR:CE2	2.56	0.41
1:AA:1328:C:H5''	13:AM:27:THR:HG21	2.03	0.41
1:AA:1409:C:O2'	33:BA:1914:C:N4	2.46	0.41
1:AA:1498:U:H1'	1:AA:1499:A:N7	2.36	0.41
2:AB:76:SER:OG	2:AB:77:GLU:N	2.54	0.41
4:AD:145:ARG:HD2	4:AD:147:LYS:HE2	2.03	0.41
5:AE:85:LYS:HG3	5:AE:93:VAL:O	2.21	0.41
10:AJ:18:ILE:HD12	10:AJ:72:ARG:HG3	2.03	0.41
10:AJ:56:HIS:HD2	10:AJ:57:VAL:H	1.69	0.41
13:AM:77:LYS:HD3	13:AM:80:MET:CE	2.51	0.41
15:AO:2:LEU:HD22	15:AO:34:GLN:HG2	2.03	0.41
16:AP:46:LYS:HE2	16:AP:47:GLU:H	1.86	0.41
16:AP:67:ILE:HG21	16:AP:72:ALA:HB2	2.03	0.41
17:AQ:30:HIS:HB2	17:AQ:37:ILE:HD11	2.03	0.41
19:AS:48:ILE:HD11	19:AS:61:VAL:HG13	2.03	0.41
20:AT:33:LYS:HA	20:AT:33:LYS:HD3	1.86	0.41
20:AT:60:GLN:HB3	20:AT:65:LEU:HD11	2.03	0.41
23:AW:398:PHE:CD1	23:AW:399:ARG:N	2.88	0.41
25:B1:12:VAL:HG23	25:B1:28:PHE:HB2	2.03	0.41
33:BA:30:G:H2'	33:BA:31:C:C6	2.56	0.41
33:BA:154:U:H2'	33:BA:155:A:C8	2.56	0.41
33:BA:192:C:H2'	33:BA:193:U:O4'	2.21	0.41
33:BA:287:G:H2'	33:BA:288:U:C6	2.56	0.41
33:BA:328:U:O3'	54:BY:65:GLN:HG3	2.20	0.41
33:BA:691:C:C4'	35:BC:42:ARG:HH12	2.33	0.41
33:BA:819:A:C4	33:BA:1189:A:C2	3.08	0.41
33:BA:894:U:C2'	33:BA:895:U:O5'	2.68	0.41
33:BA:922:C:C2	33:BA:923:G:C8	3.09	0.41
33:BA:996:A:H4'	50:BU:91:ARG:HD2	2.02	0.41
33:BA:1007:C:C6	33:BA:1008:A:C8	3.08	0.41
33:BA:1180:U:H5'	33:BA:1181:U:OP2	2.20	0.41
33:BA:1206:G:C6	33:BA:1207:C:C4	3.09	0.41
33:BA:1519:G:C6	33:BA:1520:U:C4	3.08	0.41
33:BA:1527:G:H5''	33:BA:1528:A:OP1	2.20	0.41
33:BA:1666:G:N2	33:BA:1994:C:O2	2.54	0.41
33:BA:1742:U:C4	33:BA:1743:G:C6	3.09	0.41
33:BA:1833:C:H2'	33:BA:1834:U:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1906:G:N7	33:BA:1929:G:H2'	2.35	0.41
33:BA:2037:A:H2'	33:BA:2038:G:C8	2.56	0.41
33:BA:2053:G:H5'	36:BD:150:GLN:HA	2.03	0.41
33:BA:2103:C:O2'	33:BA:2104:C:P	2.79	0.41
33:BA:2142:A:H2'	33:BA:2143:C:OP2	2.21	0.41
33:BA:2228:G:H2'	33:BA:2229:U:H6	1.85	0.41
33:BA:2230:G:C4	33:BA:2231:U:C5	3.09	0.41
33:BA:2397:G:C2	33:BA:2420:C:C2	3.09	0.41
33:BA:2561:U:H4'	44:BO:22:ILE:CD1	2.51	0.41
33:BA:2748:A:H1'	39:BG:66:THR:CG2	2.50	0.41
33:BA:2766:A:C8	33:BA:2766:A:O5'	2.74	0.41
34:BB:42:C:O2'	38:BF:63:LYS:O	2.22	0.41
34:BB:86:G:C6	34:BB:88:C:H1'	2.55	0.41
35:BC:180:MET:O	35:BC:267:VAL:N	2.49	0.41
35:BC:269:ARG:HD3	35:BC:270:ARG:H	1.85	0.41
36:BD:140:HIS:H	36:BD:140:HIS:CD2	2.38	0.41
40:BH:147:SER:O	40:BH:151:LEU:HG	2.21	0.41
41:BI:116:MET:SD	41:BI:124:MET:HB2	2.61	0.41
43:BN:125:TYR:CE2	43:BN:130:HIS:HB2	2.56	0.41
45:BP:19:LEU:HA	45:BP:27:LEU:HD13	2.02	0.41
46:BQ:36:VAL:H	46:BQ:99:GLY:H	1.69	0.41
47:BR:27:SER:HB3	47:BR:34:ILE:HG21	2.02	0.41
47:BR:37:THR:OG1	47:BR:40:LYS:HG3	2.21	0.41
53:BX:50:LEU:O	53:BX:51:PHE:HB2	2.20	0.41
54:BY:9:GLU:OE2	54:BY:21:ARG:NH2	2.47	0.41
1:AA:392:C:H2'	1:AA:393:A:C8	2.56	0.41
1:AA:880:C:H2'	1:AA:881:G:H8	1.86	0.41
1:AA:1084:G:C5	1:AA:1085:U:C4	3.09	0.41
1:AA:1120:C:H2'	1:AA:1121:U:C6	2.55	0.41
4:AD:198:LEU:HD23	4:AD:198:LEU:HA	1.85	0.41
6:AF:36:ILE:HD13	6:AF:36:ILE:H	1.85	0.41
8:AH:105:THR:OG1	8:AH:107:LYS:O	2.38	0.41
10:AJ:57:VAL:HG13	10:AJ:58:ASN:N	2.36	0.41
12:AL:19:ASN:O	12:AL:93:ARG:HD2	2.21	0.41
23:AW:399:ARG:NE	23:AW:445:GLN:HB3	2.36	0.41
23:AW:481:LYS:NZ	23:AW:520:ASP:HB2	2.36	0.41
24:B0:39:GLN:HG3	24:B0:42:THR:N	2.33	0.41
24:B0:46:ALA:HB2	24:B0:78:PHE:HB3	2.02	0.41
27:B3:38:GLU:HB2	27:B3:40:THR:HG22	2.03	0.41
31:B7:2:LYS:HA	33:BA:592:A:O2'	2.21	0.41
33:BA:753:A:H2'	33:BA:754:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1184:U:O2'	33:BA:1185:G:H5'	2.21	0.41
33:BA:2323:G:H2'	33:BA:2324:U:O4'	2.20	0.41
33:BA:2326:C:H6	33:BA:2326:C:H2'	1.69	0.41
39:BG:139:VAL:O	39:BG:143:VAL:HG23	2.21	0.41
40:BH:76:PHE:O	40:BH:79:PRO:HD3	2.21	0.41
43:BN:7:LYS:HA	43:BN:8:PRO:HD3	1.91	0.41
43:BN:35:ARG:HG2	43:BN:40:HIS:CD2	2.56	0.41
47:BR:102:PHE:H	47:BR:109:PRO:HA	1.86	0.41
1:AA:372:C:N4	1:AA:387:U:H2'	2.36	0.40
1:AA:1440:U:H5'	1:AA:1441:A:OP1	2.20	0.40
4:AD:109:THR:HG23	4:AD:112:GLU:N	2.26	0.40
7:AG:50:ALA:HB2	7:AG:57:GLU:OE2	2.21	0.40
9:AI:71:ILE:H	9:AI:71:ILE:HD12	1.86	0.40
10:AJ:34:ALA:O	10:AJ:36:VAL:HG23	2.21	0.40
10:AJ:49:PHE:CE1	14:AN:76:PHE:HZ	2.38	0.40
13:AM:72:ILE:O	13:AM:76:ILE:HG13	2.21	0.40
20:AT:14:GLU:O	20:AT:17:ARG:HB3	2.21	0.40
28:B4:42:ILE:HD11	47:BR:98:LEU:HB3	2.03	0.40
28:B4:43:THR:OG1	28:B4:47:TYR:N	2.53	0.40
33:BA:7:G:H2'	33:BA:8:C:O4'	2.20	0.40
33:BA:321:U:OP2	37:BE:130:LYS:HD3	2.20	0.40
33:BA:340:A:O2'	37:BE:162:ARG:NH1	2.54	0.40
33:BA:483:A:O2'	54:BY:56:GLY:N	2.54	0.40
33:BA:948:C:O2	33:BA:984:A:O2'	2.39	0.40
33:BA:1277:G:H2'	33:BA:1278:C:C6	2.56	0.40
33:BA:1536:C:H1'	33:BA:1537:G:N2	2.36	0.40
33:BA:1567:G:C8	35:BC:82:TYR:CE1	3.10	0.40
33:BA:1789:A:P	35:BC:220:ARG:HD3	2.61	0.40
33:BA:2038:G:C6	33:BA:2039:U:C4	3.09	0.40
33:BA:2789:C:H2'	33:BA:2893:A:N7	2.35	0.40
33:BA:2834:G:O6	33:BA:2879:A:H2'	2.20	0.40
35:BC:142:ASN:HA	35:BC:153:LEU:O	2.22	0.40
37:BE:79:ARG:HG2	37:BE:80:SER:N	2.36	0.40
46:BQ:74:THR:HA	46:BQ:89:VAL:HA	2.03	0.40
49:BT:6:GLN:HE21	49:BT:6:GLN:HB3	1.68	0.40
49:BT:77:SER:HA	49:BT:78:PRO:HD3	1.95	0.40
52:BW:15:GLN:O	52:BW:19:LEU:HD13	2.21	0.40
1:AA:52:C:H2'	1:AA:53:A:C8	2.56	0.40
1:AA:376:G:H2'	1:AA:377:G:C8	2.56	0.40
1:AA:879:C:H2'	1:AA:880:C:H6	1.85	0.40
1:AA:1323:G:H5''	1:AA:1324:A:OP2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1366:C:O3'	10:AJ:62:ARG:NH1	2.49	0.40
3:AC:10:ARG:O	3:AC:13:ILE:O	2.38	0.40
7:AG:49:LEU:HG	7:AG:123:LEU:HD12	2.03	0.40
7:AG:110:ARG:HD2	7:AG:122:GLU:HG2	2.02	0.40
12:AL:82:ARG:HB2	12:AL:97:VAL:HG22	2.03	0.40
13:AM:15:VAL:O	13:AM:29:SER:OG	2.25	0.40
19:AS:52:ASN:OD1	19:AS:54:ARG:HG3	2.21	0.40
23:AW:45:THR:HG23	23:AW:51:SER:HB2	2.02	0.40
23:AW:72:THR:HG22	23:AW:88:ASP:H	1.87	0.40
23:AW:321:VAL:HG21	23:AW:387:PHE:CE2	2.56	0.40
23:AW:484:GLU:CD	23:AW:487:ARG:HH21	2.25	0.40
33:BA:419:U:H2'	33:BA:420:C:C6	2.56	0.40
33:BA:455:C:H6	33:BA:455:C:H2'	1.75	0.40
33:BA:582:A:C2	33:BA:1259:G:C2	3.09	0.40
33:BA:1909:C:H2'	33:BA:1910:G:H8	1.85	0.40
33:BA:2341:G:H2'	33:BA:2342:C:O4'	2.22	0.40
33:BA:2467:C:H2'	33:BA:2468:A:O4'	2.22	0.40
33:BA:2736:A:H2'	33:BA:2737:G:H8	1.86	0.40
34:BB:88:C:HO2'	34:BB:90:C:N4	2.19	0.40
41:BI:123:ALA:HA	41:BI:126:ARG:CZ	2.51	0.40
42:BJ:11:VAL:HG21	42:BM:15:SER:HB2	2.01	0.40
42:BK:24:SER:O	42:BK:28:GLU:HG2	2.20	0.40
45:BP:50:PHE:CZ	45:BP:52:GLY:O	2.74	0.40
51:BV:66:HIS:HB3	51:BV:93:PHE:O	2.22	0.40
53:BX:39:THR:N	53:BX:42:GLU:HB2	2.36	0.40
1:AA:2:A:C6	1:AA:3:A:C2	3.09	0.40
1:AA:325:A:H2'	1:AA:326:G:O4'	2.22	0.40
1:AA:562:U:H1'	12:AL:11:ARG:HB3	2.04	0.40
1:AA:832:G:C2	1:AA:855:U:C2	3.08	0.40
1:AA:1360:A:H2'	1:AA:1361:G:O4'	2.21	0.40
1:AA:1414:U:H2'	1:AA:1415:G:H8	1.85	0.40
2:AB:127:LYS:HG3	2:AB:128:LEU:H	1.86	0.40
4:AD:57:LYS:HE2	4:AD:203:TYR:OH	2.22	0.40
7:AG:37:THR:O	7:AG:41:ILE:HG13	2.21	0.40
15:AO:73:ASP:OD1	15:AO:76:ARG:N	2.40	0.40
17:AQ:39:ARG:HD2	17:AQ:39:ARG:HA	1.90	0.40
21:AU:13:VAL:HG13	21:AU:15:LEU:HG	2.02	0.40
23:AW:389:GLY:O	23:AW:390:ILE:HD13	2.21	0.40
24:B0:30:VAL:HA	24:B0:60:ALA:O	2.21	0.40
32:B8:20:ASP:N	33:BA:2757:A:OP1	2.54	0.40
33:BA:279:A:N6	33:BA:361:G:H1'	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:481:G:P	54:BY:43:LYS:HE3	2.62	0.40
33:BA:608:A:C4	33:BA:621:A:C6	3.09	0.40
33:BA:1866:A:N6	33:BA:1875:G:O2'	2.50	0.40
33:BA:2735:G:C4	33:BA:2736:A:C8	3.09	0.40
41:BI:56:VAL:HG23	41:BI:70:THR:HA	2.04	0.40
43:BN:2:LYS:H	43:BN:2:LYS:CD	2.34	0.40
1:AA:502:A:OP1	12:AL:114:SER:HB3	2.21	0.40
1:AA:898:G:C6	1:AA:902:G:O6	2.74	0.40
1:AA:922:G:C6	1:AA:923:A:C6	3.10	0.40
1:AA:1191:A:H5''	3:AC:3:LYS:CE	2.49	0.40
1:AA:1241:G:N2	1:AA:1296:C:O2	2.33	0.40
2:AB:55:GLU:HA	2:AB:58:LYS:HB3	2.02	0.40
3:AC:148:ILE:HA	3:AC:201:ILE:HA	2.03	0.40
3:AC:149:LYS:HG3	3:AC:200:TRP:HE3	1.85	0.40
6:AF:91:ARG:HG2	6:AF:93:LYS:HD3	2.03	0.40
13:AM:77:LYS:HA	13:AM:80:MET:HE2	2.03	0.40
13:AM:85:TYR:OH	13:AM:89:ARG:NH2	2.54	0.40
15:AO:38:LEU:HD13	15:AO:38:LEU:HA	1.83	0.40
21:AU:33:ARG:CD	21:AU:34:ARG:H	2.33	0.40
32:B8:19:ARG:NH1	33:BA:2755:C:C4	2.90	0.40
33:BA:257:C:H2'	33:BA:258:G:O4'	2.22	0.40
33:BA:566:U:O4	51:BV:80:ARG:HD3	2.20	0.40
33:BA:1161:C:H2'	33:BA:1162:G:H8	1.86	0.40
33:BA:1218:G:C6	33:BA:1219:U:C4	3.09	0.40
33:BA:1220:G:H2'	33:BA:1221:C:C6	2.57	0.40
33:BA:1425:G:C6	33:BA:1426:G:C6	3.10	0.40
33:BA:2313:C:H2'	33:BA:2314:A:C8	2.57	0.40
33:BA:2786:U:O2'	36:BD:63:PRO:O	2.35	0.40
33:BA:2886:A:C6	33:BA:2887:A:C4	3.10	0.40
35:BC:70:LYS:HD2	35:BC:95:TYR:CG	2.56	0.40
36:BD:184:ARG:HD3	36:BD:186:LEU:HD22	2.04	0.40
38:BF:32:LYS:O	38:BF:33:ILE:HD13	2.21	0.40
46:BQ:34:LYS:HG3	46:BQ:99:GLY:O	2.21	0.40
51:BV:38:VAL:O	51:BV:53:PHE:HA	2.22	0.40
51:BV:49:ILE:HG22	51:BV:54:VAL:N	2.37	0.40
1:AA:202:G:H21	1:AA:466:A:N6	2.17	0.40
1:AA:274:A:H4'	1:AA:275:G:O5'	2.22	0.40
1:AA:641:U:H4'	8:AH:106:SER:O	2.22	0.40
1:AA:1042:A:P	1:AA:1042:A:O4'	2.80	0.40
4:AD:173:ASP:OD1	4:AD:174:ALA:N	2.54	0.40
4:AD:174:ALA:O	4:AD:177:MET:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:110:VAL:H	9:AI:110:VAL:HG22	1.65	0.40
23:AW:411:GLN:O	23:AW:411:GLN:HG2	2.21	0.40
23:AW:424:ALA:O	23:AW:441:VAL:HG13	2.22	0.40
24:B0:39:GLN:HG3	24:B0:42:THR:CB	2.45	0.40
33:BA:387:U:H4'	33:BA:388:G:O4'	2.21	0.40
33:BA:409:G:H2'	33:BA:410:G:C8	2.56	0.40
33:BA:732:C:H2'	33:BA:733:G:O4'	2.22	0.40
33:BA:858:G:N3	33:BA:2268:A:H2'	2.37	0.40
33:BA:1038:G:N2	33:BA:1118:C:C2	2.90	0.40
33:BA:1589:U:H2'	33:BA:1590:A:H8	1.86	0.40
33:BA:1818:U:HO2'	33:BA:1819:A:P	2.45	0.40
33:BA:2149:U:C3'	33:BA:2149:U:C6	3.04	0.40
33:BA:2290:G:C6	33:BA:2291:U:C4	3.10	0.40
33:BA:2680:U:OP1	36:BD:114:LYS:HE2	2.21	0.40
34:BB:78:A:H2'	34:BB:79:G:O4'	2.20	0.40
38:BF:56:LEU:HD23	38:BF:56:LEU:HA	1.84	0.40
38:BF:107:VAL:HB	38:BF:108:PRO:HD3	2.02	0.40
40:BH:132:TYR:C	40:BH:134:GLU:N	2.75	0.40
41:BI:120:ASP:HB3	41:BI:123:ALA:HB3	2.04	0.40
43:BN:121:LYS:HE3	43:BN:121:LYS:HB2	1.77	0.40
46:BQ:26:VAL:HG13	46:BQ:104:GLU:OE2	2.21	0.40
46:BQ:77:PRO:HD2	46:BQ:80:VAL:HG11	2.04	0.40
53:BX:4:GLU:OE1	53:BX:5:GLU:N	2.55	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:131:ARG:NH2	33:BA:2156:G:O2'[4_445]	1.71	0.49
3:AC:135:ARG:CG	33:BA:2157:G:OP2[4_445]	1.99	0.21
3:AC:131:ARG:CB	33:BA:2157:G:OP1[4_445]	2.11	0.09
1:AA:205:A:OP2	19:AS:24:SER:OG[2_355]	2.12	0.08
3:AC:131:ARG:NE	33:BA:2157:G:O5'[4_445]	2.12	0.08
4:AD:176:LYS:NZ	55:BZ:70:ILE:O[2_355]	2.17	0.03

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
2	AB	216/241 (90%)	175 (81%)	40 (18%)	1 (0%)	29	66
3	AC	204/233 (88%)	178 (87%)	24 (12%)	2 (1%)	15	51
4	AD	203/206 (98%)	170 (84%)	29 (14%)	4 (2%)	7	39
5	AE	148/167 (89%)	125 (84%)	19 (13%)	4 (3%)	5	33
6	AF	98/135 (73%)	77 (79%)	20 (20%)	1 (1%)	15	51
7	AG	149/179 (83%)	124 (83%)	25 (17%)	0	100	100
8	AH	127/130 (98%)	113 (89%)	13 (10%)	1 (1%)	19	56
9	AI	125/130 (96%)	109 (87%)	12 (10%)	4 (3%)	4	31
10	AJ	96/103 (93%)	77 (80%)	16 (17%)	3 (3%)	4	32
11	AK	115/129 (89%)	100 (87%)	15 (13%)	0	100	100
12	AL	121/124 (98%)	107 (88%)	12 (10%)	2 (2%)	9	42
13	AM	112/118 (95%)	96 (86%)	14 (12%)	2 (2%)	8	41
14	AN	92/101 (91%)	73 (79%)	19 (21%)	0	100	100
15	AO	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
16	AP	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	12	47
17	AQ	78/84 (93%)	65 (83%)	12 (15%)	1 (1%)	12	47
18	AR	53/75 (71%)	46 (87%)	7 (13%)	0	100	100
19	AS	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
20	AT	83/87 (95%)	73 (88%)	9 (11%)	1 (1%)	13	48
21	AU	49/71 (69%)	36 (74%)	12 (24%)	1 (2%)	7	39
23	AW	523/534 (98%)	382 (73%)	82 (16%)	59 (11%)	0	5
24	B0	77/85 (91%)	49 (64%)	24 (31%)	4 (5%)	2	21
25	B1	75/78 (96%)	65 (87%)	10 (13%)	0	100	100
26	B2	61/63 (97%)	47 (77%)	12 (20%)	2 (3%)	4	31
27	B3	56/59 (95%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	B4	54/57 (95%)	45 (83%)	8 (15%)	1 (2%)	8	40
29	B5	48/55 (87%)	43 (90%)	4 (8%)	1 (2%)	7	38
30	B6	44/46 (96%)	41 (93%)	2 (4%)	1 (2%)	6	36
31	B7	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	9	43
32	B8	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	5	33
35	BC	269/273 (98%)	234 (87%)	29 (11%)	6 (2%)	6	37
36	BD	207/209 (99%)	176 (85%)	26 (13%)	5 (2%)	6	35
37	BE	199/201 (99%)	170 (85%)	23 (12%)	6 (3%)	4	32
38	BF	175/179 (98%)	145 (83%)	27 (15%)	3 (2%)	9	42
39	BG	174/177 (98%)	141 (81%)	32 (18%)	1 (1%)	25	62
40	BH	161/165 (98%)	123 (76%)	31 (19%)	7 (4%)	2	24
41	BI	139/142 (98%)	113 (81%)	26 (19%)	0	100	100
42	BJ	28/121 (23%)	20 (71%)	8 (29%)	0	100	100
42	BK	28/121 (23%)	23 (82%)	5 (18%)	0	100	100
42	BL	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
42	BM	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	15
43	BN	140/142 (99%)	118 (84%)	20 (14%)	2 (1%)	11	45
44	BO	120/123 (98%)	97 (81%)	19 (16%)	4 (3%)	4	31
45	BP	141/144 (98%)	118 (84%)	22 (16%)	1 (1%)	22	59
46	BQ	134/136 (98%)	112 (84%)	18 (13%)	4 (3%)	4	32
47	BR	118/127 (93%)	101 (86%)	16 (14%)	1 (1%)	19	56
48	BS	114/117 (97%)	99 (87%)	14 (12%)	1 (1%)	17	54
49	BT	112/115 (97%)	93 (83%)	16 (14%)	3 (3%)	5	33
50	BU	115/118 (98%)	103 (90%)	10 (9%)	2 (2%)	9	42
51	BV	101/103 (98%)	88 (87%)	11 (11%)	2 (2%)	7	39
52	BW	108/110 (98%)	97 (90%)	10 (9%)	1 (1%)	17	54
53	BX	91/100 (91%)	62 (68%)	25 (28%)	4 (4%)	2	24
54	BY	100/104 (96%)	78 (78%)	21 (21%)	1 (1%)	15	51
55	BZ	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
All	All	6270/7019 (89%)	5201 (83%)	915 (15%)	154 (2%)	5	35

All (154) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	14	VAL
4	AD	30	LYS
4	AD	125	ASN
13	AM	46	GLU
17	AQ	12	VAL
23	AW	52	ASN
23	AW	61	GLU
23	AW	69	SER
23	AW	98	ASP
23	AW	301	PHE
23	AW	305	ALA
23	AW	309	PRO
23	AW	313	ASP
23	AW	315	VAL
23	AW	390	ILE
23	AW	398	PHE
23	AW	399	ARG
23	AW	406	PRO
23	AW	434	ASN
23	AW	440	ALA
23	AW	441	VAL
23	AW	521	VAL
23	AW	522	GLN
24	B0	18	LYS
24	B0	40	ARG
35	BC	141	HIS
36	BD	73	VAL
38	BF	135	ILE
43	BN	44	TYR
46	BQ	36	VAL
10	AJ	57	VAL
23	AW	60	MET
23	AW	68	ILE
23	AW	96	SER
23	AW	300	VAL
23	AW	356	VAL
23	AW	410	LYS
23	AW	413	LEU
23	AW	424	ALA
23	AW	433	ASN
23	AW	500	ASN
23	AW	504	ILE
23	AW	524	HIS

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Mol	Chain	Res	Type
23	AW	526	THR
35	BC	238	ASN
38	BF	11	VAL
38	BF	134	GLN
40	BH	58	THR
48	BS	68	LYS
6	AF	53	LYS
8	AH	87	ARG
10	AJ	74	VAL
12	AL	24	GLU
23	AW	18	ILE
23	AW	49	ARG
23	AW	53	GLN
23	AW	54	HIS
23	AW	62	MET
23	AW	92	HIS
23	AW	391	PRO
23	AW	404	LYS
23	AW	405	ASP
23	AW	435	ASP
23	AW	477	ALA
23	AW	492	GLN
23	AW	523	PHE
35	BC	256	THR
36	BD	170	VAL
40	BH	59	LEU
40	BH	61	ARG
40	BH	107	GLU
40	BH	108	VAL
44	BO	14	SER
44	BO	92	GLU
46	BQ	70	ASP
49	BT	50	ARG
50	BU	87	VAL
53	BX	38	ALA
9	AI	41	GLU
9	AI	57	VAL
9	AI	71	ILE
12	AL	8	ARG
16	AP	43	ALA
23	AW	295	LYS
23	AW	403	LEU

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Mol	Chain	Res	Type
23	AW	412	LEU
23	AW	480	LYS
37	BE	45	ALA
37	BE	124	PHE
39	BG	118	ALA
42	BM	10	ALA
43	BN	81	ILE
44	BO	35	VAL
47	BR	70	THR
53	BX	18	GLU
4	AD	124	VAL
5	AE	77	ASN
5	AE	97	PRO
5	AE	154	ALA
23	AW	93	GLU
23	AW	304	GLN
23	AW	467	ASN
23	AW	473	TRP
26	B2	24	GLU
26	B2	46	VAL
45	BP	111	ILE
46	BQ	43	ALA
53	BX	70	HIS
2	AB	163	ILE
4	AD	159	GLU
23	AW	320	VAL
23	AW	407	LEU
23	AW	411	GLN
24	B0	11	ASN
35	BC	140	VAL
49	BT	105	LYS
50	BU	114	ALA
54	BY	92	VAL
5	AE	104	ILE
10	AJ	36	VAL
35	BC	77	VAL
36	BD	107	VAL
36	BD	122	VAL
37	BE	175	ILE
40	BH	118	ILE
44	BO	93	GLN
13	AM	3	ILE

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Mol	Chain	Res	Type
21	AU	10	PRO
23	AW	518	TYR
35	BC	64	VAL
37	BE	148	ILE
40	BH	119	PRO
46	BQ	73	ILE
49	BT	63	ILE
9	AI	22	PRO
24	B0	50	VAL
28	B4	54	ILE
30	B6	44	VAL
32	B8	16	ILE
37	BE	83	VAL
51	BV	98	ILE
3	AC	65	VAL
23	AW	78	PRO
23	AW	382	GLY
31	B7	31	ILE
36	BD	109	VAL
37	BE	96	VAL
42	BM	11	VAL
51	BV	101	ILE
52	BW	96	ILE
53	BX	55	VAL
20	AT	66	ILE
29	B5	4	ILE
23	AW	519	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
2	AB	180/199 (90%)	149 (83%)	31 (17%)	2	13
3	AC	170/190 (90%)	145 (85%)	25 (15%)	3	18
4	AD	172/173 (99%)	148 (86%)	24 (14%)	3	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AE	113/126 (90%)	93 (82%)	20 (18%)	2	12
6	AF	87/116 (75%)	74 (85%)	13 (15%)	3	18
7	AG	124/147 (84%)	114 (92%)	10 (8%)	11	41
8	AH	104/105 (99%)	89 (86%)	15 (14%)	3	19
9	AI	105/107 (98%)	87 (83%)	18 (17%)	2	13
10	AJ	86/90 (96%)	70 (81%)	16 (19%)	1	10
11	AK	90/99 (91%)	77 (86%)	13 (14%)	3	19
12	AL	103/104 (99%)	88 (85%)	15 (15%)	3	18
13	AM	92/96 (96%)	87 (95%)	5 (5%)	22	54
14	AN	79/84 (94%)	71 (90%)	8 (10%)	7	31
15	AO	76/77 (99%)	69 (91%)	7 (9%)	9	36
16	AP	65/65 (100%)	58 (89%)	7 (11%)	6	29
17	AQ	74/78 (95%)	62 (84%)	12 (16%)	2	15
18	AR	48/65 (74%)	44 (92%)	4 (8%)	11	40
19	AS	70/79 (89%)	65 (93%)	5 (7%)	14	45
20	AT	65/66 (98%)	58 (89%)	7 (11%)	6	29
21	AU	44/61 (72%)	38 (86%)	6 (14%)	3	21
23	AW	447/458 (98%)	380 (85%)	67 (15%)	3	18
24	B0	59/63 (94%)	44 (75%)	15 (25%)	0	4
25	B1	67/68 (98%)	61 (91%)	6 (9%)	9	37
26	B2	55/55 (100%)	48 (87%)	7 (13%)	4	23
27	B3	48/49 (98%)	39 (81%)	9 (19%)	1	10
28	B4	47/48 (98%)	44 (94%)	3 (6%)	17	48
29	B5	45/49 (92%)	40 (89%)	5 (11%)	6	28
30	B6	38/38 (100%)	34 (90%)	4 (10%)	7	30
31	B7	51/52 (98%)	49 (96%)	2 (4%)	32	60
32	B8	34/34 (100%)	31 (91%)	3 (9%)	10	38
35	BC	216/218 (99%)	184 (85%)	32 (15%)	3	18
36	BD	164/164 (100%)	145 (88%)	19 (12%)	5	27
37	BE	165/165 (100%)	144 (87%)	21 (13%)	4	23
38	BF	148/150 (99%)	134 (90%)	14 (10%)	8	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	BG	137/138 (99%)	115 (84%)	22 (16%)	2	15
40	BH	123/123 (100%)	105 (85%)	18 (15%)	3	18
41	BI	109/110 (99%)	94 (86%)	15 (14%)	3	21
42	BJ	26/85 (31%)	23 (88%)	3 (12%)	5	27
42	BK	26/85 (31%)	25 (96%)	1 (4%)	33	61
42	BL	26/85 (31%)	25 (96%)	1 (4%)	33	61
42	BM	26/85 (31%)	23 (88%)	3 (12%)	5	27
43	BN	116/116 (100%)	90 (78%)	26 (22%)	1	6
44	BO	103/104 (99%)	83 (81%)	20 (19%)	1	9
45	BP	102/103 (99%)	89 (87%)	13 (13%)	4	23
46	BQ	109/109 (100%)	91 (84%)	18 (16%)	2	14
47	BR	100/103 (97%)	85 (85%)	15 (15%)	3	18
48	BS	86/87 (99%)	72 (84%)	14 (16%)	2	15
49	BT	99/100 (99%)	82 (83%)	17 (17%)	2	13
50	BU	89/90 (99%)	75 (84%)	14 (16%)	2	16
51	BV	84/84 (100%)	73 (87%)	11 (13%)	4	22
52	BW	93/93 (100%)	76 (82%)	17 (18%)	1	10
53	BX	80/84 (95%)	69 (86%)	11 (14%)	3	21
54	BY	83/85 (98%)	69 (83%)	14 (17%)	2	13
55	BZ	78/78 (100%)	73 (94%)	5 (6%)	17	48
All	All	5226/5685 (92%)	4500 (86%)	726 (14%)	3	20

All (726) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	13	VAL
2	AB	15	PHE
2	AB	19	THR
2	AB	20	ARG
2	AB	22	TRP
2	AB	26	MET
2	AB	36	LYS
2	AB	38	HIS
2	AB	49	PHE
2	AB	67	LEU

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Mol	Chain	Res	Type
2	AB	71	THR
2	AB	81	ASP
2	AB	86	CYS
2	AB	88	GLN
2	AB	90	PHE
2	AB	93	HIS
2	AB	95	TRP
2	AB	108	GLN
2	AB	115	ASP
2	AB	122	ASP
2	AB	125	PHE
2	AB	128	LEU
2	AB	130	LYS
2	AB	136	ARG
2	AB	138	ARG
2	AB	143	LEU
2	AB	158	ASP
2	AB	189	ASN
2	AB	198	VAL
2	AB	212	TYR
2	AB	219	THR
3	AC	2	GLN
3	AC	10	ARG
3	AC	15	LYS
3	AC	20	THR
3	AC	26	LYS
3	AC	28	PHE
3	AC	36	PHE
3	AC	52	SER
3	AC	54	ILE
3	AC	79	LYS
3	AC	83	VAL
3	AC	99	GLN
3	AC	100	ILE
3	AC	102	ILE
3	AC	106	ARG
3	AC	135	ARG
3	AC	143	LEU
3	AC	148	ILE
3	AC	161	ILE
3	AC	165	GLU
3	AC	166	TRP

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Mol	Chain	Res	Type
3	AC	167	TYR
3	AC	171	ARG
3	AC	184	ASN
3	AC	189	HIS
4	AD	4	LEU
4	AD	21	LYS
4	AD	25	ARG
4	AD	29	THR
4	AD	34	GLU
4	AD	39	GLN
4	AD	43	ARG
4	AD	55	ARG
4	AD	57	LYS
4	AD	103	ARG
4	AD	109	THR
4	AD	115	GLN
4	AD	119	HIS
4	AD	127	ARG
4	AD	131	ILE
4	AD	151	GLN
4	AD	153	ARG
4	AD	160	LEU
4	AD	162	GLU
4	AD	166	LYS
4	AD	172	VAL
4	AD	193	ASP
4	AD	199	ILE
4	AD	205	LYS
5	AE	9	GLU
5	AE	14	LEU
5	AE	28	ARG
5	AE	29	ILE
5	AE	31	SER
5	AE	45	VAL
5	AE	63	MET
5	AE	69	ASN
5	AE	71	ILE
5	AE	92	ARG
5	AE	99	SER
5	AE	100	GLU
5	AE	114	LEU
5	AE	120	HIS

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Mol	Chain	Res	Type
5	AE	121	ASN
5	AE	123	LEU
5	AE	125	LYS
5	AE	150	GLU
5	AE	155	LYS
5	AE	156	ARG
6	AF	7	VAL
6	AF	14	GLN
6	AF	17	GLN
6	AF	24	ARG
6	AF	36	ILE
6	AF	51	ILE
6	AF	54	LEU
6	AF	68	GLN
6	AF	69	GLU
6	AF	84	VAL
6	AF	86	ARG
6	AF	96	VAL
6	AF	97	THR
7	AG	3	ARG
7	AG	5	VAL
7	AG	6	ILE
7	AG	11	ILE
7	AG	12	LEU
7	AG	62	GLU
7	AG	69	ARG
7	AG	93	VAL
7	AG	112	ASP
7	AG	130	LYS
8	AH	9	MET
8	AH	11	THR
8	AH	17	GLN
8	AH	21	LYS
8	AH	50	VAL
8	AH	54	THR
8	AH	55	LYS
8	AH	58	LEU
8	AH	72	GLU
8	AH	76	ARG
8	AH	84	ILE
8	AH	86	LYS
8	AH	111	THR

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Mol	Chain	Res	Type
8	AH	120	LEU
8	AH	124	ILE
9	AI	11	ARG
9	AI	21	LYS
9	AI	35	GLU
9	AI	40	ARG
9	AI	45	MET
9	AI	48	ARG
9	AI	51	LEU
9	AI	54	VAL
9	AI	56	MET
9	AI	62	LEU
9	AI	67	LYS
9	AI	84	ARG
9	AI	86	LEU
9	AI	87	MET
9	AI	89	TYR
9	AI	110	VAL
9	AI	115	VAL
9	AI	128	LYS
10	AJ	14	ASP
10	AJ	15	HIS
10	AJ	18	ILE
10	AJ	19	ASP
10	AJ	25	ILE
10	AJ	32	THR
10	AJ	44	THR
10	AJ	48	ARG
10	AJ	63	ASP
10	AJ	71	LEU
10	AJ	73	LEU
10	AJ	78	GLU
10	AJ	83	THR
10	AJ	89	ARG
10	AJ	92	LEU
10	AJ	100	ILE
11	AK	17	ASP
11	AK	22	ILE
11	AK	30	ILE
11	AK	51	PHE
11	AK	55	ARG
11	AK	64	VAL

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Mol	Chain	Res	Type
11	AK	78	ILE
11	AK	82	GLU
11	AK	120	CYS
11	AK	124	LYS
11	AK	125	LYS
11	AK	127	ARG
11	AK	128	VAL
12	AL	9	LYS
12	AL	17	LYS
12	AL	23	LEU
12	AL	28	GLN
12	AL	43	LYS
12	AL	49	ARG
12	AL	57	THR
12	AL	77	SER
12	AL	81	ILE
12	AL	86	VAL
12	AL	87	LYS
12	AL	89	LEU
12	AL	102	ASP
12	AL	109	ARG
12	AL	114	SER
13	AM	18	LEU
13	AM	100	ARG
13	AM	103	THR
13	AM	104	ASN
13	AM	112	ARG
14	AN	3	GLN
14	AN	20	PHE
14	AN	25	GLU
14	AN	27	LYS
14	AN	47	LEU
14	AN	54	SER
14	AN	88	MET
14	AN	99	SER
15	AO	16	ARG
15	AO	21	THR
15	AO	39	GLN
15	AO	47	LYS
15	AO	63	ARG
15	AO	82	GLU
15	AO	86	LEU

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Mol	Chain	Res	Type
16	AP	2	VAL
16	AP	6	LEU
16	AP	18	GLN
16	AP	19	VAL
16	AP	36	VAL
16	AP	46	LYS
16	AP	80	LYS
17	AQ	3	LYS
17	AQ	12	VAL
17	AQ	15	LYS
17	AQ	16	MET
17	AQ	21	VAL
17	AQ	47	ASP
17	AQ	51	GLU
17	AQ	54	ILE
17	AQ	64	ARG
17	AQ	74	LEU
17	AQ	78	VAL
17	AQ	80	LYS
18	AR	24	ASP
18	AR	25	ILE
18	AR	54	LEU
18	AR	71	ASP
19	AS	55	GLN
19	AS	60	PHE
19	AS	61	VAL
19	AS	62	THR
19	AS	64	GLU
20	AT	27	MET
20	AT	35	TYR
20	AT	42	ASP
20	AT	48	LYS
20	AT	66	ILE
20	AT	75	LYS
20	AT	84	LYS
21	AU	4	LYS
21	AU	9	GLU
21	AU	18	PHE
21	AU	33	ARG
21	AU	38	GLU
21	AU	45	LYS
23	AW	3	LEU

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Mol	Chain	Res	Type
23	AW	14	ARG
23	AW	31	GLU
23	AW	35	LEU
23	AW	42	THR
23	AW	45	THR
23	AW	46	VAL
23	AW	49	ARG
23	AW	51	SER
23	AW	59	TRP
23	AW	60	MET
23	AW	70	ILE
23	AW	72	THR
23	AW	73	SER
23	AW	94	ASP
23	AW	97	GLU
23	AW	108	CYS
23	AW	110	LEU
23	AW	117	LYS
23	AW	127	MET
23	AW	145	ASP
23	AW	155	LEU
23	AW	178	LEU
23	AW	202	GLN
23	AW	204	VAL
23	AW	216	ASP
23	AW	231	LEU
23	AW	238	SER
23	AW	258	THR
23	AW	268	MET
23	AW	304	GLN
23	AW	307	MET
23	AW	310	LYS
23	AW	311	HIS
23	AW	332	ARG
23	AW	343	SER
23	AW	344	ASP
23	AW	353	ARG
23	AW	355	HIS
23	AW	356	VAL
23	AW	358	GLU
23	AW	369	ASN
23	AW	390	ILE

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Mol	Chain	Res	Type
23	AW	397	LEU
23	AW	398	PHE
23	AW	400	ARG
23	AW	401	ILE
23	AW	403	LEU
23	AW	404	LYS
23	AW	410	LYS
23	AW	411	GLN
23	AW	412	LEU
23	AW	433	ASN
23	AW	441	VAL
23	AW	447	ASP
23	AW	452	ARG
23	AW	453	LEU
23	AW	454	LYS
23	AW	458	ASN
23	AW	459	VAL
23	AW	462	VAL
23	AW	487	ARG
23	AW	499	ASP
23	AW	501	LEU
23	AW	518	TYR
23	AW	521	VAL
23	AW	525	GLN
24	B0	9	THR
24	B0	10	ARG
24	B0	14	ASP
24	B0	19	ARG
24	B0	23	LYS
24	B0	24	ARG
24	B0	30	VAL
24	B0	35	ILE
24	B0	36	ILE
24	B0	38	ARG
24	B0	49	ASN
24	B0	54	ARG
24	B0	63	ASP
24	B0	67	LYS
24	B0	79	ILE
25	B1	6	VAL
25	B1	24	THR
25	B1	45	PHE

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Mol	Chain	Res	Type
25	B1	53	LYS
25	B1	70	LEU
25	B1	77	TYR
26	B2	9	LYS
26	B2	17	GLU
26	B2	18	LEU
26	B2	39	GLN
26	B2	41	HIS
26	B2	57	LEU
26	B2	59	GLU
27	B3	4	ILE
27	B3	6	ILE
27	B3	8	GLN
27	B3	15	ARG
27	B3	23	LEU
27	B3	30	ARG
27	B3	31	ILE
27	B3	37	ARG
27	B3	40	THR
28	B4	9	ARG
28	B4	37	HIS
28	B4	45	ASP
29	B5	4	ILE
29	B5	9	LYS
29	B5	19	PHE
29	B5	33	LEU
29	B5	46	VAL
30	B6	3	ARG
30	B6	24	THR
30	B6	39	ARG
30	B6	44	VAL
31	B7	7	ARG
31	B7	22	LYS
32	B8	7	VAL
32	B8	9	LYS
32	B8	27	CYS
35	BC	9	SER
35	BC	12	ARG
35	BC	23	LEU
35	BC	27	LYS
35	BC	35	LYS
35	BC	38	LYS

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Mol	Chain	Res	Type
35	BC	73	ILE
35	BC	76	VAL
35	BC	93	VAL
35	BC	102	TYR
35	BC	109	LEU
35	BC	117	SER
35	BC	123	ILE
35	BC	132	ARG
35	BC	141	HIS
35	BC	142	ASN
35	BC	155	ARG
35	BC	175	LEU
35	BC	176	ARG
35	BC	193	GLU
35	BC	202	ARG
35	BC	204	LEU
35	BC	212	TRP
35	BC	215	VAL
35	BC	250	GLN
35	BC	251	THR
35	BC	252	LYS
35	BC	254	LYS
35	BC	259	ASN
35	BC	268	ARG
35	BC	269	ARG
35	BC	270	ARG
36	BD	14	ILE
36	BD	16	THR
36	BD	34	VAL
36	BD	43	ASP
36	BD	50	VAL
36	BD	60	VAL
36	BD	62	LYS
36	BD	89	GLU
36	BD	91	THR
36	BD	114	LYS
36	BD	118	PHE
36	BD	124	ARG
36	BD	129	THR
36	BD	131	ASP
36	BD	137	SER
36	BD	150	GLN

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Mol	Chain	Res	Type
36	BD	176	ASP
36	BD	201	LEU
36	BD	203	VAL
37	BE	9	GLN
37	BE	12	LEU
37	BE	41	GLN
37	BE	51	GLU
37	BE	70	SER
37	BE	78	TRP
37	BE	108	ILE
37	BE	109	LEU
37	BE	116	ASP
37	BE	118	LEU
37	BE	119	ILE
37	BE	123	LYS
37	BE	143	LEU
37	BE	144	GLU
37	BE	146	VAL
37	BE	147	LEU
37	BE	150	THR
37	BE	163	ASN
37	BE	170	ARG
37	BE	180	LEU
37	BE	189	THR
38	BF	9	ASP
38	BF	35	LEU
38	BF	39	VAL
38	BF	46	LYS
38	BF	50	ASP
38	BF	73	VAL
38	BF	80	GLN
38	BF	82	TYR
38	BF	99	PHE
38	BF	102	LEU
38	BF	109	ARG
38	BF	114	ARG
38	BF	152	ASP
38	BF	154	THR
39	BG	8	VAL
39	BG	18	ILE
39	BG	34	ARG
39	BG	37	ASN

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Mol	Chain	Res	Type
39	BG	40	VAL
39	BG	55	ASP
39	BG	59	ASP
39	BG	68	ARG
39	BG	72	ASN
39	BG	76	ILE
39	BG	78	VAL
39	BG	84	LYS
39	BG	91	VAL
39	BG	98	LYS
39	BG	120	ILE
39	BG	131	VAL
39	BG	132	LEU
39	BG	138	GLN
39	BG	140	ILE
39	BG	151	ARG
39	BG	152	ARG
39	BG	166	GLU
40	BH	3	LEU
40	BH	11	ILE
40	BH	26	VAL
40	BH	31	ARG
40	BH	46	ARG
40	BH	59	LEU
40	BH	61	ARG
40	BH	96	PHE
40	BH	106	PHE
40	BH	107	GLU
40	BH	118	ILE
40	BH	123	ILE
40	BH	126	LEU
40	BH	128	THR
40	BH	140	MET
40	BH	143	MET
40	BH	154	THR
40	BH	158	VAL
41	BI	7	TYR
41	BI	10	LEU
41	BI	12	VAL
41	BI	23	VAL
41	BI	30	GLN
41	BI	37	PHE

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Mol	Chain	Res	Type
41	BI	39	LYS
41	BI	61	TYR
41	BI	63	ASP
41	BI	71	LYS
41	BI	100	ILE
41	BI	112	LYS
41	BI	117	THR
41	BI	126	ARG
41	BI	135	MET
42	BJ	27	GLU
42	BJ	29	LYS
42	BJ	30	PHE
42	BK	28	GLU
42	BL	18	ASP
42	BM	2	ILE
42	BM	3	THR
42	BM	18	ASP
43	BN	1	MET
43	BN	2	LYS
43	BN	3	THR
43	BN	17	VAL
43	BN	18	VAL
43	BN	25	LEU
43	BN	30	THR
43	BN	34	ARG
43	BN	36	LEU
43	BN	41	LYS
43	BN	45	THR
43	BN	54	ILE
43	BN	55	ILE
43	BN	64	VAL
43	BN	69	ARG
43	BN	73	VAL
43	BN	80	HIS
43	BN	103	ILE
43	BN	111	LYS
43	BN	114	LEU
43	BN	123	LYS
43	BN	124	VAL
43	BN	129	GLU
43	BN	131	ASN
43	BN	135	GLN

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Mol	Chain	Res	Type
43	BN	140	LEU
44	BO	6	THR
44	BO	22	ILE
44	BO	28	SER
44	BO	47	ILE
44	BO	51	LYS
44	BO	54	LYS
44	BO	58	LEU
44	BO	70	ARG
44	BO	73	ASP
44	BO	82	ASN
44	BO	89	ASN
44	BO	93	GLN
44	BO	95	ILE
44	BO	100	PHE
44	BO	105	ARG
44	BO	107	LEU
44	BO	109	SER
44	BO	111	LYS
44	BO	114	LYS
44	BO	118	LEU
45	BP	3	LEU
45	BP	13	LYS
45	BP	19	LEU
45	BP	21	ARG
45	BP	27	LEU
45	BP	48	ARG
45	BP	55	MET
45	BP	59	ARG
45	BP	61	LEU
45	BP	81	ASP
45	BP	82	LEU
45	BP	85	VAL
45	BP	121	THR
46	BQ	10	ARG
46	BQ	24	THR
46	BQ	33	LEU
46	BQ	42	THR
46	BQ	70	ASP
46	BQ	73	ILE
46	BQ	75	GLU
46	BQ	78	LEU

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Mol	Chain	Res	Type
46	BQ	81	ARG
46	BQ	93	VAL
46	BQ	96	ILE
46	BQ	97	GLN
46	BQ	100	LYS
46	BQ	102	LEU
46	BQ	108	VAL
46	BQ	115	GLU
46	BQ	128	THR
46	BQ	134	THR
47	BR	1	MET
47	BR	10	LEU
47	BR	27	SER
47	BR	33	ILE
47	BR	36	THR
47	BR	51	LEU
47	BR	69	ARG
47	BR	71	ARG
47	BR	75	ILE
47	BR	76	VAL
47	BR	95	THR
47	BR	97	ILE
47	BR	99	LYS
47	BR	113	ILE
47	BR	117	ASP
48	BS	9	ARG
48	BS	17	LYS
48	BS	21	LEU
48	BS	31	THR
48	BS	33	ARG
48	BS	35	ILE
48	BS	38	GLN
48	BS	76	LYS
48	BS	78	VAL
48	BS	103	VAL
48	BS	106	LEU
48	BS	111	ARG
48	BS	112	GLU
48	BS	116	GLN
49	BT	6	GLN
49	BT	13	LYS
49	BT	14	GLN

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Mol	Chain	Res	Type
49	BT	15	ASP
49	BT	24	THR
49	BT	28	LYS
49	BT	36	LYS
49	BT	37	LYS
49	BT	38	ARG
49	BT	46	VAL
49	BT	50	ARG
49	BT	61	ARG
49	BT	75	THR
49	BT	83	ILE
49	BT	91	VAL
49	BT	92	ARG
49	BT	93	LYS
50	BU	7	VAL
50	BU	8	ILE
50	BU	10	ARG
50	BU	12	ARG
50	BU	44	TYR
50	BU	50	ARG
50	BU	59	LEU
50	BU	63	ARG
50	BU	65	ASN
50	BU	73	ILE
50	BU	88	GLU
50	BU	93	ILE
50	BU	94	LEU
50	BU	96	ASP
51	BV	4	VAL
51	BV	10	LYS
51	BV	37	GLU
51	BV	39	LEU
51	BV	46	GLU
51	BV	48	LYS
51	BV	49	ILE
51	BV	55	ASP
51	BV	63	VAL
51	BV	66	HIS
51	BV	81	LYS
52	BW	3	THR
52	BW	4	ILE
52	BW	7	HIS

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Mol	Chain	Res	Type
52	BW	24	ILE
52	BW	36	LEU
52	BW	45	VAL
52	BW	48	LYS
52	BW	68	ASP
52	BW	69	LEU
52	BW	75	PHE
52	BW	76	VAL
52	BW	81	SER
52	BW	85	ILE
52	BW	88	ARG
52	BW	95	ARG
52	BW	99	ARG
52	BW	101	SER
53	BX	2	ILE
53	BX	3	ARG
53	BX	8	LEU
53	BX	18	GLU
53	BX	31	VAL
53	BX	32	LEU
53	BX	37	ASP
53	BX	43	ILE
53	BX	49	LYS
53	BX	64	LYS
53	BX	68	LYS
54	BY	6	ARG
54	BY	18	LYS
54	BY	20	LYS
54	BY	23	LYS
54	BY	30	SER
54	BY	32	LYS
54	BY	42	LYS
54	BY	43	LYS
54	BY	61	GLU
54	BY	67	SER
54	BY	80	ASP
54	BY	82	VAL
54	BY	87	GLU
54	BY	102	ILE
55	BZ	3	THR
55	BZ	10	LYS
55	BZ	55	GLU

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Mol	Chain	Res	Type
55	BZ	61	LEU
55	BZ	66	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	108	GLN
2	AB	189	ASN
3	AC	184	ASN
4	AD	84	ASN
5	AE	121	ASN
6	AF	37	HIS
8	AH	17	GLN
10	AJ	56	HIS
11	AK	108	ASN
12	AL	28	GLN
12	AL	95	HIS
15	AO	39	GLN
16	AP	26	ASN
18	AR	53	GLN
20	AT	20	ASN
20	AT	47	GLN
20	AT	74	HIS
23	AW	21	HIS
23	AW	76	GLN
23	AW	306	ASN
23	AW	369	ASN
23	AW	409	GLN
23	AW	525	GLN
26	B2	41	HIS
35	BC	14	HIS
35	BC	85	ASN
36	BD	140	HIS
37	BE	163	ASN
39	BG	72	ASN
40	BH	57	ASN
40	BH	88	HIS
44	BO	82	ASN
48	BS	104	GLN
48	BS	116	GLN
49	BT	6	GLN
50	BU	65	ASN

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Mol	Chain	Res	Type
51	BV	66	HIS
52	BW	9	HIS
53	BX	91	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1531/1533 (99%)	278 (18%)	29 (1%)
22	AV	5/27 (18%)	3 (60%)	0
33	BA	2849/2903 (98%)	501 (17%)	53 (1%)
34	BB	117/118 (99%)	20 (17%)	3 (2%)
All	All	4502/4581 (98%)	802 (17%)	85 (1%)

All (802) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	9	G
1	AA	22	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	52	C
1	AA	63	C
1	AA	65	A
1	AA	66	A
1	AA	70	U
1	AA	71	A
1	AA	75	G
1	AA	76	G
1	AA	78	A
1	AA	81	A
1	AA	82	G
1	AA	83	C
1	AA	84	U
1	AA	85	U
1	AA	86	G
1	AA	89	U
1	AA	92	U

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Mol	Chain	Res	Type
1	AA	95	C
1	AA	116	A
1	AA	121	U
1	AA	122	G
1	AA	141	G
1	AA	143	A
1	AA	146	G
1	AA	151	A
1	AA	159	G
1	AA	163	C
1	AA	166	U
1	AA	177	G
1	AA	182	A
1	AA	183	C
1	AA	191	G
1	AA	197	A
1	AA	205	A
1	AA	207	C
1	AA	208	U
1	AA	209	U
1	AA	210	C
1	AA	233	C
1	AA	240	G
1	AA	245	U
1	AA	247	G
1	AA	250	A
1	AA	251	G
1	AA	266	G
1	AA	267	C
1	AA	279	A
1	AA	281	G
1	AA	289	G
1	AA	306	A
1	AA	315	A
1	AA	316	C
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	330	C
1	AA	332	G
1	AA	344	A
1	AA	345	C

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Mol	Chain	Res	Type
1	AA	346	G
1	AA	347	G
1	AA	352	C
1	AA	354	G
1	AA	367	U
1	AA	372	C
1	AA	384	G
1	AA	389	A
1	AA	398	U
1	AA	406	G
1	AA	412	A
1	AA	413	G
1	AA	421	U
1	AA	423	G
1	AA	429	U
1	AA	430	A
1	AA	435	A
1	AA	452	A
1	AA	459	A
1	AA	461	A
1	AA	462	G
1	AA	463	U
1	AA	465	A
1	AA	467	U
1	AA	468	A
1	AA	481	G
1	AA	484	G
1	AA	485	U
1	AA	486	U
1	AA	496	A
1	AA	508	U
1	AA	509	A
1	AA	511	C
1	AA	524	G
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	536	C
1	AA	547	A
1	AA	559	A
1	AA	564	C

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Mol	Chain	Res	Type
1	AA	572	A
1	AA	573	A
1	AA	576	C
1	AA	577	G
1	AA	588	G
1	AA	595	A
1	AA	607	A
1	AA	633	G
1	AA	653	U
1	AA	665	A
1	AA	687	A
1	AA	701	U
1	AA	702	A
1	AA	703	G
1	AA	704	A
1	AA	718	A
1	AA	722	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	733	G
1	AA	748	G
1	AA	755	G
1	AA	777	A
1	AA	794	A
1	AA	799	G
1	AA	809	G
1	AA	813	U
1	AA	814	A
1	AA	815	A
1	AA	817	C
1	AA	828	U
1	AA	841	C
1	AA	843	U
1	AA	845	A
1	AA	846	G
1	AA	849	G
1	AA	859	G
1	AA	885	G
1	AA	890	G
1	AA	891	U
1	AA	914	A

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Mol	Chain	Res	Type
1	AA	927	G
1	AA	934	C
1	AA	935	A
1	AA	960	U
1	AA	961	U
1	AA	966	G
1	AA	969	A
1	AA	972	C
1	AA	974	A
1	AA	975	A
1	AA	977	A
1	AA	983	A
1	AA	992	U
1	AA	994	A
1	AA	1003	G
1	AA	1004	A
1	AA	1008	U
1	AA	1018	G
1	AA	1022	A
1	AA	1024	G
1	AA	1025	U
1	AA	1030	U
1	AA	1031	C
1	AA	1032	G
1	AA	1033	G
1	AA	1034	G
1	AA	1036	A
1	AA	1037	C
1	AA	1042	A
1	AA	1050	G
1	AA	1053	G
1	AA	1054	C
1	AA	1064	G
1	AA	1065	U
1	AA	1085	U
1	AA	1086	U
1	AA	1087	G
1	AA	1094	G
1	AA	1095	U
1	AA	1101	A
1	AA	1102	A
1	AA	1124	G

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Mol	Chain	Res	Type
1	AA	1127	G
1	AA	1129	C
1	AA	1133	G
1	AA	1135	U
1	AA	1136	C
1	AA	1137	C
1	AA	1139	G
1	AA	1146	A
1	AA	1154	G
1	AA	1159	U
1	AA	1160	G
1	AA	1167	A
1	AA	1168	U
1	AA	1181	G
1	AA	1182	G
1	AA	1183	U
1	AA	1184	G
1	AA	1196	A
1	AA	1200	C
1	AA	1201	A
1	AA	1202	U
1	AA	1212	U
1	AA	1213	A
1	AA	1215	G
1	AA	1224	U
1	AA	1225	A
1	AA	1226	C
1	AA	1227	A
1	AA	1240	U
1	AA	1241	G
1	AA	1257	A
1	AA	1258	G
1	AA	1261	A
1	AA	1278	G
1	AA	1279	G
1	AA	1280	A
1	AA	1281	C
1	AA	1285	A
1	AA	1286	U
1	AA	1287	A
1	AA	1297	G
1	AA	1298	U

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Mol	Chain	Res	Type
1	AA	1300	G
1	AA	1301	U
1	AA	1305	G
1	AA	1317	C
1	AA	1318	A
1	AA	1319	A
1	AA	1320	C
1	AA	1323	G
1	AA	1336	C
1	AA	1337	G
1	AA	1340	A
1	AA	1347	G
1	AA	1348	U
1	AA	1353	G
1	AA	1362	A
1	AA	1364	U
1	AA	1371	G
1	AA	1380	U
1	AA	1381	U
1	AA	1397	C
1	AA	1398	A
1	AA	1413	A
1	AA	1419	G
1	AA	1441	A
1	AA	1446	A
1	AA	1448	C
1	AA	1451	U
1	AA	1452	C
1	AA	1453	G
1	AA	1469	C
1	AA	1475	G
1	AA	1487	G
1	AA	1491	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1503	A
1	AA	1506	U
1	AA	1517	G
1	AA	1519	A
1	AA	1529	G

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Mol	Chain	Res	Type
1	AA	1530	G
22	AV	18	G
22	AV	19	U
22	AV	20	A
33	BA	10	A
33	BA	12	U
33	BA	15	G
33	BA	28	A
33	BA	35	G
33	BA	42	A
33	BA	46	G
33	BA	61	C
33	BA	63	A
33	BA	71	A
33	BA	72	U
33	BA	74	A
33	BA	75	G
33	BA	84	A
33	BA	101	A
33	BA	103	A
33	BA	118	A
33	BA	119	A
33	BA	120	U
33	BA	125	A
33	BA	126	A
33	BA	135	U
33	BA	137	U
33	BA	138	U
33	BA	139	U
33	BA	140	C
33	BA	142	A
33	BA	162	U
33	BA	163	C
33	BA	181	A
33	BA	188	G
33	BA	196	A
33	BA	199	A
33	BA	205	G
33	BA	216	A
33	BA	221	A
33	BA	222	A
33	BA	228	C

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Mol	Chain	Res	Type
33	BA	230	G
33	BA	248	G
33	BA	255	A
33	BA	265	A
33	BA	266	G
33	BA	271	G
33	BA	272	A
33	BA	276	U
33	BA	285	G
33	BA	302	C
33	BA	311	A
33	BA	329	G
33	BA	330	A
33	BA	335	C
33	BA	343	C
33	BA	345	A
33	BA	346	A
33	BA	347	A
33	BA	353	C
33	BA	361	G
33	BA	363	G
33	BA	371	A
33	BA	372	G
33	BA	373	U
33	BA	383	C
33	BA	386	G
33	BA	396	G
33	BA	399	U
33	BA	403	U
33	BA	404	A
33	BA	405	U
33	BA	411	G
33	BA	412	A
33	BA	424	G
33	BA	443	A
33	BA	455	C
33	BA	458	G
33	BA	459	U
33	BA	480	A
33	BA	481	G
33	BA	490	C
33	BA	491	G

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Mol	Chain	Res	Type
33	BA	504	A
33	BA	505	A
33	BA	508	A
33	BA	509	C
33	BA	527	C
33	BA	528	A
33	BA	532	A
33	BA	533	G
33	BA	544	C
33	BA	546	U
33	BA	547	A
33	BA	548	G
33	BA	549	G
33	BA	550	C
33	BA	563	A
33	BA	573	U
33	BA	575	A
33	BA	586	A
33	BA	588	U
33	BA	603	A
33	BA	604	G
33	BA	614	A
33	BA	615	U
33	BA	627	A
33	BA	628	G
33	BA	637	A
33	BA	645	C
33	BA	646	U
33	BA	647	G
33	BA	653	U
33	BA	654	A
33	BA	655	A
33	BA	656	G
33	BA	668	A
33	BA	670	A
33	BA	686	U
33	BA	702	U
33	BA	705	A
33	BA	714	U
33	BA	717	C
33	BA	726	G
33	BA	730	A

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Mol	Chain	Res	Type
33	BA	747	U
33	BA	752	A
33	BA	761	A
33	BA	764	A
33	BA	775	G
33	BA	776	G
33	BA	782	A
33	BA	783	A
33	BA	784	G
33	BA	785	G
33	BA	789	A
33	BA	794	A
33	BA	805	G
33	BA	812	C
33	BA	819	A
33	BA	827	U
33	BA	828	U
33	BA	831	G
33	BA	845	A
33	BA	846	U
33	BA	847	U
33	BA	859	G
33	BA	860	U
33	BA	876	C
33	BA	877	A
33	BA	879	G
33	BA	881	G
33	BA	884	U
33	BA	895	U
33	BA	896	A
33	BA	897	C
33	BA	900	A
33	BA	901	C
33	BA	902	C
33	BA	907	G
33	BA	910	A
33	BA	914	G
33	BA	915	C
33	BA	931	U
33	BA	941	A
33	BA	946	C
33	BA	957	C

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Mol	Chain	Res	Type
33	BA	958	U
33	BA	961	C
33	BA	974	G
33	BA	983	A
33	BA	985	C
33	BA	989	G
33	BA	995	C
33	BA	996	A
33	BA	1005	C
33	BA	1012	U
33	BA	1013	C
33	BA	1021	A
33	BA	1022	G
33	BA	1025	G
33	BA	1026	G
33	BA	1027	A
33	BA	1033	U
33	BA	1046	A
33	BA	1047	G
33	BA	1060	U
33	BA	1061	U
33	BA	1066	U
33	BA	1070	A
33	BA	1071	G
33	BA	1074	G
33	BA	1078	U
33	BA	1083	U
33	BA	1084	A
33	BA	1088	A
33	BA	1098	A
33	BA	1102	C
33	BA	1103	A
33	BA	1112	G
33	BA	1128	G
33	BA	1130	U
33	BA	1131	G
33	BA	1132	U
33	BA	1133	A
33	BA	1135	C
33	BA	1136	G
33	BA	1139	G
33	BA	1142	A

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Mol	Chain	Res	Type
33	BA	1157	G
33	BA	1168	G
33	BA	1169	A
33	BA	1174	U
33	BA	1175	A
33	BA	1176	U
33	BA	1180	U
33	BA	1186	G
33	BA	1210	G
33	BA	1212	G
33	BA	1236	G
33	BA	1237	A
33	BA	1238	G
33	BA	1248	G
33	BA	1250	G
33	BA	1252	G
33	BA	1253	A
33	BA	1256	G
33	BA	1266	G
33	BA	1267	U
33	BA	1271	G
33	BA	1272	A
33	BA	1276	A
33	BA	1282	U
33	BA	1300	G
33	BA	1301	A
33	BA	1306	C
33	BA	1341	G
33	BA	1345	C
33	BA	1346	G
33	BA	1352	U
33	BA	1365	A
33	BA	1368	G
33	BA	1378	A
33	BA	1379	U
33	BA	1380	G
33	BA	1383	A
33	BA	1386	C
33	BA	1395	A
33	BA	1396	U
33	BA	1397	U
33	BA	1413	A

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Mol	Chain	Res	Type
33	BA	1416	G
33	BA	1419	A
33	BA	1420	A
33	BA	1421	G
33	BA	1428	C
33	BA	1434	A
33	BA	1435	G
33	BA	1437	C
33	BA	1451	C
33	BA	1453	A
33	BA	1459	G
33	BA	1461	C
33	BA	1482	G
33	BA	1490	A
33	BA	1497	U
33	BA	1498	C
33	BA	1502	A
33	BA	1504	A
33	BA	1507	C
33	BA	1508	A
33	BA	1509	A
33	BA	1510	G
33	BA	1512	C
33	BA	1515	A
33	BA	1522	A
33	BA	1523	U
33	BA	1524	G
33	BA	1533	C
33	BA	1535	A
33	BA	1536	C
33	BA	1565	C
33	BA	1569	A
33	BA	1578	U
33	BA	1581	G
33	BA	1584	U
33	BA	1585	C
33	BA	1602	U
33	BA	1603	A
33	BA	1608	A
33	BA	1609	A
33	BA	1610	A
33	BA	1647	U

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Mol	Chain	Res	Type
33	BA	1648	U
33	BA	1668	A
33	BA	1674	G
33	BA	1688	U
33	BA	1694	C
33	BA	1714	U
33	BA	1715	G
33	BA	1729	U
33	BA	1730	C
33	BA	1732	C
33	BA	1733	G
33	BA	1738	G
33	BA	1744	A
33	BA	1756	G
33	BA	1758	U
33	BA	1759	A
33	BA	1764	C
33	BA	1773	A
33	BA	1774	C
33	BA	1780	A
33	BA	1781	U
33	BA	1782	U
33	BA	1791	A
33	BA	1800	C
33	BA	1801	A
33	BA	1808	A
33	BA	1816	C
33	BA	1819	A
33	BA	1822	C
33	BA	1829	A
33	BA	1833	C
33	BA	1839	G
33	BA	1858	A
33	BA	1869	G
33	BA	1871	A
33	BA	1884	G
33	BA	1906	G
33	BA	1913	A
33	BA	1914	C
33	BA	1927	A
33	BA	1929	G
33	BA	1930	G

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Mol	Chain	Res	Type
33	BA	1937	A
33	BA	1938	A
33	BA	1955	U
33	BA	1963	U
33	BA	1964	G
33	BA	1966	A
33	BA	1967	C
33	BA	1970	A
33	BA	1971	U
33	BA	1972	G
33	BA	1991	U
33	BA	1993	U
33	BA	1996	C
33	BA	1997	C
33	BA	2020	A
33	BA	2022	U
33	BA	2023	C
33	BA	2030	A
33	BA	2031	A
33	BA	2032	G
33	BA	2033	A
33	BA	2034	U
33	BA	2043	C
33	BA	2049	G
33	BA	2055	C
33	BA	2056	G
33	BA	2060	A
33	BA	2061	G
33	BA	2062	A
33	BA	2069	G
33	BA	2093	G
33	BA	2104	C
33	BA	2107	G
33	BA	2109	U
33	BA	2110	G
33	BA	2134	A
33	BA	2135	A
33	BA	2136	G
33	BA	2137	U
33	BA	2139	U
33	BA	2140	G
33	BA	2143	C

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Mol	Chain	Res	Type
33	BA	2144	G
33	BA	2145	C
33	BA	2146	C
33	BA	2147	A
33	BA	2148	G
33	BA	2149	U
33	BA	2150	C
33	BA	2151	U
33	BA	2155	U
33	BA	2156	G
33	BA	2180	U
33	BA	2181	U
33	BA	2183	A
33	BA	2187	U
33	BA	2198	A
33	BA	2199	A
33	BA	2203	U
33	BA	2204	G
33	BA	2210	U
33	BA	2211	A
33	BA	2212	A
33	BA	2213	U
33	BA	2214	C
33	BA	2225	A
33	BA	2226	C
33	BA	2238	G
33	BA	2239	G
33	BA	2250	G
33	BA	2273	A
33	BA	2278	A
33	BA	2283	C
33	BA	2287	A
33	BA	2288	A
33	BA	2305	U
33	BA	2307	G
33	BA	2308	G
33	BA	2309	A
33	BA	2312	U
33	BA	2321	U
33	BA	2322	A
33	BA	2325	G
33	BA	2327	A

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Mol	Chain	Res	Type
33	BA	2333	A
33	BA	2334	U
33	BA	2345	G
33	BA	2347	C
33	BA	2350	C
33	BA	2353	G
33	BA	2357	G
33	BA	2361	G
33	BA	2382	G
33	BA	2383	G
33	BA	2385	C
33	BA	2396	G
33	BA	2402	U
33	BA	2406	A
33	BA	2407	A
33	BA	2423	U
33	BA	2424	C
33	BA	2425	A
33	BA	2427	C
33	BA	2428	G
33	BA	2429	G
33	BA	2430	A
33	BA	2435	A
33	BA	2441	U
33	BA	2445	G
33	BA	2448	A
33	BA	2450	A
33	BA	2459	A
33	BA	2476	A
33	BA	2478	A
33	BA	2491	U
33	BA	2502	G
33	BA	2505	G
33	BA	2506	U
33	BA	2518	A
33	BA	2520	C
33	BA	2529	G
33	BA	2554	U
33	BA	2566	A
33	BA	2567	G
33	BA	2572	A
33	BA	2585	U

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Mol	Chain	Res	Type
33	BA	2586	U
33	BA	2602	A
33	BA	2603	G
33	BA	2609	U
33	BA	2613	U
33	BA	2615	U
33	BA	2629	U
33	BA	2630	G
33	BA	2632	A
33	BA	2640	G
33	BA	2663	G
33	BA	2680	U
33	BA	2689	U
33	BA	2690	U
33	BA	2714	G
33	BA	2726	A
33	BA	2727	A
33	BA	2729	G
33	BA	2733	A
33	BA	2744	G
33	BA	2748	A
33	BA	2757	A
33	BA	2762	C
33	BA	2765	A
33	BA	2769	U
33	BA	2778	A
33	BA	2791	G
33	BA	2799	A
33	BA	2800	A
33	BA	2801	G
33	BA	2818	U
33	BA	2820	A
33	BA	2823	A
33	BA	2848	G
33	BA	2849	U
33	BA	2861	U
33	BA	2867	G
33	BA	2868	A
33	BA	2873	A
33	BA	2883	A
33	BA	2884	U
33	BA	2887	A

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Mol	Chain	Res	Type
33	BA	2891	U
34	BB	3	C
34	BB	9	G
34	BB	15	A
34	BB	16	G
34	BB	25	U
34	BB	30	C
34	BB	35	C
34	BB	41	G
34	BB	44	G
34	BB	53	A
34	BB	57	A
34	BB	66	A
34	BB	67	G
34	BB	87	U
34	BB	88	C
34	BB	89	U
34	BB	90	C
34	BB	99	A
34	BB	108	A
34	BB	109	A

All (85) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	51	A
1	AA	115	G
1	AA	181	A
1	AA	246	A
1	AA	250	A
1	AA	345	C
1	AA	412	A
1	AA	422	C
1	AA	429	U
1	AA	451	A
1	AA	484	G
1	AA	495	A
1	AA	721	G
1	AA	812	G
1	AA	890	G
1	AA	913	A

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Mol	Chain	Res	Type
1	AA	965	U
1	AA	982	U
1	AA	1049	U
1	AA	1101	A
1	AA	1145	A
1	AA	1201	A
1	AA	1239	A
1	AA	1257	A
1	AA	1297	G
1	AA	1300	G
1	AA	1336	C
1	AA	1347	G
33	BA	27	G
33	BA	34	U
33	BA	60	G
33	BA	71	A
33	BA	74	A
33	BA	100	U
33	BA	119	A
33	BA	370	G
33	BA	372	G
33	BA	404	A
33	BA	442	G
33	BA	458	G
33	BA	479	A
33	BA	503	A
33	BA	504	A
33	BA	527	C
33	BA	627	A
33	BA	655	A
33	BA	704	G
33	BA	793	A
33	BA	859	G
33	BA	895	U
33	BA	900	A
33	BA	957	C
33	BA	995	C
33	BA	1020	A
33	BA	1025	G
33	BA	1247	A
33	BA	1253	A
33	BA	1275	A

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Mol	Chain	Res	Type
33	BA	1378	A
33	BA	1458	U
33	BA	1509	A
33	BA	1522	A
33	BA	1818	U
33	BA	1857	G
33	BA	1870	C
33	BA	1970	A
33	BA	2033	A
33	BA	2060	A
33	BA	2092	U
33	BA	2103	C
33	BA	2146	C
33	BA	2149	U
33	BA	2150	C
33	BA	2211	A
33	BA	2225	A
33	BA	2326	C
33	BA	2423	U
33	BA	2726	A
33	BA	2756	U
33	BA	2798	U
33	BA	2867	G
34	BB	52	A
34	BB	56	G
34	BB	66	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is 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
56	GNP	AW	601	57	29,34,34	1.84	7 (24%)	33,54,54	2.47	11 (33%)

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
56	GNP	AW	601	57	-	6/14/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	AW	601	GNP	PB-O3A	-5.61	1.52	1.59
56	AW	601	GNP	C6-N1	3.80	1.39	1.33
56	AW	601	GNP	PB-O2B	-3.34	1.47	1.56
56	AW	601	GNP	PG-O1G	3.07	1.51	1.46
56	AW	601	GNP	PG-O2G	-2.25	1.50	1.56
56	AW	601	GNP	PG-O3G	-2.24	1.50	1.56
56	AW	601	GNP	C8-N7	-2.23	1.30	1.34

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	AW	601	GNP	C5-C6-N1	-8.64	111.61	123.43
56	AW	601	GNP	C2-N1-C6	5.58	124.80	115.93
56	AW	601	GNP	O2B-PB-O1B	4.18	118.69	109.92
56	AW	601	GNP	PB-O3A-PA	-3.79	119.27	132.62
56	AW	601	GNP	C2-N3-C4	-3.34	111.55	115.36
56	AW	601	GNP	O1G-PG-N3B	-3.26	106.96	111.77
56	AW	601	GNP	O3G-PG-O1G	-2.83	106.33	113.45
56	AW	601	GNP	C3'-C2'-C1'	2.22	104.32	100.98
56	AW	601	GNP	N3-C2-N1	-2.18	124.31	127.22
56	AW	601	GNP	O2G-PG-O3G	2.09	113.21	107.64
56	AW	601	GNP	C2'-C3'-C4'	2.03	106.59	102.64

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	AW	601	GNP	PG-N3B-PB-O1B
56	AW	601	GNP	C5'-O5'-PA-O3A
56	AW	601	GNP	C3'-C4'-C5'-O5'
56	AW	601	GNP	O4'-C4'-C5'-O5'
56	AW	601	GNP	C5'-O5'-PA-O1A
56	AW	601	GNP	C5'-O5'-PA-O2A

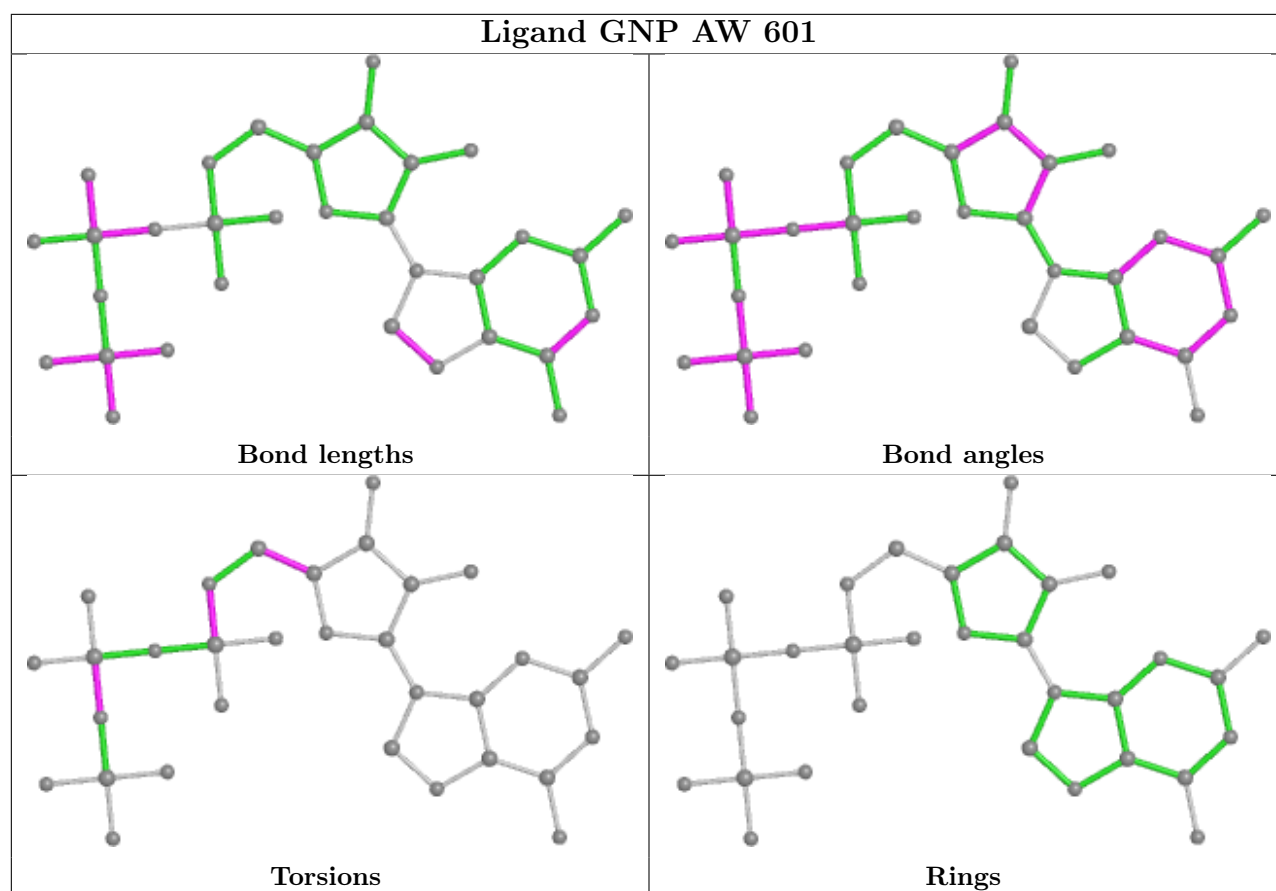
There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	AW	601	GNP	7	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 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	AA	1532/1533 (99%)	0.13	44 (2%) 51 39	72, 119, 232, 344	0
2	AB	218/241 (90%)	1.59	78 (35%) 0 0	124, 181, 235, 328	0
3	AC	206/233 (88%)	0.73	22 (10%) 6 5	88, 129, 167, 218	0
4	AD	205/206 (99%)	0.73	21 (10%) 6 5	88, 120, 177, 250	0
5	AE	150/167 (89%)	0.57	8 (5%) 26 20	88, 123, 176, 253	0
6	AF	100/135 (74%)	0.88	17 (17%) 1 1	106, 153, 182, 204	0
7	AG	151/179 (84%)	1.45	40 (26%) 0 0	132, 178, 218, 300	0
8	AH	129/130 (99%)	0.92	21 (16%) 1 1	108, 137, 177, 228	0
9	AI	127/130 (97%)	1.40	33 (25%) 0 0	102, 145, 212, 252	0
10	AJ	98/103 (95%)	1.11	21 (21%) 0 0	95, 124, 243, 282	0
11	AK	117/129 (90%)	0.29	6 (5%) 28 21	81, 116, 155, 200	0
12	AL	123/124 (99%)	0.71	12 (9%) 7 6	83, 103, 188, 250	0
13	AM	114/118 (96%)	1.98	47 (41%) 0 0	137, 194, 233, 273	0
14	AN	96/101 (95%)	0.94	16 (16%) 1 1	93, 161, 212, 250	0
15	AO	88/89 (98%)	0.75	11 (12%) 3 4	100, 137, 190, 275	0
16	AP	82/82 (100%)	2.03	35 (42%) 0 0	78, 105, 160, 252	0
17	AQ	80/84 (95%)	1.59	27 (33%) 0 0	96, 139, 204, 301	0
18	AR	55/75 (73%)	1.25	12 (21%) 0 0	91, 119, 176, 247	0
19	AS	79/92 (85%)	3.05	53 (67%) 0 0	158, 201, 238, 282	0
20	AT	85/87 (97%)	0.53	5 (5%) 22 15	96, 126, 172, 184	0
21	AU	51/71 (71%)	3.71	34 (66%) 0 0	158, 215, 255, 264	0
22	AV	6/27 (22%)	9.39	6 (100%) 0 0	221, 256, 294, 306	0
23	AW	525/534 (98%)	1.02	95 (18%) 1 1	35, 99, 188, 267	0
24	B0	79/85 (92%)	0.93	13 (16%) 1 1	61, 105, 177, 200	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	B1	77/78 (98%)	0.98	7 (9%) 9 7	68, 83, 132, 154	0
26	B2	63/63 (100%)	0.35	5 (7%) 12 9	72, 100, 145, 187	0
27	B3	58/59 (98%)	1.09	6 (10%) 6 5	67, 92, 143, 174	0
28	B4	56/57 (98%)	0.07	1 (1%) 68 57	44, 65, 108, 150	0
29	B5	50/55 (90%)	2.68	28 (56%) 0 0	133, 176, 209, 228	0
30	B6	46/46 (100%)	0.22	1 (2%) 62 50	48, 60, 84, 197	0
31	B7	64/65 (98%)	0.62	2 (3%) 49 36	63, 85, 109, 128	0
32	B8	38/38 (100%)	1.00	3 (7%) 12 9	82, 104, 135, 178	0
33	BA	2853/2903 (98%)	0.05	124 (4%) 35 26	28, 79, 260, 445	0
34	BB	118/118 (100%)	-0.09	0 100 100	71, 127, 173, 221	0
35	BC	271/273 (99%)	0.10	1 (0%) 92 88	47, 77, 100, 151	0
36	BD	209/209 (100%)	0.05	2 (0%) 82 73	48, 64, 108, 162	0
37	BE	201/201 (100%)	0.28	9 (4%) 33 24	45, 94, 146, 200	0
38	BF	177/179 (98%)	1.16	39 (22%) 0 0	117, 157, 214, 286	0
39	BG	176/177 (99%)	0.79	20 (11%) 5 4	71, 108, 162, 189	0
40	BH	163/165 (98%)	3.70	111 (68%) 0 0	135, 263, 334, 394	0
41	BI	141/142 (99%)	5.14	113 (80%) 0 0	185, 276, 378, 452	0
42	BJ	30/121 (24%)	3.60	19 (63%) 0 0	222, 260, 328, 407	0
42	BK	30/121 (24%)	5.67	28 (93%) 0 0	222, 263, 318, 343	0
42	BL	30/121 (24%)	3.84	24 (80%) 0 0	187, 275, 348, 365	0
42	BM	30/121 (24%)	3.39	21 (70%) 0 0	206, 255, 324, 352	0
43	BN	142/142 (100%)	0.58	5 (3%) 44 33	56, 72, 105, 173	0
44	BO	122/123 (99%)	0.47	4 (3%) 46 35	48, 75, 107, 196	0
45	BP	143/144 (99%)	0.91	22 (15%) 2 1	55, 100, 149, 201	0
46	BQ	136/136 (100%)	0.84	13 (9%) 8 6	65, 92, 133, 188	0
47	BR	120/127 (94%)	0.23	3 (2%) 57 45	39, 64, 85, 233	0
48	BS	116/117 (99%)	1.68	46 (39%) 0 0	91, 125, 157, 180	0
49	BT	114/115 (99%)	0.16	4 (3%) 44 33	61, 83, 133, 164	0
50	BU	117/118 (99%)	-0.16	3 (2%) 56 43	44, 69, 116, 219	0
51	BV	103/103 (100%)	0.28	4 (3%) 39 28	51, 93, 151, 334	0
52	BW	110/110 (100%)	0.16	3 (2%) 54 42	42, 61, 101, 181	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
53	BX	93/100 (93%)	0.74	12 (12%) 3 3	52, 88, 150, 197	0
54	BY	102/104 (98%)	1.03	16 (15%) 2 1	68, 95, 169, 203	0
55	BZ	94/94 (100%)	0.40	6 (6%) 19 13	83, 112, 151, 177	0
All	All	10889/11600 (93%)	0.67	1382 (12%) 3 4	28, 105, 249, 452	0

All (1382) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
40	BH	88	HIS	25.4
41	BI	59	THR	20.6
42	BK	11	VAL	18.2
33	BA	2157	G	17.4
33	BA	885	C	16.7
41	BI	66	PHE	16.6
41	BI	67	THR	16.5
41	BI	20	SER	16.0
23	AW	476	CYS	15.8
42	BL	6	GLN	14.8
42	BJ	8	ILE	14.2
41	BI	5	GLN	14.0
41	BI	118	GLY	13.0
2	AB	17	HIS	12.6
40	BH	50	VAL	12.5
33	BA	1508	A	12.4
41	BI	6	ALA	12.2
41	BI	41	PHE	12.2
41	BI	54	ILE	12.0
22	AV	18	G	11.9
40	BH	14	GLU	11.8
22	AV	19	U	11.7
23	AW	477	ALA	11.6
42	BK	21	GLU	11.6
33	BA	1728	C	11.5
40	BH	45	GLY	11.2
41	BI	32	VAL	11.2
40	BH	103	ASN	11.0
21	AU	24	LYS	11.0
41	BI	21	PRO	10.9
40	BH	17	GLU	10.7
23	AW	519	PRO	10.7
41	BI	68	PHE	10.6

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Mol	Chain	Res	Type	RSRZ
41	BI	30	GLN	10.6
23	AW	478	ASP	10.5
42	BK	29	LYS	10.4
22	AV	20	A	10.2
40	BH	46	ARG	10.0
40	BH	84	TYR	10.0
40	BH	137	ALA	9.9
41	BI	40	ALA	9.8
42	BL	1	SER	9.8
41	BI	33	ASN	9.7
4	AD	24	VAL	9.6
41	BI	119	ALA	9.6
23	AW	475	GLU	9.6
23	AW	514	ALA	9.5
41	BI	58	ILE	9.5
18	AR	19	GLU	9.4
42	BM	9	GLU	9.3
33	BA	1727	C	9.3
23	AW	487	ARG	9.3
5	AE	9	GLU	9.3
33	BA	1093	G	9.2
42	BM	8	ILE	9.1
42	BK	12	ALA	9.1
41	BI	65	SER	9.1
21	AU	27	VAL	9.0
24	B0	6	GLY	9.0
42	BJ	7	ILE	9.0
33	BA	880	G	8.9
41	BI	12	VAL	8.9
41	BI	42	ASN	8.7
19	AS	56	HIS	8.7
33	BA	1730	C	8.7
40	BH	116	GLU	8.5
40	BH	109	LYS	8.5
41	BI	53	PRO	8.4
19	AS	55	GLN	8.4
23	AW	515	GLN	8.4
22	AV	15	A	8.4
42	BK	10	ALA	8.4
23	AW	482	PHE	8.3
1	AA	209	U	8.3
23	AW	520	ASP	8.3

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Mol	Chain	Res	Type	RSRZ
41	BI	34	ILE	8.2
40	BH	146	ALA	8.2
41	BI	29	GLN	8.1
41	BI	13	ALA	8.0
4	AD	23	GLY	8.0
23	AW	474	VAL	7.9
13	AM	36	ALA	7.9
41	BI	39	LYS	7.8
23	AW	486	LYS	7.8
42	BL	22	LEU	7.8
41	BI	63	ASP	7.8
41	BI	61	TYR	7.8
21	AU	20	ARG	7.8
41	BI	105	LEU	7.7
51	BV	50	GLY	7.7
41	BI	31	GLY	7.6
41	BI	55	PRO	7.6
42	BK	18	ASP	7.6
42	BJ	3	THR	7.5
23	AW	521	VAL	7.5
19	AS	57	VAL	7.5
40	BH	16	SER	7.5
23	AW	493	LEU	7.5
23	AW	518	TYR	7.4
23	AW	489	ASN	7.4
41	BI	78	LEU	7.4
42	BK	22	LEU	7.4
48	BS	89	ASP	7.3
41	BI	111	THR	7.3
41	BI	60	VAL	7.3
21	AU	23	GLU	7.3
42	BK	7	ILE	7.2
42	BK	2	ILE	7.2
41	BI	24	GLY	7.2
40	BH	42	ARG	7.2
40	BH	18	VAL	7.1
41	BI	69	VAL	7.1
33	BA	139	U	7.1
23	AW	485	PHE	7.1
21	AU	26	GLY	7.1
9	AI	3	ASN	7.1
9	AI	89	TYR	7.1

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Mol	Chain	Res	Type	RSRZ
22	AV	16	A	7.1
22	AV	17	U	7.1
33	BA	2156	G	7.0
19	AS	49	ALA	7.0
33	BA	2179	C	7.0
38	BF	116	LEU	6.9
41	BI	90	GLY	6.9
40	BH	158	VAL	6.9
33	BA	884	U	6.8
42	BK	3	THR	6.8
2	AB	29	PHE	6.8
10	AJ	91	ASP	6.8
40	BH	49	GLY	6.8
19	AS	29	PRO	6.8
13	AM	37	GLY	6.7
21	AU	28	LEU	6.6
33	BA	1094	U	6.6
41	BI	112	LYS	6.6
41	BI	136	GLY	6.6
40	BH	68	PRO	6.6
42	BL	3	THR	6.6
21	AU	3	ILE	6.6
41	BI	45	THR	6.6
33	BA	2133	G	6.5
42	BM	19	VAL	6.5
23	AW	54	HIS	6.5
40	BH	89	PRO	6.5
41	BI	79	LEU	6.5
23	AW	517	ARG	6.5
40	BH	37	LYS	6.5
41	BI	120	ASP	6.5
41	BI	49	GLU	6.5
41	BI	77	VAL	6.4
40	BH	62	ARG	6.3
23	AW	483	GLU	6.3
29	B5	23	THR	6.3
40	BH	135	ALA	6.3
21	AU	42	THR	6.3
17	AQ	14	ASP	6.3
21	AU	25	ALA	6.3
33	BA	1726	C	6.3
40	BH	36	ASP	6.3

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Mol	Chain	Res	Type	RSRZ
42	BK	25	ALA	6.2
41	BI	17	ALA	6.2
33	BA	1067	A	6.2
21	AU	38	GLU	6.2
40	BH	154	THR	6.2
23	AW	502	ALA	6.1
23	AW	494	ALA	6.1
19	AS	38	THR	6.1
23	AW	488	LYS	6.1
2	AB	19	THR	6.1
17	AQ	82	VAL	6.0
19	AS	39	ILE	6.0
42	BJ	30	PHE	6.0
2	AB	152	ASP	6.0
40	BH	15	VAL	6.0
41	BI	115	ASP	6.0
33	BA	896	A	5.9
19	AS	50	VAL	5.9
38	BF	44	ALA	5.9
23	AW	492	GLN	5.9
1	AA	211	G	5.9
23	AW	479	ALA	5.9
13	AM	83	GLY	5.9
19	AS	73	PHE	5.9
33	BA	881	G	5.9
9	AI	42	THR	5.9
42	BJ	28	GLU	5.9
40	BH	159	ARG	5.9
41	BI	38	CYS	5.9
29	B5	22	THR	5.9
41	BI	109	ALA	5.9
42	BK	4	LYS	5.9
41	BI	28	GLY	5.8
33	BA	2103	C	5.8
16	AP	47	GLU	5.8
40	BH	4	ASN	5.8
40	BH	128	THR	5.8
21	AU	37	TYR	5.8
41	BI	141	ASP	5.8
2	AB	87	ASP	5.7
13	AM	84	CYS	5.7
29	B5	8	ILE	5.7

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Mol	Chain	Res	Type	RSRZ
45	BP	115	GLU	5.7
33	BA	548	G	5.6
7	AG	61	PHE	5.6
40	BH	38	MET	5.6
13	AM	35	ALA	5.6
33	BA	274	C	5.6
41	BI	95	ASP	5.6
23	AW	467	ASN	5.6
4	AD	27	ILE	5.6
40	BH	86	MET	5.6
41	BI	37	PHE	5.6
12	AL	123	ALA	5.6
17	AQ	52	CYS	5.6
41	BI	64	ARG	5.6
13	AM	28	ARG	5.6
40	BH	113	PHE	5.6
33	BA	1065	U	5.5
40	BH	52	MET	5.5
33	BA	1729	U	5.5
29	B5	6	GLU	5.5
41	BI	84	GLY	5.5
23	AW	470	THR	5.5
46	BQ	1	MET	5.5
33	BA	2153	C	5.5
1	AA	841	C	5.5
23	AW	524	HIS	5.4
40	BH	20	LYS	5.4
13	AM	81	ASP	5.4
42	BL	13	ALA	5.4
41	BI	108	ILE	5.4
2	AB	118	THR	5.4
9	AI	38	PHE	5.4
33	BA	2109	U	5.4
14	AN	35	ALA	5.3
42	BJ	10	ALA	5.3
33	BA	2107	G	5.3
33	BA	1095	A	5.3
42	BK	9	GLU	5.3
21	AU	34	ARG	5.3
42	BM	3	THR	5.3
40	BH	29	ASP	5.3
42	BK	28	GLU	5.3

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Mol	Chain	Res	Type	RSRZ
33	BA	1078	U	5.3
1	AA	844	G	5.3
17	AQ	76	ARG	5.3
40	BH	77	VAL	5.3
8	AH	1	SER	5.2
41	BI	70	THR	5.2
2	AB	26	MET	5.2
16	AP	22	ALA	5.2
33	BA	882	G	5.2
41	BI	16	MET	5.2
9	AI	127	SER	5.2
40	BH	27	VAL	5.2
14	AN	56	PRO	5.2
40	BH	26	VAL	5.1
21	AU	41	THR	5.1
42	BL	23	ILE	5.1
19	AS	9	PHE	5.1
13	AM	38	ILE	5.1
48	BS	24	THR	5.1
17	AQ	13	SER	5.1
41	BI	87	SER	5.1
42	BJ	20	VAL	5.1
19	AS	10	ILE	5.1
21	AU	14	ALA	5.1
2	AB	150	ILE	5.1
41	BI	19	PRO	5.1
41	BI	62	ALA	5.1
48	BS	115	LEU	5.0
45	BP	91	ASP	5.0
33	BA	879	G	5.0
13	AM	23	GLY	5.0
42	BK	1	SER	5.0
29	B5	51	ALA	5.0
41	BI	18	ASN	5.0
42	BJ	1	SER	5.0
23	AW	501	LEU	4.9
42	BK	6	GLN	4.9
2	AB	126	ASP	4.9
42	BK	8	ILE	4.9
19	AS	40	PHE	4.9
40	BH	112	ALA	4.9
23	AW	503	TYR	4.9

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Mol	Chain	Res	Type	RSRZ
41	BI	86	LYS	4.9
27	B3	58	GLU	4.9
41	BI	125	THR	4.9
23	AW	522	GLN	4.9
41	BI	80	LYS	4.9
25	B1	75	GLU	4.9
29	B5	21	THR	4.9
8	AH	129	ALA	4.9
19	AS	31	ARG	4.9
45	BP	82	LEU	4.9
29	B5	52	LYS	4.9
45	BP	92	LEU	4.8
19	AS	26	ASP	4.8
40	BH	21	GLY	4.8
40	BH	1	MET	4.8
21	AU	22	CYS	4.8
38	BF	22	ASN	4.8
23	AW	490	GLU	4.8
42	BM	15	SER	4.8
41	BI	139	VAL	4.8
7	AG	75	LYS	4.8
7	AG	71	THR	4.8
23	AW	511	LEU	4.8
39	BG	31	GLU	4.7
2	AB	115	ASP	4.7
19	AS	48	ILE	4.7
40	BH	9	GLN	4.7
2	AB	16	GLY	4.7
40	BH	57	ASN	4.7
21	AU	21	SER	4.7
38	BF	79	ARG	4.7
21	AU	33	ARG	4.7
40	BH	85	SER	4.7
40	BH	105	LYS	4.7
26	B2	63	ALA	4.7
41	BI	52	LEU	4.7
7	AG	82	SER	4.7
27	B3	38	GLU	4.7
40	BH	58	THR	4.7
13	AM	57	ASP	4.7
38	BF	45	ASP	4.7
1	AA	845	A	4.6

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Mol	Chain	Res	Type	RSRZ
13	AM	58	GLU	4.6
41	BI	56	VAL	4.6
13	AM	45	SER	4.6
42	BM	1	SER	4.6
33	BA	2105	U	4.6
42	BK	15	SER	4.6
23	AW	516	GLU	4.6
45	BP	142	ILE	4.6
45	BP	144	GLU	4.6
13	AM	62	PHE	4.6
21	AU	32	ARG	4.6
16	AP	44	SER	4.6
26	B2	62	GLY	4.6
40	BH	53	ARG	4.6
25	B1	77	TYR	4.6
33	BA	2134	A	4.6
33	BA	2150	C	4.6
43	BN	142	ILE	4.6
21	AU	29	ALA	4.6
21	AU	19	LYS	4.6
23	AW	512	ARG	4.6
40	BH	144	LYS	4.5
48	BS	26	LEU	4.5
29	B5	17	GLY	4.5
33	BA	2108	A	4.5
42	BM	29	LYS	4.5
40	BH	114	GLU	4.5
41	BI	92	PRO	4.5
42	BK	5	ASP	4.5
40	BH	25	ALA	4.5
40	BH	110	ALA	4.5
42	BL	7	ILE	4.5
33	BA	1871	A	4.5
9	AI	128	LYS	4.5
19	AS	2	ARG	4.5
7	AG	151	ALA	4.4
41	BI	85	ILE	4.4
7	AG	15	PRO	4.4
23	AW	466	VAL	4.4
40	BH	13	ALA	4.4
33	BA	367	G	4.4
33	BA	368	A	4.4

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Mol	Chain	Res	Type	RSRZ
13	AM	44	ILE	4.4
5	AE	12	GLU	4.4
41	BI	1	ALA	4.4
41	BI	14	ALA	4.4
15	AO	17	ASP	4.4
29	B5	42	VAL	4.4
21	AU	40	PRO	4.4
9	AI	129	ARG	4.4
21	AU	16	ARG	4.4
16	AP	23	ASP	4.4
23	AW	358	GLU	4.3
42	BM	28	GLU	4.3
40	BH	39	THR	4.3
16	AP	52	LEU	4.3
19	AS	3	SER	4.3
33	BA	1870	C	4.3
7	AG	84	TYR	4.3
39	BG	165	ASP	4.3
33	BA	883	G	4.3
23	AW	334	VAL	4.3
45	BP	136	GLU	4.3
7	AG	65	LEU	4.3
40	BH	51	TYR	4.3
29	B5	41	VAL	4.2
40	BH	97	LYS	4.2
9	AI	39	GLY	4.2
2	AB	186	VAL	4.2
33	BA	2106	U	4.2
42	BK	19	VAL	4.2
39	BG	51	PHE	4.2
48	BS	92	PHE	4.2
33	BA	2148	G	4.2
33	BA	275	C	4.2
40	BH	117	LEU	4.2
40	BH	32	GLY	4.2
13	AM	9	PRO	4.2
40	BH	3	LEU	4.2
41	BI	8	VAL	4.2
41	BI	74	PRO	4.2
23	AW	496	ASP	4.2
16	AP	53	ASP	4.2
21	AU	36	PHE	4.2

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Mol	Chain	Res	Type	RSRZ
21	AU	30	GLU	4.2
42	BM	30	PHE	4.2
38	BF	176	PHE	4.1
3	AC	190	THR	4.1
19	AS	70	LEU	4.1
29	B5	9	LYS	4.1
41	BI	137	LEU	4.1
46	BQ	6	ARG	4.1
38	BF	115	GLY	4.1
18	AR	73	HIS	4.1
42	BJ	24	SER	4.1
2	AB	38	HIS	4.1
40	BH	142	THR	4.1
21	AU	35	GLU	4.1
41	BI	2	LYS	4.1
40	BH	111	ALA	4.1
41	BI	44	LYS	4.1
9	AI	91	GLU	4.1
23	AW	526	THR	4.1
42	BL	27	GLU	4.1
16	AP	3	THR	4.1
48	BS	93	ASP	4.1
33	BA	1092	C	4.0
23	AW	431	ILE	4.0
33	BA	2146	C	4.0
7	AG	133	ALA	4.0
23	AW	525	GLN	4.0
16	AP	80	LYS	4.0
41	BI	11	GLN	4.0
1	AA	412	A	4.0
42	BJ	23	ILE	4.0
42	BJ	22	LEU	4.0
40	BH	134	GLU	4.0
29	B5	34	GLU	4.0
41	BI	128	ILE	4.0
6	AF	64	VAL	4.0
42	BM	10	ALA	4.0
41	BI	43	ALA	3.9
13	AM	94	LEU	3.9
29	B5	30	PRO	3.9
19	AS	74	ALA	3.9
33	BA	2110	G	3.9

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Mol	Chain	Res	Type	RSRZ
41	BI	46	ASP	3.9
7	AG	4	ARG	3.9
1	AA	1362	A	3.9
49	BT	114	ASN	3.9
13	AM	3	ILE	3.9
40	BH	91	ALA	3.9
41	BI	36	GLU	3.9
6	AF	59	TYR	3.9
40	BH	153	ARG	3.9
7	AG	5	VAL	3.9
21	AU	4	LYS	3.9
23	AW	471	ALA	3.9
41	BI	27	LEU	3.9
48	BS	50	ALA	3.9
13	AM	46	GLU	3.9
41	BI	88	GLY	3.9
33	BA	1068	G	3.9
33	BA	1171	G	3.9
2	AB	34	ARG	3.9
40	BH	115	GLY	3.9
19	AS	47	THR	3.9
2	AB	36	LYS	3.9
19	AS	8	PRO	3.9
48	BS	40	ILE	3.9
54	BY	86	PHE	3.9
41	BI	50	LYS	3.8
42	BL	18	ASP	3.8
50	BU	86	SER	3.8
23	AW	473	TRP	3.8
40	BH	10	ALA	3.8
2	AB	32	GLY	3.8
33	BA	1175	A	3.8
17	AQ	19	SER	3.8
14	AN	53	ASP	3.8
23	AW	484	GLU	3.8
40	BH	47	GLU	3.8
7	AG	77	ARG	3.8
1	AA	208	U	3.8
42	BL	15	SER	3.8
8	AH	122	GLY	3.8
17	AQ	5	ARG	3.8
4	AD	170	LEU	3.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
19	AS	58	PRO	3.8
23	AW	497	GLY	3.8
29	B5	20	TYR	3.8
19	AS	30	LEU	3.8
42	BJ	19	VAL	3.8
16	AP	51	ARG	3.8
33	BA	1731	G	3.8
33	BA	2180	U	3.8
23	AW	468	VAL	3.7
23	AW	402	ARG	3.7
29	B5	4	ILE	3.7
13	AM	54	THR	3.7
6	AF	8	PHE	3.7
42	BK	30	PHE	3.7
33	BA	1077	A	3.7
17	AQ	79	GLU	3.7
42	BM	18	ASP	3.7
13	AM	1	ALA	3.7
19	AS	32	THR	3.7
41	BI	71	LYS	3.7
45	BP	143	GLU	3.7
6	AF	62	MET	3.7
19	AS	69	LYS	3.7
33	BA	2102	G	3.7
42	BL	17	MET	3.7
3	AC	160	GLU	3.7
1	AA	461	A	3.7
17	AQ	77	VAL	3.7
18	AR	63	TYR	3.7
23	AW	359	ALA	3.7
29	B5	24	LYS	3.7
46	BQ	3	GLN	3.7
19	AS	41	PRO	3.7
10	AJ	30	LYS	3.7
2	AB	8	MET	3.7
40	BH	147	SER	3.7
41	BI	47	SER	3.7
17	AQ	74	LEU	3.7
47	BR	120	GLU	3.7
1	AA	1032	G	3.7
14	AN	19	TYR	3.7
40	BH	145	GLU	3.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
38	BF	78	ILE	3.7
7	AG	79	VAL	3.7
38	BF	43	ILE	3.6
40	BH	31	ARG	3.6
17	AQ	50	ASN	3.6
41	BI	91	LYS	3.6
4	AD	26	ALA	3.6
2	AB	111	LYS	3.6
42	BK	17	MET	3.6
42	BL	2	ILE	3.6
40	BH	74	ASP	3.6
16	AP	67	ILE	3.6
40	BH	106	PHE	3.6
42	BJ	2	ILE	3.6
19	AS	28	LYS	3.6
13	AM	33	LEU	3.6
13	AM	39	ALA	3.6
38	BF	173	ASP	3.6
40	BH	123	ILE	3.6
2	AB	147	LEU	3.6
6	AF	61	LEU	3.6
42	BL	24	SER	3.6
2	AB	138	ARG	3.6
2	AB	205	ALA	3.6
45	BP	108	ALA	3.6
11	AK	128	VAL	3.6
41	BI	9	LYS	3.6
42	BL	26	MET	3.6
19	AS	21	ALA	3.6
33	BA	2402	U	3.6
3	AC	203	LYS	3.5
33	BA	1872	A	3.5
8	AH	67	GLY	3.5
38	BF	31	GLU	3.5
23	AW	508	MET	3.5
33	BA	276	U	3.5
6	AF	25	TYR	3.5
6	AF	37	HIS	3.5
50	BU	87	VAL	3.5
41	BI	114	ALA	3.5
33	BA	1724	G	3.5
38	BF	30	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
42	BL	10	ALA	3.5
46	BQ	7	THR	3.5
48	BS	81	ARG	3.5
10	AJ	93	ALA	3.5
40	BH	104	ALA	3.5
41	BI	98	GLY	3.5
4	AD	193	ASP	3.5
2	AB	37	VAL	3.5
1	AA	1493	A	3.5
27	B3	1	ALA	3.5
19	AS	75	PRO	3.5
33	BA	1509	A	3.5
42	BJ	15	SER	3.5
23	AW	510	ASN	3.4
48	BS	62	LEU	3.4
4	AD	17	ASP	3.4
4	AD	34	GLU	3.4
15	AO	16	ARG	3.4
33	BA	1079	C	3.4
42	BL	28	GLU	3.4
1	AA	1212	U	3.4
19	AS	27	LYS	3.4
41	BI	132	ALA	3.4
14	AN	52	ARG	3.4
6	AF	6	ILE	3.4
40	BH	136	ILE	3.4
3	AC	169	GLU	3.4
13	AM	63	VAL	3.4
41	BI	76	ALA	3.4
33	BA	2147	A	3.4
40	BH	99	PHE	3.4
40	BH	143	MET	3.4
2	AB	50	ASN	3.4
48	BS	85	LYS	3.4
33	BA	2139	U	3.4
2	AB	68	PHE	3.4
15	AO	87	ARG	3.4
11	AK	12	ARG	3.4
40	BH	22	ALA	3.4
33	BA	897	C	3.4
42	BL	21	GLU	3.4
51	BV	44	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
6	AF	9	MET	3.4
33	BA	364	C	3.4
40	BH	44	ALA	3.4
40	BH	133	GLU	3.4
41	BI	73	PRO	3.4
2	AB	71	THR	3.4
20	AT	85	LEU	3.4
19	AS	54	ARG	3.4
41	BI	23	VAL	3.4
33	BA	2149	U	3.4
9	AI	20	ILE	3.4
1	AA	1031	C	3.4
2	AB	51	GLU	3.3
23	AW	523	PHE	3.3
1	AA	1016	A	3.3
48	BS	35	ILE	3.3
23	AW	434	ASN	3.3
42	BL	16	VAL	3.3
2	AB	59	ILE	3.3
6	AF	5	GLU	3.3
42	BJ	27	GLU	3.3
42	BM	12	ALA	3.3
40	BH	43	LYS	3.3
29	B5	16	THR	3.3
13	AM	4	ALA	3.3
53	BX	6	ARG	3.3
2	AB	24	PRO	3.3
42	BM	27	GLU	3.3
42	BM	7	ILE	3.3
42	BK	14	MET	3.3
2	AB	28	PRO	3.3
23	AW	292	SER	3.3
6	AF	63	ASN	3.3
48	BS	49	VAL	3.3
23	AW	432	SER	3.3
17	AQ	62	GLU	3.3
10	AJ	8	ILE	3.3
40	BH	160	ASP	3.3
40	BH	102	ALA	3.3
3	AC	145	ALA	3.3
2	AB	112	ARG	3.3
15	AO	14	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
24	B0	45	HIS	3.2
5	AE	102	THR	3.2
23	AW	430	PRO	3.2
16	AP	66	THR	3.2
41	BI	35	MET	3.2
49	BT	34	GLY	3.2
41	BI	97	VAL	3.2
17	AQ	63	CYS	3.2
10	AJ	35	GLN	3.2
23	AW	379	PHE	3.2
45	BP	118	THR	3.2
10	AJ	49	PHE	3.2
33	BA	1083	U	3.2
21	AU	13	VAL	3.2
23	AW	507	SER	3.2
6	AF	60	VAL	3.2
2	AB	66	ILE	3.2
40	BH	138	ARG	3.2
33	BA	2144	G	3.2
45	BP	123	ARG	3.2
9	AI	40	ARG	3.1
12	AL	16	ALA	3.1
19	AS	14	LEU	3.1
18	AR	26	ALA	3.1
4	AD	165	GLU	3.1
38	BF	70	ARG	3.1
40	BH	107	GLU	3.1
54	BY	88	ASP	3.1
3	AC	165	GLU	3.1
45	BP	141	LYS	3.1
39	BG	42	VAL	3.1
33	BA	138	U	3.1
40	BH	95	LEU	3.1
46	BQ	2	LEU	3.1
54	BY	59	GLU	3.1
1	AA	1033	G	3.1
4	AD	35	GLN	3.1
42	BM	17	MET	3.1
23	AW	527	ARG	3.1
40	BH	83	ALA	3.1
54	BY	78	LYS	3.1
23	AW	428	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
46	BQ	33	LEU	3.1
40	BH	127	ALA	3.1
13	AM	7	ASN	3.1
38	BF	80	GLN	3.1
42	BL	9	GLU	3.1
19	AS	12	LEU	3.1
48	BS	88	LYS	3.1
48	BS	100	HIS	3.1
38	BF	73	VAL	3.1
38	BF	163	GLU	3.1
38	BF	112	ASP	3.1
40	BH	96	PHE	3.1
38	BF	165	GLY	3.1
33	BA	2585	U	3.1
41	BI	48	ILE	3.1
46	BQ	68	PHE	3.1
4	AD	172	VAL	3.1
10	AJ	74	VAL	3.1
1	AA	205	A	3.1
33	BA	1725	U	3.0
48	BS	37	ALA	3.0
48	BS	90	VAL	3.0
16	AP	50	THR	3.0
18	AR	20	ILE	3.0
21	AU	39	LYS	3.0
48	BS	63	LYS	3.0
16	AP	39	PHE	3.0
23	AW	481	LYS	3.0
5	AE	86	GLY	3.0
46	BQ	4	PRO	3.0
16	AP	73	ALA	3.0
33	BA	363	G	3.0
38	BF	15	LEU	3.0
16	AP	8	ARG	3.0
42	BJ	29	LYS	3.0
40	BH	129	LEU	3.0
23	AW	433	ASN	3.0
7	AG	73	GLU	3.0
2	AB	64	GLY	3.0
18	AR	54	LEU	3.0
33	BA	1723	G	3.0
54	BY	31	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
16	AP	21	VAL	3.0
7	AG	70	PRO	3.0
29	B5	26	LYS	3.0
24	B0	84	GLU	3.0
1	AA	972	C	3.0
1	AA	1043	G	3.0
15	AO	62	ARG	3.0
23	AW	504	ILE	3.0
19	AS	4	LEU	3.0
2	AB	151	LYS	3.0
7	AG	1	PRO	3.0
23	AW	406	PRO	3.0
53	BX	92	ASN	3.0
40	BH	24	SER	3.0
48	BS	116	GLN	3.0
2	AB	206	ILE	3.0
7	AG	90	VAL	3.0
42	BM	11	VAL	3.0
16	AP	1	MET	3.0
39	BG	94	ARG	3.0
41	BI	22	PRO	3.0
8	AH	2	MET	3.0
2	AB	142	LYS	3.0
33	BA	277	G	3.0
23	AW	498	GLY	3.0
31	B7	47	ALA	3.0
13	AM	40	GLU	3.0
38	BF	76	PHE	3.0
18	AR	41	SER	2.9
1	AA	1030	U	2.9
10	AJ	99	GLN	2.9
16	AP	65	ALA	2.9
33	BA	1174	U	2.9
23	AW	500	ASN	2.9
8	AH	120	LEU	2.9
9	AI	31	GLN	2.9
13	AM	10	ASP	2.9
19	AS	64	GLU	2.9
29	B5	35	LEU	2.9
10	AJ	102	LEU	2.9
3	AC	129	PHE	2.9
8	AH	53	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
33	BA	846	U	2.9
7	AG	123	LEU	2.9
48	BS	25	ARG	2.9
20	AT	52	GLU	2.9
25	B1	46	VAL	2.9
9	AI	27	ILE	2.9
16	AP	60	TRP	2.9
12	AL	24	GLU	2.9
33	BA	2188	U	2.9
48	BS	58	ILE	2.9
23	AW	435	ASP	2.9
42	BM	13	ALA	2.9
4	AD	159	GLU	2.9
48	BS	80	GLU	2.9
13	AM	41	ASP	2.9
8	AH	51	GLU	2.9
46	BQ	5	LYS	2.9
20	AT	66	ILE	2.9
48	BS	39	VAL	2.9
14	AN	59	GLN	2.9
21	AU	6	ARG	2.9
40	BH	56	ARG	2.9
17	AQ	46	HIS	2.9
9	AI	86	LEU	2.9
10	AJ	63	ASP	2.9
33	BA	2155	U	2.9
13	AM	93	GLY	2.8
23	AW	469	ALA	2.9
9	AI	50	PRO	2.8
54	BY	4	ILE	2.8
7	AG	72	VAL	2.8
16	AP	2	VAL	2.8
33	BA	1625	C	2.8
7	AG	149	ALA	2.8
41	BI	93	ASN	2.8
42	BM	5	ASP	2.8
18	AR	47	ARG	2.8
26	B2	16	THR	2.8
40	BH	140	MET	2.8
13	AM	82	LEU	2.8
9	AI	28	VAL	2.8
4	AD	28	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
23	AW	339	ASP	2.8
13	AM	34	ALA	2.8
38	BF	72	SER	2.8
29	B5	50	GLU	2.8
41	BI	122	GLU	2.8
29	B5	47	ILE	2.8
33	BA	1090	A	2.8
10	AJ	50	THR	2.8
38	BF	158	THR	2.8
1	AA	1214	C	2.8
43	BN	74	TYR	2.8
33	BA	547	A	2.8
33	BA	914	G	2.8
48	BS	117	PHE	2.8
29	B5	46	VAL	2.8
52	BW	110	ARG	2.8
39	BG	48	THR	2.8
19	AS	60	PHE	2.8
33	BA	1172	C	2.8
42	BJ	6	GLN	2.8
40	BH	94	ARG	2.8
1	AA	4	U	2.8
2	AB	191	ASP	2.8
23	AW	405	ASP	2.8
9	AI	88	GLU	2.8
40	BH	163	GLU	2.8
53	BX	70	HIS	2.8
13	AM	110	GLY	2.8
29	B5	25	ASN	2.8
1	AA	1044	A	2.8
16	AP	24	SER	2.8
36	BD	209	ALA	2.8
2	AB	110	ILE	2.8
19	AS	65	MET	2.8
14	AN	2	LYS	2.8
17	AQ	15	LYS	2.8
24	B0	8	SER	2.8
2	AB	212	TYR	2.8
9	AI	30	ASN	2.8
38	BF	117	SER	2.8
42	BM	2	ILE	2.8
48	BS	7	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
53	BX	69	ARG	2.8
16	AP	6	LEU	2.8
16	AP	74	LEU	2.8
23	AW	506	THR	2.8
4	AD	162	GLU	2.7
1	AA	1138	G	2.7
1	AA	1309	G	2.7
16	AP	7	ALA	2.7
40	BH	59	LEU	2.7
38	BF	174	PHE	2.7
40	BH	76	PHE	2.7
33	BA	1073	A	2.7
38	BF	82	TYR	2.7
2	AB	216	VAL	2.7
7	AG	78	ARG	2.7
14	AN	58	ARG	2.7
19	AS	59	VAL	2.7
23	AW	53	GLN	2.7
40	BH	2	ALA	2.7
41	BI	123	ALA	2.7
3	AC	191	THR	2.7
53	BX	1	MET	2.7
1	AA	1317	C	2.7
17	AQ	60	ILE	2.7
23	AW	429	ARG	2.7
13	AM	32	ILE	2.7
38	BF	164	GLU	2.7
48	BS	97	PHE	2.7
29	B5	13	SER	2.7
19	AS	36	ARG	2.7
38	BF	118	ALA	2.7
19	AS	20	LYS	2.7
23	AW	463	TYR	2.7
3	AC	156	LEU	2.7
23	AW	409	GLN	2.7
1	AA	1492	A	2.7
1	AA	989	U	2.7
16	AP	34	GLU	2.7
27	B3	19	HIS	2.7
40	BH	155	LEU	2.7
19	AS	45	GLY	2.7
19	AS	15	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
8	AH	93	LYS	2.7
16	AP	38	PHE	2.7
40	BH	69	PHE	2.7
53	BX	3	ARG	2.7
8	AH	102	VAL	2.7
33	BA	2151	U	2.7
40	BH	131	THR	2.7
7	AG	45	ALA	2.7
2	AB	189	ASN	2.7
19	AS	52	ASN	2.7
38	BF	29	ARG	2.6
16	AP	18	GLN	2.6
3	AC	196	GLY	2.6
13	AM	61	LYS	2.6
1	AA	151	A	2.6
16	AP	17	TYR	2.6
2	AB	52	ALA	2.6
40	BH	148	ALA	2.6
23	AW	499	ASP	2.6
14	AN	11	LYS	2.6
14	AN	18	LYS	2.6
33	BA	2104	C	2.6
7	AG	7	GLY	2.6
10	AJ	12	ALA	2.6
3	AC	82	ASP	2.6
15	AO	1	SER	2.6
1	AA	1020	G	2.6
7	AG	3	ARG	2.6
53	BX	2	ILE	2.6
9	AI	22	PRO	2.6
12	AL	12	ALA	2.6
1	AA	1167	A	2.6
48	BS	78	VAL	2.6
33	BA	102	U	2.6
3	AC	186	SER	2.6
16	AP	35	ARG	2.6
50	BU	88	GLU	2.6
10	AJ	90	LEU	2.6
9	AI	57	VAL	2.6
33	BA	279	A	2.6
24	B0	49	ASN	2.6
41	BI	135	MET	2.6

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Mol	Chain	Res	Type	RSRZ
33	BA	1066	U	2.6
9	AI	15	ALA	2.6
9	AI	66	VAL	2.6
52	BW	73	LYS	2.6
19	AS	19	GLU	2.6
23	AW	399	ARG	2.6
53	BX	4	GLU	2.6
44	BO	8	LEU	2.6
19	AS	17	LYS	2.6
19	AS	72	GLU	2.6
12	AL	14	LYS	2.6
12	AL	15	VAL	2.6
14	AN	46	LYS	2.6
23	AW	326	GLU	2.6
38	BF	172	PHE	2.6
33	BA	1847	A	2.6
48	BS	51	ALA	2.6
54	BY	2	ALA	2.6
18	AR	21	ASP	2.6
13	AM	6	ILE	2.6
41	BI	107	GLU	2.6
42	BK	26	MET	2.6
48	BS	74	VAL	2.6
14	AN	12	ARG	2.5
33	BA	1075	C	2.5
33	BA	1076	C	2.5
3	AC	52	SER	2.5
8	AH	9	MET	2.5
23	AW	52	ASN	2.5
41	BI	57	VAL	2.5
20	AT	3	ILE	2.5
25	B1	76	LYS	2.5
41	BI	89	SER	2.5
48	BS	38	GLN	2.5
3	AC	20	THR	2.5
42	BK	20	VAL	2.5
8	AH	3	GLN	2.5
40	BH	82	ILE	2.5
2	AB	117	GLU	2.5
25	B1	66	VAL	2.5
55	BZ	41	GLU	2.5
23	AW	465	SER	2.5

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Mol	Chain	Res	Type	RSRZ
5	AE	17	VAL	2.5
4	AD	108	ALA	2.5
24	B0	51	GLY	2.5
38	BF	69	ALA	2.5
16	AP	57	ILE	2.5
17	AQ	54	ILE	2.5
7	AG	62	GLU	2.5
4	AD	106	PHE	2.5
19	AS	43	MET	2.5
42	BM	4	LYS	2.5
55	BZ	34	LYS	2.5
33	BA	2183	A	2.5
48	BS	70	ALA	2.5
41	BI	138	VAL	2.5
3	AC	131	ARG	2.5
33	BA	1734	G	2.5
48	BS	2	ASP	2.5
54	BY	80	ASP	2.5
39	BG	7	PRO	2.5
1	AA	1248	A	2.5
12	AL	69	GLU	2.5
33	BA	504	A	2.5
47	BR	28	LEU	2.5
42	BK	27	GLU	2.5
9	AI	62	LEU	2.5
8	AH	74	ILE	2.5
23	AW	342	ILE	2.5
48	BS	27	VAL	2.5
33	BA	2143	C	2.5
21	AU	50	SER	2.5
54	BY	3	LYS	2.5
45	BP	114	GLY	2.5
33	BA	1737	G	2.5
15	AO	41	HIS	2.5
37	BE	134	LEU	2.5
8	AH	49	LYS	2.5
13	AM	100	ARG	2.5
27	B3	4	ILE	2.5
41	BI	82	ALA	2.5
2	AB	56	LEU	2.4
2	AB	188	THR	2.4
9	AI	34	LEU	2.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
33	BA	899	A	2.4
39	BG	40	VAL	2.4
40	BH	7	ASP	2.4
38	BF	129	MET	2.4
48	BS	53	THR	2.4
13	AM	91	ARG	2.4
25	B1	34	SER	2.4
40	BH	156	ALA	2.4
38	BF	99	PHE	2.4
8	AH	128	VAL	2.4
1	AA	1011	C	2.4
4	AD	180	THR	2.4
38	BF	42	ALA	2.4
23	AW	495	LEU	2.4
19	AS	68	HIS	2.4
12	AL	50	LYS	2.4
26	B2	5	GLU	2.4
1	AA	207	C	2.4
37	BE	201	ALA	2.4
13	AM	30	LYS	2.4
21	AU	15	LEU	2.4
23	AW	455	SER	2.4
10	AJ	47	GLU	2.4
3	AC	148	ILE	2.4
33	BA	365	U	2.4
37	BE	9	GLN	2.4
42	BL	25	ALA	2.4
17	AQ	17	GLU	2.4
26	B2	1	MET	2.4
2	AB	18	GLN	2.4
2	AB	113	LEU	2.4
32	B8	24	ARG	2.4
33	BA	1848	A	2.4
37	BE	6	LYS	2.4
42	BL	29	LYS	2.4
2	AB	198	VAL	2.4
48	BS	28	VAL	2.4
53	BX	82	LYS	2.4
19	AS	80	ARG	2.4
23	AW	436	LEU	2.4
24	B0	40	ARG	2.4
54	BY	70	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
33	BA	1744	A	2.4
33	BA	1914	C	2.4
33	BA	2211	A	2.4
9	AI	7	GLY	2.4
4	AD	42	ALA	2.4
33	BA	2187	U	2.4
3	AC	161	ILE	2.4
7	AG	16	LYS	2.4
55	BZ	68	LYS	2.4
2	AB	14	HIS	2.4
4	AD	18	LEU	2.4
7	AG	146	ALA	2.4
54	BY	12	VAL	2.4
1	AA	206	C	2.4
23	AW	327	LYS	2.4
29	B5	3	GLY	2.3
7	AG	106	ALA	2.3
40	BH	141	ALA	2.3
45	BP	113	ALA	2.3
33	BA	1091	G	2.3
39	BG	18	ILE	2.3
52	BW	104	THR	2.3
2	AB	134	LEU	2.3
2	AB	199	ILE	2.3
42	BK	23	ILE	2.3
2	AB	69	VAL	2.3
17	AQ	73	THR	2.3
38	BF	96	TRP	2.3
2	AB	31	PHE	2.3
2	AB	145	ASN	2.3
41	BI	3	LYS	2.3
48	BS	34	HIS	2.3
9	AI	32	ARG	2.3
39	BG	176	LYS	2.3
2	AB	201	GLY	2.3
6	AF	21	MET	2.3
23	AW	423	GLY	2.3
38	BF	156	THR	2.3
48	BS	69	ASP	2.3
33	BA	1057	A	2.3
29	B5	10	LEU	2.3
13	AM	95	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
13	AM	86	ARG	2.3
17	AQ	64	ARG	2.3
37	BE	119	ILE	2.3
21	AU	43	GLU	2.3
1	AA	843	U	2.3
24	B0	83	ALA	2.3
1	AA	68	G	2.3
42	BM	6	GLN	2.3
39	BG	129	GLU	2.3
42	BL	14	MET	2.3
41	BI	106	GLN	2.3
33	BA	895	U	2.3
33	BA	2181	U	2.3
33	BA	142	A	2.3
33	BA	715	A	2.3
45	BP	75	ALA	2.3
18	AR	43	ILE	2.3
42	BK	24	SER	2.3
39	BG	147	LEU	2.3
23	AW	298	GLY	2.3
2	AB	130	LYS	2.3
8	AH	127	TYR	2.3
1	AA	988	G	2.3
2	AB	67	LEU	2.3
2	AB	116	LEU	2.3
3	AC	51	VAL	2.3
45	BP	125	LEU	2.3
48	BS	36	TYR	2.3
2	AB	149	GLY	2.3
10	AJ	31	ARG	2.3
6	AF	1	MET	2.3
39	BG	173	ALA	2.3
42	BJ	17	MET	2.3
2	AB	127	LYS	2.3
23	AW	324	LYS	2.3
5	AE	101	GLY	2.3
7	AG	33	GLY	2.3
19	AS	7	GLY	2.3
40	BH	90	GLY	2.3
7	AG	148	LYS	2.3
54	BY	71	ILE	2.3
8	AH	103	VAL	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	AA	1009	U	2.2
33	BA	141	G	2.2
33	BA	1733	G	2.2
38	BF	97	GLU	2.2
14	AN	1	ALA	2.2
16	AP	5	ARG	2.2
24	B0	82	GLU	2.2
2	AB	153	MET	2.2
13	AM	111	PRO	2.2
2	AB	13	VAL	2.2
6	AF	7	VAL	2.2
7	AG	68	VAL	2.2
32	B8	25	VAL	2.2
1	AA	842	U	2.2
33	BA	2189	U	2.2
2	AB	136	ARG	2.2
54	BY	93	ARG	2.2
40	BH	34	THR	2.2
3	AC	150	VAL	2.2
16	AP	33	ILE	2.2
33	BA	2182	U	2.2
41	BI	104	GLN	2.2
48	BS	48	LEU	2.2
41	BI	127	SER	2.2
51	BV	46	GLU	2.2
54	BY	25	LYS	2.2
10	AJ	10	LEU	2.2
23	AW	3	LEU	2.2
33	BA	1089	A	2.2
39	BG	132	LEU	2.2
2	AB	73	ARG	2.2
9	AI	63	TYR	2.2
13	AM	113	LYS	2.2
28	B4	56	LYS	2.2
33	BA	2903	U	2.2
7	AG	21	LEU	2.2
9	AI	29	ILE	2.2
43	BN	73	VAL	2.2
55	BZ	40	ILE	2.2
45	BP	119	PRO	2.2
33	BA	2152	G	2.2
11	AK	15	VAL	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
48	BS	15	ARG	2.2
2	AB	12	GLY	2.2
23	AW	513	LEU	2.2
2	AB	20	ARG	2.2
2	AB	121	GLN	2.2
33	BA	549	G	2.2
8	AH	125	ILE	2.2
48	BS	83	LEU	2.2
21	AU	48	LYS	2.2
53	BX	68	LYS	2.2
14	AN	94	GLY	2.2
2	AB	21	TYR	2.2
10	AJ	92	LEU	2.2
15	AO	86	LEU	2.2
16	AP	48	GLU	2.2
33	BA	2145	C	2.2
4	AD	150	LYS	2.2
30	B6	46	LYS	2.2
9	AI	125	GLN	2.2
46	BQ	60	GLN	2.2
7	AG	13	PRO	2.2
12	AL	4	ASN	2.2
13	AM	97	ARG	2.2
15	AO	42	PHE	2.2
18	AR	46	THR	2.2
38	BF	166	ARG	2.2
8	AH	28	SER	2.2
23	AW	491	SER	2.2
33	BA	1743	G	2.2
39	BG	115	GLN	2.2
27	B3	5	LYS	2.2
43	BN	90	GLU	2.2
31	B7	23	HIS	2.2
37	BE	188	MET	2.2
24	B0	50	VAL	2.2
33	BA	2602	A	2.2
10	AJ	66	GLU	2.2
14	AN	51	PRO	2.2
45	BP	88	GLY	2.2
54	BY	11	ILE	2.2
3	AC	188	ALA	2.2
33	BA	366	C	2.2

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Mol	Chain	Res	Type	RSRZ
43	BN	19	ASP	2.2
3	AC	110	LEU	2.2
17	AQ	22	VAL	2.2
29	B5	11	VAL	2.2
37	BE	138	LEU	2.2
17	AQ	4	ILE	2.2
18	AR	25	ILE	2.2
17	AQ	53	GLY	2.1
33	BA	546	U	2.2
33	BA	2185	U	2.2
37	BE	4	VAL	2.1
45	BP	89	VAL	2.1
51	BV	33	VAL	2.1
39	BG	23	ILE	2.1
2	AB	187	ASP	2.1
11	AK	26	PHE	2.1
42	BL	5	ASP	2.1
1	AA	1022	A	2.1
7	AG	140	VAL	2.1
14	AN	31	SER	2.1
21	AU	7	GLU	2.1
5	AE	13	LYS	2.1
11	AK	125	LYS	2.1
45	BP	107	PHE	2.1
1	AA	152	A	2.1
1	AA	1019	A	2.1
16	AP	69	ASP	2.1
45	BP	140	GLY	2.1
54	BY	46	LYS	2.1
2	AB	107	ARG	2.1
8	AH	44	PHE	2.1
41	BI	7	TYR	2.1
45	BP	135	ILE	2.1
2	AB	44	LYS	2.1
9	AI	122	ARG	2.1
10	AJ	101	SER	2.1
40	BH	66	GLY	2.1
37	BE	7	ASP	2.1
33	BA	1913	A	2.1
2	AB	144	GLU	2.1
48	BS	112	GLU	2.1
2	AB	213	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
4	AD	16	THR	2.1
24	B0	76	ARG	2.1
15	AO	19	ASN	2.1
13	AM	16	ILE	2.1
38	BF	175	PRO	2.1
7	AG	46	LEU	2.1
7	AG	52	ARG	2.1
7	AG	131	GLY	2.1
7	AG	150	PHE	2.1
23	AW	5	PRO	2.1
46	BQ	69	PRO	2.1
53	BX	72	GLN	2.1
17	AQ	3	LYS	2.1
12	AL	70	GLY	2.1
40	BH	11	ILE	2.1
44	BO	51	LYS	2.1
48	BS	52	SER	2.1
48	BS	87	ILE	2.1
15	AO	21	THR	2.1
19	AS	63	ASP	2.1
39	BG	59	ASP	2.1
2	AB	30	ILE	2.1
29	B5	44	GLN	2.1
35	BC	74	PRO	2.1
2	AB	99	MET	2.1
13	AM	17	ALA	2.1
3	AC	167	TYR	2.1
9	AI	36	GLN	2.1
9	AI	33	SER	2.1
23	AW	472	ARG	2.1
6	AF	57	ALA	2.1
9	AI	61	ASP	2.1
10	AJ	75	ASP	2.1
55	BZ	62	THR	2.1
33	BA	1583	A	2.1
44	BO	7	MET	2.1
40	BH	122	GLN	2.1
17	AQ	51	GLU	2.1
19	AS	5	LYS	2.1
19	AS	11	ASP	2.1
40	BH	101	LYS	2.1
20	AT	82	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
46	BQ	17	ASN	2.1
42	BJ	16	VAL	2.1
42	BL	30	PHE	2.1
10	AJ	9	ARG	2.0
13	AM	53	ASP	2.0
41	BI	117	THR	2.0
7	AG	74	VAL	2.0
2	AB	55	GLU	2.0
12	AL	23	LEU	2.0
17	AQ	43	LEU	2.0
25	B1	6	VAL	2.0
36	BD	19	GLY	2.0
39	BG	172	GLU	2.0
5	AE	95	MET	2.0
6	AF	4	TYR	2.0
2	AB	114	LYS	2.0
40	BH	6	GLN	2.0
2	AB	200	PRO	2.0
12	AL	66	ILE	2.0
46	BQ	53	MET	2.0
13	AM	64	VAL	2.0
23	AW	190	THR	2.0
39	BG	35	THR	2.0
24	B0	18	LYS	2.0
49	BT	26	GLU	2.0
16	AP	58	ALA	2.0
23	AW	401	ILE	2.0
7	AG	124	SER	2.0
53	BX	24	MET	2.0
8	AH	90	GLU	2.0
24	B0	7	GLY	2.0
1	AA	188	C	2.0
1	AA	877	G	2.0
48	BS	46	GLU	2.0
32	B8	29	ALA	2.0
33	BA	163	C	2.0
41	BI	113	ALA	2.0
44	BO	9	ASN	2.0
17	AQ	80	LYS	2.0
47	BR	119	SER	2.0
49	BT	111	GLU	2.0
55	BZ	1	MET	2.0

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Mol	Chain	Res	Type	RSRZ
11	AK	13	LYS	2.0
39	BG	88	LEU	2.0
38	BF	127	TYR	2.0
2	AB	70	GLY	2.0
48	BS	33	ARG	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

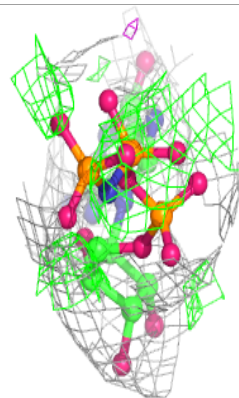
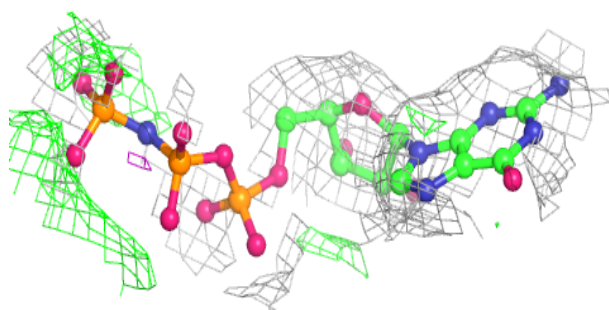
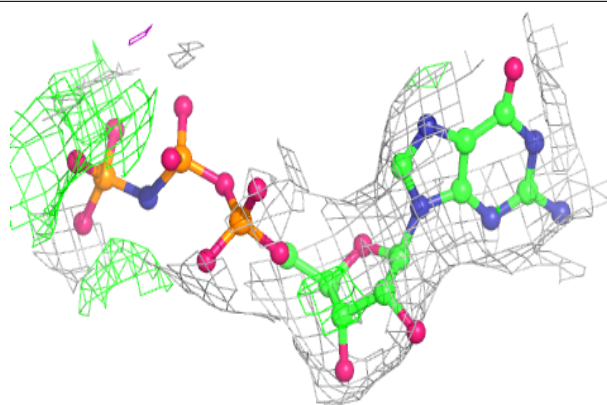
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	AW	602	1/1	0.76	0.20	36,36,36,36	0
56	GNP	AW	601	32/32	0.92	0.21	81,97,115,121	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around GNP AW 601:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.