



Full wwPDB X-ray Structure Validation Report

Jun 16, 2014 – 06:31 PM BST

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 validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

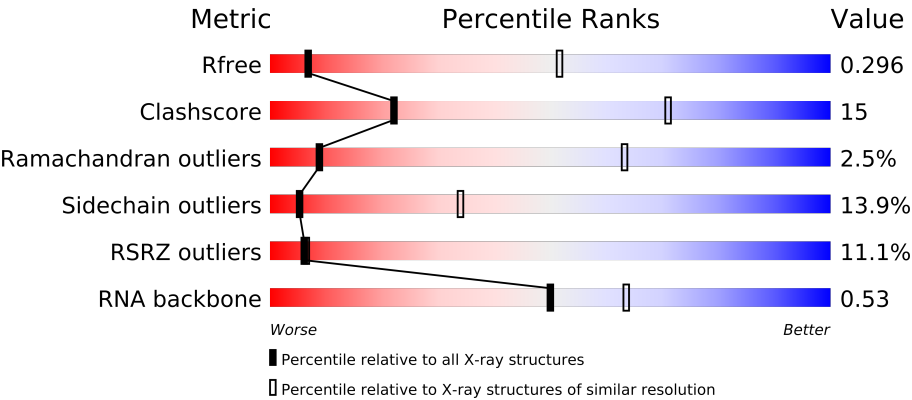
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1323
EDS : stable23397
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23397

1 Overall quality at a glance

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_{free}	66092	1098 (4.00-3.40)
Clashscore	79885	1009 (3.94-3.46)
Ramachandran outliers	78287	1016 (3.98-3.42)
Sidechain outliers	78261	1014 (3.98-3.42)
RSRZ outliers	66119	1099 (4.00-3.40)
RNA backbone	1838	1008 (4.52-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	AA	1533	
2	AB	241	
3	AC	233	
4	AD	206	
5	AE	167	
6	AF	135	
7	AG	179	
8	AH	130	
9	AI	130	
10	AJ	103	
11	AK	129	
12	AL	124	


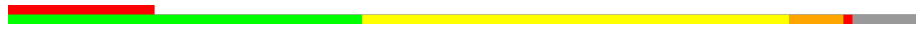


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Mol	Chain	Length	Quality of chain
13	AM	118	
14	AN	101	
15	AO	89	
16	AP	82	
17	AQ	84	
18	AR	75	
19	AS	92	
20	AT	87	
21	AU	71	
22	AV	27	
23	AW	534	
24	B0	85	
25	B1	78	
26	B2	63	
27	B3	59	
28	B4	57	
29	B5	55	
30	B6	46	
31	B7	65	
32	B8	38	
33	BA	2903	
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	
53	BX	100	
54	BY	104	
55	BZ	94	

2 Entry composition

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

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			

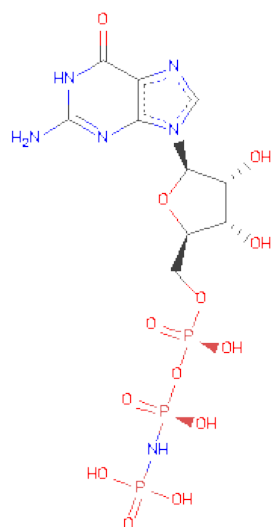
- Molecule 54 is a protein called 50S ribosomal protein L24.

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 PHOSPHOAMINOPHOSPHONICACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
56	AW	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

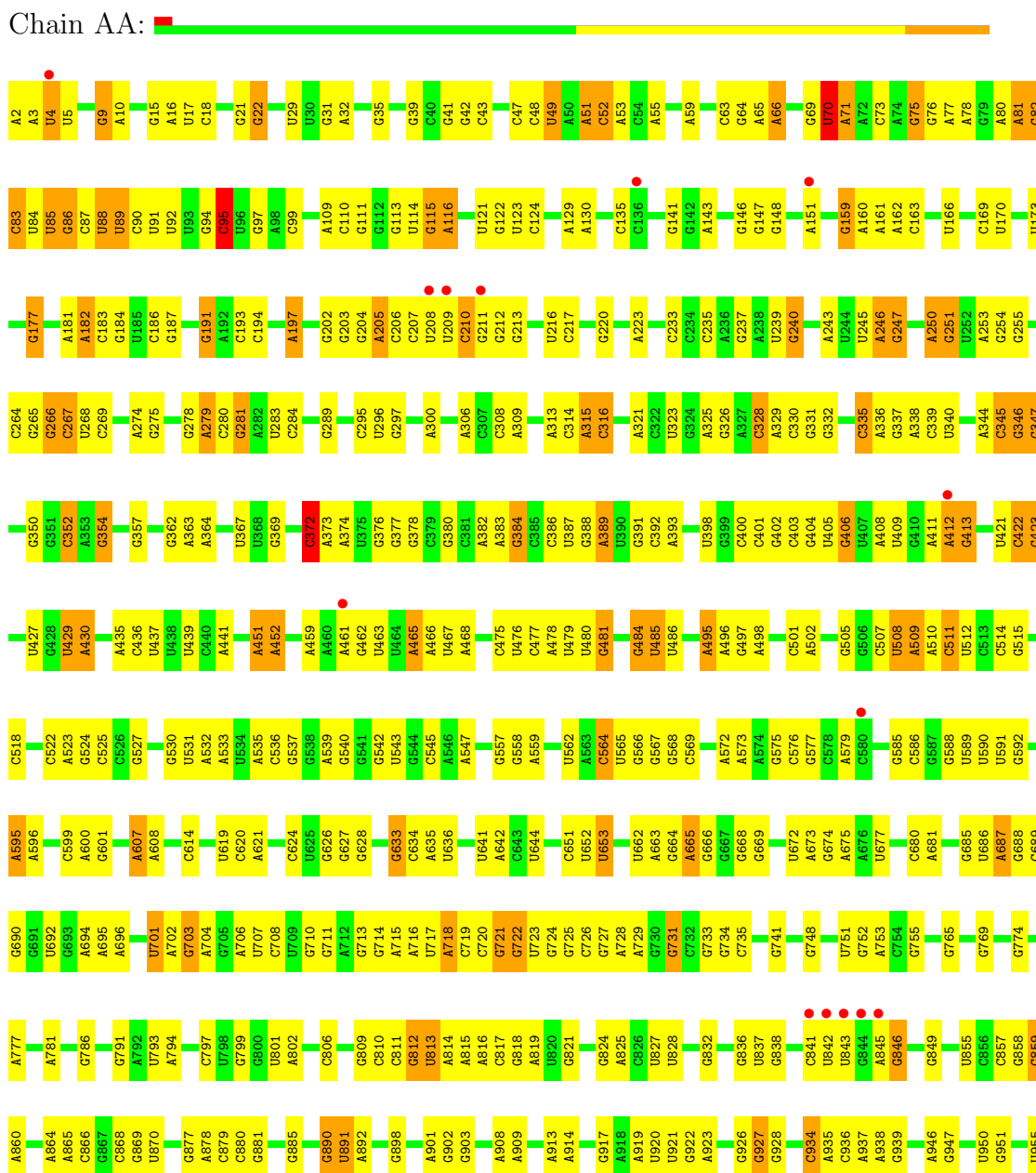
- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

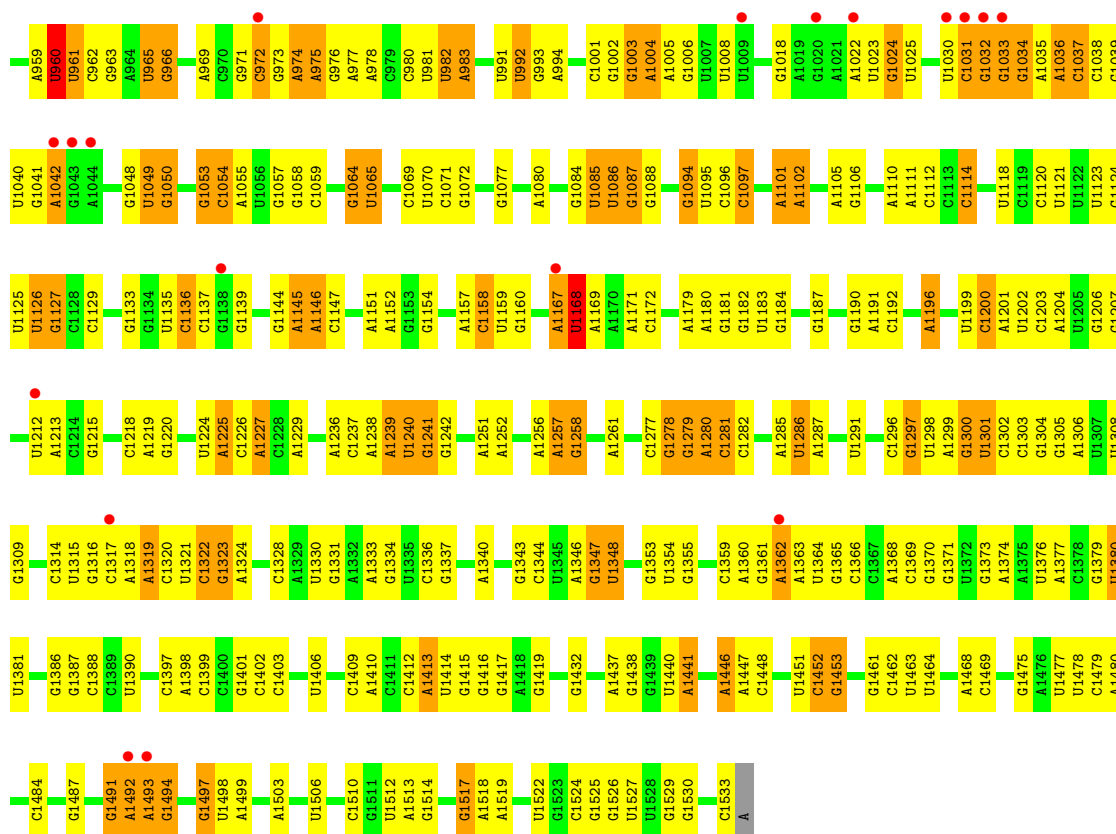
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AW	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

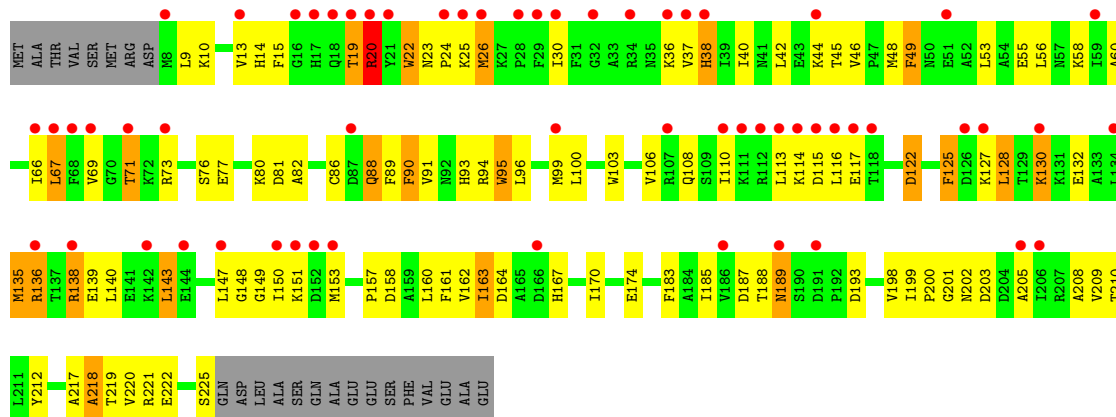
• Molecule 1: 16S rRNA





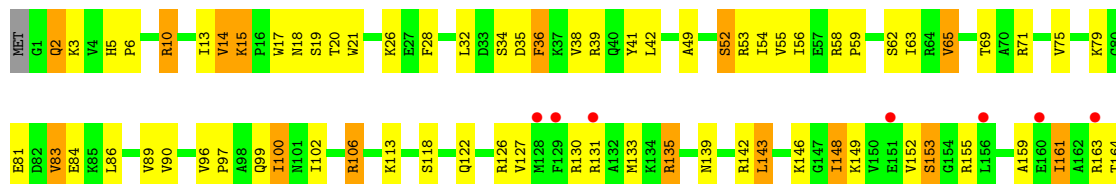
• Molecule 2: 30S ribosomal protein S2

Chain AB:



• Molecule 3: 30S ribosomal protein S3

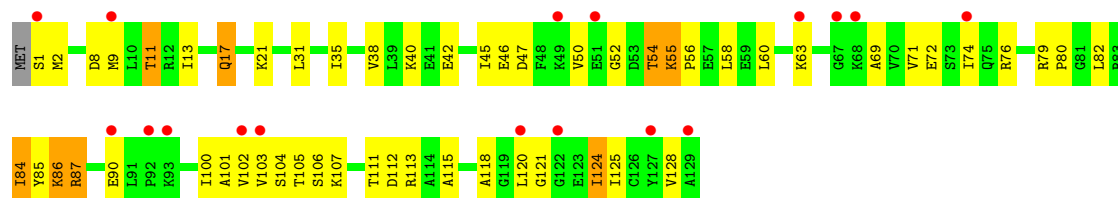
Chain AC:



HIS
TYR
ARG
TRP
LEU
SER
LEU
ARG
SER
PHE
SER
HIS
GLN
ALA
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LYS
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PRO
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LEU
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TYR
LEU
ASN

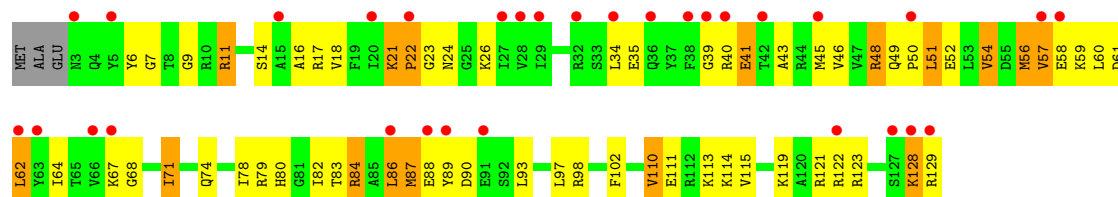
• Molecule 8: 30S ribosomal protein S8

Chain AH:



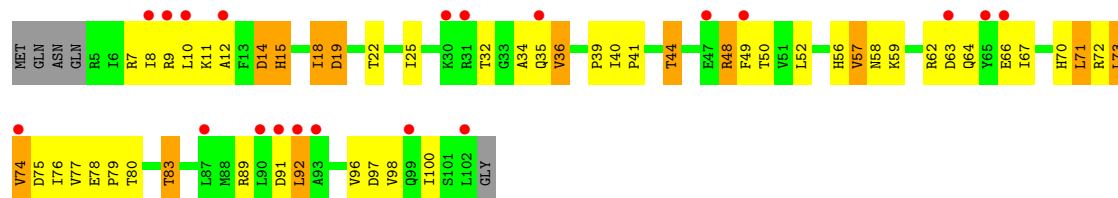
• Molecule 9: 30S ribosomal protein S9

Chain AI:



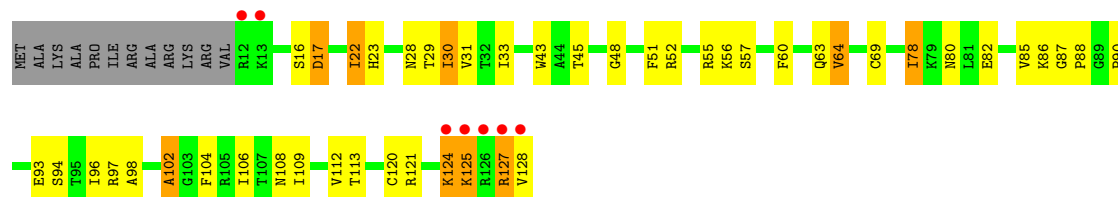
• Molecule 10: 30S ribosomal protein S10

Chain AJ:



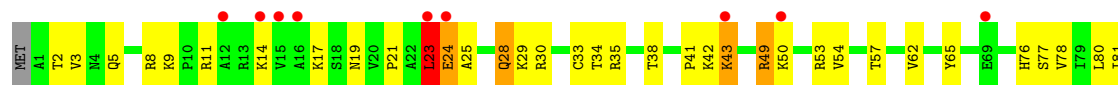
• Molecule 11: 30S ribosomal protein S11

Chain AK:



• Molecule 12: 30S ribosomal protein S12

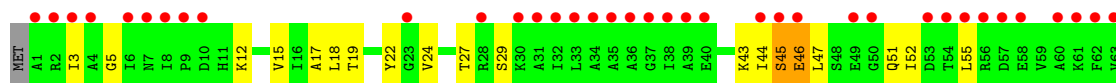
Chain AL:





- Molecule 13: 30S ribosomal protein S13

Chain AM:



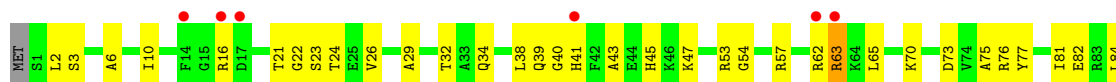
- Molecule 14: 30S ribosomal protein S14

Chain AN:



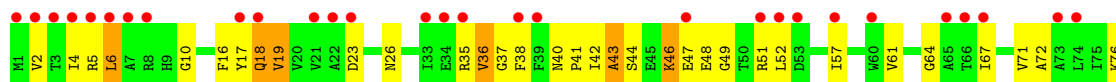
- Molecule 15: 30S ribosomal protein S15

Chain AO:



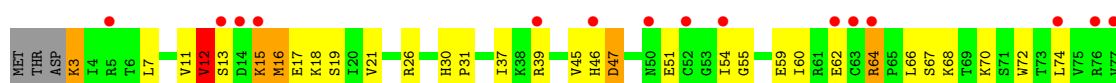
- Molecule 16: 30S ribosomal protein S16

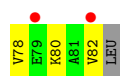
Chain AP:



- Molecule 17: 30S ribosomal protein S17

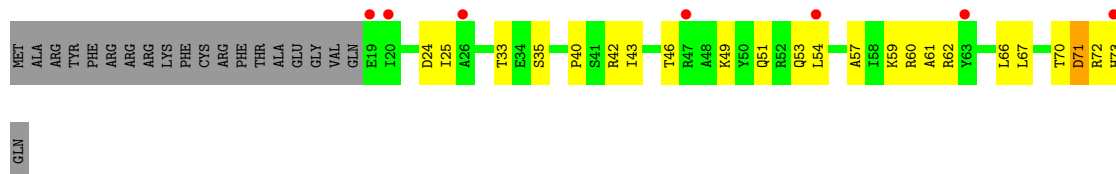
Chain AQ:





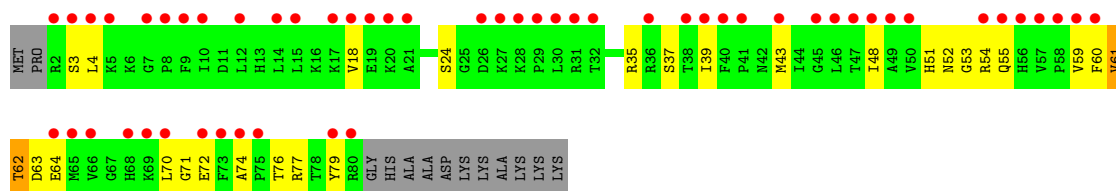
- Molecule 18: 30S ribosomal protein S18

Chain AR:



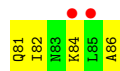
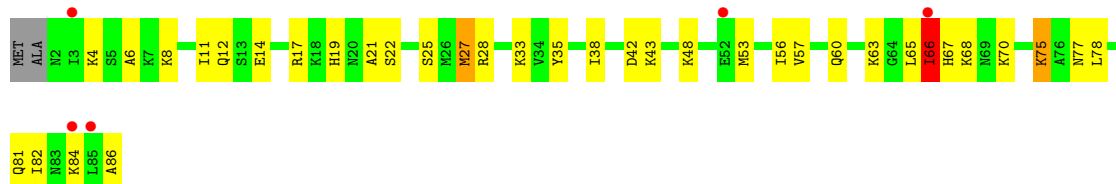
- Molecule 19: 30S ribosomal protein S19

Chain AS:



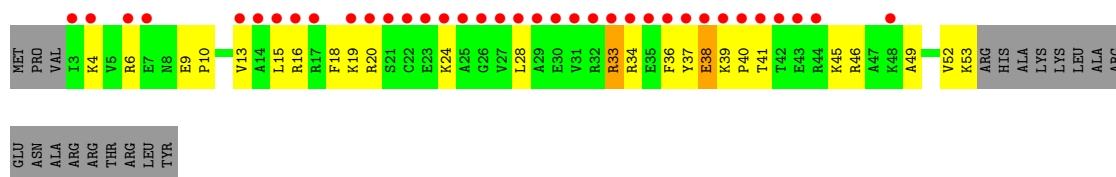
- Molecule 20: 30S ribosomal protein S20

Chain AT:



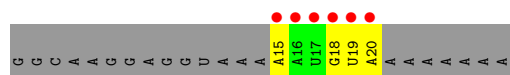
- Molecule 21: 30S ribosomal protein S21

Chain AU:



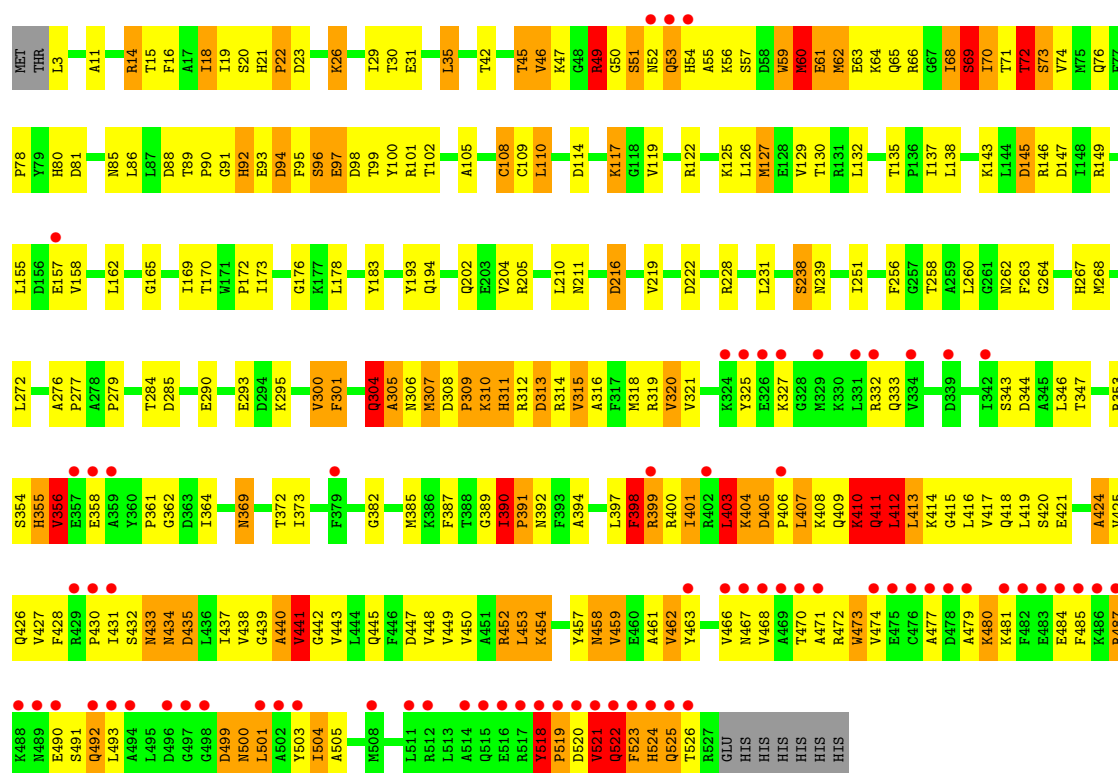
- Molecule 22: messenger RNA

Chain AV:



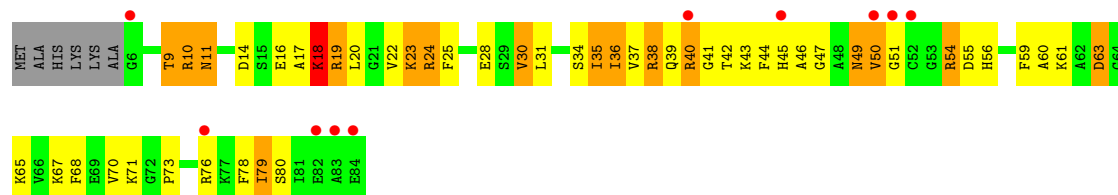
- Molecule 23: Peptide chain release factor 3

Chain AW:



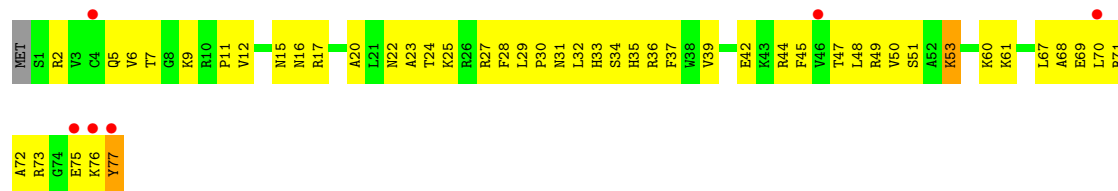
• Molecule 24: 50S ribosomal protein L27

Chain B0:



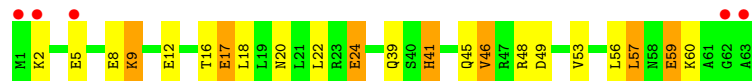
• Molecule 25: 50S ribosomal protein L28

Chain B1:



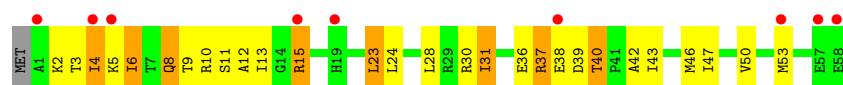
• Molecule 26: 50S ribosomal protein L29

Chain B2:



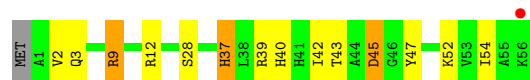
• Molecule 27: 50S ribosomal protein L30

Chain B3: 



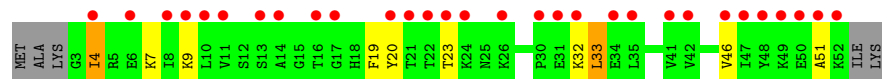
- Molecule 28: 50S ribosomal protein L32

Chain B4: 



- Molecule 29: 50S ribosomal protein L33

Chain B5: 



- Molecule 30: 50S ribosomal protein L34

Chain B6: 



- Molecule 31: 50S ribosomal protein L35

Chain B7: 



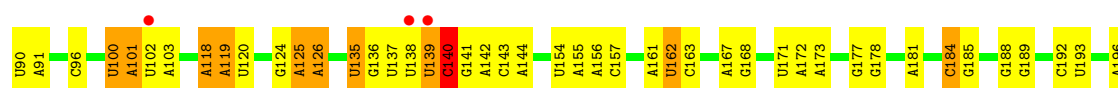
- Molecule 32: 50S ribosomal protein L36

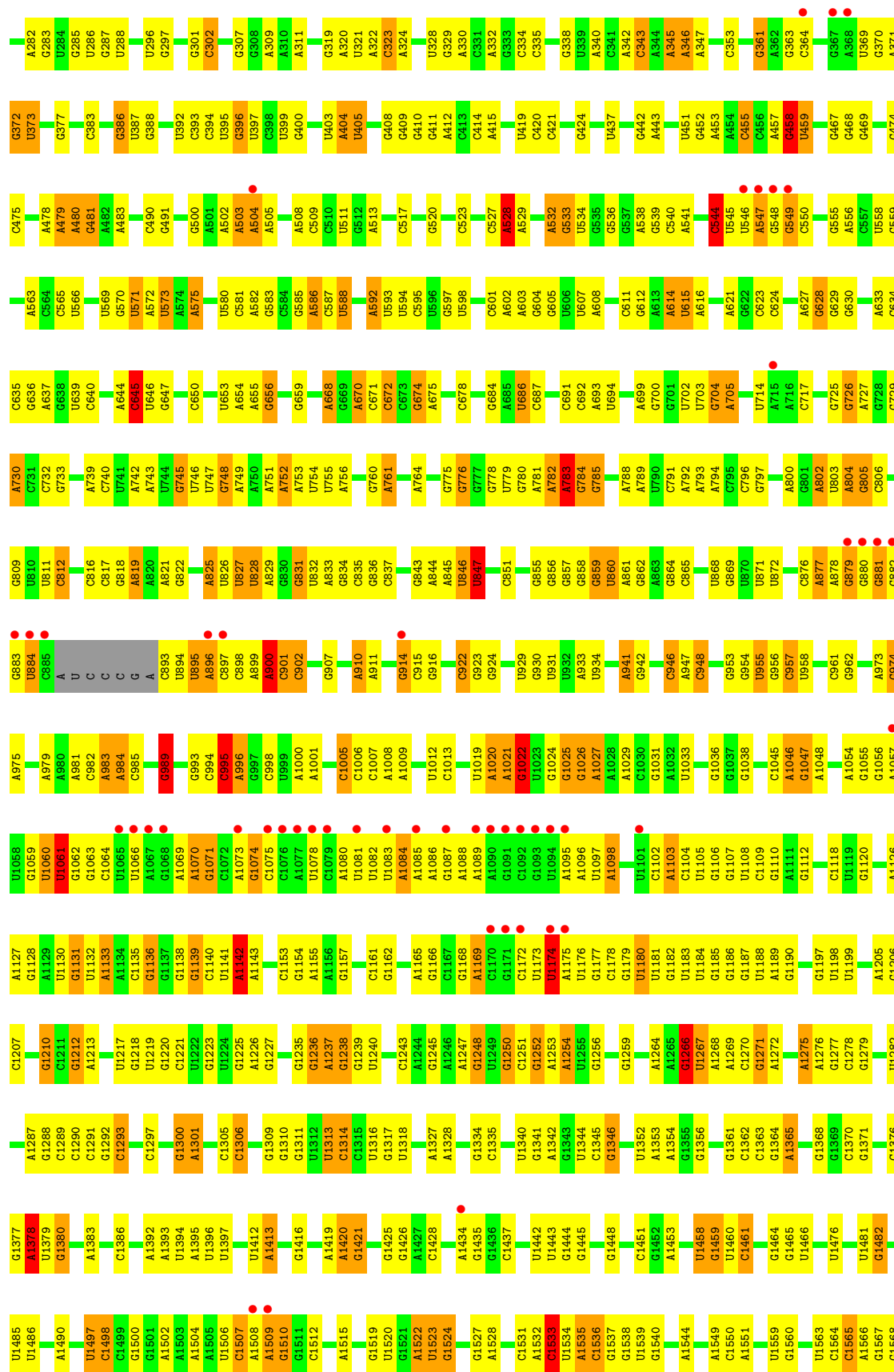
Chain B8: 



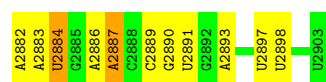
- Molecule 33: 23S rRNA

Chain BA: 



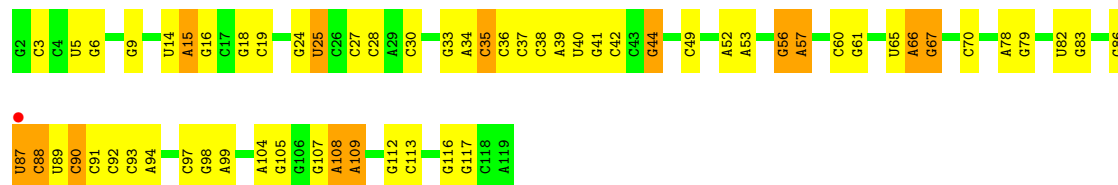


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U2698	C2704	C2708	C2714	C2719	U2720	A2721	C2722	C2723	A2726	A2727	U2728	C2729	C2730	A2733	C2734	C2735	A2736	C2737	A2740	C2741	C2742	U2743	C2744	C2747	A2748	C2755	U2756	A2757	U2758	C2759	C2762	A2765	A2766	U2769	A2778	U2784	C2785	U2786	C2787	C2788	C2789	U2790	C2791	U2792	C2793	C2794	C2795	C2796	C2797	C2798	C2799	C2800	C2801	C2802	C2803	C2804	C2805	C2806	C2807	C2808	C2809	C2810	C2811	C2812	C2813	C2814	C2815	C2816	C2817	C2818	C2819	C2820	C2821	C2822	C2823	C2824	C2825	C2826	C2827	C2828	C2829	C2830	C2831	C2832	C2833	C2834	C2835	C2836	C2837	C2838	C2839	C2840	C2841	C2842	C2843	C2844	C2845	C2846	C2847	C2848	C2849	C2850	C2851	C2852	C2853	C2854	C2855	C2856	C2857	C2858	C2859	C2860	C2861	C2862	C2863	C2864	C2865	C2866	C2867	C2868	C2869	C2870	C2871	C2872	C2873	C2874	C2875	C2876	C2877	C2878	C2879	C2880	C2881	C2882	C2883	C2884	C2885	C2886	C2887	C2888	C2889	C2890	C2891	C2892	C2893	C2894	C2895	C2896	C2897	C2898	C2899	C2900	C2901	C2902	C2903	C2904	C2905	C2906	C2907	C2908	C2909	C2910	C2911	C2912	C2913	C2914	C2915	C2916	C2917	C2918	C2919	C2920	C2921	C2922	C2923	C2924	C2925	C2926	C2927	C2928	C2929	C2930	C2931	C2932	C2933	C2934	C2935	C2936	C2937	C2938	C2939	C2940	C2941	C2942	C2943	C2944	C2945	C2946	C2947	C2948	C2949	C2950	C2951	C2952	C2953	C2954	C2955	C2956	C2957	C2958	C2959	C2960	C2961	C2962	C2963	C2964	C2965	C2966	C2967	C2968	C2969	C2970	C2971	C2972	C2973	C2974	C2975	C2976	C2977	C2978	C2979	C2980	C2981	C2982	C2983	C2984	C2985	C2986	C2987	C2988	C2989	C2990	C2991	C2992	C2993	C2994	C2995	C2996	C2997	C2998	C2999	C3000	C3001	C3002	C3003	C3004	C3005	C3006	C3007	C3008	C3009	C3010	C3011	C3012	C3013	C3014	C3015	C3016	C3017	C3018	C3019	C3020	C3021	C3022	C3023	C3024	C3025	C3026	C3027	C3028	C3029	C3030	C3031	C3032	C3033	C3034	C3035	C3036	C3037	C3038	C3039	C3040	C3041	C3042	C3043	C3044	C3045	C3046	C3047	C3048	C3049	C3050	C3051	C3052	C3053	C3054	C3055	C3056	C3057	C3058	C3059	C3060	C3061	C3062	C3063	C3064	C3065	C3066	C3067	C3068	C3069	C3070	C3071	C3072	C3073	C3074	C3075	C3076	C3077	C3078	C3079	C3080	C3081	C3082	C3083	C3084	C3085	C3086	C3087	C3088	C3089	C3090	C3091	C3092	C3093	C3094	C3095	C3096	C3097	C3098	C3099	C3100	C3101	C3102	C3103	C3104	C3105	C3106	C3107	C3108	C3109	C3110	C3111	C3112	C3113	C3114	C3115	C3116	C3117	C3118	C3119	C3120	C3121	C3122	C3123	C3124	C3125	C3126	C3127	C3128	C3129	C3130	C3131	C3132	C3133	C3134	C3135	C3136	C3137	C3138	C3139	C3140	C3141	C3142	C3143	C3144	C3145	C3146	C3147	C3148	C3149	C3150	C3151	C3152	C3153	C3154	C3155	C3156	C3157	C3158	C3159	C3160	C3161	C3162	C3163	C3164	C3165	C3166	C3167	C3168	C3169	C3170	C3171	C3172	C3173	C3174	C3175	C3176	C3177	C3178	C3179	C3180	C3181	C3182	C3183	C3184	C3185	C3186	C3187	C3188	C3189	C3190	C3191	C3192	C3193	C3194	C3195	C3196	C3197	C3198	C3199	C3200	C3201	C3202	C3203	C3204	C3205	C3206	C3207	C3208	C3209	C3210	C3211	C3212	C3213	C3214	C3215	C3216	C3217	C3218	C3219	C3220	C3221	C3222	C3223	C3224	C3225	C3226	C3227	C3228	C3229	C3230	C3231	C3232	C3233	C3234	C3235	C3236	C3237	C3238	C3239	C3240	C3241	C3242	C3243	C3244	C3245	C3246	C3247	C3248	C3249	C3250	C3251	C3252	C3253	C3254	C3255	C3256	C3257	C3258	C3259	C3260	C3261	C3262	C3263	C3264	C3265	C3266	C3267	C3268	C3269	C3270	C3271	C3272	C3273	C3274	C3275	C3276	C3277	C3278	C3279	C3280	C3281	C3282	C3283	C3284	C3285	C3286	C3287	C3288	C3289	C3290	C3291	C3292	C3293	C3294	C3295	C3296	C3297	C3298	C3299	C3300	C3301	C3302	C3303	C3304	C3305	C3306	C3307	C3308	C3309	C3310	C3311	C3312	C3313	C3314	C3315	C3316	C3317	C3318	C3319	C3320	C3321	C3322	C3323	C3324	C3325	C3326	C3327	C3328	C3329	C3330	C3331	C3332	C3333	C3334	C3335	C3336	C3337	C3338	C3339	C3340	C3341	C3342	C3343	C3344	C3345	C3346	C3347	C3348	C3349	C3350	C3351	C3352	C3353	C3354	C3355	C3356	C3357	C3358	C3359	C3360	C3361	C3362	C3363	C3364	C3365	C3366	C3367	C3368	C3369	C3370	C3371	C3372	C3373	C3374	C3375	C3376	C3377	C3378	C3379	C3380	C3381	C3382	C3383	C3384	C3385	C3386	C3387	C3388	C3389	C3390	C3391	C3392	C3393	C3394	C3395	C3396	C3397	C3398	C3399	C3400	C3401	C3402	C3403	C3404	C3405	C3406	C3407	C3408	C3409	C3410	C3411	C3412	C3413	C3414	C3415	C3416	C3417	C3418	C3419	C3420	C3421	C3422	C3423	C3424	C3425	C3426	C3427	C3428	C3429	C3430	C3431	C3432	C3433	C3434	C3435	C3436	C3437	C3438	C3439	C3440	C3441	C3442	C3443	C3444	C3445	C3446	C3447	C3448	C3449	C3450	C3451	C3452	C3453	C3454	C3455	C3456	C3457	C3458	C3459	C3460	C3461	C3462	C3463	C3464	C3465	C3466	C3467	C3468	C3469	C3470	C3471	C3472	C3473	C3474	C3475	C3476	C3477	C3478	C3479	C3480	C3481	C3482	C3483	C3484	C3485	C3486	C3487	C3488	C3489	C3490	C3491	C3492	C3493	C3494	C3495	C3496	C3497	C3498	C3499	C3500	C3501	C3502	C3503	C3504	C3505	C3506	C3507	C3508	C3509	C3510	C3511	C3512	C3513	C3514	C3515	C3516	C3517	C3518	C3519	C3520	C3521	C3522	C3523	C3524	C3525	C3526	C3527	C3528	C3529	C3530	C3531	C3532	C3533	C3534	C3535	C3536	C3537	C3538	C3539	C3540	C3541	C3542	C3543	C3544	C3545	C3546	C3547	C3548	C3549	C3550	C3551	C3552	C3553	C3554	C3555	C3556	C3557	C3558	C3559	C3560	C3561	C3562	C3563	C3564	C3565	C3566	C3567	C3568	C3569	C3570	C3571	C3572	C3573	C3574	C3575	C3576	C3577	C3578	C3579	C3580	C3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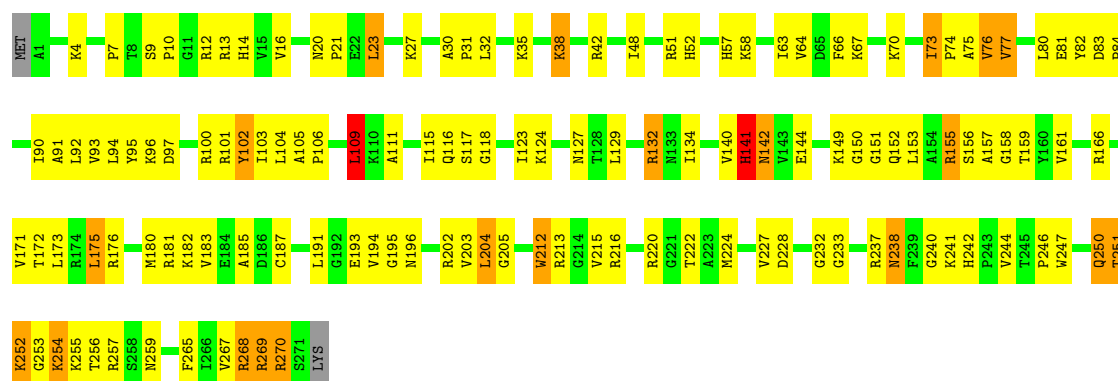
• Molecule 34: 5S rRNA

Chain BB:



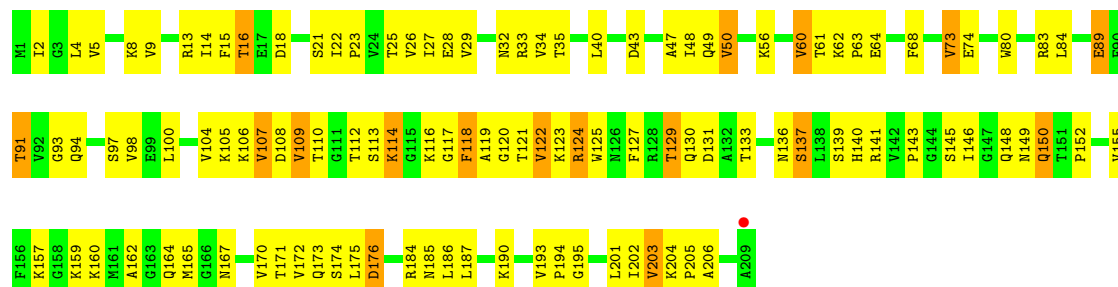
• Molecule 35: 50S ribosomal protein L2

Chain BC:



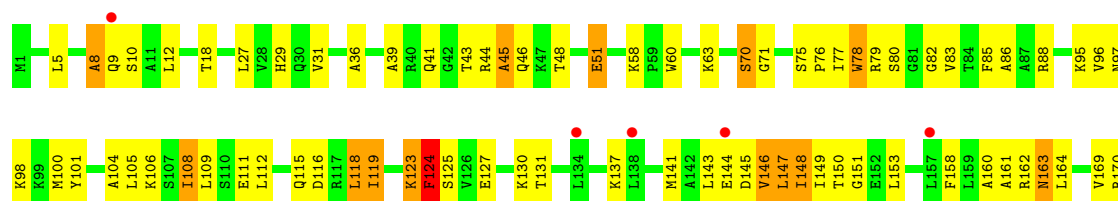
• Molecule 36: 50S ribosomal protein L3

Chain BD:



• Molecule 37: 50S ribosomal protein L4

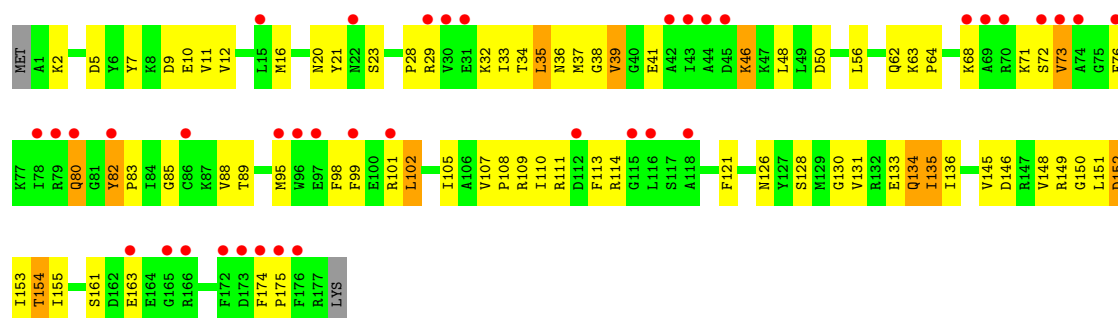
Chain BE:





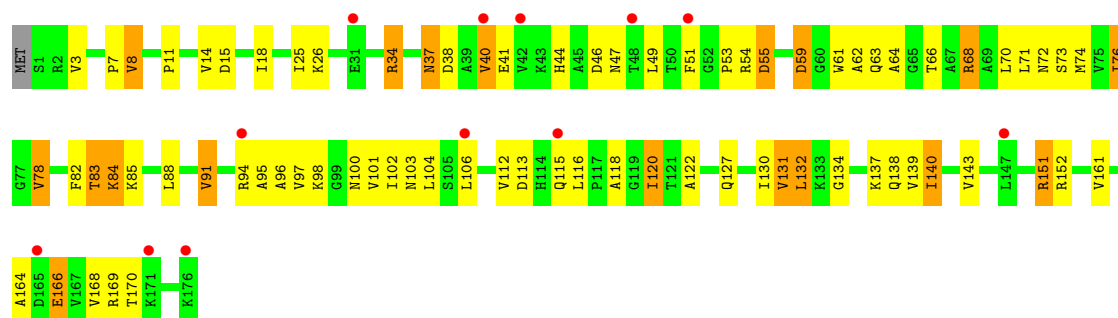
• Molecule 38: 50S ribosomal protein L5

Chain BF:



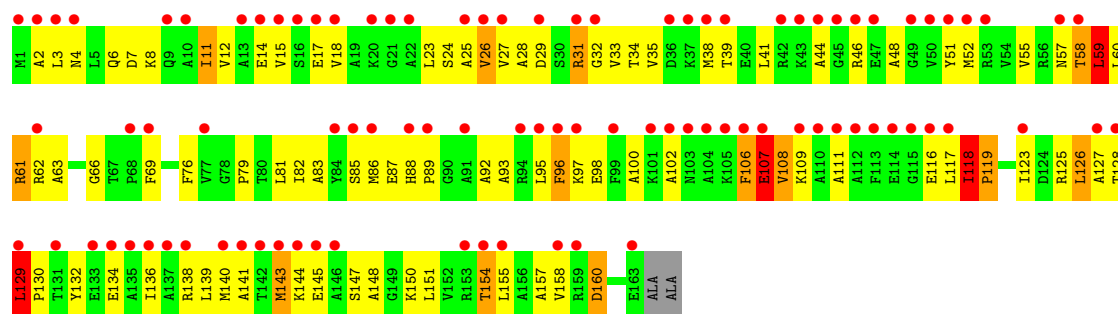
• Molecule 39: 50S ribosomal protein L6

Chain BG:



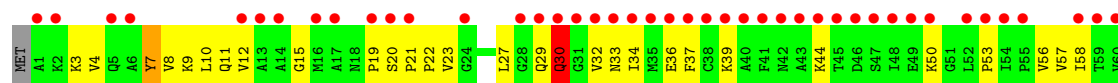
• Molecule 40: 50S ribosomal protein L10

Chain BH:

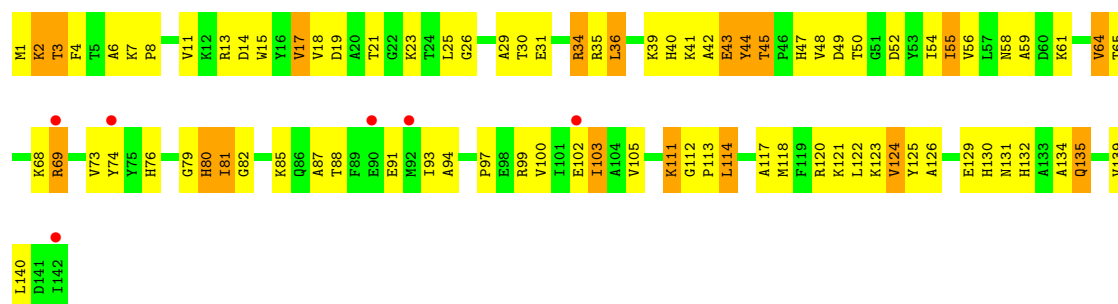


• Molecule 41: 50S ribosomal protein L11

Chain BI:



Chain BN: 



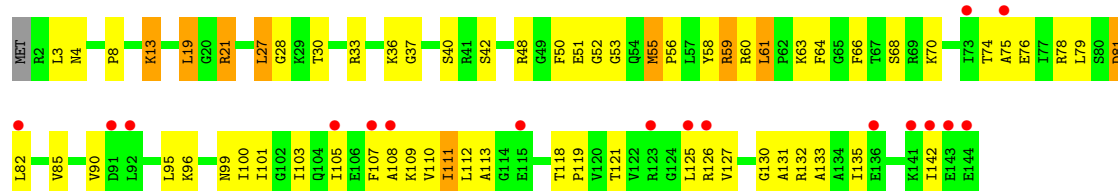
- Molecule 44: 50S ribosomal protein L14

Chain BO: 



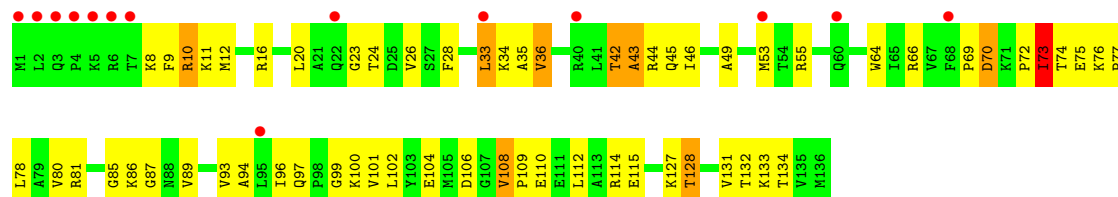
- Molecule 45: 50S ribosomal protein L15

Chain BP: 



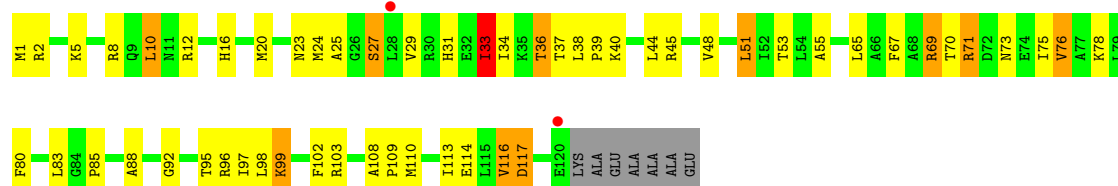
- Molecule 46: 50S ribosomal protein L16

Chain BQ: 

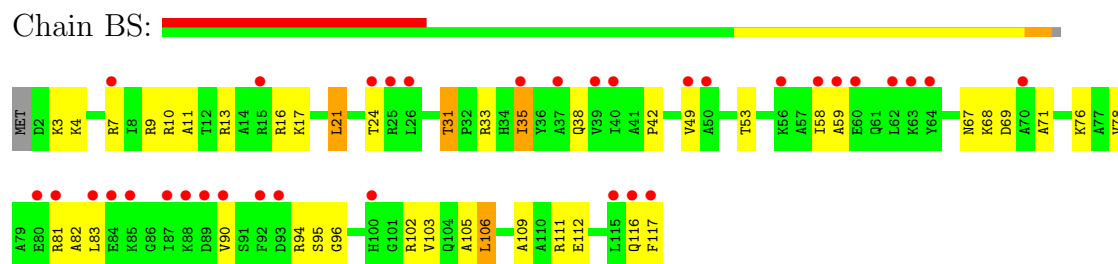


- Molecule 47: 50S ribosomal protein L17

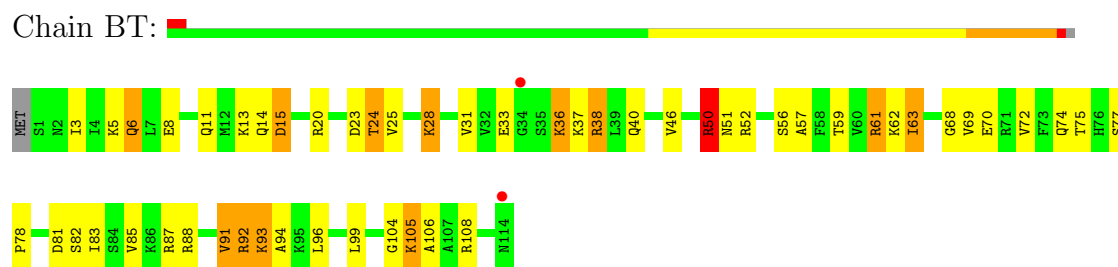
Chain BR: 



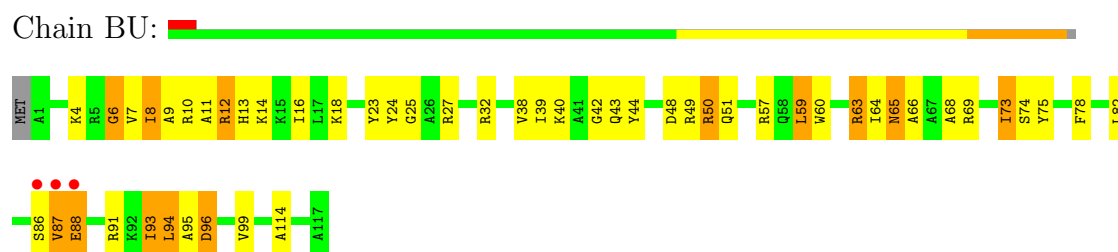
- Molecule 48: 50S ribosomal protein L18



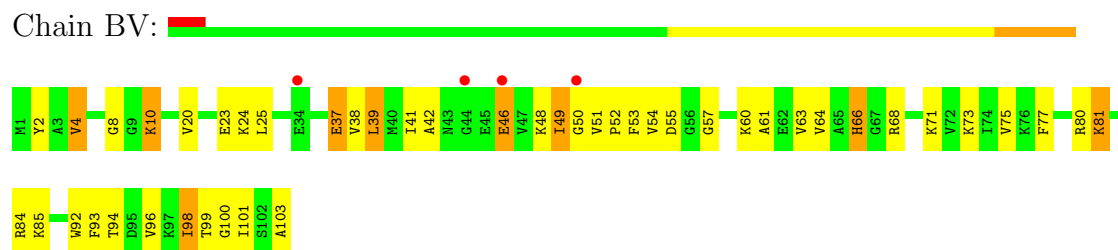
- Molecule 49: 50S ribosomal protein L19



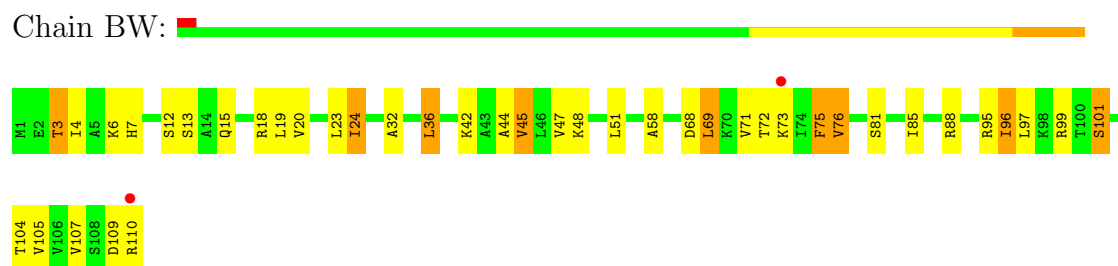
- Molecule 50: 50S ribosomal protein L20



- Molecule 51: 50S ribosomal protein L21

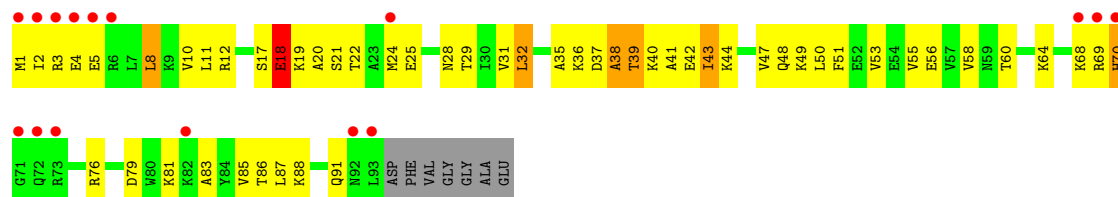


- Molecule 52: 50S ribosomal protein L22



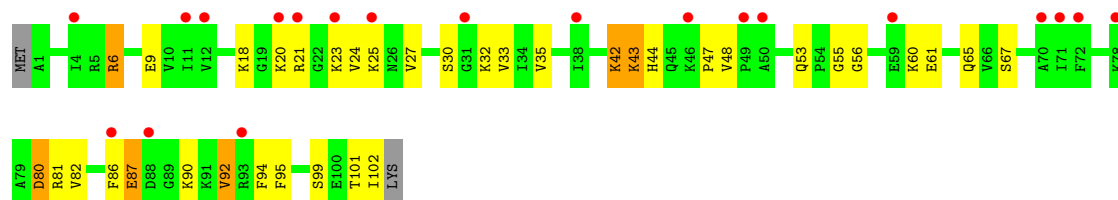
- Molecule 53: 50S ribosomal protein L23

Chain BX:



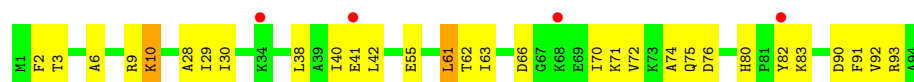
- Molecule 54: 50S ribosomal protein L24

Chain BY:



- Molecule 55: 50S ribosomal protein L25

Chain BZ:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 3.49Å)	Xtriage
Refinement program	CNS 1.2, phenix	Depositor
R, R_{free}	0.240 , 0.290 0.253 , 0.296	Depositor DCC
R_{free} test set	16644 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	83.9	Xtriage
Anisotropy	0.485	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 65.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	7 of 329524 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	146665	wwPDB-VP
Average B, all atoms (Å ²)	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.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	AU	425	0	449	22	0
22	AV	129	0	65	2	0
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

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including

hydrogens) of the entry. The overall clashscore for this entry is 15.

All (3630) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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	Distance(Å)	Clash(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
12:AL:78:VAL:HG21	23:AW:407:LEU:HB2	1.51	0.89
1:AA:690:G:O6	11:AK:52:ARG:NH2	2.05	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
33:BA:1060:U:H4'	33:BA:1061:U:H5'	1.58	0.85
23:AW:439:GLY:HA2	23:AW:440:ALA:HB2	1.56	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
40:BH:59:LEU:HD23	40:BH:62:ARG:HD2	1.60	0.83
33:BA:503:A:H5''	33:BA:504:A:H3'	1.60	0.83
10:AJ:50:THR:HG22	10:AJ:64:GLN:HG2	1.60	0.83
40:BH:25:ALA:CB	40:BH:85:SER:OG	2.26	0.83
33:BA:1914:C:C5	33:BA:1915:U:C5	2.67	0.83
33:BA:71:A:O2'	33:BA:72:U:OP2	1.95	0.83
37:BE:51:GLU:OE2	37:BE:88:ARG:NH1	2.11	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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
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: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
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
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:41:G:H2'	1:AA:42:G:H8	1.48	0.79
1:AA:82:G:O6	1:AA:87:C:N4	2.16	0.79
2:AB:187:ASP:HB2	2:AB:203:ASP:HB3	1.64	0.78
1:AA:978:A:OP2	1:AA:1362:A:N6	2.17	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
50:BU:91:ARG:HH21	50:BU:93:ILE:HG12	1.48	0.78
33:BA:242:G:N2	33:BA:255:A:OP2	2.15	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
27:B3:5:LYS:HG3	27:B3:36:GLU:HG2	1.65	0.77
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
1:AA:1366:C:O2'	10:AJ:62:ARG:NH2	2.18	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:674:G:H5''	37:BE:71:GLY:H	1.49	0.77
12:AL:30:ARG:HH11	23:AW:408:LYS:HG3	1.48	0.77
7:AG:14:ASP:HB3	7:AG:19:SER:H	1.50	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
33:BA:2150:C:C2'	33:BA:2151:U:C5	2.67	0.77
24:B0:45:HIS:HB2	24:B0:50:VAL:HG13	1.67	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
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
33:BA:2107:G:C6	33:BA:2183:A:C6	2.73	0.76
4:AD:109:THR:HG23	4:AD:112:GLU:H	1.51	0.76
37:BE:5:LEU:HD12	37:BE:10:SER:HB3	1.67	0.76
23:AW:62:MET:HG2	23:AW:454:LYS:HG2	1.65	0.76
3:AC:13:ILE:HD11	3:AC:177:LEU:HB3	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
23:AW:26:LYS:NZ	23:AW:89:THR:O	2.18	0.75
20:AT:4:LYS:HD3	20:AT:6:ALA:H	1.52	0.75
23:AW:399:ARG:HH12	23:AW:448:VAL:HG11	1.52	0.75
33:BA:1056:G:H8	33:BA:1056:G:O5'	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
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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AW:59:TRP:CE2	23:AW:69:SER:OG	2.41	0.74
49:BT:50:ARG:HB3	49:BT:57:ALA:N	2.00	0.74
33:BA:1248:G:OP2	37:BE:44:ARG:NH1	2.18	0.74
33:BA:962:G:H21	33:BA:2250:G:H1	1.33	0.74
33:BA:558:U:H5''	43:BN:111:LYS:HE2	1.69	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
35:BC:144:GLU:HA	35:BC:151:GLY:HA2	1.68	0.74
1:AA:1452:C:H4'	1:AA:1453:G:C2	2.23	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
33:BA:2532:G:N2	33:BA:2663:G:O2'	2.21	0.73
33:BA:704:G:H2'	33:BA:726:G:H22	1.53	0.73
8:AH:86:LYS:HG3	8:AH:90:GLU:HB3	1.71	0.73
33:BA:1509:A:O2'	33:BA:1510:G:O5'	2.04	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:1057:A:N6	33:BA:1087:G:OP2	2.22	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
43:BN:31:GLU:HA	43:BN:34:ARG:HG2	1.69	0.72
31:B7:24:LYS:HD2	45:BP:64:PHE:HB3	1.71	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
23:AW:260:LEU:HD21	33:BA:2655:G:H5'	1.72	0.72
1:AA:677:U:H3	1:AA:713:G:H22	1.37	0.72
23:AW:300:VAL:H	23:AW:318:MET:HG3	1.54	0.72
33:BA:2150:C:C2'	33:BA:2151:U:C6	2.72	0.72
1:AA:429:U:H3'	4:AD:8:LEU:HD23	1.70	0.72
2:AB:40:ILE:HG21	2:AB:201:GLY:H	1.52	0.72
35:BC:16:VAL:HB	35:BC:203:VAL:HG23	1.72	0.72
1:AA:651:C:N4	1:AA:753:A:OP2	2.18	0.72
7:AG:110:ARG:NH1	7:AG:122:GLU:OE2	2.22	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:BC:124:LYS:HB3	35:BC:127:ASN:HD22	1.54	0.72
23:AW:76:GLN:HE21	23:AW:85:ASN:HD21	1.37	0.72
33:BA:1693:U:O2'	35:BC:13:ARG:NH2	2.23	0.72
33:BA:1165:A:H2'	33:BA:1166:G:H8	1.55	0.72
23:AW:312:ARG:O	23:AW:314:ARG:N	2.22	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
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
1:AA:205:A:H4'	1:AA:205:A:OP1	1.90	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
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:OG	37:BE:70:SER:O	2.07	0.71
2:AB:99:MET:HA	2:AB:106:VAL:HG21	1.72	0.71
23:AW:60:MET:SD	23:AW:61:GLU:N	2.64	0.71
42:BM:3:THR:OG1	42:BM:4:LYS:N	2.22	0.71
33:BA:1996:C:OP1	44:BO:31:ARG:NE	2.23	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
24:B0:31:LEU:HD22	33:BA:2354:C:H4'	1.71	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
34:BB:15:A:H1'	34:BB:109:A:C8	2.26	0.71
1:AA:687:A:N6	1:AA:703:G:O2'	2.23	0.71
39:BG:96:ALA:HB3	39:BG:103:ASN:HB3	1.72	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:2757:A:N1	39:BG:66:THR:HG21	2.05	0.71
33:BA:1779:U:H5	33:BA:1784:A:N7	1.89	0.71
33:BA:1097:U:H1'	41:BI:8:VAL:HG12	1.72	0.70
1:AA:974:A:H4'	1:AA:975:A:H5'	1.72	0.70
33:BA:2047:C:O2'	33:BA:2823:A:N1	2.23	0.70
1:AA:1241:G:H2'	1:AA:1242:G:H8	1.56	0.70
4:AD:117:VAL:HG13	4:AD:122:ILE:HD11	1.73	0.70
1:AA:511:C:O2	1:AA:540:G:N2	2.22	0.70
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
33:BA:2149:U:H2'	33:BA:2150:C:O2'	1.91	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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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
33:BA:74:A:H4'	33:BA:75:G:O5'	1.92	0.70
6:AF:3:HIS:H	6:AF:92:THR:HG23	1.57	0.70
33:BA:2845:U:O3'	49:BT:52:ARG:NH1	2.25	0.69
24:B0:18:LYS:HG2	33:BA:2269:G:O2'	1.92	0.69
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
14:AN:44:VAL:HG23	14:AN:45:LEU:H	1.57	0.69
1:AA:1105:A:H2'	1:AA:1106:G:H8	1.55	0.69
12:AL:78:VAL:HG21	23:AW:407:LEU:CB	2.22	0.69
38:BF:128:SER:HA	38:BF:154:THR:HA	1.72	0.69
33:BA:2060:A:H3'	37:BE:63:LYS:HZ3	1.56	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
23:AW:138:LEU:HD11	23:AW:272:LEU:HD23	1.73	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
23:AW:59:TRP:CZ2	23:AW:69:SER:CB	2.75	0.69
1:AA:374:A:H5''	1:AA:452:A:C2	2.27	0.69
32:B8:9:LYS:HG3	32:B8:16:ILE:HG13	1.74	0.69
20:AT:38:ILE:HD11	20:AT:82:ILE:HG22	1.72	0.69
51:BV:49:ILE:HG13	51:BV:52:PRO:HA	1.73	0.69
33:BA:783:A:H8	33:BA:784:G:H4'	1.56	0.69
33:BA:41:C:H2'	33:BA:42:A:O4'	1.93	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
43:BN:6:ALA:HB3	43:BN:45:THR:HG21	1.74	0.69
5:AE:80:LEU:HD23	5:AE:122:VAL:HG11	1.74	0.69
39:BG:34:ARG:HH11	39:BG:34:ARG:H	1.40	0.69
1:AA:1441:A:H62	1:AA:1461:G:H21	1.39	0.69
33:BA:2304:G:H22	33:BA:2312:U:H3	1.39	0.69
54:BY:6:ARG:NH2	54:BY:25:LYS:O	2.26	0.69
33:BA:900:A:O2'	33:BA:901:C:OP1	2.10	0.69
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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:332:A:O2'	33:BA:334:C:OP2	2.11	0.68
23:AW:26:LYS:HE2	23:AW:89:THR:O	1.92	0.68
1:AA:599:C:H5''	8:AH:87:ARG:HA	1.73	0.68
39:BG:59:ASP:HB3	39:BG:63:GLN:HG3	1.74	0.68
14:AN:8:ARG:HB3	14:AN:12:ARG:HH12	1.58	0.68
33:BA:2598:A:H5''	35:BC:233:GLY:HA3	1.74	0.68
33:BA:458:G:O2'	33:BA:459:U:OP2	2.10	0.68
24:B0:39:GLN:C	24:B0:41:GLY:H	1.96	0.68
24:B0:28:GLU:HB3	24:B0:31:LEU:HD21	1.74	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
24:B0:23:LYS:HG2	33:BA:855:G:H21	1.57	0.68
23:AW:47:LYS:HE2	23:AW:66:ARG:O	1.93	0.68
33:BA:2104:C:H2'	33:BA:2105:U:O4'	1.94	0.68
9:AI:6:TYR:HE2	9:AI:17:ARG:HB2	1.59	0.68
4:AD:200:VAL:HG12	5:AE:102:THR:HG23	1.76	0.68
23:AW:399:ARG:NE	23:AW:445:GLN:OE1	2.20	0.68
43:BN:111:LYS:HD2	43:BN:112:GLY:H	1.58	0.68
33:BA:1266:G:O2'	33:BA:1267:U:OP2	2.11	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
23:AW:474:VAL:HG22	23:AW:501:LEU:HD12	1.75	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
39:BG:97:VAL:HG22	39:BG:102:ILE:HG12	1.75	0.67
49:BT:15:ASP:N	49:BT:15:ASP:OD1	2.28	0.67
5:AE:12:GLU:OE1	5:AE:67:ARG:NH1	2.26	0.67
50:BU:88:GLU:HG2	51:BV:49:ILE:HG12	1.75	0.67
34:BB:56:G:H5'	38:BF:23:SER:HB2	1.74	0.67
4:AD:124:VAL:O	4:AD:126:GLY:N	2.26	0.67
50:BU:6:GLY:HA2	50:BU:9:ALA:H	1.60	0.67
33:BA:140:C:H5'	33:BA:141:G:H21	1.58	0.67
35:BC:255:LYS:O	35:BC:257:ARG:N	2.28	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
39:BG:88:LEU:HD22	39:BG:161:VAL:HG22	1.77	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
33:BA:2150:C:H2'	33:BA:2151:U:H5	1.56	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
1:AA:83:C:N3	1:AA:86:G:N2	2.42	0.67
1:AA:1512:U:H2'	1:AA:1513:A:H8	1.59	0.67
33:BA:1791:A:O2'	35:BC:205:GLY:HA2	1.95	0.67
1:AA:1088:G:H21	1:AA:1167:A:H62	1.43	0.67
11:AK:124:LYS:HG2	21:AU:34:ARG:HG2	1.77	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
40:BH:88:HIS:HB2	40:BH:89:PRO:HD3	1.76	0.66
33:BA:1654:A:H2'	33:BA:1655:A:H8	1.58	0.66
23:AW:472:ARG:HD2	23:AW:503:TYR:HB3	1.76	0.66
33:BA:878:A:N6	33:BA:879:G:N3	2.43	0.66
1:AA:812:G:O2'	1:AA:813:U:OP2	2.09	0.66
31:B7:53:ASP:HA	31:B7:56:LEU:HD23	1.77	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:403:LEU:HD12	23:AW:407:LEU:HD23	1.76	0.66
23:AW:210:LEU:O	23:AW:228:ARG:NH1	2.28	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
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
15:AO:24:THR:HG23	15:AO:65:LEU:HD12	1.78	0.66
11:AK:78:ILE:HB	11:AK:104:PHE:HE1	1.60	0.66
19:AS:51:HIS:CD2	19:AS:53:GLY:H	2.13	0.66
36:BD:73:VAL:HG23	36:BD:74:GLU:H	1.60	0.66
33:BA:1594:U:H2'	33:BA:1595:C:C6	2.31	0.65
33:BA:1169:A:H61	33:BA:1180:U:H3	1.43	0.65
5:AE:148:SER:HB2	5:AE:151:MET:HB2	1.79	0.65
46:BQ:110:GLU:OE2	46:BQ:114:ARG:NH2	2.30	0.65
23:AW:59:TRP:HZ2	23:AW:69:SER:HB3	1.61	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:951:G:OP2	13:AM:100:ARG:NH2	2.29	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
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
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
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
23:AW:401:ILE:HD11	23:AW:438:VAL:HG21	1.78	0.65
11:AK:23:HIS:HB3	11:AK:30:ILE:HG23	1.78	0.65
8:AH:82:LEU:HD12	12:AL:3:VAL:HG11	1.77	0.65
33:BA:784:G:O2'	33:BA:785:G:H5''	1.97	0.65
50:BU:42:GLY:HA3	51:BV:75:VAL:HG21	1.77	0.65
1:AA:1406:U:O2	1:AA:1517:G:N2	2.29	0.65
17:AQ:47:ASP:N	17:AQ:47:ASP:OD2	2.30	0.65
1:AA:1280:A:OP1	10:AJ:9:ARG:NH1	2.30	0.65
23:AW:403:LEU:HG	23:AW:412:LEU:HG	1.77	0.65
54:BY:80:ASP:HB3	54:BY:95:PHE:HD2	1.62	0.65
14:AN:87:ALA:HB2	14:AN:92:ILE:HD12	1.78	0.65
35:BC:242:HIS:O	35:BC:244:VAL:HG13	1.97	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
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
12:AL:62:VAL:HG21	12:AL:94:TYR:HE2	1.60	0.64
33:BA:1923:U:H2'	33:BA:1924:C:C6	2.32	0.64
12:AL:78:VAL:HG21	23:AW:407:LEU:HD12	1.79	0.64
1:AA:1492:A:H5''	12:AL:43:LYS:HG3	1.79	0.64
1:AA:211:G:C2	1:AA:212:G:H1'	2.33	0.64
33:BA:2557:G:H2'	33:BA:2558:C:C6	2.31	0.64
8:AH:42:GLU:HG3	8:AH:100:ILE:HD13	1.77	0.64
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
50:BU:91:ARG:NH1	51:BV:10:LYS:HB3	2.13	0.64
12:AL:62:VAL:HG21	12:AL:94:TYR:CE2	2.33	0.64
55:BZ:72:VAL:HG12	55:BZ:93:ARG:HA	1.78	0.64
23:AW:158:VAL:HG13	23:AW:162:LEU:HD12	1.79	0.64
1:AA:1126:U:H1'	1:AA:1281:C:H1'	1.79	0.64
36:BD:118:PHE:HD2	36:BD:119:ALA:H	1.44	0.64
43:BN:17:VAL:HG12	43:BN:139:VAL:HG23	1.80	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
40:BH:52:MET:HG3	40:BH:95:LEU:HD11	1.80	0.64
13:AM:44:ILE:HA	13:AM:47:LEU:HB2	1.79	0.64
1:AA:1054:C:H1'	1:AA:1196:A:C5	2.33	0.64
33:BA:1889:A:N3	33:BA:2086:U:O2'	2.26	0.64
1:AA:352:C:H4'	1:AA:354:G:OP1	1.98	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
53:BX:39:THR:HB	53:BX:41:ALA:H	1.63	0.64
25:B1:9:LYS:NZ	33:BA:396:G:OP2	2.30	0.64
23:AW:149:ARG:NH1	23:AW:157:GLU:OE1	2.31	0.64
41:BI:19:PRO:HB2	41:BI:22:PRO:HD2	1.78	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:920:U:H2'	1:AA:921:U:C6	2.32	0.64
1:AA:3:A:N1	1:AA:628:G:O2'	2.31	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
55:BZ:76:ASP:H	55:BZ:90:ASP:HB2	1.63	0.64
33:BA:1392:A:N7	53:BX:19:LYS:HD2	2.13	0.64
33:BA:1007:C:OP1	43:BN:39:LYS:NZ	2.30	0.64
9:AI:50:PRO:HB3	9:AI:83:THR:HG23	1.79	0.64
4:AD:10:LEU:HD22	4:AD:62:ARG:HG3	1.80	0.64
52:BW:3:THR:O	52:BW:3:THR:OG1	2.12	0.64
2:AB:103:TRP:NE1	2:AB:150:ILE:HD11	2.13	0.63
53:BX:5:GLU:HA	53:BX:8:LEU:HD23	1.78	0.63
9:AI:51:LEU:HA	9:AI:54:VAL:HG23	1.79	0.63
23:AW:56:LYS:HB2	23:AW:57:SER:HA	1.80	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
37:BE:148:ILE:HA	37:BE:187:VAL:HB	1.78	0.63
33:BA:135:U:H3	33:BA:144:A:H61	1.43	0.63
1:AA:477:C:H2'	1:AA:478:A:C8	2.33	0.63
33:BA:1914:C:C2'	33:BA:1915:U:O4'	2.34	0.63
33:BA:1183:U:H2'	33:BA:1184:U:C6	2.33	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
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
1:AA:212:G:H2'	1:AA:213:G:H8	1.63	0.63
37:BE:161:ALA:HA	37:BE:164:LEU:HB2	1.81	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
54:BY:27:VAL:HG23	54:BY:33:VAL:HG12	1.79	0.63
1:AA:345:C:O2'	1:AA:346:G:O5'	2.15	0.63
12:AL:30:ARG:NH1	23:AW:408:LYS:CG	2.59	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
17:AQ:11:VAL:HG12	17:AQ:13:SER:H	1.64	0.63
4:AD:124:VAL:C	4:AD:126:GLY:H	2.02	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
4:AD:106:PHE:HB3	4:AD:144:ILE:HD11	1.80	0.63
33:BA:2788:C:H2'	33:BA:2789:C:C6	2.33	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
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
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:26:LYS:HG3	56:AW:601:GNP:O1B	1.99	0.63
6:AF:89:VAL:HG22	6:AF:90:MET:H	1.64	0.63
10:AJ:40:ILE:HB	10:AJ:73:LEU:HB2	1.81	0.63
30:B6:21:ARG:HG2	30:B6:31:LEU:HG	1.80	0.63
16:AP:6:LEU:HG	16:AP:17:TYR:HB3	1.81	0.63
45:BP:76:GLU:HB2	45:BP:111:ILE:HD12	1.81	0.63
2:AB:53:LEU:HD13	2:AB:56:LEU:HD12	1.80	0.63
33:BA:1812:U:H2'	33:BA:1813:G:H8	1.63	0.62
33:BA:900:A:H2	33:BA:901:C:H5	1.46	0.62
10:AJ:12:ALA:HB2	10:AJ:96:VAL:HG13	1.81	0.62
8:AH:104:SER:HB2	8:AH:125:ILE:HD11	1.79	0.62
39:BG:84:LYS:HB2	39:BG:132:LEU:H	1.64	0.62
28:B4:9:ARG:HB2	28:B4:12:ARG:NH2	2.13	0.62
49:BT:105:LYS:HA	49:BT:108:ARG:HH21	1.62	0.62
28:B4:47:TYR:CE2	28:B4:52:LYS:HB2	2.33	0.62
23:AW:304:GLN:O	23:AW:306:ASN:N	2.32	0.62
33:BA:1458:U:H4'	33:BA:1459:G:O5'	1.98	0.62
33:BA:184:C:H2'	33:BA:185:G:H8	1.64	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
27:B3:8:GLN:O	27:B3:10:ARG:N	2.32	0.62
4:AD:197:HIS:O	4:AD:201:GLU:HB2	1.99	0.62
46:BQ:12:MET:HB2	46:BQ:72:PRO:HD2	1.81	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:AM:106:ARG:HH12	13:AM:109:LYS:HD3	1.64	0.62
52:BW:109:ASP:OD1	52:BW:110:ARG:N	2.32	0.62
33:BA:974:G:N7	33:BA:989:G:C5	2.67	0.62
1:AA:1512:U:H2'	1:AA:1513:A:C8	2.35	0.62
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.35	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
23:AW:80:HIS:ND1	23:AW:81:ASP:OD1	2.27	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
49:BT:5:LYS:HA	49:BT:8:GLU:HB2	1.82	0.62
41:BI:135:MET:SD	41:BI:135:MET:N	2.73	0.62
1:AA:412:A:H5'	1:AA:413:G:OP1	2.00	0.62
38:BF:134:GLN:O	38:BF:136:ILE:N	2.31	0.62
23:AW:314:ARG:CZ	23:AW:421:GLU:HB2	2.29	0.62
51:BV:49:ILE:HB	51:BV:51:VAL:O	2.00	0.62
6:AF:67:PRO:HG2	6:AF:70:VAL:HG22	1.80	0.62
42:BJ:27:GLU:HA	42:BJ:29:LYS:HG3	1.80	0.62
36:BD:15:PHE:H	49:BT:11:GLN:HE22	1.47	0.62
38:BF:64:PRO:HA	38:BF:88:VAL:HG22	1.82	0.62
33:BA:1181:U:H2'	33:BA:1182:G:C8	2.33	0.62
11:AK:22:ILE:HD11	11:AK:85: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
33:BA:1914:C:C5	33:BA:1915:U:C4	2.88	0.61
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
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
35:BC:250:GLN:HG2	35:BC:254:LYS:HG3	1.82	0.61
24:B0:43:LYS:HD2	24:B0:79:ILE:HD11	1.82	0.61
33:BA:2375:G:N2	33:BA:2378:A:OP2	2.30	0.61
32:B8:7:VAL:O	32:B8:35:GLN:NE2	2.33	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
35:BC:83:ASP:HB2	35:BC:90:ILE:HD12	1.81	0.61
24:B0:49:ASN:HB2	24:B0:60:ALA:HA	1.82	0.61
1:AA:430:A:OP2	4:AD:7:LYS:HG2	2.00	0.61
43:BN:44:TYR:HB2	50:BU:63:ARG:HB3	1.81	0.61
10:AJ:11:LYS:HG3	10:AJ:97:ASP:HB3	1.82	0.61
37:BE:149:ILE:HD12	37:BE:175:ILE:HB	1.82	0.61
50:BU:68:ALA:HB1	50:BU:73:ILE:HG23	1.81	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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
33:BA:1105:U:H2'	33:BA:1106:G:H8	1.66	0.61
34:BB:66:A:H4'	34:BB:67:G:OP1	2.01	0.61
33:BA:1894:C:H2'	33:BA:1895:C:H6	1.66	0.61
33:BA:1800:C:OP2	35:BC:181:ARG:NH1	2.33	0.61
1:AA:1387:G:H2'	1:AA:1388:C:C6	2.35	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
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
1:AA:1492:A:N1	33:BA:1913:A:H2	1.98	0.61
42:BJ:13:ALA:O	42:BJ:17:MET:HB2	2.01	0.61
33:BA:503:A:H4'	33:BA:504:A:O5'	1.99	0.61
1:AA:82:G:O4'	1:AA:89:U:O2'	2.19	0.61
1:AA:2:A:N6	1:AA:3:A:N1	2.49	0.61
26:B2:45:GLN:O	26:B2:46:VAL:HB	2.00	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
33:BA:1082:U:H5'	41:BI:118:GLY:HA2	1.82	0.61
1:AA:1005:A:OP2	1:AA:1024:G:N2	2.33	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
1:AA:509:A:N3	1:AA:543:U:O2'	2.32	0.61
1:AA:1527:U:OP2	21:AU:38:GLU:HG2	2.00	0.61
1:AA:992:U:O2'	1:AA:993:G:N2	2.34	0.61
33:BA:172:A:H2'	33:BA:173:A:C8	2.36	0.61
1:AA:1191:A:H5''	3:AC:3:LYS:HE3	1.82	0.61
1:AA:1492:A:C6	33:BA:1913:A:C2	2.88	0.61
1:AA:591:U:H2'	1:AA:592:G:H8	1.65	0.61
33:BA:580:U:H2'	33:BA:581:C:C6	2.36	0.61
2:AB:113:LEU:HD13	2:AB:143:LEU:HD12	1.83	0.61
33:BA:364:C:H6	33:BA:364:C:O5'	1.84	0.61
44:BO:103:VAL:O	44:BO:122:VAL:HB	2.01	0.61
15:AO:84:LEU:HB3	15:AO:86:LEU:HD22	1.83	0.61
51:BV:25:LEU:H	51:BV:94:THR:HG21	1.66	0.60
38:BF:7:TYR:OH	38:BF:29:ARG:HB3	2.01	0.60
25:B1:67:LEU:HD13	25:B1:77:TYR:CE1	2.36	0.60
33:BA:2150:C:N3	33:BA:2151:U:O4	2.34	0.60
33:BA:1069:A:O2'	33:BA:1070:A:H5''	2.00	0.60
9:AI:56:MET:HB3	9:AI:60:LEU:HD23	1.82	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
41:BI:33:ASN:HB3	41:BI:36:GLU:HB2	1.83	0.60
1:AA:1002:G:H1	1:AA:1038:C:H42	1.49	0.60
36:BD:184:ARG:HB3	36:BD:186:LEU:HD13	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
7:AG:135:LYS:HD2	7:AG:138:GLU:HB2	1.83	0.60
1:AA:70:U:HO2'	1:AA:71:A:H8	1.49	0.60
26:B2:5:GLU:O	26:B2:8:GLU:HB2	2.00	0.60
23:AW:300:VAL:HG12	23:AW:301:PHE:H	1.66	0.60
33:BA:1894:C:H2'	33:BA:1895:C:C6	2.37	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
1:AA:251:G:N1	1:AA:266:G:O6	2.34	0.60
53:BX:38:ALA:HB1	53:BX:43:ILE:HG22	1.81	0.60
52:BW:42:LYS:O	52:BW:45:VAL:HG13	2.02	0.60
36:BD:157:LYS:HD2	43:BN:79:GLY:O	2.01	0.60
45:BP:110:VAL:HB	45:BP:127:VAL:HG23	1.84	0.60
1:AA:1105:A:H2'	1:AA:1106:G:C8	2.35	0.60
33:BA:877:A:H1'	33:BA:900:A:N6	2.16	0.60
19:AS:35:ARG:NH2	19:AS:71:GLY:O	2.34	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
33:BA:1914:C:C6	33:BA:1915:U:C5	2.89	0.60
23:AW:59:TRP:CZ2	23:AW:69:SER:OG	2.55	0.60
40:BH:11:ILE:CG2	40:BH:66:GLY:HA3	2.29	0.60
23:AW:472:ARG:HH21	23:AW:505:ALA:HB2	1.66	0.60
12:AL:49:ARG:HG2	12:AL:89:LEU:HD21	1.83	0.60
35:BC:171:VAL:HG23	35:BC:185:ALA:HB2	1.84	0.60
40:BH:138:ARG:HG2	42:BK:22:LEU:HD11	1.83	0.60
38:BF:108:PRO:HA	38:BF:113:PHE:CD2	2.36	0.60
1:AA:982:U:H4'	1:AA:983:A:O5'	2.01	0.60
45:BP:79:LEU:H	45:BP:113:ALA:HB3	1.66	0.60
33:BA:639:U:H2'	33:BA:640:C:C6	2.37	0.60
3:AC:184:ASN:HD22	3:AC:185:THR:H	1.50	0.60
23:AW:427:VAL:HG12	23:AW:438:VAL:HG22	1.83	0.60
1:AA:1297:G:H5'	1:AA:1302:C:H42	1.67	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
48:BS:11:ALA:HB2	48:BS:96:GLY:N	2.17	0.60
1:AA:422:C:O2'	1:AA:423:G:O5'	2.19	0.60
33:BA:197:A:N6	33:BA:2430:A:H2'	2.16	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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
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
23:AW:518:TYR:CD1	23:AW:519:PRO:HA	2.36	0.60
33:BA:923:G:H2'	33:BA:924:G:H8	1.65	0.60
10:AJ:10:LEU:HB3	10:AJ:18:ILE:HD11	1.82	0.60
1:AA:411:A:C5	1:AA:413:G:H1'	2.37	0.60
23:AW:35:LEU:HD11	23:AW:262:ASN:HD21	1.67	0.60
33:BA:2233:U:H2'	33:BA:2234:G:C8	2.37	0.60
33:BA:859:G:O2'	33:BA:860:U:O5'	2.18	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
23:AW:522:GLN:HB2	23:AW:524:HIS:H	1.67	0.59
6:AF:47:LEU:HD13	6:AF:51:ILE:HG22	1.84	0.59
1:AA:922:G:H4'	5:AE:24:VAL:HA	1.83	0.59
23:AW:63:GLU:HB2	23:AW:450:VAL:HG11	1.83	0.59
23:AW:53:GLN:O	23:AW:55:ALA:N	2.32	0.59
1:AA:369:G:OP2	1:AA:388:G:N2	2.27	0.59
33:BA:2149:U:H3'	33:BA:2150:C:H4'	1.84	0.59
1:AA:73:C:H41	1:AA:94:G:H22	1.50	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
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
1:AA:1147:C:H4'	9:AI:6:TYR:CE1	2.38	0.59
6:AF:6:ILE:HD11	6:AF:71:ILE:HD11	1.82	0.59
33:BA:1290:C:H2'	33:BA:1291:C:H6	1.67	0.59
33:BA:118:A:N3	33:BA:178:G:H1'	2.17	0.59
23:AW:147:ASP:HB3	39:BG:91:VAL:HG11	1.84	0.59
33:BA:582:A:H2'	33:BA:583:G:C8	2.37	0.59
5:AE:91:SER:OG	5:AE:129:SER:O	2.15	0.59
33:BA:1442:U:H2'	33:BA:1443:U:C6	2.37	0.59
23:AW:59:TRP:NE1	23:AW:69:SER:HA	2.18	0.59
3:AC:10:ARG:HB3	3:AC:15:LYS:HB2	1.84	0.59
33:BA:2105:U:C4	33:BA:2106:U:O4	2.55	0.59
32:B8:22:VAL:HG11	32:B8:36:ARG:HG2	1.84	0.59
32:B8:11:CYS:SG	32:B8:33:HIS:ND1	2.71	0.59
33:BA:2149:U:O3'	33:BA:2150:C:C4'	2.30	0.59
23:AW:105:ALA:O	23:AW:319:ARG:NH1	2.32	0.59
1:AA:1152:A:H5'	10:AJ:15:HIS:CD2	2.38	0.59
42:BJ:13:ALA:O	42:BJ:14:MET:HG2	2.02	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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
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
5:AE:103:GLY:HA2	5:AE:121:ASN:HA	1.85	0.59
5:AE:35:LEU:HD21	5:AE:136:VAL:HG11	1.83	0.59
33:BA:2152:G:H2'	33:BA:2153:C:O4'	2.01	0.59
7:AG:14:ASP:OD2	7:AG:43:TYR:OH	2.15	0.59
33:BA:910:A:N3	33:BA:2264:C:O2'	2.34	0.59
24:B0:39:GLN:HG2	24:B0:40:ARG:N	2.18	0.59
35:BC:124:LYS:HB3	35:BC:127:ASN:ND2	2.18	0.59
33:BA:900:A:H3'	33:BA:902:C:H41	1.68	0.59
33:BA:900:A:C2	33:BA:901:C:H5	2.21	0.59
33:BA:395:U:O2'	33:BA:396:G:N7	2.34	0.59
24:B0:37:VAL:HG13	24:B0:55:ASP:O	2.01	0.59
47:BR:69:ARG:O	47:BR:71:ARG:N	2.32	0.59
33:BA:136:G:H1	33:BA:143:C:H42	1.51	0.59
3:AC:139:ASN:HA	3:AC:142:ARG:HB2	1.84	0.59
32:B8:15:LYS:HE3	32:B8:17:VAL:HG22	1.84	0.59
7:AG:78:ARG:NH1	7:AG:81:GLY:O	2.35	0.59
30:B6:9:VAL:HG12	33:BA:1309:G:OP1	2.02	0.59
3:AC:126:ARG:HH12	3:AC:192:TYR:HE2	1.49	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
35:BC:180:MET:HG3	35:BC:268:ARG:HB3	1.85	0.59
44:BO:18:ARG:H	44:BO:45:GLU:HB2	1.67	0.59
43:BN:132:HIS:O	43:BN:135:GLN:HG2	2.03	0.59
7:AG:62:GLU:OE1	7:AG:69:ARG:NH2	2.35	0.59
33:BA:538:A:H2'	33:BA:539:G:O4'	2.03	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
1:AA:250:A:H4'	1:AA:251:G:O5'	2.02	0.59
1:AA:1035:A:H2'	1:AA:1036:A:O4'	2.02	0.59
1:AA:402:G:C6	1:AA:403:C:C4	2.91	0.59
25:B1:69:GLU:O	25:B1:71:ARG:N	2.36	0.59
43:BN:100:VAL:O	43:BN:103:ILE:HD13	2.03	0.59
11:AK:94:SER:HA	11:AK:97:ARG:HG2	1.84	0.59
23:AW:401:ILE:HG22	23:AW:461:ALA:HB1	1.84	0.58
23:AW:59:TRP:O	23:AW:64:LYS:HD2	2.03	0.58
33:BA:1059:G:N2	41:BI:127:SER:O	2.25	0.58
24:B0:39:GLN:HG3	24:B0:42:THR:H	1.67	0.58
8:AH:87:ARG:O	8:AH:121:GLY:HA3	2.04	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1654:A:H2'	33:BA:1655:A:C8	2.39	0.58
33:BA:668:A:H2'	33:BA:670:A:H62	1.68	0.58
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
54:BY:53:GLN:N	54:BY:53:GLN:OE1	2.36	0.58
45:BP:81:ASP:HB3	45:BP:100:ILE:HD12	1.85	0.58
19:AS:3:SER:HB2	19:AS:4:LEU:HD12	1.84	0.58
23:AW:145:ASP:OD2	56:AW:601:GNP:C2	2.51	0.58
23:AW:50:GLY:HA3	33:BA:2655:G:H8	1.68	0.58
36:BD:68:PHE:CB	36:BD:73:VAL:HG12	2.33	0.58
42:BJ:3:THR:HG22	42:BJ:6:GLN:HB2	1.83	0.58
33:BA:1045:C:H5''	33:BA:1046:A:H5'	1.85	0.58
3:AC:152:VAL:HG12	3:AC:197:VAL:HG13	1.84	0.58
38:BF:38:GLY:HA2	38:BF:85:GLY:HA3	1.85	0.58
33:BA:674:G:H5''	37:BE:71:GLY:N	2.18	0.58
37:BE:149:ILE:HD11	37:BE:172:ALA:HA	1.86	0.58
27:B3:12:ALA:HA	27:B3:15:ARG:HD3	1.86	0.58
53:BX:44:LYS:O	53:BX:48:GLN:HG2	2.03	0.58
52:BW:72:THR:O	52:BW:73:LYS:HD2	2.02	0.58
44:BO:111:LYS:HE2	44:BO:111:LYS:H	1.67	0.58
33:BA:819:A:OP2	33:BA:1187:G:N2	2.23	0.58
33:BA:27:G:H1'	33:BA:513:A:H62	1.68	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
37:BE:158:PHE:HA	37:BE:169:VAL:HG21	1.85	0.58
16:AP:18:GLN:HE21	16:AP:35:ARG:HD2	1.69	0.58
33:BA:899:A:H2'	33:BA:900:A:C8	2.38	0.58
1:AA:980:C:O3'	14:AN:12:ARG:NH2	2.37	0.58
1:AA:383:A:C5	1:AA:384:G:H1'	2.38	0.58
1:AA:210:C:O2'	1:AA:211:G:N2	2.36	0.58
43:BN:118:MET:HA	43:BN:121:LYS:HE2	1.86	0.58
33:BA:1243:C:H1'	45:BP:4:ASN:O	2.03	0.58
36:BD:13:ARG:HE	36:BD:21:SER:HG	1.48	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
1:AA:662:U:H2'	1:AA:663:A:C8	2.39	0.58
40:BH:57:ASN:C	40:BH:59:LEU:H	2.06	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
53:BX:39:THR:O	53:BX:40:LYS:HB2	2.04	0.58
38:BF:10:GLU:C	38:BF:12:VAL:H	2.06	0.58
23:AW:59:TRP:CE3	23:AW:59:TRP:HA	2.39	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1054:C:H1'	1:AA:1196:A:N7	2.17	0.58
33:BA:1844:C:H5'	35:BC:253:GLY:O	2.04	0.58
5:AE:87:VAL:HG12	5:AE:92:ARG:HA	1.86	0.58
53:BX:76:ARG:NH2	53:BX:79:ASP:OD1	2.37	0.58
4:AD:25:ARG:NH1	4:AD:30:LYS:HE3	2.19	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
1:AA:1171:A:H2'	1:AA:1172:C:C6	2.39	0.58
44:BO:2:ILE:O	44:BO:3:GLN:HG2	2.03	0.58
33:BA:1666:G:H4'	44:BO:6:THR:HG23	1.86	0.58
33:BA:993:G:OP1	50:BU:49:ARG:NE	2.31	0.58
36:BD:121:THR:HB	36:BD:127:PHE:CD1	2.39	0.58
14:AN:21:ALA:N	14:AN:24:ALA:HB3	2.19	0.58
23:AW:314:ARG:NH2	23:AW:418:GLN:HA	2.19	0.58
51:BV:49:ILE:HG22	51:BV:54:VAL:HG13	1.86	0.58
21:AU:33:ARG:HD3	21:AU:34:ARG:H	1.67	0.58
33:BA:2680:U:OP1	36:BD:114:LYS:HG3	2.02	0.58
33:BA:2580:U:OP1	36:BD:137:SER:OG	2.20	0.58
1:AA:1101:A:H4'	1:AA:1102:A:O5'	2.04	0.58
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
10:AJ:8:ILE:HB	10:AJ:74:VAL:HB	1.86	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
23:AW:399:ARG:HG3	23:AW:438:VAL:O	2.05	0.57
23:AW:68:ILE:HG23	23:AW:68:ILE:O	2.03	0.57
35:BC:13:ARG:HG2	35:BC:14:HIS:CD2	2.39	0.57
4:AD:63:ILE:HG23	4:AD:64:TYR:CD1	2.39	0.57
33:BA:1425:G:H2'	33:BA:1426:G:C8	2.39	0.57
23:AW:97:GLU:O	23:AW:99:THR:N	2.37	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
36:BD:119:ALA:HB1	36:BD:123:LYS:HB3	1.86	0.57
33:BA:90:U:H2'	33:BA:91:A:C8	2.39	0.57
50:BU:23:TYR:HB3	50:BU:27:ARG:HB3	1.86	0.57
33:BA:2107:G:C6	33:BA:2183:A:C5	2.91	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
52:BW:24:ILE:HG23	52:BW:71:VAL:HG11	1.87	0.57
51:BV:42:ALA:HA	51:BV:46:GLU:HB2	1.84	0.57
3:AC:118:SER:O	3:AC:122:GLN:HG2	2.04	0.57
47:BR:38:LEU:HB3	47:BR:39:PRO:HD3	1.87	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1549:A:H2'	33:BA:1550:C:C6	2.39	0.57
33:BA:2146:C:H4'	33:BA:2147:A:OP1	2.02	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
40:BH:157:ALA:O	40:BH:160:ASP:N	2.37	0.57
44:BO:106:GLU:OE1	44:BO:106:GLU:N	2.37	0.57
2:AB:22:TRP:CZ3	2:AB:24:PRO:HA	2.39	0.57
47:BR:44:LEU:O	47:BR:48:VAL:HG23	2.05	0.57
40:BH:155:LEU:HD22	42:BL:22:LEU:HB3	1.87	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
37:BE:27:LEU:O	37:BE:31:VAL:HG23	2.04	0.57
33:BA:2548:U:O2	44:BO:23:LYS:NZ	2.36	0.57
33:BA:244:A:C2	33:BA:245:G:H1'	2.39	0.57
9:AI:18:VAL:HG22	9:AI:64:ILE:HG23	1.86	0.57
1:AA:1203:C:H2'	1:AA:1204:A:H8	1.68	0.57
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
49:BT:50:ARG:HD2	49:BT:51:ASN:H	1.70	0.57
2:AB:164:ASP:HB2	2:AB:203:ASP:HB2	1.86	0.57
26:B2:48:ARG:CZ	33:BA:75:G:H4'	2.35	0.57
33:BA:2726:A:HO2'	33:BA:2727:A:P	2.27	0.57
1:AA:922:G:H2'	1:AA:923:A:C8	2.39	0.57
36:BD:32:ASN:HB3	36:BD:50:VAL:HG11	1.85	0.57
2:AB:73:ARG:HA	2:AB:76:SER:HB3	1.87	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
33:BA:31:C:O3'	33:BA:1238:G:H5'	2.05	0.57
1:AA:1410:A:C6	1:AA:1491:G:O6	2.58	0.57
40:BH:51:TYR:HB2	40:BH:89:PRO:HD2	1.85	0.57
1:AA:974:A:OP1	1:AA:974:A:H8	1.87	0.57
1:AA:971:G:H5''	1:AA:972:C:H5''	1.87	0.57
1:AA:765:G:H1	1:AA:812:G:H2'	1.70	0.57
33:BA:1818:U:H3'	35:BC:155:ARG:HB2	1.87	0.57
1:AA:983:A:H5'	14:AN:2:LYS:NZ	2.20	0.57
44:BO:23:LYS:HB3	44:BO:40:LYS:HB3	1.86	0.57
6:AF:40:GLU:OE1	6:AF:100:SER:OG	2.20	0.57
5:AE:149:PRO:HG2	5:AE:150:GLU:HG2	1.85	0.57
48:BS:67:ASN:C	48:BS:69:ASP:H	2.07	0.57
2:AB:71:THR:HB	2:AB:167:HIS:HE1	1.69	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:501:C:H2'	1:AA:502:A:C8	2.40	0.57
1:AA:182:A:N1	1:AA:223:A:O2'	2.32	0.57
46:BQ:42:THR:O	46:BQ:44:ARG:N	2.37	0.57
37:BE:76:PRO:HA	37:BE:82:GLY:HA2	1.87	0.57
33:BA:962:G:N2	33:BA:2250:G:H1	2.02	0.57
46:BQ:72:PRO:O	46:BQ:89:VAL:HG13	2.05	0.57
1:AA:197:A:N1	1:AA:220:G:O2'	2.35	0.57
33:BA:1497:U:H5''	33:BA:1498:C:OP2	2.05	0.57
46:BQ:66:ARG:HB2	46:BQ:101:VAL:O	2.05	0.57
38:BF:33:ILE:HD12	38:BF:155:ILE:HG13	1.87	0.57
21:AU:36:PHE:HB3	21:AU:40:PRO:HD3	1.86	0.57
24:B0:23:LYS:HD3	33:BA:855:G:N3	2.20	0.56
38:BF:110:ILE:HG12	38:BF:136:ILE:HG21	1.87	0.56
27:B3:8:GLN:HB3	27:B3:31:ILE:HA	1.86	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
44:BO:13:ASN:O	44:BO:15:GLY:N	2.38	0.56
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
6:AF:62:MET:HG3	6:AF:64:VAL:HG23	1.87	0.56
55:BZ:2:PHE:O	55:BZ:62:THR:OG1	2.22	0.56
1:AA:9:G:H5'	5:AE:107:GLY:HA3	1.87	0.56
7:AG:56:SER:OG	7:AG:57:GLU:N	2.37	0.56
35:BC:95:TYR:HE1	35:BC:101:ARG:HD2	1.70	0.56
1:AA:1363:A:O2'	1:AA:1365:G:N7	2.38	0.56
33:BA:17:G:H2'	33:BA:18:U:C6	2.40	0.56
23:AW:64:LYS:CE	23:AW:71:THR:H	2.17	0.56
36:BD:121:THR:O	36:BD:122:VAL:HB	2.04	0.56
23:AW:394:ALA:HB2	23:AW:525:GLN:HG2	1.86	0.56
33:BA:878:A:C6	33:BA:879:G:H1'	2.41	0.56
14:AN:8:ARG:HB3	14:AN:12:ARG:NH1	2.19	0.56
1:AA:1088:G:H21	1:AA:1167:A:N6	2.02	0.56
36:BD:146:ILE:HD12	36:BD:155:VAL:HG21	1.86	0.56
33:BA:197:A:H62	33:BA:2430:A:H2'	1.70	0.56
33:BA:1485:U:H2'	33:BA:1486:U:C6	2.41	0.56
33:BA:1212:G:O2'	33:BA:1236:G:N2	2.38	0.56
5:AE:110:MET:HG3	5:AE:139:THR:HG21	1.88	0.56
24:B0:63:ASP:N	24:B0:63:ASP:OD1	2.37	0.56
1:AA:537:G:H5''	12:AL:109:ARG:NH1	2.19	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
11:AK:63:GLN:HG3	11:AK:98:ALA:HB2	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:721:G:H4'	1:AA:722:G:O5'	2.05	0.56
4:AD:73:ASN:HA	4:AD:76:LYS:HE2	1.86	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
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
11:AK:22:ILE:HG22	11:AK:31:VAL:HG22	1.86	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
1:AA:82:G:N2	1:AA:88:U:HO2'	2.04	0.56
33:BA:704:G:H1'	33:BA:727:A:N6	2.20	0.56
23:AW:108:CYS:HA	23:AW:135:THR:HG23	1.88	0.56
33:BA:1819:A:H5''	35:BC:159:THR:HG21	1.87	0.56
3:AC:142:ARG:HB3	3:AC:143:LEU:HD13	1.87	0.56
1:AA:35:G:O2'	12:AL:114:SER:O	2.19	0.56
1:AA:202:G:H21	1:AA:466:A:H61	1.53	0.56
33:BA:2377:A:O2'	48:BS:117:PHE:O	2.19	0.56
4:AD:149:LYS:NZ	4:AD:176:LYS:O	2.38	0.56
33:BA:974:G:O2'	33:BA:975:A:OP2	2.23	0.56
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
12:AL:43:LYS:HD3	12:AL:43:LYS:H	1.70	0.56
33:BA:2804:U:H2'	33:BA:2805:C:C6	2.40	0.56
33:BA:1392:A:H61	53:BX:18:GLU:HG2	1.71	0.56
1:AA:412:A:H4'	1:AA:413:G:O5'	2.05	0.56
36:BD:108:ASP:HA	36:BD:173:GLN:HA	1.87	0.56
33:BA:1327:A:H2'	33:BA:1328:A:O4'	2.05	0.56
33:BA:864:G:C6	33:BA:865:C:N4	2.74	0.56
33:BA:372:G:O2'	33:BA:373:U:P	2.63	0.56
33:BA:2345:G:H4'	33:BA:2346:A:H5''	1.87	0.56
33:BA:2209:G:C2	33:BA:2216:G:C2	2.92	0.56
33:BA:1657:U:H2'	33:BA:1658:C:H6	1.70	0.56
23:AW:428:PHE:HB2	23:AW:437:ILE:HB	1.87	0.56
38:BF:128:SER:OG	38:BF:154:THR:HB	2.06	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
33:BA:1914:C:C6	33:BA:1915:U:C6	2.93	0.56
12:AL:24:GLU:CD	12:AL:29:LYS:HZ1	2.10	0.56
23:AW:525:GLN:N	23:AW:525:GLN:HE21	2.04	0.56
33:BA:1029:A:OP1	46:BQ:127:LYS:NZ	2.27	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1792:G:O2'	33:BA:1830:C:OP1	2.23	0.56
33:BA:1084:A:C2	33:BA:1105:U:H1'	2.41	0.55
9:AI:22:PRO:HA	9:AI:60:LEU:HA	1.88	0.55
1:AA:115:G:H4'	1:AA:116:A:O5'	2.06	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
33:BA:2591:C:P	35:BC:237:ARG:HG3	2.46	0.55
23:AW:59:TRP:NE1	23:AW:69:SER:CB	2.69	0.55
1:AA:408:A:OP1	4:AD:109:THR:HG21	2.07	0.55
35:BC:173:LEU:HD22	35:BC:183:VAL:HG21	1.88	0.55
1:AA:972:C:OP2	10:AJ:59:LYS:HE3	2.05	0.55
1:AA:950:U:H2'	1:AA:951:G:C8	2.41	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
6:AF:22:ILE:HD11	6:AF:60:VAL:HG11	1.89	0.55
42:BJ:21:GLU:HB3	42:BK:7:ILE:HD11	1.88	0.55
1:AA:624:C:H4'	16:AP:10:GLY:O	2.07	0.55
2:AB:82:ALA:HB3	2:AB:217:ALA:HB1	1.88	0.55
29:B5:7:LYS:HA	29:B5:23:THR:HG22	1.88	0.55
1:AA:376:G:H5''	16:AP:5:ARG:HB2	1.87	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
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
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
33:BA:1316:U:H2'	33:BA:1317:G:C8	2.41	0.55
2:AB:20:ARG:CZ	2:AB:20:ARG:HA	2.36	0.55
33:BA:1794:A:H2'	33:BA:1795:C:C6	2.41	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:659:G:H4'	37:BE:95:LYS:HB3	1.87	0.55
33:BA:645:C:N4	33:BA:2350:C:O2'	2.38	0.55
33:BA:247:G:H4'	33:BA:386:G:C5	2.41	0.55
41:BI:27:LEU:HD21	41:BI:34:ILE:HG23	1.88	0.55
23:AW:399:ARG:CZ	23:AW:445:GLN:HB3	2.37	0.55
1:AA:1361:G:N2	1:AA:1362:A:N7	2.54	0.55
23:AW:472:ARG:HG3	23:AW:504:ILE:HA	1.89	0.55
33:BA:2311:A:H5'	33:BA:2312:U:OP2	2.06	0.55
36:BD:118:PHE:C	36:BD:120:GLY:H	2.09	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
53:BX:36:LYS:O	53:BX:81:LYS:HD2	2.07	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
1:AA:1125:U:C4	1:AA:1127:G:C4	2.95	0.55
33:BA:1444:G:H2'	33:BA:1445:G:H8	1.71	0.55
33:BA:2485:G:H5''	46:BQ:45:GLN:HE21	1.71	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
1:AA:591:U:H2'	1:AA:592:G:C8	2.42	0.55
33:BA:645:C:H2'	33:BA:645:C:O2	2.06	0.55
1:AA:1437:A:H5''	20:AT:28:ARG:NH1	2.21	0.55
44:BO:39:ILE:HG23	44:BO:41:ILE:HD13	1.89	0.55
1:AA:714:G:H2'	1:AA:715:A:C8	2.41	0.55
33:BA:634:C:H2'	33:BA:635:C:C6	2.42	0.55
26:B2:41:HIS:CE1	33:BA:96:C:H4'	2.41	0.55
25:B1:31:ASN:CG	25:B1:33:HIS:HE2	2.07	0.55
36:BD:184:ARG:NH1	49:BT:6:GLN:HE22	2.05	0.55
33:BA:167:A:H2'	33:BA:168:G:O4'	2.07	0.55
33:BA:1757:A:H3'	33:BA:1758:U:C5'	2.37	0.55
7:AG:12:LEU:HD22	7:AG:12:LEU:H	1.72	0.55
17:AQ:45:VAL:HG11	17:AQ:60:ILE:HD12	1.88	0.55
33:BA:2147:A:H3'	33:BA:2148:G: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
43:BN:36:LEU:O	43:BN:121:LYS:NZ	2.37	0.55
33:BA:1420:A:H5'	33:BA:1421:G:OP2	2.07	0.55
31:B7:12:ARG:NH1	33:BA:250:G:OP2	2.37	0.55
27:B3:46:MET:O	27:B3:50:VAL:HG22	2.07	0.55
55:BZ:9:ARG:HG2	55:BZ:41:GLU:HB3	1.89	0.55
23:AW:490:GLU:HA	23:AW:493:LEU:HD12	1.89	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
25:B1:73:ARG:HD2	25:B1:75:GLU:HG3	1.88	0.54
1:AA:507:C:H3'	1:AA:508:U:H5''	1.88	0.54
44:BO:105:ARG:H	44:BO:105:ARG:HD3	1.72	0.54
53:BX:29:THR:CA	53:BX:86:THR:HA	2.34	0.54
23:AW:472:ARG:HA	23:AW:473:TRP:HB2	1.89	0.54
33:BA:704:G:H2'	33:BA:726:G:N2	2.20	0.54
33:BA:1654:A:O2'	36:BD:118:PHE:CG	2.58	0.54
33:BA:580:U:H2'	33:BA:581:C:H6	1.72	0.54
4:AD:63:ILE:HG23	4:AD:64:TYR:HD1	1.71	0.54
1:AA:501:C:H2'	1:AA:502:A:H8	1.72	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1444:G:H2'	33:BA:1445:G:C8	2.42	0.54
24:B0:47:GLY:HA3	24:B0:80:SER:HB3	1.88	0.54
4:AD:123:MET:HB3	4:AD:128:VAL:HA	1.87	0.54
3:AC:19:SER:HB2	3:AC:39:ARG:NH2	2.21	0.54
23:AW:432:SER:O	23:AW:434:ASN:N	2.34	0.54
1:AA:441:A:H1'	1:AA:497:G:N2	2.22	0.54
33:BA:2149:U:H3'	33:BA:2150:C:O4'	2.07	0.54
39:BG:83:THR:HA	39:BG:84:LYS:NZ	2.23	0.54
23:AW:473:TRP:HA	23:AW:524:HIS:O	2.08	0.54
2:AB:95:TRP:CZ2	2:AB:100:LEU:HD23	2.43	0.54
33:BA:1024:G:C8	33:BA:1025:G:H2'	2.41	0.54
23:AW:479:ALA:O	23:AW:481:LYS:N	2.39	0.54
36:BD:40:LEU:HD12	36:BD:40:LEU:H	1.72	0.54
14:AN:98:ALA:HB1	14:AN:100:TRP:HZ3	1.72	0.54
33:BA:572:A:H5''	33:BA:573:U:OP2	2.07	0.54
33:BA:2857:G:N2	33:BA:2860:A:OP2	2.39	0.54
12:AL:78:VAL:HB	23:AW:407:LEU:HD12	1.90	0.54
24:B0:16:GLU:HG3	33:BA:2356:U:H4'	1.89	0.54
36:BD:68:PHE:HB3	36:BD:73:VAL:HG12	1.90	0.54
33:BA:2052:A:C8	36:BD:146:ILE:HD11	2.42	0.54
44:BO:18:ARG:HB2	44:BO:45:GLU:HG2	1.90	0.54
2:AB:71:THR:HG21	2:AB:94:ARG:HD3	1.88	0.54
17:AQ:46:HIS:HA	17:AQ:70:LYS:HE3	1.89	0.54
55:BZ:80:HIS:HB3	55:BZ:83:LYS:O	2.08	0.54
33:BA:2064:C:H2'	33:BA:2065:C:C6	2.43	0.54
33:BA:251:A:OP1	45:BP:58:TYR:OH	2.20	0.54
50:BU:63:ARG:HH12	50:BU:96:ASP:HB2	1.71	0.54
33:BA:1236:G:O2'	33:BA:1237:A:H8	1.91	0.54
33:BA:691:C:H4'	35:BC:42:ARG:HH12	1.72	0.54
3:AC:146:LYS:HB2	3:AC:202:PHE:CD2	2.43	0.54
34:BB:112:G:H2'	34:BB:113:C:H6	1.72	0.54
33:BA:404:A:H1'	33:BA:405:U:OP2	2.08	0.54
40:BH:25:ALA:HB3	40:BH:85:SER:HG	1.64	0.54
40:BH:17:GLU:HG2	40:BH:88:HIS:CE1	2.42	0.54
40:BH:57:ASN:C	40:BH:59:LEU:N	2.61	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
1:AA:892:A:O2'	1:AA:1415:G:H4'	2.07	0.54
33:BA:1970:A:H5'	33:BA:1972:G:H1'	1.89	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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1370:G:O5'	9:AI:110:VAL:HG21	2.08	0.54
23:AW:91:GLY:O	23:AW:92:HIS:HB2	2.08	0.54
33:BA:923:G:H2'	33:BA:924:G:C8	2.42	0.54
3:AC:13:ILE:O	3:AC:15:LYS:N	2.40	0.54
38:BF:35:LEU:HA	38:BF:153:ILE:HA	1.90	0.54
34:BB:66:A:OP2	34:BB:108:A:N6	2.40	0.54
53:BX:43:ILE:HD11	53:BX:58:VAL:HG21	1.88	0.54
1:AA:404:G:H2'	1:AA:405:U:H6	1.72	0.54
36:BD:4:LEU:HD23	36:BD:29:VAL:HG11	1.89	0.54
47:BR:85:PRO:HA	47:BR:88:ALA:HB2	1.90	0.54
33:BA:307:G:N2	33:BA:309:A:H3'	2.22	0.54
35:BC:76:VAL:HG22	35:BC:96:LYS:HZ2	1.71	0.54
40:BH:28:ALA:H	40:BH:111:ALA:HB2	1.70	0.54
33:BA:611:C:H2'	33:BA:612:G:O4'	2.08	0.54
40:BH:32:GLY:HA2	40:BH:108:VAL:HG22	1.89	0.54
12:AL:78:VAL:HG21	23:AW:407:LEU:CG	2.37	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
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
23:AW:15:THR:OG1	23:AW:362:GLY:O	2.13	0.54
5:AE:56:PRO:O	5:AE:59:ILE:HG13	2.07	0.54
4:AD:143:SER:HB3	4:AD:178:GLU:HB2	1.90	0.54
33:BA:692:C:H2'	33:BA:693:A:C8	2.43	0.54
1:AA:720:C:H5''	18:AR:40:PRO:HB3	1.90	0.54
37:BE:124:PHE:O	37:BE:125:SER:HB2	2.08	0.54
1:AA:235:C:H1'	17:AQ:62:GLU:OE2	2.08	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
51:BV:10:LYS:NZ	51:BV:23:GLU:OE1	2.38	0.54
33:BA:1061:U:H6	41:BI:9:LYS:HG3	1.73	0.54
36:BD:146:ILE:HA	36:BD:159:LYS:HE2	1.89	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:1252:G:H1'	50:BU:32:ARG:HH22	1.71	0.54
45:BP:96:LYS:HD3	45:BP:103:ILE:HA	1.90	0.54
1:AA:514:C:H2'	1:AA:515:G:C8	2.42	0.54
33:BA:1270:C:H5''	33:BA:1271:G:H5'	1.89	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
48:BS:49:VAL:HG21	48:BS:82:ALA:HA	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:AS:62:THR:HG22	19:AS:63:ASP:H	1.72	0.54
50:BU:91:ARG:NH2	50:BU:93:ILE:HG12	2.20	0.54
23:AW:472:ARG:HG3	23:AW:504:ILE:N	2.22	0.54
35:BC:66:PHE:HB3	35:BC:150:GLY:O	2.08	0.54
33:BA:140:C:O2	33:BA:140:C:H2'	2.07	0.54
1:AA:793:U:O4	1:AA:1517:G:H8	1.90	0.54
1:AA:369:G:N2	1:AA:393:A:H1'	2.23	0.54
33:BA:1656:C:H2'	33:BA:1657:U:H6	1.73	0.54
9:AI:24:ASN:HA	9:AI:58:GLU:O	2.08	0.54
23:AW:347:THR:O	23:AW:354:SER:HB3	2.08	0.54
23:AW:129:VAL:O	23:AW:132:LEU:HB2	2.09	0.54
47:BR:36:THR:OG1	47:BR:37:THR:N	2.40	0.54
1:AA:1190:G:H5'	3:AC:175:HIS:NE2	2.23	0.54
33:BA:2415:G:H4'	45:BP:66:PHE:HB2	1.89	0.54
23:AW:310:LYS:O	23:AW:311:HIS:ND1	2.41	0.54
38:BF:134:GLN:C	38:BF:136:ILE:H	2.10	0.53
1:AA:680:C:H2'	1:AA:681:A:C8	2.43	0.53
33:BA:993:G:OP2	50:BU:50:ARG:NH2	2.41	0.53
51:BV:2:TYR:H	51:BV:42:ALA:HB3	1.73	0.53
47:BR:24:MET:HG2	47:BR:44:LEU:HD22	1.89	0.53
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
51:BV:38:VAL:HG22	51:BV:54:VAL:HG22	1.90	0.53
14:AN:63:CYS:HB2	14:AN:79:SER:OG	2.07	0.53
33:BA:215:G:C4'	33:BA:216:A:H4'	2.38	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:2322:A:H2'	33:BA:2323:G:O4'	2.08	0.53
1:AA:129:A:O2'	1:AA:130:A:H8	1.91	0.53
33:BA:2276:G:OP2	46:BQ:85:GLY:N	2.40	0.53
41:BI:32:VAL:HG22	41:BI:66:PHE:CD2	2.44	0.53
33:BA:630:G:N2	33:BA:633:A:OP2	2.37	0.53
12:AL:30:ARG:HH11	23:AW:408:LYS:CG	2.19	0.53
1:AA:1493:A:C2'	1:AA:1494:G:OP1	2.57	0.53
23:AW:49:ARG:NH2	33:BA:2664:G:O6	2.41	0.53
1:AA:1241:G:H2'	1:AA:1242:G:C8	2.40	0.53
31:B7:12:ARG:HD3	45:BP:61:LEU:O	2.08	0.53
11:AK:108:ASN:HB3	21:AU:6:ARG:HG2	1.89	0.53
20:AT:66:ILE:O	20:AT:70:LYS:HB3	2.08	0.53
20:AT:8:LYS:O	20:AT:12:GLN:HB2	2.08	0.53
35:BC:251:THR:HG22	35:BC:252:LYS:H	1.73	0.53
31:B7:54:LEU:HG	31:B7:58:ILE:HD11	1.90	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AW:26:LYS:O	23:AW:29:ILE:HG22	2.09	0.53
33:BA:2046:G:H2'	33:BA:2047:C:H6	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
33:BA:324:A:N6	33:BA:338:G:O2'	2.39	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
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
6:AF:26:THR:HG22	6:AF:36:ILE:HG21	1.91	0.53
36:BD:125:TRP:CG	36:BD:160:LYS:HB3	2.44	0.53
46:BQ:74:THR:HG21	46:BQ:86:LYS:HE3	1.89	0.53
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
40:BH:144:LYS:HB2	40:BH:148:ALA:H	1.74	0.53
1:AA:908:A:H2'	1:AA:909:A:C8	2.44	0.53
33:BA:1225:G:C2	33:BA:1226:A:C2	2.97	0.53
44:BO:113:MET:O	44:BO:116:ILE:HG13	2.09	0.53
45:BP:30:THR:O	45:BP:33:ARG:HG2	2.09	0.53
42:BJ:15:SER:HB3	42:BM:11:VAL:HG12	1.90	0.53
49:BT:33:GLU:HB2	49:BT:38:ARG:HH11	1.73	0.53
33:BA:1914:C:C4	33:BA:1915:U:C4	2.96	0.53
49:BT:50:ARG:CD	49:BT:56:SER:HB3	2.29	0.53
23:AW:45:THR:N	23:AW:56:LYS:O	2.41	0.53
53:BX:83:ALA:HB1	53:BX:85:VAL:HG23	1.91	0.53
23:AW:522:GLN:HB2	23:AW:523:PHE:CB	2.37	0.53
33:BA:2060:A:H3'	37:BE:63:LYS:NZ	2.21	0.53
50:BU:86:SER:HB2	51:BV:50:GLY:O	2.09	0.53
21:AU:33:ARG:HE	21:AU:34:ARG:HG3	1.74	0.53
33:BA:2052:A:OP1	36:BD:145:SER:HA	2.08	0.53
1:AA:1237:C:H3'	1:AA:1238:A:H5'	1.90	0.53
33:BA:2224:G:H4'	33:BA:2226:C:C2	2.43	0.53
12:AL:34:THR:HG22	12:AL:35:ARG:HG2	1.89	0.53
35:BC:118:GLY:O	35:BC:129:LEU:HD23	2.09	0.53
18:AR:57:ALA:HA	18:AR:60:ARG:HD3	1.91	0.53
31:B7:3:ILE:HD11	33:BA:592:A:N3	2.23	0.53
33:BA:1056:G:H4'	40:BH:34:THR:CG2	2.38	0.53
40:BH:44:ALA:HA	40:BH:48:ALA:HB3	1.91	0.53
39:BG:84:LYS:CB	39:BG:132:LEU:H	2.21	0.53
9:AI:83:THR:HG21	9:AI:102:PHE:HB3	1.90	0.53
51:BV:66:HIS:CD2	51:BV:66:HIS:H	2.26	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1036:A:H2'	1:AA:1037:C:C4	2.44	0.53
27:B3:11:SER:OG	27:B3:13:ILE:HG12	2.09	0.53
33:BA:1665:A:H5''	44:BO:66:LYS:HG3	1.90	0.53
21:AU:52:VAL:HG13	21:AU:53:LYS:H	1.73	0.53
33:BA:2329:U:H2'	33:BA:2330:G:C8	2.43	0.53
33:BA:686:U:H2'	33:BA:788:A:N1	2.24	0.53
27:B3:9:THR:HB	27:B3:53:MET:O	2.09	0.53
1:AA:373:A:H1'	1:AA:481:G:H1'	1.90	0.53
33:BA:1918:A:O2'	33:BA:1920:C:N4	2.42	0.53
1:AA:978:A:HO2'	1:AA:1322:C:H5	1.55	0.53
33:BA:1279:G:H4'	47:BR:31:HIS:CD2	2.43	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
36:BD:106:LYS:HB3	36:BD:206:ALA:CB	2.37	0.53
1:AA:380:G:C2	1:AA:384:G:C6	2.97	0.53
38:BF:56:LEU:HD13	38:BF:88:VAL:HG23	1.90	0.53
33:BA:859:G:O2'	33:BA:860:U:P	2.67	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
36:BD:175:LEU:HD22	36:BD:190:LYS:O	2.09	0.53
33:BA:544:C:H5'	33:BA:545:U:OP2	2.09	0.53
1:AA:564:C:C4	1:AA:565:U:C4	2.97	0.53
40:BH:57:ASN:O	40:BH:59:LEU:N	2.42	0.52
23:AW:472:ARG:HG3	23:AW:504:ILE:CA	2.39	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
1:AA:812:G:HO2'	1:AA:813:U:P	2.28	0.52
35:BC:159:THR:O	35:BC:194:VAL:HG12	2.08	0.52
1:AA:514:C:H2'	1:AA:515:G:H8	1.74	0.52
32:B8:4:ARG:HB2	33:BA:2466:C:OP1	2.09	0.52
47:BR:73:ASN:HA	47:BR:76:VAL:HG12	1.91	0.52
1:AA:816:A:OP1	1:AA:1526:G:O2'	2.21	0.52
1:AA:254:G:OP1	17:AQ:67:SER:OG	2.24	0.52
1:AA:1123:U:O2'	10:AJ:39:PRO:O	2.26	0.52
23:AW:408:LYS:HB3	23:AW:409:GLN:O	2.08	0.52
33:BA:1165:A:H2'	33:BA:1166:G:C8	2.40	0.52
54:BY:6:ARG:O	54:BY:24:VAL:HB	2.10	0.52
33:BA:394:C:H2'	33:BA:395:U:C6	2.44	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
36:BD:114:LYS:HE3	36:BD:114:LYS:O	2.08	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:755:U:H2'	33:BA:756:A:C8	2.44	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
33:BA:2104:C:H42	33:BA:2185:U:H3	1.58	0.52
1:AA:1347:G:O2'	1:AA:1348:U:P	2.67	0.52
48:BS:3:LYS:HG3	48:BS:4:LYS:H	1.75	0.52
33:BA:1962:C:O2'	33:BA:1964:G:OP2	2.26	0.52
33:BA:2485:G:H5''	46:BQ:45:GLN:NE2	2.24	0.52
49:BT:61:ARG:HG2	49:BT:70:GLU:HG2	1.89	0.52
1:AA:1257:A:H4'	1:AA:1258:G:OP2	2.10	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
34:BB:24:G:O2'	34:BB:27:C:N4	2.42	0.52
33:BA:559:G:OP1	43:BN:111:LYS:HE3	2.10	0.52
1:AA:1347:G:H22	1:AA:1374:A:P	2.32	0.52
33:BA:1022:G:H22	33:BA:1142:A:H2	1.51	0.52
1:AA:404:G:H4'	1:AA:439:U:H3	1.75	0.52
33:BA:2325:G:C6	33:BA:2326:C:N4	2.77	0.52
1:AA:926:G:N2	22:AV:15:A:H4'	2.24	0.52
38:BF:34:THR:HG22	38:BF:89:THR:HA	1.90	0.52
33:BA:1266:G:O2'	33:BA:2012:G:N1	2.38	0.52
33:BA:171:U:H2'	33:BA:172:A:H8	1.74	0.52
25:B1:16:ASN:HD22	33:BA:2081:U:H5''	1.75	0.52
2:AB:125:PHE:HD2	2:AB:125:PHE:N	2.07	0.52
33:BA:1095:A:C2	41:BI:29:GLN:HB3	2.44	0.52
33:BA:2848:G:H2'	33:BA:2867:G:N2	2.23	0.52
33:BA:2046:G:H2'	33:BA:2047:C:C6	2.45	0.52
1:AA:1227:A:O2'	13:AM:114:PRO:HG2	2.09	0.52
47:BR:48:VAL:HA	47:BR:51:LEU:HD22	1.91	0.52
11:AK:57:SER:O	11:AK:90:PRO:HG3	2.09	0.52
39:BG:106:LEU:HD13	39:BG:151:ARG:HB2	1.92	0.52
33:BA:2013:A:H4'	52:BW:96:ILE:HG22	1.92	0.52
33:BA:974:G:C6	33:BA:989:G:C6	2.98	0.52
24:B0:23:LYS:HE2	33:BA:923:G:N3	2.24	0.52
39:BG:84:LYS:HB3	39:BG:132:LEU:O	2.10	0.52
37:BE:60:TRP:CZ2	37:BE:70:SER:HB3	2.44	0.52
23:AW:499:ASP:O	23:AW:500:ASN:HB3	2.10	0.52
6:AF:3:HIS:HB3	6:AF:95:ALA:HB2	1.92	0.52
51:BV:66:HIS:HB3	51:BV:94:THR:HG22	1.91	0.52
33:BA:2683:C:O2	44:BO:70:ARG:NH2	2.33	0.52
10:AJ:12:ALA:HB3	10:AJ:18:ILE:HG12	1.92	0.52
40:BH:144:LYS:HD2	40:BH:148:ALA:HB2	1.91	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:116:LEU:HB3	4:AD:121:ALA:HB3	1.92	0.52
33:BA:1539:U:H2'	33:BA:1540:G:H8	1.75	0.52
39:BG:3:VAL:O	39:BG:68:ARG:HG3	2.10	0.52
33:BA:1060:U:O4'	33:BA:1062:G:H5'	2.09	0.52
1:AA:1225:A:N3	1:AA:1225:A:H2'	2.23	0.52
23:AW:521:VAL:HG22	23:AW:522:GLN:HG2	1.92	0.52
50:BU:86:SER:O	51:BV:51:VAL:HA	2.09	0.52
1:AA:77:A:H62	1:AA:90:C:N4	2.06	0.52
1:AA:1145:A:O2'	1:AA:1146:A:O5'	2.28	0.52
34:BB:112:G:H2'	34:BB:113:C:C6	2.45	0.52
10:AJ:36:VAL:HG22	10:AJ:76:ILE:HG12	1.92	0.52
25:B1:7:THR:HG21	25:B1:53:LYS:HD3	1.91	0.52
36:BD:25:THR:HG21	36:BD:193:VAL:HG22	1.92	0.52
1:AA:109:A:C6	1:AA:326:G:C6	2.98	0.52
4:AD:84:ASN:HB3	4:AD:87:GLU:HG2	1.92	0.52
3:AC:159:ALA:HB1	3:AC:161:ILE:HD13	1.92	0.52
7:AG:71:THR:HG22	7:AG:72:VAL:HG13	1.92	0.52
34:BB:37:C:C5	34:BB:38:C:C4	2.98	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
26:B2:46:VAL:HA	26:B2:49:ASP:HB2	1.91	0.52
25:B1:76:LYS:HG3	25:B1:77:TYR:H	1.75	0.52
33:BA:483:A:C8	54:BY:44:HIS:CD2	2.97	0.52
10:AJ:7:ARG:HA	10:AJ:75:ASP:HA	1.91	0.52
1:AA:579:A:O2'	15:AO:53:ARG:NH1	2.42	0.52
50:BU:60:TRP:O	50:BU:64:ILE:HG12	2.10	0.52
40:BH:7:ASP:O	40:BH:11:ILE:HG12	2.09	0.52
51:BV:4:VAL:HG23	51:BV:39:LEU:HG	1.92	0.52
33:BA:2105:U:C4	33:BA:2106:U:C4	2.98	0.52
35:BC:244:VAL:HG12	35:BC:250:GLN:HA	1.92	0.52
42:BJ:26:MET:HE2	42:BJ:29:LYS:HD3	1.91	0.52
33:BA:1141:U:H4'	33:BA:1142:A:O4'	2.10	0.52
1:AA:664:G:H22	1:AA:741:G:H1	1.58	0.52
40:BH:129:LEU:HB3	40:BH:132:TYR:CE1	2.44	0.52
5:AE:22:LYS:HB3	5:AE:29:ILE:HG23	1.92	0.52
40:BH:102:ALA:O	40:BH:107:GLU:HB2	2.09	0.52
7:AG:24:LYS:O	7:AG:28:ILE:HG12	2.10	0.52
33:BA:2339:C:H2'	33:BA:2340:A:C8	2.45	0.52
33:BA:270:A:N1	33:BA:369:U:O2'	2.34	0.52
38:BF:111:ARG:NH1	38:BF:133:GLU:OE2	2.43	0.52
23:AW:59:TRP:CD2	23:AW:64:LYS:HD3	2.45	0.51
1:AA:1126:U:O2	1:AA:1126:U:H2'	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:955:U:H3	1:AA:1225:A:N6	2.07	0.51
23:AW:369:ASN:ND2	23:AW:373:ILE:H	2.08	0.51
21:AU:33:ARG:NE	21:AU:34:ARG:HG3	2.25	0.51
9:AI:9:GLY:N	9:AI:84:ARG:HH12	2.08	0.51
51:BV:20:VAL:HG22	51:BV:98:ILE:HD11	1.91	0.51
33:BA:834:G:C6	33:BA:835:C:C4	2.98	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
23:AW:290:GLU:HB2	23:AW:293:GLU:HG3	1.92	0.51
1:AA:607:A:H2'	1:AA:608:A:H8	1.75	0.51
33:BA:1313:U:H2'	33:BA:1610:A:C2	2.45	0.51
33:BA:1172:C:C4	33:BA:1173:U:H1'	2.45	0.51
38:BF:134:GLN:OE1	38:BF:134:GLN:N	2.38	0.51
23:AW:470:THR:HA	23:AW:471:ALA:HB3	1.91	0.51
36:BD:68:PHE:HB3	36:BD:73:VAL:HA	1.90	0.51
54:BY:94:PHE:HA	54:BY:101:THR:HA	1.92	0.51
10:AJ:10:LEU:HD11	10:AJ:98:VAL:HG12	1.92	0.51
34:BB:65:U:H3'	34:BB:108:A:N6	2.26	0.51
26:B2:49:ASP:O	26:B2:53:VAL:HG23	2.09	0.51
16:AP:35:ARG:HH21	16:AP:51:ARG:NH1	2.07	0.51
25:B1:60:LYS:HE3	33:BA:372:G:N9	2.25	0.51
33:BA:404:A:H4'	33:BA:405:U:O5'	2.10	0.51
12:AL:2:THR:HB	12:AL:5:GLN:HB2	1.92	0.51
41:BI:63:ASP:OD1	41:BI:63:ASP:N	2.43	0.51
35:BC:157:ALA:HB1	35:BC:196:ASN:HB3	1.92	0.51
1:AA:1479:C:H2'	1:AA:1480:A:H8	1.76	0.51
10:AJ:19:ASP:OD2	10:AJ:72:ARG:NH2	2.43	0.51
31:B7:22:LYS:HA	31:B7:47:ALA:O	2.10	0.51
1:AA:1510:C:C2	1:AA:1526:G:N2	2.78	0.51
23:AW:173:ILE:HG21	23:AW:219:VAL:HG11	1.93	0.51
1:AA:1096:C:H2'	1:AA:1097:C:C6	2.46	0.51
1:AA:71:A:H61	1:AA:99:C:H1'	1.76	0.51
33:BA:675:A:C4	33:BA:804:A:C2	2.99	0.51
24:B0:9:THR:HG23	24:B0:10:ARG:HD3	1.92	0.51
15:AO:70:LYS:HA	15:AO:77:TYR:HB2	1.91	0.51
36:BD:176:ASP:N	36:BD:176:ASP:OD2	2.42	0.51
33:BA:2233:U:H2'	33:BA:2234:G:H8	1.74	0.51
38:BF:37:MET:HG2	38:BF:151:LEU:HB3	1.91	0.51
1:AA:114:U:H2'	1:AA:115:G:C8	2.45	0.51
33:BA:1026:G:H2'	33:BA:1027:A:C8	2.45	0.51
33:BA:2267:A:H5''	33:BA:2268:A:H5'	1.92	0.51
33:BA:320:A:H4'	33:BA:322:A:N7	2.26	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:AQ:15:LYS:HZ1	17:AQ:17:GLU:HB2	1.75	0.51
43:BN:74:TYR:HB2	43:BN:87:ALA:O	2.10	0.51
33:BA:1838:C:H4'	33:BA:1839:G:C8	2.46	0.51
12:AL:78:VAL:CB	23:AW:407:LEU:HD12	2.40	0.51
12:AL:41:PRO:HA	12:AL:89:LEU:HD13	1.92	0.51
1:AA:1513:A:H2'	1:AA:1514:G:H8	1.74	0.51
13:AM:105:ALA:HB3	13:AM:109:LYS:HD2	1.93	0.51
1:AA:1192:C:OP2	3:AC:3:LYS:NZ	2.33	0.51
29:B5:7:LYS:HE3	31:B7:33:THR:HG21	1.93	0.51
2:AB:125:PHE:N	2:AB:125:PHE:CD2	2.78	0.51
23:AW:290:GLU:N	23:AW:293:GLU:OE2	2.44	0.51
36:BD:97:SER:OG	36:BD:98:VAL:N	2.43	0.51
12:AL:23:LEU:C	12:AL:25:ALA:H	2.13	0.51
35:BC:144:GLU:HB2	35:BC:187:CYS:HB3	1.91	0.51
33:BA:2747:G:O6	33:BA:2755:C:H5''	2.10	0.51
28:B4:47:TYR:HA	28:B4:52:LYS:HA	1.93	0.51
34:BB:66:A:H61	34:BB:107:G:H2'	1.75	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
1:AA:1203:C:H2'	1:AA:1204:A:C8	2.45	0.51
1:AA:216:U:H2'	1:AA:217:C:C6	2.46	0.51
1:AA:129:A:HO2'	1:AA:130:A:H8	1.57	0.51
33:BA:1219:U:H2'	33:BA:1220:G:C8	2.45	0.51
33:BA:953:G:H5''	46:BQ:16:ARG:NH1	2.26	0.51
33:BA:601:C:O2'	33:BA:605:G:OP1	2.23	0.51
16:AP:61:VAL:O	16:AP:64:GLY:N	2.42	0.51
39:BG:70:LEU:O	39:BG:74:MET:HG3	2.10	0.51
55:BZ:61:LEU:HD11	55:BZ:74:ALA:HB2	1.93	0.51
50:BU:91:ARG:HH11	51:BV:10:LYS:HB3	1.76	0.51
40:BH:58:THR:C	40:BH:60:LEU:N	2.63	0.51
33:BA:883:G:O3'	33:BA:896:A:N6	2.40	0.51
1:AA:1239:A:H1'	1:AA:1241:G:C4	2.45	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
3:AC:32:LEU:HD21	14:AN:92:ILE:HG12	1.92	0.51
55:BZ:72:VAL:HG21	55:BZ:91:PHE:HB3	1.92	0.51
4:AD:71:PHE:O	4:AD:74:TYR:HB2	2.11	0.51
1:AA:1005:A:H2'	1:AA:1006:G:O4'	2.11	0.51
1:AA:403:C:H2'	1:AA:404:G:H8	1.76	0.51
1:AA:1314:C:N4	19:AS:3:SER:O	2.40	0.51
38:BF:10:GLU:O	38:BF:12:VAL:N	2.31	0.51
1:AA:1437:A:H2'	1:AA:1438:G:H8	1.76	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
41:BI:72:THR:HG21	41:BI:112:LYS:HB3	1.92	0.51
25:B1:5:GLN:HG3	25:B1:49:ARG:O	2.10	0.51
1:AA:976:G:OP1	14:AN:70:HIS:ND1	2.31	0.51
23:AW:64:LYS:HG2	23:AW:70:ILE:HB	1.92	0.51
33:BA:880:G:O6	33:BA:898:C:N3	2.44	0.51
34:BB:60:C:H2'	34:BB:61:G:H8	1.76	0.51
10:AJ:57:VAL:HG22	10:AJ:58:ASN:H	1.76	0.51
33:BA:955:U:H5''	46:BQ:86:LYS:HD2	1.91	0.51
33:BA:629:G:N3	33:BA:639:U:O2'	2.42	0.51
33:BA:2134:A:O2'	33:BA:2135:A:H8	1.93	0.51
12:AL:34:THR:N	12:AL:53:ARG:O	2.43	0.51
34:BB:87:U:H5'	34:BB:88:C:OP2	2.10	0.51
3:AC:5:HIS:ND1	14:AN:88:MET:HB3	2.25	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
28:B4:39:ARG:HG3	33:BA:2884:U:O4	2.10	0.51
7:AG:30:MET:SD	7:AG:35:LYS:HB2	2.50	0.51
23:AW:11:ALA:O	23:AW:14:ARG:NH2	2.43	0.51
33:BA:587:C:H5'	37:BE:85:PHE:CE2	2.46	0.51
36:BD:122:VAL:HA	36:BD:127:PHE:N	2.20	0.51
23:AW:437:ILE:HD12	23:AW:504:ILE:HD13	1.92	0.51
40:BH:23:LEU:HG	40:BH:24:SER:H	1.76	0.51
5:AE:153:ALA:HA	5:AE:156:ARG:HB2	1.92	0.51
33:BA:832:U:H2'	33:BA:833:A:C8	2.46	0.51
3:AC:6:PRO:HB3	3:AC:174:LEU:CD1	2.41	0.51
24:B0:71:LYS:HB3	24:B0:73:PRO:HD2	1.93	0.51
1:AA:1354:U:H2'	1:AA:1355:G:C8	2.46	0.51
21:AU:24:LYS:HA	21:AU:28:LEU:HD12	1.93	0.51
33:BA:2470:G:OP1	46:BQ:55:ARG:NH1	2.44	0.51
24:B0:39:GLN:C	24:B0:41:GLY:N	2.64	0.51
33:BA:2728:U:H5'	44:BO:70:ARG:NH2	2.26	0.51
33:BA:1181:U:H2'	33:BA:1182:G:H8	1.75	0.51
8:AH:45:ILE:HD13	8:AH:60:LEU:HD22	1.92	0.51
40:BH:136:ILE:HA	40:BH:139:LEU:HD12	1.93	0.51
33:BA:1930:G:H22	33:BA:1969:A:P	2.34	0.51
1:AA:1308:U:OP1	13:AM:96:VAL:N	2.33	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:742:A:H2'	33:BA:743:A:C8	2.46	0.51
33:BA:1056:G:C8	33:BA:1056:G:O5'	2.59	0.50
24:B0:23:LYS:HZ3	33:BA:923:G:H21	1.57	0.50
33:BA:884:U:H6	33:BA:884:U:O5'	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:B0:17:ALA:HA	24:B0:35:ILE:HG23	1.92	0.50
51:BV:39:LEU:HA	51:BV:49:ILE:HG21	1.93	0.50
34:BB:40:U:N3	34:BB:44:G:OP2	2.42	0.50
35:BC:166:ARG:HB3	35:BC:171:VAL:HG22	1.93	0.50
33:BA:1082:U:C5'	41:BI:118:GLY:HA2	2.40	0.50
32:B8:10:LEU:HD12	32:B8:33:HIS:CD2	2.46	0.50
11:AK:93:GLU:OE2	11:AK:97:ARG:NH2	2.44	0.50
40:BH:144:LYS:HB3	40:BH:147:SER:OG	2.11	0.50
2:AB:125:PHE:HD2	2:AB:125:PHE:H	1.59	0.50
1:AA:203:G:H1'	1:AA:465:A:H61	1.76	0.50
45:BP:130:GLY:O	45:BP:133:ALA:HB3	2.10	0.50
54:BY:90:LYS:HB2	54:BY:92:VAL:HG23	1.93	0.50
11:AK:86:LYS:HB2	11:AK:112:VAL:HG23	1.94	0.50
34:BB:91:C:H2'	34:BB:92:C:C6	2.46	0.50
1:AA:1180:A:OP2	9:AI:98:ARG:NH2	2.40	0.50
1:AA:362:G:N7	23:AW:408:LYS:NZ	2.59	0.50
33:BA:2148:G:H2'	33:BA:2149:U:O5'	2.10	0.50
39:BG:120:ILE:HD13	39:BG:143:VAL:HG21	1.93	0.50
33:BA:1657:U:H2'	33:BA:1658:C:C6	2.46	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
1:AA:692:U:H2'	1:AA:694:A:OP2	2.11	0.50
14:AN:19:TYR:O	14:AN:22:LYS:HB3	2.12	0.50
38:BF:41:GLU:HB2	38:BF:48:LEU:HD23	1.93	0.50
1:AA:818:G:O2'	1:AA:819:A:H5'	2.11	0.50
1:AA:672:U:H2'	1:AA:673:A:C8	2.46	0.50
1:AA:59:A:N6	1:AA:331:G:H1'	2.26	0.50
46:BQ:36:VAL:HG22	55:BZ:82:TYR:HB2	1.94	0.50
39:BG:94:ARG:HG3	39:BG:127:GLN:OE1	2.10	0.50
33:BA:2073:C:H5''	35:BC:227:VAL:HG12	1.92	0.50
5:AE:148:SER:CB	5:AE:151:MET:HB2	2.41	0.50
36:BD:172:VAL:HG12	36:BD:173:GLN:O	2.11	0.50
33:BA:864:G:O2'	33:BA:914:G:O6	2.29	0.50
36:BD:8:LYS:NZ	36:BD:193:VAL:O	2.35	0.50
1:AA:1478:U:H2'	1:AA:1479:C:C6	2.47	0.50
33:BA:479:A:H4'	33:BA:480:A:OP1	2.11	0.50
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.47	0.50
33:BA:974:G:C5	33:BA:989:G:C6	2.99	0.50
23:AW:64:LYS:HE2	23:AW:71:THR:N	2.21	0.50
1:AA:364:A:OP1	23:AW:410:LYS:NZ	2.45	0.50
33:BA:882:G:H2'	33:BA:883:G:C8	2.45	0.50
1:AA:1126:U:H1'	1:AA:1281:C:Cl'	2.42	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:BC:183:VAL:HG12	35:BC:187:CYS:SG	2.52	0.50
39:BG:102:ILE:O	39:BG:113:ASP:HA	2.12	0.50
33:BA:1047:G:HO2'	33:BA:1048:A:H8	1.58	0.50
38:BF:36:ASN:O	38:BF:151:LEU:HB2	2.11	0.50
33:BA:1252:G:H1'	50:BU:32:ARG:NH2	2.26	0.50
1:AA:857:C:H2'	1:AA:858:G:O4'	2.12	0.50
33:BA:2394:C:H5''	45:BP:63:LYS:HE2	1.94	0.50
12:AL:30:ARG:NH1	23:AW:408:LYS:CE	2.73	0.50
33:BA:974:G:C5	33:BA:989:G:C2	2.99	0.50
33:BA:2149:U:H6	33:BA:2149:U:H3'	1.76	0.50
33:BA:1106:G:H5''	40:BH:59:LEU:CD1	2.41	0.50
24:B0:40:ARG:H	24:B0:56:HIS:HB3	1.77	0.50
14:AN:52:ARG:HG3	14:AN:58:ARG:NH1	2.26	0.50
33:BA:1796:U:H2'	33:BA:1797:G:C8	2.47	0.50
28:B4:47:TYR:CE1	28:B4:52:LYS:HD3	2.47	0.50
2:AB:22:TRP:CG	2:AB:22:TRP:O	2.64	0.50
46:BQ:66:ARG:NH1	46:BQ:104:GLU:OE1	2.45	0.50
1:AA:376:G:H2'	1:AA:377:G:H8	1.76	0.50
20:AT:77:ASN:O	20:AT:81:GLN:HG3	2.12	0.50
41:BI:89:SER:HB3	41:BI:92:PRO:HG3	1.93	0.50
3:AC:69:THR:HG21	3:AC:75:VAL:HG21	1.92	0.50
1:AA:267:C:OP2	17:AQ:68:LYS:HD2	2.11	0.50
11:AK:17:ASP:HB3	11:AK:80:ASN:OD1	2.12	0.50
32:B8:29:ALA:O	39:BG:169:ARG:NH2	2.44	0.50
50:BU:60:TRP:CE2	50:BU:93:ILE:HB	2.46	0.50
1:AA:689:C:OP1	11:AK:45:THR:OG1	2.27	0.50
33:BA:2489:U:C4	33:BA:2490:G:C6	3.00	0.50
54:BY:24:VAL:HG22	54:BY:35:VAL:HG22	1.94	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:1269:A:H2'	33:BA:1270:C:C6	2.47	0.50
33:BA:2225:A:H4'	33:BA:2226:C:O5'	2.12	0.50
1:AA:1258:G:OP2	1:AA:1258:G:H8	1.95	0.50
47:BR:96:ARG:HH12	47:BR:116:VAL:HG21	1.77	0.50
33:BA:941:A:H2'	33:BA:942:G:C8	2.47	0.50
44:BO:16:ALA:HB2	44:BO:86:LEU:HD11	1.94	0.50
33:BA:2423:U:O2'	33:BA:2424:C:OP2	2.29	0.50
34:BB:93:C:H2'	34:BB:94:A:C8	2.47	0.50
33:BA:1533:C:H42	33:BA:1538:G:H1	1.60	0.50
49:BT:24:THR:HB	49:BT:87:ARG:HB3	1.93	0.50
1:AA:937:A:H1'	1:AA:1379:G:N2	2.26	0.50
33:BA:1061:U:O4	41:BI:11:GLN:NE2	2.45	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:42:G:C6	1:AA:43:C:C4	2.99	0.50
2:AB:163:ILE:HG13	2:AB:164:ASP:H	1.75	0.50
14:AN:53:ASP:OD2	14:AN:58:ARG:NH1	2.45	0.50
13:AM:106:ARG:HH21	13:AM:112:ARG:HB3	1.76	0.50
1:AA:926:G:H5''	1:AA:927:G:O5'	2.12	0.50
3:AC:59:PRO:HG2	3:AC:62:SER:HB3	1.92	0.50
23:AW:333:GLN:NE2	23:AW:372:THR:O	2.35	0.50
3:AC:166:TRP:H	3:AC:166:TRP:HE3	1.58	0.50
43:BN:64:VAL:HG11	43:BN:69:ARG:H	1.77	0.50
33:BA:1902:C:C5	33:BA:1903:G:C8	2.99	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
24:B0:40:ARG:HB3	33:BA:2336:A:H61	1.75	0.50
35:BC:149:LYS:HD3	35:BC:152:GLN:OE1	2.10	0.50
4:AD:61:ARG:NH2	4:AD:67:LEU:HD22	2.26	0.50
33:BA:2740:A:H2'	33:BA:2741:A:C8	2.47	0.50
33:BA:659:G:O5'	37:BE:95:LYS:HD3	2.11	0.50
33:BA:1567:G:H2'	35:BC:84:PRO:HG3	1.92	0.50
42:BM:13:ALA:O	42:BM:18:ASP:HB2	2.12	0.50
33:BA:1695:G:H1'	35:BC:7:PRO:O	2.12	0.50
33:BA:623:C:H2'	33:BA:624:C:C6	2.47	0.50
55:BZ:6:ALA:HB2	55:BZ:42:LEU:HD23	1.94	0.50
16:AP:4:ILE:O	16:AP:71:VAL:HG21	2.12	0.50
13:AM:71:GLU:O	13:AM:74:MET:HB3	2.12	0.50
33:BA:836:G:C5	33:BA:837:C:C4	3.00	0.50
33:BA:2364:C:H2'	33:BA:2365:G:O4'	2.11	0.50
54:BY:86:PHE:CD1	54:BY:101:THR:HG21	2.47	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
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
36:BD:110:THR:HA	36:BD:171:THR:HB	1.94	0.50
16:AP:37:GLY:HA3	16:AP:52:LEU:HA	1.93	0.50
8:AH:17:GLN:NE2	8:AH:71:VAL:H	2.09	0.50
1:AA:1493:A:O2'	1:AA:1494:G:OP1	2.30	0.49
1:AA:710:G:H2'	1:AA:711:G:H8	1.77	0.49
33:BA:1179:G:H3'	33:BA:1180:U:H4'	1.94	0.49
24:B0:38:ARG:NH2	33:BA:2262:U:H5''	2.26	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
35:BC:95:TYR:CE1	35:BC:101:ARG:HD2	2.47	0.49
13:AM:70:ARG:O	13:AM:74:MET:HB2	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:AT:67:HIS:HB3	20:AT:68:LYS:HZ2	1.77	0.49
1:AA:781:A:O2'	1:AA:1522:U:O2	2.29	0.49
33:BA:78:U:H2'	33:BA:79:C:C6	2.46	0.49
2:AB:132:GLU:O	2:AB:136:ARG:HB2	2.12	0.49
33:BA:345:A:O2'	33:BA:346:A:N7	2.36	0.49
1:AA:297:G:N2	1:AA:300:A:OP2	2.44	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:1277:G:H5'	47:BR:20:MET:CE	2.40	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
51:BV:54:VAL:HG23	51:BV:57:GLY:HA3	1.95	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
33:BA:1539:U:H2'	33:BA:1540:G:C8	2.47	0.49
48:BS:58:ILE:HD11	48:BS:81:ARG:NH2	2.28	0.49
16:AP:43:ALA:O	16:AP:46:LYS:HD2	2.12	0.49
52:BW:6:LYS:HB3	52:BW:104:THR:HG23	1.95	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
33:BA:1197:G:H2'	33:BA:1198:U:C6	2.48	0.49
20:AT:53:MET:O	20:AT:57:VAL:HG23	2.12	0.49
33:BA:974:G:C5	33:BA:989:G:N1	2.80	0.49
33:BA:2107:G:N7	33:BA:2183:A:N1	2.60	0.49
1:AA:1491:G:H2'	1:AA:1492:A:OP2	2.12	0.49
40:BH:48:ALA:HA	40:BH:51:TYR:HE2	1.77	0.49
33:BA:895:U:O2'	33:BA:896:A:OP1	2.30	0.49
23:AW:314:ARG:NH1	23:AW:421:GLU:HB2	2.27	0.49
33:BA:1857:G:N2	33:BA:1884:G:H2'	2.27	0.49
39:BG:51:PHE:CD2	39:BG:68:ARG:HG2	2.47	0.49
33:BA:1219:U:H2'	33:BA:1220:G:H8	1.78	0.49
37:BE:145:ASP:HB3	37:BE:184:ASP:HB2	1.94	0.49
27:B3:40:THR:HG23	27:B3:43:ILE:HG23	1.95	0.49
1:AA:728:A:H2'	1:AA:729:A:C8	2.48	0.49
33:BA:805:G:N2	33:BA:829:A:OP1	2.46	0.49
1:AA:243:A:C2	1:AA:246:A:C8	3.00	0.49
37:BE:97:ASN:HB2	37:BE:100:MET:HG3	1.95	0.49
9:AI:74:GLN:O	9:AI:78:ILE:HG12	2.11	0.49
1:AA:1053:G:O6	1:AA:1199:U:H2'	2.12	0.49
12:AL:28:GLN:HG3	12:AL:80:LEU:HD21	1.92	0.49
33:BA:895:U:HO2'	33:BA:896:A:P	2.28	0.49
33:BA:1509:A:O2'	33:BA:1510:G:O4'	2.30	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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
33:BA:1141:U:H2'	43:BN:65:THR:CG2	2.42	0.49
36:BD:114:LYS:NZ	36:BD:116:LYS:HE2	2.27	0.49
55:BZ:62:THR:HA	55:BZ:71:LYS:HA	1.93	0.49
33:BA:614:A:O2'	33:BA:615:U:H5'	2.13	0.49
20:AT:43:LYS:HE2	20:AT:86:ALA:HB1	1.95	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
9:AI:34:LEU:HG	9:AI:39:GLY:HA3	1.94	0.49
33:BA:533:G:C5	33:BA:534:U:C4	3.00	0.49
50:BU:8:ILE:O	50:BU:11:ALA:HB3	2.13	0.49
33:BA:588:U:H1'	37:BE:85:PHE:CG	2.48	0.49
33:BA:528:A:C2	33:BA:2042:A:H2'	2.47	0.49
1:AA:404:G:H2'	1:AA:405:U:C6	2.48	0.49
33:BA:1757:A:H3'	33:BA:1758:U:H5'	1.94	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:392:U:H2'	33:BA:393:C:H6	1.76	0.49
33:BA:377:G:H1	33:BA:397:U:H3	1.59	0.49
3:AC:106:ARG:H	3:AC:106:ARG:HD3	1.78	0.49
23:AW:194:GLN:HB2	23:AW:205:ARG:HH12	1.76	0.49
33:BA:2180:U:H2'	33:BA:2181:U:C5	2.48	0.49
2:AB:25:LYS:HE2	2:AB:193:ASP:HB2	1.95	0.49
33:BA:2182:U:C2'	33:BA:2183:A:OP1	2.61	0.49
51:BV:8:GLY:O	51:BV:10:LYS:HE3	2.12	0.49
43:BN:45:THR:OG1	43:BN:48:VAL:HB	2.12	0.49
23:AW:355:HIS:HA	23:AW:356:VAL:CG2	2.41	0.49
33:BA:1829:A:O2'	35:BC:14:HIS:CE1	2.66	0.49
1:AA:642:A:N7	8:AH:106:SER:HA	2.28	0.49
50:BU:73:ILE:HG13	50:BU:74:SER:N	2.27	0.49
33:BA:2561:U:O3'	44:BO:40:LYS:HE2	2.12	0.49
1:AA:688:G:H5'	11:AK:48:GLY:HA2	1.95	0.49
1:AA:247:G:C6	1:AA:278:G:C2	3.00	0.49
1:AA:786:G:C2	1:AA:797:C:C2	3.01	0.49
33:BA:827:U:H2'	33:BA:2068:U:C2	2.47	0.49
1:AA:1236:A:H4'	1:AA:1304:G:H4'	1.95	0.49
33:BA:228:C:H4'	33:BA:229:C:H5''	1.95	0.49
51:BV:77:PHE:HD2	51:BV:84:ARG:HB3	1.78	0.49
28:B4:2:VAL:HG23	33:BA:2015:A:C6	2.47	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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:2150:C:O2'	33:BA:2151:U:P	2.70	0.49
23:AW:72:THR:HG21	23:AW:102:THR:HG21	1.94	0.49
23:AW:59:TRP:HE3	23:AW:59:TRP:HA	1.75	0.49
23:AW:485:PHE:C	23:AW:487:ARG:H	2.16	0.49
33:BA:994:C:O2	51:BV:10:LYS:HE2	2.13	0.49
41:BI:8:VAL:HG22	41:BI:58:ILE:HG13	1.94	0.49
12:AL:49:ARG:NH1	12:AL:88:ASP:OD1	2.44	0.49
51:BV:66:HIS:CG	51:BV:94:THR:HG22	2.47	0.49
23:AW:211:ASN:HA	23:AW:228:ARG:NH1	2.28	0.49
35:BC:106:PRO:HA	35:BC:141:HIS:NE2	2.27	0.49
3:AC:17:TRP:CD1	14:AN:93:PRO:HA	2.48	0.49
32:B8:2:LYS:HB2	32:B8:35:GLN:HG2	1.95	0.49
25:B1:60:LYS:HE3	33:BA:372:G:C8	2.48	0.49
33:BA:1024:G:P	33:BA:1025:G:H3'	2.52	0.49
1:AA:585:G:C6	1:AA:586:C:C4	3.00	0.49
33:BA:760:G:H2'	33:BA:761:A:O4'	2.12	0.49
33:BA:597:G:H2'	33:BA:598:U:C6	2.47	0.49
33:BA:2272:U:H6	33:BA:2272:U:O5'	1.95	0.49
45:BP:42:SER:O	45:BP:42:SER:OG	2.31	0.49
8:AH:38:VAL:HG11	8:AH:102:VAL:HG22	1.95	0.49
35:BC:92:LEU:HD13	35:BC:102:TYR:CE1	2.47	0.49
33:BA:2838:G:H1'	47:BR:45:ARG:NH1	2.26	0.49
1:AA:824:G:H2'	1:AA:825:A:H8	1.78	0.49
31:B7:39:ARG:HH11	33:BA:2362:C:H5''	1.77	0.49
48:BS:24:THR:HG22	48:BS:42:PRO:HD3	1.93	0.49
33:BA:2310:C:H2'	38:BF:76:PHE:CE1	2.48	0.49
2:AB:30:ILE:HD11	2:AB:38:HIS:CG	2.48	0.49
32:B8:30:GLU:HG3	32:B8:32:LYS:H	1.76	0.49
42:BM:3:THR:O	42:BM:7:ILE:HG12	2.13	0.49
24:B0:51:GLY:HA3	24:B0:59:PHE:CZ	2.48	0.49
33:BA:859:G:HO2'	33:BA:860:U:P	2.35	0.49
36:BD:114:LYS:HZ2	36:BD:116:LYS:HE2	1.76	0.49
33:BA:565:C:H2'	33:BA:566:U:O4'	2.12	0.49
40:BH:100:ALA:HB2	40:BH:125:ARG:CZ	2.43	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
23:AW:415:GLY:HA2	23:AW:457:TYR:CZ	2.48	0.49
13:AM:19:THR:HA	13:AM:24:VAL:HG23	1.94	0.49
23:AW:408:LYS:HG2	23:AW:409:GLN:HB2	1.95	0.49
33:BA:1565:C:HO2'	33:BA:1566:A:H2'	1.76	0.49
9:AI:59:LYS:HD2	9:AI:60:LEU:HD22	1.95	0.49
1:AA:1239:A:H4'	1:AA:1240:U:C5'	2.43	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1003:G:N2	1:AA:1005:A:H5'	2.28	0.49
1:AA:1437:A:H5''	20:AT:28:ARG:HH12	1.78	0.49
27:B3:43:ILE:O	27:B3:47:ILE:HG12	2.12	0.49
1:AA:308:C:H2'	1:AA:309:A:H8	1.77	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
9:AI:23:GLY:H	9:AI:61:ASP:H	1.61	0.49
33:BA:2469:A:N6	33:BA:2481:G:O2'	2.46	0.49
33:BA:2207:C:C2	33:BA:2218:G:C2	3.01	0.49
33:BA:1005:C:H2'	33:BA:1006:C:C6	2.48	0.49
1:AA:497:G:H2'	1:AA:498:A:C8	2.48	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
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
33:BA:2502:G:H5''	33:BA:2503:A:H5''	1.95	0.49
17:AQ:64:ARG:HD3	17:AQ:64:ARG:H	1.77	0.49
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.48	0.49
50:BU:65:ASN:ND2	50:BU:69:ARG:HD3	2.28	0.49
24:B0:23:LYS:HE3	24:B0:24:ARG:HG3	1.95	0.48
1:AA:1359:C:H5	14:AN:74:ARG:HH12	1.61	0.48
33:BA:558:U:H5'	43:BN:114:LEU:HD12	1.95	0.48
33:BA:1353:A:H2'	33:BA:1354:A:C8	2.48	0.48
51:BV:61:ALA:HB1	51:BV:98:ILE:H	1.78	0.48
1:AA:1478:U:H2'	1:AA:1479:C:H6	1.78	0.48
14:AN:15:LEU:O	14:AN:54:SER:OG	2.20	0.48
34:BB:93:C:H2'	34:BB:94:A:H8	1.78	0.48
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.77	0.48
51:BV:64:VAL:HG23	51:BV:96:VAL:HA	1.94	0.48
33:BA:616:A:H4'	37:BE:101:TYR:CE2	2.48	0.48
3:AC:153:SER:CB	3:AC:164:THR:HG22	2.43	0.48
23:AW:94:ASP:HB3	23:AW:443:VAL:H	1.77	0.48
47:BR:2:ARG:HA	47:BR:5:LYS:HD2	1.93	0.48
41:BI:7:TYR:HB3	41:BI:57:VAL:HG13	1.95	0.48
24:B0:23:LYS:HD2	24:B0:24:ARG:H	1.77	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
33:BA:983:A:C6	33:BA:984:A:C2	3.01	0.48
54:BY:86:PHE:CG	54:BY:101:THR:HG21	2.48	0.48
45:BP:76:GLU:HB2	45:BP:111:ILE:CD1	2.43	0.48
40:BH:23:LEU:HD22	40:BH:92:ALA:O	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
50:BU:73:ILE:HG13	50:BU:74:SER:H	1.78	0.48
1:AA:392:C:H2'	1:AA:393:A:H8	1.78	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
38:BF:131:VAL:HG22	38:BF:151:LEU:H	1.78	0.48
33:BA:372:G:O2'	33:BA:373:U:OP2	2.31	0.48
33:BA:1926:U:O2	33:BA:1929:G:N1	2.46	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
33:BA:1716:U:H2'	33:BA:1717:A:H8	1.78	0.48
33:BA:37:C:O2'	37:BE:45:ALA:HA	2.12	0.48
33:BA:745:G:H2'	33:BA:746:U:H5'	1.95	0.48
12:AL:30:ARG:HH12	23:AW:408:LYS:HG3	1.68	0.48
23:AW:59:TRP:CE2	23:AW:69:SER:CB	2.96	0.48
33:BA:1154:G:OP2	50:BU:57:ARG:NH1	2.46	0.48
24:B0:23:LYS:HB3	33:BA:856:G:H1'	1.95	0.48
48:BS:67:ASN:OD1	48:BS:67:ASN:N	2.46	0.48
24:B0:9:THR:HG23	24:B0:10:ARG:NH1	2.27	0.48
15:AO:77:TYR:OH	15:AO:87:ARG:HG2	2.13	0.48
36:BD:33:ARG:NH2	36:BD:74:GLU:O	2.46	0.48
34:BB:65:U:H3'	34:BB:108:A:H61	1.77	0.48
7:AG:134:VAL:O	7:AG:138:GLU:HG2	2.13	0.48
33:BA:2334:U:H3	48:BS:16:ARG:HG2	1.78	0.48
46:BQ:28:PHE:HB3	46:BQ:64:TRP:CE2	2.48	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
5:AE:114:LEU:HA	5:AE:114:LEU:HD12	1.73	0.48
51:BV:81:LYS:HD3	51:BV:81:LYS:HA	1.57	0.48
25:B1:27:ARG:NH2	33:BA:1365:A:O5'	2.40	0.48
2:AB:44:LYS:O	2:AB:48:MET:HB2	2.13	0.48
23:AW:448:VAL:HG13	23:AW:452:ARG:NH2	2.28	0.48
23:AW:452:ARG:HD3	23:AW:452:ARG:HA	1.63	0.48
36:BD:21:SER:HB2	44:BO:73:ASP:HA	1.95	0.48
33:BA:2302:U:H2'	33:BA:2303:G:H8	1.77	0.48
23:AW:300:VAL:HG13	23:AW:316:ALA:HB1	1.96	0.48
44:BO:31:ARG:HB3	44:BO:32:TYR:CE1	2.49	0.48
23:AW:117:LYS:O	23:AW:149:ARG:NH2	2.46	0.48
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.48	0.48
44:BO:13:ASN:OD1	44:BO:14:SER:N	2.42	0.48
33:BA:1306:C:H5''	33:BA:1606:C:N4	2.28	0.48
33:BA:322:A:H3'	37:BE:163:ASN:HD21	1.79	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1570:A:C6	33:BA:1571:A:C6	3.02	0.48
42:BJ:4:LYS:O	42:BJ:8:ILE:HG12	2.13	0.48
1:AA:1031:C:H4'	1:AA:1032:G:C4	2.48	0.48
33:BA:63:A:C2	33:BA:64:A:C5	3.01	0.48
23:AW:16:PHE:CZ	23:AW:276:ALA:HB1	2.48	0.48
33:BA:2881:U:H2'	33:BA:2882:A:C8	2.47	0.48
33:BA:594:U:H2'	33:BA:595:C:C6	2.48	0.48
16:AP:80:LYS:HB2	16:AP:80:LYS:HZ2	1.78	0.48
33:BA:828:U:H4'	33:BA:831:G:N1	2.29	0.48
7:AG:94:ARG:CZ	7:AG:98:LEU:HD21	2.43	0.48
7:AG:93:VAL:HG23	7:AG:94:ARG:H	1.77	0.48
34:BB:35:C:H2'	34:BB:36:C:O4'	2.13	0.48
6:AF:50:PRO:HD3	18:AR:73:HIS:HB3	1.95	0.48
46:BQ:35:ALA:O	46:BQ:36:VAL:HB	2.14	0.48
45:BP:33:ARG:HE	45:BP:40:SER:HA	1.78	0.48
38:BF:128:SER:HA	38:BF:153:ILE:O	2.13	0.48
33:BA:1392:A:C6	33:BA:1393:A:C6	3.01	0.48
40:BH:23:LEU:HD13	40:BH:92:ALA:HB1	1.95	0.48
4:AD:64:TYR:CE2	4:AD:93:LEU:HB3	2.48	0.48
2:AB:95:TRP:HZ2	2:AB:100:LEU:HD23	1.77	0.48
1:AA:1065:U:H5''	1:AA:1190:G:N2	2.29	0.48
9:AI:9:GLY:H	9:AI:84:ARG:HH12	1.62	0.48
33:BA:319:G:H2'	33:BA:320:A:O4'	2.14	0.48
1:AA:308:C:H2'	1:AA:309:A:C8	2.49	0.48
26:B2:56:LEU:HA	26:B2:59:GLU:HG2	1.95	0.48
43:BN:21:THR:HG23	43:BN:61:LYS:HB3	1.95	0.48
33:BA:1522:A:H1'	33:BA:1524:G:C5	2.48	0.48
45:BP:75:ALA:HB2	45:BP:105:ILE:HG12	1.96	0.48
33:BA:2572:A:N7	36:BD:150:GLN:HB3	2.28	0.48
1:AA:938:A:C6	1:AA:939:G:C5	3.01	0.48
23:AW:50:GLY:HA3	33:BA:2655:G:N7	2.28	0.48
33:BA:2205:A:OP1	35:BC:67:LYS:NZ	2.46	0.48
39:BG:62:ALA:O	39:BG:66:THR:HG23	2.13	0.48
23:AW:500:ASN:HB2	23:AW:501:LEU:CG	2.42	0.48
6:AF:6:ILE:H	6:AF:62:MET:HB3	1.78	0.48
26:B2:17:GLU:HB2	26:B2:53:VAL:HG11	1.96	0.48
1:AA:1145:A:O2'	1:AA:1146:A:H8	1.97	0.48
23:AW:279:PRO:HG3	23:AW:362:GLY:HA3	1.96	0.48
33:BA:1838:C:H4'	33:BA:1839:G:H8	1.77	0.48
1:AA:673:A:H4'	6:AF:86:ARG:HE	1.78	0.48
27:B3:6:ILE:HG21	27:B3:47:ILE:HD12	1.96	0.48
35:BC:81:GLU:OE1	35:BC:102:TYR:OH	2.20	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
36:BD:149:ASN:OD1	36:BD:150:GLN:N	2.45	0.48
3:AC:21:TRP:HB3	3:AC:58:ARG:H	1.79	0.48
37:BE:105:LEU:HB2	37:BE:200:LEU:HD11	1.96	0.48
25:B1:36:ARG:HG3	25:B1:47:THR:HB	1.94	0.48
33:BA:1774:C:O2	35:BC:10:PRO:HB2	2.12	0.48
33:BA:825:A:H2'	33:BA:826:U:C6	2.49	0.48
23:AW:448:VAL:HG22	23:AW:452:ARG:HH21	1.79	0.48
23:AW:145:ASP:CG	56:AW:601:GNP:HN1	2.17	0.48
23:AW:71:THR:HG22	23:AW:72:THR:N	2.28	0.48
24:B0:23:LYS:HG3	24:B0:24:ARG:O	2.13	0.48
1:AA:73:C:N4	1:AA:97:G:H1	2.04	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
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
36:BD:186:LEU:HD11	49:BT:3:ILE:HG12	1.96	0.48
33:BA:566:U:H5	51:BV:80:ARG:HG2	1.78	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
55:BZ:28:ALA:N	55:BZ:40:ILE:O	2.46	0.48
33:BA:1394:U:H4'	33:BA:1603:A:H4'	1.94	0.48
33:BA:586:A:N1	33:BA:809:G:O2'	2.37	0.48
33:BA:259:G:HO2'	33:BA:621:A:HO2'	1.62	0.48
43:BN:88:THR:HG22	43:BN:91:GLU:CD	2.33	0.48
43:BN:88:THR:O	43:BN:91:GLU:N	2.47	0.48
25:B1:2:ARG:O	25:B1:11:PRO:HD3	2.13	0.48
39:BG:73:SER:HA	39:BG:76:ILE:HG22	1.96	0.48
23:AW:419:LEU:HD12	23:AW:452:ARG:NH2	2.27	0.48
23:AW:64:LYS:NZ	23:AW:71:THR:O	2.38	0.48
1:AA:1492:A:N6	33:BA:1913:A:C2	2.82	0.48
40:BH:60:LEU:O	40:BH:62:ARG:N	2.46	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
32:B8:16:ILE:HA	32:B8:24:ARG:O	2.13	0.48
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
1:AA:1227:A:OP2	13:AM:109:LYS:HE2	2.14	0.48
24:B0:43:LYS:HB3	24:B0:79:ILE:HD11	1.96	0.48
21:AU:19:LYS:HB2	21:AU:20:ARG:HH11	1.78	0.48
48:BS:4:LYS:CD	48:BS:7:ARG:HH21	2.26	0.48
33:BA:833:A:H2'	33:BA:834:G:C8	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:BQ:11:LYS:NZ	46:BQ:87:GLY:O	2.30	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
33:BA:703:U:H2'	33:BA:704:G:O4'	2.14	0.48
8:AH:79:ARG:HB2	8:AH:80:PRO:HD2	1.95	0.48
7:AG:129:ASN:C	7:AG:134:VAL:HG21	2.35	0.48
33:BA:1378:A:C4	33:BA:1380:G:N7	2.82	0.48
35:BC:180:MET:HG3	35:BC:268:ARG:HH11	1.79	0.48
23:AW:96:SER:HA	23:AW:97:GLU:CB	2.43	0.48
7:AG:3:ARG:HG3	7:AG:4:ARG:H	1.79	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
26:B2:56:LEU:HA	26:B2:59:GLU:CG	2.44	0.48
55:BZ:75:GLN:HB2	55:BZ:92:VAL:HG23	1.95	0.48
33:BA:2220:U:H2'	33:BA:2221:G:C8	2.49	0.48
33:BA:752:A:H62	33:BA:2609:U:H3	1.60	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
1:AA:1380:U:C5	7:AG:2:ARG:HA	2.48	0.48
33:BA:2007:U:H2'	33:BA:2008:C:C6	2.49	0.48
1:AA:51:A:H4'	1:AA:52:C:O5'	2.13	0.48
53:BX:56:GLU:HA	53:BX:88:LYS:HE2	1.95	0.48
35:BC:20:ASN:O	35:BC:23:LEU:HB2	2.13	0.48
42:BL:21:GLU:O	42:BL:24:SER:OG	2.22	0.48
33:BA:1568:G:H4'	35:BC:58:LYS:CB	2.36	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
46:BQ:26:VAL:HA	46:BQ:104:GLU:OE1	2.13	0.48
36:BD:108:ASP:N	36:BD:204:LYS:O	2.46	0.48
3:AC:153:SER:HB3	3:AC:164:THR:HG22	1.96	0.48
33:BA:301:G:P	54:BY:81:ARG:HH12	2.37	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
1:AA:239:U:H5''	1:AA:240:G:OP2	2.14	0.48
35:BC:224:MET:HB3	35:BC:228:ASP:HB2	1.96	0.48
33:BA:1055:G:H4'	40:BH:33:VAL:HA	1.96	0.48
2:AB:26:MET:HG2	2:AB:188:THR:HA	1.96	0.48
33:BA:2294:G:H5''	48:BS:10:ARG:HD3	1.96	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
33:BA:1559:U:H4'	33:BA:1560:G:OP2	2.14	0.48
33:BA:587:C:OP2	45:BP:21:ARG:NH1	2.48	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:AI:83:THR:HG22	9:AI:97:LEU:HD21	1.96	0.47
33:BA:2848:G:H2'	33:BA:2867:G:H22	1.79	0.47
33:BA:2444:G:OP2	37:BE:63:LYS:HD2	2.14	0.47
1:AA:542:G:H2'	1:AA:543:U:H6	1.79	0.47
25:B1:68:ALA:O	25:B1:72:ALA:HB2	2.13	0.47
18:AR:40:PRO:HG2	18:AR:43:ILE:HG12	1.96	0.47
33:BA:686:U:H2'	33:BA:788:A:C2	2.49	0.47
33:BA:342:A:H2'	33:BA:343:C:O4'	2.14	0.47
14:AN:20:PHE:HB2	14:AN:54:SER:OG	2.14	0.47
33:BA:2416:C:N4	33:BA:2417:C:H41	2.12	0.47
14:AN:3:GLN:HA	14:AN:6:LYS:HE2	1.96	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
34:BB:28:C:OP1	48:BS:31:THR:HG21	2.14	0.47
1:AA:497:G:H5''	23:AW:480:LYS:HE2	1.95	0.47
12:AL:78:VAL:HG21	23:AW:407:LEU:CD1	2.42	0.47
33:BA:974:G:N7	33:BA:989:G:N1	2.61	0.47
33:BA:2845:U:H5''	49:BT:51:ASN:O	2.14	0.47
40:BH:60:LEU:O	40:BH:63:ALA:N	2.48	0.47
37:BE:48:THR:N	37:BE:51:GLU:HG3	2.29	0.47
33:BA:881:G:H2'	33:BA:882:G:C8	2.49	0.47
53:BX:29:THR:HA	53:BX:86:THR:CA	2.42	0.47
9:AI:49:GLN:N	9:AI:50:PRO:HD2	2.29	0.47
51:BV:25:LEU:H	51:BV:94:THR:CG2	2.27	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
3:AC:63:ILE:HG12	3:AC:65:VAL:HG23	1.96	0.47
10:AJ:35:GLN:HG2	10:AJ:77:VAL:HB	1.96	0.47
1:AA:707:U:H2'	1:AA:708:C:C6	2.48	0.47
37:BE:119:ILE:O	37:BE:119:ILE:HG12	2.15	0.47
43:BN:59:ALA:H	43:BN:126:ALA:HA	1.79	0.47
33:BA:979:A:H2'	33:BA:982:C:H42	1.80	0.47
1:AA:1463:U:H2'	1:AA:1464:U:C6	2.48	0.47
33:BA:816:C:H2'	33:BA:817:C:H6	1.79	0.47
33:BA:1103:A:H5'	33:BA:1104:C:OP2	2.14	0.47
40:BH:51:TYR:HB2	40:BH:89:PRO:HG2	1.96	0.47
1:AA:1302:C:OP1	13:AM:12:LYS:HE2	2.15	0.47
33:BA:893:C:H2'	33:BA:894:U:O4'	2.14	0.47
48:BS:102:ARG:HA	48:BS:105:ALA:HB3	1.95	0.47
1:AA:706:A:H4'	11:AK:30:ILE:HD12	1.94	0.47
33:BA:1022:G:C6	33:BA:1140:C:C4	3.02	0.47
19:AS:35:ARG:NH2	19:AS:74:ALA:O	2.47	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
47:BR:69:ARG:C	47:BR:71:ARG:H	2.16	0.47
33:BA:1731:G:O2'	33:BA:1732:C:H3'	2.15	0.47
25:B1:39:VAL:HG22	25:B1:44:ARG:O	2.14	0.47
41:BI:53:PRO:HD2	41:BI:77:VAL:HG21	1.96	0.47
33:BA:1300:G:H5''	33:BA:1301:A:H5'	1.96	0.47
33:BA:2889:C:H2'	33:BA:2890:G:O4'	2.14	0.47
2:AB:60:ALA:HB2	2:AB:220:VAL:HG13	1.96	0.47
33:BA:84:A:H4'	33:BA:85:G:O5'	2.13	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:883:G:O2'	33:BA:896:A:N7	2.37	0.47
3:AC:14:VAL:O	3:AC:15:LYS:HD2	2.15	0.47
17:AQ:55:GLY:HA3	17:AQ:82:VAL:HG11	1.96	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
51:BV:41:ILE:HD13	51:BV:103:ALA:HA	1.96	0.47
1:AA:666:G:H5'	1:AA:726:C:H1'	1.96	0.47
14:AN:82:LYS:HE2	14:AN:85:GLU:HG3	1.96	0.47
43:BN:91:GLU:O	43:BN:94:ALA:HB3	2.13	0.47
1:AA:1330:U:H4'	13:AM:22:TYR:CE1	2.49	0.47
1:AA:774:G:N2	1:AA:806:C:C2	2.83	0.47
50:BU:78:PHE:CZ	50:BU:82:LEU:HD11	2.49	0.47
33:BA:2398:U:H2'	33:BA:2399:G:C8	2.50	0.47
33:BA:1370:C:H2'	33:BA:1371:G:O4'	2.15	0.47
23:AW:20:SER:HB3	23:AW:26:LYS:HG2	1.97	0.47
40:BH:11:ILE:HG23	40:BH:63:ALA:HA	1.96	0.47
33:BA:2867:G:O2'	33:BA:2868:A:H8	1.98	0.47
35:BC:182:LYS:N	35:BC:265:PHE:O	2.43	0.47
46:BQ:64:TRP:CZ3	46:BQ:106:ASP:HB2	2.50	0.47
9:AI:9:GLY:HA2	9:AI:80:HIS:ND1	2.29	0.47
33:BA:1363:C:H2'	33:BA:1364:G:H8	1.79	0.47
33:BA:2691:C:C4	33:BA:2719:G:N2	2.83	0.47
33:BA:1671:U:N3	33:BA:1674:G:OP2	2.38	0.47
34:BB:116:G:H2'	34:BB:117:G:H8	1.78	0.47
1:AA:147:G:H2'	1:AA:148:G:C8	2.49	0.47
36:BD:60:VAL:HG23	36:BD:64:GLU:HB2	1.95	0.47
2:AB:66:ILE:O	2:AB:160:LEU:HA	2.14	0.47
33:BA:1071:G:H1'	33:BA:1089:A:N7	2.29	0.47
33:BA:1531:C:H2'	33:BA:1532:A:C8	2.50	0.47
18:AR:61:ALA:HB3	18:AR:67:LEU:HD12	1.96	0.47
33:BA:1106:G:H5''	40:BH:59:LEU:HD11	1.97	0.47
2:AB:162:VAL:HG23	2:AB:163:ILE:O	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:204:G:H3'	1:AA:205:A:C5'	2.43	0.47
23:AW:491:SER:N	23:AW:492:GLN:HB2	2.30	0.47
1:AA:478:A:H2'	1:AA:479:U:O4'	2.15	0.47
33:BA:1141:U:H6	43:BN:65:THR:HG22	1.79	0.47
45:BP:90:VAL:HG13	45:BP:95:LEU:HD21	1.96	0.47
36:BD:91:THR:C	36:BD:93:GLY:N	2.67	0.47
33:BA:826:U:O2'	45:BP:53:GLY:HA3	2.15	0.47
2:AB:209:VAL:HG23	2:AB:210:THR:H	1.79	0.47
25:B1:17:ARG:HD2	25:B1:23:ALA:HA	1.95	0.47
47:BR:117:ASP:OD2	47:BR:117:ASP:N	2.47	0.47
36:BD:61:THR:OG1	36:BD:63:PRO:HD2	2.15	0.47
13:AM:92:ARG:HG2	13:AM:92:ARG:HH11	1.80	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
23:AW:146:ARG:CZ	33:BA:2659:G:O6	2.63	0.47
33:BA:1056:G:O2'	33:BA:1086:A:H8	1.98	0.47
39:BG:122:ALA:HB2	39:BG:132:LEU:HB3	1.97	0.47
24:B0:30:VAL:HG11	33:BA:2352:A:C6	2.50	0.47
33:BA:882:G:C2	33:BA:895:U:O2	2.67	0.47
43:BN:31:GLU:OE2	43:BN:35:ARG:NH1	2.46	0.47
33:BA:2756:U:H1'	33:BA:2757:A:H5''	1.97	0.47
32:B8:9:LYS:HE2	32:B8:9:LYS:HB2	1.72	0.47
54:BY:6:ARG:HA	54:BY:6:ARG:HD2	1.54	0.47
33:BA:900:A:O2'	33:BA:901:C:P	2.71	0.47
23:AW:307:MET:CG	23:AW:308:ASP:HA	2.44	0.47
23:AW:127:MET:HG3	23:AW:162:LEU:HD22	1.96	0.47
53:BX:19:LYS:O	53:BX:20:ALA:C	2.53	0.47
33:BA:1837:C:H4'	33:BA:1928:A:H4'	1.96	0.47
1:AA:1386:G:H2'	1:AA:1387:G:C8	2.49	0.47
33:BA:1020:A:H4'	33:BA:1021:A:O5'	2.14	0.47
45:BP:78:ARG:NH1	45:BP:113:ALA:HB1	2.28	0.47
32:B8:36:ARG:HD3	33:BA:2742:G:OP1	2.14	0.47
33:BA:1550:C:H2'	33:BA:1551:A:H8	1.79	0.47
47:BR:48:VAL:O	47:BR:51:LEU:N	2.47	0.47
33:BA:2197:U:O2'	33:BA:2198:A:C8	2.66	0.47
33:BA:687:C:N3	33:BA:788:A:H5'	2.30	0.47
33:BA:1728:C:O2	33:BA:1731:G:N2	2.37	0.47
33:BA:2310:C:H2'	38:BF:76:PHE:HE1	1.79	0.47
23:AW:276:ALA:HA	23:AW:277:PRO:HD3	1.80	0.47
36:BD:149:ASN:O	36:BD:152:PRO:HD2	2.15	0.47
1:AA:123:U:H2'	1:AA:124:C:H6	1.79	0.47
15:AO:32:THR:HG23	15:AO:62:ARG:NH1	2.29	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
53:BX:22:THR:O	53:BX:25:GLU:HB3	2.14	0.47
1:AA:484:G:H4'	1:AA:485:U:O5'	2.15	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
35:BC:103:ILE:HG22	35:BC:104:LEU:O	2.15	0.47
31:B7:7:ARG:HA	31:B7:7:ARG:HD2	1.59	0.47
29:B5:33:LEU:H	29:B5:51:ALA:HB3	1.80	0.47
41:BI:100:ILE:HG22	41:BI:101:SER:H	1.79	0.47
50:BU:91:ARG:HB3	50:BU:94:LEU:H	1.79	0.47
33:BA:2489:U:HO2'	33:BA:2491:U:H5	1.60	0.47
50:BU:87:VAL:HB	51:BV:52:PRO:HD3	1.97	0.47
33:BA:878:A:N6	33:BA:900:A:H1'	2.29	0.47
34:BB:60:C:H2'	34:BB:61:G:C8	2.50	0.47
1:AA:765:G:N2	1:AA:812:G:O2'	2.48	0.47
33:BA:1799:G:H22	33:BA:1818:U:H2'	1.79	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
54:BY:60:LYS:HA	54:BY:60:LYS:HD2	1.68	0.47
33:BA:1334:G:C6	33:BA:1335:C:C4	3.03	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
1:AA:975:A:O2'	14:AN:71:GLY:HA2	2.15	0.47
33:BA:2314:A:H2'	33:BA:2315:G:H8	1.80	0.47
24:B0:10:ARG:O	24:B0:11:ASN:HB2	2.14	0.47
39:BG:54:ARG:HD3	39:BG:55:ASP:N	2.29	0.47
33:BA:1509:A:O2'	33:BA:1510:G:C8	2.65	0.47
35:BC:4:LYS:HG2	35:BC:16:VAL:HG22	1.97	0.47
33:BA:1054:A:O3'	40:BH:31:ARG:HA	2.13	0.47
1:AA:716:A:H2'	1:AA:717:U:O4'	2.14	0.47
1:AA:1347:G:O2'	1:AA:1348:U:OP2	2.33	0.47
33:BA:1236:G:HO2'	33:BA:1237:A:H8	1.60	0.47
18:AR:40:PRO:HB2	18:AR:42:ARG:HG2	1.97	0.47
16:AP:57:ILE:O	16:AP:61:VAL:HG23	2.14	0.47
7:AG:35:LYS:HA	7:AG:38:ALA:HB3	1.96	0.47
33:BA:2470:G:H2'	33:BA:2471:A:H8	1.80	0.47
33:BA:2886:A:C2	33:BA:2887:A:H1'	2.50	0.47
38:BF:16:MET:O	38:BF:20:ASN:HA	2.15	0.47
33:BA:2576:G:O2'	33:BA:2579:C:OP2	2.27	0.47
36:BD:2:ILE:HG13	36:BD:100:LEU:HD21	1.97	0.47
23:AW:172:PRO:HD3	23:AW:256:PHE:CG	2.50	0.47
33:BA:1710:G:C2	33:BA:1749:A:C2	3.03	0.47
12:AL:23:LEU:O	12:AL:25:ALA:N	2.47	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1063:G:H2'	33:BA:1064:C:O4'	2.14	0.47
33:BA:812:C:H5''	33:BA:1250:G:O2'	2.15	0.47
27:B3:4:ILE:HG12	27:B3:5:LYS:N	2.29	0.47
33:BA:2391:G:O6	33:BA:2425:A:H8	1.97	0.47
33:BA:2822:G:OP1	36:BD:164:GLN:NE2	2.44	0.47
33:BA:1353:A:C8	33:BA:1378:A:N6	2.83	0.47
1:AA:1152:A:H5'	10:AJ:15:HIS:HD2	1.79	0.47
47:BR:67:PHE:O	47:BR:71:ARG:HA	2.14	0.47
43:BN:55:ILE:HD12	43:BN:132:HIS:HD2	1.79	0.47
4:AD:60:VAL:O	4:AD:63:ILE:HG22	2.14	0.47
33:BA:2793:C:O2	33:BA:2803:G:N2	2.37	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
51:BV:61:ALA:HB2	51:BV:98:ILE:HA	1.96	0.47
15:AO:40:GLY:O	15:AO:43:ALA:HB3	2.15	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:2148:G:C2'	33:BA:2149:U:O5'	2.63	0.46
33:BA:2250:G:H21	33:BA:2496:C:H5''	1.80	0.46
1:AA:878:A:H5''	8:AH:80:PRO:HG2	1.97	0.46
36:BD:159:LYS:HD3	36:BD:160:LYS:N	2.30	0.46
33:BA:1020:A:C2	33:BA:1141:U:C2	3.03	0.46
40:BH:4:ASN:O	40:BH:8:LYS:HG3	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
1:AA:123:U:H2'	1:AA:124:C:C6	2.50	0.46
49:BT:31:VAL:HG11	49:BT:40:GLN:HB2	1.97	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
33:BA:2243:U:H2'	33:BA:2244:U:C6	2.51	0.46
2:AB:80:LYS:HD3	2:AB:90:PHE:CE1	2.50	0.46
16:AP:19:VAL:HG13	16:AP:36:VAL:O	2.15	0.46
8:AH:101:ALA:HB3	8:AH:112:ASP:HB3	1.97	0.46
46:BQ:46:ILE:O	46:BQ:49:ALA:HB3	2.14	0.46
14:AN:61:ASN:HB3	14:AN:72:PHE:CE1	2.49	0.46
23:AW:403:LEU:HD21	23:AW:459:VAL:HG12	1.97	0.46
33:BA:1914:C:C3'	33:BA:1915:U:C5'	2.91	0.46
49:BT:50:ARG:H	49:BT:50:ARG:HG3	1.44	0.46
23:AW:50:GLY:CA	33:BA:2655:G:N7	2.78	0.46
1:AA:82:G:N2	1:AA:88:U:O2'	2.49	0.46
2:AB:163:ILE:HD12	2:AB:185:ILE:HG12	1.97	0.46
2:AB:110:ILE:HG12	2:AB:150:ILE:HG13	1.97	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:AI:56:MET:HB3	9:AI:60:LEU:CD2	2.46	0.46
9:AI:6:TYR:CE2	9:AI:17:ARG:HB2	2.46	0.46
33:BA:2103:C:N4	33:BA:2185:U:O4	2.47	0.46
49:BT:33:GLU:HB3	49:BT:36:LYS:O	2.15	0.46
33:BA:1570:A:H2'	33:BA:1571:A:C8	2.51	0.46
33:BA:2230:G:H2'	33:BA:2231:U:H6	1.80	0.46
33:BA:2071:A:H2'	33:BA:2072:C:C6	2.50	0.46
50:BU:39:ILE:O	50:BU:43:GLN:HG3	2.14	0.46
33:BA:414:C:H2'	33:BA:415:A:C8	2.51	0.46
1:AA:237:G:H5''	17:AQ:26:ARG:NH2	2.29	0.46
33:BA:2825:G:H5''	33:BA:2825:G:N3	2.30	0.46
16:AP:42:ILE:O	16:AP:44:SER:N	2.48	0.46
8:AH:31:LEU:O	8:AH:35:ILE:HG12	2.16	0.46
33:BA:1131:G:N2	33:BA:2024:G:H21	2.14	0.46
33:BA:1708:C:H2'	33:BA:1709:U:C6	2.49	0.46
33:BA:2840:C:H2'	33:BA:2841:C:C6	2.50	0.46
33:BA:282:A:H2'	33:BA:283:G:C8	2.50	0.46
33:BA:1153:C:H5'	50:BU:75:TYR:HE2	1.81	0.46
1:AA:82:G:C8	1:AA:89:U:H1'	2.51	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
36:BD:120:GLY:HA2	36:BD:162:ALA:CB	2.45	0.46
43:BN:4:PHE:HD1	43:BN:44:TYR:CE2	2.33	0.46
33:BA:1045:C:H5'	33:BA:1047:G:O4'	2.16	0.46
38:BF:130:GLY:HA2	38:BF:152:ASP:HA	1.97	0.46
33:BA:1656:C:H2'	33:BA:1657:U:C6	2.50	0.46
36:BD:5:VAL:HG21	36:BD:80:TRP:CD2	2.50	0.46
9:AI:87:MET:SD	9:AI:88:GLU:N	2.89	0.46
33:BA:1853:A:N1	33:BA:2087:G:H1'	2.29	0.46
52:BW:97:LEU:H	52:BW:97:LEU:HD22	1.80	0.46
1:AA:160:A:H2'	1:AA:161:A:O4'	2.15	0.46
33:BA:2834:G:O3'	36:BD:56:LYS:NZ	2.47	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
45:BP:109:LYS:HG2	45:BP:126:ARG:HB3	1.97	0.46
23:AW:449:VAL:HG23	23:AW:463:TYR:OH	2.15	0.46
24:B0:23:LYS:HD3	33:BA:855:G:H1'	1.97	0.46
1:AA:1359:C:O2'	1:AA:1361:G:N7	2.48	0.46
23:AW:523:PHE:O	23:AW:525:GLN:NE2	2.49	0.46
36:BD:117:GLY:HA2	36:BD:164:GLN:NE2	2.30	0.46
39:BG:61:TRP:CE3	39:BG:61:TRP:HA	2.49	0.46
4:AD:124:VAL:C	4:AD:126:GLY:N	2.69	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:2557:G:H2'	33:BA:2558:C:H6	1.81	0.46
1:AA:346:G:N2	1:AA:347:G:C8	2.84	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
35:BC:180:MET:HB2	35:BC:267:VAL:HB	1.96	0.46
5:AE:59:ILE:O	5:AE:62:ALA:HB3	2.15	0.46
33:BA:1080:A:H4'	41:BI:126:ARG:HB2	1.97	0.46
6:AF:20:GLY:O	6:AF:24:ARG:HD3	2.16	0.46
33:BA:2335:A:OP1	48:BS:13:ARG:HD2	2.15	0.46
15:AO:54:GLY:O	15:AO:57:ARG:HB3	2.15	0.46
33:BA:1126:A:H4'	33:BA:1127:A:O5'	2.15	0.46
33:BA:868:U:C4	33:BA:869:G:N7	2.84	0.46
33:BA:1174:U:O2	33:BA:1174:U:H2'	2.14	0.46
33:BA:2813:A:H2'	33:BA:2814:A:C8	2.50	0.46
15:AO:73:ASP:OD1	15:AO:75:ALA:HB3	2.15	0.46
33:BA:2677:G:H2'	33:BA:2678:C:H6	1.79	0.46
23:AW:315:VAL:HG11	23:AW:346:LEU:HD12	1.98	0.46
23:AW:22:PRO:HA	56:AW:601:GNP:O2G	2.15	0.46
1:AA:1302:C:H5''	1:AA:1303:C:OP2	2.15	0.46
45:BP:21:ARG:HD3	45:BP:21:ARG:HA	1.64	0.46
43:BN:40:HIS:C	50:BU:66:ALA:HB1	2.36	0.46
32:B8:9:LYS:HD3	32:B8:9:LYS:H	1.80	0.46
23:AW:491:SER:HB2	23:AW:492:GLN:HB2	1.98	0.46
35:BC:250:GLN:CD	35:BC:250:GLN:H	2.17	0.46
33:BA:2578:G:N7	36:BD:145:SER:HB2	2.31	0.46
23:AW:306:ASN:HD21	23:AW:313:ASP:HB2	1.80	0.46
1:AA:337:G:H2'	1:AA:338:A:H8	1.80	0.46
35:BC:180:MET:HB2	35:BC:268:ARG:H	1.80	0.46
35:BC:70:LYS:NZ	35:BC:97:ASP:OD2	2.49	0.46
38:BF:71:LYS:HA	38:BF:71:LYS:HD3	1.81	0.46
20:AT:27:MET:CE	20:AT:57:VAL:HG22	2.45	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
53:BX:17:SER:H	53:BX:21:SER:CB	2.28	0.46
3:AC:96:VAL:HB	3:AC:97:PRO:HD2	1.98	0.46
1:AA:902:G:O2'	1:AA:903:G:H5'	2.16	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
2:AB:148:GLY:HA2	2:AB:151:LYS:HE2	1.98	0.46
12:AL:78:VAL:HG12	12:AL:101:LEU:HD23	1.96	0.46
33:BA:2846:G:P	49:BT:52:ARG:HH12	2.39	0.46
33:BA:995:C:O2'	33:BA:996:A:P	2.74	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:975:A:N1	1:AA:1366:C:O2'	2.46	0.46
53:BX:28:ASN:HA	53:BX:91:GLN:HE22	1.81	0.46
33:BA:2849:U:OP1	49:BT:92:ARG:NH1	2.48	0.46
16:AP:38:PHE:CE2	16:AP:51:ARG:HB3	2.50	0.46
33:BA:1669:A:H5''	33:BA:2550:G:OP1	2.15	0.46
2:AB:222:GLU:OE1	2:AB:225:SER:HA	2.16	0.46
1:AA:169:C:H2'	1:AA:170:U:H6	1.80	0.46
44:BO:59:LYS:HE2	44:BO:89:ASN:ND2	2.31	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:1652:A:N7	33:BA:1653:G:C6	2.84	0.46
36:BD:13:ARG:NE	36:BD:21:SER:OG	2.32	0.46
33:BA:1061:U:O2'	33:BA:1070:A:H4'	2.16	0.46
46:BQ:33:LEU:CD2	46:BQ:128:THR:HB	2.46	0.46
42:BM:2:ILE:HD12	42:BM:5:ASP:HB2	1.97	0.46
51:BV:49:ILE:HD13	51:BV:49:ILE:H	1.81	0.46
33:BA:2636:C:H2'	33:BA:2637:U:C6	2.51	0.46
39:BG:104:LEU:HB2	39:BG:112:VAL:CG2	2.45	0.46
33:BA:954:G:C5	33:BA:955:U:C5	3.04	0.46
33:BA:639:U:H2'	33:BA:640:C:H6	1.78	0.46
43:BN:105:VAL:HG11	43:BN:122:LEU:CD2	2.45	0.46
36:BD:172:VAL:HG23	36:BD:194:PRO:HD3	1.97	0.46
16:AP:10:GLY:HA3	16:AP:16:PHE:N	2.30	0.46
39:BG:25:ILE:HG22	39:BG:78:VAL:HG21	1.97	0.46
33:BA:1947:C:H2'	33:BA:1948:G:H8	1.79	0.46
33:BA:816:C:H2'	33:BA:817:C:C6	2.51	0.46
1:AA:868:C:H2'	1:AA:869:G:O4'	2.15	0.46
33:BA:208:C:H2'	33:BA:209:C:C6	2.50	0.46
1:AA:1058:G:H2'	1:AA:1059:C:O4'	2.16	0.46
46:BQ:53:MET:HE2	46:BQ:53:MET:HB2	1.59	0.46
23:AW:30:THR:HG23	23:AW:86:LEU:HD21	1.97	0.46
5:AE:131:ASN:O	5:AE:135:VAL:HG12	2.16	0.46
43:BN:80:HIS:HB2	43:BN:81:ILE:HG22	1.98	0.46
33:BA:1805:A:H5''	35:BC:247:TRP:CE2	2.51	0.46
25:B1:15:ASN:OD1	25:B1:25:LYS:HD3	2.15	0.46
3:AC:34:SER:O	3:AC:38:VAL:HG13	2.16	0.46
1:AA:363:A:OP1	12:AL:29:LYS:HE2	2.16	0.46
3:AC:13:ILE:HB	3:AC:14:VAL:HG23	1.97	0.46
33:BA:452:G:C6	33:BA:453:A:C6	3.03	0.46
1:AA:1054:C:O2'	1:AA:1055:A:H5''	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:734:G:C2	1:AA:735:C:C2	3.03	0.46
54:BY:48:VAL:O	54:BY:53:GLN:HB3	2.16	0.46
36:BD:110:THR:HB	36:BD:202:ILE:HB	1.98	0.46
33:BA:1005:C:H2'	33:BA:1006:C:H6	1.80	0.46
48:BS:53:THR:O	48:BS:59:ALA:HB2	2.16	0.46
25:B1:35:HIS:HB3	25:B1:37:PHE:CE2	2.51	0.46
19:AS:52:ASN:HB2	19:AS:76:THR:HA	1.98	0.46
1:AA:1401:G:H2'	1:AA:1402:C:O4'	2.16	0.46
49:BT:81:ASP:OD2	49:BT:82:SER:N	2.48	0.46
1:AA:15:G:C6	1:AA:16:A:C5	3.03	0.46
1:AA:811:C:O2'	1:AA:901:A:N1	2.47	0.46
46:BQ:108:VAL:HG13	46:BQ:109:PRO:HD2	1.96	0.46
33:BA:286:U:H2'	33:BA:287:G:C8	2.51	0.46
1:AA:981:U:O3'	14:AN:62:ARG:NH2	2.49	0.46
11:AK:87:GLY:N	11:AK:113:THR:HG22	2.09	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
46:BQ:33:LEU:HD22	46:BQ:128:THR:HB	1.98	0.46
24:B0:11:ASN:ND2	33:BA:2264:C:H41	2.14	0.46
11:AK:16:SER:O	11:AK:78:ILE:HA	2.16	0.46
33:BA:1205:A:H4'	33:BA:1206:G:OP2	2.16	0.46
1:AA:991:U:H5''	1:AA:992:U:OP1	2.16	0.46
41:BI:32:VAL:HG22	41:BI:66:PHE:CG	2.51	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
2:AB:14:HIS:O	2:AB:202:ASN:HB2	2.16	0.46
33:BA:1534:U:H5'	33:BA:1535:A:OP1	2.15	0.46
33:BA:1059:G:H5''	33:BA:1060:U:H3'	1.98	0.46
46:BQ:35:ALA:O	46:BQ:128:THR:HA	2.16	0.46
37:BE:5:LEU:HA	37:BE:5:LEU:HD23	1.65	0.46
4:AD:58:GLN:O	4:AD:62:ARG:HG2	2.16	0.46
3:AC:113:LYS:HD3	3:AC:184:ASN:CG	2.35	0.46
45:BP:95:LEU:HD23	45:BP:100:ILE:HD11	1.98	0.46
4:AD:23:GLY:HA2	4:AD:108:ALA:HB1	1.98	0.46
1:AA:1479:C:H2'	1:AA:1480:A:C8	2.51	0.46
1:AA:858:G:O2'	1:AA:859:G:H5'	2.16	0.46
1:AA:246:A:H4'	1:AA:247:G:OP1	2.15	0.46
53:BX:11:LEU:HD11	53:BX:47:VAL:HG22	1.98	0.46
23:AW:94:ASP:HB3	23:AW:442:GLY:HA3	1.98	0.46
33:BA:2417:C:C2	33:BA:2418:A:C8	3.04	0.46
23:AW:169:ILE:HG22	23:AW:170:THR:HG23	1.97	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1110:A:H8	1:AA:1110:A:O5'	1.99	0.46
3:AC:86:LEU:O	3:AC:90:VAL:HG23	2.15	0.46
33:BA:34:U:H4'	33:BA:35:G:OP2	2.14	0.46
36:BD:104:VAL:HG11	36:BD:205:PRO:HB3	1.98	0.46
43:BN:19:ASP:OD2	43:BN:58:ASN:HB2	2.15	0.45
1:AA:1281:C:H5''	1:AA:1282:C:C5	2.38	0.45
4:AD:7:LYS:HG3	4:AD:8:LEU:HD22	1.97	0.45
51:BV:49:ILE:O	51:BV:49:ILE:HG12	2.17	0.45
5:AE:12:GLU:HB3	5:AE:38:VAL:HG12	1.98	0.45
33:BA:2305:U:C4	33:BA:2306:C:C4	3.04	0.45
22:AV:15:A:N3	22:AV:15:A:H2'	2.30	0.45
9:AI:90:ASP:OD2	9:AI:93:LEU:HG	2.16	0.45
33:BA:2784:U:H2'	33:BA:2785:C:C6	2.51	0.45
33:BA:2259:U:H2'	33:BA:2260:C:H6	1.81	0.45
7:AG:23:ALA:O	7:AG:26:VAL:HG22	2.16	0.45
2:AB:10:LYS:HE3	2:AB:10:LYS:HB2	1.69	0.45
5:AE:106:ALA:HB2	5:AE:124:ALA:HB3	1.97	0.45
1:AA:635:A:H2'	1:AA:636:U:C6	2.51	0.45
33:BA:265:A:H4'	33:BA:266:G:OP1	2.16	0.45
33:BA:2758:A:H2'	33:BA:2759:G:H5'	1.98	0.45
23:AW:68:ILE:HD11	56:AW:601:GNP:H5'1	1.98	0.45
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
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
39:BG:8:VAL:HB	39:BG:49:LEU:H	1.81	0.45
38:BF:39:VAL:HG12	38:BF:85:GLY:HA2	1.98	0.45
55:BZ:70:ILE:HA	55:BZ:70:ILE:HD13	1.83	0.45
33:BA:2154:A:C4	33:BA:2155:U:H1'	2.52	0.45
33:BA:2137:U:O4	33:BA:2154:A:C6	2.69	0.45
33:BA:2897:U:H2'	33:BA:2898:U:C6	2.51	0.45
39:BG:71:LEU:HD13	39:BG:74:MET:SD	2.57	0.45
33:BA:1139:G:O2'	33:BA:1143:A:N1	2.40	0.45
1:AA:148:G:O2'	1:AA:1446:A:N3	2.37	0.45
9:AI:86:LEU:O	9:AI:93:LEU:HD11	2.15	0.45
37:BE:108:ILE:HG13	37:BE:181:ILE:HG12	1.98	0.45
5:AE:44:ARG:HG2	5:AE:72:ASN:OD1	2.17	0.45
1:AA:719:C:N4	18:AR:59:LYS:HE2	2.31	0.45
7:AG:121:ASN:O	7:AG:125:ASP:HB2	2.15	0.45
3:AC:163:ARG:NH1	3:AC:165:GLU:OE2	2.49	0.45
33:BA:1361:G:H2'	33:BA:1362:C:C6	2.51	0.45
12:AL:102:ASP:OD1	23:AW:407:LEU:CD1	2.44	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1070:A:C2	33:BA:1097:U:H4'	2.52	0.45
53:BX:28:ASN:OD1	53:BX:29:THR:HG22	2.16	0.45
24:B0:28:GLU:O	24:B0:31:LEU:HG	2.16	0.45
35:BC:158:GLY:H	35:BC:194:VAL:HG13	1.80	0.45
8:AH:79:ARG:HG3	8:AH:82:LEU:H	1.80	0.45
1:AA:345:C:HO2'	1:AA:346:G:P	2.39	0.45
33:BA:1082:U:O3'	40:BH:41:LEU:HD13	2.16	0.45
23:AW:310:LYS:HE2	23:AW:310:LYS:HB3	1.67	0.45
1:AA:908:A:C2	1:AA:909:A:C5	3.04	0.45
39:BG:38:ASP:N	39:BG:38:ASP:OD1	2.48	0.45
41:BI:64:ARG:HD2	41:BI:64:ARG:HA	1.64	0.45
38:BF:2:LYS:O	38:BF:5:ASP:N	2.49	0.45
53:BX:50:LEU:H	53:BX:50:LEU:HD12	1.81	0.45
39:BG:100:ASN:O	39:BG:116:LEU:HB2	2.15	0.45
24:B0:22:VAL:O	24:B0:25:PHE:HD2	1.99	0.45
26:B2:16:THR:O	26:B2:20:ASN:HB2	2.16	0.45
23:AW:146:ARG:HH11	33:BA:2657:A:P	2.38	0.45
1:AA:1410:A:N1	1:AA:1491:G:O6	2.50	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:1818:U:O4	35:BC:152:GLN:HG2	2.17	0.45
35:BC:105:ALA:O	35:BC:195:GLY:N	2.40	0.45
1:AA:717:U:C4	1:AA:734:G:N7	2.84	0.45
4:AD:61:ARG:HH21	4:AD:67:LEU:CD2	2.30	0.45
1:AA:1300:G:O2'	1:AA:1301:U:P	2.74	0.45
33:BA:2741:A:H2'	33:BA:2742:G:O4'	2.16	0.45
1:AA:403:C:H2'	1:AA:404:G:C8	2.51	0.45
21:AU:36:PHE:HB3	21:AU:40:PRO:CD	2.46	0.45
53:BX:60:THR:HB	53:BX:81:LYS:HE2	1.98	0.45
1:AA:1144:G:N2	1:AA:1146:A:H62	2.15	0.45
33:BA:1476:U:H4'	33:BA:1732:C:O2'	2.16	0.45
50:BU:8:ILE:H	50:BU:8:ILE:HG12	1.52	0.45
33:BA:1569:A:N6	33:BA:1570:A:C6	2.84	0.45
37:BE:106:LYS:HG3	37:BE:200:LEU:HD12	1.99	0.45
33:BA:1847:A:H2'	33:BA:1848:A:C8	2.52	0.45
25:B1:17:ARG:NH1	33:BA:201:C:OP1	2.50	0.45
1:AA:484:G:H4'	1:AA:485:U:C5'	2.46	0.45
41:BI:100:ILE:HD12	41:BI:105:LEU:HD11	1.98	0.45
33:BA:2228:G:H2'	33:BA:2229:U:C6	2.51	0.45
33:BA:843:G:H2'	33:BA:844:A:C8	2.52	0.45
24:B0:20:LEU:HD13	33:BA:2355:G:H4'	1.99	0.45
33:BA:1590:A:H2'	33:BA:1591:A:C8	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
49:BT:62:LYS:HB3	49:BT:69:VAL:HG13	1.97	0.45
4:AD:137:SER:HB2	4:AD:140:ASP:OD1	2.17	0.45
33:BA:2554:U:H2'	33:BA:2555:U:C6	2.52	0.45
27:B3:42:ALA:O	33:BA:851:C:O2'	2.34	0.45
23:AW:413:LEU:O	23:AW:417:VAL:N	2.32	0.45
8:AH:115:ALA:HA	8:AH:118:ALA:HB3	1.98	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
2:AB:46:VAL:HA	2:AB:49:PHE:CE2	2.52	0.45
1:AA:49:U:H3	1:AA:362:G:H1'	1.81	0.45
33:BA:27:G:H1'	33:BA:513:A:N6	2.30	0.45
1:AA:81:A:H2	1:AA:88:U:H3	1.64	0.45
23:AW:314:ARG:NH1	23:AW:418:GLN:O	2.50	0.45
33:BA:784:G:C6	35:BC:227:VAL:HG11	2.52	0.45
28:B4:45:ASP:O	28:B4:52:LYS:HE3	2.17	0.45
11:AK:28:ASN:HB2	11:AK:56:LYS:HE3	1.99	0.45
45:BP:79:LEU:HD23	45:BP:79:LEU:HA	1.70	0.45
33:BA:859:G:H2'	33:BA:916:G:H1	1.82	0.45
33:BA:1047:G:O2'	33:BA:1110:G:N2	2.50	0.45
1:AA:662:U:O2'	1:AA:836:G:O5'	2.35	0.45
1:AA:537:G:H5''	12:AL:109:ARG:HH12	1.82	0.45
40:BH:132:TYR:C	40:BH:134:GLU:H	2.20	0.45
23:AW:430:PRO:HD2	23:AW:435:ASP:O	2.17	0.45
33:BA:1131:G:O2'	33:BA:1133:A:N7	2.40	0.45
39:BG:15:ASP:OD2	39:BG:26:LYS:N	2.49	0.45
34:BB:82:U:H2'	34:BB:83:G:H8	1.82	0.45
36:BD:28:GLU:HA	36:BD:185:ASN:O	2.17	0.45
35:BC:132:ARG:HD3	35:BC:132:ARG:HA	1.58	0.45
1:AA:1086:U:H5'	1:AA:1087:G:OP2	2.17	0.45
1:AA:335:C:H2'	1:AA:336:A:H8	1.81	0.45
3:AC:41:TYR:OH	3:AC:89:VAL:HG21	2.17	0.45
1:AA:1151:A:H5''	10:AJ:44:THR:OG1	2.17	0.45
30:B6:1:MET:HE3	30:B6:2:LYS:H	1.82	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
25:B1:20:ALA:HB3	25:B1:22:ASN:OD1	2.16	0.45
7:AG:74:VAL:HG11	7:AG:143:MET:HG3	1.99	0.45
2:AB:147:LEU:HB3	2:AB:150:ILE:CG2	2.47	0.45
23:AW:522:GLN:OE1	23:AW:524:HIS:ND1	2.48	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
12:AL:42:LYS:HG3	12:AL:88:ASP:O	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AW:308:ASP:CG	23:AW:309:PRO:HD2	2.37	0.45
1:AA:507:C:C3'	1:AA:508:U:H5''	2.47	0.45
2:AB:95:TRP:HH2	2:AB:100:LEU:HB2	1.82	0.45
33:BA:694:U:OP1	33:BA:1569:A:H1'	2.16	0.45
33:BA:2230:G:C5	33:BA:2231:U:C5	3.05	0.45
1:AA:919:A:O5'	1:AA:919:A:H8	1.98	0.45
33:BA:1676:A:H2'	33:BA:1677:A:O4'	2.17	0.45
4:AD:202:LEU:O	4:AD:205:LYS:HE2	2.15	0.45
1:AA:1085:U:H1'	1:AA:1094:G:C6	2.52	0.45
33:BA:139:U:C5	53:BX:1:MET:HG2	2.52	0.45
44:BO:102:PRO:HB3	44:BO:121:GLU:HB3	1.99	0.45
1:AA:1114:C:C2	1:AA:1187:G:C2	3.05	0.45
33:BA:532:A:OP2	50:BU:40:LYS:HD3	2.16	0.45
13:AM:73:SER:HA	13:AM:76:ILE:HD12	1.96	0.45
33:BA:1746:A:H2'	33:BA:1747:U:C6	2.52	0.45
13:AM:84:CYS:O	13:AM:88:LEU:HG	2.16	0.45
17:AQ:13:SER:HB3	17:AQ:16:MET:HE1	1.98	0.45
49:BT:59:THR:OG1	49:BT:72:VAL:HG12	2.16	0.45
33:BA:1008:A:N6	33:BA:1136:G:C6	2.85	0.45
46:BQ:10:ARG:HH12	46:BQ:89:VAL:H	1.65	0.45
33:BA:1289:C:H2'	33:BA:1290:C:H6	1.81	0.45
33:BA:118:A:C8	33:BA:119:A:C8	3.05	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:1138:G:H2'	33:BA:1139:G:O4'	2.16	0.45
1:AA:1343:G:O3'	9:AI:123:ARG:HB3	2.16	0.45
14:AN:60:ARG:O	14:AN:61:ASN:HB2	2.17	0.45
25:B1:29:LEU:HD23	33:BA:2231:U:OP1	2.16	0.45
33:BA:1709:U:C2	33:BA:1750:G:N2	2.85	0.45
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.17	0.45
40:BH:12:VAL:HG13	40:BH:69:PHE:HZ	1.81	0.45
4:AD:6:PRO:HB2	4:AD:9:LYS:HB2	1.99	0.45
16:AP:23:ASP:HB3	16:AP:26:ASN:HD22	1.81	0.45
12:AL:33:CYS:H	12:AL:54:VAL:HG13	1.82	0.45
43:BN:13:ARG:HA	43:BN:13:ARG:HD3	1.63	0.45
33:BA:239:C:H2'	33:BA:240:C:O4'	2.17	0.45
55:BZ:29:ILE:HD12	55:BZ:38:LEU:O	2.17	0.45
33:BA:781:A:OP1	35:BC:216:ARG:NH2	2.49	0.45
2:AB:170:ILE:O	2:AB:174:GLU:HB2	2.16	0.45
10:AJ:67:ILE:HG13	14:AN:95:LEU:HD13	1.99	0.45
19:AS:18:VAL:HG11	19:AS:43:MET:HG2	1.99	0.45
42:BL:11:VAL:HG21	42:BM:28:GLU:OE1	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AW:398:PHE:O	23:AW:399:ARG:HB2	2.17	0.45
23:AW:46:VAL:O	23:AW:49:ARG:HB2	2.17	0.45
9:AI:83:THR:HG21	9:AI:102:PHE:CB	2.47	0.45
33:BA:1509:A:O2'	33:BA:1510:G:P	2.74	0.45
33:BA:1509:A:O2'	33:BA:1510:G:H8	2.00	0.45
33:BA:321:U:H5''	37:BE:131:THR:HG23	1.99	0.45
32:B8:9:LYS:CD	32:B8:9:LYS:H	2.30	0.45
1:AA:928:G:C2	1:AA:1390:U:O2	2.70	0.45
40:BH:117:LEU:O	40:BH:119:PRO:HD2	2.17	0.45
33:BA:1212:G:HO2'	33:BA:1213:A:P	2.38	0.45
25:B1:61:LYS:NZ	33:BA:372:G:OP1	2.50	0.45
25:B1:32:LEU:HD23	25:B1:49:ARG:HE	1.81	0.45
3:AC:49:ALA:HB1	3:AC:75:VAL:HG22	1.99	0.45
50:BU:65:ASN:HD21	50:BU:69:ARG:NH2	2.15	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:1118:U:H1'	1:AA:1179:A:C4	2.52	0.45
38:BF:146:ASP:HB2	38:BF:149:ARG:HH21	1.82	0.45
40:BH:126:LEU:HD13	40:BH:127:ALA:H	1.81	0.45
28:B4:28:SER:HB2	28:B4:37:HIS:NE2	2.31	0.45
33:BA:871:U:H2'	33:BA:872:U:C6	2.51	0.45
42:BL:15:SER:OG	42:BL:16:VAL:N	2.50	0.45
33:BA:555:G:HO2'	33:BA:556:A:H8	1.65	0.45
44:BO:73:ASP:O	49:BT:74:GLN:HG3	2.17	0.45
40:BH:51:TYR:HB2	40:BH:89:PRO:CD	2.47	0.45
33:BA:1097:U:C5	33:BA:1098:A:H1'	2.52	0.45
8:AH:85:TYR:O	8:AH:86:LYS:HD2	2.17	0.45
1:AA:681:A:C2	1:AA:710:G:C2	3.05	0.45
1:AA:1461:G:H2'	1:AA:1462:C:C6	2.52	0.45
43:BN:42:ALA:O	43:BN:44:TYR:HB3	2.17	0.45
1:AA:983:A:H5'	14:AN:2:LYS:HZ1	1.80	0.45
43:BN:36:LEU:HD21	43:BN:122:LEU:HB2	1.98	0.45
38:BF:33:ILE:HG12	38:BF:95:MET:HG3	1.99	0.45
33:BA:1316:U:H2'	33:BA:1317:G:H8	1.79	0.45
33:BA:2197:U:O2'	33:BA:2198:A:O5'	2.34	0.45
33:BA:2109:U:C4	33:BA:2181:U:O4	2.70	0.45
41:BI:123:ALA:HA	41:BI:126:ARG:NE	2.32	0.45
33:BA:1006:C:C2	33:BA:1138:G:N2	2.85	0.45
43:BN:81:ILE:HG12	43:BN:82:GLY:H	1.81	0.45
33:BA:1589:U:H2'	33:BA:1590:A:C8	2.52	0.45
2:AB:130:LYS:NZ	2:AB:130:LYS:HA	2.30	0.45
27:B3:37:ARG:HH12	33:BA:929:U:H4'	1.82	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:801:U:H2'	1:AA:802:A:C8	2.52	0.45
1:AA:1306:A:N6	1:AA:1331:G:H1'	2.31	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
33:BA:49:A:N6	33:BA:177:G:C4	2.85	0.45
49:BT:20:ARG:HB3	49:BT:23:ASP:OD1	2.16	0.45
7:AG:144:ALA:C	7:AG:146:ALA:H	2.21	0.45
49:BT:57:ALA:HB2	49:BT:74:GLN:HA	1.98	0.45
39:BG:130:ILE:HG22	39:BG:132:LEU:HD22	1.99	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
33:BA:878:A:C6	33:BA:900:A:H1'	2.51	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
1:AA:1348:U:H4'	9:AI:121:ARG:HG3	1.99	0.45
33:BA:38:A:N3	37:BE:43:THR:HB	2.32	0.45
15:AO:29:ALA:HA	15:AO:84:LEU:HD21	1.98	0.45
40:BH:32:GLY:HA2	40:BH:108:VAL:CG2	2.47	0.45
33:BA:2093:G:H1'	33:BA:2198:A:H2	1.82	0.45
33:BA:2328:A:H2'	33:BA:2329:U:C6	2.52	0.45
17:AQ:66:LEU:HD23	17:AQ:66:LEU:HA	1.81	0.45
36:BD:110:THR:N	36:BD:202:ILE:O	2.49	0.45
1:AA:1053:G:N7	1:AA:1200:C:H5''	2.32	0.45
2:AB:44:LYS:HA	2:AB:44:LYS:HD2	1.72	0.45
16:AP:23:ASP:HB3	16:AP:26:ASN:ND2	2.32	0.45
1:AA:695:A:H2'	1:AA:696:A:C8	2.51	0.45
1:AA:340:U:C2	1:AA:350:G:N2	2.85	0.45
1:AA:1168:U:H5''	1:AA:1169:A:OP2	2.17	0.45
39:BG:37:ASN:HB3	39:BG:40:VAL:HG13	1.99	0.45
33:BA:1607:C:H5''	33:BA:1608:A:H5'	1.98	0.45
33:BA:1239:G:H2'	33:BA:1240:U:O4'	2.16	0.45
33:BA:1223:G:C6	33:BA:1227:G:C6	3.05	0.45
23:AW:145:ASP:O	23:AW:176:GLY:HA2	2.17	0.44
1:AA:1321:U:C4	1:AA:1322:C:N4	2.85	0.44
1:AA:205:A:H3'	1:AA:206:C:C6	2.51	0.44
24:B0:17:ALA:O	24:B0:18:LYS:HB2	2.17	0.44
54:BY:94:PHE:HD1	54:BY:99:SER:HA	1.81	0.44
2:AB:53:LEU:HA	2:AB:56:LEU:HB3	1.98	0.44
35:BC:172:THR:HG22	35:BC:182:LYS:HG2	1.97	0.44
21:AU:39:LYS:N	21:AU:40:PRO:HD2	2.32	0.44
40:BH:136:ILE:H	40:BH:136:ILE:HD12	1.81	0.44
33:BA:933:A:H5'	33:BA:934:U:OP2	2.16	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AW:125:LYS:O	23:AW:129:VAL:HG23	2.18	0.44
1:AA:253:A:H2'	1:AA:254:G:C8	2.51	0.44
38:BF:133:GLU:H	38:BF:150:GLY:HA3	1.82	0.44
33:BA:2308:G:H2'	33:BA:2310:C:H41	1.82	0.44
33:BA:2881:U:H2'	33:BA:2882:A:H8	1.82	0.44
45:BP:51:GLU:OE1	45:BP:56:PRO:HA	2.17	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
36:BD:27:ILE:HB	36:BD:187:LEU:HB3	1.99	0.44
33:BA:861:A:H2'	33:BA:862:G:O4'	2.17	0.44
37:BE:147:LEU:HB3	37:BE:186:VAL:HG23	1.98	0.44
55:BZ:10:LYS:HD3	55:BZ:10:LYS:H	1.82	0.44
41:BI:44:LYS:HD2	41:BI:44:LYS:HA	1.77	0.44
27:B3:23:LEU:HA	27:B3:23:LEU:HD12	1.86	0.44
50:BU:59:LEU:HD23	50:BU:59:LEU:HA	1.83	0.44
31:B7:26:ALA:O	31:B7:43:LEU:HD13	2.17	0.44
33:BA:2094:A:C2	33:BA:2196:C:C2	3.04	0.44
41:BI:20:SER:HB3	41:BI:21:PRO:HD3	1.99	0.44
37:BE:137:LYS:O	37:BE:141:MET:HG3	2.17	0.44
4:AD:169:TRP:HB2	4:AD:183:ARG:O	2.15	0.44
33:BA:1103:A:H5''	33:BA:1104:C:C5	2.52	0.44
33:BA:1568:G:C4'	35:BC:58:LYS:HB3	2.38	0.44
20:AT:78:LEU:HD23	20:AT:78:LEU:HA	1.54	0.44
33:BA:1818:U:O2'	33:BA:1819:A:P	2.75	0.44
23:AW:304:GLN:HG2	23:AW:305:ALA:N	2.31	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:CE	44:BO:111:LYS:H	2.30	0.44
23:AW:100:TYR:CE1	23:AW:129:VAL:HG21	2.52	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
33:BA:586:A:C2	33:BA:1254:A:C2	3.06	0.44
33:BA:2690:U:O2'	33:BA:2872:A:H1'	2.17	0.44
51:BV:71:LYS:HE3	51:BV:73:LYS:HE3	1.99	0.44
8:AH:8:ASP:HA	8:AH:11:THR:HG22	1.98	0.44
33:BA:1177:G:H2'	33:BA:1178:C:O4'	2.16	0.44
8:AH:46:GLU:HA	8:AH:63:LYS:HD2	2.00	0.44
33:BA:1275:A:H3'	33:BA:1645:G:O2'	2.16	0.44
5:AE:15:ILE:HD12	5:AE:109:ALA:HA	1.99	0.44
24:B0:44:PHE:O	24:B0:78:PHE:HA	2.17	0.44
17:AQ:12:VAL:O	17:AQ:13:SER:HB2	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:899:A:C2'	33:BA:900:A:H8	2.28	0.44
1:AA:1219:A:H2'	1:AA:1220:G:H8	1.82	0.44
33:BA:2561:U:H4'	44:BO:22:ILE:HD11	1.97	0.44
1:AA:130:A:O2'	1:AA:264:C:H5'	2.16	0.44
33:BA:2197:U:C2'	33:BA:2198:A:H2'	2.47	0.44
25:B1:16:ASN:ND2	33:BA:2081:U:H5''	2.32	0.44
9:AI:21:LYS:HE3	9:AI:21:LYS:HB3	1.72	0.44
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.53	0.44
47:BR:8:ARG:O	47:BR:10:LEU:HD22	2.17	0.44
47:BR:8:ARG:HD2	47:BR:10:LEU:HD11	2.00	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
54:BY:42:LYS:N	54:BY:42:LYS:HD3	2.32	0.44
1:AA:1277:C:O2'	1:AA:1279:G:H1'	2.17	0.44
19:AS:39:ILE:HD13	19:AS:61:VAL:HG12	1.98	0.44
53:BX:69:ARG:HB3	53:BX:70:HIS:H	1.60	0.44
33:BA:2031:A:C6	33:BA:2498:C:H1'	2.52	0.44
2:AB:40:ILE:HG21	2:AB:201:GLY:N	2.27	0.44
33:BA:2727:A:O2'	44:BO:70:ARG:NH2	2.50	0.44
53:BX:8:LEU:HA	53:BX:8:LEU:HD13	1.46	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
1:AA:376:G:C2	1:AA:389:A:C2	3.05	0.44
33:BA:612:G:C2	33:BA:614:A:H1'	2.51	0.44
41:BI:30:GLN:HG2	41:BI:32:VAL:H	1.83	0.44
35:BC:129:LEU:HD12	35:BC:191:LEU:HD21	2.00	0.44
33:BA:2423:U:O2'	33:BA:2424:C:P	2.76	0.44
42:BL:17:MET:O	42:BL:21:GLU:HG3	2.17	0.44
33:BA:271:G:H1'	33:BA:272:A:C8	2.52	0.44
24:B0:20:LEU:CD1	33:BA:2355:G:H4'	2.47	0.44
16:AP:40:ASN:HA	16:AP:41:PRO:HD2	1.88	0.44
13:AM:93:GLY:HA2	13:AM:108:ARG:NH1	2.33	0.44
8:AH:54:THR:HG23	8:AH:55:LYS:HD3	1.99	0.44
4:AD:151:GLN:H	4:AD:154:VAL:CG1	2.31	0.44
35:BC:153:LEU:H	35:BC:153:LEU:HG	1.44	0.44
40:BH:25:ALA:CA	40:BH:85:SER:HG	2.31	0.44
23:AW:19:ILE:HA	23:AW:89:THR:OG1	2.18	0.44
38:BF:110:ILE:HD11	38:BF:136:ILE:HD13	1.99	0.44
43:BN:114:LEU:HD23	43:BN:114:LEU:HA	1.80	0.44
1:AA:962:C:H2'	1:AA:963:G:H8	1.83	0.44
35:BC:156:SER:O	35:BC:194:VAL:HG11	2.18	0.44
1:AA:479:U:O2'	1:AA:480:U:H5'	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:923:A:OP1	5:AE:25:LYS:HG2	2.17	0.44
1:AA:595:A:C5	1:AA:641:U:C4	3.05	0.44
46:BQ:10:ARG:NH1	46:BQ:89:VAL:H	2.15	0.44
33:BA:859:G:H2'	33:BA:916:G:N1	2.33	0.44
1:AA:664:G:H2'	1:AA:666:G:OP1	2.18	0.44
33:BA:1656:C:C2	33:BA:1657:U:C5	3.05	0.44
37:BE:75:SER:O	37:BE:78:TRP:HB2	2.17	0.44
33:BA:2137:U:H6	33:BA:2137:U:O5'	2.01	0.44
1:AA:859:G:H2'	1:AA:860:A:C8	2.53	0.44
33:BA:1340:U:C5	33:BA:1603:A:C8	3.06	0.44
33:BA:585:G:H5''	33:BA:586:A:OP1	2.17	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
2:AB:116:LEU:HD12	2:AB:140:LEU:HD11	1.99	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
1:AA:685:G:H2'	1:AA:686:U:C6	2.53	0.44
33:BA:1465:G:H2'	33:BA:1466:U:O4'	2.18	0.44
23:AW:89:THR:HA	23:AW:90:PRO:HD2	1.59	0.44
33:BA:2182:U:H2'	33:BA:2183:A:OP1	2.17	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
23:AW:472:ARG:CD	23:AW:503:TYR:HB3	2.44	0.44
35:BC:171:VAL:HG23	35:BC:185:ALA:CB	2.47	0.44
10:AJ:11:LYS:HE2	10:AJ:71:LEU:HD21	1.99	0.44
6:AF:9:MET:HA	6:AF:58:HIS:O	2.17	0.44
33:BA:1830:C:H6	33:BA:1830:C:O5'	2.01	0.44
37:BE:123:LYS:HG3	37:BE:124:PHE:H	1.82	0.44
33:BA:77:G:C6	33:BA:78:U:C4	3.06	0.44
27:B3:40:THR:O	27:B3:43:ILE:HG13	2.18	0.44
9:AI:16:ALA:CB	9:AI:78:ILE:HD13	2.48	0.44
25:B1:39:VAL:HG21	25:B1:42:GLU:HB2	1.99	0.44
34:BB:116:G:H2'	34:BB:117:G:C8	2.51	0.44
5:AE:23:THR:HA	5:AE:28:ARG:HA	2.00	0.44
39:BG:168:VAL:O	39:BG:170:THR:HG23	2.18	0.44
48:BS:94:ARG:H	48:BS:94:ARG:HG3	1.50	0.44
14:AN:27:LYS:HB2	14:AN:27:LYS:HE3	1.91	0.44
13:AM:46:GLU:O	13:AM:46:GLU:HG3	2.17	0.44
1:AA:255:G:H4'	17:AQ:18:LYS:HD2	1.98	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
1:AA:186:C:O4'	20:AT:75:LYS:HD2	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1376:C:N4	33:BA:1377:G:C6	2.86	0.44
1:AA:567:G:H2'	1:AA:568:G:O4'	2.18	0.44
33:BA:644:A:H61	33:BA:2349:G:H21	1.66	0.44
23:AW:452:ARG:O	23:AW:459:VAL:HG23	2.16	0.44
36:BD:106:LYS:H	36:BD:106:LYS:HD2	1.82	0.44
23:AW:428:PHE:N	23:AW:437:ILE:O	2.46	0.44
4:AD:8:LEU:O	4:AD:12:ARG:HG3	2.18	0.44
23:AW:474:VAL:CG2	23:AW:501:LEU:H	2.31	0.44
10:AJ:80:THR:HB	10:AJ:83:THR:CG2	2.47	0.44
36:BD:68:PHE:HB2	36:BD:73:VAL:HG12	1.99	0.44
43:BN:4:PHE:N	43:BN:44:TYR:OH	2.51	0.44
40:BH:24:SER:HB2	40:BH:116:GLU:CD	2.38	0.44
1:AA:391:G:C6	1:AA:392:C:C4	3.06	0.44
3:AC:155:ARG:HH11	3:AC:192:TYR:HB2	1.82	0.44
33:BA:1212:G:HO2'	33:BA:1236:G:N2	2.14	0.44
11:AK:60:PHE:O	11:AK:64:VAL:HG13	2.17	0.44
4:AD:84:ASN:O	4:AD:88:ASN:ND2	2.45	0.44
37:BE:18:THR:HG22	37:BE:106:LYS:HE3	2.00	0.44
1:AA:1111:A:N1	3:AC:176:THR:OG1	2.43	0.44
1:AA:110:C:H2'	1:AA:111:G:O4'	2.17	0.44
33:BA:7:G:H4'	43:BN:15:TRP:CZ2	2.53	0.44
41:BI:109:ALA:HA	41:BI:128:ILE:HD12	2.00	0.44
1:AA:505:G:C6	1:AA:535:A:C2	3.05	0.44
33:BA:1342:A:O2'	33:BA:1344:U:OP2	2.26	0.44
24:B0:16:GLU:HB2	24:B0:17:ALA:H	1.34	0.44
44:BO:70:ARG:HD3	44:BO:76:VAL:HG22	2.00	0.44
1:AA:1219:A:H2'	1:AA:1220:G:C8	2.53	0.44
33:BA:2591:C:OP1	35:BC:237:ARG:HG3	2.18	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
1:AA:607:A:H2'	1:AA:608:A:C8	2.52	0.44
33:BA:2572:A:OP1	33:BA:2574:G:H4'	2.18	0.44
33:BA:817:C:C2	33:BA:818:G:C8	3.06	0.44
1:AA:589:U:H2'	1:AA:590:U:C6	2.52	0.44
33:BA:800:A:H8	33:BA:800:A:OP1	2.00	0.44
33:BA:156:A:H2'	33:BA:157:C:C6	2.53	0.44
1:AA:187:G:C2	1:AA:191:G:C6	3.06	0.44
37:BE:153:LEU:HB2	37:BE:171:ASP:HB3	1.99	0.44
23:AW:407:LEU:HD22	23:AW:409:GLN:HG3	2.00	0.44
1:AA:69:G:H5'	1:AA:70:U:OP1	2.17	0.44
9:AI:43:ALA:O	9:AI:46:VAL:HG22	2.18	0.44
23:AW:503:TYR:O	23:AW:504:ILE:HB	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:AF:52:ASN:O	6:AF:53:LYS:HB2	2.18	0.44
33:BA:42:A:N6	33:BA:437:U:H3	2.16	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
33:BA:1019:U:O2'	33:BA:1021:A:N7	2.42	0.44
33:BA:520:G:H5'	52:BW:73:LYS:NZ	2.33	0.44
33:BA:1187:G:OP1	51:BV:85:LYS:NZ	2.51	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
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
33:BA:569:U:C4	33:BA:570:G:C6	3.05	0.44
17:AQ:3:LYS:HB3	17:AQ:3:LYS:HE3	1.81	0.44
33:BA:2730:C:H4'	36:BD:174:SER:HB3	2.00	0.44
44:BO:8:LEU:HB2	44:BO:82:ASN:HB2	1.99	0.44
33:BA:1527:G:N1	33:BA:1544:A:OP2	2.40	0.44
1:AA:727:G:C2	1:AA:731:G:C2	3.05	0.44
1:AA:29:U:H5'	1:AA:296:U:OP1	2.18	0.44
39:BG:84:LYS:HB2	39:BG:85:LYS:H	1.62	0.43
39:BG:53:PRO:HB3	39:BG:61:TRP:H	1.83	0.43
55:BZ:76:ASP:N	55:BZ:90:ASP:HB2	2.33	0.43
4:AD:57:LYS:HG3	4:AD:58:GLN:N	2.32	0.43
33:BA:184:C:H2'	33:BA:185:G:C8	2.50	0.43
1:AA:9:G:H2'	1:AA:10:A:H8	1.83	0.43
1:AA:77:A:N6	1:AA:91:U:O4	2.51	0.43
18:AR:70:THR:OG1	18:AR:72:ARG:HG2	2.18	0.43
1:AA:673:A:H2'	1:AA:674:G:C8	2.53	0.43
31:B7:29:ARG:HD2	33:BA:2394:C:OP2	2.18	0.43
20:AT:67:HIS:HB3	20:AT:68:LYS:NZ	2.33	0.43
46:BQ:43:ALA:O	46:BQ:46:ILE:HG12	2.18	0.43
42:BK:4:LYS:O	42:BK:8:ILE:HG12	2.17	0.43
33:BA:671:C:H2'	33:BA:672:C:H6	1.83	0.43
27:B3:24:LEU:HD21	33:BA:930:G:H1'	2.00	0.43
47:BR:78:LYS:HG2	47:BR:83:LEU:HD13	2.00	0.43
1:AA:21:G:H2'	1:AA:22:G:C8	2.53	0.43
7:AG:64:ALA:HB1	7:AG:126:ALA:HB3	2.00	0.43
41:BI:56:VAL:HG21	41:BI:68:PHE:HD2	1.82	0.43
23:AW:410:LYS:HA	23:AW:414:LYS:H	1.84	0.43
23:AW:390:ILE:HA	23:AW:391:PRO:HD3	1.72	0.43
2:AB:164:ASP:CB	2:AB:203:ASP:HB2	2.48	0.43
13:AM:85:TYR:O	13:AM:88:LEU:HB2	2.18	0.43
1:AA:1225:A:H1'	19:AS:77:ARG:HD2	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:2258:C:O2'	33:BA:2426:A:H4'	2.18	0.43
33:BA:1509:A:HO2'	33:BA:1510:G:H8	1.64	0.43
33:BA:740:C:H5''	33:BA:1784:A:OP1	2.19	0.43
23:AW:307:MET:HE2	23:AW:309:PRO:HD3	2.00	0.43
40:BH:18:VAL:HA	40:BH:86:MET:HE2	2.00	0.43
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
48:BS:90:VAL:O	48:BS:117:PHE:HB3	2.18	0.43
40:BH:134:GLU:O	40:BH:136:ILE:N	2.51	0.43
5:AE:55:VAL:O	5:AE:59:ILE:HG23	2.18	0.43
1:AA:55:A:C6	23:AW:311:HIS:CE1	3.06	0.43
34:BB:24:G:H4'	34:BB:25:U:H5	1.82	0.43
1:AA:1031:C:O2'	1:AA:1032:G:N2	2.51	0.43
40:BH:35:VAL:O	40:BH:39:THR:HG23	2.17	0.43
1:AA:484:G:H4'	1:AA:485:U:H5'	2.00	0.43
33:BA:700:G:C6	33:BA:733:G:N2	2.86	0.43
1:AA:634:C:H2'	1:AA:635:A:C8	2.52	0.43
33:BA:569:U:H2'	33:BA:570:G:O4'	2.17	0.43
1:AA:1039:G:C6	1:AA:1040:U:C4	3.06	0.43
23:AW:466:VAL:HG12	23:AW:468:VAL:HG23	2.00	0.43
5:AE:33:THR:HG22	5:AE:51:LYS:HE2	1.99	0.43
6:AF:48:ALA:HB2	18:AR:66:LEU:O	2.18	0.43
30:B6:34:ARG:NH1	30:B6:39:ARG:HG2	2.33	0.43
5:AE:96:GLN:HA	5:AE:97:PRO:HD2	1.50	0.43
33:BA:1074:G:H4'	33:BA:1074:G:OP1	2.17	0.43
53:BX:86:THR:O	53:BX:87:LEU:HG	2.19	0.43
23:AW:471:ALA:HA	23:AW:472:ARG:O	2.18	0.43
35:BC:67:LYS:HG2	35:BC:150:GLY:HA2	2.00	0.43
1:AA:427:U:OP1	4:AD:12:ARG:NH2	2.51	0.43
6:AF:92:THR:HG22	6:AF:93:LYS:N	2.33	0.43
1:AA:972:C:O2'	10:AJ:57:VAL:HA	2.18	0.43
11:AK:102:ALA:HB3	11:AK:104:PHE:H	1.83	0.43
50:BU:63:ARG:CZ	50:BU:96:ASP:HA	2.47	0.43
45:BP:95:LEU:HD13	45:BP:101:ILE:HD11	2.00	0.43
33:BA:1045:C:C5'	33:BA:1046:A:H5'	2.47	0.43
1:AA:129:A:O2'	1:AA:130:A:C8	2.70	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
7:AG:117:LEU:O	7:AG:121:ASN:ND2	2.49	0.43
1:AA:865:A:H2'	1:AA:866:C:C6	2.53	0.43
1:AA:335:C:H2'	1:AA:336:A:C8	2.54	0.43
1:AA:1206:G:H2'	1:AA:1207:G:O4'	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:AK:106:ILE:HG12	11:AK:109:ILE:HD11	2.01	0.43
33:BA:2505:G:O2'	33:BA:2506:U:H5'	2.17	0.43
52:BW:32:ALA:O	52:BW:36:LEU:HB2	2.19	0.43
38:BF:46:LYS:HD2	38:BF:46:LYS:H	1.83	0.43
26:B2:9:LYS:O	26:B2:12:GLU:N	2.51	0.43
20:AT:21:ALA:O	20:AT:25:SER:HB2	2.19	0.43
43:BN:56:VAL:O	43:BN:124:VAL:O	2.35	0.43
23:AW:420:SER:HB3	23:AW:426:GLN:OE1	2.18	0.43
1:AA:497:G:OP1	23:AW:480:LYS:HE2	2.18	0.43
12:AL:29:LYS:O	12:AL:80:LEU:HD12	2.18	0.43
23:AW:49:ARG:HB3	23:AW:50:GLY:H	1.35	0.43
38:BF:135:ILE:HD11	38:BF:145:VAL:HG11	2.00	0.43
33:BA:2867:G:O2'	33:BA:2868:A:P	2.77	0.43
20:AT:78:LEU:O	20:AT:82:ILE:HG23	2.17	0.43
35:BC:32:LEU:HD23	35:BC:32:LEU:HA	1.70	0.43
5:AE:121:ASN:N	5:AE:121:ASN:HD22	2.16	0.43
36:BD:109:VAL:HA	36:BD:203:VAL:HA	2.00	0.43
2:AB:139:GLU:O	2:AB:143:LEU:HG	2.18	0.43
23:AW:319:ARG:HA	23:AW:364:ILE:HD13	1.98	0.43
3:AC:122:GLN:HB3	3:AC:127:VAL:CG2	2.48	0.43
33:BA:1287:A:H5'	47:BR:103:ARG:HD2	1.99	0.43
42:BK:3:THR:O	42:BK:7:ILE:HG12	2.18	0.43
1:AA:325:A:N6	1:AA:326:G:C2	2.87	0.43
34:BB:91:C:H2'	34:BB:92:C:H6	1.83	0.43
33:BA:2109:U:H2'	33:BA:2110:G:H5'	1.99	0.43
33:BA:207:A:H2'	33:BA:208:C:O4'	2.19	0.43
45:BP:131:ALA:O	45:BP:135:ILE:HG12	2.18	0.43
33:BA:1036:G:C6	33:BA:1120:G:C5	3.06	0.43
33:BA:2654:A:OP1	33:BA:2654:A:H8	2.02	0.43
33:BA:2540:C:H2'	33:BA:2541:A:O4'	2.18	0.43
33:BA:2286:G:H5''	33:BA:2287:A:O5'	2.19	0.43
3:AC:81:GLU:O	3:AC:84:GLU:HB3	2.18	0.43
45:BP:118:THR:HA	45:BP:119:PRO:HD3	1.81	0.43
12:AL:21:PRO:C	12:AL:23:LEU:H	2.21	0.43
33:BA:947:A:H2'	33:BA:948:C:C6	2.53	0.43
1:AA:382:A:H2'	1:AA:383:A:C8	2.54	0.43
24:B0:37:VAL:HG12	24:B0:38:ARG:HD3	2.00	0.43
10:AJ:10:LEU:CD1	10:AJ:98:VAL:HG12	2.48	0.43
33:BA:244:A:H2'	33:BA:245:G:O4'	2.19	0.43
9:AI:18:VAL:HG11	9:AI:82:ILE:HG12	2.01	0.43
1:AA:908:A:C2	1:AA:909:A:C4	3.07	0.43
33:BA:1219:U:OP2	50:BU:18:LYS:NZ	2.41	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1905:C:H4'	33:BA:1929:G:H8	1.83	0.43
33:BA:479:A:H4'	33:BA:480:A:H5'	1.99	0.43
47:BR:96:ARG:HD3	47:BR:98:LEU:HD21	1.99	0.43
43:BN:64:VAL:HG13	43:BN:68:LYS:HB2	2.01	0.43
33:BA:1650:A:C2	33:BA:2008:C:N3	2.86	0.43
33:BA:733:G:O5'	33:BA:733:G:H8	2.00	0.43
33:BA:2677:G:H2'	33:BA:2678:C:C6	2.54	0.43
1:AA:686:U:H1'	11:AK:43:TRP:CZ2	2.54	0.43
1:AA:177:G:OP2	20:AT:63:LYS:NZ	2.52	0.43
1:AA:1309:G:P	13:AM:90:HIS:HE2	2.41	0.43
50:BU:64:ILE:HD11	50:BU:95:ALA:CB	2.48	0.43
24:B0:76:ARG:O	24:B0:78:PHE:HD2	2.01	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
33:BA:1022:G:C5	33:BA:1140:C:C4	3.06	0.43
45:BP:78:ARG:CZ	45:BP:113:ALA:HB1	2.48	0.43
27:B3:15:ARG:N	27:B3:15:ARG:HD2	2.34	0.43
33:BA:1317:G:H2'	33:BA:1318:U:O4'	2.19	0.43
33:BA:2155:U:C4	33:BA:2156:G:C6	3.06	0.43
33:BA:307:G:H2'	33:BA:309:A:OP2	2.18	0.43
40:BH:28:ALA:CB	40:BH:111:ALA:HB2	2.49	0.43
31:B7:22:LYS:HE2	33:BA:630:G:OP1	2.19	0.43
33:BA:836:G:N7	33:BA:837:C:N4	2.66	0.43
49:BT:23:ASP:OD2	49:BT:88:ARG:HA	2.18	0.43
1:AA:295:C:C4	1:AA:296:U:C4	3.07	0.43
33:BA:2404:U:H2'	33:BA:2405:G:O4'	2.19	0.43
2:AB:45:THR:HG23	2:AB:200:PRO:HG2	2.00	0.43
33:BA:1851:U:C4	33:BA:1852:U:C4	3.06	0.43
33:BA:1038:G:C2	33:BA:1118:C:C2	3.07	0.43
1:AA:400:C:O2'	1:AA:401:C:H5'	2.18	0.43
37:BE:146:VAL:HA	37:BE:185:LYS:O	2.18	0.43
23:AW:216:ASP:OD2	23:AW:216:ASP:N	2.52	0.43
33:BA:2291:U:H2'	33:BA:2292:U:C6	2.54	0.43
9:AI:48:ARG:HH21	9:AI:52:GLU:HA	1.83	0.43
34:BB:14:U:OP2	34:BB:70:C:O2'	2.36	0.43
33:BA:1460:U:H5"	33:BA:1461:C:OP2	2.18	0.43
33:BA:1448:G:C2	33:BA:1464:G:C2	3.06	0.43
2:AB:9:LEU:HD12	2:AB:42:LEU:HD22	1.99	0.43
1:AA:49:U:O4	1:AA:362:G:N2	2.51	0.43
23:AW:401:ILE:HD12	23:AW:416:LEU:HD11	2.00	0.43
33:BA:1063:G:H1	33:BA:1075:C:H42	1.66	0.43
36:BD:117:GLY:N	36:BD:165:MET:O	2.47	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
51:BV:37:GLU:HB2	51:BV:53:PHE:CE1	2.53	0.43
33:BA:452:G:N2	33:BA:458:G:C4	2.86	0.43
51:BV:66:HIS:HB3	51:BV:94:THR:HA	1.99	0.43
1:AA:380:G:N2	1:AA:384:G:C6	2.86	0.43
33:BA:1290:C:C2	33:BA:1291:C:C5	3.07	0.43
36:BD:91:THR:O	36:BD:93:GLY:N	2.51	0.43
33:BA:1288:G:C4	33:BA:1327:A:C2	3.06	0.43
1:AA:1064:G:N2	1:AA:1190:G:O2'	2.52	0.43
33:BA:2340:A:H2'	33:BA:2341:G:C8	2.54	0.43
1:AA:936:C:H2'	1:AA:937:A:O4'	2.18	0.43
33:BA:826:U:H1'	45:BP:53:GLY:H	1.83	0.43
33:BA:748:G:O6	33:BA:751:A:H5'	2.19	0.43
40:BH:33:VAL:HG12	40:BH:35:VAL:H	1.83	0.43
26:B2:20:ASN:O	26:B2:24:GLU:HB2	2.18	0.43
33:BA:2692:G:H2'	33:BA:2693:G:H8	1.84	0.43
33:BA:205:G:O2'	33:BA:206:U:OP2	2.36	0.43
13:AM:52:ILE:HD12	13:AM:55:LEU:HD12	2.00	0.43
35:BC:73:ILE:HA	35:BC:74:PRO:HD3	1.85	0.43
33:BA:88:G:C2	33:BA:89:A:C8	3.06	0.43
33:BA:2433:A:H5''	33:BA:2434:A:OP1	2.18	0.43
33:BA:408:G:H1	33:BA:419:U:H3	1.66	0.43
49:BT:93:LYS:HG3	49:BT:94:ALA:N	2.34	0.43
1:AA:751:U:H1'	15:AO:22:GLY:O	2.18	0.43
23:AW:411:GLN:N	23:AW:414:LYS:HB3	2.13	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
9:AI:46:VAL:HA	9:AI:49:GLN:HG3	2.01	0.43
23:AW:472:ARG:CG	23:AW:504:ILE:H	2.28	0.43
23:AW:114:ASP:HB3	23:AW:117:LYS:HB2	2.01	0.43
33:BA:2805:C:H2'	33:BA:2806:C:O4'	2.19	0.43
42:BM:14:MET:HG2	42:BM:17:MET:HG2	2.00	0.43
52:BW:24:ILE:HA	52:BW:24:ILE:HD12	1.73	0.43
33:BA:1288:G:C8	33:BA:1327:A:C6	3.06	0.43
33:BA:2793:C:H2'	33:BA:2794:C:C6	2.54	0.43
23:AW:434:ASN:HB3	23:AW:435:ASP:H	1.41	0.43
3:AC:183:TYR:HE1	3:AC:198:LYS:HB3	1.84	0.43
33:BA:2330:G:C2	33:BA:2386:A:C2	3.07	0.43
7:AG:71:THR:O	7:AG:90:VAL:HG12	2.18	0.43
34:BB:38:C:H2'	34:BB:39:A:C8	2.54	0.43
43:BN:64:VAL:HG11	43:BN:69:ARG:N	2.33	0.43
33:BA:751:A:H5''	33:BA:752:A:OP1	2.19	0.43
13:AM:92:ARG:NH1	19:AS:79:TYR:CZ	2.86	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1652:A:OP1	47:BR:8:ARG:HD3	2.18	0.43
1:AA:866:C:C4'	1:AA:919:A:H5'	2.49	0.43
33:BA:1356:G:C2	33:BA:1376:C:O2	2.71	0.43
43:BN:11:VAL:HG11	43:BN:50:THR:HA	2.01	0.43
4:AD:89:LEU:HD22	4:AD:199:ILE:HD12	2.01	0.43
33:BA:729:G:H2'	33:BA:1775:U:H1'	2.00	0.43
6:AF:45:ARG:HG2	6:AF:46:GLN:N	2.33	0.43
33:BA:2721:A:H2'	33:BA:2722:G:O4'	2.18	0.43
33:BA:2551:C:C4	33:BA:2552:U:C4	3.07	0.43
3:AC:18:ASN:O	3:AC:55:VAL:HA	2.19	0.43
33:BA:2379:G:H4'	48:BS:21:LEU:HD11	2.00	0.43
2:AB:161:PHE:HA	2:AB:183:PHE:O	2.19	0.43
23:AW:472:ARG:HA	23:AW:473:TRP:CB	2.46	0.43
33:BA:558:U:OP1	43:BN:113:PRO:HD2	2.18	0.43
52:BW:20:VAL:O	52:BW:23:LEU:HB2	2.18	0.43
35:BC:80:LEU:HD11	35:BC:109:LEU:HB2	2.01	0.43
1:AA:595:A:H61	1:AA:641:U:H2'	1.84	0.43
33:BA:2547:A:H2'	33:BA:2548:U:C6	2.54	0.43
1:AA:202:G:N2	1:AA:216:U:O2	2.52	0.43
33:BA:2092:U:H4'	33:BA:2093:G:O5'	2.18	0.43
33:BA:1225:G:N1	33:BA:1226:A:N1	2.67	0.43
41:BI:112:LYS:HB3	41:BI:115:ASP:HB3	2.01	0.43
20:AT:53:MET:O	20:AT:56:ILE:HG22	2.18	0.43
33:BA:540:C:H2'	33:BA:541:A:H8	1.84	0.43
33:BA:781:A:O2'	33:BA:1788:C:O2	2.34	0.43
27:B3:3:THR:HA	27:B3:37:ARG:O	2.19	0.43
37:BE:118:LEU:HD23	37:BE:186:VAL:O	2.18	0.43
3:AC:2:GLN:H	3:AC:2:GLN:CD	2.23	0.43
47:BR:99:LYS:HG3	47:BR:99:LYS:H	1.62	0.43
33:BA:1264:A:H2'	33:BA:2014:A:N6	2.33	0.43
47:BR:55:ALA:HA	47:BR:80:PHE:CZ	2.54	0.43
33:BA:587:C:N3	45:BP:33:ARG:NH2	2.67	0.43
9:AI:46:VAL:O	9:AI:49:GLN:HB2	2.18	0.43
23:AW:428:PHE:HB3	23:AW:504:ILE:HD11	2.01	0.43
2:AB:96:LEU:H	2:AB:99:MET:HE3	1.84	0.43
14:AN:12:ARG:HG2	14:AN:53:ASP:HB3	2.01	0.43
33:BA:1798:U:C4	33:BA:1819:A:C2	3.07	0.43
25:B1:28:PHE:HB3	33:BA:396:G:H1'	2.01	0.43
33:BA:1927:A:H2'	33:BA:1928:A:C8	2.54	0.43
37:BE:27:LEU:HG	37:BE:104:ALA:HB2	2.01	0.43
46:BQ:26:VAL:HG13	46:BQ:104:GLU:CD	2.39	0.43
33:BA:2015:A:H3'	33:BA:2016:U:H6	1.84	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1652:A:C2	33:BA:2006:C:N3	2.87	0.43
10:AJ:44:THR:HG23	10:AJ:70:HIS:HA	2.01	0.43
1:AA:791:G:N2	1:AA:1497:G:O3'	2.50	0.43
4:AD:56:GLU:OE2	4:AD:194:ILE:HA	2.19	0.43
2:AB:127:LYS:HD2	2:AB:127:LYS:HA	1.72	0.43
12:AL:113:ARG:NH2	12:AL:120:ARG:HG2	2.34	0.43
35:BC:222:THR:HA	35:BC:232:GLY:HA2	2.00	0.43
37:BE:111:GLU:OE1	37:BE:115:GLN:NE2	2.45	0.43
23:AW:71:THR:CG2	23:AW:72:THR:H	2.31	0.42
33:BA:1104:C:H2'	33:BA:1105:U:C6	2.54	0.42
23:AW:490:GLU:HA	23:AW:493:LEU:HB2	2.00	0.42
1:AA:600:A:H2'	1:AA:601:G:C8	2.54	0.42
11:AK:22:ILE:H	11:AK:22:ILE:HD13	1.84	0.42
23:AW:114:ASP:CG	23:AW:143:LYS:HD2	2.40	0.42
33:BA:1046:A:N6	40:BH:8:LYS:HE2	2.34	0.42
23:AW:96:SER:HB3	23:AW:99:THR:H	1.84	0.42
33:BA:1236:G:O2'	33:BA:1237:A:C8	2.70	0.42
1:AA:357:G:O2'	23:AW:311:HIS:CE1	2.72	0.42
33:BA:592:A:C6	33:BA:593:U:C4	3.06	0.42
39:BG:74:MET:O	39:BG:78:VAL:HG22	2.19	0.42
34:BB:88:C:O2'	34:BB:90:C:N4	2.51	0.42
33:BA:621:A:OP2	45:BP:99:ASN:ND2	2.52	0.42
33:BA:2221:G:H2'	33:BA:2222:C:C6	2.54	0.42
38:BF:21:TYR:HE2	38:BF:28:PRO:HD3	1.84	0.42
45:BP:55:MET:HA	45:BP:56:PRO:HD3	1.79	0.42
6:AF:20:GLY:O	6:AF:23:GLU:HB3	2.19	0.42
43:BN:81:ILE:HG12	43:BN:82:GLY:N	2.34	0.42
14:AN:62:ARG:HG2	14:AN:69:PRO:HB3	2.00	0.42
12:AL:33:CYS:HB3	12:AL:76:HIS:O	2.18	0.42
5:AE:94:PHE:CZ	5:AE:96:GLN:HG2	2.54	0.42
33:BA:571:U:C4	33:BA:575:A:C5	3.08	0.42
1:AA:1057:G:O3'	3:AC:196:GLY:HA3	2.19	0.42
36:BD:112:THR:O	36:BD:195:GLY:HA2	2.19	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
17:AQ:7:LEU:O	17:AQ:59:GLU:HA	2.19	0.42
33:BA:1641:A:H2'	33:BA:1642:G:O4'	2.18	0.42
23:AW:405:ASP:O	23:AW:407:LEU:N	2.53	0.42
23:AW:20:SER:CB	23:AW:26:LYS:HG2	2.49	0.42
33:BA:2846:G:OP1	49:BT:52:ARG:NH1	2.51	0.42
40:BH:14:GLU:CD	40:BH:57:ASN:HD22	2.23	0.42
45:BP:127:VAL:HG11	45:BP:142:ILE:HG21	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1073:A:H3'	33:BA:1074:G:C5'	2.38	0.42
8:AH:84:ILE:HG22	8:AH:124:ILE:HD11	2.00	0.42
1:AA:522:C:H41	12:AL:49:ARG:HH22	1.67	0.42
14:AN:53:ASP:HA	14:AN:58:ARG:HH11	1.84	0.42
52:BW:12:SER:OG	52:BW:13:SER:N	2.52	0.42
1:AA:1036:A:H2'	1:AA:1037:C:C5	2.54	0.42
38:BF:10:GLU:C	38:BF:12:VAL:N	2.72	0.42
55:BZ:80:HIS:ND1	55:BZ:83:LYS:HB2	2.33	0.42
1:AA:1477:U:H2'	1:AA:1478:U:C6	2.54	0.42
49:BT:24:THR:HG23	49:BT:24:THR:O	2.17	0.42
7:AG:94:ARG:O	7:AG:97:ALA:HB3	2.20	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
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:1592:C:H2'	33:BA:1593:A:C8	2.54	0.42
38:BF:174:PHE:HA	38:BF:175:PRO:HD3	1.82	0.42
52:BW:75:PHE:N	52:BW:75:PHE:CD1	2.87	0.42
17:AQ:30:HIS:HA	17:AQ:31:PRO:HD3	1.75	0.42
52:BW:51:LEU:HA	52:BW:105:VAL:HG11	2.01	0.42
45:BP:36:LYS:HB3	45:BP:37:GLY:H	1.61	0.42
33:BA:1722:A:H2'	33:BA:1723:G:C8	2.54	0.42
23:AW:72:THR:CG2	23:AW:88:ASP:H	2.32	0.42
33:BA:2846:G:P	49:BT:52:ARG:NH1	2.92	0.42
25:B1:50:VAL:HG12	25:B1:51:SER:O	2.19	0.42
33:BA:883:G:C5	33:BA:884:U:C4	3.07	0.42
44:BO:76:VAL:HB	49:BT:72:VAL:CG2	2.49	0.42
11:AK:127:ARG:HB2	21:AU:33:ARG:HH22	1.84	0.42
6:AF:6:ILE:HD12	6:AF:62:MET:HG2	2.01	0.42
1:AA:878:A:C5'	8:AH:80:PRO:HG2	2.48	0.42
14:AN:92:ILE:HA	14:AN:93:PRO:HD3	1.75	0.42
23:AW:114:ASP:OD2	23:AW:143:LYS:NZ	2.45	0.42
33:BA:956:G:P	46:BQ:86:LYS:HG3	2.59	0.42
33:BA:372:G:H2'	33:BA:400:G:O6	2.18	0.42
1:AA:1125:U:OP2	1:AA:1145:A:N6	2.52	0.42
33:BA:1522:A:O2'	33:BA:1523:U:O5'	2.36	0.42
1:AA:652:U:O4	1:AA:752:G:H2'	2.20	0.42
33:BA:2800:A:H3'	33:BA:2801:G:C5'	2.49	0.42
43:BN:81:ILE:HG23	43:BN:82:GLY:H	1.84	0.42
53:BX:51:PHE:O	53:BX:53:VAL:HG13	2.19	0.42
33:BA:540:C:H2'	33:BA:541:A:C8	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:BC:30:ALA:N	35:BC:31:PRO:HD2	2.34	0.42
2:AB:67:LEU:HD21	2:AB:91:VAL:HG23	2.01	0.42
1:AA:113:G:C2	1:AA:315:A:C2	3.06	0.42
33:BA:1199:U:H5'	50:BU:4:LYS:HG2	2.01	0.42
33:BA:2811:G:H2'	33:BA:2812:G:O4'	2.20	0.42
33:BA:1346:G:C2	33:BA:1601:G:C2	3.08	0.42
1:AA:864:A:H2	1:AA:917:G:N3	2.17	0.42
1:AA:837:U:H2'	1:AA:838:G:C8	2.54	0.42
1:AA:475:C:H2'	1:AA:476:U:C6	2.54	0.42
9:AI:14:SER:OG	9:AI:68:GLY:O	2.30	0.42
33:BA:1153:C:H2'	33:BA:1154:G:O4'	2.19	0.42
33:BA:1056:G:H5'	40:BH:34:THR:OG1	2.20	0.42
33:BA:856:G:H2'	33:BA:857:G:C8	2.54	0.42
1:AA:88:U:H2'	1:AA:88:U:O2	2.19	0.42
2:AB:153:MET:CE	2:AB:157:PRO:HG3	2.49	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
35:BC:181:ARG:HG2	35:BC:182:LYS:N	2.34	0.42
43:BN:49:ASP:CG	43:BN:121:LYS:HZ3	2.20	0.42
33:BA:1550:C:H2'	33:BA:1551:A:C8	2.54	0.42
4:AD:145:ARG:O	4:AD:149:LYS:HG3	2.20	0.42
2:AB:20:ARG:NH1	2:AB:20:ARG:HA	2.34	0.42
33:BA:821:A:H5''	33:BA:822:G:O5'	2.19	0.42
1:AA:373:A:C1'	1:AA:481:G:H1'	2.49	0.42
1:AA:59:A:H61	1:AA:331:G:H1'	1.85	0.42
1:AA:797:C:OP1	11:AK:125:LYS:HG3	2.19	0.42
25:B1:2:ARG:HG3	33:BA:1364:G:OP1	2.19	0.42
33:BA:1651:G:N2	33:BA:2007:U:C2	2.87	0.42
40:BH:35:VAL:HA	40:BH:38:MET:HB2	2.00	0.42
37:BE:119:ILE:HD13	37:BE:119:ILE:H	1.85	0.42
21:AU:46:ARG:HA	21:AU:49:ALA:HB3	2.02	0.42
33:BA:1835:G:H1'	33:BA:1931:U:C2	2.53	0.42
33:BA:1107:G:H2'	33:BA:1108:U:C6	2.54	0.42
23:AW:320:VAL:HG12	23:AW:361:PRO:HA	2.01	0.42
33:BA:2428:G:H21	45:BP:60:ARG:HD3	1.85	0.42
30:B6:25:LYS:HE3	30:B6:25:LYS:HB2	1.87	0.42
1:AA:1524:C:H2'	1:AA:1525:G:C8	2.54	0.42
1:AA:620:C:H2'	1:AA:621:A:O4'	2.18	0.42
43:BN:117:ALA:HA	43:BN:120:ARG:NH2	2.34	0.42
1:AA:1368:A:O2'	1:AA:1369:C:H5'	2.19	0.42
37:BE:151:GLY:HA3	37:BE:191:ASP:OD1	2.19	0.42
1:AA:668:G:H2'	1:AA:669:G:H8	1.85	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:1250:G:OP2	45:BP:21:ARG:NH2	2.53	0.42
21:AU:38:GLU:O	21:AU:41:THR:OG1	2.26	0.42
6:AF:44:ARG:HG3	6:AF:58:HIS:ND1	2.35	0.42
3:AC:143:LEU:HD22	3:AC:143:LEU:H	1.84	0.42
50:BU:24:TYR:CD1	50:BU:25:GLY:N	2.87	0.42
1:AA:182:A:N7	1:AA:184:G:C5	2.88	0.42
21:AU:36:PHE:O	21:AU:37:TYR:HB3	2.19	0.42
1:AA:114:U:O2'	1:AA:115:G:H5'	2.20	0.42
33:BA:167:A:C2	33:BA:168:G:H1'	2.54	0.42
17:AQ:46:HIS:N	17:AQ:72:TRP:O	2.34	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
11:AK:17:ASP:HA	11:AK:80:ASN:O	2.19	0.42
33:BA:1669:A:O3'	33:BA:2549:G:H5'	2.19	0.42
33:BA:210:C:H2'	33:BA:211:C:C6	2.55	0.42
37:BE:112:LEU:HD13	37:BE:186:VAL:HG11	2.02	0.42
36:BD:22:ILE:HA	36:BD:23:PRO:HD3	1.91	0.42
33:BA:1973:G:C6	33:BA:1974:C:C4	3.07	0.42
49:BT:28:LYS:HE3	49:BT:28:LYS:N	2.35	0.42
47:BR:12:ARG:HE	47:BR:16:HIS:CE1	2.38	0.42
33:BA:802:A:C5	33:BA:803:U:C4	3.06	0.42
33:BA:2584:U:H2'	33:BA:2585:U:H5'	2.00	0.42
33:BA:2033:A:H4'	33:BA:2034:U:OP1	2.20	0.42
23:AW:419:LEU:HG	23:AW:452:ARG:HH12	1.84	0.42
23:AW:20:SER:N	23:AW:26:LYS:NZ	2.67	0.42
1:AA:70:U:C2	1:AA:94:G:C5	3.07	0.42
24:B0:17:ALA:HA	24:B0:35:ILE:CG2	2.49	0.42
33:BA:1054:A:O2'	40:BH:31:ARG:N	2.53	0.42
54:BY:95:PHE:O	54:BY:99:SER:HA	2.20	0.42
33:BA:2790:U:H5'	33:BA:2893:A:N7	2.35	0.42
33:BA:1837:C:H1'	33:BA:1928:A:H1'	2.02	0.42
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.34	0.42
33:BA:2376:A:H2'	33:BA:2377:A:O4'	2.19	0.42
20:AT:8:LYS:HA	20:AT:11:ILE:HG22	2.01	0.42
24:B0:70:VAL:C	24:B0:71:LYS:HD2	2.39	0.42
33:BA:1716:U:H2'	33:BA:1717:A:C8	2.54	0.42
1:AA:148:G:H1'	1:AA:1447:A:H1'	2.02	0.42
1:AA:110:C:C4	1:AA:111:G:C5	3.08	0.42
23:AW:425:VAL:HB	23:AW:426:GLN:H	1.67	0.42
15:AO:23:SER:HB3	15:AO:26:VAL:HG23	2.00	0.42
33:BA:1960:A:C6	33:BA:1961:C:C4	3.08	0.42
33:BA:2107:G:C5	33:BA:2183:A:N1	2.88	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:80:A:C2	1:AA:81:A:H1'	2.54	0.42
33:BA:703:U:O2	33:BA:730:A:C2	2.72	0.42
23:AW:314:ARG:HB2	23:AW:369:ASN:HB3	2.02	0.42
17:AQ:13:SER:HB3	17:AQ:16:MET:CE	2.50	0.42
35:BC:204:LEU:HB3	35:BC:205:GLY:H	1.57	0.42
33:BA:1182:G:H2'	33:BA:1183:U:O4'	2.20	0.42
35:BC:80:LEU:HD23	35:BC:91:ALA:HB2	2.01	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
24:B0:68:PHE:CE1	24:B0:79:ILE:HD12	2.54	0.42
1:AA:1191:A:OP1	3:AC:3:LYS:HD3	2.20	0.42
1:AA:377:G:H2'	1:AA:378:G:C8	2.55	0.42
33:BA:2678:C:H2'	33:BA:2679:A:O4'	2.19	0.42
1:AA:1085:U:H1'	1:AA:1094:G:C5	2.55	0.42
23:AW:193:TYR:HA	23:AW:263:PHE:CE1	2.53	0.42
49:BT:25:VAL:HA	49:BT:85:VAL:O	2.20	0.42
10:AJ:50:THR:HG22	10:AJ:64:GLN:CG	2.41	0.42
2:AB:135:MET:HA	2:AB:138:ARG:HG2	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
14:AN:52:ARG:HD3	14:AN:52:ARG:HA	1.70	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
1:AA:1406:U:H1'	1:AA:1518:A:H4'	2.01	0.42
40:BH:95:LEU:HD13	40:BH:95:LEU:HA	1.92	0.42
1:AA:1229:A:OP2	13:AM:112:ARG:HD3	2.20	0.42
44:BO:18:ARG:HB2	44:BO:45:GLU:CG	2.49	0.42
1:AA:405:U:O4	4:AD:1:ALA:N	2.52	0.42
47:BR:108:ALA:O	47:BR:110:MET:HG2	2.19	0.42
3:AC:179:ALA:HB1	3:AC:202:PHE:CE1	2.53	0.42
3:AC:148:ILE:HG12	3:AC:149:LYS:N	2.35	0.42
33:BA:2820:A:OP1	47:BR:2:ARG:NH2	2.53	0.42
33:BA:979:A:H2'	33:BA:982:C:N4	2.35	0.42
1:AA:866:C:H4'	1:AA:919:A:H5'	2.02	0.42
4:AD:169:TRP:CD2	4:AD:185:PRO:HB3	2.55	0.42
23:AW:264:GLY:HA2	23:AW:267:HIS:CE1	2.54	0.42
4:AD:2:ARG:CZ	4:AD:114:ARG:HD2	2.49	0.42
33:BA:1245:G:OP1	45:BP:13:LYS:HE3	2.19	0.42
46:BQ:73:ILE:O	46:BQ:73:ILE:HG22	2.19	0.42
48:BS:83:LEU:HA	48:BS:83:LEU:HD13	1.92	0.42
36:BD:89:GLU:HG3	36:BD:94:GLN:OE1	2.19	0.42
47:BR:33:ILE:HG23	47:BR:114:GLU:HB3	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:AL:119:LYS:NZ	23:AW:431:ILE:O	2.41	0.42
33:BA:2638:G:H1'	33:BA:2778:A:H61	1.85	0.42
23:AW:22:PRO:HG3	23:AW:91:GLY:C	2.40	0.42
50:BU:57:ARG:HA	50:BU:60:TRP:CE3	2.54	0.42
1:AA:689:C:OP2	11:AK:52:ARG:NH1	2.51	0.42
33:BA:1278:C:H2'	33:BA:1279:G:C8	2.54	0.42
40:BH:24:SER:HB3	40:BH:86:MET:HE1	2.02	0.42
1:AA:1069:C:H4'	1:AA:1192:C:O2	2.20	0.42
44:BO:111:LYS:HG3	44:BO:112:PHE:CE2	2.54	0.42
33:BA:572:A:OP2	51:BV:80:ARG:NH2	2.53	0.42
42:BM:11:VAL:O	42:BM:11:VAL:HG12	2.20	0.42
38:BF:133:GLU:HA	38:BF:148:VAL:O	2.19	0.42
51:BV:61:ALA:HA	51:BV:99:THR:H	1.84	0.42
33:BA:78:U:H2'	33:BA:79:C:H6	1.85	0.42
2:AB:19:THR:HB	2:AB:37:VAL:HB	2.01	0.42
33:BA:301:G:O5'	54:BY:81:ARG:NH1	2.53	0.42
1:AA:633:G:H2'	1:AA:634:C:C6	2.55	0.42
1:AA:339:C:H2'	1:AA:340:U:C6	2.54	0.42
19:AS:48:ILE:H	19:AS:48:ILE:HG13	1.53	0.42
6:AF:11:HIS:HA	6:AF:12:PRO:HD2	1.83	0.42
15:AO:41:HIS:CE1	15:AO:45:HIS:CD2	3.08	0.42
4:AD:131:ILE:H	4:AD:131:ILE:HD13	1.85	0.42
42:BL:14:MET:CE	42:BL:14:MET:HA	2.50	0.42
42:BL:8:ILE:HA	42:BL:8:ILE:HD13	1.92	0.42
46:BQ:8:LYS:HB3	46:BQ:9:PHE:CD2	2.54	0.42
33:BA:1734:G:H2'	33:BA:1735:A:C8	2.55	0.42
12:AL:38:THR:HG22	12:AL:50:LYS:HA	2.01	0.42
41:BI:50:LYS:HE2	41:BI:50:LYS:HB2	1.88	0.42
50:BU:64:ILE:HD13	50:BU:64:ILE:HA	1.76	0.42
33:BA:1084:A:H5'	40:BH:55:VAL:HG13	2.01	0.42
33:BA:2822:G:H2'	33:BA:2823:A:H5''	2.01	0.42
43:BN:44:TYR:CE2	50:BU:99:VAL:HG21	2.50	0.42
53:BX:20:ALA:O	53:BX:24:MET:HB2	2.19	0.42
4:AD:101:VAL:HG13	4:AD:106:PHE:HB2	2.01	0.42
28:B4:47:TYR:CD2	28:B4:52:LYS:HB2	2.55	0.42
1:AA:509:A:C6	1:AA:510:A:C6	3.08	0.42
25:B1:68:ALA:C	25:B1:69:GLU:O	2.57	0.42
45:BP:95:LEU:HB2	45:BP:101:ILE:CD1	2.50	0.42
33:BA:483:A:O4'	54:BY:44:HIS:HB3	2.20	0.42
33:BA:2134:A:O2'	33:BA:2135:A:C8	2.68	0.42
3:AC:71:ARG:O	3:AC:75:VAL:HG23	2.20	0.42
33:BA:1902:C:H4'	35:BC:241:LYS:O	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:37:C:H4'	33:BA:451:U:OP1	2.20	0.42
29:B5:32:LYS:HA	29:B5:51:ALA:O	2.20	0.42
33:BA:1789:A:OP1	35:BC:220:ARG:HD3	2.20	0.42
41:BI:15:GLY:HA2	41:BI:50:LYS:HB3	2.00	0.42
1:AA:1417:G:N2	1:AA:1484:C:N4	2.67	0.42
23:AW:285:ASP:N	23:AW:285:ASP:OD1	2.53	0.42
1:AA:436:C:H2'	1:AA:437:U:C6	2.55	0.42
1:AA:1256:A:N1	1:AA:1278:G:N2	2.68	0.42
54:BY:47:PRO:HB3	54:BY:55:GLY:N	2.35	0.42
51:BV:68:ARG:HD3	51:BV:92:TRP:CE2	2.54	0.42
34:BB:18:G:C6	34:BB:19:C:C4	3.08	0.42
42:BL:19:VAL:O	42:BL:23:ILE:HB	2.19	0.42
39:BG:82:PHE:N	39:BG:134:GLY:O	2.53	0.42
23:AW:401:ILE:HA	23:AW:462:VAL:O	2.20	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
33:BA:253:C:H2'	33:BA:254:G:O4'	2.20	0.41
33:BA:2273:A:H2'	33:BA:2274:A:H8	1.76	0.41
33:BA:1000:A:N6	33:BA:1155:A:C8	2.88	0.41
1:AA:1023:U:H2'	1:AA:1024:G:C8	2.55	0.41
33:BA:1109:C:C4	33:BA:1110:G:C2	3.08	0.41
51:BV:41:ILE:O	51:BV:46:GLU:HB2	2.19	0.41
5:AE:54:GLU:HB3	5:AE:56:PRO:HD2	2.02	0.41
33:BA:2340:A:H2'	33:BA:2341:G:H8	1.85	0.41
38:BF:111:ARG:HA	38:BF:111:ARG:HD3	1.59	0.41
34:BB:86:G:N1	34:BB:88:C:H1'	2.35	0.41
1:AA:1180:A:P	9:AI:98:ARG:HH22	2.43	0.41
1:AA:674:G:H2'	1:AA:675:A:C8	2.54	0.41
8:AH:17:GLN:NE2	8:AH:69:ALA:HB1	2.35	0.41
2:AB:205:ALA:O	2:AB:209:VAL:HG22	2.20	0.41
33:BA:200:U:H2'	33:BA:201:C:O4'	2.20	0.41
2:AB:80:LYS:HB2	2:AB:90:PHE:CD1	2.54	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
1:AA:406:G:N2	1:AA:437:U:C2	2.87	0.41
33:BA:2527:C:H2'	33:BA:2528:U:O4'	2.19	0.41
33:BA:1310:G:H3'	33:BA:1311:G:C8	2.55	0.41
12:AL:14:LYS:HB2	12:AL:14:LYS:HE3	1.88	0.41
36:BD:113:SER:O	36:BD:167:ASN:HA	2.20	0.41
33:BA:2595:G:O6	35:BC:238:ASN:ND2	2.53	0.41
33:BA:536:G:H21	43:BN:47:HIS:CG	2.38	0.41
38:BF:121:PHE:HA	38:BF:126:ASN:O	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
43:BN:99:ARG:O	43:BN:102:GLU:HB2	2.19	0.41
33:BA:2149:U:C4'	33:BA:2150:C:OP2	2.66	0.41
24:B0:19:ARG:HH12	33:BA:922:C:H1'	1.86	0.41
33:BA:1566:A:C6	35:BC:212:TRP:CZ3	3.09	0.41
33:BA:806:C:O2	33:BA:2444:G:O2'	2.38	0.41
34:BB:56:G:H4'	34:BB:57:A:O5'	2.20	0.41
10:AJ:41:PRO:HA	10:AJ:72:ARG:HH11	1.85	0.41
21:AU:19:LYS:HB2	21:AU:20:ARG:NH1	2.34	0.41
33:BA:2305:U:C5	38:BF:151:LEU:HA	2.55	0.41
52:BW:96:ILE:HG13	52:BW:96:ILE:O	2.19	0.41
36:BD:48:ILE:HG23	36:BD:84:LEU:HD21	2.02	0.41
33:BA:319:G:C6	33:BA:320:A:C5	3.08	0.41
14:AN:20:PHE:C	14:AN:22:LYS:H	2.24	0.41
38:BF:72:SER:HB2	38:BF:80:GLN:HB2	2.01	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
49:BT:104:GLY:C	49:BT:106:ALA:H	2.23	0.41
30:B6:16:HIS:ND1	33:BA:684:G:OP1	2.50	0.41
40:BH:150:LYS:HA	40:BH:154:THR:OG1	2.20	0.41
2:AB:122:ASP:OD1	2:AB:122:ASP:N	2.53	0.41
47:BR:25:ALA:O	47:BR:29:VAL:HG23	2.20	0.41
30:B6:18:PHE:HA	30:B6:43:THR:HG21	2.01	0.41
33:BA:2472:G:H2'	33:BA:2475:C:H42	1.85	0.41
33:BA:628:G:C6	33:BA:636:G:C2	3.08	0.41
33:BA:998:C:OP2	50:BU:57:ARG:NH2	2.50	0.41
24:B0:24:ARG:HD3	24:B0:65:LYS:HE2	2.01	0.41
2:AB:163:ILE:HD12	2:AB:163:ILE:HA	1.81	0.41
55:BZ:30:ILE:HG12	55:BZ:91:PHE:HB2	2.01	0.41
33:BA:1392:A:N6	53:BX:18:GLU:HG2	2.34	0.41
53:BX:5:GLU:O	53:BX:8:LEU:HB2	2.20	0.41
40:BH:24:SER:OG	40:BH:117:LEU:N	2.53	0.41
1:AA:1005:A:O5'	1:AA:1005:A:H8	2.04	0.41
1:AA:1001:C:H2'	1:AA:1002:G:C8	2.54	0.41
33:BA:2:G:H2'	33:BA:3:U:C6	2.56	0.41
33:BA:1839:G:C5	33:BA:1840:G:C8	3.09	0.41
42:BM:18:ASP:O	42:BM:21:GLU:HB2	2.20	0.41
33:BA:1651:G:C2	33:BA:2007:U:C2	3.08	0.41
1:AA:1525:G:OP1	11:AK:121:ARG:NH2	2.52	0.41
33:BA:1735:A:H2'	33:BA:1736:U:O4'	2.20	0.41
46:BQ:132:THR:HG22	46:BQ:133:LYS:N	2.35	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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:BC:51:ARG:NH2	35:BC:246:PRO:HG2	2.34	0.41
36:BD:129:THR:HG23	36:BD:130:GLN:O	2.21	0.41
18:AR:49:LYS:HG2	18:AR:53:GLN:HE21	1.85	0.41
35:BC:75:ALA:HB3	35:BC:115:ILE:HG22	2.01	0.41
33:BA:2151:U:N3	33:BA:2152:G:C5	2.88	0.41
40:BH:58:THR:O	40:BH:60:LEU:HG	2.20	0.41
13:AM:84:CYS:HB2	19:AS:72:GLU:HB3	2.01	0.41
26:B2:8:GLU:H	26:B2:60:LYS:NZ	2.19	0.41
35:BC:67:LYS:HG2	35:BC:150:GLY:CA	2.50	0.41
33:BA:739:A:H1'	33:BA:740:C:H5	1.84	0.41
10:AJ:56:HIS:HD2	10:AJ:57:VAL:N	2.18	0.41
25:B1:30:PRO:HA	33:BA:396:G:O3'	2.20	0.41
52:BW:3:THR:OG1	52:BW:58:ALA:HB2	2.21	0.41
10:AJ:19:ASP:HA	10:AJ:22:THR:HB	2.01	0.41
1:AA:983:A:O2'	1:AA:1050:G:OP1	2.29	0.41
46:BQ:64:TRP:HB2	46:BQ:104:GLU:HB2	2.03	0.41
1:AA:265:G:H5''	17:AQ:66:LEU:O	2.21	0.41
33:BA:1522:A:O2'	33:BA:1523:U:P	2.78	0.41
33:BA:2230:G:H2'	33:BA:2231:U:C6	2.55	0.41
33:BA:1708:C:H2'	33:BA:1709:U:H6	1.85	0.41
33:BA:500:G:N2	33:BA:502:A:H3'	2.35	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:2357:G:N2	33:BA:2360:G:OP2	2.46	0.41
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.21	0.41
33:BA:2146:C:C4'	33:BA:2147:A:OP1	2.67	0.41
1:AA:70:U:O2'	1:AA:71:A:H8	2.04	0.41
33:BA:2757:A:N3	33:BA:2757:A:H2'	2.36	0.41
23:AW:183:TYR:CZ	23:AW:210:LEU:HD13	2.56	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
35:BC:265:PHE:CD1	35:BC:265:PHE:N	2.88	0.41
39:BG:8:VAL:HB	39:BG:49:LEU:HB2	2.03	0.41
37:BE:193:VAL:O	37:BE:197:GLU:HB2	2.20	0.41
11:AK:60:PHE:O	11:AK:63:GLN:HB3	2.20	0.41
33:BA:2347:C:H4'	33:BA:2347:C:OP1	2.21	0.41
25:B1:32:LEU:HD23	25:B1:49:ARG:NE	2.35	0.41
36:BD:5:VAL:HG22	36:BD:202:ILE:HD13	2.03	0.41
16:AP:76:LYS:HZ3	16:AP:80:LYS:HB2	1.85	0.41
35:BC:20:ASN:HA	35:BC:21:PRO:HD2	1.92	0.41
23:AW:172:PRO:HD3	23:AW:256:PHE:CD1	2.55	0.41
19:AS:48:ILE:HD12	19:AS:59:VAL:O	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
52:BW:36:LEU:HA	52:BW:36:LEU:HD12	1.71	0.41
1:AA:1368:A:OP2	9:AI:113:LYS:NZ	2.37	0.41
46:BQ:76:LYS:HA	46:BQ:77:PRO:HD3	1.90	0.41
4:AD:3:TYR:O	4:AD:4:LEU:HB2	2.21	0.41
36:BD:35:THR:N	36:BD:49:GLN:O	2.50	0.41
46:BQ:20:LEU:HD13	46:BQ:20:LEU:HA	1.78	0.41
3:AC:42:LEU:HA	3:AC:42:LEU:HD12	1.88	0.41
33:BA:796:C:H2'	33:BA:797:G:C8	2.55	0.41
23:AW:165:GLY:HA3	23:AW:251:ILE:HG22	2.02	0.41
33:BA:974:G:N7	33:BA:989:G:C6	2.89	0.41
33:BA:2846:G:H1	33:BA:2870:C:H42	1.67	0.41
1:AA:75:G:H1	1:AA:95:C:H42	1.69	0.41
3:AC:15:LYS:HE3	3:AC:180:ASP:OD1	2.20	0.41
15:AO:63:ARG:HD3	15:AO:87:ARG:HH22	1.85	0.41
7:AG:110:ARG:HB3	7:AG:118:ARG:HB3	2.03	0.41
33:BA:784:G:N7	33:BA:792:A:N7	2.69	0.41
52:BW:44:ALA:O	52:BW:47:VAL:HG12	2.19	0.41
1:AA:812:G:O2'	1:AA:813:U:P	2.75	0.41
53:BX:39:THR:OG1	53:BX:42:GLU:HB2	2.20	0.41
42:BJ:27:GLU:HG2	42:BJ:29:LYS:HZ1	1.85	0.41
33:BA:2708:G:H1'	47:BR:71:ARG:NH2	2.35	0.41
9:AI:62:LEU:HD12	9:AI:64:ILE:HD11	2.03	0.41
1:AA:665:A:C8	1:AA:725:G:C2	3.09	0.41
3:AC:35:ASP:OD2	3:AC:39:ARG:NE	2.52	0.41
40:BH:143:MET:O	40:BH:148:ALA:HB3	2.20	0.41
1:AA:1479:C:C2	1:AA:1480:A:C8	3.09	0.41
33:BA:2395:C:OP1	45:BP:63:LYS:NZ	2.51	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
33:BA:1597:A:H5''	33:BA:1598:A:H5'	2.02	0.41
1:AA:1432:G:H1'	1:AA:1468:A:N6	2.35	0.41
23:AW:325:TYR:OH	23:AW:327:LYS:HA	2.20	0.41
33:BA:2150:C:O2'	33:BA:2151:U:C6	2.72	0.41
23:AW:45:THR:HB	23:AW:46:VAL:H	1.50	0.41
33:BA:910:A:C6	33:BA:911:A:C6	3.08	0.41
33:BA:2443:C:H2'	33:BA:2444:G:C8	2.56	0.41
33:BA:946:C:H2'	33:BA:947:A:H8	1.86	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
40:BH:139:LEU:HD21	42:BJ:25:ALA:HB3	2.03	0.41
2:AB:188:THR:OG1	2:AB:188:THR:O	2.30	0.41
33:BA:981:A:H5''	33:BA:982:C:OP2	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
41:BI:105:LEU:HA	41:BI:108:ILE:HB	2.02	0.41
33:BA:1828:G:O6	35:BC:220:ARG:HD2	2.19	0.41
46:BQ:108:VAL:HG13	46:BQ:112:LEU:HB3	2.02	0.41
33:BA:1500:G:O2'	35:BC:100:ARG:NH1	2.54	0.41
32:B8:6:SER:HB2	33:BA:1031:G:H4'	2.03	0.41
1:AA:959:A:H5''	1:AA:960:U:OP2	2.21	0.41
1:AA:523:A:H8	1:AA:523:A:O5'	2.03	0.41
18:AR:46:THR:HG23	18:AR:51:GLN:HB2	2.01	0.41
1:AA:842:U:HO2'	1:AA:846:G:H1	1.68	0.41
1:AA:66:A:H4'	1:AA:173:U:C5	2.56	0.41
23:AW:403:LEU:HA	23:AW:461:ALA:HA	2.02	0.41
33:BA:71:A:HO2'	33:BA:72:U:P	2.39	0.41
15:AO:77:TYR:CZ	15:AO:81:ILE:HD13	2.55	0.41
9:AI:59:LYS:NZ	9:AI:60:LEU:HD22	2.36	0.41
4:AD:14:GLU:OE2	4:AD:55:ARG:NH1	2.53	0.41
33:BA:780:G:H21	33:BA:783:A:H62	1.68	0.41
23:AW:491:SER:CA	23:AW:492:GLN:HB2	2.51	0.41
11:AK:78:ILE:H	11:AK:78:ILE:HG13	1.68	0.41
2:AB:89:PHE:HB3	2:AB:149:GLY:CA	2.48	0.41
1:AA:1005:A:C2	1:AA:1006:G:H1'	2.56	0.41
33:BA:819:A:H5'	33:BA:973:A:N1	2.36	0.41
2:AB:73:ARG:HA	2:AB:76:SER:CB	2.51	0.41
33:BA:749:A:H4'	33:BA:1271:G:N3	2.36	0.41
40:BH:143:MET:C	40:BH:145:GLU:H	2.24	0.41
1:AA:937:A:H1'	1:AA:1379:G:H22	1.85	0.41
38:BF:73:VAL:HG21	38:BF:76:PHE:HD1	1.85	0.41
35:BC:52:HIS:HA	35:BC:216:ARG:HB2	2.03	0.41
2:AB:170:ILE:HG13	2:AB:170:ILE:H	1.67	0.41
33:BA:2292:U:H2'	33:BA:2293:G:C8	2.55	0.41
1:AA:668:G:C4	1:AA:669:G:C8	3.09	0.41
9:AI:128:LYS:HD2	9:AI:129:ARG:H	1.85	0.41
15:AO:2:LEU:HD12	15:AO:3:SER:H	1.86	0.41
12:AL:115:LYS:H	12:AL:115:LYS:HG3	1.55	0.41
33:BA:602:A:C2	33:BA:656:G:C6	3.09	0.41
1:AA:193:C:H2'	1:AA:194:C:H6	1.85	0.41
4:AD:166:LYS:HA	4:AD:167:PRO:HD3	1.78	0.41
39:BG:101:VAL:HG12	39:BG:115:GLN:HA	2.03	0.41
33:BA:467:G:H2'	33:BA:468:G:O4'	2.20	0.41
23:AW:398:PHE:CD1	23:AW:399:ARG:N	2.88	0.41
1:AA:1409:C:O2'	33:BA:1914:C:N4	2.46	0.41
33:BA:996:A:H4'	50:BU:91:ARG:HD2	2.02	0.41
33:BA:922:C:C2	33:BA:923:G:C8	3.09	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:BQ:36:VAL:H	46:BQ:99:GLY:H	1.69	0.41
1:AA:73:C:H41	1:AA:94:G:N2	2.17	0.41
33:BA:894:U:C2'	33:BA:895:U:O5'	2.68	0.41
1:AA:1321:U:H5'	13:AM:85:TYR:CE2	2.56	0.41
33:BA:2748:A:H1'	39:BG:66:THR:CG2	2.50	0.41
10:AJ:56:HIS:HD2	10:AJ:57:VAL:H	1.69	0.41
1:AA:383:A:C6	1:AA:384:G:H1'	2.56	0.41
33:BA:2103:C:O2'	33:BA:2104:C:P	2.79	0.41
33:BA:1180:U:H5'	33:BA:1181:U:OP2	2.20	0.41
35:BC:269:ARG:HD3	35:BC:270:ARG:H	1.85	0.41
25:B1:12:VAL:HG23	25:B1:28:PHE:HB2	2.03	0.41
33:BA:1007:C:C6	33:BA:1008:A:C8	3.08	0.41
33:BA:1206:G:C6	33:BA:1207:C:C4	3.09	0.41
10:AJ:18:ILE:HD12	10:AJ:72:ARG:HG3	2.03	0.41
34:BB:42:C:O2'	38:BF:63:LYS:O	2.22	0.41
35:BC:180:MET:O	35:BC:267:VAL:N	2.49	0.41
43:BN:125:TYR:CE2	43:BN:130:HIS:HB2	2.56	0.41
33:BA:819:A:C4	33:BA:1189:A:C2	3.08	0.41
33:BA:1666:G:N2	33:BA:1994:C:O2	2.54	0.41
33:BA:2561:U:H4'	44:BO:22:ILE:CD1	2.51	0.41
2:AB:76:SER:OG	2:AB:77:GLU:N	2.54	0.41
33:BA:30:G:H2'	33:BA:31:C:C6	2.56	0.41
4:AD:145:ARG:HD2	4:AD:147:LYS:HE2	2.03	0.41
33:BA:691:C:C4'	35:BC:42:ARG:HH12	2.33	0.41
47:BR:37:THR:OG1	47:BR:40:LYS:HG3	2.21	0.41
40:BH:147:SER:O	40:BH:151:LEU:HG	2.21	0.41
34:BB:86:G:C6	34:BB:88:C:H1'	2.55	0.41
33:BA:1906:G:N7	33:BA:1929:G:H2'	2.35	0.41
16:AP:46:LYS:HE2	16:AP:47:GLU:H	1.86	0.41
1:AA:824:G:H2'	1:AA:825:A:C8	2.55	0.41
33:BA:2766:A:C8	33:BA:2766:A:O5'	2.74	0.41
33:BA:2053:G:H5'	36:BD:150:GLN:HA	2.03	0.41
1:AA:774:G:C2	1:AA:806:C:C2	3.09	0.41
33:BA:2230:G:C4	33:BA:2231:U:C5	3.09	0.41
1:AA:890:G:C2'	1:AA:891:U:OP2	2.69	0.41
33:BA:287:G:H2'	33:BA:288:U:C6	2.56	0.41
53:BX:50:LEU:O	53:BX:51:PHE:HB2	2.20	0.41
33:BA:2228:G:H2'	33:BA:2229:U:H6	1.85	0.41
1:AA:1168:U:H2'	1:AA:1168:U:O2	2.21	0.41
19:AS:48:ILE:HD11	19:AS:61:VAL:HG13	2.03	0.41
33:BA:1527:G:H5''	33:BA:1528:A:OP1	2.20	0.41
1:AA:1040:U:H2'	1:AA:1041:G:C8	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:AQ:30:HIS:HB2	17:AQ:37:ILE:HD11	2.03	0.41
15:AO:2:LEU:HD22	15:AO:34:GLN:HG2	2.03	0.41
20:AT:60:GLN:HB3	20:AT:65:LEU:HD11	2.03	0.41
33:BA:2142:A:H2'	33:BA:2143:C:OP2	2.21	0.41
33:BA:2397:G:C2	33:BA:2420:C:C2	3.09	0.41
1:AA:1328:C:H5''	13:AM:27:THR:HG21	2.03	0.41
36:BD:140:HIS:CD2	36:BD:140:HIS:H	2.38	0.41
20:AT:33:LYS:HD3	20:AT:33:LYS:HA	1.86	0.41
13:AM:77:LYS:HD3	13:AM:80:MET:CE	2.51	0.41
33:BA:154:U:H2'	33:BA:155:A:C8	2.56	0.41
54:BY:9:GLU:OE2	54:BY:21:ARG:NH2	2.47	0.41
16:AP:67:ILE:HG21	16:AP:72:ALA:HB2	2.03	0.41
1:AA:283:U:C4	1:AA:284:C:C4	3.09	0.41
33:BA:328:U:O3'	54:BY:65:GLN:HG3	2.20	0.41
33:BA:192:C:H2'	33:BA:193:U:O4'	2.21	0.41
33:BA:2037:A:H2'	33:BA:2038:G:C8	2.56	0.41
1:AA:1498:U:H1'	1:AA:1499:A:N7	2.36	0.41
45:BP:19:LEU:HA	45:BP:27:LEU:HD13	2.02	0.41
41:BI:116:MET:SD	41:BI:124:MET:HB2	2.61	0.41
1:AA:159:G:N2	1:AA:162:A:OP2	2.49	0.41
33:BA:1519:G:C6	33:BA:1520:U:C4	3.08	0.41
1:AA:626:G:C6	1:AA:627:G:C5	3.09	0.41
5:AE:85:LYS:HG3	5:AE:93:VAL:O	2.21	0.41
47:BR:27:SER:HB3	47:BR:34:ILE:HG21	2.02	0.41
33:BA:1833:C:H2'	33:BA:1834:U:H6	1.85	0.41
33:BA:1742:U:C4	33:BA:1743:G:C6	3.09	0.41
23:AW:399:ARG:NE	23:AW:445:GLN:HB3	2.36	0.41
39:BG:139:VAL:O	39:BG:143:VAL:HG23	2.21	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
43:BN:35:ARG:HG2	43:BN:40:HIS:CD2	2.56	0.41
10:AJ:57:VAL:HG13	10:AJ:58:ASN:N	2.36	0.41
33:BA:1184:U:O2'	33:BA:1185:G:H5'	2.21	0.41
6:AF:36:ILE:HD13	6:AF:36:ILE:H	1.85	0.41
4:AD:198:LEU:HA	4:AD:198:LEU:HD23	1.85	0.41
1:AA:392:C:H2'	1:AA:393:A:C8	2.56	0.41
23:AW:481:LYS:NZ	23:AW:520:ASP:HB2	2.36	0.41
33:BA:2323:G:H2'	33:BA:2324:U:O4'	2.20	0.41
31:B7:2:LYS:HA	33:BA:592:A:O2'	2.21	0.41
33:BA:2326:C:H2'	33:BA:2326:C:H6	1.69	0.41
27:B3:38:GLU:HB2	27:B3:40:THR:HG22	2.03	0.41
1:AA:1084:G:C5	1:AA:1085:U:C4	3.09	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
40:BH:76:PHE:O	40:BH:79:PRO:HD3	2.21	0.41
33:BA:753:A:H2'	33:BA:754:U:C6	2.56	0.41
1:AA:1120:C:H2'	1:AA:1121:U:C6	2.55	0.41
1:AA:880:C:H2'	1:AA:881:G:H8	1.86	0.41
12:AL:19:ASN:O	12:AL:93:ARG:HD2	2.21	0.41
43:BN:7:LYS:HA	43:BN:8:PRO:HD3	1.91	0.41
8:AH:105:THR:OG1	8:AH:107:LYS:O	2.38	0.41
47:BR:102:PHE:H	47:BR:109:PRO:HA	1.86	0.41
33:BA:1277:G:H2'	33:BA:1278:C:C6	2.56	0.40
4:AD:109:THR:HG23	4:AD:112:GLU:N	2.26	0.40
33:BA:321:U:OP2	37:BE:130:LYS:HD3	2.20	0.40
1:AA:1440:U:H5'	1:AA:1441:A:OP1	2.20	0.40
33:BA:948:C:O2	33:BA:984:A:O2'	2.39	0.40
33:BA:2789:C:H2'	33:BA:2893:A:N7	2.35	0.40
28:B4:43:THR:OG1	28:B4:47:TYR:N	2.53	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
7:AG:50:ALA:HB2	7:AG:57:GLU:OE2	2.21	0.40
33:BA:483:A:O2'	54:BY:56:GLY:N	2.54	0.40
10:AJ:34:ALA:O	10:AJ:36:VAL:HG23	2.21	0.40
28:B4:42:ILE:HD11	47:BR:98:LEU:HB3	2.03	0.40
33:BA:1567:G:C8	35:BC:82:TYR:CE1	3.10	0.40
33:BA:2834:G:O6	33:BA:2879:A:H2'	2.20	0.40
33:BA:1789:A:P	35:BC:220:ARG:HD3	2.61	0.40
13:AM:72:ILE:O	13:AM:76:ILE:HG13	2.21	0.40
35:BC:142:ASN:HA	35:BC:153:LEU:O	2.22	0.40
33:BA:7:G:H2'	33:BA:8:C:O4'	2.20	0.40
33:BA:2038:G:C6	33:BA:2039:U:C4	3.09	0.40
49:BT:77:SER:HA	49:BT:78:PRO:HD3	1.95	0.40
33:BA:340:A:O2'	37:BE:162:ARG:NH1	2.54	0.40
52:BW:15:GLN:O	52:BW:19:LEU:HD13	2.21	0.40
9:AI:71:ILE:H	9:AI:71:ILE:HD12	1.86	0.40
20:AT:14:GLU:O	20:AT:17:ARG:HB3	2.21	0.40
33:BA:1536:C:H1'	33:BA:1537:G:N2	2.36	0.40
1:AA:372:C:N4	1:AA:387:U:H2'	2.36	0.40
37:BE:79:ARG:HG2	37:BE:80:SER:N	2.36	0.40
10:AJ:49:PHE:CE1	14:AN:76:PHE:HZ	2.38	0.40
23:AW:72:THR:HG22	23:AW:88:ASP:H	1.87	0.40
23:AW:484:GLU:CD	23:AW:487:ARG:HH21	2.25	0.40
23:AW:45:THR:HG23	23:AW:51:SER:HB2	2.02	0.40
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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:110:ARG:HD2	7:AG:122:GLU:HG2	2.02	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
33:BA:582:A:C2	33:BA:1259:G:C2	3.09	0.40
1:AA:376:G:H2'	1:AA:377:G:C8	2.56	0.40
33:BA:2341:G:H2'	33:BA:2342:C:O4'	2.22	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
1:AA:52:C:H2'	1:AA:53:A:C8	2.56	0.40
19:AS:52:ASN:OD1	19:AS:54:ARG:HG3	2.21	0.40
33:BA:419:U:H2'	33:BA:420:C:C6	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
33:BA:455:C:H2'	33:BA:455:C:H6	1.75	0.40
33:BA:2736:A:H2'	33:BA:2737:G:H8	1.86	0.40
33:BA:2467:C:H2'	33:BA:2468:A:O4'	2.22	0.40
42:BJ:11:VAL:HG21	42:BM:15:SER:HB2	2.01	0.40
45:BP:50:PHE:CZ	45:BP:52:GLY:O	2.74	0.40
23:AW:321:VAL:HG21	23:AW:387:PHE:CE2	2.56	0.40
12:AL:82:ARG:HB2	12:AL:97:VAL:HG22	2.03	0.40
7:AG:49:LEU:HG	7:AG:123:LEU:HD12	2.03	0.40
13:AM:15:VAL:O	13:AM:29:SER:OG	2.25	0.40
33:BA:1909:C:H2'	33:BA:1910:G:H8	1.85	0.40
42:BK:24:SER:O	42:BK:28:GLU:HG2	2.20	0.40
24:B0:30:VAL:HA	24:B0:60:ALA:O	2.21	0.40
23:AW:389:GLY:O	23:AW:390:ILE:HD13	2.21	0.40
1:AA:1360:A:H2'	1:AA:1361:G:O4'	2.21	0.40
32:B8:20:ASP:N	33:BA:2757:A:OP1	2.54	0.40
1:AA:2:A:C6	1:AA:3:A:C2	3.09	0.40
4:AD:57:LYS:HE2	4:AD:203:TYR:OH	2.22	0.40
1:AA:1414:U:H2'	1:AA:1415:G:H8	1.85	0.40
33:BA:481:G:P	54:BY:43:LYS:HE3	2.62	0.40
1:AA:325:A:H2'	1:AA:326:G:O4'	2.22	0.40
33:BA:608:A:C4	33:BA:621:A:C6	3.09	0.40
15:AO:73:ASP:OD1	15:AO:76:ARG:N	2.40	0.40
41:BI:56:VAL:HG23	41:BI:70:THR:HA	2.04	0.40
2:AB:127:LYS:HG3	2:AB:128:LEU:H	1.86	0.40
33:BA:2735:G:C4	33:BA:2736:A:C8	3.09	0.40
7:AG:37:THR:O	7:AG:41:ILE:HG13	2.21	0.40
17:AQ:39:ARG:HA	17:AQ:39:ARG:HD2	1.90	0.40
43:BN:2:LYS:H	43:BN:2:LYS:CD	2.34	0.40
33:BA:1866:A:N6	33:BA:1875:G:O2'	2.50	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:AU:13:VAL:HG13	21:AU:15:LEU:HG	2.02	0.40
1:AA:832:G:C2	1:AA:855:U:C2	3.08	0.40
1:AA:562:U:H1'	12:AL:11:ARG:HB3	2.04	0.40
33:BA:279:A:N6	33:BA:361:G:H1'	2.35	0.40
46:BQ:34:LYS:HG3	46:BQ:99:GLY:O	2.21	0.40
13:AM:85:TYR:OH	13:AM:89:ARG:NH2	2.54	0.40
33:BA:2313:C:H2'	33:BA:2314:A:C8	2.57	0.40
32:B8:19:ARG:NH1	33:BA:2755:C:C4	2.90	0.40
1:AA:1241:G:N2	1:AA:1296:C:O2	2.33	0.40
6:AF:91:ARG:HG2	6:AF:93:LYS:HD3	2.03	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
21:AU:33:ARG:CD	21:AU:34:ARG:H	2.33	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
36:BD:184:ARG:HD3	36:BD:186:LEU:HD22	2.04	0.40
33:BA:1425:G:C6	33:BA:1426:G:C6	3.10	0.40
1:AA:502:A:OP1	12:AL:114:SER:HB3	2.21	0.40
38:BF:32:LYS:O	38:BF:33:ILE:HD13	2.21	0.40
35:BC:70:LYS:HD2	35:BC:95:TYR:CG	2.56	0.40
33:BA:566:U:O4	51:BV:80:ARG:HD3	2.20	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
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: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
1:AA:898:G:C6	1:AA:902:G:O6	2.74	0.40
13:AM:77:LYS:HA	13:AM:80:MET:HE2	2.03	0.40
15:AO:38:LEU:HD13	15:AO:38:LEU:HA	1.83	0.40
33:BA:1161:C:H2'	33:BA:1162:G:H8	1.86	0.40
33:BA:257:C:H2'	33:BA:258:G:O4'	2.22	0.40
2:AB:55:GLU:HA	2:AB:58:LYS:HB3	2.02	0.40
33:BA:2149:U:C6	33:BA:2149:U:C3'	3.04	0.40
23:AW:411:GLN:HG2	23:AW:411:GLN:O	2.21	0.40
24:B0:39:GLN:HG3	24:B0:42:THR:CB	2.45	0.40
33:BA:1818:U:HO2'	33:BA:1819:A:P	2.45	0.40
53:BX:4:GLU:OE1	53:BX:5:GLU:N	2.55	0.40
1:AA:641:U:H4'	8:AH:106:SER:O	2.22	0.40
38:BF:56:LEU:HA	38:BF:56:LEU:HD23	1.84	0.40
38:BF:107:VAL:HB	38:BF:108:PRO:HD3	2.02	0.40
43:BN:121:LYS:HE3	43:BN:121:LYS:HB2	1.77	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BA:2680:U:OP1	36:BD:114:LYS:HE2	2.21	0.40
46:BQ:26:VAL:HG13	46:BQ:104:GLU:OE2	2.21	0.40
1:AA:202:G:H21	1:AA:466:A:N6	2.17	0.40
40:BH:132:TYR:C	40:BH:134:GLU:N	2.75	0.40
9:AI:110:VAL:H	9:AI:110:VAL:HG22	1.65	0.40
33:BA:858:G:N3	33:BA:2268:A:H2'	2.37	0.40
41:BI:120:ASP:HB3	41:BI:123:ALA:HB3	2.04	0.40
33:BA:732:C:H2'	33:BA:733:G:O4'	2.22	0.40
33:BA:1589:U:H2'	33:BA:1590:A:H8	1.86	0.40
33:BA:1038:G:N2	33:BA:1118:C:C2	2.90	0.40
33:BA:2290:G:C6	33:BA:2291:U:C4	3.10	0.40
46:BQ:77:PRO:HD2	46:BQ:80:VAL:HG11	2.04	0.40
23:AW:424:ALA:O	23:AW:441:VAL:HG13	2.22	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
34:BB:78:A:H2'	34:BB:79:G:O4'	2.20	0.40
1:AA:1042:A:P	1:AA:1042:A:O4'	2.80	0.40
1:AA:274:A:H4'	1:AA:275:G:O5'	2.22	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

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	Distance(Å)	Clash(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%)	38	88
3	AC	204/233 (88%)	178 (87%)	24 (12%)	2 (1%)	22	81
4	AD	203/206 (98%)	170 (84%)	29 (14%)	4 (2%)	11	68
5	AE	148/167 (89%)	125 (84%)	19 (13%)	4 (3%)	8	62
6	AF	98/135 (73%)	77 (79%)	20 (20%)	1 (1%)	22	81
7	AG	149/179 (83%)	124 (83%)	25 (17%)	0	100	100
8	AH	127/130 (98%)	113 (89%)	13 (10%)	1 (1%)	27	83
9	AI	125/130 (96%)	109 (87%)	12 (10%)	4 (3%)	6	58
10	AJ	96/103 (93%)	77 (80%)	16 (17%)	3 (3%)	7	59
11	AK	115/129 (89%)	100 (87%)	15 (13%)	0	100	100
12	AL	121/124 (98%)	107 (88%)	12 (10%)	2 (2%)	14	71
13	AM	112/118 (95%)	96 (86%)	14 (12%)	2 (2%)	13	70
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%)	18	76
17	AQ	78/84 (93%)	65 (83%)	12 (15%)	1 (1%)	18	76
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%)	19	78
21	AU	49/71 (69%)	36 (74%)	12 (24%)	1 (2%)	11	68
23	AW	523/534 (98%)	382 (73%)	82 (16%)	59 (11%)	1	16
24	B0	77/85 (91%)	49 (64%)	24 (31%)	4 (5%)	3	42
25	B1	75/78 (96%)	65 (87%)	10 (13%)	0	100	100
26	B2	61/63 (97%)	47 (77%)	12 (20%)	2 (3%)	6	57
27	B3	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
28	B4	54/57 (95%)	45 (83%)	8 (15%)	1 (2%)	12	69
29	B5	48/55 (87%)	43 (90%)	4 (8%)	1 (2%)	11	67
30	B6	44/46 (96%)	41 (93%)	2 (4%)	1 (2%)	10	65
31	B7	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	14	72
32	B8	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	8	61
35	BC	269/273 (98%)	234 (87%)	29 (11%)	6 (2%)	10	66
36	BD	207/209 (99%)	176 (85%)	26 (13%)	5 (2%)	9	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	BE	199/201 (99%)	170 (85%)	23 (12%)	6 (3%)	7	59
38	BF	175/179 (98%)	145 (83%)	27 (15%)	3 (2%)	14	71
39	BG	174/177 (98%)	141 (81%)	32 (18%)	1 (1%)	33	86
40	BH	161/165 (98%)	123 (76%)	31 (19%)	7 (4%)	4	48
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%)	2	32
43	BN	140/142 (99%)	118 (84%)	20 (14%)	2 (1%)	16	74
44	BO	120/123 (98%)	97 (81%)	19 (16%)	4 (3%)	6	57
45	BP	141/144 (98%)	118 (84%)	22 (16%)	1 (1%)	30	85
46	BQ	134/136 (98%)	112 (84%)	18 (13%)	4 (3%)	7	59
47	BR	118/127 (93%)	101 (86%)	16 (14%)	1 (1%)	27	83
48	BS	114/117 (97%)	99 (87%)	14 (12%)	1 (1%)	25	82
49	BT	112/115 (97%)	93 (83%)	16 (14%)	3 (3%)	8	62
50	BU	115/118 (98%)	103 (90%)	10 (9%)	2 (2%)	14	71
51	BV	101/103 (98%)	88 (87%)	11 (11%)	2 (2%)	11	68
52	BW	108/110 (98%)	97 (90%)	10 (9%)	1 (1%)	25	82
53	BX	91/100 (91%)	62 (68%)	25 (28%)	4 (4%)	4	48
54	BY	100/104 (96%)	78 (78%)	21 (21%)	1 (1%)	22	81
55	BZ	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
All	All	6270/7019 (89%)	5201 (83%)	915 (15%)	154 (2%)	9	63

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

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Mol	Chain	Res	Type
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
23	AW	526	THR
35	BC	238	ASN
38	BF	11	VAL
38	BF	134	GLN
40	BH	58	THR
48	BS	68	LYS

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Mol	Chain	Res	Type
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
23	AW	412	LEU
23	AW	480	LYS
37	BE	45	ALA
37	BE	124	PHE
39	BG	118	ALA
42	BM	10	ALA

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Mol	Chain	Res	Type
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
21	AU	10	PRO
23	AW	518	TYR
35	BC	64	VAL
37	BE	148	ILE
40	BH	119	PRO
46	BQ	73	ILE

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Mol	Chain	Res	Type
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%)	3	21
3	AC	170/190 (90%)	145 (85%)	25 (15%)	4	30
4	AD	172/173 (99%)	148 (86%)	24 (14%)	5	33
5	AE	113/126 (90%)	93 (82%)	20 (18%)	3	20
6	AF	87/116 (75%)	74 (85%)	13 (15%)	4	30
7	AG	124/147 (84%)	114 (92%)	10 (8%)	17	64
8	AH	104/105 (99%)	89 (86%)	15 (14%)	5	31
9	AI	105/107 (98%)	87 (83%)	18 (17%)	3	22
10	AJ	86/90 (96%)	70 (81%)	16 (19%)	2	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AK	90/99 (91%)	77 (86%)	13 (14%)	5	31
12	AL	103/104 (99%)	88 (85%)	15 (15%)	5	31
13	AM	92/96 (96%)	87 (95%)	5 (5%)	31	79
14	AN	79/84 (94%)	71 (90%)	8 (10%)	11	52
15	AO	76/77 (99%)	69 (91%)	7 (9%)	13	57
16	AP	65/65 (100%)	58 (89%)	7 (11%)	9	48
17	AQ	74/78 (95%)	62 (84%)	12 (16%)	3	25
18	AR	48/65 (74%)	44 (92%)	4 (8%)	16	62
19	AS	70/79 (89%)	65 (93%)	5 (7%)	21	70
20	AT	65/66 (98%)	58 (89%)	7 (11%)	9	48
21	AU	44/61 (72%)	38 (86%)	6 (14%)	5	35
23	AW	447/458 (98%)	380 (85%)	67 (15%)	4	30
24	B0	59/63 (94%)	44 (75%)	15 (25%)	1	7
25	B1	67/68 (98%)	61 (91%)	6 (9%)	14	58
26	B2	55/55 (100%)	48 (87%)	7 (13%)	6	38
27	B3	48/49 (98%)	39 (81%)	9 (19%)	2	16
28	B4	47/48 (98%)	44 (94%)	3 (6%)	25	74
29	B5	45/49 (92%)	40 (89%)	5 (11%)	9	46
30	B6	38/38 (100%)	34 (90%)	4 (10%)	10	49
31	B7	51/52 (98%)	49 (96%)	2 (4%)	43	85
32	B8	34/34 (100%)	31 (91%)	3 (9%)	14	60
35	BC	216/218 (99%)	184 (85%)	32 (15%)	4	30
36	BD	164/164 (100%)	145 (88%)	19 (12%)	8	43
37	BE	165/165 (100%)	144 (87%)	21 (13%)	6	38
38	BF	148/150 (99%)	134 (90%)	14 (10%)	12	55
39	BG	137/138 (99%)	115 (84%)	22 (16%)	3	26
40	BH	123/123 (100%)	105 (85%)	18 (15%)	5	31
41	BI	109/110 (99%)	94 (86%)	15 (14%)	5	34
42	BJ	26/85 (31%)	23 (88%)	3 (12%)	8	44
42	BK	26/85 (31%)	25 (96%)	1 (4%)	44	86
42	BL	26/85 (31%)	25 (96%)	1 (4%)	44	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	BM	26/85 (31%)	23 (88%)	3 (12%)	8	44
43	BN	116/116 (100%)	90 (78%)	26 (22%)	1	10
44	BO	103/104 (99%)	83 (81%)	20 (19%)	2	14
45	BP	102/103 (99%)	89 (87%)	13 (13%)	6	38
46	BQ	109/109 (100%)	91 (84%)	18 (16%)	3	24
47	BR	100/103 (97%)	85 (85%)	15 (15%)	4	30
48	BS	86/87 (99%)	72 (84%)	14 (16%)	3	25
49	BT	99/100 (99%)	82 (83%)	17 (17%)	3	21
50	BU	89/90 (99%)	75 (84%)	14 (16%)	4	27
51	BV	84/84 (100%)	73 (87%)	11 (13%)	6	37
52	BW	93/93 (100%)	76 (82%)	17 (18%)	2	17
53	BX	80/84 (95%)	69 (86%)	11 (14%)	5	34
54	BY	83/85 (98%)	69 (83%)	14 (17%)	3	23
55	BZ	78/78 (100%)	73 (94%)	5 (6%)	25	74
All	All	5226/5685 (92%)	4500 (86%)	726 (14%)	5	34

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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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

Some 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

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

5.3.3 RNA ⓘ

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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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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 ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	34,34,34	2.44	9 (26%)	48,54,54	5.28	11 (22%)

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	-	0/18/38/38	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	AW	601	GNP	PB-N3B	-6.81	1.58	1.64
56	AW	601	GNP	PG-N3B	-6.67	1.58	1.64
56	AW	601	GNP	PB-O3A	-5.68	1.52	1.59
56	AW	601	GNP	PA-O3A	-4.43	1.52	1.59
56	AW	601	GNP	PG-O1G	4.28	1.51	1.46
56	AW	601	GNP	PB-O2B	-3.18	1.47	1.56
56	AW	601	GNP	PG-O2G	-2.13	1.50	1.56
56	AW	601	GNP	PG-O3G	-2.12	1.50	1.56
56	AW	601	GNP	C6-N1	2.03	1.39	1.36

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	AW	601	GNP	C6-C5-N7	-33.78	129.59	134.14
56	AW	601	GNP	C6-N1-C2	8.14	124.80	120.20
56	AW	601	GNP	PB-N3B-PG	-4.98	121.69	130.07
56	AW	601	GNP	O2B-PB-O1B	4.16	118.69	109.90
56	AW	601	GNP	PA-O3A-PB	-3.73	119.27	132.05
56	AW	601	GNP	O1G-PG-N3B	-3.22	106.96	111.83
56	AW	601	GNP	C2-N3-C4	-3.13	111.55	115.30
56	AW	601	GNP	O3G-PG-O1G	-2.73	106.33	113.51
56	AW	601	GNP	C3'-C2'-C1'	2.17	104.32	100.92
56	AW	601	GNP	N2-C2-N1	-2.08	115.59	117.82
56	AW	601	GNP	C5-C4-N3	2.06	128.44	126.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 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, 95th 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 ²)	Q<0.9
1	AA	1532/1533 (99%)	0.09	32 (2%) 60 38	72, 119, 232, 344	0
2	AB	218/241 (90%)	1.42	59 (27%) 1 2	124, 181, 235, 328	0
3	AC	206/233 (88%)	0.71	12 (5%) 22 15	88, 129, 167, 218	0
4	AD	205/206 (99%)	0.78	17 (8%) 11 9	88, 120, 177, 250	0
5	AE	150/167 (89%)	0.64	7 (4%) 30 20	88, 123, 176, 253	0
6	AF	100/135 (74%)	0.97	16 (16%) 3 3	106, 153, 182, 204	0
7	AG	151/179 (84%)	1.48	45 (29%) 1 2	132, 178, 218, 300	0
8	AH	129/130 (99%)	0.96	17 (13%) 4 4	108, 137, 177, 228	0
9	AI	127/130 (97%)	1.39	31 (24%) 1 2	102, 145, 212, 252	0
10	AJ	98/103 (95%)	1.16	20 (20%) 1 2	95, 124, 243, 282	0
11	AK	117/129 (90%)	0.36	7 (5%) 21 15	81, 116, 155, 200	0
12	AL	123/124 (99%)	0.72	10 (8%) 12 10	83, 103, 188, 250	0
13	AM	114/118 (96%)	1.93	48 (42%) 1 1	137, 194, 233, 273	0
14	AN	96/101 (95%)	1.12	15 (15%) 3 4	93, 161, 212, 250	0
15	AO	88/89 (98%)	0.83	8 (9%) 9 8	100, 137, 190, 275	0
16	AP	82/82 (100%)	1.78	31 (37%) 1 1	78, 105, 160, 252	0
17	AQ	80/84 (95%)	1.27	17 (21%) 1 2	96, 139, 204, 301	0
18	AR	55/75 (73%)	1.02	7 (12%) 4 5	91, 119, 176, 247	0
19	AS	79/92 (85%)	2.91	54 (68%) 0 1	158, 201, 238, 282	0
20	AT	85/87 (97%)	0.68	5 (5%) 22 15	96, 126, 172, 184	0
21	AU	51/71 (71%)	3.55	36 (70%) 0 1	158, 215, 255, 264	0
22	AV	6/27 (22%)	9.94	6 (100%) 0 0	221, 256, 294, 306	0
23	AW	525/534 (98%)	0.93	72 (13%) 4 4	35, 99, 188, 267	0
24	B0	79/85 (92%)	0.99	10 (12%) 4 5	61, 105, 177, 200	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
25	B1	77/78 (98%)	1.09	6 (7%)	13 10	68, 83, 132, 154	0
26	B2	63/63 (100%)	0.57	5 (7%)	13 10	72, 100, 145, 187	0
27	B3	58/59 (98%)	1.10	9 (15%)	3 4	67, 92, 143, 174	0
28	B4	56/57 (98%)	0.31	1 (1%)	65 43	44, 65, 108, 150	0
29	B5	50/55 (90%)	2.60	30 (60%)	0 1	133, 176, 209, 228	0
30	B6	46/46 (100%)	0.40	1 (2%)	59 37	48, 60, 84, 197	0
31	B7	64/65 (98%)	0.80	4 (6%)	19 13	63, 85, 109, 128	0
32	B8	38/38 (100%)	1.16	3 (7%)	13 10	82, 104, 135, 178	0
33	BA	2853/2903 (98%)	0.01	109 (3%)	38 25	28, 79, 260, 445	0
34	BB	118/118 (100%)	-0.16	1 (0%)	83 63	71, 127, 173, 221	0
35	BC	271/273 (99%)	0.27	0	100 100	47, 77, 100, 151	0
36	BD	209/209 (100%)	0.22	1 (0%)	88 73	48, 64, 108, 162	0
37	BE	201/201 (100%)	0.44	6 (2%)	48 29	45, 94, 146, 200	0
38	BF	177/179 (98%)	1.21	38 (21%)	1 2	117, 157, 214, 286	0
39	BG	176/177 (99%)	0.78	12 (6%)	17 12	71, 108, 162, 189	0
40	BH	163/165 (98%)	2.73	93 (57%)	0 1	135, 263, 334, 394	0
41	BI	141/142 (99%)	3.32	95 (67%)	0 1	185, 276, 378, 452	0
42	BJ	30/121 (24%)	3.14	22 (73%)	0 1	222, 260, 328, 407	0
42	BK	30/121 (24%)	4.91	25 (83%)	0 1	222, 263, 318, 343	0
42	BL	30/121 (24%)	3.12	22 (73%)	0 1	187, 275, 348, 365	0
42	BM	30/121 (24%)	2.86	21 (70%)	0 1	206, 255, 324, 352	0
43	BN	142/142 (100%)	0.77	6 (4%)	35 22	56, 72, 105, 173	0
44	BO	122/123 (99%)	0.63	3 (2%)	54 34	48, 75, 107, 196	0
45	BP	143/144 (99%)	0.97	17 (11%)	5 6	55, 100, 149, 201	0
46	BQ	136/136 (100%)	0.99	14 (10%)	7 7	65, 92, 133, 188	0
47	BR	120/127 (94%)	0.38	2 (1%)	67 44	39, 64, 85, 233	0
48	BS	116/117 (99%)	1.54	34 (29%)	1 2	91, 125, 157, 180	0
49	BT	114/115 (99%)	0.28	2 (1%)	65 43	61, 83, 133, 164	0
50	BU	117/118 (99%)	0.10	3 (2%)	53 33	44, 69, 116, 219	0
51	BV	103/103 (100%)	0.48	4 (3%)	37 24	51, 93, 151, 334	0
52	BW	110/110 (100%)	0.39	2 (1%)	65 43	42, 61, 101, 181	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
53	BX	93/100 (93%)	0.92	16 (17%) 2 3	52, 88, 150, 197	0
54	BY	102/104 (98%)	1.16	20 (19%) 2 2	68, 95, 169, 203	0
55	BZ	94/94 (100%)	0.54	4 (4%) 34 22	83, 112, 151, 177	0
All	All	10889/11600 (93%)	0.64	1213 (11%) 6 6	28, 105, 249, 452	0

All (1213) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
40	BH	88	HIS	20.2
33	BA	2157	G	17.8
33	BA	885	C	16.2
22	AV	19	U	14.8
42	BK	11	VAL	13.9
22	AV	20	A	12.3
42	BL	6	GLN	12.0
23	AW	476	CYS	11.5
42	BJ	8	ILE	11.3
22	AV	18	G	11.1
33	BA	1508	A	10.7
33	BA	1728	C	10.3
21	AU	24	LYS	10.2
2	AB	17	HIS	10.0
42	BK	21	GLU	10.0
33	BA	1093	G	9.1
42	BK	12	ALA	9.0
41	BI	67	THR	9.0
41	BI	5	GLN	9.0
23	AW	487	ARG	8.9
40	BH	17	GLU	8.7
41	BI	59	THR	8.7
40	BH	14	GLU	8.4
42	BK	29	LYS	8.2
41	BI	54	ILE	8.1
22	AV	15	A	8.1
42	BM	9	GLU	8.1
41	BI	41	PHE	8.1
5	AE	9	GLU	8.0
23	AW	477	ALA	8.0
18	AR	19	GLU	8.0
40	BH	137	ALA	7.8
33	BA	1730	C	7.8

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Mol	Chain	Res	Type	RSRZ
21	AU	27	VAL	7.8
42	BM	8	ILE	7.8
42	BK	10	ALA	7.8
13	AM	36	ALA	7.8
33	BA	880	G	7.7
41	BI	118	GLY	7.7
1	AA	209	U	7.5
19	AS	56	HIS	7.5
23	AW	519	PRO	7.5
41	BI	40	ALA	7.4
42	BJ	7	ILE	7.3
33	BA	1727	C	7.3
40	BH	46	ARG	7.3
41	BI	112	LYS	7.2
9	AI	89	TYR	7.2
41	BI	78	LEU	7.2
33	BA	1094	U	7.1
21	AU	20	ARG	7.1
4	AD	24	VAL	7.0
42	BK	7	ILE	7.0
41	BI	6	ALA	7.0
42	BK	4	LYS	6.9
41	BI	66	PHE	6.9
40	BH	103	ASN	6.8
38	BF	116	LEU	6.8
22	AV	16	A	6.8
40	BH	116	GLU	6.8
40	BH	50	VAL	6.8
21	AU	28	LEU	6.7
19	AS	49	ALA	6.7
33	BA	139	U	6.7
23	AW	475	GLU	6.7
19	AS	55	GLN	6.7
23	AW	478	ASP	6.6
42	BK	2	ILE	6.6
22	AV	17	U	6.6
41	BI	105	LEU	6.5
40	BH	109	LYS	6.5
23	AW	54	HIS	6.5
19	AS	29	PRO	6.5
41	BI	20	SER	6.5
41	BI	39	LYS	6.4

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Mol	Chain	Res	Type	RSRZ
40	BH	84	TYR	6.4
42	BL	22	LEU	6.4
19	AS	57	VAL	6.3
41	BI	49	GLU	6.3
40	BH	146	ALA	6.2
33	BA	1067	A	6.2
33	BA	2109	U	6.2
23	AW	514	ALA	6.2
42	BK	22	LEU	6.2
1	AA	211	G	6.2
21	AU	26	GLY	6.2
40	BH	45	GLY	6.2
40	BH	20	LYS	6.2
23	AW	486	LYS	6.1
21	AU	23	GLU	6.1
29	B5	52	LYS	6.1
33	BA	884	U	6.1
41	BI	111	THR	6.1
41	BI	21	PRO	6.1
40	BH	42	ARG	6.1
42	BK	3	THR	6.1
41	BI	53	PRO	6.0
23	AW	518	TYR	6.0
19	AS	39	ILE	6.0
21	AU	34	ARG	6.0
48	BS	89	ASP	5.9
41	BI	119	ALA	5.9
23	AW	488	LYS	5.9
41	BI	13	ALA	5.9
21	AU	38	GLU	5.8
33	BA	1095	A	5.8
13	AM	37	GLY	5.8
42	BK	9	GLU	5.8
41	BI	61	TYR	5.8
51	BV	50	GLY	5.7
21	AU	37	TYR	5.7
46	BQ	1	MET	5.7
21	AU	25	ALA	5.7
33	BA	2179	C	5.6
40	BH	135	ALA	5.6
2	AB	29	PHE	5.6
38	BF	44	ALA	5.6

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Mol	Chain	Res	Type	RSRZ
4	AD	23	GLY	5.6
42	BK	18	ASP	5.6
41	BI	68	PHE	5.5
13	AM	35	ALA	5.5
23	AW	515	GLN	5.4
33	BA	548	G	5.4
29	B5	8	ILE	5.4
33	BA	1065	U	5.4
2	AB	26	MET	5.4
38	BF	79	ARG	5.4
19	AS	28	LYS	5.4
1	AA	841	C	5.4
41	BI	108	ILE	5.3
33	BA	2156	G	5.3
13	AM	84	CYS	5.3
25	B1	75	GLU	5.3
21	AU	32	ARG	5.3
41	BI	109	ALA	5.3
40	BH	86	MET	5.3
40	BH	37	LYS	5.3
7	AG	84	TYR	5.3
41	BI	77	VAL	5.3
19	AS	31	ARG	5.3
23	AW	482	PHE	5.3
7	AG	151	ALA	5.3
13	AM	58	GLU	5.2
40	BH	1	MET	5.2
42	BL	1	SER	5.2
23	AW	493	LEU	5.2
42	BJ	3	THR	5.2
41	BI	79	LEU	5.1
4	AD	27	ILE	5.1
42	BK	8	ILE	5.1
1	AA	844	G	5.1
21	AU	33	ARG	5.1
29	B5	51	ALA	5.1
29	B5	9	LYS	5.0
41	BI	29	GLN	5.0
12	AL	123	ALA	5.0
23	AW	483	GLU	5.0
42	BJ	28	GLU	5.0
1	AA	845	A	5.0

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Mol	Chain	Res	Type	RSRZ
24	B0	6	GLY	5.0
33	BA	1729	U	5.0
33	BA	2133	G	5.0
1	AA	412	A	5.0
19	AS	38	THR	5.0
21	AU	3	ILE	5.0
21	AU	22	CYS	5.0
41	BI	34	ILE	4.9
40	BH	18	VAL	4.9
21	AU	30	GLU	4.9
25	B1	77	TYR	4.9
42	BK	6	GLN	4.9
40	BH	113	PHE	4.9
21	AU	35	GLU	4.9
33	BA	274	C	4.9
23	AW	517	ARG	4.9
21	AU	42	THR	4.9
33	BA	2107	G	4.8
19	AS	10	ILE	4.8
23	AW	521	VAL	4.8
41	BI	12	VAL	4.8
42	BJ	10	ALA	4.8
45	BP	92	LEU	4.8
21	AU	29	ALA	4.8
40	BH	38	MET	4.8
41	BI	16	MET	4.8
42	BK	14	MET	4.8
41	BI	32	VAL	4.8
19	AS	73	PHE	4.7
13	AM	28	ARG	4.7
40	BH	62	ARG	4.7
9	AI	3	ASN	4.7
23	AW	479	ALA	4.7
23	AW	474	VAL	4.7
19	AS	48	ILE	4.7
41	BI	42	ASN	4.7
41	BI	38	CYS	4.7
41	BI	45	THR	4.7
23	AW	520	ASP	4.7
13	AM	38	ILE	4.7
19	AS	30	LEU	4.6
41	BI	80	LYS	4.6

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Mol	Chain	Res	Type	RSRZ
1	AA	1493	A	4.6
33	BA	2153	C	4.6
19	AS	50	VAL	4.6
26	B2	63	ALA	4.6
21	AU	36	PHE	4.6
42	BL	3	THR	4.6
29	B5	22	THR	4.6
29	B5	34	GLU	4.6
41	BI	30	GLN	4.6
33	BA	1726	C	4.6
17	AQ	52	CYS	4.6
19	AS	27	LYS	4.6
29	B5	6	GLU	4.6
33	BA	2150	C	4.6
19	AS	2	ARG	4.6
29	B5	23	THR	4.6
42	BM	19	VAL	4.6
33	BA	2108	A	4.5
2	AB	150	ILE	4.5
42	BJ	22	LEU	4.5
14	AN	35	ALA	4.5
16	AP	22	ALA	4.5
27	B3	58	GLU	4.5
10	AJ	91	ASP	4.5
19	AS	40	PHE	4.5
40	BH	89	PRO	4.5
40	BH	97	LYS	4.5
48	BS	62	LEU	4.5
19	AS	9	PHE	4.5
41	BI	52	LEU	4.4
41	BI	63	ASP	4.4
33	BA	2134	A	4.4
33	BA	1092	C	4.4
21	AU	19	LYS	4.4
9	AI	91	GLU	4.4
42	BJ	20	VAL	4.3
40	BH	52	MET	4.3
41	BI	64	ARG	4.3
48	BS	24	THR	4.3
33	BA	1078	U	4.3
16	AP	80	LYS	4.3
21	AU	14	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
42	BL	13	ALA	4.3
2	AB	152	ASP	4.3
23	AW	485	PHE	4.3
21	AU	16	ARG	4.3
23	AW	358	GLU	4.3
40	BH	144	LYS	4.3
40	BH	68	PRO	4.3
42	BK	17	MET	4.2
13	AM	23	GLY	4.2
41	BI	58	ILE	4.2
48	BS	115	LEU	4.2
42	BM	29	LYS	4.2
14	AN	56	PRO	4.2
46	BQ	6	ARG	4.2
45	BP	144	GLU	4.2
19	AS	69	LYS	4.2
38	BF	176	PHE	4.2
40	BH	105	LYS	4.2
7	AG	61	PHE	4.2
33	BA	896	A	4.2
42	BM	28	GLU	4.2
45	BP	82	LEU	4.2
9	AI	129	ARG	4.2
48	BS	63	LYS	4.2
40	BH	9	GLN	4.2
2	AB	19	THR	4.1
9	AI	128	LYS	4.1
29	B5	20	TYR	4.1
41	BI	115	ASP	4.1
23	AW	494	ALA	4.1
2	AB	111	LYS	4.1
19	AS	70	LEU	4.1
54	BY	78	LYS	4.1
13	AM	44	ILE	4.1
23	AW	524	HIS	4.1
3	AC	165	GLU	4.1
13	AM	3	ILE	4.0
33	BA	1175	A	4.0
41	BI	90	GLY	4.0
45	BP	115	GLU	4.0
9	AI	38	PHE	4.0
19	AS	47	THR	4.0

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Mol	Chain	Res	Type	RSRZ
41	BI	69	VAL	4.0
42	BK	25	ALA	4.0
29	B5	21	THR	4.0
9	AI	42	THR	4.0
2	AB	147	LEU	4.0
29	B5	17	GLY	4.0
17	AQ	76	ARG	4.0
41	BI	120	ASP	4.0
41	BI	125	THR	4.0
33	BA	1090	A	4.0
38	BF	78	ILE	4.0
42	BL	7	ILE	4.0
13	AM	9	PRO	3.9
40	BH	3	LEU	3.9
13	AM	57	ASP	3.9
23	AW	490	GLU	3.9
41	BI	33	ASN	3.9
19	AS	58	PRO	3.9
1	AA	1362	A	3.9
21	AU	39	LYS	3.9
33	BA	275	C	3.9
40	BH	128	THR	3.9
41	BI	86	LYS	3.9
42	BM	3	THR	3.9
8	AH	129	ALA	3.9
48	BS	26	LEU	3.9
29	B5	50	GLU	3.9
40	BH	21	GLY	3.9
43	BN	142	ILE	3.9
19	AS	26	ASP	3.9
33	BA	2402	U	3.9
42	BL	23	ILE	3.9
1	AA	1212	U	3.9
40	BH	158	VAL	3.9
1	AA	1492	A	3.9
45	BP	91	ASP	3.9
33	BA	2103	C	3.9
33	BA	879	G	3.9
13	AM	4	ALA	3.8
7	AG	75	LYS	3.8
23	AW	492	GLN	3.8
40	BH	134	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
41	BI	17	ALA	3.8
33	BA	2106	U	3.8
41	BI	50	LYS	3.8
42	BJ	19	VAL	3.8
11	AK	12	ARG	3.8
23	AW	334	VAL	3.8
33	BA	2110	G	3.8
41	BI	55	PRO	3.8
33	BA	2189	U	3.8
13	AM	54	THR	3.8
40	BH	16	SER	3.8
38	BF	82	TYR	3.8
33	BA	138	U	3.8
40	BH	159	ARG	3.8
41	BI	136	GLY	3.8
14	AN	19	TYR	3.7
29	B5	24	LYS	3.7
7	AG	15	PRO	3.7
17	AQ	82	VAL	3.7
41	BI	62	ALA	3.7
40	BH	114	GLU	3.7
33	BA	2149	U	3.7
41	BI	74	PRO	3.7
13	AM	62	PHE	3.7
19	AS	8	PRO	3.7
26	B2	62	GLY	3.7
42	BM	27	GLU	3.7
16	AP	52	LEU	3.7
41	BI	95	ASP	3.7
21	AU	40	PRO	3.7
33	BA	881	G	3.7
42	BJ	23	ILE	3.7
2	AB	118	THR	3.7
41	BI	14	ALA	3.7
2	AB	16	GLY	3.7
42	BK	5	ASP	3.6
33	BA	2105	U	3.6
5	AE	12	GLU	3.6
6	AF	62	MET	3.6
40	BH	133	GLU	3.6
45	BP	142	ILE	3.6
42	BL	27	GLU	3.6

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Mol	Chain	Res	Type	RSRZ
8	AH	67	GLY	3.6
48	BS	85	LYS	3.6
29	B5	30	PRO	3.6
41	BI	44	LYS	3.6
42	BJ	2	ILE	3.6
13	AM	83	GLY	3.6
41	BI	141	ASP	3.6
23	AW	522	GLN	3.6
2	AB	138	ARG	3.6
40	BH	145	GLU	3.6
13	AM	46	GLU	3.6
23	AW	467	ASN	3.6
40	BH	36	ASP	3.6
1	AA	1031	C	3.6
21	AU	41	THR	3.6
38	BF	45	ASP	3.6
47	BR	120	GLU	3.6
40	BH	117	LEU	3.5
40	BH	138	ARG	3.5
9	AI	39	GLY	3.5
23	AW	516	GLU	3.5
38	BF	80	GLN	3.5
40	BH	15	VAL	3.5
33	BA	2102	G	3.5
40	BH	112	ALA	3.5
16	AP	23	ASP	3.5
33	BA	2602	A	3.5
7	AG	65	LEU	3.5
16	AP	47	GLU	3.5
23	AW	466	VAL	3.5
45	BP	136	GLU	3.5
45	BP	123	ARG	3.5
41	BI	65	SER	3.5
2	AB	34	ARG	3.5
41	BI	60	VAL	3.5
13	AM	33	LEU	3.5
33	BA	2146	C	3.5
10	AJ	30	LYS	3.5
33	BA	276	U	3.5
42	BL	17	MET	3.5
10	AJ	102	LEU	3.5
45	BP	143	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
21	AU	4	LYS	3.5
41	BI	128	ILE	3.5
48	BS	88	LYS	3.5
27	B3	38	GLU	3.5
54	BY	86	PHE	3.5
40	BH	49	GLY	3.5
23	AW	512	ARG	3.4
23	AW	497	GLY	3.4
6	AF	61	LEU	3.4
41	BI	73	PRO	3.4
3	AC	131	ARG	3.4
40	BH	53	ARG	3.4
23	AW	511	LEU	3.4
38	BF	115	GLY	3.4
19	AS	21	ALA	3.4
16	AP	1	MET	3.4
42	BK	28	GLU	3.4
1	AA	1030	U	3.4
1	AA	1032	G	3.4
16	AP	3	THR	3.4
23	AW	470	THR	3.4
23	AW	501	LEU	3.4
6	AF	64	VAL	3.4
13	AM	1	ALA	3.4
2	AB	112	ARG	3.4
19	AS	41	PRO	3.4
7	AG	77	ARG	3.4
33	BA	547	A	3.4
38	BF	173	ASP	3.4
53	BX	6	ARG	3.4
19	AS	4	LEU	3.4
38	BF	43	ILE	3.4
2	AB	38	HIS	3.4
19	AS	14	LEU	3.4
2	AB	151	LYS	3.4
38	BF	97	GLU	3.4
4	AD	162	GLU	3.3
48	BS	92	PHE	3.3
14	AN	52	ARG	3.3
23	AW	53	GLN	3.3
20	AT	85	LEU	3.3
15	AO	87	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
48	BS	58	ILE	3.3
6	AF	25	TYR	3.3
7	AG	71	THR	3.3
16	AP	67	ILE	3.3
2	AB	126	ASP	3.3
23	AW	431	ILE	3.3
23	AW	484	GLU	3.3
42	BK	19	VAL	3.3
2	AB	28	PRO	3.3
23	AW	508	MET	3.3
41	BI	84	GLY	3.3
2	AB	73	ARG	3.3
33	BA	2585	U	3.3
6	AF	59	TYR	3.3
41	BI	31	GLY	3.3
18	AR	73	HIS	3.3
42	BL	9	GLU	3.3
42	BM	17	MET	3.3
7	AG	82	SER	3.3
41	BI	139	VAL	3.3
40	BH	51	TYR	3.3
40	BH	22	ALA	3.3
11	AK	128	VAL	3.3
13	AM	39	ALA	3.3
19	AS	65	MET	3.3
41	BI	48	ILE	3.3
40	BH	154	THR	3.3
2	AB	115	ASP	3.3
39	BG	31	GLU	3.3
17	AQ	14	ASP	3.2
4	AD	26	ALA	3.2
33	BA	1079	C	3.2
33	BA	2139	U	3.2
42	BK	13	ALA	3.2
7	AG	4	ARG	3.2
29	B5	35	LEU	3.2
33	BA	2148	G	3.2
1	AA	461	A	3.2
23	AW	525	GLN	3.2
4	AD	165	GLU	3.2
13	AM	6	ILE	3.2
33	BA	1744	A	3.2

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Mol	Chain	Res	Type	RSRZ
26	B2	1	MET	3.2
46	BQ	33	LEU	3.2
9	AI	40	ARG	3.2
13	AM	81	ASP	3.2
40	BH	77	VAL	3.2
33	BA	1174	U	3.2
13	AM	61	LYS	3.2
33	BA	2180	U	3.2
42	BL	26	MET	3.2
13	AM	45	SER	3.2
2	AB	107	ARG	3.2
2	AB	205	ALA	3.2
41	BI	122	GLU	3.2
33	BA	1073	A	3.2
46	BQ	3	GLN	3.2
8	AH	122	GLY	3.2
24	B0	45	HIS	3.2
40	BH	110	ALA	3.2
53	BX	69	ARG	3.2
23	AW	502	ALA	3.2
42	BM	10	ALA	3.2
6	AF	5	GLU	3.1
14	AN	58	ARG	3.1
40	BH	25	ALA	3.1
40	BH	26	VAL	3.1
48	BS	40	ILE	3.1
54	BY	59	GLU	3.1
23	AW	326	GLU	3.1
2	AB	142	LYS	3.1
40	BH	13	ALA	3.1
6	AF	37	HIS	3.1
23	AW	489	ASN	3.1
33	BA	1077	A	3.1
13	AM	94	LEU	3.1
45	BP	108	ALA	3.1
40	BH	27	VAL	3.1
40	BH	142	THR	3.1
40	BH	140	MET	3.1
41	BI	91	LYS	3.1
16	AP	51	ARG	3.1
42	BJ	30	PHE	3.1
42	BM	1	SER	3.1

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Mol	Chain	Res	Type	RSRZ
7	AG	45	ALA	3.1
10	AJ	8	ILE	3.1
12	AL	24	GLU	3.1
13	AM	113	LYS	3.1
40	BH	136	ILE	3.1
15	AO	62	ARG	3.1
41	BI	92	PRO	3.1
48	BS	81	ARG	3.1
33	BA	882	G	3.1
42	BL	28	GLU	3.1
33	BA	1083	U	3.1
24	B0	84	GLU	3.1
50	BU	87	VAL	3.1
33	BA	1509	A	3.1
40	BH	99	PHE	3.1
7	AG	79	VAL	3.0
25	B1	76	LYS	3.0
1	AA	1317	C	3.0
9	AI	20	ILE	3.0
19	AS	43	MET	3.0
40	BH	102	ALA	3.0
1	AA	4	U	3.0
23	AW	359	ALA	3.0
33	BA	102	U	3.0
7	AG	133	ALA	3.0
40	BH	4	ASN	3.0
2	AB	71	THR	3.0
16	AP	8	ARG	3.0
40	BH	143	MET	3.0
2	AB	186	VAL	3.0
42	BJ	17	MET	3.0
29	B5	32	LYS	3.0
4	AD	34	GLU	3.0
33	BA	1171	G	3.0
18	AR	47	ARG	3.0
19	AS	74	ALA	3.0
27	B3	1	ALA	3.0
42	BK	1	SER	3.0
42	BM	7	ILE	3.0
41	BI	71	LYS	3.0
53	BX	70	HIS	3.0
7	AG	13	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
29	B5	10	LEU	3.0
33	BA	1068	G	3.0
23	AW	526	THR	3.0
2	AB	36	LYS	3.0
42	BJ	1	SER	3.0
9	AI	88	GLU	3.0
18	AR	63	TYR	3.0
40	BH	104	ALA	3.0
2	AB	8	MET	3.0
38	BF	22	ASN	3.0
17	AQ	74	LEU	3.0
23	AW	503	TYR	3.0
29	B5	41	VAL	3.0
33	BA	2188	U	3.0
41	BI	85	ILE	3.0
16	AP	5	ARG	3.0
39	BG	51	PHE	3.0
45	BP	141	LYS	2.9
13	AM	34	ALA	2.9
40	BH	10	ALA	2.9
4	AD	159	GLU	2.9
16	AP	6	LEU	2.9
39	BG	165	ASP	2.9
43	BN	74	TYR	2.9
23	AW	324	LYS	2.9
33	BA	1075	C	2.9
42	BL	21	GLU	2.9
29	B5	42	VAL	2.9
17	AQ	63	CYS	2.9
33	BA	883	G	2.9
29	B5	16	THR	2.9
41	BI	2	LYS	2.9
7	AG	149	ALA	2.9
40	BH	96	PHE	2.9
20	AT	52	GLU	2.9
1	AA	208	U	2.9
3	AC	129	PHE	2.9
8	AH	120	LEU	2.9
33	BA	2143	C	2.9
7	AG	20	GLU	2.9
33	BA	2151	U	2.9
40	BH	115	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
33	BA	367	G	2.9
42	BM	4	LYS	2.9
10	AJ	93	ALA	2.9
40	BH	123	ILE	2.9
7	AG	148	LYS	2.9
17	AQ	79	GLU	2.9
19	AS	36	ARG	2.9
42	BM	12	ALA	2.9
46	BQ	2	LEU	2.9
33	BA	546	U	2.9
19	AS	3	SER	2.9
19	AS	12	LEU	2.9
4	AD	170	LEU	2.9
43	BN	90	GLU	2.9
14	AN	11	LYS	2.9
2	AB	87	ASP	2.9
33	BA	1625	C	2.9
40	BH	31	ARG	2.9
41	BI	43	ALA	2.9
13	AM	32	ILE	2.8
33	BA	1724	G	2.8
42	BL	2	ILE	2.8
19	AS	15	LEU	2.8
42	BM	2	ILE	2.8
7	AG	150	PHE	2.8
1	AA	843	U	2.8
6	AF	6	ILE	2.8
50	BU	88	GLU	2.8
33	BA	1091	G	2.8
8	AH	93	LYS	2.8
9	AI	34	LEU	2.8
41	BI	1	ALA	2.8
48	BS	50	ALA	2.8
29	B5	47	ILE	2.8
38	BF	73	VAL	2.8
41	BI	24	GLY	2.8
2	AB	206	ILE	2.8
46	BQ	7	THR	2.8
19	AS	60	PHE	2.8
42	BM	30	PHE	2.8
23	AW	402	ARG	2.8
13	AM	40	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
19	AS	17	LYS	2.8
14	AN	46	LYS	2.8
46	BQ	5	LYS	2.8
7	AG	78	ARG	2.8
38	BF	15	LEU	2.8
45	BP	73	ILE	2.8
41	BI	70	THR	2.8
41	BI	123	ALA	2.8
21	AU	21	SER	2.8
23	AW	379	PHE	2.8
23	AW	498	GLY	2.8
33	BA	1731	G	2.8
38	BF	31	GLU	2.8
14	AN	59	GLN	2.8
38	BF	70	ARG	2.8
34	BB	87	U	2.8
16	AP	7	ALA	2.8
24	B0	76	ARG	2.8
41	BI	137	LEU	2.8
52	BW	110	ARG	2.8
2	AB	110	ILE	2.8
3	AC	156	LEU	2.8
7	AG	21	LEU	2.8
19	AS	32	THR	2.8
12	AL	16	ALA	2.8
7	AG	16	LYS	2.8
19	AS	64	GLU	2.8
42	BM	15	SER	2.7
8	AH	90	GLU	2.7
17	AQ	39	ARG	2.7
1	AA	1167	A	2.7
1	AA	1043	G	2.7
2	AB	24	PRO	2.7
10	AJ	12	ALA	2.7
31	B7	47	ALA	2.7
21	AU	48	LYS	2.7
23	AW	339	ASP	2.7
1	AA	972	C	2.7
2	AB	32	GLY	2.7
19	AS	20	LYS	2.7
33	BA	1870	C	2.7
10	AJ	90	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
23	AW	468	VAL	2.7
40	BH	129	LEU	2.7
42	BL	16	VAL	2.7
13	AM	7	ASN	2.7
18	AR	20	ILE	2.7
40	BH	29	ASP	2.7
40	BH	91	ALA	2.7
19	AS	59	VAL	2.7
6	AF	9	MET	2.7
21	AU	43	GLU	2.7
9	AI	15	ALA	2.7
16	AP	74	LEU	2.7
41	BI	76	ALA	2.7
48	BS	64	TYR	2.7
19	AS	45	GLY	2.7
42	BJ	27	GLU	2.7
9	AI	32	ARG	2.7
7	AG	123	LEU	2.7
16	AP	34	GLU	2.7
40	BH	95	LEU	2.7
1	AA	842	U	2.7
21	AU	13	VAL	2.7
23	AW	327	LYS	2.7
5	AE	17	VAL	2.7
48	BS	25	ARG	2.7
33	BA	368	A	2.7
2	AB	37	VAL	2.7
7	AG	143	MET	2.7
14	AN	18	LYS	2.7
40	BH	101	LYS	2.7
38	BF	174	PHE	2.7
14	AN	12	ARG	2.7
48	BS	100	HIS	2.7
33	BA	2144	G	2.7
38	BF	112	ASP	2.7
16	AP	21	VAL	2.7
23	AW	481	LYS	2.7
33	BA	1089	A	2.7
7	AG	73	GLU	2.7
33	BA	1725	U	2.7
10	AJ	99	GLN	2.7
12	AL	12	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
26	B2	5	GLU	2.7
25	B1	4	CYS	2.7
33	BA	1871	A	2.7
41	BI	114	ALA	2.7
4	AD	17	ASP	2.6
41	BI	37	PHE	2.6
7	AG	3	ARG	2.6
48	BS	93	ASP	2.6
38	BF	69	ALA	2.6
40	BH	111	ALA	2.6
23	AW	332	ARG	2.6
39	BG	115	GLN	2.6
11	AK	125	LYS	2.6
21	AU	15	LEU	2.6
40	BH	106	PHE	2.6
16	AP	17	TYR	2.6
29	B5	49	LYS	2.6
42	BL	18	ASP	2.6
33	BA	277	G	2.6
15	AO	16	ARG	2.6
23	AW	469	ALA	2.6
42	BL	10	ALA	2.6
54	BY	21	ARG	2.6
33	BA	1583	A	2.6
9	AI	57	VAL	2.6
29	B5	11	VAL	2.6
41	BI	46	ASP	2.6
33	BA	364	C	2.6
40	BH	39	THR	2.6
53	BX	1	MET	2.6
14	AN	2	LYS	2.6
53	BX	4	GLU	2.6
40	BH	2	ALA	2.6
41	BI	107	GLU	2.6
29	B5	46	VAL	2.6
23	AW	329	MET	2.6
33	BA	914	G	2.6
10	AJ	47	GLU	2.6
18	AR	26	ALA	2.6
1	AA	1138	G	2.6
12	AL	43	LYS	2.6
19	AS	54	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
40	BH	107	GLU	2.6
46	BQ	4	PRO	2.6
16	AP	73	ALA	2.6
16	AP	81	ALA	2.6
33	BA	2147	A	2.6
42	BJ	24	SER	2.6
17	AQ	5	ARG	2.6
29	B5	26	LYS	2.6
40	BH	43	LYS	2.6
9	AI	22	PRO	2.5
16	AP	65	ALA	2.5
26	B2	2	LYS	2.5
27	B3	19	HIS	2.5
38	BF	175	PRO	2.5
2	AB	144	GLU	2.5
12	AL	69	GLU	2.5
30	B6	46	LYS	2.5
36	BD	209	ALA	2.5
8	AH	51	GLU	2.5
10	AJ	66	GLU	2.5
44	BO	8	LEU	2.5
48	BS	60	GLU	2.5
13	AM	60	ALA	2.5
2	AB	136	ARG	2.5
12	AL	14	LYS	2.5
41	BI	106	GLN	2.5
46	BQ	68	PHE	2.5
48	BS	116	GLN	2.5
2	AB	30	ILE	2.5
2	AB	44	LYS	2.5
3	AC	203	LYS	2.5
33	BA	1076	C	2.5
32	B8	11	CYS	2.5
38	BF	172	PHE	2.5
13	AM	8	ILE	2.5
38	BF	76	PHE	2.5
24	B0	40	ARG	2.5
2	AB	21	TYR	2.5
17	AQ	13	SER	2.5
41	BI	35	MET	2.5
54	BY	31	GLY	2.5
18	AR	54	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
2	AB	191	ASP	2.5
41	BI	87	SER	2.5
53	BX	72	GLN	2.5
38	BF	30	VAL	2.5
48	BS	35	ILE	2.5
2	AB	153	MET	2.5
23	AW	471	ALA	2.5
17	AQ	62	GLU	2.5
20	AT	66	ILE	2.5
55	BZ	41	GLU	2.5
21	AU	6	ARG	2.5
48	BS	7	ARG	2.5
6	AF	4	TYR	2.5
7	AG	46	LEU	2.5
23	AW	496	ASP	2.5
6	AF	60	VAL	2.5
9	AI	5	TYR	2.5
41	BI	82	ALA	2.5
48	BS	90	VAL	2.5
54	BY	4	ILE	2.5
32	B8	29	ALA	2.4
39	BG	176	LYS	2.4
50	BU	86	SER	2.4
1	AA	1033	G	2.4
10	AJ	49	PHE	2.4
42	BM	13	ALA	2.4
23	AW	342	ILE	2.4
2	AB	134	LEU	2.4
53	BX	71	GLY	2.4
42	BM	11	VAL	2.4
38	BF	96	TRP	2.4
41	BI	36	GLU	2.4
4	AD	35	GLN	2.4
48	BS	56	LYS	2.4
9	AI	27	ILE	2.4
9	AI	122	ARG	2.4
20	AT	3	ILE	2.4
33	BA	1066	U	2.4
33	BA	1914	C	2.4
19	AS	46	LEU	2.4
45	BP	125	LEU	2.4
21	AU	31	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
38	BF	163	GLU	2.4
2	AB	116	LEU	2.4
1	AA	1044	A	2.4
4	AD	172	VAL	2.4
19	AS	19	GLU	2.4
13	AM	55	LEU	2.4
16	AP	66	THR	2.4
23	AW	429	ARG	2.4
48	BS	83	LEU	2.4
3	AC	151	GLU	2.4
16	AP	33	ILE	2.4
19	AS	68	HIS	2.4
42	BM	6	GLN	2.4
39	BG	94	ARG	2.4
24	B0	82	GLU	2.4
48	BS	49	VAL	2.4
19	AS	72	GLU	2.4
40	BH	47	GLU	2.4
8	AH	49	LYS	2.4
24	B0	52	CYS	2.4
27	B3	5	LYS	2.4
42	BK	15	SER	2.4
2	AB	113	LEU	2.4
11	AK	127	ARG	2.4
32	B8	24	ARG	2.4
13	AM	93	GLY	2.4
24	B0	83	ALA	2.4
10	AJ	74	VAL	2.4
38	BF	118	ALA	2.4
6	AF	21	MET	2.4
33	BA	715	A	2.4
10	AJ	10	LEU	2.4
29	B5	31	GLU	2.4
13	AM	2	ARG	2.4
13	AM	10	ASP	2.4
2	AB	127	LYS	2.4
6	AF	8	PHE	2.4
38	BF	99	PHE	2.4
42	BJ	15	SER	2.4
10	AJ	31	ARG	2.4
14	AN	53	ASP	2.4
29	B5	4	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
13	AM	30	LYS	2.4
38	BF	86	CYS	2.4
52	BW	73	LYS	2.4
55	BZ	34	LYS	2.4
13	AM	63	VAL	2.4
9	AI	62	LEU	2.4
23	AW	399	ARG	2.4
23	AW	463	TYR	2.4
41	BI	19	PRO	2.4
48	BS	117	PHE	2.4
8	AH	68	LYS	2.4
9	AI	86	LEU	2.4
33	BA	1723	G	2.4
42	BM	18	ASP	2.4
17	AQ	77	VAL	2.4
33	BA	504	A	2.4
33	BA	1872	A	2.4
54	BY	25	LYS	2.4
9	AI	127	SER	2.3
9	AI	28	VAL	2.3
12	AL	23	LEU	2.3
54	BY	11	ILE	2.3
17	AQ	50	ASN	2.3
37	BE	134	LEU	2.3
10	AJ	65	TYR	2.3
19	AS	75	PRO	2.3
38	BF	42	ALA	2.3
53	BX	82	LYS	2.3
4	AD	18	LEU	2.3
19	AS	66	VAL	2.3
45	BP	107	PHE	2.3
38	BF	166	ARG	2.3
43	BN	102	GLU	2.3
53	BX	3	ARG	2.3
16	AP	2	VAL	2.3
49	BT	114	ASN	2.3
16	AP	35	ARG	2.3
13	AM	82	LEU	2.3
42	BL	25	ALA	2.3
2	AB	117	GLU	2.3
42	BJ	29	LYS	2.3
51	BV	44	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
38	BF	74	ALA	2.3
42	BK	26	MET	2.3
3	AC	190	THR	2.3
14	AN	9	GLU	2.3
33	BA	2183	A	2.3
42	BK	30	PHE	2.3
46	BQ	60	GLN	2.3
42	BL	14	MET	2.3
42	BL	29	LYS	2.3
55	BZ	68	LYS	2.3
5	AE	86	GLY	2.3
38	BF	95	MET	2.3
16	AP	4	ILE	2.3
7	AG	145	GLU	2.3
40	BH	163	GLU	2.3
13	AM	53	ASP	2.3
54	BY	23	LYS	2.3
39	BG	42	VAL	2.3
42	BJ	6	GLN	2.3
21	AU	44	ARG	2.3
4	AD	28	ASP	2.3
7	AG	109	LYS	2.3
53	BX	93	LEU	2.3
16	AP	18	GLN	2.3
8	AH	63	LYS	2.3
43	BN	92	MET	2.3
53	BX	24	MET	2.3
49	BT	34	GLY	2.3
53	BX	73	ARG	2.3
54	BY	12	VAL	2.3
17	AQ	15	LYS	2.3
2	AB	99	MET	2.3
9	AI	66	VAL	2.3
19	AS	5	LYS	2.3
21	AU	17	ARG	2.3
13	AM	91	ARG	2.2
40	BH	153	ARG	2.2
45	BP	126	ARG	2.2
48	BS	87	ILE	2.2
25	B1	70	LEU	2.2
7	AG	39	GLU	2.2
2	AB	25	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
2	AB	68	PHE	2.2
25	B1	46	VAL	2.2
42	BM	5	ASP	2.2
16	AP	60	TRP	2.2
54	BY	38	ILE	2.2
23	AW	325	TYR	2.2
23	AW	430	PRO	2.2
3	AC	169	GLU	2.2
53	BX	68	LYS	2.2
16	AP	39	PHE	2.2
7	AG	62	GLU	2.2
7	AG	70	PRO	2.2
33	BA	1847	A	2.2
53	BX	92	ASN	2.2
7	AG	22	LEU	2.2
13	AM	86	ARG	2.2
24	B0	50	VAL	2.2
47	BR	28	LEU	2.2
2	AB	59	ILE	2.2
19	AS	7	GLY	2.2
53	BX	2	ILE	2.2
7	AG	72	VAL	2.2
45	BP	75	ALA	2.2
33	BA	549	G	2.2
41	BI	28	GLY	2.2
41	BI	132	ALA	2.2
3	AC	167	TYR	2.2
3	AC	160	GLU	2.2
40	BH	131	THR	2.2
33	BA	1745	A	2.2
42	BJ	16	VAL	2.2
1	AA	1009	U	2.2
3	AC	128	MET	2.2
7	AG	100	MET	2.2
24	B0	51	GLY	2.2
28	B4	56	LYS	2.2
40	BH	127	ALA	2.2
38	BF	165	GLY	2.2
48	BS	15	ARG	2.2
33	BA	897	C	2.2
7	AG	146	ALA	2.2
13	AM	100	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
16	AP	53	ASP	2.2
23	AW	52	ASN	2.2
42	BL	24	SER	2.2
31	B7	18	LYS	2.2
54	BY	20	LYS	2.2
54	BY	46	LYS	2.2
17	AQ	54	ILE	2.2
2	AB	20	ARG	2.2
10	AJ	9	ARG	2.2
40	BH	94	ARG	2.2
33	BA	1087	G	2.2
2	AB	166	ASP	2.2
12	AL	15	VAL	2.2
23	AW	357	GLU	2.2
33	BA	1170	C	2.2
48	BS	80	GLU	2.2
10	AJ	87	LEU	2.2
12	AL	50	LYS	2.2
19	AS	80	ARG	2.2
9	AI	45	MET	2.2
40	BH	69	PHE	2.2
31	B7	23	HIS	2.2
54	BY	70	ALA	2.2
7	AG	11	ILE	2.2
11	AK	126	ARG	2.2
40	BH	85	SER	2.2
54	BY	49	PRO	2.2
8	AH	9	MET	2.2
13	AM	50	GLY	2.2
15	AO	14	PHE	2.2
39	BG	147	LEU	2.2
41	BI	88	GLY	2.2
54	BY	71	ILE	2.2
54	BY	72	PHE	2.1
10	AJ	63	ASP	2.1
43	BN	69	ARG	2.1
23	AW	157	GLU	2.1
37	BE	157	LEU	2.1
51	BV	34	GLU	2.1
11	AK	124	LYS	2.1
16	AP	57	ILE	2.1
4	AD	203	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
48	BS	37	ALA	2.1
2	AB	114	LYS	2.1
23	AW	331	LEU	2.1
8	AH	127	TYR	2.1
38	BF	101	ARG	2.1
42	BJ	25	ALA	2.1
1	AA	1022	A	2.1
7	AG	83	THR	2.1
9	AI	29	ILE	2.1
33	BA	1848	A	2.1
39	BG	106	LEU	2.1
29	B5	14	ALA	2.1
31	B7	64	ALA	2.1
48	BS	59	ALA	2.1
8	AH	103	VAL	2.1
21	AU	7	GLU	2.1
41	BI	81	LYS	2.1
46	BQ	53	MET	2.1
7	AG	140	VAL	2.1
15	AO	17	ASP	2.1
23	AW	523	PHE	2.1
33	BA	1057	A	2.1
7	AG	85	GLN	2.1
40	BH	44	ALA	2.1
46	BQ	40	ARG	2.1
8	AH	74	ILE	2.1
27	B3	4	ILE	2.1
1	AA	1042	A	2.1
38	BF	68	LYS	2.1
33	BA	2145	C	2.1
2	AB	130	LYS	2.1
41	BI	124	MET	2.1
2	AB	18	GLN	2.1
15	AO	63	ARG	2.1
2	AB	66	ILE	2.1
13	AM	111	PRO	2.1
15	AO	86	LEU	2.1
17	AQ	46	HIS	2.1
55	BZ	82	TYR	2.1
10	AJ	35	GLN	2.1
6	AF	63	ASN	2.1
11	AK	13	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
39	BG	171	LYS	2.1
41	BI	47	SER	2.1
7	AG	80	GLY	2.1
42	BJ	9	GLU	2.1
37	BE	9	GLN	2.1
20	AT	84	LYS	2.1
2	AB	51	GLU	2.1
4	AD	46	ARG	2.1
7	AG	5	VAL	2.1
33	BA	1737	G	2.1
54	BY	50	ALA	2.1
1	AA	136	C	2.1
42	BL	15	SER	2.1
6	AF	65	GLU	2.1
15	AO	41	HIS	2.1
29	B5	48	TYR	2.1
9	AI	58	GLU	2.1
23	AW	406	PRO	2.1
44	BO	71	ARG	2.1
48	BS	84	GLU	2.1
9	AI	36	GLN	2.1
4	AD	193	ASP	2.1
33	BA	1172	C	2.1
16	AP	38	PHE	2.1
39	BG	48	THR	2.1
9	AI	63	TYR	2.1
27	B3	15	ARG	2.1
37	BE	188	MET	2.1
46	BQ	22	GLN	2.1
33	BA	1101	U	2.1
44	BO	49	ARG	2.1
40	BH	155	LEU	2.1
54	BY	88	ASP	2.1
5	AE	109	ALA	2.0
40	BH	141	ALA	2.0
48	BS	70	ALA	2.0
2	AB	13	VAL	2.0
7	AG	90	VAL	2.0
41	BI	98	GLY	2.0
1	AA	1020	G	2.0
46	BQ	95	LEU	2.0
9	AI	67	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
5	AE	102	THR	2.0
27	B3	57	GLU	2.0
29	B5	13	SER	2.0
37	BE	138	LEU	2.0
33	BA	1085	A	2.0
48	BS	39	VAL	2.0
53	BX	5	GLU	2.0
6	AF	1	MET	2.0
27	B3	53	MET	2.0
42	BJ	14	MET	2.0
3	AC	163	ARG	2.0
8	AH	102	VAL	2.0
19	AS	18	VAL	2.0
38	BF	29	ARG	2.0
54	BY	93	ARG	2.0
33	BA	1734	G	2.0
40	BH	32	GLY	2.0
40	BH	57	ASN	2.0
45	BP	105	ILE	2.0
2	AB	67	LEU	2.0
9	AI	50	PRO	2.0
39	BG	40	VAL	2.0
13	AM	56	ARG	2.0
38	BF	72	SER	2.0
40	BH	58	THR	2.0
2	AB	189	ASN	2.0
1	AA	151	A	2.0
7	AG	10	LYS	2.0
13	AM	49	GLU	2.0
19	AS	79	TYR	2.0
2	AB	69	VAL	2.0
1	AA	580	C	2.0
14	AN	1	ALA	2.0
33	BA	1081	U	2.0
37	BE	144	GLU	2.0
7	AG	52	ARG	2.0
8	AH	92	PRO	2.0
8	AH	1	SER	2.0
5	AE	13	LYS	2.0
13	AM	31	ALA	2.0
33	BA	1434	A	2.0
51	BV	46	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
7	AG	7	GLY	2.0
10	AJ	92	LEU	2.0
14	AN	8	ARG	2.0
17	AQ	64	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	GNP	AW	601	32/32	0.22	0.30	81,97,115,121	0
57	MG	AW	602	1/1	0.19	-0.97	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.