



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 04:28 PM UTC

PDB ID : 8EVT / pdb_00008evt
EMDB ID : EMD-28636
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES) refined against a composite map
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-20
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

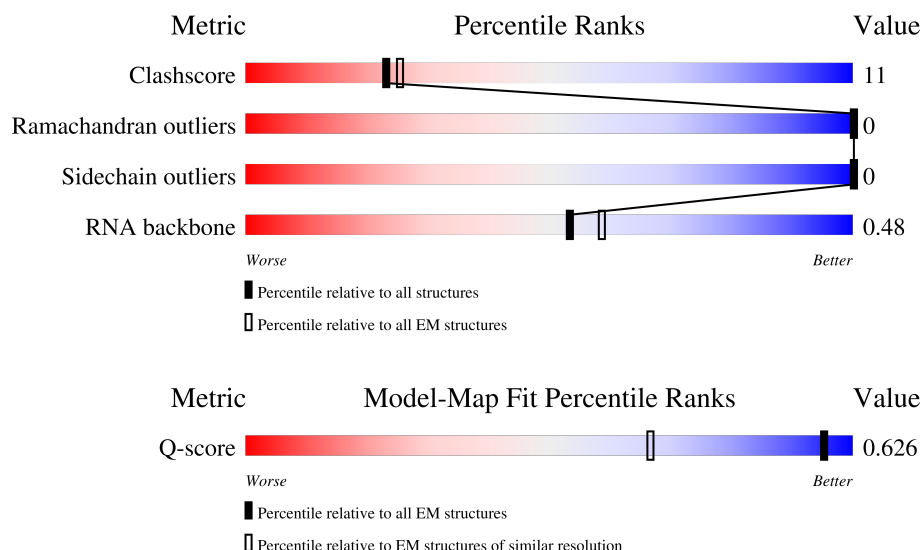
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.20 Å.

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



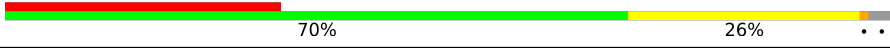
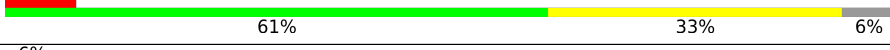
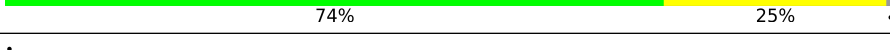
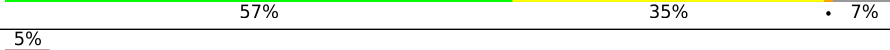
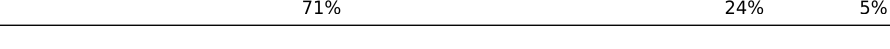
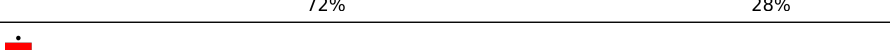
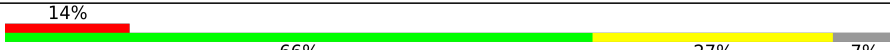
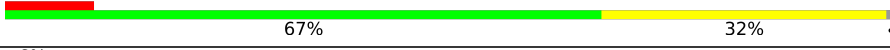
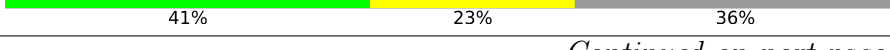
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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

Mol	Chain	Length	Quality of chain
1	BA	252	5% 54% 28% 18%
2	BB	255	10% 55% 29% 16%
3	BC	254	66% 19% 15%

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Mol	Chain	Length	Quality of chain
4	BE	261	
5	BG	236	
6	BH	190	
7	BI	200	
8	BJ	197	
9	BL	156	
10	BN	151	
11	BO	137	
12	BV	87	
13	BW	130	
14	BX	145	
15	BY	135	
16	Ba	119	
17	Bb	82	
18	Be	63	
19	BD	240	
20	BF	225	
21	BK	105	
22	BP	142	
23	BQ	143	
24	BR	136	
25	BS	146	
26	BT	144	
27	BU	121	
28	BZ	108	

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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3360	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	221	
47	AJ	174	
48	AL	199	
49	AM	138	
50	AN	204	
51	AO	199	
52	AP	184	
53	AQ	186	

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Mol	Chain	Length	Quality of chain
54	AR	189	
55	AS	178	
56	AT	160	
57	AU	121	
58	AV	137	
59	AW	155	
60	AX	142	
61	AY	127	
62	AZ	136	
63	Aa	149	
64	Ab	59	
65	Ac	105	
66	Ad	113	
67	Ae	130	
68	Af	107	
69	Ag	121	
70	Ah	120	
71	Ai	100	
72	Aj	88	
73	Ak	78	
74	Al	51	
75	Am	128	
76	An	25	
77	Ao	106	
78	Ap	92	

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Mol	Chain	Length	Quality of chain
79	E	217	100% 63% 37%
80	EC	202	15% 14% 9% 72%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 202928 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	BA	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 2 is a protein called RPS1A isoform 1.

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

- Molecule 3 is a protein called RPS2 isoform 1.

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

- Molecule 4 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 5 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BG	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 6 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	BH	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 7 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BL	155	Total	C	N	O	S	0	0
			1244	798	235	208	3		

- Molecule 10 is a protein called 40S ribosomal protein S13.

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

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BO	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 12 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 13 is a protein called RPS22A isoform 1.

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

- Molecule 14 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BY	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 16 is a protein called RPS26B isoform 1.

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

- Molecule 17 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 19 is a protein called RPS3 isoform 1.

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

- Molecule 20 is a protein called Rps5p.

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

- Molecule 21 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BK	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 22 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BP	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 23 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BR	121	Total	C	N	O	S	0	0
			975	611	183	179	2		

- Molecule 25 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BT	141	Total	C	N	O	S	0	0
			1095	685	206	202	2		

- Molecule 27 is a protein called RPS20 isoform 1.

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

- Molecule 28 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BZ	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 29 is a protein called RPS28A isoform 1.

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

- Molecule 30 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bd	53	Total	C	N	O	S	0	0
			443	275	92	72	4		

- Molecule 31 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bg	312	Total	C	N	O	S	0	0
			2401	1522	410	461	8		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bf	57	Total	C	N	O	S	0	0
			454	288	86	77	3		

- Molecule 33 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BM	121	Total	C	N	O	S	0	0
			913	574	162	175	2		

- Molecule 34 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B5	1782	Total	C	N	O	P	1	0
			38004	17005	6718	12499	1782		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B5	1280	4AC	C	conflict	GB 1329886537
B5	1773	4AC	C	conflict	GB 1329886537

- Molecule 35 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AA	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 36 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	386	Total	C	N	O	S	0	0
			3080	1955	584	533	8		

- Molecule 37 is a protein called RPL4A isoform 1.

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

- Molecule 38 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	3192	Total	C	N	O	P	0	0
			68319	30539	12310	22278	3192		

- Molecule 39 is a RNA chain called 5s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 40 is a RNA chain called 5.8 S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 41 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AD	292	Total	C	N	O	S	0	0
			2341	1478	408	453	2		

- Molecule 42 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AG	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 45 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AH	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 46 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AI	205	Total	C	N	O	S	0	0
			1672	1063	316	288	5		

- Molecule 47 is a protein called RPL11A isoform 1.

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

- Molecule 48 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	AP	175	Total	C	N	O		
			1388	862	277	249	0	0

- Molecule 53 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	AR	188	Total	C	N	O		
			1521	935	326	260	0	0

- Molecule 55 is a protein called 60S ribosomal protein L20.

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

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 59 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AW	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AX	121	Total	C	N	O	S	0	0
			968	623	170	173	2		

- Molecule 61 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AY	126	Total	C	N	O	S	0	0
			993	625	192	176			

- Molecule 62 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L28.

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

- Molecule 64 is a protein called RPL29 isoform 1.

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

- Molecule 65 is a protein called 60S ribosomal protein L30.

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

- Molecule 66 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Ad	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 67 is a protein called RPL32 isoform 1.

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

- Molecule 68 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 73 is a protein called RPL38 isoform 1.

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

- Molecule 74 is a protein called 60S ribosomal protein L39.

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

- Molecule 75 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 76 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 79 is a protein called RPL1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	E	217	Total	C	N	O	S	0	0
			1718	1097	299	312	10		

- Molecule 80 is a RNA chain called TSV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	EC	57	Total	C	N	O	P	0	0
			1209	541	213	398	57		

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	BN	1	Total	Mg	0
			1	1	
81	Ba	1	Total	Mg	0
			1	1	
81	B5	73	Total	Mg	0
			73	73	
81	AB	1	Total	Mg	0
			1	1	
81	AC	1	Total	Mg	0
			1	1	
81	A1	180	Total	Mg	0
			180	180	

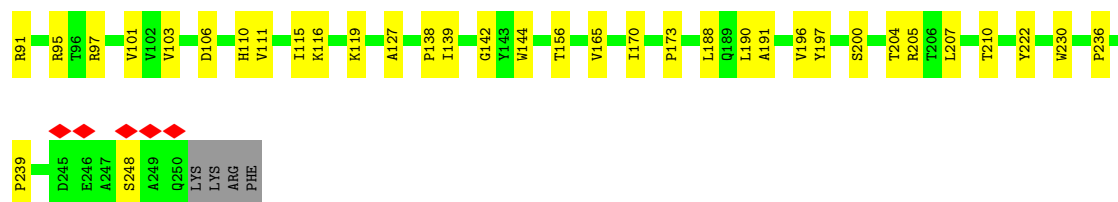
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Mol	Chain	Residues	Atoms		AltConf
81	A3	2	Total 2	Mg 2	0
81	A4	4	Total 4	Mg 4	0
81	AN	2	Total 2	Mg 2	0
81	AO	1	Total 1	Mg 1	0
81	AP	1	Total 1	Mg 1	0
81	Ae	2	Total 2	Mg 2	0
81	Af	1	Total 1	Mg 1	0
81	Ah	1	Total 1	Mg 1	0
81	Aj	1	Total 1	Mg 1	0

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

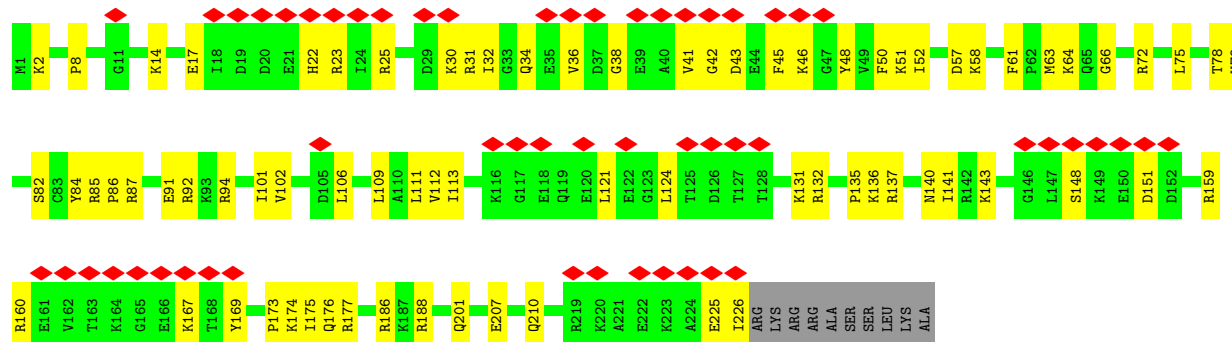
Mol	Chain	Residues	Atoms		AltConf
82	Ao	1	Total 1	Zn 1	0



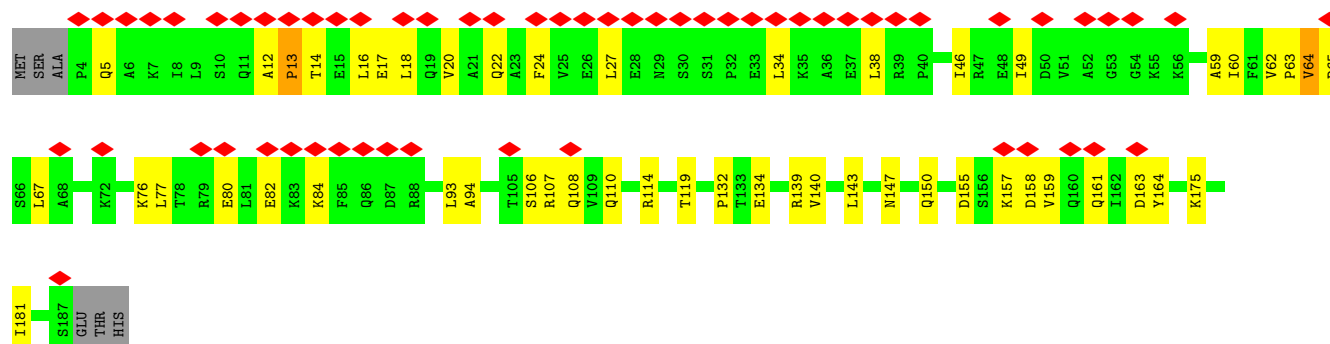
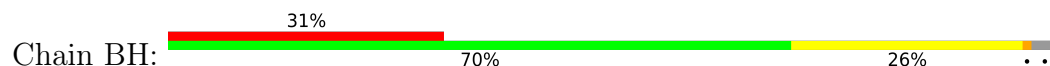
• Molecule 4: 40S ribosomal protein S4-A



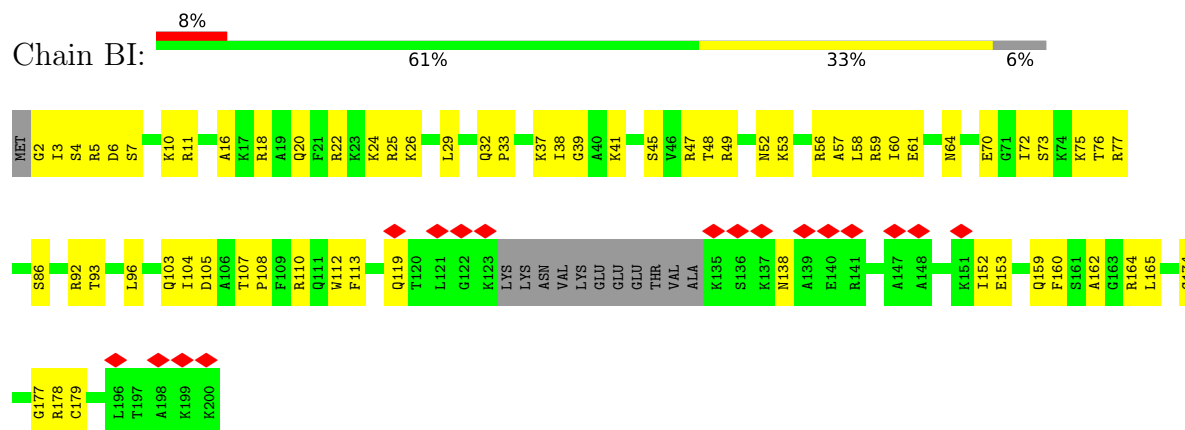
• Molecule 5: 40S ribosomal protein S6-A



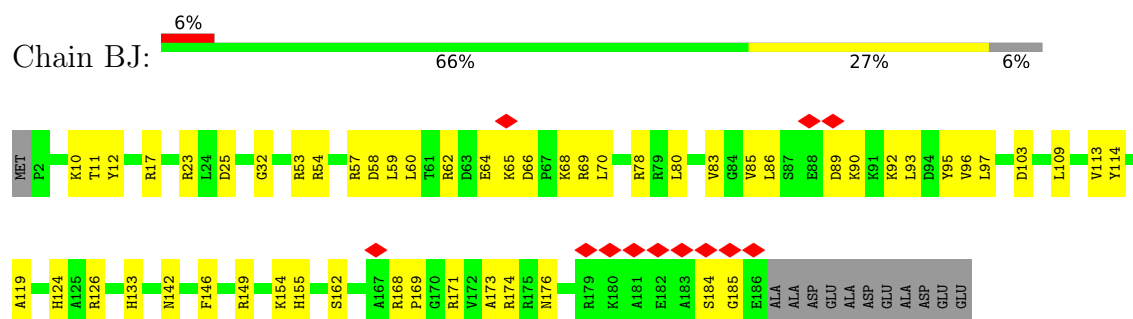
• Molecule 6: 40S ribosomal protein S7-A



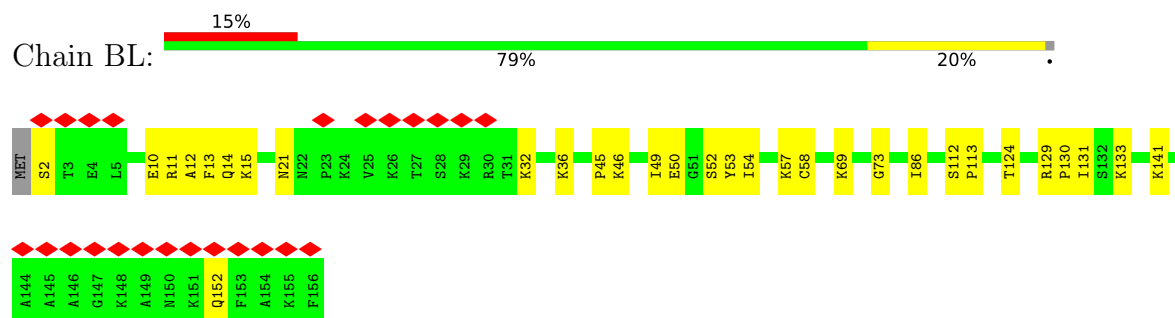
- Molecule 7: 40S ribosomal protein S8-A



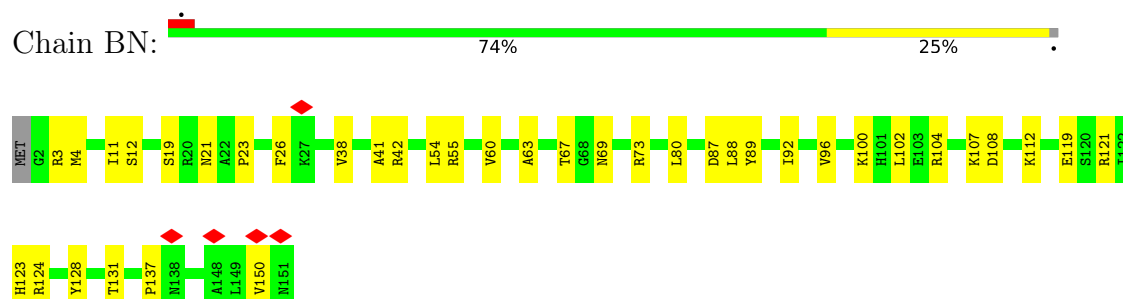
- Molecule 8: 40S ribosomal protein S9-A



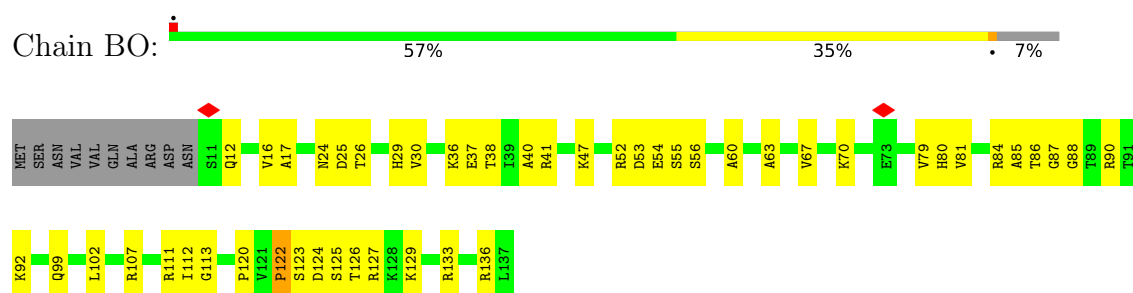
- Molecule 9: 40S ribosomal protein S11-A



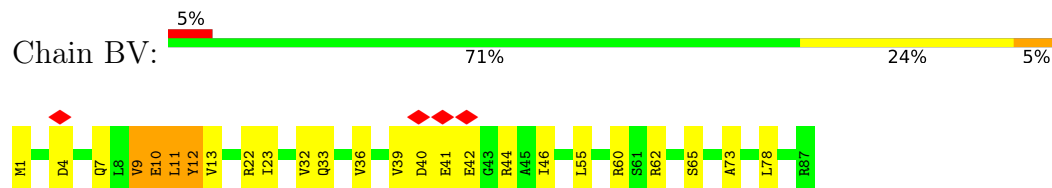
- Molecule 10: 40S ribosomal protein S13



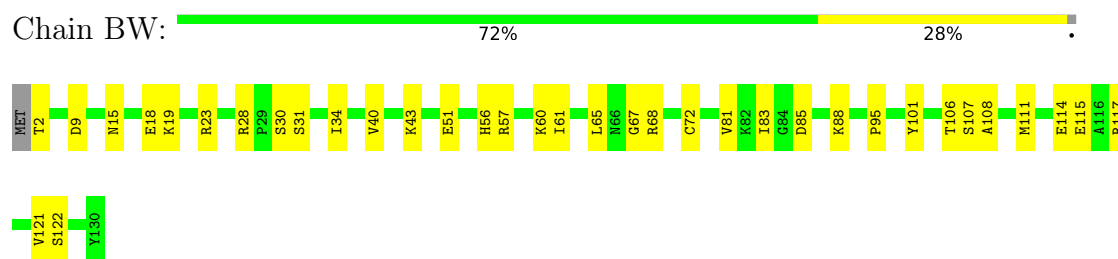
- Molecule 11: 40S ribosomal protein S14-A



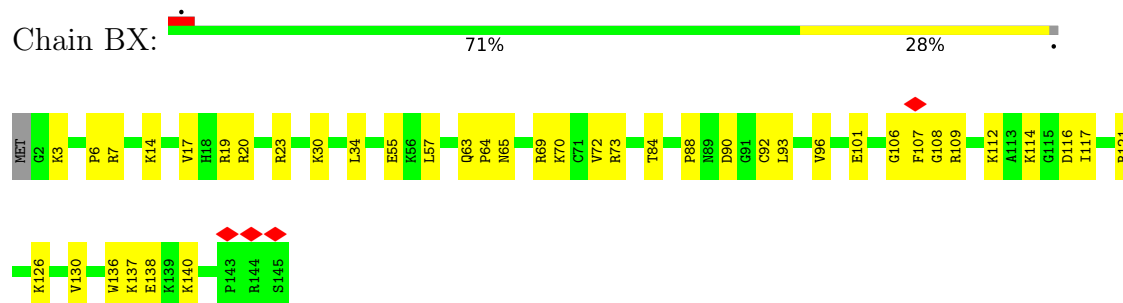
- Molecule 12: 40S ribosomal protein S21-A



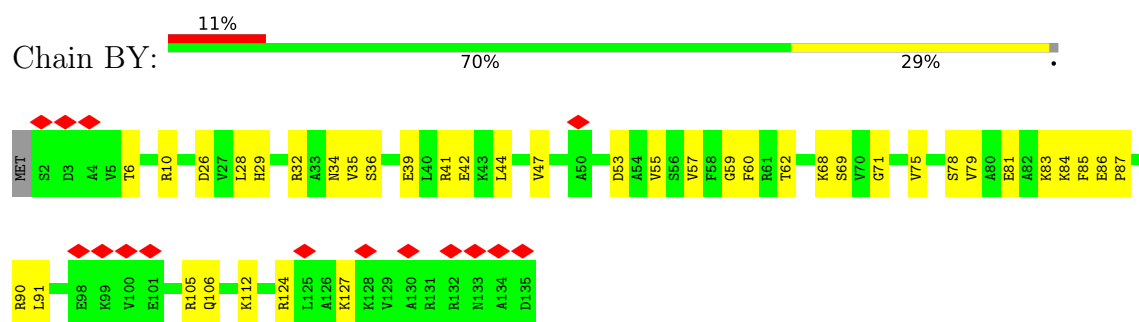
- Molecule 13: RPS22A isoform 1



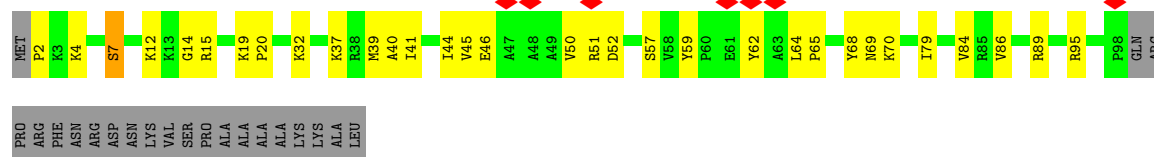
- Molecule 14: 40S ribosomal protein S23-A



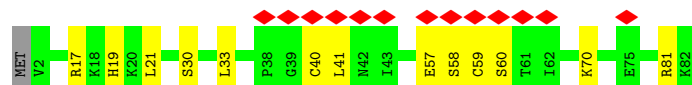
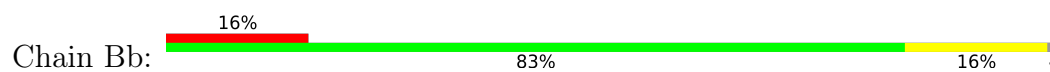
- Molecule 15: 40S ribosomal protein S24-A



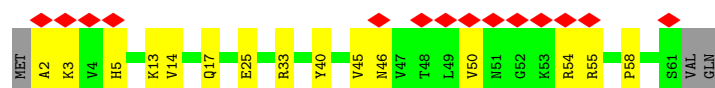
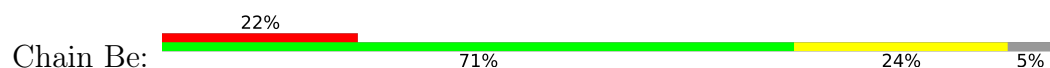
- Molecule 16: RPS26B isoform 1



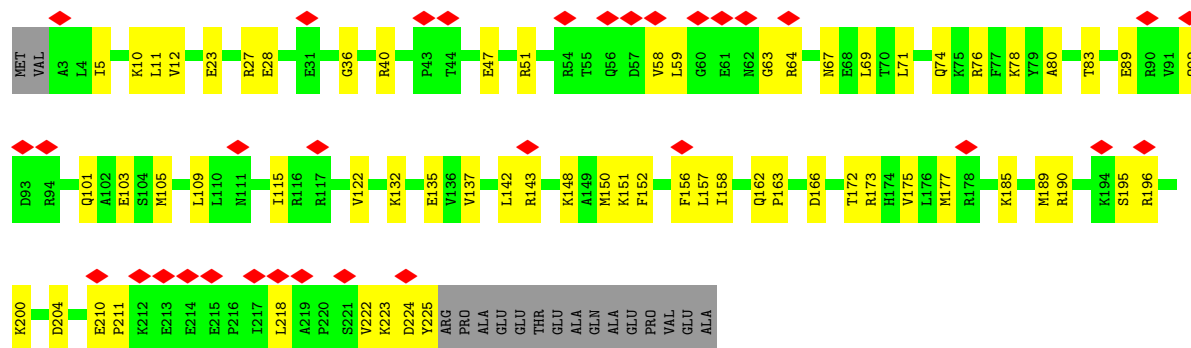
- Molecule 17: 40S ribosomal protein S27-A



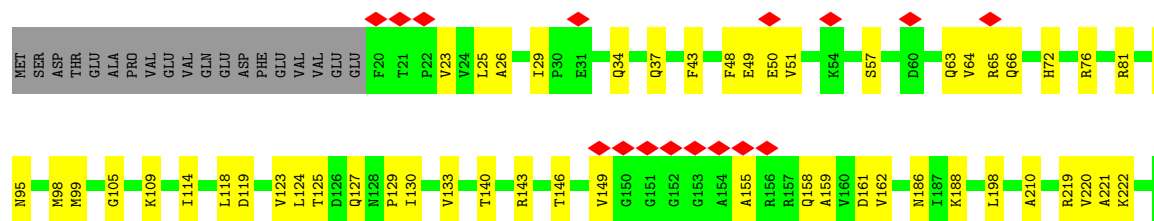
- Molecule 18: 40S ribosomal protein S30-A



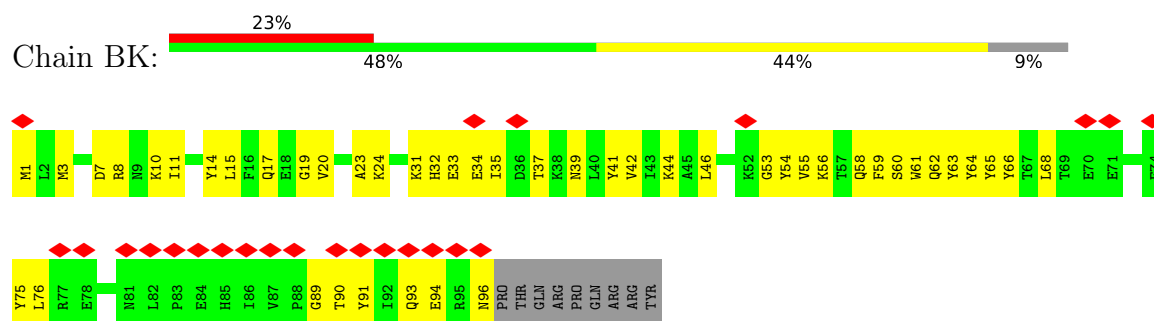
- Molecule 19: RPS3 isoform 1



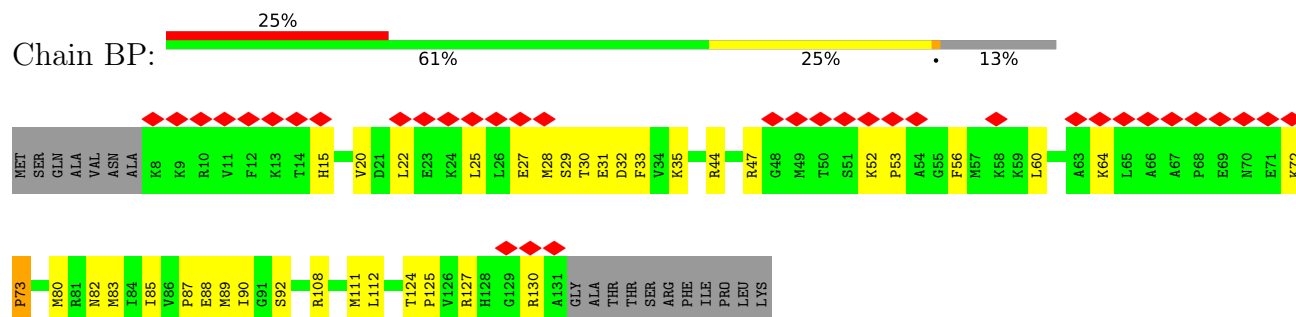
- Molecule 20: Rps5p



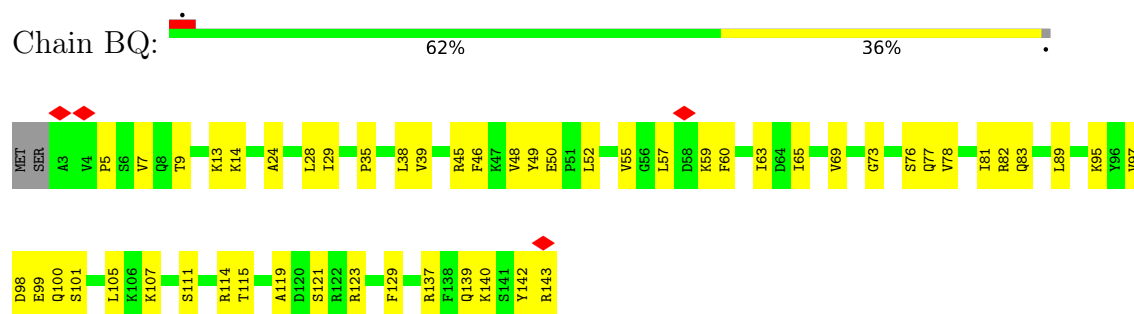
- Molecule 21: 40S ribosomal protein S10-A



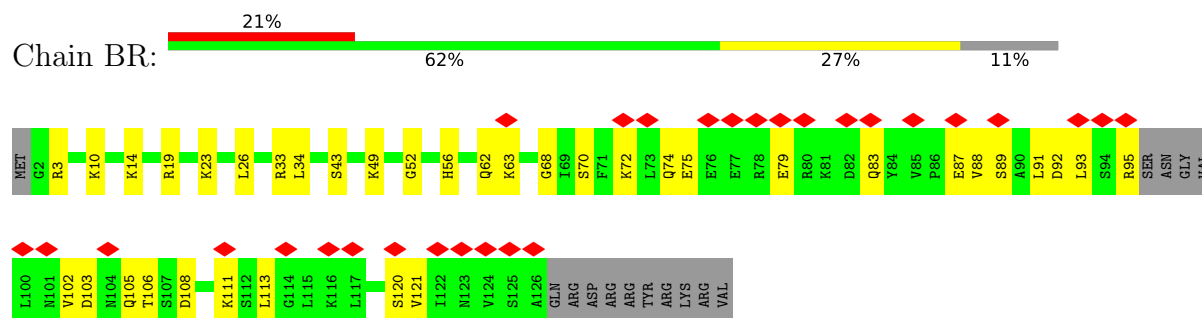
- Molecule 22: RPS15 isoform 1



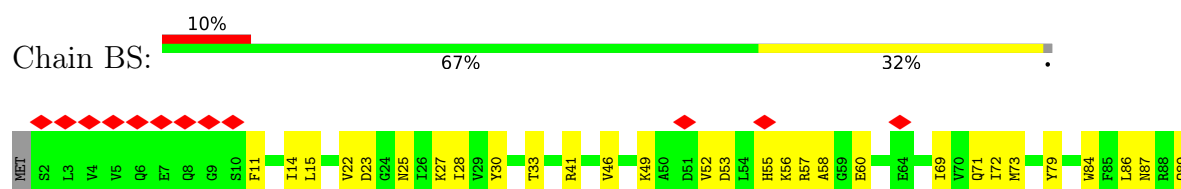
- Molecule 23: 40S ribosomal protein S16-A



- Molecule 24: 40S ribosomal protein S17-A

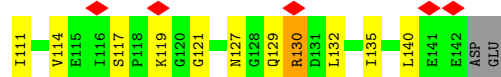
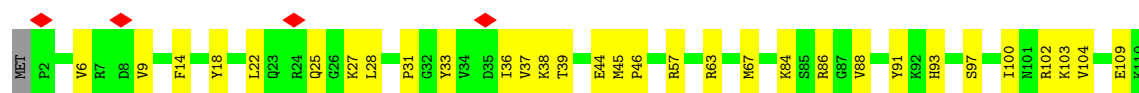


- Molecule 25: 40S ribosomal protein S18-A

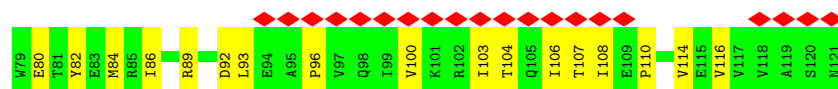
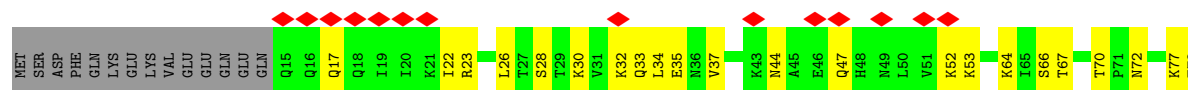




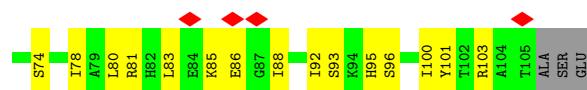
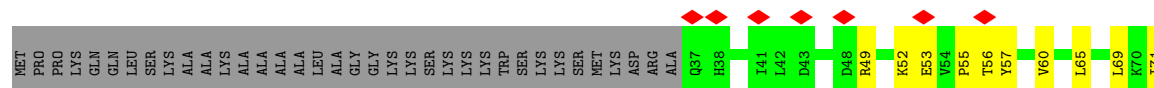
- Molecule 26: 40S ribosomal protein S19-A



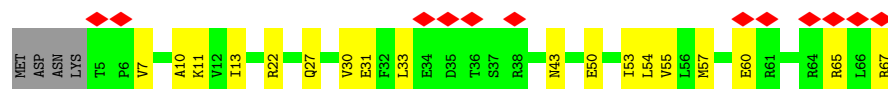
- Molecule 27: RPS20 isoform 1



- Molecule 28: RPS25A isoform 1

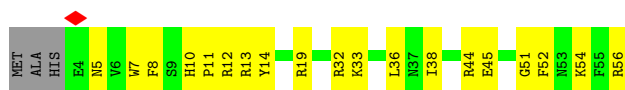


- Molecule 29: RPS28A isoform 1

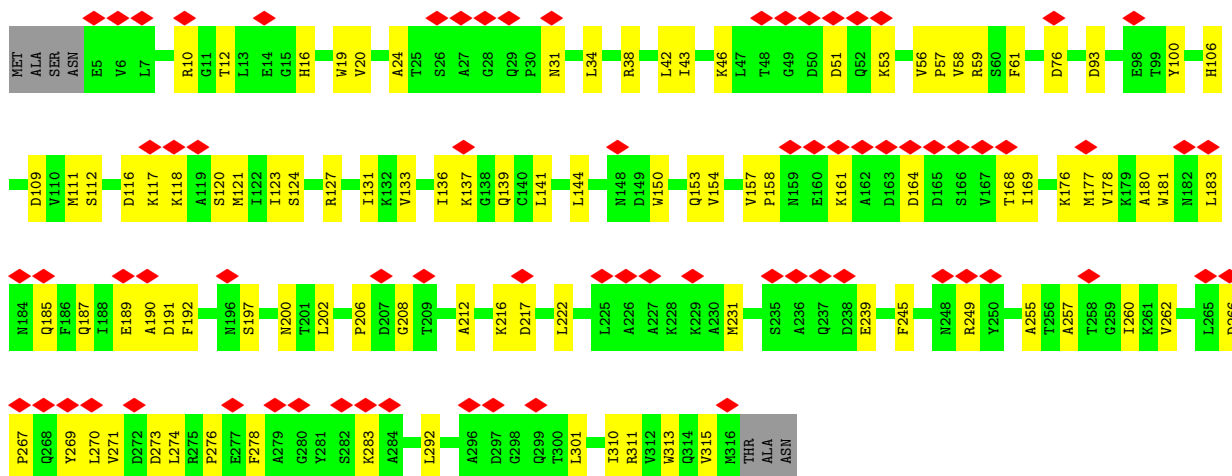


- Molecule 30: RPS29A isoform 1

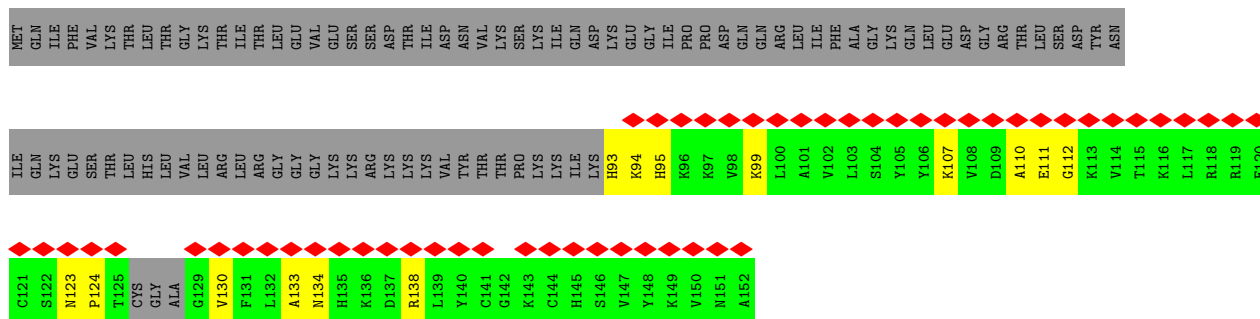




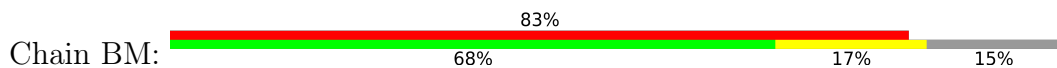
- Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 32: Ubiquitin-40S ribosomal protein S31

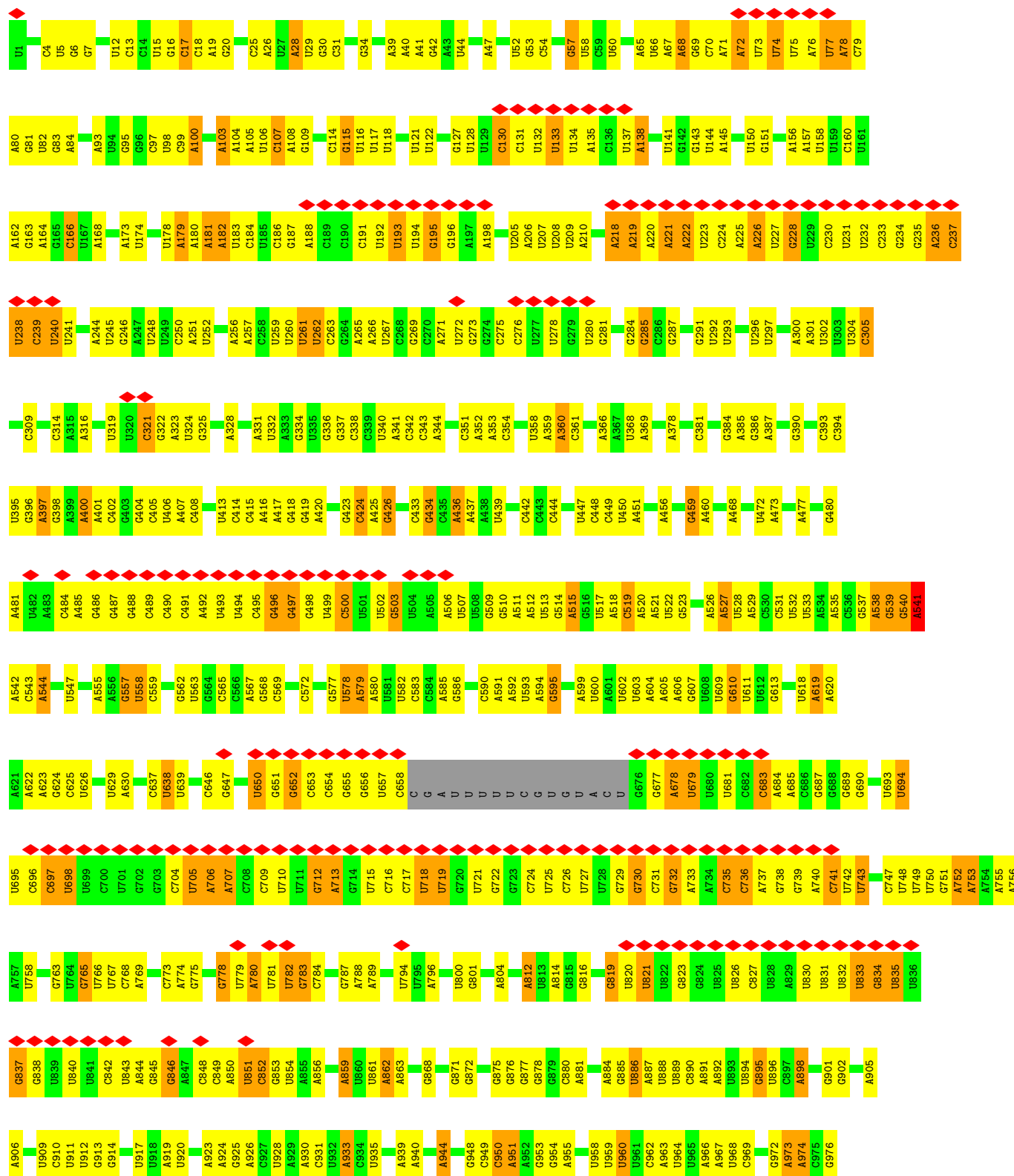


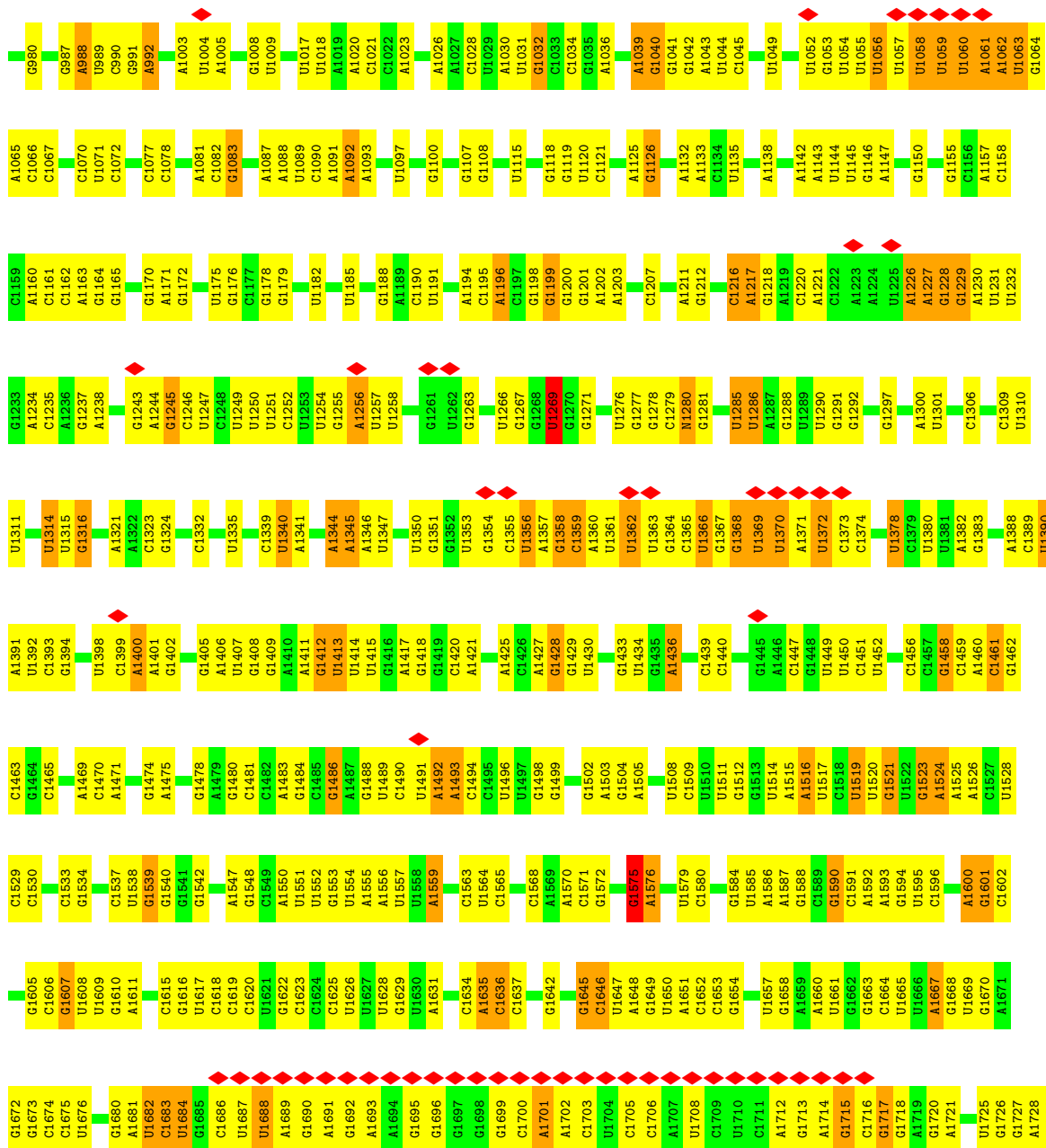
- Molecule 33: 40S ribosomal protein S12



● Molecule 34: 18S rRNA

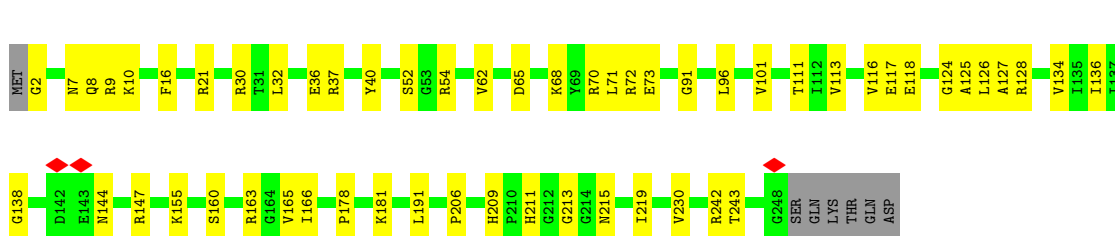
Chain B5: 



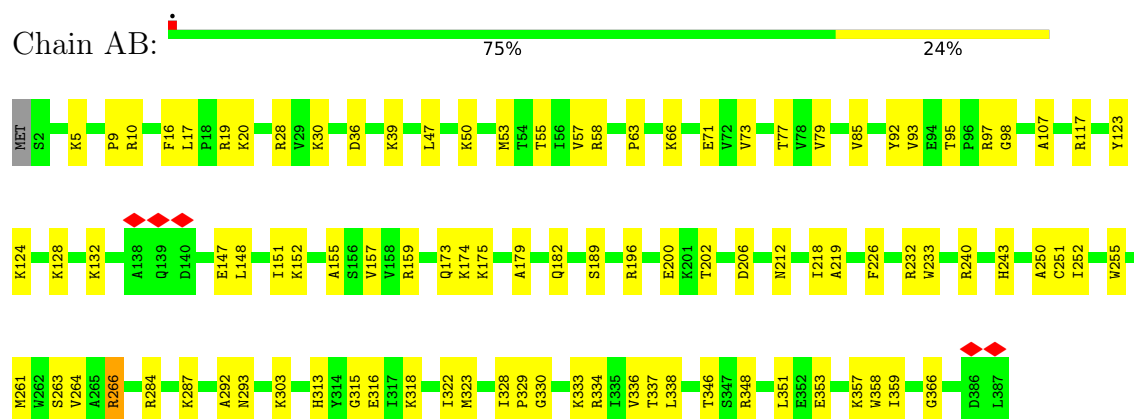


• Molecule 35: 60S ribosomal protein L2-A

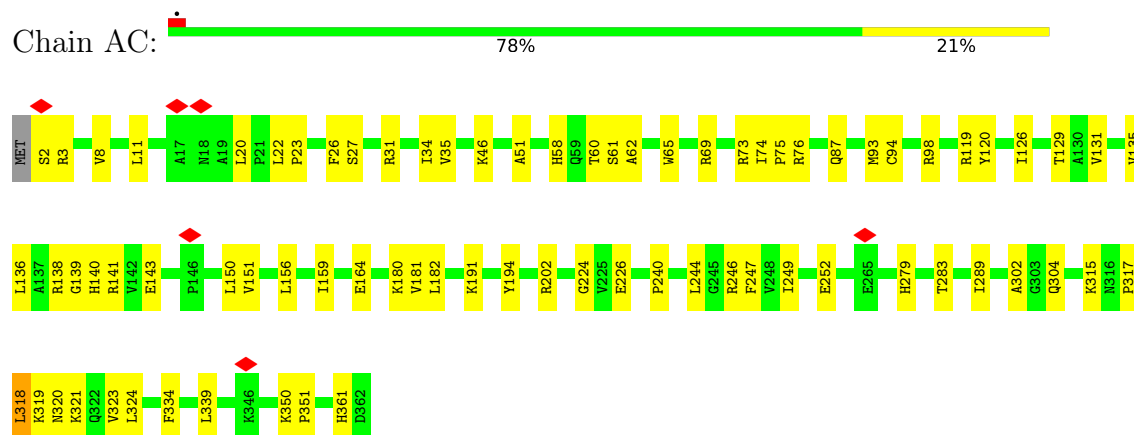
Chain AA:



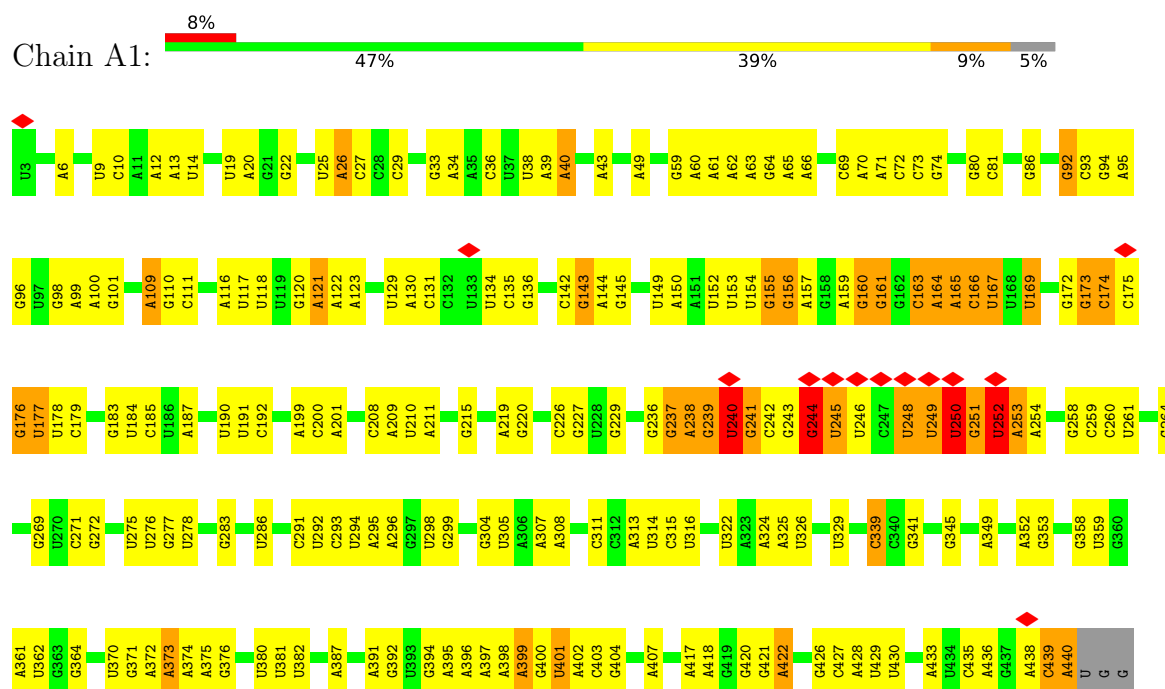
• Molecule 36: 60S ribosomal protein L3



• Molecule 37: RPL4A isoform 1

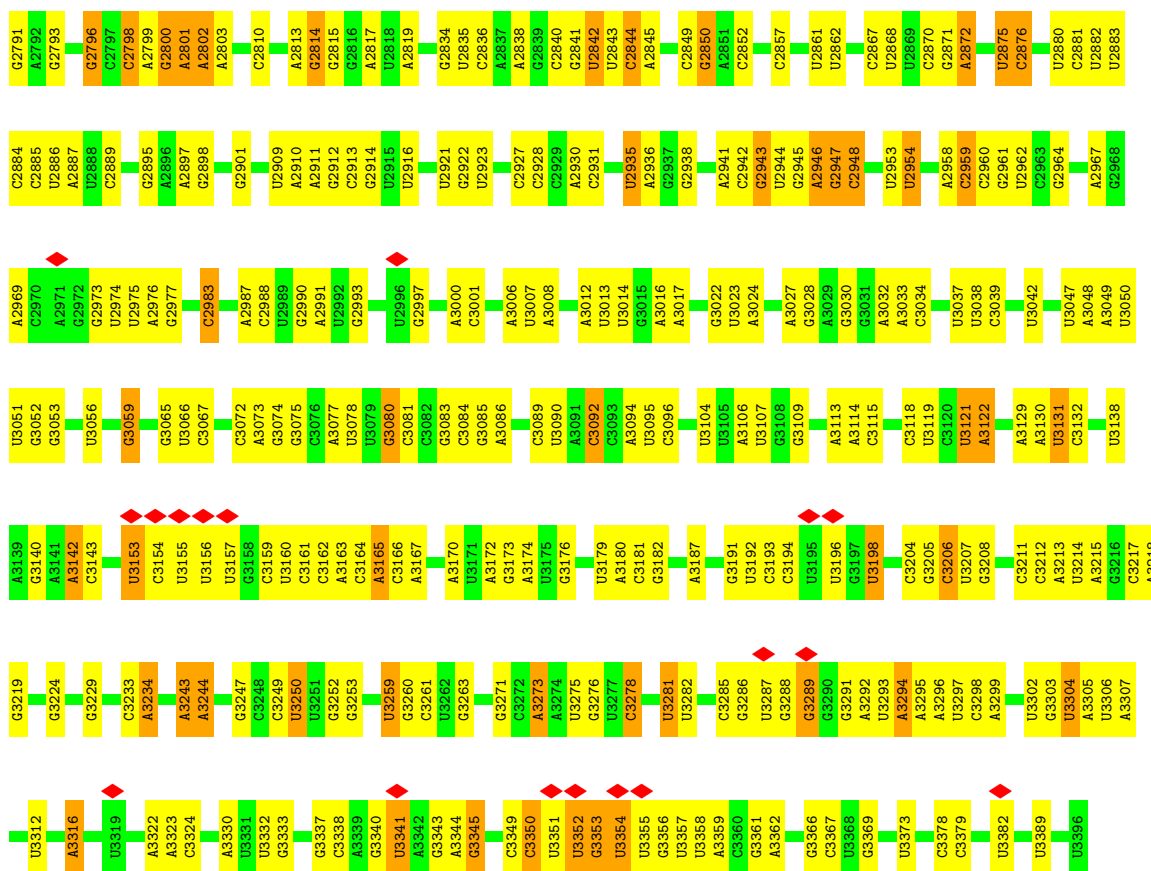


• Molecule 38: 25S rRNA

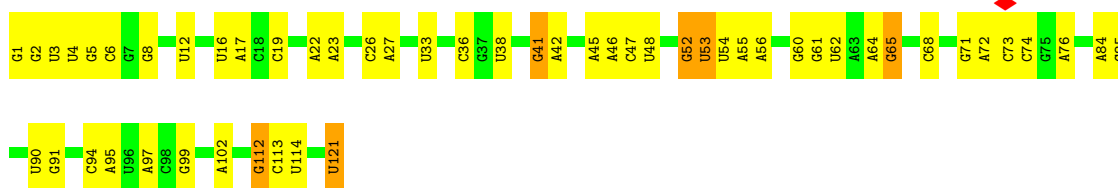




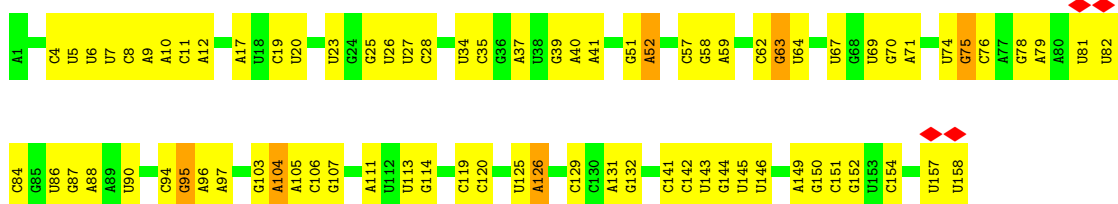




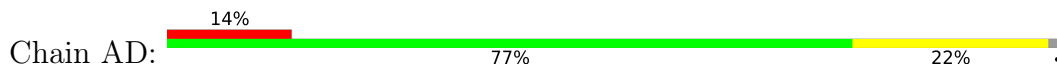
• Molecule 39: 5s rRNA

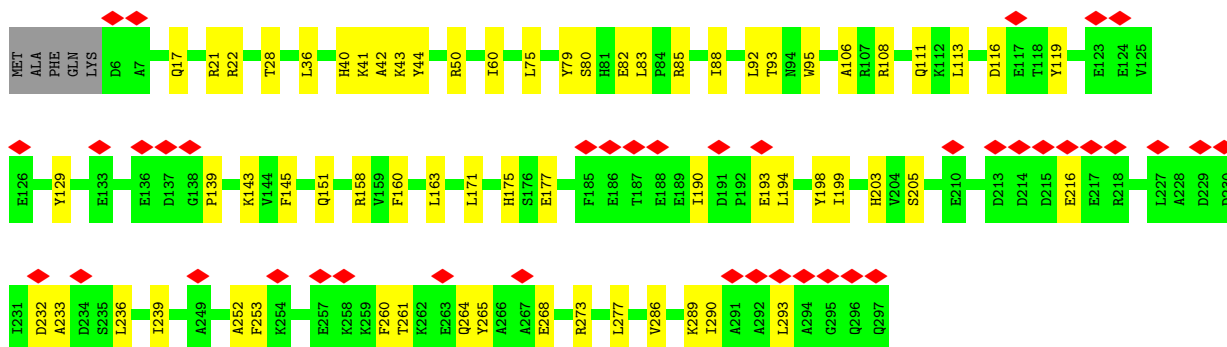


• Molecule 40: 5.8 S rRNA

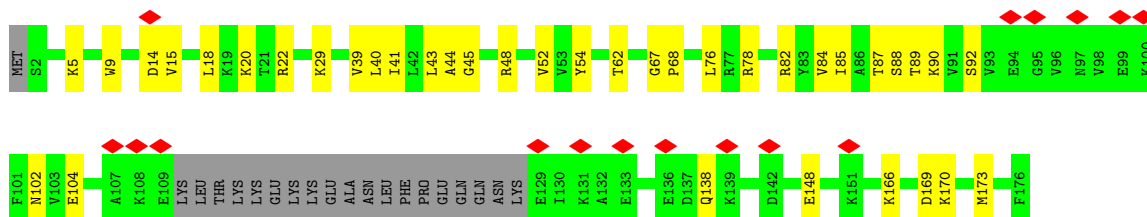


• Molecule 41: RPL5 isoform 1

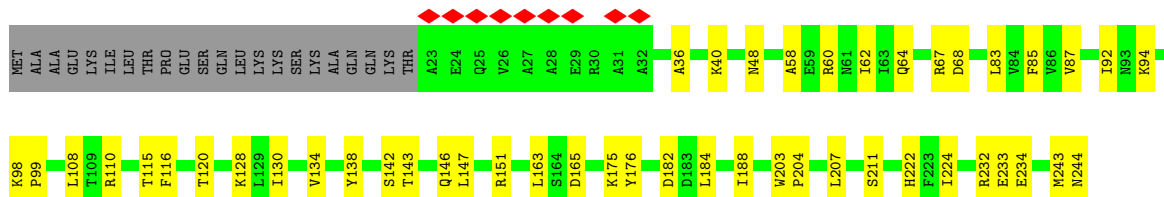




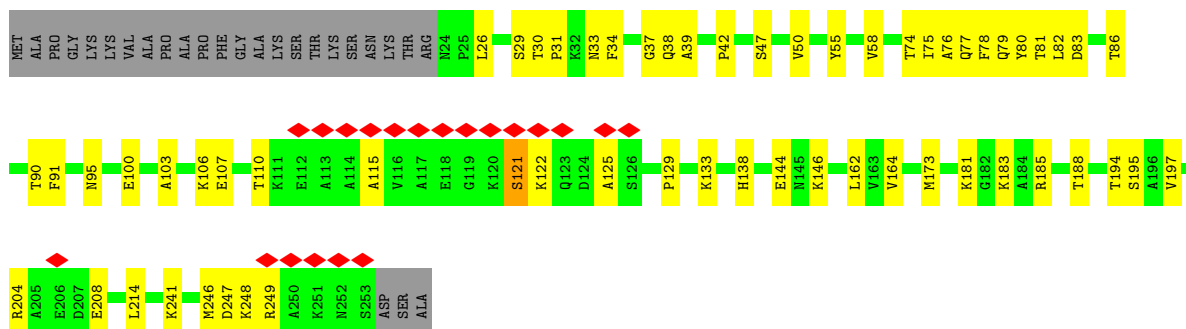
• Molecule 42: 60S ribosomal protein L6-A



• Molecule 43: 60S ribosomal protein L7-A

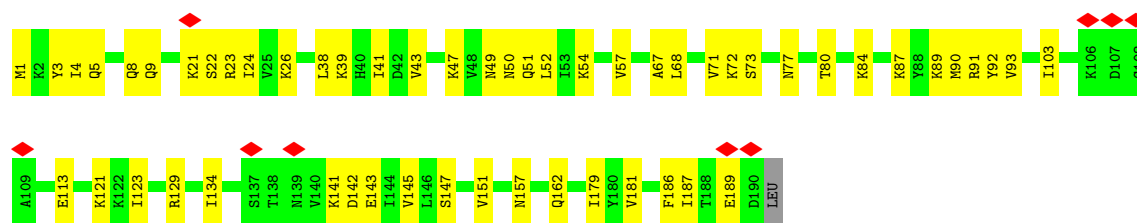


• Molecule 44: 60S ribosomal protein L8-A

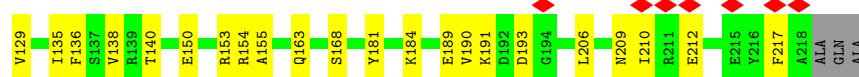
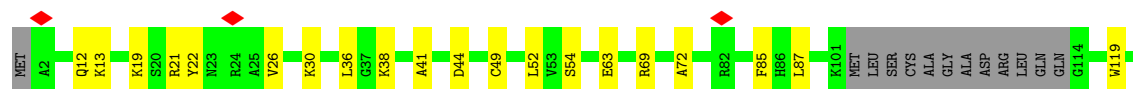
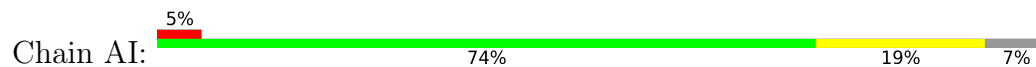


• Molecule 45: 60S ribosomal protein L9-A

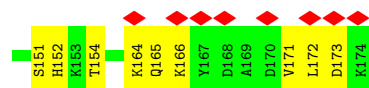
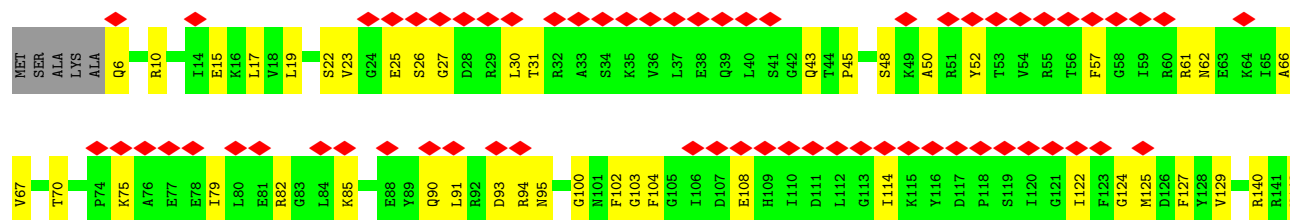
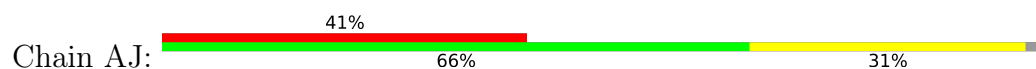




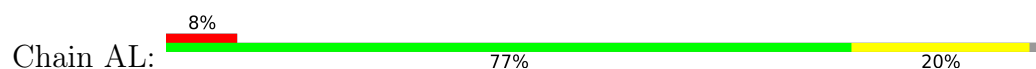
• Molecule 46: RPL10 isoform 1



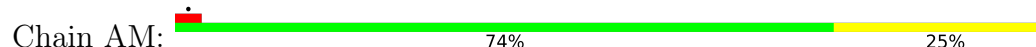
• Molecule 47: RPL11A isoform 1



• Molecule 48: 60S ribosomal protein L13-A



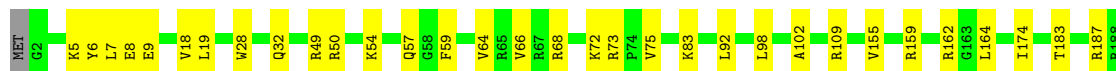
• Molecule 49: 60S ribosomal protein L14-A





- Molecule 50: 60S ribosomal protein L15-A

Chain AN: 82% 17%



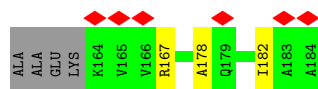
- Molecule 51: 60S ribosomal protein L16-A

Chain AO: 77% 22%



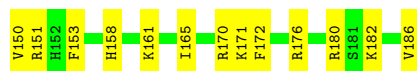
- Molecule 52: 60S ribosomal protein L17-A

Chain AP: 78% 17% 5%



- Molecule 53: 60S ribosomal protein L18-A

Chain AQ: 75% 24%



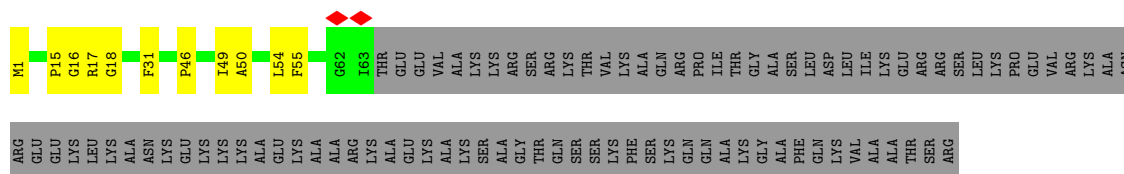
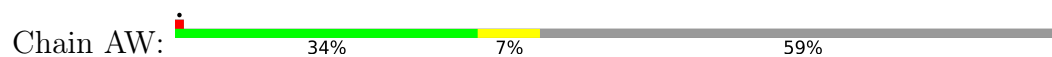
- Molecule 54: 60S ribosomal protein L19-A

Chain AR: 18% 79% 21%

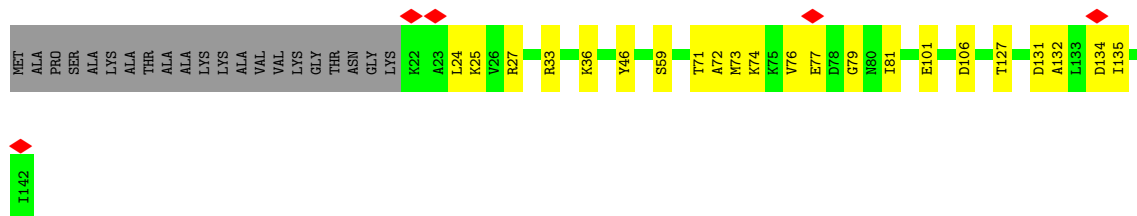




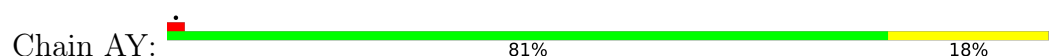
- Molecule 59: RPL24A isoform 1



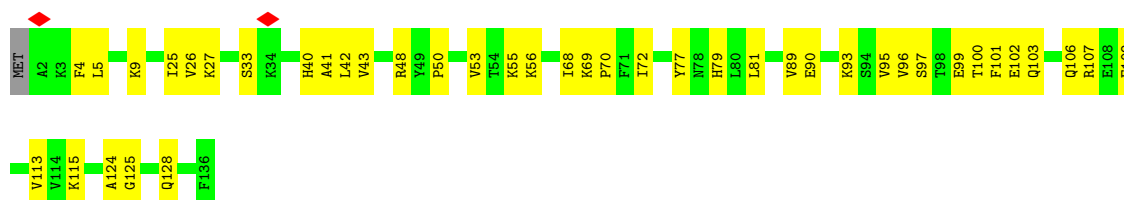
- Molecule 60: 60S ribosomal protein L25



- Molecule 61: 60S ribosomal protein L26-A



- Molecule 62: 60S ribosomal protein L27-A

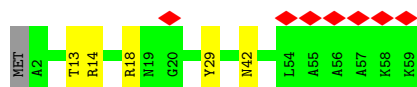


- Molecule 63: 60S ribosomal protein L28





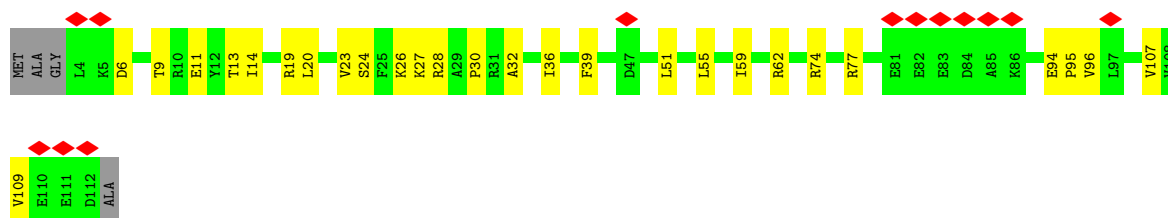
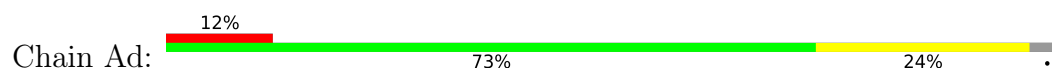
- Molecule 64: RPL29 isoform 1



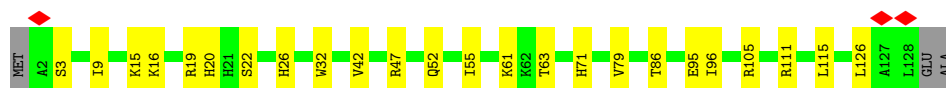
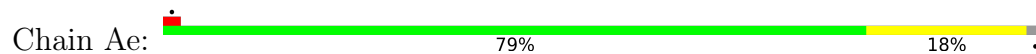
- Molecule 65: 60S ribosomal protein L30



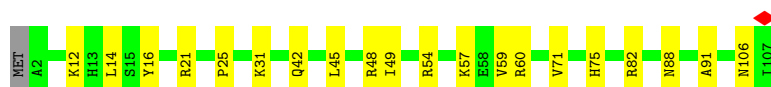
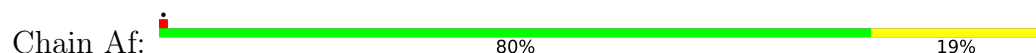
- Molecule 66: 60S ribosomal protein L31-A



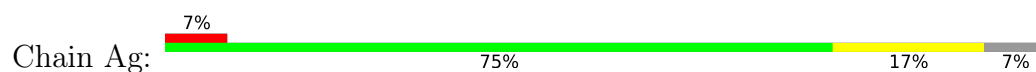
- Molecule 67: RPL32 isoform 1



- Molecule 68: 60S ribosomal protein L33-A

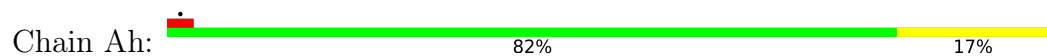


- Molecule 69: 60S ribosomal protein L34-A

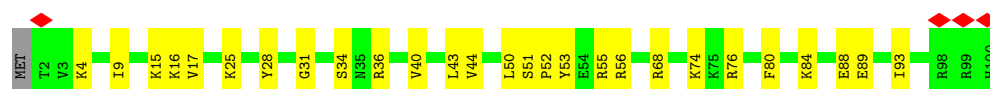




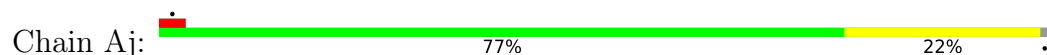
- Molecule 70: 60S ribosomal protein L35-A



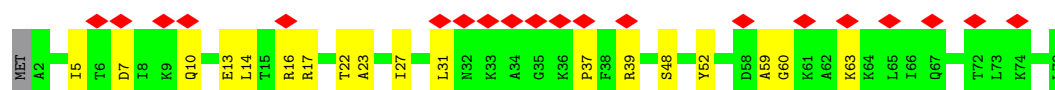
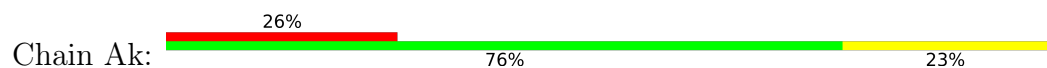
- Molecule 71: 60S ribosomal protein L36-A



- Molecule 72: 60S ribosomal protein L37-A



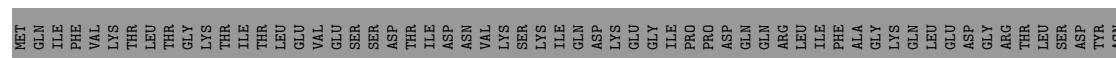
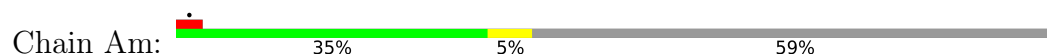
- Molecule 73: RPL38 isoform 1

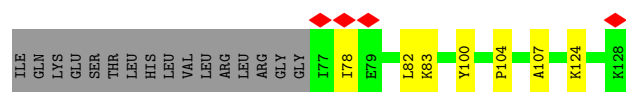


- Molecule 74: 60S ribosomal protein L39

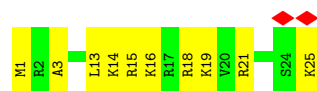


- Molecule 75: Ubiquitin-60S ribosomal protein L40

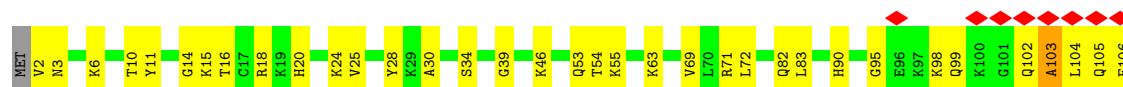




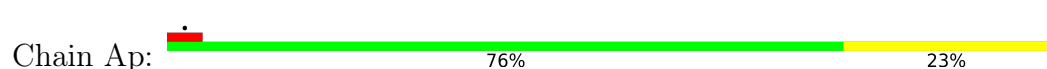
- Molecule 76: 60S ribosomal protein L41-A



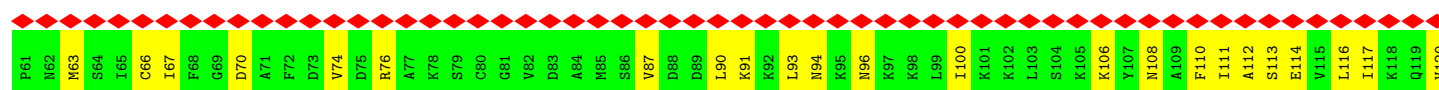
- Molecule 77: 60S ribosomal protein L42-A



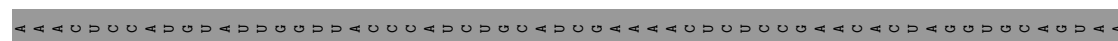
- Molecule 78: 60S ribosomal protein L43-A



- Molecule 79: RPL1A isoform 1



- Molecule 80: TSV IRES





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	300118	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	10.371	Depositor
Minimum map value	-0.362	Depositor
Average map value	0.144	Depositor
Map value standard deviation	0.326	Depositor
Recommended contour level	1.1	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 4AC, 1MA, A2M, 5MC, OMU, OMC, HIC, X SX, MA6, MG, UR3, 7MG, OMG

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	BA	0.14	0/1653	0.41	2/2261 (0.1%)
2	BB	0.17	0/1735	0.42	0/2335
3	BC	0.16	0/1665	0.34	0/2263
4	BE	0.16	0/2109	0.37	0/2839
5	BG	0.12	0/1844	0.31	0/2464
6	BH	0.18	0/1506	0.44	2/2028 (0.1%)
7	BI	0.18	0/1514	0.43	0/2021
8	BJ	0.83	3/1519 (0.2%)	0.48	2/2035 (0.1%)
9	BL	0.15	0/1272	0.34	0/1712
10	BN	0.15	0/1215	0.37	0/1638
11	BO	0.19	0/952	0.43	0/1279
12	BV	0.80	6/693 (0.9%)	0.59	1/935 (0.1%)
13	BW	0.17	0/1038	0.39	0/1395
14	BX	0.17	0/1139	0.41	0/1518
15	BY	0.16	0/1087	0.43	0/1449
16	Ba	0.18	0/782	0.49	0/1047
17	Bb	0.15	0/620	0.44	0/838
18	Be	0.15	0/483	0.37	0/643
19	BD	0.15	0/1759	0.32	0/2368
20	BF	0.18	0/1629	0.40	0/2202
21	BK	0.18	0/837	0.44	0/1131
22	BP	0.94	5/1012 (0.5%)	1.14	4/1356 (0.3%)
23	BQ	0.17	0/1125	0.36	0/1510
24	BR	0.14	0/984	0.36	0/1318
25	BS	0.19	0/1211	0.45	0/1628
26	BT	0.19	0/1113	0.45	1/1494 (0.1%)
27	BU	0.16	0/865	0.39	0/1169
28	BZ	0.14	0/566	0.33	0/761
29	Bc	0.13	0/499	0.34	0/670
30	Bd	0.17	0/453	0.39	0/602
31	Bg	0.13	0/2454	0.35	0/3340
32	Bf	0.10	0/462	0.41	0/617

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.11	0/921	0.37	0/1245
34	B5	0.20	1/41880 (0.0%)	0.34	4/65248 (0.0%)
35	AA	0.17	0/1912	0.39	0/2569
36	AB	0.16	0/3138	0.37	0/4217
37	AC	0.16	0/2800	0.37	0/3790
38	A1	0.21	0/75445	0.37	10/117621 (0.0%)
39	A3	0.16	0/2883	0.30	0/4491
40	A4	0.19	0/3746	0.33	0/5832
41	AD	0.14	0/2390	0.35	0/3225
42	AE	0.14	0/1260	0.35	0/1694
43	AF	0.16	0/1821	0.37	0/2451
44	AG	0.16	0/1830	0.39	0/2469
45	AH	0.19	0/1531	0.39	0/2062
46	AI	0.16	0/1708	0.34	0/2290
47	AJ	0.13	0/1374	0.37	0/1842
48	AL	0.15	0/1568	0.38	0/2106
49	AM	0.13	0/1068	0.29	0/1438
50	AN	0.16	0/1757	0.36	0/2354
51	AO	0.16	0/1585	0.36	0/2128
52	AP	0.16	0/1410	0.36	0/1893
53	AQ	0.14	0/1465	0.35	0/1965
54	AR	0.13	0/1538	0.33	0/2050
55	AS	0.19	0/1481	0.42	0/1990
56	AT	0.15	0/1300	0.34	0/1743
57	AU	0.17	0/812	0.43	0/1099
58	AV	0.23	0/1018	0.52	0/1369
59	AW	0.15	0/533	0.32	0/707
60	AX	0.15	0/983	0.35	0/1325
61	AY	0.14	0/1004	0.36	0/1341
62	AZ	0.14	0/1118	0.33	0/1497
63	Aa	0.17	0/1204	0.41	0/1612
64	Ab	0.15	0/473	0.43	0/629
65	Ac	0.18	0/751	0.39	0/1008
66	Ad	0.15	0/904	0.31	0/1213
67	Ae	0.15	0/1041	0.37	0/1394
68	Af	0.19	0/868	0.37	0/1168
69	Ag	0.18	0/890	0.41	0/1189
70	Ah	0.14	0/978	0.32	0/1301
71	Ai	0.16	0/778	0.41	0/1034
72	Aj	0.18	0/696	0.38	0/923
73	Ak	0.22	0/618	0.37	0/826
74	Al	0.14	0/443	0.35	0/588
75	Am	0.15	0/423	0.34	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.13	0/234	0.30	0/300
77	Ao	0.34	0/860	0.55	2/1136 (0.2%)
78	Ap	0.15	0/701	0.39	0/934
79	E	0.17	0/1745	0.41	0/2342
80	EC	0.27	2/1349 (0.1%)	0.31	0/2096
All	All	0.22	17/216030 (0.0%)	0.38	28/317172 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	BH	0	1
11	BO	0	1
14	BX	0	1
16	Ba	0	1
20	BF	0	1
36	AB	0	1
37	AC	0	1
41	AD	0	1
43	AF	0	1
44	AG	0	3
54	AR	0	1
62	AZ	0	1
All	All	0	14

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	BJ	169	PRO	N-CD	-28.31	1.08	1.47
22	BP	73	PRO	CB-CG	21.20	2.55	1.49
22	BP	73	PRO	CG-CD	-16.38	0.95	1.50
8	BJ	169	PRO	CG-CD	-12.93	1.06	1.50
12	BV	10	GLU	CA-C	-9.59	1.41	1.52
12	BV	13	VAL	N-CA	-7.75	1.40	1.46
22	BP	73	PRO	N-CA	-7.04	1.38	1.47
12	BV	11	LEU	N-CA	-6.78	1.38	1.46
12	BV	10	GLU	N-CA	-6.66	1.38	1.46
22	BP	73	PRO	N-CD	6.48	1.56	1.47
12	BV	12	TYR	C-O	-6.25	1.16	1.23
80	EC	6843	U	C1'-N1	6.17	1.56	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	EC	6842	U	C1'-N1	6.03	1.56	1.47
8	BJ	169	PRO	N-CA	-5.44	1.40	1.47
12	BV	9	VAL	C-N	-5.38	1.26	1.33
22	BP	73	PRO	CA-CB	-5.11	1.46	1.53
34	B5	1269	OMU	O3'-P	5.03	1.61	1.56

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BP	73	PRO	CB-CG-CD	-33.14	0.05	106.10
22	BP	73	PRO	CA-N-CD	-14.00	92.40	112.00
34	B5	1575	7MG	OP1-P-O3'	-13.20	68.40	108.00
34	B5	1575	7MG	O3'-P-O5'	12.23	122.35	104.00
22	BP	73	PRO	N-CA-CB	-10.32	94.37	103.35
12	BV	10	GLU	N-CA-C	-9.35	91.65	108.48
8	BJ	169	PRO	N-CD-CG	8.89	116.54	103.20
22	BP	73	PRO	CA-CB-CG	-8.85	87.69	104.50
8	BJ	169	PRO	CA-CB-CG	-8.62	88.13	104.50
34	B5	1575	7MG	P-O3'-C3'	-6.92	109.82	120.20
38	A1	250	U	C2'-C3'-O3'	6.79	119.69	109.50
38	A1	240	U	C2'-C3'-O3'	6.68	119.52	109.50
77	Ao	103	ALA	CA-C-N	-6.10	114.66	122.77
77	Ao	103	ALA	C-N-CA	-6.10	114.66	122.77
38	A1	240	U	C4'-C3'-O3'	5.90	118.25	109.40
38	A1	244	G	C4'-C3'-O3'	5.73	121.60	113.00
38	A1	161	G	C3'-C2'-O2'	5.60	119.10	110.70
38	A1	2266	U	C4'-C3'-O3'	-5.56	104.66	113.00
26	BT	130	ARG	CA-CB-CG	5.48	125.06	114.10
38	A1	252	U	C2'-C3'-O3'	-5.45	105.52	113.70
1	BA	4	PRO	CA-C-N	5.41	131.43	121.70
1	BA	4	PRO	C-N-CA	5.41	131.43	121.70
6	BH	13	PRO	CA-C-N	5.34	131.31	121.70
6	BH	13	PRO	C-N-CA	5.34	131.31	121.70
38	A1	250	U	C3'-C2'-O2'	5.31	122.57	114.60
38	A1	2504	U	C2'-C3'-O3'	-5.31	105.74	113.70
34	B5	1575	7MG	OP2-P-O3'	5.23	123.69	108.00
38	A1	2268	U	C1'-C2'-O2'	-5.05	100.83	108.40

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	AB	266	ARG	Sidechain
37	AC	318	LEU	Peptide
41	AD	43	LYS	Peptide
43	AF	232	ARG	Peptide
44	AG	121	SER	Peptide
44	AG	30	THR	Peptide
44	AG	76	ALA	Peptide
54	AR	131	ALA	Peptide
62	AZ	124	ALA	Peptide
20	BF	43	PHE	Peptide
6	BH	64	VAL	Peptide
11	BO	122	PRO	Peptide
14	BX	88	PRO	Peptide
16	Ba	7	SER	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	49	0
2	BB	1709	0	1784	63	0
3	BC	1635	0	1723	40	0
4	BE	2068	0	2153	53	0
5	BG	1820	0	1918	57	0
6	BH	1481	0	1572	43	0
7	BI	1489	0	1525	59	0
8	BJ	1494	0	1573	44	0
9	BL	1244	0	1314	24	0
10	BN	1192	0	1255	31	0
11	BO	941	0	979	46	0
12	BV	684	0	672	24	0
13	BW	1021	0	1060	31	0
14	BX	1121	0	1196	32	0
15	BY	1073	0	1132	41	0
16	Ba	769	0	818	33	0
17	Bb	610	0	633	10	0
18	Be	475	0	525	17	0
19	BD	1734	0	1817	54	0
20	BF	1609	0	1675	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	BK	817	0	804	40	0
22	BP	991	0	1035	34	0
23	BQ	1105	0	1166	46	0
24	BR	975	0	1039	31	0
25	BS	1192	0	1222	39	0
26	BT	1095	0	1114	38	0
27	BU	855	0	917	36	0
28	BZ	558	0	598	18	0
29	Bc	497	0	535	15	0
30	Bd	443	0	436	19	0
31	Bg	2401	0	2356	72	0
32	Bf	454	0	465	11	0
33	BM	913	0	955	18	0
34	B5	38004	0	19140	742	0
35	AA	1878	0	1946	45	0
36	AB	3080	0	3158	68	0
37	AC	2748	0	2859	59	0
38	A1	68319	0	34394	1188	0
39	A3	2579	0	1304	44	0
40	A4	3353	0	1695	59	0
41	AD	2341	0	2290	53	0
42	AE	1239	0	1326	34	0
43	AF	1784	0	1862	36	0
44	AG	1798	0	1894	50	0
45	AH	1510	0	1576	44	0
46	AI	1672	0	1711	32	0
47	AJ	1353	0	1383	46	0
48	AL	1543	0	1608	31	0
49	AM	1053	0	1149	29	0
50	AN	1720	0	1779	35	0
51	AO	1555	0	1659	30	0
52	AP	1388	0	1423	34	0
53	AQ	1441	0	1543	35	0
54	AR	1521	0	1617	42	0
55	AS	1445	0	1487	40	0
56	AT	1276	0	1323	35	0
57	AU	796	0	812	12	0
58	AV	1003	0	1048	24	0
59	AW	521	0	551	11	0
60	AX	968	0	1036	15	0
61	AY	993	0	1081	21	0
62	AZ	1092	0	1155	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	Aa	1173	0	1215	40	0
64	Ab	462	0	491	13	0
65	Ac	743	0	797	17	0
66	Ad	890	0	938	20	0
67	Ae	1020	0	1090	20	0
68	Af	850	0	880	18	0
69	Ag	880	0	945	22	0
70	Ah	969	0	1078	19	0
71	Ai	771	0	849	38	0
72	Aj	681	0	687	16	0
73	Ak	612	0	682	15	0
74	Al	436	0	475	18	0
75	Am	417	0	459	6	0
76	An	233	0	284	8	0
77	Ao	847	0	914	35	0
78	Ap	694	0	738	14	0
79	E	1718	0	1811	77	0
80	EC	1209	0	615	34	0
81	A1	180	0	0	0	0
81	A3	2	0	0	0	0
81	A4	4	0	0	0	0
81	AB	1	0	0	0	0
81	AC	1	0	0	0	0
81	AN	2	0	0	0	0
81	AO	1	0	0	0	0
81	AP	1	0	0	0	0
81	Ae	2	0	0	0	0
81	Af	1	0	0	0	0
81	Ah	1	0	0	0	0
81	Aj	1	0	0	0	0
81	B5	73	0	0	0	0
81	BN	1	0	0	0	0
81	Ba	1	0	0	0	0
82	Ao	1	0	0	0	0
All	All	202928	0	150346	3857	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (3857) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:E:60:ARG:O	79:E:63:MET:CE	1.66	1.38
52:AP:128:ARG:NH2	52:AP:136:ILE:CD1	1.86	1.37
34:B5:1575:7MG:H2'	34:B5:1576:A:C8	1.61	1.33
79:E:60:ARG:HB2	79:E:63:MET:SD	1.67	1.33
52:AP:128:ARG:HH21	52:AP:136:ILE:CD1	1.44	1.29
79:E:60:ARG:O	79:E:63:MET:HE1	1.24	1.27
52:AP:128:ARG:NH2	52:AP:136:ILE:HD13	0.91	1.24
4:BE:115:THR:OG1	4:BE:118:GLU:OE1	1.56	1.22
38:A1:2457:G:N2	38:A1:2486:A:C2	2.08	1.21
45:AH:113:GLU:OE1	45:AH:123:ILE:HG21	1.44	1.15
42:AE:170:LYS:HD2	42:AE:173:MET:CE	1.77	1.14
79:E:60:ARG:CB	79:E:63:MET:SD	2.36	1.12
38:A1:1222:G:H21	38:A1:1286:A:N6	1.49	1.10
58:AV:108:GLU:OE1	58:AV:128:ARG:HG3	1.51	1.10
28:BZ:83:LEU:HD22	28:BZ:88:ILE:HD11	1.14	1.07
11:BO:107:ARG:HH12	16:Ba:52:ASP:CG	1.63	1.03
52:AP:128:ARG:HE	52:AP:136:ILE:HG21	1.25	1.00
38:A1:169:U:H5	38:A1:253:A:N1	1.60	1.00
38:A1:2264:U:H2'	38:A1:2265:C:H6	1.25	0.99
79:E:60:ARG:C	79:E:63:MET:HE1	1.87	0.99
51:AO:163[A]:SER:O	51:AO:166[A]:GLU:HG3	1.63	0.98
34:B5:1585:U:H3	34:B5:1611:A:H2	1.05	0.98
38:A1:2457:G:N2	38:A1:2486:A:H2	1.49	0.95
11:BO:107:ARG:NH1	16:Ba:52:ASP:OD1	1.99	0.95
38:A1:169:U:C5	38:A1:253:A:N1	2.35	0.95
26:BT:127:ASN:HA	26:BT:130:ARG:HG2	1.46	0.94
38:A1:1222:G:N2	38:A1:1286:A:H62	1.66	0.94
54:AR:43:LYS:NZ	54:AR:44:LEU:HD21	1.83	0.93
34:B5:1575:7MG:H2'	34:B5:1576:A:H8	1.28	0.93
34:B5:69:G:H1	34:B5:82:U:H3	1.10	0.92
38:A1:1222:G:H21	38:A1:1286:A:H62	0.99	0.92
38:A1:241:G:H2'	38:A1:242:C:H5'	1.49	0.92
44:AG:246:MET:HE2	44:AG:249:ARG:NH2	1.83	0.92
11:BO:99:GLN:NE2	16:Ba:45:VAL:O	2.03	0.92
52:AP:128:ARG:HH22	52:AP:136:ILE:HD13	1.22	0.91
38:A1:172:G:H1	38:A1:245:U:H3	1.15	0.91
45:AH:113:GLU:OE1	45:AH:123:ILE:CG2	2.17	0.91
45:AH:89:LYS:HB3	45:AH:143:GLU:OE2	1.70	0.91
47:AJ:25:GLU:HG3	47:AJ:26:SER:H	1.36	0.90
54:AR:31:GLU:OE2	54:AR:43:LYS:NZ	2.04	0.90
3:BC:52:THR:HB	3:BC:54:GLU:OE1	1.72	0.90
38:A1:236:G:H2'	38:A1:237:G:O4'	1.71	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Ah:102:GLU:OE1	70:Ah:102:GLU:N	2.05	0.89
58:AV:81:GLN:O	58:AV:98:ASN:ND2	2.05	0.89
12:BV:10:GLU:HG3	12:BV:12:TYR:O	1.73	0.89
23:BQ:100:GLN:OE1	23:BQ:100:GLN:N	2.05	0.88
38:A1:174:C:H2'	38:A1:175:C:C6	2.08	0.88
22:BP:72:LYS:HA	22:BP:73:PRO:HG2	1.56	0.88
55:AS:25:PHE:HD1	56:AT:150:THR:HG1	1.21	0.87
38:A1:169:U:H5	38:A1:253:A:C2	1.91	0.87
38:A1:175:C:H2'	38:A1:176:G:H5'	1.56	0.87
51:AO:22[A]:VAL:HG22	51:AO:122[A]:GLN:OE1	1.74	0.87
24:BR:75:GLU:O	24:BR:79:GLU:OE1	1.93	0.86
38:A1:164:A:H5'	38:A1:164:A:H8	1.40	0.86
71:Ai:51:SER:O	71:Ai:55:ARG:NE	2.07	0.86
36:AB:212:ASN:ND2	36:AB:353:GLU:OE1	2.08	0.86
3:BC:142:GLY:HA2	12:BV:1:MET:HE1	1.55	0.86
79:E:155:ILE:HG23	79:E:167:VAL:HG11	1.57	0.86
54:AR:43:LYS:HZ1	54:AR:44:LEU:HD21	1.36	0.85
34:B5:1356:U:H3	34:B5:1367:G:H1	1.25	0.85
14:BX:114:LYS:HD2	14:BX:117:ILE:HD12	1.59	0.84
15:BY:32:ARG:NH2	15:BY:39:GLU:OE2	2.10	0.84
31:Bg:109:ASP:HB3	31:Bg:111:MET:CE	2.08	0.84
38:A1:2673:A:H5''	47:AJ:95:ASN:HD22	1.42	0.84
77:Ao:99:GLN:O	77:Ao:102:GLN:OE1	1.96	0.83
38:A1:174:C:H2'	38:A1:175:C:H6	1.42	0.83
18:Be:25:GLU:OE2	34:B5:540:G:N2	2.11	0.83
38:A1:163:C:H2'	38:A1:164:A:H5''	1.59	0.83
71:Ai:52:PRO:CA	71:Ai:55:ARG:HH21	1.92	0.83
1:BA:15:GLN:HE21	24:BR:93:LEU:HD23	1.43	0.82
34:B5:868:G:H1	34:B5:960:U:H3	1.23	0.82
79:E:60:ARG:O	79:E:63:MET:HE2	1.74	0.82
38:A1:240:U:H1'	38:A1:241:G:OP1	1.78	0.82
9:BL:21:ASN:HD21	9:BL:32:LYS:H	1.28	0.82
31:Bg:222:LEU:HB3	31:Bg:231:MET:HE3	1.62	0.82
46:AI:30:LYS:HE3	46:AI:63:GLU:HA	1.61	0.81
38:A1:2442:G:C6	38:A1:2506:U:C4	2.68	0.81
6:BH:64:VAL:HG23	6:BH:67:LEU:HD23	1.61	0.81
42:AE:170:LYS:CD	42:AE:173:MET:CE	2.59	0.81
6:BH:5:GLN:HE22	6:BH:22:GLN:HB2	1.46	0.81
38:A1:496:C:O2	38:A1:617:G:N2	2.13	0.81
23:BQ:100:GLN:HE21	31:Bg:56:VAL:HB	1.45	0.81
77:Ao:103:ALA:C	77:Ao:104:LEU:HD12	2.06	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2506:U:H2'	38:A1:2507:C:O4'	1.81	0.80
72:Aj:21:ARG:NH2	72:Aj:41:ALA:O	2.11	0.80
26:BT:130:ARG:HH22	34:B5:1359:C:H4'	1.46	0.80
38:A1:177:U:O2	38:A1:241:G:N2	2.15	0.80
27:BU:44:ASN:HA	27:BU:47:GLN:HE22	1.45	0.80
34:B5:992:A:O2'	34:B5:1785:U:O2	1.99	0.80
34:B5:1339:C:O2'	34:B5:1341:A:N7	2.14	0.80
42:AE:170:LYS:HD2	42:AE:173:MET:HE1	1.63	0.80
26:BT:130:ARG:NH2	34:B5:1359:C:H4'	1.97	0.79
79:E:34:LEU:HD11	79:E:183:ILE:HG22	1.64	0.79
38:A1:241:G:H2'	38:A1:242:C:C5'	2.13	0.79
79:E:60:ARG:O	79:E:63:MET:SD	2.40	0.79
11:BO:107:ARG:NH1	16:Ba:52:ASP:CG	2.40	0.79
38:A1:2767:U:OP1	77:Ao:34:SER:OG	2.00	0.79
38:A1:2264:U:H2'	38:A1:2265:C:C6	2.15	0.79
5:BG:131:LYS:HD2	34:B5:166:C:H4'	1.63	0.79
34:B5:519:C:N4	34:B5:533:U:O2	2.14	0.79
48:AL:174:ARG:HG3	71:Ai:9:ILE:HD12	1.63	0.79
23:BQ:98:ASP:OD1	23:BQ:99:GLU:N	2.16	0.79
34:B5:1672:G:H2'	34:B5:1673:G:C8	2.18	0.79
38:A1:1566:A:H3'	38:A1:1567:U:H5''	1.65	0.79
62:AZ:95:VAL:HG21	62:AZ:113:VAL:HG11	1.65	0.79
31:Bg:109:ASP:CB	31:Bg:111:MET:HE3	2.13	0.78
31:Bg:109:ASP:HB2	31:Bg:111:MET:HE3	1.64	0.78
27:BU:33:GLN:CD	27:BU:33:GLN:H	1.91	0.78
42:AE:170:LYS:CD	42:AE:173:MET:HE2	2.14	0.78
77:Ao:28:TYR:HD1	77:Ao:71:ARG:NH2	1.81	0.78
58:AV:87:ARG:HH22	58:AV:137:VAL:HG21	1.45	0.78
69:Ag:101:VAL:O	69:Ag:104:VAL:HG12	1.82	0.78
15:BY:10:ARG:HH21	34:B5:778:G:H22	1.32	0.78
46:AI:38:LYS:HG3	46:AI:41:ALA:HB2	1.65	0.78
8:BJ:119:ALA:O	8:BJ:124:HIS:ND1	2.17	0.78
30:Bd:14:TYR:HH	34:B5:1553:G:HO2'	1.24	0.78
38:A1:1138:U:H3'	64:Ab:14:ARG:HH21	1.49	0.78
21:BK:19:GLY:HA2	21:BK:68:LEU:HD12	1.66	0.77
34:B5:65:A:H2	34:B5:84:A:H62	1.32	0.77
6:BH:24:PHE:HE1	6:BH:77:LEU:HD21	1.49	0.77
38:A1:118:U:O2	38:A1:121:A:H5''	1.83	0.77
38:A1:175:C:C2'	38:A1:176:G:H5'	2.13	0.77
38:A1:174:C:H42	38:A1:243:G:H1	1.30	0.77
41:AD:216:GLU:OE1	41:AD:216:GLU:N	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AN:183:THR:HG22	50:AN:187:ARG:HB3	1.67	0.77
7:BI:152:ILE:HG13	7:BI:153:GLU:H	1.49	0.77
27:BU:30:LYS:HB2	27:BU:33:GLN:OE1	1.85	0.77
38:A1:2268:U:OP2	38:A1:2268:U:H6	1.67	0.76
38:A1:2960:C:H2'	38:A1:2961:G:C8	2.21	0.76
38:A1:175:C:H42	38:A1:242:C:N4	1.82	0.76
58:AV:108:GLU:OE1	58:AV:128:ARG:CG	2.30	0.76
6:BH:134:GLU:HG2	6:BH:155:ASP:OD2	1.84	0.76
7:BI:20:GLN:NE2	7:BI:22:ARG:O	2.19	0.76
47:AJ:25:GLU:HG3	47:AJ:26:SER:N	2.00	0.76
38:A1:2798:C:H5''	38:A1:2800:G:H5'	1.66	0.76
5:BG:79:LYS:HD3	5:BG:86:PRO:HG2	1.66	0.76
38:A1:1639:C:OP2	69:Ag:74:ARG:NH2	2.18	0.75
80:EC:6851:G:H1	80:EC:6878:G:HO2'	0.76	0.75
34:B5:238:U:C6	34:B5:238:U:H5''	2.22	0.75
42:AE:170:LYS:HD2	42:AE:173:MET:HE2	1.64	0.75
38:A1:2434:U:H5	38:A1:2594:C:OP2	1.69	0.75
45:AH:4:ILE:HG22	45:AH:5:GLN:OE1	1.85	0.75
47:AJ:61:ARG:O	77:Ao:104:LEU:HB2	1.85	0.75
38:A1:1575:A:C8	38:A1:1575:A:H3'	2.22	0.75
40:A4:75:G:OP2	61:AY:74:TYR:OH	2.05	0.75
34:B5:239:C:C4	34:B5:835:U:H5''	2.22	0.75
4:BE:129:VAL:HG22	4:BE:139:VAL:HG12	1.67	0.75
38:A1:1010:G:N2	46:AI:193:ASP:OD2	2.19	0.75
21:BK:17:GLN:O	21:BK:90:THR:OG1	2.04	0.74
47:AJ:62:ASN:HB2	77:Ao:104:LEU:HD13	1.68	0.74
54:AR:40:ALA:O	54:AR:43:LYS:HG3	1.88	0.74
38:A1:243:G:H2'	38:A1:244:G:C1'	2.17	0.74
31:Bg:127:ARG:HA	31:Bg:150:TRP:HB2	1.67	0.74
34:B5:973:A:H4'	38:A1:848:A:C8	2.21	0.74
38:A1:1940:G:H21	38:A1:3362:A:H8	1.32	0.74
38:A1:2457:G:N3	38:A1:2486:A:N1	2.35	0.74
23:BQ:95:LYS:O	31:Bg:59:ARG:NH2	2.21	0.74
34:B5:218:A:N6	34:B5:844:A:O2'	2.20	0.74
38:A1:1138:U:H3'	64:Ab:14:ARG:NH2	2.03	0.74
79:E:177:ASP:OD1	79:E:178:VAL:N	2.20	0.74
4:BE:6:LYS:NZ	34:B5:95:G:OP1	2.21	0.74
7:BI:104:ILE:HG13	7:BI:105:ASP:H	1.51	0.74
6:BH:64:VAL:HG23	6:BH:67:LEU:CD2	2.18	0.74
38:A1:1565:G:H2'	38:A1:1566:A:O4'	1.88	0.74
34:B5:1291:G:N2	34:B5:1324:G:H22	1.85	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:4:SER:OG	7:BI:6:ASP:OD1	2.06	0.73
18:Be:2:ALA:N	34:B5:1754:A:HO2'	1.87	0.73
24:BR:102:VAL:HG13	24:BR:106:THR:HB	1.69	0.73
34:B5:237:C:H4'	34:B5:238:U:OP1	1.88	0.73
34:B5:1474:G:H2'	34:B5:1475:A:C8	2.22	0.73
38:A1:1631:C:OP2	62:AZ:48:ARG:NH2	2.22	0.73
36:AB:240:ARG:NH2	38:A1:1907:C:O2	2.22	0.73
38:A1:1717:U:H2'	38:A1:1718:G:C8	2.24	0.73
28:BZ:83:LEU:CD2	28:BZ:88:ILE:HD11	2.07	0.73
35:AA:36:GLU:HG3	35:AA:91:GLY:HA2	1.71	0.73
34:B5:821:U:O4	34:B5:852:C:N3	2.22	0.73
34:B5:1595:U:H3	34:B5:1600:A:H2	1.34	0.73
38:A1:2508:U:H2'	38:A1:2509:U:C6	2.24	0.73
49:AM:19:ARG:HA	49:AM:69:THR:HG22	1.71	0.73
14:BX:69:ARG:HG3	14:BX:117:ILE:HG12	1.69	0.73
38:A1:179:C:H42	38:A1:237:G:H1	1.37	0.72
38:A1:2508:U:H3'	38:A1:2508:U:OP2	1.88	0.72
38:A1:243:G:H2'	38:A1:244:G:H1'	1.70	0.72
54:AR:134:HIS:HE1	54:AR:136:ARG:HE	1.36	0.72
71:AI:50:LEU:HB2	71:AI:55:ARG:HD2	1.71	0.72
38:A1:2504:U:H3'	38:A1:2505:U:C6	2.25	0.72
6:BH:46:ILE:HG12	6:BH:60:ILE:HG13	1.72	0.72
26:BT:129:GLN:NE2	34:B5:1358:G:O2'	2.23	0.72
38:A1:3050:U:O2'	59:AW:16:GLY:O	2.07	0.72
38:A1:243:G:H3'	38:A1:244:G:C8	2.24	0.72
52:AP:128:ARG:NE	52:AP:136:ILE:HG21	2.04	0.72
61:AY:74:TYR:CD2	61:AY:77:LYS:HG2	2.24	0.72
55:AS:81:TYR:CE1	55:AS:90:MET:HE3	2.25	0.72
22:BP:72:LYS:CA	22:BP:73:PRO:HG2	2.20	0.72
38:A1:2213:A:H2'	38:A1:2214:A:C8	2.24	0.72
77:Ao:104:LEU:HD12	77:Ao:104:LEU:N	2.05	0.72
34:B5:647:G:H21	34:B5:687:G:H1	1.38	0.72
38:A1:952:A:OP1	64:Ab:18:ARG:NH2	2.23	0.72
54:AR:109:TYR:HB3	54:AR:115:ILE:HG12	1.70	0.71
27:BU:70:THR:OG1	27:BU:72:ASN:OD1	2.08	0.71
34:B5:1344:A:H2'	34:B5:1345:A:C8	2.25	0.71
39:A3:2:G:H5'	41:AD:273:ARG:HD3	1.72	0.71
50:AN:18:VAL:HG13	50:AN:19:LEU:HD12	1.70	0.71
71:AI:52:PRO:HA	71:AI:55:ARG:HH21	1.53	0.71
38:A1:2534:G:H1	38:A1:2545:C:H42	1.39	0.71
6:BH:64:VAL:HA	6:BH:67:LEU:CD2	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BY:57:VAL:HB	15:BY:60:PHE:HE2	1.56	0.71
23:BQ:7:VAL:HG12	23:BQ:95:LYS:HE2	1.73	0.71
28:BZ:95:HIS:ND1	28:BZ:96:SER:O	2.23	0.71
37:AC:31:ARG:HG3	37:AC:120:TYR:OH	1.89	0.71
38:A1:838:G:O6	78:Ap:4:ARG:NH2	2.23	0.71
34:B5:1171:A:H2'	34:B5:1172:G:C8	2.26	0.71
36:AB:95:THR:HG22	36:AB:97:ARG:H	1.56	0.71
13:BW:57:ARG:HG2	34:B5:862:A:H4'	1.71	0.71
34:B5:895:G:H1	34:B5:917:U:H3	1.38	0.71
38:A1:2185:G:O2'	38:A1:2314:U:OP2	2.06	0.71
39:A3:64:A:N7	46:AI:209:ASN:ND2	2.38	0.71
3:BC:95:ARG:NH1	3:BC:97:ARG:HE	1.89	0.70
19:BD:101:GLN:HE21	19:BD:122:VAL:HG13	1.55	0.70
31:Bg:178:VAL:HB	31:Bg:192:PHE:HB2	1.72	0.70
38:A1:845:G:H21	38:A1:848:A:H2	1.37	0.70
79:E:49:PHE:HE1	79:E:51:GLY:HA3	1.55	0.70
38:A1:1724:U:H1'	38:A1:1725:C:C6	2.27	0.70
5:BG:225:GLU:HG3	5:BG:226:ILE:HG13	1.73	0.70
7:BI:76:THR:HG23	7:BI:105:ASP:HB2	1.74	0.70
13:BW:9:ASP:OD1	34:B5:1036:A:O2'	2.09	0.70
24:BR:14:LYS:NZ	24:BR:68:GLY:O	2.23	0.70
79:E:177:ASP:OD1	79:E:178:VAL:HG23	1.92	0.70
38:A1:2457:G:H1'	38:A1:2486:A:H61	1.56	0.70
55:AS:22:PRO:O	56:AT:146:ASN:ND2	2.21	0.70
64:Ab:13:THR:OG1	64:Ab:14:ARG:NH1	2.24	0.70
5:BG:160:ARG:NH2	34:B5:68:A:OP1	2.24	0.70
38:A1:159:A:O2'	38:A1:160:G:H5'	1.92	0.70
9:BL:129:ARG:HD3	34:B5:115:G:H5'	1.74	0.70
38:A1:3017:A:N1	38:A1:3037:U:H5	1.90	0.70
52:AP:4:TYR:HE2	52:AP:16:SER:HB2	1.56	0.70
12:BV:10:GLU:CG	12:BV:12:TYR:O	2.40	0.70
38:A1:656:A:H2'	38:A1:657:A:C8	2.27	0.70
49:AM:60:LEU:HD13	55:AS:152:LEU:HD11	1.72	0.70
30:Bd:32:ARG:NH2	34:B5:1596:C:O2	2.25	0.70
35:AA:68:LYS:HD3	35:AA:70:ARG:HE	1.57	0.70
19:BD:40:ARG:HG2	27:BU:110:PRO:HB3	1.74	0.69
31:Bg:109:ASP:CB	31:Bg:111:MET:CE	2.70	0.69
38:A1:662:U:H2'	38:A1:663:OMC:C6	2.27	0.69
38:A1:2204:C:HO2'	38:A1:2205:U:H6	1.38	0.69
54:AR:43:LYS:NZ	54:AR:44:LEU:CD2	2.55	0.69
2:BB:33:LYS:NZ	2:BB:42:ASN:OD1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:64:VAL:HG12	20:BF:65:ARG:H	1.56	0.69
47:AJ:26:SER:HA	47:AJ:30:LEU:HD23	1.74	0.69
62:AZ:5:LEU:HD11	65:Ac:35:ARG:HD2	1.74	0.69
34:B5:1369:U:H1'	34:B5:1372:U:H2'	1.73	0.69
38:A1:541:U:H3	38:A1:550:A:H61	1.39	0.69
2:BB:38:PHE:CD1	2:BB:73:LEU:HD13	2.28	0.69
45:AH:90:MET:HE2	45:AH:179:ILE:HG22	1.73	0.69
23:BQ:13:LYS:HG3	23:BQ:14:LYS:H	1.58	0.69
31:Bg:262:VAL:HG13	31:Bg:271:VAL:HB	1.73	0.69
34:B5:1687:U:O2	34:B5:1715:G:N2	2.26	0.69
38:A1:238:A:H3'	38:A1:239:G:C8	2.27	0.69
38:A1:1863:G:N1	38:A1:1866:C:OP2	2.22	0.69
7:BI:110:ARG:NH2	7:BI:160:PHE:O	2.20	0.69
38:A1:3278:C:OP1	68:Af:54:ARG:NH2	2.23	0.69
46:AI:150:GLU:OE2	46:AI:153:ARG:NH2	2.25	0.69
8:BJ:78:ARG:NH2	34:B5:763:G:OP1	2.25	0.69
14:BX:130:VAL:HG13	14:BX:140:LYS:HD2	1.75	0.69
25:BS:110:ARG:NH1	25:BS:114:GLU:OE2	2.26	0.69
36:AB:97:ARG:NH2	38:A1:3244:A:OP1	2.26	0.69
38:A1:1019:G:N2	38:A1:1034:U:OP1	2.25	0.69
38:A1:1222:G:H1	38:A1:1285:G:HO2'	1.39	0.69
38:A1:2356:A:H61	38:A1:2983:C:H5	1.39	0.69
38:A1:2786:G:N2	63:Aa:58:MET:SD	2.63	0.69
80:EC:6833:G:N2	80:EC:6833:G:OP2	2.26	0.69
34:B5:871:G:H2'	34:B5:872:G:C8	2.28	0.69
38:A1:2506:U:O2	38:A1:2507:C:H1'	1.93	0.69
44:AG:246:MET:HE2	44:AG:249:ARG:HH21	1.56	0.69
13:BW:15:ASN:ND2	13:BW:72:CYS:O	2.24	0.68
15:BY:35:VAL:HG23	15:BY:36:SER:H	1.56	0.68
26:BT:45:MET:HE3	26:BT:46:PRO:HD2	1.73	0.68
5:BG:136:LYS:NZ	5:BG:174:LYS:O	2.26	0.68
6:BH:67:LEU:HD11	6:BH:94:ALA:HB2	1.73	0.68
25:BS:71:GLN:HG3	25:BS:79:TYR:OH	1.94	0.68
38:A1:174:C:N4	38:A1:243:G:H1	1.92	0.68
38:A1:2219:A:H2'	38:A1:2220:A2M:H8	1.73	0.68
79:E:55:LEU:HB2	79:E:153:SER:HB2	1.75	0.68
24:BR:49:LYS:NZ	34:B5:1390:U:OP2	2.27	0.68
38:A1:252:U:H4'	38:A1:252:U:OP1	1.93	0.68
19:BD:222:VAL:HG12	31:Bg:192:PHE:HA	1.76	0.68
34:B5:514:G:H1	34:B5:543:C:H5	1.39	0.68
14:BX:30:LYS:HE2	14:BX:34:LEU:HD11	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BU:106:ILE:HG13	27:BU:107:THR:HG22	1.75	0.68
38:A1:967:A:OP1	63:Aa:47:LYS:NZ	2.26	0.68
38:A1:1661:G:H2'	38:A1:1662:G:C8	2.29	0.68
38:A1:2550:U:H1'	44:AG:38:GLN:CD	2.19	0.68
51:AO:61[A]:ALA:HA	51:AO:70[A]:PRO:HD2	1.73	0.68
52:AP:4:TYR:HE1	52:AP:18:ARG:HD2	1.58	0.68
34:B5:1474:G:H2'	34:B5:1475:A:H8	1.56	0.68
38:A1:1694:U:H5	38:A1:1752:A:N1	1.92	0.68
38:A1:1696:A:H2'	38:A1:1697:A:C8	2.28	0.68
80:EC:6832:G:H3'	80:EC:6833:G:H21	1.58	0.68
31:Bg:120:SER:HA	31:Bg:136:ILE:HD11	1.74	0.68
34:B5:821:U:N3	34:B5:852:C:O2	2.26	0.68
38:A1:567:G:H2'	38:A1:568:G:C8	2.28	0.68
50:AN:155:VAL:O	50:AN:162:ARG:NH2	2.25	0.68
54:AR:166:ASN:HA	54:AR:170:ARG:HD3	1.76	0.68
79:E:60:ARG:CA	79:E:63:MET:HE1	2.24	0.68
19:BD:175:VAL:HG12	19:BD:177:MET:HE3	1.75	0.68
38:A1:2464:U:H2'	38:A1:2465:G:C8	2.29	0.68
44:AG:75:ILE:HD11	50:AN:18:VAL:HG23	1.75	0.68
8:BJ:17:ARG:O	8:BJ:23:ARG:NH2	2.27	0.68
10:BN:55:ARG:NH1	34:B5:958:U:O2'	2.27	0.67
38:A1:664:U:H2'	38:A1:665:A:C8	2.29	0.67
38:A1:1645:U:H3	38:A1:1810:A:H61	1.40	0.67
16:Ba:84:VAL:O	34:B5:1797:A:N6	2.27	0.67
27:BU:80:GLU:HG2	30:Bd:54:LYS:NZ	2.08	0.67
39:A3:42:A:O2'	47:AJ:140:ARG:NE	2.27	0.67
79:E:6:SER:HA	79:E:9:VAL:HG12	1.76	0.67
19:BD:210:GLU:OE2	24:BR:19:ARG:NH1	2.27	0.67
38:A1:1575:A:C8	38:A1:1575:A:C3'	2.78	0.67
48:AL:4:SER:O	63:Aa:44:ASN:ND2	2.28	0.67
77:Ao:11:TYR:OH	77:Ao:18:ARG:NH1	2.27	0.67
21:BK:32:HIS:ND1	21:BK:33:GLU:O	2.27	0.67
38:A1:655:C:H2'	38:A1:656:A:H8	1.58	0.67
73:Ak:13:GLU:OE1	73:Ak:16:ARG:NH2	2.27	0.67
34:B5:407:A:H2'	34:B5:408:C:C6	2.29	0.67
34:B5:1290:U:H2'	34:B5:1291:G:C8	2.30	0.67
38:A1:163:C:C2'	38:A1:164:A:H5''	2.24	0.67
38:A1:3092:C:O2'	38:A1:3094:A:OP2	2.13	0.67
35:AA:52:SER:HB3	35:AA:191:LEU:HD12	1.75	0.67
38:A1:129:U:H2'	38:A1:130:A:C8	2.30	0.67
38:A1:299:G:C4	71:Ai:31:GLY:HA3	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AU:13:LYS:HE2	57:AU:15:PHE:HZ	1.60	0.67
7:BI:5:ARG:NH1	7:BI:29:LEU:O	2.27	0.67
44:AG:82:LEU:HG	44:AG:86:THR:HG23	1.75	0.67
79:E:13:VAL:HG12	79:E:17:LEU:HD23	1.76	0.67
2:BB:70:LEU:HD12	2:BB:73:LEU:HD11	1.77	0.67
38:A1:1565:G:O5'	38:A1:1565:G:H8	1.78	0.67
53:AQ:170:ARG:HH11	63:Aa:56:VAL:HG23	1.60	0.67
79:E:60:ARG:H	79:E:63:MET:HE1	1.59	0.67
6:BH:108:GLN:NE2	34:B5:743:U:O4'	2.27	0.66
34:B5:1291:G:H22	34:B5:1324:G:H22	1.42	0.66
38:A1:1784:G:OP1	69:Ag:19:LYS:NZ	2.28	0.66
79:E:148:VAL:O	79:E:152:ARG:HG2	1.95	0.66
11:BO:24:ASN:ND2	34:B5:902:G:N7	2.43	0.66
26:BT:28:LEU:HA	26:BT:111:ILE:HD11	1.76	0.66
32:Bf:94:LYS:NZ	34:B5:1232:U:OP2	2.27	0.66
34:B5:1058:U:H3'	34:B5:1059:U:H5''	1.75	0.66
35:AA:62:VAL:HG22	35:AA:73:GLU:HG3	1.77	0.66
38:A1:439:C:OP2	38:A1:440:A:N6	2.28	0.66
34:B5:1309:C:O2	34:B5:1316:G:N2	2.16	0.66
36:AB:152:LYS:HD3	36:AB:189:SER:HA	1.77	0.66
38:A1:1223:A:H2'	38:A1:1224:C:H6	1.59	0.66
38:A1:2895:G:O2'	75:Am:100:TYR:O	2.12	0.66
43:AF:36:ALA:O	43:AF:40:LYS:HG3	1.95	0.66
3:BC:40:LYS:HE2	3:BC:248:SER:HB2	1.77	0.66
3:BC:45:VAL:HG21	3:BC:68:ILE:HG23	1.76	0.66
5:BG:167:LYS:O	34:B5:72:A:N6	2.29	0.66
20:BF:63:GLN:NE2	20:BF:66:GLN:OE1	2.28	0.66
33:BM:61:VAL:HB	33:BM:121:VAL:HB	1.76	0.66
38:A1:3295:A:H2'	38:A1:3296:A:C8	2.31	0.66
38:A1:3344:A:C2	38:A1:3361:G:N2	2.62	0.66
1:BA:183:ARG:HG3	1:BA:188:LEU:HD23	1.76	0.66
31:Bg:123:ILE:HD13	31:Bg:169:ILE:HG21	1.76	0.66
31:Bg:200:ASN:ND2	31:Bg:239:GLU:OE2	2.28	0.66
38:A1:2552:C:N3	65:Ac:53:LYS:NZ	2.43	0.66
44:AG:74:THR:HG22	44:AG:164:VAL:HG22	1.77	0.66
38:A1:417:A:H2'	38:A1:418:A:C8	2.31	0.66
15:BY:44:LEU:HA	15:BY:47:VAL:HG12	1.78	0.66
15:BY:55:VAL:HG22	15:BY:75:VAL:HG22	1.77	0.66
15:BY:105:ARG:NH2	34:B5:459:G:OP2	2.27	0.66
34:B5:1237:G:H2'	34:B5:1238:A:H8	1.61	0.66
36:AB:261:MET:HB2	36:AB:264:VAL:HG23	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1659:U:H2'	38:A1:1660:C:C6	2.30	0.66
39:A3:47:C:OP1	41:AD:95:TRP:N	2.28	0.66
12:BV:22:ARG:NH2	13:BW:19:LYS:O	2.29	0.66
38:A1:900:G:H1'	38:A1:1589:A:N6	2.11	0.66
38:A1:1095:U:N3	56:AT:127:GLN:OE1	2.28	0.66
2:BB:158:SER:O	2:BB:162:ARG:NE	2.24	0.66
8:BJ:176:ASN:ND2	34:B5:511:A:OP2	2.29	0.66
34:B5:1291:G:H22	34:B5:1324:G:H1	1.43	0.66
45:AH:1:MET:HE2	45:AH:3:TYR:HE1	1.61	0.66
50:AN:5:LYS:HG3	71:AI:40:VAL:HG11	1.78	0.66
71:AI:51:SER:C	71:AI:55:ARG:HE	2.03	0.66
19:BD:28:GLU:HA	21:BK:58:GLN:HE22	1.61	0.66
20:BF:109:LYS:NZ	34:B5:1474:G:OP1	2.27	0.66
23:BQ:50:GLU:OE1	23:BQ:82:ARG:NH2	2.28	0.66
38:A1:1596:C:H2'	38:A1:1597:C:C6	2.31	0.66
45:AH:4:ILE:HG22	45:AH:5:GLN:CD	2.21	0.66
55:AS:8:GLN:HB3	55:AS:64:ILE:HD11	1.76	0.66
5:BG:31:ARG:HB3	5:BG:101:ILE:HD13	1.78	0.65
13:BW:2:THR:N	34:B5:1034:C:HO2'	1.94	0.65
34:B5:509:G:H2'	34:B5:510:G:C8	2.31	0.65
38:A1:164:A:H2'	38:A1:165:A:C1'	2.25	0.65
38:A1:649:A2M:OP2	38:A1:2868:U:O2'	2.14	0.65
38:A1:2960:C:H2'	38:A1:2961:G:H8	1.60	0.65
40:A4:58:G:O6	72:Aj:63:ARG:NH1	2.29	0.65
20:BF:81:ARG:NH2	34:B5:1615:C:OP1	2.28	0.65
38:A1:655:C:H2'	38:A1:656:A:C8	2.30	0.65
38:A1:2218:G:OP2	71:AI:68:ARG:NH2	2.30	0.65
38:A1:2406:C:H2'	38:A1:2407:C:C6	2.32	0.65
4:BE:148:ARG:NH2	5:BG:201:GLN:OE1	2.29	0.65
26:BT:86:ARG:NH2	34:B5:1601:G:OP1	2.28	0.65
31:Bg:292:LEU:HD12	31:Bg:301:LEU:HD11	1.76	0.65
34:B5:591:A:H2'	34:B5:592:A:C8	2.31	0.65
47:AJ:108:GLU:HB2	47:AJ:122:ILE:HG13	1.77	0.65
66:Ad:9:THR:HG23	66:Ad:109:VAL:HB	1.78	0.65
5:BG:66:GLY:HA2	34:B5:1681:A:H1'	1.78	0.65
7:BI:58:LEU:HD21	34:B5:1676:U:H5''	1.77	0.65
34:B5:162:A:H3'	34:B5:163:G:H21	1.60	0.65
34:B5:221:A:O2'	34:B5:222:A:O5'	2.13	0.65
62:AZ:125:GLY:O	62:AZ:128:GLN:NE2	2.29	0.65
79:E:114:GLU:HA	79:E:117:ILE:HG13	1.78	0.65
34:B5:407:A:H2'	34:B5:408:C:H6	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1132:C:H2'	38:A1:1133:A2M:H8	1.78	0.65
61:AY:74:TYR:HD2	61:AY:77:LYS:HG2	1.61	0.65
79:E:60:ARG:HB3	79:E:63:MET:SD	2.34	0.65
37:AC:35:VAL:HG21	37:AC:244:LEU:HD21	1.79	0.65
38:A1:1348:U:OP1	53:AQ:39:ARG:NH1	2.30	0.65
38:A1:2468:A:O2'	38:A1:2477:G:N2	2.29	0.65
39:A3:121:U:C2	41:AD:268:GLU:HG3	2.32	0.65
62:AZ:81:LEU:HD22	69:Ag:90:ILE:HD13	1.78	0.65
38:A1:176:G:H2'	38:A1:177:U:C6	2.32	0.65
38:A1:2768:U:H2'	38:A1:2769:A:H8	1.61	0.65
55:AS:77:VAL:HG11	55:AS:106:LEU:HD22	1.78	0.65
62:AZ:101:PHE:O	62:AZ:107:ARG:NH2	2.28	0.65
77:Ao:28:TYR:HB3	77:Ao:69:VAL:HB	1.79	0.65
20:BF:94:THR:HG22	20:BF:114:ILE:HG13	1.79	0.65
34:B5:924:A:H2'	34:B5:925:G:C8	2.32	0.65
34:B5:1061:A:H5'	34:B5:1062:A:H5''	1.79	0.65
35:AA:209:HIS:CE1	35:AA:211:HIS:HD2	2.15	0.65
45:AH:90:MET:O	45:AH:143:GLU:HG3	1.97	0.65
55:AS:42:TRP:O	55:AS:46:GLN:HG2	1.96	0.65
38:A1:1559:A:OP1	60:AX:33:ARG:NE	2.25	0.65
56:AT:102:ARG:O	56:AT:106:LEU:HG	1.97	0.65
24:BR:70:SER:HA	24:BR:74:GLN:HE21	1.62	0.64
40:A4:151:C:C5	60:AX:24:LEU:HD21	2.32	0.64
34:B5:1251:U:HO2'	34:B5:1252:C:H6	1.45	0.64
37:AC:191:LYS:NZ	38:A1:341:G:OP2	2.29	0.64
75:Am:78:ILE:O	75:Am:83:LYS:NZ	2.23	0.64
8:BJ:59:LEU:HD22	8:BJ:69:ARG:HA	1.80	0.64
38:A1:1139:G:OP2	64:Ab:14:ARG:NH2	2.28	0.64
38:A1:2509:U:H2'	38:A1:2510:U:O4'	1.97	0.64
15:BY:106:GLN:NE2	34:B5:442:C:OP2	2.30	0.64
34:B5:209:U:H2'	34:B5:210:A:H8	1.61	0.64
38:A1:159:A:C2'	38:A1:160:G:H5'	2.27	0.64
38:A1:1281:G:N2	38:A1:1282:G:O6	2.31	0.64
73:Ak:39:ARG:HH21	73:Ak:59:ALA:HB1	1.62	0.64
29:Bc:27:GLN:NE2	29:Bc:65:ARG:O	2.31	0.64
38:A1:164:A:H2'	38:A1:165:A:H1'	1.80	0.64
38:A1:3291:G:H2'	38:A1:3292:A:C8	2.33	0.64
44:AG:162:LEU:HD23	50:AN:7:LEU:HD11	1.79	0.64
38:A1:3016:A:H2'	38:A1:3017:A:C8	2.33	0.64
71:Ai:51:SER:C	71:Ai:55:ARG:NE	2.55	0.64
6:BH:63:PRO:C	6:BH:65:PRO:HD3	2.23	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Ba:45:VAL:HG13	16:Ba:46:GLU:N	2.13	0.64
27:BU:44:ASN:HA	27:BU:47:GLN:NE2	2.11	0.64
58:AV:120:LYS:NZ	58:AV:124:ASP:OD1	2.25	0.64
78:Ap:51:ALA:HB3	78:Ap:54:ILE:HD12	1.79	0.64
1:BA:70:PRO:HB2	1:BA:94:GLY:HA3	1.79	0.64
2:BB:194:ASN:HD22	2:BB:210:ILE:HG22	1.62	0.64
34:B5:625:C:H2'	34:B5:626:U:C6	2.33	0.64
34:B5:1357:A:H2'	34:B5:1358:G:H8	1.63	0.64
38:A1:243:G:H5''	38:A1:243:G:H8	1.63	0.64
40:A4:126:A:O2'	40:A4:129:C:N4	2.30	0.64
43:AF:138:TYR:CD2	43:AF:233:GLU:HB2	2.32	0.64
52:AP:128:ARG:HE	52:AP:136:ILE:CG2	2.08	0.64
4:BE:19:LEU:HD11	4:BE:108:ARG:HD2	1.79	0.63
14:BX:30:LYS:NZ	34:B5:1132:A:OP1	2.30	0.63
35:AA:30:ARG:HH21	35:AA:72:ARG:HH22	1.46	0.63
39:A3:38:U:N3	39:A3:41:G:OP2	2.27	0.63
1:BA:30:GLN:HE22	1:BA:32:HIS:HB2	1.63	0.63
3:BC:222:TYR:CE1	12:BV:10:GLU:OE2	2.50	0.63
14:BX:73:ARG:NH1	14:BX:84:THR:OG1	2.29	0.63
16:Ba:45:VAL:HG13	16:Ba:46:GLU:H	1.62	0.63
31:Bg:249:ARG:HH12	31:Bg:315:VAL:HG11	1.63	0.63
40:A4:9:A:H2'	40:A4:10:A:C8	2.33	0.63
63:Aa:112:ILE:HB	63:Aa:130:VAL:HG12	1.79	0.63
79:E:55:LEU:HD22	79:E:182:GLN:HG2	1.80	0.63
15:BY:34:ASN:O	34:B5:521:A:O2'	2.16	0.63
26:BT:84:LYS:NZ	34:B5:1563:C:OP1	2.23	0.63
34:B5:851:U:OP2	54:AR:170:ARG:NH1	2.32	0.63
37:AC:20:LEU:HD11	37:AC:252:GLU:HG3	1.81	0.63
38:A1:656:A:H2'	38:A1:657:A:H8	1.63	0.63
77:Ao:2:VAL:N	77:Ao:90:HIS:O	2.31	0.63
6:BH:24:PHE:CE1	6:BH:77:LEU:HD21	2.33	0.63
38:A1:176:G:N1	38:A1:241:G:N1	2.46	0.63
38:A1:1228:C:H2'	38:A1:1229:G:C8	2.33	0.63
61:AY:3:LYS:HD2	61:AY:8:VAL:HG13	1.80	0.63
3:BC:103:VAL:HG12	3:BC:190:LEU:HD12	1.81	0.63
15:BY:78:SER:OG	15:BY:81:GLU:OE1	2.10	0.63
24:BR:3:ARG:NH1	34:B5:1414:U:H5''	2.14	0.63
38:A1:1203:A:H2'	38:A1:1204:A:C8	2.34	0.63
38:A1:3206:C:OP1	55:AS:166:LYS:NZ	2.31	0.63
44:AG:91:PHE:CE2	44:AG:185:ARG:HG2	2.33	0.63
47:AJ:25:GLU:CG	47:AJ:26:SER:H	2.10	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:31:ARG:H	5:BG:34:GLN:HE21	1.44	0.63
10:BN:11:ILE:HG13	10:BN:12:SER:H	1.62	0.63
24:BR:3:ARG:HH11	34:B5:1414:U:H5''	1.62	0.63
38:A1:2679:A:O2'	47:AJ:52:TYR:OH	2.17	0.63
40:A4:57:C:H4'	40:A4:63:G:N7	2.13	0.63
45:AH:9:GLN:HB3	45:AH:52:LEU:HD11	1.79	0.63
3:BC:81:MET:HB2	3:BC:101:VAL:HG23	1.80	0.63
38:A1:1498:A:H2'	38:A1:1499:C:C6	2.34	0.63
38:A1:2506:U:C2	38:A1:2507:C:H1'	2.33	0.63
38:A1:2256:A:H4'	38:A1:2257:C:OP2	1.99	0.63
38:A1:179:C:N4	38:A1:237:G:H1	1.95	0.63
38:A1:831:G:O2'	38:A1:1864:A:N3	2.29	0.63
38:A1:3291:G:H2'	38:A1:3292:A:H8	1.63	0.63
10:BN:104:ARG:NH2	34:B5:951:A:OP1	2.31	0.62
21:BK:23:ALA:O	21:BK:64:TYR:HB2	1.99	0.62
34:B5:1041:G:H2'	34:B5:1042:G:C8	2.34	0.62
38:A1:2927:C:H2'	38:A1:2928:C:C6	2.34	0.62
38:A1:2945:G:O2'	38:A1:2948:OMC:OP2	2.16	0.62
62:AZ:103:GLN:HB2	62:AZ:106:GLN:NE2	2.13	0.62
3:BC:205:ARG:NH2	34:B5:7:G:N7	2.47	0.62
11:BO:90:ARG:NH2	34:B5:902:G:OP1	2.32	0.62
20:BF:51:VAL:HG11	20:BF:130:ILE:HG22	1.81	0.62
27:BU:80:GLU:HG2	30:Bd:54:LYS:HZ3	1.63	0.62
38:A1:501:A:H2'	38:A1:502:U:C6	2.34	0.62
11:BO:123:SER:HB2	34:B5:885:G:H21	1.65	0.62
19:BD:11:LEU:HD12	27:BU:86:ILE:HG12	1.81	0.62
38:A1:970:A:OP1	64:Ab:18:ARG:HD2	1.99	0.62
38:A1:2796:G:N7	77:Ao:63:LYS:NZ	2.46	0.62
46:AI:72:ALA:HB2	46:AI:155:ALA:HB2	1.81	0.62
62:AZ:72:ILE:HD11	62:AZ:107:ARG:HG3	1.81	0.62
15:BY:10:ARG:HH21	34:B5:778:G:N2	1.96	0.62
37:AC:320:ASN:ND2	38:A1:505:G:OP1	2.24	0.62
38:A1:243:G:H5'	38:A1:244:G:OP2	1.99	0.62
38:A1:1563:C:H2'	38:A1:1564:U:H4'	1.80	0.62
45:AH:1:MET:HE2	45:AH:3:TYR:CE1	2.33	0.62
5:BG:23:ARG:HH11	5:BG:42:GLY:HA2	1.64	0.62
14:BX:137:LYS:C	14:BX:138:GLU:OE1	2.43	0.62
31:Bg:137:LYS:HB2	31:Bg:139:GLN:HE22	1.64	0.62
38:A1:585:A:H2'	38:A1:586:C:C6	2.35	0.62
16:Ba:19:LYS:HD3	16:Ba:20:PRO:HD2	1.82	0.62
38:A1:994:G:N2	38:A1:995:U:O4	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1576:G:H2'	38:A1:1577:G:H5'	1.80	0.62
38:A1:2482:U:H2'	38:A1:2483:G:C8	2.35	0.62
79:E:60:ARG:N	79:E:63:MET:HE1	2.14	0.62
38:A1:500:C:P	68:Af:48:ARG:HH22	2.23	0.62
38:A1:2219:A:H2'	38:A1:2220:A2M:C8	2.29	0.62
38:A1:2264:U:O2'	38:A1:2265:C:H5'	1.99	0.62
38:A1:3016:A:H2'	38:A1:3017:A:H8	1.64	0.62
38:A1:3295:A:H2'	38:A1:3296:A:H8	1.64	0.62
41:AD:95:TRP:HD1	41:AD:158:ARG:HA	1.64	0.62
6:BH:114:ARG:NH1	34:B5:637:C:O2	2.22	0.62
10:BN:107:LYS:NZ	34:B5:1018:U:OP1	2.32	0.62
30:Bd:13:ARG:NH2	34:B5:1554:U:OP1	2.32	0.62
38:A1:173:G:H1	38:A1:244:G:N2	1.98	0.62
38:A1:242:C:H2'	38:A1:243:G:C8	2.35	0.62
38:A1:1495:U:H5	38:A1:1835:A:N1	1.97	0.62
41:AD:236:LEU:HD12	41:AD:239:ILE:HD11	1.81	0.62
38:A1:2369:G:H2'	38:A1:2370:G:C8	2.35	0.62
38:A1:3165:A:H2'	38:A1:3166:C:C6	2.34	0.62
40:A4:26:U:H2'	40:A4:27:U:C6	2.35	0.62
41:AD:177:GLU:HB2	41:AD:190:ILE:HD12	1.82	0.62
9:BL:69:LYS:NZ	34:B5:304:U:O2	2.31	0.62
34:B5:1059:U:OP1	34:B5:1059:U:H6	1.83	0.62
38:A1:1134:G:O2'	38:A1:2642:A:N3	2.30	0.62
19:BD:166:ASP:O	19:BD:190:ARG:NH2	2.32	0.61
32:Bf:124:PRO:O	33:BM:50:LYS:NZ	2.34	0.61
38:A1:2152:A:H2'	38:A1:2153:U:H6	1.64	0.61
38:A1:2445:A:C6	38:A1:2503:G:C6	2.88	0.61
13:BW:106:THR:HG21	13:BW:121:VAL:HB	1.81	0.61
34:B5:782:U:H4'	34:B5:783:G:H5''	1.82	0.61
34:B5:939:A:H2'	34:B5:940:A:C8	2.35	0.61
34:B5:1061:A:H5''	34:B5:1062:A:N3	2.15	0.61
34:B5:1683:C:O2'	34:B5:1684:U:O5'	2.17	0.61
37:AC:126:ILE:O	37:AC:129:THR:OG1	2.18	0.61
38:A1:1573:G:C8	38:A1:1574:C:C6	2.88	0.61
8:BJ:64:GLU:O	8:BJ:65:LYS:HG2	2.01	0.61
34:B5:321:C:N4	34:B5:1667:A:OP1	2.33	0.61
36:AB:315:GLY:HA2	38:A1:3379:C:H4'	1.81	0.61
38:A1:1212:A:O2'	55:AS:92:LYS:NZ	2.33	0.61
38:A1:1447:G:OP1	52:AP:65:SER:OG	2.17	0.61
79:E:57:ASN:OD1	79:E:182:GLN:NE2	2.33	0.61
9:BL:73:GLY:HA3	9:BL:86:ILE:HD12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:34:GLN:HG3	23:BQ:57:LEU:HD12	1.81	0.61
26:BT:91:TYR:HB2	34:B5:1590:G:OP1	2.01	0.61
34:B5:1126:OMG:OP2	76:An:18:ARG:NH2	2.33	0.61
38:A1:562:C:H5''	55:AS:71:LYS:HD2	1.82	0.61
38:A1:3343:G:H21	38:A1:3362:A:H2	1.48	0.61
41:AD:36:LEU:HD13	41:AD:50:ARG:HD2	1.82	0.61
13:BW:107:SER:HA	34:B5:804:A:C8	2.35	0.61
34:B5:885:G:H2'	34:B5:886:U:C6	2.36	0.61
38:A1:2196:C:O2'	38:A1:2270:A:N3	2.32	0.61
38:A1:2697:A:H2'	38:A1:2698:G:H8	1.64	0.61
47:AJ:19:LEU:HD21	47:AJ:125:MET:HE3	1.83	0.61
5:BG:174:LYS:HG3	34:B5:78:A:H2	1.65	0.61
6:BH:14:THR:O	6:BH:18:LEU:HD13	2.00	0.61
9:BL:21:ASN:ND2	9:BL:32:LYS:H	1.97	0.61
34:B5:1115:U:H5''	76:An:14:LYS:HD2	1.83	0.61
36:AB:28:ARG:NH2	38:A1:3140:G:N7	2.48	0.61
38:A1:1138:U:O5'	64:Ab:14:ARG:NH2	2.32	0.61
38:A1:2699:G:H5''	56:AT:16:GLN:OE1	1.99	0.61
62:AZ:25:ILE:HG23	62:AZ:41:ALA:HB1	1.82	0.61
2:BB:179:SER:HA	2:BB:183:GLN:HB2	1.82	0.61
34:B5:1755:A:H8	34:B5:1755:A:OP1	1.84	0.61
38:A1:86:G:O2'	38:A1:98:G:O6	2.14	0.61
44:AG:183:LYS:HB2	44:AG:194:THR:HG23	1.81	0.61
56:AT:8:ARG:O	56:AT:11:THR:OG1	2.17	0.61
71:AI:51:SER:O	71:AI:55:ARG:CD	2.48	0.61
5:BG:43:ASP:HA	5:BG:46:LYS:HE3	1.83	0.61
14:BX:107:PHE:CG	14:BX:114:LYS:HE3	2.36	0.61
34:B5:71:A:N6	34:B5:72:A:N3	2.48	0.61
38:A1:2253:G:H1'	38:A1:2254:U:H5'	1.81	0.61
41:AD:205:SER:HB3	41:AD:236:LEU:HD23	1.81	0.61
79:E:165:LEU:HD23	79:E:167:VAL:HG23	1.83	0.61
79:E:196:LYS:H	79:E:200:ASN:ND2	1.98	0.61
38:A1:243:G:H3'	38:A1:244:G:H8	1.66	0.61
38:A1:339:C:OP1	38:A1:1380:G:O2'	2.17	0.61
38:A1:2251:G:N1	38:A1:2266:U:C2	2.69	0.61
41:AD:289:LYS:HD2	46:AI:206:LEU:HD12	1.82	0.61
66:Ad:51:LEU:HB3	66:Ad:55:LEU:HD23	1.83	0.61
2:BB:77:GLU:O	2:BB:80:SER:OG	2.17	0.61
25:BS:69:ILE:O	25:BS:73:MET:HG3	2.01	0.61
34:B5:1061:A:H5''	34:B5:1062:A:C2	2.36	0.61
37:AC:34:ILE:HG21	37:AC:120:TYR:CD2	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:40:A:H2'	40:A4:41:A:C8	2.36	0.61
44:AG:37:GLY:O	44:AG:38:GLN:OE1	2.18	0.61
38:A1:1565:G:C4	38:A1:1566:A:C8	2.88	0.60
1:BA:53:THR:OG1	1:BA:161:PRO:O	2.16	0.60
20:BF:72:HIS:NE2	34:B5:1610:G:OP1	2.30	0.60
38:A1:945:C:H2'	38:A1:946:U:C6	2.35	0.60
38:A1:1564:U:H3'	38:A1:1565:G:C8	2.36	0.60
62:AZ:33:SER:H	62:AZ:40:HIS:HE1	1.50	0.60
3:BC:119:LYS:NZ	34:B5:1291:G:OP1	2.34	0.60
31:Bg:249:ARG:HH22	31:Bg:315:VAL:HG11	1.66	0.60
34:B5:12:U:H2'	34:B5:13:C:C6	2.35	0.60
34:B5:1346:A:H62	34:B5:1370:U:H6	1.49	0.60
38:A1:129:U:H2'	38:A1:130:A:H8	1.66	0.60
38:A1:3353:G:O2'	38:A1:3354:U:O4'	2.19	0.60
46:AI:54:SER:HB2	46:AI:135:ILE:HD11	1.83	0.60
34:B5:1160:A:H2'	34:B5:1161:C:C6	2.35	0.60
34:B5:1234:A:OP2	34:B5:1245:G:O2'	2.14	0.60
37:AC:138:ARG:NH1	38:A1:1384:U:H5'	2.16	0.60
38:A1:2767:U:H2'	38:A1:2768:U:C6	2.36	0.60
54:AR:8:LYS:NZ	54:AR:22:VAL:O	2.34	0.60
58:AV:23:MET:HE2	58:AV:100:GLY:HA3	1.83	0.60
34:B5:218:A:N6	34:B5:844:A:HO2'	1.98	0.60
38:A1:1243:G:N2	38:A1:1248:C:OP2	2.34	0.60
38:A1:1268:G:O2'	38:A1:1270:A:OP2	2.19	0.60
40:A4:141:C:OP1	50:AN:109:ARG:NH2	2.35	0.60
54:AR:134:HIS:CE1	54:AR:136:ARG:HB3	2.37	0.60
58:AV:27:ASP:OD1	58:AV:101:VAL:HA	2.01	0.60
4:BE:251:GLU:OE2	4:BE:254:ARG:NH2	2.35	0.60
34:B5:1591:C:H2'	34:B5:1592:A:C8	2.37	0.60
38:A1:120:G:H4'	38:A1:121:A:O5'	2.02	0.60
35:AA:111:THR:HB	35:AA:136:ILE:HD13	1.84	0.60
36:AB:79:VAL:HG21	36:AB:338:LEU:HD11	1.81	0.60
37:AC:150:LEU:HD23	37:AC:249:ILE:HG12	1.83	0.60
38:A1:3192:U:H2'	38:A1:3193:C:C6	2.36	0.60
53:AQ:122:ILE:HG23	53:AQ:126:GLN:HB2	1.82	0.60
67:Ae:86:THR:HG22	67:Ae:115:LEU:HD13	1.83	0.60
15:BY:124:ARG:HA	15:BY:127:LYS:HE2	1.83	0.60
34:B5:1524:A:H2'	34:B5:1525:A:C8	2.36	0.60
38:A1:1046:A:H2'	38:A1:1049:C:C5	2.36	0.60
38:A1:1814:A:H2	38:A1:1816:A:H1'	1.66	0.60
38:A1:2107:A:H2	38:A1:3344:A:H8	1.50	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2257:C:H3'	38:A1:2258:U:H5''	1.82	0.60
38:A1:2550:U:H1'	44:AG:38:GLN:NE2	2.17	0.60
40:A4:71:A:O2'	61:AY:52:ARG:NH2	2.35	0.60
79:E:48:ARG:HA	79:E:159:LEU:HD23	1.84	0.60
38:A1:33:G:OP1	50:AN:73:ARG:NH1	2.34	0.60
38:A1:1565:G:O5'	38:A1:1565:G:C8	2.54	0.60
38:A1:1874:A:OP2	54:AR:21:LYS:NZ	2.32	0.60
38:A1:2193:U:H5''	38:A1:2194:G:H5'	1.83	0.60
38:A1:3294:A:H2'	38:A1:3295:A:O4'	2.01	0.60
63:Aa:86:LYS:HG3	63:Aa:90:TYR:CE2	2.37	0.60
15:BY:112:LYS:NZ	34:B5:57:G:OP1	2.30	0.60
19:BD:28:GLU:HG2	19:BD:69:LEU:HD21	1.84	0.60
37:AC:34:ILE:HG21	37:AC:120:TYR:HD2	1.66	0.60
38:A1:177:U:H2'	38:A1:178:U:C6	2.37	0.60
38:A1:2457:G:C2	38:A1:2486:A:N1	2.69	0.60
38:A1:3302:U:H3	38:A1:3312:U:H3	1.48	0.60
54:AR:181:ARG:NH1	54:AR:182:ASP:OD1	2.35	0.60
76:An:15:ARG:O	76:An:19:LYS:HG3	2.02	0.60
5:BG:113:ILE:HD11	5:BG:124:LEU:HD13	1.82	0.59
7:BI:48:THR:OG1	7:BI:52:ASN:O	2.20	0.59
9:BL:133:LYS:NZ	34:B5:324:U:OP1	2.30	0.59
11:BO:17:ALA:HB2	11:BO:79:VAL:HG11	1.83	0.59
21:BK:44:LYS:HD2	34:B5:1217:A:H5''	1.84	0.59
31:Bg:185:GLN:NE2	31:Bg:187:GLN:HE22	2.00	0.59
38:A1:531:G:H2'	38:A1:532:A:C8	2.37	0.59
38:A1:2700:G:H5''	56:AT:17:ARG:HG2	1.84	0.59
38:A1:2882:U:H2'	38:A1:2883:U:C6	2.36	0.59
54:AR:175:GLN:OE1	54:AR:176:ARG:NH1	2.34	0.59
6:BH:110:GLN:NE2	34:B5:816:G:O2'	2.35	0.59
34:B5:209:U:H2'	34:B5:210:A:C8	2.38	0.59
38:A1:1565:G:H8	38:A1:1565:G:C5'	2.15	0.59
51:AO:187[A]:GLU:HA	51:AO:192[A]:LYS:HE3	1.84	0.59
62:AZ:41:ALA:HB2	62:AZ:77:TYR:HE1	1.67	0.59
71:Ai:52:PRO:HA	71:Ai:55:ARG:HE	1.67	0.59
5:BG:137:ARG:HH12	34:B5:144:U:H5	1.48	0.59
34:B5:193:U:O2'	34:B5:195:G:OP2	2.14	0.59
34:B5:538:A:N3	34:B5:538:A:H2'	2.17	0.59
38:A1:1657:C:O2'	38:A1:1797:A:OP2	2.13	0.59
42:AE:40:LEU:HD13	42:AE:84:VAL:HG11	1.83	0.59
2:BB:48:VAL:HG21	2:BB:61:LEU:HD11	1.85	0.59
16:Ba:39:MET:HG3	16:Ba:41:ILE:HD11	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BP:85:ILE:HA	22:BP:89:MET:HE2	1.84	0.59
40:A4:8:C:H2'	40:A4:9:A:C8	2.37	0.59
77:Ao:28:TYR:HD1	77:Ao:71:ARG:HH21	1.49	0.59
79:E:91:LYS:O	79:E:94:ASN:ND2	2.35	0.59
3:BC:165:VAL:HG11	3:BC:210:THR:HA	1.83	0.59
22:BP:108:ARG:HH22	25:BS:119:ILE:HA	1.67	0.59
27:BU:26:LEU:HB3	27:BU:34:LEU:HD11	1.85	0.59
36:AB:313:HIS:O	36:AB:333:LYS:HE3	2.03	0.59
38:A1:627:U:H2'	38:A1:628:A:C8	2.38	0.59
45:AH:92:TYR:HB2	45:AH:142:ASP:HB3	1.83	0.59
5:BG:30:LYS:O	5:BG:102:VAL:N	2.27	0.59
7:BI:152:ILE:HG13	7:BI:153:GLU:N	2.16	0.59
10:BN:55:ARG:NH1	34:B5:960:U:O5'	2.35	0.59
34:B5:778:G:H2'	34:B5:779:U:H2'	1.84	0.59
38:A1:177:U:H2'	38:A1:178:U:H6	1.67	0.59
38:A1:326:U:OP1	48:AL:31:LYS:NZ	2.34	0.59
38:A1:2232:A:H2'	38:A1:2233:A:C8	2.37	0.59
38:A1:2664:C:OP2	47:AJ:142:LYS:NZ	2.28	0.59
41:AD:260:PHE:HD1	41:AD:264:GLN:HE21	1.50	0.59
53:AQ:8:LYS:HB3	53:AQ:11:LYS:HE3	1.84	0.59
78:Ap:46:THR:OG1	78:Ap:57:CYS:SG	2.60	0.59
1:BA:90:ALA:HA	1:BA:95:ALA:HB3	1.83	0.59
5:BG:52:ILE:HD13	5:BG:102:VAL:HG21	1.84	0.59
34:B5:276:C:O2'	34:B5:278:U:OP2	2.20	0.59
34:B5:1062:A:H4'	34:B5:1062:A:OP1	2.03	0.59
34:B5:1533:C:H4'	34:B5:1539:G:N1	2.18	0.59
38:A1:1497:C:O2'	38:A1:1602:A:N3	2.33	0.59
38:A1:1504:A:N1	38:A1:1515:A:O2'	2.35	0.59
38:A1:2588:U:OP1	44:AG:241:LYS:NZ	2.36	0.59
54:AR:134:HIS:CE1	54:AR:136:ARG:HE	2.19	0.59
34:B5:319:U:H4'	34:B5:323:A:C8	2.37	0.59
38:A1:1167:U:H2'	38:A1:1168:U:O4'	2.03	0.59
38:A1:3252:G:H2'	38:A1:3253:G:C8	2.38	0.59
66:Ad:11:GLU:OE1	66:Ad:96:VAL:HG21	2.03	0.59
71:AI:52:PRO:HA	71:AI:55:ARG:NH2	2.17	0.59
25:BS:41:ARG:NH2	26:BT:36:ILE:O	2.36	0.59
34:B5:300:A:H2'	34:B5:301:A:C8	2.38	0.59
38:A1:1015:U:O4	38:A1:1036:A:N6	2.35	0.59
39:A3:4:U:H2'	39:A3:5:G:H8	1.68	0.59
5:BG:121:LEU:HD13	5:BG:124:LEU:HD12	1.85	0.59
14:BX:70:LYS:NZ	34:B5:567:A:OP1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1648:A:H2'	34:B5:1649:G:C8	2.38	0.59
37:AC:74:ILE:HD12	37:AC:75:PRO:HD2	1.84	0.59
38:A1:175:C:H42	38:A1:242:C:H41	1.51	0.59
38:A1:1915:A:H2'	38:A1:1916:U:C6	2.38	0.59
44:AG:247:ASP:OD1	44:AG:248:LYS:HD2	2.03	0.59
47:AJ:94:ARG:HG2	47:AJ:95:ASN:H	1.67	0.59
54:AR:43:LYS:HZ2	54:AR:44:LEU:HD21	1.66	0.59
79:E:116:LEU:HB3	79:E:120:VAL:HG23	1.84	0.59
80:EC:6950:C:H2'	80:EC:6951:C:C6	2.37	0.59
2:BB:150:VAL:HG23	34:B5:1067:C:H5''	1.84	0.58
4:BE:22:LYS:N	34:B5:773:C:OP1	2.36	0.58
10:BN:124:ARG:NH2	34:B5:967:A:OP2	2.35	0.58
34:B5:156:A:H2'	34:B5:157:A:O4'	2.03	0.58
38:A1:2596:U:H2'	38:A1:2597:U:C6	2.38	0.58
38:A1:2724:OMU:OP1	56:AT:78:LYS:NZ	2.36	0.58
42:AE:166:LYS:N	42:AE:169:ASP:OD2	2.32	0.58
47:AJ:50:ALA:HB3	47:AJ:61:ARG:HA	1.85	0.58
61:AY:52:ARG:O	61:AY:70:ILE:HB	2.03	0.58
22:BP:52:LYS:HB3	22:BP:53:PRO:HD3	1.84	0.58
34:B5:108:A:H2'	34:B5:109:G:C8	2.38	0.58
38:A1:100:A:H3'	38:A1:101:G:H21	1.69	0.58
38:A1:2265:C:H2'	38:A1:2266:U:C6	2.38	0.58
45:AH:41:ILE:HG21	45:AH:71:VAL:HG21	1.85	0.58
48:AL:182:ILE:O	48:AL:186:ARG:HG3	2.03	0.58
80:EC:6951:C:H2'	80:EC:6952:U:O4'	2.03	0.58
2:BB:116:LYS:HG3	34:B5:931:C:H5''	1.85	0.58
2:BB:132:ASP:HB2	2:BB:221:PRO:HB3	1.86	0.58
20:BF:146:THR:HG21	20:BF:220:VAL:HG12	1.84	0.58
25:BS:87:ASN:HD22	25:BS:100:THR:N	2.01	0.58
38:A1:2438:A:H2'	38:A1:2439:A:C8	2.38	0.58
38:A1:2550:U:H1'	44:AG:38:GLN:OE1	2.04	0.58
23:BQ:137:ARG:HB2	34:B5:1580:C:H4'	1.86	0.58
34:B5:894:U:H2'	34:B5:895:G:C8	2.39	0.58
38:A1:164:A:H5'	38:A1:164:A:C8	2.31	0.58
38:A1:173:G:N1	38:A1:244:G:N2	2.52	0.58
66:Ad:74:ARG:HD3	66:Ad:94:GLU:OE2	2.04	0.58
12:BV:62:ARG:HH22	34:B5:1039:A:H4'	1.69	0.58
14:BX:65:ASN:ND2	14:BX:116:ASP:OD2	2.35	0.58
34:B5:1588:G:H1	34:B5:1608:U:H3	1.52	0.58
34:B5:1591:C:H2'	34:B5:1592:A:H8	1.67	0.58
38:A1:1392:G:O2'	38:A1:1417:G:N2	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2762:A:H2'	38:A1:2763:U:H6	1.68	0.58
41:AD:160:PHE:HA	41:AD:163:LEU:HB3	1.86	0.58
44:AG:78:PHE:O	44:AG:79:GLN:HG3	2.03	0.58
19:BD:142:LEU:HD13	19:BD:150:MET:HE3	1.85	0.58
38:A1:1251:A:N7	38:A1:1263:A:N6	2.51	0.58
38:A1:1567:U:H5''	38:A1:1567:U:H6	1.69	0.58
38:A1:3165:A:H2'	38:A1:3166:C:H6	1.68	0.58
41:AD:80:SER:OG	41:AD:92:LEU:O	2.19	0.58
52:AP:33:ALA:HB1	52:AP:117:ILE:HG12	1.85	0.58
4:BE:86:PHE:CZ	4:BE:87:MET:HE3	2.38	0.58
7:BI:56:ARG:HH22	34:B5:332:U:P	2.26	0.58
13:BW:106:THR:HG22	13:BW:108:ALA:H	1.69	0.58
26:BT:22:LEU:HD13	26:BT:28:LEU:HD13	1.86	0.58
28:BZ:56:THR:HA	28:BZ:103:ARG:HD3	1.86	0.58
31:Bg:31:ASN:HD21	31:Bg:46:LYS:HG3	1.69	0.58
38:A1:496:C:N3	38:A1:617:G:N1	2.40	0.58
38:A1:968:G:H2'	38:A1:969:C:C6	2.39	0.58
38:A1:2258:U:O2'	38:A1:2259:A:O4'	2.22	0.58
38:A1:2441:A:N1	38:A1:2506:U:O4	2.36	0.58
38:A1:2467:G:H4'	79:E:28:PHE:HE1	1.68	0.58
41:AD:111:GLN:HE22	41:AD:252:ALA:HA	1.67	0.58
56:AT:26:HIS:CE1	56:AT:29:THR:HG23	2.39	0.58
5:BG:31:ARG:HH22	34:B5:1682:U:P	2.26	0.58
6:BH:14:THR:O	6:BH:18:LEU:CD1	2.51	0.58
9:BL:58:CYS:HG	9:BL:112:SER:HG	1.52	0.58
14:BX:72:VAL:HG11	14:BX:96:VAL:HG11	1.85	0.58
34:B5:1564:U:H2'	34:B5:1565:C:C6	2.39	0.58
36:AB:16:PHE:HB2	36:AB:19:ARG:HH21	1.69	0.58
38:A1:2702:A:OP1	56:AT:23:GLY:HA2	2.03	0.58
53:AQ:176:ARG:HA	53:AQ:182:LYS:O	2.03	0.58
61:AY:70:ILE:HD13	61:AY:82:VAL:HG22	1.84	0.58
3:BC:47:ALA:O	3:BC:49:LYS:NZ	2.37	0.58
4:BE:11:ARG:NH1	4:BE:21:ASP:OD1	2.37	0.58
11:BO:133:ARG:NH1	34:B5:1786:G:OP2	2.36	0.58
14:BX:121:ARG:NH2	34:B5:1135:U:OP2	2.37	0.58
23:BQ:46:PHE:HA	23:BQ:49:TYR:HB2	1.85	0.58
34:B5:585:A:H2'	34:B5:586:G:C8	2.38	0.58
34:B5:1713:G:H2'	34:B5:1714:A:C8	2.39	0.58
39:A3:95:A:N3	55:AS:119:ARG:HD2	2.19	0.58
66:Ad:11:GLU:OE2	66:Ad:74:ARG:NH1	2.36	0.58
77:Ao:46:LYS:HE2	77:Ao:54:THR:HB	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:BL:2:SER:HB3	9:BL:53:TYR:HB3	1.86	0.58
16:Ba:70:LYS:NZ	34:B5:933:A:OP1	2.30	0.58
19:BD:63:GLY:O	21:BK:91:TYR:OH	2.15	0.58
34:B5:82:U:H2'	34:B5:83:G:O4'	2.04	0.58
38:A1:407:A:C2	40:A4:17:A:H1'	2.39	0.58
38:A1:418:A:N1	40:A4:5:U:H5	2.02	0.58
38:A1:1534:A:H2'	38:A1:1535:A:C8	2.38	0.58
38:A1:2206:G:H1'	38:A1:2207:A:C8	2.38	0.58
41:AD:41:LYS:HB2	56:AT:68:THR:O	2.04	0.58
52:AP:128:ARG:HH22	52:AP:136:ILE:CD1	1.91	0.58
73:Ak:5:ILE:HD12	73:Ak:10:GLN:HE22	1.68	0.58
33:BM:54:ARG:NH2	33:BM:56:GLU:OE2	2.37	0.57
34:B5:256:A:H2'	34:B5:257:A:O4'	2.04	0.57
36:AB:36:ASP:H	36:AB:39:LYS:NZ	2.00	0.57
46:AI:184:LYS:HG2	46:AI:190:VAL:HG23	1.86	0.57
51:AO:189[A]:ASP:O	51:AO:193[A]:GLN:HG3	2.04	0.57
6:BH:139:ARG:HB3	13:BW:51:GLU:OE2	2.04	0.57
19:BD:115:ILE:HG13	19:BD:142:LEU:HD22	1.86	0.57
20:BF:76:ARG:NH2	23:BQ:121:SER:OG	2.37	0.57
38:A1:741:U:H5'	53:AQ:74:GLU:OE2	2.04	0.57
38:A1:2697:A:H2'	38:A1:2698:G:C8	2.38	0.57
65:Ac:74:ASN:HB2	65:Ac:86:ARG:HB3	1.85	0.57
8:BJ:133:HIS:ND1	8:BJ:162:SER:OG	2.32	0.57
26:BT:119:LYS:NZ	34:B5:1368:G:OP1	2.38	0.57
34:B5:415:C:O2'	34:B5:418:G:O6	2.21	0.57
34:B5:513:U:H2'	34:B5:514:G:C8	2.39	0.57
38:A1:528:U:H2'	38:A1:529:A:C8	2.38	0.57
56:AT:64:VAL:HG13	56:AT:72:VAL:HG13	1.85	0.57
70:Ah:41:LEU:HD23	70:Ah:44:ILE:HD11	1.86	0.57
13:BW:111:MET:SD	13:BW:115:GLU:HG2	2.45	0.57
20:BF:161:ASP:OD2	29:Bc:54:LEU:HD12	2.04	0.57
38:A1:314:U:H2'	38:A1:315:C:C6	2.39	0.57
38:A1:1390:A:N6	38:A1:1418:A:O2'	2.38	0.57
38:A1:1809:A:H2'	38:A1:1810:A:O4'	2.04	0.57
38:A1:2542:U:H4'	38:A1:2543:U:H5'	1.85	0.57
71:Ai:51:SER:O	71:Ai:55:ARG:HD3	2.05	0.57
4:BE:19:LEU:HD22	34:B5:788:A:H2'	1.86	0.57
5:BG:175:ILE:HG12	34:B5:78:A:H1'	1.85	0.57
38:A1:2961:G:H2'	38:A1:2962:U:C6	2.39	0.57
40:A4:6:U:H2'	40:A4:7:U:C6	2.39	0.57
44:AG:133:LYS:HD2	44:AG:138:HIS:HE1	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AH:1:MET:HG2	45:AH:3:TYR:CE1	2.40	0.57
77:Ao:105:GLN:O	77:Ao:106:PHE:HB2	2.04	0.57
25:BS:28:ILE:HA	25:BS:58:ALA:HB2	1.87	0.57
34:B5:684:A:H2'	34:B5:685:A:C8	2.39	0.57
34:B5:1091:A:H4'	34:B5:1092:A:O4'	2.05	0.57
35:AA:21:ARG:HD3	38:A1:824:C:H5''	1.86	0.57
38:A1:40:A:H5''	63:Aa:35:ALA:HB1	1.85	0.57
38:A1:1573:G:H3'	38:A1:1574:C:H5''	1.86	0.57
38:A1:2367:A:H2'	38:A1:2368:A:C8	2.40	0.57
38:A1:2502:A:C5	38:A1:2503:G:N7	2.73	0.57
2:BB:168:ILE:HG12	2:BB:197:ILE:HD12	1.87	0.57
5:BG:2:LYS:HG2	5:BG:17:GLU:HG3	1.85	0.57
25:BS:49:LYS:NZ	25:BS:79:TYR:O	2.37	0.57
31:Bg:239:GLU:HB3	31:Bg:257:ALA:HB2	1.85	0.57
34:B5:162:A:H3'	34:B5:163:G:N2	2.20	0.57
34:B5:304:U:H2'	34:B5:305:C:C6	2.39	0.57
34:B5:950:C:H2'	34:B5:951:A:C8	2.40	0.57
38:A1:3113:A:OP1	45:AH:73:SER:OG	2.20	0.57
39:A3:73:C:H41	55:AS:19:VAL:HG21	1.70	0.57
1:BA:20:ALA:HB2	24:BR:91:LEU:HD21	1.87	0.57
11:BO:40:ALA:HB2	11:BO:70:LYS:HG2	1.87	0.57
34:B5:1146:G:H2'	34:B5:1147:A:C8	2.38	0.57
38:A1:121:A:C2	44:AG:100:GLU:OE2	2.58	0.57
38:A1:643:U:O2'	38:A1:1153:A:N1	2.36	0.57
39:A3:45:A:OP1	41:AD:151:GLN:NE2	2.23	0.57
45:AH:47:LYS:NZ	49:AM:4:ASP:OD2	2.38	0.57
77:Ao:25:VAL:HG22	77:Ao:72:LEU:HD13	1.87	0.57
36:AB:17:LEU:HD21	36:AB:233:TRP:HH2	1.70	0.57
38:A1:1340:G:OP2	67:Ae:61:LYS:NZ	2.33	0.57
38:A1:1603:A:OP1	54:AR:38:ARG:NH2	2.25	0.57
38:A1:3042:U:OP2	38:A1:3092:C:N4	2.30	0.57
39:A3:4:U:H2'	39:A3:5:G:C8	2.40	0.57
42:AE:76:LEU:N	42:AE:138:GLN:OE1	2.37	0.57
44:AG:83:ASP:OD1	44:AG:86:THR:HG22	2.05	0.57
70:Ah:102:GLU:HG2	70:Ah:103:LYS:N	2.19	0.57
21:BK:11:ILE:HD11	21:BK:37:THR:HG21	1.85	0.57
34:B5:1648:A:H2'	34:B5:1649:G:H8	1.70	0.57
38:A1:1799:A:H2'	38:A1:1800:A:C8	2.40	0.57
38:A1:2506:U:H3'	38:A1:2506:U:C6	2.40	0.57
18:Be:46:ASN:ND2	34:B5:503:G:O2'	2.33	0.56
20:BF:119:ASP:O	20:BF:123:VAL:HG23	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1622:G:H2'	34:B5:1623:C:C6	2.40	0.56
37:AC:119:ARG:NH2	38:A1:696:C:OP2	2.36	0.56
38:A1:240:U:H3	38:A1:241:G:N2	2.02	0.56
38:A1:400:G:H4'	38:A1:401:U:H5''	1.87	0.56
38:A1:428:A:H2'	38:A1:429:U:C6	2.40	0.56
38:A1:1222:G:N2	38:A1:1286:A:N6	2.32	0.56
42:AE:20:LYS:NZ	42:AE:22:ARG:HE	2.02	0.56
52:AP:128:ARG:HH21	52:AP:136:ILE:CG1	2.16	0.56
77:Ao:10:THR:HA	77:Ao:20:HIS:HD2	1.69	0.56
3:BC:55:GLU:OE2	3:BC:239:PRO:HD2	2.06	0.56
21:BK:59:PHE:CZ	21:BK:62:GLN:HA	2.40	0.56
24:BR:26:LEU:HD21	24:BR:62:GLN:HG3	1.87	0.56
38:A1:3094:A:OP1	58:AV:14:SER:OG	2.24	0.56
40:A4:154:C:H5''	44:AG:181:LYS:HG2	1.85	0.56
4:BE:230:GLU:OE2	4:BE:235:TYR:OH	2.17	0.56
5:BG:188:ARG:NH1	34:B5:284:G:O6	2.37	0.56
7:BI:75:LYS:NZ	34:B5:259:U:OP1	2.26	0.56
25:BS:143:ARG:HH21	34:B5:1461:C:H3'	1.70	0.56
34:B5:844:A:H2'	34:B5:845:G:C8	2.40	0.56
34:B5:1345:A:N1	34:B5:1380:U:H5	2.04	0.56
34:B5:1732:A:H2'	34:B5:1733:C:C6	2.40	0.56
38:A1:1208:U:O2'	38:A1:3115:C:N4	2.38	0.56
38:A1:2656:A:H4'	77:Ao:98:LYS:HD2	1.88	0.56
38:A1:3033:A:H2'	38:A1:3034:C:O2	2.05	0.56
38:A1:3089:C:H2'	38:A1:3090:U:O4'	2.06	0.56
39:A3:121:U:OP2	41:AD:265:TYR:OH	2.17	0.56
60:AX:59:SER:OG	60:AX:101:GLU:OE1	2.23	0.56
77:Ao:105:GLN:OE1	77:Ao:105:GLN:N	2.38	0.56
27:BU:108:ILE:HD12	27:BU:114:VAL:HG21	1.88	0.56
38:A1:716:A:C6	63:Aa:117:ARG:HG3	2.41	0.56
38:A1:1176:C:H2'	38:A1:1177:G:N2	2.20	0.56
38:A1:1667:A:H2'	38:A1:1668:G:C8	2.40	0.56
38:A1:1786:G:H2'	38:A1:1787:A:C8	2.41	0.56
38:A1:2218:G:H2'	38:A1:2219:A:H8	1.70	0.56
42:AE:170:LYS:HD3	42:AE:173:MET:HE2	1.87	0.56
4:BE:21:ASP:OD2	4:BE:24:SER:OG	2.19	0.56
19:BD:175:VAL:CG1	19:BD:177:MET:HE3	2.36	0.56
34:B5:71:A:H2'	34:B5:72:A:H4'	1.86	0.56
34:B5:261:U:H1'	34:B5:262:U:H5	1.70	0.56
38:A1:176:G:H2'	38:A1:177:U:H6	1.70	0.56
1:BA:7:PHE:HA	1:BA:191:ARG:HH21	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:107:THR:O	7:BI:110:ARG:HG2	2.05	0.56
11:BO:16:VAL:O	11:BO:30:VAL:HA	2.06	0.56
11:BO:81:VAL:HG11	11:BO:102:LEU:HD13	1.86	0.56
20:BF:23:VAL:H	20:BF:34:GLN:NE2	2.03	0.56
28:BZ:81:ARG:O	28:BZ:85:LYS:HG3	2.06	0.56
34:B5:968:U:H2'	34:B5:969:C:O4'	2.05	0.56
36:AB:57:VAL:HG22	36:AB:73:VAL:HG22	1.86	0.56
38:A1:152:U:OP1	70:Ah:106:LYS:NZ	2.34	0.56
38:A1:1560:G:O2'	38:A1:1561:G:O4'	2.24	0.56
40:A4:4:C:H2'	40:A4:5:U:O2	2.06	0.56
45:AH:50:ASN:ND2	49:AM:4:ASP:OD1	2.39	0.56
53:AQ:92:ARG:HG3	63:Aa:77:LYS:HE3	1.88	0.56
7:BI:49:ARG:O	7:BI:52:ASN:ND2	2.37	0.56
10:BN:4:MET:HE1	10:BN:121:ARG:HG3	1.86	0.56
11:BO:129:LYS:HB2	34:B5:990:C:H5''	1.87	0.56
26:BT:39:THR:HA	26:BT:100:ILE:HD12	1.87	0.56
37:AC:181:VAL:O	37:AC:182:LEU:HG	2.06	0.56
38:A1:2480:A:OP2	79:E:106:LYS:NZ	2.38	0.56
40:A4:40:A:H2'	40:A4:41:A:H8	1.70	0.56
42:AE:45:GLY:O	42:AE:48:ARG:NH1	2.38	0.56
44:AG:146:LYS:HG3	44:AG:173:MET:HE3	1.88	0.56
5:BG:160:ARG:NH1	34:B5:66:U:O2	2.39	0.56
6:BH:76:LYS:O	6:BH:80:GLU:HG2	2.04	0.56
8:BJ:149:ARG:HG2	34:B5:765:G:O6	2.06	0.56
21:BK:32:HIS:CD2	21:BK:42:VAL:HG21	2.41	0.56
24:BR:10:LYS:NZ	34:B5:1316:G:O2'	2.39	0.56
37:AC:191:LYS:HG2	37:AC:194:TYR:OH	2.06	0.56
38:A1:100:A:H2'	38:A1:101:G:N3	2.21	0.56
38:A1:650:OMC:H2'	38:A1:651:G:C8	2.41	0.56
38:A1:1223:A:H2'	38:A1:1224:C:C6	2.41	0.56
38:A1:2442:G:C6	38:A1:2506:U:C5	2.94	0.56
17:Bb:30:SER:OG	34:B5:959:U:O2	2.24	0.56
26:BT:38:LYS:O	26:BT:39:THR:OG1	2.23	0.56
38:A1:631:U:H2'	38:A1:632:G:C8	2.41	0.56
38:A1:3013:U:H2'	38:A1:3014:U:C6	2.41	0.56
41:AD:22:ARG:NE	41:AD:28:THR:OG1	2.36	0.56
67:Ae:79:VAL:HG13	67:Ae:111:ARG:HG2	1.88	0.56
68:Af:75:HIS:HB2	68:Af:82:ARG:HG3	1.87	0.56
2:BB:216:LYS:NZ	34:B5:886:U:OP2	2.38	0.56
14:BX:92:CYS:HG	14:BX:136:TRP:CD1	2.24	0.56
22:BP:15:HIS:HB3	22:BP:22:LEU:HD11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:92:ARG:HG3	38:A1:3345:G:H5'	1.87	0.55
14:BX:3:LYS:HE2	14:BX:7:ARG:HH21	1.71	0.55
36:AB:71:GLU:OE2	59:AW:1:MET:N	2.27	0.55
38:A1:2494:A:H5''	38:A1:2495:C:H5''	1.88	0.55
38:A1:2769:A:H5'	77:Ao:71:ARG:HH12	1.71	0.55
40:A4:150:G:OP1	60:AX:27:ARG:NH2	2.39	0.55
5:BG:177:ARG:NH2	34:B5:143:G:O6	2.34	0.55
15:BY:34:ASN:ND2	34:B5:532:U:O2	2.38	0.55
19:BD:58:VAL:HG13	19:BD:59:LEU:HD12	1.87	0.55
38:A1:1717:U:H2'	38:A1:1718:G:H8	1.71	0.55
38:A1:2144:A:H1'	38:A1:2281:A2M:N6	2.22	0.55
38:A1:2197:OMC:N4	38:A1:2241:U:H2'	2.22	0.55
62:AZ:25:ILE:HA	62:AZ:43:VAL:HG12	1.87	0.55
10:BN:23:PRO:HD2	10:BN:26:PHE:HB2	1.88	0.55
15:BY:39:GLU:HA	15:BY:42:GLU:HG3	1.88	0.55
34:B5:712:G:H5''	34:B5:713:A:N7	2.21	0.55
38:A1:156:G:OP2	71:Ai:25:LYS:HB3	2.06	0.55
38:A1:1138:U:P	64:Ab:14:ARG:HH12	2.29	0.55
38:A1:1233:G:N2	38:A1:1234:G:O6	2.39	0.55
38:A1:2897:A:OP2	75:Am:124:LYS:NZ	2.30	0.55
3:BC:138:PRO:HB3	12:BV:11:LEU:HD21	1.89	0.55
19:BD:51:ARG:HG2	19:BD:89:GLU:OE2	2.06	0.55
20:BF:57:SER:HA	29:Bc:53:ILE:HB	1.88	0.55
38:A1:29:C:H4'	38:A1:62:A:H4'	1.89	0.55
38:A1:169:U:C5	38:A1:253:A:C2	2.84	0.55
38:A1:1620:U:H2'	38:A1:1621:A:C8	2.42	0.55
38:A1:2909:U:H2'	38:A1:2910:A:O4'	2.07	0.55
51:AO:163[A]:SER:C	51:AO:166[A]:GLU:HG3	2.31	0.55
9:BL:10:GLU:CD	9:BL:12:ALA:H	2.14	0.55
22:BP:60:LEU:HG	22:BP:64:LYS:HZ3	1.71	0.55
34:B5:238:U:H5''	34:B5:238:U:H6	1.69	0.55
34:B5:976:G:N1	34:B5:1023:A:O2'	2.35	0.55
37:AC:138:ARG:HH21	37:AC:240:PRO:HG2	1.72	0.55
38:A1:728:G:H5''	53:AQ:43:PRO:HB2	1.89	0.55
38:A1:1083:G:H2'	38:A1:1084:A:C8	2.42	0.55
38:A1:1410:U:O2'	67:Ae:95:GLU:OE1	2.23	0.55
43:AF:87:VAL:HG11	43:AF:243:MET:HE1	1.88	0.55
56:AT:39:ILE:HD12	56:AT:102:ARG:HE	1.72	0.55
65:Ac:24:THR:HG22	65:Ac:91:SER:HB3	1.89	0.55
65:Ac:54:SER:HA	65:Ac:57:GLU:OE1	2.06	0.55
69:Ag:51:LEU:CD1	69:Ag:54:ILE:HD12	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:176:GLN:NE2	34:B5:65:A:OP1	2.36	0.55
10:BN:63:ALA:O	10:BN:67:THR:OG1	2.23	0.55
19:BD:105:MET:HE3	19:BD:109:LEU:HD21	1.89	0.55
31:Bg:12:THR:HG22	31:Bg:311:ARG:HG3	1.88	0.55
34:B5:1358:G:H2'	34:B5:1359:C:O4'	2.06	0.55
35:AA:215:ASN:ND2	38:A1:2969:A:N7	2.53	0.55
37:AC:65:TRP:HB3	37:AC:69:ARG:HD3	1.89	0.55
41:AD:261:THR:OG1	41:AD:264:GLN:OE1	2.21	0.55
58:AV:87:ARG:NH2	58:AV:137:VAL:HG21	2.20	0.55
79:E:165:LEU:CD2	79:E:167:VAL:HG23	2.37	0.55
1:BA:83:GLN:HG2	1:BA:99:ALA:HB1	1.88	0.55
25:BS:52:VAL:HG21	25:BS:69:ILE:HD11	1.89	0.55
33:BM:59:LEU:HB3	33:BM:123:VAL:HB	1.87	0.55
34:B5:1755:A:H2'	34:B5:1756[A]:A:C8	2.41	0.55
38:A1:1563:C:H6	38:A1:1563:C:C5'	2.20	0.55
38:A1:1615:C:H2'	38:A1:1616:U:C6	2.42	0.55
38:A1:2427:U:H2'	38:A1:2428:U:C6	2.42	0.55
4:BE:71:LYS:HG3	4:BE:91:THR:HB	1.88	0.55
5:BG:32:ILE:HD11	5:BG:63:MET:HB3	1.88	0.55
7:BI:2:GLY:N	34:B5:393:C:OP2	2.39	0.55
15:BY:36:SER:HB3	15:BY:39:GLU:HG2	1.89	0.55
34:B5:1357:A:H2'	34:B5:1358:G:C8	2.41	0.55
34:B5:1391:A:H2'	34:B5:1392:U:C6	2.41	0.55
37:AC:315:LYS:HB2	37:AC:323:VAL:HG21	1.89	0.55
38:A1:897:U:H2'	38:A1:898:OMU:H6	1.89	0.55
38:A1:1562:C:H2'	38:A1:1563:C:C6	2.41	0.55
38:A1:2206:G:H1'	38:A1:2207:A:N7	2.22	0.55
38:A1:2544:U:H2'	38:A1:2545:C:C6	2.42	0.55
39:A3:16:U:H2'	39:A3:17:A:C8	2.42	0.55
45:AH:57:VAL:HG23	45:AH:68:LEU:HD13	1.88	0.55
79:E:60:ARG:C	79:E:63:MET:CE	2.59	0.55
34:B5:1171:A:H2'	34:B5:1172:G:H8	1.70	0.55
38:A1:651:G:O2'	38:A1:1435:A:OP1	2.25	0.55
38:A1:1155:C:OP2	43:AF:94:LYS:NZ	2.40	0.55
38:A1:3160:U:H2'	38:A1:3161:C:C6	2.42	0.55
42:AE:41:ILE:HB	42:AE:85:ILE:HB	1.89	0.55
47:AJ:10:ARG:NH2	47:AJ:151:SER:O	2.32	0.55
75:Am:104:PRO:HG2	75:Am:107:ALA:HB2	1.89	0.55
2:BB:130:SER:HB2	2:BB:180:THR:HG22	1.88	0.55
2:BB:180:THR:O	2:BB:183:GLN:N	2.40	0.55
34:B5:520:A:H2'	34:B5:521:A:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:9:ARG:NH2	38:A1:912:G:OP2	2.38	0.55
38:A1:370:U:H4'	38:A1:404:G:H5'	1.87	0.55
38:A1:1120:A:H2'	38:A1:1121:U:H6	1.72	0.55
3:BC:101:VAL:HG12	3:BC:115:ILE:HD12	1.90	0.54
4:BE:251:GLU:O	4:BE:255:ARG:HG2	2.07	0.54
9:BL:58:CYS:SG	9:BL:112:SER:OG	2.62	0.54
36:AB:250:ALA:HB3	38:A1:2880:U:H1'	1.89	0.54
38:A1:2842:U:OP1	38:A1:2844:C:N4	2.39	0.54
55:AS:26:ARG:O	56:AT:150:THR:HB	2.06	0.54
26:BT:9:VAL:HG22	26:BT:140:LEU:HG	1.89	0.54
34:B5:30:G:H2'	34:B5:31:C:C6	2.42	0.54
34:B5:1071:U:H2'	34:B5:1072:C:C6	2.42	0.54
34:B5:1291:G:H22	34:B5:1324:G:N2	2.04	0.54
38:A1:2407:C:H2'	38:A1:2408:U:H6	1.72	0.54
79:E:55:LEU:HB3	79:E:182:GLN:HE21	1.72	0.54
80:EC:6870:A:O2'	80:EC:6871:A:OP2	2.19	0.54
7:BI:5:ARG:NH2	34:B5:334:G:O6	2.40	0.54
34:B5:887:A:H2'	34:B5:888:U:H6	1.72	0.54
38:A1:717:C:OP1	38:A1:751:A:O2'	2.25	0.54
38:A1:2946:A2M:H5''	38:A1:2947:G:H5'	1.88	0.54
5:BG:92:ARG:NH1	34:B5:1674:C:OP1	2.38	0.54
14:BX:3:LYS:HE2	14:BX:7:ARG:NH2	2.23	0.54
22:BP:47:ARG:NH2	34:B5:1555:A:OP2	2.35	0.54
25:BS:135:GLY:HA3	34:B5:1559:A:O5'	2.07	0.54
34:B5:219:A:H62	34:B5:830:U:H3	1.55	0.54
34:B5:898:A:N1	34:B5:911:U:O2'	2.37	0.54
34:B5:1144:U:H2'	34:B5:1145:U:C6	2.42	0.54
34:B5:1450:U:H2'	34:B5:1451:C:C6	2.43	0.54
35:AA:209:HIS:CE1	35:AA:211:HIS:CD2	2.95	0.54
38:A1:164:A:H2'	38:A1:165:A:O4'	2.08	0.54
38:A1:2268:U:H3	38:A1:2272:G:H22	1.55	0.54
38:A1:3066:U:H2'	38:A1:3067:C:C6	2.43	0.54
79:E:138:VAL:HG22	79:E:147:LYS:HG2	1.88	0.54
19:BD:80:ALA:O	19:BD:83:THR:OG1	2.25	0.54
19:BD:109:LEU:HD22	19:BD:115:ILE:HD13	1.89	0.54
24:BR:92:ASP:OD1	24:BR:93:LEU:N	2.38	0.54
34:B5:52:U:H2'	34:B5:53:G:C8	2.42	0.54
34:B5:1237:G:H2'	34:B5:1238:A:C8	2.40	0.54
37:AC:318:LEU:HD11	43:AF:146:GLN:HA	1.90	0.54
38:A1:1110:U:H2'	38:A1:1111:U:C6	2.42	0.54
43:AF:233:GLU:HG2	43:AF:234:GLU:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AO:163[A]:SER:O	51:AO:166[A]:GLU:CG	2.46	0.54
1:BA:126:PRO:HG2	1:BA:151:SER:HB2	1.89	0.54
11:BO:41:ARG:NH1	34:B5:896:U:O2	2.36	0.54
15:BY:29:HIS:HB2	15:BY:32:ARG:HB3	1.89	0.54
38:A1:1185:C:OP1	49:AM:59:ASN:ND2	2.39	0.54
38:A1:2228:A:H2'	38:A1:2229:A:C8	2.43	0.54
38:A1:2439:A:H3'	38:A1:2440:G:O4'	2.07	0.54
38:A1:2767:U:O2'	77:Ao:30:ALA:O	2.24	0.54
47:AJ:43:GLN:NE2	47:AJ:70:THR:O	2.39	0.54
58:AV:57:MET:HE3	58:AV:126:TRP:CH2	2.42	0.54
5:BG:132:ARG:NH1	34:B5:150:U:O4'	2.41	0.54
31:Bg:127:ARG:HG2	31:Bg:150:TRP:CD1	2.43	0.54
31:Bg:187:GLN:NE2	31:Bg:189:GLU:OE2	2.40	0.54
34:B5:845:G:H2'	34:B5:846:G:H5''	1.90	0.54
34:B5:850:A:H3'	54:AR:170:ARG:HH22	1.71	0.54
36:AB:58:ARG:HA	36:AB:357:LYS:HG3	1.89	0.54
38:A1:238:A:C8	38:A1:238:A:H5''	2.42	0.54
44:AG:81:THR:HG21	44:AG:181:LYS:HE3	1.90	0.54
4:BE:106:LYS:NZ	34:B5:789:A:O2'	2.41	0.54
21:BK:68:LEU:HD21	21:BK:76:LEU:HD12	1.89	0.54
41:AD:83:LEU:HG	41:AD:88:ILE:HB	1.90	0.54
50:AN:5:LYS:HB3	71:Ai:36:ARG:HH21	1.72	0.54
73:Ak:5:ILE:HG23	73:Ak:10:GLN:NE2	2.22	0.54
77:Ao:3:ASN:ND2	77:Ao:95:GLY:O	2.41	0.54
5:BG:36:VAL:N	5:BG:50:PHE:O	2.33	0.54
11:BO:80:HIS:HA	11:BO:113:GLY:O	2.08	0.54
21:BK:60:SER:HB3	21:BK:65:TYR:CE1	2.43	0.54
22:BP:124:THR:OG1	34:B5:1182:U:H4'	2.08	0.54
34:B5:1220:C:H2'	34:B5:1221:A:H8	1.72	0.54
34:B5:1645:G:H2'	34:B5:1646:C:H6	1.73	0.54
38:A1:209:A:H4'	38:A1:211:A:N7	2.23	0.54
38:A1:595:G:O6	42:AE:22:ARG:NH2	2.35	0.54
40:A4:8:C:H2'	40:A4:9:A:H8	1.73	0.54
55:AS:152:LEU:HB2	55:AS:172:TYR:CZ	2.43	0.54
3:BC:230:TRP:CG	13:BW:68:ARG:HD2	2.43	0.54
8:BJ:53:ARG:HG2	8:BJ:57:ARG:HH21	1.73	0.54
34:B5:693:U:H5''	34:B5:694:U:H5'	1.90	0.54
38:A1:275:U:H2'	38:A1:276:U:C6	2.43	0.54
38:A1:375:A:OP2	61:AY:89:LYS:NZ	2.36	0.54
38:A1:2930:A:H2'	38:A1:2931:C:C6	2.42	0.54
45:AH:21:LYS:HD2	49:AM:8:LYS:HZ3	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:51:GLY:HA3	24:BR:113:LEU:HD11	1.90	0.53
2:BB:76:SER:OG	2:BB:78:ASP:OD2	2.24	0.53
31:Bg:112:SER:HB3	31:Bg:154:VAL:HG22	1.90	0.53
34:B5:1553:G:N1	34:B5:1556:A:OP2	2.37	0.53
38:A1:240:U:C1'	38:A1:241:G:OP1	2.54	0.53
38:A1:2148:U:H2'	38:A1:2149:A:C5	2.43	0.53
38:A1:3121:U:H1'	38:A1:3122:A:H5''	1.90	0.53
40:A4:52:A:H5'	74:A1:21:ARG:HD3	1.89	0.53
69:Ag:51:LEU:HD11	69:Ag:54:ILE:HD12	1.89	0.53
2:BB:111:ARG:HB3	16:Ba:68:TYR:HB2	1.90	0.53
3:BC:111:VAL:HG13	3:BC:191:ALA:HA	1.91	0.53
4:BE:45:ILE:HG13	4:BE:61:VAL:HG21	1.89	0.53
4:BE:94:ALA:O	4:BE:95:THR:OG1	2.25	0.53
15:BY:6:THR:HG23	15:BY:28:LEU:HB2	1.90	0.53
21:BK:3:MET:HB3	21:BK:8:ARG:HH21	1.73	0.53
23:BQ:98:ASP:O	23:BQ:101:SER:OG	2.26	0.53
26:BT:88:VAL:HG23	34:B5:1172:G:H21	1.73	0.53
31:Bg:133:VAL:O	31:Bg:141:LEU:N	2.40	0.53
34:B5:158:U:O2'	34:B5:160:C:OP2	2.24	0.53
34:B5:749:U:H2'	34:B5:750:U:C6	2.43	0.53
37:AC:304:GLN:HE22	38:A1:594:U:H3	1.57	0.53
38:A1:545:U:H5'	38:A1:546:C:H5'	1.90	0.53
38:A1:2801:A:O2'	38:A1:2802:A:H2'	2.08	0.53
41:AD:106:ALA:HA	41:AD:171:LEU:HD23	1.90	0.53
73:Ak:27:ILE:HG23	73:Ak:39:ARG:HD3	1.91	0.53
77:Ao:6:LYS:HA	77:Ao:25:VAL:HB	1.89	0.53
10:BN:11:ILE:HD11	34:B5:1072:C:H4'	1.89	0.53
19:BD:23:GLU:OE1	21:BK:61:TRP:NE1	2.25	0.53
22:BP:15:HIS:O	22:BP:22:LEU:HD12	2.07	0.53
34:B5:97:C:H2'	34:B5:98:U:C6	2.43	0.53
34:B5:1350:U:H2'	34:B5:1351:G:H8	1.73	0.53
34:B5:1680:G:O2'	34:B5:1720:G:N2	2.40	0.53
36:AB:250:ALA:HB1	38:A1:2947:G:C2	2.43	0.53
38:A1:1114:U:OP1	63:Aa:23:GLY:N	2.31	0.53
38:A1:1498:A:H2'	38:A1:1499:C:H6	1.72	0.53
38:A1:2494:A:H1'	79:E:162:VAL:HG23	1.90	0.53
49:AM:23:ILE:O	49:AM:30:GLY:N	2.41	0.53
54:AR:21:LYS:HD2	54:AR:53:LYS:O	2.08	0.53
62:AZ:89:VAL:HG23	62:AZ:93:LYS:HB3	1.91	0.53
80:EC:6851:G:N1	80:EC:6878:G:O2'	2.16	0.53
5:BG:173:PRO:O	34:B5:78:A:O2'	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BX:70:LYS:HG3	14:BX:93:LEU:HD22	1.90	0.53
16:Ba:40:ALA:HB3	16:Ba:69:ASN:OD1	2.09	0.53
34:B5:424:C:O2'	34:B5:426:G:OP1	2.24	0.53
34:B5:629:U:H2'	34:B5:630:A:H8	1.73	0.53
34:B5:739:G:N2	34:B5:739:G:OP2	2.42	0.53
38:A1:229:G:H5''	61:AY:4:GLN:HB2	1.91	0.53
38:A1:760:G:N2	38:A1:770:G:O2'	2.41	0.53
38:A1:1039:U:H2'	38:A1:1040:A:C8	2.43	0.53
38:A1:3153:U:H5	38:A1:3293:U:H3	1.54	0.53
56:AT:13:TYR:HA	56:AT:16:GLN:HG2	1.90	0.53
8:BJ:10:LYS:HE3	8:BJ:12:TYR:CZ	2.44	0.53
23:BQ:29:ILE:HD13	23:BQ:52:LEU:HD21	1.89	0.53
23:BQ:143:ARG:NH1	34:B5:1463:C:O3'	2.41	0.53
33:BM:57:ALA:HA	33:BM:124:LYS:HB3	1.91	0.53
34:B5:358:U:O2'	34:B5:360:A:OP1	2.20	0.53
38:A1:169:U:C4	38:A1:253:A:N1	2.77	0.53
38:A1:1049:C:OP1	46:AI:21:ARG:NH2	2.40	0.53
38:A1:2204:C:O2'	38:A1:2205:U:H5''	2.09	0.53
38:A1:2478:C:OP2	38:A1:2480:A:N6	2.41	0.53
49:AM:25:LYS:HB2	49:AM:62:GLN:HB2	1.90	0.53
80:EC:6869:C:H1'	80:EC:6870:A:H5'	1.89	0.53
20:BF:76:ARG:NH2	23:BQ:121:SER:H	2.06	0.53
33:BM:62:LEU:H	33:BM:86:VAL:HG21	1.74	0.53
40:A4:63:G:H22	40:A4:97:A:H2	1.57	0.53
63:Aa:19:LYS:HB3	63:Aa:25:HIS:HB2	1.91	0.53
71:Ai:52:PRO:CA	71:Ai:55:ARG:HE	2.21	0.53
1:BA:39:ASN:OD1	1:BA:40:ALA:N	2.41	0.53
4:BE:103:TYR:HB2	4:BE:182:TYR:OH	2.09	0.53
4:BE:211:LYS:HB3	4:BE:217:THR:HG22	1.91	0.53
7:BI:162:ALA:HA	38:A1:3352:U:H2'	1.90	0.53
15:BY:62:THR:HG22	34:B5:531:C:O2	2.09	0.53
27:BU:33:GLN:CD	27:BU:33:GLN:N	2.64	0.53
32:Bf:107:LYS:HB2	32:Bf:110:ALA:HB2	1.90	0.53
38:A1:1311:G:N2	51:AO:86[A]:GLY:O	2.30	0.53
38:A1:1781:C:H2'	38:A1:1782:U:C6	2.42	0.53
38:A1:2218:G:H2'	38:A1:2219:A:C8	2.43	0.53
38:A1:2459:A:H62	38:A1:2461:A:H61	1.56	0.53
39:A3:8:G:O6	41:AD:21:ARG:NH2	2.36	0.53
48:AL:79:GLU:OE2	48:AL:112:ASN:ND2	2.38	0.53
56:AT:157:GLU:OE1	56:AT:157:GLU:HA	2.09	0.53
63:Aa:86:LYS:HG3	63:Aa:90:TYR:HE2	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Ao:15:LYS:HE2	77:Ao:18:ARG:HD3	1.91	0.53
1:BA:41:ARG:HE	1:BA:45:VAL:HB	1.74	0.53
20:BF:49:GLU:O	20:BF:50:GLU:HG3	2.09	0.53
31:Bg:197:SER:OG	31:Bg:217:ASP:N	2.42	0.53
34:B5:17:C:H2'	34:B5:18:C:C6	2.44	0.53
37:AC:319:LYS:NZ	38:A1:505:G:OP2	2.40	0.53
38:A1:737:G:H2'	38:A1:738:A:C8	2.44	0.53
41:AD:95:TRP:HZ3	41:AD:199:ILE:N	2.06	0.53
47:AJ:90:GLN:NE2	47:AJ:173:ASP:OD2	2.42	0.53
53:AQ:71:LEU:HD13	53:AQ:99:THR:HG21	1.90	0.53
54:AR:43:LYS:HZ1	54:AR:44:LEU:CD2	2.15	0.53
7:BI:76:THR:HG21	7:BI:104:ILE:HD12	1.91	0.53
19:BD:137:VAL:HG22	19:BD:151:LYS:HG2	1.90	0.53
25:BS:11:PHE:HD1	25:BS:60:GLU:HG3	1.72	0.53
34:B5:1516:A:O2'	34:B5:1517:U:H5'	2.09	0.53
38:A1:1801:U:H2'	38:A1:1802:C:C6	2.44	0.53
38:A1:2662:G:H2'	38:A1:2663:G:C8	2.44	0.53
38:A1:2768:U:H2'	38:A1:2769:A:C8	2.42	0.53
38:A1:2883:U:H2'	38:A1:2884:C:H6	1.74	0.53
40:A4:103:G:OP2	40:A4:105:A:O2'	2.22	0.53
41:AD:60:ILE:HD11	41:AD:93:THR:HA	1.91	0.53
56:AT:151:LEU:HG	56:AT:152:ALA:H	1.74	0.53
3:BC:156:THR:HG23	13:BW:95:PRO:HB2	1.90	0.53
10:BN:54:LEU:HB3	10:BN:60:VAL:HB	1.91	0.53
34:B5:116:U:H2'	34:B5:117:U:C6	2.44	0.53
38:A1:36:C:OP2	50:AN:83:LYS:NZ	2.41	0.53
38:A1:1573:G:H2'	38:A1:1574:C:O4'	2.09	0.53
38:A1:2520:A:H2'	38:A1:2521:U:C6	2.44	0.53
47:AJ:23:VAL:HG12	47:AJ:25:GLU:H	1.74	0.53
1:BA:57:LEU:HD21	1:BA:176:LEU:HB3	1.91	0.52
14:BX:101:GLU:OE1	14:BX:101:GLU:N	2.28	0.52
30:Bd:32:ARG:HH22	34:B5:1596:C:H3'	1.73	0.52
38:A1:74:G:H5''	48:AL:104:ARG:HH11	1.73	0.52
38:A1:130:A:H2'	38:A1:131:C:C6	2.44	0.52
38:A1:358:G:N2	38:A1:361:A:OP2	2.37	0.52
38:A1:818:C:O2'	38:A1:2138:A:N1	2.34	0.52
38:A1:2419:A:H2'	38:A1:2420:C:C6	2.44	0.52
38:A1:2426:U:H2'	38:A1:2427:U:C6	2.44	0.52
38:A1:2720:G:OP1	53:AQ:180:ARG:NH1	2.42	0.52
41:AD:119:TYR:OH	41:AD:139:PRO:O	2.23	0.52
47:AJ:100:GLY:HA3	47:AJ:154:THR:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:Ag:57:LEU:HB3	69:Ag:61:GLN:HG3	1.91	0.52
5:BG:207:GLU:O	5:BG:210:GLN:NE2	2.42	0.52
11:BO:53:ASP:HB2	11:BO:56:SER:HB3	1.90	0.52
15:BY:26:ASP:HB2	15:BY:68:LYS:NZ	2.25	0.52
31:Bg:117:LYS:O	31:Bg:118:LYS:HG2	2.09	0.52
31:Bg:255:ALA:HB2	31:Bg:292:LEU:HD22	1.91	0.52
32:Bf:94:LYS:HE3	34:B5:1231:U:C6	2.44	0.52
34:B5:1503:A:H2'	34:B5:1504:G:O4'	2.10	0.52
36:AB:284:ARG:HB3	36:AB:323:MET:HB3	1.91	0.52
38:A1:619:A:OP1	52:AP:167:ARG:NH1	2.42	0.52
38:A1:674:G:O6	53:AQ:56:LYS:NZ	2.41	0.52
38:A1:1575:A:H3'	38:A1:1575:A:H8	1.70	0.52
38:A1:2357:A:H2'	38:A1:2358:A:C8	2.44	0.52
44:AG:55:TYR:HA	44:AG:58:VAL:HG12	1.90	0.52
50:AN:28:TRP:O	50:AN:32:GLN:HG2	2.09	0.52
7:BI:73:SER:HB3	34:B5:257:A:H1'	1.90	0.52
15:BY:53:ASP:HB3	15:BY:79:VAL:HG22	1.92	0.52
16:Ba:89:ARG:NH2	34:B5:1089:U:OP1	2.42	0.52
34:B5:698:U:C4	34:B5:741:C:C4	2.97	0.52
34:B5:887:A:H2'	34:B5:888:U:C6	2.45	0.52
38:A1:3298:C:C2	38:A1:3299:A:C8	2.97	0.52
44:AG:185:ARG:O	44:AG:188:THR:HG22	2.09	0.52
52:AP:4:TYR:CE2	52:AP:16:SER:HB2	2.40	0.52
54:AR:160:GLU:HA	54:AR:163:ARG:NH1	2.24	0.52
13:BW:23:ARG:HH12	13:BW:67:GLY:N	2.07	0.52
18:Be:50:VAL:HA	18:Be:54:ARG:HA	1.90	0.52
19:BD:64:ARG:HA	21:BK:91:TYR:CE2	2.45	0.52
34:B5:1350:U:H2'	34:B5:1351:G:C8	2.44	0.52
34:B5:1382:A:HO2'	34:B5:1383:G:H8	1.57	0.52
35:AA:54:ARG:NH2	38:A1:2176:U:OP1	2.32	0.52
38:A1:252:U:H4'	38:A1:253:A:O5'	2.09	0.52
38:A1:1597:C:H2'	38:A1:1598:G:C8	2.44	0.52
38:A1:2506:U:C4	38:A1:2507:C:C5	2.98	0.52
48:AL:28:GLN:HB3	50:AN:201:ARG:HD2	1.91	0.52
72:Aj:54:LYS:O	72:Aj:58:THR:HB	2.09	0.52
11:BO:99:GLN:HE22	16:Ba:45:VAL:HA	1.74	0.52
21:BK:31:LYS:NZ	21:BK:32:HIS:O	2.33	0.52
21:BK:94:GLU:O	21:BK:96:ASN:ND2	2.43	0.52
23:BQ:100:GLN:NE2	31:Bg:57:PRO:O	2.42	0.52
24:BR:108:ASP:HA	24:BR:111:LYS:HG2	1.92	0.52
26:BT:63:ARG:O	26:BT:67:MET:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BT:130:ARG:NH1	34:B5:1360:A:OP1	2.43	0.52
34:B5:1592:A:H2'	34:B5:1593:A:H8	1.74	0.52
34:B5:1714:A:H2'	34:B5:1715:G:C8	2.44	0.52
35:AA:40:TYR:HA	35:AA:91:GLY:HA3	1.91	0.52
38:A1:173:G:C6	38:A1:244:G:N2	2.77	0.52
38:A1:796:U:H2'	38:A1:797:U:C6	2.45	0.52
38:A1:1560:G:O6	60:AX:36:LYS:NZ	2.41	0.52
38:A1:2444:C:H2'	38:A1:2445:A:C8	2.44	0.52
38:A1:2462:A:H1'	38:A1:2494:A:N6	2.25	0.52
38:A1:2673:A:O2'	47:AJ:104:PHE:O	2.28	0.52
61:AY:116:LYS:HG2	61:AY:126:LEU:HD11	1.91	0.52
63:Aa:90:TYR:CD1	63:Aa:100:PRO:HG3	2.44	0.52
73:Ak:31:LEU:HA	73:Ak:37:PRO:HA	1.91	0.52
5:BG:85:ARG:O	5:BG:87:ARG:NH1	2.42	0.52
37:AC:361:HIS:O	55:AS:28:ARG:NH1	2.41	0.52
38:A1:1108:U:H2'	38:A1:1109:U:C6	2.45	0.52
38:A1:2466:G:OP1	79:E:108:ASN:ND2	2.42	0.52
38:A1:2901:G:O2'	38:A1:3024:A:N1	2.38	0.52
38:A1:3296:A:H2'	38:A1:3297:U:H6	1.74	0.52
7:BI:38:ILE:HG12	7:BI:96:LEU:HD11	1.92	0.52
34:B5:381:C:O2'	34:B5:755:A:N1	2.37	0.52
36:AB:358:TRP:CD2	59:AW:1:MET:HE1	2.44	0.52
38:A1:517:G:OP1	43:AF:67:ARG:NH2	2.41	0.52
38:A1:1447:G:H3'	52:AP:67:ILE:HD11	1.90	0.52
38:A1:2406:C:H2'	38:A1:2407:C:H6	1.72	0.52
38:A1:3034:C:H5	45:AH:121:LYS:H	1.57	0.52
38:A1:3066:U:H2'	38:A1:3067:C:H6	1.74	0.52
46:AI:85:PHE:HA	46:AI:140:THR:HG22	1.90	0.52
63:Aa:24:LYS:O	63:Aa:26:ARG:HG2	2.09	0.52
1:BA:41:ARG:HD2	24:BR:103:ASP:OD2	2.08	0.52
15:BY:10:ARG:HD2	15:BY:26:ASP:OD2	2.10	0.52
36:AB:117:ARG:CZ	36:AB:175:LYS:HD3	2.39	0.52
36:AB:159:ARG:HG2	36:AB:182:GLN:HA	1.90	0.52
38:A1:1203:A:H2'	38:A1:1204:A:H8	1.73	0.52
38:A1:1641:U:O2'	38:A1:1642:A:H3'	2.10	0.52
44:AG:37:GLY:C	44:AG:38:GLN:CD	2.78	0.52
69:Ag:58:ARG:H	69:Ag:61:GLN:HE21	1.57	0.52
69:Ag:58:ARG:O	69:Ag:61:GLN:HG2	2.10	0.52
73:Ak:31:LEU:HD23	73:Ak:37:PRO:HB3	1.92	0.52
9:BL:13:PHE:HD2	9:BL:15:LYS:HE3	1.74	0.52
13:BW:101:TYR:CE1	13:BW:114:GLU:OE2	2.63	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BT:102:ARG:NH2	34:B5:1502:G:N7	2.57	0.52
27:BU:64:LYS:NZ	34:B5:1486:G:OP1	2.42	0.52
33:BM:42:ALA:HB3	33:BM:122:VAL:HB	1.92	0.52
37:AC:2:SER:OG	37:AC:3:ARG:N	2.42	0.52
38:A1:708:G:N2	38:A1:711:A:OP2	2.42	0.52
38:A1:2344:U:H2'	38:A1:2345:A:C8	2.45	0.52
38:A1:2404:A:N7	38:A1:2872:A:N6	2.57	0.52
79:E:49:PHE:CE1	79:E:51:GLY:HA3	2.39	0.52
79:E:53:LEU:HD21	79:E:189:PHE:HD2	1.75	0.52
5:BG:58:LYS:NZ	5:BG:106:LEU:O	2.39	0.52
9:BL:11:ARG:NH2	34:B5:342:C:H1'	2.24	0.52
21:BK:24:LYS:NZ	21:BK:63:TYR:OH	2.42	0.52
30:Bd:19:ARG:HD2	30:Bd:32:ARG:HD3	1.92	0.52
34:B5:1125:A:O2'	34:B5:1776:A:OP1	2.22	0.52
38:A1:120:G:N3	38:A1:121:A:N6	2.58	0.52
38:A1:1188:U:OP1	38:A1:1210:U:O2'	2.13	0.52
38:A1:1235:U:O4	38:A1:1251:A:N6	2.43	0.52
38:A1:2471:U:O2	38:A1:2475:G:O6	2.27	0.52
38:A1:2883:U:H2'	38:A1:2884:C:C6	2.45	0.52
38:A1:3343:G:H2'	38:A1:3344:A:C2	2.45	0.52
45:AH:21:LYS:HG3	45:AH:22:SER:H	1.75	0.52
51:AO:121[A]:PRO:HA	51:AO:124[A]:LEU:HD12	1.92	0.52
1:BA:127:ARG:NH2	1:BA:150:ASP:O	2.42	0.51
2:BB:171:ILE:HD13	2:BB:196:GLU:HG2	1.91	0.51
4:BE:100:ARG:HB2	4:BE:114:ILE:HD13	1.92	0.51
12:BV:4:ASP:N	12:BV:4:ASP:OD1	2.43	0.51
20:BF:25:LEU:HD12	20:BF:29:ILE:HG13	1.92	0.51
20:BF:99:MET:HE3	34:B5:1165:G:H5''	1.91	0.51
21:BK:35:ILE:HG22	21:BK:37:THR:HG22	1.92	0.51
23:BQ:48:VAL:HG13	23:BQ:78:VAL:HG13	1.93	0.51
24:BR:52:GLY:HA3	34:B5:1389:C:O2'	2.10	0.51
26:BT:18:TYR:HD1	26:BT:135:ILE:HG13	1.74	0.51
34:B5:526:A:H2'	34:B5:527:A:O4'	2.11	0.51
38:A1:283:G:O6	38:A1:304:G:H1'	2.09	0.51
38:A1:3233:C:H2'	38:A1:3234:A:C8	2.44	0.51
65:Ac:17:VAL:HG11	65:Ac:92:ILE:HD12	1.91	0.51
70:Ah:68:GLN:HE22	70:Ah:71:LYS:HD2	1.75	0.51
7:BI:11:ARG:O	9:BL:133:LYS:NZ	2.44	0.51
7:BI:41:LYS:HA	7:BI:60:ILE:HA	1.91	0.51
38:A1:12:A:H2'	38:A1:13:A:C8	2.45	0.51
38:A1:508:U:H2'	38:A1:509:U:C6	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1621:A:H2'	38:A1:1622:U:C6	2.45	0.51
38:A1:2152:A:H2'	38:A1:2153:U:C6	2.45	0.51
38:A1:2592:G:H4'	38:A1:2594:C:C2	2.46	0.51
38:A1:3357:U:H2'	38:A1:3358:U:C6	2.45	0.51
48:AL:50:PRO:O	48:AL:52:ASP:N	2.42	0.51
54:AR:167:ARG:NH2	54:AR:171:ASP:OD2	2.43	0.51
56:AT:91:LEU:HD12	56:AT:96:ILE:HD11	1.92	0.51
1:BA:200:ASP:OD2	24:BR:89:SER:HA	2.10	0.51
2:BB:73:LEU:HD12	2:BB:74:GLN:HG2	1.92	0.51
3:BC:82:ASN:HB2	3:BC:207:LEU:HD23	1.93	0.51
6:BH:143:LEU:HD12	6:BH:147:ASN:HB3	1.92	0.51
8:BJ:66:ASP:HB3	8:BJ:69:ARG:HB3	1.91	0.51
20:BF:109:LYS:HZ3	34:B5:1474:G:P	2.31	0.51
25:BS:86:LEU:HD22	25:BS:99:HIS:HB2	1.92	0.51
34:B5:980:G:H4'	34:B5:1776:A:H4'	1.91	0.51
34:B5:1055:U:H2'	34:B5:1056:U:C6	2.44	0.51
34:B5:1309:C:N3	34:B5:1316:G:N1	2.38	0.51
34:B5:1705:C:H2'	34:B5:1706:C:C6	2.45	0.51
37:AC:51:ALA:O	40:A4:26:U:O2'	2.27	0.51
37:AC:156:LEU:HD12	37:AC:159:ILE:HD12	1.91	0.51
38:A1:1404:G:O6	67:Ae:16:LYS:NZ	2.42	0.51
38:A1:2840:C:H2'	38:A1:2841:G:O4'	2.11	0.51
54:AR:43:LYS:HE3	54:AR:44:LEU:HG	1.92	0.51
66:Ad:11:GLU:HB2	66:Ad:107:VAL:HG22	1.91	0.51
78:Ap:59:CYS:C	78:Ap:61:LYS:H	2.18	0.51
79:E:30:GLU:HG3	79:E:209:SER:HB3	1.92	0.51
2:BB:47:LEU:O	11:BO:37:GLU:HG3	2.10	0.51
25:BS:30:TYR:O	25:BS:33:THR:OG1	2.28	0.51
31:Bg:106:HIS:NE2	31:Bg:124:SER:OG	2.32	0.51
34:B5:193:U:OP1	34:B5:195:G:N2	2.43	0.51
37:AC:180:LYS:HD3	37:AC:202:ARG:HG3	1.91	0.51
38:A1:1119:C:H2'	38:A1:1120:A:H8	1.74	0.51
38:A1:1721:U:OP2	54:AR:124:TYR:OH	2.28	0.51
38:A1:2206:G:O4'	38:A1:2208:A:N6	2.44	0.51
44:AG:91:PHE:O	44:AG:95:ASN:ND2	2.36	0.51
58:AV:81:GLN:HG2	58:AV:83:LYS:H	1.75	0.51
79:E:70:ASP:O	79:E:74:VAL:HG23	2.10	0.51
9:BL:2:SER:O	9:BL:52:SER:OG	2.18	0.51
29:Bc:13:ILE:HD11	29:Bc:31:GLU:HB3	1.92	0.51
34:B5:58:U:O2'	34:B5:451:A:N3	2.42	0.51
34:B5:1107:G:O2'	34:B5:1108:G:H5'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1579:U:H2'	34:B5:1580:C:C6	2.46	0.51
38:A1:959:C:O2	38:A1:2614:G:O2'	2.26	0.51
38:A1:1574:C:H2'	38:A1:1575:A:OP1	2.10	0.51
38:A1:1593:A:H2'	38:A1:1594:A:C8	2.46	0.51
38:A1:2508:U:OP2	38:A1:2508:U:H6	1.93	0.51
40:A4:52:A:N6	74:A1:27:ILE:HD13	2.26	0.51
41:AD:108:ARG:CZ	41:AD:253:PHE:HB2	2.41	0.51
52:AP:53:ASP:OD1	52:AP:55:GLN:HG2	2.11	0.51
54:AR:172:ARG:HD2	54:AR:176:ARG:HG3	1.93	0.51
63:Aa:89:GLN:NE2	63:Aa:89:GLN:O	2.43	0.51
2:BB:153:HIS:HE1	34:B5:1044:U:H5''	1.74	0.51
5:BG:140:ASN:ND2	34:B5:168:A:OP1	2.40	0.51
9:BL:14:GLN:HB3	9:BL:54:ILE:HG13	1.93	0.51
34:B5:1285:U:H4'	34:B5:1286:U:O5'	2.10	0.51
34:B5:1525:A:H2'	34:B5:1526:A:C8	2.46	0.51
35:AA:242:ARG:NH2	35:AA:243:THR:O	2.44	0.51
38:A1:2264:U:C2'	38:A1:2265:C:H5'	2.41	0.51
38:A1:2680:A:C2	47:AJ:57:PHE:HB3	2.46	0.51
46:AI:87:LEU:HD13	46:AI:138:VAL:HG22	1.93	0.51
23:BQ:97:VAL:HG12	23:BQ:98:ASP:H	1.76	0.51
34:B5:31:C:O2'	34:B5:547:U:OP1	2.26	0.51
34:B5:1359:C:H3'	34:B5:1360:A:C8	2.46	0.51
38:A1:1742:U:H2'	38:A1:1743:G:C8	2.46	0.51
44:AG:107:GLU:O	44:AG:110:THR:OG1	2.22	0.51
73:Ak:7:ASP:HB3	73:Ak:10:GLN:HG3	1.92	0.51
9:BL:53:TYR:CD2	9:BL:113:PRO:HG2	2.45	0.51
16:Ba:44:ILE:HG21	16:Ba:65:PRO:HG2	1.93	0.51
19:BD:172:THR:HG23	19:BD:185:LYS:HG2	1.93	0.51
34:B5:1628:U:H2'	34:B5:1629:G:C8	2.45	0.51
34:B5:1660:A:H2'	34:B5:1661:U:C6	2.45	0.51
37:AC:3:ARG:HB3	37:AC:22:LEU:H	1.76	0.51
38:A1:153:U:O2'	38:A1:154:U:H5'	2.10	0.51
40:A4:142:C:H2'	40:A4:143:U:C6	2.45	0.51
41:AD:95:TRP:HZ3	41:AD:198:TYR:C	2.18	0.51
42:AE:82:ARG:NH2	68:Af:106:ASN:OD1	2.44	0.51
48:AL:48:PRO:HA	48:AL:137:GLN:HB2	1.93	0.51
52:AP:67:ILE:HD12	52:AP:82:ARG:CZ	2.41	0.51
67:Ae:9:ILE:HG12	67:Ae:63:THR:HG23	1.93	0.51
14:BX:57:LEU:HD11	14:BX:73:ARG:HG2	1.92	0.51
20:BF:64:VAL:HG12	20:BF:65:ARG:N	2.25	0.51
26:BT:25:GLN:HG2	26:BT:27:LYS:HZ3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BT:39:THR:OG1	34:B5:1478:G:OP1	2.29	0.51
34:B5:544:A:OP2	34:B5:544:A:H8	1.94	0.51
34:B5:1407:U:H2'	34:B5:1408:G:O4'	2.11	0.51
35:AA:71:LEU:HD12	38:A1:1651:U:H5''	1.91	0.51
38:A1:1364:C:OP1	43:AF:110:ARG:NH2	2.38	0.51
38:A1:1760:A:H2'	38:A1:1761:C:O4'	2.11	0.51
46:AI:206:LEU:O	46:AI:210:ILE:HD12	2.11	0.51
80:EC:6847:G:O2'	80:EC:6848:U:OP1	2.27	0.51
5:BG:57:ASP:OD1	5:BG:61:PHE:N	2.44	0.51
37:AC:334:PHE:HA	37:AC:339:LEU:HD12	1.92	0.51
38:A1:164:A:H8	38:A1:164:A:C5'	2.19	0.51
38:A1:353:G:O2'	38:A1:364:G:O6	2.27	0.51
38:A1:631:U:H2'	38:A1:632:G:H8	1.75	0.51
38:A1:2506:U:C6	38:A1:2506:U:C3'	2.93	0.51
45:AH:41:ILE:HG22	45:AH:43:VAL:HG13	1.93	0.51
51:AO:18[A]:ARG:O	51:AO:22[A]:VAL:HG23	2.10	0.51
77:Ao:104:LEU:N	77:Ao:104:LEU:CD1	2.71	0.51
78:Ap:38:ASP:HA	78:Ap:45:LYS:HA	1.93	0.51
2:BB:180:THR:HG23	2:BB:183:GLN:HE21	1.75	0.50
3:BC:116:LYS:HG2	3:BC:127:ALA:HB3	1.93	0.50
11:BO:88:GLY:O	11:BO:92:LYS:NZ	2.40	0.50
23:BQ:14:LYS:O	23:BQ:123:ARG:NH2	2.44	0.50
32:Bf:99:LYS:H	32:Bf:99:LYS:HD2	1.76	0.50
34:B5:366:A:OP1	34:B5:758:U:O2'	2.19	0.50
34:B5:698:U:N3	34:B5:741:C:C4	2.79	0.50
38:A1:916:G:H5'	38:A1:917:A:OP1	2.10	0.50
38:A1:1084:A:H2'	38:A1:1085:A:C8	2.46	0.50
38:A1:1658:G:H2'	38:A1:1659:U:C6	2.46	0.50
40:A4:12:A:OP1	52:AP:3:ARG:NH2	2.30	0.50
40:A4:37:A:H5''	40:A4:39:G:O4'	2.11	0.50
47:AJ:17:LEU:HD11	47:AJ:127:PHE:HD1	1.76	0.50
72:Aj:14:LYS:HZ1	74:Al:51:ILE:HD11	1.76	0.50
3:BC:230:TRP:CD2	13:BW:68:ARG:HD2	2.46	0.50
21:BK:53:GLY:O	21:BK:55:VAL:N	2.44	0.50
22:BP:108:ARG:H	22:BP:111:MET:HE3	1.76	0.50
23:BQ:99:GLU:HB3	31:Bg:57:PRO:O	2.11	0.50
34:B5:226:A:H61	34:B5:838:G:N2	2.10	0.50
34:B5:250:C:H2'	34:B5:251:A:H8	1.76	0.50
34:B5:1297:G:N2	34:B5:1300:A:OP2	2.33	0.50
36:AB:323:MET:HE1	36:AB:359:ILE:HD13	1.92	0.50
38:A1:737:G:H2'	38:A1:738:A:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1472:U:H5''	54:AR:24:LEU:HD12	1.93	0.50
38:A1:2438:A:H2'	38:A1:2439:A:H8	1.76	0.50
38:A1:2655:U:H4'	38:A1:2656:A:O4'	2.11	0.50
38:A1:3006:A:H2'	38:A1:3007:U:O4'	2.11	0.50
38:A1:3072:C:H2'	38:A1:3073:A:O4'	2.11	0.50
46:AI:12:GLN:NE2	46:AI:129:VAL:O	2.44	0.50
15:BY:60:PHE:H	15:BY:71:GLY:HA2	1.76	0.50
22:BP:83:MET:HE2	22:BP:89:MET:HE1	1.93	0.50
31:Bg:123:ILE:HD11	31:Bg:183:LEU:HD21	1.92	0.50
34:B5:1417:A:H2'	34:B5:1418:G:O4'	2.10	0.50
34:B5:1552:U:H2'	34:B5:1553:G:O4'	2.11	0.50
38:A1:500:C:P	68:Af:48:ARG:NH2	2.84	0.50
38:A1:640:U:H2'	38:A1:641:C:C6	2.47	0.50
38:A1:1621:A:H2'	38:A1:1622:U:H6	1.77	0.50
38:A1:1807:G:O2'	38:A1:2559:U:O4	2.28	0.50
38:A1:2723:U:H2'	38:A1:2724:OMU:H6	1.94	0.50
41:AD:232:ASP:OD1	41:AD:233:ALA:N	2.44	0.50
45:AH:80:THR:HG23	45:AH:84:LYS:HE2	1.92	0.50
49:AM:50:LYS:HG3	49:AM:85:TRP:CD1	2.45	0.50
51:AO:22[A]:VAL:HG21	51:AO:120[A]:VAL:HG11	1.93	0.50
53:AQ:170:ARG:NH1	63:Aa:56:VAL:HG23	2.23	0.50
62:AZ:9:LYS:HB3	62:AZ:25:ILE:HD12	1.92	0.50
6:BH:63:PRO:HB2	6:BH:65:PRO:HD3	1.92	0.50
8:BJ:173:ALA:HB2	34:B5:511:A:H5'	1.93	0.50
21:BK:3:MET:HE3	21:BK:41:TYR:HB3	1.92	0.50
22:BP:64:LYS:HD2	22:BP:92:SER:HB3	1.93	0.50
25:BS:14:ILE:HG22	25:BS:23:ASP:HA	1.93	0.50
31:Bg:93:ASP:HB2	31:Bg:100:TYR:CZ	2.46	0.50
31:Bg:267:PRO:HG2	31:Bg:269:TYR:CD1	2.46	0.50
34:B5:239:C:N4	34:B5:835:U:H5''	2.27	0.50
34:B5:953:G:H2'	34:B5:954:G:C8	2.47	0.50
34:B5:1776:A:H2'	34:B5:1777:G:C8	2.47	0.50
35:AA:65:ASP:OD2	35:AA:72:ARG:HD3	2.12	0.50
35:AA:117:GLU:HG2	35:AA:124:GLY:H	1.77	0.50
38:A1:191:U:H2'	38:A1:192:C:C6	2.47	0.50
38:A1:671:U:H2'	38:A1:672:A:H8	1.77	0.50
38:A1:733:G:N2	38:A1:736:A:OP2	2.42	0.50
38:A1:963:G:O2'	63:Aa:29:PRO:O	2.29	0.50
38:A1:1601:U:OP1	54:AR:42:ARG:NH2	2.42	0.50
38:A1:1615:C:H2'	38:A1:1616:U:H6	1.75	0.50
38:A1:2180:G:H2'	38:A1:2181:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2676:A:H5'	38:A1:2677:G:C8	2.47	0.50
48:AL:59:ARG:HD2	48:AL:69:VAL:HG12	1.94	0.50
49:AM:135:LEU:HD21	51:AO:178[A]:VAL:HA	1.94	0.50
52:AP:4:TYR:CE1	52:AP:18:ARG:HD2	2.44	0.50
61:AY:74:TYR:CE2	61:AY:77:LYS:HG2	2.46	0.50
78:Ap:84:ARG:NH1	78:Ap:88:GLU:HG3	2.25	0.50
79:E:66:CYS:HB3	79:E:110:PHE:CD2	2.47	0.50
2:BB:113:MET:HG2	2:BB:142:PHE:CE1	2.46	0.50
8:BJ:154:LYS:HG3	8:BJ:155:HIS:CD2	2.46	0.50
10:BN:96:VAL:HG13	10:BN:100:LYS:NZ	2.27	0.50
19:BD:40:ARG:NE	19:BD:47:GLU:OE2	2.39	0.50
20:BF:48:PHE:HD2	20:BF:64:VAL:HG13	1.76	0.50
38:A1:1721:U:O2'	38:A1:1723:A:N7	2.44	0.50
38:A1:2141:U:H5'	38:A1:2977:G:H4'	1.94	0.50
40:A4:78:G:H2'	40:A4:79:A:C8	2.47	0.50
44:AG:162:LEU:HA	50:AN:7:LEU:HD21	1.93	0.50
64:Ab:14:ARG:N	64:Ab:14:ARG:HD2	2.26	0.50
66:Ad:36:ILE:HD12	66:Ad:59:ILE:HD11	1.92	0.50
72:Aj:25:ARG:HD3	74:Al:50:ASN:O	2.12	0.50
73:Ak:60:GLY:O	73:Ak:63:LYS:HG2	2.11	0.50
4:BE:246:LEU:HB3	4:BE:250:GLU:HG3	1.94	0.50
24:BR:23:LYS:HB3	24:BR:34:LEU:HD11	1.93	0.50
38:A1:1061:A:H1'	56:AT:101:CYS:SG	2.52	0.50
38:A1:1565:G:H1	38:A1:1574:C:N4	2.09	0.50
38:A1:2550:U:C1'	44:AG:38:GLN:NE2	2.74	0.50
38:A1:2674:A:C6	47:AJ:124:GLY:HA3	2.47	0.50
40:A4:67:U:H5''	72:Aj:85:LYS:O	2.11	0.50
47:AJ:62:ASN:O	77:Ao:103:ALA:HA	2.12	0.50
7:BI:57:ALA:HB2	7:BI:177:GLY:HA2	1.94	0.50
23:BQ:39:VAL:O	23:BQ:45:ARG:NE	2.41	0.50
23:BQ:69:VAL:HG11	23:BQ:81:ILE:HD11	1.94	0.50
34:B5:1409:G:N1	34:B5:1412:G:OP2	2.45	0.50
37:AC:11:LEU:HD13	37:AC:159:ILE:HD11	1.93	0.50
38:A1:818:C:H2'	38:A1:819:U:O4'	2.12	0.50
38:A1:1899:G:O2'	38:A1:2334:U:O4	2.27	0.50
38:A1:1935:G:H2'	38:A1:1936:A:H8	1.77	0.50
38:A1:2484:A:H8	38:A1:2485:A:C8	2.30	0.50
44:AG:81:THR:HG21	44:AG:181:LYS:HB2	1.94	0.50
71:Ai:52:PRO:CG	71:Ai:55:ARG:HH21	2.24	0.50
3:BC:222:TYR:HE1	12:BV:10:GLU:OE2	1.95	0.50
7:BI:33:PRO:HA	34:B5:331:A:H5'	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:109:LEU:HB2	8:BJ:146:PHE:HB3	1.94	0.50
15:BY:62:THR:HA	15:BY:69:SER:HA	1.93	0.50
36:AB:147:GLU:O	36:AB:151:ILE:HG13	2.12	0.50
38:A1:248:U:H1'	38:A1:250:U:C5	2.47	0.50
38:A1:2213:A:H2'	38:A1:2214:A:H8	1.73	0.50
38:A1:2459:A:N6	38:A1:2487:U:H1'	2.27	0.50
57:AU:50:LEU:HD22	57:AU:54:VAL:CG1	2.42	0.50
77:Ao:53:GLN:HE21	77:Ao:55:LYS:H	1.60	0.50
1:BA:90:ALA:HB2	1:BA:97:PRO:HB3	1.92	0.50
2:BB:30:PHE:HE2	2:BB:93:GLY:O	1.94	0.50
5:BG:14:LYS:HG2	5:BG:124:LEU:HG	1.94	0.50
7:BI:104:ILE:HG13	7:BI:105:ASP:N	2.24	0.50
10:BN:38:VAL:O	10:BN:42:ARG:HG2	2.12	0.50
26:BT:31:PRO:HB3	26:BT:103:LYS:HD3	1.93	0.50
27:BU:77:LYS:NZ	34:B5:1195:C:OP1	2.32	0.50
31:Bg:157:VAL:HG22	31:Bg:168:THR:O	2.12	0.50
34:B5:179:A:H2'	34:B5:180:A:O4'	2.12	0.50
34:B5:1691:A:H2'	34:B5:1692:G:C8	2.46	0.50
38:A1:373:A:N1	38:A1:394:G:H4'	2.27	0.50
38:A1:394:G:N1	38:A1:397:A:OP2	2.42	0.50
38:A1:1553:U:H4'	38:A1:1554:U:H5'	1.93	0.50
38:A1:2407:C:H2'	38:A1:2408:U:C6	2.47	0.50
38:A1:2740:A:H2'	38:A1:2741:C:O4'	2.11	0.50
47:AJ:93:ASP:HB3	47:AJ:172:LEU:HD12	1.94	0.50
53:AQ:147:ARG:HB3	53:AQ:150:VAL:HG23	1.92	0.50
55:AS:77:VAL:HG13	55:AS:126:VAL:HG22	1.93	0.50
2:BB:68:VAL:HG13	2:BB:73:LEU:HD23	1.93	0.49
6:BH:12:ALA:HB3	6:BH:13:PRO:HD3	1.94	0.49
12:BV:32:VAL:HG22	12:BV:60:ARG:HD2	1.93	0.49
15:BY:35:VAL:HG23	15:BY:36:SER:N	2.26	0.49
31:Bg:112:SER:HB2	31:Bg:153:GLN:HA	1.94	0.49
34:B5:220:A:H62	34:B5:831:U:H3	1.58	0.49
34:B5:1082:C:H5'	34:B5:1083:G:OP2	2.11	0.49
34:B5:1132:A:H2'	34:B5:1133:A:C8	2.47	0.49
34:B5:1622:G:H2'	34:B5:1623:C:H6	1.77	0.49
34:B5:1687:U:H3	34:B5:1715:G:H1	1.59	0.49
39:A3:26:C:H2'	39:A3:27:A:O4'	2.12	0.49
50:AN:66:VAL:HG21	50:AN:98:LEU:HB3	1.93	0.49
54:AR:43:LYS:HD2	54:AR:44:LEU:HD23	1.92	0.49
57:AU:19:VAL:HG12	57:AU:105:LEU:HD13	1.94	0.49
2:BB:62:LYS:HD3	2:BB:90:GLU:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:31:SER:H	13:BW:34:ILE:HD12	1.75	0.49
29:Bc:30:VAL:HG11	29:Bc:54:LEU:HD11	1.94	0.49
34:B5:239:C:HO2'	34:B5:240:U:H6	1.60	0.49
34:B5:386:G:H2'	34:B5:387:A:C8	2.47	0.49
34:B5:604:A:H2'	34:B5:605:A:O4'	2.12	0.49
34:B5:652:G:H4'	34:B5:653:C:O4'	2.11	0.49
34:B5:1291:G:H2'	34:B5:1292:G:H8	1.76	0.49
34:B5:1391:A:H2'	34:B5:1392:U:H6	1.77	0.49
34:B5:1483:A:H2'	34:B5:1484:G:C8	2.47	0.49
35:AA:2:GLY:C	38:A1:925:A:H61	2.20	0.49
36:AB:63:PRO:HD2	36:AB:348:ARG:HH21	1.76	0.49
37:AC:34:ILE:HD11	38:A1:673:U:O3'	2.11	0.49
38:A1:396:A:O2'	38:A1:399:A:OP1	2.28	0.49
38:A1:2881:C:H2'	38:A1:2882:U:C6	2.48	0.49
41:AD:95:TRP:CZ3	41:AD:198:TYR:C	2.91	0.49
43:AF:48:ASN:ND2	43:AF:182:ASP:OD2	2.45	0.49
44:AG:195:SER:OG	44:AG:197:VAL:O	2.29	0.49
4:BE:62:LYS:HD2	4:BE:66:MET:HG2	1.94	0.49
19:BD:36:GLY:HA3	19:BD:51:ARG:NH2	2.27	0.49
19:BD:76:ARG:O	19:BD:76:ARG:NH1	2.41	0.49
34:B5:884:A:H2'	34:B5:885:G:C8	2.47	0.49
35:AA:2:GLY:HA3	38:A1:2415:C:OP1	2.12	0.49
38:A1:241:G:C8	38:A1:241:G:H3'	2.48	0.49
38:A1:761:A:C2	38:A1:771:A:H1'	2.47	0.49
38:A1:2129:U:H2'	38:A1:2130:G:C8	2.46	0.49
38:A1:2696:A:H2'	38:A1:2697:A:C8	2.47	0.49
7:BI:47:ARG:HH12	34:B5:398:G:P	2.36	0.49
8:BJ:53:ARG:HG3	8:BJ:97:LEU:HD22	1.93	0.49
11:BO:36:LYS:NZ	34:B5:894:U:H4'	2.28	0.49
15:BY:10:ARG:HG2	34:B5:780:A:N7	2.28	0.49
28:BZ:74:SER:OG	34:B5:1534:G:OP2	2.21	0.49
34:B5:447:U:H2'	34:B5:448:C:O4'	2.11	0.49
34:B5:1609:U:H2'	34:B5:1610:G:O4'	2.12	0.49
38:A1:26:A:H2'	38:A1:27:C:H6	1.76	0.49
38:A1:996:A:H2'	38:A1:997:A:O4'	2.12	0.49
38:A1:1337:A:H2'	38:A1:1338:C:C6	2.47	0.49
38:A1:1351:U:O4	38:A1:1353:U:O2'	2.30	0.49
38:A1:1671:C:OP1	54:AR:60:LYS:NZ	2.44	0.49
38:A1:2676:A:N1	47:AJ:22:SER:OG	2.42	0.49
38:A1:2683:U:H2'	38:A1:2684:C:C6	2.47	0.49
38:A1:3000:A:H2'	38:A1:3001:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3358:U:H2'	38:A1:3359:A:H8	1.76	0.49
41:AD:260:PHE:HA	41:AD:264:GLN:NE2	2.27	0.49
45:AH:186:PHE:HB2	45:AH:189:GLU:HB2	1.94	0.49
48:AL:168:ARG:HE	48:AL:172:LEU:HG	1.76	0.49
79:E:19:TYR:HE2	79:E:211:GLY:HA2	1.76	0.49
79:E:49:PHE:CD1	79:E:51:GLY:N	2.81	0.49
80:EC:6852:U:H2'	80:EC:6853:G:C4	2.47	0.49
2:BB:26:ARG:NH2	34:B5:896:U:OP1	2.44	0.49
3:BC:138:PRO:HB2	12:BV:11:LEU:HD23	1.94	0.49
22:BP:85:ILE:HA	22:BP:89:MET:CE	2.43	0.49
28:BZ:86:GLU:OE1	28:BZ:86:GLU:N	2.40	0.49
34:B5:962:C:H2'	34:B5:963:A:O4'	2.13	0.49
38:A1:121:A:C2	44:AG:129:PRO:HG3	2.47	0.49
38:A1:1194:G:H2'	38:A1:1195:A:C8	2.48	0.49
38:A1:1627:U:H1'	38:A1:1817:G:O6	2.13	0.49
38:A1:2160:G:H2'	38:A1:2161:G:H8	1.77	0.49
62:AZ:103:GLN:HB2	62:AZ:106:GLN:HE22	1.77	0.49
76:An:13:LEU:HA	76:An:16:LYS:HE3	1.95	0.49
34:B5:1220:C:H2'	34:B5:1221:A:C8	2.47	0.49
34:B5:1226:A:H1'	34:B5:1227:A:H5''	1.95	0.49
34:B5:1496:U:H4'	34:B5:1519:U:O2'	2.12	0.49
34:B5:1594:G:OP2	34:B5:1596:C:N4	2.46	0.49
38:A1:177:U:H3	38:A1:239:G:H22	1.59	0.49
38:A1:1129:A:OP1	46:AI:13:LYS:NZ	2.30	0.49
38:A1:1636:U:O2	38:A1:1710:C:H4'	2.12	0.49
38:A1:2413:A:H2'	38:A1:2414:G:H8	1.78	0.49
53:AQ:63:SER:OG	53:AQ:90:ASP:HB2	2.12	0.49
77:Ao:10:THR:HA	77:Ao:20:HIS:CD2	2.46	0.49
79:E:35:GLN:HB3	79:E:205:VAL:HB	1.94	0.49
1:BA:98:ILE:HD11	1:BA:116:LYS:HD2	1.94	0.49
4:BE:182:TYR:HD1	4:BE:192:ILE:HG12	1.77	0.49
6:BH:80:GLU:C	6:BH:84:LYS:HZ2	2.20	0.49
8:BJ:89:ASP:O	8:BJ:90:LYS:HG2	2.13	0.49
12:BV:73:ALA:HB1	12:BV:78:LEU:HB2	1.93	0.49
20:BF:63:GLN:HE22	20:BF:66:GLN:HB2	1.78	0.49
34:B5:585:A:H2'	34:B5:586:G:H8	1.77	0.49
34:B5:610:G:H2'	34:B5:610:G:N3	2.28	0.49
34:B5:1642:G:H5'	76:An:1:MET:HB2	1.94	0.49
38:A1:215:G:H5''	61:AY:12:ARG:HG3	1.94	0.49
38:A1:244:G:H2'	38:A1:244:G:N3	2.28	0.49
38:A1:664:U:H2'	38:A1:665:A:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:9:A:H2'	40:A4:10:A:H8	1.77	0.49
42:AE:90:LYS:NZ	42:AE:92:SER:HA	2.28	0.49
2:BB:98:THR:O	2:BB:232:HIS:NE2	2.35	0.49
2:BB:157:GLN:C	2:BB:159:SER:H	2.21	0.49
31:Bg:131:ILE:HG12	31:Bg:154:VAL:HG11	1.94	0.49
31:Bg:283:LYS:N	34:B5:1394:G:OP1	2.45	0.49
34:B5:1511:U:H2'	34:B5:1512:G:C8	2.47	0.49
34:B5:1753:A:H2'	34:B5:1754:A:O4'	2.12	0.49
35:AA:138:GLY:HA3	35:AA:147:ARG:CZ	2.43	0.49
38:A1:98:G:N7	48:AL:13:HIS:NE2	2.57	0.49
38:A1:541:U:H3	38:A1:550:A:N6	2.08	0.49
38:A1:947:G:H5''	67:Ae:55:ILE:HB	1.95	0.49
38:A1:1597:C:H2'	38:A1:1598:G:H8	1.77	0.49
38:A1:1688:U:H2'	38:A1:1689:U:C6	2.47	0.49
38:A1:2258:U:O2'	38:A1:2259:A:O5'	2.30	0.49
38:A1:2289:U:H2'	38:A1:2290:C:C6	2.47	0.49
38:A1:3322:A:H2'	38:A1:3323:A:C8	2.47	0.49
55:AS:152:LEU:HB2	55:AS:172:TYR:CE2	2.47	0.49
79:E:76:ARG:NH2	79:E:143:ASP:HA	2.27	0.49
2:BB:86:LEU:HB3	2:BB:98:THR:HB	1.95	0.49
6:BH:161:GLN:OE1	6:BH:161:GLN:N	2.45	0.49
7:BI:107:THR:HB	7:BI:108:PRO:HD3	1.95	0.49
12:BV:36:VAL:HG11	12:BV:78:LEU:HD13	1.95	0.49
25:BS:87:ASN:ND2	25:BS:100:THR:O	2.45	0.49
34:B5:222:A:OP2	34:B5:236:A:N6	2.46	0.49
34:B5:1087:A:H2'	34:B5:1088:A:C8	2.47	0.49
34:B5:1498:G:H2'	34:B5:1499:G:H8	1.78	0.49
34:B5:1787:C:H2'	34:B5:1788:G:C8	2.48	0.49
38:A1:241:G:C8	38:A1:241:G:O5'	2.65	0.49
51:AO:29[A]:ASN:O	68:Af:12:LYS:NZ	2.33	0.49
70:Ah:31:LEU:HB3	70:Ah:44:ILE:HD13	1.95	0.49
80:EC:6875:C:H2'	80:EC:6876:A:C8	2.48	0.49
5:BG:41:VAL:HG21	5:BG:50:PHE:HD2	1.77	0.49
6:BH:17:GLU:HA	6:BH:20:VAL:HG12	1.93	0.49
16:Ba:95:ARG:HG2	34:B5:1797:A:H5'	1.93	0.49
27:BU:100:VAL:O	27:BU:104:THR:OG1	2.18	0.49
28:BZ:49:ARG:HG2	28:BZ:69:LEU:HD11	1.94	0.49
28:BZ:52:LYS:NZ	28:BZ:53:GLU:OE2	2.46	0.49
30:Bd:36:LEU:HD12	30:Bd:38:ILE:HD12	1.95	0.49
34:B5:1528:U:H2'	34:B5:1529:C:C6	2.47	0.49
34:B5:1760:G:OP1	80:EC:6946:A:N6	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:209:HIS:HE1	35:AA:211:HIS:CD2	2.31	0.49
36:AB:219:ALA:HB2	36:AB:336:VAL:HG23	1.93	0.49
38:A1:1392:G:H1'	38:A1:1418:A:N6	2.28	0.49
38:A1:1630:U:H3	38:A1:1817:G:N2	2.10	0.49
38:A1:2456:A:H2'	38:A1:2457:G:C8	2.47	0.49
38:A1:2787:G:O3'	63:Aa:57:GLY:HA2	2.12	0.49
41:AD:198:TYR:CE1	41:AD:203:HIS:HB3	2.47	0.49
52:AP:122:ALA:HB3	52:AP:143:PRO:HB2	1.94	0.49
53:AQ:79:LYS:HA	53:AQ:136:ASN:ND2	2.28	0.49
55:AS:96:ASP:CG	55:AS:97:VAL:H	2.21	0.49
58:AV:23:MET:HE1	58:AV:78:VAL:HG22	1.95	0.49
60:AX:131:ASP:OD1	60:AX:132:ALA:N	2.46	0.49
69:Ag:8:ARG:HB2	69:Ag:34:HIS:CD2	2.47	0.49
2:BB:70:LEU:HD23	2:BB:79:HIS:CG	2.48	0.48
27:BU:53:LYS:HB3	27:BU:92:ASP:HB2	1.94	0.48
31:Bg:270:LEU:HD21	31:Bg:273:ASP:HB2	1.95	0.48
34:B5:58:U:OP1	34:B5:456:A:O2'	2.25	0.48
34:B5:821:U:C4	34:B5:852:C:N3	2.81	0.48
38:A1:109:A:N1	38:A1:322:U:O2'	2.36	0.48
38:A1:528:U:H2'	38:A1:529:A:H8	1.77	0.48
38:A1:1362:G:H2'	38:A1:1363:A:C8	2.48	0.48
38:A1:1642:A:N3	38:A1:1822:C:O2'	2.43	0.48
38:A1:2357:A:H2'	38:A1:2358:A:H8	1.78	0.48
38:A1:2495:C:H2'	38:A1:2496:C:C6	2.48	0.48
38:A1:3332:U:H2'	38:A1:3333:G:O4'	2.13	0.48
39:A3:90:U:H2'	39:A3:91:G:O4'	2.13	0.48
39:A3:113:C:H2'	39:A3:114:U:O4'	2.12	0.48
41:AD:194:LEU:HD11	41:AD:198:TYR:CZ	2.48	0.48
41:AD:293:LEU:HD11	46:AI:210:ILE:HG21	1.95	0.48
44:AG:121:SER:OG	44:AG:122:LYS:N	2.45	0.48
55:AS:81:TYR:CE1	55:AS:88:HIS:HB2	2.47	0.48
58:AV:33:ASN:OD1	58:AV:64:LYS:N	2.43	0.48
71:Ai:50:LEU:HB2	71:Ai:55:ARG:CD	2.42	0.48
80:EC:6948:U:H2'	80:EC:6949:G:H5''	1.95	0.48
2:BB:26:ARG:HG2	2:BB:50:LYS:HE2	1.95	0.48
9:BL:124:THR:HB	9:BL:141:LYS:HB3	1.94	0.48
12:BV:41:GLU:O	12:BV:42:GLU:HG3	2.13	0.48
26:BT:127:ASN:HA	26:BT:130:ARG:CG	2.31	0.48
33:BM:83:GLU:O	33:BM:83:GLU:HG2	2.13	0.48
34:B5:143:G:H2'	34:B5:144:U:C6	2.47	0.48
34:B5:919:A:H2'	34:B5:920:U:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1039:A:O2'	34:B5:1040:G:H8	1.96	0.48
34:B5:1649:G:H2'	34:B5:1650:U:C6	2.48	0.48
38:A1:101:G:OP2	38:A1:101:G:N2	2.44	0.48
38:A1:422:A:C2	38:A1:2363:A:H4'	2.49	0.48
38:A1:616:G:H2'	38:A1:617:G:H8	1.79	0.48
45:AH:67:ALA:O	45:AH:71:VAL:HG23	2.14	0.48
45:AH:147:SER:HB3	45:AH:187:ILE:HD11	1.95	0.48
62:AZ:26:VAL:HG12	62:AZ:27:LYS:HG3	1.94	0.48
65:Ac:16:LEU:O	65:Ac:20:SER:OG	2.25	0.48
65:Ac:103:THR:HG22	65:Ac:105:ALA:H	1.78	0.48
67:Ae:96:ILE:HG21	67:Ae:105:ARG:HG2	1.93	0.48
25:BS:143:ARG:NH2	34:B5:1462:G:N7	2.55	0.48
27:BU:35:GLU:OE2	27:BU:89:ARG:NH2	2.47	0.48
34:B5:220:A:N6	34:B5:831:U:H3	2.10	0.48
34:B5:1031:U:H4'	34:B5:1032:G:OP2	2.14	0.48
34:B5:1291:G:H2'	34:B5:1292:G:C8	2.48	0.48
34:B5:1701:A:H2'	34:B5:1702:A:C8	2.48	0.48
36:AB:66:LYS:NZ	58:AV:9:THR:OG1	2.40	0.48
38:A1:240:U:O2'	38:A1:241:G:C5	2.67	0.48
38:A1:1737:U:O2	69:Ag:52:GLN:NE2	2.47	0.48
38:A1:2252:A:H61	38:A1:2265:C:N4	2.11	0.48
38:A1:2376:G:H2'	38:A1:2377:G:C8	2.48	0.48
38:A1:2958:A:H2'	38:A1:2959:OMC:H6	1.77	0.48
54:AR:68:GLN:OE1	54:AR:71:ARG:NH2	2.46	0.48
63:Aa:76:ASP:OD1	63:Aa:77:LYS:HG2	2.12	0.48
71:Ai:89:GLU:O	71:Ai:93:ILE:HD12	2.14	0.48
2:BB:195:LYS:NZ	2:BB:198:GLU:OE1	2.45	0.48
4:BE:67:GLN:OE1	4:BE:69:HIS:NE2	2.46	0.48
23:BQ:73:GLY:H	23:BQ:76:SER:HG	1.58	0.48
24:BR:56:HIS:NE2	34:B5:1401:A:OP1	2.27	0.48
26:BT:44:GLU:OE2	26:BT:45:MET:HG2	2.13	0.48
34:B5:1211:A:H2'	34:B5:1212:G:O4'	2.13	0.48
35:AA:2:GLY:N	38:A1:2608:G:OP1	2.46	0.48
36:AB:93:VAL:HG12	36:AB:155:ALA:H	1.77	0.48
38:A1:155:G:H5''	38:A1:156:G:H2'	1.95	0.48
38:A1:716:A:C5	63:Aa:117:ARG:HG3	2.49	0.48
38:A1:1002:A:N1	38:A1:1050:U:O2'	2.44	0.48
38:A1:1119:C:H2'	38:A1:1120:A:C8	2.48	0.48
38:A1:1688:U:C2	38:A1:1689:U:C5	3.01	0.48
38:A1:2747:A:H2'	38:A1:2748:A:C8	2.48	0.48
66:Ad:6:ASP:O	66:Ad:77:ARG:NE	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Ae:32:TRP:CH2	67:Ae:52:GLN:HG2	2.48	0.48
79:E:112:ALA:O	79:E:138:VAL:N	2.45	0.48
79:E:191:VAL:HG11	79:E:198:TRP:CD2	2.49	0.48
1:BA:204:TYR:OH	1:BA:206:ASP:OD1	2.30	0.48
3:BC:200:SER:HB3	3:BC:204:THR:HG21	1.95	0.48
6:BH:150:GLN:O	6:BH:181:ILE:HA	2.14	0.48
7:BI:7:SER:O	7:BI:18:ARG:NH2	2.46	0.48
11:BO:124:ASP:OD1	34:B5:928:U:H4'	2.14	0.48
21:BK:1:MET:N	34:B5:1217:A:OP1	2.35	0.48
34:B5:1449:U:H2'	34:B5:1450:U:C6	2.47	0.48
34:B5:1585:U:N3	34:B5:1611:A:H2	1.89	0.48
34:B5:1738:U:H2'	34:B5:1739:C:C6	2.48	0.48
36:AB:148:LEU:HD11	36:AB:196:ARG:HD3	1.95	0.48
38:A1:500:C:OP1	68:Af:48:ARG:NH2	2.37	0.48
38:A1:1037:C:H2'	38:A1:1038:C:C6	2.49	0.48
38:A1:1184:A:H2'	38:A1:1185:C:C6	2.48	0.48
38:A1:2836:C:H5	38:A1:2852:C:H42	1.60	0.48
38:A1:2843:U:H5''	38:A1:2844:C:H5	1.79	0.48
39:A3:42:A:HO2'	47:AJ:140:ARG:HE	1.60	0.48
46:AI:36:LEU:HD11	46:AI:69:ARG:HD2	1.93	0.48
53:AQ:170:ARG:NH2	53:AQ:171:LYS:HD2	2.28	0.48
1:BA:71:GLU:O	1:BA:96:THR:OG1	2.30	0.48
1:BA:180:GLU:CD	1:BA:191:ARG:HH12	2.22	0.48
3:BC:188:LEU:HD13	3:BC:196:VAL:HG11	1.94	0.48
4:BE:254:ARG:NH2	34:B5:787:G:OP1	2.40	0.48
19:BD:157:LEU:HD23	19:BD:189:MET:HB2	1.94	0.48
19:BD:196:ARG:HA	19:BD:200:LYS:NZ	2.28	0.48
19:BD:223:LYS:HG2	31:Bg:191:ASP:HB2	1.96	0.48
24:BR:70:SER:HA	24:BR:74:GLN:NE2	2.27	0.48
25:BS:53:ASP:HB3	25:BS:56:LYS:HG2	1.95	0.48
31:Bg:216:LYS:HA	31:Bg:239:GLU:OE1	2.14	0.48
34:B5:1370:U:H3	34:B5:1374:C:H41	1.61	0.48
38:A1:955:U:H2'	38:A1:956:U:C6	2.48	0.48
38:A1:1354:G:O2'	38:A1:1355:A:OP1	2.30	0.48
38:A1:2552:C:C2	65:Ac:53:LYS:NZ	2.82	0.48
38:A1:2916:U:H5	38:A1:2935:U:HO2'	1.59	0.48
38:A1:3249:C:H2'	38:A1:3250:U:O4'	2.14	0.48
45:AH:49:ASN:C	45:AH:51:GLN:H	2.20	0.48
45:AH:91:ARG:NH2	45:AH:141:LYS:O	2.46	0.48
46:AI:44:ASP:OD1	46:AI:181:TYR:OH	2.29	0.48
1:BA:76:ILE:HD13	1:BA:98:ILE:HB	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:20:VAL:HG11	6:BH:46:ILE:HD13	1.95	0.48
11:BO:126:THR:HG21	34:B5:888:U:H1'	1.95	0.48
22:BP:80:MET:HG2	22:BP:83:MET:HB2	1.96	0.48
32:Bf:93:HIS:NE2	34:B5:1247:U:OP1	2.47	0.48
36:AB:128:LYS:HG3	38:A1:3294:A:H5'	1.95	0.48
38:A1:1696:A:H2'	38:A1:1697:A:H8	1.77	0.48
38:A1:2416:U:H2'	38:A1:2417:OMU:H6	1.96	0.48
38:A1:2675:C:H3'	38:A1:2676:A:H2'	1.95	0.48
41:AD:60:ILE:HB	41:AD:80:SER:HB2	1.96	0.48
42:AE:14:ASP:OD1	42:AE:15:VAL:N	2.46	0.48
46:AI:135:ILE:HG22	46:AI:136:PHE:CD1	2.48	0.48
80:EC:6862:G:H2'	80:EC:6864:A:N7	2.29	0.48
2:BB:153:HIS:HB2	2:BB:155:TYR:CE2	2.49	0.48
21:BK:14:TYR:OH	21:BK:34:GLU:OE2	2.31	0.48
26:BT:14:PHE:HZ	26:BT:132:LEU:HG	1.79	0.48
34:B5:902:G:O2'	34:B5:1008:G:H4'	2.13	0.48
34:B5:1357:A:O2'	34:B5:1358:G:H5'	2.14	0.48
34:B5:1469:A:H2'	34:B5:1470:C:C6	2.48	0.48
34:B5:1600:A:H1'	34:B5:1601:G:H5''	1.96	0.48
38:A1:240:U:C2	38:A1:241:G:C2	3.02	0.48
38:A1:1812:G:C2'	38:A1:1817:G:H21	2.25	0.48
38:A1:2186:U:H5'	38:A1:2314:U:OP2	2.14	0.48
38:A1:2282:U:O2	38:A1:2310:U:H4'	2.13	0.48
42:AE:87:THR:HG22	42:AE:89:THR:H	1.79	0.48
45:AH:21:LYS:HB3	45:AH:24:ILE:HB	1.95	0.48
48:AL:80:VAL:HG12	48:AL:85:LEU:O	2.13	0.48
49:AM:132:LYS:HA	49:AM:135:LEU:HD12	1.95	0.48
50:AN:8:GLU:HB2	50:AN:50:ARG:NH2	2.28	0.48
51:AO:65[A]:ASN:HB3	51:AO:68[A]:ARG:HG2	1.96	0.48
55:AS:27:MET:HE1	55:AS:44:PHE:CB	2.44	0.48
62:AZ:50:PRO:HD3	62:AZ:68:ILE:HG12	1.95	0.48
62:AZ:106:GLN:HA	62:AZ:109:GLU:HG3	1.95	0.48
73:Ak:60:GLY:HA2	73:Ak:63:LYS:NZ	2.29	0.48
79:E:113:SER:HA	79:E:138:VAL:H	1.79	0.48
4:BE:103:TYR:O	4:BE:182:TYR:OH	2.29	0.48
20:BF:186:ASN:HD21	20:BF:188:LYS:HB2	1.78	0.48
34:B5:183:U:H2'	34:B5:184:C:H6	1.79	0.48
34:B5:1132:A:H2'	34:B5:1133:A:H8	1.77	0.48
34:B5:1361:U:O2'	34:B5:1362:U:O5'	2.31	0.48
34:B5:1461:C:H2'	34:B5:1462:G:H8	1.79	0.48
34:B5:1734:U:H2'	34:B5:1735:U:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1787:A:H2'	38:A1:1788:C:O4'	2.13	0.48
38:A1:2947:G:OP2	38:A1:2947:G:H4'	2.14	0.48
38:A1:3047:U:O2'	38:A1:3048:A:H5'	2.14	0.48
38:A1:3095:U:H2'	38:A1:3096:C:C6	2.48	0.48
39:A3:112:G:H2'	39:A3:113:C:C6	2.49	0.48
46:AI:19:LYS:HD2	46:AI:26:VAL:HB	1.96	0.48
49:AM:32:LEU:HB3	49:AM:85:TRP:HH2	1.79	0.48
58:AV:89:ASP:OD1	58:AV:91:VAL:HG12	2.13	0.48
79:E:60:ARG:C	79:E:63:MET:SD	2.96	0.48
5:BG:186:ARG:NH2	34:B5:269:G:N7	2.62	0.48
8:BJ:114:TYR:HA	8:BJ:119:ALA:HB3	1.96	0.48
10:BN:19:SER:OG	10:BN:21:ASN:O	2.31	0.48
10:BN:102:LEU:HD11	10:BN:112:LYS:HA	1.95	0.48
19:BD:132:LYS:HG3	19:BD:156:PHE:HB3	1.95	0.48
24:BR:95:ARG:HH12	24:BR:120:SER:CB	2.27	0.48
30:Bd:5:ASN:OD1	30:Bd:8:PHE:HB2	2.14	0.48
34:B5:162:A:H2'	34:B5:163:G:N3	2.29	0.48
34:B5:225:A:N6	34:B5:837:G:H21	2.11	0.48
36:AB:92:TYR:HB2	36:AB:157:VAL:HB	1.95	0.48
38:A1:251:G:H4'	38:A1:252:U:OP2	2.13	0.48
38:A1:627:U:H2'	38:A1:628:A:H8	1.77	0.48
38:A1:772:U:H2'	38:A1:773:G:O4'	2.13	0.48
38:A1:1021:G:H2'	38:A1:1031:C:N3	2.29	0.48
38:A1:2251:G:H2'	38:A1:2252:A:H8	1.79	0.48
38:A1:3162:C:H2'	38:A1:3163:A:H8	1.78	0.48
38:A1:3273:A:H4'	42:AE:44:ALA:HB1	1.96	0.48
44:AG:90:THR:HG23	44:AG:214:LEU:HD21	1.95	0.48
50:AN:73:ARG:HG2	50:AN:75:VAL:HG13	1.95	0.48
20:BF:133:VAL:HG12	20:BF:198:LEU:HD13	1.96	0.47
25:BS:109:LEU:O	25:BS:113:LEU:HD23	2.14	0.47
34:B5:207:U:H2'	34:B5:208:U:C6	2.49	0.47
34:B5:1175:U:H2'	34:B5:1176:G:C8	2.49	0.47
34:B5:1636:C:H4'	34:B5:1637:C:H3'	1.96	0.47
34:B5:1691:A:H2'	34:B5:1692:G:H8	1.79	0.47
35:AA:209:HIS:HE1	35:AA:211:HIS:HD2	1.58	0.47
37:AC:27:SER:O	37:AC:279:HIS:NE2	2.43	0.47
38:A1:1913:A:N3	38:A1:2120:A:H2'	2.30	0.47
38:A1:3324:C:OP1	66:Ad:19:ARG:NH1	2.44	0.47
46:AI:52:LEU:HD11	46:AI:163:GLN:HB3	1.95	0.47
7:BI:4:SER:HB2	7:BI:24:LYS:HD3	1.96	0.47
7:BI:56:ARG:NH1	7:BI:174:GLY:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:41:ALA:HB3	10:BN:80:LEU:HD13	1.96	0.47
13:BW:101:TYR:HE1	13:BW:114:GLU:OE2	1.97	0.47
19:BD:142:LEU:HB2	19:BD:148:LYS:NZ	2.29	0.47
26:BT:6:VAL:HG21	26:BT:132:LEU:HB3	1.96	0.47
31:Bg:93:ASP:HB2	31:Bg:100:TYR:CE2	2.48	0.47
38:A1:314:U:H2'	38:A1:315:C:H6	1.79	0.47
38:A1:345:G:OP1	38:A1:1429:G:N1	2.47	0.47
38:A1:577:C:H2'	38:A1:579:G:H5''	1.95	0.47
38:A1:1805:C:H2'	38:A1:1806:A:H8	1.79	0.47
38:A1:2220:A2M:H8	38:A1:2220:A2M:O5'	2.14	0.47
38:A1:3198:U:O4	45:AH:26:LYS:HB2	2.14	0.47
39:A3:3:U:H2'	39:A3:4:U:C6	2.49	0.47
40:A4:52:A:H62	74:A1:27:ILE:HD13	1.79	0.47
43:AF:151:ARG:HD2	43:AF:207:LEU:HD23	1.96	0.47
68:Af:14:LEU:HD11	68:Af:31:LYS:HB2	1.95	0.47
71:Ai:50:LEU:CB	71:Ai:55:ARG:HD2	2.43	0.47
71:Ai:52:PRO:HA	71:Ai:55:ARG:NE	2.29	0.47
34:B5:39:A:O2'	34:B5:40:A:OP2	2.27	0.47
34:B5:1439:C:H2'	34:B5:1440:C:H6	1.79	0.47
37:AC:321:LYS:HD3	37:AC:324:LEU:HD23	1.97	0.47
38:A1:508:U:OP1	43:AF:211:SER:OG	2.20	0.47
38:A1:523:A:O2'	55:AS:69:PRO:HD2	2.14	0.47
38:A1:939:U:O2'	38:A1:2402:A:N1	2.44	0.47
38:A1:1120:A:H2'	38:A1:1121:U:C6	2.48	0.47
38:A1:1286:A:N3	38:A1:1287:A:H1'	2.28	0.47
38:A1:1682:U:O2	57:AU:82:LYS:HD2	2.14	0.47
38:A1:2741:C:O2	77:Ao:20:HIS:HE1	1.98	0.47
38:A1:2835:U:H2'	38:A1:2836:C:O2	2.14	0.47
38:A1:2836:C:H5	38:A1:2852:C:N4	2.11	0.47
38:A1:3164:C:O2'	38:A1:3165:A:H8	1.97	0.47
71:Ai:4:LYS:O	71:Ai:16:LYS:NZ	2.33	0.47
7:BI:47:ARG:NH2	34:B5:398:G:OP2	2.38	0.47
17:Bb:19:HIS:CD2	17:Bb:21:LEU:H	2.32	0.47
19:BD:103:GLU:OE2	19:BD:173:ARG:NE	2.47	0.47
19:BD:224:ASP:OD1	19:BD:225:TYR:N	2.47	0.47
20:BF:98:MET:HB2	20:BF:105:GLY:O	2.15	0.47
31:Bg:260:ILE:HB	31:Bg:274:LEU:HB2	1.97	0.47
36:AB:173:GLN:O	36:AB:174:LYS:HB2	2.14	0.47
38:A1:241:G:C8	38:A1:241:G:C3'	2.96	0.47
38:A1:1069:C:H2'	38:A1:1070:U:H6	1.79	0.47
38:A1:1284:C:H2'	38:A1:1285:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1471:U:H2'	38:A1:1472:U:C6	2.50	0.47
38:A1:1616:U:H2'	38:A1:1617:G:C8	2.49	0.47
38:A1:2426:U:H2'	38:A1:2427:U:H6	1.79	0.47
38:A1:3305:A:H2'	38:A1:3306:U:O4'	2.14	0.47
39:A3:3:U:H2'	39:A3:4:U:H6	1.78	0.47
42:AE:39:VAL:HG23	42:AE:87:THR:HB	1.96	0.47
43:AF:142:SER:O	43:AF:146:GLN:HG3	2.14	0.47
45:AH:23:ARG:HE	45:AH:39:LYS:HA	1.78	0.47
47:AJ:6:GLN:HE21	47:AJ:10:ARG:HD3	1.80	0.47
64:Ab:13:THR:HG1	64:Ab:14:ARG:NH1	2.10	0.47
79:E:11:GLU:HA	79:E:14:LYS:HG2	1.96	0.47
5:BG:148:SER:OG	5:BG:151:ASP:HB2	2.14	0.47
19:BD:150:MET:HG3	19:BD:152:PHE:CE1	2.50	0.47
25:BS:11:PHE:HZ	25:BS:25:ASN:H	1.62	0.47
25:BS:46:VAL:HG11	25:BS:73:MET:HG2	1.96	0.47
34:B5:30:G:H2'	34:B5:31:C:H6	1.80	0.47
34:B5:590:C:H2'	34:B5:591:A:C8	2.50	0.47
35:AA:37:ARG:NH2	38:A1:2526:C:OP1	2.34	0.47
36:AB:266:ARG:NH2	38:A1:2392:C:H1'	2.30	0.47
37:AC:34:ILE:HD12	37:AC:120:TYR:CE2	2.49	0.47
38:A1:1565:G:C2	38:A1:1566:A:C4	3.02	0.47
38:A1:3106:A:H2'	38:A1:3107:U:O4'	2.15	0.47
39:A3:64:A:H5'	39:A3:65:G:H5''	1.94	0.47
51:AO:16[A]:VAL:HG23	51:AO:80[A]:PHE:HD1	1.80	0.47
62:AZ:26:VAL:HG11	62:AZ:96:VAL:HG13	1.96	0.47
12:BV:7:GLN:O	12:BV:9:VAL:HG13	2.14	0.47
15:BY:57:VAL:HB	15:BY:60:PHE:CE2	2.43	0.47
22:BP:90:ILE:HD11	22:BP:112:LEU:HD21	1.96	0.47
32:Bf:133:ALA:HB2	34:B5:1252:C:O4'	2.14	0.47
34:B5:226:A:H4'	34:B5:228:G:C8	2.50	0.47
34:B5:1269:OMU:H5''	34:B5:1269:OMU:O2	2.14	0.47
38:A1:174:C:H2'	38:A1:175:C:O4'	2.14	0.47
38:A1:184:U:H2'	38:A1:185:C:C6	2.49	0.47
38:A1:873:C:H5''	38:A1:874:U:O5'	2.14	0.47
38:A1:1771:C:H2'	38:A1:1772:U:O4'	2.15	0.47
38:A1:2491:A:H5''	79:E:213:ALA:HA	1.95	0.47
38:A1:2506:U:C4	38:A1:2507:C:C6	3.03	0.47
38:A1:2762:A:H2'	38:A1:2763:U:C6	2.48	0.47
41:AD:75:LEU:HD21	41:AD:113:LEU:HD11	1.97	0.47
41:AD:82:GLU:O	41:AD:85:ARG:HG2	2.15	0.47
79:E:33:GLU:HB3	79:E:207:LYS:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:EC:6851:G:O2'	80:EC:6852:U:O4'	2.29	0.47
2:BB:29:TRP:CE2	2:BB:47:LEU:HD13	2.50	0.47
2:BB:195:LYS:HD2	2:BB:195:LYS:HA	1.63	0.47
4:BE:105:VAL:HG21	4:BE:245:LYS:H	1.78	0.47
7:BI:26:LYS:HG3	7:BI:29:LEU:HD23	1.97	0.47
8:BJ:25:ASP:OD2	18:Be:54:ARG:NH2	2.48	0.47
15:BY:86:GLU:OE2	15:BY:90:ARG:NH1	2.34	0.47
19:BD:27:ARG:NH2	34:B5:1436:A:OP2	2.35	0.47
20:BF:125:THR:O	20:BF:127:GLN:N	2.47	0.47
27:BU:22:ILE:HG22	27:BU:93:LEU:HB2	1.96	0.47
31:Bg:249:ARG:HH12	31:Bg:315:VAL:CG1	2.28	0.47
33:BM:45:LEU:N	34:B5:1228:G:OP2	2.47	0.47
36:AB:50:LYS:NZ	36:AB:330:GLY:O	2.36	0.47
36:AB:77:THR:HG21	36:AB:328:ILE:HG12	1.97	0.47
37:AC:46:LYS:NZ	38:A1:691:A:OP1	2.48	0.47
38:A1:208:C:H2'	38:A1:209:A:O4'	2.15	0.47
38:A1:591:G:C2	42:AE:18:LEU:HD22	2.50	0.47
38:A1:799:G:O2'	48:AL:18:TRP:NE1	2.42	0.47
38:A1:921:A:N6	38:A1:1846:C:OP2	2.48	0.47
38:A1:1562:C:O2'	38:A1:1563:C:O5'	2.31	0.47
38:A1:1935:G:H2'	38:A1:1936:A:C8	2.50	0.47
38:A1:2268:U:OP2	38:A1:2268:U:C6	2.58	0.47
38:A1:2578:U:H2'	38:A1:2579:G:O4'	2.15	0.47
38:A1:2767:U:H2'	38:A1:2768:U:H6	1.79	0.47
38:A1:2813:A:H2'	38:A1:2814:G:O4'	2.15	0.47
40:A4:97:A:O2'	70:Ah:59:ASN:ND2	2.47	0.47
43:AF:58:ALA:O	43:AF:62:ILE:HD12	2.14	0.47
43:AF:92:ILE:HD12	53:AQ:4:ASP:HB2	1.97	0.47
43:AF:203:TRP:CD1	43:AF:204:PRO:HD2	2.49	0.47
44:AG:75:ILE:CD1	50:AN:18:VAL:HG23	2.44	0.47
69:Ag:101:VAL:O	69:Ag:104:VAL:CG1	2.58	0.47
74:Al:43:ASN:HB3	74:Al:46:ARG:HE	1.79	0.47
79:E:138:VAL:HG11	79:E:144:LEU:HD13	1.97	0.47
80:EC:6832:G:H3'	80:EC:6833:G:N2	2.26	0.47
2:BB:70:LEU:HD23	2:BB:79:HIS:HB3	1.96	0.47
6:BH:119:THR:HG21	34:B5:638:U:H5''	1.96	0.47
10:BN:73:ARG:HD3	34:B5:859:A:C5	2.50	0.47
23:BQ:14:LYS:NZ	34:B5:1610:G:N7	2.62	0.47
23:BQ:129:PHE:CE1	27:BU:78:THR:HA	2.50	0.47
23:BQ:143:ARG:C	34:B5:1195:C:H42	2.23	0.47
27:BU:32:LYS:HB3	27:BU:33:GLN:NE2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1740:A:H2'	34:B5:1741:U:C6	2.49	0.47
36:AB:55:THR:HG23	38:A1:3049:A:O2'	2.15	0.47
38:A1:98:G:OP1	48:AL:16:LYS:NZ	2.36	0.47
38:A1:163:C:C3'	38:A1:164:A:H5''	2.44	0.47
38:A1:250:U:O2'	38:A1:251:G:P	2.73	0.47
38:A1:1174:G:N2	51:AO:87[A]:MET:SD	2.88	0.47
38:A1:2651:G:H5''	38:A1:2652:U:O4'	2.14	0.47
39:A3:1:G:C2	39:A3:2:G:C8	3.03	0.47
39:A3:73:C:N4	55:AS:19:VAL:HG21	2.30	0.47
40:A4:96:A:O2'	70:Ah:60:GLU:OE1	2.32	0.47
56:AT:150:THR:HG22	56:AT:151:LEU:N	2.30	0.47
61:AY:116:LYS:HB3	61:AY:126:LEU:HD21	1.97	0.47
66:Ad:20:LEU:HD11	66:Ad:32:ALA:HB2	1.97	0.47
74:Al:28:ARG:HA	74:Al:33:ASN:ND2	2.30	0.47
2:BB:111:ARG:NH1	34:B5:930:A:O2'	2.46	0.47
6:BH:140:VAL:N	13:BW:51:GLU:OE2	2.48	0.47
10:BN:128:TYR:O	10:BN:131:THR:OG1	2.30	0.47
17:Bb:33:LEU:HD23	17:Bb:81:ARG:HA	1.97	0.47
31:Bg:93:ASP:HB2	31:Bg:100:TYR:OH	2.15	0.47
31:Bg:260:ILE:O	31:Bg:274:LEU:N	2.47	0.47
34:B5:340:U:H2'	34:B5:341:A:C8	2.49	0.47
34:B5:538:A:O2'	34:B5:541:A2M:H8	2.15	0.47
34:B5:694:U:H3'	34:B5:695:U:C6	2.50	0.47
34:B5:1382:A:O2'	34:B5:1383:G:H8	1.98	0.47
34:B5:1570:A:H2'	34:B5:1571:C:O4'	2.14	0.47
36:AB:226:PHE:O	38:A1:1886:A:O2'	2.25	0.47
38:A1:123:A:C6	38:A1:150:A:C5	3.03	0.47
38:A1:160:G:H2'	38:A1:161:G:O4'	2.15	0.47
38:A1:191:U:H2'	38:A1:192:C:H6	1.80	0.47
38:A1:380:U:H2'	38:A1:381:U:C6	2.50	0.47
38:A1:929:A:H2'	38:A1:930:U:C6	2.49	0.47
38:A1:1341:U:H2'	38:A1:1342:C:C6	2.49	0.47
67:Ae:9:ILE:HA	67:Ae:63:THR:HG21	1.97	0.47
68:Af:16:TYR:CG	68:Af:25:PRO:HA	2.50	0.47
2:BB:179:SER:HB3	2:BB:187:LYS:HE3	1.97	0.47
25:BS:41:ARG:NH1	34:B5:1565:C:OP1	2.45	0.47
34:B5:138:A:N6	34:B5:266:A:H61	2.12	0.47
34:B5:528:U:H2'	34:B5:529:A:O4'	2.15	0.47
36:AB:366:GLY:HA3	38:A1:3330:A:H4'	1.96	0.47
37:AC:8:VAL:HG23	37:AC:151:VAL:HG12	1.97	0.47
37:AC:23:PRO:HD2	37:AC:26:PHE:CD2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:307:A:H2'	38:A1:308:A:C8	2.50	0.47
38:A1:345:G:O2'	40:A4:25:G:N3	2.47	0.47
38:A1:600:G:N2	38:A1:602:A:H3'	2.30	0.47
38:A1:1719:G:N7	54:AR:121:HIS:HE1	2.13	0.47
38:A1:2148:U:H2'	38:A1:2149:A:C8	2.50	0.47
39:A3:94:C:H2'	39:A3:95:A:C8	2.50	0.47
45:AH:129:ARG:H	45:AH:157:ASN:ND2	2.13	0.47
47:AJ:164:LYS:HE2	47:AJ:171:VAL:HG22	1.97	0.47
79:E:94:ASN:HD22	79:E:123:LEU:HD13	1.80	0.47
79:E:125:GLY:N	79:E:126:PRO:HD2	2.30	0.47
4:BE:141:THR:OG1	4:BE:143:ASP:OD1	2.26	0.46
4:BE:147:ILE:HG21	4:BE:169:ILE:HG13	1.96	0.46
18:Be:3:LYS:HE2	18:Be:5:HIS:HB2	1.97	0.46
27:BU:28:SER:HB3	27:BU:34:LEU:HD22	1.97	0.46
28:BZ:74:SER:O	28:BZ:78:ILE:HG12	2.15	0.46
34:B5:221:A:H2'	34:B5:222:A:C5	2.51	0.46
34:B5:1077:C:H2'	34:B5:1078:C:H6	1.80	0.46
34:B5:1712:A:H3'	34:B5:1713:G:H8	1.79	0.46
38:A1:61:A:N1	50:AN:189:LYS:NZ	2.60	0.46
38:A1:63:A:H5''	50:AN:174:ILE:HG21	1.97	0.46
38:A1:744:A:H4'	53:AQ:142:GLY:O	2.14	0.46
38:A1:792:G:H2'	38:A1:793:C:C6	2.50	0.46
38:A1:976:U:H2'	38:A1:977:C:O4'	2.15	0.46
38:A1:1147:G:OP1	67:Ae:47:ARG:NH1	2.44	0.46
38:A1:1659:U:H2'	38:A1:1660:C:H6	1.77	0.46
38:A1:1694:U:O2'	38:A1:1695:U:H5'	2.15	0.46
38:A1:2722:U:O2'	56:AT:88:ARG:O	2.29	0.46
38:A1:3259:U:H5''	38:A1:3261:C:H5	1.79	0.46
39:A3:52:G:O2'	39:A3:53:U:OP1	2.33	0.46
40:A4:84:C:O3'	61:AY:113:LYS:NZ	2.48	0.46
44:AG:144:GLU:OE2	50:AN:6:TYR:OH	2.24	0.46
45:AH:89:LYS:HG2	45:AH:145:VAL:HG13	1.96	0.46
55:AS:92:LYS:HE2	55:AS:109:ASP:OD1	2.15	0.46
62:AZ:99:GLU:HA	62:AZ:102:GLU:HG3	1.96	0.46
63:Aa:45:MET:HE1	63:Aa:52:TYR:CG	2.50	0.46
1:BA:29:VAL:HG22	1:BA:149:LEU:HB3	1.97	0.46
3:BC:139:ILE:HD13	3:BC:191:ALA:HB1	1.97	0.46
8:BJ:113:VAL:HG12	8:BJ:119:ALA:HB2	1.97	0.46
11:BO:122:PRO:HB3	34:B5:887:A:H1'	1.96	0.46
12:BV:10:GLU:O	12:BV:11:LEU:C	2.57	0.46
17:Bb:40:CYS:SG	17:Bb:41:LEU:N	2.88	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:57:GLU:O	17:Bb:60:SER:OG	2.32	0.46
23:BQ:5:PRO:HG2	23:BQ:24:ALA:HB2	1.97	0.46
24:BR:87:GLU:OE1	24:BR:88:VAL:HG23	2.15	0.46
28:BZ:93:SER:HB3	28:BZ:100:ILE:HD13	1.96	0.46
33:BM:36:LEU:HG	33:BM:36:LEU:O	2.15	0.46
34:B5:368:U:H2'	34:B5:369:A:O4'	2.14	0.46
34:B5:607:G:H5'	34:B5:613:G:N2	2.30	0.46
38:A1:242:C:H2'	38:A1:243:G:H8	1.77	0.46
38:A1:1895:A:O2'	38:A1:3053:G:H4'	2.14	0.46
38:A1:1923:C:H5''	76:An:25:LYS:HE3	1.97	0.46
38:A1:2597:U:H2'	38:A1:2598:G:H8	1.80	0.46
49:AM:14:LEU:H	49:AM:19:ARG:NH2	2.14	0.46
54:AR:90:PRO:O	54:AR:93:VAL:HG22	2.15	0.46
61:AY:109:LEU:HD22	61:AY:115:ARG:NH2	2.30	0.46
69:Ag:59:PRO:HA	69:Ag:62:TYR:HD2	1.79	0.46
79:E:175:GLU:HG3	79:E:177:ASP:OD1	2.15	0.46
80:EC:6836:U:H3	80:EC:6877:C:H41	1.62	0.46
2:BB:39:GLU:HB2	2:BB:74:GLN:HA	1.98	0.46
6:BH:64:VAL:HA	6:BH:67:LEU:HD23	1.97	0.46
20:BF:158:GLN:NE2	20:BF:159:ALA:O	2.48	0.46
22:BP:108:ARG:H	22:BP:111:MET:CE	2.28	0.46
31:Bg:16:HIS:CE1	31:Bg:43:ILE:HD12	2.51	0.46
34:B5:301:A:H2'	34:B5:302:U:O4'	2.14	0.46
34:B5:472:U:O2'	34:B5:769:A:N3	2.43	0.46
34:B5:650:U:H2'	34:B5:651:G:O4'	2.15	0.46
34:B5:705:U:O2'	34:B5:732:G:O2'	2.25	0.46
34:B5:1170:G:C2	34:B5:1171:A:C8	3.03	0.46
34:B5:1450:U:H2'	34:B5:1451:C:H6	1.81	0.46
38:A1:39:A:H5''	63:Aa:35:ALA:HB2	1.97	0.46
38:A1:872:U:H2'	38:A1:873:C:C6	2.49	0.46
38:A1:2352:A:H5''	52:AP:83:TRP:O	2.15	0.46
38:A1:3027:A:H2'	38:A1:3028:G:O4'	2.15	0.46
38:A1:3160:U:H2'	38:A1:3161:C:H6	1.80	0.46
40:A4:6:U:H2'	40:A4:7:U:H6	1.80	0.46
41:AD:193:GLU:HG2	41:AD:194:LEU:N	2.30	0.46
43:AF:83:LEU:HD11	43:AF:116:PHE:HB3	1.96	0.46
47:AJ:45:PRO:HB2	47:AJ:67:VAL:HG22	1.97	0.46
47:AJ:102:PHE:CZ	47:AJ:129:VAL:HG11	2.51	0.46
55:AS:27:MET:HE1	55:AS:44:PHE:HB3	1.97	0.46
79:E:76:ARG:HD3	79:E:144:LEU:HD23	1.97	0.46
3:BC:170:ILE:HB	3:BC:197:TYR:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:99:GLN:HE21	16:Ba:46:GLU:HG3	1.81	0.46
13:BW:23:ARG:NH1	13:BW:65:LEU:O	2.48	0.46
16:Ba:32:LYS:O	16:Ba:37:LYS:NZ	2.46	0.46
19:BD:218:LEU:HD23	19:BD:218:LEU:H	1.80	0.46
26:BT:117:SER:HB3	26:BT:121:GLY:O	2.15	0.46
31:Bg:274:LEU:HD22	31:Bg:313:TRP:NE1	2.31	0.46
34:B5:404:G:H2'	34:B5:405:C:C6	2.50	0.46
34:B5:1592:A:H2'	34:B5:1593:A:C8	2.50	0.46
38:A1:238:A:H3'	38:A1:239:G:H8	1.74	0.46
38:A1:292:U:OP2	50:AN:68:ARG:NH2	2.47	0.46
38:A1:1062:A:H4'	56:AT:105:PHE:CE1	2.50	0.46
38:A1:1074:U:O2'	64:Ab:42:ASN:OD1	2.21	0.46
38:A1:2445:A:C6	38:A1:2503:G:N1	2.83	0.46
38:A1:2646:C:H5''	46:AI:119:TRP:CG	2.51	0.46
38:A1:2723:U:H2'	38:A1:2724:OMU:C6	2.44	0.46
40:A4:27:U:H2'	40:A4:28:C:H6	1.79	0.46
43:AF:120:THR:HB	56:AT:132:PRO:HB2	1.97	0.46
43:AF:138:TYR:CE2	43:AF:233:GLU:HB2	2.50	0.46
49:AM:21:VAL:HB	49:AM:63:VAL:HG22	1.97	0.46
54:AR:134:HIS:CE1	54:AR:136:ARG:HH21	2.34	0.46
1:BA:200:ASP:HA	1:BA:203:PHE:CD2	2.51	0.46
3:BC:95:ARG:HH12	3:BC:97:ARG:HE	1.61	0.46
4:BE:86:PHE:CE2	4:BE:87:MET:HE3	2.51	0.46
20:BF:149:VAL:O	20:BF:155:ALA:HB1	2.16	0.46
26:BT:33:TYR:CD2	26:BT:37:VAL:HG11	2.50	0.46
29:Bc:22:ARG:HD3	34:B5:1162:C:H4'	1.96	0.46
34:B5:103:A:H4'	34:B5:105:A:C8	2.49	0.46
34:B5:292:U:H2'	34:B5:293:U:C6	2.50	0.46
34:B5:538:A:H8	34:B5:541:A2M:H2'	1.81	0.46
34:B5:579:A:O2'	34:B5:580:A:H5''	2.15	0.46
34:B5:1120:U:H2'	34:B5:1121:C:H6	1.80	0.46
34:B5:1492:A:O2'	34:B5:1493:A:H5''	2.16	0.46
38:A1:264:G:OP1	71:AI:34:SER:HB2	2.16	0.46
38:A1:1814:A:C2	38:A1:1816:A:H1'	2.48	0.46
38:A1:2101:C:O2'	38:A1:2102:U:H5''	2.15	0.46
38:A1:3191:G:H2'	38:A1:3192:U:C6	2.50	0.46
43:AF:108:LEU:HD21	43:AF:115:THR:HG22	1.96	0.46
45:AH:90:MET:HG2	45:AH:181:VAL:HA	1.97	0.46
60:AX:72:ALA:O	60:AX:76:VAL:HG23	2.15	0.46
73:Ak:14:LEU:HD12	73:Ak:17:ARG:HD3	1.98	0.46
3:BC:138:PRO:HB2	12:BV:11:LEU:CD2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BC:236:PRO:O	12:BV:33:GLN:NE2	2.48	0.46
5:BG:45:PHE:HB3	5:BG:48:TYR:HB2	1.98	0.46
8:BJ:168:ARG:HH21	8:BJ:174:ARG:CZ	2.28	0.46
22:BP:56:PHE:O	22:BP:60:LEU:HB2	2.16	0.46
31:Bg:20:VAL:HG11	31:Bg:310:ILE:HG12	1.98	0.46
31:Bg:161:LYS:HB2	31:Bg:164:ASP:OD2	2.16	0.46
33:BM:47:GLU:CD	34:B5:1229:G:H1	2.24	0.46
34:B5:706:A:H4'	34:B5:707:A:OP2	2.16	0.46
34:B5:890:C:H2'	34:B5:891:A:H8	1.80	0.46
34:B5:1120:U:H2'	34:B5:1121:C:C6	2.51	0.46
34:B5:1619:C:H2'	34:B5:1620:C:H6	1.80	0.46
37:AC:61:SER:OG	38:A1:929:A:OP1	2.32	0.46
38:A1:240:U:N3	38:A1:241:G:C2	2.83	0.46
38:A1:291:C:H2'	38:A1:292:U:C6	2.51	0.46
38:A1:728:G:H2'	38:A1:729:C:H6	1.81	0.46
38:A1:947:G:H2'	38:A1:948:C:C6	2.50	0.46
38:A1:976:U:OP1	53:AQ:144:ARG:NH2	2.46	0.46
38:A1:1037:C:H2'	38:A1:1038:C:H6	1.80	0.46
38:A1:1069:C:H2'	38:A1:1070:U:C6	2.50	0.46
38:A1:1566:A:C8	38:A1:1566:A:H5''	2.50	0.46
38:A1:2497:U:O2	38:A1:2498:U:N3	2.49	0.46
38:A1:3159:C:H2'	38:A1:3160:U:C6	2.51	0.46
45:AH:93:VAL:HG22	75:Am:82:LEU:HD12	1.97	0.46
46:AI:210:ILE:HG13	46:AI:217:PHE:CE2	2.50	0.46
48:AL:11:LYS:O	48:AL:13:HIS:ND1	2.49	0.46
69:Ag:79:SER:HB3	69:Ag:80:ARG:HH11	1.81	0.46
70:Ah:102:GLU:N	70:Ah:102:GLU:CD	2.70	0.46
74:Al:6:SER:OG	74:Al:9:ILE:HG12	2.16	0.46
77:Ao:99:GLN:C	77:Ao:102:GLN:OE1	2.58	0.46
79:E:60:ARG:H	79:E:63:MET:CE	2.28	0.46
6:BH:16:LEU:HD23	6:BH:16:LEU:C	2.41	0.46
8:BJ:93:LEU:HA	8:BJ:96:VAL:HG22	1.97	0.46
11:BO:84:ARG:NH1	11:BO:85:ALA:O	2.48	0.46
11:BO:122:PRO:HB3	34:B5:887:A:C1'	2.46	0.46
12:BV:55:LEU:HD13	12:BV:65:SER:HB2	1.98	0.46
22:BP:56:PHE:CD2	22:BP:83:MET:HE1	2.51	0.46
23:BQ:55:VAL:HG11	23:BQ:105:LEU:HD23	1.98	0.46
25:BS:27:LYS:HA	25:BS:57:ARG:HA	1.96	0.46
27:BU:100:VAL:HA	27:BU:103:ILE:HG22	1.98	0.46
34:B5:16:G:H2'	34:B5:17:C:C6	2.50	0.46
34:B5:1504:G:H2'	34:B5:1505:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:252:ILE:HG12	38:A1:2393:G:H4'	1.98	0.46
36:AB:334:ARG:HH21	38:A1:3304:U:H1'	1.80	0.46
38:A1:1243:G:H2'	38:A1:1244:A:H8	1.79	0.46
38:A1:1293:U:O2'	38:A1:1294:A:H5'	2.15	0.46
38:A1:1364:C:H5''	53:AQ:3:ILE:HD13	1.97	0.46
38:A1:3162:C:H2'	38:A1:3163:A:C8	2.51	0.46
48:AL:9:ILE:HG12	63:Aa:34:MET:HE1	1.98	0.46
56:AT:28:SER:O	56:AT:32:LYS:HG3	2.15	0.46
1:BA:121:VAL:HG23	1:BA:141:ILE:HG21	1.98	0.46
6:BH:34:LEU:HD12	6:BH:38:LEU:HB3	1.98	0.46
7:BI:72:ILE:HD13	7:BI:112:TRP:CD2	2.50	0.46
7:BI:103:GLN:HA	7:BI:165:LEU:O	2.16	0.46
8:BJ:59:LEU:O	8:BJ:69:ARG:HD2	2.15	0.46
14:BX:69:ARG:NH2	34:B5:569:C:H41	2.13	0.46
20:BF:118:LEU:HD22	20:BF:129:PRO:HB2	1.98	0.46
22:BP:20:VAL:HG11	22:BP:25:LEU:HB2	1.98	0.46
25:BS:96:LYS:HB2	25:BS:98:TYR:CE1	2.51	0.46
34:B5:76:A:O2'	34:B5:77:U:H5'	2.15	0.46
34:B5:97:C:H2'	34:B5:98:U:H6	1.81	0.46
34:B5:223:U:H2'	34:B5:224:C:C6	2.51	0.46
34:B5:324:U:H2'	34:B5:325:G:C8	2.51	0.46
35:AA:118:GLU:HG3	35:AA:125:ALA:HB3	1.98	0.46
38:A1:1128:U:H2'	38:A1:1129:A:O4'	2.16	0.46
38:A1:2204:C:O2'	38:A1:2205:U:H6	1.98	0.46
48:AL:42:ARG:O	48:AL:46:ILE:HG12	2.15	0.46
49:AM:5:SER:O	49:AM:6:ILE:HD13	2.16	0.46
49:AM:16:GLU:OE2	49:AM:69:THR:HG21	2.16	0.46
50:AN:6:TYR:CE1	71:Ai:43:LEU:HD23	2.51	0.46
1:BA:118:PRO:HG2	1:BA:141:ILE:HD13	1.97	0.46
2:BB:204:ILE:O	34:B5:1064:G:O2'	2.34	0.46
16:Ba:2:PRO:HG3	34:B5:1143:A:OP2	2.16	0.46
16:Ba:86:VAL:HG23	34:B5:1795:U:OP1	2.16	0.46
20:BF:124:LEU:O	20:BF:125:THR:C	2.58	0.46
23:BQ:107:LYS:O	23:BQ:111:SER:OG	2.30	0.46
25:BS:53:ASP:HB3	25:BS:56:LYS:CG	2.46	0.46
30:Bd:10:HIS:ND1	30:Bd:11:PRO:HD2	2.31	0.46
34:B5:1647:U:H2'	34:B5:1648:A:C8	2.51	0.46
34:B5:1732:A:H2'	34:B5:1733:C:H6	1.78	0.46
38:A1:1202:A:C2	38:A1:2857:C:H5'	2.51	0.46
38:A1:1528:G:O2'	38:A1:1588:A:N3	2.43	0.46
38:A1:1622:U:H2'	38:A1:1623:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2491:A:H5'	79:E:207:LYS:HG3	1.97	0.46
38:A1:2547:A:H2'	38:A1:2548:C:C6	2.51	0.46
38:A1:2585:G:H2'	38:A1:2585:G:N3	2.31	0.46
38:A1:2953:U:H2'	38:A1:2954:U:H2'	1.97	0.46
38:A1:3296:A:H2'	38:A1:3297:U:C6	2.50	0.46
46:AI:191:LYS:HE2	46:AI:212:GLU:HG3	1.98	0.46
47:AJ:75:LYS:O	47:AJ:79:ILE:HG12	2.16	0.46
48:AL:37:ASN:O	48:AL:41:THR:HG23	2.16	0.46
48:AL:56:PRO:HG3	48:AL:74:GLY:C	2.41	0.46
50:AN:159:ARG:HB3	50:AN:164:LEU:HB2	1.98	0.46
62:AZ:27:LYS:HB2	62:AZ:42:LEU:HB2	1.98	0.46
5:BG:51:LYS:HB3	5:BG:112:VAL:HG23	1.97	0.46
8:BJ:32:GLY:HA3	18:Be:40:TYR:CG	2.51	0.46
16:Ba:59:TYR:HB2	16:Ba:62:TYR:HB2	1.98	0.46
18:Be:45:VAL:HG11	34:B5:502:U:O2'	2.16	0.46
20:BF:99:MET:CE	34:B5:1165:G:H5''	2.46	0.46
30:Bd:45:GLU:OE1	34:B5:1433:G:N2	2.49	0.46
34:B5:413:U:H2'	34:B5:414:OMC:H6	1.80	0.46
34:B5:602:U:H2'	34:B5:603:U:C6	2.51	0.46
34:B5:689:G:H2'	34:B5:690:G:H8	1.81	0.46
38:A1:1224:C:H41	38:A1:1285:G:H21	1.63	0.46
38:A1:2207:A:O2'	38:A1:2208:A:OP2	2.32	0.46
38:A1:2507:C:C4	38:A1:2508:U:O4	2.69	0.46
38:A1:2546:C:N4	38:A1:2547:A:H62	2.14	0.46
38:A1:2673:A:OP1	47:AJ:95:ASN:ND2	2.49	0.46
38:A1:3204:C:H2'	38:A1:3205:G:C8	2.50	0.46
39:A3:121:U:C5	41:AD:260:PHE:CE1	3.03	0.46
45:AH:103:ILE:HD11	45:AH:134:ILE:HG21	1.98	0.46
2:BB:149:GLN:NE2	2:BB:151:LYS:HG3	2.31	0.45
4:BE:59:ARG:NH2	15:BY:87:PRO:HG3	2.30	0.45
4:BE:163:ASP:HB3	4:BE:166:SER:O	2.15	0.45
5:BG:102:VAL:HG11	5:BG:109:LEU:HD11	1.98	0.45
7:BI:25:ARG:HA	34:B5:400:A:H5''	1.97	0.45
28:BZ:55:PRO:O	28:BZ:56:THR:OG1	2.30	0.45
34:B5:522:U:H2'	34:B5:523:G:O4'	2.16	0.45
34:B5:684:A:H2'	34:B5:685:A:H8	1.80	0.45
34:B5:800:U:H2'	34:B5:801:G:C8	2.51	0.45
34:B5:837:G:H2'	34:B5:838:G:H8	1.81	0.45
34:B5:1266:U:H2'	34:B5:1267:G:C8	2.50	0.45
34:B5:1688:U:H3'	34:B5:1689:A:H8	1.81	0.45
37:AC:74:ILE:HG12	37:AC:94:CYS:SG	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:AC:350:LYS:HD3	37:AC:351:PRO:O	2.14	0.45
38:A1:1083:G:H2'	38:A1:1084:A:H8	1.81	0.45
38:A1:1566:A:H61	38:A1:1571:A:N6	2.13	0.45
38:A1:2351:U:H2'	38:A1:2352:A:H8	1.81	0.45
43:AF:163:LEU:O	43:AF:165:ASP:N	2.49	0.45
49:AM:73:PRO:HG2	49:AM:76:ALA:HB2	1.98	0.45
1:BA:110:TYR:HA	1:BA:115:PHE:CD1	2.52	0.45
4:BE:87:MET:O	4:BE:122:LYS:HE3	2.17	0.45
4:BE:133:LYS:NZ	34:B5:252:U:OP1	2.31	0.45
8:BJ:142:ASN:OD1	34:B5:767:U:H5	2.00	0.45
9:BL:13:PHE:CD2	9:BL:15:LYS:HE3	2.50	0.45
10:BN:107:LYS:HZ3	34:B5:1018:U:P	2.39	0.45
10:BN:108:ASP:OD1	34:B5:878:G:O2'	2.27	0.45
14:BX:63:GLN:NE2	14:BX:64:PRO:HA	2.31	0.45
34:B5:517:U:H3	34:B5:535:A:H61	1.63	0.45
34:B5:1216:C:H4'	34:B5:1217:A:C8	2.50	0.45
34:B5:1772:C:H2'	34:B5:1773:4AC:H6	1.98	0.45
36:AB:10:ARG:NH1	36:AB:263:SER:O	2.31	0.45
38:A1:418:A:N1	40:A4:5:U:C5	2.84	0.45
38:A1:748:U:H2'	38:A1:749:C:C6	2.51	0.45
38:A1:954:U:H5	38:A1:967:A:N1	2.15	0.45
38:A1:1139:G:OP2	64:Ab:14:ARG:NE	2.46	0.45
38:A1:1709:C:H2'	38:A1:1710:C:C6	2.51	0.45
38:A1:2354:C:OP1	52:AP:86:LYS:NZ	2.43	0.45
38:A1:2438:A:C2	38:A1:2510:U:O2	2.69	0.45
40:A4:69:U:H2'	40:A4:70:G:O4'	2.16	0.45
51:AO:27[A]:LEU:O	51:AO:101[A]:ARG:NH1	2.49	0.45
2:BB:148:ASN:OD1	34:B5:1066:C:O2'	2.33	0.45
5:BG:64:LYS:NZ	5:BG:82:SER:OG	2.49	0.45
9:BL:130:PRO:O	34:B5:336:G:H5'	2.17	0.45
11:BO:127:ARG:NH2	34:B5:1787:C:OP1	2.48	0.45
16:Ba:12:LYS:HG3	16:Ba:15:ARG:HB2	1.97	0.45
34:B5:130:C:H1'	34:B5:133:U:H5	1.81	0.45
34:B5:150:U:H2'	34:B5:151:G:O4'	2.17	0.45
34:B5:488:G:N1	34:B5:500:C:O5'	2.39	0.45
34:B5:1044:U:H2'	34:B5:1045:C:C6	2.51	0.45
34:B5:1160:A:H2'	34:B5:1161:C:H6	1.77	0.45
34:B5:1353:U:HO2'	34:B5:1354:G:H8	1.64	0.45
34:B5:1490:C:H1'	34:B5:1492:A:C6	2.51	0.45
36:AB:53:MET:HE2	38:A1:3049:A:C8	2.50	0.45
36:AB:85:VAL:HG22	36:AB:202:THR:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:92:G:OP1	77:Ao:46:LYS:NZ	2.36	0.45
38:A1:244:G:H8	38:A1:244:G:O5'	1.99	0.45
38:A1:426:G:H2'	38:A1:427:C:C6	2.51	0.45
38:A1:589:A:H8	38:A1:590:G:C8	2.35	0.45
38:A1:2561:A:O2'	38:A1:2562:A:H8	1.99	0.45
38:A1:3113:A:H2'	38:A1:3114:A:O4'	2.16	0.45
61:AY:55:GLU:HB2	61:AY:108:LYS:HB3	1.98	0.45
63:Aa:36:GLY:HA3	63:Aa:40:HIS:CE1	2.52	0.45
71:Ai:84:LYS:O	71:Ai:88:GLU:OE1	2.34	0.45
80:EC:6837:G:C6	80:EC:6847:G:N1	2.84	0.45
1:BA:111:ILE:HD11	34:B5:1292:G:H21	1.82	0.45
2:BB:153:HIS:NE2	34:B5:1045:C:OP1	2.33	0.45
3:BC:138:PRO:CB	12:BV:11:LEU:CD2	2.95	0.45
6:BH:82:GLU:OE1	6:BH:164:TYR:OH	2.30	0.45
17:Bb:70:LYS:HG3	34:B5:1049:U:H5''	1.98	0.45
34:B5:888:U:H2'	34:B5:889:U:C6	2.52	0.45
34:B5:1521:G:O2'	34:B5:1523:G:OP2	2.34	0.45
35:AA:206:PRO:HG3	35:AA:213:GLY:HA3	1.98	0.45
36:AB:346:THR:HG22	36:AB:351:LEU:HD11	1.98	0.45
38:A1:120:G:C2	38:A1:121:A:N6	2.85	0.45
38:A1:616:G:H2'	38:A1:617:G:C8	2.51	0.45
38:A1:716:A:OP1	63:Aa:137:LYS:NZ	2.50	0.45
38:A1:871:U:H2'	38:A1:872:U:C6	2.51	0.45
38:A1:1915:A:H2'	38:A1:1916:U:H6	1.79	0.45
38:A1:2416:U:H2'	38:A1:2417:OMU:C6	2.46	0.45
38:A1:2469:G:N1	38:A1:2477:G:O6	2.49	0.45
38:A1:3243:A:OP1	51:AO:159[A]:LYS:NZ	2.43	0.45
38:A1:3324:C:H4'	66:Ad:13:THR:HG23	1.98	0.45
39:A3:42:A:HO2'	47:AJ:140:ARG:NE	2.14	0.45
58:AV:15:LEU:HD13	58:AV:51:ALA:HB3	1.98	0.45
59:AW:18:GLY:HA3	59:AW:31:PHE:O	2.17	0.45
67:Ae:3:SER:HB2	67:Ae:71:HIS:CE1	2.51	0.45
79:E:160:LYS:HG3	79:E:162:VAL:HG12	1.99	0.45
1:BA:198:MET:HG2	1:BA:200:ASP:H	1.80	0.45
2:BB:64:ARG:CZ	11:BO:36:LYS:HD3	2.46	0.45
34:B5:271:A:C2	34:B5:285:G:C6	3.04	0.45
34:B5:689:G:H2'	34:B5:690:G:C8	2.51	0.45
34:B5:990:C:H2'	34:B5:991:G:O4'	2.17	0.45
36:AB:284:ARG:NH1	36:AB:293:ASN:O	2.49	0.45
37:AC:181:VAL:HG11	37:AC:224:GLY:HA3	1.97	0.45
38:A1:433:A:OP2	68:Af:57:LYS:HE2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:879:U:O2	38:A1:2357:A:H1'	2.17	0.45
38:A1:1092:C:O2'	38:A1:1093:A:OP1	2.27	0.45
38:A1:1264:G:H4'	38:A1:1278:A:N7	2.31	0.45
38:A1:1742:U:H2'	38:A1:1743:G:H8	1.80	0.45
38:A1:1925:U:O2'	38:A1:1927:G:N7	2.48	0.45
38:A1:2107:A:C2	38:A1:3344:A:H8	2.33	0.45
38:A1:2911:A:H4'	38:A1:2912:G:C8	2.51	0.45
38:A1:3193:C:H2'	38:A1:3194:C:C6	2.51	0.45
39:A3:16:U:H2'	39:A3:17:A:H8	1.80	0.45
44:AG:33:ASN:O	44:AG:39:ALA:HB3	2.17	0.45
53:AQ:40:THR:OG1	53:AQ:45:ASN:ND2	2.48	0.45
53:AQ:153:PHE:O	53:AQ:161:LYS:HE2	2.17	0.45
70:Ah:70:TYR:O	70:Ah:76:GLN:NE2	2.49	0.45
74:Al:9:ILE:HG22	74:Al:13:MET:SD	2.56	0.45
79:E:148:VAL:HA	79:E:151:VAL:HG12	1.98	0.45
19:BD:135:GLU:HB2	19:BD:157:LEU:HD13	1.99	0.45
21:BK:46:LEU:HD13	21:BK:66:TYR:CD2	2.51	0.45
26:BT:130:ARG:HH22	34:B5:1359:C:C4'	2.21	0.45
31:Bg:116:ASP:CG	31:Bg:121:MET:H	2.24	0.45
34:B5:1542:G:N2	34:B5:1568:C:H1'	2.32	0.45
34:B5:1664:C:H2'	34:B5:1665:U:O4'	2.17	0.45
35:AA:113:VAL:HG12	35:AA:166:ILE:HD13	1.98	0.45
36:AB:30:LYS:HD2	38:A1:3138:U:OP2	2.17	0.45
38:A1:176:G:N1	38:A1:241:G:C6	2.74	0.45
38:A1:226:C:H2'	38:A1:227:G:O4'	2.17	0.45
38:A1:975:C:H2'	38:A1:976:U:C6	2.52	0.45
38:A1:1073:U:H2'	38:A1:1074:U:C6	2.52	0.45
38:A1:1306:G:O2'	38:A1:1307:G:H5''	2.16	0.45
38:A1:1478:C:H2'	38:A1:1479:U:C6	2.52	0.45
38:A1:1739:U:HO2'	69:Ag:56:THR:HG1	1.60	0.45
38:A1:3213:A:H2'	38:A1:3214:U:O4'	2.16	0.45
41:AD:143:LYS:HD2	41:AD:145:PHE:CE1	2.51	0.45
41:AD:286:VAL:O	41:AD:290:ILE:HG12	2.16	0.45
53:AQ:170:ARG:HG2	63:Aa:56:VAL:HG21	1.98	0.45
54:AR:134:HIS:HE1	54:AR:136:ARG:HB3	1.77	0.45
55:AS:25:PHE:HD1	56:AT:150:THR:OG1	1.93	0.45
61:AY:39:LEU:HD22	61:AY:43:TYR:HE2	1.81	0.45
67:Ae:126:LEU:HA	67:Ae:126:LEU:HD23	1.81	0.45
4:BE:87:MET:SD	4:BE:123:LEU:HB2	2.57	0.45
13:BW:40:VAL:HA	13:BW:43:LYS:HE3	1.97	0.45
13:BW:114:GLU:HA	13:BW:117:ARG:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BY:83:LYS:HA	15:BY:91:LEU:HD11	1.98	0.45
34:B5:747:C:H2'	34:B5:748:U:C6	2.52	0.45
34:B5:1645:G:H2'	34:B5:1646:C:C6	2.52	0.45
34:B5:1674:C:H2'	34:B5:1675:C:C6	2.52	0.45
37:AC:139:GLY:O	37:AC:141:ARG:NH1	2.49	0.45
37:AC:140:HIS:CD2	37:AC:247:PHE:H	2.35	0.45
38:A1:821:U:H2'	38:A1:822:G:H8	1.82	0.45
38:A1:840:C:H2'	38:A1:841:A:C8	2.52	0.45
38:A1:938:C:C5	63:Aa:26:ARG:HD2	2.52	0.45
38:A1:943:U:H3'	63:Aa:13:GLY:HA2	1.99	0.45
38:A1:1542:G:H2'	38:A1:1543:G:C8	2.51	0.45
38:A1:1555:U:H5'	38:A1:1556:C:OP2	2.17	0.45
38:A1:1666:G:H2'	38:A1:1667:A:H8	1.82	0.45
38:A1:2167:A:H2'	38:A1:2168:A:C8	2.52	0.45
38:A1:2441:A:H2'	38:A1:2442:G:O4'	2.16	0.45
38:A1:2930:A:H2'	38:A1:2931:C:H6	1.82	0.45
38:A1:2941:A:O5'	38:A1:2943:G:H4'	2.16	0.45
43:AF:151:ARG:NH2	43:AF:244:ASN:O	2.50	0.45
51:AO:108[A]:ILE:HD12	51:AO:160[A]:ARG:CZ	2.47	0.45
57:AU:78:TYR:O	57:AU:82:LYS:HG2	2.17	0.45
62:AZ:97:SER:O	62:AZ:100:THR:HG22	2.17	0.45
70:Ah:13:SER:H	70:Ah:16:GLN:NE2	2.14	0.45
78:Ap:76:ALA:O	78:Ap:80:ARG:HG3	2.16	0.45
80:EC:6865:G:H2'	80:EC:6866:C:O2	2.17	0.45
1:BA:79:ARG:NH2	1:BA:164:ASN:O	2.46	0.45
3:BC:222:TYR:O	12:BV:23:ILE:HG21	2.16	0.45
5:BG:38:GLY:HA2	5:BG:41:VAL:HB	1.99	0.45
13:BW:30:SER:HB2	13:BW:61:ILE:HG13	1.98	0.45
32:Bf:111:GLU:N	32:Bf:112:GLY:HA2	2.31	0.45
33:BM:54:ARG:HB2	33:BM:57:ALA:HB2	1.99	0.45
34:B5:989:U:H2'	34:B5:990:C:C6	2.52	0.45
35:AA:147:ARG:HG2	35:AA:155:LYS:NZ	2.31	0.45
38:A1:1596:C:O2'	38:A1:1696:A:N3	2.44	0.45
38:A1:1798:A:H2'	38:A1:1799:A:C8	2.52	0.45
38:A1:1817:G:H2'	38:A1:1818:U:O4'	2.16	0.45
38:A1:3192:U:H2'	38:A1:3193:C:H6	1.80	0.45
41:AD:129:TYR:CD1	41:AD:177:GLU:HB3	2.52	0.45
45:AH:38:LEU:HD13	45:AH:71:VAL:HG13	1.98	0.45
46:AI:52:LEU:HB3	46:AI:136:PHE:HB2	1.98	0.45
52:AP:178:ALA:O	52:AP:182:ILE:HG12	2.17	0.45
65:Ac:43:ILE:HB	65:Ac:90:VAL:CG1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:EC:6946:A:H2'	80:EC:6947:A:N3	2.32	0.45
1:BA:75:ALA:HB1	1:BA:174:TRP:CH2	2.51	0.45
2:BB:103:MET:HE3	2:BB:215:VAL:HG23	1.99	0.45
14:BX:126:LYS:HD3	34:B5:30:G:H5''	1.98	0.45
19:BD:92:GLN:CD	19:BD:92:GLN:H	2.24	0.45
19:BD:162:GLN:HB3	34:B5:1332:C:O2'	2.17	0.45
22:BP:108:ARG:NH2	25:BS:119:ILE:HA	2.32	0.45
34:B5:205:U:C2	34:B5:206:A:C8	3.04	0.45
34:B5:1090:C:H2'	34:B5:1091:A:H5''	1.98	0.45
34:B5:1254:U:H2'	34:B5:1255:G:C8	2.52	0.45
34:B5:1776:A:H2'	34:B5:1777:G:H8	1.82	0.45
36:AB:250:ALA:HB1	38:A1:2947:G:N3	2.32	0.45
38:A1:166:C:N4	38:A1:167:U:O4	2.50	0.45
38:A1:1412:G:OP1	67:Ae:105:ARG:NH1	2.46	0.45
38:A1:1729:A:C6	78:Ap:42:CYS:HA	2.52	0.45
38:A1:2526:C:H2'	38:A1:2527:G:H8	1.82	0.45
38:A1:2612:U:H2'	38:A1:2613:U:O4'	2.17	0.45
38:A1:2747:A:H5'	41:AD:175:HIS:HA	1.99	0.45
38:A1:3074:G:H4'	66:Ad:62:ARG:HD2	1.99	0.45
39:A3:60:G:H2'	39:A3:61:G:H8	1.81	0.45
41:AD:40:HIS:CE1	41:AD:42:ALA:HB3	2.51	0.45
45:AH:8:GLN:HB3	45:AH:72:LYS:HD3	1.97	0.45
45:AH:162:GLN:NE2	45:AH:181:VAL:H	2.15	0.45
46:AI:49:CYS:HB3	46:AI:168:SER:HB3	1.98	0.45
62:AZ:96:VAL:HA	62:AZ:100:THR:HG21	1.99	0.45
72:Aj:75:LYS:HB3	72:Aj:75:LYS:HE3	1.85	0.45
79:E:67:ILE:HD13	79:E:111:ILE:HD12	1.99	0.45
79:E:114:GLU:OE1	79:E:114:GLU:N	2.49	0.45
79:E:151:VAL:O	79:E:154:THR:OG1	2.31	0.45
1:BA:144:ILE:HG12	1:BA:158:VAL:HB	1.98	0.45
8:BJ:25:ASP:CG	18:Be:54:ARG:HH22	2.25	0.45
19:BD:105:MET:O	19:BD:109:LEU:HG	2.17	0.45
19:BD:142:LEU:O	19:BD:143:ARG:HG2	2.17	0.45
28:BZ:49:ARG:HA	28:BZ:52:LYS:HG2	1.99	0.45
31:Bg:19:TRP:HB2	31:Bg:38:ARG:HG3	1.99	0.45
34:B5:174:U:H3	34:B5:266:A:H62	1.64	0.45
34:B5:181:A:H2'	34:B5:182:A:H8	1.82	0.45
34:B5:886:U:C2	34:B5:887:A:C8	3.04	0.45
36:AB:316:GLU:HB2	36:AB:318:LYS:HE3	1.99	0.45
36:AB:357:LYS:HE2	36:AB:357:LYS:HB3	1.75	0.45
38:A1:238:A:C8	38:A1:238:A:C5'	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1668:G:H2'	38:A1:1669:C:O4'	2.17	0.45
38:A1:2292:U:H2'	38:A1:2293:C:C6	2.52	0.45
38:A1:2390:A:H2'	38:A1:2391:G:O4'	2.17	0.45
38:A1:3084:C:H2'	38:A1:3085:G:O4'	2.15	0.45
39:A3:84:A:H2'	39:A3:85:G:C8	2.52	0.45
40:A4:10:A:H2'	40:A4:11:C:C6	2.52	0.45
43:AF:143:THR:O	43:AF:147:LEU:HB2	2.17	0.45
52:AP:128:ARG:HH21	52:AP:136:ILE:HD13	0.62	0.45
1:BA:3:LEU:HD23	1:BA:3:LEU:HA	1.88	0.44
5:BG:50:PHE:HB3	5:BG:111:LEU:HB3	1.99	0.44
6:BH:132:PRO:HB2	6:BH:158:ASP:OD1	2.17	0.44
7:BI:77:ARG:HH22	38:A1:3354:U:H2'	1.82	0.44
7:BI:86:SER:OG	34:B5:328:A:N3	2.41	0.44
15:BY:10:ARG:NH2	34:B5:778:G:H22	2.08	0.44
19:BD:211:PRO:HG3	24:BR:19:ARG:HB2	1.99	0.44
27:BU:52:LYS:HB3	27:BU:93:LEU:HD23	1.98	0.44
31:Bg:158:PRO:HD2	31:Bg:208:GLY:HA2	1.99	0.44
33:BM:118:ALA:C	33:BM:120:VAL:H	2.23	0.44
34:B5:1017:U:H2'	34:B5:1018:U:C6	2.52	0.44
34:B5:1198:G:OP1	34:B5:1199:G:O2'	2.23	0.44
34:B5:1280:4AC:H2'	34:B5:1281:G:C8	2.52	0.44
34:B5:1606:C:H2'	34:B5:1607:G:C8	2.52	0.44
34:B5:1647:U:H2'	34:B5:1648:A:H8	1.83	0.44
36:AB:218:ILE:HB	36:AB:337:THR:OG1	2.16	0.44
37:AC:60:THR:HG22	37:AC:62:ALA:H	1.82	0.44
38:A1:74:G:OP1	48:AL:104:ARG:HG3	2.17	0.44
38:A1:1566:A:H3'	38:A1:1567:U:C5'	2.38	0.44
38:A1:1594:A:H1'	38:A1:1615:C:H1'	1.99	0.44
38:A1:1666:G:H2'	38:A1:1667:A:C8	2.51	0.44
38:A1:2611:U:H2'	38:A1:2612:U:C6	2.52	0.44
38:A1:3118:C:H2'	38:A1:3119:U:O4'	2.17	0.44
39:A3:62:U:H5''	41:AD:277:LEU:HD12	1.99	0.44
40:A4:74:U:C4	61:AY:74:TYR:HD1	2.35	0.44
42:AE:29:LYS:HB3	42:AE:29:LYS:HE3	1.82	0.44
67:Ae:20:HIS:CG	67:Ae:42:VAL:HG21	2.52	0.44
70:Ah:41:LEU:HD12	70:Ah:41:LEU:HA	1.80	0.44
8:BJ:85:VAL:HG13	8:BJ:103:ASP:HB3	1.99	0.44
25:BS:110:ARG:O	25:BS:114:GLU:OE1	2.34	0.44
27:BU:70:THR:HG23	27:BU:72:ASN:O	2.17	0.44
31:Bg:249:ARG:NH1	31:Bg:315:VAL:HG11	2.32	0.44
34:B5:852:C:H2'	34:B5:853:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1340:U:O4'	34:B5:1378:U:H5''	2.16	0.44
35:AA:7:ASN:O	38:A1:2163:C:H4'	2.17	0.44
35:AA:10:LYS:HA	35:AA:16:PHE:CD2	2.52	0.44
36:AB:107:ALA:HB1	36:AB:200:GLU:OE2	2.17	0.44
38:A1:529:A:H2'	38:A1:530:G:O4'	2.16	0.44
38:A1:954:U:C5	38:A1:967:A:N1	2.85	0.44
38:A1:1337:A:H2'	38:A1:1338:C:H6	1.81	0.44
38:A1:2294:U:OP2	58:AV:71:LYS:NZ	2.50	0.44
38:A1:2379:U:H2'	38:A1:2380:U:C6	2.53	0.44
38:A1:2594:C:H2'	38:A1:2595:A:O4'	2.16	0.44
38:A1:2615:G:H2'	38:A1:2616:C:H6	1.82	0.44
38:A1:2875:U:O2'	38:A1:2876:C:O5'	2.29	0.44
38:A1:3229:G:P	49:AM:137:LYS:HZ1	2.40	0.44
38:A1:3273:A:H5''	42:AE:45:GLY:CA	2.47	0.44
44:AG:47:SER:HA	44:AG:50:VAL:HG23	1.99	0.44
51:AO:89[A]:SER:O	51:AO:95[A]:GLY:HA3	2.16	0.44
53:AQ:165:ILE:HD11	53:AQ:172:PHE:HB3	2.00	0.44
57:AU:90:ARG:O	57:AU:91:ASP:OD1	2.34	0.44
62:AZ:70:PRO:HG3	62:AZ:115:LYS:HB2	1.99	0.44
7:BI:164:ARG:HH12	38:A1:3354:U:H3	1.63	0.44
8:BJ:65:LYS:HA	8:BJ:70:LEU:HD11	2.00	0.44
8:BJ:171:ARG:NH1	34:B5:537:G:N7	2.65	0.44
14:BX:6:PRO:HG3	14:BX:14:LYS:HG2	1.98	0.44
16:Ba:4:LYS:NZ	34:B5:1795:U:OP2	2.49	0.44
20:BF:95:ASN:HB3	34:B5:1611:A:O3'	2.16	0.44
20:BF:143:ARG:HB3	29:Bc:55:VAL:HG23	2.00	0.44
25:BS:84:TRP:HA	25:BS:89:GLN:NE2	2.32	0.44
30:Bd:5:ASN:HA	30:Bd:7:TRP:CZ3	2.53	0.44
33:BM:113:ARG:HG3	33:BM:114:LYS:H	1.82	0.44
34:B5:395:U:H2'	34:B5:396:G:O4'	2.17	0.44
34:B5:826:U:H2'	34:B5:827:C:H6	1.83	0.44
34:B5:842:C:H2'	34:B5:843:U:O4'	2.16	0.44
34:B5:1388:A:H4'	34:B5:1389:C:O4'	2.18	0.44
35:AA:144:ASN:HB2	35:AA:160:SER:HB2	1.99	0.44
38:A1:237:G:N3	38:A1:237:G:H2'	2.31	0.44
38:A1:718:G:C2	38:A1:721:G:H1'	2.53	0.44
38:A1:787:G:H2'	38:A1:788:C:C6	2.52	0.44
38:A1:819:U:H2'	38:A1:820:A:H8	1.80	0.44
38:A1:992:A:O2'	38:A1:993:G:H5'	2.17	0.44
38:A1:1195:A:H2'	38:A1:1309:U:O2	2.17	0.44
38:A1:1449:A2M:H2'	38:A1:1450:OMG:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1791:C:H2'	38:A1:1792:C:C6	2.52	0.44
38:A1:2251:G:H2'	38:A1:2252:A:C8	2.51	0.44
39:A3:121:U:H5	41:AD:260:PHE:CD1	2.35	0.44
40:A4:64:U:H5'	70:Ah:49:LYS:HD2	1.99	0.44
53:AQ:93:ILE:HG23	53:AQ:113:LYS:HE2	2.00	0.44
63:Aa:90:TYR:CG	63:Aa:100:PRO:HG3	2.52	0.44
16:Ba:50:VAL:HG13	16:Ba:64:LEU:HD11	1.99	0.44
24:BR:43:SER:OG	34:B5:1332:C:OP1	2.19	0.44
27:BU:66:SER:HA	27:BU:80:GLU:O	2.17	0.44
31:Bg:76:ASP:N	31:Bg:76:ASP:OD1	2.51	0.44
34:B5:74:U:OP1	34:B5:80:A:O2'	2.30	0.44
34:B5:186:C:H2'	34:B5:187:G:O4'	2.18	0.44
34:B5:296:U:H2'	34:B5:297:U:C6	2.52	0.44
34:B5:393:C:H2'	34:B5:394:C:C6	2.53	0.44
34:B5:512:A:H2'	34:B5:513:U:C6	2.52	0.44
34:B5:1291:G:H1	34:B5:1324:G:H1	1.66	0.44
34:B5:1365:C:H2'	34:B5:1366:U:O4'	2.17	0.44
34:B5:1439:C:H2'	34:B5:1440:C:C6	2.52	0.44
36:AB:329:PRO:HA	38:A1:3047:U:H5'	2.00	0.44
37:AC:60:THR:HG23	38:A1:364:G:OP1	2.18	0.44
38:A1:671:U:H2'	38:A1:672:A:C8	2.52	0.44
38:A1:1246:G:O2'	38:A1:1247:U:O3'	2.30	0.44
38:A1:1565:G:C8	38:A1:1565:G:C5'	3.00	0.44
46:AI:36:LEU:HD11	46:AI:69:ARG:HH11	1.82	0.44
58:AV:18:PRO:HA	58:AV:51:ALA:HA	1.99	0.44
77:Ao:82:GLN:O	77:Ao:83:LEU:HD23	2.17	0.44
79:E:145:TYR:HA	79:E:148:VAL:HG22	1.99	0.44
2:BB:82:ARG:HD3	2:BB:105:PHE:HE1	1.82	0.44
4:BE:4:GLY:HA3	34:B5:93:A:O2'	2.17	0.44
4:BE:241:GLY:O	4:BE:244:ILE:HG12	2.18	0.44
6:BH:62:VAL:HG22	6:BH:93:LEU:O	2.17	0.44
7:BI:113:PHE:HE1	7:BI:119:GLN:HB3	1.82	0.44
11:BO:136:ARG:HD3	11:BO:136:ARG:H	1.82	0.44
13:BW:51:GLU:O	13:BW:61:ILE:HA	2.17	0.44
19:BD:71:LEU:HB3	21:BK:20:VAL:HG21	1.99	0.44
21:BK:33:GLU:O	21:BK:34:GLU:HG2	2.17	0.44
31:Bg:51:ASP:O	31:Bg:53:LYS:N	2.50	0.44
34:B5:28:A2M:H2'	34:B5:29:U:C6	2.53	0.44
34:B5:239:C:O2'	34:B5:240:U:H6	2.00	0.44
34:B5:262:U:H2'	34:B5:263:C:C6	2.52	0.44
34:B5:514:G:O2'	34:B5:515:A:H8	2.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:891:A:H2'	34:B5:892:A:H8	1.83	0.44
34:B5:1125:A:C5	34:B5:1126:OMG:H1'	2.52	0.44
34:B5:1480:G:H2'	34:B5:1481:C:O4'	2.17	0.44
36:AB:123:TYR:CZ	36:AB:124:LYS:HG3	2.52	0.44
38:A1:22:G:H1'	40:A4:104:A:N3	2.32	0.44
38:A1:710:A:H2'	38:A1:711:A:C8	2.53	0.44
38:A1:792:G:H2'	38:A1:793:C:H6	1.82	0.44
38:A1:1159:A:O2'	38:A1:1160:C:H5'	2.18	0.44
38:A1:1222:G:N2	38:A1:1285:G:HO2'	2.14	0.44
38:A1:1766:G:H2'	38:A1:1767:C:C6	2.52	0.44
38:A1:1900:A:O2'	38:A1:1906:G:N7	2.44	0.44
38:A1:2838:A:OP1	46:AI:154:ARG:NH2	2.34	0.44
38:A1:3182:G:H4'	51:AO:161[A]:LYS:HG2	1.99	0.44
39:A3:45:A:H2'	39:A3:46:A:C8	2.53	0.44
40:A4:144:G:H5'	50:AN:57:GLN:NE2	2.33	0.44
40:A4:145:U:H2'	40:A4:146:U:C6	2.53	0.44
41:AD:93:THR:HG22	41:AD:158:ARG:HH11	1.83	0.44
52:AP:40:GLU:OE1	52:AP:42:THR:N	2.47	0.44
60:AX:134:ASP:OD1	60:AX:135:ILE:N	2.51	0.44
79:E:49:PHE:CE1	79:E:51:GLY:CA	2.99	0.44
7:BI:41:LYS:HG3	7:BI:60:ILE:HG22	2.00	0.44
11:BO:17:ALA:HA	11:BO:30:VAL:HG22	1.99	0.44
13:BW:81:VAL:O	13:BW:122:SER:OG	2.34	0.44
14:BX:108:GLY:HA2	34:B5:600:U:OP2	2.18	0.44
20:BF:49:GLU:O	20:BF:51:VAL:HG23	2.18	0.44
27:BU:22:ILE:CG2	27:BU:93:LEU:HB2	2.48	0.44
28:BZ:57:TYR:O	28:BZ:103:ARG:HG3	2.17	0.44
34:B5:397:A:H2'	34:B5:398:G:O4'	2.17	0.44
34:B5:416:A:H3'	34:B5:417:A:H8	1.82	0.44
34:B5:1059:U:HO2'	34:B5:1060:U:H6	1.64	0.44
34:B5:1668:G:H5'	38:A1:1936:A:H5'	1.98	0.44
34:B5:1674:C:H2'	34:B5:1675:C:H6	1.83	0.44
36:AB:124:LYS:HG2	38:A1:3316:A:N1	2.32	0.44
36:AB:132:LYS:NZ	38:A1:3292:A:H4'	2.33	0.44
37:AC:22:LEU:HA	37:AC:23:PRO:HD3	1.79	0.44
38:A1:80:G:H2'	38:A1:81:C:H6	1.83	0.44
38:A1:249:U:C2	38:A1:251:G:O3'	2.70	0.44
38:A1:1019:G:N2	38:A1:1020:G:O6	2.50	0.44
38:A1:1280:C:O2'	38:A1:1281:G:OP1	2.24	0.44
38:A1:1460:A:H5'	66:Ad:51:LEU:O	2.18	0.44
38:A1:1724:U:O4	54:AR:125:LYS:NZ	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2289:U:H2'	38:A1:2290:C:H6	1.82	0.44
42:AE:62:THR:HB	42:AE:78:ARG:HB3	1.98	0.44
51:AO:127[A]:LEU:HD22	55:AS:156:VAL:HG13	2.00	0.44
1:BA:120:LEU:HD11	1:BA:144:ILE:HG13	1.99	0.44
1:BA:139:VAL:HG23	1:BA:141:ILE:HG13	1.99	0.44
4:BE:21:ASP:OD1	4:BE:21:ASP:N	2.49	0.44
7:BI:3:ILE:HD11	7:BI:32:GLN:OE1	2.17	0.44
8:BJ:54:ARG:O	8:BJ:58:ASP:OD1	2.36	0.44
14:BX:109:ARG:O	14:BX:112:LYS:HB2	2.17	0.44
17:Bb:19:HIS:HD2	17:Bb:21:LEU:H	1.64	0.44
19:BD:12:VAL:HG11	30:Bd:36:LEU:HD22	2.00	0.44
19:BD:67:ASN:HB2	21:BK:91:TYR:CZ	2.53	0.44
22:BP:47:ARG:HH21	34:B5:1555:A:P	2.40	0.44
34:B5:518:A:O2'	34:B5:519:C:H5'	2.18	0.44
38:A1:73:C:C4	71:Ai:15:LYS:HD3	2.52	0.44
38:A1:93:C:OP2	38:A1:2764:C:O2'	2.30	0.44
38:A1:945:C:H2'	38:A1:946:U:H6	1.78	0.44
38:A1:2160:G:H2'	38:A1:2161:G:C8	2.52	0.44
38:A1:2661:G:H2'	38:A1:2662:G:C8	2.53	0.44
39:A3:6:C:O2'	41:AD:50:ARG:NH2	2.50	0.44
43:AF:222:HIS:CE1	43:AF:224:ILE:HD12	2.53	0.44
48:AL:64:LYS:HE2	48:AL:65:TYR:CZ	2.53	0.44
49:AM:47:ASP:OD1	49:AM:49:PRO:HG3	2.18	0.44
49:AM:65:LEU:HG	55:AS:172:TYR:OH	2.17	0.44
56:AT:136:ARG:HD2	56:AT:139:ARG:NH2	2.33	0.44
71:Ai:50:LEU:HB3	71:Ai:55:ARG:HD3	1.99	0.44
80:EC:6875:C:N3	80:EC:6876:A:N6	2.60	0.44
1:BA:40:ALA:O	24:BR:105:GLN:HG2	2.18	0.44
5:BG:85:ARG:HB3	5:BG:87:ARG:HH12	1.83	0.44
34:B5:972:G:O2'	38:A1:847:A:N6	2.51	0.44
34:B5:1760:G:H1'	34:B5:1781:MA6:H2	1.99	0.44
38:A1:63:A:H2'	38:A1:64:G:O4'	2.18	0.44
38:A1:179:C:N3	38:A1:237:G:N2	2.62	0.44
38:A1:243:G:H5''	38:A1:243:G:C8	2.47	0.44
38:A1:701:G:H2'	38:A1:702:C:C6	2.53	0.44
38:A1:753:C:H2'	38:A1:754:G:H8	1.82	0.44
38:A1:1709:C:H2'	38:A1:1710:C:H6	1.82	0.44
38:A1:2115:G:H22	38:A1:2120:A:H1'	1.82	0.44
38:A1:2361:A:H2'	38:A1:2362:C:H6	1.81	0.44
38:A1:2726:C:O2'	38:A1:2727:A:H2'	2.18	0.44
38:A1:2777:G:C2	63:Aa:60:TYR:CE2	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3212:C:H2'	38:A1:3213:A:O4'	2.18	0.44
47:AJ:82:ARG:O	47:AJ:85:LYS:HG2	2.18	0.44
49:AM:48:GLY:HA3	49:AM:53:VAL:HB	1.99	0.44
57:AU:13:LYS:HE2	57:AU:15:PHE:CZ	2.46	0.44
68:Af:42:GLN:HA	68:Af:45:LEU:HG	1.99	0.44
68:Af:49:ILE:HD11	68:Af:71:VAL:CG2	2.47	0.44
79:E:87:VAL:HG12	79:E:116:LEU:HD11	2.00	0.44
5:BG:17:GLU:OE1	5:BG:17:GLU:N	2.51	0.44
6:BH:46:ILE:HA	6:BH:59:ALA:O	2.18	0.44
6:BH:159:VAL:C	6:BH:163:ASP:OD2	2.60	0.44
7:BI:178:ARG:NH1	34:B5:207:U:O2	2.51	0.44
8:BJ:62:ARG:CZ	8:BJ:68:LYS:HD3	2.48	0.44
16:Ba:14:GLY:C	16:Ba:15:ARG:HD2	2.42	0.44
25:BS:140:THR:HG21	34:B5:1176:G:O6	2.18	0.44
34:B5:121:U:H2'	34:B5:122:U:C6	2.52	0.44
34:B5:472:U:H2'	34:B5:473:A:C8	2.53	0.44
34:B5:683:C:H2'	34:B5:684:A:H8	1.82	0.44
34:B5:1175:U:H2'	34:B5:1176:G:H8	1.83	0.44
34:B5:1508:U:H2'	34:B5:1509:C:C6	2.53	0.44
37:AC:98:ARG:NH2	38:A1:804:C:OP1	2.50	0.44
38:A1:2201:G:H2'	38:A1:2202:C:C6	2.52	0.44
43:AF:85:PHE:CZ	43:AF:147:LEU:HD21	2.53	0.44
49:AM:118:PHE:O	49:AM:122:VAL:HG23	2.18	0.44
53:AQ:116:LYS:NZ	63:Aa:88:ASP:OD2	2.50	0.44
58:AV:90:GLY:O	59:AW:16:GLY:HA2	2.18	0.44
80:EC:6863:C:H3'	80:EC:6864:A:C8	2.53	0.44
4:BE:128:LYS:HG2	4:BE:140:VAL:HB	2.00	0.43
4:BE:187:ARG:HD3	34:B5:752:A:OP1	2.17	0.43
5:BG:75:LEU:O	5:BG:94:ARG:HA	2.17	0.43
15:BY:35:VAL:HB	15:BY:39:GLU:OE2	2.18	0.43
21:BK:60:SER:HB3	21:BK:65:TYR:HE1	1.82	0.43
34:B5:1353:U:O2'	34:B5:1354:G:O4'	2.35	0.43
34:B5:1625:C:H2'	34:B5:1626:U:H6	1.83	0.43
38:A1:1157:G:H2'	38:A1:1158:A:O4'	2.18	0.43
38:A1:1213:G:H4'	55:AS:90:MET:HB2	1.98	0.43
38:A1:2459:A:H62	38:A1:2461:A:N6	2.15	0.43
38:A1:2674:A:N1	47:AJ:124:GLY:HA3	2.33	0.43
38:A1:3000:A:H2'	38:A1:3001:C:H6	1.83	0.43
38:A1:3358:U:H2'	38:A1:3359:A:C8	2.53	0.43
39:A3:47:C:H2'	39:A3:48:U:C6	2.53	0.43
39:A3:56:A:H4'	47:AJ:152:HIS:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:AG:29:SER:HB3	44:AG:31:PRO:HD3	2.00	0.43
49:AM:59:ASN:H	49:AM:62:GLN:HE21	1.66	0.43
57:AU:80:THR:HG21	57:AU:95:PHE:HD2	1.82	0.43
65:Ac:13:LYS:O	65:Ac:17:VAL:HG23	2.18	0.43
66:Ad:14:ILE:HD12	66:Ad:39:PHE:CG	2.53	0.43
79:E:59:PRO:O	79:E:171:ASN:ND2	2.51	0.43
2:BB:61:LEU:O	2:BB:63:GLY:N	2.51	0.43
10:BN:69:ASN:HB2	10:BN:73:ARG:HD2	2.01	0.43
13:BW:106:THR:HG23	13:BW:122:SER:O	2.17	0.43
14:BX:55:GLU:HG2	14:BX:73:ARG:HB2	2.00	0.43
32:Bf:123:ASN:O	32:Bf:130:VAL:HG12	2.18	0.43
34:B5:751:G:H2'	34:B5:752:A:C8	2.53	0.43
34:B5:888:U:O2	34:B5:988:A:O2'	2.35	0.43
34:B5:1226:A:H61	34:B5:1256:A:H5''	1.82	0.43
35:AA:101:VAL:HG22	35:AA:165:VAL:HG22	2.00	0.43
35:AA:127:ALA:HB2	35:AA:134:VAL:HG23	2.01	0.43
36:AB:251:CYS:SG	38:A1:2944:U:H1'	2.58	0.43
38:A1:149:U:OP1	50:AN:49:ARG:NH1	2.39	0.43
38:A1:565:U:H2'	38:A1:566:G:H8	1.83	0.43
38:A1:1146:C:H4'	38:A1:1331:U:C4	2.52	0.43
38:A1:1174:G:H1'	38:A1:1181:U:N3	2.33	0.43
38:A1:1240:A:H2'	38:A1:1241:U:H4'	2.00	0.43
38:A1:1495:U:C5	38:A1:1835:A:N1	2.81	0.43
38:A1:1565:G:H1	38:A1:1574:C:H42	1.65	0.43
38:A1:2361:A:H2'	38:A1:2362:C:C6	2.53	0.43
40:A4:27:U:H2'	40:A4:28:C:C6	2.53	0.43
42:AE:5:LYS:HA	42:AE:5:LYS:HD2	1.88	0.43
42:AE:87:THR:HG22	42:AE:88:SER:N	2.33	0.43
42:AE:102:ASN:ND2	42:AE:104:GLU:OE2	2.51	0.43
45:AH:87:LYS:HD3	45:AH:89:LYS:HE2	2.00	0.43
55:AS:96:ASP:OD2	55:AS:101:ALA:HB3	2.18	0.43
56:AT:48:ILE:HB	56:AT:95:HIS:CE1	2.53	0.43
56:AT:75:ILE:HG23	56:AT:86:GLU:HG3	2.00	0.43
80:EC:6845:G:H2'	80:EC:6846:C:C6	2.53	0.43
4:BE:157:ASN:OD1	4:BE:222:LEU:HD21	2.18	0.43
22:BP:25:LEU:HA	22:BP:28:MET:HE2	2.00	0.43
24:BR:102:VAL:O	24:BR:121:VAL:HA	2.18	0.43
25:BS:114:GLU:HA	25:BS:117:LYS:HB2	2.01	0.43
28:BZ:65:LEU:HB3	28:BZ:71:ILE:HD11	2.00	0.43
29:Bc:10:ALA:O	29:Bc:54:LEU:HD23	2.18	0.43
34:B5:5:U:H2'	34:B5:6:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1310:U:H2'	34:B5:1311:U:C6	2.53	0.43
34:B5:1727:G:H2'	34:B5:1728:A:C8	2.53	0.43
35:AA:242:ARG:NH1	38:A1:2154:U:OP1	2.52	0.43
36:AB:5:LYS:O	36:AB:5:LYS:HG2	2.19	0.43
38:A1:183:G:H2'	38:A1:184:U:C6	2.53	0.43
38:A1:634:C:H5'	68:Af:21:ARG:O	2.18	0.43
38:A1:1477:A:OP1	38:A1:3075:G:O2'	2.27	0.43
38:A1:1670:C:H4'	38:A1:1859:A:O3'	2.18	0.43
38:A1:1833:G:H21	74:A1:4:GLN:HE22	1.66	0.43
38:A1:1922:A:H2'	38:A1:1923:C:O4'	2.18	0.43
38:A1:2107:A:H2'	38:A1:2108:C:O4'	2.19	0.43
38:A1:2424:A:H2'	38:A1:2425:G:O4'	2.18	0.43
38:A1:3095:U:H2'	38:A1:3096:C:H6	1.83	0.43
48:AL:157:ARG:NH2	63:Aa:146:GLU:OE1	2.47	0.43
49:AM:43:LYS:HD3	49:AM:59:ASN:HA	2.00	0.43
55:AS:30:PHE:CE2	55:AS:103:VAL:HG21	2.53	0.43
1:BA:82:GLY:O	1:BA:86:VAL:HG12	2.19	0.43
7:BI:76:THR:CG2	7:BI:105:ASP:HB2	2.47	0.43
9:BL:57:LYS:HE2	9:BL:131:ILE:HG23	2.00	0.43
11:BO:25:ASP:N	11:BO:55:SER:HB3	2.33	0.43
16:Ba:7:SER:O	16:Ba:7:SER:OG	2.35	0.43
16:Ba:51:ARG:HH21	29:Bc:60:GLU:HB3	1.83	0.43
22:BP:127:ARG:NH1	22:BP:130:ARG:HE	2.16	0.43
28:BZ:60:VAL:HG12	28:BZ:80:LEU:HD21	2.00	0.43
34:B5:875:G:H2'	34:B5:877:G:OP1	2.18	0.43
34:B5:1163:A:H2'	34:B5:1164:G:O4'	2.18	0.43
34:B5:1207:C:H42	34:B5:1456:C:H5	1.66	0.43
34:B5:1280:4AC:H2'	34:B5:1281:G:H8	1.83	0.43
34:B5:1575:7MG:C2'	34:B5:1576:A:H8	2.15	0.43
35:AA:128:ARG:NE	38:A1:2177:G:OP2	2.42	0.43
38:A1:149:U:P	50:AN:49:ARG:HH12	2.39	0.43
38:A1:709:A:H2'	38:A1:710:A:O4'	2.19	0.43
38:A1:2440:G:C2	38:A1:2441:A:C5	3.07	0.43
38:A1:2457:G:C2	38:A1:2486:A:C2	2.95	0.43
38:A1:2656:A:C4	38:A1:2658:G:N7	2.87	0.43
38:A1:3285:C:H2'	38:A1:3286:G:C8	2.53	0.43
40:A4:94:C:HO2'	40:A4:95:G:H8	1.67	0.43
43:AF:175:LYS:HE3	43:AF:176:TYR:CZ	2.54	0.43
43:AF:184:LEU:O	43:AF:188:ILE:HG12	2.19	0.43
60:AX:25:LYS:HD3	60:AX:27:ARG:NH2	2.34	0.43
63:Aa:75:LEU:HB3	63:Aa:118:ILE:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Ah:14:LYS:HE2	70:Ah:14:LYS:HB2	1.84	0.43
2:BB:112:SER:HA	2:BB:115:ARG:HH12	1.83	0.43
3:BC:106:ASP:OD1	3:BC:110:HIS:HB2	2.18	0.43
4:BE:112:HIS:NE2	4:BE:237:SER:O	2.51	0.43
7:BI:72:ILE:HG21	7:BI:112:TRP:CE2	2.54	0.43
10:BN:89:TYR:CD2	10:BN:150:VAL:HG12	2.53	0.43
26:BT:93:HIS:ND1	34:B5:1525:A:OP1	2.47	0.43
31:Bg:176:LYS:O	31:Bg:177:MET:HE2	2.19	0.43
34:B5:436:A2M:H8	34:B5:436:A2M:O5'	2.18	0.43
34:B5:1118:G:P	76:An:21:ARG:HH22	2.40	0.43
34:B5:1251:U:O2'	34:B5:1252:C:H5''	2.18	0.43
34:B5:1277:G:H22	34:B5:1434:U:H3	1.66	0.43
35:AA:181:LYS:HB2	38:A1:860:G:C5	2.54	0.43
37:AC:131:VAL:O	37:AC:135:VAL:HG23	2.19	0.43
38:A1:277:G:H2'	38:A1:278:U:C6	2.54	0.43
38:A1:359:U:O3'	72:Aj:25:ARG:NH2	2.49	0.43
38:A1:843:A:H2'	38:A1:844:G:O4'	2.19	0.43
38:A1:1389:G:O2'	38:A1:1418:A:N1	2.41	0.43
38:A1:1646:G:O2'	38:A1:1808:G:N2	2.43	0.43
38:A1:1744:G:H2'	38:A1:1745:C:C6	2.53	0.43
38:A1:1831:U:O2'	40:A4:114:G:OP1	2.21	0.43
38:A1:1915:A:H4'	54:AR:83:GLY:O	2.18	0.43
38:A1:1950:U:H3	38:A1:2096:A:N6	2.17	0.43
38:A1:2318:U:H2'	38:A1:2319:U:O4'	2.18	0.43
38:A1:2974:U:H2'	38:A1:2975:U:C6	2.53	0.43
50:AN:64:VAL:CG1	50:AN:102:ALA:HB1	2.49	0.43
53:AQ:122:ILE:HG22	53:AQ:123:THR:O	2.18	0.43
73:Ak:22:THR:HG22	73:Ak:23:ALA:N	2.33	0.43
74:Al:24:PRO:HB2	74:Al:27:ILE:HD12	2.00	0.43
2:BB:149:GLN:HE21	2:BB:151:LYS:HG3	1.83	0.43
8:BJ:83:VAL:HG13	8:BJ:85:VAL:HG23	1.99	0.43
22:BP:15:HIS:H	22:BP:22:LEU:CD1	2.32	0.43
23:BQ:83:GLN:NE2	23:BQ:115:THR:O	2.52	0.43
25:BS:139:LYS:HE3	34:B5:1179:G:O6	2.19	0.43
27:BU:67:THR:HG22	34:B5:1199:G:O6	2.18	0.43
29:Bc:11:LYS:HB2	29:Bc:33:LEU:HD21	2.01	0.43
31:Bg:180:ALA:HB3	31:Bg:190:ALA:HB3	1.99	0.43
34:B5:487:G:N2	34:B5:488:G:N3	2.67	0.43
34:B5:1344:A:H4'	34:B5:1345:A:OP1	2.17	0.43
34:B5:1553:G:N2	34:B5:1555:A:H3'	2.34	0.43
34:B5:1663:G:H2'	34:B5:1664:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:95:THR:HB	36:AB:98:GLY:O	2.18	0.43
36:AB:206:ASP:HB3	36:AB:287:LYS:HZ1	1.83	0.43
36:AB:255:TRP:CD1	38:A1:2395:G:H5''	2.53	0.43
38:A1:240:U:N3	38:A1:241:G:N2	2.66	0.43
38:A1:1343:A:H2'	38:A1:1344:G:C8	2.53	0.43
38:A1:2111:G:C8	59:AW:49:ILE:HG22	2.53	0.43
38:A1:2405:C:O2	38:A1:2819:A:N1	2.52	0.43
38:A1:2535:A:C2	38:A1:2536:A:H1'	2.53	0.43
38:A1:2964:G:N2	38:A1:2967:A:OP2	2.49	0.43
42:AE:39:VAL:HA	42:AE:52:VAL:O	2.19	0.43
44:AG:74:THR:O	44:AG:77:GLN:NE2	2.51	0.43
47:AJ:15:GLU:OE2	47:AJ:140:ARG:NH2	2.51	0.43
60:AX:46:TYR:HB3	70:Ah:75:TYR:O	2.18	0.43
67:Ae:9:ILE:HG12	67:Ae:63:THR:CG2	2.48	0.43
72:Aj:87:SER:OG	72:Aj:88:ALA:N	2.52	0.43
4:BE:139:VAL:HG13	4:BE:150:PRO:HG3	2.00	0.43
11:BO:87:GLY:HA3	11:BO:120:PRO:HG2	2.00	0.43
34:B5:718:U:H2'	34:B5:719:U:H5''	2.00	0.43
34:B5:1008:G:H2'	34:B5:1009:U:C6	2.53	0.43
34:B5:1461:C:H2'	34:B5:1462:G:C8	2.53	0.43
34:B5:1586:A:H2'	34:B5:1587:A:O4'	2.19	0.43
38:A1:19:U:H2'	38:A1:20:A:C8	2.54	0.43
38:A1:241:G:H2'	38:A1:242:C:O5'	2.18	0.43
38:A1:845:G:O2'	38:A1:847:A:N1	2.33	0.43
38:A1:1563:C:C2'	38:A1:1564:U:H4'	2.46	0.43
38:A1:1597:C:OP1	69:Ag:8:ARG:NH1	2.52	0.43
38:A1:1622:U:H2'	38:A1:1623:G:C8	2.54	0.43
38:A1:2504:U:O5'	38:A1:2504:U:H6	2.02	0.43
38:A1:2566:C:H2'	38:A1:2567:C:H6	1.83	0.43
38:A1:2568:C:O2'	38:A1:2569:A:O4'	2.31	0.43
38:A1:2656:A:C5	38:A1:2658:G:C8	3.07	0.43
38:A1:2681:U:OP1	47:AJ:50:ALA:HA	2.19	0.43
39:A3:12:U:OP2	39:A3:68:C:O2'	2.36	0.43
39:A3:99:G:O2'	43:AF:128:LYS:NZ	2.40	0.43
43:AF:147:LEU:HD11	43:AF:207:LEU:HD21	2.01	0.43
45:AH:1:MET:CG	45:AH:3:TYR:CE1	3.01	0.43
52:AP:40:GLU:OE2	52:AP:112:LEU:O	2.36	0.43
53:AQ:158:HIS:ND1	53:AQ:186:VAL:HG23	2.34	0.43
70:Ah:31:LEU:HB3	70:Ah:44:ILE:CD1	2.48	0.43
70:Ah:102:GLU:CG	70:Ah:103:LYS:N	2.82	0.43
72:Aj:17:THR:O	72:Aj:25:ARG:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:107:GLY:HA2	4:BE:189:LEU:HG	2.00	0.43
11:BO:112:ILE:HB	16:Ba:57:SER:HB2	2.01	0.43
13:BW:28:ARG:HD3	13:BW:60:LYS:HE2	2.00	0.43
13:BW:56:HIS:O	34:B5:861:U:O2'	2.33	0.43
15:BY:41:ARG:HG3	15:BY:57:VAL:HG22	2.01	0.43
20:BF:29:ILE:HG21	23:BQ:57:LEU:HD11	2.01	0.43
21:BK:32:HIS:HD2	21:BK:42:VAL:HG21	1.84	0.43
26:BT:18:TYR:CD1	26:BT:135:ILE:HG13	2.53	0.43
34:B5:590:C:H2'	34:B5:591:A:H8	1.84	0.43
34:B5:646:C:H2'	34:B5:647:G:O4'	2.19	0.43
34:B5:837:G:H2'	34:B5:838:G:C8	2.53	0.43
38:A1:426:G:OP1	67:Ae:15:LYS:NZ	2.33	0.43
38:A1:863:C:H2'	38:A1:864:G:O4'	2.19	0.43
38:A1:947:G:C5'	67:Ae:55:ILE:HB	2.48	0.43
38:A1:1576:G:C2'	38:A1:1577:G:H5'	2.48	0.43
38:A1:1727:G:OP1	78:Ap:44:LYS:NZ	2.43	0.43
38:A1:2150:G:H22	38:A1:2313:A:H2	1.66	0.43
38:A1:2526:C:H2'	38:A1:2527:G:C8	2.54	0.43
38:A1:3131:U:H2'	38:A1:3132:C:C6	2.54	0.43
49:AM:45:LEU:HD13	55:AS:97:VAL:HG11	2.00	0.43
62:AZ:48:ARG:NH2	62:AZ:69:LYS:HD2	2.34	0.43
69:Ag:101:VAL:C	69:Ag:104:VAL:HG12	2.44	0.43
5:BG:159:ARG:NH2	34:B5:79:C:OP1	2.41	0.43
7:BI:16:ALA:HB2	34:B5:354:C:H5''	1.99	0.43
7:BI:39:GLY:HA2	7:BI:61:GLU:HG2	2.00	0.43
8:BJ:126:ARG:HD3	18:Be:33:ARG:HD3	2.01	0.43
13:BW:81:VAL:HG13	13:BW:85:ASP:OD1	2.19	0.43
14:BX:19:ARG:O	14:BX:23:ARG:HG3	2.19	0.43
20:BF:161:ASP:OD1	20:BF:162:VAL:N	2.52	0.43
21:BK:7:ASP:HA	21:BK:10:LYS:HE3	2.01	0.43
34:B5:44:U:H5	34:B5:437:A:N1	2.16	0.43
34:B5:1449:U:H2'	34:B5:1450:U:H6	1.83	0.43
34:B5:1669:U:H2'	34:B5:1670:G:O4'	2.19	0.43
36:AB:232:ARG:NH1	36:AB:266:ARG:O	2.46	0.43
38:A1:271:C:H2'	38:A1:272:G:O4'	2.19	0.43
38:A1:612:U:H2'	38:A1:613:G:H8	1.84	0.43
38:A1:775:A:H8	38:A1:775:A:OP2	2.01	0.43
38:A1:1086:C:H2'	38:A1:1087:G:O4'	2.19	0.43
38:A1:1143:A:H5'	38:A1:1368:U:H1'	2.01	0.43
38:A1:1482:A:H5''	38:A1:1858:A:C6	2.54	0.43
38:A1:2462:A:H2'	38:A1:2463:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2712:U:H2'	38:A1:2713:U:C6	2.53	0.43
41:AD:111:GLN:HA	41:AD:116:ASP:OD2	2.19	0.43
61:AY:82:VAL:HG12	61:AY:83:ASP:O	2.18	0.43
80:EC:6850:C:H1'	80:EC:6851:G:N7	2.33	0.43
80:EC:6852:U:O2'	80:EC:6853:G:O4'	2.32	0.43
8:BJ:86:LEU:HD22	8:BJ:96:VAL:HG12	2.00	0.43
24:BR:72:LYS:HA	24:BR:75:GLU:HG3	2.01	0.43
31:Bg:206:PRO:HD3	31:Bg:245:PHE:HB3	2.01	0.43
34:B5:650:U:H2'	34:B5:651:G:C8	2.54	0.43
34:B5:1119:G:H2'	34:B5:1120:U:C6	2.54	0.43
34:B5:1649:G:H2'	34:B5:1650:U:H6	1.84	0.43
34:B5:1717:G:H2'	34:B5:1718:G:H8	1.83	0.43
35:AA:230:VAL:HG11	38:A1:2424:A:N1	2.33	0.43
36:AB:292:ALA:HA	36:AB:303:LYS:O	2.18	0.43
37:AC:136:LEU:HD21	37:AC:143:GLU:HG3	2.01	0.43
37:AC:283:THR:HG22	37:AC:289:ILE:HD11	2.00	0.43
38:A1:177:U:H3'	38:A1:178:U:C5	2.54	0.43
38:A1:238:A:C5'	38:A1:238:A:H8	2.31	0.43
38:A1:258:G:H2'	38:A1:259:C:H6	1.83	0.43
38:A1:381:U:H2'	38:A1:382:U:C6	2.54	0.43
38:A1:960:U:H4'	38:A1:963:G:N1	2.33	0.43
38:A1:1821:U:C2	69:Ag:67:LYS:HG2	2.54	0.43
38:A1:2200:U:H2'	38:A1:2201:G:O4'	2.18	0.43
38:A1:2466:G:H4'	79:E:60:ARG:HH11	1.82	0.43
38:A1:2661:G:H2'	38:A1:2662:G:H8	1.84	0.43
38:A1:3059:G:H4'	38:A1:3373:U:O2'	2.18	0.43
42:AE:40:LEU:HD11	42:AE:54:TYR:HB2	2.00	0.43
50:AN:73:ARG:HB2	50:AN:92:LEU:HD12	2.01	0.43
60:AX:71:THR:O	60:AX:74:LYS:HG3	2.19	0.43
60:AX:106:ASP:OD2	60:AX:127:THR:HG21	2.18	0.43
80:EC:6834:U:H2'	80:EC:6874:A:C8	2.54	0.43
6:BH:107:ARG:HA	34:B5:743:U:OP1	2.19	0.42
11:BO:84:ARG:HG2	11:BO:85:ALA:O	2.18	0.42
11:BO:84:ARG:HH12	11:BO:86:THR:HA	1.84	0.42
12:BV:39:VAL:HA	12:BV:44:ARG:O	2.19	0.42
15:BY:35:VAL:O	15:BY:36:SER:HB2	2.19	0.42
18:Be:55:ARG:NH2	34:B5:557:G:H4'	2.33	0.42
22:BP:31:GLU:O	22:BP:35:LYS:HG2	2.19	0.42
24:BR:63:LYS:NZ	31:Bg:283:LYS:O	2.42	0.42
27:BU:89:ARG:HH22	34:B5:1383:G:P	2.41	0.42
34:B5:539:G:H8	34:B5:539:G:OP2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:683:C:H2'	34:B5:684:A:C8	2.54	0.42
34:B5:1081:A:H2	34:B5:1082:C:H42	1.67	0.42
34:B5:1146:G:N3	34:B5:1635:A:H2	2.17	0.42
34:B5:1251:U:O2'	34:B5:1252:C:H6	1.99	0.42
34:B5:1699:G:N2	34:B5:1700:C:H1'	2.34	0.42
38:A1:316:U:O4	71:AI:28:TYR:HA	2.18	0.42
38:A1:1340:G:H2'	38:A1:1341:U:C6	2.53	0.42
38:A1:1404:G:N2	38:A1:1407:A:OP2	2.39	0.42
38:A1:1941:C:H2'	38:A1:1942:U:C6	2.54	0.42
38:A1:3285:C:H2'	38:A1:3286:G:H8	1.84	0.42
40:A4:39:G:H1'	40:A4:104:A:N6	2.34	0.42
42:AE:170:LYS:HD2	42:AE:173:MET:HE3	1.87	0.42
43:AF:151:ARG:HE	43:AF:244:ASN:HA	1.84	0.42
44:AG:34:PHE:CD1	44:AG:42:PRO:HD3	2.54	0.42
44:AG:204:ARG:O	44:AG:208:GLU:HG2	2.18	0.42
65:Ac:30:THR:HG23	65:Ac:42:ILE:HD12	2.01	0.42
79:E:196:LYS:HB2	79:E:200:ASN:CG	2.43	0.42
1:BA:190:ASP:HB3	1:BA:193:GLN:NE2	2.34	0.42
2:BB:38:PHE:CD1	2:BB:73:LEU:CD1	3.00	0.42
14:BX:106:GLY:O	34:B5:599:A:H4'	2.19	0.42
21:BK:89:GLY:N	21:BK:90:THR:HA	2.34	0.42
23:BQ:83:GLN:HE22	23:BQ:119:ALA:HA	1.84	0.42
23:BQ:114:ARG:NH1	34:B5:1411:A:OP1	2.37	0.42
33:BM:119:SER:HB3	34:B5:1228:G:OP1	2.19	0.42
34:B5:15:U:H2'	34:B5:16:G:O4'	2.19	0.42
34:B5:100:A2M:H8	34:B5:100:A2M:O5'	2.19	0.42
34:B5:183:U:H2'	34:B5:184:C:C6	2.54	0.42
34:B5:220:A:H2	34:B5:843:U:H1'	1.83	0.42
38:A1:175:C:N4	38:A1:242:C:N4	2.61	0.42
38:A1:209:A:H4'	38:A1:211:A:C8	2.53	0.42
38:A1:291:C:OP1	50:AN:68:ARG:HB3	2.19	0.42
38:A1:585:A:H2'	38:A1:586:C:H6	1.80	0.42
38:A1:1181:U:O4	51:AO:21[A]:SER:OG	2.30	0.42
38:A1:1740:U:H1'	38:A1:1741:A:H2	1.83	0.42
38:A1:2309:A:N3	38:A1:2961:G:O2'	2.46	0.42
38:A1:2566:C:H2'	38:A1:2567:C:C6	2.55	0.42
38:A1:3065:G:H2'	38:A1:3066:U:C6	2.54	0.42
46:AI:206:LEU:O	46:AI:209:ASN:N	2.52	0.42
50:AN:9:GLU:HG3	71:AI:44:VAL:HG11	1.99	0.42
53:AQ:83:VAL:O	53:AQ:103:ALA:HA	2.18	0.42
55:AS:24:LEU:HD21	56:AT:141:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Ai:50:LEU:CB	71:Ai:55:ARG:CD	2.97	0.42
8:BJ:92:LYS:HB2	8:BJ:95:TYR:HD2	1.83	0.42
16:Ba:45:VAL:CG1	16:Ba:46:GLU:N	2.81	0.42
17:Bb:58:SER:OG	17:Bb:59:CYS:N	2.53	0.42
20:BF:123:VAL:HG22	28:BZ:92:ILE:HD13	2.02	0.42
21:BK:90:THR:O	21:BK:93:GLN:HB2	2.19	0.42
22:BP:30:THR:OG1	22:BP:88:GLU:OE1	2.29	0.42
23:BQ:98:ASP:OD1	31:Bg:58:VAL:HA	2.20	0.42
26:BT:88:VAL:HG22	34:B5:1601:G:N2	2.34	0.42
27:BU:23:ARG:HH22	34:B5:1347:U:P	2.42	0.42
34:B5:181:A:H2'	34:B5:182:A:C8	2.54	0.42
34:B5:224:C:N4	34:B5:838:G:H1	2.17	0.42
34:B5:698:U:O4	34:B5:741:C:N3	2.52	0.42
34:B5:909:U:H2'	34:B5:910:C:C6	2.54	0.42
34:B5:1392:U:H2'	34:B5:1393:C:C6	2.54	0.42
34:B5:1405:G:H2'	34:B5:1406:A:C8	2.54	0.42
37:AC:3:ARG:HA	37:AC:3:ARG:HD2	1.76	0.42
38:A1:391:A:H2'	38:A1:392:G:O4'	2.19	0.42
38:A1:511:G:H2'	38:A1:512:U:O4'	2.20	0.42
38:A1:798:G:OP1	63:Aa:33:GLY:N	2.47	0.42
38:A1:2265:C:C2	38:A1:2266:U:C5	3.07	0.42
38:A1:3337:G:H2'	38:A1:3338:C:C6	2.55	0.42
47:AJ:114:ILE:HG13	47:AJ:114:ILE:O	2.19	0.42
59:AW:46:PRO:HB2	59:AW:54:LEU:HD12	2.01	0.42
72:Aj:14:LYS:NZ	74:Al:51:ILE:HD11	2.33	0.42
1:BA:125:ASP:OD1	1:BA:164:ASN:ND2	2.52	0.42
3:BC:138:PRO:CB	12:BV:11:LEU:HD21	2.49	0.42
5:BG:22:HIS:HA	5:BG:25:ARG:HG2	2.01	0.42
9:BL:36:LYS:HD3	34:B5:248:U:H4'	2.01	0.42
11:BO:40:ALA:HB2	11:BO:70:LYS:CG	2.49	0.42
11:BO:63:ALA:O	11:BO:67:VAL:HG23	2.19	0.42
18:Be:55:ARG:HG3	18:Be:58:PRO:HG3	2.01	0.42
22:BP:33:PHE:CD2	22:BP:87:PRO:HD3	2.54	0.42
34:B5:272:U:O3'	34:B5:273:G:H8	2.02	0.42
34:B5:519:C:H2'	34:B5:520:A:O4'	2.19	0.42
34:B5:1226:A:N6	34:B5:1256:A:O4'	2.52	0.42
34:B5:1367:G:H2'	34:B5:1368:G:O4'	2.19	0.42
34:B5:1393:C:H2'	34:B5:1394:G:H8	1.84	0.42
34:B5:1767:G:H4'	34:B5:1768:G:C4	2.54	0.42
35:AA:116:VAL:HB	35:AA:126:LEU:HB2	2.00	0.42
37:AC:164:GLU:N	37:AC:164:GLU:OE1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:258:G:H2'	38:A1:259:C:C6	2.54	0.42
38:A1:974:G:H2'	38:A1:975:C:H6	1.84	0.42
38:A1:1283:C:HO2'	38:A1:1284:C:P	2.42	0.42
38:A1:1541:G:H2'	38:A1:1542:G:O4'	2.19	0.42
38:A1:1573:G:C8	38:A1:1574:C:C5	3.07	0.42
38:A1:1660:C:H2'	38:A1:1661:G:H8	1.85	0.42
38:A1:2733:A:H2'	38:A1:2734:A:O4'	2.19	0.42
38:A1:2861:U:H2'	38:A1:2862:U:O4'	2.18	0.42
41:AD:17:GLN:HB2	56:AT:20:ARG:HG2	2.01	0.42
44:AG:26:LEU:HB3	62:AZ:53:VAL:HG21	2.00	0.42
55:AS:79:VAL:HG11	55:AS:106:LEU:HD21	2.02	0.42
57:AU:19:VAL:O	57:AU:23:THR:OG1	2.24	0.42
57:AU:99:LYS:HB2	57:AU:102:GLU:HG2	2.02	0.42
58:AV:79:VAL:HG12	58:AV:122:CYS:SG	2.60	0.42
80:EC:6868:C:N4	80:EC:6869:C:H41	2.17	0.42
5:BG:78:THR:OG1	5:BG:79:LYS:N	2.52	0.42
13:BW:83:ILE:HG12	34:B5:749:U:H5''	2.01	0.42
15:BY:86:GLU:OE2	15:BY:90:ARG:HD2	2.20	0.42
17:Bb:17:ARG:NH2	34:B5:1070:C:H5'	2.33	0.42
23:BQ:140:LYS:HE2	23:BQ:142:TYR:CZ	2.55	0.42
24:BR:83:GLN:HG3	24:BR:83:GLN:O	2.19	0.42
31:Bg:144:LEU:HB3	31:Bg:181:TRP:CZ3	2.54	0.42
34:B5:19:A:H2'	34:B5:20:G:O4'	2.19	0.42
34:B5:880:C:H2'	34:B5:881:A:O4'	2.19	0.42
34:B5:1278:G:H2'	34:B5:1279:C:O4'	2.19	0.42
38:A1:768:C:N4	38:A1:769:G:C6	2.87	0.42
38:A1:2445:A:C2	38:A1:2503:G:C2	3.07	0.42
38:A1:2529:A:H2'	38:A1:2530:G:O4'	2.19	0.42
38:A1:2987:A:H2'	38:A1:2988:C:C6	2.55	0.42
38:A1:3306:U:H2'	38:A1:3307:A:H5''	2.02	0.42
40:A4:26:U:H2'	40:A4:27:U:H6	1.83	0.42
41:AD:40:HIS:CE1	56:AT:69:LYS:HA	2.54	0.42
44:AG:37:GLY:C	44:AG:38:GLN:OE1	2.62	0.42
49:AM:43:LYS:NZ	49:AM:59:ASN:HD22	2.17	0.42
51:AO:137[A]:THR:HB	51:AO:140[A]:LYS:HE3	2.00	0.42
53:AQ:151:ARG:O	53:AQ:161:LYS:HE3	2.19	0.42
62:AZ:90:GLU:OE1	62:AZ:93:LYS:HE3	2.20	0.42
77:Ao:14:GLY:C	77:Ao:16:THR:H	2.28	0.42
2:BB:82:ARG:NH1	2:BB:188:LEU:O	2.53	0.42
4:BE:173:ILE:HG22	4:BE:179:LYS:HD3	2.01	0.42
7:BI:37:LYS:C	7:BI:59:ARG:HA	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BX:112:LYS:NZ	34:B5:18:C:O3'	2.46	0.42
20:BF:64:VAL:CG1	20:BF:65:ARG:H	2.30	0.42
21:BK:76:LEU:HD23	21:BK:76:LEU:HA	1.87	0.42
25:BS:134:ARG:HD3	34:B5:1559:A:C6	2.54	0.42
34:B5:53:G:H2'	34:B5:54:C:C6	2.54	0.42
34:B5:618:U:H5''	34:B5:1030:A:C5	2.54	0.42
34:B5:1458:G:H2'	34:B5:1458:G:N3	2.35	0.42
34:B5:1529:C:H2'	34:B5:1530:C:C6	2.54	0.42
38:A1:507:U:H2'	38:A1:508:U:C6	2.55	0.42
38:A1:594:U:H2'	38:A1:609:G:O6	2.19	0.42
38:A1:886:C:OP1	38:A1:1851:G:H5''	2.19	0.42
38:A1:1208:U:H4'	38:A1:1209:G:OP1	2.19	0.42
38:A1:2291:A:H2'	38:A1:2292:U:C6	2.54	0.42
38:A1:2364:G:H22	38:A1:2396:G:H1'	1.83	0.42
38:A1:2662:G:H2'	38:A1:2663:G:H8	1.84	0.42
38:A1:2683:U:H2'	38:A1:2684:C:H6	1.84	0.42
38:A1:3286:G:H2'	38:A1:3287:U:C6	2.54	0.42
39:A3:71:G:H2'	39:A3:72:A:C8	2.54	0.42
40:A4:143:U:H2'	40:A4:144:G:O4'	2.19	0.42
43:AF:130:ILE:HD12	43:AF:134:VAL:HG11	2.02	0.42
44:AG:103:ALA:O	44:AG:107:GLU:HG2	2.18	0.42
71:AI:74:LYS:HD2	71:AI:80:PHE:HD1	1.83	0.42
1:BA:200:ASP:HA	1:BA:203:PHE:CE2	2.54	0.42
3:BC:56:ILE:HA	3:BC:61:LEU:HD12	2.00	0.42
4:BE:42:LEU:N	4:BE:84:ALA:O	2.47	0.42
4:BE:127:LYS:N	4:BE:140:VAL:O	2.45	0.42
7:BI:26:LYS:HE3	34:B5:396:G:O6	2.20	0.42
20:BF:34:GLN:O	20:BF:37:GLN:HG3	2.20	0.42
20:BF:146:THR:HG22	20:BF:221:ALA:HA	2.02	0.42
22:BP:29:SER:HB2	22:BP:32:ASP:HB2	2.01	0.42
34:B5:1196:A:C8	34:B5:1602:C:H4'	2.55	0.42
34:B5:1323:C:H2'	34:B5:1324:G:O4'	2.19	0.42
35:AA:8:GLN:NE2	38:A1:2164:A:OP1	2.53	0.42
38:A1:25:U:H4'	38:A1:26:A:N7	2.35	0.42
38:A1:36:C:H4'	38:A1:808:A:C2	2.54	0.42
38:A1:781:G:OP1	53:AQ:151:ARG:HD2	2.19	0.42
38:A1:837:A:H5'	78:AP:9:GLY:C	2.45	0.42
38:A1:952:A:H4'	38:A1:968:G:N2	2.34	0.42
38:A1:1494:U:OP1	74:AI:44:TRP:HB3	2.20	0.42
38:A1:1503:A:C4	38:A1:1504:A:C8	3.08	0.42
38:A1:1701:C:H2'	38:A1:1702:U:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2283:G:H1'	38:A1:2285:C:N4	2.34	0.42
38:A1:2673:A:H4'	47:AJ:103:GLY:C	2.44	0.42
38:A1:2849:C:H2'	38:A1:2850:G:O4'	2.19	0.42
38:A1:2958:A:H2'	38:A1:2959:OMC:C6	2.54	0.42
39:A3:97:A:OP1	55:AS:40:ARG:NH2	2.42	0.42
44:AG:78:PHE:C	44:AG:80:TYR:H	2.28	0.42
47:AJ:27:GLY:O	47:AJ:31:THR:HG23	2.19	0.42
55:AS:151:PRO:O	55:AS:152:LEU:HD23	2.20	0.42
56:AT:26:HIS:CE1	56:AT:28:SER:HB2	2.55	0.42
65:Ac:14:LEU:O	65:Ac:18:ILE:HG12	2.20	0.42
66:Ad:27:LYS:C	66:Ad:30:PRO:HD2	2.45	0.42
78:Ap:37:TYR:HB2	78:Ap:47:VAL:HB	2.01	0.42
1:BA:69:ASN:HB2	1:BA:72:ASP:OD2	2.20	0.42
1:BA:122:ILE:HA	1:BA:144:ILE:O	2.20	0.42
8:BJ:64:GLU:O	8:BJ:65:LYS:CG	2.66	0.42
8:BJ:83:VAL:HA	8:BJ:149:ARG:HA	2.01	0.42
8:BJ:90:LYS:HB2	8:BJ:95:TYR:CG	2.55	0.42
11:BO:120:PRO:HB2	34:B5:887:A:H5''	2.02	0.42
14:BX:17:VAL:HG22	14:BX:20:ARG:HH22	1.85	0.42
21:BK:14:TYR:CE2	21:BK:34:GLU:HG3	2.54	0.42
25:BS:15:LEU:HD23	25:BS:22:VAL:O	2.20	0.42
26:BT:97:SER:OG	34:B5:1504:G:OP1	2.38	0.42
32:Bf:134:ASN:HA	32:Bf:138:ARG:O	2.20	0.42
33:BM:50:LYS:HD2	33:BM:50:LYS:HA	1.79	0.42
34:B5:1062:A:H2'	34:B5:1063:U:O5'	2.19	0.42
34:B5:1203:A:C2	34:B5:1556:A:C4	3.08	0.42
34:B5:1773:4AC:OP1	76:An:3:ALA:HB3	2.20	0.42
38:A1:142:C:H2'	38:A1:143:G:O4'	2.20	0.42
38:A1:735:A:H2'	38:A1:736:A:C8	2.55	0.42
38:A1:2223:A:H2'	38:A1:2224:A:C8	2.55	0.42
38:A1:2499:U:H2'	38:A1:2500:A:C4	2.54	0.42
38:A1:2606:G:H2'	38:A1:2606:G:N3	2.35	0.42
38:A1:2843:U:H5''	38:A1:2844:C:C5	2.55	0.42
38:A1:3180:A:C4	51:AO:114[A]:LYS:HA	2.54	0.42
38:A1:3211:C:H2'	38:A1:3212:C:O4'	2.19	0.42
38:A1:3302:U:H2'	38:A1:3303:G:C8	2.54	0.42
38:A1:3340:G:O3'	38:A1:3341:U:H3'	2.20	0.42
40:A4:104:A:C8	40:A4:105:A:C8	3.07	0.42
45:AH:4:ILE:HG22	45:AH:5:GLN:NE2	2.35	0.42
46:AI:184:LYS:HG3	46:AI:189:GLU:OE1	2.20	0.42
51:AO:8[A]:VAL:HG12	51:AO:117[A]:ARG:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:AQ:122:ILE:CG2	53:AQ:126:GLN:HB2	2.49	0.42
56:AT:65:TYR:CD1	56:AT:75:ILE:HG13	2.55	0.42
56:AT:152:ALA:HB1	56:AT:153:PRO:HD2	2.02	0.42
57:AU:53:ALA:HB1	57:AU:69:ALA:HB2	2.01	0.42
59:AW:50:ALA:HA	59:AW:55:PHE:CG	2.55	0.42
61:AY:51:ARG:HD2	61:AY:115:ARG:HH11	1.83	0.42
80:EC:6847:G:O2'	80:EC:6848:U:P	2.77	0.42
2:BB:111:ARG:NH2	34:B5:930:A:N3	2.55	0.42
3:BC:91:ARG:HH11	34:B5:1147:A:H5''	1.84	0.42
10:BN:92:ILE:HB	10:BN:150:VAL:HG11	2.02	0.42
10:BN:112:LYS:HE2	34:B5:974:A2M:H4'	2.02	0.42
10:BN:119:GLU:O	10:BN:123:HIS:ND1	2.52	0.42
11:BO:47:LYS:HD3	11:BO:47:LYS:HA	1.73	0.42
11:BO:124:ASP:OD1	11:BO:124:ASP:N	2.52	0.42
18:Be:55:ARG:NH2	34:B5:558:U:P	2.92	0.42
19:BD:175:VAL:HG12	19:BD:177:MET:CE	2.45	0.42
22:BP:44:ARG:NH1	22:BP:82:ASN:O	2.30	0.42
22:BP:125:PRO:HG3	25:BS:129:TRP:CH2	2.54	0.42
26:BT:109:GLU:HG2	26:BT:114:VAL:HG23	2.02	0.42
27:BU:17:GLN:HA	27:BU:96:PRO:HG3	2.00	0.42
29:Bc:7:VAL:HG12	29:Bc:57:MET:HA	2.01	0.42
34:B5:117:U:H2'	34:B5:118:U:O4'	2.20	0.42
34:B5:384:G:H2'	34:B5:385:A:C8	2.55	0.42
34:B5:448:C:H2'	34:B5:449:C:H6	1.85	0.42
34:B5:735:C:O2'	34:B5:736:C:OP2	2.30	0.42
34:B5:1488:G:O2'	34:B5:1494:C:O2	2.25	0.42
34:B5:1785:U:H2'	34:B5:1786:G:C8	2.55	0.42
38:A1:176:G:O6	38:A1:241:G:O6	2.38	0.42
38:A1:1455:U:H1'	66:Ad:26:LYS:NZ	2.34	0.42
38:A1:1549:U:H2'	38:A1:1550:C:C6	2.55	0.42
38:A1:1571:A:C2	38:A1:1573:G:C6	3.08	0.42
38:A1:1739:U:O2'	69:Ag:56:THR:OG1	2.30	0.42
43:AF:64:GLN:HG3	43:AF:68:ASP:OD2	2.20	0.42
60:AX:33:ARG:HD2	60:AX:33:ARG:HA	1.76	0.42
68:Af:16:TYR:CD1	68:Af:25:PRO:HA	2.54	0.42
4:BE:12:LEU:O	34:B5:756:A:H1'	2.20	0.42
4:BE:256:ARG:HG3	4:BE:259:GLN:NE2	2.35	0.42
6:BH:64:VAL:CG2	6:BH:67:LEU:HD23	2.43	0.42
7:BI:56:ARG:NH2	34:B5:331:A:H5''	2.35	0.42
11:BO:26:THR:HG21	11:BO:60:ALA:HB2	2.02	0.42
15:BY:41:ARG:HG2	15:BY:55:VAL:HG12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BP:44:ARG:HD3	34:B5:1556:A:OP1	2.20	0.42
23:BQ:73:GLY:HA3	34:B5:1608:U:O3'	2.19	0.42
27:BU:33:GLN:O	27:BU:37:VAL:HG23	2.19	0.42
30:Bd:12:ARG:HH22	34:B5:1451:C:P	2.43	0.42
34:B5:106:U:C2'	34:B5:107:C:H5'	2.50	0.42
34:B5:496:G:N3	34:B5:496:G:H2'	2.35	0.42
34:B5:1227:A:H4'	34:B5:1228:G:H5'	2.01	0.42
34:B5:1564:U:H2'	34:B5:1565:C:H6	1.82	0.42
35:AA:211:HIS:ND1	35:AA:219:ILE:HG23	2.34	0.42
38:A1:240:U:O2'	38:A1:241:G:N7	2.53	0.42
38:A1:259:C:H2'	38:A1:260:C:H6	1.85	0.42
38:A1:629:U:H2'	38:A1:630:A:C8	2.55	0.42
38:A1:774:G:C2'	38:A1:775:A:H5'	2.49	0.42
38:A1:2347:OMU:H2'	38:A1:2348:A:O4'	2.20	0.42
38:A1:2442:G:O6	38:A1:2506:U:C4	2.73	0.42
38:A1:2457:G:O4'	38:A1:2482:U:O2'	2.36	0.42
38:A1:2689:A:N3	38:A1:2689:A:H2'	2.35	0.42
38:A1:3051:U:C2	38:A1:3052:G:C8	3.08	0.42
38:A1:3343:G:H2'	38:A1:3344:A:H2	1.83	0.42
66:Ad:55:LEU:HB2	66:Ad:95:PRO:HD3	2.00	0.42
71:Ai:52:PRO:HG3	71:Ai:55:ARG:NH2	2.35	0.42
79:E:19:TYR:HA	79:E:23:THR:HG22	2.01	0.42
1:BA:171:GLY:HA3	1:BA:203:PHE:HD1	1.85	0.41
3:BC:144:TRP:CE2	3:BC:173:PRO:HG3	2.55	0.41
7:BI:159:GLN:HB3	7:BI:164:ARG:O	2.20	0.41
13:BW:18:GLU:OE2	13:BW:67:GLY:HA2	2.20	0.41
19:BD:135:GLU:HB2	19:BD:157:LEU:CD1	2.50	0.41
20:BF:219:ARG:HG2	80:EC:6841:U:O3'	2.20	0.41
25:BS:41:ARG:NE	26:BT:46:PRO:HD3	2.35	0.41
25:BS:46:VAL:HG22	25:BS:72:ILE:HG22	2.01	0.41
28:BZ:60:VAL:HB	28:BZ:101:TYR:HB2	2.01	0.41
34:B5:40:A:H2'	34:B5:41:A:O4'	2.20	0.41
34:B5:69:G:H2'	34:B5:70:C:C6	2.55	0.41
34:B5:1226:A:H4'	34:B5:1227:A:OP1	2.18	0.41
34:B5:1250:U:O2'	34:B5:1251:U:H5'	2.19	0.41
35:AA:178:PRO:HG2	78:Ap:26:VAL:CG2	2.50	0.41
37:AC:138:ARG:HD2	37:AC:140:HIS:CD2	2.55	0.41
38:A1:9:U:H2'	38:A1:10:C:O4'	2.20	0.41
38:A1:38:U:H2'	38:A1:39:A:O4'	2.20	0.41
38:A1:293:C:H2'	38:A1:294:U:O4'	2.20	0.41
38:A1:359:U:H4'	38:A1:817:A2M:N6	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:498:A:O2'	38:A1:3273:A:N1	2.51	0.41
38:A1:1460:A:H2'	38:A1:1461:A:C8	2.54	0.41
38:A1:2265:C:O2'	38:A1:2266:U:H5'	2.20	0.41
38:A1:2351:U:H2'	38:A1:2352:A:C8	2.55	0.41
40:A4:149:A:H2'	40:A4:150:G:C8	2.55	0.41
44:AG:90:THR:OG1	44:AG:214:LEU:HD11	2.20	0.41
44:AG:115:ALA:CB	44:AG:125:ALA:HB2	2.49	0.41
53:AQ:55:SER:O	53:AQ:59:ARG:HG2	2.20	0.41
63:Aa:114:GLY:O	63:Aa:137:LYS:NZ	2.52	0.41
65:Ac:21:GLY:O	65:Ac:22:LYS:HD2	2.19	0.41
71:Ai:52:PRO:CB	71:Ai:55:ARG:HH21	2.33	0.41
5:BG:8:PRO:HB3	34:B5:164:A:O3'	2.20	0.41
8:BJ:184:SER:OG	8:BJ:185:GLY:N	2.52	0.41
9:BL:45:PRO:O	9:BL:49:ILE:HG12	2.19	0.41
11:BO:24:ASN:O	11:BO:54:GLU:HB2	2.20	0.41
16:Ba:79:ILE:HD13	34:B5:1794:A:H1'	2.01	0.41
31:Bg:217:ASP:N	31:Bg:217:ASP:OD1	2.53	0.41
34:B5:1142:A:H2'	34:B5:1143:A:C8	2.55	0.41
38:A1:418:A:H4'	38:A1:629:U:O3'	2.20	0.41
38:A1:1470:U:H2'	38:A1:1471:U:C6	2.55	0.41
38:A1:1504:A:OP1	52:AP:23:ARG:NH1	2.53	0.41
38:A1:1827:C:H2'	38:A1:1828:A:C8	2.55	0.41
38:A1:1831:U:H2'	38:A1:1832:C:C6	2.55	0.41
38:A1:2213:A:N1	38:A1:2429:G:H1'	2.35	0.41
38:A1:2368:A:H2'	38:A1:2369:G:H8	1.84	0.41
38:A1:3007:U:H2'	38:A1:3008:A:C8	2.55	0.41
38:A1:3066:U:C2	38:A1:3067:C:C5	3.08	0.41
38:A1:3322:A:H2'	38:A1:3323:A:H8	1.84	0.41
42:AE:67:GLY:O	42:AE:68:PRO:C	2.63	0.41
51:AO:129[A]:LEU:HG	51:AO:133[A]:ARG:HB2	2.02	0.41
52:AP:60:PHE:HB3	52:AP:64:ASN:HB3	2.01	0.41
55:AS:80:ARG:HB2	55:AS:124:LEU:HD11	2.01	0.41
68:Af:59:VAL:HG23	68:Af:60:ARG:H	1.85	0.41
72:Aj:39:TYR:CD1	72:Aj:40:PRO:HA	2.55	0.41
73:Ak:14:LEU:HD21	73:Ak:52:TYR:CG	2.55	0.41
80:EC:6842:U:H4'	80:EC:6843:U:H5''	2.02	0.41
1:BA:190:ASP:HB3	1:BA:193:GLN:HE22	1.86	0.41
2:BB:26:ARG:HG2	2:BB:50:LYS:HG2	2.02	0.41
3:BC:88:LYS:HG3	34:B5:1301:U:H5'	2.02	0.41
7:BI:45:SER:OG	7:BI:53:LYS:HD3	2.21	0.41
11:BO:125:SER:HB3	34:B5:926:A:H2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:85:ASP:O	13:BW:88:LYS:HG3	2.20	0.41
15:BY:26:ASP:HB2	15:BY:68:LYS:HZ2	1.86	0.41
18:Be:55:ARG:CG	18:Be:58:PRO:HG3	2.50	0.41
26:BT:44:GLU:CD	26:BT:45:MET:HG2	2.44	0.41
27:BU:22:ILE:HD11	27:BU:116:VAL:HG22	2.02	0.41
29:Bc:50:GLU:OE1	29:Bc:50:GLU:N	2.48	0.41
31:Bg:276:PRO:HG2	31:Bg:278:PHE:CZ	2.55	0.41
34:B5:826:U:H2'	34:B5:827:C:C6	2.55	0.41
34:B5:1547:A:H2'	34:B5:1548:G:O4'	2.20	0.41
36:AB:358:TRP:CE2	59:AW:1:MET:HE1	2.54	0.41
37:AC:76:ARG:HA	37:AC:87:GLN:O	2.20	0.41
38:A1:70:A:N1	38:A1:313:A:O2'	2.50	0.41
38:A1:166:C:C4	38:A1:167:U:C4	3.09	0.41
38:A1:655:C:H5''	67:Ae:26:HIS:HB3	2.03	0.41
38:A1:1139:G:O3'	43:AF:94:LYS:HA	2.20	0.41
38:A1:1231:A:H5'	38:A1:1232:C:OP1	2.21	0.41
38:A1:1664:G:H2'	38:A1:1665:C:C6	2.56	0.41
38:A1:1719:G:H2'	38:A1:1720:U:O4'	2.20	0.41
38:A1:2615:G:H2'	38:A1:2616:C:C6	2.55	0.41
40:A4:75:G:H5'	74:Al:30:ARG:HA	2.02	0.41
43:AF:60:ARG:HA	43:AF:60:ARG:HD2	1.80	0.41
49:AM:31:LYS:HE2	49:AM:53:VAL:HG22	2.03	0.41
66:Ad:23:VAL:O	66:Ad:28:ARG:HD3	2.20	0.41
68:Af:16:TYR:OH	68:Af:91:ALA:HB2	2.21	0.41
2:BB:203:ASP:O	34:B5:1064:G:H1'	2.19	0.41
5:BG:61:PHE:CD2	5:BG:72:ARG:HD3	2.55	0.41
5:BG:169:TYR:HB3	34:B5:72:A:N1	2.35	0.41
7:BI:10:LYS:HD2	34:B5:323:A:OP2	2.21	0.41
7:BI:138:ASN:HD22	7:BI:138:ASN:HA	1.67	0.41
9:BL:152:GLN:CD	10:BN:137:PRO:HD3	2.45	0.41
10:BN:3:ARG:HD2	34:B5:955:A:P	2.61	0.41
10:BN:55:ARG:HH11	34:B5:960:U:P	2.43	0.41
10:BN:87:ASP:OD1	10:BN:88:LEU:N	2.54	0.41
11:BO:29:HIS:CE1	11:BO:38:THR:HG23	2.56	0.41
12:BV:40:ASP:HB3	12:BV:46:ILE:HD11	2.01	0.41
17:Bb:17:ARG:HH21	34:B5:1070:C:H5'	1.85	0.41
19:BD:142:LEU:CD1	19:BD:150:MET:HE3	2.50	0.41
20:BF:57:SER:HB2	29:Bc:53:ILE:O	2.21	0.41
21:BK:54:TYR:CE2	21:BK:75:TYR:CD2	3.08	0.41
22:BP:27:GLU:HG3	22:BP:88:GLU:HA	2.01	0.41
27:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:406:U:H2'	34:B5:407:A:C8	2.54	0.41
34:B5:752:A:H2'	34:B5:753:A:C8	2.54	0.41
34:B5:1042:G:H2'	34:B5:1043:A:H8	1.85	0.41
34:B5:1360:A:O5'	34:B5:1360:A:H8	2.04	0.41
34:B5:1695:G:H2'	34:B5:1696:G:C8	2.55	0.41
34:B5:1714:A:H2'	34:B5:1715:G:H8	1.85	0.41
34:B5:1785:U:H2'	34:B5:1786:G:H8	1.85	0.41
38:A1:199:A:C4	38:A1:201:A:C8	3.09	0.41
38:A1:260:C:H2'	38:A1:261:U:C6	2.54	0.41
38:A1:926:A:H2'	38:A1:927:C:C6	2.55	0.41
38:A1:1048:A:H2'	46:AI:22:TYR:CZ	2.56	0.41
38:A1:1072:G:H2'	38:A1:1073:U:C6	2.55	0.41
38:A1:1664:G:H2'	38:A1:1665:C:H6	1.86	0.41
38:A1:2201:G:H2'	38:A1:2202:C:H6	1.86	0.41
38:A1:2252:A:C6	38:A1:2265:C:N3	2.89	0.41
38:A1:2261:G:O2'	38:A1:2263:C:N4	2.54	0.41
38:A1:2427:U:H2'	38:A1:2428:U:H6	1.85	0.41
38:A1:2442:G:O6	38:A1:2506:U:C5	2.73	0.41
38:A1:2506:U:C2	38:A1:2507:C:C1'	3.01	0.41
38:A1:3023:U:H2'	38:A1:3024:A:H8	1.84	0.41
38:A1:3281:U:H2'	38:A1:3282:U:C6	2.55	0.41
42:AE:43:LEU:HD11	42:AE:85:ILE:HG12	2.03	0.41
45:AH:77:ASN:HB3	45:AH:151:VAL:HG11	2.02	0.41
47:AJ:48:SER:OG	47:AJ:66:ALA:HB3	2.19	0.41
55:AS:46:GLN:HE22	55:AS:52:LYS:CB	2.34	0.41
65:Ac:77:LEU:O	65:Ac:81:VAL:HG22	2.20	0.41
4:BE:87:MET:HE1	4:BE:228:ILE:HG22	2.03	0.41
21:BK:39:ASN:O	21:BK:42:VAL:HG22	2.20	0.41
21:BK:64:TYR:HB3	21:BK:66:TYR:CE2	2.56	0.41
22:BP:25:LEU:HA	22:BP:25:LEU:HD12	1.90	0.41
27:BU:84:MET:HE2	30:Bd:51:GLY:HA3	2.02	0.41
31:Bg:42:LEU:HB2	31:Bg:61:PHE:HB2	2.03	0.41
34:B5:625:C:H2'	34:B5:626:U:H6	1.82	0.41
34:B5:948:G:H2'	34:B5:949:C:C6	2.55	0.41
34:B5:953:G:H2'	34:B5:954:G:H8	1.84	0.41
34:B5:973:A:H4'	38:A1:848:A:H8	1.77	0.41
34:B5:1178:G:H5'	34:B5:1190:C:H42	1.86	0.41
34:B5:1393:C:H2'	34:B5:1394:G:C8	2.55	0.41
34:B5:1398:U:N3	34:B5:1400:A:N1	2.69	0.41
35:AA:147:ARG:HG2	35:AA:155:LYS:HZ3	1.84	0.41
38:A1:395:A:H2'	38:A1:396:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:429:U:H4'	68:Af:88:ASN:O	2.20	0.41
38:A1:1373:A:H2'	38:A1:1374:G:C8	2.55	0.41
38:A1:1573:G:N7	38:A1:1574:C:C5	2.88	0.41
38:A1:2429:G:H2'	38:A1:2430:A:C8	2.54	0.41
38:A1:2441:A:N1	38:A1:2506:U:C4	2.88	0.41
38:A1:2656:A:C8	38:A1:2658:G:C8	3.09	0.41
43:AF:98:LYS:HB3	43:AF:99:PRO:HD3	2.01	0.41
48:AL:157:ARG:HH22	63:Aa:146:GLU:CD	2.28	0.41
53:AQ:64:VAL:HA	53:AQ:67:ILE:HD12	2.02	0.41
59:AW:17:ARG:HA	59:AW:17:ARG:HD2	1.84	0.41
63:Aa:96:LYS:C	63:Aa:98:THR:H	2.27	0.41
65:Ac:38:LYS:HE3	65:Ac:93:LEU:HD12	2.02	0.41
69:Ag:104:VAL:HG13	69:Ag:105:VAL:N	2.36	0.41
70:Ah:84:LYS:HB2	70:Ah:84:LYS:HE3	1.90	0.41
72:Aj:43:LYS:HE3	72:Aj:43:LYS:HB2	1.76	0.41
79:E:90:LEU:HD13	79:E:93:LEU:HD22	2.02	0.41
80:EC:6844:A:C8	80:EC:6845:G:N7	2.88	0.41
1:BA:56:LYS:HD2	1:BA:56:LYS:HA	1.90	0.41
1:BA:171:GLY:HA3	1:BA:203:PHE:CD1	2.56	0.41
2:BB:28:GLU:HG3	2:BB:30:PHE:HD1	1.84	0.41
2:BB:61:LEU:HD13	2:BB:96:LEU:HD21	2.03	0.41
15:BY:84:LYS:HZ2	15:BY:85:PHE:HE1	1.69	0.41
19:BD:5:ILE:HG23	19:BD:10:LYS:HB2	2.02	0.41
19:BD:204:ASP:OD1	19:BD:204:ASP:N	2.54	0.41
20:BF:26:ALA:CB	23:BQ:28:LEU:HD22	2.50	0.41
23:BQ:139:GLN:NE2	34:B5:1465:C:OP1	2.38	0.41
34:B5:237:C:C6	34:B5:834:G:H4'	2.56	0.41
34:B5:812:A:H62	34:B5:859:A:H5'	1.86	0.41
34:B5:876:G:H1'	34:B5:944:A:O4'	2.20	0.41
34:B5:1288:G:N7	34:B5:1314:U:O2'	2.47	0.41
36:AB:57:VAL:HG21	59:AW:15:PRO:HG2	2.03	0.41
36:AB:79:VAL:CG2	36:AB:322:ILE:HB	2.51	0.41
37:AC:302:ALA:HB2	53:AQ:39:ARG:CZ	2.50	0.41
37:AC:317:PRO:C	37:AC:319:LYS:H	2.28	0.41
38:A1:698:U:H2'	38:A1:699:A:O4'	2.21	0.41
38:A1:1493:G:O6	74:Al:2:ALA:N	2.54	0.41
38:A1:1856:C:H2'	38:A1:1857:C:C6	2.55	0.41
38:A1:1912:U:H2'	38:A1:1913:A:O4'	2.20	0.41
38:A1:2354:C:H2'	38:A1:2355:G:O4'	2.20	0.41
38:A1:2515:A:H5''	50:AN:28:TRP:CD1	2.55	0.41
38:A1:2659:G:H4'	38:A1:2751:G:O2'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2976:A:H2'	38:A1:2977:G:O4'	2.20	0.41
38:A1:3297:U:H2'	38:A1:3298:C:H6	1.86	0.41
40:A4:11:C:O2'	52:AP:4:TYR:O	2.33	0.41
40:A4:119:C:H2'	40:A4:120:C:H6	1.85	0.41
41:AD:44:TYR:CD2	56:AT:35:LYS:HG2	2.56	0.41
44:AG:26:LEU:HB3	62:AZ:53:VAL:CG2	2.51	0.41
51:AO:143[A]:THR:OG1	51:AO:150[A]:GLU:OE1	2.29	0.41
54:AR:136:ARG:HE	54:AR:136:ARG:HB3	1.62	0.41
54:AR:160:GLU:HA	54:AR:163:ARG:HH11	1.84	0.41
63:Aa:125:VAL:O	63:Aa:145:VAL:HA	2.21	0.41
74:Al:51:ILE:HD13	74:Al:51:ILE:HA	1.89	0.41
2:BB:70:LEU:HD13	2:BB:84:ILE:HD11	2.02	0.41
6:BH:24:PHE:O	6:BH:27:LEU:HG	2.21	0.41
8:BJ:80:LEU:HA	8:BJ:83:VAL:HG12	2.03	0.41
29:Bc:27:GLN:HG2	29:Bc:43:ASN:OD1	2.20	0.41
34:B5:480:G:H2'	34:B5:481:A:C8	2.56	0.41
34:B5:496:G:H3'	34:B5:497:G:H8	1.86	0.41
34:B5:765:G:H1'	34:B5:768:C:OP1	2.21	0.41
37:AC:58:HIS:NE2	37:AC:98:ARG:HD3	2.36	0.41
38:A1:80:G:OP1	50:AN:193:ARG:NH1	2.54	0.41
38:A1:130:A:H2'	38:A1:131:C:H6	1.86	0.41
38:A1:1332:A:H2'	38:A1:1333:C:C6	2.55	0.41
38:A1:1357:G:H2'	38:A1:1358:C:C6	2.56	0.41
38:A1:2441:A:C2	38:A1:2442:G:C8	3.09	0.41
38:A1:2538:U:H3	38:A1:2543:U:H3	1.68	0.41
38:A1:2765:C:O3'	77:Ao:39:GLY:HA3	2.19	0.41
38:A1:2784:G:H2'	38:A1:2785:A:O4'	2.20	0.41
38:A1:3083:G:H2'	38:A1:3084:C:O4'	2.20	0.41
38:A1:3119:U:H4'	75:Am:104:PRO:HG3	2.02	0.41
39:A3:22:A:H2'	39:A3:23:A:C8	2.56	0.41
39:A3:94:C:H2'	39:A3:95:A:H8	1.84	0.41
40:A4:7:U:H2'	40:A4:8:C:C6	2.55	0.41
40:A4:131:A:H2'	40:A4:132:G:H8	1.85	0.41
46:Al:36:LEU:HD21	46:Al:69:ARG:NH1	2.35	0.41
49:AM:32:LEU:HB3	49:AM:85:TRP:CH2	2.55	0.41
63:Aa:28:HIS:CD2	63:Aa:32:ARG:HG2	2.55	0.41
67:Ae:19:ARG:O	67:Ae:22:SER:OG	2.34	0.41
77:Ao:25:VAL:HG22	77:Ao:72:LEU:CD1	2.49	0.41
3:BC:82:ASN:HB2	3:BC:207:LEU:CD2	2.50	0.41
7:BI:60:ILE:HD11	7:BI:179:CYS:SG	2.61	0.41
7:BI:93:THR:O	7:BI:93:THR:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:128:TYR:CE1	34:B5:964:U:H5''	2.56	0.41
14:BX:140:LYS:HB2	14:BX:140:LYS:HE2	1.83	0.41
16:Ba:59:TYR:CB	16:Ba:62:TYR:HB2	2.50	0.41
19:BD:158:ILE:CD1	19:BD:163:PRO:HB2	2.51	0.41
21:BK:11:ILE:HD13	21:BK:42:VAL:HA	2.02	0.41
23:BQ:9:THR:HA	34:B5:1340:U:O4	2.20	0.41
31:Bg:202:LEU:HA	31:Bg:212:ALA:O	2.20	0.41
34:B5:271:A:H2'	34:B5:272:U:O4'	2.21	0.41
34:B5:833:U:H5'	34:B5:834:G:H3'	2.02	0.41
34:B5:1413:U:H4'	34:B5:1414:U:OP2	2.21	0.41
34:B5:1686:C:H2'	34:B5:1687:U:C6	2.56	0.41
35:AA:32:LEU:HD13	35:AA:163:ARG:HD3	2.03	0.41
35:AA:96:LEU:O	78:Ap:87:ARG:HD3	2.21	0.41
37:AC:93:MET:HB2	38:A1:658:G:N2	2.36	0.41
38:A1:184:U:H2'	38:A1:185:C:H6	1.85	0.41
38:A1:663:OMC:H2'	38:A1:664:U:C6	2.56	0.41
38:A1:993:G:N3	38:A1:2637:A:H2'	2.35	0.41
38:A1:1765:U:H2'	38:A1:1766:G:C4'	2.51	0.41
38:A1:2389:C:H2'	38:A1:2390:A:H8	1.86	0.41
38:A1:2430:A:H2'	38:A1:2431:C:C6	2.55	0.41
38:A1:3007:U:OP1	51:AO:73[A]:PHE:HA	2.21	0.41
38:A1:3288:G:O2'	38:A1:3289:G:H8	2.03	0.41
41:AD:79:TYR:O	41:AD:82:GLU:HG2	2.20	0.41
43:AF:233:GLU:HG2	43:AF:234:GLU:N	2.35	0.41
43:AF:233:GLU:OE2	55:AS:35:VAL:HG22	2.20	0.41
49:AM:21:VAL:HB	49:AM:63:VAL:CG2	2.51	0.41
52:AP:10:ASN:HB3	52:AP:13:LYS:HG2	2.03	0.41
52:AP:129:THR:HG23	52:AP:131:ARG:HD3	2.03	0.41
58:AV:17:LEU:HD21	58:AV:98:ASN:CG	2.46	0.41
2:BB:70:LEU:HA	2:BB:73:LEU:HG	2.03	0.41
2:BB:176:VAL:HG12	2:BB:177:GLN:H	1.86	0.41
4:BE:7:LYS:HD3	34:B5:450:U:H5'	2.01	0.41
6:BH:157:LYS:HD2	6:BH:158:ASP:HB2	2.03	0.41
7:BI:37:LYS:HD3	7:BI:37:LYS:HA	1.77	0.41
7:BI:64:ASN:ND2	7:BI:73:SER:OG	2.53	0.41
8:BJ:97:LEU:HD23	8:BJ:97:LEU:HA	1.90	0.41
11:BO:52:ARG:HE	34:B5:905:A:H4'	1.86	0.41
15:BY:10:ARG:HG2	34:B5:780:A:C8	2.55	0.41
15:BY:112:LYS:HE3	15:BY:112:LYS:HB3	1.84	0.41
18:Be:13:LYS:NZ	18:Be:17:GLN:HE22	2.19	0.41
20:BF:188:LYS:HB3	20:BF:188:LYS:HE2	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:219:ARG:HG3	20:BF:222:LYS:HE2	2.03	0.41
21:BK:56:LYS:HD3	21:BK:58:GLN:HG3	2.03	0.41
23:BQ:46:PHE:O	23:BQ:50:GLU:HG3	2.21	0.41
23:BQ:60:PHE:CZ	23:BQ:89:LEU:HD22	2.56	0.41
23:BQ:63:ILE:HG22	23:BQ:65:ILE:HG13	2.01	0.41
25:BS:91:ASP:OD1	25:BS:93:THR:HG22	2.21	0.41
30:Bd:33:LYS:O	30:Bd:36:LEU:HD23	2.21	0.41
31:Bg:24:ALA:HB3	31:Bg:34:LEU:HB3	2.03	0.41
33:BM:81:ASP:O	33:BM:83:GLU:N	2.47	0.41
34:B5:244:A:H2'	34:B5:245:U:C6	2.56	0.41
34:B5:275:C:H2'	34:B5:276:C:C6	2.55	0.41
34:B5:433:C:H2'	34:B5:434:G:O4'	2.21	0.41
34:B5:848:C:H2'	34:B5:849:C:C6	2.56	0.41
34:B5:948:G:H2'	34:B5:949:C:H6	1.84	0.41
34:B5:1157:A:H2'	34:B5:1160:A:N7	2.35	0.41
34:B5:1451:C:H2'	34:B5:1452:U:C6	2.55	0.41
34:B5:1617:U:H2'	34:B5:1618:C:C6	2.55	0.41
34:B5:1652:C:H2'	34:B5:1653:C:C6	2.56	0.41
34:B5:1654:G:C6	34:B5:1745:G:C6	3.09	0.41
34:B5:1680:G:H1'	34:B5:1721:A:N6	2.36	0.41
38:A1:612:U:H2'	38:A1:613:G:C8	2.55	0.41
38:A1:723:U:O2'	64:Ab:29:TYR:OH	2.38	0.41
38:A1:789:A:H2'	38:A1:790:U:C6	2.55	0.41
38:A1:844:G:H3'	38:A1:845:G:H8	1.85	0.41
38:A1:855:U:H5''	54:AR:95:TRP:CG	2.56	0.41
38:A1:947:G:H2'	38:A1:948:C:H6	1.86	0.41
38:A1:949:C:O2'	38:A1:971:G:H5''	2.21	0.41
38:A1:974:G:H2'	38:A1:975:C:C6	2.56	0.41
38:A1:1266:G:H2'	38:A1:1267:U:H3'	2.02	0.41
38:A1:1340:G:H2'	38:A1:1341:U:H6	1.86	0.41
38:A1:1491:A:H5'	72:Aj:12:HIS:O	2.21	0.41
38:A1:1517:G:OP1	74:Al:22:PRO:HG3	2.21	0.41
38:A1:1546:A:H2'	38:A1:1547:G:O4'	2.20	0.41
38:A1:1660:C:H2'	38:A1:1661:G:C8	2.55	0.41
38:A1:1700:G:H2'	38:A1:1701:C:C6	2.56	0.41
38:A1:1856:C:H2'	38:A1:1857:C:H6	1.86	0.41
38:A1:2533:G:H2'	38:A1:2534:G:O4'	2.20	0.41
38:A1:2574:G:N7	62:AZ:56:LYS:NZ	2.68	0.41
38:A1:2993:G:H2'	38:A1:3142:A:N6	2.36	0.41
38:A1:3366:G:H2'	38:A1:3367:C:C6	2.55	0.41
39:A3:61:G:H2'	39:A3:62:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:19:C:H2'	40:A4:20:U:C6	2.54	0.41
42:AE:52:VAL:HA	42:AE:67:GLY:HA3	2.01	0.41
48:AL:85:LEU:HD13	48:AL:120:GLN:HE21	1.85	0.41
54:AR:106:LEU:HD23	54:AR:106:LEU:HA	1.94	0.41
58:AV:29:SER:OG	58:AV:102:ILE:HD12	2.20	0.41
60:AX:73:MET:O	60:AX:77:GLU:OE1	2.38	0.41
61:AY:119:ILE:HG22	61:AY:124:GLY:HA3	2.02	0.41
66:Ad:74:ARG:NH2	66:Ad:109:VAL:HG11	2.36	0.41
72:Aj:52:LYS:HG2	72:Aj:55:ARG:NH2	2.36	0.41
73:Ak:5:ILE:HG23	73:Ak:10:GLN:HE22	1.84	0.41
79:E:96:ASN:O	79:E:100:ILE:HG13	2.21	0.41
79:E:196:LYS:H	79:E:200:ASN:HD21	1.69	0.41
2:BB:176:VAL:HG12	2:BB:177:GLN:N	2.35	0.41
6:BH:49:ILE:HG12	6:BH:175:LYS:HG2	2.03	0.41
8:BJ:53:ARG:O	8:BJ:57:ARG:HB2	2.21	0.41
15:BY:59:GLY:O	34:B5:523:G:H5''	2.20	0.41
19:BD:190:ARG:HH12	19:BD:195:SER:HB3	1.86	0.41
21:BK:15:LEU:HD23	21:BK:76:LEU:HD11	2.02	0.41
26:BT:57:ARG:HG3	26:BT:104:VAL:HG21	2.03	0.41
34:B5:250:C:H2'	34:B5:251:A:C8	2.55	0.41
34:B5:1725:U:H2'	34:B5:1726:G:C8	2.56	0.41
38:A1:144:A:H2'	38:A1:145:G:O4'	2.21	0.41
38:A1:435:C:H2'	38:A1:436:A:H8	1.86	0.41
38:A1:594:U:O2'	38:A1:595:G:H5'	2.20	0.41
38:A1:1324:U:H5''	55:AS:1:MET:N	2.36	0.41
38:A1:1561:G:O2'	38:A1:1562:C:P	2.79	0.41
38:A1:2096:A:H3'	38:A1:2097:U:C6	2.55	0.41
38:A1:2251:G:C6	38:A1:2266:U:N3	2.89	0.41
38:A1:2419:A:OP2	38:A1:2606:G:N2	2.39	0.41
38:A1:2834:G:H2'	38:A1:2835:U:H6	1.86	0.41
38:A1:2881:C:H2'	38:A1:2882:U:H6	1.85	0.41
38:A1:3159:C:H2'	38:A1:3160:U:H6	1.85	0.41
38:A1:3208:G:O2'	55:AS:161:LYS:NZ	2.35	0.41
42:AE:92:SER:N	42:AE:148:GLU:OE1	2.54	0.41
47:AJ:165:GLN:O	47:AJ:166:LYS:C	2.64	0.41
62:AZ:55:LYS:HB2	62:AZ:55:LYS:HE2	1.80	0.41
71:Ai:76:ARG:NE	71:Ai:76:ARG:HA	2.35	0.41
78:Ap:7:LYS:HB3	78:Ap:7:LYS:HE3	1.84	0.41
80:EC:6872:A:N7	80:EC:6873:A:N6	2.69	0.41
1:BA:109:ASN:H	3:BC:64:LYS:NZ	2.18	0.40
5:BG:84:TYR:OH	5:BG:91:GLU:OE1	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:135:PRO:HB2	5:BG:141:ILE:HG13	2.03	0.40
6:BH:14:THR:C	6:BH:18:LEU:HD13	2.46	0.40
9:BL:46:LYS:O	9:BL:50:GLU:HG3	2.21	0.40
19:BD:135:GLU:OE1	19:BD:137:VAL:HG23	2.21	0.40
20:BF:140:THR:OG1	20:BF:210:ALA:HB1	2.21	0.40
25:BS:11:PHE:HZ	25:BS:25:ASN:N	2.19	0.40
30:Bd:56:ARG:HD3	34:B5:1335:U:H1'	2.03	0.40
31:Bg:10:ARG:HH12	31:Bg:51:ASP:HA	1.85	0.40
34:B5:1065:A:H2'	34:B5:1066:C:O4'	2.21	0.40
34:B5:1713:G:H2'	34:B5:1714:A:H8	1.82	0.40
35:AA:144:ASN:N	35:AA:144:ASN:OD1	2.54	0.40
36:AB:20:LYS:HB2	38:A1:2991:A:P	2.61	0.40
38:A1:362:U:O4	72:Aj:24:ARG:NH2	2.54	0.40
38:A1:953:G:O2'	38:A1:1116:G:H5'	2.20	0.40
38:A1:2162:U:H2'	38:A1:2163:C:O4'	2.21	0.40
38:A1:2282:U:OP1	38:A1:2973:G:O2'	2.30	0.40
38:A1:2307:G:O2'	38:A1:2310:U:OP2	2.30	0.40
38:A1:2913:C:O2'	38:A1:3013:U:H4'	2.20	0.40
52:AP:67:ILE:HG23	52:AP:82:ARG:NE	2.36	0.40
60:AX:79:GLY:HA3	60:AX:81:ILE:HD12	2.03	0.40
66:Ad:24:SER:HB2	66:Ad:27:LYS:HG2	2.02	0.40
71:Ai:53:TYR:CB	71:Ai:56:ARG:NH2	2.84	0.40
74:Al:15:LYS:O	74:Al:19:GLN:HG3	2.21	0.40
79:E:183:ILE:O	79:E:187:VAL:HG23	2.21	0.40
1:BA:89:PHE:O	1:BA:93:THR:OG1	2.40	0.40
5:BG:140:ASN:OD1	5:BG:143:LYS:NZ	2.46	0.40
8:BJ:60:LEU:HD23	8:BJ:60:LEU:HA	1.93	0.40
8:BJ:171:ARG:C	8:BJ:171:ARG:HD2	2.46	0.40
19:BD:78:LYS:HE2	19:BD:78:LYS:HA	2.02	0.40
34:B5:74:U:OP1	34:B5:76:A:N6	2.49	0.40
34:B5:99:C:OP2	34:B5:378:A:O2'	2.29	0.40
34:B5:343:C:H2'	34:B5:344:A:H8	1.84	0.40
34:B5:629:U:H2'	34:B5:630:A:C8	2.54	0.40
34:B5:891:A:H2'	34:B5:892:A:C8	2.56	0.40
34:B5:1729:C:H2'	34:B5:1730:A:O4'	2.21	0.40
37:AC:73:ARG:NH1	38:A1:2814:G:OP1	2.45	0.40
37:AC:136:LEU:HD23	37:AC:136:LEU:HA	1.94	0.40
38:A1:673:U:H2'	38:A1:674:G:C8	2.56	0.40
38:A1:767:U:H4'	48:AL:186:ARG:NH2	2.36	0.40
38:A1:873:C:H2'	38:A1:875:G:O4'	2.21	0.40
38:A1:1169:A:H2'	38:A1:1170:A:C8	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1478:C:H2'	38:A1:1479:U:H6	1.86	0.40
38:A1:1542:G:H2'	38:A1:1543:G:H8	1.85	0.40
38:A1:1610:G:H2'	38:A1:1611:G:O4'	2.21	0.40
38:A1:1825:G:OP1	73:Ak:48:SER:HB3	2.22	0.40
38:A1:2449:A:H5''	38:A1:2450:G:OP1	2.20	0.40
38:A1:2535:A:H2'	38:A1:2536:A:O4'	2.20	0.40
38:A1:3094:A:H2'	38:A1:3095:U:C6	2.56	0.40
50:AN:54:LYS:HB2	50:AN:59:PHE:CE1	2.56	0.40
50:AN:64:VAL:HG11	50:AN:102:ALA:HB1	2.03	0.40
68:Af:59:VAL:HG23	68:Af:60:ARG:N	2.36	0.40
69:Ag:79:SER:C	69:Ag:80:ARG:HD2	2.47	0.40
79:E:55:LEU:HB3	79:E:182:GLN:NE2	2.34	0.40
80:EC:6947:A:H3'	80:EC:6948:U:C6	2.56	0.40
2:BB:28:GLU:HG3	2:BB:30:PHE:CD1	2.56	0.40
2:BB:65:VAL:HG22	2:BB:87:ARG:HB2	2.03	0.40
6:BH:14:THR:O	6:BH:18:LEU:HD12	2.22	0.40
16:Ba:45:VAL:CG1	16:Ba:46:GLU:H	2.32	0.40
18:Be:14:VAL:HA	18:Be:17:GLN:HE21	1.85	0.40
20:BF:149:VAL:O	20:BF:149:VAL:HG23	2.22	0.40
29:Bc:67:ARG:HD3	29:Bc:67:ARG:HA	1.92	0.40
34:B5:593:U:H4'	34:B5:595:G:H4'	2.03	0.40
34:B5:819:G:C5	34:B5:853:G:C2	3.09	0.40
34:B5:887:A:C4	34:B5:888:U:C5	3.09	0.40
34:B5:1420:C:H2'	34:B5:1421:A:O4'	2.22	0.40
34:B5:1429:G:H2'	34:B5:1430:U:C6	2.56	0.40
34:B5:1489:U:O2'	34:B5:1492:A:N3	2.51	0.40
34:B5:1575:7MG:O5'	34:B5:1575:7MG:H81	2.21	0.40
36:AB:47:LEU:HD11	36:AB:179:ALA:HB3	2.04	0.40
38:A1:69:C:H2'	38:A1:70:A:O4'	2.21	0.40
38:A1:429:U:H2'	38:A1:430:U:H6	1.85	0.40
38:A1:767:U:H4'	48:AL:186:ARG:HH22	1.85	0.40
38:A1:821:U:H2'	38:A1:822:G:C8	2.56	0.40
38:A1:1070:U:H2'	38:A1:1071:U:O4'	2.21	0.40
38:A1:1354:G:H1'	42:AE:9:TRP:CD1	2.55	0.40
38:A1:1583:A:H3'	38:A1:1584:U:H6	1.86	0.40
38:A1:1636:U:O2'	62:AZ:79:HIS:ND1	2.40	0.40
38:A1:1910:A:H2'	38:A1:1911:A:C8	2.56	0.40
38:A1:2117:A:H4'	38:A1:3081:C:O4'	2.21	0.40
38:A1:2674:A:C2	47:AJ:124:GLY:HA3	2.56	0.40
38:A1:2725:U:H3'	38:A1:2726:C:O2	2.20	0.40
38:A1:2738:A:H2'	38:A1:2739:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2961:G:H2'	38:A1:2962:U:H6	1.83	0.40
41:AD:236:LEU:HA	41:AD:239:ILE:HG12	2.03	0.40
45:AH:9:GLN:HE21	45:AH:54:LYS:NZ	2.19	0.40
48:AL:119:TYR:O	48:AL:123:ILE:HG23	2.22	0.40
52:AP:127:ARG:HB2	52:AP:139:TYR:O	2.20	0.40
54:AR:43:LYS:HZ2	54:AR:44:LEU:CD2	2.28	0.40
70:Ah:95:PHE:O	70:Ah:99:GLN:HG2	2.21	0.40
79:E:191:VAL:HA	79:E:194:LEU:HD12	2.02	0.40
80:EC:6846:C:H2'	80:EC:6847:G:C8	2.56	0.40
4:BE:11:ARG:HD3	4:BE:21:ASP:O	2.22	0.40
4:BE:114:ILE:HB	4:BE:118:GLU:HB2	2.04	0.40
8:BJ:11:THR:HG23	34:B5:472:U:H5''	2.03	0.40
11:BO:12:GLN:NE2	11:BO:111:ARG:HG3	2.36	0.40
16:Ba:41:ILE:HD12	16:Ba:68:TYR:CD2	2.56	0.40
23:BQ:73:GLY:O	23:BQ:77:GLN:HG3	2.21	0.40
25:BS:27:LYS:HE3	25:BS:55:HIS:ND1	2.36	0.40
27:BU:80:GLU:OE1	30:Bd:44:ARG:NE	2.45	0.40
33:BM:97:LEU:HD12	33:BM:97:LEU:HA	1.96	0.40
34:B5:730:G:N2	34:B5:732:G:H4'	2.37	0.40
34:B5:884:A:H2'	34:B5:885:G:H8	1.86	0.40
34:B5:901:G:C6	34:B5:902:G:C6	3.10	0.40
34:B5:1550:A:H2'	34:B5:1551:U:C6	2.56	0.40
34:B5:1690:G:H2'	34:B5:1691:A:C8	2.57	0.40
34:B5:1717:G:H2'	34:B5:1718:G:C8	2.57	0.40
36:AB:9:PRO:HG3	38:A1:2914:G:H5'	2.04	0.40
37:AC:226:GLU:OE1	37:AC:246:ARG:NH1	2.50	0.40
38:A1:240:U:C2'	38:A1:241:G:OP1	2.70	0.40
38:A1:595:G:H2'	38:A1:596:C:C6	2.56	0.40
38:A1:1049:C:H2'	38:A1:1050:U:C6	2.57	0.40
38:A1:1464:G:H22	38:A1:1467:A:P	2.44	0.40
38:A1:1602:A:H2'	38:A1:1603:A:C8	2.56	0.40
38:A1:2552:C:OP1	69:Ag:102:LYS:NZ	2.47	0.40
38:A1:2570:U:H1'	38:A1:2573:G:C2	2.57	0.40
38:A1:2885:C:O2'	38:A1:2886:U:H5'	2.21	0.40
38:A1:3166:C:C2	38:A1:3167:A:C8	3.10	0.40
44:AG:86:THR:O	44:AG:90:THR:OG1	2.32	0.40
47:AJ:91:LEU:HD23	47:AJ:91:LEU:HA	1.93	0.40
57:AU:89:LEU:HA	57:AU:89:LEU:HD23	1.88	0.40
58:AV:75:PRO:HG2	58:AV:104:ASN:HA	2.03	0.40
77:Ao:6:LYS:O	77:Ao:24:LYS:HD2	2.22	0.40
6:BH:106:SER:OG	34:B5:697:C:OP2	2.23	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:70:GLU:HB3	7:BI:112:TRP:CH2	2.56	0.40
10:BN:23:PRO:HD2	10:BN:26:PHE:CB	2.52	0.40
14:BX:90:ASP:OD1	34:B5:567:A:O2'	2.36	0.40
14:BX:92:CYS:O	14:BX:96:VAL:HG23	2.21	0.40
18:Be:17:GLN:NE2	34:B5:563:U:H4'	2.37	0.40
19:BD:71:LEU:HD23	19:BD:74:GLN:HE21	1.86	0.40
20:BF:76:ARG:HH21	23:BQ:121:SER:H	1.68	0.40
23:BQ:35:PRO:HD2	23:BQ:38:LEU:HD12	2.03	0.40
23:BQ:59:LYS:CD	23:BQ:105:LEU:HD21	2.52	0.40
24:BR:33:ARG:NE	31:Bg:109:ASP:OD2	2.38	0.40
31:Bg:249:ARG:NH2	31:Bg:315:VAL:HG11	2.33	0.40
31:Bg:266:ASP:HB2	31:Bg:267:PRO:HD3	2.03	0.40
32:Bf:94:LYS:HG2	32:Bf:95:HIS:H	1.86	0.40
34:B5:304:U:H2'	34:B5:305:C:H6	1.82	0.40
34:B5:488:G:H22	34:B5:500:C:P	2.44	0.40
34:B5:678:A:H3'	34:B5:679:U:C6	2.57	0.40
34:B5:1229:G:N2	34:B5:1255:G:O2'	2.54	0.40
38:A1:26:A:H2'	38:A1:27:C:C6	2.56	0.40
38:A1:94:G:H2'	38:A1:95:A:C8	2.56	0.40
38:A1:96:G:H4'	48:AL:15:ARG:CZ	2.51	0.40
38:A1:238:A:H5''	38:A1:238:A:H8	1.87	0.40
38:A1:324:A:H2'	38:A1:325:A:C8	2.57	0.40
38:A1:629:U:H2'	38:A1:630:A:H8	1.86	0.40
38:A1:649:A2M:H2'	38:A1:650:OMC:C6	2.57	0.40
38:A1:1204:A:H2'	38:A1:1205:A:O4'	2.21	0.40
38:A1:1676:A:C6	38:A1:1677:G:N7	2.90	0.40
38:A1:1785:U:H2'	38:A1:1786:G:C8	2.56	0.40
38:A1:1949:G:H5''	54:AR:104:ARG:NH2	2.36	0.40
38:A1:2425:G:OP1	50:AN:72:LYS:NZ	2.54	0.40
38:A1:2445:A:N1	38:A1:2503:G:C6	2.88	0.40
38:A1:2601:A:H2'	38:A1:2602:G:C8	2.56	0.40
38:A1:3038:U:H2'	38:A1:3039:C:O4'	2.22	0.40
38:A1:3039:C:OP1	58:AV:88:ARG:NH1	2.47	0.40
38:A1:3077:A:N6	38:A1:3080:G:C5	2.90	0.40
38:A1:3349:C:H2'	38:A1:3350:C:O4'	2.21	0.40
44:AG:103:ALA:HA	44:AG:106:LYS:HE3	2.04	0.40
45:AH:23:ARG:NE	45:AH:39:LYS:HA	2.36	0.40
48:AL:67:ARG:HG3	48:AL:68:LYS:HG3	2.04	0.40
48:AL:105:ASN:CG	71:AI:17:VAL:HG11	2.46	0.40
51:AO:60[A]:LYS:HE2	51:AO:60[A]:LYS:HB3	1.88	0.40
62:AZ:4:PHE:CZ	65:Ac:35:ARG:HA	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Aa:47:LYS:HD3	63:Aa:48:TYR:CZ	2.57	0.40
71:Ai:52:PRO:N	71:Ai:55:ARG:HH21	2.19	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	185 (91%)	19 (9%)	0	100	100
2	BB	212/255 (83%)	185 (87%)	27 (13%)	0	100	100
3	BC	215/254 (85%)	208 (97%)	7 (3%)	0	100	100
4	BE	258/261 (99%)	241 (93%)	17 (7%)	0	100	100
5	BG	224/236 (95%)	215 (96%)	9 (4%)	0	100	100
6	BH	182/190 (96%)	163 (90%)	19 (10%)	0	100	100
7	BI	184/200 (92%)	165 (90%)	19 (10%)	0	100	100
8	BJ	183/197 (93%)	172 (94%)	11 (6%)	0	100	100
9	BL	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
10	BN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
11	BO	125/137 (91%)	109 (87%)	16 (13%)	0	100	100
12	BV	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
13	BW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
14	BX	142/145 (98%)	127 (89%)	15 (11%)	0	100	100
15	BY	132/135 (98%)	125 (95%)	7 (5%)	0	100	100
16	Ba	95/119 (80%)	79 (83%)	16 (17%)	0	100	100
17	Bb	79/82 (96%)	63 (80%)	16 (20%)	0	100	100
18	Be	58/63 (92%)	54 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	BD	221/240 (92%)	208 (94%)	13 (6%)	0	100	100
20	BF	204/225 (91%)	183 (90%)	21 (10%)	0	100	100
21	BK	94/105 (90%)	82 (87%)	12 (13%)	0	100	100
22	BP	122/142 (86%)	108 (88%)	14 (12%)	0	100	100
23	BQ	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
24	BR	117/136 (86%)	117 (100%)	0	0	100	100
25	BS	143/146 (98%)	133 (93%)	10 (7%)	0	100	100
26	BT	139/144 (96%)	122 (88%)	17 (12%)	0	100	100
27	BU	105/121 (87%)	100 (95%)	5 (5%)	0	100	100
28	BZ	67/108 (62%)	65 (97%)	2 (3%)	0	100	100
29	Bc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
30	Bd	51/56 (91%)	51 (100%)	0	0	100	100
31	Bg	310/319 (97%)	272 (88%)	38 (12%)	0	100	100
32	Bf	53/152 (35%)	41 (77%)	12 (23%)	0	100	100
33	BM	119/143 (83%)	90 (76%)	29 (24%)	0	100	100
35	AA	245/254 (96%)	231 (94%)	14 (6%)	0	100	100
36	AB	383/387 (99%)	366 (96%)	17 (4%)	0	100	100
37	AC	359/362 (99%)	337 (94%)	22 (6%)	0	100	100
41	AD	290/297 (98%)	277 (96%)	13 (4%)	0	100	100
42	AE	152/176 (86%)	140 (92%)	12 (8%)	0	100	100
43	AF	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
44	AG	228/256 (89%)	211 (92%)	17 (8%)	0	100	100
45	AH	188/191 (98%)	172 (92%)	16 (8%)	0	100	100
46	AI	201/221 (91%)	188 (94%)	13 (6%)	0	100	100
47	AJ	167/174 (96%)	148 (89%)	19 (11%)	0	100	100
48	AL	191/199 (96%)	175 (92%)	16 (8%)	0	100	100
49	AM	134/138 (97%)	130 (97%)	4 (3%)	0	100	100
50	AN	201/204 (98%)	188 (94%)	13 (6%)	0	100	100
51	AO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
52	AP	171/184 (93%)	165 (96%)	6 (4%)	0	100	100
53	AQ	183/186 (98%)	176 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	AR	186/189 (98%)	178 (96%)	8 (4%)	0	100	100
55	AS	170/178 (96%)	162 (95%)	8 (5%)	0	100	100
56	AT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
57	AU	98/121 (81%)	95 (97%)	3 (3%)	0	100	100
58	AV	134/137 (98%)	131 (98%)	3 (2%)	0	100	100
59	AW	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
60	AX	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
61	AY	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
62	AZ	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
63	Aa	146/149 (98%)	133 (91%)	13 (9%)	0	100	100
64	Ab	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
65	Ac	95/105 (90%)	90 (95%)	5 (5%)	0	100	100
66	Ad	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
67	Ae	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
68	Af	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
69	Ag	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
70	Ah	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
71	Ai	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
72	Aj	85/88 (97%)	79 (93%)	6 (7%)	0	100	100
73	Ak	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
74	Al	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
75	Am	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	91 (88%)	12 (12%)	0	100	100
78	Ap	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
79	E	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
All	All	11086/12103 (92%)	10325 (93%)	761 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	173/210 (82%)	173 (100%)	0	100	100
2	BB	191/224 (85%)	191 (100%)	0	100	100
3	BC	176/205 (86%)	176 (100%)	0	100	100
4	BE	221/222 (100%)	221 (100%)	0	100	100
5	BG	193/201 (96%)	193 (100%)	0	100	100
6	BH	165/170 (97%)	165 (100%)	0	100	100
7	BI	150/161 (93%)	150 (100%)	0	100	100
8	BJ	158/166 (95%)	158 (100%)	0	100	100
9	BL	136/137 (99%)	136 (100%)	0	100	100
10	BN	127/128 (99%)	127 (100%)	0	100	100
11	BO	96/105 (91%)	96 (100%)	0	100	100
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	110 (100%)	0	100	100
14	BX	119/120 (99%)	119 (100%)	0	100	100
15	BY	112/113 (99%)	112 (100%)	0	100	100
16	Ba	83/100 (83%)	83 (100%)	0	100	100
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	110/124 (89%)	110 (100%)	0	100	100
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	BU	100/114 (88%)	100 (100%)	0	100	100
28	BZ	61/89 (68%)	61 (100%)	0	100	100
29	Bc	56/60 (93%)	56 (100%)	0	100	100
30	Bd	47/49 (96%)	47 (100%)	0	100	100
31	Bg	256/262 (98%)	256 (100%)	0	100	100
32	Bf	49/135 (36%)	49 (100%)	0	100	100
33	BM	98/119 (82%)	98 (100%)	0	100	100
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	321/322 (100%)	321 (100%)	0	100	100
37	AC	288/289 (100%)	288 (100%)	0	100	100
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	134/153 (88%)	134 (100%)	0	100	100
43	AF	186/205 (91%)	186 (100%)	0	100	100
44	AG	189/208 (91%)	189 (100%)	0	100	100
45	AH	170/171 (99%)	170 (100%)	0	100	100
46	AI	176/187 (94%)	176 (100%)	0	100	100
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100
58	AV	104/105 (99%)	104 (100%)	0	100	100
59	AW	55/129 (43%)	55 (100%)	0	100	100
60	AX	105/118 (89%)	105 (100%)	0	100	100
61	AY	109/110 (99%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	AZ	115/116 (99%)	115 (100%)	0	100	100
63	Aa	118/119 (99%)	118 (100%)	0	100	100
64	Ab	46/47 (98%)	46 (100%)	0	100	100
65	Ac	81/88 (92%)	81 (100%)	0	100	100
66	Ad	96/97 (99%)	96 (100%)	0	100	100
67	Ae	109/111 (98%)	109 (100%)	0	100	100
68	Af	90/91 (99%)	90 (100%)	0	100	100
69	Ag	95/103 (92%)	95 (100%)	0	100	100
70	Ah	104/105 (99%)	104 (100%)	0	100	100
71	Ai	81/82 (99%)	81 (100%)	0	100	100
72	Aj	70/71 (99%)	70 (100%)	0	100	100
73	Ak	68/69 (99%)	68 (100%)	0	100	100
74	Al	45/46 (98%)	45 (100%)	0	100	100
75	Am	47/116 (40%)	47 (100%)	0	100	100
76	An	23/23 (100%)	23 (100%)	0	100	100
77	Ao	90/91 (99%)	90 (100%)	0	100	100
78	Ap	71/72 (99%)	71 (100%)	0	100	100
79	E	198/198 (100%)	198 (100%)	0	100	100
All	All	9468/10186 (93%)	9468 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (152) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	15	GLN
1	BA	30	GLN
1	BA	168	HIS
2	BB	149	GLN
2	BB	183	GLN
2	BB	194	ASN
2	BB	199	ASN
2	BB	209	ASN
2	BB	220	GLN
3	BC	82	ASN

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Mol	Chain	Res	Type
3	BC	150	GLN
3	BC	233	GLN
4	BE	98	ASN
4	BE	223	ASN
4	BE	259	GLN
5	BG	22	HIS
5	BG	34	GLN
5	BG	139	ASN
6	BH	5	GLN
6	BH	22	GLN
6	BH	110	GLN
7	BI	64	ASN
7	BI	159	GLN
8	BJ	48	GLN
8	BJ	74	ASN
9	BL	21	ASN
9	BL	92	HIS
9	BL	98	ASN
9	BL	104	HIS
9	BL	106	ASN
10	BN	105	ASN
11	BO	29	HIS
11	BO	65	GLN
11	BO	99	GLN
12	BV	29	HIS
13	BW	12	ASN
14	BX	75	GLN
15	BY	34	ASN
16	Ba	25	ASN
17	Bb	5	GLN
17	Bb	9	HIS
18	Be	17	GLN
18	Be	46	ASN
19	BD	67	ASN
19	BD	74	GLN
19	BD	101	GLN
19	BD	159	HIS
20	BF	34	GLN
20	BF	35	GLN
20	BF	122	ASN
20	BF	186	ASN
20	BF	224	ASN

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Mol	Chain	Res	Type
21	BK	28	ASN
22	BP	103	ASN
22	BP	104	GLN
23	BQ	21	HIS
23	BQ	83	GLN
23	BQ	103	ASN
25	BS	6	GLN
25	BS	13	HIS
25	BS	74	GLN
25	BS	89	GLN
25	BS	103	ASN
26	BT	25	GLN
26	BT	43	ASN
26	BT	70	GLN
26	BT	129	GLN
26	BT	138	GLN
27	BU	15	GLN
31	Bg	101	GLN
31	Bg	139	GLN
31	Bg	147	HIS
31	Bg	148	ASN
31	Bg	174	ASN
31	Bg	185	GLN
31	Bg	196	ASN
31	Bg	288	HIS
32	Bf	145	HIS
35	AA	211	HIS
36	AB	182	GLN
36	AB	231	HIS
36	AB	293	ASN
37	AC	160	GLN
37	AC	304	GLN
41	AD	111	GLN
43	AF	64	GLN
43	AF	146	GLN
43	AF	186	HIS
45	AH	9	GLN
45	AH	51	GLN
45	AH	157	ASN
45	AH	162	GLN
45	AH	183	HIS
46	AI	51	HIS

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Mol	Chain	Res	Type
46	AI	59	GLN
46	AI	92	HIS
46	AI	100	ASN
47	AJ	6	GLN
47	AJ	90	GLN
47	AJ	95	ASN
47	AJ	132	ASN
48	AL	106	GLN
48	AL	120	GLN
49	AM	62	GLN
49	AM	119	GLN
50	AN	15	GLN
50	AN	138	GLN
50	AN	156	HIS
50	AN	182	ASN
51	AO	50[A]	ASN
51	AO	182[A]	ASN
52	AP	133	HIS
53	AQ	45	ASN
53	AQ	136	ASN
53	AQ	145	ASN
54	AR	134	HIS
54	AR	141	HIS
55	AS	46	GLN
55	AS	49	HIS
56	AT	5	HIS
56	AT	103	GLN
56	AT	112	ASN
57	AU	88	GLN
57	AU	101	ASN
58	AV	98	ASN
58	AV	104	ASN
59	AW	32	GLN
59	AW	59	HIS
62	AZ	36	HIS
62	AZ	40	HIS
62	AZ	106	GLN
62	AZ	122	HIS
62	AZ	128	GLN
63	Aa	89	GLN
67	Ae	71	HIS
69	Ag	33	GLN

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Mol	Chain	Res	Type
69	Ag	61	GLN
70	Ah	16	GLN
70	Ah	59	ASN
70	Ah	68	GLN
70	Ah	99	GLN
72	Aj	13	ASN
72	Aj	57	HIS
73	Ak	10	GLN
74	Al	4	GLN
77	Ao	38	GLN
77	Ao	53	GLN
79	E	94	ASN
79	E	119	GLN
79	E	127	GLN
79	E	182	GLN
79	E	200	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1780/1798 (98%)	416 (23%)	18 (1%)
38	A1	3186/3360 (94%)	613 (19%)	34 (1%)
39	A3	120/121 (99%)	13 (10%)	1 (0%)
40	A4	157/158 (99%)	28 (17%)	0
80	EC	55/202 (27%)	25 (45%)	1 (1%)
All	All	5298/5639 (93%)	1095 (20%)	54 (1%)

All (1095) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	4	C
34	B5	17	C
34	B5	25	C
34	B5	26	A
34	B5	34	G
34	B5	42	G
34	B5	47	A
34	B5	57	G
34	B5	60	U
34	B5	67	A
34	B5	68	A

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Mol	Chain	Res	Type
34	B5	72	A
34	B5	73	U
34	B5	74	U
34	B5	75	U
34	B5	77	U
34	B5	78	A
34	B5	81	G
34	B5	103	A
34	B5	104	A
34	B5	107	C
34	B5	114	C
34	B5	115	G
34	B5	127	G
34	B5	128	U
34	B5	130	C
34	B5	131	C
34	B5	132	U
34	B5	133	U
34	B5	134	U
34	B5	135	A
34	B5	137	U
34	B5	138	A
34	B5	141	U
34	B5	145	A
34	B5	166	C
34	B5	173	A
34	B5	178	U
34	B5	179	A
34	B5	181	A
34	B5	182	A
34	B5	188	A
34	B5	191	C
34	B5	192	U
34	B5	193	U
34	B5	194	U
34	B5	195	G
34	B5	196	G
34	B5	198	A
34	B5	218	A
34	B5	219	A
34	B5	222	A
34	B5	226	A

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Mol	Chain	Res	Type
34	B5	227	U
34	B5	228	G
34	B5	230	C
34	B5	231	U
34	B5	232	U
34	B5	233	C
34	B5	234	G
34	B5	235	G
34	B5	236	A
34	B5	237	C
34	B5	238	U
34	B5	239	C
34	B5	240	U
34	B5	241	U
34	B5	246	G
34	B5	260	U
34	B5	261	U
34	B5	262	U
34	B5	265	A
34	B5	267	U
34	B5	280	U
34	B5	281	G
34	B5	285	G
34	B5	287	G
34	B5	291	G
34	B5	305	C
34	B5	309	C
34	B5	314	C
34	B5	316	A
34	B5	321	C
34	B5	322	G
34	B5	337	G
34	B5	338	C
34	B5	351	C
34	B5	352	A
34	B5	353	A
34	B5	359	A
34	B5	360	A
34	B5	361	C
34	B5	390	G
34	B5	397	A
34	B5	400	A

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Mol	Chain	Res	Type
34	B5	401	A
34	B5	402	C
34	B5	419	G
34	B5	423	G
34	B5	424	C
34	B5	425	A
34	B5	426	G
34	B5	434	G
34	B5	439	U
34	B5	444	C
34	B5	459	G
34	B5	460	A
34	B5	468	A
34	B5	477	A
34	B5	484	C
34	B5	485	A
34	B5	486	G
34	B5	489	C
34	B5	490	C
34	B5	491	C
34	B5	492	A
34	B5	493	U
34	B5	494	U
34	B5	495	C
34	B5	496	G
34	B5	497	G
34	B5	498	G
34	B5	499	U
34	B5	500	C
34	B5	503	G
34	B5	506	A
34	B5	507	U
34	B5	515	A
34	B5	519	C
34	B5	527	A
34	B5	538	A
34	B5	539	G
34	B5	540	G
34	B5	541	A2M
34	B5	542	A
34	B5	544	A
34	B5	555	A

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Mol	Chain	Res	Type
34	B5	557	G
34	B5	558	U
34	B5	559	C
34	B5	565	C
34	B5	568	G
34	B5	572	C
34	B5	577	G
34	B5	578	OMU
34	B5	579	A
34	B5	582	U
34	B5	583	C
34	B5	594	A
34	B5	595	G
34	B5	606	A
34	B5	609	U
34	B5	610	G
34	B5	611	U
34	B5	619	A2M
34	B5	620	A
34	B5	622	A
34	B5	623	A
34	B5	624	G
34	B5	638	U
34	B5	639	U
34	B5	650	U
34	B5	652	G
34	B5	654	C
34	B5	655	G
34	B5	656	G
34	B5	657	U
34	B5	658	C
34	B5	677	G
34	B5	678	A
34	B5	679	U
34	B5	681	U
34	B5	683	C
34	B5	694	U
34	B5	696	C
34	B5	697	C
34	B5	698	U
34	B5	704	C
34	B5	705	U

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Mol	Chain	Res	Type
34	B5	707	A
34	B5	709	C
34	B5	710	U
34	B5	712	G
34	B5	713	A
34	B5	715	U
34	B5	716	C
34	B5	717	C
34	B5	718	U
34	B5	719	U
34	B5	721	U
34	B5	722	G
34	B5	724	C
34	B5	725	U
34	B5	726	C
34	B5	727	U
34	B5	729	G
34	B5	730	G
34	B5	731	C
34	B5	732	G
34	B5	733	A
34	B5	735	C
34	B5	736	C
34	B5	737	A
34	B5	738	G
34	B5	740	A
34	B5	741	C
34	B5	742	U
34	B5	743	U
34	B5	753	A
34	B5	765	G
34	B5	766	U
34	B5	774	A
34	B5	775	G
34	B5	778	G
34	B5	780	A
34	B5	781	U
34	B5	782	U
34	B5	783	G
34	B5	784	C
34	B5	794	U
34	B5	812	A

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Mol	Chain	Res	Type
34	B5	814	A
34	B5	819	G
34	B5	820	U
34	B5	821	U
34	B5	823	G
34	B5	832	U
34	B5	833	U
34	B5	834	G
34	B5	835	U
34	B5	837	G
34	B5	840	U
34	B5	846	G
34	B5	851	U
34	B5	852	C
34	B5	854	U
34	B5	856	A
34	B5	859	A
34	B5	862	A
34	B5	863	A
34	B5	886	U
34	B5	895	G
34	B5	898	A
34	B5	906	A
34	B5	913	G
34	B5	914	G
34	B5	923	A
34	B5	933	A
34	B5	935	U
34	B5	944	A
34	B5	951	A
34	B5	960	U
34	B5	966	A
34	B5	973	A
34	B5	987	G
34	B5	988	A
34	B5	992	A
34	B5	1003	A
34	B5	1004	U
34	B5	1005	A
34	B5	1020	A
34	B5	1021	C
34	B5	1026	A

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Mol	Chain	Res	Type
34	B5	1028	C
34	B5	1032	G
34	B5	1039	A
34	B5	1040	G
34	B5	1052	U
34	B5	1053	G
34	B5	1054	U
34	B5	1056	U
34	B5	1057	U
34	B5	1058	U
34	B5	1059	U
34	B5	1060	U
34	B5	1061	A
34	B5	1062	A
34	B5	1063	U
34	B5	1083	G
34	B5	1092	A
34	B5	1093	A
34	B5	1097	U
34	B5	1100	G
34	B5	1138	A
34	B5	1150	G
34	B5	1155	G
34	B5	1158	C
34	B5	1185	U
34	B5	1188	G
34	B5	1194	A
34	B5	1196	A
34	B5	1199	G
34	B5	1200	G
34	B5	1201	G
34	B5	1202	A
34	B5	1216	C
34	B5	1217	A
34	B5	1218	G
34	B5	1226	A
34	B5	1227	A
34	B5	1228	G
34	B5	1229	G
34	B5	1230	A
34	B5	1235	C
34	B5	1243	G

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Mol	Chain	Res	Type
34	B5	1244	A
34	B5	1245	G
34	B5	1246	C
34	B5	1249	U
34	B5	1256	A
34	B5	1257	U
34	B5	1258	U
34	B5	1263	G
34	B5	1269	OMU
34	B5	1276	U
34	B5	1286	U
34	B5	1306	C
34	B5	1314	U
34	B5	1315	U
34	B5	1316	G
34	B5	1321	A
34	B5	1340	U
34	B5	1345	A
34	B5	1355	C
34	B5	1356	U
34	B5	1358	G
34	B5	1359	C
34	B5	1362	U
34	B5	1363	U
34	B5	1364	G
34	B5	1366	U
34	B5	1368	G
34	B5	1369	U
34	B5	1370	U
34	B5	1371	A
34	B5	1372	U
34	B5	1373	C
34	B5	1378	U
34	B5	1390	U
34	B5	1399	C
34	B5	1400	A
34	B5	1402	G
34	B5	1412	G
34	B5	1413	U
34	B5	1415	U
34	B5	1425	A
34	B5	1427	A

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Mol	Chain	Res	Type
34	B5	1428	OMG
34	B5	1436	A
34	B5	1447	C
34	B5	1459	C
34	B5	1460	A
34	B5	1461	C
34	B5	1471	A
34	B5	1486	G
34	B5	1491	U
34	B5	1492	A
34	B5	1493	A
34	B5	1514	U
34	B5	1515	A
34	B5	1516	A
34	B5	1519	U
34	B5	1520	U
34	B5	1521	G
34	B5	1523	G
34	B5	1524	A
34	B5	1537	C
34	B5	1538	U
34	B5	1539	G
34	B5	1540	G
34	B5	1557	U
34	B5	1559	A
34	B5	1575	7MG
34	B5	1576	A
34	B5	1584	G
34	B5	1590	G
34	B5	1600	A
34	B5	1601	G
34	B5	1605	G
34	B5	1607	G
34	B5	1616	G
34	B5	1631	A
34	B5	1634	C
34	B5	1635	A
34	B5	1636	C
34	B5	1646	C
34	B5	1651	A
34	B5	1657	U
34	B5	1658	G

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Mol	Chain	Res	Type
34	B5	1667	A
34	B5	1682	U
34	B5	1683	C
34	B5	1684	U
34	B5	1688	U
34	B5	1693	A
34	B5	1701	A
34	B5	1703	C
34	B5	1708	U
34	B5	1715	G
34	B5	1716	C
34	B5	1717	G
34	B5	1755	A
34	B5	1757	G
34	B5	1760	G
34	B5	1762	A
34	B5	1766	A
34	B5	1767	G
34	B5	1769	U
34	B5	1771	U
34	B5	1780	G
34	B5	1792	G
34	B5	1793	G
34	B5	1794	A
34	B5	1795	U
34	B5	1796	C
34	B5	1799	U
38	A1	6	A
38	A1	14	U
38	A1	26	A
38	A1	34	A
38	A1	40	A
38	A1	43	A
38	A1	49	A
38	A1	59	G
38	A1	60	A
38	A1	65	A
38	A1	66	A
38	A1	71	A
38	A1	72	C
38	A1	92	G
38	A1	99	A

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Mol	Chain	Res	Type
38	A1	109	A
38	A1	110	G
38	A1	111	C
38	A1	116	A
38	A1	117	U
38	A1	121	A
38	A1	122	A
38	A1	134	U
38	A1	135	C
38	A1	136	G
38	A1	143	G
38	A1	155	G
38	A1	156	G
38	A1	157	A
38	A1	160	G
38	A1	163	C
38	A1	164	A
38	A1	165	A
38	A1	166	C
38	A1	167	U
38	A1	169	U
38	A1	173	G
38	A1	174	C
38	A1	176	G
38	A1	177	U
38	A1	187	A
38	A1	190	U
38	A1	200	C
38	A1	210	U
38	A1	219	A
38	A1	220	G
38	A1	237	G
38	A1	238	A
38	A1	239	G
38	A1	240	U
38	A1	241	G
38	A1	244	G
38	A1	245	U
38	A1	246	U
38	A1	248	U
38	A1	249	U
38	A1	250	U

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Mol	Chain	Res	Type
38	A1	251	G
38	A1	252	U
38	A1	253	A
38	A1	254	A
38	A1	269	G
38	A1	286	U
38	A1	295	A
38	A1	296	A
38	A1	298	U
38	A1	305	U
38	A1	311	C
38	A1	329	U
38	A1	339	C
38	A1	349	A
38	A1	352	A
38	A1	371	G
38	A1	372	A
38	A1	373	A
38	A1	374	A
38	A1	376	G
38	A1	387	A
38	A1	398	A
38	A1	399	A
38	A1	401	U
38	A1	402	A
38	A1	403	C
38	A1	420	G
38	A1	421	G
38	A1	422	A
38	A1	438	A
38	A1	439	C
38	A1	440	A
38	A1	495	G
38	A1	520	U
38	A1	521	A
38	A1	523	A
38	A1	535	G
38	A1	540	U
38	A1	542	G
38	A1	545	U
38	A1	547	G
38	A1	548	G

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Mol	Chain	Res	Type
38	A1	550	A
38	A1	552	G
38	A1	554	A
38	A1	557	A
38	A1	559	A
38	A1	579	G
38	A1	592	A
38	A1	602	A
38	A1	604	G
38	A1	611	A
38	A1	612	U
38	A1	620	U
38	A1	621	A
38	A1	649	A2M
38	A1	660	A
38	A1	677	A
38	A1	681	U
38	A1	691	A
38	A1	705	A
38	A1	715	A
38	A1	725	G
38	A1	736	A
38	A1	765	C
38	A1	766	U
38	A1	767	U
38	A1	771	A
38	A1	774	G
38	A1	775	A
38	A1	777	U
38	A1	778	U
38	A1	781	G
38	A1	784	A
38	A1	785	G
38	A1	786	A
38	A1	799	G
38	A1	806	A
38	A1	813	G
38	A1	817	A2M
38	A1	830	A
38	A1	844	G
38	A1	849	C
38	A1	861	C

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Mol	Chain	Res	Type
38	A1	874	U
38	A1	879	U
38	A1	896	A
38	A1	907	G
38	A1	908	OMG
38	A1	914	A
38	A1	916	G
38	A1	917	A
38	A1	921	A
38	A1	923	C
38	A1	924	G
38	A1	925	A
38	A1	934	G
38	A1	937	G
38	A1	943	U
38	A1	944	C
38	A1	959	C
38	A1	960	U
38	A1	964	G
38	A1	974	G
38	A1	980	A
38	A1	981	U
38	A1	995	U
38	A1	1000	C
38	A1	1002	A
38	A1	1010	G
38	A1	1015	U
38	A1	1016	C
38	A1	1017	C
38	A1	1018	G
38	A1	1019	G
38	A1	1021	G
38	A1	1022	U
38	A1	1023	C
38	A1	1033	U
38	A1	1034	U
38	A1	1035	G
38	A1	1045	C
38	A1	1047	A
38	A1	1064	A
38	A1	1072	G
38	A1	1081	U

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Mol	Chain	Res	Type
38	A1	1082	U
38	A1	1087	G
38	A1	1093	A
38	A1	1094	U
38	A1	1095	U
38	A1	1097	G
38	A1	1098	A
38	A1	1103	A
38	A1	1104	G
38	A1	1117	G
38	A1	1131	G
38	A1	1144	U
38	A1	1153	A
38	A1	1159	A
38	A1	1160	C
38	A1	1168	U
38	A1	1180	A
38	A1	1181	U
38	A1	1182	A
38	A1	1192	C
38	A1	1193	A
38	A1	1201	C
38	A1	1206	G
38	A1	1208	U
38	A1	1219	C
38	A1	1221	A
38	A1	1222	G
38	A1	1223	A
38	A1	1225	A
38	A1	1227	C
38	A1	1228	C
38	A1	1230	G
38	A1	1231	A
38	A1	1232	C
38	A1	1233	G
38	A1	1235	U
38	A1	1236	G
38	A1	1237	G
38	A1	1239	C
38	A1	1240	A
38	A1	1241	U
38	A1	1242	G

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Mol	Chain	Res	Type
38	A1	1243	G
38	A1	1244	A
38	A1	1245	A
38	A1	1246	G
38	A1	1247	U
38	A1	1249	G
38	A1	1251	A
38	A1	1252	A
38	A1	1263	A
38	A1	1264	G
38	A1	1265	U
38	A1	1267	U
38	A1	1268	G
38	A1	1270	A
38	A1	1271	A
38	A1	1276	U
38	A1	1277	C
38	A1	1278	A
38	A1	1279	C
38	A1	1281	G
38	A1	1283	C
38	A1	1285	G
38	A1	1286	A
38	A1	1287	A
38	A1	1292	C
38	A1	1293	U
38	A1	1307	G
38	A1	1309	U
38	A1	1317	A
38	A1	1325	U
38	A1	1331	U
38	A1	1348	U
38	A1	1349	G
38	A1	1350	A
38	A1	1351	U
38	A1	1352	A
38	A1	1353	U
38	A1	1355	A
38	A1	1356	U
38	A1	1357	G
38	A1	1386	A
38	A1	1393	A

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Mol	Chain	Res	Type
38	A1	1399	A
38	A1	1400	G
38	A1	1419	A
38	A1	1434	G
38	A1	1437	OMC
38	A1	1443	G
38	A1	1446	A
38	A1	1455	U
38	A1	1481	A
38	A1	1488	G
38	A1	1490	A
38	A1	1508	C
38	A1	1523	U
38	A1	1527	C
38	A1	1539	A
38	A1	1555	U
38	A1	1556	C
38	A1	1558	A
38	A1	1562	C
38	A1	1563	C
38	A1	1564	U
38	A1	1565	G
38	A1	1566	A
38	A1	1567	U
38	A1	1568	U
38	A1	1569	U
38	A1	1572	U
38	A1	1573	G
38	A1	1574	C
38	A1	1575	A
38	A1	1583	A
38	A1	1587	A
38	A1	1589	A
38	A1	1593	A
38	A1	1594	A
38	A1	1605	A
38	A1	1613	A
38	A1	1621	A
38	A1	1628	C
38	A1	1630	U
38	A1	1631	C
38	A1	1643	A

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Mol	Chain	Res	Type
38	A1	1657	C
38	A1	1677	G
38	A1	1714	A
38	A1	1724	U
38	A1	1736	G
38	A1	1738	C
38	A1	1741	A
38	A1	1750	A
38	A1	1751	G
38	A1	1761	C
38	A1	1762	C
38	A1	1763	U
38	A1	1764	U
38	A1	1765	U
38	A1	1766	G
38	A1	1775	G
38	A1	1797	A
38	A1	1813	A
38	A1	1815	U
38	A1	1817	G
38	A1	1820	U
38	A1	1821	U
38	A1	1842	A
38	A1	1846	C
38	A1	1849	C
38	A1	1850	A
38	A1	1851	G
38	A1	1878	G
38	A1	1880	U
38	A1	1893	A
38	A1	1906	G
38	A1	1932	A
38	A1	1936	A
38	A1	1948	G
38	A1	1950	U
38	A1	1952	G
38	A1	1953	G
38	A1	1955	U
38	A1	2095	G
38	A1	2102	U
38	A1	2112	U
38	A1	2113	A

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Mol	Chain	Res	Type
38	A1	2122	G
38	A1	2131	A
38	A1	2144	A
38	A1	2158	A
38	A1	2169	G
38	A1	2188	A
38	A1	2194	G
38	A1	2205	U
38	A1	2206	G
38	A1	2207	A
38	A1	2208	A
38	A1	2209	U
38	A1	2210	G
38	A1	2242	A
38	A1	2249	G
38	A1	2254	U
38	A1	2255	A
38	A1	2256	A
38	A1	2257	C
38	A1	2258	U
38	A1	2259	A
38	A1	2262	A
38	A1	2263	C
38	A1	2266	U
38	A1	2267	C
38	A1	2268	U
38	A1	2269	U
38	A1	2270	A
38	A1	2272	G
38	A1	2273	G
38	A1	2274	U
38	A1	2281	A2M
38	A1	2282	U
38	A1	2307	G
38	A1	2308	C
38	A1	2310	U
38	A1	2313	A
38	A1	2314	U
38	A1	2315	G
38	A1	2318	U
38	A1	2334	U
38	A1	2335	G

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Mol	Chain	Res	Type
38	A1	2336	U
38	A1	2340	U
38	A1	2366	C
38	A1	2373	A
38	A1	2374	C
38	A1	2375	G
38	A1	2383	C
38	A1	2388	U
38	A1	2391	G
38	A1	2393	G
38	A1	2397	A
38	A1	2402	A
38	A1	2403	G
38	A1	2404	A
38	A1	2411	U
38	A1	2412	G
38	A1	2445	A
38	A1	2447	A
38	A1	2450	G
38	A1	2452	G
38	A1	2453	U
38	A1	2454	G
38	A1	2455	U
38	A1	2456	A
38	A1	2458	A
38	A1	2459	A
38	A1	2460	U
38	A1	2461	A
38	A1	2463	G
38	A1	2467	G
38	A1	2468	A
38	A1	2469	G
38	A1	2472	U
38	A1	2474	G
38	A1	2475	G
38	A1	2477	G
38	A1	2479	C
38	A1	2482	U
38	A1	2486	A
38	A1	2487	U
38	A1	2490	C
38	A1	2491	A

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Mol	Chain	Res	Type
38	A1	2493	U
38	A1	2495	C
38	A1	2497	U
38	A1	2498	U
38	A1	2499	U
38	A1	2501	U
38	A1	2502	A
38	A1	2504	U
38	A1	2505	U
38	A1	2506	U
38	A1	2508	U
38	A1	2509	U
38	A1	2511	A
38	A1	2514	U
38	A1	2515	A
38	A1	2523	A
38	A1	2524	A
38	A1	2530	G
38	A1	2532	U
38	A1	2537	U
38	A1	2538	U
38	A1	2539	C
38	A1	2540	A
38	A1	2541	U
38	A1	2542	U
38	A1	2544	U
38	A1	2546	C
38	A1	2549	G
38	A1	2552	C
38	A1	2560	C
38	A1	2561	A
38	A1	2569	A
38	A1	2570	U
38	A1	2571	U
38	A1	2572	C
38	A1	2573	G
38	A1	2576	G
38	A1	2585	G
38	A1	2586	G
38	A1	2593	A
38	A1	2606	G
38	A1	2607	G

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Mol	Chain	Res	Type
38	A1	2614	G
38	A1	2619	OMG
38	A1	2635	A
38	A1	2652	U
38	A1	2656	A
38	A1	2658	G
38	A1	2672	G
38	A1	2674	A
38	A1	2677	G
38	A1	2678	A
38	A1	2681	U
38	A1	2688	U
38	A1	2689	A
38	A1	2691	A
38	A1	2702	A
38	A1	2703	A
38	A1	2704	A
38	A1	2705	A
38	A1	2712	U
38	A1	2714	G
38	A1	2719	U
38	A1	2726	C
38	A1	2728	G
38	A1	2729	OMU
38	A1	2737	C
38	A1	2752	U
38	A1	2753	G
38	A1	2755	C
38	A1	2762	A
38	A1	2777	G
38	A1	2778	G
38	A1	2796	G
38	A1	2798	C
38	A1	2799	A
38	A1	2800	G
38	A1	2801	A
38	A1	2802	A
38	A1	2803	A
38	A1	2810	C
38	A1	2814	G
38	A1	2817	A
38	A1	2842	U

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Mol	Chain	Res	Type
38	A1	2844	C
38	A1	2845	A
38	A1	2850	G
38	A1	2867	C
38	A1	2871	G
38	A1	2872	A
38	A1	2875	U
38	A1	2876	C
38	A1	2887	A
38	A1	2889	C
38	A1	2898	G
38	A1	2923	U
38	A1	2935	U
38	A1	2936	A
38	A1	2938	G
38	A1	2942	C
38	A1	2943	G
38	A1	2947	G
38	A1	2954	U
38	A1	2983	C
38	A1	2990	G
38	A1	2997	G
38	A1	3012	A
38	A1	3022	G
38	A1	3030	G
38	A1	3032	A
38	A1	3056	U
38	A1	3059	G
38	A1	3078	U
38	A1	3080	G
38	A1	3086	A
38	A1	3092	C
38	A1	3104	U
38	A1	3109	G
38	A1	3122	A
38	A1	3129	A
38	A1	3130	A
38	A1	3131	U
38	A1	3142	A
38	A1	3143	C
38	A1	3153	U
38	A1	3154	C

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Mol	Chain	Res	Type
38	A1	3155	U
38	A1	3156	U
38	A1	3157	U
38	A1	3165	A
38	A1	3170	A
38	A1	3172	A
38	A1	3173	G
38	A1	3174	A
38	A1	3176	G
38	A1	3179	U
38	A1	3181	C
38	A1	3187	A
38	A1	3196	U
38	A1	3198	U
38	A1	3206	C
38	A1	3207	U
38	A1	3215	A
38	A1	3217	C
38	A1	3218	A
38	A1	3219	G
38	A1	3224	G
38	A1	3234	A
38	A1	3243	A
38	A1	3244	A
38	A1	3247	G
38	A1	3250	U
38	A1	3259	U
38	A1	3260	G
38	A1	3263	G
38	A1	3271	G
38	A1	3273	A
38	A1	3275	U
38	A1	3276	G
38	A1	3278	C
38	A1	3281	U
38	A1	3289	G
38	A1	3294	A
38	A1	3304	U
38	A1	3316	A
38	A1	3341	U
38	A1	3345	G
38	A1	3350	C

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Mol	Chain	Res	Type
38	A1	3351	U
38	A1	3352	U
38	A1	3353	G
38	A1	3354	U
38	A1	3355	U
38	A1	3356	G
38	A1	3369	G
38	A1	3378	C
38	A1	3382	U
38	A1	3389	U
39	A3	19	C
39	A3	33	U
39	A3	36	C
39	A3	41	G
39	A3	53	U
39	A3	54	U
39	A3	55	A
39	A3	65	G
39	A3	74	C
39	A3	76	A
39	A3	102	A
39	A3	112	G
39	A3	121	U
40	A4	23	U
40	A4	34	U
40	A4	35	C
40	A4	51	G
40	A4	52	A
40	A4	59	A
40	A4	62	C
40	A4	63	G
40	A4	75	G
40	A4	76	C
40	A4	81	U
40	A4	82	U
40	A4	83	C
40	A4	86	U
40	A4	87	G
40	A4	88	A
40	A4	90	U
40	A4	95	G
40	A4	104	A

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Mol	Chain	Res	Type
40	A4	106	C
40	A4	107	G
40	A4	111	A
40	A4	113	U
40	A4	125	U
40	A4	126	A
40	A4	152	G
40	A4	157	U
40	A4	158	U
80	EC	6834	U
80	EC	6835	U
80	EC	6837	G
80	EC	6841	U
80	EC	6843	U
80	EC	6844	A
80	EC	6845	G
80	EC	6848	U
80	EC	6849	A
80	EC	6850	C
80	EC	6851	G
80	EC	6852	U
80	EC	6854	U
80	EC	6855	A
80	EC	6857	C
80	EC	6860	A
80	EC	6861	G
80	EC	6869	C
80	EC	6870	A
80	EC	6871	A
80	EC	6872	A
80	EC	6873	A
80	EC	6876	A
80	EC	6950	C
80	EC	6954	C

All (54) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	B5	221	A
34	B5	239	C
34	B5	240	U
34	B5	706	A

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Mol	Chain	Res	Type
34	B5	752	A
34	B5	819	G
34	B5	862	A
34	B5	912	U
34	B5	950	C
34	B5	1226	A
34	B5	1285	U
34	B5	1344	A
34	B5	1369	U
34	B5	1458	G
34	B5	1539	G
34	B5	1575	7MG
34	B5	1600	A
34	B5	1645	G
38	A1	116	A
38	A1	164	A
38	A1	173	G
38	A1	238	A
38	A1	240	U
38	A1	244	G
38	A1	249	U
38	A1	250	U
38	A1	251	G
38	A1	252	U
38	A1	873	C
38	A1	916	G
38	A1	959	C
38	A1	1092	C
38	A1	1218	U
38	A1	1280	C
38	A1	1292	C
38	A1	1354	G
38	A1	1566	A
38	A1	1567	U
38	A1	1568	U
38	A1	1574	C
38	A1	2204	C
38	A1	2207	A
38	A1	2241	U
38	A1	2255	A
38	A1	2256	A
38	A1	2372	A

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Mol	Chain	Res	Type
38	A1	2504	U
38	A1	2505	U
38	A1	2541	U
38	A1	2801	A
38	A1	2875	U
38	A1	3121	U
39	A3	52	G
80	EC	6847	G

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

66 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	OMC	A1	2948	38	19,22,23	0.78	0	25,31,34	0.90	1 (4%)
38	OMC	A1	663	38	19,22,23	0.80	0	25,31,34	0.81	0
38	A2M	A1	2946	38,81	22,25,26	1.48	5 (22%)	30,36,39	2.15	8 (26%)
38	OMG	A1	1450	38	23,26,27	1.19	3 (13%)	32,38,41	2.01	6 (18%)
38	A2M	A1	2280	38	22,25,26	1.48	4 (18%)	30,36,39	2.10	9 (30%)
34	OMU	B5	578	34	19,22,23	1.20	3 (15%)	25,31,34	1.85	5 (20%)
38	A2M	A1	876	38	22,25,26	1.53	4 (18%)	30,36,39	1.97	7 (23%)
38	OMU	A1	2729	38	19,22,23	1.26	4 (21%)	25,31,34	1.85	4 (16%)
34	7MG	B5	1575	34	23,26,27	5.86	5 (21%)	27,39,42	3.55	7 (25%)
36	HIC	AB	243	36	10,11,12	1.49	1 (10%)	9,14,16	1.29	2 (22%)
38	A2M	A1	1133	38	22,25,26	1.51	4 (18%)	30,36,39	2.09	9 (30%)
34	OMG	B5	1271	34	23,26,27	1.18	3 (13%)	32,38,41	1.97	6 (18%)
38	A2M	A1	649	38	22,25,26	1.49	4 (18%)	30,36,39	2.06	7 (23%)
38	OMG	A1	2922	38	23,26,27	1.19	3 (13%)	32,38,41	1.96	6 (18%)
38	A2M	A1	2220	38	22,25,26	1.54	5 (22%)	30,36,39	1.89	9 (30%)
34	OMG	B5	562	34	23,26,27	1.18	3 (13%)	32,38,41	2.01	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	OMU	A1	2417	38	19,22,23	1.23	3 (15%)	25,31,34	1.82	5 (20%)
38	OMU	A1	898	38	19,22,23	1.25	3 (15%)	25,31,34	1.83	5 (20%)
38	OMC	A1	2337	38	19,22,23	0.76	0	25,31,34	0.82	1 (4%)
34	OMC	B5	414	34	19,22,23	0.80	0	25,31,34	0.82	0
38	A2M	A1	1449	38,81	22,25,26	1.50	4 (18%)	30,36,39	2.07	7 (23%)
34	MA6	B5	1781	34	23,26,27	1.52	5 (21%)	33,38,41	2.06	10 (30%)
38	OMC	A1	2197	38	19,22,23	0.76	0	25,31,34	0.87	0
34	OMC	B5	1639	34	19,22,23	0.77	0	25,31,34	0.80	0
34	A2M	B5	28	81,34	22,25,26	1.49	4 (18%)	30,36,39	2.09	9 (30%)
34	OMG	B5	1428	81,34	23,26,27	1.19	3 (13%)	32,38,41	1.96	6 (18%)
34	A2M	B5	796	34	22,25,26	1.48	4 (18%)	30,36,39	2.11	10 (33%)
38	A2M	A1	807	38	22,25,26	1.51	4 (18%)	30,36,39	2.05	8 (26%)
38	5MC	A1	2870	38	19,22,23	1.63	3 (15%)	26,32,35	1.29	2 (7%)
38	OMG	A1	2619	38	23,26,27	1.19	3 (13%)	32,38,41	1.93	6 (18%)
34	OMC	B5	1007	34	19,22,23	0.77	0	25,31,34	0.82	0
34	A2M	B5	436	34	22,25,26	1.51	4 (18%)	30,36,39	2.07	8 (26%)
34	4AC	B5	1280	34	21,24,25	0.97	1 (4%)	28,34,37	1.15	4 (14%)
38	OMC	A1	1437	38,81	19,22,23	0.78	0	25,31,34	1.00	2 (8%)
38	OMG	A1	2288	38	23,26,27	1.18	3 (13%)	32,38,41	2.06	6 (18%)
38	OMG	A1	867	38	23,26,27	1.13	3 (13%)	32,38,41	2.02	7 (21%)
38	OMG	A1	2793	38	23,26,27	1.19	3 (13%)	32,38,41	2.05	6 (18%)
34	OMG	B5	1126	34	23,26,27	1.16	3 (13%)	32,38,41	2.03	6 (18%)
38	OMC	A1	2959	38	19,22,23	0.81	0	25,31,34	0.90	1 (4%)
38	OMG	A1	908	38	23,26,27	1.20	3 (13%)	32,38,41	2.01	6 (18%)
34	XSX	B5	1191	34	24,28,29	0.99	0	30,40,43	2.22	4 (13%)
34	A2M	B5	974	34	22,25,26	1.47	5 (22%)	30,36,39	2.06	10 (33%)
38	1MA	A1	645	38,81	21,25,26	1.36	4 (19%)	30,37,40	1.66	5 (16%)
34	A2M	B5	420	34	22,25,26	1.51	4 (18%)	30,36,39	2.09	8 (26%)
38	A2M	A1	2281	38	22,25,26	1.44	4 (18%)	30,36,39	2.33	11 (36%)
38	OMG	A1	2815	38	23,26,27	1.18	3 (13%)	32,38,41	2.04	7 (21%)
38	OMU	A1	2724	38	19,22,23	1.22	3 (15%)	25,31,34	1.90	6 (24%)
34	A2M	B5	619	81,34	22,25,26	1.45	5 (22%)	30,36,39	2.01	9 (30%)
34	OMG	B5	1572	34	23,26,27	1.19	3 (13%)	32,38,41	1.99	6 (18%)
38	OMU	A1	2347	38	19,22,23	1.25	3 (15%)	25,31,34	1.75	5 (20%)
38	A2M	A1	2640	38	22,25,26	1.50	4 (18%)	30,36,39	2.01	8 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	A2M	A1	817	38,81	22,25,26	1.48	4 (18%)	30,36,39	2.12	10 (33%)
38	1MA	A1	2142	38,81	21,25,26	1.34	5 (23%)	30,37,40	1.65	5 (16%)
34	OMU	B5	1269	34	19,22,23	1.27	4 (21%)	25,31,34	1.86	5 (20%)
38	OMU	A1	1888	38	19,22,23	1.26	2 (10%)	25,31,34	1.91	6 (24%)
38	OMU	A1	2921	38	19,22,23	1.22	3 (15%)	25,31,34	1.84	5 (20%)
34	A2M	B5	100	81,34	22,25,26	1.47	4 (18%)	30,36,39	2.13	8 (26%)
34	A2M	B5	541	34	22,25,26	1.50	4 (18%)	30,36,39	2.10	7 (23%)
38	OMU	A1	2421	38	19,22,23	1.22	4 (21%)	25,31,34	1.83	5 (20%)
38	UR3	A1	2634	38	19,22,23	0.98	0	26,32,35	1.74	3 (11%)
38	OMG	A1	805	38	23,26,27	1.17	3 (13%)	32,38,41	2.04	6 (18%)
38	OMG	A1	2791	38	23,26,27	1.17	3 (13%)	32,38,41	2.00	6 (18%)
34	MA6	B5	1782	34	23,26,27	1.52	5 (21%)	33,38,41	2.08	10 (30%)
38	OMC	A1	650	38	19,22,23	0.81	0	25,31,34	0.98	1 (4%)
34	4AC	B5	1773	34	21,24,25	0.97	1 (4%)	28,34,37	2.19	6 (21%)
38	5MC	A1	2278	38,81	19,22,23	1.63	3 (15%)	26,32,35	1.12	3 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMC	A1	2948	38	-	0/9/27/28	0/2/2/2
38	OMC	A1	663	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2946	38,81	-	1/9/27/28	0/3/3/3
38	OMG	A1	1450	38	-	0/9/27/28	0/3/3/3
38	A2M	A1	2280	38	-	1/9/27/28	0/3/3/3
34	OMU	B5	578	34	-	0/9/27/28	0/2/2/2
38	A2M	A1	876	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2729	38	-	3/9/27/28	0/2/2/2
34	7MG	B5	1575	34	-	0/7/37/38	0/3/3/3
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
38	A2M	A1	1133	38	-	0/9/27/28	0/3/3/3
34	OMG	B5	1271	34	-	1/9/27/28	0/3/3/3
38	A2M	A1	649	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	A2M	A1	2220	38	-	1/9/27/28	0/3/3/3
34	OMG	B5	562	34	-	0/9/27/28	0/3/3/3
38	OMU	A1	2417	38	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMU	A1	898	38	-	0/9/27/28	0/2/2/2
38	OMC	A1	2337	38	-	1/9/27/28	0/2/2/2
34	OMC	B5	414	34	-	1/9/27/28	0/2/2/2
38	A2M	A1	1449	38,81	-	0/9/27/28	0/3/3/3
34	MA6	B5	1781	34	-	0/11/29/30	0/3/3/3
38	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
34	OMC	B5	1639	34	-	0/9/27/28	0/2/2/2
34	A2M	B5	28	81,34	-	1/9/27/28	0/3/3/3
34	OMG	B5	1428	81,34	-	1/9/27/28	0/3/3/3
34	A2M	B5	796	34	-	1/9/27/28	0/3/3/3
38	A2M	A1	807	38	-	0/9/27/28	0/3/3/3
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
38	OMG	A1	2619	38	-	1/9/27/28	0/3/3/3
34	OMC	B5	1007	34	-	1/9/27/28	0/2/2/2
34	A2M	B5	436	34	-	0/9/27/28	0/3/3/3
34	4AC	B5	1280	34	-	0/11/29/30	0/2/2/2
38	OMC	A1	1437	38,81	-	3/9/27/28	0/2/2/2
38	OMG	A1	2288	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	867	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2793	38	-	1/9/27/28	0/3/3/3
34	OMG	B5	1126	34	-	1/9/27/28	0/3/3/3
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2
38	OMG	A1	908	38	-	0/9/27/28	0/3/3/3
34	XSX	B5	1191	34	-	5/16/34/35	0/2/2/2
34	A2M	B5	974	34	-	1/9/27/28	0/3/3/3
38	1MA	A1	645	38,81	-	1/7/25/26	0/3/3/3
34	A2M	B5	420	34	-	0/9/27/28	0/3/3/3
38	A2M	A1	2281	38	-	2/9/27/28	0/3/3/3
38	OMG	A1	2815	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2724	38	-	0/9/27/28	0/2/2/2
34	A2M	B5	619	81,34	-	3/9/27/28	0/3/3/3
34	OMG	B5	1572	34	-	0/9/27/28	0/3/3/3
38	OMU	A1	2347	38	-	2/9/27/28	0/2/2/2
38	A2M	A1	2640	38	-	0/9/27/28	0/3/3/3
38	A2M	A1	817	38,81	-	2/9/27/28	0/3/3/3
38	1MA	A1	2142	38,81	-	0/7/25/26	0/3/3/3
34	OMU	B5	1269	34	-	3/9/27/28	0/2/2/2
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
34	A2M	B5	100	81,34	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	A2M	B5	541	34	-	4/9/27/28	0/3/3/3
38	OMU	A1	2421	38	-	1/9/27/28	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	OMG	A1	805	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2791	38	-	0/9/27/28	0/3/3/3
34	MA6	B5	1782	34	-	3/11/29/30	0/3/3/3
38	OMC	A1	650	38	-	0/9/27/28	0/2/2/2
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
38	5MC	A1	2278	38,81	-	0/7/25/26	0/2/2/2

All (190) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	7MG	C1'-N9	-27.38	0.97	1.46
38	A1	2278	5MC	C5-C4	5.88	1.48	1.44
38	A1	2870	5MC	C5-C4	5.63	1.48	1.44
38	A1	1449	A2M	C5-C4	4.75	1.47	1.39
38	A1	876	A2M	C5-C4	4.72	1.47	1.39
34	B5	541	A2M	C5-C4	4.69	1.47	1.39
34	B5	1781	MA6	C5-C4	4.69	1.47	1.39
38	A1	2220	A2M	C5-C4	4.68	1.47	1.39
38	A1	1133	A2M	C5-C4	4.66	1.47	1.39
34	B5	436	A2M	C5-C4	4.65	1.47	1.39
38	A1	807	A2M	C5-C4	4.65	1.47	1.39
38	A1	649	A2M	C5-C4	4.64	1.47	1.39
38	A1	2946	A2M	C5-C4	4.62	1.47	1.39
34	B5	420	A2M	C5-C4	4.62	1.47	1.39
34	B5	1782	MA6	C5-C4	4.60	1.47	1.39
38	A1	2640	A2M	C5-C4	4.59	1.47	1.39
34	B5	28	A2M	C5-C4	4.53	1.47	1.39
34	B5	796	A2M	C5-C4	4.52	1.47	1.39
34	B5	100	A2M	C5-C4	4.49	1.47	1.39
38	A1	2281	A2M	C5-C4	4.48	1.47	1.39
38	A1	817	A2M	C5-C4	4.48	1.47	1.39
34	B5	974	A2M	C5-C4	4.44	1.47	1.39
38	A1	2280	A2M	C5-C4	4.44	1.47	1.39
34	B5	619	A2M	C5-C4	4.27	1.46	1.39
34	B5	1575	7MG	C5-C4	3.30	1.47	1.37
38	A1	2288	OMG	C5-C4	3.13	1.47	1.38
38	A1	908	OMG	C5-C4	3.12	1.47	1.38
34	B5	1428	OMG	C5-C4	3.12	1.47	1.38
38	A1	645	1MA	C5-C4	3.11	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	645	1MA	C6-N6	3.10	1.35	1.28
38	A1	2870	5MC	C6-C5	3.09	1.39	1.34
38	A1	2619	OMG	C5-C4	3.08	1.47	1.38
34	B5	1572	OMG	C5-C4	3.06	1.47	1.38
38	A1	1450	OMG	C5-C4	3.05	1.47	1.38
34	B5	1781	MA6	C5-C6	3.05	1.49	1.41
38	A1	2922	OMG	C5-C4	3.05	1.47	1.38
34	B5	1782	MA6	C5-C6	3.04	1.49	1.41
38	A1	2142	1MA	C6-N6	3.03	1.35	1.28
34	B5	1271	OMG	C5-C4	3.03	1.47	1.38
38	A1	805	OMG	C5-C4	3.02	1.47	1.38
38	A1	2791	OMG	C5-C4	3.01	1.47	1.38
34	B5	562	OMG	C5-C4	2.99	1.47	1.38
38	A1	2793	OMG	C5-C4	2.99	1.46	1.38
38	A1	2815	OMG	C5-C4	2.97	1.46	1.38
34	B5	1126	OMG	C5-C4	2.95	1.46	1.38
38	A1	2142	1MA	C5-C4	2.95	1.46	1.38
38	A1	2278	5MC	C6-C5	2.93	1.39	1.34
36	AB	243	HIC	CD2-CG	2.88	1.41	1.36
38	A1	898	OMU	C4-N3	-2.88	1.33	1.38
38	A1	2729	OMU	C4-N3	-2.88	1.33	1.38
38	A1	2347	OMU	C4-N3	-2.85	1.33	1.38
34	B5	1269	OMU	C4-N3	-2.84	1.33	1.38
38	A1	867	OMG	C5-C4	2.84	1.46	1.38
38	A1	1449	A2M	C5-C6	2.80	1.48	1.41
38	A1	2417	OMU	C4-N3	-2.77	1.33	1.38
34	B5	436	A2M	C5-C6	2.75	1.48	1.41
34	B5	28	A2M	C5-C6	2.75	1.48	1.41
38	A1	2724	OMU	C4-N3	-2.75	1.33	1.38
38	A1	1888	OMU	C4-N3	-2.74	1.33	1.38
38	A1	2793	OMG	C6-N1	-2.74	1.33	1.38
38	A1	807	A2M	C5-C6	2.73	1.48	1.41
38	A1	649	A2M	C5-C6	2.73	1.48	1.41
38	A1	817	A2M	C5-C6	2.72	1.48	1.41
34	B5	796	A2M	C5-C6	2.72	1.48	1.41
38	A1	2280	A2M	C5-C6	2.71	1.48	1.41
38	A1	2640	A2M	C5-C6	2.70	1.48	1.41
38	A1	2921	OMU	C4-N3	-2.68	1.34	1.38
38	A1	876	A2M	C5-C6	2.68	1.48	1.41
38	A1	1133	A2M	C5-C6	2.67	1.48	1.41
34	B5	420	A2M	C5-C6	2.65	1.48	1.41
34	B5	100	A2M	C5-C6	2.65	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2922	OMG	C6-N1	-2.64	1.33	1.38
38	A1	1450	OMG	C6-N1	-2.62	1.33	1.38
34	B5	1575	7MG	C6-N1	-2.61	1.34	1.38
34	B5	578	OMU	C4-N3	-2.61	1.34	1.38
34	B5	541	A2M	C5-C6	2.61	1.48	1.41
34	B5	562	OMG	C6-N1	-2.60	1.34	1.38
38	A1	2619	OMG	C6-N1	-2.60	1.34	1.38
38	A1	2815	OMG	C6-N1	-2.59	1.34	1.38
38	A1	2220	A2M	C5-N7	-2.58	1.34	1.39
38	A1	908	OMG	C6-N1	-2.57	1.34	1.38
34	B5	1428	OMG	C6-N1	-2.56	1.34	1.38
34	B5	974	A2M	C5-C6	2.56	1.48	1.41
34	B5	619	A2M	C5-C6	2.55	1.48	1.41
38	A1	2421	OMU	C4-N3	-2.55	1.34	1.38
34	B5	1572	OMG	C6-N1	-2.55	1.34	1.38
34	B5	1271	OMG	C6-N1	-2.55	1.34	1.38
38	A1	2640	A2M	C5-N7	-2.54	1.34	1.39
38	A1	2791	OMG	C6-N1	-2.54	1.34	1.38
38	A1	2220	A2M	C5-C6	2.54	1.48	1.41
38	A1	805	OMG	C6-N1	-2.53	1.34	1.38
34	B5	1126	OMG	C6-N1	-2.53	1.34	1.38
38	A1	876	A2M	C5-N7	-2.51	1.34	1.39
34	B5	1280	4AC	C4-N4	-2.51	1.36	1.39
34	B5	541	A2M	C5-N7	-2.51	1.34	1.39
38	A1	2288	OMG	C6-N1	-2.50	1.34	1.38
38	A1	2946	A2M	C5-C6	2.50	1.47	1.41
38	A1	2281	A2M	C5-C6	2.48	1.47	1.41
38	A1	2946	A2M	C5-N7	-2.47	1.34	1.39
38	A1	2921	OMU	C2-N3	-2.45	1.33	1.38
38	A1	807	A2M	C5-N7	-2.44	1.34	1.39
34	B5	420	A2M	C5-N7	-2.44	1.34	1.39
34	B5	100	A2M	C5-N7	-2.43	1.34	1.39
38	A1	1888	OMU	C2-N3	-2.42	1.33	1.38
38	A1	867	OMG	C6-N1	-2.41	1.34	1.38
38	A1	1133	A2M	C5-N7	-2.41	1.34	1.39
38	A1	1449	A2M	C5-N7	-2.40	1.34	1.39
34	B5	436	A2M	C5-N7	-2.39	1.34	1.39
34	B5	619	A2M	C4-N9	-2.35	1.32	1.37
38	A1	2417	OMU	C2-N3	-2.34	1.33	1.38
38	A1	2142	1MA	C5-N7	-2.33	1.34	1.39
34	B5	619	A2M	C5-N7	-2.33	1.34	1.39
38	A1	2280	A2M	C5-N7	-2.33	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	796	A2M	C5-N7	-2.32	1.34	1.39
34	B5	1782	MA6	C8-N7	2.32	1.36	1.31
38	A1	898	OMU	C2-N3	-2.32	1.33	1.38
38	A1	649	A2M	C5-N7	-2.32	1.34	1.39
34	B5	974	A2M	C5-N7	-2.30	1.34	1.39
34	B5	974	A2M	C4-N9	-2.29	1.32	1.37
34	B5	28	A2M	C5-N7	-2.29	1.34	1.39
38	A1	817	A2M	C8-N7	2.28	1.36	1.31
34	B5	1428	OMG	C5-N7	-2.28	1.34	1.39
38	A1	2729	OMU	C2-N3	-2.28	1.34	1.38
34	B5	28	A2M	C8-N7	2.27	1.36	1.31
34	B5	1269	OMU	C2-N3	-2.26	1.34	1.38
34	B5	1782	MA6	C5-N7	-2.25	1.35	1.39
34	B5	1773	4AC	C4-N4	-2.25	1.36	1.39
34	B5	578	OMU	C2-N3	-2.24	1.34	1.38
34	B5	1269	OMU	C2-N1	2.24	1.42	1.38
34	B5	1575	7MG	C8-N9	2.23	1.47	1.45
34	B5	420	A2M	C8-N7	2.23	1.36	1.31
34	B5	1781	MA6	C8-N7	2.23	1.36	1.31
34	B5	974	A2M	C8-N7	2.22	1.36	1.31
38	A1	2220	A2M	C4-N9	-2.22	1.33	1.37
38	A1	2281	A2M	C5-N7	-2.22	1.35	1.39
34	B5	1781	MA6	C5-N7	-2.21	1.35	1.39
38	A1	2280	A2M	C8-N7	2.21	1.35	1.31
38	A1	2281	A2M	C8-N7	2.21	1.35	1.31
38	A1	908	OMG	C5-N7	-2.21	1.34	1.39
38	A1	2870	5MC	C6-N1	-2.21	1.34	1.38
38	A1	807	A2M	C8-N7	2.20	1.35	1.31
34	B5	796	A2M	C8-N7	2.20	1.35	1.31
34	B5	1782	MA6	C4-N9	-2.19	1.33	1.37
34	B5	619	A2M	C8-N7	2.19	1.35	1.31
38	A1	1450	OMG	C5-N7	-2.18	1.34	1.39
38	A1	2421	OMU	C2-N1	2.18	1.41	1.38
38	A1	2417	OMU	C5-C4	-2.17	1.39	1.43
38	A1	2724	OMU	C2-N3	-2.16	1.34	1.38
38	A1	2640	A2M	C8-N7	2.16	1.35	1.31
38	A1	649	A2M	C8-N7	2.15	1.35	1.31
38	A1	2619	OMG	C5-N7	-2.14	1.34	1.39
38	A1	2347	OMU	C2-N3	-2.14	1.34	1.38
38	A1	2288	OMG	C5-N7	-2.14	1.34	1.39
38	A1	2724	OMU	C5-C4	-2.14	1.39	1.43
34	B5	436	A2M	C8-N7	2.13	1.35	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2220	A2M	C8-N7	2.13	1.35	1.31
38	A1	645	1MA	C5-N7	-2.13	1.34	1.39
38	A1	817	A2M	C5-N7	-2.13	1.35	1.39
34	B5	100	A2M	C8-N7	2.13	1.35	1.31
38	A1	2421	OMU	C5-C4	-2.13	1.39	1.43
38	A1	898	OMU	C5-C4	-2.12	1.39	1.43
38	A1	1133	A2M	C8-N7	2.12	1.35	1.31
38	A1	876	A2M	C8-N7	2.11	1.35	1.31
38	A1	2793	OMG	C5-N7	-2.11	1.34	1.39
38	A1	2815	OMG	C5-N7	-2.10	1.34	1.39
38	A1	2729	OMU	C2-N1	2.10	1.41	1.38
38	A1	2729	OMU	C5-C4	-2.10	1.39	1.43
34	B5	1269	OMU	C5-C4	-2.09	1.39	1.43
38	A1	805	OMG	C5-N7	-2.09	1.34	1.39
38	A1	2922	OMG	C5-N7	-2.09	1.34	1.39
38	A1	2278	5MC	C6-N1	-2.09	1.34	1.38
34	B5	1575	7MG	C5-N7	-2.09	1.33	1.35
34	B5	1781	MA6	C4-N9	-2.08	1.33	1.37
38	A1	2142	1MA	C2-N3	2.07	1.34	1.30
34	B5	1126	OMG	C5-N7	-2.07	1.34	1.39
34	B5	541	A2M	C8-N7	2.06	1.35	1.31
34	B5	1271	OMG	C5-N7	-2.06	1.34	1.39
38	A1	2347	OMU	C5-C4	-2.06	1.39	1.43
34	B5	578	OMU	C5-C4	-2.05	1.39	1.43
38	A1	2946	A2M	C4-N9	-2.05	1.33	1.37
38	A1	1449	A2M	C8-N7	2.04	1.35	1.31
34	B5	562	OMG	C5-N7	-2.04	1.35	1.39
38	A1	2921	OMU	C5-C4	-2.03	1.39	1.43
38	A1	2791	OMG	C5-N7	-2.03	1.35	1.39
38	A1	2946	A2M	C8-N7	2.03	1.35	1.31
38	A1	645	1MA	C2-N3	2.03	1.34	1.30
38	A1	2421	OMU	C2-N3	-2.02	1.34	1.38
34	B5	1572	OMG	C5-N7	-2.02	1.35	1.39
38	A1	2142	1MA	C4-N9	-2.01	1.32	1.38
38	A1	867	OMG	C5-N7	-2.01	1.35	1.39

All (372) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1575	7MG	O4'-C1'-N9	-12.60	92.13	109.30
34	B5	1191	XSX	C3-C1-N3	9.28	128.38	112.16
34	B5	1575	7MG	N9-C4-N3	9.21	138.95	125.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1773	4AC	N4-C4-N3	7.88	126.65	113.87
38	A1	2634	UR3	C4-N3-C2	-7.02	118.93	124.58
38	A1	2288	OMG	C5-C4-N3	-6.44	118.15	128.39
34	B5	100	A2M	C5-C4-N3	-6.30	118.04	126.72
34	B5	1428	OMG	C5-C4-N3	-6.30	118.37	128.39
38	A1	2793	OMG	C5-C4-N3	-6.29	118.37	128.39
38	A1	1450	OMG	C5-C4-N3	-6.29	118.39	128.39
38	A1	908	OMG	C5-C4-N3	-6.25	118.44	128.39
34	B5	541	A2M	C5-C4-N3	-6.23	118.13	126.72
38	A1	2815	OMG	C5-C4-N3	-6.22	118.49	128.39
34	B5	420	A2M	C5-C4-N3	-6.10	118.32	126.72
38	A1	2922	OMG	C5-C4-N3	-6.09	118.69	128.39
34	B5	796	A2M	C5-C4-N3	-6.08	118.35	126.72
38	A1	1449	A2M	C5-C4-N3	-6.06	118.37	126.72
34	B5	1572	OMG	C5-C4-N3	-6.05	118.77	128.39
38	A1	649	A2M	C5-C4-N3	-6.04	118.40	126.72
34	B5	1271	OMG	C5-C4-N3	-6.03	118.79	128.39
34	B5	562	OMG	C5-C4-N3	-6.03	118.80	128.39
38	A1	2640	A2M	C5-C4-N3	-6.02	118.42	126.72
34	B5	1575	7MG	C5-C4-N3	-6.02	116.83	128.13
38	A1	805	OMG	C5-C4-N3	-6.00	118.85	128.39
38	A1	2619	OMG	C5-C4-N3	-5.99	118.85	128.39
38	A1	2791	OMG	C5-C4-N3	-5.99	118.85	128.39
38	A1	876	A2M	C5-C4-N3	-5.94	118.54	126.72
34	B5	436	A2M	C5-C4-N3	-5.89	118.61	126.72
38	A1	867	OMG	C5-C4-N3	-5.89	119.02	128.39
34	B5	1126	OMG	C5-C4-N3	-5.88	119.03	128.39
34	B5	28	A2M	C5-C4-N3	-5.87	118.64	126.72
38	A1	807	A2M	C5-C4-N3	-5.87	118.64	126.72
38	A1	2280	A2M	C5-C4-N3	-5.87	118.64	126.72
38	A1	1133	A2M	C5-C4-N3	-5.76	118.78	126.72
38	A1	817	A2M	C5-C4-N3	-5.67	118.92	126.72
38	A1	2946	A2M	C5-C4-N3	-5.64	118.96	126.72
34	B5	619	A2M	C5-C4-N3	-5.51	119.14	126.72
34	B5	1191	XSX	C4-N3-C2	-5.48	118.22	124.66
38	A1	2281	A2M	C5-C4-N3	-5.45	119.22	126.72
38	A1	2220	A2M	C5-C4-N3	-5.36	119.34	126.72
34	B5	1781	MA6	C5-C4-N3	-5.31	119.40	126.72
38	A1	867	OMG	C2-N3-C4	5.28	121.39	112.30
34	B5	974	A2M	C5-C4-N3	-5.27	119.47	126.72
34	B5	1782	MA6	C5-C4-N3	-5.26	119.47	126.72
38	A1	2815	OMG	C2-N3-C4	5.22	121.29	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2288	OMG	C2-N3-C4	5.18	121.22	112.30
34	B5	1126	OMG	C2-N3-C4	5.16	121.18	112.30
38	A1	1450	OMG	C2-N3-C4	5.11	121.10	112.30
34	B5	1271	OMG	C2-N3-C4	5.09	121.06	112.30
38	A1	805	OMG	C2-N3-C4	5.09	121.06	112.30
34	B5	562	OMG	C2-N3-C4	5.08	121.06	112.30
38	A1	2793	OMG	C2-N3-C4	5.07	121.03	112.30
34	B5	1572	OMG	C2-N3-C4	5.07	121.03	112.30
38	A1	645	1MA	C5-C4-N3	-5.05	119.84	127.27
38	A1	2729	OMU	C4-N3-C2	-5.00	120.40	126.61
38	A1	2142	1MA	C5-C4-N3	-5.00	119.91	127.27
34	B5	541	A2M	N3-C4-N9	5.00	135.67	127.17
34	B5	1428	OMG	C2-N3-C4	5.00	120.90	112.30
34	B5	578	OMU	C4-N3-C2	-4.96	120.46	126.61
38	A1	2791	OMG	C2-N3-C4	4.95	120.83	112.30
38	A1	2619	OMG	C2-N3-C4	4.95	120.82	112.30
38	A1	2922	OMG	C2-N3-C4	4.94	120.80	112.30
38	A1	908	OMG	C2-N3-C4	4.91	120.76	112.30
38	A1	1888	OMU	C4-N3-C2	-4.90	120.53	126.61
34	B5	100	A2M	N3-C4-N9	4.89	135.49	127.17
38	A1	649	A2M	N3-C4-N9	4.88	135.46	127.17
38	A1	2921	OMU	C4-N3-C2	-4.85	120.59	126.61
38	A1	2724	OMU	C4-N3-C2	-4.85	120.59	126.61
38	A1	2288	OMG	N9-C4-N3	4.84	135.63	125.95
38	A1	2281	A2M	O4'-C1'-N9	4.84	117.38	108.09
38	A1	2417	OMU	C4-N3-C2	-4.83	120.62	126.61
34	B5	420	A2M	N3-C4-N9	4.83	135.38	127.17
38	A1	898	OMU	C4-N3-C2	-4.82	120.62	126.61
38	A1	908	OMG	N9-C4-N3	4.81	135.56	125.95
38	A1	1449	A2M	N3-C4-N9	4.79	135.31	127.17
34	B5	1773	4AC	C5-C4-N4	-4.77	114.91	122.94
38	A1	2421	OMU	C4-N3-C2	-4.73	120.74	126.61
34	B5	1269	OMU	C4-N3-C2	-4.72	120.76	126.61
34	B5	1428	OMG	N9-C4-N3	4.68	135.31	125.95
38	A1	1450	OMG	N9-C4-N3	4.68	135.31	125.95
34	B5	796	A2M	N3-C4-N9	4.66	135.09	127.17
38	A1	2281	A2M	N3-C4-N9	4.64	135.06	127.17
38	A1	2793	OMG	N9-C4-N3	4.64	135.22	125.95
34	B5	1575	7MG	C2-N3-C4	4.60	120.23	112.30
38	A1	2946	A2M	N3-C4-N9	4.59	134.97	127.17
38	A1	876	A2M	N3-C4-N9	4.58	134.96	127.17
38	A1	2921	OMU	N3-C2-N1	4.58	120.85	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	436	A2M	N3-C4-N9	4.58	134.95	127.17
38	A1	2347	OMU	C4-N3-C2	-4.58	120.93	126.61
38	A1	898	OMU	N3-C2-N1	4.56	120.82	114.89
38	A1	2946	A2M	C2'-C1'-N9	-4.55	106.27	113.75
38	A1	1133	A2M	N3-C4-N9	4.54	134.89	127.17
38	A1	2729	OMU	N3-C2-N1	4.54	120.80	114.89
38	A1	807	A2M	N3-C4-N9	4.53	134.87	127.17
38	A1	2640	A2M	N3-C4-N9	4.52	134.86	127.17
38	A1	2280	A2M	N3-C4-N9	4.52	134.86	127.17
34	B5	1572	OMG	N9-C4-N3	4.48	134.92	125.95
38	A1	2417	OMU	N3-C2-N1	4.48	120.73	114.89
38	A1	805	OMG	N9-C4-N3	4.45	134.86	125.95
38	A1	2142	1MA	C2-N3-C4	4.44	121.23	112.53
38	A1	817	A2M	N3-C4-N9	4.44	134.71	127.17
38	A1	2922	OMG	N9-C4-N3	4.43	134.81	125.95
38	A1	2791	OMG	N9-C4-N3	4.43	134.80	125.95
38	A1	645	1MA	C2-N3-C4	4.42	121.20	112.53
38	A1	1888	OMU	N3-C2-N1	4.41	120.64	114.89
38	A1	2619	OMG	N9-C4-N3	4.41	134.78	125.95
38	A1	2724	OMU	N3-C2-N1	4.41	120.63	114.89
34	B5	28	A2M	N3-C4-N9	4.39	134.63	127.17
34	B5	1781	MA6	C2-N1-C6	4.37	122.51	111.83
34	B5	1271	OMG	N9-C4-N3	4.33	134.60	125.95
38	A1	2347	OMU	N3-C2-N1	4.27	120.45	114.89
34	B5	619	A2M	N3-C4-N9	4.27	134.43	127.17
34	B5	1782	MA6	C4-C5-N7	-4.26	105.71	110.58
34	B5	1782	MA6	C2-N1-C6	4.24	122.19	111.83
38	A1	2815	OMG	N9-C4-N3	4.24	134.44	125.95
38	A1	2421	OMU	N3-C2-N1	4.24	120.41	114.89
34	B5	562	OMG	N9-C4-N3	4.22	134.39	125.95
34	B5	578	OMU	N3-C2-N1	4.22	120.38	114.89
38	A1	867	OMG	N9-C4-N3	4.21	134.37	125.95
34	B5	1269	OMU	N3-C2-N1	4.20	120.36	114.89
34	B5	1781	MA6	C4-C5-N7	-4.18	105.80	110.58
34	B5	1126	OMG	N9-C4-N3	4.18	134.32	125.95
38	A1	2220	A2M	N3-C4-N9	4.13	134.20	127.17
34	B5	1575	7MG	N9-C8-N7	-4.13	97.52	103.37
34	B5	974	A2M	N3-C4-N9	4.02	134.01	127.17
38	A1	2870	5MC	C5-C6-N1	-3.99	118.98	123.31
34	B5	578	OMU	C5-C4-N3	3.92	120.29	114.80
38	A1	1888	OMU	C5-C4-N3	3.90	120.27	114.80
34	B5	1781	MA6	N3-C4-N9	3.90	133.81	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	817	A2M	C2-N3-C4	3.85	121.22	111.83
38	A1	2729	OMU	C5-C4-N3	3.83	120.16	114.80
34	B5	619	A2M	C2-N3-C4	3.82	121.16	111.83
38	A1	2280	A2M	C2-N3-C4	3.81	121.14	111.83
34	B5	1269	OMU	C5-C4-N3	3.81	120.13	114.80
34	B5	541	A2M	C2-N3-C4	3.80	121.11	111.83
34	B5	100	A2M	C2-N3-C4	3.79	121.10	111.83
38	A1	2421	OMU	C5-C4-N3	3.79	120.11	114.80
34	B5	28	A2M	C2-N3-C4	3.79	121.08	111.83
38	A1	2417	OMU	C5-C4-N3	3.78	120.10	114.80
38	A1	649	A2M	C2-N3-C4	3.78	121.05	111.83
34	B5	28	A2M	C4-C5-N7	-3.78	106.27	110.58
34	B5	1782	MA6	N3-C4-N9	3.75	133.54	127.17
38	A1	807	A2M	C2-N3-C4	3.74	120.96	111.83
38	A1	2724	OMU	C5-C4-N3	3.74	120.04	114.80
34	B5	796	A2M	C4-C5-N7	-3.73	106.31	110.58
38	A1	1449	A2M	C2-N3-C4	3.72	120.91	111.83
38	A1	2921	OMU	C5-C4-N3	3.72	120.01	114.80
38	A1	898	OMU	C5-C4-N3	3.71	120.00	114.80
38	A1	2640	A2M	C2-N3-C4	3.71	120.89	111.83
34	B5	796	A2M	C2-N3-C4	3.69	120.86	111.83
38	A1	2815	OMG	C6-C5-N7	3.69	137.01	130.29
38	A1	2280	A2M	C4-C5-N7	-3.68	106.37	110.58
34	B5	1773	4AC	CM7-C7-N4	3.68	121.21	115.27
34	B5	420	A2M	C2-N3-C4	3.67	120.81	111.83
34	B5	436	A2M	C4-C5-N7	-3.67	106.38	110.58
34	B5	562	OMG	C6-C5-N7	3.67	136.97	130.29
34	B5	436	A2M	C2-N3-C4	3.66	120.78	111.83
34	B5	1126	OMG	C6-C5-N7	3.66	136.95	130.29
38	A1	867	OMG	C6-C5-N7	3.65	136.92	130.29
38	A1	2347	OMU	C5-C4-N3	3.62	119.88	114.80
38	A1	1133	A2M	C2-N3-C4	3.62	120.68	111.83
38	A1	2640	A2M	C4-C5-N7	-3.59	106.48	110.58
34	B5	1781	MA6	C2-N3-C4	3.58	120.58	111.83
38	A1	876	A2M	C4-C5-N7	-3.57	106.50	110.58
38	A1	817	A2M	C4-C5-N7	-3.57	106.50	110.58
34	B5	974	A2M	C2-N3-C4	3.57	120.55	111.83
38	A1	2281	A2M	C2-N3-C4	3.57	120.54	111.83
34	B5	1782	MA6	C2-N3-C4	3.56	120.53	111.83
38	A1	1449	A2M	C4-C5-N7	-3.56	106.51	110.58
38	A1	1133	A2M	C4-C5-N7	-3.56	106.52	110.58
38	A1	2946	A2M	C2-N3-C4	3.54	120.47	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	100	A2M	C4-C5-N7	-3.53	106.55	110.58
38	A1	817	A2M	N3-C2-N1	-3.49	123.30	128.58
34	B5	619	A2M	N3-C2-N1	-3.48	123.31	128.58
34	B5	974	A2M	C4-C5-N7	-3.48	106.61	110.58
38	A1	807	A2M	C4-C5-N7	-3.47	106.62	110.58
38	A1	876	A2M	C2-N3-C4	3.46	120.28	111.83
34	B5	1271	OMG	C6-C5-N7	3.45	136.57	130.29
38	A1	805	OMG	C6-C5-N7	3.42	136.51	130.29
34	B5	974	A2M	N3-C2-N1	-3.41	123.42	128.58
38	A1	2220	A2M	C2-N3-C4	3.40	120.13	111.83
34	B5	420	A2M	C4-C5-N7	-3.35	106.75	110.58
38	A1	2791	OMG	C6-C5-N7	3.34	136.38	130.29
34	B5	541	A2M	C4-C5-N7	-3.33	106.77	110.58
38	A1	2281	A2M	C2'-C1'-N9	-3.33	108.27	113.75
38	A1	2793	OMG	C6-C5-N7	3.32	136.34	130.29
34	B5	619	A2M	C4-C5-N7	-3.32	106.78	110.58
38	A1	2281	A2M	N3-C2-N1	-3.31	123.58	128.58
38	A1	649	A2M	C4-C5-N7	-3.30	106.81	110.58
38	A1	2220	A2M	C4-C5-N7	-3.30	106.81	110.58
34	B5	1773	4AC	C6-C5-C4	3.29	120.97	117.00
34	B5	1781	MA6	N1-C2-N3	-3.29	123.61	128.58
38	A1	2280	A2M	N3-C2-N1	-3.27	123.64	128.58
38	A1	2278	5MC	C5-C6-N1	-3.27	119.77	123.31
34	B5	1572	OMG	C6-C5-N7	3.27	136.23	130.29
38	A1	2922	OMG	C6-C5-N7	3.26	136.23	130.29
38	A1	2142	1MA	N9-C4-N3	3.25	134.31	126.90
38	A1	2634	UR3	C5-C4-N3	3.24	119.30	115.04
38	A1	2220	A2M	N3-C2-N1	-3.24	123.68	128.58
34	B5	28	A2M	N3-C2-N1	-3.23	123.70	128.58
38	A1	2619	OMG	C6-C5-N7	3.21	136.13	130.29
38	A1	2421	OMU	O4-C4-C5	-3.21	119.63	125.16
38	A1	1450	OMG	C6-C5-N7	3.21	136.12	130.29
38	A1	2281	A2M	C4-N9-C8	3.20	109.10	105.74
38	A1	649	A2M	N3-C2-N1	-3.20	123.74	128.58
34	B5	1782	MA6	N1-C2-N3	-3.19	123.75	128.58
38	A1	2288	OMG	C6-C5-N7	3.18	136.08	130.29
38	A1	2946	A2M	C4-C5-N7	-3.17	106.96	110.58
34	B5	541	A2M	N3-C2-N1	-3.15	123.81	128.58
34	B5	436	A2M	N3-C2-N1	-3.14	123.83	128.58
34	B5	1280	4AC	C6-C5-C4	3.14	120.78	117.00
38	A1	2870	5MC	C5-C4-N3	-3.11	118.57	121.75
38	A1	1449	A2M	N3-C2-N1	-3.11	123.88	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2946	A2M	N3-C2-N1	-3.10	123.89	128.58
38	A1	1133	A2M	N3-C2-N1	-3.09	123.90	128.58
34	B5	578	OMU	O4-C4-C5	-3.09	119.83	125.16
38	A1	2417	OMU	O4-C4-C5	-3.07	119.87	125.16
38	A1	807	A2M	N3-C2-N1	-3.07	123.94	128.58
38	A1	645	1MA	N9-C4-N3	3.07	133.89	126.90
38	A1	2724	OMU	O4-C4-C5	-3.05	119.91	125.16
38	A1	2281	A2M	C4-C5-N7	-3.04	107.11	110.58
34	B5	1191	XSX	C5-C4-N3	3.01	119.80	115.64
34	B5	420	A2M	N3-C2-N1	-3.00	124.04	128.58
38	A1	2729	OMU	O4-C4-C5	-3.00	119.99	125.16
38	A1	908	OMG	C6-C5-N7	2.99	135.73	130.29
36	AB	243	HIC	NE2-CE1-ND1	-2.96	111.53	112.66
38	A1	2640	A2M	N3-C2-N1	-2.95	124.12	128.58
34	B5	1428	OMG	C6-C5-N7	2.94	135.64	130.29
38	A1	1888	OMU	O4-C4-C5	-2.94	120.09	125.16
38	A1	898	OMU	O4-C4-C5	-2.91	120.14	125.16
38	A1	2815	OMG	C4-C5-N7	-2.90	106.08	110.67
34	B5	1782	MA6	C5-N7-C8	2.89	108.00	103.45
34	B5	100	A2M	N3-C2-N1	-2.89	124.21	128.58
38	A1	2278	5MC	C5-C4-N3	-2.88	118.80	121.75
34	B5	1269	OMU	O4-C4-C5	-2.86	120.22	125.16
34	B5	1781	MA6	C5-N7-C8	2.86	107.95	103.45
38	A1	817	A2M	C4-N9-C8	2.86	108.74	105.74
34	B5	100	A2M	C2'-C1'-N9	-2.86	109.05	113.75
38	A1	2347	OMU	O4-C4-C5	-2.85	120.25	125.16
34	B5	796	A2M	N3-C2-N1	-2.84	124.29	128.58
38	A1	2921	OMU	O4-C4-C5	-2.83	120.28	125.16
34	B5	562	OMG	C4-C5-N7	-2.83	106.19	110.67
34	B5	974	A2M	C2'-C1'-N9	-2.82	109.10	113.75
38	A1	1437	OMC	O2-C2-N3	-2.81	117.90	122.33
38	A1	650	OMC	O2-C2-N3	-2.79	117.94	122.33
38	A1	876	A2M	N3-C2-N1	-2.77	124.39	128.58
34	B5	1269	OMU	C1'-N1-C2	2.76	122.55	117.59
34	B5	619	A2M	C4-N9-C8	2.74	108.61	105.74
34	B5	1575	7MG	C5-C6-N1	2.73	115.75	110.94
38	A1	2280	A2M	C5-N7-C8	2.73	107.74	103.45
38	A1	2280	A2M	C4-N9-C8	2.70	108.57	105.74
38	A1	1133	A2M	C2'-C1'-N9	-2.69	109.32	113.75
34	B5	1781	MA6	C4-N9-C8	2.68	108.55	105.74
38	A1	2791	OMG	C4-C5-N7	-2.67	106.44	110.67
34	B5	28	A2M	C5-N7-C8	2.67	107.65	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	796	A2M	C5-N7-C8	2.66	107.63	103.45
38	A1	2793	OMG	C4-C5-N7	-2.66	106.46	110.67
34	B5	1773	4AC	C5-C4-N3	-2.66	118.44	122.60
34	B5	1782	MA6	C4-N9-C8	2.66	108.53	105.74
34	B5	436	A2M	C5-N7-C8	2.65	107.62	103.45
34	B5	974	A2M	C4-N9-C8	2.65	108.52	105.74
34	B5	1126	OMG	C4-C5-N7	-2.63	106.50	110.67
34	B5	1782	MA6	C6-C5-N7	2.63	137.63	133.43
34	B5	1271	OMG	C4-C5-N7	-2.62	106.52	110.67
38	A1	1449	A2M	C5-N7-C8	2.62	107.56	103.45
38	A1	867	OMG	C4-C5-N7	-2.61	106.53	110.67
38	A1	817	A2M	C5-N7-C8	2.60	107.54	103.45
38	A1	2288	OMG	C4-C5-N7	-2.58	106.59	110.67
38	A1	2922	OMG	C4-C5-N7	-2.58	106.59	110.67
38	A1	876	A2M	C5-N7-C8	2.55	107.46	103.45
34	B5	796	A2M	C4-N9-C8	2.55	108.41	105.74
38	A1	649	A2M	C4-N9-C8	2.55	108.41	105.74
34	B5	100	A2M	C5-N7-C8	2.55	107.45	103.45
38	A1	2946	A2M	C4-N9-C8	2.54	108.41	105.74
38	A1	2724	OMU	C1'-N1-C2	2.54	122.16	117.59
38	A1	1450	OMG	C4-C5-N7	-2.54	106.65	110.67
38	A1	1133	A2M	C4-N9-C8	2.54	108.40	105.74
38	A1	805	OMG	C4-C5-N7	-2.53	106.66	110.67
38	A1	2724	OMU	O2-C2-N1	-2.53	119.50	122.80
38	A1	645	1MA	C4-C5-N7	-2.53	106.66	110.67
38	A1	1133	A2M	C5-N7-C8	2.53	107.42	103.45
34	B5	420	A2M	C2'-C1'-N9	-2.52	109.60	113.75
38	A1	817	A2M	C6-C5-N7	2.50	136.91	132.09
34	B5	1781	MA6	C6-C5-N7	2.48	137.40	133.43
38	A1	2619	OMG	C4-C5-N7	-2.48	106.74	110.67
38	A1	2640	A2M	C5-N7-C8	2.47	107.33	103.45
38	A1	2948	OMC	O2-C2-N3	-2.47	118.44	122.33
38	A1	807	A2M	C5-N7-C8	2.46	107.32	103.45
34	B5	436	A2M	C4-N9-C8	2.46	108.33	105.74
34	B5	420	A2M	C4-N9-C8	2.45	108.31	105.74
38	A1	2921	OMU	O2-C2-N1	-2.45	119.61	122.80
38	A1	2959	OMC	O2-C2-N3	-2.44	118.48	122.33
34	B5	1572	OMG	C4-C5-N7	-2.44	106.80	110.67
38	A1	649	A2M	C5-N7-C8	2.44	107.29	103.45
38	A1	908	OMG	C4-C5-N7	-2.44	106.81	110.67
34	B5	420	A2M	C5-N7-C8	2.44	107.28	103.45
38	A1	2220	A2M	C2-N1-C6	2.43	122.73	118.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1428	OMG	C4-C5-N7	-2.43	106.82	110.67
34	B5	541	A2M	C5-N7-C8	2.42	107.25	103.45
34	B5	619	A2M	C6-C5-N7	2.41	136.74	132.09
34	B5	974	A2M	C6-C5-N7	2.39	136.70	132.09
34	B5	974	A2M	C5-N7-C8	2.38	107.20	103.45
38	A1	645	1MA	C6-C5-N7	2.37	136.35	132.16
38	A1	1888	OMU	O2-C2-N1	-2.37	119.71	122.80
34	B5	578	OMU	O2-C2-N1	-2.35	119.73	122.80
34	B5	28	A2M	C6-C5-N7	2.35	136.63	132.09
34	B5	796	A2M	C2'-C1'-N9	-2.34	109.89	113.75
38	A1	2278	5MC	O2-C2-N3	-2.34	118.64	122.33
38	A1	2281	A2M	C5-N7-C8	2.34	107.12	103.45
34	B5	619	A2M	C5-N7-C8	2.33	107.11	103.45
34	B5	28	A2M	C4-N9-C8	2.32	108.17	105.74
38	A1	2946	A2M	C5-N7-C8	2.30	107.06	103.45
38	A1	805	OMG	O6-C6-C5	-2.29	120.50	126.53
34	B5	100	A2M	C4-N9-C8	2.28	108.13	105.74
38	A1	867	OMG	O6-C6-C5	-2.26	120.57	126.53
38	A1	1449	A2M	C4-N9-C8	2.26	108.11	105.74
38	A1	1437	OMC	C1'-N1-C2	2.26	123.42	118.44
34	B5	1280	4AC	C5-C4-N3	-2.25	119.07	122.60
34	B5	974	A2M	C2-N1-C6	2.25	122.42	118.73
38	A1	1450	OMG	O6-C6-C5	-2.25	120.60	126.53
38	A1	807	A2M	C4-N9-C8	2.24	108.09	105.74
38	A1	2142	1MA	C4-C5-N7	-2.23	107.13	110.67
34	B5	1782	MA6	N9-C8-N7	-2.23	110.77	113.94
34	B5	541	A2M	C4-N9-C8	2.23	108.08	105.74
38	A1	2280	A2M	C6-C5-N7	2.22	136.37	132.09
38	A1	2417	OMU	O2-C2-N1	-2.21	119.91	122.80
38	A1	908	OMG	O6-C6-C5	-2.21	120.71	126.53
38	A1	2280	A2M	N9-C8-N7	-2.20	110.81	113.94
34	B5	1280	4AC	N4-C4-N3	2.20	117.44	113.87
38	A1	817	A2M	N9-C8-N7	-2.19	110.83	113.94
34	B5	1191	XSX	C1-N3-C2	2.18	120.86	117.64
38	A1	2288	OMG	O6-C6-C5	-2.18	120.77	126.53
38	A1	2421	OMU	O2-C2-N1	-2.18	119.96	122.80
38	A1	898	OMU	O2-C2-N1	-2.18	119.96	122.80
38	A1	807	A2M	C6-C5-N7	2.17	136.28	132.09
38	A1	2220	A2M	C4-N9-C8	2.16	108.00	105.74
38	A1	1133	A2M	C6-C5-N7	2.15	136.24	132.09
34	B5	436	A2M	C6-C5-N7	2.14	136.22	132.09
34	B5	1428	OMG	O6-C6-C5	-2.13	120.91	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1781	MA6	N9-C8-N7	-2.13	110.91	113.94
38	A1	2220	A2M	C5-N7-C8	2.12	106.79	103.45
38	A1	2791	OMG	O6-C6-C5	-2.12	120.93	126.53
38	A1	2281	A2M	N9-C8-N7	-2.11	110.94	113.94
34	B5	796	A2M	C6-C5-N7	2.11	136.15	132.09
38	A1	876	A2M	C4-N9-C8	2.10	107.95	105.74
38	A1	2281	A2M	C6-C5-N7	2.10	136.14	132.09
38	A1	2640	A2M	C6-C5-N7	2.10	136.14	132.09
34	B5	1572	OMG	O6-C6-C5	-2.09	121.01	126.53
34	B5	1280	4AC	O2-C2-N3	-2.08	119.05	122.33
38	A1	2142	1MA	C6-C5-N7	2.08	135.84	132.16
38	A1	2922	OMG	O6-C6-C5	-2.08	121.04	126.53
38	A1	2347	OMU	O2-C2-N1	-2.08	120.09	122.80
34	B5	1126	OMG	O6-C6-C5	-2.07	121.07	126.53
38	A1	2619	OMG	O6-C6-C5	-2.07	121.07	126.53
34	B5	1773	4AC	C1'-N1-C2	2.06	122.98	118.44
34	B5	28	A2M	C2'-C1'-N9	-2.06	110.37	113.75
38	A1	867	OMG	C5-C6-N1	2.05	118.48	113.25
38	A1	1888	OMU	C2'-C1'-N1	-2.04	110.36	114.24
36	AB	243	HIC	CB-CG-CD2	-2.04	125.03	129.96
34	B5	1271	OMG	O6-C6-C5	-2.04	121.15	126.53
34	B5	1575	7MG	O6-C6-C5	-2.04	122.62	127.62
34	B5	619	A2M	N9-C8-N7	-2.03	111.05	113.94
34	B5	796	A2M	N9-C8-N7	-2.03	111.05	113.94
38	A1	2815	OMG	C5-C6-N1	2.03	118.41	113.25
38	A1	2337	OMC	O2-C2-N3	-2.02	119.14	122.33
38	A1	2640	A2M	C4-N9-C8	2.02	107.86	105.74
38	A1	2793	OMG	O6-C6-C5	-2.02	121.20	126.53
38	A1	2220	A2M	C6-C5-N7	2.01	135.97	132.09
38	A1	2634	UR3	C3U-N3-C2	2.01	120.83	117.33
38	A1	817	A2M	O3'-C3'-C4'	-2.01	105.31	111.08
38	A1	2815	OMG	O6-C6-C5	-2.00	121.25	126.53
34	B5	562	OMG	O6-C6-C5	-2.00	121.25	126.53

There are no chirality outliers.

All (65) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	28	A2M	C1'-C2'-O2'-CM'
34	B5	100	A2M	C1'-C2'-O2'-CM'
34	B5	414	OMC	C1'-C2'-O2'-CM2
34	B5	796	A2M	C1'-C2'-O2'-CM'

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Mol	Chain	Res	Type	Atoms
34	B5	974	A2M	C1'-C2'-O2'-CM'
34	B5	1191	XSX	C3-C1-N3-C2
34	B5	1271	OMG	C1'-C2'-O2'-CM2
34	B5	1773	4AC	N3-C4-N4-C7
38	A1	867	OMG	C1'-C2'-O2'-CM2
38	A1	1437	OMC	C1'-C2'-O2'-CM2
38	A1	2197	OMC	C2'-C1'-N1-C2
38	A1	2197	OMC	C2'-C1'-N1-C6
38	A1	2220	A2M	C1'-C2'-O2'-CM'
38	A1	2280	A2M	C1'-C2'-O2'-CM'
38	A1	2337	OMC	C1'-C2'-O2'-CM2
38	A1	2417	OMU	C1'-C2'-O2'-CM2
38	A1	2421	OMU	C1'-C2'-O2'-CM2
38	A1	2619	OMG	C1'-C2'-O2'-CM2
38	A1	2729	OMU	C1'-C2'-O2'-CM2
38	A1	2729	OMU	C3'-C4'-C5'-O5'
38	A1	2729	OMU	O4'-C4'-C5'-O5'
38	A1	2946	A2M	C1'-C2'-O2'-CM'
34	B5	1191	XSX	C3-C1-N3-C4
34	B5	541	A2M	O4'-C4'-C5'-O5'
34	B5	1782	MA6	O4'-C4'-C5'-O5'
34	B5	541	A2M	C3'-C4'-C5'-O5'
34	B5	619	A2M	O4'-C4'-C5'-O5'
34	B5	619	A2M	C3'-C4'-C5'-O5'
38	A1	2197	OMC	O4'-C4'-C5'-O5'
34	B5	1191	XSX	N4-C7-C9-O10
38	A1	2870	5MC	C2'-C1'-N1-C6
38	A1	1437	OMC	C3'-C4'-C5'-O5'
38	A1	1437	OMC	O4'-C4'-C5'-O5'
34	B5	541	A2M	C4'-C5'-O5'-P
34	B5	1782	MA6	C5-C6-N6-C9
38	A1	2347	OMU	C3'-C4'-C5'-O5'
34	B5	1191	XSX	N4-C7-C9-O11
34	B5	1773	4AC	O7-C7-N4-C4
34	B5	1773	4AC	CM7-C7-N4-C4
34	B5	1269	OMU	O4'-C4'-C5'-O5'
38	A1	817	A2M	C4'-C5'-O5'-P
34	B5	1269	OMU	O4'-C1'-N1-C6
38	A1	2870	5MC	O4'-C1'-N1-C6
38	A1	2870	5MC	O4'-C1'-N1-C2
38	A1	2870	5MC	C2'-C1'-N1-C2
34	B5	1269	OMU	O4'-C1'-N1-C2

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Mol	Chain	Res	Type	Atoms
34	B5	1428	OMG	C4'-C5'-O5'-P
38	A1	649	A2M	C4'-C5'-O5'-P
34	B5	1782	MA6	C3'-C4'-C5'-O5'
38	A1	2197	OMC	C3'-C4'-C5'-O5'
38	A1	2197	OMC	O4'-C1'-N1-C6
34	B5	1126	OMG	C4'-C5'-O5'-P
38	A1	2197	OMC	O4'-C1'-N1-C2
34	B5	1007	OMC	C1'-C2'-O2'-CM2
38	A1	2793	OMG	C3'-C2'-O2'-CM2
34	B5	619	A2M	C2'-C1'-N9-C8
38	A1	645	1MA	C2'-C1'-N9-C8
34	B5	541	A2M	O4'-C1'-N9-C8
34	B5	1191	XSX	C3-C7-C9-O11
38	A1	2281	A2M	O4'-C4'-C5'-O5'
38	A1	2347	OMU	O4'-C4'-C5'-O5'
34	B5	1773	4AC	C5-C4-N4-C7
38	A1	805	OMG	C3'-C2'-O2'-CM2
38	A1	2281	A2M	C2'-C1'-N9-C8
38	A1	817	A2M	O4'-C4'-C5'-O5'

There are no ring outliers.

29 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2948	OMC	1	0
38	A1	663	OMC	2	0
38	A1	2946	A2M	1	0
38	A1	1450	OMG	1	0
34	B5	1575	7MG	4	0
38	A1	1133	A2M	1	0
38	A1	649	A2M	2	0
38	A1	2220	A2M	3	0
38	A1	2417	OMU	2	0
38	A1	898	OMU	1	0
34	B5	414	OMC	1	0
38	A1	1449	A2M	1	0
34	B5	1781	MA6	1	0
38	A1	2197	OMC	1	0
34	B5	28	A2M	1	0
34	B5	436	A2M	1	0
34	B5	1280	4AC	2	0
34	B5	1126	OMG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2959	OMC	2	0
34	B5	974	A2M	1	0
38	A1	2281	A2M	1	0
38	A1	2724	OMU	3	0
38	A1	2347	OMU	1	0
38	A1	817	A2M	1	0
34	B5	1269	OMU	1	0
34	B5	100	A2M	1	0
34	B5	541	A2M	2	0
38	A1	650	OMC	2	0
34	B5	1773	4AC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 273 ligands modelled in this entry, 273 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	A1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	2439:A	O3'	2440:G	P	6.91

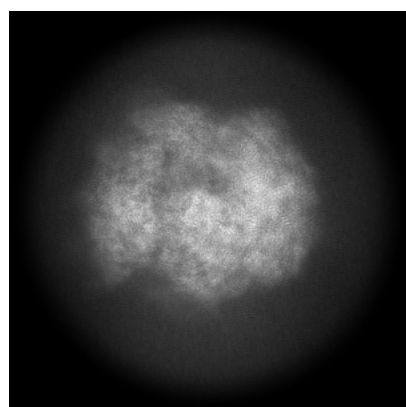
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28636. These allow visual inspection of the internal detail of the map and identification of artifacts.

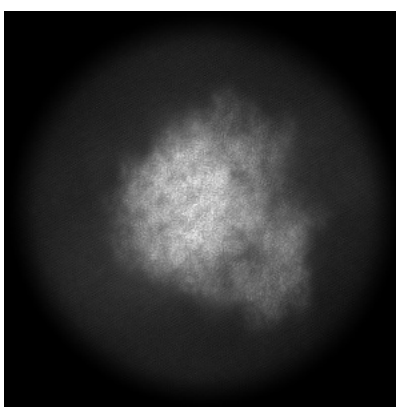
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

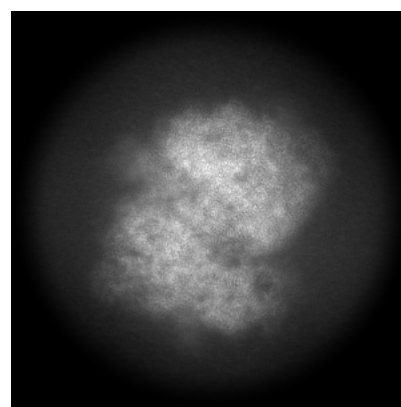
6.1.1 Primary map



X



Y

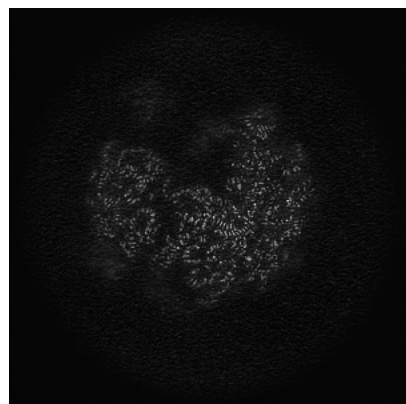


Z

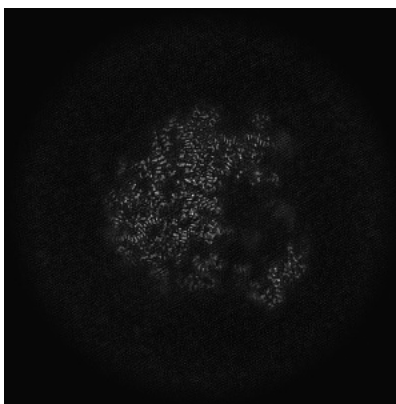
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

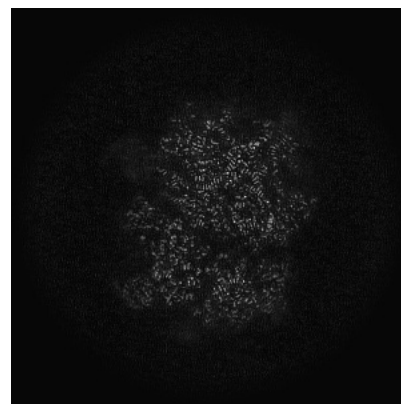
6.2.1 Primary map



X Index: 200



Y Index: 200

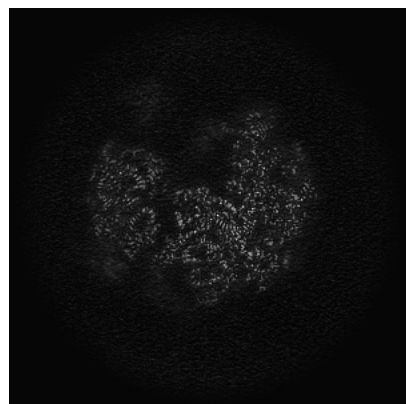


Z Index: 200

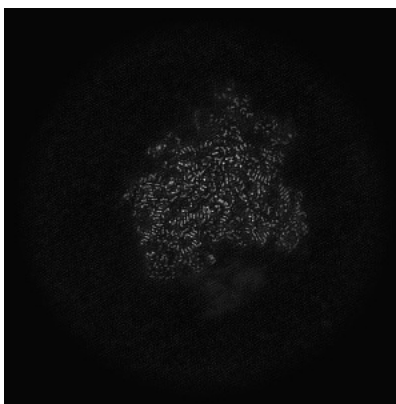
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

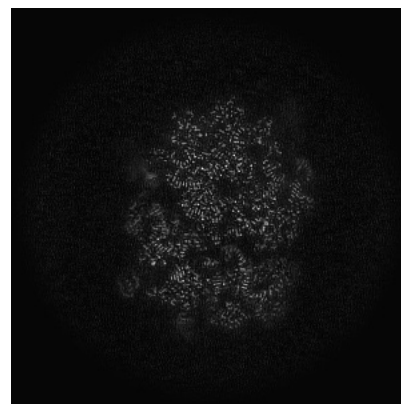
6.3.1 Primary map



X Index: 201



Y Index: 246

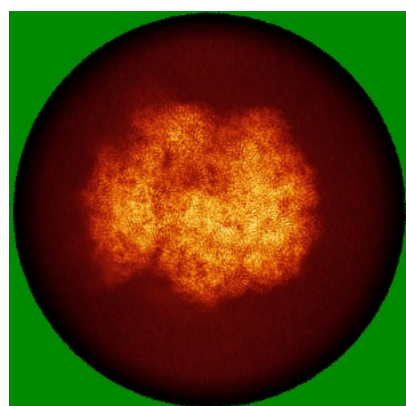


Z Index: 191

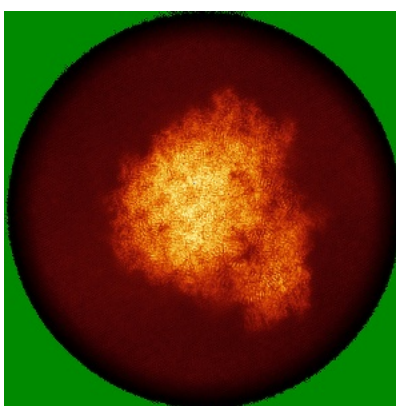
The images above show the largest variance slices of the map in three orthogonal directions.

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

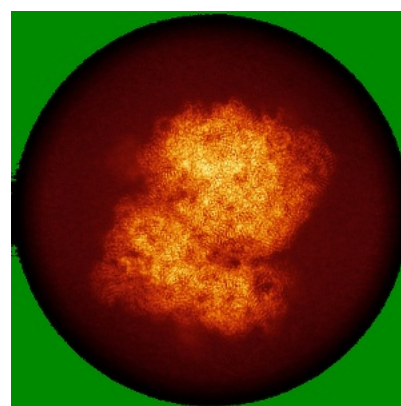
6.4.1 Primary map



X



Y

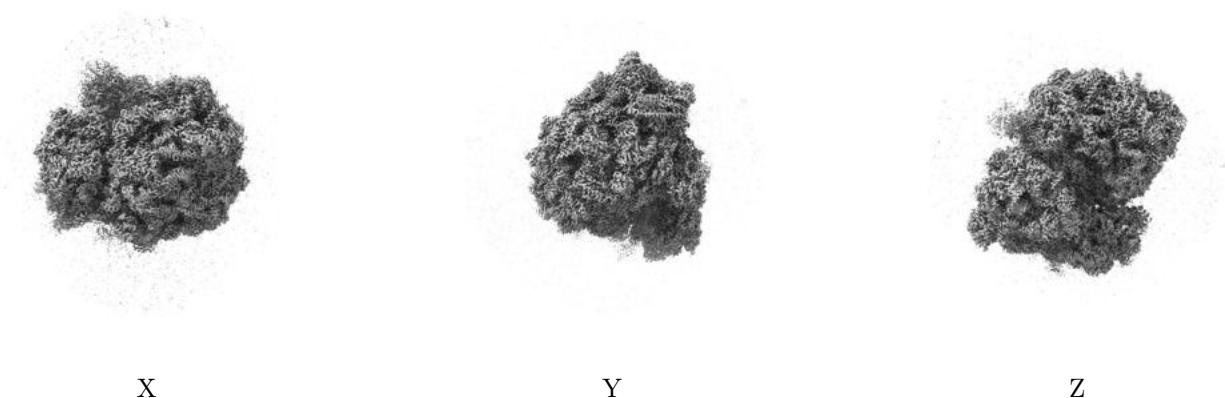


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

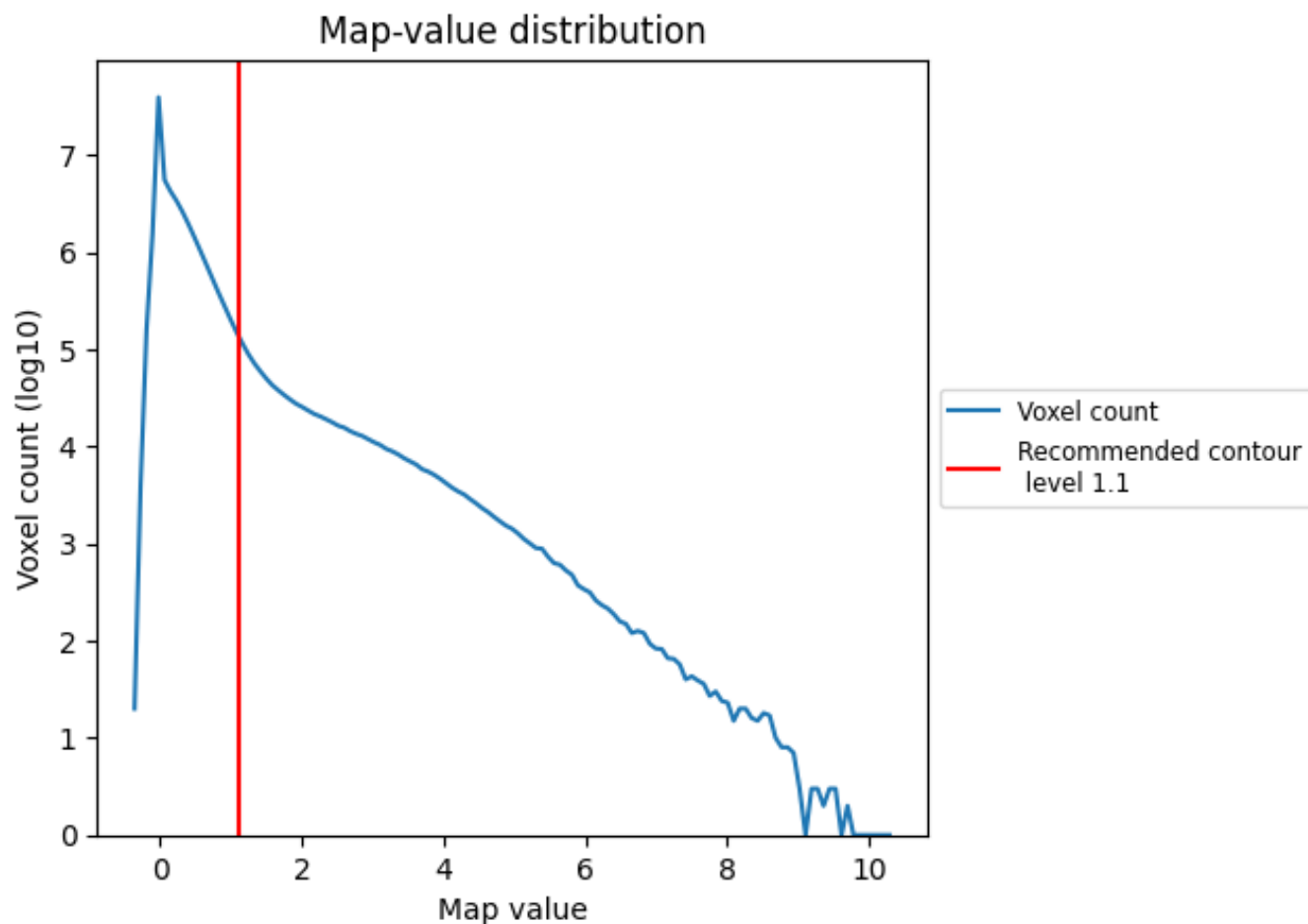
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

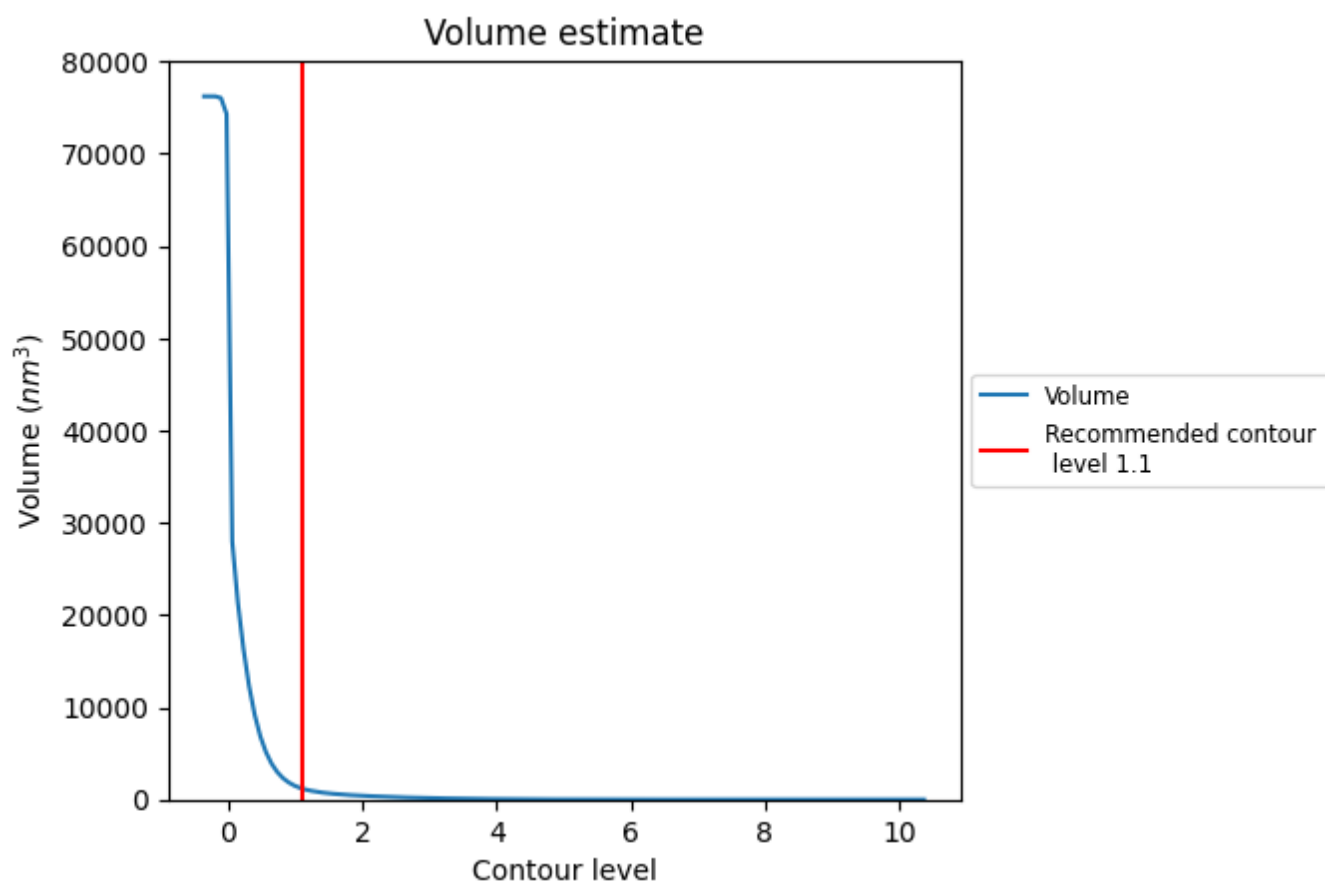
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

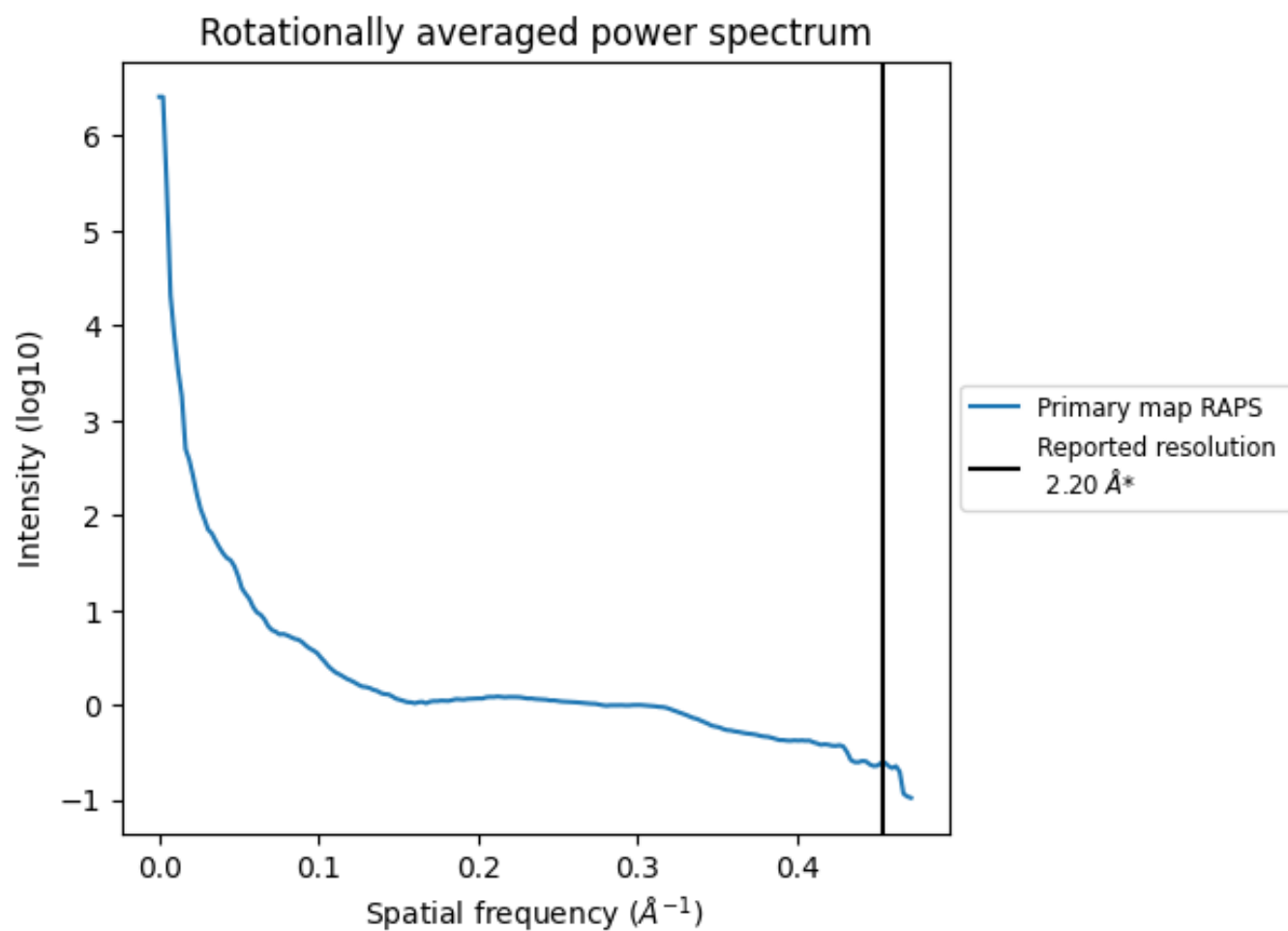
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1196 nm³; this corresponds to an approximate mass of 1081 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

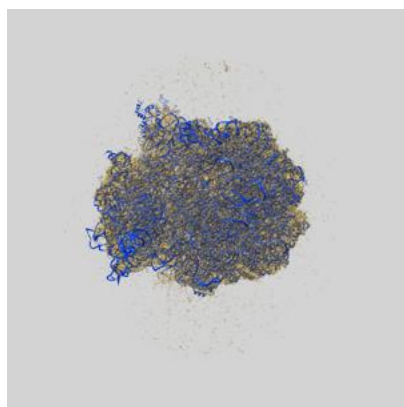
8 Fourier-Shell correlation

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

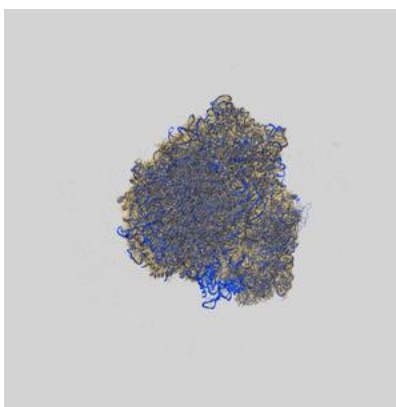
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28636 and PDB model 8EVT. Per-residue inclusion information can be found in section 3 on page 20.

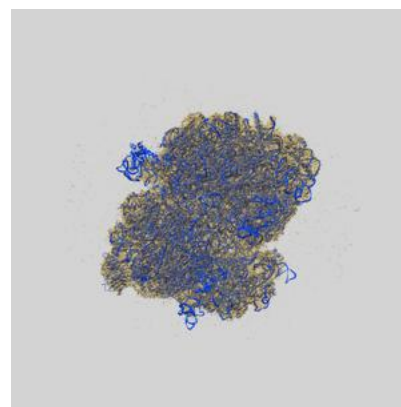
9.1 Map-model overlay [i](#)



X



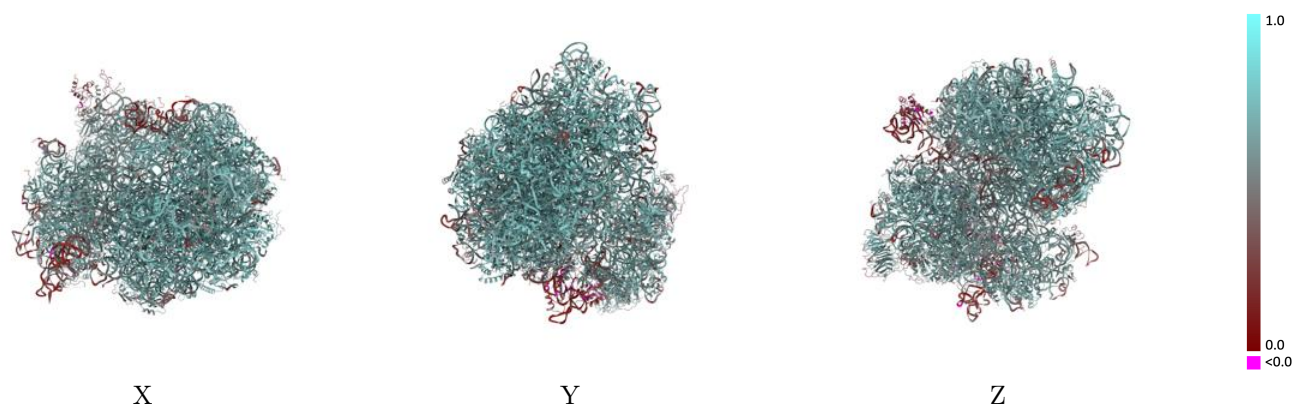
Y



Z

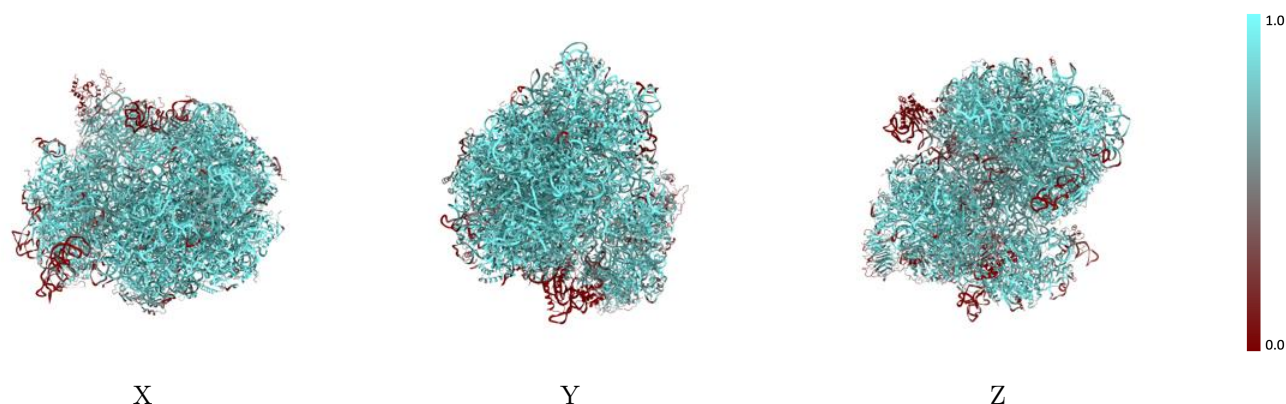
The images above show the 3D surface view of the map at the recommended contour level 1.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



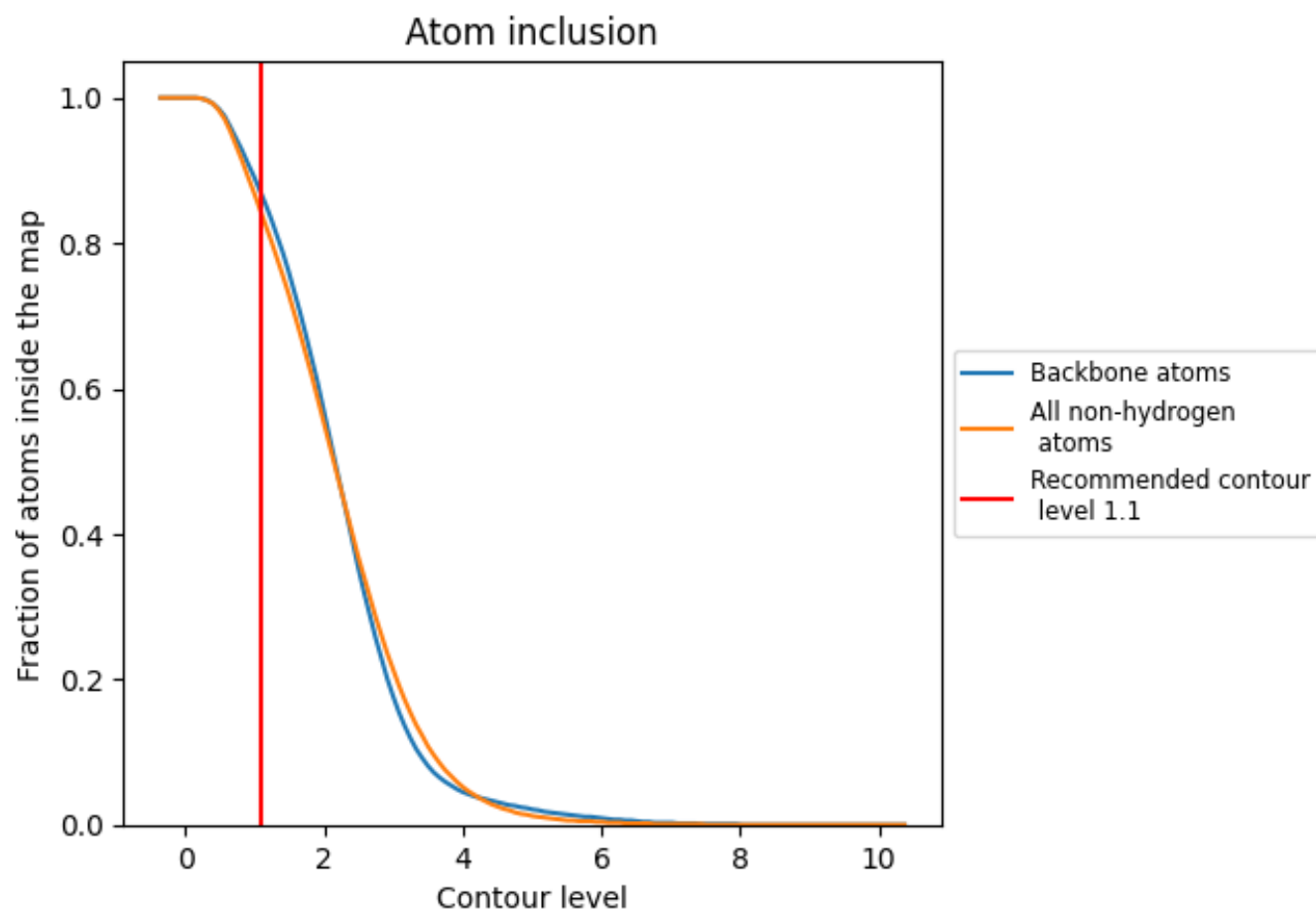
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 87% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8390	 0.6260
A1	 0.8920	 0.6480
A3	 0.9400	 0.6580
A4	 0.9490	 0.6850
AA	 0.9610	 0.7190
AB	 0.9250	 0.6990
AC	 0.9200	 0.7070
AD	 0.7360	 0.5960
AE	 0.7680	 0.6210
AF	 0.9130	 0.7040
AG	 0.8180	 0.6430
AH	 0.8330	 0.6540
AI	 0.8560	 0.6670
AJ	 0.5090	 0.4710
AL	 0.8800	 0.6800
AM	 0.8630	 0.6640
AN	 0.9820	 0.7440
AO	 0.9300	 0.7110
AP	 0.9020	 0.7050
AQ	 0.9570	 0.7340
AR	 0.7830	 0.6120
AS	 0.8990	 0.6900
AT	 0.8810	 0.6790
AU	 0.6570	 0.5680
AV	 0.9000	 0.6860
AW	 0.8990	 0.6860
AX	 0.8930	 0.6890
AY	 0.8930	 0.6870
AZ	 0.8560	 0.6440
Aa	 0.9330	 0.7150
Ab	 0.8140	 0.6180
Ac	 0.8610	 0.6390
Ad	 0.8260	 0.6540
Ae	 0.9310	 0.7200
Af	 0.9560	 0.7220



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Chain	Atom inclusion	Q-score
Ag	 0.8840	 0.6760
Ah	 0.8740	 0.6830
Ai	 0.8590	 0.6430
Aj	 0.9620	 0.7320
Ak	 0.6130	 0.5660
Al	 0.9570	 0.7100
Am	 0.8690	 0.6650
An	 0.7970	 0.6160
Ao	 0.8490	 0.6660
Ap	 0.9030	 0.6920
B5	 0.8330	 0.5860
BA	 0.8020	 0.6140
BB	 0.7640	 0.5900
BC	 0.8840	 0.6550
BD	 0.6770	 0.5700
BE	 0.8910	 0.6450
BF	 0.8140	 0.6200
BG	 0.6330	 0.5420
BH	 0.5790	 0.5120
BI	 0.8180	 0.6070
BJ	 0.8540	 0.6330
BK	 0.6040	 0.5160
BL	 0.8000	 0.5940
BM	 0.0530	 0.2660
BN	 0.8880	 0.6450
BO	 0.8490	 0.6000
BP	 0.6210	 0.5310
BQ	 0.8970	 0.6700
BR	 0.6670	 0.5590
BS	 0.7630	 0.5830
BT	 0.8220	 0.6210
BU	 0.5750	 0.5300
BV	 0.8510	 0.6330
BW	 0.9640	 0.7000
BX	 0.8900	 0.6430
BY	 0.7570	 0.5990
BZ	 0.7600	 0.6010
Ba	 0.8490	 0.6000
Bb	 0.7800	 0.6020
Bc	 0.6750	 0.5490
Bd	 0.9100	 0.6460
Be	 0.7040	 0.5640

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Chain	Atom inclusion	Q-score
Bf	 0.0900	 0.2390
Bg	 0.6440	 0.5650
E	 0.0120	 0.1830
EC	 0.4360	 0.3750