



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 02:54 PM UTC

PDB ID : 8EWB / pdb_00008ewb
EMDB ID : EMD-28642
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2 and GDP, Structure III
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-22
Resolution : 2.87 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

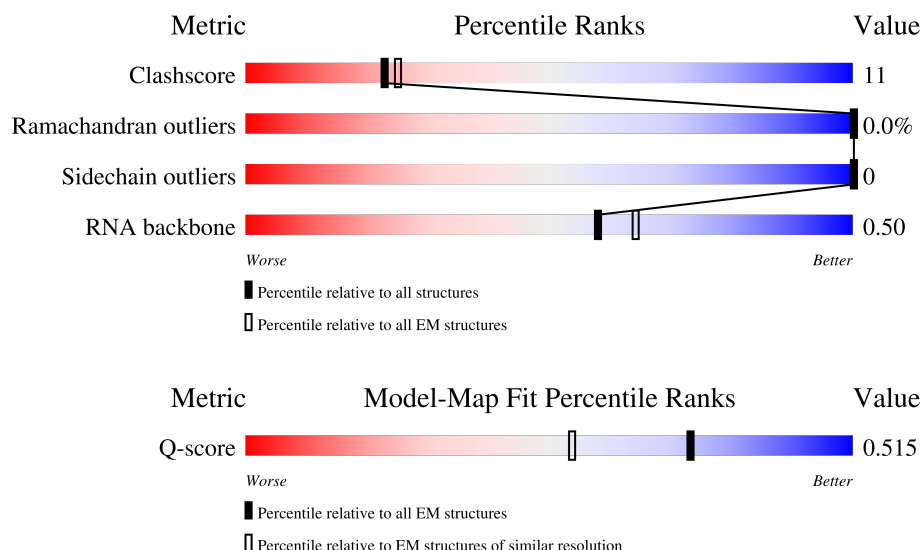
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.87 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	12062 (2.37 - 3.37)

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	
2	BB	255	
3	BC	254	

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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	

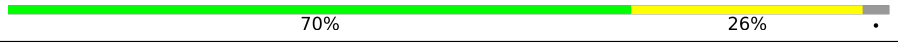
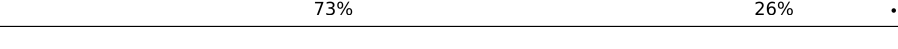
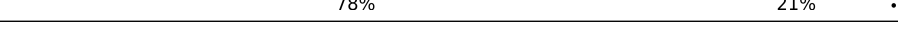
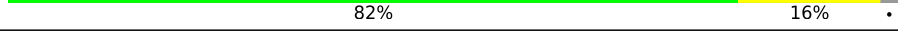
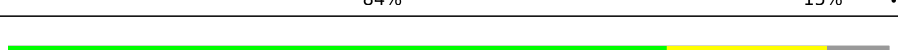
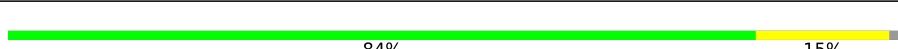
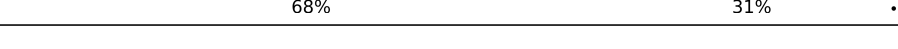
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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3360	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	221	
47	AJ	174	
48	AL	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	12% 61% 39%
80	DC	842	58% 40%
81	V	312	42% 19% 39%
82	EC	202	14% 37% 25% 24%

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 213196 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	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	125	Total	C	N	O	S	0	0
			1000	625	188	185	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	75	Total	C	N	O	S	0	0
			605	386	116	99	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BM	124	Total	C	N	O	S	0	0
			935	587	165	181	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
			38005	17006	6718	12499	1782		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B5	1191	B8N	U	conflict	GB 1329886537
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
			3081	1956	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	3198	Total	C	N	O	P	0	0
			68445	30596	12331	22320	3198		

- 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 protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	DC	824	Total	C	N	O	S	0	0
			6419	4085	1096	1208	30		

- Molecule 81 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 82 is a RNA chain called Taura syndrome virus (TSV) internal ribosome entry site (IRES) RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	EC	153	Total	C	N	O	P	0	0
			3261	1457	580	1071	153		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EC	6953	U	-	expression tag	GB 14701764
EC	6954	A	-	expression tag	GB 14701764
EC	6955	A	-	expression tag	GB 14701764
EC	6956	A	-	expression tag	GB 14701764
EC	6957	A	-	expression tag	GB 14701764
EC	6958	C	-	expression tag	GB 14701764
EC	6959	C	-	expression tag	GB 14701764

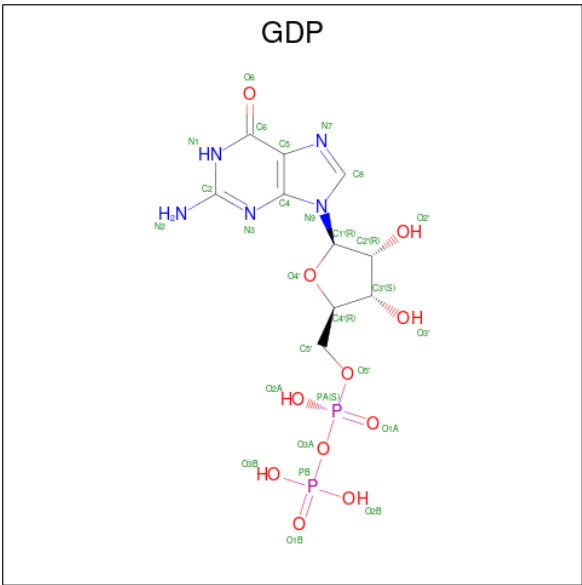
- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
83	Ba	1	Total Mg 1 1	0
83	B5	63	Total Mg 63 63	0
83	AB	1	Total Mg 1 1	0
83	A1	173	Total Mg 173 173	0
83	A3	1	Total Mg 1 1	0
83	A4	1	Total Mg 1 1	0
83	AP	1	Total Mg 1 1	0
83	Aj	1	Total Mg 1 1	0

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

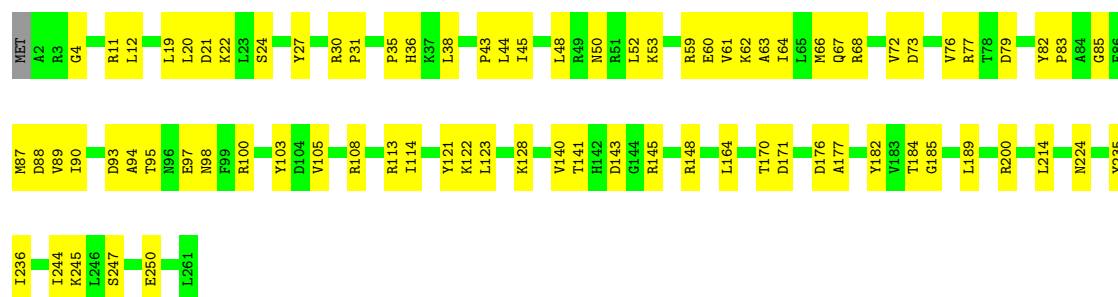
Mol	Chain	Residues	Atoms	AltConf
84	Ao	1	Total Zn 1 1	0

- Molecule 85 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



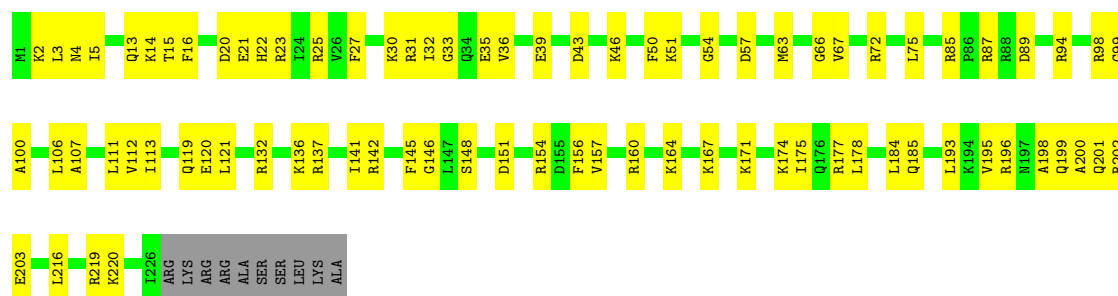
Mol	Chain	Residues	Atoms					AltConf
85	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

Chain BE:  69% 31%



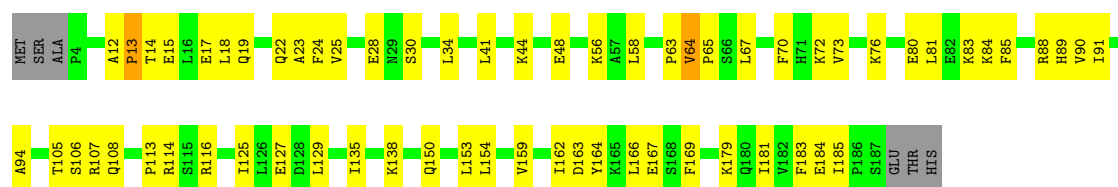
- Molecule 5: 40S ribosomal protein S6-A

Chain BG:  61% 34% .



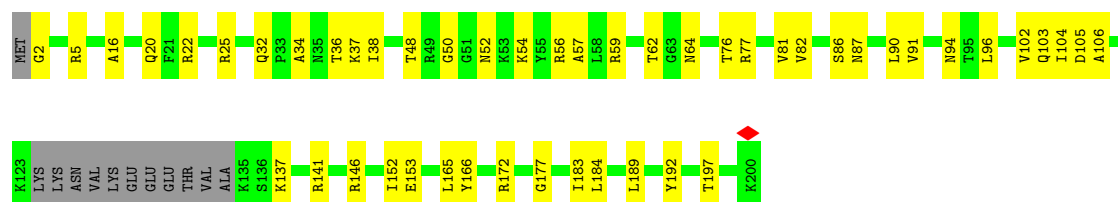
- Molecule 6: 40S ribosomal protein S7-A

Chain BH:  63% 33% . .



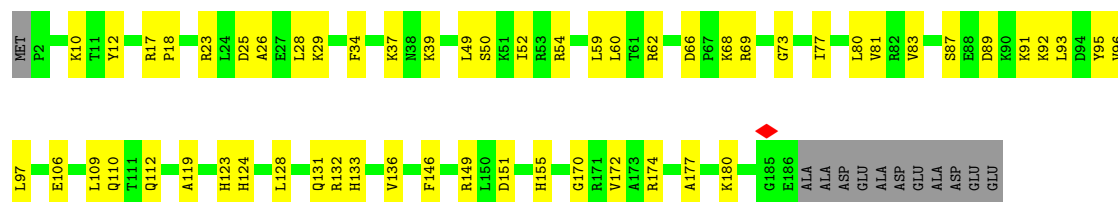
- Molecule 7: 40S ribosomal protein S8-A

Chain BI:  70% 24% 6%

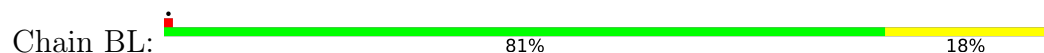


- Molecule 8: 40S ribosomal protein S9-A

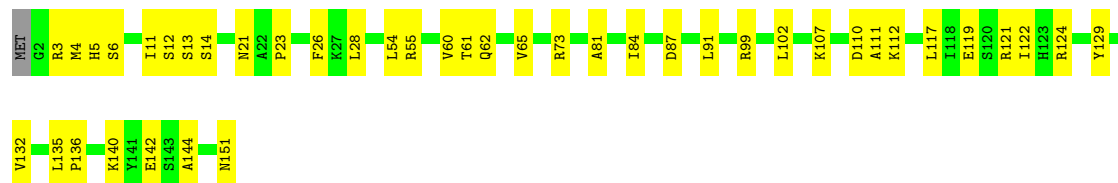
Chain BJ:  65% 28% 6%



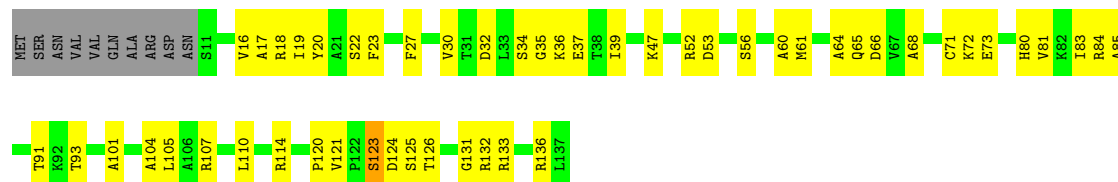
• Molecule 9: 40S ribosomal protein S11-A



• Molecule 10: 40S ribosomal protein S13



• Molecule 11: 40S ribosomal protein S14-A

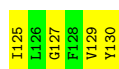


• Molecule 12: 40S ribosomal protein S21-A



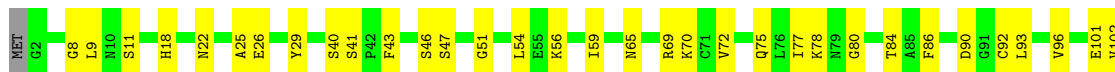
• Molecule 13: RPS22A isoform 1





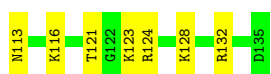
• Molecule 14: 40S ribosomal protein S23-A

Chain BX: 68% 32%



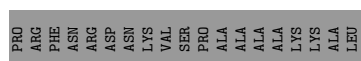
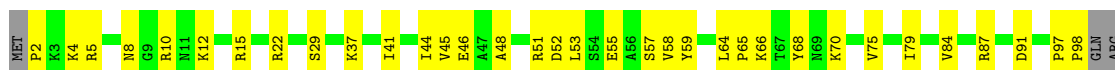
• Molecule 15: 40S ribosomal protein S24-A

Chain BY: 70% 30%



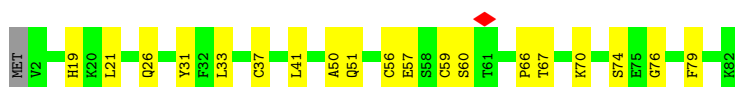
• Molecule 16: RPS26B isoform 1

Chain Ba: 53% 29% 18%



• Molecule 17: 40S ribosomal protein S27-A

Chain Bb: 76% 23%



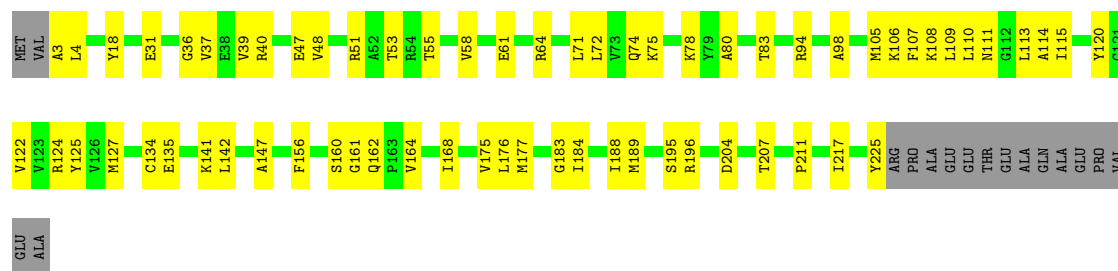
• Molecule 18: 40S ribosomal protein S30-A

Chain Be: 60% 35% 5%



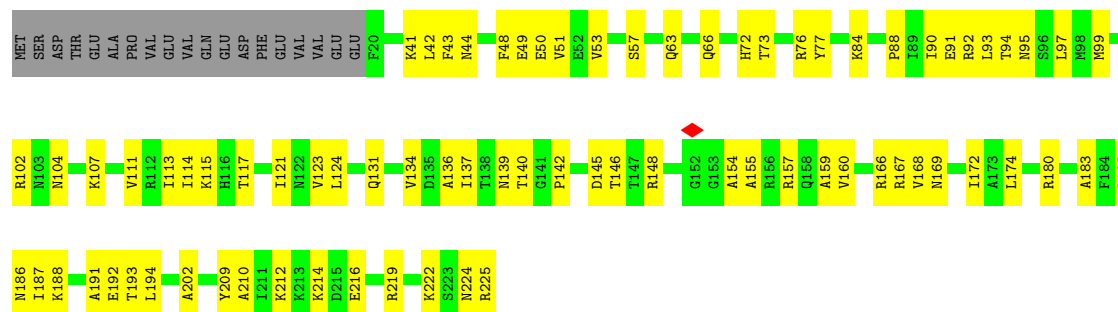
• Molecule 19: RPS3 isoform 1

Chain BD: 66% 27% 7%



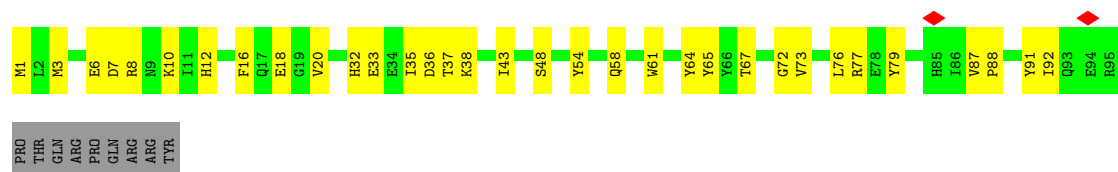
• Molecule 20: Rps5p

Chain BF: 57% 35% 8%



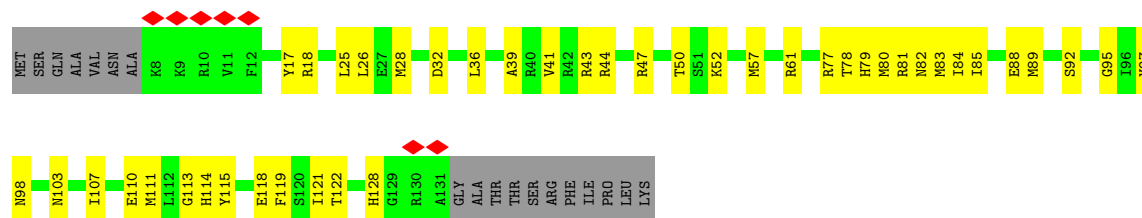
• Molecule 21: 40S ribosomal protein S10-A

Chain BK: 60% 31% 9%



• Molecule 22: RPS15 isoform 1

Chain BP: 5% 57% 30% 13%



• Molecule 23: 40S ribosomal protein S16-A

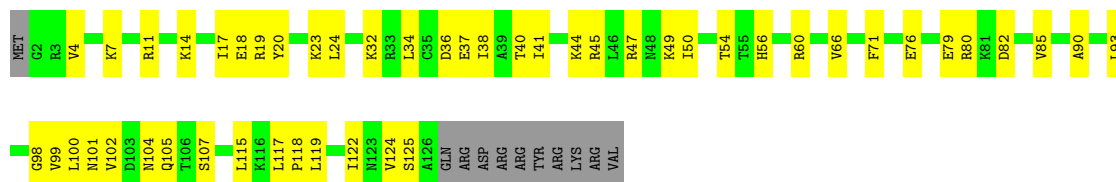
Chain BQ: 70% 29%





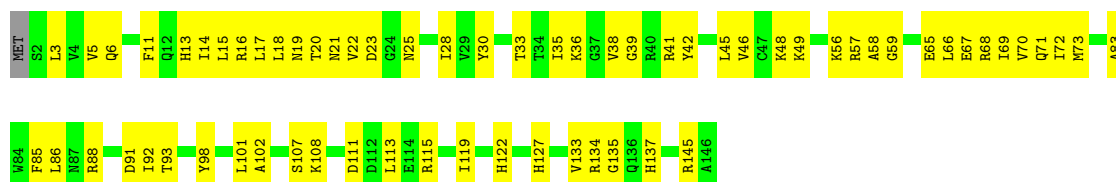
- Molecule 24: 40S ribosomal protein S17-A

Chain BR: 56% 36% 8%



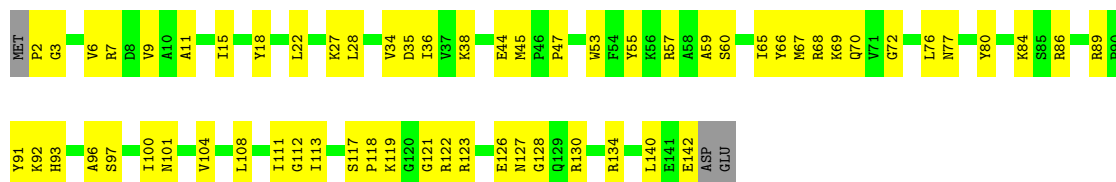
- Molecule 25: 40S ribosomal protein S18-A

Chain BS: 55% 45% .



- Molecule 26: 40S ribosomal protein S19-A

Chain BT: 56% 42% .



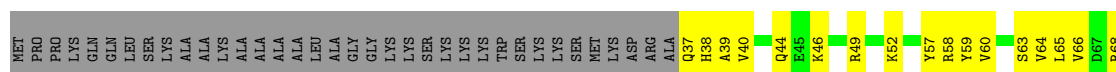
- Molecule 27: RPS20 isoform 1

Chain BU: 54% 35% 12%



- Molecule 28: RPS25A isoform 1

Chain BZ: 32% 31% 36%



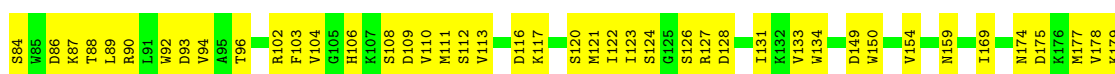
- Molecule 29: RPS28A isoform 1



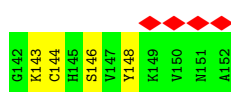
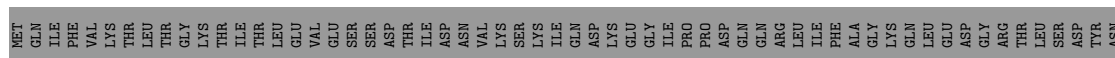
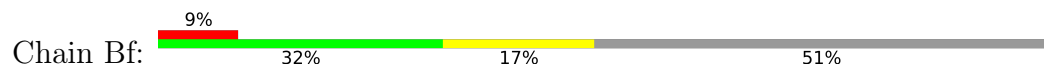
- Molecule 30: RPS29A isoform 1



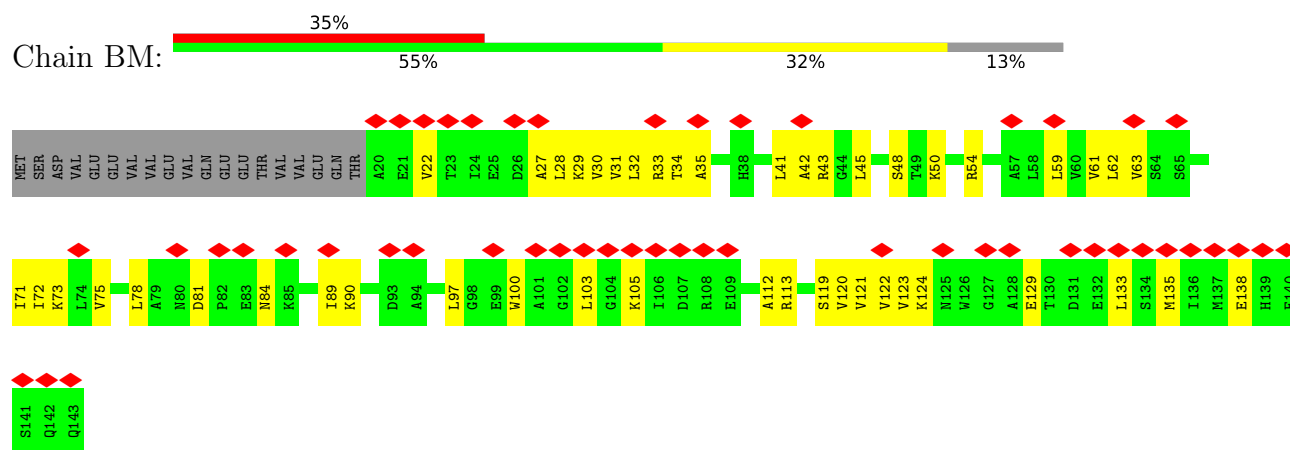
- Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein



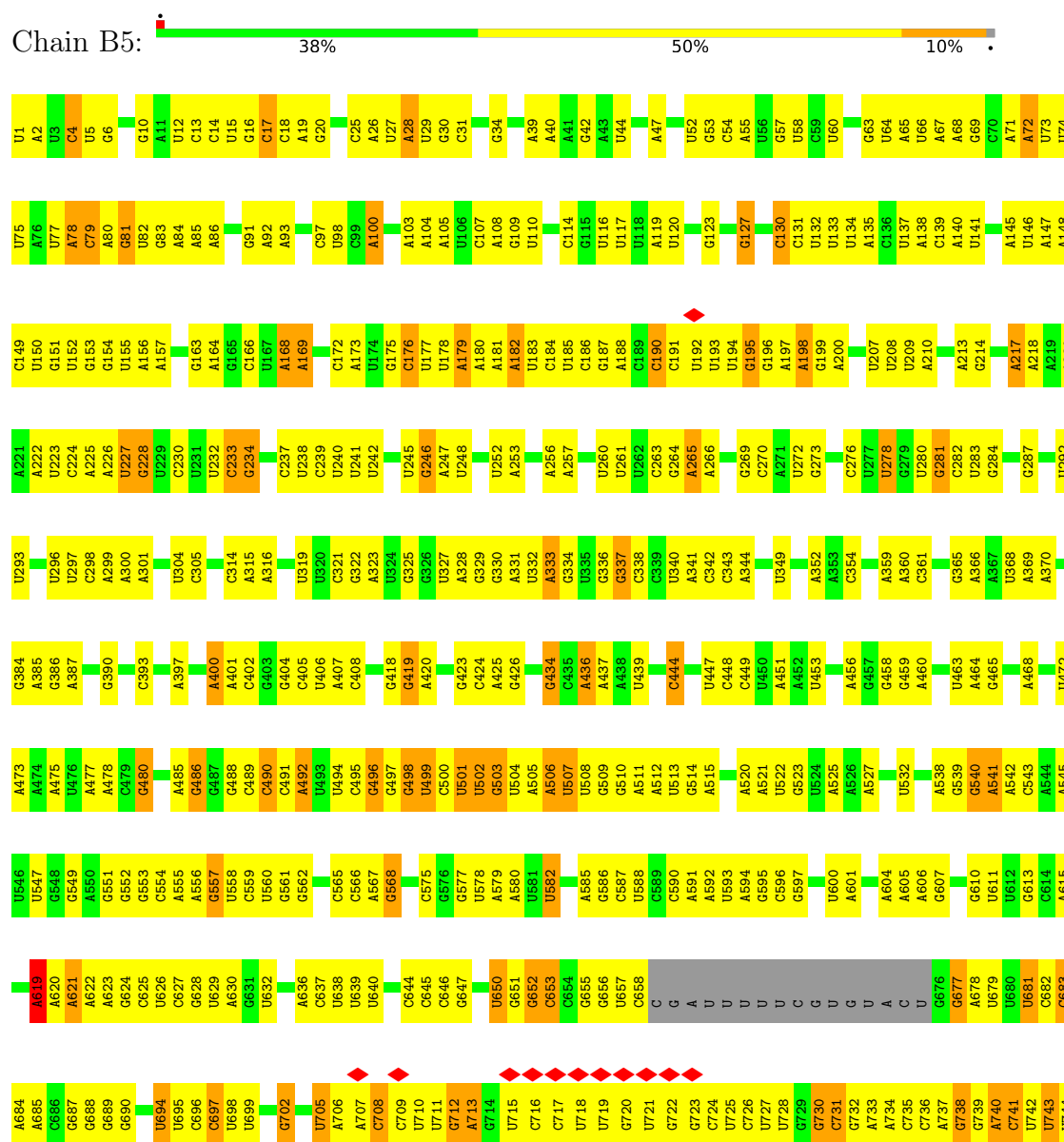
- Molecule 32: Ubiquitin-40S ribosomal protein S31



- Molecule 33: 40S ribosomal protein S12



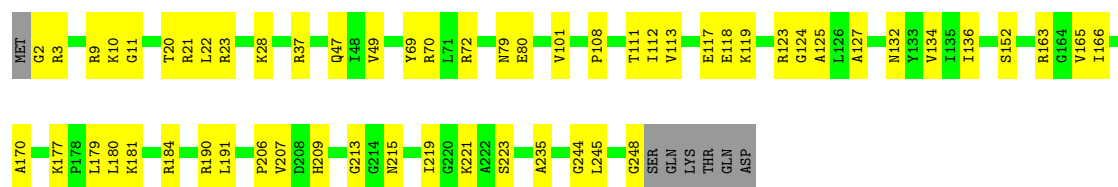
• Molecule 34: 18S rRNA



G1720	G1642	C1571	G1502	C1431	A1360	M1280	G1218	G1150	A1065	G980	A907	U839	A752
G1727	U1643	G1572	A1503	U1442	U1361	G1281	A1219	A1151	C1066	G987	U908	U840	A753
A1728	C1644	G1575	G1504	U1443	U1362	C1284	C1220	G1152	C1067	A988	U909	U841	A754
A1732	G1646	A1576	A1505	U1444	U1363	U1286	C1222	G1154	U989	C990	G914	U842	A755
C1733	U1647	A1577	U1508	G1446	C1365	U1286	G1224	G1155	C1072	G991	U917	U844	A756
A1648	U1578	U1577	U1511	C1447	U1366	G1291	U1226	C1158	A1076	A992	U918	A844	A757
G1649	U1579	U1578	G1512	G1448	G1367	G1292	U1225	C1159	A1226	A993	U918	G846	U758
U1650	C1580	U1579	G1513	U1449	U1368	G1292	G1227	A1160	U1079	U996	U919	G847	U759
A1651	U1581	U1580	U1514	U1450	U1369	G1293	G1228	C1161	U1080	G997	U920	C848	A760
C1652	U1582	U1581	G1515	C1451	U1370	G1294	G1229	C1162	A1081	U1004	U921	C849	G765
C1653	C1553	A1583	A1516	U1452	A1371	G1297	G1230	C1163	C1082	U1005	U922	A850	U766
A1754	G1584	G1584	U1517	G1453	U1372	U1297	G1231	G1164	C1083	A1086	A923	U851	U766
A1755	U1556	U1585	U1518	G1454	C1373	A1300	U1233	G1165	A1087	A1086	A924	C852	U766
A1756	U1557	A1596	C1518	G1455	A1374	U1301	G1232	G1166	A1088	A1087	A925	G853	A769
U1758	G1588	U1596	U1519	C1456	C1376	U1302	G1233	G1167	U1092	G1008	A926	U859	C773
C1759	U1589	C1589	G1521	G1458	U1377	G1308	G1234	G1169	A1092	G1011	U928	U860	A774
G1760	G1590	G1590	U1522	C1459	U1378	C1309	A1236	G1170	A1096	U1012	U929	U861	G775
G1761	C1591	C1591	G1523	A1460	G1379	U1314	G1237	C1173	U1095	A1020	A933	A863	G778
A1762	A1592	A1592	A1524	C1461	U1380	U1315	G1238	C1174	C1096	C1021	A934	U864	U779
U1765	G1594	G1594	A1525	G1462	A1382	G1316	U1239	U1175	U1097	C1022	U935	A865	A780
A1766	U1595	U1595	A1526	U1465	G1383	G1241	G1242	G1176	U1097	A1023	G936	G866	U781
A1767	C1596	C1596	C1529	G1466	A1384	U1320	A1242	G1179	G1100	A1026	A939	G867	U782
G1768	A1597	A1597	C1533	C1467	G1385	A1321	G1243	G1179	A1027	A1026	A940	G868	C784
U1769	U1598	U1598	U1533	C1468	G1386	A1322	A1244	U1182	U1103	C1028	U947	G871	A789
U1770	C1599	C1599	U1537	A1469	G1387	C1323	G1245	U1183	G1107	C1029	U947	G872	U794
U1771	A1600	A1600	C1537	G1470	G1388	G1324	G1246	A1184	G1108	A1030	G948	U873	U795
C1772	G1601	G1601	G1540	A1471	C1389	U1328	U1247	U1187	G1114	C1033	C949	C874	A796
A1773	C1606	C1606	G1541	C1472	U1390	A1329	G1248	U1187	G1115	C1034	A952	G878	U796
G1774	G1607	G1607	G1542	U1473	C1393	G1330	U1249	U1188	A1116	G1037	A955	G879	U797
A1776	U1608	U1608	A1543	G1474	G1394	A1331	U1250	G1188	U1120	U1038	C956	U880	A809
U1777	G1609	G1609	U1544	C1476	A1395	A1331	U1251	U1188	G1122	G1040	C957	U886	G810
G1780	G1610	G1610	A1545	G1477	U1398	U1335	C1252	B8M1191	G1123	G1041	U958	U887	A809
A1781	A1611	A1611	G1548	G1478	C1399	U1335	U1254	A1194	G1124	G1042	U959	U888	G810
A1782	U1612	U1612	C1549	A1479	A1400	C1338	G1255	C1195	A1125	A1043	U960	U889	U813
C1783	A1613	A1613	U1550	G1480	A1401	U1340	A1256	C1196	G1126	A1044	U961	A891	A814
G1785	C1615	C1615	U1551	C1482	G1405	A1341	U1257	A1196	U1056	G1046	A966	U892	G819
G1786	G1616	G1616	U1552	A1483	U1406	U1342	U1258	C1197	A1143	U1057	A967	U894	U820
G1787	U1617	U1617	G1553	G1484	G1409	U1343	U1260	G1199	A1124	U1058	U968	U895	U821
G1788	C1618	C1618	U1554	C1485	A1410	U1344	G1261	G1200	A1125	A1043	C962	U896	U822
G1789	C1619	C1619	U1555	G1486	A1411	A1345	U1262	G1201	G1126	C1045	A963	C897	G823
U1792	U1620	U1620	U1557	A1487	U1412	A1346	G1263	A1202	U1130	G1047	A966	U897	G824
G1793	G1621	G1621	U1558	G1488	U1413	U1347	G1264	C1205	A1131	U1047	A966	U898	G825
A1794	C1622	C1622	U1559	U1489	C1426	A1348	U1265	U1206	A1132	G1050	A967	U899	U826
U1795	G1623	G1623	U1560	C1490	A1427	U1349	G1267	C1207	A1133	U1051	U968	U896	U827
C1796	U1624	U1624	U1561	U1491	C1428	U1350	G1268	C1208	A1138	U1052	C969	C897	G823
U1797	U1628	U1628	U1562	A1492	G1429	G1351	U1269	C1209	A1142	U1056	A970	U898	G824
U1798	G1629	G1629	C1563	C1493	U1430	U1352	G1270	C1210	A1143	U1057	A971	U899	U825
U1799	U1630	U1630	U1564	C1495	U1433	U1353	G1271	A1211	A1144	U1058	A972	U900	U826
U1799	A1631	A1631	C1565	U1496	G1433	G1354	G1271	G1212	U1145	U1059	A974	G901	C827
U1799	U1636	U1636	U1567	G1498	U1437	U1355	C1274	G1213	U1146	U1060	C975	U903	U833
G1715	C1636	C1636	U1568	G1499	G1438	U1356	A1275	U1214	G1147	A1061	G976	G904	G834
G1716	U1569	U1569	C1500	C1500	G1439	A1357	U1276	C1215	A1147	A1062	G976	A905	U835
G1717	C1641	C1641	A1570	C1501	C1440	C1359	G1277	C1216	G1148	A1062	A979	A906	U836

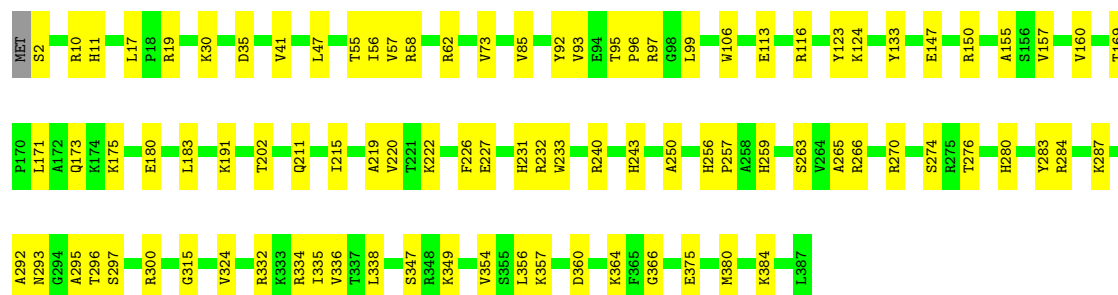
• Molecule 35: 60S ribosomal protein L2-A

Chain AA:  75% 22%



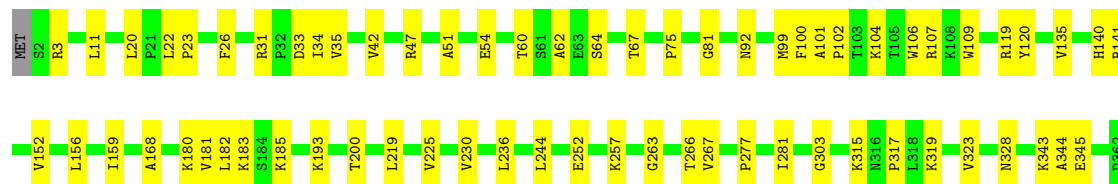
• Molecule 36: 60S ribosomal protein L3

Chain AB:  76% 24%

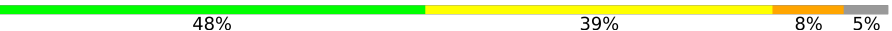


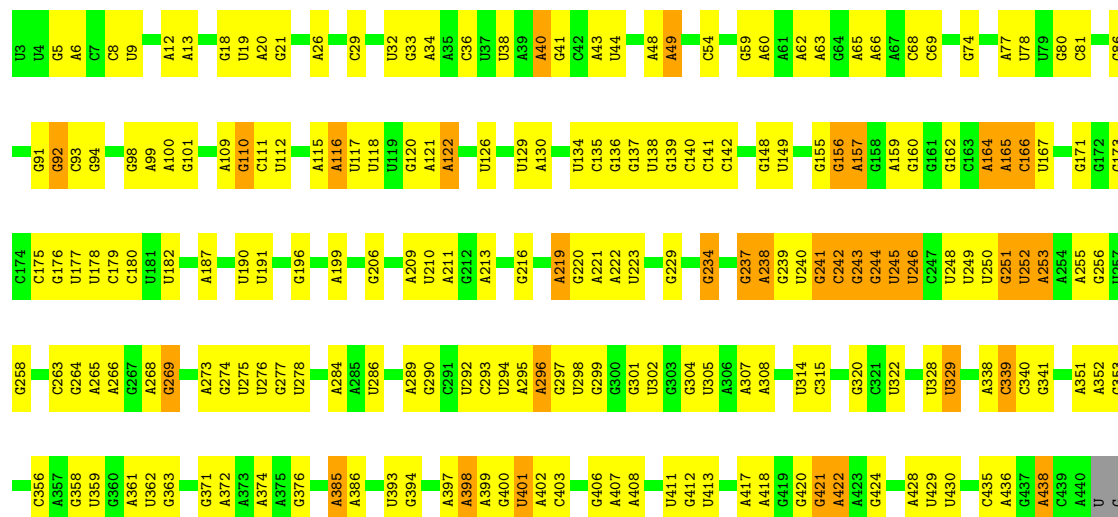
• Molecule 37: RPL4A isoform 1

Chain AC:  81% 18%



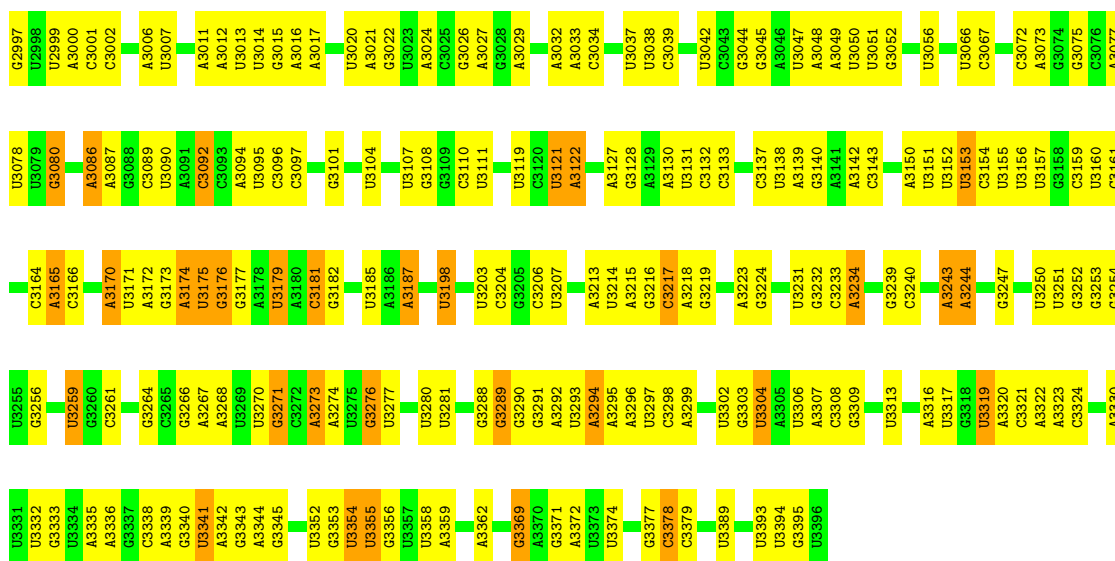
• Molecule 38: 25S rRNA

Chain A1:  48% 39% 8% 5%



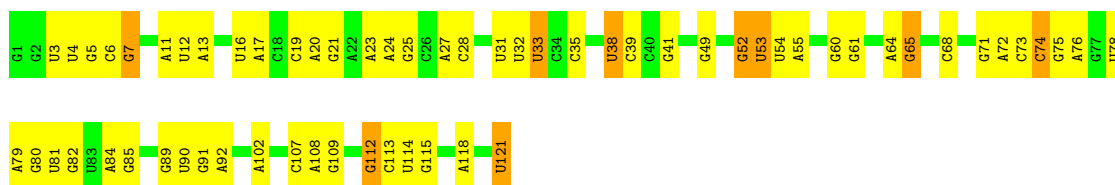
U1689	C1596	U1415	G1237	C1156	G1072	G993	G910	G809	U719	G632	A557
C1597	C1598	A1326	G1238	G1157	G1073	G994	C911	A810	G727	C636	U558
U1694	U1695	C1327	C1239	A1158	U1074	U995	G912	U811	G728	U640	A559
A1696	U1523	A1418	A1240	A1159	A1075	U996	A913	G812	A996	C641	G560
A1697	U1524	A1330	U1241	U1167	U1081	A997	A914	G813	C729	U642	C561
C1698	A1525	A1331	G1242	U1168	U1082	A998	A915	U814	U734	U643	C562
A1699	G1525	A1332	G1243	U1169	G1083	G999	G916	G815	A735	U644	U565
G1700	A1534	C1333	A1244	A1170	U1084	C1000	A917	A816	A736	G644	G566
U1717	A1535	U1335	G1246	A1171	G1085	G1001	A921	A817	A737	A645	G567
G1718	A1536	U1336	G1247	G1174	A1085	A1002	U922	U821	A738	A646	G568
U1721	A1537	A1337	G1248	C1175	U1088	U1008	G923	G822	G742	C650	A569
U1722	U1435	G1340	A1251	G1176	G1089	A1009	G924	G823	U748	C651	A570
A1723	C1437	U1341	U1253	G1177	U1090	G1010	A925	C824	C749	C655	U571
U1724	A1446	U1347	U1254	U1179	C1092	A1011	A929	U825	C753	A657	A572
C1725	G1447	U1348	C1255	A1180	U1093	G1012	A930	A830	C758	U662	C576
C1726	U1448	G1349	G1256	U1181	U1094	U1013	G934	G831	U759	C663	C577
G1727	A1449	A1350	C1257	A1182	U1095	U1015	G937	U834	G760	U664	A578
G1728	G1450	A1351	U1258	C1183	U1096	C1016	U939	G835	A761	A665	G579
A1729	U1455	U1352	A1259	A1184	U1097	C1017	U943	G845	A666	A666	C584
U1737	A1456	G1353	G1261	G1186	A1098	G1018	C944	A846	U762	C667	C585
U1740	A1460	A1355	U1262	C1192	A1103	G1020	C945	A847	C765	U671	U506
A1741	A1461	U1356	A1263	A1193	G1104	G1021	C946	A848	U766	A672	U507
G1747	G1464	A1363	U1269	G1194	U1108	U1022	U947	C849	G767	U673	C515
G1748	C1465	C1364	A1270	A1195	U1109	G	G948	G857	U674	U674	C516
A1749	G1466	G1368	A1271	C1196	U1110	A	C949	G860	G674	C675	A516
A1750	A1467	U1369	C1272	A1197	U1111	A	G950	C861	A771	C676	G617
G1751	A1468	C1376	A1273	C1201	U1114	U	A951	G866	U772	A677	G518
A1752	C1469	G1377	U1277	A1202	U1117	G	A952	A867	A775	G677	A521
U1757	U1472	U1378	C1278	A1203	C1117	A1030	U955	U871	U776	U679	A522
G1758	U1567	G1379	C1279	A1204	C1118	C1031	U956	U872	U777	U681	A523
C1759	U1568	G1380	U1279	A1205	C1119	C1032	U957	U873	A601	U682	U528
U1645	U1570	A1381	G1282	G1206	A1120	U1033	C959	C874	A602	U683	A529
G1646	A1571	G1382	C1283	G1207	U1121	U1034	U964	U875	A603	U684	G530
C1761	U1572	C1385	A1286	U1211	U1128	G1035	A964	A690	A608	U605	G531
C1762	G1573	A1386	A1287	A1212	A1129	C1037	A965	A876	A609	A532	A532
U1763	U1574	G1387	U1287	U1218	A1130	C1038	U966	A794	G609	A533	U534
U1764	A1481	U1388	A1290	U1219	G1131	U1039	A967	G785	G610	U534	A534
U1765	G1482	G1389	A1291	C1219	C1132	A1040	G968	A796	A611	G535	G535
G1766	G1483	C1390	C1292	G1222	A1133	U1041	C975	G787	U612	U536	U536
U1767	G1486	G1392	U1293	A1223	G1134	U1042	U976	C788	G616	U540	U540
C1768	G1487	A1399	G1295	C1224	U1138	C1043	U977	A791	G617	U541	G542
G1769	U1492	G1400	G1306	C1227	G1140	A1046	U979	G792	C618	G543	C543
U1770	G1493	G1404	G1307	C1228	C1141	A1047	A980	A793	A619	U620	G547
C1771	U1494	U1404	U1308	G1229	G1142	A1048	U981	G798	A621	G548	G548
U1772	C1495	A1407	U1309	G1230	A1143	U1049	U982	G799	A622	U549	U549
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U1774	A1497	C1409	G1311	C1232	U1150	A1062	U987	G805	G714	A551	A551
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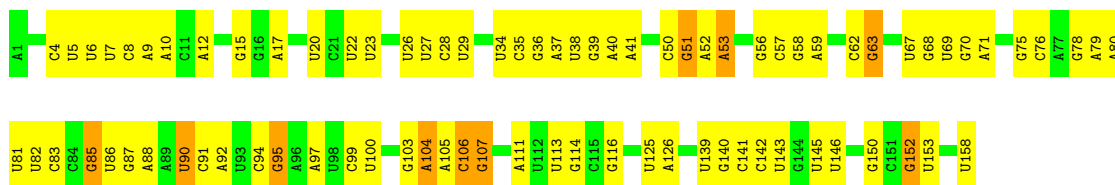
• Molecule 39: 5s rRNA

Chain A3: 49% 44% 7%



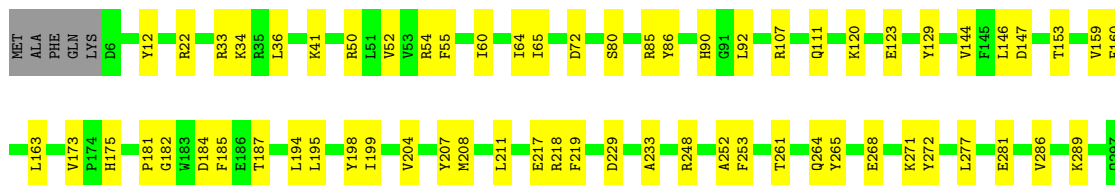
• Molecule 40: 5.8 S rRNA

Chain A4: 48% 46% 6%



• Molecule 41: RPL5 isoform 1

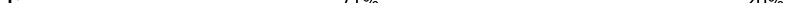
Chain AD: 77% 22% 1%

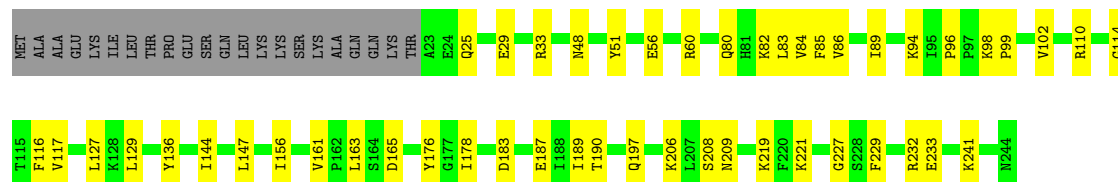


• Molecule 42: 60S ribosomal protein L6-A

Chain AE: 67% 22% 11%

- Molecule 43: 60S ribosomal protein L7-A

Chain AF: 



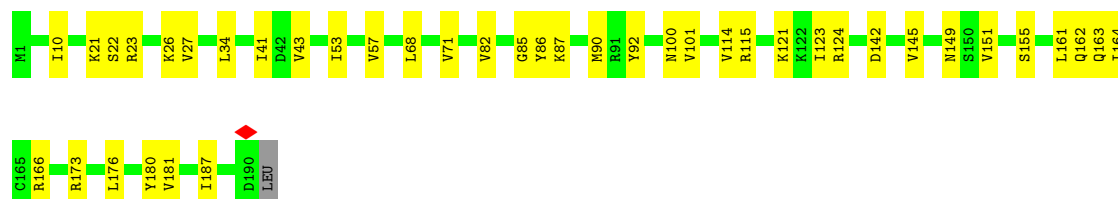
- Molecule 44: 60S ribosomal protein L8-A

Chain AG:

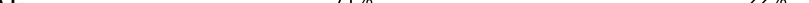


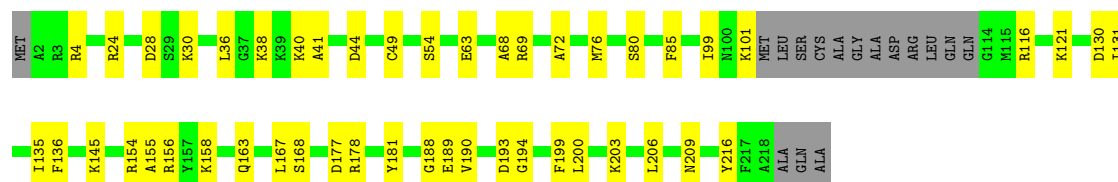
- Molecule 45: 60S ribosomal protein L9-A

Chain AH: 78% 21%

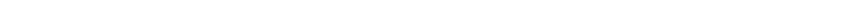


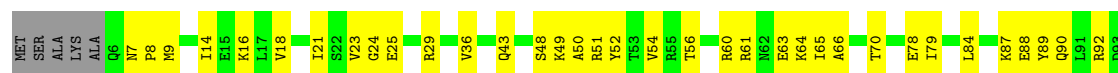
- Molecule 46: RPL10 isoform 1

Chain AI:  71% 22% 7%

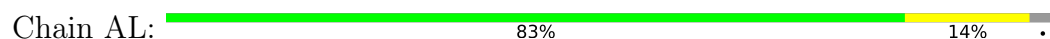


- Molecule 47: RPL11A isoform 1

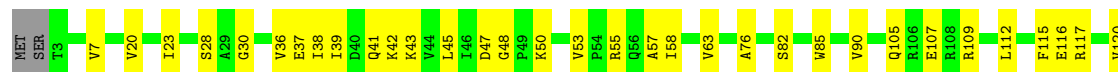
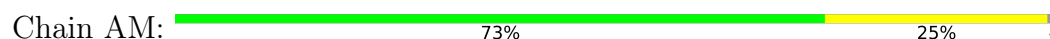
Chain A.J:  60% 37%



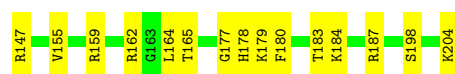
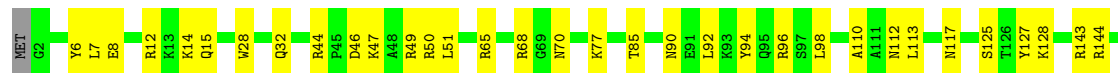
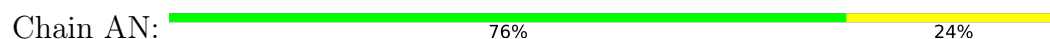
• Molecule 48: 60S ribosomal protein L13-A



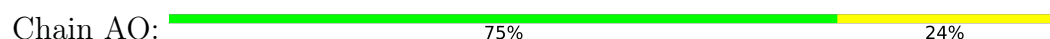
• Molecule 49: 60S ribosomal protein L14-A



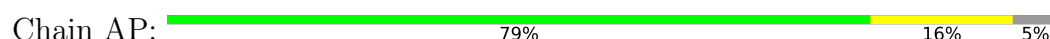
• Molecule 50: 60S ribosomal protein L15-A

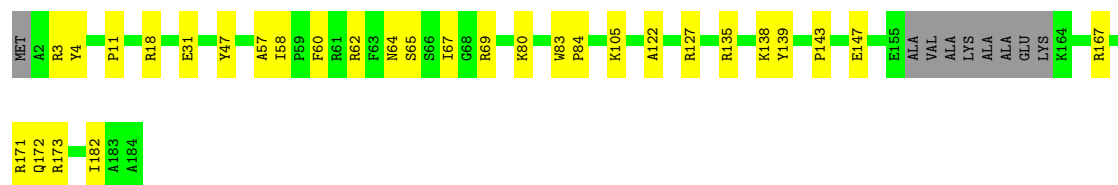


• Molecule 51: 60S ribosomal protein L16-A



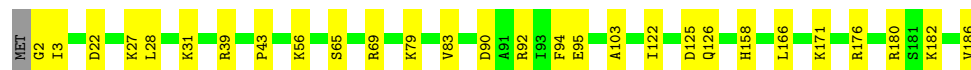
• Molecule 52: 60S ribosomal protein L17-A





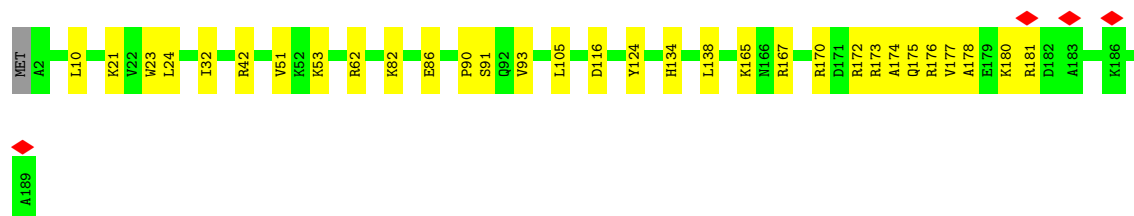
- Molecule 53: 60S ribosomal protein L18-A

Chain AQ: 84% 15% .



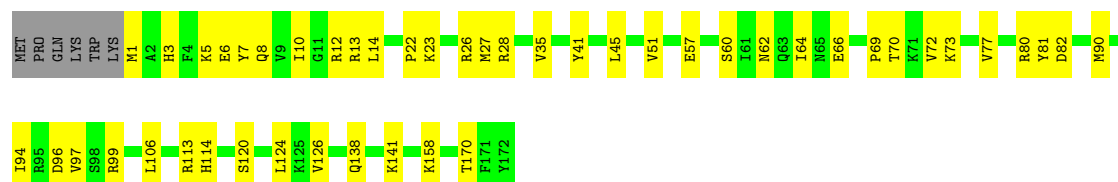
- Molecule 54: 60S ribosomal protein L19-A

Chain AR: 83% 16% .



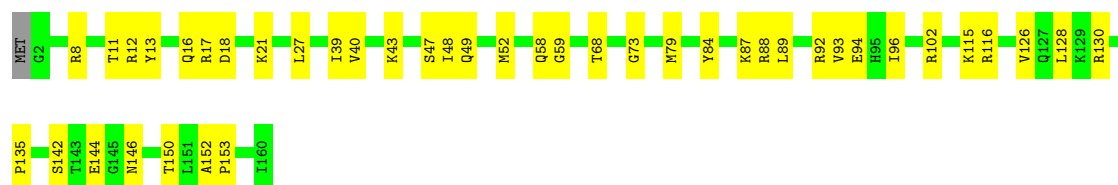
- Molecule 55: 60S ribosomal protein L20

Chain AS: 70% 26% .



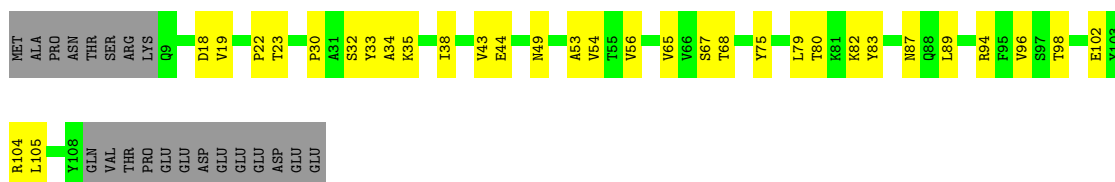
- Molecule 56: 60S ribosomal protein L21-A

Chain AT: 73% 26% .

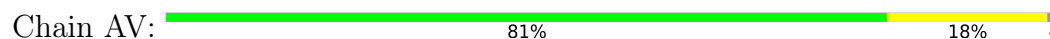


- Molecule 57: 60S ribosomal protein L22-A

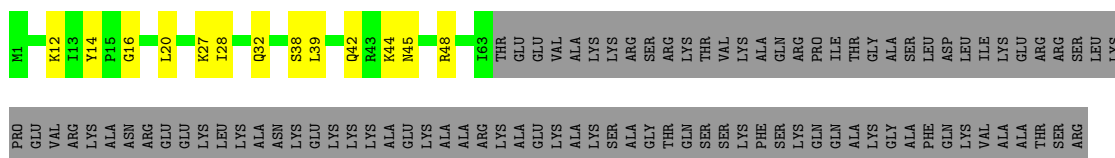
Chain AU: 56% 26% 17%



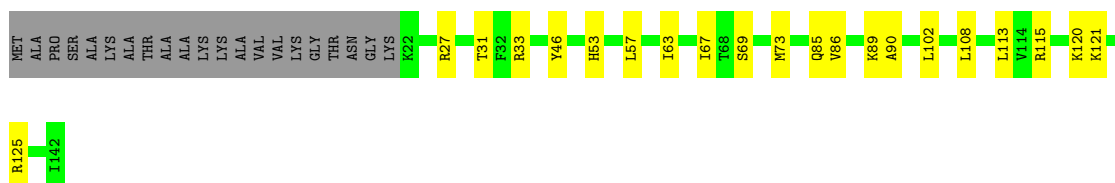
- Molecule 58: 60S ribosomal protein L23-A



- Molecule 59: RPL24A isoform 1



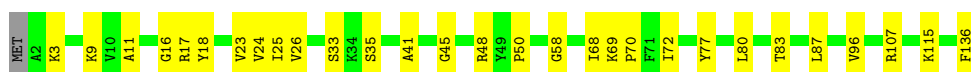
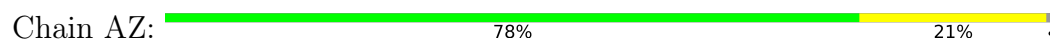
- Molecule 60: 60S ribosomal protein L25



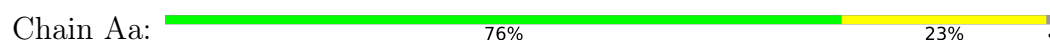
- Molecule 61: 60S ribosomal protein L26-A



- Molecule 62: 60S ribosomal protein L27-A



- Molecule 63: 60S ribosomal protein L28





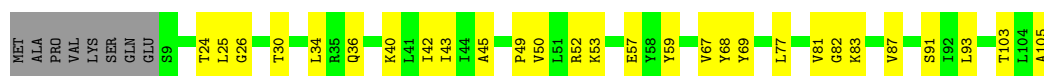
- Molecule 64: RPL29 isoform 1

Chain Ab: 90% 8% .



- Molecule 65: 60S ribosomal protein L30

Chain Ac: 66% 27% 8% .



- Molecule 66: 60S ribosomal protein L31-A

Chain Ad: 81% 16% .



- Molecule 67: RPL32 isoform 1

Chain Ae: 82% 16% .



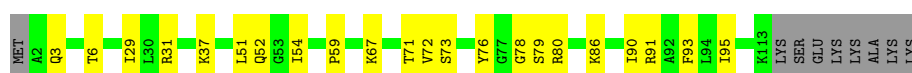
- Molecule 68: 60S ribosomal protein L33-A

Chain Af: 84% 15% .



- Molecule 69: 60S ribosomal protein L34-A

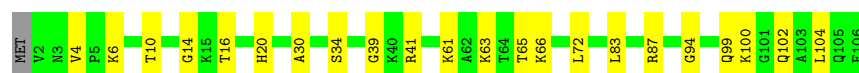
Chain Ag: 74% 18% 7% .



- Molecule 70: 60S ribosomal protein L35-A

Chain Ah: 84% 15% .

Chain Ao:  78% 21% .

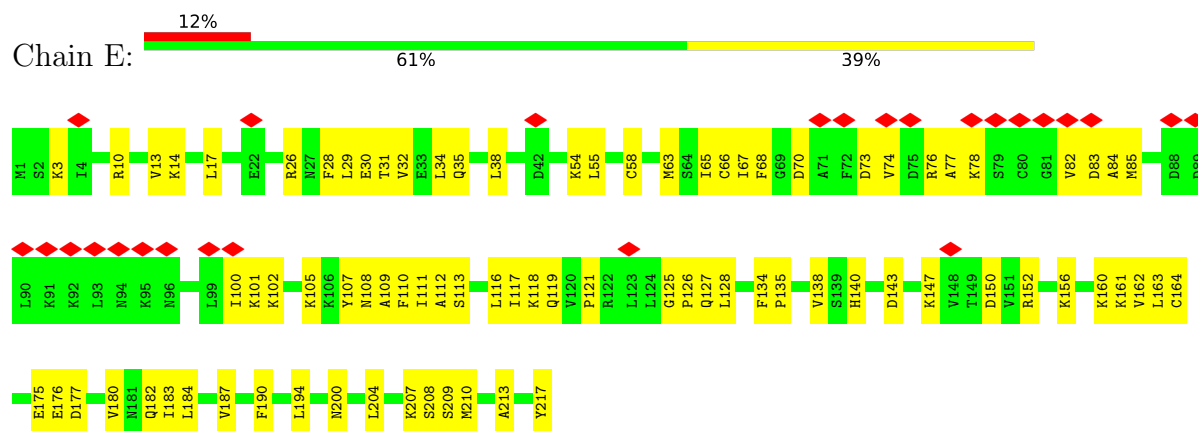


- Molecule 78: 60S ribosomal protein L43-A

Chain Ap:  77% 22% .

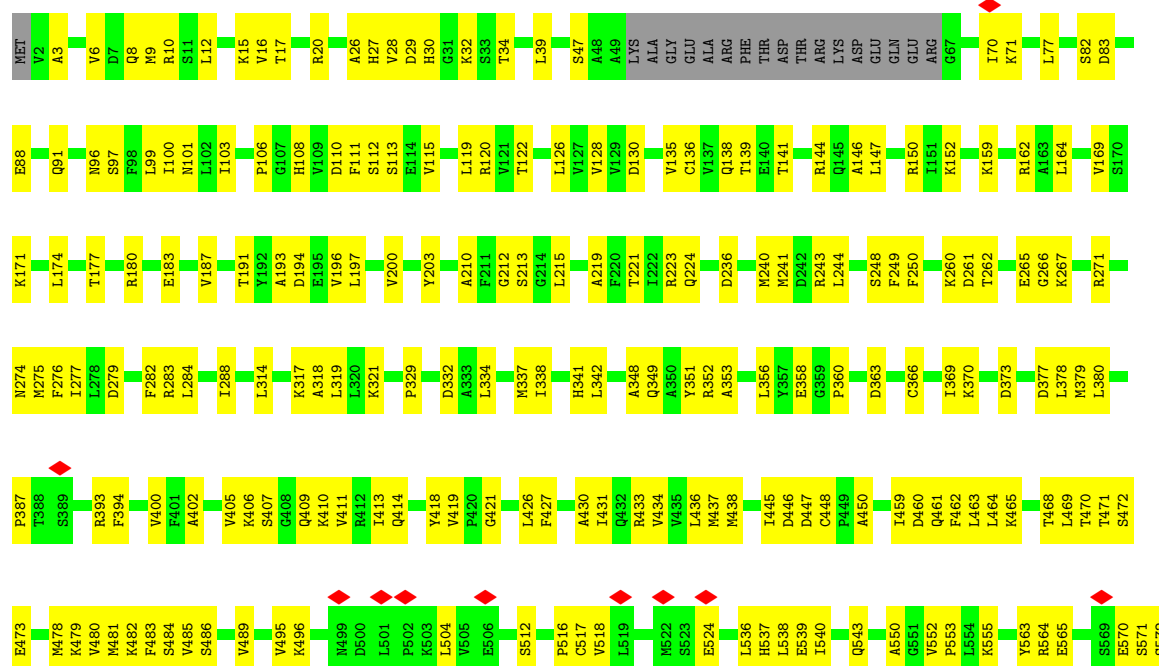


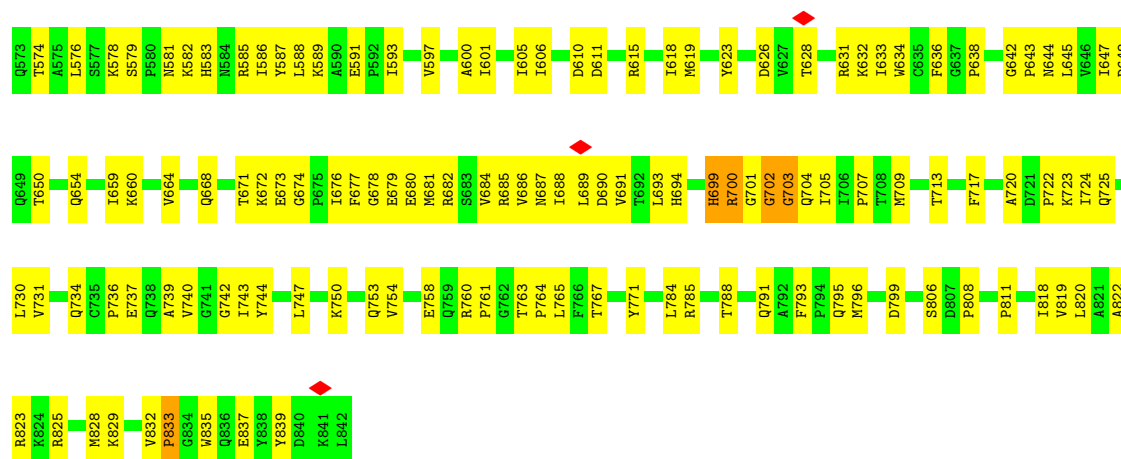
- Molecule 79: RPL1A isoform 1



- Molecule 80: Elongation factor 2

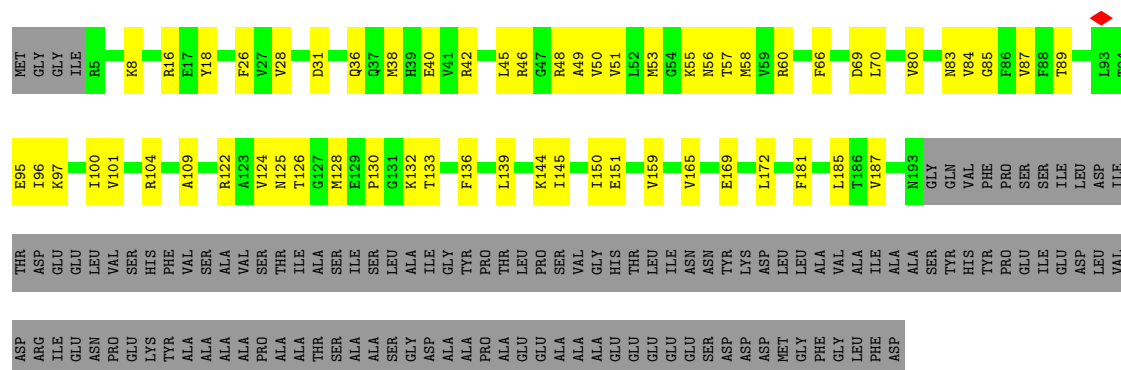
Chain DC:  58% 40% ..





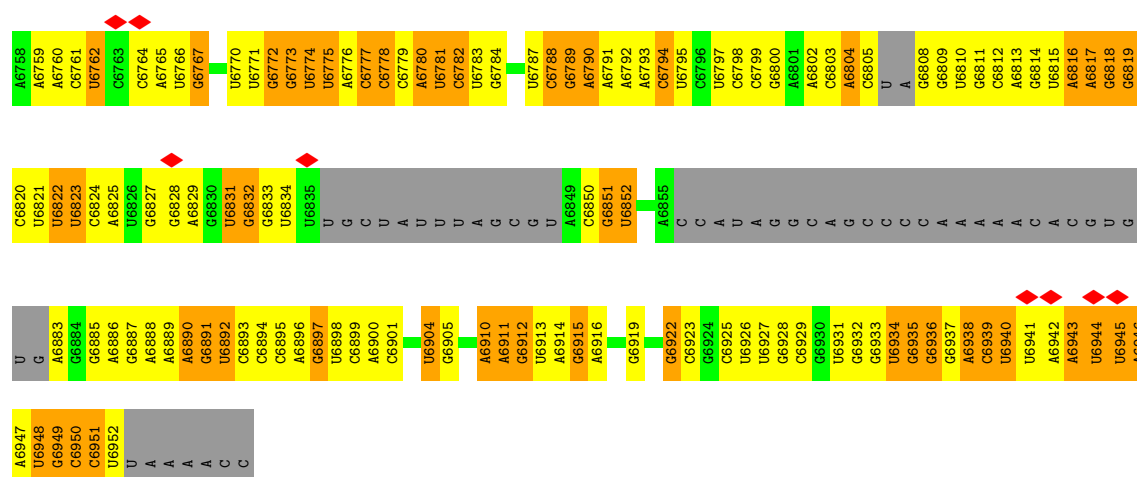
- Molecule 81: 60S acidic ribosomal protein P0

Chain V: 42% 19% 39%



- Molecule 82: Taura syndrome virus (TSV) internal ribosome entry site (IRES) RNA

Chain EC: 14% 37% 25% 24%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20205	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)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.399	Depositor
Minimum map value	-1.080	Depositor
Average map value	0.037	Depositor
Map value standard deviation	0.185	Depositor
Recommended contour level	0.3	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: 1MA, HIC, MA6, UR3, OMG, B8N, 5MC, G7M, DDE, 4AC, OMC, OMU, MG, GDP, ZN, A2M

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	0.15	0/1653	0.29	0/2261
2	BB	0.18	0/1735	0.39	0/2335
3	BC	0.16	0/1665	0.27	0/2263
4	BE	0.16	0/2109	0.32	0/2839
5	BG	0.12	0/1844	0.27	0/2464
6	BH	0.66	4/1506 (0.3%)	0.84	8/2028 (0.4%)
7	BI	0.17	0/1514	0.37	0/2021
8	BJ	0.15	0/1519	0.29	0/2035
9	BL	0.17	0/1272	0.31	0/1712
10	BN	0.18	0/1215	0.32	0/1638
11	BO	0.19	0/952	0.38	0/1279
12	BV	0.16	0/693	0.36	0/935
13	BW	0.17	0/1038	0.30	0/1395
14	BX	0.17	0/1139	0.33	0/1518
15	BY	0.13	0/1087	0.29	0/1449
16	Ba	0.19	0/782	0.40	0/1047
17	Bb	0.15	0/620	0.35	0/838
18	Be	0.14	0/483	0.34	0/643
19	BD	0.13	0/1759	0.30	0/2368
20	BF	0.13	0/1629	0.33	0/2202
21	BK	0.12	0/837	0.37	0/1131
22	BP	0.12	0/1012	0.36	0/1356
23	BQ	0.12	0/1125	0.28	0/1510
24	BR	0.17	0/1010	0.48	0/1355
25	BS	0.12	0/1211	0.35	0/1628
26	BT	0.13	0/1113	0.32	0/1494
27	BU	0.15	0/865	0.33	0/1169
28	BZ	0.13	0/566	0.35	0/761
29	Bc	0.11	0/499	0.28	0/670
30	Bd	0.13	0/453	0.27	0/602
31	Bg	0.12	0/2454	0.33	0/3340
32	Bf	0.10	0/616	0.31	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.12	0/943	0.35	0/1274
34	B5	0.19	0/41880	0.28	0/65248
35	AA	0.21	0/1912	0.33	0/2569
36	AB	0.18	0/3139	0.28	0/4219
37	AC	0.19	0/2800	0.32	0/3790
38	A1	0.22	0/75561	0.30	0/117806
39	A3	0.18	0/2883	0.25	0/4491
40	A4	0.23	0/3746	0.29	0/5832
41	AD	0.16	0/2390	0.28	0/3225
42	AE	0.16	0/1260	0.30	0/1694
43	AF	0.18	0/1821	0.28	0/2451
44	AG	0.19	0/1830	0.38	0/2469
45	AH	0.16	0/1531	0.30	0/2062
46	AI	0.16	0/1708	0.27	0/2290
47	AJ	0.14	0/1374	0.35	0/1842
48	AL	0.19	0/1568	0.30	0/2106
49	AM	0.18	0/1068	0.30	0/1438
50	AN	0.22	0/1757	0.29	0/2354
51	AO	0.18	0/1585	0.28	0/2128
52	AP	0.18	0/1410	0.28	0/1893
53	AQ	0.19	0/1465	0.29	0/1965
54	AR	0.17	0/1538	0.26	0/2050
55	AS	0.19	0/1481	0.35	0/1990
56	AT	0.18	0/1300	0.28	0/1743
57	AU	0.16	0/812	0.36	0/1099
58	AV	0.18	0/1018	0.30	0/1369
59	AW	0.17	0/533	0.26	0/707
60	AX	0.19	0/983	0.29	0/1325
61	AY	0.18	0/1004	0.28	0/1341
62	AZ	0.19	0/1118	0.30	0/1497
63	Aa	0.21	0/1204	0.30	0/1612
64	Ab	0.17	0/473	0.30	0/629
65	Ac	0.20	0/751	0.27	0/1008
66	Ad	0.17	0/904	0.28	0/1213
67	Ae	0.19	0/1041	0.28	0/1394
68	Af	0.20	0/868	0.31	0/1168
69	Ag	0.21	0/890	0.34	0/1189
70	Ah	0.19	0/978	0.30	0/1301
71	Ai	0.18	0/778	0.33	0/1034
72	Aj	0.21	0/696	0.30	0/923
73	Ak	0.17	0/618	0.30	0/826
74	Al	0.21	0/443	0.38	0/588
75	Am	0.16	0/423	0.29	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.26	0/234	0.77	1/300 (0.3%)
77	Ao	0.19	0/860	0.35	0/1136
78	Ap	0.19	0/701	0.30	0/934
79	E	0.14	0/1745	0.40	0/2342
80	DC	0.22	1/6521 (0.0%)	0.43	3/8830 (0.0%)
81	V	0.13	0/1498	0.32	0/2025
82	EC	0.13	0/3643	0.31	0/5666
All	All	0.20	5/226662 (0.0%)	0.31	12/332050 (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
43	AF	0	1
44	AG	0	1
76	An	0	1
All	All	0	5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	BH	13	PRO	CG-CD	-19.03	0.86	1.50
6	BH	13	PRO	CB-CG	13.20	2.15	1.49
80	DC	833	PRO	CG-CD	-7.15	1.26	1.50
6	BH	13	PRO	CA-CB	-6.86	1.44	1.54
6	BH	13	PRO	N-CD	5.98	1.56	1.47

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	BH	13	PRO	N-CD-CG	-19.50	73.94	103.20
6	BH	13	PRO	CA-CB-CG	-14.48	76.98	104.50
6	BH	13	PRO	CB-CG-CD	-14.25	60.49	106.10
6	BH	13	PRO	N-CA-CB	-13.90	87.14	102.85
80	DC	702	GLY	N-CA-C	-13.56	99.75	114.67
80	DC	833	PRO	N-CD-CG	-7.64	91.75	103.20
80	DC	703	GLY	N-CA-C	-6.00	105.54	112.50
6	BH	13	PRO	CA-C-N	5.83	132.19	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	BH	13	PRO	C-N-CA	5.83	132.19	121.70
6	BH	13	PRO	CB-CA-C	5.50	118.15	110.17
76	An	15	ARG	CB-CG-CD	-5.34	99.03	111.30
6	BH	13	PRO	CA-N-CD	-5.28	104.61	112.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	AF	232	ARG	Peptide
44	AG	30	THR	Peptide
76	An	15	ARG	Sidechain
6	BH	64	VAL	Peptide
11	BO	123	SER	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	56	0
2	BB	1709	0	1784	57	0
3	BC	1635	0	1723	31	0
4	BE	2068	0	2154	55	0
5	BG	1820	0	1918	61	0
6	BH	1481	0	1572	44	0
7	BI	1489	0	1525	38	0
8	BJ	1494	0	1573	38	0
9	BL	1244	0	1314	19	0
10	BN	1192	0	1255	34	0
11	BO	941	0	979	41	0
12	BV	684	0	672	25	0
13	BW	1021	0	1060	30	0
14	BX	1121	0	1196	36	0
15	BY	1073	0	1132	36	0
16	Ba	769	0	818	35	0
17	Bb	610	0	633	15	0
18	Be	475	0	525	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	BD	1734	0	1817	55	0
20	BF	1609	0	1675	61	0
21	BK	817	0	804	27	0
22	BP	991	0	1035	44	0
23	BQ	1105	0	1166	29	0
24	BR	1000	0	1063	44	0
25	BS	1192	0	1222	60	0
26	BT	1095	0	1114	52	0
27	BU	855	0	917	34	0
28	BZ	558	0	598	27	0
29	Bc	497	0	535	21	0
30	Bd	443	0	436	18	0
31	Bg	2401	0	2356	91	0
32	Bf	605	0	654	27	0
33	BM	935	0	975	37	0
34	B5	38005	0	19140	852	0
35	AA	1878	0	1946	48	0
36	AB	3081	0	3162	70	0
37	AC	2748	0	2859	51	0
38	A1	68445	0	34456	1073	0
39	A3	2579	0	1304	48	0
40	A4	3353	0	1695	51	0
41	AD	2341	0	2290	52	0
42	AE	1239	0	1326	31	0
43	AF	1784	0	1862	31	0
44	AG	1798	0	1894	32	0
45	AH	1510	0	1576	32	0
46	AI	1672	0	1711	34	0
47	AJ	1353	0	1383	45	0
48	AL	1543	0	1608	26	0
49	AM	1053	0	1149	30	0
50	AN	1720	0	1779	41	0
51	AO	1555	0	1659	36	0
52	AP	1388	0	1423	28	0
53	AQ	1441	0	1543	24	0
54	AR	1521	0	1617	31	0
55	AS	1445	0	1487	35	0
56	AT	1276	0	1323	32	0
57	AU	796	0	812	21	0
58	AV	1003	0	1048	16	0
59	AW	521	0	551	9	0
60	AX	968	0	1036	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	AY	993	0	1081	24	0
62	AZ	1092	0	1155	21	0
63	Aa	1173	0	1215	34	0
64	Ab	462	0	491	4	0
65	Ac	743	0	797	22	0
66	Ad	890	0	938	11	0
67	Ae	1020	0	1090	18	0
68	Af	850	0	880	13	0
69	Ag	880	0	945	21	0
70	Ah	969	0	1078	17	0
71	Ai	771	0	849	15	0
72	Aj	681	0	687	20	0
73	Ak	612	0	682	19	0
74	Al	436	0	475	11	0
75	Am	417	0	459	8	0
76	An	233	0	281	15	0
77	Ao	847	0	914	19	0
78	Ap	694	0	738	17	0
79	E	1718	0	1811	69	0
80	DC	6419	0	6493	264	0
81	V	1473	0	1514	53	0
82	EC	3261	0	1648	80	0
83	A1	173	0	0	0	0
83	A3	1	0	0	0	0
83	A4	1	0	0	0	0
83	AB	1	0	0	0	0
83	AP	1	0	0	0	0
83	Aj	1	0	0	0	0
83	B5	63	0	0	0	0
83	Ba	1	0	0	0	0
84	Ao	1	0	0	0	0
85	DC	28	0	11	7	0
All	All	213196	0	159694	4100	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 (4100) 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)
38:A1:237:G:HO2'	38:A1:238:A:H8	1.02	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1356:U:H3	34:B5:1367:G:H1	1.03	0.98
34:B5:1756[A]:A:H3'	38:A1:2256:A2M:H61	1.27	0.98
38:A1:3234:A:N6	38:A1:3253:G:H1	1.62	0.97
34:B5:1756[A]:A:H1'	80:DC:703:GLY:HA2	1.46	0.96
34:B5:1588:G:H1	34:B5:1608:U:H3	1.01	0.94
34:B5:976:G:H1	34:B5:1023:A:HO2'	1.17	0.92
13:BW:2:THR:N	34:B5:1034:C:HO2'	1.72	0.88
5:BG:160:ARG:HH21	5:BG:171:LYS:HD2	1.38	0.86
18:Be:55:ARG:HH22	34:B5:557:G:H4'	1.40	0.86
76:An:13:LEU:HG	76:An:17:ARG:HH21	1.39	0.86
20:BF:145:ASP:OD1	20:BF:146:THR:N	2.09	0.85
25:BS:39:GLY:H	34:B5:1566:U:H5''	1.42	0.84
80:DC:578:LYS:HD2	80:DC:582:LYS:HG3	1.59	0.84
38:A1:3234:A:H61	38:A1:3253:G:H1	0.88	0.84
38:A1:2491:A:H1'	79:E:35:GLN:HG3	1.60	0.83
34:B5:821:U:O4	34:B5:852:C:N3	2.10	0.83
82:EC:6800:G:N1	82:EC:6883:A:C2	2.47	0.83
34:B5:1575:G7M:O2'	34:B5:1576:A:O4'	1.98	0.82
34:B5:1756[A]:A:H1'	80:DC:703:GLY:CA	2.09	0.82
31:Bg:122:ILE:HB	31:Bg:134:TRP:HB2	1.61	0.81
39:A3:23:A:HO2'	39:A3:121:U:HO3'	1.26	0.81
25:BS:48:LYS:HD3	26:BT:35:ASP:HB3	1.62	0.81
40:A4:141:C:O2	50:AN:112:ASN:ND2	2.14	0.81
11:BO:125:SER:HB3	34:B5:926:A:H2	1.46	0.80
16:Ba:41:ILE:HG22	16:Ba:66:LYS:HE2	1.61	0.80
81:V:48:ARG:HH22	81:V:96:ILE:HG13	1.46	0.80
38:A1:2457:G:H21	38:A1:2483:G:H1'	1.46	0.80
80:DC:413:ILE:HB	80:DC:427:PHE:HB2	1.62	0.80
32:Bf:134:ASN:HA	32:Bf:139:LEU:HA	1.65	0.79
38:A1:171:G:H1	38:A1:246:U:H3	1.29	0.79
38:A1:173:G:H1	38:A1:244:G:H22	1.31	0.79
34:B5:868:G:H1	34:B5:960:U:H3	1.30	0.78
35:AA:21:ARG:HE	35:AA:22:LEU:HG	1.48	0.78
46:AI:130:ASP:OD1	46:AI:131:ILE:N	2.17	0.78
82:EC:6800:G:H1	82:EC:6883:A:H2	1.29	0.78
31:Bg:83:ALA:HB2	31:Bg:113:VAL:HG13	1.66	0.78
38:A1:1661:G:H2'	38:A1:1662:G:C8	2.19	0.77
81:V:139:LEU:HD11	81:V:169:GLU:HA	1.64	0.77
5:BG:13:GLN:NE2	34:B5:151:G:N3	2.33	0.77
20:BF:94:THR:HG22	20:BF:114:ILE:HG13	1.67	0.77
34:B5:69:G:H1	34:B5:82:U:H3	1.32	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AU:98:THR:OG1	57:AU:102:GLU:OE1	2.01	0.77
6:BH:108:GLN:OE1	34:B5:810:G:N2	2.17	0.77
26:BT:86:ARG:NH1	34:B5:1601:G:OP1	2.18	0.77
34:B5:1209:C:N3	34:B5:1455:G:N2	2.34	0.76
34:B5:1756[A]:A:H3'	38:A1:2256:A2M:N6	2.00	0.76
35:AA:101:VAL:HG22	35:AA:165:VAL:HG22	1.68	0.76
25:BS:69:ILE:HG22	25:BS:73:MET:HE1	1.68	0.76
80:DC:734:GLN:HG2	80:DC:767:THR:HG22	1.66	0.76
22:BP:43:ARG:NH2	34:B5:1553:G:N7	2.34	0.76
38:A1:1243:G:N2	38:A1:1270:A:O2'	2.19	0.76
38:A1:2842:U:OP1	38:A1:2844:C:N4	2.19	0.76
58:AV:33:ASN:HD21	58:AV:64:LYS:HE2	1.50	0.76
18:Be:33:ARG:HH12	34:B5:478:A:H5'	1.52	0.75
31:Bg:102:ARG:NH1	34:B5:1342:C:OP1	2.19	0.75
38:A1:2468:A:O2'	38:A1:2477:G:N2	2.19	0.75
36:AB:240:ARG:NH2	38:A1:1907:C:O2	2.19	0.75
82:EC:6777:C:O2	82:EC:6818:G:N1	2.19	0.75
34:B5:992:A:O2'	34:B5:1785:U:O2	2.04	0.75
79:E:116:LEU:HD12	79:E:119:GLN:HB3	1.67	0.75
19:BD:105:MET:HE2	19:BD:122:VAL:HG21	1.69	0.74
38:A1:182:U:H3	38:A1:234:G:H1	1.35	0.74
38:A1:2895:G:O2'	75:Am:100:TYR:O	2.04	0.74
80:DC:495:VAL:HG12	80:DC:504:LEU:HD13	1.70	0.74
80:DC:739:ALA:HB1	80:DC:788:THR:HB	1.69	0.74
47:AJ:61:ARG:HB2	77:Ao:104:LEU:HD13	1.70	0.74
19:BD:106:LYS:HD2	19:BD:175:VAL:HG22	1.68	0.74
38:A1:2478:C:OP2	38:A1:2480:A:N6	2.19	0.74
34:B5:1213:G:H1	34:B5:1450:U:H3	1.33	0.74
80:DC:496:LYS:HB2	80:DC:553:PRO:HB2	1.68	0.74
80:DC:82:SER:O	80:DC:96:ASN:ND2	2.20	0.73
5:BG:2:LYS:NZ	34:B5:154:G:OP1	2.21	0.73
22:BP:18:ARG:NH2	34:B5:1548:G:OP1	2.21	0.73
80:DC:8:GLN:NE2	80:DC:9:MET:SD	2.61	0.73
1:BA:135:GLU:OE1	34:B5:1321:A:N6	2.21	0.73
38:A1:3092:C:O2'	38:A1:3094:A:OP2	2.05	0.73
80:DC:518:VAL:HB	80:DC:537:HIS:HE1	1.54	0.73
34:B5:851:U:OP1	54:AR:165:LYS:NZ	2.21	0.73
38:A1:799:G:O2'	48:AL:18:TRP:NE1	2.22	0.73
38:A1:2673:A:OP1	47:AJ:95:ASN:ND2	2.22	0.73
27:BU:62:VAL:HG22	27:BU:85:ARG:HG3	1.71	0.73
9:BL:152:GLN:HB3	10:BN:136:PRO:HA	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:AJ:115:LYS:HG3	47:AJ:116:TYR:H	1.54	0.73
4:BE:72:VAL:HG22	4:BE:90:ILE:HG12	1.70	0.73
39:A3:5:G:OP1	47:AJ:143:ARG:NH2	2.21	0.73
20:BF:51:VAL:O	20:BF:131:GLN:NE2	2.22	0.72
80:DC:150:ARG:HH12	80:DC:196:VAL:HB	1.53	0.72
34:B5:1:U:H1'	34:B5:370:A:H5'	1.70	0.72
30:Bd:7:TRP:NE1	34:B5:1451:C:O2'	2.22	0.72
80:DC:465:LYS:HD2	80:DC:516:PRO:HA	1.70	0.72
20:BF:183:ALA:HB2	20:BF:193:THR:HG21	1.71	0.72
31:Bg:254:ALA:HB3	31:Bg:261:LYS:HB2	1.71	0.72
34:B5:1339:C:O2'	34:B5:1341:A:N7	2.23	0.72
34:B5:1591:C:H2'	34:B5:1592:A:H8	1.53	0.72
34:B5:1672:G:H2'	34:B5:1673:G:C8	2.23	0.72
36:AB:315:GLY:HA2	38:A1:3379:C:H4'	1.70	0.72
82:EC:6922:G:H1	82:EC:6931:U:H3	1.35	0.72
33:BM:135:MET:HA	33:BM:138:GLU:HG2	1.69	0.72
34:B5:1218:G:N2	34:B5:1444:A:OP2	2.21	0.72
80:DC:436:LEU:HD13	80:DC:438:MET:HE3	1.70	0.72
24:BR:49:LYS:NZ	34:B5:1390:U:OP2	2.23	0.72
58:AV:81:GLN:O	58:AV:98:ASN:ND2	2.23	0.72
36:AB:297:SER:HA	36:AB:300:ARG:HH12	1.55	0.71
80:DC:586:ILE:HD11	80:DC:688:ILE:HB	1.70	0.71
38:A1:1863:G:N1	38:A1:1866:C:OP2	2.19	0.71
79:E:117:ILE:HG22	79:E:118:LYS:HG2	1.72	0.71
15:BY:37:LYS:HG3	34:B5:522:U:H5''	1.73	0.71
26:BT:72:GLY:HA3	34:B5:1498:G:H5''	1.72	0.71
38:A1:1132:C:H2'	38:A1:1133:A2M:H8	1.71	0.71
38:A1:3160:U:H3	38:A1:3290:G:H1	1.39	0.71
1:BA:111:ILE:HD11	34:B5:1292:G:H21	1.53	0.71
29:Bc:66:LEU:HG	29:Bc:67:ARG:HG2	1.72	0.71
38:A1:245:U:H6	38:A1:245:U:H5''	1.54	0.71
82:EC:6892:U:O2'	82:EC:6943:A:N6	2.23	0.71
38:A1:714:G:HO2'	38:A1:753:C:HO2'	1.39	0.71
8:BJ:119:ALA:O	8:BJ:124:HIS:ND1	2.23	0.71
34:B5:1041:G:H2'	34:B5:1042:G:C8	2.26	0.71
79:E:54:LYS:NZ	79:E:150:ASP:OD1	2.18	0.71
34:B5:509:G:H2'	34:B5:510:G:C8	2.25	0.71
38:A1:785:G:N7	63:Aa:77:LYS:NZ	2.35	0.71
38:A1:3042:U:OP2	38:A1:3092:C:N4	2.24	0.71
34:B5:1673:G:O6	34:B5:1728:A:N1	2.25	0.70
31:Bg:34:LEU:HD21	31:Bg:42:LEU:HD23	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2474:G:N2	38:A1:2475:G:O6	2.24	0.70
21:BK:8:ARG:O	21:BK:12:HIS:ND1	2.24	0.70
30:Bd:13:ARG:NH1	34:B5:1554:U:OP1	2.23	0.70
36:AB:124:LYS:NZ	38:A1:3297:U:O4	2.23	0.70
38:A1:2207:A:H4'	38:A1:2208:A:H5'	1.74	0.70
26:BT:7:ARG:NH1	26:BT:67:MET:SD	2.64	0.70
42:AE:69:PHE:HB2	42:AE:138:GLN:HE21	1.56	0.70
52:AP:122:ALA:HB3	52:AP:143:PRO:HB2	1.73	0.70
25:BS:137:HIS:ND1	34:B5:1175:U:OP2	2.24	0.70
34:B5:871:G:H2'	34:B5:872:G:C8	2.26	0.70
81:V:16:ARG:NH1	81:V:69:ASP:OD2	2.24	0.70
34:B5:1393:C:N3	34:B5:1405:G:N1	2.34	0.70
22:BP:78:THR:HA	34:B5:1241:G:H4'	1.74	0.70
82:EC:6815:U:H3'	82:EC:6816:A:H5''	1.73	0.70
7:BI:104:ILE:HG13	7:BI:105:ASP:H	1.55	0.70
34:B5:490:C:N4	34:B5:492:A:O4'	2.25	0.69
34:B5:1561:U:H2'	34:B5:1562:G:H8	1.57	0.69
34:B5:163:G:N2	34:B5:163:G:OP2	2.23	0.69
34:B5:1160:A:H2'	34:B5:1161:C:H6	1.56	0.69
34:B5:1426:C:H3'	34:B5:1427:A:H4'	1.74	0.69
82:EC:6774:U:H2'	82:EC:6775:U:H4'	1.74	0.69
38:A1:2185:G:O2'	38:A1:2314:U:OP2	2.10	0.69
40:A4:38:U:O2'	70:Ah:83:LYS:NZ	2.24	0.69
10:BN:5:HIS:HB3	10:BN:117:LEU:HD23	1.75	0.69
38:A1:518:G:OP2	38:A1:518:G:N2	2.20	0.69
38:A1:845:G:H21	38:A1:848:A:H2	1.41	0.69
5:BG:66:GLY:HA2	34:B5:1681:A:H1'	1.75	0.69
3:BC:80:VAL:HG11	3:BC:125:ILE:HD12	1.75	0.69
39:A3:64:A:N7	46:AI:209:ASN:ND2	2.41	0.69
48:AL:123:ILE:HD11	70:Ah:116:TYR:HD2	1.55	0.69
49:AM:37:GLU:HG2	55:AS:72:VAL:HG21	1.72	0.69
50:AN:183:THR:HG22	50:AN:187:ARG:HB3	1.75	0.69
80:DC:686:VAL:HG21	80:DC:713:THR:HG23	1.74	0.69
82:EC:6787:U:OP1	82:EC:6804:A:N6	2.26	0.69
3:BC:170:ILE:HB	3:BC:197:TYR:HB2	1.74	0.69
34:B5:480:G:O6	34:B5:508:U:O2	2.11	0.69
34:B5:1505:A:H1'	34:B5:1562:G:H21	1.58	0.69
34:B5:1756[A]:A:H2'	38:A1:2256:A2M:N7	2.08	0.69
38:A1:655:C:H2'	38:A1:656:A:H8	1.56	0.69
73:Ak:32:ASN:HB3	73:Ak:36:LYS:HE3	1.74	0.69
80:DC:479:LYS:HB2	80:DC:481:MET:HE2	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1756[A]:A:H5'	38:A1:2256:A2M:N6	2.08	0.69
36:AB:284:ARG:NH1	36:AB:293:ASN:O	2.26	0.69
80:DC:811:PRO:HB3	80:DC:820:LEU:HD21	1.73	0.69
39:A3:31:U:O2'	41:AD:218:ARG:NH2	2.26	0.69
41:AD:111:GLN:HE22	41:AD:252:ALA:HA	1.56	0.69
38:A1:784:A:OP2	53:AQ:69:ARG:NH1	2.25	0.68
59:AW:12:LYS:O	59:AW:32:GLN:NE2	2.25	0.68
34:B5:591:A:H2'	34:B5:592:A:C8	2.28	0.68
34:B5:1291:G:H1	34:B5:1324:G:H22	1.42	0.68
36:AB:160:VAL:HB	36:AB:183:LEU:HD21	1.73	0.68
34:B5:1237:G:H2'	34:B5:1238:A:H8	1.57	0.68
38:A1:3016:A:H2'	38:A1:3017:A:H8	1.57	0.68
80:DC:601:ILE:HG22	80:DC:606:ILE:HB	1.75	0.68
52:AP:31:GLU:HG2	52:AP:60:PHE:HA	1.75	0.68
20:BF:92:ARG:NH2	34:B5:1613:U:OP1	2.26	0.68
34:B5:71:A:N6	34:B5:72:A:N3	2.42	0.68
21:BK:43:ILE:HD12	21:BK:64:TYR:HD2	1.58	0.68
30:Bd:36:LEU:HB3	30:Bd:38:ILE:HG22	1.75	0.68
32:Bf:105:TYR:CE1	32:Bf:131:PHE:HB3	2.28	0.68
36:AB:169:THR:HG22	36:AB:171:LEU:HD13	1.75	0.68
34:B5:814:A:H3'	54:AR:167:ARG:HG3	1.75	0.68
48:AL:4:SER:O	63:Aa:44:ASN:ND2	2.26	0.68
51:AO:22[A]:VAL:HG21	51:AO:120[A]:VAL:HG11	1.76	0.68
19:BD:75:LYS:HZ1	21:BK:18:GLU:HB3	1.59	0.68
31:Bg:192:PHE:HB3	31:Bg:223:TRP:CE2	2.27	0.68
31:Bg:200:ASN:H	31:Bg:215:GLY:HA2	1.59	0.68
34:B5:486:G:N2	34:B5:488:G:N7	2.42	0.68
40:A4:75:G:OP2	61:AY:74:TYR:OH	2.11	0.68
41:AD:144:VAL:HG23	41:AD:173:VAL:HG22	1.76	0.68
4:BE:45:ILE:HG13	4:BE:61:VAL:HG21	1.76	0.68
6:BH:48:GLU:OE1	6:BH:56:LYS:NZ	2.22	0.68
22:BP:44:ARG:NH1	22:BP:82:ASN:O	2.27	0.68
32:Bf:78:LYS:N	34:B5:1271:OMG:OP1	2.27	0.68
38:A1:1627:U:O2	38:A1:1817:G:O6	2.11	0.67
47:AJ:18:VAL:HG22	47:AJ:70:THR:HG22	1.75	0.67
5:BG:43:ASP:O	5:BG:46:LYS:NZ	2.27	0.67
34:B5:78:A:H2'	34:B5:79:C:C5	2.29	0.67
38:A1:3340:G:H3'	38:A1:3341:U:H5''	1.75	0.67
6:BH:154:LEU:HD11	6:BH:183:PHE:HD2	1.58	0.67
38:A1:3252:G:H2'	38:A1:3253:G:C8	2.29	0.67
47:AJ:52:TYR:HA	47:AJ:61:ARG:HG2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:AM:55:ARG:NH1	49:AM:76:ALA:O	2.27	0.67
8:BJ:66:ASP:HB3	8:BJ:69:ARG:HB3	1.75	0.67
38:A1:1747:G:H21	73:Ak:2:ALA:HB3	1.59	0.67
38:A1:2553:U:C4	69:Ag:95:ILE:HG22	2.30	0.67
4:BE:44:LEU:HD23	4:BE:82:TYR:HB3	1.75	0.67
4:BE:50:ASN:O	4:BE:53:LYS:NZ	2.26	0.67
36:AB:287:LYS:O	36:AB:293:ASN:ND2	2.21	0.67
38:A1:284:A:OP2	77:Ao:41:ARG:NH1	2.28	0.67
45:AH:162:GLN:HE21	45:AH:180:TYR:HD1	1.43	0.67
46:AI:54:SER:HB2	46:AI:135:ILE:HD11	1.77	0.67
38:A1:3340:G:O2'	38:A1:3342:A:OP2	2.13	0.67
65:Ac:103:THR:HG22	65:Ac:105:ALA:H	1.59	0.67
82:EC:6759:A:H2'	82:EC:6760:A:C8	2.30	0.67
15:BY:132:ARG:NH1	34:B5:155:U:OP2	2.28	0.67
22:BP:122:THR:O	34:B5:1183:A:N6	2.28	0.67
38:A1:2469:G:N1	38:A1:2477:G:O6	2.27	0.67
68:Af:16:TYR:OH	68:Af:89:LEU:O	2.12	0.67
2:BB:27:LYS:HD3	2:BB:47:LEU:HD13	1.76	0.67
31:Bg:299:GLN:HG2	31:Bg:300:THR:HG23	1.77	0.67
4:BE:63:ALA:O	4:BE:67:GLN:NE2	2.28	0.67
31:Bg:89:LEU:HB2	31:Bg:103:PHE:HB2	1.76	0.67
34:B5:1294:G:O2'	34:B5:1321:A:N1	2.23	0.67
38:A1:649:A2M:OP2	38:A1:2868:U:O2'	2.12	0.67
47:AJ:36:VAL:HG21	47:AJ:110:ILE:HD12	1.77	0.67
80:DC:223:ARG:HA	80:DC:241:MET:HE1	1.76	0.67
2:BB:86:LEU:HB3	2:BB:98:THR:HG21	1.76	0.67
6:BH:135:ILE:HG21	6:BH:138:LYS:HE3	1.76	0.67
20:BF:77:TYR:HB3	20:BF:84:LYS:HA	1.76	0.67
38:A1:1873:U:OP1	54:AR:21:LYS:NZ	2.28	0.67
56:AT:142:SER:OG	56:AT:144:GLU:OE1	2.13	0.67
34:B5:851:U:OP2	54:AR:173:ARG:NH2	2.28	0.66
34:B5:1241:G:OP1	34:B5:1241:G:N2	2.26	0.66
73:Ak:26:LYS:NZ	73:Ak:28:ASN:OD1	2.28	0.66
2:BB:134:VAL:HG12	2:BB:219:LYS:HG2	1.75	0.66
19:BD:115:ILE:HD13	19:BD:142:LEU:HD22	1.77	0.66
21:BK:77:ARG:NH2	21:BK:87:VAL:O	2.27	0.66
34:B5:1474:G:H2'	34:B5:1475:A:H8	1.58	0.66
47:AJ:165:GLN:HG2	47:AJ:166:LYS:H	1.59	0.66
14:BX:65:ASN:ND2	14:BX:116:ASP:OD2	2.28	0.66
20:BF:117:THR:HG21	20:BF:194:LEU:HD23	1.77	0.66
34:B5:108:A:H2'	34:B5:109:G:C8	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2454:G:OP2	38:A1:2484:A:N6	2.28	0.66
51:AO:65[A]:ASN:HB3	51:AO:68[A]:ARG:HG2	1.74	0.66
77:Ao:6:LYS:HG3	77:Ao:94:GLY:HA3	1.77	0.66
14:BX:18:HIS:O	14:BX:22:ASN:ND2	2.24	0.66
34:B5:1393:C:O2	34:B5:1405:G:N2	2.17	0.66
23:BQ:128:LYS:HB2	23:BQ:137:ARG:HH22	1.61	0.66
38:A1:681:U:O2	38:A1:696:C:N4	2.22	0.66
45:AH:163:GLN:OE1	45:AH:166:ARG:NH2	2.28	0.66
80:DC:610:ASP:HB3	80:DC:615:ARG:HB3	1.77	0.66
80:DC:674:GLY:H	80:DC:678:GLY:HA2	1.60	0.66
82:EC:6800:G:N1	82:EC:6883:A:H2	1.90	0.66
34:B5:891:A:H2'	34:B5:892:A:H8	1.60	0.66
80:DC:17:THR:O	80:DC:91:GLN:NE2	2.28	0.66
7:BI:152:ILE:HG13	7:BI:153:GLU:H	1.59	0.66
24:BR:20:TYR:HE2	24:BR:34:LEU:HD11	1.61	0.66
36:AB:93:VAL:HG12	36:AB:155:ALA:H	1.61	0.66
38:A1:2383:C:OP2	51:AO:85[A]:ARG:NH2	2.28	0.66
51:AO:61[A]:ALA:HA	51:AO:70[A]:PRO:HD2	1.78	0.66
24:BR:76:GLU:HA	24:BR:79:GLU:HG3	1.78	0.66
26:BT:69:LYS:HG2	34:B5:1367:G:H5''	1.78	0.66
34:B5:1499:G:H1	34:B5:1508:U:H3	1.44	0.66
38:A1:3174:A:H61	68:Af:54:ARG:HH21	1.44	0.66
1:BA:79:ARG:NH1	1:BA:164:ASN:O	2.24	0.65
34:B5:867:G:H1	34:B5:961:U:H3	1.43	0.65
81:V:144:LYS:HZ3	81:V:145:ILE:H	1.44	0.65
20:BF:104:ASN:OD1	34:B5:1587:A:O2'	2.15	0.65
27:BU:74:GLU:OE2	34:B5:1429:G:H1'	1.97	0.65
34:B5:1594:G:OP2	34:B5:1596:C:N4	2.29	0.65
56:AT:39:ILE:HD12	56:AT:102:ARG:HD2	1.76	0.65
33:BM:43:ARG:HG2	33:BM:103:LEU:HD13	1.78	0.65
38:A1:2568:C:O2'	38:A1:2569:A:O4'	2.14	0.65
38:A1:2897:A:H5''	75:Am:125:LYS:HD2	1.78	0.65
62:AZ:72:ILE:HD11	62:AZ:107:ARG:HG2	1.78	0.65
80:DC:633:ILE:HB	80:DC:645:LEU:HD12	1.78	0.65
4:BE:141:THR:OG1	4:BE:143:ASP:OD1	2.13	0.65
31:Bg:42:LEU:HB2	31:Bg:61:PHE:HB2	1.77	0.65
34:B5:1160:A:H2'	34:B5:1161:C:C6	2.31	0.65
38:A1:576:C:OP1	43:AF:241:LYS:NZ	2.28	0.65
38:A1:627:U:H2'	38:A1:628:A:C8	2.31	0.65
38:A1:2207:A:H5'	38:A1:2208:A:H2	1.61	0.65
38:A1:2515:A:N1	38:A1:2594:C:N4	2.42	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:E:10:ARG:NH2	79:E:177:ASP:OD1	2.29	0.65
34:B5:110:U:OP1	34:B5:753:A:O2'	2.14	0.65
37:AC:20:LEU:HD11	37:AC:252:GLU:HG2	1.77	0.65
38:A1:2700:G:H5''	56:AT:17:ARG:HG2	1.77	0.65
54:AR:86:GLU:OE2	54:AR:91:SER:OG	2.12	0.65
71:AI:59:ASP:OD1	71:AI:63:ASN:ND2	2.29	0.65
79:E:147:LYS:HA	79:E:150:ASP:HB2	1.79	0.65
14:BX:70:LYS:NZ	34:B5:567:A:OP1	2.30	0.65
38:A1:1114:U:OP1	63:Aa:23:GLY:N	2.26	0.65
38:A1:1390:A:N6	38:A1:1418:A:O2'	2.30	0.65
41:AD:211:LEU:HB3	41:AD:219:PHE:HB2	1.79	0.65
58:AV:14:SER:O	58:AV:81:GLN:NE2	2.29	0.65
27:BU:26:LEU:HG	27:BU:114:VAL:HG22	1.79	0.65
34:B5:778:G:H2'	34:B5:779:U:H2'	1.79	0.65
38:A1:2960:C:H2'	38:A1:2961:G:C8	2.31	0.65
52:AP:18:ARG:NH1	52:AP:147:GLU:OE1	2.30	0.65
8:BJ:83:VAL:HA	8:BJ:149:ARG:HA	1.78	0.65
24:BR:36:ASP:OD1	24:BR:47:ARG:NH1	2.29	0.65
38:A1:1544:G:O2'	38:A1:2167:A:N3	2.28	0.65
38:A1:1899:G:O2'	38:A1:2334:U:O4	2.09	0.65
74:AI:10:LYS:HA	74:AI:13:MET:HE2	1.78	0.65
14:BX:46:SER:OG	14:BX:78:LYS:NZ	2.29	0.65
7:BI:2:GLY:N	34:B5:393:C:OP2	2.30	0.65
10:BN:62:GLN:HB2	10:BN:65:VAL:HG22	1.79	0.65
28:BZ:82:HIS:HD2	28:BZ:85:LYS:HE2	1.62	0.65
33:BM:97:LEU:HA	33:BM:100:TRP:NE1	2.11	0.65
34:B5:1683:C:O2'	34:B5:1684:U:O5'	2.15	0.65
38:A1:1601:U:OP1	54:AR:42:ARG:NH2	2.30	0.65
38:A1:1631:C:OP2	62:AZ:48:ARG:NH2	2.29	0.65
34:B5:800:U:H2'	34:B5:801:G:H8	1.62	0.64
38:A1:1447:G:N2	38:A1:2356:A:OP2	2.27	0.64
19:BD:176:LEU:HD11	34:B5:1437:U:H4'	1.79	0.64
22:BP:89:MET:O	22:BP:92:SER:OG	2.14	0.64
24:BR:101:ASN:HD21	24:BR:122:ILE:HG13	1.63	0.64
31:Bg:243:LEU:HD22	31:Bg:252:LEU:HD11	1.78	0.64
32:Bf:80:ARG:NH1	34:B5:1209:C:OP1	2.30	0.64
34:B5:1226:A:N6	34:B5:1258:U:O4	2.30	0.64
49:AM:48:GLY:HA3	49:AM:53:VAL:HB	1.78	0.64
79:E:13:VAL:HG22	79:E:17:LEU:HD23	1.80	0.64
20:BF:148:ARG:HD2	20:BF:155:ALA:HB1	1.79	0.64
29:Bc:12:VAL:HG22	29:Bc:30:VAL:HG12	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Bf:82:LYS:HD3	80:DC:631:ARG:HH21	1.62	0.64
36:AB:85:VAL:HG22	36:AB:202:THR:HG22	1.80	0.64
8:BJ:50:SER:OG	8:BJ:54:ARG:NH2	2.28	0.64
23:BQ:13:LYS:HG3	23:BQ:14:LYS:H	1.62	0.64
31:Bg:256:THR:OG1	31:Bg:259:GLY:O	2.14	0.64
35:AA:21:ARG:HG3	38:A1:824:C:H5''	1.78	0.64
38:A1:2648:G:OP1	46:AI:24:ARG:NH2	2.30	0.64
47:AJ:90:GLN:NE2	47:AJ:174:LYS:O	2.31	0.64
80:DC:171:LYS:NZ	80:DC:279:ASP:OD1	2.27	0.64
3:BC:143:TYR:O	13:BW:98:GLN:NE2	2.30	0.64
34:B5:227:U:H2'	34:B5:228:G:H8	1.61	0.64
34:B5:1213:G:N2	34:B5:1450:U:O2	2.29	0.64
36:AB:10:ARG:NH2	36:AB:263:SER:O	2.29	0.64
36:AB:226:PHE:O	38:A1:1886:A:O2'	2.15	0.64
38:A1:718:G:OP1	63:Aa:117:ARG:NH2	2.25	0.64
38:A1:959:C:O2'	38:A1:2410:U:N3	2.30	0.64
38:A1:2767:U:O2'	77:Ao:30:ALA:O	2.15	0.64
40:A4:150:G:OP1	60:AX:27:ARG:NH2	2.30	0.64
79:E:194:LEU:HD13	79:E:200:ASN:HD21	1.62	0.64
5:BG:137:ARG:HD3	5:BG:177:ARG:HD2	1.78	0.64
34:B5:146:U:H2'	34:B5:147:A:H8	1.62	0.64
38:A1:1256:G:H2'	38:A1:1257:C:C6	2.33	0.64
40:A4:103:G:OP2	40:A4:105:A:O2'	2.16	0.64
51:AO:84[A]:LEU:HD13	51:AO:102[A]:LEU:HD21	1.78	0.64
56:AT:88:ARG:NH1	64:Ab:33:LYS:O	2.31	0.64
57:AU:98:THR:HG22	57:AU:104:ARG:HH11	1.63	0.64
82:EC:6783:U:H2'	82:EC:6784:G:C8	2.33	0.64
25:BS:25:ASN:O	25:BS:57:ARG:NH1	2.30	0.64
34:B5:736:C:N4	34:B5:737:A:H62	1.96	0.64
38:A1:74:G:H5''	48:AL:104:ARG:HH11	1.61	0.64
38:A1:651:G:O2'	38:A1:1435:A:OP1	2.15	0.64
44:AG:78:PHE:O	44:AG:79:GLN:HG3	1.98	0.64
8:BJ:37:LYS:HA	18:Be:33:ARG:HB3	1.80	0.64
38:A1:412:G:OP1	52:AP:62:ARG:NH1	2.31	0.64
79:E:100:ILE:HD12	79:E:127:GLN:HB2	1.80	0.64
8:BJ:59:LEU:HD11	8:BJ:69:ARG:HA	1.79	0.64
24:BR:124:VAL:HG22	24:BR:125:SER:H	1.63	0.64
34:B5:1488:G:O2'	34:B5:1494:C:O2	2.14	0.64
38:A1:900:G:H1'	38:A1:1589:A:N6	2.13	0.64
38:A1:2483:G:N7	79:E:101:LYS:NZ	2.45	0.64
38:A1:2786:G:N2	63:Aa:58:MET:SD	2.68	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AZ:41:ALA:HB2	62:AZ:77:TYR:HE1	1.62	0.64
25:BS:36:LYS:HB3	25:BS:102:ALA:HA	1.79	0.64
38:A1:1799:A:H2'	38:A1:1800:A:C8	2.32	0.64
81:V:42:ARG:HH21	81:V:51:VAL:HB	1.63	0.64
10:BN:11:ILE:HG13	10:BN:12:SER:H	1.63	0.63
19:BD:94:ARG:NH1	19:BD:125:TYR:OH	2.30	0.63
38:A1:2555:G:N7	69:Ag:95:ILE:HD11	2.12	0.63
38:A1:3234:A:N1	38:A1:3253:G:N2	2.40	0.63
40:A4:39:G:O2'	40:A4:105:A:N1	2.31	0.63
1:BA:200:ASP:HB2	24:BR:90:ALA:HB1	1.81	0.63
38:A1:362:U:O4	72:Aj:24:ARG:NH2	2.31	0.63
49:AM:107:GLU:OE1	49:AM:107:GLU:N	2.32	0.63
51:AO:125[A]:ARG:HG3	51:AO:129[A]:LEU:HD12	1.79	0.63
56:AT:49:GLN:HA	56:AT:52:MET:HE3	1.81	0.63
79:E:63:MET:HE2	79:E:152:ARG:HG3	1.78	0.63
1:BA:150:ASP:OD2	1:BA:165:ARG:NH2	2.30	0.63
3:BC:95:ARG:HH22	3:BC:97:ARG:HH21	1.47	0.63
26:BT:38:LYS:NZ	34:B5:1564:U:OP1	2.24	0.63
31:Bg:20:VAL:HG11	31:Bg:310:ILE:HD11	1.80	0.63
38:A1:1786:G:H2'	38:A1:1787:A:C8	2.34	0.63
31:Bg:13:LEU:HB2	31:Bg:310:ILE:HB	1.79	0.63
34:B5:1182:U:H3	34:B5:1185:U:H5''	1.64	0.63
38:A1:1183:C:OP1	55:AS:158:LYS:NZ	2.32	0.63
38:A1:1211:U:O2'	55:AS:113:ARG:NH1	2.32	0.63
38:A1:1350:A:H4'	38:A1:1351:U:O5'	1.99	0.63
38:A1:1727:G:OP1	78:Ap:44:LYS:NZ	2.31	0.63
40:A4:94:C:OP1	72:Aj:75:LYS:NZ	2.31	0.63
7:BI:16:ALA:HB2	34:B5:354:C:H5''	1.80	0.63
12:BV:36:VAL:HB	12:BV:51:VAL:HG23	1.81	0.63
34:B5:65:A:H2	34:B5:84:A:H62	1.45	0.63
34:B5:198:A:H3'	34:B5:199:G:H8	1.63	0.63
38:A1:664:U:H2'	38:A1:665:A:C8	2.32	0.63
38:A1:1634:G:N7	62:AZ:17:ARG:NH1	2.46	0.63
38:A1:2697:A:H2'	38:A1:2698:G:C8	2.33	0.63
63:Aa:24:LYS:O	63:Aa:26:ARG:HG2	1.97	0.63
6:BH:150:GLN:HB3	6:BH:181:ILE:HG22	1.80	0.63
7:BI:57:ALA:HB2	7:BI:177:GLY:HA2	1.80	0.63
34:B5:736:C:H42	34:B5:737:A:H62	1.47	0.63
38:A1:655:C:H2'	38:A1:656:A:C8	2.32	0.63
73:Ak:23:ALA:HB3	73:Ak:75:VAL:HG22	1.79	0.63
80:DC:563:TYR:O	80:DC:564:ARG:NH1	2.27	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:636:PHE:O	80:DC:642:GLY:N	2.31	0.63
38:A1:879:U:O2'	52:AP:135:ARG:NH2	2.32	0.63
38:A1:1233:G:H2'	38:A1:1234:G:C8	2.34	0.63
38:A1:2697:A:H2'	38:A1:2698:G:H8	1.62	0.63
38:A1:2960:C:H2'	38:A1:2961:G:H8	1.62	0.63
34:B5:1175:U:H2'	34:B5:1176:G:C8	2.34	0.63
34:B5:1673:G:H1	34:B5:1728:A:H2	1.43	0.63
34:B5:1775:U:OP1	76:An:11:ARG:NH2	2.30	0.63
38:A1:1622:U:H2'	38:A1:1623:G:H8	1.64	0.63
38:A1:1694:U:H5	38:A1:1752:A:N1	1.97	0.63
56:AT:18:ASP:HB2	56:AT:21:LYS:HB2	1.79	0.63
81:V:69:ASP:OD1	81:V:70:LEU:N	2.32	0.63
38:A1:938:C:OP2	63:Aa:26:ARG:NH1	2.32	0.63
38:A1:2449:A:H2'	38:A1:2450:G:C8	2.34	0.63
79:E:13:VAL:HG11	79:E:180:VAL:HG12	1.80	0.63
81:V:26:PHE:HB3	81:V:87:VAL:HB	1.79	0.63
8:BJ:132:ARG:NH2	34:B5:532:U:OP1	2.32	0.62
31:Bg:174:ASN:O	31:Bg:198:ASN:ND2	2.29	0.62
33:BM:42:ALA:HB3	33:BM:122:VAL:HB	1.80	0.62
34:B5:809:A:H2'	34:B5:810:G:C8	2.34	0.62
38:A1:398:A:N7	52:AP:3:ARG:NH2	2.47	0.62
38:A1:1093:A:H5'	38:A1:1096:U:O4	1.99	0.62
1:BA:183:ARG:O	12:BV:44:ARG:NH2	2.33	0.62
15:BY:60:PHE:H	15:BY:71:GLY:HA2	1.64	0.62
19:BD:55:THR:HA	19:BD:58:VAL:HG12	1.81	0.62
50:AN:46:ASP:OD1	50:AN:47:LYS:N	2.30	0.62
5:BG:5:ILE:HG22	5:BG:111:LEU:HD12	1.81	0.62
34:B5:1672:G:H2'	34:B5:1673:G:H8	1.64	0.62
38:A1:775:A:O2'	38:A1:777:U:OP2	2.18	0.62
18:Be:55:ARG:NH2	18:Be:57:ASN:O	2.32	0.62
31:Bg:179:LYS:HD3	31:Bg:188:ILE:HD13	1.80	0.62
38:A1:177:U:O2	38:A1:241:G:C6	2.51	0.62
6:BH:127:GLU:OE2	10:BN:21:ASN:ND2	2.33	0.62
19:BD:207:THR:OG1	24:BR:40:THR:OG1	2.18	0.62
34:B5:29:U:H2'	34:B5:30:G:H8	1.65	0.62
38:A1:591:G:N2	38:A1:612:U:OP1	2.26	0.62
38:A1:1477:A:OP1	38:A1:3075:G:O2'	2.14	0.62
38:A1:2373:A:N3	38:A1:2824:G:O2'	2.30	0.62
80:DC:704:GLN:O	80:DC:707:PRO:HD2	2.00	0.62
18:Be:15:LYS:NZ	34:B5:585:A:OP1	2.32	0.62
38:A1:1348:U:OP1	53:AQ:39:ARG:NH1	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:AT:48:ILE:HD11	56:AT:94:GLU:HB2	1.81	0.62
80:DC:150:ARG:NH2	80:DC:351:TYR:O	2.26	0.62
3:BC:142:GLY:HA2	12:BV:1:MET:HE1	1.81	0.62
12:BV:79:LEU:HD13	12:BV:82:VAL:HG11	1.82	0.62
25:BS:108:LYS:HA	25:BS:111:ASP:HB2	1.82	0.62
38:A1:806:A:N3	38:A1:2812:C:O2'	2.32	0.62
38:A1:2228:A:H2'	38:A1:2229:A:C8	2.35	0.62
78:Ap:46:THR:OG1	78:Ap:57:CYS:SG	2.57	0.62
80:DC:83:ASP:HA	80:DC:96:ASN:HD21	1.63	0.62
3:BC:82:ASN:HB2	3:BC:207:LEU:HD23	1.81	0.62
33:BM:29:LYS:HA	33:BM:100:TRP:CZ3	2.35	0.62
38:A1:792:G:H5''	63:Aa:2:PRO:HD3	1.82	0.62
38:A1:3050:U:O2'	59:AW:16:GLY:O	2.14	0.62
19:BD:36:GLY:H	19:BD:51:ARG:HB2	1.65	0.62
25:BS:14:ILE:HG22	25:BS:23:ASP:HA	1.82	0.62
77:Ao:65:THR:O	77:Ao:87:ARG:NH1	2.33	0.62
10:BN:14:SER:HB3	34:B5:959:U:H5''	1.82	0.62
33:BM:78:LEU:O	33:BM:84:ASN:ND2	2.33	0.62
36:AB:180:GLU:OE2	38:A1:3002:C:O2'	2.16	0.62
38:A1:1203:A:H2'	38:A1:1204:A:C8	2.34	0.62
38:A1:1696:A:H2'	38:A1:1697:A:C8	2.35	0.62
47:AJ:50:ALA:HB2	47:AJ:65:ILE:HG12	1.82	0.62
32:Bf:143:LYS:NZ	34:B5:1254:U:OP1	2.32	0.61
37:AC:119:ARG:NH2	38:A1:696:C:OP2	2.33	0.61
38:A1:1242:G:H2'	38:A1:1243:G:C8	2.35	0.61
38:A1:2772:C:H4'	38:A1:2773:C:H5'	1.82	0.61
41:AD:208:MET:HB2	41:AD:219:PHE:HE1	1.65	0.61
80:DC:579:SER:OG	80:DC:581:ASN:OD1	2.13	0.61
80:DC:747:LEU:HA	80:DC:750:LYS:HB2	1.80	0.61
9:BL:57:LYS:HG2	9:BL:131:ILE:HD12	1.81	0.61
20:BF:63:GLN:HE22	20:BF:66:GLN:HB3	1.64	0.61
34:B5:1773:4AC:OP1	76:An:2:ARG:HB3	2.00	0.61
79:E:55:LEU:HD23	79:E:182:GLN:HG2	1.83	0.61
80:DC:409:GLN:HE22	80:DC:471:THR:HG21	1.65	0.61
69:Ag:3:GLN:HE22	69:Ag:29:ILE:HB	1.65	0.61
11:BO:136:ARG:NH2	34:B5:1785:U:OP1	2.29	0.61
27:BU:58:LEU:HB2	27:BU:88:LYS:HB3	1.82	0.61
32:Bf:135:HIS:HE2	34:B5:1250:U:HO2'	1.44	0.61
34:B5:227:U:H2'	34:B5:228:G:C8	2.35	0.61
34:B5:1490:C:H1'	34:B5:1492:A:C6	2.36	0.61
34:B5:1593:A:H2'	34:B5:1594:G:H8	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1710:U:H2'	34:B5:1711:C:C6	2.35	0.61
38:A1:1378:U:H2'	38:A1:1379:G:H8	1.65	0.61
51:AO:4[A]:GLU:OE1	51:AO:4[A]:GLU:N	2.34	0.61
54:AR:175:GLN:HG2	54:AR:176:ARG:HD3	1.82	0.61
72:Aj:29:VAL:O	72:Aj:32:LYS:NZ	2.27	0.61
5:BG:154:ARG:NH2	34:B5:78:A:OP2	2.33	0.61
10:BN:54:LEU:HB3	10:BN:60:VAL:HG21	1.83	0.61
25:BS:67:GLU:HA	25:BS:70:VAL:HG12	1.83	0.61
30:Bd:17:GLY:N	34:B5:1205:C:O2	2.33	0.61
34:B5:1146:G:H2'	34:B5:1147:A:C8	2.35	0.61
34:B5:1280:4AC:H2'	34:B5:1281:G:C8	2.35	0.61
37:AC:31:ARG:NH2	37:AC:33:ASP:OD2	2.32	0.61
38:A1:216:G:OP1	61:AY:16:ARG:NH1	2.32	0.61
38:A1:1805:C:H2'	38:A1:1806:A:H8	1.66	0.61
1:BA:198:MET:HE2	24:BR:90:ALA:HB3	1.81	0.61
19:BD:72:LEU:HD22	21:BK:65:TYR:HD2	1.66	0.61
34:B5:1619:C:H2'	34:B5:1620:C:H6	1.66	0.61
38:A1:1186:G:OP2	49:AM:42:LYS:NZ	2.28	0.61
38:A1:1448:U:H2'	38:A1:1449:A2M:H8	1.83	0.61
38:A1:3324:C:OP1	66:Ad:19:ARG:NH1	2.30	0.61
58:AV:54:LEU:HD11	58:AV:119:GLY:HA3	1.83	0.61
69:Ag:51:LEU:HB3	69:Ag:54:ILE:HD12	1.82	0.61
80:DC:126:LEU:HD12	80:DC:338:ILE:HD11	1.83	0.61
4:BE:105:VAL:HG21	4:BE:245:LYS:H	1.65	0.61
34:B5:710:U:H2'	34:B5:728:U:H3	1.64	0.61
44:AG:195:SER:OG	44:AG:197:VAL:O	2.19	0.61
62:AZ:70:PRO:HG3	62:AZ:115:LYS:HB2	1.83	0.61
18:Be:55:ARG:NH1	34:B5:557:G:OP1	2.34	0.61
34:B5:655:G:H22	34:B5:677:G:H3'	1.65	0.61
34:B5:1552:U:H2'	34:B5:1553:G:C8	2.36	0.61
34:B5:1584:G:N2	34:B5:1611:A:OP2	2.34	0.61
38:A1:307:A:H2'	38:A1:308:A:C8	2.35	0.61
80:DC:406:LYS:HB3	80:DC:409:GLN:HB2	1.82	0.61
28:BZ:57:TYR:HD2	28:BZ:60:VAL:HG22	1.65	0.61
34:B5:1488:G:H3'	34:B5:1515:A:H61	1.64	0.61
34:B5:1693:A:N1	34:B5:1709:C:N4	2.48	0.61
36:AB:219:ALA:HB2	36:AB:336:VAL:HG23	1.82	0.61
37:AC:3:ARG:HB3	37:AC:22:LEU:H	1.66	0.61
38:A1:307:A:H2'	38:A1:308:A:H8	1.65	0.61
38:A1:2160:G:H2'	38:A1:2161:G:H8	1.65	0.61
38:A1:2964:G:N2	38:A1:2967:A:OP2	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3277:U:O4	52:AP:172:GLN:NE2	2.25	0.61
1:BA:2:SER:OG	1:BA:3:LEU:N	2.32	0.61
11:BO:131:GLY:O	16:Ba:22:ARG:NH2	2.34	0.61
34:B5:1280:4AC:H2'	34:B5:1281:G:H8	1.64	0.61
38:A1:1222:G:OP2	81:V:57:THR:OG1	2.19	0.61
38:A1:2464:U:OP1	38:A1:2485:A:O2'	2.18	0.61
38:A1:3333:G:N2	38:A1:3369:G:O2'	2.34	0.61
39:A3:32:U:H5'	41:AD:218:ARG:HH22	1.66	0.61
45:AH:10:ILE:HB	45:AH:53:ILE:HB	1.83	0.61
57:AU:32:SER:OG	57:AU:83:TYR:OH	2.19	0.61
79:E:128:LEU:HD21	79:E:135:PRO:HD3	1.83	0.61
82:EC:6764:C:H2'	82:EC:6765:A:H8	1.66	0.61
3:BC:88:LYS:HD2	3:BC:95:ARG:HH21	1.65	0.60
32:Bf:121:CYS:HB3	32:Bf:130:VAL:HG11	1.83	0.60
34:B5:900:A:H3'	34:B5:901:G:H21	1.66	0.60
36:AB:147:GLU:OE1	36:AB:150:ARG:NH2	2.31	0.60
14:BX:54:LEU:HD11	14:BX:75:GLN:HB2	1.83	0.60
20:BF:139:ASN:ND2	20:BF:202:ALA:O	2.34	0.60
29:Bc:27:GLN:NE2	29:Bc:64:ARG:O	2.34	0.60
34:B5:1393:C:H2'	34:B5:1394:G:H8	1.66	0.60
34:B5:1503:A:H2'	34:B5:1504:G:C8	2.36	0.60
38:A1:627:U:H2'	38:A1:628:A:H8	1.66	0.60
38:A1:2875:U:O2'	38:A1:2876:C:O5'	2.18	0.60
47:AJ:101:ASN:HD22	47:AJ:130:VAL:HA	1.66	0.60
50:AN:159:ARG:HG2	50:AN:164:LEU:HB2	1.82	0.60
80:DC:15:LYS:HZ2	80:DC:16:VAL:H	1.49	0.60
26:BT:70:GLN:NE2	26:BT:119:LYS:O	2.28	0.60
38:A1:38:U:H4'	63:Aa:32:ARG:HD2	1.84	0.60
38:A1:831:G:O2'	38:A1:1864:A:N3	2.32	0.60
38:A1:2115:G:H22	38:A1:2120:A:H1'	1.65	0.60
38:A1:2497:U:O2'	38:A1:2498:U:O5'	2.17	0.60
38:A1:2507:C:H2'	38:A1:2508:U:C6	2.37	0.60
51:AO:178[A]:VAL:O	51:AO:182[A]:ASN:ND2	2.35	0.60
71:Ai:60:LEU:HD23	71:Ai:68:ARG:HD3	1.82	0.60
73:Ak:5:ILE:HG23	73:Ak:10:GLN:HE21	1.65	0.60
80:DC:743:ILE:HG22	80:DC:784:LEU:HD22	1.81	0.60
6:BH:63:PRO:C	6:BH:65:PRO:HD3	2.26	0.60
7:BI:56:ARG:HH22	34:B5:332:U:P	2.24	0.60
19:BD:141:LYS:HA	19:BD:147:ALA:HA	1.83	0.60
34:B5:183:U:H2'	34:B5:184:C:C6	2.37	0.60
34:B5:343:C:H2'	34:B5:344:A:H8	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:220:VAL:O	36:AB:334:ARG:NH1	2.35	0.60
19:BD:120:TYR:HB3	19:BD:124:ARG:HH21	1.65	0.60
34:B5:1171:A:H2'	34:B5:1172:G:C8	2.36	0.60
38:A1:571:U:H2'	38:A1:572:A:H8	1.67	0.60
80:DC:249:PHE:CE1	80:DC:271:ARG:HG2	2.37	0.60
1:BA:65:ALA:HB2	1:BA:181:VAL:HG23	1.82	0.60
9:BL:122:ILE:HG23	9:BL:143:SER:HB2	1.83	0.60
35:AA:10:LYS:O	38:A1:2163:C:O2'	2.18	0.60
38:A1:499:G:OP1	68:Af:48:ARG:NH2	2.34	0.60
40:A4:8:C:H2'	40:A4:9:A:H8	1.66	0.60
77:Ao:61:LYS:NZ	77:Ao:63:LYS:O	2.28	0.60
80:DC:26:ALA:HB2	80:DC:128:VAL:HB	1.84	0.60
82:EC:6828:G:H2'	82:EC:6829:A:H8	1.66	0.60
31:Bg:248:ASN:OD1	31:Bg:249:ARG:N	2.33	0.60
34:B5:436:A2M:H8	34:B5:436:A2M:O5'	2.01	0.60
44:AG:107:GLU:HA	44:AG:110:THR:HB	1.82	0.60
80:DC:701:GLY:O	80:DC:705:ILE:HG12	2.01	0.60
9:BL:37:ASN:O	34:B5:247:A:O2'	2.17	0.60
21:BK:35:ILE:HG22	21:BK:37:THR:HG22	1.83	0.60
27:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	1.84	0.60
34:B5:823:G:O6	34:B5:850:A:N6	2.34	0.60
38:A1:2677:G:H21	38:A1:2679:A:H5''	1.67	0.60
38:A1:2988:C:OP1	51:AO:65[A]:ASN:ND2	2.31	0.60
81:V:100:ILE:HB	81:V:185:LEU:HD11	1.82	0.60
5:BG:32:ILE:HD12	5:BG:54:GLY:HA2	1.83	0.60
38:A1:19:U:H2'	38:A1:20:A:C8	2.36	0.60
38:A1:2138:A:HO2'	72:Aj:2:GLY:N	2.00	0.60
38:A1:3016:A:H2'	38:A1:3017:A:C8	2.35	0.60
48:AL:3:ILE:HD13	63:Aa:45:MET:HE2	1.83	0.60
77:Ao:72:LEU:HD11	77:Ao:83:LEU:HD12	1.84	0.60
80:DC:464:LEU:O	80:DC:465:LYS:HG2	2.02	0.60
25:BS:145:ARG:NH2	34:B5:1543:A:O2'	2.31	0.60
34:B5:1351:G:H2'	34:B5:1352:G:C8	2.36	0.60
34:B5:1524:A:H2'	34:B5:1525:A:C8	2.37	0.60
35:AA:69:TYR:OH	38:A1:2557:A:OP1	2.16	0.60
46:AI:156:ARG:HG3	46:AI:163:GLN:HB2	1.84	0.60
6:BH:64:VAL:HB	6:BH:94:ALA:HB1	1.84	0.59
6:BH:114:ARG:NH1	34:B5:637:C:O2	2.33	0.59
13:BW:111:MET:HE1	13:BW:119:LYS:HD2	1.84	0.59
34:B5:183:U:H2'	34:B5:184:C:H6	1.67	0.59
34:B5:1352:G:H2'	34:B5:1353:U:O4'	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3231:U:O2	38:A1:3256:G:O6	2.20	0.59
53:AQ:122:ILE:HG23	53:AQ:126:GLN:HB2	1.84	0.59
2:BB:134:VAL:HG13	2:BB:218:LEU:HB2	1.83	0.59
32:Bf:108:VAL:HG22	32:Bf:114:VAL:HG12	1.84	0.59
34:B5:1260:U:H2'	34:B5:1261:G:C8	2.37	0.59
38:A1:424:G:O2'	67:Ae:23:ASP:OD2	2.18	0.59
38:A1:1644:C:H5''	38:A1:1645:U:H5''	1.84	0.59
50:AN:8:GLU:HB2	50:AN:50:ARG:HH22	1.67	0.59
34:B5:209:U:H2'	34:B5:210:A:H8	1.67	0.59
38:A1:1311:G:N2	51:AO:86[A]:GLY:O	2.24	0.59
38:A1:1717:U:H2'	38:A1:1718:G:C8	2.37	0.59
32:Bf:105:TYR:OH	34:B5:1252:C:H5'	2.01	0.59
33:BM:22:VAL:HG12	33:BM:135:MET:HE2	1.84	0.59
38:A1:1940:G:H21	38:A1:3362:A:H8	1.51	0.59
38:A1:3119:U:H4'	75:Am:104:PRO:HG3	1.84	0.59
79:E:58:CYS:SG	79:E:152:ARG:NE	2.75	0.59
81:V:42:ARG:O	81:V:46:ARG:HG3	2.01	0.59
34:B5:184:C:H2'	34:B5:185:U:C6	2.38	0.59
34:B5:1169:G:N1	34:B5:1575:G7M:OP2	2.35	0.59
38:A1:1799:A:H2'	38:A1:1800:A:H8	1.65	0.59
39:A3:6:C:OP2	41:AD:22:ARG:NH2	2.36	0.59
32:Bf:102:VAL:HG23	32:Bf:103:LEU:HD12	1.83	0.59
33:BM:129:GLU:HA	33:BM:133:LEU:HD21	1.84	0.59
38:A1:417:A:H2'	38:A1:418:A:C8	2.37	0.59
38:A1:1310:G:HO2'	38:A1:2380:U:HO2'	1.50	0.59
58:AV:18:PRO:HA	58:AV:51:ALA:HA	1.83	0.59
59:AW:45:ASN:HB3	59:AW:48:ARG:HG3	1.84	0.59
80:DC:20:ARG:NE	80:DC:342:LEU:O	2.35	0.59
80:DC:113:SER:OG	80:DC:517:CYS:SG	2.53	0.59
19:BD:98:ALA:HA	19:BD:188:ILE:HD12	1.83	0.59
34:B5:12:U:H2'	34:B5:13:C:C6	2.38	0.59
34:B5:520:A:H2'	34:B5:521:A:C8	2.37	0.59
38:A1:3217:C:C2	52:AP:182:ILE:HD11	2.37	0.59
58:AV:15:LEU:HD13	58:AV:51:ALA:HB3	1.84	0.59
14:BX:107:PHE:HE1	14:BX:123:LYS:HB3	1.67	0.59
35:AA:117:GLU:OE2	35:AA:163:ARG:NH2	2.35	0.59
35:AA:180:LEU:HD11	78:Ap:26:VAL:HG21	1.84	0.59
38:A1:3276:G:O6	52:AP:171:ARG:NH2	2.36	0.59
80:DC:679:GLU:HG3	80:DC:680:GLU:H	1.67	0.59
1:BA:114:SER:O	1:BA:116:LYS:NZ	2.35	0.59
9:BL:109:VAL:HG12	9:BL:137:PHE:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BX:41:SER:OG	14:BX:43:PHE:O	2.21	0.59
16:Ba:45:VAL:HG13	16:Ba:46:GLU:H	1.68	0.59
22:BP:44:ARG:HH12	22:BP:82:ASN:HB2	1.66	0.59
34:B5:156:A:H2'	34:B5:157:A:O4'	2.03	0.59
34:B5:1144:U:H2'	34:B5:1145:U:C6	2.38	0.59
38:A1:1760:A:N6	38:A1:1766:G:O6	2.36	0.59
39:A3:4:U:H2'	39:A3:5:G:C8	2.37	0.59
42:AE:60:ASP:OD2	42:AE:78:ARG:NH1	2.36	0.59
45:AH:92:TYR:HB2	45:AH:142:ASP:HB3	1.85	0.59
80:DC:108:HIS:HB2	80:DC:111:PHE:HB3	1.83	0.59
20:BF:97:LEU:HD11	20:BF:114:ILE:HD11	1.85	0.59
31:Bg:209:THR:O	31:Bg:224:ASN:ND2	2.29	0.59
33:BM:71:ILE:HG13	33:BM:72:ILE:HD12	1.84	0.59
38:A1:1241:U:N3	38:A1:1244:A:OP2	2.34	0.59
79:E:73:ASP:OD2	79:E:113:SER:OG	2.20	0.59
2:BB:64:ARG:NH2	11:BO:37:GLU:OE2	2.33	0.58
19:BD:211:PRO:HA	24:BR:19:ARG:HE	1.67	0.58
34:B5:1163:A:N3	34:B5:1613:U:O2'	2.31	0.58
34:B5:1474:G:H2'	34:B5:1475:A:C8	2.38	0.58
44:AG:162:LEU:HD23	50:AN:7:LEU:HD11	1.84	0.58
60:AX:90:ALA:O	60:AX:120:LYS:NZ	2.35	0.58
70:Ah:73:LYS:O	70:Ah:76:GLN:NE2	2.36	0.58
7:BI:32:GLN:NE2	34:B5:1727:G:H21	2.01	0.58
28:BZ:96:SER:OG	28:BZ:97:LYS:NZ	2.31	0.58
33:BM:30:VAL:HA	33:BM:33:ARG:HD3	1.85	0.58
35:AA:117:GLU:HG2	35:AA:124:GLY:H	1.68	0.58
38:A1:1227:C:O2'	38:A1:1228:C:O4'	2.21	0.58
38:A1:1914:G:O2'	54:AR:82:LYS:O	2.21	0.58
38:A1:1950:U:H3	38:A1:2096:A:N6	2.01	0.58
38:A1:2523:A:OP1	60:AX:31:THR:OG1	2.18	0.58
38:A1:2541:U:H4'	38:A1:2542:U:H5'	1.85	0.58
42:AE:13:GLU:HA	67:Ae:4:LEU:HD11	1.85	0.58
2:BB:82:ARG:NH1	2:BB:188:LEU:O	2.36	0.58
11:BO:17:ALA:N	11:BO:80:HIS:O	2.28	0.58
19:BD:160:SER:OG	34:B5:1329:A:OP2	2.18	0.58
34:B5:513:U:H2'	34:B5:514:G:C8	2.38	0.58
34:B5:699:U:O4	34:B5:741:C:N4	2.32	0.58
34:B5:1260:U:H2'	34:B5:1261:G:H8	1.68	0.58
34:B5:1591:C:H2'	34:B5:1592:A:C8	2.37	0.58
38:A1:1119:C:H2'	38:A1:1120:A:H8	1.68	0.58
38:A1:1355:A:H4'	38:A1:1356:U:H5''	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2369:G:H2'	38:A1:2370:G:C8	2.38	0.58
40:A4:142:C:H2'	40:A4:143:U:C6	2.38	0.58
42:AE:69:PHE:HB2	42:AE:138:GLN:NE2	2.19	0.58
19:BD:225:TYR:HE2	31:Bg:191:ASP:HB2	1.67	0.58
20:BF:225:ARG:NH1	29:Bc:58:GLU:OE1	2.37	0.58
34:B5:1071:U:H2'	34:B5:1072:C:C6	2.38	0.58
38:A1:428:A:H2'	38:A1:429:U:C6	2.39	0.58
45:AH:41:ILE:HG21	45:AH:71:VAL:HG21	1.84	0.58
46:AI:44:ASP:OD1	46:AI:181:TYR:OH	2.19	0.58
79:E:32:VAL:HA	79:E:208:SER:HA	1.84	0.58
79:E:134:PHE:H	79:E:156:LYS:HE2	1.69	0.58
80:DC:583:HIS:HB3	80:DC:694:HIS:HD2	1.67	0.58
80:DC:650:THR:HG21	80:DC:691:VAL:HG12	1.85	0.58
13:BW:41:MET:HG2	13:BW:129:VAL:HG21	1.84	0.58
34:B5:814:A:H5'	54:AR:167:ARG:HE	1.69	0.58
37:AC:317:PRO:C	37:AC:319:LYS:H	2.11	0.58
38:A1:129:U:H2'	38:A1:130:A:C8	2.39	0.58
38:A1:177:U:H2'	38:A1:178:U:H6	1.68	0.58
38:A1:1019:G:H1	38:A1:1033:U:H6	1.50	0.58
38:A1:2759:U:H5''	38:A1:2760:C:H5'	1.85	0.58
80:DC:676:ILE:HD13	80:DC:722:PRO:HB2	1.85	0.58
15:BY:105:ARG:NH2	34:B5:459:G:OP2	2.36	0.58
34:B5:319:U:H4'	34:B5:323:A:C8	2.38	0.58
37:AC:266:THR:HG23	37:AC:267:VAL:HG13	1.85	0.58
38:A1:728:G:H5''	53:AQ:43:PRO:HB2	1.86	0.58
38:A1:1729:A:O4'	65:Ac:52:ARG:NH1	2.36	0.58
38:A1:3319:U:H5'	38:A1:3320:A:H5'	1.85	0.58
44:AG:113:ALA:O	44:AG:116:VAL:HG12	2.03	0.58
53:AQ:28:LEU:HA	53:AQ:31:LYS:HB3	1.86	0.58
20:BF:185:ARG:NH2	34:B5:1471:A:OP1	2.33	0.58
34:B5:1393:C:H2'	34:B5:1394:G:C8	2.39	0.58
37:AC:60:THR:HG22	37:AC:62:ALA:H	1.69	0.58
38:A1:252:U:O3'	38:A1:253:A:H8	1.86	0.58
38:A1:1134:G:O2'	38:A1:2642:A:N3	2.35	0.58
38:A1:1236:G:N2	38:A1:1244:A:OP1	2.36	0.58
46:AI:76:MET:O	46:AI:80:SER:OG	2.20	0.58
46:AI:193:ASP:OD1	46:AI:194:GLY:N	2.31	0.58
50:AN:143:ARG:NH2	70:Ah:90:ARG:O	2.37	0.58
51:AO:189[A]:ASP:OD1	51:AO:190[A]:VAL:N	2.35	0.58
80:DC:30:HIS:CE1	80:DC:130:ASP:HB2	2.39	0.58
82:EC:6919:G:O6	82:EC:6934:U:O2'	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:61:LEU:HD13	2:BB:96:LEU:HD11	1.84	0.58
34:B5:1477:G:H2'	34:B5:1478:G:H8	1.69	0.58
34:B5:1785:U:H2'	34:B5:1786:G:H8	1.67	0.58
38:A1:118:U:N3	38:A1:122:A:OP2	2.32	0.58
80:DC:20:ARG:NH1	80:DC:91:GLN:OE1	2.30	0.58
17:Bb:67:THR:OG1	17:Bb:70:LYS:O	2.21	0.58
33:BM:43:ARG:HA	33:BM:121:VAL:HG23	1.85	0.58
34:B5:844:A:H2'	34:B5:845:G:H8	1.69	0.58
35:AA:215:ASN:ND2	38:A1:2969:A:N7	2.52	0.58
36:AB:35:ASP:OD2	36:AB:191:LYS:NZ	2.35	0.58
38:A1:528:U:H2'	38:A1:529:A:C8	2.38	0.58
68:Af:31:LYS:NZ	68:Af:35:VAL:O	2.37	0.58
13:BW:19:LYS:NZ	34:B5:1095:U:O2'	2.37	0.58
34:B5:184:C:H2'	34:B5:185:U:H6	1.69	0.58
34:B5:1537:C:O4'	34:B5:1572:OMG:N2	2.36	0.58
38:A1:1203:A:H2'	38:A1:1204:A:H8	1.69	0.58
38:A1:2451:G:N1	38:A1:2496:C:O2	2.36	0.58
38:A1:2470:C:H1'	79:E:26:ARG:HH21	1.69	0.58
2:BB:48:VAL:HG13	2:BB:49:ASN:H	1.68	0.57
5:BG:72:ARG:NH2	34:B5:418:G:O3'	2.37	0.57
20:BF:146:THR:O	20:BF:157:ARG:NH2	2.36	0.57
22:BP:77:ARG:H	22:BP:77:ARG:HD3	1.69	0.57
38:A1:618:C:OP1	52:AP:173:ARG:NH2	2.37	0.57
38:A1:1251:A:H2'	38:A1:1252:A:H8	1.69	0.57
38:A1:1580:A:H2'	38:A1:1581:C:H1'	1.86	0.57
38:A1:2197:OMC:OP2	38:A1:2242:A:N6	2.37	0.57
38:A1:2882:U:H2'	38:A1:2883:U:C6	2.39	0.57
38:A1:3231:U:H2'	38:A1:3232:G:H8	1.69	0.57
56:AT:13:TYR:HA	56:AT:16:GLN:HG2	1.85	0.57
64:Ab:54:LEU:HG	64:Ab:58:LYS:HD3	1.85	0.57
80:DC:27:HIS:CD2	80:DC:138:GLN:HB2	2.39	0.57
1:BA:74:VAL:HG23	1:BA:118:PRO:HB3	1.85	0.57
9:BL:155:LYS:HE2	10:BN:81:ALA:HB3	1.85	0.57
20:BF:72:HIS:NE2	34:B5:1610:G:OP1	2.20	0.57
25:BS:3:LEU:HD13	25:BS:5:VAL:HG13	1.86	0.57
34:B5:1525:A:H2'	34:B5:1526:A:C8	2.39	0.57
34:B5:1561:U:H4'	34:B5:1599:C:H4'	1.86	0.57
38:A1:620:U:O5'	52:AP:167:ARG:NH2	2.37	0.57
38:A1:1571:A:H2'	38:A1:1572:U:O4'	2.05	0.57
55:AS:60:SER:OG	55:AS:62:ASN:OD1	2.22	0.57
80:DC:823:ARG:HD2	80:DC:829:LYS:O	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BS:28:ILE:HA	25:BS:58:ALA:HB2	1.87	0.57
32:Bf:108:VAL:HG11	33:BM:73:LYS:HB3	1.86	0.57
34:B5:1592:A:H2'	34:B5:1593:A:H8	1.70	0.57
34:B5:1656:U:HO2'	38:A1:2292:U:HO2'	1.49	0.57
38:A1:166:C:H2'	38:A1:167:U:C6	2.40	0.57
38:A1:2356:A:H5'	52:AP:138:LYS:HZ2	1.70	0.57
39:A3:84:A:H2'	39:A3:85:G:C8	2.38	0.57
40:A4:8:C:H2'	40:A4:9:A:C8	2.40	0.57
50:AN:155:VAL:O	50:AN:162:ARG:NH2	2.31	0.57
6:BH:14:THR:N	6:BH:17:GLU:OE2	2.28	0.57
31:Bg:123:ILE:HG13	31:Bg:169:ILE:HG13	1.85	0.57
38:A1:815:G:OP2	72:Aj:31:LYS:NZ	2.29	0.57
38:A1:821:U:H2'	38:A1:822:G:H8	1.69	0.57
38:A1:2407:C:H2'	38:A1:2408:U:H6	1.68	0.57
16:Ba:15:ARG:NH2	34:B5:936:G:N7	2.53	0.57
16:Ba:70:LYS:NZ	34:B5:933:A:OP1	2.31	0.57
25:BS:39:GLY:N	34:B5:1566:U:H5''	2.16	0.57
34:B5:179:A:H3'	34:B5:180:A:H8	1.69	0.57
34:B5:182:A:H2'	34:B5:183:U:H6	1.70	0.57
34:B5:472:U:O2'	34:B5:769:A:N3	2.34	0.57
34:B5:1267:G:H1	34:B5:1442:U:H3	1.52	0.57
55:AS:81:TYR:CE1	55:AS:90:MET:HE3	2.39	0.57
1:BA:70:PRO:O	1:BA:95:ALA:N	2.33	0.57
13:BW:53:ILE:HB	13:BW:60:LYS:HB2	1.87	0.57
34:B5:273:G:O6	34:B5:283:U:O2	2.23	0.57
34:B5:1252:C:H2'	34:B5:1253:U:O4'	2.04	0.57
38:A1:2555:G:C5	69:Ag:95:ILE:HD11	2.40	0.57
76:An:17:ARG:HA	76:An:20:VAL:HG12	1.87	0.57
17:Bb:50:ALA:O	17:Bb:51:GLN:HG2	2.04	0.57
25:BS:16:ARG:NH2	25:BS:19:ASN:O	2.37	0.57
31:Bg:127:ARG:HA	31:Bg:150:TRP:HB2	1.87	0.57
35:AA:79:ASN:ND2	35:AA:166:ILE:O	2.35	0.57
38:A1:407:A:C2	40:A4:17:A:H1'	2.40	0.57
38:A1:594:U:OP2	38:A1:609:G:N1	2.35	0.57
39:A3:52:G:N2	47:AJ:9:MET:SD	2.76	0.57
42:AE:3:ALA:HB2	67:Ae:77:ALA:HB2	1.86	0.57
82:EC:6764:C:H2'	82:EC:6765:A:C8	2.40	0.57
82:EC:6935:G:HO2'	82:EC:6936:G:H8	1.52	0.57
1:BA:52:LYS:HD2	12:BV:82:VAL:HG23	1.87	0.57
5:BG:85:ARG:O	5:BG:87:ARG:NH1	2.38	0.57
16:Ba:5:ARG:NH2	34:B5:1796:C:OP2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BR:117:LEU:HD12	24:BR:118:PRO:HD2	1.86	0.57
34:B5:706:A:N6	34:B5:731:C:OP2	2.36	0.57
34:B5:950:C:O2'	34:B5:951:A:OP1	2.20	0.57
38:A1:29:C:H4'	38:A1:62:A:H4'	1.86	0.57
38:A1:177:U:O2	38:A1:241:G:O6	2.22	0.57
49:AM:36:VAL:HG11	49:AM:55:ARG:HH12	1.70	0.57
80:DC:213:SER:OG	85:DC:901:GDP:O6	2.18	0.57
80:DC:565:GLU:HB3	80:DC:717:PHE:CZ	2.40	0.57
80:DC:703:GLY:O	80:DC:707:PRO:CD	2.53	0.57
2:BB:113:MET:HE2	2:BB:142:PHE:HE2	1.70	0.57
26:BT:97:SER:OG	34:B5:1504:G:OP1	2.23	0.57
29:Bc:19:THR:HG23	29:Bc:25:VAL:HG13	1.85	0.57
32:Bf:102:VAL:HG21	33:BM:71:ILE:HG22	1.87	0.57
34:B5:555:A:N3	34:B5:590:C:O2'	2.34	0.57
34:B5:1564:U:H2'	34:B5:1565:C:C6	2.40	0.57
36:AB:215:ILE:HD12	36:AB:338:LEU:HB3	1.86	0.57
47:AJ:101:ASN:ND2	47:AJ:130:VAL:HA	2.20	0.57
55:AS:22:PRO:O	56:AT:146:ASN:ND2	2.28	0.57
80:DC:647:ILE:HB	80:DC:687:ASN:HA	1.85	0.57
13:BW:111:MET:HG3	13:BW:116:ALA:HB2	1.87	0.57
20:BF:124:LEU:HD23	28:BZ:58:ARG:HG2	1.85	0.57
27:BU:85:ARG:HH22	34:B5:1335:U:H5'	1.70	0.57
35:AA:3:ARG:HB3	35:AA:207:VAL:HG22	1.87	0.57
39:A3:4:U:H2'	39:A3:5:G:H8	1.69	0.57
41:AD:60:ILE:HB	41:AD:80:SER:HB2	1.87	0.57
2:BB:181:LEU:HA	2:BB:184:LEU:HB3	1.86	0.56
34:B5:924:A:H2'	34:B5:925:G:C8	2.40	0.56
38:A1:358:G:N2	38:A1:361:A:OP2	2.32	0.56
38:A1:1580:A:H62	60:AX:33:ARG:NH1	2.03	0.56
41:AD:41:LYS:HD2	56:AT:93:VAL:HG11	1.87	0.56
41:AD:64:ILE:HD12	41:AD:144:VAL:HG11	1.87	0.56
47:AJ:108:GLU:HB2	47:AJ:122:ILE:HG23	1.86	0.56
62:AZ:3:LYS:NZ	65:Ac:36:GLN:O	2.37	0.56
11:BO:35:GLY:O	34:B5:918:U:O2'	2.18	0.56
34:B5:1579:U:H2'	34:B5:1580:C:C6	2.40	0.56
36:AB:375:GLU:OE2	59:AW:14:TYR:OH	2.18	0.56
38:A1:1565:G:H1	38:A1:1574:C:N4	2.03	0.56
38:A1:2180:G:H2'	38:A1:2181:C:C6	2.39	0.56
39:A3:121:U:OP2	41:AD:265:TYR:OH	2.21	0.56
55:AS:99:ARG:NH1	55:AS:126:VAL:O	2.32	0.56
5:BG:219:ARG:NH2	34:B5:242:U:OP1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:34:PHE:O	8:BJ:110:GLN:NE2	2.39	0.56
8:BJ:149:ARG:HG2	34:B5:765:G:O6	2.06	0.56
13:BW:16:ASN:ND2	34:B5:1037:C:O2	2.38	0.56
13:BW:31:SER:HB3	34:B5:636:A:H5''	1.86	0.56
19:BD:39:VAL:HG12	19:BD:48:VAL:HG22	1.87	0.56
34:B5:5:U:H2'	34:B5:6:G:H8	1.70	0.56
36:AB:384:LYS:NZ	38:A1:3371:G:OP1	2.34	0.56
37:AC:92:ASN:HD22	37:AC:100:PHE:HB2	1.69	0.56
38:A1:26:A:N3	38:A1:328:U:O2'	2.37	0.56
38:A1:535:G:N2	38:A1:536:U:O4	2.35	0.56
38:A1:1241:U:H5'	38:A1:1242:G:OP2	2.06	0.56
38:A1:1388:U:O2'	67:Ae:99:ASN:O	2.21	0.56
38:A1:1474:A:OP1	54:AR:53:LYS:NZ	2.37	0.56
38:A1:1551:C:HO2'	38:A1:2170:U:HO2'	1.53	0.56
38:A1:1560:G:C2'	38:A1:1561:G:H5'	2.35	0.56
38:A1:2883:U:H2'	38:A1:2884:C:C6	2.40	0.56
38:A1:3185:U:O2'	55:AS:170:THR:OG1	2.23	0.56
41:AD:123:GLU:OE2	41:AD:248:ARG:NH1	2.38	0.56
63:Aa:36:GLY:HA3	63:Aa:40:HIS:CE1	2.40	0.56
73:Ak:36:LYS:HD3	73:Ak:38:PHE:CD2	2.40	0.56
80:DC:150:ARG:HH11	80:DC:194:ASP:HB3	1.70	0.56
80:DC:288:ILE:HD12	80:DC:319:LEU:HD22	1.87	0.56
80:DC:437:MET:O	80:DC:438:MET:HE2	2.04	0.56
80:DC:572:SER:O	80:DC:589:LYS:NZ	2.34	0.56
34:B5:1087:A:H2'	34:B5:1088:A:C8	2.41	0.56
34:B5:1773:4AC:P	76:An:2:ARG:NH1	2.77	0.56
37:AC:328:ASN:OD1	43:AF:48:ASN:ND2	2.38	0.56
38:A1:1560:G:H2'	38:A1:1561:G:H5'	1.88	0.56
38:A1:2213:A:H2'	38:A1:2214:A:C8	2.40	0.56
38:A1:3164:C:HO2'	38:A1:3165:A:H8	1.53	0.56
69:Ag:79:SER:OG	69:Ag:80:ARG:NH1	2.38	0.56
80:DC:576:LEU:HD21	80:DC:585:ARG:HH21	1.70	0.56
81:V:95:GLU:N	81:V:95:GLU:OE1	2.38	0.56
6:BH:22:GLN:O	6:BH:25:VAL:HG22	2.05	0.56
7:BI:20:GLN:NE2	7:BI:22:ARG:O	2.37	0.56
7:BI:184:LEU:HD23	7:BI:189:LEU:HA	1.85	0.56
12:BV:3:ASN:HD21	12:BV:7:GLN:HG3	1.71	0.56
34:B5:560:U:H2'	34:B5:561:G:H8	1.70	0.56
34:B5:646:C:H2'	34:B5:647:G:O4'	2.05	0.56
38:A1:1404:G:N2	38:A1:1407:A:OP2	2.32	0.56
38:A1:3006:A:H2'	38:A1:3007:U:O4'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:51:G:OP2	74:Al:21:ARG:NH1	2.38	0.56
76:An:2:ARG:HH11	76:An:4:LYS:HD2	1.70	0.56
81:V:51:VAL:HG22	81:V:87:VAL:HG22	1.88	0.56
5:BG:30:LYS:NZ	5:BG:35:GLU:O	2.38	0.56
10:BN:99:ARG:NH2	10:BN:119:GLU:OE2	2.38	0.56
26:BT:72:GLY:HA2	26:BT:121:GLY:HA3	1.87	0.56
31:Bg:68:VAL:HA	31:Bg:84:SER:HA	1.88	0.56
34:B5:1248:C:H2'	34:B5:1249:U:H5	1.71	0.56
34:B5:1585:U:H3	34:B5:1611:A:H2	1.53	0.56
38:A1:616:G:H2'	38:A1:617:G:H8	1.71	0.56
66:Ad:9:THR:HG23	66:Ad:76:SER:HB3	1.87	0.56
80:DC:672:LYS:HG3	80:DC:673:GLU:HG2	1.88	0.56
2:BB:59:ASP:HA	2:BB:62:LYS:HG2	1.87	0.56
21:BK:20:VAL:HG12	21:BK:67:THR:HA	1.87	0.56
21:BK:88:PRO:HB3	21:BK:91:TYR:CZ	2.41	0.56
37:AC:47:ARG:NH2	37:AC:109:TRP:O	2.34	0.56
38:A1:1410:U:O2'	67:Ae:95:GLU:OE2	2.22	0.56
38:A1:1497:C:H2'	38:A1:1498:A:H8	1.71	0.56
40:A4:39:G:H1'	40:A4:104:A:N6	2.21	0.56
54:AR:172:ARG:HG2	54:AR:176:ARG:NH2	2.20	0.56
1:BA:201:LEU:HB3	24:BR:85:VAL:HG12	1.86	0.56
4:BE:38:LEU:HD23	34:B5:298:C:H5''	1.87	0.56
22:BP:18:ARG:HB2	22:BP:36:LEU:HD13	1.88	0.56
34:B5:1496:U:HO2'	34:B5:1519:U:HO2'	1.50	0.56
38:A1:2219:A:H2'	38:A1:2220:A2M:H8	1.87	0.56
38:A1:2688:U:OP1	41:AD:12:TYR:OH	2.20	0.56
66:Ad:20:LEU:HD11	66:Ad:32:ALA:HB2	1.88	0.56
15:BY:60:PHE:O	34:B5:522:U:O2'	2.23	0.56
20:BF:48:PHE:HZ	20:BF:90:ILE:HD13	1.71	0.56
36:AB:360:ASP:OD2	36:AB:364:LYS:NZ	2.39	0.56
38:A1:400:G:H4'	38:A1:401:U:H5''	1.87	0.56
38:A1:1156:C:OP2	43:AF:94:LYS:NZ	2.32	0.56
38:A1:1667:A:H2'	38:A1:1668:G:C8	2.40	0.56
46:AI:38:LYS:N	46:AI:85:PHE:O	2.38	0.56
67:Ae:83:GLU:O	67:Ae:86:THR:OG1	2.20	0.56
5:BG:195:VAL:HG12	5:BG:199:GLN:HE22	1.71	0.56
6:BH:91:ILE:HG21	6:BH:129:LEU:HD12	1.87	0.56
34:B5:891:A:H2'	34:B5:892:A:C8	2.40	0.56
38:A1:993:G:N3	38:A1:2637:A:H2'	2.21	0.56
38:A1:2129:U:H2'	38:A1:2130:G:C8	2.41	0.56
58:AV:53:SER:N	58:AV:56:ASP:OD2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:E:68:PHE:H	79:E:112:ALA:HA	1.70	0.56
37:AC:281:ILE:HD13	53:AQ:28:LEU:HD12	1.88	0.55
38:A1:159:A:H2'	38:A1:160:G:H8	1.69	0.55
38:A1:1565:G:H1	38:A1:1574:C:H42	1.54	0.55
38:A1:2880:U:OP1	58:AV:47:ASN:ND2	2.37	0.55
43:AF:156:ILE:HD12	43:AF:161:VAL:HB	1.87	0.55
65:Ac:30:THR:HG23	65:Ac:91:SER:HB2	1.88	0.55
9:BL:124:THR:OG1	9:BL:141:LYS:HG2	2.06	0.55
34:B5:146:U:H2'	34:B5:147:A:C8	2.41	0.55
38:A1:177:U:C2	38:A1:178:U:C5	2.94	0.55
38:A1:584:G:H2'	38:A1:585:A:C8	2.42	0.55
38:A1:1084:A:H2'	38:A1:1085:A:C8	2.41	0.55
4:BE:247:SER:OG	4:BE:250:GLU:OE1	2.20	0.55
16:Ba:79:ILE:HD13	34:B5:1794:A:H1'	1.88	0.55
27:BU:71:PRO:O	30:Bd:40:ARG:NH2	2.39	0.55
34:B5:29:U:H2'	34:B5:30:G:C8	2.41	0.55
38:A1:115:A:H8	38:A1:266:A:H5'	1.71	0.55
38:A1:2745:G:N2	38:A1:2748:A:OP2	2.33	0.55
5:BG:67:VAL:HB	5:BG:99:GLY:HA2	1.88	0.55
15:BY:121:THR:HG23	15:BY:123:LYS:H	1.71	0.55
24:BR:104:ASN:O	24:BR:107:SER:OG	2.16	0.55
34:B5:222:A:H2'	34:B5:223:U:C6	2.42	0.55
34:B5:702:G:O6	34:B5:737:A:N6	2.40	0.55
34:B5:950:C:H2'	34:B5:951:A:C8	2.42	0.55
34:B5:1291:G:H22	34:B5:1324:G:N2	2.04	0.55
37:AC:99:MET:HE3	37:AC:102:PRO:HA	1.87	0.55
38:A1:1272:C:H3'	38:A1:1273:A:H8	1.71	0.55
38:A1:1618:G:O2'	40:A4:126:A:N1	2.37	0.55
38:A1:1863:G:H4'	54:AR:82:LYS:HD3	1.88	0.55
38:A1:2216:G:H22	38:A1:2229:A:H2	1.55	0.55
45:AH:115:ARG:NH1	45:AH:123:ILE:HG12	2.22	0.55
80:DC:250:PHE:HB3	80:DC:275:MET:HE1	1.87	0.55
80:DC:414:GLN:HE21	80:DC:468:THR:HB	1.72	0.55
34:B5:1297:G:N2	34:B5:1300:A:OP2	2.30	0.55
38:A1:737:G:H2'	38:A1:738:A:H8	1.71	0.55
38:A1:2662:G:H2'	38:A1:2663:G:H8	1.72	0.55
4:BE:176:ASP:OD1	4:BE:177:ALA:N	2.39	0.55
5:BG:216:LEU:HG	5:BG:220:LYS:HE3	1.89	0.55
34:B5:1171:A:H2'	34:B5:1172:G:H8	1.71	0.55
34:B5:1452:U:H2'	34:B5:1453:G:H8	1.71	0.55
80:DC:724:ILE:HD13	80:DC:818:ILE:HD12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:16:VAL:HG12	11:BO:18:ARG:HG3	1.87	0.55
25:BS:46:VAL:HG21	25:BS:73:MET:SD	2.47	0.55
34:B5:209:U:H2'	34:B5:210:A:C8	2.42	0.55
34:B5:1315:U:OP1	34:B5:1328:G:N2	2.32	0.55
36:AB:250:ALA:HB1	38:A1:2947:G:N3	2.22	0.55
38:A1:909:G:OP2	50:AN:77:LYS:NZ	2.37	0.55
38:A1:1613:A:OP1	73:AK:2:ALA:N	2.40	0.55
38:A1:2357:A:H2'	38:A1:2358:A:H8	1.72	0.55
39:A3:74:C:H2'	39:A3:75:G:C8	2.42	0.55
41:AD:146:LEU:HD22	41:AD:163:LEU:HD13	1.89	0.55
80:DC:147:LEU:HD22	80:DC:193:ALA:HB2	1.88	0.55
14:BX:26:GLU:HB2	14:BX:29:TYR:HB3	1.89	0.55
34:B5:895:G:H2'	34:B5:896:U:C6	2.41	0.55
37:AC:101:ALA:HA	38:A1:800:G:H22	1.72	0.55
38:A1:1596:C:H2'	38:A1:1597:C:C6	2.42	0.55
38:A1:1765:U:H2'	38:A1:1766:G:H4'	1.88	0.55
46:AI:189:GLU:HA	46:AI:200:LEU:HB3	1.89	0.55
80:DC:644:ASN:ND2	80:DC:681:MET:O	2.38	0.55
34:B5:16:G:H2'	34:B5:17:C:C6	2.41	0.55
34:B5:139:C:N4	34:B5:175:G:O2'	2.40	0.55
34:B5:190:C:O2'	34:B5:195:G:O6	2.25	0.55
38:A1:675:C:O2'	38:A1:679:U:OP1	2.21	0.55
38:A1:845:G:O2'	38:A1:847:A:N1	2.35	0.55
38:A1:1621:A:H2'	38:A1:1622:U:C6	2.42	0.55
38:A1:2223:A:H2'	38:A1:2224:A:C8	2.42	0.55
38:A1:2611:U:H2'	38:A1:2612:U:C6	2.42	0.55
45:AH:27:VAL:HG12	45:AH:82:VAL:HG11	1.89	0.55
45:AH:90:MET:HG2	45:AH:181:VAL:HA	1.87	0.55
71:AI:66:GLU:OE1	71:AI:70:ARG:NH1	2.40	0.55
6:BH:30:SER:O	6:BH:34:LEU:N	2.37	0.55
15:BY:112:LYS:NZ	34:B5:55:A:OP1	2.33	0.55
38:A1:269:G:H5''	50:AN:14:LYS:HE2	1.89	0.55
38:A1:2152:A:H2'	38:A1:2153:U:H6	1.71	0.55
38:A1:2352:A:H5''	52:AP:83:TRP:O	2.07	0.55
42:AE:56:LYS:NZ	42:AE:101:PHE:O	2.39	0.55
44:AG:133:LYS:HD2	44:AG:138:HIS:HE1	1.72	0.55
79:E:70:ASP:CG	79:E:140:HIS:HE2	2.14	0.55
80:DC:244:LEU:HD12	80:DC:277:ILE:HG12	1.89	0.55
80:DC:249:PHE:CE2	80:DC:261:ASP:HA	2.42	0.55
80:DC:760:ARG:NE	80:DC:763:THR:OG1	2.33	0.55
20:BF:72:HIS:CD2	20:BF:107:LYS:HD2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BZ:65:LEU:HG	28:BZ:71:ILE:HD11	1.90	0.54
38:A1:339:C:OP1	38:A1:1380:G:O2'	2.22	0.54
38:A1:966:U:H2'	38:A1:967:A:C8	2.42	0.54
38:A1:1793:C:OP2	78:Ap:49:ARG:NH2	2.33	0.54
40:A4:58:G:O6	72:Aj:63:ARG:NH1	2.40	0.54
41:AD:34:LYS:HA	56:AT:27:LEU:HD11	1.89	0.54
48:AL:123:ILE:HD11	70:Ah:116:TYR:CD2	2.39	0.54
51:AO:27[A]:LEU:O	51:AO:101[A]:ARG:NH1	2.39	0.54
1:BA:72:ASP:HB2	1:BA:118:PRO:HA	1.89	0.54
4:BE:103:TYR:O	4:BE:182:TYR:OH	2.25	0.54
7:BI:87:ASN:HB3	7:BI:90:LEU:HD13	1.89	0.54
14:BX:75:GLN:NE2	14:BX:80:GLY:O	2.40	0.54
31:Bg:205:SER:OG	31:Bg:207:ASP:OD1	2.23	0.54
37:AC:35:VAL:HG21	37:AC:244:LEU:HD21	1.89	0.54
38:A1:584:G:H2'	38:A1:585:A:H8	1.71	0.54
38:A1:2461:A:N6	38:A1:2487:U:O2	2.40	0.54
38:A1:2720:G:OP1	53:AQ:180:ARG:NH1	2.40	0.54
55:AS:13:ARG:HD3	55:AS:51:VAL:HG12	1.88	0.54
68:Af:6:ARG:NH1	68:Af:8:TYR:O	2.39	0.54
73:Ak:30:LYS:NZ	73:Ak:40:GLN:OE1	2.32	0.54
82:EC:6783:U:H2'	82:EC:6784:G:H8	1.72	0.54
4:BE:22:LYS:NZ	34:B5:758:U:OP1	2.40	0.54
13:BW:15:ASN:HD21	13:BW:71:LYS:HD2	1.71	0.54
23:BQ:97:VAL:HG12	23:BQ:98:ASP:H	1.72	0.54
25:BS:70:VAL:HA	25:BS:73:MET:HE2	1.90	0.54
34:B5:385:A:H2'	34:B5:386:G:C8	2.42	0.54
34:B5:705:U:H2'	34:B5:730:G:H22	1.72	0.54
34:B5:1179:G:OP1	80:DC:654:GLN:NE2	2.40	0.54
38:A1:2406:C:H2'	38:A1:2407:C:C6	2.42	0.54
38:A1:2469:G:O2'	38:A1:2470:C:O4'	2.18	0.54
49:AM:23:ILE:HG13	49:AM:63:VAL:HG12	1.88	0.54
80:DC:360:PRO:HB2	80:DC:363:ASP:HB2	1.89	0.54
26:BT:108:LEU:HG	26:BT:113:ILE:HB	1.88	0.54
31:Bg:197:SER:HB2	31:Bg:216:LYS:HB3	1.89	0.54
34:B5:182:A:H2'	34:B5:183:U:C6	2.42	0.54
34:B5:407:A:H2'	34:B5:408:C:C6	2.42	0.54
34:B5:1452:U:H2'	34:B5:1453:G:C8	2.43	0.54
34:B5:1642:G:O2'	34:B5:1781:MA6:O2'	2.25	0.54
37:AC:23:PRO:HD2	37:AC:26:PHE:CD2	2.42	0.54
38:A1:273:A:H2'	38:A1:274:G:H8	1.72	0.54
56:AT:40:VAL:HG21	56:AT:96:ILE:HD11	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Ac:53:LYS:O	65:Ac:57:GLU:HG3	2.08	0.54
69:Ag:54:ILE:HD11	69:Ag:78:GLY:HA2	1.90	0.54
80:DC:394:PHE:N	80:DC:460:ASP:OD2	2.40	0.54
6:BH:15:GLU:HA	6:BH:18:LEU:HD12	1.90	0.54
13:BW:80:ASN:OD1	13:BW:124:LYS:NZ	2.39	0.54
14:BX:90:ASP:HA	34:B5:568:G:H4'	1.90	0.54
18:Be:25:GLU:OE2	34:B5:540:G:N2	2.40	0.54
29:Bc:18:ARG:NH2	34:B5:1615:C:OP1	2.40	0.54
31:Bg:13:LEU:HD22	31:Bg:55:GLY:HA3	1.90	0.54
32:Bf:121:CYS:HB2	32:Bf:132:LEU:HD21	1.88	0.54
34:B5:844:A:H2'	34:B5:845:G:C8	2.42	0.54
38:A1:1688:U:H2'	38:A1:1689:U:C6	2.43	0.54
38:A1:2480:A:O2'	38:A1:2481:G:O4'	2.22	0.54
46:AI:30:LYS:HG3	46:AI:63:GLU:HG3	1.88	0.54
80:DC:77:LEU:HD22	80:DC:100:ILE:HD11	1.90	0.54
3:BC:45:VAL:HG21	3:BC:68:ILE:HG23	1.88	0.54
24:BR:44:LYS:NZ	34:B5:1387:G:N7	2.46	0.54
34:B5:1266:U:H2'	34:B5:1267:G:C8	2.42	0.54
38:A1:737:G:H2'	38:A1:738:A:C8	2.42	0.54
51:AO:189[A]:ASP:O	51:AO:193[A]:GLN:HG3	2.08	0.54
79:E:101:LYS:O	79:E:105:LYS:NZ	2.41	0.54
80:DC:468:THR:OG1	80:DC:478:MET:HB2	2.07	0.54
82:EC:6890:A:N1	82:EC:6937:G:H5''	2.23	0.54
7:BI:38:ILE:HG13	7:BI:96:LEU:HD11	1.89	0.54
11:BO:107:ARG:NH2	29:Bc:60:GLU:OE2	2.39	0.54
34:B5:939:A:H2'	34:B5:940:A:C8	2.42	0.54
34:B5:1226:A:C6	34:B5:1230:A:H1'	2.43	0.54
38:A1:3251:U:H2'	38:A1:3252:G:C8	2.42	0.54
40:A4:40:A:H2'	40:A4:41:A:C8	2.43	0.54
47:AJ:14:ILE:HG13	47:AJ:131:MET:HE1	1.89	0.54
80:DC:180:ARG:NE	80:DC:183:GLU:OE2	2.28	0.54
4:BE:185:GLY:H	4:BE:224:ASN:HB3	1.73	0.54
16:Ba:8:ASN:ND2	34:B5:1030:A:OP2	2.33	0.54
34:B5:947:U:H2'	34:B5:948:G:H8	1.73	0.54
34:B5:1208:A:H8	34:B5:1269:OMU:H6	1.72	0.54
34:B5:1427:A:O2'	34:B5:1428:OMG:OP1	2.25	0.54
38:A1:620:U:H4'	52:AP:167:ARG:HH12	1.71	0.54
38:A1:748:U:H2'	38:A1:749:C:C6	2.42	0.54
38:A1:821:U:H2'	38:A1:822:G:C8	2.42	0.54
38:A1:1055:A:N3	39:A3:81:U:O2'	2.40	0.54
38:A1:2492:C:H1'	79:E:164:CYS:SG	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:AG:75:ILE:C	44:AG:77:GLN:H	2.16	0.54
53:AQ:92:ARG:HG3	63:Aa:76:ASP:HB2	1.90	0.54
3:BC:60:SER:OG	12:BV:25:LYS:O	2.24	0.54
10:BN:11:ILE:HD11	34:B5:1072:C:H4'	1.88	0.54
21:BK:48:SER:HA	34:B5:1219:A:O2'	2.07	0.54
34:B5:1628:U:H2'	34:B5:1629:G:C8	2.43	0.54
35:AA:80:GLU:HG3	78:Ap:66:GLY:HA2	1.89	0.54
38:A1:531:G:H2'	38:A1:532:A:C8	2.43	0.54
38:A1:792:G:H2'	38:A1:793:C:C6	2.43	0.54
38:A1:952:A:H4'	38:A1:968:G:N2	2.21	0.54
38:A1:1235:U:H4'	38:A1:1236:G:H5'	1.89	0.54
38:A1:1615:C:H2'	38:A1:1616:U:C6	2.43	0.54
38:A1:1740:U:H4'	38:A1:1741:A:H5'	1.90	0.54
52:AP:58:ILE:HD12	52:AP:84:PRO:HD2	1.90	0.54
77:Ao:6:LYS:NZ	77:Ao:94:GLY:O	2.40	0.54
8:BJ:81:VAL:HG21	8:BJ:91:LYS:HE3	1.89	0.54
34:B5:1477:G:H2'	34:B5:1478:G:C8	2.42	0.54
38:A1:110:G:OP2	48:AL:73:ARG:NH2	2.30	0.54
38:A1:596:C:OP1	43:AF:33:ARG:NH1	2.41	0.54
38:A1:691:A:N1	40:A4:28:C:O2'	2.40	0.54
38:A1:991:G:N2	56:AT:59:GLY:O	2.27	0.54
38:A1:1072:G:H2'	38:A1:1073:U:C6	2.43	0.54
38:A1:1492:G:O2'	74:Al:48:LYS:NZ	2.40	0.54
38:A1:2584:G:O2'	44:AG:240:ASN:OD1	2.25	0.54
42:AE:92:SER:OG	42:AE:148:GLU:OE1	2.24	0.54
80:DC:27:HIS:HD2	80:DC:138:GLN:HB2	1.72	0.54
3:BC:156:THR:HG23	13:BW:95:PRO:HB2	1.88	0.53
9:BL:99:ARG:HG2	14:BX:9:LEU:HA	1.90	0.53
15:BY:16:PRO:HA	15:BY:19:ALA:HA	1.90	0.53
22:BP:79:HIS:HA	22:BP:97:TYR:HB3	1.90	0.53
26:BT:45:MET:SD	34:B5:1476:C:O2'	2.66	0.53
31:Bg:17:ASN:HB3	31:Bg:39:ASP:HB3	1.90	0.53
31:Bg:50:ASP:OD1	31:Bg:51:ASP:N	2.42	0.53
31:Bg:89:LEU:HD11	31:Bg:110:VAL:HG11	1.89	0.53
34:B5:79:C:H2'	34:B5:80:A:O4'	2.09	0.53
34:B5:233:C:O2'	34:B5:234:G:N2	2.37	0.53
38:A1:1010:G:N2	46:AI:193:ASP:OD1	2.37	0.53
40:A4:95:G:O2'	72:Aj:81:GLY:O	2.17	0.53
49:AM:50:LYS:HE3	49:AM:82:SER:HB2	1.89	0.53
79:E:175:GLU:OE1	79:E:177:ASP:N	2.34	0.53
80:DC:758:GLU:OE2	80:DC:767:THR:OG1	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:32:ASP:OD2	11:BO:34:SER:OG	2.22	0.53
17:Bb:51:GLN:OE1	34:B5:957:G:N2	2.40	0.53
20:BF:102:ARG:NH1	34:B5:1473:U:O2'	2.41	0.53
25:BS:115:ARG:O	25:BS:119:ILE:HG13	2.08	0.53
34:B5:705:U:H2'	34:B5:730:G:H1	1.74	0.53
34:B5:1185:U:H4'	34:B5:1186:U:H5''	1.90	0.53
38:A1:2261:G:OP1	38:A1:2306:C:N4	2.35	0.53
38:A1:3296:A:H2'	38:A1:3297:U:H6	1.72	0.53
47:AJ:54:VAL:HG13	47:AJ:56:THR:H	1.72	0.53
57:AU:94:ARG:HG2	57:AU:96:VAL:HG13	1.90	0.53
60:AX:46:TYR:HD2	70:Ah:75:TYR:HB3	1.73	0.53
80:DC:822:ALA:HA	80:DC:825:ARG:HG2	1.91	0.53
81:V:89:THR:HG21	81:V:96:ILE:HD11	1.90	0.53
2:BB:83:LYS:HE3	2:BB:106:THR:HG22	1.89	0.53
15:BY:55:VAL:HG22	15:BY:75:VAL:HG12	1.89	0.53
16:Ba:51:ARG:NH1	29:Bc:37:SER:HB3	2.23	0.53
16:Ba:51:ARG:O	16:Ba:55:GLU:HG3	2.08	0.53
20:BF:216:GLU:OE1	20:BF:219:ARG:NH2	2.41	0.53
23:BQ:94:GLN:HB2	23:BQ:102:LYS:HG3	1.91	0.53
30:Bd:15:GLY:O	30:Bd:19:ARG:NH2	2.41	0.53
34:B5:1308:G:H2'	34:B5:1309:C:C6	2.43	0.53
38:A1:876:A2M:H5''	38:A1:1890:U:H5''	1.91	0.53
38:A1:2206:G:H21	38:A1:2208:A:H62	1.56	0.53
38:A1:2273:G:O2'	38:A1:2311:G:O6	2.25	0.53
38:A1:2465:G:H1	38:A1:2491:A:N6	2.07	0.53
38:A1:2699:G:H5''	56:AT:16:GLN:NE2	2.23	0.53
38:A1:2800:G:O6	63:Aa:42:ARG:NH2	2.41	0.53
39:A3:7:G:O2'	41:AD:72:ASP:OD1	2.25	0.53
40:A4:36:G:O2'	40:A4:104:A:N1	2.35	0.53
41:AD:41:LYS:HB2	56:AT:68:THR:O	2.08	0.53
43:AF:102:VAL:HG21	43:AF:129:LEU:HD23	1.90	0.53
80:DC:197:LEU:HD22	80:DC:200:VAL:HB	1.90	0.53
10:BN:55:ARG:HD3	34:B5:960:U:H5'	1.91	0.53
18:Be:41:THR:HA	18:Be:45:VAL:HB	1.90	0.53
23:BQ:69:VAL:HB	23:BQ:81:ILE:HD11	1.89	0.53
34:B5:1358:G:H2'	34:B5:1359:C:C6	2.44	0.53
38:A1:371:G:N1	38:A1:374:A:OP2	2.37	0.53
38:A1:2357:A:H2'	38:A1:2358:A:C8	2.43	0.53
38:A1:2450:G:H5'	38:A1:2451:G:OP2	2.09	0.53
38:A1:3239:G:H2'	38:A1:3240:C:C6	2.43	0.53
51:AO:54[A]:TYR:OH	51:AO:73[A]:PHE:O	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AP:47:TYR:OH	52:AP:57:ALA:O	2.22	0.53
66:Ad:10:ARG:HD3	66:Ad:108:VAL:HG22	1.90	0.53
82:EC:6789:G:H4'	82:EC:6790:A:OP1	2.07	0.53
1:BA:66:ALA:O	12:BV:50:TYR:OH	2.25	0.53
5:BG:39:GLU:OE1	5:BG:39:GLU:N	2.39	0.53
7:BI:81:VAL:HG22	7:BI:94:ASN:HA	1.89	0.53
8:BJ:73:GLY:O	8:BJ:77:ILE:HG12	2.09	0.53
11:BO:64:ALA:HB1	11:BO:105:LEU:HD22	1.89	0.53
31:Bg:72:THR:HG22	31:Bg:81:LEU:HB2	1.89	0.53
34:B5:1559:A:H5'	34:B5:1560:U:H5'	1.91	0.53
38:A1:595:G:OP1	43:AF:33:ARG:NH2	2.42	0.53
38:A1:643:U:O2'	38:A1:1153:A:N1	2.36	0.53
38:A1:1364:C:OP1	43:AF:110:ARG:NH2	2.37	0.53
40:A4:69:U:H2'	40:A4:70:G:O4'	2.09	0.53
49:AM:112:LEU:HB3	49:AM:117:ARG:HG3	1.90	0.53
80:DC:393:ARG:HB2	80:DC:460:ASP:OD2	2.09	0.53
80:DC:411:VAL:HG21	80:DC:469:LEU:HD13	1.90	0.53
1:BA:118:PRO:HG2	1:BA:141:ILE:HD13	1.91	0.53
10:BN:13:SER:OG	10:BN:14:SER:N	2.41	0.53
34:B5:64:U:O2'	34:B5:168:A:N3	2.39	0.53
34:B5:514:G:H1	34:B5:543:C:H5	1.57	0.53
36:AB:92:TYR:HB3	36:AB:99:LEU:HG	1.91	0.53
38:A1:44:U:H5''	50:AN:85:THR:HG23	1.90	0.53
38:A1:1534:A:H2'	38:A1:1535:A:C8	2.43	0.53
54:AR:105:LEU:HD23	54:AR:138:LEU:HD23	1.91	0.53
61:AY:83:ASP:O	61:AY:84:LYS:HG2	2.08	0.53
80:DC:317:LYS:HG3	80:DC:321:LYS:NZ	2.24	0.53
4:BE:89:VAL:HG11	4:BE:164:LEU:HD21	1.90	0.53
7:BI:5:ARG:NH1	34:B5:336:G:O6	2.31	0.53
8:BJ:131:GLN:NE2	34:B5:512:A:N3	2.56	0.53
27:BU:84:MET:HE2	30:Bd:52:PHE:CZ	2.44	0.53
34:B5:979:A:N3	34:B5:1775:U:O2'	2.40	0.53
35:AA:47:GLN:HG2	35:AA:49:VAL:HG13	1.90	0.53
38:A1:2696:A:H2'	38:A1:2697:A:C8	2.43	0.53
80:DC:103:ILE:HD13	80:DC:122:THR:HG22	1.90	0.53
80:DC:407:SER:OG	80:DC:433:ARG:NH1	2.42	0.53
82:EC:6885:G:H2'	82:EC:6886:A:C8	2.43	0.53
24:BR:7:LYS:HB3	34:B5:1316:G:H5'	1.90	0.53
24:BR:79:GLU:OE2	24:BR:80:ARG:HD3	2.09	0.53
25:BS:16:ARG:HA	25:BS:21:ASN:HA	1.89	0.53
34:B5:1132:A:H2'	34:B5:1133:A:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1717:G:H2'	34:B5:1718:G:C8	2.44	0.53
34:B5:1732:A:H2'	34:B5:1733:C:C6	2.43	0.53
38:A1:1229:G:O2'	81:V:31:ASP:O	2.26	0.53
38:A1:3252:G:H2'	38:A1:3253:G:H8	1.72	0.53
51:AO:75[A]:ALA:HB3	51:AO:78[A]:ARG:HG2	1.91	0.53
54:AR:177:VAL:HG23	54:AR:178:ALA:H	1.74	0.53
62:AZ:83:THR:HG23	69:Ag:93:PHE:CZ	2.44	0.53
80:DC:12:LEU:HG	80:DC:97:SER:HB3	1.89	0.53
80:DC:20:ARG:O	80:DC:101:ASN:N	2.39	0.53
80:DC:760:ARG:HH21	80:DC:763:THR:HG21	1.73	0.53
81:V:144:LYS:NZ	81:V:145:ILE:H	2.06	0.53
2:BB:149:GLN:HE22	2:BB:154:SER:HB2	1.73	0.53
5:BG:195:VAL:O	5:BG:199:GLN:NE2	2.42	0.53
14:BX:140:LYS:NZ	34:B5:31:C:OP1	2.32	0.53
19:BD:195:SER:O	19:BD:196:ARG:HG2	2.09	0.53
28:BZ:38:HIS:NE2	28:BZ:66:VAL:O	2.36	0.53
33:BM:31:VAL:O	33:BM:34:THR:OG1	2.23	0.53
34:B5:699:U:O2'	34:B5:740:A:N1	2.30	0.53
34:B5:1606:C:H2'	34:B5:1607:G:C8	2.44	0.53
34:B5:1705:C:H2'	34:B5:1706:C:C6	2.43	0.53
38:A1:1497:C:O2'	38:A1:1602:A:N3	2.40	0.53
38:A1:2107:A:H2	38:A1:3344:A:H8	1.57	0.53
38:A1:2639:G:H2'	38:A1:2640:A2M:H8	1.91	0.53
38:A1:2897:A:OP2	75:Am:124:LYS:NZ	2.41	0.53
42:AE:50:LYS:NZ	42:AE:72:ASN:O	2.41	0.53
18:Be:55:ARG:HH21	18:Be:58:PRO:HA	1.74	0.53
19:BD:211:PRO:HG3	24:BR:19:ARG:HB2	1.90	0.53
20:BF:146:THR:HG21	20:BF:224:ASN:HD22	1.74	0.53
22:BP:18:ARG:N	25:BS:92:ILE:O	2.42	0.53
25:BS:6:GLN:NE2	28:BZ:44:GLN:HA	2.23	0.53
34:B5:1220:C:H2'	34:B5:1221:A:H8	1.73	0.53
38:A1:734:C:H3'	38:A1:735:A:H8	1.73	0.53
38:A1:1129:A:H2'	38:A1:1130:A:C8	2.44	0.53
38:A1:1497:C:H2'	38:A1:1498:A:C8	2.44	0.53
43:AF:189:ILE:HG23	43:AF:190:THR:HG23	1.91	0.53
61:AY:11:ASP:HB3	61:AY:14:LYS:HB2	1.89	0.53
80:DC:564:ARG:O	80:DC:725:GLN:N	2.39	0.53
34:B5:782:U:H4'	34:B5:783:G:H5''	1.92	0.52
34:B5:1592:A:H2'	34:B5:1593:A:C8	2.44	0.52
38:A1:126:U:OP1	50:AN:144:ARG:NH1	2.38	0.52
38:A1:421:G:O6	38:A1:2383:C:O2'	2.20	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2228:A:H2'	38:A1:2229:A:H8	1.71	0.52
40:A4:57:C:H4'	40:A4:63:G:N7	2.24	0.52
44:AG:178:ALA:HB2	44:AG:218:ILE:HG23	1.91	0.52
80:DC:150:ARG:NH1	80:DC:196:VAL:HB	2.23	0.52
80:DC:446:ASP:OD1	80:DC:447:ASP:N	2.43	0.52
80:DC:837:GLU:N	80:DC:837:GLU:OE1	2.40	0.52
8:BJ:17:ARG:NH2	34:B5:4:C:O2'	2.30	0.52
16:Ba:97:PRO:HB2	16:Ba:98:PRO:HD3	1.92	0.52
22:BP:128:HIS:NE2	34:B5:1459:C:O2	2.37	0.52
26:BT:122:ARG:NH2	34:B5:1500:C:OP1	2.27	0.52
30:Bd:31:ILE:HD11	30:Bd:40:ARG:HA	1.91	0.52
34:B5:208:U:H2'	34:B5:209:U:C6	2.45	0.52
34:B5:651:G:H2'	34:B5:652:G:H2'	1.91	0.52
34:B5:1358:G:H2'	34:B5:1359:C:H6	1.73	0.52
36:AB:123:TYR:CZ	36:AB:124:LYS:HG3	2.45	0.52
38:A1:616:G:H2'	38:A1:617:G:C8	2.43	0.52
38:A1:650:OMC:H2'	38:A1:651:G:C8	2.44	0.52
38:A1:3110:C:H2'	38:A1:3111:U:C6	2.44	0.52
38:A1:3306:U:O2'	38:A1:3308:C:OP2	2.24	0.52
57:AU:32:SER:HA	57:AU:35:LYS:HG2	1.91	0.52
57:AU:53:ALA:O	57:AU:68:THR:N	2.40	0.52
65:Ac:57:GLU:OE2	65:Ac:69:TYR:OH	2.23	0.52
80:DC:29:ASP:O	80:DC:30:HIS:ND1	2.42	0.52
80:DC:221:THR:HG23	80:DC:224:GLN:H	1.73	0.52
82:EC:6851:G:O2'	82:EC:6852:U:O5'	2.27	0.52
4:BE:31:PRO:HG3	4:BE:43:PRO:HG3	1.91	0.52
31:Bg:88:THR:HG22	31:Bg:104:VAL:HG12	1.91	0.52
34:B5:681:U:O2'	34:B5:683:C:OP2	2.27	0.52
34:B5:684:A:H2'	34:B5:685:A:C8	2.44	0.52
38:A1:251:G:O3'	38:A1:252:U:H4'	2.08	0.52
38:A1:772:U:H2'	38:A1:773:G:C8	2.43	0.52
38:A1:2579:G:OP2	38:A1:2580:A:O2'	2.22	0.52
42:AE:76:LEU:N	42:AE:138:GLN:OE1	2.39	0.52
55:AS:12:ARG:HD2	55:AS:22:PRO:HD2	1.91	0.52
66:Ad:36:ILE:HD12	66:Ad:59:ILE:HD11	1.91	0.52
73:Ak:36:LYS:HD2	73:Ak:36:LYS:O	2.08	0.52
80:DC:138:GLN:HA	80:DC:141:THR:HG22	1.91	0.52
11:BO:72:LYS:O	11:BO:73:GLU:HG3	2.10	0.52
16:Ba:44:ILE:HG21	16:Ba:65:PRO:HG2	1.90	0.52
34:B5:1231:U:H2'	34:B5:1232:U:C6	2.44	0.52
34:B5:1242:A:O2'	34:B5:1244:A:OP1	2.20	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1641:C:H2'	34:B5:1642:G:C8	2.45	0.52
38:A1:219:A:HO2'	38:A1:220:G:H21	1.56	0.52
38:A1:296:A:N3	38:A1:299:G:O2'	2.39	0.52
38:A1:656:A:H2'	38:A1:657:A:C8	2.45	0.52
38:A1:1447:G:O2'	38:A1:2355:G:O6	2.23	0.52
38:A1:1630:U:OP2	38:A1:1813:A:N6	2.41	0.52
38:A1:2836:C:H5	38:A1:2852:C:H42	1.56	0.52
21:BK:1:MET:SD	21:BK:3:MET:HB2	2.50	0.52
22:BP:115:TYR:OH	34:B5:1556:A:OP1	2.24	0.52
27:BU:96:PRO:HD2	27:BU:99:ILE:HD11	1.91	0.52
28:BZ:75:LEU:HA	28:BZ:78:ILE:HG12	1.91	0.52
34:B5:1262:U:H2'	34:B5:1263:G:C8	2.45	0.52
35:AA:28:LYS:HB2	35:AA:123:ARG:HB3	1.90	0.52
35:AA:127:ALA:HB2	35:AA:134:VAL:HG23	1.90	0.52
38:A1:2203:U:H2'	38:A1:2204:C:C6	2.45	0.52
50:AN:159:ARG:HH21	50:AN:165:THR:HG22	1.74	0.52
65:Ac:43:ILE:HG13	65:Ac:68:TYR:HB3	1.90	0.52
80:DC:314:LEU:O	80:DC:319:LEU:HD12	2.09	0.52
12:BV:39:VAL:HG13	12:BV:43:GLY:HA2	1.92	0.52
18:Be:33:ARG:HH22	34:B5:478:A:H5'	1.75	0.52
24:BR:100:LEU:HD21	24:BR:117:LEU:HD21	1.91	0.52
34:B5:1588:G:O6	34:B5:1608:U:O4	2.28	0.52
36:AB:95:THR:HG23	38:A1:3243:A:H4'	1.92	0.52
50:AN:28:TRP:O	50:AN:32:GLN:HG2	2.09	0.52
80:DC:588:LEU:HA	80:DC:689:LEU:H	1.74	0.52
5:BG:148:SER:OG	5:BG:151:ASP:OD2	2.18	0.52
34:B5:512:A:H2'	34:B5:513:U:C6	2.45	0.52
34:B5:521:A:H2'	34:B5:522:U:C6	2.43	0.52
34:B5:800:U:H2'	34:B5:801:G:C8	2.45	0.52
34:B5:1220:C:H2'	34:B5:1221:A:C8	2.45	0.52
36:AB:17:LEU:HD21	36:AB:233:TRP:HH2	1.75	0.52
38:A1:394:G:N1	38:A1:397:A:OP2	2.41	0.52
38:A1:406:G:OP1	38:A1:1415:U:O2'	2.23	0.52
38:A1:585:A:H2'	38:A1:586:C:C6	2.45	0.52
38:A1:1659:U:H2'	38:A1:1660:C:C6	2.45	0.52
45:AH:173:ARG:NH1	75:Am:125:LYS:O	2.43	0.52
3:BC:214:ALA:O	3:BC:218:ILE:HG13	2.10	0.52
14:BX:72:VAL:HG11	14:BX:96:VAL:HG11	1.92	0.52
15:BY:13:ILE:HG13	15:BY:22:GLN:HG3	1.92	0.52
32:Bf:118:ARG:NH2	34:B5:1252:C:OP1	2.23	0.52
34:B5:888:U:H2'	34:B5:889:U:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1579:U:H2'	34:B5:1580:C:H6	1.75	0.52
36:AB:58:ARG:HD2	36:AB:354:VAL:HG13	1.92	0.52
36:AB:274:SER:O	38:A1:3138:U:H5''	2.09	0.52
38:A1:567:G:H2'	38:A1:568:G:C8	2.45	0.52
38:A1:2918:G:H2'	38:A1:2919:A:H8	1.74	0.52
41:AD:52:VAL:HG21	41:AD:65:ILE:HD12	1.92	0.52
80:DC:419:VAL:HG12	80:DC:421:GLY:H	1.74	0.52
1:BA:74:VAL:HG22	1:BA:96:THR:HG23	1.92	0.52
7:BI:86:SER:OG	34:B5:328:A:N3	2.43	0.52
26:BT:118:PRO:HD2	26:BT:123:ARG:HH22	1.75	0.52
31:Bg:121:MET:HG3	31:Bg:183:LEU:HD22	1.91	0.52
32:Bf:129:GLY:H	33:BM:54:ARG:NH1	2.08	0.52
34:B5:329:G:H2'	34:B5:330:G:H8	1.75	0.52
36:AB:19:ARG:NH2	38:A1:3045:G:OP1	2.33	0.52
36:AB:380:MET:HE2	36:AB:380:MET:HA	1.92	0.52
38:A1:1290:A:H2'	38:A1:1291:A:C8	2.45	0.52
38:A1:1643:A:H2'	38:A1:1644:C:C2	2.45	0.52
38:A1:1737:U:O2	69:Ag:52:GLN:NE2	2.43	0.52
38:A1:2727:A:OP2	38:A1:2728:G:N2	2.39	0.52
38:A1:3017:A:N1	38:A1:3037:U:H5	2.08	0.52
38:A1:3266:G:OP2	42:AE:70:LYS:NZ	2.43	0.52
40:A4:12:A:H5''	52:AP:3:ARG:HB3	1.92	0.52
43:AF:233:GLU:OE1	55:AS:35:VAL:HG22	2.09	0.52
45:AH:21:LYS:HG3	45:AH:22:SER:H	1.75	0.52
49:AM:23:ILE:O	49:AM:30:GLY:N	2.42	0.52
2:BB:39:GLU:OE1	2:BB:39:GLU:N	2.43	0.52
3:BC:139:ILE:HD13	3:BC:191:ALA:HB1	1.92	0.52
12:BV:67:ASP:HA	12:BV:70:ASN:HD22	1.75	0.52
19:BD:207:THR:HG1	24:BR:40:THR:HG1	1.51	0.52
22:BP:41:VAL:HG22	22:BP:84:ILE:HG12	1.90	0.52
24:BR:32:LYS:NZ	34:B5:1388:A:OP2	2.42	0.52
25:BS:68:ARG:HG3	25:BS:71:GLN:NE2	2.25	0.52
34:B5:1171:A:O2'	34:B5:1570:A:N3	2.39	0.52
34:B5:1636:C:O2	34:B5:1765:A:N6	2.43	0.52
35:AA:181:LYS:HB2	38:A1:860:G:C5	2.44	0.52
38:A1:411:U:H2'	38:A1:412:G:H8	1.75	0.52
38:A1:884:A:OP1	72:Aj:5:THR:OG1	2.22	0.52
38:A1:1952:G:N1	38:A1:2094:C:O2'	2.36	0.52
44:AG:101:THR:N	44:AG:104:GLU:OE2	2.42	0.52
73:Ak:36:LYS:HD3	73:Ak:38:PHE:CE2	2.45	0.52
4:BE:36:HIS:CG	4:BE:85:GLY:HA3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Ba:51:ARG:HH12	29:Bc:37:SER:HB3	1.74	0.51
19:BD:3:ALA:C	19:BD:4:LEU:HD23	2.35	0.51
24:BR:56:HIS:NE2	34:B5:1401:A:OP1	2.34	0.51
29:Bc:18:ARG:NH1	29:Bc:23:GLY:O	2.39	0.51
29:Bc:22:ARG:HD3	34:B5:1162:C:H4'	1.92	0.51
33:BM:43:ARG:HH21	33:BM:103:LEU:HD22	1.75	0.51
34:B5:5:U:H2'	34:B5:6:G:C8	2.45	0.51
36:AB:113:GLU:HA	36:AB:116:ARG:HD2	1.92	0.51
38:A1:758:C:N4	38:A1:774:G:O6	2.43	0.51
38:A1:761:A:H2'	38:A1:762:U:C6	2.44	0.51
38:A1:3089:C:H2'	38:A1:3090:U:O4'	2.10	0.51
38:A1:3233:C:H2'	38:A1:3234:A:C8	2.46	0.51
38:A1:3239:G:H2'	38:A1:3240:C:H6	1.74	0.51
55:AS:94:ILE:HG22	55:AS:96:ASP:OD1	2.10	0.51
57:AU:23:THR:HG21	57:AU:30:PRO:HG3	1.92	0.51
1:BA:42:PRO:O	1:BA:43:ASP:HB2	2.11	0.51
1:BA:48:ILE:HG21	1:BA:161:PRO:HB2	1.91	0.51
18:Be:10:ARG:NH1	34:B5:566:C:O3'	2.43	0.51
30:Bd:45:GLU:OE2	34:B5:1433:G:N1	2.30	0.51
34:B5:300:A:H2'	34:B5:301:A:C8	2.44	0.51
34:B5:1609:U:H2'	34:B5:1610:G:O4'	2.10	0.51
34:B5:1710:U:H2'	34:B5:1711:C:H6	1.75	0.51
38:A1:165:A:HO2'	38:A1:166:C:H6	1.57	0.51
40:A4:29:U:H5''	48:AL:27:ASP:HB3	1.92	0.51
59:AW:38:SER:OG	59:AW:42:GLN:NE2	2.42	0.51
80:DC:688:ILE:HG21	80:DC:709:MET:HE1	1.92	0.51
11:BO:120:PRO:HB2	34:B5:887:A:H5''	1.92	0.51
19:BD:113:LEU:HD12	19:BD:114:ALA:H	1.76	0.51
24:BR:102:VAL:HG21	24:BR:119:LEU:HD11	1.93	0.51
26:BT:76:LEU:HD12	26:BT:80:TYR:HE2	1.74	0.51
38:A1:1336:U:H2'	38:A1:1337:A:H8	1.74	0.51
44:AG:70:LYS:HG2	44:AG:233:TRP:HE3	1.75	0.51
81:V:26:PHE:HZ	81:V:187:VAL:HG22	1.75	0.51
8:BJ:49:LEU:HA	8:BJ:52:ILE:HG22	1.92	0.51
9:BL:78:THR:HA	9:BL:84:ILE:HG22	1.92	0.51
18:Be:38:LEU:HA	18:Be:41:THR:HG22	1.93	0.51
19:BD:4:LEU:HD21	34:B5:1490:C:C5	2.45	0.51
34:B5:708:C:O2'	34:B5:710:U:OP2	2.24	0.51
34:B5:1352:G:N2	34:B5:1374:C:O2	2.44	0.51
34:B5:1579:U:OP1	82:EC:6904:U:N3	2.36	0.51
38:A1:2699:G:H5''	56:AT:16:GLN:HE22	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2768:U:H2'	38:A1:2769:A:H8	1.75	0.51
39:A3:12:U:OP2	39:A3:68:C:O2'	2.27	0.51
1:BA:76:ILE:HD13	1:BA:98:ILE:HB	1.92	0.51
5:BG:27:PHE:CE1	5:BG:36:VAL:HG21	2.45	0.51
15:BY:35:VAL:HG23	15:BY:36:SER:H	1.75	0.51
28:BZ:57:TYR:O	28:BZ:103:ARG:NE	2.37	0.51
32:Bf:135:HIS:CD2	34:B5:1250:U:HO2'	2.27	0.51
34:B5:30:G:H2'	34:B5:31:C:C6	2.45	0.51
38:A1:897:U:H2'	38:A1:898:OMU:H6	1.93	0.51
38:A1:2406:C:H2'	38:A1:2407:C:H6	1.75	0.51
38:A1:2768:U:H2'	38:A1:2769:A:C8	2.45	0.51
42:AE:84:VAL:O	68:Af:105:SER:OG	2.24	0.51
44:AG:144:GLU:OE2	50:AN:6:TYR:OH	2.18	0.51
47:AJ:25:GLU:HA	47:AJ:65:ILE:HG22	1.93	0.51
56:AT:152:ALA:HB1	56:AT:153:PRO:HD2	1.93	0.51
79:E:65:ILE:HB	79:E:109:ALA:HB3	1.92	0.51
80:DC:481:MET:C	80:DC:483:PHE:H	2.18	0.51
1:BA:121:VAL:HG23	1:BA:141:ILE:HG21	1.91	0.51
2:BB:132:ASP:HB3	2:BB:221:PRO:HB3	1.92	0.51
4:BE:45:ILE:HA	4:BE:61:VAL:HG11	1.93	0.51
7:BI:137:LYS:HE3	7:BI:141:ARG:HH21	1.74	0.51
31:Bg:35:SER:OG	31:Bg:45:TRP:NE1	2.36	0.51
34:B5:58:U:OP1	34:B5:456:A:O2'	2.25	0.51
34:B5:304:U:H2'	34:B5:305:C:C6	2.45	0.51
34:B5:592:A:O2'	34:B5:596:C:OP1	2.29	0.51
34:B5:1027:A:OP1	34:B5:1789:G:O2'	2.23	0.51
38:A1:1193:A:OP1	51:AO:49[A]:ARG:NH2	2.32	0.51
38:A1:1836:C:H41	74:Al:3:ALA:HB2	1.75	0.51
55:AS:90:MET:HE1	55:AS:114:HIS:CE1	2.46	0.51
66:Ad:44:MET:O	66:Ad:77:ARG:NH1	2.42	0.51
80:DC:731:VAL:HG22	80:DC:796:MET:HB3	1.92	0.51
16:Ba:2:PRO:HB3	34:B5:1142:A:H5''	1.92	0.51
18:Be:33:ARG:HH12	34:B5:478:A:C5'	2.22	0.51
21:BK:10:LYS:HG2	21:BK:35:ILE:HG23	1.93	0.51
27:BU:33:GLN:HB3	27:BU:109:GLU:OE2	2.10	0.51
32:Bf:135:HIS:NE2	34:B5:1250:U:O2'	2.32	0.51
34:B5:1188:G:O2'	34:B5:1430:U:OP1	2.27	0.51
34:B5:1237:G:H2'	34:B5:1238:A:C8	2.43	0.51
37:AC:11:LEU:HD12	37:AC:168:ALA:HB1	1.93	0.51
38:A1:12:A:H2'	38:A1:13:A:C8	2.46	0.51
43:AF:176:TYR:CZ	43:AF:197:GLN:HG2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:AI:38:LYS:HG3	46:AI:41:ALA:HB2	1.92	0.51
80:DC:119:LEU:HD21	80:DC:146:ALA:HA	1.92	0.51
2:BB:103:MET:HE1	2:BB:212:VAL:HG23	1.93	0.51
7:BI:64:ASN:ND2	34:B5:257:A:N3	2.59	0.51
20:BF:57:SER:OG	20:BF:167:ARG:NH1	2.44	0.51
37:AC:263:GLY:HA2	37:AC:267:VAL:HG23	1.93	0.51
38:A1:1810:A:H2'	38:A1:1811:G:C8	2.46	0.51
55:AS:10:ILE:HD12	55:AS:60:SER:HB3	1.93	0.51
82:EC:6823:U:H2'	82:EC:6824:C:H6	1.76	0.51
82:EC:6831:U:H1'	82:EC:6832:G:C8	2.46	0.51
10:BN:54:LEU:HB3	10:BN:60:VAL:CG2	2.41	0.51
13:BW:90:THR:HG23	13:BW:94:LEU:HD12	1.93	0.51
21:BK:73:VAL:O	21:BK:77:ARG:HG2	2.10	0.51
22:BP:85:ILE:HG13	22:BP:111:MET:HG3	1.92	0.51
34:B5:1590:G:H2'	34:B5:1591:C:C6	2.46	0.51
38:A1:649:A2M:H2'	38:A1:650:OMC:C6	2.46	0.51
38:A1:1108:U:H2'	38:A1:1109:U:C6	2.46	0.51
38:A1:2496:C:O2'	38:A1:2497:U:OP1	2.29	0.51
39:A3:118:A:H5''	41:AD:253:PHE:CZ	2.45	0.51
41:AD:80:SER:OG	41:AD:92:LEU:O	2.25	0.51
57:AU:54:VAL:HA	57:AU:67:SER:HA	1.93	0.51
62:AZ:9:LYS:HD2	62:AZ:83:THR:O	2.11	0.51
80:DC:694:HIS:O	80:DC:700:ARG:NH1	2.43	0.51
82:EC:6911:A:O2'	82:EC:6912:G:OP1	2.27	0.51
10:BN:102:LEU:HD11	10:BN:112:LYS:HA	1.93	0.51
22:BP:118:GLU:O	25:BS:122:HIS:N	2.43	0.51
23:BQ:59:LYS:HE2	23:BQ:93:HIS:CE1	2.46	0.51
25:BS:13:HIS:CD2	25:BS:14:ILE:H	2.29	0.51
27:BU:59:PRO:HG3	34:B5:1381:U:H4'	1.92	0.51
36:AB:296:THR:OG1	36:AB:357:LYS:O	2.28	0.51
38:A1:149:U:P	50:AN:49:ARG:HH12	2.33	0.51
38:A1:994:G:N2	38:A1:995:U:O4	2.38	0.51
38:A1:2430:A:H2'	38:A1:2431:C:C6	2.46	0.51
38:A1:2779:A:O2'	48:AL:180:ARG:NH2	2.44	0.51
39:A3:23:A:H2'	39:A3:24:A:C8	2.46	0.51
44:AG:70:LYS:HG2	44:AG:233:TRP:CE3	2.46	0.51
61:AY:106:ILE:HG21	61:AY:109:LEU:HD23	1.93	0.51
65:Ac:81:VAL:HG23	65:Ac:83:LYS:HG2	1.91	0.51
82:EC:6893:C:OP2	82:EC:6894:C:N4	2.41	0.51
1:BA:88:LYS:HD3	1:BA:201:LEU:HD13	1.93	0.50
6:BH:12:ALA:N	6:BH:13:PRO:HG2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:57:GLU:O	17:Bb:60:SER:OG	2.28	0.50
18:Be:31:LYS:HD3	34:B5:545:A:H2'	1.92	0.50
20:BF:166:ARG:HA	20:BF:169:ASN:HB2	1.91	0.50
20:BF:168:VAL:O	20:BF:172:ILE:HG12	2.11	0.50
34:B5:694:U:H3'	34:B5:695:U:H6	1.76	0.50
38:A1:1047:A:N3	38:A1:2633:U:O2'	2.43	0.50
38:A1:1277:C:H2'	38:A1:1278:A:H8	1.76	0.50
38:A1:2471:U:H3	38:A1:2474:G:H22	1.59	0.50
38:A1:2801:A:O2'	38:A1:2802:A:H2'	2.11	0.50
55:AS:138:GLN:HA	55:AS:141:LYS:HB2	1.93	0.50
82:EC:6890:A:H2'	82:EC:6891:G:H21	1.76	0.50
1:BA:48:ILE:HG12	1:BA:149:LEU:HD21	1.92	0.50
26:BT:76:LEU:HD12	26:BT:80:TYR:CE2	2.46	0.50
28:BZ:49:ARG:HA	28:BZ:52:LYS:HG2	1.94	0.50
34:B5:1487:A:H2'	34:B5:1488:G:C8	2.46	0.50
35:AA:21:ARG:NH1	38:A1:825:U:OP2	2.42	0.50
38:A1:2683:U:H2'	38:A1:2684:C:C6	2.47	0.50
38:A1:3067:C:H3'	54:AR:62:ARG:HH22	1.75	0.50
38:A1:3291:G:H2'	38:A1:3292:A:H8	1.75	0.50
51:AO:46[A]:GLU:HG3	51:AO:49[A]:ARG:H	1.76	0.50
69:Ag:29:ILE:HD11	69:Ag:31:ARG:HH21	1.76	0.50
80:DC:703:GLY:O	80:DC:707:PRO:HD3	2.12	0.50
1:BA:157:ASP:OD1	12:BV:60:ARG:NH1	2.40	0.50
10:BN:91:LEU:HB3	10:BN:122:ILE:HG12	1.93	0.50
14:BX:56:LYS:NZ	14:BX:93:LEU:O	2.30	0.50
14:BX:108:GLY:HA2	34:B5:600:U:OP2	2.11	0.50
25:BS:38:VAL:HG23	25:BS:42:TYR:HB3	1.94	0.50
28:BZ:60:VAL:HB	28:BZ:101:TYR:HB2	1.94	0.50
34:B5:80:A:H3'	34:B5:81:G:H5'	1.92	0.50
34:B5:907:A:H2'	34:B5:908:U:H6	1.76	0.50
34:B5:1370:U:H3	34:B5:1374:C:H41	1.58	0.50
38:A1:68:C:OP2	38:A1:301:G:N2	2.45	0.50
38:A1:1334:U:H2'	38:A1:1335:C:C6	2.46	0.50
38:A1:2492:C:H2'	38:A1:2493:U:H4'	1.93	0.50
38:A1:2615:G:H2'	38:A1:2616:C:H6	1.76	0.50
44:AG:91:PHE:CE2	44:AG:185:ARG:HG2	2.45	0.50
46:AI:177:ASP:OD1	46:AI:178:ARG:N	2.44	0.50
56:AT:8:ARG:O	56:AT:11:THR:OG1	2.29	0.50
60:AX:108:LEU:HD23	60:AX:125:ARG:HD3	1.94	0.50
82:EC:6813:A:H2'	82:EC:6814:G:C8	2.47	0.50
1:BA:11:PRO:HA	24:BR:115:LEU:HD23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:21:ASP:N	4:BE:21:ASP:OD1	2.43	0.50
5:BG:164:LYS:HZ3	5:BG:167:LYS:HB3	1.76	0.50
9:BL:133:LYS:HB2	34:B5:337:G:H3'	1.93	0.50
10:BN:73:ARG:HD3	34:B5:859:A:C5	2.47	0.50
24:BR:20:TYR:CZ	24:BR:23:LYS:HB2	2.46	0.50
27:BU:39:SER:HA	27:BU:42:VAL:HG12	1.94	0.50
27:BU:55:PRO:HA	27:BU:91:ILE:HG13	1.94	0.50
27:BU:70:THR:HG23	27:BU:72:ASN:O	2.11	0.50
33:BM:75:VAL:HG21	33:BM:120:VAL:HG11	1.93	0.50
34:B5:652:G:O3'	34:B5:682:C:N4	2.44	0.50
35:AA:2:GLY:O	38:A1:925:A:N6	2.40	0.50
37:AC:344:ALA:HB2	38:A1:516:A:H5''	1.93	0.50
38:A1:209:A:H4'	38:A1:211:A:N7	2.25	0.50
38:A1:1622:U:H2'	38:A1:1623:G:C8	2.45	0.50
38:A1:2217:U:H2'	38:A1:2218:G:H8	1.77	0.50
38:A1:2407:C:H2'	38:A1:2408:U:C6	2.46	0.50
38:A1:2662:G:H2'	38:A1:2663:G:C8	2.46	0.50
38:A1:3108:G:H1'	45:AH:166:ARG:HH21	1.75	0.50
38:A1:3295:A:H2'	38:A1:3296:A:C8	2.46	0.50
38:A1:3308:C:O2'	52:AP:69:ARG:O	2.23	0.50
46:AI:188:GLY:HA3	46:AI:216:TYR:HB2	1.92	0.50
68:Af:49:ILE:HG12	68:Af:100:ILE:HG13	1.93	0.50
68:Af:49:ILE:HD11	68:Af:71:VAL:HG22	1.94	0.50
74:Al:9:ILE:HD12	74:Al:51:ILE:HG13	1.92	0.50
80:DC:221:THR:HG22	80:DC:224:GLN:HB2	1.94	0.50
80:DC:593:ILE:HG12	80:DC:685:ARG:HB2	1.91	0.50
80:DC:615:ARG:NH2	80:DC:633:ILE:O	2.44	0.50
80:DC:736:PRO:O	80:DC:740:VAL:HG23	2.11	0.50
82:EC:6827:G:H2'	82:EC:6828:G:C8	2.46	0.50
1:BA:148:ASP:OD1	1:BA:149:LEU:N	2.37	0.50
8:BJ:25:ASP:OD1	8:BJ:26:ALA:N	2.44	0.50
20:BF:113:ILE:O	20:BF:117:THR:HG23	2.12	0.50
31:Bg:37:SER:HB2	31:Bg:39:ASP:OD1	2.12	0.50
38:A1:1616:U:H2'	38:A1:1617:G:C8	2.47	0.50
38:A1:1798:A:H2'	38:A1:1799:A:C8	2.47	0.50
38:A1:2154:U:H2'	38:A1:2155:G:H8	1.76	0.50
38:A1:2413:A:H2'	38:A1:2414:G:H8	1.77	0.50
38:A1:2881:C:H2'	38:A1:2882:U:C6	2.47	0.50
39:A3:121:U:H5''	41:AD:265:TYR:HE1	1.77	0.50
78:Ap:79:VAL:O	78:Ap:83:ILE:HG12	2.11	0.50
80:DC:110:ASP:HB2	80:DC:537:HIS:HB2	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:174:LEU:HD21	80:DC:282:PHE:HZ	1.75	0.50
80:DC:565:GLU:HB3	80:DC:717:PHE:HZ	1.76	0.50
80:DC:699:DDE:HAB2	82:EC:6952:U:H4'	1.93	0.50
81:V:60:ARG:NH2	81:V:80:VAL:O	2.44	0.50
81:V:126:THR:HG21	81:V:128:MET:HE3	1.94	0.50
82:EC:6949:G:O2'	82:EC:6950:C:OP2	2.29	0.50
5:BG:27:PHE:HE1	5:BG:36:VAL:HG11	1.77	0.50
7:BI:32:GLN:HE22	34:B5:1727:G:H21	1.60	0.50
8:BJ:149:ARG:HG3	8:BJ:151:ASP:OD1	2.11	0.50
24:BR:45:ARG:NH1	34:B5:1332:C:OP2	2.40	0.50
26:BT:84:LYS:HE3	26:BT:86:ARG:HG2	1.93	0.50
34:B5:1429:G:H2'	34:B5:1430:U:C6	2.47	0.50
38:A1:86:G:O2'	38:A1:98:G:O6	2.29	0.50
38:A1:1333:C:OP1	53:AQ:2:GLY:N	2.44	0.50
38:A1:1498:A:H2'	38:A1:1499:C:C6	2.47	0.50
39:A3:71:G:H2'	39:A3:72:A:C8	2.46	0.50
40:A4:63:G:H22	40:A4:97:A:H2	1.58	0.50
55:AS:45:LEU:HD23	55:AS:51:VAL:HG21	1.94	0.50
78:Ap:46:THR:HG1	78:Ap:57:CYS:HG	1.60	0.50
80:DC:489:VAL:HB	80:DC:538:LEU:HD11	1.94	0.50
81:V:18:TYR:CE1	81:V:50:VAL:HG11	2.46	0.50
81:V:38:MET:HE2	81:V:42:ARG:HH22	1.76	0.50
81:V:53:MET:HB3	81:V:85:GLY:HA2	1.94	0.50
81:V:55:LYS:HD3	81:V:84:VAL:H	1.76	0.50
20:BF:186:ASN:HD21	20:BF:188:LYS:HB2	1.77	0.50
34:B5:1355:C:H2'	34:B5:1356:U:H6	1.75	0.50
47:AJ:16:LYS:HE3	47:AJ:130:VAL:HG21	1.94	0.50
50:AN:183:THR:O	50:AN:183:THR:OG1	2.28	0.50
79:E:10:ARG:HD3	79:E:180:VAL:HG11	1.93	0.50
80:DC:169:VAL:HG13	80:DC:174:LEU:HD23	1.94	0.50
11:BO:47:LYS:NZ	11:BO:66:ASP:OD2	2.31	0.50
29:Bc:44:VAL:HG11	29:Bc:48:VAL:HB	1.94	0.50
32:Bf:102:VAL:HG13	33:BM:45:LEU:HD12	1.94	0.50
34:B5:256:A:H2'	34:B5:257:A:O4'	2.12	0.50
34:B5:741:C:H4'	34:B5:742:U:H5'	1.94	0.50
36:AB:57:VAL:HG22	36:AB:73:VAL:HG22	1.94	0.50
38:A1:98:G:N7	48:AL:13:HIS:NE2	2.55	0.50
38:A1:292:U:OP2	50:AN:68:ARG:NH2	2.40	0.50
38:A1:631:U:H2'	38:A1:632:G:C8	2.46	0.50
38:A1:999:G:N3	38:A1:1002:A:N6	2.59	0.50
38:A1:3013:U:H2'	38:A1:3014:U:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:A3:52:G:O2'	39:A3:53:U:OP1	2.28	0.50
62:AZ:16:GLY:C	62:AZ:18:TYR:H	2.20	0.50
82:EC:6822:U:H2'	82:EC:6823:U:H5''	1.94	0.50
5:BG:63:MET:HA	5:BG:98:ARG:HB3	1.93	0.50
10:BN:4:MET:HE3	10:BN:121:ARG:HG3	1.94	0.50
12:BV:49:GLU:N	12:BV:49:GLU:OE1	2.45	0.50
34:B5:1458:G:O2'	34:B5:1459:C:OP1	2.26	0.50
38:A1:1039:U:H2'	38:A1:1040:A:C8	2.47	0.50
38:A1:1088:U:C2	38:A1:1089:G:C8	3.00	0.50
38:A1:1615:C:H2'	38:A1:1616:U:H6	1.75	0.50
38:A1:2471:U:O2	38:A1:2475:G:O6	2.30	0.50
38:A1:3291:G:H2'	38:A1:3292:A:C8	2.47	0.50
45:AH:57:VAL:HG23	45:AH:68:LEU:HD13	1.94	0.50
60:AX:67:ILE:HD13	60:AX:121:LYS:HD3	1.94	0.50
61:AY:86:THR:HG22	61:AY:96:PRO:HA	1.94	0.50
80:DC:634:TRP:CG	80:DC:660:LYS:HE3	2.46	0.50
80:DC:753:GLN:HB3	80:DC:771:TYR:HB2	1.94	0.50
2:BB:77:GLU:OE1	11:BO:114:ARG:NH2	2.42	0.49
21:BK:92:ILE:HG13	21:BK:92:ILE:O	2.11	0.49
28:BZ:77:ARG:O	28:BZ:81:ARG:HG2	2.12	0.49
31:Bg:102:ARG:NH1	34:B5:1342:C:H5''	2.27	0.49
34:B5:17:C:H2'	34:B5:18:C:C6	2.46	0.49
34:B5:264:G:H5''	34:B5:265:A:H5'	1.94	0.49
34:B5:272:U:O2'	34:B5:284:G:N2	2.45	0.49
34:B5:404:G:H2'	34:B5:405:C:C6	2.47	0.49
34:B5:448:C:H2'	34:B5:449:C:C6	2.46	0.49
34:B5:1449:U:H2'	34:B5:1450:U:C6	2.47	0.49
34:B5:1458:G:H2'	34:B5:1458:G:N3	2.27	0.49
34:B5:1504:G:H2'	34:B5:1505:A:C8	2.47	0.49
34:B5:1693:A:H2'	34:B5:1694:A:C8	2.47	0.49
38:A1:412:G:H2'	38:A1:413:U:C6	2.47	0.49
38:A1:729:C:O2'	53:AQ:79:LYS:NZ	2.44	0.49
38:A1:1604:G:H4'	38:A1:1835:A:H4'	1.94	0.49
38:A1:2426:U:H2'	38:A1:2427:U:C6	2.47	0.49
38:A1:2632:G:H5''	56:AT:12:ARG:HB2	1.94	0.49
38:A1:3164:C:O2'	38:A1:3165:A:H8	1.93	0.49
38:A1:3215:A:H5''	68:Af:2:ALA:HB2	1.93	0.49
48:AL:53:LEU:HD22	48:AL:94:GLY:HA2	1.93	0.49
48:AL:102:GLN:HB2	48:AL:104:ARG:NH2	2.26	0.49
61:AY:74:TYR:HD2	61:AY:77:LYS:HB2	1.77	0.49
82:EC:6804:A:O2'	82:EC:6808:G:N2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:EC:6811:G:H2'	82:EC:6812:C:C6	2.46	0.49
1:BA:147:THR:OG1	1:BA:151:SER:HB2	2.12	0.49
3:BC:120:GLU:HG3	3:BC:123:GLY:H	1.77	0.49
20:BF:49:GLU:O	20:BF:50:GLU:HG3	2.12	0.49
20:BF:73:THR:OG1	20:BF:91:GLU:OE1	2.31	0.49
25:BS:28:ILE:HD11	25:BS:56:LYS:H	1.77	0.49
26:BT:22:LEU:HB3	26:BT:55:TYR:HD1	1.77	0.49
34:B5:97:C:H2'	34:B5:98:U:C6	2.48	0.49
34:B5:407:A:H2'	34:B5:408:C:H6	1.77	0.49
34:B5:925:G:H2'	34:B5:926:A:C8	2.46	0.49
38:A1:824:C:O2'	38:A1:1534:A:N3	2.39	0.49
38:A1:1138:U:OP1	64:Ab:13:THR:HG21	2.12	0.49
38:A1:3296:A:H2'	38:A1:3297:U:C6	2.47	0.49
60:AX:46:TYR:CD2	70:Ah:75:TYR:HB3	2.47	0.49
6:BH:179:LYS:NZ	34:B5:640:U:O2	2.33	0.49
8:BJ:172:VAL:HG23	34:B5:511:A:H5''	1.95	0.49
10:BN:151:ASN:ND2	65:Ac:82:GLY:HA2	2.28	0.49
16:Ba:84:VAL:O	34:B5:1797:A:N6	2.40	0.49
17:Bb:56:CYS:SG	17:Bb:57:GLU:N	2.86	0.49
22:BP:25:LEU:HA	22:BP:28:MET:HE2	1.93	0.49
31:Bg:123:ILE:HD12	31:Bg:133:VAL:HG22	1.95	0.49
34:B5:451:A:N6	34:B5:453:U:O2	2.45	0.49
34:B5:1456:C:OP1	34:B5:1457:C:O2'	2.22	0.49
35:AA:119:LYS:NZ	38:A1:2590:A:O2'	2.39	0.49
38:A1:1846:C:OP1	38:A1:1849:C:N4	2.26	0.49
40:A4:71:A:O2'	61:AY:52:ARG:NH1	2.45	0.49
42:AE:39:VAL:HG11	42:AE:158:TYR:HE2	1.76	0.49
44:AG:78:PHE:C	44:AG:80:TYR:H	2.21	0.49
61:AY:17:LYS:O	61:AY:21:THR:OG1	2.28	0.49
71:Ai:27:SER:C	71:Ai:29:LYS:H	2.20	0.49
80:DC:366:CYS:O	80:DC:369:ILE:HG22	2.12	0.49
80:DC:512:SER:HA	80:DC:518:VAL:HG13	1.93	0.49
80:DC:565:GLU:OE2	80:DC:677:PHE:HB3	2.12	0.49
5:BG:178:LEU:HD21	34:B5:78:A:C2	2.48	0.49
8:BJ:80:LEU:HD12	8:BJ:96:VAL:HG22	1.93	0.49
22:BP:97:TYR:OH	34:B5:1211:A:H1'	2.13	0.49
25:BS:135:GLY:HA3	34:B5:1559:A:O5'	2.12	0.49
26:BT:53:TRP:CH2	26:BT:100:ILE:HD11	2.46	0.49
34:B5:980:G:H4'	34:B5:1776:A:H4'	1.92	0.49
35:AA:37:ARG:NH2	38:A1:2526:C:OP1	2.30	0.49
38:A1:952:A:H4'	38:A1:968:G:H22	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1597:C:H2'	38:A1:1598:G:C8	2.48	0.49
58:AV:104:ASN:OD1	58:AV:108:GLU:N	2.45	0.49
79:E:160:LYS:HE2	79:E:162:VAL:HB	1.94	0.49
3:BC:80:VAL:HG12	3:BC:102:VAL:HG22	1.93	0.49
3:BC:116:LYS:HG2	3:BC:127:ALA:HB3	1.94	0.49
4:BE:77:ARG:NH2	34:B5:123:G:OP1	2.40	0.49
9:BL:40:LEU:HG	34:B5:246:G:C2	2.47	0.49
10:BN:124:ARG:NH2	34:B5:967:A:OP2	2.45	0.49
20:BF:99:MET:HB2	20:BF:180:ARG:CZ	2.42	0.49
26:BT:117:SER:HB3	26:BT:123:ARG:HB3	1.93	0.49
34:B5:1132:A:H2'	34:B5:1133:A:C8	2.47	0.49
37:AC:181:VAL:O	37:AC:182:LEU:HG	2.11	0.49
38:A1:662:U:H2'	38:A1:663:OMC:C6	2.47	0.49
38:A1:1682:U:O2	57:AU:82:LYS:HD2	2.12	0.49
50:AN:15:GLN:HB3	71:AI:52:PRO:HD2	1.94	0.49
50:AN:51:LEU:O	50:AN:117:ASN:ND2	2.41	0.49
60:AX:63:ILE:HD13	60:AX:86:VAL:HG12	1.94	0.49
73:AK:7:ASP:OD1	73:AK:7:ASP:N	2.40	0.49
80:DC:701:GLY:C	80:DC:703:GLY:N	2.63	0.49
82:EC:6831:U:H4'	82:EC:6832:G:OP1	2.10	0.49
2:BB:137:ILE:HD13	2:BB:215:VAL:HG22	1.94	0.49
7:BI:25:ARG:HA	34:B5:400:A:H5''	1.95	0.49
34:B5:368:U:H2'	34:B5:369:A:O4'	2.13	0.49
34:B5:580:A:O2'	34:B5:582:U:OP1	2.30	0.49
34:B5:1308:G:H2'	34:B5:1309:C:H6	1.77	0.49
38:A1:622:A:O4'	68:AF:60:ARG:NH2	2.45	0.49
38:A1:1508:C:OP1	52:AP:127:ARG:NH2	2.31	0.49
38:A1:1572:U:HO2'	38:A1:1573:G:H8	1.60	0.49
38:A1:3037:U:H2'	38:A1:3038:U:C6	2.47	0.49
56:AT:92:ARG:HB3	56:AT:94:GLU:OE1	2.11	0.49
74:AI:28:ARG:HA	74:AI:33:ASN:HD22	1.77	0.49
80:DC:348:ALA:HB1	80:DC:352:ARG:NH2	2.28	0.49
82:EC:6944:U:H3'	82:EC:6945:U:H5'	1.94	0.49
4:BE:103:TYR:CG	4:BE:189:LEU:HD11	2.47	0.49
19:BD:53:THR:HG21	19:BD:94:ARG:HD3	1.94	0.49
22:BP:57:MET:HE2	22:BP:88:GLU:HG2	1.95	0.49
25:BS:91:ASP:OD1	25:BS:92:ILE:N	2.46	0.49
26:BT:15:ILE:HG21	34:B5:1479:A:H4'	1.94	0.49
27:BU:80:GLU:OE2	30:Bd:54:LYS:NZ	2.36	0.49
33:BM:32:LEU:HD12	33:BM:35:ALA:HB3	1.93	0.49
34:B5:1489:U:OP2	34:B5:1515:A:N6	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1699:G:N2	34:B5:1700:C:H1'	2.28	0.49
36:AB:41:VAL:HG12	36:AB:183:LEU:HD12	1.94	0.49
37:AC:81:GLY:O	38:A1:356:C:O2'	2.24	0.49
38:A1:129:U:H2'	38:A1:130:A:H8	1.78	0.49
38:A1:2461:A:O2'	38:A1:2485:A:N1	2.38	0.49
38:A1:2676:A:H5'	38:A1:2677:G:C8	2.48	0.49
42:AE:87:THR:HG22	42:AE:176:PHE:HB3	1.93	0.49
62:AZ:23:VAL:HG12	62:AZ:45:GLY:HA3	1.94	0.49
80:DC:71:LYS:HD2	80:DC:387:PRO:HG2	1.94	0.49
80:DC:279:ASP:OD1	80:DC:283:ARG:NH1	2.45	0.49
80:DC:632:LYS:HB3	80:DC:648:ASP:OD1	2.13	0.49
82:EC:6812:C:H2'	82:EC:6813:A:C8	2.47	0.49
2:BB:137:ILE:HG21	2:BB:172:LEU:HD22	1.94	0.49
4:BE:95:THR:OG1	4:BE:97:GLU:OE1	2.30	0.49
7:BI:48:THR:OG1	7:BI:52:ASN:O	2.26	0.49
7:BI:146:ARG:NH2	34:B5:186:C:OP1	2.42	0.49
15:BY:124:ARG:O	15:BY:128:LYS:HG2	2.13	0.49
33:BM:81:ASP:HB2	33:BM:84:ASN:HB3	1.94	0.49
34:B5:629:U:H2'	34:B5:630:A:H8	1.78	0.49
34:B5:850:A:O2'	34:B5:851:U:OP1	2.31	0.49
34:B5:1124:A:H2'	34:B5:1125:A:O4'	2.13	0.49
36:AB:211:GLN:NE2	36:AB:283:TYR:O	2.35	0.49
37:AC:3:ARG:HH21	37:AC:22:LEU:HB3	1.78	0.49
38:A1:177:U:H2'	38:A1:178:U:C6	2.47	0.49
38:A1:229:G:H5''	61:AY:4:GLN:HB2	1.95	0.49
38:A1:1580:A:H2'	38:A1:1581:C:C1'	2.43	0.49
38:A1:2467:G:H5''	79:E:29:LEU:HD21	1.95	0.49
38:A1:3253:G:H2'	38:A1:3254:G:H8	1.77	0.49
46:AI:68:ALA:HB2	46:AI:158:LYS:HB2	1.93	0.49
55:AS:10:ILE:HG12	55:AS:26:ARG:HG3	1.94	0.49
65:Ac:45:ALA:HB2	65:Ac:77:LEU:HD12	1.95	0.49
68:Af:14:LEU:HD11	68:Af:31:LYS:HB2	1.94	0.49
70:Ah:5:LYS:HB2	70:Ah:8:GLU:OE1	2.12	0.49
70:Ah:83:LYS:O	72:Aj:73:ARG:NH2	2.46	0.49
6:BH:163:ASP:OD1	6:BH:164:TYR:N	2.46	0.49
11:BO:133:ARG:NH1	34:B5:1786:G:OP2	2.45	0.49
31:Bg:123:ILE:HG21	31:Bg:169:ILE:HG21	1.95	0.49
31:Bg:276:PRO:HG3	31:Bg:305:TYR:CZ	2.48	0.49
34:B5:632:U:O2'	34:B5:1103:U:OP1	2.24	0.49
34:B5:1151:A:H2'	34:B5:1152:A:H8	1.78	0.49
34:B5:1648:A:H2'	34:B5:1649:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:363:G:OP2	72:Aj:56:ARG:NH2	2.40	0.49
38:A1:673:U:H2'	38:A1:674:G:C8	2.48	0.49
38:A1:939:U:O2'	38:A1:2402:A:N1	2.42	0.49
38:A1:1017:C:H1'	38:A1:1035:G:H22	1.77	0.49
38:A1:1119:C:H2'	38:A1:1120:A:C8	2.46	0.49
38:A1:2901:G:O2'	38:A1:3024:A:N1	2.45	0.49
44:AG:219:ASP:HB2	44:AG:223:ALA:HB3	1.95	0.49
49:AM:20:VAL:HG21	49:AM:90:VAL:HG11	1.95	0.49
80:DC:141:THR:HA	80:DC:144:ARG:HE	1.78	0.49
1:BA:175:TYR:CD2	1:BA:199:PRO:HB3	2.47	0.49
6:BH:159:VAL:HG11	6:BH:185:ILE:HG12	1.94	0.49
8:BJ:89:ASP:OD1	8:BJ:89:ASP:N	2.46	0.49
8:BJ:106:GLU:O	8:BJ:112:GLN:NE2	2.41	0.49
15:BY:26:ASP:OD1	15:BY:26:ASP:N	2.44	0.49
18:Be:33:ARG:NH1	34:B5:478:A:H5'	2.24	0.49
20:BF:123:VAL:O	28:BZ:58:ARG:NE	2.46	0.49
21:BK:32:HIS:N	21:BK:37:THR:O	2.46	0.49
34:B5:823:G:C6	34:B5:850:A:N6	2.81	0.49
34:B5:973:A:H2'	34:B5:974:A2M:H8	1.94	0.49
34:B5:976:G:N1	34:B5:1023:A:O2'	2.31	0.49
34:B5:1484:G:H2'	34:B5:1485:C:C6	2.48	0.49
36:AB:232:ARG:NH1	36:AB:266:ARG:O	2.41	0.49
38:A1:1176:C:OP1	51:AO:25[A]:LYS:NZ	2.36	0.49
38:A1:1363:A:H2'	38:A1:1364:C:O4'	2.13	0.49
38:A1:1667:A:H2'	38:A1:1668:G:H8	1.78	0.49
38:A1:2219:A:H2'	38:A1:2220:A2M:C8	2.43	0.49
38:A1:2597:U:H2'	38:A1:2598:G:H8	1.77	0.49
38:A1:2611:U:H2'	38:A1:2612:U:H6	1.77	0.49
69:Ag:91:ARG:O	69:Ag:95:ILE:HG12	2.13	0.49
79:E:190:PHE:O	79:E:194:LEU:HG	2.13	0.49
81:V:122:ARG:HG3	81:V:124:VAL:HG12	1.93	0.49
1:BA:107:PHE:HB2	1:BA:135:GLU:HG3	1.94	0.48
5:BG:57:ASP:HA	5:BG:107:ALA:H	1.77	0.48
15:BY:44:LEU:HA	15:BY:47:VAL:HG12	1.94	0.48
19:BD:72:LEU:HG	21:BK:20:VAL:HG21	1.95	0.48
31:Bg:116:ASP:HB3	31:Bg:120:SER:HB2	1.94	0.48
34:B5:1543:A:H1'	34:B5:1569:A:C2	2.48	0.48
35:AA:11:GLY:O	38:A1:2171:G:N2	2.41	0.48
36:AB:297:SER:HA	36:AB:300:ARG:NH1	2.27	0.48
38:A1:92:G:H5'	38:A1:94:G:N7	2.28	0.48
38:A1:245:U:H5''	38:A1:245:U:C6	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1662:G:H22	38:A1:1787:A:H2	1.59	0.48
38:A1:2154:U:H2'	38:A1:2155:G:C8	2.48	0.48
38:A1:2218:G:H2'	38:A1:2219:A:H8	1.76	0.48
51:AO:113[A]:ASP:N	51:AO:113[A]:ASP:OD1	2.46	0.48
73:Ak:19:ASP:OD1	73:Ak:20:VAL:N	2.47	0.48
80:DC:418:TYR:CZ	80:DC:426:LEU:HD13	2.48	0.48
80:DC:723:LYS:HA	80:DC:808:PRO:HG3	1.94	0.48
4:BE:27:TYR:O	34:B5:447:U:O2'	2.30	0.48
7:BI:54:LYS:NZ	34:B5:333:A:OP2	2.46	0.48
20:BF:186:ASN:ND2	20:BF:188:LYS:HB2	2.28	0.48
22:BP:50:THR:H	22:BP:52:LYS:HZ1	1.61	0.48
34:B5:1061:A:H3'	34:B5:1062:A:H5''	1.95	0.48
34:B5:1214:U:H2'	34:B5:1215:C:C6	2.49	0.48
36:AB:250:ALA:HB1	38:A1:2947:G:C2	2.48	0.48
38:A1:69:C:OP1	50:AN:178:HIS:ND1	2.31	0.48
38:A1:255:A:H2'	38:A1:256:G:C8	2.48	0.48
38:A1:353:G:O6	72:Aj:55:ARG:NH2	2.36	0.48
38:A1:1083:G:H2'	38:A1:1084:A:C8	2.48	0.48
38:A1:3174:A:H61	68:Af:54:ARG:NH2	2.09	0.48
41:AD:50:ARG:HG2	41:AD:147:ASP:HB2	1.95	0.48
44:AG:247:ASP:OD1	44:AG:248:LYS:N	2.47	0.48
57:AU:34:ALA:O	57:AU:38:ILE:HD12	2.13	0.48
80:DC:6:VAL:HG22	80:DC:47:SER:HB3	1.94	0.48
80:DC:260:LYS:HD2	80:DC:260:LYS:HA	1.66	0.48
5:BG:137:ARG:NE	34:B5:169:A:OP1	2.44	0.48
11:BO:36:LYS:NZ	34:B5:894:U:O2'	2.25	0.48
15:BY:57:VAL:HB	15:BY:60:PHE:CE2	2.48	0.48
17:Bb:41:LEU:HD23	17:Bb:41:LEU:H	1.78	0.48
31:Bg:111:MET:HE3	31:Bg:127:ARG:HD3	1.95	0.48
31:Bg:117:LYS:HZ1	31:Bg:159:ASN:HB2	1.79	0.48
34:B5:538:A:N3	34:B5:538:A:H2'	2.29	0.48
34:B5:644:C:H2'	34:B5:645:C:C6	2.48	0.48
35:AA:9:ARG:HD2	38:A1:911:C:OP2	2.12	0.48
38:A1:54:C:HO2'	38:A1:1547:G:HO2'	1.60	0.48
38:A1:1569:U:H5'	38:A1:1570:U:H5''	1.94	0.48
38:A1:3259:U:H5''	38:A1:3261:C:H5	1.78	0.48
39:A3:16:U:H2'	39:A3:17:A:H8	1.77	0.48
41:AD:55:PHE:HE2	41:AD:159:VAL:HA	1.78	0.48
45:AH:41:ILE:HG22	45:AH:43:VAL:HG13	1.94	0.48
55:AS:14:LEU:HD23	55:AS:57:GLU:HG2	1.96	0.48
79:E:160:LYS:NZ	79:E:164:CYS:O	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:3:LEU:HD12	1:BA:4:PRO:HD2	1.94	0.48
1:BA:38:PHE:HB3	1:BA:47:VAL:HG13	1.95	0.48
2:BB:48:VAL:HG13	2:BB:49:ASN:N	2.28	0.48
4:BE:30:ARG:NH2	34:B5:298:C:O3'	2.46	0.48
8:BJ:170:GLY:O	8:BJ:174:ARG:HG3	2.13	0.48
12:BV:14:PRO:HB2	12:BV:23:ILE:HG23	1.94	0.48
16:Ba:45:VAL:HG13	16:Ba:46:GLU:N	2.27	0.48
18:Be:53:LYS:HG3	18:Be:54:ARG:H	1.79	0.48
22:BP:98:ASN:ND2	22:BP:121:ILE:O	2.46	0.48
34:B5:895:G:H1	34:B5:917:U:H3	1.62	0.48
34:B5:1233:G:N2	34:B5:1253:U:H1'	2.27	0.48
36:AB:366:GLY:HA3	38:A1:3330:A:H4'	1.94	0.48
37:AC:42:VAL:HG12	37:AC:236:LEU:HD21	1.94	0.48
38:A1:393:U:H2'	38:A1:394:G:O4'	2.13	0.48
38:A1:629:U:H2'	38:A1:630:A:C8	2.48	0.48
38:A1:683:U:H5'	50:AN:204:LYS:HE3	1.95	0.48
38:A1:1032:C:C4	38:A1:1033:U:H1'	2.49	0.48
38:A1:1592:G:OP2	69:Ag:37:LYS:NZ	2.31	0.48
38:A1:2471:U:H3	38:A1:2474:G:N2	2.11	0.48
38:A1:2588:U:OP1	44:AG:241:LYS:NZ	2.46	0.48
38:A1:2930:A:H2'	38:A1:2931:C:C6	2.48	0.48
40:A4:9:A:H2'	40:A4:10:A:C8	2.49	0.48
40:A4:99:C:OP1	60:AX:53:HIS:NE2	2.46	0.48
51:AO:62[A]:THR:HG22	51:AO:65[A]:ASN:H	1.78	0.48
79:E:73:ASP:HA	79:E:76:ARG:HG2	1.95	0.48
80:DC:110:ASP:OD2	80:DC:537:HIS:N	2.45	0.48
80:DC:537:HIS:HA	80:DC:540:ILE:HG22	1.95	0.48
81:V:130:PRO:O	81:V:133:THR:OG1	2.25	0.48
13:BW:56:HIS:O	34:B5:861:U:O2'	2.31	0.48
20:BF:148:ARG:HB2	20:BF:157:ARG:HH11	1.78	0.48
25:BS:14:ILE:HD12	47:AJ:119:SER:HB2	1.95	0.48
31:Bg:178:VAL:HB	31:Bg:192:PHE:HB2	1.94	0.48
34:B5:996:U:H2'	34:B5:997:G:H8	1.78	0.48
34:B5:1086:A:H2'	34:B5:1087:A:C8	2.48	0.48
34:B5:1370:U:H3	34:B5:1374:C:N4	2.11	0.48
38:A1:1032:C:N4	38:A1:1033:U:O2	2.46	0.48
38:A1:1176:C:H2'	38:A1:1177:G:N2	2.29	0.48
38:A1:2927:C:H2'	38:A1:2928:C:C6	2.48	0.48
39:A3:16:U:H2'	39:A3:17:A:C8	2.49	0.48
40:A4:4:C:H2'	40:A4:5:U:O2	2.13	0.48
57:AU:19:VAL:HG23	57:AU:105:LEU:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Aa:126:LYS:HB3	63:Aa:148:ILE:HD13	1.95	0.48
80:DC:210:ALA:HB2	80:DC:337:MET:HE1	1.95	0.48
80:DC:730:LEU:HB2	80:DC:799:ASP:HB2	1.94	0.48
5:BG:145:PHE:CE2	5:BG:156:PHE:HB3	2.49	0.48
8:BJ:28:LEU:HD23	18:Be:43:ARG:HD2	1.96	0.48
10:BN:3:ARG:HB3	10:BN:6:SER:HB3	1.94	0.48
10:BN:107:LYS:NZ	34:B5:880:C:OP1	2.46	0.48
14:BX:84:THR:HG23	14:BX:120:VAL:HG22	1.95	0.48
19:BD:71:LEU:HD23	19:BD:74:GLN:HE21	1.77	0.48
34:B5:1515:A:H4'	34:B5:1517:U:H5	1.78	0.48
38:A1:552:G:H2'	38:A1:553:U:O4'	2.12	0.48
38:A1:736:A:H2'	38:A1:737:G:O4'	2.13	0.48
38:A1:761:A:H2'	38:A1:762:U:H6	1.78	0.48
38:A1:1639:C:O2'	38:A1:1737:U:O2'	2.23	0.48
38:A1:2429:G:H2'	38:A1:2430:A:C8	2.48	0.48
40:A4:63:G:OP1	40:A4:90:U:H5''	2.14	0.48
70:Ah:45:LYS:O	70:Ah:49:LYS:HG2	2.14	0.48
79:E:190:PHE:CZ	79:E:194:LEU:HD11	2.49	0.48
80:DC:6:VAL:HA	80:DC:9:MET:HE2	1.95	0.48
80:DC:742:GLY:HA3	80:DC:788:THR:HG22	1.95	0.48
3:BC:166:THR:HB	3:BC:201:ASN:HB2	1.96	0.48
4:BE:87:MET:HE3	4:BE:123:LEU:HB3	1.96	0.48
11:BO:124:ASP:OD1	34:B5:928:U:H4'	2.14	0.48
19:BD:217:ILE:HG21	31:Bg:194:GLY:HA2	1.94	0.48
23:BQ:68:ARG:NH1	34:B5:1350:U:H5''	2.29	0.48
28:BZ:38:HIS:HA	28:BZ:70:LYS:HB3	1.96	0.48
34:B5:652:G:H4'	34:B5:653:C:H6	1.78	0.48
34:B5:956:C:OP1	34:B5:1072:C:O2'	2.30	0.48
34:B5:1214:U:H2'	34:B5:1215:C:H6	1.78	0.48
34:B5:1356:U:H2'	34:B5:1357:A:C8	2.48	0.48
38:A1:528:U:H2'	38:A1:529:A:H8	1.79	0.48
38:A1:589:A:H8	38:A1:590:G:C8	2.32	0.48
38:A1:2160:G:H2'	38:A1:2161:G:C8	2.46	0.48
38:A1:2991:A:O2'	38:A1:3309:G:N7	2.46	0.48
38:A1:3000:A:H2'	38:A1:3001:C:C6	2.48	0.48
38:A1:3273:A:H2'	38:A1:3274:A:C8	2.49	0.48
42:AE:93:VAL:O	42:AE:95:GLY:N	2.43	0.48
54:AR:23:TRP:HB3	54:AR:51:VAL:HG22	1.95	0.48
65:Ac:24:THR:HG22	65:Ac:91:SER:HB3	1.95	0.48
65:Ac:26:GLY:O	65:Ac:30:THR:OG1	2.22	0.48
73:Ak:42:LYS:HG2	73:Ak:55:VAL:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Ap:49:ARG:HB2	78:Ap:55:TRP:CZ3	2.48	0.48
80:DC:588:LEU:CB	80:DC:688:ILE:HA	2.44	0.48
4:BE:79:ASP:HB3	4:BE:82:TYR:HB2	1.95	0.48
4:BE:200:ARG:HH21	34:B5:246:G:H5'	1.79	0.48
5:BG:21:GLU:OE1	5:BG:25:ARG:NE	2.45	0.48
6:BH:44:LYS:HD2	6:BH:63:PRO:HB3	1.96	0.48
11:BO:121:VAL:O	34:B5:886:U:O2'	2.32	0.48
13:BW:75:ILE:HG13	13:BW:93:LEU:HD21	1.96	0.48
19:BD:108:LYS:HA	19:BD:111:ASN:HD22	1.78	0.48
24:BR:18:GLU:HA	24:BR:71:PHE:HA	1.96	0.48
30:Bd:7:TRP:NE1	34:B5:1451:C:HO2'	2.12	0.48
31:Bg:220:ILE:HD11	31:Bg:236:ALA:HB2	1.96	0.48
31:Bg:262:VAL:HB	31:Bg:271:VAL:HB	1.96	0.48
34:B5:625:C:H2'	34:B5:626:U:C6	2.49	0.48
34:B5:894:U:H2'	34:B5:895:G:C8	2.48	0.48
34:B5:1215:C:H2'	34:B5:1216:C:C6	2.49	0.48
34:B5:1740:A:H2'	34:B5:1741:U:C6	2.49	0.48
37:AC:23:PRO:HD2	37:AC:26:PHE:HD2	1.77	0.48
38:A1:289:A:H2'	38:A1:290:G:H8	1.78	0.48
38:A1:871:U:H2'	38:A1:872:U:C6	2.49	0.48
38:A1:1046:A:H2'	38:A1:1049:C:C5	2.49	0.48
38:A1:1194:G:H2'	38:A1:1195:A:C8	2.49	0.48
38:A1:1336:U:H2'	38:A1:1337:A:C8	2.48	0.48
38:A1:1493:G:OP2	38:A1:1493:G:N2	2.41	0.48
51:AO:77[A]:SER:OG	51:AO:106[A]:GLU:OE2	2.17	0.48
80:DC:32:LYS:NZ	85:DC:901:GDP:O3B	2.36	0.48
3:BC:95:ARG:NH1	3:BC:97:ARG:HE	2.12	0.48
12:BV:5:LYS:HE2	12:BV:7:GLN:HE22	1.76	0.48
20:BF:53:VAL:HG22	20:BF:134:VAL:HG11	1.95	0.48
25:BS:127:HIS:NE2	25:BS:133:VAL:HG21	2.29	0.48
27:BU:106:ILE:HG13	27:BU:107:THR:H	1.79	0.48
31:Bg:64:HIS:CE1	31:Bg:90:ARG:HD2	2.49	0.48
31:Bg:245:PHE:HE1	31:Bg:252:LEU:HD22	1.78	0.48
34:B5:1349:G:H2'	34:B5:1350:U:H6	1.78	0.48
37:AC:120:TYR:CE1	37:AC:277:PRO:HB3	2.48	0.48
37:AC:193:LYS:NZ	38:A1:1420:C:OP2	2.37	0.48
38:A1:179:C:H2'	38:A1:180:C:H6	1.79	0.48
38:A1:315:C:OP2	71:Ai:28:TYR:OH	2.17	0.48
38:A1:834:U:H2'	38:A1:835:G:O4'	2.14	0.48
38:A1:1460:A:H2'	38:A1:1461:A:H8	1.79	0.48
38:A1:1921:A:H2'	38:A1:1922:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2213:A:H2'	38:A1:2214:A:H8	1.77	0.48
38:A1:2427:U:H2'	38:A1:2428:U:C6	2.48	0.48
38:A1:2439:A:H2'	38:A1:2440:G:O4'	2.14	0.48
63:Aa:104:THR:OG1	63:Aa:126:LYS:O	2.28	0.48
69:Ag:86:LYS:O	69:Ag:90:ILE:HG12	2.14	0.48
73:Ak:32:ASN:CG	73:Ak:36:LYS:HG3	2.39	0.48
80:DC:539:GLU:O	80:DC:543:GLN:HG2	2.14	0.48
80:DC:606:ILE:HG12	80:DC:618:ILE:HD12	1.96	0.48
2:BB:156:ALA:HB3	2:BB:161:ILE:HD11	1.96	0.48
6:BH:58:LEU:N	6:BH:89:HIS:O	2.41	0.48
11:BO:126:THR:HG21	34:B5:888:U:H1'	1.96	0.48
14:BX:78:LYS:HA	34:B5:434:G:OP1	2.14	0.48
34:B5:130:C:O2'	34:B5:133:U:OP1	2.20	0.48
34:B5:1147:A:O2'	34:B5:1636:C:OP2	2.23	0.48
37:AC:141:ARG:NH1	38:A1:1385:C:OP1	2.41	0.48
37:AC:281:ILE:HG13	53:AQ:125:ASP:CG	2.38	0.48
38:A1:631:U:H2'	38:A1:632:G:H8	1.79	0.48
38:A1:1232:C:H5	38:A1:1261:G:H2'	1.79	0.48
38:A1:2505:U:H2'	38:A1:2506:U:H6	1.79	0.48
38:A1:2883:U:H2'	38:A1:2884:C:H6	1.77	0.48
48:AL:25:HIS:NE2	50:AN:198:SER:OG	2.38	0.48
71:Ai:5:THR:HG23	71:Ai:12:ASN:HB2	1.96	0.48
16:Ba:5:ARG:NH2	34:B5:1795:U:H3'	2.29	0.47
16:Ba:37:LYS:HE3	34:B5:933:A:OP2	2.14	0.47
19:BD:204:ASP:OD1	19:BD:204:ASP:N	2.41	0.47
22:BP:113:GLY:O	22:BP:114:HIS:ND1	2.47	0.47
23:BQ:106:LYS:HG3	23:BQ:117:LEU:HD22	1.95	0.47
25:BS:83:ALA:HA	25:BS:86:LEU:HD13	1.95	0.47
26:BT:93:HIS:ND1	34:B5:1524:A:O3'	2.47	0.47
34:B5:694:U:H3'	34:B5:695:U:C6	2.47	0.47
34:B5:1182:U:H1'	34:B5:1185:U:C4	2.49	0.47
34:B5:1285:U:H4'	34:B5:1286:U:O5'	2.14	0.47
34:B5:1617:U:H2'	34:B5:1618:C:C6	2.49	0.47
38:A1:700:C:H2'	38:A1:701:G:H8	1.78	0.47
38:A1:1948:G:C2	38:A1:2099:A:C2	3.02	0.47
38:A1:2617:U:O2'	46:AI:116:ARG:NH2	2.47	0.47
38:A1:2999:U:H2'	38:A1:3000:A:C8	2.49	0.47
45:AH:114:VAL:HB	45:AH:124:ARG:HB2	1.96	0.47
46:AI:135:ILE:HG22	46:AI:136:PHE:CD1	2.49	0.47
47:AJ:115:LYS:HG3	47:AJ:116:TYR:N	2.26	0.47
1:BA:67:ILE:HG12	1:BA:119:ARG:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:191:GLU:HG3	2:BB:194:ASN:HB2	1.95	0.47
11:BO:17:ALA:HA	11:BO:30:VAL:HG22	1.95	0.47
22:BP:80:MET:HE1	22:BP:83:MET:HG2	1.94	0.47
22:BP:110:GLU:OE1	25:BS:119:ILE:HG12	2.14	0.47
25:BS:13:HIS:CG	25:BS:14:ILE:H	2.32	0.47
25:BS:41:ARG:HG2	25:BS:85:PHE:CE1	2.50	0.47
28:BZ:37:GLN:OE1	28:BZ:38:HIS:ND1	2.48	0.47
34:B5:1114:G:O2'	34:B5:1130:G:O6	2.29	0.47
34:B5:1516:A:O2'	34:B5:1517:U:H5'	2.13	0.47
37:AC:107:ARG:HA	38:A1:664:U:H5'	1.96	0.47
38:A1:221:A:O2'	38:A1:223:U:OP2	2.30	0.47
38:A1:589:A:H1'	38:A1:1337:A:H5''	1.95	0.47
38:A1:797:U:O2	48:AL:12:ASN:ND2	2.47	0.47
38:A1:873:C:H3'	38:A1:874:U:H4'	1.96	0.47
38:A1:1009:A:H2'	38:A1:1010:G:C8	2.49	0.47
38:A1:2429:G:H2'	38:A1:2430:A:H8	1.78	0.47
38:A1:2453:U:H4'	38:A1:2461:A:H5''	1.96	0.47
38:A1:2466:G:OP1	79:E:108:ASN:ND2	2.46	0.47
38:A1:2813:A:H2'	38:A1:2814:G:O4'	2.14	0.47
38:A1:3033:A:H2'	38:A1:3034:C:O2	2.15	0.47
48:AL:48:PRO:HD3	70:Ah:115:LYS:HE3	1.94	0.47
51:AO:89[A]:SER:O	51:AO:95[A]:GLY:HA3	2.13	0.47
56:AT:115:LYS:HB3	56:AT:126:VAL:HG11	1.95	0.47
79:E:17:LEU:HD22	79:E:176:GLU:HB2	1.96	0.47
1:BA:176:LEU:O	1:BA:180:GLU:HG2	2.14	0.47
5:BG:136:LYS:NZ	5:BG:174:LYS:O	2.33	0.47
6:BH:23:ALA:HB1	6:BH:84:LYS:HD3	1.96	0.47
23:BQ:97:VAL:HG12	23:BQ:98:ASP:N	2.29	0.47
34:B5:960:U:H2'	34:B5:961:U:H6	1.79	0.47
34:B5:1202:A:H62	34:B5:1456:C:H2'	1.79	0.47
35:AA:190:ARG:HG3	35:AA:191:LEU:HD22	1.96	0.47
37:AC:51:ALA:O	40:A4:26:U:O2'	2.28	0.47
37:AC:303:GLY:H	38:A1:1347:U:H5''	1.80	0.47
38:A1:873:C:H5''	38:A1:874:U:O5'	2.14	0.47
38:A1:2232:A:H2'	38:A1:2233:A:C8	2.49	0.47
38:A1:2496:C:H3'	38:A1:2497:U:C4	2.49	0.47
38:A1:2553:U:C5	69:Ag:95:ILE:HG22	2.50	0.47
38:A1:3185:U:C5	51:AO:126[A]:VAL:HG21	2.50	0.47
38:A1:3371:G:H2'	38:A1:3372:A:C8	2.50	0.47
44:AG:91:PHE:HE1	44:AG:180:VAL:HG21	1.79	0.47
44:AG:185:ARG:O	44:AG:188:THR:HG22	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AH:161:LEU:O	45:AH:164:ILE:HG22	2.13	0.47
62:AZ:11:ALA:HB3	62:AZ:80:LEU:HD12	1.95	0.47
79:E:207:LYS:HD2	79:E:213:ALA:HA	1.95	0.47
6:BH:64:VAL:HG23	6:BH:67:LEU:HD23	1.95	0.47
14:BX:107:PHE:CE1	14:BX:123:LYS:HB3	2.49	0.47
14:BX:110:LYS:HD2	34:B5:601:A:OP2	2.15	0.47
20:BF:63:GLN:HB3	20:BF:88:PRO:HA	1.95	0.47
20:BF:222:LYS:HG2	20:BF:225:ARG:HH21	1.80	0.47
31:Bg:307:ASP:OD1	31:Bg:309:VAL:HG12	2.15	0.47
34:B5:835:U:N3	34:B5:836:U:O4	2.47	0.47
34:B5:1208:A:O2'	34:B5:1270:G:OP2	2.23	0.47
35:AA:9:ARG:NH2	38:A1:912:G:N7	2.63	0.47
35:AA:244:GLY:HA2	38:A1:2243:A:H3'	1.96	0.47
36:AB:62:ARG:NH1	38:A1:3039:C:OP1	2.42	0.47
38:A1:1128:U:H2'	38:A1:1129:A:O4'	2.14	0.47
38:A1:2116:G:OP1	38:A1:2118:C:N4	2.47	0.47
38:A1:2150:G:O2'	38:A1:2189:U:OP1	2.30	0.47
38:A1:2585:G:H2'	38:A1:2585:G:N3	2.29	0.47
38:A1:3288:G:O2'	38:A1:3289:G:H8	1.97	0.47
40:A4:53:A:OP1	74:A1:19:GLN:NE2	2.32	0.47
41:AD:36:LEU:HD13	41:AD:50:ARG:HD2	1.96	0.47
50:AN:98:LEU:HD12	50:AN:128:LYS:HD3	1.95	0.47
79:E:67:ILE:HA	79:E:111:ILE:O	2.13	0.47
1:BA:59:LEU:HD22	12:BV:79:LEU:HD11	1.95	0.47
7:BI:34:ALA:HB2	7:BI:56:ARG:HD2	1.96	0.47
7:BI:137:LYS:O	7:BI:141:ARG:HG3	2.14	0.47
11:BO:53:ASP:OD1	11:BO:56:SER:HB2	2.13	0.47
22:BP:81:ARG:HH12	22:BP:98:ASN:HB3	1.79	0.47
28:BZ:65:LEU:HD23	28:BZ:76:ALA:HA	1.94	0.47
34:B5:1174:C:H42	34:B5:1465:C:H42	1.60	0.47
34:B5:1761:U:C4	82:EC:6951:C:H5'	2.50	0.47
35:AA:177:LYS:O	38:A1:1793:C:N4	2.37	0.47
38:A1:2103:U:H2'	38:A1:2104:A:C8	2.50	0.47
39:A3:112:G:H2'	39:A3:113:C:C6	2.50	0.47
46:AI:190:VAL:HG22	46:AI:199:PHE:HD1	1.79	0.47
47:AJ:48:SER:HB3	47:AJ:66:ALA:HB3	1.97	0.47
61:AY:55:GLU:HB2	61:AY:108:LYS:HB3	1.95	0.47
70:Ah:86:ARG:O	70:Ah:90:ARG:HG2	2.14	0.47
80:DC:27:HIS:CD2	80:DC:28:VAL:H	2.32	0.47
80:DC:329:PRO:HG2	80:DC:332:ASP:HB2	1.95	0.47
80:DC:702:GLY:O	80:DC:703:GLY:C	2.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:EC:6789:G:H5''	82:EC:6851:G:N2	2.28	0.47
82:EC:6812:C:H2'	82:EC:6813:A:H8	1.79	0.47
82:EC:6897:G:H2'	82:EC:6898:U:C6	2.50	0.47
2:BB:82:ARG:HG3	2:BB:103:MET:SD	2.55	0.47
15:BY:19:ALA:HB3	15:BY:81:GLU:OE2	2.13	0.47
24:BR:20:TYR:CE2	24:BR:34:LEU:HD21	2.49	0.47
25:BS:145:ARG:HH21	34:B5:1172:G:H4'	1.79	0.47
28:BZ:64:VAL:HG22	28:BZ:68:ARG:HG3	1.95	0.47
31:Bg:66:HIS:HD2	34:B5:1386:G:O2'	1.97	0.47
34:B5:712:G:H5''	34:B5:713:A:C8	2.49	0.47
34:B5:902:G:O2'	34:B5:1008:G:H4'	2.15	0.47
34:B5:947:U:H2'	34:B5:948:G:C8	2.50	0.47
34:B5:1031:U:H4'	34:B5:1032:G:OP2	2.13	0.47
34:B5:1061:A:H5''	34:B5:1062:A:H2	1.80	0.47
34:B5:1521:G:O2'	34:B5:1523:G:OP2	2.21	0.47
34:B5:1575:G7M:O5'	34:B5:1575:G7M:H8	2.15	0.47
34:B5:1787:C:H2'	34:B5:1788:G:C8	2.49	0.47
38:A1:80:G:H2'	38:A1:81:C:H6	1.80	0.47
38:A1:1243:G:H2'	38:A1:1244:A:O4'	2.15	0.47
40:A4:78:G:H2'	40:A4:79:A:C8	2.48	0.47
46:AI:145:LYS:HD2	46:AI:167:LEU:HD21	1.96	0.47
49:AM:45:LEU:HA	49:AM:57:ALA:HA	1.97	0.47
63:Aa:134:ALA:O	63:Aa:138:ILE:HG13	2.13	0.47
73:Ak:16:ARG:HE	73:Ak:70:PRO:HG3	1.80	0.47
79:E:85:MET:HE3	79:E:85:MET:HB3	1.87	0.47
80:DC:483:PHE:C	80:DC:485:VAL:H	2.22	0.47
80:DC:570:GLU:HA	80:DC:591:GLU:OE1	2.15	0.47
80:DC:650:THR:HG23	80:DC:690:ASP:HA	1.96	0.47
82:EC:6828:G:H2'	82:EC:6829:A:C8	2.48	0.47
1:BA:190:ASP:HB2	1:BA:193:GLN:NE2	2.30	0.47
2:BB:35:PRO:HB2	2:BB:37:THR:HG22	1.96	0.47
2:BB:157:GLN:C	2:BB:159:SER:H	2.22	0.47
2:BB:164:ILE:HG23	2:BB:201:THR:HG21	1.96	0.47
6:BH:72:LYS:HG3	6:BH:73:VAL:HG13	1.96	0.47
7:BI:103:GLN:HA	7:BI:165:LEU:O	2.14	0.47
7:BI:104:ILE:HG13	7:BI:105:ASP:N	2.28	0.47
7:BI:172:ARG:NH2	34:B5:331:A:N7	2.56	0.47
10:BN:61:THR:OG1	10:BN:62:GLN:N	2.48	0.47
11:BO:91:THR:HG23	11:BO:93:THR:H	1.79	0.47
11:BO:107:ARG:NH1	16:Ba:52:ASP:OD1	2.48	0.47
19:BD:31:GLU:HA	19:BD:107:PHE:CE2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:139:ASN:O	20:BF:214:LYS:NZ	2.41	0.47
21:BK:16:PHE:CD1	21:BK:76:LEU:HD23	2.49	0.47
29:Bc:50:GLU:OE1	29:Bc:51:ASN:ND2	2.47	0.47
31:Bg:81:LEU:HD11	31:Bg:122:ILE:HD12	1.95	0.47
31:Bg:240:VAL:HA	31:Bg:256:THR:HA	1.97	0.47
33:BM:28:LEU:HD23	33:BM:100:TRP:HH2	1.79	0.47
34:B5:327:U:H2'	34:B5:328:A:C8	2.50	0.47
34:B5:503:G:H2'	34:B5:504:U:C6	2.50	0.47
34:B5:795:U:H2'	34:B5:796:A2M:H8	1.97	0.47
34:B5:1080:U:H2'	34:B5:1081:A:C8	2.49	0.47
34:B5:1550:A:H2'	34:B5:1551:U:C6	2.49	0.47
34:B5:1652:C:H2'	34:B5:1653:C:H6	1.80	0.47
35:AA:70:ARG:HD2	35:AA:72:ARG:NH2	2.30	0.47
35:AA:112:ILE:HG13	78:Ap:79:VAL:HG22	1.97	0.47
36:AB:56:ILE:HD12	36:AB:356:LEU:HD22	1.97	0.47
38:A1:8:C:H2'	38:A1:9:U:C6	2.50	0.47
38:A1:121:A:O2'	44:AG:108:ARG:NH2	2.47	0.47
38:A1:302:U:H5''	50:AN:179:LYS:HE3	1.95	0.47
38:A1:422:A:C2	38:A1:2363:A:H4'	2.49	0.47
38:A1:501:A:H2'	38:A1:502:U:C6	2.49	0.47
38:A1:674:G:O6	53:AQ:56:LYS:NZ	2.47	0.47
38:A1:992:A:O2'	38:A1:993:G:H5'	2.15	0.47
38:A1:1174:G:H1'	38:A1:1181:U:N3	2.30	0.47
38:A1:1334:U:H2'	38:A1:1335:C:H6	1.79	0.47
38:A1:1419:A:OP1	40:A4:20:U:O2'	2.33	0.47
38:A1:1883:A:H2'	38:A1:1884:A:H8	1.79	0.47
38:A1:2197:OMC:N4	38:A1:2241:U:H2'	2.30	0.47
38:A1:2261:G:H21	38:A1:2262:A:N6	2.13	0.47
38:A1:2571:U:O2'	38:A1:2572:C:O5'	2.28	0.47
38:A1:2651:G:H5''	38:A1:2652:U:O4'	2.15	0.47
38:A1:3034:C:H5	45:AH:121:LYS:HB2	1.80	0.47
47:AJ:92:ARG:HA	47:AJ:172:LEU:H	1.79	0.47
50:AN:112:ASN:OD1	50:AN:113:LEU:HG	2.15	0.47
66:Ad:13:THR:HB	66:Ad:72:ARG:HH11	1.79	0.47
77:Ao:14:GLY:C	77:Ao:16:THR:H	2.22	0.47
80:DC:171:LYS:HD3	80:DC:274:ASN:O	2.14	0.47
80:DC:485:VAL:HA	80:DC:793:PHE:CZ	2.50	0.47
80:DC:638:PRO:HD2	80:DC:642:GLY:HA3	1.95	0.47
2:BB:144:ARG:HB2	2:BB:208:GLN:HG3	1.97	0.47
5:BG:142:ARG:HH12	5:BG:151:ASP:C	2.22	0.47
6:BH:19:GLN:HA	6:BH:22:GLN:HG3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:167:GLU:N	6:BH:167:GLU:OE1	2.46	0.47
12:BV:32:VAL:HG12	12:BV:60:ARG:HD2	1.96	0.47
19:BD:162:GLN:HB3	34:B5:1332:C:O2'	2.14	0.47
20:BF:187:ILE:HG12	28:BZ:66:VAL:HB	1.96	0.47
24:BR:19:ARG:CZ	24:BR:20:TYR:HB2	2.44	0.47
33:BM:48:SER:HB3	33:BM:122:VAL:HG23	1.97	0.47
38:A1:100:A:H2'	38:A1:101:G:N3	2.29	0.47
38:A1:165:A:OP1	38:A1:165:A:H4'	2.14	0.47
38:A1:243:G:C4	38:A1:244:G:C8	3.03	0.47
38:A1:987:U:H2'	38:A1:988:U:C6	2.50	0.47
38:A1:1666:G:H2'	38:A1:1667:A:H8	1.80	0.47
38:A1:1911:A:H2	38:A1:2122:G:C8	2.33	0.47
38:A1:2424:A:OP1	50:AN:90:ASN:ND2	2.40	0.47
38:A1:2767:U:OP1	77:Ao:34:SER:HB3	2.14	0.47
38:A1:3029:A:H4'	80:DC:536:LEU:HD21	1.96	0.47
38:A1:3198:U:O4	45:AH:26:LYS:HB2	2.14	0.47
38:A1:3343:G:O2'	38:A1:3362:A:N6	2.48	0.47
48:AL:59:ARG:HD2	48:AL:69:VAL:HG12	1.97	0.47
62:AZ:136:PHE:O	69:Ag:76:TYR:OH	2.27	0.47
5:BG:72:ARG:NH2	34:B5:419:G:H5'	2.30	0.47
10:BN:129:TYR:HA	10:BN:132:VAL:HG12	1.97	0.47
13:BW:57:ARG:HB3	34:B5:863:A:H4'	1.96	0.47
14:BX:92:CYS:HG	14:BX:136:TRP:CD1	2.33	0.47
15:BY:102:LYS:HE2	34:B5:444:C:OP1	2.15	0.47
19:BD:110:LEU:HD22	19:BD:175:VAL:HG13	1.97	0.47
22:BP:107:ILE:HG23	22:BP:111:MET:HG2	1.97	0.47
34:B5:17:C:H2'	34:B5:18:C:H6	1.80	0.47
34:B5:628:G:H21	34:B5:971:A:H62	1.63	0.47
38:A1:196:G:N1	38:A1:199:A:OP2	2.41	0.47
38:A1:266:A:H2'	71:Ai:30:LYS:HE3	1.97	0.47
38:A1:915:A:H8	38:A1:2136:C:O2'	1.98	0.47
38:A1:916:G:H5'	38:A1:917:A:OP1	2.15	0.47
38:A1:2098:C:H2'	38:A1:2099:A:C8	2.50	0.47
38:A1:3152:U:OP2	38:A1:3395:G:N1	2.30	0.47
38:A1:3294:A:H2'	38:A1:3295:A:O4'	2.15	0.47
41:AD:181:PRO:HG2	41:AD:195:LEU:HD13	1.97	0.47
41:AD:184:ASP:OD1	41:AD:185:PHE:N	2.48	0.47
41:AD:286:VAL:HG23	46:AI:206:LEU:HD22	1.97	0.47
55:AS:66:GLU:HB3	55:AS:69:PRO:HG3	1.96	0.47
72:Aj:39:TYR:CD1	72:Aj:40:PRO:HA	2.50	0.47
79:E:125:GLY:H	79:E:126:PRO:HD2	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:174:LEU:O	80:DC:177:THR:OG1	2.25	0.47
80:DC:626:ASP:OD2	80:DC:628:THR:OG1	2.31	0.47
82:EC:6761:C:H2'	82:EC:6762:U:C6	2.49	0.47
15:BY:34:ASN:O	34:B5:521:A:O2'	2.33	0.47
29:Bc:9:LEU:HB3	29:Bc:33:LEU:HD13	1.96	0.47
34:B5:340:U:H2'	34:B5:341:A:C8	2.50	0.47
37:AC:345:GLU:H	37:AC:345:GLU:CD	2.22	0.47
38:A1:787:G:H2'	38:A1:788:C:C6	2.50	0.47
38:A1:835:G:O2'	38:A1:857:G:N2	2.28	0.47
38:A1:1110:U:H2'	38:A1:1111:U:C6	2.49	0.47
38:A1:2618:G:OP1	38:A1:2644:C:O2'	2.29	0.47
38:A1:2777:G:C2	63:Aa:60:TYR:CE1	3.03	0.47
38:A1:3094:A:OP1	58:AV:14:SER:OG	2.23	0.47
80:DC:659:ILE:HD13	80:DC:693:LEU:HD11	1.97	0.47
81:V:101:VAL:HG13	81:V:104:ARG:NH2	2.29	0.47
1:BA:198:MET:SD	1:BA:199:PRO:HD2	2.55	0.46
5:BG:50:PHE:HD2	5:BG:111:LEU:HD13	1.80	0.46
6:BH:81:LEU:HD13	6:BH:90:VAL:HG21	1.96	0.46
20:BF:93:LEU:HD21	20:BF:137:ILE:HD11	1.96	0.46
20:BF:99:MET:HE1	34:B5:1165:G:H5''	1.96	0.46
20:BF:117:THR:HG22	20:BF:191:ALA:O	2.16	0.46
33:BM:113:ARG:NH2	34:B5:1224:A:OP2	2.47	0.46
34:B5:82:U:H2'	34:B5:83:G:O4'	2.16	0.46
34:B5:448:C:H2'	34:B5:449:C:H6	1.80	0.46
34:B5:607:G:H5'	34:B5:613:G:N2	2.30	0.46
34:B5:1758:U:H2'	34:B5:1759:C:C6	2.50	0.46
34:B5:1770:U:H2'	34:B5:1771:U:C6	2.50	0.46
38:A1:907:G:OP1	38:A1:909:G:O2'	2.32	0.46
38:A1:1641:U:O2'	38:A1:1642:A:H3'	2.14	0.46
38:A1:1760:A:N6	38:A1:1766:G:C6	2.83	0.46
38:A1:1791:C:H2'	38:A1:1792:C:C6	2.49	0.46
49:AM:109:ARG:HA	49:AM:112:LEU:HD23	1.97	0.46
55:AS:8:GLN:HB3	55:AS:64:ILE:HD11	1.96	0.46
80:DC:162:ARG:HB3	85:DC:901:GDP:N2	2.30	0.46
80:DC:262:THR:HB	80:DC:266:GLY:HA2	1.96	0.46
80:DC:648:ASP:OD1	80:DC:648:ASP:N	2.48	0.46
81:V:48:ARG:NH2	81:V:95:GLU:HB2	2.30	0.46
5:BG:20:ASP:HB3	5:BG:22:HIS:NE2	2.29	0.46
5:BG:174:LYS:HB2	34:B5:79:C:N3	2.30	0.46
10:BN:26:PHE:CE1	10:BN:28:LEU:HB2	2.50	0.46
13:BW:57:ARG:HE	17:Bb:26:GLN:NE2	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:BQ:52:LEU:HD12	23:BQ:57:LEU:HD22	1.97	0.46
31:Bg:117:LYS:NZ	31:Bg:159:ASN:O	2.46	0.46
34:B5:91:G:H2'	34:B5:92:A:O4'	2.15	0.46
34:B5:281:G:H2'	34:B5:282:C:C6	2.49	0.46
34:B5:472:U:H2'	34:B5:473:A:C8	2.50	0.46
34:B5:587:C:H2'	34:B5:588:U:C6	2.50	0.46
34:B5:752:A:HO2'	34:B5:753:A:P	2.38	0.46
34:B5:1355:C:H2'	34:B5:1356:U:C6	2.50	0.46
34:B5:1645:G:H2'	34:B5:1646:C:H6	1.81	0.46
34:B5:1732:A:H2'	34:B5:1733:C:H6	1.80	0.46
38:A1:141:C:H2'	38:A1:142:C:C6	2.50	0.46
38:A1:175:C:N3	38:A1:242:C:N4	2.60	0.46
38:A1:568:G:H2'	38:A1:569:A:O4'	2.15	0.46
38:A1:1174:G:N2	51:AO:87[A]:MET:HE2	2.31	0.46
38:A1:2438:A:H2'	38:A1:2439:A:C8	2.50	0.46
38:A1:2447:A:H2'	38:A1:2448:G:C8	2.50	0.46
38:A1:2519:A:H2'	38:A1:2520:A:C8	2.50	0.46
38:A1:2916:U:H2'	38:A1:2917:G:H8	1.80	0.46
38:A1:3066:U:H2'	38:A1:3067:C:C6	2.50	0.46
48:AL:166:ALA:N	63:Aa:135:GLU:OE2	2.48	0.46
49:AM:37:GLU:HG3	49:AM:38:ILE:N	2.30	0.46
74:Al:13:MET:HG3	74:Al:49:MET:HE1	1.97	0.46
79:E:143:ASP:OD1	79:E:143:ASP:N	2.47	0.46
80:DC:284:LEU:O	80:DC:288:ILE:HG12	2.15	0.46
81:V:109:ALA:HA	81:V:181:PHE:CZ	2.50	0.46
1:BA:31:VAL:HA	1:BA:34:GLU:HG3	1.97	0.46
2:BB:39:GLU:HB2	2:BB:74:GLN:HA	1.96	0.46
4:BE:22:LYS:N	34:B5:773:C:OP1	2.48	0.46
4:BE:68:ARG:HD2	4:BE:76:VAL:HG11	1.96	0.46
7:BI:81:VAL:HG12	7:BI:102:VAL:HG12	1.98	0.46
11:BO:52:ARG:HD3	34:B5:905:A:H5''	1.97	0.46
27:BU:63:LEU:HD12	27:BU:84:MET:HE3	1.97	0.46
34:B5:496:G:H2'	34:B5:496:G:N3	2.31	0.46
34:B5:689:G:H2'	34:B5:690:G:H8	1.80	0.46
34:B5:1107:G:O2'	34:B5:1108:G:H5'	2.15	0.46
34:B5:1116:A:H5''	76:An:17:ARG:NH1	2.31	0.46
34:B5:1254:U:H3'	34:B5:1255:G:H8	1.79	0.46
34:B5:1717:G:H2'	34:B5:1718:G:H8	1.80	0.46
37:AC:156:LEU:HD12	37:AC:159:ILE:HD12	1.97	0.46
38:A1:63:A:N3	38:A1:78:U:O2'	2.35	0.46
38:A1:1721:U:O2'	38:A1:1723:A:N7	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2376:G:H2'	38:A1:2377:G:C8	2.51	0.46
38:A1:2482:U:H2'	38:A1:2483:G:C8	2.51	0.46
38:A1:3110:C:O2'	45:AH:155:SER:OG	2.30	0.46
38:A1:3215:A:H5'	49:AM:121:MET:HE1	1.96	0.46
38:A1:3320:A:H2'	38:A1:3321:C:C6	2.50	0.46
39:A3:27:A:H2'	39:A3:28:C:C6	2.50	0.46
47:AJ:117:ASP:OD1	47:AJ:119:SER:OG	2.32	0.46
55:AS:73:LYS:NZ	55:AS:97:VAL:O	2.44	0.46
71:AI:90:MET:HE2	71:AI:90:MET:HA	1.97	0.46
2:BB:194:ASN:HD22	2:BB:210:ILE:HG22	1.80	0.46
4:BE:35:PRO:HD2	4:BE:83:PRO:HG2	1.97	0.46
6:BH:24:PHE:O	6:BH:28:GLU:HG3	2.16	0.46
9:BL:2:SER:O	9:BL:52:SER:HB2	2.14	0.46
23:BQ:14:LYS:HD3	34:B5:1584:G:N7	2.30	0.46
25:BS:65:GLU:O	25:BS:69:ILE:HG12	2.15	0.46
26:BT:44:GLU:OE1	26:BT:44:GLU:N	2.48	0.46
26:BT:68:ARG:HG2	34:B5:1523:G:O6	2.15	0.46
34:B5:52:U:H2'	34:B5:53:G:C8	2.50	0.46
34:B5:150:U:H2'	34:B5:151:G:C8	2.50	0.46
34:B5:904:G:N2	82:EC:6946:A:O4'	2.49	0.46
34:B5:968:U:H2'	34:B5:969:C:O4'	2.15	0.46
34:B5:1081:A:O2'	34:B5:1083:G:N7	2.44	0.46
34:B5:1513:G:H1'	34:B5:1518:C:O2	2.16	0.46
34:B5:1648:A:H2'	34:B5:1649:G:H8	1.81	0.46
34:B5:1754:A:H3'	34:B5:1755:A:H8	1.81	0.46
38:A1:435:C:H2'	38:A1:436:A:H8	1.81	0.46
38:A1:1269:U:H1'	38:A1:1272:C:H5	1.79	0.46
38:A1:1646:G:O2'	38:A1:1808:G:N2	2.40	0.46
38:A1:2218:G:H2'	38:A1:2219:A:C8	2.50	0.46
38:A1:3153:U:H5	38:A1:3293:U:H3	1.64	0.46
43:AF:178:ILE:HD11	43:AF:187:GLU:HG3	1.97	0.46
48:AL:163:GLY:HA2	63:Aa:139:ARG:NH2	2.30	0.46
80:DC:174:LEU:HD21	80:DC:282:PHE:CZ	2.50	0.46
81:V:28:VAL:O	81:V:84:VAL:HA	2.16	0.46
82:EC:6798:C:H2'	82:EC:6799:C:C6	2.51	0.46
82:EC:6939:C:H1'	82:EC:6940:U:OP1	2.15	0.46
2:BB:26:ARG:O	2:BB:50:LYS:N	2.47	0.46
4:BE:148:ARG:NH1	5:BG:201:GLN:OE1	2.48	0.46
4:BE:184:THR:O	4:BE:189:LEU:HD13	2.15	0.46
5:BG:202:ARG:NH1	34:B5:127:G:N7	2.63	0.46
7:BI:62:THR:HG22	7:BI:77:ARG:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:23:PRO:HD2	10:BN:26:PHE:HB3	1.97	0.46
10:BN:124:ARG:NH1	34:B5:628:G:OP1	2.46	0.46
11:BO:60:ALA:HB1	11:BO:101:ALA:HB2	1.96	0.46
15:BY:109:LYS:HE3	34:B5:458:G:OP1	2.16	0.46
20:BF:95:ASN:O	34:B5:1611:A:O2'	2.33	0.46
20:BF:159:ALA:HB3	29:Bc:61:ARG:HH12	1.81	0.46
26:BT:47:PRO:HA	34:B5:1477:G:H4'	1.97	0.46
31:Bg:80:ALA:HB3	31:Bg:92:TRP:HB2	1.97	0.46
34:B5:315:A:N1	34:B5:349:U:O2'	2.38	0.46
34:B5:826:U:H2'	34:B5:827:C:H6	1.80	0.46
34:B5:885:G:H2'	34:B5:886:U:C6	2.51	0.46
34:B5:1120:U:H2'	34:B5:1121:C:C6	2.51	0.46
34:B5:1673:G:C6	34:B5:1728:A:N1	2.84	0.46
37:AC:343:LYS:HD2	38:A1:515:C:H5'	1.97	0.46
38:A1:36:C:H4'	38:A1:808:A:C2	2.51	0.46
38:A1:621:A:OP1	52:AP:167:ARG:NH1	2.48	0.46
38:A1:2344:U:H2'	38:A1:2345:A:C8	2.51	0.46
38:A1:2683:U:H2'	38:A1:2684:C:H6	1.81	0.46
43:AF:83:LEU:HD11	43:AF:116:PHE:HB3	1.97	0.46
47:AJ:164:LYS:HE2	47:AJ:171:VAL:H	1.80	0.46
53:AQ:65:SER:OG	53:AQ:90:ASP:OD2	2.30	0.46
54:AR:116:ASP:OD1	54:AR:116:ASP:N	2.42	0.46
73:Ak:38:PHE:HZ	73:Ak:57:ASN:HD22	1.63	0.46
80:DC:120:ARG:NH1	80:DC:481:MET:HE1	2.30	0.46
82:EC:6813:A:H2'	82:EC:6814:G:H8	1.81	0.46
1:BA:29:VAL:HG21	1:BA:37:VAL:HG21	1.97	0.46
5:BG:132:ARG:NH1	34:B5:149:C:O2'	2.47	0.46
7:BI:192:TYR:O	7:BI:197:THR:OG1	2.30	0.46
20:BF:188:LYS:HA	28:BZ:63:SER:HB2	1.98	0.46
21:BK:88:PRO:HG2	21:BK:92:ILE:HG13	1.98	0.46
23:BQ:129:PHE:CE1	27:BU:78:THR:HA	2.51	0.46
34:B5:919:A:H2'	34:B5:920:U:C6	2.50	0.46
34:B5:1619:C:H2'	34:B5:1620:C:C6	2.48	0.46
35:AA:219:ILE:HD13	35:AA:223:SER:OG	2.15	0.46
36:AB:97:ARG:NH2	38:A1:3244:A:OP1	2.44	0.46
36:AB:347:SER:C	36:AB:349:LYS:H	2.24	0.46
38:A1:32:U:H2'	38:A1:33:G:O4'	2.16	0.46
38:A1:268:A:C4	50:AN:12:ARG:HG2	2.50	0.46
38:A1:408:A:N6	40:A4:15:G:H1'	2.31	0.46
38:A1:656:A:H2'	38:A1:657:A:H8	1.81	0.46
38:A1:950:G:N1	38:A1:1368:U:OP2	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1072:G:H2'	38:A1:1073:U:H6	1.81	0.46
38:A1:1464:G:O2'	38:A1:1466:G:N7	2.46	0.46
38:A1:1757:A:H2'	38:A1:1758:G:H8	1.80	0.46
38:A1:2609:A:H2'	38:A1:2610:G:C8	2.50	0.46
38:A1:3027:A:N1	80:DC:785:ARG:HB3	2.31	0.46
39:A3:89:G:N2	39:A3:92:A:OP2	2.44	0.46
55:AS:82:ASP:HB2	55:AS:120:SER:OG	2.15	0.46
80:DC:10:ARG:NH1	80:DC:446:ASP:OD2	2.49	0.46
80:DC:402:ALA:HA	80:DC:450:ALA:HB2	1.96	0.46
81:V:136:PHE:HE1	81:V:172:LEU:HB2	1.80	0.46
82:EC:6926:U:H2'	82:EC:6927:U:C6	2.51	0.46
6:BH:166:LEU:HD23	6:BH:169:PHE:HD2	1.81	0.46
7:BI:76:THR:HG21	7:BI:104:ILE:HD12	1.98	0.46
9:BL:53:TYR:CG	9:BL:113:PRO:HG2	2.51	0.46
16:Ba:46:GLU:HB3	16:Ba:48:ALA:H	1.80	0.46
33:BM:62:LEU:HB3	33:BM:90:LYS:HG2	1.96	0.46
34:B5:86:A:H4'	34:B5:148:A:H4'	1.98	0.46
34:B5:923:A:H2'	34:B5:924:A:C8	2.50	0.46
38:A1:727:G:OP2	38:A1:742:G:N2	2.45	0.46
38:A1:966:U:H2'	38:A1:967:A:H8	1.80	0.46
38:A1:1721:U:OP2	54:AR:124:TYR:OH	2.34	0.46
38:A1:2152:A:H2'	38:A1:2153:U:C6	2.49	0.46
38:A1:2222:A:H2'	38:A1:2223:A:C8	2.51	0.46
38:A1:3047:U:O2'	38:A1:3048:A:H5'	2.16	0.46
38:A1:3298:C:C2	38:A1:3299:A:C8	3.02	0.46
52:AP:64:ASN:O	52:AP:80:LYS:NZ	2.32	0.46
66:Ad:48:ASP:OD1	66:Ad:50:ARG:NE	2.48	0.46
79:E:14:LYS:HA	79:E:17:LEU:HG	1.97	0.46
19:BD:109:LEU:HB3	19:BD:175:VAL:HG11	1.98	0.46
19:BD:156:PHE:CD2	19:BD:189:MET:HE1	2.51	0.46
24:BR:99:VAL:HG13	24:BR:99:VAL:O	2.15	0.46
26:BT:28:LEU:HA	26:BT:111:ILE:HD11	1.98	0.46
31:Bg:22:SER:OG	31:Bg:70:ASP:HA	2.15	0.46
31:Bg:239:GLU:HB3	31:Bg:257:ALA:HB2	1.98	0.46
34:B5:44:U:OP2	34:B5:437:A:N6	2.48	0.46
34:B5:1146:G:H2'	34:B5:1147:A:H8	1.80	0.46
35:AA:221:LYS:NZ	38:A1:2965:U:O2	2.34	0.46
38:A1:245:U:H2'	38:A1:246:U:C6	2.50	0.46
38:A1:3374:U:H2'	38:A1:3378:C:H41	1.81	0.46
46:AI:99:ILE:HD13	46:AI:101:LYS:HE2	1.98	0.46
46:AI:203:LYS:HE2	46:AI:203:LYS:HB2	1.74	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:AX:69:SER:O	60:AX:73:MET:HG2	2.16	0.46
62:AZ:25:ILE:HG23	62:AZ:41:ALA:HB1	1.98	0.46
79:E:105:LYS:HB2	79:E:105:LYS:HE2	1.77	0.46
80:DC:236:ASP:N	80:DC:236:ASP:OD1	2.48	0.46
80:DC:496:LYS:HG2	80:DC:555:LYS:HB2	1.97	0.46
1:BA:16:LEU:HD23	1:BA:16:LEU:H	1.81	0.46
2:BB:134:VAL:HG22	2:BB:218:LEU:HD12	1.97	0.46
8:BJ:109:LEU:HB2	8:BJ:146:PHE:HB3	1.97	0.46
10:BN:140:LYS:HE3	38:A1:847:A:OP1	2.16	0.46
13:BW:104:LEU:HD23	13:BW:125:ILE:HA	1.97	0.46
30:Bd:32:ARG:NH1	34:B5:1597:A:OP2	2.44	0.46
34:B5:100:A2M:H8	34:B5:100:A2M:O5'	2.16	0.46
34:B5:1561:U:H2'	34:B5:1562:G:C8	2.43	0.46
35:AA:206:PRO:HG3	35:AA:213:GLY:HA3	1.98	0.46
38:A1:1141:C:O2'	38:A1:1153:A:N3	2.47	0.46
38:A1:1262:G:H3'	38:A1:1262:G:OP2	2.16	0.46
38:A1:1348:U:H4'	38:A1:1350:A:H5'	1.98	0.46
38:A1:1687:U:H5''	38:A1:1688:U:H5'	1.96	0.46
38:A1:1867:A:H2'	38:A1:1868:G:C8	2.51	0.46
38:A1:2416:U:H2'	38:A1:2417:OMU:C6	2.45	0.46
38:A1:2615:G:H2'	38:A1:2616:C:C6	2.51	0.46
38:A1:3121:U:H1'	38:A1:3122:A:H5''	1.97	0.46
40:A4:6:U:H2'	40:A4:7:U:C6	2.51	0.46
41:AD:111:GLN:NE2	41:AD:252:ALA:HA	2.29	0.46
50:AN:147:ARG:HG3	70:Ah:101:THR:HG21	1.98	0.46
80:DC:373:ASP:N	80:DC:373:ASP:OD1	2.47	0.46
81:V:136:PHE:CE1	81:V:172:LEU:HB2	2.51	0.46
82:EC:6817:A:H4'	82:EC:6818:G:O5'	2.15	0.46
5:BG:89:ASP:OD2	34:B5:92:A:N6	2.49	0.46
6:BH:64:VAL:HA	6:BH:67:LEU:HD23	1.97	0.46
8:BJ:29:LYS:HA	18:Be:40:TYR:HE1	1.80	0.46
12:BV:66:ASP:OD1	12:BV:67:ASP:N	2.48	0.46
15:BY:108:ARG:NH2	34:B5:444:C:OP2	2.44	0.46
23:BQ:87:LYS:HG3	23:BQ:117:LEU:HA	1.97	0.46
31:Bg:9:LEU:HD13	31:Bg:313:TRP:HE1	1.81	0.46
31:Bg:70:ASP:HB2	31:Bg:112:SER:HA	1.98	0.46
31:Bg:102:ARG:CZ	34:B5:1342:C:H5''	2.46	0.46
33:BM:43:ARG:HE	33:BM:103:LEU:HD22	1.80	0.46
34:B5:853:G:OP1	54:AR:177:VAL:HG23	2.15	0.46
34:B5:1564:U:H2'	34:B5:1565:C:H6	1.80	0.46
38:A1:640:U:H2'	38:A1:641:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1282:G:O2'	38:A1:1283:C:H6	1.99	0.46
38:A1:1350:A:H1'	38:A1:1351:U:OP2	2.15	0.46
38:A1:1378:U:H2'	38:A1:1379:G:C8	2.47	0.46
38:A1:1897:G:O2'	58:AV:16:GLY:O	2.26	0.46
38:A1:2250:G:O6	38:A1:2267:C:N4	2.49	0.46
38:A1:2520:A:H2'	38:A1:2521:U:C6	2.51	0.46
38:A1:2618:G:O2'	38:A1:2865:U:OP1	2.18	0.46
38:A1:3280:U:O2'	38:A1:3281:U:H5''	2.16	0.46
40:A4:40:A:H2'	40:A4:41:A:H8	1.81	0.46
47:AJ:49:LYS:HA	47:AJ:64:LYS:H	1.81	0.46
48:AL:8:PRO:HB2	53:AQ:166:LEU:HG	1.97	0.46
55:AS:27:MET:HB2	55:AS:41:TYR:HD1	1.81	0.46
59:AW:20:LEU:HD21	59:AW:28:ILE:HG23	1.98	0.46
62:AZ:50:PRO:HD3	62:AZ:68:ILE:HG12	1.98	0.46
75:Am:99:CYS:HB2	75:Am:114:LYS:HE3	1.97	0.46
79:E:77:ALA:HB1	79:E:82:VAL:HG23	1.97	0.46
81:V:16:ARG:HB2	81:V:66:PHE:CZ	2.51	0.46
81:V:48:ARG:HH21	81:V:95:GLU:HB2	1.81	0.46
81:V:159:VAL:HG11	81:V:165:VAL:HG12	1.98	0.46
1:BA:59:LEU:HB2	12:BV:79:LEU:HD21	1.97	0.45
2:BB:146:GLN:N	2:BB:149:GLN:OE1	2.48	0.45
3:BC:147:ASN:HB2	12:BV:3:ASN:HA	1.98	0.45
4:BE:48:LEU:HD23	4:BE:52:LEU:HD12	1.98	0.45
4:BE:108:ARG:NH2	34:B5:789:A:OP1	2.48	0.45
5:BG:14:LYS:HD3	34:B5:152:U:H4'	1.98	0.45
8:BJ:62:ARG:CZ	8:BJ:68:LYS:HD3	2.46	0.45
19:BD:71:LEU:HD23	19:BD:74:GLN:NE2	2.31	0.45
25:BS:11:PHE:CE2	25:BS:59:GLY:HA3	2.51	0.45
32:Bf:97:LYS:NZ	34:B5:1230:A:OP2	2.40	0.45
33:BM:97:LEU:HA	33:BM:100:TRP:HE1	1.79	0.45
34:B5:1369:U:H1'	34:B5:1372:U:H2'	1.99	0.45
34:B5:1524:A:C2	34:B5:1590:G:H1'	2.51	0.45
34:B5:1590:G:H2'	34:B5:1591:C:H6	1.81	0.45
34:B5:1593:A:H2'	34:B5:1594:G:C8	2.48	0.45
38:A1:887:G:H2'	38:A1:888:A:C8	2.51	0.45
38:A1:1762:C:H3'	38:A1:1763:U:H4'	1.98	0.45
38:A1:2307:G:O2'	38:A1:2310:U:OP2	2.30	0.45
38:A1:3160:U:H2'	38:A1:3161:C:C6	2.50	0.45
39:A3:33:U:C2	41:AD:207:TYR:CD1	3.04	0.45
56:AT:79:MET:HB2	56:AT:84:TYR:CE1	2.52	0.45
58:AV:87:ARG:HB2	58:AV:89:ASP:OD1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:AY:54:ASP:OD1	61:AY:110:HIS:N	2.48	0.45
1:BA:190:ASP:HB2	1:BA:193:GLN:CD	2.41	0.45
5:BG:16:PHE:HE2	5:BG:121:LEU:HD23	1.81	0.45
19:BD:75:LYS:NZ	21:BK:20:VAL:O	2.38	0.45
31:Bg:16:HIS:CE1	31:Bg:37:SER:HG	2.34	0.45
31:Bg:93:ASP:OD1	31:Bg:94:VAL:N	2.49	0.45
31:Bg:194:GLY:C	31:Bg:221:MET:HE1	2.41	0.45
34:B5:207:U:H2'	34:B5:208:U:C6	2.50	0.45
34:B5:615:A:O2'	34:B5:621:A:N1	2.47	0.45
36:AB:266:ARG:NH2	38:A1:2392:C:H1'	2.31	0.45
37:AC:181:VAL:C	37:AC:183:LYS:H	2.25	0.45
38:A1:20:A:H2'	38:A1:21:G:C8	2.51	0.45
38:A1:68:C:O3'	50:AN:177:GLY:HA2	2.16	0.45
38:A1:273:A:H2'	38:A1:274:G:C8	2.51	0.45
38:A1:550:A:H2'	38:A1:551:A:C8	2.51	0.45
38:A1:860:G:OP1	78:Ap:17:ARG:NH2	2.47	0.45
38:A1:2514:U:O2	38:A1:2593:A:N6	2.44	0.45
38:A1:3015:G:H2'	38:A1:3016:A:H8	1.81	0.45
38:A1:3267:A:H2'	42:AE:69:PHE:CZ	2.50	0.45
39:A3:108:A:H2'	39:A3:109:G:H8	1.81	0.45
39:A3:114:U:H2'	39:A3:115:G:H8	1.81	0.45
42:AE:4:GLN:HB2	67:Ae:75:LEU:HB3	1.98	0.45
47:AJ:25:GLU:HG2	47:AJ:29:ARG:HH22	1.80	0.45
47:AJ:94:ARG:O	47:AJ:95:ASN:HB2	2.16	0.45
67:Ae:82:LEU:HD21	67:Ae:112:ALA:HB2	1.98	0.45
71:Ai:27:SER:O	71:Ai:28:TYR:HB2	2.15	0.45
71:Ai:90:MET:HE2	71:Ai:93:ILE:HD12	1.99	0.45
80:DC:380:LEU:HB2	80:DC:469:LEU:HD11	1.98	0.45
82:EC:6886:A:H2'	82:EC:6887:G:C8	2.51	0.45
3:BC:119:LYS:HE3	34:B5:1291:G:H5'	1.98	0.45
16:Ba:5:ARG:HH21	34:B5:1796:C:P	2.39	0.45
20:BF:148:ARG:HA	20:BF:157:ARG:HA	1.97	0.45
34:B5:53:G:H2'	34:B5:54:C:H6	1.82	0.45
34:B5:1170:G:C2	34:B5:1171:A:C8	3.04	0.45
34:B5:1235:C:H2'	34:B5:1236:A:H8	1.81	0.45
34:B5:1773:4AC:P	76:An:2:ARG:HH11	2.38	0.45
38:A1:74:G:H5''	48:AL:104:ARG:NH1	2.31	0.45
38:A1:340:C:H2'	38:A1:341:G:O4'	2.16	0.45
38:A1:1015:U:O4'	38:A1:1017:C:N4	2.50	0.45
38:A1:1494:U:OP1	74:Al:42:ARG:NH2	2.35	0.45
38:A1:1883:A:H2'	38:A1:1884:A:C8	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2446:U:N3	38:A1:2447:A:N7	2.64	0.45
38:A1:2466:G:H21	79:E:209:SER:HG	1.61	0.45
54:AR:178:ALA:O	54:AR:181:ARG:HG2	2.17	0.45
55:AS:77:VAL:HG11	55:AS:106:LEU:HD13	1.98	0.45
80:DC:275:MET:HE3	80:DC:276:PHE:CZ	2.51	0.45
80:DC:472:SER:OG	80:DC:473:GLU:N	2.50	0.45
80:DC:597:VAL:HG22	80:DC:623:TYR:HD2	1.81	0.45
1:BA:190:ASP:N	1:BA:190:ASP:OD1	2.49	0.45
8:BJ:17:ARG:HH22	34:B5:4:C:HO2'	1.60	0.45
17:Bb:51:GLN:HA	17:Bb:66:PRO:HB3	1.98	0.45
34:B5:213:A:H2'	34:B5:214:G:O4'	2.17	0.45
34:B5:434:G:N1	34:B5:437:A:OP2	2.46	0.45
34:B5:549:G:O2'	34:B5:556:A:N1	2.43	0.45
34:B5:1022:C:O2'	34:B5:1125:A:N1	2.38	0.45
34:B5:1198:G:OP1	34:B5:1199:G:O2'	2.28	0.45
34:B5:1494:C:H2'	34:B5:1495:C:C6	2.51	0.45
38:A1:1139:G:P	64:Ab:14:ARG:HH21	2.39	0.45
38:A1:1292:C:O2'	38:A1:1293:U:OP1	2.29	0.45
38:A1:2728:G:N7	56:AT:87:LYS:NZ	2.52	0.45
38:A1:3150:A:H2'	38:A1:3151:U:O4'	2.16	0.45
40:A4:39:G:H1'	40:A4:104:A:H61	1.80	0.45
42:AE:40:LEU:HD13	42:AE:84:VAL:HG21	1.97	0.45
43:AF:82:LYS:HB3	43:AF:82:LYS:HE2	1.83	0.45
63:Aa:77:LYS:O	63:Aa:80:THR:OG1	2.33	0.45
76:An:15:ARG:HA	76:An:18:ARG:HG2	1.97	0.45
81:V:97:LYS:HE2	81:V:187:VAL:HG21	1.97	0.45
2:BB:176:VAL:HG12	2:BB:177:GLN:H	1.82	0.45
4:BE:121:TYR:OH	4:BE:235:TYR:O	2.26	0.45
6:BH:154:LEU:HD11	6:BH:183:PHE:CD2	2.47	0.45
9:BL:82:ARG:O	9:BL:110:HIS:ND1	2.50	0.45
17:Bb:70:LYS:NZ	34:B5:1050:G:OP1	2.43	0.45
22:BP:128:HIS:HB3	34:B5:1460:A:C8	2.51	0.45
34:B5:1147:A:H2'	34:B5:1148:C:C6	2.51	0.45
34:B5:1461:C:H2'	34:B5:1462:G:H8	1.81	0.45
36:AB:250:ALA:HB3	38:A1:2880:U:H1'	1.98	0.45
37:AC:230:VAL:HG21	37:AC:257:LYS:HD3	1.98	0.45
38:A1:1269:U:O2'	38:A1:1271:A:N7	2.43	0.45
38:A1:1666:G:H2'	38:A1:1667:A:C8	2.52	0.45
38:A1:2148:U:H2'	38:A1:2149:A:C8	2.52	0.45
38:A1:2208:A:H2'	38:A1:2209:U:O4'	2.17	0.45
38:A1:2305:G:OP2	38:A1:2305:G:N2	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2356:A:H5'	52:AP:138:LYS:NZ	2.32	0.45
38:A1:2426:U:H2'	38:A1:2427:U:H6	1.81	0.45
38:A1:2999:U:H2'	38:A1:3000:A:H8	1.82	0.45
38:A1:3302:U:H2'	38:A1:3303:G:C8	2.52	0.45
44:AG:71:VAL:HG23	44:AG:235:GLY:HA3	1.98	0.45
62:AZ:33:SER:OG	62:AZ:35:SER:O	2.25	0.45
2:BB:205:PHE:CD1	34:B5:1065:A:H4'	2.51	0.45
4:BE:85:GLY:N	4:BE:88:ASP:OD2	2.49	0.45
6:BH:105:THR:O	6:BH:107:ARG:NH1	2.50	0.45
8:BJ:39:LYS:HG3	34:B5:592:A:OP1	2.17	0.45
12:BV:66:ASP:O	12:BV:70:ASN:ND2	2.50	0.45
22:BP:50:THR:H	22:BP:52:LYS:NZ	2.15	0.45
22:BP:77:ARG:HH12	34:B5:1242:A:P	2.40	0.45
25:BS:73:MET:HB3	25:BS:101:LEU:HD11	1.97	0.45
31:Bg:278:PHE:CZ	31:Bg:287:PRO:HG2	2.51	0.45
34:B5:31:C:O2'	34:B5:547:U:OP1	2.35	0.45
34:B5:245:U:O2'	34:B5:247:A:N7	2.41	0.45
34:B5:252:U:H2'	34:B5:253:A:H8	1.82	0.45
34:B5:365:G:H5'	34:B5:758:U:O2	2.16	0.45
34:B5:1468:U:H2'	34:B5:1469:A:O4'	2.17	0.45
36:AB:169:THR:CG2	36:AB:171:LEU:HD13	2.45	0.45
38:A1:137:G:H2'	38:A1:138:U:C6	2.51	0.45
38:A1:1001:G:N3	38:A1:1041:U:H5'	2.32	0.45
38:A1:1629:U:H1'	62:AZ:115:LYS:HD2	1.98	0.45
38:A1:1886:A:O4'	38:A1:3307:A:H5'	2.16	0.45
45:AH:85:GLY:HA3	45:AH:187:ILE:HD12	1.99	0.45
78:Ap:59:CYS:C	78:Ap:61:LYS:H	2.24	0.45
80:DC:20:ARG:N	80:DC:99:LEU:O	2.45	0.45
80:DC:619:MET:HE2	80:DC:685:ARG:HH12	1.80	0.45
81:V:45:LEU:HD13	81:V:49:ALA:HB3	1.97	0.45
1:BA:98:ILE:HD11	1:BA:116:LYS:HE3	1.99	0.45
2:BB:109:LYS:O	2:BB:113:MET:HG2	2.16	0.45
3:BC:178:ILE:HB	3:BC:185:LYS:HG3	1.99	0.45
4:BE:98:ASN:HB2	4:BE:114:ILE:HG13	1.99	0.45
13:BW:30:SER:HA	13:BW:34:ILE:HD12	1.97	0.45
14:BX:40:SER:O	14:BX:40:SER:OG	2.34	0.45
14:BX:59:ILE:HD12	14:BX:118:PRO:HD2	1.98	0.45
26:BT:77:ASN:OD1	26:BT:101:ASN:ND2	2.47	0.45
27:BU:40:ASN:ND2	27:BU:107:THR:OG1	2.49	0.45
34:B5:585:A:H2'	34:B5:586:G:C8	2.51	0.45
34:B5:1159:C:N4	34:B5:1285:U:O5'	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1398:U:H2'	34:B5:1400:A:C5	2.52	0.45
34:B5:1715:G:C2	34:B5:1716:C:H1'	2.52	0.45
61:AY:74:TYR:CD2	61:AY:77:LYS:HB2	2.52	0.45
79:E:31:THR:O	79:E:209:SER:N	2.50	0.45
79:E:118:LYS:C	79:E:121:PRO:HD2	2.42	0.45
82:EC:6759:A:H2'	82:EC:6760:A:H8	1.77	0.45
4:BE:60:GLU:O	4:BE:64:ILE:HD12	2.17	0.45
10:BN:61:THR:HB	34:B5:959:U:C6	2.51	0.45
11:BO:19:ILE:HB	11:BO:83:ILE:HD13	1.99	0.45
19:BD:36:GLY:N	19:BD:51:ARG:HB2	2.31	0.45
24:BR:37:GLU:HG2	24:BR:38:ILE:HD12	1.98	0.45
25:BS:133:VAL:HG22	34:B5:1545:A:H5''	1.98	0.45
31:Bg:109:ASP:C	31:Bg:126:SER:HG	2.17	0.45
34:B5:12:U:H2'	34:B5:13:C:H6	1.81	0.45
34:B5:30:G:C6	34:B5:597:G:C6	3.05	0.45
34:B5:176:C:H2'	34:B5:177:U:O4'	2.16	0.45
34:B5:447:U:H2'	34:B5:448:C:O4'	2.15	0.45
34:B5:1159:C:H42	34:B5:1285:U:P	2.40	0.45
34:B5:1471:A:H2'	34:B5:1471:A:N3	2.32	0.45
34:B5:1623:C:H2'	34:B5:1624:C:H6	1.81	0.45
38:A1:241:G:N3	38:A1:242:C:H5''	2.32	0.45
38:A1:601:U:H2'	38:A1:602:A:C8	2.52	0.45
38:A1:649:A2M:H2'	38:A1:650:OMC:H6	1.82	0.45
38:A1:715:A:N1	38:A1:781:G:O2'	2.40	0.45
38:A1:1340:G:H2'	38:A1:1341:U:C6	2.52	0.45
38:A1:1597:C:H5'	38:A1:1696:A:H1'	1.98	0.45
38:A1:1695:U:HO2'	38:A1:1749:A:H61	1.63	0.45
38:A1:1921:A:H2'	38:A1:1922:A:H8	1.81	0.45
38:A1:2526:C:H2'	38:A1:2527:G:H8	1.82	0.45
45:AH:34:LEU:HD21	45:AH:149:ASN:HB3	1.98	0.45
51:AO:3[A]:VAL:N	51:AO:4[A]:GLU:OE1	2.50	0.45
54:AR:23:TRP:HB2	54:AR:53:LYS:HD2	1.98	0.45
54:AR:24:LEU:HB3	54:AR:32:ILE:HD13	1.99	0.45
72:Aj:87:SER:OG	72:Aj:88:ALA:N	2.50	0.45
78:Ap:84:ARG:O	78:Ap:88:GLU:HG3	2.16	0.45
80:DC:215:LEU:HD12	85:DC:901:GDP:H2'	1.99	0.45
80:DC:447:ASP:OD1	80:DC:448:CYS:N	2.50	0.45
80:DC:823:ARG:HA	80:DC:828:MET:HB3	1.99	0.45
20:BF:148:ARG:HB2	20:BF:157:ARG:HG2	1.98	0.45
25:BS:113:LEU:HD22	25:BS:127:HIS:CG	2.52	0.45
26:BT:60:SER:OG	34:B5:1479:A:H5''	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BZ:40:VAL:HA	28:BZ:75:LEU:HD22	1.98	0.45
31:Bg:38:ARG:HA	31:Bg:67:ILE:HG23	1.99	0.45
32:Bf:133:ALA:HB2	34:B5:1252:C:O4'	2.17	0.45
34:B5:1202:A:N6	34:B5:1457:C:OP1	2.49	0.45
34:B5:1483:A:H2'	34:B5:1484:G:C8	2.51	0.45
34:B5:1650:U:H2'	34:B5:1651:A:C8	2.52	0.45
34:B5:1702:A:H3'	34:B5:1703:C:H6	1.81	0.45
38:A1:791:A:H2'	38:A1:792:G:H8	1.82	0.45
38:A1:1602:A:H4'	54:AR:10:LEU:HD21	1.98	0.45
38:A1:1621:A:H2'	38:A1:1622:U:H6	1.82	0.45
38:A1:1654:A:N3	69:Ag:59:PRO:HB3	2.32	0.45
38:A1:1724:U:H1'	38:A1:1725:C:C6	2.52	0.45
38:A1:2497:U:HO2'	38:A1:2498:U:P	2.40	0.45
38:A1:2727:A:C2	63:Aa:43:ILE:HG23	2.51	0.45
38:A1:3160:U:H2'	38:A1:3161:C:H6	1.81	0.45
41:AD:217:GLU:OE2	41:AD:218:ARG:HG3	2.17	0.45
41:AD:289:LYS:HD2	46:AI:206:LEU:HD23	1.98	0.45
45:AH:86:TYR:CD2	45:AH:151:VAL:HB	2.52	0.45
11:BO:61:MET:HE2	11:BO:65:GLN:NE2	2.32	0.45
11:BO:125:SER:HB3	34:B5:926:A:C2	2.37	0.45
13:BW:115:GLU:CD	13:BW:118:ARG:HH11	2.25	0.45
16:Ba:12:LYS:HG3	16:Ba:15:ARG:HB2	1.99	0.45
23:BQ:109:PHE:HD2	23:BQ:117:LEU:HD11	1.81	0.45
25:BS:134:ARG:HD3	34:B5:1559:A:N6	2.32	0.45
33:BM:32:LEU:HD11	33:BM:41:LEU:HD11	1.99	0.45
34:B5:1321:A:H4'	34:B5:1322:A:O5'	2.17	0.45
34:B5:1575:G7M:H2'	34:B5:1576:A:C8	2.51	0.45
38:A1:18:G:N2	50:AN:112:ASN:HD22	2.15	0.45
38:A1:590:G:H21	42:AE:19:LYS:HD3	1.81	0.45
38:A1:761:A:C2	38:A1:771:A:H1'	2.52	0.45
38:A1:1073:U:H2'	38:A1:1074:U:C6	2.52	0.45
38:A1:1141:C:H2'	38:A1:1142:G:O4'	2.17	0.45
38:A1:1203:A:N3	38:A1:2855:U:O2'	2.43	0.45
38:A1:1323:G:O3'	55:AS:1:MET:HB2	2.16	0.45
38:A1:1460:A:H2'	38:A1:1461:A:C8	2.51	0.45
38:A1:1565:G:C6	38:A1:1566:A:C6	3.04	0.45
39:A3:7:G:H5''	41:AD:22:ARG:HD3	1.99	0.45
46:AI:36:LEU:HD21	46:AI:69:ARG:HH11	1.81	0.45
47:AJ:60:ARG:H	47:AJ:63:GLU:CD	2.24	0.45
47:AJ:78:GLU:OE2	47:AJ:79:ILE:HG13	2.17	0.45
80:DC:180:ARG:HA	80:DC:183:GLU:OE2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:41:ARG:HA	24:BR:105:GLN:NE2	2.32	0.44
3:BC:59:HIS:CE1	3:BC:239:PRO:HD3	2.52	0.44
5:BG:142:ARG:O	5:BG:146:GLY:N	2.49	0.44
16:Ba:4:LYS:NZ	34:B5:1795:U:OP2	2.49	0.44
16:Ba:53:LEU:O	16:Ba:57:SER:HB2	2.18	0.44
22:BP:98:ASN:HB2	22:BP:122:THR:HA	1.98	0.44
27:BU:69:LYS:HG2	27:BU:80:GLU:HG3	1.99	0.44
34:B5:238:U:H3'	34:B5:239:C:C6	2.53	0.44
34:B5:498:G:H4'	34:B5:499:U:H5''	1.99	0.44
34:B5:590:C:H2'	34:B5:591:A:C8	2.52	0.44
34:B5:874:C:H2'	34:B5:875:G:C8	2.52	0.44
34:B5:1754:A:H3'	34:B5:1755:A:C8	2.53	0.44
35:AA:245:LEU:HD23	35:AA:248:GLY:C	2.41	0.44
38:A1:899:U:H2'	38:A1:900:G:H8	1.82	0.44
38:A1:1759:C:N4	38:A1:1760:A:H62	2.15	0.44
38:A1:2671:A:H2'	38:A1:2672:G:O4'	2.17	0.44
38:A1:2712:U:H2'	38:A1:2713:U:C6	2.52	0.44
38:A1:3354:U:H4'	38:A1:3355:U:OP2	2.12	0.44
38:A1:3371:G:H2'	38:A1:3372:A:H8	1.81	0.44
47:AJ:51:ARG:NH1	47:AJ:52:TYR:HB3	2.31	0.44
55:AS:23:LYS:HA	55:AS:23:LYS:HD2	1.79	0.44
80:DC:677:PHE:HD1	80:DC:819:VAL:HG22	1.81	0.44
82:EC:6897:G:H2'	82:EC:6898:U:H6	1.81	0.44
1:BA:13:ASP:OD2	1:BA:179:ARG:NH2	2.50	0.44
4:BE:170:THR:OG1	4:BE:171:ASP:N	2.50	0.44
16:Ba:64:LEU:HD12	16:Ba:65:PRO:HD2	1.99	0.44
22:BP:119:PHE:HE2	25:BS:119:ILE:HG22	1.82	0.44
23:BQ:28:LEU:HD21	23:BQ:30:LYS:HG2	1.99	0.44
25:BS:28:ILE:HD11	25:BS:56:LYS:HB2	1.98	0.44
26:BT:142:GLU:OE1	26:BT:142:GLU:N	2.47	0.44
31:Bg:297:ASP:HB3	31:Bg:299:GLN:OE1	2.17	0.44
34:B5:107:C:H2'	34:B5:108:A:H8	1.81	0.44
34:B5:743:U:H2'	34:B5:744:U:C6	2.53	0.44
34:B5:1227:A:N6	34:B5:1256:A:OP2	2.49	0.44
34:B5:1515:A:O2'	34:B5:1518:C:N4	2.49	0.44
38:A1:293:C:H2'	38:A1:294:U:O4'	2.17	0.44
38:A1:1010:G:H5'	46:AI:40:LYS:HE2	2.00	0.44
38:A1:1120:A:H2'	38:A1:1121:U:C6	2.53	0.44
38:A1:1211:U:HO2'	55:AS:113:ARG:HH11	1.62	0.44
38:A1:1222:G:H2'	81:V:57:THR:HG21	1.98	0.44
38:A1:1412:G:OP1	67:Ae:105:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1575:A:H2'	38:A1:1576:G:O4'	2.16	0.44
38:A1:2655:U:H4'	38:A1:2656:A:O4'	2.17	0.44
38:A1:2767:U:H2'	38:A1:2768:U:C6	2.52	0.44
41:AD:208:MET:HG3	41:AD:233:ALA:HB2	1.98	0.44
45:AH:101:VAL:HG22	45:AH:114:VAL:HG22	2.00	0.44
57:AU:33:TYR:HH	57:AU:80:THR:HG1	1.65	0.44
80:DC:162:ARG:HB3	85:DC:901:GDP:HN21	1.82	0.44
80:DC:550:ALA:HB1	80:DC:552:VAL:HG22	1.99	0.44
80:DC:681:MET:HB3	80:DC:684:VAL:HG21	2.00	0.44
82:EC:6777:C:N4	82:EC:6822:U:O2	2.50	0.44
1:BA:4:PRO:HG2	1:BA:7:PHE:HD2	1.83	0.44
2:BB:43:VAL:HG13	2:BB:68:VAL:HG11	1.98	0.44
15:BY:128:LYS:HA	15:BY:128:LYS:HD3	1.81	0.44
22:BP:77:ARG:NH2	34:B5:1240:U:H3'	2.33	0.44
31:Bg:116:ASP:OD1	31:Bg:117:LYS:N	2.50	0.44
34:B5:39:A:O2'	34:B5:40:A:OP2	2.30	0.44
34:B5:1269:OMU:H5''	34:B5:1269:OMU:O2	2.16	0.44
34:B5:1380:U:O2'	34:B5:1516:A:N1	2.48	0.44
38:A1:297:G:OP2	38:A1:297:G:N2	2.39	0.44
38:A1:361:A:OP1	72:Aj:26:SER:OG	2.31	0.44
38:A1:1155:C:O2'	38:A1:1197:A:N1	2.40	0.44
38:A1:1245:A:N7	38:A1:1271:A:O2'	2.51	0.44
38:A1:1616:U:H2'	38:A1:1617:G:H8	1.81	0.44
38:A1:2476:C:H2'	38:A1:2477:G:N7	2.33	0.44
38:A1:2838:A:OP1	46:AI:154:ARG:NH2	2.50	0.44
38:A1:2961:G:H2'	38:A1:2962:U:C6	2.52	0.44
38:A1:2986:U:H2'	38:A1:2987:A:H8	1.81	0.44
38:A1:3253:G:H2'	38:A1:3254:G:C8	2.52	0.44
42:AE:158:TYR:CE1	49:AM:115:PHE:HA	2.52	0.44
55:AS:26:ARG:O	56:AT:150:THR:HB	2.17	0.44
57:AU:43:VAL:HB	57:AU:49:ASN:HB2	1.98	0.44
62:AZ:41:ALA:HB2	62:AZ:77:TYR:CE1	2.48	0.44
80:DC:407:SER:HB3	80:DC:433:ARG:HA	1.99	0.44
82:EC:6892:U:H2'	82:EC:6893:C:H6	1.82	0.44
1:BA:39:ASN:OD1	1:BA:40:ALA:N	2.51	0.44
3:BC:87:GLN:OE1	34:B5:10:G:O2'	2.30	0.44
14:BX:70:LYS:HB3	14:BX:93:LEU:HD13	1.98	0.44
26:BT:118:PRO:HD2	26:BT:123:ARG:NH2	2.32	0.44
34:B5:406:U:H2'	34:B5:407:A:H8	1.83	0.44
34:B5:472:U:H2'	34:B5:473:A:H8	1.82	0.44
34:B5:1364:G:H2'	34:B5:1365:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1382:A:HO2'	34:B5:1383:G:H8	1.63	0.44
35:AA:152:SER:OG	38:A1:2157:G:N7	2.43	0.44
38:A1:269:G:OP2	50:AN:44:ARG:NH1	2.51	0.44
38:A1:532:A:H2'	38:A1:533:A:C8	2.52	0.44
38:A1:708:G:N2	38:A1:711:A:OP2	2.42	0.44
38:A1:976:U:H2'	38:A1:977:C:O4'	2.18	0.44
38:A1:1422:G:H21	42:AE:5:LYS:HD3	1.82	0.44
38:A1:2103:U:H2'	38:A1:2104:A:H8	1.82	0.44
38:A1:2180:G:H2'	38:A1:2181:C:H6	1.82	0.44
39:A3:113:C:H2'	39:A3:114:U:O4'	2.17	0.44
39:A3:118:A:H5''	41:AD:253:PHE:HZ	1.82	0.44
43:AF:80:GLN:HB2	56:AT:135:PRO:HB2	2.00	0.44
48:AL:61:PRO:O	48:AL:62:THR:OG1	2.27	0.44
65:Ac:43:ILE:HA	65:Ac:68:TYR:O	2.17	0.44
11:BO:17:ALA:HB3	11:BO:81:VAL:HA	2.00	0.44
21:BK:54:TYR:HB3	21:BK:72:GLY:HA2	2.00	0.44
24:BR:41:ILE:HD12	24:BR:50:ILE:HD12	1.99	0.44
25:BS:30:TYR:O	25:BS:33:THR:OG1	2.36	0.44
26:BT:57:ARG:HH21	34:B5:1479:A:P	2.41	0.44
26:BT:130:ARG:HG2	26:BT:134:ARG:NH1	2.32	0.44
34:B5:269:G:H2'	34:B5:270:C:C6	2.53	0.44
34:B5:1785:U:H2'	34:B5:1786:G:C8	2.51	0.44
37:AC:104:LYS:HD2	37:AC:106:TRP:CZ2	2.53	0.44
38:A1:176:G:C4	38:A1:242:C:C4	3.05	0.44
38:A1:975:C:H2'	38:A1:976:U:C6	2.52	0.44
38:A1:1769:G:H2'	38:A1:1770:G:H8	1.82	0.44
38:A1:2389:C:H2'	38:A1:2390:A:H8	1.83	0.44
38:A1:2433:U:H1'	50:AN:125:SER:HB2	1.99	0.44
41:AD:182:GLY:HA2	41:AD:194:LEU:HD23	2.00	0.44
46:AI:28:ASP:OD1	46:AI:28:ASP:N	2.50	0.44
79:E:101:LYS:HE2	79:E:105:LYS:HD3	2.00	0.44
80:DC:3:ALA:HB1	80:DC:8:GLN:NE2	2.32	0.44
4:BE:11:ARG:NH1	4:BE:20:LEU:HB3	2.32	0.44
4:BE:59:ARG:NH2	15:BY:87:PRO:HG3	2.32	0.44
4:BE:128:LYS:HG2	4:BE:140:VAL:HB	1.98	0.44
5:BG:33:GLY:HA2	5:BG:51:LYS:HE3	1.99	0.44
9:BL:27:THR:HG23	9:BL:30:ARG:H	1.82	0.44
10:BN:84:ILE:HG22	10:BN:135:LEU:HD21	1.99	0.44
18:Be:29:LYS:O	18:Be:31:LYS:NZ	2.49	0.44
19:BD:40:ARG:HD2	19:BD:47:GLU:OE2	2.18	0.44
20:BF:72:HIS:HB2	20:BF:111:VAL:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:142:PRO:O	20:BF:167:ARG:HG3	2.18	0.44
26:BT:11:ALA:HB1	34:B5:1480:G:H4'	2.00	0.44
27:BU:74:GLU:CD	34:B5:1429:G:H1'	2.42	0.44
34:B5:15:U:H2'	34:B5:16:G:O4'	2.17	0.44
34:B5:846:G:H2'	34:B5:847:A:C8	2.52	0.44
34:B5:850:A:HO2'	34:B5:851:U:P	2.40	0.44
34:B5:1116:A:H5''	76:An:17:ARG:HH11	1.81	0.44
34:B5:1409:G:N2	34:B5:1411:A:H3'	2.32	0.44
36:AB:233:TRP:CG	36:AB:265:ALA:HB1	2.53	0.44
38:A1:77:A:H5'	48:AL:100:ARG:NH1	2.32	0.44
38:A1:213:A:H1'	61:AY:3:LYS:HB2	1.99	0.44
38:A1:2203:U:H2'	38:A1:2204:C:H6	1.80	0.44
38:A1:2389:C:H2'	38:A1:2390:A:C8	2.52	0.44
38:A1:3177:G:O2'	38:A1:3179:U:OP1	2.34	0.44
42:AE:45:GLY:O	42:AE:48:ARG:HG3	2.17	0.44
50:AN:65:ARG:HD2	50:AN:127:TYR:CG	2.52	0.44
53:AQ:90:ASP:OD1	53:AQ:92:ARG:NE	2.41	0.44
79:E:74:VAL:HA	79:E:84:ALA:HB3	1.99	0.44
80:DC:32:LYS:HE3	80:DC:106:PRO:HA	2.00	0.44
82:EC:6885:G:H2'	82:EC:6886:A:H8	1.81	0.44
3:BC:44:LEU:HD12	3:BC:240:LEU:HD23	2.00	0.44
6:BH:81:LEU:O	6:BH:85:PHE:HB2	2.18	0.44
6:BH:113:PRO:HG2	6:BH:116:ARG:HD3	1.99	0.44
16:Ba:58:VAL:HG22	16:Ba:59:TYR:H	1.82	0.44
17:Bb:37:CYS:SG	17:Bb:59:CYS:HB2	2.58	0.44
19:BD:31:GLU:HA	19:BD:107:PHE:HE2	1.82	0.44
20:BF:209:TYR:HA	20:BF:212:LYS:HG2	1.99	0.44
21:BK:10:LYS:HE2	21:BK:36:ASP:H	1.82	0.44
22:BP:95:GLY:HA2	22:BP:103:ASN:O	2.17	0.44
38:A1:314:U:H2'	38:A1:315:C:C6	2.52	0.44
38:A1:1783:U:H2'	38:A1:1784:G:C8	2.53	0.44
38:A1:2941:A:O5'	38:A1:2943:G:H4'	2.18	0.44
39:A3:81:U:H2'	39:A3:82:G:H8	1.82	0.44
44:AG:29:SER:OG	44:AG:31:PRO:HD3	2.18	0.44
45:AH:21:LYS:CG	45:AH:22:SER:H	2.31	0.44
46:AI:101:LYS:HE3	46:AI:121:LYS:NZ	2.32	0.44
53:AQ:158:HIS:H	53:AQ:186:VAL:CG1	2.31	0.44
54:AR:90:PRO:O	54:AR:93:VAL:HG12	2.18	0.44
61:AY:31:LEU:HB3	61:AY:101:PRO:HG3	1.99	0.44
67:Ae:111:ARG:NH2	67:Ae:115:LEU:HD21	2.32	0.44
80:DC:600:ALA:HB1	80:DC:605:ILE:HB	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:EC:6922:G:C6	82:EC:6932:G:C6	3.06	0.44
2:BB:66:VAL:HG12	2:BB:68:VAL:HG13	2.00	0.44
5:BG:31:ARG:HA	5:BG:100:ALA:O	2.17	0.44
10:BN:112:LYS:NZ	34:B5:975:C:OP1	2.51	0.44
12:BV:4:ASP:OD1	12:BV:5:LYS:HG2	2.18	0.44
12:BV:73:ALA:HB1	12:BV:78:LEU:HB2	1.99	0.44
19:BD:80:ALA:O	19:BD:83:THR:HG22	2.17	0.44
34:B5:140:A:N6	34:B5:281:G:OP2	2.51	0.44
34:B5:329:G:H2'	34:B5:330:G:C8	2.53	0.44
34:B5:340:U:H2'	34:B5:341:A:H8	1.82	0.44
34:B5:505:A:H2'	34:B5:507:U:C2	2.52	0.44
34:B5:590:C:H2'	34:B5:591:A:H8	1.83	0.44
35:AA:177:LYS:NZ	78:Ap:33:GLN:OE1	2.50	0.44
38:A1:1062:A:H5''	38:A1:1063:G:H5'	2.00	0.44
38:A1:1211:U:H2'	38:A1:1212:A:C8	2.53	0.44
38:A1:1310:G:O2'	38:A1:2380:U:O2'	2.24	0.44
38:A1:1729:A:C6	65:Ac:49:PRO:HD3	2.53	0.44
38:A1:1831:U:H2'	38:A1:1832:C:C6	2.53	0.44
38:A1:1913:A:N3	38:A1:2120:A:H2'	2.33	0.44
39:A3:7:G:OP1	41:AD:33:ARG:NH1	2.50	0.44
47:AJ:100:GLY:HA3	47:AJ:154:THR:HG22	1.98	0.44
49:AM:23:ILE:HG21	49:AM:28:SER:HB2	2.00	0.44
57:AU:98:THR:HG22	57:AU:104:ARG:NH1	2.30	0.44
58:AV:104:ASN:HD21	58:AV:106:LYS:HB3	1.83	0.44
63:Aa:90:TYR:CD1	63:Aa:100:PRO:HG3	2.52	0.44
79:E:161:LYS:N	82:EC:6817:A:H62	2.16	0.44
80:DC:20:ARG:HB2	80:DC:100:ILE:HA	1.99	0.44
80:DC:203:TYR:OH	81:V:144:LYS:HE3	2.18	0.44
80:DC:212:GLY:HA3	80:DC:219:ALA:HA	2.00	0.44
82:EC:6797:U:H2'	82:EC:6798:C:C6	2.52	0.44
7:BI:106:ALA:HB2	7:BI:165:LEU:HG	1.99	0.44
9:BL:134:THR:OG1	34:B5:325:G:OP1	2.32	0.44
10:BN:87:ASP:OD1	10:BN:87:ASP:N	2.51	0.44
11:BO:136:ARG:HH21	34:B5:1785:U:P	2.37	0.44
16:Ba:45:VAL:O	16:Ba:46:GLU:HG2	2.17	0.44
16:Ba:87:ARG:HD2	16:Ba:91:ASP:OD2	2.18	0.44
20:BF:192:GLU:OE1	28:BZ:59:TYR:OH	2.27	0.44
22:BP:119:PHE:CE2	25:BS:119:ILE:HG22	2.53	0.44
27:BU:97:VAL:HG22	27:BU:102:ARG:NH1	2.33	0.44
30:Bd:10:HIS:NE2	34:B5:1554:U:O4	2.44	0.44
34:B5:27:U:H2'	34:B5:28:A2M:H8	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:276:C:O2'	34:B5:278:U:OP2	2.30	0.44
36:AB:173:GLN:HG2	36:AB:175:LYS:H	1.82	0.44
38:A1:1012:G:H2'	38:A1:1013:G:H8	1.83	0.44
38:A1:1232:C:C5	38:A1:1261:G:H2'	2.53	0.44
38:A1:1567:U:H3'	38:A1:1568:U:H4'	1.99	0.44
38:A1:2133:U:O4	38:A1:2147:A:H2	2.01	0.44
38:A1:2631:U:H2'	38:A1:2632:G:H8	1.82	0.44
38:A1:3214:U:OP2	49:AM:128:ARG:NH1	2.36	0.44
43:AF:163:LEU:O	43:AF:165:ASP:N	2.51	0.44
50:AN:110:ALA:HB1	50:AN:113:LEU:HD12	2.00	0.44
50:AN:180:PHE:O	50:AN:184:LYS:HG3	2.18	0.44
65:Ac:40:LYS:NZ	65:Ac:93:LEU:O	2.41	0.44
75:Am:104:PRO:HG2	75:Am:107:ALA:HB2	2.00	0.44
79:E:111:ILE:HD12	79:E:147:LYS:HE3	1.99	0.44
80:DC:88:GLU:OE1	80:DC:88:GLU:N	2.46	0.44
80:DC:240:MET:HB3	80:DC:244:LEU:HD23	2.00	0.44
80:DC:249:PHE:HE1	80:DC:271:ARG:HG2	1.79	0.44
2:BB:157:GLN:HB2	2:BB:160:HIS:CE1	2.53	0.43
3:BC:101:VAL:HG12	3:BC:115:ILE:HD12	1.99	0.43
5:BG:4:ASN:ND2	34:B5:152:U:O2	2.46	0.43
7:BI:165:LEU:HD13	7:BI:183:ILE:HD13	2.00	0.43
11:BO:22:SER:OG	11:BO:23:PHE:O	2.32	0.43
14:BX:69:ARG:HD2	14:BX:117:ILE:HG12	1.99	0.43
15:BY:36:SER:O	15:BY:40:LEU:HD13	2.18	0.43
25:BS:17:LEU:HD11	25:BS:66:LEU:HD11	1.99	0.43
25:BS:88:ARG:HB2	25:BS:98:TYR:HB2	1.99	0.43
26:BT:108:LEU:HD11	26:BT:113:ILE:HD12	2.00	0.43
27:BU:30:LYS:HB3	27:BU:33:GLN:OE1	2.17	0.43
31:Bg:177:MET:N	31:Bg:199:ILE:HD11	2.33	0.43
34:B5:108:A:H2'	34:B5:109:G:H8	1.81	0.43
34:B5:148:A:H3'	34:B5:149:C:H6	1.83	0.43
34:B5:463:U:H2'	34:B5:464:A:C8	2.53	0.43
34:B5:604:A:H2'	34:B5:605:A:O4'	2.18	0.43
34:B5:1688:U:H3'	34:B5:1689:A:H8	1.82	0.43
36:AB:233:TRP:CD1	36:AB:265:ALA:HB1	2.53	0.43
37:AC:281:ILE:HD13	53:AQ:28:LEU:CD1	2.48	0.43
38:A1:48:A:H4'	38:A1:49:A:H5'	2.00	0.43
38:A1:1234:G:C8	38:A1:1235:U:H2'	2.52	0.43
38:A1:1242:G:O2'	38:A1:1243:G:OP1	2.34	0.43
38:A1:1927:G:C8	78:Ap:16:VAL:HG12	2.53	0.43
38:A1:1947:G:H5''	54:AR:134:HIS:CB	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2974:U:H2'	38:A1:2975:U:C6	2.53	0.43
38:A1:3165:A:H2'	38:A1:3166:C:C6	2.52	0.43
38:A1:3215:A:C8	49:AM:121:MET:HE2	2.53	0.43
43:AF:51:TYR:OH	43:AF:183:ASP:OD1	2.29	0.43
43:AF:96:PRO:HB2	43:AF:99:PRO:HD2	1.99	0.43
55:AS:3:HIS:HD2	55:AS:5:LYS:NZ	2.15	0.43
63:Aa:96:LYS:NZ	63:Aa:142:GLY:O	2.50	0.43
78:Ap:8:VAL:O	78:Ap:11:THR:OG1	2.36	0.43
80:DC:461:GLN:HG2	80:DC:462:PHE:CD1	2.53	0.43
1:BA:84:ARG:NH2	24:BR:82:ASP:O	2.50	0.43
2:BB:190:PRO:HB2	2:BB:192:VAL:HG23	1.99	0.43
3:BC:157:LYS:HG2	13:BW:95:PRO:HA	1.99	0.43
11:BO:123:SER:HA	34:B5:929:A:C8	2.54	0.43
13:BW:71:LYS:HB3	13:BW:130:TYR:CE1	2.53	0.43
15:BY:37:LYS:NZ	34:B5:523:G:OP2	2.30	0.43
16:Ba:10:ARG:HH21	16:Ba:12:LYS:HD3	1.83	0.43
19:BD:109:LEU:HD23	19:BD:109:LEU:HA	1.89	0.43
23:BQ:35:PRO:HG2	23:BQ:38:LEU:HG	1.99	0.43
23:BQ:77:GLN:O	23:BQ:81:ILE:HG12	2.17	0.43
24:BR:60:ARG:HG2	24:BR:66:VAL:HG22	1.99	0.43
31:Bg:18:GLY:HA3	31:Bg:38:ARG:HB2	2.00	0.43
33:BM:63:VAL:HG21	33:BM:119:SER:HA	1.99	0.43
34:B5:151:G:H2'	34:B5:152:U:C6	2.53	0.43
34:B5:172:C:H2'	34:B5:173:A:C8	2.53	0.43
34:B5:1126:OMG:OP2	76:An:18:ARG:NH2	2.51	0.43
34:B5:1239:U:H2'	34:B5:1240:U:O4'	2.18	0.43
34:B5:1756[A]:A:H5'	38:A1:2256:A2M:H62	1.81	0.43
38:A1:979:U:H4'	38:A1:980:A:O4'	2.17	0.43
38:A1:2882:U:H2'	38:A1:2883:U:H6	1.82	0.43
38:A1:2943:G:H2'	38:A1:2944:U:O4'	2.18	0.43
38:A1:3203:U:H2'	38:A1:3204:C:C6	2.53	0.43
42:AE:62:THR:HB	42:AE:78:ARG:HB3	2.00	0.43
45:AH:53:ILE:HD12	49:AM:7:VAL:HG21	2.00	0.43
65:Ac:50:VAL:HA	65:Ac:53:LYS:HG2	2.00	0.43
77:Ao:10:THR:HG21	77:Ao:72:LEU:HD13	2.00	0.43
79:E:184:LEU:HA	79:E:187:VAL:HG22	1.99	0.43
80:DC:159:LYS:HA	85:DC:901:GDP:C6	2.52	0.43
81:V:55:LYS:HA	81:V:56:ASN:HA	1.71	0.43
82:EC:6910:A:H2'	82:EC:6911:A:C8	2.53	0.43
4:BE:12:LEU:O	34:B5:756:A:H1'	2.19	0.43
31:Bg:255:ALA:HB2	31:Bg:292:LEU:HD23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:119:A:H1'	34:B5:397:A:C5	2.53	0.43
34:B5:488:G:H2'	34:B5:492:A:H62	1.83	0.43
34:B5:1466:G:H2'	34:B5:1467:C:C6	2.52	0.43
34:B5:1773:4AC:O5'	76:An:2:ARG:NH1	2.51	0.43
38:A1:359:U:O3'	72:Aj:25:ARG:NH2	2.49	0.43
38:A1:1251:A:H2'	38:A1:1252:A:C8	2.49	0.43
38:A1:1392:G:H1'	38:A1:1418:A:N6	2.34	0.43
38:A1:1633:C:OP2	62:AZ:69:LYS:NZ	2.52	0.43
38:A1:2572:C:H4'	62:AZ:58:GLY:HA3	2.00	0.43
38:A1:2686:A:H2'	38:A1:2687:G:O4'	2.18	0.43
38:A1:3107:U:H2'	38:A1:3108:G:C8	2.53	0.43
47:AJ:84:LEU:HG	47:AJ:89:TYR:CD1	2.53	0.43
49:AM:36:VAL:HG11	49:AM:55:ARG:NH1	2.33	0.43
56:AT:17:ARG:HH11	56:AT:47:SER:HB3	1.83	0.43
57:AU:75:TYR:CZ	57:AU:79:LEU:HD11	2.52	0.43
80:DC:819:VAL:O	80:DC:823:ARG:HG2	2.18	0.43
82:EC:6898:U:H2'	82:EC:6899:C:C6	2.54	0.43
4:BE:19:LEU:HD11	4:BE:108:ARG:HD3	1.99	0.43
5:BG:20:ASP:O	5:BG:23:ARG:HG2	2.17	0.43
14:BX:69:ARG:NH2	34:B5:568:G:N7	2.67	0.43
14:BX:130:VAL:HG23	14:BX:140:LYS:HD2	2.00	0.43
15:BY:33:ALA:HB1	34:B5:532:U:O2	2.18	0.43
23:BQ:115:THR:HA	23:BQ:118:ILE:O	2.18	0.43
24:BR:93:LEU:HD13	24:BR:98:GLY:HA2	2.00	0.43
25:BS:107:SER:O	25:BS:111:ASP:N	2.47	0.43
31:Bg:106:HIS:CD2	31:Bg:110:VAL:HG22	2.52	0.43
34:B5:1669:U:H2'	34:B5:1670:G:O4'	2.18	0.43
34:B5:1756[A]:A:C8	38:A1:2256:A2M:C6	3.01	0.43
36:AB:256:HIS:HA	36:AB:257:PRO:C	2.43	0.43
38:A1:1349:G:OP2	38:A1:1349:G:N2	2.47	0.43
38:A1:1827:C:H2'	38:A1:1828:A:C8	2.54	0.43
38:A1:1856:C:H2'	38:A1:1857:C:H6	1.83	0.43
38:A1:2599:U:H2'	38:A1:2600:C:C6	2.53	0.43
38:A1:3322:A:H2'	38:A1:3323:A:C8	2.53	0.43
39:A3:64:A:H5'	39:A3:65:G:H5''	2.00	0.43
53:AQ:176:ARG:HA	53:AQ:182:LYS:O	2.18	0.43
63:Aa:117:ARG:HA	63:Aa:117:ARG:HD3	1.76	0.43
79:E:121:PRO:HG3	82:EC:6772:G:O3'	2.17	0.43
80:DC:187:VAL:HG13	81:V:130:PRO:HB2	2.00	0.43
82:EC:6794:C:O2'	82:EC:6889:A:N1	2.48	0.43
82:EC:6833:G:H2'	82:EC:6834:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:104:ALA:HA	11:BO:107:ARG:HB2	2.00	0.43
19:BD:109:LEU:O	19:BD:177:MET:HE1	2.19	0.43
21:BK:58:GLN:HB2	21:BK:65:TYR:HB2	1.98	0.43
34:B5:404:G:H2'	34:B5:405:C:H6	1.83	0.43
34:B5:901:G:H2'	34:B5:902:G:O4'	2.19	0.43
34:B5:1151:A:H2'	34:B5:1152:A:C8	2.54	0.43
34:B5:1161:C:H2'	34:B5:1162:C:H6	1.83	0.43
34:B5:1202:A:H3'	34:B5:1202:A:N3	2.34	0.43
34:B5:1439:C:H2'	34:B5:1440:C:C6	2.53	0.43
34:B5:1474:G:C2	34:B5:1475:A:C5	3.07	0.43
34:B5:1652:C:H2'	34:B5:1653:C:C6	2.54	0.43
35:AA:111:THR:HB	35:AA:136:ILE:HD13	2.00	0.43
35:AA:118:GLU:OE1	38:A1:2158:A:O2'	2.28	0.43
36:AB:30:LYS:NZ	38:A1:3139:A:OP2	2.42	0.43
38:A1:561:C:H2'	38:A1:562:C:H6	1.84	0.43
38:A1:965:A:H2	63:Aa:43:ILE:HD12	1.83	0.43
38:A1:1037:C:H2'	38:A1:1038:C:H6	1.84	0.43
38:A1:1695:U:O2'	38:A1:1749:A:N6	2.44	0.43
38:A1:2631:U:H2'	38:A1:2632:G:C8	2.54	0.43
38:A1:3150:A:HO2'	38:A1:3294:A:HO2'	1.58	0.43
41:AD:195:LEU:O	41:AD:199:ILE:HG13	2.19	0.43
42:AE:51:ARG:HD3	42:AE:158:TYR:CZ	2.54	0.43
48:AL:126:PHE:HD2	70:Ah:115:LYS:HG2	1.84	0.43
57:AU:87:ASN:HB2	57:AU:89:LEU:HD23	1.99	0.43
60:AX:85:GLN:OE1	60:AX:115:ARG:NH2	2.52	0.43
73:Ak:14:LEU:HD21	73:Ak:52:TYR:CD1	2.54	0.43
80:DC:377:ASP:OD1	80:DC:377:ASP:N	2.52	0.43
80:DC:736:PRO:HD2	80:DC:791:GLN:HB3	2.00	0.43
1:BA:167:LYS:HD2	1:BA:204:TYR:HB3	2.01	0.43
2:BB:144:ARG:HB3	2:BB:206:PRO:HB2	2.01	0.43
6:BH:80:GLU:HA	6:BH:83:LYS:HG2	2.01	0.43
11:BO:84:ARG:HG2	11:BO:85:ALA:O	2.18	0.43
14:BX:47:SER:HB3	34:B5:600:U:H1'	2.00	0.43
19:BD:61:GLU:H	19:BD:64:ARG:HB2	1.84	0.43
21:BK:76:LEU:HD12	21:BK:79:TYR:HB3	2.00	0.43
23:BQ:99:GLU:HB2	31:Bg:57:PRO:O	2.19	0.43
34:B5:343:C:H2'	34:B5:344:A:C8	2.50	0.43
34:B5:1122:G:N2	34:B5:1125:A:OP2	2.48	0.43
35:AA:181:LYS:HB2	38:A1:860:G:C6	2.53	0.43
38:A1:91:G:OP2	38:A1:93:C:N4	2.37	0.43
38:A1:792:G:H2'	38:A1:793:C:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1092:C:O2'	38:A1:1093:A:OP1	2.32	0.43
38:A1:1096:U:OP2	56:AT:116:ARG:NH2	2.34	0.43
38:A1:1098:A:OP2	56:AT:130:ARG:NE	2.39	0.43
38:A1:1659:U:H2'	38:A1:1660:C:H6	1.83	0.43
38:A1:2661:G:H2'	38:A1:2662:G:H8	1.83	0.43
38:A1:2760:C:N3	77:Ao:63:LYS:HE3	2.33	0.43
38:A1:3026:G:N2	38:A1:3029:A:OP2	2.48	0.43
52:AP:11:PRO:O	52:AP:105:LYS:NZ	2.51	0.43
59:AW:39:LEU:HD22	59:AW:44:LYS:HG3	2.01	0.43
79:E:112:ALA:O	79:E:138:VAL:HG12	2.18	0.43
80:DC:135:VAL:HG13	80:DC:139:THR:HG23	2.00	0.43
80:DC:314:LEU:HD23	80:DC:318:ALA:HB1	2.00	0.43
80:DC:571:SER:HB3	80:DC:720:ALA:HB2	2.00	0.43
81:V:169:GLU:N	81:V:169:GLU:OE1	2.52	0.43
3:BC:185:LYS:O	3:BC:189:GLN:HG3	2.18	0.43
5:BG:198:ALA:HB1	5:BG:202:ARG:HH12	1.83	0.43
9:BL:36:LYS:HD3	34:B5:248:U:H4'	2.01	0.43
15:BY:98:GLU:OE1	15:BY:98:GLU:N	2.52	0.43
19:BD:164:VAL:O	19:BD:168:ILE:HB	2.19	0.43
26:BT:34:VAL:HG12	26:BT:35:ASP:OD1	2.18	0.43
34:B5:185:U:H2'	34:B5:186:C:C6	2.53	0.43
34:B5:186:C:H2'	34:B5:187:G:O4'	2.18	0.43
34:B5:237:C:O2'	34:B5:238:U:H6	2.02	0.43
34:B5:833:U:H5'	34:B5:834:G:H5''	1.99	0.43
34:B5:1209:C:C4	34:B5:1455:G:N2	2.84	0.43
34:B5:1245:G:N2	34:B5:1248:C:OP2	2.52	0.43
34:B5:1275:A:C6	34:B5:1438:G:C5	3.06	0.43
34:B5:1556:A:H1'	34:B5:1560:U:OP2	2.19	0.43
34:B5:1783:C:OP1	76:An:1:MET:N	2.48	0.43
37:AC:34:ILE:HD11	38:A1:673:U:O3'	2.19	0.43
37:AC:67:THR:HG21	38:A1:2402:A:H2'	1.99	0.43
38:A1:551:A:O2'	38:A1:552:G:H8	2.01	0.43
38:A1:594:U:P	38:A1:609:G:H1	2.39	0.43
38:A1:1306:G:O2'	38:A1:1307:G:H5''	2.19	0.43
38:A1:1525:G:H5'	38:A1:1830:G:OP2	2.19	0.43
38:A1:1757:A:H2'	38:A1:1758:G:C8	2.53	0.43
38:A1:2144:A:H1'	38:A1:2281:A2M:N6	2.34	0.43
38:A1:2597:U:H2'	38:A1:2598:G:C8	2.54	0.43
38:A1:2953:U:H2'	38:A1:2954:U:C6	2.54	0.43
47:AJ:125:MET:SD	47:AJ:127:PHE:HE1	2.42	0.43
52:AP:60:PHE:HB3	52:AP:64:ASN:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:AX:31:THR:HG22	60:AX:33:ARG:HG3	2.01	0.43
63:Aa:59:ARG:HE	63:Aa:59:ARG:HB2	1.70	0.43
77:Ao:99:GLN:HG2	77:Ao:102:GLN:OE1	2.18	0.43
80:DC:101:ASN:O	80:DC:103:ILE:HD12	2.18	0.43
80:DC:152:LYS:NZ	80:DC:341:HIS:O	2.35	0.43
80:DC:433:ARG:NH1	80:DC:445:ILE:O	2.49	0.43
80:DC:835:TRP:CD1	80:DC:835:TRP:H	2.35	0.43
82:EC:6809:G:H2'	82:EC:6810:U:C6	2.54	0.43
2:BB:24:PHE:CE2	11:BO:39:ILE:HG12	2.54	0.43
2:BB:89:ASP:HB3	2:BB:223:PHE:CZ	2.53	0.43
13:BW:10:ALA:HB1	13:BW:27:ILE:HD13	2.00	0.43
15:BY:29:HIS:ND1	15:BY:29:HIS:O	2.51	0.43
22:BP:44:ARG:CZ	34:B5:1555:A:H4'	2.48	0.43
24:BR:20:TYR:CD2	24:BR:24:LEU:HG	2.54	0.43
27:BU:97:VAL:HG23	27:BU:101:LYS:HD3	1.99	0.43
29:Bc:30:VAL:HG11	29:Bc:54:LEU:HD12	2.00	0.43
31:Bg:149:ASP:HB2	31:Bg:175:ASP:HB3	2.00	0.43
32:Bf:96:LYS:HG2	32:Bf:98:VAL:HG13	2.00	0.43
34:B5:647:G:H1'	34:B5:688:G:N2	2.34	0.43
34:B5:909:U:H2'	34:B5:910:C:C6	2.54	0.43
34:B5:990:C:H2'	34:B5:991:G:O4'	2.19	0.43
34:B5:1254:U:C4	34:B5:1255:G:C5	3.07	0.43
34:B5:1344:A:O2'	34:B5:1345:A:OP1	2.30	0.43
34:B5:1496:U:H2'	34:B5:1497:U:H6	1.83	0.43
34:B5:1541:G:H21	34:B5:1570:A:H62	1.67	0.43
34:B5:1727:G:H2'	34:B5:1728:A:C8	2.54	0.43
34:B5:1739:C:H2'	34:B5:1740:A:C8	2.54	0.43
38:A1:277:G:H2'	38:A1:278:U:C6	2.53	0.43
38:A1:595:G:H2'	38:A1:596:C:C6	2.54	0.43
38:A1:655:C:H5''	67:Ae:26:HIS:HB3	1.99	0.43
38:A1:1624:G:H2'	38:A1:1625:A:C8	2.53	0.43
38:A1:3332:U:H2'	38:A1:3333:G:O4'	2.19	0.43
39:A3:90:U:H2'	39:A3:91:G:O4'	2.18	0.43
41:AD:90:HIS:NE2	41:AD:229:ASP:OD2	2.45	0.43
65:Ac:25:LEU:HD11	65:Ac:83:LYS:HE3	2.01	0.43
78:Ap:17:ARG:H	78:Ap:17:ARG:HG2	1.65	0.43
4:BE:97:GLU:HG3	4:BE:113:ARG:HH11	1.84	0.43
10:BN:110:ASP:OD1	10:BN:111:ALA:N	2.52	0.43
11:BO:16:VAL:O	11:BO:30:VAL:HA	2.19	0.43
13:BW:107:SER:HB2	34:B5:802:G:H21	1.84	0.43
20:BF:76:ARG:NH2	23:BQ:122:ARG:HG3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BS:6:GLN:HE22	28:BZ:44:GLN:HA	1.84	0.43
28:BZ:82:HIS:CD2	28:BZ:85:LYS:HE2	2.49	0.43
34:B5:1524:A:H2	34:B5:1590:G:H1'	1.81	0.43
38:A1:429:U:H2'	38:A1:430:U:H6	1.84	0.43
38:A1:1233:G:C6	38:A1:1234:G:C6	3.07	0.43
38:A1:1480:G:O2'	38:A1:1871:U:O4	2.32	0.43
38:A1:1596:C:H2'	38:A1:1597:C:H6	1.83	0.43
38:A1:2465:G:H22	38:A1:2491:A:N6	2.17	0.43
38:A1:2561:A:C2	44:AG:31:PRO:HA	2.54	0.43
38:A1:2909:U:H2'	38:A1:2910:A:O4'	2.19	0.43
38:A1:3175:U:H4'	38:A1:3176:G:H5'	2.00	0.43
38:A1:3182:G:H4'	51:AO:161[A]:LYS:HG2	2.00	0.43
43:AF:89:ILE:HD11	43:AF:229:PHE:HB3	2.00	0.43
45:AH:173:ARG:HE	45:AH:173:ARG:HB2	1.60	0.43
80:DC:15:LYS:NZ	80:DC:16:VAL:H	2.16	0.43
80:DC:353:ALA:HA	80:DC:356:LEU:HG	2.00	0.43
80:DC:358:GLU:OE1	80:DC:358:GLU:N	2.52	0.43
80:DC:482:LYS:C	80:DC:484:SER:H	2.26	0.43
81:V:55:LYS:HE3	81:V:83:ASN:HA	2.00	0.43
82:EC:6914:A:H2'	82:EC:6915:G:C8	2.54	0.43
3:BC:49:LYS:HB3	3:BC:243:TYR:CD2	2.54	0.43
5:BG:184:LEU:HD21	34:B5:140:A:C4	2.54	0.43
6:BH:63:PRO:O	6:BH:64:VAL:HG12	2.18	0.43
11:BO:68:ALA:HB1	11:BO:110:LEU:HD13	2.01	0.43
13:BW:57:ARG:HE	17:Bb:26:GLN:HE21	1.67	0.43
27:BU:98:GLN:HA	27:BU:102:ARG:CZ	2.49	0.43
31:Bg:126:SER:HB3	31:Bg:128:ASP:OD1	2.19	0.43
31:Bg:209:THR:HA	31:Bg:225:LEU:HD23	2.01	0.43
34:B5:553:G:OP2	34:B5:554:C:O2'	2.33	0.43
34:B5:841:U:H2'	34:B5:842:C:C6	2.54	0.43
34:B5:1471:A:H2	34:B5:1474:G:N3	2.17	0.43
34:B5:1476:C:H2'	34:B5:1477:G:H8	1.83	0.43
35:AA:108:PRO:O	35:AA:111:THR:OG1	2.23	0.43
38:A1:1601:U:P	54:AR:42:ARG:HH22	2.42	0.43
50:AN:94:TYR:CE2	50:AN:96:ARG:HB2	2.53	0.43
51:AO:43[A]:ILE:HD11	51:AO:138[A]:LEU:HD13	2.01	0.43
57:AU:82:LYS:HE3	57:AU:82:LYS:HB3	1.75	0.43
59:AW:27:LYS:HD3	59:AW:27:LYS:HA	1.84	0.43
77:Ao:4:VAL:O	77:Ao:94:GLY:N	2.41	0.43
82:EC:6781:U:O2'	82:EC:6782:C:O5'	2.33	0.43
1:BA:81:PHE:CD1	1:BA:167:LYS:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:100:ARG:HH12	4:BE:122:LYS:HA	1.83	0.42
7:BI:37:LYS:O	7:BI:59:ARG:HA	2.19	0.42
8:BJ:136:VAL:O	8:BJ:155:HIS:HB3	2.18	0.42
23:BQ:47:LYS:HB3	23:BQ:82:ARG:HD2	2.01	0.42
23:BQ:95:LYS:O	31:Bg:96:THR:OG1	2.36	0.42
24:BR:20:TYR:HD2	24:BR:24:LEU:HG	1.84	0.42
25:BS:20:THR:HG21	25:BS:35:ILE:HA	2.01	0.42
30:Bd:4:GLU:HG2	30:Bd:5:ASN:H	1.84	0.42
33:BM:61:VAL:HA	33:BM:89:ILE:O	2.19	0.42
34:B5:175:G:H1'	34:B5:266:A:N6	2.34	0.42
34:B5:826:U:H2'	34:B5:827:C:C6	2.54	0.42
34:B5:918:U:H2'	34:B5:919:A:C8	2.54	0.42
34:B5:1383:G:H2'	34:B5:1384:A:C8	2.54	0.42
34:B5:1712:A:H3'	34:B5:1713:G:H8	1.84	0.42
36:AB:280:HIS:HB3	36:AB:324:VAL:HG13	2.00	0.42
38:A1:109:A:N1	38:A1:322:U:O2'	2.50	0.42
38:A1:411:U:H2'	38:A1:412:G:C8	2.54	0.42
38:A1:848:A:H5'	38:A1:849:C:OP2	2.19	0.42
38:A1:1376:C:O2'	38:A1:1408:G:O2'	2.32	0.42
38:A1:2526:C:H2'	38:A1:2527:G:C8	2.53	0.42
38:A1:2741:C:O2'	77:Ao:20:HIS:N	2.48	0.42
41:AD:107:ARG:NH1	41:AD:120:LYS:O	2.52	0.42
46:AI:49:CYS:HB3	46:AI:168:SER:HB3	2.01	0.42
51:AO:106[A]:GLU:HG2	51:AO:147[A]:TRP:CZ2	2.54	0.42
80:DC:70:ILE:HG13	80:DC:71:LYS:HG2	2.00	0.42
80:DC:378:LEU:HD12	80:DC:378:LEU:HA	1.87	0.42
80:DC:379:MET:HA	80:DC:470:THR:HG22	2.01	0.42
2:BB:149:GLN:HE21	2:BB:151:LYS:HB3	1.84	0.42
4:BE:87:MET:SD	4:BE:236:ILE:HD13	2.59	0.42
17:Bb:31:TYR:HE2	17:Bb:33:LEU:HD21	1.83	0.42
22:BP:47:ARG:NH2	34:B5:1554:U:OP2	2.37	0.42
27:BU:19:ILE:HD12	27:BU:94:GLU:HB3	2.01	0.42
29:Bc:64:ARG:HA	29:Bc:64:ARG:HE	1.85	0.42
34:B5:780:A:H4'	34:B5:781:U:H5''	2.01	0.42
34:B5:1338:C:H2'	34:B5:1339:C:C6	2.54	0.42
34:B5:1362:U:H5'	34:B5:1363:U:C2	2.54	0.42
35:AA:132:ASN:OD1	38:A1:2178:A:H5''	2.18	0.42
36:AB:259:HIS:HB3	38:A1:2987:A:O2'	2.19	0.42
36:AB:292:ALA:HB1	36:AB:295:ALA:HB3	2.01	0.42
38:A1:1392:G:H3'	67:Ae:125:ARG:HH12	1.84	0.42
38:A1:1446:A:H5''	52:AP:65:SER:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1493:G:O6	74:A1:2:ALA:N	2.52	0.42
38:A1:1584:U:H2'	38:A1:1585:C:H6	1.84	0.42
38:A1:1699:A:H2'	38:A1:1700:G:C8	2.54	0.42
38:A1:2266:U:H2'	38:A1:2267:C:C6	2.53	0.42
38:A1:2486:A:OP1	79:E:105:LYS:HG2	2.19	0.42
38:A1:3072:C:H2'	38:A1:3073:A:O4'	2.19	0.42
41:AD:153:THR:HG23	41:AD:160:PHE:HZ	1.83	0.42
45:AH:86:TYR:CE2	45:AH:151:VAL:HB	2.54	0.42
46:AI:30:LYS:HA	46:AI:30:LYS:HD2	1.91	0.42
51:AO:138[A]:LEU:HD12	51:AO:138[A]:LEU:HA	1.79	0.42
70:Ah:28:LEU:O	70:Ah:32:LYS:N	2.42	0.42
79:E:102:LYS:HA	79:E:105:LYS:HZ3	1.85	0.42
80:DC:760:ARG:HG3	80:DC:761:PRO:HD2	2.01	0.42
2:BB:138:PHE:HB2	2:BB:214:LYS:HB3	2.02	0.42
5:BG:145:PHE:HE2	5:BG:156:PHE:HB3	1.83	0.42
14:BX:102:VAL:HB	14:BX:124:VAL:HG13	2.00	0.42
18:Be:14:VAL:HA	18:Be:17:GLN:HG2	2.01	0.42
25:BS:45:LEU:O	25:BS:49:LYS:HG2	2.19	0.42
27:BU:106:ILE:HG23	27:BU:107:THR:HG22	2.01	0.42
31:Bg:87:LYS:HG2	31:Bg:108:SER:O	2.19	0.42
31:Bg:89:LEU:HD21	31:Bg:124:SER:OG	2.20	0.42
31:Bg:239:GLU:O	31:Bg:257:ALA:N	2.47	0.42
33:BM:59:LEU:HB2	33:BM:123:VAL:HB	2.00	0.42
34:B5:107:C:H2'	34:B5:108:A:C8	2.54	0.42
34:B5:705:U:H2'	34:B5:730:G:N2	2.35	0.42
34:B5:1553:G:N1	34:B5:1556:A:OP2	2.52	0.42
36:AB:332:ARG:HH22	38:A1:3304:U:P	2.43	0.42
37:AC:22:LEU:HA	37:AC:23:PRO:HD3	1.80	0.42
38:A1:945:C:H2'	38:A1:946:U:C6	2.53	0.42
38:A1:1581:C:H2'	38:A1:1582:C:C4	2.55	0.42
38:A1:1658:G:H2'	38:A1:1659:U:C6	2.54	0.42
38:A1:2767:U:H2'	38:A1:2768:U:H6	1.84	0.42
38:A1:3020:U:H2'	38:A1:3033:A:N6	2.34	0.42
38:A1:3086:A:H3'	38:A1:3087:A:H8	1.85	0.42
38:A1:3393:U:H2'	38:A1:3394:U:C6	2.54	0.42
39:A3:79:A:H2'	39:A3:80:G:O4'	2.19	0.42
41:AD:129:TYR:HE1	41:AD:175:HIS:CD2	2.38	0.42
43:AF:84:VAL:HG23	43:AF:117:VAL:HB	2.01	0.42
43:AF:221:LYS:HB2	43:AF:227:GLY:HA3	2.02	0.42
56:AT:115:LYS:HB2	56:AT:128:LEU:HD21	2.02	0.42
79:E:34:LEU:HD11	79:E:183:ILE:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:V:128:MET:HG3	81:V:150:ILE:HD12	2.01	0.42
8:BJ:92:LYS:HB2	8:BJ:95:TYR:HD2	1.84	0.42
11:BO:20:TYR:HB3	11:BO:27:PHE:HB2	2.01	0.42
21:BK:61:TRP:CE2	30:Bd:23:VAL:HG22	2.55	0.42
23:BQ:60:PHE:CZ	23:BQ:89:LEU:HD22	2.55	0.42
24:BR:20:TYR:CE1	24:BR:23:LYS:HB2	2.54	0.42
26:BT:18:TYR:HB3	26:BT:59:ALA:HB1	2.01	0.42
31:Bg:109:ASP:O	31:Bg:126:SER:OG	2.22	0.42
34:B5:185:U:H2'	34:B5:186:C:H6	1.85	0.42
34:B5:196:G:O2'	34:B5:197:A:H8	2.02	0.42
34:B5:592:A:H2'	34:B5:593:U:O4'	2.20	0.42
34:B5:961:U:C2	34:B5:962:C:C5	3.07	0.42
34:B5:1237:G:N3	34:B5:1238:A:C8	2.87	0.42
34:B5:1484:G:H2'	34:B5:1485:C:H6	1.84	0.42
36:AB:250:ALA:HB3	38:A1:2880:U:O2	2.19	0.42
38:A1:996:A:H2'	38:A1:997:A:O4'	2.19	0.42
38:A1:1522:U:H3'	60:AX:113:LEU:HD22	2.02	0.42
38:A1:3096:C:H2'	38:A1:3097:C:C6	2.54	0.42
38:A1:3127:A:H2'	38:A1:3128:G:O4'	2.20	0.42
39:A3:3:U:O2'	39:A3:25:G:N3	2.46	0.42
44:AG:33:ASN:O	44:AG:39:ALA:HB3	2.20	0.42
47:AJ:21:ILE:HG22	47:AJ:23:VAL:HG13	2.01	0.42
48:AL:11:LYS:O	48:AL:13:HIS:ND1	2.53	0.42
79:E:38:LEU:O	79:E:163:LEU:HD12	2.20	0.42
79:E:176:GLU:O	79:E:180:VAL:HG13	2.19	0.42
81:V:48:ARG:O	81:V:89:THR:OG1	2.32	0.42
2:BB:35:PRO:HG3	2:BB:99:ASN:HA	2.02	0.42
5:BG:119:GLN:HG3	5:BG:120:GLU:H	1.83	0.42
6:BH:153:LEU:HD22	6:BH:184:GLU:OE2	2.18	0.42
7:BI:50:GLY:HA2	34:B5:397:A:H4'	2.01	0.42
14:BX:144:ARG:HA	14:BX:144:ARG:HD2	1.87	0.42
15:BY:32:ARG:NE	15:BY:35:VAL:HG12	2.35	0.42
16:Ba:45:VAL:HG12	16:Ba:64:LEU:HD21	2.01	0.42
16:Ba:75:VAL:HB	34:B5:1793:G:N1	2.34	0.42
17:Bb:74:SER:O	17:Bb:76:GLY:N	2.53	0.42
19:BD:105:MET:SD	19:BD:184:ILE:HG21	2.58	0.42
26:BT:130:ARG:O	26:BT:134:ARG:HD3	2.19	0.42
31:Bg:46:LYS:HE3	31:Bg:56:VAL:HB	2.01	0.42
33:BM:50:LYS:HE3	33:BM:50:LYS:HB2	1.95	0.42
34:B5:14:C:O2	34:B5:619:A2M:H2	2.19	0.42
34:B5:292:U:H2'	34:B5:293:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1079:U:H2'	34:B5:1080:U:C6	2.55	0.42
34:B5:1210:C:C2	34:B5:1454:G:C2	3.07	0.42
34:B5:1233:G:N1	34:B5:1253:U:O2	2.52	0.42
34:B5:1450:U:H2'	34:B5:1451:C:C6	2.55	0.42
36:AB:231:HIS:CE1	38:A1:2341:A:H5''	2.55	0.42
37:AC:11:LEU:HD11	37:AC:156:LEU:HB2	2.01	0.42
37:AC:152:VAL:HG21	37:AC:156:LEU:HD22	2.02	0.42
38:A1:698:U:H2'	38:A1:699:A:O4'	2.19	0.42
38:A1:1334:U:H5''	43:AF:206:LYS:HB3	2.01	0.42
38:A1:1486:G:H21	69:Ag:6:THR:HG22	1.84	0.42
38:A1:1909:A:H2'	38:A1:1910:A:C8	2.55	0.42
38:A1:3213:A:H2'	38:A1:3214:U:O4'	2.19	0.42
42:AE:172:HIS:ND1	42:AE:173:MET:HG3	2.34	0.42
56:AT:43:LYS:HG3	56:AT:58:GLN:HE22	1.84	0.42
57:AU:19:VAL:O	57:AU:22:PRO:HD2	2.19	0.42
79:E:66:CYS:HB3	79:E:110:PHE:CD1	2.55	0.42
80:DC:265:GLU:OE1	80:DC:267:LYS:N	2.51	0.42
80:DC:378:LEU:HD21	80:DC:405:VAL:HG12	2.00	0.42
4:BE:4:GLY:HA3	34:B5:93:A:O2'	2.19	0.42
6:BH:25:VAL:HA	6:BH:28:GLU:HG3	2.01	0.42
6:BH:162:ILE:HB	6:BH:169:PHE:HE2	1.83	0.42
13:BW:103:ILE:N	13:BW:127:GLY:O	2.46	0.42
17:Bb:33:LEU:HD22	17:Bb:79:PHE:CD2	2.54	0.42
25:BS:41:ARG:NH2	26:BT:36:ILE:O	2.43	0.42
27:BU:15:GLN:HB3	27:BU:16:GLN:OE1	2.20	0.42
34:B5:30:G:H2'	34:B5:31:C:H6	1.84	0.42
34:B5:650:U:O4	34:B5:684:A:N6	2.53	0.42
34:B5:759:U:C2	34:B5:760:A:C8	3.07	0.42
37:AC:315:LYS:HB2	37:AC:323:VAL:HG21	2.01	0.42
38:A1:602:A:H8	38:A1:602:A:OP2	2.03	0.42
38:A1:1157:G:H2'	38:A1:1158:A:O4'	2.19	0.42
38:A1:1503:A:C4	38:A1:1504:A:C8	3.07	0.42
38:A1:2361:A:H2'	38:A1:2362:C:H6	1.84	0.42
38:A1:2448:G:H3'	38:A1:2449:A:C8	2.54	0.42
38:A1:2587:U:H2'	38:A1:2588:U:C6	2.54	0.42
38:A1:2793:OMG:H5''	77:Ao:66:LYS:HG2	2.00	0.42
38:A1:2984:C:H2'	38:A1:2985:C:C6	2.54	0.42
39:A3:20:A:H2'	39:A3:21:G:C8	2.54	0.42
40:A4:142:C:H2'	40:A4:143:U:H6	1.80	0.42
42:AE:38:THR:HG22	42:AE:90:LYS:HE3	2.01	0.42
42:AE:142:ASP:O	42:AE:146:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AF:86:VAL:O	43:AF:114:GLY:HA2	2.20	0.42
46:AI:190:VAL:HG22	46:AI:199:PHE:CD1	2.54	0.42
53:AQ:83:VAL:O	53:AQ:103:ALA:HA	2.20	0.42
57:AU:18:ASP:HB2	57:AU:104:ARG:HB2	2.01	0.42
62:AZ:26:VAL:HG11	62:AZ:96:VAL:HG11	2.01	0.42
63:Aa:19:LYS:HB3	63:Aa:25:HIS:HB2	2.02	0.42
79:E:138:VAL:HB	79:E:147:LYS:HE2	2.01	0.42
80:DC:366:CYS:O	80:DC:370:LYS:HG3	2.20	0.42
2:BB:36:SER:N	2:BB:231:LEU:O	2.46	0.42
9:BL:110:HIS:HB3	9:BL:138:ASN:ND2	2.35	0.42
13:BW:106:THR:HG23	13:BW:108:ALA:H	1.84	0.42
25:BS:14:ILE:HD11	47:AJ:119:SER:H	1.84	0.42
25:BS:42:TYR:N	34:B5:1566:U:OP1	2.39	0.42
26:BT:65:ILE:HD11	26:BT:70:GLN:HA	2.01	0.42
26:BT:91:TYR:HB2	34:B5:1590:G:OP1	2.20	0.42
31:Bg:267:PRO:HG2	31:Bg:269:TYR:HE1	1.84	0.42
34:B5:53:G:H2'	34:B5:54:C:C6	2.54	0.42
34:B5:296:U:H2'	34:B5:297:U:C6	2.55	0.42
34:B5:591:A:H2'	34:B5:592:A:H8	1.83	0.42
34:B5:953:G:H2'	34:B5:954:G:C8	2.55	0.42
34:B5:1175:U:H2'	34:B5:1176:G:H8	1.81	0.42
36:AB:276:THR:HG21	38:A1:3137:C:H5''	2.01	0.42
38:A1:1143:A:H5'	38:A1:1368:U:H1'	2.00	0.42
38:A1:1572:U:O2'	38:A1:1573:G:O4'	2.37	0.42
38:A1:1650:G:H2'	38:A1:1651:U:C6	2.54	0.42
38:A1:2496:C:H2'	38:A1:2497:U:N3	2.35	0.42
38:A1:2709:C:H2'	38:A1:2710:C:C6	2.55	0.42
38:A1:2836:C:H2'	38:A1:2837:A:O4'	2.20	0.42
38:A1:2933:A:C6	38:A1:3014:U:H4'	2.54	0.42
39:A3:6:C:H5''	41:AD:54:ARG:HH21	1.85	0.42
49:AM:50:LYS:HG3	49:AM:85:TRP:CD1	2.55	0.42
63:Aa:86:LYS:HB3	63:Aa:86:LYS:HE2	1.73	0.42
65:Ac:34:LEU:HD13	65:Ac:59:TYR:HB3	2.02	0.42
72:Aj:75:LYS:HE3	72:Aj:75:LYS:HB3	1.75	0.42
80:DC:486:SER:HB2	80:DC:795:GLN:HG3	2.01	0.42
80:DC:701:GLY:C	80:DC:703:GLY:H	2.27	0.42
1:BA:79:ARG:O	1:BA:83:GLN:NE2	2.53	0.42
4:BE:94:ALA:HB3	15:BY:17:LEU:HD22	2.00	0.42
8:BJ:59:LEU:HD23	8:BJ:93:LEU:HD21	2.01	0.42
14:BX:51:GLY:O	14:BX:101:GLU:HA	2.20	0.42
20:BF:76:ARG:NH2	23:BQ:120:ASP:OD1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:255:ALA:HA	31:Bg:260:ILE:HD13	2.02	0.42
34:B5:872:G:N2	34:B5:1047:G:H4'	2.34	0.42
34:B5:878:G:H2'	34:B5:879:G:H8	1.85	0.42
34:B5:1202:A:H1'	34:B5:1207:C:N4	2.35	0.42
34:B5:1359:C:H2'	34:B5:1360:A:C8	2.54	0.42
34:B5:1612:U:H2'	34:B5:1613:U:O4'	2.20	0.42
34:B5:1642:G:H2'	34:B5:1643:U:C6	2.55	0.42
34:B5:1646:C:H2'	34:B5:1647:U:C6	2.55	0.42
36:AB:55:THR:HG23	38:A1:3049:A:O2'	2.20	0.42
38:A1:251:G:H1'	38:A1:253:A:C5	2.55	0.42
38:A1:565:U:H2'	38:A1:566:G:H8	1.85	0.42
38:A1:799:G:OP2	63:Aa:32:ARG:NH1	2.37	0.42
38:A1:999:G:H2'	38:A1:1000:C:C6	2.55	0.42
38:A1:1138:U:H2'	38:A1:1139:G:C8	2.55	0.42
38:A1:1169:A:H4'	43:AF:219:LYS:HD3	2.01	0.42
38:A1:3132:C:H2'	38:A1:3133:C:C6	2.55	0.42
39:A3:81:U:H2'	39:A3:82:G:C8	2.55	0.42
40:A4:145:U:H2'	40:A4:146:U:C6	2.54	0.42
41:AD:85:ARG:HD2	41:AD:86:TYR:CZ	2.55	0.42
41:AD:184:ASP:HB3	41:AD:187:THR:O	2.20	0.42
43:AF:25:GLN:O	43:AF:29:GLU:HG2	2.19	0.42
53:AQ:95:GLU:O	53:AQ:95:GLU:HG2	2.20	0.42
54:AR:176:ARG:HG3	54:AR:180:LYS:NZ	2.34	0.42
57:AU:43:VAL:O	57:AU:44:GLU:HG3	2.19	0.42
61:AY:51:ARG:HG2	61:AY:52:ARG:H	1.83	0.42
72:Aj:27:PHE:HA	72:Aj:34:CYS:HA	2.00	0.42
80:DC:34:THR:HG23	85:DC:901:GDP:O2A	2.20	0.42
80:DC:144:ARG:NH1	80:DC:765:LEU:HD21	2.35	0.42
80:DC:164:LEU:HD21	80:DC:282:PHE:CE1	2.55	0.42
6:BH:41:LEU:HB3	6:BH:70:PHE:CE1	2.55	0.42
8:BJ:87:SER:OG	8:BJ:89:ASP:OD1	2.31	0.42
15:BY:16:PRO:C	15:BY:19:ALA:H	2.28	0.42
15:BY:57:VAL:HB	15:BY:60:PHE:HE2	1.84	0.42
19:BD:127:MET:HE3	19:BD:127:MET:HB3	1.88	0.42
19:BD:183:GLY:HA3	34:B5:1277:G:O3'	2.19	0.42
23:BQ:140:LYS:HE2	23:BQ:142:TYR:CZ	2.55	0.42
27:BU:80:GLU:OE1	27:BU:82:TYR:OH	2.23	0.42
31:Bg:23:LEU:HD21	31:Bg:310:ILE:HD12	2.01	0.42
34:B5:103:A:H4'	34:B5:105:A:C8	2.55	0.42
34:B5:116:U:H2'	34:B5:117:U:C6	2.55	0.42
34:B5:848:C:H2'	34:B5:849:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1142:A:H2'	34:B5:1143:A:C8	2.54	0.42
34:B5:1183:A:H1'	34:B5:1210:C:O2'	2.19	0.42
34:B5:1237:G:N1	34:B5:1249:U:O4	2.53	0.42
34:B5:1461:C:H2'	34:B5:1462:G:C8	2.53	0.42
37:AC:135:VAL:HG12	37:AC:140:HIS:HB2	2.02	0.42
37:AC:193:LYS:HE2	38:A1:1419:A:H5''	2.02	0.42
38:A1:166:C:H2'	38:A1:167:U:H6	1.84	0.42
38:A1:341:G:O2'	40:A4:22:U:O4	2.33	0.42
38:A1:590:G:N2	42:AE:19:LYS:HD3	2.33	0.42
38:A1:845:G:N2	38:A1:848:A:H2	2.15	0.42
38:A1:980:A:H61	38:A1:1104:G:H21	1.68	0.42
38:A1:1411:C:OP1	67:Ae:98:HIS:N	2.44	0.42
38:A1:1464:G:N2	38:A1:1467:A:OP2	2.51	0.42
38:A1:1578:C:H2'	38:A1:1579:C:C6	2.55	0.42
38:A1:1624:G:H2'	38:A1:1625:A:H8	1.85	0.42
38:A1:2220:A2M:H8	38:A1:2220:A2M:O5'	2.19	0.42
38:A1:2438:A:H2'	38:A1:2439:A:H8	1.85	0.42
38:A1:3223:A:H2'	38:A1:3224:G:O4'	2.20	0.42
38:A1:3271:G:H8	38:A1:3271:G:OP2	2.01	0.42
40:A4:139:U:H2'	40:A4:140:G:H8	1.85	0.42
41:AD:271:LYS:HE2	41:AD:272:TYR:CE2	2.55	0.42
49:AM:105:GLN:HE21	49:AM:109:ARG:NH2	2.17	0.42
52:AP:4:TYR:CZ	52:AP:18:ARG:HG3	2.55	0.42
53:AQ:94:PHE:CE2	63:Aa:119:PRO:HD3	2.54	0.42
56:AT:17:ARG:NH1	56:AT:47:SER:HB3	2.34	0.42
58:AV:114:ILE:HD12	58:AV:133:SER:HB3	2.01	0.42
59:AW:39:LEU:HD23	59:AW:39:LEU:HA	1.83	0.42
76:An:13:LEU:HD12	76:An:16:LYS:HD3	2.02	0.42
80:DC:480:VAL:C	80:DC:482:LYS:H	2.27	0.42
2:BB:150:VAL:H	34:B5:1067:C:H5''	1.84	0.42
5:BG:193:LEU:HA	5:BG:196:ARG:HG2	2.02	0.42
8:BJ:149:ARG:HG2	34:B5:765:G:C6	2.54	0.42
9:BL:64:VAL:HG11	9:BL:131:ILE:HD11	2.01	0.42
20:BF:136:ALA:O	20:BF:140:THR:HG22	2.19	0.42
27:BU:57:ARG:HD2	34:B5:1382:A:N3	2.34	0.42
31:Bg:266:ASP:HB3	31:Bg:267:PRO:HD3	2.02	0.42
34:B5:551:G:H2'	34:B5:552:G:H8	1.85	0.42
34:B5:585:A:H2'	34:B5:586:G:H8	1.84	0.42
34:B5:1263:G:H2'	34:B5:1264:G:O4'	2.20	0.42
34:B5:1649:G:H2'	34:B5:1650:U:C6	2.54	0.42
36:AB:106:TRP:HB2	36:AB:133:TYR:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:120:G:H4'	38:A1:121:A:H5'	2.02	0.42
38:A1:532:A:H2'	38:A1:533:A:H8	1.85	0.42
38:A1:577:C:O2'	38:A1:579:G:OP1	2.37	0.42
38:A1:1037:C:H2'	38:A1:1038:C:C6	2.55	0.42
38:A1:2723:U:H2'	38:A1:2724:OMU:H6	2.02	0.42
38:A1:3231:U:H2'	38:A1:3232:G:C8	2.53	0.42
44:AG:130:TYR:CE2	44:AG:202:GLU:HG3	2.55	0.42
45:AH:176:LEU:HD23	75:Am:86:ALA:HB3	2.02	0.42
47:AJ:111:ASP:O	47:AJ:114:ILE:HG23	2.20	0.42
51:AO:4[A]:GLU:CD	51:AO:7[A]:VAL:HG22	2.43	0.42
67:Ae:111:ARG:CZ	67:Ae:115:LEU:HD21	2.50	0.42
69:Ag:67:LYS:O	69:Ag:71:THR:HG22	2.20	0.42
80:DC:120:ARG:HD2	80:DC:356:LEU:HD22	2.01	0.42
80:DC:564:ARG:HD3	80:DC:564:ARG:HA	1.90	0.42
80:DC:610:ASP:OD1	80:DC:611:ASP:N	2.53	0.42
80:DC:671:THR:HG22	80:DC:681:MET:HB2	2.02	0.42
81:V:36:GLN:O	81:V:40:GLU:HG3	2.20	0.42
2:BB:83:LYS:O	2:BB:103:MET:HG2	2.20	0.41
5:BG:3:LEU:O	5:BG:15:THR:HA	2.20	0.41
5:BG:160:ARG:NH2	34:B5:66:U:H1'	2.35	0.41
8:BJ:123:HIS:HB3	18:Be:33:ARG:NH1	2.35	0.41
19:BD:18:TYR:CZ	19:BD:37:VAL:HG13	2.55	0.41
19:BD:207:THR:O	24:BR:40:THR:OG1	2.38	0.41
24:BR:17:ILE:HD11	24:BR:54:THR:HG23	2.02	0.41
32:Bf:139:LEU:HD11	32:Bf:148:TYR:HB2	2.02	0.41
32:Bf:141:CYS:SG	32:Bf:144:CYS:N	2.79	0.41
33:BM:75:VAL:HG11	33:BM:120:VAL:HG21	2.02	0.41
34:B5:252:U:H2'	34:B5:253:A:C8	2.55	0.41
34:B5:263:C:H2'	34:B5:264:G:O4'	2.19	0.41
34:B5:384:G:H2'	34:B5:385:A:C8	2.55	0.41
34:B5:798:C:H2'	34:B5:799:A:H8	1.85	0.41
34:B5:890:C:H2'	34:B5:891:A:H8	1.84	0.41
34:B5:962:C:H2'	34:B5:963:A:O4'	2.20	0.41
35:AA:2:GLY:HA2	38:A1:2608:G:OP1	2.20	0.41
36:AB:222:LYS:NZ	38:A1:3048:A:OP2	2.36	0.41
38:A1:438:A:OP1	67:Ae:118:LYS:HE3	2.20	0.41
38:A1:644:G:H2'	38:A1:2372:A:N7	2.35	0.41
38:A1:2254:U:H2'	38:A1:2261:G:H22	1.85	0.41
38:A1:2744:U:H2'	38:A1:2745:G:C8	2.55	0.41
47:AJ:7:ASN:OD1	47:AJ:8:PRO:HD2	2.20	0.41
55:AS:80:ARG:HB2	55:AS:124:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:15:LYS:HD2	80:DC:15:LYS:HA	1.77	0.41
80:DC:582:LYS:HE2	80:DC:582:LYS:HB2	1.89	0.41
81:V:55:LYS:CD	81:V:84:VAL:H	2.33	0.41
2:BB:129:THR:OG1	2:BB:133:TYR:HB2	2.20	0.41
3:BC:141:ARG:HB3	3:BC:151:PRO:HB2	2.03	0.41
4:BE:214:LEU:HD22	4:BE:244:ILE:HD12	2.01	0.41
5:BG:22:HIS:HA	5:BG:25:ARG:HD3	2.02	0.41
6:BH:28:GLU:O	6:BH:34:LEU:HD22	2.20	0.41
8:BJ:60:LEU:HD12	8:BJ:97:LEU:HD11	2.01	0.41
18:Be:50:VAL:O	18:Be:50:VAL:HG12	2.19	0.41
19:BD:109:LEU:HD12	19:BD:175:VAL:HG21	2.02	0.41
20:BF:154:ALA:N	82:EC:6946:A:O2'	2.52	0.41
25:BS:15:LEU:O	25:BS:22:VAL:N	2.42	0.41
26:BT:9:VAL:HG22	26:BT:140:LEU:HG	2.02	0.41
26:BT:27:LYS:O	26:BT:27:LYS:HD3	2.20	0.41
27:BU:84:MET:HE2	30:Bd:52:PHE:CE2	2.55	0.41
33:BM:27:ALA:O	33:BM:31:VAL:HG13	2.20	0.41
33:BM:42:ALA:HB2	33:BM:124:LYS:HE2	2.02	0.41
34:B5:19:A:H2'	34:B5:20:G:O4'	2.20	0.41
34:B5:386:G:H2'	34:B5:387:A:C8	2.55	0.41
34:B5:1350:U:H2'	34:B5:1351:G:C8	2.55	0.41
36:AB:47:LEU:HD12	36:AB:335:ILE:HD11	2.02	0.41
36:AB:96:PRO:HB3	51:AO:153[A]:VAL:HG22	2.02	0.41
38:A1:268:A:N7	50:AN:12:ARG:NH1	2.68	0.41
38:A1:304:G:H3'	38:A1:304:G:OP2	2.20	0.41
38:A1:947:G:H2'	38:A1:948:C:C6	2.55	0.41
38:A1:955:U:H2'	38:A1:956:U:C6	2.55	0.41
38:A1:1381:A:H2'	38:A1:1382:G:H8	1.85	0.41
38:A1:1747:G:N2	73:Ak:2:ALA:HB3	2.31	0.41
38:A1:2468:A:H4'	79:E:28:PHE:CG	2.55	0.41
38:A1:2566:C:H2'	38:A1:2567:C:H6	1.85	0.41
38:A1:2796:G:N7	77:Ao:63:LYS:NZ	2.55	0.41
38:A1:3268:A:H5''	42:AE:46:ARG:NH1	2.35	0.41
38:A1:3358:U:H2'	38:A1:3359:A:H8	1.85	0.41
40:A4:85:G:OP2	61:AY:113:LYS:NZ	2.39	0.41
40:A4:152:G:H2'	40:A4:153:U:O4'	2.20	0.41
47:AJ:87:LYS:O	47:AJ:88:GLU:HG2	2.20	0.41
47:AJ:160:VAL:O	47:AJ:164:LYS:HG2	2.20	0.41
51:AO:11[A]:GLY:O	51:AO:41[A]:LEU:HD23	2.20	0.41
54:AR:175:GLN:OE1	54:AR:175:GLN:N	2.53	0.41
80:DC:524:GLU:N	80:DC:524:GLU:OE1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:570:GLU:O	80:DC:571:SER:C	2.63	0.41
81:V:69:ASP:C	81:V:70:LEU:HD12	2.45	0.41
5:BG:50:PHE:CE1	5:BG:113:ILE:HG12	2.55	0.41
5:BG:141:ILE:HD13	5:BG:157:VAL:HG22	2.02	0.41
6:BH:106:SER:OG	34:B5:697:C:OP2	2.30	0.41
7:BI:82:VAL:HG21	7:BI:166:TYR:CE1	2.55	0.41
8:BJ:18:PRO:O	8:BJ:23:ARG:NH2	2.51	0.41
14:BX:8:GLY:O	14:BX:11:SER:OG	2.26	0.41
14:BX:86:PHE:HB2	14:BX:107:PHE:HZ	1.84	0.41
15:BY:62:THR:HA	15:BY:69:SER:HA	2.02	0.41
15:BY:113:ASN:HA	15:BY:116:LYS:HD3	2.02	0.41
18:Be:27:PRO:HG3	34:B5:506:A:C4	2.55	0.41
19:BD:164:VAL:HA	19:BD:168:ILE:HD12	2.01	0.41
20:BF:41:LYS:HB2	20:BF:44:ASN:HA	2.01	0.41
26:BT:100:ILE:O	26:BT:104:VAL:HG23	2.20	0.41
28:BZ:39:ALA:HB3	28:BZ:46:LYS:HE2	2.02	0.41
31:Bg:131:ILE:HG23	31:Bg:154:VAL:HG11	2.03	0.41
32:Bf:135:HIS:CE1	34:B5:1250:U:H1'	2.56	0.41
34:B5:84:A:H2'	34:B5:85:A:O4'	2.20	0.41
34:B5:1011:G:H2'	34:B5:1012:U:C5	2.56	0.41
34:B5:1235:C:H2'	34:B5:1236:A:C8	2.55	0.41
34:B5:1584:G:H22	34:B5:1610:G:H3'	1.85	0.41
36:AB:227:GLU:HG2	36:AB:270:ARG:HD3	2.02	0.41
36:AB:266:ARG:HH21	38:A1:2391:G:N2	2.18	0.41
38:A1:156:G:OP2	71:AI:25:LYS:HB3	2.21	0.41
38:A1:1008:U:O4	38:A1:1043:C:N4	2.54	0.41
38:A1:1771:C:H2'	38:A1:1772:U:O4'	2.20	0.41
38:A1:2199:G:H2'	38:A1:2200:U:C6	2.54	0.41
38:A1:2828:G:H4'	46:AI:4:ARG:HD3	2.01	0.41
38:A1:3051:U:H2'	38:A1:3052:G:H8	1.85	0.41
41:AD:181:PRO:HG3	41:AD:198:TYR:CD2	2.55	0.41
44:AG:73:PRO:HD3	44:AG:233:TRP:CE2	2.55	0.41
56:AT:73:GLY:HA2	56:AT:89:LEU:O	2.20	0.41
67:Ae:11:LYS:O	67:Ae:12:LYS:HB2	2.20	0.41
76:An:7:LYS:HE2	76:An:11:ARG:NH2	2.35	0.41
78:Ap:41:PHE:CD2	78:Ap:62:LYS:HG2	2.55	0.41
80:DC:39:LEU:HD11	80:DC:334:LEU:HD12	2.01	0.41
80:DC:642:GLY:HA2	80:DC:643:PRO:HD3	1.88	0.41
80:DC:723:LYS:HD2	80:DC:808:PRO:HD3	2.03	0.41
80:DC:744:TYR:HE1	80:DC:754:VAL:HG21	1.85	0.41
82:EC:6948:U:H6	82:EC:6948:U:H2'	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:76:LYS:HB3	6:BH:76:LYS:HE2	1.75	0.41
13:BW:119:LYS:HG2	34:B5:687:G:H5''	2.02	0.41
16:Ba:12:LYS:NZ	34:B5:1029:U:OP2	2.53	0.41
18:Be:39:LEU:HD23	18:Be:39:LEU:HA	1.92	0.41
22:BP:25:LEU:HD12	22:BP:26:LEU:HD12	2.03	0.41
34:B5:1511:U:H2'	34:B5:1512:G:C8	2.56	0.41
34:B5:1719:A:H2'	34:B5:1720:G:O4'	2.19	0.41
37:AC:54:GLU:OE2	38:A1:329:U:N3	2.53	0.41
37:AC:60:THR:HG22	37:AC:62:ALA:N	2.35	0.41
38:A1:1169:A:H2'	38:A1:1170:A:C8	2.56	0.41
38:A1:1260:A:O2'	38:A1:1261:G:O4'	2.28	0.41
38:A1:1595:U:C2	38:A1:1596:C:C5	3.08	0.41
38:A1:1695:U:HO2'	38:A1:1749:A:N6	2.18	0.41
38:A1:2765:C:O3'	77:Ao:39:GLY:HA3	2.20	0.41
38:A1:2890:A:O2'	38:A1:2933:A:N3	2.42	0.41
38:A1:3077:A:N6	38:A1:3080:G:C5	2.89	0.41
41:AD:204:VAL:HG12	41:AD:208:MET:HE3	2.02	0.41
42:AE:172:HIS:HE1	42:AE:173:MET:HE2	1.86	0.41
42:AE:174:LEU:HD23	42:AE:174:LEU:HA	1.94	0.41
53:AQ:171:LYS:HB3	53:AQ:171:LYS:HE2	1.93	0.41
54:AR:173:ARG:HG2	54:AR:177:VAL:HG11	2.03	0.41
70:Ah:41:LEU:HD23	70:Ah:44:ILE:HD11	2.02	0.41
80:DC:187:VAL:O	80:DC:191:THR:HG22	2.20	0.41
80:DC:380:LEU:HD21	80:DC:400:VAL:HG22	2.02	0.41
80:DC:410:LYS:HA	80:DC:430:ALA:HA	2.02	0.41
80:DC:571:SER:O	80:DC:589:LYS:NZ	2.52	0.41
82:EC:6938:A:H8	82:EC:6938:A:OP2	2.04	0.41
2:BB:185:THR:O	2:BB:189:ILE:HG12	2.21	0.41
3:BC:235:LEU:HD11	12:BV:54:ALA:HB2	2.02	0.41
4:BE:73:ASP:CG	4:BE:145:ARG:HH21	2.27	0.41
5:BG:112:VAL:HG11	34:B5:164:A:H5'	2.01	0.41
7:BI:81:VAL:CG2	7:BI:91:VAL:HA	2.50	0.41
26:BT:2:PRO:HB2	26:BT:3:GLY:H	1.62	0.41
26:BT:53:TRP:HH2	26:BT:100:ILE:HD11	1.85	0.41
27:BU:52:LYS:HB3	27:BU:93:LEU:HD13	2.02	0.41
28:BZ:95:HIS:NE2	34:B5:1529:C:OP1	2.42	0.41
34:B5:1147:A:H2'	34:B5:1148:C:H6	1.86	0.41
34:B5:1346:A:H62	34:B5:1370:U:H5	1.67	0.41
34:B5:1348:A:H2'	34:B5:1349:G:C8	2.55	0.41
34:B5:1515:A:O2'	34:B5:1517:U:OP2	2.32	0.41
34:B5:1577:A:H2'	34:B5:1578:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:179:LEU:O	35:AA:184:ARG:HD2	2.20	0.41
38:A1:139:G:H2'	38:A1:140:C:C6	2.55	0.41
38:A1:1456:A:N7	66:Ad:26:LYS:HE2	2.35	0.41
38:A1:1925:U:O2'	38:A1:1927:G:N7	2.54	0.41
38:A1:2898:G:OP2	45:AH:173:ARG:NH1	2.50	0.41
38:A1:3000:A:H2'	38:A1:3001:C:H6	1.86	0.41
39:A3:28:C:OP1	47:Aj:137:ARG:NE	2.33	0.41
39:A3:39:C:O2'	47:Aj:43:GLN:HG3	2.20	0.41
40:A4:37:A:H5''	40:A4:39:G:O4'	2.20	0.41
41:AD:261:THR:O	41:AD:264:GLN:N	2.53	0.41
43:AF:85:PHE:CZ	43:AF:147:LEU:HD21	2.55	0.41
44:AG:75:ILE:C	44:AG:77:GLN:N	2.78	0.41
45:AH:22:SER:O	45:AH:23:ARG:HD3	2.20	0.41
57:AU:56:VAL:HG23	57:AU:65:VAL:HG22	2.03	0.41
61:AY:116:LYS:HD3	61:AY:126:LEU:HD11	2.02	0.41
79:E:83:ASP:HB3	79:E:107:TYR:HE2	1.86	0.41
79:E:121:PRO:HB3	82:EC:6773:G:OP1	2.21	0.41
81:V:125:ASN:HA	81:V:151:GLU:HA	2.01	0.41
1:BA:56:LYS:HA	1:BA:56:LYS:HD2	1.86	0.41
6:BH:58:LEU:HD13	6:BH:88:ARG:HB3	2.02	0.41
8:BJ:128:LEU:HD12	8:BJ:133:HIS:CD2	2.55	0.41
14:BX:25:ALA:HB1	34:B5:1108:G:H2'	2.02	0.41
24:BR:4:VAL:HG11	34:B5:1315:U:O2	2.20	0.41
25:BS:18:LEU:HD12	25:BS:18:LEU:HA	1.95	0.41
25:BS:46:VAL:HG23	25:BS:72:ILE:HB	2.01	0.41
31:Bg:19:TRP:N	31:Bg:19:TRP:CD1	2.88	0.41
34:B5:823:G:H2'	34:B5:824:G:O4'	2.21	0.41
34:B5:907:A:H2'	34:B5:908:U:C6	2.54	0.41
34:B5:1320:U:O2	34:B5:1322:A:H5'	2.20	0.41
34:B5:1642:G:H2'	34:B5:1643:U:H6	1.86	0.41
35:AA:209:HIS:CE1	35:AA:235:ALA:HB1	2.55	0.41
36:AB:259:HIS:CE1	38:A1:2366:C:H5'	2.54	0.41
38:A1:112:U:C2	38:A1:320:G:C2	3.08	0.41
38:A1:604:G:H2'	38:A1:605:U:C6	2.55	0.41
38:A1:1495:U:H5	38:A1:1835:A:N1	2.19	0.41
38:A1:2770:G:H2'	38:A1:2771:U:C6	2.55	0.41
38:A1:3302:U:O2'	38:A1:3303:G:H5'	2.20	0.41
39:A3:108:A:H2'	39:A3:109:G:C8	2.55	0.41
62:AZ:24:VAL:HG11	62:AZ:87:LEU:HD23	2.03	0.41
72:Aj:17:THR:O	72:Aj:25:ARG:HA	2.21	0.41
80:DC:136:CYS:H	80:DC:139:THR:HG22	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:597:VAL:HG11	80:DC:619:MET:HE3	2.02	0.41
80:DC:644:ASN:C	80:DC:645:LEU:HD22	2.46	0.41
80:DC:723:LYS:HE3	80:DC:806:SER:N	2.36	0.41
81:V:8:LYS:HD3	81:V:58:MET:HE1	2.03	0.41
82:EC:6788:C:OP2	82:EC:6805:C:N4	2.41	0.41
19:BD:78:LYS:HE3	21:BK:33:GLU:HG2	2.02	0.41
21:BK:12:HIS:HB3	21:BK:76:LEU:HD11	2.03	0.41
22:BP:77:ARG:NH2	34:B5:1240:U:O5'	2.51	0.41
23:BQ:72:GLY:N	34:B5:1483:A:H4'	2.36	0.41
23:BQ:79:TYR:HA	23:BQ:82:ARG:HG2	2.03	0.41
26:BT:113:ILE:HG23	26:BT:128:GLY:HA3	2.02	0.41
28:BZ:80:LEU:HD12	28:BZ:81:ARG:N	2.36	0.41
29:Bc:19:THR:OG1	29:Bc:20:GLY:N	2.53	0.41
34:B5:119:A:H2'	34:B5:120:U:O4'	2.21	0.41
34:B5:501:U:H4'	34:B5:502:U:C6	2.55	0.41
34:B5:738:G:H3'	34:B5:739:G:N2	2.35	0.41
34:B5:865:A:H2'	34:B5:866:G:O4'	2.20	0.41
34:B5:1232:U:N3	34:B5:1254:U:O4	2.54	0.41
34:B5:1369:U:O2'	34:B5:1373:C:OP1	2.25	0.41
36:AB:10:ARG:NH1	36:AB:11:HIS:O	2.53	0.41
37:AC:185:LYS:HA	37:AC:200:THR:O	2.21	0.41
37:AC:219:LEU:HD22	37:AC:225:VAL:HG11	2.01	0.41
38:A1:216:G:H4'	61:AY:19:TYR:CE2	2.56	0.41
38:A1:666:A:H2'	38:A1:667:C:O4'	2.21	0.41
38:A1:1541:G:H1'	38:A1:1557:A:C5	2.55	0.41
38:A1:1828:A:H2'	38:A1:1829:G:C8	2.56	0.41
38:A1:1840:U:H4'	38:A1:1841:A:H5''	2.03	0.41
38:A1:3181:C:O2'	51:AO:164[A]:SER:OG	2.33	0.41
48:AL:180:ARG:HG3	71:Ai:11:LEU:HD11	2.03	0.41
79:E:100:ILE:O	79:E:127:GLN:HG2	2.21	0.41
80:DC:112:SER:O	80:DC:115:VAL:HG12	2.20	0.41
80:DC:349:GLN:NE2	80:DC:369:ILE:O	2.52	0.41
80:DC:400:VAL:HG12	80:DC:450:ALA:HA	2.03	0.41
80:DC:504:LEU:HA	80:DC:550:ALA:HB2	2.02	0.41
80:DC:703:GLY:O	80:DC:707:PRO:HD2	2.21	0.41
81:V:100:ILE:HG13	81:V:101:VAL:N	2.35	0.41
2:BB:30:PHE:HB3	2:BB:96:LEU:HD13	2.03	0.41
11:BO:132:ARG:HG3	16:Ba:29:SER:OG	2.21	0.41
14:BX:51:GLY:HA2	14:BX:77:ILE:HG13	2.03	0.41
14:BX:59:ILE:HD11	14:BX:117:ILE:HG23	2.03	0.41
22:BP:18:ARG:N	25:BS:93:THR:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BP:39:ALA:N	34:B5:1549:C:OP2	2.54	0.41
26:BT:6:VAL:HB	26:BT:66:TYR:CE1	2.55	0.41
28:BZ:83:LEU:HB3	28:BZ:88:ILE:HD11	2.03	0.41
31:Bg:23:LEU:HD22	31:Bg:302:PHE:HB3	2.01	0.41
33:BM:113:ARG:NH2	34:B5:1223:A:H3'	2.36	0.41
34:B5:198:A:C2	34:B5:199:G:H1'	2.56	0.41
34:B5:464:A:C2	34:B5:465:G:C8	3.08	0.41
34:B5:1233:G:H22	34:B5:1253:U:H1'	1.84	0.41
34:B5:1363:U:HO2'	34:B5:1364:G:H8	1.61	0.41
34:B5:1614:A:H2'	34:B5:1615:C:C6	2.55	0.41
35:AA:21:ARG:NH1	38:A1:825:U:P	2.94	0.41
38:A1:44:U:H5''	50:AN:85:THR:CG2	2.50	0.41
38:A1:155:G:H5''	38:A1:156:G:H2'	2.01	0.41
38:A1:164:A:N1	38:A1:258:G:C6	2.88	0.41
38:A1:263:C:H2'	38:A1:264:G:O4'	2.21	0.41
38:A1:275:U:H2'	38:A1:276:U:C6	2.55	0.41
38:A1:675:C:H2'	38:A1:676:G:O4'	2.20	0.41
38:A1:2259:A:OP1	80:DC:829:LYS:HE2	2.21	0.41
38:A1:2419:A:H2'	38:A1:2420:C:C6	2.55	0.41
38:A1:2533:G:H2'	38:A1:2534:G:H8	1.86	0.41
38:A1:3094:A:H2'	38:A1:3095:U:C6	2.56	0.41
38:A1:3335:A:H2'	38:A1:3336:A:C8	2.55	0.41
38:A1:3343:G:H2'	38:A1:3344:A:C2	2.56	0.41
49:AM:41:GLN:NE2	49:AM:41:GLN:O	2.53	0.41
53:AQ:22:ASP:HA	53:AQ:27:LYS:HE2	2.02	0.41
54:AR:170:ARG:HD2	54:AR:174:ALA:HB2	2.02	0.41
58:AV:84:SER:HA	58:AV:94:TYR:HB3	2.02	0.41
61:AY:101:PRO:HA	61:AY:104:LEU:HD12	2.03	0.41
65:Ac:77:LEU:O	65:Ac:81:VAL:HG22	2.21	0.41
80:DC:115:VAL:O	80:DC:119:LEU:HB2	2.21	0.41
80:DC:183:GLU:O	80:DC:187:VAL:HG23	2.21	0.41
80:DC:243:ARG:HD3	80:DC:248:SER:HB2	2.03	0.41
81:V:55:LYS:HD3	81:V:84:VAL:O	2.20	0.41
82:EC:6892:U:HO2'	82:EC:6943:A:N6	2.16	0.41
82:EC:6905:G:H1	82:EC:6952:U:H3	1.67	0.41
2:BB:111:ARG:HD3	16:Ba:68:TYR:HB2	2.03	0.41
2:BB:176:VAL:C	2:BB:178:GLY:H	2.28	0.41
4:BE:24:SER:O	4:BE:24:SER:OG	2.37	0.41
6:BH:125:ILE:O	6:BH:129:LEU:HB2	2.21	0.41
13:BW:11:LEU:HD23	13:BW:11:LEU:HA	1.90	0.41
13:BW:81:VAL:O	13:BW:122:SER:OG	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BX:59:ILE:CD1	14:BX:118:PRO:HD2	2.51	0.41
18:Be:23:LYS:HD3	34:B5:586:G:OP1	2.21	0.41
19:BD:161:GLY:HA3	34:B5:1331:A:H61	1.85	0.41
20:BF:42:LEU:HB2	20:BF:48:PHE:HE1	1.86	0.41
20:BF:43:PHE:HE2	20:BF:115:LYS:HA	1.86	0.41
20:BF:160:VAL:HG23	29:Bc:43:ASN:HB3	2.03	0.41
22:BP:80:MET:HE1	22:BP:83:MET:CG	2.50	0.41
26:BT:112:GLY:O	26:BT:127:ASN:HB2	2.20	0.41
30:Bd:14:TYR:OH	34:B5:1553:G:O2'	2.33	0.41
31:Bg:46:LYS:NZ	31:Bg:48:THR:HG22	2.36	0.41
34:B5:217:A:N3	34:B5:217:A:H2'	2.36	0.41
34:B5:407:A:O2'	34:B5:1671:A:N3	2.39	0.41
34:B5:746:A:H2'	34:B5:747:C:O4'	2.21	0.41
34:B5:753:A:H2'	34:B5:754:A:C8	2.56	0.41
34:B5:888:U:H2'	34:B5:889:U:H6	1.84	0.41
34:B5:1020:A:C6	34:B5:1021:C:C5	3.09	0.41
34:B5:1044:U:H2'	34:B5:1045:C:C6	2.55	0.41
34:B5:1482:C:P	34:B5:1521:G:H22	2.43	0.41
34:B5:1483:A:H2	34:B5:1607:G:H1'	1.86	0.41
34:B5:1674:C:H2'	34:B5:1675:C:C6	2.56	0.41
34:B5:1767:G:OP1	34:B5:1770:U:H4'	2.21	0.41
37:AC:64:SER:HA	37:AC:75:PRO:HA	2.03	0.41
37:AC:180:LYS:HA	38:A1:1386:A:N3	2.36	0.41
38:A1:41:G:N2	38:A1:2803:A:N7	2.69	0.41
38:A1:116:A:H5''	38:A1:265:A:H2	1.86	0.41
38:A1:385:A:H2'	38:A1:386:A:C8	2.55	0.41
38:A1:671:U:H2'	38:A1:672:A:H8	1.86	0.41
38:A1:759:U:H2'	38:A1:760:G:O4'	2.21	0.41
38:A1:860:G:O2'	38:A1:895:A:H4'	2.21	0.41
38:A1:943:U:H3'	63:Aa:13:GLY:HA2	2.03	0.41
38:A1:1449:A2M:H2'	38:A1:1450:OMG:O4'	2.20	0.41
38:A1:1507:G:H1'	52:AP:139:TYR:CE2	2.56	0.41
38:A1:1657:C:O2'	38:A1:1797:A:OP2	2.25	0.41
38:A1:1660:C:H2'	38:A1:1661:G:H8	1.86	0.41
38:A1:1942:U:H2'	38:A1:1943:C:O4'	2.19	0.41
38:A1:2129:U:H2'	38:A1:2130:G:H8	1.84	0.41
38:A1:2347:OMU:H2'	38:A1:2348:A:O4'	2.21	0.41
38:A1:2497:U:H6	38:A1:2497:U:H2'	1.67	0.41
38:A1:2498:U:H2'	38:A1:2499:U:C6	2.56	0.41
38:A1:2806:U:H2'	38:A1:2807:U:C6	2.56	0.41
39:A3:38:U:N3	39:A3:41:G:OP2	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:A3:71:G:H2'	39:A3:72:A:H8	1.85	0.41
40:A4:26:U:H2'	40:A4:27:U:C6	2.56	0.41
40:A4:56:G:H2'	40:A4:57:C:O4'	2.21	0.41
40:A4:67:U:H2'	40:A4:68:G:H8	1.86	0.41
40:A4:106:C:H4'	40:A4:107:G:H5''	2.02	0.41
43:AF:98:LYS:HB3	43:AF:99:PRO:HD3	2.02	0.41
51:AO:25[A]:LYS:HD2	51:AO:25[A]:LYS:HA	1.86	0.41
55:AS:81:TYR:CZ	55:AS:90:MET:HE3	2.56	0.41
61:AY:115:ARG:HA	61:AY:115:ARG:HD2	1.84	0.41
65:Ac:77:LEU:HB3	65:Ac:87:VAL:HG23	2.02	0.41
69:Ag:29:ILE:HD11	69:Ag:31:ARG:NH2	2.35	0.41
69:Ag:95:ILE:HG21	69:Ag:95:ILE:HD13	1.85	0.41
74:Al:44:TRP:CE2	74:Al:45:ARG:HG3	2.56	0.41
79:E:30:GLU:OE1	79:E:210:MET:HB2	2.21	0.41
79:E:65:ILE:HD11	79:E:111:ILE:HG23	2.02	0.41
79:E:78:LYS:NZ	79:E:83:ASP:HA	2.35	0.41
79:E:204:LEU:N	79:E:217:TYR:HB2	2.36	0.41
80:DC:574:THR:HG23	80:DC:689:LEU:HD12	2.02	0.41
80:DC:638:PRO:HG3	80:DC:671:THR:HB	2.03	0.41
80:DC:644:ASN:HD21	80:DC:682:ARG:HA	1.86	0.41
82:EC:6767:G:H2'	82:EC:6767:G:N3	2.36	0.41
82:EC:6833:G:C2	82:EC:6834:U:C4	3.09	0.41
7:BI:5:ARG:NH2	34:B5:334:G:O6	2.44	0.41
8:BJ:10:LYS:HD2	8:BJ:12:TYR:CE1	2.56	0.41
8:BJ:177:ALA:O	8:BJ:180:LYS:HG3	2.21	0.41
10:BN:151:ASN:CG	65:Ac:82:GLY:HA2	2.46	0.41
11:BO:68:ALA:HA	11:BO:71:CYS:HB2	2.02	0.41
17:Bb:19:HIS:HE1	17:Bb:21:LEU:HG	1.86	0.41
24:BR:11:ARG:HA	24:BR:14:LYS:HB2	2.03	0.41
27:BU:54:GLY:N	34:B5:1345:A:OP1	2.44	0.41
32:Bf:80:ARG:HG3	34:B5:1447:C:C6	2.56	0.41
33:BM:105:LYS:O	33:BM:112:ALA:HA	2.21	0.41
34:B5:341:A:H2'	34:B5:342:C:C6	2.56	0.41
34:B5:464:A:H4'	34:B5:527:A:H2	1.86	0.41
34:B5:925:G:H2'	34:B5:926:A:H8	1.86	0.41
34:B5:1248:C:H2'	34:B5:1249:U:C5	2.54	0.41
34:B5:1315:U:H2'	34:B5:1316:G:O4'	2.21	0.41
34:B5:1439:C:H2'	34:B5:1440:C:H6	1.86	0.41
35:AA:80:GLU:HB2	35:AA:170:ALA:HA	2.03	0.41
38:A1:673:U:H2'	38:A1:674:G:H8	1.85	0.41
38:A1:715:A:H5'	63:Aa:133:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:810:A:H2'	38:A1:811:U:C6	2.56	0.41
38:A1:929:A:H1'	72:Aj:49:TRP:CE3	2.56	0.41
38:A1:1242:G:O2'	38:A1:1243:G:P	2.78	0.41
38:A1:1364:C:H5''	53:AQ:3:ILE:HD13	2.02	0.41
38:A1:1805:C:H2'	38:A1:1806:A:C8	2.51	0.41
38:A1:1877:U:H5''	38:A1:1878:G:C5'	2.51	0.41
38:A1:2661:G:H2'	38:A1:2662:G:C8	2.56	0.41
38:A1:3095:U:H2'	38:A1:3096:C:C6	2.56	0.41
38:A1:3187:A:OP1	45:AH:22:SER:HB2	2.21	0.41
38:A1:3338:C:H2'	38:A1:3339:A:H8	1.86	0.41
41:AD:129:TYR:OH	41:AD:175:HIS:O	2.33	0.41
44:AG:83:ASP:OD1	44:AG:83:ASP:N	2.53	0.41
44:AG:104:GLU:HA	44:AG:107:GLU:CD	2.46	0.41
44:AG:150:LEU:HD12	44:AG:151:VAL:H	1.86	0.41
51:AO:23[A]:VAL:O	51:AO:27[A]:LEU:HG	2.20	0.41
52:AP:67:ILE:HD13	52:AP:67:ILE:HA	1.89	0.41
61:AY:37:LYS:HA	61:AY:37:LYS:HD2	1.65	0.41
66:Ad:81:GLU:OE1	66:Ad:81:GLU:N	2.54	0.41
68:Af:9:VAL:HG23	68:Af:100:ILE:HB	2.03	0.41
69:Ag:72:VAL:HG12	69:Ag:73:SER:N	2.35	0.41
73:Ak:11:PHE:HD2	73:Ak:12:LEU:HD22	1.86	0.41
80:DC:460:ASP:N	80:DC:460:ASP:OD1	2.53	0.41
80:DC:664:VAL:O	80:DC:668:GLN:HG2	2.20	0.41
82:EC:6892:U:H2'	82:EC:6893:C:C6	2.56	0.41
2:BB:130:SER:HB2	2:BB:180:THR:HB	2.02	0.40
3:BC:121:VAL:O	3:BC:125:ILE:HG12	2.21	0.40
11:BO:123:SER:HB2	34:B5:885:G:H21	1.86	0.40
21:BK:6:GLU:HG2	21:BK:7:ASP:N	2.36	0.40
22:BP:61:ARG:NH1	22:BP:61:ARG:HB2	2.36	0.40
25:BS:145:ARG:NH2	34:B5:1172:G:O3'	2.55	0.40
29:Bc:65:ARG:HA	29:Bc:65:ARG:HD3	1.88	0.40
32:Bf:141:CYS:HB3	32:Bf:146:SER:H	1.85	0.40
34:B5:366:A:OP1	34:B5:758:U:O2'	2.30	0.40
34:B5:1174:C:H42	34:B5:1465:C:N4	2.19	0.40
34:B5:1241:G:H2'	34:B5:1242:A:O4'	2.21	0.40
34:B5:1623:C:H2'	34:B5:1624:C:C6	2.56	0.40
34:B5:1713:G:H2'	34:B5:1714:A:O4'	2.21	0.40
34:B5:1793:G:O2'	34:B5:1795:U:OP2	2.39	0.40
35:AA:125:ALA:HB1	38:A1:2177:G:C6	2.56	0.40
36:AB:92:TYR:HB2	36:AB:157:VAL:HB	2.03	0.40
38:A1:523:A:O2'	55:AS:69:PRO:HD2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:604:G:H2'	38:A1:605:U:H6	1.86	0.40
38:A1:847:A:H2'	38:A1:848:A:O4'	2.21	0.40
38:A1:1912:U:H2'	38:A1:1913:A:O4'	2.21	0.40
38:A1:1950:U:H3	38:A1:2096:A:H61	1.69	0.40
38:A1:3044:G:H2'	38:A1:3045:G:C8	2.56	0.40
38:A1:3159:C:H2'	38:A1:3160:U:C6	2.56	0.40
41:AD:268:GLU:O	41:AD:271:LYS:HG2	2.21	0.40
43:AF:116:PHE:CE1	43:AF:144:ILE:HG12	2.56	0.40
48:AL:153:ASP:OD1	48:AL:154:VAL:N	2.54	0.40
49:AM:58:ILE:HD13	49:AM:63:VAL:HG13	2.03	0.40
55:AS:5:LYS:HD2	55:AS:7:TYR:OH	2.20	0.40
60:AX:57:LEU:HD11	60:AX:89:LYS:HB2	2.03	0.40
61:AY:48:LEU:HD23	61:AY:48:LEU:HA	1.91	0.40
80:DC:688:ILE:HG13	80:DC:688:ILE:O	2.22	0.40
82:EC:6773:G:O2'	82:EC:6819:G:OP1	2.28	0.40
1:BA:67:ILE:HG22	1:BA:69:ASN:H	1.86	0.40
2:BB:143:THR:HB	2:BB:205:PHE:HE2	1.87	0.40
3:BC:147:ASN:O	12:BV:4:ASP:N	2.54	0.40
4:BE:48:LEU:HD23	4:BE:48:LEU:HA	1.95	0.40
20:BF:174:LEU:HB3	20:BF:210:ALA:HA	2.03	0.40
21:BK:38:LYS:H	21:BK:38:LYS:HG2	1.72	0.40
22:BP:17:TYR:CZ	22:BP:18:ARG:HD2	2.56	0.40
24:BR:76:GLU:HA	24:BR:79:GLU:CG	2.49	0.40
26:BT:122:ARG:HH22	34:B5:1500:C:P	2.40	0.40
31:Bg:185:GLN:HB2	31:Bg:187:GLN:OE1	2.22	0.40
34:B5:1501:C:H2'	34:B5:1502:G:C8	2.56	0.40
34:B5:1739:C:H2'	34:B5:1740:A:H8	1.85	0.40
34:B5:1758:U:H2'	34:B5:1759:C:H6	1.84	0.40
35:AA:113:VAL:HG12	35:AA:166:ILE:HD13	2.03	0.40
38:A1:1255:C:O2'	38:A1:1256:G:H8	2.03	0.40
38:A1:1838:G:H5''	38:A1:1839:A:O5'	2.22	0.40
38:A1:1867:A:H2'	38:A1:1868:G:H8	1.85	0.40
38:A1:2418:G:H5'	38:A1:2606:G:N2	2.35	0.40
43:AF:127:LEU:HD12	43:AF:136:TYR:CD2	2.56	0.40
45:AH:100:ASN:HB3	45:AH:115:ARG:HB2	2.01	0.40
49:AM:47:ASP:OD2	49:AM:55:ARG:HD2	2.21	0.40
49:AM:55:ARG:NE	55:AS:70:THR:OG1	2.53	0.40
61:AY:83:ASP:C	61:AY:85:VAL:H	2.29	0.40
65:Ac:42:ILE:HD11	65:Ac:67:VAL:HG22	2.03	0.40
66:Ad:10:ARG:HB2	66:Ad:12:TYR:CE1	2.56	0.40
67:Ae:109:LEU:HD23	67:Ae:109:LEU:HA	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:E:3:LYS:O	79:E:217:TYR:OH	2.24	0.40
80:DC:271:ARG:H	80:DC:274:ASN:HD22	1.68	0.40
80:DC:576:LEU:H	80:DC:839:TYR:HD1	1.68	0.40
1:BA:60:ALA:HB1	1:BA:144:ILE:HD13	2.03	0.40
4:BE:62:LYS:O	4:BE:66:MET:HG2	2.22	0.40
4:BE:93:ASP:N	4:BE:93:ASP:OD1	2.54	0.40
4:BE:94:ALA:O	4:BE:95:THR:OG1	2.27	0.40
5:BG:63:MET:SD	5:BG:106:LEU:HD11	2.61	0.40
5:BG:75:LEU:O	5:BG:94:ARG:HA	2.22	0.40
5:BG:200:ALA:O	5:BG:203:GLU:HG3	2.22	0.40
15:BY:15:ASN:OD1	15:BY:17:LEU:HB2	2.21	0.40
20:BF:146:THR:HG22	20:BF:157:ARG:HB3	2.03	0.40
23:BQ:16:ALA:HB2	23:BQ:72:GLY:HA3	2.02	0.40
25:BS:41:ARG:HG2	25:BS:85:PHE:CZ	2.56	0.40
26:BT:86:ARG:HD2	26:BT:92:LYS:HE2	2.02	0.40
33:BM:33:ARG:NH1	33:BM:100:TRP:HB2	2.36	0.40
34:B5:463:U:H2'	34:B5:464:A:H8	1.87	0.40
34:B5:626:U:H2'	34:B5:627:C:H6	1.86	0.40
34:B5:1349:G:H2'	34:B5:1350:U:C6	2.56	0.40
35:AA:20:THR:HG22	35:AA:23:ARG:HD2	2.03	0.40
38:A1:157:A:N7	71:Ai:26:ILE:HG12	2.36	0.40
38:A1:165:A:O2'	38:A1:166:C:H6	2.04	0.40
38:A1:219:A:O2'	38:A1:220:G:N2	2.38	0.40
38:A1:945:C:OP1	67:Ae:36:LYS:NZ	2.42	0.40
38:A1:1326:A:H2'	38:A1:1327:C:O4'	2.20	0.40
38:A1:2708:C:OP1	77:Ao:100:LYS:HD3	2.21	0.40
39:A3:11:A:H4'	39:A3:13:A:C8	2.56	0.40
40:A4:150:G:O2'	44:AG:59:GLN:NE2	2.55	0.40
41:AD:277:LEU:HD12	41:AD:281:GLU:HG2	2.02	0.40
49:AM:39:ILE:HB	49:AM:43:LYS:HB3	2.02	0.40
50:AN:70:ASN:HB3	50:AN:92:LEU:O	2.21	0.40
55:AS:6:GLU:CD	55:AS:28:ARG:HH21	2.29	0.40
60:AX:102:LEU:HD23	60:AX:102:LEU:HA	1.86	0.40
80:DC:203:TYR:CZ	81:V:144:LYS:HE3	2.56	0.40
80:DC:459:ILE:HD12	80:DC:463:LEU:HD21	2.03	0.40
82:EC:6912:G:H2'	82:EC:6913:U:C6	2.57	0.40
1:BA:200:ASP:HB2	24:BR:90:ALA:CB	2.49	0.40
2:BB:54:LEU:O	2:BB:55:LYS:HG2	2.21	0.40
5:BG:157:VAL:HG21	5:BG:175:ILE:HD11	2.04	0.40
7:BI:36:THR:OG1	7:BI:57:ALA:O	2.32	0.40
10:BN:142:GLU:C	10:BN:144:ALA:H	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BY:55:VAL:HG13	15:BY:75:VAL:HG12	2.03	0.40
19:BD:134:CYS:SG	19:BD:135:GLU:N	2.95	0.40
20:BF:117:THR:O	20:BF:121:ILE:HG12	2.21	0.40
22:BP:28:MET:HB3	22:BP:32:ASP:OD2	2.22	0.40
23:BQ:98:ASP:OD2	23:BQ:100:GLN:HB2	2.21	0.40
26:BT:86:ARG:HB2	26:BT:89:ARG:HB2	2.03	0.40
29:Bc:8:THR:HG23	29:Bc:34:GLU:OE2	2.21	0.40
31:Bg:26:SER:OG	31:Bg:75:ALA:O	2.39	0.40
31:Bg:86:ASP:OD1	31:Bg:88:THR:OG1	2.33	0.40
31:Bg:262:VAL:O	31:Bg:271:VAL:N	2.31	0.40
34:B5:783:G:O2'	34:B5:784:C:H6	2.04	0.40
34:B5:1511:U:H2'	34:B5:1512:G:H8	1.86	0.40
34:B5:1771:U:H2'	34:B5:1772:C:H6	1.86	0.40
36:AB:2:SER:OG	38:A1:2943:G:OP2	2.21	0.40
38:A1:5:G:H2'	38:A1:6:A:O4'	2.21	0.40
38:A1:40:A:O2'	38:A1:937:G:O6	2.35	0.40
38:A1:44:U:OP1	50:AN:85:THR:HG23	2.21	0.40
38:A1:412:G:H2'	38:A1:413:U:H6	1.86	0.40
38:A1:506:U:H2'	38:A1:507:U:O4'	2.22	0.40
38:A1:866:A:H2'	38:A1:867:OMG:O4'	2.22	0.40
38:A1:1144:U:H6	38:A1:1144:U:H2'	1.73	0.40
38:A1:1150:A:N7	38:A1:1310:G:H5'	2.36	0.40
38:A1:1472:U:H2'	38:A1:1473:G:H8	1.87	0.40
38:A1:1660:C:H2'	38:A1:1661:G:C8	2.56	0.40
38:A1:1792:C:HO2'	38:A1:1794:G:H8	1.66	0.40
38:A1:1947:G:H5''	54:AR:134:HIS:HB2	2.04	0.40
38:A1:2508:U:H2'	38:A1:2509:U:C6	2.57	0.40
38:A1:2573:G:H2'	38:A1:2574:G:C8	2.57	0.40
38:A1:2689:A:H2'	38:A1:2689:A:N3	2.37	0.40
38:A1:3170:A:H2'	38:A1:3171:U:C6	2.56	0.40
40:A4:97:A:O2'	70:Ah:59:ASN:ND2	2.55	0.40
43:AF:56:GLU:O	43:AF:60:ARG:HG2	2.21	0.40
43:AF:208:SER:OG	43:AF:209:ASN:N	2.54	0.40
45:AH:87:LYS:HE2	45:AH:145:VAL:HG11	2.02	0.40
46:AI:72:ALA:HB2	46:AI:155:ALA:HB2	2.03	0.40
47:AJ:24:GLY:H	47:AJ:29:ARG:HH12	1.67	0.40
58:AV:45:ARG:HD2	58:AV:46:LEU:H	1.86	0.40
63:Aa:24:LYS:O	63:Aa:25:HIS:C	2.65	0.40
79:E:10:ARG:HH22	79:E:177:ASP:HA	1.85	0.40
80:DC:587:TYR:O	80:DC:689:LEU:N	2.55	0.40
80:DC:737:GLU:OE1	80:DC:764:PRO:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:V:128:MET:HB2	81:V:132:LYS:HD2	2.04	0.40
82:EC:6778:C:H5''	82:EC:6780:A:N7	2.37	0.40
82:EC:6922:G:H2'	82:EC:6923:C:C6	2.57	0.40
2:BB:111:ARG:HB3	16:Ba:68:TYR:HB2	2.04	0.40
5:BG:185:GLN:HG3	34:B5:284:G:C6	2.56	0.40
12:BV:38:LYS:HE3	12:BV:51:VAL:HG13	2.03	0.40
15:BY:89:TYR:CD2	34:B5:525:A:H5''	2.57	0.40
19:BD:40:ARG:NE	27:BU:110:PRO:HG3	2.37	0.40
25:BS:113:LEU:HD22	25:BS:127:HIS:CD2	2.57	0.40
26:BT:77:ASN:HA	26:BT:96:ALA:HB3	2.04	0.40
26:BT:126:GLU:HG2	34:B5:1359:C:H5'	2.03	0.40
34:B5:821:U:C4	34:B5:852:C:N3	2.87	0.40
34:B5:1174:C:O2'	34:B5:1196:A:N6	2.53	0.40
34:B5:1238:A:H2'	34:B5:1239:U:O4'	2.20	0.40
34:B5:1338:C:H1'	34:B5:1410:A:C5	2.56	0.40
34:B5:1693:A:H2'	34:B5:1694:A:H8	1.87	0.40
34:B5:1755:A:O3'	38:A1:2256:A2M:N6	2.54	0.40
35:AA:79:ASN:ND2	35:AA:165:VAL:HG12	2.36	0.40
36:AB:270:ARG:NH2	38:A1:3090:U:OP1	2.41	0.40
38:A1:817:A2M:H8	72:Aj:15:SER:OG	2.22	0.40
38:A1:1167:U:H2'	38:A1:1168:U:O4'	2.22	0.40
38:A1:1184:A:H2'	38:A1:1185:C:C6	2.56	0.40
38:A1:1340:G:H2'	38:A1:1341:U:H6	1.86	0.40
38:A1:2674:A:N6	47:AJ:124:GLY:O	2.54	0.40
38:A1:3139:A:H2'	38:A1:3140:G:O4'	2.21	0.40
39:A3:39:C:O2	47:AJ:70:THR:N	2.44	0.40
39:A3:60:G:H2'	39:A3:61:G:C8	2.56	0.40
40:A4:91:C:H2'	40:A4:92:A:C8	2.56	0.40
41:AD:153:THR:HG23	41:AD:160:PHE:CZ	2.56	0.40
42:AE:171:PRO:HA	42:AE:174:LEU:HB2	2.04	0.40
47:AJ:116:TYR:HD2	47:AJ:118:PRO:HD3	1.87	0.40
49:AM:112:LEU:HD21	51:AO:197[A]:LEU:O	2.21	0.40
49:AM:116:GLU:O	49:AM:120:VAL:HG13	2.21	0.40
63:Aa:90:TYR:CG	63:Aa:100:PRO:HG3	2.56	0.40
71:Ai:34:SER:H	71:Ai:37:THR:HG22	1.85	0.40
80:DC:431:ILE:HG21	80:DC:434:VAL:HG22	2.04	0.40
80:DC:565:GLU:OE2	80:DC:679:GLU:HB3	2.21	0.40
80:DC:723:LYS:CD	80:DC:806:SER:H	2.35	0.40
80:DC:832:VAL:HA	80:DC:833:PRO:HD2	1.93	0.40
81:V:144:LYS:HA	81:V:144:LYS:HD2	1.90	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%)	189 (93%)	15 (7%)	0	100	100
2	BB	212/255 (83%)	182 (86%)	30 (14%)	0	100	100
3	BC	215/254 (85%)	204 (95%)	11 (5%)	0	100	100
4	BE	258/261 (99%)	237 (92%)	21 (8%)	0	100	100
5	BG	224/236 (95%)	210 (94%)	14 (6%)	0	100	100
6	BH	182/190 (96%)	167 (92%)	15 (8%)	0	100	100
7	BI	184/200 (92%)	163 (89%)	21 (11%)	0	100	100
8	BJ	183/197 (93%)	169 (92%)	14 (8%)	0	100	100
9	BL	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
10	BN	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
11	BO	125/137 (91%)	112 (90%)	13 (10%)	0	100	100
12	BV	85/87 (98%)	73 (86%)	12 (14%)	0	100	100
13	BW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
14	BX	142/145 (98%)	127 (89%)	15 (11%)	0	100	100
15	BY	132/135 (98%)	119 (90%)	13 (10%)	0	100	100
16	Ba	95/119 (80%)	83 (87%)	12 (13%)	0	100	100
17	Bb	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
18	Be	58/63 (92%)	49 (84%)	9 (16%)	0	100	100
19	BD	221/240 (92%)	204 (92%)	17 (8%)	0	100	100
20	BF	204/225 (91%)	184 (90%)	20 (10%)	0	100	100
21	BK	94/105 (90%)	81 (86%)	13 (14%)	0	100	100
22	BP	122/142 (86%)	112 (92%)	10 (8%)	0	100	100
23	BQ	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
24	BR	123/136 (90%)	113 (92%)	10 (8%)	0	100	100
25	BS	143/146 (98%)	129 (90%)	14 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	BT	139/144 (96%)	122 (88%)	17 (12%)	0	100	100
27	BU	105/121 (87%)	93 (89%)	12 (11%)	0	100	100
28	BZ	67/108 (62%)	62 (92%)	5 (8%)	0	100	100
29	Bc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
30	Bd	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
31	Bg	310/319 (97%)	276 (89%)	34 (11%)	0	100	100
32	Bf	73/152 (48%)	64 (88%)	9 (12%)	0	100	100
33	BM	122/143 (85%)	110 (90%)	12 (10%)	0	100	100
35	AA	245/254 (96%)	228 (93%)	17 (7%)	0	100	100
36	AB	383/387 (99%)	362 (94%)	21 (6%)	0	100	100
37	AC	359/362 (99%)	334 (93%)	25 (7%)	0	100	100
41	AD	290/297 (98%)	275 (95%)	15 (5%)	0	100	100
42	AE	152/176 (86%)	141 (93%)	11 (7%)	0	100	100
43	AF	220/244 (90%)	208 (94%)	12 (6%)	0	100	100
44	AG	228/256 (89%)	209 (92%)	19 (8%)	0	100	100
45	AH	188/191 (98%)	174 (93%)	14 (7%)	0	100	100
46	AI	201/221 (91%)	190 (94%)	11 (6%)	0	100	100
47	AJ	167/174 (96%)	143 (86%)	24 (14%)	0	100	100
48	AL	191/199 (96%)	177 (93%)	14 (7%)	0	100	100
49	AM	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
50	AN	201/204 (98%)	191 (95%)	10 (5%)	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%)	178 (97%)	5 (3%)	0	100	100
54	AR	186/189 (98%)	175 (94%)	11 (6%)	0	100	100
55	AS	170/178 (96%)	159 (94%)	11 (6%)	0	100	100
56	AT	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
57	AU	98/121 (81%)	88 (90%)	10 (10%)	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%)	113 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AY	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
62	AZ	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
63	Aa	146/149 (98%)	135 (92%)	11 (8%)	0	100	100
64	Ab	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
65	Ac	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
66	Ad	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
67	Ae	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
68	Af	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
69	Ag	110/121 (91%)	104 (94%)	6 (6%)	0	100	100
70	Ah	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
71	Ai	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
72	Aj	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
73	Ak	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
74	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	Am	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	90 (87%)	13 (13%)	0	100	100
78	Ap	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
79	E	215/217 (99%)	197 (92%)	18 (8%)	0	100	100
80	DC	819/842 (97%)	755 (92%)	63 (8%)	1 (0%)	48	74
81	V	187/312 (60%)	174 (93%)	13 (7%)	0	100	100
All	All	12121/13257 (91%)	11233 (93%)	887 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
80	DC	700	ARG

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	113/124 (91%)	113 (100%)	0	100	100
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	113 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	Bf	66/135 (49%)	66 (100%)	0	100	100
33	BM	100/119 (84%)	100 (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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
80	DC	699/714 (98%)	699 (100%)	0	100	100
81	V	160/254 (63%)	160 (100%)	0	100	100
All	All	10349/11154 (93%)	10349 (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 (135) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	23	HIS
1	BA	163	ASN
1	BA	164	ASN
2	BB	194	ASN
4	BE	36	HIS
4	BE	197	HIS
5	BG	182	GLN
6	BH	150	GLN
7	BI	32	GLN
7	BI	35	ASN
9	BL	14	GLN
9	BL	81	HIS
9	BL	106	ASN
9	BL	127	GLN

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Mol	Chain	Res	Type
10	BN	21	ASN
10	BN	62	GLN
10	BN	78	ASN
12	BV	7	GLN
12	BV	29	HIS
12	BV	81	ASN
13	BW	12	ASN
13	BW	44	HIS
13	BW	64	GLN
15	BY	110	GLN
17	Bb	26	GLN
17	Bb	42	ASN
19	BD	111	ASN
19	BD	162	GLN
20	BF	63	GLN
20	BF	66	GLN
20	BF	131	GLN
20	BF	169	ASN
20	BF	186	ASN
20	BF	224	ASN
21	BK	13	GLN
21	BK	28	ASN
21	BK	32	HIS
24	BR	31	ASN
25	BS	13	HIS
25	BS	122	HIS
27	BU	40	ASN
27	BU	47	GLN
27	BU	48	HIS
28	BZ	44	GLN
28	BZ	98	GLN
29	Bc	51	ASN
31	Bg	52	GLN
31	Bg	139	GLN
31	Bg	153	GLN
31	Bg	185	GLN
35	AA	97	ASN
35	AA	140	ASN
36	AB	121	ASN
36	AB	173	GLN
36	AB	177	HIS
36	AB	182	GLN

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Mol	Chain	Res	Type
37	AC	304	GLN
41	AD	111	GLN
43	AF	25	GLN
43	AF	52	GLN
43	AF	93	ASN
44	AG	137	ASN
44	AG	145	ASN
44	AG	191	ASN
44	AG	221	ASN
45	AH	96	HIS
45	AH	116	ASN
45	AH	162	GLN
46	AI	59	GLN
46	AI	92	HIS
46	AI	162	GLN
47	AJ	95	ASN
47	AJ	101	ASN
48	AL	17	HIS
48	AL	102	GLN
49	AM	105	GLN
50	AN	11	GLN
50	AN	32	GLN
50	AN	182	ASN
51	AO	31[A]	GLN
51	AO	90[A]	HIS
52	AP	133	HIS
52	AP	137	ASN
53	AQ	126	GLN
54	AR	166	ASN
55	AS	3	HIS
55	AS	49	HIS
55	AS	114	HIS
55	AS	157	GLN
56	AT	5	HIS
56	AT	127	GLN
56	AT	131	GLN
57	AU	49	ASN
57	AU	87	ASN
58	AV	33	ASN
58	AV	98	ASN
59	AW	32	GLN
59	AW	42	GLN

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Mol	Chain	Res	Type
59	AW	58	HIS
61	AY	81	GLN
61	AY	98	ASN
61	AY	110	HIS
62	AZ	103	GLN
62	AZ	122	HIS
63	Aa	11	HIS
65	Ac	75	ASN
67	Ae	49	ASN
67	Ae	71	HIS
68	Af	5	HIS
70	Ah	34	GLN
70	Ah	59	ASN
70	Ah	104	GLN
71	Ai	35	ASN
72	Aj	48	ASN
73	Ak	10	GLN
73	Ak	57	ASN
73	Ak	67	GLN
74	Al	4	GLN
74	Al	32	ASN
74	Al	43	ASN
79	E	181	ASN
80	DC	8	GLN
80	DC	96	ASN
80	DC	101	ASN
80	DC	108	HIS
80	DC	341	HIS
80	DC	409	GLN
80	DC	414	GLN
80	DC	452	ASN
80	DC	537	HIS
80	DC	654	GLN
80	DC	795	GLN
80	DC	800	HIS
81	V	37	GLN
81	V	137	GLN

5.3.3 RNA ⓘ

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1780/1798 (98%)	396 (22%)	12 (0%)
38	A1	3194/3360 (95%)	568 (17%)	22 (0%)
39	A3	120/121 (99%)	18 (15%)	1 (0%)
40	A4	157/158 (99%)	32 (20%)	0
82	EC	149/202 (73%)	78 (52%)	5 (3%)
All	All	5400/5639 (95%)	1092 (20%)	40 (0%)

All (1092) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
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	63	G
34	B5	67	A
34	B5	68	A
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	79	C
34	B5	81	G
34	B5	104	A
34	B5	114	C
34	B5	127	G
34	B5	130	C
34	B5	131	C
34	B5	132	U
34	B5	134	U
34	B5	135	A
34	B5	137	U
34	B5	138	A

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Mol	Chain	Res	Type
34	B5	141	U
34	B5	145	A
34	B5	153	G
34	B5	166	C
34	B5	168	A
34	B5	169	A
34	B5	176	C
34	B5	178	U
34	B5	179	A
34	B5	181	A
34	B5	182	A
34	B5	188	A
34	B5	190	C
34	B5	191	C
34	B5	192	U
34	B5	193	U
34	B5	194	U
34	B5	195	G
34	B5	198	A
34	B5	200	A
34	B5	217	A
34	B5	218	A
34	B5	220	A
34	B5	224	C
34	B5	225	A
34	B5	226	A
34	B5	227	U
34	B5	228	G
34	B5	230	C
34	B5	232	U
34	B5	233	C
34	B5	234	G
34	B5	240	U
34	B5	241	U
34	B5	246	G
34	B5	260	U
34	B5	261	U
34	B5	265	A
34	B5	278	U
34	B5	280	U
34	B5	281	G
34	B5	287	G

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Mol	Chain	Res	Type
34	B5	299	A
34	B5	314	C
34	B5	316	A
34	B5	321	C
34	B5	322	G
34	B5	333	A
34	B5	337	G
34	B5	338	C
34	B5	352	A
34	B5	359	A
34	B5	360	A
34	B5	361	C
34	B5	390	G
34	B5	400	A
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	460	A
34	B5	468	A
34	B5	475	A
34	B5	477	A
34	B5	480	G
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	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

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Mol	Chain	Res	Type
34	B5	501	U
34	B5	502	U
34	B5	503	G
34	B5	506	A
34	B5	507	U
34	B5	515	A
34	B5	539	G
34	B5	540	G
34	B5	541	A2M
34	B5	542	A
34	B5	557	G
34	B5	558	U
34	B5	559	C
34	B5	565	C
34	B5	568	G
34	B5	575	C
34	B5	577	G
34	B5	579	A
34	B5	582	U
34	B5	594	A
34	B5	595	G
34	B5	606	A
34	B5	610	G
34	B5	611	U
34	B5	619	A2M
34	B5	620	A
34	B5	621	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	653	C
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

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Mol	Chain	Res	Type
34	B5	683	C
34	B5	694	U
34	B5	696	C
34	B5	697	C
34	B5	698	U
34	B5	702	G
34	B5	705	U
34	B5	707	A
34	B5	708	C
34	B5	709	C
34	B5	711	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	720	G
34	B5	721	U
34	B5	722	G
34	B5	723	G
34	B5	724	C
34	B5	725	U
34	B5	726	C
34	B5	727	U
34	B5	730	G
34	B5	731	C
34	B5	732	G
34	B5	733	A
34	B5	734	A
34	B5	735	C
34	B5	738	G
34	B5	740	A
34	B5	741	C
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

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Mol	Chain	Res	Type
34	B5	779	U
34	B5	782	U
34	B5	783	G
34	B5	784	C
34	B5	789	A
34	B5	794	U
34	B5	813	U
34	B5	814	A
34	B5	820	U
34	B5	823	G
34	B5	824	G
34	B5	833	U
34	B5	836	U
34	B5	839	U
34	B5	840	U
34	B5	846	G
34	B5	850	A
34	B5	851	U
34	B5	859	A
34	B5	863	A
34	B5	873	U
34	B5	886	U
34	B5	893	U
34	B5	898	A
34	B5	906	A
34	B5	907	A
34	B5	914	G
34	B5	922	G
34	B5	933	A
34	B5	935	U
34	B5	951	A
34	B5	960	U
34	B5	966	A
34	B5	987	G
34	B5	988	A
34	B5	992	A
34	B5	993	A
34	B5	1004	U
34	B5	1005	A
34	B5	1026	A
34	B5	1028	C
34	B5	1039	A

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Mol	Chain	Res	Type
34	B5	1040	G
34	B5	1052	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	1076	A
34	B5	1083	G
34	B5	1092	A
34	B5	1097	U
34	B5	1100	G
34	B5	1109	G
34	B5	1126	OMG
34	B5	1138	A
34	B5	1150	G
34	B5	1153	G
34	B5	1154	G
34	B5	1155	G
34	B5	1158	C
34	B5	1159	C
34	B5	1183	A
34	B5	1185	U
34	B5	1186	U
34	B5	1194	A
34	B5	1196	A
34	B5	1199	G
34	B5	1200	G
34	B5	1201	G
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	1235	C
34	B5	1243	G
34	B5	1244	A
34	B5	1245	G
34	B5	1246	C

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Mol	Chain	Res	Type
34	B5	1249	U
34	B5	1251	U
34	B5	1252	C
34	B5	1256	A
34	B5	1257	U
34	B5	1269	OMU
34	B5	1274	C
34	B5	1276	U
34	B5	1284	C
34	B5	1286	U
34	B5	1301	U
34	B5	1314	U
34	B5	1315	U
34	B5	1316	G
34	B5	1321	A
34	B5	1340	U
34	B5	1344	A
34	B5	1345	A
34	B5	1346	A
34	B5	1352	G
34	B5	1355	C
34	B5	1358	G
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	1376	C
34	B5	1378	U
34	B5	1383	G
34	B5	1385	G
34	B5	1390	U
34	B5	1398	U
34	B5	1399	C
34	B5	1400	A
34	B5	1413	U
34	B5	1427	A
34	B5	1428	OMG

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Mol	Chain	Res	Type
34	B5	1433	G
34	B5	1446	A
34	B5	1447	C
34	B5	1459	C
34	B5	1461	C
34	B5	1471	A
34	B5	1485	C
34	B5	1491	U
34	B5	1492	A
34	B5	1493	A
34	B5	1496	U
34	B5	1516	A
34	B5	1521	G
34	B5	1523	G
34	B5	1524	A
34	B5	1533	C
34	B5	1537	C
34	B5	1540	G
34	B5	1542	G
34	B5	1557	U
34	B5	1559	A
34	B5	1560	U
34	B5	1565	C
34	B5	1568	C
34	B5	1570	A
34	B5	1576	A
34	B5	1582	U
34	B5	1584	G
34	B5	1596	C
34	B5	1600	A
34	B5	1601	G
34	B5	1619	C
34	B5	1622	G
34	B5	1631	A
34	B5	1635	A
34	B5	1645	G
34	B5	1646	C
34	B5	1651	A
34	B5	1657	U
34	B5	1658	G
34	B5	1680	G
34	B5	1682	U

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Mol	Chain	Res	Type
34	B5	1683	C
34	B5	1684	U
34	B5	1686	C
34	B5	1688	U
34	B5	1690	G
34	B5	1699	G
34	B5	1700	C
34	B5	1702	A
34	B5	1703	C
34	B5	1709	C
34	B5	1715	G
34	B5	1716	C
34	B5	1717	G
34	B5	1756[A]	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	1773	4AC
34	B5	1780	G
34	B5	1782	MA6
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	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	92	G
38	A1	99	A
38	A1	110	G
38	A1	111	C
38	A1	116	A

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Mol	Chain	Res	Type
38	A1	117	U
38	A1	122	A
38	A1	134	U
38	A1	135	C
38	A1	136	G
38	A1	148	G
38	A1	156	G
38	A1	157	A
38	A1	162	G
38	A1	164	A
38	A1	165	A
38	A1	166	C
38	A1	187	A
38	A1	190	U
38	A1	191	U
38	A1	206	G
38	A1	210	U
38	A1	219	A
38	A1	222	A
38	A1	234	G
38	A1	237	G
38	A1	238	A
38	A1	239	G
38	A1	240	U
38	A1	241	G
38	A1	242	C
38	A1	243	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
38	A1	251	G
38	A1	252	U
38	A1	253	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

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Mol	Chain	Res	Type
38	A1	329	U
38	A1	338	A
38	A1	339	C
38	A1	351	A
38	A1	352	A
38	A1	372	A
38	A1	376	G
38	A1	385	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	495	G
38	A1	521	A
38	A1	523	A
38	A1	535	G
38	A1	540	U
38	A1	542	G
38	A1	543	C
38	A1	547	G
38	A1	548	G
38	A1	549	U
38	A1	552	G
38	A1	557	A
38	A1	559	A
38	A1	560	G
38	A1	569	A
38	A1	578	A
38	A1	579	G
38	A1	589	A
38	A1	592	A
38	A1	597	G
38	A1	602	A
38	A1	604	G
38	A1	608	A
38	A1	611	A
38	A1	620	U

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Mol	Chain	Res	Type
38	A1	621	A
38	A1	636	C
38	A1	649	A2M
38	A1	677	A
38	A1	681	U
38	A1	690	A
38	A1	691	A
38	A1	705	A
38	A1	715	A
38	A1	719	U
38	A1	736	A
38	A1	761	A
38	A1	765	C
38	A1	766	U
38	A1	767	U
38	A1	770	G
38	A1	775	A
38	A1	777	U
38	A1	780	A
38	A1	781	G
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	849	C
38	A1	857	G
38	A1	861	C
38	A1	874	U
38	A1	879	U
38	A1	896	A
38	A1	897	U
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	925	A

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Mol	Chain	Res	Type
38	A1	934	G
38	A1	937	G
38	A1	943	U
38	A1	944	C
38	A1	959	C
38	A1	964	G
38	A1	980	A
38	A1	981	U
38	A1	983	A
38	A1	1000	C
38	A1	1002	A
38	A1	1010	G
38	A1	1011	A
38	A1	1014	U
38	A1	1016	C
38	A1	1017	C
38	A1	1018	G
38	A1	1019	G
38	A1	1021	G
38	A1	1031	C
38	A1	1032	C
38	A1	1033	U
38	A1	1034	U
38	A1	1035	G
38	A1	1036	A
38	A1	1047	A
38	A1	1064	A
38	A1	1066	G
38	A1	1072	G
38	A1	1075	A
38	A1	1081	U
38	A1	1082	U
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	1130	A
38	A1	1131	G

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Mol	Chain	Res	Type
38	A1	1143	A
38	A1	1144	U
38	A1	1150	A
38	A1	1153	A
38	A1	1159	A
38	A1	1179	A
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	1222	G
38	A1	1224	C
38	A1	1228	C
38	A1	1231	A
38	A1	1232	C
38	A1	1235	U
38	A1	1236	G
38	A1	1237	G
38	A1	1239	C
38	A1	1241	U
38	A1	1243	G
38	A1	1244	A
38	A1	1245	A
38	A1	1246	G
38	A1	1249	G
38	A1	1252	A
38	A1	1253	U
38	A1	1256	G
38	A1	1258	U
38	A1	1259	A
38	A1	1262	G
38	A1	1263	A
38	A1	1279	C
38	A1	1282	G
38	A1	1283	C
38	A1	1286	A
38	A1	1287	A

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Mol	Chain	Res	Type
38	A1	1293	U
38	A1	1295	G
38	A1	1307	G
38	A1	1309	U
38	A1	1317	A
38	A1	1330	A
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	1354	G
38	A1	1355	A
38	A1	1356	U
38	A1	1386	A
38	A1	1392	G
38	A1	1399	A
38	A1	1400	G
38	A1	1408	G
38	A1	1419	A
38	A1	1431	G
38	A1	1434	G
38	A1	1437	OMC
38	A1	1446	A
38	A1	1455	U
38	A1	1469	C
38	A1	1481	A
38	A1	1483	G
38	A1	1487	G
38	A1	1494	U
38	A1	1496	C
38	A1	1508	C
38	A1	1523	U
38	A1	1535	A
38	A1	1539	A
38	A1	1555	U
38	A1	1556	C
38	A1	1558	A
38	A1	1559	A
38	A1	1560	G

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Mol	Chain	Res	Type
38	A1	1561	G
38	A1	1562	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	1571	A
38	A1	1574	C
38	A1	1575	A
38	A1	1576	G
38	A1	1578	C
38	A1	1579	C
38	A1	1580	A
38	A1	1581	C
38	A1	1583	A
38	A1	1593	A
38	A1	1628	C
38	A1	1630	U
38	A1	1642	A
38	A1	1643	A
38	A1	1645	U
38	A1	1694	U
38	A1	1724	U
38	A1	1741	A
38	A1	1750	A
38	A1	1751	G
38	A1	1752	A
38	A1	1762	C
38	A1	1763	U
38	A1	1765	U
38	A1	1766	G
38	A1	1775	G
38	A1	1796	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

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Mol	Chain	Res	Type
38	A1	1846	C
38	A1	1849	C
38	A1	1850	A
38	A1	1866	C
38	A1	1878	G
38	A1	1880	U
38	A1	1886	A
38	A1	1894	U
38	A1	1906	G
38	A1	1908	A
38	A1	1932	A
38	A1	1952	G
38	A1	1953	G
38	A1	1954	G
38	A1	1955	U
38	A1	2094	C
38	A1	2110	G
38	A1	2111	G
38	A1	2112	U
38	A1	2122	G
38	A1	2131	A
38	A1	2140	U
38	A1	2144	A
38	A1	2145	A
38	A1	2158	A
38	A1	2169	G
38	A1	2176	U
38	A1	2188	A
38	A1	2197	OMC
38	A1	2201	G
38	A1	2206	G
38	A1	2207	A
38	A1	2242	A
38	A1	2249	G
38	A1	2255	A
38	A1	2256	A2M
38	A1	2260	U
38	A1	2269	U
38	A1	2270	A
38	A1	2272	G
38	A1	2273	G
38	A1	2279	A

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Mol	Chain	Res	Type
38	A1	2281	A2M
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	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	2394	G
38	A1	2397	A
38	A1	2402	A
38	A1	2403	G
38	A1	2404	A
38	A1	2411	U
38	A1	2418	G
38	A1	2435	G
38	A1	2440	G
38	A1	2442	G
38	A1	2446	U
38	A1	2450	G
38	A1	2451	G
38	A1	2452	G
38	A1	2453	U
38	A1	2454	G
38	A1	2455	U
38	A1	2458	A
38	A1	2459	A
38	A1	2461	A
38	A1	2462	A
38	A1	2463	G
38	A1	2465	G

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Mol	Chain	Res	Type
38	A1	2467	G
38	A1	2468	A
38	A1	2469	G
38	A1	2474	G
38	A1	2477	G
38	A1	2479	C
38	A1	2486	A
38	A1	2487	U
38	A1	2490	C
38	A1	2491	A
38	A1	2493	U
38	A1	2494	A
38	A1	2495	C
38	A1	2496	C
38	A1	2497	U
38	A1	2498	U
38	A1	2499	U
38	A1	2500	A
38	A1	2502	A
38	A1	2503	G
38	A1	2504	U
38	A1	2505	U
38	A1	2506	U
38	A1	2507	C
38	A1	2514	U
38	A1	2523	A
38	A1	2524	A
38	A1	2530	G
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	2543	U
38	A1	2549	G
38	A1	2552	C
38	A1	2561	A
38	A1	2562	A
38	A1	2569	A
38	A1	2571	U
38	A1	2573	G

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Mol	Chain	Res	Type
38	A1	2585	G
38	A1	2593	A
38	A1	2594	C
38	A1	2606	G
38	A1	2607	G
38	A1	2614	G
38	A1	2626	A
38	A1	2635	A
38	A1	2652	U
38	A1	2656	A
38	A1	2672	G
38	A1	2674	A
38	A1	2677	G
38	A1	2678	A
38	A1	2680	A
38	A1	2681	U
38	A1	2688	U
38	A1	2689	A
38	A1	2691	A
38	A1	2704	A
38	A1	2714	G
38	A1	2719	U
38	A1	2727	A
38	A1	2728	G
38	A1	2729	OMU
38	A1	2749	G
38	A1	2752	U
38	A1	2753	G
38	A1	2755	C
38	A1	2772	C
38	A1	2773	C
38	A1	2777	G
38	A1	2778	G
38	A1	2796	G
38	A1	2799	A
38	A1	2800	G
38	A1	2801	A
38	A1	2803	A
38	A1	2810	C
38	A1	2814	G
38	A1	2817	A
38	A1	2822	U

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Mol	Chain	Res	Type
38	A1	2828	G
38	A1	2833	A
38	A1	2842	U
38	A1	2845	A
38	A1	2856	G
38	A1	2860	U
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	2894	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	2947	G
38	A1	2977	G
38	A1	2980	U
38	A1	2983	C
38	A1	2990	G
38	A1	2997	G
38	A1	3011	A
38	A1	3012	A
38	A1	3021	A
38	A1	3022	G
38	A1	3032	A
38	A1	3056	U
38	A1	3078	U
38	A1	3080	G
38	A1	3086	A
38	A1	3092	C
38	A1	3101	G
38	A1	3104	U
38	A1	3122	A
38	A1	3130	A
38	A1	3131	U
38	A1	3142	A
38	A1	3143	C

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Mol	Chain	Res	Type
38	A1	3153	U
38	A1	3154	C
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	3175	U
38	A1	3176	G
38	A1	3179	U
38	A1	3181	C
38	A1	3187	A
38	A1	3198	U
38	A1	3206	C
38	A1	3207	U
38	A1	3216	G
38	A1	3217	C
38	A1	3218	A
38	A1	3219	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	3264	G
38	A1	3270	U
38	A1	3271	G
38	A1	3273	A
38	A1	3276	G
38	A1	3289	G
38	A1	3294	A
38	A1	3304	U
38	A1	3313	U
38	A1	3316	A
38	A1	3317	U
38	A1	3319	U
38	A1	3341	U
38	A1	3345	G

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Mol	Chain	Res	Type
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	3377	G
38	A1	3378	C
38	A1	3389	U
39	A3	7	G
39	A3	19	C
39	A3	33	U
39	A3	35	C
39	A3	38	U
39	A3	49	G
39	A3	53	U
39	A3	54	U
39	A3	55	A
39	A3	65	G
39	A3	73	C
39	A3	74	C
39	A3	76	A
39	A3	78	U
39	A3	102	A
39	A3	107	C
39	A3	112	G
39	A3	121	U
40	A4	23	U
40	A4	34	U
40	A4	35	C
40	A4	50	C
40	A4	51	G
40	A4	52	A
40	A4	53	A
40	A4	59	A
40	A4	62	C
40	A4	63	G
40	A4	76	C
40	A4	80	A
40	A4	81	U
40	A4	82	U
40	A4	83	C

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Mol	Chain	Res	Type
40	A4	85	G
40	A4	86	U
40	A4	87	G
40	A4	88	A
40	A4	90	U
40	A4	95	G
40	A4	100	U
40	A4	104	A
40	A4	106	C
40	A4	107	G
40	A4	111	A
40	A4	113	U
40	A4	114	G
40	A4	116	G
40	A4	125	U
40	A4	152	G
40	A4	158	U
82	EC	6762	U
82	EC	6766	U
82	EC	6767	G
82	EC	6770	U
82	EC	6771	U
82	EC	6772	G
82	EC	6773	G
82	EC	6774	U
82	EC	6775	U
82	EC	6776	A
82	EC	6777	C
82	EC	6778	C
82	EC	6779	C
82	EC	6780	A
82	EC	6781	U
82	EC	6782	C
82	EC	6788	C
82	EC	6789	G
82	EC	6790	A
82	EC	6791	A
82	EC	6792	A
82	EC	6793	A
82	EC	6794	C
82	EC	6795	U
82	EC	6802	A

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Mol	Chain	Res	Type
82	EC	6803	C
82	EC	6804	A
82	EC	6816	A
82	EC	6817	A
82	EC	6818	G
82	EC	6819	G
82	EC	6820	C
82	EC	6821	U
82	EC	6822	U
82	EC	6823	U
82	EC	6825	A
82	EC	6831	U
82	EC	6832	G
82	EC	6850	C
82	EC	6851	G
82	EC	6852	U
82	EC	6888	A
82	EC	6890	A
82	EC	6891	G
82	EC	6892	U
82	EC	6895	C
82	EC	6896	A
82	EC	6897	G
82	EC	6900	A
82	EC	6901	C
82	EC	6904	U
82	EC	6910	A
82	EC	6911	A
82	EC	6912	G
82	EC	6915	G
82	EC	6916	A
82	EC	6922	G
82	EC	6925	C
82	EC	6928	G
82	EC	6929	C
82	EC	6933	G
82	EC	6934	U
82	EC	6935	G
82	EC	6936	G
82	EC	6938	A
82	EC	6939	C
82	EC	6940	U

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Mol	Chain	Res	Type
82	EC	6941	U
82	EC	6942	A
82	EC	6943	A
82	EC	6944	U
82	EC	6945	U
82	EC	6946	A
82	EC	6947	A
82	EC	6948	U
82	EC	6949	G
82	EC	6950	C
82	EC	6951	C

All (40) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	B5	752	A
34	B5	819	G
34	B5	850	A
34	B5	862	A
34	B5	950	C
34	B5	1285	U
34	B5	1344	A
34	B5	1369	U
34	B5	1458	G
34	B5	1568	C
34	B5	1645	G
34	B5	1756[A]	A
38	A1	237	G
38	A1	240	U
38	A1	243	G
38	A1	245	U
38	A1	873	C
38	A1	916	G
38	A1	1092	C
38	A1	1218	U
38	A1	1242	G
38	A1	1292	C
38	A1	1350	A
38	A1	1561	G
38	A1	1581	C
38	A1	1629	U
38	A1	2241	U

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Mol	Chain	Res	Type
38	A1	2450	G
38	A1	2496	C
38	A1	2497	U
38	A1	2506	U
38	A1	2875	U
38	A1	3121	U
38	A1	3354	U
39	A3	52	G
82	EC	6789	G
82	EC	6831	U
82	EC	6911	A
82	EC	6939	C
82	EC	6943	A

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

68 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	1MA	A1	2142	38,83	21,25,26	1.34	4 (19%)	30,37,40	1.70	5 (16%)
38	A2M	A1	2220	38	22,25,26	1.50	4 (18%)	30,36,39	1.98	9 (30%)
38	OMG	A1	2793	38	23,26,27	1.18	3 (13%)	32,38,41	1.99	6 (18%)
38	OMU	A1	2729	38	19,22,23	1.25	3 (15%)	25,31,34	1.78	4 (16%)
34	A2M	B5	974	34	22,25,26	1.45	4 (18%)	30,36,39	2.12	10 (33%)
38	A2M	A1	1449	38,83	22,25,26	1.50	3 (13%)	30,36,39	2.06	7 (23%)
38	OMC	A1	650	38,83	19,22,23	0.82	0	25,31,34	0.83	0
34	OMU	B5	578	34	19,22,23	1.20	3 (15%)	25,31,34	1.79	5 (20%)
38	A2M	A1	807	38	22,25,26	1.46	5 (22%)	30,36,39	2.16	10 (33%)
34	OMG	B5	1428	34	23,26,27	1.17	3 (13%)	32,38,41	1.96	6 (18%)
34	A2M	B5	100	34,83	22,25,26	1.50	5 (22%)	30,36,39	2.03	7 (23%)
34	OMG	B5	1271	34	23,26,27	1.18	3 (13%)	32,38,41	1.98	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	HIC	AB	243	36	10,11,12	1.47	1 (10%)	9,14,16	1.31	2 (22%)
34	OMG	B5	1572	34	23,26,27	1.18	2 (8%)	32,38,41	1.96	6 (18%)
38	OMG	A1	2619	38	23,26,27	1.19	3 (13%)	32,38,41	1.94	6 (18%)
38	OMG	A1	2288	38	23,26,27	1.22	3 (13%)	32,38,41	2.02	5 (15%)
38	OMG	A1	867	38	23,26,27	1.18	3 (13%)	32,38,41	1.96	6 (18%)
38	OMC	A1	2197	38	19,22,23	0.80	0	25,31,34	0.84	0
38	OMU	A1	1888	38	19,22,23	1.29	3 (15%)	25,31,34	1.92	5 (20%)
34	A2M	B5	619	34,83	22,25,26	1.48	5 (22%)	30,36,39	2.10	9 (30%)
38	OMC	A1	663	38	19,22,23	0.80	0	25,31,34	0.75	0
38	A2M	A1	2280	38	22,25,26	1.50	4 (18%)	30,36,39	2.06	9 (30%)
38	OMC	A1	2948	38	19,22,23	0.78	0	25,31,34	0.84	1 (4%)
38	OMC	A1	1437	38,83	19,22,23	0.80	0	25,31,34	0.94	2 (8%)
34	A2M	B5	436	34	22,25,26	1.49	4 (18%)	30,36,39	2.06	8 (26%)
34	A2M	B5	796	34	22,25,26	1.48	4 (18%)	30,36,39	2.25	10 (33%)
38	1MA	A1	645	38,83	21,25,26	1.35	4 (19%)	30,37,40	1.71	5 (16%)
34	MA6	B5	1782	34	23,26,27	1.48	5 (21%)	33,38,41	2.08	11 (33%)
34	A2M	B5	541	34	22,25,26	1.49	4 (18%)	30,36,39	2.13	7 (23%)
38	OMG	A1	2815	38	23,26,27	1.19	3 (13%)	32,38,41	2.01	7 (21%)
38	5MC	A1	2278	38,83	19,22,23	1.46	3 (15%)	26,32,35	1.16	3 (11%)
38	OMG	A1	2922	38	23,26,27	1.20	3 (13%)	32,38,41	1.97	6 (18%)
38	OMU	A1	2347	38	19,22,23	1.29	3 (15%)	25,31,34	1.85	5 (20%)
38	OMU	A1	2921	38	19,22,23	1.25	3 (15%)	25,31,34	1.80	5 (20%)
38	A2M	A1	2946	38,83	22,25,26	1.46	5 (22%)	30,36,39	2.20	10 (33%)
34	4AC	B5	1773	34	21,24,25	1.06	1 (4%)	28,34,37	1.16	3 (10%)
38	OMU	A1	2724	38	19,22,23	1.27	3 (15%)	25,31,34	1.81	5 (20%)
34	A2M	B5	28	34,83	22,25,26	1.47	4 (18%)	30,36,39	2.06	10 (33%)
34	G7M	B5	1575	34,82	23,26,27	2.57	6 (26%)	34,39,42	3.06	15 (44%)
34	A2M	B5	420	34	22,25,26	1.50	4 (18%)	30,36,39	2.05	8 (26%)
80	DDE	DC	699	80	18,20,21	1.05	1 (5%)	17,28,30	0.92	1 (5%)
38	A2M	A1	1133	38	22,25,26	1.49	5 (22%)	30,36,39	2.13	9 (30%)
34	B8N	B5	1191	34	25,29,30	1.38	3 (12%)	28,42,45	2.61	6 (21%)
38	UR3	A1	2634	38	19,22,23	0.98	0	26,32,35	1.72	4 (15%)
38	A2M	A1	2256	38	22,25,26	1.48	4 (18%)	30,36,39	2.13	9 (30%)
38	A2M	A1	817	38,83	22,25,26	1.49	5 (22%)	30,36,39	2.05	8 (26%)
34	MA6	B5	1781	34	23,26,27	1.49	5 (21%)	33,38,41	2.08	11 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	OMG	A1	805	38	23,26,27	1.18	4 (17%)	32,38,41	2.02	6 (18%)
38	OMU	A1	898	38	19,22,23	1.26	3 (15%)	25,31,34	1.80	5 (20%)
34	OMG	B5	1126	34	23,26,27	1.17	3 (13%)	32,38,41	2.05	6 (18%)
38	OMC	A1	2337	38	19,22,23	0.78	0	25,31,34	0.77	0
34	OMC	B5	1639	34	19,22,23	0.78	0	25,31,34	0.70	0
38	A2M	A1	649	38,83	22,25,26	1.46	5 (22%)	30,36,39	2.09	9 (30%)
34	OMC	B5	414	34	19,22,23	0.78	0	25,31,34	0.81	0
34	OMC	B5	1007	34	19,22,23	0.81	0	25,31,34	0.86	0
38	OMC	A1	2959	38	19,22,23	0.80	0	25,31,34	0.79	0
38	A2M	A1	876	38	22,25,26	1.48	4 (18%)	30,36,39	2.02	7 (23%)
38	OMU	A1	2417	38	19,22,23	1.25	3 (15%)	25,31,34	1.77	5 (20%)
38	OMG	A1	2791	38	23,26,27	1.20	3 (13%)	32,38,41	1.98	5 (15%)
38	5MC	A1	2870	38	19,22,23	1.51	3 (15%)	26,32,35	1.26	3 (11%)
34	OMG	B5	562	34	23,26,27	1.20	3 (13%)	32,38,41	1.95	5 (15%)
38	OMG	A1	908	38	23,26,27	1.23	3 (13%)	32,38,41	2.10	6 (18%)
34	OMU	B5	1269	34,83	19,22,23	1.29	4 (21%)	25,31,34	1.81	5 (20%)
38	A2M	A1	2281	38	22,25,26	1.44	5 (22%)	30,36,39	2.16	11 (36%)
38	OMU	A1	2421	38	19,22,23	1.25	3 (15%)	25,31,34	1.83	5 (20%)
34	4AC	B5	1280	34	21,24,25	1.06	1 (4%)	28,34,37	1.02	2 (7%)
38	A2M	A1	2640	38	22,25,26	1.47	4 (18%)	30,36,39	2.03	7 (23%)
38	OMG	A1	1450	38	23,26,27	1.19	3 (13%)	32,38,41	1.98	6 (18%)

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	1MA	A1	2142	38,83	-	0/7/25/26	0/3/3/3
38	A2M	A1	2220	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2793	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2729	38	-	4/9/27/28	0/2/2/2
34	A2M	B5	974	34	-	1/9/27/28	0/3/3/3
38	A2M	A1	1449	38,83	-	0/9/27/28	0/3/3/3
38	OMC	A1	650	38,83	-	0/9/27/28	0/2/2/2
34	OMU	B5	578	34	-	0/9/27/28	0/2/2/2
38	A2M	A1	807	38	-	1/9/27/28	0/3/3/3
34	OMG	B5	1428	34	-	4/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	A2M	B5	100	34,83	-	1/9/27/28	0/3/3/3
34	OMG	B5	1271	34	-	1/9/27/28	0/3/3/3
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
34	OMG	B5	1572	34	-	2/9/27/28	0/3/3/3
38	OMG	A1	2619	38	-	1/9/27/28	0/3/3/3
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	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2
34	A2M	B5	619	34,83	-	3/9/27/28	0/3/3/3
38	OMC	A1	663	38	-	1/9/27/28	0/2/2/2
38	A2M	A1	2280	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2948	38	-	0/9/27/28	0/2/2/2
38	OMC	A1	1437	38,83	-	4/9/27/28	0/2/2/2
34	A2M	B5	436	34	-	1/9/27/28	0/3/3/3
34	A2M	B5	796	34	-	0/9/27/28	0/3/3/3
38	1MA	A1	645	38,83	-	2/7/25/26	0/3/3/3
34	MA6	B5	1782	34	-	5/11/29/30	0/3/3/3
34	A2M	B5	541	34	-	6/9/27/28	0/3/3/3
38	OMG	A1	2815	38	-	0/9/27/28	0/3/3/3
38	5MC	A1	2278	38,83	-	0/7/25/26	0/2/2/2
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2347	38	-	0/9/27/28	0/2/2/2
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2946	38,83	-	1/9/27/28	0/3/3/3
34	4AC	B5	1773	34	-	7/11/29/30	0/2/2/2
38	OMU	A1	2724	38	-	1/9/27/28	0/2/2/2
34	A2M	B5	28	34,83	-	1/9/27/28	0/3/3/3
34	G7M	B5	1575	34,82	-	0/7/25/26	0/3/3/3
34	A2M	B5	420	34	-	0/9/27/28	0/3/3/3
80	DDE	DC	699	80	-	8/20/21/23	0/1/1/1
38	A2M	A1	1133	38	-	0/9/27/28	0/3/3/3
34	B8N	B5	1191	34	-	6/16/34/35	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	A2M	A1	2256	38	-	1/9/27/28	0/3/3/3
38	A2M	A1	817	38,83	-	2/9/27/28	0/3/3/3
34	MA6	B5	1781	34	-	3/11/29/30	0/3/3/3
38	OMG	A1	805	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	898	38	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	OMG	B5	1126	34	-	2/9/27/28	0/3/3/3
38	OMC	A1	2337	38	-	1/9/27/28	0/2/2/2
34	OMC	B5	1639	34	-	1/9/27/28	0/2/2/2
38	A2M	A1	649	38,83	-	1/9/27/28	0/3/3/3
34	OMC	B5	414	34	-	0/9/27/28	0/2/2/2
34	OMC	B5	1007	34	-	1/9/27/28	0/2/2/2
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	876	38	-	1/9/27/28	0/3/3/3
38	OMU	A1	2417	38	-	1/9/27/28	0/2/2/2
38	OMG	A1	2791	38	-	1/9/27/28	0/3/3/3
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
34	OMG	B5	562	34	-	1/9/27/28	0/3/3/3
38	OMG	A1	908	38	-	0/9/27/28	0/3/3/3
34	OMU	B5	1269	34,83	-	5/9/27/28	0/2/2/2
38	A2M	A1	2281	38	-	2/9/27/28	0/3/3/3
38	OMU	A1	2421	38	-	1/9/27/28	0/2/2/2
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	A2M	A1	2640	38	-	1/9/27/28	0/3/3/3
38	OMG	A1	1450	38	-	1/9/27/28	0/3/3/3

All (200) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	C8-N7	7.70	1.46	1.33
34	B5	1575	G7M	C5-N7	-5.13	1.33	1.39
38	A1	2278	5MC	C5-C4	5.06	1.47	1.44
38	A1	2870	5MC	C5-C4	5.03	1.47	1.44
34	B5	1781	MA6	C5-C4	4.68	1.47	1.39
34	B5	541	A2M	C5-C4	4.64	1.47	1.39
34	B5	1782	MA6	C5-C4	4.59	1.47	1.39
38	A1	2220	A2M	C5-C4	4.57	1.47	1.39
34	B5	436	A2M	C5-C4	4.57	1.47	1.39
34	B5	420	A2M	C5-C4	4.52	1.47	1.39
38	A1	2280	A2M	C5-C4	4.50	1.47	1.39
34	B5	100	A2M	C5-C4	4.50	1.47	1.39
38	A1	2640	A2M	C5-C4	4.49	1.47	1.39
38	A1	2256	A2M	C5-C4	4.49	1.47	1.39
38	A1	1449	A2M	C5-C4	4.47	1.47	1.39
34	B5	796	A2M	C5-C4	4.45	1.47	1.39
38	A1	876	A2M	C5-C4	4.45	1.47	1.39
34	B5	619	A2M	C5-C4	4.40	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	817	A2M	C5-C4	4.39	1.46	1.39
38	A1	807	A2M	C5-C4	4.39	1.46	1.39
34	B5	28	A2M	C5-C4	4.38	1.46	1.39
38	A1	2946	A2M	C5-C4	4.36	1.46	1.39
38	A1	1133	A2M	C5-C4	4.32	1.46	1.39
38	A1	649	A2M	C5-C4	4.29	1.46	1.39
34	B5	974	A2M	C5-C4	4.29	1.46	1.39
38	A1	2281	A2M	C5-C4	4.19	1.46	1.39
34	B5	1575	G7M	C8-N9	4.00	1.46	1.35
34	B5	1191	B8N	C4-C5	-3.89	1.38	1.47
34	B5	1575	G7M	C5-C4	3.61	1.47	1.38
34	B5	562	OMG	C5-C4	3.11	1.47	1.38
34	B5	1271	OMG	C5-C4	3.09	1.47	1.38
38	A1	645	1MA	C6-N6	3.09	1.35	1.28
34	B5	1572	OMG	C5-C4	3.06	1.47	1.38
38	A1	908	OMG	C5-C4	3.06	1.47	1.38
34	B5	1773	4AC	C4-N4	-3.03	1.35	1.39
38	A1	2288	OMG	C5-C4	3.02	1.47	1.38
38	A1	2142	1MA	C6-N6	3.01	1.35	1.28
38	A1	2619	OMG	C5-C4	3.01	1.47	1.38
34	B5	1428	OMG	C5-C4	3.00	1.47	1.38
38	A1	2791	OMG	C5-C4	3.00	1.47	1.38
38	A1	2922	OMG	C5-C4	2.99	1.46	1.38
34	B5	1191	B8N	C6-C5	2.98	1.39	1.35
38	A1	2347	OMU	C4-N3	-2.97	1.33	1.38
38	A1	645	1MA	C5-C4	2.95	1.46	1.38
38	A1	2793	OMG	C5-C4	2.95	1.46	1.38
34	B5	1280	4AC	C4-N4	-2.94	1.35	1.39
38	A1	867	OMG	C5-C4	2.94	1.46	1.38
38	A1	1450	OMG	C5-C4	2.92	1.46	1.38
38	A1	2142	1MA	C5-C4	2.92	1.46	1.38
38	A1	1888	OMU	C4-N3	-2.92	1.33	1.38
34	B5	1575	G7M	C2'-C3'	-2.90	1.45	1.53
34	B5	1126	OMG	C5-C4	2.90	1.46	1.38
38	A1	2724	OMU	C4-N3	-2.89	1.33	1.38
38	A1	2870	5MC	C6-C5	2.89	1.39	1.34
34	B5	1269	OMU	C4-N3	-2.88	1.33	1.38
38	A1	898	OMU	C4-N3	-2.88	1.33	1.38
38	A1	805	OMG	C5-C4	2.87	1.46	1.38
38	A1	2417	OMU	C4-N3	-2.87	1.33	1.38
38	A1	2421	OMU	C4-N3	-2.86	1.33	1.38
38	A1	2815	OMG	C5-C4	2.86	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1782	MA6	C5-C6	2.85	1.48	1.41
36	AB	243	HIC	CD2-CG	2.85	1.41	1.36
34	B5	1781	MA6	C5-C6	2.84	1.48	1.41
38	A1	2729	OMU	C4-N3	-2.83	1.33	1.38
38	A1	2288	OMG	C6-N1	-2.80	1.33	1.38
38	A1	2921	OMU	C4-N3	-2.78	1.33	1.38
38	A1	908	OMG	C6-N1	-2.76	1.33	1.38
38	A1	2815	OMG	C6-N1	-2.74	1.33	1.38
38	A1	2280	A2M	C5-C6	2.71	1.48	1.41
38	A1	1449	A2M	C5-N7	-2.66	1.34	1.39
38	A1	2791	OMG	C6-N1	-2.66	1.33	1.38
38	A1	2619	OMG	C6-N1	-2.64	1.33	1.38
38	A1	2793	OMG	C6-N1	-2.64	1.33	1.38
34	B5	578	OMU	C4-N3	-2.63	1.34	1.38
34	B5	420	A2M	C5-C6	2.62	1.48	1.41
34	B5	541	A2M	C5-C6	2.62	1.48	1.41
34	B5	796	A2M	C5-C6	2.62	1.48	1.41
38	A1	2922	OMG	C6-N1	-2.61	1.34	1.38
38	A1	1449	A2M	C5-C6	2.60	1.48	1.41
38	A1	1450	OMG	C6-N1	-2.60	1.34	1.38
34	B5	1126	OMG	C6-N1	-2.58	1.34	1.38
34	B5	436	A2M	C5-N7	-2.58	1.34	1.39
38	A1	876	A2M	C5-N7	-2.58	1.34	1.39
34	B5	436	A2M	C5-C6	2.58	1.48	1.41
38	A1	649	A2M	C5-C6	2.57	1.48	1.41
38	A1	2278	5MC	C6-C5	2.57	1.38	1.34
34	B5	619	A2M	C5-C6	2.56	1.48	1.41
38	A1	817	A2M	C5-C6	2.56	1.48	1.41
38	A1	805	OMG	C6-N1	-2.56	1.34	1.38
38	A1	2256	A2M	C5-C6	2.56	1.48	1.41
34	B5	974	A2M	C5-C6	2.55	1.48	1.41
38	A1	2724	OMU	C2-N3	-2.55	1.33	1.38
34	B5	562	OMG	C6-N1	-2.55	1.34	1.38
38	A1	2946	A2M	C5-C6	2.55	1.48	1.41
34	B5	28	A2M	C5-C6	2.55	1.48	1.41
34	B5	100	A2M	C5-C6	2.55	1.48	1.41
38	A1	867	OMG	C6-N1	-2.55	1.34	1.38
38	A1	876	A2M	C5-C6	2.55	1.48	1.41
38	A1	2220	A2M	C5-C6	2.54	1.48	1.41
80	DC	699	DDE	CD2-CG	2.54	1.41	1.36
34	B5	1271	OMG	C6-N1	-2.53	1.34	1.38
38	A1	2640	A2M	C5-C6	2.53	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	1133	A2M	C5-N7	-2.53	1.34	1.39
34	B5	1428	OMG	C6-N1	-2.53	1.34	1.38
38	A1	817	A2M	C5-N7	-2.52	1.34	1.39
34	B5	100	A2M	C5-N7	-2.51	1.34	1.39
38	A1	1888	OMU	C2-N3	-2.51	1.33	1.38
38	A1	807	A2M	C5-C6	2.50	1.48	1.41
34	B5	619	A2M	C5-N7	-2.50	1.34	1.39
38	A1	1133	A2M	C5-C6	2.50	1.47	1.41
34	B5	541	A2M	C5-N7	-2.49	1.34	1.39
38	A1	2220	A2M	C5-N7	-2.48	1.34	1.39
38	A1	807	A2M	C5-N7	-2.46	1.34	1.39
38	A1	2946	A2M	C5-N7	-2.45	1.34	1.39
38	A1	649	A2M	C5-N7	-2.44	1.34	1.39
38	A1	2281	A2M	C5-N7	-2.44	1.34	1.39
38	A1	2870	5MC	C6-N1	-2.44	1.33	1.38
38	A1	2256	A2M	C5-N7	-2.43	1.34	1.39
38	A1	2421	OMU	C2-N3	-2.42	1.33	1.38
38	A1	2640	A2M	C5-N7	-2.42	1.34	1.39
38	A1	2417	OMU	C2-N3	-2.41	1.33	1.38
34	B5	1575	G7M	C6-N1	-2.41	1.34	1.38
34	B5	420	A2M	C5-N7	-2.40	1.34	1.39
38	A1	898	OMU	C2-N3	-2.40	1.33	1.38
38	A1	2281	A2M	C5-C6	2.40	1.47	1.41
34	B5	974	A2M	C5-N7	-2.38	1.34	1.39
34	B5	28	A2M	C5-N7	-2.38	1.34	1.39
38	A1	2921	OMU	C2-N3	-2.38	1.33	1.38
38	A1	2417	OMU	C5-C4	-2.37	1.38	1.43
38	A1	2347	OMU	C2-N3	-2.36	1.33	1.38
38	A1	2142	1MA	C5-N7	-2.36	1.34	1.39
34	B5	796	A2M	C5-N7	-2.36	1.34	1.39
34	B5	1572	OMG	C6-N1	-2.35	1.34	1.38
38	A1	2729	OMU	C2-N3	-2.35	1.33	1.38
38	A1	2278	5MC	C6-N1	-2.35	1.34	1.38
38	A1	2347	OMU	C5-C4	-2.31	1.38	1.43
38	A1	898	OMU	C5-C4	-2.30	1.38	1.43
38	A1	908	OMG	C5-N7	-2.29	1.34	1.39
38	A1	2280	A2M	C5-N7	-2.29	1.34	1.39
34	B5	1781	MA6	C5-N7	-2.29	1.34	1.39
34	B5	1269	OMU	C2-N3	-2.28	1.34	1.38
38	A1	2729	OMU	C5-C4	-2.28	1.38	1.43
38	A1	2281	A2M	C4-N9	-2.28	1.33	1.37
34	B5	1782	MA6	C5-N7	-2.27	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	420	A2M	C8-N7	2.27	1.36	1.31
34	B5	28	A2M	C8-N7	2.26	1.36	1.31
34	B5	1269	OMU	C2-N1	2.25	1.42	1.38
34	B5	578	OMU	C2-N3	-2.25	1.34	1.38
38	A1	2921	OMU	C5-C4	-2.24	1.38	1.43
38	A1	645	1MA	C5-N7	-2.23	1.34	1.39
38	A1	2724	OMU	C5-C4	-2.23	1.38	1.43
38	A1	2280	A2M	C8-N7	2.22	1.35	1.31
38	A1	2220	A2M	C8-N7	2.21	1.35	1.31
38	A1	2791	OMG	C5-N7	-2.21	1.34	1.39
38	A1	2288	OMG	C5-N7	-2.21	1.34	1.39
38	A1	867	OMG	C5-N7	-2.20	1.34	1.39
38	A1	2922	OMG	C5-N7	-2.20	1.34	1.39
34	B5	796	A2M	C8-N7	2.19	1.35	1.31
38	A1	2281	A2M	C8-N7	2.19	1.35	1.31
38	A1	2619	OMG	C5-N7	-2.18	1.34	1.39
38	A1	2142	1MA	C2-N3	2.18	1.34	1.30
38	A1	1450	OMG	C5-N7	-2.17	1.34	1.39
38	A1	817	A2M	C8-N7	2.17	1.35	1.31
34	B5	1782	MA6	C8-N7	2.17	1.35	1.31
38	A1	807	A2M	C4-N9	-2.17	1.33	1.37
34	B5	1191	B8N	CN1-N1	2.16	1.51	1.46
34	B5	974	A2M	C8-N7	2.16	1.35	1.31
38	A1	2815	OMG	C5-N7	-2.16	1.34	1.39
34	B5	619	A2M	C8-N7	2.16	1.35	1.31
38	A1	2256	A2M	C8-N7	2.16	1.35	1.31
38	A1	649	A2M	C8-N7	2.16	1.35	1.31
34	B5	1271	OMG	C5-N7	-2.15	1.34	1.39
34	B5	100	A2M	C8-N7	2.15	1.35	1.31
38	A1	1133	A2M	C4-N9	-2.14	1.33	1.37
38	A1	2640	A2M	C8-N7	2.14	1.35	1.31
38	A1	1888	OMU	C5-C4	-2.13	1.39	1.43
34	B5	541	A2M	C8-N7	2.13	1.35	1.31
34	B5	1781	MA6	C8-N7	2.13	1.35	1.31
34	B5	562	OMG	C5-N7	-2.13	1.34	1.39
34	B5	1428	OMG	C5-N7	-2.13	1.34	1.39
38	A1	2793	OMG	C5-N7	-2.13	1.34	1.39
34	B5	1126	OMG	C5-N7	-2.12	1.34	1.39
38	A1	805	OMG	C5-N7	-2.11	1.34	1.39
38	A1	1133	A2M	C8-N7	2.11	1.35	1.31
34	B5	619	A2M	C4-N9	-2.11	1.33	1.37
38	A1	807	A2M	C8-N7	2.10	1.35	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	578	OMU	C5-C4	-2.10	1.39	1.43
34	B5	1269	OMU	C5-C4	-2.10	1.39	1.43
38	A1	2421	OMU	C5-C4	-2.09	1.39	1.43
34	B5	436	A2M	C8-N7	2.09	1.35	1.31
38	A1	817	A2M	C4-N9	-2.07	1.33	1.37
34	B5	1782	MA6	C4-N9	-2.07	1.33	1.37
38	A1	2946	A2M	C8-N7	2.07	1.35	1.31
38	A1	876	A2M	C8-N7	2.05	1.35	1.31
38	A1	649	A2M	C4-N9	-2.04	1.33	1.37
38	A1	2946	A2M	C4-N9	-2.04	1.33	1.37
38	A1	805	OMG	C4-N9	-2.04	1.32	1.38
38	A1	645	1MA	C2-N3	2.01	1.34	1.30
34	B5	100	A2M	C4-N9	-2.01	1.33	1.37
34	B5	1781	MA6	C4-N9	-2.00	1.33	1.37

All (385) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1191	B8N	C32-C31-N3	10.82	131.06	112.16
34	B5	1575	G7M	CN7-N7-C8	-7.64	113.22	124.79
38	A1	2634	UR3	C4-N3-C2	-6.76	119.14	124.58
38	A1	908	OMG	C5-C4-N3	-6.67	117.77	128.39
34	B5	1575	G7M	N9-C8-N7	-6.58	96.51	112.48
34	B5	541	A2M	C5-C4-N3	-6.49	117.78	126.72
38	A1	2288	OMG	C5-C4-N3	-6.44	118.13	128.39
34	B5	1271	OMG	C5-C4-N3	-6.28	118.39	128.39
34	B5	562	OMG	C5-C4-N3	-6.27	118.41	128.39
38	A1	2791	OMG	C5-C4-N3	-6.25	118.44	128.39
38	A1	2815	OMG	C5-C4-N3	-6.24	118.45	128.39
34	B5	1575	G7M	C8-N7-C5	6.23	115.57	107.78
34	B5	1126	OMG	C5-C4-N3	-6.21	118.50	128.39
34	B5	1428	OMG	C5-C4-N3	-6.15	118.60	128.39
38	A1	1450	OMG	C5-C4-N3	-6.14	118.62	128.39
38	A1	2922	OMG	C5-C4-N3	-6.12	118.64	128.39
38	A1	1449	A2M	C5-C4-N3	-6.12	118.29	126.72
38	A1	2619	OMG	C5-C4-N3	-6.12	118.65	128.39
34	B5	436	A2M	C5-C4-N3	-6.04	118.39	126.72
38	A1	2793	OMG	C5-C4-N3	-6.04	118.78	128.39
38	A1	2640	A2M	C5-C4-N3	-6.02	118.43	126.72
38	A1	817	A2M	C5-C4-N3	-6.00	118.45	126.72
38	A1	876	A2M	C5-C4-N3	-5.99	118.47	126.72
34	B5	796	A2M	C5-C4-N3	-5.98	118.48	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	867	OMG	C5-C4-N3	-5.98	118.88	128.39
34	B5	619	A2M	C5-C4-N3	-5.92	118.57	126.72
34	B5	974	A2M	C5-C4-N3	-5.89	118.61	126.72
34	B5	100	A2M	C5-C4-N3	-5.87	118.63	126.72
34	B5	1575	G7M	N9-C4-N3	5.87	137.69	125.95
34	B5	28	A2M	C5-C4-N3	-5.82	118.70	126.72
38	A1	2220	A2M	C5-C4-N3	-5.80	118.73	126.72
38	A1	649	A2M	C5-C4-N3	-5.78	118.76	126.72
34	B5	1572	OMG	C5-C4-N3	-5.77	119.21	128.39
34	B5	420	A2M	C5-C4-N3	-5.76	118.79	126.72
38	A1	2280	A2M	C5-C4-N3	-5.73	118.83	126.72
38	A1	805	OMG	C5-C4-N3	-5.71	119.30	128.39
38	A1	807	A2M	C5-C4-N3	-5.71	118.85	126.72
38	A1	2946	A2M	C5-C4-N3	-5.69	118.88	126.72
34	B5	1191	B8N	C4-N3-C2	-5.68	118.63	125.62
38	A1	2256	A2M	C5-C4-N3	-5.59	119.01	126.72
34	B5	1782	MA6	C5-C4-N3	-5.58	119.04	126.72
38	A1	1133	A2M	C5-C4-N3	-5.57	119.04	126.72
34	B5	1781	MA6	C5-C4-N3	-5.46	119.20	126.72
38	A1	2281	A2M	C5-C4-N3	-5.44	119.22	126.72
34	B5	1575	G7M	C5-C4-N3	-5.40	117.95	128.15
38	A1	2142	1MA	C5-C4-N3	-5.34	119.41	127.27
38	A1	908	OMG	N9-C4-N3	5.33	136.62	125.95
38	A1	645	1MA	C5-C4-N3	-5.26	119.52	127.27
38	A1	2815	OMG	C2-N3-C4	5.19	121.24	112.30
34	B5	1126	OMG	C2-N3-C4	5.17	121.21	112.30
34	B5	541	A2M	N3-C4-N9	5.16	135.94	127.17
38	A1	2288	OMG	C2-N3-C4	5.13	121.14	112.30
38	A1	1450	OMG	C2-N3-C4	5.13	121.13	112.30
38	A1	1888	OMU	C4-N3-C2	-5.11	120.27	126.61
34	B5	1271	OMG	C2-N3-C4	5.09	121.07	112.30
38	A1	908	OMG	C2-N3-C4	5.08	121.05	112.30
34	B5	1428	OMG	C2-N3-C4	5.05	121.00	112.30
38	A1	867	OMG	C2-N3-C4	5.05	120.99	112.30
38	A1	2922	OMG	C2-N3-C4	5.04	120.99	112.30
38	A1	2791	OMG	C2-N3-C4	5.03	120.96	112.30
38	A1	805	OMG	C2-N3-C4	5.02	120.95	112.30
34	B5	562	OMG	C2-N3-C4	5.00	120.91	112.30
38	A1	2793	OMG	C2-N3-C4	4.96	120.84	112.30
38	A1	2619	OMG	C2-N3-C4	4.96	120.84	112.30
34	B5	1572	OMG	C2-N3-C4	4.89	120.73	112.30
38	A1	2421	OMU	C4-N3-C2	-4.88	120.55	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	1449	A2M	N3-C4-N9	4.88	135.47	127.17
38	A1	2347	OMU	C4-N3-C2	-4.83	120.61	126.61
38	A1	2288	OMG	N9-C4-N3	4.83	135.61	125.95
38	A1	898	OMU	C4-N3-C2	-4.81	120.64	126.61
38	A1	876	A2M	N3-C4-N9	4.81	135.35	127.17
38	A1	2724	OMU	C4-N3-C2	-4.77	120.69	126.61
34	B5	796	A2M	N3-C4-N9	4.76	135.27	127.17
34	B5	436	A2M	N3-C4-N9	4.74	135.23	127.17
34	B5	1271	OMG	N9-C4-N3	4.72	135.38	125.95
34	B5	974	A2M	N3-C4-N9	4.70	135.16	127.17
38	A1	2640	A2M	N3-C4-N9	4.69	135.15	127.17
34	B5	578	OMU	C4-N3-C2	-4.68	120.80	126.61
38	A1	2256	A2M	N3-C4-N9	4.68	135.12	127.17
38	A1	2921	OMU	C4-N3-C2	-4.68	120.81	126.61
38	A1	2729	OMU	C4-N3-C2	-4.66	120.83	126.61
38	A1	817	A2M	N3-C4-N9	4.65	135.07	127.17
34	B5	100	A2M	N3-C4-N9	4.64	135.07	127.17
38	A1	2417	OMU	C4-N3-C2	-4.64	120.85	126.61
34	B5	1428	OMG	N9-C4-N3	4.62	135.20	125.95
34	B5	619	A2M	N3-C4-N9	4.61	135.01	127.17
34	B5	1269	OMU	C4-N3-C2	-4.61	120.89	126.61
38	A1	2619	OMG	N9-C4-N3	4.59	135.14	125.95
38	A1	2142	1MA	C2-N3-C4	4.57	121.50	112.53
38	A1	1450	OMG	N9-C4-N3	4.57	135.09	125.95
38	A1	2922	OMG	N9-C4-N3	4.56	135.08	125.95
38	A1	645	1MA	C2-N3-C4	4.56	121.47	112.53
38	A1	2793	OMG	N9-C4-N3	4.55	135.04	125.95
38	A1	2791	OMG	N9-C4-N3	4.54	135.02	125.95
34	B5	1126	OMG	N9-C4-N3	4.53	135.01	125.95
34	B5	562	OMG	N9-C4-N3	4.53	135.00	125.95
34	B5	28	A2M	N3-C4-N9	4.50	134.81	127.17
38	A1	807	A2M	N3-C4-N9	4.49	134.80	127.17
38	A1	2421	OMU	N3-C2-N1	4.48	120.72	114.89
38	A1	2280	A2M	N3-C4-N9	4.48	134.78	127.17
38	A1	2946	A2M	N3-C4-N9	4.48	134.78	127.17
38	A1	2281	A2M	N3-C4-N9	4.48	134.78	127.17
38	A1	2815	OMG	N9-C4-N3	4.47	134.90	125.95
38	A1	1133	A2M	N3-C4-N9	4.47	134.77	127.17
38	A1	2220	A2M	N3-C4-N9	4.46	134.75	127.17
38	A1	649	A2M	N3-C4-N9	4.45	134.74	127.17
34	B5	420	A2M	N3-C4-N9	4.45	134.74	127.17
38	A1	1888	OMU	N3-C2-N1	4.41	120.63	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1575	G7M	C2-N3-C4	4.35	119.78	112.30
38	A1	2946	A2M	C2'-C1'-N9	-4.33	106.62	113.75
38	A1	867	OMG	N9-C4-N3	4.28	134.52	125.95
34	B5	1781	MA6	C2-N1-C6	4.27	122.26	111.83
34	B5	1782	MA6	N3-C4-N9	4.27	134.42	127.17
34	B5	1269	OMU	N3-C2-N1	4.23	120.40	114.89
34	B5	796	A2M	C2'-C1'-N9	-4.23	106.79	113.75
34	B5	1781	MA6	N3-C4-N9	4.21	134.33	127.17
38	A1	2921	OMU	N3-C2-N1	4.19	120.34	114.89
34	B5	1572	OMG	N9-C4-N3	4.18	134.31	125.95
38	A1	2724	OMU	N3-C2-N1	4.16	120.31	114.89
38	A1	2347	OMU	N3-C2-N1	4.16	120.31	114.89
34	B5	1782	MA6	C2-N1-C6	4.14	121.94	111.83
38	A1	2729	OMU	N3-C2-N1	4.13	120.26	114.89
38	A1	898	OMU	N3-C2-N1	4.09	120.21	114.89
38	A1	2417	OMU	N3-C2-N1	4.08	120.20	114.89
38	A1	1888	OMU	C5-C4-N3	4.04	120.46	114.80
34	B5	578	OMU	N3-C2-N1	4.04	120.15	114.89
38	A1	2870	5MC	C5-C6-N1	-4.03	118.94	123.31
38	A1	805	OMG	N9-C4-N3	4.03	134.01	125.95
38	A1	2724	OMU	C5-C4-N3	4.00	120.40	114.80
34	B5	541	A2M	C2-N3-C4	3.97	121.52	111.83
38	A1	2417	OMU	C5-C4-N3	3.96	120.35	114.80
34	B5	1782	MA6	C4-C5-N7	-3.92	106.10	110.58
38	A1	898	OMU	C5-C4-N3	3.89	120.25	114.80
38	A1	2347	OMU	C5-C4-N3	3.89	120.25	114.80
34	B5	578	OMU	C5-C4-N3	3.86	120.20	114.80
38	A1	2729	OMU	C5-C4-N3	3.83	120.17	114.80
38	A1	2921	OMU	C5-C4-N3	3.83	120.16	114.80
34	B5	1575	G7M	C8-N9-C4	3.81	116.52	107.09
38	A1	2421	OMU	C5-C4-N3	3.79	120.11	114.80
34	B5	974	A2M	C2-N3-C4	3.79	121.09	111.83
34	B5	1781	MA6	C4-C5-N7	-3.79	106.25	110.58
38	A1	817	A2M	C2-N3-C4	3.76	121.02	111.83
34	B5	796	A2M	C2-N3-C4	3.76	121.01	111.83
38	A1	876	A2M	C2-N3-C4	3.74	120.97	111.83
38	A1	805	OMG	C6-C5-N7	3.74	137.09	130.29
38	A1	649	A2M	C2-N3-C4	3.74	120.95	111.83
34	B5	1269	OMU	C5-C4-N3	3.73	120.03	114.80
38	A1	2946	A2M	C2-N3-C4	3.73	120.94	111.83
38	A1	649	A2M	C4-C5-N7	-3.72	106.33	110.58
38	A1	1449	A2M	C2-N3-C4	3.72	120.91	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	420	A2M	C2-N3-C4	3.68	120.83	111.83
34	B5	28	A2M	C2-N3-C4	3.68	120.82	111.83
38	A1	2640	A2M	C2-N3-C4	3.67	120.79	111.83
38	A1	2220	A2M	C2-N3-C4	3.67	120.79	111.83
34	B5	436	A2M	C2-N3-C4	3.66	120.76	111.83
34	B5	100	A2M	C2-N3-C4	3.65	120.75	111.83
38	A1	1133	A2M	C2-N3-C4	3.63	120.69	111.83
38	A1	2280	A2M	C4-C5-N7	-3.62	106.44	110.58
38	A1	807	A2M	C2'-C1'-N9	-3.61	107.81	113.75
34	B5	1781	MA6	C2-N3-C4	3.61	120.65	111.83
38	A1	2280	A2M	C2-N3-C4	3.61	120.64	111.83
38	A1	2281	A2M	C2-N3-C4	3.60	120.63	111.83
34	B5	619	A2M	C4-C5-N7	-3.60	106.47	110.58
34	B5	1575	G7M	O2'-C2'-C3'	3.59	123.34	111.82
34	B5	796	A2M	C4-C5-N7	-3.59	106.48	110.58
38	A1	2256	A2M	C2-N3-C4	3.58	120.58	111.83
34	B5	1782	MA6	C2-N3-C4	3.57	120.56	111.83
38	A1	1133	A2M	C2'-C1'-N9	-3.57	107.87	113.75
38	A1	807	A2M	C2-N3-C4	3.56	120.53	111.83
34	B5	28	A2M	C4-C5-N7	-3.56	106.51	110.58
38	A1	2142	1MA	N9-C4-N3	3.56	135.01	126.90
38	A1	2640	A2M	C4-C5-N7	-3.55	106.52	110.58
34	B5	420	A2M	C4-C5-N7	-3.54	106.53	110.58
34	B5	619	A2M	C2-N3-C4	3.53	120.45	111.83
34	B5	1575	G7M	CN7-N7-C5	3.52	131.19	126.80
34	B5	1572	OMG	C6-C5-N7	3.51	136.68	130.29
38	A1	817	A2M	C4-C5-N7	-3.47	106.61	110.58
34	B5	100	A2M	C4-C5-N7	-3.47	106.61	110.58
34	B5	974	A2M	C4-C5-N7	-3.45	106.64	110.58
38	A1	2946	A2M	C4-C5-N7	-3.44	106.64	110.58
38	A1	1449	A2M	C4-C5-N7	-3.43	106.66	110.58
38	A1	867	OMG	C6-C5-N7	3.41	136.49	130.29
38	A1	2946	A2M	N3-C2-N1	-3.39	123.45	128.58
34	B5	1781	MA6	N1-C2-N3	-3.38	123.47	128.58
34	B5	436	A2M	C4-C5-N7	-3.38	106.72	110.58
38	A1	807	A2M	C4-C5-N7	-3.38	106.72	110.58
38	A1	2815	OMG	C6-C5-N7	3.37	136.43	130.29
34	B5	541	A2M	C4-C5-N7	-3.37	106.73	110.58
34	B5	1280	4AC	N4-C4-N3	3.36	119.33	113.87
34	B5	974	A2M	N3-C2-N1	-3.36	123.49	128.58
38	A1	2220	A2M	N3-C2-N1	-3.35	123.51	128.58
38	A1	649	A2M	N3-C2-N1	-3.34	123.52	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2220	A2M	C4-C5-N7	-3.33	106.77	110.58
34	B5	1126	OMG	C6-C5-N7	3.31	136.31	130.29
38	A1	876	A2M	C4-C5-N7	-3.30	106.80	110.58
38	A1	1133	A2M	N3-C2-N1	-3.30	123.59	128.58
38	A1	2281	A2M	N3-C2-N1	-3.29	123.60	128.58
38	A1	1133	A2M	C4-C5-N7	-3.29	106.82	110.58
34	B5	541	A2M	N3-C2-N1	-3.28	123.62	128.58
38	A1	1450	OMG	C6-C5-N7	3.27	136.24	130.29
38	A1	2793	OMG	C6-C5-N7	3.26	136.23	130.29
38	A1	645	1MA	N9-C4-N3	3.26	134.33	126.90
38	A1	2791	OMG	C6-C5-N7	3.26	136.22	130.29
34	B5	796	A2M	N3-C2-N1	-3.26	123.65	128.58
38	A1	2256	A2M	N3-C2-N1	-3.26	123.65	128.58
38	A1	2256	A2M	C4-C5-N7	-3.25	106.87	110.58
34	B5	1773	4AC	N4-C4-N3	3.24	119.12	113.87
38	A1	2256	A2M	C2'-C1'-N9	-3.24	108.43	113.75
34	B5	420	A2M	N3-C2-N1	-3.22	123.71	128.58
34	B5	28	A2M	N3-C2-N1	-3.20	123.74	128.58
38	A1	2634	UR3	C5-C4-N3	3.20	119.25	115.04
38	A1	2417	OMU	O4-C4-C5	-3.19	119.66	125.16
34	B5	1191	B8N	N3-C2-N1	3.18	120.60	116.72
38	A1	817	A2M	N3-C2-N1	-3.17	123.78	128.58
38	A1	876	A2M	N3-C2-N1	-3.17	123.78	128.58
38	A1	2281	A2M	C4-N9-C8	3.15	109.05	105.74
38	A1	2921	OMU	O4-C4-C5	-3.15	119.73	125.16
38	A1	2922	OMG	C6-C5-N7	3.15	136.01	130.29
38	A1	2281	A2M	C4-C5-N7	-3.13	107.00	110.58
38	A1	2278	5MC	C5-C6-N1	-3.13	119.91	123.31
34	B5	1575	G7M	O3'-C3'-C4'	3.13	120.07	111.08
38	A1	2347	OMU	O4-C4-C5	-3.13	119.77	125.16
34	B5	562	OMG	C6-C5-N7	3.12	135.96	130.29
34	B5	1782	MA6	N1-C2-N3	-3.12	123.87	128.58
38	A1	2729	OMU	O4-C4-C5	-3.10	119.82	125.16
34	B5	100	A2M	N3-C2-N1	-3.10	123.89	128.58
38	A1	2288	OMG	C6-C5-N7	3.10	135.92	130.29
38	A1	898	OMU	O4-C4-C5	-3.09	119.83	125.16
38	A1	2280	A2M	N3-C2-N1	-3.08	123.93	128.58
34	B5	1428	OMG	C6-C5-N7	3.07	135.88	130.29
34	B5	1271	OMG	C6-C5-N7	3.07	135.87	130.29
38	A1	2619	OMG	C6-C5-N7	3.07	135.87	130.29
34	B5	578	OMU	O4-C4-C5	-3.05	119.90	125.16
38	A1	2256	A2M	C4-N9-C8	3.05	108.94	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	1449	A2M	N3-C2-N1	-3.05	123.97	128.58
38	A1	2640	A2M	N3-C2-N1	-3.02	124.00	128.58
38	A1	2421	OMU	O4-C4-C5	-3.00	119.99	125.16
38	A1	2278	5MC	C5-C4-N3	-2.98	118.70	121.75
34	B5	436	A2M	N3-C2-N1	-2.98	124.07	128.58
38	A1	1888	OMU	O4-C4-C5	-2.98	120.02	125.16
38	A1	2724	OMU	O4-C4-C5	-2.98	120.03	125.16
36	AB	243	HIC	NE2-CE1-ND1	-2.96	111.53	112.66
38	A1	807	A2M	N3-C2-N1	-2.95	124.11	128.58
34	B5	1269	OMU	O4-C4-C5	-2.93	120.11	125.16
38	A1	2281	A2M	O4'-C1'-N9	2.88	113.62	108.09
34	B5	974	A2M	C4-N9-C8	2.83	108.71	105.74
38	A1	2347	OMU	C1'-N1-C2	2.83	122.67	117.59
34	B5	974	A2M	C2'-C1'-N9	-2.81	109.13	113.75
34	B5	619	A2M	N3-C2-N1	-2.81	124.33	128.58
34	B5	796	A2M	C4-N9-C8	2.79	108.67	105.74
34	B5	1782	MA6	C4-N9-C8	2.78	108.66	105.74
34	B5	1782	MA6	C5-N7-C8	2.76	107.79	103.45
38	A1	2870	5MC	C5-C4-N3	-2.75	118.93	121.75
38	A1	805	OMG	C4-C5-N7	-2.75	106.31	110.67
38	A1	1133	A2M	C4-N9-C8	2.75	108.62	105.74
38	A1	2280	A2M	C4-N9-C8	2.74	108.62	105.74
34	B5	1575	G7M	O2'-C2'-C1'	2.74	119.53	110.10
38	A1	649	A2M	C4-N9-C8	2.72	108.59	105.74
38	A1	649	A2M	C5-N7-C8	2.72	107.72	103.45
34	B5	796	A2M	C5-N7-C8	2.70	107.69	103.45
34	B5	1781	MA6	C5-N7-C8	2.70	107.69	103.45
34	B5	619	A2M	C4-N9-C8	2.69	108.56	105.74
38	A1	2791	OMG	C4-C5-N7	-2.67	106.44	110.67
34	B5	1572	OMG	C4-C5-N7	-2.67	106.44	110.67
38	A1	867	OMG	C4-C5-N7	-2.65	106.47	110.67
34	B5	1781	MA6	C4-N9-C8	2.65	108.52	105.74
34	B5	562	OMG	C4-C5-N7	-2.63	106.50	110.67
38	A1	807	A2M	C4-N9-C8	2.61	108.48	105.74
38	A1	2946	A2M	C4-N9-C8	2.61	108.48	105.74
38	A1	2815	OMG	C4-C5-N7	-2.61	106.53	110.67
34	B5	1126	OMG	C4-C5-N7	-2.59	106.56	110.67
38	A1	908	OMG	C6-C5-N7	2.59	135.00	130.29
34	B5	28	A2M	C4-N9-C8	2.59	108.45	105.74
34	B5	619	A2M	C5-N7-C8	2.58	107.51	103.45
38	A1	2280	A2M	C5-N7-C8	2.58	107.51	103.45
34	B5	100	A2M	C4-N9-C8	2.58	108.45	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	974	A2M	C5-N7-C8	2.57	107.49	103.45
34	B5	28	A2M	C5-N7-C8	2.57	107.49	103.45
38	A1	1450	OMG	C4-C5-N7	-2.56	106.61	110.67
38	A1	2946	A2M	C5-N7-C8	2.54	107.45	103.45
34	B5	1575	G7M	O6-C6-C5	-2.54	122.34	128.01
38	A1	2256	A2M	C5-N7-C8	2.54	107.44	103.45
34	B5	420	A2M	C5-N7-C8	2.53	107.43	103.45
38	A1	2288	OMG	C4-C5-N7	-2.53	106.66	110.67
34	B5	420	A2M	C4-N9-C8	2.53	108.39	105.74
34	B5	436	A2M	C2'-C1'-N9	-2.52	109.60	113.75
38	A1	645	1MA	C4-C5-N7	-2.52	106.68	110.67
38	A1	2640	A2M	C5-N7-C8	2.52	107.41	103.45
38	A1	2922	OMG	C4-C5-N7	-2.51	106.69	110.67
34	B5	541	A2M	C5-N7-C8	2.51	107.39	103.45
38	A1	2417	OMU	O2-C2-N1	-2.50	119.54	122.80
38	A1	2793	OMG	C4-C5-N7	-2.50	106.71	110.67
34	B5	1271	OMG	C4-C5-N7	-2.50	106.71	110.67
38	A1	1449	A2M	C5-N7-C8	2.48	107.36	103.45
34	B5	1269	OMU	C1'-N1-C2	2.48	122.05	117.59
34	B5	100	A2M	C5-N7-C8	2.48	107.35	103.45
38	A1	2640	A2M	C4-N9-C8	2.44	108.30	105.74
38	A1	876	A2M	C5-N7-C8	2.43	107.28	103.45
38	A1	817	A2M	C4-N9-C8	2.43	108.29	105.74
34	B5	619	A2M	C2'-C1'-N9	-2.43	109.75	113.75
34	B5	1781	MA6	N1-C6-N6	2.43	119.82	116.86
38	A1	2619	OMG	C4-C5-N7	-2.43	106.82	110.67
34	B5	1428	OMG	C4-C5-N7	-2.43	106.83	110.67
38	A1	817	A2M	C5-N7-C8	2.42	107.26	103.45
38	A1	807	A2M	C5-N7-C8	2.42	107.25	103.45
38	A1	807	A2M	O4'-C1'-N9	2.41	112.73	108.09
38	A1	1449	A2M	C4-N9-C8	2.41	108.27	105.74
38	A1	876	A2M	C4-N9-C8	2.40	108.26	105.74
38	A1	1133	A2M	C5-N7-C8	2.39	107.21	103.45
34	B5	1191	B8N	C31-N3-C2	2.39	121.16	117.64
34	B5	436	A2M	C5-N7-C8	2.39	107.20	103.45
38	A1	2281	A2M	C5-N7-C8	2.37	107.18	103.45
38	A1	2281	A2M	C2'-C1'-N9	-2.37	109.85	113.75
34	B5	1773	4AC	C1'-N1-C2	2.37	123.67	118.44
34	B5	1575	G7M	C3'-C2'-C1'	2.37	105.94	101.46
34	B5	1575	G7M	C2'-C1'-N9	2.36	119.81	113.25
38	A1	2421	OMU	O2-C2-N1	-2.36	119.73	122.80
38	A1	1437	OMC	C1'-N1-C2	2.35	123.62	118.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	908	OMG	O6-C6-C5	-2.34	120.36	126.53
38	A1	645	1MA	C6-C5-N7	2.32	136.25	132.16
38	A1	649	A2M	C6-C5-N7	2.29	136.50	132.09
38	A1	908	OMG	C4-C5-N7	-2.28	107.05	110.67
38	A1	2278	5MC	O2-C2-N3	-2.27	118.75	122.33
80	DC	699	DDE	CAU-CBW-CBI	-2.27	106.78	111.22
38	A1	1437	OMC	O2-C2-N3	-2.27	118.76	122.33
38	A1	2281	A2M	N9-C8-N7	-2.23	110.77	113.94
38	A1	2724	OMU	C1'-N1-C2	2.23	121.60	117.59
38	A1	2220	A2M	C5-N7-C8	2.22	106.94	103.45
34	B5	1126	OMG	O6-C6-C5	-2.22	120.67	126.53
38	A1	2948	OMC	O2-C2-N3	-2.22	118.83	122.33
34	B5	1191	B8N	O4'-C1'-C2'	2.21	108.21	105.15
34	B5	436	A2M	C4-N9-C8	2.21	108.06	105.74
38	A1	898	OMU	O2-C2-N1	-2.18	119.95	122.80
34	B5	1428	OMG	O6-C6-C5	-2.18	120.78	126.53
34	B5	1280	4AC	C6-C5-C4	2.18	119.62	117.00
38	A1	649	A2M	N9-C8-N7	-2.18	110.85	113.94
38	A1	2946	A2M	C6-C5-N7	2.17	136.28	132.09
38	A1	1450	OMG	O6-C6-C5	-2.16	120.83	126.53
38	A1	2280	A2M	C6-C5-N7	2.16	136.25	132.09
34	B5	1575	G7M	C1'-N9-C8	-2.15	119.46	126.74
38	A1	2256	A2M	N9-C8-N7	-2.15	110.88	113.94
34	B5	1271	OMG	O6-C6-C5	-2.15	120.85	126.53
34	B5	28	A2M	C2'-C1'-N9	-2.15	110.21	113.75
34	B5	1773	4AC	O2-C2-N3	-2.15	118.94	122.33
34	B5	541	A2M	C4-N9-C8	2.15	107.99	105.74
38	A1	867	OMG	O6-C6-C5	-2.15	120.86	126.53
34	B5	420	A2M	C6-C5-N7	2.15	136.23	132.09
34	B5	796	A2M	N9-C8-N7	-2.14	110.90	113.94
34	B5	1191	B8N	C31-N3-C4	2.14	120.21	117.18
38	A1	2634	UR3	C6-N1-C2	-2.14	120.05	121.80
34	B5	578	OMU	O2-C2-N1	-2.14	120.02	122.80
38	A1	2220	A2M	C4-N9-C8	2.13	107.98	105.74
38	A1	2281	A2M	C6-C5-N7	2.13	136.20	132.09
38	A1	805	OMG	C2'-C1'-N9	-2.13	110.20	114.24
34	B5	1782	MA6	N9-C8-N7	-2.13	110.92	113.94
34	B5	28	A2M	C6-C5-N7	2.12	136.19	132.09
34	B5	974	A2M	N9-C8-N7	-2.12	110.92	113.94
38	A1	2793	OMG	O6-C6-C5	-2.12	120.94	126.53
38	A1	2922	OMG	O6-C6-C5	-2.12	120.94	126.53
38	A1	2870	5MC	O2-C2-N3	-2.12	118.99	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	1888	OMU	O2-C2-N1	-2.12	120.04	122.80
38	A1	2142	1MA	C4-C5-N7	-2.12	107.32	110.67
34	B5	1782	MA6	C6-C5-N7	2.12	136.81	133.43
34	B5	1781	MA6	C6-C5-N7	2.11	136.80	133.43
38	A1	2815	OMG	O6-C6-C5	-2.11	120.96	126.53
34	B5	1572	OMG	O6-C6-C5	-2.11	120.96	126.53
34	B5	974	A2M	C6-C5-N7	2.10	136.15	132.09
38	A1	2619	OMG	O6-C6-C5	-2.09	121.02	126.53
34	B5	1782	MA6	N1-C6-N6	2.08	119.39	116.86
34	B5	796	A2M	C6-C5-N7	2.08	136.09	132.09
38	A1	1133	A2M	C6-C5-N7	2.07	136.08	132.09
38	A1	2220	A2M	C2-N1-C6	2.06	122.12	118.73
38	A1	2142	1MA	N1-C2-N3	-2.04	123.57	126.00
38	A1	2280	A2M	N9-C8-N7	-2.04	111.05	113.94
34	B5	619	A2M	N9-C8-N7	-2.04	111.05	113.94
38	A1	817	A2M	C6-C5-N7	2.04	136.01	132.09
38	A1	807	A2M	C6-C5-N7	2.03	136.01	132.09
38	A1	2815	OMG	C5-C6-N1	2.03	118.42	113.25
34	B5	28	A2M	N9-C8-N7	-2.03	111.06	113.94
34	B5	1781	MA6	N9-C8-N7	-2.02	111.07	113.94
36	AB	243	HIC	CB-CG-CD2	-2.02	125.09	129.96
38	A1	2634	UR3	C3U-N3-C2	2.01	120.84	117.33
38	A1	2220	A2M	C6-C5-N7	2.01	135.97	132.09
38	A1	2921	OMU	O2-C2-N1	-2.01	120.18	122.80
38	A1	2946	A2M	N9-C8-N7	-2.01	111.09	113.94

There are no chirality outliers.

All (101) 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	562	OMG	C1'-C2'-O2'-CM2
34	B5	974	A2M	C1'-C2'-O2'-CM'
34	B5	1271	OMG	C1'-C2'-O2'-CM2
34	B5	1428	OMG	O4'-C4'-C5'-O5'
34	B5	1428	OMG	C1'-C2'-O2'-CM2
34	B5	1639	OMC	C1'-C2'-O2'-CM2
34	B5	1781	MA6	C5-C6-N6-C9
34	B5	1782	MA6	C5-C6-N6-C9
80	DC	699	DDE	CAT-CAU-CBW-NCB
34	B5	1280	4AC	N3-C4-N4-C7

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Mol	Chain	Res	Type	Atoms
34	B5	1280	4AC	C5-C4-N4-C7
34	B5	1773	4AC	O4'-C4'-C5'-O5'
34	B5	1773	4AC	N3-C4-N4-C7
34	B5	1773	4AC	C5-C4-N4-C7
34	B5	1773	4AC	O7-C7-N4-C4
34	B5	1773	4AC	CM7-C7-N4-C4
38	A1	649	A2M	C1'-C2'-O2'-CM'
38	A1	663	OMC	C1'-C2'-O2'-CM2
38	A1	867	OMG	C1'-C2'-O2'-CM2
38	A1	876	A2M	C1'-C2'-O2'-CM'
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	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	2640	A2M	C1'-C2'-O2'-CM'
38	A1	2724	OMU	C1'-C2'-O2'-CM2
38	A1	2729	OMU	C1'-C2'-O2'-CM2
38	A1	2729	OMU	O4'-C4'-C5'-O5'
38	A1	2791	OMG	C1'-C2'-O2'-CM2
34	B5	1191	B8N	C32-C31-N3-C4
34	B5	1782	MA6	O4'-C4'-C5'-O5'
34	B5	1773	4AC	C3'-C4'-C5'-O5'
38	A1	2197	OMC	O4'-C4'-C5'-O5'
38	A1	2729	OMU	C3'-C4'-C5'-O5'
34	B5	1191	B8N	C32-C31-N3-C2
80	DC	699	DDE	CAT-CAU-CBW-CBI
34	B5	541	A2M	O4'-C4'-C5'-O5'
34	B5	1428	OMG	C3'-C4'-C5'-O5'
38	A1	1437	OMC	O4'-C4'-C5'-O5'
38	A1	2197	OMC	C3'-C4'-C5'-O5'
34	B5	541	A2M	C3'-C4'-C5'-O5'
80	DC	699	DDE	CE1-CAT-CAU-CBW
34	B5	619	A2M	O4'-C4'-C5'-O5'
34	B5	619	A2M	C3'-C4'-C5'-O5'
34	B5	1191	B8N	N34-C33-C34-O36
34	B5	1782	MA6	N1-C6-N6-C9
34	B5	1782	MA6	C3'-C4'-C5'-O5'
38	A1	1437	OMC	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
38	A1	2870	5MC	C2'-C1'-N1-C6
38	A1	2281	A2M	O4'-C4'-C5'-O5'
34	B5	1572	OMG	O4'-C4'-C5'-O5'
34	B5	1781	MA6	N1-C6-N6-C9
38	A1	2281	A2M	C3'-C4'-C5'-O5'
34	B5	1191	B8N	N34-C33-C34-O35
34	B5	436	A2M	C1'-C2'-O2'-CM'
38	A1	1450	OMG	C1'-C2'-O2'-CM2
38	A1	2256	A2M	C4'-C5'-O5'-P
38	A1	2870	5MC	O4'-C1'-N1-C6
34	B5	1269	OMU	O4'-C1'-N1-C6
34	B5	1126	OMG	C3'-C4'-C5'-O5'
34	B5	1428	OMG	C4'-C5'-O5'-P
34	B5	541	A2M	C2'-C1'-N9-C4
80	DC	699	DDE	OAG-CBI-CBW-NCB
38	A1	817	A2M	C4'-C5'-O5'-P
34	B5	541	A2M	C2'-C1'-N9-C8
80	DC	699	DDE	OAG-CBI-CBW-CAU
34	B5	541	A2M	C4'-C5'-O5'-P
34	B5	1191	B8N	O4'-C1'-C5-C4
34	B5	1126	OMG	C4'-C5'-O5'-P
34	B5	1269	OMU	O4'-C1'-N1-C2
38	A1	2870	5MC	O4'-C1'-N1-C2
38	A1	645	1MA	C2'-C1'-N9-C8
38	A1	2197	OMC	O4'-C1'-N1-C6
38	A1	2870	5MC	C2'-C1'-N1-C2
80	DC	699	DDE	CA-CB-CG-ND1
38	A1	645	1MA	C2'-C1'-N9-C4
34	B5	1269	OMU	C4'-C5'-O5'-P
80	DC	699	DDE	CA-CB-CG-CD2
38	A1	2946	A2M	C1'-C2'-O2'-CM'
38	A1	807	A2M	C3'-C4'-C5'-O5'
34	B5	1191	B8N	O4'-C1'-C5-C6
34	B5	1007	OMC	C3'-C2'-O2'-CM2
34	B5	1572	OMG	C3'-C2'-O2'-CM2
34	B5	541	A2M	O4'-C1'-N9-C8
34	B5	1781	MA6	C5-C6-N6-C10
34	B5	1782	MA6	C5-C6-N6-C10
80	DC	699	DDE	NAD-CBI-CBW-CAU
34	B5	1269	OMU	O4'-C4'-C5'-O5'
38	A1	817	A2M	O4'-C4'-C5'-O5'
38	A1	2729	OMU	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
34	B5	1773	4AC	C2'-C1'-N1-C2
38	A1	1437	OMC	C2'-C1'-N1-C2
34	B5	619	A2M	C2'-C1'-N9-C8
34	B5	1269	OMU	C2'-C1'-N1-C2
38	A1	2197	OMC	O4'-C1'-N1-C2

There are no ring outliers.

35 monomers are involved in 54 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2220	A2M	3	0
38	A1	2793	OMG	1	0
34	B5	974	A2M	1	0
38	A1	1449	A2M	2	0
38	A1	650	OMC	3	0
34	B5	1428	OMG	1	0
34	B5	100	A2M	1	0
34	B5	1271	OMG	1	0
34	B5	1572	OMG	1	0
38	A1	867	OMG	1	0
38	A1	2197	OMC	2	0
34	B5	619	A2M	1	0
38	A1	663	OMC	1	0
34	B5	436	A2M	1	0
34	B5	796	A2M	1	0
38	A1	2347	OMU	1	0
34	B5	1773	4AC	4	0
38	A1	2724	OMU	1	0
34	B5	28	A2M	1	0
34	B5	1575	G7M	4	0
80	DC	699	DDE	1	0
38	A1	1133	A2M	1	0
38	A1	2256	A2M	7	0
38	A1	817	A2M	1	0
34	B5	1781	MA6	1	0
38	A1	898	OMU	1	0
34	B5	1126	OMG	1	0
38	A1	649	A2M	3	0
38	A1	876	A2M	1	0
38	A1	2417	OMU	1	0
34	B5	1269	OMU	2	0
38	A1	2281	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	B5	1280	4AC	2	0
38	A1	2640	A2M	1	0
38	A1	1450	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 244 ligands modelled in this entry, 243 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
85	GDP	DC	901	-	29,30,30	1.12	3 (10%)	45,47,47	1.92	9 (20%)

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
85	GDP	DC	901	-	-	5/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	DC	901	GDP	C5-C4	3.06	1.47	1.38
85	DC	901	GDP	C6-N1	-2.14	1.34	1.38
85	DC	901	GDP	C5-N7	-2.13	1.34	1.39

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	DC	901	GDP	C5-C4-N3	-6.76	117.63	128.39
85	DC	901	GDP	C2-N3-C4	5.33	121.48	112.30
85	DC	901	GDP	N9-C4-N3	4.78	135.52	125.95
85	DC	901	GDP	C6-C5-N7	3.20	136.11	130.29
85	DC	901	GDP	C2-N1-C6	-2.89	119.86	125.11
85	DC	901	GDP	C4-C5-N7	-2.83	106.19	110.67
85	DC	901	GDP	O6-C6-C5	-2.59	119.70	126.53
85	DC	901	GDP	C3'-C2'-C1'	2.46	106.11	101.46
85	DC	901	GDP	C5-C6-N1	2.34	119.21	113.25

There are no chirality outliers.

All (5) torsion outliers are listed below:

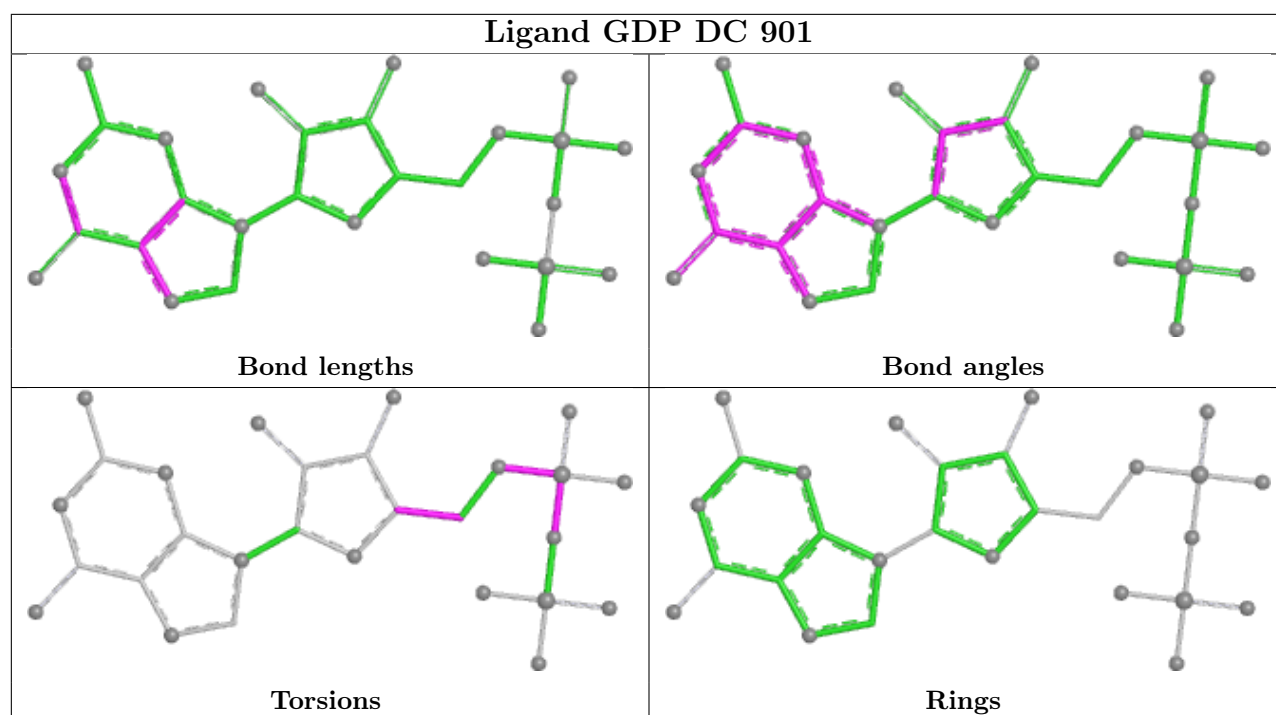
Mol	Chain	Res	Type	Atoms
85	DC	901	GDP	C5'-O5'-PA-O3A
85	DC	901	GDP	C5'-O5'-PA-O2A
85	DC	901	GDP	O4'-C4'-C5'-O5'
85	DC	901	GDP	C3'-C4'-C5'-O5'
85	DC	901	GDP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	DC	901	GDP	7	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

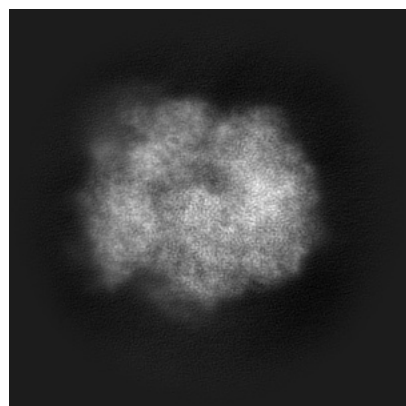
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28642. These allow visual inspection of the internal detail of the map and identification of artifacts.

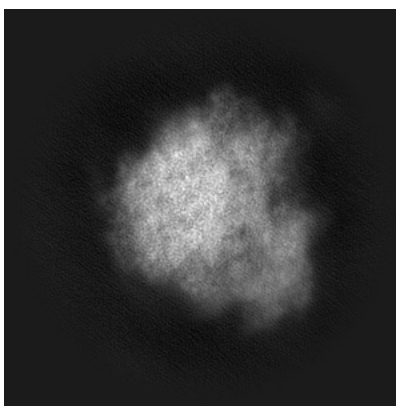
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

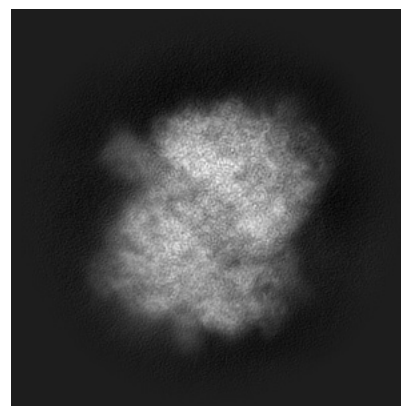
6.1.1 Primary map



X

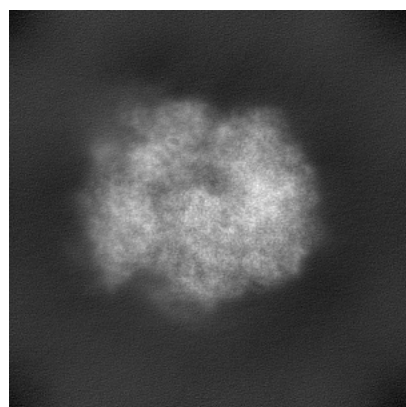


Y

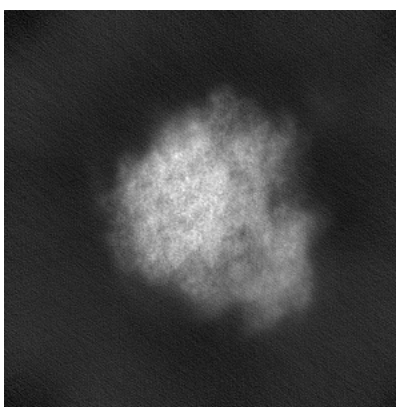


Z

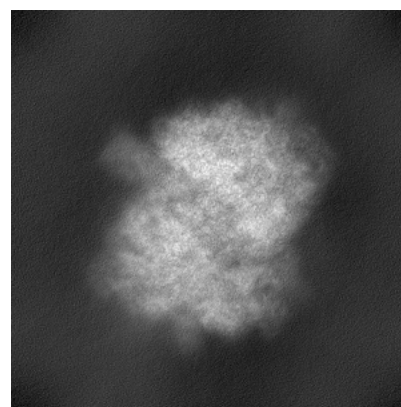
6.1.2 Raw map



X



Y

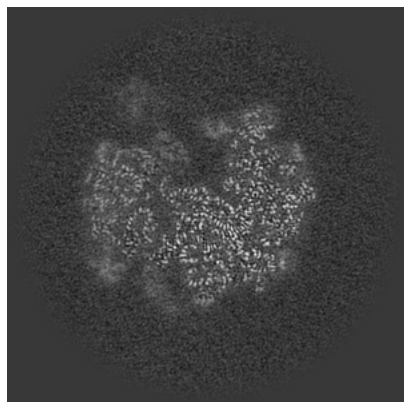


Z

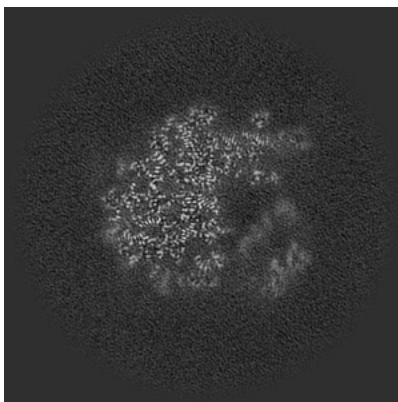
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

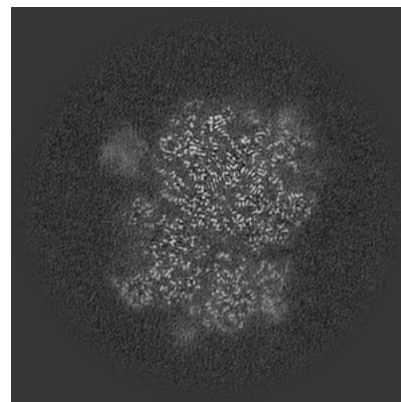
6.2.1 Primary map



X Index: 200

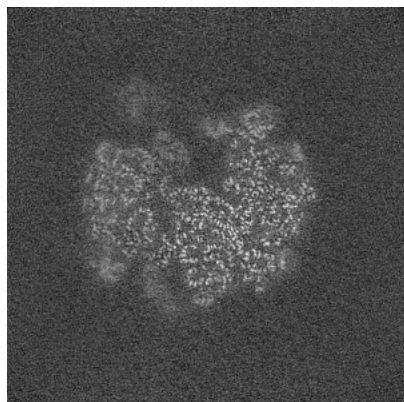


Y Index: 200

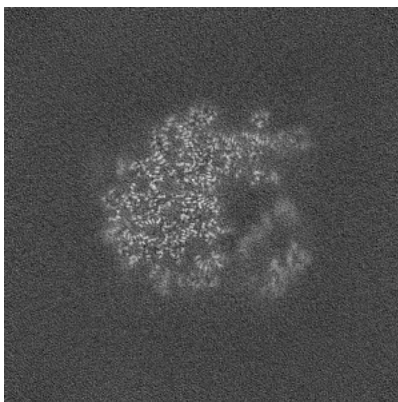


Z Index: 200

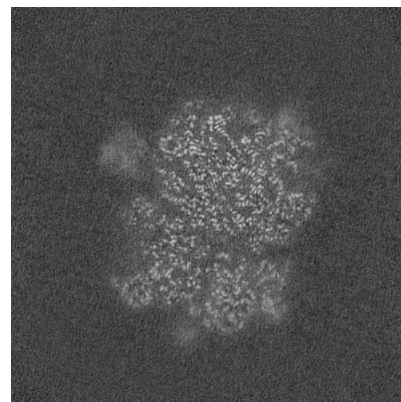
6.2.2 Raw map



X Index: 200



Y Index: 200

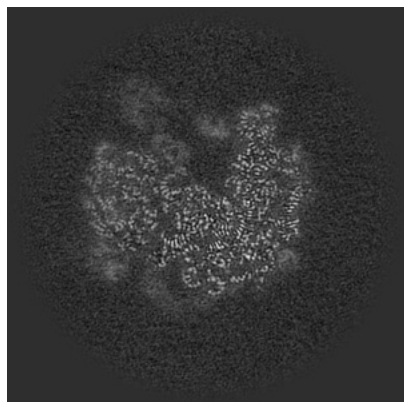


Z Index: 200

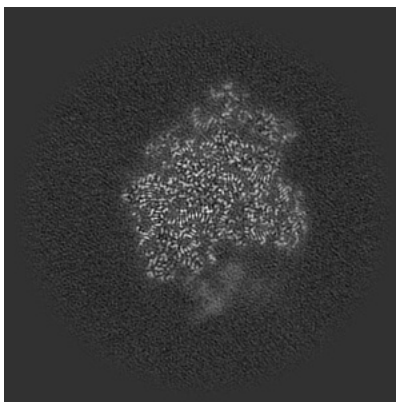
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

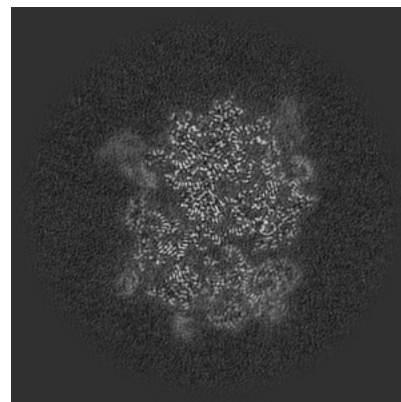
6.3.1 Primary map



X Index: 197

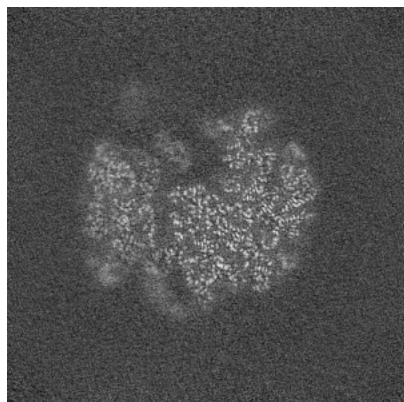


Y Index: 245

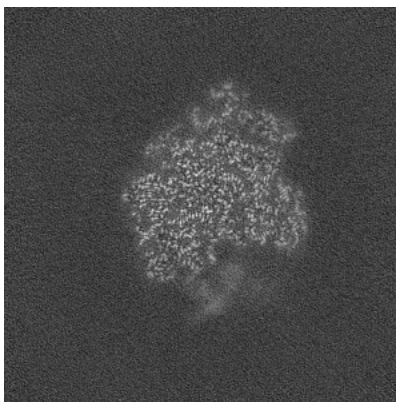


Z Index: 190

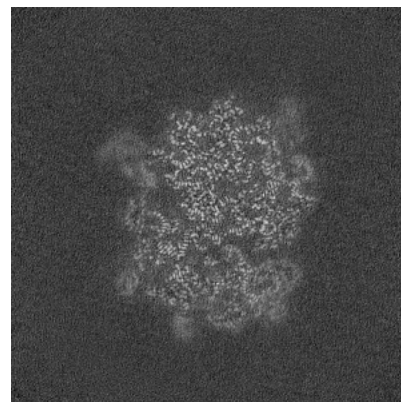
6.3.2 Raw map



X Index: 204



Y Index: 245

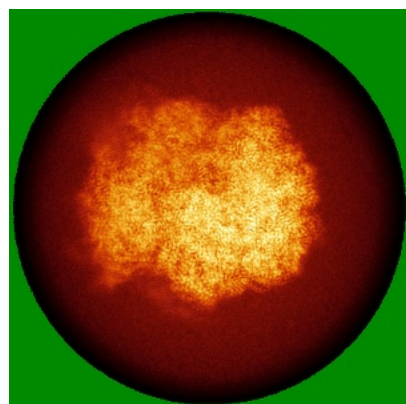


Z Index: 190

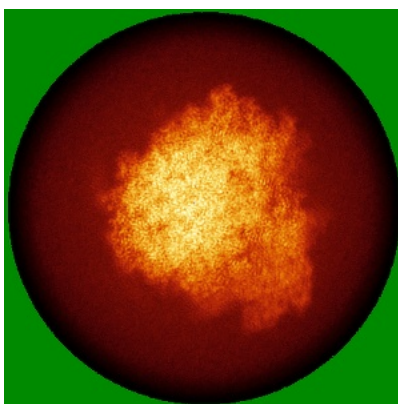
The images above show the largest variance slices of the map in three orthogonal directions.

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

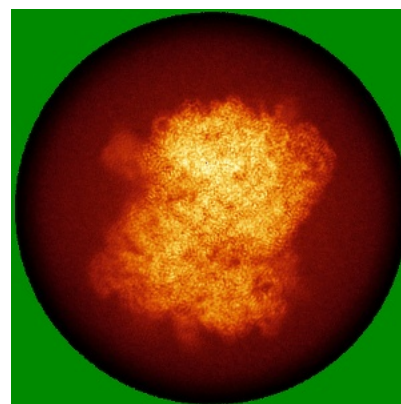
6.4.1 Primary map



X

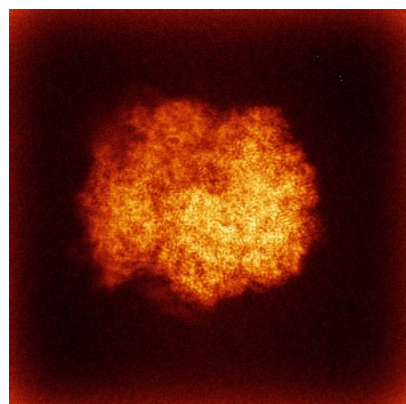


Y

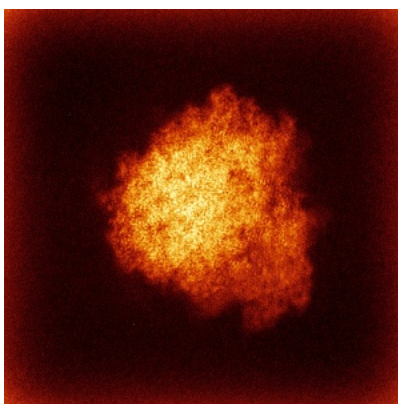


Z

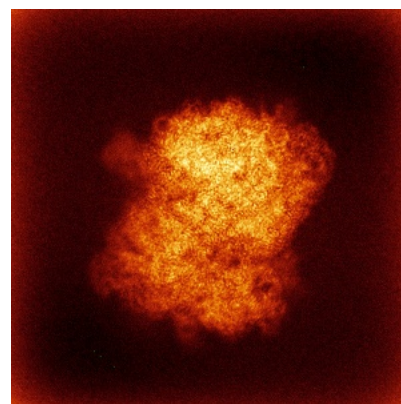
6.4.2 Raw map



X



Y

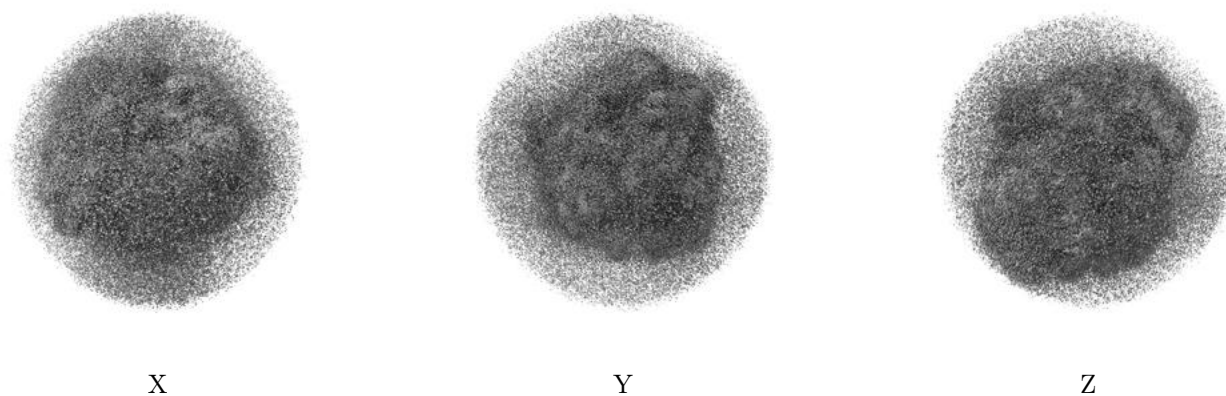


Z

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

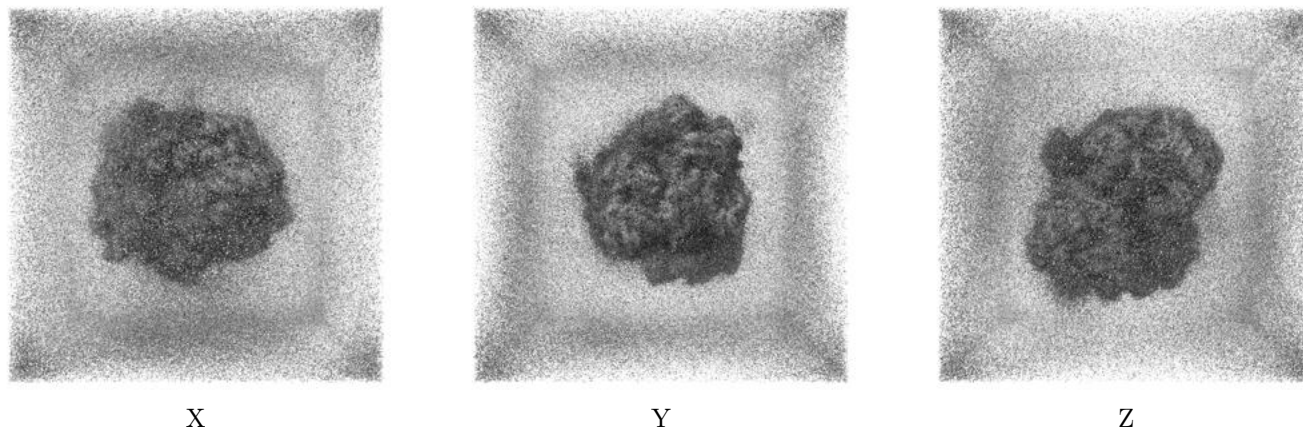
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

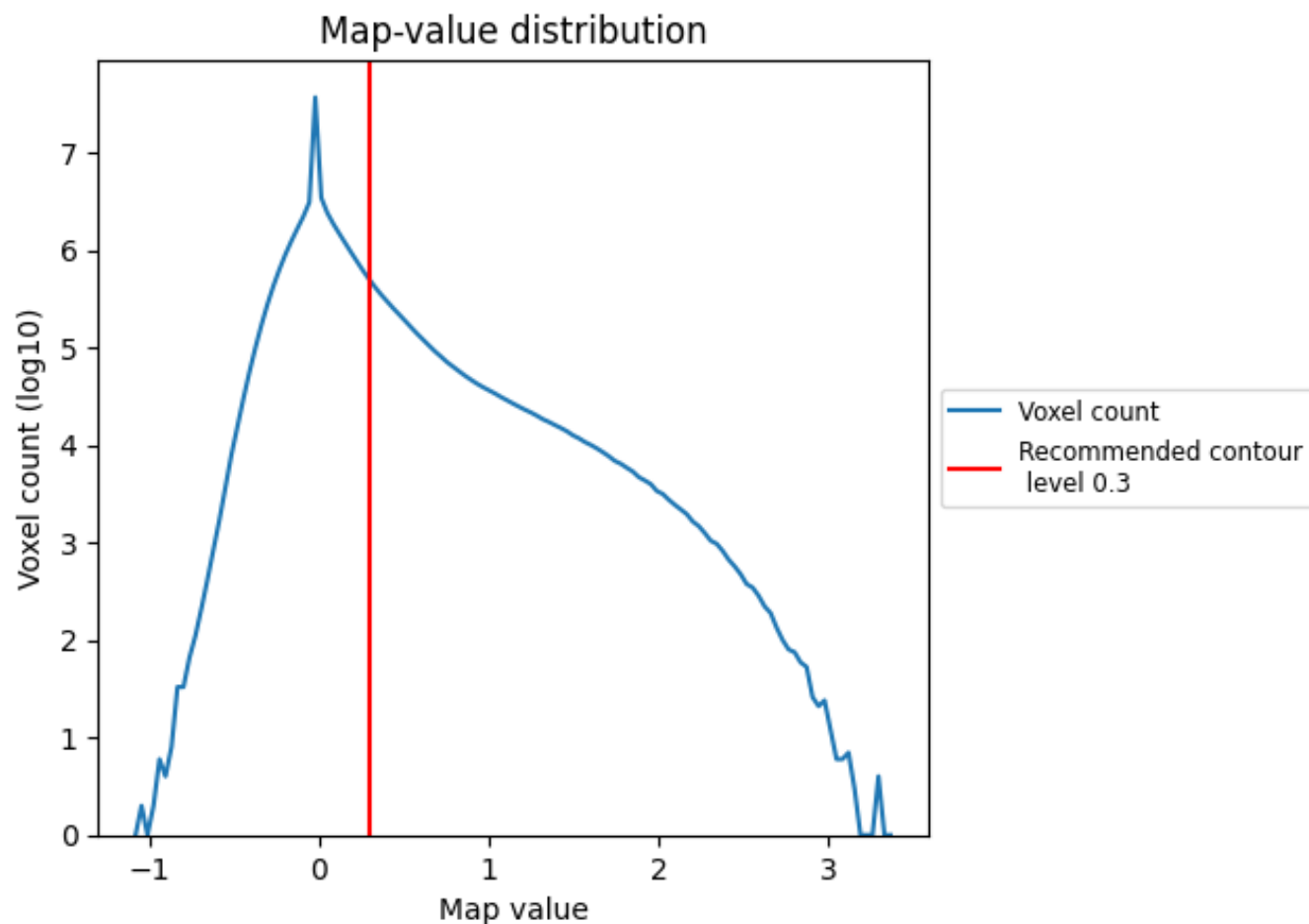
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

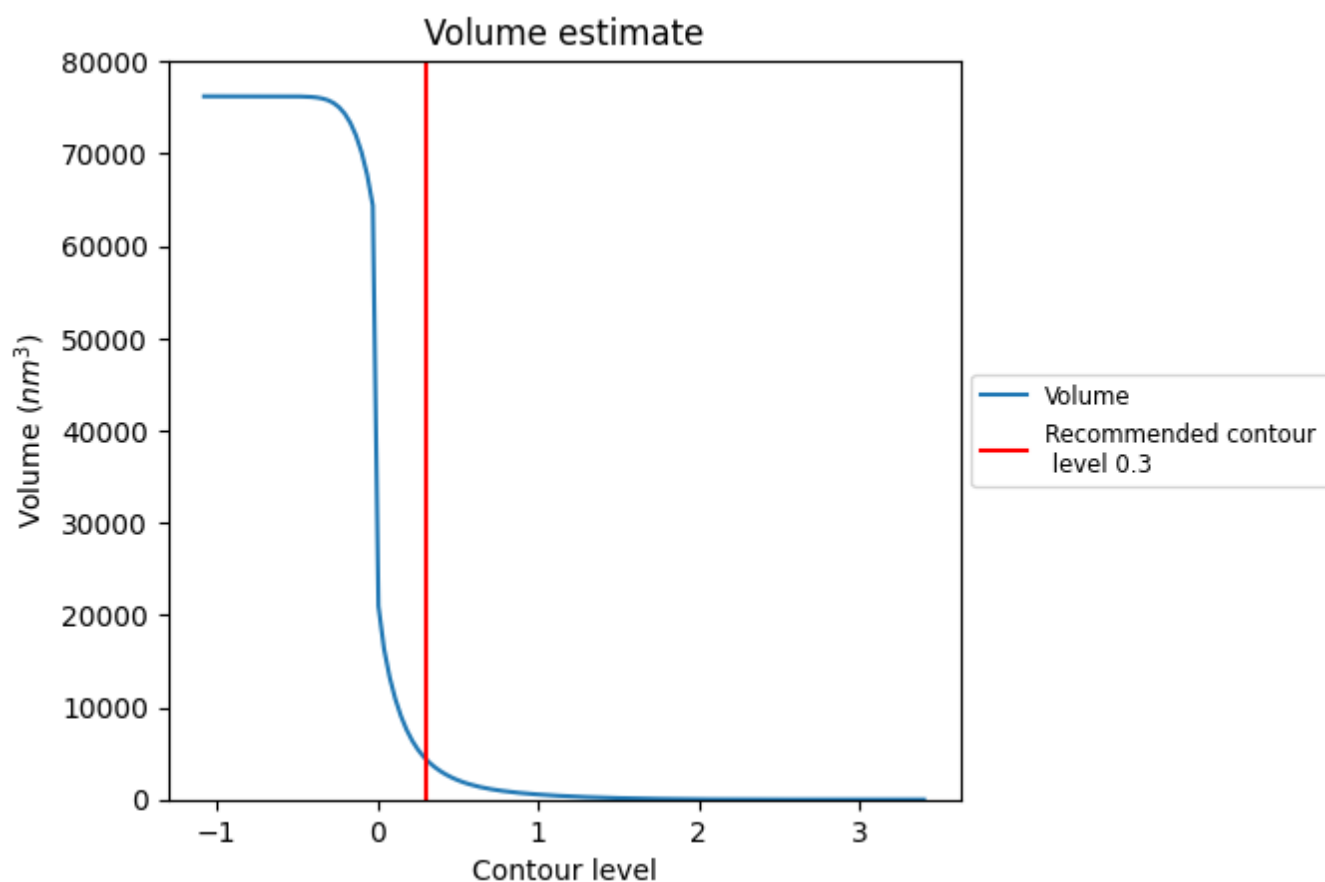
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

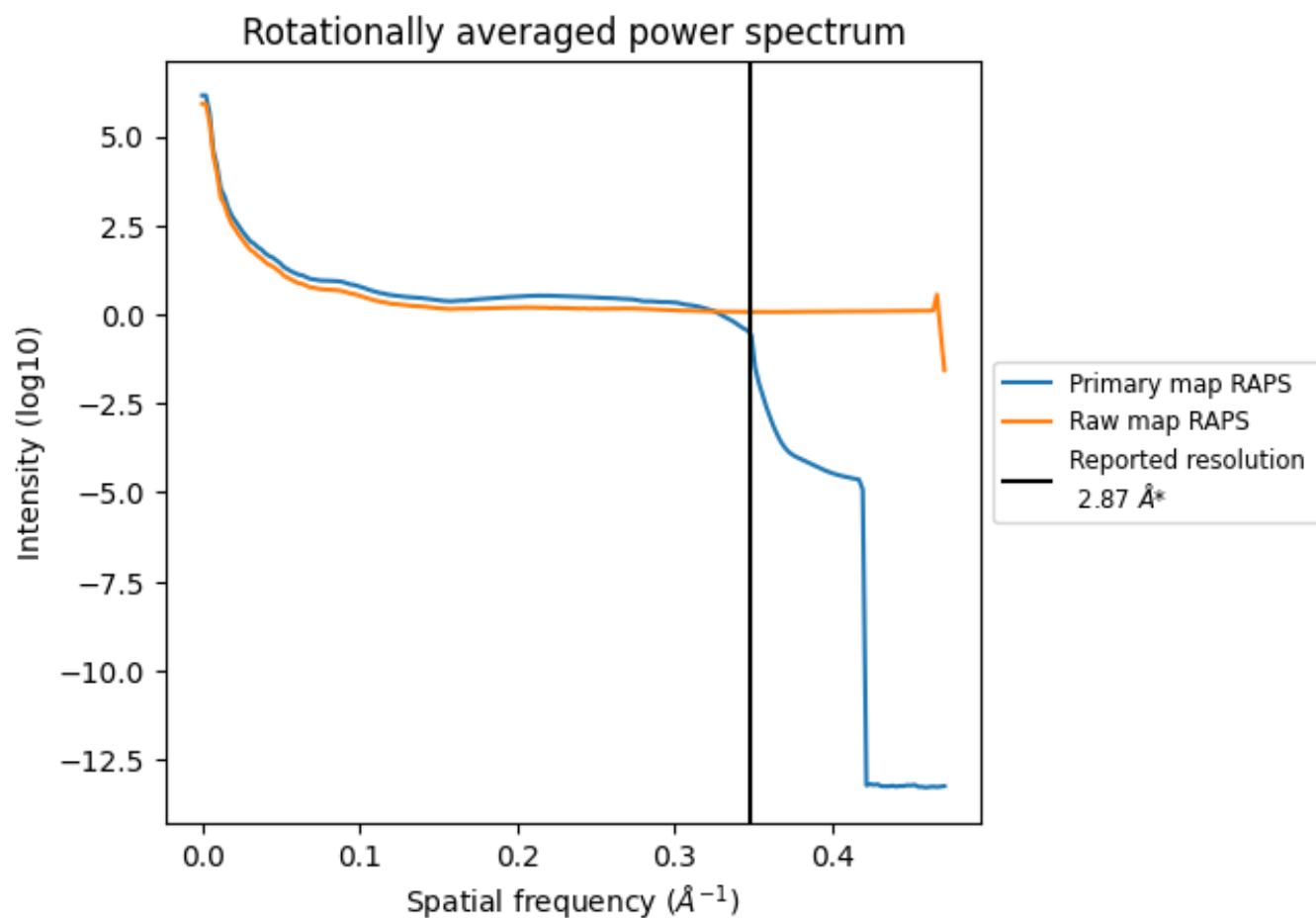
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4390 nm^3 ; this corresponds to an approximate mass of 3966 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 ⓘ

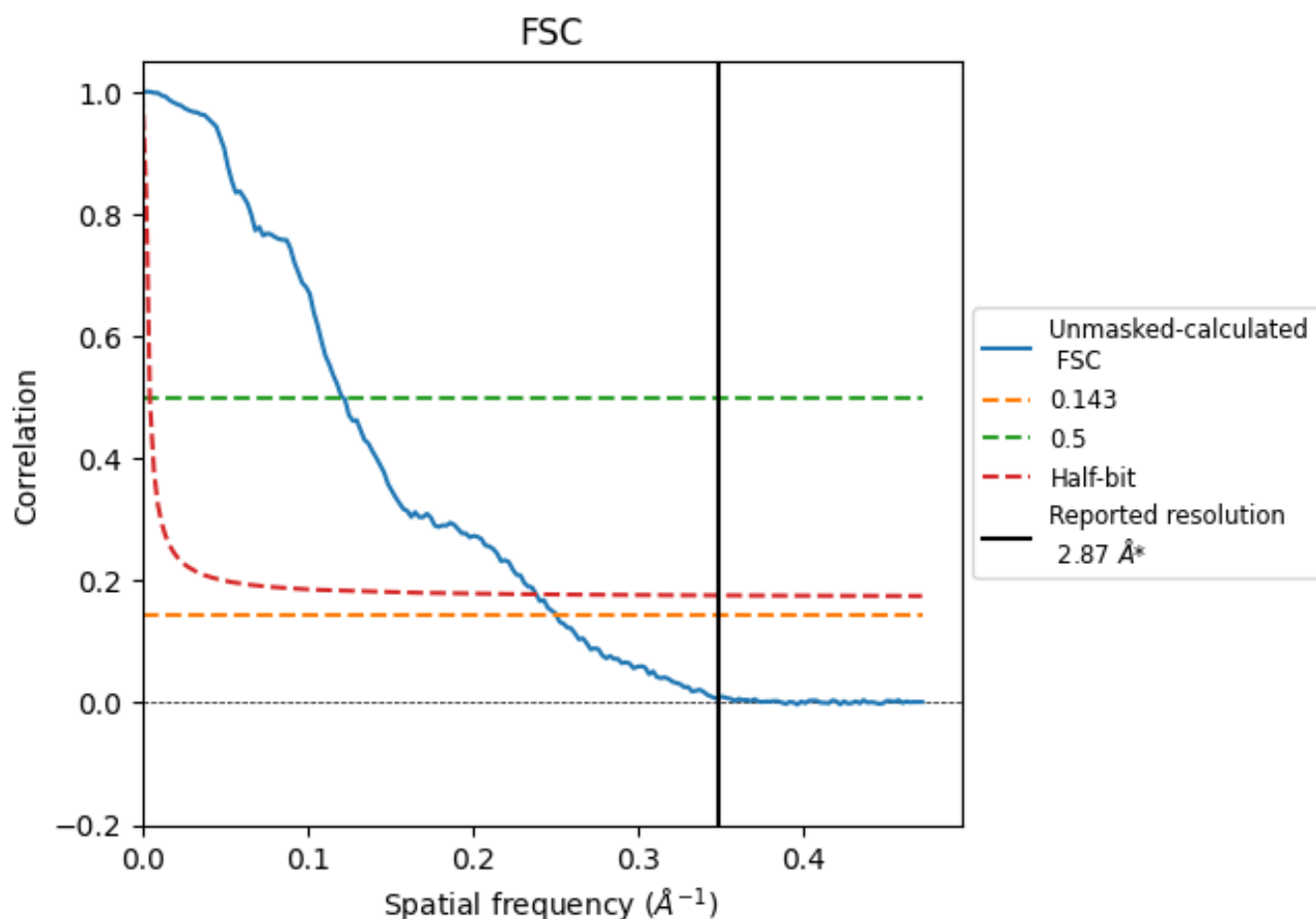


*Reported resolution corresponds to spatial frequency of 0.348 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.348 Å⁻¹

8.2 Resolution estimates [i](#)

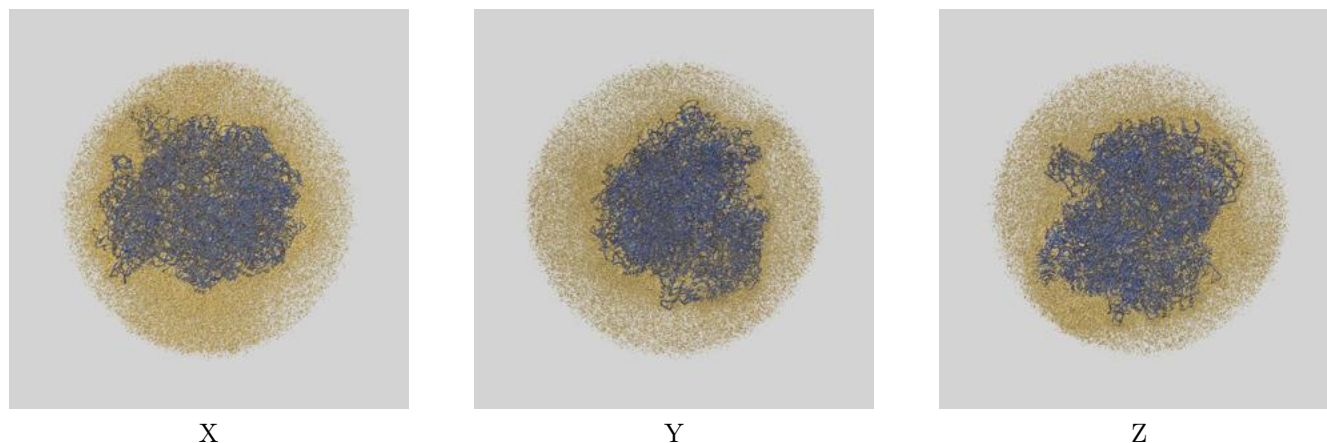
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.87	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.99	8.25	4.20

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 2.87 by more than 10 %

9 Map-model fit [i](#)

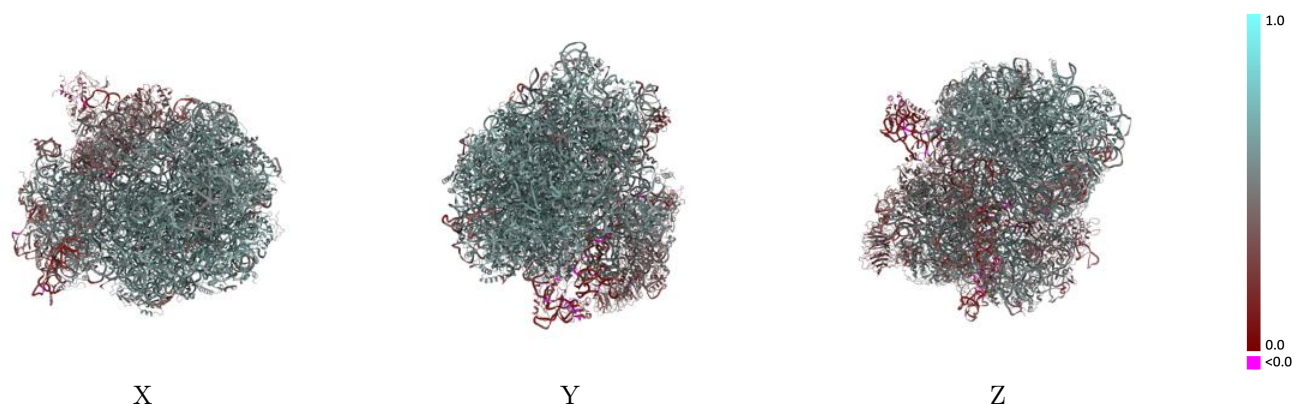
This section contains information regarding the fit between EMDB map EMD-28642 and PDB model 8EWB. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



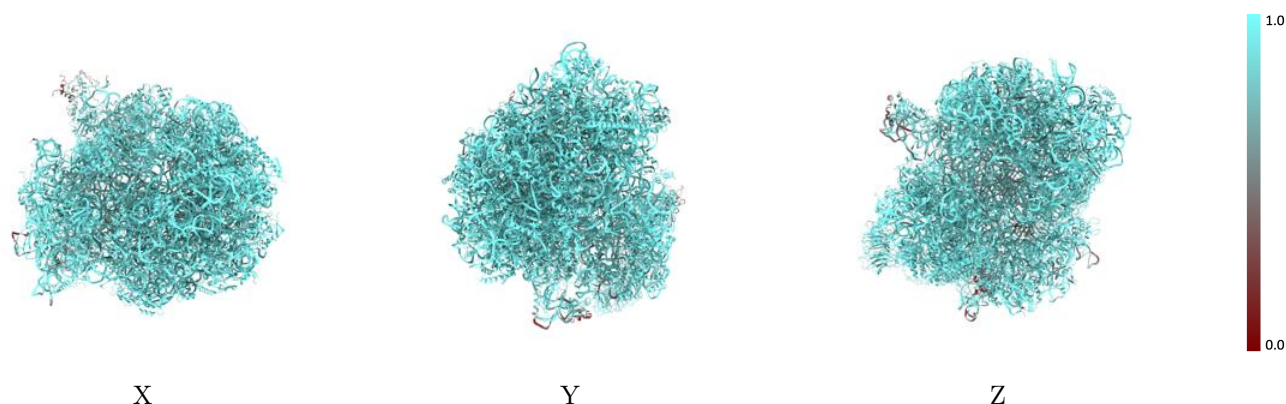
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



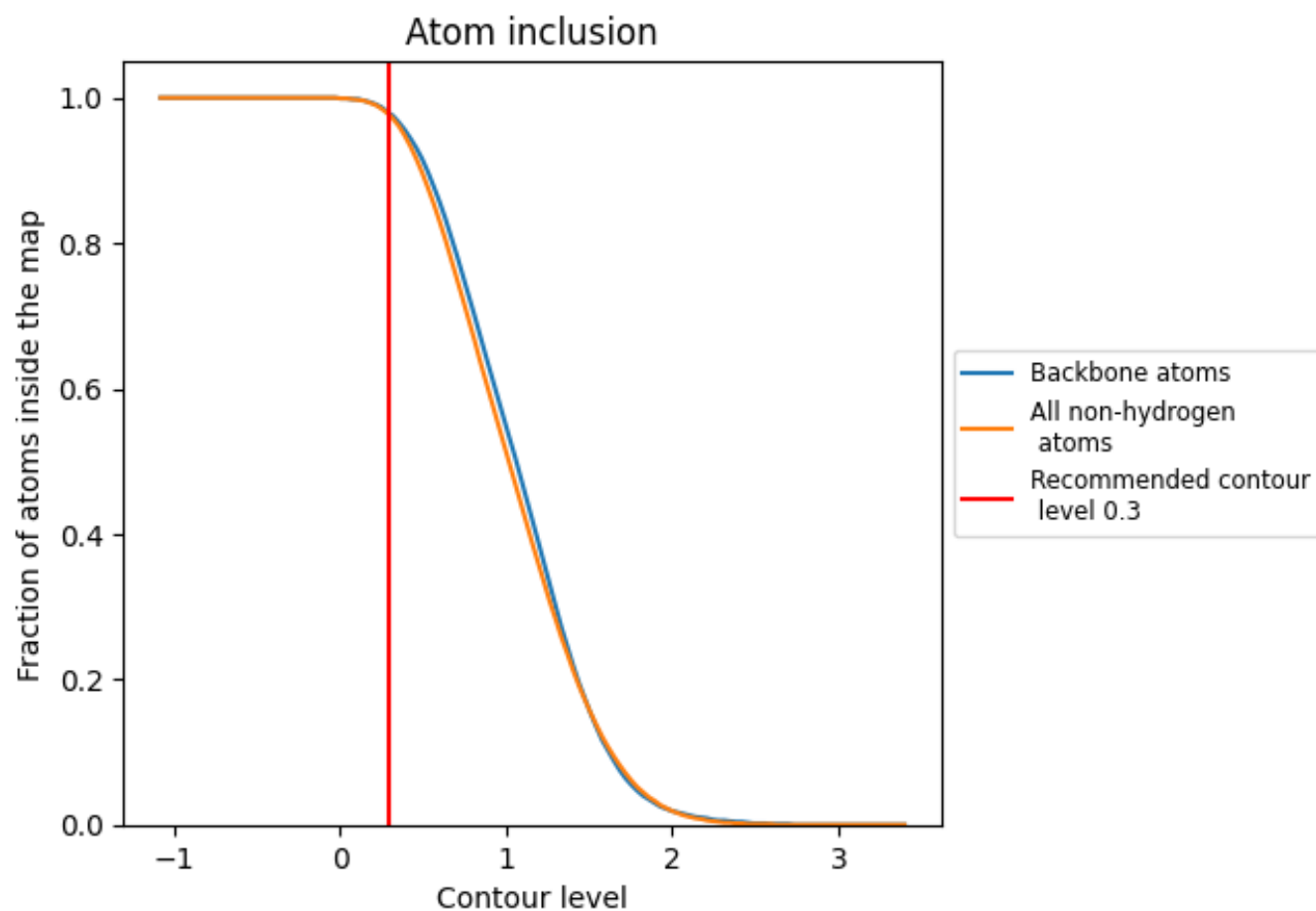
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion ⓘ



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

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9760	 0.5150
A1	 0.9920	 0.5620
A3	 1.0000	 0.5630
A4	 0.9980	 0.5870
AA	 0.9950	 0.6070
AB	 0.9970	 0.5820
AC	 0.9970	 0.5840
AD	 0.9880	 0.5280
AE	 0.9910	 0.5430
AF	 0.9970	 0.5790
AG	 0.9900	 0.5540
AH	 0.9820	 0.5450
AI	 0.9900	 0.5510
AJ	 0.9610	 0.4650
AL	 0.9950	 0.5750
AM	 0.9950	 0.5580
AN	 0.9990	 0.6090
AO	 0.9970	 0.5820
AP	 0.9940	 0.5880
AQ	 1.0000	 0.5980
AR	 0.9600	 0.5420
AS	 0.9960	 0.5690
AT	 0.9910	 0.5660
AU	 0.9830	 0.5190
AV	 0.9930	 0.5790
AW	 0.9960	 0.5880
AX	 0.9930	 0.5770
AY	 0.9950	 0.5920
AZ	 0.9950	 0.5670
Aa	 0.9980	 0.5990
Ab	 0.9890	 0.5470
Ac	 0.9890	 0.5710
Ad	 0.9720	 0.5610
Ae	 1.0000	 0.5990
Af	 0.9960	 0.5950



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Chain	Atom inclusion	Q-score
Ag	 0.9920	 0.5810
Ah	 0.9930	 0.5690
Ai	 0.9870	 0.5490
Aj	 0.9970	 0.6070
Ak	 0.9730	 0.5240
Al	 0.9980	 0.5900
Am	 0.9800	 0.5570
An	 0.9670	 0.5270
Ao	 0.9860	 0.5640
Ap	 0.9930	 0.5890
B5	 0.9760	 0.4790
BA	 0.9910	 0.5170
BB	 0.9850	 0.5300
BC	 0.9930	 0.5430
BD	 0.9730	 0.4230
BE	 0.9920	 0.5250
BF	 0.9690	 0.4220
BG	 0.9860	 0.4420
BH	 0.9680	 0.4740
BI	 0.9850	 0.5470
BJ	 0.9810	 0.5130
BK	 0.9390	 0.3340
BL	 0.9570	 0.5380
BM	 0.4890	 0.2250
BN	 0.9940	 0.5540
BO	 0.9910	 0.5420
BP	 0.8730	 0.3310
BQ	 0.9880	 0.4330
BR	 0.9820	 0.4500
BS	 0.9550	 0.3620
BT	 0.9770	 0.3940
BU	 0.9580	 0.4020
BV	 0.9850	 0.5220
BW	 0.9980	 0.5810
BX	 0.9880	 0.5450
BY	 0.9800	 0.4760
BZ	 0.9690	 0.3680
Ba	 0.9930	 0.5540
Bb	 0.9750	 0.5280
Bc	 0.9750	 0.4660
Bd	 0.9810	 0.4780
Be	 0.9700	 0.4770

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Chain	Atom inclusion	Q-score
Bf	 0.6790	 0.2920
Bg	 0.9590	 0.3420
DC	 0.9120	 0.3480
E	 0.7660	 0.2020
EC	 0.8160	 0.2150
V	 0.8950	 0.3570