



## Full wwPDB EM Validation Report ⓘ

May 19, 2025 – 05:39 AM EDT

PDB ID : 7MPI / pdb\_00007mpi  
EMDB ID : EMD-23934  
Title : Stm1 bound vacant 80S structure isolated from cbf5-D95A  
Authors : Rai, J.; Zhao, Y.; Li, H.  
Deposited on : 2021-05-04  
Resolution : 3.05 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

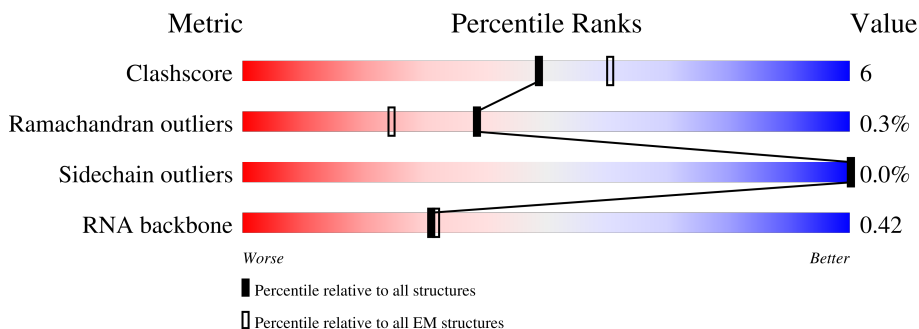
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.05 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	BA	206	
2	BB	214	
3	BC	217	
4	BD	223	
5	BE	260	
6	BF	206	
7	BG	226	


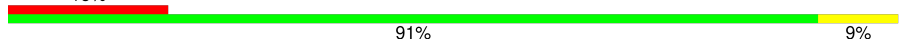




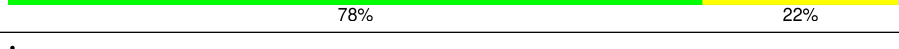
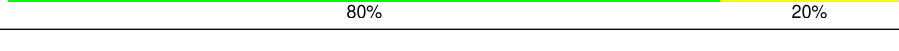
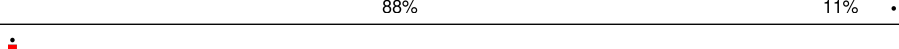
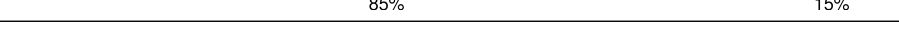
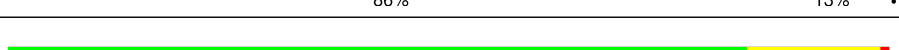

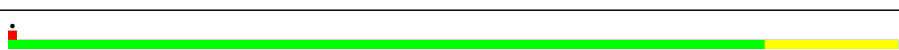

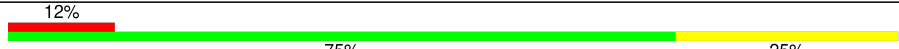





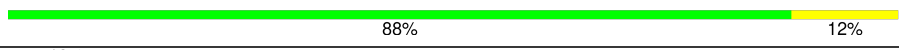
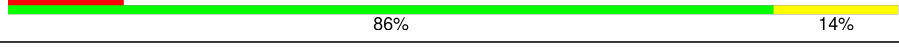



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Mol	Chain	Length	Quality of chain
8	BH	184	
9	BI	188	
10	BJ	185	
11	BK	96	
12	BL	155	
13	BM	121	
14	BN	150	
15	BO	127	
16	BP	124	
17	BQ	141	
18	BR	121	
19	BS	145	
20	BT	141	
21	BU	107	
22	BV	87	
23	BW	129	
24	BX	144	
25	BY	134	
26	BZ	69	
27	Ba	97	
28	Bb	81	
29	Bc	63	
30	Bd	53	
31	Be	60	
32	Bf	57	




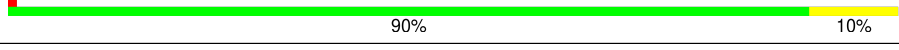


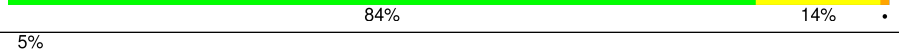
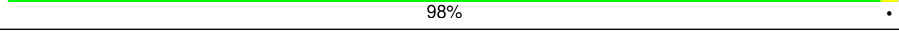
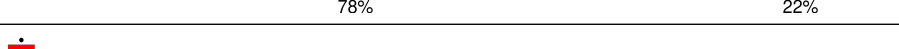
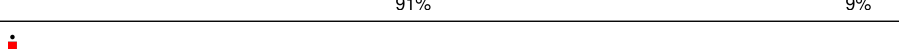
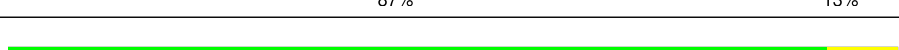
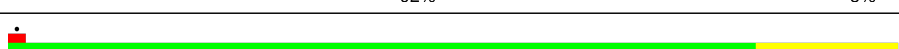
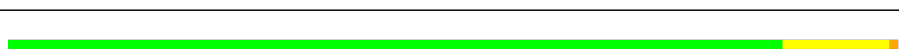
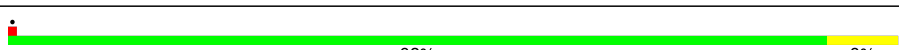
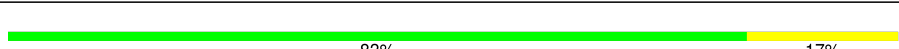




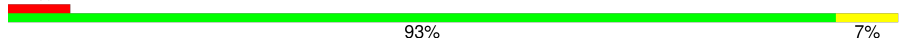
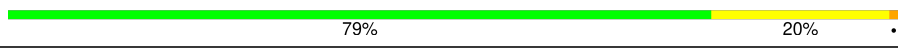
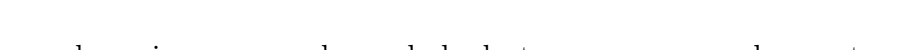
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Mol	Chain	Length	Quality of chain
33	Bg	312	
34	Bh	89	
35	B5	1781	
36	A1	3137	
37	A3	121	
38	A4	158	
39	AA	247	
40	AB	386	
41	AC	361	
42	AD	292	
43	AE	156	
44	AF	222	
45	AG	230	
46	AH	190	
47	AI	205	
48	AJ	169	
49	AL	193	
50	AM	136	
51	AN	203	
52	AO	197	
53	AP	175	
54	AQ	185	
55	AR	188	
56	AS	172	
57	AT	159	

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Mol	Chain	Length	Quality of chain
58	AU	100	
59	AV	136	
60	AW	63	
61	AX	121	
62	AY	126	
63	AZ	135	
64	Aa	148	
65	Ab	58	
66	Ac	97	
67	Ad	109	
68	Ae	127	
69	Af	106	
70	Ag	112	
71	Ah	119	
72	Ai	99	
73	Aj	87	
74	Ak	77	
75	Al	50	
76	Am	52	
77	An	25	
78	Ao	105	
79	Ap	91	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	3AU	B5	1191	X	-	-	-
35	G7M	B5	1575	X	-	-	-

## 2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 199433 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 40S ribosomal protein S1-A.

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 40S ribosomal protein S2.

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 S3.

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

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 6 is a protein called 40S ribosomal protein S5.

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

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

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

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	ASN	deletion	UNP P0CX39
BI	?	-	VAL	deletion	UNP P0CX39
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	GLU	deletion	UNP P0CX39
BI	?	-	GLU	deletion	UNP P0CX39
BI	?	-	GLU	deletion	UNP P0CX39
BI	?	-	THR	deletion	UNP P0CX39
BI	?	-	VAL	deletion	UNP P0CX39
BI	?	-	ALA	deletion	UNP P0CX39

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S12.

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

- Molecule 14 is a protein called 40S ribosomal protein S13.

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

- Molecule 15 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 16 is a protein called 40S ribosomal protein S15.

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

- Molecule 17 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S17-A.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BR	?	-	SER	deletion	UNP P02407
BR	?	-	ASN	deletion	UNP P02407
BR	?	-	GLY	deletion	UNP P02407
BR	?	-	VAL	deletion	UNP P02407

- Molecule 19 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 20 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S20.

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

- Molecule 22 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 23 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S26-B.

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

- Molecule 28 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S28-A.

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 40S ribosomal protein S29-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S30-A.

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

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

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bf	97	ALA	LYS	conflict	UNP P05759
Bf	?	-	CYS	deletion	UNP P05759
Bf	?	-	GLY	deletion	UNP P05759
Bf	?	-	ALA	deletion	UNP P05759

- Molecule 33 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 34 is a protein called Suppressor protein STM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bh	89	Total	C	N	O		0	0
			675	391	137	147			

- Molecule 35 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B5	1781	Total	C	N	O	P	1	0
			37849	16931	6657	12480	1781		

- Molecule 36 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	A1	3137	Total	C	N	O	P	0	0
			67139	30012	12094	21896	3137		

- Molecule 37 is a RNA chain called 5s rRNA.

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

- Molecule 38 is a RNA chain called 5.8 S rRNA.

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

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AB	386	Total	C	N	O	S	0	0
			3078	1953	584	533	8		

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L5.

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

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

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

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LEU	deletion	UNP Q02326
AE	?	-	THR	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326

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Chain	Residue	Modelled	Actual	Comment	Reference
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326
AE	?	-	ALA	deletion	UNP Q02326
AE	?	-	ASN	deletion	UNP Q02326
AE	?	-	LEU	deletion	UNP Q02326
AE	?	-	PHE	deletion	UNP Q02326
AE	?	-	PRO	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326
AE	?	-	GLN	deletion	UNP Q02326
AE	?	-	GLN	deletion	UNP Q02326
AE	?	-	ASN	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L10.

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

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	?	-	MET	deletion	UNP P41805
AI	?	-	LEU	deletion	UNP P41805
AI	?	-	SER	deletion	UNP P41805
AI	?	-	CYS	deletion	UNP P41805
AI	?	-	ALA	deletion	UNP P41805
AI	?	-	GLY	deletion	UNP P41805
AI	?	-	ALA	deletion	UNP P41805
AI	?	-	ASP	deletion	UNP P41805
AI	?	-	ARG	deletion	UNP P41805
AI	?	-	LEU	deletion	UNP P41805
AI	?	-	GLN	deletion	UNP P41805
AI	?	-	GLN	deletion	UNP P41805

- Molecule 48 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

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

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	VAL	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	LYS	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	GLU	deletion	UNP P05740
AP	?	-	LYS	deletion	UNP P05740

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L25.

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

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 64 is a protein called 60S ribosomal protein L28.

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

- Molecule 65 is a protein called 60S ribosomal protein L29.

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

- Molecule 66 is a protein called 60S ribosomal protein L30.

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

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 68 is a protein called 60S ribosomal protein L32.

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

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 74 is a protein called 60S ribosomal protein L38.

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

- Molecule 75 is a protein called 60S ribosomal protein L39.

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

- Molecule 76 is a protein called 60S ribosomal protein L40-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 80 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
80	BD	1	Total	Mg	0
			1	1	
80	BJ	1	Total	Mg	0
			1	1	
80	BL	1	Total	Mg	0
			1	1	
80	B5	91	Total	Mg	0
			91	91	
80	A1	242	Total	Mg	0
			242	242	
80	A3	2	Total	Mg	0
			2	2	
80	A4	9	Total	Mg	0
			9	9	
80	AB	3	Total	Mg	0
			3	3	
80	AG	1	Total	Mg	0
			1	1	
80	AL	1	Total	Mg	0
			1	1	
80	AN	2	Total	Mg	0
			2	2	
80	AO	1	Total	Mg	0
			1	1	
80	AP	1	Total	Mg	0
			1	1	
80	AR	1	Total	Mg	0
			1	1	
80	AX	1	Total	Mg	0
			1	1	
80	Ae	4	Total	Mg	0
			4	4	
80	Af	2	Total	Mg	0
			2	2	
80	Aj	2	Total	Mg	0
			2	2	

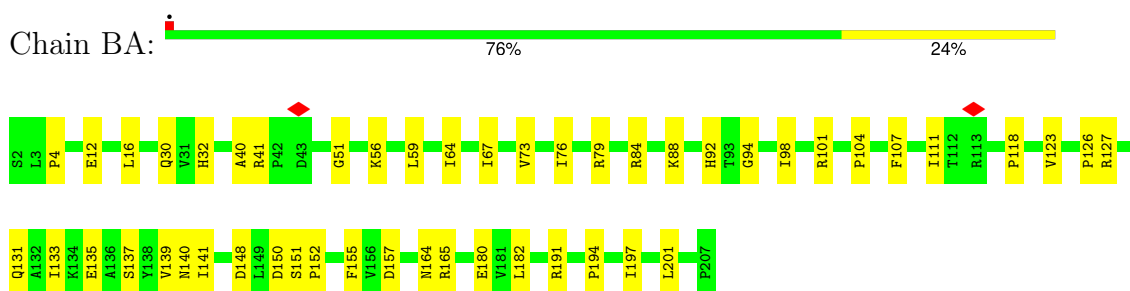
- Molecule 81 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
81	Bb	1	Total 1	Zn 1	0
81	Ao	1	Total 1	Zn 1	0

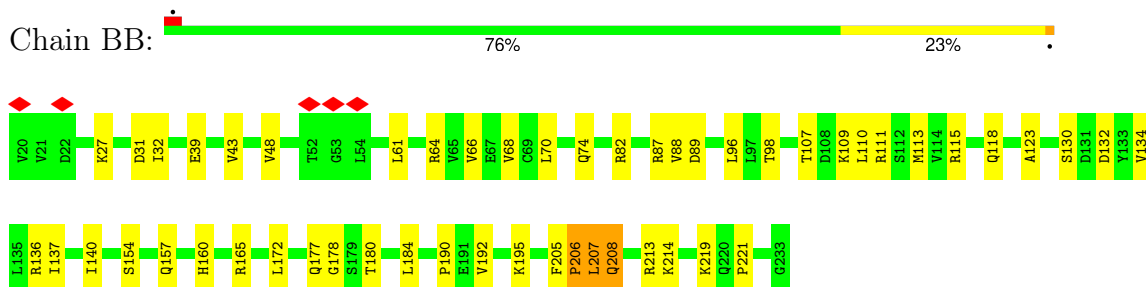
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

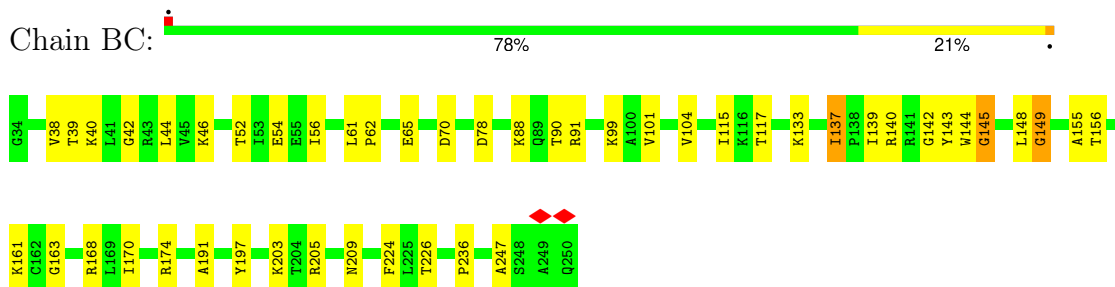
- Molecule 1: 40S ribosomal protein S0-A



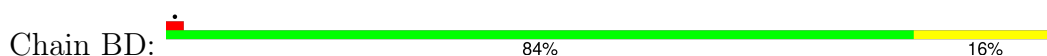
- Molecule 2: 40S ribosomal protein S1-A

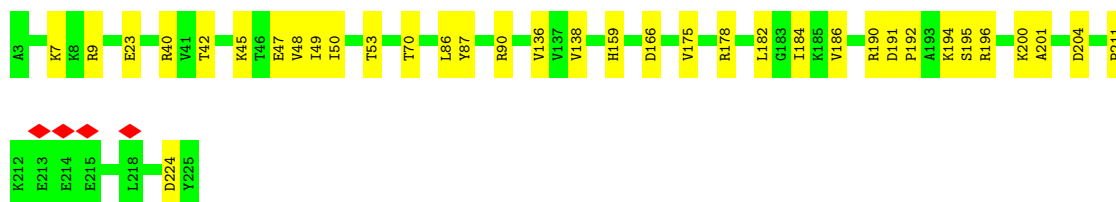


- Molecule 3: 40S ribosomal protein S2



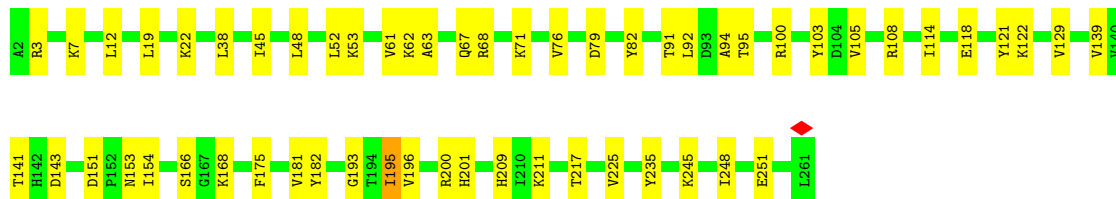
- Molecule 4: 40S ribosomal protein S3





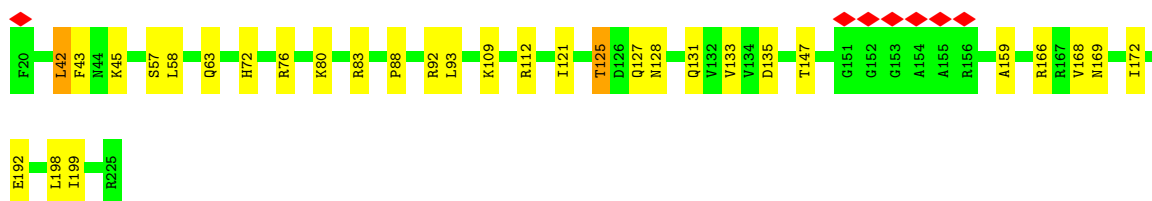
- Molecule 5: 40S ribosomal protein S4-A

Chain BE: 78% 21%



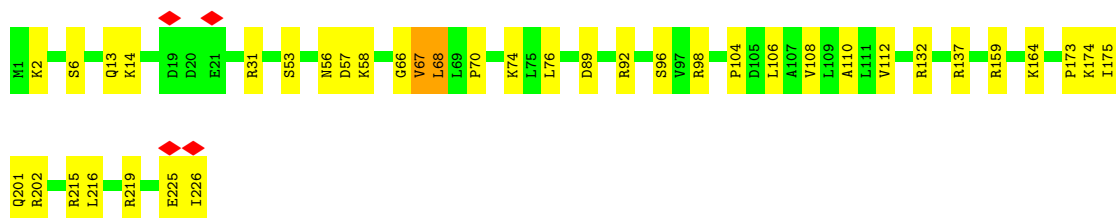
- Molecule 6: 40S ribosomal protein S5

Chain BF: 85% 14%



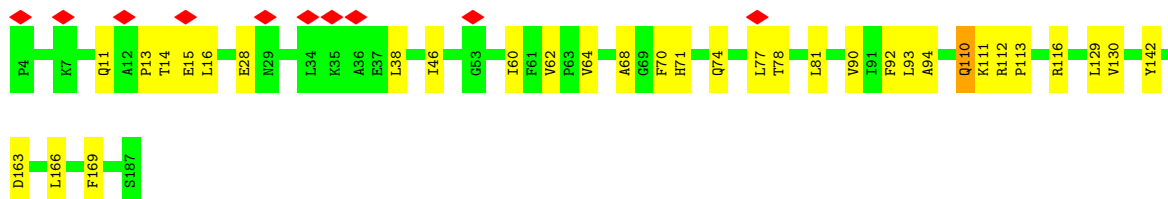
- Molecule 7: 40S ribosomal protein S6-A

Chain BG: 83% 16%

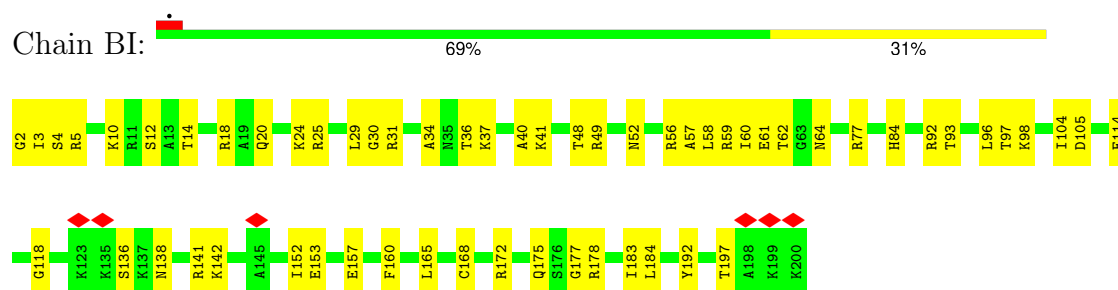


- Molecule 8: 40S ribosomal protein S7-A

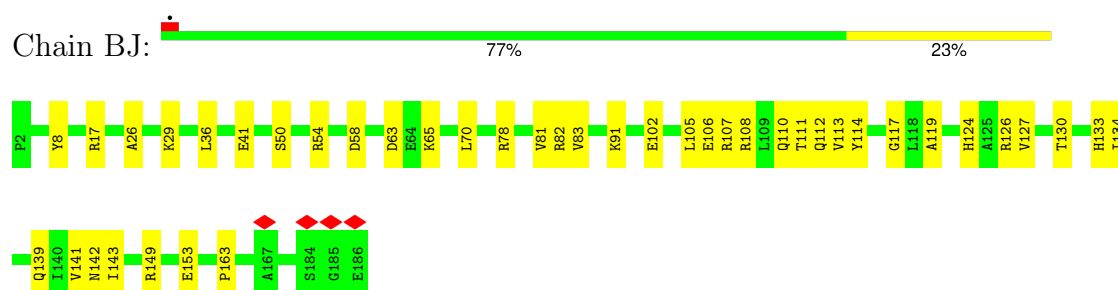
Chain BH: 5% 82% 17%



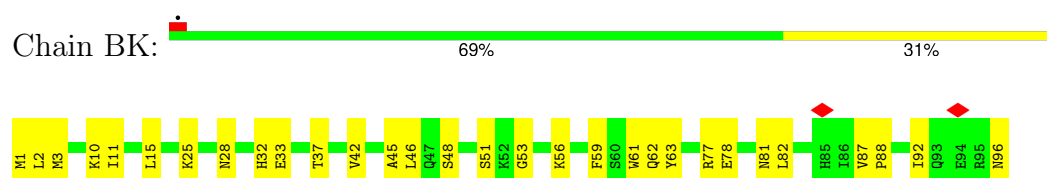
- Molecule 9: 40S ribosomal protein S8-A



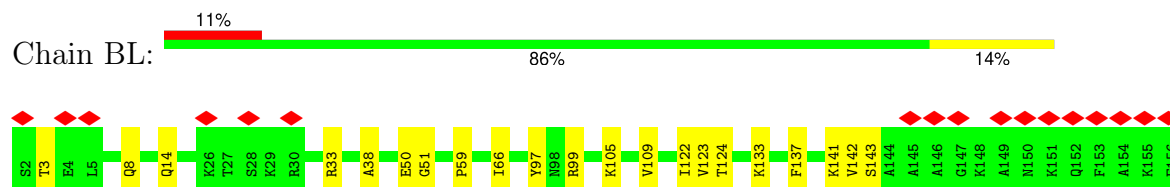
- Molecule 10: 40S ribosomal protein S9-A



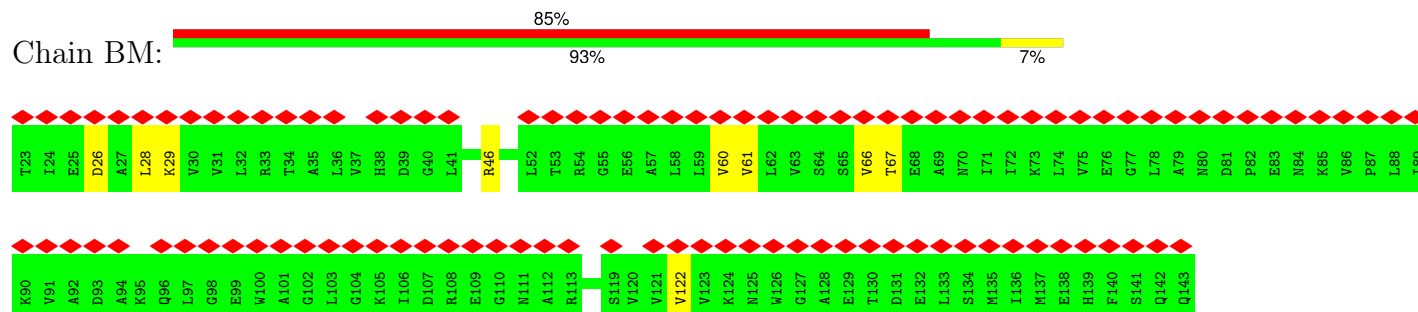
- Molecule 11: 40S ribosomal protein S10-A




- Molecule 12: 40S ribosomal protein S11-A

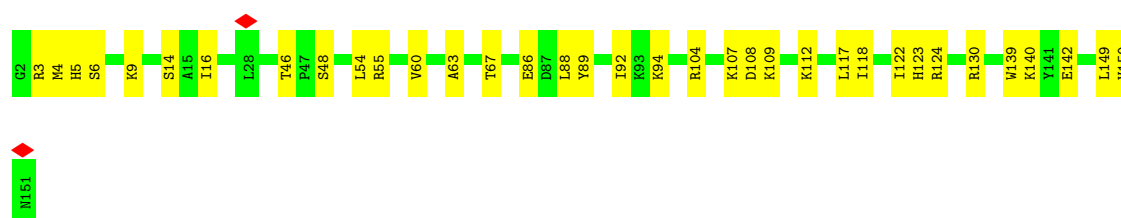


- Molecule 13: 40S ribosomal protein S12




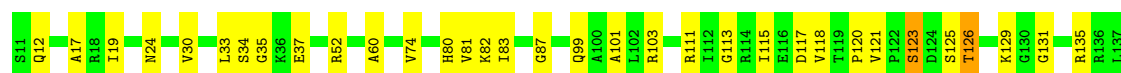
- Molecule 14: 40S ribosomal protein S13

Chain BN:  77% 23%




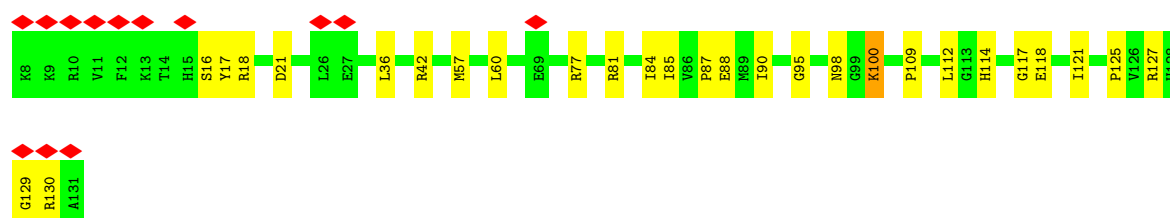
- Molecule 15: 40S ribosomal protein S14-A

Chain BO:  74% 24%




- Molecule 16: 40S ribosomal protein S15

Chain BP:  10% 77% 22%




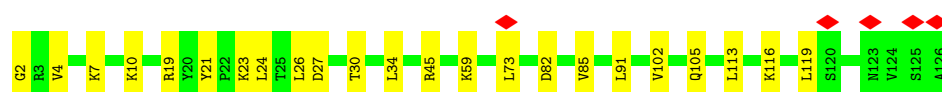
- Molecule 17: 40S ribosomal protein S16-A

Chain BQ:  74% 24%



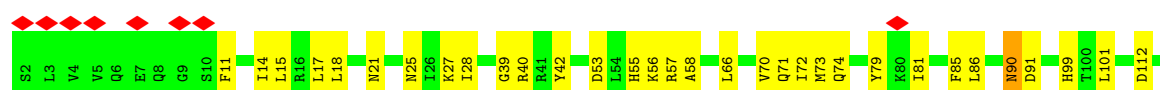
- Molecule 18: 40S ribosomal protein S17-A

Chain BR:  81% 19%



- Molecule 19: 40S ribosomal protein S18-A

Chain BS:  6% 72% 27%





- Molecule 20: 40S ribosomal protein S19-A

Chain BT: 74% 26%



- Molecule 21: 40S ribosomal protein S20

Chain BU: 7% 76% 24%



- Molecule 22: 40S ribosomal protein S21-A

Chain BV: 75% 25%



- Molecule 23: 40S ribosomal protein S22-A

Chain BW: 81% 19%



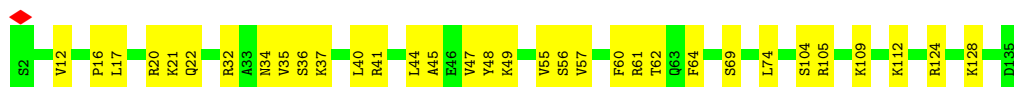
- Molecule 24: 40S ribosomal protein S23-A

Chain BX: 80% 17% ..


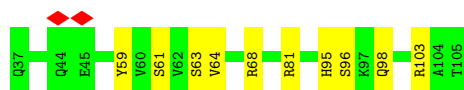


- Molecule 25: 40S ribosomal protein S24-A

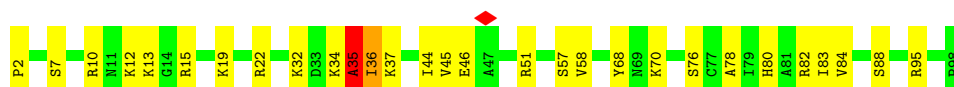
Chain BY: 75% 25%



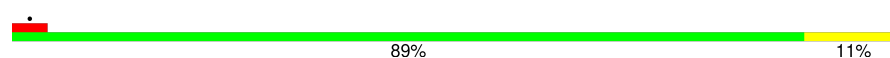
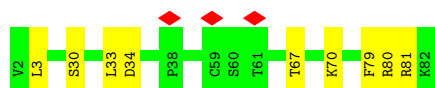
## • Molecule 26: 40S ribosomal protein S25-A

Chain BZ:  86% 14%


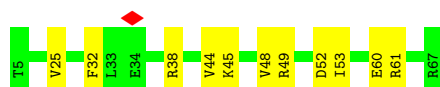
## • Molecule 27: 40S ribosomal protein S26-B

Chain Ba:  70% 28% ..


## • Molecule 28: 40S ribosomal protein S27-A

Chain Bb:  89% 11%


## • Molecule 29: 40S ribosomal protein S28-A

Chain Bc:  83% 17%

## • Molecule 30: 40S ribosomal protein S29-A

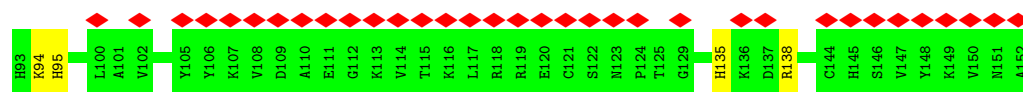
Chain Bd:  79% 21%

## • Molecule 31: 40S ribosomal protein S30-A

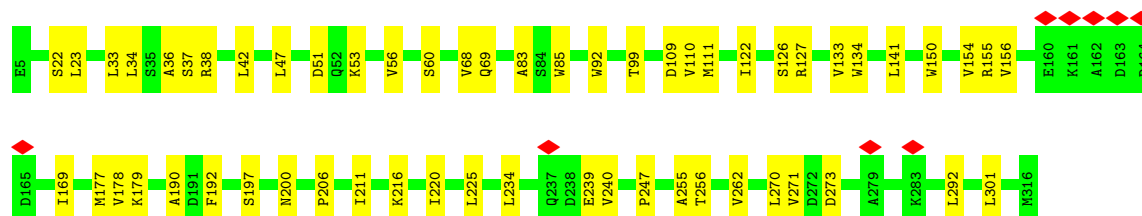
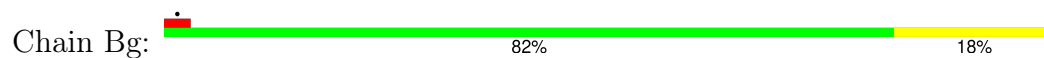
Chain Be:  85% 15%

## • Molecule 32: 40S ribosomal protein S31

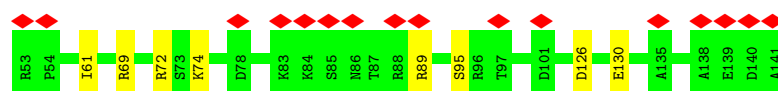
Chain Bf:  60% 93% 7%



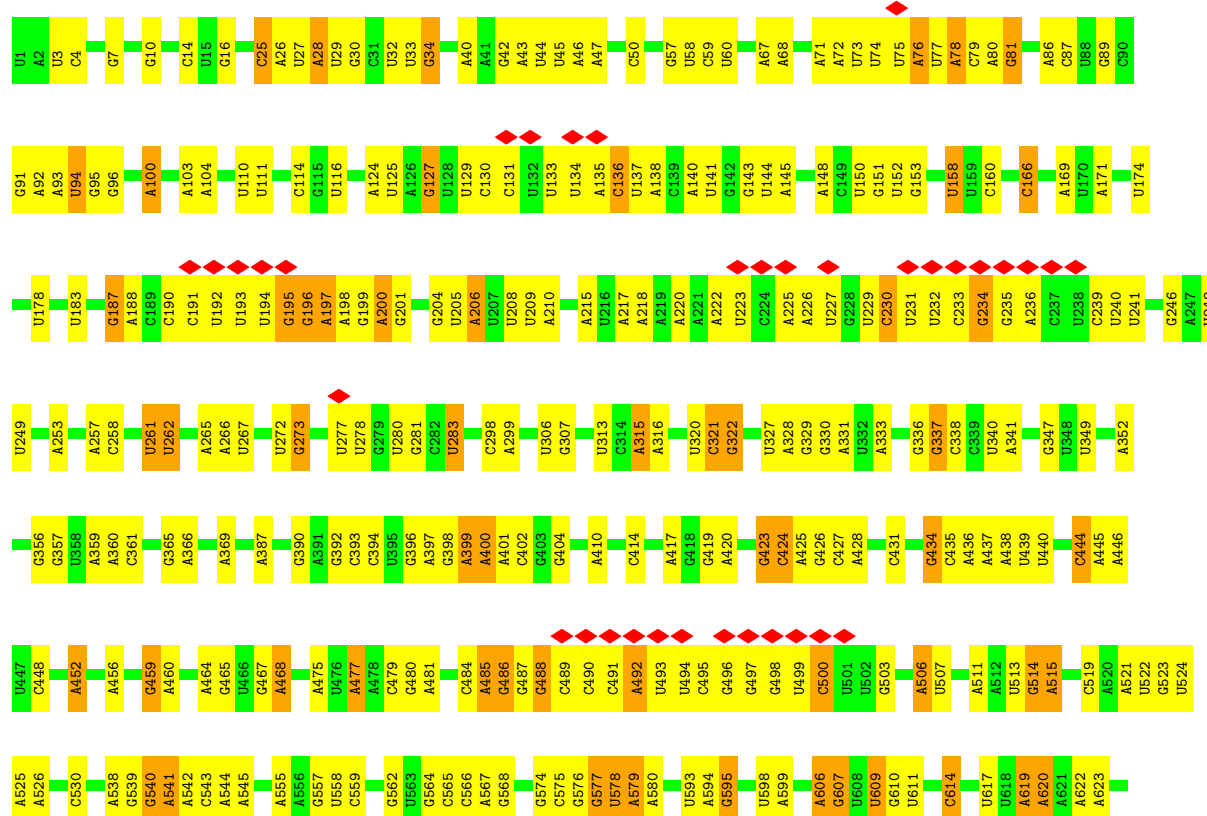
- Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 34: Suppressor protein STM1



- Molecule 35: 18S rRNA

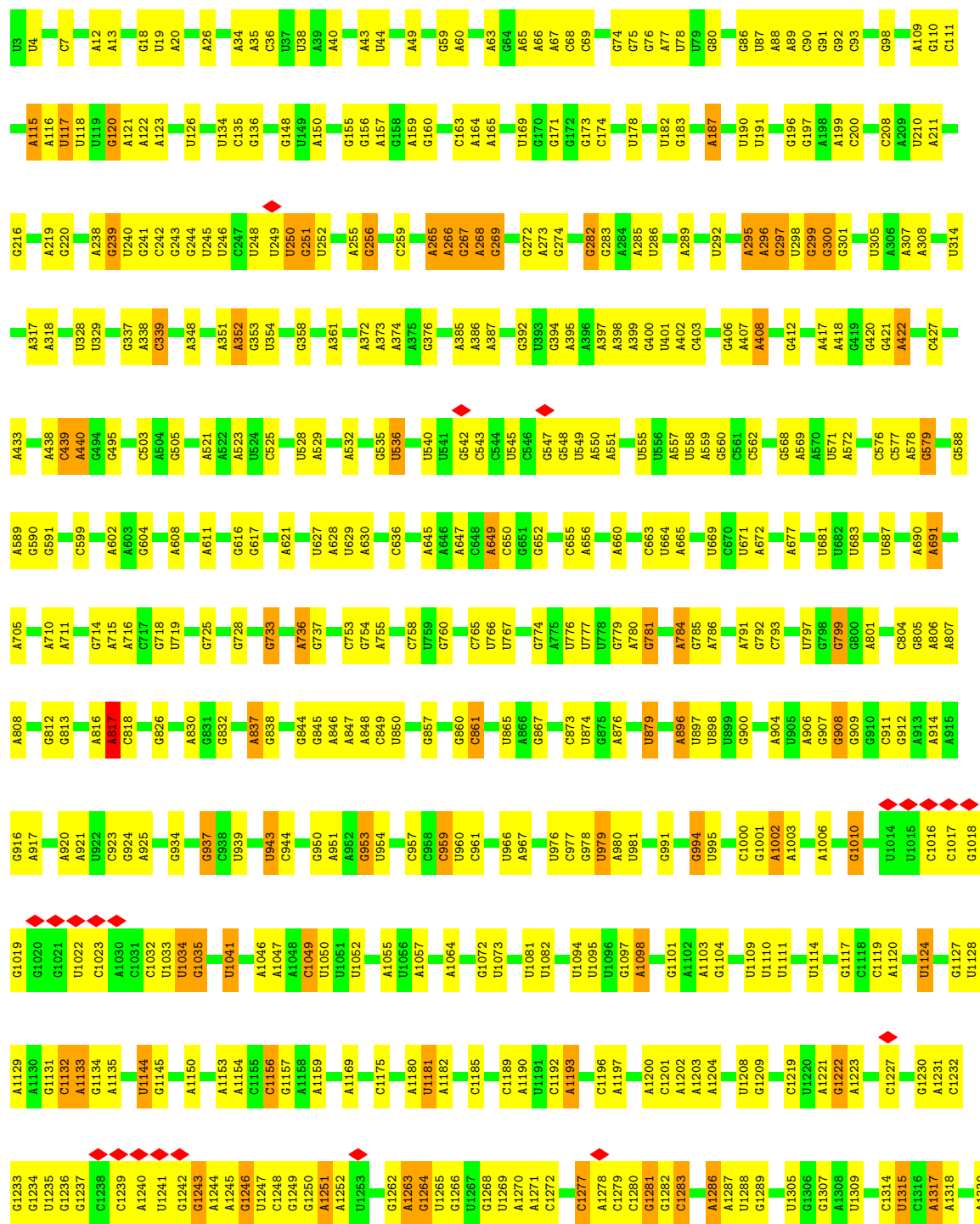




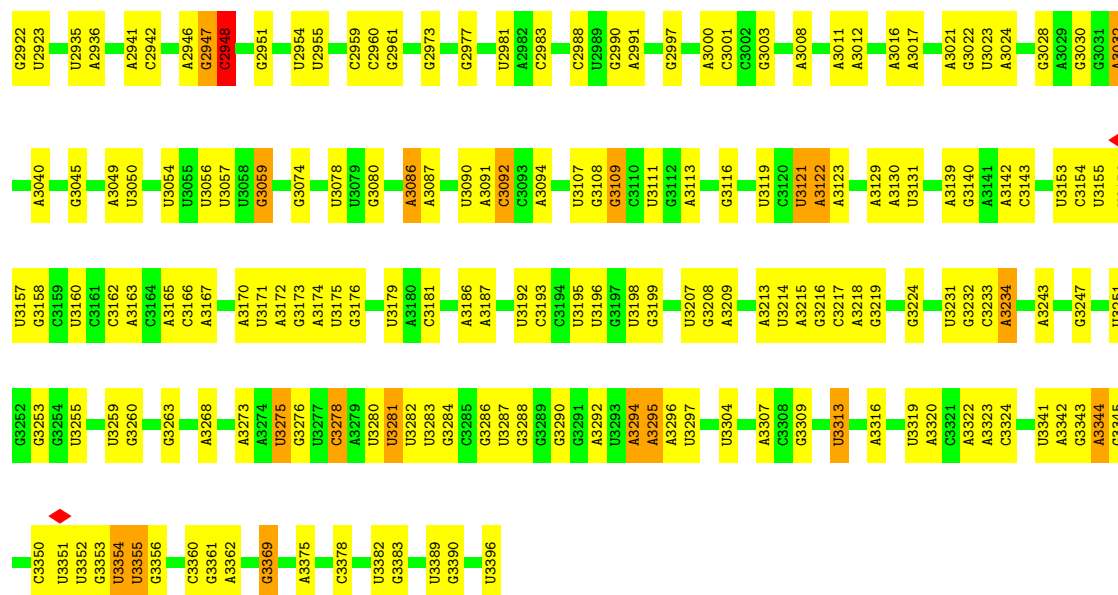
G1792  
G1793  
U1794  
U1795  
C1796  
U1797  
U1798

• Molecule 36: 25S rRNA

Chain A1:  61% 33% 5%

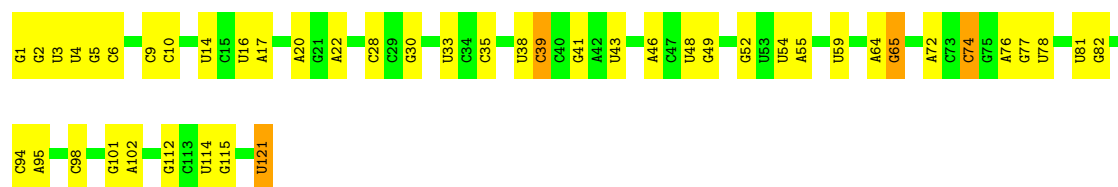






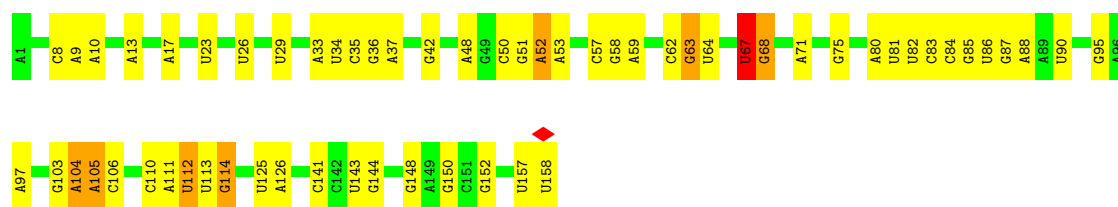
### • Molecule 37: 5S rRNA

Chain A3: 62% 35%



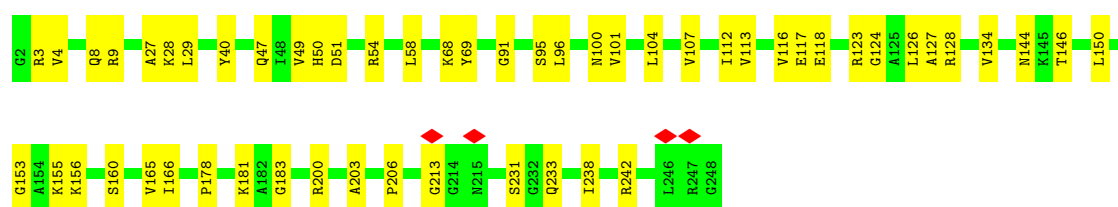
### • Molecule 38: 5.8 S rRNA

Chain A4: 62% 33%




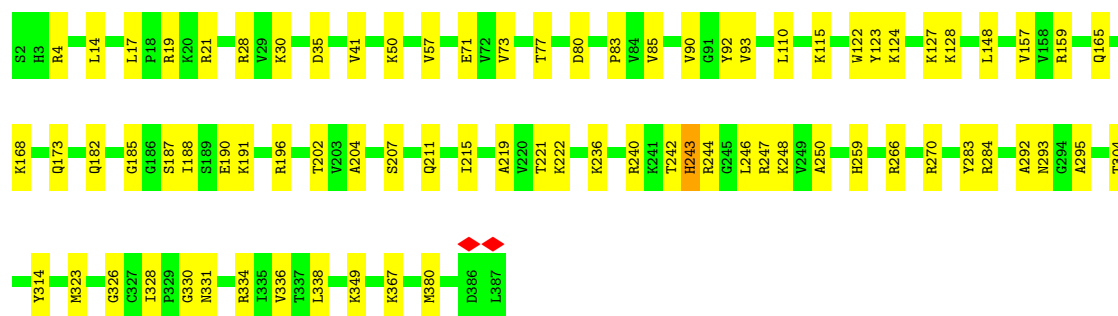
### • Molecule 39: 60S ribosomal protein L2-A

Chain AA: 78% 22%



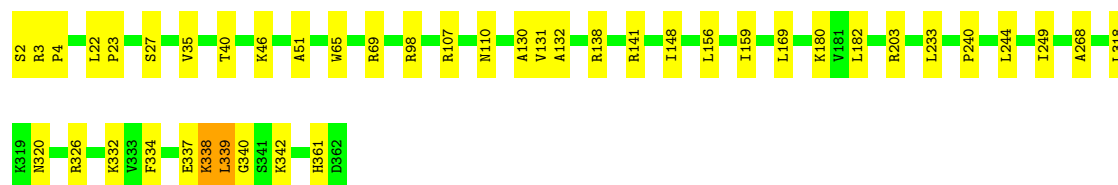
### • Molecule 40: 60S ribosomal protein L3

Chain AB:  80% 20%




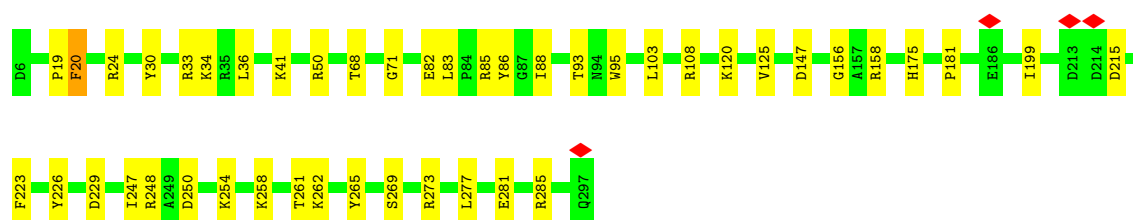
- Molecule 41: 60S ribosomal protein L4-A

Chain AC:  88% 11%




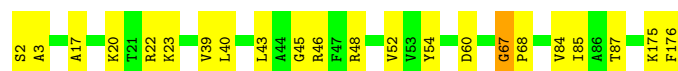
- Molecule 42: 60S ribosomal protein L5

Chain AD:  85% 15%




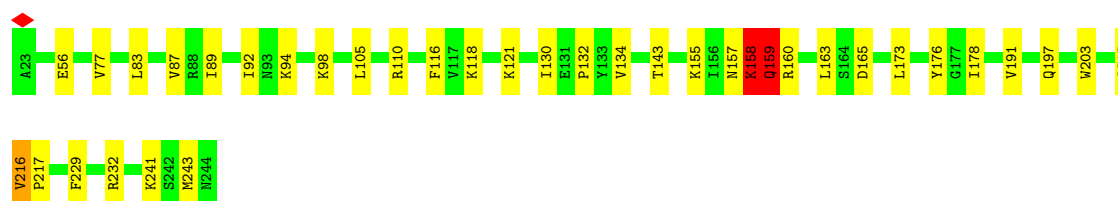
- Molecule 43: 60S ribosomal protein L6-A

Chain AE:  86% 13%

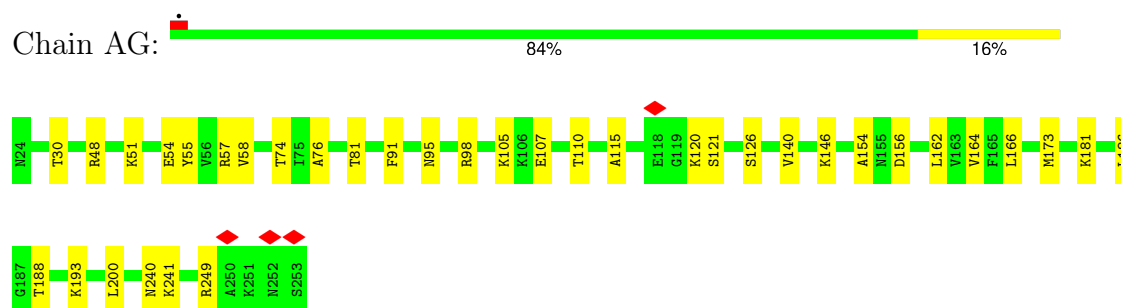


- Molecule 44: 60S ribosomal protein L7-A

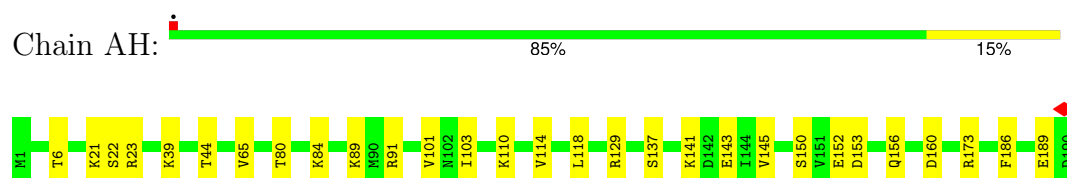
Chain AF:  83% 15%



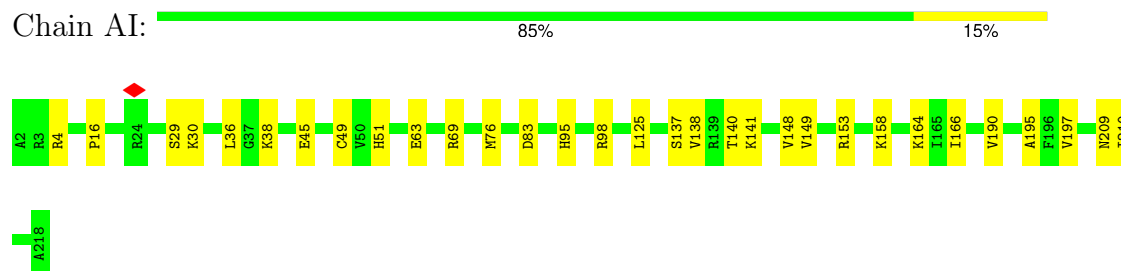
- Molecule 45: 60S ribosomal protein L8-A



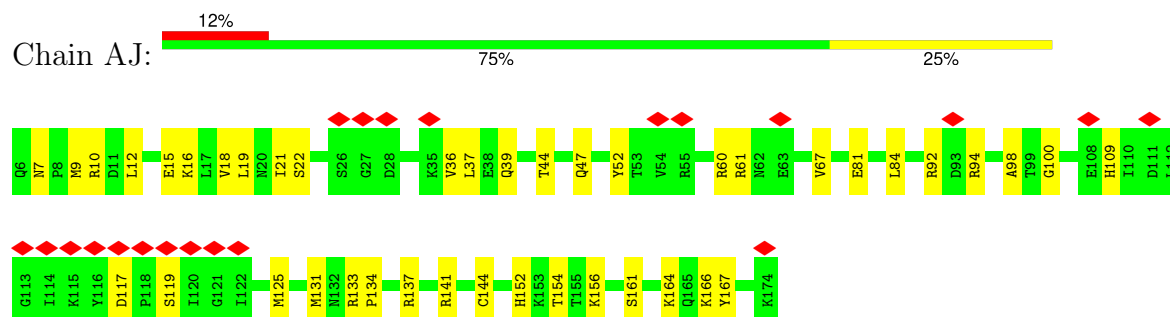
- Molecule 46: 60S ribosomal protein L9-A



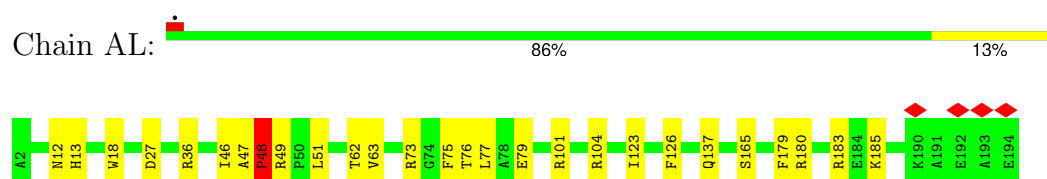
- Molecule 47: 60S ribosomal protein L10



- Molecule 48: 60S ribosomal protein L11-A

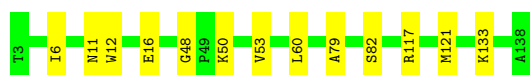


- Molecule 49: 60S ribosomal protein L13-A



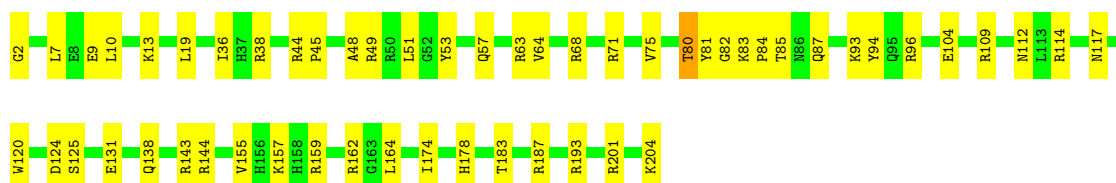
- Molecule 50: 60S ribosomal protein L14-A

Chain AM:  90% 10%



- Molecule 51: 60S ribosomal protein L15-A

Chain AN:  73% 26%



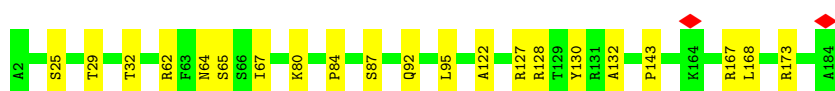
- Molecule 52: 60S ribosomal protein L16-A

Chain AO:  89% 11%



- Molecule 53: 60S ribosomal protein L17-A

Chain AP:  88% 12%




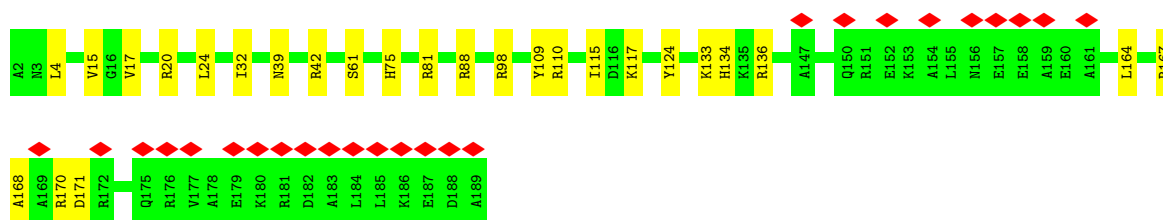
- Molecule 54: 60S ribosomal protein L18-A

Chain AQ:  88% 12%




- Molecule 55: 60S ribosomal protein L19-A

Chain AR:  13% 86% 14%




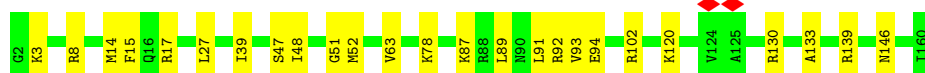
- Molecule 56: 60S ribosomal protein L20-A

Chain AS:  88% 11%



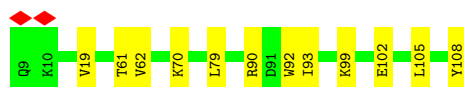
- Molecule 57: 60S ribosomal protein L21-A

Chain AT:  84% 16%



- Molecule 58: 60S ribosomal protein L22-A

Chain AU:  88% 12%




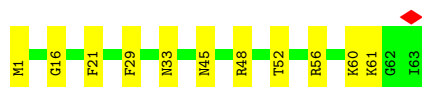
- Molecule 59: 60S ribosomal protein L23-A

Chain AV:  88% 12%



- Molecule 60: 60S ribosomal protein L24-A

Chain AW:  83% 17%




- Molecule 61: 60S ribosomal protein L25

Chain AX:  90% 10%

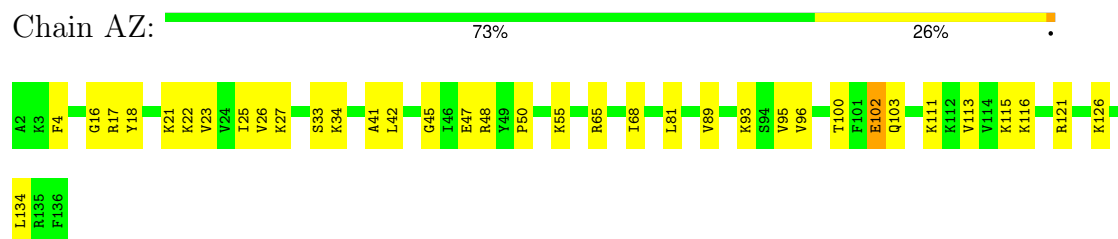


- Molecule 62: 60S ribosomal protein L26-A

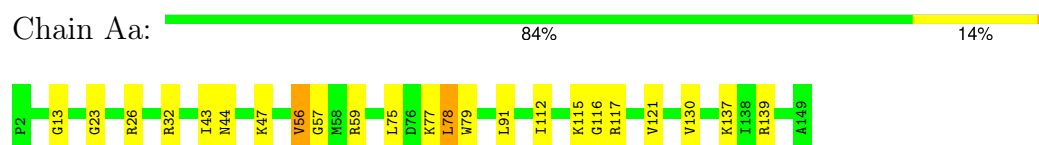
Chain AY:  86% 14%



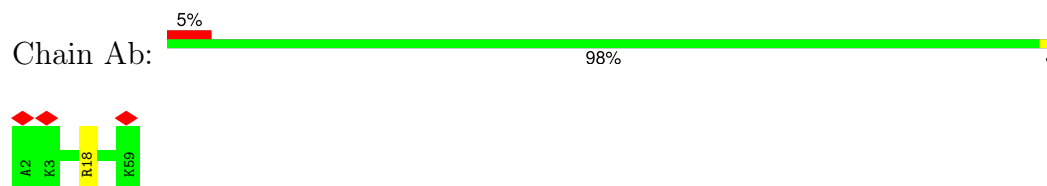
- Molecule 63: 60S ribosomal protein L27-A



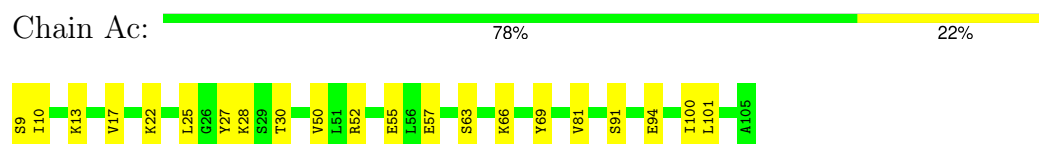
- Molecule 64: 60S ribosomal protein L28



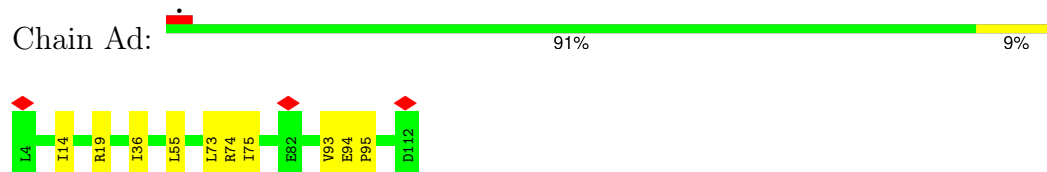
- Molecule 65: 60S ribosomal protein L29



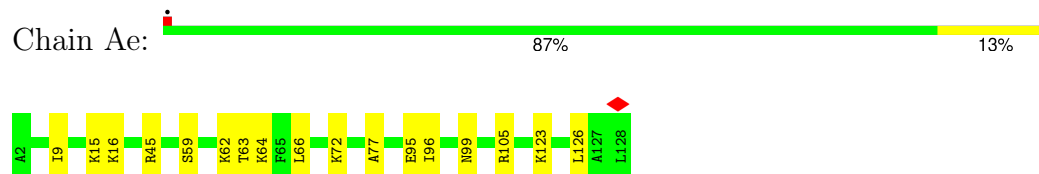
- Molecule 66: 60S ribosomal protein L30



- Molecule 67: 60S ribosomal protein L31-A

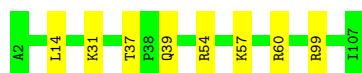


- Molecule 68: 60S ribosomal protein L32

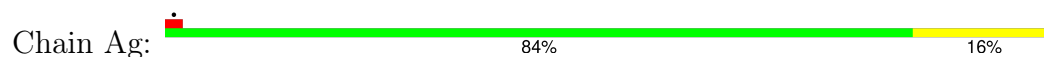


- Molecule 69: 60S ribosomal protein L33-A

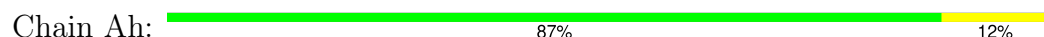




- Molecule 70: 60S ribosomal protein L34-A



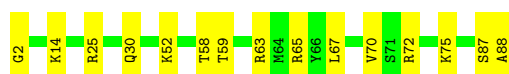
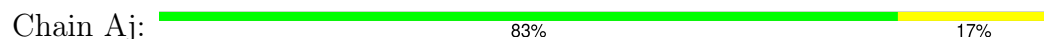
- Molecule 71: 60S ribosomal protein L35-A



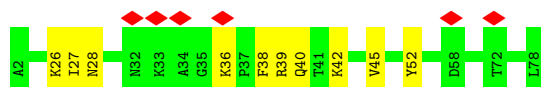
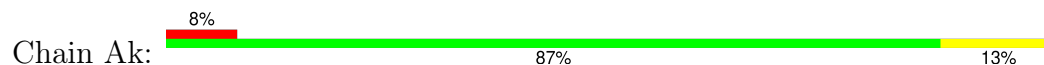
- Molecule 72: 60S ribosomal protein L36-A



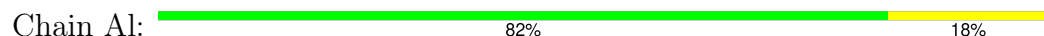
- Molecule 73: 60S ribosomal protein L37-A



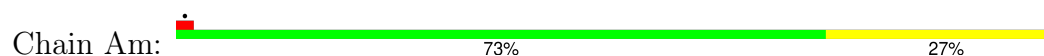
- Molecule 74: 60S ribosomal protein L38



- Molecule 75: 60S ribosomal protein L39

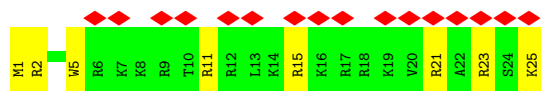


- Molecule 76: 60S ribosomal protein L40-A

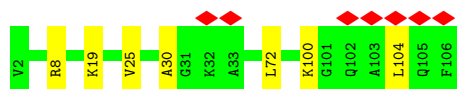




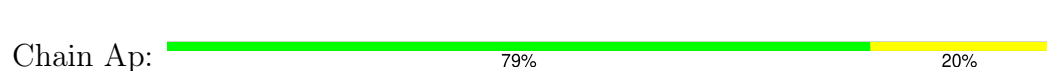
- Molecule 77: 60S ribosomal protein L41-A



- Molecule 78: 60S ribosomal protein L42-A



- Molecule 79: 60S ribosomal protein L43-A



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	404065	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	61	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0065	Depositor
Map size (Å)	463.968, 463.968, 463.968	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.074, 1.074, 1.074	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, OMC, 4AC, G7M, 1MA, MA6, 3AU, HIC, 5MC, OMU, UR3, A2M, ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	BA	0.39	0/1653	0.67	0/2261
2	BB	0.41	0/1735	0.86	3/2335 (0.1%)
3	BC	0.39	0/1665	0.74	3/2263 (0.1%)
4	BD	0.34	0/1759	0.60	0/2368
5	BE	0.38	0/2109	0.71	4/2839 (0.1%)
6	BF	0.36	0/1629	0.71	0/2202
7	BG	0.34	0/1844	0.71	3/2464 (0.1%)
8	BH	0.36	0/1506	0.75	0/2028
9	BI	0.40	0/1514	0.78	0/2021
10	BJ	0.39	0/1519	0.74	0/2035
11	BK	0.59	2/837 (0.2%)	1.11	4/1131 (0.4%)
12	BL	0.38	0/1272	0.62	0/1712
13	BM	0.28	0/921	0.78	0/1245
14	BN	0.37	0/1215	0.67	0/1638
15	BO	0.40	0/952	0.82	1/1279 (0.1%)
16	BP	0.38	0/1012	0.74	0/1356
17	BQ	0.42	0/1125	0.73	0/1510
18	BR	0.30	0/984	0.72	0/1318
19	BS	0.42	0/1211	0.77	0/1628
20	BT	0.42	0/1113	0.76	0/1494
21	BU	0.34	0/865	0.69	1/1169 (0.1%)
22	BV	0.45	0/692	0.67	2/932 (0.2%)
23	BW	0.48	0/1038	0.73	0/1395
24	BX	0.42	0/1139	0.89	5/1518 (0.3%)
25	BY	0.39	0/1087	0.72	0/1449
26	BZ	0.37	0/566	0.81	0/761
27	Ba	0.45	0/782	0.90	2/1047 (0.2%)
28	Bb	0.35	0/620	0.65	0/838
29	Bc	0.33	0/499	0.64	0/670
30	Bd	0.39	0/452	0.74	0/600
31	Be	0.28	0/483	0.56	0/643
32	Bf	0.24	0/462	0.69	0/617

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Bg	0.37	0/2454	0.70	0/3340
34	Bh	0.28	0/678	0.65	0/905
35	B5	0.40	2/41700 (0.0%)	0.48	2/64963 (0.0%)
36	A1	0.50	2/74123 (0.0%)	0.47	15/115559 (0.0%)
37	A3	0.41	0/2883	0.41	0/4491
38	A4	0.56	0/3745	0.48	1/5828 (0.0%)
39	AA	0.39	0/1912	0.58	0/2569
40	AB	0.51	0/3136	0.65	4/4213 (0.1%)
41	AC	0.50	0/2800	0.73	3/3790 (0.1%)
42	AD	0.30	0/2390	0.65	3/3225 (0.1%)
43	AE	0.46	0/1260	0.65	0/1694
44	AF	0.51	0/1821	0.73	5/2451 (0.2%)
45	AG	0.40	0/1830	0.69	0/2469
46	AH	0.40	0/1531	0.65	0/2062
47	AI	0.31	0/1708	0.61	0/2290
48	AJ	0.31	0/1374	0.73	0/1842
49	AL	0.48	0/1568	0.74	3/2106 (0.1%)
50	AM	0.46	0/1068	0.57	0/1438
51	AN	0.52	0/1757	0.69	0/2354
52	AO	0.53	0/1585	0.65	0/2128
53	AP	0.51	0/1410	0.62	0/1893
54	AQ	0.45	0/1465	0.58	0/1965
55	AR	0.41	0/1538	0.60	0/2050
56	AS	0.52	0/1481	0.69	0/1990
57	AT	0.40	0/1300	0.67	0/1743
58	AU	0.37	0/812	0.69	0/1099
59	AV	0.47	0/1018	0.64	0/1369
60	AW	0.47	0/533	0.60	0/707
61	AX	0.47	0/983	0.63	0/1325
62	AY	0.50	0/1004	0.63	0/1341
63	AZ	0.38	0/1118	0.69	2/1497 (0.1%)
64	Aa	0.46	0/1204	0.73	3/1612 (0.2%)
65	Ab	0.29	0/473	0.63	0/629
66	Ac	0.36	0/751	0.59	0/1008
67	Ad	0.50	0/904	0.56	0/1213
68	Ae	0.51	0/1041	0.61	0/1394
69	Af	0.57	0/868	0.60	0/1168
70	Ag	0.47	0/890	0.63	0/1189
71	Ah	0.42	0/978	0.63	0/1301
72	Ai	0.38	0/778	0.79	0/1034
73	Aj	0.51	0/696	0.67	0/923
74	Ak	0.33	0/618	0.60	0/826
75	Al	0.48	0/443	0.61	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Am	0.42	0/423	0.72	2/562 (0.4%)
77	An	0.29	0/234	0.64	0/300
78	Ao	0.27	0/860	0.63	0/1136
79	Ap	0.41	0/701	0.74	2/934 (0.2%)
All	All	0.45	6/212107 (0.0%)	0.57	73/311279 (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
1	BA	0	1
2	BB	0	5
3	BC	0	2
5	BE	0	1
6	BF	0	2
7	BG	0	1
8	BH	0	2
9	BI	0	1
10	BJ	0	3
11	BK	0	2
15	BO	0	1
16	BP	0	1
17	BQ	0	3
19	BS	0	2
20	BT	0	1
24	BX	0	5
26	BZ	0	1
27	Ba	0	2
35	B5	4	0
40	AB	0	1
41	AC	0	4
42	AD	0	1
43	AE	0	1
44	AF	0	3
45	AG	0	3
46	AH	0	1
48	AJ	0	3
49	AL	0	2
51	AN	0	2
52	AO	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
56	AS	0	1
63	AZ	0	1
71	Ah	0	1
72	Ai	0	1
All	All	4	62

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	BK	88	PRO	CG-CD	-11.68	1.11	1.50
11	BK	88	PRO	CB-CG	-6.46	1.17	1.49
35	B5	578	OMU	O3'-P	5.42	1.61	1.56
36	A1	2946	A2M	O3'-P	5.31	1.61	1.56
35	B5	619	A2M	O3'-P	5.05	1.61	1.56
36	A1	2281	A2M	O3'-P	5.05	1.61	1.56

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	BK	88	PRO	N-CD-CG	-18.33	75.71	103.20
36	A1	266	A	OP1-P-OP2	-13.61	78.76	119.60
11	BK	88	PRO	CB-CG-CD	13.57	149.52	106.10
11	BK	88	PRO	CA-CB-CG	-12.73	80.30	104.50
36	A1	266	A	O5'-P-OP1	-11.82	72.53	108.00
36	A1	1947	G	OP2-P-O3'	-11.57	73.30	108.00
36	A1	265	A	OP2-P-O3'	-10.32	77.04	108.00
36	A1	1947	G	OP1-P-O3'	-9.48	79.56	108.00
36	A1	1948	G	O5'-P-OP2	-9.25	80.24	108.00
36	A1	266	A	O5'-P-OP2	8.79	134.38	108.00
36	A1	1948	G	O5'-P-OP1	-8.02	83.93	108.00
44	AF	157	ASN	CA-C-N	7.87	136.57	121.54
44	AF	157	ASN	C-N-CA	7.87	136.57	121.54
36	A1	265	A	OP1-P-O3'	7.75	131.24	108.00
3	BC	137	ILE	N-CA-C	-7.33	103.18	109.19
36	A1	1948	G	OP1-P-OP2	7.12	140.97	119.60
27	Ba	35	ALA	CA-C-N	7.06	134.68	121.97
27	Ba	35	ALA	C-N-CA	7.06	134.68	121.97
24	BX	96	VAL	CA-C-N	6.65	134.25	121.54
24	BX	96	VAL	C-N-CA	6.65	134.25	121.54
3	BC	137	ILE	CB-CA-C	6.64	115.84	109.33
11	BK	88	PRO	CA-N-CD	-6.62	102.73	112.00
3	BC	149	GLY	N-CA-C	6.50	120.96	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	Aa	56	VAL	N-CA-C	-6.38	96.08	109.34
7	BG	67	VAL	CA-C-N	6.21	133.41	121.54
7	BG	67	VAL	C-N-CA	6.21	133.41	121.54
15	BO	74	VAL	N-CA-C	-6.18	106.78	112.96
40	AB	168	LYS	CA-C-N	6.17	145.04	121.95
40	AB	168	LYS	C-N-CA	6.17	145.04	121.95
42	AD	229	ASP	CA-C-N	6.07	131.02	122.46
42	AD	229	ASP	C-N-CA	6.07	131.02	122.46
7	BG	174	LYS	N-CA-C	-5.95	98.12	110.80
76	Am	80	PRO	N-CD-CG	-5.87	94.39	103.20
49	AL	48	PRO	N-CA-C	5.78	124.37	112.47
44	AF	159	GLN	N-CA-C	5.76	123.06	110.80
64	Aa	47	LYS	CA-C-N	5.71	135.83	126.86
64	Aa	47	LYS	C-N-CA	5.71	135.83	126.86
24	BX	106	GLY	CA-C-N	-5.71	111.02	121.52
24	BX	106	GLY	C-N-CA	-5.71	111.02	121.52
36	A1	299	G	C4'-C3'-O3'	5.69	117.94	109.40
2	BB	178	GLY	N-CA-C	-5.64	103.66	112.58
24	BX	130	VAL	N-CA-C	-5.60	105.95	111.88
22	BV	41	GLU	CA-C-N	5.55	130.23	122.08
22	BV	41	GLU	C-N-CA	5.55	130.23	122.08
35	B5	1358	G	C2'-C3'-O3'	5.49	121.94	113.70
35	B5	1285	U	P-O3'-C3'	5.44	128.36	120.20
2	BB	48	VAL	CA-C-N	5.43	133.75	122.41
2	BB	48	VAL	C-N-CA	5.43	133.75	122.41
76	Am	80	PRO	CA-N-CD	-5.32	104.56	112.00
42	AD	261	THR	N-CA-C	5.30	117.17	110.33
36	A1	1385	C	C2'-C3'-O3'	5.30	121.65	113.70
36	A1	299	G	P-O3'-C3'	5.29	128.13	120.20
44	AF	158	LYS	CA-C-N	5.26	131.59	121.54
44	AF	158	LYS	C-N-CA	5.26	131.59	121.54
36	A1	265	A	O3'-P-O5'	-5.25	96.12	104.00
40	AB	4	ARG	CA-C-N	5.25	131.56	121.54
40	AB	4	ARG	C-N-CA	5.25	131.56	121.54
5	BE	193	GLY	CA-C-N	5.24	131.55	121.54
5	BE	193	GLY	C-N-CA	5.24	131.55	121.54
36	A1	299	G	O4'-C1'-N9	5.22	116.03	108.20
41	AC	337	GLU	CA-C-N	5.16	131.40	121.54
41	AC	337	GLU	C-N-CA	5.16	131.40	121.54
38	A4	67	U	C2'-C3'-O3'	5.15	121.43	113.70
79	Ap	51	ALA	CA-C-N	5.14	131.36	121.54
79	Ap	51	ALA	C-N-CA	5.14	131.36	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	BE	94	ALA	CA-C-N	5.09	131.26	121.54
5	BE	94	ALA	C-N-CA	5.09	131.26	121.54
41	AC	182	LEU	CA-CB-CG	5.07	134.04	116.30
49	AL	62	THR	CA-C-N	5.07	131.09	121.97
49	AL	62	THR	C-N-CA	5.07	131.09	121.97
63	AZ	102	GLU	CA-C-N	5.05	134.11	121.80
63	AZ	102	GLU	C-N-CA	5.05	134.11	121.80
21	BU	80	GLU	CA-CB-CG	5.02	124.14	114.10

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	B5	1191	3AU	C12
35	B5	1575	G7M	C3',C2',C4'

All (62) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
40	AB	349	LYS	Peptide
41	AC	130	ALA	Peptide
41	AC	131	VAL	Peptide
41	AC	318	LEU	Peptide
41	AC	338	LYS	Peptide
42	AD	258	LYS	Peptide
43	AE	67	GLY	Peptide
44	AF	158	LYS	Peptide
44	AF	215	GLY	Peptide
44	AF	232	ARG	Peptide
45	AG	121	SER	Peptide
45	AG	30	THR	Peptide
45	AG	76	ALA	Peptide
46	AH	21	LYS	Peptide
48	AJ	109	HIS	Peptide
48	AJ	166	LYS	Peptide
48	AJ	167	TYR	Peptide
49	AL	47	ALA	Peptide
49	AL	75	PHE	Peptide
51	AN	75	VAL	Peptide
51	AN	80	THR	Peptide
52	AO	110[A]	PRO	Peptide
56	AS	22	PRO	Peptide
63	AZ	102	GLU	Peptide

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Mol	Chain	Res	Type	Group
71	Ah	90	ARG	Peptide
72	Ai	27	SER	Peptide
1	BA	94	GLY	Peptide
2	BB	177	GLN	Peptide
2	BB	205	PHE	Peptide
2	BB	206	PRO	Peptide
2	BB	208	GLN	Peptide
2	BB	27	LYS	Peptide
3	BC	144	TRP	Peptide
3	BC	145	GLY	Peptide
5	BE	195	ILE	Peptide
6	BF	125	THR	Peptide
6	BF	42	LEU	Peptide
7	BG	68	LEU	Peptide
8	BH	110	GLN	Peptide
8	BH	64	VAL	Peptide
9	BI	20	GLN	Peptide
10	BJ	117	GLY	Peptide
10	BJ	133	HIS	Peptide
10	BJ	163	PRO	Peptide
11	BK	53	GLY	Peptide
11	BK	63	TYR	Peptide
15	BO	123	SER	Peptide
16	BP	100	LYS	Peptide
17	BQ	32	ASN	Peptide
17	BQ	33	GLY	Peptide
17	BQ	40	GLU	Peptide
19	BS	81	ILE	Peptide
19	BS	90	ASN	Peptide
20	BT	30	VAL	Peptide
24	BX	130	VAL	Peptide
24	BX	137	LYS	Peptide
24	BX	138	GLU	Peptide
24	BX	88	PRO	Peptide
24	BX	97	ASP	Peptide
26	BZ	68	ARG	Peptide
27	Ba	34	LYS	Peptide
27	Ba	35	ALA	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	36	0
2	BB	1709	0	1784	33	0
3	BC	1635	0	1723	31	0
4	BD	1734	0	1817	26	0
5	BE	2068	0	2154	39	0
6	BF	1609	0	1675	26	0
7	BG	1820	0	1918	28	0
8	BH	1481	0	1572	19	0
9	BI	1489	0	1525	44	0
10	BJ	1494	0	1573	29	0
11	BK	817	0	804	18	0
12	BL	1244	0	1314	12	0
13	BM	913	0	955	6	0
14	BN	1192	0	1255	27	0
15	BO	941	0	979	24	0
16	BP	991	0	1035	18	0
17	BQ	1105	0	1166	26	0
18	BR	975	0	1039	24	0
19	BS	1192	0	1222	28	0
20	BT	1095	0	1114	27	0
21	BU	855	0	917	18	0
22	BV	684	0	671	17	0
23	BW	1021	0	1060	18	0
24	BX	1121	0	1196	15	0
25	BY	1073	0	1132	30	0
26	BZ	558	0	598	6	0
27	Ba	769	0	818	25	0
28	Bb	610	0	631	8	0
29	Bc	497	0	535	8	0
30	Bd	442	0	432	8	0
31	Be	475	0	525	7	0
32	Bf	454	0	468	3	0
33	Bg	2401	0	2356	38	0
34	Bh	675	0	654	10	0
35	B5	37849	0	19076	421	0
36	A1	67139	0	33792	500	0
37	A3	2579	0	1304	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	A4	3353	0	1695	27	0
39	AA	1878	0	1946	39	0
40	AB	3078	0	3149	51	0
41	AC	2748	0	2859	28	0
42	AD	2341	0	2290	30	0
43	AE	1239	0	1326	16	0
44	AF	1784	0	1862	24	0
45	AG	1798	0	1894	26	0
46	AH	1510	0	1576	18	0
47	AI	1672	0	1711	22	0
48	AJ	1353	0	1383	28	0
49	AL	1543	0	1608	21	0
50	AM	1053	0	1149	11	0
51	AN	1720	0	1779	38	0
52	AO	1555	0	1659	14	0
53	AP	1388	0	1423	15	0
54	AQ	1441	0	1543	16	0
55	AR	1521	0	1617	18	0
56	AS	1445	0	1487	15	0
57	AT	1276	0	1323	19	0
58	AU	796	0	812	8	0
59	AV	1003	0	1048	12	0
60	AW	521	0	551	8	0
61	AX	968	0	1036	8	0
62	AY	993	0	1081	13	0
63	AZ	1092	0	1155	22	0
64	Aa	1173	0	1215	19	0
65	Ab	462	0	491	1	0
66	Ac	743	0	797	14	0
67	Ad	890	0	938	6	0
68	Ae	1020	0	1089	12	0
69	Af	850	0	880	6	0
70	Ag	880	0	945	13	0
71	Ah	969	0	1078	11	0
72	Ai	771	0	849	5	0
73	Aj	681	0	686	11	0
74	Ak	612	0	682	7	0
75	Al	436	0	475	7	0
76	Am	417	0	459	11	0
77	An	233	0	284	11	0
78	Ao	847	0	914	6	0
79	Ap	694	0	738	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	A1	242	0	0	0	0
80	A3	2	0	0	0	0
80	A4	9	0	0	0	0
80	AB	3	0	0	0	0
80	AG	1	0	0	0	0
80	AL	1	0	0	0	0
80	AN	2	0	0	0	0
80	AO	1	0	0	0	0
80	AP	1	0	0	0	0
80	AR	1	0	0	0	0
80	AX	1	0	0	0	0
80	Ae	4	0	0	0	0
80	Af	2	0	0	0	0
80	Aj	2	0	0	0	0
80	B5	91	0	0	0	0
80	BD	1	0	0	0	0
80	BJ	1	0	0	0	0
80	BL	1	0	0	0	0
81	Ao	1	0	0	0	0
81	Bb	1	0	0	0	0
All	All	199433	0	147894	1872	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 6.

All (1872) 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)
35:B5:1354:G:O6	35:B5:1369:U:C4	2.07	1.08
35:B5:868:G:H1	35:B5:960:U:H3	1.06	1.02
35:B5:1354:G:O6	35:B5:1369:U:N3	1.91	1.02
36:A1:1222:G:H21	36:A1:1286:A:N6	1.60	0.98
35:B5:1356:U:H3	35:B5:1367:G:H1	1.12	0.98
36:A1:2414:G:H1	36:A1:2806:U:H3	1.02	0.95
36:A1:1222:G:N2	36:A1:1286:A:H62	1.65	0.95
36:A1:173:G:O6	36:A1:245:U:C2	2.21	0.94
35:B5:222:A:H62	35:B5:833:U:H3	1.16	0.93
36:A1:3234:A:H2	36:A1:3253:G:H1	1.13	0.93
36:A1:2830:G:H1	36:A1:2858:U:H3	1.24	0.86
36:A1:1222:G:H21	36:A1:1286:A:H62	0.89	0.86
35:B5:223:U:H3	35:B5:838:G:H1	0.85	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:1354:G:C6	35:B5:1369:U:N3	2.47	0.82
35:B5:895:G:H1	35:B5:917:U:H3	1.33	0.76
36:A1:1132:C:H2'	36:A1:1133:A2M:H8	1.67	0.76
36:A1:733:G:N2	36:A1:736:A:C8	2.55	0.74
36:A1:1243:G:H1	36:A1:1248:C:H5''	1.52	0.74
35:B5:1291:G:H1	35:B5:1324:G:H22	1.37	0.73
36:A1:2257:C:N4	36:A1:2259:A:H62	1.85	0.73
36:A1:2257:C:H42	36:A1:2259:A:N6	1.86	0.73
36:A1:3232:G:H1	36:A1:3255:U:H3	1.35	0.73
36:A1:2257:C:N4	36:A1:2259:A:N6	2.36	0.72
9:BI:31:ARG:HH12	9:BI:48:THR:HG22	1.53	0.72
35:B5:1588:G:H1	35:B5:1608:U:H3	1.35	0.71
35:B5:1658:G:H1	35:B5:1743:U:H3	1.36	0.71
36:A1:2250:G:H1	36:A1:2266:U:H3	1.38	0.70
23:BW:31:SER:H	23:BW:34:ILE:HD12	1.56	0.70
35:B5:1757:G:H21	36:A1:2255:A:H1'	1.57	0.70
36:A1:562:C:H5''	56:AS:71:LYS:HD2	1.74	0.70
36:A1:3275:U:O2'	69:Af:99:ARG:NH1	2.26	0.69
19:BS:135:GLY:HA3	35:B5:1559:A:H5''	1.75	0.68
36:A1:816:A:H5'	36:A1:906:A:H61	1.58	0.68
36:A1:3234:A:C2	36:A1:3253:G:N1	2.50	0.68
51:AN:80:THR:HG22	51:AN:82:GLY:H	1.57	0.68
27:Ba:82:ARG:HH22	35:B5:1152:A:H5''	1.59	0.68
18:BR:24:LEU:HB3	18:BR:34:LEU:HD11	1.76	0.67
36:A1:2392:C:O2'	40:AB:266:ARG:NH2	2.27	0.67
4:BD:204:ASP:OD1	35:B5:1330:G:N2	2.27	0.67
48:AJ:60:ARG:HH21	78:Ao:104:LEU:HB2	1.59	0.67
36:A1:1351:U:O2	36:A1:1355:A:N7	2.28	0.67
36:A1:1575:A:O2'	36:A1:1576:G:N3	2.27	0.66
59:AV:81:GLN:O	59:AV:98:ASN:ND2	2.28	0.66
4:BD:211:PRO:HD3	18:BR:19:ARG:HD3	1.76	0.66
46:AH:186:PHE:HB2	46:AH:189:GLU:HB2	1.78	0.66
23:BW:15:ASN:ND2	23:BW:72:CYS:O	2.29	0.66
61:AX:50:ALA:HB1	71:Ah:66:VAL:HG11	1.77	0.65
9:BI:98:LYS:HB3	35:B5:329:G:H5''	1.78	0.65
22:BV:38:LYS:HE2	22:BV:49:GLU:HB3	1.78	0.65
36:A1:860:G:OP1	79:Ap:17:ARG:NH1	2.30	0.65
36:A1:3343:G:H21	36:A1:3362:A:H2	1.43	0.65
36:A1:3297:U:O4	40:AB:124:LYS:NZ	2.30	0.65
23:BW:14:ILE:HG23	23:BW:65:LEU:HD21	1.79	0.65
36:A1:2852:C:N3	47:AI:158:LYS:NZ	2.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AN:155:VAL:O	51:AN:162:ARG:NH2	2.30	0.65
15:BO:131:GLY:O	27:Ba:22:ARG:NH2	2.30	0.65
43:AE:20:LYS:HZ2	43:AE:22:ARG:HE	1.44	0.64
59:AV:87:ARG:HH22	59:AV:137:VAL:HG21	1.62	0.64
36:A1:1251:A:N7	36:A1:1263:A:N6	2.45	0.64
36:A1:2736:A:OP1	57:AT:92:ARG:NH1	2.29	0.64
62:AY:70:ILE:HG12	62:AY:82:VAL:HG22	1.78	0.64
22:BV:55:LEU:HD13	22:BV:65:SER:HB2	1.78	0.64
2:BB:109:LYS:HE3	2:BB:113:MET:HE3	1.79	0.64
36:A1:2676:A:N1	48:AJ:22:SER:OG	2.31	0.64
45:AG:54:GLU:HG2	45:AG:57:ARG:HH21	1.62	0.64
49:AL:76:THR:OG1	49:AL:101:ARG:NH1	2.30	0.64
21:BU:61:LYS:HB2	21:BU:86:ILE:HB	1.79	0.64
35:B5:44:U:OP2	35:B5:437:A:N6	2.31	0.64
38:A4:29:U:H5''	49:AL:27:ASP:HB3	1.79	0.64
35:B5:1280:4AC:H2'	35:B5:1281:G:H8	1.61	0.63
35:B5:869:A:H61	35:B5:958:U:H3	1.46	0.63
36:A1:1348:U:OP1	54:AQ:39:ARG:NH1	2.32	0.63
52:AO:61[A]:ALA:HA	52:AO:70[A]:PRO:HD2	1.80	0.63
16:BP:18:ARG:NH1	19:BS:90:ASN:O	2.32	0.63
35:B5:40:A:H62	35:B5:467:G:H21	1.46	0.63
61:AX:68:THR:HA	61:AX:73:MET:HE3	1.81	0.63
3:BC:236:PRO:O	22:BV:33:GLN:NE2	2.31	0.63
36:A1:2257:C:N4	36:A1:2259:A:C5	2.66	0.63
41:AC:138:ARG:HE	41:AC:240:PRO:HD2	1.64	0.63
1:BA:111:ILE:HD11	35:B5:1292:G:H21	1.63	0.63
26:BZ:95:HIS:ND1	26:BZ:96:SER:O	2.31	0.62
35:B5:514:G:H1	35:B5:543:C:H5	1.46	0.62
35:B5:488:G:H3'	35:B5:492:A:H62	1.65	0.62
36:A1:804:C:OP1	41:AC:98:ARG:NH2	2.32	0.62
36:A1:353:G:O6	73:Aj:52:LYS:NZ	2.32	0.62
17:BQ:143:ARG:NH1	35:B5:1464:G:OP1	2.29	0.62
35:B5:1339:C:O2'	35:B5:1341:A:N7	2.32	0.62
36:A1:1863:G:N1	36:A1:1866:C:OP2	2.32	0.62
20:BT:105:LEU:HD22	20:BT:122:ARG:HG3	1.82	0.62
36:A1:2673:A:N1	36:A1:2681:U:C4	2.68	0.62
39:AA:27:ALA:O	39:AA:128:ARG:NH2	2.33	0.62
33:Bg:122:ILE:HB	33:Bg:134:TRP:HB2	1.82	0.61
35:B5:790:U:H2'	35:B5:791:A:H8	1.65	0.61
36:A1:272:G:H1'	72:Ai:82:ARG:HH12	1.64	0.61
36:A1:687:U:OP2	49:AL:36:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:1213:G:O2'	35:B5:1244:A:N7	2.33	0.61
36:A1:3268:A:OP1	43:AE:46:ARG:NH2	2.31	0.61
37:A3:2:G:H5''	42:AD:273:ARG:HH21	1.64	0.61
21:BU:33:GLN:NE2	21:BU:110:PRO:O	2.33	0.61
35:B5:1483:A:OP2	35:B5:1521:G:N2	2.32	0.61
36:A1:3160:U:H3	36:A1:3290:G:H1	1.46	0.61
9:BI:152:ILE:HD11	9:BI:157:GLU:HB3	1.83	0.61
24:BX:69:ARG:NH2	35:B5:568:G:N7	2.48	0.61
36:A1:178:U:O4	36:A1:238:A:N7	2.33	0.61
57:AT:51:GLY:HA3	57:AT:92:ARG:HG3	1.83	0.61
7:BG:70:PRO:HA	7:BG:98:ARG:HH22	1.66	0.61
37:A3:64:A:N7	47:AI:209:ASN:ND2	2.49	0.61
36:A1:1190:A:H4'	76:Am:113:ARG:HH22	1.66	0.61
36:A1:1361:U:O2	44:AF:159:GLN:NE2	2.34	0.61
2:BB:110:LEU:HD11	2:BB:213:ARG:HD2	1.82	0.61
3:BC:140:ARG:NH2	3:BC:226:THR:OG1	2.34	0.61
14:BN:5:HIS:HB3	14:BN:117:LEU:HD13	1.83	0.61
36:A1:2551:U:OP1	70:Ag:102:LYS:NZ	2.33	0.61
36:A1:784:A:OP2	54:AQ:69:ARG:NH2	2.33	0.60
44:AF:83:LEU:HD11	44:AF:116:PHE:HB3	1.83	0.60
35:B5:222:A:N6	35:B5:833:U:H3	1.94	0.60
76:Am:91:CYS:HA	76:Am:124:LYS:HD3	1.82	0.60
20:BT:122:ARG:HH21	35:B5:1499:G:H5''	1.65	0.60
21:BU:24:ILE:HG12	21:BU:116:VAL:HG12	1.83	0.60
76:Am:122:ARG:NH1	76:Am:123:PRO:O	2.35	0.60
7:BG:57:ASP:HA	7:BG:106:LEU:HA	1.83	0.60
35:B5:89:G:H21	35:B5:452:A:H5''	1.67	0.60
35:B5:979:A:N3	35:B5:1775:U:O2'	2.33	0.60
58:AU:61:THR:HG22	58:AU:62:VAL:HG23	1.82	0.60
1:BA:197:ILE:HG23	1:BA:201:LEU:HD21	1.84	0.60
10:BJ:105:LEU:HD13	10:BJ:108:ARG:HD2	1.84	0.60
33:Bg:211:ILE:HD11	33:Bg:225:LEU:HD13	1.83	0.60
5:BE:68:ARG:HE	5:BE:76:VAL:HG11	1.66	0.59
36:A1:1940:G:H21	36:A1:3362:A:H8	1.48	0.59
36:A1:2149:A:N6	36:A1:2187:G:O2'	2.30	0.59
1:BA:201:LEU:HB3	18:BR:85:VAL:HG12	1.85	0.59
20:BT:89:ARG:NH1	35:B5:1562:G:OP1	2.32	0.59
36:A1:3234:A:H2	36:A1:3253:G:N1	1.90	0.59
37:A3:1:G:N3	42:AD:269:SER:OG	2.34	0.59
40:AB:284:ARG:NH1	40:AB:293:ASN:O	2.35	0.59
17:BQ:39:VAL:HG22	17:BQ:45:ARG:HE	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1940:G:OP1	55:AR:75:HIS:ND1	2.35	0.59
18:BR:45:ARG:NH1	35:B5:1332:C:OP2	2.34	0.59
36:A1:1639:C:OP2	70:Ag:74:ARG:NH2	2.36	0.59
41:AC:65:TRP:HB3	41:AC:69:ARG:HG3	1.83	0.59
35:B5:980:G:H4'	35:B5:1776:A:H4'	1.83	0.59
36:A1:2901:G:O2'	36:A1:3024:A:N1	2.36	0.59
5:BE:100:ARG:HH12	5:BE:122:LYS:HA	1.68	0.59
7:BG:137:ARG:NH1	35:B5:144:U:O4	2.33	0.59
23:BW:106:THR:HG22	23:BW:108:ALA:H	1.68	0.59
25:BY:105:ARG:NH2	35:B5:459:G:OP2	2.36	0.59
36:A1:1727:G:OP1	79:Ap:44:LYS:NZ	2.34	0.59
6:BF:112:ARG:NH2	17:BQ:42:GLU:OE2	2.35	0.59
7:BG:13:GLN:NE2	35:B5:151:G:N3	2.50	0.59
9:BI:92:ARG:NH2	36:A1:3344:A:O2'	2.36	0.59
18:BR:26:LEU:HD23	18:BR:59:LYS:HG2	1.83	0.59
27:Ba:44:ILE:HG23	27:Ba:45:VAL:HG13	1.85	0.59
9:BI:172:ARG:NH1	35:B5:330:G:OP2	2.36	0.59
35:B5:1114:G:N2	35:B5:1115:U:O4	2.33	0.59
53:AP:64:ASN:O	53:AP:80:LYS:NZ	2.32	0.59
56:AS:22:PRO:O	57:AT:146:ASN:ND2	2.35	0.59
35:B5:976:G:N1	35:B5:1023:A:O2'	2.35	0.59
36:A1:2779:A:O2'	49:AL:180:ARG:NH2	2.34	0.59
36:A1:1156:C:OP2	44:AF:94:LYS:NZ	2.36	0.58
38:A4:37:A:OP1	71:Ah:89:ARG:NH2	2.35	0.58
38:A4:71:A:O2'	62:AY:52:ARG:NH2	2.36	0.58
67:Ad:74:ARG:HB3	67:Ad:94:GLU:HB2	1.85	0.58
1:BA:180:GLU:OE1	1:BA:191:ARG:NH2	2.35	0.58
36:A1:3234:A:N1	36:A1:3253:G:O6	2.36	0.58
39:AA:28:LYS:HB3	39:AA:123:ARG:HB3	1.85	0.58
51:AN:183:THR:HG22	51:AN:187:ARG:HB3	1.85	0.58
9:BI:157:GLU:HA	9:BI:160:PHE:HD2	1.68	0.58
27:Ba:32:LYS:O	27:Ba:37:LYS:NZ	2.37	0.58
36:A1:797:U:O2	49:AL:12:ASN:ND2	2.37	0.58
57:AT:48:ILE:HG13	57:AT:94:GLU:HG3	1.83	0.58
55:AR:39:ASN:OD1	55:AR:42:ARG:NH2	2.36	0.58
63:AZ:23:VAL:HG12	63:AZ:45:GLY:HA3	1.85	0.58
35:B5:225:A:N6	35:B5:835:U:O4	2.36	0.58
36:A1:3313:U:H4'	40:AB:173:GLN:HG3	1.85	0.58
41:AC:3:ARG:NH1	41:AC:27:SER:OG	2.37	0.58
38:A4:52:A:H62	75:Al:27:ILE:HD13	1.68	0.58
64:Aa:112:ILE:HB	64:Aa:130:VAL:HG12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:BR:59:LYS:NZ	35:B5:1393:C:OP2	2.36	0.58
36:A1:2404:A:N6	36:A1:2872:A:N7	2.52	0.58
33:Bg:126:SER:OG	33:Bg:127:ARG:N	2.36	0.58
35:B5:1210:C:H2'	35:B5:1211:A:H8	1.69	0.58
36:A1:3232:G:N2	36:A1:3255:U:O2	2.35	0.58
27:Ba:51:ARG:NH2	29:Bc:60:GLU:O	2.37	0.58
9:BI:25:ARG:HA	35:B5:400:A:H5''	1.86	0.58
36:A1:1634:G:N7	63:AZ:17:ARG:NH2	2.52	0.58
40:AB:83:PRO:O	40:AB:165:GLN:NE2	2.37	0.58
1:BA:88:LYS:NZ	1:BA:201:LEU:O	2.37	0.57
10:BJ:106:GLU:O	10:BJ:112:GLN:NE2	2.37	0.57
36:A1:267:G:OP2	36:A1:318:A:N6	2.37	0.57
36:A1:1682:U:O4	58:AU:90:ARG:NH1	2.37	0.57
36:A1:2611:U:O2'	36:A1:2803:A:N6	2.37	0.57
48:AJ:134:PRO:O	48:AJ:152:HIS:NE2	2.33	0.57
66:Ac:66:LYS:NZ	66:Ac:101:LEU:O	2.37	0.57
2:BB:39:GLU:HB2	2:BB:74:GLN:HA	1.87	0.57
35:B5:92:A:OP1	35:B5:398:G:N2	2.36	0.57
35:B5:629:U:O2	35:B5:970:A:N7	2.37	0.57
37:A3:6:C:O2'	42:AD:50:ARG:NH2	2.37	0.57
41:AC:338:LYS:O	41:AC:340:GLY:N	2.38	0.57
9:BI:178:ARG:NH2	35:B5:258:C:O2	2.37	0.57
36:A1:728:G:H5''	54:AQ:43:PRO:HB2	1.85	0.57
46:AH:103:ILE:HD11	46:AH:110:LYS:HE3	1.85	0.57
71:Ah:85:THR:HB	71:Ah:88:LEU:HB2	1.85	0.57
2:BB:132:ASP:HB3	2:BB:221:PRO:HB3	1.86	0.57
7:BG:92:ARG:NH2	35:B5:1674:C:OP1	2.31	0.57
19:BS:53:ASP:HB3	19:BS:56:LYS:HE2	1.86	0.57
2:BB:115:ARG:HH21	2:BB:208:GLN:HE22	1.52	0.57
19:BS:18:LEU:HD21	19:BS:101:LEU:HD13	1.86	0.57
4:BD:23:GLU:OE1	30:Bd:46:LYS:NZ	2.32	0.57
12:BL:105:LYS:NZ	35:B5:307:G:OP2	2.38	0.57
24:BX:48:HIS:HB3	24:BX:103:LEU:HD11	1.87	0.57
35:B5:992:A:O2'	35:B5:1785:U:O2	2.22	0.57
51:AN:143:ARG:NH2	71:Ah:90:ARG:O	2.38	0.57
62:AY:55:GLU:HB3	62:AY:108:LYS:HB3	1.87	0.57
10:BJ:119:ALA:O	10:BJ:124:HIS:ND1	2.35	0.57
36:A1:36:C:H4'	36:A1:808:A:H2	1.70	0.57
36:A1:1181:U:O4	52:AO:21[A]:SER:OG	2.20	0.57
69:Af:14:LEU:HD11	69:Af:31:LYS:HB2	1.87	0.57
7:BG:201:GLN:NE2	35:B5:125:U:OP1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:34:G:O2'	35:B5:515:A:O2'	2.23	0.57
41:AC:35:VAL:HG21	41:AC:244:LEU:HD21	1.85	0.57
66:Ac:30:THR:HG23	66:Ac:91:SER:HB2	1.85	0.57
3:BC:170:ILE:HB	3:BC:197:TYR:HB2	1.87	0.57
4:BD:166:ASP:O	4:BD:190:ARG:NH2	2.38	0.57
8:BH:62:VAL:HG22	8:BH:94:ALA:HA	1.87	0.57
35:B5:321:C:N4	35:B5:1667:A:OP2	2.38	0.57
36:A1:838:G:O6	79:Ap:4:ARG:NH2	2.37	0.57
66:Ac:13:LYS:HB3	66:Ac:100:ILE:HG22	1.87	0.57
74:Ak:45:VAL:HB	74:Ak:52:TYR:HB2	1.87	0.57
35:B5:629:U:C2	35:B5:970:A:N7	2.72	0.56
36:A1:68:C:OP2	36:A1:301:G:N2	2.38	0.56
47:AI:30:LYS:HD2	47:AI:63:GLU:HG3	1.87	0.56
6:BF:63:GLN:HB3	6:BF:88:PRO:HA	1.87	0.56
34:Bh:95:SER:HA	35:B5:1274:C:H41	1.71	0.56
36:A1:2257:C:N4	36:A1:2259:A:C6	2.73	0.56
9:BI:136:SER:HB3	9:BI:138:ASN:HD22	1.70	0.56
11:BK:10:LYS:HD2	11:BK:37:THR:HB	1.86	0.56
23:BW:80:ASN:OD1	23:BW:124:LYS:NZ	2.38	0.56
25:BY:124:ARG:HH12	25:BY:128:LYS:HD3	1.70	0.56
35:B5:1775:U:OP1	77:An:11:ARG:NH2	2.37	0.56
36:A1:120:G:N2	45:AG:126:SER:O	2.38	0.56
36:A1:1128:U:OP1	47:AI:4:ARG:NH2	2.35	0.56
52:AO:32[A]:LYS:HG2	52:AO:101[A]:ARG:HG2	1.88	0.56
53:AP:122:ALA:HB3	53:AP:143:PRO:HB2	1.87	0.56
5:BE:3:ARG:HB3	35:B5:93:A:H1'	1.86	0.56
6:BF:93:LEU:HD12	6:BF:172:ILE:HG23	1.85	0.56
18:BR:23:LYS:O	33:Bg:216:LYS:NZ	2.39	0.56
35:B5:629:U:N3	35:B5:970:A:C8	2.60	0.56
36:A1:117:U:OP2	51:AN:2:GLY:N	2.38	0.56
36:A1:1805:C:H2'	36:A1:1806:A:H8	1.70	0.56
36:A1:1809:A:OP2	63:AZ:65:ARG:NH1	2.38	0.56
36:A1:3086:A:OP1	40:AB:367:LYS:NZ	2.38	0.56
24:BX:90:ASP:O	24:BX:136:TRP:NE1	2.38	0.56
36:A1:939:U:OP2	64:Aa:26:ARG:NH2	2.38	0.56
36:A1:1057:A:OP1	44:AF:98:LYS:NZ	2.37	0.56
66:Ac:22:LYS:HG2	66:Ac:94:GLU:HB3	1.86	0.56
19:BS:27:LYS:HA	19:BS:57:ARG:HA	1.86	0.56
24:BX:65:ASN:ND2	35:B5:574:G:O6	2.35	0.56
36:A1:1317:A:O2'	52:AO:18[A]:ARG:NH2	2.37	0.56
38:A4:80:A:H4'	38:A4:82:U:H5	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:AC:334:PHE:HA	41:AC:339:LEU:HD12	1.86	0.56
70:Ag:44:CYS:HA	70:Ag:51:LEU:HD23	1.88	0.56
9:BI:2:GLY:N	35:B5:393:C:OP2	2.39	0.56
24:BX:43:PHE:HZ	24:BX:104:LEU:HB2	1.70	0.56
31:Be:41:THR:HA	31:Be:45:VAL:HB	1.87	0.56
35:B5:1658:G:N2	35:B5:1743:U:O2	2.31	0.56
37:A3:64:A:H5'	37:A3:65:G:H5''	1.87	0.56
47:AI:45:GLU:O	47:AI:141:LYS:NZ	2.38	0.56
4:BD:40:ARG:HD2	21:BU:110:PRO:HG3	1.87	0.56
5:BE:103:TYR:O	5:BE:182:TYR:OH	2.24	0.56
14:BN:46:THR:HG22	14:BN:48:SER:H	1.70	0.56
36:A1:1446:A:H5''	53:AP:65:SER:HB2	1.88	0.56
39:AA:116:VAL:HB	39:AA:126:LEU:HB2	1.88	0.56
39:AA:153:GLY:O	39:AA:155:LYS:NZ	2.38	0.56
5:BE:38:LEU:HB2	35:B5:298:C:H5''	1.88	0.56
35:B5:1488:G:O2'	35:B5:1494:C:O2	2.22	0.56
36:A1:3050:U:O2'	60:AW:16:GLY:O	2.24	0.56
2:BB:88:VAL:HA	2:BB:98:THR:HA	1.88	0.56
8:BH:113:PRO:HG2	8:BH:116:ARG:HD3	1.88	0.56
27:Ba:2:PRO:HB3	35:B5:1142:A:H5''	1.88	0.56
36:A1:896:A:H5''	39:AA:183:GLY:HA2	1.87	0.56
40:AB:77:THR:OG1	40:AB:326:GLY:O	2.23	0.56
72:AI:88:GLU:O	72:AI:92:ASN:ND2	2.38	0.56
74:AK:26:LYS:NZ	74:AK:28:ASN:OD1	2.39	0.56
17:BQ:41:PRO:HG2	17:BQ:44:LEU:HB2	1.88	0.55
17:BQ:83:GLN:NE2	17:BQ:115:THR:O	2.33	0.55
26:BZ:61:SER:H	26:BZ:64:VAL:HB	1.71	0.55
35:B5:1773:4AC:H5	77:An:2:ARG:HH21	1.71	0.55
36:A1:80:G:OP1	51:AN:193:ARG:NH1	2.38	0.55
36:A1:911:C:H42	39:AA:3:ARG:HH11	1.53	0.55
42:AD:120:LYS:O	42:AD:248:ARG:NH1	2.37	0.55
46:AH:89:LYS:HG2	46:AH:145:VAL:HG22	1.87	0.55
49:AL:49:ARG:O	49:AL:137:GLN:NE2	2.39	0.55
16:BP:127:ARG:HD2	16:BP:130:ARG:HH21	1.70	0.55
36:A1:7:C:H5''	45:AG:193:LYS:HB3	1.88	0.55
36:A1:2294:U:OP2	59:AV:71:LYS:NZ	2.39	0.55
39:AA:47:GLN:HB3	39:AA:49:VAL:HG13	1.87	0.55
51:AN:44:ARG:NH1	51:AN:120:TRP:O	2.40	0.55
66:Ac:10:ILE:HA	66:Ac:13:LYS:HB2	1.87	0.55
21:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	1.87	0.55
35:B5:987:G:N2	35:B5:1013:A:OP2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AY:42:GLN:NE2	62:AY:127:GLU:O	2.38	0.55
79:Ap:46:THR:OG1	79:Ap:57:CYS:SG	2.61	0.55
8:BH:11:GLN:HG3	8:BH:13:PRO:HD2	1.87	0.55
18:BR:2:GLY:N	35:B5:1403:C:OP1	2.40	0.55
36:A1:1055:A:N3	37:A3:81:U:O2'	2.37	0.55
47:AI:36:LEU:HD21	47:AI:69:ARG:HH11	1.71	0.55
5:BE:196:VAL:N	5:BE:209:HIS:O	2.37	0.55
9:BI:10:LYS:NZ	35:B5:322:G:O2'	2.39	0.55
10:BJ:113:VAL:HG12	10:BJ:119:ALA:HB2	1.89	0.55
25:BY:109:LYS:NZ	35:B5:459:G:OP1	2.36	0.55
35:B5:1619:C:H2'	35:B5:1620:C:H6	1.71	0.55
36:A1:1002:A:N1	36:A1:1050:U:O2'	2.40	0.55
36:A1:2196:C:O2'	36:A1:2270:A:N3	2.39	0.55
57:AT:39:ILE:HG12	57:AT:63:VAL:HG22	1.89	0.55
3:BC:38:VAL:HG13	3:BC:39:THR:HG23	1.88	0.55
3:BC:101:VAL:HG12	3:BC:115:ILE:HG22	1.89	0.55
8:BH:77:LEU:HD22	8:BH:92:PHE:HZ	1.70	0.55
10:BJ:63:ASP:OD1	23:BW:117:ARG:NH1	2.39	0.55
35:B5:941:A:O2'	35:B5:1025:A:N6	2.40	0.55
35:B5:1297:G:N2	35:B5:1300:A:OP2	2.31	0.55
36:A1:718:G:OP1	64:Aa:117:ARG:NH2	2.39	0.55
36:A1:1666:G:H1	36:A1:1783:U:H3	1.55	0.55
36:A1:1923:C:H5''	77:An:25:LYS:HD2	1.87	0.55
36:A1:2197:OMC:H5''	36:A1:2242:A:H61	1.72	0.55
59:AV:18:PRO:HA	59:AV:51:ALA:HA	1.87	0.55
63:AZ:89:VAL:HG23	63:AZ:93:LYS:HD2	1.89	0.55
7:BG:137:ARG:NH2	35:B5:143:G:N7	2.55	0.55
8:BH:68:ALA:HA	8:BH:71:HIS:HB2	1.89	0.55
10:BJ:107:ARG:NH2	10:BJ:153:GLU:OE2	2.40	0.55
33:Bg:292:LEU:HD12	33:Bg:301:LEU:HD11	1.89	0.55
35:B5:193:U:OP1	35:B5:195:G:N2	2.39	0.55
35:B5:1591:C:H2'	35:B5:1592:A:H8	1.72	0.55
36:A1:1592:G:OP1	70:Ag:58:ARG:NH2	2.38	0.55
38:A4:141:C:OP1	51:AN:109:ARG:NH2	2.40	0.55
9:BI:48:THR:OG1	9:BI:52:ASN:O	2.21	0.55
14:BN:123:HIS:ND1	36:A1:846:A:O2'	2.38	0.55
17:BQ:39:VAL:HG11	17:BQ:48:VAL:HG21	1.89	0.55
35:B5:1171:A:H2'	35:B5:1172:G:C8	2.42	0.55
35:B5:1303:U:O2'	35:B5:1322:A:OP2	2.24	0.55
5:BE:71:LYS:HG3	5:BE:91:THR:HB	1.90	0.54
6:BF:92:ARG:HH21	6:BF:168:VAL:HG12	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Bg:240:VAL:HG22	33:Bg:256:THR:HG22	1.89	0.54
55:AR:167:ARG:HE	55:AR:171:ASP:HB2	1.71	0.54
5:BE:92:LEU:HD13	25:BY:17:LEU:HD11	1.89	0.54
8:BH:28:GLU:HG3	8:BH:38:LEU:HD23	1.89	0.54
8:BH:112:ARG:NH2	35:B5:639:U:OP1	2.40	0.54
13:BM:46:ARG:NH2	35:B5:1254:U:OP2	2.40	0.54
16:BP:81:ARG:NH2	16:BP:117:GLY:O	2.40	0.54
17:BQ:32:ASN:O	17:BQ:68:ARG:NH1	2.40	0.54
35:B5:1118:G:OP1	77:An:21:ARG:NH2	2.40	0.54
19:BS:17:LEU:HD13	19:BS:66:LEU:HD23	1.89	0.54
32:Bf:138:ARG:NH1	35:B5:1235:C:O2	2.39	0.54
35:B5:1171:A:H2'	35:B5:1172:G:H8	1.72	0.54
36:A1:799:G:O2'	49:AL:18:TRP:NE1	2.39	0.54
36:A1:1447:G:N7	53:AP:25:SER:OG	2.38	0.54
36:A1:1778:G:O2'	36:A1:1780:G:OP2	2.25	0.54
67:Ad:55:LEU:HB2	67:Ad:95:PRO:HD3	1.89	0.54
73:Aj:87:SER:OG	73:Aj:88:ALA:N	2.41	0.54
2:BB:130:SER:HB2	2:BB:180:THR:HG22	1.89	0.54
13:BM:28:LEU:HD21	13:BM:61:VAL:HG11	1.88	0.54
17:BQ:29:ILE:HD13	17:BQ:52:LEU:HD21	1.90	0.54
36:A1:1669:C:H5'	70:Ag:30:LEU:HD11	1.90	0.54
36:A1:2396:G:H3'	36:A1:2398:A:H5''	1.89	0.54
36:A1:3140:G:N7	40:AB:28:ARG:NH2	2.56	0.54
40:AB:211:GLN:NE2	40:AB:283:TYR:O	2.35	0.54
6:BF:42:LEU:O	6:BF:45:LYS:N	2.38	0.54
35:B5:1022:C:H4'	35:B5:1125:A:H61	1.72	0.54
35:B5:1642:G:H4'	77:An:1:MET:HE3	1.88	0.54
36:A1:1795:U:OP2	39:AA:50:HIS:NE2	2.41	0.54
8:BH:15:GLU:HG2	8:BH:16:LEU:HD12	1.89	0.54
11:BK:77:ARG:NH2	11:BK:87:VAL:O	2.41	0.54
27:Ba:7:SER:OG	27:Ba:10:ARG:O	2.26	0.54
36:A1:173:G:O6	36:A1:245:U:O2	2.26	0.54
36:A1:2588:U:OP1	45:AG:241:LYS:NZ	2.41	0.54
41:AC:342:LYS:HE3	44:AF:56:GLU:HG3	1.90	0.54
60:AW:45:ASN:HB3	60:AW:48:ARG:HG3	1.90	0.54
62:AY:80:VAL:HG21	62:AY:104:LEU:HD11	1.90	0.54
11:BK:78:GLU:O	11:BK:81:ASN:ND2	2.41	0.54
14:BN:9:LYS:NZ	35:B5:1034:C:OP1	2.38	0.54
14:BN:104:ARG:NH2	35:B5:951:A:OP1	2.40	0.54
48:AJ:12:LEU:HB3	48:AJ:131:MET:HE2	1.90	0.54
68:Ae:123:LYS:HA	68:Ae:126:LEU:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BS:27:LYS:HE3	19:BS:55:HIS:HA	1.89	0.54
36:A1:2366:C:OP1	40:AB:259:HIS:NE2	2.37	0.54
19:BS:86:LEU:HD22	19:BS:99:HIS:HB2	1.89	0.54
19:BS:123:ARG:NH1	35:B5:1546:G:OP1	2.34	0.54
20:BT:48:GLN:OE1	35:B5:1531:G:N2	2.41	0.54
36:A1:1712:G:O6	66:Ac:28:LYS:NZ	2.41	0.54
1:BA:126:PRO:HG2	1:BA:151:SER:HB2	1.90	0.54
4:BD:40:ARG:NH2	4:BD:47:GLU:OE1	2.40	0.54
35:B5:1673:G:O6	35:B5:1728:A:N1	2.41	0.54
39:AA:150:LEU:HD11	39:AA:156:LYS:HD2	1.89	0.54
47:AI:29:SER:HB2	47:AI:125:LEU:HD12	1.89	0.54
51:AN:96:ARG:NH2	51:AN:104:GLU:OE1	2.40	0.54
63:AZ:113:VAL:HA	63:AZ:116:LYS:HE2	1.90	0.54
6:BF:72:HIS:NE2	35:B5:1610:G:OP1	2.38	0.53
35:B5:424:C:O2	35:B5:427:C:N4	2.41	0.53
36:A1:3008:A:OP2	52:AO:74[A]:ARG:NH1	2.41	0.53
66:Ac:25:LEU:HD21	66:Ac:81:VAL:HG21	1.90	0.53
2:BB:118:GLN:OE1	2:BB:208:GLN:NE2	2.41	0.53
30:Bd:32:ARG:NH2	35:B5:1596:C:O2	2.38	0.53
36:A1:1264:G:OP2	36:A1:1278:A:N6	2.41	0.53
17:BQ:136:SER:HB3	35:B5:1586:A:H5''	1.89	0.53
24:BX:70:LYS:NZ	35:B5:567:A:OP1	2.41	0.53
36:A1:89:A:N7	54:AQ:171:LYS:NZ	2.56	0.53
36:A1:2720:G:OP1	54:AQ:180:ARG:NH1	2.42	0.53
40:AB:185:GLY:O	40:AB:191:LYS:NZ	2.31	0.53
44:AF:155:LYS:HG3	44:AF:158:LYS:HA	1.90	0.53
48:AJ:161:SER:HA	48:AJ:164:LYS:HE2	1.89	0.53
60:AW:21:PHE:HB3	60:AW:29:PHE:HB2	1.90	0.53
15:BO:129:LYS:NZ	35:B5:1008:G:OP1	2.37	0.53
35:B5:1003:A:O2'	35:B5:1005:A:N7	2.34	0.53
2:BB:43:VAL:HG13	2:BB:68:VAL:HG21	1.89	0.53
5:BE:151:ASP:OD1	5:BE:153:ASN:ND2	2.42	0.53
10:BJ:41:GLU:OE2	10:BJ:126:ARG:NH2	2.39	0.53
14:BN:46:THR:HG23	14:BN:86:GLU:HG2	1.91	0.53
15:BO:24:ASN:ND2	35:B5:903:U:OP2	2.41	0.53
23:BW:17:ALA:HB3	23:BW:25:VAL:HG12	1.91	0.53
35:B5:96:G:H1	35:B5:387:A:H61	1.56	0.53
35:B5:477:A:H61	35:B5:511:A:H61	1.57	0.53
35:B5:814:A:O2'	35:B5:816:G:OP2	2.26	0.53
37:A3:72:A:O2'	37:A3:74:C:OP1	2.27	0.53
42:AD:50:ARG:NH1	42:AD:147:ASP:OD2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:AJ:98:ALA:HA	48:AJ:156:LYS:HB2	1.91	0.53
1:BA:101:ARG:NH2	35:B5:1321:A:OP2	2.42	0.53
4:BD:138:VAL:HG22	4:BD:184:ILE:HG22	1.91	0.53
12:BL:8:GLN:NE2	12:BL:14:GLN:O	2.41	0.53
13:BM:66:VAL:HG13	13:BM:67:THR:HG22	1.89	0.53
29:Bc:44:VAL:HG11	29:Bc:48:VAL:HB	1.90	0.53
36:A1:269:G:OP2	51:AN:44:ARG:NH2	2.42	0.53
36:A1:1390:A:N6	36:A1:1418:A:O2'	2.42	0.53
36:A1:2748:A:H1'	42:AD:36:LEU:HD23	1.91	0.53
48:AJ:47:GLN:HG2	48:AJ:67:VAL:HG12	1.91	0.53
12:BL:97:TYR:O	12:BL:99:ARG:NH1	2.42	0.53
20:BT:6:VAL:HG22	20:BT:136:ALA:HB2	1.90	0.53
33:Bg:22:SER:HB3	33:Bg:36:ALA:HB3	1.90	0.53
36:A1:577:C:O2'	36:A1:579:G:OP1	2.27	0.53
36:A1:1347:U:O2'	36:A1:1351:U:O2'	2.27	0.53
36:A1:3231:U:H2'	36:A1:3232:G:H8	1.74	0.53
47:AI:164:LYS:HD3	47:AI:166:ILE:HD11	1.91	0.53
20:BT:86:ARG:NH2	35:B5:1601:G:OP1	2.37	0.53
35:B5:1482:C:O5'	35:B5:1521:G:N2	2.40	0.53
36:A1:2552:C:H2'	66:Ac:50:VAL:HG11	1.91	0.53
36:A1:2948:OMC:OP1	40:AB:244:ARG:NH1	2.38	0.53
39:AA:95:SER:O	39:AA:100:ASN:ND2	2.41	0.53
2:BB:180:THR:O	2:BB:184:LEU:N	2.40	0.53
6:BF:166:ARG:HH12	29:Bc:45:LYS:HE3	1.73	0.53
15:BO:126:THR:HG21	35:B5:888:U:H1'	1.91	0.53
19:BS:15:LEU:HD12	19:BS:66:LEU:HD21	1.90	0.53
22:BV:58:TYR:OH	22:BV:62:ARG:NH1	2.41	0.53
25:BY:34:ASN:O	35:B5:521:A:O2'	2.25	0.53
35:B5:653:C:OP1	35:B5:680:U:N3	2.39	0.53
35:B5:1106:U:H2'	35:B5:1107:G:H8	1.74	0.53
36:A1:63:A:H5''	51:AN:174:ILE:HG21	1.91	0.53
36:A1:1631:C:OP2	63:AZ:48:ARG:NH2	2.41	0.53
41:AC:156:LEU:HD12	41:AC:159:ILE:HD12	1.90	0.53
78:Ao:25:VAL:HG22	78:Ao:72:LEU:HG	1.91	0.53
9:BI:152:ILE:HG13	9:BI:153:GLU:H	1.74	0.53
16:BP:85:ILE:HG22	16:BP:112:LEU:HD23	1.90	0.53
31:Be:28:LYS:NZ	35:B5:477:A:OP1	2.42	0.53
4:BD:48:VAL:HB	4:BD:86:LEU:HG	1.89	0.52
35:B5:1793:G:O2'	35:B5:1795:U:OP2	2.26	0.52
36:A1:2146:C:OP1	39:AA:200:ARG:NH1	2.40	0.52
36:A1:2727:A:O2'	36:A1:2729:OMU:OP1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AM:50:LYS:NZ	50:AM:82:SER:O	2.41	0.52
36:A1:1472:U:H5'	55:AR:4:LEU:HB2	1.90	0.52
36:A1:2981:U:OP2	40:AB:244:ARG:NH2	2.33	0.52
36:A1:3186:A:N3	46:AH:44:THR:OG1	2.40	0.52
51:AN:71:ARG:HB2	51:AN:94:TYR:HB2	1.91	0.52
71:Ah:34:GLN:HB3	71:Ah:38:ARG:HH22	1.74	0.52
1:BA:127:ARG:NH2	1:BA:150:ASP:O	2.42	0.52
3:BC:205:ARG:NH2	35:B5:7:G:N7	2.58	0.52
16:BP:129:GLY:HA3	34:Bh:74:LYS:HD2	1.90	0.52
35:B5:524:U:O2'	35:B5:526:A:N7	2.38	0.52
41:AC:110:ASN:HD22	51:AN:201:ARG:HB3	1.73	0.52
46:AH:150:SER:HB3	46:AH:153:ASP:HB2	1.91	0.52
57:AT:39:ILE:HB	57:AT:102:ARG:HG3	1.92	0.52
75:Al:3:ALA:O	75:Al:4:GLN:NE2	2.37	0.52
33:Bg:109:ASP:OD2	33:Bg:127:ARG:NH1	2.42	0.52
33:Bg:110:VAL:HA	33:Bg:126:SER:HA	1.90	0.52
35:B5:222:A:N7	35:B5:833:U:O2	2.43	0.52
35:B5:329:G:H2'	35:B5:330:G:H8	1.74	0.52
35:B5:1653:C:H4'	77:An:21:ARG:HD2	1.92	0.52
36:A1:912:G:OP2	39:AA:9:ARG:NH1	2.41	0.52
36:A1:2697:A:H2'	36:A1:2698:G:C8	2.45	0.52
43:AE:43:LEU:HD11	43:AE:85:ILE:HG13	1.90	0.52
68:Ae:59:SER:HB2	68:Ae:64:LYS:HG3	1.92	0.52
6:BF:58:LEU:HD22	6:BF:168:VAL:HG23	1.92	0.52
20:BT:36:ILE:HG13	20:BT:37:VAL:HG13	1.91	0.52
36:A1:2209:U:N3	36:A1:2230:C:OP1	2.36	0.52
36:A1:2895:G:O2'	76:Am:100:TYR:O	2.23	0.52
40:AB:85:VAL:HG22	40:AB:202:THR:HG22	1.91	0.52
46:AH:137:SER:HB2	46:AH:143:GLU:HB3	1.92	0.52
70:Ag:95:ILE:HG22	70:Ag:99:LYS:HE3	1.91	0.52
10:BJ:108:ARG:NH1	10:BJ:110:GLN:OE1	2.41	0.52
35:B5:564:G:N2	35:B5:577:G:OP1	2.42	0.52
35:B5:1515:A:O2'	35:B5:1517:U:OP2	2.26	0.52
36:A1:608:A:O3'	41:AC:326:ARG:NH1	2.42	0.52
36:A1:2816:G:N2	36:A1:2819:A:OP2	2.40	0.52
47:Al:29:SER:OG	47:Al:30:LYS:N	2.41	0.52
2:BB:107:THR:OG1	15:BO:117:ASP:OD1	2.27	0.52
3:BC:91:ARG:HH21	35:B5:1147:A:H5''	1.74	0.52
3:BC:161:LYS:NZ	35:B5:1086:A:OP2	2.43	0.52
5:BE:12:LEU:HD21	5:BE:22:LYS:HG2	1.90	0.52
33:Bg:34:LEU:HD11	33:Bg:42:LEU:HD23	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:900:A:H3'	35:B5:901:G:H21	1.75	0.52
36:A1:1277:C:O2'	36:A1:1279:C:N4	2.43	0.52
36:A1:1364:C:OP1	44:AF:110:ARG:NH2	2.34	0.52
36:A1:2661:G:H2'	36:A1:2662:G:H8	1.75	0.52
47:AI:49:CYS:HG	47:AI:51:HIS:HE2	1.55	0.52
5:BE:19:LEU:HD11	5:BE:108:ARG:HD2	1.92	0.52
9:BI:49:ARG:NH1	35:B5:399:A:OP1	2.41	0.52
19:BS:134:ARG:HB2	19:BS:136:GLN:HE22	1.74	0.52
27:Ba:12:LYS:HG3	27:Ba:15:ARG:HB2	1.91	0.52
33:Bg:42:LEU:HD11	33:Bg:68:VAL:HG11	1.91	0.52
36:A1:2433:U:H1'	51:AN:125:SER:HB3	1.92	0.52
14:BN:107:LYS:NZ	35:B5:1018:U:OP1	2.43	0.52
20:BT:6:VAL:HG21	20:BT:132:LEU:HB3	1.91	0.52
36:A1:837:A:OP2	79:Ap:4:ARG:NH1	2.40	0.52
36:A1:2896:A:OP1	76:Am:124:LYS:NZ	2.43	0.52
37:A3:81:U:H2'	37:A3:82:G:H8	1.75	0.52
43:AE:52:VAL:HA	43:AE:67:GLY:HA3	1.92	0.52
4:BD:50:ILE:HD11	4:BD:86:LEU:HD23	1.90	0.52
7:BG:132:ARG:NH1	35:B5:150:U:O4'	2.43	0.52
31:Be:24:THR:O	31:Be:26:LYS:NZ	2.39	0.52
35:B5:58:U:OP1	35:B5:456:A:O2'	2.28	0.52
35:B5:1672:G:H2'	35:B5:1673:G:C8	2.45	0.52
36:A1:427:C:OP2	68:Ae:15:LYS:NZ	2.38	0.52
36:A1:536:U:OP1	56:AS:146:LYS:NZ	2.39	0.52
38:A4:141:C:O2	51:AN:112:ASN:ND2	2.43	0.52
38:A4:150:G:OP1	61:AX:27:ARG:NH2	2.43	0.52
42:AD:83:LEU:HA	42:AD:86:TYR:HD2	1.75	0.52
63:AZ:121:ARG:HG2	63:AZ:126:LYS:HD2	1.92	0.52
2:BB:61:LEU:HA	2:BB:64:ARG:HH11	1.75	0.51
9:BI:14:THR:O	35:B5:347:G:N2	2.42	0.51
14:BN:4:MET:SD	14:BN:124:ARG:NH1	2.83	0.51
36:A1:90:C:OP1	64:Aa:59:ARG:NH1	2.42	0.51
36:A1:1695:U:O2'	36:A1:1749:A:N1	2.36	0.51
42:AD:83:LEU:HB3	42:AD:88:ILE:HB	1.92	0.51
9:BI:141:ARG:NH2	35:B5:196:G:N7	2.58	0.51
36:A1:3369:G:N2	40:AB:380:MET:O	2.42	0.51
46:AH:22:SER:OG	46:AH:39:LYS:NZ	2.43	0.51
48:AJ:52:TYR:HA	48:AJ:61:ARG:HD2	1.91	0.51
49:AL:46:ILE:HD11	49:AL:51:LEU:HA	1.91	0.51
51:AN:68:ARG:NH1	51:AN:124:ASP:O	2.39	0.51
54:AQ:25:TYR:HA	54:AQ:28:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AT:89:LEU:HB3	57:AT:91:LEU:HD13	1.92	0.51
10:BJ:139:GLN:NE2	25:BY:64:PHE:O	2.41	0.51
35:B5:33:U:N3	35:B5:468:A:N7	2.59	0.51
35:B5:871:G:H2'	35:B5:872:G:C8	2.45	0.51
36:A1:1846:C:OP1	36:A1:1849:C:N4	2.34	0.51
59:AV:10:LYS:NZ	59:AV:56:ASP:OD1	2.41	0.51
11:BK:92:ILE:HG13	11:BK:96:ASN:HA	1.91	0.51
33:Bg:197:SER:HB2	33:Bg:216:LYS:HB2	1.93	0.51
35:B5:1055:U:O2	35:B5:1064:G:O6	2.29	0.51
35:B5:1198:G:OP1	35:B5:1199:G:O2'	2.23	0.51
36:A1:216:G:OP1	62:AY:16:ARG:NH1	2.41	0.51
36:A1:2708:C:OP1	78:Ao:100:LYS:NZ	2.43	0.51
36:A1:2988:C:OP1	52:AO:65[A]:ASN:ND2	2.36	0.51
36:A1:3090:U:OP1	40:AB:270:ARG:NH2	2.37	0.51
37:A3:30:G:N2	37:A3:48:U:O2	2.43	0.51
40:AB:204:ALA:O	40:AB:207:SER:OG	2.28	0.51
63:AZ:26:VAL:HG11	63:AZ:96:VAL:HG23	1.91	0.51
6:BF:121:ILE:HA	6:BF:199:ILE:HD11	1.93	0.51
10:BJ:141:VAL:HG12	10:BJ:143:ILE:H	1.76	0.51
35:B5:29:U:H2'	35:B5:30:G:H8	1.75	0.51
35:B5:1354:G:O6	35:B5:1369:U:O4	2.26	0.51
35:B5:1504:G:N3	35:B5:1563:C:O2'	2.39	0.51
36:A1:3023:U:H2'	36:A1:3024:A:H8	1.74	0.51
36:A1:3040:A:H5''	59:AV:12:ARG:HB2	1.92	0.51
36:A1:3139:A:OP2	40:AB:30:LYS:NZ	2.41	0.51
36:A1:3199:G:H4'	50:AM:6:ILE:HD13	1.92	0.51
45:AG:162:LEU:HA	51:AN:7:LEU:HD11	1.93	0.51
48:AJ:19:LEU:HD22	48:AJ:125:MET:HE1	1.91	0.51
8:BH:163:ASP:HA	8:BH:166:LEU:HD13	1.91	0.51
25:BY:47:VAL:HG13	25:BY:48:TYR:HD1	1.76	0.51
36:A1:591:G:O2'	43:AE:17:ALA:O	2.28	0.51
36:A1:1674:G:H5''	58:AU:70:LYS:HE3	1.92	0.51
36:A1:2389:C:O2'	36:A1:3307:A:N1	2.40	0.51
42:AD:19:PRO:O	42:AD:24:ARG:NE	2.43	0.51
42:AD:85:ARG:NH1	42:AD:250:ASP:OD1	2.40	0.51
46:AH:80:THR:HG23	46:AH:84:LYS:HE3	1.92	0.51
5:BE:95:THR:HG22	25:BY:16:PRO:HD2	1.92	0.51
5:BE:196:VAL:HB	5:BE:209:HIS:HB2	1.92	0.51
7:BG:76:LEU:HD22	35:B5:1673:G:H5''	1.91	0.51
36:A1:3045:G:OP1	40:AB:19:ARG:NH2	2.41	0.51
9:BI:58:LEU:HD21	35:B5:1676:U:H5''	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BS:125:ILE:HG12	34:Bh:61:ILE:HD13	1.92	0.51
20:BT:117:SER:HB2	20:BT:123:ARG:HG2	1.92	0.51
33:Bg:177:MET:SD	33:Bg:179:LYS:NZ	2.72	0.51
5:BE:141:THR:OG1	5:BE:143:ASP:OD1	2.24	0.51
6:BF:166:ARG:NH2	35:B5:1163:A:O3'	2.44	0.51
7:BG:74:LYS:HA	7:BG:96:SER:HA	1.93	0.51
9:BI:4:SER:HB2	9:BI:24:LYS:HE2	1.91	0.51
9:BI:64:ASN:ND2	35:B5:257:A:N3	2.58	0.51
14:BN:130:ARG:NH1	14:BN:139:TRP:O	2.44	0.51
20:BT:21:PHE:HD2	20:BT:22:LEU:HD12	1.74	0.51
21:BU:26:LEU:HG	21:BU:114:VAL:HG12	1.92	0.51
35:B5:1280:4AC:H2'	35:B5:1281:G:C8	2.44	0.51
36:A1:1124:U:O2'	36:A1:2635:A:OP1	2.28	0.51
46:AH:129:ARG:NH1	46:AH:160:ASP:OD2	2.40	0.51
6:BF:80:LYS:HB2	6:BF:83:ARG:HG3	1.93	0.51
8:BH:60:ILE:O	8:BH:93:LEU:N	2.43	0.51
8:BH:129:LEU:HD21	8:BH:169:PHE:HB3	1.93	0.51
14:BN:149:LEU:HD12	14:BN:150:VAL:HG13	1.93	0.51
35:B5:223:U:O4	35:B5:838:G:O6	2.28	0.51
36:A1:255:A:H2'	36:A1:256:G:H8	1.76	0.51
36:A1:1410:U:O2'	68:Ae:95:GLU:OE1	2.27	0.51
36:A1:2660:G:O3'	36:A1:2749:G:N2	2.44	0.51
42:AD:20:PHE:O	42:AD:24:ARG:NH2	2.44	0.51
1:BA:30:GLN:HE22	1:BA:152:PRO:HA	1.74	0.50
36:A1:1448:U:H2'	36:A1:1449:A2M:H8	1.92	0.50
40:AB:57:VAL:HG22	40:AB:73:VAL:HG22	1.94	0.50
46:AH:22:SER:OG	46:AH:23:ARG:N	2.39	0.50
59:AV:54:LEU:HD21	59:AV:119:GLY:HA3	1.93	0.50
1:BA:79:ARG:HH12	1:BA:164:ASN:HB3	1.76	0.50
3:BC:78:ASP:N	3:BC:78:ASP:OD1	2.44	0.50
10:BJ:8:TYR:O	35:B5:25:C:N4	2.44	0.50
10:BJ:36:LEU:HD11	10:BJ:105:LEU:HD11	1.93	0.50
20:BT:58:ALA:HB1	20:BT:108:LEU:HD21	1.94	0.50
22:BV:73:ALA:HB1	22:BV:78:LEU:HB2	1.92	0.50
36:A1:691:A:OP1	41:AC:46:LYS:NZ	2.44	0.50
36:A1:957:C:H1'	64:Aa:43:ILE:HD11	1.93	0.50
45:AG:74:THR:HG22	45:AG:164:VAL:HG22	1.92	0.50
45:AG:81:THR:HG21	45:AG:181:LYS:HG3	1.93	0.50
5:BE:211:LYS:HB3	5:BE:217:THR:HG22	1.93	0.50
28:Bb:34:ASP:OD2	28:Bb:80:ARG:NH2	2.44	0.50
36:A1:599:C:OP1	41:AC:332:LYS:NZ	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:2697:A:H2'	36:A1:2698:G:H8	1.76	0.50
37:A3:43:U:OP1	48:AJ:137:ARG:NH1	2.38	0.50
42:AD:95:TRP:HA	42:AD:158:ARG:HG2	1.92	0.50
43:AE:87:THR:HG22	43:AE:176:PHE:HB3	1.93	0.50
49:AL:48:PRO:HB2	71:Ah:117:ALA:HB2	1.93	0.50
9:BI:34:ALA:HB2	9:BI:56:ARG:HD2	1.93	0.50
9:BI:92:ARG:HH21	36:A1:2107:A:H1'	1.76	0.50
20:BT:63:ARG:NH2	35:B5:1481:C:OP1	2.42	0.50
35:B5:699:U:O2	35:B5:741:C:N4	2.45	0.50
36:A1:503:C:O2	43:AE:23:LYS:NZ	2.41	0.50
42:AD:156:GLY:HA2	42:AD:181:PRO:HD3	1.94	0.50
1:BA:107:PHE:HB2	1:BA:135:GLU:HG2	1.93	0.50
3:BC:52:THR:OG1	3:BC:54:GLU:OE1	2.29	0.50
3:BC:78:ASP:HB3	3:BC:104:VAL:HG12	1.94	0.50
10:BJ:26:ALA:HA	10:BJ:29:LYS:HE2	1.94	0.50
17:BQ:73:GLY:H	17:BQ:76:SER:HB3	1.75	0.50
36:A1:159:A:H2'	36:A1:160:G:H8	1.77	0.50
2:BB:154:SER:O	2:BB:154:SER:OG	2.18	0.50
19:BS:123:ARG:HG3	19:BS:133:VAL:HB	1.94	0.50
35:B5:1159:C:N4	35:B5:1285:U:OP1	2.44	0.50
36:A1:250:U:H5''	36:A1:251:G:H8	1.75	0.50
36:A1:297:G:O2'	72:Ai:32:ALA:O	2.27	0.50
36:A1:664:U:H2'	36:A1:665:A:C8	2.47	0.50
38:A4:42:G:O6	73:Aj:65:ARG:NH2	2.44	0.50
3:BC:137:ILE:HG13	22:BV:26:ALA:HB3	1.93	0.50
9:BI:12:SER:HB3	9:BI:18:ARG:HE	1.76	0.50
35:B5:1284:C:OP1	35:B5:1623:C:O2'	2.27	0.50
36:A1:966:U:OP1	64:Aa:44:ASN:ND2	2.43	0.50
47:AI:76:MET:HE1	47:AI:138:VAL:HG21	1.94	0.50
47:AI:140:THR:HG21	47:AI:148:VAL:HG21	1.94	0.50
1:BA:118:PRO:HG2	1:BA:141:ILE:HD13	1.94	0.50
5:BE:151:ASP:OD2	7:BG:215:ARG:NH2	2.44	0.50
7:BG:225:GLU:HG3	7:BG:226:ILE:HG13	1.93	0.50
20:BT:39:THR:OG1	35:B5:1478:G:OP1	2.26	0.50
28:Bb:30:SER:OG	35:B5:959:U:O2	2.28	0.50
35:B5:329:G:H2'	35:B5:330:G:C8	2.47	0.50
35:B5:846:G:OP2	35:B5:848:C:N4	2.45	0.50
35:B5:1356:U:O4	35:B5:1367:G:O6	2.30	0.50
35:B5:1781:MA6:H8	35:B5:1781:MA6:OP2	2.12	0.50
36:A1:26:A:N3	36:A1:328:U:O2'	2.43	0.50
36:A1:590:G:OP1	68:Ae:62:LYS:NZ	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:647:A:N6	36:A1:2371:G:O2'	2.43	0.50
36:A1:2440:G:N1	36:A1:2505:U:OP1	2.45	0.50
36:A1:3016:A:H2'	36:A1:3017:A:H8	1.76	0.50
73:Aj:58:THR:OG1	73:Aj:59:THR:N	2.45	0.50
1:BA:148:ASP:OD2	1:BA:165:ARG:NH1	2.45	0.50
18:BR:7:LYS:N	35:B5:1316:G:OP1	2.41	0.50
25:BY:105:ARG:HH22	35:B5:444:C:H5	1.60	0.50
35:B5:878:G:H2'	35:B5:879:G:H8	1.76	0.50
36:A1:655:C:H2'	36:A1:656:A:C8	2.46	0.50
59:AV:80:ARG:NH1	59:AV:117:PRO:O	2.40	0.50
1:BA:40:ALA:O	18:BR:105:GLN:NE2	2.43	0.49
5:BE:53:LYS:O	25:BY:22:GLN:NE2	2.45	0.49
35:B5:1663:G:O6	35:B5:1738:U:O2	2.30	0.49
36:A1:433:A:OP2	69:Af:57:LYS:NZ	2.40	0.49
36:A1:2157:G:O2'	39:AA:156:LYS:NZ	2.44	0.49
36:A1:3354:U:H5'	36:A1:3355:U:H5'	1.93	0.49
40:AB:122:TRP:O	40:AB:127:LYS:NZ	2.45	0.49
63:AZ:33:SER:OG	63:AZ:34:LYS:N	2.45	0.49
32:Bf:135:HIS:NE2	35:B5:1235:C:N3	2.59	0.49
33:Bg:156:VAL:HG22	33:Bg:169:ILE:HG22	1.94	0.49
36:A1:123:A:OP1	45:AG:105:LYS:NZ	2.40	0.49
36:A1:439:C:OP2	36:A1:440:A:N6	2.45	0.49
36:A1:951:A:OP1	65:Ab:18:ARG:NH1	2.45	0.49
42:AD:223:PHE:HB3	42:AD:226:TYR:HB2	1.93	0.49
62:AY:116:LYS:HG2	62:AY:126:LEU:HD11	1.94	0.49
67:Ad:75:ILE:HG23	67:Ad:93:VAL:HG22	1.93	0.49
3:BC:46:LYS:NZ	3:BC:65:GLU:OE2	2.37	0.49
17:BQ:47:LYS:HB3	17:BQ:82:ARG:HD2	1.94	0.49
19:BS:40:ARG:NH1	35:B5:1540:G:OP2	2.44	0.49
22:BV:79:LEU:HD13	22:BV:82:VAL:HG21	1.94	0.49
35:B5:606:A:H4'	35:B5:607:G:H3'	1.94	0.49
36:A1:289:A:O2'	51:AN:93:LYS:O	2.25	0.49
36:A1:2812:C:H2'	36:A1:2813:A:C8	2.47	0.49
36:A1:3109:G:N2	46:AH:156:GLN:OE1	2.44	0.49
70:Ag:41:ARG:O	70:Ag:43:LYS:NZ	2.45	0.49
4:BD:175:VAL:HB	4:BD:182:LEU:HB3	1.93	0.49
9:BI:37:LYS:HB2	9:BI:59:ARG:HG3	1.93	0.49
11:BK:11:ILE:HG12	11:BK:42:VAL:HG12	1.95	0.49
12:BL:124:THR:HB	12:BL:141:LYS:HB3	1.95	0.49
14:BN:140:LYS:HD3	14:BN:142:GLU:HG3	1.94	0.49
35:B5:86:A:H2'	35:B5:87:C:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:850:A:H4'	35:B5:852:C:H5'	1.93	0.49
35:B5:894:U:H2'	35:B5:895:G:C8	2.47	0.49
36:A1:2257:C:C4	36:A1:2259:A:N7	2.80	0.49
36:A1:2747:A:H5'	42:AD:175:HIS:HA	1.94	0.49
36:A1:2898:G:O6	76:Am:125:LYS:NZ	2.45	0.49
37:A3:28:C:H5''	48:AJ:137:ARG:HB3	1.93	0.49
38:A4:51:G:OP2	75:Al:21:ARG:NH1	2.45	0.49
42:AD:93:THR:O	42:AD:158:ARG:NH1	2.45	0.49
44:AF:143:THR:HG22	44:AF:241:LYS:HG3	1.94	0.49
45:AG:140:VAL:HG22	45:AG:166:LEU:HD21	1.95	0.49
56:AS:109:ASP:OD1	56:AS:113:ARG:NH1	2.36	0.49
68:Ae:9:ILE:HG12	68:Ae:63:THR:HB	1.94	0.49
25:BY:41:ARG:NE	25:BY:55:VAL:O	2.39	0.49
36:A1:845:G:H21	36:A1:848:A:H2	1.60	0.49
36:A1:3016:A:H2'	36:A1:3017:A:C8	2.47	0.49
39:AA:117:GLU:HG3	39:AA:124:GLY:H	1.76	0.49
48:AJ:36:VAL:O	48:AJ:39:GLN:NE2	2.45	0.49
1:BA:59:LEU:HD22	22:BV:79:LEU:HD11	1.94	0.49
17:BQ:94:GLN:NE2	33:Bg:60:SER:O	2.46	0.49
29:Bc:32:PHE:HE2	29:Bc:38:ARG:HE	1.59	0.49
33:Bg:270:LEU:HD21	33:Bg:273:ASP:HB2	1.95	0.49
35:B5:823:G:OP2	35:B5:842:C:O2'	2.31	0.49
35:B5:1591:C:H2'	35:B5:1592:A:C8	2.47	0.49
35:B5:1785:U:H2'	35:B5:1786:G:H8	1.77	0.49
36:A1:937:G:N2	36:A1:961:C:OP1	2.45	0.49
36:A1:1114:U:OP1	64:Aa:23:GLY:N	2.41	0.49
45:AG:91:PHE:O	45:AG:95:ASN:ND2	2.46	0.49
79:Ap:27:LYS:HZ2	79:Ap:31:ILE:HD11	1.77	0.49
9:BI:98:LYS:NZ	35:B5:329:G:OP1	2.40	0.49
17:BQ:118:ILE:HG23	35:B5:1410:A:H5''	1.94	0.49
35:B5:187:G:N1	35:B5:197:A:N7	2.60	0.49
36:A1:2177:G:N2	39:AA:118:GLU:OE2	2.45	0.49
36:A1:2588:U:OP1	45:AG:48:ARG:NH2	2.44	0.49
62:AY:70:ILE:HA	62:AY:82:VAL:HA	1.95	0.49
7:BG:164:LYS:NZ	35:B5:71:A:OP2	2.38	0.49
7:BG:202:ARG:NH1	35:B5:127:G:N7	2.51	0.49
24:BX:107:PHE:HD1	24:BX:123:LYS:HB3	1.78	0.49
35:B5:651:G:H2'	35:B5:652:G:H2'	1.95	0.49
36:A1:1693:C:HO2'	36:A1:1772:U:HO2'	1.58	0.49
37:A3:114:U:H2'	37:A3:115:G:H8	1.76	0.49
46:AH:101:VAL:HG22	46:AH:114:VAL:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:AS:115:ARG:O	56:AS:117:ARG:NH2	2.45	0.49
67:Ad:36:ILE:HD12	67:Ad:73:LEU:HD11	1.95	0.49
69:Af:37:THR:HG22	69:Af:39:GLN:H	1.77	0.49
2:BB:137:ILE:HG21	2:BB:172:LEU:HD22	1.95	0.49
3:BC:90:THR:O	35:B5:1146:G:O2'	2.31	0.49
6:BF:76:ARG:NH2	17:BQ:120:ASP:OD1	2.46	0.49
7:BG:175:ILE:HG12	35:B5:78:A:H1'	1.95	0.49
18:BR:10:LYS:NZ	35:B5:1316:G:O2'	2.44	0.49
36:A1:652:G:OP1	36:A1:1436:U:O2'	2.29	0.49
36:A1:2103:U:H2'	36:A1:2104:A:H8	1.78	0.49
66:Ac:17:VAL:HG21	66:Ac:100:ILE:HD13	1.95	0.49
16:BP:98:ASN:ND2	16:BP:121:ILE:O	2.39	0.49
22:BV:53:TYR:OH	22:BV:76:ASP:OD2	2.29	0.49
27:Ba:95:ARG:HG2	35:B5:1797:A:H5'	1.94	0.49
35:B5:1290:U:H2'	35:B5:1291:G:C8	2.48	0.49
35:B5:1546:G:H2'	35:B5:1547:A:H8	1.78	0.49
36:A1:69:C:OP1	51:AN:178:HIS:ND1	2.38	0.49
36:A1:406:G:OP1	36:A1:1415:U:O2'	2.27	0.49
36:A1:2129:U:H2'	36:A1:2130:G:C8	2.48	0.49
36:A1:2428:U:H2'	36:A1:2429:G:C8	2.48	0.49
36:A1:3319:U:H5'	36:A1:3320:A:H5'	1.95	0.49
44:AF:160:ARG:HG3	44:AF:203:TRP:CD2	2.48	0.49
76:Am:104:PRO:HG2	76:Am:107:ALA:HB2	1.94	0.49
23:BW:40:VAL:HA	23:BW:43:LYS:HG2	1.95	0.48
36:A1:1560:G:O2'	36:A1:1561:G:O4'	2.31	0.48
36:A1:2767:U:O2'	78:Ao:30:ALA:O	2.27	0.48
40:AB:244:ARG:O	40:AB:248:LYS:NZ	2.33	0.48
42:AD:277:LEU:HD22	42:AD:281:GLU:HG3	1.95	0.48
58:AU:99:LYS:HB2	58:AU:102:GLU:HB2	1.94	0.48
19:BS:144:ARG:HH22	34:Bh:72:ARG:HH22	1.60	0.48
20:BT:64:HIS:HD2	20:BT:71:VAL:HG21	1.79	0.48
23:BW:6:VAL:HB	23:BW:29:PRO:HD2	1.95	0.48
33:Bg:178:VAL:HB	33:Bg:192:PHE:HB2	1.95	0.48
35:B5:10:G:H1	35:B5:1144:U:H3	1.60	0.48
35:B5:428:A:N3	35:B5:440:U:O2'	2.39	0.48
36:A1:525:C:H5''	50:AM:79:ALA:HB2	1.95	0.48
36:A1:683:U:H5'	51:AN:204:LYS:HE3	1.94	0.48
38:A4:58:G:O6	73:Aj:63:ARG:NH2	2.46	0.48
1:BA:157:ASP:OD1	22:BV:60:ARG:NE	2.39	0.48
16:BP:114:HIS:ND1	16:BP:118:GLU:OE2	2.34	0.48
25:BY:62:THR:HA	25:BY:69:SER:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1134:G:O2'	36:A1:2642:A:N3	2.38	0.48
36:A1:2635:A:N6	36:A1:2642:A:OP2	2.43	0.48
36:A1:3160:U:H5''	36:A1:3396:U:H3'	1.95	0.48
37:A3:4:U:H2'	37:A3:5:G:C8	2.49	0.48
43:AE:39:VAL:O	43:AE:87:THR:OG1	2.28	0.48
51:AN:84:PRO:HA	51:AN:87:GLN:HB2	1.95	0.48
74:Ak:36:LYS:HB3	74:Ak:38:PHE:HD2	1.78	0.48
25:BY:37:LYS:HG3	35:B5:522:U:H5''	1.95	0.48
35:B5:1474:G:H2'	35:B5:1475:A:H8	1.78	0.48
36:A1:571:U:H2'	36:A1:572:A:H8	1.78	0.48
44:AF:173:LEU:HB3	44:AF:178:ILE:HB	1.95	0.48
46:AH:6:THR:HG21	46:AH:65:VAL:HG13	1.94	0.48
56:AS:8:GLN:HB3	56:AS:64:ILE:HD11	1.93	0.48
2:BB:64:ARG:HH21	15:BO:37:GLU:HG2	1.78	0.48
2:BB:70:LEU:HD23	2:BB:82:ARG:HG3	1.96	0.48
2:BB:111:ARG:HB3	27:Ba:68:TYR:HB2	1.96	0.48
5:BE:79:ASP:HB3	5:BE:82:TYR:HB2	1.95	0.48
35:B5:110:U:OP1	35:B5:754:A:O2'	2.31	0.48
35:B5:1546:G:H2'	35:B5:1547:A:C8	2.49	0.48
36:A1:1193:A:OP2	52:AO:49[A]:ARG:NH1	2.33	0.48
36:A1:1724:U:H1'	36:A1:1725:C:C6	2.49	0.48
36:A1:2433:U:OP2	36:A1:2434:U:O2'	2.31	0.48
36:A1:2618:G:O2'	36:A1:2865:U:OP1	2.28	0.48
36:A1:2768:U:H2'	36:A1:2769:A:H8	1.77	0.48
36:A1:3234:A:N1	36:A1:3253:G:C6	2.81	0.48
38:A4:64:U:H5'	71:Ah:49:LYS:HD2	1.95	0.48
42:AD:82:GLU:OE2	42:AD:108:ARG:NH1	2.41	0.48
43:AE:40:LEU:HB3	43:AE:84:VAL:HG13	1.95	0.48
74:Ak:27:ILE:HD12	74:Ak:39:ARG:HH12	1.78	0.48
2:BB:115:ARG:H	2:BB:118:GLN:HE21	1.61	0.48
3:BC:44:LEU:HG	3:BC:247:ALA:HB2	1.96	0.48
8:BH:81:LEU:HD23	8:BH:90:VAL:HG11	1.95	0.48
13:BM:26:ASP:OD1	13:BM:26:ASP:N	2.45	0.48
21:BU:19:ILE:HB	21:BU:94:GLU:HB3	1.95	0.48
25:BY:35:VAL:HG23	25:BY:40:LEU:HD11	1.95	0.48
36:A1:1573:G:H4'	36:A1:1574:C:C4	2.49	0.48
36:A1:1717:U:H2'	36:A1:1718:G:C8	2.48	0.48
36:A1:2160:G:H2'	36:A1:2161:G:H8	1.79	0.48
36:A1:2428:U:H2'	36:A1:2429:G:H8	1.79	0.48
36:A1:2429:G:H2'	36:A1:2430:A:H8	1.77	0.48
36:A1:2523:A:H5''	45:AG:51:LYS:HE3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:A3:121:U:OP2	42:AD:265:TYR:OH	2.27	0.48
4:BD:9:ARG:NH1	35:B5:1490:C:OP2	2.46	0.48
15:BO:121:VAL:O	35:B5:886:U:O2'	2.22	0.48
16:BP:87:PRO:HA	16:BP:90:ILE:HG12	1.95	0.48
20:BT:93:HIS:NE2	20:BT:95:ASP:OD1	2.46	0.48
27:Ba:80:HIS:ND1	35:B5:1766:A:N1	2.51	0.48
27:Ba:88:SER:HA	35:B5:1628:U:H5'	1.95	0.48
35:B5:956:C:OP1	35:B5:1072:C:O2'	2.32	0.48
36:A1:1491:A:H5''	73:Aj:14:LYS:HE3	1.95	0.48
49:AL:126:PHE:O	71:Ah:114:ARG:NH2	2.47	0.48
52:AO:125[A]:ARG:HG3	52:AO:129[A]:LEU:HD12	1.95	0.48
19:BS:71:GLN:HE21	19:BS:71:GLN:HA	1.78	0.48
25:BY:124:ARG:NH2	35:B5:153:G:N7	2.57	0.48
36:A1:2661:G:H2'	36:A1:2662:G:C8	2.47	0.48
49:AL:48:PRO:HA	49:AL:137:GLN:HB2	1.95	0.48
35:B5:1525:A:H2'	35:B5:1526:A:C8	2.49	0.48
36:A1:3092:C:O2'	36:A1:3094:A:OP2	2.24	0.48
66:Ac:27:TYR:OH	66:Ac:55:GLU:OE2	2.32	0.48
1:BA:123:VAL:HG21	1:BA:133:ILE:HD11	1.96	0.48
5:BE:100:ARG:NH2	5:BE:118:GLU:O	2.47	0.48
19:BS:14:ILE:HD11	19:BS:21:ASN:HB3	1.96	0.48
25:BY:21:LYS:NZ	35:B5:783:G:OP2	2.37	0.48
25:BY:61:ARG:NH1	35:B5:530:C:O2	2.47	0.48
33:Bg:92:TRP:HD1	33:Bg:99:THR:HA	1.78	0.48
36:A1:1288:U:H2'	36:A1:1289:G:H8	1.78	0.48
36:A1:1907:C:O2	40:AB:240:ARG:NH2	2.36	0.48
36:A1:2899:C:O2	46:AH:173:ARG:NH2	2.46	0.48
41:AC:233:LEU:HA	41:AC:233:LEU:HD23	1.79	0.48
9:BI:114:GLU:HA	9:BI:118:GLY:H	1.78	0.47
23:BW:56:HIS:O	35:B5:861:U:O2'	2.31	0.47
25:BY:124:ARG:NH2	35:B5:152:U:O4	2.38	0.47
35:B5:593:U:H4'	35:B5:595:G:H4'	1.96	0.47
36:A1:408:A:N3	36:A1:655:C:O2'	2.43	0.47
61:AX:99:VAL:HG11	61:AX:124:VAL:HG11	1.96	0.47
66:Ac:57:GLU:OE2	66:Ac:69:TYR:OH	2.31	0.47
9:BI:192:TYR:O	9:BI:197:THR:OG1	2.31	0.47
14:BN:140:LYS:HZ2	14:BN:142:GLU:HA	1.79	0.47
33:Bg:37:SER:OG	33:Bg:38:ARG:N	2.47	0.47
35:B5:891:A:H2'	35:B5:892:A:C8	2.49	0.47
35:B5:1027:A:OP1	35:B5:1789:G:O2'	2.30	0.47
36:A1:394:G:N1	36:A1:397:A:OP2	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:627:U:H2'	36:A1:628:A:C8	2.49	0.47
36:A1:1748:G:OP2	74:Ak:42:LYS:NZ	2.47	0.47
36:A1:1795:U:C2	79:Ap:51:ALA:HB2	2.49	0.47
36:A1:1926:C:OP1	79:Ap:23:ARG:NH1	2.39	0.47
36:A1:2511:A:O3'	45:AG:249:ARG:NH1	2.46	0.47
36:A1:2557:A:OP1	39:AA:69:TYR:OH	2.25	0.47
39:AA:40:TYR:HA	39:AA:91:GLY:HA3	1.96	0.47
44:AF:77:VAL:HB	57:AT:139:ARG:HB2	1.95	0.47
62:AY:11:ASP:HB3	62:AY:14:LYS:HB2	1.94	0.47
4:BD:42:THR:OG1	4:BD:45:LYS:O	2.29	0.47
33:Bg:83:ALA:HB1	33:Bg:110:VAL:HG12	1.96	0.47
35:B5:1524:A:H2'	35:B5:1525:A:C8	2.50	0.47
36:A1:655:C:H2'	36:A1:656:A:H8	1.78	0.47
36:A1:1696:A:H2'	36:A1:1697:A:C8	2.49	0.47
36:A1:1721:U:OP2	55:AR:124:TYR:OH	2.26	0.47
46:AH:91:ARG:NH1	46:AH:141:LYS:O	2.46	0.47
47:AI:38:LYS:HD2	47:AI:83:ASP:HB2	1.95	0.47
3:BC:148:LEU:O	3:BC:174:ARG:NH2	2.47	0.47
4:BD:136:VAL:HG22	4:BD:186:VAL:HG22	1.97	0.47
5:BE:248:ILE:HA	5:BE:251:GLU:HB3	1.96	0.47
9:BI:41:LYS:HA	9:BI:60:ILE:HA	1.97	0.47
16:BP:42:ARG:NH2	35:B5:1549:C:OP1	2.42	0.47
40:AB:41:VAL:HA	40:AB:185:GLY:HA3	1.96	0.47
61:AX:139:ILE:HD12	61:AX:141:TYR:HE1	1.79	0.47
9:BI:3:ILE:O	9:BI:30:GLY:N	2.47	0.47
35:B5:315:A:N1	35:B5:349:U:O2'	2.41	0.47
36:A1:1175:C:O2'	52:AO:87[A]:MET:O	2.32	0.47
36:A1:1432:C:O2'	36:A1:1434:G:OP2	2.31	0.47
36:A1:2241:U:O3'	39:AA:242:ARG:NH2	2.47	0.47
36:A1:2423:U:H2'	36:A1:2424:A:C8	2.49	0.47
44:AF:121:LYS:HB2	57:AT:133:ALA:HB3	1.95	0.47
1:BA:140:ASN:ND2	22:BV:31:SER:O	2.38	0.47
6:BF:128:ASN:HB3	6:BF:131:GLN:HB3	1.96	0.47
10:BJ:106:GLU:HA	10:BJ:111:THR:HG21	1.96	0.47
12:BL:38:ALA:O	35:B5:246:G:N2	2.47	0.47
14:BN:54:LEU:HB3	14:BN:60:VAL:HB	1.96	0.47
35:B5:1210:C:H2'	35:B5:1211:A:C8	2.47	0.47
35:B5:1682:U:O4	35:B5:1720:G:N2	2.47	0.47
36:A1:1779:C:N4	36:A1:2102:U:OP1	2.47	0.47
39:AA:101:VAL:HG22	39:AA:165:VAL:HG22	1.95	0.47
53:AP:128:ARG:NH1	53:AP:130:TYR:OH	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Ad:14:ILE:HD13	67:Ad:36:ILE:HD13	1.95	0.47
68:Ae:66:LEU:HD23	68:Ae:72:LYS:HG3	1.97	0.47
1:BA:155:PHE:HE1	22:BV:30:ALA:HB1	1.79	0.47
2:BB:140:ILE:HB	2:BB:213:ARG:HD3	1.97	0.47
4:BD:224:ASP:HA	33:Bg:190:ALA:HA	1.96	0.47
22:BV:65:SER:HA	22:BV:68:SER:HB2	1.96	0.47
25:BY:36:SER:OG	25:BY:37:LYS:N	2.48	0.47
28:Bb:30:SER:OG	35:B5:959:U:OP1	2.32	0.47
35:B5:878:G:H2'	35:B5:879:G:C8	2.50	0.47
35:B5:1553:G:N1	35:B5:1556:A:OP2	2.47	0.47
35:B5:1752:U:H2'	35:B5:1753:A:C8	2.50	0.47
35:B5:1777:G:H2'	35:B5:1778:G:H8	1.79	0.47
36:A1:126:U:OP1	51:AN:144:ARG:NH1	2.46	0.47
36:A1:2160:G:H2'	36:A1:2161:G:C8	2.50	0.47
36:A1:2261:G:H1'	36:A1:2262:A:H2	1.79	0.47
36:A1:2565:U:O4	63:AZ:55:LYS:NZ	2.47	0.47
36:A1:2781:U:H4'	49:AL:185:LYS:HD3	1.97	0.47
36:A1:3278:C:OP1	69:Af:54:ARG:NH2	2.40	0.47
40:AB:292:ALA:HB1	40:AB:295:ALA:HB3	1.95	0.47
52:AO:16[A]:VAL:HG23	52:AO:41[A]:LEU:HD13	1.97	0.47
64:Aa:56:VAL:HG12	64:Aa:57:GLY:H	1.80	0.47
36:A1:2570:U:H4'	36:A1:2571:U:H2'	1.96	0.47
36:A1:2642:A:OP2	57:AT:3:LYS:NZ	2.47	0.47
4:BD:53:THR:O	4:BD:90:ARG:NH2	2.48	0.47
6:BF:192:GLU:OE2	26:BZ:63:SER:OG	2.26	0.47
7:BG:2:LYS:HB2	7:BG:108:VAL:HG23	1.97	0.47
36:A1:182:U:H2'	36:A1:183:G:H8	1.80	0.47
36:A1:781:G:OP1	54:AQ:151:ARG:NH1	2.42	0.47
36:A1:1129:A:N3	36:A1:2826:U:O2'	2.45	0.47
43:AE:40:LEU:HD11	43:AE:54:TYR:HB2	1.96	0.47
43:AE:45:GLY:O	43:AE:48:ARG:NE	2.48	0.47
79:Ap:8:VAL:O	79:Ap:11:THR:OG1	2.33	0.47
1:BA:41:ARG:HG2	18:BR:105:GLN:HB2	1.97	0.47
7:BG:31:ARG:NH2	35:B5:1681:A:O3'	2.48	0.47
8:BH:46:ILE:HD12	8:BH:60:ILE:HG12	1.97	0.47
8:BH:129:LEU:HD23	8:BH:130:VAL:HG13	1.97	0.47
9:BI:40:ALA:H	9:BI:61:GLU:HG2	1.80	0.47
14:BN:108:ASP:OD1	35:B5:878:G:O2'	2.32	0.47
15:BO:52:ARG:HE	35:B5:905:A:H5''	1.79	0.47
17:BQ:50:GLU:OE1	17:BQ:82:ARG:NH2	2.44	0.47
19:BS:39:GLY:H	35:B5:1566:U:H5''	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BT:72:GLY:HA3	35:B5:1498:G:H5''	1.97	0.47
21:BU:58:LEU:HD12	21:BU:88:LYS:HD2	1.97	0.47
35:B5:488:G:N2	35:B5:500:C:OP1	2.48	0.47
36:A1:358:G:N2	36:A1:361:A:OP2	2.43	0.47
36:A1:669:U:HO2'	36:A1:1109:U:HO2'	1.54	0.47
36:A1:2584:G:O2'	45:AG:240:ASN:OD1	2.32	0.47
45:AG:154:ALA:HB2	45:AG:186:LEU:HD12	1.97	0.47
3:BC:142:GLY:HA3	3:BC:155:ALA:HB2	1.95	0.46
4:BD:23:GLU:OE1	11:BK:61:TRP:NE1	2.38	0.46
20:BT:131:ASP:OD1	20:BT:134:ARG:NH2	2.43	0.46
35:B5:91:G:OP1	35:B5:397:A:N6	2.45	0.46
36:A1:784:A:H2'	54:AQ:69:ARG:HH21	1.80	0.46
36:A1:2103:U:H2'	36:A1:2104:A:C8	2.51	0.46
36:A1:3343:G:O2'	36:A1:3362:A:N6	2.40	0.46
36:A1:3369:G:OP2	60:AW:61:LYS:NZ	2.44	0.46
38:A4:143:U:OP1	51:AN:38:ARG:NH2	2.47	0.46
39:AA:144:ASN:HB2	39:AA:160:SER:HB2	1.97	0.46
55:AR:15:VAL:HG23	55:AR:17:VAL:HG22	1.97	0.46
5:BE:100:ARG:HB2	5:BE:114:ILE:HD13	1.97	0.46
14:BN:5:HIS:HD2	35:B5:627:C:H5''	1.80	0.46
35:B5:704:C:O2'	35:B5:734:A:N6	2.49	0.46
36:A1:664:U:H5'	41:AC:107:ARG:HA	1.96	0.46
36:A1:939:U:H5	64:Aa:26:ARG:HH12	1.62	0.46
36:A1:1810:A:H2'	36:A1:1811:G:C8	2.50	0.46
40:AB:187:SER:O	40:AB:190:GLU:N	2.48	0.46
42:AD:30:TYR:HA	42:AD:33:ARG:HB3	1.96	0.46
2:BB:190:PRO:HG2	2:BB:192:VAL:HG23	1.96	0.46
3:BC:70:ASP:OD1	3:BC:133:LYS:NZ	2.44	0.46
11:BK:32:HIS:ND1	11:BK:33:GLU:O	2.48	0.46
18:BR:21:TYR:HD2	18:BR:73:LEU:HD22	1.79	0.46
23:BW:22:LYS:HD3	28:Bb:3:LEU:HA	1.97	0.46
34:Bh:72:ARG:NH2	35:B5:1461:C:OP1	2.48	0.46
35:B5:209:U:H2'	35:B5:210:A:H8	1.81	0.46
35:B5:1087:A:H2'	35:B5:1088:A:C8	2.50	0.46
35:B5:1502:G:N2	35:B5:1505:A:OP2	2.48	0.46
36:A1:3233:C:H2'	36:A1:3234:A:C8	2.51	0.46
38:A4:9:A:H2'	38:A4:10:A:C8	2.51	0.46
47:AI:49:CYS:SG	47:AI:137:SER:OG	2.74	0.46
1:BA:30:GLN:HG2	1:BA:32:HIS:H	1.81	0.46
5:BE:129:VAL:HG22	5:BE:139:VAL:HG12	1.97	0.46
14:BN:16:ILE:HG22	35:B5:959:U:H4'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BT:114:VAL:HB	20:BT:122:ARG:HB3	1.96	0.46
21:BU:57:ARG:HD2	35:B5:1382:A:H1'	1.96	0.46
35:B5:158:U:O2'	35:B5:160:C:OP2	2.27	0.46
35:B5:438:A:O2'	35:B5:465:G:N2	2.48	0.46
35:B5:1594:G:OP2	35:B5:1596:C:N4	2.49	0.46
36:A1:91:G:OP2	36:A1:93:C:N4	2.43	0.46
36:A1:994:G:N2	36:A1:995:U:O4	2.44	0.46
36:A1:3214:U:C5	50:AM:121:MET:HG3	2.50	0.46
41:AC:361:HIS:O	56:AS:28:ARG:NH2	2.42	0.46
11:BK:3:MET:HE1	11:BK:45:ALA:HB2	1.97	0.46
12:BL:133:LYS:HB2	35:B5:337:G:H3'	1.98	0.46
14:BN:3:ARG:HB3	14:BN:6:SER:HB3	1.98	0.46
17:BQ:129:PHE:O	17:BQ:137:ARG:NH1	2.41	0.46
27:Ba:76:SER:OG	35:B5:1793:G:N2	2.44	0.46
35:B5:778:G:H2'	35:B5:779:U:H2'	1.96	0.46
35:B5:1760:G:H1'	35:B5:1781:MA6:H2	1.96	0.46
36:A1:1003:A:N1	36:A1:1049:C:O2'	2.42	0.46
37:A3:52:G:N2	48:AJ:9:MET:SD	2.88	0.46
38:A4:26:U:O2'	41:AC:51:ALA:O	2.34	0.46
38:A4:103:G:OP2	38:A4:105:A:O2'	2.27	0.46
2:BB:66:VAL:HG22	15:BO:34:SER:HB3	1.98	0.46
23:BW:14:ILE:HA	23:BW:25:VAL:HG11	1.96	0.46
27:Ba:45:VAL:HG23	27:Ba:46:GLU:H	1.80	0.46
35:B5:340:U:H2'	35:B5:341:A:H8	1.81	0.46
35:B5:1047:G:O6	35:B5:1072:C:N4	2.49	0.46
35:B5:1270:G:H2'	35:B5:1271:OMG:H8	1.81	0.46
35:B5:1474:G:H2'	35:B5:1475:A:C8	2.51	0.46
36:A1:93:C:OP2	36:A1:2764:C:O2'	2.31	0.46
36:A1:3324:C:OP1	67:Ad:19:ARG:NH1	2.45	0.46
41:AC:180:LYS:NZ	41:AC:203:ARG:O	2.46	0.46
42:AD:125:VAL:HG11	42:AD:199:ILE:HG21	1.97	0.46
6:BF:112:ARG:NE	35:B5:1529:C:OP1	2.45	0.46
7:BG:14:LYS:HB2	7:BG:14:LYS:HE3	1.78	0.46
9:BI:168:CYS:HB2	9:BI:184:LEU:HD21	1.98	0.46
11:BK:28:ASN:OD1	35:B5:1217:A:N6	2.48	0.46
27:Ba:57:SER:OG	27:Ba:58:VAL:O	2.27	0.46
35:B5:205:U:H2'	35:B5:206:A:H8	1.81	0.46
35:B5:445:A:H2'	35:B5:446:A:H8	1.81	0.46
35:B5:1587:A:H2'	35:B5:1588:G:H8	1.81	0.46
36:A1:155:G:N1	36:A1:265:A:OP2	2.40	0.46
36:A1:1010:G:H1'	47:AI:195:ALA:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1952:G:N1	36:A1:2095:G:O6	2.49	0.46
36:A1:3119:U:H4'	76:Am:104:PRO:HG3	1.97	0.46
41:AC:22:LEU:HA	41:AC:23:PRO:HD3	1.77	0.46
57:AT:78:LYS:HD3	57:AT:87:LYS:HE3	1.98	0.46
66:Ac:9:SER:OG	66:Ac:10:ILE:N	2.42	0.46
68:Ae:96:ILE:HG21	68:Ae:105:ARG:HG2	1.98	0.46
1:BA:137:SER:O	1:BA:137:SER:OG	2.34	0.46
10:BJ:83:VAL:HA	10:BJ:149:ARG:HA	1.98	0.46
26:BZ:59:TYR:OH	26:BZ:98:GLN:NE2	2.49	0.46
28:Bb:33:LEU:HD22	28:Bb:79:PHE:HD1	1.80	0.46
35:B5:148:A:N6	35:B5:166:C:O2	2.49	0.46
35:B5:261:U:H1'	35:B5:262:U:H5	1.81	0.46
36:A1:900:G:H1'	36:A1:1589:A:N6	2.31	0.46
36:A1:3158:G:H22	36:A1:3292:A:H2	1.64	0.46
36:A1:3166:C:H2'	36:A1:3167:A:H8	1.81	0.46
39:AA:8:GLN:HG2	39:AA:231:SER:HB3	1.97	0.46
40:AB:50:LYS:NZ	40:AB:330:GLY:O	2.40	0.46
40:AB:242:THR:HG21	40:AB:246:LEU:HB3	1.98	0.46
54:AQ:122:ILE:HG23	54:AQ:126:GLN:HB2	1.96	0.46
1:BA:101:ARG:HH21	35:B5:1320:U:H3'	1.81	0.46
16:BP:77:ARG:HG2	16:BP:95:GLY:HA3	1.97	0.46
35:B5:598:U:H2'	35:B5:599:A:H8	1.81	0.46
35:B5:1673:G:N1	35:B5:1728:A:C2	2.79	0.46
36:A1:77:A:OP2	49:AL:73:ARG:NH2	2.49	0.46
37:A3:98:C:OP1	56:AS:39:SER:OG	2.28	0.46
40:AB:221:THR:O	40:AB:334:ARG:NH1	2.48	0.46
55:AR:109:TYR:HB3	55:AR:115:ILE:HG12	1.96	0.46
1:BA:64:ILE:HG23	1:BA:73:VAL:HG11	1.97	0.46
5:BE:151:ASP:HB3	5:BE:154:ILE:HG13	1.98	0.46
7:BG:6:SER:HB3	7:BG:112:VAL:HG12	1.98	0.46
15:BO:17:ALA:HA	15:BO:30:VAL:HG22	1.96	0.46
30:Bd:54:LYS:NZ	35:B5:1420:C:OP1	2.47	0.46
35:B5:230:C:O2	35:B5:234:G:O2'	2.32	0.46
35:B5:273:G:O6	35:B5:283:U:O4	2.34	0.46
36:A1:2683:U:H2'	36:A1:2684:C:C6	2.51	0.46
36:A1:2683:U:H5'	48:AJ:18:VAL:HG11	1.98	0.46
40:AB:77:THR:HG21	40:AB:328:ILE:HG12	1.98	0.46
45:AG:55:TYR:HA	45:AG:58:VAL:HG12	1.98	0.46
63:AZ:21:LYS:NZ	63:AZ:47:GLU:O	2.47	0.46
3:BC:143:TYR:HB3	3:BC:145:GLY:HA3	1.97	0.45
18:BR:102:VAL:HG11	18:BR:119:LEU:HD22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Bd:22:ARG:NH1	30:Bd:36:LEU:O	2.47	0.45
34:Bh:89:ARG:NH2	35:B5:1428:OMG:O3'	2.49	0.45
35:B5:366:A:OP1	35:B5:758:U:O2'	2.31	0.45
35:B5:1680:G:O2'	35:B5:1720:G:N2	2.48	0.45
36:A1:671:U:H2'	36:A1:672:A:H8	1.81	0.45
36:A1:2146:C:H5''	39:AA:203:ALA:HB1	1.97	0.45
48:AJ:15:GLU:HG3	48:AJ:16:LYS:HG2	1.98	0.45
68:Ae:99:ASN:OD1	68:Ae:99:ASN:N	2.49	0.45
5:BE:62:LYS:HA	5:BE:62:LYS:HD2	1.79	0.45
12:BL:109:VAL:HG22	12:BL:137:PHE:HB2	1.98	0.45
16:BP:17:TYR:HD2	16:BP:36:LEU:HD23	1.81	0.45
18:BR:4:VAL:HG22	35:B5:1402:G:H4'	1.98	0.45
27:Ba:36:ILE:HD13	27:Ba:84:VAL:HG11	1.97	0.45
2:BB:214:LYS:NZ	35:B5:886:U:OP1	2.36	0.45
3:BC:99:LYS:HA	3:BC:117:THR:HA	1.99	0.45
5:BE:45:ILE:HA	5:BE:61:VAL:HG21	1.98	0.45
8:BH:14:THR:OG1	8:BH:15:GLU:N	2.48	0.45
11:BK:77:ARG:HA	11:BK:82:LEU:HD12	1.98	0.45
33:Bg:33:LEU:HB2	33:Bg:47:LEU:HD11	1.98	0.45
35:B5:849:C:OP2	55:AR:170:ARG:NH1	2.42	0.45
36:A1:120:G:H4'	36:A1:121:A:H5'	1.99	0.45
36:A1:1101:G:H1'	44:AF:105:LEU:HD22	1.97	0.45
36:A1:2723:U:H2'	36:A1:2724:OMU:H6	1.98	0.45
36:A1:2960:C:H2'	36:A1:2961:G:C8	2.51	0.45
39:AA:206:PRO:HG3	39:AA:213:GLY:HA3	1.99	0.45
42:AD:34:LYS:HA	57:AT:27:LEU:HD11	1.97	0.45
49:AL:165:SER:HA	64:Aa:139:ARG:HH22	1.80	0.45
9:BI:36:THR:OG1	9:BI:57:ALA:O	2.25	0.45
15:BO:123:SER:O	35:B5:885:G:N2	2.47	0.45
30:Bd:30:LEU:HA	30:Bd:39:CYS:HA	1.98	0.45
35:B5:16:G:H5'	35:B5:620:A:N6	2.32	0.45
35:B5:80:A:H3'	35:B5:81:G:H8	1.81	0.45
35:B5:684:A:H2'	35:B5:685:A:C8	2.51	0.45
35:B5:1641:C:O2'	77:An:1:MET:N	2.49	0.45
36:A1:44:U:OP1	51:AN:85:THR:OG1	2.28	0.45
36:A1:417:A:H2'	36:A1:418:A:C8	2.52	0.45
36:A1:1404:G:N2	36:A1:1407:A:OP2	2.40	0.45
36:A1:1530:U:O2'	38:A4:114:G:O2'	2.32	0.45
36:A1:2357:A:H2'	36:A1:2358:A:C8	2.51	0.45
60:AW:60:LYS:HE2	60:AW:60:LYS:HB2	1.69	0.45
1:BA:67:ILE:HD13	1:BA:73:VAL:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BG:58:LYS:NZ	7:BG:104:PRO:O	2.41	0.45
8:BH:110:GLN:HB3	35:B5:811:A:C6	2.52	0.45
8:BH:142:TYR:O	23:BW:42:GLN:NE2	2.46	0.45
15:BO:19:ILE:HB	15:BO:83:ILE:HD12	1.98	0.45
20:BT:39:THR:HA	20:BT:100:ILE:HD12	1.98	0.45
25:BY:37:LYS:NZ	35:B5:523:G:OP2	2.35	0.45
33:Bg:51:ASP:OD1	33:Bg:51:ASP:N	2.46	0.45
35:B5:1747:G:O2'	36:A1:2303:A:O2'	2.28	0.45
36:A1:1385:C:OP1	41:AC:141:ARG:NH1	2.48	0.45
36:A1:3123:A:OP1	52:AO:134[A]:LYS:NZ	2.40	0.45
44:AF:92:ILE:HD12	54:AQ:4:ASP:HB2	1.99	0.45
44:AF:130:ILE:HD12	44:AF:134:VAL:HG11	1.98	0.45
45:AG:162:LEU:HD21	51:AN:45:PRO:HG2	1.99	0.45
50:AM:121:MET:HE2	50:AM:121:MET:HB3	1.68	0.45
57:AT:52:MET:HE2	57:AT:52:MET:HB3	1.83	0.45
58:AU:93:ILE:HG21	58:AU:105:LEU:HD23	1.97	0.45
9:BI:5:ARG:NH1	9:BI:29:LEU:O	2.40	0.45
16:BP:16:SER:HA	16:BP:21:ASP:HA	1.97	0.45
22:BV:62:ARG:HA	22:BV:62:ARG:HD2	1.78	0.45
25:BY:41:ARG:HG3	25:BY:57:VAL:HG22	1.98	0.45
35:B5:209:U:H2'	35:B5:210:A:C8	2.51	0.45
35:B5:790:U:H2'	35:B5:791:A:C8	2.50	0.45
36:A1:505:G:OP1	41:AC:320:ASN:ND2	2.50	0.45
36:A1:2568:C:O2'	36:A1:2569:A:O4'	2.32	0.45
40:AB:35:ASP:OD2	40:AB:191:LYS:NZ	2.46	0.45
45:AG:54:GLU:HA	45:AG:57:ARG:HE	1.82	0.45
6:BF:147:THR:HG21	29:Bc:25:VAL:HG21	1.99	0.45
9:BI:5:ARG:O	35:B5:336:G:N2	2.44	0.45
35:B5:1164:G:H2'	35:B5:1165:G:H8	1.82	0.45
36:A1:38:U:H4'	64:Aa:32:ARG:HD2	1.98	0.45
36:A1:63:A:N3	36:A1:78:U:O2'	2.43	0.45
36:A1:860:G:C5	39:AA:181:LYS:HB2	2.51	0.45
37:A3:77:G:O2'	37:A3:101:G:O6	2.34	0.45
41:AC:2:SER:OG	41:AC:3:ARG:N	2.49	0.45
79:Ap:36:ARG:NH2	79:Ap:45:LYS:O	2.49	0.45
9:BI:25:ARG:HH11	35:B5:400:A:H5'	1.81	0.45
10:BJ:82:ARG:HD3	10:BJ:149:ARG:HD2	1.99	0.45
17:BQ:21:HIS:NE2	35:B5:1350:U:O2'	2.40	0.45
36:A1:2812:C:H2'	36:A1:2813:A:H8	1.81	0.45
37:A3:28:C:OP1	48:AJ:137:ARG:NE	2.41	0.45
38:A4:67:U:H2'	38:A4:68:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:AI:149:VAL:O	47:AI:153:ARG:N	2.47	0.45
48:AJ:12:LEU:HD21	48:AJ:133:ARG:HH21	1.81	0.45
7:BG:89:ASP:OD1	7:BG:89:ASP:N	2.50	0.45
9:BI:165:LEU:HD13	9:BI:183:ILE:HG12	1.98	0.45
36:A1:90:C:O2'	36:A1:282:G:OP1	2.35	0.45
36:A1:351:A:N6	75:AI:37:TYR:O	2.37	0.45
36:A1:1615:C:H2'	36:A1:1616:U:C6	2.52	0.45
36:A1:1935:G:H2'	36:A1:1936:A:H8	1.82	0.45
36:A1:2768:U:H2'	36:A1:2769:A:C8	2.52	0.45
36:A1:2960:C:H2'	36:A1:2961:G:H8	1.82	0.45
42:AD:103:LEU:HG	42:AD:247:ILE:HG21	1.98	0.45
51:AN:51:LEU:O	51:AN:117:ASN:ND2	2.41	0.45
2:BB:136:ARG:CZ	35:B5:884:A:H5''	2.46	0.45
3:BC:56:ILE:HG23	3:BC:61:LEU:HB2	1.99	0.45
10:BJ:78:ARG:NH2	35:B5:763:G:OP1	2.50	0.45
19:BS:144:ARG:NH2	19:BS:144:ARG:HA	2.31	0.45
27:Ba:70:LYS:NZ	35:B5:933:A:OP1	2.49	0.45
35:B5:1126:OMG:OP1	77:An:15:ARG:NE	2.49	0.45
36:A1:187:A:N3	36:A1:208:C:O2'	2.42	0.45
36:A1:300:G:H2'	36:A1:301:G:H8	1.81	0.45
36:A1:2219:A:H2'	36:A1:2220:A2M:H8	1.99	0.45
36:A1:2741:C:H4'	78:Ao:19:LYS:HA	1.99	0.45
36:A1:3295:A:H2'	36:A1:3296:A:C8	2.52	0.45
63:AZ:111:LYS:O	63:AZ:115:LYS:N	2.47	0.45
5:BE:105:VAL:HG21	5:BE:245:LYS:H	1.82	0.44
7:BG:216:LEU:HA	7:BG:219:ARG:HG2	1.97	0.44
14:BN:92:ILE:HG21	14:BN:149:LEU:HD11	1.98	0.44
21:BU:89:ARG:NH2	35:B5:1383:G:OP1	2.50	0.44
27:Ba:13:LYS:O	35:B5:1075:C:O2'	2.28	0.44
28:Bb:67:THR:OG1	28:Bb:70:LYS:O	2.31	0.44
30:Bd:15:GLY:O	30:Bd:18:SER:OG	2.35	0.44
33:Bg:216:LYS:HA	33:Bg:239:GLU:HG2	2.00	0.44
35:B5:851:U:H5'	35:B5:852:C:H5''	1.98	0.44
35:B5:895:G:H2'	35:B5:896:U:C6	2.52	0.44
35:B5:1470:C:OP1	35:B5:1540:G:O2'	2.32	0.44
36:A1:1650:G:OP1	39:AA:68:LYS:NZ	2.45	0.44
36:A1:1699:A:H2'	36:A1:1700:G:C8	2.52	0.44
36:A1:1894:U:O2'	36:A1:3054:U:OP1	2.29	0.44
36:A1:2429:G:H2'	36:A1:2430:A:C8	2.51	0.44
36:A1:2880:U:H5''	40:AB:236:LYS:HG2	1.98	0.44
48:AJ:117:ASP:OD1	48:AJ:119:SER:OG	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AN:159:ARG:HB3	51:AN:164:LEU:HB2	1.99	0.44
54:AQ:123:THR:OG1	54:AQ:125:ASP:OD1	2.28	0.44
63:AZ:95:VAL:O	63:AZ:100:THR:OG1	2.29	0.44
74:AK:28:ASN:HB2	74:AK:40:GLN:HB3	1.99	0.44
9:BI:62:THR:HG22	9:BI:77:ARG:HA	1.99	0.44
35:B5:76:A:N6	35:B5:80:A:O2'	2.49	0.44
35:B5:485:A:H61	35:B5:486:G:H21	1.66	0.44
35:B5:513:U:H2'	35:B5:514:G:C8	2.52	0.44
35:B5:655:G:H21	35:B5:657:U:H3	1.63	0.44
35:B5:1007:OMC:H2'	35:B5:1008:G:H8	1.82	0.44
36:A1:943:U:H3'	64:Aa:13:GLY:HA2	1.99	0.44
36:A1:1203:A:N3	36:A1:2855:U:O2'	2.49	0.44
36:A1:1447:G:H3'	53:AP:67:ILE:HD11	2.00	0.44
36:A1:2138:A:HO2'	73:Aj:2:GLY:N	2.14	0.44
38:A4:8:C:H2'	38:A4:9:A:C8	2.52	0.44
38:A4:52:A:H4'	75:Al:19:GLN:HA	1.98	0.44
47:AI:16:PRO:HA	47:AI:95:HIS:HD2	1.83	0.44
48:AJ:141:ARG:HH21	48:AJ:144:CYS:HB2	1.82	0.44
51:AN:48:ALA:HB1	51:AN:53:TYR:HB3	1.99	0.44
63:AZ:21:LYS:HD3	63:AZ:47:GLU:HA	1.99	0.44
63:AZ:27:LYS:HB3	63:AZ:42:LEU:HD12	1.99	0.44
7:BG:159:ARG:NH2	35:B5:79:C:OP1	2.50	0.44
11:BK:77:ARG:HG3	11:BK:82:LEU:HB2	1.98	0.44
14:BN:109:LYS:HD2	35:B5:975:C:H5''	1.99	0.44
35:B5:848:C:H3'	35:B5:849:C:H4'	1.99	0.44
35:B5:1174:C:O2'	35:B5:1196:A:N6	2.49	0.44
35:B5:1431:C:H5''	35:B5:1432:U:H3'	1.99	0.44
35:B5:1466:G:O2'	35:B5:1602:C:OP1	2.30	0.44
36:A1:98:G:N7	49:AL:13:HIS:NE2	2.63	0.44
36:A1:353:G:N2	36:A1:354:U:O4	2.40	0.44
36:A1:733:G:N2	36:A1:736:A:OP2	2.48	0.44
36:A1:1098:A:O2'	57:AT:130:ARG:O	2.32	0.44
36:A1:1497:C:O2'	36:A1:1602:A:N3	2.45	0.44
36:A1:1508:C:OP1	53:AP:127:ARG:NH2	2.42	0.44
36:A1:2108:C:H1'	36:A1:3344:A:C8	2.53	0.44
75:Al:6:SER:HB3	75:Al:9:ILE:HG12	1.99	0.44
20:BT:44:GLU:N	35:B5:1477:G:OP1	2.46	0.44
24:BX:19:ARG:NH2	35:B5:609:U:O2	2.50	0.44
33:Bg:262:VAL:HG13	33:Bg:271:VAL:HB	1.98	0.44
34:Bh:126:ASP:O	34:Bh:130:GLU:N	2.49	0.44
35:B5:808:U:H2'	35:B5:809:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:1041:G:H2'	35:B5:1042:G:C8	2.52	0.44
35:B5:1592:A:H2'	35:B5:1593:A:C8	2.53	0.44
35:B5:1777:G:H2'	35:B5:1778:G:C8	2.53	0.44
36:A1:19:U:H2'	36:A1:20:A:C8	2.52	0.44
36:A1:2607:G:H5'	39:AA:233:GLN:HG2	1.98	0.44
40:AB:219:ALA:HB2	40:AB:336:VAL:HG23	1.99	0.44
70:Ag:19:LYS:HA	70:Ag:19:LYS:HD3	1.79	0.44
76:Am:127:LEU:HG	76:Am:128:LYS:HG3	2.00	0.44
1:BA:92:HIS:HB3	1:BA:182:LEU:HD11	1.99	0.44
3:BC:168:ARG:NH1	35:B5:1099:U:O4	2.48	0.44
5:BE:200:ARG:HH12	35:B5:737:A:H3'	1.82	0.44
11:BK:59:PHE:CZ	11:BK:62:GLN:HA	2.53	0.44
35:B5:340:U:H2'	35:B5:341:A:C8	2.52	0.44
35:B5:897:C:O2'	35:B5:914:G:N2	2.51	0.44
36:A1:35:A:OP1	51:AN:83:LYS:N	2.41	0.44
36:A1:385:A:H2'	36:A1:386:A:C8	2.53	0.44
36:A1:817:A2M:H62	73:Aj:25:ARG:NH2	2.15	0.44
36:A1:1563:C:O2	36:A1:1564:U:O2'	2.35	0.44
36:A1:1786:G:H2'	36:A1:1787:A:C8	2.52	0.44
36:A1:2344:U:H2'	36:A1:2345:A:C8	2.53	0.44
37:A3:4:U:H2'	37:A3:5:G:H8	1.82	0.44
37:A3:39:C:H4'	48:AJ:44:THR:HG23	1.98	0.44
64:Aa:116:GLY:HA2	64:Aa:137:LYS:HZ3	1.82	0.44
79:Ap:3:LYS:HD2	79:Ap:3:LYS:HA	1.81	0.44
16:BP:90:ILE:HD12	16:BP:109:PRO:HA	1.98	0.44
17:BQ:55:VAL:HB	17:BQ:59:LYS:HD2	2.00	0.44
20:BT:86:ARG:NH1	20:BT:90:PRO:O	2.46	0.44
20:BT:111:ILE:HG13	20:BT:113:ILE:HG12	1.99	0.44
33:Bg:154:VAL:O	33:Bg:155:ARG:NE	2.51	0.44
36:A1:1466:G:N2	36:A1:1510:G:H5''	2.32	0.44
36:A1:2554:A:OP1	70:Ag:91:ARG:NH2	2.51	0.44
36:A1:2744:U:H2'	36:A1:2745:G:C8	2.52	0.44
47:AI:36:LEU:HD11	47:AI:69:ARG:HD2	1.99	0.44
48:AJ:22:SER:OG	48:AJ:22:SER:O	2.34	0.44
59:AV:104:ASN:OD1	59:AV:108:GLU:N	2.50	0.44
2:BB:195:LYS:HE3	2:BB:195:LYS:HB3	1.77	0.44
5:BE:22:LYS:N	35:B5:773:C:OP1	2.40	0.44
10:BJ:50:SER:HB3	10:BJ:54:ARG:HH21	1.82	0.44
11:BK:2:LEU:HD22	35:B5:1257:U:C2	2.53	0.44
35:B5:131:C:N4	35:B5:136:C:OP2	2.50	0.44
35:B5:1387:G:H1'	35:B5:1410:A:H61	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:1525:A:H2'	35:B5:1526:A:H8	1.83	0.44
36:A1:528:U:H2'	36:A1:529:A:C8	2.52	0.44
36:A1:2364:G:H22	36:A1:2396:G:H1'	1.83	0.44
36:A1:2392:C:H1'	40:AB:266:ARG:HH21	1.83	0.44
36:A1:2414:G:O6	36:A1:2806:U:O4	2.35	0.44
36:A1:2807:U:O2'	36:A1:2809:C:OP1	2.35	0.44
36:A1:2810:C:OP2	36:A1:2955:U:O2'	2.35	0.44
38:A4:36:G:O2'	38:A4:104:A:N1	2.44	0.44
39:AA:51:ASP:HB2	39:AA:58:LEU:HG	2.00	0.44
53:AP:29:THR:HA	53:AP:32:THR:HG22	2.00	0.44
53:AP:92:GLN:HA	53:AP:95:LEU:HB2	1.99	0.44
3:BC:163:GLY:HA3	3:BC:209:ASN:HD22	1.83	0.44
6:BF:133:VAL:HG12	6:BF:198:LEU:HD13	1.99	0.44
7:BG:66:GLY:HA3	35:B5:1681:A:C8	2.52	0.44
11:BK:25:LYS:HD2	11:BK:59:PHE:HZ	1.82	0.44
15:BO:35:GLY:O	35:B5:918:U:O2'	2.32	0.44
31:Be:25:GLU:OE2	35:B5:540:G:N2	2.50	0.44
36:A1:173:G:C6	36:A1:245:U:O2	2.70	0.44
36:A1:792:G:H2'	36:A1:793:C:C6	2.53	0.44
36:A1:1127:G:OP2	47:AI:98:ARG:NE	2.51	0.44
36:A1:2312:A:O2'	36:A1:2315:G:N3	2.44	0.44
36:A1:2660:G:H2'	36:A1:2661:G:H8	1.83	0.44
42:AD:277:LEU:HD11	42:AD:285:ARG:HH21	1.81	0.44
5:BE:22:LYS:NZ	35:B5:758:U:OP1	2.51	0.44
9:BI:36:THR:O	9:BI:96:LEU:N	2.33	0.44
19:BS:70:VAL:O	19:BS:74:GLN:HG3	2.17	0.44
25:BY:60:PHE:O	35:B5:522:U:O2'	2.35	0.44
33:Bg:220:ILE:HB	33:Bg:234:LEU:HB2	1.98	0.44
35:B5:40:A:H62	35:B5:467:G:N2	2.13	0.44
35:B5:328:A:H2'	35:B5:329:G:H8	1.83	0.44
35:B5:714:G:H2'	35:B5:715:U:H4'	1.99	0.44
35:B5:884:A:H2'	35:B5:885:G:C8	2.53	0.44
35:B5:1564:U:H2'	35:B5:1565:C:H6	1.83	0.44
35:B5:1684:U:H3	35:B5:1717:G:H1	1.66	0.44
36:A1:348:A:N3	36:A1:352:A:O2'	2.51	0.44
36:A1:2223:A:H2'	36:A1:2224:A:C8	2.53	0.44
40:AB:123:TYR:CZ	40:AB:124:LYS:HG3	2.53	0.44
41:AC:169:LEU:HD22	41:AC:249:ILE:HD13	1.98	0.44
49:AL:76:THR:O	49:AL:79:GLU:N	2.41	0.44
51:AN:138:GLN:HA	51:AN:143:ARG:HD2	2.00	0.44
52:AO:126[A]:VAL:O	56:AS:154:HIS:NE2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:31:ASP:O	2:BB:96:LEU:N	2.51	0.43
4:BD:70:THR:HA	4:BD:86:LEU:HD13	2.00	0.43
4:BD:211:PRO:HG3	18:BR:19:ARG:HB2	2.00	0.43
33:Bg:53:LYS:HE2	33:Bg:56:VAL:HG12	1.99	0.43
35:B5:1132:A:H2'	35:B5:1133:A:H8	1.83	0.43
35:B5:1359:C:H2'	35:B5:1360:A:C8	2.52	0.43
36:A1:1001:G:N2	36:A1:1041:U:OP1	2.45	0.43
36:A1:1034:U:H2'	36:A1:1035:G:C8	2.53	0.43
36:A1:1385:C:O2	43:AE:2:SER:N	2.51	0.43
37:A3:16:U:H2'	37:A3:17:A:C8	2.53	0.43
48:AJ:92:ARG:HH21	48:AJ:94:ARG:HD2	1.83	0.43
55:AR:134:HIS:CE1	55:AR:136:ARG:HB3	2.53	0.43
56:AS:139:TYR:HA	56:AS:142:GLN:HE21	1.83	0.43
64:Aa:91:LEU:HA	64:Aa:121:VAL:HG21	1.99	0.43
1:BA:84:ARG:NH2	18:BR:82:ASP:O	2.34	0.43
15:BO:125:SER:HB3	35:B5:926:A:H2	1.83	0.43
23:BW:50:PHE:HB3	23:BW:63:VAL:HG13	2.00	0.43
35:B5:1055:U:N3	35:B5:1056:U:O4	2.51	0.43
35:B5:1175:U:H3	35:B5:1464:G:H1	1.65	0.43
36:A1:12:A:H2'	36:A1:13:A:C8	2.52	0.43
36:A1:1468:A:N1	36:A1:1880:U:O2'	2.47	0.43
36:A1:2149:A:H61	36:A1:2187:G:HO2'	1.62	0.43
38:A4:84:C:H1'	62:AY:113:LYS:HG3	2.01	0.43
40:AB:215:ILE:HD12	40:AB:338:LEU:HB3	2.00	0.43
57:AT:14:MET:HE2	57:AT:14:MET:HB3	1.84	0.43
10:BJ:81:VAL:HG11	10:BJ:91:LYS:HE2	2.01	0.43
17:BQ:21:HIS:CD2	35:B5:1351:G:H5'	2.54	0.43
32:Bf:94:LYS:HG2	32:Bf:95:HIS:H	1.83	0.43
35:B5:92:A:P	35:B5:398:G:H22	2.41	0.43
35:B5:1590:G:H2'	35:B5:1591:C:C6	2.53	0.43
36:A1:171:G:N2	36:A1:246:U:O2	2.44	0.43
36:A1:2162:U:H5''	39:AA:238:ILE:HD13	1.99	0.43
36:A1:2711:C:O2'	36:A1:2744:U:OP1	2.35	0.43
52:AO:75[A]:ALA:HB3	52:AO:78[A]:ARG:HG2	2.00	0.43
64:Aa:75:LEU:HG	64:Aa:78:LEU:HD22	1.99	0.43
70:Ag:3:GLN:NE2	70:Ag:4:ARG:O	2.50	0.43
2:BB:123:ALA:HB2	2:BB:165:ARG:HG2	2.00	0.43
13:BM:60:VAL:HG12	13:BM:122:VAL:HG22	1.99	0.43
33:Bg:206:PRO:HG2	33:Bg:247:PRO:HA	2.01	0.43
36:A1:307:A:H2'	36:A1:308:A:C8	2.52	0.43
36:A1:2640:A2M:H8	36:A1:2640:A2M:O5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:3322:A:H2'	36:A1:3323:A:C8	2.54	0.43
49:AL:48:PRO:HG3	49:AL:126:PHE:HE2	1.82	0.43
50:AM:48:GLY:HA3	50:AM:53:VAL:HB	2.00	0.43
14:BN:63:ALA:O	14:BN:67:THR:OG1	2.29	0.43
14:BN:112:LYS:NZ	35:B5:975:C:OP1	2.51	0.43
21:BU:53:LYS:HB2	21:BU:92:ASP:HB2	2.00	0.43
33:Bg:23:LEU:HD22	33:Bg:33:LEU:HD11	1.99	0.43
35:B5:1320:U:N3	35:B5:1323:C:OP1	2.33	0.43
40:AB:293:ASN:HB2	40:AB:304:THR:HA	2.00	0.43
42:AD:68:THR:OG1	42:AD:71:GLY:O	2.28	0.43
59:AV:10:LYS:HD3	59:AV:125:LEU:HD22	2.01	0.43
74:Ak:26:LYS:HB3	74:Ak:42:LYS:HB2	2.01	0.43
75:Al:12:LYS:HB3	75:Al:12:LYS:HE3	1.87	0.43
25:BY:56:SER:HB3	25:BY:74:LEU:HB2	1.99	0.43
33:Bg:69:GLN:HG2	33:Bg:111:MET:HE3	2.00	0.43
36:A1:267:G:H8	36:A1:267:G:H2'	1.72	0.43
36:A1:911:C:H42	39:AA:3:ARG:HD3	1.83	0.43
36:A1:2270:A:H2'	36:A1:2271:A:C8	2.53	0.43
36:A1:2389:C:H2'	36:A1:2390:A:C8	2.53	0.43
37:A3:59:U:O2'	42:AD:273:ARG:NH2	2.50	0.43
48:AJ:100:GLY:HA3	48:AJ:154:THR:HG22	2.01	0.43
63:AZ:25:ILE:HG23	63:AZ:41:ALA:HB1	2.01	0.43
2:BB:88:VAL:HG12	2:BB:98:THR:HG22	2.00	0.43
4:BD:7:LYS:HD2	21:BU:27:THR:HG21	2.01	0.43
9:BI:57:ALA:HB2	9:BI:177:GLY:HA2	2.00	0.43
10:BJ:17:ARG:NH1	35:B5:3:U:O2	2.41	0.43
10:BJ:83:VAL:HG23	10:BJ:149:ARG:HG2	2.01	0.43
15:BO:60:ALA:HB1	15:BO:101:ALA:HB2	2.01	0.43
15:BO:99:GLN:O	15:BO:103:ARG:N	2.47	0.43
17:BQ:30:LYS:NZ	20:BT:8:ASP:OD1	2.52	0.43
21:BU:17:GLN:HA	21:BU:96:PRO:HB3	2.01	0.43
27:Ba:37:LYS:HE2	27:Ba:37:LYS:HB2	1.80	0.43
34:Bh:69:ARG:HA	34:Bh:69:ARG:HD3	1.85	0.43
35:B5:1533:C:H4'	35:B5:1539:G:C6	2.53	0.43
35:B5:1748:G:H5'	36:A1:2304:C:H5''	2.00	0.43
36:A1:589:A:O2'	36:A1:1338:C:OP1	2.36	0.43
36:A1:1157:G:O2'	36:A1:1169:A:N3	2.48	0.43
36:A1:2148:U:H2'	36:A1:2149:A:C5	2.54	0.43
36:A1:3000:A:H2'	36:A1:3001:C:C6	2.53	0.43
40:AB:14:LEU:HA	40:AB:17:LEU:HD13	2.01	0.43
40:AB:92:TYR:HB2	40:AB:157:VAL:HB	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AE:60:ASP:OD1	43:AE:60:ASP:N	2.44	0.43
4:BD:159:HIS:N	35:B5:1328:G:OP1	2.43	0.43
5:BE:195:ILE:HG13	5:BE:196:VAL:C	2.43	0.43
17:BQ:13:LYS:HD2	17:BQ:13:LYS:HA	1.88	0.43
19:BS:120:ARG:HD2	34:Bh:61:ILE:HG21	2.00	0.43
33:Bg:255:ALA:HB2	33:Bg:292:LEU:HD22	1.99	0.43
36:A1:115:A:OP2	51:AN:49:ARG:NE	2.52	0.43
36:A1:716:A:C6	64:Aa:117:ARG:HG3	2.53	0.43
36:A1:2241:U:H4'	39:AA:242:ARG:HE	1.83	0.43
36:A1:2816:G:H1	36:A1:2820:A:H62	1.66	0.43
36:A1:3344:A:H2	36:A1:3361:G:H21	1.65	0.43
44:AF:132:PRO:HA	44:AF:229:PHE:CG	2.53	0.43
54:AQ:161:LYS:HD2	54:AQ:161:LYS:HA	1.86	0.43
56:AS:77:VAL:HG11	56:AS:106:LEU:HD22	2.00	0.43
62:AY:48:LEU:HD13	62:AY:115:ARG:HH21	1.84	0.43
4:BD:196:ARG:HH11	4:BD:200:LYS:HB3	1.82	0.43
12:BL:123:VAL:HG23	12:BL:142:VAL:HA	2.01	0.43
25:BY:20:ARG:HD2	25:BY:74:LEU:HD22	2.00	0.43
28:Bb:33:LEU:HD23	28:Bb:81:ARG:HA	2.01	0.43
35:B5:1023:A:OP1	35:B5:1126:OMG:N2	2.48	0.43
36:A1:296:A:OP1	72:Ai:86:LYS:NZ	2.51	0.43
36:A1:1367:G:N2	36:A1:1368:U:O4	2.51	0.43
36:A1:2218:G:H2'	36:A1:2219:A:H8	1.83	0.43
36:A1:2991:A:O3'	40:AB:21:ARG:NH2	2.52	0.43
36:A1:3231:U:H2'	36:A1:3232:G:C8	2.54	0.43
36:A1:3344:A:N6	36:A1:3361:G:O2'	2.50	0.43
37:A3:94:C:H2'	37:A3:95:A:C8	2.53	0.43
38:A4:144:G:OP1	51:AN:57:GLN:NE2	2.50	0.43
39:AA:113:VAL:HG12	39:AA:166:ILE:HD13	2.00	0.43
39:AA:127:ALA:HB2	39:AA:134:VAL:HG23	2.00	0.43
53:AP:32:THR:HG21	53:AP:87:SER:HB3	2.00	0.43
70:Ag:66:SER:OG	70:Ag:67:LYS:N	2.47	0.43
5:BE:166:SER:O	5:BE:168:LYS:N	2.51	0.43
5:BE:181:VAL:HG13	5:BE:225:VAL:HG13	2.00	0.43
6:BF:125:THR:O	6:BF:127:GLN:N	2.52	0.43
9:BI:138:ASN:OD1	35:B5:197:A:N6	2.52	0.43
9:BI:142:LYS:NZ	35:B5:187:G:OP2	2.47	0.43
19:BS:28:ILE:HA	19:BS:58:ALA:HB2	2.01	0.43
19:BS:55:HIS:ND1	19:BS:55:HIS:O	2.52	0.43
25:BY:112:LYS:HE3	25:BY:112:LYS:HB3	1.90	0.43
35:B5:32:U:C2	35:B5:595:G:N1	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:392:G:O2'	35:B5:1673:G:N3	2.52	0.43
35:B5:628:G:H21	35:B5:971:A:H62	1.67	0.43
35:B5:873:U:O2'	35:B5:1047:G:OP1	2.35	0.43
35:B5:973:A:H4'	36:A1:848:A:C8	2.54	0.43
36:A1:1719:G:H5''	55:AR:110:ARG:HH22	1.83	0.43
36:A1:1935:G:H2'	36:A1:1936:A:C8	2.54	0.43
36:A1:2948:OMC:H5'	40:AB:243:HIC:HB2	2.00	0.43
39:AA:51:ASP:HB3	39:AA:54:ARG:HB3	2.00	0.43
43:AE:175:LYS:O	50:AM:117:ARG:NH2	2.52	0.43
46:AH:173:ARG:HB3	76:Am:127:LEU:HB2	2.01	0.43
50:AM:133:LYS:HE2	50:AM:133:LYS:HB3	1.86	0.43
3:BC:88:LYS:HG3	35:B5:1301:U:H5'	2.00	0.42
9:BI:84:HIS:NE2	9:BI:97:THR:OG1	2.50	0.42
12:BL:3:THR:OG1	12:BL:50:GLU:O	2.31	0.42
17:BQ:140:LYS:NZ	35:B5:1192:C:O3'	2.50	0.42
36:A1:1000:C:O2	36:A1:1046:A:N6	2.52	0.42
36:A1:1646:G:O2'	36:A1:1808:G:N2	2.38	0.42
44:AF:87:VAL:HG11	44:AF:243:MET:HE1	2.00	0.42
44:AF:176:TYR:CZ	44:AF:197:GLN:HG2	2.55	0.42
8:BH:78:THR:HG23	8:BH:90:VAL:HG13	2.00	0.42
10:BJ:65:LYS:HA	10:BJ:70:LEU:HD21	2.01	0.42
21:BU:77:LYS:NZ	35:B5:1195:C:OP1	2.48	0.42
25:BY:45:ALA:O	25:BY:49:LYS:N	2.52	0.42
35:B5:434:G:N1	35:B5:437:A:OP2	2.35	0.42
36:A1:754:G:H2'	36:A1:755:A:C8	2.54	0.42
42:AD:262:LYS:HA	42:AD:265:TYR:HB2	2.00	0.42
43:AE:3:ALA:HB2	68:Ae:77:ALA:HB2	2.01	0.42
2:BB:207:LEU:HD23	2:BB:207:LEU:HA	1.96	0.42
24:BX:61:SER:OG	24:BX:67:ALA:N	2.46	0.42
35:B5:655:G:H4'	35:B5:656:G:C8	2.54	0.42
35:B5:847:A:OP2	35:B5:848:C:N4	2.51	0.42
35:B5:1487:A:H2'	35:B5:1488:G:C8	2.53	0.42
36:A1:239:G:N2	71:Ah:94:LYS:O	2.53	0.42
36:A1:904:A:OP2	73:Aj:30:GLN:NE2	2.52	0.42
36:A1:1596:C:H2'	36:A1:1597:C:C6	2.55	0.42
36:A1:2727:A:OP2	36:A1:2728:G:N2	2.50	0.42
36:A1:3023:U:O2	36:A1:3032:A:N7	2.52	0.42
36:A1:3090:U:H2'	36:A1:3091:A:C8	2.55	0.42
41:AC:132:ALA:HB2	41:AC:148:ILE:HD12	2.00	0.42
51:AN:9:GLU:OE1	51:AN:13:LYS:NZ	2.45	0.42
54:AQ:67:ILE:HG12	54:AQ:81:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:AI:99:ARG:HG3	72:AI:100:HIS:CG	2.54	0.42
3:BC:149:GLY:HA2	22:BV:3:ASN:HB2	2.01	0.42
5:BE:103:TYR:HB2	5:BE:182:TYR:HE2	1.84	0.42
17:BQ:141:SER:OG	35:B5:1195:C:N4	2.52	0.42
35:B5:1087:A:H2'	35:B5:1088:A:H8	1.82	0.42
36:A1:1336:U:H2'	36:A1:1337:A:H8	1.84	0.42
36:A1:3280:U:O2'	36:A1:3281:U:O5'	2.31	0.42
37:A3:9:C:OP2	37:A3:10:C:N4	2.53	0.42
47:AI:210:ILE:HD13	47:AI:210:ILE:HA	1.90	0.42
63:AZ:50:PRO:HD3	63:AZ:68:ILE:HG12	2.01	0.42
79:Ap:38:ASP:HA	79:Ap:45:LYS:HA	2.01	0.42
1:BA:56:LYS:HE3	1:BA:56:LYS:HB3	1.84	0.42
2:BB:32:ILE:HD12	15:BO:33:LEU:HD23	2.00	0.42
20:BT:64:HIS:CD2	20:BT:71:VAL:HG21	2.54	0.42
36:A1:576:C:OP1	44:AF:241:LYS:NZ	2.41	0.42
36:A1:1875:G:N7	55:AR:20:ARG:NE	2.68	0.42
36:A1:3107:U:H2'	36:A1:3108:G:C8	2.54	0.42
36:A1:3286:G:H2'	36:A1:3287:U:H6	1.85	0.42
39:AA:178:PRO:HD2	79:Ap:26:VAL:HG12	2.02	0.42
40:AB:71:GLU:OE1	60:AW:1:MET:N	2.52	0.42
40:AB:159:ARG:HG2	40:AB:182:GLN:HA	2.02	0.42
55:AR:110:ARG:HE	55:AR:110:ARG:HB3	1.67	0.42
2:BB:87:ARG:NH1	2:BB:89:ASP:OD1	2.51	0.42
3:BC:140:ARG:NH1	22:BV:10:GLU:OE2	2.53	0.42
4:BD:195:SER:OG	4:BD:196:ARG:N	2.52	0.42
6:BF:57:SER:HA	29:Bc:53:ILE:HB	2.00	0.42
6:BF:159:ALA:O	29:Bc:61:ARG:NH2	2.47	0.42
9:BI:175:GLN:NE2	35:B5:331:A:OP2	2.53	0.42
10:BJ:29:LYS:HA	31:Be:40:TYR:CE2	2.54	0.42
10:BJ:130:THR:HA	10:BJ:142:ASN:HB2	2.01	0.42
12:BL:59:PRO:HB3	12:BL:66:ILE:HD11	2.02	0.42
12:BL:122:ILE:HG23	12:BL:143:SER:HB2	2.00	0.42
15:BO:12:GLN:HE22	15:BO:111:ARG:HE	1.67	0.42
18:BR:27:ASP:HB3	18:BR:30:THR:HG22	2.01	0.42
23:BW:17:ALA:HB1	23:BW:22:LYS:HG3	2.02	0.42
35:B5:393:C:H2'	35:B5:394:C:C6	2.54	0.42
35:B5:1220:C:H2'	35:B5:1221:A:H8	1.85	0.42
35:B5:1592:A:H2'	35:B5:1593:A:H8	1.84	0.42
35:B5:1717:G:H2'	35:B5:1718:G:C8	2.55	0.42
35:B5:1783:C:H5''	77:An:5:TRP:CD1	2.54	0.42
36:A1:87:U:H2'	36:A1:88:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:A1:1315:U:H4'	36:A1:1317:A:H1'	2.00	0.42
36:A1:3192:U:H2'	36:A1:3193:C:C6	2.54	0.42
36:A1:3294:A:OP1	40:AB:128:LYS:NZ	2.48	0.42
45:AG:98:ARG:NH1	45:AG:188:THR:O	2.52	0.42
54:AQ:158:HIS:H	54:AQ:186:VAL:HG12	1.84	0.42
55:AR:98:ARG:NH1	55:AR:133:LYS:O	2.49	0.42
3:BC:203:LYS:HG3	35:B5:14:C:H5'	2.02	0.42
19:BS:72:ILE:HG12	19:BS:79:TYR:CD2	2.54	0.42
25:BY:12:VAL:HB	35:B5:783:G:H5'	2.02	0.42
27:Ba:70:LYS:NZ	35:B5:931:C:OP2	2.36	0.42
35:B5:972:G:O2'	36:A1:847:A:N6	2.53	0.42
35:B5:1280:4AC:O2	35:B5:1428:OMG:N2	2.37	0.42
35:B5:1291:G:H22	35:B5:1324:G:N2	2.18	0.42
35:B5:1673:G:C6	35:B5:1728:A:N1	2.88	0.42
36:A1:2947:G:N3	40:AB:250:ALA:HB1	2.35	0.42
48:AJ:92:ARG:HE	48:AJ:94:ARG:HB3	1.84	0.42
51:AN:114:ARG:NH2	51:AN:157:LYS:HG2	2.34	0.42
53:AP:84:PRO:HB2	53:AP:87:SER:HB2	2.01	0.42
62:AY:82:VAL:HG12	62:AY:83:ASP:O	2.19	0.42
79:Ap:86:LEU:HA	79:Ap:89:MET:HG3	2.01	0.42
1:BA:16:LEU:HD22	18:BR:91:LEU:HD23	2.01	0.42
10:BJ:102:GLU:HA	10:BJ:105:LEU:HB2	2.01	0.42
12:BL:33:ARG:NE	12:BL:51:GLY:O	2.52	0.42
14:BN:14:SER:HB3	35:B5:959:U:H5''	2.02	0.42
16:BP:100:LYS:HE2	35:B5:1183:A:C5	2.54	0.42
27:Ba:19:LYS:HA	27:Ba:19:LYS:HD3	1.83	0.42
36:A1:196:G:N1	36:A1:199:A:OP2	2.52	0.42
36:A1:754:G:H2'	36:A1:755:A:H8	1.84	0.42
36:A1:959:C:H41	36:A1:2801:A:H5''	1.84	0.42
36:A1:1203:A:H2'	36:A1:1204:A:C8	2.55	0.42
36:A1:1523:U:H1'	61:AX:111:ASN:HB3	2.01	0.42
36:A1:1630:U:H3	36:A1:1812:G:H2'	1.84	0.42
36:A1:1666:G:H2'	36:A1:1667:A:C8	2.53	0.42
36:A1:1929:G:OP2	36:A1:1930:A:O2'	2.34	0.42
36:A1:2250:G:O6	36:A1:2266:U:O4	2.37	0.42
36:A1:2883:U:H2'	36:A1:2884:C:H6	1.85	0.42
42:AD:41:LYS:HD2	57:AT:93:VAL:HG11	2.01	0.42
44:AF:163:LEU:O	44:AF:165:ASP:N	2.53	0.42
53:AP:168:LEU:O	53:AP:173:ARG:NH1	2.53	0.42
57:AT:17:ARG:HE	57:AT:47:SER:HB3	1.85	0.42
73:Aj:67:LEU:HA	73:Aj:70:VAL:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BD:49:ILE:HD13	4:BD:87:TYR:HB2	2.00	0.42
5:BE:121:TYR:OH	5:BE:235:TYR:O	2.31	0.42
10:BJ:124:HIS:HA	10:BJ:127:VAL:HG22	2.02	0.42
35:B5:200:A:H2'	35:B5:201:G:C8	2.54	0.42
35:B5:306:U:H2'	35:B5:307:G:C8	2.55	0.42
36:A1:314:U:OP1	49:AL:104:ARG:NH2	2.48	0.42
36:A1:3121:U:H1'	36:A1:3122:A:H5''	2.02	0.42
42:AD:85:ARG:CZ	42:AD:254:LYS:HD3	2.50	0.42
55:AR:164:LEU:HA	55:AR:168:ALA:HB3	2.01	0.42
77:An:2:ARG:HD3	77:An:5:TRP:CD1	2.55	0.42
1:BA:51:GLY:HA3	18:BR:113:LEU:HD21	2.02	0.42
2:BB:134:VAL:HB	2:BB:219:LYS:HB2	2.01	0.42
6:BF:109:LYS:HE3	6:BF:109:LYS:HB2	1.92	0.42
11:BK:15:LEU:HD22	11:BK:46:LEU:HD11	2.02	0.42
21:BU:58:LEU:HD21	21:BU:90:TYR:HE1	1.85	0.42
30:Bd:32:ARG:NE	35:B5:1596:C:OP2	2.53	0.42
33:Bg:200:ASN:ND2	33:Bg:240:VAL:O	2.36	0.42
35:B5:356:G:H2'	35:B5:357:G:H8	1.85	0.42
36:A1:953:G:H4'	36:A1:954:U:O2	2.20	0.42
36:A1:1119:C:H2'	36:A1:1120:A:C8	2.55	0.42
36:A1:1404:G:O6	68:Ae:16:LYS:NZ	2.43	0.42
36:A1:1522:U:H3'	61:AX:113:LEU:HD22	2.01	0.42
36:A1:1605:A:O2'	36:A1:1607:U:OP2	2.31	0.42
36:A1:2282:U:OP1	36:A1:2973:G:O2'	2.31	0.42
36:A1:2689:A:N6	36:A1:2702:A:O2'	2.53	0.42
51:AN:63:ARG:NH2	51:AN:131:GLU:OE2	2.46	0.42
58:AU:79:LEU:HD23	58:AU:79:LEU:HA	1.84	0.42
10:BJ:124:HIS:HB2	35:B5:479:C:H5'	2.02	0.41
13:BM:26:ASP:HA	13:BM:29:LYS:HE3	2.01	0.41
14:BN:86:GLU:HA	14:BN:89:TYR:HB3	2.01	0.41
27:Ba:15:ARG:NH1	35:B5:936:G:N7	2.68	0.41
27:Ba:35:ALA:O	27:Ba:36:ILE:HG13	2.20	0.41
33:Bg:133:VAL:HG12	33:Bg:141:LEU:HD12	2.02	0.41
35:B5:27:U:H2'	35:B5:28:A2M:H8	2.02	0.41
35:B5:739:G:OP2	35:B5:739:G:N2	2.47	0.41
35:B5:1247:U:H2'	35:B5:1248:C:C6	2.55	0.41
36:A1:1144:U:OP1	36:A1:1367:G:O2'	2.37	0.41
45:AG:200:LEU:HD23	45:AG:200:LEU:HA	1.84	0.41
48:AJ:7:ASN:HB3	48:AJ:10:ARG:HB2	2.01	0.41
48:AJ:21:ILE:HG13	48:AJ:37:LEU:HD11	2.01	0.41
49:AL:123:ILE:HG22	71:Ah:118:ILE:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AT:120:LYS:HD3	57:AT:120:LYS:HA	1.72	0.41
6:BF:166:ARG:HA	6:BF:169:ASN:HB2	2.01	0.41
15:BO:82:LYS:HD3	15:BO:118:VAL:HG11	2.03	0.41
34:Bh:89:ARG:NH1	35:B5:1190:C:OP1	2.53	0.41
36:A1:1551:C:O2'	36:A1:2170:U:O2'	2.37	0.41
36:A1:1644:C:OP1	36:A1:1820:U:O2'	2.37	0.41
51:AN:10:LEU:HG	51:AN:19:LEU:HD11	2.03	0.41
14:BN:4:MET:HE2	14:BN:4:MET:HB3	1.88	0.41
15:BO:87:GLY:HA3	15:BO:120:PRO:HG2	2.03	0.41
19:BS:112:ASP:OD2	35:B5:1546:G:O2'	2.36	0.41
21:BU:68:ARG:NH1	21:BU:77:LYS:HG3	2.35	0.41
24:BX:3:LYS:NZ	35:B5:614:C:OP1	2.33	0.41
24:BX:62:LYS:NZ	35:B5:1136:U:OP1	2.43	0.41
35:B5:208:U:H2'	35:B5:209:U:C6	2.55	0.41
35:B5:751:G:H2'	35:B5:752:A:C8	2.54	0.41
35:B5:1132:A:H2'	35:B5:1133:A:C8	2.55	0.41
36:A1:292:U:OP2	51:AN:68:ARG:NH2	2.54	0.41
36:A1:616:G:H2'	36:A1:617:G:C8	2.56	0.41
36:A1:710:A:H2'	36:A1:711:A:C8	2.55	0.41
36:A1:1426:C:H4'	41:AC:40:THR:HG23	2.02	0.41
36:A1:1604:G:H4'	36:A1:1835:A:H4'	2.03	0.41
36:A1:2724:OMU:HN3	36:A1:2732:G:H1	1.66	0.41
36:A1:3057:U:O2'	36:A1:3059:G:OP1	2.38	0.41
50:AM:16:GLU:HB3	56:AS:149:LYS:HB3	2.02	0.41
4:BD:178:ARG:HD3	35:B5:579:A:C5	2.55	0.41
4:BD:191:ASP:HB3	4:BD:194:LYS:HB2	2.01	0.41
35:B5:328:A:H2'	35:B5:329:G:C8	2.55	0.41
35:B5:410:A:H2	35:B5:423:G:H22	1.67	0.41
35:B5:629:U:H3	35:B5:970:A:H8	1.53	0.41
35:B5:837:G:H2'	35:B5:838:G:C8	2.55	0.41
35:B5:1164:G:H2'	35:B5:1165:G:C8	2.55	0.41
36:A1:1110:U:H2'	36:A1:1111:U:C6	2.56	0.41
36:A1:1281:G:O6	36:A1:1283:C:N4	2.53	0.41
36:A1:1497:C:H2'	36:A1:1498:A:H8	1.86	0.41
36:A1:1742:U:H2'	36:A1:1743:G:C8	2.56	0.41
36:A1:2284:C:N4	36:A1:2308:C:OP2	2.52	0.41
45:AG:115:ALA:O	45:AG:120:LYS:N	2.51	0.41
47:AI:16:PRO:HA	47:AI:95:HIS:CD2	2.55	0.41
48:AJ:81:GLU:HA	48:AJ:84:LEU:HB2	2.03	0.41
50:AM:60:LEU:HD13	56:AS:152:LEU:HD11	2.02	0.41
1:BA:76:ILE:HD13	1:BA:98:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:104:PRO:HB3	1:BA:131:GLN:NE2	2.36	0.41
11:BK:56:LYS:HE3	11:BK:56:LYS:HB3	1.90	0.41
16:BP:84:ILE:HD13	16:BP:84:ILE:HA	1.92	0.41
19:BS:11:PHE:HZ	19:BS:25:ASN:H	1.69	0.41
28:Bb:70:LYS:HG3	35:B5:1049:U:H5'	2.03	0.41
35:B5:968:U:H2'	35:B5:969:C:O4'	2.19	0.41
35:B5:1564:U:H2'	35:B5:1565:C:C6	2.55	0.41
36:A1:791:A:H2'	36:A1:792:G:C8	2.55	0.41
36:A1:861:C:OP1	36:A1:2133:U:O2'	2.31	0.41
36:A1:879:U:H4'	53:AP:132:ALA:HB3	2.02	0.41
36:A1:978:G:N2	36:A1:979:U:O4	2.38	0.41
36:A1:1189:C:H42	36:A1:1315:U:H1'	1.85	0.41
36:A1:1288:U:H2'	36:A1:1289:G:C8	2.55	0.41
36:A1:1486:G:H21	70:Ag:6:THR:HG22	1.85	0.41
36:A1:1718:G:H4'	55:AR:117:LYS:HE2	2.02	0.41
36:A1:1888:OMU:H5'	40:AB:247:ARG:HB2	2.02	0.41
41:AC:339:LEU:HD23	41:AC:339:LEU:HA	1.89	0.41
45:AG:166:LEU:HA	45:AG:166:LEU:HD23	1.86	0.41
47:AI:190:VAL:HG13	47:AI:197:VAL:HG21	2.01	0.41
55:AR:81:ARG:HG2	55:AR:88:ARG:CZ	2.51	0.41
61:AX:63:ILE:HD13	61:AX:86:VAL:HG12	2.02	0.41
63:AZ:81:LEU:HD22	70:Ag:90:ILE:HD13	2.01	0.41
6:BF:58:LEU:HD23	6:BF:58:LEU:HA	1.92	0.41
14:BN:88:LEU:HD11	14:BN:122:ILE:HG23	2.01	0.41
17:BQ:14:LYS:NZ	35:B5:1610:G:N7	2.68	0.41
18:BR:27:ASP:OD2	33:Bg:38:ARG:NH2	2.48	0.41
35:B5:1237:G:H2'	35:B5:1238:A:H8	1.85	0.41
36:A1:1362:G:H1'	44:AF:159:GLN:HG2	2.02	0.41
36:A1:2883:U:H2'	36:A1:2884:C:C6	2.56	0.41
36:A1:3111:U:O2'	46:AH:152:GLU:OE2	2.31	0.41
39:AA:96:LEU:HD11	39:AA:107:VAL:HG12	2.03	0.41
51:AN:36:ILE:HG12	51:AN:64:VAL:HG23	2.03	0.41
55:AR:24:LEU:HD23	55:AR:32:ILE:HG21	2.02	0.41
58:AU:19:VAL:HG12	58:AU:105:LEU:HD13	2.02	0.41
59:AV:104:ASN:ND2	59:AV:108:GLU:OE1	2.42	0.41
71:Ah:5:LYS:HB2	71:Ah:8:GLU:HG3	2.02	0.41
76:Am:88:LYS:HA	76:Am:92:ASP:HB2	2.02	0.41
6:BF:131:GLN:NE2	6:BF:135:ASP:OD1	2.51	0.41
8:BH:70:PHE:O	8:BH:74:GLN:N	2.54	0.41
25:BY:32:ARG:HG2	25:BY:35:VAL:HG12	2.01	0.41
35:B5:327:U:H2'	35:B5:328:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:1021:C:H1'	35:B5:1123:C:H41	1.84	0.41
35:B5:1625:C:H2'	35:B5:1626:U:C6	2.56	0.41
36:A1:86:G:O2'	36:A1:98:G:O6	2.37	0.41
36:A1:250:U:H5''	36:A1:251:G:C8	2.56	0.41
36:A1:629:U:H2'	36:A1:630:A:C8	2.56	0.41
36:A1:1145:G:O2'	68:Ae:45:ARG:O	2.35	0.41
36:A1:2278:5MC:OP2	77:An:23:ARG:NH1	2.40	0.41
36:A1:2715:A:O2'	78:Ao:8:ARG:NH2	2.52	0.41
37:A3:81:U:H2'	37:A3:82:G:C8	2.55	0.41
38:A4:110:C:O2'	38:A4:112:U:OP2	2.35	0.41
44:AF:118:LYS:HG3	44:AF:191:VAL:HG11	2.03	0.41
45:AG:107:GLU:O	45:AG:110:THR:OG1	2.28	0.41
5:BE:63:ALA:O	5:BE:67:GLN:NE2	2.53	0.41
11:BK:1:MET:HG3	35:B5:1216:C:H5''	2.02	0.41
17:BQ:77:GLN:O	17:BQ:81:ILE:HG12	2.20	0.41
26:BZ:81:ARG:HH22	35:B5:1532:U:P	2.42	0.41
35:B5:1796:C:H5'	35:B5:1797:A:N7	2.36	0.41
36:A1:1597:C:H5'	36:A1:1696:A:H1'	2.03	0.41
36:A1:1733:G:H2'	36:A1:1734:G:C8	2.56	0.41
36:A1:1740:U:O2'	36:A1:1742:U:O4	2.33	0.41
36:A1:2440:G:H2'	36:A1:2442:G:C8	2.56	0.41
36:A1:3166:C:H2'	36:A1:3167:A:C8	2.55	0.41
37:A3:3:U:H2'	37:A3:4:U:C6	2.56	0.41
50:AM:11:ASN:OD1	50:AM:12:TRP:N	2.52	0.41
54:AQ:51:ALA:HA	54:AQ:54:LEU:HG	2.01	0.41
3:BC:39:THR:O	3:BC:42:GLY:N	2.50	0.41
4:BD:192:PRO:HB2	4:BD:201:ALA:HA	2.03	0.41
5:BE:48:LEU:HD23	5:BE:52:LEU:HD12	2.02	0.41
9:BI:104:ILE:HG13	9:BI:105:ASP:H	1.85	0.41
14:BN:55:ARG:HD3	35:B5:960:U:H5'	2.03	0.41
14:BN:94:LYS:HG2	14:BN:118:ILE:HD13	2.03	0.41
15:BO:17:ALA:N	15:BO:80:HIS:O	2.41	0.41
16:BP:57:MET:HE1	16:BP:60:LEU:HD23	2.02	0.41
16:BP:57:MET:HE2	16:BP:88:GLU:HG2	2.03	0.41
18:BR:34:LEU:HB3	33:Bg:150:TRP:HH2	1.85	0.41
19:BS:42:TYR:HA	19:BS:85:PHE:HE2	1.86	0.41
19:BS:42:TYR:HE2	19:BS:73:MET:HG2	1.85	0.41
20:BT:133:ASP:OD2	35:B5:1359:C:O2'	2.35	0.41
24:BX:73:ARG:NH1	24:BX:84:THR:OG1	2.53	0.41
27:Ba:84:VAL:O	35:B5:1797:A:N6	2.54	0.41
29:Bc:49:ARG:N	29:Bc:52:ASP:OD2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Be:31:LYS:HD2	35:B5:545:A:H2'	2.03	0.41
33:Bg:69:GLN:HB2	33:Bg:85:TRP:HE1	1.85	0.41
35:B5:1087:A:H5'	35:B5:1298:U:C5	2.56	0.41
35:B5:1160:A:H2'	35:B5:1161:C:H6	1.86	0.41
35:B5:1248:C:H2'	35:B5:1249:U:H6	1.86	0.41
35:B5:1482:C:P	35:B5:1521:G:H22	2.44	0.41
35:B5:1647:U:H2'	35:B5:1648:A:C8	2.56	0.41
35:B5:1717:G:H2'	35:B5:1718:G:H8	1.85	0.41
36:A1:76:G:N7	49:AL:101:ARG:HB3	2.36	0.41
36:A1:255:A:H2'	36:A1:256:G:C8	2.56	0.41
36:A1:268:A:N1	36:A1:295:A:H5'	2.36	0.41
36:A1:273:A:H2'	36:A1:274:G:C8	2.55	0.41
36:A1:1246:G:H5'	36:A1:1251:A:H5''	2.01	0.41
36:A1:1359:C:H2'	36:A1:1360:C:H6	1.86	0.41
36:A1:1497:C:H2'	36:A1:1498:A:C8	2.55	0.41
36:A1:2305:G:OP2	36:A1:2305:G:N2	2.40	0.41
36:A1:2662:G:H2'	36:A1:2663:G:H8	1.86	0.41
36:A1:2727:A:C2	64:Aa:43:ILE:HG23	2.56	0.41
38:A4:48:A:O2'	38:A4:50:C:OP2	2.33	0.41
38:A4:57:C:H4'	38:A4:63:G:N7	2.36	0.41
39:AA:4:VAL:HG12	39:AA:9:ARG:HG3	2.03	0.41
39:AA:104:LEU:HB3	39:AA:146:THR:HG21	2.03	0.41
40:AB:283:TYR:HB2	40:AB:323:MET:HG2	2.03	0.41
41:AC:138:ARG:O	41:AC:138:ARG:NH1	2.52	0.41
43:AE:67:GLY:HA2	43:AE:68:PRO:HD3	1.94	0.41
44:AF:216:VAL:HA	44:AF:217:PRO:HD2	1.94	0.41
54:AQ:62:VAL:HG13	54:AQ:66:ARG:HD2	2.03	0.41
56:AS:40:ARG:HA	56:AS:40:ARG:HD2	1.79	0.41
58:AU:92:TRP:O	58:AU:108:TYR:N	2.53	0.41
63:AZ:22:LYS:HE3	63:AZ:134:LEU:HG	2.02	0.41
63:AZ:34:LYS:HE2	63:AZ:34:LYS:HB2	1.83	0.41
73:Aj:72:ARG:HA	73:Aj:75:LYS:HE2	2.02	0.41
1:BA:76:ILE:HB	1:BA:123:VAL:HG12	2.03	0.41
10:BJ:58:ASP:OD2	10:BJ:58:ASP:N	2.54	0.41
11:BK:48:SER:O	11:BK:51:SER:OG	2.39	0.41
36:A1:2228:A:H2'	36:A1:2229:A:C8	2.56	0.41
36:A1:2442:G:N2	36:A1:2506:U:O4	2.54	0.41
39:AA:112:ILE:H	79:Ap:83:ILE:HD11	1.86	0.41
40:AB:148:LEU:HD11	40:AB:196:ARG:HD3	2.03	0.41
40:AB:222:LYS:HD3	40:AB:331:ASN:HB3	2.03	0.41
44:AF:89:ILE:HD11	44:AF:229:PHE:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AG:146:LYS:HG2	45:AG:173:MET:HB3	2.02	0.41
49:AL:179:PHE:O	49:AL:183:ARG:HG2	2.20	0.41
59:AV:71:LYS:HE3	59:AV:71:LYS:HB3	1.89	0.41
2:BB:88:VAL:HG11	2:BB:96:LEU:HD13	2.02	0.40
6:BF:92:ARG:HB3	6:BF:172:ILE:HD13	2.04	0.40
7:BG:56:ASN:HB2	7:BG:108:VAL:HG12	2.02	0.40
18:BR:116:LYS:HD2	18:BR:116:LYS:HA	1.77	0.40
23:BW:103:ILE:HA	23:BW:112:ASP:HA	2.02	0.40
25:BY:104:SER:OG	25:BY:105:ARG:N	2.55	0.40
35:B5:86:A:H2'	35:B5:87:C:C6	2.54	0.40
35:B5:918:U:H2'	35:B5:919:A:H8	1.86	0.40
35:B5:1763:A:H5''	35:B5:1771:U:H5''	2.02	0.40
36:A1:339:C:OP1	36:A1:1380:G:O2'	2.33	0.40
36:A1:671:U:H2'	36:A1:672:A:C8	2.56	0.40
36:A1:950:G:N1	36:A1:1368:U:OP2	2.35	0.40
36:A1:1661:G:H2'	36:A1:1662:G:C8	2.56	0.40
36:A1:2662:G:H2'	36:A1:2663:G:C8	2.57	0.40
46:AH:118:LEU:HD23	46:AH:118:LEU:HA	1.89	0.40
63:AZ:4:PHE:HE2	66:Ac:63:SER:HB3	1.86	0.40
1:BA:12:GLU:OE2	1:BA:194:PRO:HG3	2.21	0.40
1:BA:107:PHE:HB3	1:BA:139:VAL:HG21	2.03	0.40
7:BG:53:SER:OG	7:BG:110:ALA:O	2.38	0.40
10:BJ:114:TYR:HA	10:BJ:119:ALA:HB3	2.02	0.40
20:BT:63:ARG:NH2	20:BT:67:MET:HE3	2.37	0.40
23:BW:43:LYS:HE2	23:BW:44:HIS:CE1	2.56	0.40
24:BX:130:VAL:HG13	24:BX:140:LYS:HD3	2.03	0.40
35:B5:987:G:H22	35:B5:1013:A:P	2.44	0.40
35:B5:1175:U:H2'	35:B5:1176:G:C8	2.57	0.40
35:B5:1393:C:H2'	35:B5:1394:G:H8	1.87	0.40
35:B5:1490:C:H4'	35:B5:1492:A:H5''	2.03	0.40
36:A1:407:A:C2	38:A4:17:A:H1'	2.56	0.40
36:A1:3162:C:H2'	36:A1:3163:A:C8	2.56	0.40
39:AA:29:LEU:HB2	39:AA:123:ARG:HA	2.02	0.40
45:AG:156:ASP:OD1	45:AG:156:ASP:N	2.42	0.40
48:AJ:37:LEU:HD23	48:AJ:37:LEU:HA	1.86	0.40
60:AW:33:ASN:OD1	60:AW:33:ASN:N	2.53	0.40
62:AY:48:LEU:HD23	62:AY:48:LEU:HA	1.87	0.40
66:Ac:27:TYR:CE1	66:Ac:52:ARG:HD2	2.56	0.40
1:BA:139:VAL:HA	3:BC:62:PRO:HG3	2.03	0.40
2:BB:157:GLN:HB3	2:BB:160:HIS:CE1	2.56	0.40
5:BE:7:LYS:HD2	35:B5:94:U:H1'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BE:201:HIS:CE1	35:B5:799:A:H4'	2.57	0.40
15:BO:81:VAL:HG22	15:BO:115:ILE:HG12	2.02	0.40
20:BT:102:ARG:NE	35:B5:1501:C:OP2	2.47	0.40
22:BV:4:ASP:OD1	22:BV:4:ASP:N	2.54	0.40
23:BW:25:VAL:HG13	23:BW:65:LEU:HD13	2.04	0.40
24:BX:43:PHE:O	24:BX:45:GLY:N	2.54	0.40
35:B5:174:U:O4	35:B5:266:A:N7	2.54	0.40
35:B5:330:G:H2'	35:B5:331:A:C8	2.57	0.40
35:B5:1710:U:H5'	35:B5:1711:C:C5	2.56	0.40
36:A1:412:G:OP1	53:AP:62:ARG:NH1	2.55	0.40
36:A1:714:G:O2'	36:A1:753:C:O2'	2.25	0.40
64:Aa:77:LYS:C	64:Aa:79:TRP:H	2.28	0.40
6:BF:80:LYS:HD3	6:BF:80:LYS:HA	1.85	0.40
7:BG:66:GLY:HA3	35:B5:1681:A:H8	1.86	0.40
9:BI:37:LYS:HE2	9:BI:93:THR:HB	2.04	0.40
15:BO:80:HIS:ND1	15:BO:113:GLY:O	2.37	0.40
15:BO:135:ARG:HE	15:BO:135:ARG:HB3	1.52	0.40
16:BP:81:ARG:HB3	16:BP:117:GLY:HA3	2.03	0.40
21:BU:50:LEU:HD21	21:BU:96:PRO:HD2	2.04	0.40
26:BZ:103:ARG:H	26:BZ:103:ARG:HG2	1.73	0.40
27:Ba:78:ALA:HA	27:Ba:83:ILE:HD12	2.03	0.40
35:B5:396:G:N2	35:B5:399:A:OP2	2.50	0.40
36:A1:308:A:H1'	36:A1:2222:A:N3	2.36	0.40
36:A1:422:A:C2	36:A1:2363:A:H4'	2.56	0.40
36:A1:966:U:H2'	36:A1:967:A:C8	2.57	0.40
36:A1:1622:U:H2'	36:A1:1623:G:C8	2.57	0.40
36:A1:1662:G:H22	36:A1:1787:A:H2	1.69	0.40
36:A1:2586:G:O2'	45:AG:48:ARG:NH2	2.54	0.40
40:AB:110:LEU:HB2	40:AB:115:LYS:HE3	2.02	0.40
42:AD:215:ASP:OD1	42:AD:215:ASP:N	2.54	0.40
53:AP:167:ARG:HD2	69:Af:60:ARG:NH2	2.36	0.40
3:BC:139:ILE:HD13	3:BC:191:ALA:HB1	2.03	0.40
3:BC:156:THR:HG21	3:BC:224:PHE:CG	2.56	0.40
5:BE:175:PHE:HE2	5:BE:225:VAL:HG11	1.87	0.40
7:BG:74:LYS:NZ	7:BG:96:SER:HB3	2.37	0.40
17:BQ:77:GLN:HE22	35:B5:1482:C:H4'	1.86	0.40
18:BR:23:LYS:HD2	18:BR:23:LYS:HA	1.85	0.40
21:BU:33:GLN:NE2	21:BU:109:GLU:OE2	2.55	0.40
24:BX:37:ALA:O	24:BX:41:SER:OG	2.39	0.40
25:BY:44:LEU:HA	25:BY:44:LEU:HD23	1.93	0.40
31:Be:27:PRO:HD3	35:B5:506:A:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Bg:23:LEU:HD12	33:Bg:292:LEU:HA	2.03	0.40
35:B5:1051:G:N1	35:B5:1068:C:N3	2.69	0.40
35:B5:1716:C:O2'	35:B5:1717:G:O4'	2.31	0.40
36:A1:715:A:C8	64:Aa:115:LYS:HD3	2.56	0.40
36:A1:976:U:H2'	36:A1:977:C:O4'	2.22	0.40
36:A1:1689:U:H5''	55:AR:61:SER:HB3	2.04	0.40
36:A1:1813:A:H4'	36:A1:1817:G:H1'	2.02	0.40
36:A1:2653:C:O2'	36:A1:2657:A:N1	2.48	0.40
40:AB:80:ASP:OD2	40:AB:314:TYR:OH	2.39	0.40
41:AC:3:ARG:HA	41:AC:4:PRO:HD3	1.83	0.40
52:AO:127[A]:LEU:HD22	56:AS:156:VAL:HG13	2.02	0.40
57:AT:8:ARG:HG2	57:AT:15:PHE:HE2	1.87	0.40
60:AW:52:THR:O	60:AW:56:ARG:HG3	2.22	0.40
63:AZ:16:GLY:C	63:AZ:18:TYR:H	2.30	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	204/206 (99%)	181 (89%)	22 (11%)	1 (0%)	25	54
2	BB	212/214 (99%)	176 (83%)	34 (16%)	2 (1%)	14	40
3	BC	215/217 (99%)	199 (93%)	15 (7%)	1 (0%)	25	54
4	BD	221/223 (99%)	207 (94%)	14 (6%)	0	100	100
5	BE	258/260 (99%)	228 (88%)	30 (12%)	0	100	100
6	BF	204/206 (99%)	186 (91%)	17 (8%)	1 (0%)	25	54
7	BG	224/226 (99%)	205 (92%)	16 (7%)	3 (1%)	10	32
8	BH	182/184 (99%)	166 (91%)	15 (8%)	1 (0%)	25	54
9	BI	184/188 (98%)	149 (81%)	35 (19%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	BJ	183/185 (99%)	165 (90%)	17 (9%)	1 (0%)	25	54
11	BK	94/96 (98%)	77 (82%)	17 (18%)	0	100	100
12	BL	153/155 (99%)	138 (90%)	15 (10%)	0	100	100
13	BM	119/121 (98%)	85 (71%)	34 (29%)	0	100	100
14	BN	148/150 (99%)	139 (94%)	9 (6%)	0	100	100
15	BO	125/127 (98%)	109 (87%)	15 (12%)	1 (1%)	16	43
16	BP	122/124 (98%)	100 (82%)	21 (17%)	1 (1%)	16	43
17	BQ	139/141 (99%)	127 (91%)	11 (8%)	1 (1%)	19	46
18	BR	117/121 (97%)	111 (95%)	6 (5%)	0	100	100
19	BS	143/145 (99%)	129 (90%)	13 (9%)	1 (1%)	19	46
20	BT	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
21	BU	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
22	BV	83/87 (95%)	72 (87%)	11 (13%)	0	100	100
23	BW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
24	BX	142/144 (99%)	118 (83%)	21 (15%)	3 (2%)	5	21
25	BY	132/134 (98%)	124 (94%)	8 (6%)	0	100	100
26	BZ	67/69 (97%)	61 (91%)	6 (9%)	0	100	100
27	Ba	95/97 (98%)	74 (78%)	19 (20%)	2 (2%)	5	21
28	Bb	79/81 (98%)	68 (86%)	11 (14%)	0	100	100
29	Bc	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
30	Bd	51/53 (96%)	51 (100%)	0	0	100	100
31	Be	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
32	Bf	53/57 (93%)	36 (68%)	17 (32%)	0	100	100
33	Bg	310/312 (99%)	276 (89%)	34 (11%)	0	100	100
34	Bh	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
39	AA	245/247 (99%)	232 (95%)	13 (5%)	0	100	100
40	AB	383/386 (99%)	368 (96%)	14 (4%)	1 (0%)	37	64
41	AC	359/361 (99%)	321 (89%)	36 (10%)	2 (1%)	22	49
42	AD	290/292 (99%)	267 (92%)	22 (8%)	1 (0%)	37	64
43	AE	152/156 (97%)	142 (93%)	10 (7%)	0	100	100
44	AF	220/222 (99%)	206 (94%)	12 (6%)	2 (1%)	14	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	AG	228/230 (99%)	210 (92%)	18 (8%)	0	100	100
46	AH	188/190 (99%)	176 (94%)	12 (6%)	0	100	100
47	AI	201/205 (98%)	185 (92%)	16 (8%)	0	100	100
48	AJ	167/169 (99%)	146 (87%)	21 (13%)	0	100	100
49	AL	191/193 (99%)	171 (90%)	17 (9%)	3 (2%)	8	27
50	AM	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
51	AN	201/203 (99%)	185 (92%)	15 (8%)	1 (0%)	25	54
52	AO	195/197 (99%)	188 (96%)	6 (3%)	1 (0%)	25	54
53	AP	171/175 (98%)	164 (96%)	7 (4%)	0	100	100
54	AQ	183/185 (99%)	175 (96%)	8 (4%)	0	100	100
55	AR	186/188 (99%)	178 (96%)	8 (4%)	0	100	100
56	AS	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
57	AT	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
58	AU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
59	AV	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
60	AW	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
61	AX	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
62	AY	124/126 (98%)	115 (93%)	9 (7%)	0	100	100
63	AZ	133/135 (98%)	121 (91%)	11 (8%)	1 (1%)	16	43
64	Aa	146/148 (99%)	129 (88%)	16 (11%)	1 (1%)	19	46
65	Ab	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
66	Ac	95/97 (98%)	90 (95%)	5 (5%)	0	100	100
67	Ad	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
68	Ae	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
69	Af	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
70	Ag	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
71	Ah	117/119 (98%)	109 (93%)	7 (6%)	1 (1%)	14	40
72	Ai	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
73	Aj	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
74	Ak	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
75	Al	48/50 (96%)	46 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	Am	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
77	An	23/25 (92%)	23 (100%)	0	0	100	100
78	Ao	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
79	Ap	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
All	All	10956/11121 (98%)	10008 (91%)	915 (8%)	33 (0%)	38	64

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	BX	97	ASP
41	AC	339	LEU
44	AF	159	GLN
49	AL	48	PRO
51	AN	81	TYR
52	AO	111[A]	PRO
2	BB	207	LEU
7	BG	68	LEU
7	BG	173	PRO
10	BJ	134	ILE
16	BP	125	PRO
19	BS	91	ASP
49	AL	63	VAL
49	AL	77	LEU
64	Aa	78	LEU
1	BA	4	PRO
2	BB	206	PRO
8	BH	111	LYS
27	Ba	35	ALA
42	AD	20	PHE
24	BX	137	LYS
41	AC	268	ALA
27	Ba	36	ILE
71	Ah	91	ALA
3	BC	40	LYS
6	BF	43	PHE
15	BO	126	THR
17	BQ	33	GLY
44	AF	216	VAL
24	BX	96	VAL
63	AZ	103	GLN
7	BG	67	VAL

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Mol	Chain	Res	Type
40	AB	188	ILE

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	173/173 (100%)	173 (100%)	0	100	100
2	BB	191/191 (100%)	191 (100%)	0	100	100
3	BC	176/176 (100%)	176 (100%)	0	100	100
4	BD	182/182 (100%)	182 (100%)	0	100	100
5	BE	221/221 (100%)	221 (100%)	0	100	100
6	BF	173/173 (100%)	173 (100%)	0	100	100
7	BG	193/193 (100%)	193 (100%)	0	100	100
8	BH	165/165 (100%)	165 (100%)	0	100	100
9	BI	150/150 (100%)	150 (100%)	0	100	100
10	BJ	158/158 (100%)	158 (100%)	0	100	100
11	BK	89/89 (100%)	89 (100%)	0	100	100
12	BL	136/136 (100%)	136 (100%)	0	100	100
13	BM	98/98 (100%)	98 (100%)	0	100	100
14	BN	127/127 (100%)	127 (100%)	0	100	100
15	BO	96/96 (100%)	96 (100%)	0	100	100
16	BP	104/104 (100%)	104 (100%)	0	100	100
17	BQ	117/117 (100%)	117 (100%)	0	100	100
18	BR	110/110 (100%)	110 (100%)	0	100	100
19	BS	128/128 (100%)	128 (100%)	0	100	100
20	BT	113/113 (100%)	113 (100%)	0	100	100
21	BU	100/100 (100%)	100 (100%)	0	100	100
22	BV	74/74 (100%)	74 (100%)	0	100	100
23	BW	110/110 (100%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	BX	119/119 (100%)	119 (100%)	0	100	100
25	BY	112/112 (100%)	112 (100%)	0	100	100
26	BZ	61/61 (100%)	61 (100%)	0	100	100
27	Ba	83/83 (100%)	83 (100%)	0	100	100
28	Bb	70/70 (100%)	70 (100%)	0	100	100
29	Bc	56/56 (100%)	56 (100%)	0	100	100
30	Bd	47/47 (100%)	46 (98%)	1 (2%)	48	69
31	Be	51/51 (100%)	51 (100%)	0	100	100
32	Bf	49/49 (100%)	49 (100%)	0	100	100
33	Bg	256/257 (100%)	256 (100%)	0	100	100
34	Bh	68/68 (100%)	68 (100%)	0	100	100
39	AA	189/189 (100%)	189 (100%)	0	100	100
40	AB	321/321 (100%)	319 (99%)	2 (1%)	84	90
41	AC	288/288 (100%)	288 (100%)	0	100	100
42	AD	241/241 (100%)	241 (100%)	0	100	100
43	AE	134/134 (100%)	134 (100%)	0	100	100
44	AF	186/186 (100%)	186 (100%)	0	100	100
45	AG	189/189 (100%)	189 (100%)	0	100	100
46	AH	170/170 (100%)	170 (100%)	0	100	100
47	AI	176/176 (100%)	176 (100%)	0	100	100
48	AJ	147/147 (100%)	147 (100%)	0	100	100
49	AL	154/154 (100%)	154 (100%)	0	100	100
50	AM	107/107 (100%)	107 (100%)	0	100	100
51	AN	175/175 (100%)	175 (100%)	0	100	100
52	AO	160/160 (100%)	160 (100%)	0	100	100
53	AP	141/141 (100%)	141 (100%)	0	100	100
54	AQ	150/150 (100%)	150 (100%)	0	100	100
55	AR	153/153 (100%)	153 (100%)	0	100	100
56	AS	156/156 (100%)	156 (100%)	0	100	100
57	AT	136/136 (100%)	136 (100%)	0	100	100
58	AU	87/87 (100%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	AV	104/104 (100%)	104 (100%)	0	100	100
60	AW	55/55 (100%)	55 (100%)	0	100	100
61	AX	105/105 (100%)	105 (100%)	0	100	100
62	AY	109/109 (100%)	109 (100%)	0	100	100
63	AZ	115/115 (100%)	115 (100%)	0	100	100
64	Aa	118/118 (100%)	118 (100%)	0	100	100
65	Ab	46/46 (100%)	46 (100%)	0	100	100
66	Ac	81/81 (100%)	81 (100%)	0	100	100
67	Ad	96/96 (100%)	96 (100%)	0	100	100
68	Ae	109/109 (100%)	109 (100%)	0	100	100
69	Af	90/90 (100%)	90 (100%)	0	100	100
70	Ag	95/95 (100%)	95 (100%)	0	100	100
71	Ah	104/104 (100%)	104 (100%)	0	100	100
72	Ai	81/81 (100%)	81 (100%)	0	100	100
73	Aj	70/70 (100%)	70 (100%)	0	100	100
74	Ak	68/68 (100%)	68 (100%)	0	100	100
75	Al	45/45 (100%)	45 (100%)	0	100	100
76	Am	47/47 (100%)	47 (100%)	0	100	100
77	An	23/23 (100%)	23 (100%)	0	100	100
78	Ao	90/90 (100%)	90 (100%)	0	100	100
79	Ap	71/71 (100%)	71 (100%)	0	100	100
All	All	9338/9339 (100%)	9335 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	Bd	28	THR
40	AB	90	VAL
40	AB	93	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (82) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	30	GLN

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Mol	Chain	Res	Type
2	BB	101	HIS
2	BB	118	GLN
2	BB	208	GLN
3	BC	199	GLN
5	BE	50	ASN
5	BE	98	ASN
6	BF	63	GLN
6	BF	66	GLN
6	BF	95	ASN
6	BF	200	ASN
7	BG	119	GLN
8	BH	174	ASN
9	BI	94	ASN
12	BL	14	GLN
12	BL	92	HIS
14	BN	21	ASN
14	BN	49	GLN
15	BO	12	GLN
17	BQ	77	GLN
19	BS	25	ASN
19	BS	71	GLN
19	BS	103	ASN
20	BT	43	ASN
24	BX	28	ASN
26	BZ	98	GLN
28	Bb	5	GLN
28	Bb	9	HIS
28	Bb	26	GLN
33	Bg	139	GLN
33	Bg	308	ASN
34	Bh	70	ASN
39	AA	132	ASN
40	AB	121	ASN
41	AC	116	ASN
41	AC	291	ASN
41	AC	304	GLN
42	AD	244	HIS
43	AE	61	ASN
44	AF	25	GLN
44	AF	80	GLN
44	AF	93	ASN
45	AG	79	GLN

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Mol	Chain	Res	Type
45	AG	145	ASN
45	AG	192	GLN
46	AH	96	HIS
46	AH	116	ASN
46	AH	183	HIS
47	AI	59	GLN
47	AI	162	GLN
48	AJ	6	GLN
49	AL	19	GLN
49	AL	106	GLN
50	AM	126	GLN
51	AN	138	GLN
52	AO	26[A]	GLN
52	AO	122[A]	GLN
52	AO	182[A]	ASN
53	AP	54	HIS
53	AP	55	GLN
53	AP	133	HIS
55	AR	118	HIS
55	AR	134	HIS
55	AR	141	HIS
56	AS	49	HIS
57	AT	5	HIS
58	AU	25	ASN
58	AU	87	ASN
59	AV	98	ASN
61	AX	65	GLN
62	AY	110	HIS
63	AZ	36	HIS
63	AZ	78	ASN
63	AZ	122	HIS
64	Aa	120	ASN
65	Ab	43	HIS
66	Ac	71	GLN
67	Ad	21	HIS
68	Ae	60	ASN
69	Af	5	HIS
70	Ag	69	HIS
71	Ah	104	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	B5	1779/1781 (99%)	525 (29%)	11 (0%)
36	A1	3131/3137 (99%)	727 (23%)	17 (0%)
37	A3	120/121 (99%)	19 (15%)	0
38	A4	156/158 (98%)	34 (21%)	1 (0%)
All	All	5186/5197 (99%)	1305 (25%)	29 (0%)

All (1305) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	B5	4	C
35	B5	25	C
35	B5	26	A
35	B5	34	G
35	B5	42	G
35	B5	43	A
35	B5	45	U
35	B5	46	A
35	B5	47	A
35	B5	50	C
35	B5	57	G
35	B5	59	C
35	B5	60	U
35	B5	67	A
35	B5	68	A
35	B5	72	A
35	B5	73	U
35	B5	74	U
35	B5	75	U
35	B5	76	A
35	B5	77	U
35	B5	78	A
35	B5	81	G
35	B5	94	U
35	B5	95	G
35	B5	100	A2M
35	B5	103	A
35	B5	104	A
35	B5	111	U
35	B5	114	C
35	B5	116	U
35	B5	124	A
35	B5	127	G
35	B5	129	U

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Mol	Chain	Res	Type
35	B5	130	C
35	B5	133	U
35	B5	134	U
35	B5	135	A
35	B5	136	C
35	B5	137	U
35	B5	138	A
35	B5	140	A
35	B5	141	U
35	B5	145	A
35	B5	158	U
35	B5	166	C
35	B5	169	A
35	B5	171	A
35	B5	178	U
35	B5	183	U
35	B5	188	A
35	B5	190	C
35	B5	191	C
35	B5	192	U
35	B5	194	U
35	B5	195	G
35	B5	196	G
35	B5	197	A
35	B5	198	A
35	B5	199	G
35	B5	200	A
35	B5	204	G
35	B5	206	A
35	B5	215	A
35	B5	217	A
35	B5	218	A
35	B5	220	A
35	B5	226	A
35	B5	227	U
35	B5	229	U
35	B5	230	C
35	B5	231	U
35	B5	232	U
35	B5	233	C
35	B5	234	G
35	B5	235	G

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Mol	Chain	Res	Type
35	B5	236	A
35	B5	239	C
35	B5	240	U
35	B5	241	U
35	B5	248	U
35	B5	249	U
35	B5	253	A
35	B5	261	U
35	B5	262	U
35	B5	265	A
35	B5	267	U
35	B5	272	U
35	B5	273	G
35	B5	277	U
35	B5	278	U
35	B5	280	U
35	B5	281	G
35	B5	283	U
35	B5	299	A
35	B5	313	U
35	B5	315	A
35	B5	316	A
35	B5	320	U
35	B5	321	C
35	B5	322	G
35	B5	333	A
35	B5	337	G
35	B5	338	C
35	B5	352	A
35	B5	359	A
35	B5	360	A
35	B5	361	C
35	B5	365	G
35	B5	369	A
35	B5	390	G
35	B5	399	A
35	B5	400	A
35	B5	401	A
35	B5	402	C
35	B5	404	G
35	B5	417	A
35	B5	419	G

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Mol	Chain	Res	Type
35	B5	423	G
35	B5	424	C
35	B5	425	A
35	B5	426	G
35	B5	431	C
35	B5	434	G
35	B5	435	C
35	B5	439	U
35	B5	444	C
35	B5	448	C
35	B5	452	A
35	B5	459	G
35	B5	460	A
35	B5	464	A
35	B5	468	A
35	B5	475	A
35	B5	477	A
35	B5	480	G
35	B5	481	A
35	B5	484	C
35	B5	485	A
35	B5	486	G
35	B5	487	G
35	B5	489	C
35	B5	490	C
35	B5	491	C
35	B5	492	A
35	B5	493	U
35	B5	494	U
35	B5	495	C
35	B5	496	G
35	B5	497	G
35	B5	498	G
35	B5	499	U
35	B5	500	C
35	B5	503	G
35	B5	506	A
35	B5	507	U
35	B5	514	G
35	B5	515	A
35	B5	519	C
35	B5	525	A

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Mol	Chain	Res	Type
35	B5	538	A
35	B5	539	G
35	B5	540	G
35	B5	541	A2M
35	B5	542	A
35	B5	544	A
35	B5	555	A
35	B5	557	G
35	B5	558	U
35	B5	559	C
35	B5	565	C
35	B5	566	C
35	B5	575	C
35	B5	576	G
35	B5	577	G
35	B5	578	OMU
35	B5	579	A
35	B5	580	A
35	B5	594	A
35	B5	595	G
35	B5	606	A
35	B5	607	G
35	B5	609	U
35	B5	610	G
35	B5	611	U
35	B5	614	C
35	B5	617	U
35	B5	619	A2M
35	B5	620	A
35	B5	622	A
35	B5	623	A
35	B5	634	G
35	B5	635	A
35	B5	638	U
35	B5	639	U
35	B5	648	G
35	B5	650	U
35	B5	651	G
35	B5	652	G
35	B5	655	G
35	B5	656	G
35	B5	658	C

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Mol	Chain	Res	Type
35	B5	677	G
35	B5	678	A
35	B5	679	U
35	B5	681	U
35	B5	682	C
35	B5	683	C
35	B5	690	G
35	B5	693	U
35	B5	694	U
35	B5	696	C
35	B5	697	C
35	B5	700	C
35	B5	702	G
35	B5	704	C
35	B5	705	U
35	B5	707	A
35	B5	708	C
35	B5	710	U
35	B5	711	U
35	B5	712	G
35	B5	713	A
35	B5	715	U
35	B5	716	C
35	B5	717	C
35	B5	718	U
35	B5	719	U
35	B5	720	G
35	B5	721	U
35	B5	722	G
35	B5	723	G
35	B5	724	C
35	B5	725	U
35	B5	727	U
35	B5	729	G
35	B5	730	G
35	B5	731	C
35	B5	732	G
35	B5	733	A
35	B5	735	C
35	B5	736	C
35	B5	737	A
35	B5	738	G

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Mol	Chain	Res	Type
35	B5	743	U
35	B5	755	A
35	B5	765	G
35	B5	766	U
35	B5	768	C
35	B5	771	A
35	B5	774	A
35	B5	775	G
35	B5	778	G
35	B5	779	U
35	B5	781	U
35	B5	782	U
35	B5	783	G
35	B5	784	C
35	B5	789	A
35	B5	794	U
35	B5	795	U
35	B5	803	A
35	B5	807	A
35	B5	812	A
35	B5	813	U
35	B5	814	A
35	B5	815	G
35	B5	819	G
35	B5	820	U
35	B5	822	U
35	B5	823	G
35	B5	824	G
35	B5	825	U
35	B5	826	U
35	B5	828	U
35	B5	829	A
35	B5	830	U
35	B5	833	U
35	B5	834	G
35	B5	836	U
35	B5	840	U
35	B5	841	U
35	B5	843	U
35	B5	844	A
35	B5	845	G
35	B5	847	A

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Mol	Chain	Res	Type
35	B5	848	C
35	B5	849	C
35	B5	850	A
35	B5	851	U
35	B5	852	C
35	B5	853	G
35	B5	854	U
35	B5	856	A
35	B5	857	U
35	B5	859	A
35	B5	863	A
35	B5	873	U
35	B5	881	A
35	B5	886	U
35	B5	895	G
35	B5	898	A
35	B5	906	A
35	B5	912	U
35	B5	913	G
35	B5	914	G
35	B5	918	U
35	B5	933	A
35	B5	935	U
35	B5	945	U
35	B5	951	A
35	B5	952	A
35	B5	960	U
35	B5	961	U
35	B5	964	U
35	B5	966	A
35	B5	973	A
35	B5	987	G
35	B5	988	A
35	B5	991	G
35	B5	992	A
35	B5	993	A
35	B5	1004	U
35	B5	1005	A
35	B5	1020	A
35	B5	1025	A
35	B5	1026	A
35	B5	1027	A

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Mol	Chain	Res	Type
35	B5	1028	C
35	B5	1032	G
35	B5	1039	A
35	B5	1052	U
35	B5	1053	G
35	B5	1056	U
35	B5	1058	U
35	B5	1059	U
35	B5	1060	U
35	B5	1061	A
35	B5	1062	A
35	B5	1072	C
35	B5	1076	A
35	B5	1082	C
35	B5	1086	A
35	B5	1091	A
35	B5	1092	A
35	B5	1093	A
35	B5	1097	U
35	B5	1098	U
35	B5	1100	G
35	B5	1101	G
35	B5	1108	G
35	B5	1111	G
35	B5	1126	OMG
35	B5	1137	A
35	B5	1138	A
35	B5	1143	A
35	B5	1146	G
35	B5	1150	G
35	B5	1158	C
35	B5	1159	C
35	B5	1163	A
35	B5	1185	U
35	B5	1186	U
35	B5	1187	U
35	B5	1194	A
35	B5	1196	A
35	B5	1199	G
35	B5	1200	G
35	B5	1201	G
35	B5	1202	A

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Mol	Chain	Res	Type
35	B5	1203	A
35	B5	1207	C
35	B5	1217	A
35	B5	1218	G
35	B5	1226	A
35	B5	1227	A
35	B5	1229	G
35	B5	1230	A
35	B5	1241	G
35	B5	1243	G
35	B5	1244	A
35	B5	1245	G
35	B5	1248	C
35	B5	1251	U
35	B5	1252	C
35	B5	1255	G
35	B5	1256	A
35	B5	1257	U
35	B5	1269	OMU
35	B5	1270	G
35	B5	1273	G
35	B5	1276	U
35	B5	1284	C
35	B5	1285	U
35	B5	1286	U
35	B5	1287	A
35	B5	1306	C
35	B5	1314	U
35	B5	1315	U
35	B5	1316	G
35	B5	1321	A
35	B5	1340	U
35	B5	1342	C
35	B5	1344	A
35	B5	1345	A
35	B5	1347	U
35	B5	1349	G
35	B5	1352	G
35	B5	1355	C
35	B5	1358	G
35	B5	1359	C
35	B5	1361	U

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Mol	Chain	Res	Type
35	B5	1362	U
35	B5	1363	U
35	B5	1364	G
35	B5	1366	U
35	B5	1368	G
35	B5	1369	U
35	B5	1371	A
35	B5	1372	U
35	B5	1373	C
35	B5	1378	U
35	B5	1388	A
35	B5	1390	U
35	B5	1392	U
35	B5	1398	U
35	B5	1399	C
35	B5	1400	A
35	B5	1413	U
35	B5	1414	U
35	B5	1415	U
35	B5	1418	G
35	B5	1427	A
35	B5	1428	OMG
35	B5	1429	G
35	B5	1436	A
35	B5	1444	A
35	B5	1445	G
35	B5	1447	C
35	B5	1459	C
35	B5	1461	C
35	B5	1469	A
35	B5	1471	A
35	B5	1474	G
35	B5	1475	A
35	B5	1481	C
35	B5	1486	G
35	B5	1491	U
35	B5	1492	A
35	B5	1493	A
35	B5	1496	U
35	B5	1503	A
35	B5	1506	G
35	B5	1514	U

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Mol	Chain	Res	Type
35	B5	1516	A
35	B5	1523	G
35	B5	1524	A
35	B5	1537	C
35	B5	1538	U
35	B5	1539	G
35	B5	1542	G
35	B5	1557	U
35	B5	1559	A
35	B5	1575	G7M
35	B5	1576	A
35	B5	1577	A
35	B5	1582	U
35	B5	1584	G
35	B5	1590	G
35	B5	1597	A
35	B5	1600	A
35	B5	1601	G
35	B5	1605	G
35	B5	1607	G
35	B5	1619	C
35	B5	1630	U
35	B5	1633	A
35	B5	1634	C
35	B5	1635	A
35	B5	1642	G
35	B5	1643	U
35	B5	1646	C
35	B5	1651	A
35	B5	1657	U
35	B5	1658	G
35	B5	1663	G
35	B5	1680	G
35	B5	1682	U
35	B5	1683	C
35	B5	1684	U
35	B5	1689	A
35	B5	1690	G
35	B5	1691	A
35	B5	1692	G
35	B5	1693	A
35	B5	1694	A

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Mol	Chain	Res	Type
35	B5	1695	G
35	B5	1696	G
35	B5	1697	G
35	B5	1698	G
35	B5	1699	G
35	B5	1701	A
35	B5	1702	A
35	B5	1703	C
35	B5	1704	U
35	B5	1706	C
35	B5	1709	C
35	B5	1710	U
35	B5	1711	C
35	B5	1713	G
35	B5	1714	A
35	B5	1716	C
35	B5	1717	G
35	B5	1750	A
35	B5	1762	A
35	B5	1766	A
35	B5	1767	G
35	B5	1769	U
35	B5	1780	G
35	B5	1781	MA6
35	B5	1792	G
35	B5	1793	G
35	B5	1794	A
35	B5	1795	U
35	B5	1796	C
36	A1	4	U
36	A1	18	G
36	A1	34	A
36	A1	40	A
36	A1	43	A
36	A1	49	A
36	A1	59	G
36	A1	60	A
36	A1	65	A
36	A1	66	A
36	A1	67	A
36	A1	74	G
36	A1	75	G

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Mol	Chain	Res	Type
36	A1	92	G
36	A1	109	A
36	A1	110	G
36	A1	111	C
36	A1	115	A
36	A1	116	A
36	A1	117	U
36	A1	118	U
36	A1	120	G
36	A1	122	A
36	A1	134	U
36	A1	135	C
36	A1	136	G
36	A1	148	G
36	A1	150	A
36	A1	156	G
36	A1	157	A
36	A1	163	C
36	A1	164	A
36	A1	165	A
36	A1	169	U
36	A1	174	C
36	A1	187	A
36	A1	190	U
36	A1	191	U
36	A1	197	G
36	A1	200	C
36	A1	210	U
36	A1	211	A
36	A1	219	A
36	A1	220	G
36	A1	239	G
36	A1	240	U
36	A1	241	G
36	A1	242	C
36	A1	243	G
36	A1	244	G
36	A1	248	U
36	A1	249	U
36	A1	250	U
36	A1	251	G
36	A1	252	U

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Mol	Chain	Res	Type
36	A1	256	G
36	A1	259	C
36	A1	266	A
36	A1	267	G
36	A1	268	A
36	A1	269	G
36	A1	283	G
36	A1	285	A
36	A1	286	U
36	A1	295	A
36	A1	296	A
36	A1	297	G
36	A1	298	U
36	A1	299	G
36	A1	300	G
36	A1	305	U
36	A1	317	A
36	A1	329	U
36	A1	337	G
36	A1	338	A
36	A1	339	C
36	A1	352	A
36	A1	372	A
36	A1	373	A
36	A1	374	A
36	A1	376	G
36	A1	387	A
36	A1	392	G
36	A1	395	A
36	A1	398	A
36	A1	399	A
36	A1	400	G
36	A1	401	U
36	A1	402	A
36	A1	403	C
36	A1	408	A
36	A1	420	G
36	A1	421	G
36	A1	422	A
36	A1	438	A
36	A1	439	C
36	A1	440	A

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Mol	Chain	Res	Type
36	A1	495	G
36	A1	521	A
36	A1	523	A
36	A1	532	A
36	A1	535	G
36	A1	536	U
36	A1	540	U
36	A1	542	G
36	A1	543	C
36	A1	545	U
36	A1	547	G
36	A1	548	G
36	A1	549	U
36	A1	550	A
36	A1	551	A
36	A1	555	U
36	A1	557	A
36	A1	558	U
36	A1	559	A
36	A1	560	G
36	A1	568	G
36	A1	569	A
36	A1	578	A
36	A1	579	G
36	A1	602	A
36	A1	604	G
36	A1	611	A
36	A1	621	A
36	A1	636	C
36	A1	649	A2M
36	A1	660	A
36	A1	677	A
36	A1	681	U
36	A1	690	A
36	A1	691	A
36	A1	705	A
36	A1	719	U
36	A1	725	G
36	A1	733	G
36	A1	736	A
36	A1	737	G
36	A1	758	C

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Mol	Chain	Res	Type
36	A1	760	G
36	A1	765	C
36	A1	766	U
36	A1	767	U
36	A1	774	G
36	A1	776	U
36	A1	777	U
36	A1	779	G
36	A1	780	A
36	A1	781	G
36	A1	784	A
36	A1	785	G
36	A1	786	A
36	A1	799	G
36	A1	801	A
36	A1	806	A
36	A1	812	G
36	A1	813	G
36	A1	817	A2M
36	A1	818	C
36	A1	826	G
36	A1	830	A
36	A1	832	G
36	A1	837	A
36	A1	844	G
36	A1	849	C
36	A1	850	U
36	A1	857	G
36	A1	861	C
36	A1	865	U
36	A1	874	U
36	A1	879	U
36	A1	896	A
36	A1	897	U
36	A1	907	G
36	A1	908	OMG
36	A1	909	G
36	A1	914	A
36	A1	916	G
36	A1	917	A
36	A1	920	A
36	A1	921	A

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Mol	Chain	Res	Type
36	A1	923	C
36	A1	924	G
36	A1	925	A
36	A1	934	G
36	A1	937	G
36	A1	943	U
36	A1	944	C
36	A1	953	G
36	A1	959	C
36	A1	960	U
36	A1	979	U
36	A1	980	A
36	A1	981	U
36	A1	991	G
36	A1	994	G
36	A1	1002	A
36	A1	1006	A
36	A1	1010	G
36	A1	1016	C
36	A1	1017	C
36	A1	1018	G
36	A1	1019	G
36	A1	1022	U
36	A1	1023	C
36	A1	1032	C
36	A1	1033	U
36	A1	1034	U
36	A1	1035	G
36	A1	1041	U
36	A1	1047	A
36	A1	1049	C
36	A1	1052	U
36	A1	1064	A
36	A1	1072	G
36	A1	1073	U
36	A1	1081	U
36	A1	1082	U
36	A1	1094	U
36	A1	1095	U
36	A1	1097	G
36	A1	1098	A
36	A1	1103	A

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Mol	Chain	Res	Type
36	A1	1104	G
36	A1	1117	G
36	A1	1124	U
36	A1	1131	G
36	A1	1132	C
36	A1	1135	A
36	A1	1144	U
36	A1	1150	A
36	A1	1153	A
36	A1	1154	A
36	A1	1156	C
36	A1	1159	A
36	A1	1180	A
36	A1	1181	U
36	A1	1182	A
36	A1	1185	C
36	A1	1192	C
36	A1	1193	A
36	A1	1196	C
36	A1	1197	A
36	A1	1200	A
36	A1	1201	C
36	A1	1202	A
36	A1	1208	U
36	A1	1209	G
36	A1	1219	C
36	A1	1221	A
36	A1	1222	G
36	A1	1223	A
36	A1	1227	C
36	A1	1230	G
36	A1	1231	A
36	A1	1232	C
36	A1	1233	G
36	A1	1234	G
36	A1	1235	U
36	A1	1236	G
36	A1	1237	G
36	A1	1239	C
36	A1	1240	A
36	A1	1241	U
36	A1	1242	G

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Mol	Chain	Res	Type
36	A1	1243	G
36	A1	1244	A
36	A1	1245	A
36	A1	1246	G
36	A1	1247	U
36	A1	1249	G
36	A1	1250	G
36	A1	1251	A
36	A1	1252	A
36	A1	1262	G
36	A1	1263	A
36	A1	1264	G
36	A1	1265	U
36	A1	1266	G
36	A1	1268	G
36	A1	1269	U
36	A1	1270	A
36	A1	1271	A
36	A1	1272	C
36	A1	1277	C
36	A1	1281	G
36	A1	1282	G
36	A1	1283	C
36	A1	1286	A
36	A1	1287	A
36	A1	1305	U
36	A1	1307	G
36	A1	1309	U
36	A1	1315	U
36	A1	1317	A
36	A1	1318	A
36	A1	1330	A
36	A1	1332	A
36	A1	1333	C
36	A1	1346	G
36	A1	1348	U
36	A1	1349	G
36	A1	1350	A
36	A1	1351	U
36	A1	1352	A
36	A1	1353	U
36	A1	1354	G

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Mol	Chain	Res	Type
36	A1	1355	A
36	A1	1356	U
36	A1	1357	G
36	A1	1386	A
36	A1	1392	G
36	A1	1399	A
36	A1	1400	G
36	A1	1417	G
36	A1	1418	A
36	A1	1419	A
36	A1	1434	G
36	A1	1436	U
36	A1	1437	OMC
36	A1	1443	G
36	A1	1446	A
36	A1	1450	OMG
36	A1	1468	A
36	A1	1469	C
36	A1	1477	A
36	A1	1481	A
36	A1	1486	G
36	A1	1487	G
36	A1	1494	U
36	A1	1508	C
36	A1	1523	U
36	A1	1524	A
36	A1	1526	U
36	A1	1527	C
36	A1	1536	G
36	A1	1539	A
36	A1	1544	G
36	A1	1555	U
36	A1	1556	C
36	A1	1558	A
36	A1	1562	C
36	A1	1564	U
36	A1	1565	G
36	A1	1566	A
36	A1	1567	U
36	A1	1568	U
36	A1	1569	U
36	A1	1571	A

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Mol	Chain	Res	Type
36	A1	1572	U
36	A1	1574	C
36	A1	1576	G
36	A1	1578	C
36	A1	1580	A
36	A1	1581	C
36	A1	1583	A
36	A1	1587	A
36	A1	1589	A
36	A1	1590	G
36	A1	1593	A
36	A1	1596	C
36	A1	1605	A
36	A1	1627	U
36	A1	1628	C
36	A1	1629	U
36	A1	1630	U
36	A1	1631	C
36	A1	1642	A
36	A1	1643	A
36	A1	1657	C
36	A1	1683	A
36	A1	1705	U
36	A1	1714	A
36	A1	1716	U
36	A1	1724	U
36	A1	1730	G
36	A1	1736	G
36	A1	1741	A
36	A1	1742	U
36	A1	1750	A
36	A1	1751	G
36	A1	1761	C
36	A1	1762	C
36	A1	1763	U
36	A1	1764	U
36	A1	1765	U
36	A1	1766	G
36	A1	1780	G
36	A1	1795	U
36	A1	1797	A
36	A1	1813	A

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Mol	Chain	Res	Type
36	A1	1814	A
36	A1	1815	U
36	A1	1816	A
36	A1	1817	G
36	A1	1821	U
36	A1	1834	U
36	A1	1839	A
36	A1	1842	A
36	A1	1846	C
36	A1	1847	A
36	A1	1848	G
36	A1	1849	C
36	A1	1850	A
36	A1	1857	C
36	A1	1858	A
36	A1	1866	C
36	A1	1878	G
36	A1	1880	U
36	A1	1886	A
36	A1	1893	A
36	A1	1906	G
36	A1	1908	A
36	A1	1927	G
36	A1	1932	A
36	A1	1934	G
36	A1	1943	C
36	A1	1946	A
36	A1	1948	G
36	A1	1949	G
36	A1	1955	U
36	A1	2094	C
36	A1	2095	G
36	A1	2096	A
36	A1	2110	G
36	A1	2112	U
36	A1	2114	C
36	A1	2121	G
36	A1	2122	G
36	A1	2131	A
36	A1	2140	U
36	A1	2142	1MA
36	A1	2144	A

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Mol	Chain	Res	Type
36	A1	2158	A
36	A1	2159	U
36	A1	2165	G
36	A1	2169	G
36	A1	2171	G
36	A1	2175	U
36	A1	2187	G
36	A1	2188	A
36	A1	2195	C
36	A1	2197	OMC
36	A1	2205	U
36	A1	2206	G
36	A1	2207	A
36	A1	2208	A
36	A1	2209	U
36	A1	2210	G
36	A1	2234	G
36	A1	2242	A
36	A1	2244	A
36	A1	2249	G
36	A1	2253	G
36	A1	2256	A
36	A1	2257	C
36	A1	2258	U
36	A1	2260	U
36	A1	2263	C
36	A1	2264	U
36	A1	2268	U
36	A1	2269	U
36	A1	2270	A
36	A1	2272	G
36	A1	2273	G
36	A1	2276	G
36	A1	2281	A2M
36	A1	2282	U
36	A1	2287	C
36	A1	2288	OMG
36	A1	2295	A
36	A1	2298	U
36	A1	2306	C
36	A1	2307	G
36	A1	2308	C

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Mol	Chain	Res	Type
36	A1	2310	U
36	A1	2313	A
36	A1	2314	U
36	A1	2315	G
36	A1	2334	U
36	A1	2335	G
36	A1	2336	U
36	A1	2340	U
36	A1	2347	OMU
36	A1	2364	G
36	A1	2373	A
36	A1	2374	C
36	A1	2377	G
36	A1	2378	C
36	A1	2383	C
36	A1	2388	U
36	A1	2391	G
36	A1	2393	G
36	A1	2394	G
36	A1	2397	A
36	A1	2398	A
36	A1	2401	A
36	A1	2402	A
36	A1	2403	G
36	A1	2404	A
36	A1	2411	U
36	A1	2414	G
36	A1	2438	A
36	A1	2441	A
36	A1	2442	G
36	A1	2443	A
36	A1	2444	C
36	A1	2445	A
36	A1	2502	A
36	A1	2503	G
36	A1	2504	U
36	A1	2506	U
36	A1	2508	U
36	A1	2514	U
36	A1	2523	A
36	A1	2524	A
36	A1	2530	G

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Mol	Chain	Res	Type
36	A1	2531	C
36	A1	2533	G
36	A1	2538	U
36	A1	2539	C
36	A1	2540	A
36	A1	2541	U
36	A1	2542	U
36	A1	2543	U
36	A1	2544	U
36	A1	2547	A
36	A1	2548	C
36	A1	2551	U
36	A1	2552	C
36	A1	2554	A
36	A1	2560	C
36	A1	2561	A
36	A1	2569	A
36	A1	2570	U
36	A1	2571	U
36	A1	2572	C
36	A1	2573	G
36	A1	2576	G
36	A1	2580	A
36	A1	2585	G
36	A1	2586	G
36	A1	2587	U
36	A1	2590	A
36	A1	2593	A
36	A1	2606	G
36	A1	2607	G
36	A1	2614	G
36	A1	2617	U
36	A1	2626	A
36	A1	2629	U
36	A1	2635	A
36	A1	2645	G
36	A1	2649	A
36	A1	2652	U
36	A1	2656	A
36	A1	2672	G
36	A1	2674	A
36	A1	2676	A

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Mol	Chain	Res	Type
36	A1	2677	G
36	A1	2680	A
36	A1	2681	U
36	A1	2688	U
36	A1	2689	A
36	A1	2691	A
36	A1	2703	A
36	A1	2704	A
36	A1	2705	A
36	A1	2712	U
36	A1	2714	G
36	A1	2725	U
36	A1	2727	A
36	A1	2728	G
36	A1	2729	OMU
36	A1	2737	C
36	A1	2740	A
36	A1	2746	A
36	A1	2752	U
36	A1	2753	G
36	A1	2755	C
36	A1	2772	C
36	A1	2777	G
36	A1	2778	G
36	A1	2780	A
36	A1	2783	U
36	A1	2796	G
36	A1	2799	A
36	A1	2800	G
36	A1	2801	A
36	A1	2803	A
36	A1	2806	U
36	A1	2810	C
36	A1	2811	A
36	A1	2814	G
36	A1	2816	G
36	A1	2817	A
36	A1	2818	U
36	A1	2822	U
36	A1	2828	G
36	A1	2833	A
36	A1	2839	G

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Mol	Chain	Res	Type
36	A1	2842	U
36	A1	2844	C
36	A1	2845	A
36	A1	2849	C
36	A1	2855	U
36	A1	2859	U
36	A1	2862	U
36	A1	2866	U
36	A1	2867	C
36	A1	2868	U
36	A1	2872	A
36	A1	2873	U
36	A1	2875	U
36	A1	2887	A
36	A1	2889	C
36	A1	2898	G
36	A1	2914	G
36	A1	2923	U
36	A1	2935	U
36	A1	2936	A
36	A1	2941	A
36	A1	2942	C
36	A1	2947	G
36	A1	2948	OMC
36	A1	2951	G
36	A1	2954	U
36	A1	2977	G
36	A1	2983	C
36	A1	2990	G
36	A1	2997	G
36	A1	3003	G
36	A1	3011	A
36	A1	3012	A
36	A1	3021	A
36	A1	3022	G
36	A1	3028	G
36	A1	3030	G
36	A1	3032	A
36	A1	3049	A
36	A1	3056	U
36	A1	3059	G
36	A1	3074	G

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Mol	Chain	Res	Type
36	A1	3078	U
36	A1	3080	G
36	A1	3086	A
36	A1	3087	A
36	A1	3092	C
36	A1	3109	G
36	A1	3113	A
36	A1	3116	G
36	A1	3122	A
36	A1	3129	A
36	A1	3130	A
36	A1	3131	U
36	A1	3142	A
36	A1	3143	C
36	A1	3153	U
36	A1	3154	C
36	A1	3155	U
36	A1	3156	U
36	A1	3157	U
36	A1	3165	A
36	A1	3170	A
36	A1	3171	U
36	A1	3172	A
36	A1	3173	G
36	A1	3174	A
36	A1	3175	U
36	A1	3176	G
36	A1	3179	U
36	A1	3181	C
36	A1	3187	A
36	A1	3195	U
36	A1	3196	U
36	A1	3198	U
36	A1	3207	U
36	A1	3208	G
36	A1	3209	A
36	A1	3213	A
36	A1	3215	A
36	A1	3216	G
36	A1	3217	C
36	A1	3218	A
36	A1	3219	G

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Mol	Chain	Res	Type
36	A1	3224	G
36	A1	3234	A
36	A1	3243	A
36	A1	3247	G
36	A1	3251	U
36	A1	3259	U
36	A1	3260	G
36	A1	3263	G
36	A1	3273	A
36	A1	3275	U
36	A1	3276	G
36	A1	3278	C
36	A1	3281	U
36	A1	3282	U
36	A1	3283	U
36	A1	3284	G
36	A1	3288	G
36	A1	3294	A
36	A1	3295	A
36	A1	3304	U
36	A1	3309	G
36	A1	3313	U
36	A1	3316	A
36	A1	3341	U
36	A1	3342	A
36	A1	3344	A
36	A1	3345	G
36	A1	3350	C
36	A1	3351	U
36	A1	3352	U
36	A1	3353	G
36	A1	3354	U
36	A1	3355	U
36	A1	3356	G
36	A1	3360	C
36	A1	3369	G
36	A1	3375	A
36	A1	3378	C
36	A1	3382	U
36	A1	3383	G
36	A1	3389	U
36	A1	3390	G

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Mol	Chain	Res	Type
37	A3	14	U
37	A3	20	A
37	A3	22	A
37	A3	33	U
37	A3	35	C
37	A3	38	U
37	A3	39	C
37	A3	41	G
37	A3	46	A
37	A3	49	G
37	A3	54	U
37	A3	55	A
37	A3	65	G
37	A3	74	C
37	A3	76	A
37	A3	78	U
37	A3	102	A
37	A3	112	G
37	A3	121	U
38	A4	13	A
38	A4	23	U
38	A4	33	A
38	A4	34	U
38	A4	35	C
38	A4	52	A
38	A4	53	A
38	A4	59	A
38	A4	62	C
38	A4	63	G
38	A4	68	G
38	A4	75	G
38	A4	81	U
38	A4	83	C
38	A4	85	G
38	A4	86	U
38	A4	87	G
38	A4	88	A
38	A4	90	U
38	A4	95	G
38	A4	97	A
38	A4	104	A
38	A4	105	A

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Mol	Chain	Res	Type
38	A4	106	C
38	A4	111	A
38	A4	112	U
38	A4	113	U
38	A4	114	G
38	A4	125	U
38	A4	126	A
38	A4	148	G
38	A4	152	G
38	A4	157	U
38	A4	158	U

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	B5	187	G
35	B5	272	U
35	B5	401	A
35	B5	488	G
35	B5	489	C
35	B5	950	C
35	B5	1285	U
35	B5	1344	A
35	B5	1358	G
35	B5	1458	G
35	B5	1645	G
36	A1	267	G
36	A1	282	G
36	A1	299	G
36	A1	439	C
36	A1	588	G
36	A1	873	C
36	A1	916	G
36	A1	1032	C
36	A1	1280	C
36	A1	1314	C
36	A1	1354	G
36	A1	1385	C
36	A1	1575	A
36	A1	2111	G
36	A1	2585	G
36	A1	2586	G

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Mol	Chain	Res	Type
36	A1	3121	U
38	A4	67	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
40	HIC	AB	243	40	8,11,12	1.46	1 (12%)	5,14,16	0.75	0
36	A2M	A1	2280	36	18,25,26	0.82	0	20,36,39	1.38	2 (10%)
36	OMC	A1	1437	36,80	19,22,23	0.95	1 (5%)	25,31,34	1.55	5 (20%)
36	A2M	A1	1449	36,80	18,25,26	0.91	0	20,36,39	1.42	2 (10%)
36	A2M	A1	2640	36	18,25,26	0.80	0	20,36,39	1.19	2 (10%)
36	OMU	A1	2724	36	19,22,23	1.28	4 (21%)	25,31,34	1.88	5 (20%)
36	OMC	A1	2959	36	19,22,23	0.83	1 (5%)	25,31,34	1.01	1 (4%)
35	4AC	B5	1280	35	21,24,25	1.10	1 (4%)	28,34,37	1.60	6 (21%)
35	OMU	B5	578	35	19,22,23	1.29	4 (21%)	25,31,34	1.82	4 (16%)
35	A2M	B5	28	80,35	18,25,26	0.81	0	20,36,39	1.42	4 (20%)
35	OMG	B5	1126	35	19,26,27	0.91	1 (5%)	21,38,41	1.09	3 (14%)
36	OMC	A1	663	36	19,22,23	0.97	2 (10%)	25,31,34	0.88	0
36	A2M	A1	876	36	18,25,26	0.87	0	20,36,39	1.24	2 (10%)
35	A2M	B5	619	80,35	18,25,26	0.81	0	20,36,39	1.36	3 (15%)
36	OMG	A1	2791	36	19,26,27	0.88	1 (5%)	21,38,41	1.13	2 (9%)
36	OMU	A1	2921	36	19,22,23	1.23	3 (15%)	25,31,34	1.89	6 (24%)
35	A2M	B5	796	35	18,25,26	0.88	0	20,36,39	1.29	2 (10%)
35	A2M	B5	436	35	18,25,26	0.90	0	20,36,39	1.23	3 (15%)
35	G7M	B5	1575	35	20,26,27	2.55	4 (20%)	16,39,42	1.12	1 (6%)
36	5MC	A1	2870	36	19,22,23	1.35	2 (10%)	26,32,35	1.17	3 (11%)
35	MA6	B5	1781	35	19,26,27	1.00	2 (10%)	18,38,41	2.11	5 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
35	OMC	B5	414	35	19,22,23	0.89	2 (10%)	25,31,34	0.89	1 (4%)
35	A2M	B5	420	35	18,25,26	0.82	0	20,36,39	1.42	3 (15%)
36	A2M	A1	649	36	18,25,26	0.78	0	20,36,39	1.13	2 (10%)
36	5MC	A1	2278	36,80	19,22,23	1.55	3 (15%)	26,32,35	1.35	5 (19%)
36	OMU	A1	2347	36	19,22,23	1.42	4 (21%)	25,31,34	1.93	6 (24%)
35	OMU	B5	1269	80,35	19,22,23	1.31	4 (21%)	25,31,34	1.96	7 (28%)
35	A2M	B5	974	35	18,25,26	0.83	0	20,36,39	1.52	3 (15%)
36	A2M	A1	2946	36,80	18,25,26	0.79	0	20,36,39	1.49	4 (20%)
36	OMU	A1	2729	36	19,22,23	1.41	4 (21%)	25,31,34	1.82	6 (24%)
35	OMC	B5	1639	35	19,22,23	0.79	1 (5%)	25,31,34	0.89	1 (4%)
36	1MA	A1	645	36,80	17,25,26	1.34	2 (11%)	17,37,40	1.20	3 (17%)
36	A2M	A1	817	36,80	18,25,26	0.91	0	20,36,39	1.53	3 (15%)
36	1MA	A1	2142	36	17,25,26	1.42	2 (11%)	17,37,40	1.38	3 (17%)
36	OMG	A1	805	36	19,26,27	0.97	1 (5%)	21,38,41	1.16	3 (14%)
36	OMG	A1	908	36,80	19,26,27	0.96	1 (5%)	21,38,41	1.38	4 (19%)
35	4AC	B5	1773	35	21,24,25	1.17	3 (14%)	28,34,37	2.89	6 (21%)
36	OMG	A1	867	36,80	19,26,27	0.91	1 (5%)	21,38,41	1.25	3 (14%)
35	OMC	B5	1007	35	19,22,23	0.82	0	25,31,34	0.87	1 (4%)
36	A2M	A1	1133	36	18,25,26	0.92	1 (5%)	20,36,39	1.53	3 (15%)
36	A2M	A1	2281	36	18,25,26	0.79	0	20,36,39	1.85	3 (15%)
36	OMU	A1	2421	36	19,22,23	1.27	4 (21%)	25,31,34	1.74	5 (20%)
36	OMG	A1	2793	36	19,26,27	0.88	1 (5%)	21,38,41	1.13	2 (9%)
35	OMG	B5	1572	35	19,26,27	0.96	1 (5%)	21,38,41	1.07	2 (9%)
35	A2M	B5	541	35	18,25,26	0.83	0	20,36,39	1.23	3 (15%)
36	OMG	A1	1450	36	19,26,27	1.09	1 (5%)	21,38,41	1.00	2 (9%)
35	MA6	B5	1782	35	19,26,27	0.97	1 (5%)	18,38,41	1.99	4 (22%)
36	OMG	A1	2288	36	19,26,27	0.90	1 (5%)	21,38,41	1.19	3 (14%)
35	3AU	B5	1191	35	24,28,29	0.48	0	30,40,43	0.70	0
36	OMC	A1	2948	36	19,22,23	0.86	1 (5%)	25,31,34	1.18	3 (12%)
35	OMG	B5	1428	80,35	19,26,27	0.92	1 (5%)	21,38,41	1.12	2 (9%)
36	OMC	A1	650	36	19,22,23	0.88	2 (10%)	25,31,34	0.81	0
36	OMU	A1	1888	36	19,22,23	1.42	4 (21%)	25,31,34	2.00	5 (20%)
36	A2M	A1	807	36	18,25,26	0.84	0	20,36,39	1.41	2 (10%)
36	A2M	A1	2220	36	18,25,26	0.83	0	20,36,39	1.35	2 (10%)
36	OMG	A1	2619	36	19,26,27	0.86	1 (5%)	21,38,41	1.11	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
36	OMU	A1	898	36	19,22,23	1.41	4 (21%)	25,31,34	1.89	5 (20%)
36	UR3	A1	2634	36,80	19,22,23	0.98	1 (5%)	26,32,35	1.62	3 (11%)
35	OMG	B5	562	35	19,26,27	1.01	1 (5%)	21,38,41	1.13	2 (9%)
35	OMG	B5	1271	35	19,26,27	0.91	1 (5%)	21,38,41	1.02	2 (9%)
36	OMC	A1	2337	36	19,22,23	0.87	2 (10%)	25,31,34	1.19	2 (8%)
36	OMC	A1	2197	36	19,22,23	0.78	0	25,31,34	0.77	0
36	OMU	A1	2417	36	19,22,23	1.30	4 (21%)	25,31,34	1.78	4 (16%)
35	A2M	B5	100	80,35	18,25,26	0.92	1 (5%)	20,36,39	1.43	4 (20%)
36	OMG	A1	2815	36	19,26,27	0.88	1 (5%)	21,38,41	1.20	4 (19%)
36	OMG	A1	2922	36	19,26,27	0.84	1 (5%)	21,38,41	1.05	1 (4%)

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
40	HIC	AB	243	40	-	0/5/6/8	0/1/1/1
36	A2M	A1	2280	36	-	0/5/27/28	0/3/3/3
36	OMC	A1	1437	36,80	-	2/9/27/28	0/2/2/2
36	A2M	A1	1449	36,80	-	0/5/27/28	0/3/3/3
36	A2M	A1	2640	36	-	0/5/27/28	0/3/3/3
36	OMU	A1	2724	36	-	0/9/27/28	0/2/2/2
36	OMC	A1	2959	36	-	0/9/27/28	0/2/2/2
35	4AC	B5	1280	35	-	4/11/29/30	0/2/2/2
35	OMU	B5	578	35	-	3/9/27/28	0/2/2/2
35	A2M	B5	28	80,35	-	1/5/27/28	0/3/3/3
35	OMG	B5	1126	35	-	1/5/27/28	0/3/3/3
36	OMC	A1	663	36	-	0/9/27/28	0/2/2/2
36	A2M	A1	876	36	-	0/5/27/28	0/3/3/3
35	A2M	B5	619	80,35	-	2/5/27/28	0/3/3/3
36	OMG	A1	2791	36	-	0/5/27/28	0/3/3/3
36	OMU	A1	2921	36	-	0/9/27/28	0/2/2/2
35	A2M	B5	796	35	-	0/5/27/28	0/3/3/3
35	A2M	B5	436	35	-	0/5/27/28	0/3/3/3
35	G7M	B5	1575	35	3/3/5/5	2/3/25/26	0/3/3/3
36	5MC	A1	2870	36	-	4/7/25/26	0/2/2/2
35	MA6	B5	1781	35	-	5/7/29/30	0/3/3/3
35	OMC	B5	414	35	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	A2M	B5	420	35	-	0/5/27/28	0/3/3/3
36	A2M	A1	649	36	-	2/5/27/28	0/3/3/3
36	5MC	A1	2278	36,80	-	0/7/25/26	0/2/2/2
36	OMU	A1	2347	36	-	2/9/27/28	0/2/2/2
35	OMU	B5	1269	80,35	-	3/9/27/28	0/2/2/2
35	A2M	B5	974	35	-	0/5/27/28	0/3/3/3
36	A2M	A1	2946	36,80	-	1/5/27/28	0/3/3/3
36	OMU	A1	2729	36	-	3/9/27/28	0/2/2/2
35	OMC	B5	1639	35	-	0/9/27/28	0/2/2/2
36	1MA	A1	645	36,80	-	0/3/25/26	0/3/3/3
36	A2M	A1	817	36,80	-	1/5/27/28	0/3/3/3
36	1MA	A1	2142	36	-	2/3/25/26	0/3/3/3
36	OMG	A1	805	36	-	1/5/27/28	0/3/3/3
36	OMG	A1	908	36,80	-	3/5/27/28	0/3/3/3
35	4AC	B5	1773	35	-	3/11/29/30	0/2/2/2
36	OMG	A1	867	36,80	-	1/5/27/28	0/3/3/3
35	OMC	B5	1007	35	-	0/9/27/28	0/2/2/2
36	A2M	A1	1133	36	-	0/5/27/28	0/3/3/3
36	A2M	A1	2281	36	-	1/5/27/28	0/3/3/3
36	OMU	A1	2421	36	-	0/9/27/28	0/2/2/2
36	OMG	A1	2793	36	-	0/5/27/28	0/3/3/3
35	OMG	B5	1572	35	-	0/5/27/28	0/3/3/3
35	A2M	B5	541	35	-	3/5/27/28	0/3/3/3
36	OMG	A1	1450	36	-	2/5/27/28	0/3/3/3
35	MA6	B5	1782	35	-	2/7/29/30	0/3/3/3
36	OMG	A1	2288	36	-	2/5/27/28	0/3/3/3
35	3AU	B5	1191	35	1/1/7/7	2/16/34/35	0/2/2/2
36	OMC	A1	2948	36	-	0/9/27/28	0/2/2/2
35	OMG	B5	1428	80,35	-	4/5/27/28	0/3/3/3
36	OMC	A1	650	36	-	0/9/27/28	0/2/2/2
36	OMU	A1	1888	36	-	0/9/27/28	0/2/2/2
36	A2M	A1	807	36	-	1/5/27/28	0/3/3/3
36	A2M	A1	2220	36	-	1/5/27/28	0/3/3/3
36	OMG	A1	2619	36	-	0/5/27/28	0/3/3/3
36	OMU	A1	898	36	-	0/9/27/28	0/2/2/2
36	UR3	A1	2634	36,80	-	0/7/25/26	0/2/2/2
35	OMG	B5	562	35	-	0/5/27/28	0/3/3/3
35	OMG	B5	1271	35	-	0/5/27/28	0/3/3/3
36	OMC	A1	2337	36	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	OMC	A1	2197	36	-	6/9/27/28	0/2/2/2
36	OMU	A1	2417	36	-	1/9/27/28	0/2/2/2
35	A2M	B5	100	80,35	-	2/5/27/28	0/3/3/3
36	OMG	A1	2815	36	-	0/5/27/28	0/3/3/3
36	OMG	A1	2922	36	-	0/5/27/28	0/3/3/3

All (90) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	B5	1575	G7M	C8-N9	7.75	1.47	1.33
35	B5	1575	G7M	C8-N7	6.32	1.44	1.33
36	A1	2278	5MC	C5-C4	5.45	1.48	1.44
36	A1	2142	1MA	C2-N3	4.70	1.34	1.28
36	A1	2870	5MC	C5-C4	4.53	1.47	1.44
35	B5	1575	G7M	C5-C4	3.89	1.46	1.39
40	AB	243	HIC	CD2-NE2	-3.63	1.32	1.38
36	A1	1450	OMG	C6-N1	-3.61	1.32	1.37
36	A1	645	1MA	C2-N3	3.58	1.33	1.28
35	B5	562	OMG	C6-N1	-3.50	1.32	1.37
36	A1	1888	OMU	C4-N3	-3.43	1.32	1.38
36	A1	2347	OMU	C4-N3	-3.35	1.32	1.38
36	A1	898	OMU	C4-N3	-3.35	1.32	1.38
36	A1	2729	OMU	C4-N3	-3.28	1.33	1.38
36	A1	898	OMU	C2-N3	-2.94	1.32	1.38
36	A1	805	OMG	C6-N1	-2.92	1.33	1.37
36	A1	645	1MA	C6-N6	2.92	1.35	1.27
36	A1	2417	OMU	C4-N3	-2.90	1.33	1.38
36	A1	2729	OMU	C2-N3	-2.89	1.32	1.38
35	B5	1773	4AC	C4-N4	-2.83	1.35	1.39
36	A1	663	OMC	C5-C4	-2.82	1.36	1.42
36	A1	2724	OMU	C4-N3	-2.81	1.33	1.38
36	A1	1437	OMC	C5-C4	-2.81	1.36	1.42
35	B5	1280	4AC	C4-N4	-2.80	1.35	1.39
36	A1	2347	OMU	C2-N3	-2.79	1.33	1.38
35	B5	1271	OMG	C6-N1	-2.79	1.33	1.37
36	A1	867	OMG	C6-N1	-2.79	1.33	1.37
35	B5	1269	OMU	C4-N3	-2.78	1.33	1.38
35	B5	1575	G7M	C6-N1	-2.78	1.33	1.37
35	B5	1572	OMG	C6-N1	-2.77	1.33	1.37
36	A1	2921	OMU	C4-N3	-2.75	1.33	1.38
35	B5	1126	OMG	C6-N1	-2.75	1.33	1.37
36	A1	2421	OMU	C4-N3	-2.74	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	A1	1888	OMU	C2-N3	-2.72	1.33	1.38
36	A1	908	OMG	C6-N1	-2.72	1.33	1.37
36	A1	2347	OMU	C5-C4	-2.72	1.37	1.43
35	B5	578	OMU	C4-N3	-2.71	1.34	1.38
36	A1	2288	OMG	C6-N1	-2.70	1.33	1.37
36	A1	898	OMU	C5-C4	-2.69	1.37	1.43
36	A1	2870	5MC	C6-C5	2.67	1.39	1.34
36	A1	1888	OMU	C5-C4	-2.65	1.38	1.43
36	A1	2724	OMU	C5-C4	-2.59	1.38	1.43
36	A1	2815	OMG	C6-N1	-2.56	1.33	1.37
35	B5	1269	OMU	C2-N3	-2.56	1.33	1.38
35	B5	1428	OMG	C6-N1	-2.54	1.33	1.37
36	A1	2791	OMG	C6-N1	-2.54	1.33	1.37
36	A1	2793	OMG	C6-N1	-2.53	1.33	1.37
35	B5	1781	MA6	C6-C5	2.52	1.48	1.44
36	A1	2278	5MC	C6-C5	2.51	1.38	1.34
36	A1	2729	OMU	C5-C4	-2.46	1.38	1.43
36	A1	2921	OMU	C2-N3	-2.42	1.33	1.38
35	B5	578	OMU	C2-N3	-2.41	1.33	1.38
36	A1	650	OMC	C5-C4	-2.40	1.37	1.42
36	A1	2724	OMU	C2-N3	-2.39	1.33	1.38
35	B5	1782	MA6	C6-C5	2.36	1.48	1.44
36	A1	2417	OMU	C2-N1	2.36	1.42	1.38
36	A1	2922	OMG	C6-N1	-2.36	1.34	1.37
36	A1	2142	1MA	C6-N6	2.34	1.33	1.27
36	A1	2921	OMU	C5-C4	-2.33	1.38	1.43
36	A1	2278	5MC	C6-N1	-2.32	1.34	1.38
36	A1	2421	OMU	C2-N1	2.31	1.42	1.38
36	A1	2729	OMU	C2-N1	2.29	1.42	1.38
35	B5	414	OMC	C6-N1	-2.29	1.32	1.38
36	A1	2337	OMC	C5-C4	-2.26	1.37	1.42
35	B5	578	OMU	C5-C4	-2.26	1.38	1.43
35	B5	1781	MA6	C6-N1	2.26	1.35	1.32
36	A1	663	OMC	C6-N1	-2.25	1.32	1.38
36	A1	2421	OMU	C5-C4	-2.24	1.38	1.43
35	B5	1269	OMU	C5-C4	-2.24	1.38	1.43
36	A1	2417	OMU	C2-N3	-2.23	1.34	1.38
35	B5	1773	4AC	C7-N4	-2.22	1.32	1.37
36	A1	1133	A2M	O4'-C1'	2.22	1.43	1.40
35	B5	414	OMC	C5-C4	-2.19	1.37	1.42
36	A1	2948	OMC	C5-C4	-2.19	1.37	1.42
36	A1	650	OMC	C6-N1	-2.18	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	A1	2337	OMC	C6-N1	-2.18	1.32	1.38
36	A1	2417	OMU	C5-C4	-2.16	1.39	1.43
35	B5	578	OMU	C6-N1	-2.13	1.33	1.38
36	A1	898	OMU	C6-N1	-2.13	1.33	1.38
35	B5	1269	OMU	C2-N1	2.13	1.41	1.38
36	A1	2619	OMG	C6-N1	-2.11	1.34	1.37
36	A1	2724	OMU	C6-N1	-2.11	1.33	1.38
36	A1	2421	OMU	C2-N3	-2.10	1.34	1.38
35	B5	1773	4AC	C6-N1	-2.09	1.33	1.38
36	A1	2959	OMC	C5-C4	-2.08	1.38	1.42
36	A1	2634	UR3	C5-C4	-2.07	1.38	1.43
36	A1	1888	OMU	C6-N1	-2.06	1.33	1.38
35	B5	1639	OMC	C6-N1	-2.05	1.33	1.38
36	A1	2347	OMU	C6-N1	-2.03	1.33	1.38
35	B5	100	A2M	O4'-C1'	2.02	1.43	1.40

All (196) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B5	1773	4AC	N4-C4-N3	11.03	131.77	113.87
35	B5	1773	4AC	C5-C4-N4	-8.28	108.99	122.94
36	A1	2634	UR3	C4-N3-C2	-6.10	119.67	124.58
35	B5	1782	MA6	C2-N1-C6	6.09	122.82	116.84
35	B5	1781	MA6	C2-N1-C6	5.70	122.43	116.84
35	B5	1280	4AC	N4-C4-N3	5.44	122.69	113.87
35	B5	578	OMU	C4-N3-C2	-4.98	120.44	126.61
36	A1	1888	OMU	C4-N3-C2	-4.94	120.48	126.61
36	A1	898	OMU	C4-N3-C2	-4.77	120.69	126.61
36	A1	2921	OMU	C4-N3-C2	-4.77	120.69	126.61
36	A1	2724	OMU	C4-N3-C2	-4.65	120.83	126.61
36	A1	2921	OMU	N3-C2-N1	4.62	120.90	114.89
36	A1	2220	A2M	N3-C2-N1	-4.60	122.42	128.67
36	A1	2417	OMU	C4-N3-C2	-4.50	121.02	126.61
36	A1	2347	OMU	C4-N3-C2	-4.48	121.05	126.61
36	A1	2421	OMU	C4-N3-C2	-4.45	121.09	126.61
36	A1	1888	OMU	N3-C2-N1	4.45	120.68	114.89
36	A1	1437	OMC	O2-C2-N3	-4.40	115.40	122.33
35	B5	1781	MA6	N3-C2-N1	-4.36	122.75	128.67
36	A1	898	OMU	N3-C2-N1	4.32	120.52	114.89
35	B5	1269	OMU	C4-N3-C2	-4.28	121.30	126.61
36	A1	2281	A2M	C4'-O4'-C1'	-4.28	106.01	109.92
36	A1	1888	OMU	C5-C4-N3	4.17	120.64	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2724	OMU	C5-C4-N3	4.14	120.60	114.80
35	B5	578	OMU	N3-C2-N1	4.13	120.27	114.89
36	A1	2417	OMU	N3-C2-N1	4.12	120.26	114.89
36	A1	2347	OMU	N3-C2-N1	4.08	120.20	114.89
36	A1	807	A2M	N3-C2-N1	-4.07	123.14	128.67
35	B5	28	A2M	N3-C2-N1	-4.00	123.24	128.67
36	A1	2280	A2M	N3-C2-N1	-4.00	123.25	128.67
36	A1	2729	OMU	C4-N3-C2	-3.99	121.66	126.61
36	A1	2347	OMU	C5-C4-N3	3.99	120.39	114.80
36	A1	898	OMU	C5-C4-N3	3.96	120.35	114.80
36	A1	2281	A2M	N3-C2-N1	-3.94	123.33	128.67
36	A1	2421	OMU	N3-C2-N1	3.94	120.02	114.89
36	A1	1449	A2M	N3-C2-N1	-3.90	123.38	128.67
36	A1	2921	OMU	C5-C4-N3	3.87	120.22	114.80
36	A1	2421	OMU	C5-C4-N3	3.87	120.22	114.80
36	A1	2417	OMU	C5-C4-N3	3.83	120.16	114.80
36	A1	2729	OMU	C5-C4-N3	3.82	120.16	114.80
35	B5	1269	OMU	N3-C2-N1	3.82	119.87	114.89
35	B5	1269	OMU	C5-C4-N3	3.82	120.15	114.80
36	A1	1133	A2M	N3-C2-N1	-3.81	123.50	128.67
35	B5	578	OMU	C5-C4-N3	3.81	120.13	114.80
36	A1	1888	OMU	O4-C4-C5	-3.80	118.61	125.16
36	A1	876	A2M	N3-C2-N1	-3.78	123.55	128.67
35	B5	1269	OMU	C1'-N1-C2	3.77	124.36	117.59
36	A1	2729	OMU	N3-C2-N1	3.72	119.74	114.89
36	A1	817	A2M	N3-C2-N1	-3.71	123.64	128.67
36	A1	2946	A2M	N3-C2-N1	-3.70	123.65	128.67
36	A1	2724	OMU	N3-C2-N1	3.69	119.69	114.89
35	B5	796	A2M	N3-C2-N1	-3.68	123.67	128.67
35	B5	100	A2M	N3-C2-N1	-3.67	123.69	128.67
35	B5	1773	4AC	CM7-C7-N4	3.66	121.18	115.27
36	A1	2640	A2M	N3-C2-N1	-3.62	123.76	128.67
36	A1	2281	A2M	O4'-C1'-N9	3.62	113.54	108.75
36	A1	2634	UR3	C5-C4-N3	3.56	119.72	115.04
35	B5	974	A2M	N3-C2-N1	-3.53	123.88	128.67
36	A1	2724	OMU	O4-C4-C5	-3.53	119.08	125.16
35	B5	1782	MA6	N3-C2-N1	-3.46	123.97	128.67
36	A1	2347	OMU	C1'-N1-C2	3.46	123.81	117.59
35	B5	420	A2M	N3-C2-N1	-3.46	123.98	128.67
36	A1	2337	OMC	O2-C2-N3	-3.43	116.92	122.33
36	A1	2948	OMC	O2-C2-N3	-3.43	116.93	122.33
36	A1	1437	OMC	C1'-N1-C2	3.40	125.95	118.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2729	OMU	C1'-N1-C2	3.35	123.61	117.59
36	A1	817	A2M	O2'-C2'-C1'	-3.31	102.61	109.00
36	A1	2142	1MA	C5-C6-N1	3.29	118.68	113.95
35	B5	541	A2M	N3-C2-N1	-3.29	124.21	128.67
36	A1	649	A2M	N3-C2-N1	-3.28	124.22	128.67
36	A1	898	OMU	O4-C4-C5	-3.27	119.53	125.16
36	A1	1133	A2M	O4'-C1'-N9	3.23	113.03	108.75
36	A1	2347	OMU	O4-C4-C5	-3.17	119.70	125.16
36	A1	2870	5MC	C5-C6-N1	-3.17	119.87	123.31
36	A1	2724	OMU	C1'-N1-C2	3.17	123.28	117.59
36	A1	2278	5MC	O2-C2-N3	-3.17	117.34	122.33
35	B5	562	OMG	C8-N7-C5	3.15	107.91	102.55
35	B5	619	A2M	N3-C2-N1	-3.14	124.41	128.67
36	A1	2421	OMU	O4-C4-C5	-3.12	119.79	125.16
36	A1	2921	OMU	O4-C4-C5	-3.10	119.82	125.16
35	B5	1269	OMU	O4-C4-C5	-3.08	119.86	125.16
35	B5	619	A2M	C4-C5-N7	-3.04	106.13	109.34
36	A1	2791	OMG	C8-N7-C5	3.03	107.71	102.55
36	A1	2278	5MC	C5-C4-N3	-2.98	118.70	121.75
36	A1	2729	OMU	O4-C4-C5	-2.97	120.04	125.16
36	A1	867	OMG	C8-N7-C5	2.97	107.60	102.55
36	A1	2417	OMU	O4-C4-C5	-2.96	120.06	125.16
35	B5	436	A2M	N3-C2-N1	-2.95	124.67	128.67
36	A1	1437	OMC	O2-C2-N1	2.92	124.61	118.90
36	A1	1449	A2M	C4-C5-N7	-2.90	106.27	109.34
35	B5	974	A2M	O4'-C1'-N9	2.90	112.59	108.75
36	A1	908	OMG	O2'-C2'-C1'	2.90	114.60	109.00
36	A1	2870	5MC	C5-C4-N3	-2.88	118.80	121.75
35	B5	1782	MA6	C4-C5-N7	-2.88	106.30	109.34
36	A1	2729	OMU	O2-C2-N3	-2.87	116.19	121.49
35	B5	1280	4AC	O2-C2-N3	-2.87	117.80	122.33
36	A1	2946	A2M	O4'-C1'-N9	2.87	112.55	108.75
35	B5	1428	OMG	C8-N7-C5	2.86	107.42	102.55
36	A1	2922	OMG	C8-N7-C5	2.86	107.42	102.55
35	B5	1575	G7M	CN7-N7-C8	-2.84	111.74	125.43
36	A1	908	OMG	CM2-O2'-C2'	2.83	121.74	114.47
35	B5	578	OMU	O4-C4-C5	-2.83	120.28	125.16
36	A1	805	OMG	C8-N7-C5	2.78	107.28	102.55
36	A1	2815	OMG	C8-N7-C5	2.78	107.28	102.55
35	B5	436	A2M	C4-C5-N7	-2.77	106.41	109.34
36	A1	2959	OMC	O2-C2-N3	-2.77	117.96	122.33
35	B5	1781	MA6	C4-C5-N7	-2.77	106.41	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2288	OMG	C8-N7-C5	2.77	107.26	102.55
36	A1	2948	OMC	C1'-N1-C2	2.77	124.55	118.44
35	B5	1280	4AC	C5-C4-N4	-2.76	118.29	122.94
36	A1	645	1MA	C8-N7-C5	2.73	107.20	102.55
36	A1	2619	OMG	C8-N7-C5	2.73	107.20	102.55
35	B5	796	A2M	C4-C5-N7	-2.72	106.47	109.34
36	A1	2280	A2M	C4-C5-N7	-2.71	106.47	109.34
36	A1	908	OMG	C8-N7-C5	2.71	107.16	102.55
35	B5	420	A2M	O4'-C1'-N9	2.67	112.29	108.75
35	B5	100	A2M	O4'-C1'-N9	2.66	112.28	108.75
35	B5	1271	OMG	C8-N7-C5	2.66	107.08	102.55
36	A1	2278	5MC	C1'-N1-C6	-2.64	116.80	121.15
36	A1	2793	OMG	C8-N7-C5	2.64	107.04	102.55
36	A1	876	A2M	C4-C5-N7	-2.62	106.57	109.34
36	A1	867	OMG	C5-C6-N1	2.54	118.92	114.07
36	A1	817	A2M	O4'-C1'-N9	-2.54	105.37	108.75
35	B5	100	A2M	C4-C5-N7	-2.54	106.65	109.34
35	B5	1572	OMG	C8-N7-C5	2.53	106.86	102.55
35	B5	974	A2M	C4-C5-N7	-2.52	106.68	109.34
36	A1	807	A2M	C4-C5-N7	-2.49	106.70	109.34
35	B5	1126	OMG	C8-N7-C5	2.49	106.79	102.55
36	A1	1450	OMG	C8-N7-C5	2.49	106.78	102.55
35	B5	1781	MA6	N1-C6-N6	2.49	119.70	116.83
35	B5	1639	OMC	O2-C2-N3	-2.48	118.42	122.33
35	B5	1280	4AC	C6-C5-C4	2.46	119.96	117.00
35	B5	541	A2M	C4-C5-N7	-2.45	106.74	109.34
36	A1	2347	OMU	O2-C2-N3	-2.43	117.00	121.49
36	A1	1437	OMC	CM2-O2'-C2'	2.42	120.70	114.47
35	B5	1773	4AC	C6-C5-C4	2.41	119.90	117.00
36	A1	2142	1MA	C8-N7-C5	2.40	106.63	102.55
35	B5	1781	MA6	C1'-N9-C4	-2.38	122.46	126.64
35	B5	28	A2M	C4-C5-N7	-2.37	106.83	109.34
36	A1	2278	5MC	C5-C6-N1	-2.35	120.76	123.31
35	B5	1773	4AC	C1'-N1-C2	2.34	123.62	118.44
36	A1	649	A2M	C4-C5-N7	-2.33	106.88	109.34
35	B5	1428	OMG	CM2-O2'-C2'	2.33	120.45	114.47
35	B5	562	OMG	C5-C6-N1	2.32	118.50	114.07
36	A1	2870	5MC	O2-C2-N3	-2.32	118.67	122.33
35	B5	28	A2M	O4'-C1'-N9	2.31	111.81	108.75
35	B5	1007	OMC	O2-C2-N3	-2.30	118.70	122.33
35	B5	1280	4AC	C5-C4-N3	-2.30	119.00	122.60
35	B5	100	A2M	C2'-C1'-N9	-2.27	107.51	112.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2288	OMG	C5-C6-N1	2.27	118.41	114.07
36	A1	805	OMG	C5-C6-N1	2.27	118.41	114.07
35	B5	1126	OMG	C5-C6-N1	2.27	118.40	114.07
35	B5	414	OMC	O2-C2-N3	-2.25	118.78	122.33
36	A1	2793	OMG	C5-C6-N1	2.25	118.36	114.07
36	A1	2946	A2M	C1'-N9-C4	-2.24	122.70	126.64
35	B5	1269	OMU	O2-C2-N3	-2.24	117.36	121.49
35	B5	420	A2M	C4-C5-N7	-2.21	107.00	109.34
36	A1	2815	OMG	C5-C6-N1	2.20	118.27	114.07
36	A1	1437	OMC	C6-N1-C2	-2.19	116.76	120.46
36	A1	867	OMG	C2-N1-C6	-2.18	121.13	125.11
35	B5	1782	MA6	N1-C6-N6	2.17	119.34	116.83
35	B5	1773	4AC	C5-C4-N3	-2.17	119.21	122.60
35	B5	1271	OMG	C5-C6-N1	2.16	118.20	114.07
35	B5	436	A2M	C4'-O4'-C1'	2.16	111.90	109.92
35	B5	1126	OMG	O6-C6-C5	-2.16	120.04	124.32
36	A1	2921	OMU	O2-C2-N1	-2.16	119.99	122.80
36	A1	645	1MA	C5-C6-N1	2.15	117.04	113.95
36	A1	2142	1MA	N1-C2-N3	-2.15	123.21	125.90
36	A1	2921	OMU	C6-N1-C2	-2.15	118.38	121.00
36	A1	2640	A2M	C4-C5-N7	-2.14	107.08	109.34
36	A1	908	OMG	C5-C6-N1	2.14	118.15	114.07
36	A1	2278	5MC	C1'-N1-C2	2.13	123.14	118.44
36	A1	898	OMU	C1'-N1-C2	2.12	121.41	117.59
35	B5	619	A2M	C3'-C2'-C1'	2.12	106.87	102.81
36	A1	645	1MA	N1-C2-N3	-2.12	123.25	125.90
35	B5	541	A2M	O4'-C1'-N9	2.11	111.54	108.75
36	A1	2946	A2M	C4-C5-N7	-2.10	107.11	109.34
36	A1	1450	OMG	C5-C6-N1	2.10	118.08	114.07
36	A1	2948	OMC	O2-C2-N1	2.10	123.02	118.90
35	B5	1572	OMG	C5-C6-N1	2.10	118.08	114.07
36	A1	2791	OMG	C5-C6-N1	2.10	118.08	114.07
36	A1	2619	OMG	C5-C6-N1	2.09	118.06	114.07
36	A1	2815	OMG	O6-C6-C5	-2.08	120.19	124.32
35	B5	1280	4AC	C1'-N1-C2	2.08	123.03	118.44
36	A1	2288	OMG	O6-C6-C5	-2.07	120.22	124.32
35	B5	28	A2M	C2'-C1'-N9	-2.07	107.97	112.56
35	B5	1269	OMU	C1'-N1-C6	-2.06	116.37	120.78
36	A1	2815	OMG	CM2-O2'-C2'	-2.05	109.20	114.47
36	A1	2337	OMC	C1'-N1-C2	2.05	122.96	118.44
36	A1	2220	A2M	C4-C5-N7	-2.05	107.18	109.34
36	A1	1133	A2M	C4-C5-N7	-2.04	107.18	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	2634	UR3	C3U-N3-C2	2.04	120.89	117.33
36	A1	805	OMG	O6-C6-C5	-2.04	120.28	124.32
36	A1	2619	OMG	O6-C6-C5	-2.03	120.30	124.32
36	A1	2421	OMU	C1'-N1-C2	2.01	121.21	117.59
36	A1	1888	OMU	C1'-N1-C2	2.01	121.20	117.59

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	B5	1191	3AU	C12
35	B5	1575	G7M	C3'
35	B5	1575	G7M	C2'
35	B5	1575	G7M	C4'

All (73) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	B5	28	A2M	C1'-C2'-O2'-CM'
35	B5	619	A2M	O4'-C4'-C5'-O5'
35	B5	1280	4AC	N3-C4-N4-C7
35	B5	1280	4AC	C5-C4-N4-C7
35	B5	1280	4AC	O7-C7-N4-C4
35	B5	1280	4AC	CM7-C7-N4-C4
35	B5	1428	OMG	C1'-C2'-O2'-CM2
35	B5	1773	4AC	N3-C4-N4-C7
35	B5	1781	MA6	C5-C6-N6-C9
35	B5	1782	MA6	C5-C6-N6-C9
36	A1	908	OMG	O4'-C4'-C5'-O5'
36	A1	908	OMG	C1'-C2'-O2'-CM2
36	A1	1437	OMC	C1'-C2'-O2'-CM2
36	A1	1450	OMG	O4'-C4'-C5'-O5'
36	A1	2197	OMC	C2'-C1'-N1-C6
36	A1	2288	OMG	O4'-C4'-C5'-O5'
36	A1	2417	OMU	C1'-C2'-O2'-CM2
36	A1	2870	5MC	C2'-C1'-N1-C2
36	A1	2870	5MC	C2'-C1'-N1-C6
36	A1	2946	A2M	C1'-C2'-O2'-CM'
36	A1	2197	OMC	C2'-C1'-N1-C2
35	B5	619	A2M	C3'-C4'-C5'-O5'
36	A1	2729	OMU	C3'-C4'-C5'-O5'
35	B5	1191	3AU	N40-C12-C13-O31
35	B5	1575	G7M	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
36	A1	2142	1MA	O4'-C4'-C5'-O5'
36	A1	2142	1MA	C3'-C4'-C5'-O5'
36	A1	2197	OMC	O4'-C4'-C5'-O5'
36	A1	2288	OMG	C3'-C4'-C5'-O5'
36	A1	2347	OMU	C3'-C4'-C5'-O5'
35	B5	1781	MA6	N1-C6-N6-C9
35	B5	1782	MA6	N1-C6-N6-C9
35	B5	541	A2M	C3'-C4'-C5'-O5'
35	B5	1428	OMG	O4'-C4'-C5'-O5'
36	A1	908	OMG	C3'-C4'-C5'-O5'
36	A1	1450	OMG	C3'-C4'-C5'-O5'
35	B5	541	A2M	O4'-C4'-C5'-O5'
35	B5	1781	MA6	O4'-C4'-C5'-O5'
36	A1	2347	OMU	O4'-C4'-C5'-O5'
36	A1	2729	OMU	O4'-C4'-C5'-O5'
35	B5	1269	OMU	O4'-C1'-N1-C2
35	B5	1781	MA6	C3'-C4'-C5'-O5'
36	A1	2197	OMC	C3'-C4'-C5'-O5'
35	B5	1269	OMU	O4'-C1'-N1-C6
35	B5	1773	4AC	O7-C7-N4-C4
35	B5	1773	4AC	CM7-C7-N4-C4
36	A1	649	A2M	C1'-C2'-O2'-CM'
35	B5	1428	OMG	C3'-C4'-C5'-O5'
36	A1	649	A2M	C3'-C4'-C5'-O5'
36	A1	817	A2M	C4'-C5'-O5'-P
36	A1	867	OMG	O4'-C4'-C5'-O5'
35	B5	541	A2M	C4'-C5'-O5'-P
36	A1	2729	OMU	C4'-C5'-O5'-P
36	A1	2197	OMC	O4'-C1'-N1-C2
35	B5	578	OMU	C2'-C1'-N1-C6
36	A1	2197	OMC	O4'-C1'-N1-C6
36	A1	2870	5MC	O4'-C1'-N1-C6
36	A1	805	OMG	C3'-C2'-O2'-CM2
35	B5	100	A2M	C4'-C5'-O5'-P
35	B5	578	OMU	C4'-C5'-O5'-P
35	B5	1126	OMG	C4'-C5'-O5'-P
35	B5	1269	OMU	C4'-C5'-O5'-P
35	B5	1428	OMG	C4'-C5'-O5'-P
35	B5	1781	MA6	C4'-C5'-O5'-P
36	A1	807	A2M	C3'-C4'-C5'-O5'
36	A1	2220	A2M	C1'-C2'-O2'-CM'
35	B5	578	OMU	O4'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
36	A1	2870	5MC	O4'-C1'-N1-C2
35	B5	100	A2M	O4'-C4'-C5'-O5'
36	A1	2281	A2M	O4'-C4'-C5'-O5'
35	B5	1575	G7M	O4'-C4'-C5'-O5'
36	A1	1437	OMC	C2'-C1'-N1-C2
35	B5	1191	3AU	N40-C12-C13-O30

There are no ring outliers.

20 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
40	AB	243	HIC	1	0
36	A1	1449	A2M	1	0
36	A1	2640	A2M	1	0
36	A1	2724	OMU	2	0
35	B5	1280	4AC	3	0
35	B5	28	A2M	1	0
35	B5	1126	OMG	2	0
35	B5	1781	MA6	2	0
36	A1	2278	5MC	1	0
36	A1	2729	OMU	1	0
36	A1	817	A2M	1	0
35	B5	1773	4AC	1	0
35	B5	1007	OMC	1	0
36	A1	1133	A2M	1	0
36	A1	2948	OMC	2	0
35	B5	1428	OMG	2	0
36	A1	1888	OMU	1	0
36	A1	2220	A2M	1	0
35	B5	1271	OMG	1	0
36	A1	2197	OMC	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 368 ligands modelled in this entry, 368 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	A1	5
53	AP	1
9	BI	1
35	B5	1
43	AE	1
47	AI	1
32	Bf	1
18	BR	1
38	A4	1
22	BV	1
49	AL	1
40	AB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	1253:U	O3'	1260:A	P	26.01
1	AP	155:GLU	C	164:LYS	N	23.68
1	A1	1955:U	O3'	2093:A	P	22.93
1	BI	123:LYS	C	135:LYS	N	19.36
1	A1	1023:C	O3'	1030:A	P	17.87
1	B5	658:C	O3'	676:G	P	17.63
1	A1	2445:A	O3'	2501:U	P	14.79
1	AE	109:GLU	C	129:GLU	N	14.15
1	A1	440:A	O3'	494:G	P	9.78
1	AI	101:LYS	C	114:GLY	N	9.07

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Bf	125:THR	C	129:GLY	N	8.95
1	BR	95:ARG	C	100:LEU	N	6.18
1	A4	73:U	O3'	74:U	P	4.96
1	BV	11:LEU	C	12:TYR	N	4.86
1	AL	54:LEU	C	55:ARG	N	1.19
1	AB	16:PHE	C	17:LEU	N	1.14

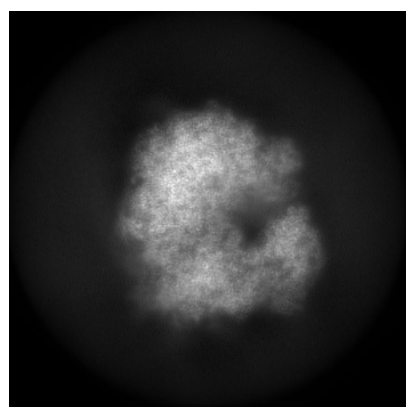
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23934. These allow visual inspection of the internal detail of the map and identification of artifacts.

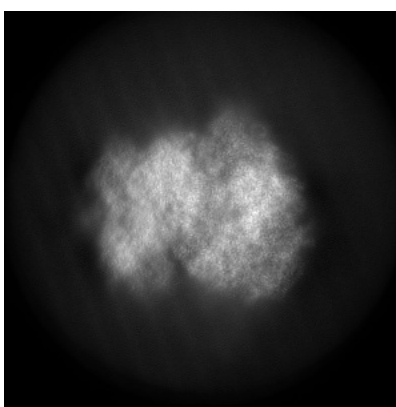
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

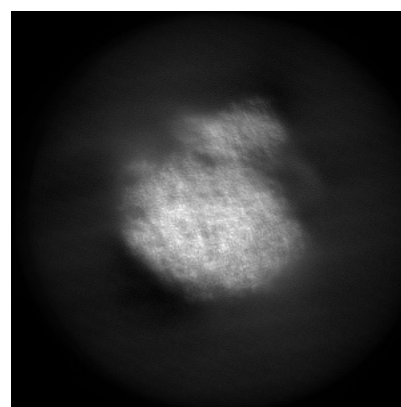
#### 6.1.1 Primary map



X



Y

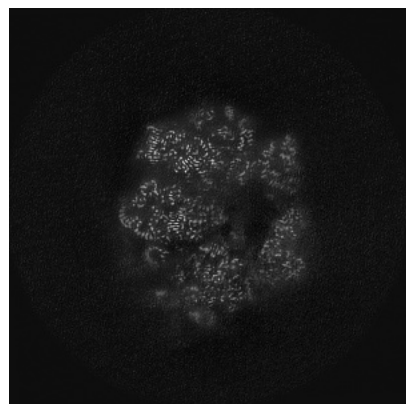


Z

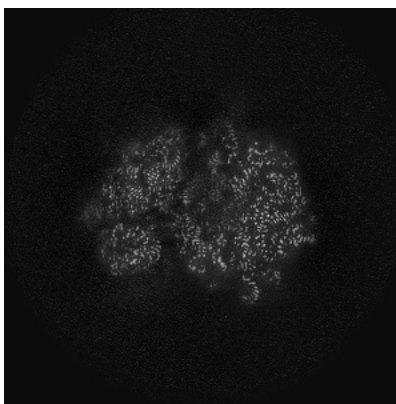
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

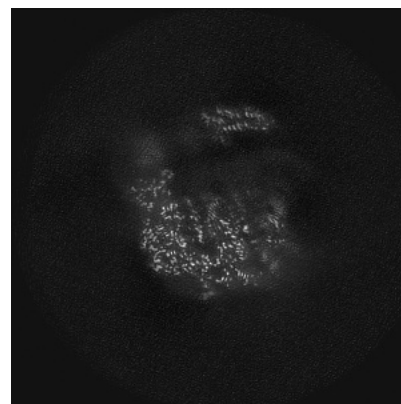
#### 6.2.1 Primary map



X Index: 216



Y Index: 216

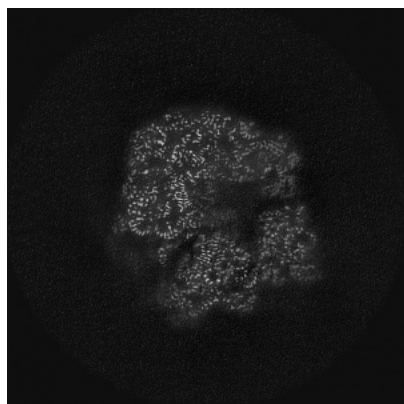


Z Index: 216

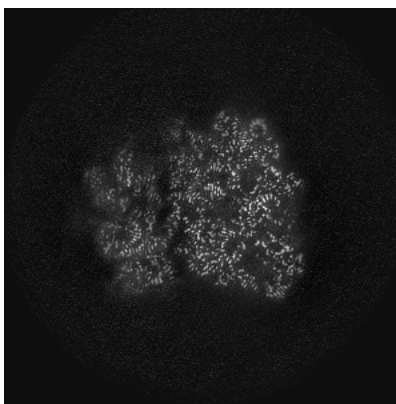
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

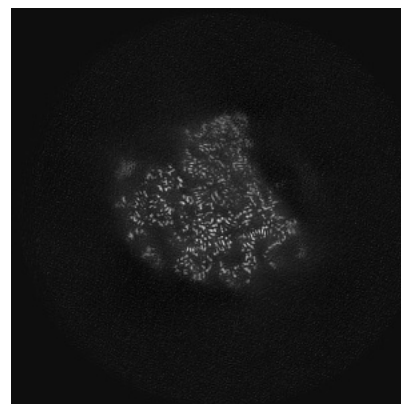
### 6.3.1 Primary map



X Index: 236



Y Index: 192

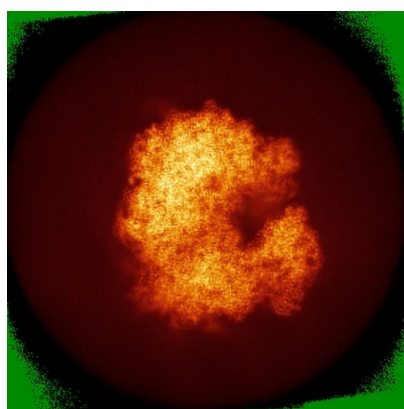


Z Index: 266

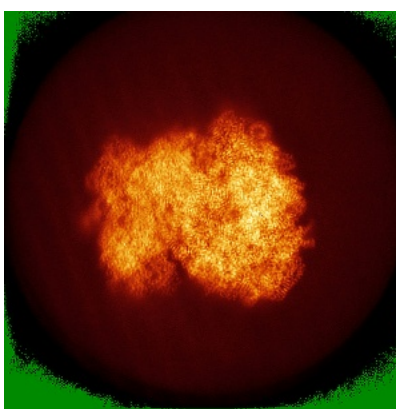
The images above show the largest variance slices of the map in three orthogonal directions.

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

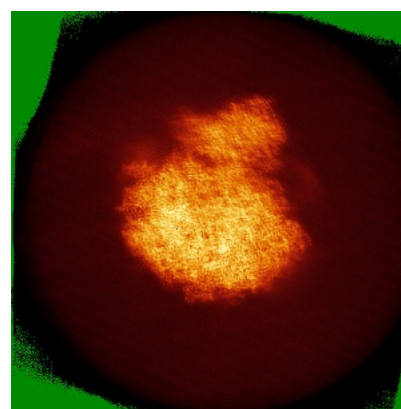
### 6.4.1 Primary map



X



Y

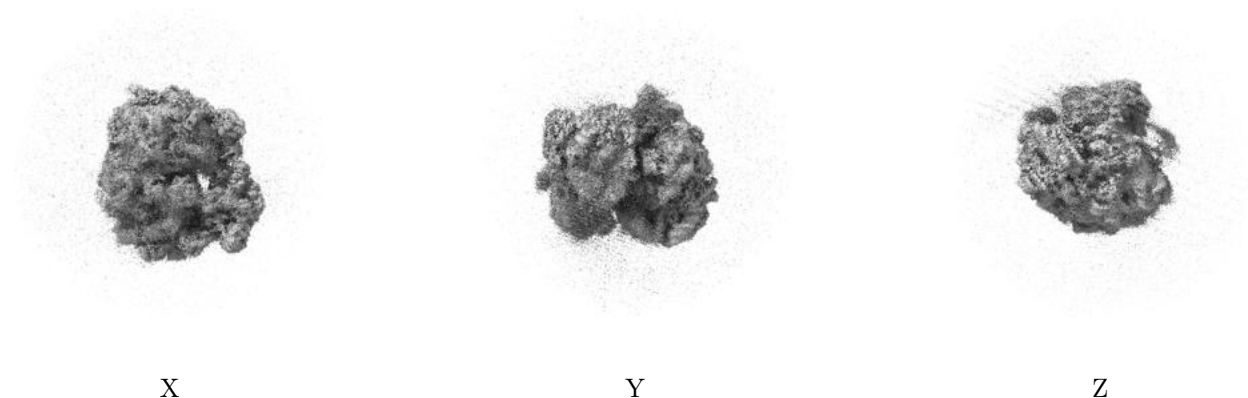


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

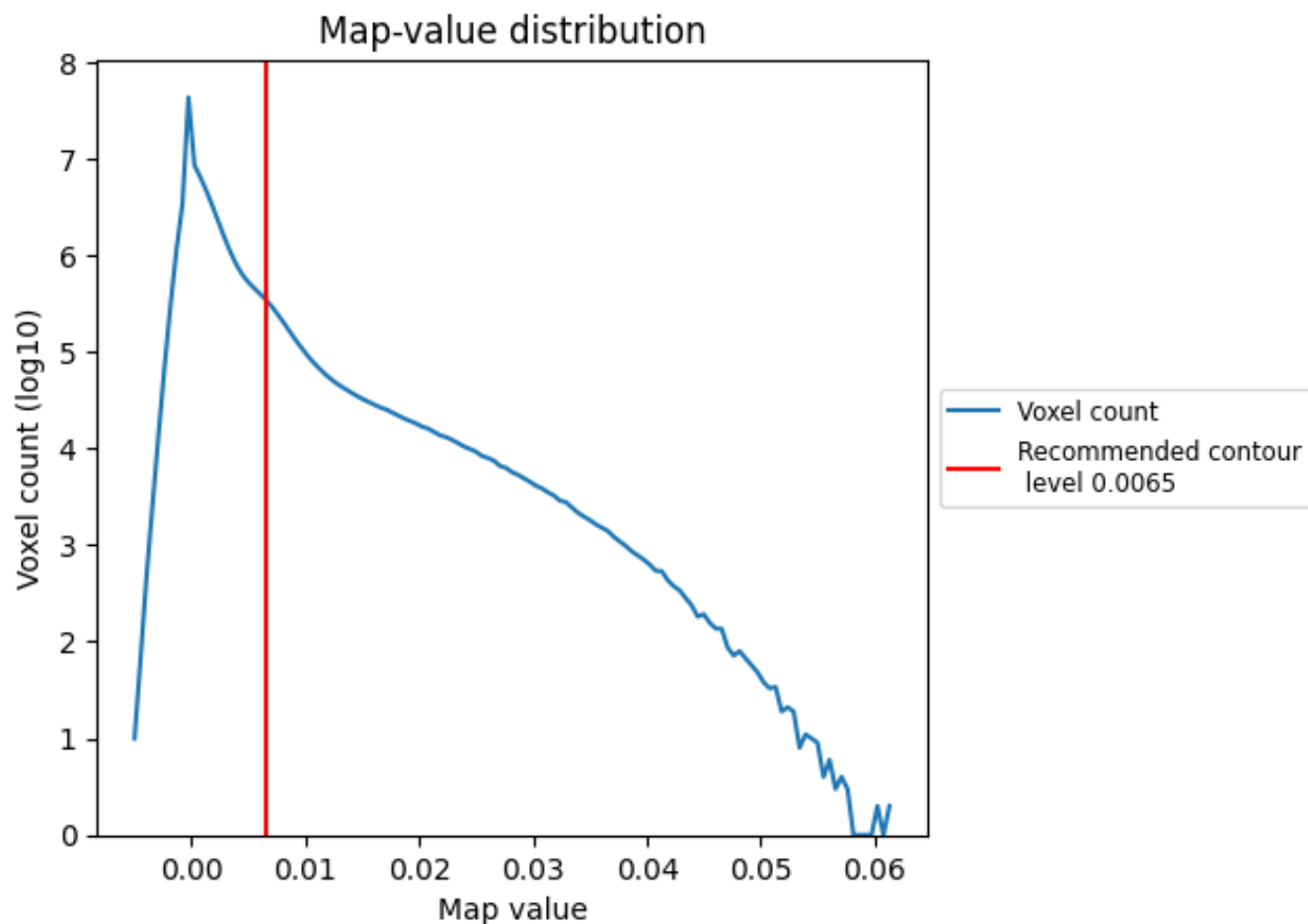
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

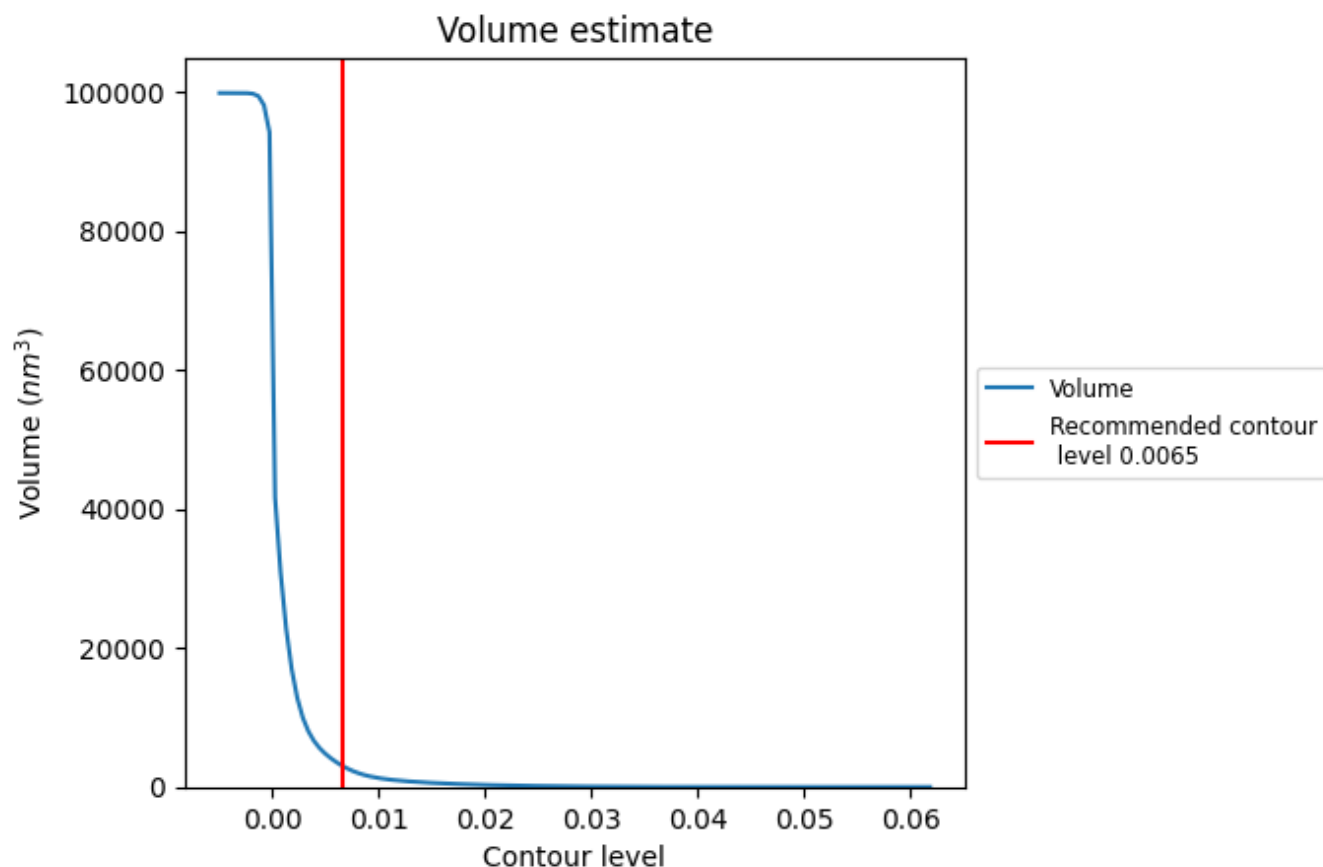
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

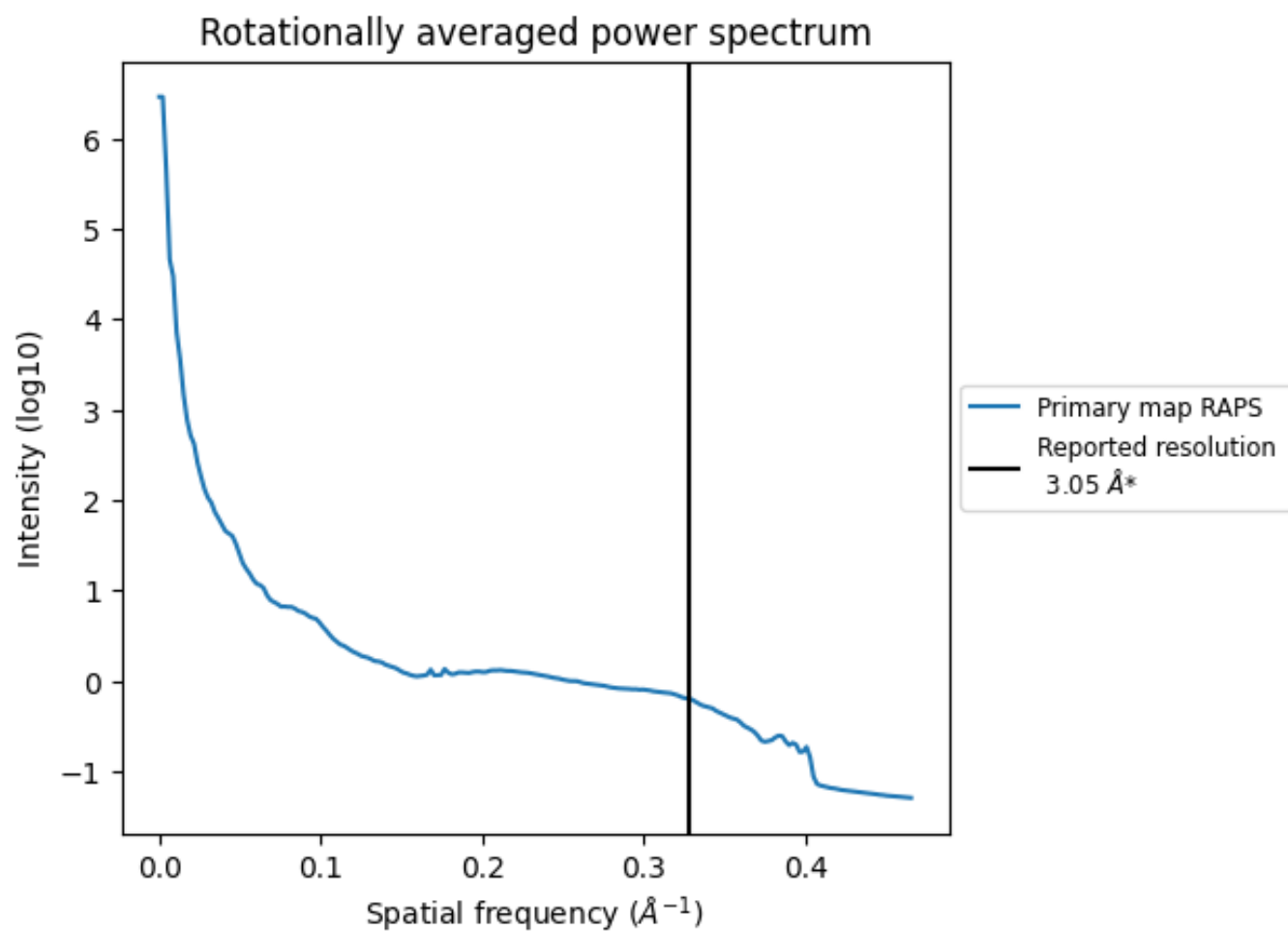
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3102  $\text{nm}^3$ ; this corresponds to an approximate mass of 2802 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 0.328 Å<sup>-1</sup>

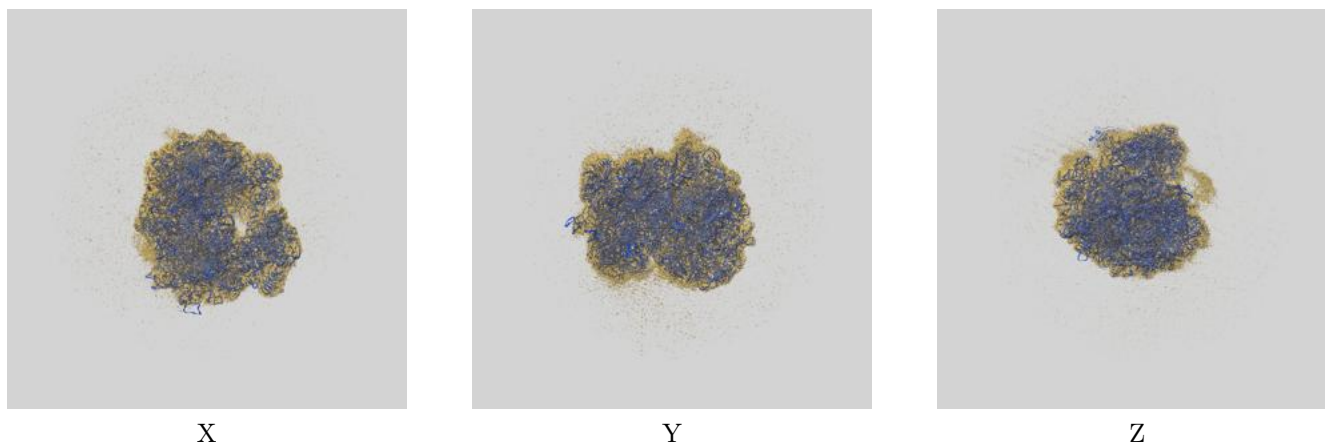
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

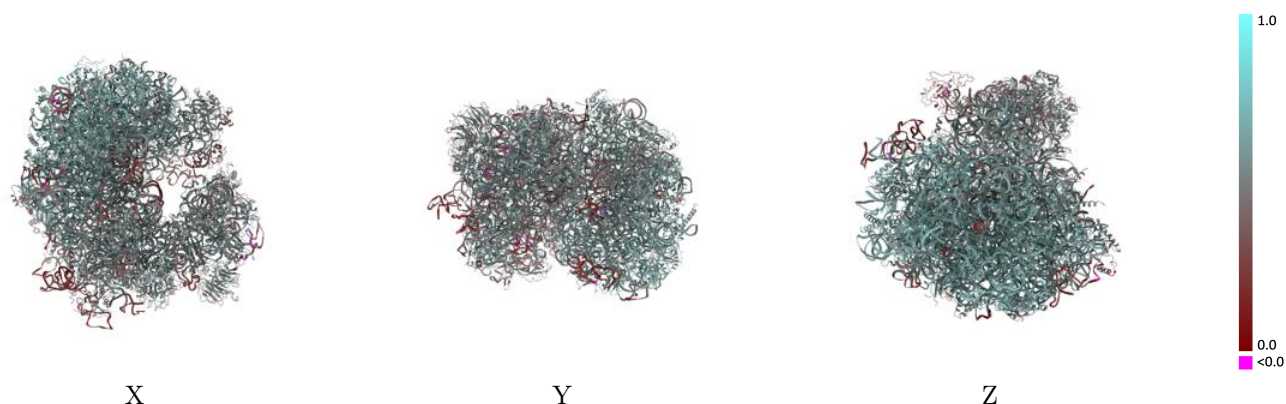
This section contains information regarding the fit between EMDB map EMD-23934 and PDB model 7MPI. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

### 9.1 Map-model overlay [i](#)



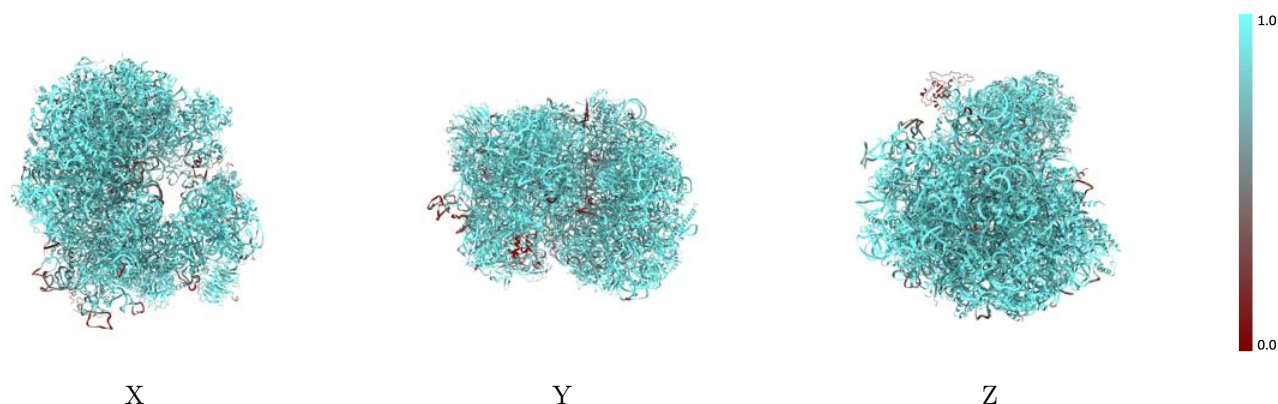
The images above show the 3D surface view of the map at the recommended contour level 0.0065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



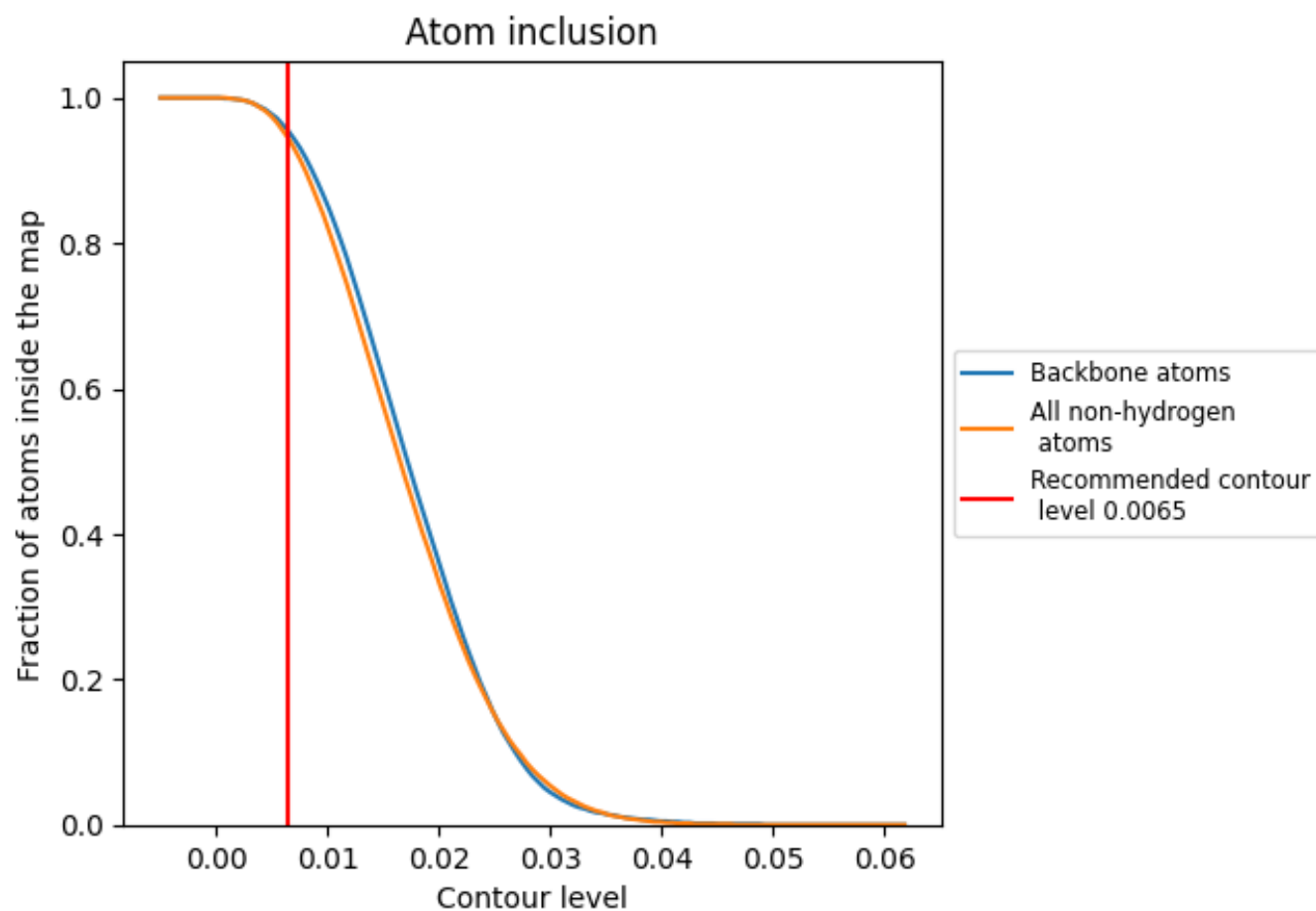
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0065).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.0065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.5380
A1	 0.9690	 0.5660
A3	 0.9990	 0.5510
A4	 0.9910	 0.6160
AA	 0.9470	 0.5690
AB	 0.9820	 0.6220
AC	 0.9770	 0.6070
AD	 0.9240	 0.4860
AE	 0.9620	 0.5840
AF	 0.9800	 0.6140
AG	 0.9630	 0.5480
AH	 0.9660	 0.5790
AI	 0.9510	 0.4970
AJ	 0.7920	 0.3910
AL	 0.9510	 0.5870
AM	 0.9810	 0.6080
AN	 0.9880	 0.6150
AO	 0.9880	 0.6260
AP	 0.9750	 0.6280
AQ	 0.9890	 0.6130
AR	 0.8470	 0.5280
AS	 0.9830	 0.6170
AT	 0.9630	 0.5730
AU	 0.9080	 0.5180
AV	 0.9520	 0.6040
AW	 0.9430	 0.6020
AX	 0.9700	 0.5920
AY	 0.9760	 0.6000
AZ	 0.9800	 0.5340
Aa	 0.9890	 0.6040
Ab	 0.9160	 0.5150
Ac	 0.9770	 0.5290
Ad	 0.9430	 0.5940
Ae	 0.9860	 0.6280
Af	 0.9950	 0.6500









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Chain	Atom inclusion	Q-score
Ag	 0.9680	 0.5780
Ah	 0.9780	 0.5920
Ai	 0.9340	 0.5470
Aj	 0.9970	 0.6350
Ak	 0.8350	 0.4790
Al	 0.9930	 0.6250
Am	 0.9650	 0.5860
An	 0.3630	 0.3240
Ao	 0.8770	 0.4870
Ap	 0.9580	 0.5750
B5	 0.9270	 0.4810
BA	 0.9310	 0.5120
BB	 0.9320	 0.4700
BC	 0.9540	 0.5270
BD	 0.9460	 0.4950
BE	 0.9800	 0.5210
BF	 0.9410	 0.4940
BG	 0.8930	 0.4890
BH	 0.8310	 0.4440
BI	 0.9340	 0.5110
BJ	 0.9670	 0.5120
BK	 0.9480	 0.4480
BL	 0.8760	 0.5080
BM	 0.1450	 0.2070
BN	 0.9450	 0.5220
BO	 0.9640	 0.4950
BP	 0.8480	 0.4610
BQ	 0.9690	 0.5320
BR	 0.7970	 0.4450
BS	 0.8920	 0.4910
BT	 0.9360	 0.5340
BU	 0.8760	 0.4500
BV	 0.9340	 0.5380
BW	 0.9860	 0.5530
BX	 0.9530	 0.5330
BY	 0.9500	 0.5150
BZ	 0.8710	 0.4960
Ba	 0.9660	 0.5260
Bb	 0.9070	 0.5020
Bc	 0.9370	 0.5010
Bd	 0.9930	 0.5480
Be	 0.9170	 0.4960

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Chain	Atom inclusion	Q-score
Bf	 0.3650	 0.2290
Bg	 0.9080	 0.4920
Bh	 0.6980	 0.3680