



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:18 PM UTC

PDB ID : 8EWC / pdb_00008ewc
EMDB ID : EMD-28643
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), Structure II
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-22
Resolution : 2.45 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

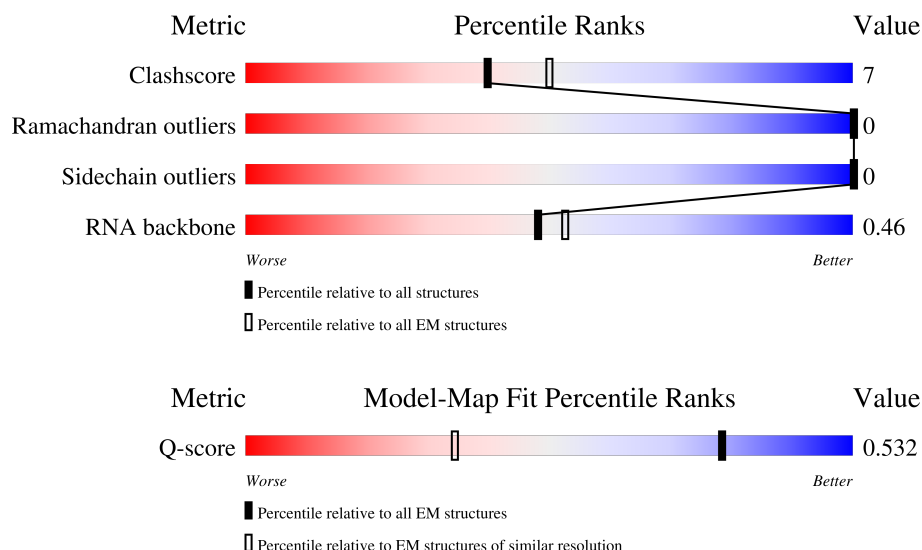
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.45 Å.

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



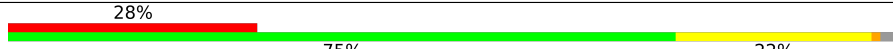
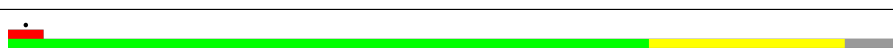
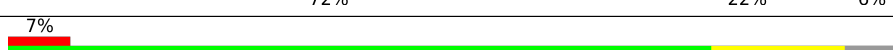
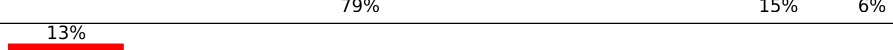
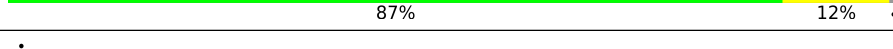
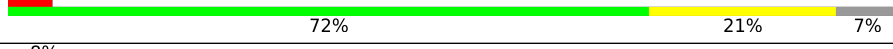
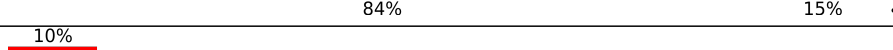
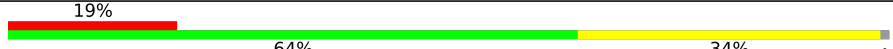
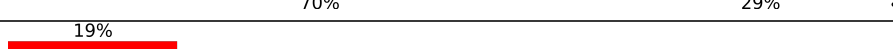
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5931 (1.96 - 2.95)

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

Mol	Chain	Length	Quality of chain
1	BA	252	6% 57% 25% 18%
2	BB	255	13% 56% 27% 16%
3	BC	254	65% 20% 15%

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

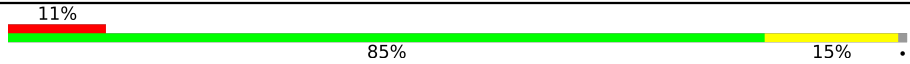
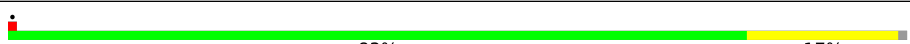
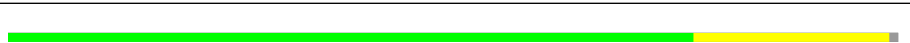
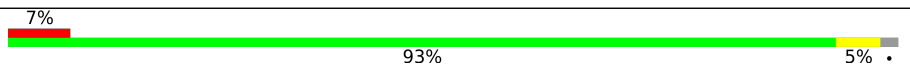
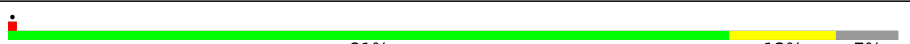
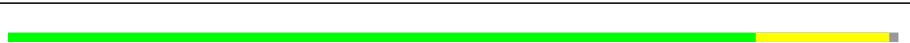
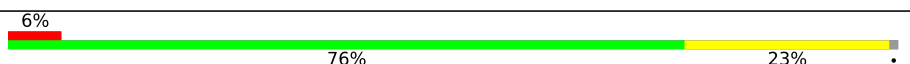
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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3360	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	221	
47	AJ	174	
48	AL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

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

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Mol	Chain	Length	Quality of chain
79	E	217	82%
			68%32%
80	EC	202	52%
			26%48%21%5%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 206055 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

- Molecule 2 is a protein called RPS1A isoform 1.

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

- Molecule 3 is a protein called RPS2 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 13 is a protein called RPS22A isoform 1.

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

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

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

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

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

- Molecule 16 is a protein called RPS26B isoform 1.

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

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

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

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

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

- Molecule 19 is a protein called RPS3 isoform 1.

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

- Molecule 20 is a protein called Rps5p.

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

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

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

- Molecule 22 is a protein called RPS15 isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 27 is a protein called RPS20 isoform 1.

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

- Molecule 28 is a protein called RPS25A isoform 1.

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

- Molecule 29 is a protein called RPS28A isoform 1.

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

- Molecule 30 is a protein called RPS29A isoform 1.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bf	75	Total	C	N	O	S	0	0
			605	386	116	99	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BM	124	Total	C	N	O	S	0	0
			935	587	165	181	2		

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

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

- Molecule 37 is a protein called RPL4A isoform 1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	3198	Total	C	N	O	P	0	0
			68445	30596	12331	22320	3198		

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

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

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

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

- Molecule 41 is a protein called RPL5 isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 46 is a protein called RPL10 isoform 1.

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

- Molecule 47 is a protein called RPL11A isoform 1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 59 is a protein called RPL24A isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 64 is a protein called RPL29 isoform 1.

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

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

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

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

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

- Molecule 67 is a protein called RPL32 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 73 is a protein called RPL38 isoform 1.

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ao	102	Total	C	N	O	S	0	0
			819	514	166	134	5		

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

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

- Molecule 79 is a protein called RPL1A isoform 1.

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

- Molecule 80 is a RNA chain called internal ribosome entry site (IRES).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	EC	192	Total	C	N	O	P	0	0
			4090	1828	729	1341	192		

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

Mol	Chain	Residues	Atoms		AltConf
81	BN	1	Total	Mg	0
			1	1	
81	Ba	1	Total	Mg	0
			1	1	
81	B5	55	Total	Mg	0
			55	55	
81	AB	2	Total	Mg	0
			2	2	
81	A1	174	Total	Mg	0
			174	174	
81	A3	2	Total	Mg	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
81	A4	4	Total 4	Mg 4	0
81	AI	1	Total 1	Mg 1	0
81	AL	1	Total 1	Mg 1	0
81	AP	1	Total 1	Mg 1	0
81	AR	1	Total 1	Mg 1	0
81	Ae	1	Total 1	Mg 1	0
81	Af	1	Total 1	Mg 1	0
81	Aj	2	Total 2	Mg 2	0

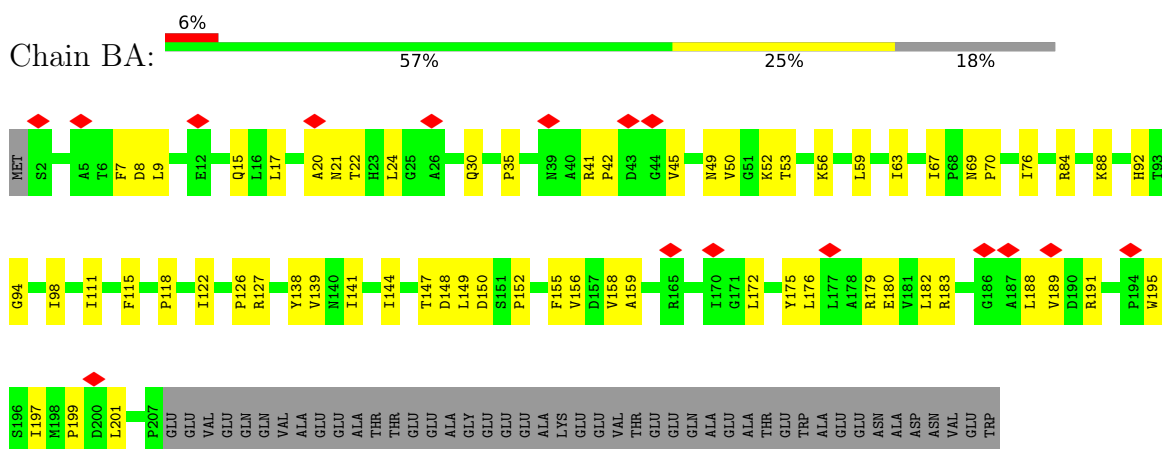
- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

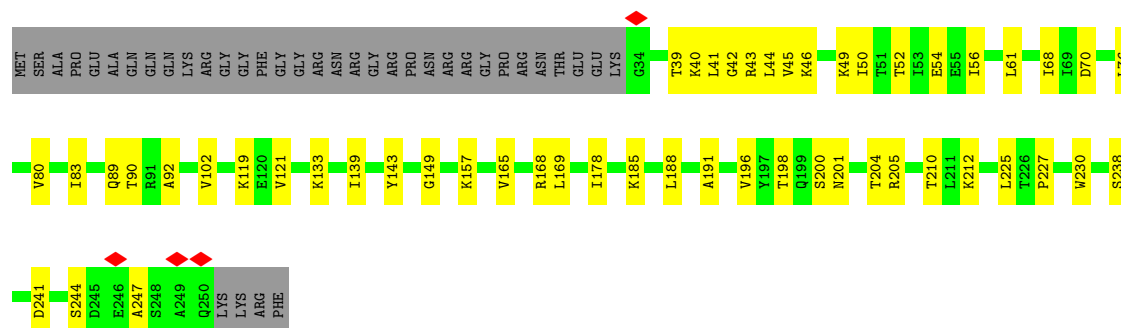
Mol	Chain	Residues	Atoms		AltConf
82	Ao	1	Total 1	Zn 1	0

3 Residue-property plots

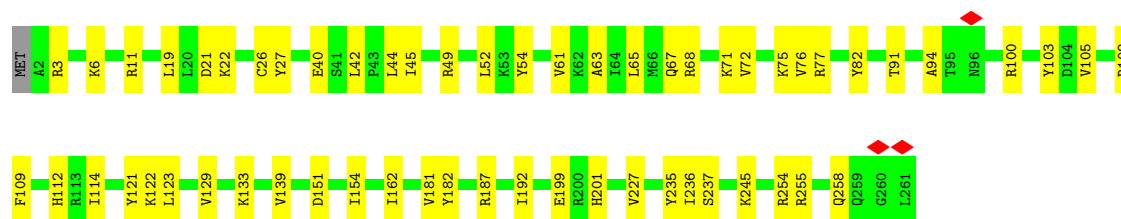
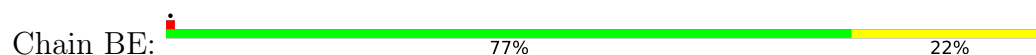
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

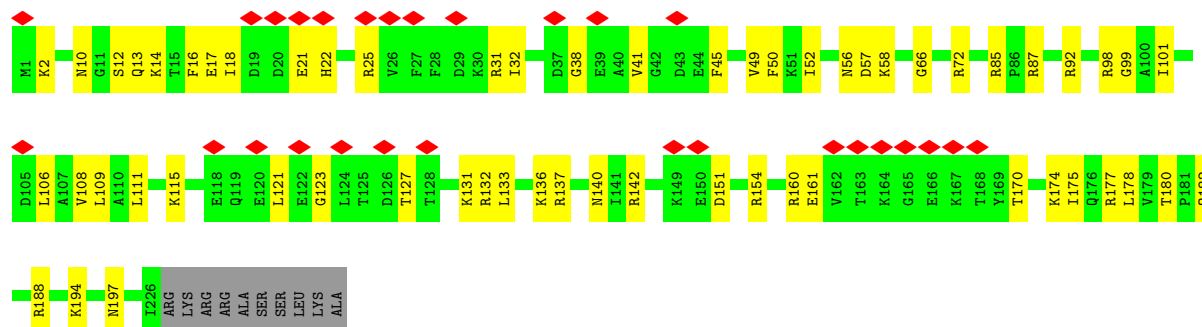




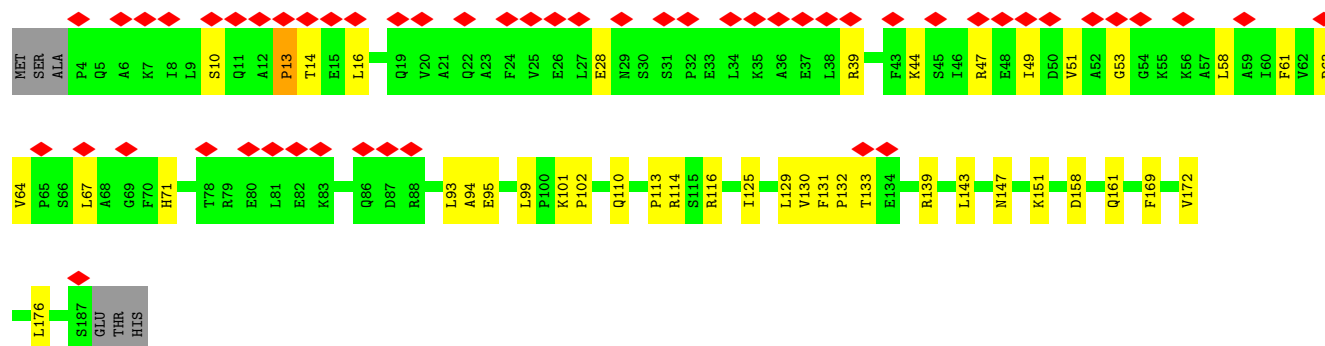
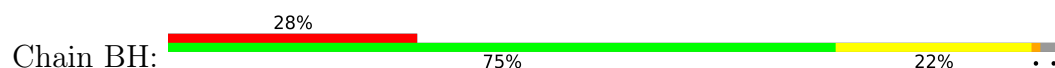
• Molecule 4: 40S ribosomal protein S4-A



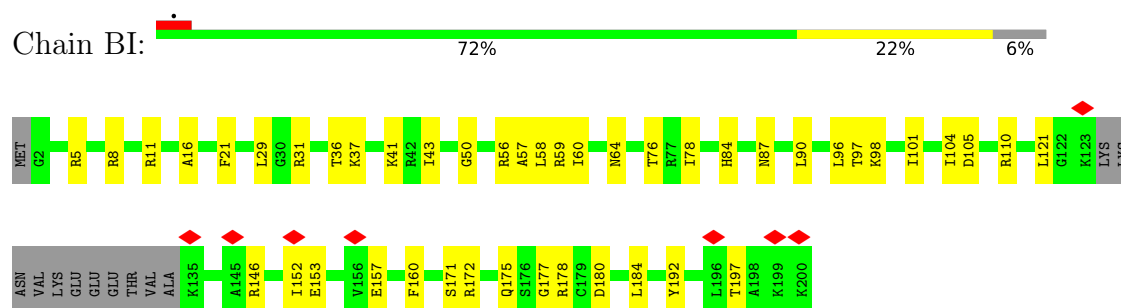
• Molecule 5: 40S ribosomal protein S6-A



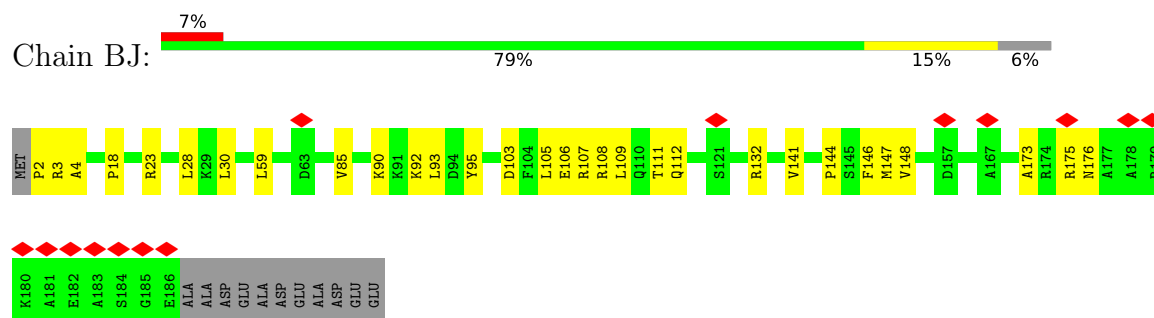
• Molecule 6: 40S ribosomal protein S7-A



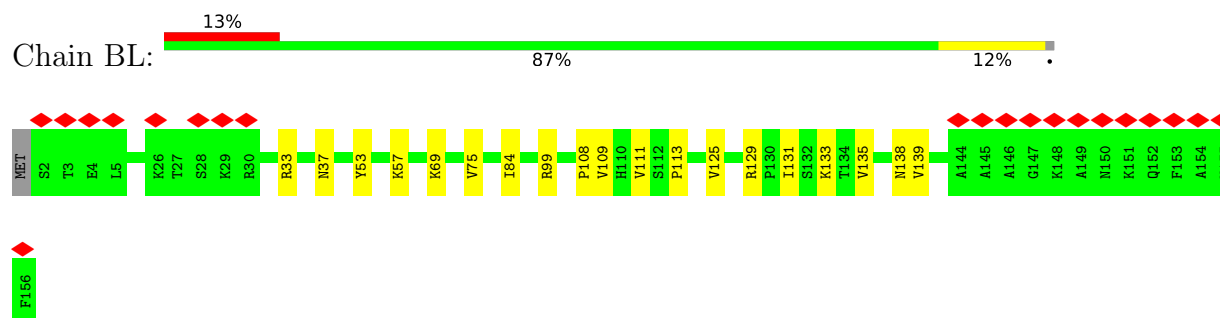
- Molecule 7: 40S ribosomal protein S8-A



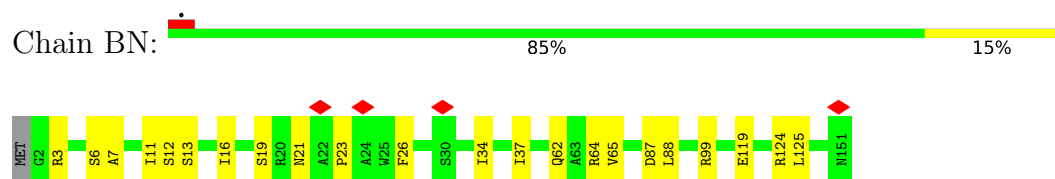
- Molecule 8: 40S ribosomal protein S9-A



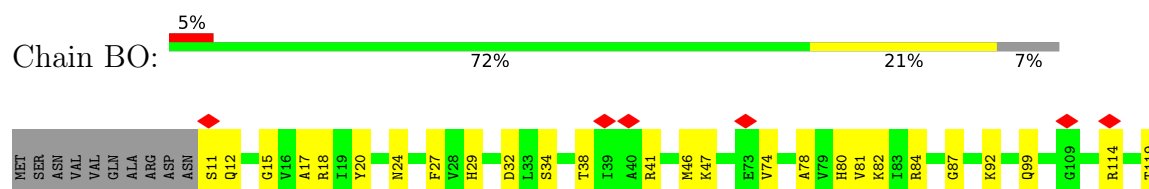
- Molecule 9: 40S ribosomal protein S11-A

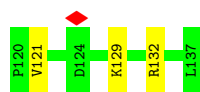


- Molecule 10: 40S ribosomal protein S13

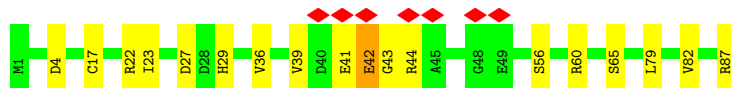
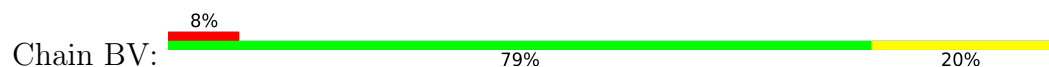


- Molecule 11: 40S ribosomal protein S14-A

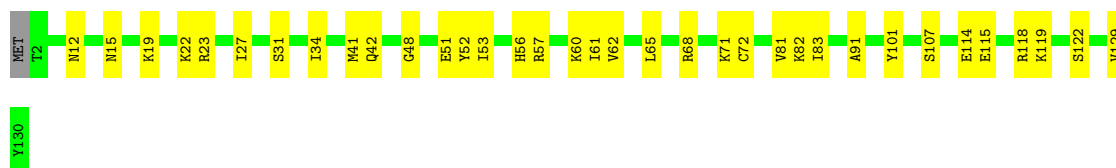
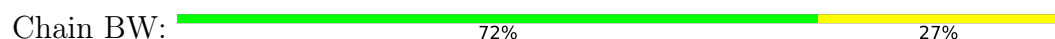




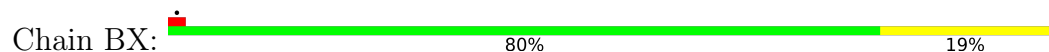
- Molecule 12: 40S ribosomal protein S21-A



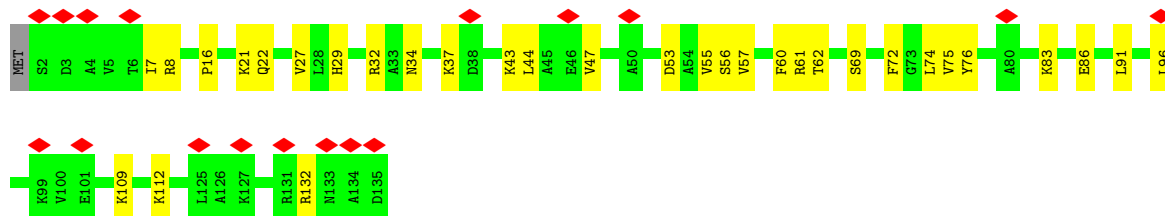
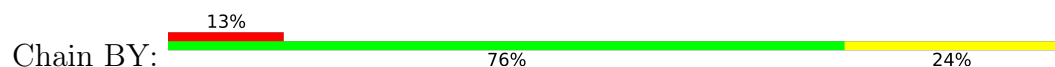
- Molecule 13: RPS22A isoform 1



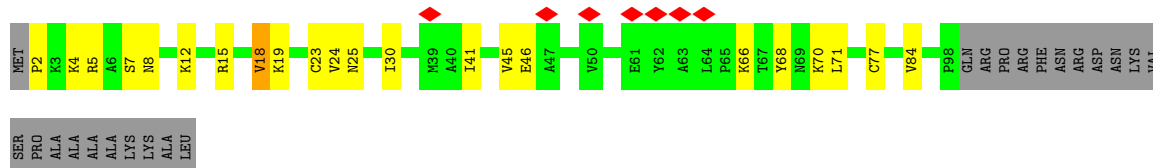
- Molecule 14: 40S ribosomal protein S23-A



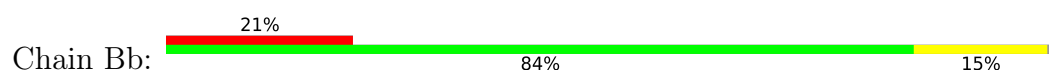
- Molecule 15: 40S ribosomal protein S24-A



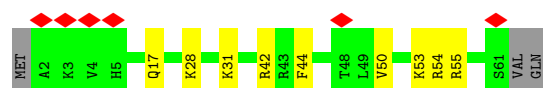
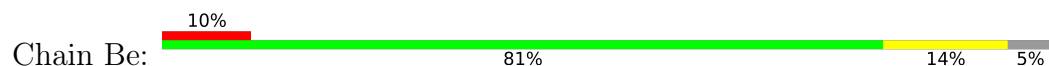
- Molecule 16: RPS26B isoform 1



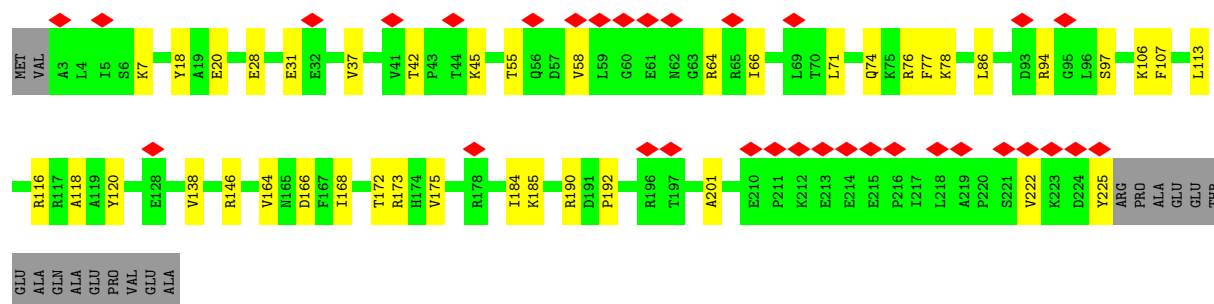
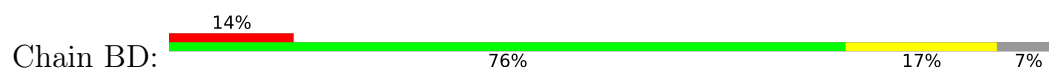
- Molecule 17: 40S ribosomal protein S27-A



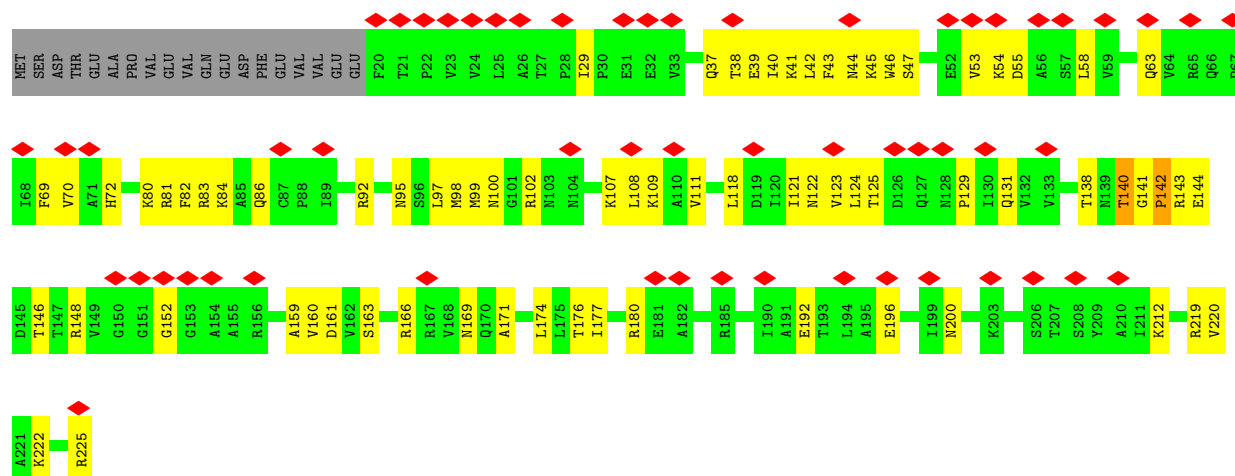
- Molecule 18: 40S ribosomal protein S30-A



- Molecule 19: RPS3 isoform 1

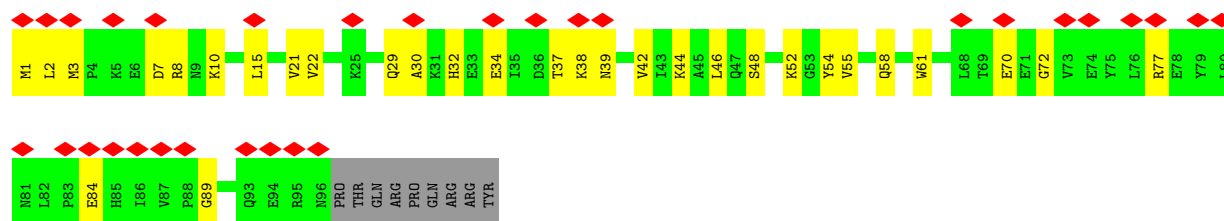


- Molecule 20: Rps5p

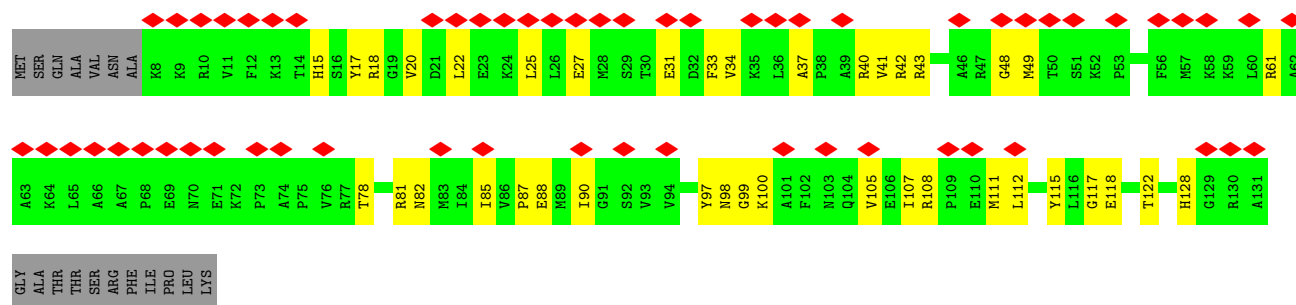
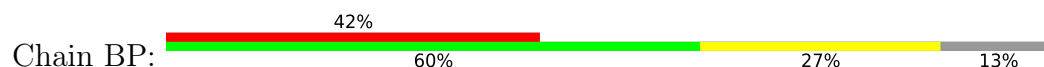


- Molecule 21: 40S ribosomal protein S10-A

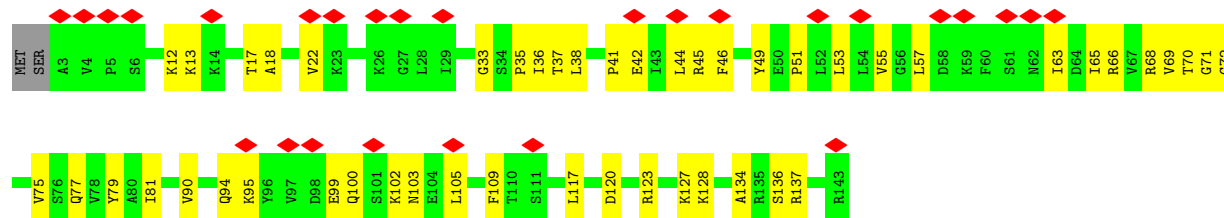




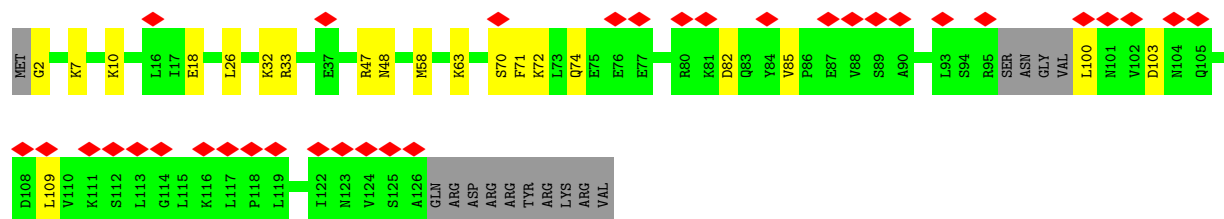
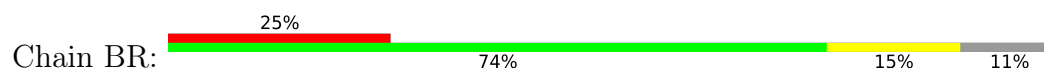
• Molecule 22: RPS15 isoform 1



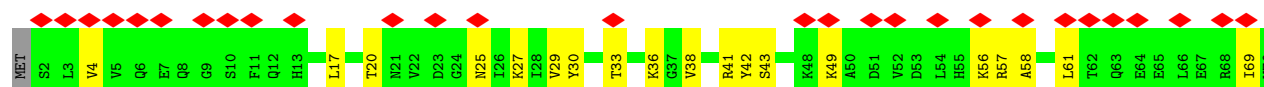
• Molecule 23: 40S ribosomal protein S16-A

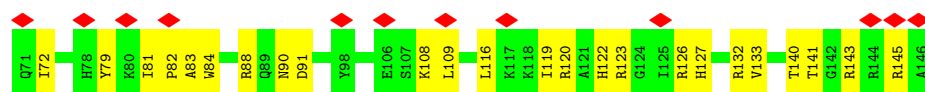


• Molecule 24: 40S ribosomal protein S17-A

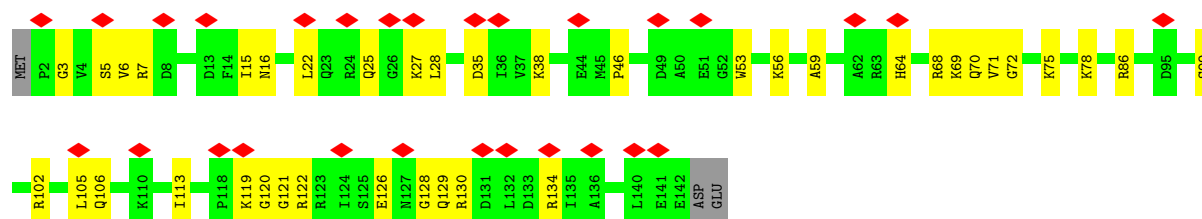
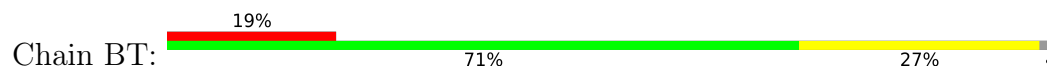


• Molecule 25: 40S ribosomal protein S18-A

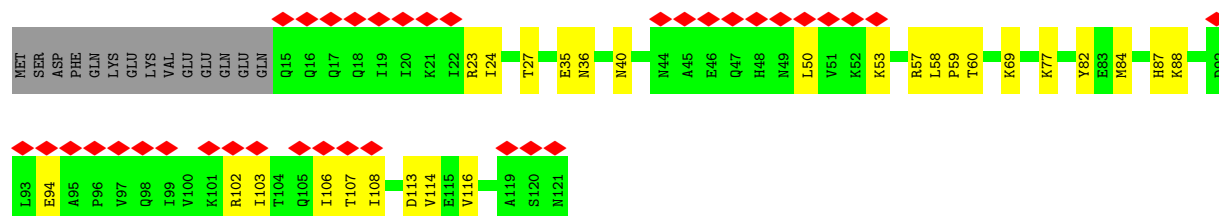




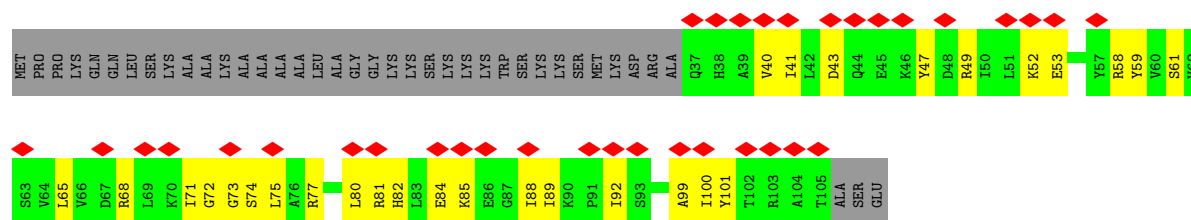
- Molecule 26: 40S ribosomal protein S19-A



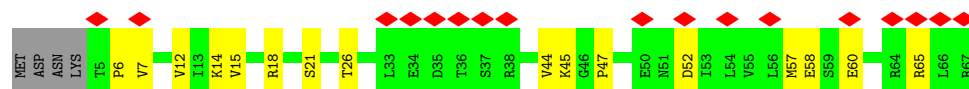
- Molecule 27: RPS20 isoform 1



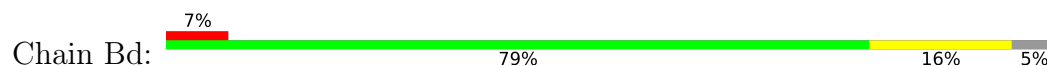
- Molecule 28: RPS25A isoform 1



- Molecule 29: RPS28A isoform 1

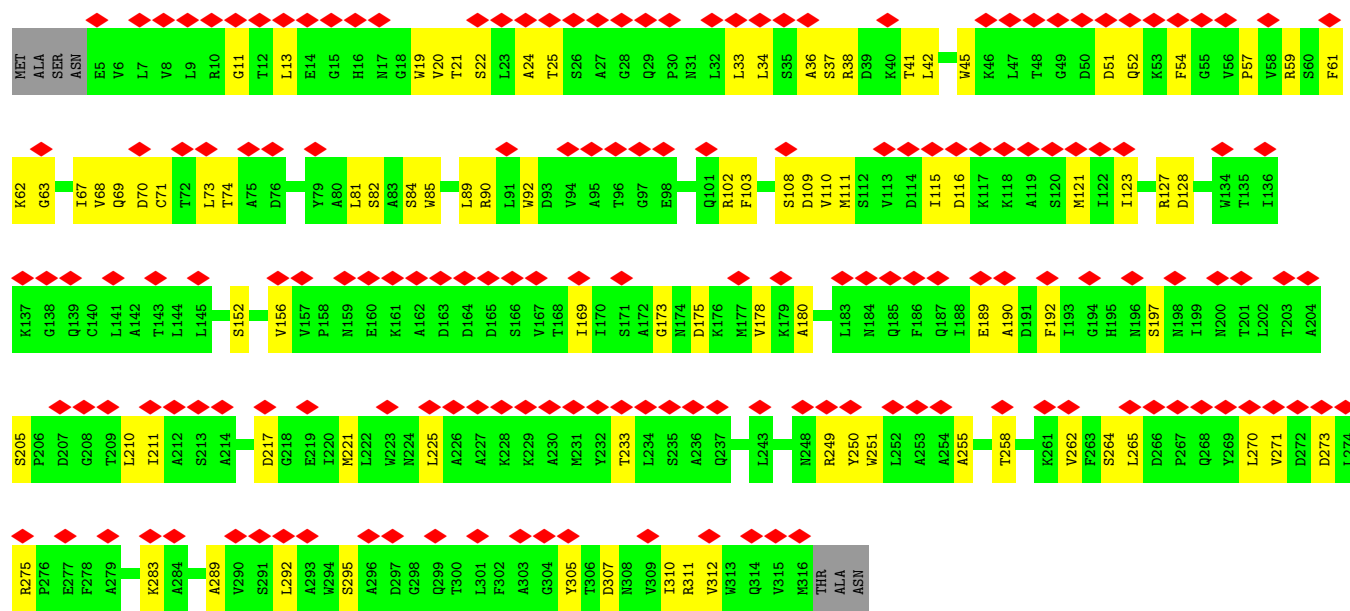
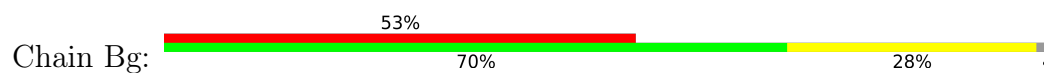


- Molecule 30: RPS29A isoform 1

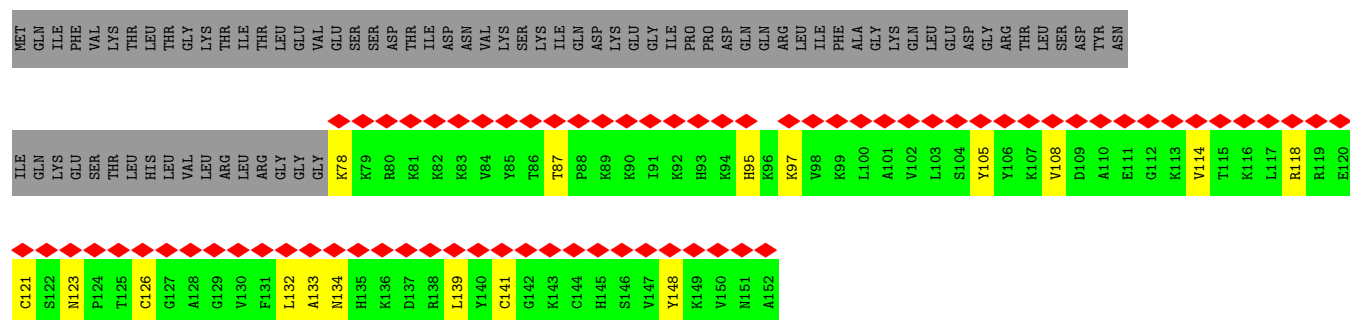
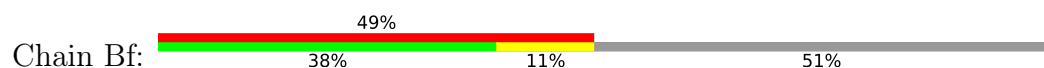




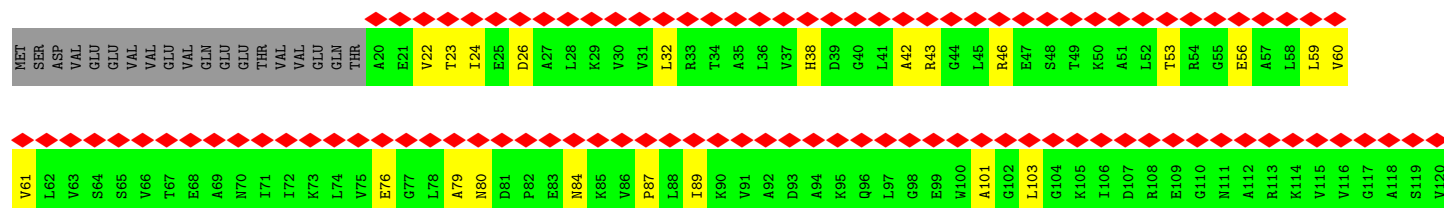
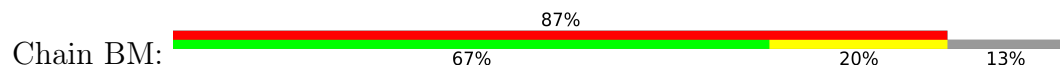
- Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 32: Ubiquitin-40S ribosomal protein S31

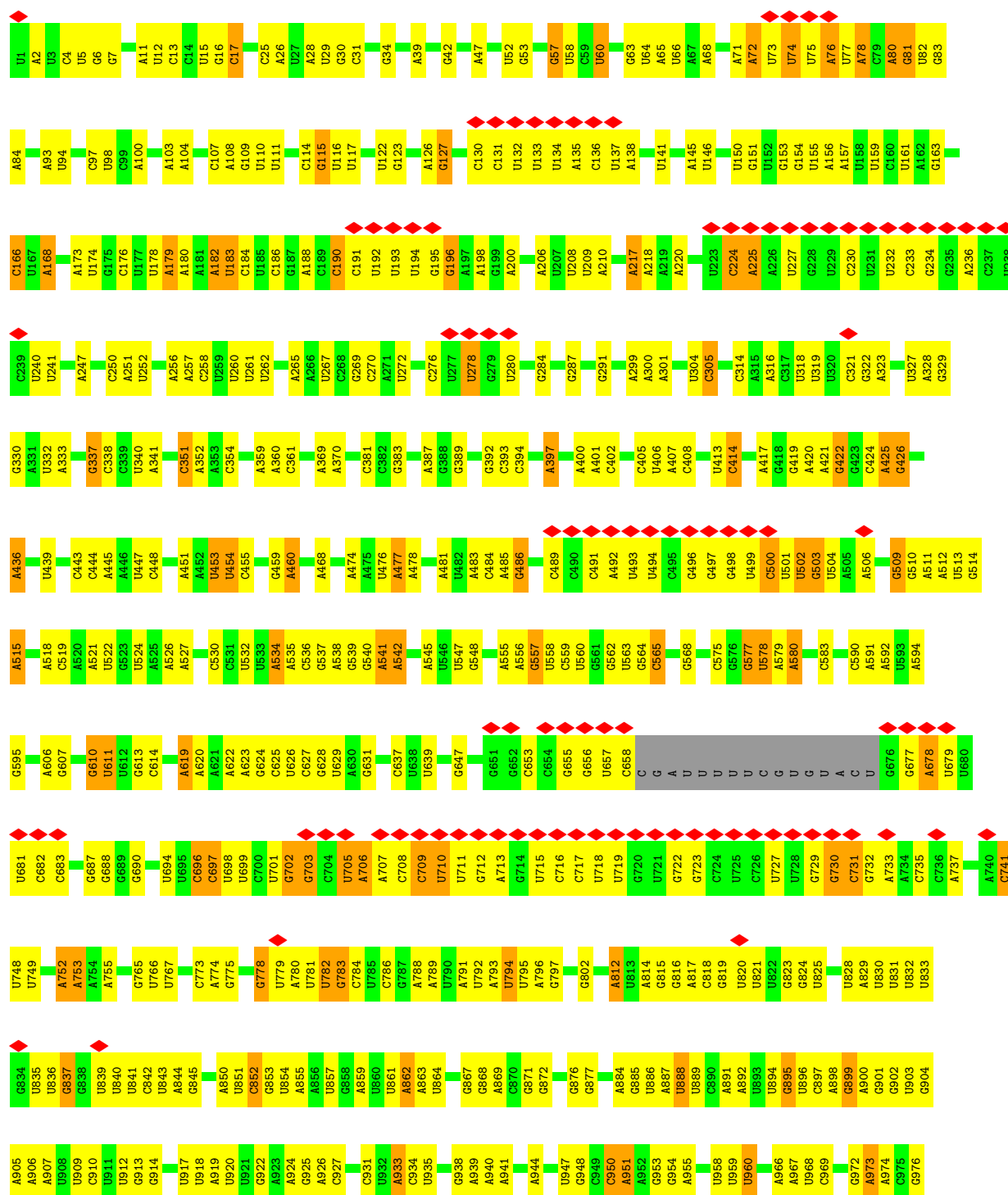


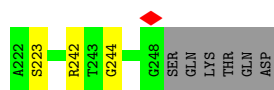
- Molecule 33: 40S ribosomal protein S12





• Molecule 34: 18S rRNA





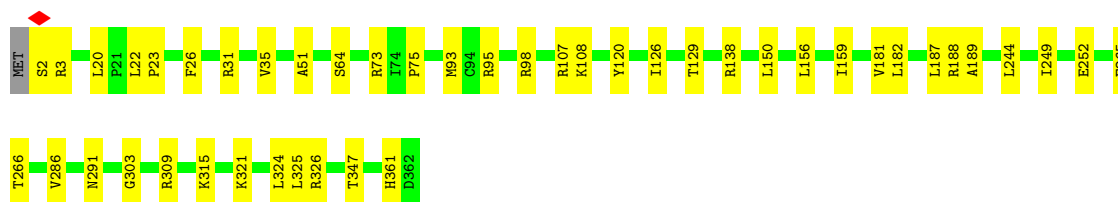
- Molecule 36: 60S ribosomal protein L3

Chain AB: 81% 18%



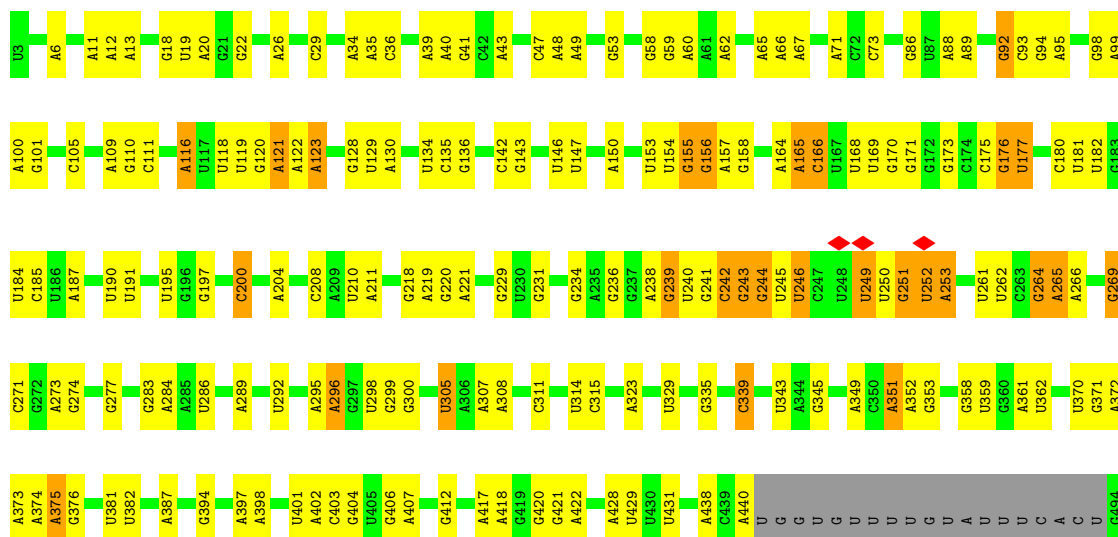
- Molecule 37: RPL4A isoform 1

Chain AC: 87% 12%



- Molecule 38: 25S rRNA

Chain A1: 56% 33% 6% 5%



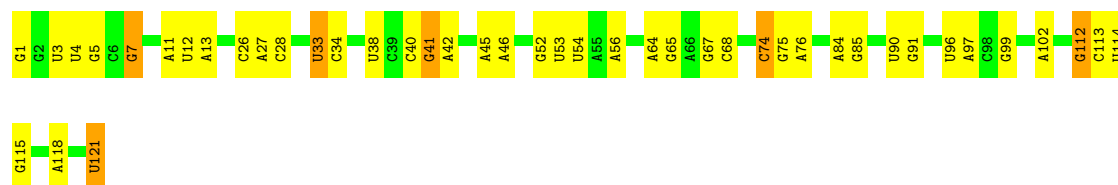
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U1720	U1724	C1725	A1729	U1737	C1738	U1739	U1740	A1741	G1744	C1745	G1748	A1749	A1750	G1751	A1752	C1762	U1763	U1764	U1765	G1766	G1775	C1779	U1785	G1786	A1787	C1791	C1792	G1796	A1797	A1798	A1799	A1800	U1801	C1802	C1805	A1806	A1809	A1810	A1813	A1814	U1815	U	U	A	G	A	C	G							
A1602	A1603	G1604	A1605	A1613	C1614	C1615	U1616	G1617	G1618	A1619	U1620	A1621	U1622	G1623	C1628	U1629	U1630	C1639	G1640	U1641	A1642	A1643	C1644	U1645	C1657	G1658	U1659	C1660	G1661	G1662	G1666	A1667	G1668	C1669	U1672	U1688	U1689	U1694	U1695	A1696	A1697	C1708	C1709	A1714	U1717	G1718	G1719								
U1495	C1496	C1497	C1498	C1499	C1502	A1503	A1504	C1508	U1523	A1524	U1525	G1526	C1527	G1528	A1534	A1535	A1539	C1551	U1555	C1556	C1562	C1563	U1564	G1565	U1566	A1566	U1567	U1568	U1569	U1570	A1571	G1573	C1574	A1575	G1576	G1577	C1578	C1579	A1580	A1583	A1588	A1589	G1590	A1593	C1596	G1597	G1598								
U1351	A1352	U1353	G1354	A1355	U1356	G1357	C1364	G1365	A1366	G1367	G1380	U1384	C1385	A1386	G1387	A1390	A1399	G1400	U1410	C1411	G1412	U1415	A1418	A1419	G1434	A1435	U1436	C1437	G1443	A1446	G1447	U1448	A1449	G1450	C1469	U1472	A1477	A1481	A1482	A1491	G1492	G1493	U1494												
G1268	U1269	C1272	A1273	A1274	C1275	U1276	C1279	C1280	G1281	G1282	U1283	C1284	G1285	A1286	A1287	A1290	A1291	C1292	U1293	A1302	U1305	G1306	G1307	A1308	U1309	G1310	G1311	C1312	G1313	A1317	A1318	U1322	G1323	U1324	U1325	C1328	U1329	A1330	U1331	U1334	C1335	U1336	A1337	G1345	G1346	U1347	U1348	G1349	A1350						
C1201	A1202	A1203	A1204	A1205	G1206	G1207	U1208	G1213	U1218	C1219	U1220	A1221	G1222	A1223	G1226	C1227	G1228	G1229	G1230	A1231	C1232	G1233	G1234	U1235	G1236	G1237	C1238	C1239	A1240	U1241	G1242	G1243	A1244	A1245	G1246	U1247	C1248	G1249	U1251	A1252	U1253	C1254	G1255	C1256	C1257	U1258	A1259	A1260	G1261	G1262	A1263	G1264	U1265	G1266	U1267
G1097	A1098	G1101	A1102	A1103	U1108	U1109	U1110	U1111	U1114	G1117	C1118	C1119	A1120	U1128	G1131	C1132	A1133	G1134	U1144	G1149	A1153	A1154	C1155	C1156	G1157	A1158	A1159	C1160	U1168	G1174	C1175	C1176	G1177	G1178	A1179	A1180	U1181	A1182	A1190	U1191	C1192	A1193	G1194	A1195	C1196	A1197									
U995	C1000	G1001	A1002	G1010	U1015	C1016	C1017	G1018	G1019	A1021	G1020	U1022	C1023	G	A	A	U	G	A1030	C1031	C1032	U1033	U1034	G1035	U1041	A1046	A1047	A1048	C1049	A1054	A1061	A1062	G1063	A1064	G1072	A1075	U1081	U1082	G1083	A1084	U1085	G1086	G1087	C1092	A1093	U1094									
U897	U898	U899	G900	G901	G907	G908	C911	G912	A913	A914	A915	G916	A917	A921	U922	C923	G924	A925	G934	G937	C938	U943	C944	C945	U946	A952	G953	C959	U960	C961	G963	C964	A965	U966	A967	C969	G974	C975	U976	A980	U981	G985	U986	A987	G993	G994									
U776	U777	G781	A784	G785	A786	C788	A791	G792	C793	G799	C804	G805	A806	A807	A808	G813	A817	C818	U819	A820	U821	G822	C823	C824	A830	A837	G838	G845	A846	A847	A848	C849	G860	C861	U862	C863	G864	G867	U874	G875	A876	U879	A896												
G678	U679	G680	U681	G684	A690	A691	U698	G699	A602	A608	G609	U620	G610	A611	A619	U627	A628	U629	A630	U631	G632	C633	U640	U643	G644	A645	A649	C650	G651	C655	C656	A657	G658	G659	A660	G661	U662	C663	U664	A665	U669	U670	U671	A672	U673	G674	A677								
A495	A498	A501	U502	G505	U508	U509	G510	G518	A519	U520	A521	A522	A523	U524	C525	U528	A529	A630	U631	G632	C633	G535	G538	C539	U540	U541	G542	C543	C544	U545	C546	G547	G548	U549	A550	A551	U552	U553	C554	A554	A557	U558	A559	U671	A672	U673	G674	A677	A578	G579					





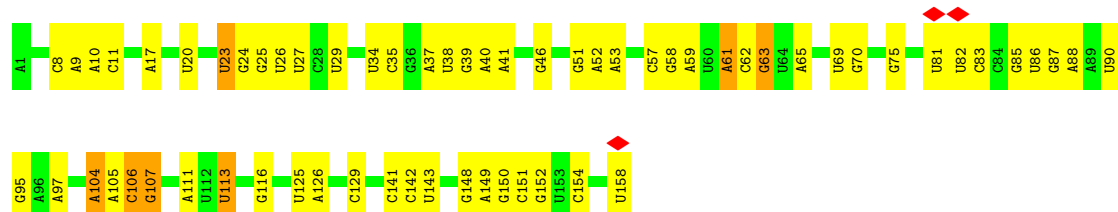
• Molecule 39: 5s rRNA

Chain A3: 64% 31% 5%



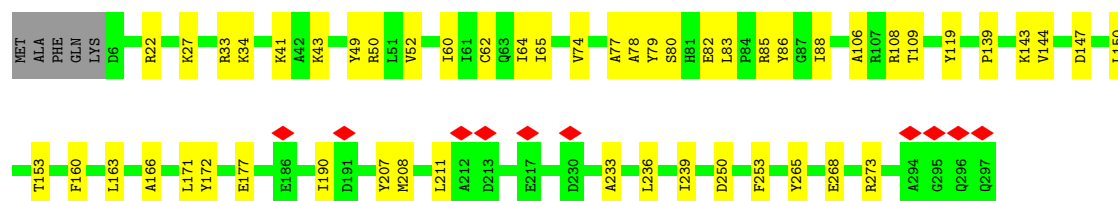
• Molecule 40: 5.8 S rRNA

Chain A4: 60% 35% .



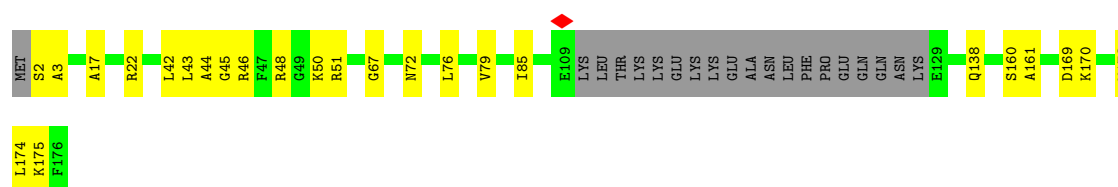
• Molecule 41: RPL5 isoform 1

Chain AD: 81% 17% .



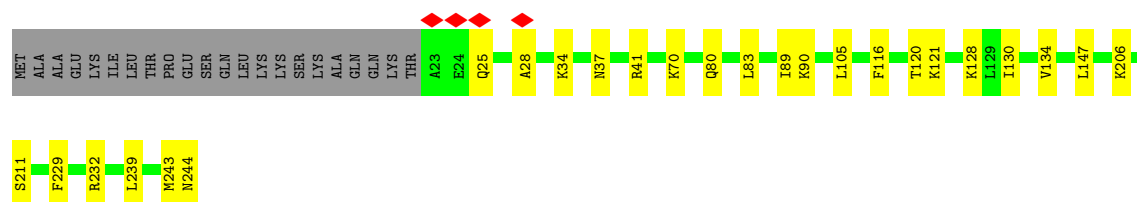
• Molecule 42: 60S ribosomal protein L6-A

Chain AE: 74% 14% 11%



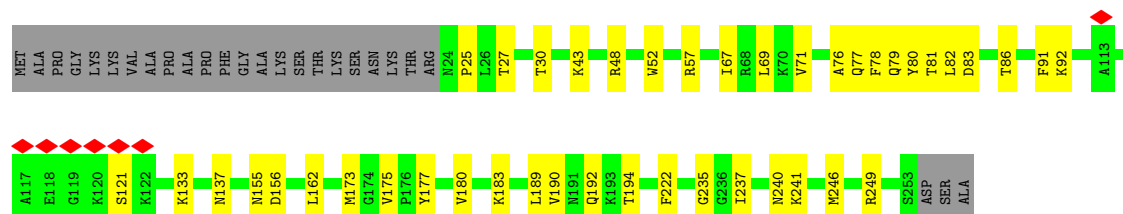
• Molecule 43: 60S ribosomal protein L7-A

Chain AF: 81% 10% 9%



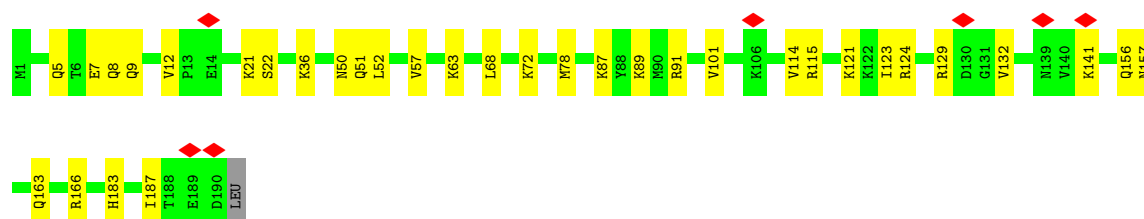
- Molecule 44: 60S ribosomal protein L8-A

Chain AG: 73% 17% 10%



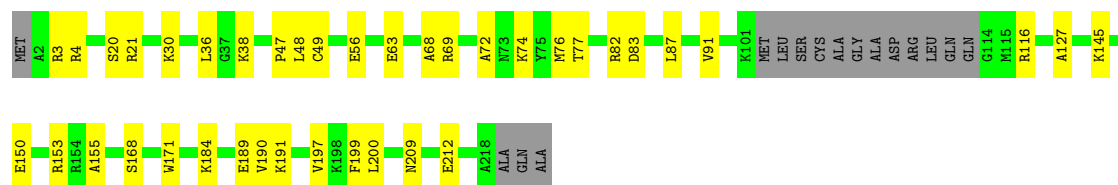
- Molecule 45: 60S ribosomal protein L9-A

Chain AH: 82% 18%



- Molecule 46: RPL10 isoform 1

Chain AI: 75% 18% 7%



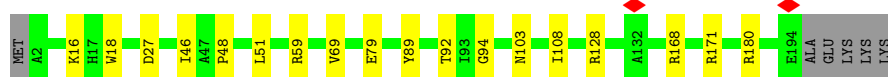
- Molecule 47: RPL11A isoform 1

Chain AJ: 7% 71% 26%



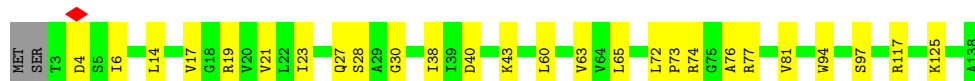
- Molecule 48: 60S ribosomal protein L13-A

Chain AL:  88% 9%



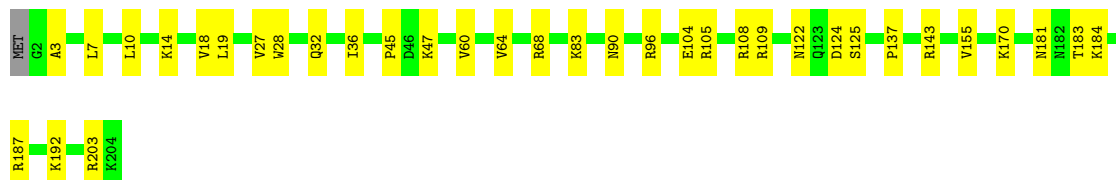
- Molecule 49: 60S ribosomal protein L14-A

Chain AM:  80% 19%



- Molecule 50: 60S ribosomal protein L15-A

Chain AN:  82% 17%



- Molecule 51: 60S ribosomal protein L16-A

Chain AO:  86% 13%



- Molecule 52: 60S ribosomal protein L17-A

Chain AP:  83% 12% 5%



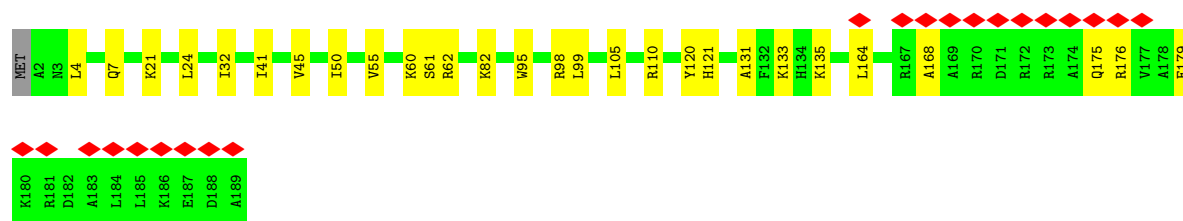
- Molecule 53: 60S ribosomal protein L18-A

Chain AQ:  88% 12%



- Molecule 54: 60S ribosomal protein L19-A

Chain AR:  11% 85% 15%



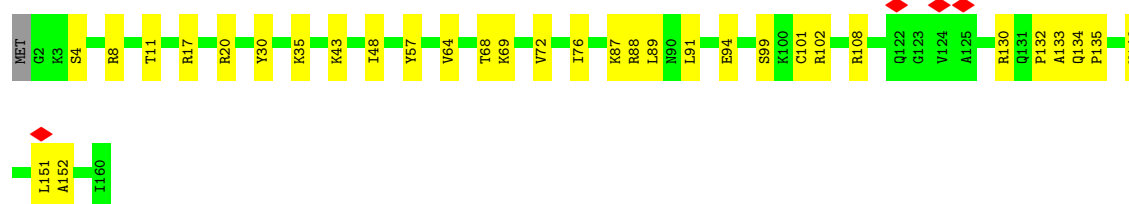
- Molecule 55: 60S ribosomal protein L20

Chain AS: 78% 19% .



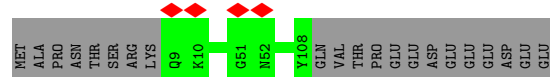
- Molecule 56: 60S ribosomal protein L21-A

Chain AT: 79% 20% .



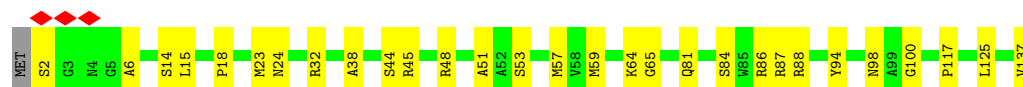
- Molecule 57: 60S ribosomal protein L22-A

Chain AU: 83% 17% .



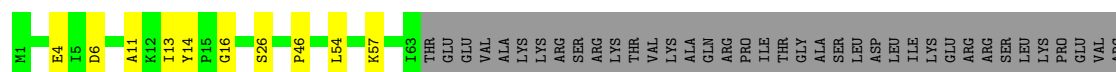
- Molecule 58: 60S ribosomal protein L23-A

Chain AV: 78% 21% .

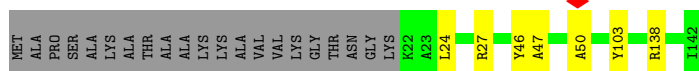
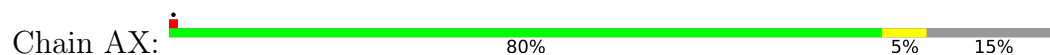


- Molecule 59: RPL24A isoform 1

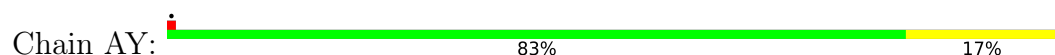
Chain AW: 34% 6% 59%



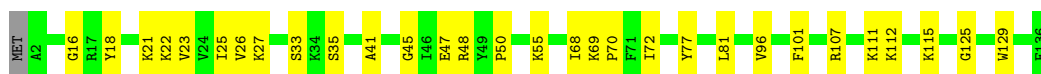
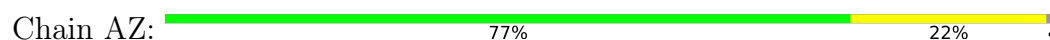
- Molecule 60: 60S ribosomal protein L25



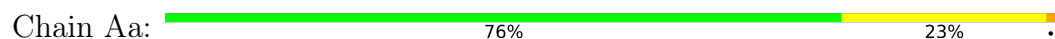
- Molecule 61: 60S ribosomal protein L26-A



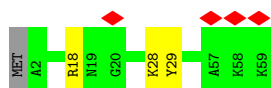
- Molecule 62: 60S ribosomal protein L27-A



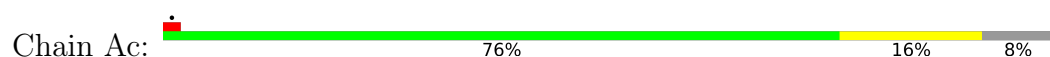
- Molecule 63: 60S ribosomal protein L28



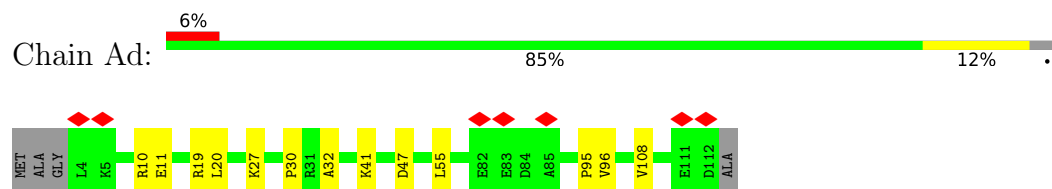
- Molecule 64: RPL29 isoform 1



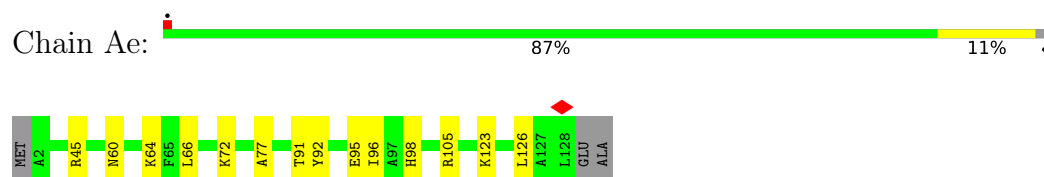
- Molecule 65: 60S ribosomal protein L30



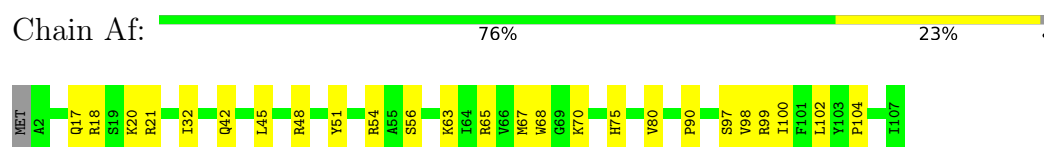
- Molecule 66: 60S ribosomal protein L31-A



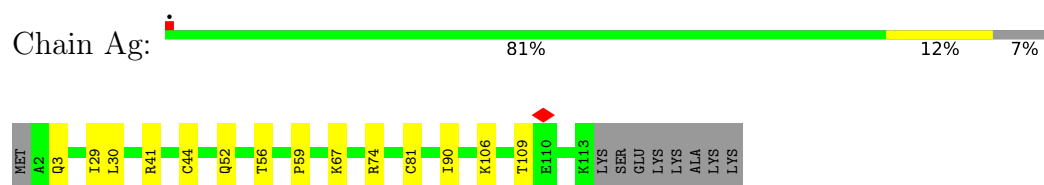
- Molecule 67: RPL32 isoform 1



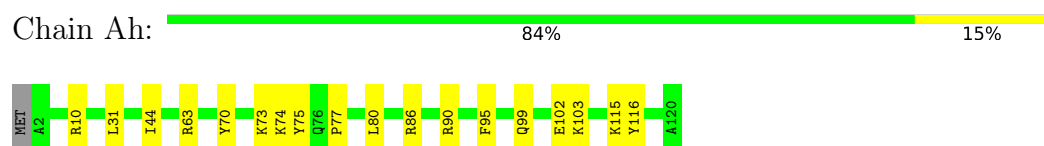
- Molecule 68: 60S ribosomal protein L33-A



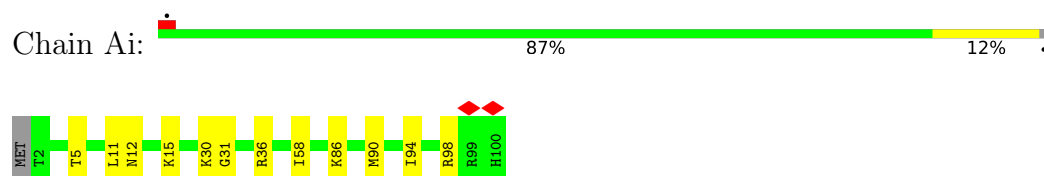
- Molecule 69: 60S ribosomal protein L34-A



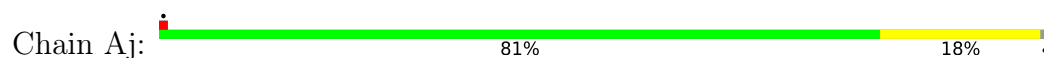
- Molecule 70: 60S ribosomal protein L35-A



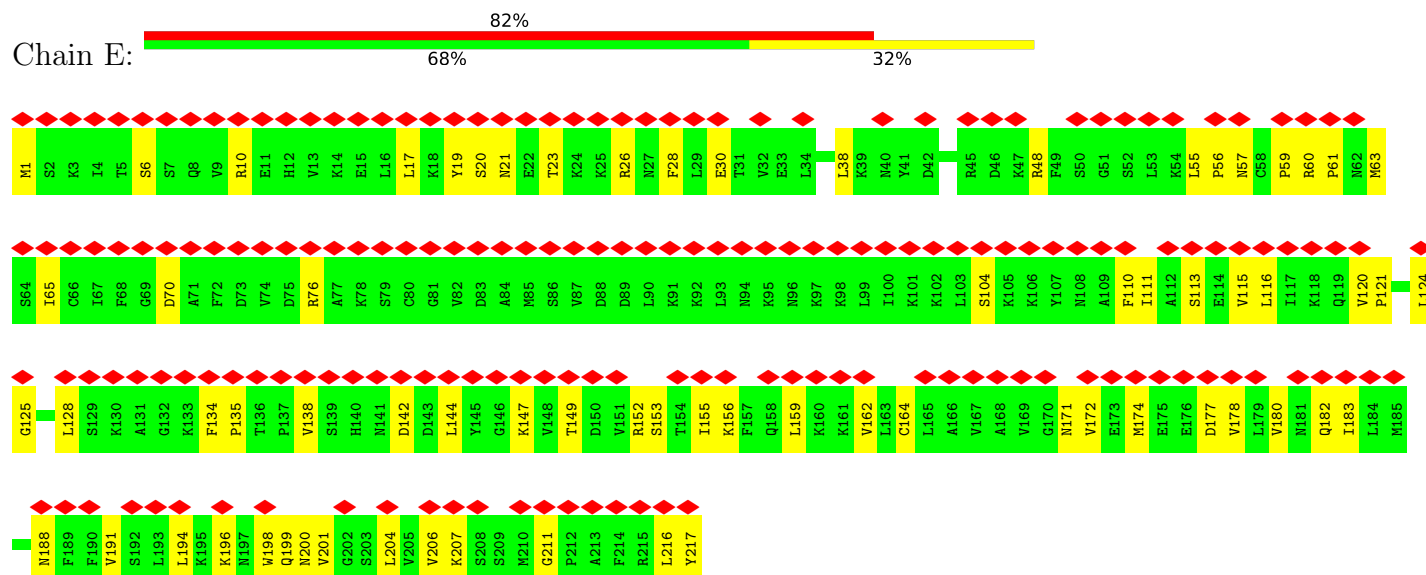
- Molecule 71: 60S ribosomal protein L36-A



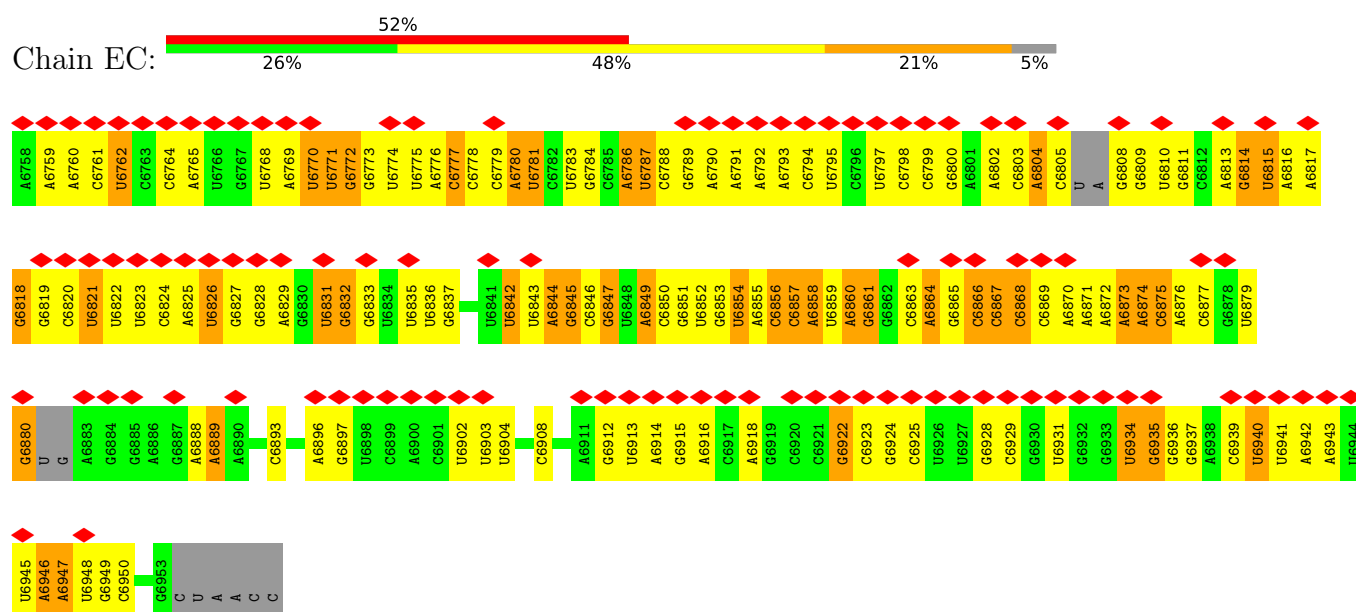
- Molecule 72: 60S ribosomal protein L37-A



- Molecule 79: RPL1A isoform 1



- Molecule 80: internal ribosome entry site (IRES)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94694	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	6.788	Depositor
Minimum map value	-2.847	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.244	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	BA	0.16	0/1653	0.43	0/2261
2	BB	0.20	0/1735	0.58	4/2335 (0.2%)
3	BC	0.17	0/1665	0.40	0/2263
4	BE	0.14	0/2109	0.40	0/2839
5	BG	0.14	0/1844	0.39	0/2464
6	BH	0.21	0/1506	0.51	2/2028 (0.1%)
7	BI	0.16	0/1514	0.46	0/2021
8	BJ	0.14	0/1519	0.41	0/2035
9	BL	0.14	0/1272	0.37	0/1712
10	BN	0.14	0/1215	0.39	0/1638
11	BO	0.17	0/952	0.47	0/1279
12	BV	0.19	0/693	0.52	1/935 (0.1%)
13	BW	0.15	0/1038	0.40	0/1395
14	BX	0.16	0/1139	0.47	0/1518
15	BY	0.15	0/1087	0.43	0/1449
16	Ba	0.19	0/782	0.61	2/1047 (0.2%)
17	Bb	0.15	0/620	0.44	0/838
18	Be	0.12	0/483	0.40	0/643
19	BD	0.15	0/1759	0.43	0/2368
20	BF	0.36	2/1629 (0.1%)	1.00	8/2202 (0.4%)
21	BK	0.18	0/837	0.56	2/1131 (0.2%)
22	BP	0.16	0/1012	0.46	0/1356
23	BQ	0.20	0/1125	0.49	0/1510
24	BR	0.18	0/984	0.43	0/1318
25	BS	0.14	0/1211	0.42	0/1628
26	BT	0.15	0/1113	0.42	0/1494
27	BU	0.18	0/865	0.45	0/1169
28	BZ	0.17	0/566	0.47	0/761
29	Bc	0.42	1/499 (0.2%)	0.74	3/670 (0.4%)
30	Bd	0.13	0/453	0.38	0/602
31	Bg	0.16	0/2454	0.45	0/3340
32	Bf	0.23	0/616	0.59	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.19	0/943	0.48	0/1274
34	B5	0.16	2/41880 (0.0%)	0.33	0/65248
35	AA	0.17	0/1912	0.39	0/2569
36	AB	0.17	0/3138	0.41	0/4217
37	AC	0.16	0/2800	0.40	0/3790
38	A1	0.18	2/75561 (0.0%)	0.36	0/117806
39	A3	0.14	0/2883	0.31	0/4491
40	A4	0.16	0/3746	0.33	0/5832
41	AD	0.15	0/2390	0.41	0/3225
42	AE	0.15	0/1260	0.40	0/1694
43	AF	0.17	0/1821	0.41	0/2451
44	AG	0.18	0/1830	0.46	0/2469
45	AH	0.17	0/1531	0.44	0/2062
46	AI	0.15	0/1708	0.36	0/2290
47	AJ	0.19	0/1374	0.52	2/1842 (0.1%)
48	AL	0.15	0/1568	0.40	0/2106
49	AM	0.14	0/1068	0.37	0/1438
50	AN	0.16	0/1757	0.40	0/2354
51	AO	0.14	0/1585	0.36	0/2128
52	AP	0.16	0/1410	0.38	0/1893
53	AQ	0.13	0/1465	0.36	0/1965
54	AR	0.14	0/1538	0.34	0/2050
55	AS	0.20	0/1481	0.46	0/1990
56	AT	0.17	0/1300	0.38	0/1743
57	AU	0.15	0/812	0.43	0/1099
58	AV	0.16	0/1018	0.39	0/1369
59	AW	0.15	0/533	0.37	0/707
60	AX	0.16	0/983	0.37	0/1325
61	AY	0.18	0/1004	0.37	0/1341
62	AZ	0.16	0/1118	0.43	0/1497
63	Aa	0.16	0/1204	0.44	0/1612
64	Ab	0.15	0/473	0.36	0/629
65	Ac	0.12	0/751	0.34	0/1008
66	Ad	0.14	0/904	0.35	0/1213
67	Ae	0.15	0/1041	0.39	0/1394
68	Af	0.16	0/868	0.35	0/1168
69	Ag	0.19	0/890	0.43	0/1189
70	Ah	0.14	0/978	0.37	0/1301
71	Ai	0.18	0/778	0.42	0/1034
72	Aj	0.17	0/696	0.44	0/923
73	Ak	0.14	0/618	0.42	0/826
74	Al	0.14	0/443	0.36	0/588
75	Am	0.14	0/423	0.37	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.17	0/234	0.39	0/300
77	Ao	0.15	0/831	0.40	0/1097
78	Ap	0.17	0/701	0.46	0/934
79	E	0.20	0/1745	0.49	0/2342
80	EC	0.18	0/4571	0.42	0/7114
All	All	0.17	7/219515 (0.0%)	0.39	24/322565 (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	2
15	BY	0	1
36	AB	0	1
41	AD	0	1
42	AE	0	1
43	AF	0	1
44	AG	0	3
54	AR	0	1
63	Aa	0	1
All	All	0	13

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	BF	142	PRO	CG-CD	-8.27	1.22	1.50
29	Bc	6	PRO	CG-CD	-7.85	1.24	1.50
34	B5	1575	G7M	O3'-P	6.58	1.62	1.56
38	A1	2256	A2M	O3'-P	6.25	1.62	1.56
20	BF	142	PRO	CB-CG	-5.27	1.23	1.49
34	B5	541	A2M	O3'-P	5.20	1.61	1.56
38	A1	2946	A2M	O3'-P	5.07	1.61	1.56

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	BF	142	PRO	N-CD-CG	-23.91	67.34	103.20
20	BF	142	PRO	CB-CG-CD	23.07	179.93	106.10
20	BF	142	PRO	CA-CB-CG	-19.83	66.83	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	Bc	6	PRO	N-CD-CG	-11.88	85.39	103.20
29	Bc	6	PRO	CA-N-CD	-7.20	101.92	112.00
20	BF	142	PRO	CA-N-CD	-6.65	102.69	112.00
21	BK	89	GLY	CA-C-N	6.14	132.74	121.70
21	BK	89	GLY	C-N-CA	6.14	132.74	121.70
29	Bc	6	PRO	CA-CB-CG	-5.77	93.53	104.50
16	Ba	18	VAL	CA-C-N	5.50	135.21	121.80
16	Ba	18	VAL	C-N-CA	5.50	135.21	121.80
2	BB	176	VAL	CA-C-N	5.25	135.37	125.66
2	BB	176	VAL	C-N-CA	5.25	135.37	125.66
12	BV	42	GLU	CA-CB-CG	5.14	124.38	114.10
6	BH	13	PRO	CA-C-N	5.07	130.82	121.70
6	BH	13	PRO	C-N-CA	5.07	130.82	121.70
20	BF	140	THR	N-CA-C	5.04	119.52	113.17
47	AJ	93	ASP	CA-C-N	5.04	134.98	125.66
47	AJ	93	ASP	C-N-CA	5.04	134.98	125.66
2	BB	147	ALA	CA-C-N	5.04	131.18	123.47
2	BB	147	ALA	C-N-CA	5.04	131.18	123.47
20	BF	142	PRO	N-CA-CB	-5.04	97.96	103.25
20	BF	140	THR	CA-C-N	5.02	129.75	121.87
20	BF	140	THR	C-N-CA	5.02	129.75	121.87

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	AB	266	ARG	Sidechain
41	AD	43	LYS	Peptide
42	AE	67	GLY	Peptide
43	AF	232	ARG	Peptide
44	AG	121	SER	Peptide
44	AG	30	THR	Peptide
44	AG	76	ALA	Peptide
54	AR	131	ALA	Peptide
63	Aa	115	LYS	Peptide
1	BA	94	GLY	Peptide
2	BB	177	GLN	Peptide
2	BB	178	GLY	Peptide
15	BY	34	ASN	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	51	0
2	BB	1709	0	1784	52	0
3	BC	1635	0	1723	38	0
4	BE	2068	0	2154	44	0
5	BG	1820	0	1918	46	0
6	BH	1481	0	1572	30	0
7	BI	1489	0	1525	33	0
8	BJ	1494	0	1573	21	0
9	BL	1244	0	1314	13	0
10	BN	1192	0	1255	16	0
11	BO	941	0	979	24	0
12	BV	684	0	672	16	0
13	BW	1021	0	1060	27	0
14	BX	1121	0	1196	20	0
15	BY	1073	0	1132	21	0
16	Ba	769	0	818	17	0
17	Bb	610	0	633	10	0
18	Be	475	0	525	8	0
19	BD	1734	0	1817	29	0
20	BF	1609	0	1675	61	0
21	BK	817	0	804	21	0
22	BP	991	0	1035	33	0
23	BQ	1105	0	1166	39	0
24	BR	975	0	1039	19	0
25	BS	1192	0	1222	37	0
26	BT	1095	0	1114	30	0
27	BU	855	0	917	22	0
28	BZ	558	0	598	27	0
29	Bc	497	0	535	11	0
30	Bd	443	0	436	11	0
31	Bg	2401	0	2356	61	0
32	Bf	605	0	654	17	0
33	BM	935	0	975	20	0
34	B5	38004	0	19140	573	0
35	AA	1878	0	1946	28	0
36	AB	3080	0	3158	57	0
37	AC	2748	0	2859	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	A1	68445	0	34457	654	0
39	A3	2579	0	1304	32	0
40	A4	3353	0	1695	37	0
41	AD	2341	0	2290	35	0
42	AE	1239	0	1326	18	0
43	AF	1784	0	1862	18	0
44	AG	1798	0	1894	28	0
45	AH	1510	0	1576	22	0
46	AI	1672	0	1711	23	0
47	AJ	1353	0	1383	30	0
48	AL	1543	0	1608	14	0
49	AM	1053	0	1149	18	0
50	AN	1720	0	1779	26	0
51	AO	1555	0	1659	18	0
52	AP	1388	0	1423	18	0
53	AQ	1441	0	1543	17	0
54	AR	1521	0	1617	19	0
55	AS	1445	0	1487	28	0
56	AT	1276	0	1323	27	0
57	AU	796	0	812	0	0
58	AV	1003	0	1048	17	0
59	AW	521	0	551	7	0
60	AX	968	0	1036	5	0
61	AY	993	0	1081	17	0
62	AZ	1092	0	1155	19	0
63	Aa	1173	0	1215	29	0
64	Ab	462	0	491	5	0
65	Ac	743	0	797	11	0
66	Ad	890	0	938	7	0
67	Ae	1020	0	1089	11	0
68	Af	850	0	880	19	0
69	Ag	880	0	945	12	0
70	Ah	969	0	1078	13	0
71	Ai	771	0	849	9	0
72	Aj	681	0	687	13	0
73	Ak	612	0	682	13	0
74	Al	436	0	475	6	0
75	Am	417	0	459	9	0
76	An	233	0	284	9	0
77	Ao	819	0	886	15	0
78	Ap	694	0	738	13	0
79	E	1718	0	1811	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	EC	4090	0	2068	55	0
81	A1	174	0	0	0	0
81	A3	2	0	0	0	0
81	A4	4	0	0	0	0
81	AB	2	0	0	0	0
81	AI	1	0	0	0	0
81	AL	1	0	0	0	0
81	AP	1	0	0	0	0
81	AR	1	0	0	0	0
81	Ae	1	0	0	0	0
81	Af	1	0	0	0	0
81	Aj	2	0	0	0	0
81	B5	55	0	0	0	0
81	BN	1	0	0	0	0
81	Ba	1	0	0	0	0
82	Ao	1	0	0	0	0
All	All	206055	0	152043	2472	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 7.

All (2472) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1222:G:N2	38:A1:1286:A:H62	1.51	1.09
38:A1:1222:G:H21	38:A1:1286:A:N6	1.60	0.99
38:A1:2138:A:HO2'	72:Aj:2:GLY:N	1.66	0.92
34:B5:1687:U:H3	34:B5:1715:G:H1	1.12	0.91
34:B5:1213:G:H1	34:B5:1450:U:H3	1.18	0.87
38:A1:1222:G:H21	38:A1:1286:A:H62	0.89	0.87
34:B5:1588:G:H1	34:B5:1608:U:H3	0.92	0.87
34:B5:1684:U:H3	34:B5:1717:G:H1	1.24	0.83
38:A1:2499:U:H3'	38:A1:2500:A:H5''	1.60	0.82
79:E:120:VAL:HB	79:E:124:LEU:HB3	1.61	0.80
51:AO:27[A]:LEU:HD21	51:AO:102[A]:LEU:HB2	1.65	0.78
79:E:125:GLY:HA2	79:E:128:LEU:HB2	1.65	0.78
34:B5:1697:G:H1	34:B5:1704:U:H3	0.82	0.77
31:Bg:289:ALA:HB2	31:Bg:311:ARG:HH22	1.48	0.76
1:BA:180:GLU:HA	1:BA:183:ARG:HB2	1.68	0.76
79:E:76:ARG:HB3	79:E:144:LEU:HD12	1.68	0.75
20:BF:98:MET:HE1	34:B5:1610:G:H4'	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:47:ARG:HH22	6:BH:176:LEU:HB2	1.52	0.73
34:B5:647:G:H21	34:B5:687:G:H1	1.36	0.73
4:BE:71:LYS:HB2	4:BE:91:THR:HB	1.71	0.73
32:Bf:78:LYS:NZ	34:B5:1432:U:O4	2.20	0.73
35:AA:215:ASN:ND2	38:A1:2969:A:N7	2.37	0.72
27:BU:69:LYS:O	30:Bd:44:ARG:NH1	2.22	0.72
46:AI:36:LEU:HD11	46:AI:69:ARG:HH11	1.55	0.72
79:E:63:MET:H	79:E:152:ARG:HH22	1.37	0.72
38:A1:170:G:OP1	48:AL:128:ARG:NH2	2.23	0.72
34:B5:1673:G:H1	34:B5:1728:A:H2	1.38	0.72
31:Bg:89:LEU:HB2	31:Bg:103:PHE:HB2	1.72	0.71
38:A1:2276:G:OP1	76:An:16:LYS:NZ	2.24	0.71
40:A4:75:G:OP2	61:AY:74:TYR:OH	2.07	0.71
15:BY:37:LYS:HG3	34:B5:522:U:H5''	1.70	0.71
33:BM:46:ARG:NH2	34:B5:1229:G:O5'	2.24	0.71
17:Bb:19:HIS:HD2	17:Bb:21:LEU:H	1.39	0.70
18:Be:53:LYS:HG2	18:Be:54:ARG:HG2	1.73	0.70
34:B5:1687:U:O4	34:B5:1715:G:O6	2.09	0.70
14:BX:125:VAL:HG12	14:BX:126:LYS:HG3	1.74	0.70
80:EC:6853:G:H22	80:EC:6875:C:H42	1.37	0.70
1:BA:189:VAL:HG23	12:BV:44:ARG:HH22	1.57	0.70
30:Bd:36:LEU:HB3	30:Bd:38:ILE:HG12	1.73	0.70
51:AO:61[A]:ALA:HA	51:AO:70[A]:PRO:HD2	1.74	0.69
21:BK:2:LEU:HA	34:B5:1257:U:H2'	1.73	0.69
32:Bf:105:TYR:HD1	32:Bf:118:ARG:HG3	1.57	0.69
17:Bb:61:THR:HG22	17:Bb:62:ILE:HD12	1.73	0.69
31:Bg:34:LEU:HB3	31:Bg:73:LEU:HD11	1.75	0.69
34:B5:1673:G:O6	34:B5:1728:A:N1	2.25	0.69
38:A1:173:G:H1	38:A1:244:G:H22	1.39	0.69
80:EC:6922:G:H1	80:EC:6931:U:H3	1.39	0.69
20:BF:70:VAL:HG22	20:BF:72:HIS:H	1.57	0.69
34:B5:190:C:H5'	34:B5:196:G:H22	1.58	0.69
33:BM:46:ARG:NH1	34:B5:1229:G:OP2	2.26	0.69
38:A1:3042:U:OP2	38:A1:3092:C:N4	2.26	0.69
34:B5:1339:C:O2'	34:B5:1341:A:N7	2.26	0.68
58:AV:32:ARG:HH21	58:AV:64:LYS:HD2	1.58	0.68
8:BJ:59:LEU:HB3	8:BJ:93:LEU:HD21	1.74	0.68
56:AT:76:ILE:HD12	56:AT:89:LEU:HD13	1.74	0.68
80:EC:6867:C:H2'	80:EC:6868:C:H6	1.58	0.68
34:B5:1656:U:HO2'	38:A1:2292:U:HO2'	1.39	0.68
38:A1:3278:C:OP1	68:Af:54:ARG:NH2	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:BQ:127:LYS:HA	23:BQ:134:ALA:HA	1.75	0.68
34:B5:1584:G:N2	34:B5:1611:A:OP2	2.27	0.68
47:AJ:49:LYS:HB3	47:AJ:62:ASN:HA	1.76	0.68
6:BH:129:LEU:HD23	6:BH:130:VAL:HG13	1.76	0.68
15:BY:7:ILE:HD12	15:BY:43:LYS:HG2	1.74	0.68
25:BS:57:ARG:NH1	28:BZ:40:VAL:O	2.27	0.67
36:AB:66:LYS:HE3	58:AV:88:ARG:HH21	1.59	0.67
38:A1:1272:C:H3'	38:A1:1273:A:H8	1.59	0.67
39:A3:40:C:O2	47:AJ:72:ARG:NH1	2.27	0.67
79:E:76:ARG:HH21	79:E:144:LEU:HG	1.58	0.67
31:Bg:178:VAL:HB	31:Bg:192:PHE:HB2	1.76	0.67
34:B5:992:A:O2'	34:B5:1785:U:O2	2.12	0.67
38:A1:784:A:OP2	53:AQ:69:ARG:NH1	2.26	0.67
54:AR:175:GLN:OE1	54:AR:176:ARG:NH1	2.27	0.67
47:AJ:39:GLN:HG2	47:AJ:115:LYS:HG3	1.77	0.67
63:Aa:86:LYS:NZ	63:Aa:90:TYR:OH	2.27	0.67
7:BI:87:ASN:HB3	7:BI:90:LEU:HG	1.77	0.67
32:Bf:78:LYS:N	34:B5:1271:OMG:OP1	2.27	0.67
37:AC:325:LEU:O	43:AF:41:ARG:NH2	2.28	0.67
34:B5:217:A:N1	34:B5:844:A:O2'	2.28	0.67
20:BF:58:LEU:HD12	20:BF:138:THR:HG22	1.77	0.67
58:AV:87:ARG:HH22	58:AV:137:VAL:HG21	1.60	0.67
5:BG:2:LYS:HB2	5:BG:108:VAL:HG22	1.76	0.66
38:A1:2193:U:H5''	38:A1:2194:G:H5'	1.77	0.66
5:BG:140:ASN:ND2	34:B5:168:A:OP1	2.28	0.66
4:BE:129:VAL:HG12	4:BE:139:VAL:HG12	1.76	0.66
25:BS:57:ARG:NH2	28:BZ:74:SER:OG	2.27	0.66
1:BA:84:ARG:NH2	24:BR:82:ASP:O	2.29	0.66
37:AC:98:ARG:NH2	38:A1:804:C:OP1	2.24	0.66
38:A1:1639:C:OP2	69:Ag:74:ARG:NH2	2.28	0.66
10:BN:124:ARG:NH2	34:B5:967:A:OP2	2.27	0.66
20:BF:37:GLN:HE21	23:BQ:53:LEU:HA	1.61	0.66
38:A1:2450:G:H1	38:A1:2497:U:H3	1.43	0.66
5:BG:66:GLY:HA2	34:B5:1681:A:H1'	1.78	0.66
12:BV:22:ARG:NH2	13:BW:19:LYS:O	2.29	0.66
36:AB:240:ARG:NH2	38:A1:1907:C:O2	2.28	0.66
51:AO:37[A]:ARG:HG3	51:AO:108[A]:ILE:HG13	1.78	0.66
3:BC:205:ARG:NH2	34:B5:7:G:N7	2.44	0.66
23:BQ:77:GLN:NE2	34:B5:1482:C:O2'	2.28	0.66
26:BT:86:ARG:NH2	34:B5:1601:G:OP1	2.29	0.65
80:EC:6770:U:H3	80:EC:6772:G:H21	1.41	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:35:PRO:HG3	12:BV:87:ARG:HH12	1.62	0.65
6:BH:158:ASP:HB3	6:BH:161:GLN:HE22	1.60	0.65
80:EC:6786:A:H61	80:EC:6810:U:H3	1.44	0.65
36:AB:296:THR:HG23	36:AB:298:PHE:H	1.61	0.65
38:A1:2185:G:O2'	38:A1:2314:U:OP2	2.13	0.65
46:AI:30:LYS:HG3	46:AI:63:GLU:HG3	1.79	0.65
59:AW:54:LEU:HA	59:AW:57:LYS:HZ3	1.61	0.65
4:BE:254:ARG:O	4:BE:258:GLN:NE2	2.28	0.65
1:BA:126:PRO:HG3	1:BA:147:THR:HG22	1.78	0.65
2:BB:89:ASP:HB3	2:BB:223:PHE:HZ	1.61	0.65
20:BF:219:ARG:HD3	20:BF:222:LYS:HE3	1.79	0.65
58:AV:14:SER:O	58:AV:81:GLN:NE2	2.29	0.65
65:Ac:36:GLN:HG3	65:Ac:38:LYS:HG3	1.77	0.65
8:BJ:30:LEU:HD12	8:BJ:105:LEU:HD12	1.78	0.65
41:AD:64:ILE:HG13	41:AD:109:THR:HG21	1.79	0.65
39:A3:7:G:OP1	41:AD:33:ARG:NH1	2.29	0.65
38:A1:2854:U:OP2	46:AI:3:ARG:NH2	2.28	0.65
79:E:26:ARG:HG2	79:E:28:PHE:H	1.62	0.65
7:BI:172:ARG:HE	7:BI:175:GLN:HG3	1.60	0.64
30:Bd:56:ARG:NH2	34:B5:1334:U:O2	2.30	0.64
13:BW:51:GLU:HG3	17:Bb:8:LEU:HD21	1.79	0.64
63:Aa:56:VAL:HG12	63:Aa:57:GLY:H	1.62	0.64
6:BH:49:ILE:HD13	6:BH:172:VAL:HG23	1.78	0.64
20:BF:225:ARG:NH2	29:Bc:57:MET:SD	2.71	0.64
26:BT:122:ARG:NH1	34:B5:1499:G:OP1	2.31	0.64
38:A1:845:G:H21	38:A1:848:A:H2	1.45	0.64
28:BZ:77:ARG:NH2	34:B5:1533:C:OP2	2.31	0.64
31:Bg:262:VAL:HG13	31:Bg:271:VAL:HB	1.80	0.64
38:A1:2497:U:H1'	38:A1:2498:U:H5'	1.79	0.64
2:BB:69:CYS:SG	11:BO:114:ARG:NH1	2.70	0.64
16:Ba:2:PRO:HB3	34:B5:1142:A:H5''	1.79	0.64
18:Be:31:LYS:HD3	34:B5:545:A:H2'	1.80	0.64
38:A1:2542:U:H4'	38:A1:2543:U:H5'	1.80	0.64
40:A4:58:G:O6	72:Aj:63:ARG:NH1	2.31	0.64
79:E:70:ASP:HB3	79:E:115:VAL:HG11	1.80	0.64
25:BS:132:ARG:NH2	34:B5:1173:C:OP1	2.30	0.64
36:AB:83:PRO:O	36:AB:165:GLN:NE2	2.31	0.64
36:AB:173:GLN:NE2	38:A1:3313:U:OP1	2.30	0.64
41:AD:22:ARG:HH21	41:AD:27:LYS:HB3	1.63	0.64
5:BG:154:ARG:NE	34:B5:78:A:N7	2.44	0.64
34:B5:1672:G:H2'	34:B5:1673:G:C8	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1245:A:H5'	38:A1:1246:G:H5''	1.80	0.64
2:BB:168:ILE:HG12	2:BB:197:ILE:HD12	1.80	0.64
25:BS:140:THR:HA	25:BS:143:ARG:HH11	1.63	0.64
39:A3:11:A:N7	56:AT:20:ARG:NH2	2.44	0.64
34:B5:900:A:H3'	34:B5:901:G:H21	1.63	0.63
22:BP:40:ARG:NH2	34:B5:1551:U:O4	2.31	0.63
26:BT:105:LEU:HD13	26:BT:122:ARG:HD2	1.78	0.63
38:A1:1491:A:H5''	72:Aj:14:LYS:HE2	1.80	0.63
46:AI:38:LYS:HE3	46:AI:83:ASP:HB3	1.80	0.63
79:E:149:THR:HA	79:E:152:ARG:HG2	1.80	0.63
5:BG:142:ARG:HH21	5:BG:151:ASP:H	1.46	0.63
34:B5:1594:G:OP2	34:B5:1596:C:N4	2.31	0.63
38:A1:3092:C:O2'	38:A1:3094:A:OP2	2.15	0.63
11:BO:87:GLY:HA2	11:BO:92:LYS:HG2	1.79	0.63
13:BW:53:ILE:HB	13:BW:60:LYS:HB2	1.80	0.63
14:BX:30:LYS:NZ	34:B5:1132:A:OP1	2.31	0.63
20:BF:109:LYS:NZ	34:B5:1474:G:OP1	2.32	0.63
22:BP:78:THR:HA	34:B5:1241:G:H4'	1.81	0.63
38:A1:994:G:N2	38:A1:995:U:O4	2.30	0.63
38:A1:2720:G:OP1	53:AQ:180:ARG:NH2	2.31	0.63
28:BZ:74:SER:HA	28:BZ:77:ARG:HB2	1.80	0.63
31:Bg:42:LEU:HB2	31:Bg:61:PHE:HB2	1.81	0.63
38:A1:284:A:OP2	77:Ao:41:ARG:NH1	2.32	0.63
2:BB:126:THR:OG1	2:BB:136:ARG:NH1	2.32	0.63
31:Bg:250:TYR:HE2	31:Bg:265:LEU:HB3	1.63	0.63
1:BA:111:ILE:HD11	34:B5:1292:G:H21	1.64	0.62
5:BG:22:HIS:HE1	36:AB:298:PHE:HA	1.64	0.62
46:AI:77:THR:HG22	46:AI:82:ARG:HA	1.80	0.62
47:AJ:50:ALA:HB3	47:AJ:61:ARG:HA	1.81	0.62
15:BY:29:HIS:HB2	15:BY:32:ARG:HB2	1.81	0.62
26:BT:7:ARG:NH1	34:B5:1364:G:O2'	2.32	0.62
27:BU:77:LYS:NZ	34:B5:1195:C:OP1	2.32	0.62
33:BM:101:ALA:HB1	33:BM:121:VAL:HG21	1.80	0.62
25:BS:81:ILE:HG22	25:BS:83:ALA:H	1.63	0.62
34:B5:58:U:O2'	34:B5:451:A:N3	2.32	0.62
36:AB:60:LEU:HD21	36:AB:62:ARG:HE	1.64	0.62
37:AC:2:SER:OG	37:AC:3:ARG:N	2.33	0.62
80:EC:6771:U:O2'	80:EC:6777:C:N3	2.32	0.62
14:BX:96:VAL:HA	14:BX:127:VAL:HG21	1.82	0.62
34:B5:907:A:N3	34:B5:997:G:O2'	2.31	0.62
38:A1:2908:G:O2'	75:Am:114:LYS:NZ	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:34:ALA:O	2:BB:41:ARG:NH1	2.33	0.62
8:BJ:3:ARG:NH2	34:B5:39:A:OP1	2.33	0.62
23:BQ:13:LYS:HD2	23:BQ:79:TYR:HB3	1.82	0.62
14:BX:24:TRP:HE3	14:BX:30:LYS:HD2	1.64	0.62
34:B5:1295:G:H1	34:B5:1302:U:H3	1.47	0.62
38:A1:619:A:OP1	52:AP:167:ARG:NH1	2.33	0.62
56:AT:48:ILE:HG13	56:AT:94:GLU:HG2	1.82	0.62
34:B5:1585:U:H3	34:B5:1611:A:H2	1.48	0.62
38:A1:708:G:N2	38:A1:711:A:OP2	2.30	0.62
21:BK:15:LEU:HD13	21:BK:21:VAL:HG23	1.82	0.62
34:B5:844:A:H2'	34:B5:845:G:H8	1.65	0.62
36:AB:244:ARG:NH1	38:A1:2948:OMC:OP1	2.33	0.62
42:AE:175:LYS:O	49:AM:117:ARG:NH2	2.32	0.62
38:A1:362:U:O4	72:Aj:24:ARG:NH2	2.32	0.61
14:BX:6:PRO:HG3	14:BX:14:LYS:HD3	1.83	0.61
33:BM:22:VAL:HG23	33:BM:135:MET:HE1	1.81	0.61
34:B5:705:U:H2'	34:B5:730:G:H1	1.64	0.61
4:BE:94:ALA:HB1	15:BY:16:PRO:HB2	1.82	0.61
7:BI:98:LYS:HB3	34:B5:329:G:H5''	1.83	0.61
21:BK:77:ARG:HD3	21:BK:84:GLU:HA	1.81	0.61
22:BP:100:LYS:HD2	34:B5:1211:A:H4'	1.83	0.61
38:A1:242:C:H2'	38:A1:243:G:C8	2.36	0.61
38:A1:1348:U:OP1	53:AQ:39:ARG:NH1	2.33	0.61
31:Bg:258:THR:OG1	31:Bg:275:ARG:NH1	2.33	0.61
66:Ad:55:LEU:HB2	66:Ad:95:PRO:HD3	1.83	0.61
38:A1:3268:A:OP1	42:AE:46:ARG:NH2	2.33	0.61
40:A4:9:A:H2'	40:A4:10:A:C8	2.36	0.61
79:E:6:SER:OG	79:E:10:ARG:NH1	2.34	0.61
34:B5:1183:A:N3	34:B5:1210:C:O2'	2.30	0.61
39:A3:7:G:H8	41:AD:22:ARG:HH11	1.47	0.61
34:B5:972:G:O2'	38:A1:847:A:N6	2.34	0.61
35:AA:37:ARG:NH2	38:A1:2526:C:OP1	2.34	0.61
37:AC:150:LEU:HD23	37:AC:249:ILE:HG12	1.81	0.61
3:BC:44:LEU:HD22	3:BC:49:LYS:HD2	1.83	0.61
34:B5:1208:A:O2'	34:B5:1270:G:OP2	2.18	0.61
55:AS:46:GLN:NE2	55:AS:51:VAL:O	2.34	0.61
3:BC:52:THR:OG1	3:BC:54:GLU:OE1	2.19	0.60
15:BY:7:ILE:HG23	15:BY:27:VAL:HG12	1.83	0.60
24:BR:2:GLY:N	34:B5:1403:C:OP1	2.34	0.60
25:BS:41:ARG:NH1	34:B5:1565:C:OP1	2.32	0.60
35:AA:9:ARG:NH2	38:A1:912:G:OP2	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AH:163:GLN:HB3	45:AH:166:ARG:HH21	1.65	0.60
62:AZ:22:LYS:NZ	62:AZ:129:TRP:O	2.32	0.60
73:Ak:24:THR:HG22	73:Ak:76:ASN:HB3	1.83	0.60
80:EC:6787:U:H3	80:EC:6809:G:H1	1.48	0.60
38:A1:1750:A:OP1	73:Ak:44:LYS:NZ	2.28	0.60
34:B5:871:G:H2'	34:B5:872:G:C8	2.36	0.60
38:A1:2960:C:H2'	38:A1:2961:G:C8	2.37	0.60
38:A1:3291:G:H2'	38:A1:3292:A:H8	1.65	0.60
1:BA:21:ASN:HD22	1:BA:24:LEU:HD11	1.67	0.60
34:B5:1552:U:O2'	34:B5:1597:A:N3	2.29	0.60
36:AB:57:VAL:HG22	36:AB:73:VAL:HG22	1.82	0.60
38:A1:1813:A:H4'	38:A1:1817:G:H1'	1.83	0.60
5:BG:197:ASN:ND2	34:B5:126:A:OP2	2.33	0.60
34:B5:1515:A:O2'	34:B5:1518:C:N4	2.35	0.60
38:A1:1132:C:H2'	38:A1:1133:A2M:H8	1.83	0.60
38:A1:1311:G:N2	51:AO:86[A]:GLY:O	2.33	0.60
38:A1:2588:U:OP1	44:AG:241:LYS:NZ	2.29	0.60
38:A1:3050:U:O2'	59:AW:16:GLY:O	2.18	0.60
80:EC:6849:A:N6	80:EC:6880:G:N3	2.50	0.60
1:BA:41:ARG:NH1	24:BR:103:ASP:OD2	2.34	0.60
1:BA:127:ARG:NH2	1:BA:150:ASP:O	2.34	0.60
10:BN:3:ARG:HB3	10:BN:6:SER:HB3	1.83	0.60
25:BS:56:LYS:HZ3	25:BS:61:LEU:HD23	1.66	0.60
26:BT:69:LYS:NZ	34:B5:1366:U:O3'	2.35	0.60
38:A1:651:G:O2'	38:A1:1435:A:OP1	2.19	0.60
72:Aj:60:GLY:HA2	72:Aj:64:MET:HE2	1.83	0.60
79:E:138:VAL:HG13	79:E:147:LYS:HG3	1.83	0.60
8:BJ:3:ARG:NH1	8:BJ:4:ALA:O	2.34	0.60
22:BP:61:ARG:NH2	22:BP:88:GLU:O	2.34	0.60
35:AA:178:PRO:HG2	78:Ap:26:VAL:HG23	1.83	0.60
37:AC:20:LEU:HD11	37:AC:252:GLU:HG3	1.83	0.60
60:AX:103:TYR:O	60:AX:138:ARG:NH2	2.34	0.60
44:AG:52:TRP:O	44:AG:57:ARG:NH1	2.34	0.60
54:AR:21:LYS:HE3	54:AR:55:VAL:HA	1.83	0.60
79:E:204:LEU:H	79:E:217:TYR:HB3	1.67	0.60
34:B5:536:C:H3'	34:B5:537:G:H8	1.65	0.60
79:E:65:ILE:HD11	79:E:111:ILE:HG12	1.84	0.60
38:A1:2584:G:O2'	44:AG:240:ASN:OD1	2.20	0.60
40:A4:106:C:H4'	40:A4:107:G:H5''	1.84	0.60
2:BB:88:VAL:HG12	2:BB:98:THR:HG22	1.83	0.59
5:BG:85:ARG:O	5:BG:87:ARG:NH1	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:BQ:71:GLY:O	23:BQ:77:GLN:NE2	2.31	0.59
26:BT:134:ARG:HH22	34:B5:1360:A:H5''	1.66	0.59
38:A1:525:C:OP2	49:AM:77:ARG:NH1	2.34	0.59
38:A1:1324:U:OP1	55:AS:1:MET:N	2.35	0.59
38:A1:1419:A:OP1	40:A4:20:U:O2'	2.20	0.59
37:AC:361:HIS:O	55:AS:28:ARG:NH1	2.35	0.59
38:A1:3275:U:O2'	68:Af:99:ARG:NH1	2.35	0.59
38:A1:3319:U:H5'	38:A1:3320:A:H5'	1.83	0.59
63:Aa:112:ILE:HB	63:Aa:130:VAL:HG12	1.84	0.59
4:BE:123:LEU:HD23	4:BE:236:ILE:HD11	1.84	0.59
6:BH:139:ARG:HB2	6:BH:151:LYS:HB3	1.85	0.59
10:BN:64:ARG:NH2	34:B5:862:A:OP2	2.34	0.59
31:Bg:156:VAL:HG22	31:Bg:169:ILE:HG22	1.84	0.59
34:B5:1291:G:H1	34:B5:1324:G:H22	1.49	0.59
36:AB:250:ALA:HB3	38:A1:2880:U:H1'	1.84	0.59
38:A1:3205:G:OP2	38:A1:3206:C:N4	2.33	0.59
38:A1:2895:G:O2'	75:Am:100:TYR:O	2.18	0.59
79:E:38:LEU:HD12	79:E:200:ASN:HB3	1.85	0.59
2:BB:122:GLU:OE2	2:BB:213:ARG:NH2	2.35	0.59
38:A1:1447:G:N7	52:AP:25:SER:OG	2.34	0.59
5:BG:132:ARG:NH1	34:B5:150:U:O4'	2.36	0.59
11:BO:29:HIS:HD2	11:BO:41:ARG:HD3	1.68	0.59
38:A1:1717:U:H2'	38:A1:1718:G:C8	2.37	0.59
22:BP:98:ASN:HB2	22:BP:122:THR:HA	1.84	0.59
27:BU:23:ARG:NH2	34:B5:1347:U:OP2	2.35	0.59
33:BM:76:GLU:OE2	33:BM:80:ASN:ND2	2.36	0.59
38:A1:508:U:OP1	43:AF:211:SER:OG	2.16	0.59
38:A1:1306:G:O6	38:A1:2366:C:O2'	2.21	0.59
6:BH:143:LEU:HD12	6:BH:147:ASN:HB2	1.85	0.59
13:BW:22:LYS:HD3	17:Bb:3:LEU:HD12	1.85	0.59
19:BD:31:GLU:HG3	19:BD:107:PHE:HE1	1.68	0.59
34:B5:1188:G:H3'	34:B5:1189:A:H8	1.68	0.59
38:A1:1940:G:H21	38:A1:3362:A:H8	1.49	0.59
79:E:57:ASN:OD1	79:E:182:GLN:NE2	2.35	0.59
80:EC:6833:G:O2'	80:EC:6872:A:N6	2.34	0.59
5:BG:180:THR:HG22	5:BG:182:GLN:H	1.68	0.59
7:BI:110:ARG:NH1	7:BI:121:LEU:O	2.33	0.59
20:BF:196:GLU:OE2	20:BF:200:ASN:ND2	2.36	0.59
24:BR:33:ARG:NH1	31:Bg:109:ASP:OD2	2.36	0.59
31:Bg:25:THR:HG21	31:Bg:295:SER:HA	1.84	0.59
38:A1:655:C:H2'	38:A1:656:A:H8	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2724:OMU:OP2	38:A1:2726:C:N4	2.36	0.59
4:BE:19:LEU:HD11	4:BE:108:ARG:HD2	1.83	0.58
22:BP:97:TYR:OH	34:B5:1211:A:N3	2.34	0.58
38:A1:3199:G:H4'	49:AM:6:ILE:HD13	1.84	0.58
79:E:59:PRO:O	79:E:171:ASN:ND2	2.36	0.58
13:BW:27:ILE:HB	13:BW:61:ILE:HB	1.85	0.58
19:BD:116:ARG:NH2	19:BD:120:TYR:OH	2.36	0.58
20:BF:81:ARG:HD2	34:B5:1615:C:H2'	1.85	0.58
22:BP:82:ASN:OD1	34:B5:1555:A:O2'	2.18	0.58
43:AF:83:LEU:HD11	43:AF:116:PHE:HB3	1.85	0.58
45:AH:132:VAL:HG11	45:AH:157:ASN:HD22	1.67	0.58
5:BG:13:GLN:NE2	34:B5:151:G:N3	2.51	0.58
12:BV:17:CYS:HB2	12:BV:56:SER:HB3	1.84	0.58
31:Bg:41:THR:HG22	31:Bg:62:LYS:HG3	1.85	0.58
38:A1:2213:A:H2'	38:A1:2214:A:C8	2.38	0.58
38:A1:2466:G:O2'	79:E:60:ARG:NH1	2.36	0.58
1:BA:49:ASN:HA	24:BR:109:LEU:HD11	1.85	0.58
21:BK:10:LYS:HD2	21:BK:37:THR:HB	1.85	0.58
21:BK:29:GLN:OE1	21:BK:39:ASN:ND2	2.32	0.58
27:BU:59:PRO:HG3	34:B5:1381:U:H4'	1.84	0.58
38:A1:723:U:HO2'	64:Ab:29:TYR:HH	1.51	0.58
38:A1:1551:C:HO2'	38:A1:2170:U:HO2'	1.50	0.58
51:AO:65[A]:ASN:HB3	51:AO:68[A]:ARG:HG2	1.84	0.58
47:AJ:43:GLN:NE2	47:AJ:70:THR:O	2.35	0.58
30:Bd:24:CYS:HG	34:B5:1433:G:HO2'	1.51	0.58
59:AW:4:GLU:HB2	59:AW:13:ILE:HB	1.85	0.58
80:EC:6842:U:H5''	80:EC:6844:A:H5'	1.86	0.58
1:BA:69:ASN:ND2	3:BC:244:SER:O	2.36	0.58
2:BB:165:ARG:NH1	34:B5:947:U:OP1	2.37	0.58
5:BG:22:HIS:CE1	36:AB:298:PHE:HA	2.39	0.58
26:BT:129:GLN:HE22	34:B5:1359:C:H4'	1.68	0.58
34:B5:1354:G:O6	34:B5:1369:U:O2	2.21	0.58
34:B5:1393:C:H2'	34:B5:1394:G:H8	1.68	0.58
34:B5:1592:A:H2'	34:B5:1593:A:H8	1.68	0.58
75:Am:127:LEU:HG	75:Am:128:LYS:HG3	1.86	0.58
19:BD:78:LYS:NZ	21:BK:34:GLU:OE1	2.37	0.58
20:BF:92:ARG:NH1	20:BF:169:ASN:OD1	2.36	0.58
32:Bf:121:CYS:SG	32:Bf:123:ASN:ND2	2.76	0.58
34:B5:1575:G7M:O2'	34:B5:1576:A:O4'	2.17	0.58
2:BB:82:ARG:HH22	2:BB:191:GLU:HG3	1.69	0.58
34:B5:126:A:H62	34:B5:291:G:H21	1.50	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1291:G:H22	34:B5:1324:G:H22	1.52	0.58
38:A1:664:U:H2'	38:A1:665:A:C8	2.39	0.58
48:AL:180:ARG:HD3	71:AI:11:LEU:HD11	1.86	0.58
58:AV:23:MET:HE3	58:AV:100:GLY:HA3	1.86	0.58
23:BQ:75:VAL:HG12	34:B5:1609:U:H5''	1.85	0.57
27:BU:57:ARG:HD2	34:B5:1382:A:H1'	1.86	0.57
34:B5:110:U:OP1	34:B5:753:A:O2'	2.22	0.57
38:A1:649:A2M:OP2	38:A1:2868:U:O2'	2.22	0.57
52:AP:122:ALA:HB3	52:AP:143:PRO:HB2	1.86	0.57
2:BB:103:MET:HE3	2:BB:215:VAL:HG23	1.85	0.57
31:Bg:197:SER:OG	31:Bg:217:ASP:N	2.37	0.57
34:B5:1778:G:O6	76:An:8:LYS:NZ	2.37	0.57
35:AA:118:GLU:OE2	38:A1:2177:G:N2	2.36	0.57
43:AF:121:LYS:HB2	56:AT:133:ALA:HB3	1.86	0.57
2:BB:176:VAL:O	2:BB:177:GLN:HG2	2.04	0.57
7:BI:152:ILE:HG13	7:BI:153:GLU:H	1.68	0.57
19:BD:76:ARG:HB2	21:BK:22:VAL:HG11	1.86	0.57
34:B5:1488:G:O2'	34:B5:1494:C:O2	2.19	0.57
38:A1:417:A:H2'	38:A1:418:A:C8	2.38	0.57
38:A1:2197:OMC:H5''	38:A1:2242:A:H61	1.69	0.57
2:BB:27:LYS:NZ	2:BB:48:VAL:O	2.37	0.57
20:BF:102:ARG:NH1	34:B5:1471:A:O2'	2.38	0.57
29:Bc:26:THR:N	29:Bc:44:VAL:O	2.36	0.57
38:A1:799:G:O2'	48:AL:18:TRP:NE1	2.37	0.57
38:A1:3067:C:H3'	54:AR:62:ARG:HH22	1.69	0.57
38:A1:3354:U:H5'	38:A1:3355:U:H5'	1.86	0.57
44:AG:81:THR:OG1	44:AG:155:ASN:ND2	2.37	0.57
46:AI:150:GLU:OE2	46:AI:153:ARG:NH1	2.38	0.57
68:Af:32:ILE:HG12	68:Af:100:ILE:HD13	1.87	0.57
18:Be:42:ARG:NH2	34:B5:590:C:OP2	2.37	0.57
24:BR:63:LYS:NZ	31:Bg:283:LYS:O	2.37	0.57
38:A1:740:G:O2'	53:AQ:74:GLU:OE2	2.22	0.57
47:AJ:60:ARG:NH1	77:Ao:103:ALA:O	2.38	0.57
61:AY:74:TYR:HE2	61:AY:77:LYS:HG3	1.68	0.57
68:Af:56:SER:O	68:Af:63:LYS:NZ	2.36	0.57
34:B5:852:C:H2'	34:B5:853:G:C8	2.39	0.57
38:A1:1661:G:H2'	38:A1:1662:G:C8	2.40	0.57
38:A1:2468:A:O2'	38:A1:2477:G:N2	2.35	0.57
45:AH:5:GLN:HE22	45:AH:7:GLU:HB2	1.70	0.57
9:BL:129:ARG:HD3	34:B5:115:G:H5'	1.87	0.57
20:BF:63:GLN:NE2	20:BF:86:GLN:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1062:A:H3'	34:B5:1063:U:H6	1.70	0.57
38:A1:3116:G:OP1	38:A1:3116:G:N2	2.38	0.57
47:AJ:92:ARG:HA	47:AJ:172:LEU:H	1.69	0.57
79:E:162:VAL:HG12	79:E:164:CYS:H	1.69	0.57
2:BB:153:HIS:HE1	34:B5:1044:U:H5''	1.70	0.57
19:BD:164:VAL:HA	19:BD:168:ILE:HD13	1.86	0.57
23:BQ:12:LYS:HG2	23:BQ:17:THR:HG23	1.85	0.57
28:BZ:61:SER:HA	28:BZ:99:ALA:HB3	1.85	0.57
31:Bg:24:ALA:HB3	31:Bg:73:LEU:HD13	1.86	0.57
34:B5:812:A:H62	34:B5:859:A:H5'	1.69	0.57
34:B5:1192:C:H2'	34:B5:1193:A:C8	2.39	0.57
65:Ac:95:ALA:HB2	65:Ac:101:LEU:HD13	1.86	0.57
68:Af:18:ARG:NH2	68:Af:20:LYS:O	2.38	0.57
19:BD:106:LYS:HG3	19:BD:175:VAL:HG22	1.87	0.57
34:B5:1202:A:N6	34:B5:1457:C:OP1	2.38	0.57
34:B5:1229:G:N2	34:B5:1255:G:O2'	2.37	0.57
36:AB:244:ARG:NH2	38:A1:2981:U:OP2	2.37	0.57
38:A1:2897:A:OP2	75:Am:124:LYS:NZ	2.36	0.57
47:AJ:14:ILE:HD12	47:AJ:77:GLU:HG3	1.86	0.57
20:BF:143:ARG:HD3	20:BF:144:GLU:HG2	1.86	0.57
38:A1:1119:C:H2'	38:A1:1120:A:H8	1.70	0.57
38:A1:1779:C:N4	38:A1:2102:U:OP1	2.33	0.57
39:A3:13:A:OP2	39:A3:67:G:N2	2.37	0.57
3:BC:238:SER:OG	3:BC:241:ASP:OD2	2.22	0.56
23:BQ:100:GLN:HA	23:BQ:103:ASN:HB2	1.87	0.56
34:B5:1295:G:N2	34:B5:1302:U:O2	2.31	0.56
38:A1:1669:C:H5'	69:Ag:30:LEU:HD11	1.86	0.56
26:BT:126:GLU:O	26:BT:130:ARG:NH1	2.38	0.56
34:B5:71:A:N6	34:B5:72:A:N3	2.53	0.56
34:B5:1588:G:O6	34:B5:1608:U:O4	2.23	0.56
38:A1:1223:A:N6	38:A1:1285:G:H21	2.04	0.56
40:A4:85:G:N1	61:AY:112:ASP:OD2	2.36	0.56
11:BO:18:ARG:HD2	34:B5:918:U:H4'	1.87	0.56
15:BY:132:ARG:NH2	34:B5:157:A:OP2	2.38	0.56
19:BD:28:GLU:HA	21:BK:58:GLN:HE22	1.69	0.56
24:BR:26:LEU:HD22	24:BR:58:MET:HE3	1.86	0.56
27:BU:58:LEU:HB2	27:BU:88:LYS:HB3	1.87	0.56
34:B5:1760:G:H1'	34:B5:1781:MA6:H2	1.86	0.56
38:A1:1493:G:O6	74:A1:2:ALA:N	2.38	0.56
38:A1:2219:A:H2'	38:A1:2220:A2M:H8	1.86	0.56
38:A1:2836:C:H5	38:A1:2852:C:H42	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:EC:6939:C:N4	80:EC:6940:U:H3	2.02	0.56
1:BA:183:ARG:NH1	1:BA:191:ARG:O	2.38	0.56
20:BF:123:VAL:HG11	28:BZ:59:TYR:HB2	1.88	0.56
38:A1:1323:G:H4'	55:AS:1:MET:HE3	1.85	0.56
38:A1:1740:U:H4'	38:A1:1741:A:H5'	1.86	0.56
42:AE:51:ARG:NH1	42:AE:161:ALA:O	2.38	0.56
45:AH:101:VAL:HG22	45:AH:114:VAL:HG22	1.87	0.56
19:BD:138:VAL:HG22	19:BD:184:ILE:HG22	1.87	0.56
23:BQ:18:ALA:HB2	23:BQ:69:VAL:HG23	1.87	0.56
24:BR:70:SER:HA	24:BR:74:GLN:HE21	1.71	0.56
38:A1:591:G:O2'	42:AE:17:ALA:O	2.23	0.56
38:A1:2284:C:N4	38:A1:2308:C:OP2	2.38	0.56
1:BA:35:PRO:O	1:BA:52:LYS:NZ	2.38	0.56
26:BT:70:GLN:HG3	26:BT:120:GLY:HA3	1.86	0.56
34:B5:591:A:H2'	34:B5:592:A:C8	2.40	0.56
35:AA:3:ARG:HD3	38:A1:911:C:H42	1.69	0.56
7:BI:56:ARG:HH22	34:B5:332:U:P	2.27	0.56
15:BY:56:SER:HB3	15:BY:74:LEU:HB2	1.87	0.56
34:B5:1575:G7M:H2'	34:B5:1576:A:C8	2.40	0.56
37:AC:73:ARG:NH1	38:A1:2814:G:OP1	2.31	0.56
38:A1:251:G:H1'	38:A1:253:A:C5	2.41	0.56
38:A1:3234:A:H61	38:A1:3253:G:H1	1.54	0.56
71:AI:5:THR:HG23	71:AI:12:ASN:HB2	1.86	0.56
5:BG:188:ARG:NH1	34:B5:284:G:N7	2.53	0.56
28:BZ:72:GLY:H	28:BZ:75:LEU:HD12	1.71	0.56
34:B5:1641:C:H2'	34:B5:1642:G:C8	2.41	0.56
38:A1:2896:A:O2'	75:Am:122:ARG:NH2	2.39	0.56
47:AJ:82:ARG:HH21	47:AJ:112:LEU:HB3	1.71	0.56
2:BB:158:SER:O	2:BB:162:ARG:NE	2.39	0.56
4:BE:22:LYS:N	34:B5:773:C:OP1	2.38	0.56
31:Bg:111:MET:SD	31:Bg:127:ARG:NH2	2.79	0.56
38:A1:2631:U:OP1	38:A1:2757:U:O2'	2.22	0.56
2:BB:83:LYS:NZ	2:BB:105:PHE:O	2.39	0.55
3:BC:139:ILE:HD13	3:BC:191:ALA:HB1	1.88	0.55
6:BH:44:LYS:HE2	6:BH:95:GLU:HG3	1.88	0.55
23:BQ:37:THR:O	23:BQ:45:ARG:NH1	2.39	0.55
38:A1:129:U:H2'	38:A1:130:A:C8	2.41	0.55
38:A1:2767:U:O2'	77:Ao:30:ALA:O	2.20	0.55
40:A4:8:C:H2'	40:A4:9:A:C8	2.40	0.55
40:A4:25:G:N7	61:AY:13:ARG:NH1	2.52	0.55
1:BA:41:ARG:HD3	1:BA:42:PRO:HD2	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:113:PRO:HG2	6:BH:116:ARG:HD3	1.88	0.55
10:BN:3:ARG:NH1	34:B5:955:A:OP1	2.37	0.55
17:Bb:20:LYS:NZ	34:B5:959:U:OP2	2.38	0.55
22:BP:17:TYR:HD1	22:BP:18:ARG:HG2	1.71	0.55
22:BP:20:VAL:HG21	22:BP:25:LEU:HD13	1.89	0.55
22:BP:85:ILE:HD13	22:BP:111:MET:HB3	1.88	0.55
34:B5:868:G:H1	34:B5:960:U:H3	1.52	0.55
37:AC:95:ARG:HG3	38:A1:343:U:H1'	1.89	0.55
38:A1:155:G:H5''	38:A1:156:G:H2'	1.87	0.55
38:A1:242:C:H2'	38:A1:243:G:H8	1.71	0.55
38:A1:307:A:H2'	38:A1:308:A:C8	2.42	0.55
38:A1:655:C:H2'	38:A1:656:A:C8	2.41	0.55
15:BY:109:LYS:NZ	34:B5:459:G:OP1	2.38	0.55
20:BF:141:GLY:HA2	20:BF:171:ALA:HB2	1.89	0.55
38:A1:627:U:H2'	38:A1:628:A:C8	2.42	0.55
38:A1:3016:A:H2'	38:A1:3017:A:C8	2.41	0.55
27:BU:60:THR:H	34:B5:1382:A:H5''	1.71	0.55
34:B5:1521:G:O2'	34:B5:1523:G:OP2	2.24	0.55
38:A1:1054:A:H5''	38:A1:2637:A:H61	1.71	0.55
38:A1:1410:U:O2'	67:Ae:95:GLU:OE1	2.24	0.55
20:BF:99:MET:SD	20:BF:180:ARG:NH2	2.80	0.55
20:BF:140:THR:HG23	20:BF:171:ALA:HB1	1.89	0.55
34:B5:250:C:H2'	34:B5:251:A:H8	1.72	0.55
34:B5:699:U:H1'	34:B5:741:C:H41	1.71	0.55
34:B5:1360:A:N6	34:B5:1361:U:O2	2.40	0.55
38:A1:1799:A:H2'	38:A1:1800:A:C8	2.41	0.55
45:AH:57:VAL:HG23	45:AH:68:LEU:HD13	1.89	0.55
50:AN:183:THR:HG22	50:AN:187:ARG:HB3	1.88	0.55
1:BA:155:PHE:O	12:BV:60:ARG:NH2	2.38	0.55
23:BQ:120:ASP:O	23:BQ:123:ARG:NH1	2.40	0.55
34:B5:1591:C:H2'	34:B5:1592:A:H8	1.72	0.55
34:B5:1613:U:H2'	34:B5:1614:A:H8	1.70	0.55
34:B5:702:G:O2'	34:B5:703:G:N7	2.38	0.55
36:AB:269:GLN:NE2	38:A1:3306:U:OP1	2.28	0.55
38:A1:2451:G:H2'	38:A1:2452:G:C8	2.42	0.55
66:Ad:20:LEU:HD11	66:Ad:32:ALA:HB2	1.89	0.55
15:BY:57:VAL:HB	15:BY:60:PHE:HE2	1.72	0.55
34:B5:973:A:H4'	38:A1:848:A:H8	1.72	0.55
34:B5:1174:C:O2'	34:B5:1196:A:N6	2.39	0.55
34:B5:1226:A:H1'	34:B5:1227:A:H5''	1.88	0.55
38:A1:1497:C:O2'	38:A1:1602:A:N3	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:Ag:3:GLN:HE22	69:Ag:29:ILE:HB	1.72	0.55
34:B5:509:G:H2'	34:B5:510:G:C8	2.42	0.55
35:AA:40:TYR:HA	35:AA:91:GLY:HA3	1.88	0.55
40:A4:141:C:OP1	50:AN:109:ARG:NH2	2.40	0.55
62:AZ:72:ILE:HD11	62:AZ:107:ARG:HG3	1.89	0.55
7:BI:58:LEU:HD21	34:B5:1676:U:H5''	1.87	0.55
7:BI:64:ASN:ND2	34:B5:257:A:N3	2.55	0.55
28:BZ:73:GLY:H	34:B5:1534:G:H2'	1.71	0.55
34:B5:1553:G:N1	34:B5:1556:A:OP2	2.40	0.55
47:AJ:30:LEU:HD21	47:AJ:47:GLN:HG2	1.89	0.55
50:AN:68:ARG:NH1	50:AN:124:ASP:O	2.28	0.55
80:EC:6939:C:C4	80:EC:6940:U:N3	2.75	0.55
13:BW:56:HIS:O	34:B5:861:U:O2'	2.25	0.54
23:BQ:42:GLU:HA	23:BQ:45:ARG:HG2	1.89	0.54
32:Bf:123:ASN:OD1	32:Bf:148:TYR:OH	2.26	0.54
38:A1:2456:A:H4'	38:A1:2483:G:H5'	1.89	0.54
62:AZ:50:PRO:HD3	62:AZ:68:ILE:HG12	1.87	0.54
73:Ak:5:ILE:HD12	73:Ak:10:GLN:HE22	1.72	0.54
79:E:125:GLY:HA2	79:E:128:LEU:CB	2.36	0.54
79:E:201:VAL:HB	79:E:204:LEU:HD11	1.88	0.54
24:BR:47:ARG:NH1	24:BR:48:ASN:OD1	2.40	0.54
31:Bg:21:THR:H	31:Bg:37:SER:HA	1.71	0.54
34:B5:1146:G:H2'	34:B5:1147:A:C8	2.42	0.54
38:A1:3237:U:H3	38:A1:3250:U:H3	1.54	0.54
39:A3:1:G:O3'	41:AD:273:ARG:NH1	2.40	0.54
39:A3:96:U:H2'	39:A3:97:A:H8	1.71	0.54
4:BE:68:ARG:HH21	4:BE:76:VAL:HG21	1.71	0.54
6:BH:110:GLN:HE22	34:B5:816:G:H21	1.54	0.54
9:BL:33:ARG:NH1	9:BL:53:TYR:O	2.30	0.54
14:BX:3:LYS:NZ	34:B5:614:C:OP1	2.38	0.54
22:BP:81:ARG:NH1	22:BP:97:TYR:O	2.38	0.54
34:B5:1290:U:H2'	34:B5:1291:G:C8	2.42	0.54
34:B5:1354:G:O6	34:B5:1369:U:C2	2.60	0.54
27:BU:87:HIS:ND1	34:B5:1383:G:OP1	2.40	0.54
28:BZ:80:LEU:HB2	28:BZ:101:TYR:HE2	1.72	0.54
34:B5:894:U:H2'	34:B5:895:G:C8	2.42	0.54
38:A1:370:U:H4'	38:A1:404:G:H5'	1.89	0.54
63:Aa:96:LYS:NZ	63:Aa:142:GLY:O	2.40	0.54
7:BI:50:GLY:HA2	34:B5:397:A:H4'	1.90	0.54
14:BX:70:LYS:HB3	14:BX:93:LEU:HD22	1.89	0.54
38:A1:1448:U:H2'	38:A1:1449:A2M:H8	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AN:137:PRO:O	50:AN:143:ARG:NH1	2.40	0.54
70:Ah:102:GLU:HG2	70:Ah:103:LYS:N	2.23	0.54
5:BG:98:ARG:NH1	5:BG:101:ILE:O	2.39	0.54
13:BW:71:LYS:NZ	34:B5:1099:U:OP1	2.39	0.54
22:BP:37:ALA:HB1	22:BP:41:VAL:HB	1.89	0.54
36:AB:128:LYS:HG3	38:A1:3294:A:H5'	1.90	0.54
38:A1:633:C:O2'	68:Af:21:ARG:O	2.23	0.54
38:A1:2160:G:H2'	38:A1:2161:G:H8	1.72	0.54
58:AV:18:PRO:HA	58:AV:51:ALA:HA	1.88	0.54
79:E:124:LEU:HG	79:E:128:LEU:HG	1.89	0.54
6:BH:44:LYS:HB2	6:BH:63:PRO:HG3	1.89	0.54
13:BW:83:ILE:HG23	34:B5:749:U:H5''	1.90	0.54
16:Ba:84:VAL:O	34:B5:1797:A:N6	2.41	0.54
34:B5:705:U:O2	34:B5:730:G:N2	2.40	0.54
34:B5:976:G:N1	34:B5:1023:A:O2'	2.36	0.54
34:B5:1654:G:H4'	76:An:24:SER:HB3	1.90	0.54
38:A1:299:G:C4	71:Ai:31:GLY:HA3	2.43	0.54
45:AH:87:LYS:HB2	45:AH:187:ILE:HG12	1.90	0.54
49:AM:38:ILE:O	55:AS:95:ARG:NH2	2.40	0.54
70:Ah:70:TYR:HA	70:Ah:73:LYS:HD3	1.90	0.54
5:BG:133:LEU:O	34:B5:166:C:O2'	2.25	0.54
7:BI:110:ARG:NH2	7:BI:160:PHE:O	2.41	0.54
19:BD:192:PRO:HB2	19:BD:201:ALA:HA	1.90	0.54
38:A1:116:A:OP2	71:Ai:36:ARG:NH2	2.40	0.54
38:A1:1914:G:O2'	54:AR:82:LYS:O	2.26	0.54
39:A3:11:A:N1	39:A3:67:G:O2'	2.41	0.54
42:AE:44:ALA:HA	42:AE:48:ARG:HG2	1.90	0.54
35:AA:174:ARG:NH2	38:A1:2179:C:O2'	2.40	0.54
49:AM:60:LEU:HD13	55:AS:152:LEU:HD11	1.89	0.54
77:Ao:10:THR:HG21	77:Ao:72:LEU:HD13	1.89	0.54
20:BF:72:HIS:NE2	34:B5:1610:G:OP1	2.40	0.54
33:BM:42:ALA:HB3	33:BM:122:VAL:HB	1.88	0.54
34:B5:836:U:C4	34:B5:837:G:O6	2.61	0.54
34:B5:1126:OMG:OP1	76:An:15:ARG:NH1	2.41	0.54
38:A1:358:G:N2	38:A1:361:A:OP2	2.36	0.54
38:A1:1302:A:N7	38:A1:2857:C:O2'	2.39	0.54
38:A1:2697:A:H2'	38:A1:2698:G:C8	2.43	0.54
41:AD:50:ARG:HG2	41:AD:147:ASP:HB2	1.89	0.54
46:AI:91:VAL:HG12	46:AI:127:ALA:HB1	1.90	0.54
58:AV:6:ALA:HB1	58:AV:125:LEU:HD11	1.90	0.54
1:BA:35:PRO:HD3	12:BV:87:ARG:HH22	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:51:VAL:HG12	6:BH:53:GLY:H	1.73	0.53
11:BO:121:VAL:O	34:B5:886:U:O2'	2.25	0.53
20:BF:124:LEU:HB3	20:BF:125:THR:HG23	1.90	0.53
26:BT:25:GLN:HG2	26:BT:27:LYS:HG3	1.90	0.53
34:B5:947:U:H2'	34:B5:948:G:H8	1.72	0.53
38:A1:1223:A:H62	38:A1:1285:G:N2	2.06	0.53
38:A1:1689:U:H5''	54:AR:61:SER:HB3	1.89	0.53
3:BC:200:SER:HB3	3:BC:204:THR:HG21	1.90	0.53
4:BE:133:LYS:NZ	34:B5:252:U:OP1	2.40	0.53
6:BH:16:LEU:HD21	6:BH:58:LEU:HD11	1.91	0.53
34:B5:153:G:H2'	34:B5:154:G:H8	1.73	0.53
34:B5:973:A:H4'	38:A1:848:A:C8	2.43	0.53
38:A1:1724:U:H1'	38:A1:1725:C:C6	2.42	0.53
38:A1:2335:G:N2	38:A1:2339:C:O2'	2.42	0.53
77:Ao:28:TYR:HB3	77:Ao:69:VAL:HB	1.89	0.53
8:BJ:107:ARG:HH21	8:BJ:148:VAL:HG23	1.73	0.53
23:BQ:22:VAL:HG22	23:BQ:65:ILE:HD12	1.88	0.53
38:A1:1672:U:OP2	54:AR:60:LYS:NZ	2.42	0.53
38:A1:3109:G:N2	45:AH:156:GLN:OE1	2.40	0.53
44:AG:67:ILE:HD12	44:AG:237:ILE:HD11	1.89	0.53
45:AH:50:ASN:ND2	49:AM:4:ASP:OD1	2.40	0.53
79:E:55:LEU:HB2	79:E:153:SER:HB2	1.90	0.53
79:E:180:VAL:HA	79:E:183:ILE:HG12	1.90	0.53
15:BY:62:THR:HA	15:BY:69:SER:HA	1.90	0.53
23:BQ:41:PRO:HD2	23:BQ:44:LEU:HB2	1.90	0.53
34:B5:1381:U:H2'	34:B5:1382:A:C8	2.43	0.53
36:AB:291:GLU:OE1	36:AB:292:ALA:N	2.34	0.53
37:AC:265:GLU:HG2	37:AC:266:THR:HG23	1.90	0.53
38:A1:2676:A:H5'	38:A1:2677:G:C8	2.44	0.53
3:BC:119:LYS:NZ	34:B5:1291:G:OP1	2.42	0.53
20:BF:212:LYS:NZ	80:EC:6845:G:OP2	2.41	0.53
22:BP:81:ARG:NH2	22:BP:117:GLY:O	2.42	0.53
32:Bf:87:THR:O	34:B5:1445:G:N2	2.33	0.53
34:B5:1359:C:H2'	34:B5:1360:A:C8	2.44	0.53
38:A1:1208:U:O2'	38:A1:3115:C:N4	2.42	0.53
38:A1:2727:A:OP2	38:A1:2728:G:N2	2.38	0.53
79:E:20:SER:HB3	79:E:172:VAL:HG21	1.91	0.53
11:BO:132:ARG:NH1	34:B5:1789:G:OP2	2.31	0.53
13:BW:119:LYS:HG2	34:B5:687:G:H5''	1.91	0.53
25:BS:122:HIS:ND1	34:B5:1558:U:OP1	2.34	0.53
28:BZ:92:ILE:HG23	28:BZ:100:ILE:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1246:G:H1'	38:A1:1264:G:H2'	1.89	0.53
38:A1:1667:A:H2'	38:A1:1668:G:C8	2.44	0.53
38:A1:1729:A:O4'	65:Ac:52:ARG:NH1	2.33	0.53
38:A1:3343:G:H21	38:A1:3362:A:H2	1.57	0.53
4:BE:181:VAL:HG12	4:BE:227:VAL:HA	1.91	0.53
13:BW:82:LYS:NZ	34:B5:748:U:OP1	2.38	0.53
20:BF:143:ARG:HH21	29:Bc:7:VAL:HG23	1.72	0.53
21:BK:46:LEU:HD11	21:BK:55:VAL:HG21	1.89	0.53
23:BQ:55:VAL:HG11	23:BQ:105:LEU:HG	1.90	0.53
38:A1:1324:U:H4'	55:AS:2:ALA:HA	1.91	0.53
62:AZ:33:SER:OG	62:AZ:35:SER:O	2.25	0.53
79:E:206:VAL:H	79:E:216:LEU:HD13	1.73	0.53
1:BA:41:ARG:HB3	1:BA:45:VAL:HB	1.90	0.53
19:BD:71:LEU:HG	19:BD:74:GLN:HE21	1.73	0.53
22:BP:118:GLU:HB2	25:BS:122:HIS:HB3	1.90	0.53
34:B5:1280:4AC:H2'	34:B5:1281:G:H8	1.74	0.53
34:B5:1388:A:H61	34:B5:1409:G:H21	1.57	0.53
34:B5:1592:A:H2'	34:B5:1593:A:C8	2.44	0.53
34:B5:1776:A:H2'	34:B5:1777:G:C8	2.43	0.53
36:AB:128:LYS:NZ	38:A1:3294:A:OP1	2.41	0.53
38:A1:171:G:H22	38:A1:246:U:H3	1.55	0.53
38:A1:585:A:H5''	68:Af:70:LYS:HE3	1.90	0.53
50:AN:18:VAL:HG13	50:AN:19:LEU:HD12	1.91	0.53
79:E:48:ARG:HA	79:E:159:LEU:HD23	1.89	0.53
7:BI:5:ARG:NH1	7:BI:29:LEU:O	2.39	0.53
34:B5:884:A:H2'	34:B5:885:G:C8	2.44	0.53
34:B5:1220:C:H2'	34:B5:1221:A:H8	1.72	0.53
36:AB:284:ARG:NH1	36:AB:293:ASN:O	2.42	0.53
38:A1:528:U:H2'	38:A1:529:A:C8	2.44	0.53
38:A1:571:U:H2'	38:A1:572:A:H8	1.74	0.53
38:A1:2357:A:H2'	38:A1:2358:A:C8	2.43	0.53
79:E:17:LEU:O	79:E:21:ASN:HB2	2.08	0.53
80:EC:6777:C:O3'	80:EC:6818:G:N2	2.42	0.53
10:BN:19:SER:OG	10:BN:21:ASN:O	2.26	0.53
31:Bg:123:ILE:HG12	31:Bg:169:ILE:HG21	1.91	0.53
34:B5:1307:U:H3	34:B5:1318:G:H21	1.56	0.53
38:A1:2256:A2M:OP1	38:A1:2256:A2M:H8	2.09	0.53
2:BB:203:ASP:N	2:BB:203:ASP:OD1	2.42	0.52
3:BC:45:VAL:HG21	3:BC:68:ILE:HG23	1.91	0.52
6:BH:114:ARG:NH2	34:B5:637:C:O2	2.41	0.52
13:BW:42:GLN:NE2	13:BW:48:GLY:O	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:107:SER:HB2	34:B5:802:G:H21	1.73	0.52
17:Bb:33:LEU:HD22	17:Bb:79:PHE:HB2	1.89	0.52
19:BD:166:ASP:O	19:BD:190:ARG:NH2	2.40	0.52
33:BM:56:GLU:HB3	33:BM:124:LYS:HA	1.92	0.52
34:B5:778:G:H2'	34:B5:779:U:H2'	1.91	0.52
35:AA:21:ARG:HD3	38:A1:824:C:H5''	1.91	0.52
38:A1:3291:G:H2'	38:A1:3292:A:C8	2.44	0.52
13:BW:23:ARG:NE	13:BW:65:LEU:O	2.33	0.52
19:BD:225:TYR:HB2	31:Bg:189:GLU:HA	1.92	0.52
26:BT:38:LYS:HA	26:BT:46:PRO:HA	1.90	0.52
27:BU:108:ILE:HD12	27:BU:114:VAL:HG11	1.91	0.52
34:B5:319:U:H4'	34:B5:323:A:C8	2.43	0.52
34:B5:953:G:H2'	34:B5:954:G:C8	2.44	0.52
34:B5:1280:4AC:H2'	34:B5:1281:G:C8	2.45	0.52
37:AC:35:VAL:HG21	37:AC:244:LEU:HD21	1.91	0.52
38:A1:249:U:H3	38:A1:251:G:H2'	1.73	0.52
42:AE:72:ASN:HB3	42:AE:160:SER:HA	1.91	0.52
52:AP:41:LEU:HD21	52:AP:99:ALA:HB2	1.91	0.52
54:AR:164:LEU:HD12	54:AR:168:ALA:HB3	1.91	0.52
79:E:19:TYR:O	79:E:23:THR:OG1	2.27	0.52
3:BC:40:LYS:HG2	3:BC:247:ALA:HB1	1.91	0.52
8:BJ:173:ALA:HB2	34:B5:511:A:H5'	1.91	0.52
13:BW:115:GLU:HA	13:BW:118:ARG:HE	1.75	0.52
20:BF:53:VAL:HG12	20:BF:55:ASP:H	1.73	0.52
25:BS:122:HIS:O	25:BS:126:ARG:HG2	2.09	0.52
31:Bg:22:SER:HB3	31:Bg:36:ALA:HB3	1.90	0.52
34:B5:71:A:H2'	34:B5:72:A:H4'	1.90	0.52
34:B5:1772:C:H2'	34:B5:1773:4AC:H6	1.91	0.52
38:A1:406:G:OP1	38:A1:1415:U:O2'	2.24	0.52
38:A1:1666:G:H2'	38:A1:1667:A:H8	1.75	0.52
38:A1:2478:C:OP2	38:A1:2480:A:N6	2.42	0.52
38:A1:2573:G:H2'	38:A1:2574:G:H8	1.74	0.52
44:AG:162:LEU:HA	50:AN:7:LEU:HD11	1.90	0.52
80:EC:6866:C:H5''	80:EC:6867:C:H5	1.75	0.52
1:BA:175:TYR:CG	1:BA:199:PRO:HB3	2.45	0.52
8:BJ:18:PRO:O	8:BJ:23:ARG:NH2	2.43	0.52
28:BZ:40:VAL:HG13	28:BZ:41:ILE:HG23	1.90	0.52
34:B5:752:A:H2	34:B5:797:G:H1	1.56	0.52
35:AA:117:GLU:HG2	35:AA:122:ASP:OD1	2.09	0.52
38:A1:29:C:H4'	38:A1:62:A:H4'	1.92	0.52
38:A1:640:U:OP1	63:Aa:21:ARG:NH1	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1241:U:N3	38:A1:1244:A:OP2	2.42	0.52
38:A1:1696:A:H2'	38:A1:1697:A:C8	2.44	0.52
38:A1:3174:A:OP1	68:Af:97:SER:OG	2.24	0.52
39:A3:28:C:OP1	47:Aj:137:ARG:NH1	2.42	0.52
41:AD:77:ALA:O	41:AD:108:ARG:NH1	2.39	0.52
42:AE:42:LEU:HD22	42:AE:79:VAL:HG11	1.92	0.52
44:AG:77:GLN:NE2	44:AG:177:TYR:OH	2.42	0.52
47:Aj:93:ASP:O	47:Aj:94:ARG:HG2	2.10	0.52
52:AP:16:SER:O	52:AP:101:ASN:ND2	2.42	0.52
78:Ap:46:THR:OG1	78:Ap:57:CYS:SG	2.63	0.52
20:BF:100:ASN:ND2	34:B5:1166:A:OP1	2.42	0.52
21:BK:8:ARG:NH2	34:B5:1257:U:O3'	2.43	0.52
34:B5:1198:G:OP1	34:B5:1199:G:O2'	2.27	0.52
36:AB:219:ALA:HB2	36:AB:336:VAL:HG23	1.92	0.52
38:A1:969:C:O2'	64:Ab:18:ARG:NH2	2.42	0.52
38:A1:1596:C:H2'	38:A1:1597:C:C6	2.45	0.52
38:A1:1621:A:H2'	38:A1:1622:U:C6	2.44	0.52
38:A1:2219:A:H2'	38:A1:2220:A2M:C8	2.39	0.52
51:AO:65[A]:ASN:OD1	51:AO:67[A]:THR:OG1	2.24	0.52
3:BC:188:LEU:HD13	3:BC:196:VAL:HG11	1.90	0.52
4:BE:68:ARG:HE	4:BE:76:VAL:HG11	1.74	0.52
20:BF:80:LYS:HB2	20:BF:83:ARG:HG2	1.92	0.52
38:A1:53:G:OP2	72:Aj:48:ASN:ND2	2.39	0.52
38:A1:3322:A:H2'	38:A1:3323:A:C8	2.45	0.52
43:AF:34:LYS:HA	43:AF:37:ASN:HB2	1.92	0.52
3:BC:83:ILE:HG21	3:BC:121:VAL:HG13	1.91	0.52
21:BK:48:SER:OG	34:B5:1220:C:OP1	2.26	0.52
24:BR:32:LYS:HB2	24:BR:47:ARG:HH11	1.74	0.52
25:BS:36:LYS:NZ	34:B5:1568:C:OP1	2.38	0.52
26:BT:22:LEU:HD22	26:BT:28:LEU:HD11	1.91	0.52
31:Bg:38:ARG:HA	31:Bg:67:ILE:HG23	1.91	0.52
34:B5:1477:G:H2'	34:B5:1478:G:H8	1.75	0.52
34:B5:1691:A:H2'	34:B5:1692:G:H8	1.75	0.52
38:A1:988:U:OP1	43:AF:121:LYS:NZ	2.41	0.52
38:A1:1786:G:H2'	38:A1:1787:A:C8	2.45	0.52
38:A1:2701:U:OP1	56:AT:17:ARG:NH1	2.42	0.52
78:Ap:8:VAL:O	78:Ap:11:THR:OG1	2.27	0.52
80:EC:6934:U:O2'	80:EC:6935:G:O4'	2.27	0.52
5:BG:18:ILE:HD11	5:BG:45:PHE:HE1	1.74	0.52
34:B5:625:C:H2'	34:B5:626:U:C6	2.45	0.52
34:B5:1164:G:H2'	34:B5:1165:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:113:VAL:HG12	35:AA:166:ILE:HD13	1.92	0.52
36:AB:93:VAL:HG12	36:AB:155:ALA:H	1.74	0.52
45:AH:9:GLN:HB3	45:AH:52:LEU:HD11	1.91	0.52
61:AY:116:LYS:HG2	61:AY:126:LEU:HD11	1.92	0.52
19:BD:64:ARG:NH1	21:BK:70:GLU:OE2	2.41	0.52
27:BU:24:ILE:HG12	27:BU:116:VAL:HG12	1.91	0.52
34:B5:794:U:H5'	34:B5:795:U:H5	1.73	0.52
34:B5:844:A:H2'	34:B5:845:G:C8	2.44	0.52
34:B5:1619:C:H2'	34:B5:1620:C:H6	1.75	0.52
35:AA:83:HIS:HB3	78:Ap:64:VAL:HG12	1.92	0.52
38:A1:120:G:H4'	38:A1:121:A:H5'	1.91	0.52
38:A1:520:U:OP2	43:AF:70:LYS:NZ	2.39	0.52
38:A1:631:U:H2'	38:A1:632:G:C8	2.44	0.52
38:A1:1504:A:OP1	52:AP:23:ARG:NH1	2.42	0.52
38:A1:2462:A:H1'	38:A1:2494:A:H61	1.75	0.52
38:A1:3358:U:H2'	38:A1:3359:A:H8	1.75	0.52
49:AM:21:VAL:HB	49:AM:63:VAL:HG13	1.92	0.52
16:Ba:24:VAL:HG11	16:Ba:71:LEU:HD23	1.92	0.52
19:BD:18:TYR:HE1	19:BD:37:VAL:HG13	1.75	0.52
20:BF:38:THR:HG23	20:BF:39:GLU:HG2	1.90	0.52
26:BT:15:ILE:HG13	26:BT:59:ALA:HB3	1.92	0.52
31:Bg:69:GLN:H	31:Bg:84:SER:HA	1.74	0.52
34:B5:5:U:H2'	34:B5:6:G:H8	1.75	0.52
34:B5:979:A:N3	34:B5:1775:U:O2'	2.41	0.52
38:A1:353:G:O6	72:Aj:55:ARG:NH2	2.41	0.52
38:A1:1001:G:O2'	38:A1:1041:U:OP2	2.24	0.52
38:A1:2960:C:H2'	38:A1:2961:G:H8	1.72	0.52
38:A1:3295:A:H2'	38:A1:3296:A:C8	2.45	0.52
40:A4:65:A:O2'	70:Ah:10:ARG:NH2	2.43	0.52
43:AF:25:GLN:HG3	43:AF:28:ALA:HB3	1.92	0.52
80:EC:6783:U:H2'	80:EC:6784:G:C8	2.46	0.52
5:BG:2:LYS:HG2	5:BG:17:GLU:HG3	1.92	0.51
8:BJ:106:GLU:O	8:BJ:112:GLN:NE2	2.43	0.51
23:BQ:127:LYS:HD3	34:B5:1605:G:C8	2.45	0.51
35:AA:36:GLU:HG3	35:AA:91:GLY:HA2	1.92	0.51
38:A1:900:G:H1'	38:A1:1589:A:N6	2.24	0.51
38:A1:1144:U:OP1	38:A1:1367:G:O2'	2.22	0.51
43:AF:130:ILE:HD12	43:AF:134:VAL:HG11	1.93	0.51
63:Aa:75:LEU:HB3	63:Aa:118:ILE:HG23	1.93	0.51
80:EC:6808:G:H2'	80:EC:6809:G:C8	2.45	0.51
22:BP:115:TYR:OH	34:B5:1556:A:OP1	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BS:49:LYS:NZ	25:BS:79:TYR:O	2.40	0.51
34:B5:65:A:H2	34:B5:84:A:H62	1.58	0.51
34:B5:74:U:OP1	34:B5:76:A:N6	2.43	0.51
38:A1:2482:U:H3	38:A1:2486:A:H62	1.59	0.51
38:A1:3252:G:H2'	38:A1:3253:G:C8	2.45	0.51
55:AS:71:LYS:O	55:AS:73:LYS:NZ	2.38	0.51
80:EC:6826:U:H2'	80:EC:6827:G:C8	2.45	0.51
23:BQ:33:GLY:H	23:BQ:66:ARG:HH12	1.57	0.51
34:B5:565:C:OP2	34:B5:577:G:O2'	2.28	0.51
34:B5:821:U:O4	34:B5:852:C:N3	2.43	0.51
38:A1:12:A:H2'	38:A1:13:A:C8	2.46	0.51
38:A1:58:G:H4'	50:AN:155:VAL:HG12	1.93	0.51
38:A1:1016:C:H42	38:A1:1034:U:H1'	1.76	0.51
38:A1:2568:C:O2'	38:A1:2569:A:O4'	2.23	0.51
41:AD:83:LEU:HB3	41:AD:88:ILE:HB	1.91	0.51
56:AT:8:ARG:O	56:AT:11:THR:OG1	2.25	0.51
1:BA:179:ARG:HD2	1:BA:183:ARG:HH21	1.75	0.51
4:BE:44:LEU:HD13	4:BE:65:LEU:HD21	1.91	0.51
7:BI:172:ARG:NH1	34:B5:330:G:OP2	2.43	0.51
25:BS:4:VAL:HG21	28:BZ:81:ARG:HD3	1.91	0.51
38:A1:1366:A:O2'	67:Ae:45:ARG:NH2	2.44	0.51
42:AE:169:ASP:HB3	42:AE:174:LEU:HD11	1.91	0.51
50:AN:181:ASN:HA	50:AN:184:LYS:HE3	1.91	0.51
55:AS:2:ALA:O	55:AS:3:HIS:ND1	2.44	0.51
62:AZ:101:PHE:O	62:AZ:107:ARG:NH2	2.44	0.51
23:BQ:95:LYS:O	31:Bg:59:ARG:NH1	2.43	0.51
23:BQ:99:GLU:O	23:BQ:103:ASN:N	2.34	0.51
34:B5:1588:G:N2	34:B5:1608:U:O2	2.33	0.51
36:AB:261:MET:HB2	36:AB:264:VAL:HG23	1.92	0.51
36:AB:279:ASN:ND2	38:A1:3098:G:OP1	2.37	0.51
38:A1:1062:A:O2'	56:AT:108:ARG:NH2	2.43	0.51
38:A1:1351:U:O2'	38:A1:1355:A:N6	2.39	0.51
38:A1:1534:A:H2'	38:A1:1535:A:C8	2.45	0.51
38:A1:3294:A:H2'	38:A1:3295:A:O4'	2.11	0.51
40:A4:97:A:OP1	70:Ah:63:ARG:NH2	2.42	0.51
56:AT:68:THR:HG22	56:AT:69:LYS:H	1.74	0.51
58:AV:15:LEU:HD23	58:AV:53:SER:HB3	1.93	0.51
14:BX:66:SER:HB2	34:B5:565:C:H1'	1.92	0.51
15:BY:60:PHE:O	34:B5:522:U:O2'	2.28	0.51
23:BQ:94:GLN:HB2	23:BQ:102:LYS:HG3	1.92	0.51
34:B5:163:G:OP2	34:B5:163:G:N2	2.33	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:891:A:H2'	34:B5:892:A:C8	2.45	0.51
37:AC:347:THR:O	38:A1:520:U:N3	2.44	0.51
38:A1:966:U:OP1	63:Aa:44:ASN:ND2	2.41	0.51
38:A1:1412:G:OP1	67:Ae:105:ARG:NH1	2.42	0.51
38:A1:2413:A:H2'	38:A1:2414:G:H8	1.76	0.51
38:A1:2848:G:OP1	75:Am:100:TYR:OH	2.24	0.51
55:AS:99:ARG:NH1	55:AS:126:VAL:O	2.44	0.51
5:BG:85:ARG:N	34:B5:161:U:OP1	2.37	0.51
31:Bg:11:GLY:HA2	31:Bg:52:GLN:HA	1.93	0.51
34:B5:12:U:H2'	34:B5:13:C:C6	2.46	0.51
34:B5:1210:C:H2'	34:B5:1211:A:H8	1.74	0.51
36:AB:226:PHE:O	38:A1:1886:A:O2'	2.28	0.51
38:A1:100:A:H3'	38:A1:101:G:H21	1.76	0.51
38:A1:901:G:OP1	72:Aj:12:HIS:NE2	2.44	0.51
65:Ac:30:THR:HG23	65:Ac:91:SER:HB2	1.93	0.51
70:Ah:31:LEU:HB3	70:Ah:44:ILE:HG12	1.92	0.51
3:BC:41:LEU:HD21	3:BC:61:LEU:HB3	1.92	0.51
26:BT:70:GLN:NE2	26:BT:119:LYS:O	2.44	0.51
37:AC:303:GLY:H	38:A1:1347:U:H5''	1.74	0.51
38:A1:1237:G:H1	38:A1:1251:A:H2	1.58	0.51
38:A1:2366:C:H2'	38:A1:2367:A:H8	1.74	0.51
38:A1:3023:U:H2'	38:A1:3024:A:H8	1.75	0.51
39:A3:64:A:N7	46:AI:209:ASN:ND2	2.58	0.51
62:AZ:23:VAL:HG12	62:AZ:45:GLY:HA3	1.92	0.51
1:BA:172:LEU:HG	1:BA:176:LEU:HD13	1.92	0.51
1:BA:182:LEU:HB3	1:BA:188:LEU:HD13	1.93	0.51
25:BS:123:ARG:NH2	34:B5:1546:G:OP1	2.39	0.51
34:B5:126:A:H62	34:B5:291:G:N2	2.09	0.51
34:B5:1593:A:H2'	34:B5:1594:G:H8	1.76	0.51
34:B5:1717:G:H2'	34:B5:1718:G:C8	2.46	0.51
35:AA:221:LYS:NZ	38:A1:2965:U:O2	2.44	0.51
36:AB:66:LYS:HD2	36:AB:67:PHE:HD1	1.76	0.51
38:A1:1390:A:N6	38:A1:1418:A:O2'	2.44	0.51
80:EC:6815:U:H2'	80:EC:6816:A:C4	2.45	0.51
1:BA:67:ILE:HD12	1:BA:70:PRO:HA	1.92	0.51
14:BX:74:VAL:HG11	14:BX:104:LEU:HD11	1.93	0.51
18:Be:50:VAL:HA	18:Be:54:ARG:HA	1.93	0.51
28:BZ:80:LEU:HB2	28:BZ:101:TYR:CE2	2.46	0.51
34:B5:701:U:N3	34:B5:702:G:O6	2.44	0.51
34:B5:980:G:H4'	34:B5:1776:A:H4'	1.93	0.51
34:B5:1297:G:N2	34:B5:1300:A:OP2	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1650:U:H2'	34:B5:1651:A:C8	2.46	0.51
38:A1:1482:A:H5''	38:A1:1858:A:C6	2.46	0.51
42:AE:3:ALA:HB2	67:Ae:77:ALA:HB2	1.93	0.51
53:AQ:23:ASN:HB3	53:AQ:26:LEU:HB3	1.93	0.51
55:AS:135:VAL:HG12	55:AS:141:LYS:HG3	1.93	0.51
34:B5:1661:U:H2'	34:B5:1662:G:C8	2.46	0.50
38:A1:992:A:H5''	56:AT:43:LYS:HG3	1.93	0.50
38:A1:1203:A:H2'	38:A1:1204:A:C8	2.45	0.50
43:AF:120:THR:HB	56:AT:132:PRO:HB2	1.92	0.50
79:E:138:VAL:HG11	79:E:144:LEU:HD23	1.92	0.50
79:E:207:LYS:HE2	79:E:211:GLY:H	1.76	0.50
4:BE:112:HIS:NE2	4:BE:237:SER:O	2.44	0.50
23:BQ:69:VAL:HG11	23:BQ:81:ILE:HD11	1.93	0.50
23:BQ:123:ARG:HE	34:B5:1337:A:H4'	1.76	0.50
26:BT:113:ILE:HA	26:BT:128:GLY:HA2	1.93	0.50
38:A1:1597:C:H5'	38:A1:1696:A:H1'	1.93	0.50
63:Aa:19:LYS:HB3	63:Aa:25:HIS:HB2	1.93	0.50
73:Ak:7:ASP:HB3	73:Ak:10:GLN:HE21	1.75	0.50
79:E:20:SER:OG	79:E:30:GLU:OE1	2.28	0.50
80:EC:6809:G:H2'	80:EC:6810:U:C6	2.46	0.50
1:BA:179:ARG:O	1:BA:183:ARG:N	2.42	0.50
4:BE:100:ARG:HG2	4:BE:114:ILE:HG21	1.92	0.50
5:BG:58:LYS:NZ	5:BG:106:LEU:O	2.38	0.50
16:Ba:66:LYS:HE2	16:Ba:68:TYR:HE1	1.76	0.50
34:B5:886:U:H2'	34:B5:887:A:H8	1.77	0.50
34:B5:925:G:H2'	34:B5:926:A:C8	2.46	0.50
38:A1:1108:U:H2'	38:A1:1109:U:C6	2.47	0.50
38:A1:1334:U:H5''	43:AF:206:LYS:HB3	1.93	0.50
38:A1:1477:A:OP1	38:A1:3075:G:O2'	2.24	0.50
61:AY:73:VAL:HA	61:AY:80:VAL:HG12	1.94	0.50
4:BE:255:ARG:NE	34:B5:786:C:O2'	2.45	0.50
7:BI:146:ARG:NH2	34:B5:186:C:OP1	2.42	0.50
26:BT:35:ASP:OD1	26:BT:53:TRP:NE1	2.41	0.50
31:Bg:67:ILE:O	31:Bg:85:TRP:N	2.43	0.50
34:B5:1477:G:H2'	34:B5:1478:G:C8	2.46	0.50
38:A1:98:G:OP1	48:AL:16:LYS:NZ	2.43	0.50
38:A1:1524:A:O2'	38:A1:1526:U:OP2	2.23	0.50
38:A1:2812:C:H2'	38:A1:2813:A:C8	2.46	0.50
41:AD:60:ILE:HB	41:AD:80:SER:HB2	1.94	0.50
47:AJ:100:GLY:HA3	47:AJ:154:THR:HG22	1.93	0.50
55:AS:125:LYS:HE3	55:AS:127:ALA:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:E:196:LYS:HB3	79:E:199:GLN:HB2	1.92	0.50
7:BI:178:ARG:NH1	34:B5:258:C:O2	2.44	0.50
11:BO:24:ASN:ND2	34:B5:903:U:O4	2.44	0.50
27:BU:106:ILE:HG13	27:BU:107:THR:HG22	1.94	0.50
38:A1:93:C:OP2	38:A1:2764:C:O2'	2.23	0.50
38:A1:177:U:H3	38:A1:239:G:H22	1.58	0.50
38:A1:2812:C:H2'	38:A1:2813:A:H8	1.76	0.50
50:AN:96:ARG:NH1	50:AN:104:GLU:OE1	2.45	0.50
68:Af:42:GLN:HA	68:Af:45:LEU:HG	1.93	0.50
11:BO:20:TYR:HB3	11:BO:27:PHE:HB2	1.94	0.50
19:BD:172:THR:O	19:BD:173:ARG:NH1	2.45	0.50
32:Bf:139:LEU:HB3	32:Bf:148:TYR:HB2	1.93	0.50
33:BM:61:VAL:HG23	33:BM:89:ILE:HG23	1.94	0.50
36:AB:187:SER:OG	36:AB:190:GLU:OE1	2.21	0.50
38:A1:1019:G:N2	38:A1:1020:G:N7	2.58	0.50
38:A1:1061:A:H4'	56:AT:102:ARG:HH21	1.76	0.50
3:BC:56:ILE:HG23	3:BC:61:LEU:HB2	1.94	0.50
20:BF:84:LYS:O	20:BF:92:ARG:NH2	2.45	0.50
28:BZ:65:LEU:HB3	28:BZ:71:ILE:HD11	1.93	0.50
31:Bg:82:SER:HB3	31:Bg:92:TRP:HE1	1.76	0.50
34:B5:183:U:H2'	34:B5:184:C:C6	2.47	0.50
34:B5:1171:A:O2'	34:B5:1570:A:N3	2.40	0.50
34:B5:1697:G:O6	34:B5:1704:U:O4	2.30	0.50
38:A1:89:A:OP1	63:Aa:60:TYR:N	2.42	0.50
38:A1:1281:G:N2	38:A1:1282:G:O6	2.44	0.50
38:A1:1387:G:HO2'	42:AE:2:SER:N	2.10	0.50
69:Ag:41:ARG:HG2	69:Ag:56:THR:HG21	1.94	0.50
26:BT:129:GLN:OE1	34:B5:1359:C:O2'	2.26	0.50
34:B5:1488:G:H3'	34:B5:1515:A:H61	1.77	0.50
38:A1:359:U:O2'	72:Aj:16:HIS:ND1	2.34	0.50
38:A1:567:G:H2'	38:A1:568:G:C8	2.46	0.50
38:A1:974:G:H5'	53:AQ:16:ARG:HG3	1.94	0.50
38:A1:2197:OMC:N4	38:A1:2241:U:H2'	2.27	0.50
38:A1:2697:A:H2'	38:A1:2698:G:H8	1.76	0.50
41:AD:166:ALA:HB1	41:AD:171:LEU:HD11	1.94	0.50
62:AZ:21:LYS:NZ	62:AZ:47:GLU:O	2.45	0.50
5:BG:160:ARG:HH21	34:B5:66:U:H1'	1.77	0.50
9:BL:57:LYS:HG2	9:BL:131:ILE:HD12	1.94	0.50
10:BN:23:PRO:HD2	10:BN:26:PHE:HB2	1.94	0.50
31:Bg:270:LEU:HD21	31:Bg:273:ASP:HB2	1.94	0.50
34:B5:1391:A:H2'	34:B5:1392:U:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:821:U:H2'	38:A1:822:G:H8	1.76	0.50
20:BF:122:ASN:HD21	20:BF:129:PRO:HG3	1.76	0.49
21:BK:3:MET:SD	34:B5:1257:U:O2'	2.66	0.49
34:B5:476:U:OP1	34:B5:477:A:O2'	2.23	0.49
38:A1:1472:U:H5''	54:AR:24:LEU:HD12	1.93	0.49
38:A1:2255:A:H62	38:A1:2260:U:H3	1.60	0.49
42:AE:170:LYS:HG3	42:AE:173:MET:HB2	1.92	0.49
49:AM:23:ILE:O	49:AM:30:GLY:N	2.44	0.49
55:AS:152:LEU:HB2	55:AS:172:TYR:CE2	2.47	0.49
73:AK:10:GLN:HA	73:AK:13:GLU:HG2	1.94	0.49
2:BB:137:ILE:HG21	2:BB:172:LEU:HD11	1.94	0.49
8:BJ:144:PRO:HD2	34:B5:474:A:H5''	1.94	0.49
22:BP:27:GLU:HG3	22:BP:88:GLU:HA	1.95	0.49
23:BQ:46:PHE:HA	23:BQ:49:TYR:CD2	2.47	0.49
28:BZ:77:ARG:HH22	34:B5:1532:U:H3'	1.76	0.49
34:B5:447:U:H2'	34:B5:448:C:O4'	2.11	0.49
34:B5:1364:G:H2'	34:B5:1365:C:C6	2.47	0.49
34:B5:1776:A:H2'	34:B5:1777:G:H8	1.77	0.49
38:A1:1178:G:N3	38:A1:1328:C:O2'	2.45	0.49
38:A1:1659:U:H2'	38:A1:1660:C:C6	2.47	0.49
38:A1:2534:G:H2'	38:A1:2535:A:C8	2.47	0.49
38:A1:2946:A2M:H5''	38:A1:2947:G:H5'	1.93	0.49
8:BJ:176:ASN:ND2	34:B5:511:A:OP2	2.45	0.49
20:BF:95:ASN:O	34:B5:1611:A:O2'	2.22	0.49
36:AB:83:PRO:HB2	36:AB:202:THR:HB	1.94	0.49
37:AC:31:ARG:HG3	37:AC:120:TYR:HE1	1.77	0.49
38:A1:36:C:OP2	50:AN:83:LYS:NZ	2.45	0.49
38:A1:963:G:O2'	63:Aa:29:PRO:O	2.28	0.49
38:A1:1411:C:OP1	67:Ae:98:HIS:N	2.39	0.49
38:A1:2447:A:H2'	38:A1:2448:G:H8	1.78	0.49
40:A4:142:C:H2'	40:A4:143:U:C6	2.47	0.49
43:AF:239:LEU:HG	43:AF:243:MET:HE2	1.94	0.49
80:EC:6828:G:H2'	80:EC:6829:A:C8	2.48	0.49
7:BI:8:ARG:HH21	7:BI:21:PHE:HB2	1.77	0.49
25:BS:90:ASN:HB3	34:B5:1548:G:H4'	1.94	0.49
26:BT:71:VAL:HG13	26:BT:75:LYS:HB2	1.95	0.49
31:Bg:11:GLY:HA3	31:Bg:54:PHE:HB2	1.93	0.49
31:Bg:19:TRP:HB2	31:Bg:38:ARG:HG3	1.92	0.49
34:B5:1648:A:H2'	34:B5:1649:G:C8	2.47	0.49
38:A1:171:G:H1	38:A1:246:U:H3	1.58	0.49
38:A1:1694:U:H5	38:A1:1752:A:N1	2.09	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Ae:96:ILE:HG21	67:Ae:105:ARG:HG2	1.93	0.49
67:Ae:123:LYS:HA	67:Ae:126:LEU:HD12	1.95	0.49
3:BC:230:TRP:CD2	13:BW:68:ARG:HD2	2.48	0.49
9:BL:133:LYS:HB2	34:B5:337:G:H3'	1.93	0.49
34:B5:1357:A:H2'	34:B5:1358:G:C8	2.48	0.49
34:B5:1780:G:N3	38:A1:2262:A:O2'	2.44	0.49
38:A1:2204:C:H2'	38:A1:2205:U:C6	2.48	0.49
3:BC:165:VAL:HG13	3:BC:204:THR:HG22	1.94	0.49
5:BG:10:ASN:ND2	5:BG:127:THR:O	2.46	0.49
15:BY:61:ARG:NH1	34:B5:530:C:O2	2.45	0.49
34:B5:950:C:H2'	34:B5:951:A:C8	2.48	0.49
36:AB:308:MET:HE2	38:A1:3329:U:H5''	1.95	0.49
37:AC:315:LYS:NZ	38:A1:609:G:OP2	2.36	0.49
41:AD:150:LEU:HD12	47:AJ:143:ARG:HG3	1.95	0.49
5:BG:14:LYS:HD2	5:BG:123:GLY:HA3	1.94	0.49
38:A1:650:OMC:H2'	38:A1:651:G:C8	2.48	0.49
38:A1:952:A:H4'	38:A1:968:G:N2	2.27	0.49
38:A1:1194:G:H2'	38:A1:1195:A:C8	2.48	0.49
38:A1:2160:G:H2'	38:A1:2161:G:C8	2.48	0.49
38:A1:2747:A:H2'	38:A1:2748:A:C8	2.48	0.49
25:BS:27:LYS:HA	25:BS:57:ARG:HA	1.94	0.49
32:Bf:121:CYS:HB2	32:Bf:132:LEU:HD21	1.93	0.49
34:B5:1291:G:H22	34:B5:1324:G:N2	2.10	0.49
34:B5:1561:U:H2'	34:B5:1562:G:H8	1.78	0.49
38:A1:407:A:C2	40:A4:17:A:H1'	2.47	0.49
38:A1:643:U:O2'	38:A1:1153:A:N1	2.43	0.49
38:A1:3275:U:H5'	68:Af:68:TRP:HZ2	1.78	0.49
45:AH:115:ARG:HG2	45:AH:123:ILE:HD12	1.93	0.49
51:AO:126[A]:VAL:HG23	51:AO:127[A]:LEU:HD12	1.95	0.49
63:Aa:24:LYS:O	63:Aa:26:ARG:HG2	2.12	0.49
80:EC:6804:A:O2'	80:EC:6808:G:N1	2.35	0.49
5:BG:98:ARG:NH1	5:BG:99:GLY:O	2.45	0.49
29:Bc:12:VAL:N	29:Bc:52:ASP:O	2.40	0.49
33:BM:24:ILE:HD12	33:BM:135:MET:HG3	1.94	0.49
38:A1:119:U:O3'	44:AG:133:LYS:NZ	2.46	0.49
38:A1:1239:C:H3'	38:A1:1240:A:H8	1.77	0.49
38:A1:2108:C:H1'	38:A1:3344:A:C8	2.48	0.49
38:A1:2767:U:H2'	38:A1:2768:U:C6	2.48	0.49
41:AD:62:CYS:HB2	41:AD:78:ALA:HB3	1.94	0.49
46:AI:68:ALA:HB1	46:AI:155:ALA:HB1	1.94	0.49
2:BB:121:ILE:HB	2:BB:141:ALA:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:40:CYS:SG	17:Bb:41:LEU:N	2.86	0.49
21:BK:52:LYS:HG3	34:B5:1220:C:H4'	1.95	0.49
23:BQ:35:PRO:HD2	23:BQ:38:LEU:HB2	1.95	0.49
31:Bg:250:TYR:CE2	31:Bg:265:LEU:HB3	2.47	0.49
34:B5:29:U:H2'	34:B5:30:G:H8	1.78	0.49
37:AC:138:ARG:NH2	38:A1:1384:U:OP1	2.46	0.49
38:A1:273:A:H2'	38:A1:274:G:C8	2.48	0.49
38:A1:723:U:O2'	64:Ab:29:TYR:OH	2.24	0.49
38:A1:876:A2M:H5''	38:A1:1890:U:H5''	1.95	0.49
38:A1:1322:U:O2	55:AS:108:GLN:NE2	2.39	0.49
41:AD:49:TYR:HB3	41:AD:144:VAL:HG12	1.94	0.49
46:AI:190:VAL:HG13	46:AI:197:VAL:HG21	1.94	0.49
47:AJ:21:ILE:HG22	47:AJ:125:MET:HA	1.94	0.49
48:AL:59:ARG:HD2	48:AL:69:VAL:HG12	1.95	0.49
68:Af:51:TYR:HB2	68:Af:98:VAL:HG12	1.95	0.49
1:BA:63:ILE:HD13	12:BV:36:VAL:HG22	1.95	0.48
1:BA:122:ILE:HA	1:BA:144:ILE:HB	1.94	0.48
2:BB:108:ASP:OD1	2:BB:108:ASP:N	2.46	0.48
5:BG:49:VAL:HB	5:BG:115:LYS:HB3	1.95	0.48
6:BH:67:LEU:HD11	6:BH:94:ALA:HB2	1.94	0.48
9:BL:37:ASN:O	34:B5:247:A:O2'	2.25	0.48
11:BO:84:ARG:HG3	11:BO:119:THR:HA	1.95	0.48
13:BW:81:VAL:O	13:BW:122:SER:OG	2.30	0.48
20:BF:42:LEU:HG	20:BF:43:PHE:H	1.78	0.48
36:AB:85:VAL:HG22	36:AB:202:THR:HG22	1.95	0.48
37:AC:187:LEU:HD23	38:A1:1419:A:C8	2.48	0.48
38:A1:966:U:H2'	38:A1:967:A:C8	2.48	0.48
38:A1:3276:G:O6	52:AP:171:ARG:NH2	2.40	0.48
39:A3:121:U:H5''	41:AD:265:TYR:HE1	1.77	0.48
80:EC:6780:A:H2'	80:EC:6781:U:H6	1.78	0.48
2:BB:33:LYS:HG3	2:BB:95:ASN:HD21	1.77	0.48
5:BG:92:ARG:O	34:B5:405:C:O2'	2.29	0.48
13:BW:57:ARG:HG2	34:B5:862:A:H4'	1.94	0.48
34:B5:406:U:H2'	34:B5:407:A:H8	1.78	0.48
38:A1:2639:G:H2'	38:A1:2640:A2M:H8	1.94	0.48
43:AF:80:GLN:HB2	56:AT:135:PRO:HB2	1.95	0.48
45:AH:8:GLN:HB3	45:AH:72:LYS:HG3	1.94	0.48
65:Ac:100:ILE:HG23	65:Ac:101:LEU:HD12	1.95	0.48
72:Aj:87:SER:OG	72:Aj:88:ALA:N	2.46	0.48
2:BB:153:HIS:NE2	34:B5:1045:C:OP1	2.36	0.48
15:BY:8:ARG:HB2	34:B5:780:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:174:LEU:HA	20:BF:177:ILE:HG22	1.96	0.48
25:BS:29:VAL:HG13	25:BS:43:SER:HB2	1.95	0.48
26:BT:78:LYS:NZ	34:B5:1522:U:O3'	2.47	0.48
34:B5:1072:C:H2'	34:B5:1073:G:C8	2.48	0.48
34:B5:1584:G:O2'	34:B5:1610:G:O6	2.26	0.48
34:B5:1693:A:N1	34:B5:1709:C:N4	2.60	0.48
38:A1:874:U:N3	38:A1:2978:U:OP1	2.31	0.48
42:AE:50:LYS:NZ	42:AE:72:ASN:O	2.39	0.48
43:AF:89:ILE:HD11	43:AF:229:PHE:HB3	1.96	0.48
61:AY:48:LEU:HD13	61:AY:115:ARG:HH21	1.78	0.48
2:BB:34:ALA:H	2:BB:41:ARG:HB3	1.78	0.48
7:BI:84:HIS:NE2	7:BI:97:THR:OG1	2.34	0.48
9:BL:69:LYS:NZ	34:B5:304:U:O2	2.47	0.48
11:BO:46:MET:HG2	34:B5:899:G:H4'	1.96	0.48
34:B5:903:U:O2'	34:B5:905:A:N7	2.37	0.48
34:B5:1673:G:C6	34:B5:1728:A:N1	2.80	0.48
36:AB:50:LYS:HA	36:AB:79:VAL:HG12	1.95	0.48
36:AB:328:ILE:HD12	36:AB:336:VAL:HG21	1.95	0.48
36:AB:366:GLY:HA2	38:A1:3086:A:H4'	1.95	0.48
42:AE:43:LEU:HD11	42:AE:85:ILE:HG12	1.95	0.48
6:BH:129:LEU:HD21	6:BH:169:PHE:HB3	1.96	0.48
17:Bb:19:HIS:CD2	17:Bb:21:LEU:H	2.25	0.48
20:BF:97:LEU:HG	34:B5:1473:U:H5	1.79	0.48
24:BR:18:GLU:HA	24:BR:71:PHE:HB3	1.95	0.48
38:A1:1329:U:OP1	68:Af:17:GLN:NE2	2.46	0.48
38:A1:1799:A:H2'	38:A1:1800:A:H8	1.79	0.48
38:A1:2228:A:H2'	38:A1:2229:A:C8	2.48	0.48
38:A1:2597:U:O2	50:AN:125:SER:OG	2.24	0.48
48:AL:79:GLU:OE2	48:AL:103:ASN:ND2	2.32	0.48
79:E:116:LEU:HD22	79:E:120:VAL:HG13	1.95	0.48
80:EC:6855:A:H3'	80:EC:6856:C:H5''	1.95	0.48
1:BA:138:TYR:OH	34:B5:1296:A:OP1	2.24	0.48
2:BB:116:LYS:HG3	34:B5:931:C:H5''	1.95	0.48
2:BB:132:ASP:HB3	2:BB:221:PRO:HB3	1.95	0.48
5:BG:52:ILE:HD11	5:BG:109:LEU:HD11	1.96	0.48
5:BG:136:LYS:NZ	5:BG:174:LYS:O	2.38	0.48
31:Bg:251:TRP:HD1	31:Bg:264:SER:HA	1.79	0.48
32:Bf:95:HIS:CD2	34:B5:1252:C:H41	2.32	0.48
34:B5:1405:G:H2'	34:B5:1406:A:C8	2.49	0.48
38:A1:47:C:OP2	38:A1:48:A:O2'	2.27	0.48
38:A1:394:G:N1	38:A1:397:A:OP2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1618:G:O2'	40:A4:126:A:N1	2.46	0.48
38:A1:2116:G:OP1	38:A1:2118:C:N4	2.47	0.48
39:A3:3:U:H2'	39:A3:4:U:C6	2.49	0.48
39:A3:74:C:H2'	39:A3:75:G:C8	2.48	0.48
49:AM:14:LEU:HG	55:AS:149:LYS:HE2	1.96	0.48
80:EC:6780:A:H2'	80:EC:6781:U:C6	2.47	0.48
80:EC:6846:C:N4	80:EC:6847:G:O6	2.46	0.48
11:BO:38:THR:OG1	34:B5:895:G:N3	2.44	0.48
22:BP:31:GLU:HA	22:BP:34:VAL:HG12	1.95	0.48
22:BP:42:ARG:NH2	34:B5:1550:A:OP2	2.47	0.48
25:BS:116:LEU:HD23	25:BS:119:ILE:HD11	1.95	0.48
25:BS:122:HIS:NE2	25:BS:126:ARG:HD3	2.29	0.48
28:BZ:73:GLY:O	28:BZ:77:ARG:N	2.46	0.48
34:B5:836:U:H2'	34:B5:837:G:C8	2.48	0.48
34:B5:1210:C:H2'	34:B5:1211:A:C8	2.48	0.48
34:B5:1712:A:H3'	34:B5:1713:G:H8	1.78	0.48
36:AB:108:GLU:HG3	36:AB:137:TYR:HB2	1.96	0.48
36:AB:159:ARG:HG2	36:AB:182:GLN:HA	1.94	0.48
38:A1:129:U:H2'	38:A1:130:A:H8	1.78	0.48
44:AG:183:LYS:HB2	44:AG:194:THR:HG23	1.95	0.48
50:AN:27:VAL:HB	50:AN:122:ASN:HD21	1.79	0.48
10:BN:13:SER:HB2	17:Bb:21:LEU:HD11	1.95	0.48
19:BD:66:ILE:HD11	19:BD:86:LEU:HB3	1.96	0.48
22:BP:48:GLY:O	22:BP:49:MET:HE2	2.14	0.48
32:Bf:133:ALA:HB2	34:B5:1252:C:H4'	1.94	0.48
36:AB:123:TYR:CZ	36:AB:124:LYS:HG3	2.48	0.48
38:A1:1364:C:H5''	53:AQ:3:ILE:HD13	1.95	0.48
38:A1:2768:U:H2'	38:A1:2769:A:H8	1.79	0.48
40:A4:9:A:H2'	40:A4:10:A:H8	1.77	0.48
56:AT:99:SER:OG	56:AT:101:CYS:SG	2.61	0.48
79:E:76:ARG:NH2	79:E:142:ASP:O	2.46	0.48
80:EC:6814:G:O2'	80:EC:6815:U:OP1	2.28	0.48
10:BN:99:ARG:NH2	10:BN:119:GLU:OE2	2.38	0.48
22:BP:122:THR:HG21	34:B5:1454:G:H4'	1.95	0.48
23:BQ:90:VAL:HG21	23:BQ:117:LEU:HD21	1.95	0.48
33:BM:23:THR:HG21	33:BM:26:ASP:HB2	1.96	0.48
34:B5:183:U:H2'	34:B5:184:C:H6	1.79	0.48
34:B5:208:U:H2'	34:B5:209:U:C6	2.49	0.48
34:B5:1208:A:H8	34:B5:1269:OMU:H6	1.78	0.48
38:A1:1666:G:H2'	38:A1:1667:A:C8	2.48	0.48
40:A4:8:C:H2'	40:A4:9:A:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:AJ:37:LEU:O	47:AJ:41:SER:OG	2.29	0.48
68:Af:67:MET:HE1	68:Af:90:PRO:HD3	1.96	0.48
4:BE:77:ARG:NH2	34:B5:122:U:O3'	2.47	0.48
8:BJ:175:ARG:NH2	34:B5:538:A:OP1	2.47	0.48
13:BW:12:ASN:ND2	34:B5:1095:U:O2	2.39	0.48
20:BF:124:LEU:HG	28:BZ:58:ARG:HG3	1.95	0.48
38:A1:716:A:C5	63:Aa:117:ARG:HG3	2.48	0.48
38:A1:1098:A:OP2	56:AT:130:ARG:NE	2.40	0.48
38:A1:1313:G:O2'	38:A1:1318:A:N1	2.45	0.48
38:A1:2759:U:H5''	38:A1:2760:C:H5'	1.95	0.48
46:AI:49:CYS:HB3	46:AI:168:SER:HB3	1.96	0.48
65:Ac:24:THR:HG22	65:Ac:91:SER:HB3	1.96	0.48
7:BI:16:ALA:HB2	34:B5:354:C:H5''	1.95	0.47
8:BJ:109:LEU:HB2	8:BJ:146:PHE:HB3	1.96	0.47
13:BW:15:ASN:ND2	13:BW:72:CYS:O	2.34	0.47
25:BS:127:HIS:CE1	25:BS:133:VAL:HG11	2.49	0.47
27:BU:58:LEU:HD23	34:B5:1516:A:H5''	1.95	0.47
31:Bg:45:TRP:HA	31:Bg:57:PRO:HA	1.96	0.47
34:B5:1142:A:H2'	34:B5:1143:A:C8	2.49	0.47
34:B5:1642:G:H2'	34:B5:1643:U:H6	1.78	0.47
38:A1:717:C:OP1	38:A1:751:A:O2'	2.27	0.47
38:A1:769:G:O2'	48:AL:168:ARG:NH1	2.40	0.47
38:A1:967:A:OP1	63:Aa:47:LYS:NZ	2.47	0.47
38:A1:2499:U:H6	38:A1:2500:A:H2'	1.79	0.47
40:A4:150:G:OP1	60:AX:27:ARG:NH2	2.47	0.47
45:AH:129:ARG:O	45:AH:132:VAL:HG12	2.14	0.47
61:AY:60:ARG:HB2	61:AY:103:LYS:HD3	1.95	0.47
63:Aa:90:TYR:CG	63:Aa:100:PRO:HG3	2.49	0.47
72:Aj:66:TYR:OH	72:Aj:73:ARG:NH2	2.47	0.47
20:BF:72:HIS:HA	20:BF:107:LYS:HE2	1.95	0.47
22:BP:33:PHE:HZ	22:BP:112:LEU:HB3	1.79	0.47
25:BS:17:LEU:O	25:BS:20:THR:OG1	2.25	0.47
25:BS:25:ASN:HB3	28:BZ:40:VAL:HG21	1.97	0.47
34:B5:443:C:O2'	34:B5:445:A:N7	2.45	0.47
38:A1:1615:C:H2'	38:A1:1616:U:C6	2.49	0.47
38:A1:2115:G:H22	38:A1:2120:A:H1'	1.79	0.47
38:A1:2366:C:H2'	38:A1:2367:A:C8	2.49	0.47
52:AP:113:TYR:HB3	52:AP:153:LYS:HZ1	1.79	0.47
80:EC:6828:G:H2'	80:EC:6829:A:H8	1.79	0.47
32:Bf:132:LEU:HD22	32:Bf:141:CYS:HA	1.95	0.47
34:B5:276:C:O2'	34:B5:278:U:OP2	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:146:THR:N	35:AA:158:ILE:O	2.47	0.47
37:AC:126:ILE:O	37:AC:129:THR:OG1	2.29	0.47
38:A1:128:G:OP2	70:Ah:74:LYS:NZ	2.46	0.47
38:A1:197:G:O2'	38:A1:218:G:N2	2.47	0.47
38:A1:629:U:H2'	38:A1:630:A:C8	2.49	0.47
38:A1:1176:C:H2'	38:A1:1177:G:N2	2.30	0.47
38:A1:1629:U:C5	62:AZ:112:LYS:HG3	2.50	0.47
38:A1:2988:C:OP1	51:AO:65[A]:ASN:ND2	2.44	0.47
44:AG:78:PHE:O	44:AG:79:GLN:HG3	2.14	0.47
77:Ao:35:LEU:HA	77:Ao:40:LYS:HG2	1.95	0.47
5:BG:32:ILE:HA	5:BG:52:ILE:HG23	1.95	0.47
9:BL:57:LYS:O	9:BL:138:ASN:ND2	2.44	0.47
34:B5:1041:G:H2'	34:B5:1042:G:C8	2.50	0.47
34:B5:1164:G:H2'	34:B5:1165:G:C8	2.49	0.47
38:A1:2503:G:H2'	38:A1:2504:U:C6	2.49	0.47
38:A1:3358:U:H2'	38:A1:3359:A:C8	2.49	0.47
3:BC:43:ARG:HA	3:BC:46:LYS:HZ2	1.79	0.47
18:Be:28:LYS:NZ	34:B5:542:A:OP1	2.41	0.47
24:BR:7:LYS:NZ	34:B5:1316:G:OP1	2.39	0.47
34:B5:155:U:O2'	34:B5:157:A:N7	2.40	0.47
34:B5:1158:C:O2'	34:B5:1581:C:OP2	2.33	0.47
34:B5:1227:A:H61	34:B5:1256:A:H5''	1.79	0.47
34:B5:1441:C:O2'	34:B5:1447:C:N4	2.47	0.47
34:B5:1785:U:H2'	34:B5:1786:G:H8	1.78	0.47
36:AB:288:GLY:N	36:AB:320:ASP:OD1	2.44	0.47
38:A1:1119:C:H2'	38:A1:1120:A:C8	2.48	0.47
38:A1:1809:A:H2'	38:A1:1810:A:O4'	2.15	0.47
38:A1:1836:C:O2'	38:A1:1842:A:N1	2.42	0.47
38:A1:2404:A:N7	38:A1:2872:A:N6	2.62	0.47
38:A1:3302:U:H3	38:A1:3312:U:H3	1.61	0.47
49:AM:14:LEU:H	49:AM:19:ARG:NH2	2.12	0.47
79:E:17:LEU:HG	79:E:172:VAL:HG23	1.96	0.47
5:BG:131:LYS:HD2	34:B5:166:C:H4'	1.95	0.47
8:BJ:106:GLU:HA	8:BJ:111:THR:HG21	1.97	0.47
20:BF:140:THR:O	20:BF:142:PRO:HD3	2.15	0.47
21:BK:30:ALA:HA	21:BK:38:LYS:HG2	1.96	0.47
38:A1:335:G:OP2	61:AY:14:LYS:NZ	2.37	0.47
38:A1:656:A:H2'	38:A1:657:A:C8	2.50	0.47
38:A1:837:A:OP1	78:Ap:5:THR:OG1	2.27	0.47
38:A1:1336:U:H2'	38:A1:1337:A:H8	1.79	0.47
38:A1:2597:U:H2'	38:A1:2598:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2882:U:H2'	38:A1:2883:U:C6	2.50	0.47
44:AG:91:PHE:HE1	44:AG:180:VAL:HG21	1.78	0.47
68:Af:75:HIS:HB3	68:Af:80:VAL:HG12	1.95	0.47
7:BI:36:THR:O	7:BI:96:LEU:N	2.42	0.47
25:BS:143:ARG:HH21	34:B5:1461:C:H3'	1.79	0.47
32:Bf:133:ALA:O	32:Bf:139:LEU:HD12	2.14	0.47
33:BM:43:ARG:HA	33:BM:121:VAL:HG22	1.97	0.47
33:BM:53:THR:HA	33:BM:84:ASN:HD21	1.79	0.47
34:B5:939:A:H2'	34:B5:940:A:C8	2.49	0.47
34:B5:1087:A:H2'	34:B5:1088:A:C8	2.50	0.47
34:B5:1469:A:H4'	34:B5:1541:G:H5'	1.95	0.47
34:B5:1515:A:O2'	34:B5:1517:U:OP2	2.31	0.47
35:AA:223:SER:OG	38:A1:2244:A:O2'	2.32	0.47
36:AB:266:ARG:NH2	38:A1:2392:C:H1'	2.29	0.47
36:AB:315:GLY:HA2	38:A1:3379:C:H4'	1.96	0.47
38:A1:673:U:H2'	38:A1:674:G:C8	2.50	0.47
38:A1:1597:C:H2'	38:A1:1598:G:C8	2.50	0.47
38:A1:2152:A:H2'	38:A1:2153:U:H6	1.79	0.47
38:A1:2369:G:H2'	38:A1:2370:G:C8	2.49	0.47
40:A4:57:C:H4'	40:A4:63:G:N7	2.29	0.47
43:AF:147:LEU:HD12	43:AF:244:ASN:HD22	1.80	0.47
61:AY:3:LYS:HD2	61:AY:8:VAL:HG13	1.96	0.47
77:Ao:7:THR:OG1	77:Ao:22:GLN:OE1	2.32	0.47
80:EC:6759:A:H2'	80:EC:6760:A:C8	2.50	0.47
80:EC:6810:U:H2'	80:EC:6811:G:C8	2.49	0.47
1:BA:59:LEU:O	1:BA:63:ILE:HG12	2.15	0.47
4:BE:72:VAL:N	4:BE:75:LYS:O	2.42	0.47
5:BG:92:ARG:NH1	34:B5:1674:C:OP1	2.47	0.47
6:BH:158:ASP:O	6:BH:161:GLN:NE2	2.47	0.47
22:BP:105:VAL:HG23	25:BS:120:ARG:HH11	1.79	0.47
23:BQ:36:ILE:HG12	23:BQ:49:TYR:HE1	1.80	0.47
31:Bg:63:GLY:HA3	31:Bg:90:ARG:NH1	2.29	0.47
34:B5:1187:U:H3	34:B5:1198:G:H1	1.63	0.47
34:B5:1228:G:OP1	34:B5:1228:G:N2	2.48	0.47
38:A1:412:G:OP1	52:AP:62:ARG:NH1	2.48	0.47
38:A1:531:G:H2'	38:A1:532:A:C8	2.50	0.47
38:A1:2203:U:H2'	38:A1:2204:C:C6	2.50	0.47
38:A1:2661:G:H2'	38:A1:2662:G:H8	1.80	0.47
38:A1:2838:A:H4'	46:AI:74:LYS:HD3	1.97	0.47
41:AD:236:LEU:HD12	41:AD:239:ILE:HD11	1.96	0.47
50:AN:36:ILE:HG12	50:AN:64:VAL:HG23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:AT:132:PRO:O	56:AT:134:GLN:NE2	2.48	0.47
63:Aa:3:SER:O	63:Aa:6:THR:OG1	2.29	0.47
69:Ag:44:CYS:HB2	69:Ag:81:CYS:HB3	1.97	0.47
80:EC:6873:A:H2'	80:EC:6874:A:H2'	1.97	0.47
2:BB:180:THR:O	2:BB:184:LEU:N	2.46	0.47
4:BE:40:GLU:OE1	4:BE:103:TYR:OH	2.30	0.47
5:BG:132:ARG:HG3	5:BG:133:LEU:HD12	1.97	0.47
11:BO:99:GLN:NE2	16:Ba:45:VAL:HA	2.30	0.47
15:BY:44:LEU:HA	15:BY:47:VAL:HG12	1.97	0.47
25:BS:30:TYR:O	25:BS:33:THR:OG1	2.30	0.47
34:B5:515:A:N6	34:B5:537:G:O2'	2.42	0.47
34:B5:521:A:H2'	34:B5:522:U:C6	2.50	0.47
38:A1:92:G:H5'	38:A1:94:G:N7	2.30	0.47
38:A1:1492:G:O2'	74:A1:48:LYS:NZ	2.48	0.47
38:A1:3121:U:H1'	38:A1:3122:A:H5''	1.96	0.47
45:AH:5:GLN:NE2	45:AH:7:GLU:OE1	2.48	0.47
2:BB:149:GLN:NE2	2:BB:151:LYS:O	2.42	0.47
2:BB:190:PRO:HB2	2:BB:192:VAL:HG13	1.97	0.47
5:BG:175:ILE:HG12	34:B5:78:A:H1'	1.97	0.47
13:BW:52:TYR:HA	13:BW:61:ILE:HD13	1.97	0.47
19:BD:94:ARG:O	19:BD:97:SER:OG	2.32	0.47
26:BT:7:ARG:NH1	34:B5:1365:C:O4'	2.48	0.47
34:B5:1642:G:H2'	34:B5:1643:U:C6	2.50	0.47
36:AB:99:LEU:O	38:A1:3004:C:O2'	2.25	0.47
38:A1:1101:G:H1'	43:AF:105:LEU:HD23	1.97	0.47
38:A1:1616:U:H2'	38:A1:1617:G:C8	2.50	0.47
38:A1:2947:G:OP1	38:A1:2982:A:N6	2.41	0.47
38:A1:3343:G:O2'	38:A1:3362:A:N6	2.48	0.47
47:AJ:47:GLN:HB3	47:AJ:64:LYS:HD2	1.97	0.47
76:An:2:ARG:HB3	76:An:5:TRP:CD1	2.50	0.47
2:BB:92:GLN:HE21	2:BB:95:ASN:HD22	1.63	0.46
2:BB:228:LEU:HG	2:BB:232:HIS:HD2	1.80	0.46
3:BC:168:ARG:HD2	34:B5:1097:U:H1'	1.97	0.46
7:BI:192:TYR:O	7:BI:197:THR:OG1	2.34	0.46
31:Bg:33:LEU:HB3	31:Bg:45:TRP:HB2	1.96	0.46
34:B5:108:A:H2'	34:B5:109:G:C8	2.50	0.46
34:B5:269:G:H2'	34:B5:270:C:C6	2.50	0.46
36:AB:375:GLU:OE2	59:AW:14:TYR:OH	2.27	0.46
37:AC:291:ASN:HD21	38:A1:1349:G:H4'	1.80	0.46
38:A1:498:A:O2'	38:A1:3273:A:N1	2.45	0.46
38:A1:631:U:H2'	38:A1:632:G:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1945:A:H2'	38:A1:1946:A:C8	2.49	0.46
14:BX:63:GLN:HA	34:B5:1755:A:H5''	1.97	0.46
32:Bf:108:VAL:HG22	32:Bf:114:VAL:HG23	1.97	0.46
34:B5:1237:G:N1	34:B5:1249:U:O4	2.48	0.46
34:B5:1393:C:H2'	34:B5:1394:G:C8	2.49	0.46
34:B5:1606:C:H2'	34:B5:1607:G:C8	2.51	0.46
38:A1:1084:A:H2'	38:A1:1085:A:C8	2.50	0.46
38:A1:1244:A:O2'	38:A1:1272:C:OP1	2.32	0.46
38:A1:2935:U:O4	58:AV:44:SER:OG	2.33	0.46
46:AI:184:LYS:HD3	46:AI:199:PHE:HE1	1.81	0.46
4:BE:121:TYR:OH	4:BE:235:TYR:O	2.26	0.46
11:BO:11:SER:OG	11:BO:12:GLN:N	2.49	0.46
11:BO:129:LYS:HB2	34:B5:990:C:H5''	1.97	0.46
20:BF:42:LEU:HD23	20:BF:46:TRP:HD1	1.79	0.46
22:BP:99:GLY:O	34:B5:1211:A:O2'	2.27	0.46
31:Bg:217:ASP:N	31:Bg:217:ASP:OD1	2.48	0.46
34:B5:5:U:H2'	34:B5:6:G:C8	2.50	0.46
34:B5:15:U:H2'	34:B5:16:G:O4'	2.15	0.46
38:A1:728:G:H5''	53:AQ:43:PRO:HB2	1.97	0.46
38:A1:1764:U:H3'	38:A1:1765:U:H4'	1.97	0.46
38:A1:2180:G:H2'	38:A1:2181:C:C6	2.51	0.46
38:A1:3119:U:H4'	75:Am:104:PRO:HG3	1.98	0.46
59:AW:46:PRO:HB2	59:AW:54:LEU:HD23	1.96	0.46
73:Ak:63:LYS:O	73:Ak:67:GLN:NE2	2.48	0.46
79:E:128:LEU:HB3	79:E:135:PRO:HG3	1.97	0.46
80:EC:6787:U:O2'	80:EC:6805:C:N4	2.48	0.46
4:BE:19:LEU:HD23	34:B5:788:A:C4	2.50	0.46
4:BE:45:ILE:HA	4:BE:61:VAL:HG11	1.98	0.46
20:BF:54:LYS:NZ	20:BF:131:GLN:OE1	2.38	0.46
20:BF:159:ALA:HB3	20:BF:225:ARG:HD3	1.98	0.46
26:BT:3:GLY:HA2	34:B5:1360:A:H2'	1.96	0.46
33:BM:53:THR:HA	33:BM:84:ASN:ND2	2.31	0.46
38:A1:1240:A:N6	38:A1:1245:A:OP1	2.39	0.46
38:A1:2573:G:H2'	38:A1:2574:G:C8	2.51	0.46
44:AG:190:VAL:HG23	44:AG:192:GLN:HG2	1.97	0.46
63:Aa:77:LYS:O	63:Aa:80:THR:OG1	2.29	0.46
2:BB:24:PHE:HA	2:BB:27:LYS:HD2	1.97	0.46
5:BG:56:ASN:HB2	34:B5:154:G:H1'	1.98	0.46
5:BG:72:ARG:HH21	34:B5:419:G:H5'	1.80	0.46
23:BQ:128:LYS:HB2	23:BQ:137:ARG:HH22	1.81	0.46
24:BR:10:LYS:NZ	34:B5:1401:A:O3'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	1.97	0.46
28:BZ:73:GLY:HA3	34:B5:1534:G:C8	2.49	0.46
34:B5:895:G:H1	34:B5:917:U:H3	1.61	0.46
34:B5:1171:A:H2'	34:B5:1172:G:C8	2.50	0.46
34:B5:1683:C:O2'	34:B5:1684:U:O5'	2.27	0.46
38:A1:180:C:H2'	38:A1:181:U:O4'	2.15	0.46
38:A1:518:G:OP2	38:A1:518:G:N2	2.35	0.46
38:A1:821:U:H2'	38:A1:822:G:C8	2.51	0.46
49:AM:27:GLN:NE2	49:AM:28:SER:OG	2.49	0.46
49:AM:40:ASP:OD2	49:AM:43:LYS:N	2.49	0.46
16:Ba:4:LYS:NZ	34:B5:1795:U:OP2	2.41	0.46
21:BK:1:MET:SD	34:B5:1216:C:H3'	2.56	0.46
21:BK:32:HIS:CD2	21:BK:42:VAL:HG11	2.51	0.46
26:BT:7:ARG:NH2	34:B5:1364:G:N3	2.63	0.46
34:B5:1230:A:H61	34:B5:1255:G:H1'	1.80	0.46
38:A1:1528:G:O2'	38:A1:1588:A:N3	2.44	0.46
38:A1:2424:A:OP1	50:AN:90:ASN:ND2	2.49	0.46
38:A1:2464:U:OP1	38:A1:2485:A:O2'	2.33	0.46
39:A3:84:A:H2'	39:A3:85:G:C8	2.51	0.46
41:AD:119:TYR:OH	41:AD:139:PRO:O	2.26	0.46
41:AD:153:THR:HG23	41:AD:160:PHE:HZ	1.81	0.46
1:BA:92:HIS:HB3	1:BA:182:LEU:HD11	1.98	0.46
28:BZ:82:HIS:O	28:BZ:85:LYS:HG2	2.16	0.46
34:B5:1647:U:H2'	34:B5:1648:A:C8	2.51	0.46
34:B5:1777:G:O6	76:An:8:LYS:NZ	2.48	0.46
38:A1:1174:G:N2	51:AO:87[A]:MET:HE2	2.31	0.46
38:A1:3013:U:H2'	38:A1:3014:U:C6	2.51	0.46
79:E:113:SER:OG	79:E:138:VAL:O	2.26	0.46
80:EC:6804:A:H4'	80:EC:6805:C:H5'	1.98	0.46
7:BI:37:LYS:HB2	7:BI:59:ARG:HG3	1.96	0.46
23:BQ:68:ARG:NH1	23:BQ:70:THR:OG1	2.49	0.46
34:B5:179:A:H3'	34:B5:180:A:H8	1.79	0.46
34:B5:877:G:H22	34:B5:951:A:H2	1.63	0.46
34:B5:1188:G:H3'	34:B5:1189:A:C8	2.49	0.46
34:B5:1409:G:N1	34:B5:1412:G:OP2	2.49	0.46
34:B5:1484:G:H2'	34:B5:1485:C:C6	2.51	0.46
38:A1:19:U:H2'	38:A1:20:A:C8	2.51	0.46
38:A1:273:A:H2'	38:A1:274:G:H8	1.80	0.46
38:A1:2883:U:H2'	38:A1:2884:C:H6	1.81	0.46
38:A1:2945:G:O2'	38:A1:2948:OMC:OP2	2.26	0.46
38:A1:3000:A:H2'	38:A1:3001:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3296:A:H2'	38:A1:3297:U:H6	1.80	0.46
53:AQ:116:LYS:NZ	63:Aa:88:ASP:OD2	2.38	0.46
54:AR:105:LEU:HD13	54:AR:135:LYS:HE2	1.96	0.46
79:E:194:LEU:HD13	79:E:200:ASN:HB2	1.97	0.46
1:BA:201:LEU:HD23	24:BR:85:VAL:HB	1.98	0.46
4:BE:49:ARG:NH2	34:B5:448:C:OP1	2.29	0.46
6:BH:93:LEU:HD22	6:BH:125:ILE:HG23	1.98	0.46
25:BS:41:ARG:NE	26:BT:46:PRO:HD3	2.31	0.46
26:BT:72:GLY:HA3	34:B5:1498:G:H5''	1.97	0.46
34:B5:1471:A:H2	34:B5:1474:G:N3	2.14	0.46
38:A1:1718:G:H2'	38:A1:1719:G:C8	2.50	0.46
52:AP:41:LEU:HD22	52:AP:150:VAL:HG11	1.96	0.46
79:E:188:ASN:HA	79:E:191:VAL:HG22	1.98	0.46
2:BB:150:VAL:HG22	34:B5:1067:C:H5''	1.98	0.46
3:BC:157:LYS:NZ	13:BW:91:ALA:O	2.38	0.46
7:BI:37:LYS:C	7:BI:59:ARG:HA	2.41	0.46
23:BQ:72:GLY:H	34:B5:1483:A:H4'	1.81	0.46
28:BZ:84:GLU:OE1	28:BZ:84:GLU:N	2.49	0.46
32:Bf:121:CYS:HB3	32:Bf:126:CYS:HB3	1.77	0.46
34:B5:1524:A:N3	34:B5:1590:G:O2'	2.49	0.46
35:AA:44:ILE:HD11	35:AA:85:GLY:HA2	1.98	0.46
38:A1:1498:A:H2'	38:A1:1499:C:C6	2.51	0.46
38:A1:2406:C:H2'	38:A1:2407:C:C6	2.51	0.46
38:A1:2953:U:H2'	38:A1:2954:U:H2'	1.97	0.46
40:A4:126:A:O2'	40:A4:129:C:N4	2.48	0.46
44:AG:27:THR:HG21	62:AZ:55:LYS:HD3	1.98	0.46
44:AG:173:MET:HB2	44:AG:175:VAL:HG23	1.97	0.46
79:E:156:LYS:HB3	79:E:156:LYS:HE2	1.64	0.46
1:BA:8:ASP:OD1	1:BA:9:LEU:N	2.47	0.45
2:BB:134:VAL:HB	2:BB:219:LYS:HB2	1.98	0.45
13:BW:41:MET:HG2	13:BW:129:VAL:HG11	1.98	0.45
14:BX:53:VAL:HG22	14:BX:72:VAL:HG11	1.97	0.45
34:B5:209:U:H2'	34:B5:210:A:H8	1.81	0.45
34:B5:1071:U:H2'	34:B5:1072:C:C6	2.51	0.45
34:B5:1648:A:H2'	34:B5:1649:G:H8	1.82	0.45
35:AA:108:PRO:HG3	78:Ap:90:VAL:HG21	1.97	0.45
35:AA:108:PRO:HB2	78:Ap:86:LEU:HD22	1.98	0.45
38:A1:1657:C:O2'	38:A1:1797:A:OP2	2.24	0.45
38:A1:2499:U:C6	38:A1:2500:A:H2'	2.51	0.45
44:AG:189:LEU:HD12	44:AG:190:VAL:HG13	1.98	0.45
62:AZ:41:ALA:HB2	62:AZ:77:TYR:HE1	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:EC:6770:U:H3	80:EC:6772:G:N2	2.13	0.45
1:BA:76:ILE:HG13	1:BA:98:ILE:HB	1.98	0.45
5:BG:178:LEU:HD21	34:B5:78:A:C6	2.51	0.45
6:BH:47:ARG:O	6:BH:47:ARG:HG3	2.15	0.45
7:BI:101:ILE:HD12	7:BI:184:LEU:HD11	1.99	0.45
7:BI:104:ILE:HG13	7:BI:105:ASP:H	1.80	0.45
11:BO:17:ALA:HB3	11:BO:81:VAL:HA	1.98	0.45
16:Ba:7:SER:O	16:Ba:7:SER:OG	2.32	0.45
30:Bd:15:GLY:HA3	34:B5:1204:A:H61	1.80	0.45
34:B5:407:A:H2'	34:B5:408:C:C6	2.51	0.45
34:B5:1114:G:O2'	34:B5:1130:G:O6	2.28	0.45
34:B5:1508:U:H2'	34:B5:1509:C:C6	2.52	0.45
35:AA:117:GLU:OE2	35:AA:163:ARG:NH2	2.47	0.45
38:A1:428:A:H2'	38:A1:429:U:C6	2.51	0.45
38:A1:2423:U:H2'	38:A1:2424:A:C8	2.52	0.45
38:A1:3193:C:H2'	38:A1:3194:C:C6	2.52	0.45
47:AJ:16:LYS:HD3	47:AJ:72:ARG:NH2	2.31	0.45
80:EC:6936:G:H2'	80:EC:6937:G:C8	2.52	0.45
1:BA:156:VAL:O	12:BV:65:SER:OG	2.34	0.45
3:BC:225:LEU:HD13	12:BV:23:ILE:HD11	1.98	0.45
5:BG:16:PHE:HE2	5:BG:121:LEU:HD13	1.81	0.45
13:BW:31:SER:H	13:BW:34:ILE:HD12	1.81	0.45
16:Ba:8:ASN:HB3	34:B5:1791:A:H3'	1.97	0.45
19:BD:42:THR:OG1	19:BD:45:LYS:O	2.24	0.45
21:BK:44:LYS:HE2	34:B5:1217:A:H5''	1.99	0.45
23:BQ:136:SER:HB2	34:B5:1586:A:H5''	1.98	0.45
34:B5:11:A:N3	34:B5:1300:A:O2'	2.48	0.45
34:B5:1239:U:H3	34:B5:1246:C:H42	1.62	0.45
38:A1:716:A:C6	63:Aa:117:ARG:HG3	2.52	0.45
38:A1:2157:G:N2	38:A1:2177:G:O2'	2.49	0.45
38:A1:2961:G:H2'	38:A1:2962:U:C6	2.50	0.45
54:AR:98:ARG:NH1	54:AR:133:LYS:O	2.48	0.45
22:BP:128:HIS:HE1	34:B5:1459:C:H1'	1.82	0.45
34:B5:224:C:N4	34:B5:225:A:H62	2.15	0.45
34:B5:824:G:H2'	34:B5:825:U:H6	1.81	0.45
34:B5:1451:C:H2'	34:B5:1452:U:H6	1.81	0.45
36:AB:73:VAL:O	58:AV:86:ARG:NH2	2.50	0.45
36:AB:229:VAL:HG21	36:AB:249:VAL:HG23	1.98	0.45
36:AB:250:ALA:HB1	38:A1:2947:G:N3	2.32	0.45
38:A1:173:G:H1	38:A1:244:G:N2	2.11	0.45
38:A1:1134:G:O2'	38:A1:2642:A:N3	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2611:U:H2'	38:A1:2612:U:C6	2.51	0.45
38:A1:2660:G:O3'	38:A1:2749:G:N2	2.49	0.45
38:A1:2883:U:H2'	38:A1:2884:C:C6	2.51	0.45
42:AE:76:LEU:N	42:AE:138:GLN:OE1	2.48	0.45
67:Ae:91:THR:HG23	67:Ae:92:TYR:CD2	2.51	0.45
2:BB:216:LYS:NZ	34:B5:885:G:OP1	2.40	0.45
3:BC:50:ILE:HG21	3:BC:56:ILE:HD11	1.99	0.45
5:BG:57:ASP:HA	5:BG:106:LEU:HA	1.99	0.45
5:BG:161:GLU:HG3	5:BG:170:THR:HB	1.99	0.45
22:BP:90:ILE:HD13	22:BP:107:ILE:HG22	1.97	0.45
29:Bc:18:ARG:HE	34:B5:1616:G:H4'	1.82	0.45
34:B5:190:C:N4	34:B5:196:G:OP2	2.41	0.45
34:B5:655:G:N2	34:B5:678:A:OP2	2.42	0.45
34:B5:947:U:H2'	34:B5:948:G:C8	2.50	0.45
34:B5:1609:U:H2'	34:B5:1610:G:O4'	2.17	0.45
38:A1:269:G:OP1	50:AN:47:LYS:NZ	2.44	0.45
38:A1:761:A:C2	38:A1:771:A:H1'	2.51	0.45
38:A1:938:C:OP2	63:Aa:26:ARG:NH1	2.49	0.45
38:A1:1213:G:H4'	55:AS:90:MET:HB2	1.98	0.45
41:AD:143:LYS:HG3	41:AD:172:TYR:HD2	1.82	0.45
45:AH:36:LYS:HB2	45:AH:78:MET:SD	2.56	0.45
46:AI:191:LYS:HZ1	46:AI:212:GLU:HG3	1.82	0.45
48:AL:89:TYR:O	48:AL:92:THR:OG1	2.33	0.45
61:AY:85:VAL:HG12	61:AY:97:ILE:HB	1.99	0.45
65:Ac:43:ILE:HG13	65:Ac:68:TYR:HB3	1.98	0.45
4:BE:187:ARG:NH2	34:B5:791:A:OP1	2.45	0.45
7:BI:121:LEU:HD22	7:BI:157:GLU:HB3	1.98	0.45
14:BX:107:PHE:HD1	14:BX:123:LYS:HB3	1.82	0.45
15:BY:55:VAL:HG12	15:BY:75:VAL:HG22	1.98	0.45
20:BF:41:LYS:NZ	20:BF:47:SER:OG	2.48	0.45
20:BF:108:LEU:HA	20:BF:111:VAL:HG12	1.97	0.45
31:Bg:205:SER:OG	31:Bg:210:LEU:O	2.32	0.45
34:B5:536:C:H3'	34:B5:537:G:C8	2.50	0.45
38:A1:345:G:O2'	40:A4:25:G:N3	2.47	0.45
38:A1:748:U:H2'	38:A1:749:C:C6	2.51	0.45
38:A1:1791:C:H2'	38:A1:1792:C:C6	2.52	0.45
38:A1:1805:C:H2'	38:A1:1806:A:H8	1.81	0.45
38:A1:1899:G:O2'	38:A1:2334:U:O4	2.29	0.45
38:A1:2368:A:H2'	38:A1:2369:G:C8	2.52	0.45
50:AN:105:ARG:HG2	50:AN:108:ARG:HH22	1.82	0.45
51:AO:26[A]:GLN:HG3	51:AO:31[A]:GLN:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:AR:45:VAL:HG22	54:AR:50:ILE:HB	1.99	0.45
63:Aa:36:GLY:HA3	63:Aa:40:HIS:CE1	2.52	0.45
1:BA:115:PHE:HZ	3:BC:39:THR:HG22	1.82	0.45
3:BC:201:ASN:ND2	34:B5:1097:U:O4	2.49	0.45
3:BC:230:TRP:CE2	13:BW:68:ARG:HB3	2.52	0.45
16:Ba:41:ILE:HD11	16:Ba:66:LYS:HE2	1.99	0.45
24:BR:72:LYS:HE3	24:BR:72:LYS:HB2	1.72	0.45
28:BZ:68:ARG:NH1	80:EC:6864:A:O4'	2.49	0.45
32:Bf:97:LYS:NZ	34:B5:1230:A:OP1	2.32	0.45
34:B5:888:U:H2'	34:B5:889:U:C6	2.52	0.45
34:B5:1308:G:H2'	34:B5:1309:C:C6	2.51	0.45
38:A1:1128:U:OP1	46:AI:4:ARG:NH1	2.38	0.45
38:A1:1688:U:H2'	38:A1:1689:U:C6	2.52	0.45
47:AJ:45:PRO:HB3	47:AJ:69:VAL:HG22	1.98	0.45
1:BA:15:GLN:HE21	24:BR:100:LEU:HD21	1.81	0.45
3:BC:143:TYR:OH	3:BC:149:GLY:O	2.33	0.45
3:BC:165:VAL:HG11	3:BC:210:THR:HA	1.99	0.45
6:BH:71:HIS:HD2	6:BH:131:PHE:CD1	2.35	0.45
7:BI:11:ARG:HD3	34:B5:318:U:H4'	1.98	0.45
8:BJ:85:VAL:HG23	8:BJ:103:ASP:HB3	1.98	0.45
20:BF:219:ARG:HH11	20:BF:222:LYS:HE3	1.81	0.45
34:B5:16:G:H2'	34:B5:17:C:C6	2.51	0.45
34:B5:80:A:H3'	34:B5:81:G:H8	1.82	0.45
34:B5:1308:G:H2'	34:B5:1309:C:H6	1.82	0.45
36:AB:106:TRP:O	36:AB:137:TYR:OH	2.29	0.45
38:A1:2661:G:H2'	38:A1:2662:G:C8	2.52	0.45
61:AY:51:ARG:HD2	61:AY:115:ARG:HH11	1.82	0.45
62:AZ:16:GLY:C	62:AZ:18:TYR:H	2.25	0.45
79:E:26:ARG:HD3	79:E:28:PHE:CD2	2.52	0.45
2:BB:149:GLN:HG3	34:B5:1066:C:O3'	2.16	0.45
6:BH:47:ARG:HG2	6:BH:61:PHE:HE2	1.81	0.45
7:BI:78:ILE:HD13	7:BI:104:ILE:HG22	1.99	0.45
26:BT:106:GLN:NE2	34:B5:1500:C:OP1	2.50	0.45
34:B5:1647:U:H2'	34:B5:1648:A:H8	1.82	0.45
37:AC:108:LYS:HG3	50:AN:203:ARG:HG3	1.99	0.45
38:A1:2447:A:H2'	38:A1:2448:G:C8	2.51	0.45
38:A1:3308:C:O2'	52:AP:69:ARG:O	2.21	0.45
44:AG:137:ASN:OD1	50:AN:3:ALA:N	2.47	0.45
47:AJ:45:PRO:HB2	47:AJ:67:VAL:HG22	1.98	0.45
62:AZ:70:PRO:HG3	62:AZ:115:LYS:HB2	1.99	0.45
72:Aj:21:ARG:NH1	72:Aj:41:ALA:O	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:124:ARG:HD2	34:B5:628:G:OP1	2.17	0.45
22:BP:17:TYR:CD1	22:BP:18:ARG:HG2	2.51	0.45
27:BU:50:LEU:HD23	27:BU:94:GLU:H	1.81	0.45
31:Bg:180:ALA:HB3	31:Bg:190:ALA:HB3	1.99	0.45
31:Bg:249:ARG:HD2	31:Bg:251:TRP:CH2	2.52	0.45
34:B5:97:C:H1'	34:B5:426:G:H5'	1.99	0.45
34:B5:153:G:H2'	34:B5:154:G:C8	2.52	0.45
34:B5:340:U:H2'	34:B5:341:A:C8	2.52	0.45
34:B5:1670:G:O2'	34:B5:1731:A:N6	2.48	0.45
38:A1:1604:G:H4'	38:A1:1835:A:H4'	1.97	0.45
38:A1:1620:U:H2'	38:A1:1621:A:C8	2.52	0.45
38:A1:2930:A:H2'	38:A1:2931:C:C6	2.51	0.45
38:A1:3275:U:H5'	68:Af:68:TRP:CZ2	2.52	0.45
41:AD:82:GLU:O	41:AD:85:ARG:HG2	2.16	0.45
41:AD:208:MET:HG3	41:AD:233:ALA:HB2	1.99	0.45
67:Ae:91:THR:HG23	67:Ae:92:TYR:HD2	1.82	0.45
80:EC:6923:C:H2'	80:EC:6924:G:C8	2.52	0.45
1:BA:56:LYS:HE2	1:BA:158:VAL:HG13	2.00	0.44
2:BB:89:ASP:HB3	2:BB:223:PHE:CZ	2.46	0.44
3:BC:90:THR:HA	34:B5:1146:G:H4'	1.99	0.44
4:BE:26:CYS:SG	8:BJ:2:PRO:HB3	2.57	0.44
25:BS:126:ARG:HB2	25:BS:133:VAL:HG12	1.99	0.44
26:BT:16:ASN:OD1	26:BT:56:LYS:NZ	2.47	0.44
34:B5:1222:C:H2'	34:B5:1223:A:C8	2.53	0.44
37:AC:107:ARG:HA	38:A1:664:U:H5'	1.99	0.44
38:A1:2662:G:H2'	38:A1:2663:G:C8	2.51	0.44
38:A1:3023:U:H2'	38:A1:3024:A:C8	2.52	0.44
41:AD:64:ILE:HD12	41:AD:144:VAL:HG11	1.99	0.44
54:AR:175:GLN:HA	54:AR:179:GLU:HB2	1.99	0.44
2:BB:207:LEU:HD23	2:BB:210:ILE:HG12	1.98	0.44
6:BH:28:GLU:HG2	6:BH:39:ARG:HH21	1.81	0.44
13:BW:122:SER:O	34:B5:748:U:O2'	2.34	0.44
18:Be:55:ARG:NH2	34:B5:557:G:OP2	2.50	0.44
34:B5:436:A2M:H8	34:B5:436:A2M:O5'	2.16	0.44
34:B5:1314:U:H4'	34:B5:1315:U:H5	1.82	0.44
35:AA:244:GLY:HA3	38:A1:2242:A:H5''	1.98	0.44
38:A1:1155:C:O2'	38:A1:1197:A:N1	2.48	0.44
38:A1:1643:A:H2'	38:A1:1644:C:C2	2.53	0.44
38:A1:2922:OMG:C2	38:A1:2952:G:H1'	2.52	0.44
38:A1:2991:A:O2'	38:A1:3309:G:N7	2.51	0.44
45:AH:91:ARG:NH2	45:AH:141:LYS:O	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:AQ:68:ALA:HA	53:AQ:71:LEU:HD12	1.98	0.44
78:Ap:44:LYS:HD2	78:Ap:59:CYS:SG	2.57	0.44
2:BB:29:TRP:CE2	2:BB:47:LEU:HD13	2.52	0.44
11:BO:15:GLY:N	11:BO:78:ALA:O	2.44	0.44
23:BQ:51:PRO:HA	23:BQ:109:PHE:CE1	2.53	0.44
26:BT:5:SER:OG	26:BT:6:VAL:N	2.50	0.44
31:Bg:108:SER:HB2	31:Bg:128:ASP:HB2	1.99	0.44
34:B5:451:A:N6	34:B5:453:U:O2	2.50	0.44
37:AC:188:ARG:HG2	37:AC:189:ALA:H	1.83	0.44
38:A1:200:C:H5'	38:A1:221:A:C2	2.52	0.44
38:A1:229:G:H5''	61:AY:4:GLN:HB2	1.98	0.44
38:A1:754:G:H2'	38:A1:755:A:H8	1.82	0.44
38:A1:975:C:H2'	38:A1:976:U:C6	2.53	0.44
44:AG:78:PHE:C	44:AG:80:TYR:H	2.25	0.44
8:BJ:28:LEU:HD23	18:Be:44:PHE:HE2	1.82	0.44
23:BQ:77:GLN:O	23:BQ:81:ILE:N	2.38	0.44
25:BS:145:ARG:HE	34:B5:1172:G:H5''	1.82	0.44
31:Bg:20:VAL:HG21	31:Bg:310:ILE:HG13	1.99	0.44
31:Bg:74:THR:HG22	31:Bg:115:ILE:HG12	2.00	0.44
31:Bg:90:ARG:HH21	31:Bg:102:ARG:HH11	1.65	0.44
31:Bg:109:ASP:OD1	31:Bg:110:VAL:N	2.47	0.44
34:B5:454:U:H5''	34:B5:455:C:H5	1.82	0.44
34:B5:968:U:H2'	34:B5:969:C:O4'	2.18	0.44
37:AC:51:ALA:O	40:A4:26:U:O2'	2.33	0.44
37:AC:64:SER:HA	37:AC:75:PRO:HA	2.00	0.44
38:A1:165:A:H2'	38:A1:166:C:C6	2.52	0.44
38:A1:945:C:H2'	38:A1:946:U:C6	2.52	0.44
38:A1:1347:U:H2'	38:A1:1355:A:H61	1.80	0.44
38:A1:1737:U:O2	69:Ag:52:GLN:NE2	2.45	0.44
38:A1:1738:C:H2'	38:A1:1739:U:C6	2.53	0.44
38:A1:2376:G:H2'	38:A1:2377:G:C8	2.53	0.44
38:A1:2446:U:H5''	71:Ai:98:ARG:HH12	1.83	0.44
41:AD:41:LYS:HB2	56:AT:68:THR:O	2.17	0.44
56:AT:151:LEU:HG	56:AT:152:ALA:H	1.82	0.44
73:Ak:19:ASP:OD2	73:Ak:19:ASP:N	2.50	0.44
1:BA:41:ARG:NH2	24:BR:103:ASP:HB3	2.32	0.44
4:BE:105:VAL:HG21	4:BE:245:LYS:H	1.83	0.44
5:BG:194:LYS:HD3	34:B5:127:G:H4'	1.99	0.44
30:Bd:10:HIS:ND1	34:B5:1452:U:OP1	2.50	0.44
31:Bg:175:ASP:OD1	31:Bg:175:ASP:N	2.51	0.44
33:BM:32:LEU:HD21	33:BM:59:LEU:HD21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:250:ALA:HB1	38:A1:2947:G:C2	2.53	0.44
38:A1:753:C:H2'	38:A1:754:G:H8	1.83	0.44
38:A1:761:A:H2'	38:A1:762:U:C6	2.53	0.44
38:A1:1260:A:H2'	38:A1:1261:G:C4	2.52	0.44
41:AD:65:ILE:HG12	41:AD:74:VAL:HG23	2.00	0.44
52:AP:36:ILE:HD13	52:AP:95:LEU:HD11	1.98	0.44
53:AQ:71:LEU:HD13	53:AQ:99:THR:HG21	2.00	0.44
79:E:134:PHE:HA	79:E:135:PRO:HD3	1.78	0.44
80:EC:6844:A:H1'	80:EC:6845:G:C8	2.51	0.44
80:EC:6939:C:N4	80:EC:6940:U:N3	2.65	0.44
20:BF:163:SER:HB3	20:BF:166:ARG:HB3	2.00	0.44
31:Bg:152:SER:H	31:Bg:173:GLY:HA2	1.83	0.44
33:BM:87:PRO:HB3	33:BM:140:PHE:CD1	2.52	0.44
34:B5:60:U:H5'	34:B5:455:C:N4	2.33	0.44
34:B5:1591:C:H2'	34:B5:1592:A:C8	2.51	0.44
36:AB:215:ILE:HD12	36:AB:338:LEU:HB3	2.00	0.44
38:A1:36:C:H4'	38:A1:808:A:C2	2.53	0.44
38:A1:1915:A:H2'	38:A1:1916:U:C6	2.53	0.44
38:A1:2927:C:H2'	38:A1:2928:C:C6	2.53	0.44
38:A1:3153:U:H5	38:A1:3293:U:H3	1.65	0.44
44:AG:162:LEU:HD21	50:AN:45:PRO:HG2	1.98	0.44
49:AM:65:LEU:HG	55:AS:172:TYR:OH	2.17	0.44
74:Al:44:TRP:CE2	74:Al:45:ARG:HG3	2.53	0.44
77:Ao:15:LYS:HG2	77:Ao:18:ARG:HH21	1.82	0.44
2:BB:121:ILE:HG12	2:BB:161:ILE:HG23	1.99	0.44
14:BX:73:ARG:HE	14:BX:82:LYS:HB3	1.83	0.44
23:BQ:63:ILE:HD12	23:BQ:65:ILE:HD11	2.00	0.44
34:B5:392:G:OP1	34:B5:1729:C:O2'	2.32	0.44
34:B5:699:U:O2	34:B5:741:C:N4	2.50	0.44
34:B5:791:A:H2'	34:B5:792:U:C6	2.52	0.44
38:A1:2451:G:H2'	38:A1:2452:G:H8	1.82	0.44
38:A1:2801:A:O2'	38:A1:2802:A:H2'	2.18	0.44
38:A1:3162:C:H2'	38:A1:3163:A:H8	1.83	0.44
38:A1:3184:A:N3	38:A1:3187:A:O2'	2.47	0.44
50:AN:28:TRP:O	50:AN:32:GLN:HG2	2.18	0.44
50:AN:192:LYS:HE3	50:AN:192:LYS:HB2	1.64	0.44
56:AT:89:LEU:HD23	56:AT:91:LEU:HD21	2.00	0.44
65:Ac:17:VAL:HG11	65:Ac:92:ILE:HD12	2.00	0.44
80:EC:6896:A:H2	80:EC:6935:G:H1	1.66	0.44
3:BC:80:VAL:HG12	3:BC:102:VAL:HG22	2.00	0.44
9:BL:108:PRO:HB2	9:BL:135:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:11:ILE:HG13	10:BN:12:SER:H	1.82	0.44
19:BD:222:VAL:HG12	31:B _g :192:PHE:HA	1.99	0.44
21:BK:54:TYR:HD1	21:BK:72:GLY:HA2	1.83	0.44
34:B5:1196:A:OP2	34:B5:1464:G:N2	2.38	0.44
34:B5:1494:C:H2'	34:B5:1495:C:C6	2.52	0.44
34:B5:1530:C:H2'	34:B5:1531:G:C8	2.53	0.44
34:B5:1714:A:H2'	34:B5:1715:G:C8	2.52	0.44
35:AA:204:MET:HG2	38:A1:914:A:C2	2.53	0.44
38:A1:296:A:N3	38:A1:299:G:O2'	2.50	0.44
38:A1:662:U:H2'	38:A1:663:OMC:C6	2.52	0.44
38:A1:1236:G:O3'	38:A1:1245:A:O2'	2.36	0.44
38:A1:2283:G:H1'	38:A1:2285:C:N4	2.33	0.44
38:A1:2352:A:H5''	52:AP:83:TRP:O	2.17	0.44
38:A1:2771:U:H5''	77:Ao:15:LYS:HE2	1.99	0.44
38:A1:3242:G:OP1	51:AO:159[A]:LYS:NZ	2.43	0.44
39:A3:12:U:OP2	39:A3:68:C:O2'	2.34	0.44
39:A3:96:U:OP1	55:AS:43:TYR:OH	2.30	0.44
44:AG:71:VAL:HG23	44:AG:235:GLY:HA3	1.99	0.44
44:AG:246:MET:HA	44:AG:249:ARG:HG2	2.00	0.44
6:BH:64:VAL:HG22	6:BH:94:ALA:HB1	1.98	0.44
15:BY:76:TYR:OH	15:BY:86:GLU:OE2	2.33	0.44
25:BS:109:LEU:HD12	25:BS:109:LEU:HA	1.87	0.44
27:BU:58:LEU:HD22	27:BU:88:LYS:HD3	2.00	0.44
34:B5:406:U:H2'	34:B5:407:A:C8	2.53	0.44
34:B5:830:U:H2'	34:B5:831:U:C6	2.53	0.44
34:B5:1156:C:H2'	34:B5:1157:A:C8	2.52	0.44
34:B5:1388:A:H61	34:B5:1409:G:N2	2.14	0.44
38:A1:105:C:O2'	38:A1:684:G:O2'	2.27	0.44
38:A1:351:A:N6	74:Al:37:TYR:O	2.49	0.44
38:A1:673:U:H2'	38:A1:674:G:H8	1.83	0.44
38:A1:792:G:H2'	38:A1:793:C:C6	2.53	0.44
38:A1:2144:A:H1'	38:A1:2281:A2M:N6	2.32	0.44
38:A1:3072:C:H2'	38:A1:3073:A:O4'	2.17	0.44
39:A3:56:A:H4'	47:AJ:152:HIS:HB2	2.00	0.44
41:AD:79:TYR:O	41:AD:82:GLU:HG2	2.18	0.44
45:AH:21:LYS:HG3	45:AH:22:SER:H	1.82	0.44
79:E:1:MET:O	79:E:198:TRP:NE1	2.46	0.44
1:BA:30:GLN:HE22	1:BA:152:PRO:HA	1.84	0.43
3:BC:89:GLN:O	34:B5:1145:U:O2'	2.29	0.43
5:BG:38:GLY:HA2	5:BG:41:VAL:HG22	2.00	0.43
20:BF:225:ARG:NH1	29:Bc:58:GLU:OE1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1184:A:O2'	34:B5:1186:U:H5'	2.18	0.43
34:B5:1511:U:H2'	34:B5:1512:G:C8	2.53	0.43
38:A1:11:A:H2'	38:A1:12:A:C8	2.53	0.43
38:A1:501:A:H2'	38:A1:502:U:C6	2.53	0.43
38:A1:718:G:OP1	63:Aa:117:ARG:NH2	2.45	0.43
38:A1:1629:U:O4	62:AZ:111:LYS:HB2	2.17	0.43
38:A1:1802:C:O2'	69:Ag:59:PRO:O	2.32	0.43
38:A1:2451:G:N2	38:A1:2496:C:O2'	2.50	0.43
65:Ac:16:LEU:HD21	65:Ac:97:ASP:HB2	1.99	0.43
66:Ad:27:LYS:HA	66:Ad:30:PRO:HD2	2.00	0.43
76:An:13:LEU:HD21	76:An:17:ARG:HH22	1.83	0.43
80:EC:6946:A:H2'	80:EC:6947:A:C8	2.54	0.43
4:BE:44:LEU:HD12	4:BE:82:TYR:HB3	1.99	0.43
5:BG:50:PHE:CG	5:BG:111:LEU:HD23	2.53	0.43
16:Ba:70:LYS:NZ	34:B5:933:A:OP1	2.37	0.43
20:BF:118:LEU:HA	20:BF:121:ILE:HG22	1.99	0.43
33:BM:60:VAL:HG11	33:BM:79:ALA:HB2	1.99	0.43
34:B5:107:C:OP1	34:B5:383:G:O2'	2.34	0.43
34:B5:393:C:H2'	34:B5:394:C:C6	2.52	0.43
34:B5:1349:G:H2'	34:B5:1350:U:C6	2.53	0.43
38:A1:589:A:H8	38:A1:590:G:C8	2.36	0.43
38:A1:1446:A:H5''	52:AP:65:SER:HB2	2.00	0.43
38:A1:1708:C:H2'	38:A1:1709:C:H6	1.83	0.43
38:A1:1720:U:OP2	54:AR:120:TYR:OH	2.24	0.43
38:A1:3160:U:H2'	38:A1:3161:C:H6	1.82	0.43
39:A3:99:G:H4'	43:AF:128:LYS:HE3	2.00	0.43
39:A3:118:A:H5''	41:AD:253:PHE:CZ	2.53	0.43
40:A4:23:U:H5''	61:AY:13:ARG:HG3	1.99	0.43
41:AD:108:ARG:CZ	41:AD:253:PHE:HB2	2.48	0.43
47:AJ:11:ASP:N	47:AJ:11:ASP:OD1	2.51	0.43
62:AZ:26:VAL:HG11	62:AZ:96:VAL:HB	2.00	0.43
63:Aa:90:TYR:CD1	63:Aa:100:PRO:HG3	2.52	0.43
66:Ad:41:LYS:HE2	66:Ad:47:ASP:HA	2.00	0.43
4:BE:45:ILE:HG13	4:BE:61:VAL:HG21	1.99	0.43
4:BE:49:ARG:HE	4:BE:49:ARG:HB3	1.61	0.43
20:BF:80:LYS:O	34:B5:1615:C:N4	2.50	0.43
34:B5:329:G:H2'	34:B5:330:G:H8	1.83	0.43
34:B5:351:C:H5	34:B5:631:G:H5''	1.84	0.43
34:B5:938:G:N2	34:B5:941:A:OP2	2.45	0.43
38:A1:264:G:O2'	38:A1:265:A:OP2	2.33	0.43
38:A1:289:A:OP2	50:AN:170:LYS:NZ	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1046:A:H2'	38:A1:1049:C:C5	2.53	0.43
38:A1:2205:U:H2'	38:A1:2206:G:N3	2.33	0.43
38:A1:2353:G:H5''	52:AP:86:LYS:HB2	2.00	0.43
38:A1:3159:C:H2'	38:A1:3160:U:H6	1.84	0.43
38:A1:3212:C:H2'	38:A1:3213:A:O4'	2.19	0.43
38:A1:3296:A:H2'	38:A1:3297:U:C6	2.53	0.43
40:A4:37:A:H5''	40:A4:39:G:O4'	2.18	0.43
49:AM:17:VAL:HG11	49:AM:74:ARG:HA	1.99	0.43
62:AZ:26:VAL:HG12	62:AZ:27:LYS:HG3	2.00	0.43
80:EC:6770:U:N3	80:EC:6821:U:O4	2.52	0.43
1:BA:50:VAL:HA	1:BA:53:THR:HB	2.00	0.43
4:BE:77:ARG:HH22	34:B5:123:G:P	2.41	0.43
6:BH:133:THR:OG1	6:BH:158:ASP:O	2.35	0.43
34:B5:272:U:O2'	34:B5:284:G:N2	2.51	0.43
34:B5:919:A:H2'	34:B5:920:U:C6	2.54	0.43
34:B5:1474:G:H2'	34:B5:1475:A:C8	2.54	0.43
36:AB:380:MET:HG2	36:AB:383:LEU:HD21	2.00	0.43
38:A1:176:G:H2'	38:A1:177:U:O4'	2.19	0.43
38:A1:2367:A:H2'	38:A1:2368:A:C8	2.54	0.43
38:A1:2407:C:H2'	38:A1:2408:U:H6	1.83	0.43
45:AH:12:VAL:HB	45:AH:51:GLN:HA	1.99	0.43
47:AJ:87:LYS:HA	47:AJ:87:LYS:HD2	1.90	0.43
63:Aa:74:ASN:HB3	63:Aa:115:LYS:HB3	1.99	0.43
2:BB:66:VAL:HG23	11:BO:34:SER:HA	1.99	0.43
3:BC:70:ASP:OD1	3:BC:133:LYS:NZ	2.32	0.43
4:BE:3:ARG:HB3	34:B5:93:A:H1'	2.00	0.43
12:BV:41:GLU:HG2	12:BV:42:GLU:OE1	2.18	0.43
20:BF:40:ILE:HG23	20:BF:69:PHE:CZ	2.53	0.43
31:Bg:68:VAL:HA	31:Bg:84:SER:HA	2.00	0.43
33:BM:103:LEU:HD11	34:B5:1227:A:H2'	1.99	0.43
34:B5:792:U:H2'	34:B5:793:A:O4'	2.17	0.43
34:B5:828:U:H2'	34:B5:829:A:C8	2.54	0.43
34:B5:854:U:O4	34:B5:855:A:N6	2.52	0.43
34:B5:1125:A:C5	34:B5:1126:OMG:H1'	2.53	0.43
34:B5:1369:U:H4'	34:B5:1372:U:N3	2.33	0.43
34:B5:1550:A:H2'	34:B5:1551:U:C6	2.53	0.43
36:AB:231:HIS:CE1	38:A1:2341:A:H5''	2.53	0.43
38:A1:1306:G:C6	51:AO:62[A]:THR:HA	2.53	0.43
38:A1:2167:A:H2'	38:A1:2168:A:C8	2.54	0.43
49:AM:73:PRO:HG2	49:AM:76:ALA:HB2	2.00	0.43
58:AV:2:SER:OG	58:AV:57:MET:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:182:TYR:HD1	4:BE:192:ILE:HG12	1.83	0.43
6:BH:132:PRO:HB2	6:BH:161:GLN:HE21	1.83	0.43
16:Ba:12:LYS:HG3	16:Ba:15:ARG:HB2	2.00	0.43
16:Ba:25:ASN:ND2	16:Ba:77:CYS:SG	2.88	0.43
19:BD:146:ARG:HE	34:B5:1427:A:N6	2.17	0.43
25:BS:88:ARG:NH1	25:BS:108:LYS:HG2	2.34	0.43
34:B5:841:U:H2'	34:B5:842:C:C6	2.54	0.43
34:B5:1672:G:H2'	34:B5:1673:G:H8	1.83	0.43
38:A1:41:G:N2	38:A1:2803:A:N7	2.67	0.43
38:A1:595:G:O6	42:AE:22:ARG:NH2	2.37	0.43
38:A1:737:G:H2'	38:A1:738:A:H8	1.83	0.43
38:A1:787:G:H2'	38:A1:788:C:C6	2.54	0.43
38:A1:791:A:H2'	38:A1:792:G:H8	1.84	0.43
38:A1:3273:A:H5''	42:AE:45:GLY:HA2	2.00	0.43
44:AG:25:PRO:HB2	62:AZ:125:GLY:H	1.84	0.43
45:AH:132:VAL:HG11	45:AH:157:ASN:ND2	2.32	0.43
47:AJ:108:GLU:HB3	47:AJ:122:ILE:HG23	2.00	0.43
55:AS:83:SER:OG	55:AS:84:ARG:N	2.51	0.43
80:EC:6948:U:H2'	80:EC:6949:G:H5''	2.01	0.43
4:BE:122:LYS:HG2	4:BE:162:ILE:HB	2.00	0.43
23:BQ:137:ARG:HB2	34:B5:1580:C:H4'	2.01	0.43
27:BU:36:ASN:O	27:BU:40:ASN:ND2	2.51	0.43
34:B5:209:U:H2'	34:B5:210:A:C8	2.53	0.43
34:B5:304:U:H2'	34:B5:305:C:C6	2.53	0.43
34:B5:629:U:OP2	34:B5:969:C:N4	2.38	0.43
34:B5:891:A:H2'	34:B5:892:A:H8	1.81	0.43
34:B5:909:U:H2'	34:B5:910:C:C6	2.54	0.43
34:B5:1183:A:H2'	34:B5:1184:A:C8	2.53	0.43
34:B5:1254:U:H3'	34:B5:1255:G:H8	1.83	0.43
34:B5:1291:G:N2	34:B5:1324:G:H22	2.17	0.43
34:B5:1325:A:H2'	34:B5:1326:A:H8	1.82	0.43
34:B5:1775:U:P	76:An:11:ARG:HH22	2.42	0.43
36:AB:215:ILE:HD11	36:AB:324:VAL:HG11	2.01	0.43
38:A1:671:U:H2'	38:A1:672:A:C8	2.54	0.43
38:A1:993:G:N3	38:A1:2637:A:H2'	2.34	0.43
38:A1:1719:G:N7	54:AR:121:HIS:HE1	2.16	0.43
38:A1:2218:G:H2'	38:A1:2219:A:H8	1.82	0.43
38:A1:2419:A:H2'	38:A1:2420:C:C6	2.54	0.43
38:A1:2622:C:H42	46:AI:116:ARG:HH12	1.65	0.43
38:A1:3011:A:N1	38:A1:3043:C:O2'	2.47	0.43
58:AV:32:ARG:HG3	58:AV:65:GLY:HA2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Ad:10:ARG:HG2	66:Ad:108:VAL:HG22	2.00	0.43
80:EC:6799:C:H2'	80:EC:6800:G:C8	2.54	0.43
8:BJ:92:LYS:HB2	8:BJ:95:TYR:HD2	1.83	0.43
8:BJ:108:ARG:HG2	8:BJ:147:MET:HE1	2.00	0.43
19:BD:55:THR:HA	19:BD:58:VAL:HG12	2.01	0.43
20:BF:44:ASN:HB3	20:BF:45:LYS:HD3	2.01	0.43
27:BU:35:GLU:OE2	34:B5:1383:G:O2'	2.28	0.43
31:Bg:51:ASP:O	31:Bg:54:PHE:N	2.52	0.43
34:B5:512:A:H2'	34:B5:513:U:C6	2.53	0.43
34:B5:1335:U:H2'	34:B5:1336:A:H8	1.84	0.43
34:B5:1760:G:OP1	80:EC:6946:A:N6	2.52	0.43
38:A1:791:A:H2'	38:A1:792:G:C8	2.53	0.43
38:A1:1083:G:H2'	38:A1:1084:A:C8	2.54	0.43
38:A1:1158:A:OP2	43:AF:90:LYS:NZ	2.43	0.43
38:A1:2232:A:H2'	38:A1:2233:A:C8	2.53	0.43
38:A1:2465:G:H21	79:E:60:ARG:HH22	1.66	0.43
38:A1:3007:U:H2'	38:A1:3008:A:C8	2.53	0.43
49:AM:72:LEU:HD11	49:AM:81:VAL:HG22	2.01	0.43
55:AS:22:PRO:O	56:AT:146:ASN:ND2	2.47	0.43
55:AS:77:VAL:HG21	55:AS:106:LEU:HD22	1.99	0.43
65:Ac:51:LEU:HD11	69:Ag:90:ILE:HG22	2.01	0.43
79:E:104:SER:HA	79:E:110:PHE:HZ	1.84	0.43
3:BC:212:LYS:NZ	34:B5:1298:U:O3'	2.52	0.43
19:BD:113:LEU:HD22	19:BD:118:ALA:HB2	2.01	0.43
22:BP:33:PHE:CZ	22:BP:112:LEU:HB3	2.54	0.43
25:BS:69:ILE:HA	25:BS:72:ILE:HD12	2.00	0.43
27:BU:102:ARG:HG3	27:BU:103:ILE:HG23	2.00	0.43
31:Bg:22:SER:HB2	31:Bg:70:ASP:HA	2.00	0.43
38:A1:39:A:H5''	63:Aa:35:ALA:HB2	2.01	0.43
38:A1:2768:U:H2'	38:A1:2769:A:C8	2.54	0.43
39:A3:4:U:H2'	39:A3:5:G:C8	2.54	0.43
41:AD:177:GLU:HG3	41:AD:190:ILE:HD13	2.01	0.43
51:AO:113[A]:ASP:OD1	51:AO:113[A]:ASP:N	2.52	0.43
56:AT:64:VAL:HG13	56:AT:72:VAL:HG13	2.01	0.43
64:Ab:28:LYS:HD3	64:Ab:29:TYR:CE2	2.54	0.43
70:Ah:77:PRO:HD2	70:Ah:80:LEU:HD12	2.00	0.43
73:Ak:32:ASN:HD21	73:Ak:36:LYS:HG2	1.83	0.43
75:Am:79:GLU:HB3	75:Am:82:LEU:HB2	2.01	0.43
16:Ba:45:VAL:HG13	16:Ba:46:GLU:H	1.84	0.43
20:BF:160:VAL:HG11	29:Bc:45:LYS:HB2	2.00	0.43
23:BQ:90:VAL:HG13	23:BQ:102:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:95:THR:HG22	36:AB:97:ARG:H	1.84	0.43
37:AC:23:PRO:HD2	37:AC:26:PHE:CD2	2.54	0.43
38:A1:627:U:H2'	38:A1:628:A:H8	1.82	0.43
38:A1:669:U:H1'	38:A1:1110:U:H4'	2.01	0.43
38:A1:819:U:H2'	38:A1:820:A:H8	1.83	0.43
38:A1:952:A:OP1	64:Ab:18:ARG:NH2	2.36	0.43
38:A1:1941:C:H2'	38:A1:1942:U:C6	2.54	0.43
38:A1:2767:U:H2'	38:A1:2768:U:H6	1.83	0.43
41:AD:106:ALA:HB2	41:AD:166:ALA:HA	2.01	0.43
61:AY:87:LYS:HB2	61:AY:97:ILE:HD11	2.00	0.43
62:AZ:48:ARG:HG2	62:AZ:69:LYS:HB3	2.00	0.43
71:Ai:58:ILE:HG12	71:Ai:94:ILE:HD11	2.00	0.43
77:Ao:4:VAL:O	77:Ao:94:GLY:N	2.50	0.43
79:E:56:PRO:HG2	79:E:178:VAL:HG13	2.00	0.43
1:BA:15:GLN:HG2	24:BR:100:LEU:HD21	2.01	0.42
9:BL:109:VAL:HG21	9:BL:125:VAL:HG11	2.01	0.42
15:BY:53:ASP:HB3	15:BY:96:LEU:HD21	2.01	0.42
19:BD:76:ARG:HH11	19:BD:77:PHE:HA	1.84	0.42
22:BP:87:PRO:HA	22:BP:90:ILE:HG12	2.01	0.42
31:Bg:13:LEU:HB2	31:Bg:310:ILE:HB	2.01	0.42
31:Bg:36:ALA:HB2	31:Bg:71:CYS:SG	2.59	0.42
34:B5:31:C:O2'	34:B5:547:U:OP1	2.36	0.42
34:B5:842:C:H2'	34:B5:843:U:O4'	2.18	0.42
34:B5:1661:U:H2'	34:B5:1662:G:H8	1.83	0.42
36:AB:84:VAL:HB	36:AB:162:VAL:HB	2.00	0.42
37:AC:291:ASN:ND2	38:A1:1349:G:H4'	2.34	0.42
38:A1:431:U:OP1	68:Af:65:ARG:NH1	2.41	0.42
38:A1:1034:U:H2'	38:A1:1035:G:C8	2.54	0.42
38:A1:1616:U:H2'	38:A1:1617:G:H8	1.84	0.42
38:A1:1785:U:H2'	38:A1:1786:G:C8	2.53	0.42
38:A1:2206:G:O2'	38:A1:2207:A:H5''	2.19	0.42
38:A1:2586:G:O2'	44:AG:48:ARG:NH2	2.52	0.42
39:A3:38:U:N3	39:A3:41:G:OP2	2.35	0.42
67:Ae:66:LEU:HD23	67:Ae:72:LYS:HG3	2.00	0.42
70:Ah:86:ARG:O	70:Ah:90:ARG:HG2	2.19	0.42
1:BA:148:ASP:OD1	1:BA:149:LEU:N	2.45	0.42
4:BE:21:ASP:OD1	4:BE:21:ASP:N	2.51	0.42
9:BL:99:ARG:HG2	14:BX:9:LEU:HA	2.01	0.42
10:BN:16:ILE:HA	34:B5:959:U:H5'	2.01	0.42
20:BF:177:ILE:HD12	20:BF:180:ARG:HH11	1.83	0.42
25:BS:38:VAL:HG13	25:BS:42:TYR:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:255:ALA:HB2	31:Bg:292:LEU:HD23	2.01	0.42
34:B5:97:C:H2'	34:B5:98:U:C6	2.53	0.42
38:A1:261:U:H2'	38:A1:262:U:C6	2.54	0.42
38:A1:1613:A:OP1	73:Ak:2:ALA:N	2.52	0.42
38:A1:1821:U:C2	69:Ag:67:LYS:HG3	2.54	0.42
38:A1:2700:G:H5''	56:AT:17:ARG:HG2	2.01	0.42
38:A1:3186:A:OP1	55:AS:154:HIS:ND1	2.52	0.42
44:AG:82:LEU:HD13	44:AG:222:PHE:HE2	1.83	0.42
45:AH:114:VAL:HB	45:AH:124:ARG:HB2	2.01	0.42
50:AN:10:LEU:HG	50:AN:19:LEU:HD11	2.01	0.42
69:Ag:106:LYS:HA	69:Ag:109:THR:HG22	2.01	0.42
1:BA:17:LEU:O	1:BA:22:THR:OG1	2.36	0.42
3:BC:76:LEU:HD23	3:BC:133:LYS:HE3	2.01	0.42
4:BE:27:TYR:OH	34:B5:460:A:O2'	2.30	0.42
5:BG:137:ARG:HD2	5:BG:177:ARG:HD2	2.01	0.42
6:BH:101:LYS:HA	6:BH:102:PRO:HD3	1.94	0.42
11:BO:32:ASP:OD2	11:BO:34:SER:OG	2.31	0.42
20:BF:97:LEU:HD12	20:BF:176:THR:HG23	1.99	0.42
34:B5:524:U:O2'	34:B5:526:A:N7	2.51	0.42
34:B5:1193:A:H8	34:B5:1193:A:OP1	2.02	0.42
34:B5:1714:A:H2'	34:B5:1715:G:H8	1.84	0.42
37:AC:315:LYS:HA	38:A1:505:G:H5''	2.01	0.42
38:A1:22:G:H1'	40:A4:104:A:N3	2.34	0.42
38:A1:899:U:H2'	38:A1:900:G:H8	1.83	0.42
38:A1:1556:C:O2'	38:A1:2169:G:N2	2.53	0.42
38:A1:1597:C:H2'	38:A1:1598:G:H8	1.85	0.42
38:A1:1639:C:O5'	69:Ag:52:GLN:HG2	2.19	0.42
38:A1:2534:G:H2'	38:A1:2535:A:H8	1.83	0.42
38:A1:3359:A:H2'	38:A1:3360:C:C6	2.54	0.42
46:AI:76:MET:HE1	46:AI:87:LEU:HD12	2.01	0.42
47:AJ:60:ARG:N	47:AJ:63:GLU:OE2	2.39	0.42
71:AI:86:LYS:HD2	71:AI:90:MET:HE3	2.00	0.42
79:E:120:VAL:HG22	79:E:121:PRO:HD3	2.01	0.42
7:BI:43:ILE:HB	34:B5:260:U:H5	1.85	0.42
7:BI:57:ALA:HB2	7:BI:177:GLY:HA2	2.00	0.42
11:BO:41:ARG:NH2	34:B5:897:C:O2	2.52	0.42
15:BY:112:LYS:NZ	34:B5:57:G:OP1	2.46	0.42
28:BZ:52:LYS:HG3	28:BZ:53:GLU:HG2	2.01	0.42
34:B5:64:U:O2'	34:B5:168:A:N3	2.44	0.42
34:B5:256:A:H2'	34:B5:257:A:O4'	2.19	0.42
34:B5:329:G:H2'	34:B5:330:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:73:C:C2	71:Ai:15:LYS:HD2	2.54	0.42
38:A1:1110:U:H2'	38:A1:1111:U:C6	2.54	0.42
38:A1:1447:G:H3'	52:AP:67:ILE:HD11	2.01	0.42
38:A1:2499:U:H3'	38:A1:2500:A:C5'	2.39	0.42
38:A1:2709:C:H2'	38:A1:2710:C:C6	2.54	0.42
38:A1:3162:C:H2'	38:A1:3163:A:C8	2.55	0.42
42:AE:43:LEU:HD13	68:Af:102:LEU:HB2	2.02	0.42
44:AG:156:ASP:OD1	44:AG:156:ASP:N	2.50	0.42
45:AH:89:LYS:HE2	45:AH:183:HIS:HB3	2.00	0.42
50:AN:14:LYS:HA	50:AN:19:LEU:HD22	2.02	0.42
54:AR:7:GLN:HG3	54:AR:41:ILE:HD11	2.01	0.42
80:EC:6888:A:H2'	80:EC:6889:A:C4	2.55	0.42
2:BB:103:MET:HE2	2:BB:188:LEU:HD11	2.02	0.42
10:BN:6:SER:OG	10:BN:7:ALA:N	2.52	0.42
11:BO:47:LYS:HD3	11:BO:47:LYS:HA	1.84	0.42
14:BX:19:ARG:NH2	34:B5:610:G:O2'	2.52	0.42
25:BS:58:ALA:HA	25:BS:61:LEU:HD12	2.00	0.42
34:B5:182:A:H2'	34:B5:183:U:C6	2.54	0.42
34:B5:486:G:H22	34:B5:500:C:H4'	1.83	0.42
34:B5:1160:A:H2'	34:B5:1161:C:C6	2.55	0.42
34:B5:1552:U:H2'	34:B5:1553:G:C8	2.54	0.42
37:AC:286:VAL:HG13	53:AQ:32:LEU:HB2	2.01	0.42
38:A1:252:U:O2'	38:A1:253:A:N7	2.53	0.42
38:A1:551:A:O2'	38:A1:552:G:H8	2.01	0.42
38:A1:671:U:H2'	38:A1:672:A:H8	1.83	0.42
38:A1:1235:U:H4'	38:A1:1236:G:H5'	2.01	0.42
38:A1:1563:C:O2'	38:A1:1564:U:OP1	2.32	0.42
46:AI:20:SER:OG	46:AI:21:ARG:N	2.52	0.42
55:AS:12:ARG:HB3	55:AS:24:LEU:HD23	2.01	0.42
10:BN:87:ASP:HB3	34:B5:867:G:H21	1.84	0.42
13:BW:62:VAL:HG21	17:Bb:7:LEU:HB2	2.01	0.42
34:B5:1317:C:H2'	34:B5:1318:G:O4'	2.20	0.42
34:B5:1773:4AC:H5	76:An:2:ARG:HH21	1.84	0.42
38:A1:292:U:OP2	50:AN:68:ARG:NH2	2.50	0.42
38:A1:359:U:HO2'	72:Aj:16:HIS:CE1	2.30	0.42
38:A1:1114:U:OP1	63:Aa:23:GLY:N	2.33	0.42
38:A1:1290:A:H2'	38:A1:1291:A:C8	2.54	0.42
38:A1:2451:G:H22	38:A1:2496:C:H1'	1.85	0.42
38:A1:3324:C:OP1	66:Ad:19:ARG:NH1	2.35	0.42
39:A3:26:C:H2'	39:A3:27:A:O4'	2.20	0.42
39:A3:112:G:H2'	39:A3:113:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:26:U:H2'	40:A4:27:U:C6	2.54	0.42
41:AD:34:LYS:HE3	56:AT:30:TYR:CE1	2.54	0.42
53:AQ:176:ARG:HA	53:AQ:182:LYS:O	2.20	0.42
79:E:177:ASP:OD1	79:E:178:VAL:N	2.52	0.42
1:BA:201:LEU:N	24:BR:85:VAL:HG23	2.34	0.42
3:BC:169:LEU:HD23	3:BC:198:THR:HG22	2.01	0.42
20:BF:148:ARG:NH1	20:BF:152:GLY:O	2.52	0.42
22:BP:18:ARG:NH2	25:BS:91:ASP:O	2.52	0.42
27:BU:113:ASP:OD1	27:BU:113:ASP:N	2.50	0.42
33:BM:87:PRO:HB3	33:BM:140:PHE:CG	2.54	0.42
34:B5:924:A:H2'	34:B5:925:G:C8	2.55	0.42
34:B5:1189:A:N6	34:B5:1190:C:H41	2.18	0.42
38:A1:1569:U:H5'	38:A1:1570:U:H5''	2.02	0.42
38:A1:3346:U:H2'	38:A1:3347:A:C8	2.55	0.42
39:A3:33:U:H2'	39:A3:34:C:C6	2.55	0.42
40:A4:10:A:H2'	40:A4:11:C:C6	2.55	0.42
40:A4:142:C:H4'	50:AN:60:VAL:HG21	2.01	0.42
40:A4:149:A:H2'	40:A4:150:G:C8	2.55	0.42
46:AI:48:LEU:HD21	46:AI:145:LYS:HG3	2.02	0.42
49:AM:94:TRP:O	49:AM:97:SER:OG	2.38	0.42
80:EC:6857:C:O2'	80:EC:6858:A:OP1	2.30	0.42
3:BC:42:GLY:HA2	3:BC:68:ILE:HD11	2.02	0.42
4:BE:100:ARG:HG2	4:BE:114:ILE:HD13	2.01	0.42
4:BE:151:ASP:HB3	4:BE:154:ILE:HG13	2.02	0.42
6:BH:99:LEU:HD23	6:BH:99:LEU:HA	1.92	0.42
16:Ba:23:CYS:HB2	16:Ba:30:ILE:HD11	2.00	0.42
20:BF:29:ILE:HG21	23:BQ:57:LEU:HD21	2.02	0.42
20:BF:108:LEU:HD21	23:BQ:44:LEU:HD11	2.01	0.42
20:BF:146:THR:HG21	20:BF:220:VAL:HG12	2.01	0.42
22:BP:43:ARG:HH12	34:B5:1551:U:H3'	1.85	0.42
25:BS:141:THR:HG21	34:B5:1173:C:H3'	2.02	0.42
28:BZ:88:ILE:HG13	28:BZ:89:ILE:HG23	2.02	0.42
34:B5:421:A:H2'	34:B5:422:G:H5''	2.02	0.42
34:B5:1560:U:H2'	34:B5:1561:U:O4'	2.20	0.42
37:AC:93:MET:HB2	38:A1:658:G:N2	2.35	0.42
38:A1:94:G:H2'	38:A1:95:A:C8	2.55	0.42
38:A1:2427:U:H2'	38:A1:2428:U:C6	2.54	0.42
38:A1:2722:U:O2'	56:AT:88:ARG:O	2.30	0.42
38:A1:2776:C:H5'	38:A1:2777:G:C2	2.54	0.42
58:AV:38:ALA:HB3	58:AV:59:MET:HB2	2.01	0.42
58:AV:117:PRO:HD3	59:AW:26:SER:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:176:VAL:HG12	2:BB:177:GLN:H	1.85	0.42
6:BH:44:LYS:N	6:BH:61:PHE:O	2.41	0.42
14:BX:107:PHE:CE2	14:BX:114:LYS:HB2	2.54	0.42
34:B5:752:A:H2'	34:B5:753:A:C8	2.55	0.42
34:B5:1524:A:H2'	34:B5:1525:A:C8	2.55	0.42
34:B5:1530:C:H2'	34:B5:1531:G:H8	1.85	0.42
35:AA:113:VAL:HG23	35:AA:134:VAL:HB	2.02	0.42
38:A1:86:G:O2'	38:A1:98:G:O6	2.33	0.42
38:A1:375:A:H5''	61:AY:95:VAL:HG21	2.02	0.42
38:A1:1084:A:H5''	56:AT:35:LYS:HD3	2.01	0.42
38:A1:1660:C:H2'	38:A1:1661:G:C8	2.55	0.42
38:A1:1798:A:H2'	38:A1:1799:A:C8	2.55	0.42
38:A1:1863:G:N1	38:A1:1866:C:OP2	2.38	0.42
38:A1:2881:C:H2'	38:A1:2882:U:C6	2.55	0.42
40:A4:46:G:O2'	40:A4:61:A:N1	2.48	0.42
40:A4:69:U:H2'	40:A4:70:G:O4'	2.20	0.42
40:A4:113:U:H5''	74:Al:7:PHE:HB2	2.01	0.42
47:AJ:106:ILE:O	47:AJ:125:MET:N	2.46	0.42
53:AQ:147:ARG:HB3	53:AQ:150:VAL:HG23	2.01	0.42
55:AS:10:ILE:HG12	55:AS:26:ARG:HB2	2.01	0.42
62:AZ:81:LEU:HD22	69:Ag:90:ILE:HG12	2.01	0.42
63:Aa:45:MET:HE3	63:Aa:45:MET:HB3	1.87	0.42
74:Al:5:LYS:HE2	74:Al:13:MET:HE1	2.01	0.42
1:BA:7:PHE:HZ	12:BV:43:GLY:HA3	1.85	0.42
4:BE:6:LYS:NZ	34:B5:94:U:H5''	2.35	0.42
4:BE:199:GLU:HG3	4:BE:201:HIS:NE2	2.35	0.42
15:BY:83:LYS:HD2	15:BY:91:LEU:HD22	2.01	0.42
20:BF:69:PHE:CD1	23:BQ:46:PHE:HZ	2.38	0.42
33:BM:38:HIS:HD1	33:BM:126:TRP:C	2.26	0.42
34:B5:824:G:H2'	34:B5:825:U:C6	2.55	0.42
35:AA:112:ILE:HG13	78:Ap:79:VAL:HG22	2.02	0.42
37:AC:326:ARG:NH2	38:A1:608:A:O3'	2.53	0.42
38:A1:277:G:H5''	77:Ao:49:GLY:HA2	2.02	0.42
38:A1:656:A:H2'	38:A1:657:A:H8	1.85	0.42
38:A1:2407:C:H2'	38:A1:2408:U:C6	2.55	0.42
38:A1:2477:G:H5'	38:A1:2487:U:C2	2.55	0.42
38:A1:2696:A:H2'	38:A1:2697:A:C8	2.55	0.42
38:A1:3089:C:H2'	38:A1:3090:U:O4'	2.20	0.42
39:A3:3:U:H2'	39:A3:4:U:H6	1.84	0.42
39:A3:90:U:H2'	39:A3:91:G:O4'	2.20	0.42
47:AJ:21:ILE:HD12	47:AJ:33:ALA:HB1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:AQ:62:VAL:HG13	53:AQ:66:ARG:HD2	2.02	0.42
60:AX:47:ALA:HB3	60:AX:50:ALA:HB2	2.02	0.42
73:Ak:17:ARG:HB3	73:Ak:19:ASP:OD2	2.20	0.42
1:BA:7:PHE:CZ	12:BV:43:GLY:HA3	2.54	0.41
9:BL:53:TYR:CD2	9:BL:113:PRO:HG2	2.55	0.41
10:BN:62:GLN:HB2	10:BN:65:VAL:HG22	2.01	0.41
12:BV:39:VAL:HB	12:BV:43:GLY:HA2	2.01	0.41
26:BT:99:SER:HA	26:BT:102:ARG:HH12	1.85	0.41
34:B5:896:U:H2'	34:B5:897:C:C6	2.55	0.41
34:B5:1291:G:H1	34:B5:1324:G:H1	1.68	0.41
34:B5:1458:G:H5''	34:B5:1459:C:OP2	2.20	0.41
34:B5:1483:A:N3	34:B5:1607:G:O2'	2.40	0.41
34:B5:1613:U:H2'	34:B5:1614:A:C8	2.52	0.41
35:AA:101:VAL:HG22	35:AA:165:VAL:HG22	2.02	0.41
38:A1:184:U:H2'	38:A1:185:C:C6	2.55	0.41
38:A1:1020:G:H3'	38:A1:1021:G:H8	1.85	0.41
38:A1:2129:U:H2'	38:A1:2130:G:C8	2.55	0.41
38:A1:2344:U:H2'	38:A1:2345:A:C8	2.55	0.41
38:A1:3044:G:H2'	38:A1:3045:G:C8	2.55	0.41
38:A1:3214:U:O2	49:AM:125:LYS:NZ	2.52	0.41
40:A4:142:C:H2'	40:A4:143:U:H6	1.85	0.41
41:AD:86:TYR:OH	41:AD:250:ASP:O	2.30	0.41
41:AD:160:PHE:HA	41:AD:163:LEU:HB3	2.02	0.41
51:AO:77[A]:SER:HB2	51:AO:104[A]:VAL:HG12	2.02	0.41
52:AP:113:TYR:HB3	52:AP:153:LYS:NZ	2.34	0.41
78:Ap:59:CYS:C	78:Ap:61:LYS:H	2.28	0.41
1:BA:139:VAL:HG13	1:BA:141:ILE:HG13	2.03	0.41
2:BB:50:LYS:HD3	2:BB:50:LYS:HA	1.89	0.41
11:BO:15:GLY:O	11:BO:80:HIS:N	2.53	0.41
20:BF:166:ARG:HH22	34:B5:1163:A:H4'	1.84	0.41
30:Bd:10:HIS:HB3	34:B5:1451:C:OP1	2.20	0.41
34:B5:30:G:H2'	34:B5:31:C:C6	2.55	0.41
34:B5:97:C:O2	34:B5:425:A:O2'	2.35	0.41
34:B5:116:U:H2'	34:B5:117:U:C6	2.55	0.41
34:B5:706:A:N6	34:B5:731:C:H5'	2.34	0.41
34:B5:902:G:O2'	34:B5:1008:G:H4'	2.19	0.41
34:B5:1027:A:OP1	34:B5:1789:G:O2'	2.31	0.41
34:B5:1307:U:H3	34:B5:1318:G:N2	2.17	0.41
34:B5:1732:A:H2'	34:B5:1733:C:C6	2.55	0.41
38:A1:142:C:H2'	38:A1:143:G:O4'	2.19	0.41
38:A1:863:C:H2'	38:A1:864:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:938:C:C5	63:Aa:26:ARG:HD2	2.55	0.41
38:A1:1495:U:H5	38:A1:1835:A:N1	2.17	0.41
38:A1:2533:G:H2'	38:A1:2534:G:C8	2.54	0.41
38:A1:3273:A:H2'	38:A1:3274:A:C8	2.55	0.41
40:A4:29:U:H5''	48:AL:27:ASP:HB3	2.02	0.41
45:AH:63:LYS:HD3	45:AH:63:LYS:HA	1.88	0.41
54:AR:4:LEU:HD22	54:AR:32:ILE:HG22	2.02	0.41
55:AS:93:GLU:OE1	55:AS:135:VAL:HG13	2.20	0.41
80:EC:6814:G:O2'	80:EC:6815:U:H5''	2.20	0.41
2:BB:127:VAL:HG13	2:BB:176:VAL:HG11	2.02	0.41
2:BB:144:ARG:HB2	2:BB:208:GLN:HB3	2.02	0.41
7:BI:76:THR:HG21	7:BI:104:ILE:HD12	2.03	0.41
12:BV:4:ASP:N	12:BV:4:ASP:OD1	2.53	0.41
20:BF:37:GLN:HG2	23:BQ:53:LEU:HA	2.01	0.41
25:BS:82:PRO:HB2	25:BS:84:TRP:CD1	2.56	0.41
29:Bc:14:LYS:NZ	29:Bc:15:VAL:O	2.52	0.41
34:B5:502:U:H5	34:B5:503:G:C5	2.38	0.41
34:B5:1202:A:H62	34:B5:1456:C:H3'	1.85	0.41
34:B5:1713:G:H2'	34:B5:1714:A:C8	2.55	0.41
38:A1:339:C:OP1	38:A1:1380:G:O2'	2.33	0.41
38:A1:1157:G:H2'	38:A1:1158:A:O4'	2.20	0.41
38:A1:2426:U:H2'	38:A1:2427:U:C6	2.55	0.41
38:A1:2631:U:OP2	56:AT:4:SER:OG	2.34	0.41
38:A1:2875:U:O2'	38:A1:2876:C:O5'	2.32	0.41
39:A3:91:G:N2	46:AI:56:GLU:OE2	2.47	0.41
59:AW:6:ASP:HB3	59:AW:11:ALA:H	1.85	0.41
68:Af:48:ARG:HG2	68:Af:104:PRO:HD3	2.02	0.41
80:EC:6761:C:H2'	80:EC:6762:U:C6	2.55	0.41
1:BA:88:LYS:HD2	1:BA:201:LEU:HD13	2.02	0.41
2:BB:82:ARG:HB3	2:BB:105:PHE:CE1	2.55	0.41
5:BG:12:SER:OG	5:BG:123:GLY:O	2.31	0.41
7:BI:31:ARG:NH1	34:B5:332:U:OP1	2.51	0.41
9:BL:75:VAL:HG22	9:BL:84:ILE:HD12	2.02	0.41
12:BV:27:ASP:O	12:BV:29:HIS:N	2.54	0.41
19:BD:7:LYS:HD2	27:BU:27:THR:HG21	2.02	0.41
22:BP:108:ARG:H	22:BP:111:MET:HG2	1.86	0.41
22:BP:118:GLU:O	25:BS:122:HIS:N	2.53	0.41
26:BT:64:HIS:CD2	26:BT:68:ARG:HD3	2.55	0.41
34:B5:782:U:H4'	34:B5:783:G:H5''	2.03	0.41
34:B5:1171:A:H2'	34:B5:1172:G:H8	1.85	0.41
36:AB:92:TYR:HB3	36:AB:99:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:67:A:H61	38:A1:271:C:HO2'	1.67	0.41
38:A1:153:U:H4'	38:A1:158:G:H4'	2.03	0.41
38:A1:270:U:H2'	38:A1:271:C:H6	1.84	0.41
38:A1:838:G:O6	78:Ap:4:ARG:NH1	2.51	0.41
38:A1:1234:G:H3'	38:A1:1235:U:H2'	2.02	0.41
38:A1:1265:U:H2'	38:A1:1266:G:C8	2.55	0.41
38:A1:1622:U:H2'	38:A1:1623:G:H8	1.85	0.41
38:A1:2152:A:H2'	38:A1:2153:U:C6	2.55	0.41
38:A1:3034:C:H5	45:AH:121:LYS:H	1.68	0.41
38:A1:3298:C:C2	38:A1:3299:A:C8	3.08	0.41
53:AQ:29:LEU:HD23	53:AQ:29:LEU:HA	1.87	0.41
55:AS:155:ARG:HD3	55:AS:172:TYR:CD1	2.54	0.41
79:E:171:ASN:H	79:E:174:MET:HE2	1.86	0.41
1:BA:56:LYS:NZ	1:BA:159:ALA:H	2.18	0.41
3:BC:227:PRO:HA	3:BC:230:TRP:CD2	2.55	0.41
4:BE:11:ARG:HD3	4:BE:21:ASP:O	2.21	0.41
4:BE:63:ALA:O	4:BE:67:GLN:HG2	2.20	0.41
11:BO:17:ALA:N	11:BO:80:HIS:O	2.32	0.41
11:BO:18:ARG:HA	11:BO:82:LYS:HB2	2.01	0.41
27:BU:53:LYS:HE3	27:BU:53:LYS:HB3	1.90	0.41
34:B5:340:U:H2'	34:B5:341:A:H8	1.85	0.41
34:B5:534:A:H2'	34:B5:535:A:C8	2.56	0.41
34:B5:626:U:H2'	34:B5:627:C:H6	1.85	0.41
34:B5:1405:G:H2'	34:B5:1406:A:H8	1.85	0.41
34:B5:1735:U:H2'	34:B5:1736:G:H8	1.85	0.41
38:A1:1336:U:H2'	38:A1:1337:A:C8	2.55	0.41
38:A1:2441:A:H2'	38:A1:2442:G:H4'	2.03	0.41
38:A1:3295:A:H2'	38:A1:3296:A:H8	1.85	0.41
39:A3:4:U:H2'	39:A3:5:G:H8	1.85	0.41
51:AO:8[A]:VAL:HG22	51:AO:34[A]:VAL:HB	2.01	0.41
51:AO:8[A]:VAL:HG12	51:AO:117[A]:ARG:HG3	2.02	0.41
52:AP:85:ALA:O	52:AP:89:LYS:HG2	2.20	0.41
79:E:153:SER:O	79:E:155:ILE:HG12	2.21	0.41
14:BX:40:SER:O	14:BX:40:SER:OG	2.32	0.41
20:BF:192:GLU:O	20:BF:196:GLU:N	2.53	0.41
31:Bg:81:LEU:HD23	31:Bg:81:LEU:HA	1.93	0.41
31:Bg:102:ARG:NH2	34:B5:1342:C:OP1	2.54	0.41
31:Bg:305:TYR:HB3	31:Bg:307:ASP:H	1.84	0.41
34:B5:869:A:H61	34:B5:958:U:H3	1.67	0.41
34:B5:934:C:C4	34:B5:1077:C:H4'	2.56	0.41
34:B5:1077:C:H2'	34:B5:1078:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1315:U:OP1	34:B5:1328:G:N2	2.43	0.41
34:B5:1564:U:H2'	34:B5:1565:C:C6	2.55	0.41
37:AC:309:ARG:NH2	38:A1:610:G:N7	2.67	0.41
38:A1:35:A:H2'	38:A1:36:C:H6	1.86	0.41
38:A1:381:U:H2'	38:A1:382:U:C6	2.56	0.41
38:A1:1751:G:H5'	73:Ak:26:LYS:HE2	2.02	0.41
40:A4:148:G:H2'	40:A4:149:A:C8	2.55	0.41
56:AT:57:TYR:CD2	56:AT:89:LEU:HD21	2.55	0.41
65:Ac:40:LYS:HB3	65:Ac:101:LEU:HD21	2.02	0.41
80:EC:6764:C:H2'	80:EC:6765:A:C8	2.55	0.41
2:BB:24:PHE:CE1	11:BO:74:VAL:HG13	2.55	0.41
7:BI:41:LYS:HA	7:BI:60:ILE:HA	2.02	0.41
7:BI:171:SER:HB3	7:BI:180:ASP:H	1.86	0.41
8:BJ:141:VAL:HA	34:B5:767:U:H6	1.86	0.41
12:BV:79:LEU:HD13	12:BV:82:VAL:HG21	2.01	0.41
19:BD:185:LYS:HB3	19:BD:185:LYS:HE2	1.88	0.41
20:BF:97:LEU:HA	20:BF:176:THR:HG21	2.01	0.41
31:Bg:116:ASP:CG	31:Bg:121:MET:H	2.29	0.41
34:B5:82:U:H2'	34:B5:83:G:O4'	2.21	0.41
34:B5:327:U:H2'	34:B5:328:A:C8	2.55	0.41
34:B5:564:G:N2	34:B5:580:A:OP2	2.41	0.41
34:B5:817:A:H2'	34:B5:818:C:C6	2.55	0.41
34:B5:1220:C:H2'	34:B5:1221:A:C8	2.54	0.41
34:B5:1512:G:H2'	34:B5:1513:G:C8	2.56	0.41
34:B5:1619:C:H2'	34:B5:1620:C:C6	2.53	0.41
38:A1:314:U:H2'	38:A1:315:C:C6	2.55	0.41
38:A1:737:G:H2'	38:A1:738:A:C8	2.56	0.41
38:A1:943:U:H3'	63:Aa:13:GLY:HA2	2.02	0.41
38:A1:1190:A:H4'	75:Am:113:ARG:HH22	1.85	0.41
38:A1:1239:C:H3'	38:A1:1240:A:C8	2.55	0.41
38:A1:1621:A:H2'	38:A1:1622:U:H6	1.85	0.41
38:A1:1622:U:H2'	38:A1:1623:G:C8	2.56	0.41
38:A1:1660:C:H2'	38:A1:1661:G:H8	1.84	0.41
38:A1:2357:A:H2'	38:A1:2358:A:H8	1.83	0.41
38:A1:2533:G:H2'	38:A1:2534:G:H8	1.85	0.41
38:A1:3234:A:N6	38:A1:3253:G:H1	2.18	0.41
39:A3:114:U:H2'	39:A3:115:G:H8	1.86	0.41
47:AJ:148:VAL:HG23	47:AJ:153:LYS:HG2	2.03	0.41
48:AL:59:ARG:HG2	48:AL:108:ILE:HG13	2.03	0.41
70:Ah:102:GLU:OE1	70:Ah:102:GLU:N	2.45	0.41
2:BB:61:LEU:HD23	2:BB:96:LEU:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:118:GLN:O	34:B5:931:C:O2'	2.37	0.41
6:BH:58:LEU:HD13	6:BH:58:LEU:HA	1.91	0.41
28:BZ:58:ARG:NH1	28:BZ:59:TYR:HB3	2.35	0.41
31:Bg:13:LEU:HB3	31:Bg:45:TRP:CZ3	2.56	0.41
32:Bf:118:ARG:HH21	32:Bf:134:ASN:H	1.68	0.41
34:B5:300:A:H2'	34:B5:301:A:C8	2.55	0.41
38:A1:1644:C:H5''	38:A1:1645:U:H5''	2.02	0.41
38:A1:2266:U:H2'	38:A1:2267:C:C6	2.56	0.41
38:A1:2429:G:H2'	38:A1:2430:A:C8	2.55	0.41
39:A3:27:A:O3'	47:AJ:141:ARG:NH1	2.53	0.41
58:AV:84:SER:HA	58:AV:94:TYR:HB3	2.01	0.41
60:AX:46:TYR:HD1	70:Ah:75:TYR:HB3	1.84	0.41
67:Ae:60:ASN:O	67:Ae:64:LYS:N	2.52	0.41
2:BB:103:MET:H	2:BB:215:VAL:HB	1.85	0.41
3:BC:92:ALA:O	34:B5:1424:A:O2'	2.38	0.41
8:BJ:90:LYS:HB2	8:BJ:95:TYR:CG	2.56	0.41
16:Ba:5:ARG:HH21	34:B5:1795:U:H3'	1.86	0.41
16:Ba:18:VAL:O	16:Ba:19:LYS:HG2	2.21	0.41
19:BD:31:GLU:HG3	19:BD:107:PHE:CE1	2.53	0.41
19:BD:31:GLU:OE1	19:BD:31:GLU:N	2.52	0.41
20:BF:82:PHE:HE1	29:Bc:47:PRO:HB2	1.86	0.41
31:Bg:221:MET:HG3	31:Bg:233:THR:HB	2.03	0.41
32:Bf:118:ARG:HH21	32:Bf:134:ASN:N	2.19	0.41
34:B5:269:G:H2'	34:B5:270:C:H6	1.86	0.41
34:B5:696:C:H1'	34:B5:697:C:H2'	2.03	0.41
34:B5:743:U:H2'	34:B5:744:U:C6	2.56	0.41
34:B5:1055:U:H2'	34:B5:1056:U:C6	2.55	0.41
34:B5:1146:G:H2'	34:B5:1147:A:H8	1.86	0.41
34:B5:1638:G:H2'	34:B5:1639:OMC:O4'	2.21	0.41
36:AB:15:GLY:O	38:A1:3009:G:N2	2.44	0.41
36:AB:106:TRP:HB2	36:AB:133:TYR:CE1	2.56	0.41
38:A1:123:A:C6	38:A1:150:A:C5	3.09	0.41
38:A1:283:G:N2	38:A1:305:U:H5''	2.36	0.41
38:A1:299:G:H2'	38:A1:300:G:H8	1.86	0.41
38:A1:1283:C:H2'	38:A1:1284:C:C6	2.56	0.41
38:A1:1324:U:H5'	55:AS:1:MET:C	2.46	0.41
38:A1:1945:A:H2'	38:A1:1946:A:H8	1.85	0.41
38:A1:3095:U:H2'	38:A1:3096:C:C6	2.56	0.41
38:A1:3233:C:H2'	38:A1:3234:A:C8	2.55	0.41
38:A1:3302:U:H2'	38:A1:3303:G:C8	2.56	0.41
41:AD:52:VAL:HG21	41:AD:65:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:AD:207:TYR:CZ	41:AD:211:LEU:HD11	2.56	0.41
46:AI:189:GLU:HG2	46:AI:200:LEU:HD23	2.03	0.41
48:AL:46:ILE:HD11	48:AL:51:LEU:HA	2.03	0.41
54:AR:95:TRP:CZ2	54:AR:99:LEU:HD22	2.55	0.41
54:AR:110:ARG:HE	54:AR:110:ARG:HB3	1.68	0.41
58:AV:24:ASN:N	58:AV:98:ASN:O	2.43	0.41
62:AZ:25:ILE:HG23	62:AZ:41:ALA:HB1	2.03	0.41
63:Aa:76:ASP:OD1	63:Aa:76:ASP:N	2.51	0.41
73:Ak:46:ARG:HD3	73:Ak:47:GLY:O	2.21	0.41
77:Ao:18:ARG:HH11	77:Ao:18:ARG:HG3	1.86	0.41
77:Ao:78:LYS:HE2	77:Ao:78:LYS:HB3	1.88	0.41
79:E:113:SER:HA	79:E:138:VAL:H	1.86	0.41
80:EC:6853:G:H2'	80:EC:6854:U:O4'	2.19	0.41
1:BA:115:PHE:CZ	3:BC:39:THR:HG22	2.56	0.41
1:BA:118:PRO:HG2	1:BA:141:ILE:HD13	2.03	0.41
2:BB:222:LYS:HB3	2:BB:222:LYS:HE3	1.88	0.41
4:BE:52:LEU:HD12	4:BE:54:TYR:CZ	2.56	0.41
9:BL:111:VAL:HG22	9:BL:139:VAL:HG21	2.03	0.41
29:Bc:60:GLU:OE1	29:Bc:60:GLU:N	2.53	0.41
31:Bg:69:GLN:HB2	31:Bg:85:TRP:CD1	2.56	0.41
33:BM:43:ARG:HH11	33:BM:103:LEU:HD22	1.85	0.41
34:B5:794:U:H5''	34:B5:795:U:C5	2.55	0.41
34:B5:855:A:C2	34:B5:857:U:H1'	2.55	0.41
34:B5:1035:G:H2'	34:B5:1036:A:H8	1.86	0.41
34:B5:1349:G:H2'	34:B5:1350:U:H6	1.85	0.41
34:B5:1467:C:H2'	34:B5:1468:U:C6	2.56	0.41
34:B5:1482:C:P	34:B5:1521:G:H22	2.44	0.41
34:B5:1704:U:H2'	34:B5:1705:C:C6	2.56	0.41
35:AA:135:ILE:HB	35:AA:149:ARG:HB3	2.03	0.41
36:AB:283:TYR:CZ	36:AB:325:LYS:HB2	2.56	0.41
37:AC:156:LEU:HD12	37:AC:159:ILE:HD12	2.02	0.41
38:A1:101:G:OP2	38:A1:101:G:N2	2.52	0.41
38:A1:679:U:H2'	38:A1:680:G:C8	2.56	0.41
38:A1:1046:A:O2'	38:A1:1048:A:OP2	2.28	0.41
38:A1:1082:U:H2'	38:A1:1083:G:O4'	2.21	0.41
38:A1:2723:U:OP1	56:AT:87:LYS:HD3	2.20	0.41
38:A1:3159:C:H2'	38:A1:3160:U:C6	2.56	0.41
38:A1:3273:A:H5''	42:AE:45:GLY:CA	2.51	0.41
38:A1:3286:G:H2'	38:A1:3287:U:C6	2.56	0.41
44:AG:69:LEU:HD23	44:AG:69:LEU:HA	1.88	0.41
48:AL:94:GLY:HA3	70:Ah:116:TYR:OH	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Ao:15:LYS:HG2	77:Ao:18:ARG:NH2	2.36	0.41
80:EC:6831:U:H4'	80:EC:6832:G:OP1	2.19	0.41
2:BB:36:SER:HA	2:BB:41:ARG:HD3	2.03	0.40
4:BE:199:GLU:OE1	4:BE:199:GLU:N	2.54	0.40
13:BW:101:TYR:HE1	13:BW:114:GLU:HG3	1.85	0.40
14:BX:30:LYS:HE2	14:BX:34:LEU:HD11	2.03	0.40
14:BX:69:ARG:HA	14:BX:69:ARG:HD3	1.73	0.40
15:BY:21:LYS:HE2	15:BY:21:LYS:HB3	1.81	0.40
34:B5:1172:G:H2'	34:B5:1173:C:C6	2.56	0.40
34:B5:1439:C:H2'	34:B5:1440:C:H6	1.86	0.40
37:AC:22:LEU:HA	37:AC:23:PRO:HD3	1.83	0.40
38:A1:176:G:H5'	38:A1:176:G:H8	1.87	0.40
38:A1:1149:G:OP2	68:Af:21:ARG:NH2	2.50	0.40
38:A1:1748:G:OP2	73:Ak:42:LYS:NZ	2.45	0.40
38:A1:2478:C:O2'	38:A1:2479:C:H5'	2.21	0.40
44:AG:92:LYS:HB3	44:AG:92:LYS:HE2	1.83	0.40
46:AI:72:ALA:HB2	46:AI:155:ALA:HB2	2.03	0.40
66:Ad:11:GLU:OE1	66:Ad:96:VAL:HG21	2.21	0.40
1:BA:20:ALA:HB3	1:BA:172:LEU:HD22	2.03	0.40
1:BA:195:TRP:CZ3	1:BA:197:ILE:HG22	2.55	0.40
15:BY:22:GLN:HB2	15:BY:72:PHE:CE2	2.56	0.40
21:BK:7:ASP:HA	21:BK:10:LYS:HE3	2.04	0.40
34:B5:250:C:H2'	34:B5:251:A:C8	2.52	0.40
34:B5:607:G:H5'	34:B5:613:G:N2	2.36	0.40
34:B5:1161:C:H2'	34:B5:1162:C:C6	2.56	0.40
34:B5:1382:A:O2'	34:B5:1383:G:H8	2.04	0.40
34:B5:1561:U:H4'	34:B5:1599:C:H4'	2.03	0.40
36:AB:175:LYS:HE2	38:A1:3313:U:H5'	2.02	0.40
37:AC:321:LYS:HA	37:AC:324:LEU:HB3	2.02	0.40
38:A1:349:A:C4	40:A4:24:G:H1'	2.56	0.40
38:A1:1203:A:H2'	38:A1:1204:A:H8	1.86	0.40
38:A1:1744:G:H2'	38:A1:1745:C:C6	2.56	0.40
38:A1:2535:A:C4	38:A1:2536:A:H1'	2.57	0.40
38:A1:3192:U:H2'	38:A1:3193:C:C6	2.56	0.40
41:AD:83:LEU:HD22	41:AD:88:ILE:HD12	2.02	0.40
46:AI:47:PRO:HB3	46:AI:171:TRP:CH2	2.56	0.40
55:AS:27:MET:HB3	55:AS:27:MET:HE2	1.83	0.40
79:E:60:ARG:HA	79:E:61:PRO:HD3	1.82	0.40
80:EC:6797:U:H2'	80:EC:6798:C:C6	2.56	0.40
2:BB:111:ARG:HB3	16:Ba:68:TYR:HB2	2.03	0.40
5:BG:21:GLU:O	5:BG:25:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:31:ARG:HD3	5:BG:101:ILE:HG13	2.02	0.40
6:BH:10:SER:O	6:BH:10:SER:OG	2.38	0.40
6:BH:13:PRO:HB2	6:BH:14:THR:HG22	2.03	0.40
8:BJ:132:ARG:NH2	34:B5:532:U:OP1	2.43	0.40
10:BN:34:ILE:HA	10:BN:37:ILE:HD12	2.01	0.40
10:BN:88:LEU:HD13	10:BN:125:LEU:HD23	2.03	0.40
19:BD:71:LEU:HA	19:BD:74:GLN:HG2	2.02	0.40
31:Bg:211:ILE:HB	31:Bg:225:LEU:HD21	2.03	0.40
34:B5:208:U:H2'	34:B5:209:U:H6	1.84	0.40
34:B5:926:A:H2'	34:B5:927:C:C6	2.56	0.40
35:AA:181:LYS:HB2	38:A1:860:G:C5	2.56	0.40
36:AB:182:GLN:NE2	36:AB:184:ASN:OD1	2.50	0.40
38:A1:1242:G:H3'	38:A1:1243:G:H8	1.86	0.40
38:A1:2108:C:H1'	38:A1:3344:A:H8	1.86	0.40
38:A1:2261:G:O2'	38:A1:2263:C:N4	2.54	0.40
38:A1:2718:U:OP1	77:Ao:13:LYS:NZ	2.53	0.40
38:A1:3007:U:H2'	38:A1:3008:A:H8	1.87	0.40
39:A3:121:U:C2	41:AD:268:GLU:HG3	2.56	0.40
44:AG:83:ASP:OD1	44:AG:86:THR:HG22	2.21	0.40
61:AY:48:LEU:HD23	61:AY:48:LEU:HA	1.87	0.40
70:Ah:95:PHE:O	70:Ah:99:GLN:HG2	2.22	0.40
78:Ap:17:ARG:H	78:Ap:17:ARG:HG2	1.65	0.40
3:BC:178:ILE:HB	3:BC:185:LYS:HG3	2.04	0.40
7:BI:157:GLU:HA	7:BI:160:PHE:HB2	2.03	0.40
18:Be:17:GLN:NE2	34:B5:563:U:H4'	2.35	0.40
20:BF:169:ASN:HB3	34:B5:1613:U:OP1	2.22	0.40
28:BZ:43:ASP:O	28:BZ:47:TYR:N	2.48	0.40
28:BZ:49:ARG:HA	28:BZ:52:LYS:HG2	2.03	0.40
34:B5:52:U:H2'	34:B5:53:G:C8	2.57	0.40
34:B5:413:U:H2'	34:B5:414:OMC:C6	2.57	0.40
34:B5:850:A:H2'	34:B5:851:U:C6	2.56	0.40
34:B5:1254:U:H3'	34:B5:1255:G:C8	2.56	0.40
34:B5:1429:G:H2'	34:B5:1430:U:C6	2.56	0.40
36:AB:137:TYR:CE1	36:AB:144:ILE:HG13	2.56	0.40
36:AB:296:THR:OG1	36:AB:297:SER:N	2.54	0.40
37:AC:181:VAL:O	37:AC:182:LEU:HG	2.21	0.40
38:A1:698:U:H2'	38:A1:699:A:O4'	2.20	0.40
38:A1:770:G:OP1	48:AL:171:ARG:NE	2.51	0.40
38:A1:1497:C:H2'	38:A1:1498:A:C8	2.56	0.40
38:A1:1719:G:H5''	54:AR:110:ARG:NH1	2.37	0.40
38:A1:2217:U:H2'	38:A1:2218:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2218:G:H2'	38:A1:2219:A:C8	2.57	0.40
38:A1:2413:A:H2'	38:A1:2414:G:C8	2.55	0.40
38:A1:2742:C:H2'	38:A1:2743:A:H8	1.86	0.40
38:A1:3006:A:H2'	38:A1:3007:U:O4'	2.22	0.40
38:A1:3057:U:H5'	38:A1:3086:A:H61	1.86	0.40
44:AG:43:LYS:HA	44:AG:43:LYS:HD3	1.82	0.40
47:AJ:32:ARG:NH2	47:AJ:120:ILE:O	2.46	0.40
48:AL:48:PRO:HD3	70:Ah:115:LYS:HE2	2.04	0.40
51:AO:136[A]:THR:HG21	51:AO:141[A]:LEU:HD12	2.04	0.40
58:AV:45:ARG:HB3	58:AV:48:ARG:HB3	2.02	0.40
4:BE:42:LEU:HB2	4:BE:109:PHE:CD2	2.56	0.40
4:BE:75:LYS:HE3	4:BE:75:LYS:HB3	1.98	0.40
5:BG:17:GLU:OE1	5:BG:17:GLU:N	2.55	0.40
14:BX:5:LYS:HD3	34:B5:611:U:H5''	2.03	0.40
19:BD:20:GLU:HG2	21:BK:61:TRP:CD2	2.56	0.40
20:BF:161:ASP:N	20:BF:161:ASP:OD1	2.53	0.40
22:BP:15:HIS:HE1	22:BP:22:LEU:HB3	1.85	0.40
26:BT:70:GLN:HB2	26:BT:121:GLY:H	1.86	0.40
27:BU:84:MET:HG3	30:Bd:52:PHE:CD1	2.56	0.40
29:Bc:21:SER:OG	29:Bc:65:ARG:NH2	2.55	0.40
30:Bd:34:TYR:OH	34:B5:1487:A:OP1	2.28	0.40
30:Bd:44:ARG:HH12	34:B5:1280:4AC:H5'	1.87	0.40
31:Bg:54:PHE:CE2	31:Bg:312:VAL:HG11	2.57	0.40
34:B5:709:C:H5'	34:B5:710:U:H5	1.87	0.40
34:B5:828:U:H2'	34:B5:829:A:H8	1.86	0.40
35:AA:242:ARG:NH1	38:A1:2154:U:OP1	2.54	0.40
38:A1:266:A:C6	71:Ai:30:LYS:HA	2.56	0.40
38:A1:1242:G:H3'	38:A1:1243:G:C8	2.55	0.40
38:A1:2347:OMU:H2'	38:A1:2348:A:O4'	2.22	0.40
39:A3:45:A:H2'	39:A3:46:A:C8	2.57	0.40
40:A4:40:A:H2'	40:A4:41:A:C8	2.56	0.40
40:A4:151:C:C5	60:AX:24:LEU:HD11	2.56	0.40
51:AO:36[A]:VAL:HB	51:AO:108[A]:ILE:HG12	2.04	0.40
53:AQ:36:LEU:HD23	53:AQ:36:LEU:HA	1.96	0.40
78:Ap:79:VAL:O	78:Ap:83:ILE:HG12	2.22	0.40
80:EC:6860:A:H3'	80:EC:6861:G:C8	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	185 (91%)	19 (9%)	0	100	100
2	BB	212/255 (83%)	183 (86%)	29 (14%)	0	100	100
3	BC	215/254 (85%)	207 (96%)	8 (4%)	0	100	100
4	BE	258/261 (99%)	238 (92%)	20 (8%)	0	100	100
5	BG	224/236 (95%)	211 (94%)	13 (6%)	0	100	100
6	BH	182/190 (96%)	171 (94%)	11 (6%)	0	100	100
7	BI	184/200 (92%)	167 (91%)	17 (9%)	0	100	100
8	BJ	183/197 (93%)	170 (93%)	13 (7%)	0	100	100
9	BL	153/156 (98%)	139 (91%)	14 (9%)	0	100	100
10	BN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
11	BO	125/137 (91%)	112 (90%)	13 (10%)	0	100	100
12	BV	85/87 (98%)	71 (84%)	14 (16%)	0	100	100
13	BW	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
14	BX	142/145 (98%)	128 (90%)	14 (10%)	0	100	100
15	BY	132/135 (98%)	123 (93%)	9 (7%)	0	100	100
16	Ba	95/119 (80%)	80 (84%)	15 (16%)	0	100	100
17	Bb	79/82 (96%)	70 (89%)	9 (11%)	0	100	100
18	Be	58/63 (92%)	52 (90%)	6 (10%)	0	100	100
19	BD	221/240 (92%)	209 (95%)	12 (5%)	0	100	100
20	BF	204/225 (91%)	186 (91%)	18 (9%)	0	100	100
21	BK	94/105 (90%)	82 (87%)	12 (13%)	0	100	100
22	BP	122/142 (86%)	109 (89%)	13 (11%)	0	100	100
23	BQ	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
24	BR	117/136 (86%)	112 (96%)	5 (4%)	0	100	100
25	BS	143/146 (98%)	130 (91%)	13 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	BT	139/144 (96%)	125 (90%)	14 (10%)	0	100	100
27	BU	105/121 (87%)	100 (95%)	5 (5%)	0	100	100
28	BZ	67/108 (62%)	64 (96%)	3 (4%)	0	100	100
29	Bc	61/67 (91%)	54 (88%)	7 (12%)	0	100	100
30	Bd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
31	Bg	310/319 (97%)	276 (89%)	34 (11%)	0	100	100
32	Bf	73/152 (48%)	67 (92%)	6 (8%)	0	100	100
33	BM	122/143 (85%)	107 (88%)	15 (12%)	0	100	100
35	AA	245/254 (96%)	232 (95%)	13 (5%)	0	100	100
36	AB	383/387 (99%)	361 (94%)	22 (6%)	0	100	100
37	AC	359/362 (99%)	340 (95%)	19 (5%)	0	100	100
41	AD	290/297 (98%)	273 (94%)	17 (6%)	0	100	100
42	AE	152/176 (86%)	142 (93%)	10 (7%)	0	100	100
43	AF	220/244 (90%)	211 (96%)	9 (4%)	0	100	100
44	AG	228/256 (89%)	211 (92%)	17 (8%)	0	100	100
45	AH	188/191 (98%)	173 (92%)	15 (8%)	0	100	100
46	AI	201/221 (91%)	188 (94%)	13 (6%)	0	100	100
47	AJ	167/174 (96%)	152 (91%)	15 (9%)	0	100	100
48	AL	191/199 (96%)	175 (92%)	16 (8%)	0	100	100
49	AM	134/138 (97%)	129 (96%)	5 (4%)	0	100	100
50	AN	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
51	AO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
52	AP	171/184 (93%)	167 (98%)	4 (2%)	0	100	100
53	AQ	183/186 (98%)	177 (97%)	6 (3%)	0	100	100
54	AR	186/189 (98%)	179 (96%)	7 (4%)	0	100	100
55	AS	170/178 (96%)	162 (95%)	8 (5%)	0	100	100
56	AT	157/160 (98%)	147 (94%)	10 (6%)	0	100	100
57	AU	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
58	AV	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
59	AW	61/155 (39%)	61 (100%)	0	0	100	100
60	AX	119/142 (84%)	113 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AY	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
62	AZ	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
63	Aa	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
64	Ab	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
65	Ac	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
66	Ad	107/113 (95%)	103 (96%)	4 (4%)	0	100	100
67	Ae	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
68	Af	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
69	Ag	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
70	Ah	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
71	Ai	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
72	Aj	85/88 (97%)	81 (95%)	4 (5%)	0	100	100
73	Ak	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
74	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	Am	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
76	An	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
77	Ao	100/106 (94%)	91 (91%)	9 (9%)	0	100	100
78	Ap	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
79	E	215/217 (99%)	204 (95%)	11 (5%)	0	100	100
All	All	11106/12103 (92%)	10380 (94%)	726 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	173/210 (82%)	173 (100%)	0	100	100
2	BB	191/224 (85%)	191 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	BC	176/205 (86%)	176 (100%)	0	100	100
4	BE	221/222 (100%)	221 (100%)	0	100	100
5	BG	193/201 (96%)	193 (100%)	0	100	100
6	BH	165/170 (97%)	165 (100%)	0	100	100
7	BI	150/161 (93%)	150 (100%)	0	100	100
8	BJ	158/166 (95%)	158 (100%)	0	100	100
9	BL	136/137 (99%)	136 (100%)	0	100	100
10	BN	127/128 (99%)	127 (100%)	0	100	100
11	BO	96/105 (91%)	96 (100%)	0	100	100
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	110 (100%)	0	100	100
14	BX	119/120 (99%)	119 (100%)	0	100	100
15	BY	112/113 (99%)	112 (100%)	0	100	100
16	Ba	83/100 (83%)	83 (100%)	0	100	100
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	110/124 (89%)	110 (100%)	0	100	100
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	113 (100%)	0	100	100
27	BU	100/114 (88%)	100 (100%)	0	100	100
28	BZ	61/89 (68%)	61 (100%)	0	100	100
29	Bc	56/60 (93%)	56 (100%)	0	100	100
30	Bd	47/49 (96%)	47 (100%)	0	100	100
31	Bg	256/262 (98%)	256 (100%)	0	100	100
32	Bf	66/135 (49%)	66 (100%)	0	100	100
33	BM	100/119 (84%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	320/322 (99%)	320 (100%)	0	100	100
37	AC	288/289 (100%)	288 (100%)	0	100	100
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	134/153 (88%)	134 (100%)	0	100	100
43	AF	186/205 (91%)	186 (100%)	0	100	100
44	AG	189/208 (91%)	189 (100%)	0	100	100
45	AH	170/171 (99%)	170 (100%)	0	100	100
46	AI	176/187 (94%)	176 (100%)	0	100	100
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100
58	AV	104/105 (99%)	104 (100%)	0	100	100
59	AW	55/129 (43%)	55 (100%)	0	100	100
60	AX	105/118 (89%)	105 (100%)	0	100	100
61	AY	109/110 (99%)	109 (100%)	0	100	100
62	AZ	115/116 (99%)	115 (100%)	0	100	100
63	Aa	118/119 (99%)	118 (100%)	0	100	100
64	Ab	46/47 (98%)	46 (100%)	0	100	100
65	Ac	81/88 (92%)	81 (100%)	0	100	100
66	Ad	96/97 (99%)	96 (100%)	0	100	100
67	Ae	109/111 (98%)	109 (100%)	0	100	100
68	Af	90/91 (99%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Ag	95/103 (92%)	95 (100%)	0	100	100
70	Ah	104/105 (99%)	104 (100%)	0	100	100
71	Ai	81/82 (99%)	81 (100%)	0	100	100
72	Aj	70/71 (99%)	70 (100%)	0	100	100
73	Ak	68/69 (99%)	68 (100%)	0	100	100
74	Al	45/46 (98%)	45 (100%)	0	100	100
75	Am	47/116 (40%)	47 (100%)	0	100	100
76	An	23/23 (100%)	23 (100%)	0	100	100
77	Ao	87/91 (96%)	87 (100%)	0	100	100
78	Ap	71/72 (99%)	71 (100%)	0	100	100
79	E	198/198 (100%)	198 (100%)	0	100	100
All	All	9483/10186 (93%)	9483 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (117) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	15	GLN
1	BA	21	ASN
1	BA	131	GLN
1	BA	140	ASN
2	BB	40	ASN
2	BB	92	GLN
2	BB	124	ASN
2	BB	149	GLN
3	BC	108	ASN
4	BE	153	ASN
4	BE	197	HIS
4	BE	259	GLN
5	BG	190	GLN
5	BG	201	GLN
6	BH	42	GLN
6	BH	71	HIS
6	BH	110	GLN
6	BH	161	GLN
6	BH	174	ASN
7	BI	119	GLN

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Mol	Chain	Res	Type
9	BL	14	GLN
9	BL	21	ASN
10	BN	78	ASN
11	BO	24	ASN
12	BV	70	ASN
14	BX	10	ASN
14	BX	18	HIS
14	BX	75	GLN
16	Ba	8	ASN
18	Be	17	GLN
19	BD	62	ASN
19	BD	162	GLN
19	BD	165	ASN
20	BF	37	GLN
20	BF	95	ASN
20	BF	122	ASN
20	BF	139	ASN
20	BF	158	GLN
22	BP	15	HIS
23	BQ	94	GLN
24	BR	74	GLN
24	BR	83	GLN
25	BS	13	HIS
26	BT	70	GLN
26	BT	129	GLN
27	BU	15	GLN
27	BU	36	ASN
27	BU	44	ASN
27	BU	47	GLN
27	BU	48	HIS
27	BU	98	GLN
27	BU	105	GLN
28	BZ	98	GLN
29	Bc	43	ASN
30	Bd	48	ASN
30	Bd	53	ASN
31	Bg	31	ASN
31	Bg	196	ASN
31	Bg	288	HIS
32	Bf	134	ASN
33	BM	84	ASN
37	AC	87	GLN

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Mol	Chain	Res	Type
37	AC	291	ASN
37	AC	296	GLN
43	AF	25	GLN
43	AF	64	GLN
43	AF	197	GLN
43	AF	225	GLN
43	AF	231	ASN
43	AF	244	ASN
44	AG	77	GLN
44	AG	95	ASN
44	AG	243	GLN
45	AH	5	GLN
45	AH	51	GLN
45	AH	59	ASN
45	AH	125	ASN
45	AH	157	ASN
46	AI	175	ASN
48	AL	99	HIS
48	AL	114	GLN
48	AL	160	GLN
49	AM	27	GLN
49	AM	105	GLN
50	AN	34	ASN
50	AN	95	GLN
51	AO	50[A]	ASN
51	AO	193[A]	GLN
52	AP	50	GLN
52	AP	96	GLN
52	AP	133	HIS
54	AR	118	HIS
55	AS	65	ASN
55	AS	68	HIS
56	AT	98	HIS
56	AT	103	GLN
56	AT	127	GLN
57	AU	49	ASN
57	AU	101	ASN
61	AY	4	GLN
63	Aa	25	HIS
65	Ac	75	ASN
66	Ad	57	GLN
66	Ad	105	GLN

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Mol	Chain	Res	Type
67	Ae	104	ASN
68	Af	5	HIS
69	Ag	61	GLN
70	Ah	68	GLN
72	Aj	13	ASN
72	Aj	57	HIS
73	Ak	10	GLN
73	Ak	67	GLN
74	Al	11	GLN
75	Am	120	GLN
77	Ao	90	HIS
79	E	197	ASN
79	E	200	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1780/1798 (98%)	445 (25%)	13 (0%)
38	A1	3194/3360 (95%)	634 (19%)	29 (0%)
39	A3	120/121 (99%)	13 (10%)	1 (0%)
40	A4	157/158 (99%)	30 (19%)	0
80	EC	189/202 (93%)	102 (53%)	10 (5%)
All	All	5440/5639 (96%)	1224 (22%)	53 (0%)

All (1224) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
34	B5	4	C
34	B5	17	C
34	B5	25	C
34	B5	26	A
34	B5	34	G
34	B5	42	G
34	B5	47	A
34	B5	57	G
34	B5	60	U
34	B5	63	G
34	B5	68	A
34	B5	72	A
34	B5	73	U

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Mol	Chain	Res	Type
34	B5	74	U
34	B5	75	U
34	B5	76	A
34	B5	77	U
34	B5	78	A
34	B5	80	A
34	B5	81	G
34	B5	103	A
34	B5	104	A
34	B5	111	U
34	B5	114	C
34	B5	115	G
34	B5	127	G
34	B5	130	C
34	B5	131	C
34	B5	132	U
34	B5	133	U
34	B5	134	U
34	B5	135	A
34	B5	136	C
34	B5	137	U
34	B5	138	A
34	B5	141	U
34	B5	145	A
34	B5	146	U
34	B5	156	A
34	B5	159	U
34	B5	166	C
34	B5	168	A
34	B5	173	A
34	B5	174	U
34	B5	176	C
34	B5	178	U
34	B5	179	A
34	B5	182	A
34	B5	183	U
34	B5	188	A
34	B5	190	C
34	B5	191	C
34	B5	192	U
34	B5	193	U
34	B5	194	U

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Mol	Chain	Res	Type
34	B5	195	G
34	B5	196	G
34	B5	198	A
34	B5	200	A
34	B5	206	A
34	B5	217	A
34	B5	218	A
34	B5	220	A
34	B5	224	C
34	B5	225	A
34	B5	227	U
34	B5	230	C
34	B5	232	U
34	B5	233	C
34	B5	234	G
34	B5	236	A
34	B5	240	U
34	B5	241	U
34	B5	261	U
34	B5	262	U
34	B5	265	A
34	B5	267	U
34	B5	278	U
34	B5	280	U
34	B5	287	G
34	B5	299	A
34	B5	305	C
34	B5	314	C
34	B5	316	A
34	B5	321	C
34	B5	322	G
34	B5	333	A
34	B5	337	G
34	B5	338	C
34	B5	351	C
34	B5	352	A
34	B5	359	A
34	B5	360	A
34	B5	361	C
34	B5	369	A
34	B5	370	A
34	B5	381	C

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Mol	Chain	Res	Type
34	B5	387	A
34	B5	389	G
34	B5	397	A
34	B5	400	A
34	B5	401	A
34	B5	402	C
34	B5	417	A
34	B5	422	G
34	B5	424	C
34	B5	425	A
34	B5	426	G
34	B5	439	U
34	B5	444	C
34	B5	453	U
34	B5	454	U
34	B5	460	A
34	B5	468	A
34	B5	477	A
34	B5	478	A
34	B5	481	A
34	B5	483	A
34	B5	484	C
34	B5	485	A
34	B5	486	G
34	B5	489	C
34	B5	491	C
34	B5	492	A
34	B5	493	U
34	B5	494	U
34	B5	496	G
34	B5	497	G
34	B5	498	G
34	B5	499	U
34	B5	500	C
34	B5	502	U
34	B5	503	G
34	B5	504	U
34	B5	506	A
34	B5	509	G
34	B5	514	G
34	B5	515	A
34	B5	518	A

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Mol	Chain	Res	Type
34	B5	519	C
34	B5	527	A
34	B5	534	A
34	B5	539	G
34	B5	540	G
34	B5	541	A2M
34	B5	542	A
34	B5	548	G
34	B5	555	A
34	B5	556	A
34	B5	557	G
34	B5	558	U
34	B5	559	C
34	B5	560	U
34	B5	565	C
34	B5	568	G
34	B5	575	C
34	B5	577	G
34	B5	578	OMU
34	B5	579	A
34	B5	580	A
34	B5	583	C
34	B5	594	A
34	B5	595	G
34	B5	606	A
34	B5	610	G
34	B5	611	U
34	B5	619	A2M
34	B5	620	A
34	B5	622	A
34	B5	623	A
34	B5	624	G
34	B5	639	U
34	B5	653	C
34	B5	656	G
34	B5	657	U
34	B5	658	C
34	B5	677	G
34	B5	678	A
34	B5	679	U
34	B5	681	U
34	B5	682	C

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Mol	Chain	Res	Type
34	B5	683	C
34	B5	688	G
34	B5	690	G
34	B5	694	U
34	B5	696	C
34	B5	697	C
34	B5	698	U
34	B5	702	G
34	B5	703	G
34	B5	705	U
34	B5	706	A
34	B5	707	A
34	B5	708	C
34	B5	709	C
34	B5	710	U
34	B5	711	U
34	B5	712	G
34	B5	713	A
34	B5	715	U
34	B5	716	C
34	B5	717	C
34	B5	718	U
34	B5	719	U
34	B5	722	G
34	B5	723	G
34	B5	727	U
34	B5	729	G
34	B5	730	G
34	B5	731	C
34	B5	732	G
34	B5	733	A
34	B5	735	C
34	B5	737	A
34	B5	741	C
34	B5	743	U
34	B5	753	A
34	B5	755	A
34	B5	765	G
34	B5	766	U
34	B5	774	A
34	B5	775	G
34	B5	778	G

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Mol	Chain	Res	Type
34	B5	781	U
34	B5	782	U
34	B5	783	G
34	B5	784	C
34	B5	789	A
34	B5	794	U
34	B5	812	A
34	B5	814	A
34	B5	815	G
34	B5	820	U
34	B5	823	G
34	B5	832	U
34	B5	833	U
34	B5	835	U
34	B5	837	G
34	B5	839	U
34	B5	840	U
34	B5	852	C
34	B5	863	A
34	B5	864	U
34	B5	876	G
34	B5	888	U
34	B5	895	G
34	B5	898	A
34	B5	899	G
34	B5	904	G
34	B5	906	A
34	B5	912	U
34	B5	913	G
34	B5	914	G
34	B5	922	G
34	B5	933	A
34	B5	935	U
34	B5	944	A
34	B5	951	A
34	B5	960	U
34	B5	966	A
34	B5	973	A
34	B5	987	G
34	B5	988	A
34	B5	992	A
34	B5	993	A

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Mol	Chain	Res	Type
34	B5	998	A
34	B5	1004	U
34	B5	1005	A
34	B5	1020	A
34	B5	1021	C
34	B5	1026	A
34	B5	1028	C
34	B5	1032	G
34	B5	1039	A
34	B5	1052	U
34	B5	1054	U
34	B5	1056	U
34	B5	1057	U
34	B5	1058	U
34	B5	1059	U
34	B5	1060	U
34	B5	1061	A
34	B5	1062	A
34	B5	1063	U
34	B5	1064	G
34	B5	1076	A
34	B5	1083	G
34	B5	1092	A
34	B5	1097	U
34	B5	1098	U
34	B5	1100	G
34	B5	1109	G
34	B5	1138	A
34	B5	1150	G
34	B5	1158	C
34	B5	1159	C
34	B5	1164	G
34	B5	1172	G
34	B5	1185	U
34	B5	1186	U
34	B5	1194	A
34	B5	1196	A
34	B5	1199	G
34	B5	1200	G
34	B5	1201	G
34	B5	1207	C
34	B5	1209	C

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Mol	Chain	Res	Type
34	B5	1212	G
34	B5	1217	A
34	B5	1218	G
34	B5	1226	A
34	B5	1227	A
34	B5	1229	G
34	B5	1230	A
34	B5	1237	G
34	B5	1243	G
34	B5	1244	A
34	B5	1245	G
34	B5	1246	C
34	B5	1248	C
34	B5	1249	U
34	B5	1251	U
34	B5	1252	C
34	B5	1254	U
34	B5	1255	G
34	B5	1256	A
34	B5	1257	U
34	B5	1258	U
34	B5	1259	U
34	B5	1260	U
34	B5	1269	OMU
34	B5	1286	U
34	B5	1291	G
34	B5	1306	C
34	B5	1307	U
34	B5	1314	U
34	B5	1315	U
34	B5	1321	A
34	B5	1329	A
34	B5	1340	U
34	B5	1344	A
34	B5	1345	A
34	B5	1347	U
34	B5	1355	C
34	B5	1356	U
34	B5	1362	U
34	B5	1363	U
34	B5	1364	G
34	B5	1367	G

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Mol	Chain	Res	Type
34	B5	1368	G
34	B5	1369	U
34	B5	1370	U
34	B5	1371	A
34	B5	1372	U
34	B5	1373	C
34	B5	1378	U
34	B5	1382	A
34	B5	1383	G
34	B5	1385	G
34	B5	1388	A
34	B5	1390	U
34	B5	1399	C
34	B5	1400	A
34	B5	1402	G
34	B5	1403	C
34	B5	1413	U
34	B5	1414	U
34	B5	1415	U
34	B5	1418	G
34	B5	1427	A
34	B5	1428	OMG
34	B5	1432	U
34	B5	1436	A
34	B5	1445	G
34	B5	1447	C
34	B5	1458	G
34	B5	1459	C
34	B5	1461	C
34	B5	1469	A
34	B5	1471	A
34	B5	1472	C
34	B5	1473	U
34	B5	1484	G
34	B5	1491	U
34	B5	1492	A
34	B5	1493	A
34	B5	1496	U
34	B5	1506	G
34	B5	1516	A
34	B5	1521	G
34	B5	1523	G

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Mol	Chain	Res	Type
34	B5	1524	A
34	B5	1531	G
34	B5	1534	G
34	B5	1537	C
34	B5	1540	G
34	B5	1541	G
34	B5	1542	G
34	B5	1549	C
34	B5	1557	U
34	B5	1559	A
34	B5	1568	C
34	B5	1575	G7M
34	B5	1576	A
34	B5	1584	G
34	B5	1600	A
34	B5	1601	G
34	B5	1605	G
34	B5	1607	G
34	B5	1619	C
34	B5	1631	A
34	B5	1634	C
34	B5	1635	A
34	B5	1637	C
34	B5	1651	A
34	B5	1657	U
34	B5	1658	G
34	B5	1666	U
34	B5	1667	A
34	B5	1680	G
34	B5	1683	C
34	B5	1684	U
34	B5	1688	U
34	B5	1700	C
34	B5	1701	A
34	B5	1703	C
34	B5	1709	C
34	B5	1713	G
34	B5	1715	G
34	B5	1716	C
34	B5	1717	G
34	B5	1755	A
34	B5	1757	G

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Mol	Chain	Res	Type
34	B5	1762	A
34	B5	1766	A
34	B5	1767	G
34	B5	1769	U
34	B5	1780	G
34	B5	1792	G
34	B5	1793	G
34	B5	1794	A
34	B5	1795	U
34	B5	1796	C
34	B5	1799	U
38	A1	6	A
38	A1	18	G
38	A1	26	A
38	A1	34	A
38	A1	40	A
38	A1	43	A
38	A1	49	A
38	A1	59	G
38	A1	60	A
38	A1	65	A
38	A1	66	A
38	A1	71	A
38	A1	88	A
38	A1	92	G
38	A1	99	A
38	A1	109	A
38	A1	110	G
38	A1	111	C
38	A1	116	A
38	A1	118	U
38	A1	121	A
38	A1	122	A
38	A1	123	A
38	A1	134	U
38	A1	135	C
38	A1	136	G
38	A1	146	U
38	A1	147	U
38	A1	154	U
38	A1	155	G
38	A1	156	G

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Mol	Chain	Res	Type
38	A1	157	A
38	A1	164	A
38	A1	165	A
38	A1	166	C
38	A1	169	U
38	A1	175	C
38	A1	176	G
38	A1	177	U
38	A1	182	U
38	A1	187	A
38	A1	190	U
38	A1	191	U
38	A1	195	U
38	A1	200	C
38	A1	204	A
38	A1	208	C
38	A1	210	U
38	A1	211	A
38	A1	219	A
38	A1	220	G
38	A1	231	G
38	A1	234	G
38	A1	236	G
38	A1	238	A
38	A1	239	G
38	A1	240	U
38	A1	242	C
38	A1	243	G
38	A1	244	G
38	A1	245	U
38	A1	246	U
38	A1	249	U
38	A1	250	U
38	A1	251	G
38	A1	252	U
38	A1	253	A
38	A1	265	A
38	A1	269	G
38	A1	286	U
38	A1	295	A
38	A1	296	A
38	A1	298	U

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Mol	Chain	Res	Type
38	A1	305	U
38	A1	311	C
38	A1	323	A
38	A1	329	U
38	A1	339	C
38	A1	351	A
38	A1	352	A
38	A1	371	G
38	A1	372	A
38	A1	373	A
38	A1	374	A
38	A1	375	A
38	A1	376	G
38	A1	387	A
38	A1	398	A
38	A1	401	U
38	A1	402	A
38	A1	403	C
38	A1	420	G
38	A1	421	G
38	A1	422	A
38	A1	438	A
38	A1	440	A
38	A1	495	G
38	A1	510	G
38	A1	521	A
38	A1	523	A
38	A1	535	G
38	A1	538	G
38	A1	540	U
38	A1	542	G
38	A1	545	U
38	A1	546	C
38	A1	547	G
38	A1	548	G
38	A1	550	A
38	A1	551	A
38	A1	552	G
38	A1	554	A
38	A1	557	A
38	A1	559	A
38	A1	578	A

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Mol	Chain	Res	Type
38	A1	579	G
38	A1	592	A
38	A1	602	A
38	A1	611	A
38	A1	620	U
38	A1	621	A
38	A1	649	A2M
38	A1	660	A
38	A1	677	A
38	A1	679	U
38	A1	681	U
38	A1	690	A
38	A1	691	A
38	A1	705	A
38	A1	711	A
38	A1	715	A
38	A1	719	U
38	A1	725	G
38	A1	758	C
38	A1	760	G
38	A1	761	A
38	A1	766	U
38	A1	767	U
38	A1	775	A
38	A1	776	U
38	A1	777	U
38	A1	781	G
38	A1	784	A
38	A1	785	G
38	A1	786	A
38	A1	799	G
38	A1	806	A
38	A1	808	A
38	A1	813	G
38	A1	817	A2M
38	A1	818	C
38	A1	830	A
38	A1	849	C
38	A1	861	C
38	A1	874	U
38	A1	879	U
38	A1	896	A

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Mol	Chain	Res	Type
38	A1	897	U
38	A1	907	G
38	A1	908	OMG
38	A1	914	A
38	A1	916	G
38	A1	917	A
38	A1	921	A
38	A1	923	C
38	A1	924	G
38	A1	925	A
38	A1	934	G
38	A1	937	G
38	A1	943	U
38	A1	944	C
38	A1	953	G
38	A1	959	C
38	A1	960	U
38	A1	961	C
38	A1	964	G
38	A1	980	A
38	A1	981	U
38	A1	994	G
38	A1	995	U
38	A1	1000	C
38	A1	1002	A
38	A1	1010	G
38	A1	1015	U
38	A1	1016	C
38	A1	1017	C
38	A1	1018	G
38	A1	1019	G
38	A1	1021	G
38	A1	1023	C
38	A1	1032	C
38	A1	1033	U
38	A1	1034	U
38	A1	1035	G
38	A1	1047	A
38	A1	1064	A
38	A1	1072	G
38	A1	1075	A
38	A1	1081	U

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Mol	Chain	Res	Type
38	A1	1082	U
38	A1	1087	G
38	A1	1093	A
38	A1	1094	U
38	A1	1097	G
38	A1	1098	A
38	A1	1103	A
38	A1	1117	G
38	A1	1131	G
38	A1	1144	U
38	A1	1153	A
38	A1	1154	A
38	A1	1155	C
38	A1	1159	A
38	A1	1160	C
38	A1	1168	U
38	A1	1180	A
38	A1	1181	U
38	A1	1182	A
38	A1	1192	C
38	A1	1193	A
38	A1	1201	C
38	A1	1206	G
38	A1	1208	U
38	A1	1219	C
38	A1	1221	A
38	A1	1222	G
38	A1	1223	A
38	A1	1226	G
38	A1	1227	C
38	A1	1230	G
38	A1	1232	C
38	A1	1233	G
38	A1	1235	U
38	A1	1236	G
38	A1	1239	C
38	A1	1241	U
38	A1	1243	G
38	A1	1244	A
38	A1	1245	A
38	A1	1246	G
38	A1	1248	C

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Mol	Chain	Res	Type
38	A1	1249	G
38	A1	1252	A
38	A1	1254	C
38	A1	1256	G
38	A1	1258	U
38	A1	1261	G
38	A1	1262	G
38	A1	1263	A
38	A1	1265	U
38	A1	1268	G
38	A1	1279	C
38	A1	1280	C
38	A1	1281	G
38	A1	1282	G
38	A1	1283	C
38	A1	1285	G
38	A1	1286	A
38	A1	1287	A
38	A1	1292	C
38	A1	1293	U
38	A1	1305	U
38	A1	1307	G
38	A1	1309	U
38	A1	1317	A
38	A1	1325	U
38	A1	1330	A
38	A1	1331	U
38	A1	1345	G
38	A1	1348	U
38	A1	1349	G
38	A1	1350	A
38	A1	1351	U
38	A1	1352	A
38	A1	1353	U
38	A1	1355	A
38	A1	1356	U
38	A1	1357	G
38	A1	1386	A
38	A1	1399	A
38	A1	1400	G
38	A1	1419	A
38	A1	1434	G

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Mol	Chain	Res	Type
38	A1	1437	OMC
38	A1	1443	G
38	A1	1446	A
38	A1	1469	C
38	A1	1481	A
38	A1	1482	A
38	A1	1502	C
38	A1	1508	C
38	A1	1523	U
38	A1	1527	C
38	A1	1539	A
38	A1	1555	U
38	A1	1556	C
38	A1	1562	C
38	A1	1563	C
38	A1	1564	U
38	A1	1565	G
38	A1	1566	A
38	A1	1567	U
38	A1	1568	U
38	A1	1569	U
38	A1	1572	U
38	A1	1573	G
38	A1	1575	A
38	A1	1576	G
38	A1	1578	C
38	A1	1579	C
38	A1	1580	A
38	A1	1583	A
38	A1	1590	G
38	A1	1593	A
38	A1	1605	A
38	A1	1628	C
38	A1	1629	U
38	A1	1630	U
38	A1	1641	U
38	A1	1642	A
38	A1	1643	A
38	A1	1657	C
38	A1	1714	A
38	A1	1724	U
38	A1	1738	C

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Mol	Chain	Res	Type
38	A1	1741	A
38	A1	1750	A
38	A1	1751	G
38	A1	1762	C
38	A1	1763	U
38	A1	1765	U
38	A1	1766	G
38	A1	1775	G
38	A1	1796	G
38	A1	1797	A
38	A1	1813	A
38	A1	1814	A
38	A1	1815	U
38	A1	1816	A
38	A1	1817	G
38	A1	1821	U
38	A1	1842	A
38	A1	1846	C
38	A1	1849	C
38	A1	1850	A
38	A1	1858	A
38	A1	1866	C
38	A1	1867	A
38	A1	1878	G
38	A1	1879	A
38	A1	1880	U
38	A1	1886	A
38	A1	1899	G
38	A1	1906	G
38	A1	1932	A
38	A1	1935	G
38	A1	1948	G
38	A1	1953	G
38	A1	1954	G
38	A1	1955	U
38	A1	2095	G
38	A1	2102	U
38	A1	2112	U
38	A1	2114	C
38	A1	2122	G
38	A1	2126	A
38	A1	2131	A

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Mol	Chain	Res	Type
38	A1	2140	U
38	A1	2144	A
38	A1	2158	A
38	A1	2159	U
38	A1	2169	G
38	A1	2188	A
38	A1	2197	OMC
38	A1	2198	A
38	A1	2205	U
38	A1	2206	G
38	A1	2207	A
38	A1	2208	A
38	A1	2209	U
38	A1	2242	A
38	A1	2249	G
38	A1	2253	G
38	A1	2254	U
38	A1	2256	A2M
38	A1	2257	C
38	A1	2258	U
38	A1	2259	A
38	A1	2260	U
38	A1	2263	C
38	A1	2267	C
38	A1	2269	U
38	A1	2272	G
38	A1	2273	G
38	A1	2281	A2M
38	A1	2307	G
38	A1	2309	A
38	A1	2310	U
38	A1	2313	A
38	A1	2314	U
38	A1	2315	G
38	A1	2334	U
38	A1	2335	G
38	A1	2336	U
38	A1	2340	U
38	A1	2373	A
38	A1	2374	C
38	A1	2375	G
38	A1	2383	C

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Mol	Chain	Res	Type
38	A1	2388	U
38	A1	2391	G
38	A1	2393	G
38	A1	2394	G
38	A1	2397	A
38	A1	2398	A
38	A1	2402	A
38	A1	2403	G
38	A1	2404	A
38	A1	2411	U
38	A1	2412	G
38	A1	2439	A
38	A1	2440	G
38	A1	2442	G
38	A1	2447	A
38	A1	2450	G
38	A1	2451	G
38	A1	2453	U
38	A1	2454	G
38	A1	2455	U
38	A1	2459	A
38	A1	2460	U
38	A1	2461	A
38	A1	2463	G
38	A1	2465	G
38	A1	2467	G
38	A1	2468	A
38	A1	2471	U
38	A1	2474	G
38	A1	2475	G
38	A1	2477	G
38	A1	2479	C
38	A1	2480	A
38	A1	2483	G
38	A1	2486	A
38	A1	2487	U
38	A1	2490	C
38	A1	2491	A
38	A1	2492	C
38	A1	2493	U
38	A1	2495	C
38	A1	2496	C

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Mol	Chain	Res	Type
38	A1	2497	U
38	A1	2498	U
38	A1	2499	U
38	A1	2500	A
38	A1	2501	U
38	A1	2502	A
38	A1	2503	G
38	A1	2504	U
38	A1	2505	U
38	A1	2506	U
38	A1	2507	C
38	A1	2513	U
38	A1	2514	U
38	A1	2515	A
38	A1	2522	G
38	A1	2523	A
38	A1	2524	A
38	A1	2530	G
38	A1	2536	A
38	A1	2537	U
38	A1	2538	U
38	A1	2539	C
38	A1	2540	A
38	A1	2541	U
38	A1	2542	U
38	A1	2543	U
38	A1	2544	U
38	A1	2546	C
38	A1	2547	A
38	A1	2552	C
38	A1	2555	G
38	A1	2561	A
38	A1	2562	A
38	A1	2569	A
38	A1	2570	U
38	A1	2571	U
38	A1	2573	G
38	A1	2576	G
38	A1	2585	G
38	A1	2587	U
38	A1	2593	A
38	A1	2606	G

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Mol	Chain	Res	Type
38	A1	2607	G
38	A1	2614	G
38	A1	2626	A
38	A1	2629	U
38	A1	2652	U
38	A1	2656	A
38	A1	2674	A
38	A1	2677	G
38	A1	2688	U
38	A1	2689	A
38	A1	2691	A
38	A1	2703	A
38	A1	2704	A
38	A1	2705	A
38	A1	2712	U
38	A1	2719	U
38	A1	2727	A
38	A1	2728	G
38	A1	2729	OMU
38	A1	2737	C
38	A1	2749	G
38	A1	2752	U
38	A1	2753	G
38	A1	2755	C
38	A1	2762	A
38	A1	2777	G
38	A1	2778	G
38	A1	2796	G
38	A1	2799	A
38	A1	2800	G
38	A1	2801	A
38	A1	2803	A
38	A1	2810	C
38	A1	2814	G
38	A1	2817	A
38	A1	2842	U
38	A1	2844	C
38	A1	2845	A
38	A1	2849	C
38	A1	2871	G
38	A1	2872	A
38	A1	2875	U

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Mol	Chain	Res	Type
38	A1	2876	C
38	A1	2887	A
38	A1	2889	C
38	A1	2898	G
38	A1	2923	U
38	A1	2925	C
38	A1	2935	U
38	A1	2936	A
38	A1	2938	G
38	A1	2942	C
38	A1	2947	G
38	A1	2977	G
38	A1	2983	C
38	A1	2990	G
38	A1	2997	G
38	A1	3011	A
38	A1	3012	A
38	A1	3022	G
38	A1	3028	G
38	A1	3032	A
38	A1	3056	U
38	A1	3059	G
38	A1	3074	G
38	A1	3078	U
38	A1	3079	U
38	A1	3086	A
38	A1	3092	C
38	A1	3109	G
38	A1	3113	A
38	A1	3122	A
38	A1	3129	A
38	A1	3130	A
38	A1	3131	U
38	A1	3141	A
38	A1	3142	A
38	A1	3143	C
38	A1	3153	U
38	A1	3154	C
38	A1	3155	U
38	A1	3156	U
38	A1	3157	U
38	A1	3164	C

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Mol	Chain	Res	Type
38	A1	3165	A
38	A1	3170	A
38	A1	3172	A
38	A1	3173	G
38	A1	3174	A
38	A1	3175	U
38	A1	3176	G
38	A1	3179	U
38	A1	3181	C
38	A1	3187	A
38	A1	3196	U
38	A1	3198	U
38	A1	3206	C
38	A1	3207	U
38	A1	3210	A
38	A1	3215	A
38	A1	3217	C
38	A1	3218	A
38	A1	3219	G
38	A1	3229	G
38	A1	3234	A
38	A1	3243	A
38	A1	3246	G
38	A1	3247	G
38	A1	3250	U
38	A1	3256	G
38	A1	3257	C
38	A1	3259	U
38	A1	3260	G
38	A1	3263	G
38	A1	3273	A
38	A1	3275	U
38	A1	3276	G
38	A1	3280	U
38	A1	3281	U
38	A1	3289	G
38	A1	3294	A
38	A1	3304	U
38	A1	3307	A
38	A1	3312	U
38	A1	3316	A
38	A1	3319	U

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Mol	Chain	Res	Type
38	A1	3323	A
38	A1	3342	A
38	A1	3345	G
38	A1	3350	C
38	A1	3351	U
38	A1	3352	U
38	A1	3353	G
38	A1	3354	U
38	A1	3355	U
38	A1	3356	G
38	A1	3369	G
38	A1	3378	C
38	A1	3382	U
38	A1	3389	U
38	A1	3390	G
39	A3	7	G
39	A3	33	U
39	A3	41	G
39	A3	42	A
39	A3	52	G
39	A3	53	U
39	A3	54	U
39	A3	65	G
39	A3	74	C
39	A3	76	A
39	A3	102	A
39	A3	112	G
39	A3	121	U
40	A4	23	U
40	A4	34	U
40	A4	35	C
40	A4	38	U
40	A4	51	G
40	A4	52	A
40	A4	53	A
40	A4	59	A
40	A4	61	A
40	A4	62	C
40	A4	63	G
40	A4	81	U
40	A4	82	U
40	A4	83	C

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Mol	Chain	Res	Type
40	A4	86	U
40	A4	87	G
40	A4	88	A
40	A4	90	U
40	A4	95	G
40	A4	104	A
40	A4	105	A
40	A4	106	C
40	A4	107	G
40	A4	111	A
40	A4	113	U
40	A4	116	G
40	A4	125	U
40	A4	152	G
40	A4	154	C
40	A4	158	U
80	EC	6762	U
80	EC	6768	U
80	EC	6769	A
80	EC	6770	U
80	EC	6771	U
80	EC	6772	G
80	EC	6773	G
80	EC	6774	U
80	EC	6775	U
80	EC	6776	A
80	EC	6777	C
80	EC	6778	C
80	EC	6779	C
80	EC	6780	A
80	EC	6781	U
80	EC	6786	A
80	EC	6787	U
80	EC	6788	C
80	EC	6789	G
80	EC	6790	A
80	EC	6791	A
80	EC	6792	A
80	EC	6793	A
80	EC	6794	C
80	EC	6795	U
80	EC	6802	A

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Mol	Chain	Res	Type
80	EC	6803	C
80	EC	6804	A
80	EC	6813	A
80	EC	6814	G
80	EC	6815	U
80	EC	6817	A
80	EC	6818	G
80	EC	6819	G
80	EC	6820	C
80	EC	6821	U
80	EC	6822	U
80	EC	6823	U
80	EC	6824	C
80	EC	6825	A
80	EC	6826	U
80	EC	6831	U
80	EC	6832	G
80	EC	6835	U
80	EC	6836	U
80	EC	6837	G
80	EC	6842	U
80	EC	6843	U
80	EC	6844	A
80	EC	6845	G
80	EC	6847	G
80	EC	6849	A
80	EC	6850	C
80	EC	6851	G
80	EC	6852	U
80	EC	6854	U
80	EC	6856	C
80	EC	6858	A
80	EC	6859	U
80	EC	6860	A
80	EC	6861	G
80	EC	6863	C
80	EC	6864	A
80	EC	6865	G
80	EC	6866	C
80	EC	6867	C
80	EC	6868	C
80	EC	6869	C

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Mol	Chain	Res	Type
80	EC	6870	A
80	EC	6871	A
80	EC	6873	A
80	EC	6874	A
80	EC	6875	C
80	EC	6877	C
80	EC	6879	U
80	EC	6880	G
80	EC	6889	A
80	EC	6893	C
80	EC	6897	G
80	EC	6902	U
80	EC	6903	U
80	EC	6904	U
80	EC	6908	C
80	EC	6912	G
80	EC	6913	U
80	EC	6914	A
80	EC	6915	G
80	EC	6916	A
80	EC	6918	A
80	EC	6922	G
80	EC	6925	C
80	EC	6928	G
80	EC	6929	C
80	EC	6935	G
80	EC	6940	U
80	EC	6941	U
80	EC	6942	A
80	EC	6943	A
80	EC	6945	U
80	EC	6946	A
80	EC	6947	A
80	EC	6950	C

All (53) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	B5	224	C
34	B5	369	A
34	B5	501	U
34	B5	559	C

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Mol	Chain	Res	Type
34	B5	706	A
34	B5	722	G
34	B5	752	A
34	B5	819	G
34	B5	862	A
34	B5	950	C
34	B5	1226	A
34	B5	1285	U
34	B5	1344	A
38	A1	122	A
38	A1	168	U
38	A1	210	U
38	A1	241	G
38	A1	249	U
38	A1	264	G
38	A1	374	A
38	A1	588	G
38	A1	916	G
38	A1	959	C
38	A1	1015	U
38	A1	1018	G
38	A1	1092	C
38	A1	1218	U
38	A1	1229	G
38	A1	1292	C
38	A1	1354	G
38	A1	1563	C
38	A1	1629	U
38	A1	2241	U
38	A1	2496	C
38	A1	2500	A
38	A1	2501	U
38	A1	2504	U
38	A1	2506	U
38	A1	2586	G
38	A1	2875	U
38	A1	3121	U
38	A1	3303	G
39	A3	52	G
80	EC	6789	G
80	EC	6817	A
80	EC	6831	U

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Mol	Chain	Res	Type
80	EC	6835	U
80	EC	6844	A
80	EC	6857	C
80	EC	6858	A
80	EC	6863	C
80	EC	6876	A
80	EC	6934	U

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

67 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
34	OMG	B5	1271	34	23,26,27	1.18	3 (13%)	32,38,41	1.92	6 (18%)
38	OMG	A1	2619	38	23,26,27	1.18	3 (13%)	32,38,41	1.97	6 (18%)
34	A2M	B5	796	34	22,25,26	1.51	4 (18%)	30,36,39	2.17	9 (30%)
34	OMG	B5	1126	34	23,26,27	1.17	3 (13%)	32,38,41	2.00	6 (18%)
34	4AC	B5	1280	34	21,24,25	1.07	1 (4%)	28,34,37	1.10	2 (7%)
38	OMG	A1	867	81,38	23,26,27	1.19	3 (13%)	32,38,41	1.97	6 (18%)
38	A2M	A1	2280	38	22,25,26	1.49	4 (18%)	30,36,39	2.08	9 (30%)
34	A2M	B5	541	34	22,25,26	1.54	4 (18%)	30,36,39	2.28	7 (23%)
38	A2M	A1	2256	38	22,25,26	1.55	4 (18%)	30,36,39	2.25	11 (36%)
34	A2M	B5	420	34	22,25,26	1.49	4 (18%)	30,36,39	2.12	10 (33%)
38	OMU	A1	2347	38	19,22,23	1.27	4 (21%)	25,31,34	1.78	5 (20%)
34	A2M	B5	619	81,34	22,25,26	1.50	5 (22%)	30,36,39	2.00	9 (30%)
34	XSX	B5	1191	34	24,28,29	1.38	5 (20%)	30,40,43	4.69	7 (23%)
38	OMU	A1	2421	38	19,22,23	1.25	4 (21%)	25,31,34	1.78	5 (20%)
34	OMU	B5	1269	34	19,22,23	1.28	4 (21%)	25,31,34	1.82	5 (20%)
34	A2M	B5	28	34	22,25,26	1.51	4 (18%)	30,36,39	2.06	8 (26%)
38	A2M	A1	649	38	22,25,26	1.50	4 (18%)	30,36,39	2.03	8 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	OMC	A1	2948	38	19,22,23	0.80	0	25,31,34	0.95	2 (8%)
38	A2M	A1	2220	38	22,25,26	1.53	5 (22%)	30,36,39	1.99	9 (30%)
34	OMG	B5	1428	81,34	23,26,27	1.19	3 (13%)	32,38,41	1.98	6 (18%)
34	A2M	B5	100	81,34	22,25,26	1.51	4 (18%)	30,36,39	2.03	7 (23%)
38	OMG	A1	2793	38	23,26,27	1.18	3 (13%)	32,38,41	1.98	6 (18%)
34	OMC	B5	1639	34	19,22,23	0.78	0	25,31,34	0.80	1 (4%)
38	A2M	A1	1449	81,38	22,25,26	1.49	4 (18%)	30,36,39	2.05	8 (26%)
38	OMC	A1	2197	38	19,22,23	0.77	0	25,31,34	0.84	0
38	OMU	A1	898	38	19,22,23	1.24	3 (15%)	25,31,34	1.74	4 (16%)
38	OMG	A1	2791	38	23,26,27	1.18	3 (13%)	32,38,41	1.99	6 (18%)
36	HIC	AB	243	36	10,11,12	1.49	1 (10%)	9,14,16	1.35	2 (22%)
38	5MC	A1	2870	38	19,22,23	1.59	3 (15%)	26,32,35	1.31	3 (11%)
38	OMG	A1	2922	38	23,26,27	1.20	3 (13%)	32,38,41	2.03	6 (18%)
38	OMU	A1	2729	38	19,22,23	1.26	4 (21%)	25,31,34	1.73	5 (20%)
38	A2M	A1	817	81,38	22,25,26	1.51	5 (22%)	30,36,39	2.07	9 (30%)
34	OMG	B5	562	34	23,26,27	1.18	3 (13%)	32,38,41	1.96	6 (18%)
38	OMU	A1	2724	38	19,22,23	1.21	3 (15%)	25,31,34	1.77	5 (20%)
38	A2M	A1	2946	81,38	22,25,26	1.50	5 (22%)	30,36,39	2.17	9 (30%)
38	OMG	A1	908	81,38	23,26,27	1.21	3 (13%)	32,38,41	2.03	6 (18%)
38	OMU	A1	1888	38	19,22,23	1.28	3 (15%)	25,31,34	1.88	4 (16%)
38	A2M	A1	2281	38	22,25,26	1.40	5 (22%)	30,36,39	2.40	11 (36%)
38	A2M	A1	876	38	22,25,26	1.49	4 (18%)	30,36,39	2.00	8 (26%)
38	1MA	A1	645	81,38	21,25,26	1.34	4 (19%)	30,37,40	1.70	6 (20%)
38	OMU	A1	2417	38	19,22,23	1.22	3 (15%)	25,31,34	1.75	5 (20%)
38	OMC	A1	650	38	19,22,23	0.78	0	25,31,34	0.76	0
34	4AC	B5	1773	34	21,24,25	0.96	1 (4%)	28,34,37	1.96	5 (17%)
34	A2M	B5	974	34	22,25,26	1.49	4 (18%)	30,36,39	2.04	8 (26%)
34	MA6	B5	1781	34	23,26,27	1.53	5 (21%)	33,38,41	2.08	10 (30%)
38	A2M	A1	807	38	22,25,26	1.51	4 (18%)	30,36,39	2.05	8 (26%)
38	OMC	A1	663	38	19,22,23	0.80	0	25,31,34	0.84	0
38	OMG	A1	805	38	23,26,27	1.19	3 (13%)	32,38,41	2.01	6 (18%)
38	OMG	A1	2288	38	23,26,27	1.19	3 (13%)	32,38,41	2.00	6 (18%)
34	A2M	B5	436	34	22,25,26	1.50	4 (18%)	30,36,39	2.13	8 (26%)
38	OMU	A1	2921	38	19,22,23	1.22	3 (15%)	25,31,34	1.81	5 (20%)
34	OMU	B5	578	34	19,22,23	1.20	2 (10%)	25,31,34	1.82	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	OMC	B5	414	34	19,22,23	0.81	0	25,31,34	0.85	1 (4%)
38	5MC	A1	2278	81,38	19,22,23	1.57	3 (15%)	26,32,35	1.23	3 (11%)
34	G7M	B5	1575	34	23,26,27	2.54	6 (26%)	34,39,42	3.10	14 (41%)
34	MA6	B5	1782	34	23,26,27	1.52	5 (21%)	33,38,41	2.10	10 (30%)
38	A2M	A1	1133	38	22,25,26	1.48	4 (18%)	30,36,39	2.23	9 (30%)
38	OMC	A1	2337	38	19,22,23	0.78	0	25,31,34	0.77	0
38	UR3	A1	2634	38	19,22,23	1.00	1 (5%)	26,32,35	1.76	2 (7%)
38	OMC	A1	1437	81,38	19,22,23	0.81	0	25,31,34	1.14	2 (8%)
38	OMG	A1	2815	38	23,26,27	1.17	3 (13%)	32,38,41	1.97	5 (15%)
38	OMG	A1	1450	38	23,26,27	1.19	3 (13%)	32,38,41	1.98	6 (18%)
38	1MA	A1	2142	81,38	21,25,26	1.33	4 (19%)	30,37,40	1.70	3 (10%)
34	OMC	B5	1007	34	19,22,23	0.81	0	25,31,34	0.95	1 (4%)
38	OMC	A1	2959	38	19,22,23	0.80	0	25,31,34	0.85	1 (4%)
34	OMG	B5	1572	34	23,26,27	1.18	3 (13%)	32,38,41	1.97	6 (18%)
38	A2M	A1	2640	38	22,25,26	1.51	4 (18%)	30,36,39	2.07	8 (26%)

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
34	OMG	B5	1271	34	-	1/9/27/28	0/3/3/3
38	OMG	A1	2619	38	-	1/9/27/28	0/3/3/3
34	A2M	B5	796	34	-	0/9/27/28	0/3/3/3
34	OMG	B5	1126	34	-	1/9/27/28	0/3/3/3
34	4AC	B5	1280	34	-	4/11/29/30	0/2/2/2
38	OMG	A1	867	81,38	-	0/9/27/28	0/3/3/3
38	A2M	A1	2280	38	-	1/9/27/28	0/3/3/3
34	A2M	B5	541	34	-	4/9/27/28	0/3/3/3
38	A2M	A1	2256	38	-	2/9/27/28	0/3/3/3
34	A2M	B5	420	34	-	1/9/27/28	0/3/3/3
38	OMU	A1	2347	38	-	2/9/27/28	0/2/2/2
34	A2M	B5	619	81,34	-	2/9/27/28	0/3/3/3
34	XSX	B5	1191	34	-	6/16/34/35	0/2/2/2
38	OMU	A1	2421	38	-	1/9/27/28	0/2/2/2
34	OMU	B5	1269	34	-	3/9/27/28	0/2/2/2
34	A2M	B5	28	34	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	A2M	A1	649	38	-	1/9/27/28	0/3/3/3
38	OMC	A1	2948	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2220	38	-	1/9/27/28	0/3/3/3
34	OMG	B5	1428	81,34	-	3/9/27/28	0/3/3/3
34	A2M	B5	100	81,34	-	0/9/27/28	0/3/3/3
38	OMG	A1	2793	38	-	1/9/27/28	0/3/3/3
34	OMC	B5	1639	34	-	1/9/27/28	0/2/2/2
38	A2M	A1	1449	81,38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
38	OMU	A1	898	38	-	0/9/27/28	0/2/2/2
38	OMG	A1	2791	38	-	0/9/27/28	0/3/3/3
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2729	38	-	2/9/27/28	0/2/2/2
38	A2M	A1	817	81,38	-	1/9/27/28	0/3/3/3
34	OMG	B5	562	34	-	1/9/27/28	0/3/3/3
38	OMU	A1	2724	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2946	81,38	-	0/9/27/28	0/3/3/3
38	OMG	A1	908	81,38	-	0/9/27/28	0/3/3/3
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2281	38	-	0/9/27/28	0/3/3/3
38	A2M	A1	876	38	-	0/9/27/28	0/3/3/3
38	1MA	A1	645	81,38	-	2/7/25/26	0/3/3/3
38	OMU	A1	2417	38	-	1/9/27/28	0/2/2/2
38	OMC	A1	650	38	-	0/9/27/28	0/2/2/2
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
34	A2M	B5	974	34	-	0/9/27/28	0/3/3/3
34	MA6	B5	1781	34	-	1/11/29/30	0/3/3/3
38	A2M	A1	807	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	663	38	-	0/9/27/28	0/2/2/2
38	OMG	A1	805	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	2288	38	-	0/9/27/28	0/3/3/3
34	A2M	B5	436	34	-	0/9/27/28	0/3/3/3
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
34	OMU	B5	578	34	-	0/9/27/28	0/2/2/2
34	OMC	B5	414	34	-	1/9/27/28	0/2/2/2
38	5MC	A1	2278	81,38	-	1/7/25/26	0/2/2/2
34	G7M	B5	1575	34	-	0/7/25/26	0/3/3/3
34	MA6	B5	1782	34	-	3/11/29/30	0/3/3/3
38	A2M	A1	1133	38	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMC	A1	2337	38	-	0/9/27/28	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	OMC	A1	1437	81,38	-	4/9/27/28	0/2/2/2
38	OMG	A1	2815	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	1450	38	-	0/9/27/28	0/3/3/3
38	1MA	A1	2142	81,38	-	0/7/25/26	0/3/3/3
34	OMC	B5	1007	34	-	0/9/27/28	0/2/2/2
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2
34	OMG	B5	1572	34	-	0/9/27/28	0/3/3/3
38	A2M	A1	2640	38	-	1/9/27/28	0/3/3/3

All (202) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	C8-N7	7.70	1.46	1.33
38	A1	2278	5MC	C5-C4	5.55	1.48	1.44
38	A1	2870	5MC	C5-C4	5.43	1.48	1.44
34	B5	541	A2M	C5-C4	4.94	1.47	1.39
34	B5	1575	G7M	C5-N7	-4.79	1.33	1.39
34	B5	1781	MA6	C5-C4	4.78	1.47	1.39
34	B5	1782	MA6	C5-C4	4.77	1.47	1.39
38	A1	2256	A2M	C5-C4	4.72	1.47	1.39
38	A1	2220	A2M	C5-C4	4.71	1.47	1.39
34	B5	796	A2M	C5-C4	4.68	1.47	1.39
34	B5	28	A2M	C5-C4	4.67	1.47	1.39
34	B5	436	A2M	C5-C4	4.67	1.47	1.39
34	B5	100	A2M	C5-C4	4.65	1.47	1.39
38	A1	807	A2M	C5-C4	4.65	1.47	1.39
38	A1	2640	A2M	C5-C4	4.63	1.47	1.39
38	A1	649	A2M	C5-C4	4.62	1.47	1.39
34	B5	974	A2M	C5-C4	4.61	1.47	1.39
38	A1	876	A2M	C5-C4	4.61	1.47	1.39
38	A1	1449	A2M	C5-C4	4.60	1.47	1.39
38	A1	2280	A2M	C5-C4	4.60	1.47	1.39
38	A1	2946	A2M	C5-C4	4.59	1.47	1.39
34	B5	420	A2M	C5-C4	4.57	1.47	1.39
34	B5	619	A2M	C5-C4	4.55	1.47	1.39
38	A1	1133	A2M	C5-C4	4.52	1.47	1.39
38	A1	817	A2M	C5-C4	4.46	1.47	1.39
34	B5	1575	G7M	C8-N9	4.22	1.47	1.35
38	A1	2281	A2M	C5-C4	4.15	1.46	1.39
34	B5	1575	G7M	C5-C4	3.85	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1191	XSX	C2-N1	3.67	1.43	1.38
38	A1	908	OMG	C5-C4	3.20	1.47	1.38
38	A1	2288	OMG	C5-C4	3.17	1.47	1.38
34	B5	1428	OMG	C5-C4	3.16	1.47	1.38
34	B5	1781	MA6	C5-C6	3.16	1.49	1.41
34	B5	1271	OMG	C5-C4	3.14	1.47	1.38
38	A1	2619	OMG	C5-C4	3.14	1.47	1.38
34	B5	1782	MA6	C5-C6	3.14	1.49	1.41
38	A1	2791	OMG	C5-C4	3.13	1.47	1.38
34	B5	1572	OMG	C5-C4	3.13	1.47	1.38
38	A1	1450	OMG	C5-C4	3.12	1.47	1.38
34	B5	562	OMG	C5-C4	3.12	1.47	1.38
38	A1	867	OMG	C5-C4	3.11	1.47	1.38
38	A1	2922	OMG	C5-C4	3.10	1.47	1.38
38	A1	2870	5MC	C6-C5	3.07	1.39	1.34
38	A1	2815	OMG	C5-C4	3.06	1.47	1.38
38	A1	645	1MA	C6-N6	3.06	1.35	1.28
38	A1	2793	OMG	C5-C4	3.05	1.47	1.38
38	A1	2142	1MA	C5-C4	3.05	1.47	1.38
34	B5	1280	4AC	C4-N4	-3.03	1.35	1.39
38	A1	805	OMG	C5-C4	3.03	1.47	1.38
34	B5	1126	OMG	C5-C4	3.02	1.47	1.38
38	A1	2142	1MA	C6-N6	3.00	1.35	1.28
38	A1	645	1MA	C5-C4	2.97	1.46	1.38
36	AB	243	HIC	CD2-CG	2.92	1.41	1.36
38	A1	1888	OMU	C4-N3	-2.83	1.33	1.38
34	B5	541	A2M	C5-C6	2.77	1.48	1.41
34	B5	28	A2M	C5-C6	2.76	1.48	1.41
38	A1	2347	OMU	C4-N3	-2.75	1.33	1.38
38	A1	2256	A2M	C5-C6	2.74	1.48	1.41
38	A1	2421	OMU	C4-N3	-2.72	1.33	1.38
38	A1	817	A2M	C5-C6	2.72	1.48	1.41
38	A1	898	OMU	C4-N3	-2.71	1.34	1.38
38	A1	2278	5MC	C6-C5	2.71	1.39	1.34
34	B5	1269	OMU	C4-N3	-2.70	1.34	1.38
38	A1	2729	OMU	C4-N3	-2.70	1.34	1.38
34	B5	796	A2M	C5-C6	2.70	1.48	1.41
38	A1	2417	OMU	C4-N3	-2.69	1.34	1.38
34	B5	100	A2M	C5-C6	2.69	1.48	1.41
34	B5	974	A2M	C5-C6	2.69	1.48	1.41
38	A1	649	A2M	C5-C6	2.68	1.48	1.41
38	A1	2280	A2M	C5-C6	2.68	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2921	OMU	C4-N3	-2.67	1.34	1.38
34	B5	420	A2M	C5-C6	2.67	1.48	1.41
38	A1	2640	A2M	C5-C6	2.67	1.48	1.41
34	B5	619	A2M	C5-C6	2.66	1.48	1.41
38	A1	807	A2M	C5-C6	2.66	1.48	1.41
38	A1	2946	A2M	C5-C6	2.65	1.48	1.41
38	A1	1449	A2M	C5-C6	2.64	1.48	1.41
34	B5	436	A2M	C5-C6	2.64	1.48	1.41
38	A1	1133	A2M	C5-C6	2.64	1.48	1.41
38	A1	876	A2M	C5-C6	2.62	1.48	1.41
38	A1	2724	OMU	C4-N3	-2.61	1.34	1.38
38	A1	2922	OMG	C6-N1	-2.58	1.34	1.38
34	B5	578	OMU	C4-N3	-2.58	1.34	1.38
38	A1	908	OMG	C6-N1	-2.55	1.34	1.38
38	A1	2220	A2M	C5-C6	2.52	1.48	1.41
38	A1	2815	OMG	C6-N1	-2.51	1.34	1.38
38	A1	2288	OMG	C6-N1	-2.51	1.34	1.38
38	A1	2220	A2M	C5-N7	-2.51	1.34	1.39
38	A1	867	OMG	C6-N1	-2.50	1.34	1.38
38	A1	2619	OMG	C6-N1	-2.49	1.34	1.38
38	A1	805	OMG	C6-N1	-2.49	1.34	1.38
34	B5	436	A2M	C5-N7	-2.49	1.34	1.39
38	A1	1450	OMG	C6-N1	-2.49	1.34	1.38
38	A1	2793	OMG	C6-N1	-2.48	1.34	1.38
34	B5	562	OMG	C6-N1	-2.48	1.34	1.38
38	A1	807	A2M	C5-N7	-2.47	1.34	1.39
34	B5	1126	OMG	C6-N1	-2.46	1.34	1.38
38	A1	2791	OMG	C6-N1	-2.46	1.34	1.38
38	A1	649	A2M	C5-N7	-2.45	1.34	1.39
34	B5	1428	OMG	C6-N1	-2.45	1.34	1.38
34	B5	1269	OMU	C2-N1	2.44	1.42	1.38
34	B5	541	A2M	C5-N7	-2.44	1.34	1.39
38	A1	2640	A2M	C5-N7	-2.44	1.34	1.39
34	B5	1572	OMG	C6-N1	-2.43	1.34	1.38
34	B5	1191	XSX	O2-C2	2.43	1.27	1.22
34	B5	1271	OMG	C6-N1	-2.41	1.34	1.38
38	A1	1888	OMU	C2-N3	-2.41	1.33	1.38
38	A1	1449	A2M	C5-N7	-2.40	1.34	1.39
34	B5	100	A2M	C5-N7	-2.39	1.34	1.39
34	B5	1191	XSX	O10-C9	-2.38	1.23	1.30
38	A1	2281	A2M	C5-C6	2.37	1.47	1.41
34	B5	619	A2M	C5-N7	-2.37	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2280	A2M	C5-N7	-2.36	1.34	1.39
38	A1	1133	A2M	C5-N7	-2.35	1.34	1.39
34	B5	28	A2M	C8-N7	2.34	1.36	1.31
38	A1	876	A2M	C5-N7	-2.34	1.34	1.39
34	B5	796	A2M	C5-N7	-2.33	1.34	1.39
38	A1	2946	A2M	C5-N7	-2.32	1.34	1.39
34	B5	28	A2M	C5-N7	-2.31	1.34	1.39
38	A1	2256	A2M	C8-N7	2.31	1.36	1.31
38	A1	2256	A2M	C5-N7	-2.30	1.34	1.39
34	B5	420	A2M	C8-N7	2.30	1.36	1.31
38	A1	2922	OMG	C5-N7	-2.30	1.34	1.39
34	B5	1782	MA6	C8-N7	2.29	1.36	1.31
34	B5	619	A2M	C8-N7	2.29	1.36	1.31
34	B5	1575	G7M	C6-N1	-2.29	1.34	1.38
38	A1	817	A2M	C8-N7	2.28	1.36	1.31
34	B5	974	A2M	C8-N7	2.28	1.36	1.31
38	A1	908	OMG	C5-N7	-2.27	1.34	1.39
38	A1	2946	A2M	C8-N7	2.27	1.36	1.31
34	B5	1781	MA6	C8-N7	2.27	1.36	1.31
34	B5	420	A2M	C5-N7	-2.27	1.34	1.39
38	A1	2281	A2M	C5-N7	-2.26	1.35	1.39
38	A1	2421	OMU	C2-N3	-2.26	1.34	1.38
38	A1	817	A2M	C5-N7	-2.26	1.35	1.39
38	A1	2729	OMU	C2-N1	2.26	1.42	1.38
38	A1	2280	A2M	C8-N7	2.26	1.36	1.31
34	B5	796	A2M	C8-N7	2.26	1.36	1.31
38	A1	2142	1MA	C5-N7	-2.25	1.34	1.39
34	B5	974	A2M	C5-N7	-2.25	1.35	1.39
38	A1	817	A2M	C4-N9	-2.24	1.33	1.37
38	A1	2921	OMU	C2-N3	-2.23	1.34	1.38
38	A1	2724	OMU	C2-N3	-2.23	1.34	1.38
34	B5	1269	OMU	C2-N3	-2.23	1.34	1.38
38	A1	1133	A2M	C8-N7	2.23	1.36	1.31
34	B5	100	A2M	C8-N7	2.23	1.36	1.31
38	A1	2278	5MC	C6-N1	-2.22	1.34	1.38
34	B5	1575	G7M	C2'-C3'	-2.22	1.47	1.53
38	A1	2729	OMU	C5-C4	-2.21	1.38	1.43
38	A1	2281	A2M	C4-N9	-2.21	1.33	1.37
38	A1	2347	OMU	C2-N1	2.20	1.41	1.38
38	A1	2288	OMG	C5-N7	-2.20	1.34	1.39
38	A1	2870	5MC	C6-N1	-2.20	1.34	1.38
38	A1	645	1MA	C5-N7	-2.20	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2347	OMU	C2-N3	-2.19	1.34	1.38
38	A1	2417	OMU	C2-N3	-2.19	1.34	1.38
34	B5	578	OMU	C2-N3	-2.18	1.34	1.38
34	B5	436	A2M	C8-N7	2.18	1.35	1.31
34	B5	1191	XSX	C6-C5	2.18	1.40	1.35
34	B5	1428	OMG	C5-N7	-2.17	1.34	1.39
38	A1	898	OMU	C5-C4	-2.17	1.39	1.43
38	A1	2220	A2M	C8-N7	2.17	1.35	1.31
38	A1	649	A2M	C8-N7	2.16	1.35	1.31
34	B5	1191	XSX	C5-C4	-2.16	1.38	1.43
38	A1	807	A2M	C8-N7	2.16	1.35	1.31
38	A1	898	OMU	C2-N3	-2.16	1.34	1.38
38	A1	2417	OMU	C5-C4	-2.16	1.39	1.43
34	B5	1773	4AC	C4-N4	-2.15	1.36	1.39
38	A1	876	A2M	C8-N7	2.15	1.35	1.31
38	A1	2347	OMU	C5-C4	-2.15	1.39	1.43
38	A1	1449	A2M	C8-N7	2.15	1.35	1.31
34	B5	541	A2M	C8-N7	2.14	1.35	1.31
38	A1	2220	A2M	C4-N9	-2.14	1.33	1.37
38	A1	1450	OMG	C5-N7	-2.14	1.34	1.39
38	A1	2281	A2M	C8-N7	2.13	1.35	1.31
38	A1	2142	1MA	C2-N3	2.12	1.34	1.30
38	A1	2619	OMG	C5-N7	-2.12	1.34	1.39
38	A1	2724	OMU	C5-C4	-2.11	1.39	1.43
34	B5	1781	MA6	C4-N9	-2.11	1.33	1.37
38	A1	867	OMG	C5-N7	-2.11	1.34	1.39
38	A1	2640	A2M	C8-N7	2.10	1.35	1.31
38	A1	2793	OMG	C5-N7	-2.09	1.34	1.39
38	A1	2634	UR3	C2-N1	2.09	1.41	1.38
38	A1	2921	OMU	C5-C4	-2.09	1.39	1.43
38	A1	805	OMG	C5-N7	-2.09	1.34	1.39
38	A1	2421	OMU	C5-C4	-2.09	1.39	1.43
38	A1	2791	OMG	C5-N7	-2.07	1.34	1.39
34	B5	1782	MA6	C5-N7	-2.07	1.35	1.39
38	A1	1888	OMU	C5-C4	-2.06	1.39	1.43
34	B5	1269	OMU	C5-C4	-2.06	1.39	1.43
38	A1	645	1MA	C2-N3	2.05	1.34	1.30
38	A1	2729	OMU	C2-N3	-2.05	1.34	1.38
34	B5	1126	OMG	C5-N7	-2.05	1.35	1.39
38	A1	2815	OMG	C5-N7	-2.03	1.35	1.39
34	B5	562	OMG	C5-N7	-2.03	1.35	1.39
34	B5	1271	OMG	C5-N7	-2.02	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	619	A2M	C4-N9	-2.02	1.33	1.37
34	B5	1572	OMG	C5-N7	-2.02	1.35	1.39
34	B5	1781	MA6	C5-N7	-2.02	1.35	1.39
38	A1	2421	OMU	C2-N1	2.02	1.41	1.38
34	B5	1782	MA6	C4-N9	-2.01	1.33	1.37
38	A1	2946	A2M	C4-N9	-2.00	1.33	1.37

All (385) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1191	XSX	C3-C1-N3	24.10	154.29	112.16
34	B5	1575	G7M	CN7-N7-C8	-7.90	112.83	124.79
34	B5	541	A2M	C5-C4-N3	-7.13	116.90	126.72
34	B5	1773	4AC	N4-C4-N3	7.09	125.38	113.87
38	A1	2634	UR3	C4-N3-C2	-7.07	118.89	124.58
38	A1	2922	OMG	C5-C4-N3	-6.47	118.09	128.39
38	A1	908	OMG	C5-C4-N3	-6.41	118.20	128.39
38	A1	2288	OMG	C5-C4-N3	-6.39	118.22	128.39
34	B5	1575	G7M	N9-C8-N7	-6.35	97.07	112.48
34	B5	1428	OMG	C5-C4-N3	-6.27	118.41	128.39
38	A1	2619	OMG	C5-C4-N3	-6.22	118.49	128.39
38	A1	2791	OMG	C5-C4-N3	-6.18	118.55	128.39
38	A1	867	OMG	C5-C4-N3	-6.17	118.57	128.39
38	A1	1450	OMG	C5-C4-N3	-6.15	118.60	128.39
34	B5	1575	G7M	C8-N7-C5	6.14	115.45	107.78
34	B5	562	OMG	C5-C4-N3	-6.08	118.71	128.39
34	B5	1572	OMG	C5-C4-N3	-6.07	118.74	128.39
34	B5	436	A2M	C5-C4-N3	-6.06	118.37	126.72
38	A1	2815	OMG	C5-C4-N3	-6.06	118.75	128.39
34	B5	1126	OMG	C5-C4-N3	-6.02	118.81	128.39
38	A1	2793	OMG	C5-C4-N3	-6.01	118.82	128.39
38	A1	2640	A2M	C5-C4-N3	-6.01	118.44	126.72
38	A1	805	OMG	C5-C4-N3	-6.00	118.84	128.39
38	A1	807	A2M	C5-C4-N3	-5.99	118.47	126.72
34	B5	100	A2M	C5-C4-N3	-5.97	118.49	126.72
34	B5	796	A2M	C5-C4-N3	-5.96	118.51	126.72
38	A1	2280	A2M	C5-C4-N3	-5.94	118.53	126.72
38	A1	1449	A2M	C5-C4-N3	-5.93	118.55	126.72
34	B5	28	A2M	C5-C4-N3	-5.91	118.57	126.72
34	B5	1271	OMG	C5-C4-N3	-5.90	118.99	128.39
38	A1	649	A2M	C5-C4-N3	-5.87	118.64	126.72
34	B5	1575	G7M	N9-C4-N3	5.86	137.67	125.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2256	A2M	C5-C4-N3	-5.82	118.70	126.72
38	A1	876	A2M	C5-C4-N3	-5.80	118.73	126.72
38	A1	1133	A2M	C5-C4-N3	-5.75	118.79	126.72
34	B5	541	A2M	N3-C4-N9	5.73	136.91	127.17
34	B5	974	A2M	C5-C4-N3	-5.69	118.88	126.72
38	A1	2946	A2M	C5-C4-N3	-5.68	118.90	126.72
34	B5	420	A2M	C5-C4-N3	-5.67	118.91	126.72
34	B5	619	A2M	C5-C4-N3	-5.67	118.92	126.72
34	B5	1575	G7M	C5-C4-N3	-5.54	117.69	128.15
38	A1	2281	A2M	C5-C4-N3	-5.47	119.19	126.72
38	A1	817	A2M	C5-C4-N3	-5.43	119.24	126.72
34	B5	1782	MA6	C5-C4-N3	-5.37	119.32	126.72
38	A1	2220	A2M	C5-C4-N3	-5.26	119.48	126.72
38	A1	2922	OMG	C2-N3-C4	5.20	121.26	112.30
38	A1	2142	1MA	C5-C4-N3	-5.18	119.64	127.27
34	B5	1781	MA6	C5-C4-N3	-5.14	119.64	126.72
38	A1	2791	OMG	C2-N3-C4	5.13	121.14	112.30
38	A1	805	OMG	C2-N3-C4	5.12	121.12	112.30
38	A1	2288	OMG	C2-N3-C4	5.12	121.11	112.30
34	B5	1126	OMG	C2-N3-C4	5.11	121.10	112.30
38	A1	2815	OMG	C2-N3-C4	5.11	121.09	112.30
38	A1	2793	OMG	C2-N3-C4	5.09	121.07	112.30
38	A1	2619	OMG	C2-N3-C4	5.09	121.07	112.30
38	A1	867	OMG	C2-N3-C4	5.08	121.06	112.30
38	A1	1450	OMG	C2-N3-C4	5.07	121.03	112.30
34	B5	1428	OMG	C2-N3-C4	5.06	121.02	112.30
38	A1	908	OMG	C2-N3-C4	5.06	121.02	112.30
38	A1	645	1MA	C5-C4-N3	-5.02	119.88	127.27
34	B5	562	OMG	C2-N3-C4	5.00	120.91	112.30
34	B5	1572	OMG	C2-N3-C4	4.99	120.90	112.30
34	B5	1271	OMG	C2-N3-C4	4.97	120.86	112.30
38	A1	908	OMG	N9-C4-N3	4.96	135.88	125.95
38	A1	2288	OMG	N9-C4-N3	4.89	135.73	125.95
34	B5	578	OMU	C4-N3-C2	-4.86	120.57	126.61
34	B5	1428	OMG	N9-C4-N3	4.81	135.58	125.95
38	A1	1888	OMU	C4-N3-C2	-4.79	120.67	126.61
38	A1	2640	A2M	N3-C4-N9	4.78	135.29	127.17
38	A1	2281	A2M	N3-C4-N9	4.72	135.19	127.17
38	A1	1133	A2M	C2'-C1'-N9	-4.72	105.99	113.75
38	A1	2921	OMU	C4-N3-C2	-4.71	120.76	126.61
34	B5	100	A2M	N3-C4-N9	4.70	135.17	127.17
34	B5	796	A2M	N3-C4-N9	4.69	135.14	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	436	A2M	N3-C4-N9	4.69	135.14	127.17
38	A1	2280	A2M	N3-C4-N9	4.67	135.11	127.17
38	A1	807	A2M	N3-C4-N9	4.67	135.11	127.17
38	A1	1450	OMG	N9-C4-N3	4.67	135.28	125.95
38	A1	2421	OMU	C4-N3-C2	-4.67	120.82	126.61
38	A1	1449	A2M	N3-C4-N9	4.66	135.09	127.17
38	A1	2619	OMG	N9-C4-N3	4.61	135.18	125.95
38	A1	649	A2M	N3-C4-N9	4.60	135.00	127.17
38	A1	876	A2M	N3-C4-N9	4.59	134.98	127.17
34	B5	1575	G7M	C2-N3-C4	4.58	120.19	112.30
38	A1	2922	OMG	N9-C4-N3	4.58	135.11	125.95
38	A1	867	OMG	N9-C4-N3	4.56	135.07	125.95
38	A1	2791	OMG	N9-C4-N3	4.56	135.07	125.95
34	B5	28	A2M	N3-C4-N9	4.56	134.92	127.17
38	A1	645	1MA	C2-N3-C4	4.56	121.47	112.53
34	B5	1781	MA6	C4-C5-N7	-4.55	105.38	110.58
38	A1	2724	OMU	C4-N3-C2	-4.55	120.97	126.61
38	A1	2417	OMU	C4-N3-C2	-4.53	120.99	126.61
34	B5	1269	OMU	C4-N3-C2	-4.51	121.02	126.61
38	A1	2347	OMU	C4-N3-C2	-4.51	121.02	126.61
38	A1	2142	1MA	C2-N3-C4	4.50	121.35	112.53
34	B5	420	A2M	N3-C4-N9	4.49	134.80	127.17
34	B5	562	OMG	N9-C4-N3	4.49	134.93	125.95
38	A1	1133	A2M	N3-C4-N9	4.49	134.80	127.17
38	A1	2256	A2M	N3-C4-N9	4.47	134.78	127.17
34	B5	974	A2M	N3-C4-N9	4.47	134.76	127.17
34	B5	1781	MA6	C2-N1-C6	4.45	122.69	111.83
34	B5	1126	OMG	N9-C4-N3	4.42	134.80	125.95
38	A1	898	OMU	C4-N3-C2	-4.42	121.12	126.61
38	A1	2946	A2M	N3-C4-N9	4.41	134.67	127.17
34	B5	1782	MA6	C4-C5-N7	-4.39	105.56	110.58
34	B5	1572	OMG	N9-C4-N3	4.39	134.73	125.95
34	B5	619	A2M	N3-C4-N9	4.38	134.62	127.17
34	B5	1782	MA6	C2-N1-C6	4.37	122.50	111.83
38	A1	2815	OMG	N9-C4-N3	4.36	134.67	125.95
38	A1	2793	OMG	N9-C4-N3	4.36	134.66	125.95
38	A1	2921	OMU	N3-C2-N1	4.35	120.55	114.89
38	A1	805	OMG	N9-C4-N3	4.35	134.65	125.95
38	A1	1888	OMU	N3-C2-N1	4.31	120.50	114.89
38	A1	2281	A2M	O4'-C1'-N9	4.29	116.33	108.09
34	B5	1271	OMG	N9-C4-N3	4.29	134.52	125.95
38	A1	2281	A2M	C2'-C1'-N9	-4.26	106.74	113.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	541	A2M	C2-N3-C4	4.25	122.20	111.83
38	A1	2421	OMU	N3-C2-N1	4.24	120.41	114.89
38	A1	2417	OMU	N3-C2-N1	4.21	120.38	114.89
38	A1	817	A2M	N3-C4-N9	4.21	134.32	127.17
34	B5	578	OMU	N3-C2-N1	4.19	120.34	114.89
38	A1	2729	OMU	N3-C2-N1	4.17	120.32	114.89
38	A1	2729	OMU	C4-N3-C2	-4.17	121.44	126.61
38	A1	2870	5MC	C5-C6-N1	-4.15	118.81	123.31
38	A1	2220	A2M	N3-C4-N9	4.14	134.20	127.17
34	B5	1191	XSX	C6-N1-C2	-4.13	118.42	121.80
38	A1	898	OMU	N3-C2-N1	4.09	120.22	114.89
38	A1	2347	OMU	N3-C2-N1	4.09	120.22	114.89
38	A1	2256	A2M	O2'-C2'-C1'	4.07	116.72	108.99
38	A1	2724	OMU	N3-C2-N1	4.06	120.17	114.89
34	B5	1773	4AC	C5-C4-N4	-3.96	116.27	122.94
34	B5	1575	G7M	CN7-N7-C5	3.94	131.71	126.80
34	B5	1191	XSX	O2-C2-N3	-3.93	116.69	121.98
34	B5	1269	OMU	N3-C2-N1	3.92	120.00	114.89
38	A1	1888	OMU	C5-C4-N3	3.92	120.29	114.80
34	B5	1269	OMU	C5-C4-N3	3.91	120.27	114.80
38	A1	2724	OMU	C5-C4-N3	3.88	120.23	114.80
34	B5	578	OMU	C5-C4-N3	3.87	120.22	114.80
38	A1	2421	OMU	C5-C4-N3	3.85	120.19	114.80
34	B5	1280	4AC	N4-C4-N3	3.84	120.10	113.87
34	B5	1782	MA6	N3-C4-N9	3.81	133.65	127.17
38	A1	2921	OMU	C5-C4-N3	3.80	120.12	114.80
38	A1	2347	OMU	C5-C4-N3	3.79	120.11	114.80
38	A1	2280	A2M	C2-N3-C4	3.78	121.06	111.83
34	B5	1191	XSX	C1-N3-C4	3.78	124.41	117.10
34	B5	28	A2M	C2-N3-C4	3.77	121.04	111.83
38	A1	2256	A2M	C2-N3-C4	3.76	121.01	111.83
34	B5	436	A2M	C2-N3-C4	3.76	121.00	111.83
38	A1	2417	OMU	C5-C4-N3	3.75	120.05	114.80
38	A1	1449	A2M	C2-N3-C4	3.75	120.98	111.83
34	B5	100	A2M	C2-N3-C4	3.74	120.98	111.83
38	A1	2640	A2M	C2-N3-C4	3.74	120.97	111.83
38	A1	2946	A2M	C2-N3-C4	3.74	120.96	111.83
38	A1	649	A2M	C2-N3-C4	3.73	120.95	111.83
34	B5	796	A2M	C2-N3-C4	3.73	120.95	111.83
38	A1	1133	A2M	C2-N3-C4	3.71	120.89	111.83
38	A1	817	A2M	C2-N3-C4	3.71	120.89	111.83
38	A1	2220	A2M	N3-C2-N1	-3.70	122.97	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	898	OMU	C5-C4-N3	3.70	119.98	114.80
34	B5	796	A2M	C2'-C1'-N9	-3.70	107.67	113.75
34	B5	420	A2M	C2-N3-C4	3.68	120.81	111.83
38	A1	876	A2M	C2-N3-C4	3.67	120.80	111.83
34	B5	974	A2M	C2-N3-C4	3.67	120.80	111.83
38	A1	2281	A2M	C2-N3-C4	3.66	120.78	111.83
34	B5	1782	MA6	C2-N3-C4	3.65	120.74	111.83
38	A1	2729	OMU	C5-C4-N3	3.63	119.89	114.80
34	B5	1575	G7M	O3'-C3'-C4'	3.60	121.43	111.08
34	B5	619	A2M	C4-C5-N7	-3.60	106.47	110.58
34	B5	1575	G7M	C8-N9-C4	3.60	116.00	107.09
38	A1	817	A2M	C4-C5-N7	-3.60	106.47	110.58
34	B5	619	A2M	C2-N3-C4	3.59	120.59	111.83
34	B5	1781	MA6	N3-C4-N9	3.59	133.27	127.17
34	B5	28	A2M	C4-C5-N7	-3.58	106.49	110.58
38	A1	649	A2M	C4-C5-N7	-3.57	106.50	110.58
38	A1	2142	1MA	N9-C4-N3	3.56	135.02	126.90
38	A1	807	A2M	C2-N3-C4	3.56	120.53	111.83
38	A1	2280	A2M	C4-C5-N7	-3.56	106.51	110.58
38	A1	2281	A2M	C4-N9-C8	3.56	109.47	105.74
38	A1	807	A2M	C4-C5-N7	-3.54	106.53	110.58
34	B5	420	A2M	C2'-C1'-N9	-3.54	107.93	113.75
34	B5	1781	MA6	C2-N3-C4	3.52	120.44	111.83
34	B5	796	A2M	C4-C5-N7	-3.51	106.57	110.58
34	B5	420	A2M	C4-C5-N7	-3.50	106.58	110.58
34	B5	974	A2M	C4-C5-N7	-3.49	106.59	110.58
38	A1	2220	A2M	C2-N3-C4	3.49	120.35	111.83
38	A1	817	A2M	N3-C2-N1	-3.48	123.31	128.58
38	A1	1449	A2M	C4-C5-N7	-3.48	106.60	110.58
34	B5	436	A2M	C4-C5-N7	-3.48	106.61	110.58
38	A1	1133	A2M	C4-C5-N7	-3.48	106.61	110.58
38	A1	2946	A2M	C4-C5-N7	-3.48	106.61	110.58
38	A1	2256	A2M	C4-C5-N7	-3.47	106.62	110.58
38	A1	805	OMG	C6-C5-N7	3.47	136.60	130.29
34	B5	100	A2M	C4-C5-N7	-3.46	106.62	110.58
38	A1	2815	OMG	C6-C5-N7	3.45	136.57	130.29
38	A1	2946	A2M	N3-C2-N1	-3.44	123.37	128.58
38	A1	876	A2M	C4-C5-N7	-3.44	106.65	110.58
38	A1	2281	A2M	N3-C2-N1	-3.41	123.43	128.58
38	A1	2793	OMG	C6-C5-N7	3.39	136.46	130.29
34	B5	1126	OMG	C6-C5-N7	3.38	136.44	130.29
38	A1	2640	A2M	C4-C5-N7	-3.38	106.72	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1271	OMG	C6-C5-N7	3.35	136.39	130.29
34	B5	1782	MA6	N1-C2-N3	-3.33	123.53	128.58
38	A1	2280	A2M	N3-C2-N1	-3.33	123.54	128.58
38	A1	1133	A2M	N3-C2-N1	-3.33	123.55	128.58
38	A1	649	A2M	N3-C2-N1	-3.32	123.55	128.58
34	B5	974	A2M	N3-C2-N1	-3.32	123.56	128.58
38	A1	1449	A2M	N3-C2-N1	-3.31	123.56	128.58
34	B5	1572	OMG	C6-C5-N7	3.30	136.30	130.29
38	A1	2634	UR3	C5-C4-N3	3.30	119.39	115.04
34	B5	541	A2M	N3-C2-N1	-3.29	123.60	128.58
34	B5	1575	G7M	O2'-C2'-C3'	3.29	122.36	111.82
34	B5	420	A2M	N3-C2-N1	-3.29	123.61	128.58
38	A1	2946	A2M	C2'-C1'-N9	-3.28	108.35	113.75
34	B5	28	A2M	N3-C2-N1	-3.28	123.62	128.58
34	B5	562	OMG	C6-C5-N7	3.27	136.25	130.29
38	A1	2791	OMG	C6-C5-N7	3.26	136.23	130.29
34	B5	436	A2M	N3-C2-N1	-3.25	123.66	128.58
38	A1	876	A2M	N3-C2-N1	-3.24	123.68	128.58
38	A1	2220	A2M	C4-C5-N7	-3.24	106.88	110.58
34	B5	1781	MA6	N1-C2-N3	-3.24	123.68	128.58
38	A1	2256	A2M	N3-C2-N1	-3.23	123.69	128.58
38	A1	867	OMG	C6-C5-N7	3.23	136.17	130.29
34	B5	541	A2M	C4-C5-N7	-3.23	106.89	110.58
34	B5	100	A2M	N3-C2-N1	-3.22	123.71	128.58
38	A1	645	1MA	N9-C4-N3	3.22	134.23	126.90
34	B5	796	A2M	N3-C2-N1	-3.21	123.73	128.58
34	B5	1773	4AC	CM7-C7-N4	3.18	120.40	115.27
38	A1	2640	A2M	N3-C2-N1	-3.15	123.81	128.58
38	A1	2619	OMG	C6-C5-N7	3.15	136.03	130.29
34	B5	1191	XSX	C4-N3-C2	-3.13	120.98	124.66
38	A1	2724	OMU	O4-C4-C5	-3.13	119.77	125.16
38	A1	2922	OMG	C6-C5-N7	3.12	135.96	130.29
38	A1	1450	OMG	C6-C5-N7	3.12	135.96	130.29
38	A1	2417	OMU	O4-C4-C5	-3.11	119.80	125.16
38	A1	2921	OMU	O4-C4-C5	-3.10	119.82	125.16
34	B5	619	A2M	N3-C2-N1	-3.06	123.95	128.58
34	B5	1781	MA6	C5-N7-C8	3.06	108.25	103.45
38	A1	2421	OMU	O4-C4-C5	-3.05	119.90	125.16
38	A1	2278	5MC	O2-C2-N3	-3.05	117.53	122.33
38	A1	2347	OMU	O4-C4-C5	-3.04	119.92	125.16
34	B5	1269	OMU	O4-C4-C5	-3.04	119.92	125.16
38	A1	2729	OMU	O4-C4-C5	-3.04	119.92	125.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	AB	243	HIC	NE2-CE1-ND1	-3.03	111.50	112.66
38	A1	898	OMU	O4-C4-C5	-3.03	119.93	125.16
34	B5	1782	MA6	C5-N7-C8	3.00	108.16	103.45
38	A1	1888	OMU	O4-C4-C5	-2.99	120.00	125.16
34	B5	578	OMU	O4-C4-C5	-2.98	120.02	125.16
38	A1	2281	A2M	C4-C5-N7	-2.96	107.19	110.58
34	B5	1575	G7M	O3'-C3'-C2'	2.96	121.31	111.82
34	B5	436	A2M	C2'-C1'-N9	-2.94	108.92	113.75
38	A1	817	A2M	C4-N9-C8	2.92	108.81	105.74
34	B5	1428	OMG	C6-C5-N7	2.91	135.58	130.29
38	A1	2288	OMG	C6-C5-N7	2.88	135.54	130.29
34	B5	1773	4AC	C6-C5-C4	2.87	120.46	117.00
38	A1	2870	5MC	C5-C4-N3	-2.87	118.81	121.75
38	A1	2278	5MC	C5-C4-N3	-2.84	118.85	121.75
34	B5	1781	MA6	C6-C5-N7	2.83	137.95	133.43
38	A1	2220	A2M	C2-N1-C6	2.82	123.37	118.73
38	A1	1437	OMC	O2-C2-N3	-2.79	117.93	122.33
34	B5	420	A2M	C4-N9-C8	2.79	108.67	105.74
38	A1	908	OMG	C6-C5-N7	2.78	135.35	130.29
38	A1	807	A2M	N3-C2-N1	-2.77	124.39	128.58
38	A1	2278	5MC	C5-C6-N1	-2.75	120.33	123.31
34	B5	1269	OMU	C1'-N1-C2	2.73	122.50	117.59
34	B5	1773	4AC	C5-C4-N3	-2.72	118.35	122.60
38	A1	2347	OMU	C1'-N1-C2	2.72	122.47	117.59
38	A1	2922	OMG	C4-C5-N7	-2.70	106.40	110.67
34	B5	1781	MA6	C4-N9-C8	2.68	108.55	105.74
38	A1	805	OMG	C4-C5-N7	-2.67	106.43	110.67
38	A1	1437	OMC	C1'-N1-C2	2.67	124.34	118.44
38	A1	2815	OMG	C4-C5-N7	-2.67	106.44	110.67
34	B5	974	A2M	C4-N9-C8	2.65	108.53	105.74
34	B5	619	A2M	C4-N9-C8	2.65	108.52	105.74
34	B5	1782	MA6	C6-C5-N7	2.64	137.64	133.43
38	A1	2280	A2M	C5-N7-C8	2.63	107.59	103.45
38	A1	649	A2M	C5-N7-C8	2.63	107.58	103.45
38	A1	2793	OMG	C4-C5-N7	-2.62	106.53	110.67
34	B5	1572	OMG	C4-C5-N7	-2.61	106.53	110.67
38	A1	2280	A2M	C4-N9-C8	2.60	108.46	105.74
34	B5	420	A2M	C5-N7-C8	2.59	107.52	103.45
34	B5	1126	OMG	C4-C5-N7	-2.59	106.57	110.67
34	B5	562	OMG	C4-C5-N7	-2.58	106.58	110.67
34	B5	619	A2M	C5-N7-C8	2.58	107.50	103.45
38	A1	867	OMG	C4-C5-N7	-2.58	106.59	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1782	MA6	C4-N9-C8	2.57	108.44	105.74
38	A1	2791	OMG	C4-C5-N7	-2.57	106.60	110.67
38	A1	2946	A2M	C4-N9-C8	2.56	108.43	105.74
34	B5	28	A2M	C5-N7-C8	2.56	107.47	103.45
38	A1	2948	OMC	O2-C2-N3	-2.56	118.30	122.33
38	A1	817	A2M	C5-N7-C8	2.56	107.47	103.45
34	B5	1271	OMG	C4-C5-N7	-2.55	106.63	110.67
38	A1	2619	OMG	C4-C5-N7	-2.54	106.65	110.67
38	A1	1449	A2M	C5-N7-C8	2.54	107.44	103.45
38	A1	1133	A2M	C5-N7-C8	2.52	107.42	103.45
34	B5	974	A2M	C5-N7-C8	2.52	107.41	103.45
38	A1	876	A2M	C4-N9-C8	2.52	108.38	105.74
34	B5	796	A2M	C5-N7-C8	2.52	107.40	103.45
34	B5	100	A2M	C5-N7-C8	2.51	107.40	103.45
34	B5	436	A2M	C5-N7-C8	2.51	107.40	103.45
38	A1	1133	A2M	C4-N9-C8	2.51	108.37	105.74
38	A1	876	A2M	C5-N7-C8	2.51	107.39	103.45
38	A1	649	A2M	C4-N9-C8	2.50	108.37	105.74
38	A1	2946	A2M	C5-N7-C8	2.49	107.36	103.45
38	A1	817	A2M	C6-C5-N7	2.47	136.86	132.09
34	B5	796	A2M	C4-N9-C8	2.47	108.33	105.74
38	A1	807	A2M	C5-N7-C8	2.47	107.33	103.45
34	B5	1575	G7M	C1'-N9-C8	-2.46	118.42	126.74
34	B5	100	A2M	C4-N9-C8	2.43	108.29	105.74
38	A1	2281	A2M	N9-C8-N7	-2.43	110.49	113.94
38	A1	1450	OMG	C4-C5-N7	-2.43	106.83	110.67
34	B5	541	A2M	C1'-N9-C8	-2.42	121.72	127.09
34	B5	28	A2M	C4-N9-C8	2.41	108.27	105.74
34	B5	541	A2M	C5-N7-C8	2.41	107.23	103.45
38	A1	2256	A2M	C5-N7-C8	2.40	107.22	103.45
34	B5	1575	G7M	O6-C6-C5	-2.40	122.66	128.01
38	A1	2281	A2M	C5-N7-C8	2.39	107.21	103.45
38	A1	2288	OMG	C4-C5-N7	-2.39	106.89	110.67
38	A1	2640	A2M	C5-N7-C8	2.38	107.19	103.45
38	A1	645	1MA	C4-C5-N7	-2.38	106.90	110.67
34	B5	578	OMU	O2-C2-N1	-2.38	119.70	122.80
38	A1	2256	A2M	O3'-C3'-C2'	2.37	117.83	111.19
38	A1	1449	A2M	C4-N9-C8	2.37	108.23	105.74
38	A1	2640	A2M	C4-N9-C8	2.34	108.19	105.74
38	A1	645	1MA	C6-C5-N7	2.33	136.28	132.16
34	B5	1428	OMG	C4-C5-N7	-2.33	106.98	110.67
38	A1	807	A2M	C4-N9-C8	2.33	108.18	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	908	OMG	C4-C5-N7	-2.32	106.99	110.67
38	A1	2729	OMU	C6-N1-C2	-2.31	118.19	121.00
38	A1	2640	A2M	C2'-C1'-N9	-2.31	109.95	113.75
38	A1	2256	A2M	C4-N9-C8	2.31	108.16	105.74
38	A1	2220	A2M	C4-N9-C8	2.29	108.15	105.74
34	B5	1007	OMC	O2-C2-N3	-2.29	118.72	122.33
34	B5	1428	OMG	O6-C6-C5	-2.29	120.48	126.53
38	A1	2256	A2M	C5'-C4'-C3'	-2.28	107.00	115.21
38	A1	2921	OMU	O2-C2-N1	-2.27	119.84	122.80
34	B5	1781	MA6	N9-C8-N7	-2.26	110.72	113.94
38	A1	645	1MA	N1-C2-N3	-2.25	123.32	126.00
38	A1	1450	OMG	O6-C6-C5	-2.24	120.63	126.53
34	B5	414	OMC	O2-C2-N3	-2.21	118.85	122.33
34	B5	1782	MA6	N9-C8-N7	-2.21	110.80	113.94
38	A1	817	A2M	N9-C8-N7	-2.20	110.81	113.94
38	A1	2946	A2M	C6-C5-N7	2.19	136.32	132.09
34	B5	619	A2M	C6-C5-N7	2.18	136.30	132.09
38	A1	2417	OMU	O2-C2-N1	-2.18	119.96	122.80
34	B5	420	A2M	C6-C5-N7	2.18	136.28	132.09
38	A1	2288	OMG	O6-C6-C5	-2.16	120.83	126.53
38	A1	908	OMG	O6-C6-C5	-2.16	120.84	126.53
34	B5	1126	OMG	O6-C6-C5	-2.15	120.85	126.53
34	B5	974	A2M	C6-C5-N7	2.15	136.23	132.09
38	A1	2619	OMG	O6-C6-C5	-2.14	120.88	126.53
34	B5	1191	XSX	C1'-N1-C2	2.14	120.54	117.04
38	A1	2220	A2M	C5-N7-C8	2.14	106.81	103.45
34	B5	28	A2M	C6-C5-N7	2.13	136.21	132.09
34	B5	1280	4AC	C6-C5-C4	2.13	119.57	117.00
38	A1	2791	OMG	O6-C6-C5	-2.13	120.92	126.53
38	A1	2256	A2M	C6-C5-N7	2.13	136.19	132.09
38	A1	2793	OMG	O6-C6-C5	-2.12	120.93	126.53
38	A1	1133	A2M	C6-C5-N7	2.11	136.16	132.09
34	B5	436	A2M	C4-N9-C8	2.11	107.95	105.74
38	A1	2870	5MC	O2-C2-N3	-2.11	119.01	122.33
34	B5	420	A2M	N9-C8-N7	-2.11	110.95	113.94
38	A1	649	A2M	C6-C5-N7	2.11	136.15	132.09
34	B5	562	OMG	O6-C6-C5	-2.10	121.00	126.53
34	B5	1572	OMG	O6-C6-C5	-2.09	121.01	126.53
38	A1	2280	A2M	C6-C5-N7	2.08	136.11	132.09
38	A1	2724	OMU	O2-C2-N1	-2.08	120.09	122.80
34	B5	1271	OMG	O6-C6-C5	-2.08	121.05	126.53
38	A1	2922	OMG	O6-C6-C5	-2.06	121.08	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2959	OMC	O2-C2-N3	-2.06	119.08	122.33
34	B5	1191	XSX	C1-N3-C2	-2.06	114.60	117.64
38	A1	2220	A2M	C6-C5-N7	2.06	136.06	132.09
38	A1	867	OMG	O6-C6-C5	-2.06	121.10	126.53
34	B5	1575	G7M	C3'-C2'-C1'	2.06	105.36	101.46
38	A1	2281	A2M	C6-C5-N7	2.05	136.05	132.09
38	A1	876	A2M	C6-C5-N7	2.05	136.03	132.09
34	B5	619	A2M	N9-C8-N7	-2.04	111.04	113.94
38	A1	807	A2M	O4'-C1'-N9	2.04	112.00	108.09
38	A1	1449	A2M	C6-C5-N7	2.03	136.01	132.09
38	A1	805	OMG	O6-C6-C5	-2.03	121.17	126.53
38	A1	2421	OMU	O2-C2-N1	-2.02	120.16	122.80
34	B5	796	A2M	C6-C5-N7	2.02	135.98	132.09
38	A1	2280	A2M	N9-C8-N7	-2.02	111.08	113.94
38	A1	2948	OMC	C1'-N1-C2	2.01	122.88	118.44
34	B5	1639	OMC	O2-C2-N3	-2.01	119.16	122.33
36	AB	243	HIC	CB-CG-CD2	-2.01	125.12	129.96

There are no chirality outliers.

All (69) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	28	A2M	C1'-C2'-O2'-CM'
34	B5	541	A2M	C2'-C1'-N9-C8
34	B5	541	A2M	C2'-C1'-N9-C4
34	B5	562	OMG	C1'-C2'-O2'-CM2
34	B5	1191	XSX	C3-C1-N3-C2
34	B5	1191	XSX	C3-C1-N3-C4
34	B5	1271	OMG	C1'-C2'-O2'-CM2
34	B5	1280	4AC	N3-C4-N4-C7
34	B5	1280	4AC	C5-C4-N4-C7
34	B5	1280	4AC	O7-C7-N4-C4
34	B5	1280	4AC	CM7-C7-N4-C4
34	B5	1773	4AC	N3-C4-N4-C7
34	B5	1773	4AC	C5-C4-N4-C7
34	B5	1773	4AC	O7-C7-N4-C4
34	B5	1773	4AC	CM7-C7-N4-C4
38	A1	1437	OMC	C1'-C2'-O2'-CM2
38	A1	1437	OMC	O4'-C4'-C5'-O5'
38	A1	2197	OMC	C2'-C1'-N1-C2
38	A1	2197	OMC	C2'-C1'-N1-C6
38	A1	2220	A2M	C1'-C2'-O2'-CM'

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Mol	Chain	Res	Type	Atoms
38	A1	2256	A2M	C1'-C2'-O2'-CM'
38	A1	2280	A2M	C1'-C2'-O2'-CM'
38	A1	2417	OMU	C1'-C2'-O2'-CM2
38	A1	2421	OMU	C1'-C2'-O2'-CM2
38	A1	2619	OMG	C1'-C2'-O2'-CM2
38	A1	1437	OMC	C3'-C4'-C5'-O5'
34	B5	1191	XSX	N4-C7-C9-O10
34	B5	541	A2M	O4'-C4'-C5'-O5'
34	B5	619	A2M	O4'-C4'-C5'-O5'
34	B5	1428	OMG	O4'-C4'-C5'-O5'
34	B5	1782	MA6	O4'-C4'-C5'-O5'
38	A1	2729	OMU	O4'-C4'-C5'-O5'
38	A1	2729	OMU	C3'-C4'-C5'-O5'
34	B5	541	A2M	C3'-C4'-C5'-O5'
34	B5	619	A2M	C3'-C4'-C5'-O5'
38	A1	2197	OMC	O4'-C4'-C5'-O5'
38	A1	2870	5MC	C2'-C1'-N1-C6
34	B5	1782	MA6	C5-C6-N6-C9
38	A1	2347	OMU	C3'-C4'-C5'-O5'
34	B5	1269	OMU	O4'-C1'-N1-C2
34	B5	1428	OMG	C3'-C4'-C5'-O5'
38	A1	817	A2M	C4'-C5'-O5'-P
34	B5	1782	MA6	C3'-C4'-C5'-O5'
34	B5	1269	OMU	O4'-C1'-N1-C6
34	B5	414	OMC	C1'-C2'-O2'-CM2
38	A1	2197	OMC	C3'-C4'-C5'-O5'
34	B5	1191	XSX	C1-C3-C7-N4
38	A1	2870	5MC	O4'-C1'-N1-C6
38	A1	2278	5MC	O4'-C4'-C5'-O5'
38	A1	2870	5MC	O4'-C1'-N1-C2
38	A1	2197	OMC	O4'-C1'-N1-C6
38	A1	2870	5MC	C2'-C1'-N1-C2
34	B5	1191	XSX	N4-C7-C9-O11
34	B5	1269	OMU	C4'-C5'-O5'-P
34	B5	420	A2M	O4'-C4'-C5'-O5'
34	B5	1639	OMC	O4'-C4'-C5'-O5'
34	B5	1428	OMG	C4'-C5'-O5'-P
38	A1	2197	OMC	O4'-C1'-N1-C2
38	A1	645	1MA	C2'-C1'-N9-C8
38	A1	649	A2M	C1'-C2'-O2'-CM'
38	A1	2640	A2M	C1'-C2'-O2'-CM'
34	B5	1781	MA6	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
38	A1	2793	OMG	C3'-C2'-O2'-CM2
38	A1	645	1MA	C2'-C1'-N9-C4
34	B5	1191	XSX	C3-C7-C9-O10
38	A1	2347	OMU	O4'-C4'-C5'-O5'
34	B5	1126	OMG	C4'-C5'-O5'-P
38	A1	2256	A2M	C4'-C5'-O5'-P
38	A1	1437	OMC	C2'-C1'-N1-C2

There are no ring outliers.

26 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	B5	1271	OMG	1	0
34	B5	1126	OMG	2	0
34	B5	1280	4AC	3	0
38	A1	2256	A2M	1	0
38	A1	2347	OMU	1	0
34	B5	1269	OMU	1	0
38	A1	649	A2M	1	0
38	A1	2948	OMC	2	0
38	A1	2220	A2M	2	0
34	B5	1639	OMC	1	0
38	A1	1449	A2M	1	0
38	A1	2197	OMC	2	0
38	A1	2922	OMG	1	0
38	A1	2724	OMU	1	0
38	A1	2946	A2M	1	0
38	A1	2281	A2M	1	0
38	A1	876	A2M	1	0
38	A1	650	OMC	1	0
34	B5	1773	4AC	2	0
34	B5	1781	MA6	1	0
38	A1	663	OMC	1	0
34	B5	436	A2M	1	0
34	B5	414	OMC	1	0
34	B5	1575	G7M	2	0
38	A1	1133	A2M	1	0
38	A1	2640	A2M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 248 ligands modelled in this entry, 248 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](#)

There are no chain breaks in this entry.

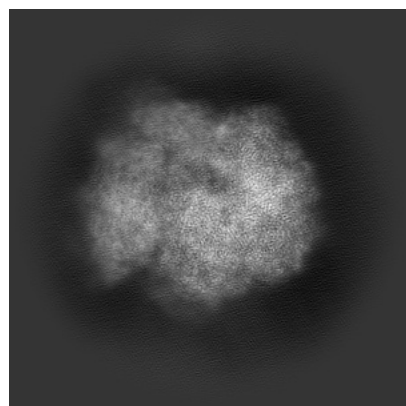
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28643. These allow visual inspection of the internal detail of the map and identification of artifacts.

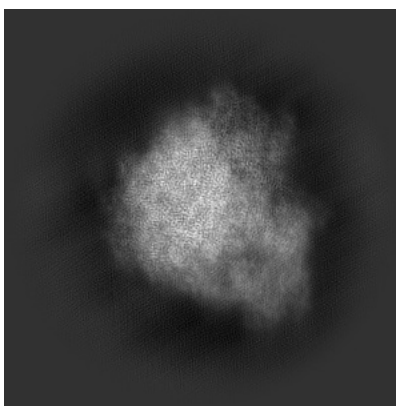
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

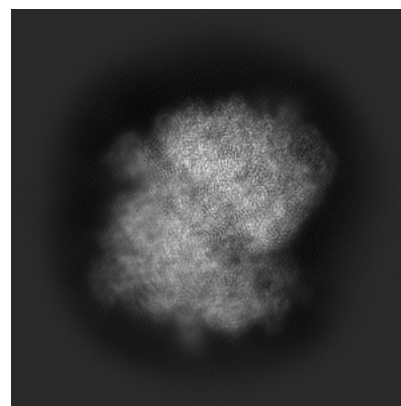
6.1.1 Primary map



X

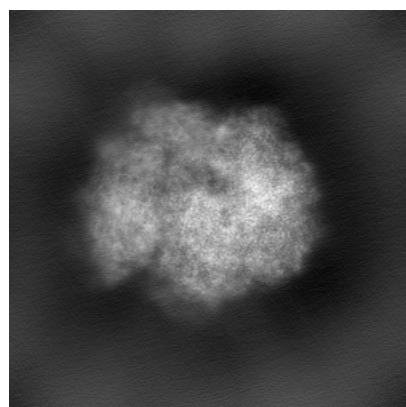


Y

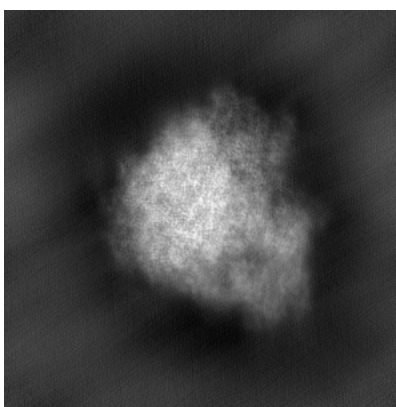


Z

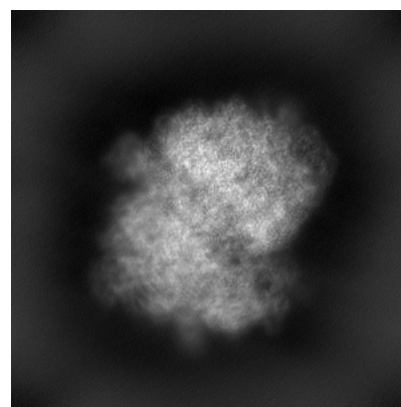
6.1.2 Raw map



X



Y

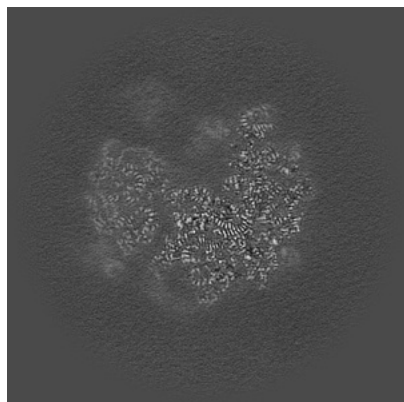


Z

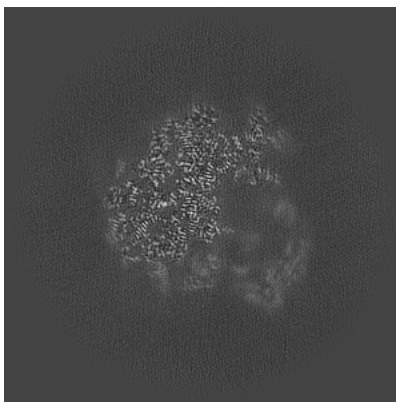
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

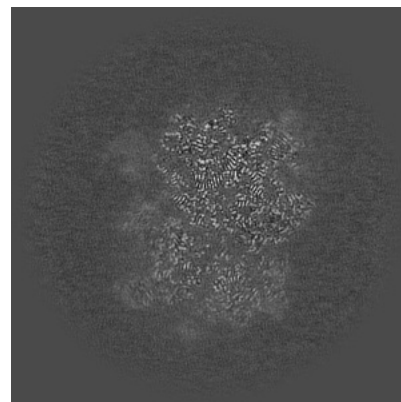
6.2.1 Primary map



X Index: 200

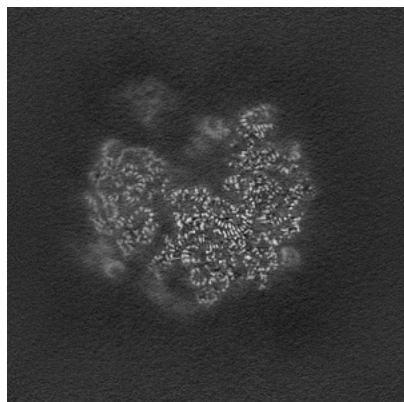


Y Index: 200

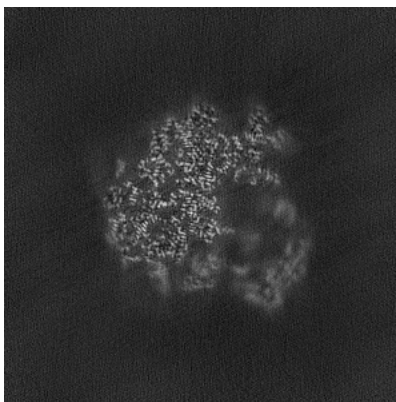


Z Index: 200

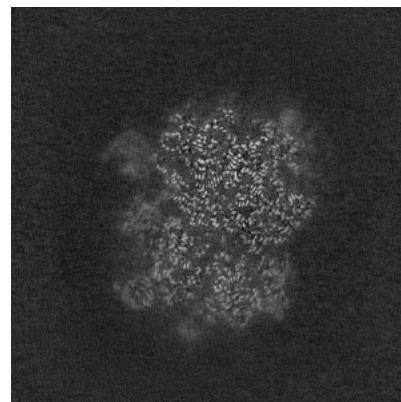
6.2.2 Raw map



X Index: 200



Y Index: 200

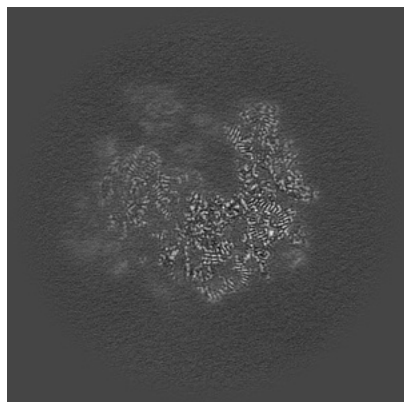


Z Index: 200

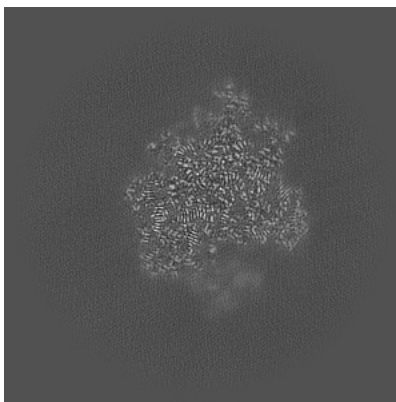
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

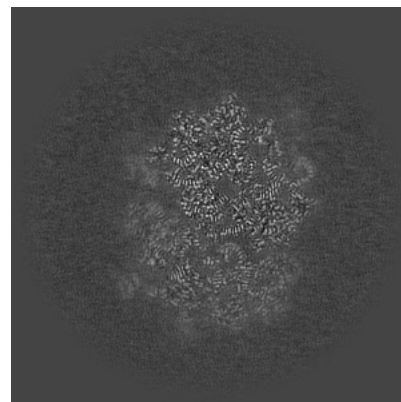
6.3.1 Primary map



X Index: 188

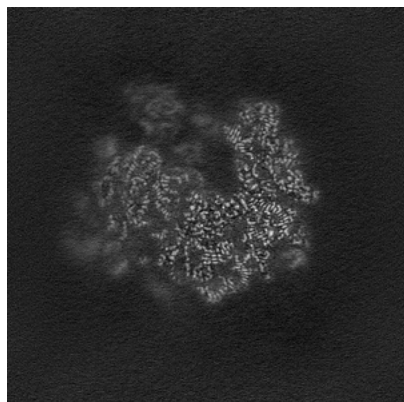


Y Index: 245

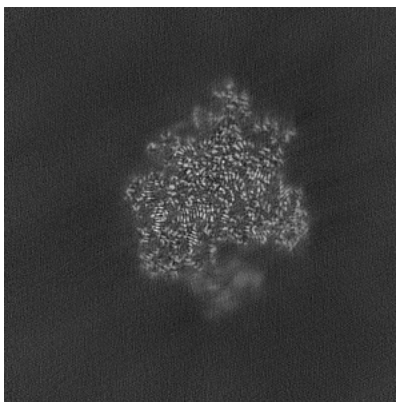


Z Index: 191

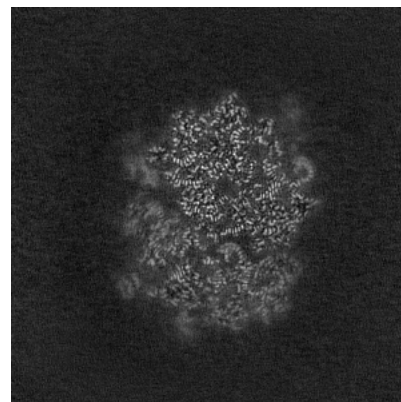
6.3.2 Raw map



X Index: 188



Y Index: 245

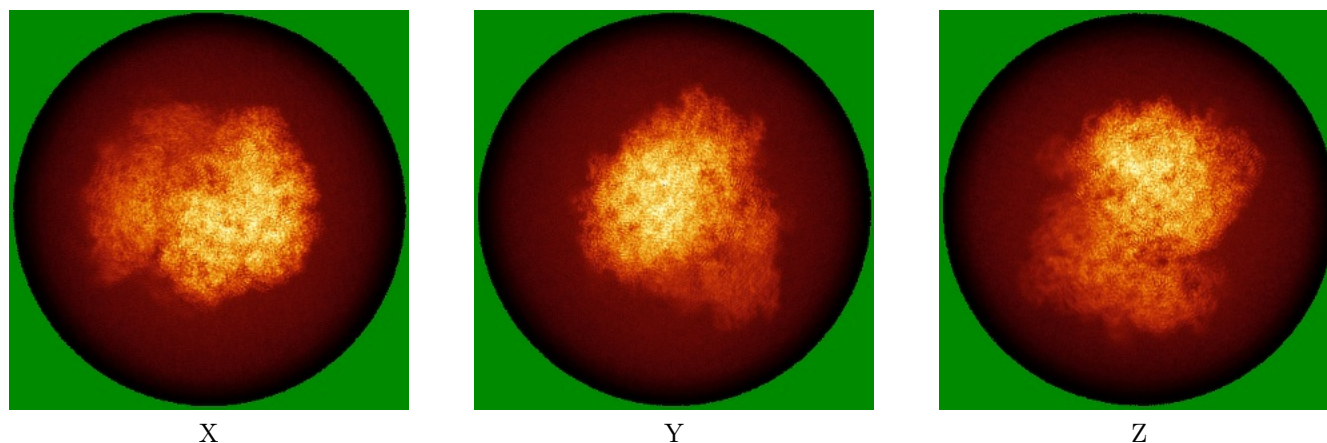


Z Index: 191

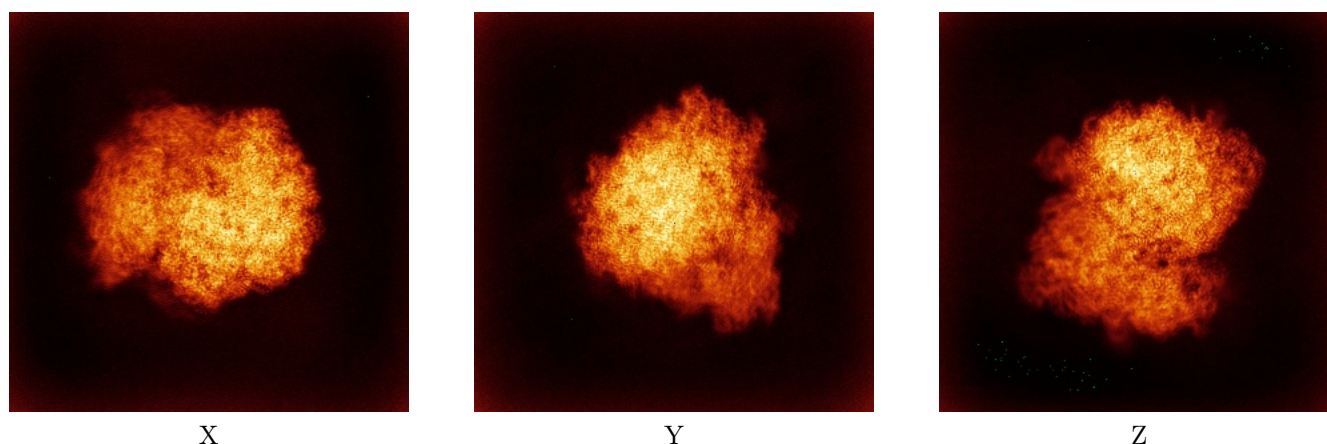
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

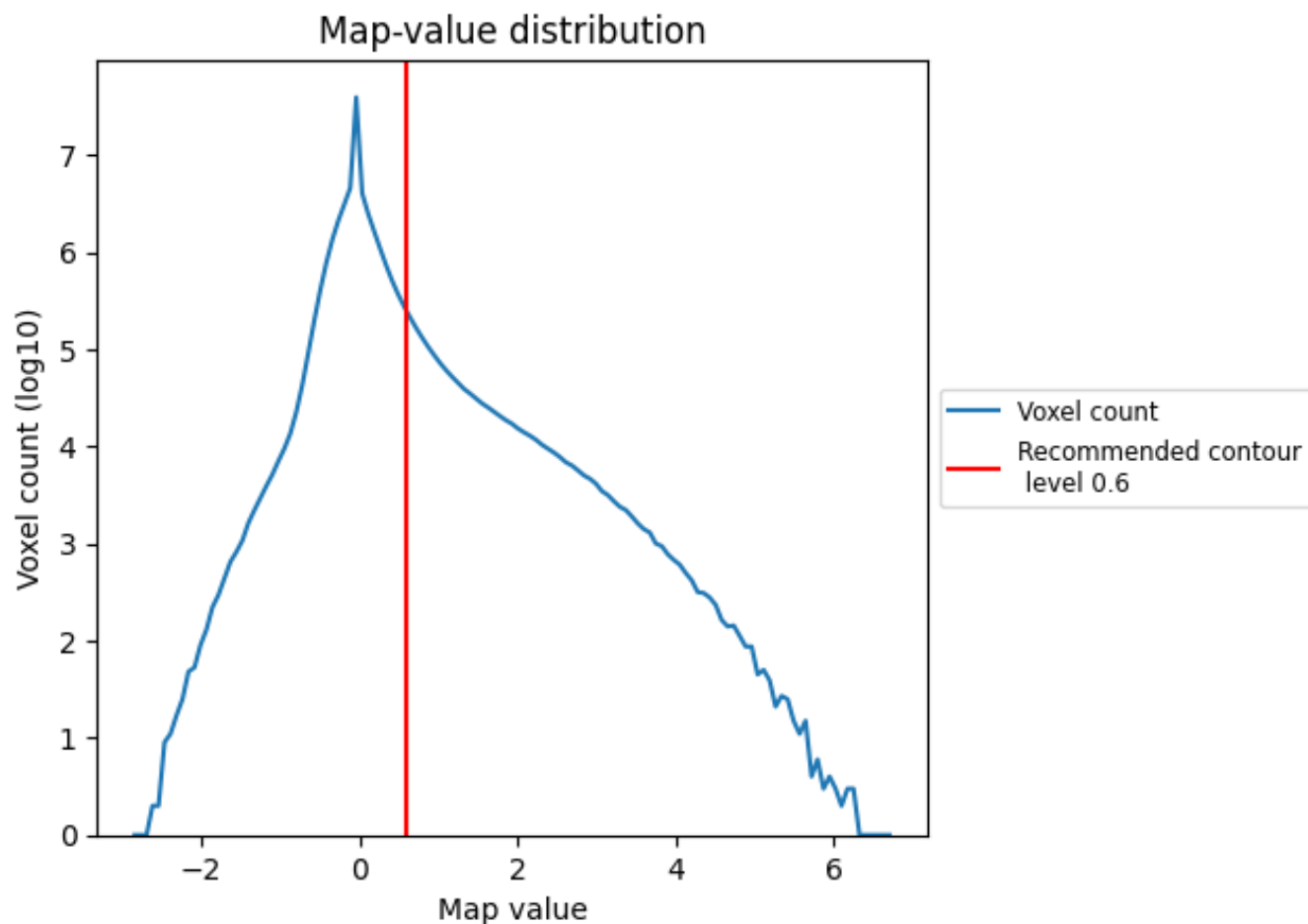
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

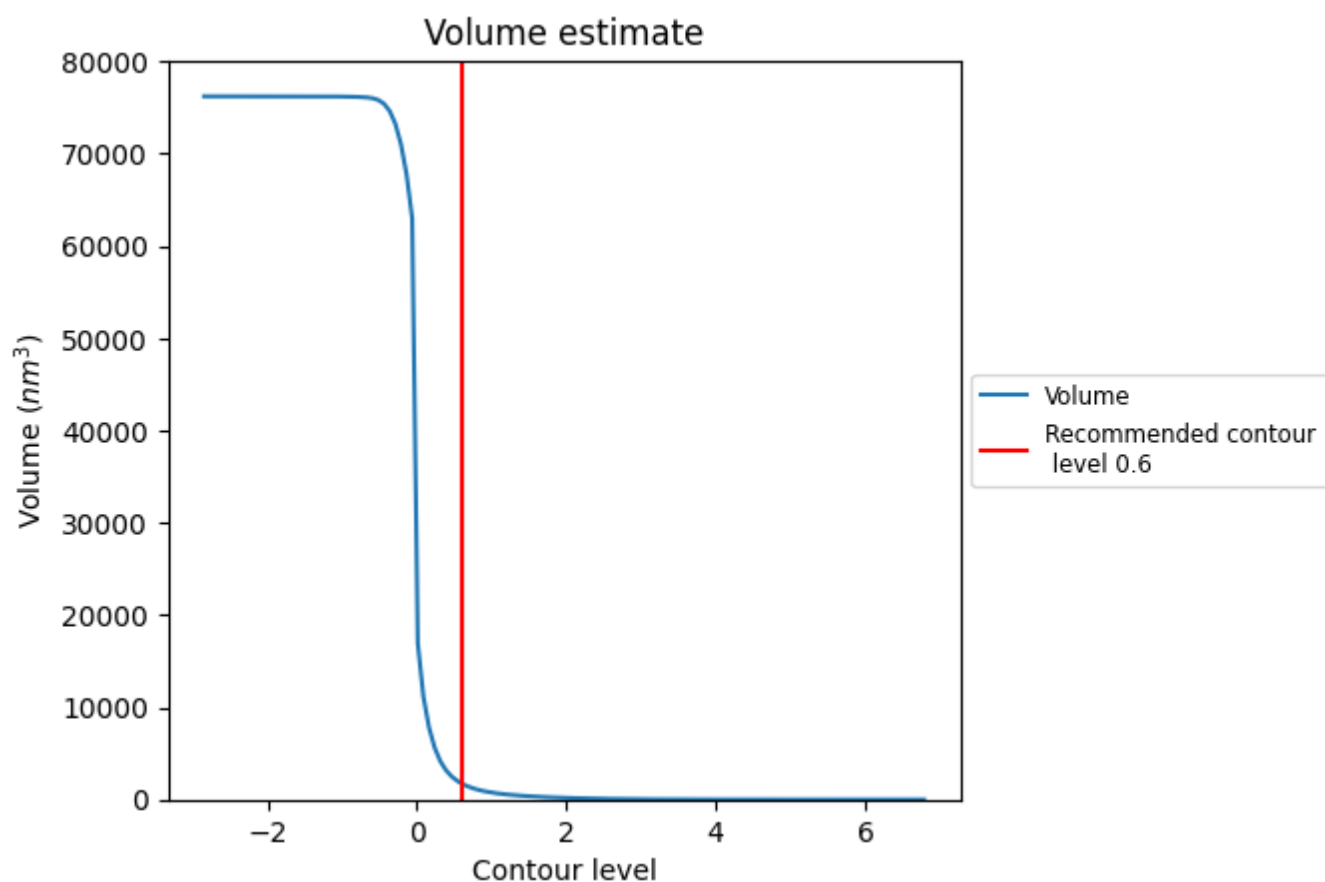
This section contains the results of statistical analysis of the map.

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.

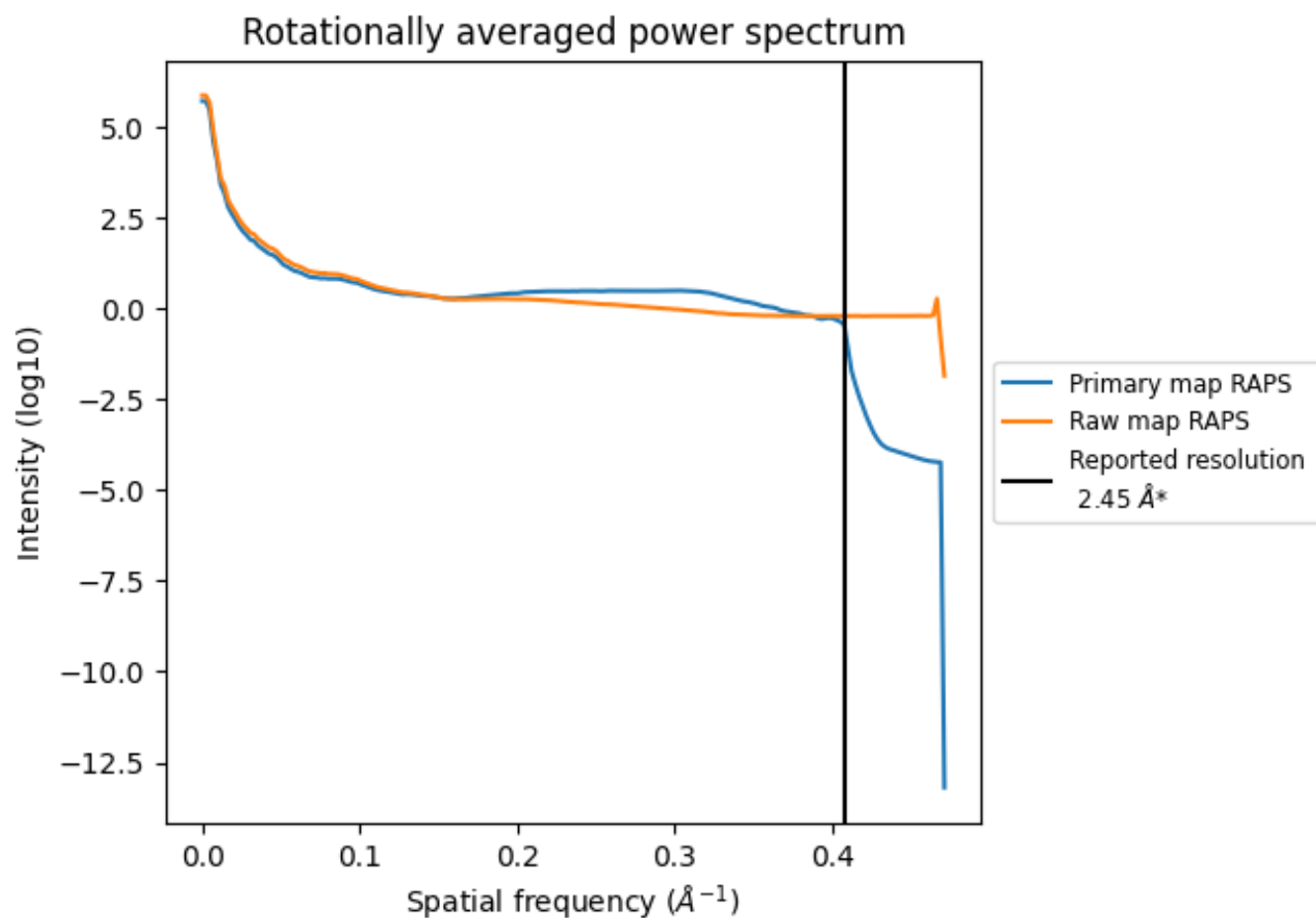
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1747 nm³; this corresponds to an approximate mass of 1578 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 ⓘ

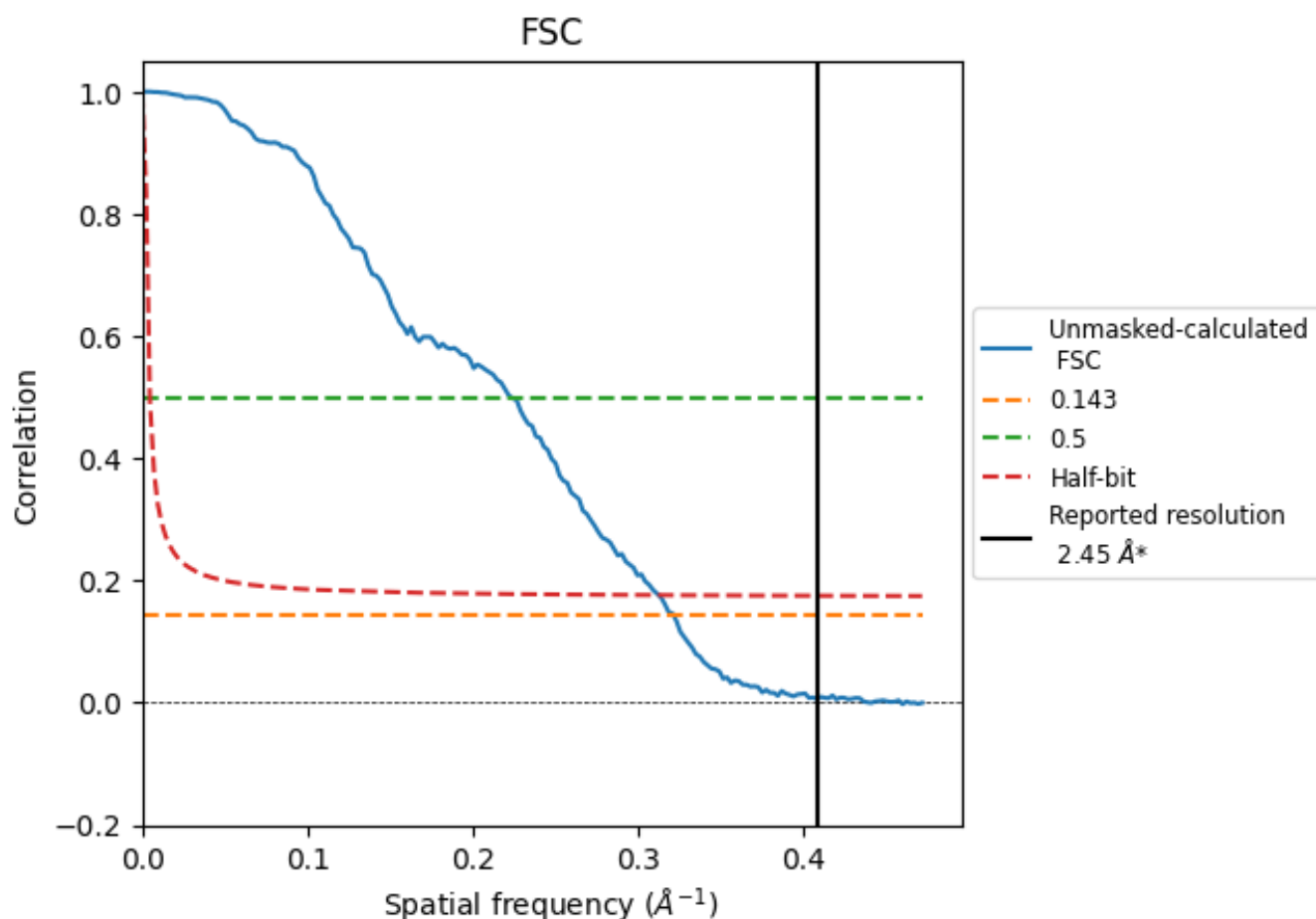


*Reported resolution corresponds to spatial frequency of 0.408 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.408 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

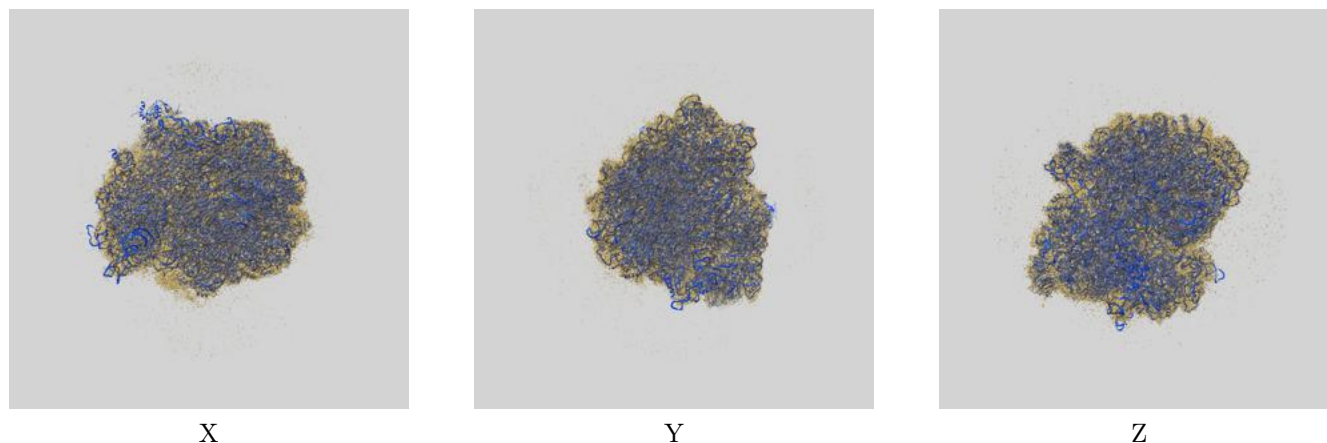
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.45	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.11	4.48	3.20

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.11 differs from the reported value 2.45 by more than 10 %

9 Map-model fit [i](#)

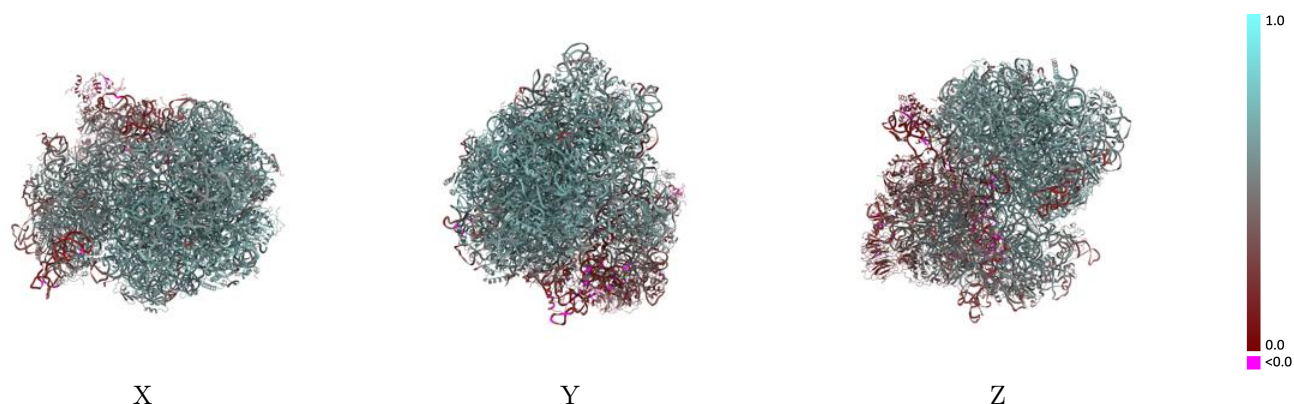
This section contains information regarding the fit between EMDB map EMD-28643 and PDB model 8EWC. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



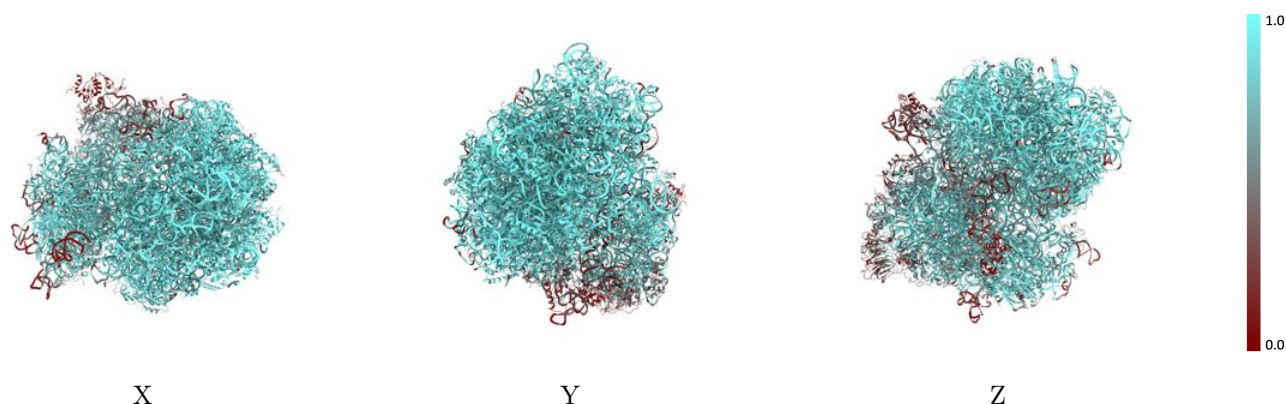
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



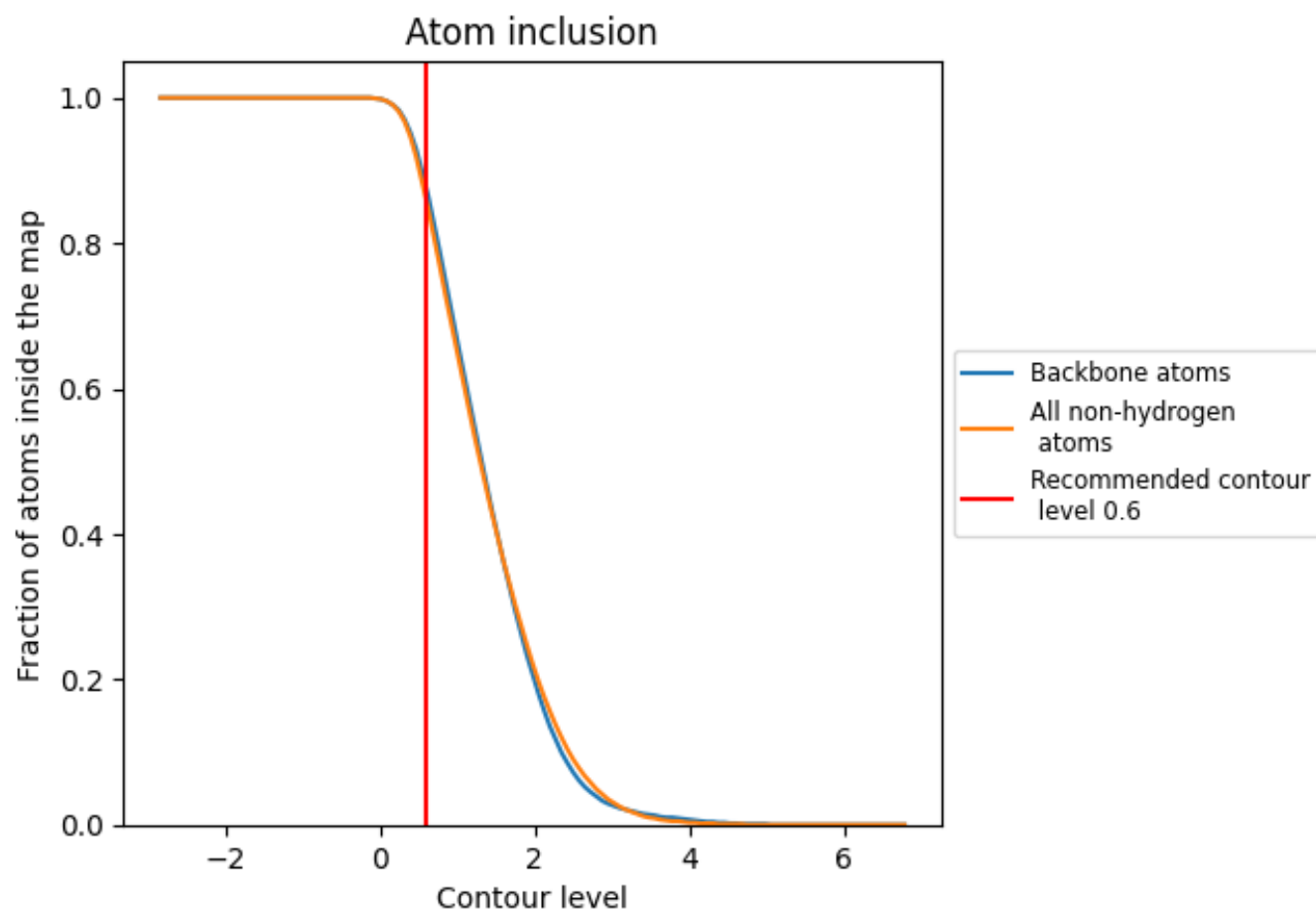
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

9.4 Atom inclusion ⓘ



At the recommended contour level, 87% of all backbone atoms, 86% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8560	 0.5320
A1	 0.9440	 0.5950
A3	 0.9810	 0.5940
A4	 0.9770	 0.6300
AA	 0.9850	 0.6470
AB	 0.9580	 0.6110
AC	 0.9590	 0.6350
AD	 0.8660	 0.5590
AE	 0.8750	 0.5550
AF	 0.9450	 0.6200
AG	 0.8930	 0.5640
AH	 0.8800	 0.5640
AI	 0.9390	 0.6070
AJ	 0.7980	 0.4840
AL	 0.9420	 0.6180
AM	 0.9220	 0.5810
AN	 0.9870	 0.6520
AO	 0.9620	 0.6120
AP	 0.9660	 0.6320
AQ	 0.9790	 0.6520
AR	 0.8470	 0.5650
AS	 0.9390	 0.6030
AT	 0.9300	 0.6050
AU	 0.8400	 0.5560
AV	 0.9450	 0.6300
AW	 0.9620	 0.6230
AX	 0.9410	 0.6210
AY	 0.9310	 0.6140
AZ	 0.9180	 0.5850
Aa	 0.9630	 0.6390
Ab	 0.9070	 0.5760
Ac	 0.9330	 0.5970
Ad	 0.8990	 0.5950
Ae	 0.9600	 0.6380
Af	 0.9760	 0.6270



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Chain	Atom inclusion	Q-score
Ag	 0.9450	 0.6160
Ah	 0.9390	 0.6130
Ai	 0.9260	 0.5790
Aj	 0.9820	 0.6630
Ak	 0.8010	 0.5490
Al	 0.9690	 0.6440
Am	 0.9010	 0.5930
An	 0.9430	 0.5910
Ao	 0.9380	 0.6110
Ap	 0.9490	 0.6250
B5	 0.8480	 0.4770
BA	 0.7360	 0.4440
BB	 0.6710	 0.4100
BC	 0.8860	 0.5330
BD	 0.6830	 0.4160
BE	 0.9020	 0.5360
BF	 0.5660	 0.3430
BG	 0.7130	 0.4590
BH	 0.5720	 0.4180
BI	 0.8610	 0.5520
BJ	 0.8110	 0.5010
BK	 0.5160	 0.3440
BL	 0.8290	 0.5430
BM	 0.0350	 0.1880
BN	 0.8560	 0.5260
BO	 0.7650	 0.4370
BP	 0.4320	 0.3160
BQ	 0.6350	 0.3480
BR	 0.6340	 0.3830
BS	 0.5320	 0.3280
BT	 0.6020	 0.3420
BU	 0.5440	 0.3580
BV	 0.8040	 0.4770
BW	 0.9170	 0.5690
BX	 0.9110	 0.5720
BY	 0.7540	 0.4800
BZ	 0.4430	 0.2850
Ba	 0.8040	 0.4850
Bb	 0.7070	 0.4540
Bc	 0.5790	 0.3590
Bd	 0.8110	 0.4610
Be	 0.7910	 0.4810

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Chain	Atom inclusion	Q-score
Bf	 0.0540	 0.1130
Bg	 0.3850	 0.2590
E	 0.2180	 0.2120
EC	 0.3940	 0.1630