



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 11:19 PM UTC

PDB ID : 8EVP / pdb_00008evp
EMDB ID : EMD-28632
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), Structure I
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-20
Resolution : 2.38 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:

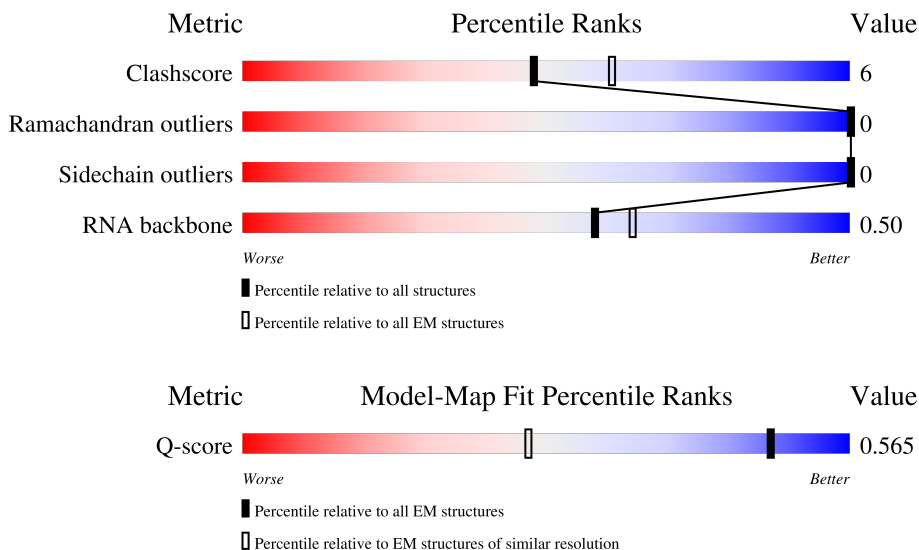
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.38 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.






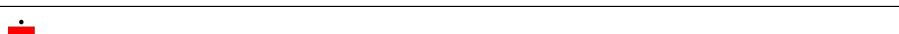
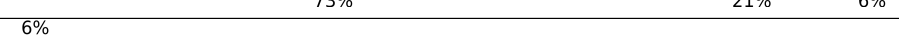
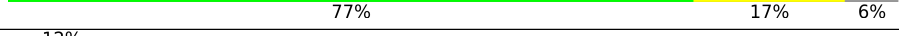



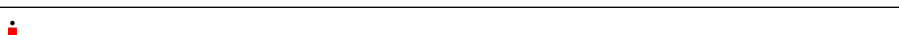
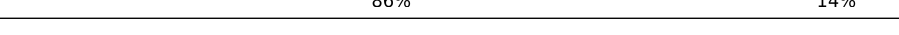




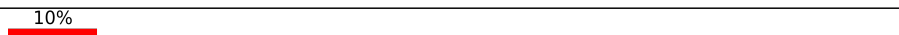






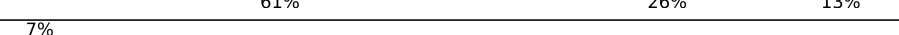


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4811 (1.88 - 2.88)

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

Mol	Chain	Length	Quality of chain
1	BA	252	
2	BB	255	
3	BC	254	

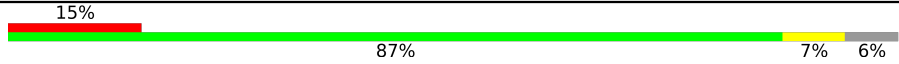







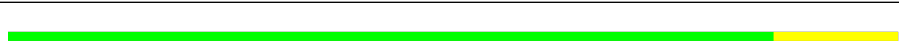

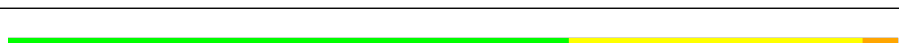


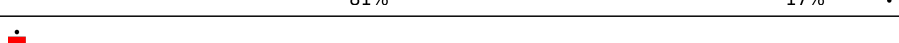
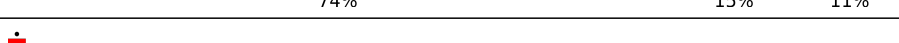
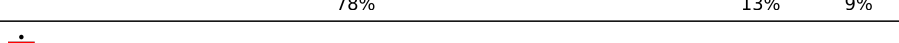
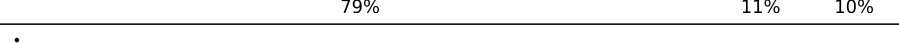
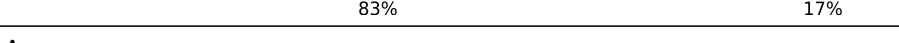
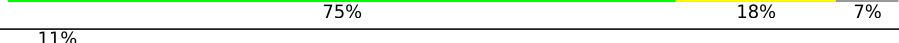






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Mol	Chain	Length	Quality of chain
4	BE	261	
5	BG	236	
6	BH	190	
7	BI	200	
8	BJ	197	
9	BL	156	
10	BN	151	
11	BO	137	
12	BV	87	
13	BW	130	
14	BX	145	
15	BY	135	
16	Ba	119	
17	Bb	82	
18	Be	63	
19	BD	240	
20	BF	225	
21	BK	105	
22	BP	142	
23	BQ	143	
24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

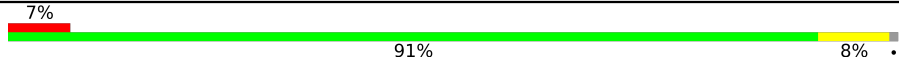







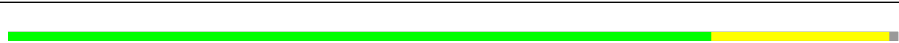

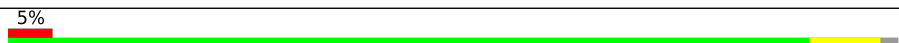


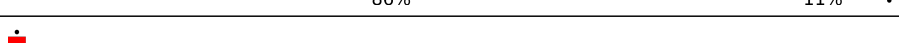
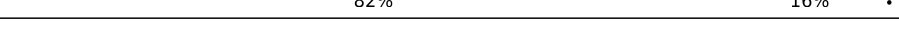
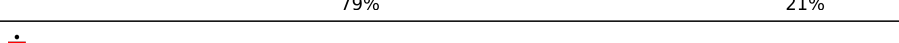
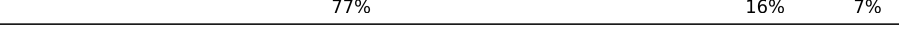
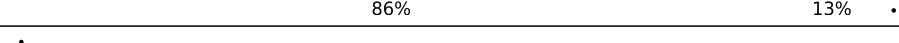
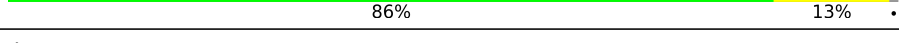






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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1799	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3360	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	221	
47	AJ	174	
48	AL	199	
49	AM	138	
50	AN	204	
51	AO	199	
52	AP	184	
53	AQ	186	

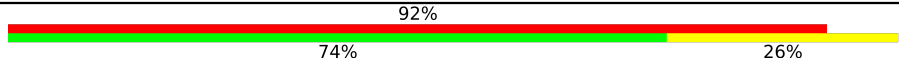

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Mol	Chain	Length	Quality of chain
54	AR	189	
55	AS	178	
56	AT	160	
57	AU	121	
58	AV	137	
59	AW	155	
60	AX	142	
61	AY	127	
62	AZ	136	
63	Aa	149	
64	Ab	59	
65	Ac	105	
66	Ad	113	
67	Ae	130	
68	Af	107	
69	Ag	121	
70	Ah	120	
71	Ai	100	
72	Aj	88	
73	Ak	78	
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	
80	EC	202	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 205919 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
			Total	C	N	O	S		
1	BA	206	1612	1034	285	291	2	0	0

- Molecule 2 is a protein called RPS1A isoform 1.

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

- Molecule 3 is a protein called RPS2 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 16 is a protein called RPS26B isoform 1.

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

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

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

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

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

- Molecule 19 is a protein called RPS3 isoform 1.

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

- Molecule 20 is a protein called Rps5p.

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

- 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	57	Total	C	N	O	S	0	0
			454	288	86	77	3		

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

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

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

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

- 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
			Total	C	N	O	S		
42	AE	156	1239	800	222	216	1	0	0

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

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

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

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

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

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

- Molecule 46 is a protein called RPL10 isoform 1.

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

- Molecule 47 is a protein called RPL11A isoform 1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 59 is a protein called RPL24A isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 64 is a protein called RPL29 isoform 1.

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

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

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

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

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

- Molecule 67 is a protein called RPL32 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 73 is a protein called RPL38 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 79 is a protein called RPL1A isoform 1.

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

- Molecule 80 is a RNA chain called Internal ribosome entry site.

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	BE	1	Total	Mg	0
			1	1	
81	BN	1	Total	Mg	0
			1	1	
81	Ba	1	Total	Mg	0
			1	1	
81	B5	60	Total	Mg	0
			60	60	
81	AC	1	Total	Mg	0
			1	1	
81	A1	182	Total	Mg	0
			182	182	
81	A3	2	Total	Mg	0
			2	2	
81	A4	5	Total	Mg	0
			5	5	
81	AD	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
81	AL	1	Total 1	Mg 1	0
81	AP	1	Total 1	Mg 1	0

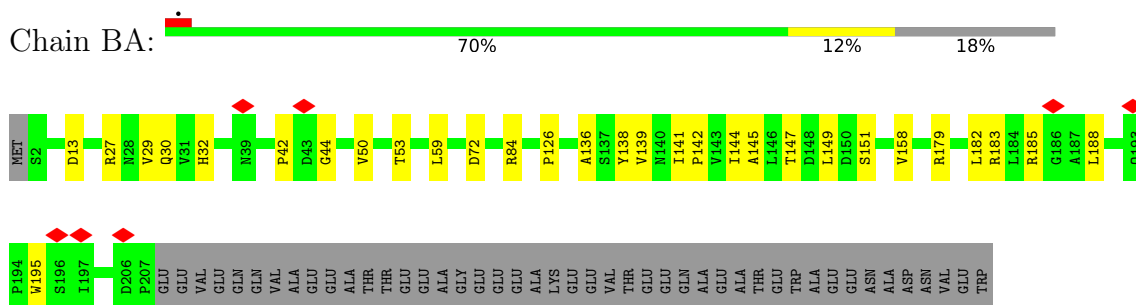
- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

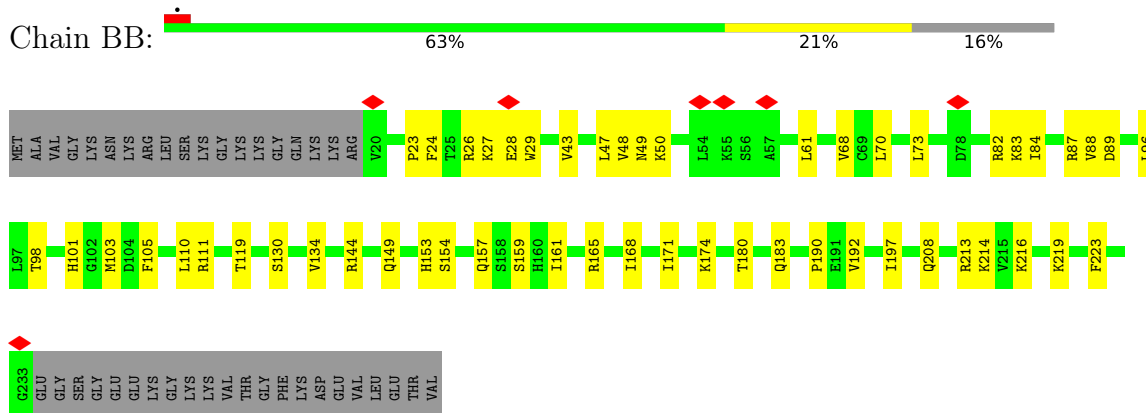
3 Residue-property plots [i](#)

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

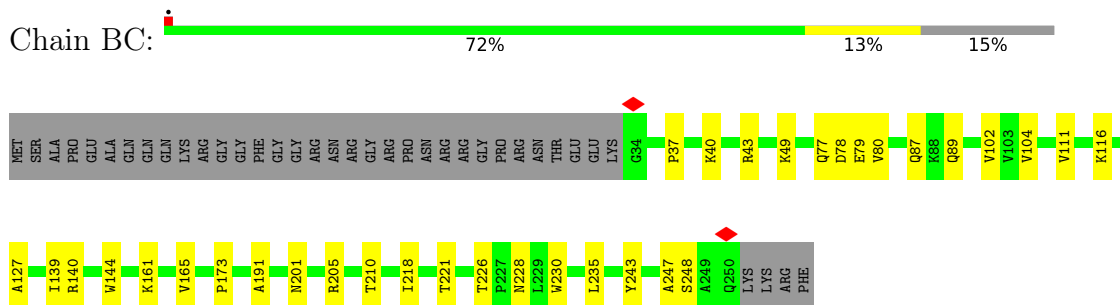
- Molecule 1: 40S ribosomal protein S0-A




- Molecule 2: RPS1A isoform 1

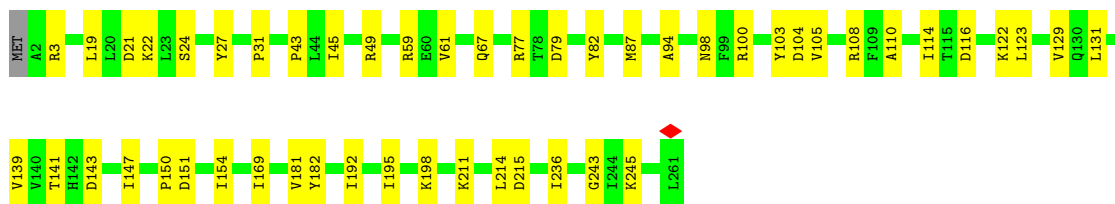


- Molecule 3: RPS2 isoform 1




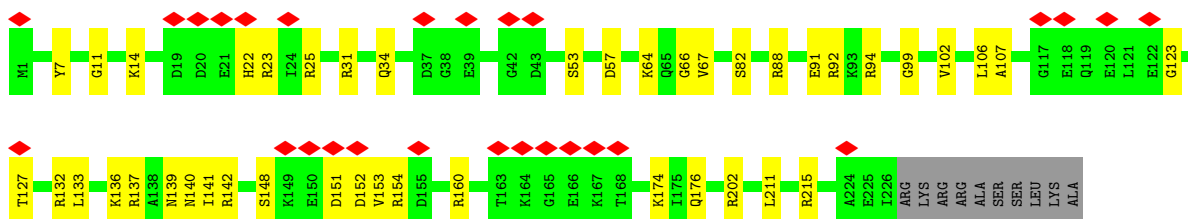
- Molecule 4: 40S ribosomal protein S4-A

Chain BE:  80% 19%




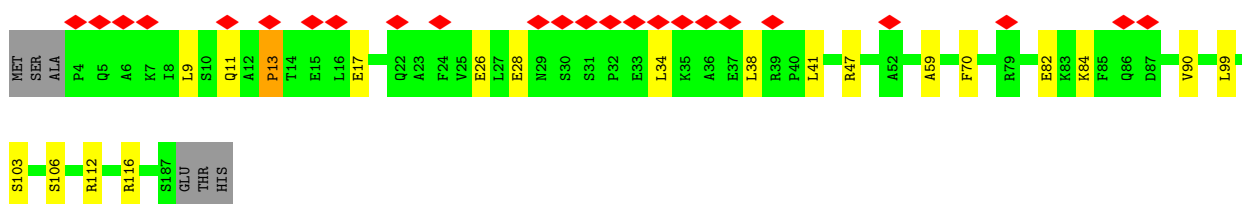
• Molecule 5: 40S ribosomal protein S6-A

Chain BG:  11% 78% 18%




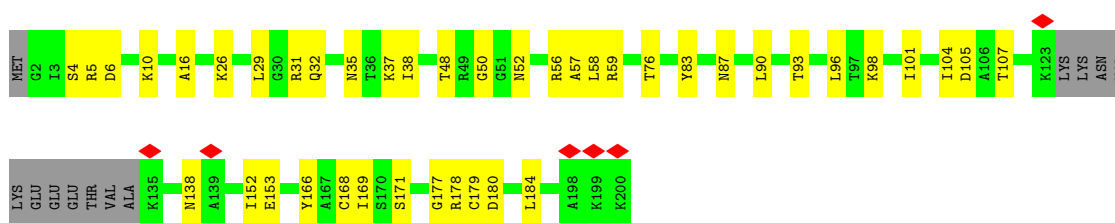
• Molecule 6: 40S ribosomal protein S7-A

Chain BH:  13% 86% 10%




• Molecule 7: 40S ribosomal protein S8-A

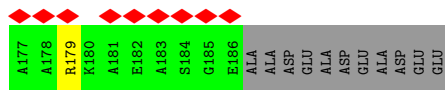
Chain BI:  73% 21% 6%



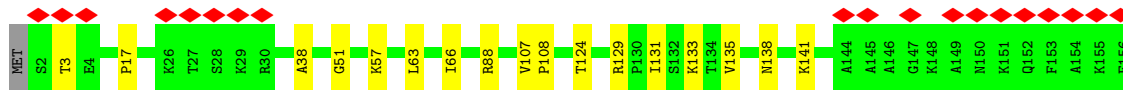
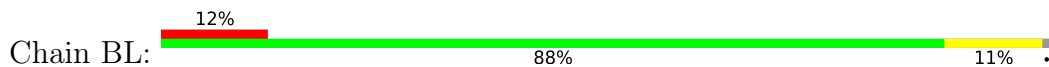
• Molecule 8: 40S ribosomal protein S9-A

Chain BJ:  6% 77% 17% 6%

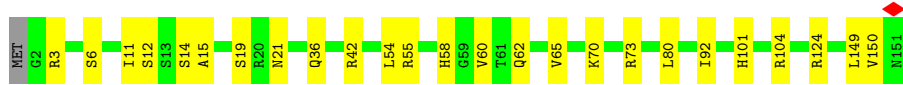
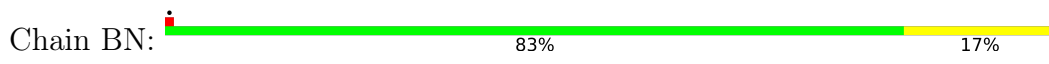




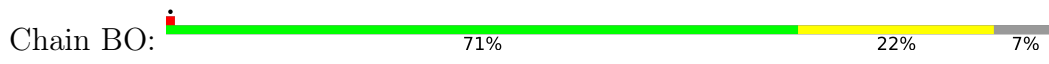
• Molecule 9: 40S ribosomal protein S11-A



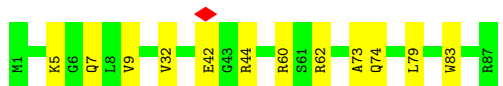
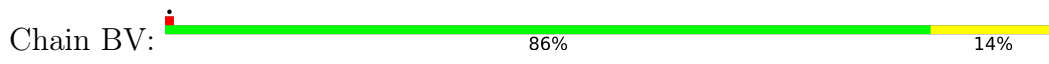
• Molecule 10: 40S ribosomal protein S13



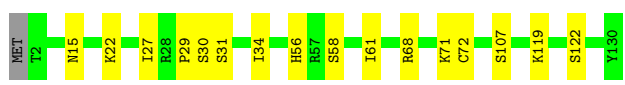
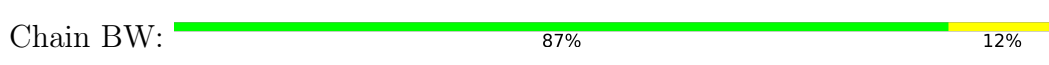
• Molecule 11: 40S ribosomal protein S14-A



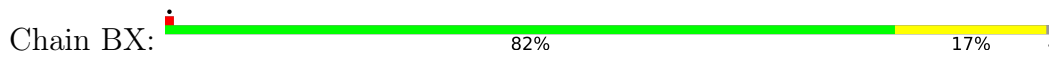
• Molecule 12: 40S ribosomal protein S21-A

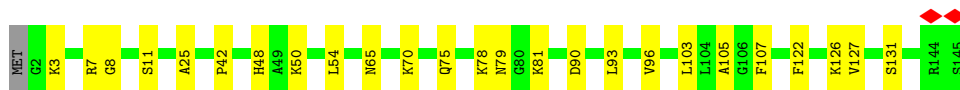


• Molecule 13: RPS22A isoform 1

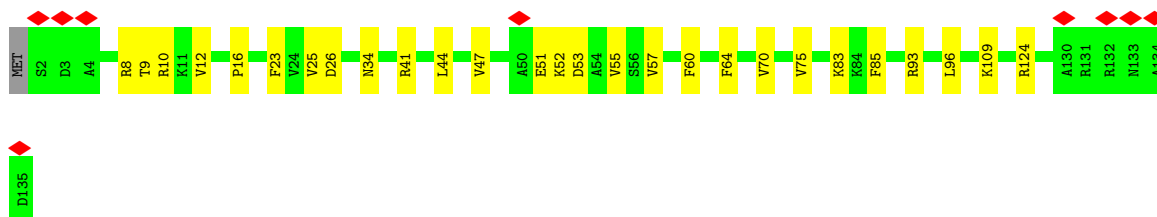
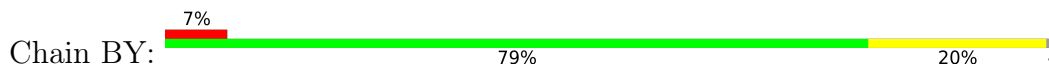


• Molecule 14: 40S ribosomal protein S23-A

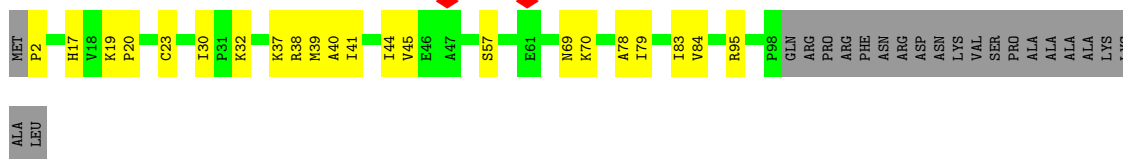




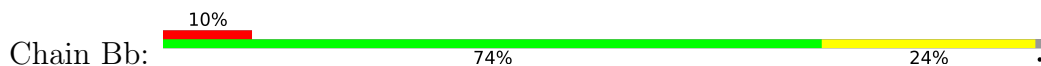
• Molecule 15: 40S ribosomal protein S24-A



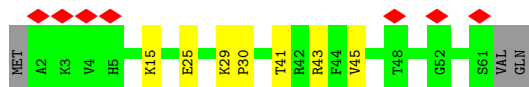
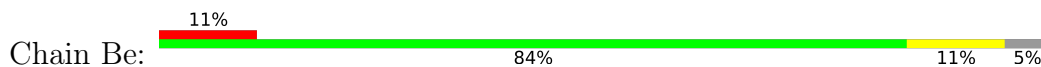
• Molecule 16: RPS26B isoform 1



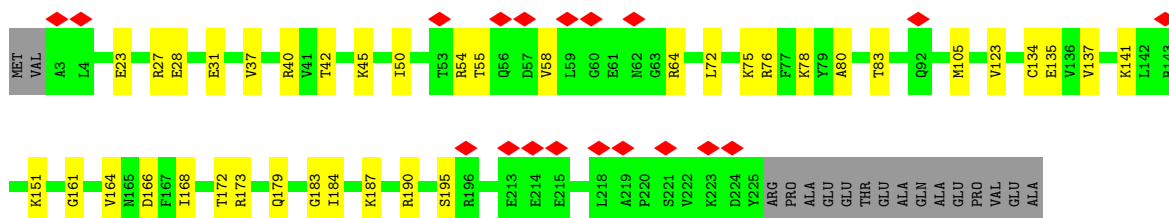
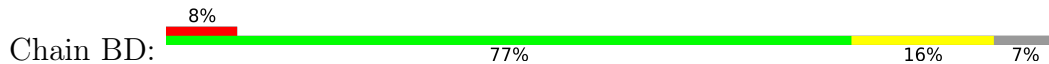
• Molecule 17: 40S ribosomal protein S27-A



• Molecule 18: 40S ribosomal protein S30-A

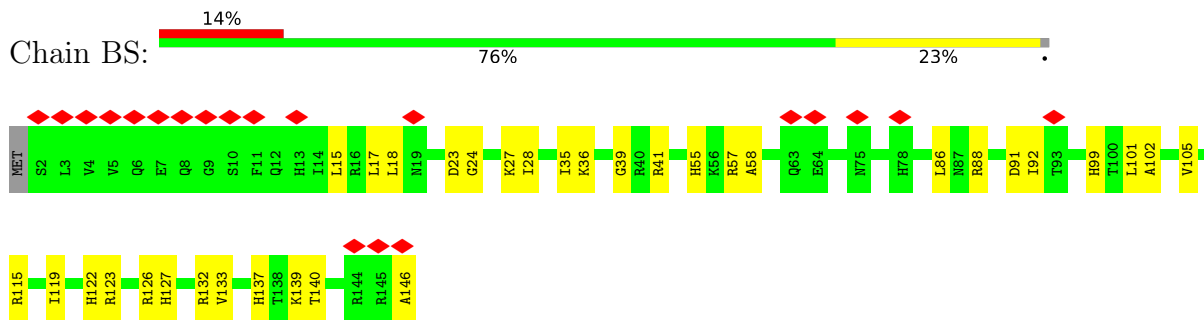


• Molecule 19: RPS3 isoform 1

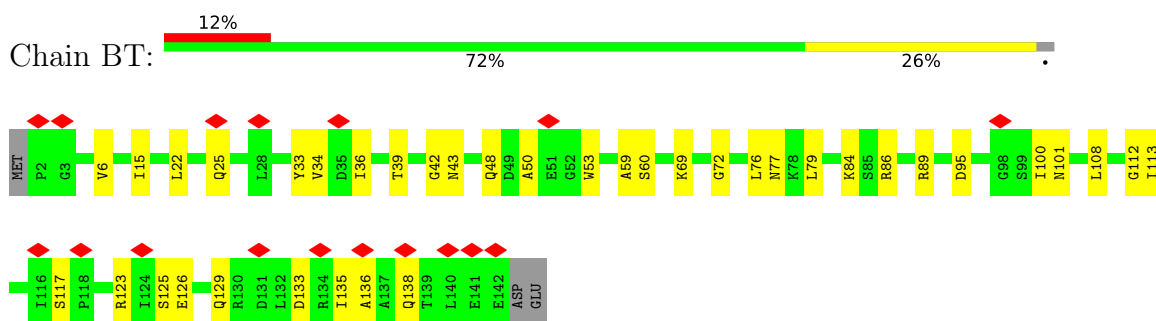


TYR
ARG
LYS
ARG
VAL

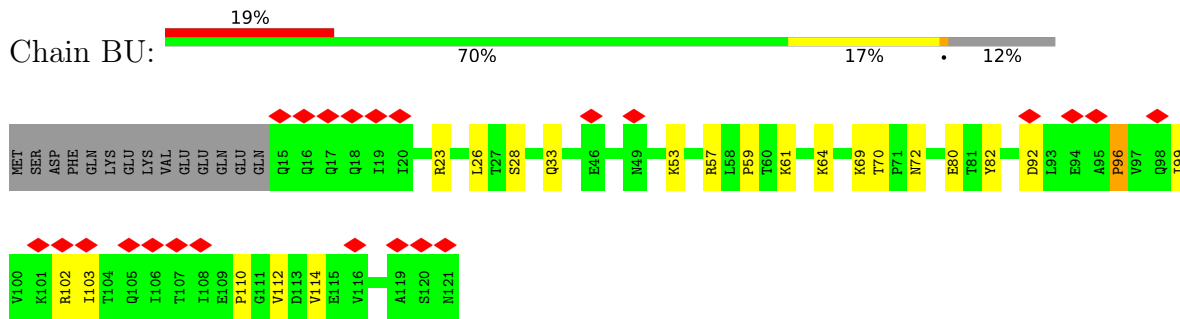
• Molecule 25: 40S ribosomal protein S18-A



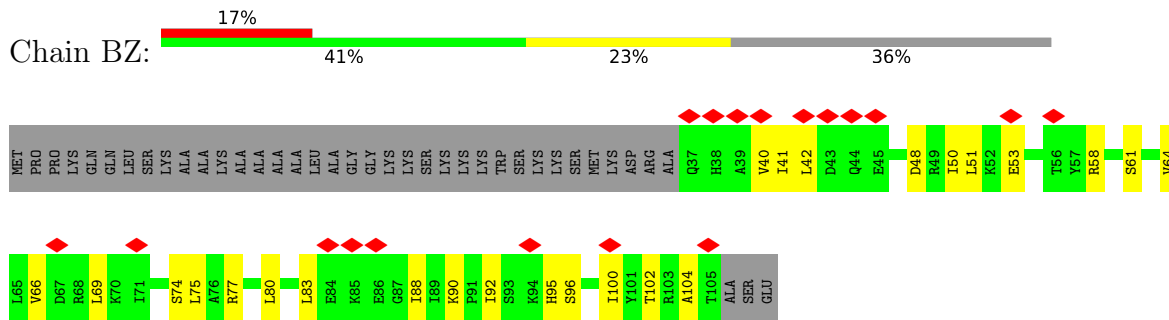
• Molecule 26: 40S ribosomal protein S19-A



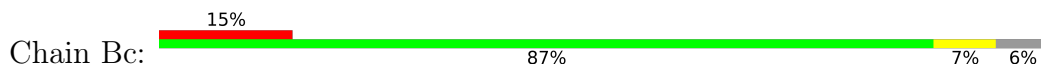
• Molecule 27: RPS20 isoform 1

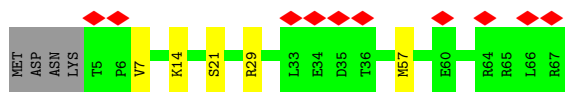


• Molecule 28: RPS25A isoform 1

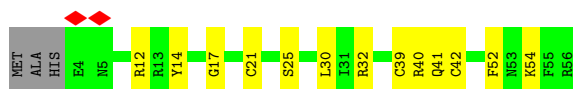


• Molecule 29: RPS28A isoform 1

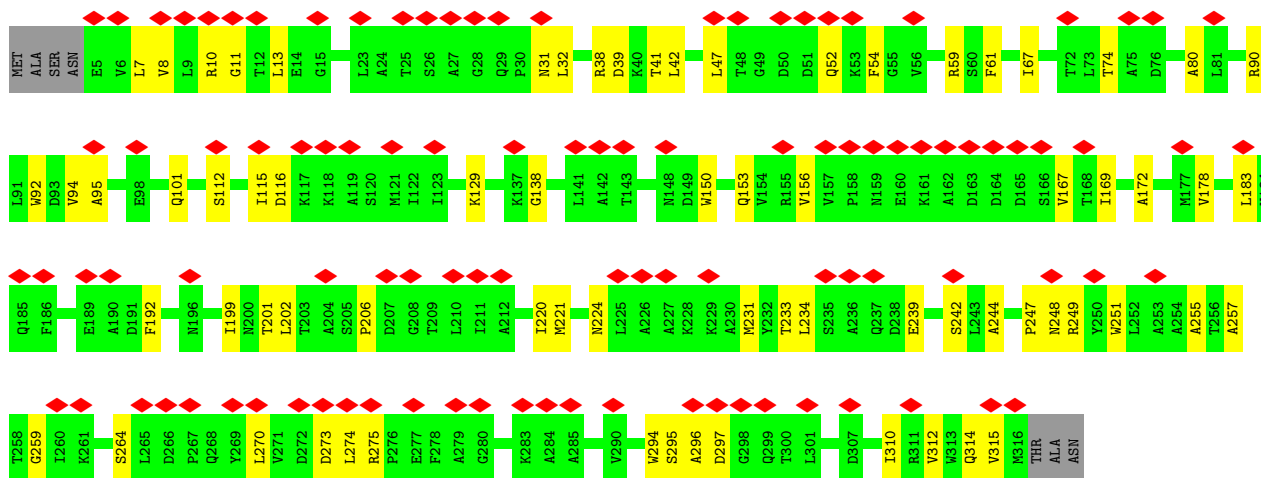
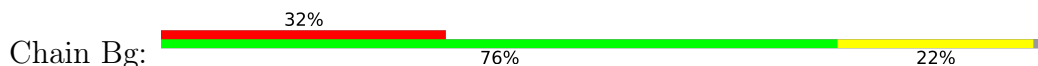




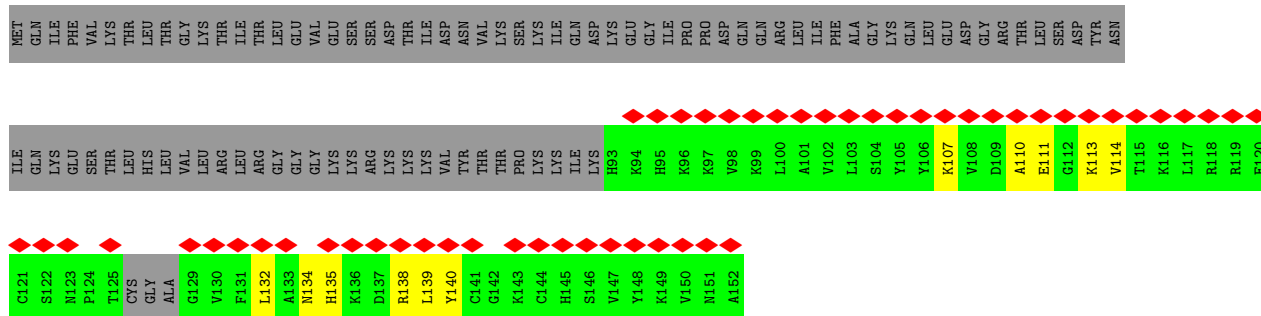
• Molecule 30: RPS29A isoform 1



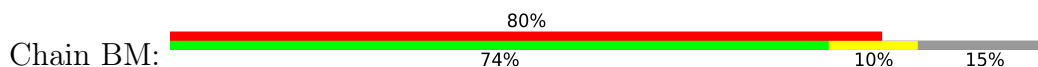
• Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein

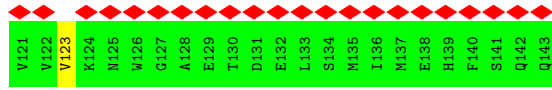
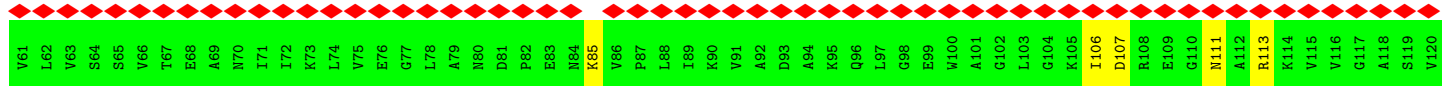


• Molecule 32: Ubiquitin-40S ribosomal protein S31

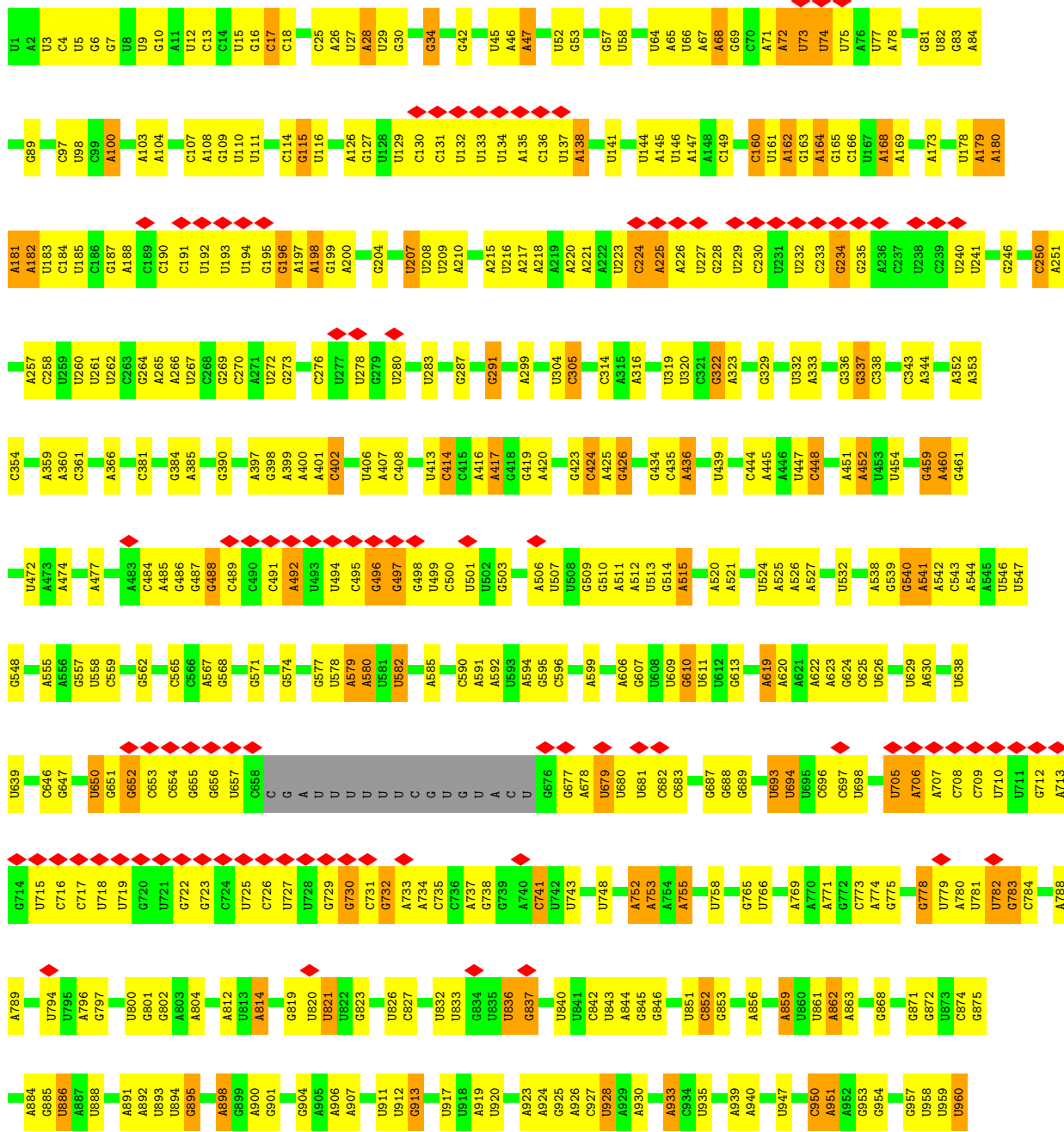


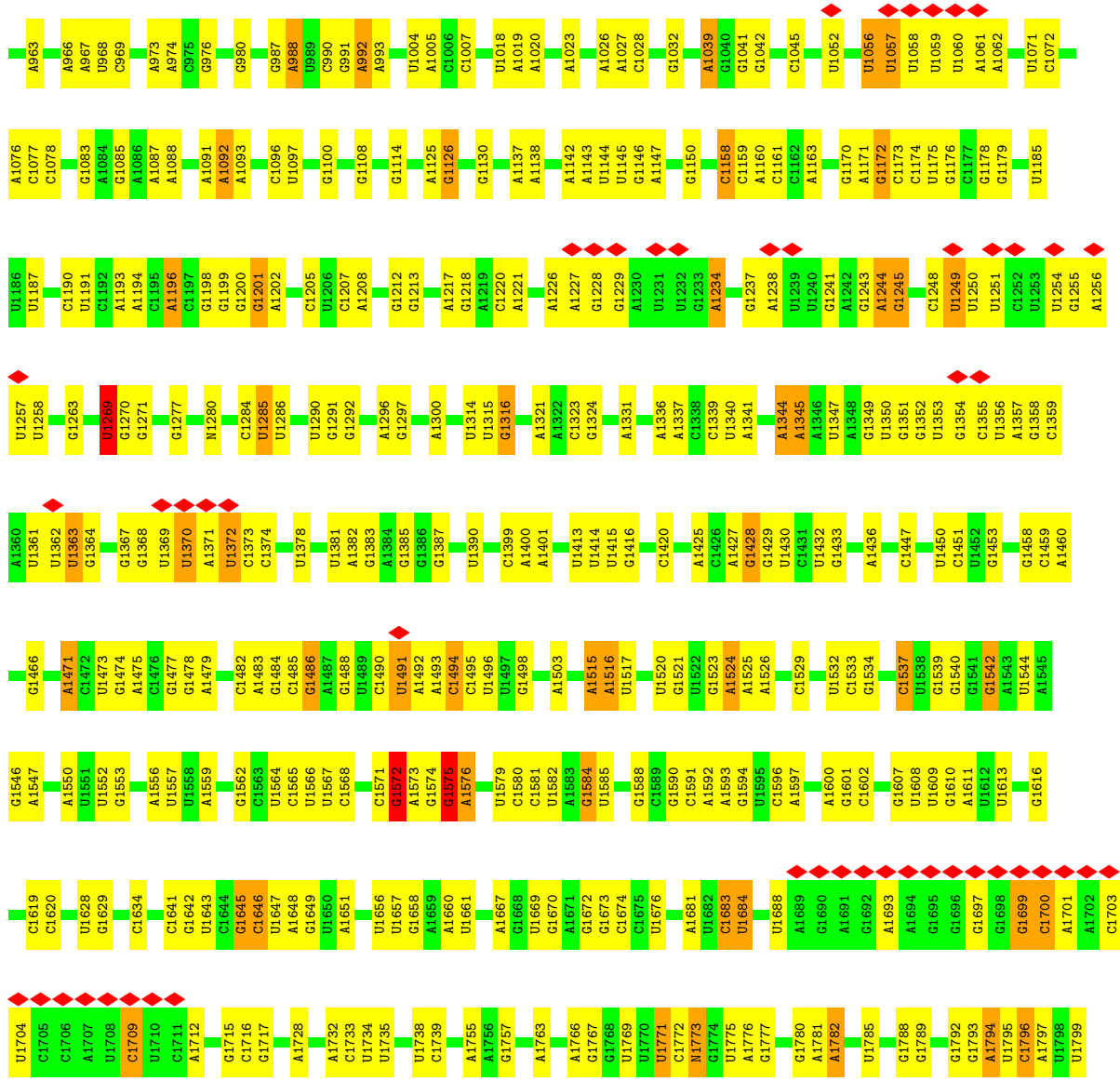
• Molecule 33: 40S ribosomal protein S12



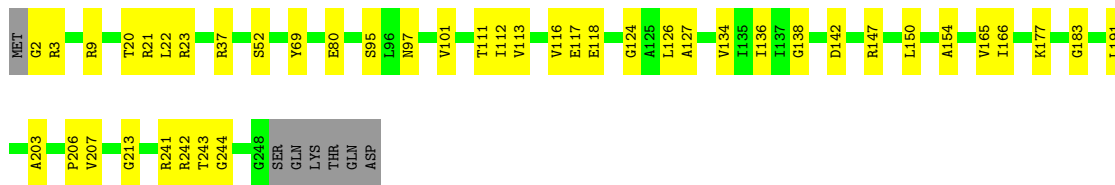
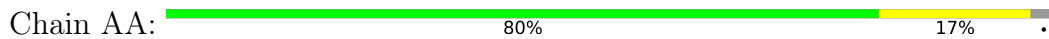


• Molecule 34: 18S rRNA

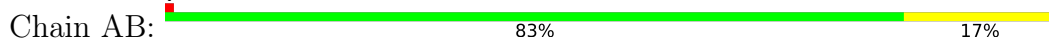


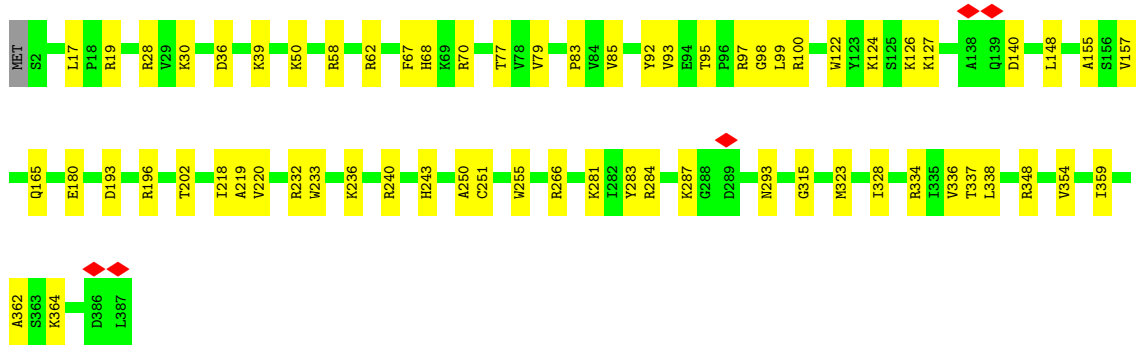


- Molecule 35: 60S ribosomal protein L2-A

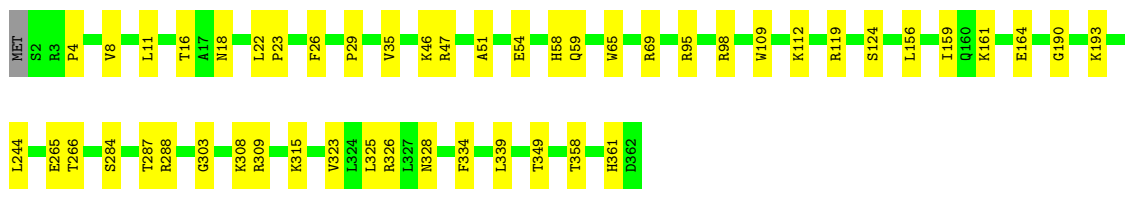
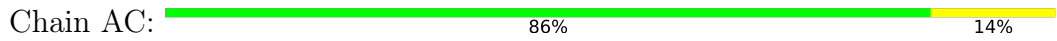


- Molecule 36: 60S ribosomal protein L3

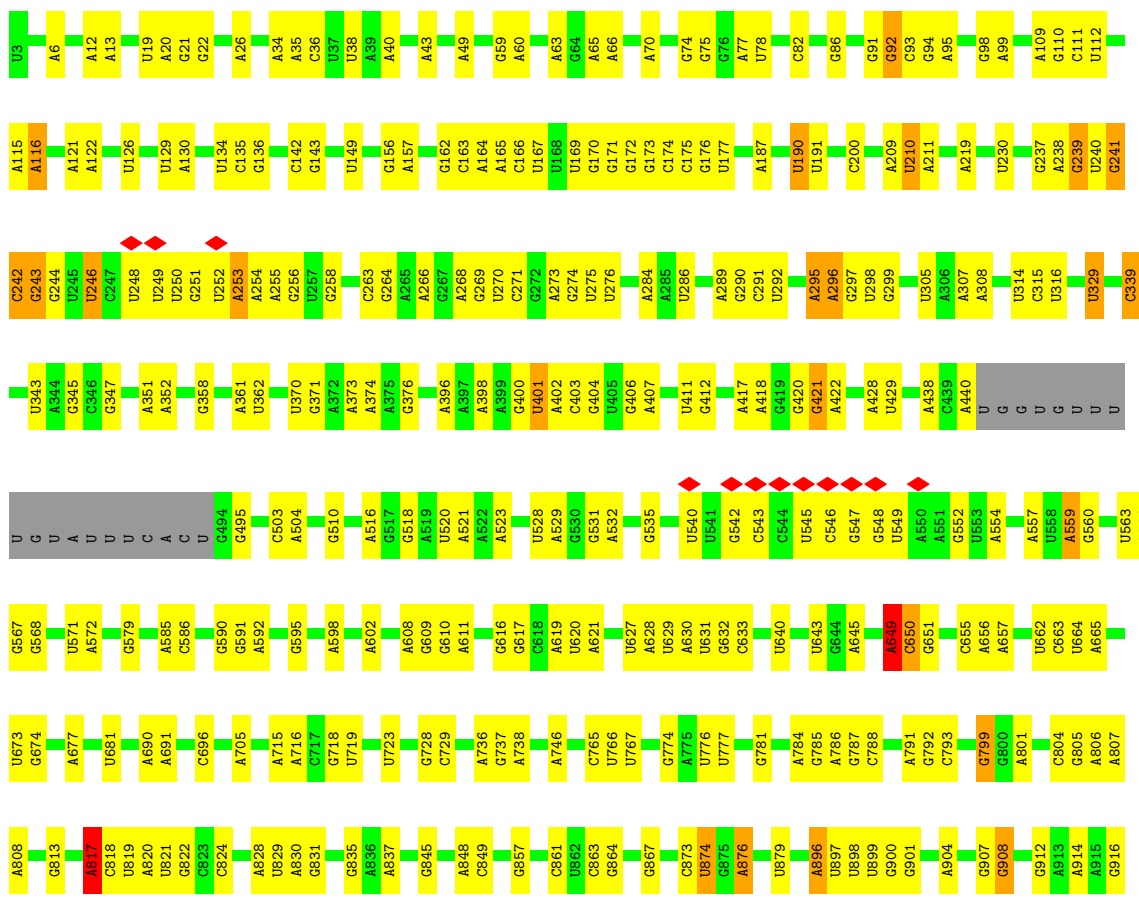


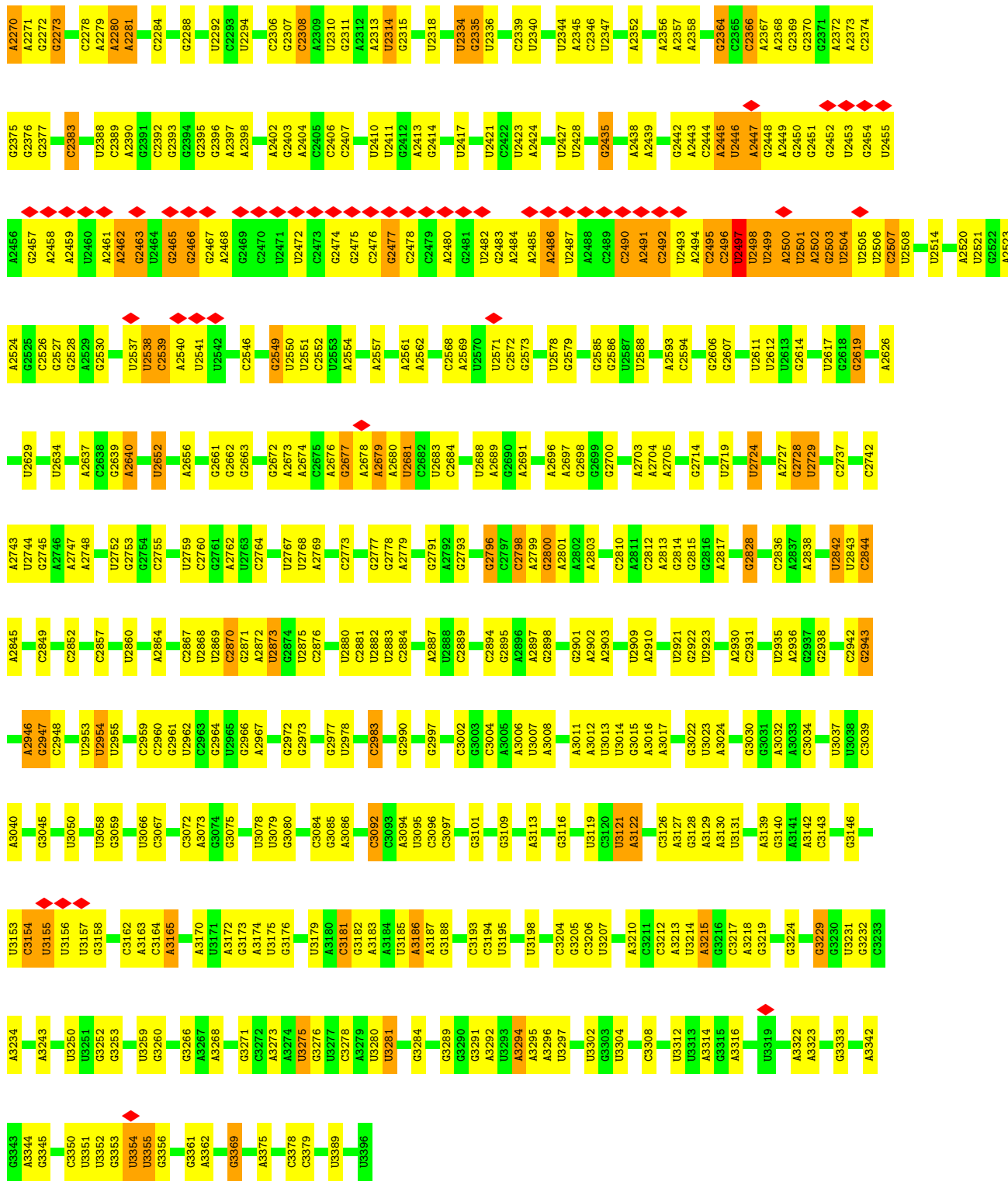


• Molecule 37: RPL4A isoform 1



• Molecule 38: 25S rRNA

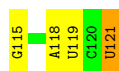




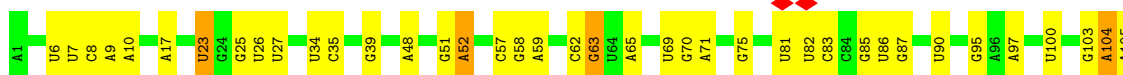
● Molecule 39: 5s rRNA

Chain A3:

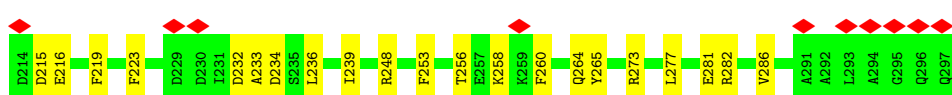
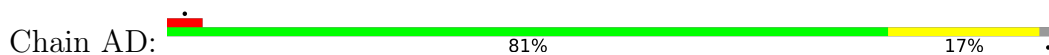




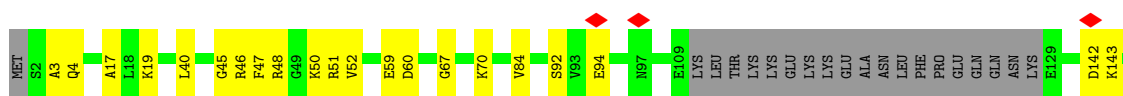
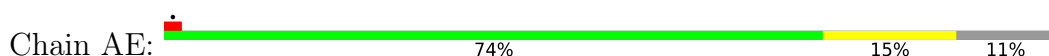
• Molecule 40: 5.8 S rRNA



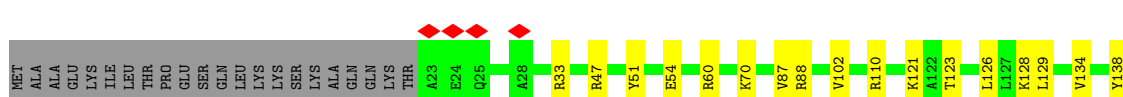
• Molecule 41: RPL5 isoform 1



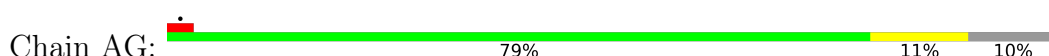
• Molecule 42: 60S ribosomal protein L6-A

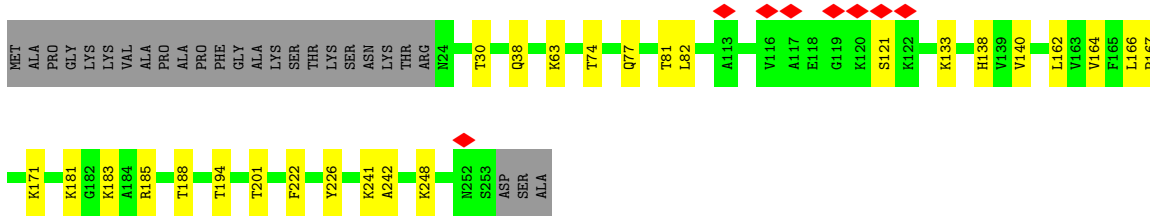


• Molecule 43: 60S ribosomal protein L7-A

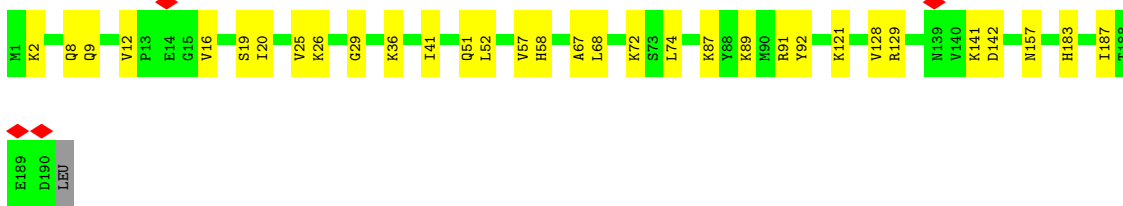
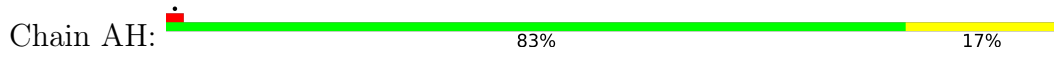


• Molecule 44: 60S ribosomal protein L8-A

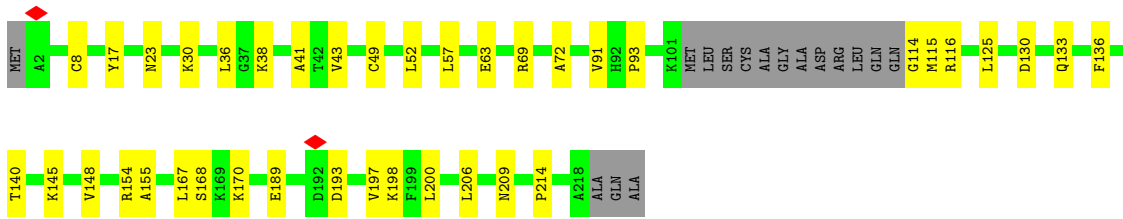
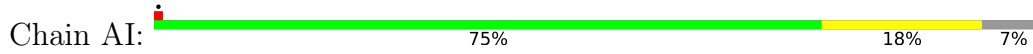




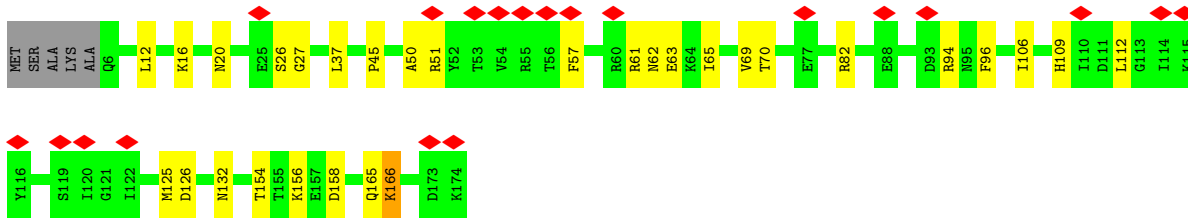
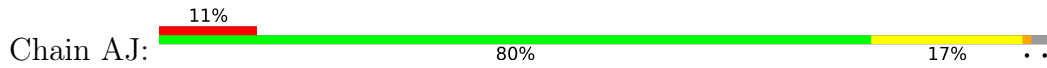
• Molecule 45: 60S ribosomal protein L9-A



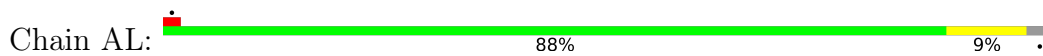
• Molecule 46: RPL10 isoform 1




• Molecule 47: RPL11A isoform 1



• Molecule 48: 60S ribosomal protein L13-A



• Molecule 49: 60S ribosomal protein L14-A

Chain AM:  80% 18%




- Molecule 50: 60S ribosomal protein L15-A

Chain AN:  88% 11%




- Molecule 51: 60S ribosomal protein L16-A

Chain AO:  85% 14%




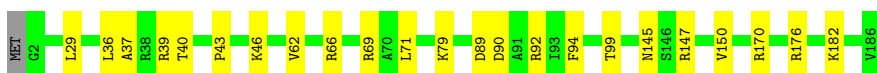
- Molecule 52: 60S ribosomal protein L17-A

Chain AP:  78% 17% 5%




- Molecule 53: 60S ribosomal protein L18-A

Chain AQ:  87% 12%




- Molecule 54: 60S ribosomal protein L19-A

Chain AR:  7% 91% 8%

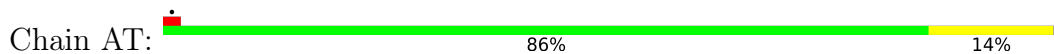


- Molecule 55: 60S ribosomal protein L20

Chain AS:  82% 15%



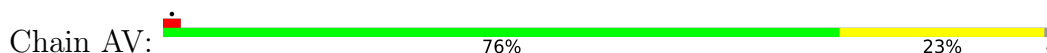
• Molecule 56: 60S ribosomal protein L21-A



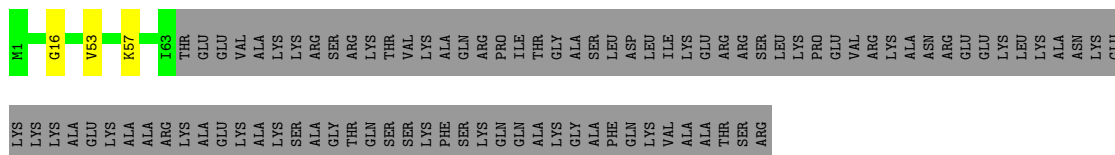
• Molecule 57: 60S ribosomal protein L22-A



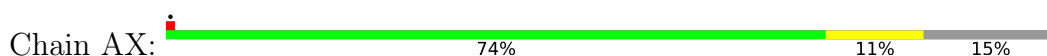
• Molecule 58: 60S ribosomal protein L23-A



• Molecule 59: RPL24A isoform 1




• Molecule 60: 60S ribosomal protein L25

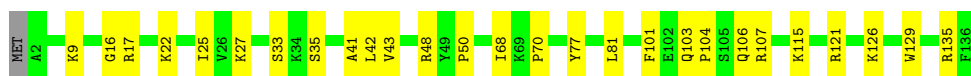


• Molecule 61: 60S ribosomal protein L26-A




- Molecule 62: 60S ribosomal protein L27-A

Chain AZ:  79% 20%



- Molecule 63: 60S ribosomal protein L28

Chain Aa:  80% 19%



- Molecule 64: RPL29 isoform 1

Chain Ab:  5% 90% 8%




- Molecule 65: 60S ribosomal protein L30

Chain Ac:  87% 6% 8%




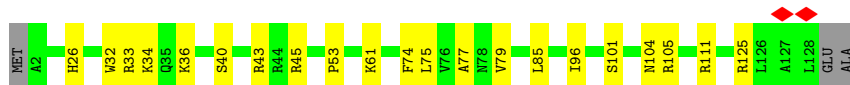
- Molecule 66: 60S ribosomal protein L31-A

Chain Ad:  6% 86% 11%




- Molecule 67: RPL32 isoform 1

Chain Ae:  82% 16%

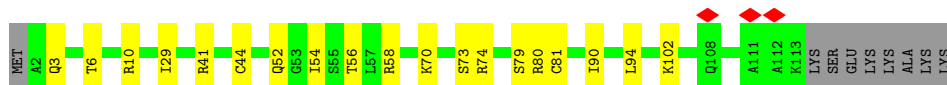
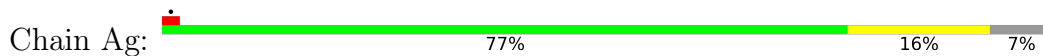


- Molecule 68: 60S ribosomal protein L33-A

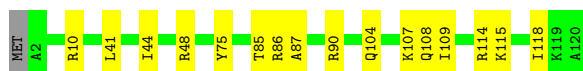
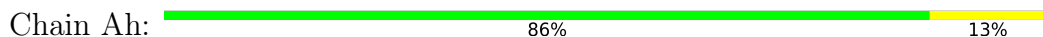
Chain Af:  79% 21%



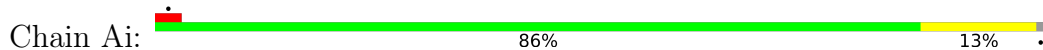
- Molecule 69: 60S ribosomal protein L34-A



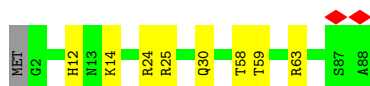
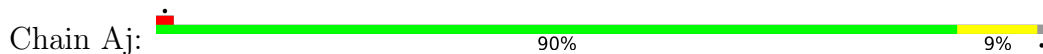
- Molecule 70: 60S ribosomal protein L35-A



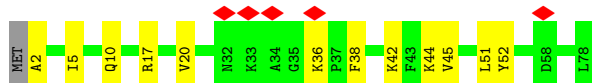
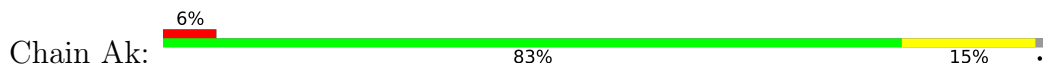
- Molecule 71: 60S ribosomal protein L36-A



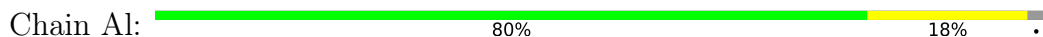
- Molecule 72: 60S ribosomal protein L37-A



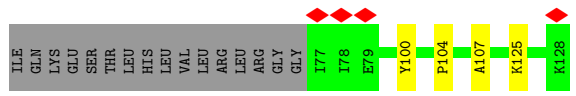
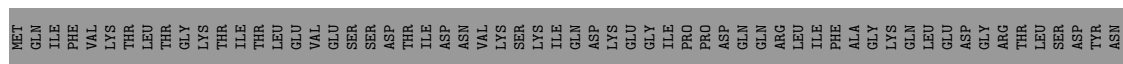
- Molecule 73: RPL38 isoform 1



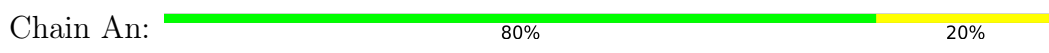
- Molecule 74: 60S ribosomal protein L39



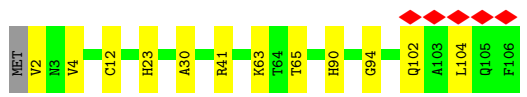
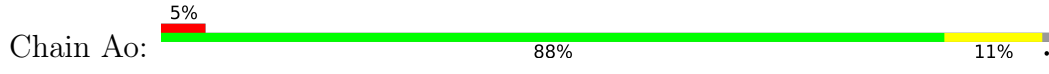
- Molecule 75: Ubiquitin-60S ribosomal protein L40



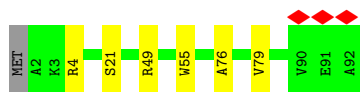
- Molecule 76: 60S ribosomal protein L41-A



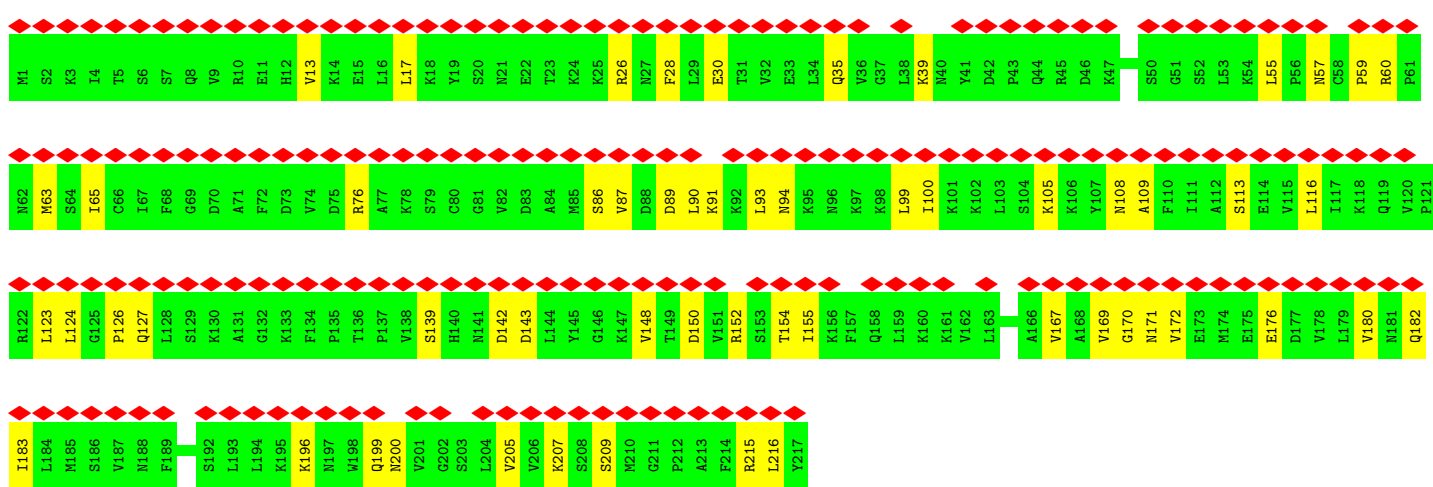
- Molecule 77: 60S ribosomal protein L42-A



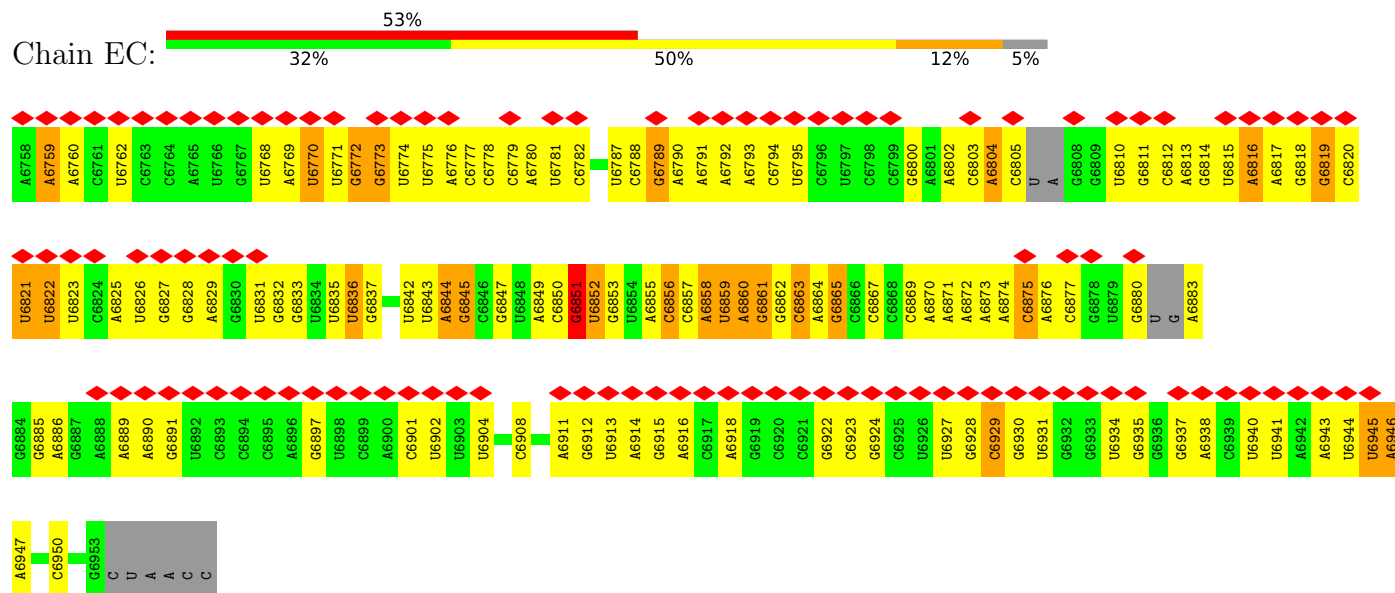
- Molecule 78: 60S ribosomal protein L43-A



- Molecule 79: RPL1A isoform 1



- Molecule 80: Internal ribosome entry site



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	112542	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	7.298	Depositor
Minimum map value	-3.391	Depositor
Average map value	0.017	Depositor
Map value standard deviation	0.255	Depositor
Recommended contour level	0.6	Depositor
Map size (\AA)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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: OMG, UR3, MA6, OMC, MG, ZN, 1MA, A2M, 5MC, XSX, HIC, 4AC, G7M, OMU

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	0.19	0/1653	0.53	0/2261
2	BB	0.20	0/1735	0.55	0/2335
3	BC	0.16	0/1665	0.39	0/2263
4	BE	0.16	0/2109	0.45	0/2839
5	BG	0.13	0/1844	0.40	0/2464
6	BH	0.20	0/1506	0.53	2/2028 (0.1%)
7	BI	0.18	0/1514	0.53	0/2021
8	BJ	0.15	0/1519	0.43	0/2035
9	BL	0.16	0/1272	0.37	0/1712
10	BN	0.16	0/1215	0.46	0/1638
11	BO	0.21	0/952	0.56	0/1279
12	BV	0.17	0/693	0.44	0/935
13	BW	0.16	0/1038	0.39	0/1395
14	BX	0.18	0/1139	0.49	0/1518
15	BY	0.16	0/1087	0.46	0/1449
16	Ba	0.20	0/782	0.57	0/1047
17	Bb	0.15	0/620	0.46	0/838
18	Be	0.12	0/483	0.43	0/643
19	BD	0.16	0/1759	0.43	0/2368
20	BF	0.17	0/1629	0.47	0/2202
21	BK	0.19	0/837	0.56	0/1131
22	BP	0.16	0/1012	0.45	0/1356
23	BQ	0.17	0/1125	0.46	0/1510
24	BR	0.18	0/984	0.46	0/1318
25	BS	0.16	0/1211	0.47	0/1628
26	BT	0.18	0/1113	0.59	2/1494 (0.1%)
27	BU	0.19	0/865	0.52	1/1169 (0.1%)
28	BZ	0.18	0/566	0.49	0/761
29	Bc	0.15	0/499	0.45	0/670
30	Bd	0.17	0/453	0.43	0/602
31	Bg	0.16	0/2454	0.47	0/3340
32	Bf	0.17	0/462	0.62	2/617 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.17	0/921	0.51	0/1245
34	B5	0.18	1/41880 (0.0%)	0.34	4/65248 (0.0%)
35	AA	0.18	0/1912	0.41	0/2569
36	AB	0.18	0/3138	0.41	0/4217
37	AC	0.19	0/2800	0.46	0/3790
38	A1	0.21	2/75561 (0.0%)	0.36	3/117806 (0.0%)
39	A3	0.16	0/2883	0.31	0/4491
40	A4	0.19	0/3746	0.33	0/5832
41	AD	0.15	0/2390	0.42	0/3225
42	AE	0.16	0/1260	0.40	0/1694
43	AF	0.18	0/1821	0.44	0/2451
44	AG	0.18	0/1830	0.47	0/2469
45	AH	0.17	0/1531	0.44	0/2062
46	AI	0.16	0/1708	0.38	1/2290 (0.0%)
47	AJ	0.22	0/1374	0.61	0/1842
48	AL	0.18	0/1568	0.45	0/2106
49	AM	0.16	0/1068	0.38	0/1438
50	AN	0.19	0/1757	0.40	0/2354
51	AO	0.17	0/1585	0.39	0/2128
52	AP	0.17	0/1410	0.41	0/1893
53	AQ	0.16	0/1465	0.38	0/1965
54	AR	0.15	0/1538	0.37	0/2050
55	AS	0.19	0/1481	0.43	0/1990
56	AT	0.20	0/1300	0.45	0/1743
57	AU	0.16	0/812	0.44	0/1099
58	AV	0.18	0/1018	0.43	0/1369
59	AW	0.16	0/533	0.38	0/707
60	AX	0.19	0/983	0.43	0/1325
61	AY	0.17	0/1004	0.40	0/1341
62	AZ	0.16	0/1118	0.37	0/1497
63	Aa	0.19	0/1204	0.48	0/1612
64	Ab	0.17	0/473	0.43	0/629
65	Ac	0.16	0/751	0.40	0/1008
66	Ad	0.16	0/904	0.35	0/1213
67	Ae	0.17	0/1041	0.38	0/1394
68	Af	0.20	0/868	0.42	0/1168
69	Ag	0.23	0/890	0.50	0/1189
70	Ah	0.15	0/978	0.35	0/1301
71	Ai	0.22	0/778	0.47	0/1034
72	Aj	0.21	0/696	0.48	0/923
73	Ak	0.15	0/618	0.39	0/826
74	Al	0.18	0/443	0.42	0/588
75	Am	0.16	0/423	0.37	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.21	0/234	0.66	0/300
77	Ao	0.17	0/860	0.51	0/1136
78	Ap	0.18	0/701	0.43	0/934
79	E	0.17	0/1745	0.44	0/2342
80	EC	0.16	0/4571	0.40	1/7114 (0.0%)
All	All	0.19	3/219368 (0.0%)	0.39	16/322375 (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
20	BF	0	1
43	AF	0	1
44	AG	0	2
47	AJ	0	1
All	All	0	5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	O3'-P	7.19	1.63	1.56
38	A1	2256	A2M	O3'-P	5.81	1.62	1.56
38	A1	2946	A2M	O3'-P	5.11	1.61	1.56

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BT	34	VAL	CA-C-N	7.62	139.57	126.32
26	BT	34	VAL	C-N-CA	7.62	139.57	126.32
6	BH	13	PRO	CA-C-N	6.92	134.16	121.70
6	BH	13	PRO	C-N-CA	6.92	134.16	121.70
34	B5	1057	U	C2'-C3'-O3'	6.57	119.35	109.50
27	BU	96	PRO	N-CD-CG	-5.98	94.23	103.20
32	Bf	111	GLU	CA-C-N	5.93	132.37	121.70
32	Bf	111	GLU	C-N-CA	5.93	132.37	121.70
34	B5	1574	G	C4'-C3'-O3'	5.73	121.60	113.00
34	B5	1575	G7M	O3'-P-O5'	5.49	114.43	104.00
80	EC	6851	G	P-O3'-C3'	5.32	128.18	120.20
38	A1	2497	U	P-O3'-C3'	5.26	128.09	120.20
46	AI	214	PRO	CA-N-CD	-5.20	104.73	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2497	U	C4'-C3'-O3'	5.19	117.18	109.40
34	B5	1057	U	P-O3'-C3'	5.16	127.94	120.20
38	A1	406	G	O4'-C1'-N9	5.09	115.84	108.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	AF	232	ARG	Peptide
44	AG	121	SER	Peptide
44	AG	30	THR	Peptide
47	AJ	166	LYS	Peptide
20	BF	124	LEU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	20	0
2	BB	1709	0	1784	38	0
3	BC	1635	0	1723	22	0
4	BE	2068	0	2154	38	0
5	BG	1820	0	1918	32	0
6	BH	1481	0	1572	12	0
7	BI	1489	0	1525	30	0
8	BJ	1494	0	1573	25	0
9	BL	1244	0	1314	10	0
10	BN	1192	0	1255	20	0
11	BO	941	0	979	19	0
12	BV	684	0	672	9	0
13	BW	1021	0	1060	13	0
14	BX	1121	0	1196	20	0
15	BY	1073	0	1132	22	0
16	Ba	769	0	818	15	0
17	Bb	610	0	633	16	0
18	Be	475	0	525	5	0
19	BD	1734	0	1817	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	BF	1609	0	1675	33	0
21	BK	817	0	804	21	0
22	BP	991	0	1035	32	0
23	BQ	1105	0	1166	29	0
24	BR	975	0	1039	13	0
25	BS	1192	0	1222	26	0
26	BT	1095	0	1114	24	0
27	BU	855	0	917	16	0
28	BZ	558	0	598	17	0
29	Bc	497	0	535	4	0
30	Bd	443	0	436	13	0
31	Bg	2401	0	2356	41	0
32	Bf	454	0	465	8	0
33	BM	913	0	955	9	0
34	B5	38004	0	19142	437	0
35	AA	1878	0	1946	30	0
36	AB	3080	0	3158	49	0
37	AC	2748	0	2859	36	0
38	A1	68445	0	34455	602	0
39	A3	2579	0	1304	27	0
40	A4	3353	0	1695	32	0
41	AD	2341	0	2290	34	0
42	AE	1239	0	1326	19	0
43	AF	1784	0	1862	20	0
44	AG	1798	0	1894	16	0
45	AH	1510	0	1576	18	0
46	AI	1672	0	1711	23	0
47	AJ	1353	0	1383	20	0
48	AL	1543	0	1608	16	0
49	AM	1053	0	1149	17	0
50	AN	1720	0	1779	19	0
51	AO	1555	0	1659	21	0
52	AP	1388	0	1423	20	0
53	AQ	1441	0	1543	16	0
54	AR	1521	0	1617	17	0
55	AS	1445	0	1487	24	0
56	AT	1276	0	1323	19	0
57	AU	796	0	812	9	0
58	AV	1003	0	1048	21	0
59	AW	521	0	551	2	0
60	AX	968	0	1036	11	0
61	AY	993	0	1081	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	AZ	1092	0	1155	19	0
63	Aa	1173	0	1215	27	0
64	Ab	462	0	491	6	0
65	Ac	743	0	797	4	0
66	Ad	890	0	938	7	0
67	Ae	1020	0	1090	17	0
68	Af	850	0	880	17	0
69	Ag	880	0	945	17	0
70	Ah	969	0	1078	12	0
71	Ai	771	0	849	10	0
72	Aj	681	0	687	8	0
73	Ak	612	0	682	10	0
74	Al	436	0	475	9	0
75	Am	417	0	459	4	0
76	An	233	0	281	5	0
77	Ao	847	0	914	9	0
78	Ap	694	0	738	6	0
79	E	1718	0	1811	40	0
80	EC	4090	0	2068	41	0
81	A1	182	0	0	0	0
81	A3	2	0	0	0	0
81	A4	5	0	0	0	0
81	AC	1	0	0	0	0
81	AD	1	0	0	0	0
81	AL	1	0	0	0	0
81	AP	1	0	0	0	0
81	B5	60	0	0	0	0
81	BE	1	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	205919	0	151860	2063	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (2063) 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:A1:2457:G:N2	38:A1:2486:A:C2	1.94	1.35
34:B5:1588:G:H1	34:B5:1608:U:H3	0.99	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1697:G:H1	34:B5:1704:U:H3	0.96	0.90
38:A1:2457:G:N2	38:A1:2486:A:H2	1.62	0.87
38:A1:2457:G:C2	38:A1:2486:A:C2	2.73	0.77
11:BO:20:TYR:HB3	11:BO:27:PHE:HB2	1.66	0.76
5:BG:154:ARG:NH1	34:B5:78:A:N7	2.34	0.75
32:Bf:134:ASN:HD21	32:Bf:139:LEU:HD23	1.49	0.75
68:Af:49:ILE:HD11	68:Af:71:VAL:HG23	1.70	0.74
38:A1:3215:A:H5'	49:AM:121:MET:HE1	1.68	0.74
24:BR:106:THR:HA	24:BR:109:LEU:HD23	1.69	0.73
38:A1:2444:C:H42	38:A1:2503:G:H22	1.37	0.73
38:A1:2457:G:C2	38:A1:2486:A:N1	2.57	0.72
44:AG:77:GLN:HE22	44:AG:167:PRO:HG2	1.54	0.72
55:AS:8:GLN:HE21	55:AS:26:ARG:HE	1.36	0.72
4:BE:87:MET:HE1	4:BE:236:ILE:HG21	1.72	0.71
11:BO:82:LYS:HE3	11:BO:118:VAL:HG11	1.72	0.71
50:AN:96:ARG:NH1	50:AN:104:GLU:OE2	2.24	0.70
34:B5:895:G:H1	34:B5:917:U:H3	1.38	0.70
50:AN:183:THR:HG22	50:AN:187:ARG:HB3	1.72	0.70
58:AV:32:ARG:HB2	58:AV:64:LYS:HG3	1.73	0.70
26:BT:77:ASN:HB3	26:BT:95:ASP:HB3	1.74	0.70
38:A1:3229:G:OP1	49:AM:137:LYS:NZ	2.24	0.70
58:AV:81:GLN:O	58:AV:98:ASN:ND2	2.25	0.70
38:A1:2457:G:N3	38:A1:2486:A:N1	2.40	0.69
4:BE:87:MET:HE2	4:BE:123:LEU:HB2	1.74	0.69
34:B5:992:A:O2'	34:B5:1785:U:O2	2.10	0.69
55:AS:89:ASN:HD21	56:AT:156:TYR:H	1.38	0.69
79:E:60:ARG:O	79:E:152:ARG:NH2	2.25	0.69
34:B5:868:G:H1	34:B5:960:U:H3	1.41	0.69
46:AI:30:LYS:HD2	46:AI:63:GLU:HG3	1.74	0.68
2:BB:28:GLU:HG3	2:BB:50:LYS:HD3	1.75	0.68
2:BB:88:VAL:HG11	2:BB:96:LEU:HD23	1.75	0.68
40:A4:75:G:OP2	61:AY:74:TYR:OH	2.11	0.68
38:A1:1916:U:H4'	54:AR:85:ARG:HH21	1.59	0.68
10:BN:62:GLN:HB2	10:BN:65:VAL:HG22	1.75	0.68
40:A4:58:G:O6	72:Aj:63:ARG:NH1	2.26	0.68
10:BN:70:LYS:NZ	34:B5:963:A:N7	2.42	0.68
65:Ac:30:THR:HG23	65:Ac:91:SER:HB3	1.76	0.68
15:BY:8:ARG:HH21	34:B5:780:A:H62	1.42	0.67
47:AJ:61:ARG:HB3	77:Ao:104:LEU:HD12	1.74	0.67
5:BG:31:ARG:H	5:BG:34:GLN:HE21	1.41	0.67
38:A1:801:A:H61	48:AL:19:GLN:HE22	1.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3302:U:H3	38:A1:3312:U:H3	1.40	0.67
38:A1:1258:U:N3	38:A1:1261:G:OP2	2.26	0.67
38:A1:1016:C:H41	38:A1:1035:G:H22	1.42	0.67
80:EC:6810:U:H2'	80:EC:6811:G:H8	1.60	0.67
36:AB:287:LYS:O	36:AB:293:ASN:ND2	2.28	0.67
73:Ak:5:ILE:HD11	73:Ak:52:TYR:HB3	1.76	0.67
13:BW:15:ASN:HD21	13:BW:72:CYS:H	1.41	0.66
14:BX:70:LYS:NZ	34:B5:567:A:OP1	2.29	0.66
34:B5:1585:U:H3	34:B5:1611:A:H2	1.42	0.66
36:AB:240:ARG:NH2	38:A1:1907:C:O2	2.29	0.66
45:AH:91:ARG:NH1	45:AH:141:LYS:O	2.29	0.66
31:Bg:13:LEU:HB2	31:Bg:310:ILE:HB	1.77	0.66
34:B5:514:G:H1	34:B5:543:C:H5	1.44	0.66
38:A1:171:G:H22	38:A1:246:U:H3	1.41	0.66
40:A4:135:G:OP2	60:AX:56:ARG:NH2	2.28	0.66
34:B5:1245:G:N2	34:B5:1250:U:O4	2.29	0.66
38:A1:2500:A:H2'	38:A1:2501:U:H5''	1.78	0.66
45:AH:57:VAL:HG23	45:AH:68:LEU:HD13	1.78	0.66
36:AB:28:ARG:NH2	38:A1:3140:G:N7	2.43	0.66
38:A1:1364:C:OP1	43:AF:110:ARG:NH2	2.30	0.65
58:AV:87:ARG:HH22	58:AV:137:VAL:HG21	1.60	0.65
17:Bb:51:GLN:OE1	34:B5:957:G:N2	2.29	0.65
31:Bg:116:ASP:HA	31:Bg:156:VAL:HG11	1.78	0.65
56:AT:88:ARG:NH1	64:Ab:33:LYS:O	2.27	0.65
25:BS:57:ARG:NH2	34:B5:1533:C:OP1	2.29	0.65
34:B5:1174:C:O2'	34:B5:1196:A:N6	2.30	0.65
55:AS:8:GLN:HE22	55:AS:10:ILE:HD11	1.61	0.65
23:BQ:75:VAL:HG22	34:B5:1609:U:H5''	1.79	0.65
80:EC:6800:G:H22	80:EC:6883:A:H2	1.45	0.65
5:BG:66:GLY:HA2	34:B5:1681:A:H1'	1.79	0.65
38:A1:595:G:OP1	43:AF:33:ARG:NH2	2.30	0.65
34:B5:1245:G:H1	34:B5:1250:U:H3	1.44	0.65
5:BG:14:LYS:HZ2	5:BG:123:GLY:H	1.42	0.65
38:A1:284:A:OP2	77:Ao:41:ARG:NH1	2.29	0.65
60:AX:91:ASN:H	60:AX:94:GLN:HE21	1.45	0.65
7:BI:152:ILE:HG13	7:BI:153:GLU:H	1.61	0.65
11:BO:124:ASP:OD2	34:B5:927:C:O2'	2.15	0.65
34:B5:1291:G:H22	34:B5:1324:G:H1	1.45	0.65
38:A1:1261:G:OP2	38:A1:1261:G:N2	2.29	0.65
38:A1:2528:G:H5''	44:AG:248:LYS:HE3	1.79	0.65
43:AF:239:LEU:HG	43:AF:243:MET:HE2	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Ba:44:ILE:HG23	16:Ba:45:VAL:HG23	1.79	0.64
31:Bg:249:ARG:HH22	31:Bg:315:VAL:HG21	1.62	0.64
38:A1:2185:G:O2'	38:A1:2314:U:OP2	2.13	0.64
38:A1:845:G:H21	38:A1:848:A:H2	1.42	0.64
38:A1:2779:A:O2'	48:AL:180:ARG:NH2	2.30	0.64
27:BU:59:PRO:HG3	34:B5:1381:U:H4'	1.78	0.64
47:AJ:165:GLN:HG3	47:AJ:166:LYS:H	1.63	0.64
34:B5:1656:U:HO2'	38:A1:2292:U:HO2'	1.46	0.64
38:A1:2447:A:H2'	38:A1:2448:G:C8	2.33	0.64
13:BW:31:SER:H	13:BW:34:ILE:HD12	1.62	0.64
27:BU:70:THR:OG1	27:BU:72:ASN:OD1	2.16	0.64
1:BA:183:ARG:HG3	1:BA:188:LEU:HD23	1.80	0.64
16:Ba:2:PRO:HB3	34:B5:1142:A:H5''	1.79	0.64
40:A4:48:A:H5''	70:Ah:48:ARG:HH12	1.62	0.64
4:BE:49:ARG:NH2	34:B5:448:C:OP1	2.31	0.64
2:BB:144:ARG:HB2	2:BB:208:GLN:HB3	1.78	0.64
34:B5:1339:C:O2'	34:B5:1341:A:N7	2.28	0.64
34:B5:1594:G:OP2	34:B5:1596:C:N4	2.31	0.64
31:Bg:101:GLN:HE21	31:Bg:138:GLY:HA3	1.63	0.63
8:BJ:17:ARG:NH2	34:B5:4:C:O2'	2.32	0.63
38:A1:1272:C:H3'	38:A1:1273:A:H8	1.64	0.63
38:A1:1757:A:OP1	57:AU:94:ARG:NH2	2.30	0.63
20:BF:222:LYS:NZ	29:Bc:57:MET:SD	2.72	0.63
38:A1:1311:G:N2	51:AO:86[A]:GLY:O	2.22	0.63
80:EC:6836:U:OP2	80:EC:6847:G:N2	2.32	0.63
10:BN:124:ARG:NH2	34:B5:967:A:OP2	2.27	0.63
23:BQ:125:GLU:OE2	34:B5:1416:G:O2'	2.13	0.63
36:AB:124:LYS:NZ	38:A1:3297:U:O4	2.32	0.63
80:EC:6787:U:OP1	80:EC:6804:A:N6	2.29	0.63
34:B5:852:C:OP2	54:AR:173:ARG:NH1	2.32	0.63
38:A1:173:G:H2'	38:A1:174:C:H5'	1.81	0.63
23:BQ:14:LYS:NZ	34:B5:1610:G:N7	2.47	0.63
37:AC:309:ARG:NH2	38:A1:610:G:N7	2.47	0.63
38:A1:3268:A:OP1	42:AE:46:ARG:NH2	2.28	0.63
3:BC:139:ILE:HD13	3:BC:191:ALA:HB1	1.81	0.62
24:BR:26:LEU:HD11	24:BR:62:GLN:HG3	1.81	0.62
36:AB:67:PHE:HD1	36:AB:70:ARG:HD2	1.64	0.62
36:AB:95:THR:HG22	36:AB:97:ARG:H	1.65	0.62
38:A1:2796:G:N7	77:Ao:63:LYS:NZ	2.47	0.62
38:A1:362:U:O4	72:Aj:24:ARG:NH2	2.32	0.62
37:AC:98:ARG:NH2	38:A1:804:C:OP1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:160:ARG:NH2	34:B5:68:A:OP1	2.32	0.62
38:A1:2448:G:H1	38:A1:2499:U:H3	1.45	0.62
34:B5:225:A:H2'	34:B5:226:A:H8	1.63	0.62
38:A1:1497:C:O2'	38:A1:1602:A:N3	2.32	0.62
34:B5:187:G:H21	34:B5:198:A:H62	1.46	0.62
38:A1:2901:G:O2'	38:A1:3024:A:N1	2.31	0.62
13:BW:56:HIS:O	34:B5:861:U:O2'	2.17	0.62
19:BD:42:THR:OG1	19:BD:45:LYS:O	2.16	0.62
38:A1:2727:A:OP2	38:A1:2728:G:N2	2.33	0.62
19:BD:31:GLU:O	19:BD:54:ARG:NH2	2.33	0.62
34:B5:1775:U:OP1	76:An:11:ARG:NH2	2.33	0.62
11:BO:127:ARG:NH2	34:B5:1788:G:OP1	2.33	0.62
38:A1:1949:G:OP2	54:AR:135:LYS:NZ	2.33	0.62
38:A1:2499:U:H2'	38:A1:2500:A:C4	2.35	0.62
23:BQ:142:TYR:O	23:BQ:143:ARG:NH1	2.33	0.61
38:A1:967:A:OP1	63:Aa:47:LYS:NZ	2.33	0.61
45:AH:41:ILE:HD11	45:AH:67:ALA:HB1	1.82	0.61
15:BY:83:LYS:HE2	15:BY:96:LEU:HD13	1.82	0.61
34:B5:1693:A:N1	34:B5:1709:C:N4	2.48	0.61
56:AT:68:THR:HG22	56:AT:69:LYS:H	1.64	0.61
32:Bf:132:LEU:HD13	32:Bf:140:TYR:H	1.65	0.61
36:AB:148:LEU:HD13	36:AB:196:ARG:HD3	1.81	0.61
44:AG:81:THR:HG21	44:AG:181:LYS:HG3	1.81	0.61
5:BG:136:LYS:NZ	5:BG:174:LYS:O	2.34	0.61
10:BN:54:LEU:HB3	10:BN:60:VAL:HB	1.83	0.61
55:AS:6:GLU:OE1	55:AS:28:ARG:NH2	2.34	0.61
36:AB:193:ASP:OD1	36:AB:196:ARG:NH2	2.27	0.61
35:AA:116:VAL:HB	35:AA:126:LEU:HB2	1.82	0.61
38:A1:1940:G:H21	38:A1:3362:A:H8	1.49	0.61
61:AY:101:PRO:HA	61:AY:104:LEU:HD12	1.83	0.61
21:BK:62:GLN:HE22	30:Bd:25:SER:HB3	1.65	0.61
24:BR:14:LYS:HG3	24:BR:69:ILE:HG13	1.82	0.61
79:E:65:ILE:HD11	79:E:148:VAL:HG13	1.83	0.61
80:EC:6833:G:O2'	80:EC:6872:A:N6	2.33	0.61
22:BP:97:TYR:HE1	34:B5:1453:G:H1'	1.66	0.61
28:BZ:77:ARG:NH2	34:B5:1533:C:OP2	2.33	0.61
34:B5:1772:C:OP2	76:An:2:ARG:NH2	2.33	0.61
38:A1:784:A:OP2	53:AQ:69:ARG:NH1	2.33	0.61
38:A1:2284:C:N4	38:A1:2308:C:OP2	2.32	0.61
11:BO:40:ALA:HB2	11:BO:70:LYS:HD2	1.82	0.60
15:BY:26:ASP:HB3	15:BY:70:VAL:HG13	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Aa:112:ILE:HB	63:Aa:130:VAL:HG12	1.82	0.60
8:BJ:139:GLN:NE2	15:BY:64:PHE:O	2.33	0.60
25:BS:123:ARG:NH2	34:B5:1547:A:OP1	2.35	0.60
36:AB:79:VAL:HG21	36:AB:338:LEU:HD11	1.83	0.60
41:AD:186:GLU:HG2	41:AD:187:THR:HG23	1.83	0.60
15:BY:55:VAL:HG22	15:BY:75:VAL:HG22	1.84	0.60
2:BB:190:PRO:HG2	2:BB:192:VAL:HG23	1.84	0.60
6:BH:26:GLU:OE2	6:BH:84:LYS:NZ	2.34	0.60
30:Bd:30:LEU:HA	30:Bd:39:CYS:HA	1.83	0.60
31:Bg:178:VAL:HB	31:Bg:192:PHE:HB2	1.83	0.60
35:AA:101:VAL:HG22	35:AA:165:VAL:HG22	1.81	0.60
34:B5:1213:G:H1	34:B5:1450:U:H3	1.48	0.60
38:A1:258:G:OP1	48:AL:81:LYS:NZ	2.31	0.60
38:A1:351:A:N6	74:A1:37:TYR:O	2.35	0.60
39:A3:1:G:O3'	41:AD:273:ARG:NH2	2.34	0.60
79:E:63:MET:HE1	79:E:108:ASN:HB2	1.83	0.60
21:BK:18:GLU:HA	21:BK:90:THR:HG22	1.84	0.60
25:BS:132:ARG:NH1	25:BS:146:ALA:O	2.34	0.60
34:B5:1575:G7M:H2'	34:B5:1576:A:C8	2.36	0.60
34:B5:900:A:H3'	34:B5:901:G:H21	1.65	0.60
38:A1:874:U:N3	38:A1:2978:U:OP1	2.30	0.60
38:A1:1281:G:N2	38:A1:1282:G:O6	2.35	0.60
20:BF:40:ILE:HG12	20:BF:67:PRO:HB2	1.84	0.60
25:BS:139:LYS:NZ	34:B5:1179:G:O6	2.28	0.60
38:A1:1226:G:O6	38:A1:1228:C:N4	2.35	0.60
38:A1:2551:U:OP1	69:Ag:102:LYS:NZ	2.34	0.60
51:AO:61[A]:ALA:HA	51:AO:70[A]:PRO:HD2	1.83	0.60
1:BA:84:ARG:NH2	24:BR:82:ASP:O	2.35	0.59
37:AC:35:VAL:HG21	37:AC:244:LEU:HD21	1.84	0.59
38:A1:3275:U:O2'	68:Af:99:ARG:NH2	2.35	0.59
3:BC:77:GLN:NE2	3:BC:79:GLU:OE2	2.36	0.59
32:Bf:135:HIS:ND1	34:B5:1250:U:O2'	2.36	0.59
35:AA:80:GLU:HG2	78:Ap:76:ALA:HB1	1.82	0.59
38:A1:1348:U:OP1	53:AQ:39:ARG:NH1	2.34	0.59
38:A1:1661:G:H2'	38:A1:1662:G:C8	2.37	0.59
7:BI:98:LYS:HB3	34:B5:329:G:H5''	1.85	0.59
8:BJ:144:PRO:HD2	34:B5:474:A:H5''	1.82	0.59
23:BQ:65:ILE:HD13	23:BQ:85:ILE:HG13	1.85	0.59
34:B5:705:U:H2'	34:B5:730:G:H1	1.67	0.59
38:A1:1639:C:OP2	69:Ag:74:ARG:NH2	2.35	0.59
2:BB:88:VAL:HG12	2:BB:98:THR:HG22	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:41:LEU:HB3	6:BH:70:PHE:CE1	2.38	0.59
11:BO:125:SER:OG	11:BO:126:THR:N	2.36	0.59
19:BD:168:ILE:HD13	19:BD:187:LYS:HE3	1.84	0.59
62:AZ:25:ILE:HA	62:AZ:43:VAL:HG12	1.85	0.59
75:Am:104:PRO:HG2	75:Am:107:ALA:HB2	1.84	0.59
3:BC:80:VAL:HG12	3:BC:102:VAL:HG22	1.83	0.59
3:BC:161:LYS:NZ	34:B5:1085:G:OP1	2.35	0.59
12:BV:62:ARG:HH22	34:B5:1039:A:H4'	1.68	0.59
20:BF:63:GLN:HE22	20:BF:66:GLN:HB3	1.67	0.59
38:A1:38:U:H4'	63:Aa:32:ARG:HD2	1.84	0.59
38:A1:619:A:OP1	52:AP:167:ARG:NH1	2.34	0.59
77:Ao:102:GLN:HE22	77:Ao:104:LEU:HD23	1.68	0.59
27:BU:33:GLN:NE2	27:BU:110:PRO:O	2.36	0.59
34:B5:110:U:OP1	34:B5:753:A:O2'	2.20	0.59
31:Bg:59:ARG:NH1	31:Bg:95:ALA:O	2.36	0.58
34:B5:69:G:H1	34:B5:82:U:H3	1.51	0.58
34:B5:680:U:H2'	34:B5:682:C:H41	1.67	0.58
37:AC:361:HIS:O	55:AS:28:ARG:NH1	2.36	0.58
38:A1:1632:A:OP1	62:AZ:48:ARG:NH2	2.33	0.58
6:BH:9:LEU:HD11	6:BH:17:GLU:HG3	1.84	0.58
26:BT:76:LEU:HB3	26:BT:101:ASN:HD22	1.66	0.58
31:Bg:224:ASN:ND2	31:Bg:231:MET:SD	2.76	0.58
36:AB:362:ALA:O	36:AB:364:LYS:NZ	2.36	0.58
9:BL:57:LYS:HD3	9:BL:131:ILE:HG23	1.84	0.58
34:B5:65:A:H2	34:B5:84:A:H62	1.51	0.58
53:AQ:170:ARG:NH1	63:Aa:57:GLY:O	2.36	0.58
2:BB:27:LYS:HB2	2:BB:47:LEU:HD12	1.85	0.58
2:BB:111:ARG:NH2	34:B5:930:A:O2'	2.36	0.58
11:BO:18:ARG:NH1	11:BO:31:THR:OG1	2.36	0.58
34:B5:488:G:H5''	34:B5:492:A:H62	1.68	0.58
79:E:30:GLU:O	79:E:171:ASN:ND2	2.37	0.58
25:BS:139:LYS:HG3	25:BS:140:THR:HG23	1.85	0.58
34:B5:871:G:H2'	34:B5:872:G:C8	2.38	0.58
38:A1:664:U:H2'	38:A1:665:A:C8	2.38	0.58
38:A1:1717:U:H2'	38:A1:1718:G:C8	2.39	0.58
40:A4:52:A:H5'	74:Al:21:ARG:HD3	1.84	0.58
41:AD:107:ARG:HD2	41:AD:248:ARG:HG2	1.86	0.58
66:Ad:55:LEU:HB2	66:Ad:95:PRO:HD3	1.86	0.58
4:BE:151:ASP:HB3	4:BE:154:ILE:HG13	1.85	0.58
7:BI:16:ALA:HB2	34:B5:354:C:H5''	1.86	0.58
34:B5:58:U:O2'	34:B5:451:A:N3	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2836:C:H5	38:A1:2852:C:H42	1.51	0.58
38:A1:3182:G:H4'	51:AO:161[A]:LYS:HD3	1.85	0.58
79:E:93:LEU:HD11	79:E:99:LEU:HD23	1.86	0.58
34:B5:782:U:H4'	34:B5:783:G:H5''	1.86	0.58
79:E:155:ILE:HG23	79:E:167:VAL:HG11	1.86	0.58
5:BG:176:GLN:NE2	34:B5:65:A:OP1	2.36	0.58
35:AA:111:THR:HB	35:AA:136:ILE:HD13	1.84	0.58
36:AB:17:LEU:HD21	36:AB:233:TRP:HH2	1.68	0.58
36:AB:220:VAL:O	36:AB:334:ARG:NH1	2.37	0.58
34:B5:1537:C:OP2	34:B5:1572:OMG:N2	2.36	0.57
38:A1:1269:U:N3	38:A1:1272:C:OP2	2.36	0.57
42:AE:47:PHE:HB3	42:AE:50:LYS:HG3	1.84	0.57
55:AS:147:ASP:OD2	55:AS:149:LYS:NZ	2.36	0.57
79:E:105:LYS:O	79:E:108:ASN:ND2	2.37	0.57
36:AB:219:ALA:HB2	36:AB:336:VAL:HG23	1.84	0.57
40:A4:100:U:O2'	60:AX:89:LYS:NZ	2.30	0.57
60:AX:111:ASN:HB2	60:AX:123:TYR:HB2	1.87	0.57
38:A1:400:G:H4'	38:A1:401:U:H5''	1.87	0.57
38:A1:2895:G:O2'	75:Am:100:TYR:O	2.22	0.57
8:BJ:59:LEU:HD22	8:BJ:69:ARG:HA	1.86	0.57
16:Ba:37:LYS:O	16:Ba:38:ARG:NH1	2.37	0.57
7:BI:35:ASN:O	7:BI:37:LYS:NZ	2.36	0.57
17:Bb:20:LYS:NZ	34:B5:958:U:OP2	2.33	0.57
20:BF:27:THR:HG23	23:BQ:28:LEU:HD12	1.87	0.57
22:BP:111:MET:HG2	25:BS:119:ILE:HG23	1.85	0.57
25:BS:28:ILE:HA	25:BS:58:ALA:HB2	1.85	0.57
32:Bf:107:LYS:HB3	32:Bf:110:ALA:HB2	1.86	0.57
33:BM:60:VAL:HG12	33:BM:85:LYS:HD2	1.86	0.57
37:AC:4:PRO:HG2	37:AC:22:LEU:HD22	1.85	0.57
80:EC:6922:G:H1	80:EC:6931:U:H3	1.52	0.57
2:BB:83:LYS:NZ	2:BB:105:PHE:O	2.37	0.57
31:Bg:80:ALA:HB3	31:Bg:92:TRP:HB2	1.85	0.57
38:A1:1448:U:H2'	38:A1:1449:A2M:H8	1.87	0.57
38:A1:1824:U:O3'	73:Ak:17:ARG:NH2	2.37	0.57
71:Ai:5:THR:HG23	71:Ai:12:ASN:HB2	1.86	0.57
76:An:15:ARG:HA	76:An:18:ARG:HG2	1.86	0.57
7:BI:104:ILE:HG13	7:BI:105:ASP:H	1.70	0.57
34:B5:509:G:H2'	34:B5:510:G:C8	2.39	0.57
41:AD:119:TYR:OH	41:AD:139:PRO:O	2.22	0.57
38:A1:2838:A:OP1	46:AI:154:ARG:NH2	2.38	0.57
38:A1:2207:A:N6	38:A1:2233:A:OP2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2842:U:OP1	38:A1:2844:C:N4	2.37	0.57
51:AO:27[A]:LEU:O	51:AO:101[A]:ARG:NH1	2.38	0.57
31:Bg:42:LEU:HB2	31:Bg:61:PHE:HB2	1.86	0.56
31:Bg:167:VAL:HG23	31:Bg:183:LEU:HB2	1.85	0.56
34:B5:250:C:H2'	34:B5:251:A:H8	1.70	0.56
34:B5:1229:G:N2	34:B5:1255:G:O2'	2.38	0.56
40:A4:9:A:H2'	40:A4:10:A:C8	2.40	0.56
4:BE:19:LEU:HD11	4:BE:108:ARG:HD2	1.85	0.56
19:BD:123:VAL:HG23	19:BD:134:CYS:HB3	1.87	0.56
20:BF:109:LYS:NZ	34:B5:1474:G:OP1	2.33	0.56
34:B5:1515:A:H4'	34:B5:1517:U:H5	1.69	0.56
38:A1:1799:A:H2'	38:A1:1800:A:C8	2.40	0.56
38:A1:2953:U:H2'	38:A1:2954:U:H2'	1.87	0.56
39:A3:64:A:N7	46:AI:209:ASN:ND2	2.51	0.56
61:AY:74:TYR:CD2	61:AY:77:LYS:HG2	2.40	0.56
5:BG:53:SER:HG	34:B5:163:G:HO2'	1.53	0.56
13:BW:119:LYS:HG2	34:B5:687:G:H5''	1.86	0.56
27:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	1.87	0.56
31:Bg:270:LEU:HD21	31:Bg:273:ASP:HB2	1.86	0.56
34:B5:1354:G:O6	34:B5:1369:U:O2	2.23	0.56
34:B5:1699:G:N2	34:B5:1700:C:O2'	2.38	0.56
38:A1:2501:U:H3'	38:A1:2502:A:C8	2.39	0.56
38:A1:2960:C:H2'	38:A1:2961:G:C8	2.41	0.56
25:BS:41:ARG:NH1	34:B5:1565:C:OP1	2.33	0.56
34:B5:190:C:O4'	34:B5:196:G:N2	2.37	0.56
19:BD:141:LYS:HE2	19:BD:179:GLN:HB3	1.87	0.56
22:BP:85:ILE:HD12	22:BP:89:MET:HE3	1.87	0.56
38:A1:1695:U:O2'	38:A1:1749:A:N1	2.33	0.56
45:AH:19:SER:HB3	45:AH:26:LYS:HG2	1.88	0.56
46:AI:52:LEU:HB3	46:AI:136:PHE:HB2	1.88	0.56
26:BT:15:ILE:HG23	26:BT:59:ALA:HB3	1.87	0.56
34:B5:225:A:H2'	34:B5:226:A:C8	2.40	0.56
34:B5:1474:G:H2'	34:B5:1475:A:H8	1.70	0.56
38:A1:411:U:H2'	38:A1:412:G:H8	1.71	0.56
62:AZ:70:PRO:HG3	62:AZ:115:LYS:HB2	1.88	0.56
2:BB:89:ASP:HB3	2:BB:223:PHE:HE1	1.71	0.56
34:B5:1041:G:H2'	34:B5:1042:G:C8	2.41	0.56
37:AC:54:GLU:OE2	38:A1:329:U:N3	2.39	0.56
38:A1:1689:U:O2'	54:AR:59:SER:OG	2.23	0.56
53:AQ:89:ASP:OD1	53:AQ:90:ASP:N	2.37	0.56
38:A1:358:G:N2	38:A1:361:A:OP2	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1174:G:N2	51:AO:87[A]:MET:SD	2.79	0.56
39:A3:1:G:H2'	39:A3:2:G:H8	1.70	0.56
62:AZ:17:ARG:HD3	69:Ag:73:SER:HB3	1.87	0.56
79:E:76:ARG:HH22	79:E:143:ASP:HA	1.71	0.56
4:BE:98:ASN:ND2	4:BE:116:ASP:OD1	2.38	0.56
38:A1:2383:C:OP2	51:AO:85[A]:ARG:NH2	2.38	0.56
45:AH:92:TYR:HB2	45:AH:142:ASP:HB3	1.86	0.56
79:E:126:PRO:HB2	79:E:127:GLN:HE21	1.71	0.56
5:BG:202:ARG:NH2	34:B5:127:G:O6	2.39	0.56
7:BI:138:ASN:HD21	34:B5:197:A:H61	1.53	0.55
25:BS:86:LEU:HG	25:BS:99:HIS:HB2	1.88	0.55
38:A1:1474:A:O2'	66:Ad:57:GLN:NE2	2.35	0.55
41:AD:122:VAL:O	41:AD:248:ARG:NH2	2.39	0.55
52:AP:56:ARG:NH2	52:AP:75:GLU:OE2	2.35	0.55
2:BB:130:SER:HB2	2:BB:180:THR:HG22	1.89	0.55
34:B5:591:A:H2'	34:B5:592:A:C8	2.41	0.55
38:A1:170:G:H5''	70:Ah:109:ILE:HD12	1.88	0.55
46:AI:193:ASP:OD2	46:AI:198:LYS:NZ	2.40	0.55
23:BQ:47:LYS:HG3	23:BQ:82:ARG:HD2	1.89	0.55
34:B5:1488:G:O2'	34:B5:1494:C:O2	2.23	0.55
63:Aa:56:VAL:HG12	63:Aa:57:GLY:H	1.70	0.55
80:EC:6885:G:H2'	80:EC:6886:A:H8	1.71	0.55
2:BB:61:LEU:HD22	2:BB:96:LEU:HD21	1.89	0.55
34:B5:891:A:H2'	34:B5:892:A:H8	1.71	0.55
38:A1:559:A:O2'	49:AM:84:LYS:NZ	2.34	0.55
38:A1:2492:C:OP1	79:E:215:ARG:NH1	2.40	0.55
8:BJ:119:ALA:O	8:BJ:124:HIS:ND1	2.30	0.55
16:Ba:32:LYS:O	16:Ba:37:LYS:NZ	2.38	0.55
34:B5:1533:C:H4'	34:B5:1539:G:C6	2.42	0.55
38:A1:1747:G:H21	73:Ak:2:ALA:HB3	1.72	0.55
38:A1:2880:U:OP1	58:AV:47:ASN:ND2	2.39	0.55
69:Ag:41:ARG:HG2	69:Ag:56:THR:HG21	1.89	0.55
79:E:55:LEU:HD22	79:E:182:GLN:HG2	1.88	0.55
80:EC:6804:A:H4'	80:EC:6805:C:H5'	1.88	0.55
6:BH:34:LEU:HA	6:BH:38:LEU:HB3	1.88	0.55
11:BO:87:GLY:HA3	11:BO:120:PRO:HG2	1.87	0.55
20:BF:119:ASP:HB3	28:BZ:100:ILE:HG12	1.88	0.55
28:BZ:95:HIS:NE2	34:B5:1529:C:OP1	2.40	0.55
38:A1:1592:G:OP1	69:Ag:58:ARG:NH2	2.34	0.55
38:A1:2700:G:H5''	56:AT:17:ARG:HG2	1.88	0.55
38:A1:2864:A:OP1	46:AI:114:GLY:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Af:31:LYS:NZ	68:Af:78:SER:O	2.39	0.55
1:BA:29:VAL:HG13	1:BA:149:LEU:HB3	1.88	0.55
11:BO:84:ARG:NH1	11:BO:85:ALA:O	2.39	0.55
15:BY:9:THR:HG22	15:BY:25:VAL:HG22	1.89	0.55
26:BT:112:GLY:O	26:BT:125:SER:OG	2.23	0.55
34:B5:851:U:H2'	54:AR:173:ARG:HH22	1.71	0.55
38:A1:969:C:O2'	64:Ab:18:ARG:NH2	2.36	0.55
38:A1:2160:G:H2'	38:A1:2161:G:H8	1.71	0.55
38:A1:2443:A:H2'	38:A1:2444:C:C6	2.41	0.55
38:A1:1203:A:H2'	38:A1:1204:A:C8	2.42	0.55
38:A1:1390:A:N6	38:A1:1418:A:O2'	2.40	0.55
38:A1:1618:G:O2'	40:A4:126:A:N1	2.39	0.55
38:A1:2673:A:O2'	47:AJ:126:ASP:OD1	2.23	0.55
50:AN:181:ASN:OD1	50:AN:184:LYS:NZ	2.40	0.55
57:AU:19:VAL:HG23	57:AU:105:LEU:HD22	1.89	0.55
60:AX:90:ALA:O	60:AX:120:LYS:NZ	2.40	0.55
70:Ah:104:GLN:OE1	70:Ah:108:GLN:NE2	2.40	0.55
79:E:65:ILE:HG22	79:E:109:ALA:HB3	1.89	0.55
4:BE:141:THR:OG1	4:BE:143:ASP:OD1	2.25	0.55
10:BN:42:ARG:HH11	10:BN:80:LEU:HD21	1.71	0.55
34:B5:1474:G:H2'	34:B5:1475:A:C8	2.42	0.55
37:AC:325:LEU:HD13	38:A1:598:A:H4'	1.89	0.55
38:A1:1805:C:H2'	38:A1:1806:A:H8	1.72	0.55
80:EC:6826:U:H2'	80:EC:6827:G:C8	2.41	0.55
38:A1:268:A:C4	50:AN:12:ARG:HG2	2.41	0.54
38:A1:2498:U:H2'	38:A1:2499:U:C6	2.43	0.54
38:A1:3280:U:O2'	38:A1:3281:U:O5'	2.24	0.54
48:AL:123:ILE:HG22	70:Ah:118:ILE:HG12	1.87	0.54
2:BB:26:ARG:NH1	2:BB:49:ASN:OD1	2.41	0.54
48:AL:167:PHE:N	63:Aa:135:GLU:OE1	2.37	0.54
48:AL:174:ARG:HB3	71:Ai:9:ILE:HD12	1.89	0.54
62:AZ:68:ILE:O	62:AZ:115:LYS:NZ	2.35	0.54
5:BG:22:HIS:HA	5:BG:25:ARG:HG2	1.89	0.54
7:BI:48:THR:OG1	7:BI:52:ASN:O	2.25	0.54
31:Bg:156:VAL:HA	31:Bg:169:ILE:HA	1.89	0.54
32:Bf:113:LYS:HE2	32:Bf:114:VAL:HG22	1.88	0.54
38:A1:2107:A:H2	38:A1:3344:A:H8	1.55	0.54
38:A1:3116:G:OP1	38:A1:3116:G:N2	2.41	0.54
40:A4:52:A:H62	74:Al:27:ILE:HD13	1.72	0.54
41:AD:50:ARG:HG2	41:AD:147:ASP:HB2	1.88	0.54
41:AD:85:ARG:NH2	41:AD:86:TYR:OH	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AF:121:LYS:HB2	56:AT:133:ALA:HB3	1.90	0.54
46:AI:17:TYR:OH	46:AI:23:ASN:ND2	2.36	0.54
55:AS:99:ARG:NH2	55:AS:126:VAL:O	2.40	0.54
4:BE:79:ASP:HB3	4:BE:82:TYR:HB2	1.89	0.54
38:A1:1264:G:N2	38:A1:1265:U:O4	2.34	0.54
63:Aa:36:GLY:HA3	63:Aa:40:HIS:CE1	2.43	0.54
34:B5:1160:A:H2'	34:B5:1161:C:H6	1.72	0.54
80:EC:6815:U:H3'	80:EC:6816:A:H5''	1.89	0.54
1:BA:182:LEU:HD23	1:BA:185:ARG:HH21	1.73	0.54
7:BI:57:ALA:HB2	7:BI:177:GLY:HA2	1.90	0.54
11:BO:36:LYS:NZ	11:BO:37:GLU:OE2	2.40	0.54
14:BX:3:LYS:HE2	14:BX:7:ARG:HH22	1.72	0.54
16:Ba:78:ALA:HA	16:Ba:83:ILE:HD12	1.88	0.54
34:B5:445:A:H1'	34:B5:525:A:H5'	1.89	0.54
34:B5:1284:C:H4'	34:B5:1285:U:H5'	1.88	0.54
38:A1:728:G:H5''	53:AQ:43:PRO:HB2	1.89	0.54
7:BI:168:CYS:HB2	7:BI:184:LEU:HD21	1.89	0.54
9:BL:133:LYS:HB2	34:B5:337:G:H3'	1.89	0.54
26:BT:22:LEU:HA	26:BT:25:GLN:HB2	1.88	0.54
38:A1:2213:A:H2'	38:A1:2214:A:C8	2.43	0.54
41:AD:38:THR:HG22	56:AT:30:TYR:HB3	1.89	0.54
79:E:87:VAL:HG11	79:E:116:LEU:HD11	1.88	0.54
2:BB:149:GLN:HE22	2:BB:154:SER:HB3	1.72	0.54
2:BB:214:LYS:NZ	34:B5:886:U:OP1	2.36	0.54
14:BX:79:ASN:HB3	14:BX:81:LYS:HD3	1.90	0.54
35:AA:69:TYR:OH	38:A1:2557:A:OP1	2.24	0.54
38:A1:631:U:H2'	38:A1:632:G:C8	2.43	0.54
19:BD:76:ARG:HD2	21:BK:63:TYR:CD2	2.42	0.54
30:Bd:42:CYS:SG	34:B5:1433:G:N2	2.77	0.54
34:B5:71:A:N6	34:B5:72:A:N3	2.55	0.54
38:A1:1244:A:H1'	38:A1:1271:A:H4'	1.89	0.54
4:BE:31:PRO:HG3	4:BE:43:PRO:HG3	1.90	0.54
19:BD:78:LYS:NZ	21:BK:34:GLU:OE1	2.41	0.54
21:BK:82:LEU:HD12	21:BK:83:PRO:HD2	1.90	0.54
23:BQ:13:LYS:NZ	23:BQ:120:ASP:OD2	2.41	0.54
38:A1:2677:G:N2	38:A1:2679:A:O2'	2.41	0.54
58:AV:57:MET:HE1	58:AV:105:PRO:HA	1.90	0.54
37:AC:161:LYS:HB2	37:AC:164:GLU:HG2	1.90	0.53
38:A1:1132:C:H2'	38:A1:1133:A2M:H8	1.89	0.53
38:A1:2681:U:OP2	47:AJ:51:ARG:NH1	2.40	0.53
41:AD:120:LYS:O	41:AD:248:ARG:NH1	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:21:ARG:HD3	38:A1:824:C:H5''	1.90	0.53
38:A1:1935:G:H2'	38:A1:1936:A:H8	1.73	0.53
38:A1:2193:U:H5''	38:A1:2194:G:H5'	1.91	0.53
41:AD:60:ILE:H	41:AD:80:SER:HB3	1.73	0.53
6:BH:41:LEU:HB3	6:BH:70:PHE:HE1	1.73	0.53
11:BO:17:ALA:HB3	11:BO:81:VAL:HA	1.91	0.53
11:BO:47:LYS:NZ	11:BO:66:ASP:OD2	2.35	0.53
19:BD:179:GLN:HE21	34:B5:579:A:H62	1.56	0.53
38:A1:3016:A:H2'	38:A1:3017:A:C8	2.43	0.53
4:BE:129:VAL:HG22	4:BE:139:VAL:HG12	1.89	0.53
24:BR:28:PHE:HA	24:BR:31:ASN:HB2	1.91	0.53
31:Bg:259:GLY:HA3	31:Bg:275:ARG:HH21	1.73	0.53
34:B5:1126:OMG:OP2	76:An:18:ARG:NH2	2.38	0.53
34:B5:1772:C:H2'	34:B5:1773:4AC:H6	1.91	0.53
37:AC:46:LYS:NZ	38:A1:691:A:OP1	2.42	0.53
38:A1:307:A:H2'	38:A1:308:A:C8	2.43	0.53
39:A3:13:A:OP2	39:A3:67:G:N2	2.41	0.53
62:AZ:81:LEU:HD22	69:Ag:90:ILE:HG12	1.90	0.53
8:BJ:109:LEU:HB2	8:BJ:146:PHE:HB3	1.90	0.53
34:B5:5:U:H2'	34:B5:6:G:H8	1.73	0.53
37:AC:190:GLY:O	37:AC:193:LYS:NZ	2.38	0.53
38:A1:1825:G:H5'	73:Ak:17:ARG:HH21	1.73	0.53
38:A1:3344:A:C2	38:A1:3361:G:N2	2.71	0.53
42:AE:92:SER:OG	42:AE:94:GLU:OE1	2.27	0.53
68:Af:14:LEU:HD11	68:Af:31:LYS:HB2	1.90	0.53
10:BN:36:GLN:OE1	10:BN:58:HIS:NE2	2.42	0.53
22:BP:90:ILE:HD11	22:BP:112:LEU:HD21	1.90	0.53
33:BM:46:ARG:NH2	34:B5:1229:G:O2'	2.42	0.53
35:AA:150:LEU:HD12	35:AA:154:ALA:HB3	1.90	0.53
38:A1:36:C:OP2	50:AN:83:LYS:NZ	2.41	0.53
38:A1:3181:C:OP2	51:AO:171[A]:LYS:NZ	2.34	0.53
2:BB:43:VAL:HG12	11:BO:33:LEU:HD21	1.90	0.53
30:Bd:32:ARG:NH1	34:B5:1597:A:OP2	2.38	0.53
31:Bg:248:ASN:ND2	31:Bg:297:ASP:O	2.42	0.53
34:B5:821:U:O4	34:B5:852:C:N3	2.41	0.53
38:A1:112:U:OP1	70:Ah:107:LYS:NZ	2.42	0.53
38:A1:655:C:H2'	38:A1:656:A:H8	1.73	0.53
79:E:90:LEU:HD13	79:E:124:LEU:HD11	1.91	0.53
5:BG:57:ASP:HA	5:BG:107:ALA:H	1.74	0.53
18:Be:15:LYS:NZ	34:B5:585:A:OP1	2.41	0.53
34:B5:800:U:H2'	34:B5:801:G:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1150:A:O2'	68:Af:21:ARG:NH2	2.41	0.53
38:A1:1389:G:H5''	67:Ae:101:SER:HB3	1.91	0.53
38:A1:1477:A:OP1	38:A1:3075:G:O2'	2.21	0.53
38:A1:2478:C:OP2	38:A1:2480:A:N6	2.40	0.53
48:AL:64:LYS:O	48:AL:67:ARG:NH1	2.41	0.53
49:AM:14:LEU:HD23	55:AS:149:LYS:HB3	1.89	0.53
34:B5:1023:A:OP1	34:B5:1126:OMG:N2	2.38	0.53
34:B5:1316:G:O2'	34:B5:1401:A:O2'	2.27	0.53
37:AC:112:LYS:HE2	50:AN:202:TYR:HB3	1.91	0.53
37:AC:156:LEU:HD12	37:AC:159:ILE:HD12	1.90	0.53
38:A1:655:C:H2'	38:A1:656:A:C8	2.43	0.53
38:A1:2767:U:O2'	77:Ao:30:ALA:O	2.23	0.53
38:A1:3322:A:H2'	38:A1:3323:A:C8	2.44	0.53
44:AG:162:LEU:HD23	50:AN:7:LEU:HD11	1.91	0.53
52:AP:52:LEU:HD11	52:AP:92:GLN:HE22	1.74	0.53
34:B5:234:G:N1	34:B5:235:G:N3	2.56	0.53
38:A1:651:G:O2'	38:A1:1435:A:OP1	2.26	0.53
38:A1:1001:G:O2'	38:A1:1041:U:OP2	2.27	0.53
38:A1:2197:OMC:H5''	38:A1:2242:A:H61	1.72	0.53
38:A1:3092:C:O2'	38:A1:3094:A:OP2	2.19	0.53
47:AJ:82:ARG:HH21	47:AJ:112:LEU:HD22	1.74	0.53
34:B5:1163:A:N3	34:B5:1613:U:O2'	2.38	0.52
36:AB:62:ARG:NH1	38:A1:3039:C:OP1	2.39	0.52
38:A1:86:G:O2'	38:A1:98:G:O6	2.27	0.52
38:A1:673:U:H2'	38:A1:674:G:C8	2.44	0.52
38:A1:1447:G:N7	52:AP:25:SER:OG	2.42	0.52
51:AO:65[A]:ASN:HB3	51:AO:68[A]:ARG:HG2	1.91	0.52
58:AV:18:PRO:HA	58:AV:51:ALA:HA	1.91	0.52
5:BG:211:LEU:HD11	5:BG:215:ARG:HE	1.73	0.52
28:BZ:90:LYS:HG3	28:BZ:104:ALA:HA	1.90	0.52
31:Bg:295:SER:OG	31:Bg:296:ALA:N	2.41	0.52
34:B5:1171:A:H2'	34:B5:1172:G:C8	2.44	0.52
36:AB:250:ALA:HB3	38:A1:2880:U:H1'	1.91	0.52
38:A1:943:U:H3'	63:Aa:13:GLY:HA2	1.91	0.52
42:AE:172:HIS:ND1	68:Af:40:ASP:OD1	2.42	0.52
21:BK:1:MET:O	21:BK:44:LYS:NZ	2.43	0.52
27:BU:64:LYS:NZ	34:B5:1486:G:OP1	2.42	0.52
38:A1:1071:U:H3	38:A1:1087:G:H1	1.56	0.52
38:A1:1235:U:H4'	38:A1:1236:G:H3'	1.92	0.52
38:A1:1786:G:H2'	38:A1:1787:A:C8	2.45	0.52
38:A1:3119:U:H4'	75:Am:104:PRO:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:Ag:3:GLN:HE22	69:Ag:29:ILE:HB	1.75	0.52
2:BB:23:PRO:HB3	2:BB:26:ARG:HH21	1.75	0.52
20:BF:95:ASN:O	34:B5:1611:A:O2'	2.27	0.52
38:A1:2452:G:N7	38:A1:2462:A:N6	2.57	0.52
40:A4:8:C:H2'	40:A4:9:A:C8	2.45	0.52
2:BB:110:LEU:HD11	2:BB:213:ARG:HD2	1.90	0.52
34:B5:814:A:H3'	54:AR:167:ARG:HG3	1.91	0.52
36:AB:19:ARG:NH2	38:A1:3045:G:OP1	2.41	0.52
38:A1:1389:G:OP1	67:Ae:104:ASN:ND2	2.37	0.52
38:A1:2219:A:H2'	38:A1:2220:A2M:H8	1.91	0.52
38:A1:2883:U:H2'	38:A1:2884:C:H6	1.74	0.52
40:A4:103:G:OP2	40:A4:105:A:O2'	2.27	0.52
46:AI:38:LYS:HG3	46:AI:41:ALA:HB2	1.89	0.52
46:AI:49:CYS:HB3	46:AI:168:SER:HB3	1.91	0.52
47:AJ:16:LYS:HG3	47:AJ:70:THR:HG23	1.91	0.52
54:AR:173:ARG:HD2	54:AR:174:ALA:N	2.25	0.52
8:BJ:17:ARG:NH1	34:B5:3:U:O2	2.42	0.52
10:BN:11:ILE:HG13	10:BN:12:SER:H	1.75	0.52
34:B5:436:A2M:H8	34:B5:436:A2M:O5'	2.09	0.52
35:AA:241:ARG:NH1	38:A1:2155:G:OP1	2.43	0.52
38:A1:2768:U:H2'	38:A1:2769:A:H8	1.73	0.52
50:AN:137:PRO:O	50:AN:143:ARG:NH1	2.40	0.52
62:AZ:50:PRO:HD3	62:AZ:68:ILE:HG12	1.91	0.52
80:EC:6853:G:H22	80:EC:6875:C:H42	1.57	0.52
5:BG:174:LYS:HG3	34:B5:78:A:H2	1.75	0.52
24:BR:17:ILE:HD11	24:BR:54:THR:HG23	1.92	0.52
26:BT:89:ARG:NH1	34:B5:1562:G:OP1	2.43	0.52
31:Bg:32:LEU:HD21	31:Bg:94:VAL:HG21	1.91	0.52
34:B5:12:U:H2'	34:B5:13:C:C6	2.45	0.52
34:B5:1524:A:H2'	34:B5:1525:A:C8	2.45	0.52
34:B5:1776:A:H2'	34:B5:1777:G:C8	2.45	0.52
38:A1:650:OMC:H2'	38:A1:651:G:C8	2.45	0.52
66:Ad:20:LEU:HD11	66:Ad:32:ALA:HB2	1.90	0.52
7:BI:50:GLY:HA2	34:B5:397:A:H4'	1.90	0.52
34:B5:1220:C:H2'	34:B5:1221:A:H8	1.75	0.52
37:AC:308:LYS:NZ	38:A1:609:G:N7	2.58	0.52
38:A1:251:G:H1'	38:A1:253:A:C4	2.45	0.52
38:A1:1084:A:OP1	56:AT:35:LYS:NZ	2.37	0.52
41:AD:106:ALA:HB2	41:AD:166:ALA:HA	1.92	0.52
9:BL:124:THR:HB	9:BL:141:LYS:HB3	1.91	0.52
18:Be:25:GLU:OE1	34:B5:540:G:N2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1551:C:HO2'	38:A1:2170:U:HO2'	1.56	0.52
51:AO:84[A]:LEU:HD22	51:AO:102[A]:LEU:HD22	1.92	0.52
20:BF:52:GLU:HA	20:BF:65:ARG:HH12	1.75	0.52
43:AF:138:TYR:CD2	43:AF:233:GLU:HB2	2.45	0.52
28:BZ:58:ARG:HG3	80:EC:6863:C:H1'	1.92	0.51
34:B5:1201:G:N2	34:B5:1600:A:O5'	2.43	0.51
34:B5:1672:G:H2'	34:B5:1673:G:C8	2.45	0.51
38:A1:1243:G:N3	38:A1:1270:A:O2'	2.43	0.51
46:AI:140:THR:HG21	46:AI:148:VAL:HG11	1.92	0.51
74:AI:43:ASN:HB3	74:AI:46:ARG:HG3	1.91	0.51
79:E:13:VAL:HG11	79:E:180:VAL:HG22	1.91	0.51
1:BA:126:PRO:HG2	1:BA:151:SER:HB2	1.92	0.51
4:BE:192:ILE:HG13	4:BE:243:GLY:HA3	1.92	0.51
19:BD:80:ALA:O	19:BD:83:THR:OG1	2.26	0.51
25:BS:17:LEU:HB3	25:BS:18:LEU:HD12	1.93	0.51
38:A1:339:C:OP1	38:A1:1380:G:O2'	2.24	0.51
38:A1:1220:U:O4	38:A1:1286:A:O2'	2.25	0.51
1:BA:144:ILE:HG13	1:BA:158:VAL:HB	1.91	0.51
3:BC:201:ASN:ND2	34:B5:607:G:O2'	2.44	0.51
10:BN:11:ILE:HD11	34:B5:1072:C:H4'	1.91	0.51
13:BW:22:LYS:HG2	17:Bb:3:LEU:HA	1.93	0.51
21:BK:25:LYS:HD2	21:BK:59:PHE:HZ	1.74	0.51
26:BT:33:TYR:O	26:BT:36:ILE:HG22	2.11	0.51
38:A1:591:G:O2'	42:AE:17:ALA:O	2.26	0.51
38:A1:1682:U:O4	57:AU:90:ARG:NH1	2.40	0.51
38:A1:2450:G:H2'	38:A1:2451:G:C8	2.45	0.51
46:AI:43:VAL:HG21	46:AI:197:VAL:HB	1.92	0.51
3:BC:78:ASP:HB3	3:BC:104:VAL:HG12	1.91	0.51
13:BW:71:LYS:NZ	34:B5:1096:C:OP2	2.42	0.51
34:B5:416:A:H3'	34:B5:417:A:H8	1.75	0.51
34:B5:1291:G:N2	34:B5:1324:G:H22	2.08	0.51
34:B5:1641:C:H2'	34:B5:1642:G:C8	2.44	0.51
35:AA:112:ILE:HG13	78:Ap:79:VAL:HG22	1.92	0.51
38:A1:370:U:H4'	38:A1:404:G:H5'	1.93	0.51
38:A1:520:U:OP2	43:AF:70:LYS:NZ	2.36	0.51
38:A1:571:U:H2'	38:A1:572:A:H8	1.76	0.51
38:A1:831:G:O2'	38:A1:1864:A:N3	2.39	0.51
38:A1:1119:C:H2'	38:A1:1120:A:H8	1.75	0.51
39:A3:38:U:N3	39:A3:41:G:OP2	2.39	0.51
11:BO:17:ALA:HA	11:BO:30:VAL:HG22	1.92	0.51
31:Bg:31:ASN:HA	31:Bg:47:LEU:HD12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1645:G:H2'	34:B5:1646:C:H6	1.75	0.51
36:AB:36:ASP:HB3	36:AB:39:LYS:HE2	1.93	0.51
36:AB:93:VAL:HG12	36:AB:155:ALA:H	1.76	0.51
38:A1:1620:U:H2'	38:A1:1621:A:C8	2.46	0.51
42:AE:51:ARG:HE	42:AE:163:PHE:HB2	1.74	0.51
72:Aj:25:ARG:HE	74:A1:51:ILE:HG13	1.74	0.51
80:EC:6852:U:H2'	80:EC:6853:G:C8	2.45	0.51
15:BY:109:LYS:NZ	34:B5:459:G:OP1	2.35	0.51
34:B5:1237:G:H2'	34:B5:1238:A:H8	1.76	0.51
38:A1:1107:C:OP2	64:Ab:22:LYS:NZ	2.43	0.51
48:AL:126:PHE:O	70:Ah:114:ARG:NH2	2.38	0.51
54:AR:105:LEU:HD23	54:AR:138:LEU:HD23	1.93	0.51
16:Ba:19:LYS:HD3	16:Ba:20:PRO:HD2	1.92	0.51
21:BK:25:LYS:HB3	21:BK:62:GLN:HB3	1.92	0.51
28:BZ:61:SER:HA	28:BZ:80:LEU:HD21	1.93	0.51
34:B5:800:U:H2'	34:B5:801:G:C8	2.46	0.51
34:B5:1542:G:H22	34:B5:1568:C:H1'	1.76	0.51
38:A1:2960:C:H2'	38:A1:2961:G:H8	1.74	0.51
47:AJ:125:MET:HG2	47:AJ:126:ASP:H	1.75	0.51
52:AP:16:SER:O	52:AP:101:ASN:ND2	2.44	0.51
53:AQ:62:VAL:HG13	53:AQ:66:ARG:HD2	1.92	0.51
2:BB:27:LYS:HD2	2:BB:47:LEU:HG	1.93	0.51
3:BC:43:ARG:HE	3:BC:248:SER:H	1.57	0.51
8:BJ:31:ALA:HA	8:BJ:36:LEU:HD12	1.93	0.51
34:B5:272:U:H5'	34:B5:273:G:H5'	1.93	0.51
34:B5:939:A:H2'	34:B5:940:A:C8	2.46	0.51
34:B5:1553:G:N1	34:B5:1556:A:OP2	2.43	0.51
34:B5:1575:G7M:H2'	34:B5:1576:A:H8	1.75	0.51
55:AS:8:GLN:HB3	55:AS:62:ASN:HB2	1.93	0.51
1:BA:126:PRO:HD3	1:BA:145:ALA:HB1	1.92	0.51
2:BB:48:VAL:HG21	2:BB:61:LEU:HD11	1.93	0.51
38:A1:3266:G:OP2	42:AE:70:LYS:NZ	2.43	0.51
49:AM:60:LEU:HD13	55:AS:152:LEU:HD11	1.92	0.51
57:AU:18:ASP:HA	57:AU:62:VAL:HG22	1.92	0.51
4:BE:27:TYR:O	34:B5:447:U:O2'	2.27	0.51
8:BJ:9:SER:OG	34:B5:771:A:OP1	2.29	0.51
19:BD:137:VAL:HG22	19:BD:151:LYS:HG2	1.93	0.51
28:BZ:40:VAL:HG23	28:BZ:41:ILE:HG12	1.93	0.51
34:B5:609:U:H4'	34:B5:610:G:H5'	1.91	0.51
20:BF:51:VAL:HG11	20:BF:130:ILE:HG22	1.93	0.50
38:A1:2451:G:H8	38:A1:2451:G:O5'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:AJ:96:PHE:HB2	47:AJ:156:LYS:HE3	1.92	0.50
47:AJ:106:ILE:HD11	47:AJ:109:HIS:ND1	2.25	0.50
71:Ai:95:ALA:HB1	71:Ai:99:ARG:HH21	1.75	0.50
7:BI:166:TYR:HB3	7:BI:184:LEU:HD12	1.92	0.50
34:B5:89:G:H21	34:B5:452:A:H5'	1.76	0.50
34:B5:1591:C:H2'	34:B5:1592:A:H8	1.75	0.50
36:AB:232:ARG:NH1	36:AB:266:ARG:O	2.44	0.50
38:A1:1152:G:OP2	38:A1:1152:G:N2	2.39	0.50
38:A1:1718:G:H2'	38:A1:1719:G:C8	2.46	0.50
38:A1:2747:A:H2'	38:A1:2748:A:C8	2.47	0.50
42:AE:51:ARG:HB3	42:AE:159:LEU:HD23	1.93	0.50
50:AN:159:ARG:HB3	50:AN:164:LEU:HB2	1.93	0.50
8:BJ:157:ASP:OD1	8:BJ:158:PHE:N	2.42	0.50
10:BN:104:ARG:NH2	34:B5:951:A:OP1	2.34	0.50
38:A1:63:A:N3	38:A1:78:U:O2'	2.40	0.50
38:A1:2798:C:H5''	38:A1:2800:G:H5'	1.91	0.50
40:A4:23:U:H5''	61:AY:13:ARG:HG3	1.93	0.50
4:BE:182:TYR:HD1	4:BE:192:ILE:HG12	1.75	0.50
7:BI:26:LYS:HG2	7:BI:29:LEU:HD23	1.93	0.50
19:BD:183:GLY:H	34:B5:1277:G:H4'	1.76	0.50
34:B5:1290:U:H2'	34:B5:1291:G:C8	2.47	0.50
36:AB:77:THR:HG21	36:AB:328:ILE:HG12	1.93	0.50
38:A1:129:U:H2'	38:A1:130:A:C8	2.47	0.50
38:A1:2697:A:H2'	38:A1:2698:G:C8	2.46	0.50
38:A1:3193:C:H2'	38:A1:3194:C:C6	2.47	0.50
7:BI:10:LYS:NZ	34:B5:322:G:O2'	2.44	0.50
38:A1:2549:G:O2'	44:AG:38:GLN:NE2	2.44	0.50
52:AP:122:ALA:HB3	52:AP:143:PRO:HB2	1.94	0.50
29:Bc:14:LYS:HB3	29:Bc:29:ARG:HB3	1.93	0.50
34:B5:146:U:H2'	34:B5:147:A:H8	1.77	0.50
34:B5:1488:G:H3'	34:B5:1515:A:H61	1.76	0.50
38:A1:901:G:OP1	72:Aj:12:HIS:NE2	2.37	0.50
38:A1:1740:U:H4'	38:A1:1741:A:H5'	1.94	0.50
38:A1:2496:C:O2'	38:A1:2497:U:O5'	2.29	0.50
38:A1:3252:G:H2'	38:A1:3253:G:C8	2.47	0.50
80:EC:6770:U:H3	80:EC:6772:G:H21	1.58	0.50
1:BA:27:ARG:HE	1:BA:44:GLY:HA3	1.77	0.50
1:BA:139:VAL:HG23	1:BA:141:ILE:HG13	1.93	0.50
12:BV:5:LYS:NZ	12:BV:7:GLN:OE1	2.45	0.50
31:Bg:220:ILE:HB	31:Bg:234:LEU:HB2	1.94	0.50
36:AB:58:ARG:HD2	36:AB:354:VAL:HG13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:AC:265:GLU:HG2	37:AC:266:THR:HG23	1.93	0.50
38:A1:528:U:H2'	38:A1:529:A:C8	2.47	0.50
38:A1:1596:C:O2'	38:A1:1696:A:N3	2.45	0.50
38:A1:1688:U:H2'	38:A1:1689:U:C6	2.47	0.50
38:A1:3354:U:H4'	38:A1:3355:U:H4'	1.92	0.50
34:B5:17:C:H2'	34:B5:18:C:C6	2.47	0.50
34:B5:52:U:H2'	34:B5:53:G:C8	2.47	0.50
34:B5:651:G:H22	34:B5:682:C:H42	1.59	0.50
34:B5:852:C:O2'	34:B5:853:G:O4'	2.30	0.50
34:B5:953:G:H2'	34:B5:954:G:H8	1.76	0.50
38:A1:776:U:OP1	64:Ab:41:ARG:NH1	2.45	0.50
38:A1:900:G:H1'	38:A1:1589:A:N6	2.26	0.50
38:A1:2491:A:O3'	79:E:35:GLN:NE2	2.37	0.50
38:A1:2697:A:H2'	38:A1:2698:G:H8	1.77	0.50
20:BF:187:ILE:HG12	28:BZ:66:VAL:HG11	1.93	0.50
21:BK:92:ILE:HD11	21:BK:96:ASN:HA	1.93	0.50
26:BT:43:ASN:ND2	34:B5:1477:G:OP1	2.43	0.50
34:B5:73:U:O2'	34:B5:74:U:O4'	2.30	0.50
34:B5:891:A:H2'	34:B5:892:A:C8	2.47	0.50
38:A1:1593:A:H2'	38:A1:1594:A:C8	2.47	0.50
38:A1:1597:C:H2'	38:A1:1598:G:C8	2.47	0.50
51:AO:35[A]:VAL:HG21	51:AO:80[A]:PHE:HE2	1.77	0.50
23:BQ:73:GLY:H	23:BQ:76:SER:HB2	1.77	0.49
31:Bg:90:ARG:HH22	34:B5:1341:A:H4'	1.75	0.49
38:A1:1687:U:O4	57:AU:45:GLY:N	2.43	0.49
38:A1:2588:U:OP1	44:AG:241:LYS:NZ	2.44	0.49
55:AS:12:ARG:HB3	55:AS:24:LEU:HA	1.94	0.49
62:AZ:22:LYS:NZ	62:AZ:129:TRP:O	2.36	0.49
77:Ao:4:VAL:O	77:Ao:94:GLY:N	2.44	0.49
4:BE:103:TYR:O	4:BE:182:TYR:OH	2.29	0.49
5:BG:94:ARG:NH2	34:B5:406:U:O2'	2.45	0.49
8:BJ:132:ARG:NH2	34:B5:532:U:OP1	2.43	0.49
25:BS:88:ARG:NH1	25:BS:91:ASP:OD1	2.45	0.49
34:B5:1370:U:H3	34:B5:1374:C:H41	1.60	0.49
37:AC:358:THR:HG21	56:AT:148:PRO:HG2	1.94	0.49
38:A1:1242:G:H22	38:A1:1270:A:H1'	1.76	0.49
38:A1:2228:A:H2'	38:A1:2229:A:C8	2.48	0.49
38:A1:2768:U:H2'	38:A1:2769:A:C8	2.47	0.49
38:A1:3294:A:H2'	38:A1:3295:A:O4'	2.12	0.49
41:AD:277:LEU:HB3	41:AD:281:GLU:HG3	1.94	0.49
4:BE:3:ARG:NH1	34:B5:402:C:OP1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:19:SER:OG	10:BN:21:ASN:O	2.29	0.49
16:Ba:84:VAL:O	34:B5:1797:A:N6	2.42	0.49
38:A1:673:U:H2'	38:A1:674:G:H8	1.77	0.49
38:A1:1724:U:H1'	38:A1:1725:C:C6	2.47	0.49
19:BD:190:ARG:HH12	19:BD:195:SER:HB3	1.78	0.49
22:BP:76:VAL:O	22:BP:95:GLY:N	2.44	0.49
34:B5:1213:G:O2'	34:B5:1244:A:N7	2.45	0.49
35:AA:183:GLY:HA2	38:A1:896:A:H5''	1.93	0.49
38:A1:307:A:H2'	38:A1:308:A:H8	1.77	0.49
38:A1:2629:U:O4	56:AT:2:GLY:N	2.44	0.49
58:AV:109:MET:SD	58:AV:132:ASN:ND2	2.78	0.49
20:BF:190:ILE:HG12	34:B5:1473:U:C5	2.48	0.49
24:BR:102:VAL:HG21	24:BR:119:LEU:HD23	1.93	0.49
34:B5:513:U:H2'	34:B5:514:G:C8	2.46	0.49
34:B5:953:G:H2'	34:B5:954:G:C8	2.47	0.49
34:B5:1146:G:H2'	34:B5:1147:A:C8	2.48	0.49
36:AB:83:PRO:O	36:AB:165:GLN:NE2	2.43	0.49
38:A1:567:G:H2'	38:A1:568:G:C8	2.47	0.49
41:AD:215:ASP:OD1	41:AD:215:ASP:N	2.45	0.49
68:Af:53:TYR:HE1	68:Af:67:MET:HG3	1.78	0.49
24:BR:102:VAL:HB	24:BR:106:THR:HG23	1.95	0.49
34:B5:590:C:H2'	34:B5:591:A:C8	2.48	0.49
38:A1:633:C:O2'	68:Af:21:ARG:O	2.24	0.49
38:A1:718:G:OP1	63:Aa:117:ARG:NH2	2.38	0.49
49:AM:109:ARG:HA	49:AM:112:LEU:HD13	1.95	0.49
3:BC:116:LYS:HG2	3:BC:127:ALA:HB3	1.94	0.49
17:Bb:36:LYS:HB2	17:Bb:78:SER:HB3	1.94	0.49
19:BD:105:MET:HG3	19:BD:184:ILE:HD13	1.93	0.49
22:BP:42:ARG:NH2	34:B5:1550:A:OP2	2.45	0.49
34:B5:319:U:H4'	34:B5:323:A:C8	2.48	0.49
34:B5:924:A:H2'	34:B5:925:G:C8	2.47	0.49
38:A1:2538:U:OP1	38:A1:2539:C:N4	2.45	0.49
38:A1:3175:U:OP1	68:Af:10:LYS:NZ	2.34	0.49
2:BB:153:HIS:NE2	34:B5:1045:C:OP1	2.31	0.49
3:BC:87:GLN:OE1	34:B5:10:G:O2'	2.28	0.49
14:BX:90:ASP:HA	34:B5:568:G:H4'	1.94	0.49
35:AA:118:GLU:OE2	38:A1:2177:G:N2	2.42	0.49
38:A1:292:U:OP2	50:AN:68:ARG:NH2	2.45	0.49
48:AL:180:ARG:HD3	71:Ai:11:LEU:HD11	1.94	0.49
61:AY:74:TYR:HD2	61:AY:77:LYS:HG2	1.76	0.49
16:Ba:70:LYS:NZ	34:B5:933:A:OP1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1142:A:H2'	34:B5:1143:A:C8	2.48	0.49
34:B5:1297:G:N2	34:B5:1300:A:OP2	2.29	0.49
38:A1:531:G:H2'	38:A1:532:A:C8	2.48	0.49
38:A1:994:G:N2	38:A1:995:U:O4	2.38	0.49
38:A1:3231:U:H2'	38:A1:3232:G:H8	1.76	0.49
44:AG:185:ARG:O	44:AG:188:THR:OG1	2.30	0.49
5:BG:92:ARG:NH1	34:B5:1674:C:OP1	2.38	0.49
25:BS:127:HIS:CD2	25:BS:133:VAL:HG11	2.48	0.49
34:B5:1697:G:O6	34:B5:1704:U:O4	2.31	0.49
35:AA:95:SER:OG	35:AA:97:ASN:OD1	2.29	0.49
38:A1:75:G:H5'	48:AL:58:VAL:HB	1.95	0.49
38:A1:655:C:H5''	67:Ae:26:HIS:HB3	1.94	0.49
38:A1:1108:U:H2'	38:A1:1109:U:C6	2.48	0.49
38:A1:1114:U:OP1	63:Aa:23:GLY:N	2.36	0.49
38:A1:1245:A:N7	38:A1:1271:A:O2'	2.45	0.49
38:A1:2444:C:N4	38:A1:2503:G:H22	2.07	0.49
38:A1:3183:A:H2	38:A1:3188:G:H4'	1.78	0.49
79:E:169:VAL:HG11	79:E:183:ILE:HG22	1.95	0.49
80:EC:6844:A:H1'	80:EC:6845:G:C8	2.48	0.49
7:BI:105:ASP:HB3	7:BI:107:THR:HG22	1.95	0.48
19:BD:40:ARG:HG2	27:BU:110:PRO:HB3	1.95	0.48
24:BR:24:LEU:HD13	24:BR:34:LEU:HD12	1.95	0.48
26:BT:129:GLN:NE2	34:B5:1358:G:O2'	2.46	0.48
38:A1:1412:G:OP1	67:Ae:105:ARG:NH1	2.43	0.48
38:A1:2152:A:H2'	38:A1:2153:U:H6	1.77	0.48
52:AP:102:ALA:HB1	52:AP:107:LEU:HB2	1.95	0.48
58:AV:38:ALA:HB3	58:AV:59:MET:HB2	1.94	0.48
2:BB:29:TRP:CE2	2:BB:47:LEU:HD13	2.47	0.48
3:BC:111:VAL:HG21	3:BC:218:ILE:HD12	1.96	0.48
22:BP:16:SER:HA	22:BP:21:ASP:HA	1.95	0.48
24:BR:32:LYS:NZ	34:B5:1387:G:OP1	2.38	0.48
25:BS:36:LYS:HB3	25:BS:102:ALA:HA	1.95	0.48
32:Bf:134:ASN:ND2	32:Bf:138:ARG:O	2.41	0.48
34:B5:1114:G:O2'	34:B5:1130:G:O6	2.29	0.48
35:AA:206:PRO:HG3	35:AA:213:GLY:HA3	1.95	0.48
38:A1:627:U:H2'	38:A1:628:A:C8	2.48	0.48
38:A1:1240:A:H2'	38:A1:1241:U:C6	2.49	0.48
4:BE:45:ILE:HG13	4:BE:61:VAL:HG21	1.95	0.48
4:BE:67:GLN:HE22	15:BY:85:PHE:HE1	1.60	0.48
25:BS:92:ILE:HG21	25:BS:115:ARG:HH12	1.77	0.48
30:Bd:54:LYS:NZ	34:B5:1420:C:OP1	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:5:U:H2'	34:B5:6:G:C8	2.48	0.48
34:B5:209:U:H2'	34:B5:210:A:H8	1.78	0.48
37:AC:59:GLN:NE2	38:A1:347:G:OP1	2.46	0.48
38:A1:643:U:O2'	38:A1:1153:A:N1	2.41	0.48
38:A1:716:A:C5	63:Aa:117:ARG:HG3	2.49	0.48
38:A1:723:U:O2'	64:Ab:29:TYR:OH	2.31	0.48
38:A1:1447:G:H3'	52:AP:67:ILE:HD11	1.95	0.48
41:AD:256:THR:OG1	41:AD:258:LYS:NZ	2.39	0.48
13:BW:107:SER:OG	34:B5:802:G:N2	2.42	0.48
17:Bb:19:HIS:HD2	17:Bb:21:LEU:H	1.62	0.48
34:B5:1357:A:H2'	34:B5:1358:G:H8	1.77	0.48
38:A1:1684:U:OP1	57:AU:86:LYS:NZ	2.45	0.48
38:A1:2724:OMU:OP1	56:AT:78:LYS:NZ	2.44	0.48
38:A1:2745:G:N2	38:A1:2748:A:OP2	2.45	0.48
41:AD:116:ASP:OD1	41:AD:117:GLU:N	2.47	0.48
50:AN:5:LYS:HG3	71:Ai:40:VAL:HG11	1.95	0.48
2:BB:70:LEU:HD13	2:BB:84:ILE:HG13	1.95	0.48
4:BE:131:LEU:HD12	34:B5:251:A:H2	1.78	0.48
5:BG:64:LYS:NZ	5:BG:82:SER:OG	2.46	0.48
25:BS:27:LYS:HE2	25:BS:55:HIS:HA	1.95	0.48
35:AA:2:GLY:O	38:A1:925:A:N6	2.38	0.48
38:A1:1696:A:H2'	38:A1:1697:A:C8	2.48	0.48
39:A3:84:A:H2'	39:A3:85:G:C8	2.48	0.48
69:Ag:79:SER:HB3	69:Ag:80:ARG:HH11	1.79	0.48
80:EC:6759:A:H2'	80:EC:6760:A:C8	2.49	0.48
3:BC:205:ARG:NH2	34:B5:7:G:O6	2.47	0.48
7:BI:87:ASN:HB3	7:BI:90:LEU:HG	1.95	0.48
14:BX:96:VAL:HA	14:BX:127:VAL:HG21	1.96	0.48
27:BU:26:LEU:HG	27:BU:114:VAL:HG12	1.94	0.48
34:B5:590:C:H2'	34:B5:591:A:H8	1.79	0.48
36:AB:315:GLY:HA2	38:A1:3379:C:H4'	1.95	0.48
41:AD:34:LYS:HE2	41:AD:38:THR:HG21	1.95	0.48
41:AD:160:PHE:HA	41:AD:163:LEU:HB3	1.95	0.48
13:BW:30:SER:HB2	13:BW:61:ILE:HG13	1.95	0.48
32:Bf:140:TYR:HH	34:B5:1234:A:HO2'	1.58	0.48
34:B5:16:G:H2'	34:B5:17:C:C6	2.49	0.48
38:A1:12:A:H2'	38:A1:13:A:C8	2.48	0.48
38:A1:428:A:H2'	38:A1:429:U:C6	2.49	0.48
38:A1:1659:U:H2'	38:A1:1660:C:C6	2.48	0.48
38:A1:2465:G:O2'	79:E:60:ARG:NH1	2.47	0.48
42:AE:45:GLY:O	42:AE:48:ARG:NH1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:AY:29:VAL:O	61:AY:32:SER:OG	2.29	0.48
62:AZ:33:SER:OG	62:AZ:35:SER:O	2.24	0.48
74:A1:28:ARG:NH2	74:A1:36:ARG:O	2.42	0.48
2:BB:82:ARG:HG2	2:BB:105:PHE:CE1	2.48	0.48
5:BG:123:GLY:O	5:BG:127:THR:OG1	2.32	0.48
20:BF:40:ILE:HG23	20:BF:67:PRO:HG2	1.96	0.48
34:B5:647:G:H21	34:B5:687:G:H1	1.60	0.48
36:AB:218:ILE:HB	36:AB:337:THR:HB	1.96	0.48
37:AC:47:ARG:NH2	37:AC:109:TRP:O	2.38	0.48
37:AC:95:ARG:HG3	38:A1:343:U:H1'	1.96	0.48
47:AJ:132:ASN:HA	47:AJ:154:THR:HG21	1.96	0.48
79:E:207:LYS:NZ	79:E:209:SER:O	2.46	0.48
9:BL:129:ARG:HD3	34:B5:115:G:H5'	1.96	0.48
15:BY:34:ASN:O	34:B5:521:A:O2'	2.31	0.48
22:BP:41:VAL:HG22	22:BP:84:ILE:HD13	1.95	0.48
22:BP:98:ASN:ND2	22:BP:121:ILE:O	2.29	0.48
28:BZ:53:GLU:OE2	80:EC:6865:G:N1	2.38	0.48
34:B5:1071:U:H2'	34:B5:1072:C:C6	2.48	0.48
34:B5:1591:C:H2'	34:B5:1592:A:C8	2.48	0.48
38:A1:1145:G:O2'	67:Ae:45:ARG:O	2.29	0.48
38:A1:1181:U:H6	51:AO:122[A]:GLN:HE21	1.61	0.48
41:AD:211:LEU:HD12	41:AD:223:PHE:HE2	1.79	0.48
4:BE:211:LYS:NZ	4:BE:215:ASP:OD1	2.47	0.48
11:BO:88:GLY:O	11:BO:92:LYS:NZ	2.27	0.48
17:Bb:67:THR:OG1	17:Bb:70:LYS:O	2.32	0.48
26:BT:69:LYS:HG2	34:B5:1367:G:H5''	1.95	0.48
34:B5:29:U:H2'	34:B5:30:G:H8	1.79	0.48
34:B5:209:U:H2'	34:B5:210:A:C8	2.49	0.48
38:A1:2501:U:H3'	38:A1:2502:A:H8	1.79	0.48
63:Aa:26:ARG:HB2	63:Aa:29:PRO:HG3	1.96	0.48
80:EC:6773:G:O2'	80:EC:6819:G:OP1	2.31	0.48
5:BG:142:ARG:NH1	5:BG:148:SER:O	2.47	0.47
6:BH:47:ARG:HB3	6:BH:59:ALA:HB3	1.96	0.47
23:BQ:25:GLY:HA3	23:BQ:64:ASP:OD2	2.14	0.47
25:BS:15:LEU:HD13	25:BS:17:LEU:HD13	1.96	0.47
26:BT:72:GLY:HA3	34:B5:1498:G:H5''	1.95	0.47
34:B5:980:G:H4'	34:B5:1776:A:H4'	1.96	0.47
34:B5:1158:C:O2'	34:B5:1581:C:OP2	2.30	0.47
34:B5:1477:G:H2'	34:B5:1478:G:C8	2.48	0.47
35:AA:142:ASP:OD1	35:AA:142:ASP:N	2.46	0.47
36:AB:30:LYS:NZ	38:A1:3139:A:OP2	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2476:C:N4	38:A1:2477:G:O6	2.47	0.47
38:A1:2680:A:OP1	47:AJ:51:ARG:NH2	2.46	0.47
77:Ao:2:VAL:N	77:Ao:90:HIS:O	2.47	0.47
20:BF:95:ASN:HA	20:BF:98:MET:HE2	1.96	0.47
31:Bg:38:ARG:HG3	31:Bg:67:ILE:HG12	1.96	0.47
34:B5:688:G:H2'	34:B5:689:G:H8	1.79	0.47
34:B5:1056:U:H3'	34:B5:1056:U:OP2	2.14	0.47
37:AC:58:HIS:HE1	38:A1:933:A:C8	2.33	0.47
37:AC:328:ASN:ND2	43:AF:182:ASP:OD2	2.46	0.47
38:A1:126:U:OP1	50:AN:144:ARG:NH1	2.47	0.47
38:A1:411:U:H2'	38:A1:412:G:C8	2.49	0.47
38:A1:1667:A:H2'	38:A1:1668:G:C8	2.49	0.47
38:A1:1799:A:H2'	38:A1:1800:A:H8	1.78	0.47
38:A1:2167:A:H2'	38:A1:2168:A:C8	2.49	0.47
38:A1:2364:G:H22	38:A1:2396:G:H1'	1.80	0.47
38:A1:2499:U:H2'	38:A1:2500:A:C5	2.50	0.47
62:AZ:121:ARG:HE	62:AZ:126:LYS:HD2	1.79	0.47
2:BB:216:LYS:NZ	34:B5:885:G:OP1	2.39	0.47
11:BO:121:VAL:O	34:B5:886:U:O2'	2.31	0.47
15:BY:51:GLU:HG3	15:BY:53:ASP:H	1.79	0.47
28:BZ:61:SER:H	28:BZ:64:VAL:HG12	1.79	0.47
34:B5:126:A:H62	34:B5:291:G:H21	1.60	0.47
37:AC:119:ARG:NH2	38:A1:696:C:OP2	2.44	0.47
37:AC:159:ILE:HG23	37:AC:164:GLU:HG3	1.96	0.47
38:A1:268:A:N1	38:A1:295:A:H5'	2.29	0.47
38:A1:1378:U:H2'	38:A1:1379:G:H8	1.78	0.47
38:A1:2435:G:O2'	50:AN:24:ARG:NH1	2.41	0.47
67:Ae:79:VAL:HG13	67:Ae:111:ARG:HG2	1.95	0.47
17:Bb:19:HIS:CD2	17:Bb:21:LEU:H	2.31	0.47
19:BD:172:THR:O	19:BD:173:ARG:NH1	2.41	0.47
20:BF:109:LYS:HB2	20:BF:109:LYS:HE3	1.69	0.47
23:BQ:128:LYS:HB2	23:BQ:137:ARG:HH22	1.80	0.47
26:BT:108:LEU:HB3	26:BT:113:ILE:HB	1.96	0.47
34:B5:923:A:H2'	34:B5:924:A:C8	2.49	0.47
35:AA:80:GLU:HG2	78:Ap:76:ALA:CB	2.45	0.47
38:A1:631:U:H2'	38:A1:632:G:H8	1.77	0.47
38:A1:662:U:H2'	38:A1:663:OMC:C6	2.49	0.47
38:A1:876:A2M:H5''	38:A1:1890:U:H5''	1.96	0.47
38:A1:959:C:O2'	38:A1:2410:U:N3	2.45	0.47
38:A1:1621:A:H2'	38:A1:1622:U:C6	2.49	0.47
38:A1:3034:C:H41	45:AH:121:LYS:HG2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:BL:66:ILE:HD11	9:BL:138:ASN:HB2	1.96	0.47
23:BQ:39:VAL:O	23:BQ:45:ARG:NH1	2.47	0.47
34:B5:71:A:H2'	34:B5:72:A:H4'	1.97	0.47
34:B5:625:C:H2'	34:B5:626:U:C6	2.50	0.47
35:AA:9:ARG:NH2	38:A1:912:G:OP2	2.35	0.47
35:AA:113:VAL:HG12	35:AA:166:ILE:HD13	1.96	0.47
38:A1:3291:G:H2'	38:A1:3292:A:H8	1.80	0.47
39:A3:121:U:OP2	41:AD:265:TYR:OH	2.29	0.47
40:A4:149:A:H2'	40:A4:150:G:C8	2.50	0.47
49:AM:48:GLY:HA3	49:AM:53:VAL:HB	1.96	0.47
10:BN:14:SER:HB2	34:B5:959:U:H5''	1.97	0.47
25:BS:126:ARG:HB2	25:BS:133:VAL:HG12	1.97	0.47
26:BT:42:GLY:HA2	26:BT:84:LYS:HG3	1.96	0.47
26:BT:50:ALA:HA	26:BT:53:TRP:HD1	1.79	0.47
27:BU:96:PRO:HD2	27:BU:99:ILE:HB	1.96	0.47
34:B5:1471:A:H2	34:B5:1474:G:N3	2.11	0.47
38:A1:2406:C:O2'	38:A1:2619:OMG:N2	2.47	0.47
38:A1:2457:G:O2'	38:A1:2482:U:O2	2.32	0.47
38:A1:2869:U:O2'	38:A1:2873:U:OP1	2.33	0.47
38:A1:2930:A:H2'	38:A1:2931:C:C6	2.49	0.47
45:AH:16:VAL:HG12	45:AH:29:GLY:HA3	1.97	0.47
79:E:57:ASN:OD1	79:E:182:GLN:NE2	2.46	0.47
2:BB:165:ARG:NH1	34:B5:947:U:OP1	2.48	0.47
4:BE:22:LYS:N	34:B5:773:C:OP1	2.46	0.47
4:BE:182:TYR:CD1	4:BE:192:ILE:HG12	2.49	0.47
7:BI:76:THR:HG21	7:BI:104:ILE:HD12	1.97	0.47
20:BF:63:GLN:NE2	20:BF:66:GLN:HB3	2.29	0.47
22:BP:40:ARG:NH2	34:B5:1553:G:O6	2.45	0.47
34:B5:199:G:H2'	34:B5:200:A:H8	1.80	0.47
34:B5:1160:A:H2'	34:B5:1161:C:C6	2.50	0.47
34:B5:1178:G:H5'	34:B5:1190:C:H42	1.80	0.47
34:B5:1619:C:H2'	34:B5:1620:C:H6	1.80	0.47
38:A1:82:C:H4'	50:AN:204:LYS:HE3	1.96	0.47
38:A1:503:C:H2'	38:A1:504:A:H8	1.79	0.47
38:A1:1597:C:H5'	38:A1:1696:A:H1'	1.97	0.47
38:A1:1612:A:H5''	73:AK:51:LEU:HD22	1.95	0.47
38:A1:1694:U:H5	38:A1:1752:A:N1	2.12	0.47
38:A1:1950:U:H3	38:A1:2096:A:H62	1.63	0.47
38:A1:2197:OMC:N4	38:A1:2241:U:H2'	2.29	0.47
38:A1:2219:A:H2'	38:A1:2220:A2M:C8	2.45	0.47
38:A1:2366:C:H2'	38:A1:2367:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2413:A:H2'	38:A1:2414:G:H8	1.80	0.47
38:A1:2526:C:H2'	38:A1:2527:G:C8	2.50	0.47
39:A3:4:U:H2'	39:A3:5:G:C8	2.50	0.47
41:AD:65:ILE:HG12	41:AD:74:VAL:HG22	1.97	0.47
61:AY:27:ARG:HA	61:AY:30:LEU:HD12	1.96	0.47
79:E:59:PRO:HA	79:E:170:GLY:HA2	1.96	0.47
2:BB:119:THR:HG21	2:BB:161:ILE:HD11	1.95	0.47
14:BX:54:LEU:HD11	14:BX:75:GLN:HB2	1.97	0.47
23:BQ:12:LYS:NZ	23:BQ:17:THR:OG1	2.43	0.47
34:B5:884:A:H2'	34:B5:885:G:C8	2.50	0.47
34:B5:1175:U:H2'	34:B5:1176:G:C8	2.50	0.47
34:B5:1466:G:O2'	34:B5:1602:C:OP1	2.23	0.47
38:A1:1090:G:H2'	38:A1:1091:A:H8	1.79	0.47
39:A3:12:U:OP2	39:A3:68:C:O2'	2.32	0.47
40:A4:142:C:H2'	40:A4:143:U:C6	2.49	0.47
42:AE:59:GLU:OE1	42:AE:59:GLU:N	2.48	0.47
56:AT:39:ILE:HD12	56:AT:102:ARG:HD3	1.96	0.47
34:B5:276:C:O2'	34:B5:278:U:OP2	2.25	0.47
36:AB:126:LYS:NZ	38:A1:3294:A:OP2	2.39	0.47
38:A1:255:A:H2'	38:A1:256:G:C8	2.50	0.47
38:A1:1196:C:OP1	38:A1:1309:U:O2'	2.28	0.47
38:A1:1534:A:H2'	38:A1:1535:A:C8	2.49	0.47
38:A1:1750:A:OP1	73:Ak:44:LYS:NZ	2.35	0.47
38:A1:2495:C:H2'	38:A1:2496:C:C6	2.50	0.47
44:AG:74:THR:HG22	44:AG:164:VAL:HG22	1.97	0.47
51:AO:189[A]:ASP:OD1	51:AO:190[A]:VAL:N	2.48	0.47
3:BC:230:TRP:CD2	13:BW:68:ARG:HD2	2.50	0.47
15:BY:57:VAL:HB	15:BY:60:PHE:CE2	2.51	0.47
17:Bb:38:PRO:HD3	17:Bb:77:THR:HG22	1.96	0.47
23:BQ:22:VAL:HG22	23:BQ:65:ILE:HG12	1.96	0.47
26:BT:76:LEU:HD23	26:BT:79:LEU:HD13	1.97	0.47
26:BT:133:ASP:OD2	34:B5:1359:C:O2'	2.33	0.47
31:Bg:39:ASP:OD1	31:Bg:41:THR:OG1	2.26	0.47
38:A1:1230:G:N2	38:A1:1260:A:O2'	2.48	0.47
38:A1:1506:A:OP2	52:AP:127:ARG:NH1	2.47	0.47
38:A1:1657:C:O2'	38:A1:1797:A:OP2	2.24	0.47
38:A1:1737:U:O2	69:Ag:52:GLN:NE2	2.48	0.47
38:A1:2639:G:H2'	38:A1:2640:A2M:H8	1.96	0.47
38:A1:2812:C:H2'	38:A1:2813:A:C8	2.49	0.47
43:AF:88:ARG:HA	43:AF:134:VAL:HG12	1.96	0.47
51:AO:12[A]:LYS:HD3	51:AO:37[A]:ARG:HH22	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:AV:83:LYS:NZ	58:AV:84:SER:O	2.40	0.47
80:EC:6944:U:H2'	80:EC:6945:U:H4'	1.97	0.47
2:BB:180:THR:O	2:BB:183:GLN:N	2.48	0.46
6:BH:28:GLU:HG2	6:BH:34:LEU:HD13	1.97	0.46
18:Be:43:ARG:NH2	34:B5:590:C:OP1	2.48	0.46
31:Bg:172:ALA:HB1	31:Bg:199:ILE:HG21	1.96	0.46
36:AB:140:ASP:N	36:AB:140:ASP:OD1	2.47	0.46
38:A1:1627:U:N3	38:A1:1817:G:O6	2.48	0.46
38:A1:3023:U:H2'	38:A1:3024:A:H8	1.79	0.46
41:AD:260:PHE:HB3	41:AD:264:GLN:NE2	2.30	0.46
10:BN:42:ARG:HH12	10:BN:80:LEU:HD11	1.80	0.46
19:BD:135:GLU:HB3	19:BD:187:LYS:HB3	1.97	0.46
20:BF:118:LEU:HD22	20:BF:129:PRO:HB2	1.96	0.46
20:BF:185:ARG:NE	34:B5:1471:A:OP1	2.48	0.46
21:BK:59:PHE:CZ	21:BK:62:GLN:HA	2.50	0.46
38:A1:1073:U:H2'	38:A1:1074:U:C6	2.50	0.46
38:A1:1366:A:O2'	67:Ae:45:ARG:NH2	2.48	0.46
38:A1:2767:U:H2'	38:A1:2768:U:C6	2.50	0.46
43:AF:180:SER:H	43:AF:183:ASP:HB2	1.81	0.46
46:AI:57:LEU:HD12	46:AI:130:ASP:HA	1.96	0.46
52:AP:84:PRO:HB2	52:AP:87:SER:HB2	1.96	0.46
79:E:89:ASP:OD1	79:E:89:ASP:N	2.48	0.46
14:BX:107:PHE:HE2	34:B5:571:G:H4'	1.81	0.46
34:B5:250:C:H2'	34:B5:251:A:C8	2.50	0.46
34:B5:653:C:OP1	34:B5:679:U:N3	2.47	0.46
38:A1:543:C:O2'	38:A1:549:U:N3	2.48	0.46
38:A1:1760:A:O2'	38:A1:1763:U:O4	2.29	0.46
38:A1:2678:A:H61	47:AJ:57:PHE:HZ	1.63	0.46
40:A4:57:C:H4'	40:A4:63:G:N7	2.30	0.46
10:BN:15:ALA:H	17:Bb:20:LYS:HE3	1.80	0.46
23:BQ:69:VAL:HG11	23:BQ:81:ILE:HD11	1.96	0.46
23:BQ:122:ARG:HG2	34:B5:1584:G:H5''	1.98	0.46
24:BR:27:ASP:HB3	24:BR:30:THR:HG22	1.97	0.46
34:B5:1588:G:O6	34:B5:1608:U:O4	2.34	0.46
38:A1:729:C:O2'	53:AQ:79:LYS:NZ	2.48	0.46
38:A1:1213:G:H4'	55:AS:90:MET:HB2	1.97	0.46
38:A1:1634:G:N7	62:AZ:17:ARG:NH2	2.59	0.46
38:A1:1638:A:N1	38:A1:1736:G:O2'	2.47	0.46
38:A1:2843:U:H5''	38:A1:2844:C:H5	1.80	0.46
38:A1:2883:U:H2'	38:A1:2884:C:C6	2.51	0.46
40:A4:65:A:O3'	70:Ah:10:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AH:9:GLN:HB3	45:AH:52:LEU:HD11	1.97	0.46
80:EC:6812:C:H2'	80:EC:6813:A:C8	2.51	0.46
6:BH:99:LEU:HD12	6:BH:112:ARG:HG3	1.98	0.46
8:BJ:114:TYR:HA	8:BJ:119:ALA:HB3	1.97	0.46
14:BX:42:PRO:O	14:BX:79:ASN:ND2	2.49	0.46
31:Bg:153:GLN:HG3	31:Bg:201:THR:HA	1.97	0.46
31:Bg:242:SER:H	31:Bg:255:ALA:HB3	1.81	0.46
34:B5:1187:U:H3	34:B5:1198:G:H1	1.63	0.46
37:AC:29:PRO:O	37:AC:124:SER:OG	2.24	0.46
38:A1:297:G:O6	50:AN:12:ARG:NH1	2.42	0.46
38:A1:314:U:H2'	38:A1:315:C:C6	2.51	0.46
38:A1:1232:C:N4	38:A1:1262:G:OP1	2.49	0.46
38:A1:1827:C:H2'	38:A1:1828:A:C8	2.50	0.46
1:BA:136:ALA:HB1	1:BA:141:ILE:HB	1.98	0.46
19:BD:75:LYS:HD3	21:BK:20:VAL:HG23	1.97	0.46
25:BS:23:ASP:OD1	25:BS:24:GLY:N	2.49	0.46
31:Bg:10:ARG:HD3	31:Bg:314:GLN:HG3	1.96	0.46
34:B5:496:G:H3'	34:B5:497:G:H8	1.80	0.46
34:B5:512:A:H2'	34:B5:513:U:C6	2.51	0.46
34:B5:706:A:H5''	34:B5:734:A:H62	1.81	0.46
36:AB:85:VAL:HG22	36:AB:202:THR:HG22	1.96	0.46
37:AC:51:ALA:O	40:A4:26:U:O2'	2.30	0.46
38:A1:1119:C:H2'	38:A1:1120:A:C8	2.50	0.46
38:A1:2505:U:H4'	71:AI:56:ARG:HD3	1.97	0.46
40:A4:8:C:H2'	40:A4:9:A:H8	1.80	0.46
60:AX:91:ASN:H	60:AX:94:GLN:NE2	2.11	0.46
4:BE:59:ARG:NH2	34:B5:448:C:H41	2.13	0.46
5:BG:133:LEU:HB2	34:B5:66:U:C4	2.51	0.46
26:BT:135:ILE:HA	26:BT:138:GLN:HG2	1.98	0.46
28:BZ:48:ASP:HA	28:BZ:51:LEU:HG	1.97	0.46
34:B5:580:A:O2'	34:B5:582:U:OP1	2.32	0.46
34:B5:752:A:H2	34:B5:797:G:H1	1.63	0.46
36:AB:284:ARG:NH1	36:AB:293:ASN:O	2.47	0.46
38:A1:1194:G:H2'	38:A1:1195:A:C8	2.50	0.46
47:AJ:20:ASN:HB3	47:AJ:126:ASP:HB3	1.98	0.46
62:AZ:9:LYS:HB3	62:AZ:25:ILE:HD12	1.98	0.46
8:BJ:23:ARG:NH1	8:BJ:27:GLU:OE2	2.41	0.46
11:BO:112:ILE:H	16:Ba:57:SER:HA	1.80	0.46
25:BS:35:ILE:HG23	25:BS:102:ALA:HB2	1.97	0.46
28:BZ:95:HIS:ND1	28:BZ:96:SER:O	2.37	0.46
34:B5:100:A2M:H8	34:B5:100:A2M:O5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:792:G:H5'	63:Aa:2:PRO:HD3	1.97	0.46
38:A1:1039:U:H2'	38:A1:1040:A:C8	2.51	0.46
38:A1:1290:A:H2'	38:A1:1291:A:C8	2.51	0.46
38:A1:2357:A:H2'	38:A1:2358:A:H8	1.81	0.46
39:A3:4:U:H2'	39:A3:5:G:H8	1.80	0.46
44:AG:171:LYS:HE2	44:AG:226:TYR:HB3	1.97	0.46
55:AS:90:MET:HE1	55:AS:114:HIS:NE2	2.31	0.46
61:AY:51:ARG:HG2	61:AY:52:ARG:H	1.81	0.46
63:Aa:24:LYS:O	63:Aa:26:ARG:HG2	2.16	0.46
76:An:2:ARG:HG3	76:An:4:LYS:H	1.79	0.46
80:EC:6946:A:H2'	80:EC:6947:A:C8	2.51	0.46
3:BC:165:VAL:HG11	3:BC:210:THR:HA	1.97	0.46
5:BG:141:ILE:HD11	5:BG:153:VAL:HB	1.98	0.46
7:BI:38:ILE:HG12	7:BI:96:LEU:HD11	1.98	0.46
15:BY:10:ARG:HH12	34:B5:778:G:H22	1.64	0.46
33:BM:36:LEU:HD13	33:BM:41:LEU:HB3	1.97	0.46
34:B5:15:U:H2'	34:B5:16:G:O4'	2.16	0.46
34:B5:1732:A:H2'	34:B5:1733:C:C6	2.50	0.46
38:A1:273:A:H2'	38:A1:274:G:C8	2.50	0.46
38:A1:1616:U:H2'	38:A1:1617:G:C8	2.51	0.46
38:A1:1624:G:O2'	38:A1:1643:A:N1	2.47	0.46
39:A3:114:U:H2'	39:A3:115:G:H8	1.81	0.46
49:AM:11:ASN:OD1	49:AM:11:ASN:N	2.49	0.46
53:AQ:37:ALA:O	53:AQ:46:LYS:NZ	2.48	0.46
57:AU:43:VAL:HG12	57:AU:44:GLU:OE1	2.15	0.46
68:Af:10:LYS:HB2	68:Af:33:GLU:HG3	1.98	0.46
16:Ba:17:HIS:NE2	34:B5:1789:G:OP1	2.40	0.46
27:BU:53:LYS:HB2	27:BU:92:ASP:HB2	1.98	0.46
34:B5:688:G:H2'	34:B5:689:G:C8	2.51	0.46
34:B5:698:U:N3	34:B5:741:C:C4	2.84	0.46
34:B5:1144:U:H2'	34:B5:1145:U:C6	2.50	0.46
34:B5:1353:U:HO2'	34:B5:1354:G:H8	1.64	0.46
36:AB:251:CYS:SG	38:A1:2943:G:N2	2.88	0.46
38:A1:966:U:H2'	38:A1:967:A:C8	2.51	0.46
38:A1:1615:C:H2'	38:A1:1616:U:C6	2.51	0.46
38:A1:1899:G:O2'	38:A1:2334:U:O4	2.23	0.46
43:AF:87:VAL:HG11	43:AF:243:MET:HE1	1.99	0.46
47:AJ:26:SER:OG	47:AJ:27:GLY:N	2.48	0.46
79:E:76:ARG:NH1	79:E:142:ASP:O	2.35	0.46
79:E:148:VAL:O	79:E:152:ARG:HG2	2.16	0.46
1:BA:138:TYR:OH	34:B5:1296:A:OP1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:82:ARG:HH21	2:BB:103:MET:HE2	1.81	0.45
21:BK:8:ARG:O	21:BK:12:HIS:ND1	2.49	0.45
34:B5:384:G:H2'	34:B5:385:A:C8	2.51	0.45
36:AB:50:LYS:HA	36:AB:79:VAL:HG12	1.98	0.45
38:A1:93:C:OP2	38:A1:2764:C:O2'	2.30	0.45
38:A1:115:A:H8	38:A1:266:A:H5'	1.81	0.45
38:A1:518:G:OP2	38:A1:518:G:N2	2.43	0.45
38:A1:799:G:H2'	38:A1:801:A:H62	1.81	0.45
38:A1:1452:A:N3	38:A1:2346:C:O2'	2.47	0.45
38:A1:2376:G:H2'	38:A1:2377:G:C8	2.51	0.45
38:A1:3040:A:H5''	58:AV:12:ARG:HB2	1.99	0.45
38:A1:3126:C:H4'	45:AH:129:ARG:HH22	1.81	0.45
39:A3:99:G:H4'	43:AF:128:LYS:HD2	1.99	0.45
62:AZ:27:LYS:HB2	62:AZ:42:LEU:HB2	1.97	0.45
7:BI:178:ARG:NH1	34:B5:258:C:O2	2.49	0.45
15:BY:41:ARG:NH2	15:BY:52:LYS:O	2.47	0.45
30:Bd:14:TYR:HH	34:B5:1553:G:HO2'	1.57	0.45
34:B5:187:G:N2	34:B5:198:A:H62	2.14	0.45
34:B5:844:A:H2'	34:B5:845:G:H8	1.81	0.45
37:AC:326:ARG:NH2	38:A1:608:A:O3'	2.50	0.45
38:A1:92:G:H5'	38:A1:94:G:N7	2.31	0.45
38:A1:1486:G:H21	69:Ag:6:THR:HG22	1.81	0.45
38:A1:1596:C:H2'	38:A1:1597:C:C6	2.51	0.45
38:A1:2964:G:N2	38:A1:2967:A:OP2	2.39	0.45
40:A4:9:A:H2'	40:A4:10:A:H8	1.79	0.45
44:AG:183:LYS:HB2	44:AG:194:THR:HG23	1.98	0.45
46:AI:170:LYS:NZ	56:AT:159:PHE:O	2.47	0.45
48:AL:4:SER:O	63:Aa:44:ASN:ND2	2.48	0.45
53:AQ:36:LEU:O	53:AQ:40:THR:OG1	2.32	0.45
68:Af:17:GLN:O	68:Af:24:ASN:N	2.49	0.45
3:BC:226:THR:OG1	3:BC:228:ASN:OD1	2.21	0.45
14:BX:48:HIS:HB3	14:BX:103:LEU:HD11	1.98	0.45
34:B5:381:C:O2'	34:B5:755:A:N1	2.46	0.45
34:B5:973:A:H4'	38:A1:848:A:H8	1.80	0.45
34:B5:1544:U:H3	34:B5:1567:U:H3	1.63	0.45
34:B5:1642:G:H2'	34:B5:1643:U:H6	1.80	0.45
37:AC:349:THR:OG1	38:A1:520:U:O4	2.34	0.45
38:A1:70:A:H5'	63:Aa:64:GLN:HE22	1.81	0.45
38:A1:1176:C:H2'	38:A1:1177:G:N2	2.31	0.45
38:A1:3006:A:H2'	38:A1:3007:U:O4'	2.17	0.45
43:AF:102:VAL:HG21	43:AF:129:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:AI:72:ALA:HB2	46:AI:155:ALA:HB2	1.98	0.45
46:AI:189:GLU:HG2	46:AI:200:LEU:HD23	1.99	0.45
55:AS:46:GLN:NE2	55:AS:51:VAL:O	2.43	0.45
63:Aa:75:LEU:HB3	63:Aa:118:ILE:HG23	1.99	0.45
68:Af:18:ARG:NH2	68:Af:20:LYS:O	2.45	0.45
1:BA:179:ARG:HG3	1:BA:195:TRP:NE1	2.30	0.45
3:BC:89:GLN:O	34:B5:1145:U:O2'	2.27	0.45
34:B5:1432:U:H4'	34:B5:1433:G:H5''	1.97	0.45
38:A1:3291:G:H2'	38:A1:3292:A:C8	2.52	0.45
41:AD:234:ASP:OD1	41:AD:234:ASP:N	2.48	0.45
58:AV:80:ARG:HB2	58:AV:99:ALA:HB3	1.99	0.45
79:E:205:VAL:HG22	79:E:216:LEU:H	1.80	0.45
5:BG:152:ASP:OD1	5:BG:152:ASP:N	2.49	0.45
7:BI:56:ARG:HH22	34:B5:332:U:P	2.40	0.45
23:BQ:13:LYS:HG3	23:BQ:14:LYS:H	1.80	0.45
31:Bg:172:ALA:HB3	31:Bg:202:LEU:HD22	1.97	0.45
33:BM:31:VAL:HA	33:BM:34:THR:HG22	1.99	0.45
34:B5:836:U:H2'	34:B5:837:G:C8	2.52	0.45
36:AB:236:LYS:HB2	36:AB:236:LYS:HE2	1.68	0.45
38:A1:3162:C:H2'	38:A1:3163:A:H8	1.81	0.45
63:Aa:19:LYS:HB3	63:Aa:25:HIS:HB2	1.98	0.45
71:AI:60:LEU:HD23	71:AI:68:ARG:HG3	1.98	0.45
79:E:196:LYS:HB3	79:E:199:GLN:HB2	1.99	0.45
80:EC:6929:C:H2'	80:EC:6930:G:C8	2.52	0.45
4:BE:77:ARG:HA	4:BE:77:ARG:HD3	1.80	0.45
7:BI:4:SER:OG	7:BI:6:ASP:OD1	2.29	0.45
10:BN:101:HIS:HA	10:BN:104:ARG:HH21	1.82	0.45
19:BD:28:GLU:HG3	21:BK:58:GLN:HG3	1.97	0.45
34:B5:424:C:O2'	34:B5:426:G:OP1	2.30	0.45
38:A1:19:U:H2'	38:A1:20:A:C8	2.52	0.45
38:A1:129:U:H2'	38:A1:130:A:H8	1.81	0.45
38:A1:993:G:N3	38:A1:2637:A:H2'	2.31	0.45
38:A1:1336:U:H2'	38:A1:1337:A:H8	1.82	0.45
41:AD:41:LYS:NZ	56:AT:32:LYS:O	2.36	0.45
45:AH:20:ILE:HG12	45:AH:25:VAL:HG13	1.98	0.45
79:E:17:LEU:HD22	79:E:172:VAL:HG23	1.97	0.45
80:EC:6861:G:H2'	80:EC:6862:G:C8	2.52	0.45
3:BC:49:LYS:HB3	3:BC:243:TYR:HD2	1.80	0.45
34:B5:223:U:H2'	34:B5:224:C:H6	1.81	0.45
34:B5:1575:G7M:O2'	34:B5:1576:A:H5''	2.17	0.45
38:A1:1393:A:OP1	67:Ae:125:ARG:NH2	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2223:A:H2'	38:A1:2224:A:C8	2.52	0.45
47:AJ:37:LEU:HD13	47:AJ:69:VAL:HG12	1.99	0.45
50:AN:155:VAL:O	50:AN:162:ARG:NH2	2.35	0.45
52:AP:27:LYS:HD3	52:AP:63:PHE:HB3	1.98	0.45
1:BA:50:VAL:HA	1:BA:53:THR:HB	1.99	0.45
4:BE:100:ARG:HH12	4:BE:122:LYS:HA	1.82	0.45
19:BD:166:ASP:O	19:BD:190:ARG:NH2	2.43	0.45
19:BD:179:GLN:NE2	34:B5:579:A:N7	2.65	0.45
22:BP:97:TYR:HB2	22:BP:102:PHE:CE1	2.52	0.45
22:BP:115:TYR:N	22:BP:118:GLU:OE2	2.50	0.45
23:BQ:28:LEU:HG	23:BQ:30:LYS:HG2	1.99	0.45
34:B5:406:U:H2'	34:B5:407:A:H8	1.82	0.45
34:B5:973:A:H4'	38:A1:848:A:C8	2.52	0.45
38:A1:289:A:H2'	38:A1:290:G:H8	1.82	0.45
38:A1:407:A:C2	40:A4:17:A:H1'	2.52	0.45
38:A1:417:A:H2'	38:A1:418:A:C8	2.51	0.45
38:A1:1110:U:H2'	38:A1:1111:U:C6	2.51	0.45
38:A1:1666:G:H2'	38:A1:1667:A:H8	1.82	0.45
42:AE:52:VAL:HA	42:AE:67:GLY:HA3	1.99	0.45
1:BA:72:ASP:OD2	3:BC:40:LYS:NZ	2.40	0.45
3:BC:140:ARG:HB3	3:BC:221:THR:HG22	1.99	0.45
8:BJ:108:ARG:HH12	8:BJ:110:GLN:HE21	1.65	0.45
22:BP:43:ARG:NH2	34:B5:1552:U:OP2	2.37	0.45
22:BP:79:HIS:HA	22:BP:97:TYR:HB3	1.99	0.45
28:BZ:74:SER:OG	34:B5:1534:G:OP2	2.35	0.45
34:B5:27:U:H2'	34:B5:28:A2M:H8	1.98	0.45
34:B5:129:U:O4'	34:B5:264:G:N1	2.50	0.45
36:AB:92:TYR:HB2	36:AB:157:VAL:HB	1.99	0.45
36:AB:250:ALA:HB1	38:A1:2947:G:N3	2.32	0.45
38:A1:1498:A:H2'	38:A1:1499:C:C6	2.52	0.45
39:A3:71:G:H2'	39:A3:72:A:C8	2.52	0.45
43:AF:51:TYR:HA	43:AF:54:GLU:HG2	1.99	0.45
44:AG:140:VAL:HG22	44:AG:166:LEU:HD21	1.98	0.45
49:AM:23:ILE:HA	49:AM:63:VAL:HG12	1.99	0.45
49:AM:32:LEU:HD11	49:AM:94:TRP:CD1	2.52	0.45
51:AO:20[A]:ALA:HB2	51:AO:80[A]:PHE:CE1	2.52	0.45
52:AP:8:SER:O	52:AP:8:SER:OG	2.32	0.45
6:BH:103:SER:HB3	6:BH:106:SER:HB3	1.97	0.45
10:BN:42:ARG:NH1	10:BN:80:LEU:HD21	2.32	0.45
20:BF:92:ARG:NH2	20:BF:169:ASN:OD1	2.37	0.45
26:BT:48:GLN:HE22	34:B5:1532:U:H1'	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BU:57:ARG:HD2	34:B5:1382:A:N3	2.31	0.45
28:BZ:83:LEU:HD22	28:BZ:88:ILE:HD11	1.99	0.45
31:Bg:8:VAL:HB	31:Bg:10:ARG:NH1	2.32	0.45
34:B5:592:A:O2'	34:B5:596:C:OP1	2.34	0.45
35:AA:20:THR:HA	35:AA:23:ARG:HG3	1.98	0.45
36:AB:281:LYS:HD2	36:AB:283:TYR:HE1	1.82	0.45
38:A1:1054:A:H5''	38:A1:2637:A:H61	1.82	0.45
38:A1:2406:C:H2'	38:A1:2407:C:H6	1.81	0.45
38:A1:2423:U:H2'	38:A1:2424:A:C8	2.52	0.45
38:A1:3016:A:H2'	38:A1:3017:A:H8	1.81	0.45
40:A4:71:A:OP2	61:AY:51:ARG:NH1	2.44	0.45
44:AG:82:LEU:HD13	44:AG:222:PHE:HE2	1.82	0.45
79:E:26:ARG:HG3	79:E:28:PHE:HB3	1.98	0.45
80:EC:6813:A:H2'	80:EC:6814:G:C8	2.52	0.45
1:BA:142:PRO:HG3	12:BV:32:VAL:HB	1.98	0.44
4:BE:105:VAL:HG21	4:BE:245:LYS:H	1.81	0.44
13:BW:29:PRO:HB2	13:BW:58:SER:HB2	1.99	0.44
34:B5:127:G:O2'	34:B5:179:A:OP2	2.33	0.44
34:B5:496:G:H3'	34:B5:497:G:C8	2.52	0.44
38:A1:316:U:O2'	71:AI:30:LYS:NZ	2.28	0.44
38:A1:737:G:H2'	38:A1:738:A:C8	2.52	0.44
38:A1:904:A:OP2	72:Aj:30:GLN:NE2	2.49	0.44
38:A1:1339:C:OP1	67:Ae:61:LYS:NZ	2.46	0.44
38:A1:2617:U:O2'	46:AI:116:ARG:NH2	2.50	0.44
52:AP:168:LEU:O	52:AP:173:ARG:NH1	2.51	0.44
69:Ag:10:ARG:HD2	74:AI:4:GLN:HE21	1.82	0.44
80:EC:6890:A:H2'	80:EC:6891:G:C8	2.52	0.44
5:BG:139:ASN:HA	5:BG:142:ARG:HB2	1.99	0.44
8:BJ:168:ARG:HD2	8:BJ:168:ARG:HA	1.68	0.44
9:BL:108:PRO:HB2	9:BL:135:VAL:HG22	1.99	0.44
12:BV:74:GLN:NE2	12:BV:83:TRP:O	2.41	0.44
23:BQ:16:ALA:HB2	23:BQ:72:GLY:HA3	1.98	0.44
31:Bg:251:TRP:CD1	31:Bg:264:SER:HG	2.34	0.44
34:B5:17:C:H2'	34:B5:18:C:H6	1.81	0.44
34:B5:47:A:N7	34:B5:98:U:O2'	2.50	0.44
34:B5:898:A:N1	34:B5:911:U:O2'	2.46	0.44
34:B5:1091:A:H4'	34:B5:1092:A:O4'	2.17	0.44
34:B5:1564:U:H2'	34:B5:1565:C:C6	2.52	0.44
34:B5:1647:U:H2'	34:B5:1648:A:C8	2.52	0.44
37:AC:287:THR:HG23	37:AC:288:ARG:HD2	1.99	0.44
38:A1:1569:U:H5'	38:A1:1570:U:H5''	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3095:U:H2'	38:A1:3096:C:C6	2.51	0.44
40:A4:69:U:H2'	40:A4:70:G:O4'	2.18	0.44
42:AE:4:GLN:NE2	67:Ae:75:LEU:H	2.15	0.44
45:AH:12:VAL:HB	45:AH:51:GLN:HA	1.99	0.44
45:AH:128:VAL:HA	45:AH:157:ASN:HD21	1.83	0.44
49:AM:40:ASP:OD1	49:AM:43:LYS:N	2.51	0.44
70:Ah:86:ARG:O	70:Ah:90:ARG:HG2	2.18	0.44
10:BN:55:ARG:HH22	17:Bb:51:GLN:NE2	2.15	0.44
14:BX:107:PHE:O	34:B5:599:A:H5''	2.17	0.44
15:BY:57:VAL:HB	15:BY:60:PHE:HE2	1.81	0.44
20:BF:140:THR:HG23	20:BF:210:ALA:HB1	1.98	0.44
38:A1:209:A:H4'	38:A1:211:A:C8	2.53	0.44
38:A1:799:G:O2'	48:AL:18:TRP:NE1	2.49	0.44
38:A1:952:A:H4'	38:A1:968:G:N2	2.32	0.44
38:A1:952:A:OP1	64:Ab:18:ARG:NH2	2.36	0.44
38:A1:1195:A:H1'	38:A1:1319:G:H4'	2.00	0.44
38:A1:1553:U:H4'	38:A1:1554:U:H5'	2.00	0.44
38:A1:2103:U:O3'	54:AR:85:ARG:NH1	2.46	0.44
38:A1:2256:A2M:N1	80:EC:6908:C:O2'	2.41	0.44
38:A1:2367:A:H2'	38:A1:2368:A:C8	2.53	0.44
38:A1:2438:A:H2'	38:A1:2439:A:C8	2.53	0.44
38:A1:2611:U:H2'	38:A1:2612:U:C6	2.52	0.44
52:AP:33:ALA:HB1	52:AP:117:ILE:HG12	1.99	0.44
69:Ag:54:ILE:HG23	69:Ag:70:LYS:HA	2.00	0.44
20:BF:143:ARG:HA	20:BF:167:ARG:HD3	1.99	0.44
21:BK:35:ILE:HG22	21:BK:37:THR:HG22	1.99	0.44
22:BP:123:TYR:OH	25:BS:122:HIS:NE2	2.40	0.44
34:B5:1220:C:H2'	34:B5:1221:A:C8	2.52	0.44
34:B5:1525:A:H2'	34:B5:1526:A:C8	2.53	0.44
37:AC:16:THR:HG22	37:AC:18:ASN:H	1.83	0.44
38:A1:1447:G:OP1	52:AP:65:SER:OG	2.33	0.44
38:A1:2103:U:H2'	38:A1:2104:A:C8	2.51	0.44
38:A1:2744:U:H2'	38:A1:2745:G:C8	2.52	0.44
38:A1:2972:G:H2'	38:A1:2973:G:H8	1.82	0.44
38:A1:3296:A:H2'	38:A1:3297:U:H6	1.82	0.44
40:A4:106:C:H4'	40:A4:107:G:H5''	1.98	0.44
45:AH:87:LYS:HB2	45:AH:187:ILE:HD13	1.99	0.44
55:AS:77:VAL:HG13	55:AS:126:VAL:HG22	1.98	0.44
79:E:94:ASN:HA	79:E:100:ILE:HD11	1.99	0.44
8:BJ:115:LYS:HA	8:BJ:115:LYS:HD3	1.85	0.44
20:BF:203:LYS:HB2	20:BF:203:LYS:HE3	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BU:28:SER:HB3	27:BU:112:VAL:HA	1.99	0.44
30:Bd:40:ARG:HG3	30:Bd:41:GLN:HG3	1.99	0.44
34:B5:1490:C:OP1	34:B5:1491:U:O2'	2.25	0.44
34:B5:1546:G:H2'	34:B5:1547:A:C8	2.53	0.44
34:B5:1579:U:H2'	34:B5:1580:C:C6	2.52	0.44
38:A1:791:A:H2'	38:A1:792:G:H8	1.83	0.44
38:A1:1334:U:H5''	43:AF:206:LYS:HB3	2.00	0.44
38:A1:1565:G:H22	38:A1:1574:C:N4	2.16	0.44
38:A1:1643:A:H2'	38:A1:1644:C:C2	2.52	0.44
38:A1:1765:U:O4	54:AR:43:LYS:NZ	2.42	0.44
38:A1:2438:A:H2'	38:A1:2439:A:H8	1.82	0.44
38:A1:2683:U:H2'	38:A1:2684:C:C6	2.53	0.44
38:A1:2759:U:H5''	38:A1:2760:C:H5'	2.00	0.44
49:AM:21:VAL:HG23	49:AM:65:LEU:HD23	1.98	0.44
54:AR:167:ARG:HA	54:AR:167:ARG:HD2	1.83	0.44
62:AZ:101:PHE:O	62:AZ:107:ARG:NH2	2.42	0.44
73:Ak:20:VAL:HG11	73:Ak:45:VAL:HG13	1.99	0.44
4:BE:27:TYR:OH	34:B5:460:A:O2'	2.24	0.44
4:BE:108:ARG:NH1	34:B5:788:A:N7	2.65	0.44
8:BJ:28:LEU:HD12	8:BJ:28:LEU:HA	1.86	0.44
22:BP:98:ASN:HB2	22:BP:122:THR:HA	2.00	0.44
31:Bg:297:ASP:OD1	31:Bg:297:ASP:N	2.46	0.44
33:BM:42:ALA:HB1	33:BM:47:GLU:HG2	1.98	0.44
34:B5:220:A:H5''	34:B5:832:U:H1'	1.98	0.44
34:B5:730:G:H21	34:B5:732:G:H4'	1.82	0.44
34:B5:950:C:O2'	34:B5:951:A:OP1	2.29	0.44
35:AA:117:GLU:HG2	35:AA:124:GLY:H	1.82	0.44
38:A1:210:U:C2	38:A1:230:U:H4'	2.53	0.44
38:A1:273:A:H2'	38:A1:274:G:H8	1.81	0.44
38:A1:1175:C:O2	51:AO:87[A]:MET:HG2	2.18	0.44
38:A1:1565:G:H22	38:A1:1574:C:H42	1.66	0.44
38:A1:1915:A:H2'	38:A1:1916:U:C6	2.53	0.44
38:A1:2180:G:H2'	38:A1:2181:C:C6	2.51	0.44
38:A1:2261:G:OP1	38:A1:2306:C:N4	2.48	0.44
38:A1:2864:A:H4'	46:AI:115:MET:HE3	1.99	0.44
39:A3:96:U:H2'	39:A3:97:A:H8	1.82	0.44
49:AM:72:LEU:HD11	49:AM:81:VAL:HG22	1.99	0.44
59:AW:53:VAL:O	59:AW:57:LYS:HG3	2.17	0.44
80:EC:6821:U:H3'	80:EC:6822:U:H4'	2.00	0.44
80:EC:6937:G:H2'	80:EC:6938:A:H8	1.81	0.44
17:Bb:15:GLU:O	17:Bb:29:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BR:69:ILE:O	24:BR:74:GLN:NE2	2.51	0.44
31:Bg:11:GLY:HA2	31:Bg:52:GLN:HA	1.99	0.44
31:Bg:221:MET:HG2	31:Bg:233:THR:HG23	1.99	0.44
34:B5:651:G:H2'	34:B5:652:G:H2'	1.98	0.44
34:B5:919:A:H2'	34:B5:920:U:C6	2.53	0.44
34:B5:1175:U:H2'	34:B5:1176:G:H8	1.83	0.44
34:B5:1494:C:H2'	34:B5:1495:C:C6	2.52	0.44
38:A1:746:A:OP1	53:AQ:145:ASN:ND2	2.50	0.44
38:A1:1597:C:H2'	38:A1:1598:G:H8	1.82	0.44
38:A1:2232:A:H2'	38:A1:2233:A:C8	2.52	0.44
38:A1:3121:U:H1'	38:A1:3122:A:H5''	1.99	0.44
38:A1:3154:C:H4'	38:A1:3155:U:H5''	1.99	0.44
54:AR:144:GLN:NE2	54:AR:148:ASP:OD1	2.51	0.44
72:Aj:14:LYS:HD3	74:Al:51:ILE:HD11	1.99	0.44
4:BE:181:VAL:HG11	4:BE:195:ILE:HD11	1.99	0.44
5:BG:140:ASN:ND2	34:B5:168:A:OP1	2.43	0.44
5:BG:142:ARG:HH22	5:BG:151:ASP:H	1.64	0.44
6:BH:11:GLN:HG3	6:BH:13:PRO:HD2	1.99	0.44
34:B5:304:U:H2'	34:B5:305:C:C6	2.53	0.44
34:B5:406:U:H2'	34:B5:407:A:C8	2.53	0.44
34:B5:1237:G:N1	34:B5:1249:U:O4	2.51	0.44
38:A1:1083:G:H2'	38:A1:1084:A:C8	2.53	0.44
38:A1:2882:U:H2'	38:A1:2883:U:C6	2.53	0.44
40:A4:63:G:H22	40:A4:97:A:H2	1.66	0.44
56:AT:102:ARG:HA	56:AT:102:ARG:HD2	1.85	0.44
61:AY:73:VAL:HG13	61:AY:80:VAL:HG12	1.99	0.44
1:BA:59:LEU:HD22	12:BV:79:LEU:HD11	1.99	0.44
23:BQ:75:VAL:HA	23:BQ:78:VAL:HG12	2.00	0.44
30:Bd:12:ARG:HH22	34:B5:1451:C:P	2.41	0.44
34:B5:885:G:H2'	34:B5:886:U:C6	2.53	0.44
38:A1:1798:A:H2'	38:A1:1799:A:C8	2.53	0.44
38:A1:2357:A:H2'	38:A1:2358:A:C8	2.52	0.44
38:A1:3015:G:H2'	38:A1:3016:A:H8	1.83	0.44
40:A4:26:U:H2'	40:A4:27:U:C6	2.53	0.44
46:AI:145:LYS:HD2	46:AI:167:LEU:HD21	2.00	0.44
2:BB:110:LEU:HD21	2:BB:213:ARG:HG3	2.00	0.43
3:BC:40:LYS:HG2	3:BC:247:ALA:HB1	2.00	0.43
19:BD:161:GLY:HA3	34:B5:1331:A:H61	1.83	0.43
30:Bd:17:GLY:N	34:B5:1205:C:O2	2.42	0.43
31:Bg:90:ARG:NH2	34:B5:1341:A:H4'	2.33	0.43
31:Bg:112:SER:HB2	31:Bg:153:GLN:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:343:C:H2'	34:B5:344:A:H8	1.83	0.43
34:B5:650:U:H2'	34:B5:651:G:O4'	2.18	0.43
36:AB:323:MET:HE1	36:AB:359:ILE:HD13	1.98	0.43
38:A1:640:U:OP1	63:Aa:21:ARG:NH1	2.46	0.43
38:A1:964:G:H5'	63:Aa:29:PRO:HB2	1.99	0.43
38:A1:1055:A:N3	39:A3:81:U:O2'	2.46	0.43
38:A1:1660:C:H2'	38:A1:1661:G:H8	1.82	0.43
38:A1:2352:A:H5''	52:AP:83:TRP:O	2.18	0.43
43:AF:47:ARG:NH2	43:AF:177:GLY:O	2.51	0.43
67:Ae:40:SER:HB3	67:Ae:43:ARG:HB3	2.00	0.43
80:EC:6855:A:H3'	80:EC:6856:C:H5''	2.00	0.43
9:BL:17:PRO:HG3	9:BL:63:LEU:HD11	1.99	0.43
14:BX:70:LYS:HB3	14:BX:93:LEU:HD13	2.00	0.43
18:Be:41:THR:HA	18:Be:45:VAL:HG22	1.99	0.43
22:BP:60:LEU:HD13	22:BP:76:VAL:HG11	1.99	0.43
31:Bg:206:PRO:HG2	31:Bg:247:PRO:HA	2.00	0.43
34:B5:524:U:O2'	34:B5:526:A:N7	2.45	0.43
34:B5:888:U:O2	34:B5:988:A:O2'	2.34	0.43
38:A1:190:U:OP1	61:AY:37:LYS:NZ	2.52	0.43
38:A1:2270:A:H2'	38:A1:2271:A:C8	2.53	0.43
38:A1:2696:A:H2'	38:A1:2697:A:C8	2.53	0.43
38:A1:3039:C:OP1	58:AV:88:ARG:NH1	2.47	0.43
38:A1:3095:U:H2'	38:A1:3096:C:H6	1.83	0.43
39:A3:94:C:H2'	39:A3:95:A:C8	2.53	0.43
45:AH:8:GLN:HB3	45:AH:72:LYS:HD2	1.99	0.43
51:AO:116[A]:LYS:NZ	55:AS:165:TYR:O	2.49	0.43
68:Af:75:HIS:HB3	68:Af:80:VAL:HG12	2.00	0.43
5:BG:102:VAL:HG13	5:BG:106:LEU:HD12	2.00	0.43
8:BJ:175:ARG:HG2	8:BJ:179:ARG:CZ	2.49	0.43
14:BX:8:GLY:O	14:BX:11:SER:OG	2.34	0.43
19:BD:23:GLU:HG2	19:BD:27:ARG:HE	1.82	0.43
23:BQ:77:GLN:HE22	34:B5:1482:C:H4'	1.83	0.43
34:B5:826:U:H2'	34:B5:827:C:C6	2.54	0.43
38:A1:2203:U:H2'	38:A1:2204:C:C6	2.53	0.43
38:A1:2446:U:H2'	38:A1:2447:A:C4	2.53	0.43
55:AS:23:LYS:HD3	55:AS:23:LYS:HA	1.83	0.43
56:AT:152:ALA:HB1	56:AT:153:PRO:HD2	1.99	0.43
8:BJ:108:ARG:HG2	8:BJ:145:SER:HA	1.99	0.43
20:BF:48:PHE:CD1	20:BF:130:ILE:HG21	2.53	0.43
29:Bc:21:SER:OG	34:B5:1619:C:O4'	2.35	0.43
34:B5:912:U:OP1	34:B5:913:G:O2'	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:92:TYR:HB3	36:AB:99:LEU:HG	1.99	0.43
37:AC:8:VAL:HG23	37:AC:16:THR:HB	2.01	0.43
38:A1:737:G:H2'	38:A1:738:A:H8	1.83	0.43
41:AD:277:LEU:O	41:AD:282:ARG:NH2	2.51	0.43
44:AG:133:LYS:HD2	44:AG:138:HIS:HE1	1.83	0.43
51:AO:35[A]:VAL:HB	51:AO:104[A]:VAL:HG13	1.98	0.43
58:AV:15:LEU:HD13	58:AV:51:ALA:HB3	2.00	0.43
58:AV:104:ASN:HD21	58:AV:108:GLU:HB2	1.84	0.43
70:Ah:85:THR:HG22	70:Ah:87:ALA:H	1.83	0.43
2:BB:171:ILE:HD12	2:BB:197:ILE:HD13	1.99	0.43
7:BI:169:ILE:HD12	7:BI:179:CYS:HB3	2.00	0.43
8:BJ:173:ALA:HB2	34:B5:511:A:H5'	2.00	0.43
18:Be:29:LYS:HD3	18:Be:30:PRO:HD2	2.00	0.43
20:BF:33:VAL:HG22	23:BQ:53:LEU:HD11	1.99	0.43
27:BU:23:ARG:NH2	34:B5:1347:U:OP2	2.40	0.43
27:BU:69:LYS:NZ	27:BU:80:GLU:OE2	2.46	0.43
34:B5:1344:A:H2'	34:B5:1345:A:C8	2.54	0.43
38:A1:116:A:OP2	71:Ai:36:ARG:NH2	2.51	0.43
38:A1:242:C:O2'	38:A1:243:G:H8	2.01	0.43
38:A1:291:C:OP1	50:AN:68:ARG:NE	2.40	0.43
38:A1:629:U:H2'	38:A1:630:A:C8	2.54	0.43
38:A1:2273:G:O2'	38:A1:2311:G:O6	2.34	0.43
38:A1:2406:C:H2'	38:A1:2407:C:C6	2.53	0.43
38:A1:3066:U:H2'	38:A1:3067:C:C6	2.53	0.43
39:A3:72:A:O2'	39:A3:74:C:OP1	2.30	0.43
39:A3:91:G:H2'	39:A3:92:A:C8	2.53	0.43
42:AE:3:ALA:HB2	67:Ae:77:ALA:HB2	2.00	0.43
42:AE:60:ASP:OD1	42:AE:60:ASP:N	2.51	0.43
44:AG:133:LYS:HG3	44:AG:201:THR:HG23	1.99	0.43
47:AJ:50:ALA:HB3	47:AJ:62:ASN:H	1.83	0.43
49:AM:15:VAL:HG22	49:AM:65:LEU:HD11	1.99	0.43
67:Ae:74:PHE:HD2	67:Ae:85:LEU:HD11	1.82	0.43
73:Ak:36:LYS:HB3	73:Ak:38:PHE:HD2	1.83	0.43
79:E:60:ARG:NH2	79:E:63:MET:SD	2.91	0.43
79:E:139:SER:HB3	79:E:142:ASP:HB2	1.99	0.43
79:E:150:ASP:O	79:E:154:THR:HG23	2.18	0.43
4:BE:147:ILE:HG21	4:BE:169:ILE:HG13	2.00	0.43
7:BI:171:SER:HB2	7:BI:180:ASP:HB2	1.99	0.43
14:BX:65:ASN:ND2	34:B5:574:G:O6	2.52	0.43
19:BD:55:THR:HA	19:BD:58:VAL:HG12	2.00	0.43
34:B5:852:C:H2'	34:B5:853:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1208:A:H8	34:B5:1269:OMU:H6	1.84	0.43
38:A1:239:G:H21	38:A1:241:G:H1	1.67	0.43
38:A1:1925:U:O2'	38:A1:1927:G:N7	2.49	0.43
38:A1:2497:U:H6	38:A1:2497:U:H2'	1.70	0.43
38:A1:3204:C:H2'	38:A1:3205:G:C8	2.54	0.43
39:A3:71:G:H2'	39:A3:72:A:H8	1.83	0.43
41:AD:40:HIS:CE1	41:AD:42:ALA:HB3	2.53	0.43
43:AF:163:LEU:HD13	43:AF:169:ILE:HD11	2.01	0.43
45:AH:36:LYS:HE3	45:AH:74:LEU:HB3	1.99	0.43
55:AS:152:LEU:HB2	55:AS:172:TYR:CE2	2.53	0.43
62:AZ:16:GLY:O	69:Ag:74:ARG:HG3	2.18	0.43
2:BB:174:LYS:HE2	2:BB:174:LYS:HB3	1.75	0.43
10:BN:73:ARG:HD2	34:B5:859:A:C6	2.53	0.43
19:BD:72:LEU:HD22	21:BK:65:TYR:CD2	2.54	0.43
26:BT:6:VAL:HG22	26:BT:136:ALA:HB2	2.00	0.43
28:BZ:42:LEU:HB2	28:BZ:75:LEU:HD11	2.01	0.43
31:Bg:129:LYS:HA	31:Bg:150:TRP:HA	2.01	0.43
34:B5:207:U:H2'	34:B5:208:U:C6	2.54	0.43
34:B5:1248:C:C2	34:B5:1249:U:H5	2.37	0.43
35:AA:244:GLY:HA3	38:A1:2242:A:H5''	1.99	0.43
37:AC:65:TRP:HB3	37:AC:69:ARG:HD3	2.01	0.43
38:A1:649:A2M:H5''	38:A1:649:A2M:H8	2.01	0.43
38:A1:1084:A:H2'	38:A1:1085:A:C8	2.53	0.43
38:A1:1184:A:H2'	38:A1:1185:C:C6	2.54	0.43
38:A1:2356:A:H61	38:A1:2983:C:H5	1.65	0.43
38:A1:2497:U:H1'	38:A1:2498:U:H5'	1.99	0.43
62:AZ:104:PRO:HA	62:AZ:107:ARG:HG2	2.00	0.43
65:Ac:49:PRO:HG2	65:Ac:52:ARG:HB3	2.01	0.43
1:BA:13:ASP:OD1	1:BA:179:ARG:NH2	2.44	0.43
14:BX:25:ALA:HB1	34:B5:1108:G:H2'	2.00	0.43
15:BY:124:ARG:NH1	34:B5:149:C:OP2	2.44	0.43
17:Bb:36:LYS:NZ	17:Bb:43:ILE:HD11	2.34	0.43
17:Bb:81:ARG:HB3	17:Bb:82:LYS:NZ	2.33	0.43
34:B5:179:A:H3'	34:B5:180:A:H8	1.84	0.43
34:B5:1212:G:H2'	34:B5:1213:G:H8	1.83	0.43
35:AA:138:GLY:HA3	35:AA:147:ARG:CZ	2.49	0.43
38:A1:270:U:H2'	38:A1:271:C:H6	1.84	0.43
38:A1:899:U:H2'	38:A1:900:G:H8	1.84	0.43
38:A1:1718:G:H2'	38:A1:1719:G:H8	1.82	0.43
38:A1:3017:A:N1	38:A1:3037:U:H5	2.17	0.43
48:AL:11:LYS:O	48:AL:13:HIS:ND1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AP:119:VAL:HG22	52:AP:146:ILE:HG23	2.01	0.43
20:BF:217:LEU:HD23	20:BF:217:LEU:HA	1.92	0.43
22:BP:28:MET:SD	22:BP:28:MET:N	2.92	0.43
25:BS:137:HIS:ND1	34:B5:1175:U:OP2	2.52	0.43
34:B5:161:U:H2'	34:B5:162:A:C8	2.54	0.43
34:B5:181:A:H2'	34:B5:182:A:C8	2.53	0.43
38:A1:1141:C:O2'	38:A1:1153:A:N3	2.47	0.43
38:A1:1791:C:H2'	38:A1:1792:C:C6	2.54	0.43
38:A1:2961:G:H2'	38:A1:2962:U:C6	2.54	0.43
38:A1:3296:A:H2'	38:A1:3297:U:C6	2.54	0.43
41:AD:286:VAL:HG13	46:AI:206:LEU:HD11	2.00	0.43
51:AO:12[A]:LYS:HD3	51:AO:37[A]:ARG:NH2	2.34	0.43
5:BG:132:ARG:HD2	5:BG:132:ARG:HA	1.88	0.43
22:BP:96:ILE:HD12	22:BP:116:LEU:HB3	2.01	0.43
26:BT:60:SER:HB3	34:B5:1479:A:H5''	2.01	0.43
34:B5:164:A:H2'	34:B5:165:G:H8	1.83	0.43
34:B5:520:A:H2'	34:B5:521:A:C8	2.54	0.43
34:B5:1027:A:OP1	34:B5:1789:G:O2'	2.26	0.43
34:B5:1763:A:H5''	34:B5:1771:U:H5'	2.01	0.43
36:AB:250:ALA:HB1	38:A1:2947:G:C2	2.54	0.43
38:A1:787:G:H2'	38:A1:788:C:C6	2.53	0.43
38:A1:981:U:O4	38:A1:1106:G:H5'	2.19	0.43
38:A1:3013:U:H2'	38:A1:3014:U:C6	2.54	0.43
38:A1:3212:C:H2'	38:A1:3213:A:O4'	2.19	0.43
41:AD:232:ASP:OD1	41:AD:233:ALA:N	2.50	0.43
43:AF:123:THR:HA	43:AF:126:LEU:HD12	2.01	0.43
51:AO:113[A]:ASP:N	51:AO:113[A]:ASP:OD1	2.50	0.43
58:AV:104:ASN:OD1	58:AV:108:GLU:N	2.52	0.43
15:BY:41:ARG:HG2	15:BY:55:VAL:HG12	2.01	0.42
34:B5:183:U:H2'	34:B5:184:C:H6	1.84	0.42
34:B5:1087:A:H2'	34:B5:1088:A:C8	2.54	0.42
38:A1:172:G:H2'	38:A1:173:G:H8	1.84	0.42
38:A1:656:A:H2'	38:A1:657:A:C8	2.54	0.42
38:A1:2742:C:H2'	38:A1:2743:A:H8	1.84	0.42
38:A1:2897:A:H5''	75:Am:125:LYS:HD2	2.00	0.42
39:A3:112:G:H2'	39:A3:113:C:C6	2.54	0.42
58:AV:24:ASN:ND2	58:AV:97:ASP:OD2	2.43	0.42
69:Ag:102:LYS:HE2	69:Ag:102:LYS:HB3	1.91	0.42
79:E:180:VAL:HA	79:E:183:ILE:HG12	2.00	0.42
80:EC:6859:U:O2'	80:EC:6860:A:H5''	2.19	0.42
4:BE:3:ARG:HG2	34:B5:399:A:H4'	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:137:ARG:HH12	34:B5:144:U:H5	1.67	0.42
9:BL:88:ARG:HD3	9:BL:107:VAL:HG21	2.01	0.42
10:BN:149:LEU:HD12	10:BN:150:VAL:HG13	2.01	0.42
16:Ba:23:CYS:HB2	16:Ba:30:ILE:HD11	2.01	0.42
34:B5:108:A:H2'	34:B5:109:G:C8	2.54	0.42
34:B5:607:G:H5'	34:B5:613:G:N2	2.34	0.42
34:B5:1642:G:H2'	34:B5:1643:U:C6	2.55	0.42
34:B5:1669:U:H2'	34:B5:1670:G:O4'	2.19	0.42
35:AA:3:ARG:HB3	35:AA:207:VAL:HG22	2.02	0.42
35:AA:37:ARG:NH2	38:A1:2526:C:OP1	2.38	0.42
38:A1:263:C:H2'	38:A1:264:G:O4'	2.19	0.42
38:A1:590:G:H21	42:AE:19:LYS:HE2	1.84	0.42
38:A1:1257:C:H2'	38:A1:1258:U:C6	2.54	0.42
49:AM:23:ILE:O	49:AM:30:GLY:N	2.52	0.42
72:Aj:58:THR:OG1	72:Aj:59:THR:N	2.51	0.42
80:EC:6789:G:OP2	80:EC:6805:C:N4	2.52	0.42
4:BE:100:ARG:HB2	4:BE:114:ILE:HD13	2.00	0.42
5:BG:88:ARG:HB3	5:BG:91:GLU:HB2	2.00	0.42
7:BI:37:LYS:HE3	7:BI:93:THR:HG22	2.01	0.42
20:BF:74:ALA:O	23:BQ:122:ARG:NH2	2.53	0.42
22:BP:77:ARG:HG3	34:B5:1241:G:H5''	2.01	0.42
26:BT:86:ARG:O	26:BT:89:ARG:NH2	2.52	0.42
34:B5:223:U:H2'	34:B5:224:C:C6	2.53	0.42
34:B5:407:A:H2'	34:B5:408:C:H6	1.84	0.42
34:B5:990:C:H2'	34:B5:991:G:O4'	2.19	0.42
34:B5:1369:U:H1'	34:B5:1372:U:H2'	2.01	0.42
34:B5:1542:G:N2	34:B5:1568:C:H1'	2.33	0.42
36:AB:122:TRP:CE2	36:AB:127:LYS:HE3	2.53	0.42
38:A1:94:G:H2'	38:A1:95:A:C8	2.55	0.42
38:A1:1699:A:H2'	38:A1:1700:G:C8	2.54	0.42
38:A1:1699:A:H2'	38:A1:1700:G:H8	1.84	0.42
38:A1:2097:U:H2'	38:A1:2098:C:C6	2.54	0.42
53:AQ:71:LEU:HD22	53:AQ:99:THR:HG21	2.01	0.42
54:AR:105:LEU:HD22	54:AR:135:LYS:HG3	2.00	0.42
58:AV:54:LEU:N	58:AV:81:GLN:OE1	2.49	0.42
2:BB:134:VAL:HB	2:BB:219:LYS:HB2	2.02	0.42
19:BD:37:VAL:HG23	19:BD:50:ILE:HA	2.01	0.42
19:BD:64:ARG:NH1	21:BK:70:GLU:OE1	2.52	0.42
19:BD:75:LYS:HE2	21:BK:21:VAL:HA	2.01	0.42
34:B5:1546:G:H2'	34:B5:1547:A:H8	1.85	0.42
35:AA:22:LEU:HD12	35:AA:191:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:649:A2M:OP2	38:A1:2868:U:O2'	2.37	0.42
38:A1:990:U:H1'	56:AT:101:CYS:HB2	2.00	0.42
38:A1:2507:C:H2'	38:A1:2508:U:C6	2.55	0.42
38:A1:2966:G:H2'	38:A1:2967:A:C8	2.54	0.42
38:A1:3186:A:N6	45:AH:58:HIS:O	2.44	0.42
52:AP:138:LYS:HB2	52:AP:140:GLU:HG3	2.02	0.42
60:AX:47:ALA:HB3	60:AX:50:ALA:HB2	2.02	0.42
65:Ac:51:LEU:HD11	69:Ag:90:ILE:HG22	2.01	0.42
65:Ac:55:GLU:HB2	69:Ag:94:LEU:HD11	2.00	0.42
69:Ag:44:CYS:HB2	69:Ag:81:CYS:HB3	2.02	0.42
1:BA:30:GLN:HG3	1:BA:32:HIS:H	1.84	0.42
2:BB:24:PHE:HD2	2:BB:47:LEU:HD21	1.84	0.42
10:BN:92:ILE:HD13	10:BN:149:LEU:HD11	2.01	0.42
13:BW:122:SER:O	34:B5:748:U:O2'	2.33	0.42
15:BY:23:PHE:HZ	15:BY:75:VAL:HG23	1.84	0.42
34:B5:107:C:H2'	34:B5:108:A:C8	2.54	0.42
34:B5:1738:U:H2'	34:B5:1739:C:C6	2.54	0.42
38:A1:1921:A:H2'	38:A1:1922:A:C8	2.55	0.42
38:A1:2662:G:H2'	38:A1:2663:G:C8	2.54	0.42
41:AD:216:GLU:HA	41:AD:219:PHE:HB3	2.00	0.42
10:BN:3:ARG:HB3	10:BN:6:SER:HB3	2.02	0.42
17:Bb:51:GLN:C	17:Bb:66:PRO:HB3	2.45	0.42
19:BD:23:GLU:CD	21:BK:61:TRP:HE1	2.26	0.42
20:BF:23:VAL:HG12	20:BF:34:GLN:HE21	1.85	0.42
34:B5:1357:A:H2'	34:B5:1358:G:C8	2.54	0.42
35:AA:52:SER:HB3	35:AA:191:LEU:HD12	2.01	0.42
35:AA:203:ALA:HB1	38:A1:2146:C:H5''	2.01	0.42
37:AC:284:SER:O	37:AC:284:SER:OG	2.35	0.42
37:AC:303:GLY:H	38:A1:1347:U:H5''	1.85	0.42
38:A1:516:A:O3'	43:AF:60:ARG:NH2	2.43	0.42
38:A1:716:A:C6	63:Aa:117:ARG:HG3	2.54	0.42
38:A1:938:C:OP2	63:Aa:26:ARG:NH1	2.52	0.42
38:A1:1047:A:H2'	38:A1:1048:A:C8	2.55	0.42
38:A1:1622:U:H2'	38:A1:1623:G:H8	1.85	0.42
38:A1:1660:C:H2'	38:A1:1661:G:C8	2.55	0.42
38:A1:3162:C:H2'	38:A1:3163:A:C8	2.55	0.42
42:AE:84:VAL:O	68:Af:105:SER:OG	2.27	0.42
66:Ad:36:ILE:HD12	66:Ad:59:ILE:HD11	2.01	0.42
78:Ap:49:ARG:HB2	78:Ap:55:TRP:CZ3	2.54	0.42
17:Bb:33:LEU:HD23	17:Bb:81:ARG:HA	2.02	0.42
25:BS:36:LYS:HB2	25:BS:36:LYS:HE2	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1628:U:H2'	34:B5:1629:G:C8	2.54	0.42
38:A1:421:G:O6	38:A1:2383:C:O2'	2.28	0.42
38:A1:837:A:OP2	78:Ap:4:ARG:NE	2.43	0.42
38:A1:1663:C:H2'	38:A1:1664:G:H8	1.85	0.42
38:A1:1921:A:H2'	38:A1:1922:A:H8	1.84	0.42
38:A1:2189:U:O3'	78:Ap:21:SER:OG	2.35	0.42
49:AM:17:VAL:HG11	49:AM:74:ARG:HA	2.01	0.42
66:Ad:102:LYS:HB3	66:Ad:102:LYS:HE2	1.78	0.42
80:EC:6828:G:H2'	80:EC:6829:A:H8	1.85	0.42
2:BB:89:ASP:HB3	2:BB:223:PHE:CE1	2.53	0.42
4:BE:45:ILE:HA	4:BE:61:VAL:HG11	2.01	0.42
14:BX:48:HIS:CD2	14:BX:105:ALA:HB2	2.55	0.42
38:A1:36:C:H4'	38:A1:808:A:C2	2.55	0.42
38:A1:828:A:H2'	38:A1:829:U:C6	2.55	0.42
38:A1:1666:G:H2'	38:A1:1667:A:C8	2.54	0.42
38:A1:2672:G:H5'	47:AJ:94:ARG:HH21	1.83	0.42
46:AI:91:VAL:HG12	46:AI:133:GLN:HE21	1.84	0.42
55:AS:6:GLU:HG2	55:AS:64:ILE:HD12	2.02	0.42
5:BG:57:ASP:HA	5:BG:106:LEU:HA	2.01	0.42
20:BF:144:GLU:HG2	20:BF:161:ASP:HA	2.01	0.42
23:BQ:71:GLY:HA2	34:B5:1483:A:H4'	2.01	0.42
28:BZ:50:ILE:HG13	28:BZ:69:LEU:HD21	2.00	0.42
28:BZ:92:ILE:HD11	28:BZ:102:THR:HG22	2.01	0.42
34:B5:34:G:O2'	34:B5:515:A:O2'	2.37	0.42
38:A1:149:U:P	50:AN:49:ARG:HH12	2.43	0.42
38:A1:835:G:O2'	38:A1:857:G:N2	2.40	0.42
38:A1:3164:C:O2'	38:A1:3165:A:H8	2.03	0.42
38:A1:3214:U:OP2	49:AM:128:ARG:NH2	2.43	0.42
39:A3:73:C:H41	55:AS:19:VAL:HG11	1.85	0.42
41:AD:236:LEU:HA	41:AD:239:ILE:HG22	2.02	0.42
48:AL:46:ILE:HD11	48:AL:51:LEU:HA	2.02	0.42
53:AQ:29:LEU:HD23	53:AQ:29:LEU:HA	1.95	0.42
53:AQ:176:ARG:HA	53:AQ:182:LYS:O	2.20	0.42
63:Aa:95:SER:OG	63:Aa:96:LYS:O	2.37	0.42
80:EC:6860:A:H3'	80:EC:6861:G:C8	2.54	0.42
4:BE:198:LYS:HE2	4:BE:198:LYS:HB2	1.89	0.42
8:BJ:108:ARG:HH12	8:BJ:110:GLN:NE2	2.18	0.42
14:BX:50:LYS:HG3	34:B5:435:C:H5''	2.02	0.42
14:BX:78:LYS:HG3	14:BX:79:ASN:OD1	2.19	0.42
14:BX:107:PHE:CE2	34:B5:571:G:H4'	2.55	0.42
21:BK:8:ARG:HE	21:BK:12:HIS:CE1	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BP:97:TYR:CE1	34:B5:1453:G:H1'	2.51	0.42
22:BP:115:TYR:OH	34:B5:1556:A:OP1	2.32	0.42
34:B5:413:U:H2'	34:B5:414:OMC:H6	1.85	0.42
34:B5:842:C:H2'	34:B5:843:U:O4'	2.20	0.42
34:B5:874:C:H2'	34:B5:875:G:C8	2.55	0.42
34:B5:968:U:H2'	34:B5:969:C:O4'	2.20	0.42
34:B5:1170:G:N2	34:B5:1571:C:O2'	2.53	0.42
34:B5:1592:A:H2'	34:B5:1593:A:C8	2.55	0.42
36:AB:99:LEU:O	38:A1:3004:C:O2'	2.21	0.42
36:AB:266:ARG:NH2	38:A1:2392:C:O2'	2.47	0.42
38:A1:407:A:H4'	38:A1:1397:C:H5'	2.02	0.42
38:A1:585:A:H2'	38:A1:586:C:C6	2.55	0.42
38:A1:1594:A:H1'	38:A1:1615:C:H1'	2.01	0.42
38:A1:2586:G:O6	44:AG:242:ALA:N	2.45	0.42
38:A1:2881:C:H2'	38:A1:2882:U:C6	2.55	0.42
38:A1:3067:C:H5'	54:AR:58:HIS:CE1	2.55	0.42
38:A1:3127:A:H2'	38:A1:3128:G:O4'	2.20	0.42
40:A4:141:C:OP1	50:AN:109:ARG:NH2	2.49	0.42
43:AF:151:ARG:HD2	43:AF:207:LEU:HD23	2.01	0.42
51:AO:55[A]:HIS:HD1	51:AO:58[A]:LEU:HD12	1.83	0.42
60:AX:82:LEU:HD12	60:AX:126:LEU:HD21	2.02	0.42
62:AZ:41:ALA:HB2	62:AZ:77:TYR:HE1	1.84	0.42
68:Af:8:TYR:CE1	68:Af:99:ARG:HG2	2.55	0.42
80:EC:6885:G:H2'	80:EC:6886:A:C8	2.54	0.42
4:BE:139:VAL:HG13	4:BE:150:PRO:HG3	2.01	0.41
6:BH:116:ARG:HD2	34:B5:856:A:C6	2.55	0.41
7:BI:37:LYS:C	7:BI:59:ARG:HA	2.45	0.41
7:BI:83:TYR:HB3	7:BI:101:ILE:HB	2.02	0.41
8:BJ:106:GLU:HA	8:BJ:111:THR:HG21	2.02	0.41
19:BD:164:VAL:HG23	19:BD:168:ILE:HD12	2.02	0.41
20:BF:63:GLN:H	20:BF:89:ILE:HG23	1.85	0.41
22:BP:78:THR:HA	34:B5:1241:G:H4'	2.02	0.41
33:BM:28:LEU:HA	33:BM:31:VAL:HG12	2.02	0.41
34:B5:64:U:O2'	34:B5:168:A:N3	2.45	0.41
34:B5:546:U:H2'	34:B5:547:U:C6	2.55	0.41
34:B5:1291:G:H2'	34:B5:1292:G:H8	1.84	0.41
34:B5:1361:U:O2	34:B5:1363:U:N3	2.53	0.41
36:AB:100:ARG:HH11	38:A1:3146:G:H4'	1.84	0.41
38:A1:585:A:H4'	68:Af:72:THR:HG23	2.01	0.41
38:A1:791:A:H2'	38:A1:792:G:C8	2.55	0.41
38:A1:2828:G:H5'	46:AI:8:CYS:SG	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2909:U:H2'	38:A1:2910:A:O4'	2.20	0.41
38:A1:3308:C:O2'	52:AP:69:ARG:O	2.25	0.41
44:AG:63:LYS:HE3	44:AG:63:LYS:HB2	1.92	0.41
48:AL:49:ARG:O	48:AL:137:GLN:NE2	2.52	0.41
48:AL:126:PHE:HD2	70:Ah:115:LYS:HE3	1.85	0.41
63:Aa:34:MET:HE3	63:Aa:34:MET:HB3	1.87	0.41
79:E:39:LYS:N	79:E:200:ASN:O	2.42	0.41
79:E:105:LYS:HA	79:E:105:LYS:HD2	1.88	0.41
2:BB:87:ARG:HD3	2:BB:101:HIS:ND1	2.35	0.41
5:BG:7:TYR:O	5:BG:11:GLY:N	2.49	0.41
22:BP:24:LYS:HG3	22:BP:25:LEU:HD12	2.00	0.41
33:BM:106:ILE:HG13	33:BM:107:ASP:H	1.85	0.41
34:B5:97:C:H2'	34:B5:98:U:C6	2.55	0.41
34:B5:182:A:H2'	34:B5:183:U:C6	2.55	0.41
34:B5:1648:A:H2'	34:B5:1649:G:C8	2.55	0.41
34:B5:1660:A:H2'	34:B5:1661:U:C6	2.54	0.41
36:AB:180:GLU:OE2	38:A1:3002:C:O2'	2.28	0.41
37:AC:334:PHE:HA	37:AC:339:LEU:HD12	2.02	0.41
38:A1:21:G:H3'	38:A1:22:G:H8	1.84	0.41
38:A1:91:G:OP2	38:A1:93:C:N4	2.38	0.41
79:E:86:SER:OG	79:E:89:ASP:OD1	2.33	0.41
1:BA:126:PRO:HG3	1:BA:147:THR:HG22	2.02	0.41
8:BJ:176:ASN:ND2	34:B5:511:A:OP2	2.51	0.41
22:BP:83:MET:HE2	22:BP:116:LEU:HD11	2.02	0.41
26:BT:39:THR:HA	26:BT:100:ILE:HD12	2.01	0.41
32:Bf:135:HIS:HB2	32:Bf:138:ARG:HE	1.84	0.41
34:B5:629:U:H2'	34:B5:630:A:H8	1.85	0.41
34:B5:646:C:H2'	34:B5:647:G:O4'	2.20	0.41
34:B5:950:C:H2'	34:B5:951:A:C8	2.54	0.41
34:B5:1350:U:H2'	34:B5:1351:G:C8	2.55	0.41
34:B5:1429:G:H2'	34:B5:1430:U:C6	2.56	0.41
34:B5:1734:U:H2'	34:B5:1735:U:C6	2.55	0.41
36:AB:62:ARG:H	36:AB:68:HIS:HD2	1.67	0.41
38:A1:371:G:H4'	38:A1:396:A:N1	2.35	0.41
38:A1:2160:G:H2'	38:A1:2161:G:C8	2.53	0.41
38:A1:3050:U:O2'	59:AW:16:GLY:O	2.38	0.41
38:A1:3252:G:H2'	38:A1:3253:G:H8	1.85	0.41
38:A1:3333:G:N2	38:A1:3369:G:O2'	2.53	0.41
70:Ah:41:LEU:O	70:Ah:44:ILE:HG12	2.21	0.41
73:Ak:5:ILE:HG23	73:Ak:10:GLN:NE2	2.35	0.41
7:BI:58:LEU:HD21	34:B5:1676:U:H5''	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:47:PHE:CD2	8:BJ:51:LYS:HE2	2.55	0.41
13:BW:107:SER:HA	34:B5:804:A:C8	2.55	0.41
15:BY:44:LEU:HA	15:BY:47:VAL:HG12	2.02	0.41
31:Bg:244:ALA:O	31:Bg:294:TRP:NE1	2.41	0.41
34:B5:82:U:H2'	34:B5:83:G:O4'	2.20	0.41
34:B5:472:U:O2'	34:B5:769:A:N3	2.53	0.41
34:B5:976:G:N1	34:B5:1023:A:O2'	2.45	0.41
34:B5:1609:U:H2'	34:B5:1610:G:O4'	2.20	0.41
35:AA:242:ARG:NH2	35:AA:243:THR:O	2.53	0.41
38:A1:1312:C:O2'	51:AO:83[A]:ALA:O	2.39	0.41
38:A1:1497:C:H2'	38:A1:1498:A:H8	1.84	0.41
38:A1:1609:C:OP2	60:AX:109:LYS:NZ	2.49	0.41
38:A1:1635:G:N2	38:A1:1638:A:OP2	2.36	0.41
40:A4:148:G:H2'	40:A4:149:A:C8	2.56	0.41
55:AS:6:GLU:OE2	55:AS:99:ARG:NH1	2.53	0.41
57:AU:54:VAL:HG23	57:AU:67:SER:HB2	2.01	0.41
80:EC:6836:U:O3'	80:EC:6874:A:O2'	2.38	0.41
11:BO:124:ASP:HB3	34:B5:928:U:H4'	2.02	0.41
14:BX:126:LYS:HA	14:BX:131:SER:HA	2.02	0.41
16:Ba:79:ILE:HD13	34:B5:1794:A:H1'	2.02	0.41
22:BP:121:ILE:HD11	22:BP:123:TYR:CZ	2.55	0.41
25:BS:101:LEU:O	25:BS:105:VAL:HG23	2.21	0.41
31:Bg:74:THR:HG22	31:Bg:115:ILE:HD13	2.01	0.41
34:B5:397:A:H2'	34:B5:398:G:C8	2.56	0.41
34:B5:1349:G:H2'	34:B5:1350:U:H6	1.85	0.41
34:B5:1358:G:H2'	34:B5:1359:C:C6	2.55	0.41
37:AC:315:LYS:HB2	37:AC:323:VAL:HG21	2.03	0.41
38:A1:345:G:O2'	40:A4:25:G:N3	2.51	0.41
38:A1:664:U:H2'	38:A1:665:A:H8	1.84	0.41
38:A1:975:C:H2'	38:A1:976:U:C6	2.55	0.41
38:A1:1302:A:N7	38:A1:2857:C:O2'	2.49	0.41
38:A1:1351:U:O4	38:A1:1353:U:O2'	2.35	0.41
41:AD:153:THR:HG23	41:AD:160:PHE:HZ	1.84	0.41
47:AJ:12:LEU:HD21	47:AJ:158:ASP:HB3	2.03	0.41
54:AR:24:LEU:HB3	54:AR:32:ILE:HD13	2.02	0.41
66:Ad:78:LYS:HE3	66:Ad:90:PHE:CZ	2.55	0.41
67:Ae:32:TRP:CZ2	67:Ae:53:PRO:HD2	2.55	0.41
67:Ae:96:ILE:HG21	67:Ae:105:ARG:HG2	2.02	0.41
68:Af:51:TYR:HB3	68:Af:67:MET:HB2	2.01	0.41
79:E:91:LYS:HA	79:E:123:LEU:HD22	2.02	0.41
1:BA:42:PRO:HD2	24:BR:105:GLN:NE2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:168:ILE:HG12	2:BB:197:ILE:HD12	2.01	0.41
4:BE:214:LEU:HD23	4:BE:214:LEU:HA	1.93	0.41
16:Ba:39:MET:HG3	16:Ba:41:ILE:HD11	2.03	0.41
26:BT:126:GLU:OE1	34:B5:1358:G:O2'	2.30	0.41
34:B5:1354:G:N2	34:B5:1372:U:OP2	2.54	0.41
38:A1:821:U:H2'	38:A1:822:G:H8	1.84	0.41
38:A1:2389:C:H2'	38:A1:2390:A:H8	1.86	0.41
38:A1:2503:G:H2'	38:A1:2504:U:C5	2.55	0.41
38:A1:2526:C:H2'	38:A1:2527:G:H8	1.85	0.41
38:A1:2578:U:H2'	38:A1:2579:G:O4'	2.21	0.41
38:A1:2652:U:OP1	77:Ao:65:THR:OG1	2.37	0.41
39:A3:81:U:H2'	39:A3:82:G:H8	1.85	0.41
41:AD:54:ARG:HD3	41:AD:54:ARG:HA	1.91	0.41
42:AE:154:LEU:HD12	42:AE:157:GLN:HB2	2.02	0.41
43:AF:156:ILE:HD12	43:AF:161:VAL:HB	2.01	0.41
45:AH:89:LYS:HB2	45:AH:183:HIS:HB3	2.02	0.41
53:AQ:147:ARG:HB3	53:AQ:150:VAL:HG23	2.03	0.41
57:AU:59:ASP:OD1	57:AU:62:VAL:N	2.43	0.41
80:EC:6851:G:O2'	80:EC:6852:U:O5'	2.24	0.41
4:BE:104:ASP:HB3	4:BE:110:ALA:HB2	2.03	0.41
7:BI:31:ARG:NH1	34:B5:332:U:OP1	2.44	0.41
13:BW:27:ILE:HB	13:BW:61:ILE:HB	2.02	0.41
15:BY:10:ARG:NH1	34:B5:778:G:H22	2.18	0.41
19:BD:179:GLN:HG2	34:B5:579:A:C6	2.55	0.41
23:BQ:42:GLU:O	23:BQ:45:ARG:HG2	2.21	0.41
31:Bg:172:ALA:HB2	31:Bg:202:LEU:HD13	2.02	0.41
34:B5:160:C:H2'	34:B5:161:U:O4'	2.21	0.41
34:B5:1336:A:H2'	34:B5:1337:A:C8	2.56	0.41
36:AB:67:PHE:CD1	36:AB:70:ARG:HD2	2.51	0.41
37:AC:11:LEU:HD21	37:AC:156:LEU:HB2	2.01	0.41
38:A1:3084:C:H2'	38:A1:3085:G:O4'	2.20	0.41
40:A4:52:A:N6	74:A1:27:ILE:HD13	2.36	0.41
23:BQ:45:ARG:HB3	23:BQ:49:TYR:CE2	2.56	0.41
26:BT:117:SER:HA	26:BT:123:ARG:HH21	1.85	0.41
30:Bd:21:CYS:HA	30:Bd:30:LEU:HD21	2.03	0.41
34:B5:894:U:H2'	34:B5:895:G:C8	2.56	0.41
34:B5:1683:C:O2'	34:B5:1684:U:O5'	2.32	0.41
38:A1:296:A:N3	38:A1:299:G:O2'	2.52	0.41
38:A1:2204:C:H2'	38:A1:2205:U:O4'	2.20	0.41
38:A1:2661:G:H2'	38:A1:2662:G:H8	1.86	0.41
39:A3:118:A:H5''	41:AD:253:PHE:CZ	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:AX:64:GLU:OE1	60:AX:85:GLN:NE2	2.53	0.41
66:Ad:25:PHE:HB3	66:Ad:65:LYS:HG3	2.01	0.41
2:BB:68:VAL:HG13	2:BB:73:LEU:HD11	2.03	0.41
5:BG:23:ARG:HG2	5:BG:23:ARG:HH11	1.86	0.41
8:BJ:136:VAL:HG11	8:BJ:146:PHE:CE2	2.56	0.41
12:BV:7:GLN:O	12:BV:9:VAL:HG13	2.21	0.41
12:BV:32:VAL:HG22	12:BV:60:ARG:HD2	2.03	0.41
12:BV:42:GLU:OE1	12:BV:44:ARG:NH1	2.53	0.41
14:BX:42:PRO:HG2	14:BX:122:PHE:HZ	1.86	0.41
15:BY:93:ARG:NE	34:B5:526:A:OP1	2.45	0.41
16:Ba:40:ALA:HB3	16:Ba:69:ASN:HB3	2.03	0.41
20:BF:20:PHE:HA	20:BF:35:GLN:HE22	1.85	0.41
20:BF:63:GLN:HB3	20:BF:88:PRO:HA	2.02	0.41
22:BP:96:ILE:HD11	22:BP:116:LEU:HD22	2.03	0.41
23:BQ:49:TYR:HB3	23:BQ:53:LEU:HD12	2.02	0.41
23:BQ:106:LYS:HB2	23:BQ:106:LYS:HE3	1.91	0.41
27:BU:70:THR:O	30:Bd:40:ARG:NH1	2.43	0.41
27:BU:102:ARG:NH1	27:BU:103:ILE:HB	2.36	0.41
31:Bg:7:LEU:HB2	31:Bg:274:LEU:HD21	2.02	0.41
33:BM:41:LEU:HD12	33:BM:123:VAL:HA	2.02	0.41
34:B5:17:C:O2'	34:B5:1137:A:N1	2.44	0.41
34:B5:107:C:H2'	34:B5:108:A:H8	1.85	0.41
34:B5:407:A:H2'	34:B5:408:C:C6	2.55	0.41
34:B5:1018:U:H2'	34:B5:1019:A:C8	2.56	0.41
34:B5:1077:C:H2'	34:B5:1078:C:H6	1.86	0.41
34:B5:1237:G:H2'	34:B5:1238:A:C8	2.56	0.41
35:AA:127:ALA:HB2	35:AA:134:VAL:HG23	2.01	0.41
36:AB:255:TRP:CD1	38:A1:2395:G:H5''	2.56	0.41
36:AB:348:ARG:CZ	38:A1:3037:U:H5''	2.51	0.41
37:AC:23:PRO:HD2	37:AC:26:PHE:CD2	2.55	0.41
38:A1:22:G:H1'	40:A4:104:A:N3	2.36	0.41
38:A1:166:C:H2'	38:A1:167:U:C6	2.56	0.41
38:A1:275:U:H2'	38:A1:276:U:C6	2.56	0.41
38:A1:799:G:OP2	63:Aa:32:ARG:NH1	2.44	0.41
38:A1:863:C:H2'	38:A1:864:G:O4'	2.21	0.41
38:A1:1144:U:OP1	38:A1:1367:G:O2'	2.33	0.41
38:A1:1243:G:H21	38:A1:1271:A:H5'	1.85	0.41
38:A1:1748:G:OP2	73:Ak:42:LYS:NZ	2.49	0.41
38:A1:2152:A:H2'	38:A1:2153:U:C6	2.55	0.41
38:A1:2294:U:OP2	58:AV:71:LYS:NZ	2.41	0.41
38:A1:2466:G:OP2	79:E:105:LYS:NZ	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2520:A:H2'	38:A1:2521:U:C6	2.56	0.41
38:A1:3072:C:H2'	38:A1:3073:A:O4'	2.20	0.41
38:A1:3295:A:H2'	38:A1:3296:A:C8	2.56	0.41
39:A3:119:U:P	41:AD:258:LYS:HZ1	2.43	0.41
40:A4:6:U:H2'	40:A4:7:U:C6	2.56	0.41
42:AE:40:LEU:HD13	42:AE:84:VAL:HG21	2.03	0.41
47:AJ:63:GLU:HG2	47:AJ:65:ILE:HG23	2.03	0.41
54:AR:173:ARG:O	54:AR:177:VAL:HG22	2.21	0.41
58:AV:13:ILE:HG23	58:AV:85:TRP:CG	2.56	0.41
62:AZ:103:GLN:HB2	62:AZ:106:GLN:OE1	2.21	0.41
67:Ae:34:LYS:O	67:Ae:36:LYS:NZ	2.52	0.41
77:Ao:12:CYS:HB2	77:Ao:23:HIS:CE1	2.56	0.41
80:EC:6923:C:H2'	80:EC:6924:G:C8	2.56	0.41
4:BE:94:ALA:HB1	15:BY:16:PRO:HB2	2.02	0.41
12:BV:73:ALA:HB3	12:BV:79:LEU:HD12	2.03	0.41
21:BK:7:ASP:HA	21:BK:10:LYS:HG2	2.03	0.41
22:BP:81:ARG:NH2	22:BP:117:GLY:O	2.54	0.41
23:BQ:48:VAL:HG12	23:BQ:82:ARG:HB3	2.01	0.41
33:BM:111:ASN:HB3	33:BM:113:ARG:HB3	2.03	0.41
34:B5:1323:C:H2'	34:B5:1324:G:C8	2.56	0.41
38:A1:142:C:H2'	38:A1:143:G:O4'	2.21	0.41
38:A1:251:G:H1'	38:A1:253:A:C5	2.55	0.41
38:A1:297:G:H8	71:Ai:31:GLY:HA2	1.86	0.41
38:A1:817:A2M:H62	72:Aj:25:ARG:NH2	2.19	0.41
38:A1:992:A:H5''	56:AT:43:LYS:HD2	2.02	0.41
38:A1:2335:G:N2	38:A1:2339:C:O2'	2.54	0.41
38:A1:2500:A:H2'	38:A1:2501:U:H6	1.86	0.41
38:A1:3185:U:O2'	55:AS:170:THR:OG1	2.32	0.41
39:A3:108:A:H2'	39:A3:109:G:H8	1.86	0.41
41:AD:8:LYS:HD3	41:AD:8:LYS:HA	1.85	0.41
46:AI:93:PRO:HB2	46:AI:125:LEU:HB3	2.03	0.41
47:AJ:45:PRO:HB3	47:AJ:69:VAL:HB	2.02	0.41
53:AQ:90:ASP:OD2	53:AQ:92:ARG:NH2	2.38	0.41
55:AS:26:ARG:O	56:AT:150:THR:HB	2.20	0.41
61:AY:27:ARG:NH1	61:AY:76:LEU:O	2.53	0.41
79:E:113:SER:HB3	79:E:116:LEU:HD13	2.03	0.41
80:EC:6858:A:H4'	80:EC:6859:U:O5'	2.21	0.41
3:BC:37:PRO:HB2	3:BC:43:ARG:HG3	2.03	0.40
7:BI:37:LYS:HA	7:BI:37:LYS:HD3	1.78	0.40
9:BL:3:THR:HG22	9:BL:51:GLY:HA2	2.03	0.40
15:BY:12:VAL:HA	15:BY:23:PHE:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Ba:95:ARG:NH1	34:B5:1796:C:O2'	2.54	0.40
22:BP:118:GLU:HB2	25:BS:122:HIS:H	1.85	0.40
31:Bg:239:GLU:HB3	31:Bg:257:ALA:HB2	2.03	0.40
34:B5:71:A:C2	34:B5:73:U:H5'	2.56	0.40
34:B5:1382:A:O2'	34:B5:1383:G:H5''	2.21	0.40
34:B5:1484:G:H2'	34:B5:1485:C:C6	2.55	0.40
35:AA:177:LYS:O	38:A1:1793:C:N4	2.35	0.40
36:AB:62:ARG:H	36:AB:68:HIS:CD2	2.38	0.40
36:AB:95:THR:HB	36:AB:98:GLY:O	2.21	0.40
38:A1:563:U:H2'	38:A1:564:G:H8	1.86	0.40
38:A1:819:U:H2'	38:A1:820:A:H8	1.86	0.40
38:A1:945:C:H2'	38:A1:946:U:C6	2.56	0.40
38:A1:1524:A:O2'	38:A1:1526:U:OP2	2.27	0.40
38:A1:1785:U:H2'	38:A1:1786:G:C8	2.55	0.40
38:A1:2344:U:H2'	38:A1:2345:A:C8	2.57	0.40
38:A1:2369:G:H2'	38:A1:2370:G:C8	2.57	0.40
38:A1:3096:C:H2'	38:A1:3097:C:C6	2.56	0.40
40:A4:39:G:O2'	40:A4:105:A:N1	2.49	0.40
55:AS:110:MET:HE3	55:AS:110:MET:HB3	1.94	0.40
56:AT:44:ALA:HB2	56:AT:53:PRO:HG2	2.03	0.40
80:EC:6923:C:H2'	80:EC:6924:G:H8	1.87	0.40
4:BE:21:ASP:OD2	4:BE:24:SER:OG	2.36	0.40
5:BG:67:VAL:HG23	5:BG:99:GLY:HA2	2.03	0.40
7:BI:5:ARG:NH1	34:B5:336:G:O6	2.45	0.40
20:BF:72:HIS:NE2	34:B5:1610:G:OP1	2.49	0.40
20:BF:203:LYS:NZ	80:EC:6862:G:H4'	2.36	0.40
21:BK:25:LYS:HD2	21:BK:59:PHE:CZ	2.56	0.40
22:BP:56:PHE:CD2	22:BP:83:MET:HE1	2.57	0.40
25:BS:55:HIS:CE1	25:BS:57:ARG:HH21	2.38	0.40
31:Bg:54:PHE:CD2	31:Bg:312:VAL:HG21	2.55	0.40
34:B5:269:G:H2'	34:B5:270:C:C6	2.57	0.40
34:B5:366:A:OP1	34:B5:758:U:O2'	2.33	0.40
38:A1:792:G:H2'	38:A1:793:C:C6	2.56	0.40
38:A1:1542:G:H2'	38:A1:1543:G:C8	2.56	0.40
38:A1:1935:G:H2'	38:A1:1936:A:C8	2.53	0.40
38:A1:2427:U:H2'	38:A1:2428:U:C6	2.56	0.40
38:A1:2463:G:N7	38:A1:2490:C:N4	2.70	0.40
45:AH:2:LYS:HD3	45:AH:2:LYS:HA	1.88	0.40
46:AI:36:LEU:HD11	46:AI:69:ARG:HH11	1.85	0.40
52:AP:18:ARG:NH1	52:AP:147:GLU:OE1	2.53	0.40
2:BB:157:GLN:C	2:BB:159:SER:H	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:56:CYS:SG	17:Bb:59:CYS:N	2.89	0.40
29:Bc:7:VAL:HG23	29:Bc:57:MET:HA	2.04	0.40
34:B5:693:U:H5''	34:B5:694:U:H5'	2.03	0.40
34:B5:1647:U:H2'	34:B5:1648:A:H8	1.86	0.40
38:A1:35:A:H2'	38:A1:36:C:H6	1.87	0.40
38:A1:616:G:H2'	38:A1:617:G:H8	1.86	0.40
38:A1:1354:G:O2'	38:A1:1355:A:OP1	2.33	0.40
38:A1:1622:U:H2'	38:A1:1623:G:C8	2.56	0.40
38:A1:2946:A2M:H5''	38:A1:2947:G:H5'	2.03	0.40
39:A3:53:U:O2'	39:A3:55:A:N7	2.53	0.40
42:AE:142:ASP:OD1	42:AE:143:LYS:N	2.55	0.40
60:AX:46:TYR:CD1	70:Ah:75:TYR:HB3	2.56	0.40
79:E:176:GLU:O	79:E:180:VAL:HG23	2.21	0.40
3:BC:235:LEU:HD12	3:BC:235:LEU:HA	1.93	0.40
7:BI:32:GLN:HE21	34:B5:1728:A:H1'	1.86	0.40
9:BL:38:ALA:O	34:B5:246:G:N2	2.54	0.40
11:BO:122:PRO:HB2	11:BO:123:SER:O	2.21	0.40
20:BF:99:MET:SD	20:BF:180:ARG:NH1	2.95	0.40
25:BS:39:GLY:N	34:B5:1566:U:H5''	2.36	0.40
30:Bd:14:TYR:OH	34:B5:1553:G:O2'	2.33	0.40
34:B5:9:U:N3	34:B5:12:U:OP2	2.39	0.40
34:B5:138:A:N6	34:B5:266:A:H61	2.20	0.40
38:A1:166:C:H2'	38:A1:167:U:H6	1.85	0.40
38:A1:616:G:H2'	38:A1:617:G:C8	2.56	0.40
38:A1:1120:A:H2'	38:A1:1121:U:H6	1.87	0.40
38:A1:1211:U:H2'	38:A1:1212:A:C8	2.57	0.40
38:A1:1244:A:H4'	38:A1:1245:A:N7	2.37	0.40
38:A1:2266:U:H2'	38:A1:2267:C:C6	2.56	0.40
38:A1:2902:A:H2'	38:A1:2903:A:O4'	2.21	0.40
38:A1:3007:U:H2'	38:A1:3008:A:C8	2.57	0.40
38:A1:3322:A:H2'	38:A1:3323:A:H8	1.84	0.40
39:A3:94:C:H2'	39:A3:95:A:H8	1.86	0.40
53:AQ:94:PHE:CE2	63:Aa:119:PRO:HD3	2.57	0.40
54:AR:19:LYS:HB2	54:AR:19:LYS:HE3	1.96	0.40
67:Ae:32:TRP:O	67:Ae:33:ARG:NH1	2.50	0.40
80:EC:6929:C:H2'	80:EC:6930:G:H8	1.84	0.40
3:BC:144:TRP:CE2	3:BC:173:PRO:HG3	2.57	0.40
6:BH:82:GLU:HG3	6:BH:90:VAL:HG12	2.03	0.40
22:BP:44:ARG:NH2	22:BP:82:ASN:O	2.43	0.40
22:BP:56:PHE:CE2	22:BP:83:MET:HE1	2.57	0.40
27:BU:61:LYS:NZ	34:B5:1516:A:H5''	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:215:A:H2'	34:B5:216:U:O4'	2.22	0.40
34:B5:861:U:H3'	34:B5:862:A:C8	2.56	0.40
34:B5:1125:A:C5	34:B5:1126:OMG:H1'	2.57	0.40
38:A1:172:G:H2'	38:A1:173:G:C8	2.56	0.40
38:A1:1910:A:H2'	38:A1:1911:A:C8	2.56	0.40
38:A1:2445:A:N1	38:A1:2502:A:H2	2.19	0.40
38:A1:2661:G:H2'	38:A1:2662:G:C8	2.57	0.40
58:AV:15:LEU:HD23	58:AV:53:SER:HB3	2.02	0.40
58:AV:63:LYS:HD3	58:AV:63:LYS:HA	1.87	0.40
62:AZ:135:ARG:HA	62:AZ:135:ARG:HD3	1.72	0.40
63:Aa:90:TYR:CG	63:Aa:100:PRO:HG3	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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%)	186 (91%)	18 (9%)	0	100	100
2	BB	212/255 (83%)	185 (87%)	27 (13%)	0	100	100
3	BC	215/254 (85%)	206 (96%)	9 (4%)	0	100	100
4	BE	258/261 (99%)	244 (95%)	14 (5%)	0	100	100
5	BG	224/236 (95%)	215 (96%)	9 (4%)	0	100	100
6	BH	182/190 (96%)	170 (93%)	12 (7%)	0	100	100
7	BI	184/200 (92%)	168 (91%)	16 (9%)	0	100	100
8	BJ	183/197 (93%)	168 (92%)	15 (8%)	0	100	100
9	BL	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
10	BN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
11	BO	125/137 (91%)	112 (90%)	13 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	BV	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
13	BW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
14	BX	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
15	BY	132/135 (98%)	124 (94%)	8 (6%)	0	100	100
16	Ba	95/119 (80%)	79 (83%)	16 (17%)	0	100	100
17	Bb	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
18	Be	58/63 (92%)	53 (91%)	5 (9%)	0	100	100
19	BD	221/240 (92%)	209 (95%)	12 (5%)	0	100	100
20	BF	204/225 (91%)	191 (94%)	13 (6%)	0	100	100
21	BK	94/105 (90%)	83 (88%)	11 (12%)	0	100	100
22	BP	122/142 (86%)	111 (91%)	11 (9%)	0	100	100
23	BQ	139/143 (97%)	133 (96%)	6 (4%)	0	100	100
24	BR	117/136 (86%)	110 (94%)	7 (6%)	0	100	100
25	BS	143/146 (98%)	129 (90%)	14 (10%)	0	100	100
26	BT	139/144 (96%)	127 (91%)	12 (9%)	0	100	100
27	BU	105/121 (87%)	100 (95%)	5 (5%)	0	100	100
28	BZ	67/108 (62%)	62 (92%)	5 (8%)	0	100	100
29	Bc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
30	Bd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
31	Bg	310/319 (97%)	275 (89%)	35 (11%)	0	100	100
32	Bf	53/152 (35%)	39 (74%)	14 (26%)	0	100	100
33	BM	119/143 (83%)	95 (80%)	24 (20%)	0	100	100
35	AA	245/254 (96%)	232 (95%)	13 (5%)	0	100	100
36	AB	383/387 (99%)	367 (96%)	16 (4%)	0	100	100
37	AC	359/362 (99%)	335 (93%)	24 (7%)	0	100	100
41	AD	290/297 (98%)	276 (95%)	14 (5%)	0	100	100
42	AE	152/176 (86%)	141 (93%)	11 (7%)	0	100	100
43	AF	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
44	AG	228/256 (89%)	212 (93%)	16 (7%)	0	100	100
45	AH	188/191 (98%)	172 (92%)	16 (8%)	0	100	100
46	AI	201/221 (91%)	191 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	AJ	167/174 (96%)	142 (85%)	25 (15%)	0	100	100
48	AL	191/199 (96%)	179 (94%)	12 (6%)	0	100	100
49	AM	134/138 (97%)	130 (97%)	4 (3%)	0	100	100
50	AN	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
51	AO	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
52	AP	171/184 (93%)	167 (98%)	4 (2%)	0	100	100
53	AQ	183/186 (98%)	178 (97%)	5 (3%)	0	100	100
54	AR	186/189 (98%)	177 (95%)	9 (5%)	0	100	100
55	AS	170/178 (96%)	160 (94%)	10 (6%)	0	100	100
56	AT	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
57	AU	98/121 (81%)	94 (96%)	4 (4%)	0	100	100
58	AV	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
59	AW	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
60	AX	119/142 (84%)	115 (97%)	4 (3%)	0	100	100
61	AY	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
62	AZ	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
63	Aa	146/149 (98%)	130 (89%)	16 (11%)	0	100	100
64	Ab	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
65	Ac	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
66	Ad	107/113 (95%)	100 (94%)	7 (6%)	0	100	100
67	Ae	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
68	Af	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
69	Ag	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
70	Ah	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
71	Ai	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
72	Aj	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
73	Ak	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
74	Al	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
75	Am	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	94 (91%)	9 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	Ap	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
79	E	215/217 (99%)	205 (95%)	10 (5%)	0	100	100
All	All	11086/12103 (92%)	10364 (94%)	722 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	49/135 (36%)	49 (100%)	0	100	100
33	BM	98/119 (82%)	98 (100%)	0	100	100
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	321/322 (100%)	321 (100%)	0	100	100
37	AC	288/289 (100%)	288 (100%)	0	100	100
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	134/153 (88%)	134 (100%)	0	100	100
43	AF	186/205 (91%)	186 (100%)	0	100	100
44	AG	189/208 (91%)	189 (100%)	0	100	100
45	AH	170/171 (99%)	170 (100%)	0	100	100
46	AI	176/187 (94%)	176 (100%)	0	100	100
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
69	Ag	95/103 (92%)	95 (100%)	0	100	100
70	Ah	104/105 (99%)	104 (100%)	0	100	100
71	Ai	81/82 (99%)	81 (100%)	0	100	100
72	Aj	70/71 (99%)	70 (100%)	0	100	100
73	Ak	68/69 (99%)	68 (100%)	0	100	100
74	Al	45/46 (98%)	45 (100%)	0	100	100
75	Am	47/116 (40%)	47 (100%)	0	100	100
76	An	23/23 (100%)	23 (100%)	0	100	100
77	Ao	90/91 (99%)	90 (100%)	0	100	100
78	Ap	71/72 (99%)	71 (100%)	0	100	100
79	E	198/198 (100%)	198 (100%)	0	100	100
All	All	9468/10186 (93%)	9468 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (178) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	140	ASN

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Mol	Chain	Res	Type
2	BB	183	GLN
3	BC	89	GLN
3	BC	110	HIS
3	BC	201	ASN
3	BC	233	GLN
4	BE	57	ASN
4	BE	188	ASN
4	BE	197	HIS
4	BE	223	ASN
4	BE	224	ASN
4	BE	231	GLN
5	BG	4	ASN
5	BG	13	GLN
5	BG	34	GLN
5	BG	65	GLN
5	BG	139	ASN
6	BH	5	GLN
6	BH	11	GLN
7	BI	9	HIS
7	BI	32	GLN
7	BI	52	ASN
7	BI	103	GLN
7	BI	111	GLN
7	BI	138	ASN
7	BI	159	GLN
8	BJ	38	ASN
8	BJ	110	GLN
9	BL	81	HIS
9	BL	92	HIS
10	BN	49	GLN
10	BN	105	ASN
11	BO	12	GLN
11	BO	99	GLN
13	BW	12	ASN
13	BW	15	ASN
13	BW	16	ASN
13	BW	42	GLN
13	BW	56	HIS
13	BW	70	ASN
13	BW	92	ASN
14	BX	18	HIS
15	BY	15	ASN

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Mol	Chain	Res	Type
15	BY	22	GLN
15	BY	29	HIS
18	Be	17	GLN
19	BD	62	ASN
19	BD	67	ASN
19	BD	179	GLN
20	BF	34	GLN
20	BF	35	GLN
20	BF	37	GLN
20	BF	86	GLN
20	BF	100	ASN
20	BF	104	ASN
20	BF	116	HIS
20	BF	122	ASN
20	BF	200	ASN
21	BK	62	GLN
22	BP	103	ASN
23	BQ	32	ASN
23	BQ	83	GLN
23	BQ	139	GLN
24	BR	31	ASN
24	BR	48	ASN
24	BR	62	GLN
24	BR	74	GLN
25	BS	12	GLN
25	BS	75	ASN
25	BS	103	ASN
25	BS	127	HIS
25	BS	136	GLN
26	BT	101	ASN
26	BT	106	GLN
27	BU	15	GLN
27	BU	44	ASN
30	Bd	41	GLN
30	Bd	53	ASN
31	Bg	29	GLN
31	Bg	101	GLN
31	Bg	200	ASN
31	Bg	224	ASN
32	Bf	134	ASN
35	AA	38	HIS
35	AA	47	GLN

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Mol	Chain	Res	Type
35	AA	50	HIS
35	AA	140	ASN
35	AA	215	ASN
36	AB	68	HIS
36	AB	121	ASN
36	AB	198	HIS
36	AB	224	HIS
36	AB	279	ASN
36	AB	345	ASN
37	AC	9	HIS
37	AC	58	HIS
37	AC	116	ASN
37	AC	296	GLN
37	AC	361	HIS
41	AD	63	GLN
41	AD	111	GLN
42	AE	4	GLN
42	AE	167	ASN
43	AF	112	ASN
43	AF	157	ASN
43	AF	166	ASN
43	AF	209	ASN
44	AG	24	ASN
44	AG	28	HIS
44	AG	38	GLN
44	AG	77	GLN
44	AG	145	ASN
45	AH	50	ASN
45	AH	102	ASN
45	AH	157	ASN
46	AI	23	ASN
46	AI	51	HIS
46	AI	59	GLN
46	AI	73	ASN
46	AI	92	HIS
46	AI	100	ASN
46	AI	208	ASN
48	AL	19	GLN
49	AM	41	GLN
49	AM	126	GLN
50	AN	138	GLN
50	AN	156	HIS

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Mol	Chain	Res	Type
50	AN	182	ASN
50	AN	194	GLN
51	AO	26[A]	GLN
51	AO	31[A]	GLN
51	AO	42[A]	ASN
52	AP	92	GLN
52	AP	120	ASN
53	AQ	9	GLN
53	AQ	126	GLN
54	AR	7	GLN
55	AS	8	GLN
55	AS	89	ASN
56	AT	5	HIS
57	AU	9	GLN
57	AU	87	ASN
58	AV	98	ASN
60	AX	65	GLN
60	AX	85	GLN
60	AX	94	GLN
61	AY	81	GLN
62	AZ	36	HIS
62	AZ	78	ASN
62	AZ	122	HIS
62	AZ	123	GLN
63	Aa	11	HIS
63	Aa	14	HIS
63	Aa	64	GLN
63	Aa	65	GLN
64	Ab	11	ASN
64	Ab	45	HIS
64	Ab	48	HIS
66	Ad	21	HIS
68	Af	26	ASN
69	Ag	69	HIS
70	Ah	34	GLN
70	Ah	99	GLN
70	Ah	104	GLN
70	Ah	108	GLN
72	Aj	13	ASN
72	Aj	69	HIS
73	Ak	40	GLN
74	Al	4	GLN

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Mol	Chain	Res	Type
74	Al	43	ASN
75	Am	109	ASN
75	Am	117	HIS
77	Ao	23	HIS
77	Ao	102	GLN
79	E	40	ASN
79	E	108	ASN
79	E	127	GLN
79	E	182	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1780/1799 (98%)	403 (22%)	12 (0%)
38	A1	3194/3360 (95%)	606 (18%)	27 (0%)
39	A3	120/121 (99%)	12 (10%)	1 (0%)
40	A4	157/158 (99%)	26 (16%)	0
80	EC	189/202 (93%)	87 (46%)	11 (5%)
All	All	5440/5640 (96%)	1134 (20%)	51 (0%)

All (1134) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	17	C
34	B5	25	C
34	B5	26	A
34	B5	34	G
34	B5	42	G
34	B5	45	U
34	B5	46	A
34	B5	47	A
34	B5	57	G
34	B5	67	A
34	B5	68	A
34	B5	72	A
34	B5	73	U
34	B5	74	U
34	B5	75	U
34	B5	77	U
34	B5	81	G
34	B5	103	A

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Mol	Chain	Res	Type
34	B5	104	A
34	B5	111	U
34	B5	114	C
34	B5	115	G
34	B5	116	U
34	B5	130	C
34	B5	131	C
34	B5	132	U
34	B5	133	U
34	B5	134	U
34	B5	135	A
34	B5	136	C
34	B5	137	U
34	B5	138	A
34	B5	141	U
34	B5	145	A
34	B5	160	C
34	B5	162	A
34	B5	164	A
34	B5	166	C
34	B5	168	A
34	B5	169	A
34	B5	173	A
34	B5	178	U
34	B5	179	A
34	B5	180	A
34	B5	181	A
34	B5	182	A
34	B5	185	U
34	B5	188	A
34	B5	191	C
34	B5	192	U
34	B5	193	U
34	B5	194	U
34	B5	195	G
34	B5	196	G
34	B5	198	A
34	B5	204	G
34	B5	207	U
34	B5	217	A
34	B5	218	A
34	B5	221	A

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Mol	Chain	Res	Type
34	B5	225	A
34	B5	227	U
34	B5	228	G
34	B5	229	U
34	B5	230	C
34	B5	232	U
34	B5	233	C
34	B5	234	G
34	B5	240	U
34	B5	241	U
34	B5	250	C
34	B5	257	A
34	B5	260	U
34	B5	261	U
34	B5	262	U
34	B5	265	A
34	B5	267	U
34	B5	280	U
34	B5	283	U
34	B5	287	G
34	B5	291	G
34	B5	299	A
34	B5	305	C
34	B5	314	C
34	B5	316	A
34	B5	320	U
34	B5	322	G
34	B5	333	A
34	B5	337	G
34	B5	338	C
34	B5	352	A
34	B5	353	A
34	B5	359	A
34	B5	360	A
34	B5	361	C
34	B5	390	G
34	B5	400	A
34	B5	401	A
34	B5	402	C
34	B5	417	A
34	B5	419	G
34	B5	423	G

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Mol	Chain	Res	Type
34	B5	424	C
34	B5	425	A
34	B5	426	G
34	B5	434	G
34	B5	439	U
34	B5	444	C
34	B5	448	C
34	B5	452	A
34	B5	454	U
34	B5	459	G
34	B5	460	A
34	B5	461	G
34	B5	477	A
34	B5	484	C
34	B5	485	A
34	B5	486	G
34	B5	487	G
34	B5	488	G
34	B5	489	C
34	B5	491	C
34	B5	492	A
34	B5	494	U
34	B5	495	C
34	B5	496	G
34	B5	497	G
34	B5	498	G
34	B5	499	U
34	B5	500	C
34	B5	501	U
34	B5	503	G
34	B5	506	A
34	B5	507	U
34	B5	515	A
34	B5	527	A
34	B5	538	A
34	B5	539	G
34	B5	540	G
34	B5	541	A2M
34	B5	542	A
34	B5	544	A
34	B5	548	G
34	B5	555	A

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Mol	Chain	Res	Type
34	B5	557	G
34	B5	558	U
34	B5	559	C
34	B5	565	C
34	B5	577	G
34	B5	579	A
34	B5	580	A
34	B5	582	U
34	B5	594	A
34	B5	595	G
34	B5	606	A
34	B5	610	G
34	B5	611	U
34	B5	619	A2M
34	B5	620	A
34	B5	622	A
34	B5	623	A
34	B5	624	G
34	B5	638	U
34	B5	639	U
34	B5	650	U
34	B5	652	G
34	B5	654	C
34	B5	655	G
34	B5	656	G
34	B5	657	U
34	B5	677	G
34	B5	678	A
34	B5	679	U
34	B5	681	U
34	B5	683	C
34	B5	693	U
34	B5	694	U
34	B5	696	C
34	B5	697	C
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	712	G

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Mol	Chain	Res	Type
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	725	U
34	B5	726	C
34	B5	727	U
34	B5	729	G
34	B5	730	G
34	B5	731	C
34	B5	732	G
34	B5	733	A
34	B5	735	C
34	B5	737	A
34	B5	738	G
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
34	B5	779	U
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	820	U
34	B5	821	U
34	B5	823	G
34	B5	833	U
34	B5	836	U

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Mol	Chain	Res	Type
34	B5	837	G
34	B5	840	U
34	B5	846	G
34	B5	852	C
34	B5	859	A
34	B5	863	A
34	B5	886	U
34	B5	893	U
34	B5	895	G
34	B5	898	A
34	B5	904	G
34	B5	906	A
34	B5	907	A
34	B5	913	G
34	B5	926	A
34	B5	928	U
34	B5	933	A
34	B5	935	U
34	B5	951	A
34	B5	960	U
34	B5	966	A
34	B5	987	G
34	B5	988	A
34	B5	992	A
34	B5	993	A
34	B5	1004	U
34	B5	1005	A
34	B5	1020	A
34	B5	1026	A
34	B5	1028	C
34	B5	1032	G
34	B5	1039	A
34	B5	1052	U
34	B5	1056	U
34	B5	1057	U
34	B5	1058	U
34	B5	1059	U
34	B5	1060	U
34	B5	1061	A
34	B5	1062	A
34	B5	1076	A
34	B5	1083	G

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Mol	Chain	Res	Type
34	B5	1092	A
34	B5	1093	A
34	B5	1097	U
34	B5	1100	G
34	B5	1138	A
34	B5	1150	G
34	B5	1158	C
34	B5	1159	C
34	B5	1172	G
34	B5	1173	C
34	B5	1185	U
34	B5	1193	A
34	B5	1194	A
34	B5	1196	A
34	B5	1199	G
34	B5	1200	G
34	B5	1201	G
34	B5	1202	A
34	B5	1207	C
34	B5	1217	A
34	B5	1218	G
34	B5	1226	A
34	B5	1227	A
34	B5	1228	G
34	B5	1234	A
34	B5	1243	G
34	B5	1244	A
34	B5	1245	G
34	B5	1249	U
34	B5	1251	U
34	B5	1254	U
34	B5	1256	A
34	B5	1257	U
34	B5	1258	U
34	B5	1263	G
34	B5	1269	OMU
34	B5	1270	G
34	B5	1286	U
34	B5	1314	U
34	B5	1315	U
34	B5	1316	G
34	B5	1321	A

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Mol	Chain	Res	Type
34	B5	1340	U
34	B5	1344	A
34	B5	1345	A
34	B5	1352	G
34	B5	1355	C
34	B5	1356	U
34	B5	1362	U
34	B5	1363	U
34	B5	1364	G
34	B5	1368	G
34	B5	1370	U
34	B5	1371	A
34	B5	1372	U
34	B5	1373	C
34	B5	1378	U
34	B5	1385	G
34	B5	1390	U
34	B5	1399	C
34	B5	1400	A
34	B5	1413	U
34	B5	1414	U
34	B5	1415	U
34	B5	1425	A
34	B5	1427	A
34	B5	1428	OMG
34	B5	1436	A
34	B5	1447	C
34	B5	1459	C
34	B5	1460	A
34	B5	1471	A
34	B5	1486	G
34	B5	1491	U
34	B5	1492	A
34	B5	1493	A
34	B5	1494	C
34	B5	1496	U
34	B5	1503	A
34	B5	1515	A
34	B5	1516	A
34	B5	1520	U
34	B5	1521	G
34	B5	1523	G

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Mol	Chain	Res	Type
34	B5	1524	A
34	B5	1537	C
34	B5	1540	G
34	B5	1542	G
34	B5	1557	U
34	B5	1559	A
34	B5	1572	OMG
34	B5	1573	A
34	B5	1575	G7M
34	B5	1576	A
34	B5	1582	U
34	B5	1584	G
34	B5	1590	G
34	B5	1601	G
34	B5	1607	G
34	B5	1616	G
34	B5	1634	C
34	B5	1645	G
34	B5	1646	C
34	B5	1651	A
34	B5	1657	U
34	B5	1658	G
34	B5	1667	A
34	B5	1683	C
34	B5	1684	U
34	B5	1688	U
34	B5	1699	G
34	B5	1700	C
34	B5	1701	A
34	B5	1703	C
34	B5	1709	C
34	B5	1712	A
34	B5	1715	G
34	B5	1716	C
34	B5	1717	G
34	B5	1755	A
34	B5	1757	G
34	B5	1766	A
34	B5	1767	G
34	B5	1769	U
34	B5	1771	U
34	B5	1780	G

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Mol	Chain	Res	Type
34	B5	1782	MA6
34	B5	1792	G
34	B5	1793	G
34	B5	1794	A
34	B5	1795	U
34	B5	1796	C
34	B5	1799	U
38	A1	6	A
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	74	G
38	A1	77	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	121	A
38	A1	122	A
38	A1	134	U
38	A1	135	C
38	A1	136	G
38	A1	156	G
38	A1	157	A
38	A1	162	G
38	A1	163	C
38	A1	164	A
38	A1	165	A
38	A1	169	U
38	A1	175	C
38	A1	176	G
38	A1	177	U
38	A1	187	A
38	A1	190	U

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Mol	Chain	Res	Type
38	A1	191	U
38	A1	200	C
38	A1	210	U
38	A1	219	A
38	A1	237	G
38	A1	238	A
38	A1	239	G
38	A1	240	U
38	A1	241	G
38	A1	242	C
38	A1	243	G
38	A1	244	G
38	A1	246	U
38	A1	248	U
38	A1	249	U
38	A1	250	U
38	A1	252	U
38	A1	253	A
38	A1	254	A
38	A1	269	G
38	A1	286	U
38	A1	295	A
38	A1	296	A
38	A1	298	U
38	A1	305	U
38	A1	329	U
38	A1	339	C
38	A1	352	A
38	A1	373	A
38	A1	374	A
38	A1	376	G
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

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Mol	Chain	Res	Type
38	A1	521	A
38	A1	523	A
38	A1	535	G
38	A1	540	U
38	A1	542	G
38	A1	545	U
38	A1	546	C
38	A1	547	G
38	A1	548	G
38	A1	552	G
38	A1	554	A
38	A1	557	A
38	A1	559	A
38	A1	560	G
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	677	A
38	A1	681	U
38	A1	690	A
38	A1	705	A
38	A1	715	A
38	A1	719	U
38	A1	736	A
38	A1	765	C
38	A1	766	U
38	A1	767	U
38	A1	774	G
38	A1	777	U
38	A1	781	G
38	A1	785	G
38	A1	786	A
38	A1	799	G
38	A1	806	A
38	A1	813	G
38	A1	817	A2M
38	A1	818	C
38	A1	830	A

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Mol	Chain	Res	Type
38	A1	849	C
38	A1	861	C
38	A1	874	U
38	A1	879	U
38	A1	896	A
38	A1	897	U
38	A1	907	G
38	A1	908	OMG
38	A1	914	A
38	A1	916	G
38	A1	917	A
38	A1	921	A
38	A1	923	C
38	A1	924	G
38	A1	925	A
38	A1	934	G
38	A1	937	G
38	A1	943	U
38	A1	944	C
38	A1	959	C
38	A1	974	G
38	A1	980	A
38	A1	981	U
38	A1	982	C
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	1020	G
38	A1	1022	U
38	A1	1023	C
38	A1	1032	C
38	A1	1033	U
38	A1	1034	U
38	A1	1035	G
38	A1	1045	C
38	A1	1047	A

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Mol	Chain	Res	Type
38	A1	1064	A
38	A1	1072	G
38	A1	1075	A
38	A1	1081	U
38	A1	1082	U
38	A1	1093	A
38	A1	1094	U
38	A1	1097	G
38	A1	1098	A
38	A1	1103	A
38	A1	1104	G
38	A1	1117	G
38	A1	1131	G
38	A1	1144	U
38	A1	1153	A
38	A1	1155	C
38	A1	1159	A
38	A1	1160	C
38	A1	1178	G
38	A1	1179	A
38	A1	1180	A
38	A1	1181	U
38	A1	1182	A
38	A1	1192	C
38	A1	1193	A
38	A1	1196	C
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	1228	C
38	A1	1231	A
38	A1	1232	C
38	A1	1233	G
38	A1	1235	U
38	A1	1236	G
38	A1	1237	G

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Mol	Chain	Res	Type
38	A1	1239	C
38	A1	1241	U
38	A1	1242	G
38	A1	1243	G
38	A1	1244	A
38	A1	1245	A
38	A1	1246	G
38	A1	1252	A
38	A1	1255	C
38	A1	1256	G
38	A1	1257	C
38	A1	1258	U
38	A1	1259	A
38	A1	1262	G
38	A1	1263	A
38	A1	1265	U
38	A1	1266	G
38	A1	1270	A
38	A1	1272	C
38	A1	1277	C
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	1293	U
38	A1	1307	G
38	A1	1309	U
38	A1	1317	A
38	A1	1330	A
38	A1	1331	U
38	A1	1348	U
38	A1	1349	G
38	A1	1350	A
38	A1	1351	U
38	A1	1352	A
38	A1	1353	U
38	A1	1354	G
38	A1	1355	A

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Mol	Chain	Res	Type
38	A1	1356	U
38	A1	1357	G
38	A1	1386	A
38	A1	1392	G
38	A1	1393	A
38	A1	1399	A
38	A1	1400	G
38	A1	1419	A
38	A1	1434	G
38	A1	1437	OMC
38	A1	1443	G
38	A1	1446	A
38	A1	1455	U
38	A1	1468	A
38	A1	1469	C
38	A1	1481	A
38	A1	1484	U
38	A1	1487	G
38	A1	1496	C
38	A1	1502	C
38	A1	1508	C
38	A1	1512	U
38	A1	1523	U
38	A1	1555	U
38	A1	1556	C
38	A1	1558	A
38	A1	1562	C
38	A1	1564	U
38	A1	1565	G
38	A1	1566	A
38	A1	1567	U
38	A1	1568	U
38	A1	1569	U
38	A1	1572	U
38	A1	1575	A
38	A1	1576	G
38	A1	1579	C
38	A1	1580	A
38	A1	1581	C
38	A1	1583	A
38	A1	1593	A
38	A1	1605	A

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Mol	Chain	Res	Type
38	A1	1628	C
38	A1	1629	U
38	A1	1630	U
38	A1	1642	A
38	A1	1643	A
38	A1	1688	U
38	A1	1724	U
38	A1	1725	C
38	A1	1738	C
38	A1	1741	A
38	A1	1750	A
38	A1	1751	G
38	A1	1761	C
38	A1	1762	C
38	A1	1763	U
38	A1	1764	U
38	A1	1765	U
38	A1	1766	G
38	A1	1775	G
38	A1	1779	C
38	A1	1797	A
38	A1	1813	A
38	A1	1815	U
38	A1	1817	G
38	A1	1820	U
38	A1	1821	U
38	A1	1842	A
38	A1	1846	C
38	A1	1849	C
38	A1	1850	A
38	A1	1851	G
38	A1	1866	C
38	A1	1878	G
38	A1	1880	U
38	A1	1893	A
38	A1	1906	G
38	A1	1932	A
38	A1	1936	A
38	A1	1948	G
38	A1	1950	U
38	A1	1952	G
38	A1	1953	G

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Mol	Chain	Res	Type
38	A1	1954	G
38	A1	1955	U
38	A1	2095	G
38	A1	2102	U
38	A1	2111	G
38	A1	2112	U
38	A1	2113	A
38	A1	2114	C
38	A1	2122	G
38	A1	2131	A
38	A1	2140	U
38	A1	2144	A
38	A1	2145	A
38	A1	2146	C
38	A1	2158	A
38	A1	2159	U
38	A1	2169	G
38	A1	2184	U
38	A1	2188	A
38	A1	2192	C
38	A1	2201	G
38	A1	2205	U
38	A1	2206	G
38	A1	2207	A
38	A1	2210	G
38	A1	2218	G
38	A1	2242	A
38	A1	2249	G
38	A1	2256	A2M
38	A1	2257	C
38	A1	2260	U
38	A1	2262	A
38	A1	2269	U
38	A1	2270	A
38	A1	2272	G
38	A1	2273	G
38	A1	2279	A
38	A1	2280	A2M
38	A1	2281	A2M
38	A1	2307	G
38	A1	2308	C
38	A1	2310	U

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Mol	Chain	Res	Type
38	A1	2313	A
38	A1	2314	U
38	A1	2315	G
38	A1	2318	U
38	A1	2334	U
38	A1	2335	G
38	A1	2336	U
38	A1	2340	U
38	A1	2364	G
38	A1	2366	C
38	A1	2372	A
38	A1	2373	A
38	A1	2374	C
38	A1	2375	G
38	A1	2383	C
38	A1	2388	U
38	A1	2393	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	2435	G
38	A1	2442	G
38	A1	2445	A
38	A1	2446	U
38	A1	2447	A
38	A1	2449	A
38	A1	2453	U
38	A1	2454	G
38	A1	2455	U
38	A1	2458	A
38	A1	2459	A
38	A1	2461	A
38	A1	2462	A
38	A1	2463	G
38	A1	2465	G
38	A1	2467	G
38	A1	2468	A
38	A1	2472	U
38	A1	2474	G

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Mol	Chain	Res	Type
38	A1	2475	G
38	A1	2477	G
38	A1	2483	G
38	A1	2484	A
38	A1	2485	A
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	2494	A
38	A1	2495	C
38	A1	2496	C
38	A1	2497	U
38	A1	2498	U
38	A1	2499	U
38	A1	2500	A
38	A1	2501	U
38	A1	2502	A
38	A1	2503	G
38	A1	2504	U
38	A1	2506	U
38	A1	2507	C
38	A1	2514	U
38	A1	2523	A
38	A1	2524	A
38	A1	2530	G
38	A1	2537	U
38	A1	2538	U
38	A1	2539	C
38	A1	2540	A
38	A1	2541	U
38	A1	2546	C
38	A1	2549	G
38	A1	2550	U
38	A1	2552	C
38	A1	2554	A
38	A1	2561	A
38	A1	2562	A
38	A1	2568	C
38	A1	2569	A

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Mol	Chain	Res	Type
38	A1	2571	U
38	A1	2572	C
38	A1	2573	G
38	A1	2585	G
38	A1	2593	A
38	A1	2594	C
38	A1	2606	G
38	A1	2607	G
38	A1	2614	G
38	A1	2626	A
38	A1	2652	U
38	A1	2656	A
38	A1	2674	A
38	A1	2676	A
38	A1	2677	G
38	A1	2679	A
38	A1	2681	U
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	2714	G
38	A1	2719	U
38	A1	2728	G
38	A1	2729	OMU
38	A1	2737	C
38	A1	2752	U
38	A1	2753	G
38	A1	2755	C
38	A1	2762	A
38	A1	2773	C
38	A1	2777	G
38	A1	2778	G
38	A1	2796	G
38	A1	2798	C
38	A1	2799	A
38	A1	2800	G
38	A1	2801	A
38	A1	2803	A
38	A1	2810	C

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Mol	Chain	Res	Type
38	A1	2814	G
38	A1	2817	A
38	A1	2828	G
38	A1	2842	U
38	A1	2844	C
38	A1	2845	A
38	A1	2849	C
38	A1	2860	U
38	A1	2867	C
38	A1	2871	G
38	A1	2872	A
38	A1	2873	U
38	A1	2875	U
38	A1	2876	C
38	A1	2887	A
38	A1	2889	C
38	A1	2894	C
38	A1	2898	G
38	A1	2923	U
38	A1	2935	U
38	A1	2936	A
38	A1	2938	G
38	A1	2942	C
38	A1	2943	G
38	A1	2947	G
38	A1	2954	U
38	A1	2955	U
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	3030	G
38	A1	3032	A
38	A1	3058	U
38	A1	3059	G
38	A1	3078	U
38	A1	3079	U
38	A1	3080	G
38	A1	3086	A

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Mol	Chain	Res	Type
38	A1	3092	C
38	A1	3101	G
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	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	3158	G
38	A1	3165	A
38	A1	3170	A
38	A1	3172	A
38	A1	3173	G
38	A1	3174	A
38	A1	3176	G
38	A1	3179	U
38	A1	3181	C
38	A1	3186	A
38	A1	3187	A
38	A1	3195	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	3224	G
38	A1	3229	G
38	A1	3234	A
38	A1	3243	A
38	A1	3250	U
38	A1	3259	U
38	A1	3260	G

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Mol	Chain	Res	Type
38	A1	3271	G
38	A1	3273	A
38	A1	3275	U
38	A1	3276	G
38	A1	3278	C
38	A1	3281	U
38	A1	3284	G
38	A1	3289	G
38	A1	3294	A
38	A1	3304	U
38	A1	3314	A
38	A1	3316	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	3375	A
38	A1	3378	C
38	A1	3389	U
39	A3	11	A
39	A3	20	A
39	A3	41	G
39	A3	53	U
39	A3	54	U
39	A3	55	A
39	A3	65	G
39	A3	76	A
39	A3	78	U
39	A3	102	A
39	A3	112	G
39	A3	121	U
40	A4	23	U
40	A4	34	U
40	A4	35	C
40	A4	51	G
40	A4	52	A

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Mol	Chain	Res	Type
40	A4	59	A
40	A4	62	C
40	A4	63	G
40	A4	81	U
40	A4	82	U
40	A4	83	C
40	A4	85	G
40	A4	86	U
40	A4	87	G
40	A4	90	U
40	A4	95	G
40	A4	104	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	157	U
40	A4	158	U
80	EC	6759	A
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	6782	C
80	EC	6788	C
80	EC	6789	G
80	EC	6790	A
80	EC	6791	A

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Mol	Chain	Res	Type
80	EC	6792	A
80	EC	6793	A
80	EC	6794	C
80	EC	6795	U
80	EC	6802	A
80	EC	6803	C
80	EC	6804	A
80	EC	6816	A
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	6825	A
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	6849	A
80	EC	6850	C
80	EC	6851	G
80	EC	6852	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	6867	C
80	EC	6869	C
80	EC	6870	A
80	EC	6871	A
80	EC	6873	A

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Mol	Chain	Res	Type
80	EC	6875	C
80	EC	6877	C
80	EC	6880	G
80	EC	6889	A
80	EC	6897	G
80	EC	6901	C
80	EC	6902	U
80	EC	6904	U
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	6927	U
80	EC	6928	G
80	EC	6929	C
80	EC	6935	G
80	EC	6940	U
80	EC	6941	U
80	EC	6943	A
80	EC	6945	U
80	EC	6946	A
80	EC	6950	C

All (51) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	B5	224	C
34	B5	486	G
34	B5	752	A
34	B5	819	G
34	B5	862	A
34	B5	950	C
34	B5	1057	U
34	B5	1226	A
34	B5	1285	U
34	B5	1344	A
34	B5	1458	G
34	B5	1645	G
38	A1	237	G
38	A1	238	A

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Mol	Chain	Res	Type
38	A1	240	U
38	A1	242	C
38	A1	873	C
38	A1	916	G
38	A1	1014	U
38	A1	1092	C
38	A1	1218	U
38	A1	1236	G
38	A1	1240	A
38	A1	1292	C
38	A1	1354	G
38	A1	1568	U
38	A1	2241	U
38	A1	2466	G
38	A1	2496	C
38	A1	2497	U
38	A1	2498	U
38	A1	2499	U
38	A1	2501	U
38	A1	2503	G
38	A1	2504	U
38	A1	2506	U
38	A1	2870	5MC
38	A1	2954	U
38	A1	3121	U
39	A3	52	G
80	EC	6789	G
80	EC	6831	U
80	EC	6844	A
80	EC	6851	G
80	EC	6857	C
80	EC	6858	A
80	EC	6863	C
80	EC	6876	A
80	EC	6901	C
80	EC	6911	A
80	EC	6934	U

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

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$
38	OMU	A1	2724	38	19,22,23	1.22	3 (15%)	25,31,34	1.82	5 (20%)
34	OMG	B5	1126	34	23,26,27	1.18	3 (13%)	32,38,41	2.00	6 (18%)
38	OMU	A1	2347	38	19,22,23	1.29	4 (21%)	25,31,34	1.84	5 (20%)
38	A2M	A1	2220	38	22,25,26	1.54	5 (22%)	30,36,39	1.94	8 (26%)
34	OMC	B5	1007	34	19,22,23	0.78	0	25,31,34	0.91	1 (4%)
38	OMC	A1	663	38	19,22,23	0.79	0	25,31,34	0.80	0
38	A2M	A1	1449	81,38	22,25,26	1.48	4 (18%)	30,36,39	2.03	7 (23%)
34	OMC	B5	414	34	19,22,23	0.81	0	25,31,34	0.80	1 (4%)
34	A2M	B5	436	34	22,25,26	1.51	4 (18%)	30,36,39	2.06	7 (23%)
38	5MC	A1	2278	81,38	19,22,23	1.55	3 (15%)	26,32,35	1.22	3 (11%)
38	OMU	A1	2421	38	19,22,23	1.23	3 (15%)	25,31,34	1.82	5 (20%)
38	OMG	A1	2793	38	23,26,27	1.18	3 (13%)	32,38,41	2.02	6 (18%)
38	1MA	A1	645	81,38	21,25,26	1.34	4 (19%)	30,37,40	1.66	6 (20%)
36	HIC	AB	243	36	10,11,12	1.49	1 (10%)	9,14,16	1.48	1 (11%)
38	1MA	A1	2142	81,38	21,25,26	1.33	4 (19%)	30,37,40	1.72	4 (13%)
38	A2M	A1	2640	38	22,25,26	1.48	3 (13%)	30,36,39	2.06	7 (23%)
34	G7M	B5	1575	34	23,26,27	2.59	9 (39%)	34,39,42	2.96	12 (35%)
38	OMG	A1	867	38	23,26,27	1.18	3 (13%)	32,38,41	2.01	6 (18%)
34	4AC	B5	1773	34	21,24,25	0.99	1 (4%)	28,34,37	1.97	7 (25%)
34	OMC	B5	1639	34	19,22,23	0.76	0	25,31,34	0.76	0
38	OMC	A1	650	38	19,22,23	0.77	0	25,31,34	0.83	1 (4%)
38	OMC	A1	1437	81,38	19,22,23	0.83	0	25,31,34	1.32	4 (16%)
34	A2M	B5	796	34	22,25,26	1.49	4 (18%)	30,36,39	2.29	9 (30%)
34	OMG	B5	1428	34	23,26,27	1.19	3 (13%)	32,38,41	1.95	6 (18%)
38	OMG	A1	908	38	23,26,27	1.20	3 (13%)	32,38,41	2.06	6 (18%)
38	OMG	A1	1450	38	23,26,27	1.19	3 (13%)	32,38,41	1.96	6 (18%)
38	OMC	A1	2337	38	19,22,23	0.78	0	25,31,34	0.79	0
34	4AC	B5	1280	34	21,24,25	1.01	1 (4%)	28,34,37	1.09	4 (14%)
38	UR3	A1	2634	38	19,22,23	0.97	0	26,32,35	1.73	2 (7%)
38	OMC	A1	2197	38	19,22,23	0.78	0	25,31,34	0.86	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	A2M	B5	28	81,34	22,25,26	1.49	4 (18%)	30,36,39	2.08	9 (30%)
34	A2M	B5	100	81,34	22,25,26	1.50	3 (13%)	30,36,39	2.06	7 (23%)
38	A2M	A1	1133	81,38	22,25,26	1.48	4 (18%)	30,36,39	2.24	10 (33%)
38	OMG	A1	2922	38	23,26,27	1.19	3 (13%)	32,38,41	1.94	6 (18%)
38	OMC	A1	2948	38	19,22,23	0.80	0	25,31,34	1.01	1 (4%)
38	OMU	A1	898	38	19,22,23	1.26	3 (15%)	25,31,34	1.82	5 (20%)
34	A2M	B5	541	34	22,25,26	1.50	4 (18%)	30,36,39	2.16	8 (26%)
38	A2M	A1	649	38	22,25,26	1.44	3 (13%)	30,36,39	1.99	7 (23%)
38	OMU	A1	1888	38	19,22,23	1.26	3 (15%)	25,31,34	1.89	5 (20%)
38	OMU	A1	2729	38	19,22,23	1.33	4 (21%)	25,31,34	1.83	7 (28%)
38	A2M	A1	2256	80,38	22,25,26	1.50	5 (22%)	30,36,39	2.15	10 (33%)
38	OMG	A1	2619	38	23,26,27	1.20	3 (13%)	32,38,41	1.98	6 (18%)
38	A2M	A1	817	81,38	22,25,26	1.48	5 (22%)	30,36,39	2.04	9 (30%)
34	A2M	B5	619	81,34	22,25,26	1.48	5 (22%)	30,36,39	2.05	9 (30%)
34	XSX	B5	1191	34	24,28,29	0.98	0	30,40,43	2.48	4 (13%)
38	A2M	A1	2281	38	22,25,26	1.37	4 (18%)	30,36,39	2.42	12 (40%)
34	OMG	B5	562	34	23,26,27	1.19	3 (13%)	32,38,41	1.94	6 (18%)
34	OMG	B5	1271	34	23,26,27	1.18	3 (13%)	32,38,41	1.94	6 (18%)
34	MA6	B5	1782	34	23,26,27	1.51	5 (21%)	33,38,41	2.08	10 (30%)
38	OMG	A1	2815	38	23,26,27	1.20	3 (13%)	32,38,41	1.98	6 (18%)
34	A2M	B5	420	34	22,25,26	1.50	4 (18%)	30,36,39	2.07	10 (33%)
34	OMU	B5	1269	34	19,22,23	1.27	4 (21%)	25,31,34	1.87	5 (20%)
38	A2M	A1	876	38	22,25,26	1.47	3 (13%)	30,36,39	2.00	7 (23%)
34	A2M	B5	974	34	22,25,26	1.47	5 (22%)	30,36,39	2.01	11 (36%)
34	MA6	B5	1781	34	23,26,27	1.53	5 (21%)	33,38,41	2.12	10 (30%)
38	OMG	A1	2288	38	23,26,27	1.19	3 (13%)	32,38,41	1.97	6 (18%)
38	OMU	A1	2417	38	19,22,23	1.22	3 (15%)	25,31,34	1.79	5 (20%)
38	A2M	A1	2946	81,38	22,25,26	1.49	5 (22%)	30,36,39	2.14	11 (36%)
38	5MC	A1	2870	38	19,22,23	1.58	3 (15%)	26,32,35	1.30	3 (11%)
34	OMG	B5	1572	34	23,26,27	1.19	3 (13%)	32,38,41	1.96	6 (18%)
38	OMC	A1	2959	38	19,22,23	0.81	0	25,31,34	0.83	1 (4%)
38	A2M	A1	807	38	22,25,26	1.48	4 (18%)	30,36,39	2.10	8 (26%)
38	OMU	A1	2921	81,38	19,22,23	1.24	3 (15%)	25,31,34	1.85	5 (20%)
38	OMG	A1	805	38	23,26,27	1.19	3 (13%)	32,38,41	2.03	7 (21%)
38	A2M	A1	2280	38	22,25,26	1.48	4 (18%)	30,36,39	2.10	9 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	OMU	B5	578	34	19,22,23	1.21	3 (15%)	25,31,34	1.82	5 (20%)
38	OMG	A1	2791	38	23,26,27	1.18	3 (13%)	32,38,41	1.98	6 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMU	A1	2724	38	-	1/9/27/28	0/2/2/2
34	OMG	B5	1126	34	-	1/9/27/28	0/3/3/3
38	OMU	A1	2347	38	-	2/9/27/28	0/2/2/2
38	A2M	A1	2220	38	-	1/9/27/28	0/3/3/3
34	OMC	B5	1007	34	-	0/9/27/28	0/2/2/2
38	OMC	A1	663	38	-	1/9/27/28	0/2/2/2
38	A2M	A1	1449	81,38	-	0/9/27/28	0/3/3/3
34	OMC	B5	414	34	-	1/9/27/28	0/2/2/2
34	A2M	B5	436	34	-	0/9/27/28	0/3/3/3
38	5MC	A1	2278	81,38	-	0/7/25/26	0/2/2/2
38	OMU	A1	2421	38	-	1/9/27/28	0/2/2/2
38	OMG	A1	2793	38	-	0/9/27/28	0/3/3/3
38	1MA	A1	645	81,38	-	2/7/25/26	0/3/3/3
36	HIC	AB	243	36	-	1/5/6/8	0/1/1/1
38	1MA	A1	2142	81,38	-	0/7/25/26	0/3/3/3
38	A2M	A1	2640	38	-	0/9/27/28	0/3/3/3
34	G7M	B5	1575	34	-	0/7/25/26	0/3/3/3
38	OMG	A1	867	38	-	0/9/27/28	0/3/3/3
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
34	OMC	B5	1639	34	-	0/9/27/28	0/2/2/2
38	OMC	A1	650	38	-	1/9/27/28	0/2/2/2
38	OMC	A1	1437	81,38	-	3/9/27/28	0/2/2/2
34	A2M	B5	796	34	-	0/9/27/28	0/3/3/3
34	OMG	B5	1428	34	-	3/9/27/28	0/3/3/3
38	OMG	A1	908	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	1450	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2337	38	-	0/9/27/28	0/2/2/2
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
34	A2M	B5	28	81,34	-	0/9/27/28	0/3/3/3
34	A2M	B5	100	81,34	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	A2M	A1	1133	81,38	-	0/9/27/28	0/3/3/3
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2948	38	-	1/9/27/28	0/2/2/2
38	OMU	A1	898	38	-	0/9/27/28	0/2/2/2
34	A2M	B5	541	34	-	4/9/27/28	0/3/3/3
38	A2M	A1	649	38	-	1/9/27/28	0/3/3/3
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2
38	OMU	A1	2729	38	-	3/9/27/28	0/2/2/2
38	A2M	A1	2256	80,38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2619	38	-	3/9/27/28	0/3/3/3
38	A2M	A1	817	81,38	-	1/9/27/28	0/3/3/3
34	A2M	B5	619	81,34	-	3/9/27/28	0/3/3/3
34	XSX	B5	1191	34	-	3/16/34/35	0/2/2/2
38	A2M	A1	2281	38	-	0/9/27/28	0/3/3/3
34	OMG	B5	562	34	-	0/9/27/28	0/3/3/3
34	OMG	B5	1271	34	-	1/9/27/28	0/3/3/3
34	MA6	B5	1782	34	-	3/11/29/30	0/3/3/3
38	OMG	A1	2815	38	-	0/9/27/28	0/3/3/3
34	A2M	B5	420	34	-	1/9/27/28	0/3/3/3
34	OMU	B5	1269	34	-	5/9/27/28	0/2/2/2
38	A2M	A1	876	38	-	1/9/27/28	0/3/3/3
34	A2M	B5	974	34	-	0/9/27/28	0/3/3/3
34	MA6	B5	1781	34	-	0/11/29/30	0/3/3/3
38	OMG	A1	2288	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2417	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2946	81,38	-	0/9/27/28	0/3/3/3
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
34	OMG	B5	1572	34	-	3/9/27/28	0/3/3/3
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	807	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2921	81,38	-	0/9/27/28	0/2/2/2
38	OMG	A1	805	38	-	1/9/27/28	0/3/3/3
38	A2M	A1	2280	38	-	2/9/27/28	0/3/3/3
34	OMU	B5	578	34	-	0/9/27/28	0/2/2/2
38	OMG	A1	2791	38	-	1/9/27/28	0/3/3/3

All (196) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	C8-N7	7.56	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2870	5MC	C5-C4	5.57	1.48	1.44
38	A1	2278	5MC	C5-C4	5.48	1.48	1.44
34	B5	1575	G7M	C5-N7	-5.02	1.33	1.39
34	B5	541	A2M	C5-C4	4.75	1.47	1.39
34	B5	1781	MA6	C5-C4	4.73	1.47	1.39
34	B5	1782	MA6	C5-C4	4.70	1.47	1.39
34	B5	436	A2M	C5-C4	4.66	1.47	1.39
38	A1	2220	A2M	C5-C4	4.62	1.47	1.39
38	A1	876	A2M	C5-C4	4.59	1.47	1.39
34	B5	100	A2M	C5-C4	4.58	1.47	1.39
38	A1	2946	A2M	C5-C4	4.54	1.47	1.39
34	B5	420	A2M	C5-C4	4.54	1.47	1.39
34	B5	796	A2M	C5-C4	4.53	1.47	1.39
38	A1	2256	A2M	C5-C4	4.53	1.47	1.39
38	A1	807	A2M	C5-C4	4.53	1.47	1.39
38	A1	1449	A2M	C5-C4	4.51	1.47	1.39
34	B5	28	A2M	C5-C4	4.50	1.47	1.39
34	B5	619	A2M	C5-C4	4.50	1.47	1.39
38	A1	2280	A2M	C5-C4	4.50	1.47	1.39
38	A1	2640	A2M	C5-C4	4.49	1.47	1.39
38	A1	1133	A2M	C5-C4	4.49	1.47	1.39
34	B5	974	A2M	C5-C4	4.41	1.46	1.39
38	A1	649	A2M	C5-C4	4.40	1.46	1.39
38	A1	817	A2M	C5-C4	4.38	1.46	1.39
38	A1	2281	A2M	C5-C4	3.90	1.46	1.39
34	B5	1575	G7M	C8-N9	3.79	1.45	1.35
34	B5	1575	G7M	C5-C4	3.37	1.46	1.38
34	B5	1781	MA6	C5-C6	3.18	1.49	1.41
34	B5	1428	OMG	C5-C4	3.18	1.47	1.38
34	B5	1575	G7M	C2'-C3'	-3.16	1.44	1.53
34	B5	1271	OMG	C5-C4	3.14	1.47	1.38
34	B5	562	OMG	C5-C4	3.11	1.47	1.38
34	B5	1572	OMG	C5-C4	3.09	1.47	1.38
38	A1	2791	OMG	C5-C4	3.08	1.47	1.38
38	A1	2922	OMG	C5-C4	3.07	1.47	1.38
38	A1	908	OMG	C5-C4	3.06	1.47	1.38
34	B5	1782	MA6	C5-C6	3.05	1.49	1.41
38	A1	2288	OMG	C5-C4	3.05	1.47	1.38
34	B5	1126	OMG	C5-C4	3.05	1.47	1.38
38	A1	2619	OMG	C5-C4	3.05	1.47	1.38
38	A1	2815	OMG	C5-C4	3.03	1.47	1.38
38	A1	2729	OMU	C4-N3	-3.02	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2142	1MA	C5-C4	3.01	1.47	1.38
38	A1	1450	OMG	C5-C4	2.99	1.46	1.38
38	A1	645	1MA	C5-C4	2.99	1.46	1.38
38	A1	2142	1MA	C6-N6	2.98	1.35	1.28
38	A1	2793	OMG	C5-C4	2.96	1.46	1.38
38	A1	805	OMG	C5-C4	2.96	1.46	1.38
38	A1	645	1MA	C6-N6	2.95	1.35	1.28
38	A1	867	OMG	C5-C4	2.94	1.46	1.38
36	AB	243	HIC	CD2-CG	2.93	1.41	1.36
38	A1	2870	5MC	C6-C5	2.93	1.39	1.34
38	A1	898	OMU	C4-N3	-2.93	1.33	1.38
38	A1	2921	OMU	C4-N3	-2.87	1.33	1.38
38	A1	2347	OMU	C4-N3	-2.86	1.33	1.38
38	A1	1888	OMU	C4-N3	-2.84	1.33	1.38
38	A1	2417	OMU	C4-N3	-2.81	1.33	1.38
38	A1	2278	5MC	C6-C5	2.77	1.39	1.34
38	A1	2220	A2M	C5-C6	2.75	1.48	1.41
34	B5	541	A2M	C5-C6	2.74	1.48	1.41
38	A1	2256	A2M	C5-C6	2.73	1.48	1.41
38	A1	2815	OMG	C6-N1	-2.72	1.33	1.38
38	A1	2421	OMU	C4-N3	-2.71	1.34	1.38
34	B5	420	A2M	C5-C6	2.71	1.48	1.41
38	A1	2724	OMU	C4-N3	-2.71	1.34	1.38
34	B5	1280	4AC	C4-N4	-2.70	1.35	1.39
34	B5	796	A2M	C5-C6	2.70	1.48	1.41
34	B5	100	A2M	C5-N7	-2.68	1.34	1.39
34	B5	28	A2M	C5-C6	2.68	1.48	1.41
38	A1	2791	OMG	C6-N1	-2.67	1.33	1.38
38	A1	2793	OMG	C6-N1	-2.67	1.33	1.38
38	A1	1449	A2M	C5-N7	-2.65	1.34	1.39
34	B5	1269	OMU	C4-N3	-2.64	1.34	1.38
38	A1	807	A2M	C5-C6	2.64	1.48	1.41
38	A1	908	OMG	C6-N1	-2.63	1.33	1.38
34	B5	1126	OMG	C6-N1	-2.62	1.33	1.38
34	B5	619	A2M	C5-C6	2.62	1.48	1.41
38	A1	2619	OMG	C6-N1	-2.62	1.33	1.38
38	A1	2280	A2M	C5-C6	2.62	1.48	1.41
34	B5	436	A2M	C5-C6	2.61	1.48	1.41
38	A1	817	A2M	C5-C6	2.61	1.48	1.41
38	A1	1133	A2M	C5-C6	2.60	1.48	1.41
38	A1	2640	A2M	C5-C6	2.60	1.48	1.41
38	A1	2922	OMG	C6-N1	-2.60	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	578	OMU	C4-N3	-2.60	1.34	1.38
38	A1	805	OMG	C6-N1	-2.59	1.34	1.38
38	A1	2288	OMG	C6-N1	-2.58	1.34	1.38
38	A1	1450	OMG	C6-N1	-2.58	1.34	1.38
34	B5	1428	OMG	C6-N1	-2.56	1.34	1.38
34	B5	974	A2M	C5-C6	2.55	1.48	1.41
34	B5	436	A2M	C5-N7	-2.55	1.34	1.39
38	A1	867	OMG	C6-N1	-2.54	1.34	1.38
34	B5	562	OMG	C6-N1	-2.54	1.34	1.38
38	A1	649	A2M	C5-C6	2.51	1.48	1.41
38	A1	1449	A2M	C5-C6	2.51	1.48	1.41
34	B5	100	A2M	C5-C6	2.51	1.48	1.41
38	A1	2640	A2M	C5-N7	-2.50	1.34	1.39
38	A1	649	A2M	C5-N7	-2.49	1.34	1.39
38	A1	2946	A2M	C5-N7	-2.48	1.34	1.39
38	A1	1133	A2M	C5-N7	-2.48	1.34	1.39
34	B5	1271	OMG	C6-N1	-2.47	1.34	1.38
38	A1	2946	A2M	C5-C6	2.47	1.47	1.41
38	A1	876	A2M	C5-N7	-2.47	1.34	1.39
38	A1	876	A2M	C5-C6	2.45	1.47	1.41
38	A1	2729	OMU	C2-N1	2.45	1.42	1.38
34	B5	1575	G7M	C2'-C1'	-2.45	1.45	1.53
38	A1	807	A2M	C5-N7	-2.44	1.34	1.39
38	A1	2280	A2M	C5-N7	-2.43	1.34	1.39
34	B5	974	A2M	C5-N7	-2.42	1.34	1.39
34	B5	541	A2M	C5-N7	-2.40	1.34	1.39
34	B5	420	A2M	C5-N7	-2.39	1.34	1.39
38	A1	2220	A2M	C5-N7	-2.38	1.34	1.39
34	B5	796	A2M	C5-N7	-2.38	1.34	1.39
38	A1	2256	A2M	C8-N7	2.38	1.36	1.31
34	B5	1773	4AC	C4-N4	-2.37	1.36	1.39
38	A1	1888	OMU	C2-N3	-2.37	1.33	1.38
38	A1	817	A2M	C5-N7	-2.37	1.34	1.39
34	B5	1572	OMG	C6-N1	-2.36	1.34	1.38
34	B5	28	A2M	C5-N7	-2.36	1.34	1.39
34	B5	619	A2M	C5-N7	-2.35	1.34	1.39
38	A1	2281	A2M	C5-C6	2.35	1.47	1.41
38	A1	2921	OMU	C2-N3	-2.35	1.33	1.38
38	A1	2281	A2M	C4-N9	-2.35	1.32	1.37
34	B5	1575	G7M	C6-N1	-2.33	1.34	1.38
38	A1	2142	1MA	C5-N7	-2.33	1.34	1.39
38	A1	898	OMU	C2-N3	-2.33	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2220	A2M	C8-N7	2.30	1.36	1.31
38	A1	2421	OMU	C2-N3	-2.29	1.34	1.38
38	A1	2347	OMU	C2-N3	-2.29	1.34	1.38
34	B5	1269	OMU	C2-N1	2.29	1.42	1.38
34	B5	420	A2M	C8-N7	2.29	1.36	1.31
38	A1	908	OMG	C5-N7	-2.28	1.34	1.39
38	A1	2729	OMU	C2-N3	-2.27	1.34	1.38
38	A1	2815	OMG	C5-N7	-2.27	1.34	1.39
38	A1	2281	A2M	C5-N7	-2.27	1.34	1.39
34	B5	796	A2M	C8-N7	2.27	1.36	1.31
38	A1	2619	OMG	C5-N7	-2.26	1.34	1.39
38	A1	2347	OMU	C2-N1	2.26	1.42	1.38
38	A1	2417	OMU	C2-N3	-2.26	1.34	1.38
38	A1	2724	OMU	C5-C4	-2.25	1.38	1.43
38	A1	817	A2M	C4-N9	-2.25	1.33	1.37
38	A1	2288	OMG	C5-N7	-2.25	1.34	1.39
38	A1	898	OMU	C5-C4	-2.23	1.38	1.43
38	A1	2220	A2M	C4-N9	-2.23	1.33	1.37
38	A1	2417	OMU	C5-C4	-2.22	1.38	1.43
38	A1	2729	OMU	C5-C4	-2.22	1.38	1.43
34	B5	619	A2M	C8-N7	2.22	1.35	1.31
34	B5	1269	OMU	C2-N3	-2.22	1.34	1.38
34	B5	578	OMU	C2-N3	-2.21	1.34	1.38
38	A1	2922	OMG	C5-N7	-2.21	1.34	1.39
38	A1	645	1MA	C5-N7	-2.20	1.34	1.39
38	A1	2280	A2M	C8-N7	2.19	1.35	1.31
38	A1	2724	OMU	C2-N3	-2.19	1.34	1.38
34	B5	1782	MA6	C5-N7	-2.19	1.35	1.39
38	A1	2256	A2M	C5-N7	-2.19	1.35	1.39
34	B5	541	A2M	C8-N7	2.18	1.35	1.31
34	B5	1269	OMU	C5-C4	-2.18	1.39	1.43
34	B5	28	A2M	C8-N7	2.17	1.35	1.31
38	A1	805	OMG	C5-N7	-2.17	1.34	1.39
38	A1	2278	5MC	C6-N1	-2.17	1.34	1.38
34	B5	1781	MA6	C5-N7	-2.17	1.35	1.39
38	A1	1133	A2M	C8-N7	2.16	1.35	1.31
38	A1	2347	OMU	C5-C4	-2.16	1.39	1.43
34	B5	562	OMG	C5-N7	-2.16	1.34	1.39
34	B5	436	A2M	C8-N7	2.15	1.35	1.31
38	A1	1450	OMG	C5-N7	-2.15	1.34	1.39
34	B5	1782	MA6	C4-N9	-2.15	1.33	1.37
38	A1	2791	OMG	C5-N7	-2.14	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1782	MA6	C8-N7	2.14	1.35	1.31
34	B5	974	A2M	C8-N7	2.14	1.35	1.31
38	A1	2256	A2M	C4-N9	-2.13	1.33	1.37
38	A1	2946	A2M	C4-N9	-2.13	1.33	1.37
38	A1	2870	5MC	C6-N1	-2.13	1.34	1.38
38	A1	2946	A2M	C8-N7	2.12	1.35	1.31
38	A1	2793	OMG	C5-N7	-2.12	1.34	1.39
34	B5	1575	G7M	O2'-C2'	-2.12	1.37	1.43
38	A1	807	A2M	C8-N7	2.12	1.35	1.31
38	A1	2921	OMU	C5-C4	-2.12	1.39	1.43
38	A1	867	OMG	C5-N7	-2.11	1.34	1.39
38	A1	1888	OMU	C5-C4	-2.11	1.39	1.43
38	A1	2421	OMU	C5-C4	-2.11	1.39	1.43
34	B5	1428	OMG	C5-N7	-2.09	1.34	1.39
34	B5	1126	OMG	C5-N7	-2.09	1.34	1.39
38	A1	645	1MA	C4-N9	-2.08	1.32	1.38
34	B5	1572	OMG	C5-N7	-2.06	1.34	1.39
38	A1	1449	A2M	C8-N7	2.06	1.35	1.31
34	B5	1271	OMG	C5-N7	-2.06	1.34	1.39
38	A1	817	A2M	C8-N7	2.06	1.35	1.31
34	B5	974	A2M	C4-N9	-2.06	1.33	1.37
34	B5	1781	MA6	C4-N9	-2.06	1.33	1.37
34	B5	1781	MA6	C8-N7	2.05	1.35	1.31
34	B5	578	OMU	C5-C4	-2.05	1.39	1.43
38	A1	2142	1MA	C2-N3	2.04	1.34	1.30
34	B5	1575	G7M	C4-N9	-2.03	1.32	1.38
34	B5	619	A2M	C4-N9	-2.02	1.33	1.37

All (393) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1191	XSX	C3-C1-N3	11.43	132.13	112.16
34	B5	1575	G7M	CN7-N7-C8	-7.87	112.87	124.79
34	B5	1773	4AC	N4-C4-N3	7.05	125.31	113.87
38	A1	2634	UR3	C4-N3-C2	-6.90	119.02	124.58
34	B5	1575	G7M	N9-C8-N7	-6.55	96.59	112.48
38	A1	908	OMG	C5-C4-N3	-6.52	118.02	128.39
34	B5	541	A2M	C5-C4-N3	-6.48	117.79	126.72
34	B5	1575	G7M	C8-N7-C5	6.29	115.64	107.78
38	A1	2619	OMG	C5-C4-N3	-6.27	118.42	128.39
38	A1	2791	OMG	C5-C4-N3	-6.26	118.42	128.39
38	A1	2815	OMG	C5-C4-N3	-6.22	118.49	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2793	OMG	C5-C4-N3	-6.22	118.49	128.39
38	A1	2288	OMG	C5-C4-N3	-6.16	118.58	128.39
34	B5	1428	OMG	C5-C4-N3	-6.15	118.61	128.39
38	A1	2922	OMG	C5-C4-N3	-6.13	118.63	128.39
34	B5	1126	OMG	C5-C4-N3	-6.12	118.66	128.39
34	B5	796	A2M	C5-C4-N3	-6.09	118.34	126.72
34	B5	100	A2M	C5-C4-N3	-6.08	118.35	126.72
38	A1	867	OMG	C5-C4-N3	-6.08	118.72	128.39
38	A1	805	OMG	C5-C4-N3	-6.05	118.76	128.39
38	A1	1450	OMG	C5-C4-N3	-6.01	118.83	128.39
34	B5	1271	OMG	C5-C4-N3	-5.99	118.85	128.39
34	B5	562	OMG	C5-C4-N3	-5.99	118.86	128.39
34	B5	1572	OMG	C5-C4-N3	-5.94	118.94	128.39
38	A1	807	A2M	C5-C4-N3	-5.90	118.59	126.72
38	A1	2640	A2M	C5-C4-N3	-5.90	118.59	126.72
38	A1	876	A2M	C5-C4-N3	-5.88	118.63	126.72
34	B5	28	A2M	C5-C4-N3	-5.87	118.64	126.72
38	A1	1133	A2M	C5-C4-N3	-5.84	118.67	126.72
34	B5	619	A2M	C5-C4-N3	-5.84	118.67	126.72
38	A1	649	A2M	C5-C4-N3	-5.84	118.67	126.72
38	A1	1449	A2M	C5-C4-N3	-5.83	118.69	126.72
34	B5	436	A2M	C5-C4-N3	-5.79	118.74	126.72
38	A1	2280	A2M	C5-C4-N3	-5.73	118.83	126.72
38	A1	2220	A2M	C5-C4-N3	-5.71	118.85	126.72
34	B5	420	A2M	C5-C4-N3	-5.69	118.88	126.72
38	A1	817	A2M	C5-C4-N3	-5.55	119.08	126.72
38	A1	2946	A2M	C5-C4-N3	-5.42	119.26	126.72
38	A1	2281	A2M	C5-C4-N3	-5.37	119.32	126.72
34	B5	1781	MA6	C5-C4-N3	-5.37	119.32	126.72
34	B5	974	A2M	C5-C4-N3	-5.33	119.38	126.72
38	A1	2256	A2M	C5-C4-N3	-5.32	119.39	126.72
38	A1	2142	1MA	C5-C4-N3	-5.29	119.48	127.27
34	B5	541	A2M	N3-C4-N9	5.24	136.08	127.17
34	B5	1575	G7M	N9-C4-N3	5.20	136.36	125.95
38	A1	908	OMG	C2-N3-C4	5.19	121.23	112.30
34	B5	1782	MA6	C5-C4-N3	-5.18	119.59	126.72
38	A1	2793	OMG	C2-N3-C4	5.12	121.11	112.30
38	A1	867	OMG	C2-N3-C4	5.10	121.08	112.30
38	A1	2288	OMG	C2-N3-C4	5.09	121.07	112.30
34	B5	1575	G7M	C5-C4-N3	-5.09	118.53	128.15
38	A1	2791	OMG	C2-N3-C4	5.07	121.04	112.30
38	A1	2815	OMG	C2-N3-C4	5.06	121.02	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2619	OMG	C2-N3-C4	5.04	120.97	112.30
38	A1	805	OMG	C2-N3-C4	5.03	120.97	112.30
38	A1	1450	OMG	C2-N3-C4	5.02	120.94	112.30
34	B5	1126	OMG	C2-N3-C4	5.02	120.94	112.30
34	B5	1271	OMG	C2-N3-C4	5.01	120.92	112.30
34	B5	1191	XSX	C4-N3-C2	-5.00	118.78	124.66
34	B5	1428	OMG	C2-N3-C4	4.97	120.86	112.30
38	A1	908	OMG	N9-C4-N3	4.96	135.88	125.95
34	B5	1572	OMG	C2-N3-C4	4.95	120.82	112.30
34	B5	562	OMG	C2-N3-C4	4.93	120.78	112.30
38	A1	1888	OMU	C4-N3-C2	-4.92	120.50	126.61
34	B5	100	A2M	N3-C4-N9	4.92	135.53	127.17
38	A1	2922	OMG	C2-N3-C4	4.90	120.73	112.30
38	A1	2921	OMU	C4-N3-C2	-4.89	120.54	126.61
38	A1	645	1MA	C5-C4-N3	-4.89	120.07	127.27
38	A1	2421	OMU	C4-N3-C2	-4.85	120.59	126.61
38	A1	2640	A2M	N3-C4-N9	4.81	135.35	127.17
38	A1	2281	A2M	O4'-C1'-N9	4.76	117.24	108.09
38	A1	898	OMU	C4-N3-C2	-4.75	120.72	126.61
34	B5	578	OMU	C4-N3-C2	-4.74	120.72	126.61
38	A1	2793	OMG	N9-C4-N3	4.73	135.42	125.95
38	A1	2619	OMG	N9-C4-N3	4.73	135.41	125.95
38	A1	807	A2M	N3-C4-N9	4.71	135.18	127.17
34	B5	796	A2M	N3-C4-N9	4.71	135.18	127.17
38	A1	876	A2M	N3-C4-N9	4.69	135.15	127.17
38	A1	1449	A2M	N3-C4-N9	4.69	135.15	127.17
34	B5	796	A2M	C2'-C1'-N9	-4.69	106.04	113.75
38	A1	2281	A2M	N3-C4-N9	4.68	135.12	127.17
38	A1	2724	OMU	C4-N3-C2	-4.68	120.80	126.61
38	A1	2791	OMG	N9-C4-N3	4.68	135.31	125.95
38	A1	2288	OMG	N9-C4-N3	4.67	135.29	125.95
38	A1	649	A2M	N3-C4-N9	4.65	135.07	127.17
34	B5	28	A2M	N3-C4-N9	4.64	135.06	127.17
34	B5	1781	MA6	C4-C5-N7	-4.64	105.28	110.58
34	B5	1428	OMG	N9-C4-N3	4.61	135.16	125.95
38	A1	2417	OMU	C4-N3-C2	-4.59	120.92	126.61
38	A1	2142	1MA	C2-N3-C4	4.59	121.52	112.53
34	B5	619	A2M	N3-C4-N9	4.58	134.95	127.17
38	A1	2922	OMG	N9-C4-N3	4.57	135.08	125.95
38	A1	2815	OMG	N9-C4-N3	4.57	135.08	125.95
38	A1	1133	A2M	N3-C4-N9	4.55	134.91	127.17
38	A1	2280	A2M	N3-C4-N9	4.53	134.87	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	817	A2M	N3-C4-N9	4.52	134.86	127.17
38	A1	1450	OMG	N9-C4-N3	4.52	134.99	125.95
34	B5	420	A2M	N3-C4-N9	4.51	134.83	127.17
34	B5	1126	OMG	N9-C4-N3	4.50	134.95	125.95
34	B5	562	OMG	N9-C4-N3	4.50	134.95	125.95
34	B5	1575	G7M	C2-N3-C4	4.49	120.04	112.30
38	A1	1888	OMU	N3-C2-N1	4.48	120.72	114.89
38	A1	2921	OMU	N3-C2-N1	4.46	120.70	114.89
34	B5	436	A2M	N3-C4-N9	4.46	134.75	127.17
38	A1	645	1MA	C2-N3-C4	4.44	121.24	112.53
34	B5	1781	MA6	C2-N1-C6	4.44	122.67	111.83
38	A1	2347	OMU	C4-N3-C2	-4.44	121.10	126.61
38	A1	805	OMG	N9-C4-N3	4.43	134.81	125.95
34	B5	1782	MA6	C2-N1-C6	4.42	122.62	111.83
34	B5	1782	MA6	C4-C5-N7	-4.42	105.53	110.58
38	A1	898	OMU	N3-C2-N1	4.41	120.64	114.89
38	A1	867	OMG	N9-C4-N3	4.40	134.75	125.95
34	B5	974	A2M	N3-C4-N9	4.39	134.63	127.17
34	B5	1269	OMU	C4-N3-C2	-4.38	121.18	126.61
34	B5	1271	OMG	N9-C4-N3	4.37	134.69	125.95
38	A1	2281	A2M	C2'-C1'-N9	-4.35	106.60	113.75
38	A1	1133	A2M	C2'-C1'-N9	-4.34	106.61	113.75
38	A1	2417	OMU	N3-C2-N1	4.32	120.52	114.89
38	A1	2729	OMU	N3-C2-N1	4.32	120.51	114.89
38	A1	2946	A2M	N3-C4-N9	4.29	134.46	127.17
34	B5	1572	OMG	N9-C4-N3	4.26	134.47	125.95
38	A1	2729	OMU	C4-N3-C2	-4.22	121.38	126.61
38	A1	2347	OMU	N3-C2-N1	4.19	120.34	114.89
38	A1	2421	OMU	N3-C2-N1	4.16	120.30	114.89
38	A1	2724	OMU	N3-C2-N1	4.10	120.22	114.89
34	B5	578	OMU	N3-C2-N1	4.06	120.18	114.89
38	A1	2421	OMU	C5-C4-N3	4.05	120.47	114.80
34	B5	1773	4AC	C5-C4-N4	-4.04	116.14	122.94
38	A1	2256	A2M	N3-C4-N9	4.04	134.03	127.17
38	A1	2220	A2M	N3-C4-N9	4.02	134.00	127.17
38	A1	2870	5MC	C5-C6-N1	-3.97	119.00	123.31
38	A1	2921	OMU	C5-C4-N3	3.97	120.36	114.80
34	B5	541	A2M	C2-N3-C4	3.96	121.50	111.83
34	B5	1269	OMU	N3-C2-N1	3.95	120.04	114.89
38	A1	898	OMU	C5-C4-N3	3.95	120.33	114.80
38	A1	2220	A2M	C4-C5-N7	-3.94	106.08	110.58
38	A1	2724	OMU	C5-C4-N3	3.91	120.28	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2946	A2M	C2'-C1'-N9	-3.88	107.36	113.75
34	B5	1781	MA6	N3-C4-N9	3.85	133.72	127.17
34	B5	796	A2M	C2-N3-C4	3.82	121.17	111.83
34	B5	578	OMU	C5-C4-N3	3.81	120.14	114.80
38	A1	1888	OMU	C5-C4-N3	3.81	120.13	114.80
38	A1	2417	OMU	C5-C4-N3	3.79	120.11	114.80
38	A1	2640	A2M	C2-N3-C4	3.78	121.06	111.83
34	B5	1575	G7M	C8-N9-C4	3.78	116.44	107.09
34	B5	1575	G7M	CN7-N7-C5	3.76	131.48	126.80
34	B5	28	A2M	C2-N3-C4	3.75	121.00	111.83
38	A1	817	A2M	C2-N3-C4	3.75	120.99	111.83
38	A1	2347	OMU	C5-C4-N3	3.75	120.05	114.80
34	B5	619	A2M	C2-N3-C4	3.72	120.92	111.83
34	B5	1782	MA6	N3-C4-N9	3.72	133.49	127.17
38	A1	2281	A2M	C4-N9-C8	3.72	109.64	105.74
34	B5	1269	OMU	C5-C4-N3	3.71	120.00	114.80
38	A1	2280	A2M	C2-N3-C4	3.71	120.89	111.83
38	A1	876	A2M	C2-N3-C4	3.70	120.88	111.83
38	A1	1133	A2M	C2-N3-C4	3.70	120.87	111.83
34	B5	100	A2M	C2-N3-C4	3.70	120.87	111.83
38	A1	649	A2M	C2-N3-C4	3.70	120.87	111.83
38	A1	2256	A2M	C4-C5-N7	-3.70	106.36	110.58
38	A1	1449	A2M	C2-N3-C4	3.69	120.85	111.83
34	B5	420	A2M	C2-N3-C4	3.68	120.82	111.83
38	A1	807	A2M	C2-N3-C4	3.68	120.81	111.83
38	A1	2142	1MA	N9-C4-N3	3.65	135.22	126.90
34	B5	436	A2M	C2-N3-C4	3.64	120.72	111.83
38	A1	2280	A2M	C4-C5-N7	-3.63	106.43	110.58
36	AB	243	HIC	NE2-CE1-ND1	-3.62	111.28	112.66
38	A1	2256	A2M	C2-N3-C4	3.62	120.68	111.83
34	B5	796	A2M	C4-C5-N7	-3.61	106.46	110.58
34	B5	1781	MA6	C2-N3-C4	3.60	120.62	111.83
38	A1	1437	OMC	O2-C2-N3	-3.59	116.67	122.33
38	A1	2281	A2M	C2-N3-C4	3.59	120.60	111.83
38	A1	2946	A2M	C2-N3-C4	3.58	120.58	111.83
34	B5	619	A2M	C4-C5-N7	-3.53	106.54	110.58
38	A1	817	A2M	N3-C2-N1	-3.53	123.24	128.58
34	B5	1782	MA6	C2-N3-C4	3.53	120.45	111.83
34	B5	974	A2M	C2-N3-C4	3.51	120.39	111.83
38	A1	2729	OMU	C5-C4-N3	3.50	119.71	114.80
38	A1	1133	A2M	C4-C5-N7	-3.50	106.58	110.58
34	B5	1269	OMU	C1'-N1-C2	3.50	123.87	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	28	A2M	C4-C5-N7	-3.48	106.60	110.58
34	B5	420	A2M	C4-C5-N7	-3.46	106.62	110.58
38	A1	805	OMG	C6-C5-N7	3.45	136.56	130.29
38	A1	2220	A2M	C2-N3-C4	3.44	120.24	111.83
38	A1	867	OMG	C6-C5-N7	3.43	136.53	130.29
34	B5	974	A2M	N3-C2-N1	-3.39	123.45	128.58
34	B5	1126	OMG	C6-C5-N7	3.38	136.44	130.29
38	A1	2256	A2M	N3-C2-N1	-3.38	123.47	128.58
38	A1	2946	A2M	N3-C2-N1	-3.37	123.48	128.58
34	B5	1271	OMG	C6-C5-N7	3.37	136.42	130.29
38	A1	807	A2M	C4-C5-N7	-3.36	106.74	110.58
38	A1	2280	A2M	N3-C2-N1	-3.36	123.50	128.58
34	B5	1572	OMG	C6-C5-N7	3.36	136.40	130.29
38	A1	2640	A2M	N3-C2-N1	-3.35	123.52	128.58
38	A1	876	A2M	N3-C2-N1	-3.34	123.52	128.58
38	A1	2946	A2M	C4-C5-N7	-3.34	106.77	110.58
34	B5	28	A2M	N3-C2-N1	-3.32	123.56	128.58
38	A1	2347	OMU	C1'-N1-C2	3.31	123.55	117.59
34	B5	436	A2M	C4-C5-N7	-3.31	106.80	110.58
38	A1	2634	UR3	C5-C4-N3	3.30	119.39	115.04
38	A1	1450	OMG	C6-C5-N7	3.30	136.30	130.29
34	B5	974	A2M	C4-C5-N7	-3.30	106.81	110.58
34	B5	1781	MA6	N1-C2-N3	-3.29	123.59	128.58
34	B5	436	A2M	N3-C2-N1	-3.28	123.62	128.58
34	B5	796	A2M	N3-C2-N1	-3.28	123.62	128.58
34	B5	420	A2M	N3-C2-N1	-3.27	123.64	128.58
38	A1	2640	A2M	C4-C5-N7	-3.26	106.86	110.58
38	A1	876	A2M	C4-C5-N7	-3.26	106.86	110.58
34	B5	1782	MA6	N1-C2-N3	-3.26	123.65	128.58
38	A1	1133	A2M	N3-C2-N1	-3.26	123.65	128.58
38	A1	1449	A2M	N3-C2-N1	-3.26	123.65	128.58
34	B5	100	A2M	C4-C5-N7	-3.26	106.86	110.58
38	A1	817	A2M	C4-C5-N7	-3.24	106.87	110.58
34	B5	541	A2M	C4-C5-N7	-3.24	106.88	110.58
38	A1	2724	OMU	O4-C4-C5	-3.23	119.59	125.16
38	A1	1437	OMC	C1'-N1-C2	3.23	125.57	118.44
38	A1	649	A2M	N3-C2-N1	-3.23	123.70	128.58
38	A1	2815	OMG	C6-C5-N7	3.22	136.15	130.29
34	B5	541	A2M	N3-C2-N1	-3.22	123.71	128.58
38	A1	649	A2M	C4-C5-N7	-3.21	106.91	110.58
34	B5	619	A2M	N3-C2-N1	-3.20	123.74	128.58
34	B5	562	OMG	C6-C5-N7	3.20	136.11	130.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2281	A2M	N3-C2-N1	-3.20	123.74	128.58
34	B5	1781	MA6	C5-N7-C8	3.19	108.46	103.45
38	A1	2729	OMU	C1'-N1-C2	3.19	123.31	117.59
38	A1	1449	A2M	C4-C5-N7	-3.17	106.96	110.58
34	B5	1773	4AC	C6-C5-C4	3.17	120.82	117.00
38	A1	2421	OMU	O4-C4-C5	-3.15	119.72	125.16
38	A1	2791	OMG	C6-C5-N7	3.12	135.98	130.29
34	B5	100	A2M	N3-C2-N1	-3.12	123.86	128.58
38	A1	2417	OMU	O4-C4-C5	-3.11	119.79	125.16
38	A1	2278	5MC	C5-C6-N1	-3.11	119.94	123.31
38	A1	645	1MA	N9-C4-N3	3.11	133.97	126.90
34	B5	1428	OMG	C6-C5-N7	3.10	135.93	130.29
34	B5	1575	G7M	O3'-C3'-C4'	3.10	119.98	111.08
38	A1	2793	OMG	C6-C5-N7	3.10	135.93	130.29
38	A1	2922	OMG	C6-C5-N7	3.09	135.92	130.29
38	A1	2619	OMG	C6-C5-N7	3.07	135.88	130.29
38	A1	2921	OMU	O4-C4-C5	-3.07	119.86	125.16
38	A1	898	OMU	O4-C4-C5	-3.07	119.87	125.16
34	B5	1269	OMU	O4-C4-C5	-3.06	119.88	125.16
38	A1	2948	OMC	O2-C2-N3	-3.03	117.55	122.33
38	A1	2288	OMG	C6-C5-N7	3.03	135.81	130.29
38	A1	807	A2M	N3-C2-N1	-3.02	124.01	128.58
34	B5	1782	MA6	C5-N7-C8	3.02	108.20	103.45
34	B5	974	A2M	C4-N9-C8	3.01	108.90	105.74
34	B5	578	OMU	O4-C4-C5	-3.01	119.97	125.16
38	A1	817	A2M	C4-N9-C8	2.97	108.86	105.74
38	A1	2347	OMU	O4-C4-C5	-2.96	120.06	125.16
38	A1	2278	5MC	O2-C2-N3	-2.95	117.67	122.33
38	A1	2870	5MC	C5-C4-N3	-2.93	118.75	121.75
38	A1	2281	A2M	C4-C5-N7	-2.93	107.23	110.58
34	B5	436	A2M	C2'-C1'-N9	-2.89	109.00	113.75
38	A1	1888	OMU	O4-C4-C5	-2.88	120.19	125.16
38	A1	2280	A2M	C4-N9-C8	2.85	108.73	105.74
34	B5	1191	XSX	C5-C4-N3	2.84	119.57	115.64
38	A1	908	OMG	C6-C5-N7	2.83	135.44	130.29
34	B5	1575	G7M	C2'-C1'-N9	2.82	121.10	113.25
38	A1	2256	A2M	C4-N9-C8	2.81	108.69	105.74
38	A1	2280	A2M	C5-N7-C8	2.77	107.80	103.45
38	A1	2729	OMU	O4-C4-C5	-2.72	120.47	125.16
38	A1	805	OMG	C4-C5-N7	-2.71	106.37	110.67
34	B5	420	A2M	C2'-C1'-N9	-2.70	109.30	113.75
34	B5	420	A2M	C4-N9-C8	2.70	108.58	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1280	4AC	N4-C4-N3	2.70	118.25	113.87
34	B5	1782	MA6	C4-N9-C8	2.70	108.57	105.74
34	B5	1781	MA6	C4-N9-C8	2.70	108.57	105.74
38	A1	2278	5MC	C5-C4-N3	-2.70	118.99	121.75
34	B5	619	A2M	C4-N9-C8	2.69	108.56	105.74
34	B5	1126	OMG	C4-C5-N7	-2.69	106.41	110.67
34	B5	1782	MA6	C6-C5-N7	2.68	137.72	133.43
34	B5	1781	MA6	C6-C5-N7	2.67	137.70	133.43
38	A1	867	OMG	C4-C5-N7	-2.65	106.46	110.67
34	B5	1572	OMG	C4-C5-N7	-2.63	106.50	110.67
34	B5	796	A2M	C5-N7-C8	2.63	107.58	103.45
34	B5	1773	4AC	C5-C4-N3	-2.62	118.50	122.60
34	B5	28	A2M	C4-N9-C8	2.61	108.48	105.74
34	B5	1271	OMG	C4-C5-N7	-2.59	106.56	110.67
38	A1	2640	A2M	C4-N9-C8	2.59	108.46	105.74
38	A1	2256	A2M	C5-N7-C8	2.59	107.51	103.45
38	A1	2946	A2M	C4-N9-C8	2.58	108.45	105.74
34	B5	420	A2M	C5-N7-C8	2.57	107.49	103.45
34	B5	1575	G7M	C3'-C2'-C1'	2.55	106.30	101.46
34	B5	619	A2M	C5-N7-C8	2.55	107.46	103.45
38	A1	1133	A2M	C5-N7-C8	2.55	107.46	103.45
34	B5	28	A2M	C5-N7-C8	2.53	107.43	103.45
38	A1	2281	A2M	N9-C8-N7	-2.53	110.34	113.94
38	A1	2815	OMG	C4-C5-N7	-2.53	106.66	110.67
38	A1	2619	OMG	C4-C5-N7	-2.52	106.67	110.67
38	A1	2922	OMG	C4-C5-N7	-2.52	106.68	110.67
34	B5	1280	4AC	C6-C5-C4	2.51	120.02	117.00
34	B5	974	A2M	C5-N7-C8	2.51	107.39	103.45
38	A1	1133	A2M	C4-N9-C8	2.50	108.36	105.74
34	B5	562	OMG	C4-C5-N7	-2.49	106.73	110.67
38	A1	807	A2M	C5-N7-C8	2.49	107.36	103.45
38	A1	2791	OMG	C4-C5-N7	-2.49	106.73	110.67
38	A1	2220	A2M	C5-N7-C8	2.48	107.35	103.45
38	A1	807	A2M	C4-N9-C8	2.47	108.33	105.74
38	A1	1450	OMG	C4-C5-N7	-2.46	106.78	110.67
34	B5	796	A2M	C4-N9-C8	2.45	108.31	105.74
34	B5	1428	OMG	C4-C5-N7	-2.44	106.80	110.67
38	A1	2256	A2M	C6-C5-N7	2.43	136.78	132.09
38	A1	1449	A2M	C4-N9-C8	2.43	108.29	105.74
38	A1	2870	5MC	O2-C2-N3	-2.43	118.50	122.33
38	A1	2946	A2M	C5-N7-C8	2.42	107.26	103.45
34	B5	1191	XSX	C1-N3-C4	2.42	121.79	117.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1773	4AC	CM7-C7-N4	2.41	119.16	115.27
38	A1	2417	OMU	O2-C2-N1	-2.41	119.66	122.80
38	A1	908	OMG	C4-C5-N7	-2.40	106.87	110.67
34	B5	541	A2M	C5-N7-C8	2.40	107.22	103.45
38	A1	2281	A2M	C5-N7-C8	2.39	107.21	103.45
38	A1	650	OMC	O2-C2-N3	-2.39	118.56	122.33
38	A1	2640	A2M	C5-N7-C8	2.39	107.20	103.45
38	A1	2729	OMU	O2-C2-N3	-2.38	117.10	121.49
38	A1	1449	A2M	C5-N7-C8	2.38	107.19	103.45
38	A1	817	A2M	C5-N7-C8	2.38	107.19	103.45
38	A1	645	1MA	C6-C5-N7	2.38	136.36	132.16
38	A1	2793	OMG	C4-C5-N7	-2.38	106.91	110.67
34	B5	541	A2M	O4'-C1'-N9	2.37	112.64	108.09
38	A1	645	1MA	C4-C5-N7	-2.37	106.92	110.67
34	B5	100	A2M	C5-N7-C8	2.36	107.17	103.45
38	A1	2288	OMG	C4-C5-N7	-2.35	106.95	110.67
38	A1	1437	OMC	O2-C2-N1	2.35	123.50	118.90
38	A1	649	A2M	C4-N9-C8	2.34	108.20	105.74
38	A1	649	A2M	C5-N7-C8	2.34	107.13	103.45
38	A1	2921	OMU	O2-C2-N1	-2.34	119.75	122.80
34	B5	1773	4AC	O2-C2-N3	-2.33	118.65	122.33
38	A1	1133	A2M	O4'-C1'-N9	2.33	112.57	108.09
34	B5	100	A2M	C4-N9-C8	2.32	108.18	105.74
38	A1	2220	A2M	C6-C5-N7	2.31	136.54	132.09
38	A1	2220	A2M	N3-C2-N1	-2.30	125.10	128.58
38	A1	876	A2M	C5-N7-C8	2.29	107.05	103.45
38	A1	817	A2M	C6-C5-N7	2.28	136.49	132.09
34	B5	1781	MA6	N9-C8-N7	-2.26	110.73	113.94
34	B5	974	A2M	C2-N1-C6	2.26	122.44	118.73
38	A1	876	A2M	C4-N9-C8	2.25	108.10	105.74
34	B5	1007	OMC	O2-C2-N3	-2.25	118.78	122.33
38	A1	2280	A2M	N9-C8-N7	-2.25	110.74	113.94
38	A1	2793	OMG	O6-C6-C5	-2.25	120.60	126.53
38	A1	2729	OMU	C6-N1-C2	-2.24	118.27	121.00
38	A1	908	OMG	O6-C6-C5	-2.24	120.61	126.53
34	B5	1773	4AC	C1'-N1-C2	2.24	123.39	118.44
38	A1	2724	OMU	C1'-N1-C2	2.23	121.61	117.59
34	B5	1782	MA6	N9-C8-N7	-2.23	110.77	113.94
34	B5	436	A2M	C5-N7-C8	2.23	106.95	103.45
38	A1	2280	A2M	C6-C5-N7	2.22	136.37	132.09
34	B5	578	OMU	O2-C2-N1	-2.21	119.93	122.80
34	B5	28	A2M	C2'-C1'-N9	-2.20	110.13	113.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2281	A2M	C4'-O4'-C1'	-2.20	104.62	109.47
34	B5	1428	OMG	O6-C6-C5	-2.19	120.74	126.53
34	B5	619	A2M	C6-C5-N7	2.18	136.30	132.09
38	A1	867	OMG	O6-C6-C5	-2.18	120.79	126.53
38	A1	807	A2M	O4'-C1'-N9	2.17	112.26	108.09
34	B5	541	A2M	C4-N9-C8	2.16	108.01	105.74
38	A1	2288	OMG	O6-C6-C5	-2.16	120.82	126.53
38	A1	2256	A2M	N9-C8-N7	-2.16	110.87	113.94
34	B5	562	OMG	O6-C6-C5	-2.14	120.88	126.53
38	A1	2281	A2M	C6-C5-N7	2.14	136.22	132.09
34	B5	420	A2M	C6-C5-N7	2.14	136.21	132.09
38	A1	1450	OMG	O6-C6-C5	-2.14	120.89	126.53
34	B5	1575	G7M	O2'-C2'-C3'	2.14	118.67	111.82
34	B5	974	A2M	N9-C8-N7	-2.13	110.91	113.94
34	B5	1572	OMG	O6-C6-C5	-2.13	120.91	126.53
34	B5	414	OMC	O2-C2-N3	-2.13	118.98	122.33
34	B5	974	A2M	C6-C5-N7	2.12	136.18	132.09
34	B5	796	A2M	C6-C5-N7	2.11	136.15	132.09
38	A1	2946	A2M	O4'-C1'-N9	2.11	112.13	108.09
38	A1	1888	OMU	O2-C2-N1	-2.10	120.06	122.80
38	A1	2619	OMG	O6-C6-C5	-2.10	121.00	126.53
38	A1	2946	A2M	C6-C5-N7	2.10	136.13	132.09
34	B5	28	A2M	C6-C5-N7	2.09	136.12	132.09
38	A1	805	OMG	O6-C6-C5	-2.09	121.03	126.53
38	A1	2959	OMC	O2-C2-N3	-2.09	119.04	122.33
34	B5	1280	4AC	C5-C4-N3	-2.08	119.34	122.60
38	A1	2142	1MA	C4-C5-N7	-2.08	107.37	110.67
38	A1	645	1MA	N1-C2-N3	-2.08	123.53	126.00
34	B5	1280	4AC	O2-C2-N3	-2.07	119.06	122.33
38	A1	1133	A2M	C6-C5-N7	2.07	136.09	132.09
38	A1	2922	OMG	O6-C6-C5	-2.07	121.08	126.53
38	A1	817	A2M	N9-C8-N7	-2.06	111.02	113.94
34	B5	420	A2M	N9-C8-N7	-2.06	111.02	113.94
38	A1	805	OMG	C2'-C1'-N9	-2.05	110.34	114.24
38	A1	2421	OMU	O2-C2-N1	-2.05	120.13	122.80
38	A1	898	OMU	O2-C2-N1	-2.04	120.14	122.80
34	B5	974	A2M	C2'-C1'-N9	-2.04	110.40	113.75
38	A1	1437	OMC	C1'-N1-C6	-2.04	116.42	120.78
34	B5	1271	OMG	O6-C6-C5	-2.04	121.16	126.53
34	B5	619	A2M	N9-C8-N7	-2.03	111.05	113.94
38	A1	2946	A2M	C2-N1-C6	2.03	122.07	118.73
38	A1	2256	A2M	C2-N1-C6	2.03	122.07	118.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2220	A2M	C4-N9-C8	2.02	107.86	105.74
34	B5	1126	OMG	O6-C6-C5	-2.02	121.20	126.53
38	A1	2791	OMG	O6-C6-C5	-2.02	121.21	126.53
38	A1	2815	OMG	O6-C6-C5	-2.00	121.25	126.53

There are no chirality outliers.

All (72) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	414	OMC	C1'-C2'-O2'-CM2
34	B5	420	A2M	C1'-C2'-O2'-CM'
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	1428	OMG	C1'-C2'-O2'-CM2
34	B5	1572	OMG	O4'-C4'-C5'-O5'
34	B5	1572	OMG	C1'-C2'-O2'-CM2
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
34	B5	1782	MA6	O4'-C4'-C5'-O5'
38	A1	649	A2M	C1'-C2'-O2'-CM'
38	A1	650	OMC	C1'-C2'-O2'-CM2
38	A1	663	OMC	C1'-C2'-O2'-CM2
38	A1	876	A2M	C1'-C2'-O2'-CM'
38	A1	1437	OMC	C1'-C2'-O2'-CM2
38	A1	2197	OMC	C2'-C1'-N1-C2
38	A1	2197	OMC	C2'-C1'-N1-C6
38	A1	2220	A2M	C1'-C2'-O2'-CM'
38	A1	2619	OMG	C1'-C2'-O2'-CM2
38	A1	2724	OMU	C1'-C2'-O2'-CM2
38	A1	2791	OMG	C1'-C2'-O2'-CM2
38	A1	2948	OMC	C1'-C2'-O2'-CM2
38	A1	2280	A2M	C3'-C4'-C5'-O5'
38	A1	2729	OMU	C3'-C4'-C5'-O5'
38	A1	2280	A2M	O4'-C4'-C5'-O5'
38	A1	2729	OMU	O4'-C4'-C5'-O5'
34	B5	619	A2M	O4'-C4'-C5'-O5'
34	B5	1782	MA6	C3'-C4'-C5'-O5'
34	B5	1191	XSX	N4-C7-C9-O10
38	A1	2870	5MC	C2'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
34	B5	541	A2M	O4'-C4'-C5'-O5'
34	B5	619	A2M	C3'-C4'-C5'-O5'
34	B5	1269	OMU	C3'-C4'-C5'-O5'
34	B5	1572	OMG	C3'-C4'-C5'-O5'
38	A1	2197	OMC	O4'-C4'-C5'-O5'
38	A1	2347	OMU	C3'-C4'-C5'-O5'
34	B5	541	A2M	C3'-C4'-C5'-O5'
34	B5	1269	OMU	O4'-C4'-C5'-O5'
38	A1	817	A2M	C4'-C5'-O5'-P
34	B5	1428	OMG	O4'-C4'-C5'-O5'
38	A1	2619	OMG	O4'-C4'-C5'-O5'
34	B5	1269	OMU	O4'-C1'-N1-C6
34	B5	1269	OMU	O4'-C1'-N1-C2
38	A1	2347	OMU	O4'-C4'-C5'-O5'
34	B5	1191	XSX	N4-C7-C9-O11
38	A1	2619	OMG	C3'-C4'-C5'-O5'
38	A1	2421	OMU	C1'-C2'-O2'-CM2
38	A1	2870	5MC	O4'-C1'-N1-C6
38	A1	2870	5MC	C2'-C1'-N1-C2
38	A1	2256	A2M	O4'-C4'-C5'-O5'
38	A1	805	OMG	C3'-C2'-O2'-CM2
34	B5	541	A2M	C4'-C5'-O5'-P
38	A1	2729	OMU	C4'-C5'-O5'-P
38	A1	2870	5MC	O4'-C1'-N1-C2
34	B5	1126	OMG	C3'-C4'-C5'-O5'
38	A1	2197	OMC	C3'-C4'-C5'-O5'
38	A1	2197	OMC	O4'-C1'-N1-C6
38	A1	645	1MA	C2'-C1'-N9-C8
38	A1	645	1MA	C2'-C1'-N9-C4
34	B5	1428	OMG	C4'-C5'-O5'-P
38	A1	2197	OMC	O4'-C1'-N1-C2
34	B5	1269	OMU	C4'-C5'-O5'-P
34	B5	541	A2M	O4'-C1'-N9-C8
34	B5	1191	XSX	C3-C7-C9-O11
34	B5	1782	MA6	C4'-C5'-O5'-P
34	B5	619	A2M	C2'-C1'-N9-C8
36	AB	243	HIC	CA-CB-CG-ND1
38	A1	1437	OMC	C2'-C1'-N1-C2
38	A1	1437	OMC	O4'-C4'-C5'-O5'

There are no ring outliers.

23 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2724	OMU	1	0
34	B5	1126	OMG	3	0
38	A1	2220	A2M	2	0
38	A1	663	OMC	1	0
38	A1	1449	A2M	1	0
34	B5	414	OMC	1	0
34	B5	436	A2M	1	0
38	A1	2640	A2M	1	0
34	B5	1575	G7M	3	0
34	B5	1773	4AC	1	0
38	A1	650	OMC	1	0
38	A1	2197	OMC	2	0
34	B5	28	A2M	1	0
34	B5	100	A2M	1	0
38	A1	1133	A2M	1	0
38	A1	649	A2M	2	0
38	A1	2256	A2M	1	0
38	A1	2619	OMG	1	0
38	A1	817	A2M	1	0
34	B5	1269	OMU	1	0
38	A1	876	A2M	1	0
38	A1	2946	A2M	1	0
34	B5	1572	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 257 ligands modelled in this entry, 257 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.

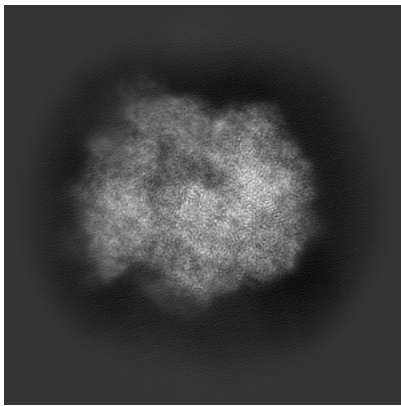
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28632. These allow visual inspection of the internal detail of the map and identification of artifacts.

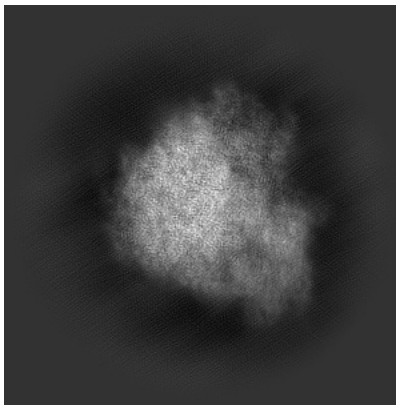
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

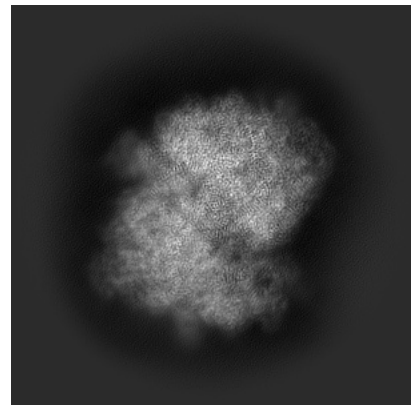
6.1.1 Primary map



X

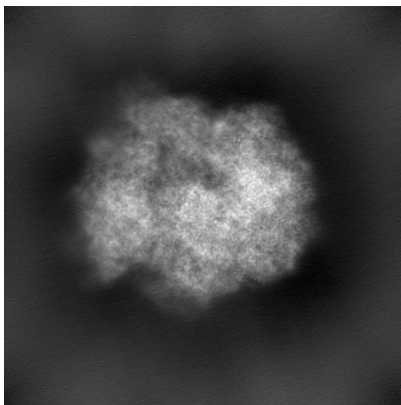


Y

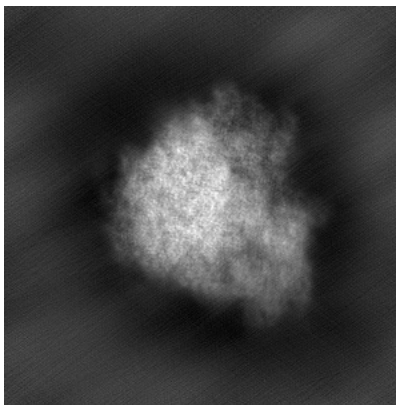


Z

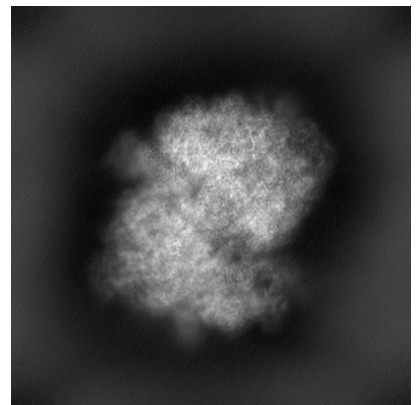
6.1.2 Raw map



X



Y

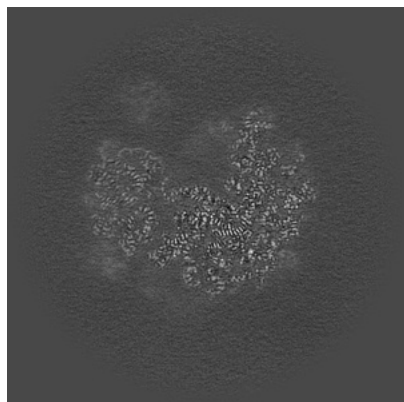


Z

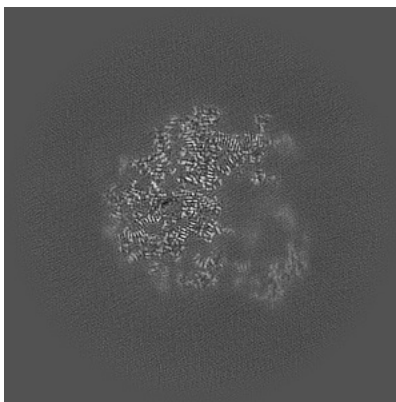
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

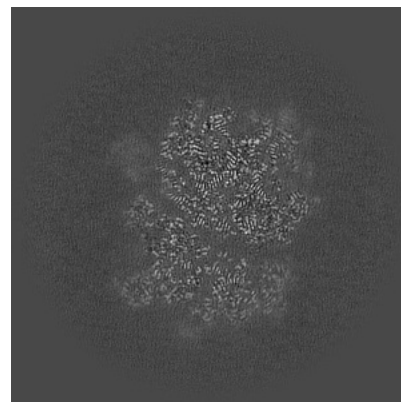
6.2.1 Primary map



X Index: 200

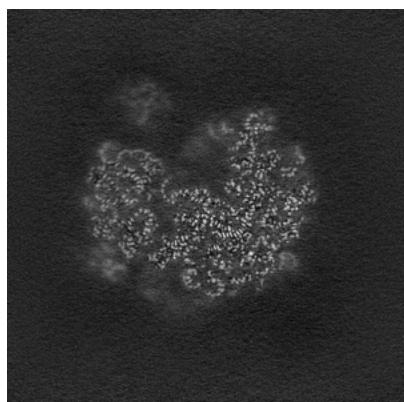


Y Index: 200

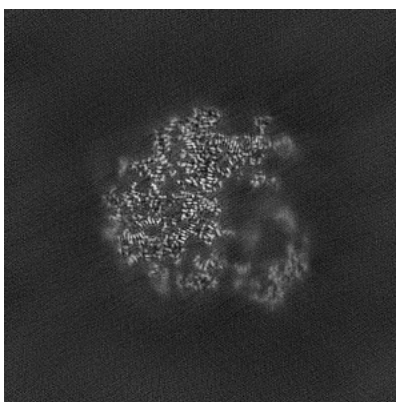


Z Index: 200

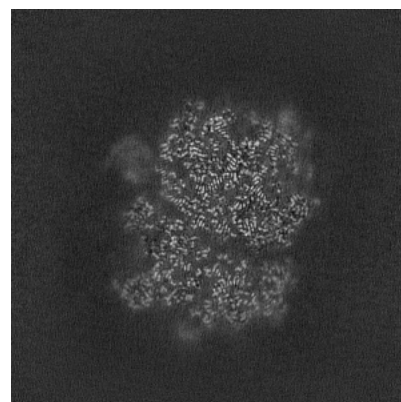
6.2.2 Raw map



X Index: 200



Y Index: 200

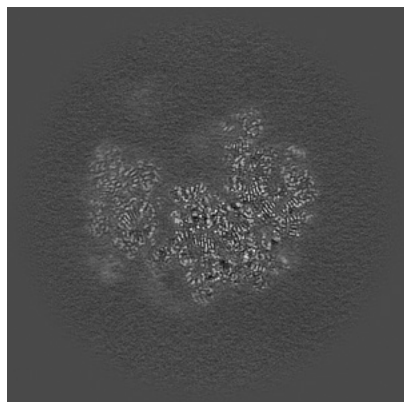


Z Index: 200

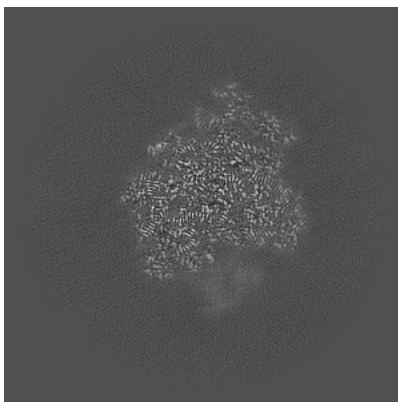
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

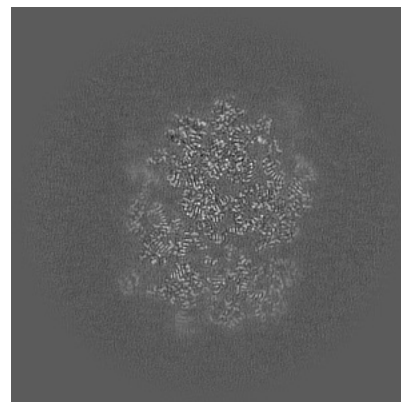
6.3.1 Primary map



X Index: 205

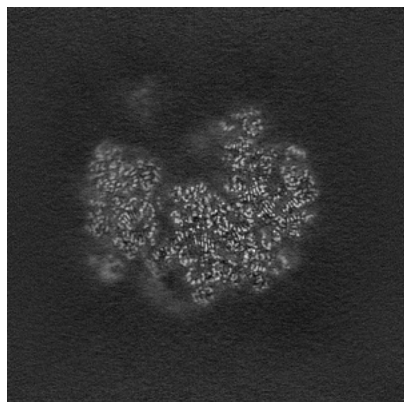


Y Index: 246

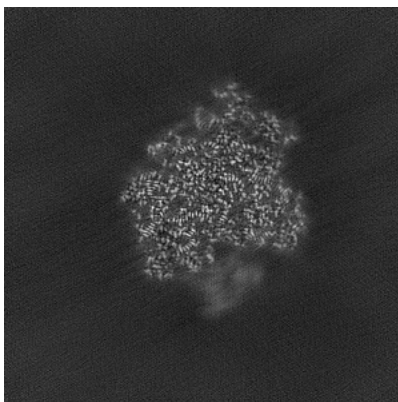


Z Index: 191

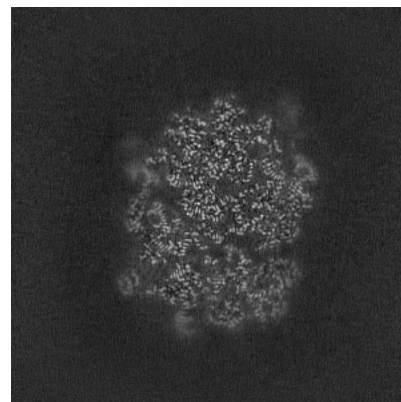
6.3.2 Raw map



X Index: 205



Y Index: 246

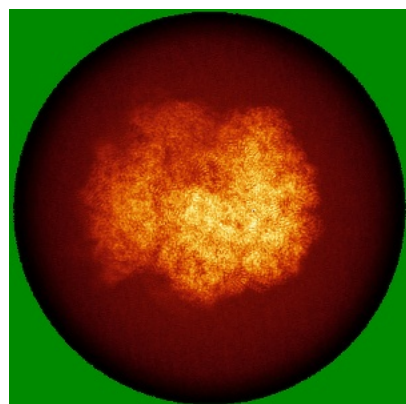


Z Index: 191

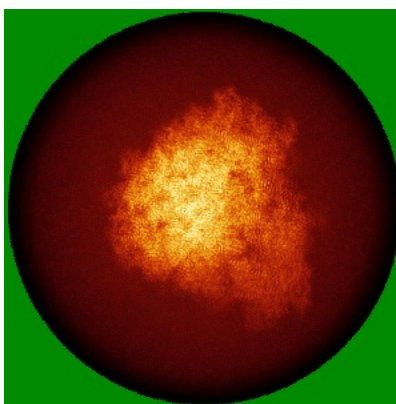
The images above show the largest variance slices of the map in three orthogonal directions.

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

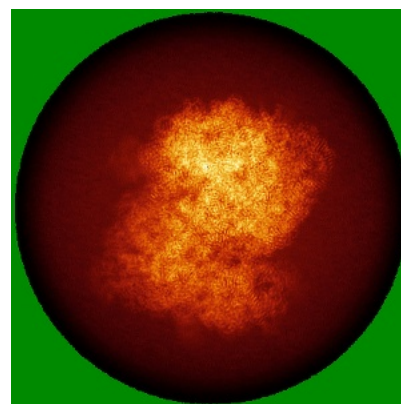
6.4.1 Primary map



X

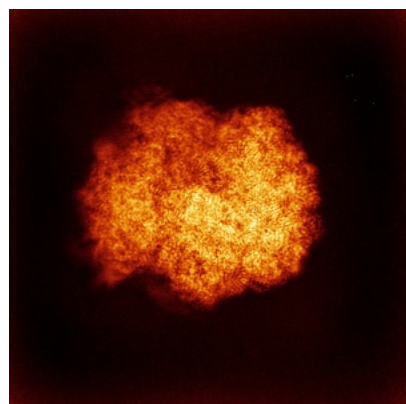


Y

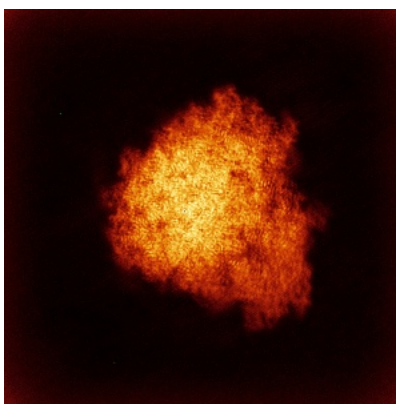


Z

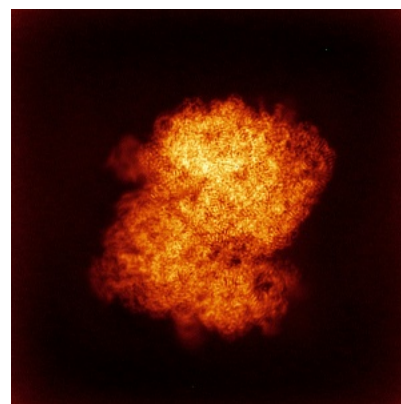
6.4.2 Raw map



X



Y



Z

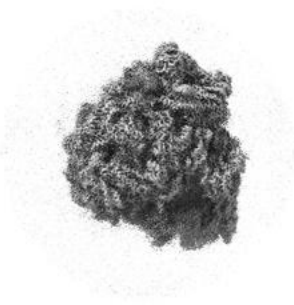
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

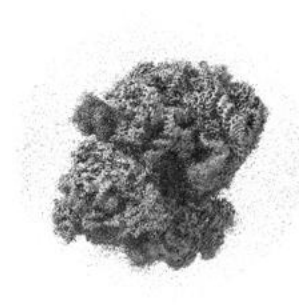
6.5.1 Primary map



X



Y



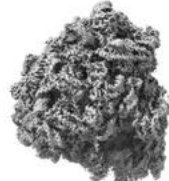
Z

The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

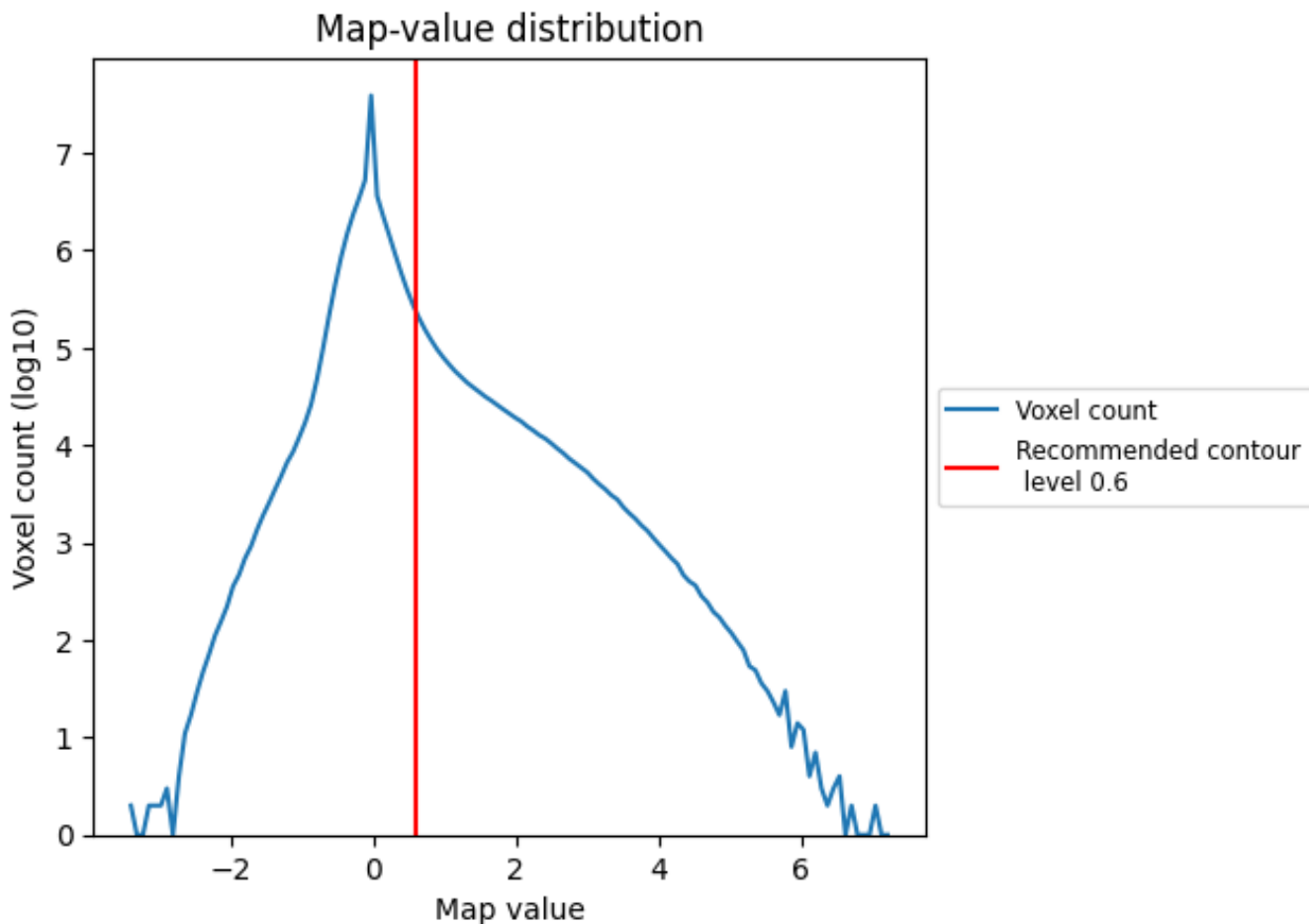
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

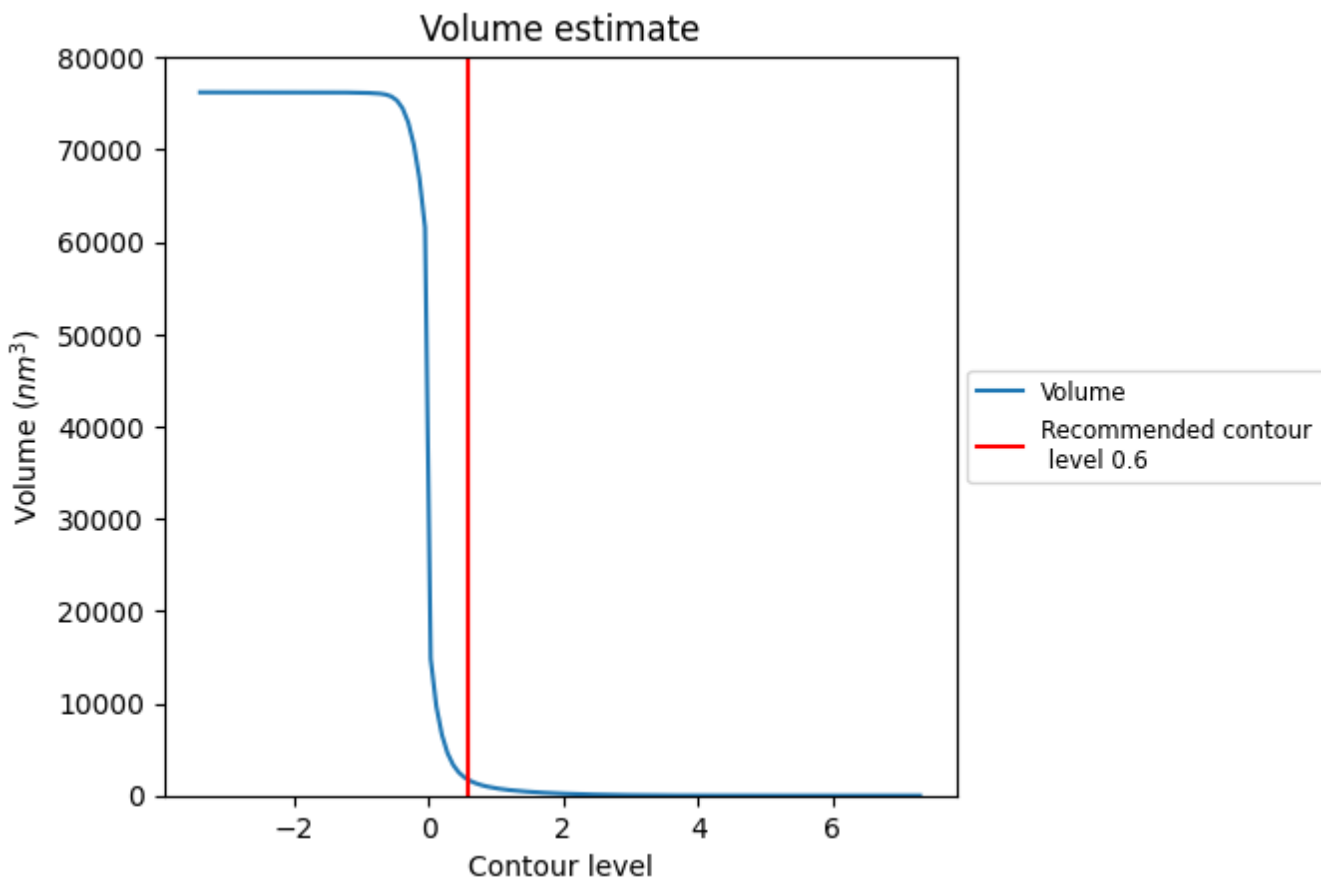
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

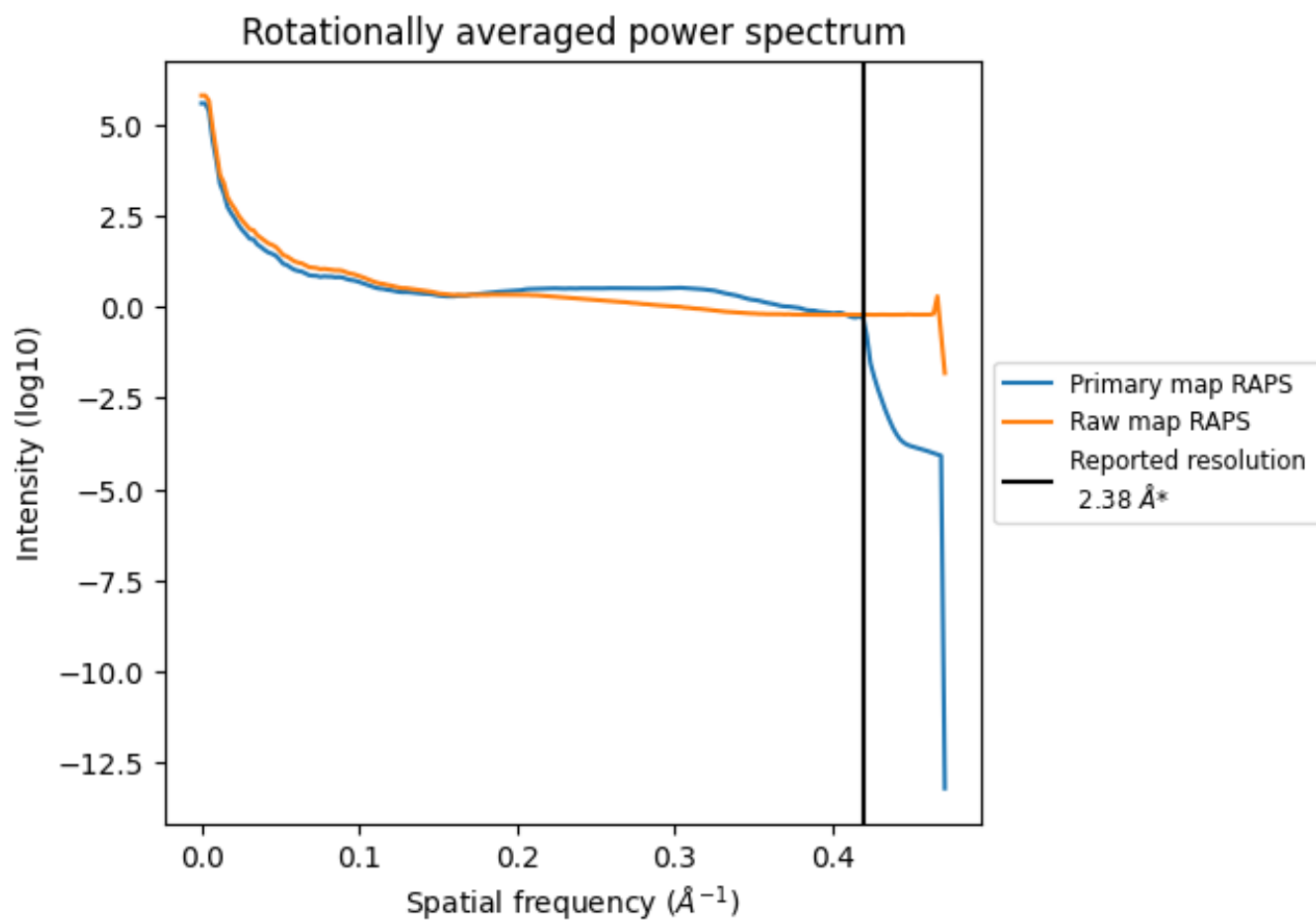
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1679 nm³; this corresponds to an approximate mass of 1517 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 i

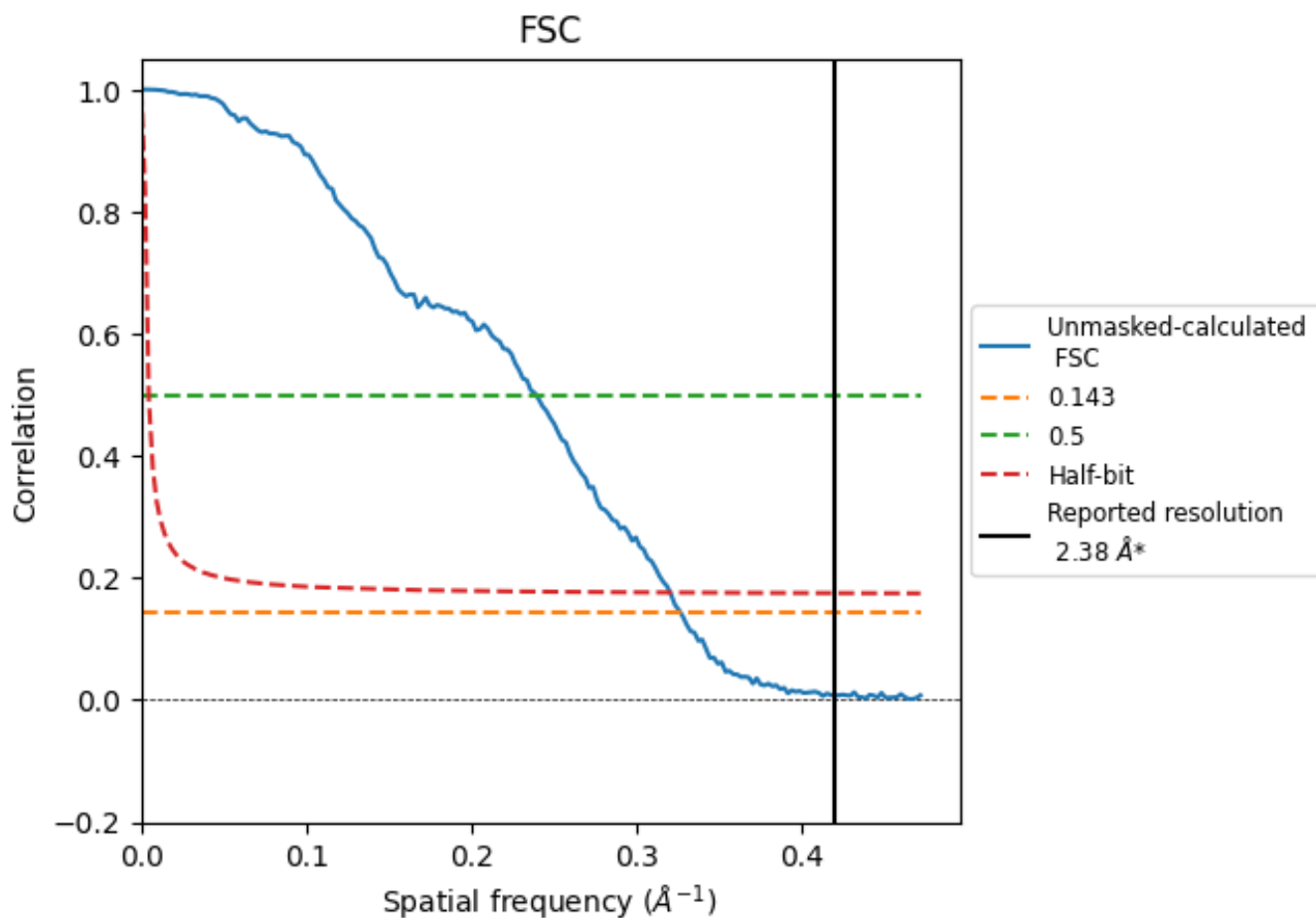


*Reported resolution corresponds to spatial frequency of 0.420 Å⁻¹

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 0.420 Å⁻¹

8.2 Resolution estimates [i](#)

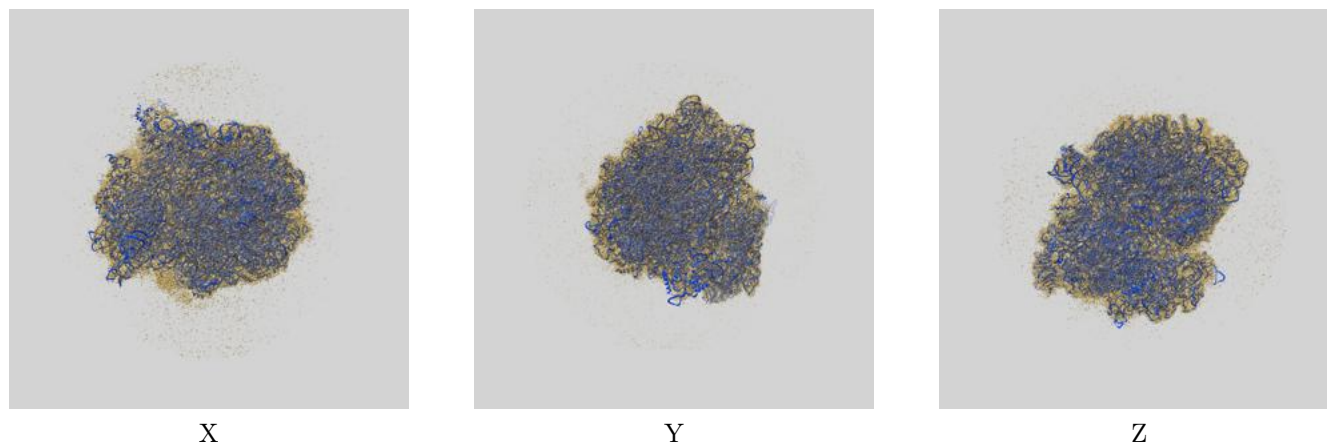
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.38	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.06	4.19	3.12

*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 3.06 differs from the reported value 2.38 by more than 10 %

9 Map-model fit [i](#)

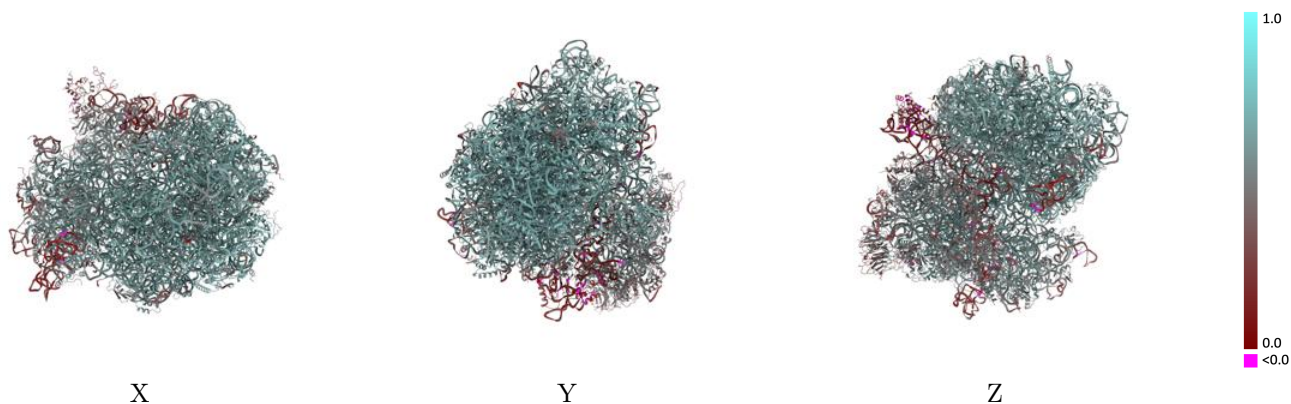
This section contains information regarding the fit between EMDB map EMD-28632 and PDB model 8EVP. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



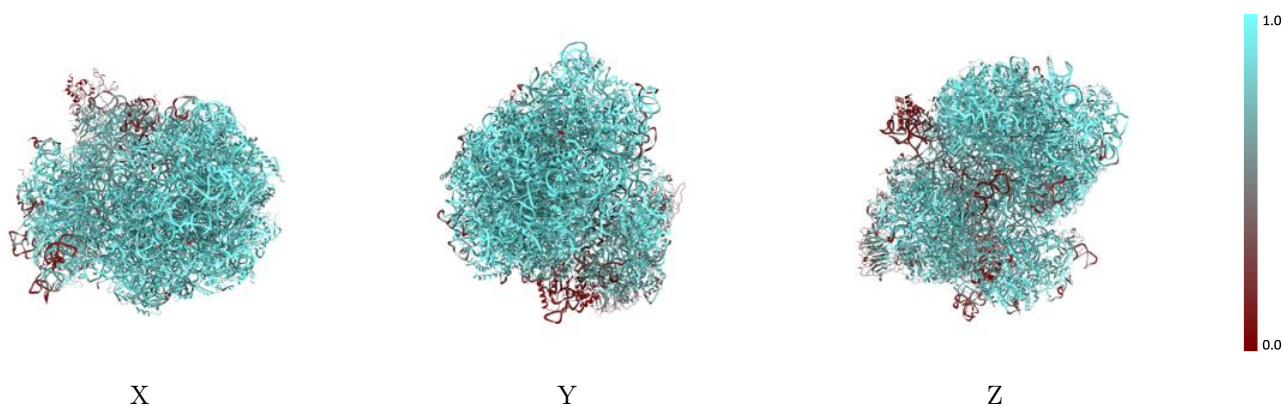
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



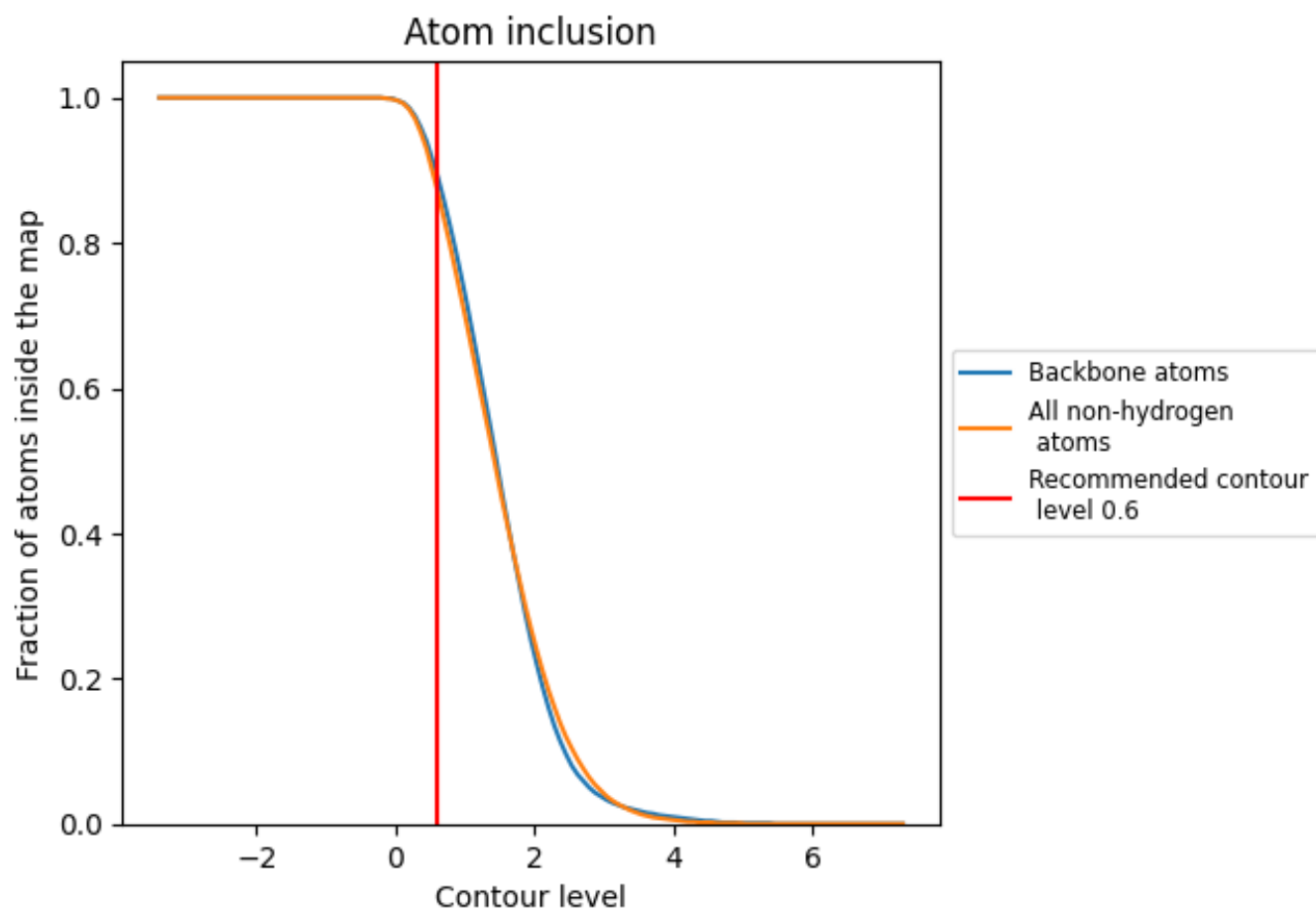
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 90% of all backbone atoms, 88% 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	 0.8750	 0.5650
A1	 0.9390	 0.6040
A3	 0.9820	 0.6100
A4	 0.9730	 0.6340
AA	 0.9810	 0.6660
AB	 0.9490	 0.6220
AC	 0.9580	 0.6390
AD	 0.8710	 0.5650
AE	 0.8710	 0.5700
AF	 0.9500	 0.6400
AG	 0.8920	 0.5810
AH	 0.8940	 0.5930
AI	 0.9330	 0.6150
AJ	 0.7510	 0.4710
AL	 0.9310	 0.6260
AM	 0.9200	 0.6030
AN	 0.9870	 0.6620
AO	 0.9600	 0.6330
AP	 0.9500	 0.6330
AQ	 0.9820	 0.6660
AR	 0.8780	 0.5910
AS	 0.9350	 0.6210
AT	 0.9380	 0.6160
AU	 0.8310	 0.5360
AV	 0.9430	 0.6340
AW	 0.9600	 0.6340
AX	 0.9420	 0.6240
AY	 0.9230	 0.6130
AZ	 0.9360	 0.6040
Aa	 0.9560	 0.6450
Ab	 0.9270	 0.6080
Ac	 0.9430	 0.6250
Ad	 0.8840	 0.5900
Ae	 0.9620	 0.6520
Af	 0.9640	 0.6410











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Chain	Atom inclusion	Q-score
Ag	 0.9400	 0.6180
Ah	 0.9420	 0.6230
Ai	 0.9170	 0.5930
Aj	 0.9680	 0.6580
Ak	 0.7810	 0.5550
Al	 0.9780	 0.6530
Am	 0.8930	 0.6150
An	 0.9340	 0.5920
Ao	 0.9020	 0.6070
Ap	 0.9400	 0.6370
B5	 0.8700	 0.5300
BA	 0.8620	 0.5530
BB	 0.8560	 0.5560
BC	 0.9340	 0.6080
BD	 0.7480	 0.4850
BE	 0.9100	 0.5800
BF	 0.7220	 0.4750
BG	 0.7310	 0.4860
BH	 0.7250	 0.4970
BI	 0.8860	 0.5880
BJ	 0.8660	 0.5570
BK	 0.5850	 0.3940
BL	 0.8570	 0.5810
BM	 0.0820	 0.2560
BN	 0.9300	 0.6100
BO	 0.9000	 0.5730
BP	 0.5180	 0.3960
BQ	 0.7750	 0.4850
BR	 0.7780	 0.4970
BS	 0.6730	 0.4460
BT	 0.7490	 0.4730
BU	 0.6440	 0.4400
BV	 0.9080	 0.5810
BW	 0.9630	 0.6390
BX	 0.9150	 0.6060
BY	 0.7900	 0.5040
BZ	 0.6220	 0.4250
Ba	 0.9000	 0.5700
Bb	 0.8450	 0.5610
Bc	 0.6960	 0.4810
Bd	 0.8840	 0.5350
Be	 0.8000	 0.5130

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Chain	Atom inclusion	Q-score
Bf	 0.1190	 0.2320
Bg	 0.5440	 0.4010
E	 0.1450	 0.1950
EC	 0.3860	 0.2180