



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 04:08 AM UTC

PDB ID : 8EVR / pdb_00008evr
EMDB ID : EMD-28634
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2, GDP, and sordarin, Structure II
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-20
Resolution : 2.87 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

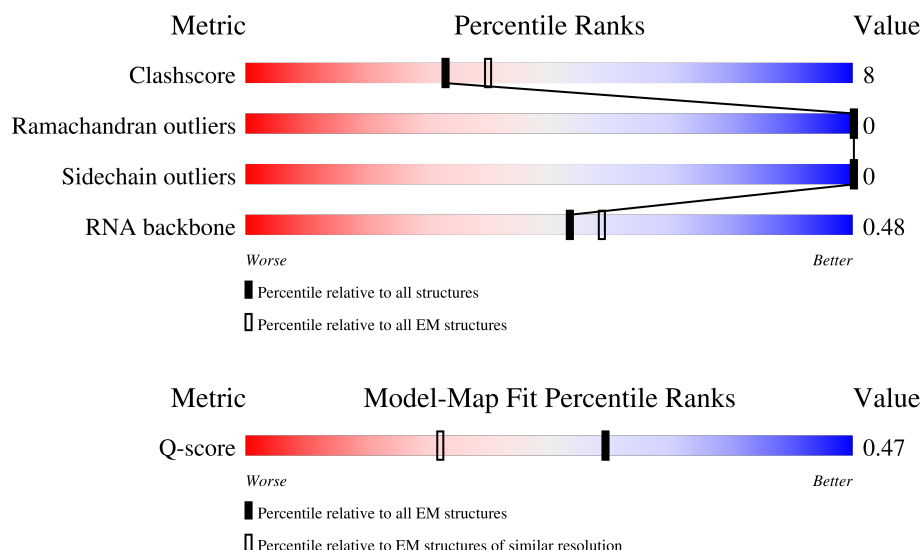
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.87 Å.

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



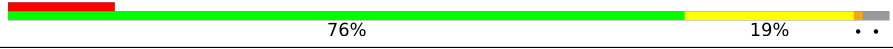
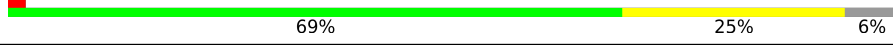
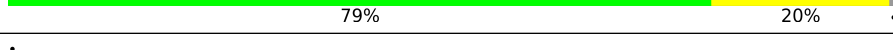
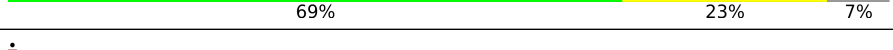
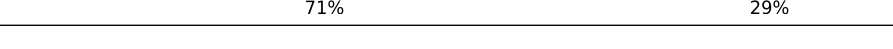
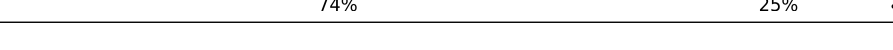
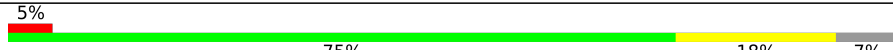
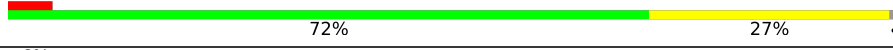
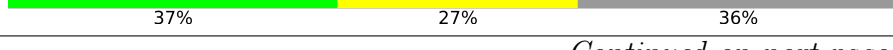
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12062 (2.37 - 3.37)

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

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

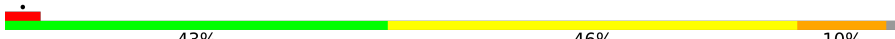
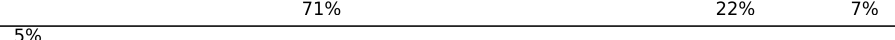
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Mol	Chain	Length	Quality of chain
4	BE	261	
5	BG	236	
6	BH	190	
7	BI	200	
8	BJ	197	
9	BL	156	
10	BN	151	
11	BO	137	
12	BV	87	
13	BW	130	
14	BX	145	
15	BY	135	
16	Ba	119	
17	Bb	82	
18	Be	63	
19	BD	240	
20	BF	225	
21	BK	105	
22	BP	142	
23	BQ	143	
24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

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

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

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Mol	Chain	Length	Quality of chain
79	E	217	
80	DC	842	
81	V	312	
82	EC	202	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	W9C	DC	902	X	-	-	-

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 213962 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

- Molecule 2 is a protein called RPS1A isoform 1.

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

- Molecule 3 is a protein called RPS2 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 13 is a protein called RPS22A isoform 1.

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

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

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

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

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

- Molecule 16 is a protein called RPS26B isoform 1.

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

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

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

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

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

- Molecule 19 is a protein called RPS3 isoform 1.

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

- Molecule 20 is a protein called Rps5p.

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

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

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

- Molecule 22 is a protein called RPS15 isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 27 is a protein called RPS20 isoform 1.

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

- Molecule 28 is a protein called RPS25A isoform 1.

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

- Molecule 29 is a protein called RPS28A isoform 1.

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

- Molecule 30 is a protein called RPS29A isoform 1.

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

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

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

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

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 37 is a protein called RPL4A isoform 1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	3198	Total	C	N	O	P	0	0
			68444	30595	12331	22320	3198		

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

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

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

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

- Molecule 41 is a protein called RPL5 isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 46 is a protein called RPL10 isoform 1.

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

- Molecule 47 is a protein called RPL11A isoform 1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 59 is a protein called RPL24A isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 64 is a protein called RPL29 isoform 1.

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

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

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

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

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

- Molecule 67 is a protein called RPL32 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 73 is a protein called RPL38 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 79 is a protein called RPL1A isoform 1.

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

- Molecule 80 is a protein called Elongation factor 2.

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

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

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

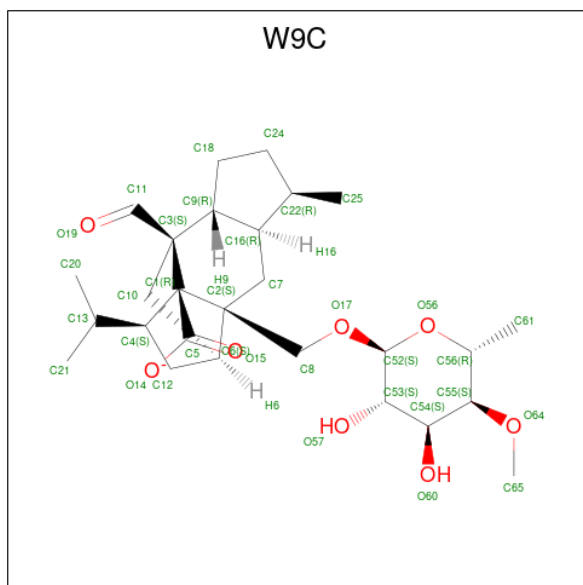
- Molecule 82 is a RNA chain called TSV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	EC	191	Total	C	N	O	P	0	0
			4045	1806	718	1330	191		

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

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

- Molecule 86 is (1S,3S,3aR,4S,4aR,7R,7aR,8aS)-8a-{[(6-deoxy-4-O-methyl- α -D-altropyranosyl)oxy]methyl}-4-formyl-7-methyl-3-(propan-2-yl)decahydro-1,4-methano-s-indacene-3a(1H)-carboxylate (CCD ID: W9C) (formula: $C_{27}H_{41}O_8$).

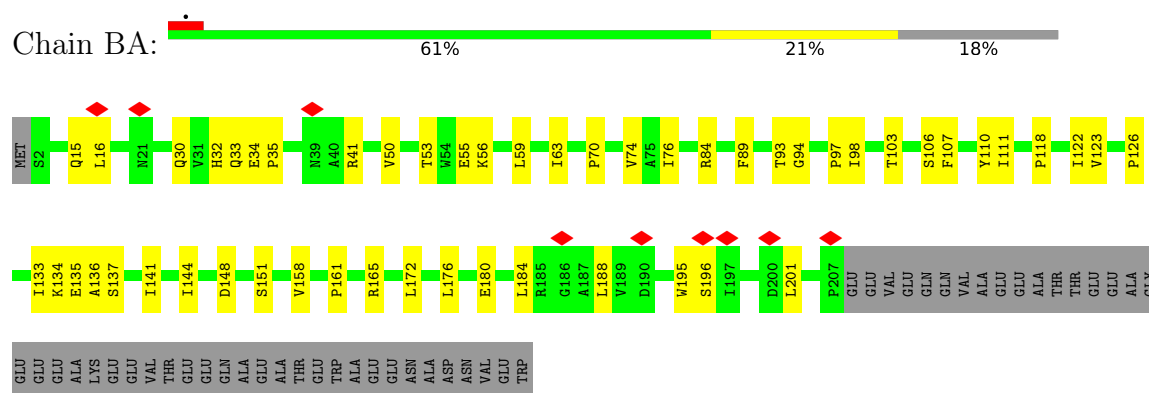


Mol	Chain	Residues	Atoms			AltConf
86	DC	1	Total	C	O	0
			35	27	8	

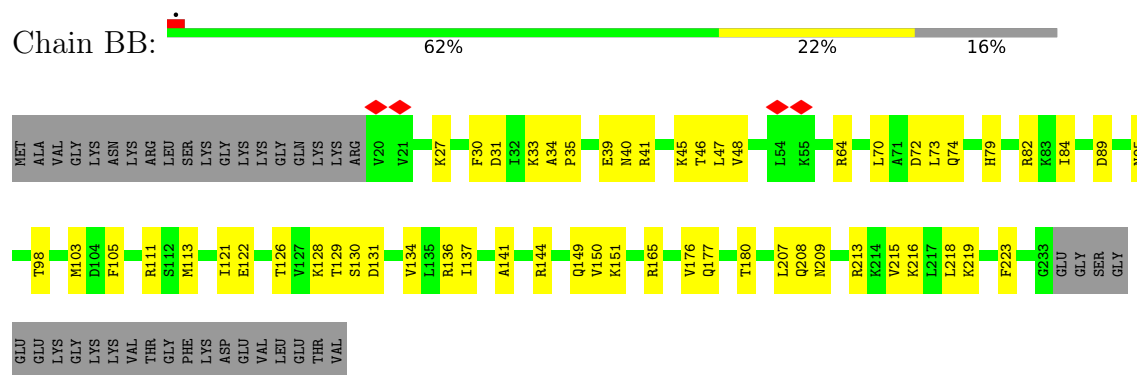
3 Residue-property plots

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

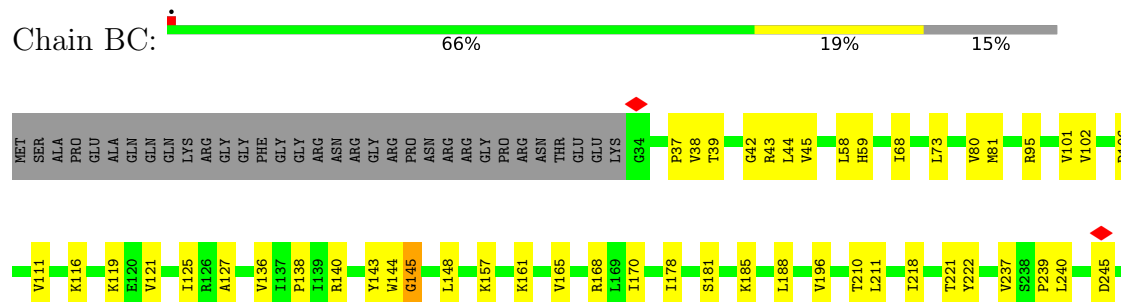
• Molecule 1: 40S ribosomal protein S0-A

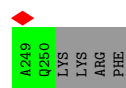


• Molecule 2: RPS1A isoform 1



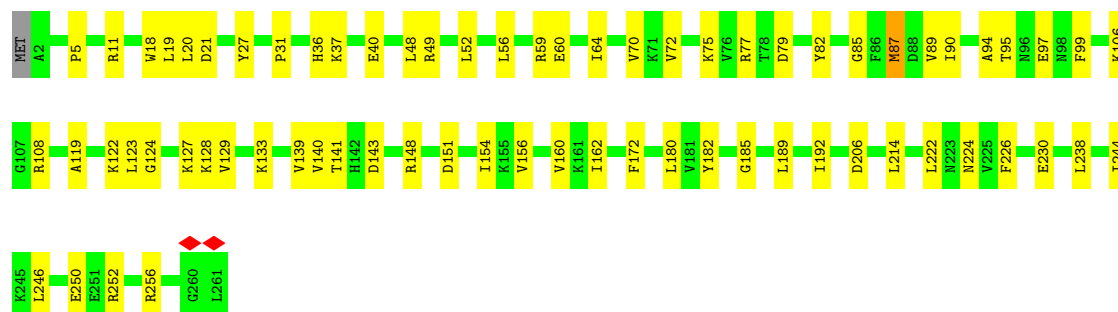
• Molecule 3: RPS2 isoform 1





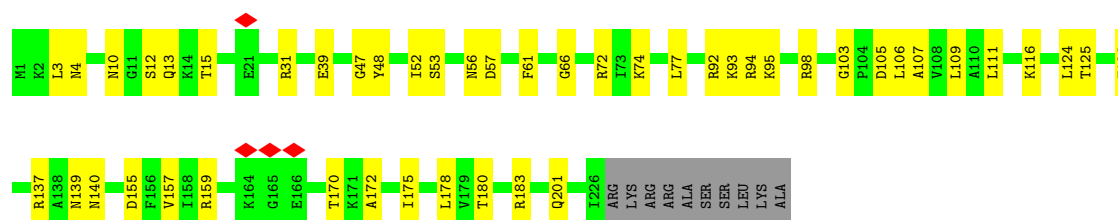
• Molecule 4: 40S ribosomal protein S4-A

Chain BE: 73% 26%



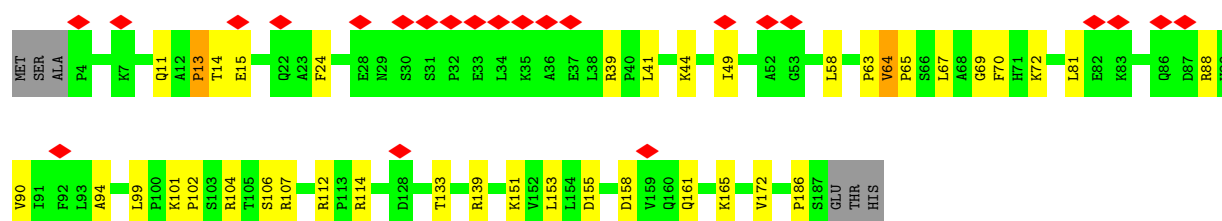
• Molecule 5: 40S ribosomal protein S6-A

Chain BG: 76% 20%



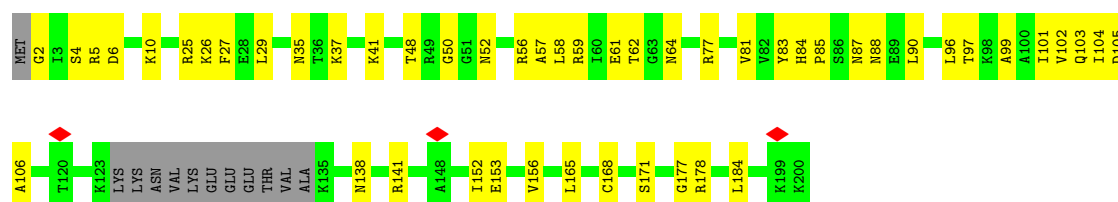
• Molecule 6: 40S ribosomal protein S7-A

Chain BH: 12% 76% 19%

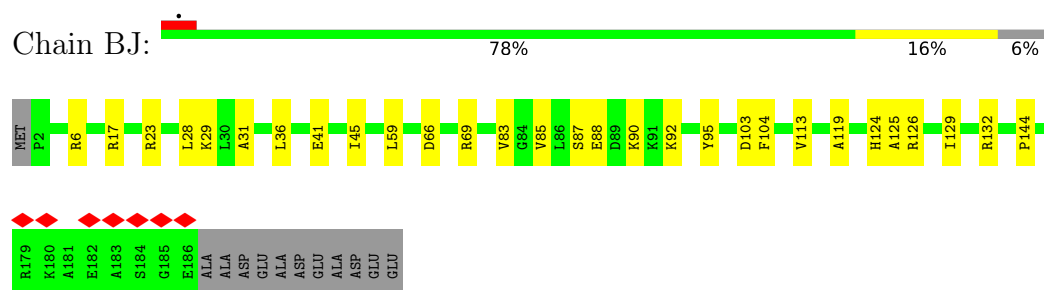


• Molecule 7: 40S ribosomal protein S8-A

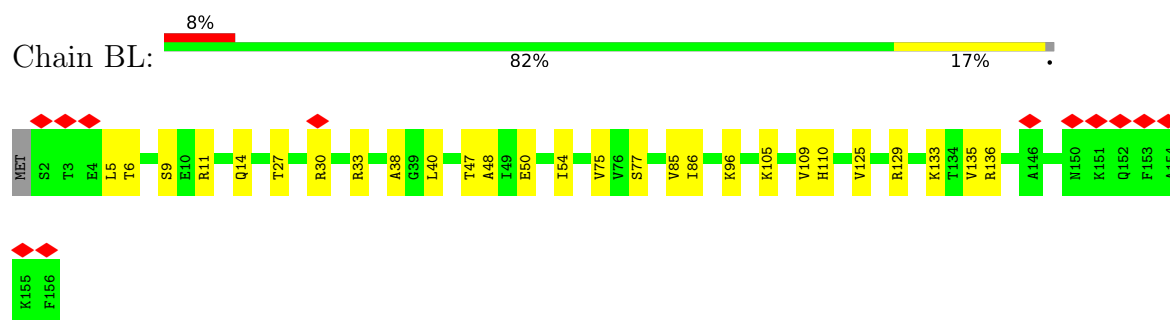
Chain BI: 69% 25% 6%



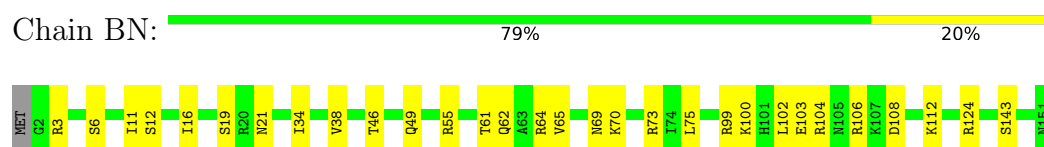
- Molecule 8: 40S ribosomal protein S9-A



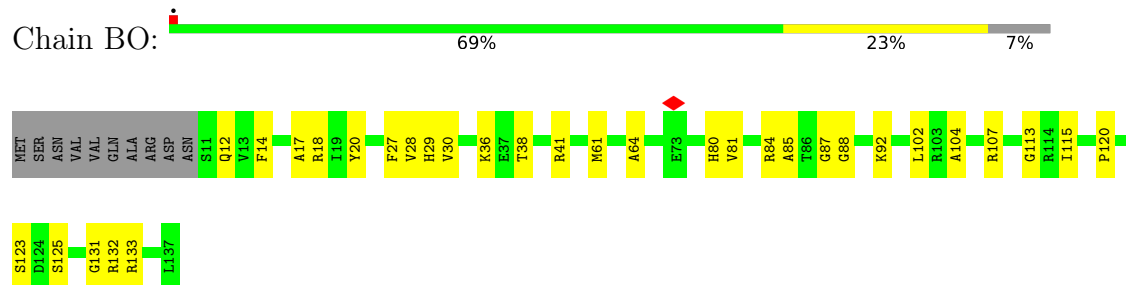
- Molecule 9: 40S ribosomal protein S11-A



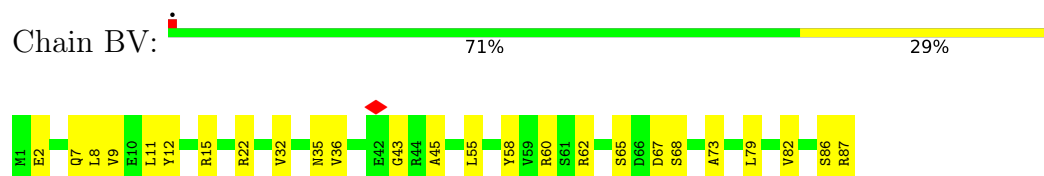
- Molecule 10: 40S ribosomal protein S13



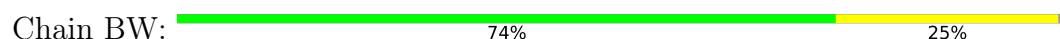
- Molecule 11: 40S ribosomal protein S14-A



- Molecule 12: 40S ribosomal protein S21-A



- Molecule 13: RPS22A isoform 1





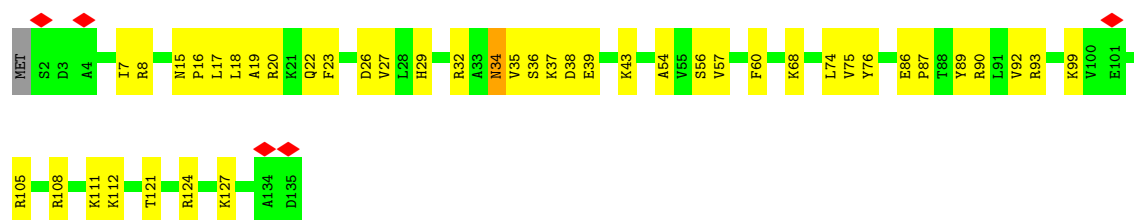
- Molecule 14: 40S ribosomal protein S23-A

Chain BX: 80% 19% .



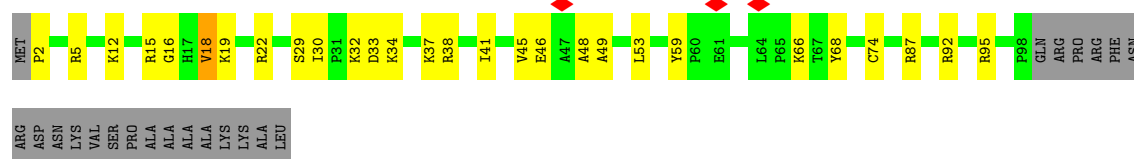
- Molecule 15: 40S ribosomal protein S24-A

Chain BY: 67% 31% ..



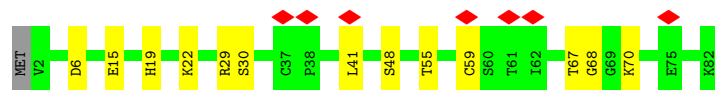
- Molecule 16: RPS26B isoform 1

Chain Ba: 58% 23% 18% .



- Molecule 17: 40S ribosomal protein S27-A

Chain Bb: 9% 83% 16% .

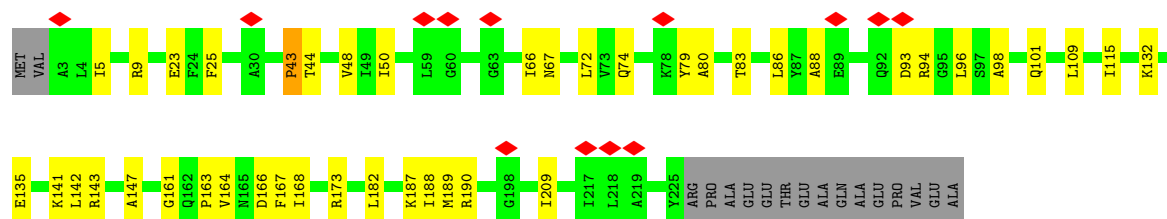
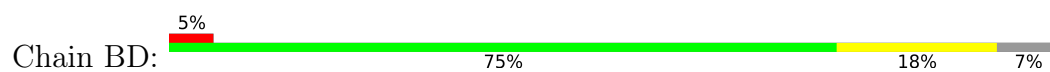


- Molecule 18: 40S ribosomal protein S30-A

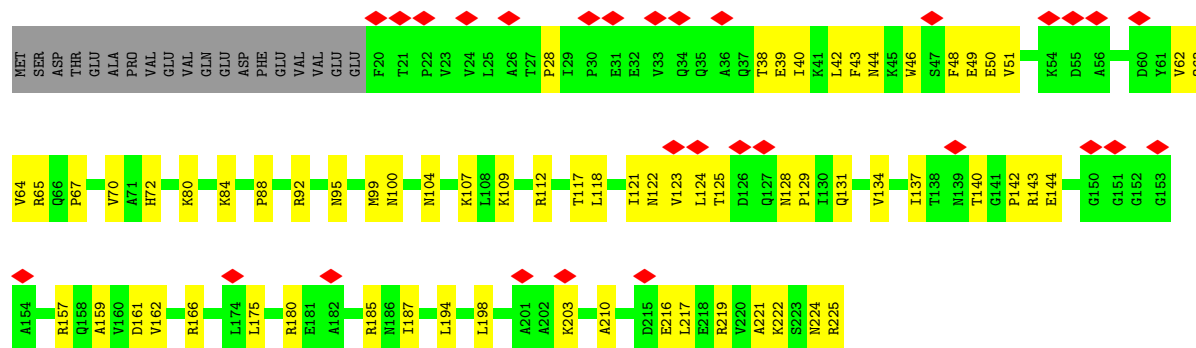
Chain Be: 83% 13% 5%



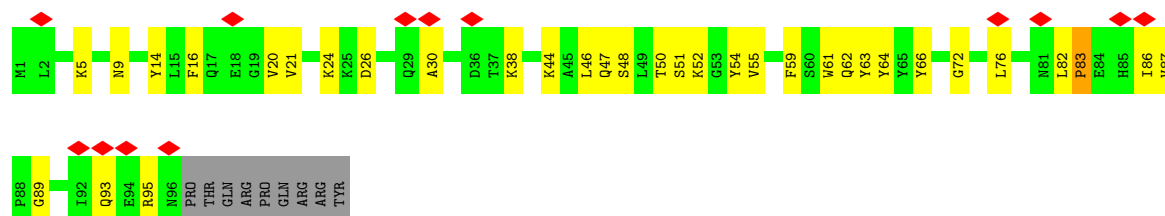
- Molecule 19: RPS3 isoform 1



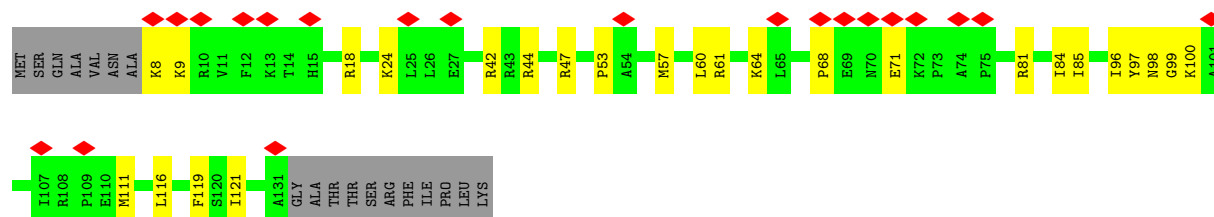
• Molecule 20: Rps5p



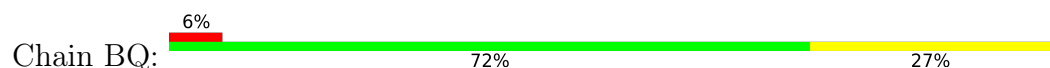
• Molecule 21: 40S ribosomal protein S10-A

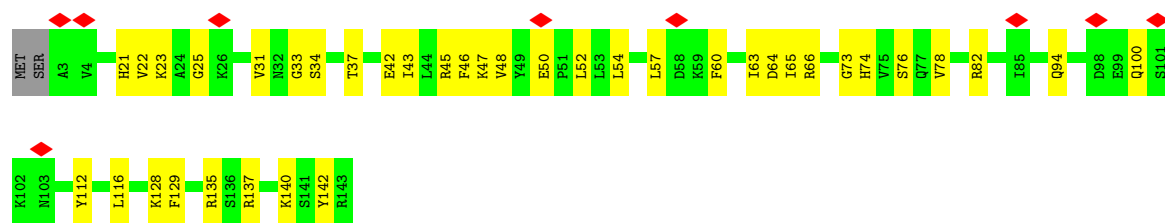


• Molecule 22: RPS15 isoform 1

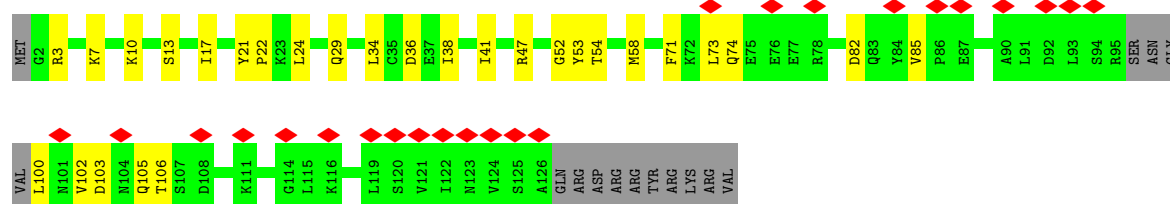


• Molecule 23: 40S ribosomal protein S16-A

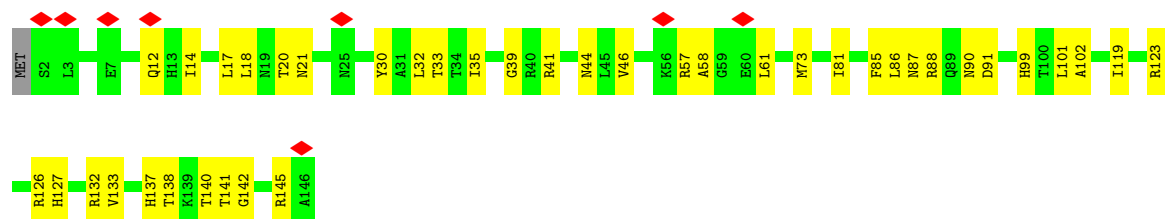
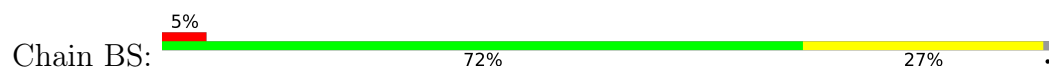




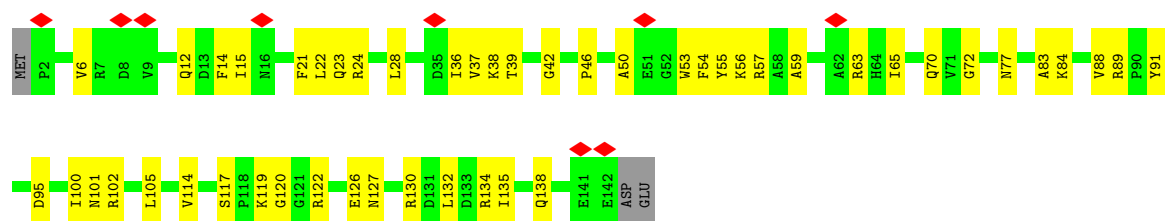
- Molecule 24: 40S ribosomal protein S17-A



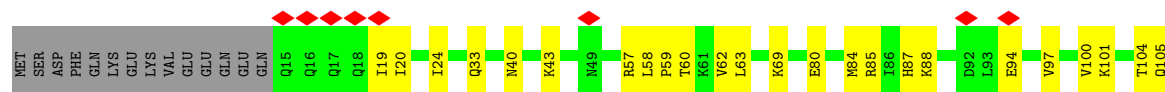
- Molecule 25: 40S ribosomal protein S18-A



- Molecule 26: 40S ribosomal protein S19-A

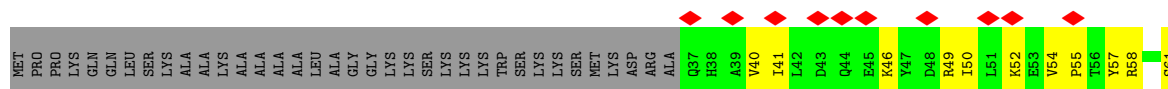


- Molecule 27: RPS20 isoform 1

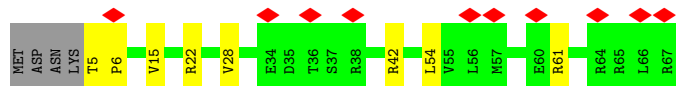
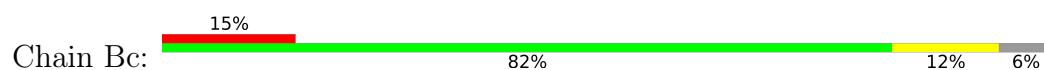




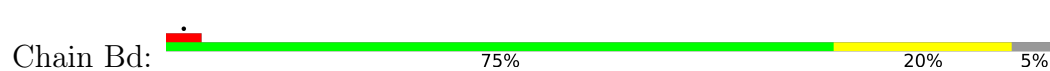
• Molecule 28: RPS25A isoform 1



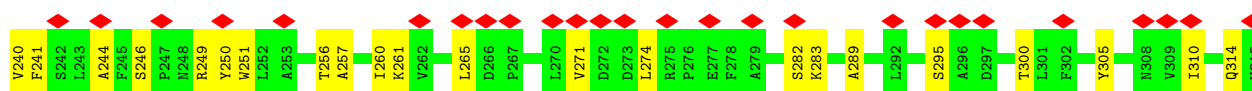
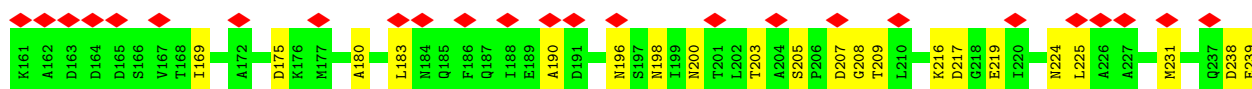
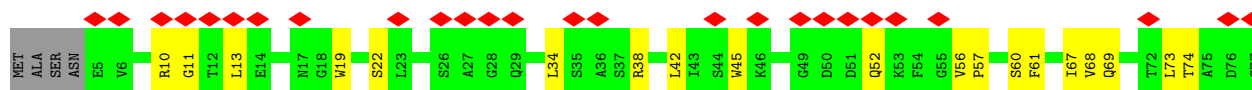
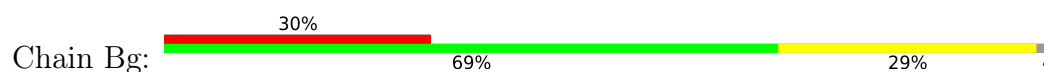
• Molecule 29: RPS28A isoform 1



• Molecule 30: RPS29A isoform 1

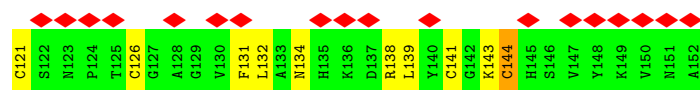
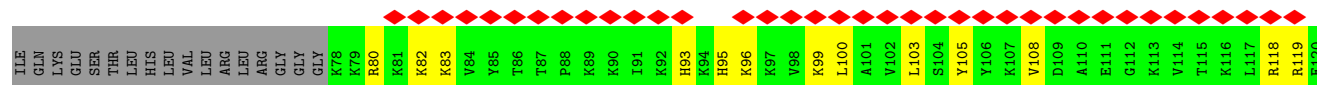
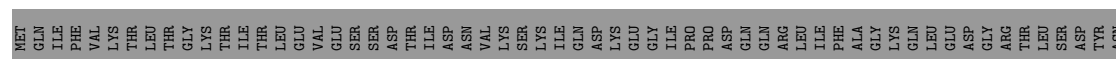
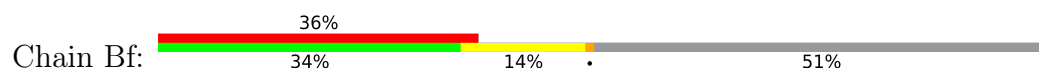


• Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein

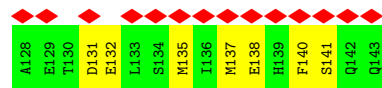
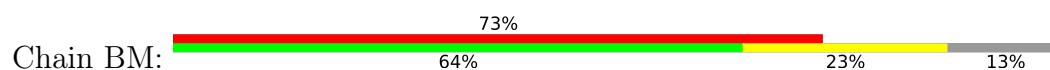




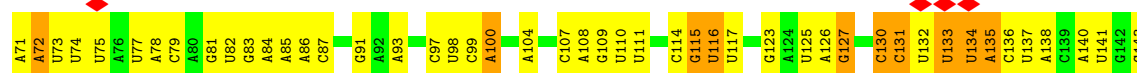
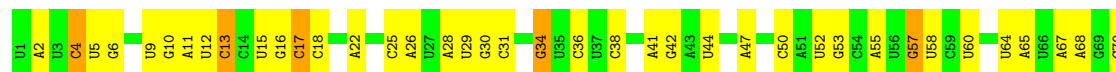
• Molecule 32: Ubiquitin-40S ribosomal protein S31

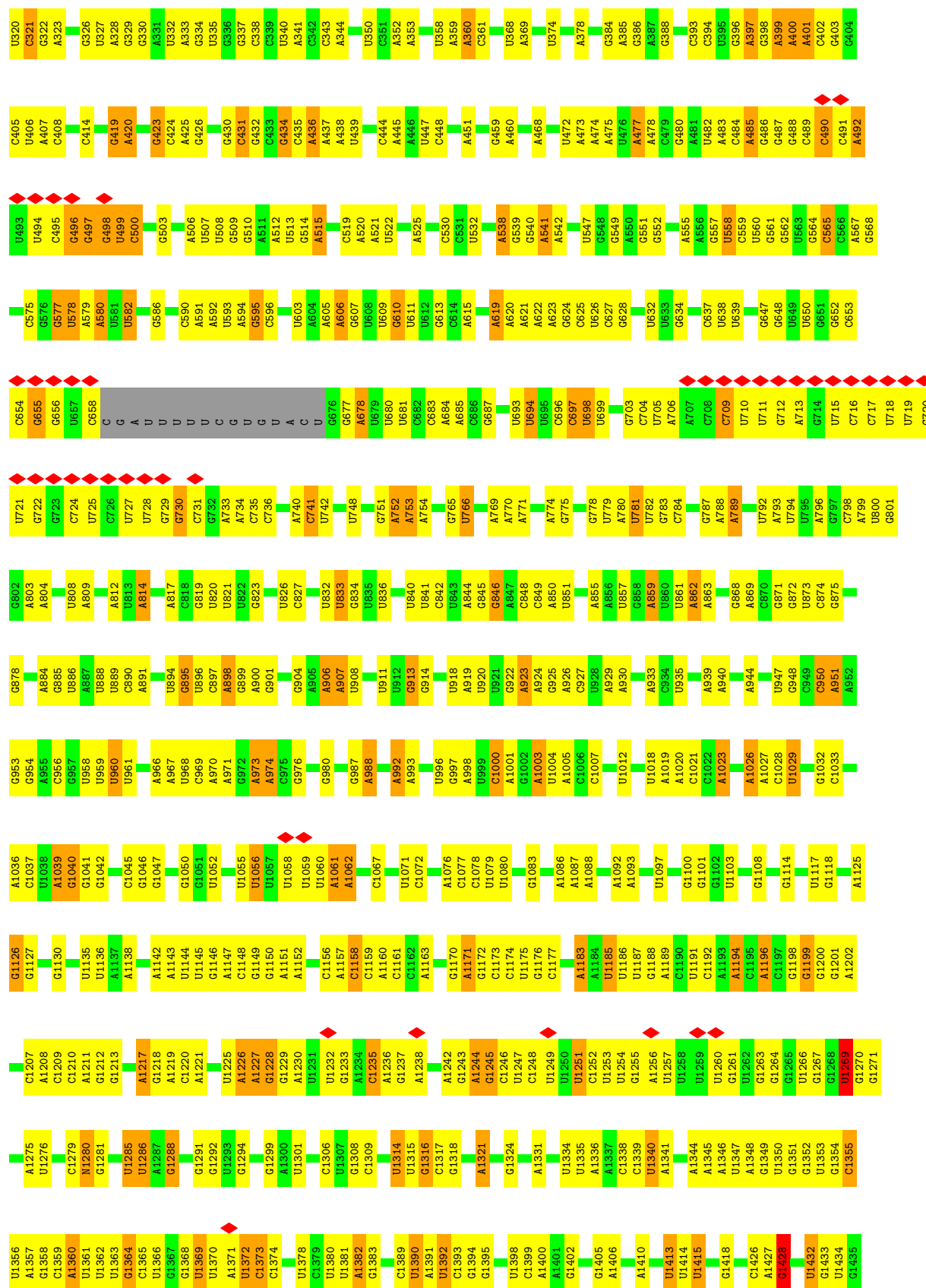


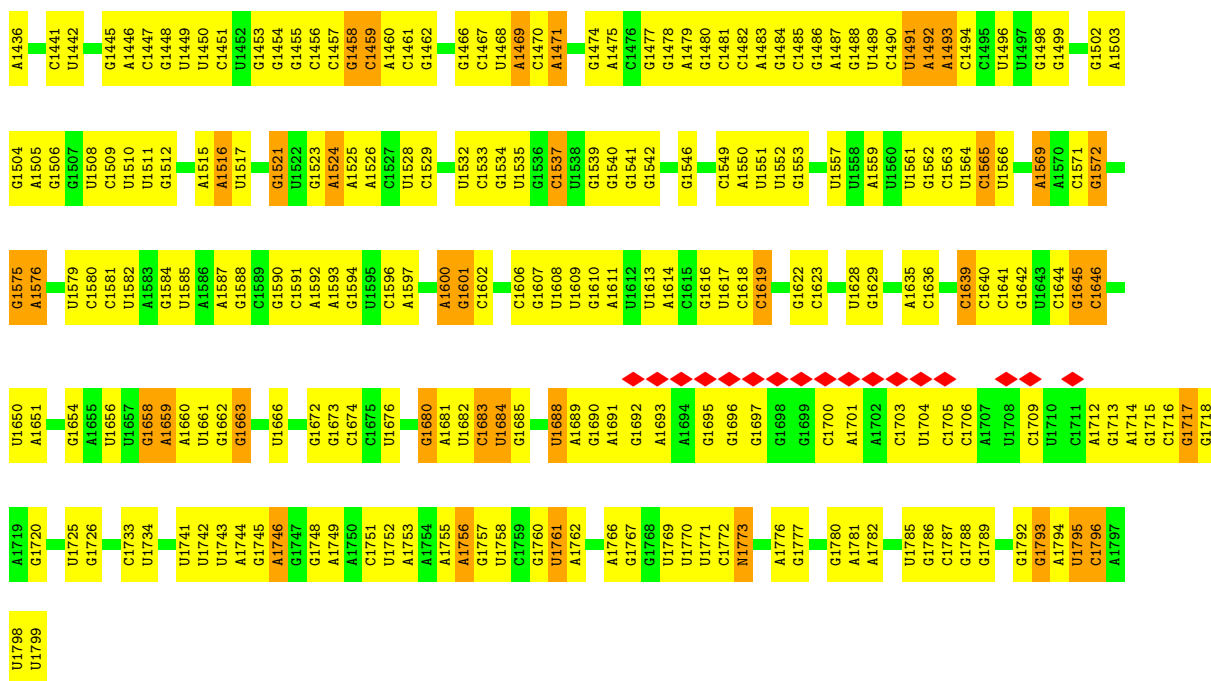
• Molecule 33: 40S ribosomal protein S12



• Molecule 34: 18S rRNA

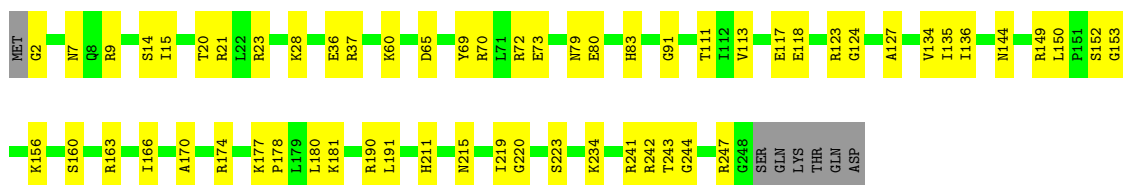






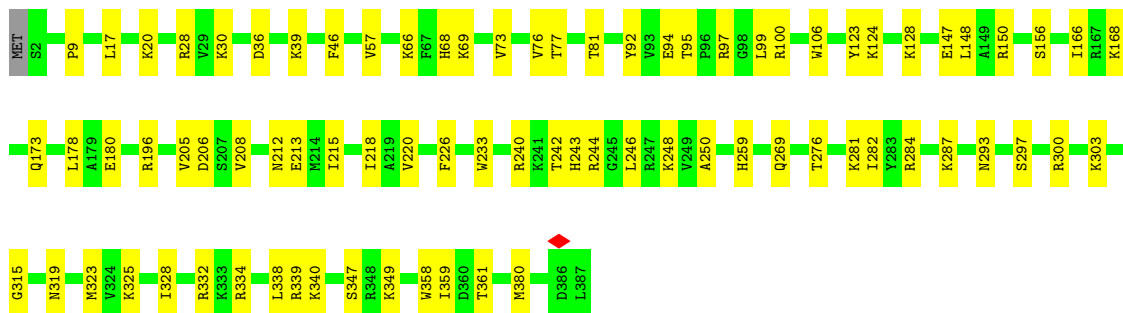
• Molecule 35: 60S ribosomal protein L2-A

Chain AA: 74% 23%



• Molecule 36: 60S ribosomal protein L3

Chain AB: 79% 21%

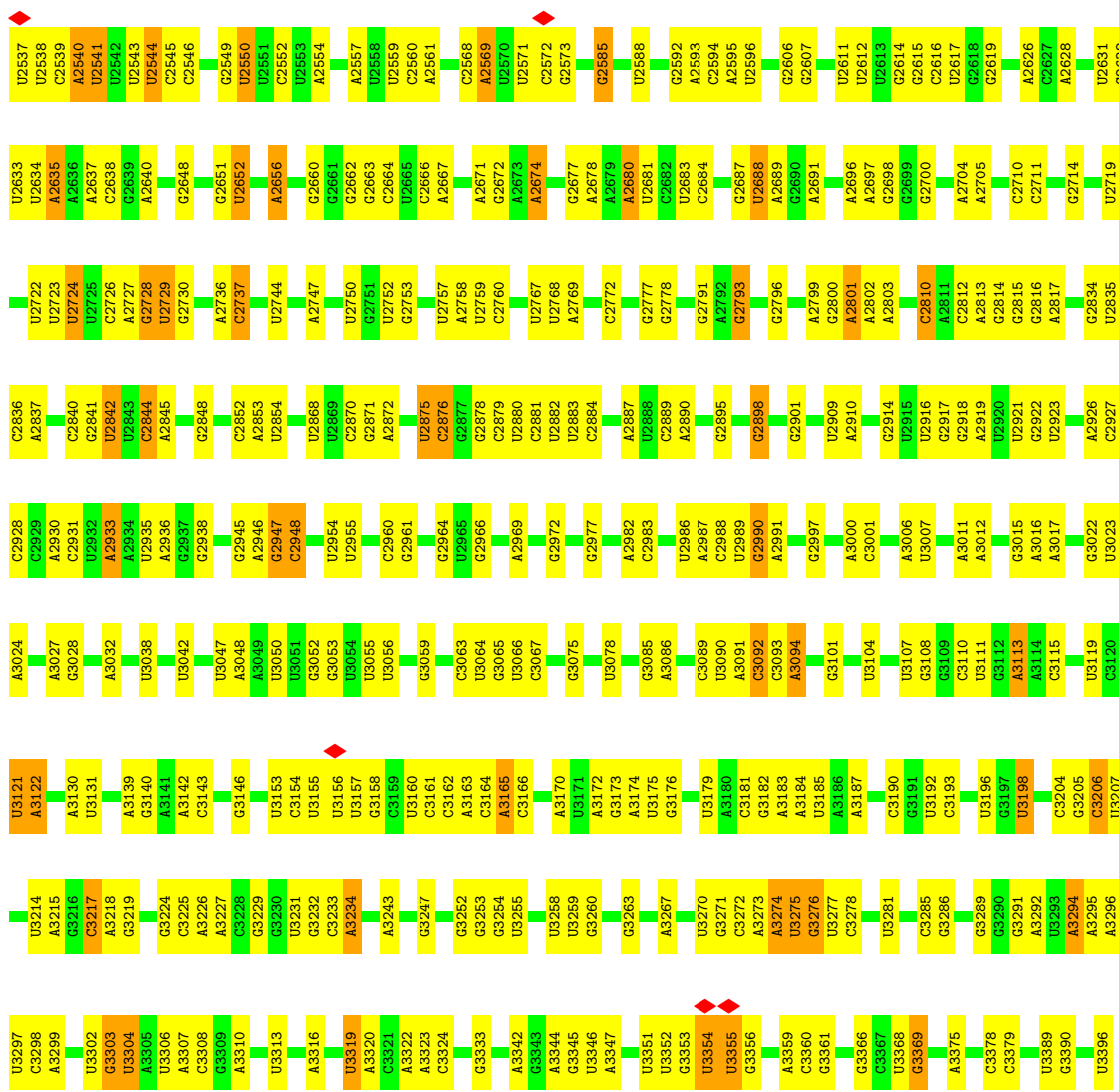


• Molecule 37: RPL4A isoform 1

Chain AC: 85% 14%



U2464	C2389	A2279	C2196	A2093	G1863	U1765	U1659	U1570	A1462	G1357	G1268
G2465	A2390	A2280	C2197	C2094	A1864	G1766	C1660	U1571	A1468	C1364	A1271
G2466	G2393	U2282	G2201	G2095	A1865	C1767	G1661	G1573	G1367	G1272	C1273
A2468	A2397	G2283	U2202	A2106	C1866	G1768	C1662	C1574	A1475	U1368	A1273
G2469	A2397	C2284	C2204	A2107	U1873	G1769	C1663	G1575	G1476	C1277	C1278
C2470	A2402	C2285	U2205	G2111	G1878	C1781	G1665	A1576	A1477	A1278	A1279
U2471	G2403	G2288	U2206	U2112	A1879	U1782	G1666	C1579	A1481	G1378	C1279
U2472	A2404	U2211	A2207	A2113	U1880	U1783	G1667	C1579	A1482	G1379	C1280
C2473	C2405	G2214	A2213	G2114	U1881	U1784	G1668	A1583	G1483	C1380	C1281
G2475	C2407	G2215	A2214	G2115	A1886	U1785	G1669	A1584	G1484	C1381	C1282
C2476	U2408	G2216	A2215	G2116	A1887	G1786	G1670	A1585	G1485	C1382	C1283
G2477	G2409	U2217	A2216	G2117	U1888	A1787	G1671	A1586	G1486	A1386	C1284
C2478	U2410	G2218	G2218	A2118	C1893	C1791	U1882	A1587	G1487	A1286	A1287
U2479	A2411	A2219	A2219	A2119	A1893	C1792	U1883	A1588	G1488	A1288	A1289
A2480	G2412	A2220	A2220	G2120	G1897	C1793	U1884	U1595	A1491	A1389	A1290
G2481	U2310	A2221	A2221	G2121	U1897	U1795	U1885	C1596	G1492	C1391	A1291
A2482	C2311	G2222	A2222	G2122	G1906	G1796	U1886	G1597	G1493	C1392	C1292
U2483	A2312	U2129	U2225	U2129	C1907	U1797	U1887	G1598	C1496	A1399	U1293
C2484	A2313	G2130	U2226	A2130	A1910	A1798	A1696	A1603	C1497	A1400	A1294
A2485	U2314	G2131	A2227	G2131	A1911	A1799	A1697	A1604	A1498	A1401	G1295
U2486	U2315	A2131	A2228	A2131	A1912	A1800	C1698	A1605	C1499	G1500	C1296
A2487	G2315	U2132	A2229	A2132	A1913	U1801	A1699	U1606	G1501	G1404	U1299
U2490	U2334	U2140	A2232	U2140	G1914	C1802	U1699	U1607	U1501	A1407	A1304
A2491	G2335	U2141	A2233	A2141	A1915	C1805	U1717	A1612	C1508	A1407	U1305
U2492	U2336	A2142	A2233	A2142	U1916	A1806	G1718	A1613	C1508	A1411	U1306
U2493	C2337	A2143	A2233	A2143	U1917	G1807	U1719	C1614	G1513	A1411	G1307
A2494	U2340	A2144	A2241	A2144	U1925	U1808	U1720	C1615	G1513	U1415	A1308
C2495	U2341	U2152	A2242	U2152	G1926	G1808	U1721	C1616	G1517	A1418	U1309
U2496	A2345	U2153	A2245	U2153	G1927	G1812	U1724	U1616	U1522	A1419	G1311
U2497	C2346	U2154	C2249	U2154	U1928	A1813	A1729	G1617	U1523	A1428	A1317
U2498	U2347	G2155	G2249	G2155	A1930	A1814	G1730	A1619	U1533	G1429	C1328
A2499	U2348	C2156	A2252	C2156	U1931	U1815	U1731	U1620	U1534	U1430	U1329
U2500	G2351	G2157	A2253	G2157	A1932	A1816	G1736	A1621	A1534	G1431	A1330
A2501	A2352	A2158	U2254	A2158	U1949	G1817	U1737	U1622	A1535	C1432	U1331
G2502	U2353	G2160	A2255	G2160	U1953	U1818	C1738	G1623	G1536	A1433	G1332
U2503	G2355	G2161	A2256	G2161	G1954	U1819	U1739	G1624	A1539	A1434	C1333
C2444	A2356	U2162	C2257	U2162	U1955	U1820	U1740	A1625	U1553	U1435	U1336
U2505	A2357	A2167	U2258	A2167	A1955	U1821	A1741	U1626	U1554	A1437	A1337
U2506	A2358	G2168	A2259	G2168	U1955	C1822	U1742	U1627	U1555	A1446	G1340
U2507	U2359	A2169	U2260	A2169	U1955	G1829	U1746	U1628	C1556	G1447	U1341
U2508	G2363	G2176	A2261	G2176	U1955	G1830	G1747	U1629	A1557	U1448	U1342
A2511	C2364	G2177	A2262	G2177	U1955	U1831	U1750	U1630	A1558	A1449	U1343
U2514	U2365	A2178	C2265	A2178	U1955	C1836	G1751	C1631	A1559	G1450	U1344
A2515	G2366	C2179	U2266	C2179	U1955	U1840	A1752	G1640	G1560	C1451	U1345
C2523	A2373	A2183	C2267	A2183	U1955	U1841	A1753	U1641	G1561	A1452	A1350
A2524	C2374	U2184	U2268	U2184	U1955	A1842	A1754	A1642	C1562	A1453	U1351
G2525	G2375	G2185	U2269	G2185	U1955	A1843	U1755	A1643	C1563	A1454	A1352
C2526	A2376	A2186	A2270	A2186	U1955	A1844	C1756	C1644	U1564	U1455	U1353
U2527	G2377	U2187	A2271	U2187	U1955	C1846	A1760	U1645	G1565	U1456	A1354
U2460	C2383	U2188	G2272	A2188	U1955	U1847	G1761	G1646	A1566	U1458	A1355
A2461	U2388	U2193	A2273	U2193	U1955	C1849	U1762	C1657	U1567	C1459	G1356
G2462	U2388	G2194	C2277	U2194	U1955	A1850	U1763	C1658	U1568	A1461	A1357
A2535	U2388	C2195	A2278	C2195	U1955	U1850	U1764	G1659	U1569	A1461	A1358



• Molecule 39: 5s rRNA

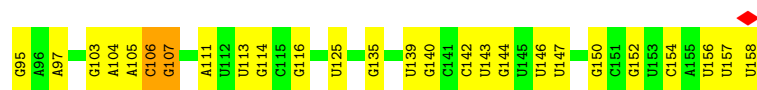
Chain A3: 60% 36%



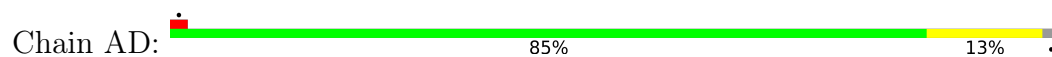
• Molecule 40: 5.8 S rRNA

Chain A4: 57% 39%

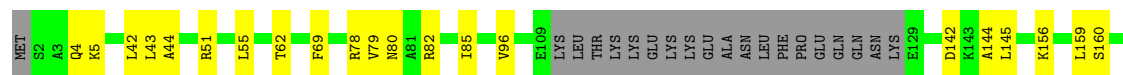
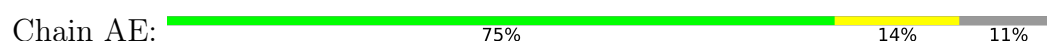




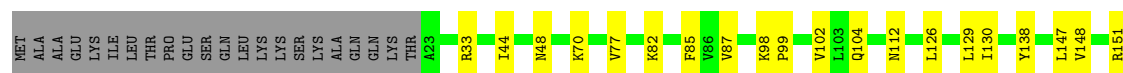
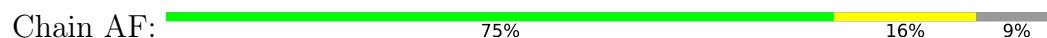
- Molecule 41: RPL5 isoform 1



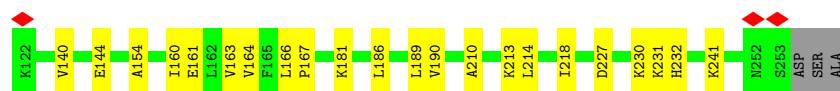
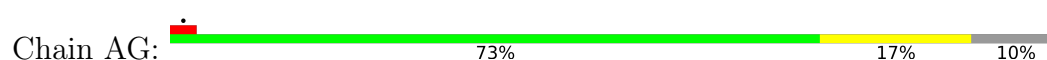
- Molecule 42: 60S ribosomal protein L6-A



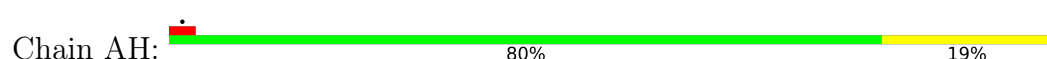
- Molecule 43: 60S ribosomal protein L7-A

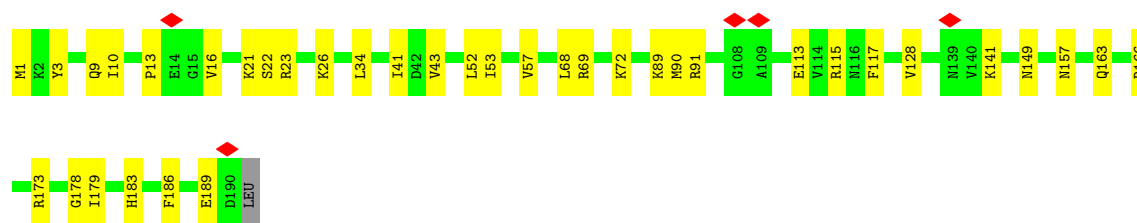


- Molecule 44: 60S ribosomal protein L8-A



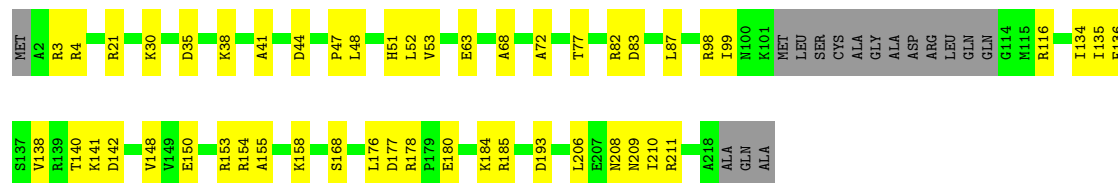
- Molecule 45: 60S ribosomal protein L9-A





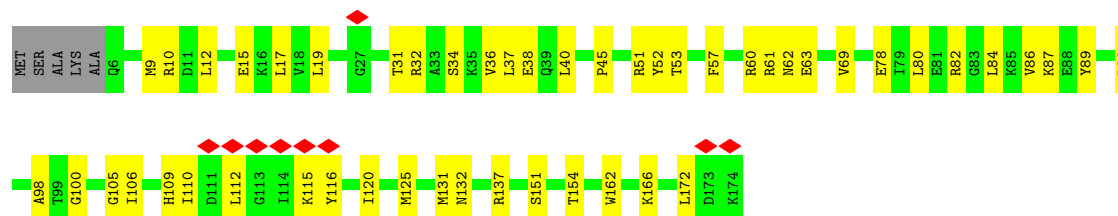
- Molecule 46: RPL10 isoform 1

Chain AI: 71% 22% 7%



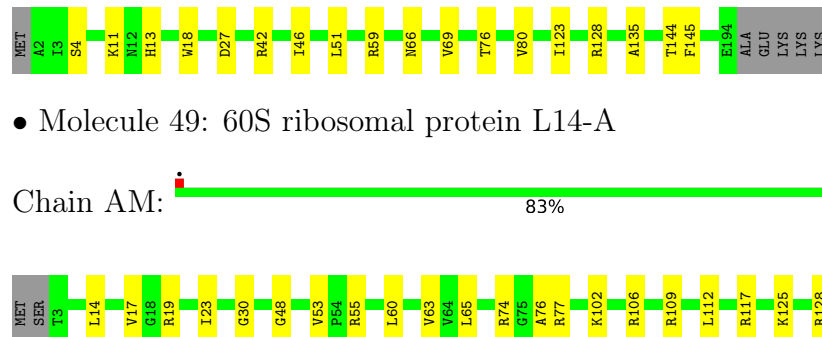
- Molecule 47: RPL11A isoform 1

Chain AJ: 5% 68% 29%



- Molecule 48: 60S ribosomal protein L13-A

Chain AL: 88% 9%



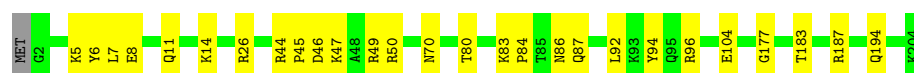
- Molecule 49: 60S ribosomal protein L14-A

Chain AM: 83% 16%

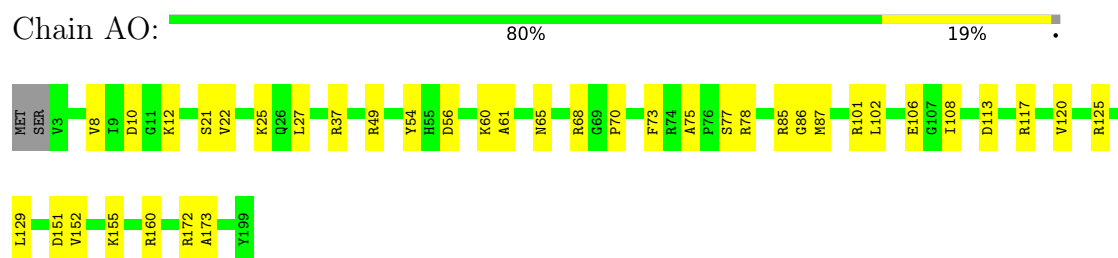


- Molecule 50: 60S ribosomal protein L15-A

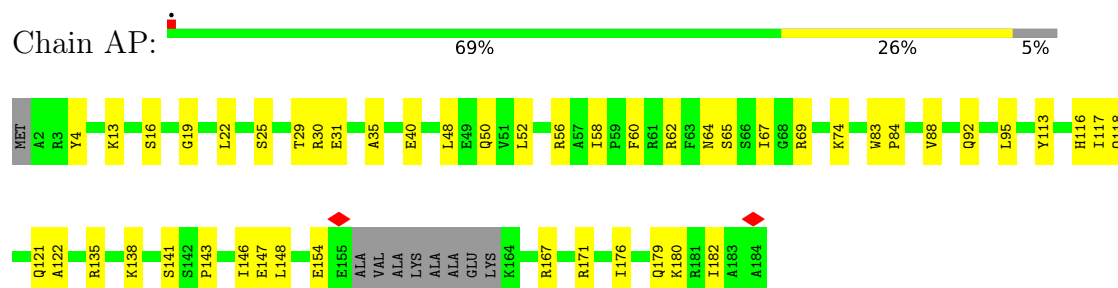
Chain AN: 86% 13%



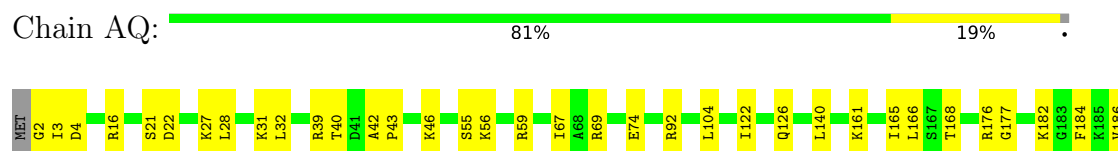
- Molecule 51: 60S ribosomal protein L16-A



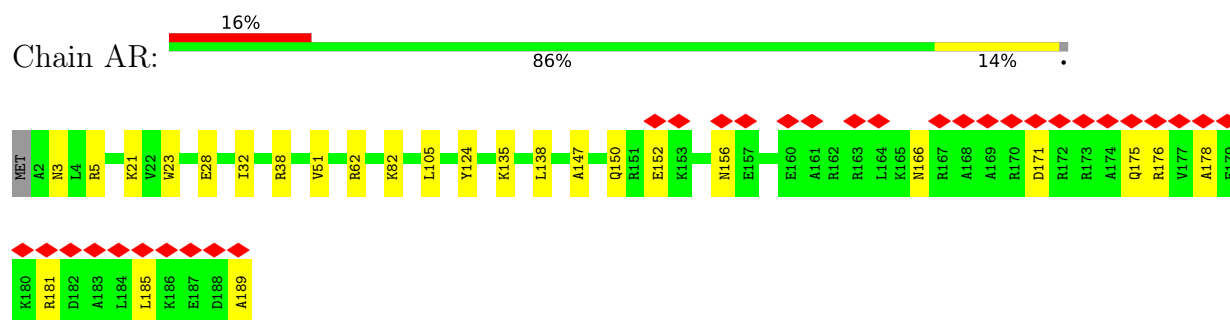
- Molecule 52: 60S ribosomal protein L17-A



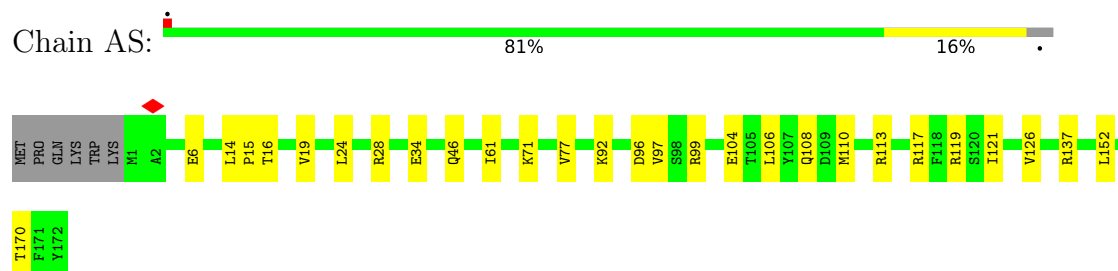
- Molecule 53: 60S ribosomal protein L18-A



- Molecule 54: 60S ribosomal protein L19-A

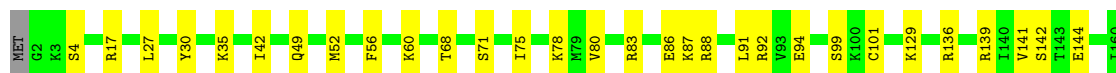


- Molecule 55: 60S ribosomal protein L20



- Molecule 56: 60S ribosomal protein L21-A

Chain AT:  81% 19%



- Molecule 57: 60S ribosomal protein L22-A

Chain AU:  69% 14% 17%



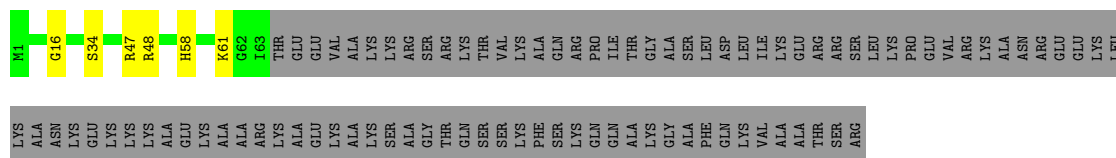
- Molecule 58: 60S ribosomal protein L23-A

Chain AV:  80% 20%



- Molecule 59: RPL24A isoform 1

Chain AW:  37% 59%



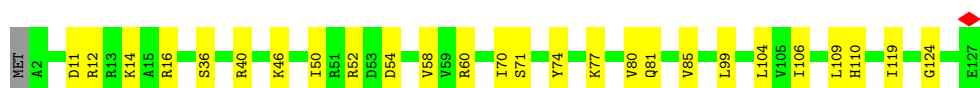
- Molecule 60: 60S ribosomal protein L25

Chain AX:  71% 14% 15%



- Molecule 61: 60S ribosomal protein L26-A

Chain AY:  79% 20%



- Molecule 62: 60S ribosomal protein L27-A

Chain AZ:  78% 21%



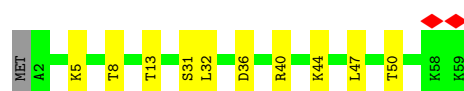
- Molecule 63: 60S ribosomal protein L28

Chain Aa:  78% 21%



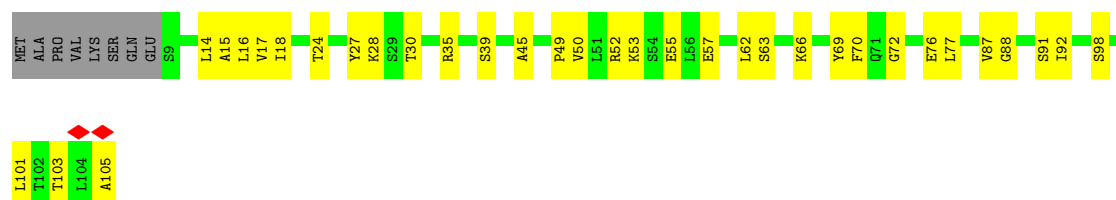
- Molecule 64: RPL29 isoform 1

Chain Ab:  81% 17%



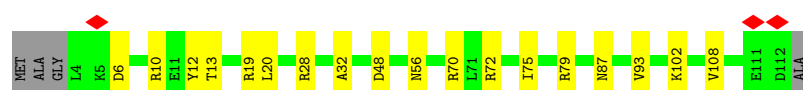
- Molecule 65: 60S ribosomal protein L30

Chain Ac:  60% 32% 8%



- Molecule 66: 60S ribosomal protein L31-A

Chain Ad:  81% 16%



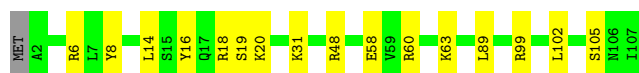
- Molecule 67: RPL32 isoform 1

Chain Ae:  85% 12%



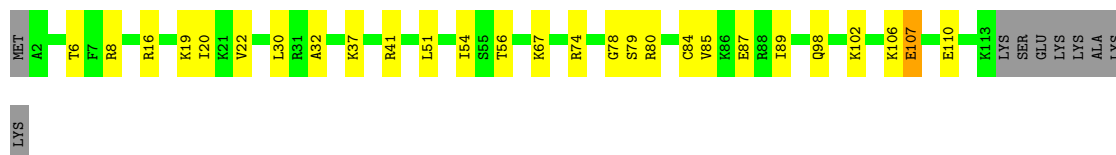
- Molecule 68: 60S ribosomal protein L33-A

Chain Af:  84% 15%



- Molecule 69: 60S ribosomal protein L34-A

Chain Ag: 70% 21% 7%



- Molecule 70: 60S ribosomal protein L35-A

Chain Ah: 81% 18%



- Molecule 71: 60S ribosomal protein L36-A

Chain Ai: 87% 12%



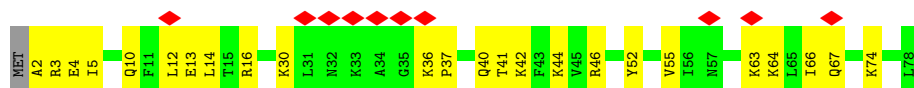
- Molecule 72: 60S ribosomal protein L37-A

Chain Aj: 83% 16%



- Molecule 73: RPL38 isoform 1

Chain Ak: 13% 68% 31%



- Molecule 74: 60S ribosomal protein L39

Chain Al: 78% 20%



- Molecule 75: Ubiquitin-60S ribosomal protein L40

Chain Am:  34% 7% 59%

MET GLN ILE PHE VAL LYS THR LEU THR GLY LYS THR ILE THR LEU GLU VAL GLU SER ASP THR ILE ASP ASN VAL LYS SER LYS ILE GLN ASP LYS GLU GLY ILE PRO PRO ASP GLN GLN ARG ARG LEU ILE PHE ALA GLY LYS LYS LYS LEU GLU ASP GLY ARG ARG THR LEU SER ASP TYR ASN

ILE GLN LYS GLU SER THR LEU HIS VAL LEU ARG ARG GLY I77 I78 I79 K98 C99 Y100 P104 A107 R113 K114 T118 K128

- Molecule 76: 60S ribosomal protein L41-A

Chain An:  68% 32%

K1 R2 A3 K4 W5 R6 K7 R11 R18 R23 S24 K25

- Molecule 77: 60S ribosomal protein L42-A

Chain Ao:  5% 84% 15%

MET V2 V3 V4 B8 G14 K15 T16 A30 R41 R45 R46 K66 L72 G94 G98 Q99 K100 G101 Q102 A103 L104 Q105 F106

- Molecule 78: 60S ribosomal protein L43-A

Chain Ap:  80% 18%

MET A2 K3 K4 T5 R17 V26 Q32 Y37 K44 K45 T46 K49 G50 A51 I54 C57 V64 A65 G66 A68 A76 V79 A92

- Molecule 79: RPL1A isoform 1

Chain E:  25% 72% 28%

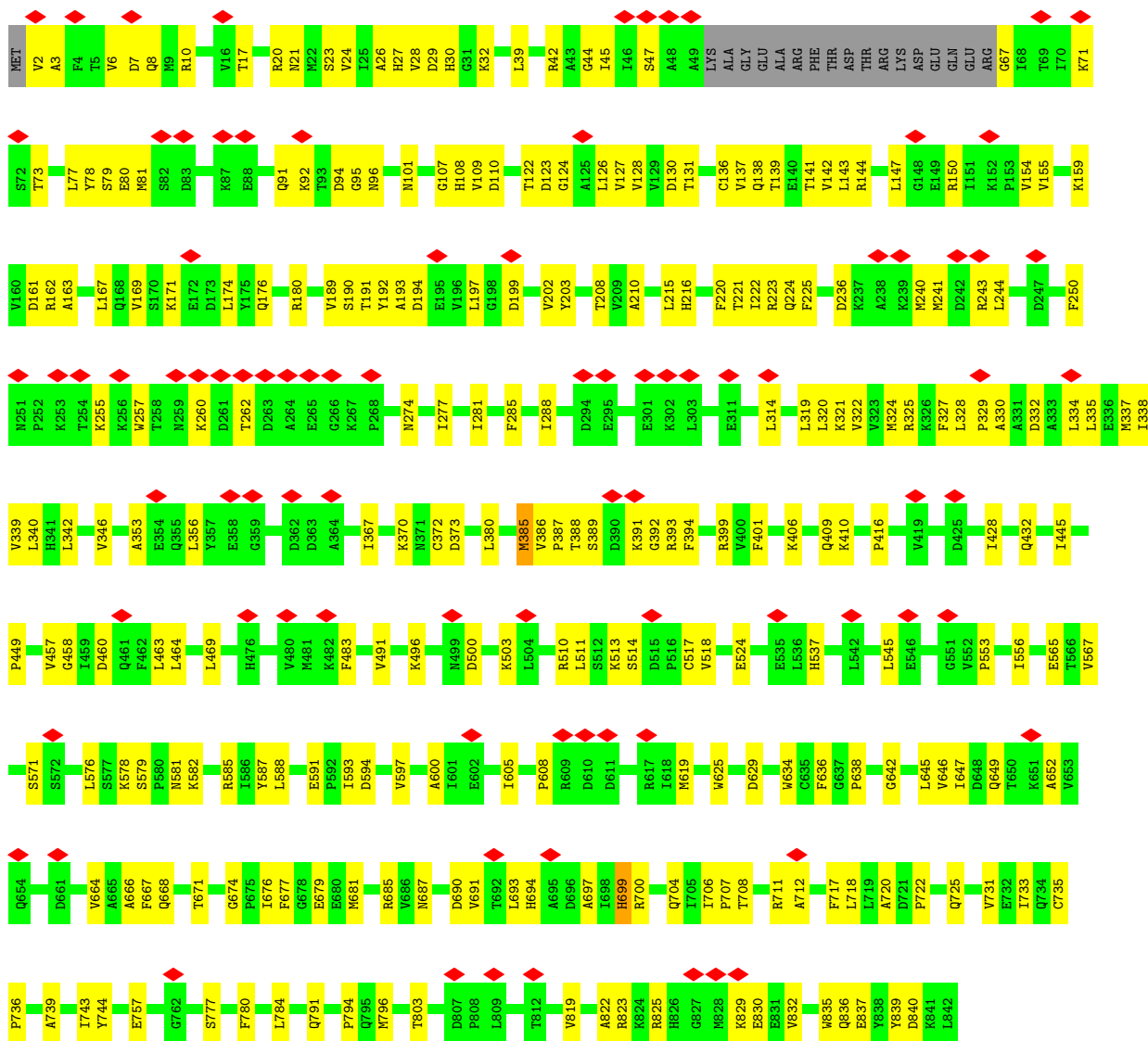
M1 S2 K3 I4 T5 S6 S7 V9 H12 V13 K14 E15 L16 L17 K18 T23 K24 K25 R26 T31 L34 L38 K39 M40 S50 K54 L55 P56 P59 R60 P61 M62 F68 F72 D73 R76 A77 K78 S79 C80 G81 V82 D83 A84 M85 S86 V87 D88

D89 L90 K91 K92 L93 N94 I100 K101 K105 A109 F110 I111 A112 S113 E114 V115 L116 I117 K118 Q119 R122 L123 L124 G125 P126 Q127 L128 S129 K130 K133 F134 V138 S139 H140 N141 D142 D143 L144 Y145 G146 K147 V148 T149 D150 V151 R152 L159 K160 R161 V162 L163 C164 S165

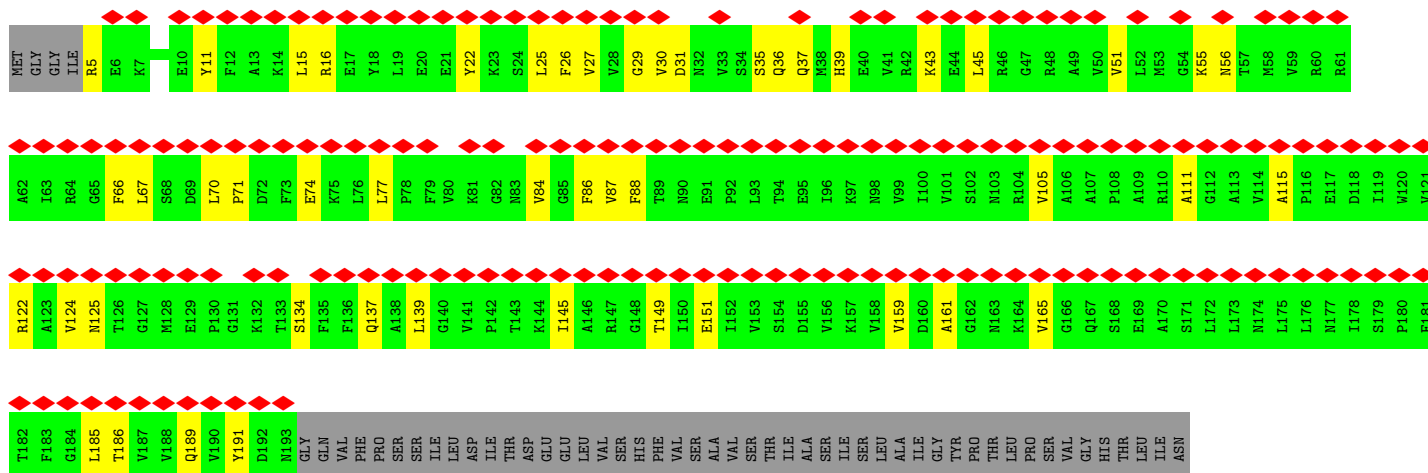
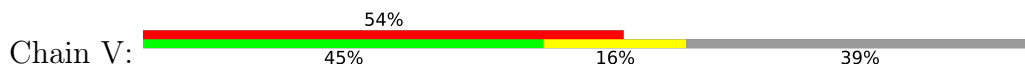
A166 V167 A168 V169 G170 N171 V172 E173 M174 E175 L179 V180 N181 Q182 I183 L184 V191 L194 M197 N200 L204 V205 S209 A213 F214 R215 L216 Y217

- Molecule 80: Elongation factor 2

Chain DC:  10% 67% 31%



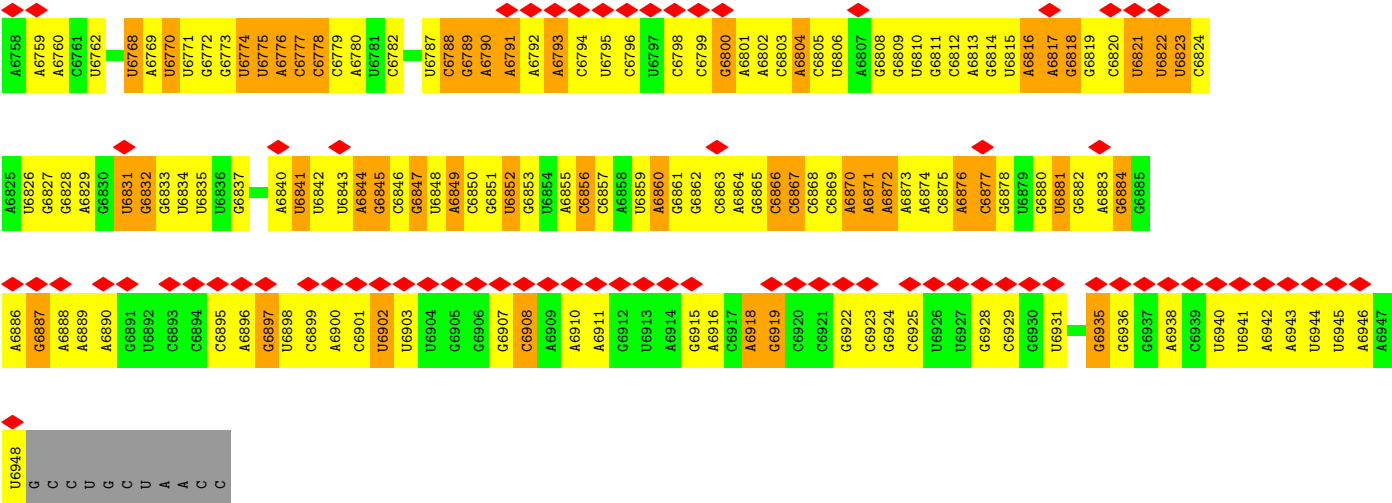
• Molecule 81: 60S acidic ribosomal protein P0



ASN TYR
TYR LYS
LYS ASP
ASP MET
LEU LEU
ALA PHE
VAL GLY
ALA LEU
ALA PHE
ALA TLE
ALA TLE
SER SER
TYR TYR
HIS TYR
PRO PRO
GLU GLU
TLE TLE
GLU ASP
ASP LEU
VAL VAL
ASP ASP
ARG ARG
TLE TLE
GLU GLU
ASN ASN
PRO PRO
GLU GLU
LYS LYS
TYR TYR
ALA ALA
ALA ALA
ALA ALA
PRO PRO
ALA ALA
ALA ALA
THR THR
SER SER
ALA ALA
SER SER
GLY GLY
ASP ASP
ALA ALA
ALA ALA
PRO PRO
ALA ALA
GLU GLU
ALA ALA
ALA ALA
GLU GLU
GLU GLU
GLU GLU

SER
ASP
ASP
ASP
MET
GLY
PHE
GLY
PHE
ASP

● Molecule 82: TSV IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47514	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	4.410	Depositor
Minimum map value	-1.730	Depositor
Average map value	0.058	Depositor
Map value standard deviation	0.237	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: A2M, OMC, MG, GDP, UR3, ZN, 1MA, W9C, OMG, G7M, X SX, DDE, HIC, 5MC, MA6, OMU, 4AC

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	0.40	2/1653 (0.1%)	0.77	4/2261 (0.2%)
2	BB	0.20	0/1735	0.51	0/2335
3	BC	0.22	0/1665	0.45	0/2263
4	BE	0.18	0/2109	0.47	1/2839 (0.0%)
5	BG	0.14	0/1844	0.36	0/2464
6	BH	0.21	0/1506	0.55	2/2028 (0.1%)
7	BI	0.17	0/1514	0.45	0/2021
8	BJ	0.15	0/1519	0.37	0/2035
9	BL	0.15	0/1272	0.37	1/1712 (0.1%)
10	BN	0.19	0/1215	0.50	0/1638
11	BO	0.21	0/952	0.48	0/1279
12	BV	0.20	0/693	0.58	2/935 (0.2%)
13	BW	0.17	0/1038	0.40	0/1395
14	BX	0.16	0/1139	0.45	0/1518
15	BY	0.18	0/1087	0.45	0/1449
16	Ba	0.24	0/782	0.65	2/1047 (0.2%)
17	Bb	0.17	0/620	0.53	0/838
18	Be	0.15	0/483	0.49	0/643
19	BD	0.19	0/1759	0.51	2/2368 (0.1%)
20	BF	0.22	0/1629	0.48	0/2202
21	BK	0.61	2/837 (0.2%)	1.10	4/1131 (0.4%)
22	BP	0.18	0/1012	0.46	0/1356
23	BQ	0.17	0/1125	0.40	0/1510
24	BR	0.18	0/984	0.48	0/1318
25	BS	0.19	0/1211	0.47	0/1628
26	BT	0.17	0/1113	0.45	0/1494
27	BU	0.17	0/865	0.42	0/1169
28	BZ	0.20	0/566	0.54	0/761
29	Bc	0.23	0/499	0.58	0/670
30	Bd	0.16	0/452	0.40	0/600
31	Bg	0.17	0/2454	0.47	0/3340

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Bf	0.16	0/616	0.49	1/817 (0.1%)
33	BM	0.22	0/943	0.62	4/1274 (0.3%)
34	B5	0.18	1/41880 (0.0%)	0.33	0/65248
35	AA	0.22	0/1912	0.46	0/2569
36	AB	0.19	0/3139	0.40	0/4219
37	AC	0.19	0/2800	0.41	0/3790
38	A1	0.21	1/75586 (0.0%)	0.34	2/117845 (0.0%)
39	A3	0.18	0/2883	0.31	0/4491
40	A4	0.19	0/3746	0.31	0/5832
41	AD	0.17	0/2390	0.38	0/3225
42	AE	0.16	0/1260	0.38	0/1694
43	AF	0.18	0/1821	0.37	0/2451
44	AG	0.18	0/1830	0.44	0/2469
45	AH	0.21	0/1531	0.47	0/2062
46	AI	0.17	0/1708	0.36	0/2290
47	AJ	0.21	0/1374	0.54	0/1842
48	AL	0.18	0/1568	0.38	0/2106
49	AM	0.16	0/1068	0.33	0/1438
50	AN	0.19	0/1757	0.36	0/2354
51	AO	0.17	0/1585	0.35	0/2128
52	AP	0.20	0/1410	0.42	0/1893
53	AQ	0.18	0/1465	0.37	0/1965
54	AR	0.16	0/1538	0.37	0/2050
55	AS	0.21	0/1481	0.43	0/1990
56	AT	0.19	0/1300	0.37	0/1743
57	AU	0.20	0/812	0.55	2/1099 (0.2%)
58	AV	0.19	0/1018	0.42	0/1369
59	AW	0.19	0/533	0.43	0/707
60	AX	0.19	0/983	0.41	0/1325
61	AY	0.20	0/1004	0.44	0/1341
62	AZ	0.18	0/1118	0.42	0/1497
63	Aa	0.21	0/1204	0.45	0/1612
64	Ab	0.21	0/473	0.43	0/629
65	Ac	0.19	0/751	0.43	0/1008
66	Ad	0.18	0/904	0.40	0/1213
67	Ae	0.18	0/1041	0.36	0/1394
68	Af	0.21	0/868	0.40	0/1168
69	Ag	0.23	0/890	0.47	1/1189 (0.1%)
70	Ah	0.16	0/978	0.35	0/1301
71	Ai	0.20	0/778	0.47	0/1034
72	Aj	0.18	0/696	0.36	0/923
73	Ak	0.17	0/618	0.41	0/826
74	Al	0.23	0/443	0.50	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Am	0.20	0/423	0.48	0/562
76	An	0.17	0/234	0.40	0/300
77	Ao	0.22	0/860	0.56	0/1136
78	Ap	0.18	0/701	0.39	0/934
79	E	0.16	0/1745	0.44	0/2342
80	DC	0.21	0/6521	0.51	3/8830 (0.0%)
81	V	0.19	0/1498	0.50	0/2025
82	EC	0.16	0/4521	0.38	0/7039
All	All	0.20	6/227538 (0.0%)	0.39	31/333423 (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
3	BC	0	2
6	BH	0	1
15	BY	0	1
44	AG	0	2
47	AJ	0	1
76	An	0	1
All	All	0	8

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BA	97	PRO	CB-CG	-11.29	0.93	1.49
21	BK	83	PRO	CB-CG	-11.22	0.93	1.49
21	BK	83	PRO	CG-CD	-9.76	1.17	1.50
1	BA	97	PRO	CG-CD	-8.70	1.21	1.50
34	B5	1575	G7M	O3'-P	6.09	1.62	1.56
38	A1	2729	OMU	O3'-P	5.15	1.61	1.56

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BA	97	PRO	N-CD-CG	-18.30	75.76	103.20
21	BK	83	PRO	N-CD-CG	-17.68	76.67	103.20
21	BK	83	PRO	CB-CG-CD	17.59	162.40	106.10
1	BA	97	PRO	CA-CB-CG	-17.15	71.92	104.50
21	BK	83	PRO	CA-CB-CG	-16.80	72.59	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BA	97	PRO	CB-CG-CD	11.16	141.81	106.10
33	BM	82	PRO	CA-N-CD	-9.09	99.28	112.00
6	BH	13	PRO	CA-C-N	8.18	136.42	121.70
6	BH	13	PRO	C-N-CA	8.18	136.42	121.70
80	DC	385	MET	CG-SD-CE	-7.59	84.20	100.90
1	BA	97	PRO	CA-N-CD	-7.51	101.48	112.00
21	BK	83	PRO	CA-N-CD	-7.41	101.62	112.00
80	DC	385	MET	CB-CG-SD	6.76	132.98	112.70
33	BM	82	PRO	N-CD-CG	-6.58	93.32	103.20
32	Bf	144	CYS	CA-CB-SG	6.31	128.92	114.40
57	AU	90	ARG	CA-C-N	6.10	135.76	125.02
57	AU	90	ARG	C-N-CA	6.10	135.76	125.02
19	BD	43	PRO	CA-C-N	5.81	132.65	121.54
19	BD	43	PRO	C-N-CA	5.81	132.65	121.54
80	DC	385	MET	CA-CB-CG	-5.78	102.54	114.10
38	A1	240	U	P-O3'-C3'	5.70	128.74	120.20
16	Ba	18	VAL	CA-C-N	5.64	135.56	121.80
16	Ba	18	VAL	C-N-CA	5.64	135.56	121.80
4	BE	87	MET	CA-CB-CG	5.50	125.10	114.10
9	BL	5	LEU	CA-CB-CG	5.36	135.07	116.30
69	Ag	107	GLU	N-CA-CB	5.31	118.02	110.16
33	BM	82	PRO	CB-CG-CD	-5.30	89.14	106.10
38	A1	239	G	C2'-C3'-O3'	5.13	117.19	109.50
12	BV	11	LEU	CA-C-N	5.04	131.18	121.54
12	BV	11	LEU	C-N-CA	5.04	131.18	121.54
33	BM	82	PRO	CA-CB-CG	-5.02	94.97	104.50

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
44	AG	121	SER	Peptide
44	AG	30	THR	Peptide
47	AJ	166	LYS	Peptide
76	An	23	ARG	Sidechain
3	BC	144	TRP	Peptide
3	BC	145	GLY	Peptide
6	BH	64	VAL	Peptide
15	BY	34	ASN	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	44	0
2	BB	1709	0	1784	39	0
3	BC	1635	0	1723	32	0
4	BE	2068	0	2154	51	0
5	BG	1820	0	1918	37	0
6	BH	1481	0	1572	28	0
7	BI	1489	0	1525	39	0
8	BJ	1494	0	1573	26	0
9	BL	1244	0	1314	17	0
10	BN	1192	0	1255	26	0
11	BO	941	0	979	24	0
12	BV	684	0	672	18	0
13	BW	1021	0	1060	21	0
14	BX	1121	0	1196	22	0
15	BY	1073	0	1132	37	0
16	Ba	769	0	818	23	0
17	Bb	610	0	633	8	0
18	Be	475	0	525	8	0
19	BD	1734	0	1817	29	0
20	BF	1609	0	1675	56	0
21	BK	817	0	804	28	0
22	BP	991	0	1035	20	0
23	BQ	1105	0	1166	32	0
24	BR	975	0	1039	30	0
25	BS	1192	0	1222	31	0
26	BT	1095	0	1114	37	0
27	BU	855	0	917	22	0
28	BZ	558	0	598	20	0
29	Bc	497	0	535	6	0
30	Bd	442	0	432	11	0
31	Bg	2401	0	2356	64	0
32	Bf	605	0	654	18	0
33	BM	935	0	975	23	0
34	B5	38004	0	19142	671	0
35	AA	1878	0	1946	47	0
36	AB	3081	0	3162	56	0
37	AC	2748	0	2859	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	A1	68444	0	34451	800	0
39	A3	2579	0	1304	37	0
40	A4	3353	0	1695	39	0
41	AD	2341	0	2290	30	0
42	AE	1239	0	1326	18	0
43	AF	1784	0	1862	27	0
44	AG	1798	0	1894	30	0
45	AH	1510	0	1576	24	0
46	AI	1672	0	1711	33	0
47	AJ	1353	0	1383	33	0
48	AL	1543	0	1608	15	0
49	AM	1053	0	1149	16	0
50	AN	1720	0	1779	21	0
51	AO	1555	0	1659	28	0
52	AP	1388	0	1423	37	0
53	AQ	1441	0	1543	29	0
54	AR	1521	0	1617	20	0
55	AS	1445	0	1487	18	0
56	AT	1276	0	1323	23	0
57	AU	796	0	812	10	0
58	AV	1003	0	1048	18	0
59	AW	521	0	551	5	0
60	AX	968	0	1036	16	0
61	AY	993	0	1081	17	0
62	AZ	1092	0	1155	25	0
63	Aa	1173	0	1215	25	0
64	Ab	462	0	491	11	0
65	Ac	743	0	797	25	0
66	Ad	890	0	938	13	0
67	Ae	1020	0	1089	11	0
68	Af	850	0	880	10	0
69	Ag	880	0	945	17	0
70	Ah	969	0	1078	18	0
71	Ai	771	0	849	10	0
72	Aj	681	0	687	12	0
73	Ak	612	0	682	20	0
74	Al	436	0	475	10	0
75	Am	417	0	459	8	0
76	An	233	0	284	6	0
77	Ao	847	0	914	16	0
78	Ap	694	0	738	14	0
79	E	1718	0	1811	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	DC	6419	0	6491	182	0
81	V	1473	0	1514	34	0
82	EC	4045	0	2039	72	0
83	A1	173	0	0	0	0
83	A3	2	0	0	0	0
83	A4	4	0	0	0	0
83	AB	1	0	0	0	0
83	AL	1	0	0	0	0
83	AO	1	0	0	0	0
83	B5	33	0	0	0	0
83	Ba	1	0	0	0	0
83	DC	1	0	0	0	0
84	Ao	1	0	0	0	0
85	DC	28	0	12	4	0
86	DC	35	0	0	0	0
All	All	213962	0	160055	3065	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 8.

All (3065) 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:N1	2.05	1.03
34:B5:1187:U:H3	34:B5:1198:G:H1	0.99	0.98
38:A1:3234:A:N6	38:A1:3253:G:H1	1.63	0.97
34:B5:1158:C:H42	34:B5:1163:A:H61	1.05	0.95
38:A1:2482:U:H3	38:A1:2486:A:H62	1.13	0.94
34:B5:126:A:H62	34:B5:291:G:H21	1.17	0.91
38:A1:1237:G:H1	38:A1:1251:A:H61	1.01	0.90
38:A1:1237:G:H1	38:A1:1251:A:N6	1.70	0.89
34:B5:1213:G:H1	34:B5:1450:U:H3	0.88	0.88
47:AJ:12:LEU:HG	47:AJ:131:MET:HE2	1.55	0.87
34:B5:1588:G:H1	34:B5:1608:U:H3	1.18	0.86
80:DC:823:ARG:HG2	80:DC:830:GLU:HA	1.57	0.86
38:A1:3234:A:H61	38:A1:3253:G:H1	0.89	0.85
34:B5:430:G:H21	80:DC:391:LYS:HG2	1.43	0.83
34:B5:1158:C:H42	34:B5:1163:A:N6	1.77	0.83
34:B5:126:A:H62	34:B5:291:G:N2	1.76	0.83
2:BB:144:ARG:HB2	2:BB:208:GLN:HB2	1.61	0.81
35:AA:21:ARG:HD3	38:A1:824:C:H5''	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:Ab:32:LEU:O	64:Ab:40:ARG:NH1	2.14	0.81
34:B5:1697:G:H1	34:B5:1704:U:H3	1.25	0.79
34:B5:1158:C:N4	34:B5:1163:A:H61	1.80	0.79
80:DC:32:LYS:HE3	80:DC:107:GLY:H	1.49	0.78
24:BR:17:ILE:HD11	24:BR:54:THR:HG23	1.64	0.78
82:EC:6853:G:N1	82:EC:6876:A:C2	2.51	0.78
35:AA:149:ARG:NH1	35:AA:150:LEU:O	2.18	0.77
56:AT:142:SER:OG	56:AT:144:GLU:OE1	2.04	0.76
3:BC:140:ARG:HB3	3:BC:221:THR:HB	1.67	0.76
38:A1:2482:U:H3	38:A1:2486:A:N6	1.82	0.75
34:B5:1684:U:H3	34:B5:1717:G:H1	1.35	0.75
23:BQ:94:GLN:HE21	31:Bg:60:SER:HB3	1.51	0.74
38:A1:2772:C:OP2	77:Ao:15:LYS:NZ	2.19	0.74
44:AG:75:ILE:HD13	44:AG:160:ILE:HG12	1.70	0.74
64:Ab:32:LEU:HB3	64:Ab:40:ARG:HH12	1.53	0.74
76:An:7:LYS:HE2	76:An:11:ARG:HH21	1.54	0.73
38:A1:2457:G:N1	38:A1:2461:A:N7	2.36	0.73
82:EC:6922:G:H1	82:EC:6931:U:H3	1.33	0.73
15:BY:34:ASN:ND2	34:B5:521:A:N3	2.36	0.73
2:BB:103:MET:HE3	2:BB:215:VAL:HG23	1.72	0.72
2:BB:70:LEU:HD12	2:BB:84:ILE:HD11	1.72	0.72
7:BI:87:ASN:HB3	7:BI:90:LEU:HD13	1.71	0.72
34:B5:1339:C:O2'	34:B5:1341:A:N7	2.23	0.72
62:AZ:133:LYS:HE3	62:AZ:135:ARG:HH22	1.53	0.72
46:AI:72:ALA:HB2	46:AI:155:ALA:HB2	1.72	0.71
44:AG:77:GLN:HE22	44:AG:167:PRO:HG2	1.55	0.71
25:BS:132:ARG:NH2	34:B5:1173:C:OP1	2.24	0.71
58:AV:81:GLN:O	58:AV:98:ASN:ND2	2.23	0.71
34:B5:913:G:H1	38:A1:2206:G:H5''	1.53	0.71
11:BO:61:MET:HG2	11:BO:104:ALA:HB2	1.73	0.71
34:B5:766:U:H3	34:B5:770:A:H62	1.38	0.71
34:B5:992:A:O2'	34:B5:1785:U:O2	2.08	0.71
13:BW:15:ASN:ND2	13:BW:72:CYS:O	2.24	0.71
25:BS:145:ARG:NH2	34:B5:1569:A:N3	2.39	0.71
79:E:128:LEU:HD21	79:E:134:PHE:HA	1.72	0.71
31:Bg:89:LEU:HB2	31:Bg:103:PHE:HB2	1.71	0.70
34:B5:628:G:H21	34:B5:971:A:H62	1.39	0.70
34:B5:1654:G:N2	34:B5:1745:G:O2'	2.20	0.70
52:AP:58:ILE:HD12	52:AP:84:PRO:HD2	1.74	0.70
66:Ad:20:LEU:HB3	66:Ad:28:ARG:HD2	1.74	0.70
80:DC:28:VAL:HG22	80:DC:108:HIS:HA	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2482:U:C2	38:A1:2486:A:N6	2.60	0.69
13:BW:57:ARG:HG2	34:B5:862:A:H4'	1.74	0.69
80:DC:215:LEU:HD23	85:DC:901:GDP:HN21	1.57	0.69
26:BT:122:ARG:NH1	34:B5:1499:G:OP1	2.26	0.69
38:A1:2667:A:OP1	47:AJ:51:ARG:NH2	2.25	0.69
7:BI:85:PRO:HA	9:BL:11:ARG:HG2	1.75	0.69
3:BC:81:MET:HB2	3:BC:101:VAL:HG13	1.72	0.69
23:BQ:100:GLN:NE2	31:Bg:57:PRO:O	2.25	0.69
15:BY:108:ARG:HA	15:BY:111:LYS:HE3	1.75	0.69
34:B5:1426:C:O2'	34:B5:1428:OMG:OP2	2.10	0.69
38:A1:2700:G:H5''	56:AT:17:ARG:HG2	1.75	0.69
80:DC:21:ASN:OD1	80:DC:101:ASN:ND2	2.25	0.69
6:BH:11:GLN:HG3	6:BH:13:PRO:HD2	1.75	0.68
22:BP:8:LYS:HG3	22:BP:9:LYS:H	1.58	0.68
79:E:38:LEU:HD11	79:E:159:LEU:HD11	1.73	0.68
80:DC:393:ARG:NH1	80:DC:460:ASP:OD2	2.26	0.68
23:BQ:42:GLU:HA	23:BQ:45:ARG:HG3	1.75	0.68
80:DC:110:ASP:HB3	80:DC:537:HIS:HB2	1.75	0.68
20:BF:166:ARG:NH2	34:B5:1163:A:O2'	2.26	0.68
38:A1:1656:A:OP2	69:Ag:37:LYS:NZ	2.26	0.68
25:BS:86:LEU:HD22	25:BS:99:HIS:HB2	1.75	0.68
34:B5:151:G:H22	34:B5:163:G:H1	1.42	0.68
80:DC:578:LYS:HE2	80:DC:582:LYS:HB3	1.74	0.68
38:A1:1765:U:H2'	38:A1:1766:G:H4'	1.76	0.68
38:A1:3275:U:O2'	68:Af:99:ARG:NH1	2.27	0.68
1:BA:41:ARG:NH1	24:BR:105:GLN:OE1	2.27	0.68
70:Ah:101:THR:OG1	70:Ah:104:GLN:NE2	2.27	0.68
49:AM:109:ARG:HA	49:AM:112:LEU:HD23	1.76	0.68
79:E:56:PRO:HD2	79:E:182:GLN:HG2	1.76	0.68
1:BA:136:ALA:HB1	1:BA:141:ILE:HB	1.77	0.67
1:BA:201:LEU:HD21	24:BR:85:VAL:HA	1.77	0.67
34:B5:1488:G:H3'	34:B5:1515:A:H61	1.59	0.67
52:AP:116:HIS:NE2	52:AP:147:GLU:OE2	2.27	0.67
10:BN:64:ARG:NH2	34:B5:862:A:OP2	2.28	0.67
16:Ba:12:LYS:HD3	16:Ba:16:GLY:H	1.58	0.67
82:EC:6817:A:H4'	82:EC:6818:G:H5'	1.76	0.67
14:BX:121:ARG:NH2	34:B5:1135:U:OP2	2.28	0.67
32:Bf:143:LYS:HD2	34:B5:1253:U:H4'	1.76	0.67
82:EC:6788:C:N4	82:EC:6805:C:OP2	2.27	0.67
26:BT:70:GLN:HG3	26:BT:120:GLY:HA3	1.77	0.67
34:B5:1267:G:H1	34:B5:1442:U:H3	1.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2261:G:H1'	38:A1:2262:A:H2	1.59	0.66
58:AV:14:SER:O	58:AV:81:GLN:NE2	2.28	0.66
38:A1:1132:C:H2'	38:A1:1133:A2M:H8	1.76	0.66
10:BN:104:ARG:NH2	34:B5:951:A:OP1	2.29	0.66
38:A1:2710:C:OP2	77:Ao:100:LYS:NZ	2.27	0.66
40:A4:97:A:O2'	70:Ah:59:ASN:ND2	2.29	0.66
79:E:34:LEU:HD11	79:E:183:ILE:HB	1.78	0.66
8:BJ:132:ARG:NH2	34:B5:532:U:OP1	2.27	0.66
14:BX:69:ARG:HG3	14:BX:117:ILE:HG12	1.76	0.66
14:BX:95:PHE:O	14:BX:142:LYS:NZ	2.28	0.66
38:A1:1015:U:O2	38:A1:1035:G:O6	2.14	0.66
38:A1:2474:G:N2	38:A1:2475:G:O6	2.27	0.66
43:AF:87:VAL:HG11	43:AF:243:MET:HE1	1.76	0.66
14:BX:70:LYS:NZ	34:B5:567:A:OP1	2.28	0.66
38:A1:2219:A:H2'	38:A1:2220:A2M:H8	1.76	0.66
40:A4:75:G:OP2	61:AY:74:TYR:OH	2.14	0.66
36:AB:240:ARG:NH2	38:A1:1907:C:O2	2.29	0.66
34:B5:431:C:H1'	80:DC:391:LYS:HD2	1.77	0.66
38:A1:2457:G:N2	38:A1:2486:A:C2	2.61	0.65
52:AP:176:ILE:HA	52:AP:179:GLN:HE21	1.62	0.65
58:AV:29:SER:O	58:AV:66:LYS:NZ	2.29	0.65
63:Aa:56:VAL:HG12	63:Aa:57:GLY:H	1.61	0.65
19:BD:109:LEU:HD21	19:BD:182:LEU:HD12	1.77	0.65
34:B5:91:G:OP1	34:B5:397:A:N6	2.29	0.65
34:B5:1594:G:OP2	34:B5:1596:C:N4	2.29	0.65
38:A1:411:U:H2'	38:A1:412:G:H8	1.59	0.65
80:DC:432:GLN:HB3	80:DC:457:VAL:HG23	1.78	0.65
80:DC:823:ARG:NH1	80:DC:829:LYS:O	2.30	0.65
10:BN:64:ARG:NH1	34:B5:861:U:OP1	2.29	0.65
23:BQ:22:VAL:HG22	23:BQ:65:ILE:HG12	1.77	0.65
34:B5:871:G:H2'	34:B5:872:G:C8	2.30	0.65
26:BT:105:LEU:HD13	26:BT:122:ARG:HD3	1.77	0.65
32:Bf:96:LYS:NZ	34:B5:1251:U:OP2	2.29	0.65
38:A1:655:C:H2'	38:A1:656:A:H8	1.61	0.65
38:A1:1448:U:H2'	38:A1:1449:A2M:H8	1.79	0.65
40:A4:29:U:H5''	48:AL:27:ASP:HB3	1.77	0.65
8:BJ:59:LEU:HD11	8:BJ:69:ARG:HA	1.78	0.65
35:AA:83:HIS:HB3	78:Ap:64:VAL:HG12	1.76	0.65
55:AS:14:LEU:HD12	55:AS:15:PRO:HD2	1.79	0.65
21:BK:48:SER:O	21:BK:52:LYS:NZ	2.30	0.65
31:Bg:42:LEU:HB2	31:Bg:61:PHE:HB2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2185:G:O2'	38:A1:2314:U:OP2	2.15	0.65
4:BE:60:GLU:OE2	15:BY:20:ARG:NH2	2.29	0.65
27:BU:59:PRO:HG3	34:B5:1381:U:H4'	1.78	0.65
38:A1:1639:C:OP2	69:Ag:74:ARG:NH1	2.30	0.65
44:AG:189:LEU:HD12	44:AG:190:VAL:HG13	1.79	0.65
79:E:109:ALA:HA	79:E:133:LYS:HG2	1.79	0.65
6:BH:49:ILE:HD12	6:BH:172:VAL:HG23	1.79	0.65
13:BW:115:GLU:HA	13:BW:118:ARG:HG2	1.79	0.64
38:A1:2767:U:O2'	77:Ao:30:ALA:O	2.14	0.64
7:BI:61:GLU:HG2	7:BI:62:THR:HG23	1.77	0.64
33:BM:56:GLU:OE2	33:BM:124:LYS:NZ	2.30	0.64
66:Ad:75:ILE:HG12	66:Ad:93:VAL:HG13	1.79	0.64
5:BG:66:GLY:HA2	34:B5:1681:A:H1'	1.79	0.64
36:AB:57:VAL:HG22	36:AB:73:VAL:HG22	1.78	0.64
38:A1:2895:G:O2'	75:Am:100:TYR:O	2.16	0.64
80:DC:744:TYR:OH	80:DC:757:GLU:OE1	2.14	0.64
17:Bb:19:HIS:HB3	17:Bb:22:LYS:HG2	1.79	0.64
27:BU:62:VAL:HG12	27:BU:85:ARG:HG3	1.79	0.64
28:BZ:90:LYS:NZ	28:BZ:103:ARG:O	2.31	0.64
38:A1:3050:U:O2'	59:AW:16:GLY:O	2.14	0.64
52:AP:30:ARG:NH1	52:AP:31:GLU:OE2	2.30	0.64
57:AU:9:GLN:N	57:AU:68:THR:O	2.29	0.64
20:BF:51:VAL:O	20:BF:131:GLN:NE2	2.30	0.64
47:AJ:52:TYR:HA	47:AJ:61:ARG:HD2	1.80	0.64
80:DC:406:LYS:HG2	80:DC:409:GLN:HB2	1.80	0.64
12:BV:22:ARG:NH2	13:BW:19:LYS:O	2.31	0.64
33:BM:42:ALA:HB2	33:BM:124:LYS:HE2	1.80	0.64
38:A1:1831:U:O2'	40:A4:114:G:OP1	2.14	0.64
15:BY:36:SER:OG	15:BY:39:GLU:OE1	2.16	0.64
24:BR:22:PRO:O	31:Bg:216:LYS:NZ	2.29	0.64
32:Bf:100:LEU:HD11	32:Bf:103:LEU:HB2	1.80	0.64
38:A1:1513:G:OP1	54:AR:5:ARG:NH1	2.31	0.64
3:BC:80:VAL:HG22	3:BC:102:VAL:HG22	1.80	0.64
13:BW:80:ASN:OD1	13:BW:124:LYS:NZ	2.29	0.64
32:Bf:132:LEU:HD22	32:Bf:141:CYS:HA	1.80	0.64
35:AA:69:TYR:OH	38:A1:2557:A:OP1	2.16	0.64
36:AB:380:MET:O	38:A1:3369:G:N1	2.29	0.64
50:AN:183:THR:HG22	50:AN:187:ARG:HB3	1.80	0.64
82:EC:6846:C:N4	82:EC:6847:G:O6	2.31	0.64
38:A1:98:G:N7	48:AL:13:HIS:NE2	2.46	0.64
49:AM:48:GLY:HA3	49:AM:53:VAL:HB	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BR:29:GLN:OE1	31:Bg:38:ARG:NH1	2.31	0.63
38:A1:524:U:OP1	49:AM:77:ARG:NH2	2.27	0.63
26:BT:50:ALA:HA	26:BT:53:TRP:HD1	1.63	0.63
34:B5:65:A:H2	34:B5:84:A:H62	1.45	0.63
34:B5:126:A:N6	34:B5:291:G:H21	1.92	0.63
34:B5:1213:G:N2	34:B5:1450:U:O2	2.27	0.63
38:A1:351:A:N6	74:Al:37:TYR:O	2.30	0.63
38:A1:1348:U:OP1	53:AQ:39:ARG:NH1	2.30	0.63
34:B5:1591:C:H2'	34:B5:1592:A:H8	1.63	0.63
38:A1:879:U:O2'	52:AP:135:ARG:NH2	2.30	0.63
38:A1:2482:U:N3	38:A1:2486:A:N6	2.42	0.63
40:A4:135:G:H5''	60:AX:49:LYS:HD2	1.79	0.63
33:BM:23:THR:HB	33:BM:26:ASP:HB2	1.80	0.63
34:B5:1477:G:H2'	34:B5:1478:G:C8	2.34	0.63
48:AL:123:ILE:HG22	70:Ah:118:ILE:HG12	1.78	0.63
15:BY:86:GLU:OE2	15:BY:90:ARG:NE	2.31	0.63
15:BY:89:TYR:OH	15:BY:90:ARG:NH1	2.32	0.63
38:A1:2469:G:N1	38:A1:2477:G:O6	2.31	0.63
47:AJ:17:LEU:HD13	47:AJ:80:LEU:HD12	1.80	0.63
60:AX:50:ALA:HB1	70:Ah:66:VAL:HG11	1.80	0.63
79:E:116:LEU:HD12	79:E:119:GLN:HB3	1.79	0.63
80:DC:718:LEU:HB3	80:DC:835:TRP:HE3	1.62	0.63
29:Bc:22:ARG:HE	34:B5:1619:C:H1'	1.63	0.63
38:A1:595:G:OP1	43:AF:33:ARG:NH2	2.31	0.63
20:BF:175:LEU:HD12	20:BF:198:LEU:HD22	1.81	0.63
24:BR:10:LYS:NZ	34:B5:1316:G:O2'	2.32	0.63
34:B5:321:C:H42	34:B5:1666:U:H5''	1.64	0.63
80:DC:676:ILE:HD11	80:DC:722:PRO:HB2	1.79	0.63
25:BS:88:ARG:NH2	25:BS:91:ASP:OD1	2.32	0.63
38:A1:1627:U:N3	38:A1:1817:G:O6	2.32	0.63
38:A1:2193:U:H5''	38:A1:2194:G:H5'	1.79	0.63
39:A3:8:G:O6	41:AD:21:ARG:NH2	2.32	0.63
14:BX:142:LYS:HD2	14:BX:143:PRO:HD2	1.81	0.63
20:BF:161:ASP:HB3	29:Bc:54:LEU:HD11	1.81	0.63
49:AM:55:ARG:NH1	49:AM:76:ALA:O	2.23	0.63
10:BN:69:ASN:HB2	10:BN:73:ARG:HD2	1.82	0.62
31:Bg:11:GLY:HA2	31:Bg:52:GLN:HA	1.81	0.62
34:B5:973:A:H2'	34:B5:974:A2M:H8	1.81	0.62
34:B5:1654:G:H21	34:B5:1746:A:H62	1.47	0.62
38:A1:2722:U:O2'	56:AT:88:ARG:O	2.17	0.62
80:DC:150:ARG:NH2	80:DC:194:ASP:OD2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:711:ARG:NH2	80:DC:837:GLU:O	2.32	0.62
15:BY:36:SER:OG	15:BY:38:ASP:OD1	2.17	0.62
36:AB:349:LYS:NZ	38:A1:3038:U:OP1	2.32	0.62
43:AF:168:ILE:O	43:AF:172:ASN:ND2	2.32	0.62
11:BO:88:GLY:O	11:BO:92:LYS:NZ	2.32	0.62
34:B5:71:A:N6	34:B5:72:A:N3	2.47	0.62
38:A1:1565:G:N2	38:A1:1575:A:N7	2.46	0.62
8:BJ:175:ARG:NH2	34:B5:538:A:OP1	2.31	0.62
31:Bg:91:LEU:HD12	31:Bg:101:GLN:HB3	1.82	0.62
34:B5:1466:G:O2'	34:B5:1602:C:OP1	2.17	0.62
35:AA:152:SER:OG	38:A1:2157:G:N7	2.30	0.62
38:A1:718:G:OP1	63:Aa:117:ARG:NH2	2.31	0.62
67:Ae:89:THR:HG22	67:Ae:117:ILE:HG13	1.81	0.62
3:BC:157:LYS:NZ	13:BW:91:ALA:O	2.30	0.62
26:BT:57:ARG:NE	34:B5:1479:A:OP1	2.32	0.62
39:A3:23:A:O2'	39:A3:121:U:O3'	2.17	0.62
55:AS:77:VAL:HG11	55:AS:106:LEU:HD22	1.81	0.62
80:DC:20:ARG:NH2	80:DC:339:VAL:O	2.31	0.62
34:B5:176:C:N4	34:B5:266:A:OP2	2.32	0.62
38:A1:1603:A:OP1	54:AR:38:ARG:NH2	2.33	0.62
60:AX:77:GLU:HG3	60:AX:133:LEU:HD12	1.80	0.62
79:E:160:LYS:HE2	79:E:162:VAL:HB	1.81	0.62
8:BJ:17:ARG:HH22	34:B5:4:C:H1'	1.64	0.62
38:A1:3042:U:OP2	38:A1:3092:C:N4	2.33	0.62
26:BT:89:ARG:HH12	34:B5:1467:C:H1'	1.65	0.62
34:B5:272:U:O2'	34:B5:284:G:N2	2.32	0.62
39:A3:45:A:OP1	41:AD:151:GLN:NE2	2.32	0.62
5:BG:137:ARG:HB3	5:BG:140:ASN:HB2	1.81	0.62
9:BL:77:SER:HB3	9:BL:85:VAL:HB	1.82	0.62
11:BO:36:LYS:HD2	34:B5:919:A:H1'	1.82	0.62
43:AF:44:ILE:HD12	43:AF:180:SER:HB3	1.82	0.62
47:AJ:131:MET:HE1	47:AJ:162:TRP:CD2	2.35	0.62
75:Am:104:PRO:HG2	75:Am:107:ALA:HB2	1.81	0.62
15:BY:15:ASN:HD22	15:BY:22:GLN:HE22	1.44	0.62
21:BK:5:LYS:O	21:BK:9:ASN:ND2	2.33	0.62
34:B5:900:A:H3'	34:B5:901:G:H21	1.65	0.62
38:A1:2842:U:OP1	38:A1:2844:C:N4	2.31	0.61
34:B5:814:A:OP1	54:AR:166:ASN:ND2	2.33	0.61
37:AC:35:VAL:HG21	37:AC:244:LEU:HD21	1.82	0.61
38:A1:170:G:OP1	48:AL:128:ARG:NH2	2.33	0.61
41:AD:257:GLU:OE2	41:AD:259:LYS:NZ	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:222:ILE:HD11	80:DC:244:LEU:HB2	1.82	0.61
1:BA:55:GLU:HB3	12:BV:79:LEU:HD12	1.82	0.61
3:BC:37:PRO:HB2	3:BC:43:ARG:HD3	1.81	0.61
35:AA:215:ASN:ND2	38:A1:2969:A:N7	2.48	0.61
20:BF:142:PRO:HB3	20:BF:217:LEU:HD22	1.83	0.61
34:B5:1237:G:N1	34:B5:1249:U:O4	2.33	0.61
38:A1:2438:A:H2'	38:A1:2439:A:H8	1.65	0.61
81:V:26:PHE:HB3	81:V:87:VAL:HB	1.82	0.61
2:BB:113:MET:SD	2:BB:209:ASN:ND2	2.74	0.61
2:BB:129:THR:OG1	2:BB:131:ASP:O	2.19	0.61
18:Be:24:THR:OG1	18:Be:26:LYS:NZ	2.34	0.61
38:A1:1646:G:O2'	38:A1:1808:G:N2	2.33	0.61
55:AS:99:ARG:NH1	55:AS:126:VAL:O	2.33	0.61
79:E:60:ARG:HB3	79:E:171:ASN:HD21	1.65	0.61
4:BE:246:LEU:HB3	4:BE:250:GLU:OE2	2.01	0.61
20:BF:121:ILE:HG13	20:BF:129:PRO:HB3	1.82	0.61
37:AC:308:LYS:NZ	38:A1:609:G:N7	2.48	0.61
45:AH:10:ILE:HB	45:AH:53:ILE:HB	1.81	0.61
27:BU:101:LYS:NZ	27:BU:105:GLN:OE1	2.31	0.61
28:BZ:61:SER:OG	28:BZ:99:ALA:O	2.17	0.61
34:B5:800:U:H2'	34:B5:801:G:H8	1.66	0.61
38:A1:2697:A:H2'	38:A1:2698:G:C8	2.36	0.61
66:Ad:70:ARG:HD2	66:Ad:102:LYS:HE3	1.83	0.61
80:DC:23:SER:HB3	80:DC:122:THR:HG21	1.82	0.61
13:BW:44:HIS:NE2	13:BW:112:ASP:OD2	2.32	0.61
33:BM:62:LEU:HD11	33:BM:75:VAL:HG21	1.81	0.61
34:B5:1183:A:N3	34:B5:1210:C:O2'	2.33	0.61
38:A1:1661:G:H2'	38:A1:1662:G:C8	2.35	0.61
38:A1:1812:G:O6	62:AZ:64:LYS:NZ	2.34	0.61
47:AJ:100:GLY:HA3	47:AJ:154:THR:HG22	1.83	0.61
81:V:74:GLU:HA	81:V:77:LEU:HD23	1.82	0.61
16:Ba:32:LYS:O	16:Ba:37:LYS:NZ	2.34	0.61
38:A1:3092:C:O2'	38:A1:3094:A:OP2	2.19	0.61
4:BE:148:ARG:NH1	5:BG:201:GLN:OE1	2.34	0.61
20:BF:92:ARG:NH2	34:B5:1613:U:OP1	2.34	0.61
38:A1:1759:C:N4	38:A1:1760:A:H62	1.99	0.61
40:A4:103:G:OP2	40:A4:105:A:O2'	2.19	0.61
2:BB:39:GLU:CD	2:BB:40:ASN:H	2.10	0.60
17:Bb:15:GLU:O	17:Bb:29:ARG:NH2	2.34	0.60
51:AO:61[A]:ALA:HA	51:AO:70[A]:PRO:HD2	1.82	0.60
36:AB:284:ARG:HB3	36:AB:323:MET:HE3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:287:LYS:O	36:AB:293:ASN:ND2	2.33	0.60
38:A1:394:G:N1	38:A1:397:A:OP2	2.33	0.60
38:A1:3354:U:H5'	38:A1:3355:U:H5'	1.82	0.60
62:AZ:33:SER:OG	62:AZ:35:SER:O	2.17	0.60
80:DC:71:LYS:NZ	80:DC:387:PRO:O	2.32	0.60
2:BB:105:PHE:CD1	2:BB:213:ARG:HA	2.36	0.60
30:Bd:22:ARG:NH2	30:Bd:36:LEU:O	2.34	0.60
53:AQ:92:ARG:HG3	63:Aa:76:ASP:HB2	1.83	0.60
27:BU:20:ILE:HG13	27:BU:97:VAL:HG13	1.82	0.60
34:B5:956:C:OP1	34:B5:1072:C:O2'	2.20	0.60
34:B5:1220:C:H2'	34:B5:1221:A:H8	1.67	0.60
38:A1:938:C:OP2	63:Aa:26:ARG:NH1	2.35	0.60
81:V:159:VAL:HG11	81:V:165:VAL:HG12	1.83	0.60
15:BY:27:VAL:HG23	15:BY:29:HIS:HD2	1.66	0.60
21:BK:44:LYS:HE2	34:B5:1217:A:H5''	1.83	0.60
34:B5:1210:C:H2'	34:B5:1211:A:H8	1.67	0.60
38:A1:576:C:OP1	43:AF:241:LYS:NZ	2.33	0.60
38:A1:1696:A:H2'	38:A1:1697:A:C8	2.37	0.60
38:A1:1873:U:OP1	54:AR:21:LYS:NZ	2.35	0.60
34:B5:445:A:H1'	34:B5:525:A:H5'	1.83	0.60
34:B5:1477:G:H2'	34:B5:1478:G:H8	1.67	0.60
50:AN:5:LYS:HG3	71:Ai:40:VAL:HG11	1.84	0.60
80:DC:92:LYS:HE2	80:DC:346:VAL:HG11	1.82	0.60
7:BI:83:TYR:HD2	7:BI:101:ILE:HD13	1.67	0.60
1:BA:148:ASP:OD2	1:BA:165:ARG:NH1	2.35	0.60
1:BA:201:LEU:HD11	24:BR:85:VAL:HB	1.82	0.60
23:BQ:21:HIS:NE2	34:B5:1350:U:O2'	2.34	0.60
36:AB:303:LYS:NZ	36:AB:359:ILE:O	2.34	0.60
34:B5:388:G:OP2	34:B5:423:G:O2'	2.19	0.60
34:B5:1175:U:H2'	34:B5:1176:G:C8	2.36	0.60
34:B5:1656:U:O2'	38:A1:2292:U:O2'	2.20	0.60
82:EC:6852:U:H2'	82:EC:6853:G:C8	2.37	0.60
10:BN:3:ARG:HB3	10:BN:6:SER:HB3	1.84	0.60
15:BY:92:VAL:HG11	15:BY:99:LYS:HG3	1.84	0.60
34:B5:947:U:H2'	34:B5:948:G:H8	1.65	0.60
36:AB:226:PHE:O	38:A1:1886:A:O2'	2.19	0.60
38:A1:655:C:H2'	38:A1:656:A:C8	2.36	0.60
38:A1:1192:C:OP1	75:Am:113:ARG:NH2	2.35	0.60
38:A1:2502:A:N1	44:AG:232:HIS:ND1	2.42	0.60
73:Ak:64:LYS:HA	73:Ak:67:GLN:HE21	1.67	0.60
82:EC:6789:G:N2	82:EC:6881:U:OP2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1348:A:H2'	34:B5:1349:G:C8	2.37	0.59
70:Ah:70:TYR:O	70:Ah:76:GLN:NE2	2.35	0.59
78:Ap:46:THR:OG1	78:Ap:57:CYS:SG	2.60	0.59
80:DC:169:VAL:HG11	80:DC:174:LEU:HD13	1.83	0.59
1:BA:53:THR:HG22	1:BA:161:PRO:HG2	1.84	0.59
16:Ba:2:PRO:HB3	34:B5:1142:A:H5''	1.84	0.59
34:B5:1171:A:H2'	34:B5:1172:G:C8	2.37	0.59
35:AA:9:ARG:NH2	38:A1:912:G:OP2	2.35	0.59
80:DC:697:ALA:HA	80:DC:700:ARG:HG2	1.83	0.59
14:BX:22:ASN:HD22	34:B5:1108:G:H1	1.49	0.59
31:Bg:200:ASN:ND2	31:Bg:240:VAL:O	2.33	0.59
36:AB:269:GLN:NE2	38:A1:3306:U:OP1	2.27	0.59
38:A1:1447:G:N7	52:AP:25:SER:OG	2.36	0.59
38:A1:3113:A:OP1	45:AH:69:ARG:NH1	2.35	0.59
19:BD:135:GLU:HB3	19:BD:187:LYS:HB3	1.84	0.59
35:AA:14:SER:OG	38:A1:911:C:OP1	2.18	0.59
38:A1:1388:U:O2'	67:Ae:99:ASN:O	2.19	0.59
80:DC:80:GLU:OE1	80:DC:96:ASN:ND2	2.36	0.59
10:BN:103:GLU:O	10:BN:106:ARG:NH2	2.35	0.59
16:Ba:18:VAL:HG23	16:Ba:19:LYS:H	1.67	0.59
34:B5:1483:A:OP2	34:B5:1521:G:N2	2.34	0.59
34:B5:1600:A:O2'	34:B5:1602:C:N4	2.35	0.59
38:A1:1603:A:H61	60:AX:71:THR:HG21	1.67	0.59
38:A1:1717:U:H2'	38:A1:1718:G:C8	2.37	0.59
38:A1:2880:U:OP1	58:AV:47:ASN:ND2	2.34	0.59
39:A3:109:G:H5''	41:AD:279:LYS:HE3	1.84	0.59
43:AF:163:LEU:HD13	43:AF:169:ILE:HD11	1.85	0.59
80:DC:2:VAL:N	80:DC:44:GLY:O	2.35	0.59
2:BB:34:ALA:O	2:BB:41:ARG:NH1	2.36	0.59
20:BF:162:VAL:HG13	20:BF:166:ARG:HG2	1.83	0.59
35:AA:234:LYS:NZ	38:A1:2162:U:OP1	2.35	0.59
38:A1:417:A:H2'	38:A1:418:A:C8	2.38	0.59
11:BO:20:TYR:HB3	11:BO:27:PHE:HB2	1.85	0.59
38:A1:173:G:N2	38:A1:245:U:O2	2.35	0.59
38:A1:421:G:O6	38:A1:2383:C:O2'	2.19	0.59
38:A1:2468:A:O2'	38:A1:2477:G:N2	2.35	0.59
47:AJ:10:ARG:NH2	47:AJ:151:SER:O	2.36	0.59
33:BM:116:VAL:HG21	34:B5:1227:A:H8	1.68	0.59
44:AG:144:GLU:OE1	71:Ai:36:ARG:NH1	2.35	0.59
80:DC:388:THR:OG1	80:DC:393:ARG:O	2.19	0.59
11:BO:87:GLY:HA3	11:BO:120:PRO:HG2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:BQ:25:GLY:HA3	23:BQ:64:ASP:HB2	1.84	0.59
34:B5:1488:G:O2'	34:B5:1494:C:O2	2.15	0.59
38:A1:68:C:OP2	38:A1:301:G:N2	2.34	0.59
75:Am:98:LYS:HD2	75:Am:118:THR:HG21	1.83	0.59
7:BI:2:GLY:N	34:B5:393:C:OP2	2.36	0.59
30:Bd:18:SER:OG	30:Bd:19:ARG:NH1	2.36	0.59
32:Bf:141:CYS:SG	32:Bf:144:CYS:N	2.70	0.59
34:B5:591:A:H2'	34:B5:592:A:C8	2.38	0.59
38:A1:799:G:O2'	48:AL:18:TRP:NE1	2.35	0.59
38:A1:831:G:O2'	38:A1:1864:A:N3	2.32	0.59
38:A1:1203:A:H2'	38:A1:1204:A:C8	2.38	0.59
1:BA:89:PHE:O	1:BA:93:THR:OG1	2.21	0.58
6:BH:114:ARG:NH1	34:B5:637:C:O2	2.35	0.58
36:AB:30:LYS:NZ	38:A1:3139:A:OP2	2.33	0.58
38:A1:175:C:H2'	38:A1:176:G:C8	2.38	0.58
38:A1:1225:A:H3'	38:A1:1226:G:H8	1.67	0.58
38:A1:1497:C:H2'	38:A1:1498:A:H8	1.67	0.58
38:A1:2254:U:O4	38:A1:2261:G:O2'	2.18	0.58
38:A1:2588:U:OP1	44:AG:241:LYS:NZ	2.31	0.58
38:A1:3234:A:N1	38:A1:3253:G:N2	2.42	0.58
5:BG:157:VAL:HG23	5:BG:175:ILE:HD11	1.84	0.58
34:B5:1644:C:O2'	38:A1:2262:A:H1'	2.03	0.58
36:AB:128:LYS:HG3	38:A1:3294:A:H5'	1.85	0.58
47:AJ:93:ASP:HB2	47:AJ:172:LEU:HB2	1.85	0.58
55:AS:6:GLU:OE2	55:AS:28:ARG:NH1	2.36	0.58
80:DC:677:PHE:HB3	80:DC:819:VAL:HG13	1.85	0.58
1:BA:56:LYS:HD3	12:BV:82:VAL:HG11	1.84	0.58
20:BF:99:MET:HG2	20:BF:100:ASN:H	1.67	0.58
38:A1:584:G:OP1	42:AE:82:ARG:NH2	2.36	0.58
38:A1:2533:G:H2'	38:A1:2534:G:H8	1.69	0.58
1:BA:15:GLN:HE22	24:BR:100:LEU:HD11	1.68	0.58
34:B5:488:G:H5''	34:B5:492:A:H62	1.68	0.58
34:B5:647:G:H21	34:B5:687:G:H1	1.52	0.58
38:A1:412:G:OP1	52:AP:62:ARG:NH1	2.36	0.58
22:BP:100:LYS:HD3	34:B5:1211:A:H4'	1.84	0.58
31:Bg:250:TYR:HB3	31:Bg:265:LEU:HD12	1.86	0.58
38:A1:1392:G:H1'	38:A1:1418:A:H61	1.69	0.58
82:EC:6853:G:O6	82:EC:6876:A:N1	2.36	0.58
11:BO:18:ARG:HD3	34:B5:918:U:H4'	1.84	0.58
38:A1:2960:C:H2'	38:A1:2961:G:C8	2.39	0.58
2:BB:72:ASP:OD1	16:Ba:59:TYR:OH	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:56:ARG:NH2	34:B5:332:U:OP1	2.36	0.58
13:BW:101:TYR:HE1	13:BW:114:GLU:HG3	1.69	0.58
15:BY:54:ALA:HB1	15:BY:76:TYR:HB2	1.84	0.58
34:B5:1458:G:O2'	34:B5:1459:C:OP1	2.20	0.58
38:A1:1114:U:OP1	63:Aa:23:GLY:N	2.33	0.58
38:A1:1236:G:N2	38:A1:1244:A:OP1	2.36	0.58
38:A1:1257:C:H42	38:A1:1261:G:N2	2.01	0.58
38:A1:1793:C:OP2	78:Ap:49:ARG:NH2	2.34	0.58
45:AH:186:PHE:HB2	45:AH:189:GLU:HB2	1.84	0.58
69:Ag:16:ARG:HA	69:Ag:19:LYS:HD3	1.85	0.58
6:BH:153:LEU:HD23	6:BH:186:PRO:HG3	1.86	0.58
18:Be:23:LYS:NZ	34:B5:586:G:OP1	2.30	0.58
34:B5:884:A:H2'	34:B5:885:G:C8	2.39	0.58
35:AA:80:GLU:HG3	78:Ap:66:GLY:HA2	1.86	0.58
38:A1:1390:A:N6	38:A1:1418:A:O2'	2.37	0.58
4:BE:49:ARG:NH2	34:B5:448:C:OP1	2.34	0.58
22:BP:47:ARG:HH22	34:B5:1553:G:H3'	1.68	0.58
38:A1:1135:A:OP2	64:Ab:5:LYS:NZ	2.33	0.58
80:DC:636:PHE:O	80:DC:642:GLY:N	2.35	0.58
31:Bg:13:LEU:HB2	31:Bg:310:ILE:HB	1.85	0.58
32:Bf:99:LYS:NZ	34:B5:1228:G:O2'	2.29	0.58
34:B5:58:U:O2'	34:B5:451:A:N3	2.36	0.58
38:A1:176:G:N2	38:A1:242:C:O2	2.37	0.58
38:A1:1829:G:H5''	38:A1:1830:G:H5'	1.86	0.58
68:Af:14:LEU:HD11	68:Af:31:LYS:HB2	1.86	0.58
1:BA:123:VAL:HG21	1:BA:133:ILE:HD11	1.86	0.57
20:BF:70:VAL:HB	23:BQ:46:PHE:HB2	1.86	0.57
22:BP:68:PRO:HG2	22:BP:71:GLU:HB2	1.86	0.57
38:A1:1799:A:H2'	38:A1:1800:A:C8	2.38	0.57
38:A1:2901:G:O2'	38:A1:3024:A:N1	2.37	0.57
45:AH:34:LEU:HD21	45:AH:149:ASN:HB3	1.84	0.57
80:DC:221:THR:HG23	80:DC:224:GLN:H	1.69	0.57
82:EC:6856:C:HO2'	82:EC:6872:A:HO2'	1.51	0.57
28:BZ:58:ARG:H	28:BZ:58:ARG:HD3	1.69	0.57
31:Bg:82:SER:HB3	31:Bg:92:TRP:HE1	1.69	0.57
33:BM:60:VAL:HG23	33:BM:122:VAL:HG22	1.85	0.57
34:B5:190:C:O4'	34:B5:196:G:N2	2.36	0.57
38:A1:175:C:H2'	38:A1:176:G:H8	1.69	0.57
38:A1:967:A:OP1	63:Aa:47:LYS:NZ	2.37	0.57
38:A1:2465:G:N1	38:A1:2491:A:C6	2.72	0.57
38:A1:2768:U:H2'	38:A1:2769:A:H8	1.67	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:AE:4:GLN:HG3	67:Ae:75:LEU:HB3	1.86	0.57
79:E:14:LYS:HA	79:E:17:LEU:HG	1.85	0.57
80:DC:10:ARG:HH12	80:DC:449:PRO:HD3	1.70	0.57
4:BE:192:ILE:HD13	4:BE:238:LEU:HD22	1.86	0.57
34:B5:1001:A:N6	34:B5:1761:U:OP1	2.33	0.57
34:B5:1658:G:O6	34:B5:1743:U:O2	2.22	0.57
38:A1:627:U:H2'	38:A1:628:A:C8	2.40	0.57
42:AE:62:THR:HG21	42:AE:78:ARG:HD2	1.87	0.57
80:DC:629:ASP:HB3	80:DC:647:ILE:HG21	1.86	0.57
1:BA:41:ARG:HH22	24:BR:106:THR:H	1.52	0.57
7:BI:62:THR:HG22	7:BI:77:ARG:HG2	1.85	0.57
38:A1:219:A:O2'	38:A1:220:G:N2	2.35	0.57
38:A1:2492:C:H5'	79:E:205:VAL:HG21	1.86	0.57
38:A1:2854:U:OP2	46:AI:3:ARG:NH2	2.38	0.57
56:AT:49:GLN:HA	56:AT:52:MET:HE3	1.87	0.57
58:AV:10:LYS:HE2	58:AV:13:ILE:HD12	1.86	0.57
14:BX:112:LYS:NZ	34:B5:1136:U:O4	2.34	0.57
18:Be:13:LYS:O	18:Be:17:GLN:NE2	2.38	0.57
38:A1:649:A2M:OP2	38:A1:2868:U:O2'	2.22	0.57
38:A1:2260:U:H3'	38:A1:2261:G:H8	1.69	0.57
38:A1:3016:A:H2'	38:A1:3017:A:H8	1.68	0.57
79:E:38:LEU:HB2	79:E:163:LEU:HB2	1.85	0.57
80:DC:260:LYS:NZ	80:DC:262:THR:OG1	2.37	0.57
80:DC:409:GLN:NE2	80:DC:410:LYS:O	2.37	0.57
4:BE:127:LYS:N	4:BE:140:VAL:O	2.29	0.57
4:BE:185:GLY:HA2	4:BE:189:LEU:HD12	1.86	0.57
31:Bg:240:VAL:HG12	31:Bg:256:THR:HG22	1.85	0.57
34:B5:580:A:O2'	34:B5:582:U:OP1	2.19	0.57
34:B5:1644:C:H2'	34:B5:1645:G:C8	2.39	0.57
38:A1:845:G:H21	38:A1:848:A:H2	1.50	0.57
82:EC:6774:U:OP1	82:EC:6818:G:O2'	2.22	0.57
4:BE:37:LYS:HB2	4:BE:40:GLU:HG2	1.86	0.57
11:BO:102:LEU:HG	16:Ba:53:LEU:HD11	1.86	0.57
24:BR:24:LEU:O	31:Bg:216:LYS:NZ	2.31	0.57
34:B5:250:C:H2'	34:B5:251:A:H8	1.70	0.57
35:AA:117:GLU:HG2	35:AA:124:GLY:H	1.68	0.57
37:AC:328:ASN:OD1	43:AF:48:ASN:ND2	2.37	0.57
38:A1:1553:U:H4'	38:A1:1554:U:H5'	1.85	0.57
46:AI:30:LYS:HE2	46:AI:63:GLU:HA	1.86	0.57
62:AZ:27:LYS:NZ	62:AZ:96:VAL:O	2.36	0.57
2:BB:149:GLN:HE21	2:BB:151:LYS:HB3	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:180:THR:HG23	5:BG:183:ARG:H	1.69	0.57
5:BG:201:GLN:NE2	34:B5:125:U:OP1	2.37	0.57
7:BI:4:SER:OG	7:BI:6:ASP:OD1	2.23	0.57
10:BN:19:SER:OG	10:BN:21:ASN:O	2.22	0.57
21:BK:46:LEU:HD21	21:BK:55:VAL:HG11	1.87	0.57
27:BU:85:ARG:NH2	34:B5:1334:U:O2'	2.37	0.57
34:B5:1660:A:H4'	58:AV:67:PRO:HG3	1.86	0.57
65:Ac:66:LYS:NZ	65:Ac:101:LEU:O	2.37	0.57
79:E:34:LEU:HD22	79:E:204:LEU:HD11	1.87	0.57
1:BA:70:PRO:HB2	1:BA:94:GLY:HA3	1.87	0.57
4:BE:64:ILE:HD11	15:BY:18:LEU:HG	1.86	0.57
15:BY:35:VAL:HG23	15:BY:36:SER:H	1.68	0.57
34:B5:509:G:H2'	34:B5:510:G:C8	2.40	0.57
38:A1:664:U:H2'	38:A1:665:A:C8	2.40	0.57
1:BA:84:ARG:NH2	24:BR:82:ASP:O	2.36	0.57
7:BI:35:ASN:O	7:BI:37:LYS:NZ	2.35	0.57
22:BP:96:ILE:HG12	22:BP:116:LEU:HB3	1.86	0.57
26:BT:42:GLY:HA2	26:BT:84:LYS:HG3	1.87	0.57
34:B5:590:C:H2'	34:B5:591:A:C8	2.40	0.57
34:B5:1490:C:H4'	34:B5:1492:A:H5''	1.86	0.57
34:B5:1524:A:H2'	34:B5:1525:A:C8	2.39	0.57
38:A1:2213:A:H2'	38:A1:2214:A:C8	2.40	0.57
43:AF:102:VAL:HG21	43:AF:129:LEU:HD23	1.87	0.57
47:AJ:37:LEU:HD23	47:AJ:69:VAL:HG12	1.86	0.57
65:Ac:39:SER:HG	65:Ac:91:SER:HG	1.51	0.57
80:DC:147:LEU:HD11	80:DC:189:VAL:HA	1.87	0.57
33:BM:36:LEU:HD12	33:BM:41:LEU:HD22	1.86	0.56
34:B5:34:G:O2'	34:B5:515:A:O2'	2.23	0.56
34:B5:406:U:H2'	34:B5:407:A:H8	1.71	0.56
34:B5:923:A:H2'	34:B5:924:A:C8	2.40	0.56
38:A1:339:C:OP1	38:A1:1380:G:O2'	2.21	0.56
38:A1:2213:A:H2'	38:A1:2214:A:H8	1.70	0.56
38:A1:2497:U:O2'	38:A1:2498:U:O4'	2.22	0.56
38:A1:3227:A:O2'	49:AM:133:LYS:NZ	2.32	0.56
45:AH:90:MET:HE2	45:AH:179:ILE:HG22	1.87	0.56
51:AO:27[A]:LEU:HD11	51:AO:102[A]:LEU:HD13	1.86	0.56
51:AO:54[A]:TYR:OH	51:AO:73[A]:PHE:O	2.22	0.56
80:DC:79:SER:HB2	80:DC:335:LEU:HD22	1.85	0.56
82:EC:6789:G:N2	82:EC:6790:A:O2'	2.36	0.56
34:B5:1171:A:H2'	34:B5:1172:G:H8	1.70	0.56
50:AN:84:PRO:HA	50:AN:87:GLN:HG3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:AP:40:GLU:HA	52:AP:113:TYR:HA	1.86	0.56
82:EC:6853:G:C6	82:EC:6876:A:N1	2.72	0.56
2:BB:129:THR:OG1	2:BB:131:ASP:OD1	2.22	0.56
5:BG:10:ASN:HB2	5:BG:128:THR:HA	1.87	0.56
16:Ba:38:ARG:HH21	34:B5:1798:U:H2'	1.71	0.56
34:B5:1474:G:H2'	34:B5:1475:A:H8	1.70	0.56
38:A1:1119:C:H2'	38:A1:1120:A:H8	1.70	0.56
38:A1:1227:C:O2'	38:A1:1228:C:O4'	2.22	0.56
38:A1:1613:A:OP1	73:Ak:2:ALA:N	2.38	0.56
38:A1:2478:C:OP2	38:A1:2480:A:N6	2.38	0.56
38:A1:3322:A:H2'	38:A1:3323:A:C8	2.40	0.56
39:A3:23:A:HO2'	39:A3:121:U:HO3'	1.48	0.56
39:A3:114:U:H2'	39:A3:115:G:H8	1.70	0.56
62:AZ:70:PRO:HG3	62:AZ:115:LYS:HB2	1.85	0.56
65:Ac:17:VAL:HG11	65:Ac:92:ILE:HD12	1.87	0.56
72:Aj:27:PHE:HA	72:Aj:34:CYS:HA	1.87	0.56
73:Ak:10:GLN:NE2	73:Ak:13:GLU:OE1	2.39	0.56
10:BN:55:ARG:HD3	34:B5:960:U:H5'	1.88	0.56
11:BO:131:GLY:O	16:Ba:22:ARG:NH2	2.39	0.56
25:BS:41:ARG:HG2	25:BS:85:PHE:CZ	2.40	0.56
38:A1:3119:U:H4'	75:Am:104:PRO:HG3	1.85	0.56
34:B5:1291:G:H1	34:B5:1324:G:H22	1.54	0.56
38:A1:792:G:H5''	63:Aa:2:PRO:HD3	1.87	0.56
38:A1:2793:OMG:H4'	77:Ao:66:LYS:HE3	1.87	0.56
42:AE:175:LYS:O	49:AM:117:ARG:NH2	2.38	0.56
65:Ac:50:VAL:HA	65:Ac:53:LYS:HG2	1.87	0.56
80:DC:45:ILE:HD11	80:DC:78:TYR:H	1.70	0.56
80:DC:45:ILE:HD13	80:DC:77:LEU:HA	1.87	0.56
80:DC:743:ILE:HG22	80:DC:784:LEU:HD22	1.87	0.56
82:EC:6877:C:O2	82:EC:6878:G:N2	2.38	0.56
7:BI:104:ILE:HG13	7:BI:105:ASP:H	1.71	0.56
19:BD:143:ARG:HE	34:B5:558:U:H3	1.53	0.56
24:BR:7:LYS:HA	24:BR:10:LYS:HB2	1.88	0.56
38:A1:1805:C:H2'	38:A1:1806:A:H8	1.70	0.56
80:DC:324:MET:HA	80:DC:327:PHE:HB2	1.87	0.56
5:BG:13:GLN:NE2	34:B5:151:G:N3	2.54	0.56
20:BF:28:PRO:O	23:BQ:37:THR:OG1	2.24	0.56
25:BS:58:ALA:HA	25:BS:61:LEU:HD23	1.88	0.56
26:BT:72:GLY:HA3	34:B5:1498:G:H5''	1.86	0.56
34:B5:1175:U:H2'	34:B5:1176:G:H8	1.71	0.56
38:A1:2356:A:H5'	52:AP:138:LYS:HZ2	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2568:C:O2'	38:A1:2569:A:O4'	2.23	0.56
38:A1:3310:A:OP1	52:AP:74:LYS:NZ	2.31	0.56
82:EC:6856:C:O2'	82:EC:6872:A:O2'	2.23	0.56
14:BX:37:ALA:O	14:BX:41:SER:OG	2.23	0.56
34:B5:343:C:H2'	34:B5:344:A:H8	1.71	0.56
34:B5:894:U:H2'	34:B5:895:G:C8	2.41	0.56
34:B5:1196:A:N6	34:B5:1601:G:O2'	2.38	0.56
36:AB:94:GLU:OE1	36:AB:156:SER:OG	2.23	0.56
38:A1:674:G:O6	53:AQ:56:LYS:NZ	2.38	0.56
38:A1:1846:C:OP1	38:A1:1849:C:N4	2.34	0.56
2:BB:130:SER:HB2	2:BB:180:THR:HG22	1.88	0.56
28:BZ:58:ARG:HG3	82:EC:6863:C:H1'	1.87	0.56
31:Bg:180:ALA:HB3	31:Bg:190:ALA:HB3	1.88	0.56
34:B5:480:G:O6	34:B5:508:U:O2	2.24	0.56
34:B5:609:U:H4'	34:B5:610:G:H5'	1.87	0.56
38:A1:1747:G:H21	73:Ak:2:ALA:HB3	1.70	0.56
10:BN:11:ILE:HG13	10:BN:12:SER:H	1.71	0.56
20:BF:84:LYS:NZ	34:B5:1614:A:OP2	2.38	0.56
26:BT:83:ALA:HB1	26:BT:91:TYR:HB3	1.87	0.56
27:BU:19:ILE:HB	27:BU:94:GLU:HG3	1.87	0.56
30:Bd:56:ARG:O	34:B5:1418:G:O2'	2.22	0.56
37:AC:99:MET:HE3	37:AC:102:PRO:HA	1.88	0.56
38:A1:1277:C:H2'	38:A1:1278:A:H8	1.71	0.56
38:A1:1799:A:H2'	38:A1:1800:A:H8	1.71	0.56
38:A1:3276:G:O6	52:AP:171:ARG:NH2	2.39	0.56
63:Aa:104:THR:HG21	63:Aa:112:ILE:HD11	1.88	0.56
68:Af:18:ARG:NH2	68:Af:20:LYS:O	2.39	0.56
4:BE:79:ASP:HB3	4:BE:82:TYR:HB2	1.87	0.55
6:BH:14:THR:HG22	6:BH:15:GLU:H	1.71	0.55
14:BX:74:VAL:HG21	14:BX:104:LEU:HD11	1.86	0.55
26:BT:21:PHE:HA	26:BT:24:ARG:HE	1.71	0.55
27:BU:80:GLU:OE1	30:Bd:44:ARG:NH1	2.38	0.55
34:B5:1027:A:OP1	34:B5:1789:G:O2'	2.22	0.55
34:B5:1752:U:H2'	34:B5:1753:A:H8	1.71	0.55
35:AA:37:ARG:NH2	38:A1:2526:C:OP1	2.35	0.55
35:AA:241:ARG:NH1	38:A1:2155:G:OP1	2.38	0.55
41:AD:177:GLU:HB2	41:AD:190:ILE:HD12	1.88	0.55
80:DC:385:MET:HE1	80:DC:514:SER:HA	1.88	0.55
80:DC:666:ALA:HB2	80:DC:706:ILE:HA	1.88	0.55
2:BB:89:ASP:HB3	2:BB:223:PHE:HE1	1.71	0.55
4:BE:230:GLU:OE1	4:BE:230:GLU:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:161:GLY:HA3	34:B5:1331:A:H61	1.72	0.55
27:BU:63:LEU:HB3	27:BU:84:MET:HB3	1.88	0.55
34:B5:1202:A:N6	34:B5:1457:C:OP1	2.39	0.55
38:A1:1311:G:N2	51:AO:86[A]:GLY:O	2.29	0.55
12:BV:86:SER:HA	17:Bb:6:ASP:HB2	1.87	0.55
38:A1:2439:A:H3'	38:A1:2440:G:H5''	1.87	0.55
38:A1:2836:C:H5	38:A1:2852:C:H42	1.53	0.55
41:AD:128:GLU:O	41:AD:164:LYS:NZ	2.38	0.55
45:AH:57:VAL:HG23	45:AH:68:LEU:HD13	1.89	0.55
48:AL:4:SER:O	63:Aa:44:ASN:ND2	2.39	0.55
27:BU:69:LYS:NZ	27:BU:80:GLU:OE2	2.40	0.55
34:B5:868:G:H1	34:B5:960:U:H3	1.54	0.55
34:B5:996:U:H2'	34:B5:997:G:H8	1.71	0.55
35:AA:65:ASP:OD2	35:AA:70:ARG:NH1	2.40	0.55
40:A4:60:U:OP1	60:AX:54:TYR:OH	2.23	0.55
46:AI:44:ASP:OD2	46:AI:185:ARG:NH1	2.28	0.55
47:AJ:38:GLU:HB3	47:AJ:45:PRO:HD3	1.88	0.55
61:AY:71:SER:N	61:AY:81:GLN:O	2.38	0.55
62:AZ:117:ALA:O	62:AZ:121:ARG:HG3	2.07	0.55
71:AI:70:ARG:HG2	71:AI:87:VAL:HG21	1.88	0.55
80:DC:190:SER:HB3	81:V:145:ILE:HD12	1.89	0.55
80:DC:578:LYS:HD2	80:DC:585:ARG:HD3	1.88	0.55
8:BJ:113:VAL:HG21	8:BJ:129:ILE:HD11	1.88	0.55
9:BL:105:LYS:NZ	34:B5:307:G:OP2	2.35	0.55
34:B5:1012:U:H4'	35:AA:247:ARG:HB3	1.87	0.55
34:B5:1288:G:N7	34:B5:1314:U:O2'	2.31	0.55
35:AA:60:LYS:HE2	35:AA:73:GLU:OE2	2.06	0.55
38:A1:1750:A:OP1	73:Ak:44:LYS:NZ	2.38	0.55
38:A1:1786:G:H2'	38:A1:1787:A:C8	2.41	0.55
58:AV:104:ASN:OD1	58:AV:108:GLU:N	2.38	0.55
5:BG:53:SER:HB2	34:B5:163:G:H4'	1.87	0.55
31:Bg:10:ARG:HE	31:Bg:314:GLN:HB2	1.71	0.55
32:Bf:95:HIS:NE2	34:B5:1253:U:O4	2.27	0.55
34:B5:565:C:O2'	34:B5:577:G:N2	2.40	0.55
34:B5:1650:U:H2'	34:B5:1651:A:C8	2.42	0.55
34:B5:1672:G:H2'	34:B5:1673:G:C8	2.40	0.55
34:B5:1695:G:H2'	34:B5:1696:G:C8	2.41	0.55
36:AB:220:VAL:O	36:AB:334:ARG:NH1	2.38	0.55
38:A1:1699:A:O2'	73:Ak:3:ARG:NH1	2.39	0.55
45:AH:128:VAL:HA	45:AH:157:ASN:HD21	1.71	0.55
80:DC:10:ARG:HB2	80:DC:445:ILE:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:25:ARG:NH1	34:B5:400:A:OP1	2.39	0.55
11:BO:81:VAL:HG11	11:BO:102:LEU:HD13	1.89	0.55
28:BZ:55:PRO:HG3	28:BZ:88:ILE:HD11	1.89	0.55
30:Bd:40:ARG:HD3	34:B5:1199:G:C5	2.42	0.55
34:B5:1689:A:H2'	34:B5:1690:G:C8	2.42	0.55
38:A1:178:U:H2'	38:A1:179:C:C6	2.42	0.55
38:A1:242:C:OP1	70:Ah:115:LYS:NZ	2.37	0.55
38:A1:1760:A:N6	38:A1:1766:G:C6	2.75	0.55
5:BG:15:THR:OG1	34:B5:152:U:O2'	2.25	0.55
24:BR:21:TYR:HD2	24:BR:73:LEU:HD12	1.72	0.55
33:BM:46:ARG:NH1	34:B5:1255:G:O6	2.40	0.55
38:A1:900:G:H1'	38:A1:1589:A:N6	2.22	0.55
81:V:30:VAL:HG21	81:V:185:LEU:HD13	1.89	0.55
2:BB:111:ARG:NH2	34:B5:930:A:N3	2.54	0.55
4:BE:72:VAL:HG12	4:BE:90:ILE:HG12	1.88	0.55
5:BG:139:ASN:ND2	34:B5:143:G:OP2	2.40	0.55
34:B5:329:G:H2'	34:B5:330:G:H8	1.72	0.55
34:B5:497:G:OP1	34:B5:498:G:N2	2.35	0.55
34:B5:1174:C:O2'	34:B5:1196:A:N6	2.40	0.55
34:B5:1213:G:O6	34:B5:1450:U:O4	2.25	0.55
34:B5:1369:U:H1'	34:B5:1372:U:H2'	1.88	0.55
34:B5:1591:C:H2'	34:B5:1592:A:C8	2.42	0.55
35:AA:150:LEU:HD11	35:AA:156:LYS:HB2	1.88	0.55
37:AC:317:PRO:C	37:AC:319:LYS:H	2.13	0.55
63:Aa:24:LYS:O	63:Aa:26:ARG:HG2	2.06	0.55
23:BQ:74:HIS:NE2	34:B5:1481:C:O2'	2.38	0.55
31:Bg:102:ARG:NH2	34:B5:1341:A:O3'	2.40	0.55
38:A1:117:U:O2'	38:A1:119:U:OP2	2.19	0.55
38:A1:2383:C:OP2	51:AO:85[A]:ARG:NH2	2.36	0.55
38:A1:2550:U:OP1	69:Ag:106:LYS:NZ	2.40	0.55
38:A1:3052:G:H2'	38:A1:3053:G:H8	1.72	0.55
45:AH:163:GLN:O	45:AH:166:ARG:NE	2.39	0.55
51:AO:65[A]:ASN:HB3	51:AO:68[A]:ARG:HG2	1.87	0.55
80:DC:671:THR:HA	80:DC:681:MET:SD	2.47	0.55
2:BB:134:VAL:HG12	2:BB:219:LYS:HG2	1.88	0.54
3:BC:143:TYR:HB3	3:BC:145:GLY:HA3	1.89	0.54
8:BJ:171:ARG:NH2	34:B5:513:U:O4	2.39	0.54
33:BM:36:LEU:HB2	33:BM:41:LEU:HD13	1.89	0.54
34:B5:590:C:H2'	34:B5:591:A:H8	1.72	0.54
34:B5:1209:C:N3	34:B5:1455:G:N2	2.54	0.54
34:B5:1220:C:H2'	34:B5:1221:A:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1260:U:H2'	34:B5:1261:G:H8	1.71	0.54
34:B5:1294:G:O2'	34:B5:1321:A:N1	2.40	0.54
38:A1:1596:C:H2'	38:A1:1597:C:C6	2.41	0.54
38:A1:3308:C:N3	52:AP:69:ARG:NH2	2.46	0.54
51:AO:125[A]:ARG:HG3	51:AO:129[A]:LEU:HD12	1.89	0.54
69:Ag:41:ARG:HG2	69:Ag:56:THR:HG21	1.89	0.54
34:B5:261:U:H1'	34:B5:262:U:H5	1.70	0.54
36:AB:244:ARG:O	36:AB:248:LYS:NZ	2.36	0.54
36:AB:303:LYS:HD2	36:AB:361:THR:HG21	1.89	0.54
38:A1:1208:U:O2'	38:A1:3115:C:N4	2.41	0.54
38:A1:1336:U:H2'	38:A1:1337:A:H8	1.72	0.54
38:A1:2255:A:H62	38:A1:2260:U:H3	1.55	0.54
54:AR:178:ALA:HA	54:AR:181:ARG:HG2	1.88	0.54
80:DC:154:VAL:HG12	80:DC:337:MET:HE2	1.89	0.54
2:BB:30:PHE:HE1	2:BB:48:VAL:HG12	1.73	0.54
4:BE:64:ILE:HD12	15:BY:17:LEU:HB3	1.89	0.54
8:BJ:119:ALA:O	8:BJ:124:HIS:ND1	2.26	0.54
20:BF:62:VAL:O	20:BF:65:ARG:NH1	2.37	0.54
21:BK:16:PHE:HB2	21:BK:76:LEU:HG	1.88	0.54
34:B5:16:G:H2'	34:B5:17:C:C6	2.41	0.54
34:B5:647:G:N2	34:B5:648:G:O6	2.40	0.54
34:B5:1474:G:H2'	34:B5:1475:A:C8	2.42	0.54
38:A1:1762:C:H3'	38:A1:1763:U:H4'	1.89	0.54
38:A1:2666:C:OP2	38:A1:2687:G:N1	2.33	0.54
47:AJ:36:VAL:HG21	47:AJ:110:ILE:HD12	1.87	0.54
51:AO:77[A]:SER:OG	51:AO:106[A]:GLU:OE2	2.24	0.54
74:Al:10:LYS:O	74:Al:13:MET:HB2	2.06	0.54
80:DC:320:LEU:HG	80:DC:324:MET:HE2	1.87	0.54
28:BZ:83:LEU:HB3	28:BZ:89:ILE:HG12	1.89	0.54
34:B5:653:C:OP1	34:B5:680:U:N3	2.30	0.54
38:A1:1378:U:H2'	38:A1:1379:G:H8	1.72	0.54
38:A1:1863:G:N1	38:A1:1866:C:OP2	2.29	0.54
39:A3:121:U:OP2	41:AD:265:TYR:OH	2.24	0.54
20:BF:63:GLN:HB3	20:BF:88:PRO:HA	1.90	0.54
21:BK:51:SER:OG	34:B5:1219:A:N3	2.39	0.54
21:BK:54:TYR:HB3	21:BK:72:GLY:HA2	1.88	0.54
34:B5:1253:U:H2'	34:B5:1254:U:H6	1.72	0.54
34:B5:1537:C:O4'	34:B5:1572:OMG:N2	2.38	0.54
38:A1:1497:C:H2'	38:A1:1498:A:C8	2.43	0.54
82:EC:6788:C:H3'	82:EC:6805:C:H41	1.72	0.54
10:BN:73:ARG:NH1	34:B5:859:A:O2'	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:67:THR:HG22	17:Bb:68:GLY:H	1.73	0.54
38:A1:1282:G:HO2'	38:A1:1283:C:H6	1.54	0.54
38:A1:3366:G:OP1	59:AW:61:LYS:NZ	2.39	0.54
62:AZ:23:VAL:HG12	62:AZ:45:GLY:HA3	1.90	0.54
64:Ab:32:LEU:HB3	64:Ab:40:ARG:NH1	2.21	0.54
80:DC:733:ILE:HD11	80:DC:780:PHE:HZ	1.73	0.54
20:BF:124:LEU:HG	20:BF:125:THR:HG23	1.88	0.54
25:BS:123:ARG:NH2	34:B5:1546:G:OP1	2.37	0.54
34:B5:31:C:O2'	34:B5:547:U:OP1	2.26	0.54
38:A1:3231:U:H2'	38:A1:3232:G:H8	1.73	0.54
39:A3:38:U:N3	39:A3:41:G:OP2	2.33	0.54
38:A1:2444:C:H2'	38:A1:2445:A:H8	1.71	0.54
38:A1:3091:A:N3	38:A1:3093:C:O2'	2.40	0.54
38:A1:3258:U:O2'	38:A1:3260:G:OP1	2.24	0.54
79:E:9:VAL:HA	79:E:12:HIS:CE1	2.43	0.54
80:DC:136:CYS:SG	80:DC:137:VAL:N	2.73	0.54
11:BO:17:ALA:HB3	11:BO:81:VAL:HA	1.90	0.54
19:BD:143:ARG:NE	34:B5:558:U:H3	2.05	0.54
21:BK:83:PRO:HB2	21:BK:86:ILE:HD12	1.88	0.54
28:BZ:68:ARG:HB3	82:EC:6866:C:H41	1.72	0.54
34:B5:925:G:H2'	34:B5:926:A:C8	2.43	0.54
38:A1:184:U:H3	38:A1:232:G:H1	1.56	0.54
38:A1:411:U:H2'	38:A1:412:G:C8	2.41	0.54
38:A1:2533:G:H2'	38:A1:2534:G:C8	2.43	0.54
38:A1:2875:U:O2'	38:A1:2876:C:O5'	2.22	0.54
51:AO:27[A]:LEU:O	51:AO:101[A]:ARG:NH1	2.39	0.54
2:BB:129:THR:HG22	2:BB:176:VAL:HG13	1.89	0.54
34:B5:1000:C:N4	34:B5:1003:A:OP2	2.31	0.54
34:B5:1280:4AC:H2'	34:B5:1281:G:H8	1.73	0.54
34:B5:1511:U:H2'	34:B5:1512:G:H8	1.72	0.54
38:A1:1486:G:H21	69:Ag:6:THR:HG22	1.73	0.54
38:A1:2759:U:H5''	38:A1:2760:C:H5'	1.89	0.54
79:E:181:ASN:HA	79:E:184:LEU:HG	1.89	0.54
81:V:27:VAL:HB	81:V:189:GLN:HB3	1.90	0.54
1:BA:16:LEU:HD13	1:BA:172:LEU:HD11	1.90	0.53
5:BG:3:LEU:HD22	5:BG:111:LEU:HD11	1.89	0.53
26:BT:88:VAL:HG12	26:BT:89:ARG:HD2	1.89	0.53
34:B5:1225:U:H2'	34:B5:1230:A:H4'	1.90	0.53
36:AB:92:TYR:HB3	36:AB:99:LEU:HG	1.89	0.53
38:A1:528:U:H2'	38:A1:529:A:C8	2.43	0.53
38:A1:1949:G:OP2	54:AR:135:LYS:NZ	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Ai:66:GLU:OE2	71:Ai:70:ARG:NH1	2.41	0.53
4:BE:182:TYR:HB3	4:BE:226:PHE:HB3	1.90	0.53
34:B5:146:U:H2'	34:B5:147:A:H8	1.73	0.53
34:B5:1235:C:H2'	34:B5:1236:A:H8	1.73	0.53
34:B5:1373:C:H2'	34:B5:1374:C:C6	2.43	0.53
36:AB:259:HIS:NE2	38:A1:2366:C:OP1	2.38	0.53
38:A1:307:A:H2'	38:A1:308:A:C8	2.43	0.53
38:A1:2438:A:H2'	38:A1:2439:A:C8	2.42	0.53
3:BC:237:VAL:HG12	12:BV:35:ASN:HD21	1.73	0.53
34:B5:1641:C:H2'	34:B5:1642:G:C8	2.43	0.53
38:A1:596:C:OP1	43:AF:33:ARG:NH1	2.41	0.53
38:A1:1729:A:C6	65:Ac:49:PRO:HD3	2.43	0.53
46:AI:208:ASN:HA	46:AI:211:ARG:HG2	1.90	0.53
34:B5:472:U:O2'	34:B5:769:A:N3	2.35	0.53
34:B5:1658:G:H2'	34:B5:1659:A:C8	2.42	0.53
38:A1:1257:C:H42	38:A1:1261:G:H22	1.56	0.53
38:A1:2116:G:OP1	38:A1:2118:C:N4	2.41	0.53
70:Ah:102:GLU:OE2	70:Ah:105:ARG:NH2	2.38	0.53
80:DC:155:VAL:HG23	80:DC:202:VAL:HG11	1.90	0.53
80:DC:387:PRO:HA	80:DC:394:PHE:CD1	2.43	0.53
19:BD:141:LYS:HA	19:BD:147:ALA:HA	1.89	0.53
34:B5:1646:C:H4'	38:A1:2259:A:H62	1.73	0.53
35:AA:21:ARG:NH1	38:A1:825:U:OP1	2.42	0.53
38:A1:503:C:H2'	38:A1:504:A:H8	1.72	0.53
38:A1:1084:A:H2'	38:A1:1085:A:C8	2.42	0.53
38:A1:1194:G:H2'	38:A1:1195:A:C8	2.43	0.53
38:A1:3164:C:HO2'	38:A1:3165:A:H8	1.57	0.53
39:A3:23:A:H2'	39:A3:24:A:C8	2.44	0.53
47:AJ:40:LEU:HD13	47:AJ:112:LEU:HD11	1.90	0.53
80:DC:26:ALA:HB2	80:DC:128:VAL:HB	1.90	0.53
16:Ba:5:ARG:NH2	34:B5:1795:U:OP2	2.40	0.53
20:BF:112:ARG:HH21	23:BQ:43:ILE:HG13	1.72	0.53
24:BR:17:ILE:HD12	24:BR:58:MET:HE3	1.90	0.53
25:BS:137:HIS:ND1	34:B5:1175:U:OP2	2.41	0.53
31:Bg:238:ASP:HB2	31:Bg:257:ALA:HB3	1.91	0.53
36:AB:168:LYS:O	36:AB:319:ASN:ND2	2.31	0.53
38:A1:1257:C:N4	38:A1:1261:G:H22	2.06	0.53
38:A1:1564:U:H3	38:A1:1575:A:H61	1.57	0.53
54:AR:152:GLU:OE2	54:AR:156:ASN:ND2	2.41	0.53
80:DC:6:VAL:HG12	80:DC:47:SER:HB3	1.91	0.53
26:BT:70:GLN:NE2	26:BT:119:LYS:O	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:703:G:N2	34:B5:736:C:O2	2.41	0.53
45:AH:113:GLU:OE2	45:AH:115:ARG:NH1	2.36	0.53
53:AQ:165:ILE:HD11	53:AQ:168:THR:HG22	1.91	0.53
79:E:122:ARG:NH1	82:EC:6770:U:OP2	2.41	0.53
80:DC:338:ILE:HG23	80:DC:342:LEU:HD12	1.90	0.53
3:BC:58:LEU:O	12:BV:15:ARG:NH1	2.36	0.53
6:BH:69:GLY:HA2	6:BH:72:LYS:HE2	1.91	0.53
19:BD:94:ARG:O	19:BD:101:GLN:NE2	2.42	0.53
34:B5:741:C:H4'	34:B5:742:U:H5'	1.90	0.53
36:AB:77:THR:HG21	36:AB:328:ILE:HG12	1.91	0.53
38:A1:3252:G:H2'	38:A1:3253:G:C8	2.43	0.53
80:DC:380:LEU:HD11	80:DC:469:LEU:HD22	1.91	0.53
80:DC:463:LEU:O	80:DC:513:LYS:NZ	2.39	0.53
11:BO:123:SER:OG	34:B5:885:G:N2	2.38	0.53
34:B5:1237:G:H2'	34:B5:1238:A:H8	1.74	0.53
36:AB:212:ASN:O	36:AB:281:LYS:NZ	2.35	0.53
38:A1:2160:G:H2'	38:A1:2161:G:H8	1.74	0.53
38:A1:3206:C:OP2	49:AM:102:LYS:NZ	2.42	0.53
38:A1:3324:C:OP1	66:Ad:19:ARG:NH1	2.42	0.53
46:AI:140:THR:HG21	46:AI:148:VAL:HG21	1.89	0.53
61:AY:11:ASP:HB3	61:AY:14:LYS:HB2	1.91	0.53
81:V:29:GLY:O	81:V:186:THR:OG1	2.27	0.53
7:BI:25:ARG:NH2	34:B5:386:G:OP2	2.42	0.53
20:BF:185:ARG:NH2	34:B5:1471:A:OP1	2.39	0.53
34:B5:512:A:H2'	34:B5:513:U:C6	2.44	0.53
38:A1:625:G:N2	38:A1:1401:A:OP1	2.36	0.53
38:A1:1008:U:O2'	46:AI:35:ASP:OD1	2.26	0.53
38:A1:3183:A:OP1	51:AO:37[A]:ARG:NH2	2.38	0.53
49:AM:60:LEU:HD13	55:AS:152:LEU:HD11	1.91	0.53
65:Ac:45:ALA:HB2	65:Ac:77:LEU:HD12	1.91	0.53
80:DC:67:GLY:N	85:DC:901:GDP:O1A	2.42	0.53
38:A1:775:A:OP1	64:Ab:44:LYS:NZ	2.41	0.52
4:BE:128:LYS:HA	4:BE:156:VAL:HG12	1.91	0.52
31:Bg:239:GLU:O	31:Bg:257:ALA:N	2.42	0.52
34:B5:1380:U:H6	34:B5:1516:A:H61	1.57	0.52
34:B5:1606:C:H2'	34:B5:1607:G:C8	2.44	0.52
38:A1:149:U:P	50:AN:49:ARG:HH12	2.32	0.52
38:A1:1606:U:O4'	69:Ag:8:ARG:NH2	2.41	0.52
44:AG:95:ASN:OD1	44:AG:98:ARG:NH2	2.41	0.52
56:AT:94:GLU:N	56:AT:94:GLU:OE2	2.39	0.52
78:Ap:32:GLN:O	78:Ap:37:TYR:OH	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:913:G:N2	38:A1:2206:G:OP1	2.43	0.52
36:AB:9:PRO:HG3	38:A1:2914:G:H5'	1.91	0.52
37:AC:303:GLY:H	38:A1:1347:U:H5''	1.73	0.52
40:A4:150:G:OP1	60:AX:27:ARG:NH2	2.41	0.52
61:AY:119:ILE:HG22	61:AY:124:GLY:HA3	1.91	0.52
64:Ab:5:LYS:HE3	64:Ab:8:THR:HB	1.91	0.52
71:Ai:54:GLU:OE2	71:Ai:86:LYS:NZ	2.43	0.52
81:V:86:PHE:HB3	81:V:88:PHE:HE1	1.74	0.52
6:BH:90:VAL:O	6:BH:165:LYS:NZ	2.40	0.52
33:BM:32:LEU:HB2	33:BM:100:TRP:HZ3	1.73	0.52
34:B5:5:U:H2'	34:B5:6:G:H8	1.74	0.52
34:B5:947:U:H2'	34:B5:948:G:C8	2.43	0.52
34:B5:1695:G:H2'	34:B5:1696:G:H8	1.73	0.52
38:A1:1174:G:N2	51:AO:87[A]:MET:SD	2.81	0.52
80:DC:288:ILE:HG21	80:DC:320:LEU:HD13	1.90	0.52
82:EC:6853:G:C6	82:EC:6876:A:C2	2.97	0.52
6:BH:41:LEU:HD23	6:BH:70:PHE:HD1	1.73	0.52
20:BF:203:LYS:HD2	82:EC:6862:G:H5''	1.90	0.52
24:BR:41:ILE:HD13	24:BR:47:ARG:HA	1.90	0.52
37:AC:156:LEU:HD12	37:AC:159:ILE:HD12	1.92	0.52
38:A1:19:U:H2'	38:A1:20:A:C8	2.44	0.52
38:A1:760:G:O2'	38:A1:770:G:N2	2.40	0.52
38:A1:1329:U:O3'	68:Af:19:SER:OG	2.28	0.52
38:A1:2219:A:H2'	38:A1:2220:A2M:C8	2.38	0.52
47:AJ:12:LEU:HD11	47:AJ:154:THR:HG23	1.91	0.52
65:Ac:39:SER:OG	65:Ac:91:SER:OG	2.27	0.52
10:BN:11:ILE:HD11	34:B5:1072:C:H4'	1.91	0.52
10:BN:124:ARG:NH1	34:B5:628:G:OP1	2.39	0.52
22:BP:96:ILE:HD11	22:BP:116:LEU:HD22	1.91	0.52
25:BS:32:LEU:HD22	25:BS:73:MET:HE1	1.90	0.52
25:BS:87:ASN:OD1	34:B5:1546:G:N2	2.37	0.52
26:BT:117:SER:O	26:BT:117:SER:OG	2.23	0.52
33:BM:116:VAL:HG21	34:B5:1227:A:C8	2.45	0.52
34:B5:17:C:H2'	34:B5:18:C:H6	1.74	0.52
34:B5:924:A:H2'	34:B5:925:G:C8	2.44	0.52
38:A1:37:U:O4	50:AN:83:LYS:NZ	2.42	0.52
79:E:194:LEU:O	79:E:197:ASN:ND2	2.43	0.52
80:DC:320:LEU:O	80:DC:324:MET:HG2	2.10	0.52
13:BW:107:SER:HA	34:B5:804:A:C8	2.44	0.52
20:BF:109:LYS:NZ	34:B5:1528:U:OP2	2.35	0.52
38:A1:531:G:H2'	38:A1:532:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1517:G:OP1	74:A1:41:ARG:NH1	2.41	0.52
68:Af:102:LEU:O	68:Af:105:SER:OG	2.27	0.52
79:E:149:THR:HA	79:E:152:ARG:HG2	1.92	0.52
3:BC:116:LYS:HG2	3:BC:127:ALA:HB3	1.91	0.52
8:BJ:17:ARG:O	8:BJ:23:ARG:NH2	2.43	0.52
19:BD:163:PRO:HA	19:BD:166:ASP:HB2	1.92	0.52
20:BF:42:LEU:O	20:BF:44:ASN:N	2.42	0.52
34:B5:1561:U:H2'	34:B5:1562:G:H8	1.75	0.52
38:A1:966:U:H2'	38:A1:967:A:C8	2.45	0.52
38:A1:1178:G:N3	38:A1:1328:C:O2'	2.40	0.52
38:A1:3016:A:H2'	38:A1:3017:A:C8	2.44	0.52
80:DC:130:ASP:OD1	80:DC:131:THR:N	2.43	0.52
80:DC:150:ARG:HG3	80:DC:197:LEU:HD11	1.91	0.52
80:DC:524:GLU:N	80:DC:524:GLU:OE1	2.43	0.52
80:DC:600:ALA:HA	80:DC:605:ILE:HD13	1.92	0.52
81:V:35:SER:O	81:V:39:HIS:ND1	2.42	0.52
82:EC:6788:C:O5'	82:EC:6805:C:N4	2.42	0.52
13:BW:56:HIS:O	34:B5:861:U:O2'	2.27	0.52
19:BD:23:GLU:OE1	21:BK:61:TRP:NE1	2.42	0.52
34:B5:164:A:H2'	34:B5:165:G:H8	1.74	0.52
38:A1:240:U:O2'	38:A1:241:G:O5'	2.19	0.52
38:A1:249:U:H1'	38:A1:251:G:H2'	1.92	0.52
38:A1:1010:G:N2	46:A1:193:ASP:OD1	2.42	0.52
38:A1:1108:U:H2'	38:A1:1109:U:C6	2.44	0.52
38:A1:1807:G:O2'	38:A1:2559:U:O4	2.28	0.52
39:A3:44:C:OP2	47:AJ:137:ARG:NH1	2.28	0.52
40:A4:9:A:H2'	40:A4:10:A:C8	2.45	0.52
3:BC:39:THR:HG23	3:BC:42:GLY:H	1.73	0.52
4:BE:27:TYR:O	34:B5:447:U:O2'	2.28	0.52
16:Ba:45:VAL:HG13	16:Ba:46:GLU:H	1.75	0.52
20:BF:42:LEU:HG	20:BF:43:PHE:H	1.74	0.52
25:BS:123:ARG:O	25:BS:127:HIS:ND1	2.37	0.52
35:AA:178:PRO:HG2	78:Ap:26:VAL:HG23	1.92	0.52
36:AB:215:ILE:HD13	36:AB:282:ILE:HD11	1.93	0.52
38:A1:3344:A:C2	38:A1:3361:G:N2	2.73	0.52
43:AF:77:VAL:HB	56:AT:139:ARG:HG2	1.92	0.52
62:AZ:97:SER:O	62:AZ:100:THR:HG22	2.10	0.52
73:Ak:5:ILE:HD11	73:Ak:52:TYR:HD2	1.74	0.52
80:DC:576:LEU:HD12	80:DC:585:ARG:NH2	2.25	0.52
8:BJ:90:LYS:HB2	8:BJ:95:TYR:CG	2.45	0.51
9:BL:27:THR:HG23	9:BL:30:ARG:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:4:SER:HG	34:B5:1101:G:HO2'	1.54	0.51
14:BX:70:LYS:HG2	14:BX:93:LEU:HD22	1.91	0.51
26:BT:15:ILE:HG23	26:BT:59:ALA:HB3	1.91	0.51
34:B5:1354:G:N2	34:B5:1372:U:O3'	2.43	0.51
34:B5:1394:G:H2'	34:B5:1395:G:C8	2.45	0.51
34:B5:1511:U:H2'	34:B5:1512:G:C8	2.45	0.51
37:AC:3:ARG:HH22	37:AC:24:ALA:HA	1.74	0.51
38:A1:2357:A:H2'	38:A1:2358:A:H8	1.75	0.51
38:A1:2986:U:H2'	38:A1:2987:A:H8	1.74	0.51
40:A4:8:C:H2'	40:A4:9:A:C8	2.44	0.51
51:AO:22[A]:VAL:HG11	51:AO:120[A]:VAL:HG11	1.91	0.51
71:Ai:5:THR:HG23	71:Ai:12:ASN:HB2	1.92	0.51
4:BE:214:LEU:HD13	4:BE:244:ILE:HG21	1.92	0.51
5:BG:53:SER:OG	34:B5:163:G:O2'	2.27	0.51
9:BL:6:THR:HB	9:BL:9:SER:HB3	1.91	0.51
34:B5:488:G:H1	34:B5:500:C:P	2.33	0.51
35:AA:177:LYS:O	38:A1:1793:C:N4	2.38	0.51
38:A1:799:G:OP2	63:Aa:32:ARG:NH1	2.38	0.51
38:A1:1124:U:O2'	38:A1:2635:A:OP1	2.27	0.51
38:A1:2469:G:H4'	79:E:26:ARG:HG2	1.92	0.51
80:DC:649:GLN:HG2	80:DC:687:ASN:HB2	1.93	0.51
82:EC:6860:A:H61	82:EC:6870:A:H1'	1.74	0.51
2:BB:79:HIS:HD2	2:BB:82:ARG:HH21	1.58	0.51
3:BC:245:ASP:OD1	3:BC:245:ASP:N	2.42	0.51
5:BG:72:ARG:HH12	34:B5:419:G:H5'	1.75	0.51
5:BG:92:ARG:NH1	34:B5:1674:C:OP1	2.43	0.51
11:BO:29:HIS:CD2	11:BO:41:ARG:HB2	2.45	0.51
20:BF:80:LYS:NZ	34:B5:1413:U:OP2	2.40	0.51
21:BK:52:LYS:HG3	34:B5:1220:C:H4'	1.91	0.51
27:BU:60:THR:H	34:B5:1382:A:H5''	1.76	0.51
36:AB:297:SER:O	36:AB:300:ARG:NH2	2.44	0.51
38:A1:651:G:O2'	38:A1:1435:A:OP1	2.28	0.51
38:A1:2947:G:OP1	38:A1:2982:A:N6	2.41	0.51
80:DC:483:PHE:HZ	80:DC:517:CYS:HA	1.75	0.51
82:EC:6918:A:H3'	82:EC:6919:G:H8	1.75	0.51
4:BE:36:HIS:CG	4:BE:85:GLY:HA3	2.45	0.51
20:BF:219:ARG:HE	82:EC:6841:U:H1'	1.74	0.51
31:Bg:102:ARG:NH1	34:B5:1341:A:O2'	2.43	0.51
34:B5:431:C:H2'	34:B5:432:G:H8	1.76	0.51
34:B5:1087:A:H2'	34:B5:1088:A:C8	2.45	0.51
34:B5:1454:G:H2'	34:B5:1455:G:C8	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1533:C:H4'	34:B5:1539:G:C6	2.45	0.51
34:B5:1714:A:H2'	34:B5:1715:G:H8	1.75	0.51
38:A1:284:A:OP2	77:Ao:41:ARG:NH1	2.36	0.51
38:A1:2494:A:H5''	38:A1:2495:C:H6	1.74	0.51
38:A1:2988:C:OP1	51:AO:65[A]:ASN:ND2	2.40	0.51
81:V:37:GLN:NE2	81:V:105:VAL:O	2.42	0.51
2:BB:30:PHE:CE1	2:BB:48:VAL:HG12	2.45	0.51
4:BE:19:LEU:HD13	34:B5:788:A:C6	2.45	0.51
5:BG:48:TYR:HE1	5:BG:116:LYS:HD3	1.75	0.51
14:BX:3:LYS:HE2	14:BX:7:ARG:HH22	1.76	0.51
19:BD:5:ILE:HG13	19:BD:9:ARG:HE	1.75	0.51
31:Bg:13:LEU:HD12	31:Bg:45:TRP:CE3	2.45	0.51
31:Bg:122:ILE:HB	31:Bg:134:TRP:HB2	1.93	0.51
31:Bg:156:VAL:HG22	31:Bg:169:ILE:HG22	1.91	0.51
31:Bg:289:ALA:HA	31:Bg:305:TYR:HA	1.91	0.51
34:B5:1349:G:H2'	34:B5:1350:U:C6	2.46	0.51
34:B5:1564:U:H2'	34:B5:1565:C:C6	2.46	0.51
38:A1:271:C:O2	71:Ai:82:ARG:NH2	2.28	0.51
38:A1:2106:A:H2'	38:A1:2107:A:C8	2.45	0.51
23:BQ:66:ARG:NH2	34:B5:1365:C:OP1	2.38	0.51
25:BS:145:ARG:NH1	34:B5:1569:A:O2'	2.43	0.51
37:AC:107:ARG:HH12	38:A1:1428:A:H5''	1.75	0.51
37:AC:315:LYS:HA	38:A1:505:G:H5''	1.92	0.51
38:A1:1560:G:O2'	38:A1:1561:G:O4'	2.23	0.51
38:A1:1759:C:N4	38:A1:1760:A:N6	2.58	0.51
40:A4:156:U:OP2	44:AG:84:ARG:NH1	2.44	0.51
6:BH:158:ASP:OD1	6:BH:161:GLN:NE2	2.44	0.51
15:BY:23:PHE:HE2	15:BY:75:VAL:HG12	1.75	0.51
15:BY:124:ARG:HA	15:BY:127:LYS:HE2	1.92	0.51
31:Bg:38:ARG:HA	31:Bg:67:ILE:HG23	1.92	0.51
38:A1:253:A:H5''	38:A1:253:A:C8	2.46	0.51
38:A1:2260:U:H3'	38:A1:2261:G:C8	2.45	0.51
40:A4:83:C:N3	61:AY:52:ARG:NH2	2.50	0.51
55:AS:92:LYS:NZ	55:AS:110:MET:SD	2.73	0.51
80:DC:199:ASP:OD1	80:DC:199:ASP:N	2.44	0.51
80:DC:216:HIS:HB3	80:DC:324:MET:HE3	1.93	0.51
80:DC:581:ASN:N	80:DC:704:GLN:OE1	2.44	0.51
4:BE:108:ARG:NH2	34:B5:788:A:OP2	2.29	0.51
8:BJ:41:GLU:OE2	8:BJ:126:ARG:NH2	2.44	0.51
14:BX:109:ARG:HB3	14:BX:112:LYS:HB2	1.92	0.51
20:BF:122:ASN:OD1	20:BF:123:VAL:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:12:U:H2'	34:B5:13:C:C6	2.46	0.51
34:B5:1394:G:H2'	34:B5:1395:G:H8	1.76	0.51
34:B5:1480:G:H2'	34:B5:1481:C:O4'	2.11	0.51
34:B5:1683:C:O2'	34:B5:1684:U:O5'	2.27	0.51
36:AB:95:THR:HG22	36:AB:97:ARG:H	1.76	0.51
38:A1:190:U:H2'	61:AY:60:ARG:HH12	1.75	0.51
38:A1:947:G:H5''	67:Ae:55:ILE:HB	1.92	0.51
38:A1:1667:A:H2'	38:A1:1668:G:C8	2.45	0.51
38:A1:3296:A:H2'	38:A1:3297:U:H6	1.75	0.51
80:DC:39:LEU:HD12	80:DC:334:LEU:HD23	1.93	0.51
80:DC:410:LYS:HD3	80:DC:428:ILE:HG23	1.93	0.51
82:EC:6813:A:H2'	82:EC:6814:G:C8	2.46	0.51
82:EC:6923:C:H2'	82:EC:6924:G:H8	1.76	0.51
10:BN:46:THR:HG23	10:BN:49:GLN:H	1.75	0.51
31:Bg:80:ALA:HB3	31:Bg:92:TRP:HB2	1.92	0.51
35:AA:174:ARG:NH2	38:A1:2179:C:O2'	2.44	0.51
38:A1:1493:G:C8	74:Al:13:MET:HE1	2.46	0.51
47:AJ:78:GLU:OE1	47:AJ:82:ARG:NH2	2.42	0.51
80:DC:634:TRP:HB2	80:DC:646:VAL:HG13	1.92	0.51
82:EC:6826:U:H2'	82:EC:6827:G:C8	2.46	0.51
4:BE:75:LYS:NZ	34:B5:123:G:OP1	2.32	0.51
13:BW:27:ILE:HB	13:BW:61:ILE:HB	1.93	0.51
34:B5:1226:A:N6	34:B5:1230:A:N3	2.60	0.51
36:AB:100:ARG:HD2	38:A1:3146:G:H4'	1.93	0.51
38:A1:728:G:H5''	53:AQ:43:PRO:HB2	1.93	0.51
53:AQ:21:SER:O	53:AQ:27:LYS:NZ	2.45	0.51
53:AQ:122:ILE:HG23	53:AQ:126:GLN:HB2	1.93	0.51
62:AZ:133:LYS:HE3	62:AZ:135:ARG:NH2	2.23	0.51
80:DC:203:TYR:O	80:DC:208:THR:OG1	2.30	0.51
82:EC:6791:A:O5'	82:EC:6849:A:N6	2.44	0.51
82:EC:6804:A:H4'	82:EC:6805:C:H5'	1.92	0.51
15:BY:32:ARG:NH2	15:BY:39:GLU:OE2	2.44	0.50
33:BM:43:ARG:HH12	33:BM:103:LEU:HA	1.75	0.50
34:B5:1551:U:H2'	34:B5:1552:U:H6	1.75	0.50
37:AC:101:ALA:HA	38:A1:800:G:H22	1.75	0.50
37:AC:315:LYS:HB2	37:AC:323:VAL:HG21	1.94	0.50
38:A1:1392:G:H1'	38:A1:1418:A:N6	2.26	0.50
38:A1:3113:A:H4'	45:AH:69:ARG:HG3	1.93	0.50
44:AG:89:GLU:HA	44:AG:92:LYS:HE2	1.93	0.50
80:DC:593:ILE:HD13	80:DC:645:LEU:HD23	1.94	0.50
28:BZ:77:ARG:NH1	34:B5:1532:U:OP2	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:17:C:H2'	34:B5:18:C:C6	2.46	0.50
34:B5:490:C:C5	34:B5:492:A:H5''	2.47	0.50
34:B5:496:G:H5'	34:B5:499:U:C4	2.45	0.50
38:A1:650:OMC:H2'	38:A1:651:G:C8	2.46	0.50
41:AD:33:ARG:NH1	41:AD:50:ARG:HH12	2.09	0.50
61:AY:58:VAL:HA	61:AY:104:LEU:HD13	1.93	0.50
79:E:100:ILE:HD12	79:E:127:GLN:HB2	1.92	0.50
10:BN:108:ASP:OD1	34:B5:878:G:O2'	2.27	0.50
11:BO:38:THR:HG21	34:B5:895:G:H21	1.75	0.50
28:BZ:66:VAL:HG12	28:BZ:71:ILE:HG23	1.93	0.50
34:B5:164:A:H2'	34:B5:165:G:C8	2.46	0.50
36:AB:147:GLU:OE1	36:AB:150:ARG:NH2	2.42	0.50
38:A1:426:G:H5'	67:Ae:50:ILE:HG22	1.93	0.50
38:A1:1015:U:C2	38:A1:1035:G:O6	2.64	0.50
38:A1:1798:A:H2'	38:A1:1799:A:C8	2.46	0.50
38:A1:2631:U:OP2	56:AT:4:SER:OG	2.29	0.50
65:Ac:70:PHE:HE2	65:Ac:76:GLU:HG3	1.76	0.50
80:DC:20:ARG:NE	80:DC:342:LEU:O	2.43	0.50
80:DC:591:GLU:HG3	80:DC:685:ARG:HB3	1.93	0.50
81:V:70:LEU:HD12	81:V:71:PRO:HD2	1.93	0.50
11:BO:17:ALA:HA	11:BO:30:VAL:HG22	1.92	0.50
34:B5:1210:C:H2'	34:B5:1211:A:C8	2.45	0.50
34:B5:1291:G:H22	34:B5:1324:G:N2	2.09	0.50
35:AA:244:GLY:HA3	38:A1:2242:A:H5''	1.94	0.50
38:A1:40:A:H5''	63:Aa:35:ALA:HB1	1.92	0.50
38:A1:1083:G:H2'	38:A1:1084:A:C8	2.47	0.50
38:A1:1612:A:P	73:Ak:46:ARG:HH11	2.35	0.50
38:A1:3359:A:H2'	38:A1:3360:C:C6	2.47	0.50
82:EC:6799:C:H2'	82:EC:6800:G:H4'	1.93	0.50
12:BV:32:VAL:HG12	12:BV:60:ARG:HD2	1.92	0.50
14:BX:42:PRO:O	14:BX:79:ASN:ND2	2.41	0.50
15:BY:26:ASP:OD1	15:BY:26:ASP:N	2.44	0.50
21:BK:64:TYR:HB3	21:BK:66:TYR:CE2	2.47	0.50
21:BK:87:VAL:HG23	21:BK:93:GLN:HE22	1.77	0.50
38:A1:1822:C:H2'	38:A1:1823:A:H8	1.77	0.50
38:A1:2494:A:H5''	38:A1:2495:C:C6	2.46	0.50
38:A1:2722:U:H4'	56:AT:88:ARG:HB2	1.94	0.50
41:AD:93:THR:OG1	41:AD:158:ARG:NH1	2.44	0.50
57:AU:19:VAL:HG23	57:AU:105:LEU:HD22	1.93	0.50
80:DC:681:MET:HE3	80:DC:717:PHE:CD1	2.47	0.50
81:V:115:ALA:HB3	81:V:161:ALA:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:66:ASP:HB3	8:BJ:69:ARG:HB3	1.93	0.50
19:BD:141:LYS:NZ	34:B5:1275:A:N3	2.59	0.50
34:B5:1490:C:H5'	34:B5:1491:U:H2'	1.94	0.50
36:AB:66:LYS:NZ	58:AV:9:THR:O	2.36	0.50
38:A1:201:A:H2'	38:A1:202:G:H8	1.77	0.50
38:A1:700:C:H2'	38:A1:701:G:H8	1.77	0.50
38:A1:806:A:N3	38:A1:2812:C:O2'	2.38	0.50
38:A1:993:G:N3	38:A1:2637:A:H2'	2.26	0.50
38:A1:2724:OMU:OP1	56:AT:78:LYS:NZ	2.43	0.50
40:A4:37:A:OP1	70:Ah:89:ARG:NH2	2.43	0.50
44:AG:214:LEU:O	44:AG:218:ILE:HG12	2.12	0.50
54:AR:175:GLN:HG2	54:AR:176:ARG:HD2	1.94	0.50
80:DC:288:ILE:HD13	80:DC:319:LEU:HD22	1.94	0.50
80:DC:314:LEU:HB3	80:DC:319:LEU:HB2	1.92	0.50
82:EC:6790:A:H5'	82:EC:6849:A:C2	2.47	0.50
1:BA:111:ILE:HD11	34:B5:1292:G:H21	1.76	0.50
3:BC:140:ARG:HB2	3:BC:222:TYR:CE1	2.47	0.50
5:BG:57:ASP:HA	5:BG:107:ALA:H	1.77	0.50
14:BX:96:VAL:HA	14:BX:127:VAL:HG21	1.93	0.50
19:BD:72:LEU:HD12	21:BK:20:VAL:HG21	1.93	0.50
19:BD:167:PHE:HD1	19:BD:190:ARG:HH12	1.59	0.50
23:BQ:50:GLU:HG2	23:BQ:112:TYR:CZ	2.47	0.50
28:BZ:77:ARG:NH2	34:B5:1534:G:N7	2.59	0.50
28:BZ:92:ILE:HD11	28:BZ:102:THR:HB	1.94	0.50
34:B5:329:G:H2'	34:B5:330:G:C8	2.46	0.50
34:B5:520:A:H2'	34:B5:521:A:C8	2.47	0.50
34:B5:1552:U:O2'	34:B5:1597:A:N3	2.36	0.50
38:A1:567:G:H2'	38:A1:568:G:C8	2.46	0.50
38:A1:1688:U:H2'	38:A1:1689:U:C6	2.47	0.50
38:A1:3295:A:H2'	38:A1:3296:A:C8	2.47	0.50
52:AP:179:GLN:HA	52:AP:182:ILE:HG22	1.93	0.50
1:BA:76:ILE:HB	1:BA:123:VAL:HG12	1.93	0.50
4:BE:252:ARG:HD2	4:BE:256:ARG:HH12	1.77	0.50
9:BL:133:LYS:O	9:BL:136:ARG:NH1	2.45	0.50
13:BW:50:PHE:HB3	13:BW:63:VAL:HG13	1.94	0.50
34:B5:272:U:H5'	34:B5:273:G:H5'	1.93	0.50
34:B5:626:U:H2'	34:B5:627:C:H6	1.77	0.50
34:B5:1381:U:H2'	34:B5:1382:A:C8	2.47	0.50
38:A1:1925:U:O2'	38:A1:1927:G:N7	2.45	0.50
38:A1:3204:C:H2'	38:A1:3205:G:C8	2.46	0.50
39:A3:84:A:H2'	39:A3:85:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:AV:87:ARG:HH22	58:AV:137:VAL:HG21	1.77	0.50
80:DC:392:GLY:O	80:DC:510:ARG:NH2	2.44	0.50
1:BA:30:GLN:HE22	1:BA:32:HIS:HB2	1.77	0.50
11:BO:36:LYS:NZ	34:B5:920:U:O4'	2.45	0.50
20:BF:95:ASN:ND2	34:B5:1611:A:OP1	2.44	0.50
31:Bg:120:SER:O	31:Bg:121:MET:HE2	2.11	0.50
34:B5:632:U:O2'	34:B5:1103:U:OP1	2.25	0.50
34:B5:684:A:H2'	34:B5:685:A:C8	2.46	0.50
38:A1:1794:G:O2'	38:A1:1796:G:N2	2.45	0.50
38:A1:2407:C:H2'	38:A1:2408:U:H6	1.77	0.50
38:A1:2767:U:H2'	38:A1:2768:U:C6	2.46	0.50
52:AP:50:GLN:OE1	52:AP:56:ARG:NH1	2.41	0.50
56:AT:56:PHE:O	56:AT:60:LYS:NZ	2.44	0.50
61:AY:54:ASP:OD1	61:AY:110:HIS:N	2.42	0.50
15:BY:90:ARG:HA	15:BY:93:ARG:HB2	1.94	0.49
31:Bg:84:SER:OG	31:Bg:85:TRP:N	2.46	0.49
31:Bg:224:ASN:OD1	31:Bg:225:LEU:N	2.45	0.49
38:A1:179:C:N4	38:A1:237:G:H22	2.10	0.49
38:A1:549:U:OP2	38:A1:551:A:N6	2.45	0.49
38:A1:1047:A:N3	38:A1:2633:U:O2'	2.44	0.49
38:A1:2697:A:H2'	38:A1:2698:G:H8	1.73	0.49
50:AN:7:LEU:HD21	50:AN:45:PRO:HD2	1.93	0.49
51:AO:56[A]:ASP:OD1	51:AO:60[A]:LYS:NZ	2.45	0.49
70:Ah:83:LYS:O	72:Aj:73:ARG:NH2	2.45	0.49
82:EC:6775:U:OP2	82:EC:6775:U:H4'	2.11	0.49
34:B5:918:U:H2'	34:B5:919:A:H8	1.77	0.49
38:A1:999:G:H2'	38:A1:1000:C:C6	2.47	0.49
38:A1:1054:A:H5''	38:A1:2637:A:H61	1.76	0.49
38:A1:1659:U:H2'	38:A1:1660:C:C6	2.48	0.49
38:A1:2683:U:H2'	38:A1:2684:C:C6	2.47	0.49
41:AD:60:ILE:HB	41:AD:80:SER:HB2	1.94	0.49
48:AL:59:ARG:NH2	48:AL:66:ASN:O	2.44	0.49
52:AP:4:TYR:CE2	52:AP:16:SER:HB2	2.46	0.49
80:DC:17:THR:O	80:DC:91:GLN:NE2	2.45	0.49
80:DC:694:HIS:CE1	80:DC:699:DDE:HD2	2.47	0.49
1:BA:41:ARG:HH21	24:BR:106:THR:HG23	1.78	0.49
8:BJ:92:LYS:HB2	8:BJ:95:TYR:HD2	1.77	0.49
20:BF:225:ARG:HB3	29:Bc:61:ARG:NH2	2.28	0.49
30:Bd:34:TYR:OH	34:B5:1487:A:OP1	2.21	0.49
34:B5:100:A2M:H8	34:B5:100:A2M:O5'	2.12	0.49
34:B5:855:A:C2	34:B5:857:U:H1'	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1691:A:H2'	34:B5:1692:G:C8	2.47	0.49
36:AB:259:HIS:CE1	38:A1:2366:C:H5'	2.47	0.49
37:AC:219:LEU:HD22	37:AC:225:VAL:HG11	1.93	0.49
37:AC:318:LEU:H	37:AC:324:LEU:HD12	1.76	0.49
38:A1:2727:A:OP2	38:A1:2728:G:N2	2.43	0.49
38:A1:2931:C:OP1	58:AV:40:LYS:NZ	2.32	0.49
44:AG:74:THR:HG22	44:AG:164:VAL:HG22	1.92	0.49
80:DC:108:HIS:O	80:DC:138:GLN:NE2	2.44	0.49
82:EC:6776:A:N3	82:EC:6818:G:N2	2.60	0.49
8:BJ:31:ALA:HA	8:BJ:36:LEU:HD12	1.94	0.49
19:BD:164:VAL:HG23	19:BD:168:ILE:HD12	1.94	0.49
25:BS:81:ILE:HG21	25:BS:86:LEU:HD21	1.94	0.49
28:BZ:50:ILE:O	28:BZ:54:VAL:HG23	2.12	0.49
34:B5:131:C:N4	34:B5:135:A:O2'	2.45	0.49
34:B5:328:A:H2'	34:B5:329:G:C8	2.47	0.49
34:B5:950:C:H2'	34:B5:951:A:C8	2.46	0.49
35:AA:117:GLU:OE2	35:AA:163:ARG:NH2	2.39	0.49
37:AC:281:ILE:HD13	53:AQ:28:LEU:HD12	1.93	0.49
38:A1:737:G:H2'	38:A1:738:A:H8	1.77	0.49
38:A1:1491:A:H5''	72:Aj:14:LYS:HE3	1.94	0.49
38:A1:2688:U:OP1	41:AD:12:TYR:OH	2.23	0.49
80:DC:21:ASN:O	80:DC:123:ASP:N	2.43	0.49
80:DC:80:GLU:O	80:DC:81:MET:HE2	2.13	0.49
80:DC:281:ILE:HG12	80:DC:285:PHE:CE2	2.46	0.49
82:EC:6821:U:O2'	82:EC:6822:U:O3'	2.30	0.49
82:EC:6871:A:O2'	82:EC:6872:A:O4'	2.29	0.49
2:BB:121:ILE:HB	2:BB:141:ALA:HB3	1.95	0.49
21:BK:61:TRP:CE2	30:Bd:23:VAL:HG22	2.47	0.49
27:BU:24:ILE:HG22	27:BU:116:VAL:HG22	1.95	0.49
34:B5:179:A:H3'	34:B5:180:A:H8	1.77	0.49
34:B5:751:G:H2'	34:B5:752:A:C8	2.47	0.49
34:B5:1146:G:H2'	34:B5:1147:A:C8	2.47	0.49
34:B5:1466:G:H2'	34:B5:1467:C:C6	2.47	0.49
38:A1:1018:G:N2	38:A1:1019:G:O2'	2.45	0.49
38:A1:2406:C:H2'	38:A1:2407:C:H6	1.78	0.49
42:AE:43:LEU:HD11	42:AE:85:ILE:HG12	1.95	0.49
42:AE:55:LEU:HD21	42:AE:145:LEU:HD11	1.94	0.49
1:BA:41:ARG:HH12	24:BR:105:GLN:H	1.59	0.49
5:BG:31:ARG:NH2	34:B5:1681:A:O3'	2.46	0.49
7:BI:26:LYS:HG2	7:BI:29:LEU:HD23	1.94	0.49
34:B5:953:G:H2'	34:B5:954:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:12:A:H2'	38:A1:13:A:C8	2.48	0.49
38:A1:2351:U:H2'	38:A1:2352:A:H8	1.76	0.49
38:A1:3273:A:H2'	38:A1:3274:A:C8	2.47	0.49
60:AX:67:ILE:HD11	60:AX:85:GLN:HB2	1.94	0.49
78:Ap:51:ALA:HB3	78:Ap:54:ILE:HD12	1.94	0.49
16:Ba:15:ARG:HD2	16:Ba:18:VAL:HG12	1.94	0.49
19:BD:115:ILE:HD13	19:BD:142:LEU:HD22	1.95	0.49
27:BU:97:VAL:HA	27:BU:100:VAL:HG12	1.94	0.49
34:B5:328:A:H2'	34:B5:329:G:H8	1.76	0.49
34:B5:1551:U:H2'	34:B5:1552:U:C6	2.48	0.49
34:B5:1644:C:H2'	34:B5:1645:G:H8	1.77	0.49
36:AB:76:VAL:HG12	36:AB:325:LYS:HA	1.93	0.49
38:A1:67:A:O2'	38:A1:315:C:O2	2.30	0.49
38:A1:1157:G:O2'	38:A1:1169:A:N3	2.42	0.49
57:AU:20:SER:OG	57:AU:61:THR:OG1	2.30	0.49
65:Ac:15:ALA:O	65:Ac:18:ILE:HG22	2.11	0.49
66:Ad:10:ARG:NH1	66:Ad:12:TYR:OH	2.45	0.49
74:Al:9:ILE:O	74:Al:13:MET:HG2	2.12	0.49
79:E:191:VAL:O	79:E:197:ASN:ND2	2.23	0.49
80:DC:215:LEU:HD23	85:DC:901:GDP:N2	2.26	0.49
82:EC:6790:A:N6	82:EC:6798:C:OP2	2.38	0.49
2:BB:34:ALA:H	2:BB:41:ARG:HG3	1.77	0.49
4:BE:56:LEU:N	4:BE:60:GLU:OE1	2.36	0.49
4:BE:108:ARG:NH1	34:B5:789:A:OP1	2.46	0.49
8:BJ:28:LEU:HD21	18:Be:40:TYR:HA	1.94	0.49
31:Bg:205:SER:OG	31:Bg:207:ASP:OD1	2.23	0.49
34:B5:183:U:H2'	34:B5:184:C:C6	2.48	0.49
34:B5:396:G:N1	34:B5:399:A:OP2	2.46	0.49
34:B5:406:U:H2'	34:B5:407:A:C8	2.47	0.49
34:B5:898:A:N1	34:B5:911:U:O2'	2.43	0.49
34:B5:929:A:OP1	34:B5:944:A:O2'	2.30	0.49
38:A1:116:A:OP2	71:Ai:36:ARG:NH2	2.46	0.49
38:A1:733:G:N2	38:A1:736:A:OP2	2.44	0.49
38:A1:1447:G:H3'	52:AP:67:ILE:HD11	1.94	0.49
38:A1:1667:A:H2'	38:A1:1668:G:H8	1.77	0.49
40:A4:40:A:H2'	40:A4:41:A:C8	2.48	0.49
45:AH:21:LYS:HG3	45:AH:22:SER:H	1.78	0.49
80:DC:3:ALA:HB3	80:DC:45:ILE:HG23	1.94	0.49
82:EC:6899:C:H2'	82:EC:6900:A:H8	1.77	0.49
10:BN:62:GLN:NE2	34:B5:960:U:OP1	2.45	0.49
13:BW:81:VAL:O	13:BW:122:SER:OG	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BY:57:VAL:HB	15:BY:60:PHE:HE2	1.78	0.49
20:BF:40:ILE:HG22	20:BF:67:PRO:HB2	1.93	0.49
34:B5:1405:G:H2'	34:B5:1406:A:C8	2.48	0.49
34:B5:1742:U:H2'	34:B5:1743:U:O4'	2.12	0.49
35:AA:118:GLU:OE2	38:A1:2177:G:N2	2.43	0.49
38:A1:1119:C:H2'	38:A1:1120:A:C8	2.47	0.49
38:A1:1452:A:N3	38:A1:2346:C:O2'	2.46	0.49
38:A1:2545:C:H2'	38:A1:2546:C:H6	1.76	0.49
52:AP:117:ILE:HD13	52:AP:148:LEU:HB3	1.95	0.49
23:BQ:129:PHE:O	23:BQ:137:ARG:NH1	2.44	0.49
24:BR:10:LYS:HD3	24:BR:53:TYR:CE2	2.48	0.49
25:BS:14:ILE:HD11	25:BS:21:ASN:HB3	1.95	0.49
28:BZ:91:PRO:HA	28:BZ:101:TYR:HD1	1.78	0.49
34:B5:918:U:H2'	34:B5:919:A:C8	2.47	0.49
34:B5:1187:U:O2	34:B5:1198:G:N2	2.33	0.49
34:B5:1349:G:H2'	34:B5:1350:U:H6	1.77	0.49
36:AB:218:ILE:HG12	36:AB:276:THR:HG22	1.95	0.49
38:A1:428:A:H2'	38:A1:429:U:C6	2.48	0.49
38:A1:774:G:O6	38:A1:775:A:N6	2.46	0.49
38:A1:1250:G:H2'	38:A1:1251:A:H8	1.77	0.49
38:A1:2444:C:H2'	38:A1:2445:A:C8	2.48	0.49
38:A1:2960:C:H2'	38:A1:2961:G:H8	1.76	0.49
46:AI:150:GLU:HA	46:AI:153:ARG:HG2	1.94	0.49
61:AY:40:ARG:HH21	61:AY:46:LYS:HD3	1.77	0.49
62:AZ:54:THR:HG23	62:AZ:56:LYS:H	1.77	0.49
63:Aa:19:LYS:HB3	63:Aa:25:HIS:HB2	1.94	0.49
66:Ad:20:LEU:HD13	66:Ad:28:ARG:HG3	1.94	0.49
79:E:38:LEU:HD12	79:E:163:LEU:HA	1.95	0.49
7:BI:152:ILE:HG13	7:BI:153:GLU:H	1.77	0.48
34:B5:1114:G:O2'	34:B5:1130:G:O6	2.26	0.48
34:B5:1433:G:H2'	34:B5:1434:U:C6	2.48	0.48
38:A1:283:G:OP2	77:Ao:45:ARG:NH1	2.46	0.48
38:A1:1404:G:N2	38:A1:1407:A:OP2	2.31	0.48
38:A1:1534:A:H2'	38:A1:1535:A:C8	2.48	0.48
50:AN:11:GLN:HG2	50:AN:44:ARG:HH21	1.78	0.48
51:AO:151[A]:ASP:OD1	51:AO:152[A]:VAL:N	2.46	0.48
1:BA:107:PHE:HB2	1:BA:135:GLU:HG2	1.95	0.48
3:BC:81:MET:HG3	3:BC:211:LEU:HD11	1.95	0.48
8:BJ:87:SER:OG	8:BJ:88:GLU:N	2.46	0.48
13:BW:31:SER:H	13:BW:34:ILE:HD12	1.78	0.48
23:BQ:37:THR:O	23:BQ:45:ARG:NH2	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:79:ASN:ND2	35:AA:166:ILE:O	2.45	0.48
38:A1:255:A:H2'	38:A1:256:G:H8	1.78	0.48
38:A1:266:A:OP1	50:AN:5:LYS:NZ	2.46	0.48
38:A1:1244:A:H4'	38:A1:1245:A:C8	2.48	0.48
38:A1:2461:A:O2'	38:A1:2485:A:N6	2.46	0.48
38:A1:2711:C:O2'	38:A1:2744:U:OP1	2.31	0.48
38:A1:2927:C:H2'	38:A1:2928:C:C6	2.48	0.48
39:A3:108:A:H2'	39:A3:109:G:C8	2.48	0.48
40:A4:52:A:H5'	74:A1:21:ARG:HD3	1.95	0.48
43:AF:147:LEU:HD11	43:AF:207:LEU:HD21	1.94	0.48
52:AP:122:ALA:HB3	52:AP:143:PRO:HB2	1.94	0.48
80:DC:161:ASP:OD1	80:DC:162:ARG:N	2.44	0.48
82:EC:6876:A:H5'	82:EC:6877:C:O4'	2.13	0.48
1:BA:34:GLU:HG3	1:BA:35:PRO:HD3	1.95	0.48
7:BI:58:LEU:HD11	34:B5:1676:U:H5''	1.95	0.48
9:BL:33:ARG:NH1	9:BL:48:ALA:O	2.46	0.48
9:BL:109:VAL:HG11	9:BL:125:VAL:HG11	1.96	0.48
19:BD:43:PRO:O	19:BD:44:THR:HG22	2.13	0.48
33:BM:61:VAL:HG12	33:BM:89:ILE:HG13	1.95	0.48
34:B5:513:U:H2'	34:B5:514:G:C8	2.47	0.48
34:B5:1071:U:H2'	34:B5:1072:C:C6	2.48	0.48
34:B5:1335:U:H2'	34:B5:1336:A:H8	1.78	0.48
36:AB:250:ALA:HB1	38:A1:2947:G:N3	2.28	0.48
38:A1:1203:A:H2'	38:A1:1204:A:H8	1.77	0.48
38:A1:1461:A:H2'	38:A1:1462:A:H8	1.78	0.48
38:A1:2389:C:H2'	38:A1:2390:A:H8	1.77	0.48
55:AS:16:THR:HG23	55:AS:19:VAL:H	1.78	0.48
62:AZ:133:LYS:HG2	62:AZ:135:ARG:HH22	1.78	0.48
15:BY:26:ASP:HB2	15:BY:68:LYS:NZ	2.28	0.48
31:Bg:260:ILE:HB	31:Bg:274:LEU:HB2	1.96	0.48
33:BM:87:PRO:HB3	33:BM:140:PHE:CG	2.47	0.48
34:B5:1142:A:H2'	34:B5:1143:A:C8	2.49	0.48
34:B5:1151:A:H2'	34:B5:1152:A:H8	1.78	0.48
38:A1:307:A:H2'	38:A1:308:A:H8	1.78	0.48
38:A1:520:U:OP2	43:AF:70:LYS:NZ	2.42	0.48
38:A1:1729:A:O4'	65:Ac:52:ARG:NH1	2.46	0.48
38:A1:2263:C:H2'	38:A1:2264:U:O4'	2.13	0.48
38:A1:3322:A:H2'	38:A1:3323:A:H8	1.77	0.48
50:AN:46:ASP:OD1	50:AN:47:LYS:N	2.45	0.48
61:AY:36:SER:O	61:AY:40:ARG:HB2	2.13	0.48
15:BY:105:ARG:NH2	34:B5:459:G:OP2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:98:GLU:HG3	31:Bg:100:TYR:HE1	1.79	0.48
31:Bg:224:ASN:HB2	31:Bg:231:MET:HE3	1.96	0.48
33:BM:52:LEU:HD13	33:BM:78:LEU:HB2	1.95	0.48
34:B5:748:U:O2	34:B5:801:G:O6	2.31	0.48
36:AB:92:TYR:OH	36:AB:180:GLU:OE1	2.30	0.48
38:A1:784:A:OP2	53:AQ:69:ARG:NH1	2.46	0.48
38:A1:1084:A:OP1	56:AT:35:LYS:NZ	2.39	0.48
38:A1:2129:U:H2'	38:A1:2130:G:C8	2.48	0.48
38:A1:2986:U:H2'	38:A1:2987:A:C8	2.47	0.48
44:AG:144:GLU:OE2	50:AN:6:TYR:OH	2.24	0.48
55:AS:34:GLU:HG3	55:AS:61:ILE:HG12	1.96	0.48
80:DC:578:LYS:HG2	80:DC:582:LYS:HA	1.94	0.48
80:DC:735:CYS:HB2	80:DC:739:ALA:HB3	1.94	0.48
6:BH:139:ARG:HB3	13:BW:51:GLU:OE2	2.13	0.48
34:B5:521:A:H2'	34:B5:522:U:C6	2.49	0.48
34:B5:845:G:H2'	34:B5:846:G:H5''	1.96	0.48
34:B5:884:A:H2'	34:B5:885:G:H8	1.76	0.48
34:B5:1036:A:H2'	34:B5:1037:C:C6	2.48	0.48
34:B5:1585:U:H3	34:B5:1611:A:H2	1.62	0.48
34:B5:1650:U:H2'	34:B5:1651:A:H8	1.77	0.48
34:B5:1659:A:H2'	34:B5:1660:A:O4'	2.12	0.48
34:B5:1776:A:H2'	34:B5:1777:G:C8	2.48	0.48
34:B5:1785:U:H2'	34:B5:1786:G:H8	1.78	0.48
38:A1:2106:A:H2'	38:A1:2107:A:H8	1.79	0.48
38:A1:2152:A:H2'	38:A1:2153:U:H6	1.77	0.48
38:A1:3296:A:H2'	38:A1:3297:U:C6	2.49	0.48
51:AO:56[A]:ASP:O	51:AO:60[A]:LYS:NZ	2.43	0.48
58:AV:32:ARG:HH12	58:AV:64:LYS:HD3	1.79	0.48
80:DC:587:TYR:HB2	80:DC:690:ASP:HB3	1.95	0.48
25:BS:138:THR:OG1	34:B5:1459:C:OP2	2.32	0.48
34:B5:12:U:O2'	34:B5:1299:G:N3	2.44	0.48
34:B5:183:U:H2'	34:B5:184:C:H6	1.77	0.48
38:A1:269:G:H5''	50:AN:14:LYS:HE2	1.95	0.48
49:AM:23:ILE:O	49:AM:30:GLY:N	2.46	0.48
80:DC:73:THR:HG21	80:DC:386:VAL:HG13	1.95	0.48
2:BB:46:THR:OG1	2:BB:64:ARG:NH1	2.47	0.48
2:BB:126:THR:OG1	2:BB:136:ARG:NE	2.46	0.48
7:BI:84:HIS:NE2	7:BI:97:THR:OG1	2.45	0.48
31:Bg:127:ARG:HA	31:Bg:150:TRP:HB2	1.96	0.48
34:B5:385:A:H2'	34:B5:386:G:C8	2.48	0.48
34:B5:1156:C:H2'	34:B5:1157:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:249:U:OP2	38:A1:249:U:H4'	2.13	0.48
38:A1:1643:A:H2'	38:A1:1644:C:C2	2.48	0.48
38:A1:1740:U:H4'	38:A1:1741:A:H5'	1.95	0.48
38:A1:2389:C:H2'	38:A1:2390:A:C8	2.48	0.48
56:AT:27:LEU:HD23	56:AT:30:TYR:HD2	1.78	0.48
81:V:25:LEU:HB3	81:V:191:TYR:HB3	1.94	0.48
8:BJ:29:LYS:HE2	8:BJ:29:LYS:HB2	1.74	0.48
9:BL:110:HIS:HB2	9:BL:135:VAL:HG11	1.96	0.48
25:BS:18:LEU:HD21	25:BS:101:LEU:HD13	1.94	0.48
34:B5:140:A:H62	34:B5:281:G:H5''	1.79	0.48
34:B5:869:A:H61	34:B5:958:U:H3	1.61	0.48
34:B5:1308:G:H2'	34:B5:1309:C:C6	2.49	0.48
34:B5:1503:A:H2'	34:B5:1504:G:C8	2.49	0.48
37:AC:107:ARG:NH2	38:A1:1429:G:OP2	2.37	0.48
38:A1:120:G:H4'	38:A1:121:A:H5'	1.96	0.48
79:E:127:GLN:HA	82:EC:6774:U:C5	2.49	0.48
80:DC:736:PRO:HD2	80:DC:791:GLN:HB3	1.94	0.48
82:EC:6923:C:H2'	82:EC:6924:G:C8	2.49	0.48
15:BY:121:THR:OG1	34:B5:149:C:OP1	2.30	0.48
31:Bg:116:ASP:HB3	31:Bg:121:MET:H	1.79	0.48
34:B5:710:U:H2'	34:B5:728:U:H3	1.79	0.48
34:B5:841:U:H2'	34:B5:842:C:C6	2.48	0.48
34:B5:1291:G:H22	34:B5:1324:G:H22	1.61	0.48
38:A1:1460:A:H2'	38:A1:1461:A:C8	2.48	0.48
38:A1:1477:A:OP1	38:A1:3075:G:O2'	2.27	0.48
38:A1:1621:A:H2'	38:A1:1622:U:C6	2.48	0.48
38:A1:1759:C:H42	38:A1:1760:A:N6	2.12	0.48
38:A1:2534:G:H2'	38:A1:2535:A:C8	2.48	0.48
38:A1:2544:U:H2'	38:A1:2545:C:C6	2.49	0.48
38:A1:3160:U:H5''	38:A1:3396:U:H3'	1.95	0.48
42:AE:170:LYS:HD2	42:AE:173:MET:HE2	1.96	0.48
80:DC:130:ASP:CG	80:DC:159:LYS:HD3	2.39	0.48
80:DC:496:LYS:NZ	80:DC:553:PRO:HB2	2.29	0.48
6:BH:99:LEU:O	6:BH:112:ARG:NH1	2.43	0.47
10:BN:64:ARG:HD3	10:BN:70:LYS:HG2	1.95	0.47
22:BP:18:ARG:NH1	25:BS:90:ASN:OD1	2.47	0.47
31:Bg:246:SER:HB2	31:Bg:251:TRP:HB2	1.96	0.47
34:B5:400:A:H4'	34:B5:401:A:H5''	1.96	0.47
34:B5:628:G:N2	34:B5:971:A:H62	2.09	0.47
34:B5:844:A:H2'	34:B5:845:G:C8	2.49	0.47
34:B5:1125:A:OP1	76:An:18:ARG:NH2	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:AC:9:HIS:HA	37:AC:15:ALA:HA	1.96	0.47
38:A1:207:U:H2'	38:A1:208:C:H6	1.79	0.47
38:A1:562:C:H5''	55:AS:71:LYS:HE3	1.96	0.47
38:A1:1785:U:H2'	38:A1:1786:G:C8	2.48	0.47
38:A1:2267:C:H2'	38:A1:2268:U:C6	2.49	0.47
38:A1:2413:A:H2'	38:A1:2414:G:H8	1.79	0.47
38:A1:2540:A:H4'	38:A1:2541:U:H2'	1.96	0.47
38:A1:2812:C:H2'	38:A1:2813:A:C8	2.49	0.47
40:A4:57:C:H4'	40:A4:63:G:N7	2.28	0.47
48:AL:59:ARG:HD2	48:AL:69:VAL:HG12	1.95	0.47
64:Ab:36:ASP:O	64:Ab:40:ARG:HG3	2.14	0.47
79:E:68:PHE:HB2	79:E:112:ALA:HA	1.96	0.47
80:DC:123:ASP:OD2	80:DC:399:ARG:NH2	2.47	0.47
2:BB:27:LYS:HD3	2:BB:47:LEU:HD13	1.96	0.47
2:BB:136:ARG:CZ	34:B5:884:A:H5''	2.44	0.47
38:A1:26:A:N3	38:A1:328:U:O2'	2.43	0.47
38:A1:532:A:H2'	38:A1:533:A:C8	2.49	0.47
38:A1:2196:C:O2'	38:A1:2270:A:N3	2.43	0.47
38:A1:2442:G:H1	38:A1:2505:U:H3	1.62	0.47
38:A1:2453:U:O2	38:A1:2454:G:O2'	2.29	0.47
41:AD:191:ASP:HB3	41:AD:194:LEU:HB3	1.95	0.47
46:AI:135:ILE:HG22	46:AI:136:PHE:CD1	2.49	0.47
54:AR:23:TRP:HB3	54:AR:51:VAL:HG22	1.96	0.47
72:Aj:14:LYS:HE2	74:Al:51:ILE:HD11	1.96	0.47
2:BB:121:ILE:HD12	2:BB:207:LEU:HD11	1.96	0.47
7:BI:48:THR:OG1	7:BI:52:ASN:O	2.25	0.47
22:BP:53:PRO:O	22:BP:57:MET:HG3	2.14	0.47
23:BQ:23:LYS:O	23:BQ:64:ASP:N	2.44	0.47
34:B5:5:U:H2'	34:B5:6:G:C8	2.49	0.47
34:B5:85:A:N3	34:B5:148:A:O2'	2.45	0.47
34:B5:1026:A:N7	34:B5:1772:C:O2'	2.44	0.47
34:B5:1484:G:H2'	34:B5:1485:C:H6	1.79	0.47
38:A1:667:C:H4'	53:AQ:166:LEU:HD21	1.97	0.47
38:A1:1333:C:OP1	53:AQ:2:GLY:N	2.47	0.47
38:A1:2469:G:O2'	38:A1:2470:C:O4'	2.28	0.47
40:A4:8:C:H2'	40:A4:9:A:H8	1.78	0.47
80:DC:571:SER:HB3	80:DC:720:ALA:HB2	1.96	0.47
80:DC:677:PHE:HA	80:DC:823:ARG:NH2	2.29	0.47
80:DC:784:LEU:HD12	80:DC:794:PRO:HG3	1.96	0.47
2:BB:33:LYS:HE3	2:BB:95:ASN:HD21	1.78	0.47
4:BE:129:VAL:HG22	4:BE:139:VAL:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BJ:125:ALA:O	8:BJ:129:ILE:HG12	2.14	0.47
15:BY:57:VAL:HB	15:BY:60:PHE:CE2	2.49	0.47
20:BF:38:THR:HG23	20:BF:39:GLU:HG2	1.95	0.47
34:B5:182:A:H2'	34:B5:183:U:C6	2.48	0.47
34:B5:431:C:H2'	34:B5:432:G:C8	2.49	0.47
34:B5:968:U:H2'	34:B5:969:C:O4'	2.14	0.47
34:B5:1449:U:H2'	34:B5:1450:U:H6	1.80	0.47
34:B5:1704:U:H2'	34:B5:1705:C:C6	2.48	0.47
35:AA:7:ASN:HB2	38:A1:2183:A:H5''	1.96	0.47
38:A1:174:C:H2'	38:A1:175:C:C6	2.48	0.47
38:A1:207:U:H2'	38:A1:208:C:C6	2.50	0.47
38:A1:1250:G:H2'	38:A1:1251:A:C8	2.49	0.47
40:A4:63:G:H22	40:A4:97:A:H2	1.63	0.47
40:A4:106:C:H4'	40:A4:107:G:H5''	1.95	0.47
43:AF:138:TYR:CD2	43:AF:233:GLU:HB3	2.49	0.47
49:AM:19:ARG:HG2	49:AM:65:LEU:HD22	1.96	0.47
63:Aa:36:GLY:HA3	63:Aa:40:HIS:CE1	2.49	0.47
69:Ag:85:VAL:O	69:Ag:89:ILE:HG12	2.14	0.47
4:BE:48:LEU:HD11	4:BE:70:VAL:HG21	1.97	0.47
8:BJ:17:ARG:NH2	34:B5:4:C:H1'	2.29	0.47
13:BW:6:VAL:HB	13:BW:29:PRO:HD2	1.97	0.47
13:BW:40:VAL:HG11	13:BW:103:ILE:HD12	1.97	0.47
23:BQ:135:ARG:HH11	34:B5:1582:U:H5''	1.79	0.47
26:BT:28:LEU:HD21	26:BT:54:PHE:HD1	1.79	0.47
27:BU:57:ARG:HD2	34:B5:1382:A:N3	2.30	0.47
28:BZ:54:VAL:O	28:BZ:57:TYR:HB2	2.15	0.47
34:B5:209:U:H2'	34:B5:210:A:C8	2.49	0.47
34:B5:436:A2M:H8	34:B5:436:A2M:O5'	2.13	0.47
34:B5:1335:U:H2'	34:B5:1336:A:C8	2.49	0.47
34:B5:1714:A:H2'	34:B5:1715:G:C8	2.49	0.47
34:B5:1717:G:H2'	34:B5:1718:G:C8	2.49	0.47
35:AA:36:GLU:HG3	35:AA:91:GLY:HA2	1.97	0.47
38:A1:1158:A:H2'	38:A1:1159:A:H4'	1.96	0.47
38:A1:1447:G:O2'	38:A1:2355:G:O6	2.27	0.47
38:A1:2261:G:H1'	38:A1:2262:A:C2	2.45	0.47
38:A1:2930:A:H2'	38:A1:2931:C:C6	2.49	0.47
46:AI:52:LEU:HB3	46:AI:136:PHE:HB2	1.96	0.47
48:AL:144:THR:HG23	48:AL:145:PHE:CD2	2.49	0.47
73:Ak:63:LYS:HA	73:Ak:66:ILE:HG22	1.95	0.47
77:Ao:4:VAL:O	77:Ao:94:GLY:N	2.43	0.47
10:BN:99:ARG:HE	10:BN:143:SER:HB2	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:49:GLU:O	13:BW:64:GLN:NE2	2.47	0.47
24:BR:34:LEU:O	24:BR:38:ILE:HG12	2.15	0.47
25:BS:126:ARG:HB3	25:BS:133:VAL:HG12	1.96	0.47
25:BS:140:THR:HG23	25:BS:141:THR:OG1	2.15	0.47
34:B5:70:C:H2'	34:B5:71:A:C8	2.49	0.47
34:B5:156:A:H2'	34:B5:157:A:O4'	2.15	0.47
34:B5:340:U:H2'	34:B5:341:A:H8	1.80	0.47
35:AA:180:LEU:HD11	78:Ap:26:VAL:HG21	1.97	0.47
35:AA:181:LYS:HB2	38:A1:860:G:C5	2.50	0.47
38:A1:631:U:H2'	38:A1:632:G:C8	2.49	0.47
44:AG:72:PRO:HG2	44:AG:75:ILE:HG22	1.95	0.47
46:AI:177:ASP:OD1	46:AI:178:ARG:N	2.48	0.47
52:AP:13:LYS:NZ	52:AP:154:GLU:OE2	2.46	0.47
80:DC:28:VAL:HG13	80:DC:108:HIS:CE1	2.50	0.47
81:V:122:ARG:HB3	81:V:124:VAL:HG23	1.96	0.47
5:BG:56:ASN:OD1	34:B5:153:G:N2	2.44	0.47
7:BI:64:ASN:ND2	34:B5:257:A:N3	2.63	0.47
7:BI:99:ALA:HB3	34:B5:329:G:H5'	1.97	0.47
8:BJ:45:ILE:HD12	8:BJ:104:PHE:HB3	1.97	0.47
11:BO:125:SER:OG	34:B5:927:C:O2	2.32	0.47
19:BD:93:ASP:HB2	19:BD:96:LEU:HD13	1.96	0.47
20:BF:134:VAL:HA	20:BF:137:ILE:HG22	1.97	0.47
23:BQ:73:GLY:N	23:BQ:76:SER:OG	2.47	0.47
28:BZ:49:ARG:HA	28:BZ:52:LYS:HE3	1.97	0.47
31:Bg:196:ASN:N	31:Bg:219:GLU:OE2	2.35	0.47
31:Bg:203:THR:HG21	31:Bg:244:ALA:HA	1.97	0.47
34:B5:374:U:O2'	34:B5:603:U:OP1	2.33	0.47
34:B5:1364:G:H2'	34:B5:1365:C:C6	2.50	0.47
36:AB:68:HIS:CE1	36:AB:69:LYS:HG2	2.50	0.47
36:AB:166:ILE:HD13	36:AB:173:GLN:HG2	1.95	0.47
37:AC:286:VAL:HG23	53:AQ:32:LEU:HB2	1.97	0.47
38:A1:35:A:OP1	50:AN:86:ASN:ND2	2.46	0.47
38:A1:280:U:O4	77:Ao:45:ARG:NH2	2.47	0.47
38:A1:675:C:O2'	38:A1:679:U:OP1	2.30	0.47
38:A1:1750:A:OP2	73:Ak:42:LYS:NZ	2.34	0.47
38:A1:2228:A:H2'	38:A1:2229:A:C8	2.50	0.47
38:A1:2406:C:H2'	38:A1:2407:C:C6	2.50	0.47
38:A1:2674:A:H5''	47:AJ:105:GLY:HA3	1.95	0.47
38:A1:3121:U:H1'	38:A1:3122:A:H5''	1.97	0.47
38:A1:3190:C:OP1	51:AO:172[A]:ARG:NH2	2.45	0.47
40:A4:13:A:O2'	52:AP:121:GLN:O	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AF:112:ASN:ND2	43:AF:209:ASN:OD1	2.42	0.47
43:AF:170:GLU:HG3	43:AF:179:LEU:HD22	1.96	0.47
44:AG:227:ASP:HA	44:AG:230:LYS:HE3	1.95	0.47
51:AO:113[A]:ASP:N	51:AO:113[A]:ASP:OD1	2.48	0.47
54:AR:105:LEU:HD22	54:AR:135:LYS:HG3	1.97	0.47
57:AU:43:VAL:HB	57:AU:49:ASN:HB3	1.97	0.47
61:AY:85:VAL:HG11	61:AY:99:LEU:HD11	1.96	0.47
66:Ad:6:ASP:OD1	66:Ad:79:ARG:NH2	2.47	0.47
69:Ag:84:CYS:HA	69:Ag:87:GLU:HG2	1.95	0.47
78:Ap:44:LYS:HB3	78:Ap:46:THR:HG23	1.97	0.47
78:Ap:49:ARG:NH1	78:Ap:68:ALA:O	2.41	0.47
79:E:89:ASP:OD1	79:E:89:ASP:N	2.47	0.47
80:DC:147:LEU:HD22	80:DC:193:ALA:HB2	1.96	0.47
80:DC:608:PRO:HG3	80:DC:636:PHE:HD2	1.79	0.47
81:V:45:LEU:HD11	81:V:51:VAL:HG23	1.95	0.47
81:V:134:SER:HA	81:V:137:GLN:HB3	1.95	0.47
4:BE:185:GLY:H	4:BE:224:ASN:HB3	1.79	0.47
5:BG:12:SER:OG	5:BG:124:LEU:O	2.24	0.47
8:BJ:83:VAL:HG23	8:BJ:85:VAL:HG23	1.95	0.47
16:Ba:46:GLU:OE2	16:Ba:49:ALA:N	2.48	0.47
21:BK:47:GLN:HA	21:BK:50:THR:HG22	1.96	0.47
26:BT:77:ASN:HB3	26:BT:95:ASP:HB3	1.96	0.47
26:BT:130:ARG:O	26:BT:134:ARG:HG2	2.15	0.47
28:BZ:95:HIS:ND1	28:BZ:96:SER:O	2.48	0.47
31:Bg:256:THR:HG21	31:Bg:261:LYS:HD2	1.96	0.47
34:B5:70:C:H2'	34:B5:71:A:H8	1.79	0.47
34:B5:1656:U:C4	34:B5:1658:G:H1'	2.50	0.47
37:AC:341:SER:OG	38:A1:514:G:N3	2.42	0.47
38:A1:959:C:O2'	38:A1:2410:U:N3	2.44	0.47
38:A1:1169:A:H4'	43:AF:219:LYS:HD3	1.96	0.47
38:A1:1644:C:H5''	38:A1:1645:U:H5''	1.95	0.47
38:A1:1914:G:O2'	54:AR:82:LYS:O	2.31	0.47
38:A1:2232:A:H2'	38:A1:2233:A:C8	2.50	0.47
38:A1:3291:G:H2'	38:A1:3292:A:H8	1.80	0.47
58:AV:18:PRO:HA	58:AV:51:ALA:HA	1.96	0.47
80:DC:7:ASP:OD1	80:DC:8:GLN:N	2.48	0.47
80:DC:127:VAL:HG11	80:DC:143:LEU:HD13	1.96	0.47
82:EC:6815:U:H3'	82:EC:6816:A:H5''	1.96	0.47
1:BA:126:PRO:HG2	1:BA:151:SER:HB2	1.97	0.47
24:BR:103:ASP:O	24:BR:106:THR:OG1	2.32	0.47
26:BT:126:GLU:HG3	34:B5:1358:G:H4'	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:123:ILE:HD11	31:Bg:183:LEU:HD12	1.95	0.47
31:Bg:249:ARG:HG3	31:Bg:251:TRP:CD1	2.50	0.47
34:B5:127:G:H21	34:B5:178:U:H2'	1.79	0.47
34:B5:1260:U:H2'	34:B5:1261:G:C8	2.50	0.47
34:B5:1770:U:H2'	34:B5:1771:U:C6	2.50	0.47
35:AA:80:GLU:HB2	35:AA:170:ALA:HA	1.97	0.47
36:AB:213:GLU:OE2	36:AB:340:LYS:NZ	2.43	0.47
38:A1:1351:U:O2'	38:A1:1355:A:N6	2.47	0.47
38:A1:2344:U:H2'	38:A1:2345:A:C8	2.49	0.47
38:A1:3291:G:H2'	38:A1:3292:A:C8	2.50	0.47
39:A3:119:U:P	41:AD:258:LYS:HZ1	2.38	0.47
53:AQ:22:ASP:HA	53:AQ:27:LYS:HE2	1.96	0.47
67:Ae:3:SER:HB3	67:Ae:71:HIS:CE1	2.49	0.47
69:Ag:79:SER:HB3	69:Ag:80:ARG:HH11	1.79	0.47
77:Ao:100:LYS:HA	77:Ao:102:GLN:NE2	2.30	0.47
82:EC:6883:A:H2'	82:EC:6884:G:H4'	1.96	0.47
82:EC:6935:G:O2'	82:EC:6936:G:O4'	2.33	0.47
5:BG:103:GLY:H	5:BG:106:LEU:HD13	1.79	0.47
6:BH:58:LEU:HD11	6:BH:88:ARG:HH11	1.80	0.47
25:BS:39:GLY:N	34:B5:1566:U:H5''	2.30	0.47
27:BU:40:ASN:OD1	27:BU:43:LYS:NZ	2.47	0.47
31:Bg:209:THR:OG1	31:Bg:224:ASN:OD1	2.33	0.47
34:B5:607:G:H5'	34:B5:613:G:N2	2.29	0.47
34:B5:885:G:H2'	34:B5:886:U:C6	2.50	0.47
34:B5:1041:G:H2'	34:B5:1042:G:C8	2.50	0.47
34:B5:1773:4AC:OP1	76:An:3:ALA:HB3	2.15	0.47
37:AC:93:MET:HB2	38:A1:658:G:N2	2.30	0.47
38:A1:408:A:N3	38:A1:655:C:O2'	2.47	0.47
38:A1:815:G:OP2	72:Aj:31:LYS:NZ	2.34	0.47
38:A1:835:G:O2'	38:A1:857:G:N2	2.42	0.47
38:A1:1081:U:H4'	38:A1:1082:U:H5'	1.96	0.47
38:A1:3085:G:OP1	59:AW:34:SER:OG	2.30	0.47
40:A4:26:U:H2'	40:A4:27:U:C6	2.50	0.47
80:DC:139:THR:HA	80:DC:142:VAL:HG22	1.97	0.47
7:BI:10:LYS:HE3	7:BI:10:LYS:HB3	1.75	0.46
7:BI:41:LYS:NZ	34:B5:260:U:OP2	2.36	0.46
33:BM:138:GLU:HA	33:BM:141:SER:HB2	1.96	0.46
34:B5:133:U:O2	34:B5:134:U:O2'	2.33	0.46
34:B5:384:G:H2'	34:B5:385:A:C8	2.50	0.46
34:B5:1158:C:O2'	34:B5:1581:C:OP2	2.29	0.46
38:A1:358:G:N2	38:A1:361:A:OP2	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:708:G:N2	38:A1:711:A:OP2	2.44	0.46
38:A1:974:G:H5'	53:AQ:16:ARG:HG3	1.97	0.46
38:A1:1150:A:N6	38:A1:2369:G:O2'	2.47	0.46
38:A1:1336:U:H2'	38:A1:1337:A:C8	2.50	0.46
38:A1:1446:A:H5''	52:AP:65:SER:HB2	1.97	0.46
38:A1:1562:C:H2'	38:A1:1563:C:C6	2.50	0.46
38:A1:1768:U:H2'	38:A1:1769:G:C8	2.49	0.46
38:A1:2389:C:O2'	38:A1:3307:A:N1	2.48	0.46
38:A1:2853:A:H5'	46:AI:3:ARG:HH22	1.80	0.46
39:A3:108:A:H2'	39:A3:109:G:H8	1.80	0.46
58:AV:32:ARG:NH1	58:AV:64:LYS:HD3	2.30	0.46
79:E:60:ARG:HB3	79:E:171:ASN:ND2	2.30	0.46
81:V:111:ALA:HA	81:V:165:VAL:HG23	1.97	0.46
82:EC:6812:C:H2'	82:EC:6813:A:H8	1.80	0.46
3:BC:106:ASP:N	3:BC:106:ASP:OD1	2.46	0.46
5:BG:39:GLU:OE2	5:BG:47:GLY:N	2.42	0.46
28:BZ:68:ARG:NH2	82:EC:6865:G:O6	2.47	0.46
32:Bf:121:CYS:HB2	32:Bf:126:CYS:HB3	1.73	0.46
34:B5:1117:U:H2'	34:B5:1118:G:C8	2.50	0.46
38:A1:20:A:H2'	38:A1:21:G:C8	2.49	0.46
38:A1:589:A:H8	38:A1:590:G:C8	2.34	0.46
38:A1:1597:C:H2'	38:A1:1598:G:C8	2.50	0.46
38:A1:2407:C:H2'	38:A1:2408:U:C6	2.50	0.46
38:A1:2724:OMU:OP2	38:A1:2726:C:N4	2.48	0.46
38:A1:2918:G:H2'	38:A1:2919:A:H8	1.80	0.46
52:AP:29:THR:HG21	52:AP:146:ILE:HD11	1.97	0.46
52:AP:48:LEU:HD13	52:AP:92:GLN:HB3	1.97	0.46
57:AU:56:VAL:HG22	57:AU:65:VAL:HG22	1.96	0.46
65:Ac:30:THR:HG23	65:Ac:91:SER:HB2	1.97	0.46
3:BC:165:VAL:HG11	3:BC:210:THR:HA	1.96	0.46
6:BH:39:ARG:NH2	54:AR:189:ALA:O	2.48	0.46
7:BI:106:ALA:HB2	7:BI:165:LEU:HG	1.98	0.46
34:B5:334:G:H2'	34:B5:335:U:H6	1.79	0.46
34:B5:833:U:H5'	34:B5:834:G:H5''	1.97	0.46
34:B5:848:C:H2'	34:B5:849:C:C6	2.51	0.46
34:B5:939:A:H2'	34:B5:940:A:C8	2.50	0.46
34:B5:1405:G:H2'	34:B5:1406:A:H8	1.79	0.46
34:B5:1482:C:P	34:B5:1521:G:H22	2.37	0.46
34:B5:1741:U:H2'	34:B5:1742:U:C6	2.51	0.46
38:A1:158:G:H2'	38:A1:159:A:H8	1.79	0.46
38:A1:1268:G:H21	38:A1:1273:A:H62	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2728:G:N7	56:AT:87:LYS:NZ	2.62	0.46
41:AD:22:ARG:NE	41:AD:28:THR:OG1	2.45	0.46
45:AH:89:LYS:HB2	45:AH:183:HIS:HB3	1.97	0.46
66:Ad:20:LEU:HD11	66:Ad:32:ALA:HB2	1.98	0.46
73:Ak:40:GLN:NE2	73:Ak:55:VAL:HG13	2.30	0.46
80:DC:243:ARG:HD3	80:DC:257:TRP:CD2	2.51	0.46
80:DC:491:VAL:HG11	80:DC:556:ILE:HG23	1.96	0.46
1:BA:41:ARG:NH2	24:BR:106:THR:H	2.13	0.46
9:BL:40:LEU:H	34:B5:246:G:H1'	1.80	0.46
12:BV:2:GLU:HA	12:BV:8:LEU:HA	1.97	0.46
21:BK:62:GLN:NE2	30:Bd:23:VAL:O	2.49	0.46
23:BQ:140:LYS:NZ	34:B5:1192:C:O3'	2.45	0.46
27:BU:105:GLN:HG3	27:BU:106:ILE:HG23	1.98	0.46
34:B5:340:U:H2'	34:B5:341:A:C8	2.50	0.46
34:B5:1187:U:H2'	34:B5:1188:G:C8	2.51	0.46
34:B5:1592:A:H2'	34:B5:1593:A:H8	1.81	0.46
34:B5:1656:U:O4	34:B5:1745:G:N2	2.48	0.46
38:A1:1498:A:H2'	38:A1:1499:C:C6	2.50	0.46
38:A1:2447:A:N6	38:A1:2448:G:O6	2.48	0.46
38:A1:2898:G:OP2	45:AH:173:ARG:NH1	2.49	0.46
38:A1:3205:G:OP2	38:A1:3206:C:N4	2.44	0.46
39:A3:27:A:H2'	39:A3:28:C:C6	2.50	0.46
39:A3:29:C:H4'	47:AJ:9:MET:HE1	1.97	0.46
43:AF:104:GLN:NE2	53:AQ:4:ASP:OD2	2.47	0.46
56:AT:99:SER:OG	56:AT:101:CYS:SG	2.63	0.46
81:V:125:ASN:HD21	81:V:149:THR:HG23	1.80	0.46
81:V:139:LEU:HD23	81:V:139:LEU:HA	1.80	0.46
82:EC:6798:C:H2'	82:EC:6799:C:C6	2.50	0.46
7:BI:57:ALA:HB2	7:BI:177:GLY:HA2	1.98	0.46
24:BR:3:ARG:HD2	34:B5:1390:U:C6	2.51	0.46
31:Bg:200:ASN:ND2	31:Bg:241:PHE:HA	2.30	0.46
34:B5:108:A:H2'	34:B5:109:G:C8	2.50	0.46
34:B5:250:C:H2'	34:B5:251:A:C8	2.51	0.46
34:B5:874:C:H2'	34:B5:875:G:C8	2.50	0.46
34:B5:1350:U:H2'	34:B5:1351:G:C8	2.50	0.46
34:B5:1467:C:H2'	34:B5:1468:U:C6	2.51	0.46
38:A1:500:C:H4'	42:AE:80:ASN:HD21	1.80	0.46
38:A1:3066:U:H2'	38:A1:3067:C:C6	2.50	0.46
46:AI:68:ALA:HB2	46:AI:158:LYS:HB2	1.97	0.46
65:Ac:27:TYR:OH	65:Ac:55:GLU:OE1	2.31	0.46
80:DC:718:LEU:HA	80:DC:722:PRO:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:V:11:TYR:O	81:V:15:LEU:HG	2.14	0.46
82:EC:6804:A:O2'	82:EC:6808:G:N2	2.43	0.46
82:EC:6831:U:H1'	82:EC:6832:G:C8	2.50	0.46
3:BC:80:VAL:HG21	3:BC:125:ILE:HD12	1.98	0.46
8:BJ:171:ARG:HH22	34:B5:538:A:H2	1.62	0.46
20:BF:95:ASN:O	34:B5:1611:A:O2'	2.33	0.46
25:BS:132:ARG:HH12	25:BS:142:GLY:HA3	1.80	0.46
26:BT:65:ILE:HG21	26:BT:114:VAL:HG12	1.98	0.46
34:B5:255:U:H2'	34:B5:256:A:H8	1.81	0.46
34:B5:1757:G:H2'	34:B5:1758:U:H6	1.81	0.46
35:AA:20:THR:HA	35:AA:23:ARG:HG3	1.97	0.46
38:A1:406:G:OP1	38:A1:1415:U:O2'	2.26	0.46
38:A1:952:A:H4'	38:A1:968:G:N2	2.30	0.46
38:A1:1630:U:OP2	38:A1:1813:A:N6	2.43	0.46
38:A1:2463:G:H1'	79:E:162:VAL:HG21	1.97	0.46
38:A1:3015:G:H2'	38:A1:3016:A:H8	1.80	0.46
38:A1:3233:C:H2'	38:A1:3234:A:C8	2.50	0.46
44:AG:50:VAL:HG21	60:AX:27:ARG:HD3	1.96	0.46
44:AG:163:VAL:HG12	44:AG:166:LEU:HD12	1.96	0.46
58:AV:13:ILE:HD11	58:AV:121:GLU:HG2	1.97	0.46
62:AZ:46:ILE:HG23	62:AZ:68:ILE:HG23	1.97	0.46
80:DC:24:VAL:HG12	80:DC:126:LEU:HD22	1.98	0.46
6:BH:101:LYS:HD2	6:BH:102:PRO:HD2	1.98	0.46
34:B5:798:C:H2'	34:B5:799:A:H8	1.81	0.46
38:A1:255:A:H2'	38:A1:256:G:C8	2.51	0.46
38:A1:584:G:H2'	38:A1:585:A:H8	1.80	0.46
38:A1:2218:G:H2'	38:A1:2219:A:H8	1.81	0.46
41:AD:181:PRO:HG3	41:AD:198:TYR:CE2	2.50	0.46
49:AM:17:VAL:HG11	49:AM:74:ARG:HA	1.97	0.46
53:AQ:43:PRO:HA	53:AQ:46:LYS:HD2	1.98	0.46
57:AU:32:SER:OG	57:AU:83:TYR:OH	2.29	0.46
9:BL:75:VAL:HG22	9:BL:86:ILE:HG22	1.96	0.46
15:BY:20:ARG:NH1	15:BY:76:TYR:OH	2.47	0.46
23:BQ:47:LYS:HD2	23:BQ:47:LYS:HA	1.74	0.46
24:BR:36:ASP:OD1	24:BR:47:ARG:NH1	2.41	0.46
34:B5:162:A:H3'	34:B5:163:G:H8	1.80	0.46
34:B5:564:G:N2	34:B5:577:G:OP1	2.43	0.46
34:B5:922:G:H2'	34:B5:923:A:C8	2.51	0.46
34:B5:1357:A:H2'	34:B5:1358:G:H8	1.80	0.46
36:AB:106:TRP:HH2	36:AB:178:LEU:HD21	1.80	0.46
38:A1:263:C:H2'	38:A1:264:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1157:G:H2'	38:A1:1158:A:O4'	2.16	0.46
38:A1:2292:U:H2'	38:A1:2293:C:C6	2.50	0.46
46:AI:176:LEU:HD22	46:AI:180:GLU:HG2	1.98	0.46
82:EC:6834:U:O4'	82:EC:6872:A:N6	2.49	0.46
5:BG:74:LYS:HB3	5:BG:94:ARG:HD3	1.98	0.46
31:Bg:217:ASP:OD1	31:Bg:219:GLU:HG2	2.15	0.46
32:Bf:83:LYS:NZ	34:B5:1447:C:OP1	2.40	0.46
38:A1:209:A:H4'	38:A1:211:A:C8	2.51	0.46
38:A1:1020:G:H5''	38:A1:1021:G:C8	2.51	0.46
38:A1:2357:A:H2'	38:A1:2358:A:C8	2.50	0.46
40:A4:37:A:H5''	40:A4:39:G:O4'	2.15	0.46
40:A4:142:C:H2'	40:A4:143:U:C6	2.51	0.46
46:AI:38:LYS:HD3	46:AI:83:ASP:HB2	1.97	0.46
54:AR:105:LEU:HD23	54:AR:138:LEU:HD23	1.98	0.46
62:AZ:41:ALA:HB2	62:AZ:77:TYR:HE1	1.81	0.46
68:Af:6:ARG:NH1	68:Af:8:TYR:O	2.48	0.46
79:E:2:SER:OG	79:E:4:ILE:HG22	2.16	0.46
80:DC:223:ARG:HA	80:DC:241:MET:HE1	1.98	0.46
4:BE:11:ARG:NH1	4:BE:21:ASP:O	2.41	0.46
6:BH:44:LYS:HE3	6:BH:44:LYS:HB3	1.83	0.46
16:Ba:95:ARG:NH1	34:B5:1796:C:O2'	2.48	0.46
19:BD:132:LYS:N	19:BD:189:MET:O	2.49	0.46
25:BS:41:ARG:HA	25:BS:44:ASN:ND2	2.31	0.46
27:BU:101:LYS:HA	27:BU:104:THR:HG22	1.98	0.46
31:Bg:283:LYS:N	34:B5:1394:G:OP1	2.49	0.46
32:Bf:80:ARG:NH1	34:B5:1209:C:OP1	2.49	0.46
34:B5:15:U:H2'	34:B5:16:G:O4'	2.15	0.46
34:B5:605:A:OP2	34:B5:606:A:O2'	2.30	0.46
34:B5:890:C:H2'	34:B5:891:A:H8	1.81	0.46
34:B5:996:U:H2'	34:B5:997:G:C8	2.51	0.46
34:B5:1712:A:H3'	34:B5:1713:G:H8	1.81	0.46
38:A1:129:U:H2'	38:A1:130:A:C8	2.50	0.46
38:A1:184:U:H2'	38:A1:185:C:C6	2.50	0.46
38:A1:3064:U:H2'	38:A1:3065:G:H8	1.81	0.46
38:A1:3319:U:H5'	38:A1:3320:A:H5'	1.98	0.46
39:A3:77:G:N2	39:A3:102:A:OP2	2.41	0.46
46:AI:53:VAL:HG22	46:AI:134:ILE:HG12	1.98	0.46
52:AP:48:LEU:HD22	52:AP:88:VAL:HG13	1.98	0.46
79:E:94:ASN:HD21	79:E:123:LEU:HD13	1.81	0.46
80:DC:339:VAL:HG23	80:DC:340:LEU:HD12	1.98	0.46
4:BE:122:LYS:O	4:BE:162:ILE:N	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BR:13:SER:O	24:BR:17:ILE:HG12	2.16	0.45
34:B5:888:U:O2	34:B5:988:A:O2'	2.33	0.45
34:B5:980:G:H4'	34:B5:1776:A:H4'	1.96	0.45
38:A1:837:A:OP1	78:Ap:5:THR:OG1	2.31	0.45
38:A1:950:G:N1	38:A1:1368:U:OP2	2.38	0.45
38:A1:1378:U:H2'	38:A1:1379:G:C8	2.50	0.45
38:A1:1500:G:H2'	38:A1:1501:U:O4'	2.15	0.45
38:A1:2631:U:OP1	38:A1:2757:U:O2'	2.24	0.45
38:A1:3215:A:OP2	49:AM:125:LYS:NZ	2.48	0.45
45:AH:1:MET:HE3	45:AH:3:TYR:CE1	2.51	0.45
54:AR:171:ASP:O	54:AR:175:GLN:NE2	2.43	0.45
62:AZ:25:ILE:HA	62:AZ:43:VAL:HG12	1.98	0.45
64:Ab:32:LEU:CB	64:Ab:40:ARG:HH12	2.28	0.45
1:BA:76:ILE:HD13	1:BA:98:ILE:HB	1.98	0.45
1:BA:122:ILE:HG13	1:BA:144:ILE:HB	1.96	0.45
4:BE:154:ILE:HG22	4:BE:172:PHE:CD2	2.52	0.45
5:BG:98:ARG:NE	5:BG:105:ASP:OD2	2.47	0.45
11:BO:133:ARG:NH1	34:B5:1786:G:OP2	2.46	0.45
17:Bb:70:LYS:NZ	34:B5:1050:G:OP1	2.46	0.45
25:BS:46:VAL:HG21	25:BS:73:MET:HE2	1.97	0.45
31:Bg:22:SER:OG	31:Bg:69:GLN:O	2.24	0.45
34:B5:973:A:H4'	38:A1:848:A:N7	2.32	0.45
35:AA:28:LYS:HB2	35:AA:123:ARG:HB3	1.99	0.45
37:AC:18:ASN:ND2	37:AC:252:GLU:OE2	2.49	0.45
38:A1:1062:A:H5''	38:A1:1063:G:H5'	1.98	0.45
80:DC:367:ILE:HD13	80:DC:370:LYS:HD3	1.97	0.45
82:EC:6897:G:H2'	82:EC:6898:U:H6	1.82	0.45
1:BA:63:ILE:HD11	12:BV:36:VAL:HG22	1.96	0.45
5:BG:52:ILE:HG12	5:BG:109:LEU:HD21	1.98	0.45
9:BL:129:ARG:HD3	34:B5:115:G:H5'	1.97	0.45
14:BX:92:CYS:HA	14:BX:95:PHE:HD2	1.81	0.45
20:BF:131:GLN:HA	20:BF:134:VAL:HG12	1.98	0.45
29:Bc:15:VAL:HG12	29:Bc:28:VAL:HG12	1.98	0.45
34:B5:41:A:H2'	34:B5:438:A:N7	2.31	0.45
34:B5:130:C:O2'	34:B5:133:U:OP1	2.25	0.45
34:B5:780:A:H4'	34:B5:781:U:H5''	1.97	0.45
34:B5:1285:U:H4'	34:B5:1286:U:O5'	2.16	0.45
34:B5:1725:U:H2'	34:B5:1726:G:C8	2.51	0.45
35:AA:242:ARG:NH1	35:AA:243:THR:O	2.49	0.45
38:A1:1049:C:OP1	46:AI:21:ARG:NH2	2.50	0.45
38:A1:1237:G:N2	38:A1:1251:A:N1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1244:A:H4'	38:A1:1245:A:H8	1.82	0.45
38:A1:3052:G:H2'	38:A1:3053:G:C8	2.51	0.45
38:A1:3067:C:H3'	54:AR:62:ARG:HH22	1.81	0.45
38:A1:3165:A:H2'	38:A1:3166:C:C6	2.51	0.45
38:A1:3225:C:H2'	38:A1:3226:A:H8	1.81	0.45
40:A4:69:U:H2'	40:A4:70:G:O4'	2.17	0.45
41:AD:41:LYS:HB2	56:AT:68:THR:O	2.17	0.45
77:Ao:14:GLY:O	77:Ao:15:LYS:HG2	2.16	0.45
79:E:126:PRO:O	82:EC:6774:U:H5'	2.17	0.45
81:V:39:HIS:O	81:V:43:LYS:HG2	2.16	0.45
1:BA:50:VAL:O	1:BA:53:THR:OG1	2.28	0.45
1:BA:144:ILE:HG12	1:BA:158:VAL:HB	1.97	0.45
1:BA:195:TRP:CD1	1:BA:196:SER:H	2.33	0.45
7:BI:153:GLU:HB3	7:BI:156:VAL:HG12	1.99	0.45
19:BD:98:ALA:HA	19:BD:188:ILE:HD12	1.98	0.45
23:BQ:142:TYR:HE1	34:B5:1579:U:H5''	1.79	0.45
25:BS:35:ILE:HG23	25:BS:102:ALA:HB2	1.99	0.45
25:BS:127:HIS:CE1	25:BS:133:VAL:HG11	2.51	0.45
34:B5:1688:U:H2'	34:B5:1689:A:O4'	2.15	0.45
35:AA:220:GLY:O	38:A1:2245:C:O2'	2.33	0.45
38:A1:215:G:OP1	61:AY:12:ARG:NH1	2.42	0.45
38:A1:2111:G:H5''	59:AW:48:ARG:HE	1.82	0.45
38:A1:2160:G:H2'	38:A1:2161:G:C8	2.50	0.45
38:A1:2352:A:H5''	52:AP:83:TRP:O	2.16	0.45
45:AH:9:GLN:NE2	45:AH:52:LEU:HD21	2.31	0.45
45:AH:10:ILE:HD11	45:AH:72:LYS:HA	1.98	0.45
45:AH:91:ARG:NH2	45:AH:141:LYS:O	2.46	0.45
17:Bb:55:THR:OG1	17:Bb:59:CYS:O	2.35	0.45
19:BD:66:ILE:HD11	19:BD:86:LEU:HB2	1.98	0.45
19:BD:74:GLN:HA	19:BD:79:TYR:HB2	1.98	0.45
31:Bg:207:ASP:OD1	31:Bg:208:GLY:N	2.49	0.45
33:BM:31:VAL:HG23	33:BM:32:LEU:HD12	1.98	0.45
34:B5:1170:G:N2	34:B5:1571:C:O2'	2.50	0.45
34:B5:1744:A:N6	34:B5:1745:G:C2	2.84	0.45
35:AA:219:ILE:HD13	35:AA:223:SER:HB3	1.97	0.45
37:AC:286:VAL:HG11	53:AQ:31:LYS:HD3	1.97	0.45
38:A1:741:U:H4'	53:AQ:74:GLU:HB3	1.99	0.45
38:A1:792:G:H2'	38:A1:793:C:C6	2.52	0.45
38:A1:1897:G:O2'	58:AV:16:GLY:O	2.31	0.45
38:A1:2255:A:N6	38:A1:2260:U:H3	2.15	0.45
38:A1:2496:C:O2'	38:A1:2497:U:OP1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2617:U:O2'	46:AI:116:ARG:NH2	2.50	0.45
38:A1:3333:G:N2	38:A1:3369:G:O2'	2.49	0.45
39:A3:121:U:H5''	41:AD:265:TYR:HE1	1.81	0.45
48:AL:42:ARG:HH11	48:AL:51:LEU:HD12	1.81	0.45
53:AQ:166:LEU:HD23	53:AQ:166:LEU:HA	1.77	0.45
62:AZ:51:LEU:HD23	62:AZ:51:LEU:HA	1.85	0.45
73:AK:36:LYS:HD2	73:AK:37:PRO:HD2	1.98	0.45
2:BB:35:PRO:HD3	2:BB:98:THR:HG23	1.98	0.45
3:BC:188:LEU:HD13	3:BC:196:VAL:HG11	1.98	0.45
5:BG:4:ASN:ND2	34:B5:152:U:O2	2.42	0.45
6:BH:133:THR:OG1	6:BH:158:ASP:O	2.33	0.45
20:BF:104:ASN:OD1	34:B5:1587:A:O2'	2.27	0.45
20:BF:117:THR:HG21	20:BF:194:LEU:HD23	1.99	0.45
26:BT:102:ARG:NH2	34:B5:1502:G:N7	2.65	0.45
34:B5:319:U:H4'	34:B5:323:A:C8	2.51	0.45
34:B5:1208:A:O2'	34:B5:1270:G:OP2	2.22	0.45
34:B5:1266:U:H2'	34:B5:1267:G:C8	2.51	0.45
34:B5:1279:C:H2'	34:B5:1280:4AC:H6	1.98	0.45
34:B5:1360:A:N6	34:B5:1361:U:O2	2.50	0.45
34:B5:1471:A:H2	34:B5:1474:G:N3	2.15	0.45
34:B5:1654:G:H4'	76:AN:24:SER:HB3	1.97	0.45
34:B5:1654:G:C6	34:B5:1745:G:C2	3.04	0.45
35:AA:111:THR:HB	35:AA:136:ILE:HD13	1.99	0.45
38:A1:142:C:H2'	38:A1:143:G:O4'	2.16	0.45
38:A1:269:G:OP2	50:AN:44:ARG:NH2	2.50	0.45
38:A1:787:G:H2'	38:A1:788:C:C6	2.51	0.45
38:A1:1241:U:N3	38:A1:1244:A:OP2	2.49	0.45
38:A1:1367:G:OP1	67:AE:45:ARG:NH2	2.49	0.45
38:A1:1523:U:OP1	38:A1:1607:U:N3	2.48	0.45
38:A1:1629:U:H1'	62:AZ:115:LYS:HD3	1.97	0.45
38:A1:1646:G:HO2'	38:A1:1808:G:H22	1.62	0.45
38:A1:1676:A:OP2	57:AU:72:SER:OG	2.24	0.45
54:AR:147:ALA:O	54:AR:150:GLN:HG3	2.17	0.45
58:AV:24:ASN:ND2	58:AV:97:ASP:OD2	2.50	0.45
79:E:39:LYS:N	79:E:200:ASN:O	2.44	0.45
80:DC:176:GLN:O	80:DC:180:ARG:HG3	2.16	0.45
80:DC:693:LEU:HD12	80:DC:700:ARG:HB2	1.99	0.45
1:BA:103:THR:O	1:BA:106:SER:OG	2.31	0.45
2:BB:216:LYS:NZ	34:B5:885:G:OP1	2.43	0.45
16:BA:30:ILE:HD13	16:BA:74:CYS:HA	1.98	0.45
23:BQ:33:GLY:H	23:BQ:66:ARG:NH1	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BT:88:VAL:HG12	26:BT:89:ARG:HH11	1.82	0.45
26:BT:127:ASN:HA	26:BT:130:ARG:HG3	1.98	0.45
27:BU:59:PRO:HA	34:B5:1382:A:H5'	1.98	0.45
34:B5:327:U:O4	34:B5:328:A:N6	2.49	0.45
34:B5:1263:G:H2'	34:B5:1264:G:O4'	2.16	0.45
38:A1:285:A:O2'	77:Ao:45:ARG:NH1	2.49	0.45
38:A1:759:U:H2'	38:A1:760:G:O4'	2.16	0.45
38:A1:1290:A:H2'	38:A1:1291:A:C8	2.51	0.45
38:A1:2611:U:H2'	38:A1:2612:U:C6	2.52	0.45
38:A1:2631:U:H2'	38:A1:2632:G:H8	1.82	0.45
38:A1:2683:U:H2'	38:A1:2684:C:H6	1.81	0.45
38:A1:2812:C:H2'	38:A1:2813:A:H8	1.82	0.45
41:AD:116:ASP:N	41:AD:116:ASP:OD1	2.50	0.45
68:Af:58:GLU:OE1	68:Af:63:LYS:NZ	2.49	0.45
72:Aj:48:ASN:OD1	72:Aj:54:LYS:NZ	2.32	0.45
80:DC:26:ALA:HB1	80:DC:30:HIS:HB2	1.97	0.45
80:DC:94:ASP:OD1	80:DC:95:GLY:N	2.50	0.45
80:DC:399:ARG:HD3	80:DC:401:PHE:CE1	2.52	0.45
80:DC:667:PHE:O	80:DC:671:THR:HG22	2.17	0.45
80:DC:777:SER:OG	80:DC:796:MET:HE1	2.16	0.45
21:BK:24:LYS:HA	21:BK:63:TYR:HA	1.99	0.45
23:BQ:128:LYS:O	23:BQ:137:ARG:NH2	2.38	0.45
24:BR:100:LEU:HB3	24:BR:102:VAL:HG23	1.99	0.45
34:B5:182:A:H2'	34:B5:183:U:H6	1.82	0.45
34:B5:304:U:H2'	34:B5:305:C:C6	2.52	0.45
37:AC:141:ARG:NH1	38:A1:1385:C:OP1	2.49	0.45
38:A1:999:G:N3	38:A1:1002:A:N6	2.65	0.45
38:A1:2312:A:H2'	38:A1:2315:G:H21	1.82	0.45
38:A1:2427:U:H2'	38:A1:2428:U:C6	2.52	0.45
38:A1:3267:A:H2'	42:AE:69:PHE:CZ	2.52	0.45
40:A4:46:G:OP1	74:Al:18:LYS:NZ	2.42	0.45
40:A4:47:C:H1'	40:A4:61:A:H2'	1.98	0.45
80:DC:220:PHE:HB3	80:DC:328:LEU:HD13	1.98	0.45
80:DC:346:VAL:HG22	80:DC:372:CYS:SG	2.57	0.45
80:DC:725:GLN:HG3	80:DC:803:THR:HB	1.98	0.45
4:BE:87:MET:HE1	4:BE:123:LEU:N	2.32	0.45
25:BS:12:GLN:NE2	25:BS:58:ALA:O	2.50	0.45
35:AA:2:GLY:O	38:A1:925:A:N6	2.33	0.45
36:AB:36:ASP:OD2	36:AB:39:LYS:NZ	2.33	0.45
38:A1:1657:C:O2'	38:A1:1797:A:OP2	2.24	0.45
46:AI:51:HIS:CD2	46:AI:168:SER:HB2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:836:GLN:HA	80:DC:839:TYR:CE2	2.52	0.45
82:EC:6768:U:O4	82:EC:6823:U:N3	2.50	0.45
34:B5:698:U:H2'	34:B5:699:U:C6	2.51	0.45
34:B5:766:U:O4	34:B5:770:A:N7	2.50	0.45
34:B5:1658:G:H2'	34:B5:1659:A:H8	1.82	0.45
37:AC:160:GLN:NE2	37:AC:213:ASN:O	2.48	0.45
38:A1:418:A:N1	40:A4:5:U:H5	2.14	0.45
38:A1:1193:A:OP1	51:AO:49[A]:ARG:NH2	2.50	0.45
38:A1:2747:A:OP1	41:AD:176:SER:OG	2.35	0.45
38:A1:2768:U:H2'	38:A1:2769:A:C8	2.49	0.45
38:A1:2852:C:N3	46:AI:158:LYS:NZ	2.63	0.45
41:AD:119:TYR:OH	41:AD:139:PRO:O	2.29	0.45
42:AE:96:VAL:HG12	42:AE:144:ALA:HB3	1.98	0.45
63:Aa:76:ASP:OD2	63:Aa:77:LYS:HG2	2.17	0.45
78:Ap:17:ARG:H	78:Ap:17:ARG:HG2	1.60	0.45
79:E:76:ARG:HH21	79:E:144:LEU:H	1.64	0.45
80:DC:141:THR:HG22	80:DC:144:ARG:NH2	2.32	0.45
80:DC:676:ILE:HA	80:DC:832:VAL:HG23	1.99	0.45
4:BE:124:GLY:N	4:BE:160:VAL:O	2.51	0.44
6:BH:63:PRO:C	6:BH:65:PRO:HD3	2.42	0.44
15:BY:7:ILE:HG13	15:BY:43:LYS:HG2	1.98	0.44
21:BK:46:LEU:HD22	21:BK:66:TYR:CD1	2.52	0.44
22:BP:98:ASN:ND2	22:BP:121:ILE:O	2.33	0.44
34:B5:473:A:H2'	34:B5:474:A:O4'	2.17	0.44
34:B5:1055:U:H2'	34:B5:1056:U:C6	2.52	0.44
38:A1:2945:G:O2'	38:A1:2948:OMC:OP2	2.25	0.44
38:A1:3158:G:H1	38:A1:3292:A:H61	1.66	0.44
38:A1:3217:C:C2	52:AP:182:ILE:HD11	2.52	0.44
41:AD:93:THR:HG1	41:AD:158:ARG:NH1	2.15	0.44
47:AJ:115:LYS:HG3	47:AJ:116:TYR:H	1.82	0.44
54:AR:3:ASN:HD21	54:AR:5:ARG:NH1	2.14	0.44
67:Ae:95:GLU:OE1	67:Ae:120:THR:OG1	2.31	0.44
70:Ah:31:LEU:HB3	70:Ah:44:ILE:HG22	1.99	0.44
70:Ah:66:VAL:HG12	70:Ah:80:LEU:HD11	1.98	0.44
80:DC:255:LYS:HD3	80:DC:255:LYS:HA	1.87	0.44
5:BG:13:GLN:HE22	34:B5:151:G:H21	1.65	0.44
7:BI:81:VAL:HA	7:BI:102:VAL:HG12	1.99	0.44
12:BV:55:LEU:HD13	12:BV:65:SER:HB2	1.99	0.44
15:BY:127:LYS:NZ	34:B5:151:G:OP2	2.49	0.44
34:B5:393:C:H2'	34:B5:394:C:C6	2.52	0.44
34:B5:888:U:H2'	34:B5:889:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:896:U:H2'	34:B5:897:C:C6	2.51	0.44
34:B5:1163:A:N3	34:B5:1613:U:O2'	2.38	0.44
34:B5:1733:C:H2'	34:B5:1734:U:H6	1.82	0.44
35:AA:113:VAL:HG12	35:AA:166:ILE:HD13	1.99	0.44
37:AC:107:ARG:HA	38:A1:664:U:H5'	1.99	0.44
38:A1:2501:U:H2'	38:A1:2503:G:C8	2.52	0.44
39:A3:48:U:H1'	41:AD:222:LEU:HD22	1.99	0.44
67:Ae:54:LYS:H	67:Ae:57:TYR:HD2	1.65	0.44
69:Ag:20:ILE:HB	69:Ag:32:ALA:HB1	1.99	0.44
2:BB:141:ALA:HB1	2:BB:207:LEU:HD12	1.99	0.44
6:BH:106:SER:OG	34:B5:697:C:OP2	2.34	0.44
8:BJ:6:ARG:HH12	34:B5:38:C:H5''	1.83	0.44
14:BX:59:ILE:HG13	18:Be:4:VAL:HG12	1.98	0.44
15:BY:26:ASP:HB2	15:BY:68:LYS:HZ1	1.83	0.44
19:BD:67:ASN:HB3	21:BK:95:ARG:HH21	1.82	0.44
34:B5:110:U:OP1	34:B5:753:A:O2'	2.36	0.44
34:B5:1662:G:H2'	34:B5:1663:G:C8	2.52	0.44
34:B5:1755:A:H4'	34:B5:1756[A]:A:H2	1.83	0.44
38:A1:629:U:H2'	38:A1:630:A:C8	2.53	0.44
38:A1:1910:A:H2'	38:A1:1911:A:C8	2.52	0.44
38:A1:2585:G:C6	60:AX:24:LEU:HD21	2.52	0.44
38:A1:3295:A:H2'	38:A1:3296:A:H8	1.81	0.44
38:A1:3298:C:C2	38:A1:3299:A:C8	3.05	0.44
59:AW:47:ARG:HD2	59:AW:58:HIS:CE1	2.52	0.44
77:Ao:102:GLN:O	77:Ao:104:LEU:HD12	2.16	0.44
80:DC:593:ILE:HG12	80:DC:685:ARG:HB2	2.00	0.44
3:BC:111:VAL:O	3:BC:136:VAL:HA	2.18	0.44
4:BE:206:ASP:HB2	4:BE:222:LEU:HD22	1.98	0.44
5:BG:13:GLN:HE22	34:B5:151:G:N2	2.15	0.44
5:BG:77:LEU:HD12	5:BG:95:LYS:HB2	1.98	0.44
6:BH:64:VAL:HG23	6:BH:67:LEU:HD23	1.99	0.44
7:BI:141:ARG:NH1	34:B5:196:G:N7	2.65	0.44
11:BO:81:VAL:HB	11:BO:115:ILE:HG12	1.99	0.44
23:BQ:31:VAL:N	23:BQ:34:SER:O	2.42	0.44
31:Bg:114:ASP:N	31:Bg:114:ASP:OD1	2.50	0.44
34:B5:447:U:H2'	34:B5:448:C:O4'	2.17	0.44
36:AB:250:ALA:HB3	38:A1:2880:U:H1'	1.98	0.44
37:AC:65:TRP:HB3	37:AC:69:ARG:HD3	1.99	0.44
38:A1:129:U:H3	38:A1:139:G:H1	1.64	0.44
38:A1:182:U:H2'	38:A1:183:G:H8	1.81	0.44
38:A1:516:A:H2'	38:A1:517:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:737:G:H2'	38:A1:738:A:C8	2.53	0.44
38:A1:1083:G:H2'	38:A1:1084:A:H8	1.82	0.44
38:A1:1597:C:H5'	38:A1:1696:A:H1'	1.98	0.44
38:A1:1677:G:OP1	57:AU:97:SER:OG	2.30	0.44
38:A1:1750:A:H1'	38:A1:1752:A:N7	2.32	0.44
40:A4:75:G:H2'	40:A4:76:C:C6	2.53	0.44
47:AJ:45:PRO:HB3	47:AJ:69:VAL:HB	2.00	0.44
47:AJ:109:HIS:ND1	47:AJ:112:LEU:HD23	2.32	0.44
82:EC:6789:G:OP2	82:EC:6805:C:N4	2.49	0.44
4:BE:133:LYS:HA	4:BE:133:LYS:HD2	1.73	0.44
10:BN:62:GLN:HB2	10:BN:65:VAL:HG22	2.00	0.44
15:BY:8:ARG:HB2	34:B5:780:A:C8	2.52	0.44
15:BY:89:TYR:CD2	34:B5:525:A:H5''	2.52	0.44
20:BF:221:ALA:HA	20:BF:224:ASN:HD22	1.83	0.44
26:BT:39:THR:HA	26:BT:100:ILE:HD12	1.98	0.44
32:Bf:119:ARG:O	32:Bf:132:LEU:N	2.45	0.44
34:B5:1177:C:H5''	34:B5:1189:A:H61	1.82	0.44
34:B5:1253:U:H2'	34:B5:1254:U:C6	2.52	0.44
34:B5:1575:G7M:O2'	34:B5:1576:A:O4'	2.26	0.44
35:AA:14:SER:OG	35:AA:15:ILE:N	2.50	0.44
36:AB:17:LEU:HD21	36:AB:233:TRP:HH2	1.82	0.44
36:AB:242:THR:HB	36:AB:246:LEU:HB3	2.00	0.44
38:A1:662:U:H2'	38:A1:663:OMC:C6	2.52	0.44
38:A1:1522:U:OP1	60:AX:123:TYR:OH	2.32	0.44
38:A1:2463:G:H2'	38:A1:2464:U:C6	2.52	0.44
39:A3:16:U:H2'	39:A3:17:A:C8	2.52	0.44
47:AJ:19:LEU:HD11	47:AJ:125:MET:SD	2.56	0.44
52:AP:118:GLN:HG2	52:AP:147:GLU:OE2	2.17	0.44
60:AX:113:LEU:HD11	60:AX:121:LYS:HE2	1.98	0.44
79:E:59:PRO:O	79:E:171:ASN:ND2	2.44	0.44
82:EC:6867:C:H2'	82:EC:6868:C:C6	2.52	0.44
82:EC:6897:G:H2'	82:EC:6898:U:C6	2.52	0.44
1:BA:188:LEU:HD21	1:BA:195:TRP:CD1	2.53	0.44
4:BE:151:ASP:O	4:BE:154:ILE:HG12	2.18	0.44
5:BG:159:ARG:HD2	5:BG:172:ALA:HB2	1.99	0.44
7:BI:37:LYS:C	7:BI:59:ARG:HA	2.43	0.44
7:BI:103:GLN:HA	7:BI:165:LEU:O	2.17	0.44
15:BY:37:LYS:HG3	34:B5:522:U:H5''	2.00	0.44
20:BF:159:ALA:HB2	20:BF:224:ASN:HB2	2.00	0.44
23:BQ:74:HIS:HE2	34:B5:1481:C:HO2'	1.56	0.44
33:BM:137:MET:HA	33:BM:140:PHE:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:907:A:H2'	34:B5:908:U:H6	1.82	0.44
34:B5:1354:G:H1'	34:B5:1373:C:H1'	2.00	0.44
34:B5:1541:G:N2	34:B5:1569:A:OP2	2.51	0.44
37:AC:23:PRO:HD2	37:AC:26:PHE:CD2	2.52	0.44
38:A1:268:A:H61	38:A1:295:A:H3'	1.83	0.44
38:A1:945:C:H2'	38:A1:946:U:C6	2.52	0.44
38:A1:2526:C:H2'	38:A1:2527:G:C8	2.53	0.44
38:A1:3285:C:H2'	38:A1:3286:G:C8	2.53	0.44
39:A3:77:G:H5''	55:AS:46:GLN:O	2.18	0.44
50:AN:8:GLU:HB2	50:AN:50:ARG:HH22	1.82	0.44
61:AY:74:TYR:HE2	61:AY:77:LYS:HG3	1.82	0.44
79:E:105:LYS:HB2	79:E:105:LYS:HE2	1.78	0.44
79:E:125:GLY:H	79:E:126:PRO:HD2	1.83	0.44
80:DC:29:ASP:HB3	85:DC:901:GDP:H1'	1.98	0.44
1:BA:110:TYR:CD2	3:BC:38:VAL:HG11	2.52	0.44
16:Ba:33:ASP:OD1	16:Ba:34:LYS:N	2.50	0.44
20:BF:144:GLU:HA	20:BF:162:VAL:HG23	2.00	0.44
33:BM:122:VAL:HG12	33:BM:124:LYS:H	1.81	0.44
34:B5:1147:A:O2'	34:B5:1636:C:OP2	2.32	0.44
34:B5:1352:G:H2'	34:B5:1353:U:O4'	2.17	0.44
34:B5:1752:U:H2'	34:B5:1753:A:C8	2.50	0.44
37:AC:216:VAL:HA	37:AC:227:THR:HG21	1.99	0.44
38:A1:796:U:H2'	38:A1:797:U:C6	2.53	0.44
38:A1:1072:G:H2'	38:A1:1073:U:C6	2.53	0.44
38:A1:1184:A:H2'	38:A1:1185:C:C6	2.52	0.44
38:A1:1299:U:O2'	75:Am:114:LYS:O	2.28	0.44
38:A1:1641:U:O2'	38:A1:1642:A:H3'	2.17	0.44
38:A1:1666:G:H2'	38:A1:1667:A:H8	1.82	0.44
47:AJ:32:ARG:NE	47:AJ:120:ILE:O	2.51	0.44
52:AP:19:GLY:HA3	52:AP:22:LEU:HD11	1.99	0.44
61:AY:54:ASP:HB2	61:AY:70:ILE:HD12	1.98	0.44
79:E:76:ARG:HE	79:E:144:LEU:HB3	1.83	0.44
80:DC:236:ASP:OD1	80:DC:236:ASP:N	2.51	0.44
80:DC:399:ARG:HD3	80:DC:401:PHE:HE1	1.83	0.44
82:EC:6828:G:H2'	82:EC:6829:A:H8	1.82	0.44
2:BB:134:VAL:HG13	2:BB:218:LEU:HB2	1.99	0.44
2:BB:137:ILE:HD13	2:BB:215:VAL:HG22	1.99	0.44
7:BI:171:SER:OG	7:BI:178:ARG:O	2.26	0.44
10:BN:34:ILE:O	10:BN:38:VAL:HG23	2.18	0.44
22:BP:24:LYS:HA	22:BP:24:LYS:HD2	1.74	0.44
34:B5:1499:G:H1	34:B5:1508:U:H3	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1593:A:H2'	34:B5:1594:G:C8	2.53	0.44
34:B5:1680:G:O2'	34:B5:1720:G:N2	2.47	0.44
38:A1:68:C:O3'	50:AN:177:GLY:HA2	2.18	0.44
38:A1:184:U:H2'	38:A1:185:C:H6	1.83	0.44
38:A1:656:A:H2'	38:A1:657:A:C8	2.52	0.44
38:A1:966:U:OP1	63:Aa:44:ASN:ND2	2.48	0.44
38:A1:1791:C:H2'	38:A1:1792:C:C6	2.52	0.44
38:A1:2964:G:N2	38:A1:2966:G:H3'	2.33	0.44
38:A1:3302:U:H2'	38:A1:3303:G:C8	2.53	0.44
43:AF:239:LEU:HG	43:AF:243:MET:HE2	2.00	0.44
80:DC:171:LYS:HE3	80:DC:274:ASN:HB3	2.00	0.44
80:DC:511:LEU:HD13	80:DC:545:LEU:HD13	2.00	0.44
9:BL:14:GLN:HB3	9:BL:54:ILE:HG13	1.99	0.44
10:BN:124:ARG:NH2	34:B5:967:A:OP2	2.45	0.44
12:BV:7:GLN:O	12:BV:9:VAL:HG13	2.18	0.44
12:BV:58:TYR:CZ	12:BV:62:ARG:HD2	2.53	0.44
14:BX:58:GLY:N	18:Be:4:VAL:O	2.51	0.44
31:Bg:198:ASN:HD21	31:Bg:216:LYS:HE3	1.83	0.44
34:B5:485:A:H8	34:B5:486:G:O4'	2.01	0.44
34:B5:826:U:H2'	34:B5:827:C:C6	2.52	0.44
34:B5:1745:G:H4'	34:B5:1746:A:H5'	1.98	0.44
34:B5:1787:C:H2'	34:B5:1788:G:C8	2.52	0.44
38:A1:273:A:H2'	38:A1:274:G:H8	1.83	0.44
38:A1:791:A:H2'	38:A1:792:G:H8	1.82	0.44
38:A1:1432:C:O2'	38:A1:1434:G:OP2	2.36	0.44
38:A1:1721:U:OP2	54:AR:124:TYR:OH	2.24	0.44
38:A1:1768:U:H2'	38:A1:1769:G:H8	1.82	0.44
46:AI:77:THR:HG23	46:AI:82:ARG:HA	1.99	0.44
53:AQ:177:GLY:O	53:AQ:186:VAL:N	2.45	0.44
60:AX:46:TYR:HD2	70:Ah:75:TYR:HB3	1.82	0.44
62:AZ:2:ALA:N	65:Ac:63:SER:O	2.51	0.44
66:Ad:10:ARG:HD3	66:Ad:108:VAL:HG22	1.99	0.44
69:Ag:41:ARG:NH2	69:Ag:51:LEU:O	2.51	0.44
80:DC:380:LEU:HG	80:DC:469:LEU:HB2	1.99	0.44
80:DC:638:PRO:HD2	80:DC:642:GLY:HA3	2.00	0.44
4:BE:5:PRO:HD2	34:B5:398:G:H21	1.82	0.43
10:BN:73:ARG:HD3	34:B5:859:A:C5	2.53	0.43
16:Ba:46:GLU:CD	16:Ba:48:ALA:H	2.26	0.43
19:BD:173:ARG:HD3	19:BD:173:ARG:HA	1.81	0.43
24:BR:3:ARG:HH22	34:B5:1415:U:H5''	1.83	0.43
26:BT:38:LYS:O	26:BT:39:THR:OG1	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:78:A:H2'	34:B5:79:C:C6	2.53	0.43
34:B5:907:A:H2'	34:B5:908:U:C6	2.53	0.43
34:B5:1373:C:H2'	34:B5:1374:C:H6	1.82	0.43
36:AB:218:ILE:HG23	36:AB:276:THR:HG22	2.00	0.43
36:AB:347:SER:C	36:AB:349:LYS:H	2.26	0.43
38:A1:673:U:H2'	38:A1:674:G:C8	2.53	0.43
38:A1:1822:C:H2'	38:A1:1823:A:C8	2.53	0.43
38:A1:2507:C:H2'	38:A1:2508:U:C6	2.53	0.43
38:A1:2810:C:OP2	38:A1:2955:U:O2'	2.36	0.43
43:AF:151:ARG:HE	43:AF:244:ASN:HB2	1.83	0.43
70:Ah:118:ILE:C	70:Ah:119:LYS:HD2	2.43	0.43
73:Ak:5:ILE:HD11	73:Ak:52:TYR:CD2	2.52	0.43
2:BB:31:ASP:OD1	2:BB:45:LYS:HG2	2.18	0.43
6:BH:14:THR:HG22	6:BH:15:GLU:HG2	1.99	0.43
9:BL:96:LYS:NZ	34:B5:374:U:OP1	2.45	0.43
28:BZ:75:LEU:HA	28:BZ:78:ILE:HG12	2.00	0.43
34:B5:434:G:N1	34:B5:437:A:OP2	2.51	0.43
34:B5:1127:G:P	76:An:11:ARG:HH12	2.41	0.43
38:A1:1128:U:OP1	46:AI:4:ARG:NH1	2.38	0.43
38:A1:1746:U:O2'	73:Ak:4:GLU:OE1	2.26	0.43
38:A1:2526:C:H2'	38:A1:2527:G:H8	1.83	0.43
38:A1:2736:A:H2'	38:A1:2737:C:O4'	2.18	0.43
38:A1:2890:A:O2'	38:A1:2933:A:N3	2.41	0.43
38:A1:3182:G:H2'	38:A1:3183:A:C8	2.53	0.43
41:AD:33:ARG:HH12	41:AD:50:ARG:HH12	1.66	0.43
44:AG:116:VAL:HA	44:AG:120:LYS:HG2	2.00	0.43
46:AI:47:PRO:HD2	46:AI:141:LYS:HA	1.99	0.43
52:AP:167:ARG:HB2	68:Af:60:ARG:HE	1.83	0.43
53:AQ:67:ILE:HG12	53:AQ:140:LEU:HD12	2.00	0.43
53:AQ:182:LYS:NZ	63:Aa:55:LYS:O	2.42	0.43
68:Af:16:TYR:OH	68:Af:89:LEU:O	2.31	0.43
79:E:77:ALA:HB1	79:E:82:VAL:HG23	2.00	0.43
80:DC:250:PHE:HB2	80:DC:257:TRP:CZ3	2.53	0.43
82:EC:6809:G:H2'	82:EC:6810:U:C6	2.53	0.43
16:Ba:12:LYS:NZ	34:B5:1029:U:OP2	2.49	0.43
20:BF:40:ILE:HD11	23:BQ:54:LEU:HD13	2.00	0.43
21:BK:59:PHE:HE2	21:BK:62:GLN:HG3	1.84	0.43
22:BP:85:ILE:HD13	22:BP:111:MET:HG3	2.00	0.43
29:Bc:42:ARG:HD3	29:Bc:42:ARG:HA	1.82	0.43
34:B5:186:C:H2'	34:B5:187:G:O4'	2.19	0.43
34:B5:1628:U:H2'	34:B5:1629:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1684:U:H2'	34:B5:1685:G:H8	1.83	0.43
36:AB:206:ASP:OD1	36:AB:206:ASP:N	2.48	0.43
38:A1:385:A:H2'	38:A1:386:A:C8	2.53	0.43
38:A1:872:U:H2'	38:A1:873:C:C6	2.52	0.43
38:A1:1127:G:OP2	46:AI:98:ARG:NH2	2.41	0.43
38:A1:1498:A:H2'	38:A1:1499:C:H6	1.83	0.43
38:A1:2144:A:H1'	38:A1:2281:A2M:N6	2.33	0.43
38:A1:2152:A:H2'	38:A1:2153:U:C6	2.53	0.43
38:A1:2660:G:OP1	38:A1:2750:U:O2'	2.36	0.43
38:A1:2834:G:H2'	38:A1:2835:U:H6	1.83	0.43
38:A1:3027:A:O2'	80:DC:27:HIS:HE1	2.00	0.43
41:AD:108:ARG:CZ	41:AD:253:PHE:HB2	2.48	0.43
62:AZ:96:VAL:HA	62:AZ:100:THR:HG21	2.01	0.43
63:Aa:134:ALA:O	63:Aa:138:ILE:HD12	2.18	0.43
73:Ak:40:GLN:NE2	73:Ak:41:THR:O	2.52	0.43
78:Ap:3:LYS:HD2	78:Ap:3:LYS:HA	1.84	0.43
80:DC:210:ALA:HB2	80:DC:337:MET:SD	2.59	0.43
6:BH:14:THR:HG22	6:BH:15:GLU:N	2.32	0.43
16:Ba:49:ALA:HB1	16:Ba:53:LEU:HD23	1.99	0.43
20:BF:72:HIS:NE2	34:B5:1610:G:OP1	2.38	0.43
31:Bg:251:TRP:CH2	31:Bg:271:VAL:HG21	2.53	0.43
34:B5:36:C:H5''	34:B5:530:C:H5''	1.99	0.43
34:B5:368:U:H2'	34:B5:369:A:O4'	2.18	0.43
34:B5:1148:C:H2'	34:B5:1149:G:H8	1.83	0.43
34:B5:1151:A:H2'	34:B5:1152:A:C8	2.53	0.43
34:B5:1645:G:H1'	38:A1:2255:A:N1	2.34	0.43
37:AC:181:VAL:O	37:AC:182:LEU:HG	2.18	0.43
38:A1:166:C:H2'	38:A1:167:U:C6	2.53	0.43
38:A1:1836:C:H41	74:AI:3:ALA:HB2	1.83	0.43
38:A1:2615:G:H2'	38:A1:2616:C:H6	1.83	0.43
39:A3:112:G:H2'	39:A3:113:C:C6	2.54	0.43
42:AE:96:VAL:HG11	42:AE:145:LEU:HG	2.01	0.43
61:AY:106:ILE:HG21	61:AY:109:LEU:HD23	2.00	0.43
65:Ac:16:LEU:HD23	65:Ac:98:SER:HA	2.00	0.43
73:Ak:12:LEU:HB3	73:Ak:16:ARG:HH22	1.82	0.43
77:Ao:14:GLY:C	77:Ao:16:THR:H	2.25	0.43
80:DC:393:ARG:HH12	80:DC:458:GLY:H	1.66	0.43
80:DC:594:ASP:HB3	80:DC:597:VAL:HG23	2.01	0.43
22:BP:81:ARG:NH2	34:B5:1453:G:O2'	2.48	0.43
22:BP:119:PHE:CE1	25:BS:119:ILE:HG12	2.54	0.43
34:B5:407:A:H2'	34:B5:408:C:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:753:A:H2'	34:B5:754:A:C8	2.52	0.43
34:B5:808:U:H2'	34:B5:809:A:C8	2.53	0.43
38:A1:1245:A:N7	38:A1:1271:A:O2'	2.42	0.43
44:AG:78:PHE:C	44:AG:80:TYR:H	2.26	0.43
47:AJ:82:ARG:O	47:AJ:86:VAL:HG23	2.19	0.43
56:AT:136:ARG:HD2	56:AT:139:ARG:HH12	1.84	0.43
81:V:16:ARG:HD2	81:V:66:PHE:CE1	2.52	0.43
3:BC:168:ARG:HD3	3:BC:170:ILE:HD11	2.00	0.43
5:BG:159:ARG:HB3	5:BG:170:THR:OG1	2.19	0.43
20:BF:46:TRP:HE1	20:BF:122:ASN:HB3	1.82	0.43
21:BK:30:ALA:HA	21:BK:38:LYS:HD3	2.00	0.43
26:BT:6:VAL:HG21	26:BT:132:LEU:HB3	2.00	0.43
31:Bg:110:VAL:HG22	31:Bg:126:SER:HB2	2.00	0.43
34:B5:93:A:O2'	34:B5:398:G:N2	2.51	0.43
34:B5:326:G:H2'	34:B5:327:U:C6	2.54	0.43
34:B5:514:G:O2'	34:B5:515:A:H8	2.01	0.43
34:B5:1061:A:H3'	34:B5:1062:A:H5''	2.00	0.43
34:B5:1456:C:OP1	34:B5:1457:C:O2'	2.33	0.43
34:B5:1484:G:H2'	34:B5:1485:C:C6	2.54	0.43
34:B5:1606:C:H2'	34:B5:1607:G:H8	1.83	0.43
35:AA:144:ASN:HB2	35:AA:160:SER:HB2	1.99	0.43
38:A1:1221:A:O2'	81:V:5:ARG:NH1	2.51	0.43
38:A1:2107:A:H2	38:A1:3344:A:H8	1.65	0.43
38:A1:2270:A:H2'	38:A1:2271:A:C8	2.54	0.43
38:A1:3028:G:H4'	80:DC:28:VAL:HG21	1.99	0.43
38:A1:3185:U:O2'	55:AS:170:THR:OG1	2.31	0.43
39:A3:49:G:OP2	41:AD:91:GLY:N	2.51	0.43
46:AI:48:LEU:HB2	46:AI:142:ASP:OD1	2.19	0.43
47:AJ:87:LYS:HB3	47:AJ:87:LYS:HE2	1.91	0.43
52:AP:35:ALA:HB2	52:AP:58:ILE:HG23	2.00	0.43
63:Aa:90:TYR:CG	63:Aa:100:PRO:HG3	2.54	0.43
73:Ak:30:LYS:HE2	73:Ak:40:GLN:HG2	2.00	0.43
82:EC:6759:A:H2'	82:EC:6760:A:C8	2.54	0.43
2:BB:176:VAL:HG12	2:BB:177:GLN:H	1.83	0.43
3:BC:181:SER:HB3	34:B5:4:C:H4'	2.00	0.43
31:Bg:149:ASP:HB2	31:Bg:175:ASP:HB3	1.99	0.43
34:B5:1036:A:H2'	34:B5:1037:C:H6	1.82	0.43
34:B5:1469:A:H2'	34:B5:1470:C:C6	2.53	0.43
34:B5:1487:A:H2'	34:B5:1488:G:C8	2.54	0.43
34:B5:1609:U:H2'	34:B5:1610:G:O4'	2.19	0.43
47:AJ:60:ARG:HG2	47:AJ:63:GLU:OE2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:AV:80:ARG:HB2	58:AV:99:ALA:HB3	2.01	0.43
65:Ac:103:THR:HG22	65:Ac:105:ALA:H	1.83	0.43
4:BE:89:VAL:HA	4:BE:99:PHE:O	2.18	0.43
5:BG:178:LEU:HD21	34:B5:78:A:C6	2.53	0.43
31:Bg:68:VAL:HG12	31:Bg:84:SER:HB2	2.00	0.43
34:B5:477:A:H2'	34:B5:478:A:H8	1.83	0.43
34:B5:1393:C:H2'	34:B5:1394:G:C8	2.54	0.43
34:B5:1393:C:H2'	34:B5:1394:G:H8	1.82	0.43
34:B5:1639:OMC:H2'	34:B5:1640:C:O4'	2.18	0.43
34:B5:1660:A:H2'	34:B5:1661:U:C6	2.54	0.43
34:B5:1660:A:H2'	34:B5:1661:U:H6	1.83	0.43
34:B5:1776:A:H2'	34:B5:1777:G:H8	1.83	0.43
36:AB:315:GLY:HA2	38:A1:3379:C:H4'	2.00	0.43
38:A1:159:A:H2'	38:A1:160:G:H8	1.82	0.43
38:A1:1915:A:H2'	38:A1:1916:U:C6	2.54	0.43
38:A1:3006:A:H2'	38:A1:3007:U:O4'	2.18	0.43
38:A1:3217:C:O2	52:AP:182:ILE:HD11	2.18	0.43
39:A3:24:A:H2'	39:A3:25:G:C8	2.54	0.43
40:A4:139:U:H2'	40:A4:140:G:H8	1.84	0.43
40:A4:143:U:H2'	40:A4:144:G:O4'	2.18	0.43
43:AF:85:PHE:CZ	43:AF:147:LEU:HD21	2.53	0.43
43:AF:184:LEU:HD21	43:AF:202:LEU:HD21	2.00	0.43
53:AQ:161:LYS:HA	53:AQ:161:LYS:HD3	1.85	0.43
80:DC:835:TRP:HD1	80:DC:839:TYR:CE2	2.37	0.43
10:BN:100:LYS:O	10:BN:104:ARG:HG3	2.19	0.43
11:BO:80:HIS:HA	11:BO:113:GLY:O	2.19	0.43
14:BX:50:LYS:HD2	34:B5:435:C:H5''	1.99	0.43
15:BY:29:HIS:ND1	15:BY:29:HIS:O	2.51	0.43
31:Bg:117:LYS:HD2	31:Bg:117:LYS:HA	1.81	0.43
34:B5:1039:A:O2'	34:B5:1040:G:H8	2.02	0.43
34:B5:1045:C:H2'	34:B5:1046:G:H8	1.83	0.43
34:B5:1225:U:O2	34:B5:1230:A:O2'	2.35	0.43
34:B5:1254:U:H2'	34:B5:1255:G:O4'	2.19	0.43
36:AB:148:LEU:HD11	36:AB:196:ARG:HD3	2.01	0.43
38:A1:99:A:H5'	50:AN:194:GLN:HG2	2.00	0.43
38:A1:170:G:C2	38:A1:250:U:H1'	2.54	0.43
38:A1:1757:A:H2'	38:A1:1758:G:C8	2.54	0.43
38:A1:2220:A2M:N1	38:A1:2225:U:H5	2.17	0.43
38:A1:2523:A:H5''	44:AG:51:LYS:HB2	2.01	0.43
38:A1:3273:A:H4'	42:AE:44:ALA:HB1	2.00	0.43
40:A4:154:C:H5''	44:AG:181:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AN:70:ASN:HB3	50:AN:92:LEU:O	2.19	0.43
50:AN:96:ARG:NH1	50:AN:104:GLU:OE1	2.51	0.43
60:AX:63:ILE:HD11	60:AX:84:PHE:CG	2.54	0.43
62:AZ:5:LEU:HD11	65:Ac:35:ARG:HG3	2.01	0.43
70:Ah:86:ARG:O	70:Ah:90:ARG:HG2	2.18	0.43
20:BF:128:ASN:HB3	20:BF:131:GLN:HG2	2.00	0.43
23:BQ:100:GLN:NE2	31:Bg:56:VAL:HB	2.34	0.43
25:BS:30:TYR:HA	25:BS:33:THR:HG23	1.99	0.43
34:B5:116:U:H2'	34:B5:117:U:C6	2.53	0.43
34:B5:488:G:H5''	34:B5:492:A:N6	2.33	0.43
34:B5:1504:G:H2'	34:B5:1505:A:C8	2.54	0.43
34:B5:1579:U:H2'	34:B5:1580:C:C6	2.54	0.43
34:B5:1645:G:H2'	34:B5:1646:C:H6	1.84	0.43
38:A1:172:G:H2'	38:A1:173:G:H8	1.84	0.43
38:A1:293:C:H2'	38:A1:294:U:O4'	2.18	0.43
38:A1:640:U:OP1	63:Aa:21:ARG:NH2	2.48	0.43
38:A1:1626:U:H2'	38:A1:1627:U:C5	2.53	0.43
38:A1:2283:G:H1'	38:A1:2285:C:N4	2.34	0.43
38:A1:2534:G:H2'	38:A1:2535:A:H8	1.83	0.43
38:A1:2837:A:H5''	46:AI:154:ARG:HH11	1.84	0.43
38:A1:3064:U:H2'	38:A1:3065:G:C8	2.54	0.43
38:A1:3354:U:H4'	38:A1:3355:U:H4'	2.01	0.43
42:AE:51:ARG:HB3	42:AE:159:LEU:HD23	2.01	0.43
52:AP:60:PHE:HB3	52:AP:64:ASN:HB3	2.00	0.43
52:AP:141:SER:O	52:AP:143:PRO:HD3	2.19	0.43
79:E:17:LEU:HD12	79:E:18:LYS:HG3	2.00	0.43
80:DC:388:THR:HG23	80:DC:394:PHE:HA	2.01	0.43
3:BC:59:HIS:CE1	3:BC:239:PRO:HD3	2.54	0.42
4:BE:106:LYS:NZ	34:B5:788:A:OP1	2.42	0.42
21:BK:14:TYR:HE2	21:BK:21:VAL:HG23	1.82	0.42
23:BQ:63:ILE:HD12	23:BQ:63:ILE:HA	1.94	0.42
31:Bg:74:THR:HG22	31:Bg:79:TYR:H	1.83	0.42
34:B5:350:U:O2'	34:B5:970:A:N1	2.49	0.42
34:B5:1207:C:H4'	34:B5:1208:A:O4'	2.19	0.42
34:B5:1515:A:O2'	34:B5:1517:U:OP2	2.22	0.42
38:A1:87:U:H2'	38:A1:88:A:C8	2.53	0.42
38:A1:353:G:O6	72:Aj:55:ARG:NH2	2.51	0.42
38:A1:370:U:H4'	38:A1:404:G:H5'	2.01	0.42
38:A1:377:A:H1'	38:A1:392:G:N2	2.34	0.42
38:A1:972:A:H2'	38:A1:973:A:C8	2.54	0.42
38:A1:1621:A:H2'	38:A1:1622:U:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1629:U:HO2'	38:A1:1630:U:P	2.41	0.42
38:A1:2429:G:H2'	38:A1:2430:A:C8	2.54	0.42
38:A1:2592:G:H4'	38:A1:2594:C:C2	2.54	0.42
38:A1:2680:A:C2	47:AJ:57:PHE:HB3	2.54	0.42
39:A3:24:A:H2'	39:A3:25:G:H8	1.84	0.42
41:AD:144:VAL:HG21	41:AD:171:LEU:HD13	2.00	0.42
63:Aa:82:ILE:HD11	63:Aa:102:ILE:HG12	2.00	0.42
79:E:144:LEU:HA	79:E:147:LYS:HG2	2.01	0.42
8:BJ:85:VAL:HG13	8:BJ:103:ASP:HB3	2.01	0.42
9:BL:40:LEU:HG	34:B5:246:G:N3	2.34	0.42
14:BX:92:CYS:SG	14:BX:136:TRP:HB2	2.59	0.42
15:BY:16:PRO:HA	15:BY:19:ALA:HA	2.01	0.42
20:BF:219:ARG:NH2	82:EC:6844:A:O4'	2.53	0.42
27:BU:33:GLN:OE1	27:BU:33:GLN:N	2.52	0.42
34:B5:29:U:H2'	34:B5:30:G:C8	2.54	0.42
34:B5:82:U:H2'	34:B5:83:G:O4'	2.18	0.42
34:B5:593:U:H4'	34:B5:595:G:H4'	2.01	0.42
38:A1:63:A:N3	38:A1:78:U:O2'	2.42	0.42
38:A1:92:G:H5'	38:A1:94:G:N7	2.34	0.42
38:A1:1593:A:H2'	38:A1:1594:A:C8	2.54	0.42
38:A1:1682:U:O2	57:AU:82:LYS:HD2	2.19	0.42
38:A1:2376:G:H2'	38:A1:2377:G:C8	2.54	0.42
38:A1:2464:U:H2'	38:A1:2465:G:C8	2.54	0.42
38:A1:2848:G:OP1	75:Am:100:TYR:OH	2.28	0.42
38:A1:3275:U:N3	38:A1:3277:U:O4'	2.52	0.42
44:AG:161:GLU:OE2	50:AN:26:ARG:NH1	2.40	0.42
45:AH:41:ILE:HG22	45:AH:43:VAL:HG13	2.01	0.42
49:AM:23:ILE:HG13	49:AM:63:VAL:HG12	2.01	0.42
51:AO:25[A]:LYS:HD2	51:AO:25[A]:LYS:HA	1.80	0.42
62:AZ:25:ILE:HG23	62:AZ:41:ALA:HB1	2.01	0.42
80:DC:674:GLY:N	80:DC:679:GLU:O	2.50	0.42
81:V:125:ASN:HA	81:V:151:GLU:HA	2.01	0.42
5:BG:10:ASN:HD21	5:BG:125:THR:HA	1.83	0.42
14:BX:69:ARG:HB3	14:BX:86:PHE:HE1	1.85	0.42
21:BK:52:LYS:HE2	21:BK:52:LYS:HB2	1.78	0.42
21:BK:82:LEU:HD21	21:BK:87:VAL:HG12	2.01	0.42
27:BU:58:LEU:HD12	27:BU:88:LYS:HB3	2.02	0.42
34:B5:97:C:H2'	34:B5:98:U:C6	2.55	0.42
34:B5:625:C:H2'	34:B5:626:U:C6	2.54	0.42
34:B5:1079:U:H2'	34:B5:1080:U:C6	2.54	0.42
34:B5:1592:A:H2'	34:B5:1593:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:499:G:H5''	68:Af:48:ARG:HH12	1.84	0.42
38:A1:584:G:H2'	38:A1:585:A:C8	2.54	0.42
38:A1:1229:G:O2'	81:V:31:ASP:O	2.37	0.42
38:A1:1340:G:H2'	38:A1:1341:U:C6	2.53	0.42
38:A1:1783:U:H2'	38:A1:1784:G:C8	2.55	0.42
38:A1:2485:A:OP1	79:E:101:LYS:HE2	2.18	0.42
38:A1:3162:C:H2'	38:A1:3163:A:H8	1.84	0.42
39:A3:4:U:H2'	39:A3:5:G:H8	1.84	0.42
53:AQ:104:LEU:HD23	53:AQ:104:LEU:HA	1.90	0.42
70:Ah:84:LYS:O	72:Aj:73:ARG:NH2	2.52	0.42
80:DC:664:VAL:O	80:DC:668:GLN:HG2	2.20	0.42
4:BE:59:ARG:NH1	15:BY:87:PRO:HG3	2.35	0.42
19:BD:161:GLY:O	19:BD:164:VAL:HG12	2.19	0.42
34:B5:872:G:N2	34:B5:1047:G:H4'	2.34	0.42
34:B5:968:U:OP1	34:B5:1033:C:O2'	2.37	0.42
34:B5:1237:G:H2'	34:B5:1238:A:C8	2.54	0.42
34:B5:1458:G:H2'	34:B5:1458:G:N3	2.34	0.42
38:A1:1244:A:H2'	38:A1:1248:C:H5	1.84	0.42
38:A1:1458:U:O2	66:Ad:56:ASN:ND2	2.49	0.42
38:A1:1694:U:H5	38:A1:1752:A:N1	2.17	0.42
38:A1:2723:U:H2'	38:A1:2724:OMU:H6	2.02	0.42
38:A1:2840:C:H2'	38:A1:2841:G:O4'	2.20	0.42
48:AL:46:ILE:HD11	48:AL:51:LEU:HA	2.00	0.42
48:AL:135:ALA:O	70:Ah:119:LYS:HE2	2.20	0.42
54:AR:181:ARG:HA	54:AR:185:LEU:HB3	2.00	0.42
56:AT:42:ILE:HD12	56:AT:91:LEU:HD12	2.00	0.42
63:Aa:45:MET:HE1	63:Aa:52:TYR:CD1	2.54	0.42
65:Ac:72:GLY:HA3	65:Ac:76:GLU:OE2	2.20	0.42
80:DC:322:VAL:HA	80:DC:325:ARG:HH21	1.85	0.42
81:V:55:LYS:HD3	81:V:84:VAL:H	1.84	0.42
1:BA:107:PHE:N	1:BA:135:GLU:OE2	2.52	0.42
3:BC:138:PRO:HG3	12:BV:12:TYR:HE1	1.84	0.42
3:BC:161:LYS:NZ	34:B5:1086:A:OP2	2.46	0.42
7:BI:168:CYS:HB2	7:BI:184:LEU:HD21	2.01	0.42
16:Ba:41:ILE:HD12	16:Ba:68:TYR:CD2	2.54	0.42
19:BD:209:ILE:HD12	19:BD:209:ILE:HA	1.89	0.42
30:Bd:41:GLN:NE2	34:B5:1433:G:O4'	2.51	0.42
34:B5:817:A:H61	34:B5:855:A:N6	2.18	0.42
34:B5:1280:4AC:H2'	34:B5:1281:G:C8	2.54	0.42
34:B5:1682:U:HO2'	34:B5:1683:C:C5'	2.32	0.42
35:AA:2:GLY:HA3	38:A1:2415:C:OP1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:284:ARG:NH1	36:AB:293:ASN:O	2.49	0.42
38:A1:129:U:H2'	38:A1:130:A:H8	1.84	0.42
38:A1:264:G:OP1	71:AI:34:SER:HB2	2.20	0.42
38:A1:323:A:H2'	38:A1:324:A:C8	2.54	0.42
38:A1:589:A:H1'	38:A1:1337:A:H5''	2.00	0.42
38:A1:1571:A:H2'	38:A1:1572:U:O4'	2.19	0.42
38:A1:1663:C:H2'	38:A1:1664:G:H8	1.85	0.42
38:A1:1696:A:H2'	38:A1:1697:A:H8	1.81	0.42
38:A1:2107:A:O2'	38:A1:3344:A:O2'	2.33	0.42
38:A1:3192:U:H2'	38:A1:3193:C:C6	2.55	0.42
38:A1:3198:U:O4	45:AH:26:LYS:HB2	2.19	0.42
39:A3:16:U:H2'	39:A3:17:A:H8	1.85	0.42
51:AO:155[A]:LYS:HE2	51:AO:155[A]:LYS:HB2	1.88	0.42
62:AZ:133:LYS:HG2	62:AZ:135:ARG:NH2	2.34	0.42
64:Ab:47:LEU:HA	64:Ab:50:THR:HG22	2.00	0.42
65:Ac:24:THR:HG22	65:Ac:91:SER:HB3	2.02	0.42
70:Ah:31:LEU:HD11	70:Ah:43:LYS:HD3	2.01	0.42
73:Ak:74:LYS:HE2	73:Ak:74:LYS:HB3	1.75	0.42
79:E:112:ALA:HB1	79:E:116:LEU:HB3	2.02	0.42
80:DC:690:ASP:OD1	80:DC:691:VAL:N	2.52	0.42
4:BE:87:MET:HE2	4:BE:87:MET:HB2	1.74	0.42
4:BE:252:ARG:HH11	4:BE:256:ARG:HH12	1.67	0.42
7:BI:5:ARG:NH2	34:B5:334:G:O6	2.52	0.42
7:BI:83:TYR:HB3	7:BI:101:ILE:HB	2.02	0.42
10:BN:102:LEU:HD11	10:BN:112:LYS:HA	2.02	0.42
14:BX:53:VAL:HA	14:BX:74:VAL:HG12	2.00	0.42
18:Be:33:ARG:NH2	34:B5:477:A:O3'	2.52	0.42
26:BT:14:PHE:HE2	26:BT:63:ARG:HB2	1.84	0.42
31:Bg:123:ILE:HG12	31:Bg:133:VAL:HG22	2.02	0.42
31:Bg:240:VAL:HA	31:Bg:256:THR:HA	2.01	0.42
34:B5:1449:U:H2'	34:B5:1450:U:C6	2.54	0.42
34:B5:1461:C:H2'	34:B5:1462:G:C8	2.54	0.42
34:B5:1748:G:H2'	34:B5:1749:A:C8	2.55	0.42
38:A1:2416:U:H2'	38:A1:2417:OMU:H6	2.02	0.42
38:A1:2426:U:H2'	38:A1:2427:U:C6	2.55	0.42
38:A1:2730:G:H4'	53:AQ:184:PHE:CG	2.54	0.42
39:A3:111:U:H3'	41:AD:276:LYS:NZ	2.34	0.42
44:AG:140:VAL:HG22	44:AG:166:LEU:HD21	2.01	0.42
46:AI:87:LEU:HD13	46:AI:138:VAL:HG22	2.01	0.42
46:AI:206:LEU:O	46:AI:210:ILE:HG12	2.20	0.42
51:AO:10[A]:ASP:HB2	51:AO:117[A]:ARG:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AS:104:GLU:O	55:AS:108:GLN:HG2	2.19	0.42
80:DC:108:HIS:HB3	80:DC:109:VAL:H	1.65	0.42
80:DC:329:PRO:HG2	80:DC:332:ASP:HB2	2.01	0.42
81:V:55:LYS:HA	81:V:56:ASN:HA	1.78	0.42
81:V:125:ASN:ND2	81:V:151:GLU:HB2	2.34	0.42
3:BC:178:ILE:HB	3:BC:185:LYS:HD2	2.02	0.42
4:BE:89:VAL:HG21	4:BE:119:ALA:HB1	2.01	0.42
4:BE:206:ASP:HB2	4:BE:222:LEU:HD13	2.02	0.42
7:BI:138:ASN:HD21	34:B5:187:G:H2'	1.85	0.42
21:BK:24:LYS:HD3	21:BK:26:ASP:HB2	2.02	0.42
22:BP:81:ARG:NH2	22:BP:97:TYR:O	2.46	0.42
24:BR:52:GLY:HA3	34:B5:1389:C:O2'	2.20	0.42
27:BU:60:THR:HG22	34:B5:1382:A:H5''	2.00	0.42
32:Bf:105:TYR:CE1	32:Bf:131:PHE:HB3	2.55	0.42
34:B5:1441:C:O2'	34:B5:1447:C:N4	2.51	0.42
34:B5:1550:A:H2'	34:B5:1551:U:C6	2.55	0.42
34:B5:1705:C:H2'	34:B5:1706:C:C6	2.54	0.42
37:AC:126:ILE:O	37:AC:129:THR:OG1	2.36	0.42
38:A1:1046:A:H2'	38:A1:1049:C:C5	2.53	0.42
38:A1:1517:G:OP1	74:A1:22:PRO:HG3	2.20	0.42
38:A1:1840:U:H4'	38:A1:1841:A:H5''	2.01	0.42
38:A1:2476:C:H2'	38:A1:2477:G:N7	2.35	0.42
38:A1:2883:U:H2'	38:A1:2884:C:C6	2.55	0.42
38:A1:3000:A:H2'	38:A1:3001:C:C6	2.55	0.42
39:A3:7:G:OP1	41:AD:33:ARG:HD2	2.19	0.42
39:A3:71:G:H2'	39:A3:72:A:C8	2.55	0.42
52:AP:92:GLN:HA	52:AP:95:LEU:HB2	2.01	0.42
80:DC:416:PRO:HG2	80:DC:464:LEU:HD23	2.02	0.42
80:DC:840:ASP:OD1	80:DC:840:ASP:N	2.53	0.42
6:BH:139:ARG:HB2	6:BH:151:LYS:HB3	2.00	0.42
7:BI:27:PHE:HB2	34:B5:333:A:N6	2.35	0.42
11:BO:28:VAL:HG11	11:BO:64:ALA:HA	2.02	0.42
22:BP:99:GLY:O	34:B5:1211:A:H1'	2.19	0.42
23:BQ:52:LEU:HA	23:BQ:60:PHE:CE2	2.55	0.42
25:BS:17:LEU:O	25:BS:20:THR:OG1	2.29	0.42
34:B5:407:A:H2'	34:B5:408:C:C6	2.54	0.42
34:B5:551:G:H2'	34:B5:552:G:H8	1.84	0.42
34:B5:976:G:H1	34:B5:1023:A:HO2'	1.67	0.42
34:B5:1061:A:H5''	34:B5:1062:A:H2	1.85	0.42
34:B5:1160:A:H2'	34:B5:1161:C:H6	1.85	0.42
34:B5:1358:G:H2'	34:B5:1359:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1466:G:H2'	34:B5:1467:C:H6	1.85	0.42
38:A1:127:G:H2'	38:A1:128:G:H8	1.84	0.42
38:A1:640:U:H2'	38:A1:641:C:C6	2.55	0.42
38:A1:664:U:H3	38:A1:798:G:H1	1.68	0.42
38:A1:1304:A:O2'	38:A1:2884:C:O2	2.37	0.42
38:A1:2223:A:H2'	38:A1:2224:A:C8	2.55	0.42
38:A1:2801:A:O2'	38:A1:2802:A:H2'	2.19	0.42
38:A1:3232:G:H2'	38:A1:3233:C:H6	1.84	0.42
38:A1:3277:U:H3'	38:A1:3278:C:H6	1.84	0.42
52:AP:22:LEU:HD12	52:AP:146:ILE:HD13	2.01	0.42
79:E:170:GLY:HA2	79:E:179:LEU:HD11	2.01	0.42
80:DC:240:MET:HG2	80:DC:244:LEU:HG	2.02	0.42
80:DC:567:VAL:HG13	80:DC:717:PHE:CE1	2.54	0.42
82:EC:6887:G:H21	82:EC:6888:A:H62	1.66	0.42
1:BA:184:LEU:HA	12:BV:43:GLY:O	2.19	0.42
1:BA:184:LEU:O	12:BV:45:ALA:HB2	2.20	0.42
8:BJ:126:ARG:HD3	18:Be:33:ARG:HD3	2.02	0.42
12:BV:67:ASP:OD1	12:BV:68:SER:N	2.53	0.42
14:BX:69:ARG:HD3	14:BX:69:ARG:HA	1.76	0.42
16:Ba:18:VAL:O	16:Ba:19:LYS:HG2	2.19	0.42
20:BF:143:ARG:HG3	20:BF:144:GLU:OE1	2.20	0.42
32:Bf:93:HIS:NE2	34:B5:1247:U:H3'	2.34	0.42
34:B5:99:C:OP2	34:B5:378:A:O2'	2.30	0.42
38:A1:216:G:OP1	61:AY:16:ARG:NH1	2.53	0.42
38:A1:396:A:O2'	38:A1:399:A:OP1	2.27	0.42
38:A1:956:U:H2'	38:A1:957:C:C6	2.55	0.42
38:A1:1232:C:O2'	81:V:36:GLN:OE1	2.29	0.42
38:A1:1411:C:OP1	67:Ae:98:HIS:N	2.43	0.42
38:A1:1929:G:OP2	38:A1:1930:A:O2'	2.30	0.42
47:AJ:106:ILE:HD11	47:AJ:125:MET:HE2	2.02	0.42
66:Ad:13:THR:HB	66:Ad:72:ARG:HH11	1.85	0.42
67:Ae:19:ARG:HB2	67:Ae:31:ASN:O	2.19	0.42
80:DC:216:HIS:CD2	80:DC:321:LYS:HG2	2.55	0.42
4:BE:75:LYS:HD2	4:BE:77:ARG:NH2	2.35	0.42
4:BE:141:THR:OG1	4:BE:143:ASP:OD1	2.33	0.42
17:Bb:30:SER:OG	17:Bb:48:SER:OG	2.21	0.42
23:BQ:82:ARG:HE	23:BQ:116:LEU:HA	1.84	0.42
26:BT:77:ASN:OD1	26:BT:101:ASN:ND2	2.53	0.42
34:B5:55:A:H3'	34:B5:403:G:H22	1.85	0.42
34:B5:175:G:H22	34:B5:266:A:P	2.43	0.42
34:B5:1226:A:H1'	34:B5:1227:A:H5''	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1528:U:H2'	34:B5:1529:C:C6	2.55	0.42
34:B5:1617:U:H2'	34:B5:1618:C:C6	2.55	0.42
37:AC:93:MET:HB2	38:A1:658:G:H21	1.85	0.42
38:A1:283:G:OP2	38:A1:285:A:O2'	2.31	0.42
38:A1:528:U:H2'	38:A1:529:A:H8	1.84	0.42
38:A1:1282:G:OP1	81:V:56:ASN:HB2	2.20	0.42
38:A1:1757:A:H2'	38:A1:1758:G:H8	1.85	0.42
38:A1:1801:U:H2'	38:A1:1802:C:C6	2.55	0.42
38:A1:2203:U:H2'	38:A1:2204:C:C6	2.54	0.42
38:A1:2926:A:H2'	38:A1:2927:C:C6	2.54	0.42
38:A1:3285:C:H2'	38:A1:3286:G:H8	1.85	0.42
48:AL:76:THR:O	48:AL:80:VAL:HG23	2.20	0.42
55:AS:24:LEU:HD21	56:AT:141:VAL:HG11	2.02	0.42
80:DC:822:ALA:O	80:DC:825:ARG:HG2	2.19	0.42
82:EC:6777:C:H5'	82:EC:6778:C:H2'	2.02	0.42
82:EC:6812:C:H2'	82:EC:6813:A:C8	2.54	0.42
82:EC:6822:U:H2'	82:EC:6823:U:H5''	2.02	0.42
8:BJ:144:PRO:HD2	34:B5:474:A:H5''	2.02	0.41
10:BN:16:ILE:HA	34:B5:959:U:H5'	2.02	0.41
11:BO:84:ARG:HG2	11:BO:85:ALA:O	2.20	0.41
15:BY:29:HIS:ND1	15:BY:32:ARG:O	2.47	0.41
20:BF:99:MET:HB3	20:BF:180:ARG:HH22	1.85	0.41
20:BF:157:ARG:NE	20:BF:224:ASN:OD1	2.53	0.41
24:BR:71:PHE:CZ	24:BR:74:GLN:HB2	2.55	0.41
32:Bf:118:ARG:HH11	32:Bf:134:ASN:HB3	1.85	0.41
34:B5:1144:U:H2'	34:B5:1145:U:C6	2.55	0.41
34:B5:1446:A:O2'	34:B5:1448:G:N7	2.42	0.41
34:B5:1508:U:H2'	34:B5:1509:C:C6	2.54	0.41
36:AB:28:ARG:NH2	38:A1:3140:G:N7	2.59	0.41
36:AB:57:VAL:HG23	36:AB:358:TRP:HE3	1.85	0.41
38:A1:4:U:H2'	38:A1:5:G:C8	2.55	0.41
38:A1:627:U:H4'	38:A1:1399:A:H1'	2.01	0.41
38:A1:1559:A:OP1	60:AX:33:ARG:NE	2.47	0.41
38:A1:2429:G:H2'	38:A1:2430:A:H8	1.84	0.41
38:A1:2656:A:H4'	77:Ao:98:LYS:HD2	2.01	0.41
38:A1:2909:U:H2'	38:A1:2910:A:O4'	2.20	0.41
57:AU:9:GLN:HB2	57:AU:10:LYS:H	1.66	0.41
65:Ac:57:GLU:OE1	65:Ac:69:TYR:OH	2.28	0.41
79:E:54:LYS:HD3	79:E:150:ASP:HB3	2.02	0.41
6:BH:107:ARG:HD3	6:BH:107:ARG:HA	1.88	0.41
9:BL:47:THR:HA	9:BL:50:GLU:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:222:LYS:HA	20:BF:225:ARG:NE	2.35	0.41
22:BP:57:MET:O	22:BP:61:ARG:HG3	2.21	0.41
31:Bg:108:SER:HB3	31:Bg:127:ARG:HB3	2.02	0.41
34:B5:496:G:H3'	34:B5:497:G:C8	2.56	0.41
34:B5:1018:U:H2'	34:B5:1019:A:C8	2.54	0.41
34:B5:1269:OMU:H5'	34:B5:1432:U:P	2.60	0.41
34:B5:1684:U:H2'	34:B5:1685:G:C8	2.55	0.41
34:B5:1751:C:H2'	34:B5:1752:U:C6	2.55	0.41
38:A1:503:C:H2'	38:A1:504:A:C8	2.52	0.41
38:A1:1094:U:O2	38:A1:1096:U:O2'	2.34	0.41
38:A1:3015:G:H2'	38:A1:3016:A:C8	2.54	0.41
38:A1:3089:C:H2'	38:A1:3090:U:O4'	2.20	0.41
41:AD:146:LEU:HD22	41:AD:163:LEU:HD13	2.01	0.41
43:AF:98:LYS:HG2	43:AF:129:LEU:HD21	2.01	0.41
47:AJ:15:GLU:HB2	47:AJ:132:ASN:OD1	2.20	0.41
55:AS:96:ASP:OD1	55:AS:97:VAL:N	2.45	0.41
65:Ac:77:LEU:HB3	65:Ac:87:VAL:HG23	2.02	0.41
66:Ad:75:ILE:HG23	66:Ad:93:VAL:HG22	2.02	0.41
79:E:31:THR:H	79:E:209:SER:HB2	1.84	0.41
80:DC:26:ALA:HB3	80:DC:32:LYS:HD3	2.01	0.41
80:DC:731:VAL:HG13	80:DC:796:MET:HG2	2.02	0.41
81:V:35:SER:HB3	81:V:39:HIS:CE1	2.55	0.41
2:BB:89:ASP:HB3	2:BB:223:PHE:CE1	2.54	0.41
16:Ba:87:ARG:NH2	16:Ba:92:ARG:O	2.53	0.41
21:BK:16:PHE:CE2	21:BK:89:GLY:HA3	2.56	0.41
22:BP:61:ARG:HA	22:BP:64:LYS:HE3	2.02	0.41
23:BQ:82:ARG:HD2	23:BQ:116:LEU:HD22	2.02	0.41
26:BT:23:GLN:HG2	26:BT:55:TYR:CD2	2.55	0.41
34:B5:482:U:H2'	34:B5:483:A:N3	2.35	0.41
35:AA:211:HIS:CD2	35:AA:219:ILE:HG23	2.55	0.41
38:A1:177:U:H2'	38:A1:178:U:C6	2.55	0.41
38:A1:1039:U:H2'	38:A1:1040:A:C8	2.55	0.41
38:A1:1364:C:H5''	53:AQ:3:ILE:HD13	2.01	0.41
38:A1:2916:U:H2'	38:A1:2917:G:H8	1.85	0.41
39:A3:81:U:H2'	39:A3:82:G:H8	1.85	0.41
44:AG:154:ALA:HB2	44:AG:186:LEU:HD12	2.01	0.41
44:AG:210:ALA:O	44:AG:213:LYS:HG2	2.20	0.41
45:AH:22:SER:OG	45:AH:23:ARG:N	2.53	0.41
46:AI:38:LYS:HG3	46:AI:41:ALA:HB2	2.01	0.41
69:Ag:98:GLN:HE21	69:Ag:102:LYS:HG3	1.85	0.41
77:Ao:8:ARG:HD2	77:Ao:72:LEU:HD21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:DC:718:LEU:HB3	80:DC:835:TRP:CE3	2.50	0.41
81:V:86:PHE:HB3	81:V:88:PHE:CE1	2.55	0.41
3:BC:95:ARG:HD3	3:BC:119:LYS:NZ	2.34	0.41
3:BC:148:LEU:HD21	8:BJ:95:TYR:CE2	2.56	0.41
7:BI:83:TYR:CD2	7:BI:101:ILE:HD13	2.52	0.41
13:BW:4:SER:HA	34:B5:634:G:H4'	2.02	0.41
22:BP:42:ARG:NH2	34:B5:1549:C:OP1	2.53	0.41
29:Bc:5:THR:HA	29:Bc:6:PRO:HD3	1.88	0.41
31:Bg:19:TRP:HB2	31:Bg:38:ARG:HG3	2.01	0.41
31:Bg:295:SER:HB3	31:Bg:300:THR:HB	2.02	0.41
34:B5:1232:U:H2'	34:B5:1233:G:C8	2.56	0.41
34:B5:1717:G:H2'	34:B5:1718:G:H8	1.86	0.41
38:A1:5:G:H2'	38:A1:6:A:O4'	2.20	0.41
38:A1:400:G:H4'	38:A1:401:U:H5''	2.03	0.41
38:A1:2154:U:H2'	38:A1:2155:G:H8	1.86	0.41
38:A1:2878:G:H2'	38:A1:2879:C:H6	1.85	0.41
53:AQ:40:THR:HG22	53:AQ:42:ALA:H	1.85	0.41
56:AT:80:VAL:O	56:AT:83:ARG:NH1	2.53	0.41
62:AZ:83:THR:O	65:Ac:62:LEU:HD11	2.21	0.41
78:Ap:76:ALA:HA	78:Ap:79:VAL:HG12	2.03	0.41
79:E:109:ALA:HB1	79:E:133:LYS:HE3	2.03	0.41
80:DC:42:ARG:HH22	80:DC:330:ALA:H	1.68	0.41
80:DC:565:GLU:HB3	80:DC:717:PHE:CZ	2.56	0.41
82:EC:6795:U:H2'	82:EC:6796:C:H6	1.85	0.41
82:EC:6833:G:H2'	82:EC:6834:U:C6	2.55	0.41
1:BA:30:GLN:NE2	1:BA:33:GLN:HG2	2.36	0.41
2:BB:73:LEU:HD12	2:BB:74:GLN:HG2	2.03	0.41
11:BO:107:ARG:HE	11:BO:107:ARG:HB3	1.61	0.41
20:BF:48:PHE:HB2	20:BF:67:PRO:HB3	2.03	0.41
26:BT:105:LEU:HD23	26:BT:105:LEU:HA	1.88	0.41
28:BZ:46:LYS:O	28:BZ:50:ILE:HG12	2.20	0.41
34:B5:655:G:H1	34:B5:678:A:P	2.43	0.41
34:B5:868:G:N2	34:B5:960:U:O2	2.40	0.41
34:B5:1126:OMG:H2'	34:B5:1127:G:H8	1.85	0.41
34:B5:1242:A:O2'	34:B5:1244:A:OP1	2.34	0.41
38:A1:1399:A:N1	40:A4:7:U:O2'	2.50	0.41
38:A1:1666:G:H2'	38:A1:1667:A:C8	2.56	0.41
38:A1:2305:G:OP2	38:A1:2305:G:N2	2.41	0.41
38:A1:2651:G:H5''	38:A1:2652:U:O4'	2.19	0.41
39:A3:3:U:H2'	39:A3:4:U:C6	2.55	0.41
44:AG:90:THR:HA	44:AG:214:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AH:22:SER:O	45:AH:23:ARG:HD3	2.20	0.41
49:AM:14:LEU:H	49:AM:19:ARG:NH2	2.19	0.41
52:AP:52:LEU:HD23	52:AP:52:LEU:HA	1.87	0.41
66:Ad:48:ASP:HB2	66:Ad:87:ASN:HD21	1.86	0.41
80:DC:342:LEU:HD23	80:DC:342:LEU:HA	1.74	0.41
4:BE:18:TRP:HH2	4:BE:31:PRO:HD3	1.85	0.41
4:BE:94:ALA:O	4:BE:95:THR:OG1	2.38	0.41
6:BH:81:LEU:HB3	6:BH:90:VAL:HG21	2.02	0.41
20:BF:70:VAL:HG13	20:BF:72:HIS:H	1.85	0.41
26:BT:12:GLN:OE1	34:B5:1529:C:O2'	2.31	0.41
33:BM:96:GLN:HA	33:BM:99:GLU:HG2	2.02	0.41
34:B5:358:U:O2'	34:B5:360:A:OP1	2.38	0.41
34:B5:1077:C:H2'	34:B5:1078:C:H6	1.86	0.41
34:B5:1357:A:H2'	34:B5:1358:G:C8	2.56	0.41
34:B5:1656:U:H2'	34:B5:1658:G:O2'	2.20	0.41
36:AB:215:ILE:HD12	36:AB:338:LEU:HB3	2.03	0.41
36:AB:339:ARG:HG2	36:AB:340:LYS:O	2.20	0.41
38:A1:821:U:H2'	38:A1:822:G:H8	1.85	0.41
38:A1:1003:A:N1	38:A1:1049:C:O2'	2.50	0.41
38:A1:1176:C:H2'	38:A1:1177:G:N2	2.35	0.41
38:A1:1214:U:OP2	55:AS:137:ARG:NH2	2.47	0.41
38:A1:1460:A:H2'	38:A1:1461:A:H8	1.85	0.41
38:A1:1619:A:H2'	38:A1:1620:U:O4'	2.20	0.41
38:A1:1718:G:H2'	38:A1:1719:G:H8	1.84	0.41
38:A1:1783:U:H2'	38:A1:1784:G:H8	1.86	0.41
38:A1:3164:C:O2'	38:A1:3165:A:H8	2.03	0.41
38:A1:3254:G:H2'	38:A1:3255:U:O4'	2.21	0.41
40:A4:68:G:H2'	40:A4:69:U:C6	2.56	0.41
42:AE:142:ASP:HA	42:AE:145:LEU:HB2	2.03	0.41
43:AF:151:ARG:HD2	43:AF:207:LEU:HD23	2.01	0.41
44:AG:111:LYS:HB2	44:AG:111:LYS:HE3	1.79	0.41
51:AO:108[A]:ILE:HD12	51:AO:160[A]:ARG:CZ	2.50	0.41
52:AP:176:ILE:O	52:AP:180:LYS:HG2	2.19	0.41
61:AY:50:ILE:HG21	61:AY:80:VAL:HG11	2.03	0.41
63:Aa:117:ARG:HA	63:Aa:117:ARG:HD3	1.85	0.41
69:Ag:54:ILE:HD11	69:Ag:78:GLY:HA2	2.02	0.41
80:DC:27:HIS:ND1	80:DC:138:GLN:HB2	2.36	0.41
80:DC:137:VAL:O	80:DC:141:THR:HG23	2.21	0.41
80:DC:511:LEU:HD23	80:DC:518:VAL:HG11	2.02	0.41
80:DC:619:MET:HE1	80:DC:625:TRP:HB2	2.03	0.41
2:BB:128:LYS:HA	2:BB:134:VAL:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:12:GLN:HB2	11:BO:14:PHE:HE1	1.85	0.41
15:BY:112:LYS:NZ	34:B5:57:G:OP1	2.52	0.41
20:BF:216:GLU:HG2	82:EC:6845:G:H5'	2.03	0.41
26:BT:135:ILE:O	26:BT:138:GLN:HG2	2.21	0.41
32:Bf:82:LYS:HD3	80:DC:652:ALA:HB2	2.03	0.41
34:B5:44:U:OP2	34:B5:437:A:N6	2.52	0.41
34:B5:107:C:H2'	34:B5:108:A:H8	1.85	0.41
34:B5:297:U:H2'	34:B5:298:C:C6	2.56	0.41
34:B5:894:U:H2'	34:B5:895:G:H8	1.85	0.41
34:B5:1492:A:O2'	34:B5:1493:A:H5''	2.21	0.41
36:AB:123:TYR:CE2	36:AB:124:LYS:HG3	2.56	0.41
37:AC:170:LYS:HE3	37:AC:178:LEU:HD12	2.02	0.41
38:A1:68:C:N4	38:A1:314:U:O2'	2.54	0.41
38:A1:422:A:C2	38:A1:2363:A:H4'	2.56	0.41
38:A1:432:G:H2'	38:A1:433:A:H8	1.85	0.41
38:A1:500:C:H2'	38:A1:501:A:C8	2.56	0.41
38:A1:675:C:H2'	38:A1:676:G:O4'	2.21	0.41
38:A1:1249:G:H2'	38:A1:1250:G:C8	2.55	0.41
38:A1:1295:G:H1'	55:AS:113:ARG:O	2.21	0.41
38:A1:1626:U:H2'	38:A1:1627:U:H5	1.86	0.41
38:A1:1729:A:OP1	65:Ac:88:GLY:N	2.51	0.41
38:A1:2440:G:H3'	38:A1:2441:A:H8	1.86	0.41
38:A1:3110:C:H2'	38:A1:3111:U:C6	2.56	0.41
38:A1:3231:U:H2'	38:A1:3232:G:C8	2.54	0.41
39:A3:90:U:H2'	39:A3:91:G:O4'	2.20	0.41
43:AF:98:LYS:HB3	43:AF:99:PRO:HD3	2.02	0.41
55:AS:117:ARG:O	55:AS:121:ILE:HG12	2.21	0.41
62:AZ:76:ASN:OD1	62:AZ:77:TYR:N	2.53	0.41
80:DC:225:PHE:CD2	80:DC:277:ILE:HG12	2.55	0.41
82:EC:6805:C:H5''	82:EC:6806:U:H4'	2.02	0.41
3:BC:218:ILE:O	3:BC:221:THR:OG1	2.28	0.41
4:BE:18:TRP:HE3	4:BE:20:LEU:HD11	1.86	0.41
6:BH:24:PHE:HE1	6:BH:81:LEU:HD11	1.85	0.41
9:BL:38:ALA:O	34:B5:246:G:N2	2.51	0.41
21:BK:59:PHE:CE2	21:BK:62:GLN:HG3	2.56	0.41
30:Bd:10:HIS:HB2	34:B5:1451:C:H5''	2.02	0.41
31:Bg:34:LEU:HB2	31:Bg:73:LEU:HD11	2.03	0.41
34:B5:29:U:H2'	34:B5:30:G:H8	1.86	0.41
34:B5:906:A:H2'	34:B5:907:A:C8	2.56	0.41
34:B5:1338:C:H1'	34:B5:1410:A:C4	2.56	0.41
34:B5:1355:C:H2'	34:B5:1356:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:205:VAL:HA	36:AB:208:VAL:HG12	2.02	0.41
38:A1:236:G:H2'	38:A1:237:G:C8	2.56	0.41
38:A1:268:A:N1	38:A1:295:A:H5'	2.35	0.41
38:A1:345:G:O2'	40:A4:25:G:N3	2.54	0.41
38:A1:987:U:H2'	38:A1:988:U:C6	2.56	0.41
38:A1:2671:A:O2'	47:AJ:98:ALA:N	2.53	0.41
40:A4:97:A:OP1	70:Ah:63:ARG:NE	2.51	0.41
44:AG:115:ALA:O	44:AG:119:GLY:N	2.54	0.41
48:AL:11:LYS:O	48:AL:13:HIS:ND1	2.54	0.41
54:AR:28:GLU:O	54:AR:32:ILE:HD12	2.20	0.41
56:AT:68:THR:OG1	56:AT:71:SER:OG	2.28	0.41
56:AT:92:ARG:HB3	56:AT:94:GLU:OE2	2.20	0.41
60:AX:108:LEU:HD23	60:AX:125:ARG:HG2	2.03	0.41
69:Ag:107:GLU:HA	69:Ag:110:GLU:HG2	2.03	0.41
72:Aj:17:THR:OG1	72:Aj:18:LEU:N	2.53	0.41
72:Aj:39:TYR:CD1	72:Aj:40:PRO:HA	2.55	0.41
82:EC:6793:A:O2'	82:EC:6795:U:H5'	2.20	0.41
1:BA:56:LYS:HA	1:BA:56:LYS:HD2	1.81	0.41
1:BA:134:LYS:O	1:BA:137:SER:OG	2.36	0.41
4:BE:180:LEU:HD12	4:BE:192:ILE:HG22	2.03	0.41
12:BV:73:ALA:HB1	12:BV:79:LEU:HD23	2.02	0.41
15:BY:56:SER:HB3	15:BY:74:LEU:HB2	2.03	0.41
19:BD:48:VAL:HB	19:BD:86:LEU:HD22	2.03	0.41
20:BF:49:GLU:HG3	20:BF:50:GLU:HG2	2.02	0.41
20:BF:118:LEU:HG	20:BF:129:PRO:HB2	2.01	0.41
20:BF:140:THR:HG23	20:BF:210:ALA:HB1	2.02	0.41
20:BF:187:ILE:HD11	34:B5:1535:U:H2'	2.03	0.41
26:BT:36:ILE:HG13	26:BT:37:VAL:HG13	2.02	0.41
28:BZ:40:VAL:HG13	28:BZ:41:ILE:HG12	2.03	0.41
32:Bf:138:ARG:HG2	32:Bf:139:LEU:N	2.36	0.41
34:B5:64:U:O2'	34:B5:168:A:N3	2.46	0.41
34:B5:86:A:H2'	34:B5:87:C:H6	1.86	0.41
34:B5:420:A2M:H8	34:B5:420:A2M:O5'	2.21	0.41
34:B5:872:G:H2'	34:B5:873:U:O4'	2.21	0.41
35:AA:70:ARG:HD2	35:AA:72:ARG:CZ	2.51	0.41
35:AA:127:ALA:HB2	35:AA:134:VAL:HG23	2.03	0.41
35:AA:149:ARG:HH12	35:AA:153:GLY:H	1.69	0.41
36:AB:46:PHE:CE2	36:AB:81:THR:HB	2.56	0.41
36:AB:259:HIS:HB3	38:A1:2987:A:O2'	2.21	0.41
37:AC:67:THR:HG21	38:A1:2402:A:H2'	2.02	0.41
37:AC:150:LEU:HD21	37:AC:172:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:518:G:OP2	38:A1:518:G:N2	2.32	0.41
38:A1:1001:G:O2'	38:A1:1041:U:OP2	2.26	0.41
38:A1:1211:U:H2'	38:A1:1212:A:C8	2.56	0.41
38:A1:1461:A:H2'	38:A1:1462:A:C8	2.55	0.41
38:A1:1718:G:H2'	38:A1:1719:G:C8	2.56	0.41
38:A1:1730:G:C8	65:Ac:28:LYS:HD3	2.56	0.41
38:A1:2265:C:O5'	38:A1:2265:C:H6	2.04	0.41
38:A1:3214:U:OP2	49:AM:128:ARG:NH1	2.49	0.41
38:A1:3346:U:H2'	38:A1:3347:A:C8	2.55	0.41
40:A4:27:U:H2'	40:A4:28:C:C6	2.55	0.41
40:A4:40:A:H2'	40:A4:41:A:H8	1.86	0.41
40:A4:57:C:OP2	72:Aj:68:LYS:NZ	2.47	0.41
42:AE:42:LEU:HD22	42:AE:79:VAL:HG11	2.03	0.41
44:AG:231:LYS:HB3	44:AG:231:LYS:HE2	1.93	0.41
45:AH:21:LYS:HD2	45:AH:21:LYS:HA	1.96	0.41
45:AH:117:PHE:HE1	45:AH:178:GLY:HA2	1.85	0.41
47:AJ:62:ASN:HB2	77:Ao:103:ALA:HA	2.03	0.41
47:AJ:84:LEU:HB3	47:AJ:89:TYR:CD1	2.56	0.41
53:AQ:55:SER:O	53:AQ:59:ARG:HG2	2.21	0.41
56:AT:75:ILE:HG23	56:AT:86:GLU:HG3	2.03	0.41
69:Ag:22:VAL:HG11	69:Ag:30:LEU:HD23	2.02	0.41
73:Ak:14:LEU:HD21	73:Ak:52:TYR:CG	2.55	0.41
75:Am:77:ILE:HG22	75:Am:79:GLU:OE1	2.21	0.41
76:An:2:ARG:HD3	76:An:5:TRP:NE1	2.36	0.41
80:DC:124:GLY:HA3	80:DC:342:LEU:HD13	2.02	0.41
1:BA:74:VAL:HG23	1:BA:118:PRO:HB3	2.02	0.41
2:BB:122:GLU:O	2:BB:165:ARG:NE	2.49	0.41
5:BG:93:LYS:HE2	34:B5:405:C:H5''	2.03	0.41
10:BN:61:THR:HB	34:B5:959:U:H6	1.86	0.41
13:BW:16:ASN:O	13:BW:20:THR:HG22	2.20	0.41
22:BP:44:ARG:HD2	22:BP:84:ILE:HD12	2.03	0.41
26:BT:22:LEU:HD21	26:BT:28:LEU:HD13	2.01	0.41
27:BU:80:GLU:CD	30:Bd:44:ARG:HH12	2.28	0.41
31:Bg:149:ASP:OD1	31:Bg:150:TRP:N	2.53	0.41
34:B5:1185:U:H4'	34:B5:1186:U:H5''	2.03	0.41
34:B5:1189:A:H2'	34:B5:1194:A:H1'	2.03	0.41
36:AB:20:LYS:HB2	38:A1:2991:A:P	2.61	0.41
37:AC:134:LEU:HD23	37:AC:134:LEU:HA	1.90	0.41
38:A1:412:G:H2'	38:A1:413:U:C6	2.56	0.41
38:A1:748:U:H2'	38:A1:749:C:C6	2.56	0.41
38:A1:748:U:H5''	64:Ab:31:SER:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1555:U:H5'	38:A1:1556:C:OP2	2.21	0.41
38:A1:1615:C:H2'	38:A1:1616:U:C6	2.56	0.41
38:A1:2267:C:O2'	38:A1:2268:U:O5'	2.36	0.41
38:A1:2483:G:H2'	38:A1:2485:A:OP2	2.21	0.41
38:A1:3063:C:H2'	38:A1:3064:U:H6	1.86	0.41
40:A4:146:U:H2'	40:A4:147:U:C6	2.56	0.41
44:AG:78:PHE:O	44:AG:79:GLN:HG3	2.22	0.41
51:AO:12[A]:LYS:HD2	51:AO:37[A]:ARG:NH2	2.36	0.41
51:AO:172[A]:ARG:HG3	51:AO:173[A]:ALA:N	2.36	0.41
53:AQ:176:ARG:HA	53:AQ:182:LYS:O	2.21	0.41
58:AV:84:SER:HA	58:AV:94:TYR:HB3	2.03	0.41
62:AZ:97:SER:H	62:AZ:100:THR:HG22	1.85	0.41
80:DC:588:LEU:HD21	80:DC:712:ALA:HB1	2.03	0.41
1:BA:176:LEU:O	1:BA:180:GLU:HG2	2.20	0.40
2:BB:150:VAL:H	34:B5:1067:C:H5''	1.86	0.40
3:BC:121:VAL:O	3:BC:125:ILE:HG12	2.21	0.40
11:BO:132:ARG:HG3	16:Ba:29:SER:OG	2.22	0.40
20:BF:72:HIS:CD2	20:BF:107:LYS:HD2	2.56	0.40
25:BS:57:ARG:NH2	34:B5:1533:C:OP1	2.54	0.40
27:BU:87:HIS:ND1	34:B5:1383:G:OP1	2.54	0.40
34:B5:52:U:H2'	34:B5:53:G:C8	2.56	0.40
34:B5:296:U:H2'	34:B5:297:U:C6	2.56	0.40
34:B5:1622:G:H2'	34:B5:1623:C:C6	2.56	0.40
35:AA:135:ILE:HD12	35:AA:149:ARG:HD2	2.02	0.40
37:AC:135:VAL:HG12	37:AC:140:HIS:HB2	2.02	0.40
38:A1:296:A:N3	38:A1:299:G:O2'	2.54	0.40
38:A1:393:U:H2'	38:A1:394:G:O4'	2.21	0.40
38:A1:1097:G:O5'	56:AT:129:LYS:NZ	2.51	0.40
38:A1:1231:A:N6	38:A1:1277:C:OP2	2.49	0.40
38:A1:1259:A:N3	38:A1:1280:C:O2'	2.45	0.40
38:A1:1747:G:N2	73:Ak:2:ALA:HB3	2.36	0.40
38:A1:2154:U:H2'	38:A1:2155:G:C8	2.56	0.40
39:A3:81:U:H2'	39:A3:82:G:C8	2.56	0.40
43:AF:126:LEU:O	43:AF:130:ILE:HG12	2.21	0.40
47:AJ:31:THR:O	47:AJ:34:SER:OG	2.31	0.40
51:AO:8[A]:VAL:HG12	51:AO:117[A]:ARG:HG3	2.02	0.40
62:AZ:54:THR:HG22	62:AZ:57:HIS:CE1	2.56	0.40
63:Aa:96:LYS:HG3	63:Aa:122:PRO:HG2	2.04	0.40
80:DC:578:LYS:HB2	80:DC:840:ASP:OD2	2.21	0.40
80:DC:707:PRO:O	80:DC:711:ARG:HG3	2.21	0.40
82:EC:6901:C:O2'	82:EC:6902:U:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:59:LEU:O	1:BA:63:ILE:HG12	2.21	0.40
5:BG:155:ASP:N	5:BG:155:ASP:OD1	2.53	0.40
6:BH:155:ASP:OD1	6:BH:155:ASP:N	2.52	0.40
7:BI:96:LEU:HD23	7:BI:96:LEU:HA	1.92	0.40
10:BN:75:LEU:HA	10:BN:75:LEU:HD23	1.84	0.40
19:BD:50:ILE:HG23	19:BD:88:ALA:HA	2.02	0.40
21:BK:5:LYS:HE2	21:BK:5:LYS:HA	2.02	0.40
26:BT:56:LYS:HB3	26:BT:56:LYS:HE2	1.86	0.40
33:BM:135:MET:N	33:BM:135:MET:SD	2.94	0.40
34:B5:538:A:N3	34:B5:538:A:H2'	2.36	0.40
34:B5:615:A:O2'	34:B5:621:A:N1	2.42	0.40
34:B5:693:U:H5''	34:B5:694:U:H5'	2.03	0.40
34:B5:1391:A:H2'	34:B5:1392:U:C6	2.56	0.40
34:B5:1461:C:H2'	34:B5:1462:G:H8	1.87	0.40
34:B5:1550:A:C6	34:B5:1562:G:C6	3.10	0.40
34:B5:1793:G:O2'	34:B5:1795:U:OP2	2.39	0.40
37:AC:47:ARG:HA	38:A1:338:A:OP1	2.21	0.40
38:A1:127:G:H2'	38:A1:128:G:C8	2.57	0.40
38:A1:1128:U:H2'	38:A1:1129:A:O4'	2.21	0.40
38:A1:1138:U:P	64:Ab:13:THR:HG21	2.61	0.40
38:A1:1622:U:H2'	38:A1:1623:G:H8	1.85	0.40
38:A1:2197:OMC:N4	38:A1:2241:U:H2'	2.36	0.40
38:A1:2505:U:H2'	38:A1:2506:U:O4'	2.22	0.40
38:A1:3107:U:H2'	38:A1:3108:G:C8	2.55	0.40
44:AG:74:THR:HG21	71:AI:47:ILE:HG23	2.02	0.40
46:AI:4:ARG:CZ	46:AI:99:ILE:HG13	2.51	0.40
49:AM:102:LYS:O	49:AM:106:ARG:HG3	2.21	0.40
50:AN:80:THR:OG1	50:AN:87:GLN:HA	2.21	0.40
50:AN:94:TYR:CE2	50:AN:96:ARG:HB2	2.57	0.40
72:Aj:68:LYS:HG3	72:Aj:69:HIS:CE1	2.56	0.40
80:DC:353:ALA:HA	80:DC:356:LEU:HG	2.03	0.40
80:DC:579:SER:HA	80:DC:708:THR:HB	2.03	0.40
81:V:67:LEU:HD11	81:V:74:GLU:HG3	2.03	0.40
82:EC:6907:G:H3'	82:EC:6908:C:H5''	2.01	0.40
1:BA:41:ARG:NH1	24:BR:105:GLN:H	2.19	0.40
3:BC:45:VAL:HG21	3:BC:68:ILE:HG23	2.03	0.40
5:BG:61:PHE:HZ	34:B5:420:A2M:H5'	1.85	0.40
7:BI:5:ARG:NH1	34:B5:332:U:O2'	2.54	0.40
7:BI:50:GLY:HA2	34:B5:397:A:H4'	2.03	0.40
7:BI:87:ASN:OD1	7:BI:88:ASN:N	2.54	0.40
16:Ba:41:ILE:HG22	16:Ba:66:LYS:HD3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:41:LEU:H	17:Bb:41:LEU:HD23	1.86	0.40
19:BD:25:PHE:CD2	19:BD:50:ILE:HD12	2.56	0.40
20:BF:99:MET:CG	20:BF:180:ARG:HH12	2.34	0.40
22:BP:60:LEU:O	22:BP:64:LYS:HG2	2.22	0.40
25:BS:41:ARG:NH1	26:BT:46:PRO:HG3	2.36	0.40
32:Bf:93:HIS:CE1	34:B5:1245:G:H21	2.39	0.40
33:BM:131:ASP:OD1	33:BM:132:GLU:N	2.54	0.40
34:B5:560:U:H2'	34:B5:561:G:H8	1.86	0.40
34:B5:973:A:H4'	38:A1:848:A:C8	2.56	0.40
34:B5:1317:C:H2'	34:B5:1318:G:O4'	2.22	0.40
34:B5:1525:A:H2'	34:B5:1526:A:C8	2.56	0.40
38:A1:1306:G:O2'	38:A1:1307:G:H5''	2.21	0.40
38:A1:2696:A:N7	38:A1:2758:A:N6	2.70	0.40
38:A1:2767:U:H2'	38:A1:2768:U:H6	1.87	0.40
38:A1:3047:U:O2'	38:A1:3048:A:H5'	2.20	0.40
38:A1:3272:C:P	42:AE:78:ARG:HH21	2.45	0.40
39:A3:4:U:H2'	39:A3:5:G:C8	2.57	0.40
42:AE:156:LYS:O	42:AE:160:SER:OG	2.36	0.40
43:AF:148:VAL:HG12	43:AF:181:ILE:HD11	2.04	0.40
47:AJ:53:THR:HG23	47:AJ:60:ARG:HA	2.03	0.40
51:AO:75[A]:ALA:HB3	51:AO:78[A]:ARG:HG2	2.02	0.40
60:AX:81:ILE:HG22	60:AX:125:ARG:HB2	2.03	0.40
63:Aa:75:LEU:HD21	63:Aa:138:ILE:HD11	2.03	0.40
80:DC:191:THR:HG23	80:DC:192:TYR:CD2	2.56	0.40
81:V:22:TYR:HB2	81:V:88:PHE:HD2	1.86	0.40
82:EC:6844:A:H1'	82:EC:6845:G:C8	2.56	0.40
1:BA:35:PRO:HG3	12:BV:87:ARG:NH2	2.36	0.40
3:BC:44:LEU:HD12	3:BC:240:LEU:HD13	2.03	0.40
3:BC:73:LEU:HD23	3:BC:73:LEU:HA	1.92	0.40
5:BG:72:ARG:HG2	5:BG:98:ARG:HA	2.03	0.40
6:BH:64:VAL:HB	6:BH:94:ALA:HB1	2.04	0.40
6:BH:104:ARG:HG3	34:B5:803:A:C4	2.56	0.40
19:BD:80:ALA:O	19:BD:83:THR:HG22	2.21	0.40
20:BF:100:ASN:HD21	20:BF:180:ARG:HD3	1.85	0.40
23:BQ:57:LEU:HA	23:BQ:60:PHE:HD2	1.85	0.40
24:BR:3:ARG:NH1	34:B5:1415:U:OP2	2.54	0.40
26:BT:130:ARG:HG2	34:B5:1359:C:H4'	2.03	0.40
32:Bf:103:LEU:HD11	32:Bf:108:VAL:HG23	2.04	0.40
34:B5:223:U:H2'	34:B5:224:C:O4'	2.21	0.40
34:B5:709:C:N4	34:B5:730:G:O3'	2.55	0.40
34:B5:792:U:H2'	34:B5:793:A:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:960:U:H2'	34:B5:961:U:C6	2.55	0.40
35:AA:190:ARG:HG3	35:AA:191:LEU:HD22	2.04	0.40
38:A1:73:C:N3	48:AL:59:ARG:NH2	2.69	0.40
38:A1:226:C:H2'	38:A1:227:G:O4'	2.21	0.40
38:A1:432:G:H2'	38:A1:433:A:C8	2.56	0.40
38:A1:548:G:OP2	38:A1:549:U:H5'	2.21	0.40
38:A1:1120:A:H2'	38:A1:1121:U:H6	1.86	0.40
38:A1:1174:G:HO2'	51:AO:21[A]:SER:HG	1.59	0.40
38:A1:1292:C:O2'	38:A1:1293:U:OP1	2.39	0.40
38:A1:1624:G:H2'	38:A1:1625:A:C8	2.56	0.40
38:A1:1729:A:OP2	65:Ac:27:TYR:N	2.52	0.40
38:A1:2115:G:H22	38:A1:2120:A:H1'	1.86	0.40
38:A1:2413:A:H2'	38:A1:2414:G:C8	2.56	0.40
38:A1:2467:G:OP1	79:E:60:ARG:NH1	2.54	0.40
38:A1:2662:G:H2'	38:A1:2663:G:C8	2.56	0.40
38:A1:3183:A:H2'	38:A1:3184:A:C8	2.57	0.40
39:A3:95:A:N3	55:AS:119:ARG:HD2	2.37	0.40
42:AE:5:LYS:HA	42:AE:5:LYS:HD2	1.89	0.40
43:AF:82:LYS:HE3	43:AF:82:LYS:HB2	1.87	0.40
46:AI:184:LYS:HB3	46:AI:184:LYS:HE3	1.98	0.40
65:Ac:14:LEU:HD23	65:Ac:14:LEU:HA	1.92	0.40
80:DC:79:SER:OG	80:DC:81:MET:HE3	2.20	0.40
80:DC:163:ALA:O	80:DC:167:LEU:HB3	2.21	0.40
80:DC:389:SER:C	80:DC:391:LYS:H	2.29	0.40
80:DC:500:ASP:HA	80:DC:503:LYS:HG3	2.03	0.40
82:EC:6787:U:OP2	82:EC:6804:A:N6	2.53	0.40
4:BE:52:LEU:HD23	4:BE:52:LEU:HA	1.92	0.40
4:BE:95:THR:OG1	4:BE:97:GLU:OE1	2.38	0.40
20:BF:64:VAL:H	20:BF:65:ARG:HH11	1.69	0.40
23:BQ:48:VAL:HG13	23:BQ:78:VAL:HG13	2.04	0.40
26:BT:21:PHE:O	26:BT:24:ARG:HG2	2.21	0.40
31:Bg:282:SER:OG	31:Bg:283:LYS:N	2.55	0.40
33:BM:135:MET:HE2	33:BM:135:MET:HB2	1.98	0.40
34:B5:595:G:H2'	34:B5:596:C:C6	2.57	0.40
34:B5:826:U:H2'	34:B5:827:C:H6	1.85	0.40
34:B5:1340:U:C6	34:B5:1378:U:H4'	2.56	0.40
34:B5:1524:A:H2	34:B5:1590:G:H1'	1.87	0.40
34:B5:1580:C:H2'	34:B5:1581:C:C6	2.56	0.40
36:AB:332:ARG:HH22	38:A1:3304:U:P	2.44	0.40
37:AC:22:LEU:HA	37:AC:23:PRO:HD3	1.83	0.40
38:A1:179:C:H42	38:A1:237:G:H22	1.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:210:U:C2	38:A1:230:U:H4'	2.57	0.40
38:A1:1781:C:H2'	38:A1:1782:U:C6	2.57	0.40
38:A1:1821:U:N3	69:Ag:67:LYS:HD3	2.37	0.40
38:A1:2167:A:H2'	38:A1:2168:A:C8	2.56	0.40
38:A1:2194:G:H2'	38:A1:2195:C:C6	2.57	0.40
38:A1:2881:C:H2'	38:A1:2882:U:C6	2.57	0.40
38:A1:2989:U:H2'	38:A1:2990:G:O4'	2.21	0.40
38:A1:3023:U:O3'	80:DC:162:ARG:NH2	2.55	0.40
38:A1:3161:C:H2'	38:A1:3162:C:C6	2.57	0.40
39:A3:64:A:N7	46:AI:209:ASN:ND2	2.69	0.40
41:AD:184:ASP:HB3	41:AD:187:THR:O	2.22	0.40
45:AH:13:PRO:HG2	45:AH:16:VAL:HG21	2.04	0.40
80:DC:373:ASP:N	80:DC:373:ASP:OD1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	182 (89%)	22 (11%)	0	100	100
2	BB	212/255 (83%)	184 (87%)	28 (13%)	0	100	100
3	BC	215/254 (85%)	204 (95%)	11 (5%)	0	100	100
4	BE	258/261 (99%)	233 (90%)	25 (10%)	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%)	167 (91%)	17 (9%)	0	100	100
8	BJ	183/197 (93%)	172 (94%)	11 (6%)	0	100	100
9	BL	153/156 (98%)	138 (90%)	15 (10%)	0	100	100
10	BN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	BO	125/137 (91%)	111 (89%)	14 (11%)	0	100	100
12	BV	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
13	BW	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
14	BX	142/145 (98%)	126 (89%)	16 (11%)	0	100	100
15	BY	132/135 (98%)	123 (93%)	9 (7%)	0	100	100
16	Ba	95/119 (80%)	80 (84%)	15 (16%)	0	100	100
17	Bb	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
18	Be	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
19	BD	221/240 (92%)	206 (93%)	15 (7%)	0	100	100
20	BF	204/225 (91%)	186 (91%)	18 (9%)	0	100	100
21	BK	94/105 (90%)	82 (87%)	12 (13%)	0	100	100
22	BP	122/142 (86%)	112 (92%)	10 (8%)	0	100	100
23	BQ	139/143 (97%)	134 (96%)	5 (4%)	0	100	100
24	BR	117/136 (86%)	109 (93%)	8 (7%)	0	100	100
25	BS	143/146 (98%)	126 (88%)	17 (12%)	0	100	100
26	BT	139/144 (96%)	126 (91%)	13 (9%)	0	100	100
27	BU	105/121 (87%)	97 (92%)	8 (8%)	0	100	100
28	BZ	67/108 (62%)	63 (94%)	4 (6%)	0	100	100
29	Bc	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
30	Bd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
31	Bg	310/319 (97%)	278 (90%)	32 (10%)	0	100	100
32	Bf	73/152 (48%)	64 (88%)	9 (12%)	0	100	100
33	BM	122/143 (85%)	115 (94%)	7 (6%)	0	100	100
35	AA	245/254 (96%)	228 (93%)	17 (7%)	0	100	100
36	AB	383/387 (99%)	361 (94%)	22 (6%)	0	100	100
37	AC	359/362 (99%)	337 (94%)	22 (6%)	0	100	100
41	AD	290/297 (98%)	274 (94%)	16 (6%)	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%)	210 (92%)	18 (8%)	0	100	100
45	AH	188/191 (98%)	171 (91%)	17 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	AI	201/221 (91%)	195 (97%)	6 (3%)	0	100	100
47	AJ	167/174 (96%)	150 (90%)	17 (10%)	0	100	100
48	AL	191/199 (96%)	178 (93%)	13 (7%)	0	100	100
49	AM	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
50	AN	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
51	AO	195/199 (98%)	194 (100%)	1 (0%)	0	100	100
52	AP	171/184 (93%)	163 (95%)	8 (5%)	0	100	100
53	AQ	183/186 (98%)	177 (97%)	6 (3%)	0	100	100
54	AR	186/189 (98%)	178 (96%)	8 (4%)	0	100	100
55	AS	170/178 (96%)	160 (94%)	10 (6%)	0	100	100
56	AT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
57	AU	98/121 (81%)	92 (94%)	6 (6%)	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%)	114 (96%)	5 (4%)	0	100	100
61	AY	124/127 (98%)	118 (95%)	6 (5%)	0	100	100
62	AZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
63	Aa	146/149 (98%)	133 (91%)	13 (9%)	0	100	100
64	Ab	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
65	Ac	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
66	Ad	107/113 (95%)	100 (94%)	7 (6%)	0	100	100
67	Ae	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
68	Af	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
69	Ag	110/121 (91%)	105 (96%)	5 (4%)	0	100	100
70	Ah	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
71	Ai	97/100 (97%)	89 (92%)	8 (8%)	0	100	100
72	Aj	85/88 (97%)	81 (95%)	4 (5%)	0	100	100
73	Ak	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
74	Al	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
75	Am	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	Ao	103/106 (97%)	91 (88%)	12 (12%)	0	100	100
78	Ap	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
79	E	215/217 (99%)	206 (96%)	9 (4%)	0	100	100
80	DC	819/842 (97%)	759 (93%)	60 (7%)	0	100	100
81	V	187/312 (60%)	176 (94%)	11 (6%)	0	100	100
All	All	12115/13257 (91%)	11288 (93%)	827 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	110/124 (89%)	110 (100%)	0	100	100
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	113 (100%)	0	100	100
27	BU	100/114 (88%)	100 (100%)	0	100	100
28	BZ	61/89 (68%)	61 (100%)	0	100	100
29	Bc	56/60 (93%)	56 (100%)	0	100	100
30	Bd	47/49 (96%)	47 (100%)	0	100	100
31	Bg	256/262 (98%)	256 (100%)	0	100	100
32	Bf	66/135 (49%)	66 (100%)	0	100	100
33	BM	100/119 (84%)	100 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100
58	AV	104/105 (99%)	104 (100%)	0	100	100
59	AW	55/129 (43%)	55 (100%)	0	100	100
60	AX	105/118 (89%)	105 (100%)	0	100	100
61	AY	109/110 (99%)	109 (100%)	0	100	100
62	AZ	115/116 (99%)	115 (100%)	0	100	100
63	Aa	118/119 (99%)	118 (100%)	0	100	100
64	Ab	46/47 (98%)	46 (100%)	0	100	100
65	Ac	81/88 (92%)	81 (100%)	0	100	100
66	Ad	96/97 (99%)	96 (100%)	0	100	100
67	Ae	109/111 (98%)	109 (100%)	0	100	100
68	Af	90/91 (99%)	90 (100%)	0	100	100
69	Ag	95/103 (92%)	95 (100%)	0	100	100
70	Ah	104/105 (99%)	104 (100%)	0	100	100
71	Ai	81/82 (99%)	81 (100%)	0	100	100
72	Aj	70/71 (99%)	70 (100%)	0	100	100
73	Ak	68/69 (99%)	68 (100%)	0	100	100
74	Al	45/46 (98%)	45 (100%)	0	100	100
75	Am	47/116 (40%)	47 (100%)	0	100	100
76	An	23/23 (100%)	23 (100%)	0	100	100
77	Ao	90/91 (99%)	90 (100%)	0	100	100
78	Ap	71/72 (99%)	71 (100%)	0	100	100
79	E	198/198 (100%)	198 (100%)	0	100	100
80	DC	699/714 (98%)	699 (100%)	0	100	100
81	V	160/254 (63%)	160 (100%)	0	100	100
All	All	10346/11154 (93%)	10346 (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 (123) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	15	GLN
1	BA	30	GLN
1	BA	49	ASN
1	BA	69	ASN
2	BB	92	GLN
2	BB	95	ASN
2	BB	146	GLN
2	BB	149	GLN
2	BB	160	HIS
2	BB	209	ASN
3	BC	152	HIS
4	BE	50	ASN
4	BE	142	HIS
4	BE	157	ASN
4	BE	258	GLN
5	BG	176	GLN
5	BG	189	HIS
6	BH	11	GLN
6	BH	22	GLN
6	BH	160	GLN
6	BH	161	GLN
6	BH	174	ASN
7	BI	35	ASN
7	BI	159	GLN
8	BJ	123	HIS
9	BL	81	HIS
9	BL	106	ASN
9	BL	127	GLN
10	BN	49	GLN
12	BV	33	GLN
12	BV	35	ASN
14	BX	22	ASN
15	BY	15	ASN
15	BY	110	GLN
16	Ba	8	ASN
16	Ba	43	ASN
16	Ba	72	HIS
16	Ba	94	ASN
18	Be	17	GLN

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Mol	Chain	Res	Type
20	BF	100	ASN
20	BF	104	ASN
21	BK	12	HIS
21	BK	58	GLN
21	BK	93	GLN
23	BQ	8	GLN
23	BQ	94	GLN
23	BQ	100	GLN
24	BR	31	ASN
26	BT	16	ASN
26	BT	48	GLN
26	BT	93	HIS
29	Bc	43	ASN
30	Bd	37	ASN
31	Bg	106	HIS
35	AA	83	HIS
36	AB	224	HIS
36	AB	280	HIS
37	AC	237	GLN
37	AC	322	GLN
41	AD	264	GLN
42	AE	57	HIS
42	AE	97	ASN
44	AG	77	GLN
44	AG	123	GLN
44	AG	145	ASN
44	AG	191	ASN
45	AH	9	GLN
45	AH	102	ASN
45	AH	157	ASN
47	AJ	20	ASN
47	AJ	39	GLN
48	AL	120	GLN
49	AM	11	ASN
50	AN	95	GLN
50	AN	117	ASN
50	AN	156	HIS
51	AO	193[A]	GLN
52	AP	28	ASN
52	AP	55	GLN
52	AP	133	HIS
52	AP	179	GLN

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Mol	Chain	Res	Type
54	AR	3	ASN
54	AR	7	GLN
54	AR	66	HIS
54	AR	134	HIS
55	AS	74	ASN
56	AT	103	GLN
56	AT	131	GLN
58	AV	98	ASN
59	AW	58	HIS
61	AY	66	GLN
61	AY	120	GLN
62	AZ	36	HIS
62	AZ	122	HIS
64	Ab	48	HIS
65	Ac	11	ASN
66	Ad	21	HIS
66	Ad	87	ASN
68	Af	106	ASN
69	Ag	69	HIS
69	Ag	98	GLN
70	Ah	34	GLN
70	Ah	59	ASN
70	Ah	99	GLN
70	Ah	104	GLN
71	Ai	35	ASN
72	Aj	20	ASN
73	Ak	10	GLN
73	Ak	40	GLN
73	Ak	67	GLN
77	Ao	59	HIS
79	E	94	ASN
79	E	108	ASN
79	E	127	GLN
80	DC	18	ASN
80	DC	27	HIS
80	DC	91	GLN
80	DC	108	HIS
80	DC	355	GLN
80	DC	414	GLN
80	DC	603	ASN
80	DC	649	GLN
80	DC	657	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1780/1798 (98%)	414 (23%)	11 (0%)
38	A1	3194/3360 (95%)	595 (18%)	21 (0%)
39	A3	120/121 (99%)	11 (9%)	1 (0%)
40	A4	157/158 (99%)	30 (19%)	0
82	EC	187/202 (92%)	101 (54%)	7 (3%)
All	All	5438/5639 (96%)	1151 (21%)	40 (0%)

All (1151) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
34	B5	4	C
34	B5	9	U
34	B5	10	G
34	B5	11	A
34	B5	13	C
34	B5	17	C
34	B5	22	A
34	B5	25	C
34	B5	26	A
34	B5	34	G
34	B5	42	G
34	B5	47	A
34	B5	50	C
34	B5	57	G
34	B5	60	U
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	104	A
34	B5	111	U
34	B5	114	C
34	B5	115	G
34	B5	116	U
34	B5	127	G
34	B5	130	C

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Mol	Chain	Res	Type
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	154	G
34	B5	159	U
34	B5	162	A
34	B5	163	G
34	B5	164	A
34	B5	166	C
34	B5	167	U
34	B5	169	A
34	B5	178	U
34	B5	179	A
34	B5	181	A
34	B5	182	A
34	B5	185	U
34	B5	188	A
34	B5	190	C
34	B5	191	C
34	B5	192	U
34	B5	193	U
34	B5	194	U
34	B5	195	G
34	B5	196	G
34	B5	198	A
34	B5	217	A
34	B5	218	A
34	B5	223	U
34	B5	224	C
34	B5	225	A
34	B5	227	U
34	B5	228	G
34	B5	229	U
34	B5	230	C
34	B5	231	U

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Mol	Chain	Res	Type
34	B5	233	C
34	B5	234	G
34	B5	240	U
34	B5	241	U
34	B5	257	A
34	B5	261	U
34	B5	262	U
34	B5	265	A
34	B5	276	C
34	B5	278	U
34	B5	280	U
34	B5	281	G
34	B5	299	A
34	B5	314	C
34	B5	315	A
34	B5	316	A
34	B5	320	U
34	B5	321	C
34	B5	322	G
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	397	A
34	B5	399	A
34	B5	400	A
34	B5	401	A
34	B5	402	C
34	B5	419	G
34	B5	423	G
34	B5	424	C
34	B5	425	A
34	B5	426	G
34	B5	431	C
34	B5	434	G
34	B5	439	U
34	B5	444	C
34	B5	460	A
34	B5	468	A

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Mol	Chain	Res	Type
34	B5	475	A
34	B5	477	A
34	B5	484	C
34	B5	485	A
34	B5	487	G
34	B5	489	C
34	B5	490	C
34	B5	491	C
34	B5	492	A
34	B5	494	U
34	B5	495	C
34	B5	496	G
34	B5	497	G
34	B5	498	G
34	B5	499	U
34	B5	500	C
34	B5	503	G
34	B5	506	A
34	B5	507	U
34	B5	515	A
34	B5	519	C
34	B5	538	A
34	B5	539	G
34	B5	540	G
34	B5	541	A2M
34	B5	542	A
34	B5	549	G
34	B5	555	A
34	B5	557	G
34	B5	558	U
34	B5	559	C
34	B5	565	C
34	B5	568	G
34	B5	575	C
34	B5	577	G
34	B5	578	OMU
34	B5	579	A
34	B5	580	A
34	B5	582	U
34	B5	594	A
34	B5	595	G
34	B5	606	A

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Mol	Chain	Res	Type
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	658	C
34	B5	677	G
34	B5	678	A
34	B5	681	U
34	B5	683	C
34	B5	694	U
34	B5	696	C
34	B5	697	C
34	B5	698	U
34	B5	704	C
34	B5	705	U
34	B5	706	A
34	B5	709	C
34	B5	711	U
34	B5	712	G
34	B5	713	A
34	B5	715	U
34	B5	716	C
34	B5	717	C
34	B5	718	U
34	B5	719	U
34	B5	720	G
34	B5	721	U
34	B5	722	G
34	B5	724	C
34	B5	725	U
34	B5	727	U
34	B5	729	G

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Mol	Chain	Res	Type
34	B5	730	G
34	B5	731	C
34	B5	733	A
34	B5	734	A
34	B5	735	C
34	B5	740	A
34	B5	741	C
34	B5	753	A
34	B5	765	G
34	B5	766	U
34	B5	771	A
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	787	G
34	B5	789	A
34	B5	794	U
34	B5	812	A
34	B5	814	A
34	B5	819	G
34	B5	820	U
34	B5	821	U
34	B5	823	G
34	B5	832	U
34	B5	833	U
34	B5	836	U
34	B5	840	U
34	B5	846	G
34	B5	850	A
34	B5	851	U
34	B5	859	A
34	B5	862	A
34	B5	863	A
34	B5	895	G
34	B5	898	A
34	B5	899	G
34	B5	904	G

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Mol	Chain	Res	Type
34	B5	906	A
34	B5	907	A
34	B5	913	G
34	B5	914	G
34	B5	923	A
34	B5	933	A
34	B5	935	U
34	B5	951	A
34	B5	960	U
34	B5	966	A
34	B5	973	A
34	B5	987	G
34	B5	988	A
34	B5	992	A
34	B5	993	A
34	B5	998	A
34	B5	1000	C
34	B5	1003	A
34	B5	1004	U
34	B5	1005	A
34	B5	1020	A
34	B5	1021	C
34	B5	1023	A
34	B5	1026	A
34	B5	1028	C
34	B5	1029	U
34	B5	1032	G
34	B5	1039	A
34	B5	1040	G
34	B5	1052	U
34	B5	1056	U
34	B5	1058	U
34	B5	1059	U
34	B5	1060	U
34	B5	1061	A
34	B5	1062	A
34	B5	1076	A
34	B5	1083	G
34	B5	1092	A
34	B5	1093	A
34	B5	1097	U
34	B5	1100	G

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Mol	Chain	Res	Type
34	B5	1138	A
34	B5	1150	G
34	B5	1158	C
34	B5	1159	C
34	B5	1171	A
34	B5	1183	A
34	B5	1185	U
34	B5	1194	A
34	B5	1196	A
34	B5	1199	G
34	B5	1200	G
34	B5	1201	G
34	B5	1212	G
34	B5	1217	A
34	B5	1218	G
34	B5	1226	A
34	B5	1227	A
34	B5	1228	G
34	B5	1229	G
34	B5	1235	C
34	B5	1243	G
34	B5	1244	A
34	B5	1245	G
34	B5	1246	C
34	B5	1248	C
34	B5	1251	U
34	B5	1252	C
34	B5	1256	A
34	B5	1257	U
34	B5	1269	OMU
34	B5	1276	U
34	B5	1286	U
34	B5	1288	G
34	B5	1301	U
34	B5	1306	C
34	B5	1314	U
34	B5	1315	U
34	B5	1316	G
34	B5	1321	A
34	B5	1340	U
34	B5	1344	A
34	B5	1345	A

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Mol	Chain	Res	Type
34	B5	1346	A
34	B5	1347	U
34	B5	1355	C
34	B5	1360	A
34	B5	1362	U
34	B5	1363	U
34	B5	1364	G
34	B5	1366	U
34	B5	1368	G
34	B5	1370	U
34	B5	1371	A
34	B5	1372	U
34	B5	1373	C
34	B5	1382	A
34	B5	1390	U
34	B5	1392	U
34	B5	1398	U
34	B5	1399	C
34	B5	1400	A
34	B5	1402	G
34	B5	1413	U
34	B5	1414	U
34	B5	1415	U
34	B5	1427	A
34	B5	1428	OMG
34	B5	1432	U
34	B5	1436	A
34	B5	1445	G
34	B5	1459	C
34	B5	1460	A
34	B5	1469	A
34	B5	1471	A
34	B5	1486	G
34	B5	1489	U
34	B5	1491	U
34	B5	1492	A
34	B5	1493	A
34	B5	1496	U
34	B5	1506	G
34	B5	1510	U
34	B5	1516	A
34	B5	1521	G

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Mol	Chain	Res	Type
34	B5	1523	G
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	1563	C
34	B5	1565	C
34	B5	1569	A
34	B5	1576	A
34	B5	1584	G
34	B5	1600	A
34	B5	1601	G
34	B5	1616	G
34	B5	1619	C
34	B5	1635	A
34	B5	1646	C
34	B5	1658	G
34	B5	1659	A
34	B5	1663	G
34	B5	1680	G
34	B5	1683	C
34	B5	1684	U
34	B5	1688	U
34	B5	1693	A
34	B5	1700	C
34	B5	1701	A
34	B5	1703	C
34	B5	1709	C
34	B5	1716	C
34	B5	1717	G
34	B5	1746	A
34	B5	1756[A]	A
34	B5	1760	G
34	B5	1761	U
34	B5	1762	A
34	B5	1766	A
34	B5	1767	G
34	B5	1769	U
34	B5	1780	G
34	B5	1792	G

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Mol	Chain	Res	Type
34	B5	1793	G
34	B5	1794	A
34	B5	1795	U
34	B5	1796	C
34	B5	1799	U
38	A1	14	U
38	A1	26	A
38	A1	34	A
38	A1	40	A
38	A1	43	A
38	A1	49	A
38	A1	59	G
38	A1	60	A
38	A1	65	A
38	A1	66	A
38	A1	67	A
38	A1	71	A
38	A1	92	G
38	A1	109	A
38	A1	110	G
38	A1	111	C
38	A1	116	A
38	A1	118	U
38	A1	122	A
38	A1	134	U
38	A1	135	C
38	A1	136	G
38	A1	146	U
38	A1	148	G
38	A1	156	G
38	A1	157	A
38	A1	163	C
38	A1	164	A
38	A1	165	A
38	A1	166	C
38	A1	170	G
38	A1	174	C
38	A1	175	C
38	A1	178	U
38	A1	187	A
38	A1	190	U
38	A1	191	U

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Mol	Chain	Res	Type
38	A1	200	C
38	A1	206	G
38	A1	210	U
38	A1	219	A
38	A1	234	G
38	A1	237	G
38	A1	238	A
38	A1	239	G
38	A1	240	U
38	A1	241	G
38	A1	242	C
38	A1	243	G
38	A1	244	G
38	A1	245	U
38	A1	246	U
38	A1	248	U
38	A1	249	U
38	A1	250	U
38	A1	251	G
38	A1	252	U
38	A1	253	A
38	A1	254	A
38	A1	266	A
38	A1	269	G
38	A1	286	U
38	A1	295	A
38	A1	296	A
38	A1	305	U
38	A1	311	C
38	A1	329	U
38	A1	339	C
38	A1	346	C
38	A1	352	A
38	A1	370	U
38	A1	371	G
38	A1	372	A
38	A1	376	G
38	A1	387	A
38	A1	390	G
38	A1	398	A
38	A1	399	A
38	A1	401	U

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Mol	Chain	Res	Type
38	A1	402	A
38	A1	403	C
38	A1	407	A
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	521	A
38	A1	535	G
38	A1	540	U
38	A1	542	G
38	A1	545	U
38	A1	547	G
38	A1	548	G
38	A1	552	G
38	A1	557	A
38	A1	559	A
38	A1	560	G
38	A1	579	G
38	A1	591	G
38	A1	592	A
38	A1	602	A
38	A1	611	A
38	A1	620	U
38	A1	621	A
38	A1	622	A
38	A1	637	C
38	A1	649	A2M
38	A1	660	A
38	A1	677	A
38	A1	681	U
38	A1	690	A
38	A1	691	A
38	A1	705	A
38	A1	719	U
38	A1	725	G
38	A1	736	A
38	A1	758	C
38	A1	760	G
38	A1	765	C

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Mol	Chain	Res	Type
38	A1	766	U
38	A1	767	U
38	A1	774	G
38	A1	775	A
38	A1	777	U
38	A1	781	G
38	A1	785	G
38	A1	786	A
38	A1	799	G
38	A1	801	A
38	A1	806	A
38	A1	808	A
38	A1	813	G
38	A1	817	A2M
38	A1	830	A
38	A1	848	A
38	A1	849	C
38	A1	857	G
38	A1	861	C
38	A1	874	U
38	A1	879	U
38	A1	896	A
38	A1	897	U
38	A1	907	G
38	A1	908	OMG
38	A1	914	A
38	A1	916	G
38	A1	917	A
38	A1	921	A
38	A1	923	C
38	A1	934	G
38	A1	937	G
38	A1	943	U
38	A1	944	C
38	A1	959	C
38	A1	980	A
38	A1	981	U
38	A1	984	G
38	A1	994	G
38	A1	1000	C
38	A1	1002	A
38	A1	1010	G

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Mol	Chain	Res	Type
38	A1	1016	C
38	A1	1017	C
38	A1	1018	G
38	A1	1019	G
38	A1	1021	G
38	A1	1022	U
38	A1	1023	C
38	A1	1032	C
38	A1	1033	U
38	A1	1034	U
38	A1	1035	G
38	A1	1036	A
38	A1	1047	A
38	A1	1052	U
38	A1	1063	G
38	A1	1064	A
38	A1	1065	A
38	A1	1072	G
38	A1	1081	U
38	A1	1082	U
38	A1	1093	A
38	A1	1094	U
38	A1	1095	U
38	A1	1097	G
38	A1	1098	A
38	A1	1103	A
38	A1	1104	G
38	A1	1117	G
38	A1	1130	A
38	A1	1131	G
38	A1	1143	A
38	A1	1144	U
38	A1	1151	U
38	A1	1153	A
38	A1	1154	A
38	A1	1155	C
38	A1	1159	A
38	A1	1160	C
38	A1	1179	A
38	A1	1180	A
38	A1	1181	U
38	A1	1182	A

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Mol	Chain	Res	Type
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	1225	A
38	A1	1228	C
38	A1	1232	C
38	A1	1235	U
38	A1	1236	G
38	A1	1239	C
38	A1	1241	U
38	A1	1242	G
38	A1	1243	G
38	A1	1245	A
38	A1	1246	G
38	A1	1252	A
38	A1	1253	U
38	A1	1256	G
38	A1	1258	U
38	A1	1262	G
38	A1	1263	A
38	A1	1265	U
38	A1	1282	G
38	A1	1283	C
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

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Mol	Chain	Res	Type
38	A1	1354	G
38	A1	1355	A
38	A1	1356	U
38	A1	1357	G
38	A1	1386	A
38	A1	1392	G
38	A1	1399	A
38	A1	1400	G
38	A1	1418	A
38	A1	1419	A
38	A1	1431	G
38	A1	1434	G
38	A1	1437	OMC
38	A1	1446	A
38	A1	1455	U
38	A1	1468	A
38	A1	1475	A
38	A1	1481	A
38	A1	1483	G
38	A1	1488	G
38	A1	1496	C
38	A1	1508	C
38	A1	1523	U
38	A1	1533	U
38	A1	1536	G
38	A1	1539	A
38	A1	1555	U
38	A1	1556	C
38	A1	1558	A
38	A1	1562	C
38	A1	1563	C
38	A1	1564	U
38	A1	1565	G
38	A1	1567	U
38	A1	1568	U
38	A1	1569	U
38	A1	1574	C
38	A1	1575	A
38	A1	1576	G
38	A1	1579	C
38	A1	1583	A
38	A1	1589	A

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Mol	Chain	Res	Type
38	A1	1593	A
38	A1	1605	A
38	A1	1618	G
38	A1	1628	C
38	A1	1629	U
38	A1	1630	U
38	A1	1631	C
38	A1	1643	A
38	A1	1657	C
38	A1	1724	U
38	A1	1736	G
38	A1	1738	C
38	A1	1739	U
38	A1	1741	A
38	A1	1742	U
38	A1	1750	A
38	A1	1751	G
38	A1	1752	A
38	A1	1762	C
38	A1	1763	U
38	A1	1764	U
38	A1	1765	U
38	A1	1766	G
38	A1	1794	G
38	A1	1796	G
38	A1	1797	A
38	A1	1813	A
38	A1	1815	U
38	A1	1818	U
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	1866	C
38	A1	1878	G
38	A1	1880	U
38	A1	1886	A
38	A1	1893	A
38	A1	1906	G
38	A1	1932	A

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Mol	Chain	Res	Type
38	A1	1953	G
38	A1	1954	G
38	A1	1955	U
38	A1	2094	C
38	A1	2095	G
38	A1	2111	G
38	A1	2112	U
38	A1	2114	C
38	A1	2122	G
38	A1	2131	A
38	A1	2140	U
38	A1	2144	A
38	A1	2158	A
38	A1	2169	G
38	A1	2176	U
38	A1	2188	A
38	A1	2197	OMC
38	A1	2201	G
38	A1	2242	A
38	A1	2249	G
38	A1	2252	A
38	A1	2253	G
38	A1	2256	A
38	A1	2260	U
38	A1	2261	G
38	A1	2263	C
38	A1	2265	C
38	A1	2267	C
38	A1	2268	U
38	A1	2269	U
38	A1	2272	G
38	A1	2273	G
38	A1	2277	C
38	A1	2278	5MC
38	A1	2279	A
38	A1	2280	A2M
38	A1	2281	A2M
38	A1	2284	C
38	A1	2307	G
38	A1	2310	U
38	A1	2313	A
38	A1	2314	U

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Mol	Chain	Res	Type
38	A1	2315	G
38	A1	2334	U
38	A1	2335	G
38	A1	2336	U
38	A1	2340	U
38	A1	2365	C
38	A1	2366	C
38	A1	2373	A
38	A1	2374	C
38	A1	2375	G
38	A1	2383	C
38	A1	2388	U
38	A1	2393	G
38	A1	2397	A
38	A1	2402	A
38	A1	2403	G
38	A1	2404	A
38	A1	2411	U
38	A1	2418	G
38	A1	2435	G
38	A1	2438	A
38	A1	2439	A
38	A1	2440	G
38	A1	2441	A
38	A1	2442	G
38	A1	2445	A
38	A1	2447	A
38	A1	2450	G
38	A1	2453	U
38	A1	2454	G
38	A1	2455	U
38	A1	2459	A
38	A1	2460	U
38	A1	2461	A
38	A1	2462	A
38	A1	2463	G
38	A1	2467	G
38	A1	2468	A
38	A1	2469	G
38	A1	2474	G
38	A1	2477	G
38	A1	2479	C

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Mol	Chain	Res	Type
38	A1	2485	A
38	A1	2487	U
38	A1	2490	C
38	A1	2491	A
38	A1	2492	C
38	A1	2493	U
38	A1	2495	C
38	A1	2496	C
38	A1	2497	U
38	A1	2498	U
38	A1	2499	U
38	A1	2500	A
38	A1	2502	A
38	A1	2503	G
38	A1	2504	U
38	A1	2505	U
38	A1	2511	A
38	A1	2514	U
38	A1	2515	A
38	A1	2523	A
38	A1	2524	A
38	A1	2525	G
38	A1	2537	U
38	A1	2538	U
38	A1	2539	C
38	A1	2540	A
38	A1	2541	U
38	A1	2543	U
38	A1	2544	U
38	A1	2549	G
38	A1	2550	U
38	A1	2552	C
38	A1	2554	A
38	A1	2560	C
38	A1	2561	A
38	A1	2569	A
38	A1	2571	U
38	A1	2572	C
38	A1	2573	G
38	A1	2585	G
38	A1	2593	A
38	A1	2595	A

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Mol	Chain	Res	Type
38	A1	2596	U
38	A1	2606	G
38	A1	2607	G
38	A1	2614	G
38	A1	2626	A
38	A1	2628	A
38	A1	2635	A
38	A1	2638	C
38	A1	2648	G
38	A1	2652	U
38	A1	2656	A
38	A1	2664	C
38	A1	2672	G
38	A1	2674	A
38	A1	2677	G
38	A1	2678	A
38	A1	2680	A
38	A1	2681	U
38	A1	2688	U
38	A1	2689	A
38	A1	2691	A
38	A1	2704	A
38	A1	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	2777	G
38	A1	2778	G
38	A1	2796	G
38	A1	2799	A
38	A1	2800	G
38	A1	2801	A
38	A1	2803	A
38	A1	2810	C
38	A1	2814	G
38	A1	2816	G
38	A1	2817	A
38	A1	2842	U

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Mol	Chain	Res	Type
38	A1	2844	C
38	A1	2845	A
38	A1	2871	G
38	A1	2872	A
38	A1	2875	U
38	A1	2876	C
38	A1	2887	A
38	A1	2889	C
38	A1	2898	G
38	A1	2923	U
38	A1	2933	A
38	A1	2935	U
38	A1	2936	A
38	A1	2938	G
38	A1	2947	G
38	A1	2954	U
38	A1	2972	G
38	A1	2977	G
38	A1	2983	C
38	A1	2990	G
38	A1	2997	G
38	A1	3011	A
38	A1	3012	A
38	A1	3022	G
38	A1	3032	A
38	A1	3055	U
38	A1	3056	U
38	A1	3059	G
38	A1	3078	U
38	A1	3086	A
38	A1	3092	C
38	A1	3094	A
38	A1	3101	G
38	A1	3104	U
38	A1	3113	A
38	A1	3122	A
38	A1	3130	A
38	A1	3131	U
38	A1	3142	A
38	A1	3143	C
38	A1	3153	U
38	A1	3154	C

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Mol	Chain	Res	Type
38	A1	3155	U
38	A1	3156	U
38	A1	3157	U
38	A1	3165	A
38	A1	3170	A
38	A1	3172	A
38	A1	3173	G
38	A1	3174	A
38	A1	3175	U
38	A1	3176	G
38	A1	3179	U
38	A1	3181	C
38	A1	3187	A
38	A1	3196	U
38	A1	3198	U
38	A1	3206	C
38	A1	3207	U
38	A1	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	3247	G
38	A1	3259	U
38	A1	3263	G
38	A1	3270	U
38	A1	3271	G
38	A1	3274	A
38	A1	3275	U
38	A1	3276	G
38	A1	3281	U
38	A1	3289	G
38	A1	3294	A
38	A1	3303	G
38	A1	3304	U
38	A1	3313	U
38	A1	3316	A
38	A1	3319	U
38	A1	3342	A
38	A1	3345	G

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Mol	Chain	Res	Type
38	A1	3351	U
38	A1	3352	U
38	A1	3353	G
38	A1	3354	U
38	A1	3355	U
38	A1	3356	G
38	A1	3368	U
38	A1	3369	G
38	A1	3375	A
38	A1	3378	C
38	A1	3389	U
38	A1	3390	G
39	A3	53	U
39	A3	54	U
39	A3	55	A
39	A3	64	A
39	A3	65	G
39	A3	74	C
39	A3	76	A
39	A3	99	G
39	A3	102	A
39	A3	112	G
39	A3	121	U
40	A4	33	A
40	A4	34	U
40	A4	35	C
40	A4	39	G
40	A4	51	G
40	A4	52	A
40	A4	53	A
40	A4	59	A
40	A4	62	C
40	A4	63	G
40	A4	76	C
40	A4	81	U
40	A4	82	U
40	A4	83	C
40	A4	85	G
40	A4	86	U
40	A4	87	G
40	A4	88	A
40	A4	90	U

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Mol	Chain	Res	Type
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
82	EC	6762	U
82	EC	6768	U
82	EC	6769	A
82	EC	6770	U
82	EC	6771	U
82	EC	6772	G
82	EC	6773	G
82	EC	6774	U
82	EC	6775	U
82	EC	6776	A
82	EC	6777	C
82	EC	6778	C
82	EC	6779	C
82	EC	6780	A
82	EC	6782	C
82	EC	6788	C
82	EC	6789	G
82	EC	6790	A
82	EC	6791	A
82	EC	6792	A
82	EC	6793	A
82	EC	6794	C
82	EC	6800	G
82	EC	6801	A
82	EC	6802	A
82	EC	6803	C
82	EC	6804	A
82	EC	6811	G
82	EC	6816	A
82	EC	6817	A
82	EC	6818	G

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Mol	Chain	Res	Type
82	EC	6819	G
82	EC	6820	C
82	EC	6821	U
82	EC	6822	U
82	EC	6823	U
82	EC	6824	C
82	EC	6831	U
82	EC	6832	G
82	EC	6835	U
82	EC	6837	G
82	EC	6840	A
82	EC	6841	U
82	EC	6842	U
82	EC	6843	U
82	EC	6845	G
82	EC	6847	G
82	EC	6848	U
82	EC	6849	A
82	EC	6850	C
82	EC	6852	U
82	EC	6855	A
82	EC	6856	C
82	EC	6857	C
82	EC	6859	U
82	EC	6860	A
82	EC	6861	G
82	EC	6864	A
82	EC	6866	C
82	EC	6867	C
82	EC	6869	C
82	EC	6870	A
82	EC	6871	A
82	EC	6872	A
82	EC	6873	A
82	EC	6874	A
82	EC	6875	C
82	EC	6877	C
82	EC	6880	G
82	EC	6881	U
82	EC	6882	G
82	EC	6884	G
82	EC	6886	A

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Mol	Chain	Res	Type
82	EC	6887	G
82	EC	6889	A
82	EC	6890	A
82	EC	6895	C
82	EC	6896	A
82	EC	6897	G
82	EC	6902	U
82	EC	6903	U
82	EC	6908	C
82	EC	6910	A
82	EC	6911	A
82	EC	6915	G
82	EC	6916	A
82	EC	6918	A
82	EC	6919	G
82	EC	6925	C
82	EC	6928	G
82	EC	6929	C
82	EC	6935	G
82	EC	6938	A
82	EC	6940	U
82	EC	6941	U
82	EC	6942	A
82	EC	6943	A
82	EC	6944	U
82	EC	6945	U
82	EC	6946	A
82	EC	6948	U

All (40) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	B5	10	G
34	B5	752	A
34	B5	819	G
34	B5	862	A
34	B5	950	C
34	B5	1285	U
34	B5	1344	A
34	B5	1369	U
34	B5	1458	G
34	B5	1600	A

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Mol	Chain	Res	Type
34	B5	1645	G
38	A1	165	A
38	A1	237	G
38	A1	239	G
38	A1	240	U
38	A1	241	G
38	A1	244	G
38	A1	248	U
38	A1	249	U
38	A1	252	U
38	A1	253	A
38	A1	916	G
38	A1	1092	C
38	A1	1218	U
38	A1	1242	G
38	A1	1292	C
38	A1	1354	G
38	A1	1629	U
38	A1	2241	U
38	A1	2280	A2M
38	A1	2875	U
38	A1	3121	U
39	A3	52	G
82	EC	6789	G
82	EC	6831	U
82	EC	6844	A
82	EC	6851	G
82	EC	6876	A
82	EC	6889	A
82	EC	6943	A

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
34	G7M	B5	1575	34	23,26,27	2.52	6 (26%)	34,39,42	3.17	16 (47%)
38	A2M	A1	876	38	22,25,26	1.49	4 (18%)	30,36,39	2.02	8 (26%)
38	A2M	A1	2280	38	22,25,26	1.48	4 (18%)	30,36,39	2.11	8 (26%)
34	MA6	B5	1782	34	23,26,27	1.44	5 (21%)	33,38,41	2.14	11 (33%)
38	A2M	A1	817	83,38	22,25,26	1.50	5 (22%)	30,36,39	2.07	9 (30%)
34	OMU	B5	578	34	19,22,23	1.19	2 (10%)	25,31,34	1.80	5 (20%)
38	OMC	A1	2337	38	19,22,23	0.80	0	25,31,34	0.90	1 (4%)
38	OMU	A1	2417	38	19,22,23	1.25	3 (15%)	25,31,34	1.76	4 (16%)
38	1MA	A1	2142	83,38	21,25,26	1.33	4 (19%)	30,37,40	1.70	4 (13%)
34	A2M	B5	28	34,83	22,25,26	1.50	4 (18%)	30,36,39	2.05	8 (26%)
38	A2M	A1	2946	83,38	22,25,26	1.47	5 (22%)	30,36,39	2.20	10 (33%)
38	OMG	A1	805	38	23,26,27	1.19	3 (13%)	32,38,41	1.98	6 (18%)
38	OMC	A1	2959	38	19,22,23	0.80	0	25,31,34	0.82	0
34	OMC	B5	1007	34	19,22,23	0.81	0	25,31,34	0.94	1 (4%)
34	A2M	B5	974	34	22,25,26	1.49	4 (18%)	30,36,39	2.07	9 (30%)
38	A2M	A1	2640	38	22,25,26	1.50	4 (18%)	30,36,39	2.06	8 (26%)
34	OMG	B5	1572	34	23,26,27	1.19	3 (13%)	32,38,41	2.01	6 (18%)
38	OMG	A1	2619	38	23,26,27	1.19	3 (13%)	32,38,41	1.99	6 (18%)
34	OMG	B5	1428	34	23,26,27	1.19	3 (13%)	32,38,41	1.96	6 (18%)
38	A2M	A1	649	38	22,25,26	1.48	4 (18%)	30,36,39	2.03	8 (26%)
38	A2M	A1	2281	38	22,25,26	1.43	4 (18%)	30,36,39	2.22	10 (33%)
34	OMU	B5	1269	34	19,22,23	1.29	4 (21%)	25,31,34	1.90	8 (32%)
34	OMG	B5	1126	34	23,26,27	1.19	3 (13%)	32,38,41	1.95	6 (18%)
34	OMG	B5	1271	34	23,26,27	1.19	3 (13%)	32,38,41	1.93	6 (18%)
38	5MC	A1	2870	83,38	19,22,23	1.48	3 (15%)	26,32,35	1.30	3 (11%)
34	A2M	B5	420	34	22,25,26	1.48	4 (18%)	30,36,39	2.07	10 (33%)
38	OMG	A1	908	38	23,26,27	1.21	3 (13%)	32,38,41	2.00	6 (18%)
38	OMG	A1	867	38	23,26,27	1.18	3 (13%)	32,38,41	1.99	6 (18%)
34	XSX	B5	1191	34	24,28,29	1.00	1 (4%)	30,40,43	2.10	7 (23%)
34	A2M	B5	100	34,83	22,25,26	1.49	4 (18%)	30,36,39	2.06	8 (26%)
38	OMG	A1	1450	83,38	23,26,27	1.19	3 (13%)	32,38,41	1.98	6 (18%)
38	OMU	A1	2729	38	19,22,23	1.29	3 (15%)	25,31,34	1.72	5 (20%)
38	OMC	A1	663	38	19,22,23	0.81	0	25,31,34	0.78	0
34	A2M	B5	619	34,83	22,25,26	1.48	5 (22%)	30,36,39	2.03	9 (30%)
38	A2M	A1	1133	38	22,25,26	1.48	5 (22%)	30,36,39	2.15	10 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	OMC	A1	650	83,38	19,22,23	0.80	0	25,31,34	0.80	0
34	OMG	B5	562	34	23,26,27	1.19	3 (13%)	32,38,41	1.98	6 (18%)
34	MA6	B5	1781	34	23,26,27	1.55	4 (17%)	33,38,41	2.10	10 (30%)
38	OMU	A1	1888	38	19,22,23	1.28	3 (15%)	25,31,34	1.85	4 (16%)
38	A2M	A1	1449	83,38	22,25,26	1.52	4 (18%)	30,36,39	1.99	7 (23%)
34	4AC	B5	1280	34	21,24,25	1.04	1 (4%)	28,34,37	1.09	2 (7%)
38	OMU	A1	2347	38	19,22,23	1.31	4 (21%)	25,31,34	1.81	6 (24%)
38	1MA	A1	645	83,38	21,25,26	1.36	4 (19%)	30,37,40	1.71	6 (20%)
38	OMG	A1	2288	38	23,26,27	1.21	3 (13%)	32,38,41	2.03	6 (18%)
34	A2M	B5	541	34	22,25,26	1.53	4 (18%)	30,36,39	2.17	7 (23%)
38	UR3	A1	2634	38	19,22,23	0.98	0	26,32,35	1.71	3 (11%)
38	OMU	A1	2921	38	19,22,23	1.24	3 (15%)	25,31,34	1.84	5 (20%)
34	OMC	B5	1639	34	19,22,23	0.79	0	25,31,34	0.80	1 (4%)
38	A2M	A1	2220	38	22,25,26	1.51	5 (22%)	30,36,39	1.97	10 (33%)
34	A2M	B5	436	34	22,25,26	1.50	4 (18%)	30,36,39	2.08	10 (33%)
38	OMC	A1	1437	83,38	19,22,23	0.84	0	25,31,34	1.24	3 (12%)
38	OMU	A1	2724	38	19,22,23	1.23	3 (15%)	25,31,34	1.82	5 (20%)
38	OMG	A1	2793	38	23,26,27	1.19	3 (13%)	32,38,41	1.93	6 (18%)
38	OMG	A1	2815	38	23,26,27	1.19	3 (13%)	32,38,41	2.00	6 (18%)
38	OMC	A1	2948	38	19,22,23	0.83	0	25,31,34	1.10	2 (8%)
36	HIC	AB	243	36	10,11,12	1.46	1 (10%)	9,14,16	1.40	2 (22%)
38	OMC	A1	2197	38	19,22,23	0.78	0	25,31,34	0.80	0
34	A2M	B5	796	34	22,25,26	1.49	4 (18%)	30,36,39	2.28	9 (30%)
38	A2M	A1	807	38	22,25,26	1.50	5 (22%)	30,36,39	2.05	9 (30%)
38	OMG	A1	2922	38	23,26,27	1.20	3 (13%)	32,38,41	1.96	6 (18%)
38	OMU	A1	898	38	19,22,23	1.25	3 (15%)	25,31,34	1.78	5 (20%)
34	4AC	B5	1773	34	21,24,25	1.05	1 (4%)	28,34,37	1.38	5 (17%)
38	OMU	A1	2421	38	19,22,23	1.26	3 (15%)	25,31,34	1.84	5 (20%)
80	DDE	DC	699	80	18,20,21	1.02	1 (5%)	17,28,30	0.91	1 (5%)
38	OMG	A1	2791	38	23,26,27	1.18	3 (13%)	32,38,41	1.97	5 (15%)
34	OMC	B5	414	34	19,22,23	0.80	0	25,31,34	0.82	1 (4%)
38	5MC	A1	2278	83,38	19,22,23	1.47	3 (15%)	26,32,35	1.27	3 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	G7M	B5	1575	34	-	0/7/25/26	0/3/3/3
38	A2M	A1	876	38	-	1/9/27/28	0/3/3/3
38	A2M	A1	2280	38	-	2/9/27/28	0/3/3/3
34	MA6	B5	1782	34	-	5/11/29/30	0/3/3/3
38	A2M	A1	817	83,38	-	1/9/27/28	0/3/3/3
34	OMU	B5	578	34	-	4/9/27/28	0/2/2/2
38	OMC	A1	2337	38	-	1/9/27/28	0/2/2/2
38	OMU	A1	2417	38	-	1/9/27/28	0/2/2/2
38	1MA	A1	2142	83,38	-	1/7/25/26	0/3/3/3
34	A2M	B5	28	34,83	-	0/9/27/28	0/3/3/3
38	A2M	A1	2946	83,38	-	1/9/27/28	0/3/3/3
38	OMG	A1	805	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2
34	OMC	B5	1007	34	-	1/9/27/28	0/2/2/2
34	A2M	B5	974	34	-	0/9/27/28	0/3/3/3
38	A2M	A1	2640	38	-	1/9/27/28	0/3/3/3
34	OMG	B5	1572	34	-	0/9/27/28	0/3/3/3
38	OMG	A1	2619	38	-	1/9/27/28	0/3/3/3
34	OMG	B5	1428	34	-	4/9/27/28	0/3/3/3
38	A2M	A1	649	38	-	1/9/27/28	0/3/3/3
38	A2M	A1	2281	38	-	1/9/27/28	0/3/3/3
34	OMU	B5	1269	34	-	4/9/27/28	0/2/2/2
34	OMG	B5	1126	34	-	2/9/27/28	0/3/3/3
34	OMG	B5	1271	34	-	1/9/27/28	0/3/3/3
38	5MC	A1	2870	83,38	-	4/7/25/26	0/2/2/2
34	A2M	B5	420	34	-	1/9/27/28	0/3/3/3
38	OMG	A1	908	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	867	38	-	1/9/27/28	0/3/3/3
34	XSX	B5	1191	34	-	4/16/34/35	0/2/2/2
34	A2M	B5	100	34,83	-	2/9/27/28	0/3/3/3
38	OMG	A1	1450	83,38	-	1/9/27/28	0/3/3/3
38	OMU	A1	2729	38	-	3/9/27/28	0/2/2/2
38	OMC	A1	663	38	-	1/9/27/28	0/2/2/2
34	A2M	B5	619	34,83	-	3/9/27/28	0/3/3/3
38	A2M	A1	1133	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	650	83,38	-	0/9/27/28	0/2/2/2
34	OMG	B5	562	34	-	0/9/27/28	0/3/3/3
34	MA6	B5	1781	34	-	3/11/29/30	0/3/3/3
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	A2M	A1	1449	83,38	-	0/9/27/28	0/3/3/3
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	OMU	A1	2347	38	-	0/9/27/28	0/2/2/2
38	1MA	A1	645	83,38	-	0/7/25/26	0/3/3/3
38	OMG	A1	2288	38	-	0/9/27/28	0/3/3/3
34	A2M	B5	541	34	-	4/9/27/28	0/3/3/3
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
34	OMC	B5	1639	34	-	0/9/27/28	0/2/2/2
38	A2M	A1	2220	38	-	0/9/27/28	0/3/3/3
34	A2M	B5	436	34	-	1/9/27/28	0/3/3/3
38	OMC	A1	1437	83,38	-	2/9/27/28	0/2/2/2
38	OMU	A1	2724	38	-	1/9/27/28	0/2/2/2
38	OMG	A1	2793	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	2815	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2948	38	-	1/9/27/28	0/2/2/2
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
38	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
34	A2M	B5	796	34	-	0/9/27/28	0/3/3/3
38	A2M	A1	807	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	898	38	-	1/9/27/28	0/2/2/2
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
38	OMU	A1	2421	38	-	1/9/27/28	0/2/2/2
80	DDE	DC	699	80	-	6/20/21/23	0/1/1/1
38	OMG	A1	2791	38	-	1/9/27/28	0/3/3/3
34	OMC	B5	414	34	-	1/9/27/28	0/2/2/2
38	5MC	A1	2278	83,38	-	0/7/25/26	0/2/2/2

All (192) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	C8-N7	7.96	1.46	1.33
38	A1	2278	5MC	C5-C4	5.03	1.47	1.44
34	B5	541	A2M	C5-C4	4.86	1.47	1.39
34	B5	1781	MA6	C5-C4	4.85	1.47	1.39
38	A1	2870	5MC	C5-C4	4.85	1.47	1.44
34	B5	436	A2M	C5-C4	4.66	1.47	1.39
38	A1	2220	A2M	C5-C4	4.63	1.47	1.39
38	A1	1449	A2M	C5-C4	4.62	1.47	1.39
34	B5	796	A2M	C5-C4	4.60	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	974	A2M	C5-C4	4.57	1.47	1.39
34	B5	28	A2M	C5-C4	4.57	1.47	1.39
38	A1	2640	A2M	C5-C4	4.55	1.47	1.39
38	A1	876	A2M	C5-C4	4.54	1.47	1.39
34	B5	420	A2M	C5-C4	4.53	1.47	1.39
38	A1	2280	A2M	C5-C4	4.52	1.47	1.39
38	A1	807	A2M	C5-C4	4.50	1.47	1.39
34	B5	619	A2M	C5-C4	4.47	1.47	1.39
34	B5	100	A2M	C5-C4	4.47	1.47	1.39
38	A1	649	A2M	C5-C4	4.47	1.47	1.39
34	B5	1782	MA6	C5-C4	4.41	1.47	1.39
38	A1	2946	A2M	C5-C4	4.40	1.46	1.39
38	A1	817	A2M	C5-C4	4.40	1.46	1.39
38	A1	1133	A2M	C5-C4	4.37	1.46	1.39
34	B5	1575	G7M	C5-N7	-4.32	1.34	1.39
38	A1	2281	A2M	C5-C4	4.31	1.46	1.39
34	B5	1575	G7M	C8-N9	4.11	1.46	1.35
34	B5	1575	G7M	C5-C4	3.54	1.47	1.38
34	B5	1781	MA6	C5-C6	3.20	1.49	1.41
34	B5	1428	OMG	C5-C4	3.16	1.47	1.38
38	A1	908	OMG	C5-C4	3.15	1.47	1.38
38	A1	2288	OMG	C5-C4	3.13	1.47	1.38
34	B5	562	OMG	C5-C4	3.12	1.47	1.38
38	A1	1450	OMG	C5-C4	3.11	1.47	1.38
38	A1	2922	OMG	C5-C4	3.10	1.47	1.38
38	A1	2619	OMG	C5-C4	3.10	1.47	1.38
38	A1	645	1MA	C6-N6	3.09	1.35	1.28
34	B5	1271	OMG	C5-C4	3.08	1.47	1.38
34	B5	1572	OMG	C5-C4	3.06	1.47	1.38
38	A1	2793	OMG	C5-C4	3.03	1.47	1.38
38	A1	867	OMG	C5-C4	3.03	1.47	1.38
38	A1	2791	OMG	C5-C4	3.02	1.47	1.38
38	A1	2815	OMG	C5-C4	3.01	1.47	1.38
38	A1	2142	1MA	C5-C4	2.98	1.46	1.38
38	A1	2142	1MA	C6-N6	2.98	1.35	1.28
38	A1	645	1MA	C5-C4	2.98	1.46	1.38
34	B5	1126	OMG	C5-C4	2.95	1.46	1.38
34	B5	1280	4AC	C4-N4	-2.92	1.35	1.39
38	A1	2347	OMU	C4-N3	-2.92	1.33	1.38
38	A1	805	OMG	C5-C4	2.90	1.46	1.38
38	A1	2729	OMU	C4-N3	-2.90	1.33	1.38
38	A1	2421	OMU	C4-N3	-2.87	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	AB	243	HIC	CD2-CG	2.86	1.41	1.36
38	A1	2870	5MC	C6-C5	2.86	1.39	1.34
38	A1	1888	OMU	C4-N3	-2.86	1.33	1.38
38	A1	2921	OMU	C4-N3	-2.85	1.33	1.38
34	B5	1773	4AC	C4-N4	-2.81	1.35	1.39
38	A1	898	OMU	C4-N3	-2.80	1.33	1.38
34	B5	541	A2M	C5-C6	2.80	1.48	1.41
38	A1	2417	OMU	C4-N3	-2.79	1.33	1.38
38	A1	2724	OMU	C4-N3	-2.77	1.33	1.38
34	B5	28	A2M	C5-C6	2.71	1.48	1.41
38	A1	2640	A2M	C5-C6	2.71	1.48	1.41
34	B5	436	A2M	C5-C6	2.70	1.48	1.41
34	B5	1269	OMU	C4-N3	-2.68	1.34	1.38
38	A1	2815	OMG	C6-N1	-2.67	1.33	1.38
38	A1	817	A2M	C5-C6	2.66	1.48	1.41
34	B5	1782	MA6	C5-C6	2.66	1.48	1.41
34	B5	420	A2M	C5-C6	2.65	1.48	1.41
38	A1	876	A2M	C5-C6	2.65	1.48	1.41
38	A1	2278	5MC	C6-C5	2.64	1.38	1.34
38	A1	2288	OMG	C6-N1	-2.62	1.33	1.38
38	A1	1449	A2M	C5-N7	-2.62	1.34	1.39
34	B5	619	A2M	C5-C6	2.61	1.48	1.41
38	A1	2280	A2M	C5-C6	2.61	1.48	1.41
34	B5	796	A2M	C5-C6	2.61	1.48	1.41
38	A1	2793	OMG	C6-N1	-2.61	1.34	1.38
38	A1	2619	OMG	C6-N1	-2.60	1.34	1.38
38	A1	649	A2M	C5-C6	2.60	1.48	1.41
34	B5	1269	OMU	C2-N1	2.59	1.42	1.38
34	B5	974	A2M	C5-C6	2.59	1.48	1.41
34	B5	1126	OMG	C6-N1	-2.59	1.34	1.38
38	A1	807	A2M	C5-C6	2.58	1.48	1.41
34	B5	578	OMU	C4-N3	-2.57	1.34	1.38
34	B5	100	A2M	C5-N7	-2.57	1.34	1.39
38	A1	805	OMG	C6-N1	-2.56	1.34	1.38
38	A1	2922	OMG	C6-N1	-2.55	1.34	1.38
38	A1	908	OMG	C6-N1	-2.55	1.34	1.38
38	A1	1133	A2M	C5-C6	2.55	1.48	1.41
38	A1	2791	OMG	C6-N1	-2.55	1.34	1.38
34	B5	562	OMG	C6-N1	-2.53	1.34	1.38
80	DC	699	DDE	CD2-CG	2.52	1.41	1.36
38	A1	2946	A2M	C5-C6	2.52	1.48	1.41
34	B5	100	A2M	C5-C6	2.52	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	807	A2M	C5-N7	-2.52	1.34	1.39
34	B5	1271	OMG	C6-N1	-2.51	1.34	1.38
38	A1	1450	OMG	C6-N1	-2.50	1.34	1.38
38	A1	1449	A2M	C5-C6	2.50	1.48	1.41
38	A1	867	OMG	C6-N1	-2.49	1.34	1.38
38	A1	2281	A2M	C5-N7	-2.49	1.34	1.39
38	A1	2220	A2M	C5-N7	-2.49	1.34	1.39
38	A1	2921	OMU	C2-N3	-2.46	1.33	1.38
38	A1	2280	A2M	C5-N7	-2.46	1.34	1.39
34	B5	1191	XSX	C2-N1	2.45	1.41	1.38
34	B5	1572	OMG	C6-N1	-2.45	1.34	1.38
38	A1	1133	A2M	C5-N7	-2.44	1.34	1.39
34	B5	1428	OMG	C6-N1	-2.43	1.34	1.38
38	A1	2946	A2M	C5-N7	-2.42	1.34	1.39
38	A1	2220	A2M	C5-C6	2.42	1.47	1.41
38	A1	817	A2M	C5-N7	-2.42	1.34	1.39
38	A1	649	A2M	C5-N7	-2.41	1.34	1.39
38	A1	2421	OMU	C2-N3	-2.41	1.33	1.38
38	A1	898	OMU	C2-N3	-2.41	1.33	1.38
38	A1	876	A2M	C5-N7	-2.40	1.34	1.39
38	A1	2640	A2M	C5-N7	-2.39	1.34	1.39
38	A1	2870	5MC	C6-N1	-2.39	1.33	1.38
38	A1	2281	A2M	C5-C6	2.39	1.47	1.41
34	B5	436	A2M	C5-N7	-2.37	1.34	1.39
38	A1	2729	OMU	C2-N3	-2.37	1.33	1.38
34	B5	541	A2M	C5-N7	-2.36	1.34	1.39
34	B5	619	A2M	C5-N7	-2.36	1.34	1.39
34	B5	974	A2M	C5-N7	-2.36	1.34	1.39
34	B5	28	A2M	C5-N7	-2.36	1.34	1.39
34	B5	1575	G7M	C2'-C3'	-2.34	1.47	1.53
34	B5	796	A2M	C5-N7	-2.34	1.34	1.39
34	B5	420	A2M	C5-N7	-2.33	1.34	1.39
38	A1	2724	OMU	C2-N3	-2.32	1.33	1.38
38	A1	1888	OMU	C2-N3	-2.32	1.33	1.38
34	B5	1782	MA6	C5-N7	-2.31	1.34	1.39
34	B5	796	A2M	C8-N7	2.31	1.36	1.31
38	A1	908	OMG	C5-N7	-2.31	1.34	1.39
38	A1	2417	OMU	C2-N3	-2.30	1.34	1.38
38	A1	2347	OMU	C2-N3	-2.29	1.34	1.38
38	A1	2278	5MC	C6-N1	-2.29	1.34	1.38
38	A1	2142	1MA	C5-N7	-2.29	1.34	1.39
38	A1	2417	OMU	C5-C4	-2.29	1.38	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2640	A2M	C8-N7	2.28	1.36	1.31
34	B5	619	A2M	C8-N7	2.28	1.36	1.31
34	B5	436	A2M	C8-N7	2.27	1.36	1.31
38	A1	2729	OMU	C5-C4	-2.27	1.38	1.43
38	A1	898	OMU	C5-C4	-2.26	1.38	1.43
38	A1	2815	OMG	C5-N7	-2.26	1.34	1.39
34	B5	1781	MA6	C8-N7	2.25	1.36	1.31
38	A1	2142	1MA	C2-N3	2.25	1.34	1.30
34	B5	1575	G7M	C6-N1	-2.24	1.34	1.38
34	B5	578	OMU	C2-N3	-2.23	1.34	1.38
38	A1	2922	OMG	C5-N7	-2.23	1.34	1.39
38	A1	645	1MA	C5-N7	-2.23	1.34	1.39
38	A1	2347	OMU	C5-C4	-2.23	1.38	1.43
38	A1	2347	OMU	C2-N1	2.23	1.42	1.38
34	B5	1428	OMG	C5-N7	-2.22	1.34	1.39
38	A1	2288	OMG	C5-N7	-2.22	1.34	1.39
34	B5	28	A2M	C8-N7	2.22	1.36	1.31
34	B5	420	A2M	C8-N7	2.22	1.36	1.31
38	A1	2724	OMU	C5-C4	-2.22	1.38	1.43
34	B5	974	A2M	C8-N7	2.21	1.35	1.31
34	B5	1126	OMG	C5-N7	-2.20	1.34	1.39
38	A1	1888	OMU	C5-C4	-2.20	1.38	1.43
38	A1	2421	OMU	C5-C4	-2.19	1.38	1.43
38	A1	1450	OMG	C5-N7	-2.19	1.34	1.39
38	A1	2946	A2M	C8-N7	2.18	1.35	1.31
38	A1	2220	A2M	C4-N9	-2.18	1.33	1.37
38	A1	2619	OMG	C5-N7	-2.17	1.34	1.39
38	A1	817	A2M	C8-N7	2.17	1.35	1.31
34	B5	541	A2M	C8-N7	2.17	1.35	1.31
38	A1	876	A2M	C8-N7	2.17	1.35	1.31
38	A1	1133	A2M	C8-N7	2.16	1.35	1.31
38	A1	2793	OMG	C5-N7	-2.16	1.34	1.39
38	A1	1449	A2M	C8-N7	2.16	1.35	1.31
34	B5	1269	OMU	C2-N3	-2.15	1.34	1.38
38	A1	2280	A2M	C8-N7	2.15	1.35	1.31
34	B5	1271	OMG	C5-N7	-2.15	1.34	1.39
38	A1	649	A2M	C8-N7	2.14	1.35	1.31
38	A1	807	A2M	C8-N7	2.14	1.35	1.31
38	A1	805	OMG	C5-N7	-2.14	1.34	1.39
34	B5	100	A2M	C8-N7	2.14	1.35	1.31
38	A1	2281	A2M	C8-N7	2.14	1.35	1.31
38	A1	2220	A2M	C8-N7	2.13	1.35	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	645	1MA	C2-N3	2.13	1.34	1.30
38	A1	867	OMG	C5-N7	-2.13	1.34	1.39
34	B5	562	OMG	C5-N7	-2.12	1.34	1.39
34	B5	1781	MA6	C5-N7	-2.11	1.35	1.39
38	A1	2921	OMU	C5-C4	-2.11	1.39	1.43
38	A1	817	A2M	C4-N9	-2.10	1.33	1.37
38	A1	807	A2M	C4-N9	-2.09	1.33	1.37
34	B5	1782	MA6	C4-N9	-2.09	1.33	1.37
34	B5	1269	OMU	C5-C4	-2.09	1.39	1.43
34	B5	1782	MA6	C8-N7	2.09	1.35	1.31
38	A1	2791	OMG	C5-N7	-2.08	1.34	1.39
38	A1	2946	A2M	C4-N9	-2.07	1.33	1.37
38	A1	1133	A2M	C4-N9	-2.07	1.33	1.37
34	B5	619	A2M	C4-N9	-2.07	1.33	1.37
34	B5	1572	OMG	C5-N7	-2.03	1.35	1.39

All (390) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1575	G7M	CN7-N7-C8	-8.16	112.42	124.79
34	B5	1575	G7M	N9-C8-N7	-7.00	95.48	112.48
34	B5	1575	G7M	C8-N7-C5	6.79	116.27	107.78
38	A1	2634	UR3	C4-N3-C2	-6.76	119.14	124.58
34	B5	541	A2M	C5-C4-N3	-6.61	117.62	126.72
38	A1	2288	OMG	C5-C4-N3	-6.54	117.98	128.39
38	A1	2815	OMG	C5-C4-N3	-6.39	118.23	128.39
38	A1	2619	OMG	C5-C4-N3	-6.37	118.25	128.39
38	A1	908	OMG	C5-C4-N3	-6.36	118.27	128.39
38	A1	1450	OMG	C5-C4-N3	-6.27	118.42	128.39
34	B5	562	OMG	C5-C4-N3	-6.25	118.44	128.39
34	B5	1428	OMG	C5-C4-N3	-6.24	118.47	128.39
38	A1	2922	OMG	C5-C4-N3	-6.23	118.48	128.39
38	A1	867	OMG	C5-C4-N3	-6.13	118.63	128.39
34	B5	1572	OMG	C5-C4-N3	-6.10	118.68	128.39
34	B5	796	A2M	C5-C4-N3	-6.06	118.38	126.72
38	A1	2791	OMG	C5-C4-N3	-6.04	118.77	128.39
34	B5	1271	OMG	C5-C4-N3	-6.04	118.78	128.39
38	A1	1449	A2M	C5-C4-N3	-6.01	118.44	126.72
38	A1	2640	A2M	C5-C4-N3	-5.99	118.47	126.72
38	A1	2793	OMG	C5-C4-N3	-5.97	118.88	128.39
38	A1	2281	A2M	C5-C4-N3	-5.96	118.50	126.72
34	B5	28	A2M	C5-C4-N3	-5.96	118.51	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1126	OMG	C5-C4-N3	-5.94	118.94	128.39
38	A1	876	A2M	C5-C4-N3	-5.94	118.54	126.72
34	B5	100	A2M	C5-C4-N3	-5.91	118.58	126.72
38	A1	2280	A2M	C5-C4-N3	-5.91	118.58	126.72
34	B5	436	A2M	C5-C4-N3	-5.86	118.64	126.72
34	B5	420	A2M	C5-C4-N3	-5.84	118.68	126.72
38	A1	805	OMG	C5-C4-N3	-5.83	119.11	128.39
38	A1	807	A2M	C5-C4-N3	-5.79	118.74	126.72
34	B5	974	A2M	C5-C4-N3	-5.79	118.75	126.72
38	A1	649	A2M	C5-C4-N3	-5.77	118.77	126.72
38	A1	817	A2M	C5-C4-N3	-5.70	118.86	126.72
38	A1	2946	A2M	C5-C4-N3	-5.69	118.88	126.72
38	A1	1133	A2M	C5-C4-N3	-5.68	118.90	126.72
34	B5	619	A2M	C5-C4-N3	-5.63	118.97	126.72
34	B5	1191	XSX	C3-C1-N3	-5.60	102.37	112.16
34	B5	1781	MA6	C5-C4-N3	-5.54	119.08	126.72
34	B5	1575	G7M	N9-C4-N3	5.49	136.94	125.95
34	B5	1782	MA6	C5-C4-N3	-5.36	119.34	126.72
38	A1	2142	1MA	C5-C4-N3	-5.34	119.41	127.27
34	B5	1191	XSX	C4-N3-C2	-5.32	118.41	124.66
38	A1	645	1MA	C5-C4-N3	-5.30	119.47	127.27
34	B5	541	A2M	N3-C4-N9	5.28	136.15	127.17
38	A1	2220	A2M	C5-C4-N3	-5.26	119.47	126.72
38	A1	867	OMG	C2-N3-C4	5.19	121.24	112.30
38	A1	2288	OMG	C2-N3-C4	5.15	121.17	112.30
38	A1	2815	OMG	C2-N3-C4	5.13	121.13	112.30
34	B5	562	OMG	C2-N3-C4	5.09	121.07	112.30
38	A1	2619	OMG	C2-N3-C4	5.09	121.06	112.30
38	A1	2791	OMG	C2-N3-C4	5.07	121.03	112.30
38	A1	1450	OMG	C2-N3-C4	5.06	121.01	112.30
34	B5	1572	OMG	C2-N3-C4	5.03	120.96	112.30
38	A1	2288	OMG	N9-C4-N3	5.03	136.01	125.95
34	B5	1428	OMG	C2-N3-C4	5.03	120.96	112.30
38	A1	805	OMG	C2-N3-C4	5.01	120.93	112.30
38	A1	2922	OMG	C2-N3-C4	4.99	120.89	112.30
34	B5	1773	4AC	N4-C4-N3	4.98	121.96	113.87
38	A1	908	OMG	C2-N3-C4	4.98	120.87	112.30
38	A1	2281	A2M	N3-C4-N9	4.96	135.61	127.17
34	B5	1271	OMG	C2-N3-C4	4.94	120.81	112.30
34	B5	1575	G7M	C5-C4-N3	-4.94	118.82	128.15
38	A1	908	OMG	N9-C4-N3	4.90	135.75	125.95
38	A1	2921	OMU	C4-N3-C2	-4.90	120.53	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2793	OMG	C2-N3-C4	4.90	120.74	112.30
38	A1	2421	OMU	C4-N3-C2	-4.89	120.54	126.61
34	B5	1126	OMG	C2-N3-C4	4.88	120.71	112.30
34	B5	796	A2M	N3-C4-N9	4.87	135.45	127.17
38	A1	1450	OMG	N9-C4-N3	4.87	135.68	125.95
38	A1	2619	OMG	N9-C4-N3	4.77	135.50	125.95
38	A1	2724	OMU	C4-N3-C2	-4.77	120.69	126.61
34	B5	578	OMU	C4-N3-C2	-4.75	120.71	126.61
38	A1	1888	OMU	C4-N3-C2	-4.74	120.72	126.61
38	A1	2815	OMG	N9-C4-N3	4.73	135.41	125.95
38	A1	2280	A2M	N3-C4-N9	4.70	135.16	127.17
34	B5	100	A2M	N3-C4-N9	4.67	135.12	127.17
34	B5	420	A2M	N3-C4-N9	4.66	135.10	127.17
38	A1	1449	A2M	N3-C4-N9	4.65	135.08	127.17
38	A1	898	OMU	C4-N3-C2	-4.64	120.85	126.61
38	A1	649	A2M	N3-C4-N9	4.64	135.06	127.17
34	B5	1428	OMG	N9-C4-N3	4.62	135.20	125.95
34	B5	1271	OMG	N9-C4-N3	4.60	135.16	125.95
34	B5	28	A2M	N3-C4-N9	4.60	134.98	127.17
38	A1	2640	A2M	N3-C4-N9	4.59	134.97	127.17
38	A1	876	A2M	N3-C4-N9	4.59	134.97	127.17
38	A1	2142	1MA	C2-N3-C4	4.58	121.51	112.53
38	A1	2922	OMG	N9-C4-N3	4.56	135.07	125.95
38	A1	645	1MA	C2-N3-C4	4.54	121.44	112.53
34	B5	562	OMG	N9-C4-N3	4.54	135.02	125.95
34	B5	974	A2M	N3-C4-N9	4.53	134.88	127.17
38	A1	2417	OMU	C4-N3-C2	-4.53	120.99	126.61
38	A1	2946	A2M	N3-C4-N9	4.50	134.82	127.17
38	A1	2921	OMU	N3-C2-N1	4.48	120.72	114.89
38	A1	867	OMG	N9-C4-N3	4.48	134.91	125.95
38	A1	807	A2M	N3-C4-N9	4.48	134.78	127.17
34	B5	436	A2M	N3-C4-N9	4.44	134.72	127.17
34	B5	1575	G7M	C2-N3-C4	4.43	119.94	112.30
38	A1	817	A2M	N3-C4-N9	4.42	134.69	127.17
38	A1	2421	OMU	N3-C2-N1	4.42	120.64	114.89
38	A1	1133	A2M	N3-C4-N9	4.40	134.65	127.17
38	A1	2724	OMU	N3-C2-N1	4.39	120.61	114.89
38	A1	2793	OMG	N9-C4-N3	4.38	134.72	125.95
34	B5	1572	OMG	N9-C4-N3	4.38	134.71	125.95
34	B5	619	A2M	N3-C4-N9	4.37	134.60	127.17
34	B5	1781	MA6	C2-N1-C6	4.36	122.48	111.83
34	B5	1781	MA6	C4-C5-N7	-4.36	105.60	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	1888	OMU	N3-C2-N1	4.35	120.56	114.89
34	B5	1126	OMG	N9-C4-N3	4.34	134.64	125.95
38	A1	2791	OMG	N9-C4-N3	4.34	134.63	125.95
38	A1	898	OMU	N3-C2-N1	4.31	120.51	114.89
34	B5	1575	G7M	C8-N9-C4	4.31	117.76	107.09
38	A1	2347	OMU	C4-N3-C2	-4.29	121.28	126.61
34	B5	1782	MA6	N3-C4-N9	4.29	134.47	127.17
38	A1	2729	OMU	C4-N3-C2	-4.29	121.28	126.61
34	B5	1269	OMU	C4-N3-C2	-4.28	121.30	126.61
34	B5	1782	MA6	C2-N1-C6	4.27	122.27	111.83
34	B5	796	A2M	C2'-C1'-N9	-4.24	106.77	113.75
38	A1	2220	A2M	N3-C4-N9	4.23	134.36	127.17
38	A1	2417	OMU	N3-C2-N1	4.21	120.38	114.89
38	A1	2870	5MC	C5-C6-N1	-4.21	118.74	123.31
38	A1	805	OMG	N9-C4-N3	4.18	134.31	125.95
34	B5	1191	XSX	C1'-N1-C2	4.17	123.86	117.04
38	A1	2347	OMU	N3-C2-N1	4.14	120.28	114.89
34	B5	578	OMU	N3-C2-N1	4.09	120.22	114.89
34	B5	1781	MA6	N3-C4-N9	4.07	134.09	127.17
34	B5	1269	OMU	N3-C2-N1	4.01	120.11	114.89
34	B5	541	A2M	C2-N3-C4	3.99	121.57	111.83
38	A1	2729	OMU	N3-C2-N1	3.95	120.04	114.89
38	A1	2921	OMU	C5-C4-N3	3.93	120.31	114.80
38	A1	2421	OMU	C5-C4-N3	3.92	120.29	114.80
34	B5	1191	XSX	C6-N1-C2	-3.90	118.61	121.80
34	B5	578	OMU	C5-C4-N3	3.88	120.24	114.80
38	A1	2724	OMU	C5-C4-N3	3.85	120.19	114.80
34	B5	796	A2M	C2-N3-C4	3.84	121.20	111.83
38	A1	2729	OMU	C5-C4-N3	3.83	120.17	114.80
38	A1	898	OMU	C5-C4-N3	3.81	120.13	114.80
38	A1	1888	OMU	C5-C4-N3	3.80	120.12	114.80
38	A1	876	A2M	C2-N3-C4	3.77	121.03	111.83
38	A1	2220	A2M	N3-C2-N1	-3.76	122.89	128.58
38	A1	817	A2M	C2-N3-C4	3.75	121.00	111.83
34	B5	28	A2M	C2-N3-C4	3.75	121.00	111.83
38	A1	2946	A2M	C2-N3-C4	3.75	120.99	111.83
38	A1	2640	A2M	C2-N3-C4	3.74	120.96	111.83
38	A1	2281	A2M	C2-N3-C4	3.73	120.93	111.83
34	B5	1782	MA6	C2-N3-C4	3.72	120.92	111.83
34	B5	420	A2M	C2-N3-C4	3.71	120.90	111.83
38	A1	2417	OMU	C5-C4-N3	3.71	120.00	114.80
34	B5	1781	MA6	C2-N3-C4	3.71	120.89	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	974	A2M	C2-N3-C4	3.71	120.88	111.83
34	B5	1269	OMU	C5-C4-N3	3.70	119.98	114.80
38	A1	1449	A2M	C2-N3-C4	3.70	120.86	111.83
38	A1	649	A2M	C2-N3-C4	3.70	120.86	111.83
34	B5	436	A2M	C2-N3-C4	3.70	120.86	111.83
34	B5	100	A2M	C2-N3-C4	3.69	120.84	111.83
38	A1	2640	A2M	C4-C5-N7	-3.68	106.37	110.58
38	A1	2946	A2M	C2'-C1'-N9	-3.67	107.71	113.75
34	B5	1782	MA6	N1-C2-N3	-3.67	123.02	128.58
38	A1	1133	A2M	C2-N3-C4	3.66	120.77	111.83
38	A1	2280	A2M	C2-N3-C4	3.65	120.75	111.83
38	A1	2142	1MA	N9-C4-N3	3.64	135.19	126.90
38	A1	1133	A2M	C2'-C1'-N9	-3.63	107.78	113.75
34	B5	1782	MA6	C4-C5-N7	-3.62	106.44	110.58
34	B5	1575	G7M	CN7-N7-C5	3.62	131.31	126.80
34	B5	28	A2M	C4-C5-N7	-3.61	106.45	110.58
34	B5	1191	XSX	O2-C2-N3	-3.61	117.12	121.98
38	A1	2347	OMU	C5-C4-N3	3.61	119.85	114.80
38	A1	1133	A2M	C4-C5-N7	-3.60	106.46	110.58
38	A1	817	A2M	C4-C5-N7	-3.58	106.48	110.58
34	B5	619	A2M	C2-N3-C4	3.58	120.57	111.83
38	A1	1437	OMC	O2-C2-N3	-3.58	116.69	122.33
34	B5	619	A2M	C4-C5-N7	-3.58	106.49	110.58
34	B5	436	A2M	C4-C5-N7	-3.56	106.51	110.58
38	A1	807	A2M	C4-C5-N7	-3.56	106.51	110.58
34	B5	1280	4AC	N4-C4-N3	3.53	119.60	113.87
38	A1	876	A2M	C4-C5-N7	-3.52	106.55	110.58
38	A1	2220	A2M	C2-N3-C4	3.51	120.39	111.83
38	A1	807	A2M	C2-N3-C4	3.50	120.37	111.83
38	A1	805	OMG	C6-C5-N7	3.49	136.65	130.29
34	B5	1575	G7M	O2'-C2'-C3'	3.49	123.01	111.82
34	B5	1191	XSX	C1-N3-C4	3.49	123.84	117.10
34	B5	1575	G7M	O3'-C3'-C4'	3.47	121.06	111.08
38	A1	2946	A2M	N3-C2-N1	-3.45	123.37	128.58
34	B5	974	A2M	C4-C5-N7	-3.44	106.64	110.58
38	A1	2791	OMG	C6-C5-N7	3.42	136.52	130.29
34	B5	420	A2M	C4-C5-N7	-3.42	106.67	110.58
34	B5	1269	OMU	C1'-N1-C2	3.41	123.72	117.59
34	B5	796	A2M	N3-C2-N1	-3.41	123.42	128.58
38	A1	2280	A2M	C4-C5-N7	-3.39	106.71	110.58
38	A1	817	A2M	N3-C2-N1	-3.38	123.46	128.58
38	A1	649	A2M	C4-C5-N7	-3.38	106.72	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	100	A2M	C4-C5-N7	-3.38	106.72	110.58
34	B5	1781	MA6	N1-C2-N3	-3.38	123.47	128.58
34	B5	796	A2M	C4-C5-N7	-3.37	106.73	110.58
34	B5	541	A2M	C4-C5-N7	-3.37	106.73	110.58
38	A1	2634	UR3	C5-C4-N3	3.36	119.47	115.04
34	B5	974	A2M	N3-C2-N1	-3.36	123.50	128.58
38	A1	645	1MA	N9-C4-N3	3.34	134.52	126.90
38	A1	1449	A2M	C4-C5-N7	-3.34	106.76	110.58
34	B5	1572	OMG	C6-C5-N7	3.32	136.34	130.29
38	A1	867	OMG	C6-C5-N7	3.32	136.33	130.29
38	A1	2946	A2M	C4-C5-N7	-3.31	106.80	110.58
38	A1	649	A2M	N3-C2-N1	-3.30	123.58	128.58
38	A1	2347	OMU	C1'-N1-C2	3.30	123.52	117.59
38	A1	1133	A2M	N3-C2-N1	-3.28	123.61	128.58
34	B5	1126	OMG	C6-C5-N7	3.26	136.22	130.29
38	A1	876	A2M	N3-C2-N1	-3.25	123.66	128.58
36	AB	243	HIC	NE2-CE1-ND1	-3.25	111.42	112.66
34	B5	562	OMG	C6-C5-N7	3.24	136.19	130.29
34	B5	100	A2M	N3-C2-N1	-3.23	123.69	128.58
34	B5	420	A2M	N3-C2-N1	-3.22	123.71	128.58
34	B5	436	A2M	N3-C2-N1	-3.21	123.72	128.58
38	A1	2793	OMG	C6-C5-N7	3.21	136.13	130.29
34	B5	541	A2M	N3-C2-N1	-3.18	123.76	128.58
38	A1	2281	A2M	N3-C2-N1	-3.17	123.78	128.58
34	B5	28	A2M	N3-C2-N1	-3.17	123.78	128.58
38	A1	1449	A2M	N3-C2-N1	-3.17	123.79	128.58
38	A1	2640	A2M	N3-C2-N1	-3.14	123.83	128.58
38	A1	2948	OMC	O2-C2-N3	-3.13	117.39	122.33
38	A1	2417	OMU	O4-C4-C5	-3.12	119.79	125.16
38	A1	2278	5MC	O2-C2-N3	-3.11	117.42	122.33
38	A1	2220	A2M	C4-C5-N7	-3.11	107.03	110.58
34	B5	619	A2M	N3-C2-N1	-3.10	123.89	128.58
38	A1	898	OMU	O4-C4-C5	-3.10	119.82	125.16
38	A1	2724	OMU	O4-C4-C5	-3.09	119.84	125.16
34	B5	1782	MA6	C4-N9-C8	3.07	108.96	105.74
38	A1	2280	A2M	N3-C2-N1	-3.07	123.94	128.58
38	A1	2922	OMG	C6-C5-N7	3.07	135.87	130.29
38	A1	2421	OMU	O4-C4-C5	-3.06	119.89	125.16
34	B5	1271	OMG	C6-C5-N7	3.05	135.85	130.29
38	A1	2619	OMG	C6-C5-N7	3.05	135.84	130.29
38	A1	1888	OMU	O4-C4-C5	-3.04	119.93	125.16
38	A1	2815	OMG	C6-C5-N7	3.03	135.81	130.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2281	A2M	C4-C5-N7	-3.03	107.12	110.58
34	B5	1428	OMG	C6-C5-N7	3.00	135.75	130.29
38	A1	2729	OMU	O4-C4-C5	-2.99	120.00	125.16
34	B5	1781	MA6	C5-N7-C8	2.99	108.15	103.45
34	B5	1269	OMU	O4-C4-C5	-2.96	120.06	125.16
38	A1	1437	OMC	C1'-N1-C2	2.96	124.97	118.44
34	B5	578	OMU	O4-C4-C5	-2.95	120.07	125.16
38	A1	2870	5MC	C5-C4-N3	-2.95	118.73	121.75
38	A1	2921	OMU	O4-C4-C5	-2.95	120.08	125.16
38	A1	2278	5MC	C5-C4-N3	-2.94	118.74	121.75
38	A1	2281	A2M	C2'-C1'-N9	-2.89	108.99	113.75
38	A1	2281	A2M	C4-N9-C8	2.87	108.75	105.74
38	A1	2347	OMU	O4-C4-C5	-2.87	120.21	125.16
38	A1	2946	A2M	O4'-C1'-N9	2.86	113.58	108.09
38	A1	2288	OMG	C6-C5-N7	2.86	135.49	130.29
38	A1	1450	OMG	C6-C5-N7	2.83	135.44	130.29
38	A1	2281	A2M	O4'-C1'-N9	2.81	113.49	108.09
38	A1	2220	A2M	C2-N1-C6	2.79	123.32	118.73
38	A1	807	A2M	N3-C2-N1	-2.76	124.40	128.58
38	A1	908	OMG	C6-C5-N7	2.76	135.31	130.29
34	B5	974	A2M	C2'-C1'-N9	-2.75	109.22	113.75
38	A1	2278	5MC	C5-C6-N1	-2.75	120.32	123.31
34	B5	619	A2M	C4-N9-C8	2.74	108.62	105.74
38	A1	649	A2M	C4-N9-C8	2.72	108.59	105.74
34	B5	420	A2M	C4-N9-C8	2.72	108.59	105.74
34	B5	1572	OMG	C4-C5-N7	-2.71	106.37	110.67
34	B5	1782	MA6	C5-N7-C8	2.71	107.71	103.45
38	A1	2791	OMG	C4-C5-N7	-2.70	106.40	110.67
38	A1	805	OMG	C4-C5-N7	-2.66	106.45	110.67
34	B5	1781	MA6	C4-N9-C8	2.66	108.53	105.74
38	A1	2640	A2M	C5-N7-C8	2.65	107.62	103.45
34	B5	562	OMG	C4-C5-N7	-2.65	106.48	110.67
38	A1	1133	A2M	C4-N9-C8	2.64	108.51	105.74
34	B5	1007	OMC	O2-C2-N3	-2.64	118.17	122.33
34	B5	796	A2M	C4-N9-C8	2.64	108.51	105.74
38	A1	817	A2M	C4-N9-C8	2.64	108.51	105.74
38	A1	2946	A2M	C4-N9-C8	2.62	108.49	105.74
34	B5	1191	XSX	C5-C4-N3	2.59	119.22	115.64
80	DC	699	DDE	CAU-CBW-CBI	-2.58	106.18	111.22
34	B5	28	A2M	C5-N7-C8	2.58	107.50	103.45
34	B5	796	A2M	C5-N7-C8	2.58	107.50	103.45
34	B5	1782	MA6	N1-C6-N6	2.57	119.99	116.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	619	A2M	C5-N7-C8	2.57	107.49	103.45
38	A1	1133	A2M	C5-N7-C8	2.57	107.48	103.45
38	A1	867	OMG	C4-C5-N7	-2.56	106.61	110.67
38	A1	2280	A2M	C4-N9-C8	2.56	108.43	105.74
34	B5	1126	OMG	C4-C5-N7	-2.56	106.61	110.67
38	A1	2922	OMG	C4-C5-N7	-2.55	106.62	110.67
38	A1	2337	OMC	O2-C2-N3	-2.55	118.31	122.33
34	B5	420	A2M	C5-N7-C8	2.54	107.45	103.45
34	B5	1781	MA6	C6-C5-N7	2.54	137.49	133.43
34	B5	1773	4AC	C5-C4-N4	-2.52	118.69	122.94
38	A1	817	A2M	C5-N7-C8	2.51	107.40	103.45
38	A1	2793	OMG	C4-C5-N7	-2.50	106.70	110.67
38	A1	2619	OMG	C4-C5-N7	-2.50	106.71	110.67
38	A1	2815	OMG	C4-C5-N7	-2.48	106.73	110.67
34	B5	1575	G7M	O4'-C1'-N9	2.48	113.99	108.36
34	B5	100	A2M	C4-N9-C8	2.48	108.34	105.74
38	A1	876	A2M	C5-N7-C8	2.48	107.35	103.45
38	A1	649	A2M	C5-N7-C8	2.48	107.34	103.45
34	B5	436	A2M	C5-N7-C8	2.48	107.34	103.45
38	A1	807	A2M	C5-N7-C8	2.47	107.34	103.45
34	B5	100	A2M	C5-N7-C8	2.47	107.33	103.45
38	A1	2948	OMC	C1'-N1-C2	2.47	123.89	118.44
38	A1	645	1MA	C4-C5-N7	-2.46	106.77	110.67
38	A1	807	A2M	C4-N9-C8	2.46	108.32	105.74
38	A1	2280	A2M	C5-N7-C8	2.45	107.31	103.45
34	B5	974	A2M	C4-N9-C8	2.45	108.31	105.74
34	B5	1428	OMG	C4-C5-N7	-2.44	106.80	110.67
34	B5	1575	G7M	O6-C6-C5	-2.44	122.56	128.01
34	B5	541	A2M	C5-N7-C8	2.44	107.28	103.45
34	B5	974	A2M	C5-N7-C8	2.42	107.26	103.45
38	A1	2640	A2M	C4-N9-C8	2.42	108.28	105.74
34	B5	578	OMU	O2-C2-N1	-2.42	119.65	122.80
38	A1	2220	A2M	C4-N9-C8	2.42	108.28	105.74
38	A1	2946	A2M	C5-N7-C8	2.41	107.23	103.45
38	A1	2288	OMG	C4-C5-N7	-2.40	106.87	110.67
34	B5	28	A2M	C4-N9-C8	2.39	108.25	105.74
34	B5	1773	4AC	C6-C5-C4	2.39	119.88	117.00
38	A1	2281	A2M	C5-N7-C8	2.37	107.17	103.45
34	B5	1271	OMG	C4-C5-N7	-2.37	106.92	110.67
34	B5	1575	G7M	C6-C5-N7	2.32	135.08	132.17
38	A1	807	A2M	C2'-C1'-N9	-2.31	109.94	113.75
34	B5	1280	4AC	C6-C5-C4	2.31	119.79	117.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	436	A2M	C2'-C1'-N9	-2.31	109.95	113.75
38	A1	817	A2M	C6-C5-N7	2.30	136.53	132.09
38	A1	908	OMG	O6-C6-C5	-2.29	120.48	126.53
38	A1	876	A2M	C4-N9-C8	2.29	108.14	105.74
34	B5	1782	MA6	N9-C8-N7	-2.29	110.69	113.94
38	A1	1450	OMG	O6-C6-C5	-2.29	120.50	126.53
38	A1	908	OMG	C4-C5-N7	-2.28	107.06	110.67
38	A1	2921	OMU	O2-C2-N1	-2.27	119.84	122.80
38	A1	1450	OMG	C4-C5-N7	-2.27	107.08	110.67
38	A1	1437	OMC	O2-C2-N1	2.25	123.32	118.90
38	A1	1449	A2M	C5-N7-C8	2.25	106.99	103.45
38	A1	2724	OMU	O2-C2-N1	-2.24	119.88	122.80
38	A1	2421	OMU	O2-C2-N1	-2.24	119.88	122.80
38	A1	645	1MA	C6-C5-N7	2.24	136.12	132.16
34	B5	619	A2M	C6-C5-N7	2.22	136.36	132.09
38	A1	2288	OMG	O6-C6-C5	-2.19	120.76	126.53
38	A1	1133	A2M	C6-C5-N7	2.18	136.30	132.09
34	B5	1126	OMG	O6-C6-C5	-2.18	120.77	126.53
38	A1	2729	OMU	C1'-N1-C2	2.18	121.51	117.59
34	B5	1428	OMG	O6-C6-C5	-2.17	120.79	126.53
34	B5	1271	OMG	O6-C6-C5	-2.17	120.80	126.53
34	B5	1269	OMU	O2-C2-N3	-2.17	117.49	121.49
34	B5	414	OMC	O2-C2-N3	-2.17	118.92	122.33
34	B5	1782	MA6	C6-C5-N7	2.16	136.88	133.43
38	A1	2815	OMG	O6-C6-C5	-2.15	120.85	126.53
34	B5	1781	MA6	N9-C8-N7	-2.14	110.90	113.94
38	A1	2619	OMG	O6-C6-C5	-2.14	120.88	126.53
34	B5	436	A2M	C4-N9-C8	2.13	107.98	105.74
34	B5	420	A2M	C2'-C1'-N9	-2.13	110.24	113.75
38	A1	2640	A2M	C6-C5-N7	2.13	136.19	132.09
38	A1	876	A2M	C6-C5-N7	2.13	136.19	132.09
34	B5	436	A2M	C6-C5-N7	2.12	136.17	132.09
34	B5	100	A2M	C2'-C1'-N9	-2.12	110.27	113.75
34	B5	28	A2M	C6-C5-N7	2.11	136.16	132.09
38	A1	817	A2M	O3'-C3'-C4'	-2.11	105.02	111.08
34	B5	1269	OMU	CM2-O2'-C2'	-2.11	109.06	114.47
34	B5	1773	4AC	C5-C4-N3	-2.10	119.31	122.60
38	A1	867	OMG	O6-C6-C5	-2.10	120.99	126.53
34	B5	1575	G7M	C1'-N9-C4	-2.10	120.29	126.49
34	B5	619	A2M	N9-C8-N7	-2.10	110.96	113.94
38	A1	2922	OMG	O6-C6-C5	-2.09	121.02	126.53
38	A1	2870	5MC	O2-C2-N3	-2.08	119.05	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2946	A2M	C6-C5-N7	2.08	136.10	132.09
38	A1	649	A2M	C6-C5-N7	2.07	136.08	132.09
38	A1	898	OMU	O2-C2-N1	-2.07	120.10	122.80
34	B5	562	OMG	O6-C6-C5	-2.07	121.08	126.53
38	A1	2634	UR3	C6-N1-C2	-2.07	120.11	121.80
38	A1	2347	OMU	O2-C2-N3	-2.07	117.68	121.49
34	B5	974	A2M	C6-C5-N7	2.06	136.07	132.09
34	B5	1572	OMG	O6-C6-C5	-2.06	121.09	126.53
38	A1	2142	1MA	N1-C2-N3	-2.06	123.55	126.00
36	AB	243	HIC	CB-CG-CD2	-2.06	124.99	129.96
38	A1	2220	A2M	C6-C5-N7	2.06	136.06	132.09
34	B5	541	A2M	C4-N9-C8	2.05	107.89	105.74
38	A1	1449	A2M	C4-N9-C8	2.05	107.89	105.74
38	A1	2220	A2M	C2'-C1'-N9	-2.05	110.38	113.75
34	B5	420	A2M	C6-C5-N7	2.05	136.04	132.09
34	B5	1575	G7M	C3'-C2'-C1'	2.04	105.33	101.46
38	A1	805	OMG	O6-C6-C5	-2.04	121.16	126.53
38	A1	2220	A2M	C5-N7-C8	2.03	106.64	103.45
34	B5	1575	G7M	C5-C6-N1	2.03	116.03	111.84
38	A1	2281	A2M	N9-C8-N7	-2.03	111.06	113.94
38	A1	2280	A2M	C2'-C1'-N9	-2.02	110.42	113.75
38	A1	645	1MA	N1-C2-N3	-2.02	123.59	126.00
34	B5	420	A2M	N9-C8-N7	-2.02	111.07	113.94
34	B5	1773	4AC	O2-C2-N3	-2.02	119.15	122.33
34	B5	436	A2M	O4'-C1'-N9	2.02	111.96	108.09
38	A1	1133	A2M	N9-C8-N7	-2.01	111.08	113.94
34	B5	1639	OMC	O2-C2-N3	-2.01	119.16	122.33
38	A1	2793	OMG	O6-C6-C5	-2.01	121.23	126.53
34	B5	796	A2M	N9-C8-N7	-2.00	111.09	113.94
38	A1	807	A2M	C6-C5-N7	2.00	135.95	132.09
34	B5	1269	OMU	O2'-C2'-C1'	2.00	112.79	108.99

There are no chirality outliers.

All (87) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	100	A2M	C1'-C2'-O2'-CM'
34	B5	414	OMC	C1'-C2'-O2'-CM2
34	B5	420	A2M	C1'-C2'-O2'-CM'
34	B5	436	A2M	C1'-C2'-O2'-CM'
34	B5	1007	OMC	C1'-C2'-O2'-CM2
34	B5	1191	XSX	O4'-C1'-N1-C2

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Mol	Chain	Res	Type	Atoms
34	B5	1271	OMG	C1'-C2'-O2'-CM2
34	B5	1428	OMG	C1'-C2'-O2'-CM2
34	B5	1782	MA6	C5-C6-N6-C9
34	B5	1280	4AC	N3-C4-N4-C7
34	B5	1280	4AC	C5-C4-N4-C7
34	B5	1773	4AC	N3-C4-N4-C7
34	B5	1773	4AC	C5-C4-N4-C7
34	B5	1773	4AC	O7-C7-N4-C4
34	B5	1773	4AC	CM7-C7-N4-C4
38	A1	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	2337	OMC	C1'-C2'-O2'-CM2
38	A1	2417	OMU	C1'-C2'-O2'-CM2
38	A1	2421	OMU	C1'-C2'-O2'-CM2
38	A1	2619	OMG	C1'-C2'-O2'-CM2
38	A1	2640	A2M	C1'-C2'-O2'-CM'
38	A1	2724	OMU	C1'-C2'-O2'-CM2
38	A1	2729	OMU	C1'-C2'-O2'-CM2
38	A1	2791	OMG	C1'-C2'-O2'-CM2
38	A1	2946	A2M	C1'-C2'-O2'-CM'
38	A1	2948	OMC	C1'-C2'-O2'-CM2
38	A1	2280	A2M	O4'-C4'-C5'-O5'
34	B5	1191	XSX	O4'-C1'-N1-C6
34	B5	1428	OMG	O4'-C4'-C5'-O5'
34	B5	1428	OMG	C3'-C4'-C5'-O5'
34	B5	1782	MA6	O4'-C4'-C5'-O5'
38	A1	2197	OMC	O4'-C4'-C5'-O5'
38	A1	2280	A2M	C3'-C4'-C5'-O5'
38	A1	2729	OMU	O4'-C4'-C5'-O5'
34	B5	1782	MA6	N1-C6-N6-C9
34	B5	541	A2M	C3'-C4'-C5'-O5'
34	B5	1191	XSX	N4-C7-C9-O10
34	B5	541	A2M	O4'-C4'-C5'-O5'
34	B5	619	A2M	O4'-C4'-C5'-O5'
38	A1	2729	OMU	C3'-C4'-C5'-O5'
34	B5	619	A2M	C3'-C4'-C5'-O5'
34	B5	1781	MA6	C5-C6-N6-C9
34	B5	1782	MA6	C5-C6-N6-C10
38	A1	2197	OMC	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
34	B5	1126	OMG	C3'-C4'-C5'-O5'
38	A1	817	A2M	C4'-C5'-O5'-P
80	DC	699	DDE	CBI-CBW-NCB-CAB
80	DC	699	DDE	CBI-CBW-NCB-CAC
38	A1	2870	5MC	C2'-C1'-N1-C6
80	DC	699	DDE	CAU-CBW-NCB-CAB
80	DC	699	DDE	CAU-CBW-NCB-CAC
38	A1	898	OMU	C1'-C2'-O2'-CM2
34	B5	619	A2M	C2'-C1'-N9-C8
34	B5	1269	OMU	O4'-C1'-N1-C6
34	B5	578	OMU	C2'-C1'-N1-C6
34	B5	1269	OMU	O4'-C1'-N1-C2
80	DC	699	DDE	CE1-CAT-CAU-CBW
38	A1	2870	5MC	O4'-C1'-N1-C6
34	B5	541	A2M	C4'-C5'-O5'-P
34	B5	1782	MA6	C3'-C4'-C5'-O5'
34	B5	1428	OMG	C4'-C5'-O5'-P
38	A1	649	A2M	C4'-C5'-O5'-P
34	B5	1191	XSX	N4-C7-C9-O11
38	A1	2197	OMC	O4'-C1'-N1-C6
34	B5	578	OMU	O4'-C1'-N1-C6
34	B5	1269	OMU	C4'-C5'-O5'-P
38	A1	2870	5MC	O4'-C1'-N1-C2
34	B5	1126	OMG	C1'-C2'-O2'-CM2
38	A1	867	OMG	C1'-C2'-O2'-CM2
38	A1	1450	OMG	C4'-C5'-O5'-P
38	A1	2197	OMC	O4'-C1'-N1-C2
34	B5	541	A2M	O4'-C1'-N9-C8
34	B5	1781	MA6	C5-C6-N6-C10
34	B5	1781	MA6	N1-C6-N6-C9
80	DC	699	DDE	CAT-CAU-CBW-CBI
38	A1	1437	OMC	O4'-C4'-C5'-O5'
38	A1	2281	A2M	O4'-C4'-C5'-O5'
34	B5	100	A2M	C4'-C5'-O5'-P
38	A1	2142	1MA	O4'-C4'-C5'-O5'
34	B5	578	OMU	O4'-C1'-N1-C2
38	A1	2870	5MC	C2'-C1'-N1-C2
34	B5	578	OMU	C2'-C1'-N1-C2
34	B5	1269	OMU	C2'-C1'-N1-C2

There are no ring outliers.

25 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	B5	1575	G7M	1	0
38	A1	2417	OMU	1	0
34	B5	974	A2M	1	0
34	B5	1572	OMG	1	0
34	B5	1428	OMG	1	0
38	A1	649	A2M	1	0
38	A1	2281	A2M	1	0
34	B5	1269	OMU	1	0
34	B5	1126	OMG	1	0
34	B5	420	A2M	2	0
34	B5	100	A2M	1	0
38	A1	663	OMC	1	0
38	A1	1133	A2M	1	0
38	A1	650	OMC	1	0
38	A1	1449	A2M	1	0
34	B5	1280	4AC	3	0
34	B5	1639	OMC	1	0
38	A1	2220	A2M	3	0
34	B5	436	A2M	1	0
38	A1	2724	OMU	3	0
38	A1	2793	OMG	1	0
38	A1	2948	OMC	1	0
38	A1	2197	OMC	1	0
34	B5	1773	4AC	1	0
80	DC	699	DDE	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 220 ligands modelled in this entry, 218 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
85	GDP	DC	901	83	29,30,30	1.23	4 (13%)	45,47,47	1.78	7 (15%)
86	W9C	DC	902	-	34,39,39	0.68	2 (5%)	38,64,64	1.13	4 (10%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
85	GDP	DC	901	83	-	4/16/32/32	0/3/3/3
86	W9C	DC	902	-	1/1/15/16	3/21/104/104	0/7/5/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	DC	901	GDP	C5-C4	3.18	1.47	1.38
86	DC	902	W9C	O14-C5	-2.90	1.20	1.30
85	DC	901	GDP	C6-N1	-2.66	1.33	1.38
85	DC	901	GDP	C5-N7	-2.51	1.34	1.39
85	DC	901	GDP	PA-O3A	2.16	1.61	1.59
86	DC	902	W9C	C1-C5	2.01	1.55	1.50

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	DC	901	GDP	C5-C4-N3	-6.40	118.21	128.39
85	DC	901	GDP	N9-C4-N3	4.92	135.80	125.95
85	DC	901	GDP	C2-N3-C4	4.66	120.33	112.30
86	DC	902	W9C	C12-C6-C2	-4.32	98.40	105.09
86	DC	902	W9C	C20-C13-C4	2.95	120.28	112.41
85	DC	901	GDP	C6-C5-N7	2.53	134.89	130.29
85	DC	901	GDP	O6-C6-C5	-2.42	120.14	126.53
85	DC	901	GDP	C4-C5-N7	-2.38	106.90	110.67
86	DC	902	W9C	C18-C9-C16	-2.26	100.63	103.72
85	DC	901	GDP	O4'-C1'-N9	2.08	113.08	108.36
86	DC	902	W9C	C7-C2-C6	2.06	116.00	112.05

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
86	DC	902	W9C	C52

All (7) torsion outliers are listed below:

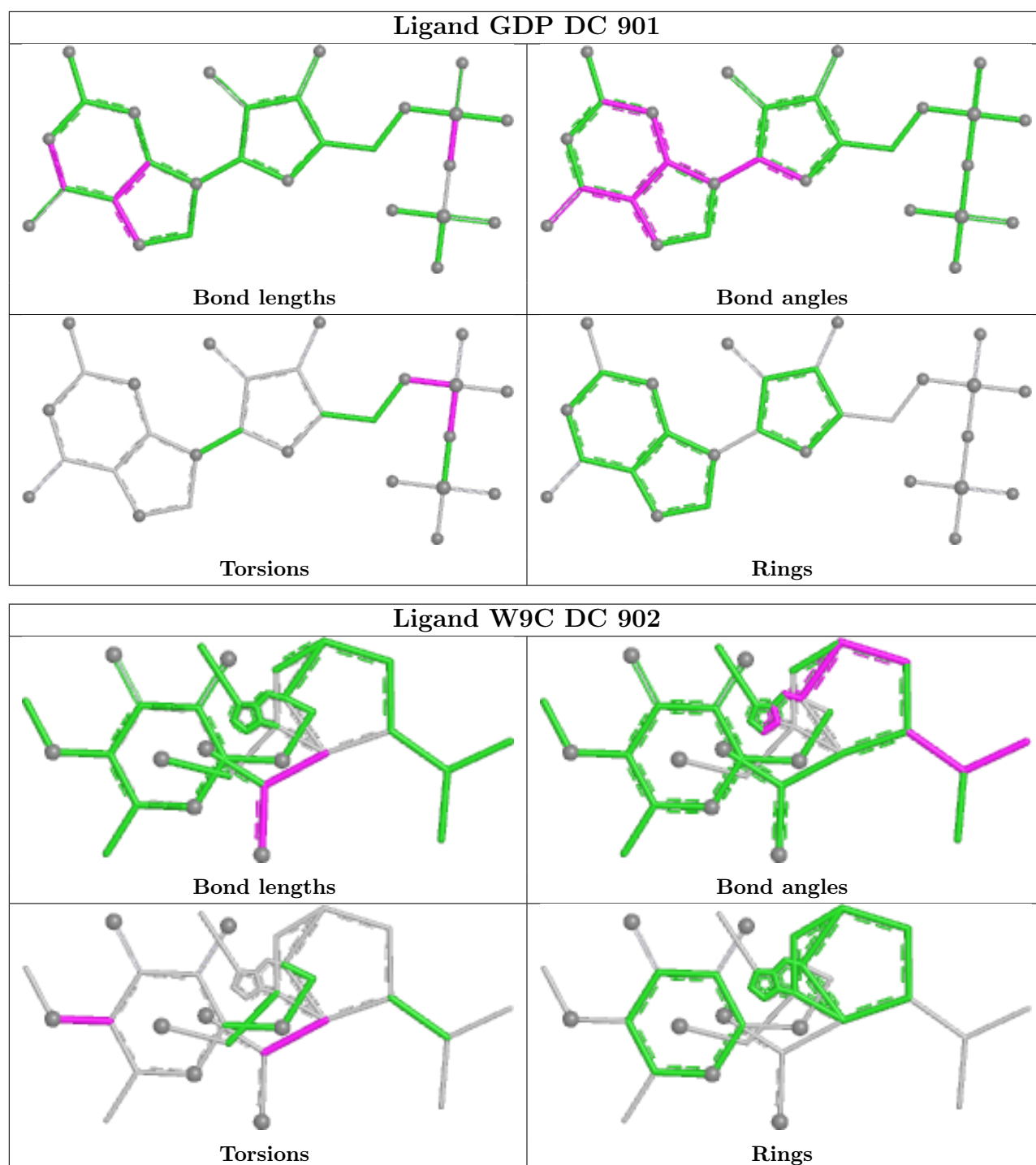
Mol	Chain	Res	Type	Atoms
85	DC	901	GDP	C5'-O5'-PA-O3A
85	DC	901	GDP	C5'-O5'-PA-O2A
86	DC	902	W9C	C2-C1-C5-O14
86	DC	902	W9C	C2-C1-C5-O15
86	DC	902	W9C	C54-C55-O64-C65
85	DC	901	GDP	PB-O3A-PA-O2A
85	DC	901	GDP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	DC	901	GDP	4	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

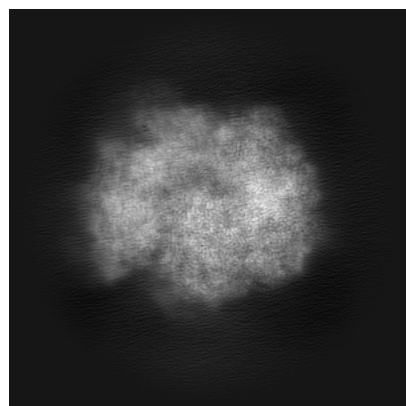
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28634. These allow visual inspection of the internal detail of the map and identification of artifacts.

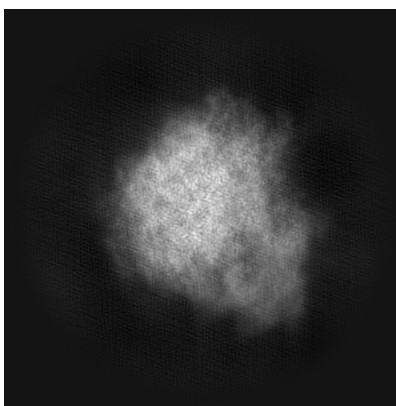
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

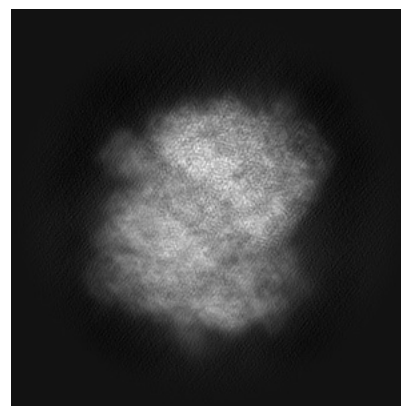
6.1.1 Primary map



X

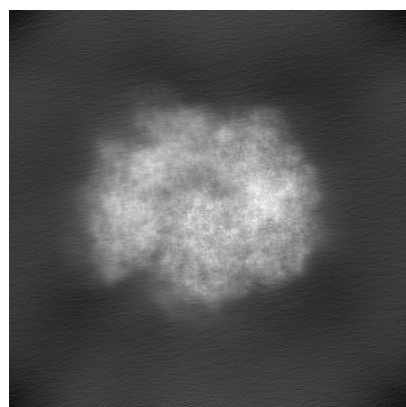


Y

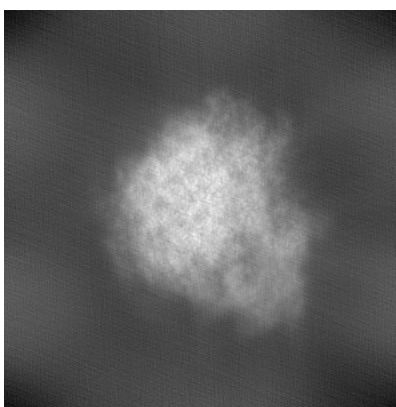


Z

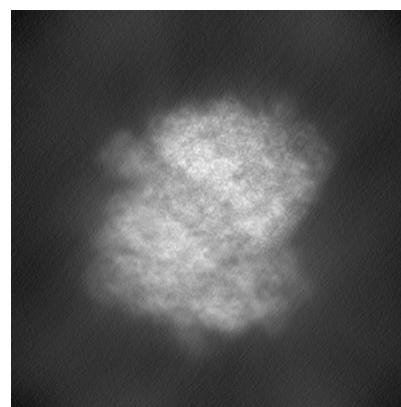
6.1.2 Raw map



X



Y

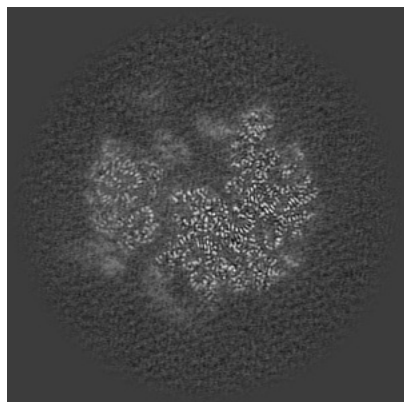


Z

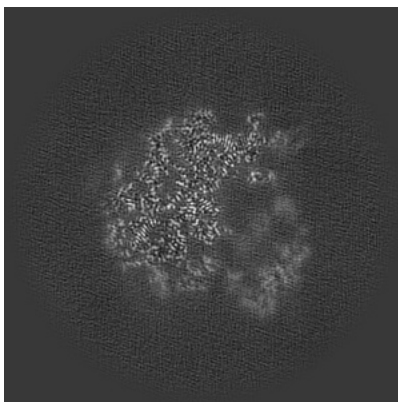
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

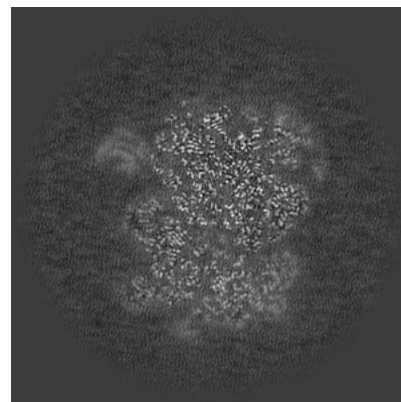
6.2.1 Primary map



X Index: 200

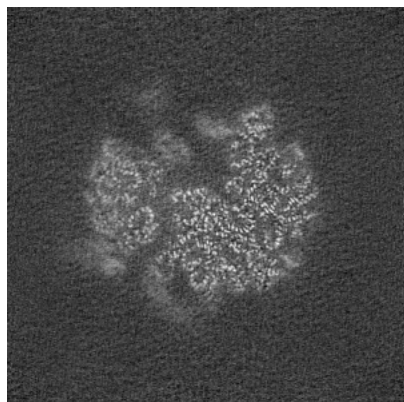


Y Index: 200

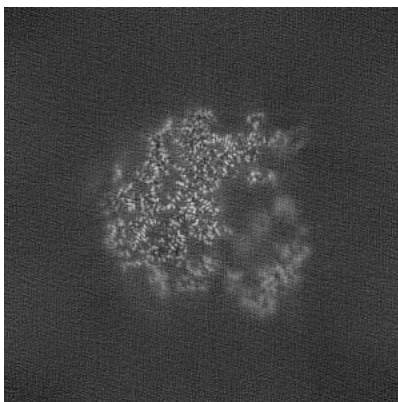


Z Index: 200

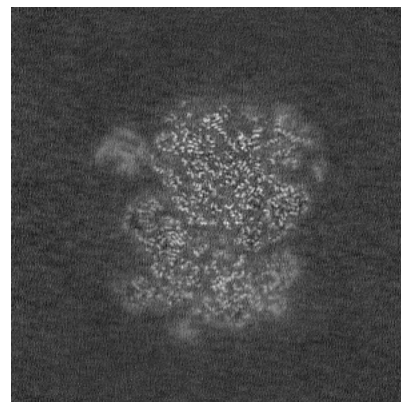
6.2.2 Raw map



X Index: 200



Y Index: 200

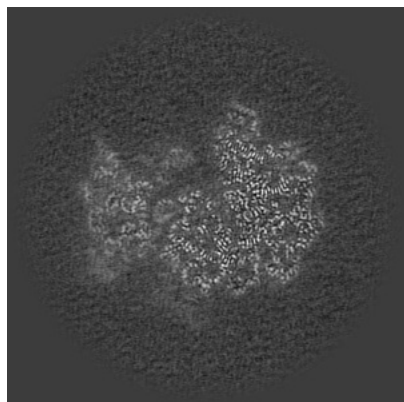


Z Index: 200

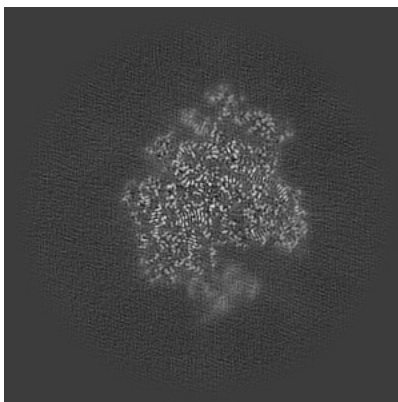
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

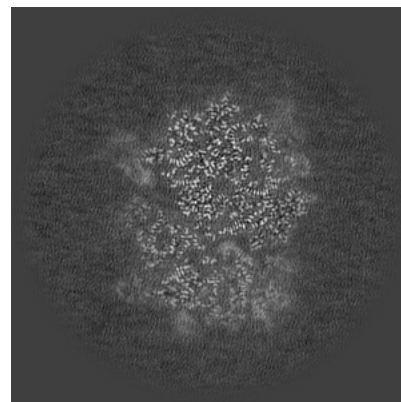
6.3.1 Primary map



X Index: 215

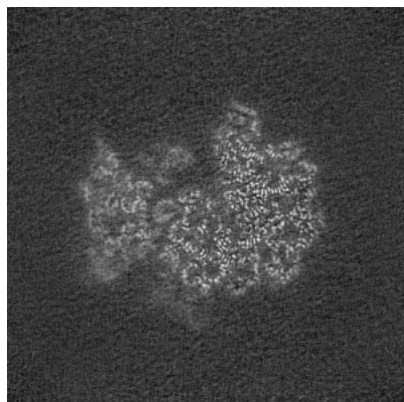


Y Index: 245

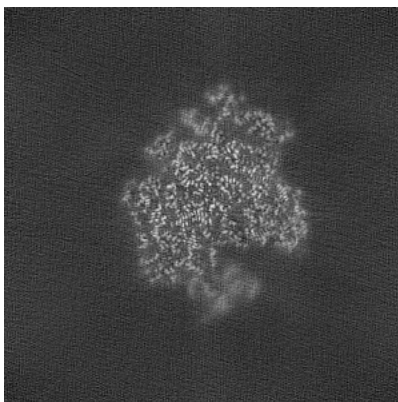


Z Index: 190

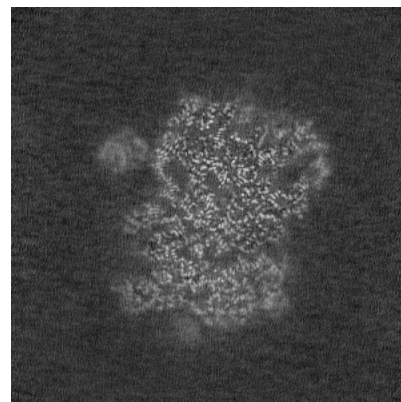
6.3.2 Raw map



X Index: 215



Y Index: 245

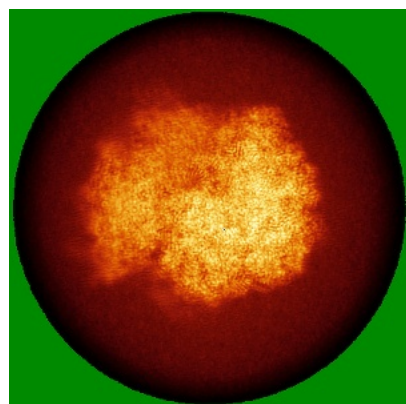


Z Index: 206

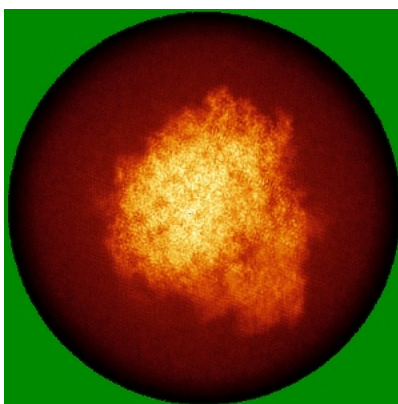
The images above show the largest variance slices of the map in three orthogonal directions.

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

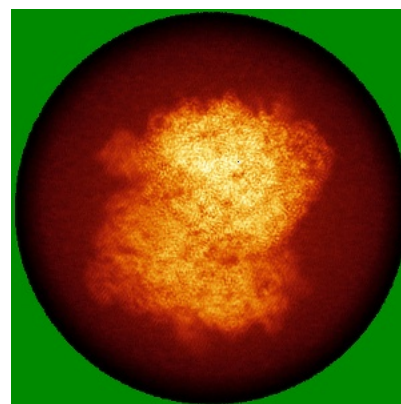
6.4.1 Primary map



X

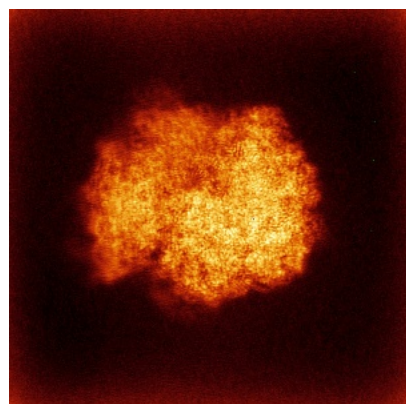


Y

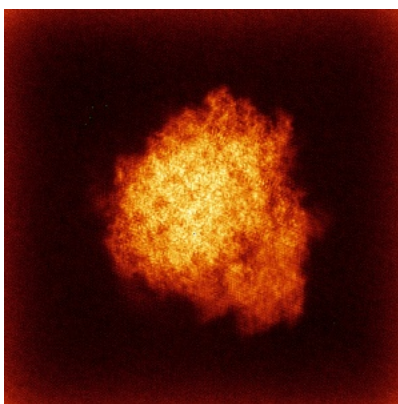


Z

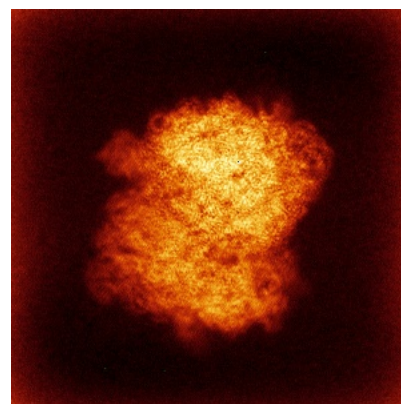
6.4.2 Raw map



X



Y

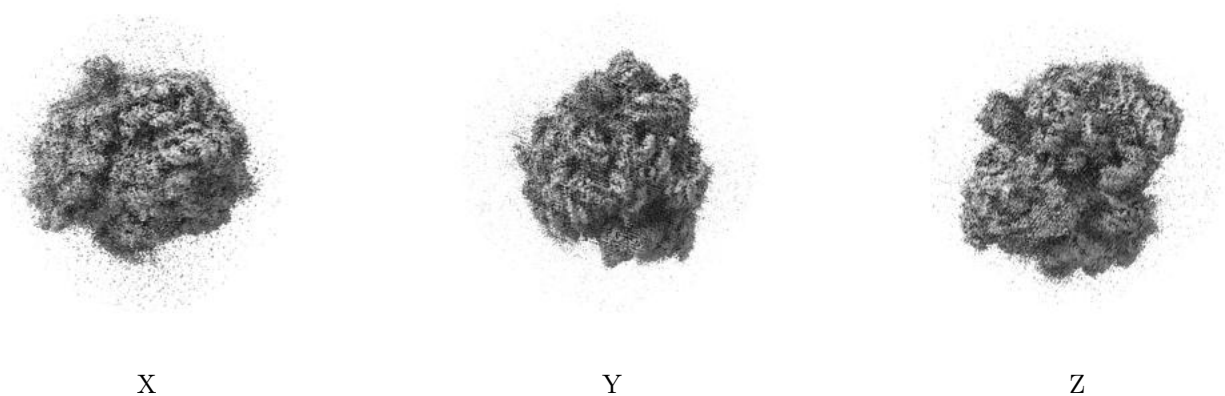


Z

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

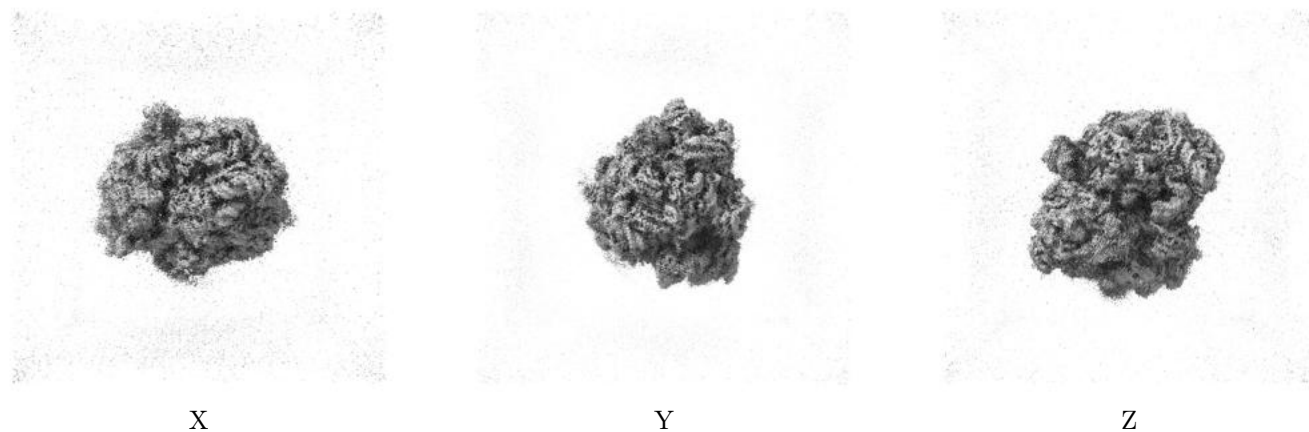
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. 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



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.

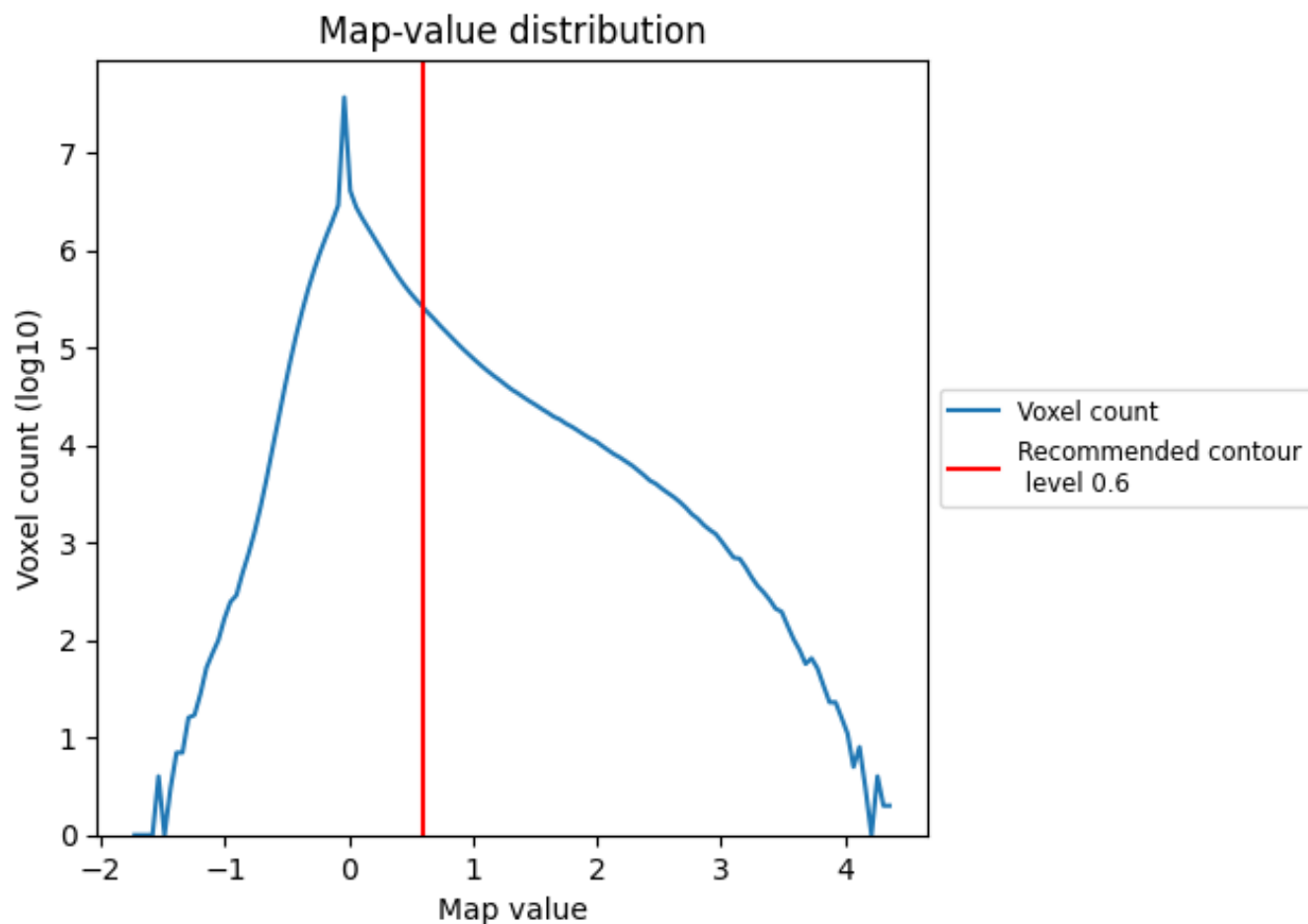
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

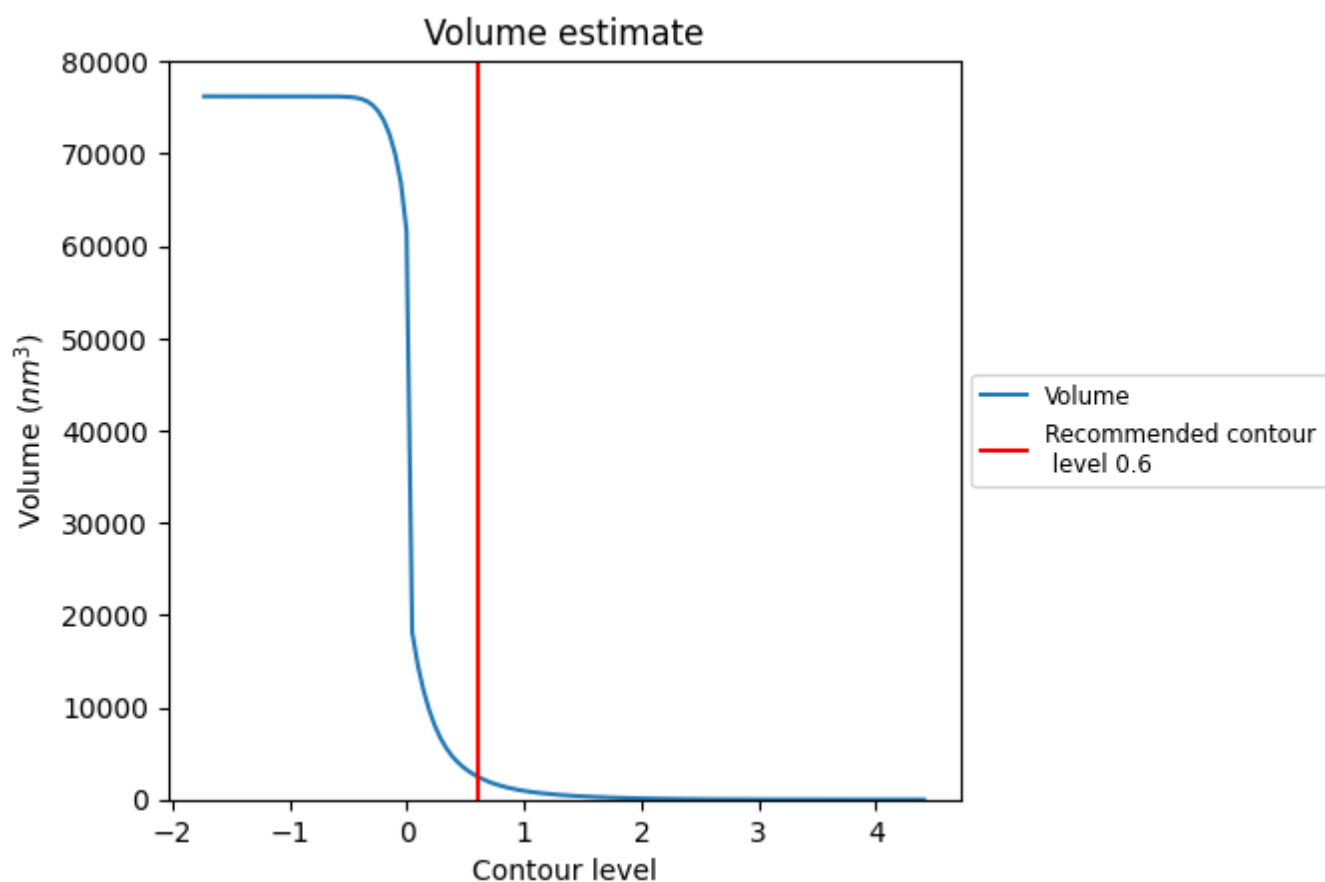
This section contains the results of statistical analysis of the map.

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.

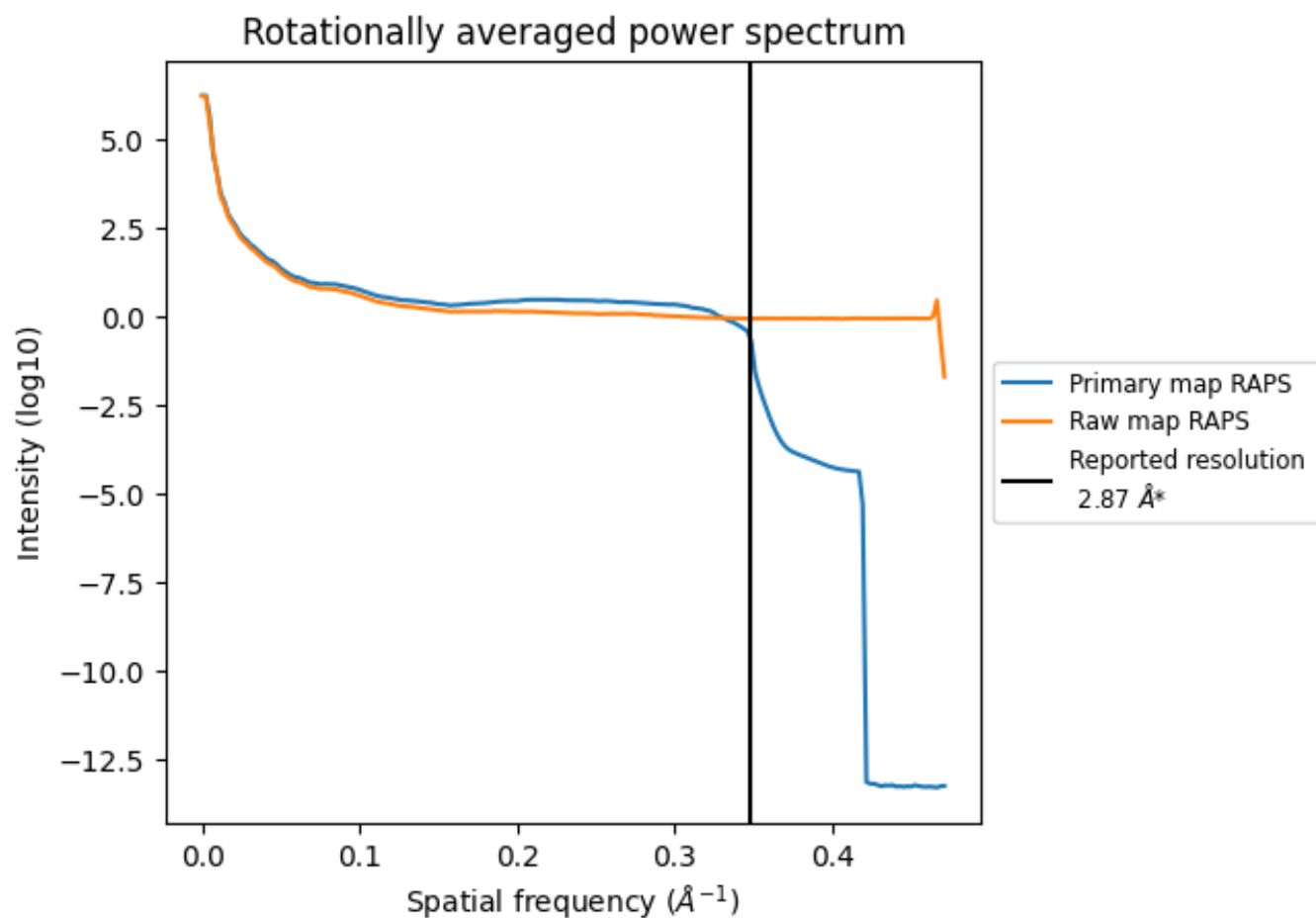
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2515 nm³; this corresponds to an approximate mass of 2272 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

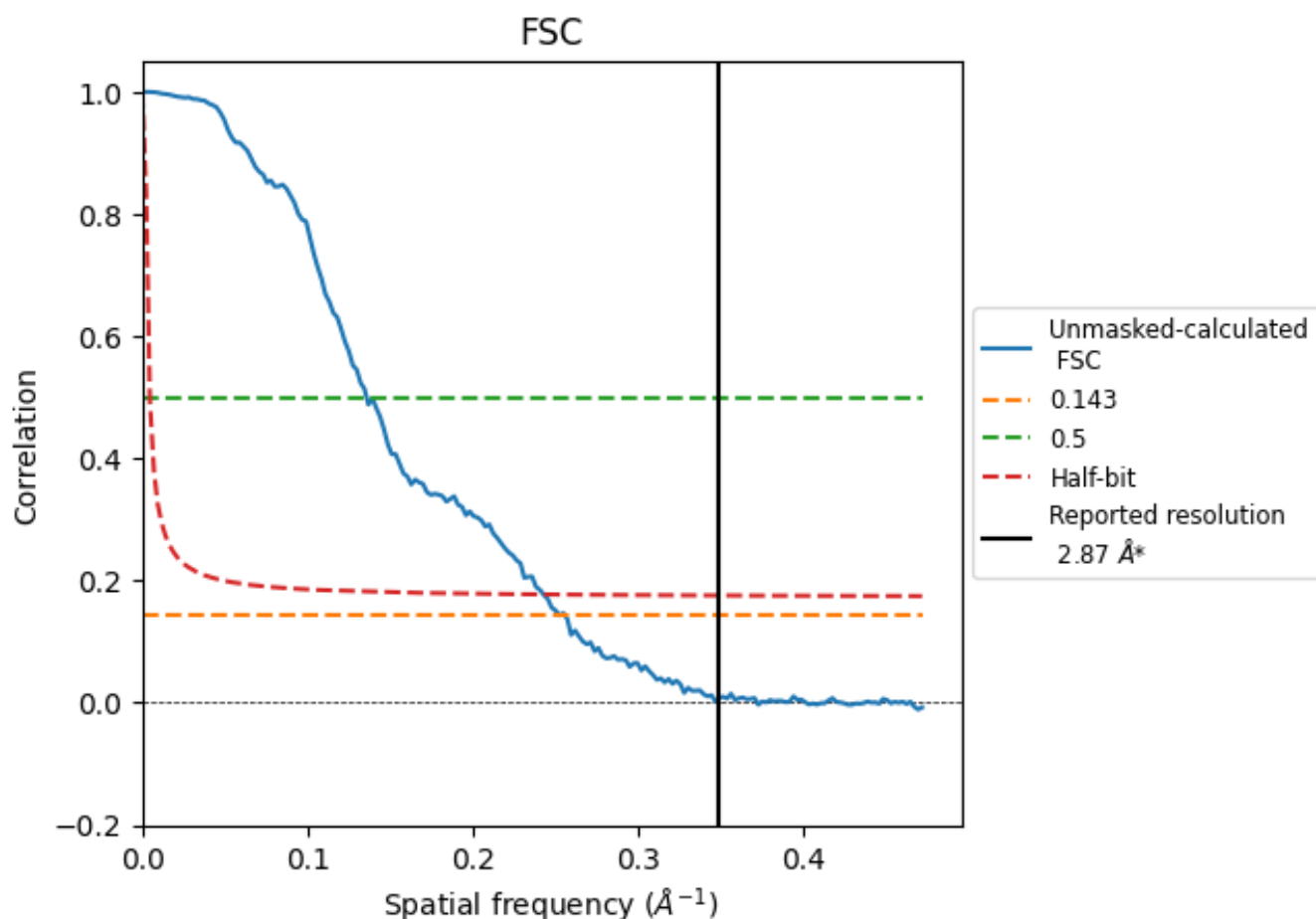


*Reported resolution corresponds to spatial frequency of $0.348 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

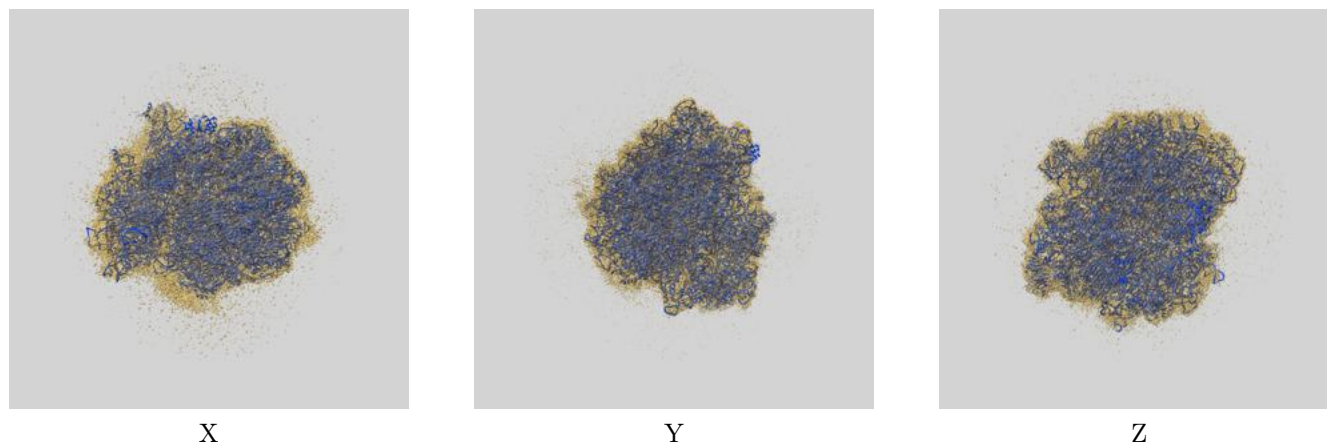
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.87	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.96	7.37	4.12

*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 3.96 differs from the reported value 2.87 by more than 10 %

9 Map-model fit [i](#)

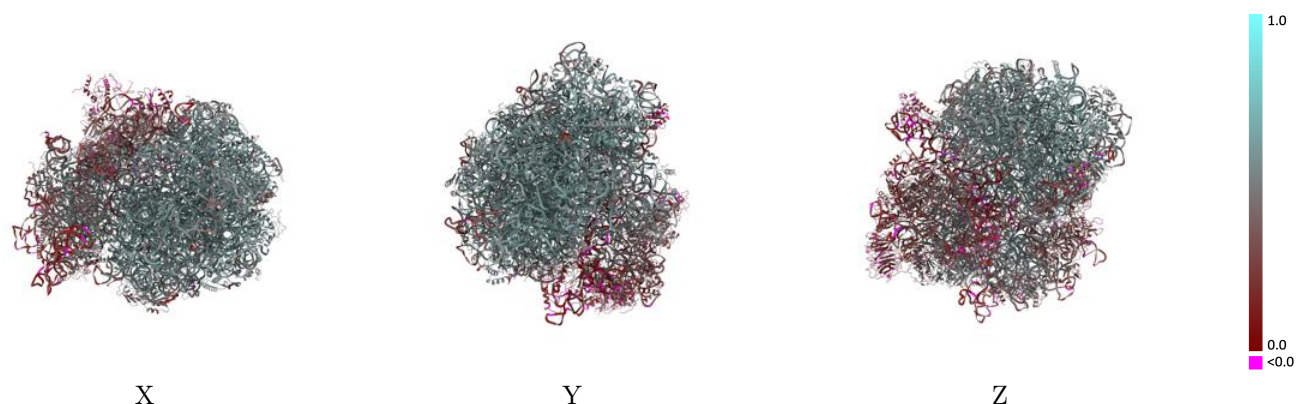
This section contains information regarding the fit between EMDB map EMD-28634 and PDB model 8EVR. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



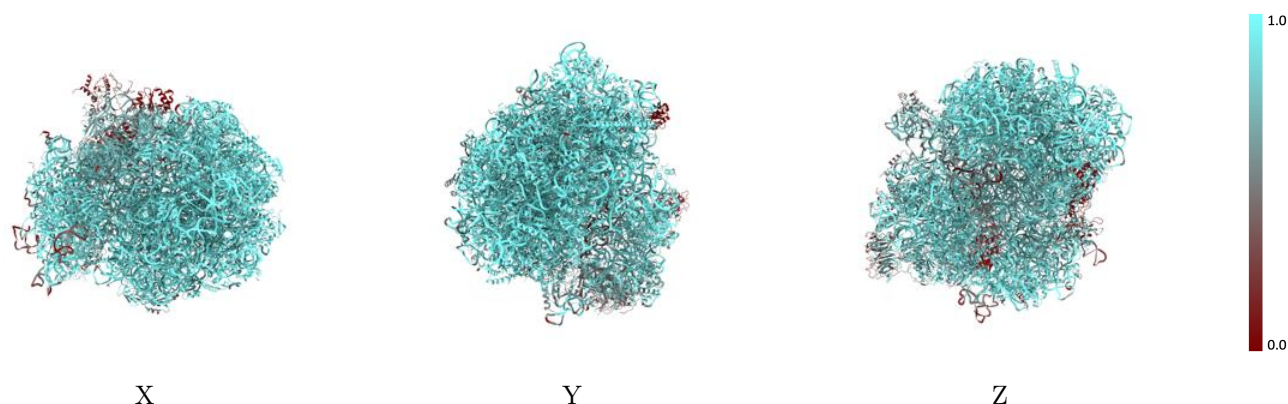
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



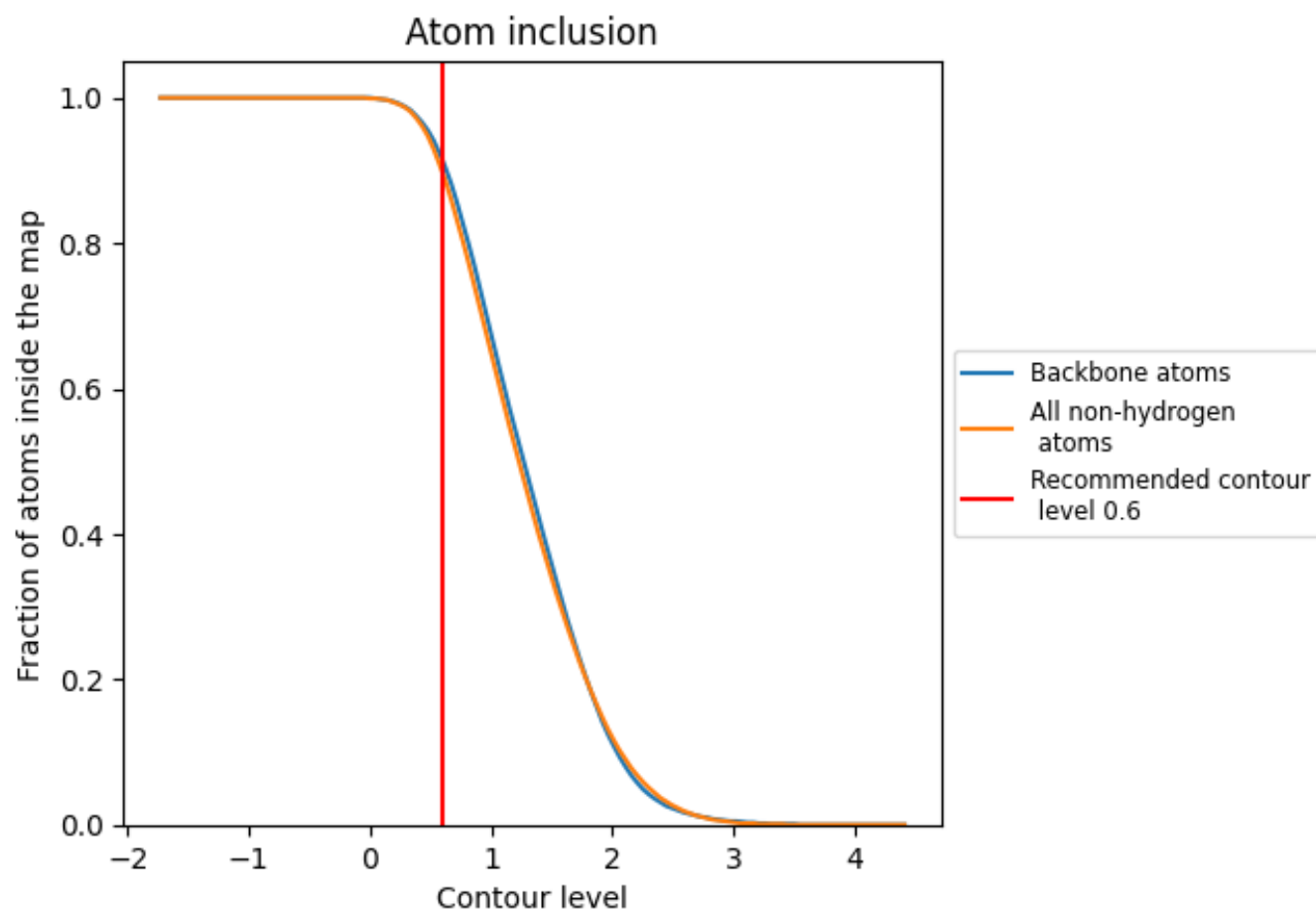
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 91% of all backbone atoms, 90% 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	 0.8960	 0.4700
A1	 0.9690	 0.5450
A3	 0.9880	 0.5370
A4	 0.9820	 0.5650
AA	 0.9650	 0.5960
AB	 0.9610	 0.5570
AC	 0.9600	 0.5680
AD	 0.9000	 0.4750
AE	 0.9400	 0.5160
AF	 0.9770	 0.5790
AG	 0.9170	 0.5240
AH	 0.9140	 0.5420
AI	 0.9570	 0.5560
AJ	 0.8430	 0.4180
AL	 0.9560	 0.5620
AM	 0.9560	 0.5510
AN	 0.9900	 0.6000
AO	 0.9620	 0.5680
AP	 0.9530	 0.5520
AQ	 0.9790	 0.5920
AR	 0.8140	 0.4660
AS	 0.9640	 0.5660
AT	 0.9600	 0.5490
AU	 0.8950	 0.4500
AV	 0.9550	 0.5720
AW	 0.9720	 0.5570
AX	 0.9420	 0.5390
AY	 0.9600	 0.5440
AZ	 0.9270	 0.5260
Aa	 0.9740	 0.5860
Ab	 0.9430	 0.5270
Ac	 0.9000	 0.5310
Ad	 0.9360	 0.5170
Ae	 0.9740	 0.5850
Af	 0.9820	 0.5850



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Chain	Atom inclusion	Q-score
Ag	 0.9400	 0.5430
Ah	 0.9640	 0.5500
Ai	 0.9600	 0.5280
Aj	 0.9860	 0.5960
Ak	 0.6730	 0.4290
Al	 0.9810	 0.5680
Am	 0.9230	 0.5480
An	 0.9580	 0.5180
Ao	 0.9050	 0.5520
Ap	 0.9700	 0.5790
B5	 0.9140	 0.4120
BA	 0.8380	 0.4370
BB	 0.8270	 0.4460
BC	 0.9330	 0.4880
BD	 0.7970	 0.3130
BE	 0.9220	 0.4430
BF	 0.6910	 0.2870
BG	 0.8690	 0.3610
BH	 0.7220	 0.3960
BI	 0.9090	 0.4430
BJ	 0.9200	 0.4600
BK	 0.7000	 0.2420
BL	 0.8850	 0.4680
BM	 0.1780	 0.1670
BN	 0.8830	 0.4760
BO	 0.8790	 0.4640
BP	 0.6790	 0.2990
BQ	 0.7860	 0.3070
BR	 0.6850	 0.3240
BS	 0.7510	 0.3010
BT	 0.8030	 0.3040
BU	 0.7410	 0.2740
BV	 0.9050	 0.4640
BW	 0.9740	 0.5400
BX	 0.9580	 0.5260
BY	 0.8900	 0.4040
BZ	 0.6720	 0.1990
Ba	 0.9040	 0.4920
Bb	 0.8000	 0.4400
Bc	 0.6500	 0.3000
Bd	 0.9030	 0.3510
Be	 0.8840	 0.4130

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Chain	Atom inclusion	Q-score
Bf	 0.2720	 0.1740
Bg	 0.5550	 0.2140
DC	 0.7140	 0.2960
E	 0.5730	 0.1810
EC	 0.5020	 0.1100
V	 0.1250	 0.2160