



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 03:06 PM UTC

PDB ID : 8T3A / pdb_00008t3a
EMDB ID : EMD-40997
Title : Hypomethylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), eEF2, GDP, sordarin, and hibernating factor Los2
Authors : Zhao, Y.; Li, H.
Deposited on : 2023-06-07
Resolution : 2.86 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

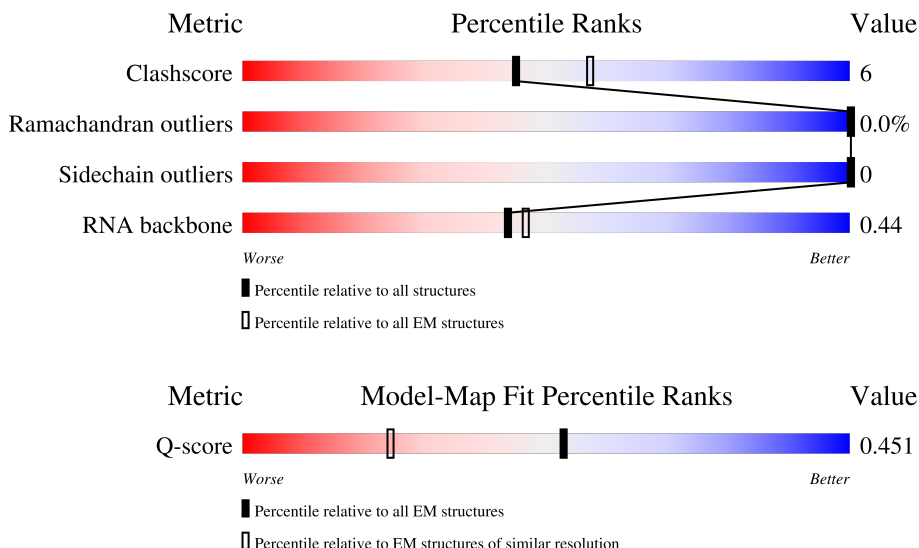
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 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	12017 (2.36 - 3.36)

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	

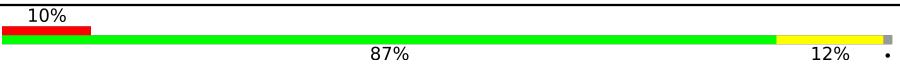
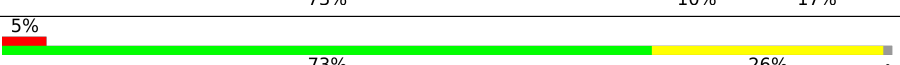
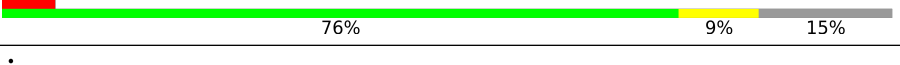
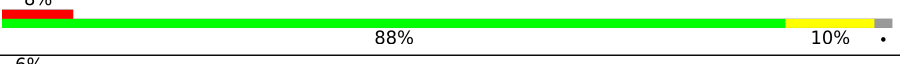
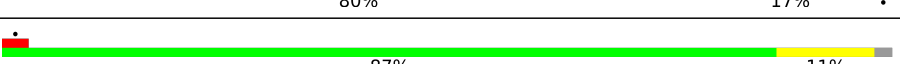
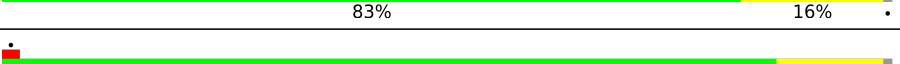
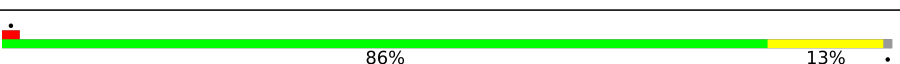
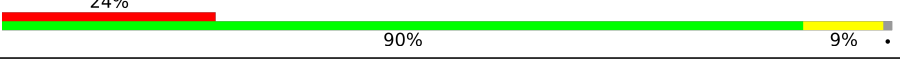
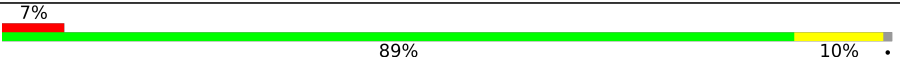
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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3394	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	222	
47	AJ	174	
48	AL	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	tE	77	
80	E	217	
81	C5	92	
82	DC	842	

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	SO1	DC	903	X	-	-	-

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 210450 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
			948	596	179	171	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	71	Total	C	N	O	0	0
			574	366	108	100		

- 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	1757	Total	C	N	O	P	1	0
			37463	16754	6635	12317	1757		

- 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	3214	Total	C	N	O	P	0	0
			68746	30711	12381	22440	3214		

- 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	167	Total	C	N	O	S	0	0
			1303	840	234	228	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	120	LYS	ASN	conflict	UNP Q02326

- 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 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AI	222	Total	C	N	O	S	0	0
			1804	1147	339	310	8		

- 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	0	0
			1543	962	315	266		

- 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	0	0
			1053	675	199	177	2		

- 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	0	0
			1720	1077	361	281	1		

- 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	197	0
			1555	1003	289	262	1		

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

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

- 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	0	0
			1441	908	290	241	2		

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

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

- 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 RNA chain called E site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	tE	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 80 is a protein called RPL1A isoform 1.

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

- Molecule 81 is a protein called LSO2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	C5	79	Total	C	N	O	S	0	0
			633	379	128	125	1		

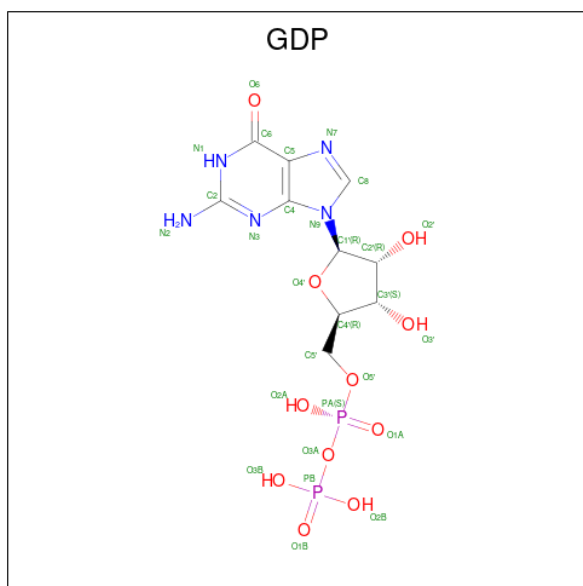
- Molecule 82 is a protein called Elongation factor 2.

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

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 84 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

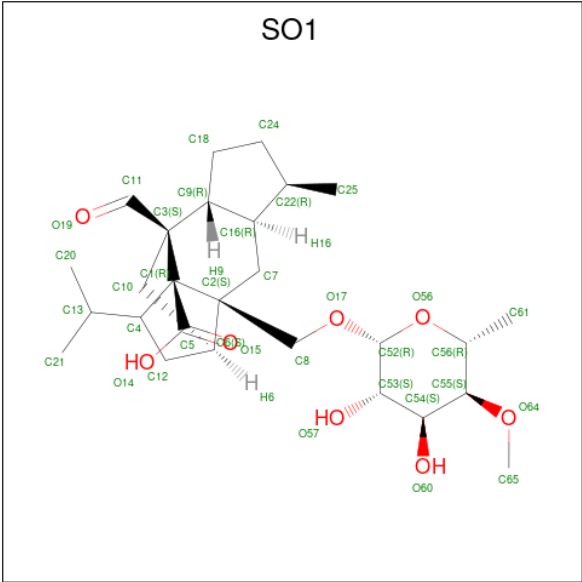


Mol	Chain	Residues	Atoms					AltConf
84	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

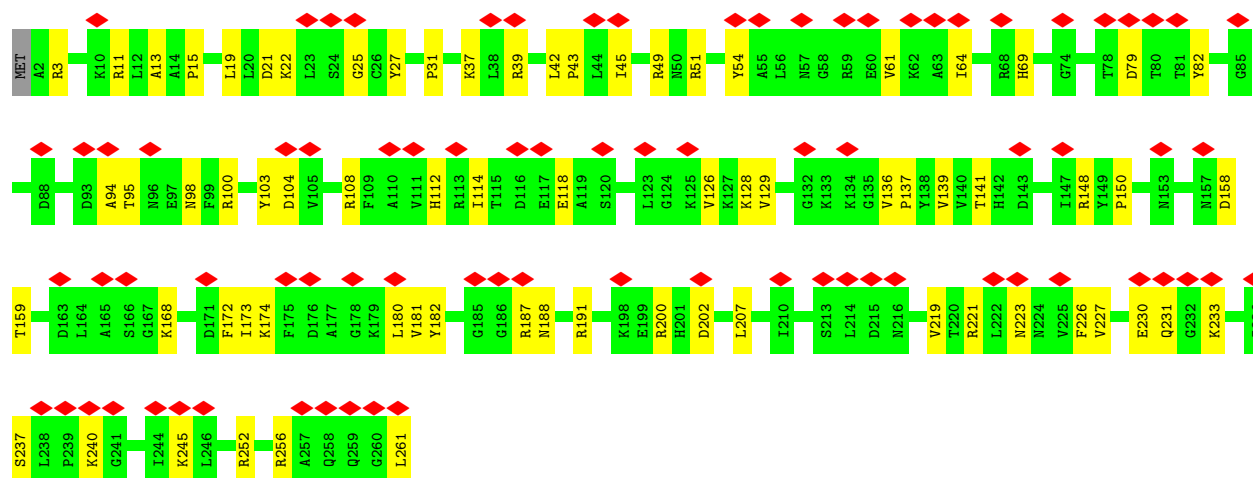
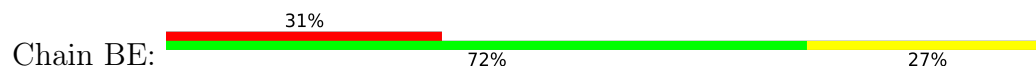
Mol	Chain	Residues	Atoms		AltConf
85	DC	1	Total	Mg	0
			1	1	

- Molecule 86 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.BETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTRPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (CCD ID: SO1) (formula: $C_{27}H_{42}O_8$).

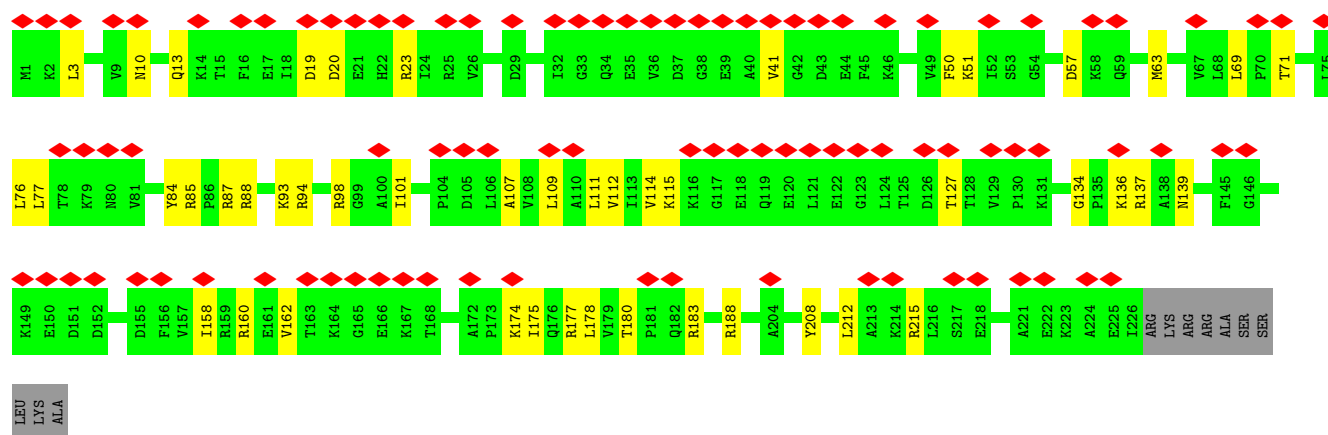
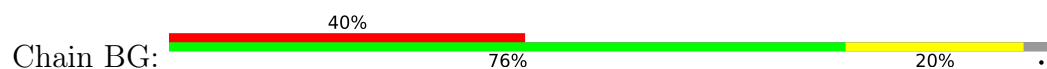


Mol	Chain	Residues	Atoms			AltConf
86	DC	1	Total	C	O	0
			35	27	8	

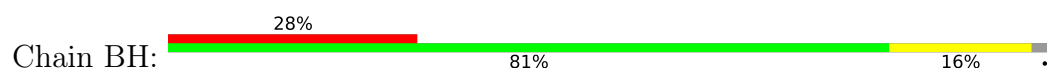
- Molecule 4: 40S ribosomal protein S4-A

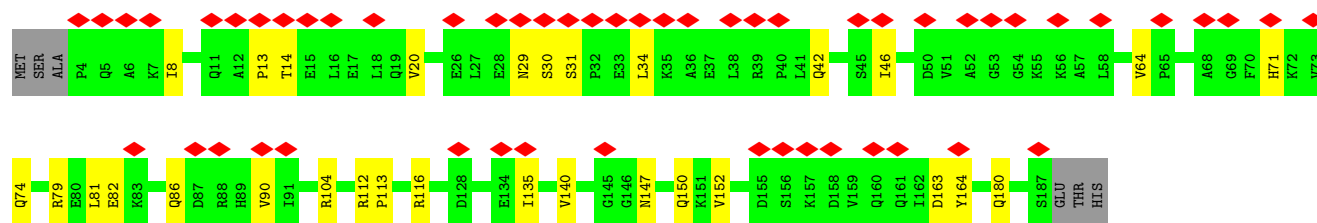


- Molecule 5: 40S ribosomal protein S6-A

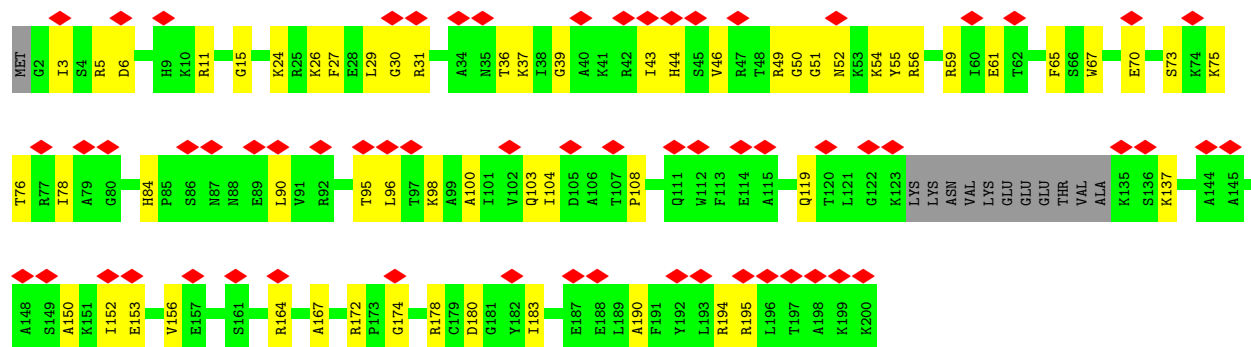


- Molecule 6: 40S ribosomal protein S7-A

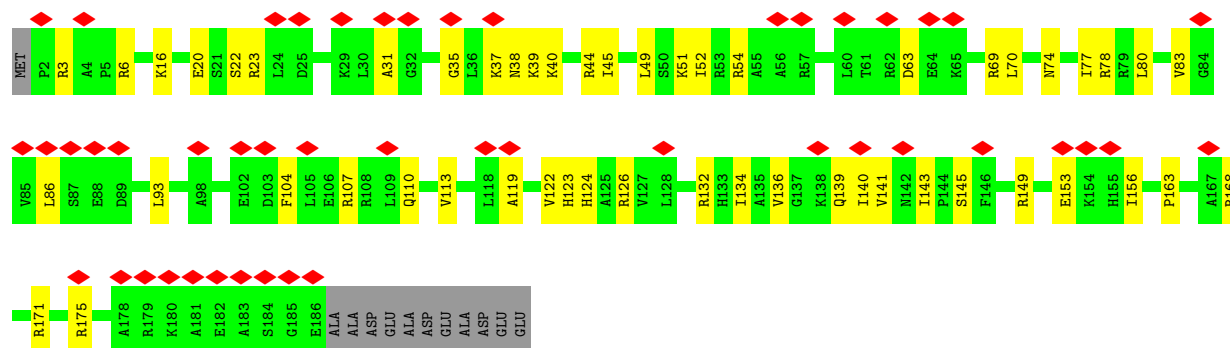




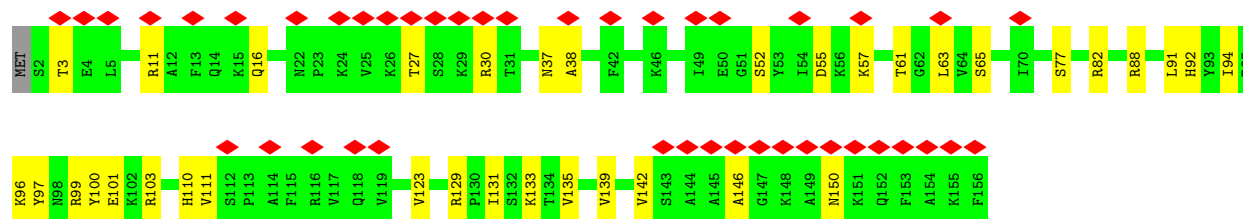
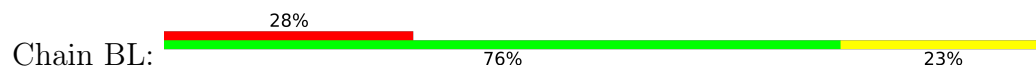
• Molecule 7: 40S ribosomal protein S8-A



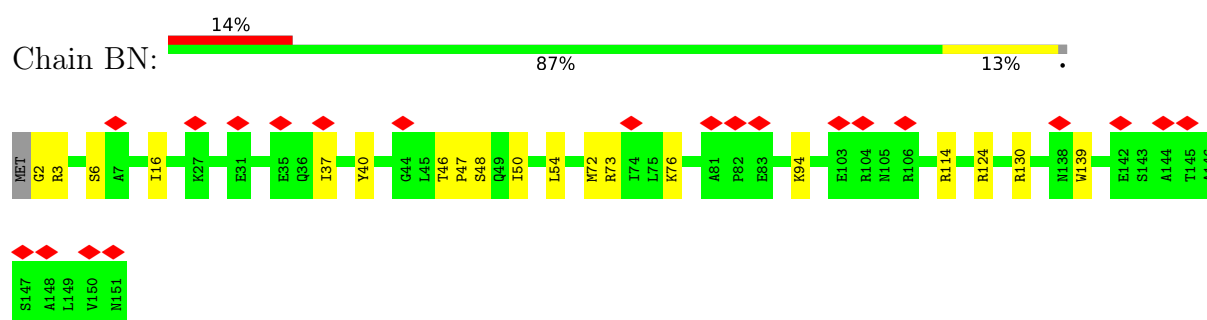
• Molecule 8: 40S ribosomal protein S9-A



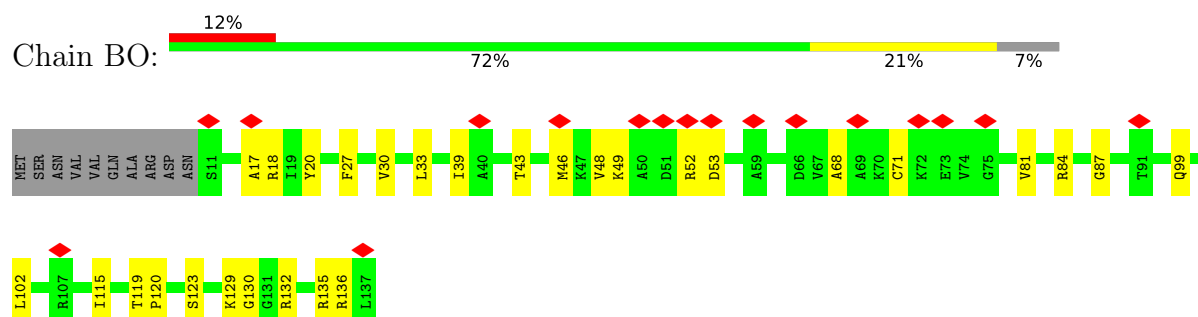
• Molecule 9: 40S ribosomal protein S11-A



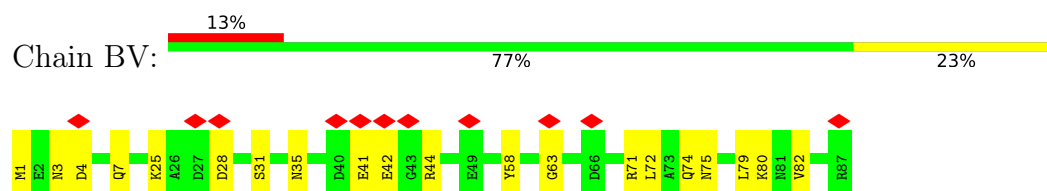
• Molecule 10: 40S ribosomal protein S13



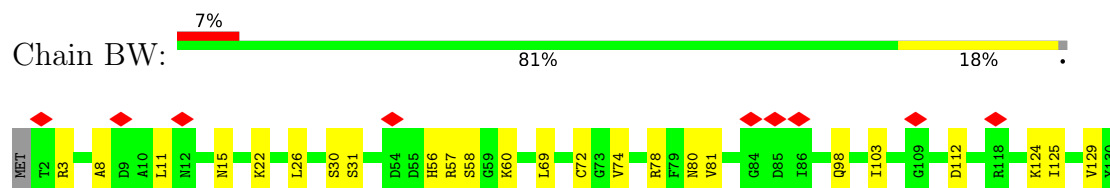
- Molecule 11: 40S ribosomal protein S14-A



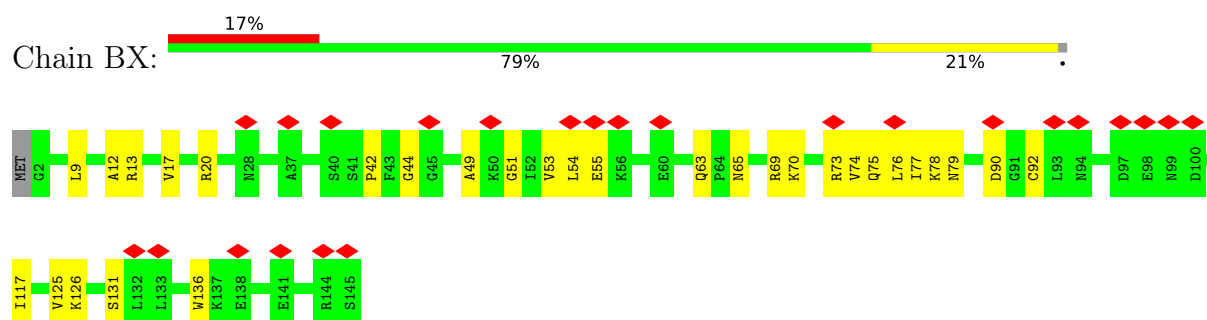
- Molecule 12: 40S ribosomal protein S21-A



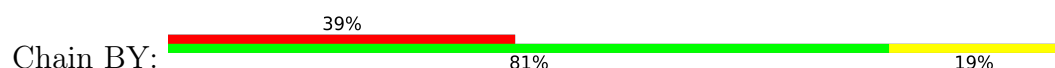
- Molecule 13: RPS22A isoform 1

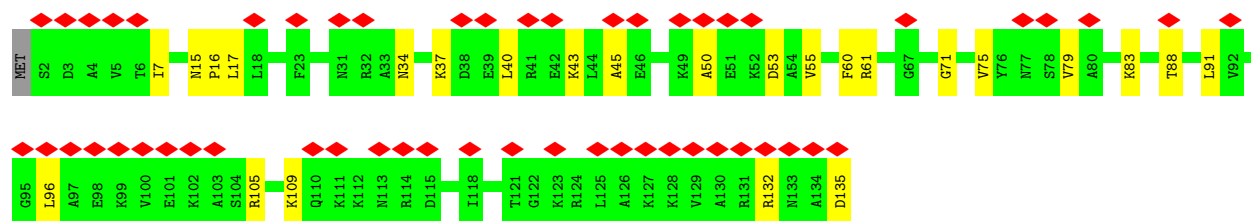


- Molecule 14: 40S ribosomal protein S23-A

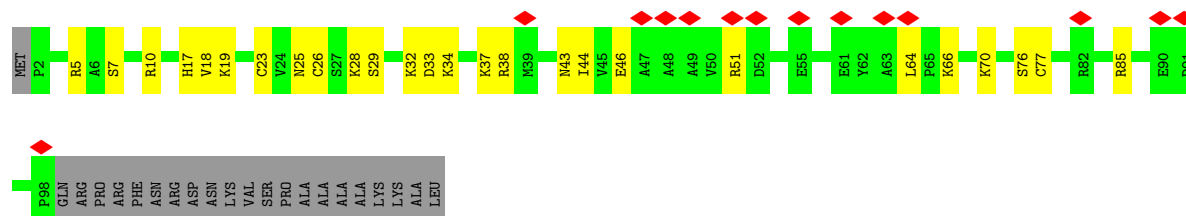


- Molecule 15: 40S ribosomal protein S24-A

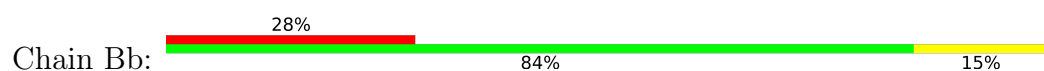




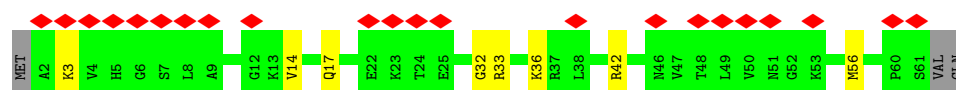
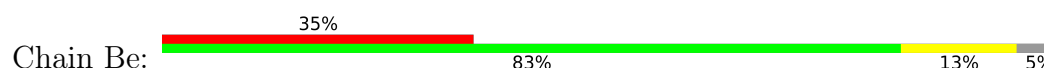
• Molecule 16: RPS26B isoform 1



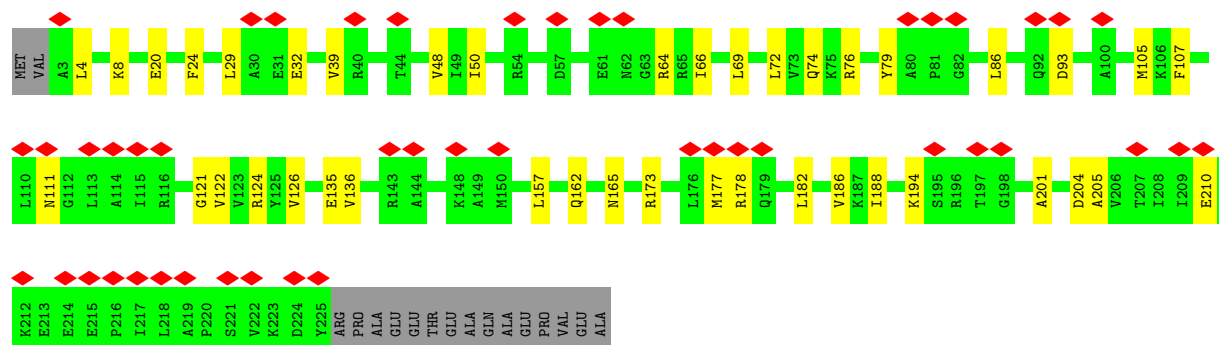
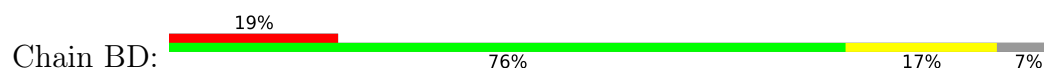
• Molecule 17: 40S ribosomal protein S27-A



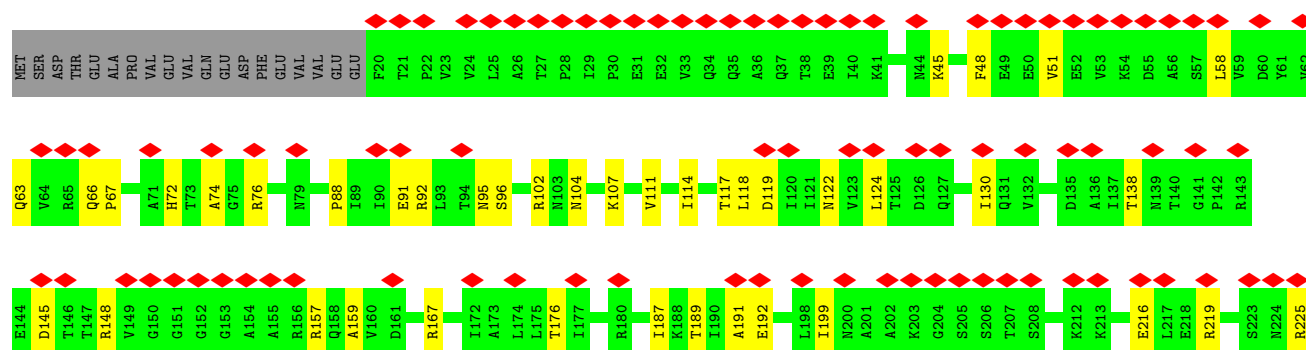
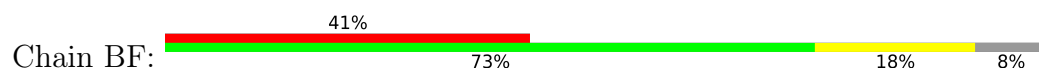
• Molecule 18: 40S ribosomal protein S30-A



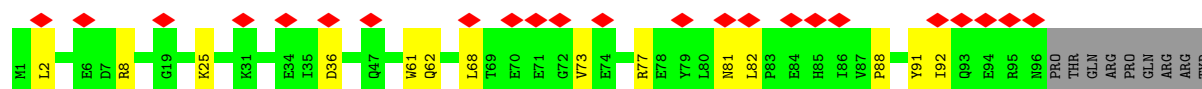
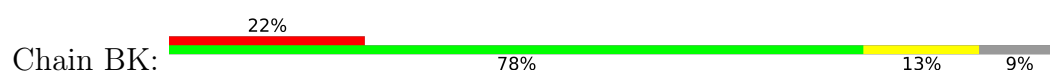
• Molecule 19: RPS3 isoform 1



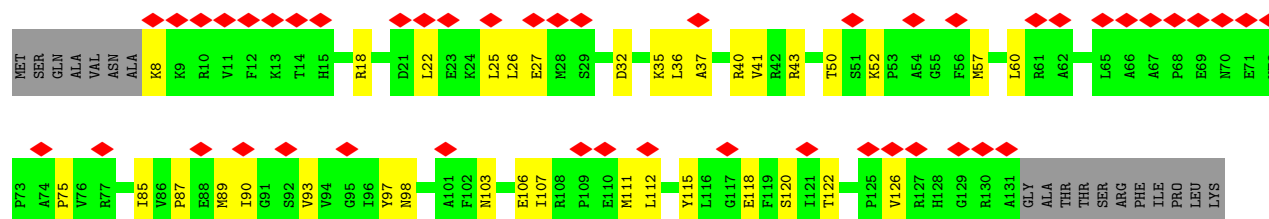
• Molecule 20: Rps5p



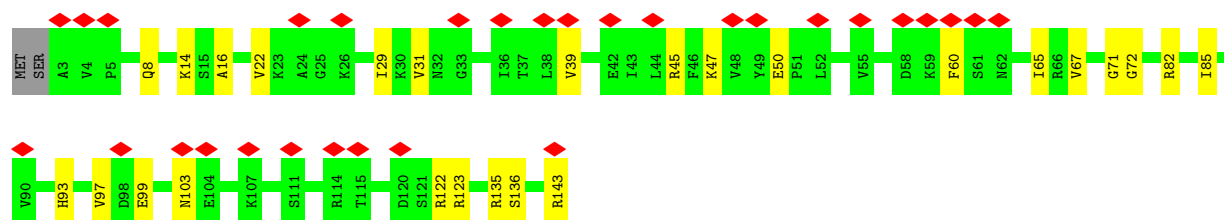
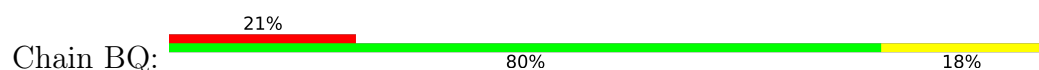
• Molecule 21: 40S ribosomal protein S10-A



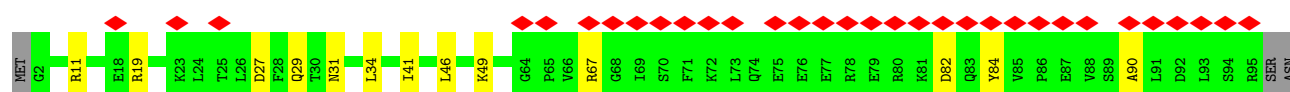
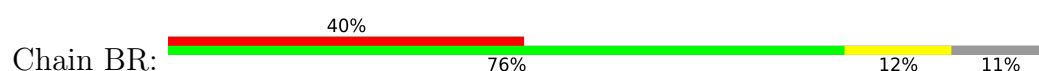
• Molecule 22: RPS15 isoform 1

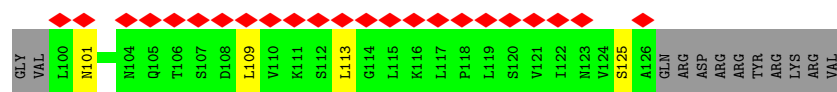


• Molecule 23: 40S ribosomal protein S16-A

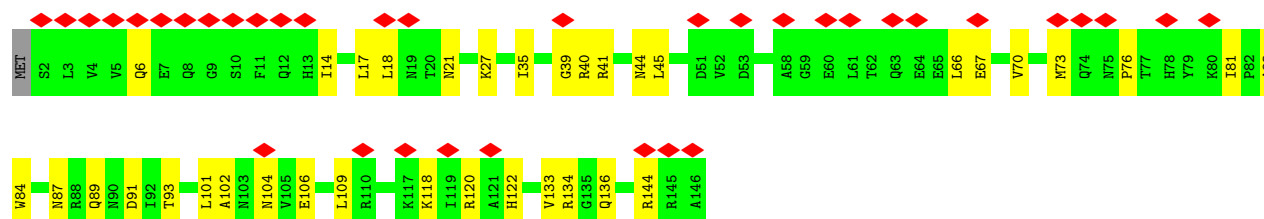
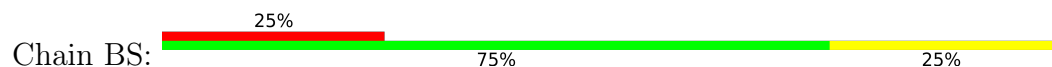


• Molecule 24: 40S ribosomal protein S17-A

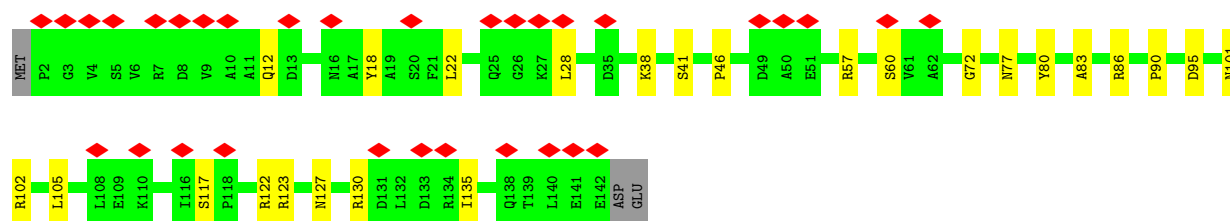
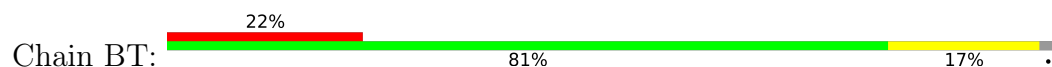




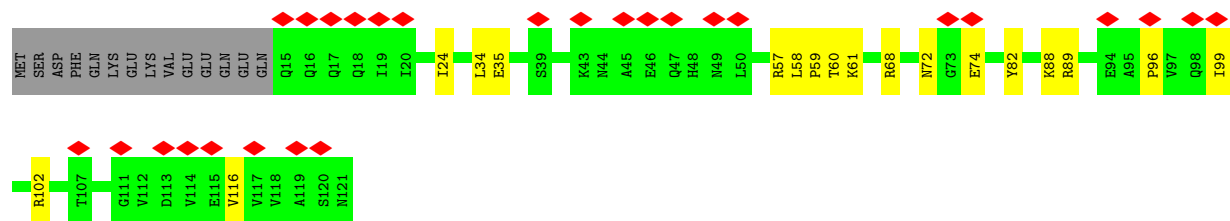
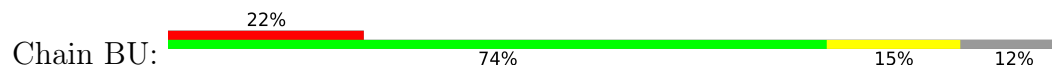
• Molecule 25: 40S ribosomal protein S18-A



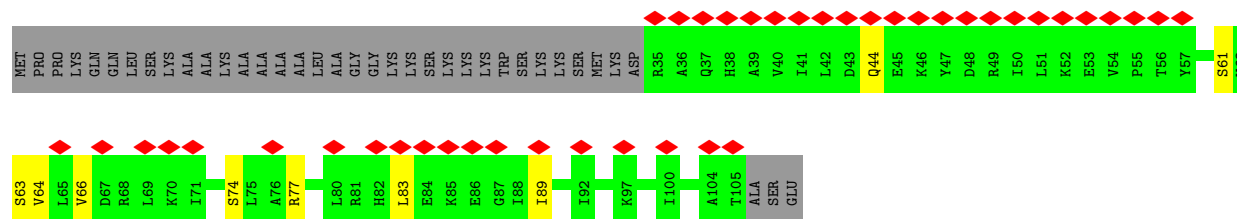
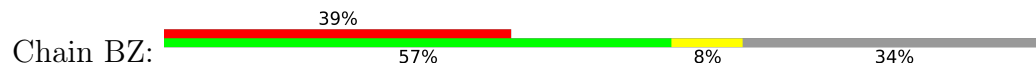
• Molecule 26: 40S ribosomal protein S19-A



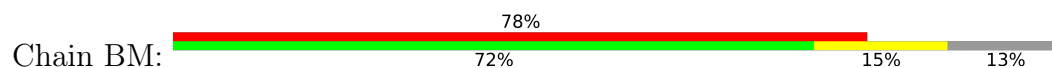
• Molecule 27: RPS20 isoform 1



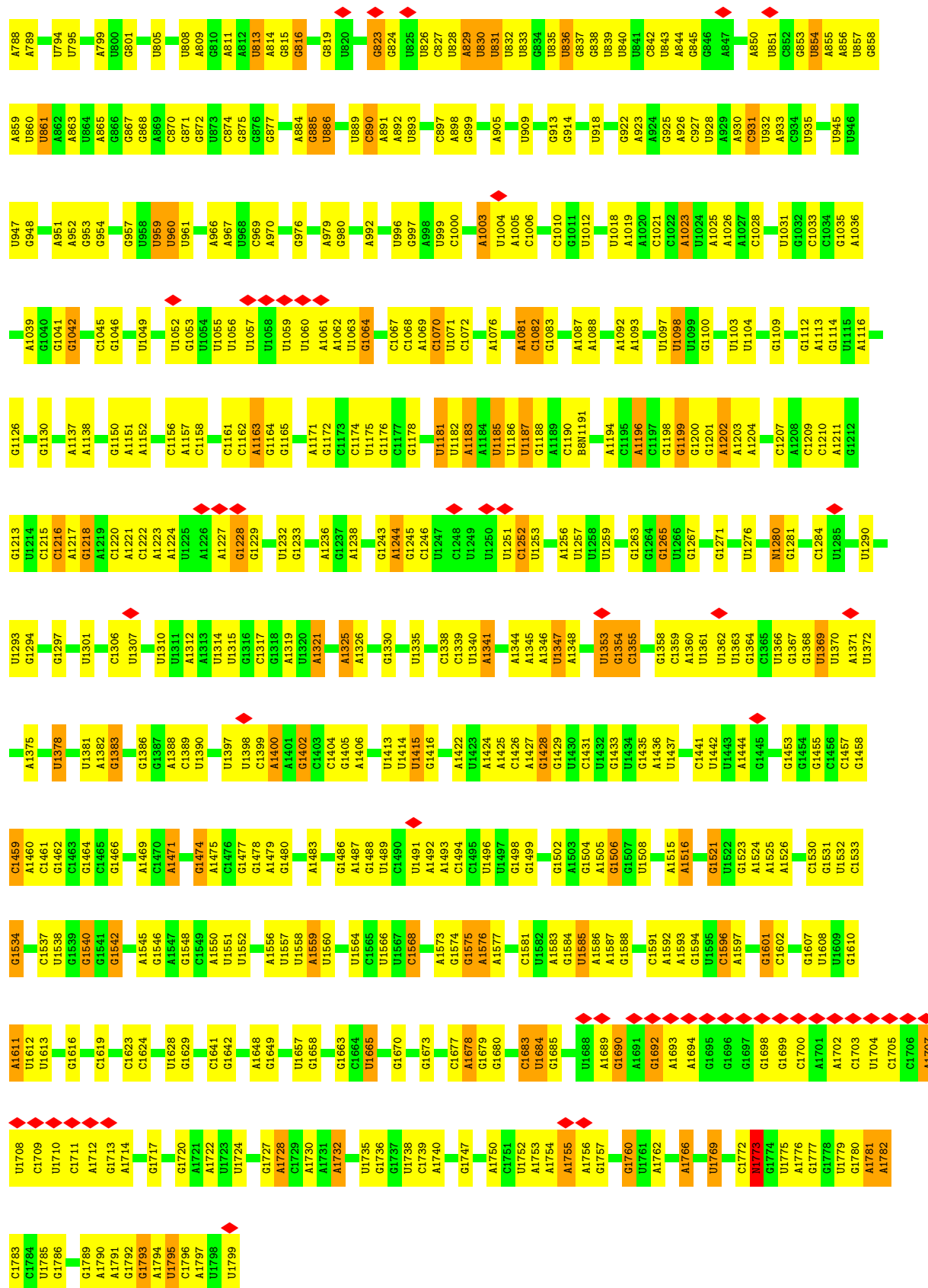
• Molecule 28: RPS25A isoform 1



• Molecule 29: RPS28A isoform 1

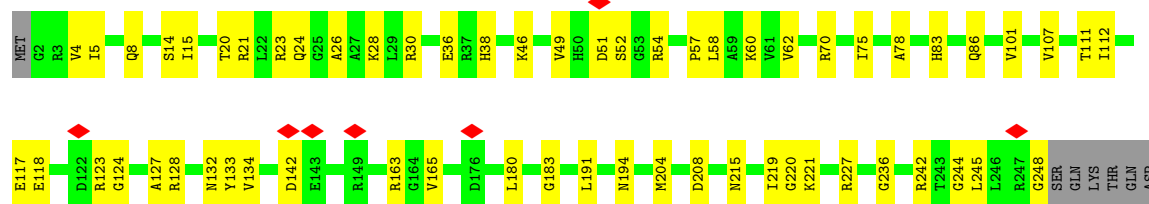






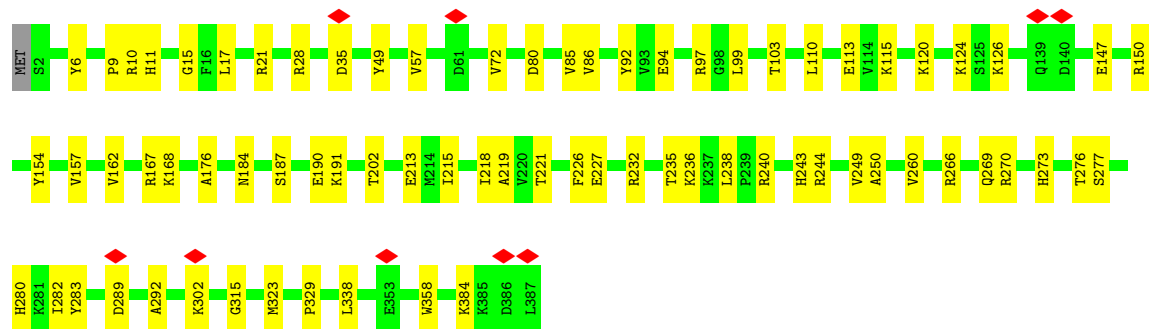
- Molecule 35: 60S ribosomal protein L2-A

Chain AA:  74% 24%



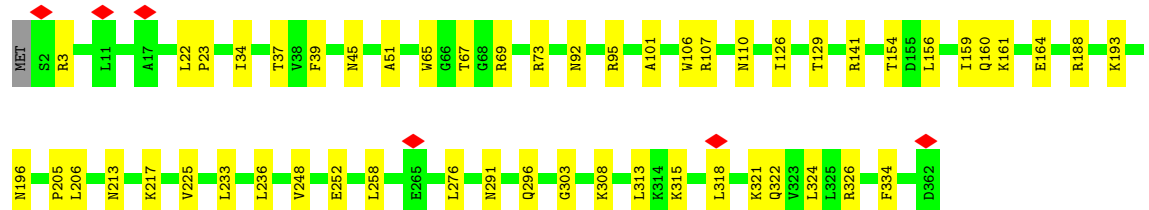
• Molecule 36: 60S ribosomal protein L3

Chain AB:  81% 19%



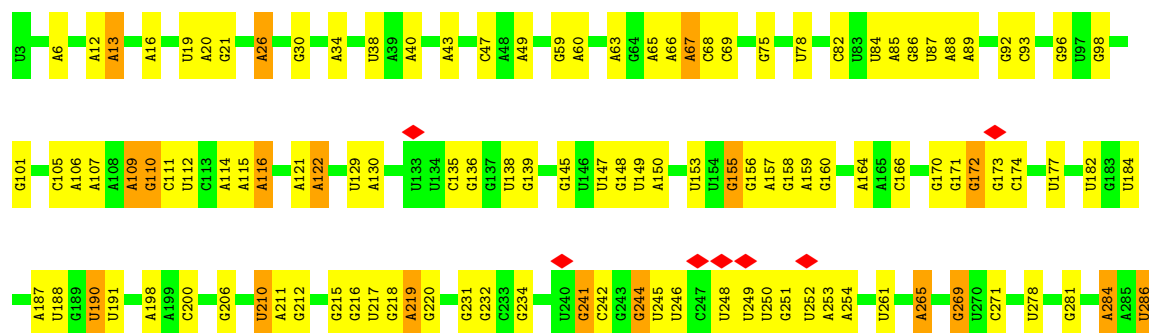
• Molecule 37: RPL4A isoform 1

Chain AC:  85% 15%



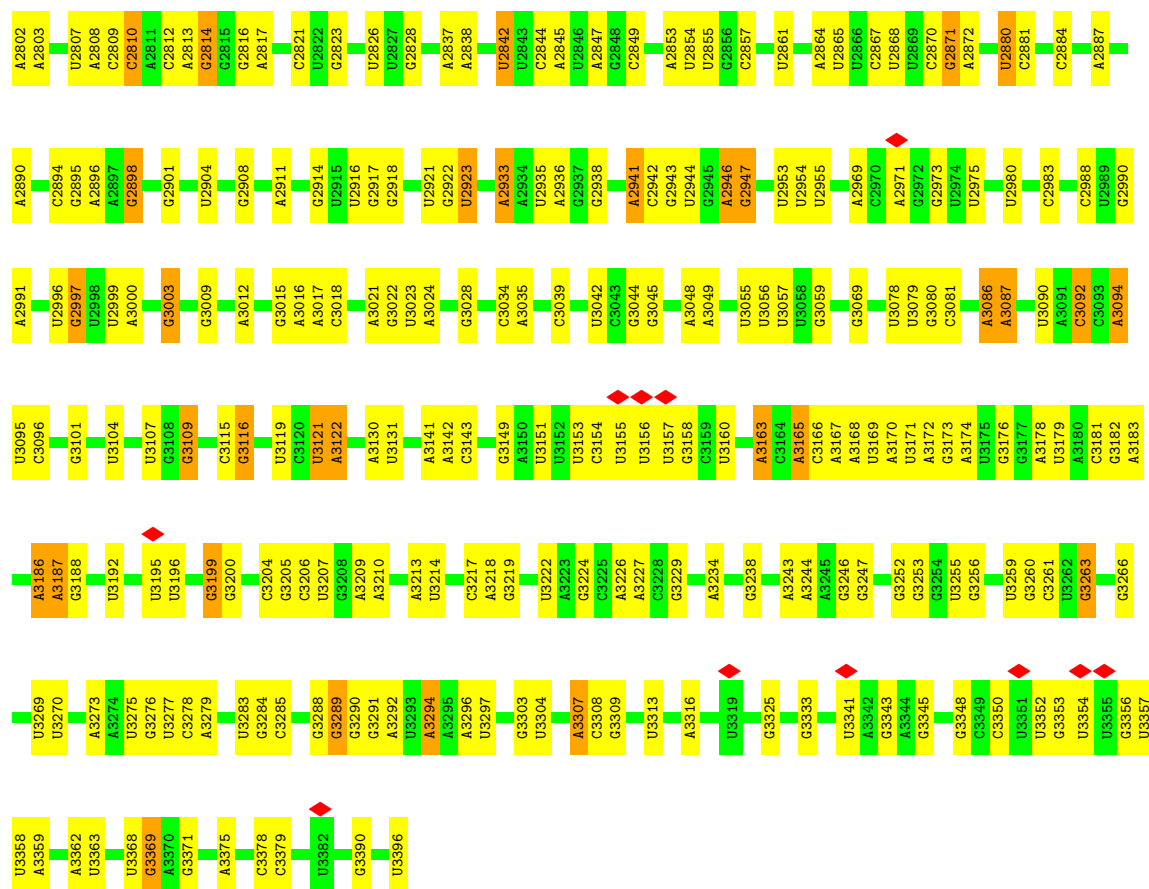
• Molecule 38: 25S rRNA

Chain A1:  54% 35% 6% 5%



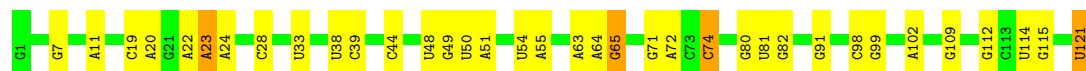






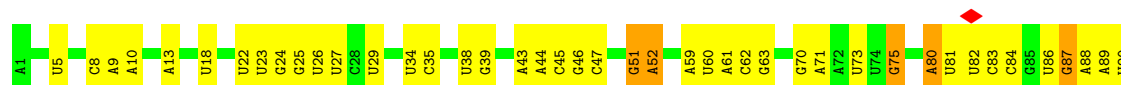
• Molecule 39: 5s rRNA

Chain A3: 70% 26%



• Molecule 40: 5.8 S rRNA

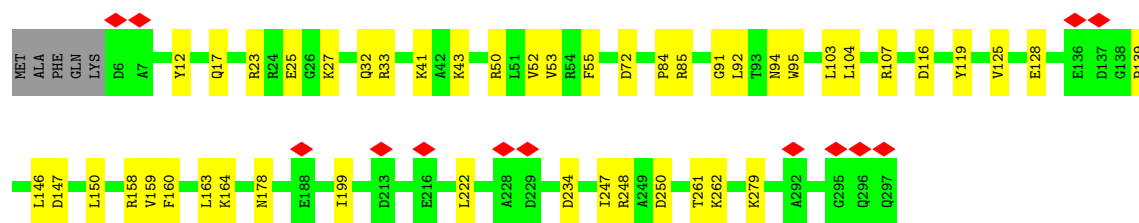
Chain A4: 59% 37%



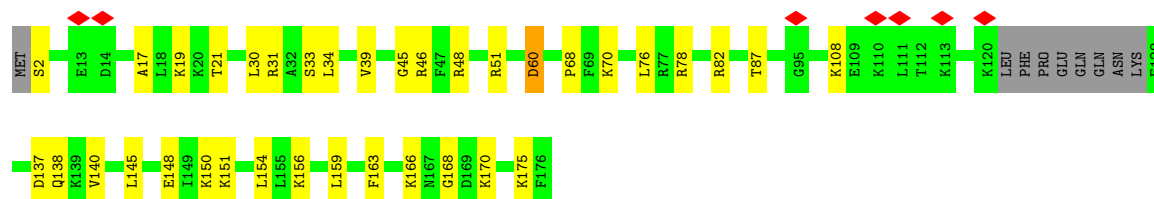
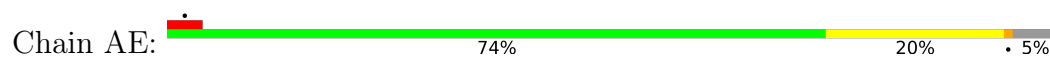
• Molecule 41: RPL5 isoform 1

Chain AD: 83% 15%

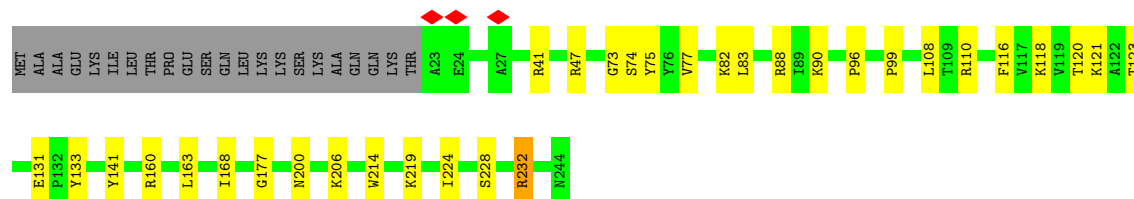
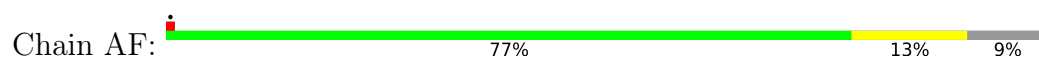




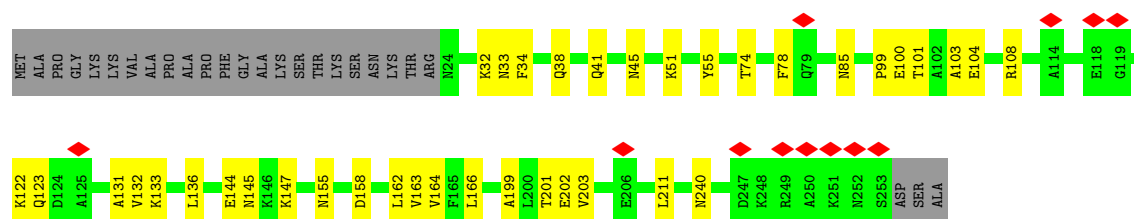
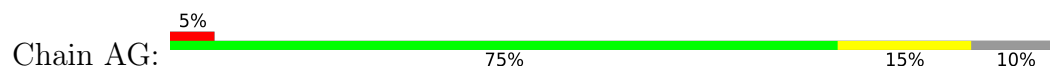
• Molecule 42: 60S ribosomal protein L6-A



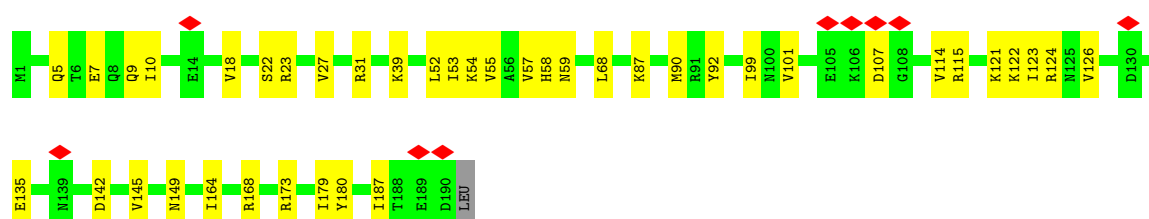
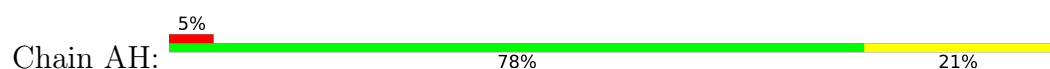
• Molecule 43: 60S ribosomal protein L7-A



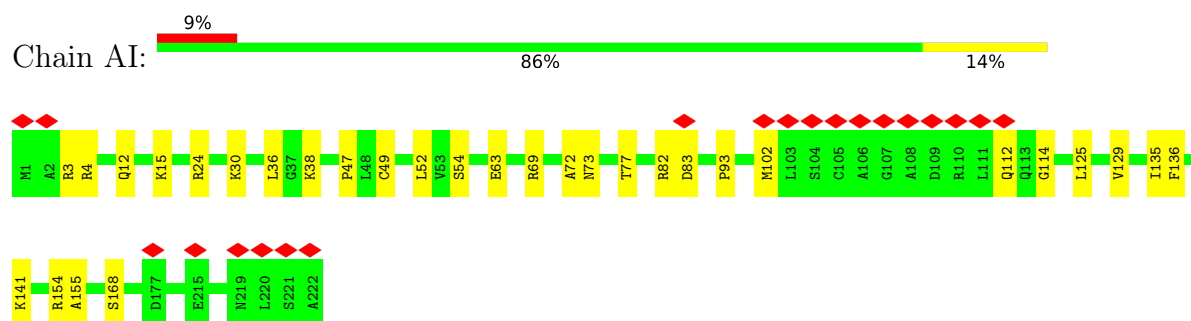
• Molecule 44: 60S ribosomal protein L8-A



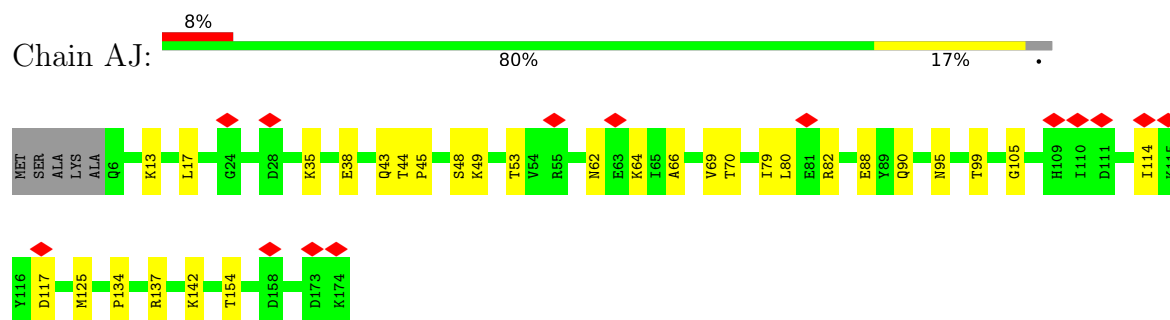
• Molecule 45: 60S ribosomal protein L9-A



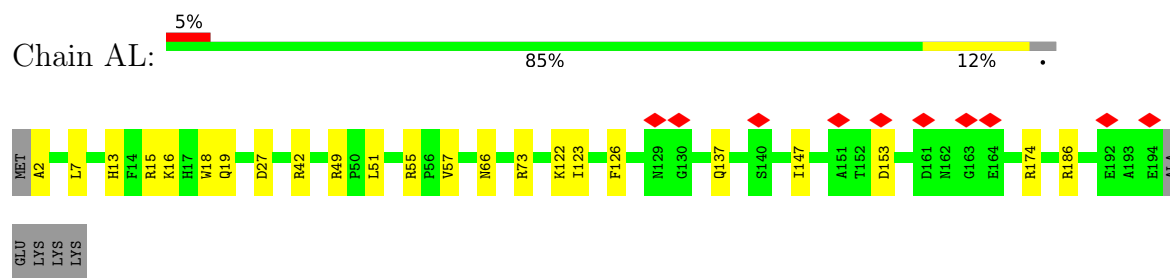
- Molecule 46: 60S ribosomal protein L10



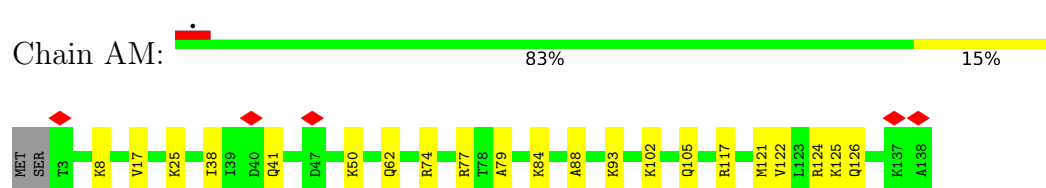
- Molecule 47: RPL11A isoform 1



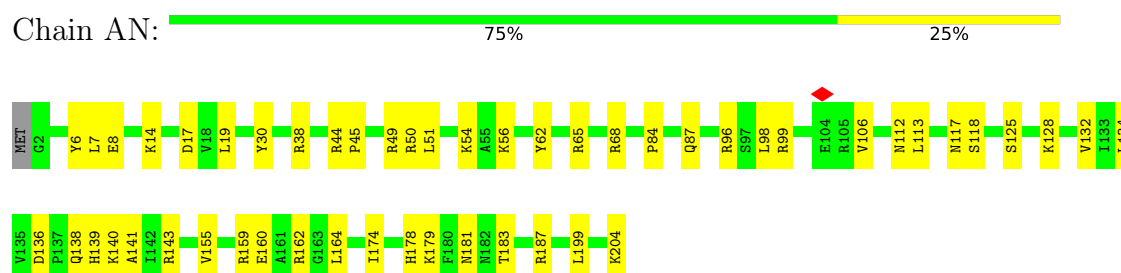
- Molecule 48: 60S ribosomal protein L13-A



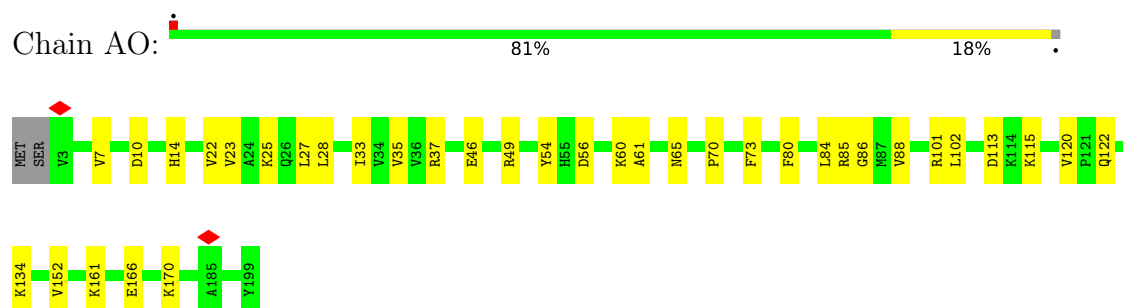
- Molecule 49: 60S ribosomal protein L14-A



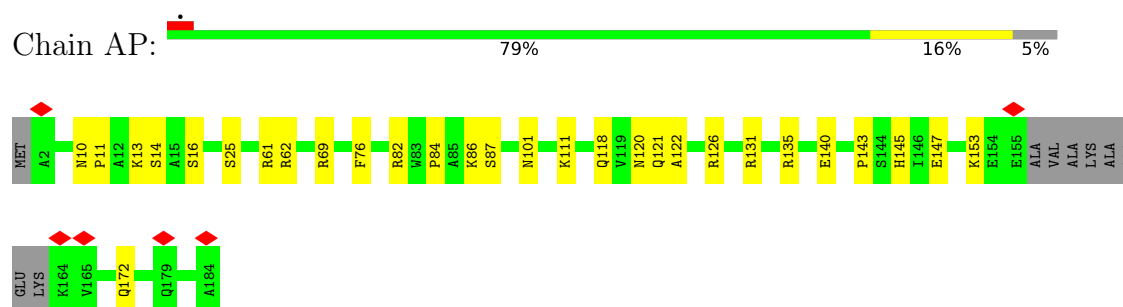
- Molecule 50: 60S ribosomal protein L15-A



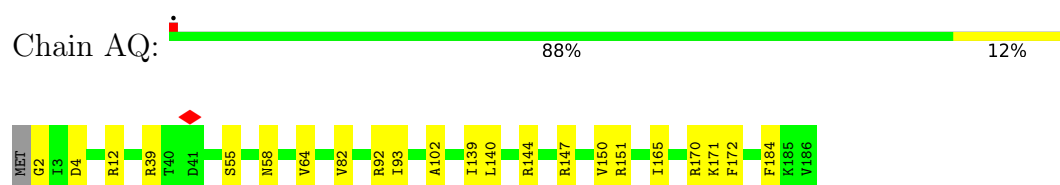
- Molecule 51: 60S ribosomal protein L16-A



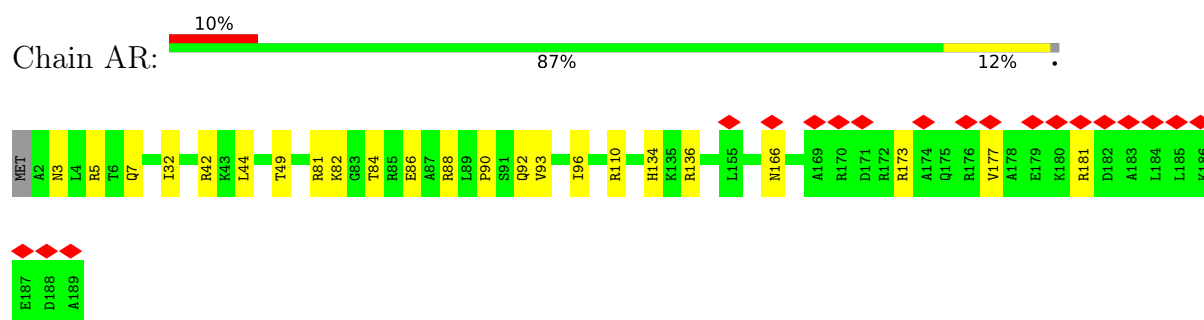
- Molecule 52: 60S ribosomal protein L17-A



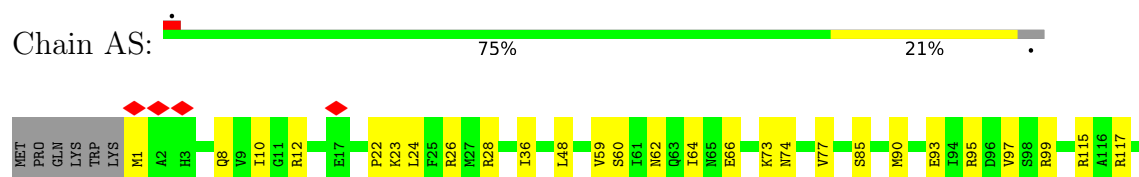
- Molecule 53: 60S ribosomal protein L18-A

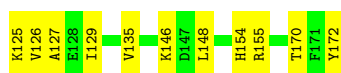


- Molecule 54: 60S ribosomal protein L19-A

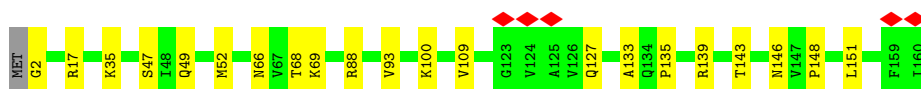
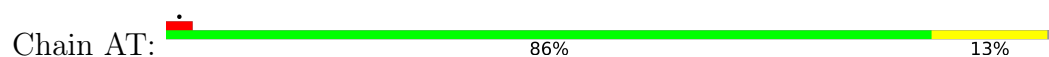


- Molecule 55: 60S ribosomal protein L20

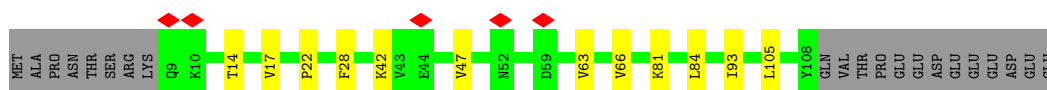
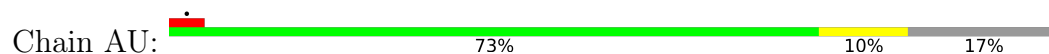




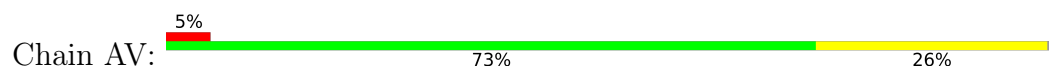
- Molecule 56: 60S ribosomal protein L21-A



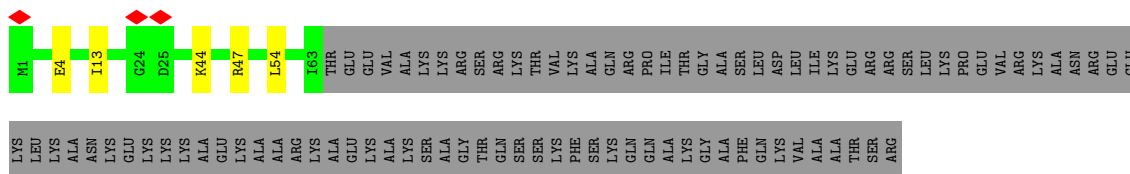
- Molecule 57: 60S ribosomal protein L22-A



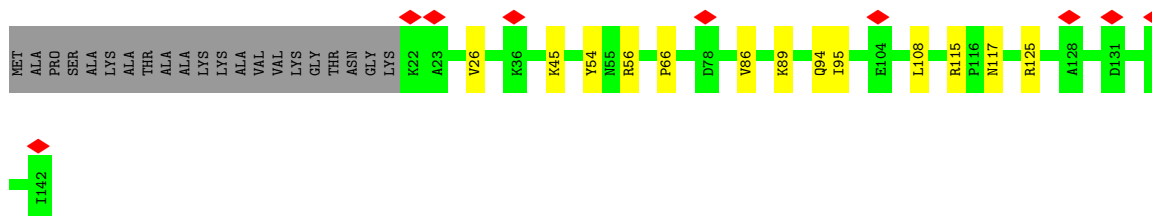
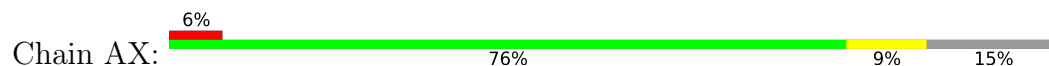
- Molecule 58: 60S ribosomal protein L23-A



- Molecule 59: RPL24A isoform 1



- Molecule 60: 60S ribosomal protein L25



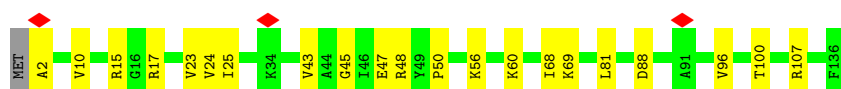
- Molecule 61: 60S ribosomal protein L26-A

Chain AY:  83% 16%



- Molecule 62: 60S ribosomal protein L27-A

Chain AZ:  84% 15%



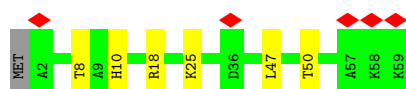
- Molecule 63: 60S ribosomal protein L28

Chain Aa:  82% 17%



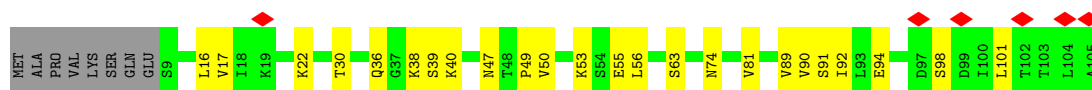
- Molecule 64: RPL29 isoform 1

Chain Ab:  8% 88% 10%



- Molecule 65: 60S ribosomal protein L30

Chain Ac:  6% 70% 23% 8%



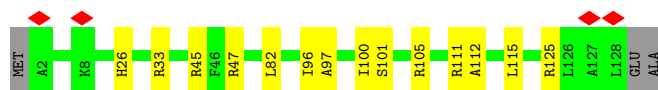
- Molecule 66: 60S ribosomal protein L31-A

Chain Ad:  10% 80% 17%

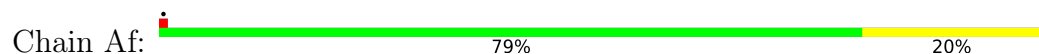


- Molecule 67: RPL32 isoform 1

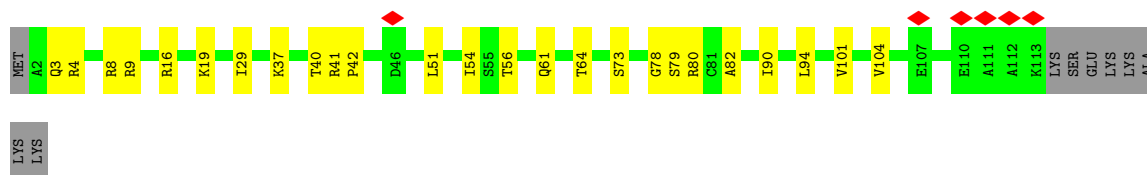
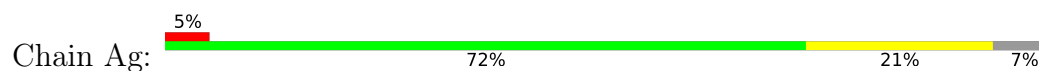
Chain Ae:  87% 11%



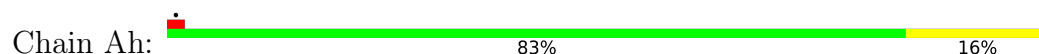
- Molecule 68: 60S ribosomal protein L33-A



- Molecule 69: 60S ribosomal protein L34-A



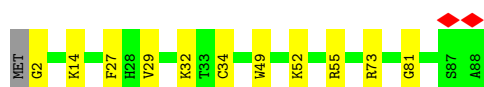
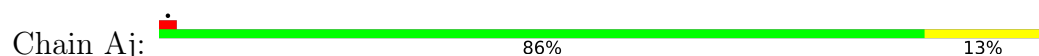
- Molecule 70: 60S ribosomal protein L35-A



- Molecule 71: 60S ribosomal protein L36-A

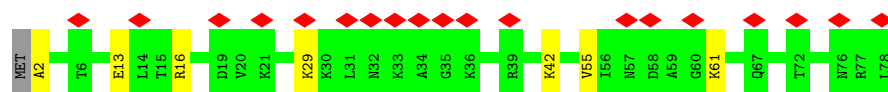


- Molecule 72: 60S ribosomal protein L37-A

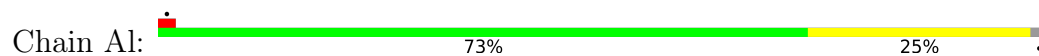


- Molecule 73: RPL38 isoform 1

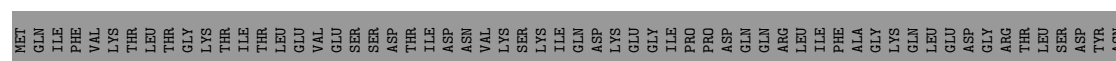
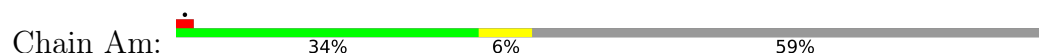




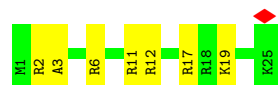
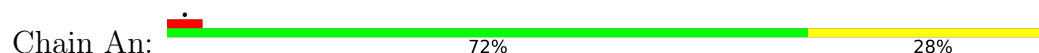
- Molecule 74: 60S ribosomal protein L39



- Molecule 75: Ubiquitin-60S ribosomal protein L40



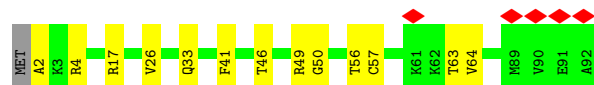
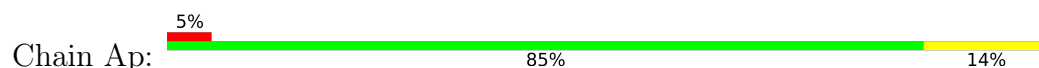
- Molecule 76: 60S ribosomal protein L41-A



- Molecule 77: 60S ribosomal protein L42-A

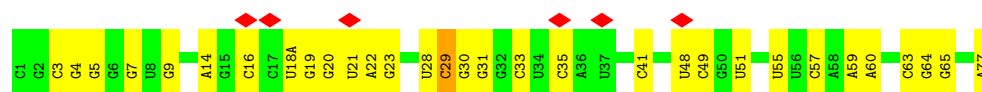


- Molecule 78: 60S ribosomal protein L43-A

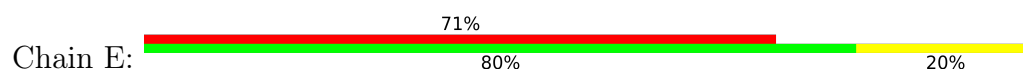


- Molecule 79: E site tRNA

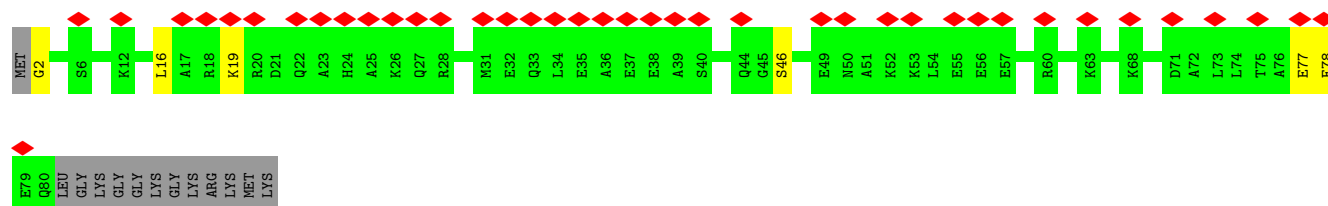
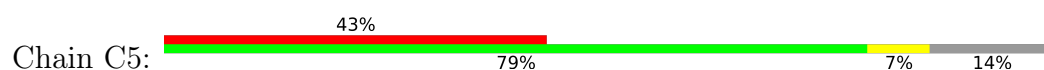




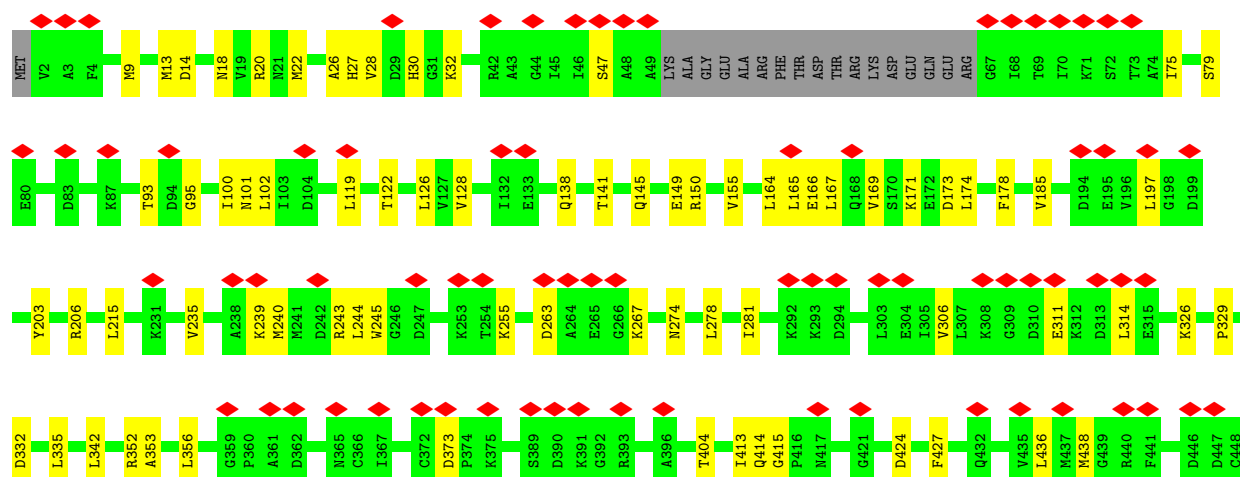
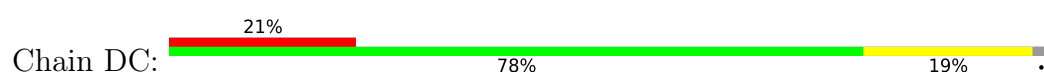
• Molecule 80: RPL1A isoform 1

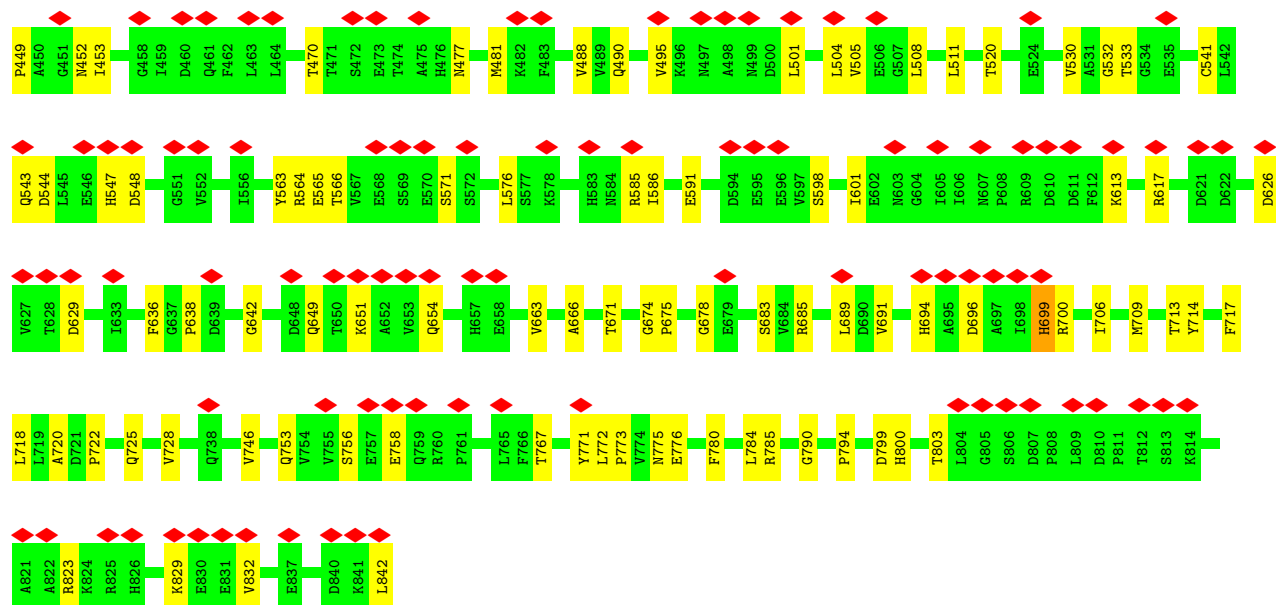


• Molecule 81: LSO2 isoform 1



• Molecule 82: Elongation factor 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	226374	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.872	Depositor
Minimum map value	-1.728	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.124	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 4AC, ZN, HIC, 5MC, OMG, SO1, MA6, OMU, B8N, MG, 1MA, UR3, GDP, DDE, PSU, G7M

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	0.20	0/1653	0.50	0/2261
2	BB	0.22	0/1735	0.62	1/2335 (0.0%)
3	BC	0.15	0/1665	0.39	0/2263
4	BE	0.19	0/2109	0.54	0/2839
5	BG	0.17	0/1844	0.45	0/2464
6	BH	0.22	0/1506	0.61	2/2028 (0.1%)
7	BI	0.22	0/1514	0.57	0/2021
8	BJ	0.19	0/1519	0.51	0/2035
9	BL	0.24	0/1272	0.56	0/1712
10	BN	0.19	0/1215	0.46	0/1638
11	BO	0.21	0/952	0.58	0/1279
12	BV	0.19	0/693	0.52	0/935
13	BW	0.17	0/1038	0.43	0/1395
14	BX	0.19	0/1139	0.50	0/1518
15	BY	0.18	0/1087	0.45	0/1449
16	Ba	0.19	0/782	0.51	0/1047
17	Bb	0.16	0/620	0.47	0/838
18	Be	0.19	0/483	0.43	0/643
19	BD	0.19	0/1759	0.45	0/2368
20	BF	0.19	0/1629	0.48	0/2202
21	BK	0.20	0/837	0.58	0/1131
22	BP	0.19	0/1012	0.51	0/1356
23	BQ	0.18	0/1125	0.46	0/1510
24	BR	0.16	0/957	0.45	0/1283
25	BS	0.18	0/1211	0.49	0/1628
26	BT	0.19	0/1113	0.51	0/1494
27	BU	0.19	0/865	0.48	0/1169
28	BZ	0.20	0/582	0.48	0/782
29	Bc	0.17	0/499	0.40	0/670
30	Bd	0.19	0/452	0.47	0/600
31	Bg	0.18	0/2454	0.49	0/3340
32	Bf	0.19	0/616	0.46	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.19	0/943	0.61	2/1274 (0.2%)
34	B5	0.17	1/41450 (0.0%)	0.36	2/64582 (0.0%)
35	AA	0.20	0/1912	0.47	0/2569
36	AB	0.22	0/3139	0.51	0/4219
37	AC	0.21	0/2800	0.49	0/3790
38	A1	0.20	0/76116	0.37	4/118677 (0.0%)
39	A3	0.17	0/2861	0.34	0/4457
40	A4	0.19	0/3724	0.35	0/5798
41	AD	0.17	0/2390	0.42	0/3225
42	AE	0.20	0/1324	0.49	2/1782 (0.1%)
43	AF	0.22	0/1821	0.49	0/2451
44	AG	0.19	0/1830	0.49	0/2469
45	AH	0.21	0/1531	0.49	0/2062
46	AI	0.16	0/1843	0.33	0/2471
47	AJ	0.20	0/1374	0.53	0/1842
48	AL	0.19	0/1568	0.41	0/2106
49	AM	0.20	0/1068	0.45	0/1438
50	AN	0.20	0/1757	0.40	0/2354
51	AO	0.20	0/1585	0.43	0/2128
52	AP	0.20	0/1410	0.42	0/1893
53	AQ	0.19	0/1465	0.47	0/1965
54	AR	0.17	0/1538	0.41	0/2050
55	AS	0.21	0/1481	0.46	0/1990
56	AT	0.19	0/1300	0.44	0/1743
57	AU	0.18	0/812	0.47	0/1099
58	AV	0.18	0/1018	0.45	0/1369
59	AW	0.18	0/533	0.41	0/707
60	AX	0.18	0/983	0.45	0/1325
61	AY	0.16	0/1004	0.39	0/1341
62	AZ	0.17	0/1118	0.43	0/1497
63	Aa	0.21	0/1204	0.47	0/1612
64	Ab	0.16	0/473	0.39	0/629
65	Ac	0.20	0/751	0.46	0/1008
66	Ad	0.19	0/904	0.42	0/1213
67	Ae	0.19	0/1041	0.43	0/1394
68	Af	0.20	0/868	0.39	0/1168
69	Ag	0.21	0/890	0.45	0/1189
70	Ah	0.17	0/978	0.43	0/1301
71	Ai	0.19	0/778	0.47	0/1034
72	Aj	0.20	0/696	0.43	0/923
73	Ak	0.16	0/618	0.45	0/826
74	Al	0.20	0/443	0.47	0/588
75	Am	0.21	0/423	0.46	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.13	0/234	0.42	0/300
77	Ao	0.19	0/860	0.50	0/1136
78	Ap	0.22	0/701	0.56	0/934
79	tE	0.16	0/1835	0.32	0/2859
80	E	0.19	0/1745	0.46	0/2342
81	C5	0.14	0/636	0.38	0/837
82	DC	0.18	0/6521	0.47	0/8830
All	All	0.19	1/224234 (0.0%)	0.41	13/328408 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	BH	0	1
11	BO	0	1
16	Ba	0	1
35	AA	0	1
37	AC	0	1
41	AD	0	1
43	AF	0	1
71	Ai	0	1
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	O3'-P	5.72	1.61	1.56

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BM	126	TRP	CA-C-N	8.90	137.72	121.70
33	BM	126	TRP	C-N-CA	8.90	137.72	121.70
42	AE	60	ASP	CA-C-N	5.65	136.12	125.66
42	AE	60	ASP	C-N-CA	5.65	136.12	125.66
38	A1	2207	A	P-O3'-C3'	5.56	128.54	120.20
38	A1	2499	U	P-O3'-C3'	5.38	128.26	120.20
34	B5	1683	C	P-O3'-C3'	5.37	128.25	120.20
34	B5	752	A	P-O3'-C3'	5.34	128.21	120.20
38	A1	2256	A	P-O3'-C3'	5.18	127.97	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	BB	178	GLY	N-CA-C	-5.15	106.83	115.80
6	BH	86	GLN	CA-C-N	5.13	135.15	125.66
6	BH	86	GLN	C-N-CA	5.13	135.15	125.66
38	A1	2772	C	P-O3'-C3'	5.12	127.88	120.20

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
35	AA	245	LEU	Peptide
37	AC	318	LEU	Peptide
41	AD	43	LYS	Peptide
43	AF	232	ARG	Peptide
71	Ai	27	SER	Peptide
6	BH	64	VAL	Peptide
11	BO	123	SER	Peptide
16	Ba	7	SER	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	35	0
2	BB	1709	0	1784	37	0
3	BC	1635	0	1723	28	0
4	BE	2068	0	2154	53	0
5	BG	1820	0	1918	37	0
6	BH	1481	0	1572	18	0
7	BI	1489	0	1525	46	0
8	BJ	1494	0	1573	40	0
9	BL	1244	0	1314	28	0
10	BN	1192	0	1255	16	0
11	BO	941	0	979	21	0
12	BV	684	0	672	18	0
13	BW	1021	0	1060	17	0
14	BX	1121	0	1196	21	0
15	BY	1073	0	1132	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	Ba	769	0	818	23	0
17	Bb	610	0	633	11	0
18	Be	475	0	525	9	0
19	BD	1734	0	1817	29	0
20	BF	1609	0	1675	30	0
21	BK	817	0	804	11	0
22	BP	991	0	1035	25	0
23	BQ	1105	0	1166	20	0
24	BR	948	0	990	15	0
25	BS	1192	0	1222	26	0
26	BT	1095	0	1114	22	0
27	BU	855	0	917	18	0
28	BZ	574	0	616	8	0
29	Bc	497	0	535	12	0
30	Bd	442	0	432	8	0
31	Bg	2401	0	2356	35	0
32	Bf	605	0	654	9	0
33	BM	935	0	975	13	0
34	B5	37463	0	18843	448	0
35	AA	1878	0	1946	44	0
36	AB	3081	0	3162	54	0
37	AC	2748	0	2859	41	0
38	A1	68746	0	34554	612	0
39	A3	2579	0	1304	18	0
40	A4	3353	0	1695	35	0
41	AD	2341	0	2290	30	0
42	AE	1303	0	1376	27	0
43	AF	1784	0	1862	26	0
44	AG	1798	0	1894	26	0
45	AH	1510	0	1576	28	0
46	AI	1804	0	1856	22	0
47	AJ	1353	0	1383	25	0
48	AL	1543	0	1608	23	0
49	AM	1053	0	1149	16	0
50	AN	1720	0	1779	41	0
51	AO	1555	0	1659	26	0
52	AP	1388	0	1423	18	0
53	AQ	1441	0	1543	18	0
54	AR	1521	0	1617	18	0
55	AS	1445	0	1487	28	0
56	AT	1276	0	1323	19	0
57	AU	796	0	812	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	AV	1003	0	1047	25	0
59	AW	521	0	551	3	0
60	AX	968	0	1036	10	0
61	AY	993	0	1081	15	0
62	AZ	1092	0	1155	15	0
63	Aa	1173	0	1215	19	0
64	Ab	462	0	489	5	0
65	Ac	743	0	797	16	0
66	Ad	890	0	938	13	0
67	Ae	1020	0	1090	13	0
68	Af	850	0	880	16	0
69	Ag	880	0	945	17	0
70	Ah	969	0	1078	16	0
71	Ai	771	0	849	7	0
72	Aj	681	0	687	10	0
73	Ak	612	0	682	6	0
74	Al	436	0	475	13	0
75	Am	417	0	459	7	0
76	An	233	0	283	8	0
77	Ao	847	0	914	7	0
78	Ap	694	0	738	11	0
79	tE	1643	0	836	16	0
80	E	1718	0	1811	29	0
81	C5	633	0	637	5	0
82	DC	6419	0	6493	109	0
83	Ao	1	0	0	0	0
84	DC	28	0	12	2	0
85	DC	1	0	0	0	0
86	DC	35	0	40	0	0
All	All	210450	0	157982	2223	0

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

All (2223) 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)
79:tE:51:U:H3	79:tE:65:G:H1	1.12	0.96
34:B5:877:G:H1	34:B5:951:A:H2	0.95	0.94
38:A1:1677:G:H1	38:A1:1691:U:H3	1.05	0.94
34:B5:1679:G:H21	34:B5:1722:A:H62	0.93	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3160:U:H3	38:A1:3290:G:H1	1.13	0.93
34:B5:1588:G:H1	34:B5:1608:U:H3	1.11	0.92
34:B5:1679:G:N2	34:B5:1722:A:H62	1.65	0.91
38:A1:1266:G:H1	38:A1:1276:U:H3	1.14	0.91
38:A1:3234:A:H2	38:A1:3253:G:H1	1.16	0.90
34:B5:1679:G:H21	34:B5:1722:A:N6	1.69	0.90
34:B5:1665:U:H3	34:B5:1736:G:H1	1.17	0.86
34:B5:1355:C:N4	34:B5:1369:U:H3	1.73	0.85
34:B5:877:G:N1	34:B5:951:A:H2	1.75	0.84
34:B5:32:U:H3	34:B5:468:A:H62	1.26	0.83
34:B5:1267:G:H1	34:B5:1442:U:H3	1.23	0.83
38:A1:182:U:H3	38:A1:234:G:H1	1.23	0.83
34:B5:1335:U:H3	34:B5:1416:G:H1	1.27	0.80
38:A1:129:U:H3	38:A1:139:G:H1	1.29	0.80
38:A1:2138:A:HO2'	72:Aj:2:GLY:N	1.79	0.80
34:B5:1175:U:H3	34:B5:1464:G:H1	1.29	0.78
38:A1:508:U:H3	38:A1:583:G:H1	1.30	0.76
34:B5:877:G:N1	34:B5:951:A:C2	2.45	0.75
34:B5:394:C:H42	34:B5:401:A:H62	1.32	0.75
38:A1:2448:G:H1	38:A1:2498:U:H3	1.35	0.71
34:B5:1499:G:H1	34:B5:1508:U:H3	1.36	0.71
51:AO:22[A]:VAL:HG11	51:AO:122[A]:GLN:HE22	1.56	0.70
38:A1:528:U:H3	38:A1:564:G:H1	1.39	0.70
34:B5:1355:C:N4	34:B5:1369:U:N3	2.40	0.70
38:A1:538:G:H1	38:A1:553:U:H3	1.38	0.69
38:A1:2458:A:H5'	38:A1:2481:G:H21	1.57	0.69
31:Bg:178:VAL:HB	31:Bg:192:PHE:HB2	1.73	0.69
38:A1:512:U:H3	38:A1:579:G:H1	1.39	0.69
31:Bg:89:LEU:HB2	31:Bg:103:PHE:HB2	1.73	0.69
7:BI:31:ARG:HH22	7:BI:46:VAL:HG11	1.58	0.69
20:BF:187:ILE:HG12	28:BZ:66:VAL:HG21	1.76	0.68
27:BU:60:THR:HG23	34:B5:1382:A:H5''	1.76	0.68
60:AX:115:ARG:HE	60:AX:117:ASN:HD21	1.42	0.68
34:B5:1677:C:H42	34:B5:1724:U:H3	1.40	0.68
58:AV:108:GLU:HG3	58:AV:128:ARG:HG3	1.76	0.68
2:BB:150:VAL:HG12	34:B5:1067:C:H5''	1.76	0.67
31:Bg:270:LEU:HD21	31:Bg:273:ASP:HB2	1.76	0.67
11:BO:20:TYR:HB3	11:BO:27:PHE:HB2	1.75	0.67
14:BX:92:CYS:SG	14:BX:136:TRP:NE1	2.68	0.67
34:B5:868:G:H1	34:B5:960:U:H3	1.42	0.66
7:BI:98:LYS:HZ1	7:BI:172:ARG:HH21	1.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1673:G:H1	34:B5:1728:A:H2	1.40	0.66
35:AA:28:LYS:HD3	35:AA:123:ARG:HE	1.62	0.65
13:BW:22:LYS:HA	17:Bb:3:LEU:HB2	1.77	0.65
38:A1:3165:A:H61	38:A1:3285:C:H42	1.45	0.65
38:A1:98:G:N7	48:AL:13:HIS:NE2	2.44	0.65
77:Ao:24:LYS:HB3	77:Ao:73:GLU:HB3	1.79	0.65
1:BA:195:TRP:HD1	1:BA:197:ILE:H	1.44	0.65
38:A1:1280:C:H2'	38:A1:1281:G:H8	1.62	0.65
64:Ab:8:THR:HG22	64:Ab:10:HIS:H	1.62	0.65
23:BQ:71:GLY:HA2	34:B5:1483:A:H4'	1.78	0.64
47:AJ:49:LYS:HB3	47:AJ:62:ASN:HA	1.77	0.64
7:BI:37:LYS:HB2	7:BI:59:ARG:HG2	1.79	0.64
5:BG:139:ASN:H	5:BG:177:ARG:HD3	1.63	0.64
34:B5:1542:G:H22	34:B5:1568:C:H1'	1.62	0.64
82:DC:20:ARG:HB2	82:DC:100:ILE:HG22	1.78	0.64
3:BC:170:ILE:HB	3:BC:197:TYR:HB2	1.80	0.64
4:BE:182:TYR:HB3	4:BE:226:PHE:HB3	1.79	0.64
20:BF:63:GLN:HE22	20:BF:66:GLN:HB3	1.63	0.64
35:AA:5:ILE:HG12	35:AA:8:GLN:HE21	1.63	0.63
58:AV:81:GLN:O	58:AV:98:ASN:ND2	2.31	0.63
38:A1:1390:A:N6	38:A1:1418:A:O2'	2.31	0.63
44:AG:163:VAL:HA	44:AG:166:LEU:HD23	1.80	0.63
1:BA:59:LEU:HB2	12:BV:79:LEU:HD11	1.80	0.63
38:A1:1389:G:H5''	67:Ae:101:SER:HB3	1.81	0.63
38:A1:2468:A:N3	38:A1:2469:G:N2	2.47	0.63
82:DC:694:HIS:H	82:DC:700:ARG:HD3	1.63	0.63
7:BI:43:ILE:HD11	7:BI:55:TYR:HB3	1.81	0.62
37:AC:291:ASN:HA	37:AC:296:GLN:HE21	1.64	0.62
38:A1:2999:U:H3	38:A1:3149:G:H1	1.47	0.62
25:BS:101:LEU:HB2	25:BS:104:ASN:HD22	1.63	0.62
34:B5:1213:G:O2'	34:B5:1244:A:N7	2.33	0.62
38:A1:2853:A:H5'	46:AI:3:ARG:HH12	1.64	0.62
34:B5:486:G:N2	34:B5:501:U:O2	2.31	0.62
38:A1:1634:G:N7	62:AZ:17:ARG:NH2	2.47	0.62
38:A1:2193:U:H5''	38:A1:2194:G:H5'	1.82	0.62
7:BI:98:LYS:HB2	34:B5:329:G:H5''	1.80	0.62
7:BI:190:ALA:HB1	7:BI:194:ARG:HH21	1.64	0.62
38:A1:1517:G:H5''	74:AI:22:PRO:HG3	1.81	0.62
38:A1:3234:A:H2	38:A1:3253:G:N1	1.95	0.62
7:BI:167:ALA:HA	7:BI:183:ILE:HA	1.82	0.61
14:BX:125:VAL:HG12	14:BX:126:LYS:HG3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BF:104:ASN:ND2	34:B5:1587:A:N3	2.48	0.61
38:A1:114:A:H5''	50:AN:49:ARG:HH21	1.64	0.61
16:Ba:34:LYS:NZ	34:B5:1791:A:N7	2.48	0.61
38:A1:845:G:N2	38:A1:848:A:OP2	2.33	0.61
25:BS:118:LYS:O	25:BS:120:ARG:NH1	2.34	0.61
38:A1:439:C:N4	38:A1:619:A:N1	2.49	0.61
70:Ah:118:ILE:HG22	70:Ah:120:ALA:H	1.66	0.61
2:BB:111:ARG:NH2	34:B5:930:A:N3	2.48	0.61
2:BB:69:CYS:SG	2:BB:70:LEU:N	2.74	0.61
35:AA:101:VAL:HG22	35:AA:165:VAL:HG22	1.83	0.61
8:BJ:143:ILE:HG22	8:BJ:145:SER:H	1.65	0.61
8:BJ:163:PRO:HB2	34:B5:512:A:H5''	1.83	0.61
9:BL:3:THR:HA	9:BL:52:SER:HB3	1.83	0.60
20:BF:216:GLU:HA	20:BF:219:ARG:HG2	1.82	0.60
34:B5:1684:U:H3	34:B5:1717:G:H1	1.48	0.60
82:DC:725:GLN:HG2	82:DC:803:THR:HB	1.83	0.60
4:BE:252:ARG:HB3	4:BE:256:ARG:HH21	1.65	0.60
20:BF:124:LEU:HD11	20:BF:199:ILE:HG21	1.81	0.60
23:BQ:29:ILE:HG23	23:BQ:65:ILE:HD11	1.82	0.60
38:A1:3348:G:H1	38:A1:3357:U:H3	1.48	0.60
19:BD:48:VAL:HB	19:BD:86:LEU:HG	1.82	0.60
36:AB:10:ARG:NH1	36:AB:11:HIS:O	2.35	0.60
54:AR:3:ASN:HD21	54:AR:5:ARG:HH21	1.48	0.60
38:A1:2468:A:H62	80:E:105:LYS:HB3	1.66	0.60
55:AS:8:GLN:HE21	55:AS:62:ASN:HD22	1.48	0.60
19:BD:177:MET:HE1	19:BD:182:LEU:HB2	1.83	0.60
20:BF:92:ARG:NH2	34:B5:1613:U:OP1	2.35	0.60
21:BK:25:LYS:HB3	21:BK:62:GLN:HB2	1.84	0.60
34:B5:1772:C:H2'	34:B5:1773:4AC:H6	1.84	0.60
35:AA:215:ASN:ND2	38:A1:2969:A:N7	2.49	0.60
38:A1:2253:G:H21	38:A1:2265:C:H42	1.50	0.60
40:A4:97:A:O2'	70:Ah:59:ASN:ND2	2.35	0.60
19:BD:178:ARG:HH21	34:B5:579:A:H8	1.49	0.60
23:BQ:65:ILE:HD13	23:BQ:85:ILE:HD13	1.84	0.60
38:A1:1128:U:OP1	46:AI:4:ARG:NH1	2.34	0.59
38:A1:2727:A:OP2	38:A1:2728:G:N2	2.35	0.59
42:AE:166:LYS:O	68:Af:6:ARG:NH2	2.35	0.59
46:AI:36:LEU:HD21	46:AI:69:ARG:HH11	1.67	0.59
48:AL:123:ILE:HG22	70:Ah:118:ILE:HG13	1.83	0.59
82:DC:79:SER:HB3	82:DC:335:LEU:HD23	1.83	0.59
5:BG:13:GLN:NE2	34:B5:151:G:N3	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:84:ARG:HG3	11:BO:119:THR:HA	1.84	0.59
31:Bg:180:ALA:HB3	31:Bg:190:ALA:HB3	1.85	0.59
38:A1:160:G:H1	38:A1:261:U:H3	1.48	0.59
38:A1:1334:U:H5''	43:AF:206:LYS:HB3	1.83	0.59
49:AM:25:LYS:HE3	49:AM:62:GLN:HG3	1.85	0.59
38:A1:67:A:N6	38:A1:271:C:O2'	2.34	0.59
38:A1:2220:A:O2'	80:E:199:GLN:NE2	2.36	0.59
23:BQ:50:GLU:HG3	23:BQ:82:ARG:HH21	1.67	0.59
38:A1:1915:A:H5''	54:AR:84:THR:HG22	1.84	0.59
38:A1:2459:A:H62	38:A1:2486:A:H61	1.51	0.59
82:DC:26:ALA:HB3	82:DC:32:LYS:HD3	1.85	0.59
82:DC:488:VAL:HG21	82:DC:794:PRO:HG2	1.85	0.59
3:BC:140:ARG:HE	12:BV:1:MET:HE1	1.66	0.59
23:BQ:99:GLU:O	23:BQ:103:ASN:ND2	2.34	0.59
38:A1:215:G:OP1	61:AY:12:ARG:NH1	2.35	0.59
36:AB:215:ILE:HD12	36:AB:338:LEU:HD12	1.85	0.59
43:AF:88:ARG:NH1	53:AQ:4:ASP:OD2	2.33	0.59
3:BC:45:VAL:HG21	3:BC:68:ILE:HG23	1.84	0.59
34:B5:1690:G:N7	34:B5:1707:A:N6	2.51	0.59
36:AB:85:VAL:HG22	36:AB:202:THR:HG22	1.85	0.59
34:B5:1673:G:O6	34:B5:1728:A:N1	2.36	0.58
38:A1:3214:U:H1'	42:AE:166:LYS:HZ1	1.67	0.58
34:B5:1055:U:H3	34:B5:1064:G:H1	1.50	0.58
34:B5:1471:A:H62	34:B5:1538:U:H3	1.50	0.58
38:A1:269:G:H5''	50:AN:14:LYS:HE3	1.85	0.58
38:A1:2908:G:O2'	75:Am:114:LYS:NZ	2.37	0.58
42:AE:154:LEU:HD11	49:AM:122:VAL:HG21	1.84	0.58
80:E:148:VAL:HB	80:E:152:ARG:HH21	1.68	0.58
1:BA:140:ASN:ND2	12:BV:31:SER:O	2.36	0.58
34:B5:1174:C:O2'	34:B5:1196:A:N6	2.36	0.58
38:A1:2842:U:OP1	38:A1:2844:C:N4	2.35	0.58
47:AJ:88:GLU:OE1	47:AJ:90:GLN:NE2	2.36	0.58
2:BB:135:LEU:HB3	2:BB:217:LEU:HD13	1.84	0.58
19:BD:204:ASP:OD2	34:B5:1330:G:N2	2.37	0.58
20:BF:145:ASP:HB3	29:Bc:45:LYS:HE3	1.85	0.58
32:Bf:118:ARG:NH1	34:B5:1252:C:O5'	2.37	0.58
38:A1:3119:U:H4'	75:Am:104:PRO:HG3	1.85	0.58
82:DC:235:VAL:HG21	82:DC:243:ARG:HH22	1.67	0.58
82:DC:571:SER:HB3	82:DC:720:ALA:HB2	1.85	0.58
3:BC:101:VAL:HG12	3:BC:115:ILE:HG12	1.85	0.58
5:BG:20:ASP:HB2	5:BG:23:ARG:HE	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:68:C:OP2	38:A1:301:G:N2	2.35	0.58
38:A1:1481:A:N3	38:A1:1858:A:O2'	2.36	0.58
38:A1:2353:G:H5''	52:AP:86:LYS:HB2	1.85	0.58
55:AS:8:GLN:HB3	55:AS:64:ILE:HD11	1.86	0.58
5:BG:114:VAL:HG13	5:BG:115:LYS:HG2	1.85	0.58
28:BZ:77:ARG:NH2	34:B5:1533:C:OP2	2.36	0.58
38:A1:89:A:N7	53:AQ:171:LYS:NZ	2.51	0.58
38:A1:351:A:N6	74:AI:37:TYR:O	2.35	0.58
38:A1:1656:A:OP2	69:Ag:37:LYS:NZ	2.37	0.58
38:A1:149:U:H5''	50:AN:54:LYS:HB3	1.85	0.58
38:A1:584:G:OP1	42:AE:82:ARG:NH2	2.37	0.58
38:A1:2427:U:H3	38:A1:2602:G:H1	1.51	0.58
7:BI:90:LEU:HG	7:BI:95:THR:HB	1.84	0.58
17:Bb:15:GLU:O	17:Bb:29:ARG:NH2	2.37	0.58
44:AG:162:LEU:HD21	50:AN:45:PRO:HG2	1.86	0.58
65:Ac:39:SER:HG	65:Ac:91:SER:HG	1.50	0.58
7:BI:39:GLY:H	7:BI:61:GLU:HB3	1.67	0.58
11:BO:99:GLN:HE21	16:Ba:46:GLU:HG2	1.68	0.58
15:BY:55:VAL:HG22	15:BY:75:VAL:HG22	1.85	0.58
38:A1:2894:C:H5'	45:AH:168:ARG:HH11	1.69	0.58
82:DC:14:ASP:HA	82:DC:449:PRO:HG3	1.86	0.58
7:BI:26:LYS:HB2	7:BI:29:LEU:HD23	1.86	0.57
8:BJ:83:VAL:HA	8:BJ:149:ARG:HA	1.85	0.57
23:BQ:8:GLN:HE22	34:B5:1378:U:H1'	1.68	0.57
40:A4:25:G:N7	61:AY:13:ARG:NH1	2.48	0.57
34:B5:104:A:H5''	34:B5:308:C:H41	1.69	0.57
38:A1:664:U:H3	38:A1:798:G:H1	1.52	0.57
8:BJ:126:ARG:HD3	18:Be:33:ARG:HD3	1.86	0.57
37:AC:160:GLN:NE2	37:AC:213:ASN:O	2.38	0.57
38:A1:158:G:H2'	38:A1:159:A:H8	1.68	0.57
45:AH:31:ARG:NH1	45:AH:149:ASN:OD1	2.38	0.57
62:AZ:50:PRO:HD3	62:AZ:68:ILE:HG12	1.85	0.57
7:BI:59:ARG:NH1	34:B5:1678:A:OP2	2.37	0.57
23:BQ:22:VAL:HG22	23:BQ:65:ILE:HG22	1.85	0.57
25:BS:87:ASN:OD1	34:B5:1546:G:N2	2.37	0.57
7:BI:5:ARG:NH1	34:B5:336:G:O6	2.37	0.57
19:BD:74:GLN:HA	19:BD:79:TYR:HB2	1.87	0.57
38:A1:2673:A:OP1	47:AJ:95:ASN:ND2	2.38	0.57
55:AS:12:ARG:HD2	55:AS:22:PRO:HD2	1.84	0.57
80:E:63:MET:SD	80:E:108:ASN:ND2	2.77	0.57
21:BK:81:ASN:ND2	33:BM:37:VAL:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:5:GLU:N	31:Bg:316:MET:SD	2.77	0.57
34:B5:871:G:H2'	34:B5:872:G:C8	2.40	0.57
35:AA:30:ARG:O	35:AA:163:ARG:NH2	2.37	0.57
50:AN:183:THR:HG22	50:AN:187:ARG:HB3	1.86	0.57
3:BC:165:VAL:HG11	3:BC:210:THR:HA	1.87	0.57
22:BP:98:ASN:HB2	22:BP:122:THR:HA	1.87	0.57
38:A1:1201:C:H42	38:A1:2857:C:H5''	1.68	0.57
38:A1:2854:U:OP2	46:AI:3:ARG:NH2	2.37	0.57
45:AH:92:TYR:HB2	45:AH:142:ASP:HB2	1.85	0.57
50:AN:17:ASP:OD2	71:AI:55:ARG:NH2	2.38	0.57
38:A1:718:G:OP1	63:Aa:117:ARG:NH2	2.38	0.57
38:A1:1408:G:OP1	67:Ae:33:ARG:NH2	2.37	0.57
40:A4:5:U:OP2	52:AP:62:ARG:NH1	2.37	0.57
7:BI:52:ASN:O	7:BI:54:LYS:NZ	2.38	0.57
34:B5:1663:G:H1	34:B5:1738:U:H3	1.51	0.57
79:tE:57:C:H5'	80:E:130:LYS:HD2	1.87	0.57
82:DC:773:PRO:HG2	82:DC:776:GLU:HB2	1.87	0.57
29:Bc:22:ARG:NH2	34:B5:1161:C:O2'	2.38	0.56
38:A1:1268:G:H4'	38:A1:1274:A:H62	1.70	0.56
38:A1:3213:A:N7	49:AM:124:ARG:NH2	2.52	0.56
34:B5:147:A:H3'	34:B5:148:A:H8	1.70	0.56
62:AZ:81:LEU:HD11	69:Ag:90:ILE:HG22	1.86	0.56
82:DC:753:GLN:HB3	82:DC:771:TYR:HB2	1.87	0.56
10:BN:16:ILE:O	13:BW:57:ARG:NH2	2.39	0.56
20:BF:76:ARG:NH1	34:B5:1583:A:O2'	2.38	0.56
24:BR:11:ARG:NH1	34:B5:1325:A:OP2	2.39	0.56
34:B5:517:U:H2'	34:B5:518:A:H8	1.69	0.56
34:B5:520:A:H2'	34:B5:521:A:H8	1.70	0.56
37:AC:45:ASN:HA	37:AC:110:ASN:HD22	1.70	0.56
38:A1:1628:C:O4'	38:A1:1814:A:N6	2.38	0.56
38:A1:1646:G:O2'	38:A1:1808:G:N2	2.35	0.56
38:A1:2635:A:OP2	46:AI:15:LYS:NZ	2.37	0.56
38:A1:3187:A:H5'	45:AH:22:SER:HA	1.87	0.56
41:AD:84:PRO:HD3	41:AD:92:LEU:HD11	1.87	0.56
74:Al:21:ARG:HH12	74:Al:24:PRO:HG3	1.68	0.56
82:DC:415:GLY:O	82:DC:477:ASN:ND2	2.38	0.56
29:Bc:18:ARG:HD2	29:Bc:23:GLY:HA2	1.85	0.56
38:A1:799:G:O2'	48:AL:18:TRP:NE1	2.38	0.56
38:A1:1491:A:H5''	72:Aj:14:LYS:HE3	1.88	0.56
82:DC:598:SER:HA	82:DC:601:ILE:HD12	1.87	0.56
38:A1:2700:G:H5''	56:AT:17:ARG:HG2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:52:A:H5'	74:A1:21:ARG:HD3	1.86	0.56
41:AD:128:GLU:O	41:AD:164:LYS:NZ	2.38	0.56
34:B5:394:C:N4	34:B5:401:A:H62	2.01	0.56
34:B5:877:G:O6	34:B5:951:A:N1	2.38	0.56
34:B5:1236:A:OP1	34:B5:1243:G:N1	2.39	0.56
82:DC:488:VAL:O	82:DC:490:GLN:NE2	2.38	0.56
1:BA:77:SER:HB2	1:BA:86:VAL:HG21	1.88	0.56
7:BI:84:HIS:HD2	7:BI:100:ALA:HB2	1.71	0.56
25:BS:41:ARG:HH11	26:BT:46:PRO:HG3	1.71	0.56
38:A1:370:U:H4'	38:A1:404:G:H5'	1.88	0.56
46:AI:93:PRO:HB2	46:AI:125:LEU:HB3	1.88	0.56
4:BE:100:ARG:NH2	4:BE:118:GLU:O	2.38	0.56
4:BE:187:ARG:NH2	34:B5:752:A:OP2	2.39	0.56
8:BJ:51:LYS:HD2	8:BJ:54:ARG:HH21	1.69	0.56
11:BO:81:VAL:HB	11:BO:115:ILE:HG12	1.88	0.56
22:BP:40:ARG:NH1	34:B5:1551:U:O4	2.39	0.56
38:A1:47:C:H5''	48:AL:16:LYS:HG2	1.88	0.56
38:A1:292:U:OP2	50:AN:68:ARG:NH2	2.38	0.56
38:A1:535:G:OP1	55:AS:146:LYS:NZ	2.36	0.56
38:A1:1447:G:N7	52:AP:25:SER:OG	2.38	0.56
31:Bg:32:LEU:HD21	31:Bg:94:VAL:HG11	1.86	0.56
31:Bg:206:PRO:HG3	31:Bg:247:PRO:HA	1.88	0.56
34:B5:1775:U:OP1	76:An:11:ARG:NH2	2.39	0.56
39:A3:44:C:OP2	47:AJ:137:ARG:NH2	2.39	0.56
58:AV:14:SER:O	58:AV:81:GLN:NE2	2.35	0.56
70:Ah:31:LEU:HB3	70:Ah:44:ILE:HG22	1.87	0.56
4:BE:42:LEU:HD21	4:BE:51:ARG:HG3	1.88	0.55
5:BG:85:ARG:NH2	34:B5:160:C:OP2	2.38	0.55
29:Bc:29:ARG:HG2	29:Bc:41:VAL:HG22	1.88	0.55
34:B5:1182:U:H3	34:B5:1185:U:H5''	1.70	0.55
34:B5:1280:4AC:H2'	34:B5:1281:G:H8	1.71	0.55
36:AB:277:SER:OG	36:AB:280:HIS:NE2	2.37	0.55
38:A1:1247:U:H3	38:A1:1275:C:H42	1.54	0.55
45:AH:18:VAL:HG22	45:AH:27:VAL:HG12	1.87	0.55
82:DC:591:GLU:OE2	82:DC:685:ARG:NH1	2.39	0.55
3:BC:145:GLY:O	13:BW:98:GLN:NE2	2.38	0.55
8:BJ:168:ARG:NH1	34:B5:513:U:OP1	2.40	0.55
22:BP:87:PRO:HG3	22:BP:112:LEU:HD11	1.89	0.55
50:AN:30:TYR:O	50:AN:65:ARG:NH1	2.38	0.55
82:DC:122:THR:O	82:DC:352:ARG:NH1	2.38	0.55
34:B5:163:G:H2'	34:B5:164:A:H8	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:381:C:O2'	34:B5:755:A:N1	2.39	0.55
34:B5:1353:U:H5'	34:B5:1354:G:H5''	1.88	0.55
36:AB:232:ARG:NH1	36:AB:266:ARG:O	2.39	0.55
37:AC:308:LYS:NZ	38:A1:609:G:N7	2.52	0.55
38:A1:655:C:H2'	38:A1:656:A:H8	1.71	0.55
38:A1:713:U:OP1	48:AL:174:ARG:NH1	2.40	0.55
38:A1:1233:G:O2'	38:A1:1236:G:N1	2.39	0.55
40:A4:133:G:OP1	60:AX:94:GLN:NE2	2.40	0.55
82:DC:481:MET:SD	82:DC:481:MET:N	2.79	0.55
3:BC:120:GLU:HG2	3:BC:123:GLY:H	1.70	0.55
20:BF:45:LYS:NZ	20:BF:119:ASP:OD1	2.39	0.55
34:B5:36:C:N3	34:B5:472:U:O4	2.39	0.55
36:AB:21:ARG:HE	36:AB:269:GLN:HE21	1.52	0.55
37:AC:206:LEU:HB3	37:AC:248:VAL:HG22	1.88	0.55
38:A1:1141:C:O2'	38:A1:1153:A:N3	2.39	0.55
38:A1:1310:G:HO2'	38:A1:2380:U:HO2'	1.55	0.55
38:A1:3034:C:H41	45:AH:121:LYS:HG2	1.72	0.55
62:AZ:47:GLU:HB2	62:AZ:69:LYS:HG3	1.87	0.55
15:BY:61:ARG:NH1	34:B5:530:C:O2	2.40	0.55
26:BT:60:SER:HG	26:BT:80:TYR:HH	1.54	0.55
34:B5:39:A:O2'	34:B5:469:C:N4	2.39	0.55
34:B5:58:U:O2'	34:B5:451:A:N3	2.40	0.55
38:A1:1064:A:H61	38:A1:1092:C:H2'	1.71	0.55
34:B5:233:C:O2'	34:B5:237:C:N4	2.40	0.55
34:B5:628:G:O3'	38:A1:846:A:N6	2.40	0.55
38:A1:2115:G:H22	38:A1:2120:A:H1'	1.71	0.55
40:A4:46:G:OP1	74:A1:18:LYS:NZ	2.39	0.55
4:BE:191:ARG:HD3	4:BE:245:LYS:HB2	1.88	0.55
8:BJ:3:ARG:NH1	34:B5:40:A:OP1	2.40	0.55
20:BF:74:ALA:O	23:BQ:122:ARG:NH2	2.40	0.55
25:BS:35:ILE:HG23	25:BS:102:ALA:HB2	1.89	0.55
36:AB:124:LYS:NZ	38:A1:3297:U:O4	2.38	0.55
38:A1:2732:G:H5'	38:A1:2761:G:H5''	1.88	0.55
42:AE:31:ARG:HB2	42:AE:34:LEU:HD13	1.88	0.55
75:Am:126:LYS:NZ	75:Am:127:LEU:O	2.40	0.55
25:BS:40:ARG:NH1	34:B5:1540:G:OP1	2.40	0.55
34:B5:1594:G:OP2	34:B5:1596:C:N4	2.40	0.55
35:AA:117:GLU:HG2	35:AA:124:GLY:H	1.70	0.55
35:AA:183:GLY:HA2	38:A1:896:A:H5''	1.87	0.55
38:A1:560:G:OP1	49:AM:84:LYS:NZ	2.40	0.55
38:A1:1483:G:O6	69:Ag:4:ARG:NH2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:AL:42:ARG:NH1	48:AL:51:LEU:O	2.40	0.55
58:AV:15:LEU:HD23	58:AV:53:SER:HB3	1.88	0.55
82:DC:694:HIS:CE1	82:DC:699:DDE:HD2	2.42	0.55
10:BN:47:PRO:HG2	10:BN:72:MET:HE3	1.88	0.55
25:BS:40:ARG:O	25:BS:44:ASN:ND2	2.40	0.55
34:B5:1773:4AC:OP2	76:An:2:ARG:NE	2.38	0.55
40:A4:135:G:OP2	60:AX:56:ARG:NH2	2.40	0.55
46:AI:47:PRO:HD2	46:AI:141:LYS:HA	1.87	0.55
9:BL:57:LYS:HB3	9:BL:131:ILE:HD12	1.89	0.55
34:B5:1769:U:OP1	81:C5:2:GLY:N	2.40	0.55
37:AC:73:ARG:NH1	38:A1:2814:G:OP1	2.40	0.55
38:A1:348:A:N3	38:A1:352:A:O2'	2.40	0.55
38:A1:1385:C:HO2'	42:AE:2:SER:N	2.04	0.55
38:A1:1576:G:N2	38:A1:1810:A:OP1	2.40	0.55
38:A1:2441:A:H3'	38:A1:2442:G:H8	1.73	0.55
38:A1:3255:U:H2'	38:A1:3256:G:H8	1.72	0.55
44:AG:74:THR:HG22	44:AG:164:VAL:HG22	1.88	0.55
46:AI:73:ASN:ND2	81:C5:77:GLU:OE2	2.39	0.55
50:AN:14:LYS:HA	50:AN:19:LEU:HD23	1.89	0.55
34:B5:250:C:H2'	34:B5:251:A:H8	1.72	0.54
36:AB:57:VAL:HB	36:AB:358:TRP:HB3	1.89	0.54
37:AC:51:ALA:HB3	40:A4:27:U:H4'	1.89	0.54
38:A1:1062:A:O2'	38:A1:1098:A:OP1	2.26	0.54
38:A1:2586:G:OP1	44:AG:240:ASN:ND2	2.40	0.54
27:BU:59:PRO:HG3	34:B5:1381:U:H4'	1.89	0.54
34:B5:1521:G:O2'	34:B5:1523:G:OP2	2.25	0.54
82:DC:311:GLU:HA	82:DC:314:LEU:HD13	1.88	0.54
7:BI:178:ARG:NH2	34:B5:207:U:O2	2.40	0.54
38:A1:899:U:H2'	38:A1:900:G:H8	1.72	0.54
42:AE:51:ARG:HE	42:AE:163:PHE:HB2	1.73	0.54
7:BI:27:PHE:HB3	34:B5:333:A:H62	1.73	0.54
8:BJ:80:LEU:HD13	8:BJ:86:LEU:HB3	1.89	0.54
35:AA:24:GLN:HG3	35:AA:49:VAL:HG21	1.90	0.54
38:A1:1106:G:H4'	64:Ab:25:LYS:HE3	1.90	0.54
38:A1:3178:A:H2'	51:AO:115[A]:LYS:HG2	1.89	0.54
38:A1:3275:U:O2'	68:Af:99:ARG:NH1	2.40	0.54
45:AH:9:GLN:HE22	45:AH:54:LYS:HE2	1.71	0.54
45:AH:59:ASN:HB2	49:AM:41:GLN:HE22	1.72	0.54
49:AM:88:ALA:O	49:AM:93:LYS:NZ	2.40	0.54
53:AQ:170:ARG:NH1	63:Aa:56:VAL:O	2.41	0.54
82:DC:543:GLN:O	82:DC:547:HIS:ND1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:144:ARG:HB3	2:BB:206:PRO:HB2	1.88	0.54
22:BP:126:VAL:HG13	34:B5:1181:PSU:H1'	1.89	0.54
34:B5:163:G:N2	34:B5:163:G:OP2	2.40	0.54
38:A1:2631:U:OP1	38:A1:2757:U:O2'	2.26	0.54
52:AP:118:GLN:NE2	52:AP:147:GLU:OE2	2.40	0.54
1:BA:195:TRP:H	24:BR:90:ALA:HA	1.72	0.54
3:BC:81:MET:HE1	3:BC:186:LYS:HB2	1.89	0.54
6:BH:82:GLU:HG3	6:BH:90:VAL:HG22	1.89	0.54
26:BT:57:ARG:NH1	26:BT:101:ASN:OD1	2.40	0.54
40:A4:75:G:OP2	61:AY:74:TYR:OH	2.25	0.54
4:BE:159:THR:HB	4:BE:173:ILE:HB	1.90	0.54
34:B5:1583:A:N6	34:B5:1612:U:OP2	2.39	0.54
37:AC:34:ILE:HD12	37:AC:37:THR:HB	1.89	0.54
37:AC:193:LYS:NZ	38:A1:1420:C:OP2	2.38	0.54
38:A1:296:A:N3	38:A1:299:G:O2'	2.39	0.54
38:A1:1178:G:N3	38:A1:1328:C:O2'	2.41	0.54
38:A1:2218:G:OP1	71:AI:68:ARG:NH1	2.40	0.54
41:AD:53:VAL:HB	41:AD:159:VAL:HG23	1.89	0.54
49:AM:102:LYS:HD2	49:AM:105:GLN:HE21	1.72	0.54
71:AI:53:TYR:OH	71:AI:86:LYS:NZ	2.41	0.54
82:DC:533:THR:O	82:DC:785:ARG:NH2	2.41	0.54
82:DC:674:GLY:H	82:DC:678:GLY:HA2	1.72	0.54
8:BJ:20:GLU:HG2	8:BJ:23:ARG:H	1.73	0.54
33:BM:61:VAL:HG12	33:BM:89:ILE:HB	1.90	0.54
34:B5:411:C:O2	34:B5:423:G:N2	2.40	0.54
34:B5:1112:G:OP1	76:AN:6:ARG:NH2	2.40	0.54
35:AA:60:LYS:HZ3	35:AA:75:ILE:HG12	1.72	0.54
38:A1:1111:U:H2'	38:A1:1112:A:H8	1.72	0.54
38:A1:1412:G:OP1	67:AE:105:ARG:NH1	2.41	0.54
38:A1:3158:G:O6	38:A1:3292:A:N1	2.41	0.54
46:AI:82:ARG:HH12	81:C5:78:GLU:HA	1.71	0.54
51:AO:27[A]:LEU:O	51:AO:101[A]:ARG:NH1	2.40	0.54
4:BE:187:ARG:NH1	34:B5:754:A:N7	2.56	0.54
25:BS:136:GLN:NE2	34:B5:1545:A:OP2	2.41	0.54
26:BT:22:LEU:HD22	26:BT:28:LEU:HD11	1.89	0.54
34:B5:1012:U:H4'	35:AA:248:GLY:HA2	1.89	0.54
38:A1:801:A:N6	48:AL:19:GLN:OE1	2.40	0.54
38:A1:1272:C:OP1	38:A1:1273:A:N6	2.40	0.54
38:A1:1551:C:HO2'	38:A1:2170:U:HO2'	1.56	0.54
38:A1:3042:U:OP2	38:A1:3092:C:N4	2.40	0.54
45:AH:57:VAL:HG23	45:AH:68:LEU:HD13	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:37:LYS:NZ	34:B5:297:U:OP1	2.37	0.54
5:BG:180:THR:HG23	5:BG:183:ARG:H	1.73	0.54
36:AB:244:ARG:NH2	38:A1:2980:U:OP2	2.41	0.54
38:A1:107:A:O2'	38:A1:324:A:N3	2.39	0.54
38:A1:3234:A:N1	38:A1:3253:G:O6	2.41	0.54
50:AN:178:HIS:O	50:AN:181:ASN:ND2	2.41	0.54
37:AC:188:ARG:NH1	38:A1:1382:G:OP2	2.40	0.53
38:A1:216:G:OP1	61:AY:16:ARG:NH1	2.40	0.53
38:A1:860:G:OP1	78:Ap:17:ARG:NH1	2.41	0.53
38:A1:3092:C:O2'	38:A1:3094:A:OP2	2.26	0.53
40:A4:143:U:OP1	50:AN:38:ARG:NH2	2.40	0.53
1:BA:52:LYS:HG2	12:BV:82:VAL:HG23	1.90	0.53
19:BD:29:LEU:HB3	19:BD:32:GLU:HB2	1.90	0.53
26:BT:122:ARG:NH1	34:B5:1499:G:OP1	2.41	0.53
35:AA:36:GLU:OE1	35:AA:163:ARG:NH1	2.40	0.53
38:A1:177:U:O2	38:A1:241:G:C6	2.62	0.53
38:A1:2510:U:H2'	38:A1:2511:A:H8	1.73	0.53
38:A1:2724:U:OP2	38:A1:2726:C:N4	2.42	0.53
44:AG:101:THR:HG23	44:AG:103:ALA:H	1.73	0.53
47:AJ:48:SER:HB2	47:AJ:66:ALA:HB3	1.90	0.53
65:Ac:50:VAL:HG23	65:Ac:53:LYS:HE3	1.90	0.53
36:AB:315:GLY:HA2	38:A1:3379:C:H4'	1.90	0.53
38:A1:1055:A:N3	39:A3:81:U:O2'	2.41	0.53
38:A1:1266:G:O6	38:A1:1276:U:O4	2.27	0.53
38:A1:2871:G:H5''	38:A1:2872:A:H5''	1.90	0.53
66:Ad:41:LYS:NZ	66:Ad:47:ASP:OD1	2.42	0.53
19:BD:50:ILE:HD11	19:BD:86:LEU:HD23	1.89	0.53
25:BS:134:ARG:HB2	25:BS:136:GLN:HE21	1.73	0.53
38:A1:1223:A:OP2	38:A1:1285:G:N2	2.39	0.53
38:A1:1302:A:N7	38:A1:2857:C:O2'	2.42	0.53
38:A1:2261:G:O2'	38:A1:2263:C:N4	2.41	0.53
38:A1:2705:A:N6	56:AT:47:SER:O	2.42	0.53
82:DC:329:PRO:HG2	82:DC:332:ASP:HB2	1.90	0.53
34:B5:114:C:N4	34:B5:245:U:O2	2.42	0.53
34:B5:754:A:H5'	34:B5:755:A:H5''	1.91	0.53
35:AA:128:ARG:NH2	38:A1:2176:U:OP2	2.41	0.53
37:AC:107:ARG:HA	38:A1:664:U:H5'	1.90	0.53
38:A1:1497:C:H2'	38:A1:1498:A:H8	1.73	0.53
38:A1:2116:G:OP1	38:A1:2118:C:N4	2.41	0.53
52:AP:84:PRO:HB2	52:AP:87:SER:HB3	1.91	0.53
10:BN:124:ARG:NH2	34:B5:967:A:OP2	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:30:SER:OG	13:BW:58:SER:O	2.26	0.53
14:BX:69:ARG:NH2	34:B5:569:C:OP2	2.41	0.53
20:BF:189:THR:HG22	20:BF:191:ALA:H	1.74	0.53
34:B5:5:U:H2'	34:B5:6:G:H8	1.73	0.53
34:B5:1317:C:O2'	34:B5:1400:A:N3	2.41	0.53
38:A1:571:U:H2'	38:A1:572:A:H8	1.73	0.53
38:A1:2552:C:H2'	65:Ac:50:VAL:HG21	1.90	0.53
53:AQ:64:VAL:HG23	53:AQ:93:ILE:HD11	1.91	0.53
7:BI:56:ARG:NH1	7:BI:174:GLY:O	2.42	0.53
31:Bg:159:ASN:ND2	31:Bg:166:SER:O	2.41	0.53
38:A1:760:G:O2'	38:A1:770:G:N2	2.41	0.53
38:A1:1606:U:O4'	69:Ag:8:ARG:NH2	2.41	0.53
41:AD:91:GLY:O	41:AD:94:ASN:ND2	2.41	0.53
66:Ad:55:LEU:HB2	66:Ad:95:PRO:HD3	1.91	0.53
82:DC:155:VAL:HG21	82:DC:185:VAL:HG11	1.91	0.53
4:BE:126:VAL:HA	4:BE:141:THR:HA	1.90	0.53
7:BI:164:ARG:NH2	38:A1:3353:G:N7	2.57	0.53
16:Ba:10:ARG:NH1	34:B5:1790:A:OP1	2.41	0.53
31:Bg:123:ILE:HG22	31:Bg:133:VAL:HG12	1.90	0.53
34:B5:131:C:H5'	34:B5:133:U:H4'	1.90	0.53
34:B5:1506:G:HO2'	34:B5:1550:A:HO2'	1.52	0.53
38:A1:673:U:H2'	38:A1:674:G:C8	2.44	0.53
51:AO:54[A]:TYR:OH	51:AO:73[A]:PHE:O	2.27	0.53
79:tE:55:U:H3	79:tE:59:A:H62	1.56	0.53
82:DC:263:ASP:OD1	82:DC:267:LYS:N	2.42	0.53
3:BC:81:MET:HG2	3:BC:211:LEU:HD11	1.91	0.53
9:BL:97:TYR:O	9:BL:99:ARG:NH1	2.41	0.53
11:BO:99:GLN:NE2	16:Ba:44:ILE:O	2.40	0.53
20:BF:148:ARG:HG3	20:BF:157:ARG:HH21	1.74	0.53
26:BT:22:LEU:HD13	26:BT:28:LEU:HD21	1.90	0.53
34:B5:1116:A:OP1	76:An:17:ARG:NH1	2.42	0.53
38:A1:2160:G:H2'	38:A1:2161:G:H8	1.74	0.53
38:A1:2574:G:O6	62:AZ:56:LYS:NZ	2.41	0.53
38:A1:2895:G:O2'	75:Am:100:TYR:O	2.26	0.53
38:A1:2941:A:H5''	38:A1:2943:G:H4'	1.91	0.53
38:A1:3291:G:H2'	38:A1:3292:A:H8	1.74	0.53
82:DC:20:ARG:NH1	82:DC:342:LEU:O	2.41	0.53
4:BE:200:ARG:NH1	4:BE:202:ASP:OD1	2.42	0.53
11:BO:132:ARG:HG3	16:Ba:29:SER:HB3	1.91	0.53
13:BW:31:SER:HB3	34:B5:636:A:H5''	1.90	0.53
34:B5:17:C:O2'	34:B5:1137:A:N1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1461:C:H2'	34:B5:1462:G:H8	1.74	0.53
35:AA:242:ARG:HG3	38:A1:2241:U:H4'	1.90	0.53
38:A1:353:G:O6	72:Aj:55:ARG:NH2	2.41	0.53
79:tE:57:C:OP2	80:E:130:LYS:NZ	2.33	0.53
36:AB:92:TYR:HB3	36:AB:99:LEU:HD22	1.90	0.52
36:AB:270:ARG:NH2	38:A1:3090:U:OP1	2.36	0.52
41:AD:103:LEU:HD11	41:AD:248:ARG:HE	1.72	0.52
45:AH:5:GLN:NE2	45:AH:7:GLU:OE1	2.42	0.52
51:AO:166[A]:GLU:OE1	51:AO:170[A]:LYS:NZ	2.42	0.52
4:BE:37:LYS:HG2	34:B5:297:U:H5''	1.91	0.52
6:BH:104:ARG:NH2	34:B5:805:U:O4	2.42	0.52
8:BJ:70:LEU:O	8:BJ:74:ASN:ND2	2.42	0.52
38:A1:938:C:OP2	63:Aa:26:ARG:NH1	2.41	0.52
57:AU:84:LEU:HD22	57:AU:93:ILE:HG13	1.92	0.52
8:BJ:123:HIS:HB3	18:Be:33:ARG:HH11	1.74	0.52
9:BL:91:LEU:HB3	9:BL:100:TYR:HD2	1.74	0.52
34:B5:523:G:O2'	34:B5:529:A:N6	2.43	0.52
35:AA:51:ASP:HB2	35:AA:58:LEU:HG	1.91	0.52
38:A1:649:A:OP2	38:A1:2868:U:O2'	2.28	0.52
38:A1:655:C:H2'	38:A1:656:A:C8	2.44	0.52
38:A1:1494:U:OP1	74:Al:42:ARG:NH1	2.38	0.52
41:AD:107:ARG:NH2	41:AD:116:ASP:OD1	2.42	0.52
52:AP:126:ARG:HA	52:AP:140:GLU:HG3	1.90	0.52
65:Ac:17:VAL:HG11	65:Ac:92:ILE:HD12	1.91	0.52
20:BF:118:LEU:O	20:BF:122:ASN:ND2	2.42	0.52
27:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	1.91	0.52
29:Bc:27:GLN:NE2	29:Bc:43:ASN:OD1	2.42	0.52
82:DC:414:GLN:NE2	82:DC:470:THR:OG1	2.43	0.52
13:BW:11:LEU:HD12	13:BW:74:VAL:HG12	1.92	0.52
33:BM:42:ALA:HB1	33:BM:47:GLU:HB3	1.91	0.52
33:BM:114:LYS:NZ	34:B5:1224:A:OP1	2.43	0.52
38:A1:845:G:O2'	38:A1:848:A:N6	2.43	0.52
38:A1:1348:U:OP1	53:AQ:39:ARG:NH1	2.42	0.52
38:A1:1618:G:O2'	40:A4:126:A:N1	2.41	0.52
38:A1:2138:A:O2'	72:Aj:2:GLY:N	2.41	0.52
58:AV:40:LYS:HG3	58:AV:57:MET:HG2	1.91	0.52
63:Aa:101:VAL:HA	63:Aa:124:ILE:HB	1.92	0.52
22:BP:37:ALA:HB1	22:BP:41:VAL:HG23	1.90	0.52
38:A1:532:A:H61	38:A1:560:G:H1	1.55	0.52
38:A1:1364:C:OP1	43:AF:110:ARG:NH2	2.41	0.52
5:BG:10:ASN:ND2	5:BG:127:THR:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BY:83:LYS:HD3	15:BY:96:LEU:HD23	1.92	0.52
18:Be:14:VAL:HA	18:Be:17:GLN:HG2	1.91	0.52
34:B5:486:G:H1	34:B5:501:U:H3	1.55	0.52
38:A1:1213:G:H4'	55:AS:90:MET:HB2	1.91	0.52
38:A1:2284:C:N4	38:A1:2308:C:OP2	2.40	0.52
41:AD:23:ARG:NH1	41:AD:23:ARG:O	2.43	0.52
51:AO:23[A]:VAL:HG12	51:AO:84[A]:LEU:HD11	1.91	0.52
52:AP:131:ARG:HB2	52:AP:135:ARG:HB2	1.92	0.52
53:AQ:55:SER:OG	53:AQ:58:ASN:ND2	2.43	0.52
80:E:31:THR:OG1	80:E:60:ARG:NH1	2.42	0.52
4:BE:54:TYR:O	15:BY:15:ASN:ND2	2.40	0.52
5:BG:63:MET:HA	5:BG:98:ARG:HB3	1.91	0.52
11:BO:81:VAL:HG11	11:BO:102:LEU:HD13	1.92	0.52
16:Ba:43:ASN:HA	16:Ba:66:LYS:HA	1.91	0.52
27:BU:35:GLU:OE2	27:BU:89:ARG:NH2	2.43	0.52
38:A1:990:PSU:H4'	56:AT:100:LYS:HB2	1.92	0.52
38:A1:1169:A:H4'	43:AF:219:LYS:HD3	1.91	0.52
38:A1:1294:A:H5''	55:AS:85:SER:HB2	1.91	0.52
38:A1:2898:G:OP2	45:AH:173:ARG:NH1	2.37	0.52
66:Ad:10:ARG:HG2	66:Ad:108:VAL:HG22	1.92	0.52
82:DC:626:ASP:N	82:DC:626:ASP:OD1	2.43	0.52
9:BL:27:THR:HG23	9:BL:30:ARG:H	1.74	0.52
10:BN:3:ARG:HB3	10:BN:6:SER:HB2	1.92	0.52
16:Ba:5:ARG:HH21	34:B5:1795:U:H3'	1.75	0.52
22:BP:97:TYR:OH	34:B5:1211:A:N3	2.41	0.52
26:BT:12:GLN:HE22	34:B5:1479:A:H1'	1.74	0.52
38:A1:1047:A:N3	38:A1:2633:U:O2'	2.42	0.52
38:A1:2737:C:H2'	38:A1:2738:A:H8	1.74	0.52
38:A1:3333:G:N2	38:A1:3369:G:O2'	2.43	0.52
82:DC:13:MET:SD	82:DC:452:ASN:ND2	2.76	0.52
4:BE:240:LYS:NZ	34:B5:786:C:OP1	2.42	0.52
5:BG:50:PHE:HB3	5:BG:111:LEU:HD22	1.91	0.52
7:BI:36:THR:O	7:BI:96:LEU:N	2.42	0.52
34:B5:434:G:N1	34:B5:437:A:OP2	2.41	0.52
35:AA:21:ARG:HD3	38:A1:824:C:H5''	1.92	0.52
48:AL:66:ASN:OD1	63:Aa:128:ARG:NH2	2.43	0.52
7:BI:67:TRP:HZ2	7:BI:152:ILE:HG12	1.76	0.51
31:Bg:13:LEU:HD21	31:Bg:55:GLY:H	1.75	0.51
34:B5:1488:G:O2'	34:B5:1494:C:O2	2.23	0.51
35:AA:14:SER:OG	38:A1:911:C:OP1	2.25	0.51
38:A1:806:A:N3	38:A1:2812:C:O2'	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:939:U:O2'	38:A1:2402:A:N1	2.39	0.51
38:A1:1481:A:N6	38:A1:1872:C:O2	2.43	0.51
38:A1:1729:A:N6	78:Ap:41:PHE:O	2.38	0.51
38:A1:2894:C:HO2'	38:A1:3107:U:HO2'	1.57	0.51
43:AF:83:LEU:HD11	43:AF:116:PHE:HB3	1.91	0.51
1:BA:107:PHE:HB2	1:BA:135:GLU:HG2	1.90	0.51
8:BJ:132:ARG:NH2	34:B5:514:G:OP1	2.43	0.51
25:BS:144:ARG:NH1	34:B5:1171:A:OP1	2.42	0.51
34:B5:925:G:H2'	34:B5:926:A:H8	1.75	0.51
37:AC:217:LYS:NZ	38:A1:210:U:O2	2.42	0.51
38:A1:2456:A:H2'	38:A1:2457:G:C4	2.45	0.51
38:A1:3261:C:OP1	49:AM:126:GLN:NE2	2.44	0.51
82:DC:629:ASP:HB3	82:DC:685:ARG:HH22	1.75	0.51
19:BD:126:VAL:HG21	19:BD:188:ILE:HD12	1.92	0.51
34:B5:976:G:N1	34:B5:1023:A:O2'	2.37	0.51
38:A1:994:G:N2	38:A1:995:U:O4	2.40	0.51
38:A1:1367:G:N2	38:A1:1368:U:O4	2.43	0.51
42:AE:39:VAL:HG13	42:AE:87:THR:HB	1.92	0.51
3:BC:148:LEU:O	3:BC:174:ARG:NH2	2.44	0.51
26:BT:77:ASN:OD1	26:BT:101:ASN:ND2	2.43	0.51
38:A1:1022:U:OP2	38:A1:1031:C:N4	2.44	0.51
82:DC:746:VAL:HG21	82:DC:784:LEU:HA	1.93	0.51
26:BT:86:ARG:NH2	34:B5:1601:G:OP1	2.43	0.51
38:A1:525:C:H5''	49:AM:79:ALA:HB2	1.91	0.51
38:A1:944:C:O2'	67:Ae:33:ARG:NH1	2.44	0.51
38:A1:1167:U:OP2	68:Af:73:ARG:NH1	2.43	0.51
38:A1:1795:U:N3	78:Ap:50:GLY:O	2.43	0.51
38:A1:3234:A:C2	38:A1:3253:G:N1	2.56	0.51
51:AO:61[A]:ALA:HA	51:AO:70[A]:PRO:HD2	1.93	0.51
57:AU:14:THR:HG22	57:AU:66:VAL:HG12	1.92	0.51
65:Ac:56:LEU:HD13	65:Ac:89:VAL:HG11	1.91	0.51
5:BG:69:LEU:HD23	5:BG:71:THR:H	1.75	0.51
15:BY:60:PHE:O	34:B5:522:U:O2'	2.28	0.51
28:BZ:74:SER:OG	34:B5:1534:G:OP2	2.29	0.51
34:B5:226:A:H1'	34:B5:837:G:H1	1.75	0.51
34:B5:748:U:O2	34:B5:801:G:O6	2.29	0.51
34:B5:1310:U:O2'	34:B5:1402:G:O2'	2.29	0.51
38:A1:838:G:N7	78:Ap:4:ARG:NH2	2.55	0.51
38:A1:1150:A:N6	38:A1:2369:G:O2'	2.44	0.51
40:A4:141:C:O3'	50:AN:62:TYR:OH	2.28	0.51
79:tE:4:G:H2'	79:tE:5:G:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:BL:91:LEU:HD12	9:BL:100:TYR:HB3	1.92	0.51
14:BX:13:ARG:HH12	34:B5:631:G:H4'	1.75	0.51
14:BX:90:ASP:HA	34:B5:568:G:H4'	1.93	0.51
19:BD:162:GLN:HG2	19:BD:165:ASN:HD22	1.74	0.51
22:BP:18:ARG:NH2	34:B5:1548:G:OP1	2.44	0.51
33:BM:68:GLU:HB3	33:BM:71:ILE:HG12	1.93	0.51
33:BM:125:ASN:ND2	33:BM:129:GLU:OE2	2.43	0.51
34:B5:155:U:O2	34:B5:157:A:N6	2.44	0.51
38:A1:617:G:OP1	42:AE:108:LYS:NZ	2.41	0.51
38:A1:1018:G:H8	38:A1:1019:G:H4'	1.76	0.51
38:A1:1833:G:H5''	74:Al:10:LYS:HD3	1.91	0.51
38:A1:2896:A:O2'	75:Am:122:ARG:NH2	2.43	0.51
69:Ag:42:PRO:HB2	69:Ag:51:LEU:HD12	1.92	0.51
80:E:76:ARG:HG3	80:E:144:LEU:HD22	1.91	0.51
19:BD:135:GLU:HB2	19:BD:157:LEU:HD21	1.93	0.51
20:BF:95:ASN:O	34:B5:1611:A:O2'	2.28	0.51
34:B5:773:C:O2'	34:B5:787:G:N2	2.43	0.51
34:B5:1018:U:H2'	34:B5:1019:A:H8	1.76	0.51
38:A1:1268:G:N2	38:A1:1273:A:N7	2.45	0.51
38:A1:1378:U:H2'	38:A1:1379:G:H8	1.76	0.51
38:A1:1435:A:H5''	38:A1:1436:U:H5''	1.92	0.51
44:AG:45:ASN:HD22	60:AX:26:VAL:HG13	1.75	0.51
82:DC:164:LEU:HD21	82:DC:174:LEU:HD22	1.91	0.51
8:BJ:74:ASN:HA	8:BJ:77:ILE:HG22	1.93	0.51
34:B5:277:U:O2'	34:B5:279:G:N2	2.44	0.51
34:B5:836:U:O4	34:B5:837:G:N2	2.44	0.51
38:A1:524:U:OP1	49:AM:77:ARG:NH2	2.44	0.51
38:A1:3269:U:H3'	42:AE:46:ARG:HH12	1.76	0.51
82:DC:780:PHE:O	82:DC:784:LEU:N	2.44	0.51
2:BB:70:LEU:HD12	2:BB:74:GLN:HG2	1.93	0.51
4:BE:27:TYR:O	34:B5:447:U:O2'	2.24	0.51
4:BE:172:PHE:HE2	4:BE:174:LYS:HE3	1.75	0.51
9:BL:38:ALA:O	34:B5:246:G:N2	2.42	0.51
14:BX:54:LEU:HD11	14:BX:75:GLN:HB2	1.93	0.51
26:BT:72:GLY:HA3	34:B5:1498:G:H5''	1.92	0.51
27:BU:89:ARG:NH2	34:B5:1383:G:OP1	2.43	0.51
32:Bf:119:ARG:NH2	32:Bf:133:ALA:O	2.44	0.51
34:B5:774:A:N6	34:B5:786:C:O2	2.38	0.51
36:AB:86:VAL:HG22	36:AB:162:VAL:HG12	1.92	0.51
38:A1:700:C:H2'	38:A1:701:G:H8	1.75	0.51
40:A4:24:G:OP1	61:AY:17:LYS:NZ	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:39:G:OP1	70:Ah:83:LYS:NZ	2.42	0.51
73:Ak:42:LYS:HG2	73:Ak:55:VAL:HG12	1.93	0.51
80:E:60:ARG:HH21	80:E:62:ASN:HB3	1.75	0.51
3:BC:139:ILE:HD12	3:BC:218:ILE:HG12	1.93	0.50
4:BE:108:ARG:NH1	34:B5:788:A:OP2	2.43	0.50
5:BG:23:ARG:NH1	5:BG:41:VAL:O	2.43	0.50
26:BT:86:ARG:NH1	26:BT:90:PRO:O	2.45	0.50
31:Bg:156:VAL:HG22	31:Bg:169:ILE:HG22	1.93	0.50
34:B5:553:G:H3'	34:B5:554:C:H2'	1.93	0.50
34:B5:1773:4AC:H5'	76:An:3:ALA:HB3	1.92	0.50
36:AB:97:ARG:NH2	38:A1:3244:A:OP1	2.44	0.50
38:A1:597:G:H2'	38:A1:598:A:H8	1.75	0.50
38:A1:2457:G:H22	38:A1:2485:A:H62	1.58	0.50
38:A1:2864:A:H5''	46:AI:114:GLY:HA2	1.94	0.50
58:AV:27:ASP:HB2	58:AV:111:GLY:HA3	1.93	0.50
6:BH:81:LEU:HB3	6:BH:90:VAL:HG11	1.92	0.50
7:BI:11:ARG:NH1	7:BI:15:GLY:O	2.44	0.50
34:B5:485:A:H61	34:B5:504:U:H1'	1.75	0.50
40:A4:8:C:H2'	40:A4:9:A:H8	1.75	0.50
69:Ag:79:SER:OG	69:Ag:80:ARG:NH1	2.44	0.50
82:DC:149:GLU:OE1	82:DC:352:ARG:NH2	2.43	0.50
19:BD:105:MET:HE2	19:BD:122:VAL:HG21	1.93	0.50
34:B5:480:G:O6	34:B5:481:A:C6	2.64	0.50
34:B5:1163:A:N3	34:B5:1613:U:O2'	2.36	0.50
36:AB:9:PRO:HD2	58:AV:45:ARG:HH11	1.76	0.50
38:A1:807:A:H61	38:A1:934:G:H22	1.58	0.50
38:A1:1631:C:OP2	62:AZ:48:ARG:NH2	2.45	0.50
46:AI:12:GLN:NE2	46:AI:129:VAL:O	2.45	0.50
48:AL:55:ARG:NH1	48:AL:73:ARG:O	2.43	0.50
52:AP:122:ALA:HB3	52:AP:143:PRO:HB2	1.93	0.50
55:AS:115:ARG:O	55:AS:117:ARG:NH1	2.44	0.50
80:E:21:ASN:HA	80:E:25:LYS:HD3	1.93	0.50
5:BG:115:LYS:NZ	34:B5:1692:G:OP2	2.44	0.50
20:BF:96:SER:HB2	20:BF:176:THR:HG21	1.92	0.50
30:Bd:14:TYR:HB2	34:B5:1597:A:C8	2.47	0.50
35:AA:70:ARG:NH2	38:A1:1580:A:OP1	2.44	0.50
37:AC:107:ARG:NH1	38:A1:1429:G:OP2	2.41	0.50
38:A1:284:A:OP2	77:Ao:41:ARG:NH1	2.44	0.50
38:A1:1659:U:H3	38:A1:1790:G:H1	1.58	0.50
38:A1:2674:A:H5''	47:AJ:105:GLY:HA3	1.94	0.50
15:BY:53:ASP:HB2	15:BY:79:VAL:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:69:LEU:HA	19:BD:72:LEU:HB2	1.94	0.50
38:A1:1193:A:OP2	51:AO:49[A]:ARG:NH1	2.41	0.50
43:AF:96:PRO:HB2	43:AF:99:PRO:HD2	1.93	0.50
45:AH:87:LYS:HB2	45:AH:187:ILE:HD13	1.93	0.50
48:AL:57:VAL:HG22	48:AL:147:ILE:HG12	1.93	0.50
67:Ae:96:ILE:HG21	67:Ae:105:ARG:HG2	1.92	0.50
1:BA:101:ARG:NH2	34:B5:1321:A:OP2	2.44	0.50
27:BU:24:ILE:HG12	27:BU:116:VAL:HG22	1.92	0.50
59:AW:47:ARG:HD3	59:AW:54:LEU:HG	1.93	0.50
82:DC:22:MET:HE1	82:DC:126:LEU:HB2	1.93	0.50
11:BO:87:GLY:HA3	11:BO:120:PRO:HG2	1.93	0.50
23:BQ:14:LYS:O	23:BQ:123:ARG:NH1	2.45	0.50
38:A1:286:U:O2'	50:AN:179:LYS:O	2.29	0.50
38:A1:411:U:H2'	38:A1:412:G:H8	1.75	0.50
47:AJ:17:LEU:HD11	47:AJ:80:LEU:HD13	1.94	0.50
6:BH:8:ILE:HA	6:BH:42:GLN:HG3	1.93	0.50
23:BQ:136:SER:HB3	34:B5:1586:A:H5''	1.92	0.50
31:Bg:151:VAL:HA	31:Bg:173:GLY:HA3	1.92	0.50
34:B5:1187:PSU:H2'	34:B5:1188:G:H8	1.77	0.50
39:A3:28:C:OP1	47:AJ:137:ARG:NH1	2.45	0.50
3:BC:56:ILE:HA	3:BC:61:LEU:HD12	1.93	0.50
34:B5:279:G:H8	34:B5:280:U:H4'	1.77	0.50
38:A1:668:G:H1	38:A1:794:U:H3	1.59	0.50
38:A1:1448:U:H2'	38:A1:1449:A:H8	1.77	0.50
38:A1:1464:G:N2	38:A1:1467:A:OP2	2.45	0.50
40:A4:8:C:H2'	40:A4:9:A:C8	2.47	0.50
52:AP:61:ARG:NH2	52:AP:76:PHE:O	2.45	0.50
3:BC:159:THR:OG1	34:B5:1098:U:OP1	2.30	0.49
34:B5:1183:A:N3	34:B5:1210:C:O2'	2.42	0.49
34:B5:1280:4AC:H2'	34:B5:1281:G:C8	2.47	0.49
37:AC:161:LYS:HB2	37:AC:164:GLU:HG2	1.93	0.49
38:A1:184:U:H3	38:A1:232:G:H1	1.59	0.49
38:A1:1134:G:O2'	38:A1:2642:A:N3	2.41	0.49
38:A1:1395:G:O2'	40:A4:18:U:O2	2.30	0.49
40:A4:80:A:O2'	40:A4:83:C:N4	2.43	0.49
55:AS:99:ARG:HG3	55:AS:126:VAL:HG11	1.94	0.49
65:Ac:55:GLU:HB3	69:Ag:94:LEU:HD21	1.94	0.49
82:DC:495:VAL:HG12	82:DC:504:LEU:HD21	1.93	0.49
5:BG:136:LYS:HA	5:BG:175:ILE:HG22	1.94	0.49
8:BJ:37:LYS:HZ1	18:Be:32:GLY:HA3	1.76	0.49
11:BO:135:ARG:HB2	16:Ba:26:CYS:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:15:ASN:ND2	13:BW:72:CYS:O	2.41	0.49
15:BY:34:ASN:ND2	34:B5:521:A:N3	2.59	0.49
34:B5:854:U:OP2	54:AR:181:ARG:NE	2.45	0.49
38:A1:153:U:H4'	38:A1:158:G:H4'	1.94	0.49
38:A1:2446:U:H2'	38:A1:2447:A:H8	1.77	0.49
43:AF:163:LEU:HA	43:AF:168:ILE:HD11	1.94	0.49
47:AJ:35:LYS:HA	47:AJ:38:GLU:HG2	1.94	0.49
55:AS:125:LYS:HE3	55:AS:127:ALA:HB2	1.95	0.49
82:DC:505:VAL:HA	82:DC:508:LEU:HD13	1.93	0.49
3:BC:142:GLY:N	3:BC:153:SER:O	2.36	0.49
10:BN:46:THR:HG22	10:BN:48:SER:H	1.77	0.49
15:BY:60:PHE:H	15:BY:71:GLY:HA2	1.77	0.49
20:BF:114:ILE:HA	20:BF:117:THR:HG22	1.94	0.49
27:BU:99:ILE:HB	27:BU:102:ARG:HH21	1.77	0.49
32:Bf:128:ALA:H	33:BM:54:ARG:HD2	1.76	0.49
34:B5:62:A:O2'	34:B5:268:C:O2	2.31	0.49
34:B5:268:C:H2'	34:B5:269:G:H8	1.77	0.49
34:B5:654:C:N4	34:B5:678:A:OP2	2.44	0.49
38:A1:522:A:O2'	55:AS:66:GLU:O	2.30	0.49
38:A1:1363:A:OP1	43:AF:160:ARG:NH1	2.39	0.49
38:A1:1717:U:H3	38:A1:1727:G:H1	1.59	0.49
38:A1:2465:G:H2'	38:A1:2466:G:C8	2.48	0.49
38:A1:2476:C:H2'	38:A1:2477:G:H21	1.77	0.49
41:AD:50:ARG:NH1	41:AD:147:ASP:OD2	2.44	0.49
62:AZ:2:ALA:N	65:Ac:63:SER:O	2.44	0.49
80:E:57:ASN:OD1	80:E:182:GLN:NE2	2.45	0.49
80:E:194:LEU:HB3	80:E:200:ASN:HD22	1.78	0.49
82:DC:18:ASN:ND2	82:DC:95:GLY:O	2.45	0.49
7:BI:103:GLN:HB3	7:BI:164:ARG:HG2	1.93	0.49
12:BV:58:TYR:HE1	34:B5:1082:C:H1'	1.77	0.49
27:BU:57:ARG:HA	27:BU:89:ARG:HG3	1.95	0.49
31:Bg:68:VAL:HG12	31:Bg:84:SER:HB2	1.94	0.49
34:B5:1218:G:H21	34:B5:1265:G:H1	1.60	0.49
36:AB:240:ARG:NH2	38:A1:1907:C:O2	2.39	0.49
38:A1:929:A:O2'	72:Aj:49:TRP:O	2.31	0.49
38:A1:1145:G:O2'	67:Ae:45:ARG:O	2.29	0.49
38:A1:1750:A:O2'	38:A1:1752:A:N6	2.45	0.49
38:A1:2722:U:O2'	56:AT:88:ARG:O	2.30	0.49
82:DC:544:ASP:O	82:DC:548:ASP:N	2.45	0.49
8:BJ:38:ASN:ND2	34:B5:594:A:OP2	2.45	0.49
26:BT:105:LEU:HD13	26:BT:122:ARG:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:AC:315:LYS:NZ	38:A1:504:A:O2'	2.46	0.49
38:A1:838:G:O6	78:Ap:4:ARG:NH1	2.39	0.49
54:AR:92:GLN:HE21	54:AR:96:ILE:HD11	1.77	0.49
62:AZ:15:ARG:NH1	69:Ag:82:ALA:O	2.45	0.49
82:DC:138:GLN:NE2	82:DC:141:THR:OG1	2.45	0.49
82:DC:823:ARG:HH22	82:DC:832:VAL:HG22	1.77	0.49
1:BA:122:ILE:HG13	1:BA:144:ILE:HB	1.93	0.49
4:BE:69:HIS:HE1	4:BE:94:ALA:H	1.60	0.49
5:BG:88:ARG:HH22	34:B5:399:A:H61	1.59	0.49
7:BI:67:TRP:HE1	7:BI:70:GLU:HG2	1.77	0.49
8:BJ:80:LEU:HA	8:BJ:83:VAL:HG12	1.95	0.49
9:BL:129:ARG:HD3	34:B5:335:U:H4'	1.94	0.49
14:BX:65:ASN:OD1	34:B5:575:C:N4	2.42	0.49
22:BP:43:ARG:HH12	34:B5:1551:U:H3'	1.77	0.49
22:BP:93:VAL:HA	22:BP:106:GLU:HA	1.94	0.49
31:Bg:176:LYS:NZ	31:Bg:196:ASN:O	2.45	0.49
31:Bg:231:MET:N	31:Bg:231:MET:SD	2.85	0.49
34:B5:292:U:H2'	34:B5:293:U:C2	2.47	0.49
34:B5:606:A:H4'	34:B5:607:G:H3'	1.94	0.49
34:B5:953:G:H2'	34:B5:954:G:H8	1.75	0.49
34:B5:1552:U:O2'	34:B5:1597:A:N3	2.41	0.49
38:A1:627:U:H2'	38:A1:628:A:C8	2.47	0.49
38:A1:969:C:O2'	64:Ab:18:ARG:NH2	2.43	0.49
38:A1:2810:C:OP2	38:A1:2955:U:O2'	2.30	0.49
42:AE:175:LYS:O	49:AM:117:ARG:NH2	2.46	0.49
44:AG:203:VAL:HG21	44:AG:211:LEU:HD22	1.95	0.49
52:AP:111:LYS:HB2	52:AP:153:LYS:HB2	1.93	0.49
68:Af:48:ARG:HG2	68:Af:104:PRO:HD3	1.95	0.49
82:DC:373:ASP:OD1	82:DC:373:ASP:N	2.45	0.49
12:BV:80:LYS:HB2	24:BR:109:LEU:HD13	1.95	0.49
26:BT:117:SER:HB2	26:BT:123:ARG:HG2	1.94	0.49
34:B5:32:U:O4	34:B5:468:A:N7	2.46	0.49
34:B5:490:C:N4	34:B5:493:U:O4'	2.46	0.49
34:B5:1202:A:N6	34:B5:1457:C:OP1	2.42	0.49
35:AA:46:LYS:HD2	35:AA:62:VAL:HG21	1.94	0.49
36:AB:126:LYS:HD2	38:A1:3294:A:H5''	1.94	0.49
38:A1:217:U:O2	61:AY:103:LYS:NZ	2.39	0.49
38:A1:1634:G:OP1	62:AZ:107:ARG:NH1	2.46	0.49
38:A1:1740:U:H4'	38:A1:1741:A:H5'	1.94	0.49
45:AH:126:VAL:HG23	45:AH:164:ILE:HD13	1.93	0.49
46:AI:49:CYS:HB3	46:AI:168:SER:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:AJ:49:LYS:HE3	47:AJ:64:LYS:HE3	1.95	0.49
51:AO:7[A]:VAL:HG22	51:AO:33[A]:ILE:HG22	1.94	0.49
61:AY:51:ARG:HD2	61:AY:115:ARG:HH11	1.78	0.49
80:E:64:SER:O	80:E:108:ASN:N	2.41	0.49
2:BB:126:THR:HB	2:BB:136:ARG:HG3	1.93	0.49
3:BC:241:ASP:OD2	12:BV:35:ASN:ND2	2.46	0.49
4:BE:13:ALA:HA	34:B5:755:A:H2	1.78	0.49
5:BG:98:ARG:NH1	5:BG:101:ILE:O	2.41	0.49
34:B5:429:G:H2'	34:B5:430:G:H8	1.77	0.49
34:B5:890:C:H2'	34:B5:891:A:H8	1.78	0.49
34:B5:1588:G:O6	34:B5:1608:U:O4	2.30	0.49
35:AA:54:ARG:NH2	38:A1:2176:U:OP1	2.42	0.49
36:AB:227:GLU:HA	38:A1:1887:A:H4'	1.95	0.49
38:A1:1606:U:O4	69:Ag:9:ARG:NE	2.41	0.49
38:A1:1666:G:H2'	38:A1:1667:A:H8	1.77	0.49
38:A1:1805:C:H2'	38:A1:1806:A:H8	1.77	0.49
42:AE:45:GLY:O	42:AE:48:ARG:NH1	2.45	0.49
45:AH:9:GLN:HB3	45:AH:52:LEU:HD11	1.94	0.49
1:BA:24:LEU:HD12	1:BA:45:VAL:HG11	1.95	0.49
1:BA:84:ARG:NH1	1:BA:203:PHE:O	2.45	0.49
4:BE:49:ARG:NH2	34:B5:448:C:OP1	2.37	0.49
18:Be:42:ARG:NH1	34:B5:589:C:OP1	2.46	0.49
28:BZ:61:SER:H	28:BZ:64:VAL:HB	1.78	0.49
34:B5:1477:G:H2'	34:B5:1478:G:H8	1.78	0.49
34:B5:1776:A:OP2	76:An:11:ARG:NH1	2.46	0.49
38:A1:1333:C:OP1	53:AQ:2:GLY:N	2.45	0.49
50:AN:8:GLU:OE1	50:AN:50:ARG:NH1	2.46	0.49
50:AN:62:TYR:HD2	50:AN:106:VAL:HG13	1.78	0.49
71:Ai:50:LEU:HD21	71:Ai:58:ILE:HD12	1.95	0.49
4:BE:136:VAL:HG21	4:BE:148:ARG:HE	1.78	0.49
4:BE:221:ARG:HG3	4:BE:223:ASN:H	1.78	0.49
25:BS:84:TRP:O	25:BS:89:GLN:NE2	2.46	0.49
38:A1:84:U:O2'	38:A1:101:G:O6	2.29	0.49
38:A1:515:C:H2'	38:A1:516:A:H8	1.78	0.49
38:A1:591:G:O2'	42:AE:17:ALA:O	2.28	0.49
38:A1:1597:C:H5'	38:A1:1696:A:H1'	1.93	0.49
38:A1:2293:C:OP2	58:AV:71:LYS:NZ	2.46	0.49
38:A1:2946:A:H5''	38:A1:2947:G:H5'	1.95	0.49
38:A1:3186:A:N6	45:AH:58:HIS:O	2.40	0.49
69:Ag:3:GLN:HE22	69:Ag:29:ILE:HB	1.78	0.49
8:BJ:136:VAL:HA	8:BJ:156:ILE:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BY:7:ILE:HG21	15:BY:43:LYS:HZ3	1.77	0.48
16:Ba:85:ARG:O	34:B5:1797:A:N6	2.45	0.48
34:B5:350:U:O2'	34:B5:970:A:N1	2.41	0.48
34:B5:1559:A:H5'	34:B5:1560:U:H5''	1.94	0.48
36:AB:283:TYR:HB2	36:AB:323:MET:HG2	1.94	0.48
38:A1:82:C:H4'	50:AN:204:LYS:HE3	1.95	0.48
38:A1:664:U:H2'	38:A1:665:A:C8	2.48	0.48
38:A1:1600:U:OP1	54:AR:42:ARG:NH1	2.46	0.48
43:AF:74:SER:OG	43:AF:75:TYR:N	2.45	0.48
73:Ak:13:GLU:HA	73:Ak:16:ARG:HE	1.78	0.48
5:BG:160:ARG:NE	34:B5:66:U:O2	2.46	0.48
10:BN:16:ILE:HG22	34:B5:959:U:H4'	1.94	0.48
13:BW:80:ASN:OD1	13:BW:124:LYS:NZ	2.41	0.48
32:Bf:109:ASP:O	33:BM:73:LYS:NZ	2.47	0.48
34:B5:1785:U:H2'	34:B5:1786:G:H8	1.78	0.48
36:AB:236:LYS:HG2	38:A1:2880:PSU:H5'	1.94	0.48
38:A1:597:G:H5''	43:AF:41:ARG:HD2	1.96	0.48
38:A1:853:G:O6	78:Ap:2:ALA:N	2.47	0.48
38:A1:3252:G:H2'	38:A1:3253:G:H8	1.78	0.48
44:AG:145:ASN:HB3	44:AG:147:LYS:HE3	1.94	0.48
82:DC:26:ALA:HB2	82:DC:128:VAL:HB	1.95	0.48
82:DC:564:ARG:HB2	82:DC:725:GLN:HB2	1.94	0.48
3:BC:123:GLY:HA2	3:BC:126:ARG:HG2	1.95	0.48
4:BE:98:ASN:HB2	4:BE:114:ILE:HG13	1.95	0.48
9:BL:37:ASN:O	34:B5:247:A:O2'	2.29	0.48
20:BF:192:GLU:OE1	28:BZ:63:SER:OG	2.31	0.48
29:Bc:14:LYS:NZ	29:Bc:15:VAL:O	2.46	0.48
32:Bf:121:CYS:HB2	32:Bf:130:VAL:HG11	1.95	0.48
34:B5:698:U:O2'	34:B5:699:U:O4'	2.31	0.48
38:A1:3343:G:O2'	38:A1:3362:A:N6	2.46	0.48
68:Af:42:GLN:HA	68:Af:45:LEU:HD13	1.94	0.48
78:Ap:46:THR:OG1	78:Ap:57:CYS:SG	2.71	0.48
2:BB:129:THR:OG1	2:BB:131:ASP:OD1	2.31	0.48
2:BB:199:ASN:HA	2:BB:202:LYS:HG2	1.94	0.48
7:BI:51:GLY:N	34:B5:397:A:OP2	2.47	0.48
19:BD:107:PHE:O	19:BD:111:ASN:ND2	2.45	0.48
30:Bd:36:LEU:HB3	30:Bd:38:ILE:HG12	1.95	0.48
34:B5:486:G:O2'	34:B5:488:G:OP2	2.31	0.48
38:A1:3199:G:OP1	49:AM:8:LYS:NZ	2.45	0.48
51:AO:14[A]:HIS:HE1	51:AO:120[A]:VAL:H	1.61	0.48
53:AQ:147:ARG:HB3	53:AQ:150:VAL:HG23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AZ:10:VAL:HG22	62:AZ:24:VAL:HG12	1.95	0.48
82:DC:544:ASP:OD1	82:DC:544:ASP:N	2.47	0.48
1:BA:143:VAL:HB	1:BA:156:VAL:HA	1.95	0.48
12:BV:25:LYS:HB2	12:BV:28:ASP:HB2	1.96	0.48
19:BD:64:ARG:HH22	21:BK:92:ILE:HD13	1.79	0.48
20:BF:58:LEU:HD21	20:BF:167:ARG:HD2	1.96	0.48
33:BM:41:LEU:HD11	33:BM:121:VAL:HG13	1.96	0.48
34:B5:811:A:O3'	34:B5:858:G:N2	2.46	0.48
36:AB:72:VAL:HG23	58:AV:88:ARG:HB3	1.94	0.48
38:A1:68:C:N4	38:A1:314:U:O2'	2.46	0.48
38:A1:1493:G:O6	74:Al:2:ALA:N	2.47	0.48
41:AD:160:PHE:HA	41:AD:163:LEU:HB3	1.95	0.48
56:AT:49:GLN:HA	56:AT:52:MET:HE3	1.94	0.48
5:BG:19:ASP:OD1	5:BG:19:ASP:N	2.45	0.48
22:BP:22:LEU:HA	22:BP:25:LEU:HB2	1.95	0.48
34:B5:467:G:O2'	34:B5:469:C:OP2	2.30	0.48
34:B5:774:A:N1	34:B5:786:C:N3	2.61	0.48
34:B5:1359:C:H2'	34:B5:1360:A:C8	2.49	0.48
38:A1:86:G:O2'	38:A1:98:G:O6	2.28	0.48
38:A1:394:G:N1	38:A1:397:A:OP2	2.41	0.48
38:A1:578:A:N6	43:AF:141:TYR:OH	2.45	0.48
38:A1:1114:U:OP1	63:Aa:23:GLY:N	2.39	0.48
82:DC:27:HIS:O	82:DC:32:LYS:NZ	2.41	0.48
1:BA:121:VAL:HG13	1:BA:141:ILE:HG21	1.96	0.48
1:BA:179:ARG:HH22	1:BA:191:ARG:HG2	1.79	0.48
4:BE:181:VAL:HG12	4:BE:227:VAL:HG22	1.96	0.48
8:BJ:40:LYS:HE3	34:B5:474:A:H62	1.77	0.48
27:BU:61:LYS:NZ	34:B5:1516:A:OP2	2.38	0.48
36:AB:187:SER:OG	36:AB:190:GLU:OE1	2.30	0.48
37:AC:156:LEU:HD12	37:AC:159:ILE:HD12	1.95	0.48
37:AC:196:ASN:ND2	61:AY:11:ASP:OD1	2.47	0.48
38:A1:406:G:OP1	38:A1:1415:U:O2'	2.30	0.48
38:A1:2127:U:O2'	38:A1:2301:U:OP1	2.32	0.48
38:A1:3353:G:O2'	38:A1:3356:G:OP2	2.32	0.48
53:AQ:170:ARG:HD2	63:Aa:57:GLY:HA3	1.95	0.48
8:BJ:6:ARG:HD3	34:B5:39:A:H5'	1.96	0.48
8:BJ:107:ARG:NH1	8:BJ:153:GLU:OE2	2.42	0.48
9:BL:77:SER:OG	34:B5:347:G:OP1	2.32	0.48
17:Bb:36:LYS:HB3	17:Bb:80:ARG:HH12	1.79	0.48
17:Bb:51:GLN:NE2	34:B5:957:G:H21	2.12	0.48
20:BF:58:LEU:HD12	20:BF:138:THR:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BP:8:LYS:HG2	47:AJ:90:GLN:HE22	1.77	0.48
25:BS:70:VAL:HA	25:BS:73:MET:HE2	1.95	0.48
34:B5:391:A:H4'	34:B5:1730:A:H4'	1.96	0.48
37:AC:322:GLN:HB2	38:A1:608:A:H5'	1.95	0.48
38:A1:591:G:N2	38:A1:612:U:OP1	2.38	0.48
38:A1:1677:G:O6	38:A1:1691:U:O4	2.31	0.48
43:AF:120:THR:H	43:AF:123:THR:HG1	1.60	0.48
43:AF:224:ILE:HA	55:AS:36:ILE:HG13	1.95	0.48
45:AH:99:ILE:HG21	45:AH:179:ILE:HD11	1.96	0.48
45:AH:115:ARG:HG2	45:AH:123:ILE:HG22	1.96	0.48
47:AJ:88:GLU:HB2	47:AJ:90:GLN:HE21	1.77	0.48
49:AM:38:ILE:O	55:AS:95:ARG:NH2	2.46	0.48
60:AX:108:LEU:HD23	60:AX:125:ARG:HE	1.78	0.48
82:DC:101:ASN:HD22	82:DC:453:ILE:HB	1.79	0.48
2:BB:100:PHE:HB3	2:BB:181:LEU:HD21	1.96	0.48
16:Ba:37:LYS:O	16:Ba:38:ARG:NH1	2.46	0.48
20:BF:72:HIS:NE2	34:B5:1610:G:OP1	2.47	0.48
34:B5:1196:A:OP2	34:B5:1464:G:N2	2.40	0.48
38:A1:581:U:H2'	38:A1:582:G:H8	1.79	0.48
38:A1:1717:U:H2'	38:A1:1718:G:C8	2.47	0.48
38:A1:1829:G:H5''	38:A1:1830:G:H5'	1.96	0.48
38:A1:2472:U:H2'	38:A1:2473:C:H4'	1.95	0.48
4:BE:188:ASN:HD21	34:B5:752:A:H5''	1.79	0.48
16:Ba:32:LYS:NZ	34:B5:932:U:O2	2.45	0.48
34:B5:1068:C:H2'	34:B5:1069:A:H8	1.79	0.48
38:A1:1054:A:H5''	38:A1:2637:A:H61	1.78	0.48
38:A1:2440:G:H2'	38:A1:2441:A:H2	1.79	0.48
58:AV:104:ASN:HD21	58:AV:108:GLU:HB2	1.79	0.48
68:Af:13:HIS:O	68:Af:95:GLY:N	2.45	0.48
72:Aj:29:VAL:O	72:Aj:32:LYS:NZ	2.42	0.48
8:BJ:78:ARG:NH2	34:B5:764:U:OP2	2.47	0.47
10:BN:94:LYS:HD2	34:B5:952:A:H5''	1.96	0.47
34:B5:1209:C:N3	34:B5:1455:G:N2	2.62	0.47
34:B5:1220:C:H2'	34:B5:1221:A:H8	1.78	0.47
34:B5:1502:G:N2	34:B5:1505:A:OP2	2.43	0.47
36:AB:289:ASP:N	36:AB:289:ASP:OD1	2.46	0.47
38:A1:612:U:H4'	42:AE:21:THR:HG21	1.95	0.47
38:A1:745:C:H2'	38:A1:746:A:H8	1.79	0.47
47:AJ:13:LYS:HE3	47:AJ:134:PRO:HD3	1.96	0.47
50:AN:113:LEU:HB2	50:AN:134:LEU:HD23	1.96	0.47
52:AP:16:SER:O	52:AP:101:ASN:ND2	2.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Af:16:TYR:OH	68:Af:89:LEU:O	2.26	0.47
70:Ah:55:LEU:HA	70:Ah:58:ILE:HB	1.95	0.47
82:DC:18:ASN:ND2	82:DC:93:THR:OG1	2.47	0.47
2:BB:87:ARG:NH1	2:BB:89:ASP:OD1	2.47	0.47
4:BE:79:ASP:HB3	4:BE:82:TYR:HB2	1.95	0.47
8:BJ:77:ILE:HD12	8:BJ:80:LEU:HD11	1.95	0.47
11:BO:136:ARG:O	34:B5:1006:C:O2'	2.33	0.47
13:BW:8:ALA:HA	13:BW:74:VAL:HG11	1.96	0.47
21:BK:36:ASP:OD1	21:BK:36:ASP:N	2.47	0.47
38:A1:1843:C:OP1	74:A1:48:LYS:NZ	2.42	0.47
38:A1:1899:G:O2'	38:A1:2334:U:O4	2.30	0.47
38:A1:3016:A:H2'	38:A1:3017:A:H8	1.79	0.47
38:A1:3039:C:O2'	58:AV:10:LYS:O	2.32	0.47
41:AD:41:LYS:HD2	56:AT:93:VAL:HG11	1.96	0.47
50:AN:98:LEU:HD12	50:AN:128:LYS:HD2	1.94	0.47
66:Ad:75:ILE:HG23	66:Ad:93:VAL:HG22	1.96	0.47
68:Af:14:LEU:HD11	68:Af:31:LYS:HB2	1.97	0.47
82:DC:167:LEU:HB3	82:DC:169:VAL:HG13	1.96	0.47
3:BC:201:ASN:ND2	34:B5:1097:U:O4	2.47	0.47
34:B5:1760:G:H1'	34:B5:1781:MA6:H2	1.96	0.47
38:A1:110:G:OP2	48:AL:73:ARG:NH2	2.43	0.47
38:A1:364:G:OP2	72:Aj:52:LYS:NZ	2.40	0.47
38:A1:1160:C:O2	67:Ae:45:ARG:NH1	2.47	0.47
38:A1:2523:A:H5''	44:AG:51:LYS:HB2	1.95	0.47
62:AZ:88:ASP:OD1	62:AZ:88:ASP:N	2.46	0.47
20:BF:111:VAL:HA	20:BF:114:ILE:HG22	1.97	0.47
34:B5:1747:G:HO2'	38:A1:2303:A:HO2'	1.60	0.47
35:AA:220:GLY:O	38:A1:2245:C:O2'	2.33	0.47
38:A1:876:A:H5''	38:A1:1890:U:H5''	1.96	0.47
38:A1:1719:G:OP1	54:AR:110:ARG:NH1	2.48	0.47
38:A1:3266:G:OP2	42:AE:70:LYS:NZ	2.46	0.47
56:AT:68:THR:HG22	56:AT:69:LYS:H	1.78	0.47
66:Ad:72:ARG:HG3	66:Ad:96:VAL:HB	1.95	0.47
80:E:6:SER:HB3	80:E:10:ARG:HH21	1.79	0.47
3:BC:143:TYR:OH	3:BC:149:GLY:O	2.32	0.47
7:BI:24:LYS:NZ	34:B5:391:A:OP1	2.42	0.47
8:BJ:69:ARG:HH21	8:BJ:93:LEU:HD12	1.80	0.47
19:BD:210:GLU:OE2	24:BR:19:ARG:NH2	2.48	0.47
34:B5:115:G:H22	34:B5:302:PSU:H1'	1.79	0.47
34:B5:623:A:N6	34:B5:1104:U:O2'	2.48	0.47
38:A1:650:C:H2'	38:A1:651:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1458:U:O2	66:Ad:56:ASN:ND2	2.48	0.47
38:A1:1785:U:H2'	38:A1:1786:G:C8	2.49	0.47
39:A3:7:G:OP1	41:AD:33:ARG:NH1	2.47	0.47
39:A3:63:A:O2'	39:A3:65:G:O4'	2.32	0.47
47:AJ:45:PRO:HB3	47:AJ:69:VAL:HB	1.96	0.47
82:DC:215:LEU:HD12	84:DC:901:GDP:H2'	1.97	0.47
82:DC:495:VAL:HG11	82:DC:501:LEU:HA	1.95	0.47
82:DC:718:LEU:HD23	82:DC:722:PRO:HG3	1.96	0.47
3:BC:40:LYS:HG2	3:BC:248:SER:HB3	1.95	0.47
5:BG:188:ARG:NH1	34:B5:285:G:OP2	2.37	0.47
8:BJ:110:GLN:NE2	8:BJ:122:VAL:O	2.47	0.47
9:BL:110:HIS:NE2	34:B5:326:G:OP1	2.42	0.47
14:BX:70:LYS:HZ3	34:B5:567:A:H5''	1.79	0.47
34:B5:1035:G:H2'	34:B5:1036:A:H8	1.80	0.47
36:AB:15:GLY:O	38:A1:3009:G:N2	2.41	0.47
39:A3:48:U:H1'	41:AD:222:LEU:HD22	1.97	0.47
40:A4:95:G:O2'	72:Aj:81:GLY:O	2.32	0.47
48:AL:7:LEU:O	63:Aa:49:HIS:NE2	2.41	0.47
51:AO:113[A]:ASP:OD1	51:AO:113[A]:ASP:N	2.47	0.47
82:DC:709:MET:SD	82:DC:713:THR:OG1	2.73	0.47
4:BE:104:ASP:OD1	4:BE:108:ARG:N	2.44	0.47
11:BO:17:ALA:HB3	11:BO:81:VAL:HA	1.95	0.47
30:Bd:10:HIS:NE2	34:B5:1204:A:N3	2.62	0.47
32:Bf:92:LYS:NZ	34:B5:1215:C:OP2	2.39	0.47
34:B5:65:A:H61	34:B5:83:G:H2'	1.79	0.47
34:B5:564:G:N1	34:B5:579:A:OP1	2.47	0.47
36:AB:11:HIS:NE2	38:A1:2881:C:OP1	2.44	0.47
37:AC:303:GLY:H	38:A1:1347:U:H5''	1.80	0.47
38:A1:38:U:H4'	63:Aa:32:ARG:HD2	1.96	0.47
38:A1:289:A:H2'	38:A1:290:G:H8	1.79	0.47
38:A1:1411:C:H2'	38:A1:1412:G:H8	1.78	0.47
38:A1:1497:C:H2'	38:A1:1498:A:C8	2.50	0.47
38:A1:1504:A:N1	38:A1:1515:A:O2'	2.42	0.47
38:A1:2465:G:H2'	38:A1:2466:G:H8	1.80	0.47
38:A1:3086:A:H3'	38:A1:3087:A:H8	1.78	0.47
43:AF:77:VAL:HB	56:AT:139:ARG:HG2	1.97	0.47
45:AH:22:SER:OG	45:AH:23:ARG:N	2.46	0.47
61:AY:125:LYS:NZ	61:AY:127:GLU:OE1	2.45	0.47
64:Ab:47:LEU:HA	64:Ab:50:THR:HG22	1.97	0.47
19:BD:8:LYS:HE3	27:BU:61:LYS:HD3	1.97	0.47
19:BD:66:ILE:HD12	19:BD:69:LEU:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BT:83:ALA:HB2	34:B5:1525:A:H4'	1.97	0.47
31:Bg:242:SER:H	31:Bg:255:ALA:HB3	1.79	0.47
34:B5:1294:G:O2'	34:B5:1321:A:N1	2.45	0.47
34:B5:1466:G:O2'	34:B5:1602:C:OP1	2.29	0.47
37:AC:321:LYS:HD3	37:AC:324:LEU:HD23	1.96	0.47
38:A1:26:A:N3	38:A1:328:U:O2'	2.45	0.47
38:A1:96:G:H4'	48:AL:15:ARG:HH11	1.80	0.47
38:A1:98:G:OP1	48:AL:16:LYS:NZ	2.45	0.47
38:A1:1601:U:OP1	54:AR:42:ARG:NH2	2.48	0.47
38:A1:2484:A:H5'	79:tE:57:C:H1'	1.97	0.47
38:A1:2559:U:OP1	44:AG:32:LYS:NZ	2.47	0.47
39:A3:28:C:H5''	47:AJ:137:ARG:HB3	1.95	0.47
40:A4:45:C:H4'	74:Al:11:GLN:HG3	1.97	0.47
42:AE:76:LEU:N	42:AE:138:GLN:OE1	2.47	0.47
46:AI:77:THR:HG21	46:AI:82:ARG:HH21	1.80	0.47
77:Ao:25:VAL:HG13	77:Ao:70:LEU:HB3	1.95	0.47
82:DC:799:ASP:N	82:DC:799:ASP:OD1	2.47	0.47
2:BB:98:THR:O	2:BB:232:HIS:NE2	2.42	0.47
5:BG:212:LEU:HD22	5:BG:215:ARG:HH21	1.79	0.47
6:BH:30:SER:O	6:BH:34:LEU:N	2.45	0.47
13:BW:56:HIS:O	34:B5:861:U:O2'	2.31	0.47
13:BW:112:ASP:OD1	13:BW:112:ASP:N	2.48	0.47
35:AA:142:ASP:OD1	35:AA:142:ASP:N	2.48	0.47
38:A1:122:A:O2'	38:A1:145:G:N2	2.46	0.47
38:A1:188:U:OP2	61:AY:46:LYS:NZ	2.45	0.47
38:A1:655:C:H5''	67:Ae:26:HIS:HB3	1.96	0.47
38:A1:996:A:N3	39:A3:80:G:O2'	2.48	0.47
38:A1:2106:A:H2'	38:A1:2107:A:H8	1.79	0.47
38:A1:2786:G:N2	63:Aa:58:MET:SD	2.85	0.47
38:A1:2901:G:O2'	38:A1:3024:A:N1	2.44	0.47
49:AM:121:MET:HE2	49:AM:125:LYS:HD2	1.97	0.47
2:BB:123:ALA:HB3	2:BB:139:ALA:HB3	1.96	0.47
15:BY:88:THR:HA	15:BY:91:LEU:HD12	1.97	0.47
19:BD:8:LYS:NZ	34:B5:1487:A:OP2	2.41	0.47
19:BD:64:ARG:NH2	21:BK:91:TYR:O	2.48	0.47
22:BP:57:MET:HA	22:BP:60:LEU:HD12	1.95	0.47
34:B5:97:C:O2	34:B5:425:A:O2'	2.33	0.47
34:B5:1474:G:H2'	34:B5:1475:A:H8	1.80	0.47
37:AC:3:ARG:HE	37:AC:22:LEU:HB2	1.80	0.47
38:A1:198:A:N3	38:A1:218:G:O2'	2.46	0.47
38:A1:768:C:OP1	48:AL:186:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2383:C:OP2	51:AO:85[A]:ARG:NH2	2.48	0.47
44:AG:144:GLU:OE2	50:AN:6:TYR:OH	2.28	0.47
52:AP:11:PRO:HA	52:AP:14:SER:HB2	1.97	0.47
60:AX:86:VAL:HG21	60:AX:95:ILE:HD11	1.97	0.47
70:Ah:84:LYS:O	72:Aj:73:ARG:NH2	2.48	0.47
2:BB:43:VAL:HG22	2:BB:73:LEU:HD11	1.97	0.46
20:BF:189:THR:HB	20:BF:192:GLU:HG3	1.96	0.46
25:BS:81:ILE:HG22	25:BS:83:ALA:H	1.81	0.46
34:B5:32:U:O2'	34:B5:594:A:N6	2.47	0.46
34:B5:953:G:H2'	34:B5:954:G:C8	2.50	0.46
34:B5:1641:C:H2'	34:B5:1642:G:C8	2.50	0.46
35:AA:8:GLN:HA	38:A1:2163:C:H4'	1.97	0.46
38:A1:212:G:OP2	61:AY:2:ALA:N	2.48	0.46
38:A1:1747:G:H21	73:Ak:2:ALA:HB3	1.79	0.46
38:A1:3288:G:O2'	38:A1:3289:G:O5'	2.33	0.46
50:AN:183:THR:O	50:AN:183:THR:OG1	2.34	0.46
1:BA:41:ARG:NH1	24:BR:125:SER:O	2.49	0.46
7:BI:44:HIS:HB3	7:BI:56:ARG:HB2	1.96	0.46
8:BJ:39:LYS:HE2	34:B5:592:A:H5''	1.98	0.46
25:BS:14:ILE:HD11	25:BS:21:ASN:HB3	1.96	0.46
31:Bg:19:TRP:HB2	31:Bg:38:ARG:HB2	1.97	0.46
31:Bg:109:ASP:HB2	31:Bg:127:ARG:HD2	1.97	0.46
36:AB:94:GLU:HG3	51:AO:152[A]:VAL:HG21	1.96	0.46
38:A1:831:G:O2'	38:A1:1864:A:N3	2.37	0.46
38:A1:2428:U:H2'	38:A1:2429:G:H8	1.80	0.46
43:AF:77:VAL:HG22	55:AS:59:VAL:HA	1.98	0.46
45:AH:23:ARG:NH1	45:AH:39:LYS:O	2.49	0.46
45:AH:107:ASP:OD1	45:AH:107:ASP:N	2.47	0.46
46:AI:52:LEU:HB3	46:AI:136:PHE:HB2	1.97	0.46
62:AZ:25:ILE:HA	62:AZ:43:VAL:HG12	1.96	0.46
68:Af:32:ILE:HG23	68:Af:100:ILE:HD13	1.97	0.46
82:DC:785:ARG:O	82:DC:790:GLY:N	2.43	0.46
4:BE:45:ILE:HG13	4:BE:61:VAL:HG21	1.96	0.46
5:BG:160:ARG:HG2	5:BG:162:VAL:HG13	1.95	0.46
7:BI:73:SER:N	34:B5:256:A:O2'	2.48	0.46
9:BL:55:ASP:HB2	9:BL:82:ARG:HH21	1.80	0.46
10:BN:37:ILE:HD11	10:BN:54:LEU:HD11	1.96	0.46
11:BO:48:VAL:HG21	11:BO:53:ASP:HB2	1.98	0.46
14:BX:63:GLN:HG3	34:B5:1755:A:H3'	1.97	0.46
23:BQ:143:ARG:NH1	79:tE:33:C:OP2	2.49	0.46
34:B5:1178:G:H5'	34:B5:1190:C:H42	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1271:G:O2'	82:DC:654:GLN:OE1	2.32	0.46
34:B5:1431:C:O2'	34:B5:1437:U:O4	2.32	0.46
38:A1:2104:A:OP2	54:AR:81:ARG:NH2	2.49	0.46
38:A1:2282:U:OP1	38:A1:2973:G:O2'	2.33	0.46
48:AL:126:PHE:HD2	70:Ah:115:LYS:HE2	1.80	0.46
58:AV:104:ASN:ND2	58:AV:108:GLU:O	2.49	0.46
63:Aa:139:ARG:HH12	63:Aa:144:VAL:HG23	1.81	0.46
71:Ai:59:ASP:HA	71:Ai:62:ARG:HG2	1.97	0.46
82:DC:585:ARG:HH22	82:DC:842:LEU:HG	1.80	0.46
2:BB:171:ILE:HA	2:BB:174:LYS:HG2	1.97	0.46
34:B5:408:C:O2'	34:B5:1732:A:O2'	2.25	0.46
36:AB:292:ALA:HB2	36:AB:302:LYS:HD3	1.97	0.46
38:A1:105:C:H2'	38:A1:106:A:H8	1.80	0.46
38:A1:875:G:O2'	38:A1:1891:A:OP1	2.33	0.46
38:A1:2413:A:H2'	38:A1:2414:G:H8	1.79	0.46
38:A1:3182:G:H4'	51:AO:161[A]:LYS:HG2	1.97	0.46
40:A4:70:G:O2'	40:A4:87:G:N2	2.48	0.46
41:AD:234:ASP:OD1	41:AD:234:ASP:N	2.49	0.46
48:AL:174:ARG:HB2	71:Ai:9:ILE:HD12	1.97	0.46
50:AN:136:ASP:HB3	50:AN:139:HIS:HB2	1.98	0.46
69:Ag:54:ILE:HD11	69:Ag:78:GLY:HA2	1.96	0.46
82:DC:75:ILE:HG13	82:DC:102:LEU:HB3	1.96	0.46
22:BP:26:LEU:HD12	22:BP:27:GLU:HB3	1.98	0.46
37:AC:315:LYS:HA	38:A1:505:G:H5''	1.96	0.46
38:A1:786:A:H4'	38:A1:787:G:H5'	1.97	0.46
47:AJ:53:THR:HB	81:C5:46:SER:HA	1.98	0.46
50:AN:51:LEU:HD13	50:AN:117:ASN:HB3	1.98	0.46
55:AS:154:HIS:HA	55:AS:170:THR:HG22	1.97	0.46
66:Ad:6:ASP:N	66:Ad:6:ASP:OD1	2.46	0.46
70:Ah:73:LYS:O	70:Ah:76:GLN:NE2	2.49	0.46
34:B5:32:U:H3	34:B5:468:A:N6	2.04	0.46
34:B5:590:C:H2'	34:B5:591:A:C8	2.51	0.46
34:B5:1171:A:H2'	34:B5:1172:G:H8	1.80	0.46
38:A1:87:U:H2'	38:A1:88:A:C8	2.50	0.46
38:A1:307:A:H2'	38:A1:308:A:C8	2.50	0.46
38:A1:975:C:O3'	53:AQ:144:ARG:NH1	2.49	0.46
38:A1:1770:G:OP1	73:Ak:29:LYS:NZ	2.49	0.46
38:A1:2697:A:H2'	38:A1:2698:G:C8	2.50	0.46
38:A1:3116:G:OP1	38:A1:3116:G:N2	2.49	0.46
38:A1:3308:C:O2'	52:AP:69:ARG:O	2.33	0.46
41:AD:261:THR:OG1	41:AD:262:LYS:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AN:84:PRO:HA	50:AN:87:GLN:HG3	1.98	0.46
58:AV:19:VAL:HB	58:AV:49:LEU:HD22	1.97	0.46
80:E:105:LYS:HG3	80:E:106:LYS:HD3	1.98	0.46
2:BB:128:LYS:HA	2:BB:134:VAL:HA	1.98	0.46
4:BE:137:PRO:HG3	5:BG:208:TYR:CZ	2.51	0.46
11:BO:130:GLY:HA2	11:BO:135:ARG:HH12	1.80	0.46
22:BP:103:ASN:HD21	22:BP:120:SER:HA	1.81	0.46
34:B5:947:U:H2'	34:B5:948:G:H8	1.81	0.46
34:B5:1591:C:H2'	34:B5:1592:A:H8	1.81	0.46
38:A1:21:G:OP2	70:Ah:86:ARG:NH2	2.49	0.46
38:A1:377:A:N6	38:A1:400:G:O2'	2.49	0.46
38:A1:2344:U:H2'	38:A1:2345:A:C8	2.51	0.46
45:AH:135:GLU:HB2	45:AH:145:VAL:HB	1.98	0.46
55:AS:93:GLU:HG2	55:AS:135:VAL:HG13	1.98	0.46
56:AT:66:ASN:ND2	56:AT:68:THR:OG1	2.48	0.46
34:B5:816:G:OP2	54:AR:166:ASN:ND2	2.49	0.46
36:AB:238:LEU:HD21	36:AB:250:ALA:HB2	1.97	0.46
38:A1:1084:A:H5''	56:AT:35:LYS:HE3	1.96	0.46
38:A1:1266:G:N2	38:A1:1276:U:O2	2.48	0.46
38:A1:1475:A:H4'	66:Ad:57:GLN:HE22	1.80	0.46
38:A1:2630:C:N4	56:AT:2:GLY:O	2.48	0.46
48:AL:49:ARG:O	48:AL:137:GLN:NE2	2.48	0.46
55:AS:22:PRO:O	56:AT:146:ASN:ND2	2.45	0.46
4:BE:15:PRO:HG3	4:BE:39:ARG:HA	1.98	0.46
16:Ba:51:ARG:HD3	29:Bc:61:ARG:HB2	1.98	0.46
21:BK:8:ARG:NH2	34:B5:1257:U:O2'	2.39	0.46
22:BP:89:MET:HG3	22:BP:107:ILE:HG21	1.96	0.46
23:BQ:16:ALA:HB2	23:BQ:72:GLY:HA3	1.98	0.46
34:B5:1041:G:H2'	34:B5:1042:G:C8	2.50	0.46
34:B5:1114:G:O2'	34:B5:1130:G:O6	2.31	0.46
38:A1:158:G:H2'	38:A1:159:A:C8	2.49	0.46
38:A1:627:U:H4'	38:A1:1399:A:H1'	1.97	0.46
38:A1:1571:A:N6	38:A1:1573:G:O5'	2.49	0.46
69:Ag:16:ARG:HA	69:Ag:19:LYS:HE2	1.97	0.46
2:BB:120:LEU:HD22	34:B5:931:C:H1'	1.98	0.46
4:BE:22:LYS:HZ3	8:BJ:6:ARG:HG2	1.81	0.46
20:BF:102:ARG:HH21	34:B5:1474:G:H5'	1.81	0.46
23:BQ:47:LYS:HD2	23:BQ:47:LYS:HA	1.78	0.46
24:BR:29:GLN:HG3	31:Bg:38:ARG:HD3	1.98	0.46
25:BS:76:PRO:HB2	25:BS:81:ILE:HG13	1.97	0.46
34:B5:29:U:H2'	34:B5:30:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:830:U:H1'	34:B5:831:U:H5	1.81	0.46
34:B5:1171:A:H2'	34:B5:1172:G:C8	2.51	0.46
34:B5:1576:A:O2'	79:tE:41:C:O2	2.34	0.46
38:A1:597:G:H2'	38:A1:598:A:C8	2.49	0.46
38:A1:1146:C:H5''	67:Ae:47:ARG:HB2	1.98	0.46
38:A1:1448:U:OP1	52:AP:82:ARG:NH2	2.49	0.46
38:A1:2441:A:H62	38:A1:2506:U:H3	1.61	0.46
40:A4:13:A:O2'	52:AP:121:GLN:O	2.32	0.46
44:AG:99:PRO:HB3	44:AG:131:ALA:HB1	1.98	0.46
46:AI:54:SER:HB2	46:AI:135:ILE:HD11	1.98	0.46
80:E:48:ARG:HH12	80:E:160:LYS:HA	1.80	0.46
82:DC:696:ASP:OD1	82:DC:696:ASP:N	2.49	0.46
4:BE:11:ARG:NH1	4:BE:21:ASP:O	2.49	0.45
5:BG:134:GLY:HA3	5:BG:158:ILE:HD12	1.99	0.45
6:BH:113:PRO:HG2	6:BH:116:ARG:HD3	1.98	0.45
7:BI:78:ILE:HA	7:BI:104:ILE:HG23	1.97	0.45
8:BJ:20:GLU:OE2	8:BJ:22:SER:OG	2.34	0.45
13:BW:3:ARG:NH1	34:B5:865:A:OP1	2.35	0.45
25:BS:39:GLY:H	34:B5:1566:U:H5''	1.81	0.45
34:B5:1477:G:H2'	34:B5:1478:G:C8	2.51	0.45
35:AA:219:ILE:HD11	38:A1:2185:G:H5'	1.98	0.45
38:A1:19:U:H2'	38:A1:20:A:C8	2.51	0.45
38:A1:1119:C:H2'	38:A1:1120:A:H8	1.80	0.45
38:A1:3358:U:H2'	38:A1:3359:A:H8	1.80	0.45
43:AF:88:ARG:HB2	43:AF:108:LEU:HB3	1.98	0.45
51:AO:22[A]:VAL:HG21	51:AO:120[A]:VAL:HG11	1.97	0.45
3:BC:78:ASP:OD1	3:BC:78:ASP:N	2.49	0.45
10:BN:73:ARG:NH1	34:B5:859:A:O2'	2.50	0.45
20:BF:148:ARG:NH2	34:B5:1162:C:O3'	2.49	0.45
31:Bg:255:ALA:HB2	31:Bg:292:LEU:HD23	1.98	0.45
34:B5:1474:G:H2'	34:B5:1475:A:C8	2.51	0.45
35:AA:83:HIS:HB3	78:Ap:64:VAL:HG12	1.98	0.45
36:AB:103:THR:HG21	36:AB:147:GLU:HG3	1.98	0.45
37:AC:92:ASN:OD1	37:AC:92:ASN:N	2.49	0.45
38:A1:631:U:H2'	38:A1:632:G:C8	2.51	0.45
38:A1:1261:G:H5''	38:A1:1262:G:C8	2.51	0.45
38:A1:2218:G:H2'	38:A1:2219:A:H8	1.81	0.45
41:AD:150:LEU:HD12	47:AJ:142:LYS:HE2	1.98	0.45
55:AS:23:LYS:HA	55:AS:23:LYS:HD2	1.81	0.45
62:AZ:23:VAL:HG12	62:AZ:45:GLY:HA3	1.97	0.45
69:Ag:101:VAL:HA	69:Ag:104:VAL:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:128:LYS:NZ	4:BE:129:VAL:O	2.49	0.45
7:BI:50:GLY:HA2	34:B5:397:A:H4'	1.99	0.45
7:BI:84:HIS:CD2	7:BI:100:ALA:HB2	2.51	0.45
8:BJ:113:VAL:HG21	8:BJ:134:ILE:HD13	1.98	0.45
9:BL:63:LEU:O	9:BL:129:ARG:NH1	2.47	0.45
11:BO:129:LYS:HG3	11:BO:135:ARG:HH22	1.80	0.45
12:BV:80:LYS:HD3	24:BR:113:LEU:HB2	1.98	0.45
20:BF:159:ALA:O	20:BF:225:ARG:NH2	2.49	0.45
25:BS:45:LEU:HD21	25:BS:81:ILE:HD11	1.98	0.45
35:AA:180:LEU:HD22	78:Ap:26:VAL:HG11	1.99	0.45
37:AC:126:ILE:HD11	37:AC:233:LEU:HG	1.98	0.45
38:A1:408:A:N3	38:A1:655:C:O2'	2.45	0.45
38:A1:656:A:H2'	38:A1:657:A:C8	2.52	0.45
38:A1:2514:U:OP2	38:A1:2586:G:N2	2.50	0.45
51:AO:46[A]:GLU:HG3	51:AO:134[A]:LYS:HD2	1.98	0.45
4:BE:128:LYS:HD2	4:BE:128:LYS:HA	1.78	0.45
9:BL:96:LYS:NZ	34:B5:610:G:OP2	2.45	0.45
15:BY:132:ARG:NH1	34:B5:154:G:OP2	2.42	0.45
22:BP:35:LYS:HG3	22:BP:36:LEU:HD12	1.99	0.45
34:B5:382:C:H2'	34:B5:383:G:H8	1.82	0.45
34:B5:632:PSU:O2'	34:B5:1103:U:OP1	2.31	0.45
34:B5:1488:G:H3'	34:B5:1515:A:H61	1.81	0.45
36:AB:232:ARG:HA	36:AB:270:ARG:HD3	1.98	0.45
40:A4:103:G:OP2	40:A4:105:A:O2'	2.26	0.45
82:DC:240:MET:HE2	82:DC:244:LEU:HD21	1.97	0.45
1:BA:112:THR:HG22	1:BA:114:SER:H	1.82	0.45
2:BB:90:GLU:HG2	2:BB:97:LEU:HD21	1.98	0.45
5:BG:77:LEU:HD13	5:BG:84:TYR:HB2	1.98	0.45
11:BO:68:ALA:HA	11:BO:71:CYS:HB2	1.98	0.45
13:BW:81:VAL:HG21	13:BW:125:ILE:HG13	1.99	0.45
34:B5:1592:A:H2'	34:B5:1593:A:H8	1.80	0.45
34:B5:1776:A:H2'	34:B5:1777:G:C8	2.52	0.45
35:AA:38:HIS:NE2	38:A1:2526:C:OP2	2.49	0.45
37:AC:101:ALA:HA	38:A1:800:G:H22	1.81	0.45
37:AC:154:THR:OG1	37:AC:252:GLU:OE1	2.33	0.45
38:A1:114:A:OP1	50:AN:54:LYS:NZ	2.49	0.45
38:A1:219:A:HO2'	38:A1:220:G:H21	1.64	0.45
38:A1:337:G:H1	40:A4:26:U:H3	1.64	0.45
38:A1:1448:U:H2'	38:A1:1449:A:C8	2.51	0.45
38:A1:1729:A:C6	65:Ac:49:PRO:HD3	2.51	0.45
38:A1:2106:A:H2'	38:A1:2107:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3172:A:H1'	51:AO:101[A]:ARG:HH21	1.82	0.45
39:A3:72:A:O2'	39:A3:74:C:OP1	2.30	0.45
52:AP:10:ASN:HB3	52:AP:13:LYS:HG2	1.98	0.45
55:AS:77:VAL:HG13	55:AS:126:VAL:HG22	1.99	0.45
69:Ag:73:SER:O	69:Ag:73:SER:OG	2.35	0.45
80:E:178:VAL:O	80:E:182:GLN:N	2.50	0.45
2:BB:103:MET:HE3	2:BB:103:MET:HB3	1.90	0.45
3:BC:84:LYS:NZ	34:B5:12:U:OP1	2.50	0.45
3:BC:205:ARG:NH1	34:B5:7:G:O6	2.50	0.45
10:BN:2:GLY:N	34:B5:1035:G:OP1	2.49	0.45
14:BX:69:ARG:HG3	14:BX:117:ILE:HG22	1.97	0.45
20:BF:91:GLU:OE2	20:BF:107:LYS:NZ	2.41	0.45
34:B5:629:U:OP2	34:B5:969:C:N4	2.41	0.45
38:A1:69:C:OP1	50:AN:178:HIS:ND1	2.35	0.45
38:A1:341:G:O2'	40:A4:22:U:O4	2.31	0.45
38:A1:1010:G:H22	38:A1:1040:A:H2	1.63	0.45
38:A1:1102:A:OP2	43:AF:200:ASN:ND2	2.41	0.45
38:A1:1157:G:O2'	38:A1:1169:A:N3	2.49	0.45
38:A1:1655:G:OP1	69:Ag:40:THR:OG1	2.33	0.45
38:A1:3163:A:N6	38:A1:3288:G:O6	2.50	0.45
38:A1:3183:A:H2	38:A1:3188:G:H4'	1.81	0.45
70:Ah:76:GLN:O	70:Ah:81:ARG:NH2	2.46	0.45
82:DC:586:ILE:HG12	82:DC:691:VAL:HG12	1.98	0.45
6:BH:71:HIS:HA	6:BH:74:GLN:HB2	1.98	0.45
33:BM:52:LEU:HD22	33:BM:78:LEU:HD23	1.97	0.45
34:B5:250:C:H2'	34:B5:251:A:C8	2.51	0.45
34:B5:486:G:N1	34:B5:501:U:N3	2.59	0.45
34:B5:1000:C:N4	34:B5:1003:A:OP2	2.50	0.45
34:B5:1353:U:H3	34:B5:1363:U:HO2'	1.62	0.45
34:B5:1441:C:O2'	82:DC:651:LYS:O	2.26	0.45
37:AC:326:ARG:NH2	38:A1:608:A:O3'	2.50	0.45
38:A1:821:U:H2'	38:A1:822:G:H8	1.81	0.45
38:A1:2673:A:H5''	47:AJ:95:ASN:HD22	1.81	0.45
39:A3:109:G:H5''	41:AD:279:LYS:HD3	1.98	0.45
82:DC:75:ILE:HD11	82:DC:102:LEU:HD23	1.99	0.45
3:BC:81:MET:HB3	3:BC:101:VAL:HG23	1.99	0.45
4:BE:95:THR:HG23	15:BY:16:PRO:HG3	1.99	0.45
6:BH:163:ASP:N	6:BH:163:ASP:OD1	2.48	0.45
9:BL:92:HIS:HB3	9:BL:101:GLU:HB3	1.98	0.45
11:BO:18:ARG:NH1	34:B5:918:U:O3'	2.50	0.45
17:Bb:28:PRO:HB3	34:B5:959:U:H5'	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1339:C:O2'	34:B5:1341:A:N7	2.47	0.45
37:AC:141:ARG:NH2	38:A1:1385:C:OP1	2.49	0.45
38:A1:63:A:H5''	50:AN:174:ILE:HG21	1.98	0.45
38:A1:1696:A:H2'	38:A1:1697:A:C8	2.52	0.45
43:AF:214:TRP:CE2	43:AF:219:LYS:HD2	2.51	0.45
43:AF:228:SER:O	43:AF:232:ARG:NH2	2.49	0.45
51:AO:14[A]:HIS:CE1	51:AO:120[A]:VAL:H	2.34	0.45
57:AU:81:LYS:HA	57:AU:84:LEU:HG	1.98	0.45
61:AY:70:ILE:HD13	61:AY:82:VAL:HG12	1.99	0.45
77:Ao:6:LYS:HG3	77:Ao:94:GLY:HA3	1.98	0.45
82:DC:30:HIS:HB3	82:DC:128:VAL:HG12	1.99	0.45
1:BA:92:HIS:ND1	24:BR:84:TYR:O	2.46	0.45
4:BE:256:ARG:O	4:BE:261:LEU:N	2.46	0.45
26:BT:102:ARG:NH2	34:B5:1502:G:N7	2.61	0.45
31:Bg:244:ALA:HB3	31:Bg:253:ALA:HB3	1.97	0.45
34:B5:686:C:H2'	34:B5:687:G:H8	1.81	0.45
38:A1:631:U:H2'	38:A1:632:G:H8	1.81	0.45
38:A1:1008:U:H2'	38:A1:1009:A:C8	2.52	0.45
4:BE:168:LYS:HD3	4:BE:168:LYS:HA	1.74	0.45
5:BG:137:ARG:HB3	5:BG:177:ARG:HD2	1.98	0.45
8:BJ:139:GLN:NE2	8:BJ:140:ILE:O	2.44	0.45
27:BU:58:LEU:HD22	27:BU:88:LYS:HB2	1.99	0.45
34:B5:394:C:H42	34:B5:401:A:N6	2.06	0.45
38:A1:129:U:H2'	38:A1:130:A:C8	2.52	0.45
38:A1:1102:A:H5''	38:A1:1103:A:H5'	1.98	0.45
38:A1:1783:U:H2'	38:A1:1784:G:C8	2.52	0.45
82:DC:413:ILE:HB	82:DC:427:PHE:HB2	1.98	0.45
82:DC:666:ALA:HB3	82:DC:709:MET:HE3	1.99	0.45
5:BG:136:LYS:NZ	34:B5:167:U:O2'	2.38	0.44
28:BZ:77:ARG:NH1	34:B5:1532:U:OP2	2.50	0.44
34:B5:867:G:H1	34:B5:961:U:H3	1.65	0.44
38:A1:172:G:O2'	38:A1:244:G:O6	2.33	0.44
38:A1:528:U:H2'	38:A1:529:A:C8	2.53	0.44
41:AD:85:ARG:NH2	41:AD:250:ASP:OD2	2.49	0.44
43:AF:121:LYS:HB2	56:AT:133:ALA:HB3	1.98	0.44
49:AM:17:VAL:HG11	49:AM:74:ARG:HA	1.98	0.44
58:AV:101:VAL:HG11	58:AV:114:ILE:HG12	1.97	0.44
65:Ac:40:LYS:HD2	65:Ac:101:LEU:HD13	1.99	0.44
72:Aj:27:PHE:HA	72:Aj:34:CYS:HA	1.99	0.44
79:tE:4:G:H2'	79:tE:5:G:C8	2.52	0.44
82:DC:165:LEU:HD12	82:DC:166:GLU:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:DC:306:VAL:HB	82:DC:326:LYS:HE3	1.99	0.44
82:DC:772:LEU:HD12	82:DC:773:PRO:HD2	1.99	0.44
4:BE:103:TYR:O	4:BE:182:TYR:OH	2.36	0.44
17:Bb:17:ARG:NH2	34:B5:1070:C:O5'	2.50	0.44
26:BT:127:ASN:OD1	26:BT:130:ARG:NH1	2.51	0.44
27:BU:96:PRO:HD2	27:BU:99:ILE:HD11	1.97	0.44
32:Bf:101:ALA:O	32:Bf:104:SER:OG	2.34	0.44
34:B5:657:U:O4	34:B5:676:G:O2'	2.30	0.44
34:B5:1081:A:O2'	34:B5:1083:G:N7	2.38	0.44
36:AB:191:LYS:HE3	36:AB:191:LYS:HB2	1.87	0.44
38:A1:500:C:H2'	38:A1:501:A:H8	1.82	0.44
38:A1:1336:U:H2'	38:A1:1337:A:H8	1.82	0.44
38:A1:1666:G:H2'	38:A1:1667:A:C8	2.52	0.44
38:A1:2433:U:H1'	50:AN:125:SER:HB3	2.00	0.44
54:AR:7:GLN:HG2	54:AR:32:ILE:HG22	2.00	0.44
65:Ac:36:GLN:HB3	65:Ac:38:LYS:HZ2	1.82	0.44
74:A1:10:LYS:HA	74:A1:13:MET:HE2	1.97	0.44
82:DC:756:SER:O	82:DC:756:SER:OG	2.34	0.44
5:BG:174:LYS:HG3	34:B5:78:A:H2	1.82	0.44
9:BL:103:ARG:NH1	34:B5:307:G:OP1	2.51	0.44
10:BN:124:ARG:NH1	34:B5:628:G:OP1	2.42	0.44
14:BX:76:LEU:HD23	14:BX:78:LYS:H	1.82	0.44
19:BD:201:ALA:HB1	19:BD:205:ALA:HB3	1.97	0.44
22:BP:40:ARG:NH1	34:B5:1552:U:O4	2.50	0.44
34:B5:69:G:O6	34:B5:82:U:O2	2.35	0.44
34:B5:406:U:H2'	34:B5:407:A:C8	2.51	0.44
34:B5:1779:U:O4	76:An:12:ARG:NH1	2.43	0.44
35:AA:118:GLU:OE2	38:A1:2177:G:N2	2.48	0.44
37:AC:205:PRO:HG2	37:AC:225:VAL:HG23	1.99	0.44
38:A1:1154:A:OP1	38:A1:1155:C:N4	2.40	0.44
38:A1:2374:C:OP1	38:A1:2823:G:O2'	2.33	0.44
45:AH:90:MET:HE2	45:AH:179:ILE:HG22	1.98	0.44
46:AI:30:LYS:HG3	46:AI:63:GLU:HG3	1.99	0.44
80:E:181:ASN:HB3	80:E:185:MET:HE1	1.99	0.44
1:BA:125:ASP:OD1	1:BA:125:ASP:N	2.48	0.44
5:BG:175:ILE:HG13	5:BG:178:LEU:HD23	1.98	0.44
9:BL:123:VAL:HG23	9:BL:142:VAL:HG22	1.98	0.44
31:Bg:260:ILE:HG12	31:Bg:292:LEU:HD21	1.99	0.44
34:B5:1525:A:H2'	34:B5:1526:A:C8	2.53	0.44
36:AB:49:TYR:O	36:AB:80:ASP:N	2.46	0.44
37:AC:3:ARG:HA	37:AC:3:ARG:HD2	1.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:155:G:N1	38:A1:265:A:OP2	2.37	0.44
38:A1:1194:G:H2'	38:A1:1195:A:C8	2.53	0.44
38:A1:1203:A:OP2	38:A1:1301:A:N6	2.42	0.44
39:A3:23:A:H1'	39:A3:121:U:H3'	1.99	0.44
48:AL:153:ASP:OD1	48:AL:153:ASP:N	2.49	0.44
68:Af:6:ARG:NH1	68:Af:8:TYR:O	2.50	0.44
80:E:44:GLN:HA	80:E:48:ARG:HH21	1.82	0.44
82:DC:758:GLU:OE2	82:DC:767:THR:OG1	2.31	0.44
7:BI:3:ILE:O	7:BI:30:GLY:N	2.51	0.44
22:BP:85:ILE:HG21	22:BP:111:MET:HG2	2.00	0.44
23:BQ:39:VAL:HB	23:BQ:45:ARG:HG3	2.00	0.44
34:B5:1680:G:O2'	34:B5:1720:G:N2	2.42	0.44
35:AA:221:LYS:NZ	38:A1:2418:G:OP1	2.49	0.44
35:AA:227:ARG:NH2	38:A1:2155:G:O3'	2.50	0.44
38:A1:2222:A:H2'	38:A1:2223:A:C8	2.52	0.44
38:A1:2452:G:H2'	38:A1:2462:A:H5'	1.98	0.44
38:A1:2812:C:H2'	38:A1:2813:A:C8	2.53	0.44
40:A4:154:C:H2'	40:A4:155:A:C8	2.52	0.44
58:AV:7:GLN:HB2	58:AV:127:PRO:HG3	1.98	0.44
63:Aa:36:GLY:HA3	63:Aa:40:HIS:CE1	2.53	0.44
82:DC:424:ASP:OD1	82:DC:424:ASP:N	2.51	0.44
82:DC:666:ALA:HB2	82:DC:706:ILE:HD13	1.98	0.44
4:BE:139:VAL:HG13	4:BE:150:PRO:HG3	1.99	0.44
5:BG:57:ASP:HA	5:BG:107:ALA:H	1.81	0.44
8:BJ:45:ILE:HD11	8:BJ:104:PHE:HB3	1.99	0.44
22:BP:118:GLU:O	25:BS:122:HIS:N	2.50	0.44
34:B5:424:C:O2	34:B5:427:C:N4	2.49	0.44
34:B5:1222:C:H2'	34:B5:1223:A:H8	1.83	0.44
36:AB:92:TYR:OH	38:A1:3003:G:O2'	2.33	0.44
38:A1:2111:G:H1'	59:AW:44:LYS:HD2	2.00	0.44
38:A1:3044:G:H2'	38:A1:3045:G:C8	2.52	0.44
43:AF:47:ARG:NH1	43:AF:177:GLY:O	2.47	0.44
54:AR:44:LEU:HB3	54:AR:49:THR:HB	1.99	0.44
55:AS:24:LEU:HD23	56:AT:148:PRO:HG3	2.00	0.44
65:Ac:81:VAL:HG21	65:Ac:90:VAL:HG21	1.99	0.44
68:Af:14:LEU:HD21	68:Af:31:LYS:HE2	1.99	0.44
80:E:120:VAL:O	80:E:125:GLY:N	2.50	0.44
82:DC:636:PHE:O	82:DC:642:GLY:N	2.50	0.44
6:BH:112:ARG:NH2	34:B5:638:U:O3'	2.50	0.44
8:BJ:63:ASP:OD1	8:BJ:63:ASP:N	2.50	0.44
22:BP:126:VAL:HB	34:B5:1459:C:H5'	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BS:17:LEU:HD21	25:BS:66:LEU:HD13	1.99	0.44
26:BT:41:SER:HB2	34:B5:1504:G:H4'	1.99	0.44
29:Bc:12:VAL:HG21	29:Bc:48:VAL:HG11	2.00	0.44
34:B5:1628:U:H2'	34:B5:1629:G:C8	2.53	0.44
34:B5:1739:C:H2'	34:B5:1740:A:C8	2.53	0.44
35:AA:244:GLY:HA3	38:A1:2242:A:H5''	1.99	0.44
36:AB:236:LYS:HE2	36:AB:236:LYS:HB2	1.75	0.44
38:A1:138:U:H2'	38:A1:139:G:H8	1.83	0.44
38:A1:1347:U:H2'	38:A1:1355:A:H61	1.83	0.44
38:A1:2660:G:OP1	38:A1:2750:U:O2'	2.36	0.44
38:A1:2997:G:H1	38:A1:3151:U:H3	1.64	0.44
40:A4:9:A:H2'	40:A4:10:A:C8	2.53	0.44
40:A4:29:U:H5''	48:AL:27:ASP:HB3	1.99	0.44
58:AV:118:VAL:HB	58:AV:136:VAL:HG22	1.99	0.44
82:DC:203:TYR:HD2	82:DC:206:ARG:HE	1.66	0.44
1:BA:124:THR:HG22	1:BA:174:TRP:HE1	1.83	0.44
8:BJ:49:LEU:HD12	8:BJ:52:ILE:HD11	1.99	0.44
8:BJ:141:VAL:HG12	8:BJ:143:ILE:H	1.83	0.44
14:BX:42:PRO:HA	14:BX:79:ASN:HD21	1.83	0.44
34:B5:551:G:H2'	34:B5:552:G:H8	1.83	0.44
34:B5:808:U:H2'	34:B5:809:A:C8	2.52	0.44
34:B5:1156:C:H2'	34:B5:1157:A:C8	2.53	0.44
34:B5:1175:U:H2'	34:B5:1176:G:H8	1.83	0.44
38:A1:307:A:H2'	38:A1:308:A:H8	1.82	0.44
38:A1:861:C:OP1	38:A1:2133:PSU:O2'	2.26	0.44
38:A1:1786:G:H2'	38:A1:1787:A:C8	2.53	0.44
38:A1:3204:C:H2'	38:A1:3205:G:C8	2.52	0.44
50:AN:99:ARG:NH2	50:AN:118:SER:O	2.39	0.44
8:BJ:119:ALA:O	8:BJ:124:HIS:ND1	2.47	0.44
13:BW:69:LEU:HD11	13:BW:72:CYS:HB2	1.99	0.44
16:Ba:70:LYS:HD3	34:B5:930:A:H5''	2.00	0.44
34:B5:979:A:N3	34:B5:1775:U:O2'	2.49	0.44
34:B5:1216:C:O2'	34:B5:1444:A:N1	2.44	0.44
34:B5:1628:U:H2'	34:B5:1629:G:H8	1.82	0.44
38:A1:1596:C:O2'	38:A1:1696:A:N3	2.49	0.44
38:A1:1660:C:H2'	38:A1:1661:G:H8	1.82	0.44
38:A1:2206:G:O2'	38:A1:2207:A:O5'	2.32	0.44
38:A1:3270:U:H2'	42:AE:46:ARG:HH11	1.82	0.44
40:A4:47:C:H1'	40:A4:61:A:H2'	2.00	0.44
42:AE:137:ASP:HA	42:AE:140:VAL:HG22	2.00	0.44
45:AH:180:TYR:OH	75:Am:90:ASN:ND2	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Af:90:PRO:HB2	68:Af:92:LYS:HG2	1.99	0.44
1:BA:11:PRO:HB3	24:BR:101:ASN:HD22	1.82	0.43
1:BA:23:HIS:O	1:BA:48:ILE:N	2.43	0.43
3:BC:107:SER:O	3:BC:141:ARG:NH1	2.51	0.43
7:BI:167:ALA:HB2	7:BI:183:ILE:HG22	2.00	0.43
8:BJ:31:ALA:HB1	18:Be:36:LYS:HZ3	1.83	0.43
25:BS:91:ASP:OD2	25:BS:93:THR:OG1	2.35	0.43
31:Bg:131:ILE:HG13	31:Bg:144:LEU:HB3	2.00	0.43
34:B5:29:U:H2'	34:B5:30:G:H8	1.82	0.43
34:B5:107:C:H2'	34:B5:108:A:C8	2.52	0.43
38:A1:109:A:N1	38:A1:322:U:O2'	2.43	0.43
38:A1:354:U:H2'	38:A1:355:A:H8	1.83	0.43
38:A1:629:U:H2'	38:A1:630:A:C8	2.53	0.43
38:A1:1948:G:H2'	38:A1:1949:G:H8	1.82	0.43
38:A1:2648:G:OP1	46:AI:24:ARG:NH2	2.51	0.43
53:AQ:165:ILE:HD11	53:AQ:172:PHE:HB3	1.99	0.43
55:AS:73:LYS:NZ	55:AS:97:VAL:O	2.51	0.43
80:E:39:LYS:N	80:E:200:ASN:O	2.50	0.43
82:DC:563:TYR:O	82:DC:564:ARG:NH1	2.51	0.43
2:BB:131:ASP:OD1	2:BB:131:ASP:N	2.43	0.43
4:BE:31:PRO:HG3	4:BE:43:PRO:HG3	2.01	0.43
7:BI:76:THR:HG22	7:BI:108:PRO:HG2	1.99	0.43
10:BN:94:LYS:HE2	10:BN:94:LYS:HB2	1.88	0.43
11:BO:43:THR:H	11:BO:46:MET:HE2	1.83	0.43
15:BY:37:LYS:HA	15:BY:40:LEU:HD12	1.99	0.43
25:BS:6:GLN:NE2	28:BZ:44:GLN:OE1	2.51	0.43
34:B5:520:A:H2'	34:B5:521:A:C8	2.52	0.43
38:A1:16:A:H4'	60:AX:45:LYS:HE2	1.99	0.43
38:A1:269:G:OP2	50:AN:44:ARG:NH1	2.51	0.43
38:A1:1646:G:HO2'	38:A1:1808:G:H22	1.62	0.43
38:A1:2197:C:H4'	38:A1:2198:A:H5'	2.00	0.43
38:A1:3015:G:H2'	38:A1:3016:A:H8	1.83	0.43
41:AD:119:TYR:OH	41:AD:139:PRO:O	2.31	0.43
42:AE:68:PRO:HG3	42:AE:145:LEU:HD23	1.99	0.43
45:AH:101:VAL:HG12	45:AH:114:VAL:HG22	2.00	0.43
46:AI:102:MET:HA	46:AI:112:GLN:HE22	1.83	0.43
82:DC:178:PHE:HB3	82:DC:245:TRP:HH2	1.82	0.43
82:DC:566:THR:OG1	82:DC:683:SER:OG	2.34	0.43
2:BB:121:ILE:HD13	2:BB:207:LEU:HD11	2.00	0.43
3:BC:169:LEU:HD13	3:BC:198:THR:HG22	2.00	0.43
4:BE:112:HIS:NE2	4:BE:237:SER:OG	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:126:VAL:HG12	4:BE:158:ASP:H	1.82	0.43
6:BH:29:ASN:OD1	6:BH:29:ASN:N	2.52	0.43
27:BU:74:GLU:OE1	34:B5:1428:G:N2	2.42	0.43
34:B5:1175:U:H2'	34:B5:1176:G:C8	2.53	0.43
35:AA:132:ASN:HD21	38:A1:2179:C:H2'	1.82	0.43
38:A1:1672:U:H2'	38:A1:1673:G:H8	1.82	0.43
38:A1:1864:A:H5'	54:AR:88:ARG:HG2	2.00	0.43
38:A1:2218:G:H2'	38:A1:2219:A:C8	2.53	0.43
38:A1:2376:G:H2'	38:A1:2377:G:C8	2.54	0.43
42:AE:60:ASP:OD2	42:AE:78:ARG:NH1	2.51	0.43
45:AH:124:ARG:HB3	45:AH:164:ILE:HD12	2.01	0.43
48:AL:122:LYS:HG2	70:Ah:118:ILE:HG23	2.01	0.43
65:Ac:22:LYS:HE2	65:Ac:94:GLU:HB3	2.00	0.43
65:Ac:30:THR:HG23	65:Ac:91:SER:HB2	2.00	0.43
68:Af:43:PHE:HE1	68:Af:107:ILE:HD11	1.83	0.43
82:DC:169:VAL:HB	82:DC:173:ASP:HB2	1.99	0.43
82:DC:591:GLU:HG3	82:DC:685:ARG:HB3	1.99	0.43
2:BB:27:LYS:HG2	2:BB:47:LEU:HD13	2.00	0.43
3:BC:176:SER:HB2	3:BC:195:ASP:HB3	2.01	0.43
4:BE:148:ARG:O	4:BE:168:LYS:NZ	2.45	0.43
9:BL:88:ARG:NH1	34:B5:306:U:OP1	2.51	0.43
14:BX:17:VAL:HA	14:BX:20:ARG:HG2	2.00	0.43
25:BS:106:GLU:HA	25:BS:109:LEU:HG	1.99	0.43
29:Bc:18:ARG:NH1	29:Bc:26:THR:OG1	2.52	0.43
34:B5:922:G:H2'	34:B5:923:A:H8	1.82	0.43
34:B5:1211:A:N6	34:B5:1453:G:O6	2.51	0.43
34:B5:1690:G:N2	34:B5:1710:U:O4	2.52	0.43
36:AB:219:ALA:HB3	36:AB:329:PRO:HG2	2.01	0.43
38:A1:2688:U:OP1	41:AD:12:TYR:OH	2.36	0.43
38:A1:3222:U:O2	38:A1:3263:G:O6	2.37	0.43
38:A1:3234:A:N1	38:A1:3253:G:C6	2.87	0.43
38:A1:3252:G:H2'	38:A1:3253:G:C8	2.53	0.43
38:A1:3291:G:H2'	38:A1:3292:A:C8	2.52	0.43
38:A1:3325:G:O2'	66:Ad:105:GLN:NE2	2.44	0.43
39:A3:39:C:H4'	47:AJ:44:THR:HG23	1.99	0.43
41:AD:32:GLN:NE2	41:AD:147:ASP:OD1	2.51	0.43
2:BB:43:VAL:HG13	2:BB:68:VAL:HG11	2.00	0.43
4:BE:69:HIS:CE1	4:BE:94:ALA:H	2.37	0.43
6:BH:79:ARG:NH1	6:BH:164:TYR:OH	2.52	0.43
27:BU:59:PRO:HA	34:B5:1382:A:H5'	2.01	0.43
29:Bc:35:ASP:OD1	29:Bc:35:ASP:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Bg:81:LEU:HB2	31:Bg:91:LEU:HD23	2.00	0.43
34:B5:1483:A:H2	34:B5:1607:G:H1'	1.84	0.43
36:AB:218:ILE:HG13	36:AB:276:THR:HG22	2.01	0.43
37:AC:23:PRO:HG2	37:AC:258:LEU:HD23	1.99	0.43
38:A1:20:A:H2'	38:A1:21:G:C8	2.52	0.43
38:A1:190:U:H2'	61:AY:60:ARG:HH12	1.83	0.43
38:A1:673:U:H2'	38:A1:674:G:H8	1.83	0.43
38:A1:824:C:O2'	38:A1:1534:A:N3	2.47	0.43
41:AD:104:LEU:HD13	41:AD:247:ILE:HG12	2.01	0.43
51:AO:35[A]:VAL:HG21	51:AO:80[A]:PHE:HE2	1.83	0.43
66:Ad:10:ARG:NE	66:Ad:12:TYR:OH	2.40	0.43
79:tE:30:G:H2'	79:tE:31:G:H8	1.83	0.43
2:BB:116:LYS:HE3	34:B5:932:U:H5''	1.99	0.43
13:BW:103:ILE:HD11	13:BW:129:VAL:HG22	2.00	0.43
20:BF:51:VAL:HG21	20:BF:130:ILE:HB	2.00	0.43
20:BF:51:VAL:HG11	20:BF:130:ILE:HG22	1.99	0.43
23:BQ:31:VAL:HG12	23:BQ:67:VAL:HB	1.99	0.43
31:Bg:108:SER:OG	31:Bg:109:ASP:N	2.50	0.43
38:A1:1914:G:O2'	54:AR:82:LYS:O	2.33	0.43
38:A1:2154:U:H2'	38:A1:2155:G:C8	2.53	0.43
38:A1:2953:U:H2'	38:A1:2954:U:H2'	2.00	0.43
51:AO:10[A]:ASP:OD2	51:AO:37[A]:ARG:NH2	2.52	0.43
54:AR:134:HIS:CD2	54:AR:136:ARG:HG2	2.54	0.43
1:BA:20:ALA:HA	1:BA:168:HIS:HB2	2.01	0.43
5:BG:76:LEU:HD13	5:BG:94:ARG:HE	1.83	0.43
7:BI:180:ASP:OD1	7:BI:180:ASP:N	2.51	0.43
9:BL:16:GLN:NE2	9:BL:61:THR:O	2.48	0.43
16:Ba:17:HIS:NE2	34:B5:1789:G:OP1	2.42	0.43
16:Ba:19:LYS:HD2	16:Ba:19:LYS:HA	1.90	0.43
23:BQ:60:PHE:HE1	23:BQ:85:ILE:HD11	1.84	0.43
34:B5:523:G:N1	34:B5:528:U:OP2	2.36	0.43
34:B5:890:C:H2'	34:B5:891:A:C8	2.54	0.43
34:B5:925:G:H2'	34:B5:926:A:C8	2.53	0.43
38:A1:533:A:O2'	38:A1:535:G:O5'	2.37	0.43
38:A1:1544:G:O2'	38:A1:2167:A:N3	2.44	0.43
38:A1:2323:G:O2'	38:A1:2325:G:OP2	2.29	0.43
41:AD:146:LEU:HD22	41:AD:163:LEU:HB2	2.01	0.43
47:AJ:79:ILE:HA	47:AJ:82:ARG:HG2	2.01	0.43
61:AY:58:VAL:HG22	61:AY:104:LEU:HD22	2.01	0.43
78:Ap:33:GLN:HG3	78:Ap:49:ARG:HD3	2.01	0.43
1:BA:35:PRO:O	1:BA:52:LYS:NZ	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:13:PRO:HA	6:BH:14:THR:HA	1.82	0.43
8:BJ:163:PRO:HG3	8:BJ:168:ARG:HG3	2.01	0.43
10:BN:114:ARG:HD3	10:BN:114:ARG:HA	1.82	0.43
14:BX:49:ALA:HA	34:B5:435:C:H5'	2.00	0.43
16:Ba:23:CYS:HB3	16:Ba:28:LYS:H	1.84	0.43
25:BS:67:GLU:HA	25:BS:70:VAL:HG22	2.00	0.43
34:B5:5:U:H2'	34:B5:6:G:C8	2.54	0.43
34:B5:947:U:H2'	34:B5:948:G:C8	2.54	0.43
35:AA:57:PRO:HG2	35:AA:78:ALA:HB3	2.01	0.43
38:A1:177:U:O2	38:A1:241:G:O6	2.37	0.43
38:A1:625:G:N2	38:A1:1401:A:OP1	2.51	0.43
38:A1:1235:U:O2'	38:A1:1244:A:O3'	2.37	0.43
38:A1:1311:G:N2	51:AO:86[A]:GLY:O	2.38	0.43
38:A1:2216:G:H22	38:A1:2229:A:H2	1.67	0.43
38:A1:2775:U:O2'	38:A1:2777:G:N1	2.51	0.43
63:Aa:73:LEU:HD21	63:Aa:78:LEU:HA	2.01	0.43
71:Ai:4:LYS:HA	71:Ai:12:ASN:HB3	2.00	0.43
82:DC:649:GLN:HB2	82:DC:689:LEU:HA	2.01	0.43
82:DC:728:VAL:HA	82:DC:773:PRO:HA	2.00	0.43
1:BA:65:ALA:HB3	1:BA:184:LEU:HD23	2.00	0.43
9:BL:129:ARG:NH2	34:B5:115:G:O5'	2.43	0.43
14:BX:131:SER:HB3	34:B5:30:G:H4'	2.00	0.43
22:BP:32:ASP:OD1	22:BP:32:ASP:N	2.47	0.43
34:B5:874:C:H2'	34:B5:875:G:C8	2.54	0.43
35:AA:14:SER:OG	35:AA:15:ILE:N	2.51	0.43
38:A1:985:U:H2'	38:A1:986:PSU:H6	1.83	0.43
38:A1:2094:C:H2'	38:A1:2095:G:H8	1.84	0.43
39:A3:19:C:H2'	39:A3:20:A:H8	1.84	0.43
44:AG:162:LEU:HD23	50:AN:7:LEU:HD11	2.01	0.43
5:BG:177:ARG:O	5:BG:183:ARG:NH1	2.52	0.43
16:Ba:64:LEU:HD12	16:Ba:64:LEU:HA	1.91	0.43
18:Be:56:MET:HB2	34:B5:556:A:H4'	2.00	0.43
34:B5:115:G:N1	34:B5:302:PSU:O4	2.51	0.43
34:B5:922:G:H2'	34:B5:923:A:C8	2.54	0.43
34:B5:1530:C:H2'	34:B5:1531:G:C8	2.53	0.43
34:B5:1592:A:H2'	34:B5:1593:A:C8	2.53	0.43
35:AA:236:GLY:N	38:A1:2183:A:O2'	2.48	0.43
36:AB:226:PHE:O	38:A1:1886:A:O2'	2.30	0.43
37:AC:321:LYS:HA	37:AC:324:LEU:HB3	2.01	0.43
38:A1:1203:A:N3	38:A1:2855:U:O2'	2.41	0.43
38:A1:1480:G:O2'	38:A1:1871:U:O4	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2697:A:H2'	38:A1:2698:G:H8	1.84	0.43
41:AD:55:PHE:HE2	41:AD:159:VAL:HB	1.83	0.43
43:AF:82:LYS:HD3	56:AT:135:PRO:HG2	2.00	0.43
44:AG:78:PHE:HB3	44:AG:155:ASN:HB2	2.00	0.43
44:AG:99:PRO:HD3	44:AG:132:VAL:HG12	2.00	0.43
81:C5:16:LEU:HA	81:C5:19:LYS:HG2	2.01	0.43
6:BH:135:ILE:HG23	6:BH:152:VAL:HG13	2.01	0.42
9:BL:99:ARG:HG2	14:BX:9:LEU:HA	2.01	0.42
13:BW:78:ARG:HB3	13:BW:124:LYS:HB3	2.00	0.42
20:BF:48:PHE:HB2	20:BF:67:PRO:HB3	2.01	0.42
31:Bg:42:LEU:HB2	31:Bg:61:PHE:HB2	2.00	0.42
31:Bg:51:ASP:OD1	31:Bg:51:ASP:N	2.47	0.42
34:B5:107:C:H2'	34:B5:108:A:H8	1.83	0.42
34:B5:980:G:H4'	34:B5:1776:A:H4'	2.00	0.42
34:B5:1164:G:H2'	34:B5:1165:G:H8	1.84	0.42
34:B5:1405:G:H2'	34:B5:1406:A:H8	1.84	0.42
34:B5:1591:C:H2'	34:B5:1592:A:C8	2.54	0.42
35:AA:4:VAL:HG13	35:AA:8:GLN:HB2	2.01	0.42
38:A1:411:U:H2'	38:A1:412:G:C8	2.53	0.42
38:A1:781:G:OP1	53:AQ:151:ARG:NH1	2.52	0.42
38:A1:872:U:O2'	38:A1:1908:A:OP1	2.36	0.42
38:A1:1660:C:H2'	38:A1:1661:G:C8	2.55	0.42
38:A1:2916:U:H2'	38:A1:2917:G:H8	1.84	0.42
39:A3:98:C:O2'	43:AF:131:GLU:OE1	2.29	0.42
40:A4:140:G:H22	50:AN:112:ASN:HB3	1.83	0.42
41:AD:50:ARG:NH2	41:AD:72:ASP:OD2	2.51	0.42
48:AL:27:ASP:OD1	48:AL:27:ASP:N	2.47	0.42
50:AN:140:LYS:HD3	50:AN:140:LYS:HA	1.87	0.42
60:AX:66:PRO:HD2	70:Ah:33:VAL:HG12	2.00	0.42
77:Ao:25:VAL:HG22	77:Ao:72:LEU:HG	2.00	0.42
1:BA:185:ARG:O	12:BV:44:ARG:NH1	2.52	0.42
2:BB:87:ARG:HG2	2:BB:101:HIS:HB2	2.01	0.42
5:BG:87:ARG:NH1	34:B5:159:U:O2	2.52	0.42
7:BI:26:LYS:HB3	34:B5:400:A:C5	2.54	0.42
9:BL:65:SER:OG	34:B5:114:C:O2'	2.32	0.42
14:BX:44:GLY:H	14:BX:78:LYS:HD3	1.84	0.42
15:BY:105:ARG:HG2	15:BY:109:LYS:HE3	2.01	0.42
19:BD:20:GLU:OE2	19:BD:76:ARG:NH2	2.51	0.42
30:Bd:19:ARG:NH2	34:B5:1597:A:OP2	2.52	0.42
34:B5:153:G:H2'	34:B5:154:G:C8	2.54	0.42
34:B5:263:C:H2'	34:B5:264:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1018:U:H2'	34:B5:1019:A:C8	2.54	0.42
38:A1:67:A:O2'	38:A1:315:C:O2	2.35	0.42
38:A1:443:G:N1	38:A1:492:C:OP2	2.51	0.42
38:A1:727:G:H22	53:AQ:139:ILE:HB	1.84	0.42
38:A1:1643:A:H2'	38:A1:1644:C:C2	2.53	0.42
38:A1:2618:G:OP1	38:A1:2644:C:O2'	2.30	0.42
38:A1:2769:A:H5''	77:Ao:80:ARG:HE	1.85	0.42
42:AE:33:SER:OG	68:Af:107:ILE:O	2.37	0.42
46:AI:72:ALA:HB2	46:AI:155:ALA:HB2	2.01	0.42
48:AL:2:ALA:HB3	63:Aa:41:HIS:HE1	1.83	0.42
54:AR:86:GLU:HA	54:AR:90:PRO:HA	2.00	0.42
59:AW:4:GLU:O	59:AW:13:ILE:N	2.43	0.42
66:Ad:25:PHE:HB3	66:Ad:65:LYS:HG2	1.99	0.42
82:DC:353:ALA:HA	82:DC:356:LEU:HG	2.00	0.42
9:BL:146:ALA:O	9:BL:150:ASN:ND2	2.41	0.42
12:BV:4:ASP:OD1	12:BV:4:ASP:N	2.52	0.42
21:BK:2:LEU:HD21	34:B5:1232:U:H4'	2.01	0.42
25:BS:133:VAL:N	34:B5:1545:A:OP1	2.46	0.42
34:B5:233:C:H5'	34:B5:234:G:H5'	2.02	0.42
34:B5:829:A:OP1	34:B5:842:C:N4	2.45	0.42
34:B5:1558:U:OP2	34:B5:1559:A:O2'	2.32	0.42
36:AB:6:TYR:HB3	58:AV:46:LEU:HD13	2.01	0.42
37:AC:65:TRP:HB3	37:AC:69:ARG:HD2	2.01	0.42
38:A1:358:G:N2	38:A1:361:A:OP2	2.36	0.42
38:A1:429:U:H2'	38:A1:430:U:H6	1.85	0.42
38:A1:1095:U:N3	56:AT:127:GLN:OE1	2.41	0.42
38:A1:1633:C:H2'	38:A1:1634:G:H8	1.83	0.42
38:A1:2349:PSU:O2'	38:A1:3307:A:N3	2.52	0.42
38:A1:2526:C:H2'	38:A1:2527:G:H8	1.84	0.42
45:AH:122:LYS:HE2	45:AH:122:LYS:HB2	1.89	0.42
57:AU:42:LYS:HG2	57:AU:47:VAL:HG22	2.01	0.42
65:Ac:47:ASN:ND2	65:Ac:74:ASN:OD1	2.53	0.42
80:E:120:VAL:O	80:E:124:LEU:N	2.52	0.42
1:BA:91:ALA:HA	24:BR:82:ASP:HA	2.02	0.42
6:BH:31:SER:HA	6:BH:34:LEU:HB3	2.00	0.42
9:BL:94:ILE:HD12	14:BX:12:ALA:HB1	2.01	0.42
19:BD:24:PHE:HZ	19:BD:72:LEU:HD13	1.85	0.42
33:BM:63:VAL:HG12	33:BM:65:SER:H	1.85	0.42
34:B5:125:U:H3	34:B5:292:U:H5	1.66	0.42
34:B5:446:A:N1	34:B5:461:G:O2'	2.51	0.42
34:B5:513:U:H2'	34:B5:514:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:590:G:H21	42:AE:19:LYS:HD2	1.84	0.42
38:A1:887:G:H2'	38:A1:888:A:C8	2.54	0.42
38:A1:1132:C:H2'	38:A1:1133:A:H8	1.84	0.42
38:A1:1799:A:H2'	38:A1:1800:A:H8	1.83	0.42
38:A1:2315:G:H2'	38:A1:2316:G:H8	1.84	0.42
38:A1:2746:A:H5''	41:AD:178:ASN:HD22	1.84	0.42
79:tE:51:U:O2	79:tE:65:G:N2	2.48	0.42
82:DC:47:SER:HB2	82:DC:438:MET:HE1	2.00	0.42
1:BA:29:VAL:HG22	1:BA:149:LEU:HD13	2.01	0.42
4:BE:3:ARG:HG2	34:B5:399:A:H4'	2.01	0.42
4:BE:3:ARG:O	34:B5:93:A:O2'	2.28	0.42
8:BJ:16:LYS:O	34:B5:21:U:O2'	2.38	0.42
10:BN:130:ARG:NH2	10:BN:139:TRP:O	2.52	0.42
34:B5:1220:C:H2'	34:B5:1221:A:C8	2.54	0.42
35:AA:20:THR:HA	35:AA:23:ARG:HG3	2.01	0.42
37:AC:106:TRP:HB2	50:AN:199:LEU:HD12	2.02	0.42
38:A1:1696:A:H2'	38:A1:1697:A:H8	1.85	0.42
38:A1:2277:C:OP1	76:An:19:LYS:NZ	2.53	0.42
44:AG:201:THR:OG1	44:AG:202:GLU:OE1	2.33	0.42
47:AJ:125:MET:HE2	47:AJ:125:MET:HB3	1.84	0.42
65:Ac:16:LEU:HD22	65:Ac:98:SER:HB2	2.01	0.42
77:Ao:10:THR:HA	77:Ao:20:HIS:HD2	1.84	0.42
2:BB:125:VAL:O	2:BB:137:ILE:N	2.53	0.42
3:BC:147:ASN:HB2	12:BV:3:ASN:HA	2.01	0.42
6:BH:116:ARG:HD2	34:B5:856:A:C6	2.54	0.42
9:BL:133:LYS:HB2	34:B5:337:G:H3'	2.01	0.42
34:B5:91:G:OP1	34:B5:397:A:N6	2.48	0.42
35:AA:83:HIS:CE1	35:AA:86:GLN:HB3	2.55	0.42
36:AB:260:VAL:HG11	36:AB:266:ARG:HD2	2.02	0.42
38:A1:1244:A:N6	38:A1:1249:G:O6	2.53	0.42
38:A1:1323:G:O3'	55:AS:1:MET:N	2.44	0.42
38:A1:2129:PSU:H2'	38:A1:2130:G:C8	2.55	0.42
38:A1:2515:A:N1	38:A1:2594:C:N4	2.63	0.42
38:A1:2837:A:H5''	46:AI:154:ARG:HH11	1.84	0.42
38:A1:3109:G:OP1	75:Am:93:LYS:NZ	2.45	0.42
80:E:53:LEU:HD22	80:E:155:ILE:HB	2.02	0.42
2:BB:155:TYR:OH	34:B5:932:U:OP2	2.30	0.42
4:BE:25:GLY:HA3	34:B5:447:U:H1'	2.00	0.42
5:BG:3:LEU:HD23	5:BG:109:LEU:HB2	2.01	0.42
5:BG:183:ARG:NH1	34:B5:141:U:O2'	2.45	0.42
16:Ba:51:ARG:HE	29:Bc:61:ARG:HH21	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1358:G:H2'	34:B5:1359:C:C6	2.54	0.42
35:AA:204:MET:HB3	35:AA:208:ASP:HB2	2.01	0.42
36:AB:120:LYS:N	38:A1:3296:A:OP1	2.47	0.42
38:A1:890:C:H2'	38:A1:891:G:H8	1.85	0.42
38:A1:1529:A:OP2	38:A1:1592:G:N2	2.47	0.42
38:A1:1595:U:O2'	38:A1:1606:U:O2	2.29	0.42
38:A1:2428:U:H2'	38:A1:2429:G:C8	2.54	0.42
38:A1:2572:C:H1'	62:AZ:60:LYS:HE2	2.02	0.42
38:A1:2742:C:H2'	38:A1:2743:A:H8	1.85	0.42
51:AO:25[A]:LYS:HA	51:AO:25[A]:LYS:HD3	1.89	0.42
66:Ad:96:VAL:HG12	66:Ad:98:VAL:HG13	2.02	0.42
82:DC:9:MET:HE2	82:DC:436:LEU:HD21	2.01	0.42
82:DC:564:ARG:O	82:DC:725:GLN:N	2.42	0.42
82:DC:565:GLU:HB3	82:DC:717:PHE:CZ	2.54	0.42
82:DC:576:LEU:HD13	82:DC:585:ARG:HH21	1.85	0.42
7:BI:73:SER:HB2	34:B5:257:A:H1'	2.01	0.42
7:BI:153:GLU:HB3	7:BI:156:VAL:HB	2.02	0.42
29:Bc:22:ARG:NH1	29:Bc:22:ARG:HA	2.35	0.42
33:BM:45:LEU:HB2	34:B5:1228:G:H5'	2.02	0.42
35:AA:107:VAL:HG22	35:AA:111:THR:HG21	2.02	0.42
36:AB:11:HIS:HE1	58:AV:45:ARG:HH22	1.67	0.42
37:AC:126:ILE:O	37:AC:129:THR:OG1	2.30	0.42
38:A1:109:A:O2'	38:A1:323:A:N6	2.52	0.42
38:A1:970:A:H2'	38:A1:971:G:C8	2.55	0.42
38:A1:1798:A:H2'	38:A1:1799:A:C8	2.55	0.42
38:A1:2519:A:H2'	38:A1:2520:A:C8	2.55	0.42
38:A1:3015:G:H2'	38:A1:3016:A:C8	2.55	0.42
42:AE:150:LYS:HE2	42:AE:156:LYS:HD2	2.02	0.42
44:AG:133:LYS:HB2	44:AG:199:ALA:HB3	2.01	0.42
49:AM:50:LYS:HA	49:AM:50:LYS:HD3	1.85	0.42
58:AV:17:LEU:HB2	58:AV:52:ALA:HB3	2.00	0.42
62:AZ:96:VAL:HA	62:AZ:100:THR:HG21	2.02	0.42
82:DC:32:LYS:NZ	84:DC:901:GDP:O2B	2.46	0.42
82:DC:278:LEU:HA	82:DC:281:ILE:HG22	2.01	0.42
9:BL:111:VAL:HG12	9:BL:139:VAL:HG21	2.00	0.42
23:BQ:135:ARG:HG3	34:B5:1585:U:H4'	2.02	0.42
26:BT:38:LYS:HA	26:BT:46:PRO:HA	2.02	0.42
34:B5:1071:U:H2'	34:B5:1072:C:C6	2.55	0.42
34:B5:1479:A:H2'	34:B5:1480:G:H8	1.85	0.42
34:B5:1739:C:H2'	34:B5:1740:A:H8	1.84	0.42
35:AA:127:ALA:HB2	35:AA:134:VAL:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:35:ASP:OD1	36:AB:184:ASN:ND2	2.53	0.42
37:AC:67:THR:HG21	38:A1:2402:A:H2'	2.01	0.42
38:A1:112:U:H5''	70:Ah:104:GLN:HE22	1.85	0.42
38:A1:946:U:H2'	38:A1:947:G:H8	1.85	0.42
38:A1:1717:U:H2'	38:A1:1718:G:H8	1.85	0.42
38:A1:2688:U:N3	41:AD:17:GLN:O	2.41	0.42
47:AJ:43:GLN:NE2	47:AJ:70:THR:O	2.53	0.42
53:AQ:140:LEU:HD12	53:AQ:140:LEU:HA	1.94	0.42
57:AU:93:ILE:HD12	57:AU:105:LEU:HD13	2.00	0.42
82:DC:150:ARG:HG3	82:DC:197:LEU:HD11	2.01	0.42
82:DC:404:THR:HG22	82:DC:449:PRO:HA	2.02	0.42
3:BC:142:GLY:HA3	3:BC:155:ALA:HB2	2.01	0.42
4:BE:180:LEU:HB2	4:BE:231:GLN:HA	2.02	0.42
11:BO:49:LYS:HD3	11:BO:49:LYS:HA	1.78	0.42
26:BT:77:ASN:HB3	26:BT:95:ASP:HB3	2.02	0.42
34:B5:116:U:O2'	34:B5:333:A:O2'	2.30	0.42
34:B5:1523:G:OP1	34:B5:1523:G:N2	2.41	0.42
34:B5:1673:G:C6	34:B5:1728:A:N1	2.88	0.42
36:AB:235:THR:HG21	36:AB:249:VAL:HG22	2.01	0.42
36:AB:384:LYS:NZ	38:A1:3371:G:OP1	2.45	0.42
38:A1:87:U:H2'	38:A1:88:A:H8	1.84	0.42
38:A1:1342:C:H5''	53:AQ:12:ARG:HG3	2.01	0.42
38:A1:1594:A:O2'	38:A1:1614:C:O2	2.38	0.42
38:A1:2988:C:OP1	51:AO:65[A]:ASN:ND2	2.47	0.42
42:AE:51:ARG:HB3	42:AE:159:LEU:HD13	2.02	0.42
57:AU:22:PRO:HB2	57:AU:28:PHE:HB2	2.02	0.42
78:Ap:56:THR:HG23	78:Ap:63:THR:HB	2.01	0.42
82:DC:119:LEU:HD21	82:DC:145:GLN:HG3	2.01	0.42
82:DC:829:LYS:HA	82:DC:829:LYS:HD2	1.89	0.42
1:BA:136:ALA:HB1	1:BA:141:ILE:HB	2.01	0.41
7:BI:61:GLU:O	7:BI:78:ILE:N	2.52	0.41
34:B5:1087:A:H2'	34:B5:1088:A:C8	2.54	0.41
34:B5:1648:A:H2'	34:B5:1649:G:C8	2.55	0.41
38:A1:116:A:H5''	38:A1:265:A:H2	1.85	0.41
38:A1:1288:U:H2'	38:A1:1289:G:H8	1.85	0.41
38:A1:2295:A:C5	58:AV:37:ILE:HG12	2.54	0.41
39:A3:114:U:H2'	39:A3:115:G:H8	1.85	0.41
53:AQ:92:ARG:HG3	63:Aa:76:ASP:HB2	2.02	0.41
58:AV:13:ILE:HG23	58:AV:85:TRP:CG	2.55	0.41
61:AY:118:LEU:HD12	61:AY:121:ARG:HD2	2.02	0.41
70:Ah:14:LYS:HE2	70:Ah:14:LYS:HB3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:DC:563:TYR:OH	82:DC:775:ASN:ND2	2.53	0.41
1:BA:101:ARG:HD2	1:BA:101:ARG:HA	1.85	0.41
4:BE:230:GLU:HB3	4:BE:233:LYS:HB3	2.02	0.41
7:BI:137:LYS:HD3	34:B5:188:A:H5'	2.03	0.41
7:BI:195:ARG:NH2	9:BL:11:ARG:HG3	2.35	0.41
8:BJ:44:ARG:HH11	34:B5:473:A:H5''	1.84	0.41
12:BV:72:LEU:HD13	12:BV:75:ASN:HD21	1.85	0.41
14:BX:55:GLU:HG2	14:BX:73:ARG:HB3	2.03	0.41
19:BD:173:ARG:HD3	19:BD:173:ARG:HA	1.90	0.41
23:BQ:136:SER:HA	34:B5:1581:C:H5'	2.02	0.41
27:BU:34:LEU:HD12	27:BU:34:LEU:HA	1.88	0.41
34:B5:1187:PSU:H2'	34:B5:1188:G:C8	2.55	0.41
34:B5:1479:A:H2'	34:B5:1480:G:C8	2.55	0.41
36:AB:110:LEU:HD23	36:AB:115:LYS:HG2	2.01	0.41
38:A1:63:A:N3	38:A1:78:U:O2'	2.40	0.41
38:A1:115:A:H2'	38:A1:265:A:H2'	2.02	0.41
38:A1:616:G:H2'	38:A1:617:G:C8	2.55	0.41
38:A1:1119:C:H2'	38:A1:1120:A:C8	2.55	0.41
38:A1:2109:U:H2'	38:A1:2110:G:C8	2.54	0.41
39:A3:81:U:H2'	39:A3:82:G:H8	1.85	0.41
42:AE:168:GLY:O	42:AE:170:LYS:NZ	2.40	0.41
52:AP:172:GLN:NE2	68:Af:60:ARG:O	2.49	0.41
58:AV:22:ILE:HG23	58:AV:33:ASN:HB2	2.02	0.41
2:BB:70:LEU:HD21	2:BB:84:ILE:HG12	2.02	0.41
7:BI:137:LYS:HE2	34:B5:197:A:H2	1.85	0.41
15:BY:7:ILE:HG12	15:BY:43:LYS:HZ3	1.85	0.41
25:BS:27:LYS:HE3	34:B5:1533:C:H5''	2.02	0.41
36:AB:221:THR:HB	36:AB:273:HIS:H	1.85	0.41
38:A1:1748:G:OP2	73:Ak:42:LYS:NZ	2.39	0.41
38:A1:2357:A:H2'	38:A1:2358:A:C8	2.55	0.41
38:A1:2366:C:H2'	38:A1:2367:A:H8	1.85	0.41
38:A1:2438:A:H3'	38:A1:2439:A:H5''	2.02	0.41
38:A1:2611:U:H2'	38:A1:2612:U:C6	2.55	0.41
40:A4:60:U:OP1	60:AX:54:TYR:OH	2.33	0.41
43:AF:73:GLY:O	56:AT:143:THR:OG1	2.33	0.41
43:AF:90:LYS:HD3	43:AF:133:TYR:HD1	1.86	0.41
44:AG:34:PHE:O	44:AG:41:GLN:NE2	2.48	0.41
79:tE:7:G:OP1	79:tE:16:C:N4	2.53	0.41
79:tE:30:G:H2'	79:tE:31:G:C8	2.55	0.41
82:DC:27:HIS:CD2	82:DC:28:VAL:H	2.39	0.41
7:BI:6:ASP:OD1	7:BI:6:ASP:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:40:TYR:HB3	10:BN:50:ILE:HD12	2.02	0.41
13:BW:26:LEU:HD21	13:BW:60:LYS:HD3	2.03	0.41
19:BD:93:ASP:OD2	19:BD:194:LYS:NZ	2.43	0.41
26:BT:18:TYR:HD1	26:BT:135:ILE:HG21	1.84	0.41
26:BT:38:LYS:NZ	34:B5:1564:U:OP1	2.47	0.41
32:Bf:118:ARG:HE	32:Bf:131:PHE:HB3	1.85	0.41
36:AB:167:ARG:NH1	36:AB:168:LYS:HG3	2.36	0.41
36:AB:213:GLU:HB2	36:AB:282:ILE:HD13	2.02	0.41
37:AC:313:LEU:HD13	38:A1:610:G:H21	1.86	0.41
38:A1:297:G:OP2	38:A1:297:G:N2	2.37	0.41
38:A1:753:C:H2'	38:A1:754:G:H8	1.85	0.41
38:A1:1083:G:H2'	38:A1:1084:A:C8	2.56	0.41
38:A1:1280:C:H2'	38:A1:1281:G:C8	2.48	0.41
40:A4:43:A:H2'	40:A4:44:A:C8	2.56	0.41
46:AI:38:LYS:HD2	46:AI:83:ASP:HB3	2.02	0.41
54:AR:93:VAL:HA	54:AR:96:ILE:HB	2.03	0.41
55:AS:10:ILE:HD12	55:AS:60:SER:HB3	2.02	0.41
55:AS:26:ARG:HH22	55:AS:28:ARG:HE	1.67	0.41
66:Ad:84:ASP:N	66:Ad:84:ASP:OD1	2.52	0.41
82:DC:495:VAL:HG11	82:DC:501:LEU:HD12	2.02	0.41
6:BH:147:ASN:OD1	6:BH:180:GLN:NE2	2.53	0.41
8:BJ:171:ARG:HG2	8:BJ:175:ARG:HH21	1.85	0.41
15:BY:45:ALA:HA	15:BY:50:ALA:HB3	2.02	0.41
16:Ba:25:ASN:ND2	16:Ba:77:CYS:SG	2.91	0.41
21:BK:68:LEU:HD21	21:BK:73:VAL:HG22	2.01	0.41
31:Bg:66:HIS:HB3	31:Bg:85:TRP:HB2	2.02	0.41
31:Bg:91:LEU:HD12	31:Bg:101:GLN:HB3	2.03	0.41
34:B5:1198:G:OP1	34:B5:1199:G:O2'	2.32	0.41
34:B5:1368:G:O2'	34:B5:1372:U:O4	2.38	0.41
36:AB:92:TYR:HB2	36:AB:157:VAL:HB	2.03	0.41
38:A1:147:U:H5'	44:AG:136:LEU:HB2	2.01	0.41
38:A1:1633:C:H2'	38:A1:1634:G:C8	2.56	0.41
42:AE:30:LEU:HD12	42:AE:34:LEU:HD22	2.02	0.41
51:AO:56[A]:ASP:O	51:AO:60[A]:LYS:NZ	2.44	0.41
80:E:60:ARG:HA	80:E:61:PRO:HD3	1.92	0.41
82:DC:613:LYS:HD3	82:DC:617:ARG:HH22	1.85	0.41
1:BA:107:PHE:HB3	1:BA:139:VAL:HG21	2.02	0.41
12:BV:3:ASN:HD21	12:BV:7:GLN:HG3	1.85	0.41
14:BX:51:GLY:HA2	14:BX:77:ILE:HG13	2.01	0.41
16:Ba:33:ASP:N	16:Ba:33:ASP:OD1	2.53	0.41
34:B5:140:A:H62	34:B5:281:G:H5''	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:823:G:OP2	34:B5:823:G:N2	2.51	0.41
34:B5:877:G:C6	34:B5:951:A:N1	2.89	0.41
34:B5:885:G:H2'	34:B5:886:U:C6	2.56	0.41
34:B5:1506:G:O2'	34:B5:1550:A:O2'	2.28	0.41
35:AA:26:ALA:HB1	35:AA:28:LYS:HE3	2.03	0.41
36:AB:150:ARG:HG3	36:AB:154:TYR:HD2	1.86	0.41
38:A1:596:C:N3	38:A1:608:A:O2'	2.53	0.41
38:A1:1493:G:OP2	38:A1:1493:G:N2	2.48	0.41
38:A1:1799:A:H2'	38:A1:1800:A:C8	2.55	0.41
38:A1:2468:A:N7	80:E:105:LYS:HE2	2.36	0.41
39:A3:71:G:H2'	39:A3:72:A:C8	2.55	0.41
41:AD:25:GLU:HB3	41:AD:27:LYS:HE3	2.03	0.41
47:AJ:117:ASP:N	47:AJ:117:ASP:OD1	2.53	0.41
52:AP:120:ASN:HB2	52:AP:145:HIS:HB2	2.03	0.41
55:AS:148:LEU:HD12	55:AS:148:LEU:HA	1.96	0.41
80:E:67:ILE:HG23	80:E:84:ALA:HB2	2.02	0.41
4:BE:64:ILE:HB	15:BY:17:LEU:HD23	2.03	0.41
6:BH:140:VAL:HG22	6:BH:150:GLN:HG3	2.03	0.41
7:BI:119:GLN:HB2	7:BI:150:ALA:HB1	2.02	0.41
22:BP:115:TYR:OH	34:B5:1556:A:OP1	2.30	0.41
34:B5:1164:G:H2'	34:B5:1165:G:C8	2.54	0.41
36:AB:113:GLU:HG2	36:AB:176:ALA:HB2	2.03	0.41
38:A1:12:A:H2'	38:A1:13:A:C8	2.56	0.41
38:A1:1729:A:N6	65:Ac:47:ASN:O	2.53	0.41
38:A1:2203:U:H2'	38:A1:2204:C:C6	2.55	0.41
38:A1:2419:A:H2'	38:A1:2420:C:C6	2.55	0.41
38:A1:3121:U:H1'	38:A1:3122:A:H5''	2.03	0.41
38:A1:3343:G:H21	38:A1:3362:A:H2	1.69	0.41
41:AD:125:VAL:HG11	41:AD:199:ILE:HG21	2.02	0.41
44:AG:158:ASP:OD1	44:AG:158:ASP:N	2.52	0.41
50:AN:155:VAL:O	50:AN:162:ARG:NH2	2.42	0.41
54:AR:173:ARG:HE	54:AR:177:VAL:HG21	1.86	0.41
82:DC:488:VAL:N	82:DC:532:GLY:O	2.52	0.41
82:DC:511:LEU:HD11	82:DC:541:CYS:HB2	2.01	0.41
2:BB:122:GLU:OE2	2:BB:213:ARG:NH2	2.52	0.41
7:BI:49:ARG:NH1	34:B5:399:A:OP1	2.54	0.41
11:BO:52:ARG:HD3	34:B5:905:A:H5''	2.03	0.41
17:Bb:3:LEU:HD12	17:Bb:4:VAL:HG23	2.02	0.41
17:Bb:70:LYS:HG2	34:B5:1049:U:H5''	2.02	0.41
27:BU:68:ARG:HB2	30:Bd:40:ARG:HH21	1.85	0.41
31:Bg:66:HIS:CE1	34:B5:1386:G:H4'	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:549:G:O2'	34:B5:556:A:N1	2.47	0.41
35:AA:52:SER:HB3	35:AA:191:LEU:HD12	2.03	0.41
36:AB:9:PRO:HG3	38:A1:2914:G:H5'	2.03	0.41
38:A1:351:A:OP1	74:A1:34:THR:OG1	2.38	0.41
38:A1:679:U:O2'	38:A1:788:C:O2	2.36	0.41
38:A1:1542:G:H2'	38:A1:1543:G:C8	2.56	0.41
40:A4:51:G:H5''	74:A1:26:TRP:HZ2	1.86	0.41
41:AD:52:VAL:HG22	41:AD:147:ASP:HB3	2.03	0.41
44:AG:100:GLU:HB2	44:AG:104:GLU:HB2	2.03	0.41
50:AN:96:ARG:NH2	50:AN:160:GLU:O	2.53	0.41
55:AS:48:LEU:HG	56:AT:151:LEU:HD23	2.02	0.41
55:AS:74:ASN:HB2	55:AS:129:ILE:HB	2.02	0.41
1:BA:70:PRO:HB2	1:BA:94:GLY:H	1.86	0.41
1:BA:101:ARG:H	24:BR:67:ARG:HH12	1.69	0.41
2:BB:61:LEU:HD21	2:BB:96:LEU:HD21	2.02	0.41
2:BB:137:ILE:HG21	2:BB:172:LEU:HD22	2.03	0.41
6:BH:20:VAL:HG21	6:BH:46:ILE:HG21	2.03	0.41
10:BN:76:LYS:NZ	34:B5:813:U:OP2	2.48	0.41
12:BV:74:GLN:NE2	12:BV:80:LYS:O	2.44	0.41
15:BY:135:ASP:OD1	15:BY:135:ASP:N	2.52	0.41
16:Ba:18:VAL:HG23	16:Ba:19:LYS:H	1.86	0.41
16:Ba:76:SER:OG	34:B5:1793:G:N2	2.44	0.41
21:BK:77:ARG:HG2	21:BK:82:LEU:HB2	2.03	0.41
23:BQ:93:HIS:HA	23:BQ:97:VAL:HG12	2.03	0.41
23:BQ:99:GLU:HB2	31:Bg:57:PRO:HB2	2.03	0.41
24:BR:27:ASP:O	24:BR:31:ASN:ND2	2.54	0.41
24:BR:49:LYS:HE2	34:B5:1389:C:H5'	2.02	0.41
26:BT:57:ARG:NE	34:B5:1479:A:OP1	2.43	0.41
27:BU:72:ASN:HD22	34:B5:1429:G:H21	1.69	0.41
34:B5:55:A:H3'	34:B5:403:G:H22	1.86	0.41
34:B5:93:A:C8	34:B5:398:G:H2'	2.56	0.41
34:B5:122:U:H2'	34:B5:123:G:C8	2.56	0.41
34:B5:386:G:H2'	34:B5:387:A:C8	2.55	0.41
34:B5:1151:A:O2'	34:B5:1766:A:N7	2.45	0.41
34:B5:1325:A:H2'	34:B5:1326:A:H8	1.86	0.41
34:B5:1405:G:H2'	34:B5:1406:A:C8	2.56	0.41
37:AC:95:ARG:NH1	38:A1:366:A:OP1	2.41	0.41
37:AC:334:PHE:HB3	38:A1:578:A:H2'	2.02	0.41
38:A1:321:C:OP1	50:AN:159:ARG:NH2	2.54	0.41
38:A1:353:G:O2'	38:A1:364:G:O6	2.37	0.41
38:A1:417:A:H2'	38:A1:418:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:499:G:H5''	68:Af:48:ARG:HH21	1.85	0.41
38:A1:662:U:H2'	38:A1:663:C:C6	2.56	0.41
38:A1:821:U:H2'	38:A1:822:G:C8	2.56	0.41
38:A1:876:A:H4'	38:A1:1890:U:H4'	2.03	0.41
38:A1:1132:C:H2'	38:A1:1133:A:C8	2.56	0.41
38:A1:1481:A:O2'	38:A1:1859:A:OP2	2.39	0.41
38:A1:1718:G:H2'	38:A1:1719:G:H8	1.86	0.41
38:A1:2609:A:H2'	38:A1:2610:G:C8	2.56	0.41
38:A1:2719:U:H2'	38:A1:2720:G:H8	1.85	0.41
38:A1:2991:A:O2'	38:A1:3309:G:N7	2.54	0.41
38:A1:3016:A:H2'	38:A1:3017:A:C8	2.56	0.41
38:A1:3028:G:H4'	82:DC:28:VAL:HG21	2.02	0.41
38:A1:3192:U:H3	38:A1:3200:G:H1	1.67	0.41
44:AG:85:ASN:OD1	44:AG:85:ASN:N	2.54	0.41
47:AJ:99:THR:O	47:AJ:154:THR:OG1	2.30	0.41
50:AN:139:HIS:HD2	50:AN:141:ALA:H	1.68	0.41
51:AO:28[A]:LEU:HD11	51:AO:88[A]:VAL:HG23	2.02	0.41
63:Aa:19:LYS:HB3	63:Aa:25:HIS:HB2	2.03	0.41
63:Aa:71:PRO:HD2	63:Aa:110:GLY:H	1.86	0.41
67:Ae:100:ILE:O	67:Ae:125:ARG:NH1	2.53	0.41
80:E:110:PHE:HB2	80:E:133:LYS:HB3	2.02	0.41
82:DC:255:LYS:HD3	82:DC:255:LYS:HA	1.97	0.41
2:BB:187:LYS:HE2	2:BB:187:LYS:HB3	1.88	0.41
4:BE:19:LEU:HD13	34:B5:788:A:C6	2.56	0.41
4:BE:207:LEU:HD12	4:BE:219:VAL:HG22	2.02	0.41
8:BJ:35:GLY:O	8:BJ:110:GLN:NE2	2.53	0.41
9:BL:135:VAL:HG21	34:B5:325:G:H5''	2.03	0.41
18:Be:3:LYS:HA	18:Be:3:LYS:HD3	1.85	0.41
19:BD:69:LEU:HA	19:BD:72:LEU:HD12	2.03	0.41
22:BP:90:ILE:HD11	22:BP:112:LEU:HD12	2.03	0.41
27:BU:58:LEU:HD21	34:B5:1347:U:H3	1.86	0.41
31:Bg:214:ALA:HB2	31:Bg:220:ILE:HG13	2.03	0.41
34:B5:870:C:H2'	34:B5:871:G:C8	2.56	0.41
36:AB:17:LEU:HD23	36:AB:17:LEU:HA	1.91	0.41
38:A1:121:A:C6	44:AG:108:ARG:HD2	2.55	0.41
38:A1:149:U:H4'	50:AN:56:LYS:HB3	2.02	0.41
38:A1:500:C:H2'	38:A1:501:A:C8	2.56	0.41
38:A1:512:U:O2	38:A1:579:G:N2	2.40	0.41
38:A1:984:G:N2	38:A1:1138:U:OP1	2.54	0.41
38:A1:1104:G:H2'	38:A1:1105:A:C8	2.56	0.41
38:A1:1203:A:H2'	38:A1:1204:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1219:C:O2'	38:A1:1286:A:N1	2.54	0.41
38:A1:1320:C:O2	55:AS:115:ARG:NH2	2.54	0.41
38:A1:2423:U:H2'	38:A1:2424:A:C8	2.56	0.41
38:A1:2769:A:H2'	38:A1:2770:G:C8	2.56	0.41
38:A1:2890:A:O2'	38:A1:2933:A:N3	2.44	0.41
40:A4:149:A:N3	44:AG:55:TYR:OH	2.45	0.41
43:AF:118:LYS:HB3	43:AF:118:LYS:HE3	1.85	0.41
50:AN:118:SER:HB2	50:AN:132:VAL:HG22	2.03	0.41
53:AQ:82:VAL:HG22	53:AQ:102:ALA:HB3	2.03	0.41
58:AV:114:ILE:HD12	58:AV:133:SER:HB3	2.03	0.41
82:DC:171:LYS:HB2	82:DC:274:ASN:HB3	2.03	0.41
2:BB:133:TYR:CE2	2:BB:217:LEU:HD11	2.57	0.40
5:BG:136:LYS:HB3	5:BG:136:LYS:HE3	1.88	0.40
5:BG:160:ARG:NH2	34:B5:68:A:OP1	2.47	0.40
12:BV:41:GLU:HG3	12:BV:42:GLU:HG3	2.03	0.40
14:BX:53:VAL:HA	14:BX:74:VAL:HG22	2.02	0.40
17:Bb:72:LYS:HD2	17:Bb:72:LYS:HA	1.79	0.40
18:Be:56:MET:HB3	34:B5:590:C:H5'	2.03	0.40
22:BP:75:PRO:HA	22:BP:93:VAL:HG13	2.03	0.40
31:Bg:23:LEU:HD12	31:Bg:33:LEU:HD11	2.03	0.40
35:AA:15:ILE:HD12	35:AA:194:ASN:HD22	1.86	0.40
37:AC:276:LEU:HD23	37:AC:276:LEU:HA	1.95	0.40
38:A1:1718:G:H2'	38:A1:1719:G:C8	2.56	0.40
38:A1:2466:G:H3'	38:A1:2467:G:H8	1.86	0.40
38:A1:2999:U:H2'	38:A1:3000:A:C8	2.56	0.40
41:AD:95:TRP:HA	41:AD:158:ARG:HG2	2.04	0.40
42:AE:148:GLU:HA	42:AE:151:LYS:HE3	2.02	0.40
44:AG:33:ASN:HB3	44:AG:38:GLN:HG2	2.03	0.40
45:AH:55:VAL:HG22	45:AH:68:LEU:HD11	2.03	0.40
50:AN:159:ARG:HB2	50:AN:164:LEU:HB2	2.02	0.40
67:Ae:111:ARG:HE	67:Ae:115:LEU:HG	1.86	0.40
79:tE:51:U:O4	79:tE:65:G:O6	2.39	0.40
80:E:88:ASP:HA	80:E:91:LYS:HZ3	1.87	0.40
82:DC:267:LYS:HB2	82:DC:267:LYS:HE2	1.90	0.40
82:DC:638:PRO:HG3	82:DC:671:THR:HB	2.03	0.40
82:DC:663:VAL:HG13	82:DC:709:MET:HE2	2.02	0.40
1:BA:154:GLU:HA	12:BV:63:GLY:HA2	2.03	0.40
4:BE:69:HIS:HD2	15:BY:17:LEU:HG	1.86	0.40
19:BD:4:LEU:HD12	19:BD:4:LEU:HA	1.98	0.40
20:BF:63:GLN:HB3	20:BF:88:PRO:HA	2.02	0.40
34:B5:93:A:H62	34:B5:396:G:N2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:591:A:H2'	34:B5:592:A:C8	2.56	0.40
34:B5:1151:A:H2'	34:B5:1152:A:C8	2.56	0.40
34:B5:1623:C:H2'	34:B5:1624:C:C6	2.56	0.40
38:A1:913:A:O2'	38:A1:2146:C:O2	2.35	0.40
38:A1:1063:G:C6	56:AT:109:VAL:HG22	2.56	0.40
38:A1:1307:G:H4'	38:A1:1308:A:H5'	2.02	0.40
38:A1:2730:G:H4'	53:AQ:184:PHE:CG	2.56	0.40
40:A4:9:A:H2'	40:A4:10:A:H8	1.86	0.40
50:AN:138:GLN:HA	50:AN:143:ARG:HD2	2.03	0.40
63:Aa:99:ALA:HA	63:Aa:100:PRO:HD3	1.98	0.40
67:Ae:97:ALA:O	67:Ae:105:ARG:NH2	2.55	0.40
69:Ag:61:GLN:O	69:Ag:64:THR:OG1	2.37	0.40
79:tE:28:U:H2'	79:tE:29:C:C6	2.56	0.40
82:DC:675:PRO:HG3	82:DC:714:TYR:CG	2.56	0.40
1:BA:11:PRO:HA	1:BA:14:ALA:HB3	2.03	0.40
1:BA:106:SER:N	1:BA:135:GLU:OE2	2.53	0.40
7:BI:75:LYS:HE2	34:B5:258:C:H4'	2.03	0.40
11:BO:30:VAL:HG13	11:BO:39:ILE:HB	2.02	0.40
12:BV:71:ARG:HD3	17:Bb:4:VAL:HG21	2.02	0.40
19:BD:136:VAL:HG22	19:BD:186:VAL:HG22	2.03	0.40
21:BK:61:TRP:NE1	30:Bd:23:VAL:HG13	2.37	0.40
30:Bd:40:ARG:HD2	34:B5:1199:G:C4	2.57	0.40
31:Bg:135:THR:HG23	31:Bg:137:LYS:H	1.86	0.40
34:B5:891:A:H2'	34:B5:892:A:C8	2.57	0.40
34:B5:1752:U:H2'	34:B5:1753:A:H8	1.85	0.40
35:AA:112:ILE:HG23	35:AA:133:TYR:HB2	2.02	0.40
38:A1:278:U:H3	38:A1:287:G:H1	1.70	0.40
38:A1:532:A:H2'	38:A1:533:A:C8	2.56	0.40
38:A1:3095:U:H2'	38:A1:3096:C:C6	2.56	0.40
45:AH:10:ILE:HB	45:AH:53:ILE:HB	2.03	0.40
47:AJ:82:ARG:HH22	47:AJ:114:ILE:HG23	1.87	0.40
57:AU:17:VAL:HB	57:AU:63:VAL:HB	2.04	0.40
58:AV:80:ARG:NH1	58:AV:117:PRO:O	2.46	0.40
60:AX:89:LYS:HE3	60:AX:89:LYS:HB2	1.83	0.40
82:DC:520:THR:HG22	82:DC:530:VAL:HG12	2.04	0.40
2:BB:27:LYS:HG2	2:BB:47:LEU:HB2	2.02	0.40
2:BB:126:THR:HA	2:BB:136:ARG:HA	2.02	0.40
2:BB:136:ARG:NH1	34:B5:884:A:O5'	2.54	0.40
2:BB:183:GLN:HG2	2:BB:187:LYS:HE3	2.04	0.40
5:BG:51:LYS:HB3	5:BG:112:VAL:HB	2.04	0.40
7:BI:65:PHE:HE2	7:BI:78:ILE:HG12	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BO:33:LEU:HD23	11:BO:33:LEU:HA	1.93	0.40
16:Ba:38:ARG:HA	16:Ba:38:ARG:HD3	1.95	0.40
17:Bb:49:HIS:HA	17:Bb:70:LYS:HA	2.02	0.40
19:BD:39:VAL:HG13	19:BD:48:VAL:HG22	2.04	0.40
24:BR:31:ASN:HA	24:BR:34:LEU:HG	2.04	0.40
24:BR:41:ILE:HG23	24:BR:46:LEU:HD23	2.03	0.40
32:Bf:79:LYS:HD2	32:Bf:79:LYS:HA	1.89	0.40
33:BM:46:ARG:NH2	34:B5:1253:U:OP2	2.55	0.40
34:B5:102:U:H3'	34:B5:360:A:H61	1.86	0.40
34:B5:1045:C:H2'	34:B5:1046:G:C8	2.56	0.40
34:B5:1404:C:H2'	34:B5:1405:G:H8	1.86	0.40
34:B5:1623:C:H2'	34:B5:1624:C:H6	1.85	0.40
34:B5:1684:U:H2'	34:B5:1685:G:C8	2.56	0.40
38:A1:856:G:OP1	54:AR:92:GLN:NE2	2.55	0.40
38:A1:1304:A:O2'	38:A1:2884:C:O2	2.34	0.40
38:A1:1336:U:H2'	38:A1:1337:A:C8	2.56	0.40
38:A1:1616:U:H2'	38:A1:1617:G:C8	2.57	0.40
38:A1:2526:C:H2'	38:A1:2527:G:C8	2.57	0.40
39:A3:81:U:H2'	39:A3:82:G:C8	2.57	0.40
44:AG:122:LYS:HB3	44:AG:123:GLN:H	1.62	0.40
67:Ae:82:LEU:HD21	67:Ae:112:ALA:HB2	2.04	0.40
70:Ah:17:LEU:HD21	70:Ah:57:VAL:HG12	2.03	0.40
73:Ak:61:LYS:HZ3	73:Ak:61:LYS:HG2	1.63	0.40
80:E:98:LYS:HB3	80:E:99:LEU:HD12	2.02	0.40
82:DC:239:LYS:HA	82:DC:239:LYS:HD2	1.82	0.40
5:BG:93:LYS:HE2	5:BG:93:LYS:HB3	1.92	0.40
19:BD:121:GLY:HA2	19:BD:124:ARG:HG2	2.02	0.40
21:BK:77:ARG:HH21	21:BK:88:PRO:HA	1.87	0.40
22:BP:50:THR:OG1	22:BP:52:LYS:NZ	2.44	0.40
25:BS:18:LEU:HD23	25:BS:18:LEU:HA	1.92	0.40
28:BZ:83:LEU:HG	28:BZ:89:ILE:HG12	2.03	0.40
31:Bg:286:GLU:HA	31:Bg:287:PRO:HD3	1.92	0.40
34:B5:169:A:O2'	34:B5:171:A:OP2	2.34	0.40
34:B5:340:U:H2'	34:B5:341:A:C8	2.56	0.40
34:B5:1727:G:H2'	34:B5:1728:A:C8	2.56	0.40
36:AB:28:ARG:H	36:AB:28:ARG:HG2	1.67	0.40
37:AC:39:PHE:HE1	37:AC:236:LEU:HA	1.86	0.40
38:A1:93:C:C2	63:Aa:55:LYS:HE2	2.56	0.40
38:A1:952:A:OP1	64:Ab:18:ARG:NH2	2.43	0.40
38:A1:1257:C:H5''	38:A1:1258:U:H5	1.86	0.40
46:AI:38:LYS:HB2	46:AI:83:ASP:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AO:27[A]:LEU:HD11	51:AO:102[A]:LEU:HB2	2.03	0.40
55:AS:155:ARG:HD3	55:AS:172:TYR:CD1	2.56	0.40
58:AV:80:ARG:HB2	58:AV:99:ALA:HB3	2.04	0.40
69:Ag:41:ARG:HG2	69:Ag:56:THR:HG21	2.03	0.40
79:tE:63:C:H2'	79:tE:64:G:C8	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	188 (92%)	16 (8%)	0	100	100
2	BB	212/255 (83%)	191 (90%)	21 (10%)	0	100	100
3	BC	215/254 (85%)	210 (98%)	5 (2%)	0	100	100
4	BE	258/261 (99%)	237 (92%)	21 (8%)	0	100	100
5	BG	224/236 (95%)	217 (97%)	7 (3%)	0	100	100
6	BH	182/190 (96%)	164 (90%)	18 (10%)	0	100	100
7	BI	184/200 (92%)	168 (91%)	16 (9%)	0	100	100
8	BJ	183/197 (93%)	170 (93%)	13 (7%)	0	100	100
9	BL	153/156 (98%)	140 (92%)	13 (8%)	0	100	100
10	BN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
11	BO	125/137 (91%)	111 (89%)	14 (11%)	0	100	100
12	BV	85/87 (98%)	76 (89%)	9 (11%)	0	100	100
13	BW	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
14	BX	142/145 (98%)	128 (90%)	14 (10%)	0	100	100
15	BY	132/135 (98%)	124 (94%)	8 (6%)	0	100	100
16	Ba	95/119 (80%)	88 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Bb	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
18	Be	58/63 (92%)	54 (93%)	4 (7%)	0	100	100
19	BD	221/240 (92%)	211 (96%)	10 (4%)	0	100	100
20	BF	204/225 (91%)	196 (96%)	8 (4%)	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%)	133 (96%)	6 (4%)	0	100	100
24	BR	117/136 (86%)	109 (93%)	8 (7%)	0	100	100
25	BS	143/146 (98%)	135 (94%)	8 (6%)	0	100	100
26	BT	139/144 (96%)	128 (92%)	11 (8%)	0	100	100
27	BU	105/121 (87%)	96 (91%)	9 (9%)	0	100	100
28	BZ	69/108 (64%)	67 (97%)	2 (3%)	0	100	100
29	Bc	61/67 (91%)	59 (97%)	2 (3%)	0	100	100
30	Bd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
31	Bg	310/319 (97%)	281 (91%)	29 (9%)	0	100	100
32	Bf	73/152 (48%)	69 (94%)	4 (6%)	0	100	100
33	BM	122/143 (85%)	115 (94%)	7 (6%)	0	100	100
35	AA	245/254 (96%)	235 (96%)	10 (4%)	0	100	100
36	AB	383/387 (99%)	360 (94%)	23 (6%)	0	100	100
37	AC	359/362 (99%)	338 (94%)	21 (6%)	0	100	100
41	AD	290/297 (98%)	273 (94%)	17 (6%)	0	100	100
42	AE	163/176 (93%)	150 (92%)	13 (8%)	0	100	100
43	AF	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
44	AG	228/256 (89%)	214 (94%)	14 (6%)	0	100	100
45	AH	188/191 (98%)	176 (94%)	12 (6%)	0	100	100
46	AI	220/222 (99%)	217 (99%)	3 (1%)	0	100	100
47	AJ	167/174 (96%)	155 (93%)	12 (7%)	0	100	100
48	AL	191/199 (96%)	184 (96%)	7 (4%)	0	100	100
49	AM	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
50	AN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
51	AO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	AP	171/184 (93%)	166 (97%)	5 (3%)	0	100	100
53	AQ	183/186 (98%)	180 (98%)	3 (2%)	0	100	100
54	AR	186/189 (98%)	178 (96%)	8 (4%)	0	100	100
55	AS	170/178 (96%)	163 (96%)	7 (4%)	0	100	100
56	AT	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
57	AU	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
58	AV	134/137 (98%)	131 (98%)	3 (2%)	0	100	100
59	AW	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
60	AX	119/142 (84%)	114 (96%)	5 (4%)	0	100	100
61	AY	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
62	AZ	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
63	Aa	146/149 (98%)	133 (91%)	13 (9%)	0	100	100
64	Ab	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
65	Ac	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
66	Ad	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
67	Ae	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
68	Af	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
69	Ag	110/121 (91%)	104 (94%)	6 (6%)	0	100	100
70	Ah	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
71	Ai	97/100 (97%)	90 (93%)	7 (7%)	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%)	46 (92%)	4 (8%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	96 (93%)	7 (7%)	0	100	100
78	Ap	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
80	E	215/217 (99%)	204 (95%)	11 (5%)	0	100	100
81	C5	77/92 (84%)	74 (96%)	3 (4%)	0	100	100
82	DC	819/842 (97%)	763 (93%)	55 (7%)	1 (0%)	48	68
All	All	12037/13038 (92%)	11352 (94%)	684 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
82	DC	800	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	173/210 (82%)	173 (100%)	0	100	100
2	BB	191/224 (85%)	191 (100%)	0	100	100
3	BC	176/205 (86%)	176 (100%)	0	100	100
4	BE	221/222 (100%)	221 (100%)	0	100	100
5	BG	193/201 (96%)	193 (100%)	0	100	100
6	BH	165/170 (97%)	165 (100%)	0	100	100
7	BI	150/161 (93%)	150 (100%)	0	100	100
8	BJ	158/166 (95%)	158 (100%)	0	100	100
9	BL	136/137 (99%)	136 (100%)	0	100	100
10	BN	127/128 (99%)	127 (100%)	0	100	100
11	BO	96/105 (91%)	96 (100%)	0	100	100
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	110 (100%)	0	100	100
14	BX	119/120 (99%)	119 (100%)	0	100	100
15	BY	112/113 (99%)	112 (100%)	0	100	100
16	Ba	83/100 (83%)	83 (100%)	0	100	100
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	101/124 (82%)	101 (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	62/89 (70%)	62 (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	137/153 (90%)	137 (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	190/190 (100%)	190 (100%)	0	100	100
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
80	E	198/198 (100%)	198 (100%)	0	100	100
81	C5	60/70 (86%)	60 (100%)	0	100	100
82	DC	699/714 (98%)	699 (100%)	0	100	100
All	All	10255/10973 (94%)	10255 (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 (193) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	23	HIS
1	BA	32	HIS

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Mol	Chain	Res	Type
1	BA	69	ASN
1	BA	83	GLN
2	BB	74	GLN
2	BB	146	GLN
2	BB	199	ASN
2	BB	220	GLN
3	BC	87	GLN
3	BC	89	GLN
3	BC	108	ASN
3	BC	220	ASN
3	BC	250	GLN
4	BE	16	HIS
4	BE	50	ASN
4	BE	69	HIS
4	BE	142	HIS
4	BE	201	HIS
4	BE	223	ASN
4	BE	224	ASN
5	BG	182	GLN
6	BH	174	ASN
7	BI	119	GLN
7	BI	175	GLN
8	BJ	74	ASN
8	BJ	112	GLN
10	BN	69	ASN
10	BN	78	ASN
11	BO	29	HIS
11	BO	99	GLN
12	BV	70	ASN
12	BV	75	ASN
13	BW	70	ASN
14	BX	48	HIS
15	BY	133	ASN
16	Ba	8	ASN
16	Ba	25	ASN
17	Bb	5	GLN
17	Bb	19	HIS
17	Bb	42	ASN
17	Bb	51	GLN
18	Be	17	GLN
19	BD	162	GLN
19	BD	165	ASN

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Mol	Chain	Res	Type
20	BF	63	GLN
20	BF	79	ASN
20	BF	86	GLN
20	BF	122	ASN
20	BF	224	ASN
21	BK	9	ASN
21	BK	29	GLN
21	BK	81	ASN
21	BK	93	GLN
22	BP	98	ASN
22	BP	104	GLN
23	BQ	8	GLN
23	BQ	32	ASN
23	BQ	100	GLN
23	BQ	103	ASN
24	BR	31	ASN
24	BR	101	ASN
25	BS	6	GLN
25	BS	25	ASN
25	BS	104	ASN
26	BT	12	GLN
26	BT	23	GLN
26	BT	64	HIS
26	BT	138	GLN
27	BU	72	ASN
28	BZ	37	GLN
28	BZ	44	GLN
29	Bc	27	GLN
29	Bc	43	ASN
30	Bd	48	ASN
31	Bg	17	ASN
32	Bf	134	ASN
33	BM	38	HIS
33	BM	80	ASN
33	BM	125	ASN
35	AA	8	GLN
35	AA	86	GLN
35	AA	100	ASN
36	AB	121	ASN
36	AB	184	ASN
36	AB	269	GLN
37	AC	9	HIS

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Mol	Chain	Res	Type
37	AC	87	GLN
37	AC	110	ASN
37	AC	291	ASN
37	AC	296	GLN
37	AC	304	GLN
37	AC	307	GLN
41	AD	178	ASN
42	AE	157	GLN
43	AF	37	ASN
43	AF	52	GLN
43	AF	64	GLN
43	AF	80	GLN
43	AF	166	ASN
43	AF	172	ASN
43	AF	186	HIS
43	AF	194	HIS
43	AF	197	GLN
43	AF	199	ASN
43	AF	231	ASN
44	AG	45	ASN
44	AG	123	GLN
44	AG	145	ASN
44	AG	240	ASN
45	AH	9	GLN
45	AH	125	ASN
45	AH	162	GLN
45	AH	183	HIS
47	AJ	47	GLN
47	AJ	68	HIS
47	AJ	90	GLN
47	AJ	95	ASN
47	AJ	152	HIS
48	AL	99	HIS
48	AL	102	GLN
48	AL	106	GLN
48	AL	137	GLN
48	AL	160	GLN
49	AM	41	GLN
49	AM	105	GLN
49	AM	119	GLN
50	AN	57	GLN
50	AN	70	ASN

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Mol	Chain	Res	Type
50	AN	87	GLN
50	AN	139	HIS
50	AN	158	HIS
50	AN	182	ASN
51	AO	14[A]	HIS
51	AO	31[A]	GLN
51	AO	42[A]	ASN
51	AO	122[A]	GLN
52	AP	34	GLN
52	AP	55	GLN
52	AP	120	ASN
53	AQ	58	ASN
54	AR	3	ASN
54	AR	47	ASN
54	AR	92	GLN
54	AR	134	HIS
55	AS	46	GLN
55	AS	62	ASN
55	AS	65	ASN
55	AS	74	ASN
56	AT	66	ASN
57	AU	25	ASN
57	AU	87	ASN
58	AV	98	ASN
58	AV	104	ASN
60	AX	55	ASN
60	AX	65	GLN
60	AX	117	ASN
61	AY	4	GLN
61	AY	98	ASN
62	AZ	40	HIS
62	AZ	78	ASN
62	AZ	106	GLN
62	AZ	122	HIS
62	AZ	123	GLN
63	Aa	62	HIS
64	Ab	19	ASN
65	Ac	36	GLN
65	Ac	75	ASN
66	Ad	57	GLN
67	Ae	31	ASN
68	Af	106	ASN

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Mol	Chain	Res	Type
70	Ah	59	ASN
70	Ah	104	GLN
72	Aj	13	ASN
72	Aj	20	ASN
73	Ak	57	ASN
77	Ao	3	ASN
80	E	108	ASN
80	E	171	ASN
80	E	182	GLN
80	E	199	GLN
80	E	200	ASN
81	C5	22	GLN
82	DC	108	HIS
82	DC	138	GLN
82	DC	186	ASN
82	DC	259	ASN
82	DC	290	ASN
82	DC	414	GLN
82	DC	573	GLN
82	DC	657	HIS
82	DC	734	GLN
82	DC	748	ASN
82	DC	775	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1754/1798 (97%)	525 (29%)	9 (0%)
38	A1	3209/3394 (94%)	770 (23%)	16 (0%)
39	A3	120/121 (99%)	18 (15%)	1 (0%)
40	A4	157/158 (99%)	30 (19%)	1 (0%)
79	tE	76/77 (98%)	15 (19%)	0
All	All	5316/5548 (95%)	1358 (25%)	27 (0%)

All (1358) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	25	C
34	B5	34	G
34	B5	42	G
34	B5	43	A

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Mol	Chain	Res	Type
34	B5	45	U
34	B5	46	A
34	B5	47	A
34	B5	57	G
34	B5	59	C
34	B5	63	G
34	B5	66	U
34	B5	68	A
34	B5	69	G
34	B5	71	A
34	B5	72	A
34	B5	73	U
34	B5	74	U
34	B5	75	U
34	B5	76	A
34	B5	77	U
34	B5	82	U
34	B5	84	A
34	B5	85	A
34	B5	86	A
34	B5	87	C
34	B5	99	C
34	B5	104	A
34	B5	111	U
34	B5	114	C
34	B5	115	G
34	B5	116	U
34	B5	117	U
34	B5	118	U
34	B5	119	A
34	B5	123	G
34	B5	124	A
34	B5	127	G
34	B5	128	U
34	B5	129	U
34	B5	130	C
34	B5	131	C
34	B5	132	U
34	B5	133	U
34	B5	134	U
34	B5	135	A
34	B5	136	C

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Mol	Chain	Res	Type
34	B5	137	U
34	B5	138	A
34	B5	139	C
34	B5	140	A
34	B5	141	U
34	B5	144	U
34	B5	145	A
34	B5	147	A
34	B5	150	U
34	B5	153	G
34	B5	154	G
34	B5	159	U
34	B5	160	C
34	B5	161	U
34	B5	164	A
34	B5	166	C
34	B5	171	A
34	B5	176	C
34	B5	178	U
34	B5	179	A
34	B5	188	A
34	B5	189	C
34	B5	190	C
34	B5	191	C
34	B5	193	U
34	B5	194	U
34	B5	195	G
34	B5	197	A
34	B5	210	A
34	B5	214	G
34	B5	215	A
34	B5	216	U
34	B5	217	A
34	B5	218	A
34	B5	220	A
34	B5	223	U
34	B5	224	C
34	B5	225	A
34	B5	226	A
34	B5	228	G
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	235	G
34	B5	238	U
34	B5	239	C
34	B5	240	U
34	B5	241	U
34	B5	242	U
34	B5	250	C
34	B5	253	A
34	B5	257	A
34	B5	260	U
34	B5	261	U
34	B5	265	A
34	B5	266	A
34	B5	272	U
34	B5	273	G
34	B5	280	U
34	B5	281	G
34	B5	285	G
34	B5	287	G
34	B5	293	U
34	B5	296	U
34	B5	299	A
34	B5	309	C
34	B5	314	C
34	B5	316	A
34	B5	320	U
34	B5	321	C
34	B5	322	G
34	B5	326	G
34	B5	330	G
34	B5	331	A
34	B5	333	A
34	B5	334	G
34	B5	337	G
34	B5	338	C
34	B5	350	U
34	B5	352	A
34	B5	359	A
34	B5	360	A
34	B5	361	C

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Mol	Chain	Res	Type
34	B5	370	A
34	B5	378	A
34	B5	381	C
34	B5	390	G
34	B5	395	U
34	B5	396	G
34	B5	397	A
34	B5	399	A
34	B5	400	A
34	B5	401	A
34	B5	402	C
34	B5	403	G
34	B5	404	G
34	B5	422	G
34	B5	424	C
34	B5	425	A
34	B5	426	G
34	B5	428	A
34	B5	434	G
34	B5	439	U
34	B5	440	U
34	B5	444	C
34	B5	448	C
34	B5	452	A
34	B5	453	U
34	B5	461	G
34	B5	469	C
34	B5	471	A
34	B5	481	A
34	B5	482	U
34	B5	483	A
34	B5	484	C
34	B5	487	G
34	B5	488	G
34	B5	489	C
34	B5	490	C
34	B5	491	C
34	B5	493	U
34	B5	495	C
34	B5	496	G
34	B5	497	G
34	B5	499	U

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Mol	Chain	Res	Type
34	B5	500	C
34	B5	501	U
34	B5	502	U
34	B5	505	A
34	B5	508	U
34	B5	511	A
34	B5	514	G
34	B5	515	A
34	B5	519	C
34	B5	520	A
34	B5	524	U
34	B5	529	A
34	B5	534	A
34	B5	538	A
34	B5	540	G
34	B5	541	A
34	B5	542	A
34	B5	543	C
34	B5	554	C
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	569	C
34	B5	572	C
34	B5	574	G
34	B5	578	U
34	B5	579	A
34	B5	580	A
34	B5	585	A
34	B5	594	A
34	B5	595	G
34	B5	606	A
34	B5	610	G
34	B5	611	U
34	B5	619	A
34	B5	620	A
34	B5	621	A
34	B5	623	A
34	B5	624	G

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Mol	Chain	Res	Type
34	B5	629	U
34	B5	635	A
34	B5	648	G
34	B5	649	U
34	B5	650	U
34	B5	652	G
34	B5	656	G
34	B5	657	U
34	B5	658	C
34	B5	679	U
34	B5	681	U
34	B5	682	C
34	B5	683	C
34	B5	684	A
34	B5	685	A
34	B5	691	C
34	B5	694	U
34	B5	696	C
34	B5	697	C
34	B5	698	U
34	B5	699	U
34	B5	700	C
34	B5	702	G
34	B5	703	G
34	B5	704	C
34	B5	731	C
34	B5	732	G
34	B5	733	A
34	B5	734	A
34	B5	735	C
34	B5	736	C
34	B5	738	G
34	B5	739	G
34	B5	740	A
34	B5	741	C
34	B5	742	U
34	B5	743	U
34	B5	745	U
34	B5	752	A
34	B5	753	A
34	B5	754	A
34	B5	755	A

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Mol	Chain	Res	Type
34	B5	765	G
34	B5	771	A
34	B5	774	A
34	B5	779	U
34	B5	780	A
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	795	U
34	B5	799	A
34	B5	813	U
34	B5	814	A
34	B5	815	G
34	B5	816	G
34	B5	819	G
34	B5	823	G
34	B5	824	G
34	B5	826	U
34	B5	827	C
34	B5	828	U
34	B5	829	A
34	B5	830	U
34	B5	831	U
34	B5	832	U
34	B5	833	U
34	B5	835	U
34	B5	836	U
34	B5	838	G
34	B5	839	U
34	B5	840	U
34	B5	843	U
34	B5	844	A
34	B5	845	G
34	B5	850	A
34	B5	851	U
34	B5	853	G
34	B5	854	U
34	B5	855	A
34	B5	857	U

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Mol	Chain	Res	Type
34	B5	860	U
34	B5	861	U
34	B5	863	A
34	B5	885	G
34	B5	886	U
34	B5	890	C
34	B5	893	U
34	B5	897	C
34	B5	898	A
34	B5	899	G
34	B5	909	U
34	B5	913	G
34	B5	914	G
34	B5	927	C
34	B5	928	U
34	B5	931	C
34	B5	933	A
34	B5	935	U
34	B5	945	U
34	B5	959	U
34	B5	960	U
34	B5	966	A
34	B5	992	A
34	B5	996	U
34	B5	997	G
34	B5	1003	A
34	B5	1004	U
34	B5	1005	A
34	B5	1010	C
34	B5	1021	C
34	B5	1023	A
34	B5	1025	A
34	B5	1026	A
34	B5	1028	C
34	B5	1031	U
34	B5	1033	C
34	B5	1039	A
34	B5	1042	G
34	B5	1052	U
34	B5	1053	G
34	B5	1056	U
34	B5	1057	U

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Mol	Chain	Res	Type
34	B5	1059	U
34	B5	1060	U
34	B5	1061	A
34	B5	1062	A
34	B5	1063	U
34	B5	1064	G
34	B5	1070	C
34	B5	1076	A
34	B5	1081	A
34	B5	1082	C
34	B5	1092	A
34	B5	1093	A
34	B5	1098	U
34	B5	1100	G
34	B5	1109	G
34	B5	1113	A
34	B5	1126	G
34	B5	1138	A
34	B5	1150	G
34	B5	1158	C
34	B5	1163	A
34	B5	1183	A
34	B5	1185	U
34	B5	1186	U
34	B5	1194	A
34	B5	1196	A
34	B5	1199	G
34	B5	1200	G
34	B5	1201	G
34	B5	1202	A
34	B5	1203	A
34	B5	1207	C
34	B5	1216	C
34	B5	1217	A
34	B5	1218	G
34	B5	1227	A
34	B5	1228	G
34	B5	1229	G
34	B5	1233	G
34	B5	1238	A
34	B5	1244	A
34	B5	1245	G

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Mol	Chain	Res	Type
34	B5	1246	C
34	B5	1251	U
34	B5	1252	C
34	B5	1256	A
34	B5	1259	U
34	B5	1263	G
34	B5	1265	G
34	B5	1276	U
34	B5	1284	C
34	B5	1293	U
34	B5	1297	G
34	B5	1301	U
34	B5	1306	C
34	B5	1307	U
34	B5	1312	A
34	B5	1314	U
34	B5	1315	U
34	B5	1319	A
34	B5	1321	A
34	B5	1325	A
34	B5	1338	C
34	B5	1340	U
34	B5	1341	A
34	B5	1344	A
34	B5	1345	A
34	B5	1346	A
34	B5	1347	U
34	B5	1348	A
34	B5	1353	U
34	B5	1354	G
34	B5	1355	C
34	B5	1361	U
34	B5	1362	U
34	B5	1364	G
34	B5	1366	U
34	B5	1367	G
34	B5	1369	U
34	B5	1370	U
34	B5	1371	A
34	B5	1375	A
34	B5	1378	U
34	B5	1383	G

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Mol	Chain	Res	Type
34	B5	1388	A
34	B5	1390	U
34	B5	1397	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	PSU
34	B5	1422	A
34	B5	1424	A
34	B5	1425	A
34	B5	1426	C
34	B5	1427	A
34	B5	1428	G
34	B5	1433	G
34	B5	1435	G
34	B5	1436	A
34	B5	1458	G
34	B5	1459	C
34	B5	1460	A
34	B5	1469	A
34	B5	1471	A
34	B5	1474	G
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	1516	A
34	B5	1521	G
34	B5	1524	A
34	B5	1534	G
34	B5	1537	C
34	B5	1540	G
34	B5	1542	G
34	B5	1557	U
34	B5	1559	A
34	B5	1568	C

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Mol	Chain	Res	Type
34	B5	1573	A
34	B5	1574	G
34	B5	1575	G7M
34	B5	1576	A
34	B5	1577	A
34	B5	1584	G
34	B5	1585	U
34	B5	1596	C
34	B5	1601	G
34	B5	1611	A
34	B5	1616	G
34	B5	1619	C
34	B5	1657	U
34	B5	1658	G
34	B5	1665	U
34	B5	1670	G
34	B5	1678	A
34	B5	1683	C
34	B5	1684	U
34	B5	1689	A
34	B5	1690	G
34	B5	1692	G
34	B5	1693	A
34	B5	1694	A
34	B5	1698	G
34	B5	1699	G
34	B5	1700	C
34	B5	1702	A
34	B5	1703	C
34	B5	1704	U
34	B5	1705	C
34	B5	1707	A
34	B5	1708	U
34	B5	1709	C
34	B5	1711	C
34	B5	1712	A
34	B5	1713	G
34	B5	1714	A
34	B5	1728	A
34	B5	1732	A
34	B5	1735	U
34	B5	1750	A

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Mol	Chain	Res	Type
34	B5	1755	A
34	B5	1756[A]	A
34	B5	1757	G
34	B5	1760	G
34	B5	1762	A
34	B5	1766	A
34	B5	1769	U
34	B5	1773	4AC
34	B5	1780	G
34	B5	1782	MA6
34	B5	1783	C
34	B5	1792	G
34	B5	1793	G
34	B5	1794	A
34	B5	1795	U
34	B5	1796	C
34	B5	1799	U
38	A1	6	A
38	A1	13	A
38	A1	26	A
38	A1	30	G
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	75	G
38	A1	85	A
38	A1	92	G
38	A1	109	A
38	A1	110	G
38	A1	111	C
38	A1	116	A
38	A1	122	A
38	A1	135	C
38	A1	136	G
38	A1	148	G
38	A1	150	A

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Mol	Chain	Res	Type
38	A1	155	G
38	A1	156	G
38	A1	157	A
38	A1	164	A
38	A1	166	C
38	A1	170	G
38	A1	171	G
38	A1	172	G
38	A1	173	G
38	A1	174	C
38	A1	187	A
38	A1	190	U
38	A1	191	U
38	A1	200	C
38	A1	206	G
38	A1	210	U
38	A1	211	A
38	A1	219	A
38	A1	231	G
38	A1	241	G
38	A1	242	C
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	265	A
38	A1	269	G
38	A1	281	G
38	A1	284	A
38	A1	286	U
38	A1	295	A
38	A1	305	U
38	A1	311	C
38	A1	337	G
38	A1	342	A
38	A1	354	U

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Mol	Chain	Res	Type
38	A1	372	A
38	A1	376	G
38	A1	398	A
38	A1	399	A
38	A1	403	C
38	A1	404	G
38	A1	421	G
38	A1	422	A
38	A1	436	A
38	A1	438	A
38	A1	439	C
38	A1	440	A
38	A1	441	U
38	A1	443	G
38	A1	444	U
38	A1	445	G
38	A1	446	U
38	A1	447	U
38	A1	448	U
38	A1	449	U
38	A1	451	U
38	A1	487	U
38	A1	488	U
38	A1	490	C
38	A1	491	A
38	A1	493	U
38	A1	494	G
38	A1	495	G
38	A1	498	A
38	A1	503	C
38	A1	521	A
38	A1	523	A
38	A1	529	A
38	A1	532	A
38	A1	533	A
38	A1	536	U
38	A1	540	U
38	A1	543	C
38	A1	544	C
38	A1	545	U
38	A1	547	G
38	A1	548	G

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Mol	Chain	Res	Type
38	A1	552	G
38	A1	555	U
38	A1	556	U
38	A1	557	A
38	A1	558	U
38	A1	559	A
38	A1	560	G
38	A1	569	A
38	A1	578	A
38	A1	579	G
38	A1	589	A
38	A1	603	A
38	A1	607	A
38	A1	610	G
38	A1	611	A
38	A1	620	U
38	A1	621	A
38	A1	622	A
38	A1	637	C
38	A1	649	A
38	A1	662	U
38	A1	667	C
38	A1	677	A
38	A1	690	A
38	A1	705	A
38	A1	712	G
38	A1	715	A
38	A1	719	U
38	A1	721	G
38	A1	734	C
38	A1	735	A
38	A1	742	G
38	A1	763	G
38	A1	766	U
38	A1	767	U
38	A1	771	A
38	A1	776	PSU
38	A1	777	U
38	A1	780	A
38	A1	781	G
38	A1	785	G
38	A1	799	G

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Mol	Chain	Res	Type
38	A1	806	A
38	A1	808	A
38	A1	817	A
38	A1	826	G
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	880	G
38	A1	884	A
38	A1	896	A
38	A1	907	G
38	A1	908	G
38	A1	914	A
38	A1	916	G
38	A1	917	A
38	A1	920	A
38	A1	921	A
38	A1	923	C
38	A1	924	G
38	A1	932	U
38	A1	933	A
38	A1	937	G
38	A1	944	C
38	A1	953	G
38	A1	959	C
38	A1	960	PSU
38	A1	963	G
38	A1	980	A
38	A1	982	C
38	A1	984	G
38	A1	994	G
38	A1	1000	C
38	A1	1006	A
38	A1	1010	G
38	A1	1013	G
38	A1	1018	G
38	A1	1019	G
38	A1	1020	G

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Mol	Chain	Res	Type
38	A1	1021	G
38	A1	1023	C
38	A1	1033	U
38	A1	1035	G
38	A1	1041	U
38	A1	1047	A
38	A1	1063	G
38	A1	1064	A
38	A1	1066	G
38	A1	1072	G
38	A1	1075	A
38	A1	1079	A
38	A1	1083	G
38	A1	1087	G
38	A1	1092	C
38	A1	1093	A
38	A1	1094	U
38	A1	1095	U
38	A1	1096	U
38	A1	1097	G
38	A1	1098	A
38	A1	1103	A
38	A1	1104	G
38	A1	1112	A
38	A1	1117	G
38	A1	1131	G
38	A1	1135	A
38	A1	1143	A
38	A1	1144	U
38	A1	1150	A
38	A1	1153	A
38	A1	1159	A
38	A1	1160	C
38	A1	1174	G
38	A1	1177	G
38	A1	1178	G
38	A1	1179	A
38	A1	1180	A
38	A1	1181	U
38	A1	1182	A
38	A1	1186	G
38	A1	1192	C

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Mol	Chain	Res	Type
38	A1	1193	A
38	A1	1196	C
38	A1	1201	C
38	A1	1208	U
38	A1	1215	U
38	A1	1218	U
38	A1	1220	U
38	A1	1221	A
38	A1	1222	G
38	A1	1227	C
38	A1	1228	C
38	A1	1230	G
38	A1	1232	C
38	A1	1233	G
38	A1	1234	G
38	A1	1236	G
38	A1	1237	G
38	A1	1238	C
38	A1	1239	C
38	A1	1241	U
38	A1	1242	G
38	A1	1243	G
38	A1	1244	A
38	A1	1246	G
38	A1	1247	U
38	A1	1248	C
38	A1	1249	G
38	A1	1250	G
38	A1	1251	A
38	A1	1252	A
38	A1	1255	C
38	A1	1256	G
38	A1	1257	C
38	A1	1258	U
38	A1	1259	A
38	A1	1260	A
38	A1	1261	G
38	A1	1263	A
38	A1	1264	G
38	A1	1265	U
38	A1	1267	U
38	A1	1268	G

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Mol	Chain	Res	Type
38	A1	1269	U
38	A1	1270	A
38	A1	1271	A
38	A1	1272	C
38	A1	1273	A
38	A1	1274	A
38	A1	1275	C
38	A1	1278	A
38	A1	1279	C
38	A1	1282	G
38	A1	1283	C
38	A1	1285	G
38	A1	1286	A
38	A1	1287	A
38	A1	1292	C
38	A1	1295	G
38	A1	1305	U
38	A1	1307	G
38	A1	1309	U
38	A1	1325	U
38	A1	1329	U
38	A1	1330	A
38	A1	1345	G
38	A1	1348	U
38	A1	1349	G
38	A1	1350	A
38	A1	1351	U
38	A1	1352	A
38	A1	1353	U
38	A1	1354	G
38	A1	1355	A
38	A1	1357	G
38	A1	1365	G
38	A1	1366	A
38	A1	1386	A
38	A1	1392	G
38	A1	1396	C
38	A1	1399	A
38	A1	1400	G
38	A1	1401	A
38	A1	1417	G
38	A1	1419	A

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Mol	Chain	Res	Type
38	A1	1434	G
38	A1	1437	C
38	A1	1443	G
38	A1	1446	A
38	A1	1455	U
38	A1	1469	C
38	A1	1475	A
38	A1	1477	A
38	A1	1481	A
38	A1	1482	A
38	A1	1483	G
38	A1	1487	G
38	A1	1488	G
38	A1	1494	U
38	A1	1496	C
38	A1	1507	G
38	A1	1522	U
38	A1	1524	A
38	A1	1535	A
38	A1	1539	A
38	A1	1547	G
38	A1	1556	C
38	A1	1557	A
38	A1	1561	G
38	A1	1562	C
38	A1	1563	C
38	A1	1564	U
38	A1	1565	G
38	A1	1566	A
38	A1	1567	U
38	A1	1569	U
38	A1	1570	U
38	A1	1571	A
38	A1	1572	U
38	A1	1573	G
38	A1	1575	A
38	A1	1577	G
38	A1	1580	A
38	A1	1582	C
38	A1	1583	A
38	A1	1587	A
38	A1	1590	G

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Mol	Chain	Res	Type
38	A1	1593	A
38	A1	1605	A
38	A1	1613	A
38	A1	1628	C
38	A1	1629	U
38	A1	1630	U
38	A1	1642	A
38	A1	1643	A
38	A1	1645	U
38	A1	1647	A
38	A1	1677	G
38	A1	1683	A
38	A1	1688	U
38	A1	1696	A
38	A1	1714	A
38	A1	1724	U
38	A1	1730	G
38	A1	1741	A
38	A1	1744	G
38	A1	1749	A
38	A1	1750	A
38	A1	1751	G
38	A1	1752	A
38	A1	1756	C
38	A1	1760	A
38	A1	1762	C
38	A1	1763	U
38	A1	1764	U
38	A1	1765	U
38	A1	1766	G
38	A1	1775	G
38	A1	1778	G
38	A1	1780	G
38	A1	1797	A
38	A1	1808	G
38	A1	1812	G
38	A1	1814	A
38	A1	1815	U
38	A1	1816	A
38	A1	1817	G
38	A1	1818	U
38	A1	1819	U

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Mol	Chain	Res	Type
38	A1	1821	U
38	A1	1840	U
38	A1	1842	A
38	A1	1847	A
38	A1	1849	C
38	A1	1850	A
38	A1	1858	A
38	A1	1866	C
38	A1	1878	G
38	A1	1879	A
38	A1	1880	U
38	A1	1886	A
38	A1	1890	U
38	A1	1893	A
38	A1	1897	G
38	A1	1899	G
38	A1	1901	A
38	A1	1906	G
38	A1	1908	A
38	A1	1954	G
38	A1	2094	C
38	A1	2095	G
38	A1	2099	A
38	A1	2101	C
38	A1	2110	G
38	A1	2111	G
38	A1	2112	U
38	A1	2114	C
38	A1	2122	G
38	A1	2126	A
38	A1	2131	A
38	A1	2140	U
38	A1	2142	1MA
38	A1	2144	A
38	A1	2145	A
38	A1	2157	G
38	A1	2158	A
38	A1	2160	G
38	A1	2169	G
38	A1	2176	U
38	A1	2188	A
38	A1	2194	G

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Mol	Chain	Res	Type
38	A1	2206	G
38	A1	2207	A
38	A1	2208	A
38	A1	2210	G
38	A1	2222	A
38	A1	2223	A
38	A1	2243	A
38	A1	2244	A
38	A1	2249	G
38	A1	2250	G
38	A1	2251	G
38	A1	2252	A
38	A1	2253	G
38	A1	2256	A
38	A1	2257	C
38	A1	2258	PSU
38	A1	2259	A
38	A1	2260	PSU
38	A1	2264	PSU
38	A1	2265	C
38	A1	2266	PSU
38	A1	2267	C
38	A1	2269	U
38	A1	2270	A
38	A1	2272	G
38	A1	2273	G
38	A1	2274	U
38	A1	2276	G
38	A1	2280	A
38	A1	2282	U
38	A1	2294	U
38	A1	2295	A
38	A1	2298	U
38	A1	2303	A
38	A1	2306	C
38	A1	2307	G
38	A1	2308	C
38	A1	2310	U
38	A1	2313	A
38	A1	2315	G
38	A1	2334	U
38	A1	2335	G

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Mol	Chain	Res	Type
38	A1	2347	U
38	A1	2363	A
38	A1	2373	A
38	A1	2374	C
38	A1	2375	G
38	A1	2383	C
38	A1	2388	U
38	A1	2389	C
38	A1	2393	G
38	A1	2394	G
38	A1	2397	A
38	A1	2401	A
38	A1	2402	A
38	A1	2403	G
38	A1	2404	A
38	A1	2411	U
38	A1	2412	G
38	A1	2419	A
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	2443	A
38	A1	2445	A
38	A1	2446	U
38	A1	2447	A
38	A1	2451	G
38	A1	2452	G
38	A1	2453	U
38	A1	2454	G
38	A1	2455	U
38	A1	2456	A
38	A1	2458	A
38	A1	2459	A
38	A1	2460	U
38	A1	2461	A
38	A1	2462	A
38	A1	2463	G
38	A1	2464	U
38	A1	2465	G

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Mol	Chain	Res	Type
38	A1	2466	G
38	A1	2468	A
38	A1	2469	G
38	A1	2470	C
38	A1	2473	C
38	A1	2474	G
38	A1	2475	G
38	A1	2476	C
38	A1	2477	G
38	A1	2481	G
38	A1	2482	U
38	A1	2484	A
38	A1	2485	A
38	A1	2486	A
38	A1	2487	U
38	A1	2490	C
38	A1	2491	A
38	A1	2492	C
38	A1	2493	U
38	A1	2494	A
38	A1	2495	C
38	A1	2496	C
38	A1	2497	U
38	A1	2498	U
38	A1	2499	U
38	A1	2500	A
38	A1	2501	U
38	A1	2502	A
38	A1	2504	U
38	A1	2505	U
38	A1	2507	C
38	A1	2508	U
38	A1	2514	U
38	A1	2515	A
38	A1	2522	G
38	A1	2523	A
38	A1	2530	G
38	A1	2535	A
38	A1	2536	A
38	A1	2537	U
38	A1	2538	U
38	A1	2539	C

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Mol	Chain	Res	Type
38	A1	2540	A
38	A1	2542	U
38	A1	2543	U
38	A1	2544	U
38	A1	2545	C
38	A1	2546	C
38	A1	2549	G
38	A1	2550	U
38	A1	2552	C
38	A1	2554	A
38	A1	2559	U
38	A1	2562	A
38	A1	2569	A
38	A1	2570	U
38	A1	2571	U
38	A1	2572	C
38	A1	2573	G
38	A1	2585	G
38	A1	2586	G
38	A1	2593	A
38	A1	2606	G
38	A1	2607	G
38	A1	2614	G
38	A1	2629	U
38	A1	2635	A
38	A1	2637	A
38	A1	2648	G
38	A1	2651	G
38	A1	2652	U
38	A1	2656	A
38	A1	2666	C
38	A1	2672	G
38	A1	2674	A
38	A1	2677	G
38	A1	2678	A
38	A1	2681	U
38	A1	2689	A
38	A1	2691	A
38	A1	2694	A
38	A1	2704	A
38	A1	2705	A
38	A1	2714	G

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Mol	Chain	Res	Type
38	A1	2719	U
38	A1	2728	G
38	A1	2729	U
38	A1	2737	C
38	A1	2740	A
38	A1	2749	G
38	A1	2752	U
38	A1	2753	G
38	A1	2755	C
38	A1	2761	G
38	A1	2762	A
38	A1	2772	C
38	A1	2773	C
38	A1	2777	G
38	A1	2778	G
38	A1	2779	A
38	A1	2780	A
38	A1	2796	G
38	A1	2800	G
38	A1	2801	A
38	A1	2802	A
38	A1	2803	A
38	A1	2807	U
38	A1	2808	A
38	A1	2809	C
38	A1	2810	C
38	A1	2814	G
38	A1	2816	G
38	A1	2817	A
38	A1	2821	C
38	A1	2828	G
38	A1	2838	A
38	A1	2842	U
38	A1	2845	A
38	A1	2847	A
38	A1	2849	C
38	A1	2861	U
38	A1	2867	C
38	A1	2871	G
38	A1	2887	A
38	A1	2898	G
38	A1	2904	U

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Mol	Chain	Res	Type
38	A1	2911	A
38	A1	2918	G
38	A1	2923	PSU
38	A1	2933	A
38	A1	2935	U
38	A1	2936	A
38	A1	2938	G
38	A1	2941	A
38	A1	2942	C
38	A1	2946	A
38	A1	2947	G
38	A1	2971	A
38	A1	2983	C
38	A1	2990	G
38	A1	2996	U
38	A1	2997	G
38	A1	3003	G
38	A1	3012	A
38	A1	3018	C
38	A1	3021	A
38	A1	3022	G
38	A1	3023	U
38	A1	3035	A
38	A1	3048	A
38	A1	3049	A
38	A1	3055	U
38	A1	3056	U
38	A1	3057	U
38	A1	3059	G
38	A1	3069	G
38	A1	3078	U
38	A1	3079	U
38	A1	3080	G
38	A1	3081	C
38	A1	3086	A
38	A1	3087	A
38	A1	3092	C
38	A1	3094	A
38	A1	3101	G
38	A1	3104	U
38	A1	3109	G
38	A1	3115	C

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Mol	Chain	Res	Type
38	A1	3116	G
38	A1	3122	A
38	A1	3130	A
38	A1	3131	U
38	A1	3141	A
38	A1	3142	A
38	A1	3143	C
38	A1	3153	U
38	A1	3155	U
38	A1	3156	U
38	A1	3157	U
38	A1	3163	A
38	A1	3165	A
38	A1	3166	C
38	A1	3167	A
38	A1	3168	A
38	A1	3169	U
38	A1	3170	A
38	A1	3171	U
38	A1	3173	G
38	A1	3174	A
38	A1	3176	G
38	A1	3179	U
38	A1	3181	C
38	A1	3186	A
38	A1	3187	A
38	A1	3195	U
38	A1	3196	U
38	A1	3199	G
38	A1	3206	C
38	A1	3207	U
38	A1	3209	A
38	A1	3210	A
38	A1	3217	C
38	A1	3218	A
38	A1	3219	G
38	A1	3224	G
38	A1	3226	A
38	A1	3227	A
38	A1	3229	G
38	A1	3238	G
38	A1	3243	A

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Mol	Chain	Res	Type
38	A1	3246	G
38	A1	3247	G
38	A1	3259	U
38	A1	3260	G
38	A1	3263	G
38	A1	3273	A
38	A1	3276	G
38	A1	3277	U
38	A1	3278	C
38	A1	3279	A
38	A1	3283	U
38	A1	3284	G
38	A1	3289	G
38	A1	3294	A
38	A1	3303	G
38	A1	3304	U
38	A1	3307	A
38	A1	3313	U
38	A1	3316	A
38	A1	3341	U
38	A1	3345	G
38	A1	3350	C
38	A1	3352	U
38	A1	3354	U
38	A1	3363	U
38	A1	3368	U
38	A1	3369	G
38	A1	3375	A
38	A1	3378	C
38	A1	3390	G
38	A1	3396	U
39	A3	11	A
39	A3	22	A
39	A3	23	A
39	A3	24	A
39	A3	33	U
39	A3	38	U
39	A3	49	G
39	A3	51	A
39	A3	54	U
39	A3	55	A
39	A3	64	A

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Mol	Chain	Res	Type
39	A3	65	G
39	A3	74	C
39	A3	91	G
39	A3	99	G
39	A3	102	A
39	A3	112	G
39	A3	121	U
40	A4	23	U
40	A4	34	U
40	A4	35	C
40	A4	38	U
40	A4	51	G
40	A4	52	A
40	A4	59	A
40	A4	62	C
40	A4	63	G
40	A4	71	A
40	A4	75	G
40	A4	80	A
40	A4	81	U
40	A4	82	U
40	A4	84	C
40	A4	86	U
40	A4	87	G
40	A4	88	A
40	A4	89	A
40	A4	90	U
40	A4	95	G
40	A4	104	A
40	A4	106	C
40	A4	111	A
40	A4	113	U
40	A4	116	G
40	A4	125	U
40	A4	131	A
40	A4	148	G
40	A4	152	G
79	tE	3	C
79	tE	9	G
79	tE	14	A
79	tE	18(A)	U
79	tE	19	G

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Mol	Chain	Res	Type
79	tE	20	G
79	tE	21	U
79	tE	22	A
79	tE	23	G
79	tE	29	C
79	tE	35	C
79	tE	48	U
79	tE	49	C
79	tE	60	A
79	tE	77	A

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	B5	117	U
34	B5	196	G
34	B5	395	U
34	B5	752	A
34	B5	889	U
34	B5	1344	A
34	B5	1683	C
34	B5	1754	A
34	B5	1755	A
38	A1	252	U
38	A1	916	G
38	A1	1560	G
38	A1	2094	C
38	A1	2206	G
38	A1	2207	A
38	A1	2222	A
38	A1	2256	A
38	A1	2440	G
38	A1	2469	G
38	A1	2499	U
38	A1	2772	C
38	A1	3022	G
38	A1	3121	U
38	A1	3154	C
38	A1	3169	U
39	A3	23	A
40	A4	88	A

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

60 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	PSU	B5	120	34	18,21,22	1.37	2 (11%)	21,30,33	1.98	4 (19%)
38	PSU	A1	1052	38	18,21,22	1.40	3 (16%)	21,30,33	1.91	4 (19%)
38	PSU	A1	2314	38	18,21,22	1.39	2 (11%)	21,30,33	2.02	4 (19%)
38	PSU	A1	776	38	18,21,22	1.42	3 (16%)	21,30,33	1.97	4 (19%)
34	PSU	B5	1187	34	18,21,22	1.37	2 (11%)	21,30,33	2.01	3 (14%)
34	4AC	B5	1280	34	21,24,25	1.05	1 (4%)	28,34,37	1.11	2 (7%)
38	5MC	A1	2278	38	19,22,23	1.53	3 (15%)	26,32,35	1.29	4 (15%)
38	PSU	A1	2349	38	18,21,22	1.45	4 (22%)	21,30,33	1.97	3 (14%)
38	PSU	A1	2351	38	18,21,22	1.41	3 (16%)	21,30,33	1.97	3 (14%)
34	PSU	B5	1415	34	18,21,22	1.42	2 (11%)	21,30,33	2.03	3 (14%)
36	HIC	AB	243	36	10,11,12	1.50	1 (10%)	9,14,16	1.43	1 (11%)
34	PSU	B5	1181	34	18,21,22	1.34	2 (11%)	21,30,33	2.03	4 (19%)
38	PSU	A1	1042	38	18,21,22	1.40	4 (22%)	21,30,33	1.86	4 (19%)
38	PSU	A1	2191	38	18,21,22	1.37	2 (11%)	21,30,33	2.02	4 (19%)
38	PSU	A1	2923	38	18,21,22	1.37	2 (11%)	21,30,33	2.02	3 (14%)
38	PSU	A1	2975	38	18,21,22	1.42	3 (16%)	21,30,33	2.01	3 (14%)
34	PSU	B5	1290	34	18,21,22	1.38	2 (11%)	21,30,33	1.99	3 (14%)
38	PSU	A1	2340	38	18,21,22	1.54	3 (16%)	21,30,33	1.96	4 (19%)
82	DDE	DC	699	-	18,20,21	1.04	1 (5%)	17,28,30	0.78	1 (5%)
39	PSU	A3	50	39	18,21,22	1.37	2 (11%)	21,30,33	2.04	4 (19%)
38	PSU	A1	2260	38	18,21,22	1.38	2 (11%)	21,30,33	1.99	3 (14%)
34	4AC	B5	1773	34	21,24,25	1.15	2 (9%)	28,34,37	1.82	8 (28%)
38	PSU	A1	2258	38	18,21,22	1.42	2 (11%)	21,30,33	2.03	3 (14%)
34	PSU	B5	632	34	18,21,22	1.39	3 (16%)	21,30,33	1.97	3 (14%)
38	PSU	A1	990	38	18,21,22	1.43	2 (11%)	21,30,33	2.01	3 (14%)
38	PSU	A1	986	38	18,21,22	1.41	3 (16%)	21,30,33	1.92	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	PSU	A1	1056	38	18,21,22	1.43	3 (16%)	21,30,33	1.99	3 (14%)
34	MA6	B5	1781	34	23,26,27	1.49	4 (17%)	33,38,41	2.07	10 (30%)
38	OMU	A1	2921	38	19,22,23	1.24	2 (10%)	25,31,34	1.82	5 (20%)
34	PSU	B5	759	34	18,21,22	1.42	2 (11%)	21,30,33	2.04	3 (14%)
38	5MC	A1	2870	38	19,22,23	1.46	3 (15%)	26,32,35	1.34	3 (11%)
38	UR3	A1	2634	38	19,22,23	0.96	0	26,32,35	1.75	4 (15%)
38	PSU	A1	2865	38	18,21,22	1.42	2 (11%)	21,30,33	2.02	5 (23%)
38	PSU	A1	960	38	18,21,22	1.45	3 (16%)	21,30,33	2.05	4 (19%)
38	PSU	A1	2735	38	18,21,22	1.41	2 (11%)	21,30,33	1.99	3 (14%)
34	PSU	B5	302	34	18,21,22	1.39	2 (11%)	21,30,33	2.03	4 (19%)
38	PSU	A1	2880	38	18,21,22	1.39	3 (16%)	21,30,33	2.05	4 (19%)
38	OMG	A1	2922	38	23,26,27	1.19	3 (13%)	32,38,41	1.93	6 (18%)
38	PSU	A1	2944	38	18,21,22	1.41	3 (16%)	21,30,33	2.04	3 (14%)
34	PSU	B5	106	34	18,21,22	1.43	3 (16%)	21,30,33	1.99	3 (14%)
34	PSU	B5	211	34	18,21,22	1.47	2 (11%)	21,30,33	1.90	4 (19%)
34	PSU	B5	766	34	18,21,22	1.40	2 (11%)	21,30,33	2.01	4 (19%)
38	PSU	A1	2264	38	18,21,22	1.52	3 (16%)	21,30,33	1.99	3 (14%)
38	PSU	A1	2826	38	18,21,22	1.41	3 (16%)	21,30,33	2.03	4 (19%)
34	PSU	B5	999	34	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
38	PSU	A1	1124	38	18,21,22	1.38	2 (11%)	21,30,33	2.04	4 (19%)
38	1MA	A1	645	38	21,25,26	1.36	4 (19%)	30,37,40	1.66	6 (20%)
38	PSU	A1	2266	38	18,21,22	1.49	3 (16%)	21,30,33	2.05	3 (14%)
38	PSU	A1	1004	38	18,21,22	1.40	3 (16%)	21,30,33	2.02	3 (14%)
38	PSU	A1	2416	38	18,21,22	1.43	3 (16%)	21,30,33	2.00	3 (14%)
34	MA6	B5	1782	34	23,26,27	1.51	4 (17%)	33,38,41	2.08	10 (30%)
40	PSU	A4	73	40	18,21,22	1.36	2 (11%)	21,30,33	1.99	3 (14%)
34	PSU	B5	466	34	18,21,22	1.35	2 (11%)	21,30,33	1.99	3 (14%)
34	B8N	B5	1191	34	25,29,30	1.38	3 (12%)	28,42,45	5.53	7 (25%)
34	G7M	B5	1575	79,34	23,26,27	2.46	7 (30%)	34,39,42	1.79	8 (23%)
38	PSU	A1	966	38	18,21,22	1.44	3 (16%)	21,30,33	2.09	3 (14%)
38	PSU	A1	1110	38	18,21,22	1.41	3 (16%)	21,30,33	1.99	3 (14%)
38	PSU	A1	2129	38	18,21,22	1.44	3 (16%)	21,30,33	2.02	3 (14%)
38	PSU	A1	2133	38	18,21,22	1.50	3 (16%)	21,30,33	2.07	5 (23%)
38	1MA	A1	2142	38	21,25,26	1.31	4 (19%)	30,37,40	1.74	4 (13%)

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	PSU	B5	120	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1052	38	-	2/7/25/26	0/2/2/2
38	PSU	A1	2314	38	-	1/7/25/26	0/2/2/2
38	PSU	A1	776	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	1187	34	-	2/7/25/26	0/2/2/2
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	5MC	A1	2278	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2349	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2351	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	1415	34	-	2/7/25/26	0/2/2/2
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
34	PSU	B5	1181	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1042	38	-	3/7/25/26	0/2/2/2
38	PSU	A1	2191	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2923	38	-	3/7/25/26	0/2/2/2
38	PSU	A1	2975	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	1290	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2340	38	-	2/7/25/26	0/2/2/2
82	DDE	DC	699	-	-	5/20/21/23	0/1/1/1
39	PSU	A3	50	39	-	0/7/25/26	0/2/2/2
38	PSU	A1	2260	38	-	2/7/25/26	0/2/2/2
34	4AC	B5	1773	34	-	6/11/29/30	0/2/2/2
38	PSU	A1	2258	38	-	2/7/25/26	0/2/2/2
34	PSU	B5	632	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	990	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	986	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1056	38	-	0/7/25/26	0/2/2/2
34	MA6	B5	1781	34	-	3/11/29/30	0/3/3/3
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
34	PSU	B5	759	34	-	0/7/25/26	0/2/2/2
38	5MC	A1	2870	38	-	2/7/25/26	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2865	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	960	38	-	4/7/25/26	0/2/2/2
38	PSU	A1	2735	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	302	34	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	PSU	A1	2880	38	-	0/7/25/26	0/2/2/2
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	PSU	A1	2944	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	106	34	-	0/7/25/26	0/2/2/2
34	PSU	B5	211	34	-	2/7/25/26	0/2/2/2
34	PSU	B5	766	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2264	38	-	3/7/25/26	0/2/2/2
38	PSU	A1	2826	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	999	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1124	38	-	0/7/25/26	0/2/2/2
38	1MA	A1	645	38	-	2/7/25/26	0/3/3/3
38	PSU	A1	2266	38	-	2/7/25/26	0/2/2/2
38	PSU	A1	1004	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2416	38	-	0/7/25/26	0/2/2/2
34	MA6	B5	1782	34	-	5/11/29/30	0/3/3/3
40	PSU	A4	73	40	-	0/7/25/26	0/2/2/2
34	PSU	B5	466	34	-	0/7/25/26	0/2/2/2
34	B8N	B5	1191	34	-	4/16/34/35	0/2/2/2
34	G7M	B5	1575	79,34	-	2/7/25/26	0/3/3/3
38	PSU	A1	966	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1110	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2129	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2133	38	-	0/7/25/26	0/2/2/2
38	1MA	A1	2142	38	-	2/7/25/26	0/3/3/3

All (157) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	O6-C6	7.51	1.37	1.23
34	B5	1575	G7M	C2-N2	5.45	1.46	1.34
38	A1	2278	5MC	C5-C4	5.29	1.48	1.44
38	A1	2870	5MC	C5-C4	4.83	1.47	1.44
34	B5	1782	MA6	C5-C4	4.77	1.47	1.39
34	B5	1781	MA6	C5-C4	4.69	1.47	1.39
34	B5	1575	G7M	C5-N7	-4.32	1.34	1.39
38	A1	2340	PSU	C6-C5	3.92	1.39	1.35
34	B5	1191	B8N	C4-C5	-3.73	1.39	1.47
34	B5	1415	PSU	C6-C5	3.70	1.39	1.35
34	B5	759	PSU	C6-C5	3.70	1.39	1.35
34	B5	211	PSU	C6-C5	3.69	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	960	PSU	C6-C5	3.65	1.39	1.35
34	B5	1575	G7M	CN7-N7	3.56	1.52	1.46
38	A1	990	PSU	C6-C5	3.56	1.39	1.35
38	A1	2264	PSU	C6-C5	3.56	1.39	1.35
38	A1	966	PSU	C6-C5	3.55	1.39	1.35
38	A1	2129	PSU	C6-C5	3.52	1.39	1.35
34	B5	120	PSU	C6-C5	3.51	1.39	1.35
38	A1	2735	PSU	C6-C5	3.48	1.39	1.35
34	B5	302	PSU	C6-C5	3.45	1.39	1.35
38	A1	1056	PSU	C6-C5	3.45	1.39	1.35
34	B5	766	PSU	C6-C5	3.44	1.39	1.35
38	A1	2258	PSU	C6-C5	3.44	1.39	1.35
38	A1	1004	PSU	C6-C5	3.42	1.39	1.35
34	B5	106	PSU	C6-C5	3.41	1.39	1.35
38	A1	2266	PSU	C6-C5	3.40	1.39	1.35
34	B5	1187	PSU	C6-C5	3.38	1.39	1.35
38	A1	2351	PSU	C6-C5	3.38	1.39	1.35
34	B5	1290	PSU	C6-C5	3.37	1.39	1.35
39	A3	50	PSU	C6-C5	3.35	1.39	1.35
38	A1	1124	PSU	C6-C5	3.33	1.39	1.35
38	A1	2133	PSU	C6-C5	3.31	1.39	1.35
34	B5	632	PSU	C6-C5	3.29	1.38	1.35
38	A1	1052	PSU	C6-C5	3.28	1.38	1.35
38	A1	1110	PSU	C6-C5	3.28	1.38	1.35
38	A1	986	PSU	C6-C5	3.26	1.38	1.35
38	A1	2260	PSU	C6-C5	3.25	1.38	1.35
38	A1	2975	PSU	C6-C5	3.25	1.38	1.35
38	A1	2349	PSU	C6-C5	3.23	1.38	1.35
38	A1	2314	PSU	C6-C5	3.20	1.38	1.35
34	B5	1773	4AC	C4-N4	-3.20	1.35	1.39
38	A1	2880	PSU	C6-C5	3.19	1.38	1.35
38	A1	2944	PSU	C6-C5	3.19	1.38	1.35
40	A4	73	PSU	C6-C5	3.18	1.38	1.35
34	B5	1191	B8N	C6-C5	3.17	1.39	1.35
34	B5	999	PSU	C6-C5	3.17	1.38	1.35
38	A1	2865	PSU	C6-C5	3.17	1.38	1.35
34	B5	1181	PSU	C6-C5	3.15	1.38	1.35
38	A1	2416	PSU	C6-C5	3.15	1.38	1.35
34	B5	1782	MA6	C5-C6	3.14	1.49	1.41
34	B5	466	PSU	C6-C5	3.13	1.38	1.35
38	A1	2191	PSU	C6-C5	3.13	1.38	1.35
38	A1	2133	PSU	C4-N3	-3.12	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	776	PSU	C6-C5	3.11	1.38	1.35
38	A1	2923	PSU	C6-C5	3.09	1.38	1.35
38	A1	2922	OMG	C5-C4	3.08	1.47	1.38
38	A1	645	1MA	C6-N6	3.01	1.35	1.28
38	A1	645	1MA	C5-C4	2.98	1.46	1.38
38	A1	2826	PSU	C6-C5	2.96	1.38	1.35
34	B5	1280	4AC	C4-N4	-2.93	1.35	1.39
38	A1	2142	1MA	C5-C4	2.93	1.46	1.38
34	B5	1575	G7M	C6-N1	-2.93	1.33	1.38
38	A1	2944	PSU	C4-N3	-2.93	1.33	1.38
34	B5	1781	MA6	C5-C6	2.89	1.48	1.41
36	AB	243	HIC	CD2-CG	2.88	1.41	1.36
38	A1	2921	OMU	C4-N3	-2.87	1.33	1.38
38	A1	2870	5MC	C6-C5	2.86	1.39	1.34
38	A1	2340	PSU	C4-N3	-2.85	1.33	1.38
38	A1	2416	PSU	C4-N3	-2.84	1.33	1.38
38	A1	2975	PSU	C4-N3	-2.84	1.33	1.38
38	A1	2880	PSU	C4-N3	-2.84	1.33	1.38
38	A1	2865	PSU	C4-N3	-2.78	1.33	1.38
38	A1	2129	PSU	C4-N3	-2.78	1.33	1.38
38	A1	1042	PSU	C4-N3	-2.78	1.33	1.38
38	A1	2142	1MA	C6-N6	2.77	1.34	1.28
38	A1	966	PSU	C4-N3	-2.77	1.33	1.38
38	A1	2266	PSU	O4'-C1'	-2.77	1.40	1.43
38	A1	960	PSU	C4-N3	-2.76	1.33	1.38
38	A1	1110	PSU	C4-N3	-2.76	1.33	1.38
38	A1	990	PSU	C4-N3	-2.76	1.33	1.38
38	A1	2826	PSU	C4-N3	-2.75	1.33	1.38
34	B5	632	PSU	C4-N3	-2.74	1.33	1.38
38	A1	2314	PSU	C4-N3	-2.73	1.33	1.38
38	A1	2735	PSU	C4-N3	-2.72	1.33	1.38
38	A1	1056	PSU	C4-N3	-2.72	1.33	1.38
38	A1	1004	PSU	C4-N3	-2.71	1.33	1.38
38	A1	2351	PSU	C4-N3	-2.70	1.33	1.38
39	A3	50	PSU	C4-N3	-2.69	1.33	1.38
38	A1	776	PSU	C4-N3	-2.68	1.33	1.38
38	A1	1124	PSU	C4-N3	-2.68	1.33	1.38
38	A1	986	PSU	C4-N3	-2.68	1.33	1.38
34	B5	1290	PSU	C4-N3	-2.68	1.33	1.38
34	B5	106	PSU	C4-N3	-2.67	1.33	1.38
38	A1	2258	PSU	C4-N3	-2.66	1.33	1.38
38	A1	2923	PSU	C4-N3	-2.66	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	759	PSU	C4-N3	-2.66	1.33	1.38
38	A1	1052	PSU	C4-N3	-2.66	1.33	1.38
38	A1	2278	5MC	C6-C5	2.65	1.38	1.34
38	A1	2191	PSU	C4-N3	-2.65	1.33	1.38
38	A1	2264	PSU	C4-N3	-2.65	1.33	1.38
34	B5	1187	PSU	C4-N3	-2.63	1.33	1.38
38	A1	2349	PSU	C4-N3	-2.63	1.33	1.38
82	DC	699	DDE	CD2-CG	2.62	1.41	1.36
38	A1	1042	PSU	C6-C5	2.60	1.38	1.35
34	B5	1415	PSU	C4-N3	-2.60	1.34	1.38
38	A1	2264	PSU	O4'-C1'	-2.60	1.40	1.43
34	B5	999	PSU	C4-N3	-2.60	1.34	1.38
34	B5	211	PSU	C4-N3	-2.59	1.34	1.38
34	B5	466	PSU	C4-N3	-2.59	1.34	1.38
34	B5	302	PSU	C4-N3	-2.59	1.34	1.38
34	B5	1181	PSU	C4-N3	-2.58	1.34	1.38
40	A4	73	PSU	C4-N3	-2.58	1.34	1.38
38	A1	2260	PSU	C4-N3	-2.57	1.34	1.38
34	B5	766	PSU	C4-N3	-2.55	1.34	1.38
38	A1	2922	OMG	C6-N1	-2.52	1.34	1.38
38	A1	2266	PSU	C4-N3	-2.52	1.34	1.38
34	B5	120	PSU	C4-N3	-2.46	1.34	1.38
38	A1	2133	PSU	C2-N3	-2.40	1.33	1.37
34	B5	1782	MA6	C8-N7	2.35	1.36	1.31
38	A1	645	1MA	C5-N7	-2.35	1.34	1.39
38	A1	2142	1MA	C2-N3	2.34	1.34	1.30
38	A1	2921	OMU	C2-N3	-2.31	1.33	1.38
34	B5	1575	G7M	C2-N1	-2.28	1.32	1.37
38	A1	1042	PSU	C2-N3	-2.27	1.33	1.37
38	A1	2278	5MC	C6-N1	-2.26	1.34	1.38
34	B5	1781	MA6	C5-N7	-2.23	1.35	1.39
38	A1	2880	PSU	C2-N3	-2.22	1.33	1.37
34	B5	1575	G7M	C4-N9	-2.19	1.32	1.38
38	A1	2416	PSU	C2-N3	-2.18	1.33	1.37
38	A1	2142	1MA	C5-N7	-2.18	1.34	1.39
38	A1	2922	OMG	C5-N7	-2.16	1.34	1.39
38	A1	2870	5MC	C6-N1	-2.15	1.34	1.38
38	A1	1042	PSU	C2-N1	-2.15	1.33	1.36
38	A1	2349	PSU	C2-N3	-2.15	1.33	1.37
34	B5	1782	MA6	C5-N7	-2.14	1.35	1.39
34	B5	1191	B8N	CN1-N1	2.13	1.50	1.46
38	A1	2340	PSU	C2-N3	-2.13	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2826	PSU	C2-N3	-2.12	1.34	1.37
34	B5	632	PSU	C2-N3	-2.11	1.34	1.37
34	B5	1781	MA6	C8-N7	2.08	1.35	1.31
38	A1	645	1MA	C4-N9	-2.07	1.32	1.38
38	A1	2349	PSU	C2-N1	-2.07	1.34	1.36
38	A1	2351	PSU	C2-N3	-2.06	1.34	1.37
38	A1	776	PSU	C2-N3	-2.05	1.34	1.37
38	A1	1052	PSU	C2-N3	-2.05	1.34	1.37
34	B5	1773	4AC	C7-N4	-2.05	1.32	1.37
38	A1	2129	PSU	C2-N3	-2.05	1.34	1.37
38	A1	966	PSU	C2-N3	-2.04	1.34	1.37
38	A1	986	PSU	C2-N3	-2.04	1.34	1.37
34	B5	106	PSU	C4-C5	2.04	1.50	1.44
38	A1	2975	PSU	C2-N3	-2.03	1.34	1.37
38	A1	2944	PSU	C2-N3	-2.02	1.34	1.37
38	A1	1056	PSU	C2-N3	-2.01	1.34	1.37
38	A1	1110	PSU	C2-N3	-2.01	1.34	1.37
38	A1	960	PSU	O4'-C1'	-2.00	1.41	1.43
38	A1	1004	PSU	C2-N3	-2.00	1.34	1.37

All (235) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1191	B8N	C32-C31-N3	28.00	161.11	112.16
38	A1	2133	PSU	N1-C2-N3	6.83	122.38	115.17
38	A1	2634	UR3	C4-N3-C2	-6.62	119.25	124.58
38	A1	966	PSU	N1-C2-N3	6.54	122.07	115.17
38	A1	2258	PSU	N1-C2-N3	6.49	122.02	115.17
38	A1	960	PSU	N1-C2-N3	6.41	121.93	115.17
39	A3	50	PSU	N1-C2-N3	6.40	121.92	115.17
38	A1	1124	PSU	N1-C2-N3	6.37	121.89	115.17
38	A1	2266	PSU	N1-C2-N3	6.37	121.89	115.17
38	A1	2826	PSU	N1-C2-N3	6.37	121.88	115.17
34	B5	759	PSU	N1-C2-N3	6.36	121.87	115.17
38	A1	2416	PSU	N1-C2-N3	6.35	121.87	115.17
38	A1	1004	PSU	N1-C2-N3	6.35	121.86	115.17
38	A1	2129	PSU	N1-C2-N3	6.35	121.86	115.17
38	A1	2865	PSU	N1-C2-N3	6.34	121.85	115.17
34	B5	1415	PSU	N1-C2-N3	6.33	121.85	115.17
34	B5	766	PSU	N1-C2-N3	6.32	121.84	115.17
38	A1	2975	PSU	N1-C2-N3	6.32	121.83	115.17
34	B5	1181	PSU	N1-C2-N3	6.31	121.82	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2314	PSU	N1-C2-N3	6.31	121.82	115.17
38	A1	990	PSU	N1-C2-N3	6.30	121.81	115.17
34	B5	106	PSU	N1-C2-N3	6.29	121.80	115.17
38	A1	2191	PSU	N1-C2-N3	6.29	121.80	115.17
38	A1	2944	PSU	N1-C2-N3	6.29	121.80	115.17
38	A1	2923	PSU	N1-C2-N3	6.28	121.80	115.17
38	A1	2260	PSU	N1-C2-N3	6.28	121.79	115.17
38	A1	1056	PSU	N1-C2-N3	6.27	121.78	115.17
34	B5	1187	PSU	N1-C2-N3	6.27	121.78	115.17
34	B5	999	PSU	N1-C2-N3	6.27	121.78	115.17
38	A1	2264	PSU	N1-C2-N3	6.25	121.77	115.17
38	A1	2340	PSU	N1-C2-N3	6.25	121.76	115.17
34	B5	466	PSU	N1-C2-N3	6.25	121.76	115.17
40	A4	73	PSU	N1-C2-N3	6.23	121.73	115.17
38	A1	2880	PSU	N1-C2-N3	6.22	121.73	115.17
34	B5	1290	PSU	N1-C2-N3	6.18	121.69	115.17
38	A1	1110	PSU	N1-C2-N3	6.18	121.69	115.17
38	A1	2351	PSU	N1-C2-N3	6.18	121.68	115.17
38	A1	2735	PSU	N1-C2-N3	6.17	121.67	115.17
38	A1	776	PSU	N1-C2-N3	6.16	121.67	115.17
38	A1	2349	PSU	N1-C2-N3	6.15	121.66	115.17
34	B5	302	PSU	N1-C2-N3	6.14	121.64	115.17
34	B5	632	PSU	N1-C2-N3	6.11	121.62	115.17
34	B5	211	PSU	N1-C2-N3	6.05	121.55	115.17
34	B5	120	PSU	N1-C2-N3	6.05	121.55	115.17
38	A1	986	PSU	N1-C2-N3	6.03	121.53	115.17
38	A1	2922	OMG	C5-C4-N3	-5.95	118.92	128.39
38	A1	1052	PSU	N1-C2-N3	5.90	121.39	115.17
34	B5	1782	MA6	C5-C4-N3	-5.66	118.93	126.72
38	A1	1042	PSU	N1-C2-N3	5.54	121.02	115.17
34	B5	1191	B8N	C4-N3-C2	-5.53	118.82	125.62
34	B5	1781	MA6	C5-C4-N3	-5.43	119.24	126.72
38	A1	2142	1MA	C5-C4-N3	-5.40	119.31	127.27
38	A1	645	1MA	C5-C4-N3	-4.96	119.96	127.27
38	A1	2922	OMG	C2-N3-C4	4.94	120.81	112.30
34	B5	1773	4AC	O2-C2-N3	-4.85	114.69	122.33
34	B5	1575	G7M	C2-N3-C4	4.80	120.57	112.30
38	A1	2921	OMU	C4-N3-C2	-4.76	120.70	126.61
38	A1	2142	1MA	C2-N3-C4	4.69	121.72	112.53
38	A1	645	1MA	C2-N3-C4	4.50	121.36	112.53
38	A1	2921	OMU	N3-C2-N1	4.50	120.75	114.89
34	B5	1782	MA6	C4-C5-N7	-4.38	105.58	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2870	5MC	C5-C6-N1	-4.37	118.57	123.31
38	A1	2922	OMG	N9-C4-N3	4.32	134.60	125.95
34	B5	1781	MA6	C2-N1-C6	4.31	122.34	111.83
34	B5	1782	MA6	C2-N1-C6	4.28	122.28	111.83
38	A1	2880	PSU	C4-N3-C2	-4.20	120.59	126.37
38	A1	2944	PSU	C4-N3-C2	-4.20	120.59	126.37
34	B5	1781	MA6	N3-C4-N9	4.15	134.23	127.17
39	A3	50	PSU	C4-N3-C2	-4.13	120.69	126.37
34	B5	1181	PSU	C4-N3-C2	-4.09	120.74	126.37
38	A1	2314	PSU	C4-N3-C2	-4.07	120.76	126.37
38	A1	1124	PSU	C4-N3-C2	-4.07	120.76	126.37
38	A1	966	PSU	C4-N3-C2	-4.07	120.77	126.37
38	A1	1110	PSU	C4-N3-C2	-4.03	120.81	126.37
38	A1	2923	PSU	C4-N3-C2	-4.03	120.82	126.37
38	A1	2129	PSU	C4-N3-C2	-4.03	120.83	126.37
34	B5	1575	G7M	C5-C4-N3	-4.02	120.55	128.15
34	B5	632	PSU	C4-N3-C2	-4.00	120.86	126.37
38	A1	2826	PSU	C4-N3-C2	-3.99	120.87	126.37
34	B5	1187	PSU	C4-N3-C2	-3.99	120.87	126.37
38	A1	960	PSU	C4-N3-C2	-3.99	120.87	126.37
34	B5	1782	MA6	N3-C4-N9	3.99	133.95	127.17
38	A1	2865	PSU	C4-N3-C2	-3.99	120.88	126.37
34	B5	1575	G7M	C6-C5-N7	3.97	137.15	132.17
34	B5	759	PSU	C4-N3-C2	-3.97	120.90	126.37
38	A1	990	PSU	C4-N3-C2	-3.97	120.90	126.37
34	B5	1773	4AC	C1'-N1-C2	3.97	127.21	118.44
34	B5	766	PSU	C4-N3-C2	-3.97	120.91	126.37
34	B5	1290	PSU	C4-N3-C2	-3.96	120.91	126.37
38	A1	2133	PSU	C4-N3-C2	-3.95	120.93	126.37
38	A1	2975	PSU	C4-N3-C2	-3.94	120.94	126.37
34	B5	1415	PSU	C4-N3-C2	-3.94	120.95	126.37
38	A1	2266	PSU	O2-C2-N1	-3.93	118.73	122.79
38	A1	1004	PSU	C4-N3-C2	-3.93	120.96	126.37
34	B5	302	PSU	C4-N3-C2	-3.92	120.96	126.37
38	A1	2191	PSU	C4-N3-C2	-3.90	121.00	126.37
34	B5	1781	MA6	C4-C5-N7	-3.90	106.13	110.58
40	A4	73	PSU	C4-N3-C2	-3.89	121.01	126.37
38	A1	2921	OMU	C5-C4-N3	3.88	120.24	114.80
38	A1	2735	PSU	C4-N3-C2	-3.88	121.03	126.37
34	B5	120	PSU	C4-N3-C2	-3.87	121.03	126.37
34	B5	999	PSU	C4-N3-C2	-3.87	121.04	126.37
38	A1	1056	PSU	C4-N3-C2	-3.86	121.05	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	466	PSU	C4-N3-C2	-3.85	121.06	126.37
38	A1	2416	PSU	C4-N3-C2	-3.85	121.07	126.37
38	A1	2266	PSU	C4-N3-C2	-3.84	121.08	126.37
34	B5	1415	PSU	O2-C2-N1	-3.82	118.85	122.79
38	A1	2260	PSU	C4-N3-C2	-3.81	121.12	126.37
34	B5	999	PSU	O2-C2-N1	-3.80	118.86	122.79
38	A1	2351	PSU	C4-N3-C2	-3.80	121.13	126.37
34	B5	1280	4AC	N4-C4-N3	3.80	120.04	113.87
38	A1	2349	PSU	C4-N3-C2	-3.79	121.14	126.37
38	A1	2258	PSU	C4-N3-C2	-3.76	121.19	126.37
34	B5	302	PSU	O2-C2-N1	-3.76	118.91	122.79
34	B5	759	PSU	O2-C2-N1	-3.76	118.91	122.79
38	A1	2142	1MA	N9-C4-N3	3.76	135.46	126.90
34	B5	1782	MA6	C2-N3-C4	3.71	120.90	111.83
34	B5	1575	G7M	C5-C6-N1	3.68	119.44	111.84
34	B5	120	PSU	O2-C2-N1	-3.67	119.00	122.79
38	A1	966	PSU	O2-C2-N1	-3.67	119.01	122.79
38	A1	2191	PSU	O2-C2-N1	-3.67	119.01	122.79
34	B5	466	PSU	O2-C2-N1	-3.66	119.01	122.79
38	A1	2258	PSU	O2-C2-N1	-3.66	119.01	122.79
34	B5	106	PSU	C4-N3-C2	-3.66	121.33	126.37
40	A4	73	PSU	O2-C2-N1	-3.63	119.04	122.79
38	A1	1052	PSU	C4-N3-C2	-3.63	121.37	126.37
34	B5	1181	PSU	O2-C2-N1	-3.63	119.04	122.79
38	A1	2264	PSU	C4-N3-C2	-3.63	121.37	126.37
38	A1	2923	PSU	O2-C2-N1	-3.63	119.05	122.79
38	A1	2260	PSU	O2-C2-N1	-3.62	119.06	122.79
38	A1	2826	PSU	O2-C2-N1	-3.60	119.08	122.79
38	A1	960	PSU	O2-C2-N1	-3.59	119.09	122.79
38	A1	1004	PSU	O2-C2-N1	-3.58	119.10	122.79
38	A1	2349	PSU	O2-C2-N1	-3.57	119.10	122.79
34	B5	1773	4AC	O2-C2-N1	3.57	125.90	118.90
34	B5	1781	MA6	C2-N3-C4	3.56	120.53	111.83
38	A1	776	PSU	C4-N3-C2	-3.56	121.47	126.37
34	B5	1187	PSU	O2-C2-N1	-3.54	119.14	122.79
38	A1	776	PSU	O2-C2-N1	-3.52	119.16	122.79
36	AB	243	HIC	NE2-CE1-ND1	-3.51	111.32	112.66
38	A1	2340	PSU	C4-N3-C2	-3.49	121.56	126.37
38	A1	2416	PSU	O2-C2-N1	-3.48	119.20	122.79
38	A1	2880	PSU	O2-C2-N1	-3.48	119.20	122.79
34	B5	1290	PSU	O2-C2-N1	-3.48	119.20	122.79
38	A1	986	PSU	C4-N3-C2	-3.47	121.59	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2865	PSU	O2-C2-N1	-3.47	119.21	122.79
38	A1	2314	PSU	O2-C2-N1	-3.47	119.21	122.79
38	A1	2975	PSU	O2-C2-N1	-3.45	119.23	122.79
38	A1	1042	PSU	C4-N3-C2	-3.45	121.62	126.37
38	A1	986	PSU	O2-C2-N1	-3.44	119.24	122.79
34	B5	106	PSU	O2-C2-N1	-3.44	119.24	122.79
34	B5	766	PSU	O2-C2-N1	-3.42	119.26	122.79
38	A1	1124	PSU	O2-C2-N1	-3.41	119.27	122.79
38	A1	2351	PSU	O2-C2-N1	-3.41	119.28	122.79
38	A1	2944	PSU	O2-C2-N1	-3.41	119.28	122.79
38	A1	1056	PSU	O2-C2-N1	-3.40	119.28	122.79
38	A1	990	PSU	O2-C2-N1	-3.39	119.29	122.79
39	A3	50	PSU	O2-C2-N1	-3.39	119.29	122.79
38	A1	2340	PSU	O2-C2-N1	-3.37	119.31	122.79
38	A1	2129	PSU	O2-C2-N1	-3.37	119.32	122.79
34	B5	211	PSU	O2-C2-N1	-3.36	119.33	122.79
38	A1	2922	OMG	C6-C5-N7	3.32	136.32	130.29
38	A1	1052	PSU	O2-C2-N1	-3.31	119.37	122.79
34	B5	211	PSU	C4-N3-C2	-3.28	121.85	126.37
38	A1	2735	PSU	O2-C2-N1	-3.28	119.41	122.79
34	B5	1781	MA6	N1-C2-N3	-3.28	123.62	128.58
34	B5	1782	MA6	N1-C2-N3	-3.27	123.64	128.58
38	A1	2634	UR3	C5-C4-N3	3.24	119.31	115.04
38	A1	645	1MA	N9-C4-N3	3.18	134.14	126.90
38	A1	2278	5MC	O2-C2-N3	-3.14	117.38	122.33
38	A1	2264	PSU	O2-C2-N1	-3.12	119.57	122.79
38	A1	1110	PSU	O2-C2-N1	-3.10	119.59	122.79
34	B5	1191	B8N	N3-C2-N1	3.08	120.48	116.72
38	A1	2278	5MC	C5-C4-N3	-3.08	118.60	121.75
38	A1	1042	PSU	O2-C2-N1	-2.97	119.72	122.79
34	B5	1782	MA6	C5-N7-C8	2.97	108.11	103.45
38	A1	2133	PSU	O2-C2-N1	-2.96	119.73	122.79
34	B5	632	PSU	O2-C2-N1	-2.90	119.79	122.79
38	A1	2870	5MC	C5-C4-N3	-2.83	118.85	121.75
38	A1	2921	OMU	O4-C4-C5	-2.82	120.30	125.16
34	B5	1575	G7M	N9-C4-N3	2.81	131.58	125.95
34	B5	1781	MA6	C5-N7-C8	2.72	107.72	103.45
34	B5	1773	4AC	C1'-N1-C6	-2.70	115.01	120.78
38	A1	1042	PSU	C6-C5-C4	-2.68	116.37	118.17
34	B5	1782	MA6	C6-C5-N7	2.62	137.61	133.43
38	A1	2634	UR3	C6-N1-C2	-2.61	119.66	121.80
34	B5	1781	MA6	C4-N9-C8	2.60	108.47	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2922	OMG	C4-C5-N7	-2.59	106.57	110.67
34	B5	1575	G7M	O6-C6-C5	-2.55	122.31	128.01
34	B5	302	PSU	C6-C5-C4	-2.54	116.46	118.17
38	A1	2278	5MC	C5-C6-N1	-2.53	120.56	123.31
34	B5	1575	G7M	O3'-C3'-C2'	2.44	119.64	111.82
34	B5	1781	MA6	N1-C6-N6	2.40	119.78	116.86
34	B5	1191	B8N	C31-N3-C2	2.39	121.17	117.64
38	A1	645	1MA	N1-C2-N3	-2.35	123.20	126.00
34	B5	1191	B8N	O4'-C1'-C2'	2.34	108.39	105.15
34	B5	1782	MA6	C4-N9-C8	2.34	108.19	105.74
34	B5	211	PSU	C6-C5-C4	-2.33	116.60	118.17
34	B5	1773	4AC	N4-C4-N3	2.32	117.64	113.87
38	A1	645	1MA	C4-C5-N7	-2.28	107.05	110.67
38	A1	986	PSU	C6-C5-C4	-2.25	116.66	118.17
34	B5	1773	4AC	CM7-C7-N4	-2.24	111.65	115.27
38	A1	2142	1MA	N1-C2-N3	-2.24	123.34	126.00
38	A1	2133	PSU	O2-C2-N3	-2.23	117.89	121.86
34	B5	1773	4AC	O7-C7-N4	2.23	125.40	121.90
34	B5	1575	G7M	C2-N1-C6	-2.21	121.11	125.11
38	A1	645	1MA	C6-C5-N7	2.20	136.06	132.16
34	B5	1773	4AC	C5-C4-N3	-2.20	119.16	122.60
38	A1	2314	PSU	C5-C6-N1	-2.19	119.10	122.14
39	A3	50	PSU	C5-C6-N1	-2.18	119.12	122.14
82	DC	699	DDE	CAU-CBW-CBI	-2.15	107.02	111.22
38	A1	2870	5MC	O2-C2-N3	-2.13	118.97	122.33
38	A1	776	PSU	C6-C5-C4	-2.10	116.75	118.17
38	A1	2826	PSU	O4'-C1'-C2'	2.10	108.06	105.15
34	B5	1781	MA6	C6-C5-N7	2.10	136.79	133.43
34	B5	120	PSU	O4'-C1'-C2'	2.10	108.06	105.15
34	B5	1181	PSU	C5-C6-N1	-2.10	119.23	122.14
38	A1	2865	PSU	O4'-C1'-C2'	2.08	108.03	105.15
34	B5	1782	MA6	N9-C8-N7	-2.07	110.99	113.94
38	A1	2340	PSU	C6-C5-C4	-2.07	116.78	118.17
38	A1	960	PSU	O4'-C1'-C2'	2.07	108.01	105.15
34	B5	1280	4AC	C6-C5-C4	2.07	119.49	117.00
38	A1	2880	PSU	C6-C5-C4	-2.07	116.78	118.17
38	A1	1052	PSU	C6-C5-C4	-2.05	116.79	118.17
38	A1	2865	PSU	C5-C6-N1	-2.05	119.30	122.14
38	A1	2133	PSU	C5-C6-N1	-2.03	119.32	122.14
34	B5	766	PSU	O4'-C1'-C2'	2.03	107.96	105.15
38	A1	2921	OMU	O2-C2-N1	-2.03	120.15	122.80
34	B5	1191	B8N	C1'-C5-C4	2.03	120.68	117.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	1124	PSU	C5-C6-N1	-2.02	119.33	122.14
38	A1	2634	UR3	C1'-N1-C2	2.01	120.34	117.04
38	A1	2278	5MC	C1'-N1-C6	-2.01	117.83	121.15
38	A1	2191	PSU	O4'-C1'-C2'	2.01	107.93	105.15
38	A1	2922	OMG	O6-C6-C5	-2.01	121.24	126.53
34	B5	1191	B8N	C31-N3-C4	2.00	120.02	117.18

There are no chirality outliers.

All (63) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	1280	4AC	N3-C4-N4-C7
34	B5	1280	4AC	C5-C4-N4-C7
34	B5	1773	4AC	O4'-C4'-C5'-O5'
34	B5	1773	4AC	N3-C4-N4-C7
34	B5	1773	4AC	C5-C4-N4-C7
34	B5	1781	MA6	C5-C6-N6-C9
34	B5	1782	MA6	O4'-C4'-C5'-O5'
34	B5	1782	MA6	C5-C6-N6-C9
38	A1	960	PSU	C2'-C1'-C5-C4
38	A1	960	PSU	O4'-C1'-C5-C4
38	A1	960	PSU	C2'-C1'-C5-C6
38	A1	1042	PSU	C2'-C1'-C5-C4
38	A1	1042	PSU	O4'-C1'-C5-C4
38	A1	1042	PSU	O4'-C1'-C5-C6
38	A1	2258	PSU	O4'-C4'-C5'-O5'
38	A1	2260	PSU	O4'-C4'-C5'-O5'
38	A1	2923	PSU	O4'-C4'-C5'-O5'
34	B5	1773	4AC	C3'-C4'-C5'-O5'
38	A1	2260	PSU	C3'-C4'-C5'-O5'
38	A1	2923	PSU	C3'-C4'-C5'-O5'
38	A1	2266	PSU	C4'-C5'-O5'-P
34	B5	1187	PSU	O4'-C4'-C5'-O5'
34	B5	1575	G7M	C3'-C4'-C5'-O5'
38	A1	1052	PSU	O4'-C4'-C5'-O5'
34	B5	1781	MA6	N1-C6-N6-C9
34	B5	1782	MA6	N1-C6-N6-C9
82	DC	699	DDE	CE1-CAT-CAU-CBW
38	A1	2258	PSU	C3'-C4'-C5'-O5'
34	B5	211	PSU	C3'-C4'-C5'-O5'
34	B5	1415	PSU	O4'-C4'-C5'-O5'
34	B5	1782	MA6	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
38	A1	2264	PSU	C3'-C4'-C5'-O5'
34	B5	1575	G7M	O4'-C4'-C5'-O5'
82	DC	699	DDE	CA-CB-CG-ND1
34	B5	1782	MA6	C5-C6-N6-C10
38	A1	2142	1MA	O4'-C4'-C5'-O5'
34	B5	211	PSU	O4'-C4'-C5'-O5'
38	A1	2142	1MA	C3'-C4'-C5'-O5'
38	A1	2264	PSU	O4'-C4'-C5'-O5'
82	DC	699	DDE	CA-CB-CG-CD2
38	A1	1052	PSU	C3'-C4'-C5'-O5'
34	B5	1781	MA6	C5-C6-N6-C10
38	A1	2340	PSU	C3'-C4'-C5'-O5'
34	B5	1191	B8N	C32-C33-C34-O35
38	A1	2266	PSU	C3'-C4'-C5'-O5'
38	A1	2314	PSU	C4'-C5'-O5'-P
34	B5	1191	B8N	O4'-C1'-C5-C4
34	B5	1415	PSU	C3'-C4'-C5'-O5'
38	A1	2340	PSU	C4'-C5'-O5'-P
34	B5	1187	PSU	C3'-C4'-C5'-O5'
38	A1	2264	PSU	C4'-C5'-O5'-P
38	A1	2923	PSU	C4'-C5'-O5'-P
38	A1	2870	5MC	O4'-C1'-N1-C6
34	B5	1773	4AC	C2'-C1'-N1-C6
38	A1	645	1MA	C2'-C1'-N9-C8
34	B5	1191	B8N	N34-C33-C34-O36
38	A1	960	PSU	O4'-C1'-C5-C6
38	A1	2870	5MC	C2'-C1'-N1-C6
38	A1	645	1MA	C2'-C1'-N9-C4
34	B5	1191	B8N	C32-C33-C34-O36
82	DC	699	DDE	CBI-CBW-NCB-CAB
82	DC	699	DDE	CBI-CBW-NCB-CAC
34	B5	1773	4AC	C2'-C1'-N1-C2

There are no ring outliers.

14 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	B5	1187	PSU	2	0
34	B5	1280	4AC	2	0
38	A1	2349	PSU	1	0
34	B5	1181	PSU	1	0
82	DC	699	DDE	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	B5	1773	4AC	3	0
34	B5	632	PSU	1	0
38	A1	990	PSU	1	0
38	A1	986	PSU	1	0
34	B5	1781	MA6	1	0
34	B5	302	PSU	2	0
38	A1	2880	PSU	1	0
38	A1	2129	PSU	1	0
38	A1	2133	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 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	$\# Z > 2$
84	GDP	DC	901	85	29,30,30	1.18	3 (10%)	45,47,47	1.81	7 (15%)
86	SO1	DC	903	-	34,39,39	0.74	2 (5%)	38,64,64	1.12	3 (7%)

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
84	GDP	DC	901	85	-	6/16/32/32	0/3/3/3
86	SO1	DC	903	-	1/1/15/16	5/21/104/104	0/7/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	DC	901	GDP	C5-C4	3.19	1.47	1.38
86	DC	903	SO1	O14-C5	-2.91	1.20	1.30
86	DC	903	SO1	C1-C5	2.56	1.56	1.50
84	DC	901	GDP	C6-N1	-2.56	1.34	1.38
84	DC	901	GDP	C5-N7	-2.22	1.34	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	DC	901	GDP	C5-C4-N3	-6.35	118.28	128.39
84	DC	901	GDP	C2-N3-C4	5.09	121.06	112.30
84	DC	901	GDP	N9-C4-N3	4.85	135.65	125.95
86	DC	903	SO1	C21-C13-C4	4.05	123.22	112.41
86	DC	903	SO1	C12-C6-C2	-3.12	100.26	105.09
84	DC	901	GDP	C6-C5-N7	2.96	135.67	130.29
84	DC	901	GDP	C3'-C2'-C1'	2.49	106.17	101.46
84	DC	901	GDP	C4-C5-N7	-2.41	106.84	110.67
84	DC	901	GDP	O6-C6-C5	-2.22	120.67	126.53
86	DC	903	SO1	C7-C2-C6	2.12	116.10	112.05

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
86	DC	903	SO1	C4

All (11) torsion outliers are listed below:

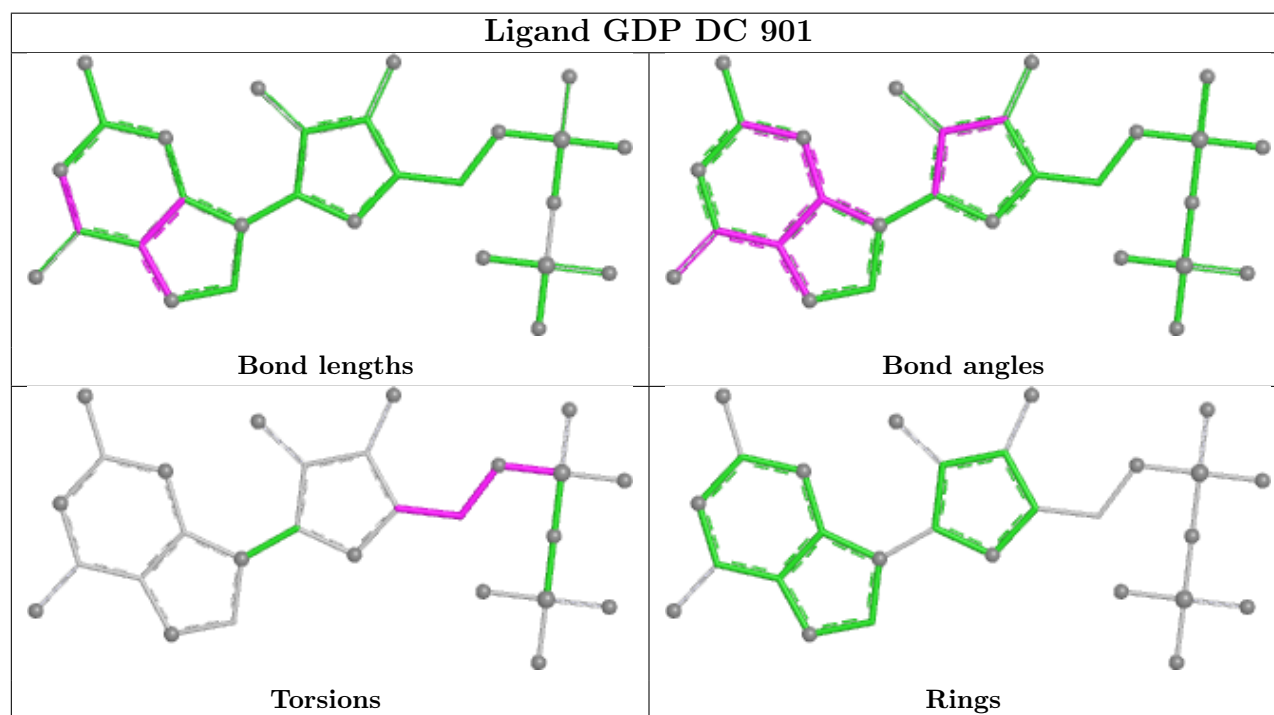
Mol	Chain	Res	Type	Atoms
84	DC	901	GDP	C5'-O5'-PA-O3A
84	DC	901	GDP	C5'-O5'-PA-O1A
84	DC	901	GDP	C5'-O5'-PA-O2A
84	DC	901	GDP	O4'-C4'-C5'-O5'
86	DC	903	SO1	C2-C1-C5-O14
86	DC	903	SO1	C2-C1-C5-O15
84	DC	901	GDP	C3'-C4'-C5'-O5'
84	DC	901	GDP	C4'-C5'-O5'-PA
86	DC	903	SO1	C20-C13-C4-C12
86	DC	903	SO1	C54-C55-O64-C65
86	DC	903	SO1	C20-C13-C4-C1

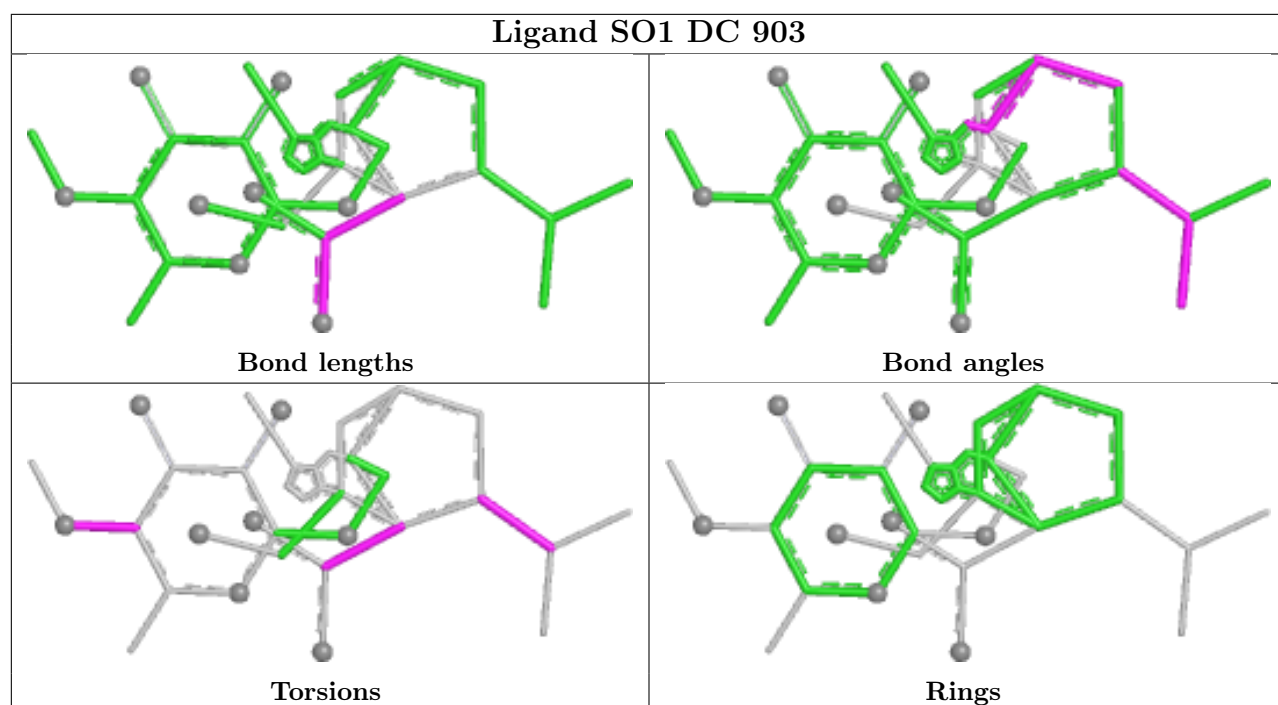
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	DC	901	GDP	2	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.

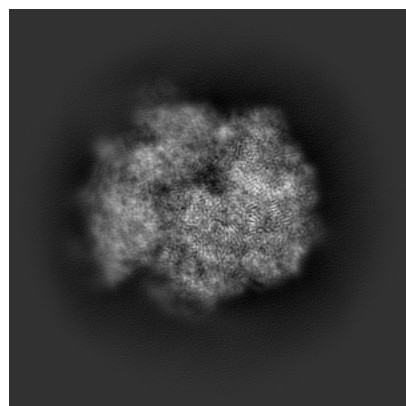
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40997. These allow visual inspection of the internal detail of the map and identification of artifacts.

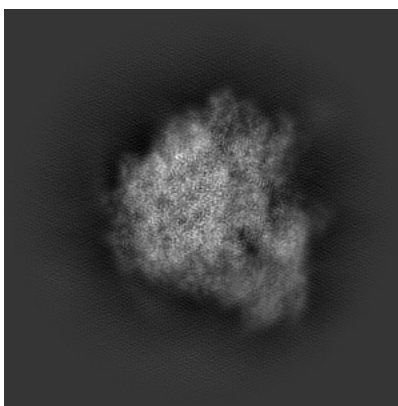
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

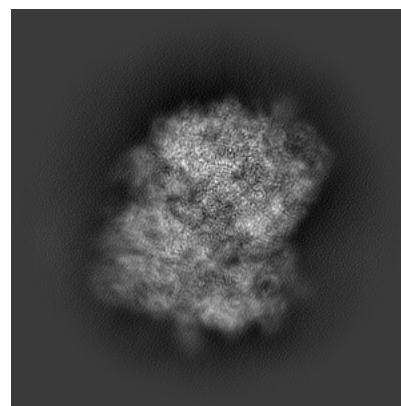
6.1.1 Primary map



X

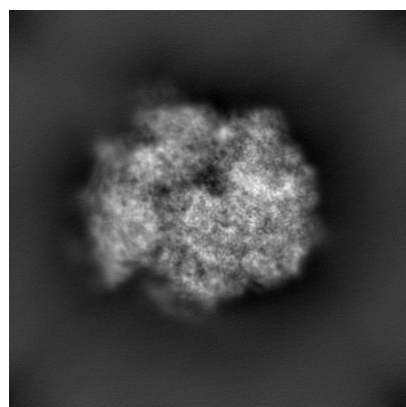


Y

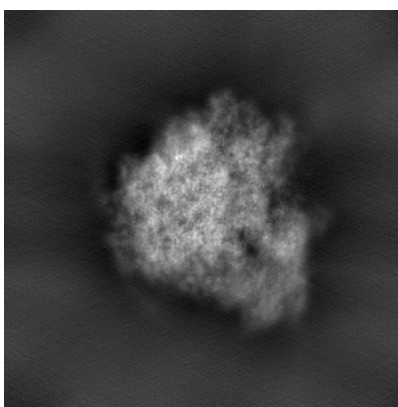


Z

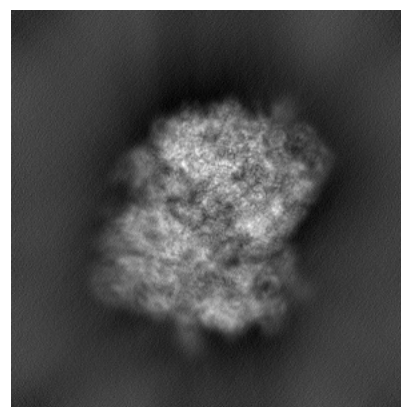
6.1.2 Raw map



X



Y

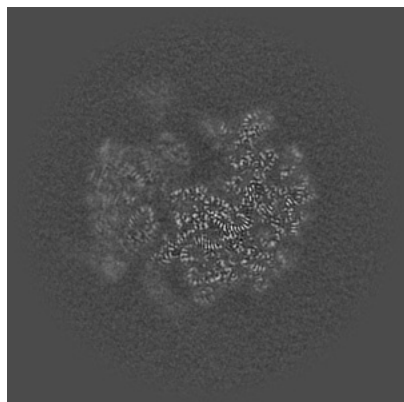


Z

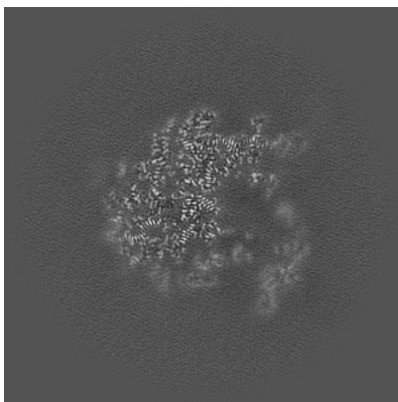
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

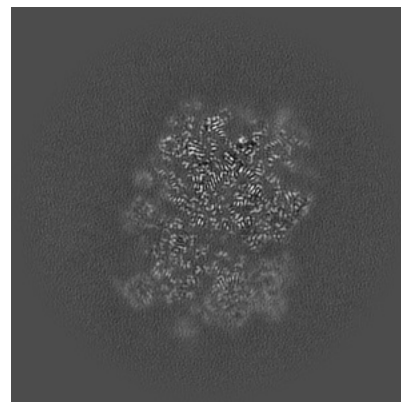
6.2.1 Primary map



X Index: 200

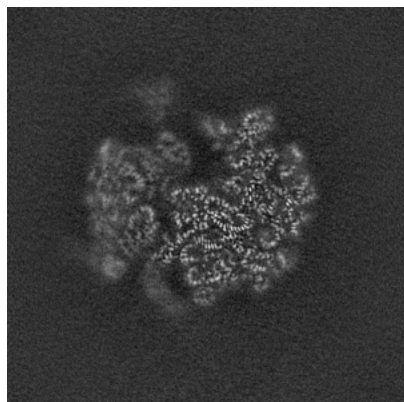


Y Index: 200

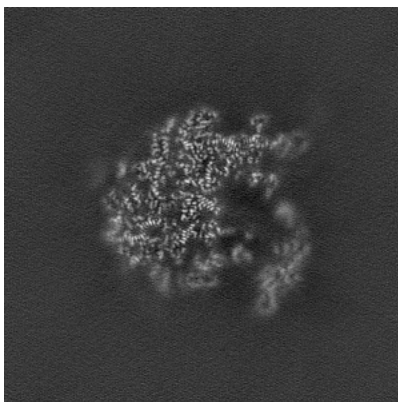


Z Index: 200

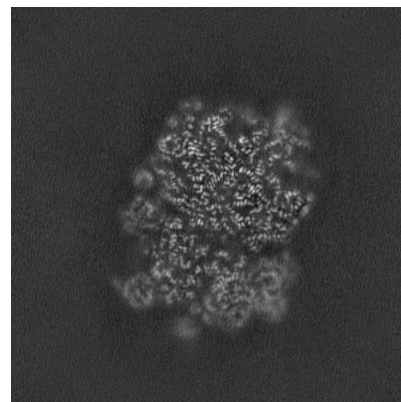
6.2.2 Raw map



X Index: 200



Y Index: 200

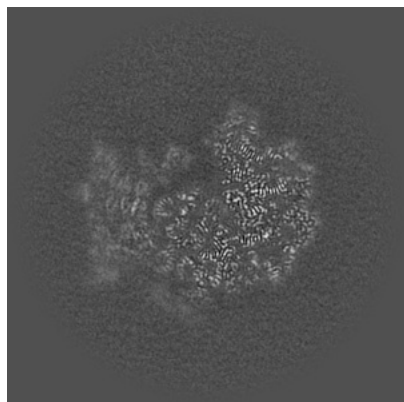


Z Index: 200

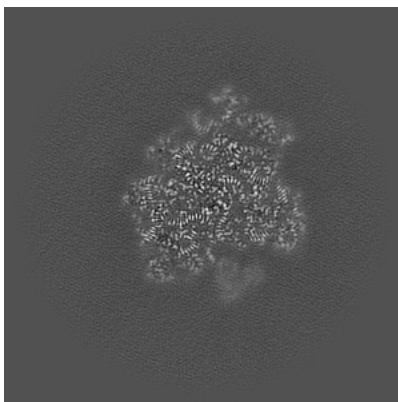
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

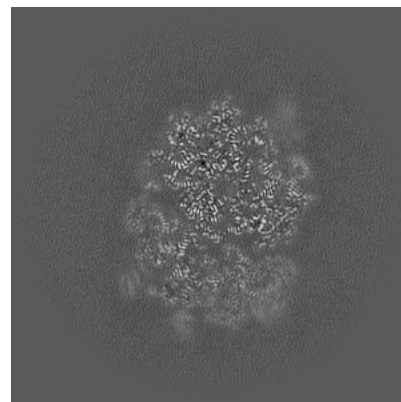
6.3.1 Primary map



X Index: 215

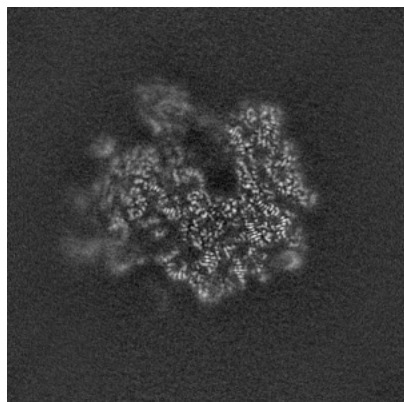


Y Index: 245

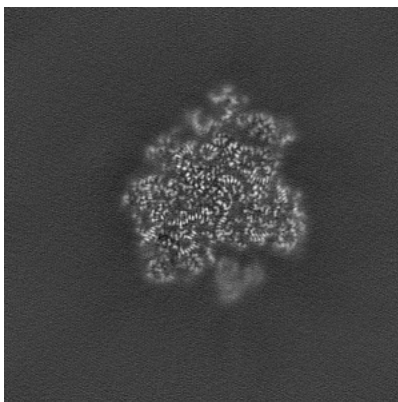


Z Index: 190

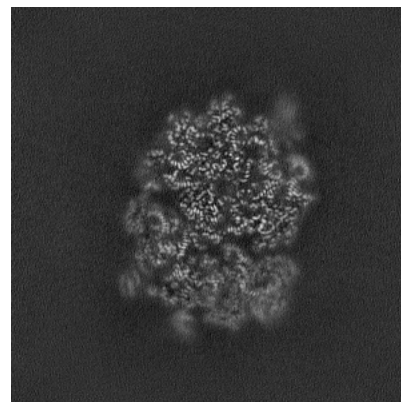
6.3.2 Raw map



X Index: 184



Y Index: 245

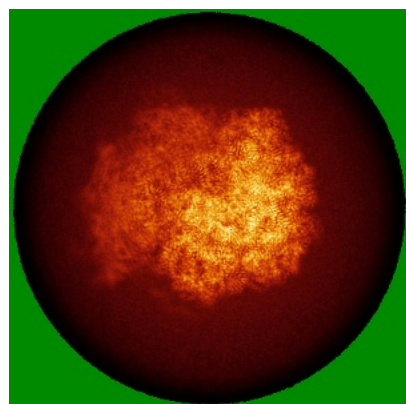


Z Index: 190

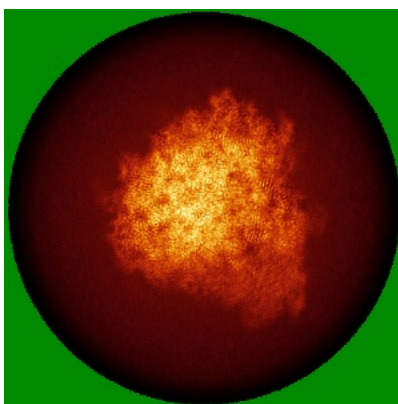
The images above show the largest variance slices of the map in three orthogonal directions.

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

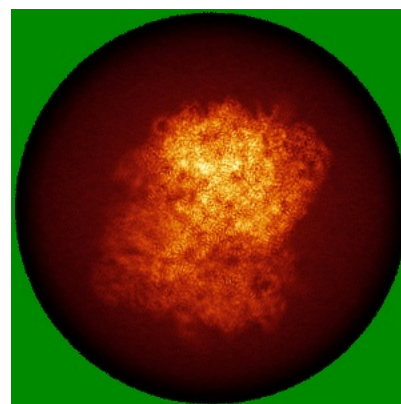
6.4.1 Primary map



X

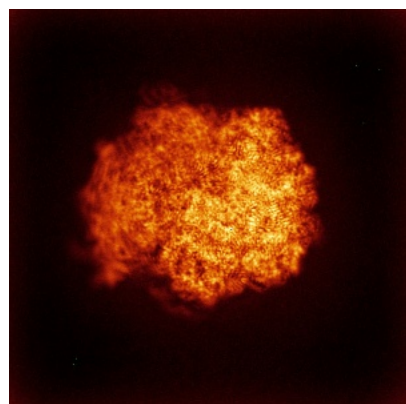


Y

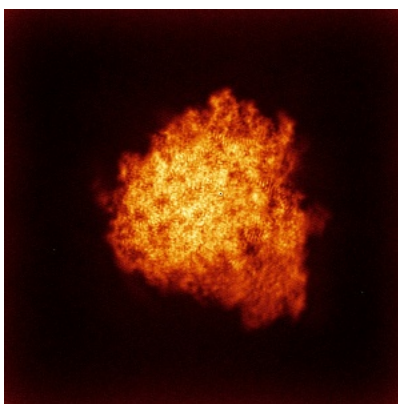


Z

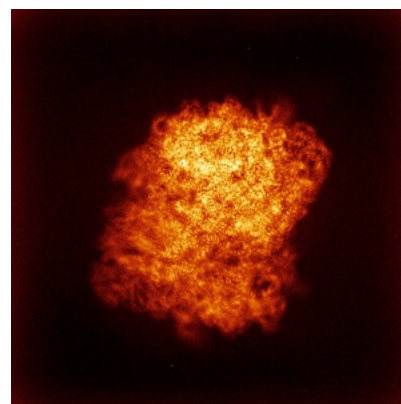
6.4.2 Raw map



X



Y

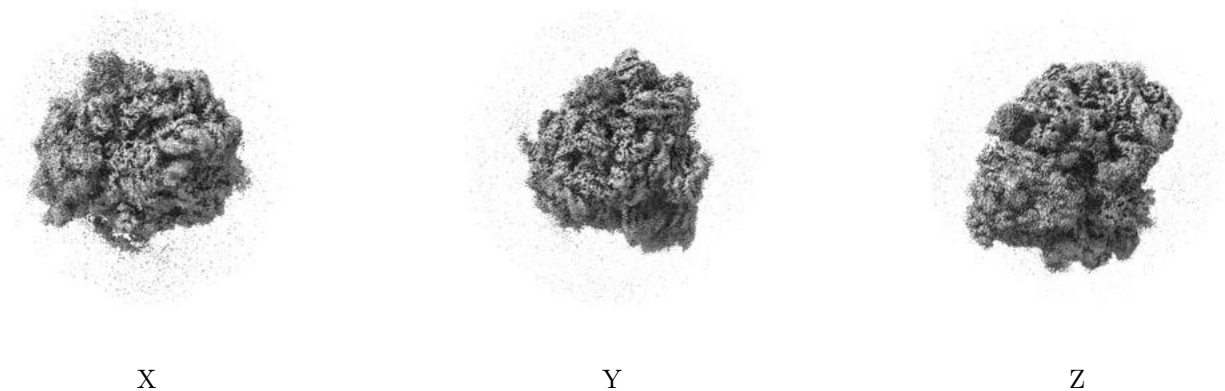


Z

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

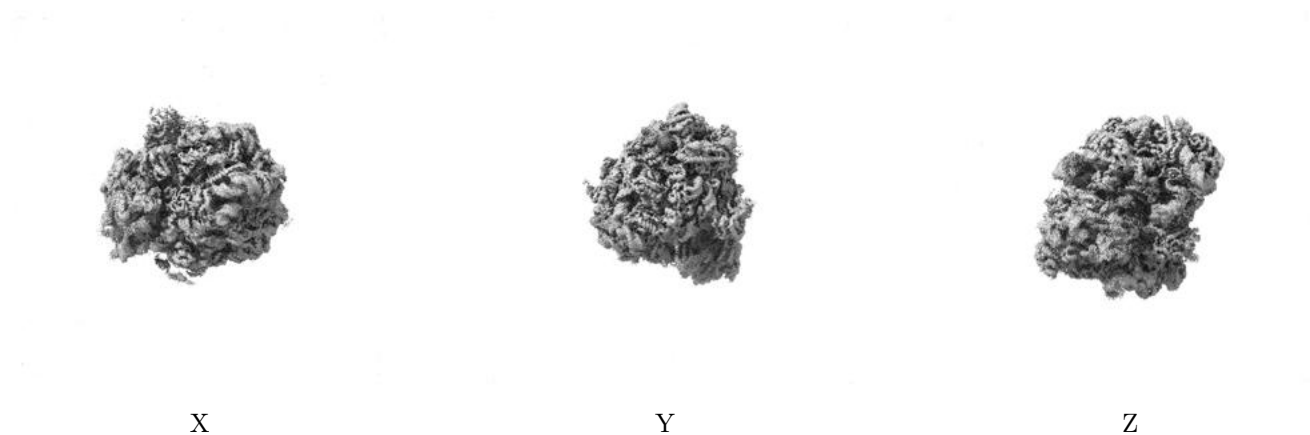
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

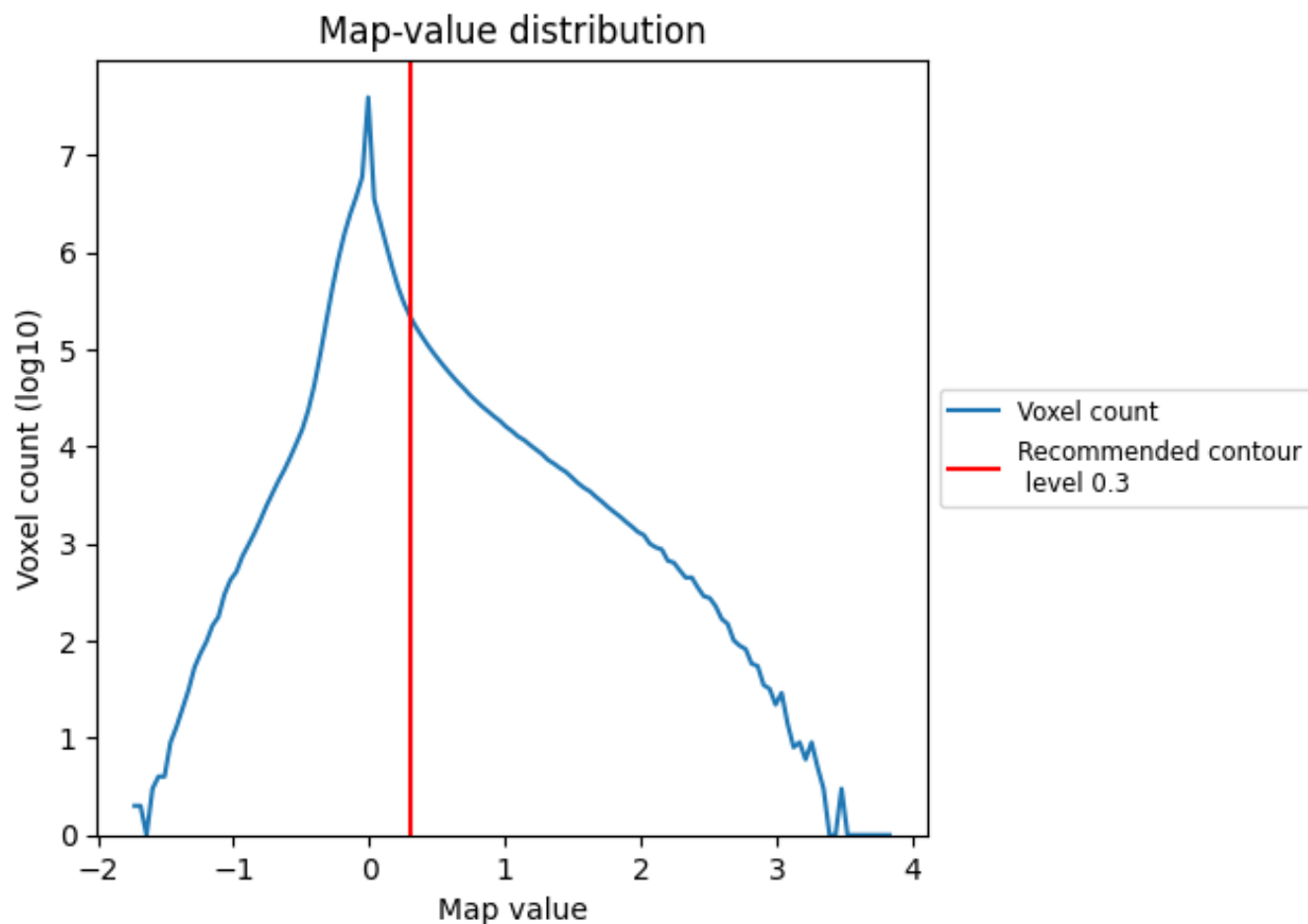
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

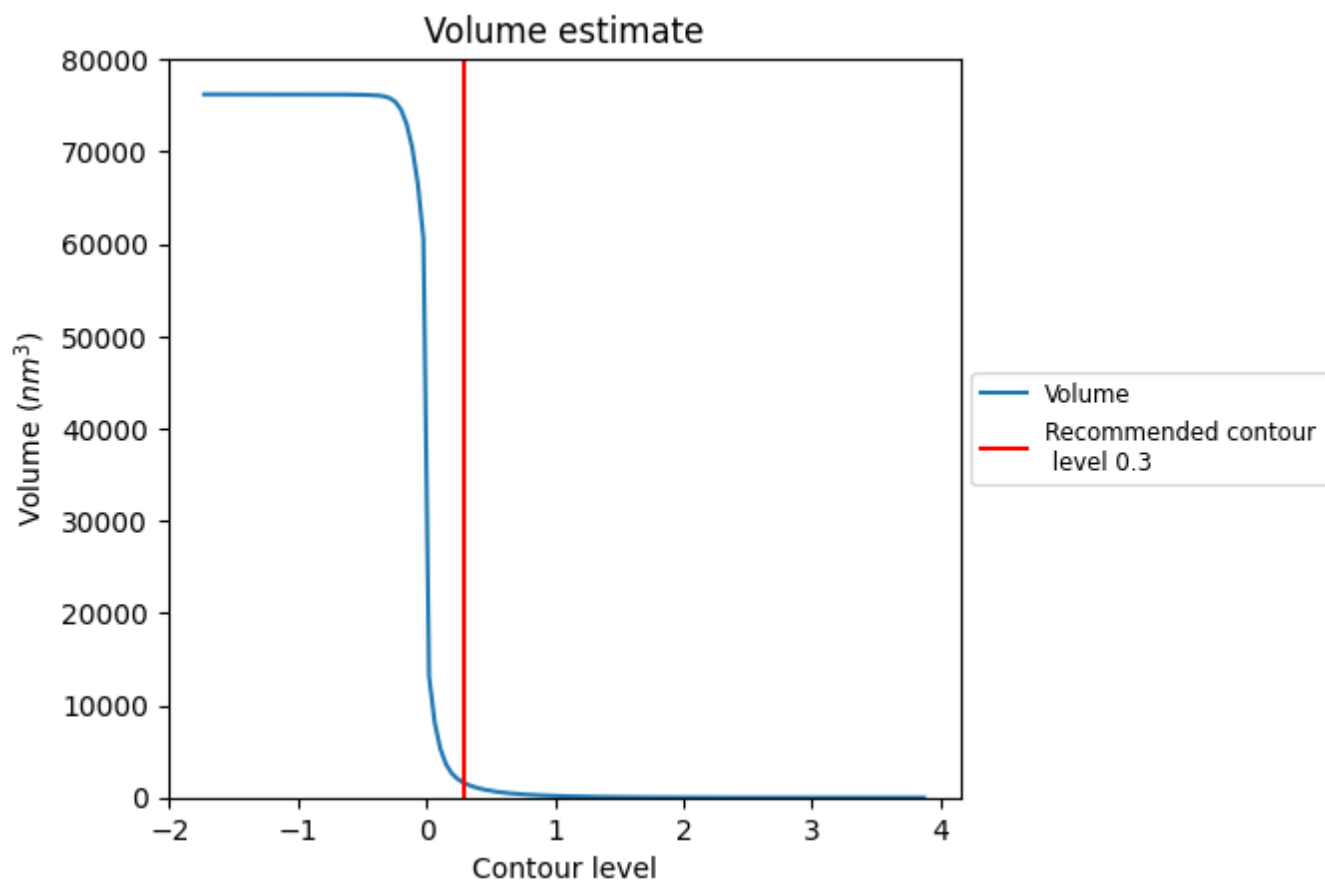
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

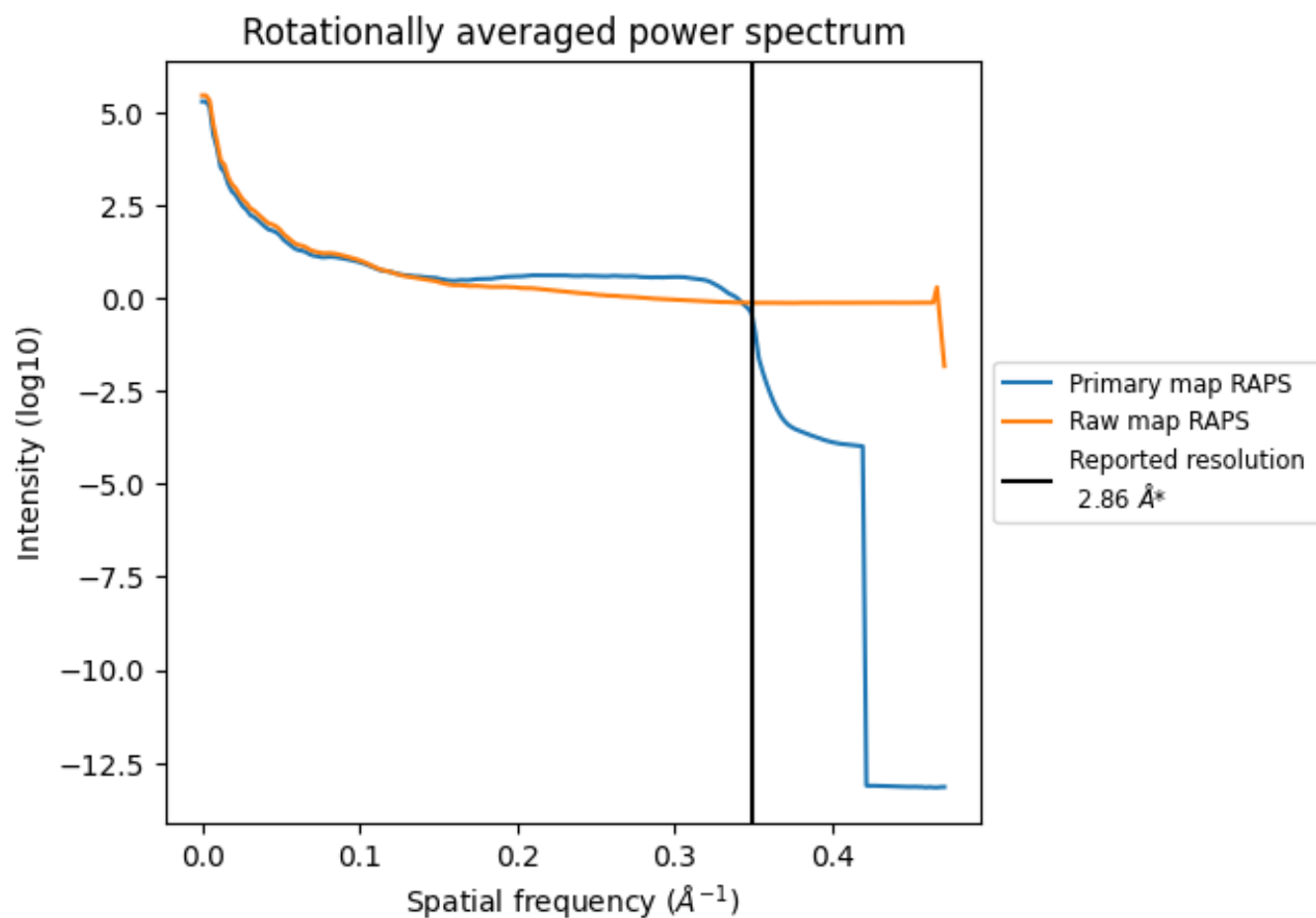
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1554 nm³; this corresponds to an approximate mass of 1404 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 ⓘ

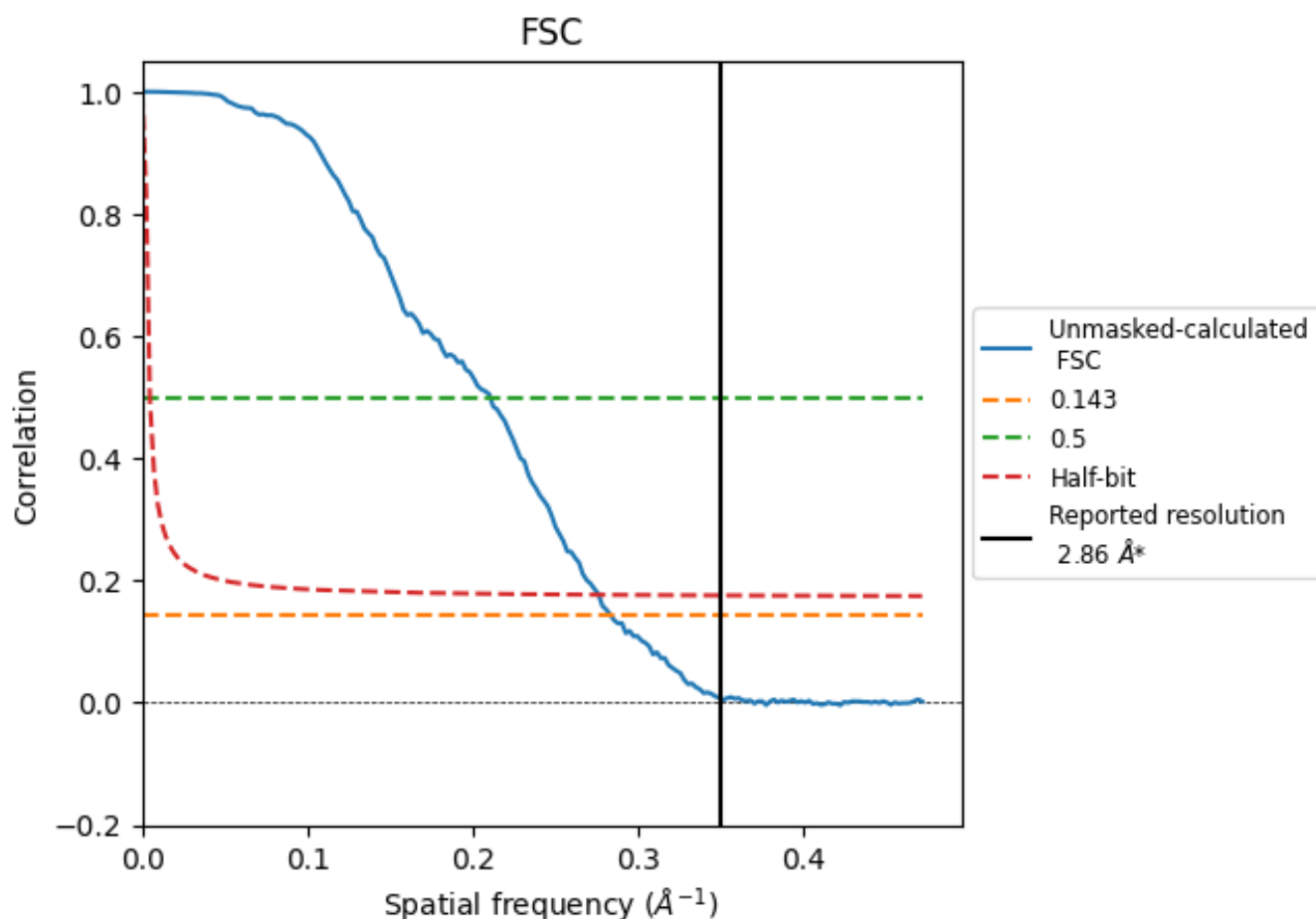


*Reported resolution corresponds to spatial frequency of 0.350 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.350 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

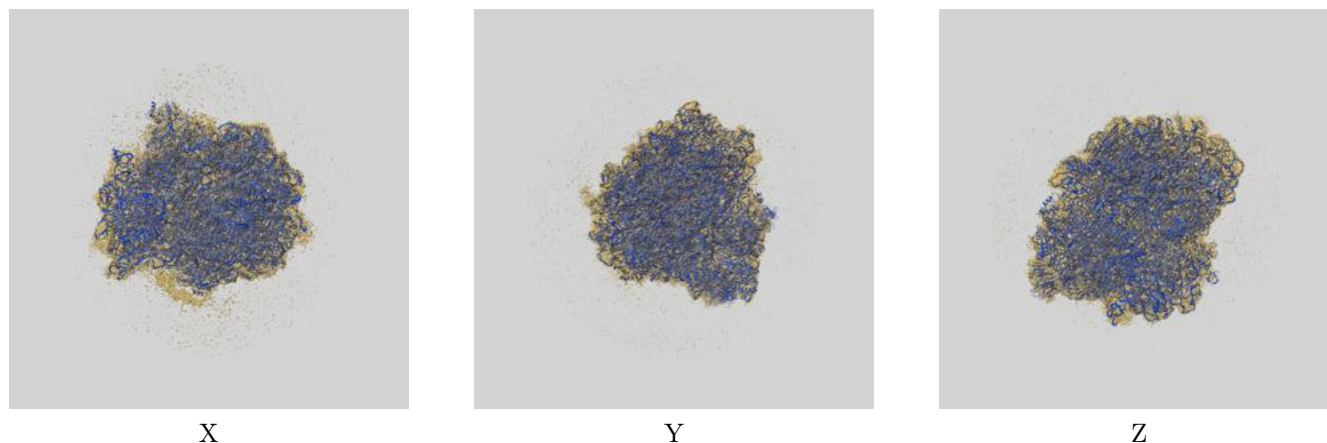
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.53	4.75	3.62

*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 3.53 differs from the reported value 2.86 by more than 10 %

9 Map-model fit [i](#)

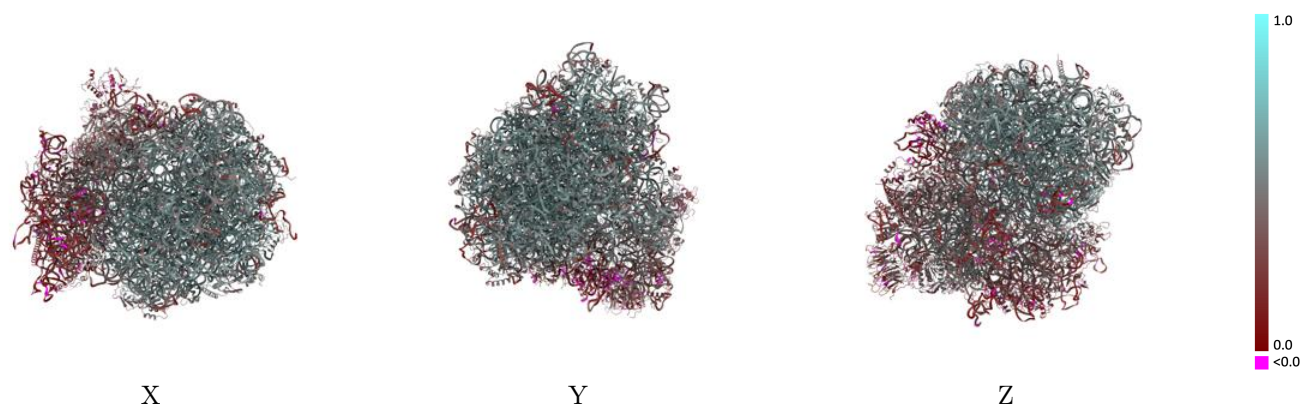
This section contains information regarding the fit between EMDB map EMD-40997 and PDB model 8T3A. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



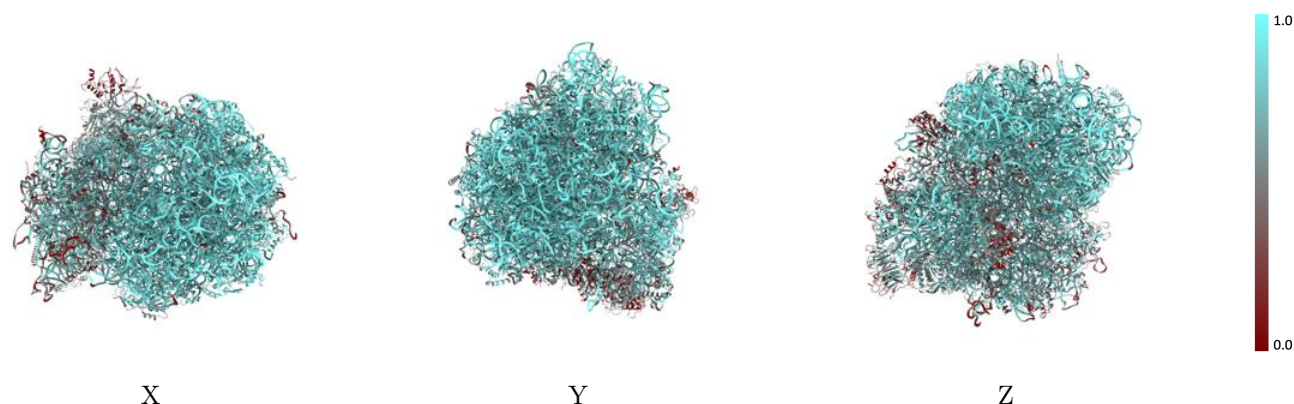
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



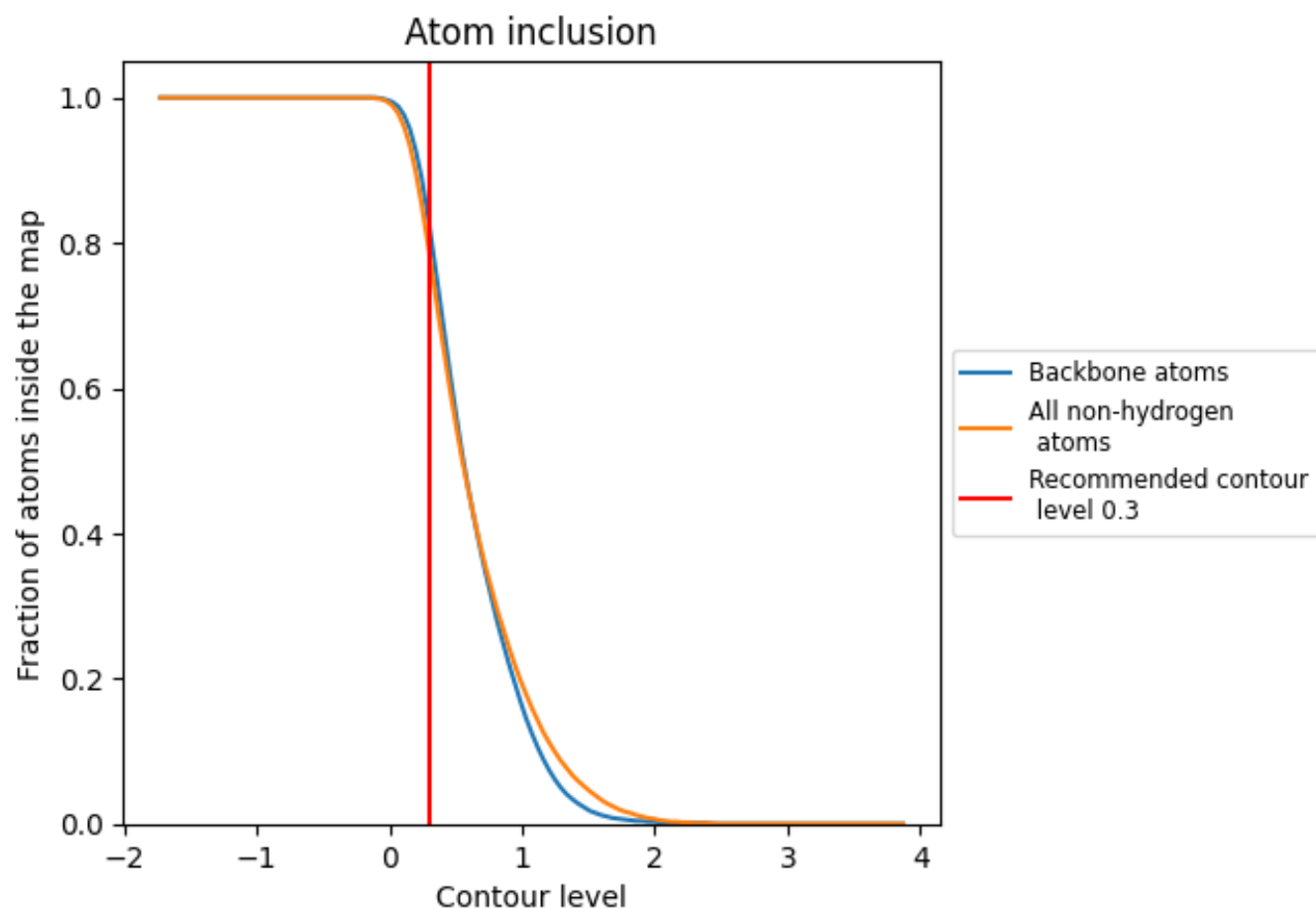
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.7860	 0.4510
A1	 0.9100	 0.5290
A3	 0.9630	 0.5490
A4	 0.9380	 0.5550
AA	 0.8260	 0.5590
AB	 0.8560	 0.5360
AC	 0.8660	 0.5360
AD	 0.8220	 0.4730
AE	 0.8260	 0.4740
AF	 0.8650	 0.5360
AG	 0.7850	 0.4730
AH	 0.7830	 0.4940
AI	 0.7550	 0.4790
AJ	 0.7520	 0.4430
AL	 0.8540	 0.5210
AM	 0.8290	 0.5000
AN	 0.8790	 0.5700
AO	 0.8530	 0.5350
AP	 0.8610	 0.5370
AQ	 0.8760	 0.5560
AR	 0.7420	 0.4830
AS	 0.8420	 0.5250
AT	 0.8490	 0.5270
AU	 0.8030	 0.4440
AV	 0.7590	 0.5180
AW	 0.8340	 0.5300
AX	 0.7990	 0.5020
AY	 0.8510	 0.5190
AZ	 0.8170	 0.4880
Aa	 0.8790	 0.5460
Ab	 0.7940	 0.5210
Ac	 0.7730	 0.5000
Ad	 0.8040	 0.4910
Ae	 0.8590	 0.5520
Af	 0.8940	 0.5700



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Chain	Atom inclusion	Q-score
Ag	 0.7910	 0.5260
Ah	 0.8270	 0.5020
Ai	 0.7910	 0.4760
Aj	 0.8990	 0.5730
Ak	 0.5990	 0.4300
Al	 0.8550	 0.5370
Am	 0.7940	 0.5220
An	 0.7970	 0.5240
Ao	 0.7970	 0.5230
Ap	 0.7520	 0.5250
B5	 0.7800	 0.3730
BA	 0.6190	 0.3790
BB	 0.5700	 0.3600
BC	 0.7280	 0.4610
BD	 0.6030	 0.3550
BE	 0.5560	 0.2690
BF	 0.4470	 0.3240
BG	 0.4930	 0.2230
BH	 0.5310	 0.3070
BI	 0.5560	 0.2720
BJ	 0.5840	 0.2310
BK	 0.5850	 0.2930
BL	 0.5570	 0.3240
BM	 0.1560	 0.1990
BN	 0.6500	 0.4220
BO	 0.6220	 0.4120
BP	 0.5210	 0.3160
BQ	 0.5860	 0.3540
BR	 0.4210	 0.2580
BS	 0.5870	 0.3080
BT	 0.6270	 0.3300
BU	 0.5590	 0.3170
BV	 0.6910	 0.3990
BW	 0.7420	 0.4640
BX	 0.6140	 0.4180
BY	 0.4900	 0.2250
BZ	 0.3380	 0.2470
Ba	 0.6960	 0.4540
Bb	 0.5670	 0.3780
Bc	 0.3980	 0.2930
Bd	 0.7850	 0.4190
Be	 0.4920	 0.2790

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Chain	Atom inclusion	Q-score
Bf	 0.1670	 0.2280
Bg	 0.4900	 0.2650
C5	 0.4320	 0.3540
DC	 0.6030	 0.3700
E	 0.2800	 0.1020
tE	 0.6810	 0.3590