



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 01:05 PM UTC

PDB ID : 8T30 / pdb_00008t30
EMDB ID : EMD-40993
Title : Hypomethylated yeast 80S bound with cycloheximide, unmodified U2921, mid rotated
Authors : Zhao, Y.; Li, H.
Deposited on : 2023-06-07
Resolution : 2.88 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

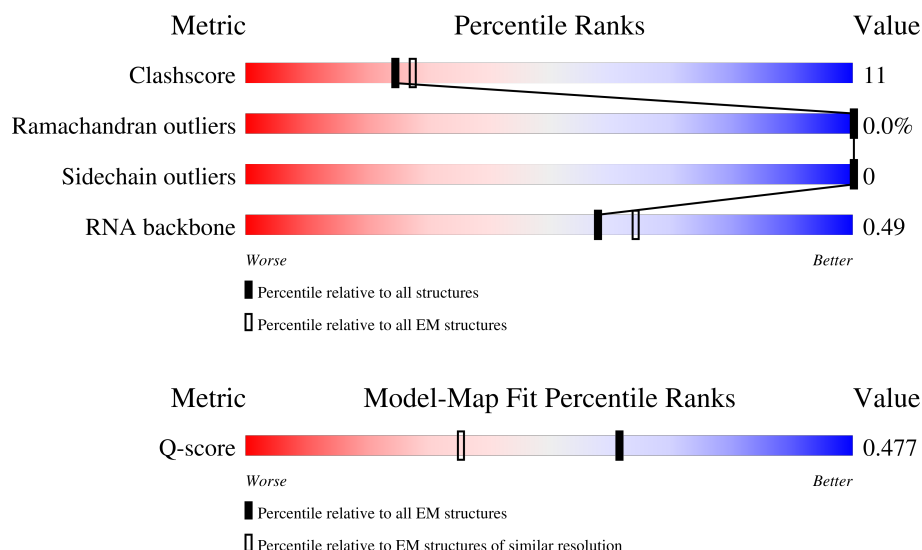
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.88 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	12111 (2.38 - 3.38)

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	17% 50% 31% 18%
2	BB	255	7% 51% 33% 16%
3	BC	254	64% 22% 15%

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

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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1798	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3395	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	221	
47	AJ	174	
48	AL	199	
49	AM	138	
50	AN	204	
51	AO	199	
52	AP	184	
53	AQ	186	

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

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 199289 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	S	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	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 29 is a protein called RPS28A isoform 1.

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

- Molecule 30 is a protein called RPS29A isoform 1.

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B5	1782	Total	C	N	O	P	1	0
			37987	16988	6718	12499	1782		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	386	Total	C	N	O	S	0	0
			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	3159	Total	C	N	O	P	0	0
			67564	30183	12164	22058	3159		

- 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 RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AI	217	Total	C	N	O	S	0	0
			1759	1114	333	305	7		

- 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		

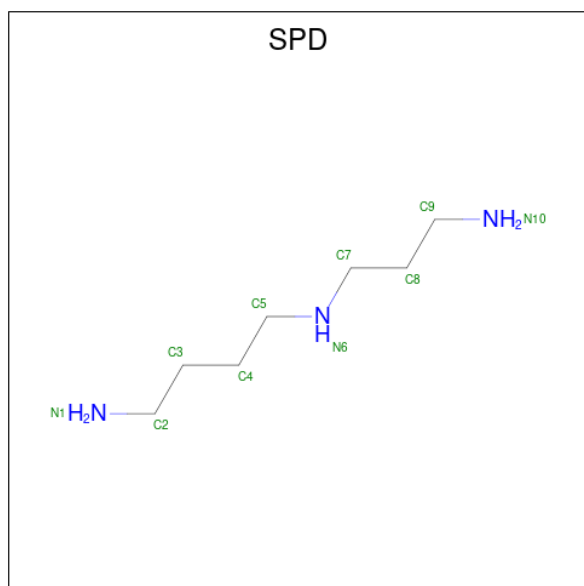
- Molecule 77 is a protein called 60S ribosomal protein L42-A.

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.

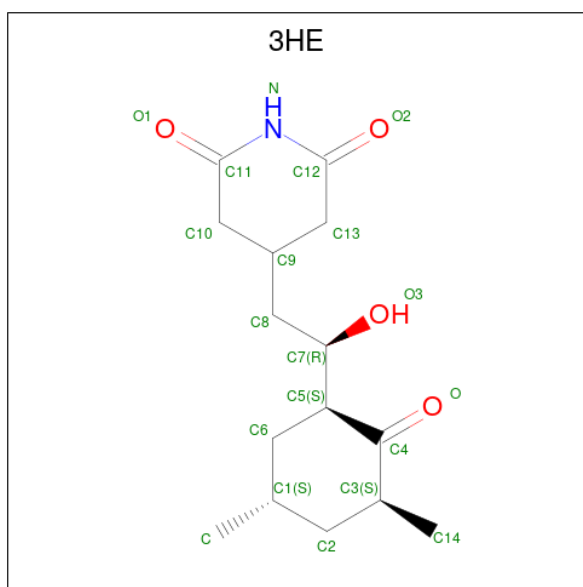
Mol	Chain	Residues	Atoms					AltConf	Trace
78	Ap	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 79 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
79	A1	1	Total	C	N	0
			10	7	3	

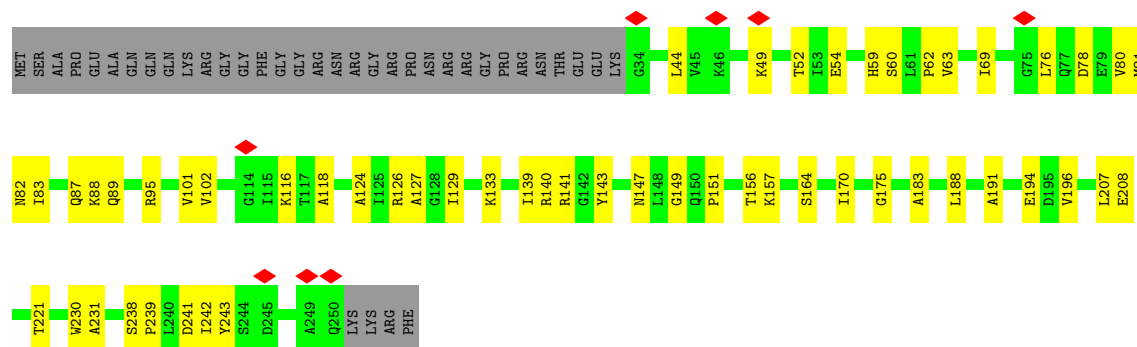
- Molecule 80 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: $C_{15}H_{23}NO_4$).



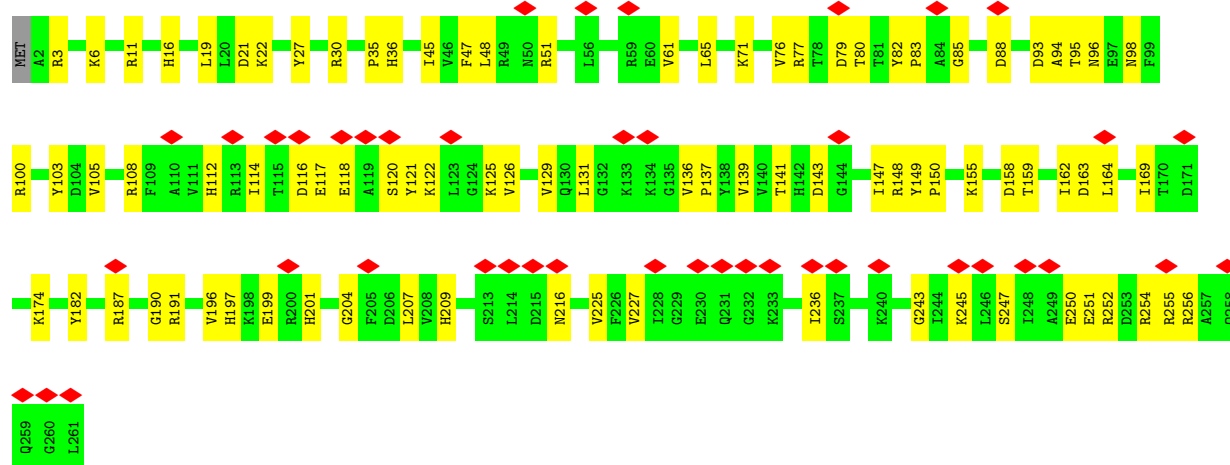
Mol	Chain	Residues	Atoms				AltConf
80	A1	1	Total	C	N	O	0
			20	15	1	4	

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

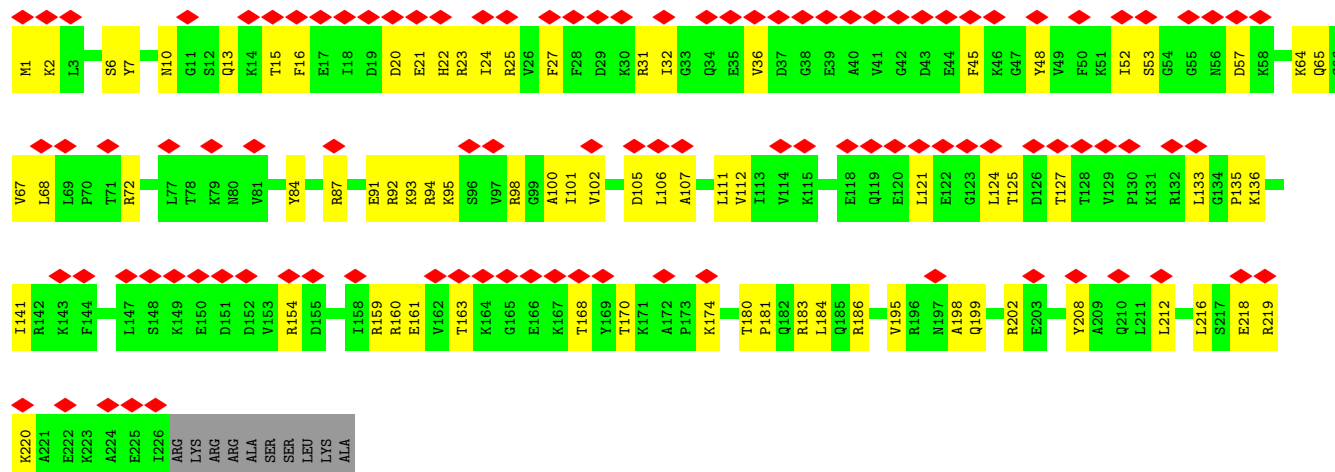
Mol	Chain	Residues	Atoms		AltConf
81	Ao	1	Total	Zn	0
			1	1	



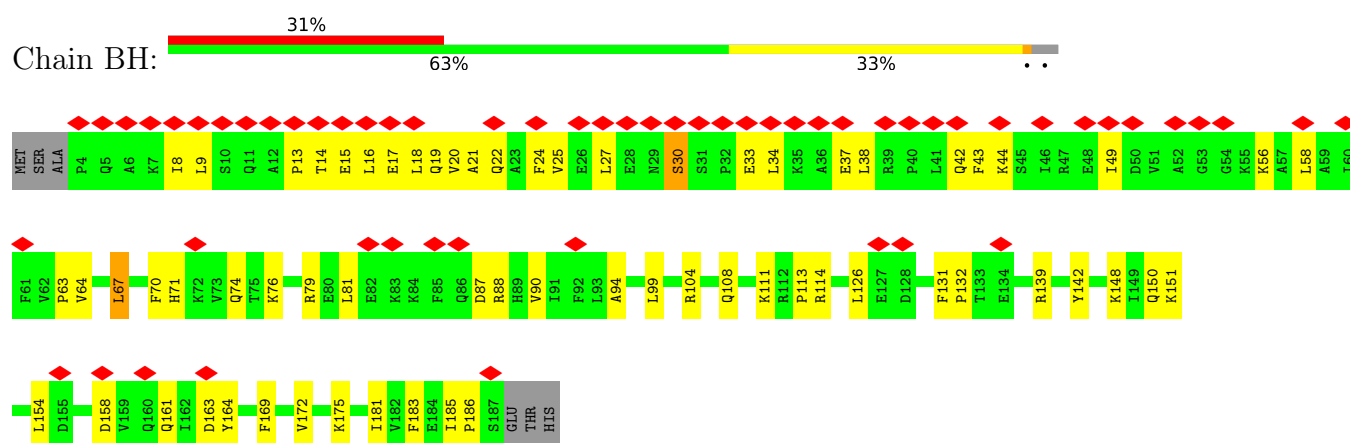
• Molecule 4: 40S ribosomal protein S4-A



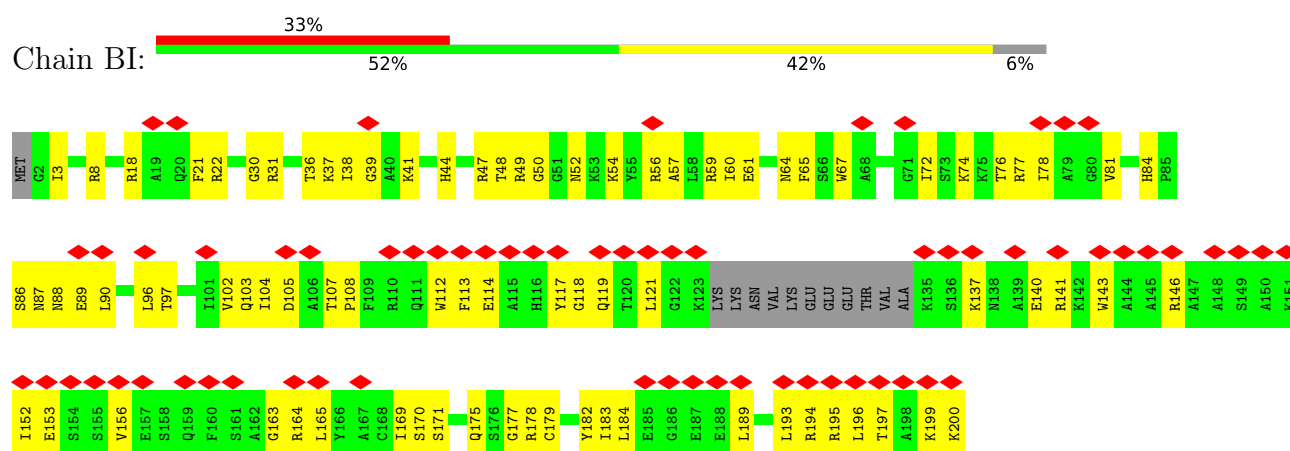
• Molecule 5: 40S ribosomal protein S6-A



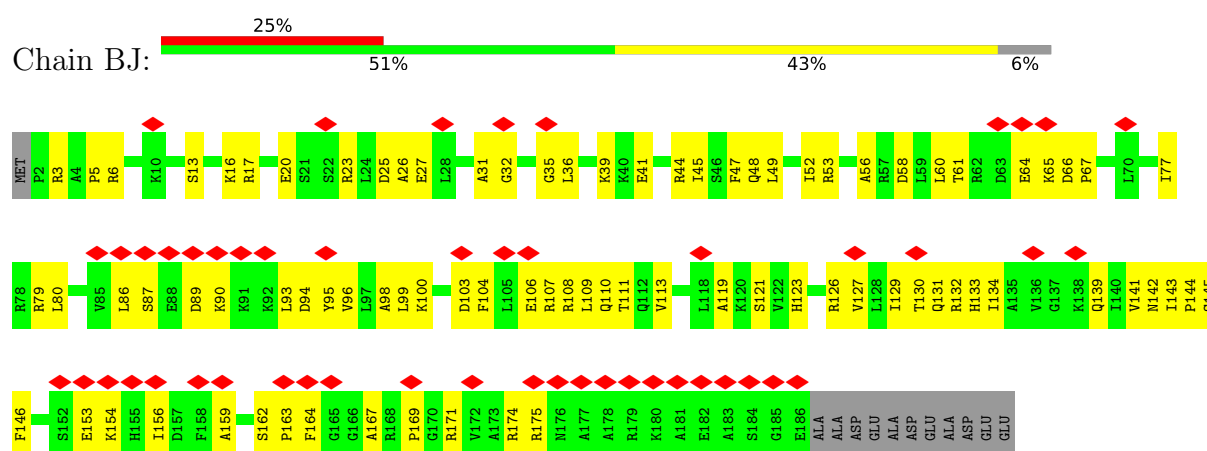
• Molecule 6: 40S ribosomal protein S7-A



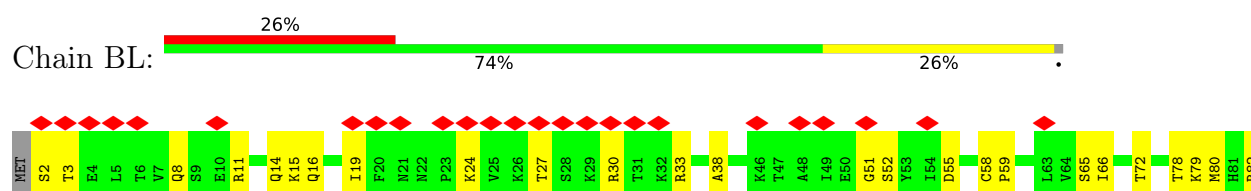
• Molecule 7: 40S ribosomal protein S8-A



• Molecule 8: 40S ribosomal protein S9-A

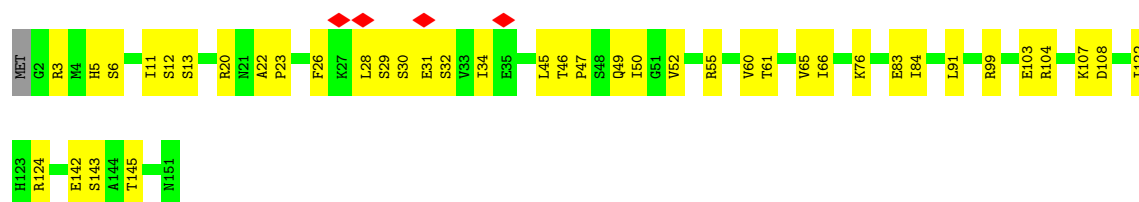
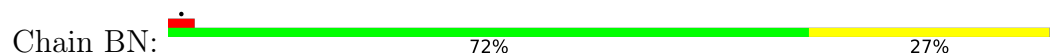


• Molecule 9: 40S ribosomal protein S11-A

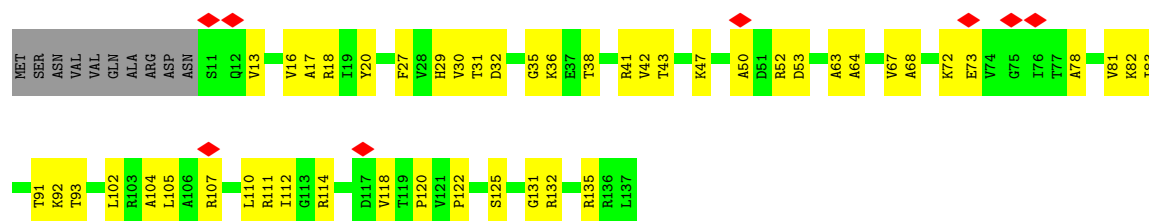




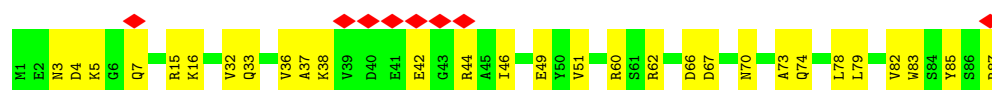
- Molecule 10: 40S ribosomal protein S13



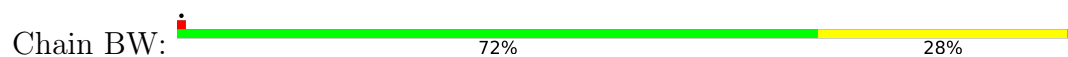
- Molecule 11: 40S ribosomal protein S14-A



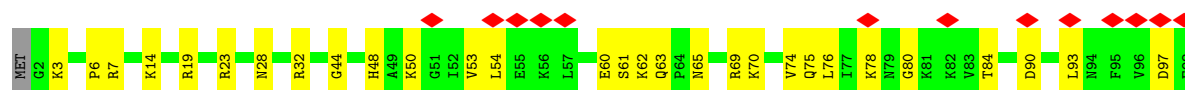
- Molecule 12: 40S ribosomal protein S21-A

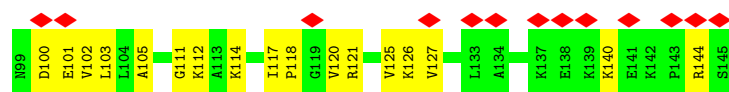


- Molecule 13: RPS22A isoform 1

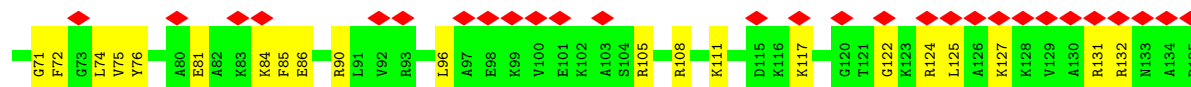
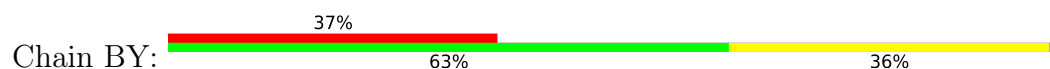


- Molecule 14: 40S ribosomal protein S23-A

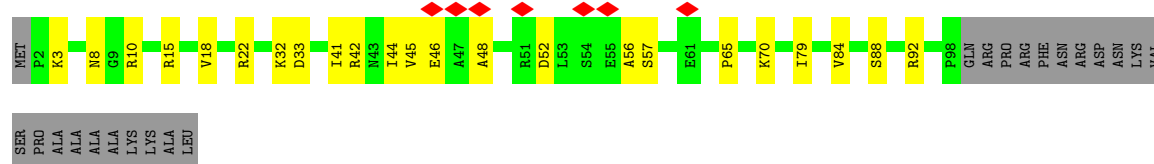




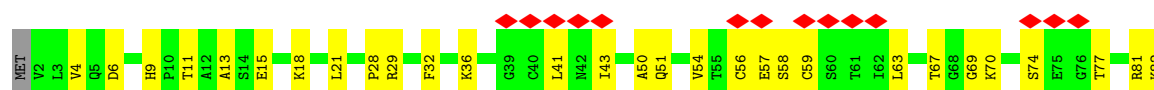
• Molecule 15: 40S ribosomal protein S24-A



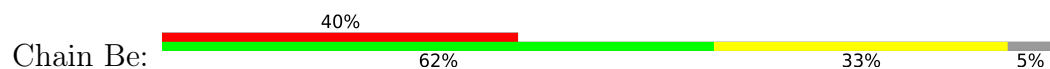
• Molecule 16: RPS26B isoform 1



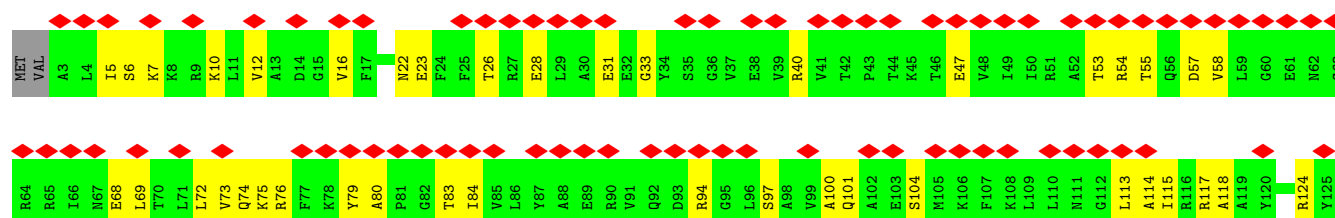
• Molecule 17: 40S ribosomal protein S27-A

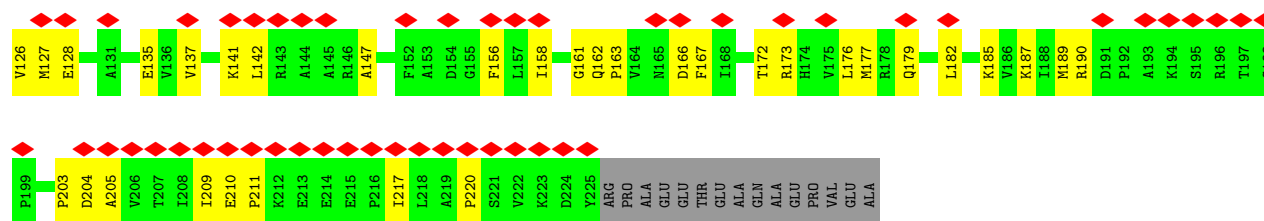


• Molecule 18: 40S ribosomal protein S30-A

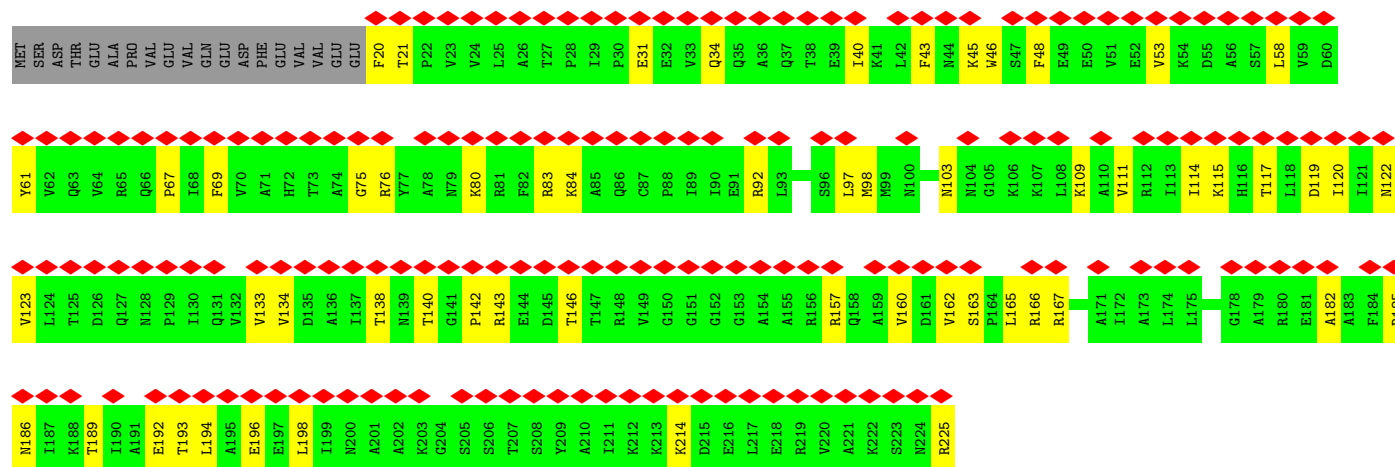
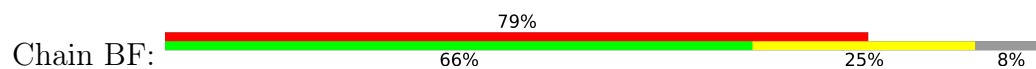


• Molecule 19: RPS3 isoform 1

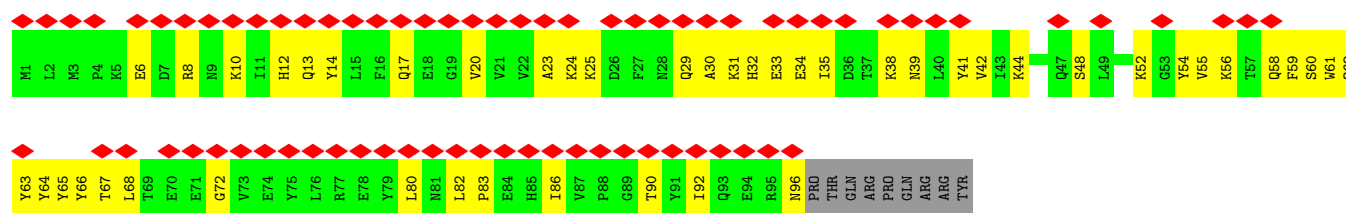
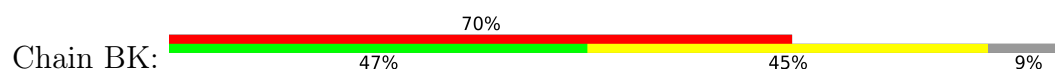




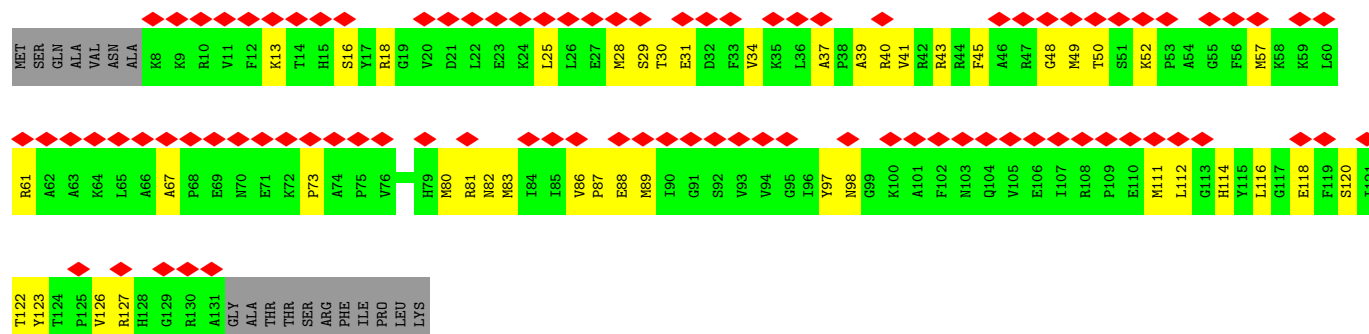
• Molecule 20: Rps5p



• Molecule 21: 40S ribosomal protein S10-A

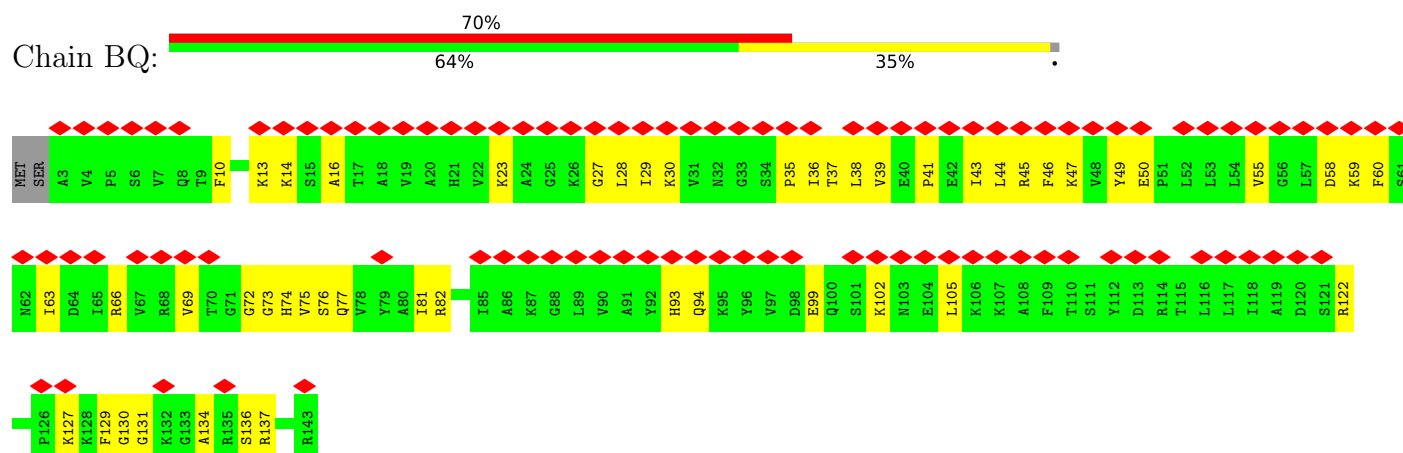


• Molecule 22: RPS15 isoform 1



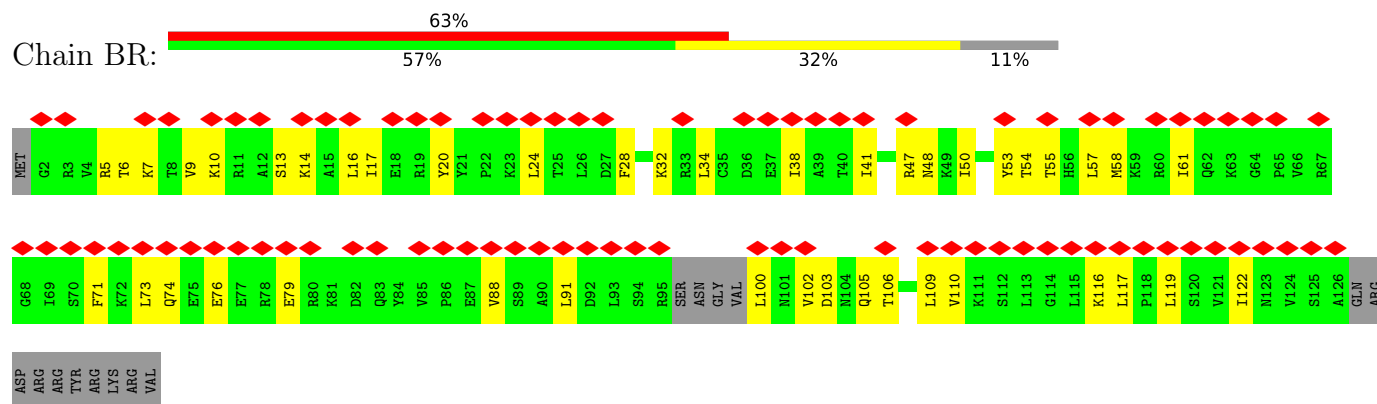
- Molecule 23: 40S ribosomal protein S16-A

Chain BQ:



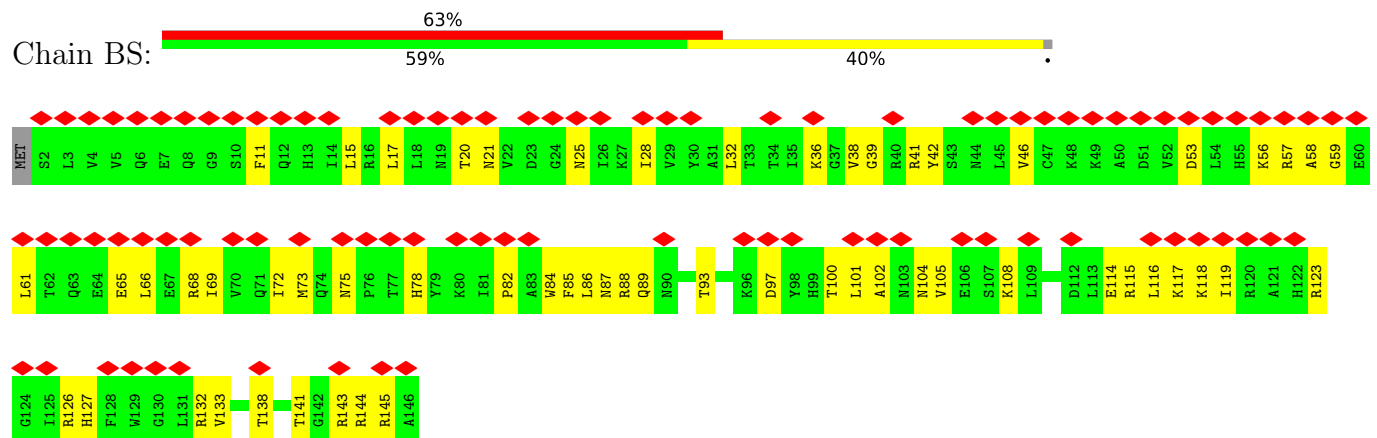
- Molecule 24: 40S ribosomal protein S17-A

Chain BR:



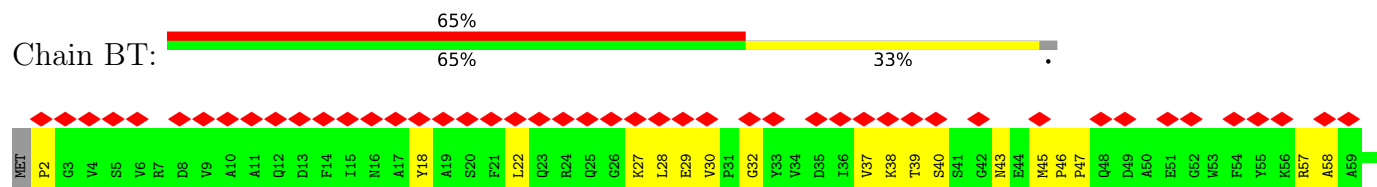
- Molecule 25: 40S ribosomal protein S18-A

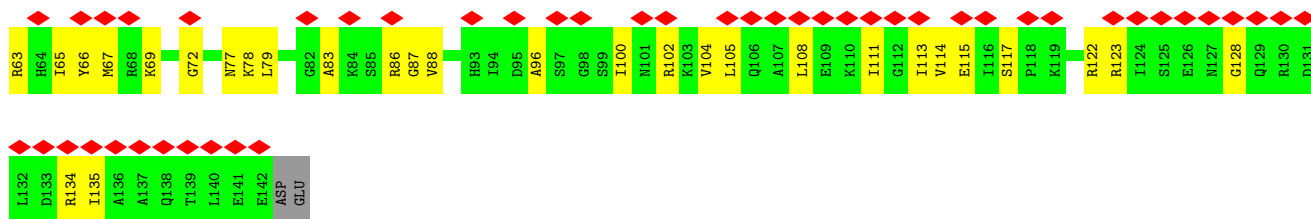
Chain BS:



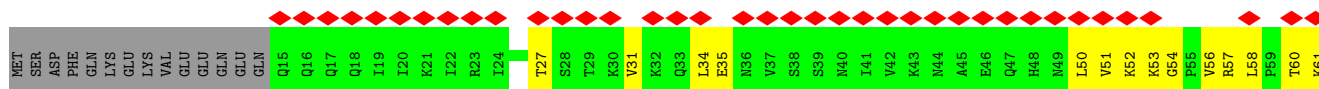
- Molecule 26: 40S ribosomal protein S19-A

Chain BT:

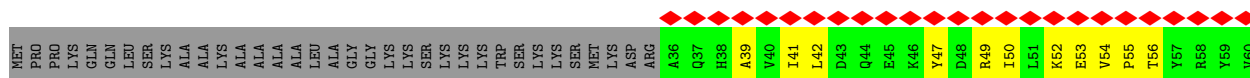




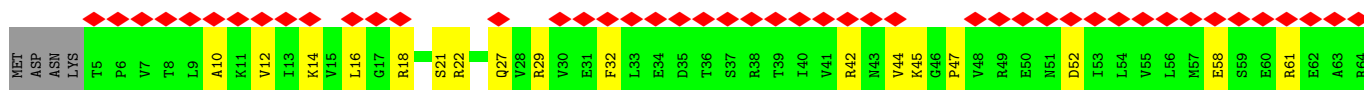
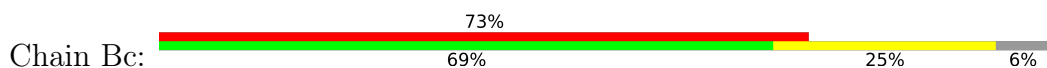
• Molecule 27: RPS20 isoform 1



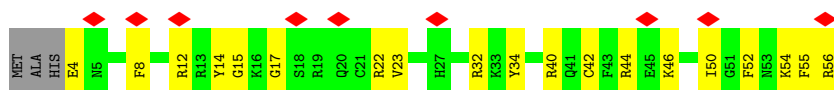
• Molecule 28: RPS25A isoform 1



• Molecule 29: RPS28A isoform 1

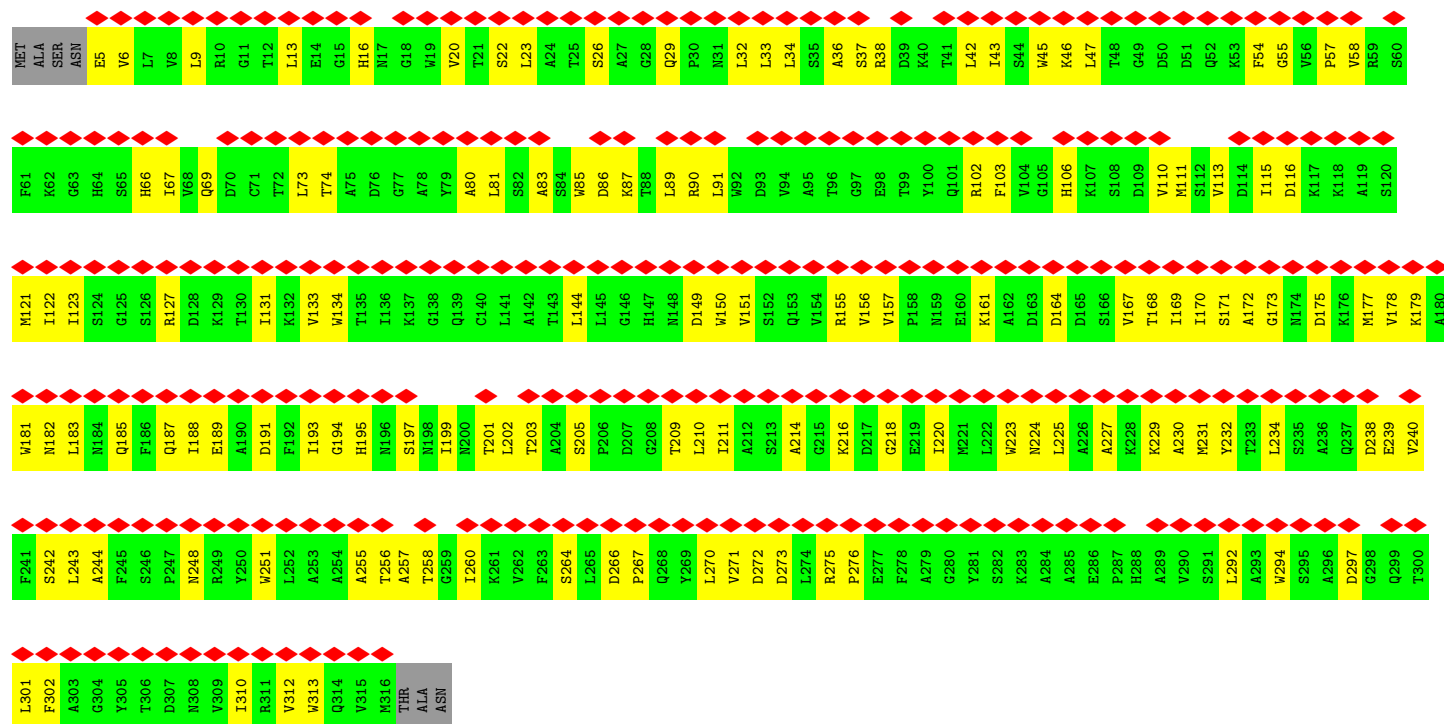


• Molecule 30: RPS29A isoform 1

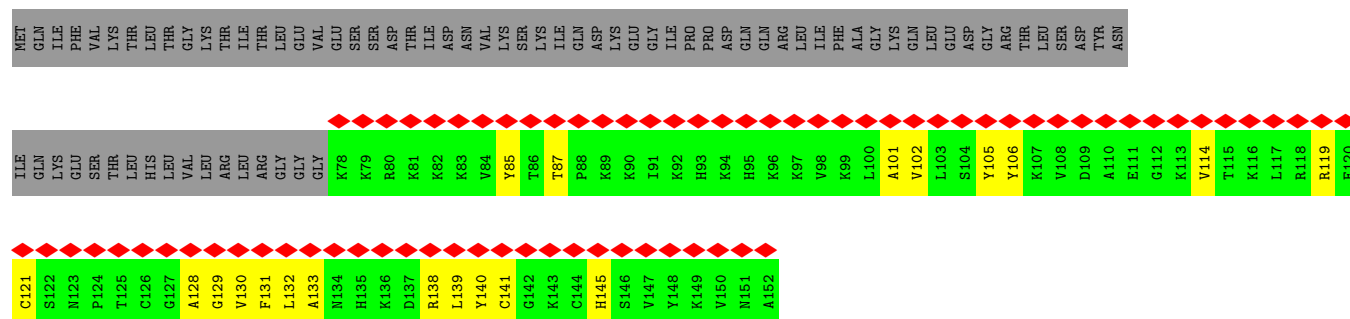
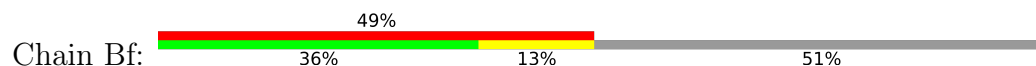


• Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein

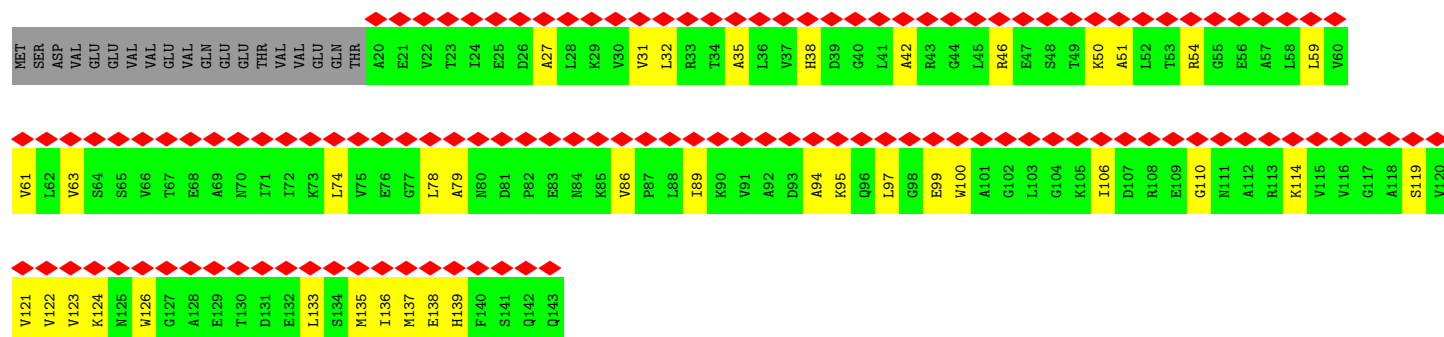




• Molecule 32: Ubiquitin-40S ribosomal protein S31

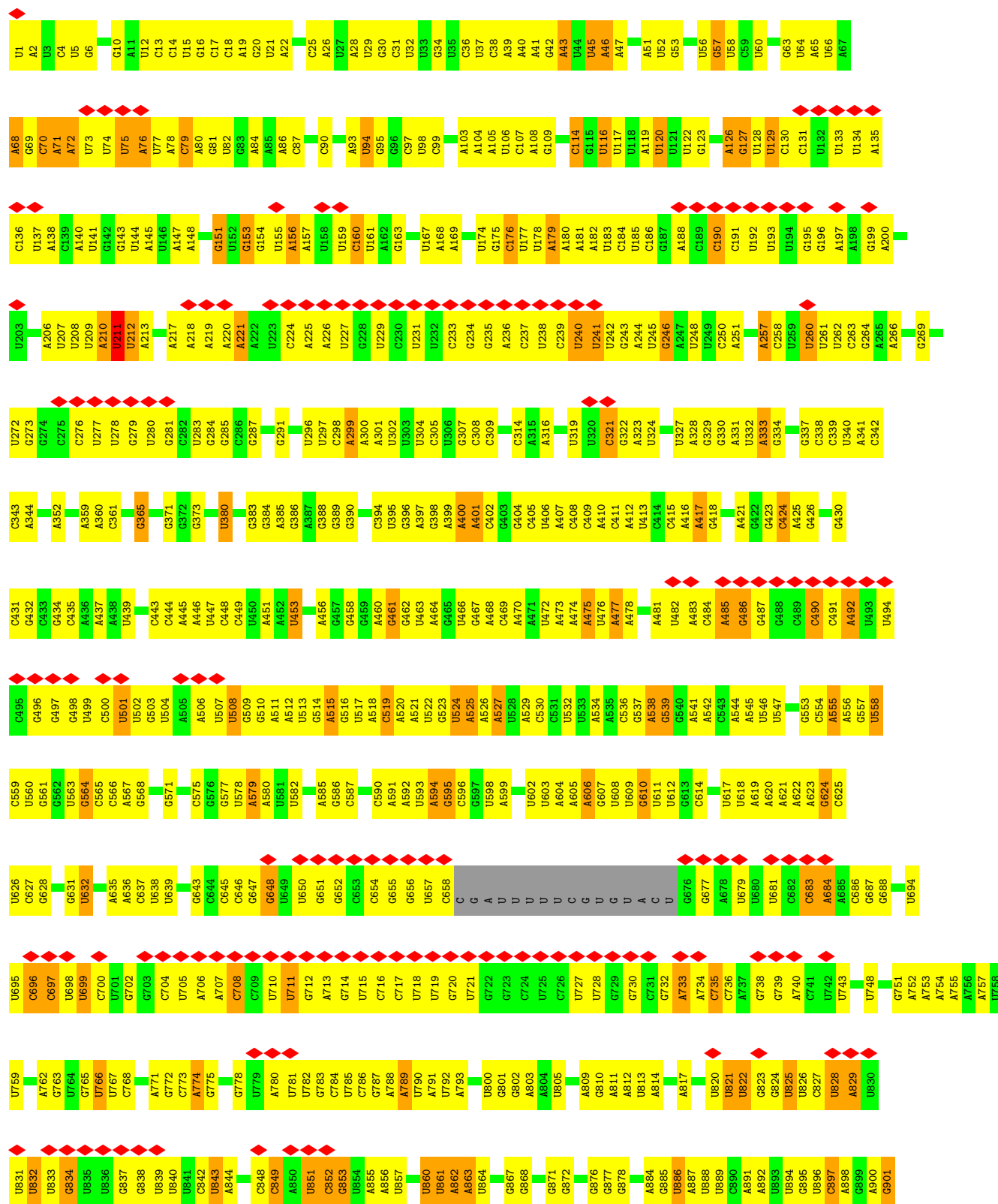


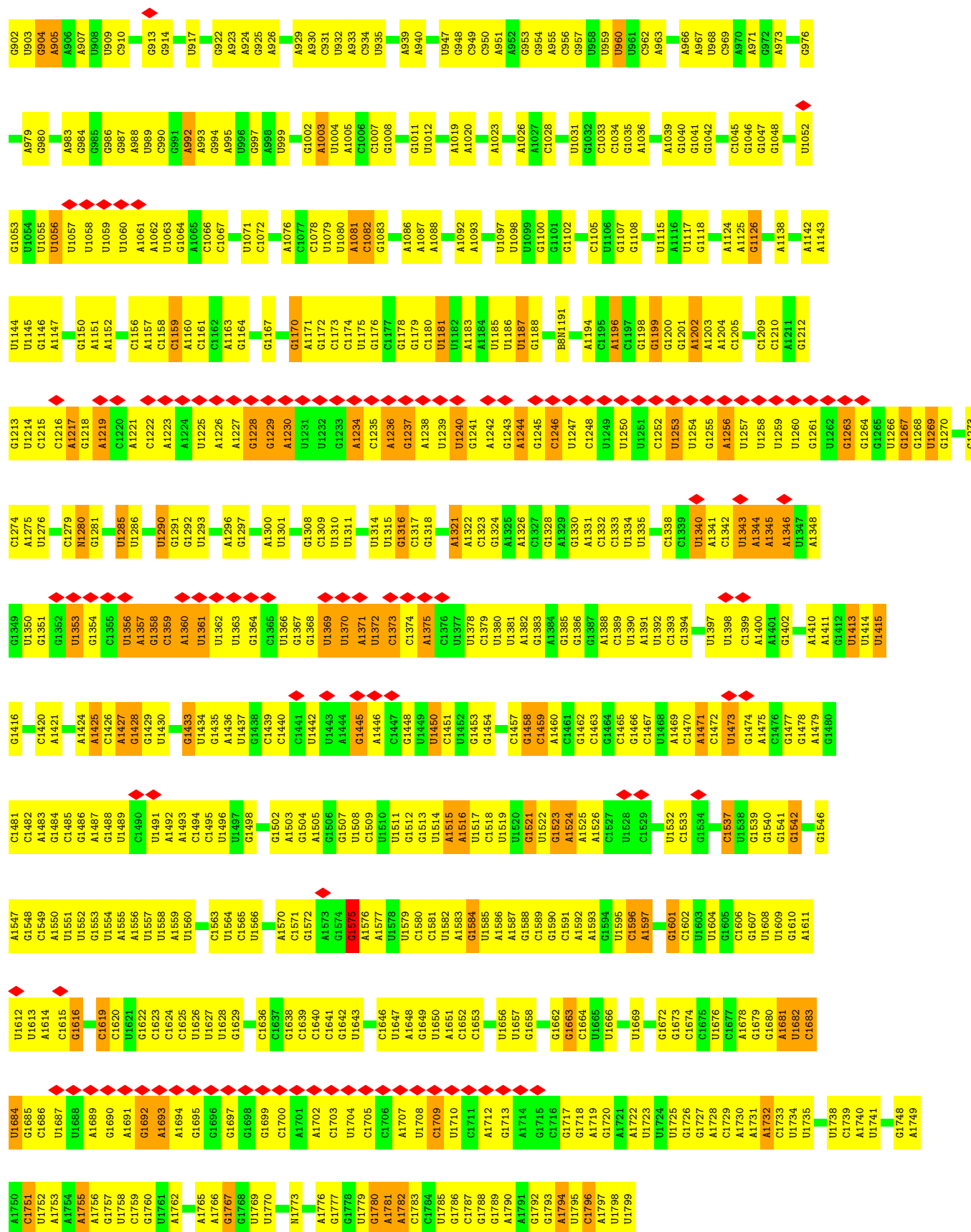
• Molecule 33: 40S ribosomal protein S12



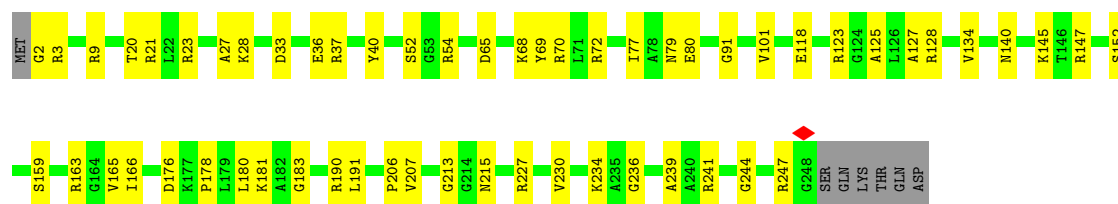
● Molecule 34: 18S rRNA

Chain B5: 



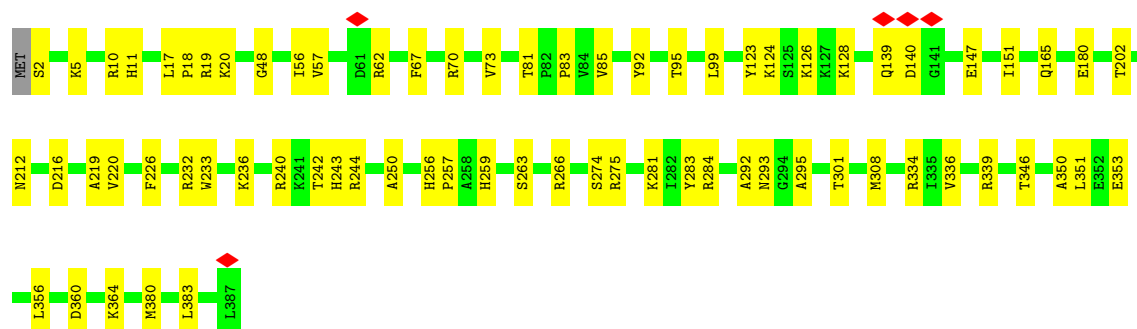


Chain AA:  75% 22%



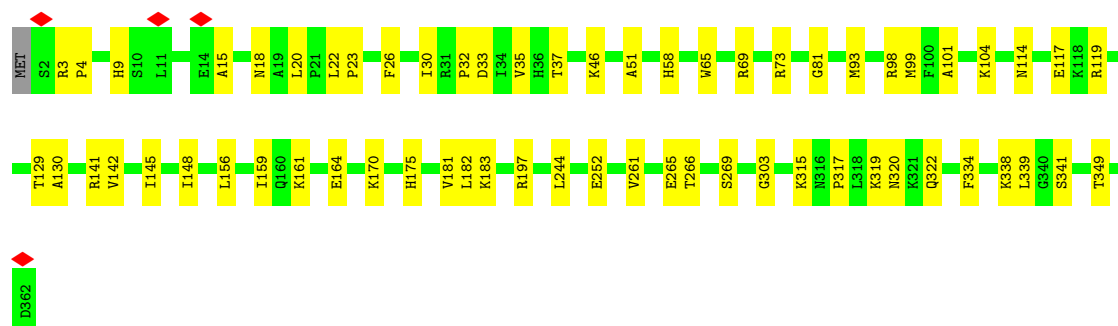
- Molecule 36: 60S ribosomal protein L3

Chain AB:  81% 19%



- Molecule 37: RPL4A isoform 1

Chain AC:  82% 17%



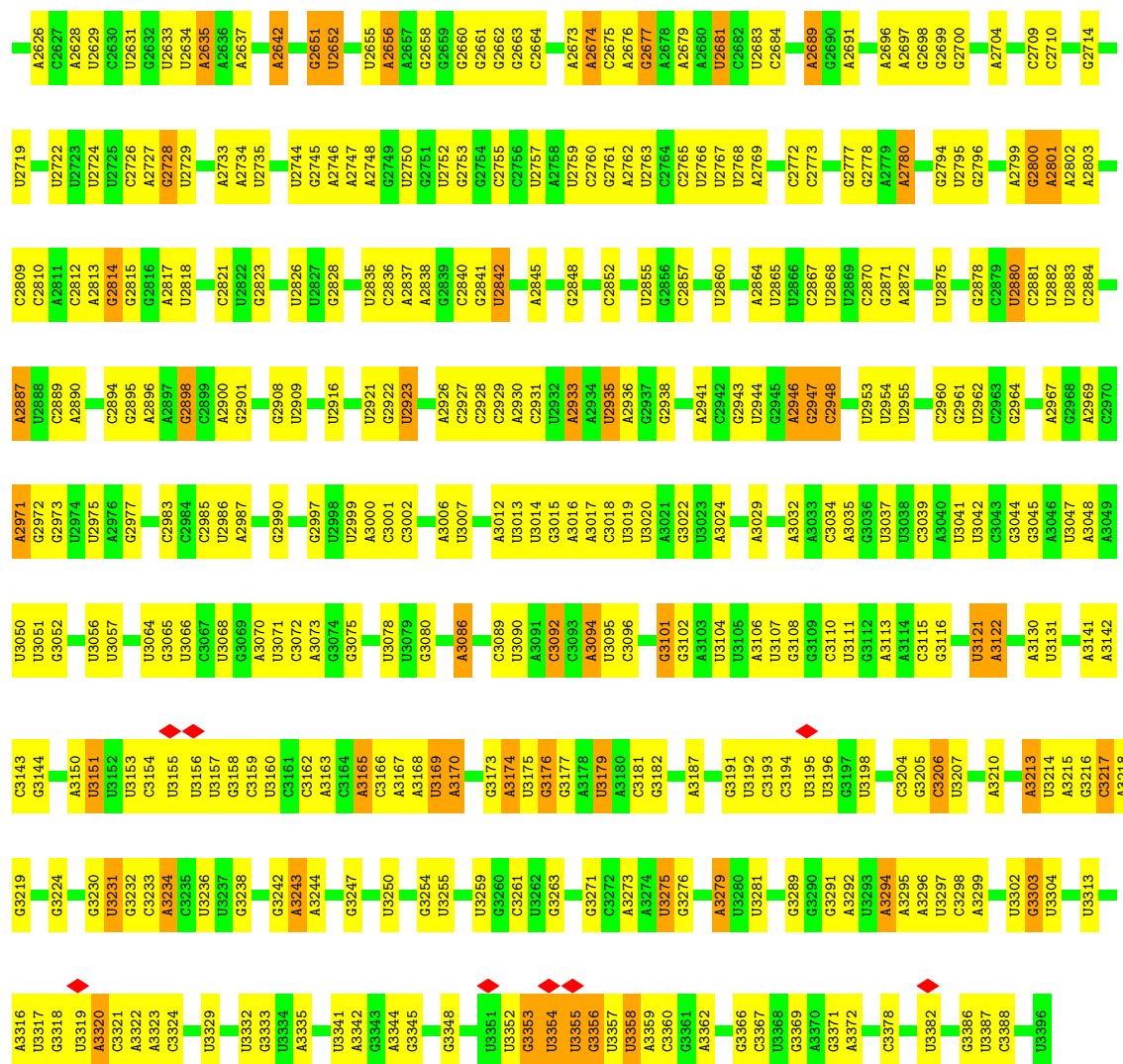
- Molecule 38: 25S rRNA

Chain A1:  48% 38% 7% 7%



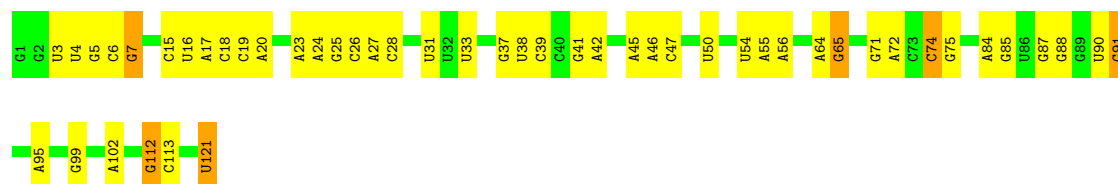


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U2408	U2411	A2412	G2413	C2414	C2415	U2416	A2419	U2420	U2423	A2424	G2425	U2426	U2427	U2428	G2429	A2430	C2431	U2432	U2433	U2434	G2435	U2436	G2437	A2438	U2439	G2440	A2441	G2442	A2443	C2444	A	U	A	G	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	
U2408	U2411	A2412	G2413	C2414	C2415	U2416	A2419	U2420	U2423	A2424	G2425	U2426	U2427	U2428	G2429	A2430	C2431	U2432	U2433	U2434	G2435	U2436	G2437	A2438	U2439	G2440	A2441	G2442	A2443	C2444	A	U	A	G	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	
U2408	U2411	A2412	G2413	C2414	C2415	U2416	A2419	U2420	U2423	A2424	G2425	U2426	U2427	U2428	G2429	A2430	C2431	U2432	U2433	U2434	G2435	U2436	G2437	A2438	U2439	G2440	A2441	G2442	A2443	C2444	A	U	A	G	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
U2408	U2411	A2412	G2413	C2414	C2415	U2416	A2419	U2420	U2423	A2424	G2425	U2426	U2427	U2428	G2429	A2430	C2431	U2432	U2433	U2434	G2435	U2436	G2437	A2438	U2439	G2440	A2441	G2442	A2443	C2444	A	U	A	G	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
U2408	U2411	A2412	G2413	C2414	C2415	U2416	A2419	U2420	U2423	A2424	G2425	U2426	U2427	U2428	G2429	A2430	C2431	U2432	U2433	U2434	G2435	U2436	G2437	A2438	U2439	G2440	A2441	G2442	A2443	C2444	A	U	A	G	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
U2408	U2411	A2412	G2413	C2414	C2415	U2416	A2419	U2420	U2423	A2424	G2425	U2426	U2427	U2428	G2429	A2430	C2431	U2432	U2433	U2434	G2435	U2436	G2437	A2438</																														



• Molecule 39: 5s rRNA

Chain A3: 60% 36% 5%



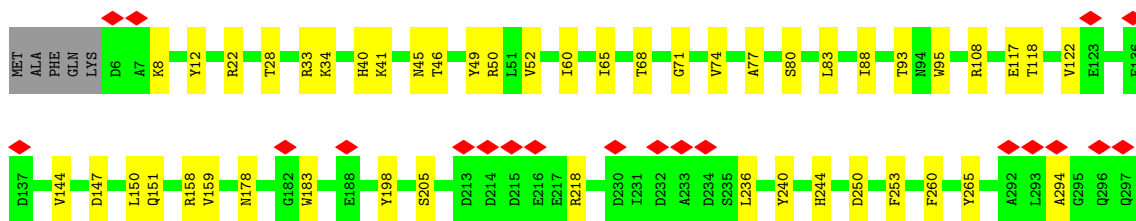
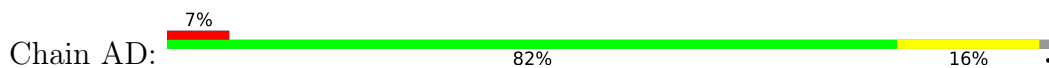
• Molecule 40: 5.8 S rRNA

Chain A4: 48% 47% 5%

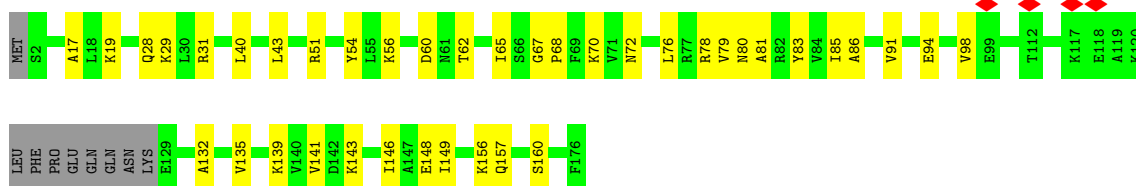
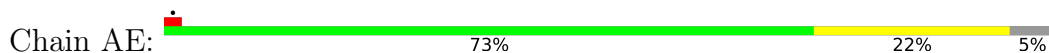




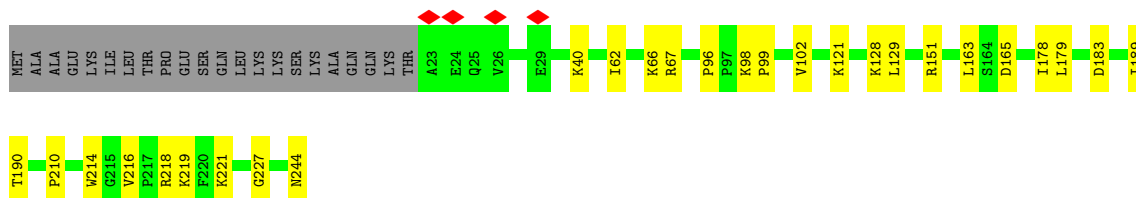
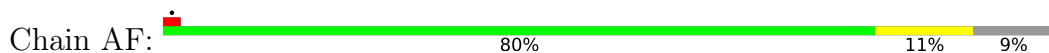
• Molecule 41: RPL5 isoform 1



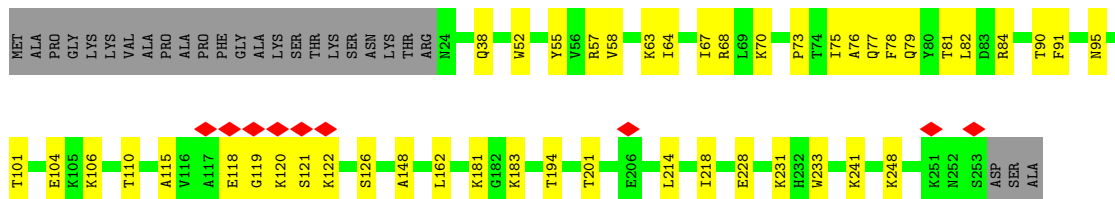
• Molecule 42: 60S ribosomal protein L6-A



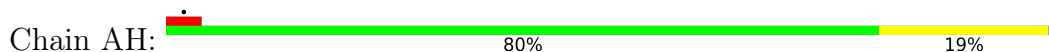
• Molecule 43: 60S ribosomal protein L7-A

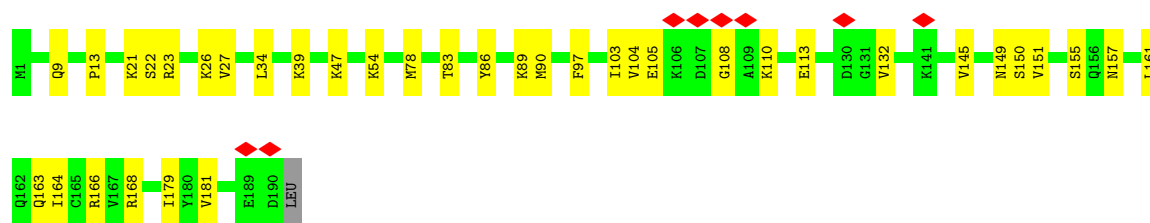


• Molecule 44: 60S ribosomal protein L8-A

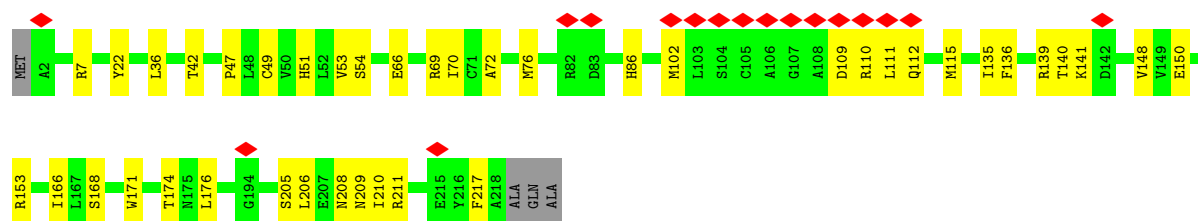
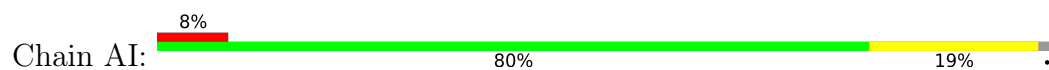


• Molecule 45: 60S ribosomal protein L9-A

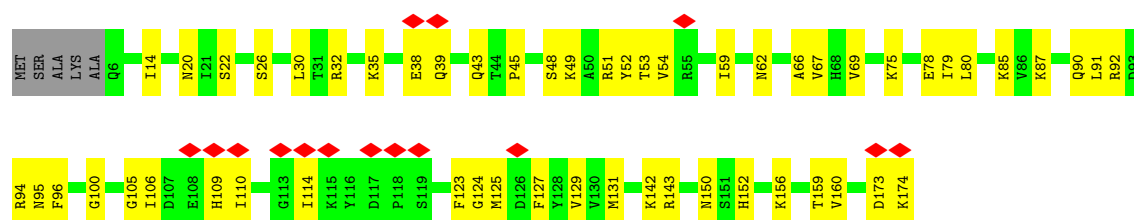




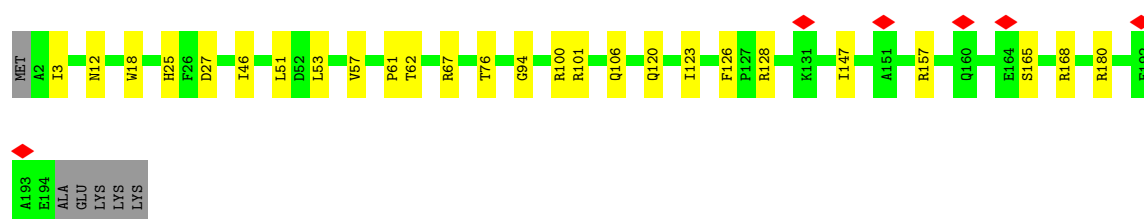
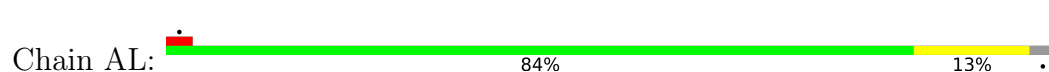
• Molecule 46: RPL10 isoform 1



• Molecule 47: RPL11A isoform 1



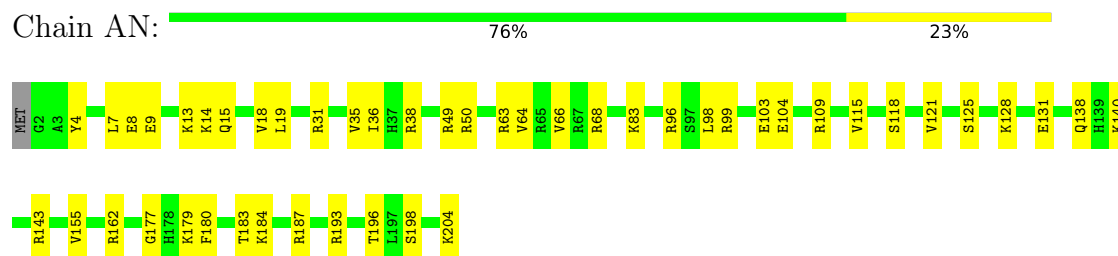
• Molecule 48: 60S ribosomal protein L13-A



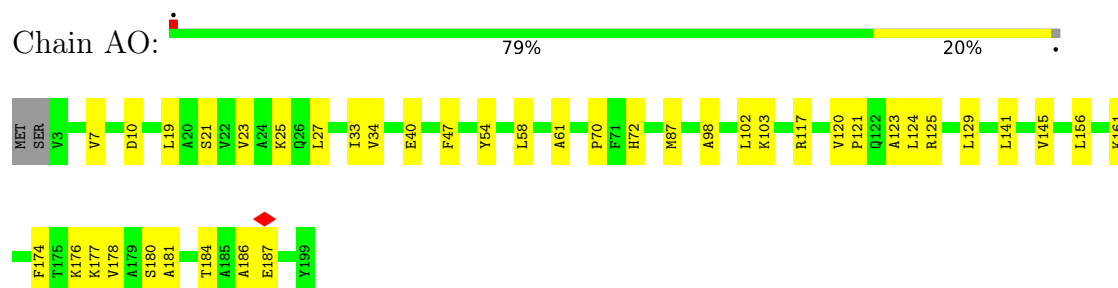
• Molecule 49: 60S ribosomal protein L14-A



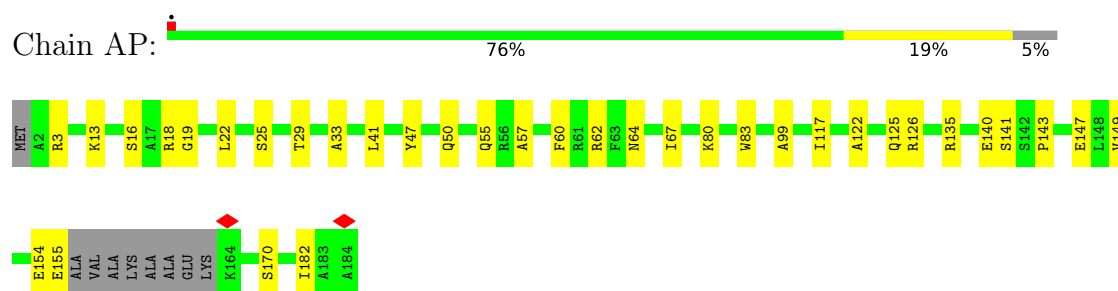
- Molecule 50: 60S ribosomal protein L15-A



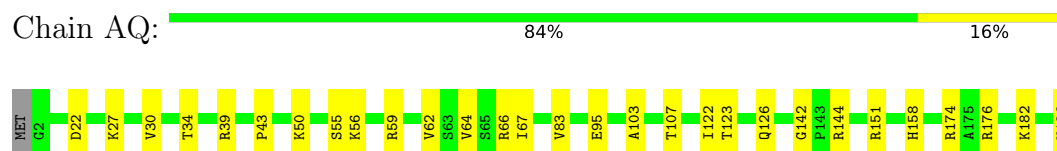
- Molecule 51: 60S ribosomal protein L16-A



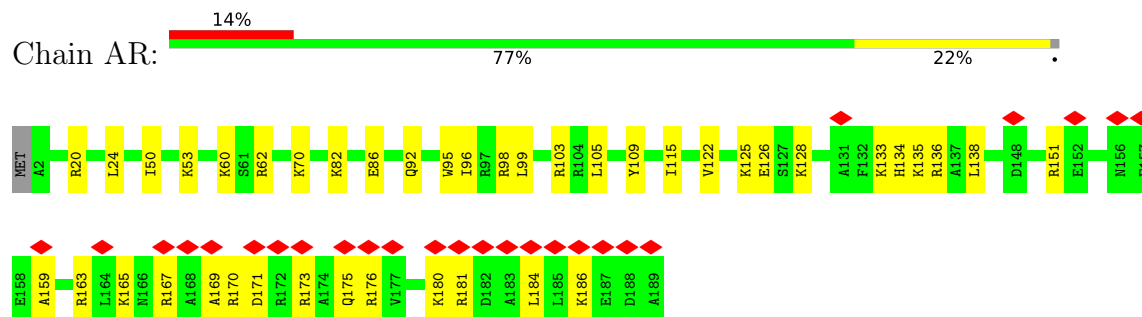
- Molecule 52: 60S ribosomal protein L17-A



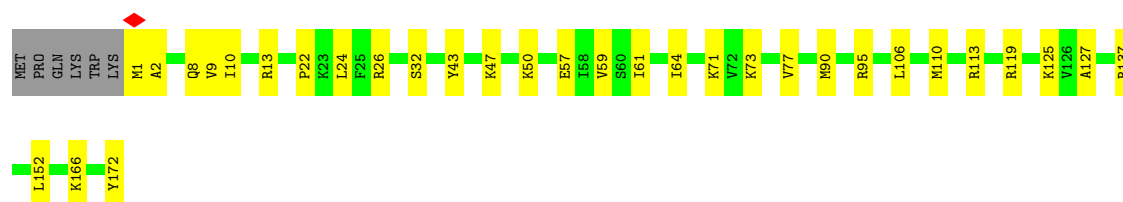
- Molecule 53: 60S ribosomal protein L18-A



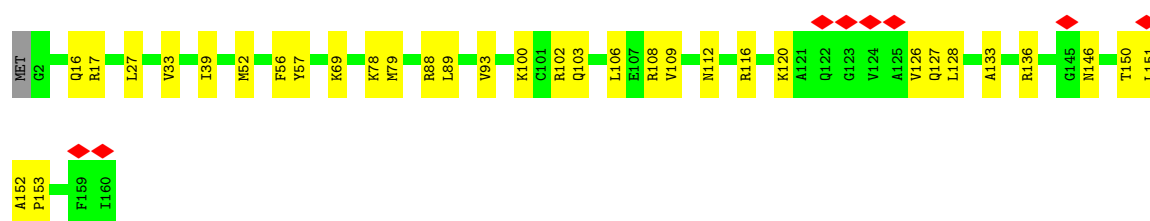
- Molecule 54: 60S ribosomal protein L19-A



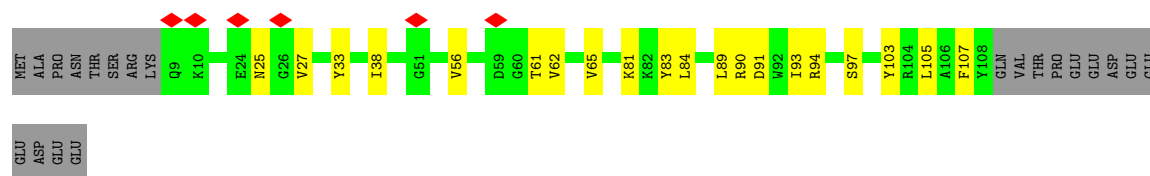
• Molecule 55: 60S ribosomal protein L20

Chain AS:  79% 18%

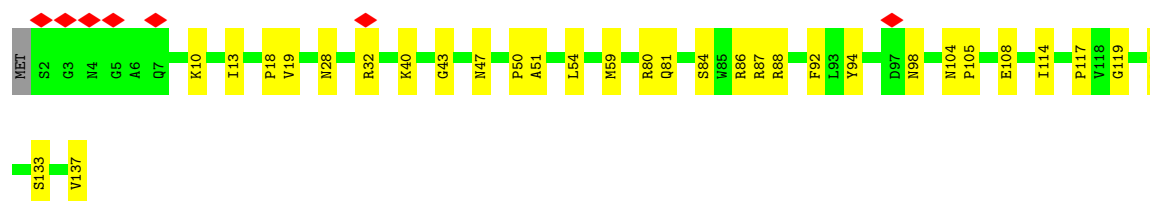
• Molecule 56: 60S ribosomal protein L21-A

Chain AT:  5% 79% 21%

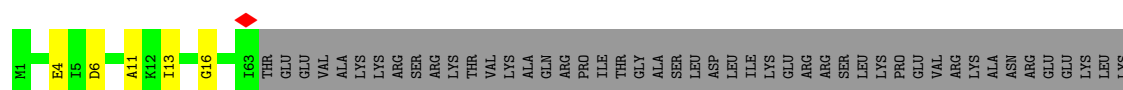
• Molecule 57: 60S ribosomal protein L22-A

Chain AU:  5% 66% 17% 17%

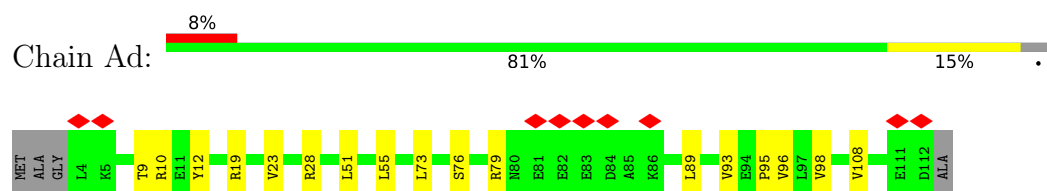
• Molecule 58: 60S ribosomal protein L23-A

Chain AV:  5% 77% 23%

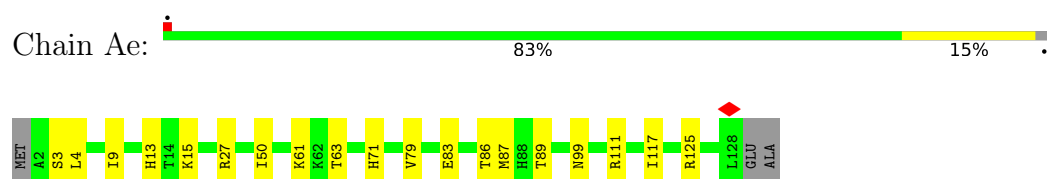
• Molecule 59: RPL24A isoform 1

Chain AW:  37% 59%

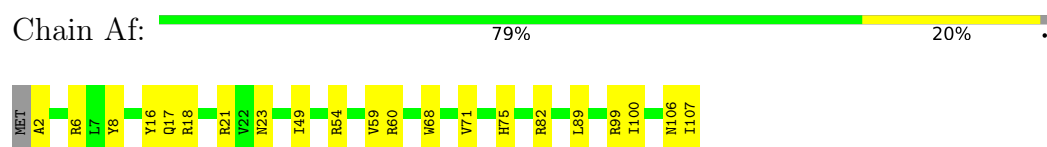
- Molecule 66: 60S ribosomal protein L31-A



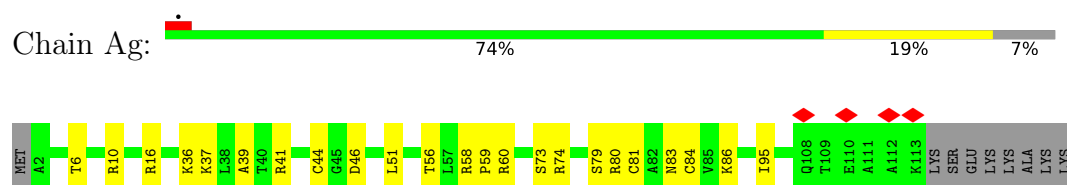
- Molecule 67: RPL32 isoform 1



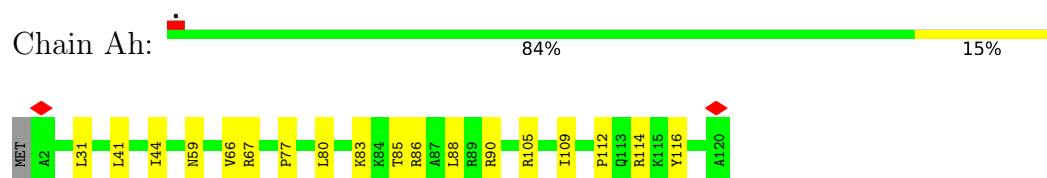
- Molecule 68: 60S ribosomal protein L33-A



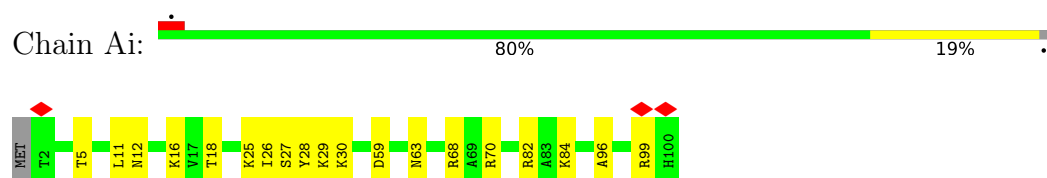
- Molecule 69: 60S ribosomal protein L34-A



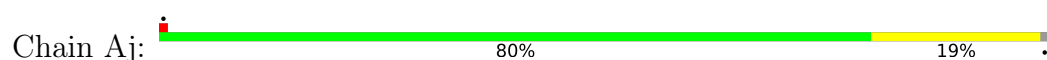
- Molecule 70: 60S ribosomal protein L35-A

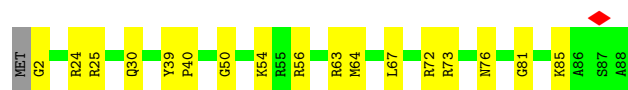


- Molecule 71: 60S ribosomal protein L36-A

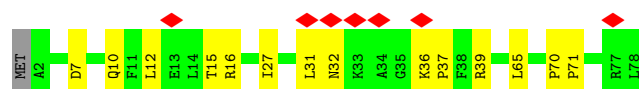
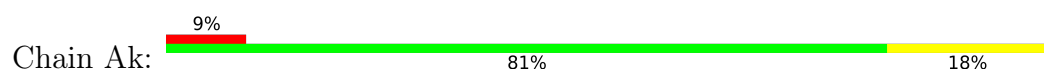


- Molecule 72: 60S ribosomal protein L37-A

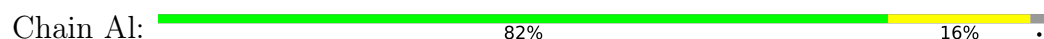




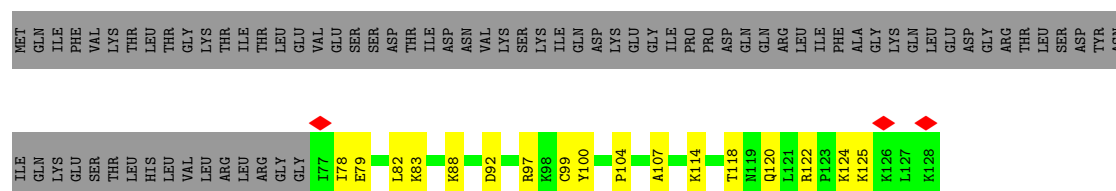
- Molecule 73: RPL38 isoform 1



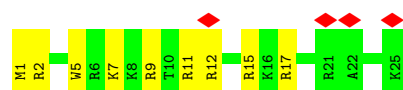
- Molecule 74: 60S ribosomal protein L39



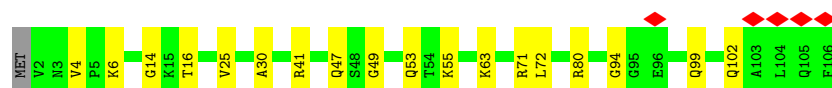
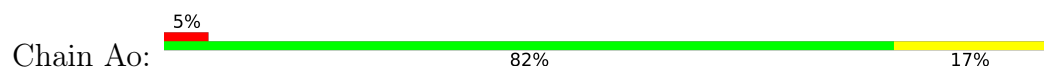
- Molecule 75: Ubiquitin-60S ribosomal protein L40



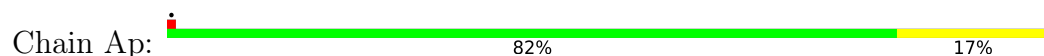
- Molecule 76: 60S ribosomal protein L41-A



- Molecule 77: 60S ribosomal protein L42-A



- Molecule 78: 60S ribosomal protein L43-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24307	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	3.779	Depositor
Minimum map value	-1.110	Depositor
Average map value	0.043	Depositor
Map value standard deviation	0.202	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, B8N, 4AC, MA6, 5MC, 1MA, 3HE, OMU, G7M, UR3, HIC, PSU, SPD, OMG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	BA	0.12	0/1653	0.36	0/2261
2	BB	0.13	0/1735	0.42	0/2335
3	BC	0.09	0/1665	0.27	0/2263
4	BE	0.10	0/2109	0.34	0/2839
5	BG	0.12	0/1844	0.39	0/2464
6	BH	0.17	0/1506	0.49	1/2028 (0.0%)
7	BI	0.11	0/1514	0.35	0/2021
8	BJ	0.12	0/1519	0.36	0/2035
9	BL	0.11	0/1272	0.34	0/1712
10	BN	0.11	0/1215	0.31	0/1638
11	BO	0.16	0/952	0.43	0/1279
12	BV	0.13	0/693	0.39	0/935
13	BW	0.13	0/1038	0.35	0/1395
14	BX	0.10	0/1139	0.31	0/1518
15	BY	0.16	0/1087	0.40	0/1449
16	Ba	0.14	0/782	0.37	0/1047
17	Bb	0.11	0/620	0.30	0/838
18	Be	0.08	0/483	0.27	0/643
19	BD	0.12	0/1759	0.36	0/2368
20	BF	0.09	0/1629	0.30	0/2202
21	BK	0.13	0/837	0.44	0/1131
22	BP	0.13	0/1012	0.40	0/1356
23	BQ	0.10	0/1125	0.32	0/1510
24	BR	0.12	0/957	0.40	0/1283
25	BS	0.10	0/1211	0.31	0/1628
26	BT	0.12	0/1113	0.36	0/1494
27	BU	0.10	0/865	0.32	0/1169
28	BZ	0.10	0/571	0.30	0/768
29	Bc	0.09	0/499	0.30	0/670
30	Bd	0.11	0/452	0.51	2/600 (0.3%)
31	Bg	0.11	0/2454	0.33	0/3340
32	Bf	0.08	0/616	0.26	0/817

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.11	0/943	0.35	0/1274
34	B5	0.12	1/42034 (0.0%)	0.29	2/65493 (0.0%)
35	AA	0.11	0/1912	0.29	0/2569
36	AB	0.10	0/3139	0.28	0/4219
37	AC	0.10	0/2800	0.29	0/3790
38	A1	0.12	0/74791	0.29	1/116610 (0.0%)
39	A3	0.10	0/2861	0.23	0/4457
40	A4	0.12	0/3724	0.30	0/5798
41	AD	0.10	0/2390	0.29	0/3225
42	AE	0.09	0/1324	0.28	0/1782
43	AF	0.10	0/1821	0.26	0/2451
44	AG	0.12	0/1830	0.30	0/2469
45	AH	0.10	0/1531	0.30	0/2062
46	AI	0.10	0/1796	0.28	0/2409
47	AJ	0.13	0/1374	0.41	0/1842
48	AL	0.09	0/1568	0.25	0/2106
49	AM	0.09	0/1068	0.25	0/1438
50	AN	0.11	0/1757	0.28	0/2354
51	AO	0.10	0/1585	0.26	0/2128
52	AP	0.10	0/1410	0.25	0/1893
53	AQ	0.11	0/1465	0.28	0/1965
54	AR	0.11	0/1538	0.28	0/2050
55	AS	0.11	0/1481	0.31	0/1990
56	AT	0.12	0/1300	0.30	0/1743
57	AU	0.10	0/812	0.30	0/1099
58	AV	0.10	0/1018	0.26	0/1369
59	AW	0.09	0/533	0.23	0/707
60	AX	0.12	0/983	0.29	0/1325
61	AY	0.10	0/1004	0.28	0/1341
62	AZ	0.11	0/1118	0.34	0/1497
63	Aa	0.13	0/1204	0.30	0/1612
64	Ab	0.09	0/473	0.25	0/629
65	Ac	0.08	0/751	0.22	0/1008
66	Ad	0.09	0/904	0.27	0/1213
67	Ae	0.09	0/1041	0.26	0/1394
68	Af	0.11	0/868	0.25	0/1168
69	Ag	0.11	0/890	0.28	0/1189
70	Ah	0.10	0/978	0.29	0/1301
71	Ai	0.10	0/778	0.31	0/1034
72	Aj	0.10	0/696	0.26	0/923
73	Ak	0.10	0/618	0.28	0/826
74	Al	0.09	0/443	0.24	0/588
75	Am	0.13	0/423	0.34	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.12	0/234	0.31	0/300
77	Ao	0.09	0/860	0.29	0/1136
78	Ap	0.10	0/701	0.31	0/934
All	All	0.12	1/212698 (0.0%)	0.30	6/312308 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	O3'-P	8.37	1.64	1.56

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1575	G7M	P-O3'-C3'	9.01	130.51	119.70
34	B5	1575	G7M	O3'-P-O5'	7.72	118.67	104.00
30	Bd	4	GLU	CA-C-N	6.89	134.10	121.70
30	Bd	4	GLU	C-N-CA	6.89	134.10	121.70
38	A1	2269	U	C2'-C3'-O3'	5.20	117.30	109.50
6	BH	67	LEU	CA-CB-CG	5.14	134.29	116.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	68	0
2	BB	1709	0	1784	71	0
3	BC	1635	0	1723	41	0
4	BE	2068	0	2154	77	0
5	BG	1820	0	1918	61	0
6	BH	1481	0	1572	54	0
7	BI	1489	0	1525	69	0
8	BJ	1494	0	1573	77	0
9	BL	1244	0	1314	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	BN	1192	0	1255	34	0
11	BO	941	0	979	49	0
12	BV	684	0	672	27	0
13	BW	1021	0	1060	30	0
14	BX	1121	0	1196	39	0
15	BY	1073	0	1132	44	0
16	Ba	769	0	818	19	0
17	Bb	610	0	633	21	0
18	Be	475	0	525	28	0
19	BD	1734	0	1817	57	0
20	BF	1609	0	1675	48	0
21	BK	817	0	804	37	0
22	BP	991	0	1035	36	0
23	BQ	1105	0	1166	46	0
24	BR	948	0	990	41	0
25	BS	1192	0	1222	52	0
26	BT	1095	0	1114	43	0
27	BU	855	0	917	37	0
28	BZ	563	0	603	16	0
29	Bc	497	0	535	15	0
30	Bd	442	0	432	22	0
31	Bg	2401	0	2356	95	0
32	Bf	605	0	654	19	0
33	BM	935	0	975	30	0
34	B5	37987	0	19105	904	0
35	AA	1878	0	1946	51	0
36	AB	3081	0	3162	56	0
37	AC	2748	0	2859	46	0
38	A1	67564	0	33965	982	0
39	A3	2579	0	1304	47	0
40	A4	3353	0	1695	62	0
41	AD	2341	0	2290	41	0
42	AE	1303	0	1376	29	0
43	AF	1784	0	1862	19	0
44	AG	1798	0	1894	32	0
45	AH	1510	0	1576	25	0
46	AI	1759	0	1799	28	0
47	AJ	1353	0	1383	43	0
48	AL	1543	0	1608	23	0
49	AM	1053	0	1149	26	0
50	AN	1720	0	1779	38	0
51	AO	1555	0	1659	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	AP	1388	0	1423	24	0
53	AQ	1441	0	1543	21	0
54	AR	1521	0	1617	34	0
55	AS	1445	0	1487	25	0
56	AT	1276	0	1323	31	0
57	AU	796	0	812	16	0
58	AV	1003	0	1048	19	0
59	AW	521	0	551	3	0
60	AX	968	0	1036	9	0
61	AY	993	0	1081	16	0
62	AZ	1092	0	1155	23	0
63	Aa	1173	0	1215	29	0
64	Ab	462	0	491	4	0
65	Ac	743	0	797	5	0
66	Ad	890	0	938	12	0
67	Ae	1020	0	1090	14	0
68	Af	850	0	880	17	0
69	Ag	880	0	945	17	0
70	Ah	969	0	1078	17	0
71	Ai	771	0	849	14	0
72	Aj	681	0	687	13	0
73	Ak	612	0	682	9	0
74	Al	436	0	475	7	0
75	Am	417	0	459	11	0
76	An	233	0	283	10	0
77	Ao	847	0	914	12	0
78	Ap	694	0	738	14	0
79	A1	10	0	19	3	0
80	A1	20	0	23	1	0
81	Ao	1	0	0	0	0
All	All	199289	0	147801	3630	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 11.

All (3630) 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)
27:BU:52:LYS:HE3	27:BU:94:GLU:H	1.28	0.96
11:BO:111:ARG:HE	11:BO:112:ILE:H	1.11	0.96
34:B5:976:G:H1	34:B5:1023:A:HO2'	1.14	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:173:G:H1	38:A1:245:U:H3	1.01	0.92
1:BA:32:HIS:HD1	1:BA:153:SER:HG	1.13	0.92
38:A1:3348:G:H1	38:A1:3357:U:H3	0.95	0.92
11:BO:111:ARG:NH2	16:Ba:56:ALA:O	2.04	0.91
19:BD:177:MET:HE1	19:BD:182:LEU:HB2	1.54	0.89
13:BW:111:MET:HE2	13:BW:116:ALA:HA	1.56	0.88
51:AO:27[A]:LEU:HD21	51:AO:102[A]:LEU:HB2	1.57	0.87
41:AD:41:LYS:HE3	56:AT:93:VAL:HG11	1.57	0.86
17:Bb:51:GLN:OE1	34:B5:957:G:N2	2.11	0.84
63:Aa:104:THR:HG21	63:Aa:112:ILE:HD11	1.57	0.83
13:BW:2:THR:N	34:B5:1034:C:HO2'	1.77	0.83
34:B5:1346:A:OP2	34:B5:1348:A:N6	2.11	0.82
38:A1:2260:PSU:H3'	38:A1:2261:G:H8	1.44	0.81
77:Ao:99:GLN:HE22	77:Ao:102:GLN:HB3	1.46	0.81
34:B5:1575:G7M:O2'	34:B5:1576:A:O4'	1.98	0.81
30:Bd:44:ARG:NH2	34:B5:1279:C:O2'	2.15	0.80
35:AA:21:ARG:HD3	38:A1:824:C:H5''	1.64	0.80
22:BP:82:ASN:ND2	34:B5:1555:A:O2'	2.14	0.79
45:AH:105:GLU:OE2	45:AH:108:GLY:N	2.15	0.79
38:A1:1213:G:H4'	55:AS:90:MET:HG3	1.65	0.79
34:B5:648:G:N2	34:B5:686:C:O2	2.16	0.79
23:BQ:46:PHE:HA	23:BQ:49:TYR:HD2	1.48	0.78
34:B5:1173:C:HO2'	34:B5:1601:G:H1	1.24	0.78
14:BX:69:ARG:HG3	14:BX:117:ILE:HG12	1.65	0.78
62:AZ:88:ASP:HB3	62:AZ:121:ARG:HH12	1.49	0.78
20:BF:133:VAL:HG12	20:BF:198:LEU:HD13	1.65	0.77
19:BD:74:GLN:HB3	19:BD:84:ILE:HG21	1.65	0.77
15:BY:131:ARG:NH1	34:B5:154:G:OP2	2.17	0.77
55:AS:8:GLN:HB3	55:AS:64:ILE:HD11	1.67	0.77
40:A4:75:G:OP2	61:AY:74:TYR:OH	2.01	0.77
6:BH:150:GLN:HB3	6:BH:181:ILE:HG22	1.66	0.77
34:B5:648:G:N1	34:B5:686:C:N3	2.32	0.77
8:BJ:153:GLU:HG2	8:BJ:154:LYS:HD3	1.66	0.76
38:A1:544:C:HO2'	38:A1:548:G:H1	1.33	0.76
10:BN:60:VAL:HG23	10:BN:66:ILE:HD12	1.67	0.76
38:A1:2138:A:HO2'	72:Aj:2:GLY:N	1.83	0.76
2:BB:27:LYS:HD3	2:BB:47:LEU:HD13	1.68	0.76
19:BD:204:ASP:OD2	34:B5:1330:G:N2	2.19	0.76
38:A1:3020:U:O2	38:A1:3034:C:N4	2.18	0.76
34:B5:1158:C:H5'	34:B5:1161:C:H41	1.51	0.75
38:A1:2679:A:O2'	47:AJ:52:TYR:OH	2.03	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3016:A:H2'	38:A1:3017:A:H8	1.51	0.75
38:A1:2442:G:H2'	38:A1:2443:A:C8	2.21	0.75
38:A1:177:U:H3	38:A1:241:G:H1	1.32	0.75
38:A1:1221:A:H3'	38:A1:1222:G:H4'	1.69	0.75
38:A1:2251:G:H1	38:A1:2266:PSU:HN3	1.32	0.74
7:BI:104:ILE:HG13	7:BI:105:ASP:H	1.51	0.74
8:BJ:106:GLU:HA	8:BJ:111:THR:HG21	1.70	0.74
34:B5:774:A:N6	34:B5:786:C:O2	2.21	0.74
5:BG:95:LYS:NZ	34:B5:421:A:OP1	2.20	0.74
58:AV:81:GLN:O	58:AV:98:ASN:ND2	2.21	0.74
38:A1:3261:C:OP1	49:AM:126:GLN:NE2	2.20	0.73
71:AI:5:THR:O	71:AI:16:LYS:NZ	2.17	0.73
3:BC:156:THR:HG23	13:BW:95:PRO:HB2	1.70	0.73
5:BG:13:GLN:NE2	34:B5:151:G:N3	2.37	0.73
19:BD:40:ARG:HB3	19:BD:47:GLU:HB3	1.67	0.73
38:A1:1192:C:N4	38:A1:1300:G:OP2	2.21	0.73
20:BF:84:LYS:NZ	34:B5:1614:A:OP2	2.21	0.73
38:A1:2253:G:H1	38:A1:2264:PSU:HN3	1.34	0.73
10:BN:46:THR:H	10:BN:49:GLN:HE21	1.36	0.73
38:A1:172:G:H1	38:A1:246:U:H3	1.37	0.73
38:A1:173:G:O6	38:A1:245:U:O4	2.06	0.73
38:A1:649:A:OP2	38:A1:2868:U:O2'	2.06	0.73
4:BE:155:LYS:NZ	34:B5:244:A:OP1	2.22	0.73
32:Bf:102:VAL:HG22	33:BM:74:LEU:HD13	1.70	0.73
38:A1:242:C:H2'	38:A1:243:G:H8	1.52	0.73
75:Am:118:THR:OG1	75:Am:120:GLN:OE1	2.07	0.73
6:BH:15:GLU:HA	6:BH:18:LEU:HB3	1.71	0.73
22:BP:45:PHE:HA	22:BP:49:MET:HE3	1.71	0.72
29:Bc:14:LYS:HB3	29:Bc:29:ARG:HB3	1.71	0.72
9:BL:33:ARG:NH1	9:BL:51:GLY:O	2.22	0.72
31:Bg:258:THR:O	31:Bg:275:ARG:NH1	2.22	0.72
38:A1:1579:C:H42	60:AX:33:ARG:HH22	1.34	0.72
38:A1:3092:C:O2'	38:A1:3094:A:OP2	2.08	0.72
10:BN:11:ILE:HG13	10:BN:12:SER:H	1.55	0.72
26:BT:72:GLY:HA3	34:B5:1498:G:H5''	1.71	0.72
50:AN:183:THR:HG22	50:AN:187:ARG:HB3	1.71	0.72
11:BO:125:SER:HB3	34:B5:926:A:H2	1.55	0.71
2:BB:222:LYS:HD3	2:BB:224:ASP:H	1.55	0.71
38:A1:718:G:OP1	63:Aa:117:ARG:NH2	2.22	0.71
31:Bg:203:THR:HG21	31:Bg:244:ALA:HA	1.72	0.71
5:BG:6:SER:HB2	5:BG:112:VAL:HG12	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BX:7:ARG:NH1	34:B5:1102:G:OP2	2.22	0.71
18:Be:43:ARG:HH22	34:B5:590:C:H5''	1.56	0.71
38:A1:655:C:H2'	38:A1:656:A:H8	1.54	0.71
55:AS:24:LEU:HD11	55:AS:59:VAL:HG21	1.71	0.71
33:BM:106:ILE:HG23	33:BM:110:GLY:HA2	1.72	0.71
38:A1:547:G:H4'	38:A1:548:G:H2'	1.71	0.71
34:B5:1504:G:N3	34:B5:1563:C:O2'	2.22	0.71
38:A1:1234:G:H3'	38:A1:1235:U:H5'	1.73	0.71
4:BE:108:ARG:NH2	34:B5:788:A:OP2	2.24	0.71
40:A4:83:C:O2	61:AY:51:ARG:NH2	2.23	0.71
46:AI:54:SER:HB2	46:AI:135:ILE:HD11	1.73	0.71
24:BR:100:LEU:HG	24:BR:119:LEU:HA	1.71	0.70
16:Ba:46:GLU:HG2	16:Ba:48:ALA:H	1.55	0.70
33:BM:46:ARG:NH2	34:B5:1253:U:OP2	2.24	0.70
34:B5:1081:A:O2'	34:B5:1083:G:N7	2.22	0.70
39:A3:121:U:OP2	41:AD:265:TYR:OH	2.07	0.70
38:A1:799:G:OP2	63:Aa:32:ARG:NH1	2.24	0.70
38:A1:1953:G:H3'	38:A1:1954:G:H3'	1.71	0.70
5:BG:219:ARG:HG3	5:BG:220:LYS:HG2	1.74	0.70
7:BI:57:ALA:HB2	7:BI:177:GLY:HA2	1.73	0.70
31:Bg:111:MET:HE3	31:Bg:127:ARG:HG3	1.73	0.70
34:B5:828:U:O2'	34:B5:829:A:O5'	2.08	0.70
9:BL:16:GLN:HG2	9:BL:19:ILE:HD13	1.74	0.70
34:B5:126:A:N6	34:B5:263:C:O2'	2.24	0.70
40:A4:58:G:O6	72:Aj:63:ARG:NH1	2.24	0.70
49:AM:48:GLY:HA3	49:AM:53:VAL:HB	1.74	0.70
11:BO:107:ARG:NH2	16:Ba:52:ASP:OD1	2.24	0.70
56:AT:39:ILE:HD13	56:AT:102:ARG:HD3	1.73	0.70
3:BC:175:GLY:O	8:BJ:53:ARG:NH1	2.25	0.70
8:BJ:132:ARG:NH2	34:B5:532:U:OP1	2.25	0.70
49:AM:72:LEU:HD12	49:AM:84:LYS:HD2	1.73	0.70
36:AB:244:ARG:NH1	38:A1:2948:C:OP1	2.25	0.69
42:AE:31:ARG:NH2	42:AE:81:ALA:O	2.25	0.69
34:B5:1356:U:H3	34:B5:1367:G:H22	1.40	0.69
34:B5:273:G:O6	34:B5:283:U:O2	2.09	0.69
34:B5:1164:G:O2'	34:B5:1612:U:O2	2.09	0.69
34:B5:1291:G:H1	34:B5:1324:G:H22	1.39	0.69
41:AD:240:TYR:O	41:AD:244:HIS:ND1	2.25	0.69
1:BA:36:TYR:OH	1:BA:56:LYS:NZ	2.26	0.69
2:BB:134:VAL:HG13	2:BB:218:LEU:HB2	1.73	0.69
18:Be:42:ARG:NH2	34:B5:590:C:OP2	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2269:U:O2'	38:A1:2270:A:OP1	2.10	0.69
15:BY:58:PHE:HE1	15:BY:90:ARG:HD3	1.57	0.69
31:Bg:89:LEU:HB2	31:Bg:103:PHE:HB2	1.73	0.69
34:B5:277:U:O2'	34:B5:279:G:N2	2.24	0.69
34:B5:501:U:H4'	34:B5:502:U:H5	1.57	0.69
34:B5:1466:G:O2'	34:B5:1602:C:OP1	2.11	0.69
6:BH:56:LYS:HB2	6:BH:88:ARG:HE	1.58	0.69
54:AR:92:GLN:O	54:AR:96:ILE:HG12	1.93	0.69
9:BL:38:ALA:O	34:B5:246:G:N2	2.26	0.69
2:BB:132:ASP:HB3	2:BB:221:PRO:HB3	1.75	0.69
32:Bf:119:ARG:HB2	32:Bf:132:LEU:HD12	1.75	0.69
60:AX:50:ALA:HB1	70:Ah:66:VAL:HG21	1.75	0.69
22:BP:48:GLY:O	22:BP:49:MET:HE2	1.93	0.69
34:B5:992:A:O2'	34:B5:1785:U:O2	2.11	0.69
5:BG:174:LYS:HG3	34:B5:78:A:H2	1.58	0.68
6:BH:108:GLN:OE1	34:B5:810:G:N2	2.26	0.68
38:A1:394:G:N1	38:A1:397:A:OP2	2.25	0.68
38:A1:590:G:H21	42:AE:19:LYS:HD3	1.58	0.68
24:BR:58:MET:HA	24:BR:61:ILE:HG12	1.75	0.68
31:Bg:177:MET:HG2	31:Bg:193:ILE:HG22	1.75	0.68
34:B5:1679:G:H21	34:B5:1722:A:H62	1.39	0.68
38:A1:446:U:O2	38:A1:488:U:N3	2.25	0.68
25:BS:42:TYR:HA	25:BS:85:PHE:HE2	1.58	0.68
38:A1:76:G:O2'	48:AL:100:ARG:NH1	2.27	0.68
56:AT:79:MET:HE1	64:Ab:21:ILE:HD12	1.74	0.68
58:AV:10:LYS:HB2	58:AV:125:LEU:HD11	1.75	0.68
20:BF:165:LEU:HD23	29:Bc:47:PRO:HG2	1.74	0.68
30:Bd:42:CYS:SG	34:B5:1433:G:N2	2.64	0.68
38:A1:1114:U:OP1	63:Aa:23:GLY:N	2.24	0.68
38:A1:1817:G:N2	38:A1:1818:U:O4	2.26	0.68
34:B5:394:C:H42	34:B5:401:A:H62	1.38	0.68
34:B5:409:C:H2'	34:B5:410:A:H8	1.59	0.68
38:A1:1717:U:H2'	38:A1:1718:G:C8	2.28	0.68
38:A1:1953:G:H1	38:A1:2093:A:N6	1.91	0.68
50:AN:96:ARG:NH1	50:AN:104:GLU:OE1	2.26	0.68
75:Am:79:GLU:O	75:Am:82:LEU:N	2.27	0.68
34:B5:1237:G:H2'	34:B5:1238:A:H8	1.58	0.68
36:AB:10:ARG:NH2	36:AB:263:SER:O	2.26	0.68
38:A1:358:G:N2	38:A1:361:A:OP2	2.24	0.68
23:BQ:94:GLN:HB2	23:BQ:102:LYS:HG3	1.75	0.68
18:Be:43:ARG:HA	18:Be:54:ARG:HH21	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:AI:42:THR:O	46:AI:139:ARG:NH2	2.27	0.68
38:A1:176:G:C2	38:A1:177:U:H1'	2.29	0.68
38:A1:3042:U:OP2	38:A1:3092:C:N4	2.25	0.68
12:BV:74:GLN:HG3	12:BV:83:TRP:HB3	1.75	0.67
34:B5:1697:G:H1	34:B5:1704:U:H3	1.43	0.67
38:A1:2895:G:O2'	75:Am:100:TYR:O	2.12	0.67
61:AY:74:TYR:CD2	61:AY:77:LYS:HG2	2.29	0.67
32:Bf:132:LEU:HD22	32:Bf:141:CYS:HA	1.75	0.67
34:B5:871:G:H2'	34:B5:872:G:C8	2.28	0.67
23:BQ:136:SER:HB3	34:B5:1586:A:H5''	1.74	0.67
67:Ae:89:THR:HG22	67:Ae:117:ILE:HD13	1.75	0.67
8:BJ:171:ARG:HD3	34:B5:513:U:H3	1.58	0.67
34:B5:163:G:N2	34:B5:163:G:OP2	2.28	0.67
34:B5:1727:G:H2'	34:B5:1728:A:C8	2.30	0.67
15:BY:37:LYS:HG3	34:B5:522:U:H5''	1.77	0.67
38:A1:1019:G:N1	38:A1:1034:U:OP1	2.28	0.67
38:A1:3206:C:OP1	55:AS:166:LYS:NZ	2.28	0.67
34:B5:1575:G7M:H2'	34:B5:1576:A:C8	2.29	0.67
38:A1:1494:U:OP1	74:AI:42:ARG:NH1	2.25	0.67
40:A4:156:U:OP2	44:AG:84:ARG:NH2	2.27	0.67
6:BH:64:VAL:O	6:BH:67:LEU:HD23	1.95	0.67
28:BZ:42:LEU:HB2	28:BZ:75:LEU:HD11	1.77	0.67
38:A1:708:G:N2	38:A1:711:A:OP2	2.24	0.67
4:BE:19:LEU:HB2	4:BE:51:ARG:HH22	1.58	0.67
23:BQ:13:LYS:HG3	23:BQ:14:LYS:H	1.60	0.67
31:Bg:151:VAL:HA	31:Bg:173:GLY:HA2	1.75	0.67
38:A1:2255:A:H62	38:A1:2261:G:H1	1.40	0.67
38:A1:3016:A:H2'	38:A1:3017:A:C8	2.29	0.67
67:Ae:86:THR:HG23	67:Ae:87:MET:HG2	1.76	0.67
8:BJ:16:LYS:H	8:BJ:16:LYS:HD2	1.60	0.67
34:B5:590:C:H2'	34:B5:591:A:H8	1.60	0.67
34:B5:1585:U:H3	34:B5:1611:A:H2	1.43	0.67
38:A1:1616:U:H2'	38:A1:1617:G:H8	1.59	0.67
38:A1:2836:C:H5	38:A1:2852:C:H42	1.43	0.67
61:AY:55:GLU:HB2	61:AY:108:LYS:HB3	1.76	0.67
9:BL:105:LYS:NZ	34:B5:307:G:OP2	2.27	0.66
56:AT:88:ARG:NH1	64:Ab:33:LYS:O	2.28	0.66
58:AV:80:ARG:NH1	58:AV:117:PRO:O	2.25	0.66
34:B5:1012:U:H4'	35:AA:247:ARG:HD3	1.77	0.66
36:AB:308:MET:HE2	38:A1:3329:U:H5''	1.78	0.66
47:AJ:14:ILE:HD13	47:AJ:131:MET:HG2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:48:VAL:HG13	2:BB:49:ASN:H	1.61	0.66
22:BP:122:THR:HG22	34:B5:1558:U:H3	1.61	0.66
31:Bg:69:GLN:OE1	31:Bg:85:TRP:NE1	2.29	0.66
34:B5:733:A:OP2	34:B5:735:C:N4	2.27	0.66
34:B5:924:A:H2'	34:B5:925:G:C8	2.30	0.66
45:AH:9:GLN:HE22	45:AH:54:LYS:HE2	1.61	0.66
1:BA:135:GLU:OE1	34:B5:1321:A:N6	2.29	0.66
31:Bg:127:ARG:HA	31:Bg:150:TRP:HB2	1.78	0.66
37:AC:46:LYS:NZ	38:A1:691:A:OP1	2.29	0.66
38:A1:284:A:OP2	77:Ao:41:ARG:NH1	2.29	0.66
26:BT:22:LEU:HD23	26:BT:28:LEU:HD22	1.78	0.66
52:AP:18:ARG:NH1	52:AP:147:GLU:OE2	2.29	0.66
2:BB:39:GLU:HB2	2:BB:74:GLN:HA	1.77	0.66
6:BH:67:LEU:HD13	6:BH:94:ALA:HB2	1.78	0.66
7:BI:84:HIS:HE2	7:BI:97:THR:HG1	1.43	0.66
17:Bb:36:LYS:HD3	17:Bb:43:ILE:HG22	1.77	0.66
31:Bg:201:THR:HB	31:Bg:214:ALA:HB3	1.75	0.66
34:B5:176:C:N4	34:B5:266:A:OP2	2.29	0.66
38:A1:1181:U:O4	51:AO:21[A]:SER:OG	2.14	0.66
38:A1:1661:G:H2'	38:A1:1662:G:C8	2.30	0.66
38:A1:2441:A:H2'	38:A1:2442:G:O4'	1.95	0.66
40:A4:103:G:OP2	40:A4:105:A:O2'	2.13	0.66
23:BQ:23:LYS:HE3	23:BQ:66:ARG:HH22	1.61	0.66
11:BO:111:ARG:HH22	16:Ba:56:ALA:C	2.01	0.65
18:Be:24:THR:O	18:Be:26:LYS:NZ	2.29	0.65
38:A1:177:U:O2	38:A1:241:G:N2	2.27	0.65
38:A1:2437:G:H1	38:A1:2510:U:H3	1.44	0.65
38:A1:1222:G:H2'	38:A1:1286:A:H61	1.60	0.65
55:AS:77:VAL:HG11	55:AS:106:LEU:HD22	1.78	0.65
5:BG:202:ARG:HH21	34:B5:179:A:H61	1.45	0.65
25:BS:28:ILE:HD11	25:BS:56:LYS:HB2	1.78	0.65
38:A1:582:G:OP1	42:AE:29:LYS:NZ	2.27	0.65
4:BE:255:ARG:NH2	34:B5:763:G:O2'	2.30	0.65
5:BG:57:ASP:HA	5:BG:106:LEU:HA	1.79	0.65
34:B5:894:U:H2'	34:B5:895:G:C8	2.31	0.65
34:B5:1198:G:OP1	34:B5:1199:G:O2'	2.13	0.65
39:A3:4:U:H2'	39:A3:5:G:H8	1.61	0.65
3:BC:126:ARG:HA	3:BC:129:ILE:HD12	1.77	0.65
14:BX:70:LYS:NZ	34:B5:567:A:OP1	2.29	0.65
35:AA:27:ALA:O	35:AA:128:ARG:NH2	2.29	0.65
2:BB:32:ILE:HD11	2:BB:46:THR:HG23	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:163:GLY:HA3	38:A1:3354:U:H3	1.62	0.65
34:B5:590:C:H2'	34:B5:591:A:C8	2.31	0.65
70:Ah:83:LYS:O	72:Aj:73:ARG:NH2	2.29	0.65
34:B5:1275:A:H5''	34:B5:1427:A:H2	1.62	0.65
38:A1:2357:A:H2'	38:A1:2358:A:H8	1.62	0.65
47:AJ:49:LYS:HB2	47:AJ:62:ASN:HA	1.79	0.65
38:A1:664:U:H2'	38:A1:665:A:C8	2.32	0.65
38:A1:1604:G:H4'	38:A1:1835:A:H4'	1.79	0.65
38:A1:1667:A:H2'	38:A1:1668:G:C8	2.31	0.65
1:BA:111:ILE:HD11	34:B5:1292:G:H21	1.62	0.65
4:BE:22:LYS:N	34:B5:773:C:OP1	2.25	0.65
4:BE:252:ARG:HE	4:BE:256:ARG:HH22	1.45	0.65
18:Be:54:ARG:NH1	18:Be:55:ARG:O	2.30	0.65
38:A1:1899:G:O2'	38:A1:2334:U:O4	2.14	0.65
38:A1:3302:U:H2'	38:A1:3303:G:C8	2.32	0.65
45:AH:104:VAL:HG13	45:AH:113:GLU:OE2	1.97	0.65
12:BV:87:ARG:NH1	17:Bb:4:VAL:O	2.31	0.64
19:BD:54:ARG:NH1	19:BD:57:ASP:OD2	2.29	0.64
33:BM:133:LEU:HG	33:BM:137:MET:HE1	1.78	0.64
34:B5:1202:A:N6	34:B5:1457:C:OP1	2.29	0.64
36:AB:220:VAL:O	36:AB:334:ARG:NH1	2.30	0.64
38:A1:2767:U:O2'	77:Ao:30:ALA:O	2.15	0.64
40:A4:8:C:H2'	40:A4:9:A:H8	1.62	0.64
8:BJ:131:GLN:HB3	34:B5:513:U:H4'	1.79	0.64
15:BY:61:ARG:NH1	34:B5:530:C:O2	2.30	0.64
34:B5:1595:U:OP2	34:B5:1596:C:N4	2.31	0.64
38:A1:2160:G:H2'	38:A1:2161:G:H8	1.63	0.64
38:A1:2260:PSU:H3'	38:A1:2261:G:C8	2.31	0.64
69:Ag:79:SER:OG	69:Ag:80:ARG:NH1	2.30	0.64
34:B5:1267:G:H1	34:B5:1442:U:H3	1.43	0.64
38:A1:242:C:H2'	38:A1:243:G:C8	2.33	0.64
38:A1:1577:G:O2'	38:A1:1578:C:O5'	2.14	0.64
73:Ak:31:LEU:HA	73:Ak:37:PRO:HA	1.77	0.64
11:BO:20:TYR:HB3	11:BO:27:PHE:HB2	1.79	0.64
34:B5:126:A:N6	34:B5:291:G:O2'	2.29	0.64
38:A1:1278:A:H5'	38:A1:1279:C:H5''	1.78	0.64
50:AN:103:GLU:HG2	50:AN:115:VAL:HG11	1.80	0.64
34:B5:1521:G:O2'	34:B5:1523:G:OP2	2.13	0.64
38:A1:63:A:N3	38:A1:78:U:O2'	2.28	0.64
38:A1:2228:A:H2'	38:A1:2229:A:C8	2.32	0.64
75:Am:99:CYS:HB2	75:Am:114:LYS:HE3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:10:ASN:ND2	5:BG:127:THR:O	2.31	0.64
19:BD:137:VAL:HB	19:BD:185:LYS:HB2	1.78	0.64
27:BU:88:LYS:NZ	34:B5:1516:A:OP1	2.30	0.64
7:BI:87:ASN:HB3	7:BI:90:LEU:HD23	1.80	0.64
11:BO:122:PRO:HB3	34:B5:887:A:H1'	1.79	0.64
19:BD:31:GLU:O	19:BD:54:ARG:NH2	2.30	0.64
38:A1:297:G:OP2	38:A1:297:G:N2	2.29	0.64
34:B5:647:G:H22	34:B5:687:G:H1	1.45	0.64
38:A1:3204:C:H2'	38:A1:3205:G:C8	2.33	0.64
46:AI:102:MET:HE1	46:AI:112:GLN:HG3	1.78	0.64
72:Aj:25:ARG:HD2	74:AI:51:ILE:HD12	1.78	0.64
8:BJ:123:HIS:NE2	18:Be:37:ARG:HD2	2.13	0.63
34:B5:1488:G:H3'	34:B5:1515:A:H61	1.60	0.63
38:A1:591:G:O2'	42:AE:17:ALA:O	2.14	0.63
38:A1:799:G:O2'	48:AL:18:TRP:NE1	2.29	0.63
46:AI:109:ASP:HA	46:AI:112:GLN:HB2	1.81	0.63
7:BI:84:HIS:NE2	7:BI:97:THR:OG1	2.32	0.63
27:BU:52:LYS:HD2	27:BU:93:LEU:HD23	1.80	0.63
38:A1:1014:U:H2'	38:A1:1017:C:H42	1.63	0.63
23:BQ:39:VAL:HB	23:BQ:45:ARG:HG3	1.80	0.63
34:B5:485:A:N1	34:B5:503:G:N2	2.47	0.63
34:B5:1236:A:H2'	34:B5:1237:G:H8	1.64	0.63
35:AA:227:ARG:NH2	38:A1:2155:G:O2'	2.32	0.63
38:A1:2413:A:H2'	38:A1:2414:G:H8	1.63	0.63
38:A1:2763:U:N3	80:A1:3402:3HE:O1	2.27	0.63
62:AZ:53:VAL:HG21	62:AZ:62:VAL:HG23	1.79	0.63
27:BU:83:GLU:OE1	30:Bd:56:ARG:NH2	2.31	0.63
6:BH:20:VAL:O	6:BH:24:PHE:HD1	1.82	0.63
6:BH:87:ASP:OD2	6:BH:88:ARG:NH2	2.32	0.63
13:BW:81:VAL:O	13:BW:122:SER:OG	2.16	0.63
14:BX:102:VAL:HG12	14:BX:127:VAL:HG23	1.81	0.63
33:BM:42:ALA:HB3	33:BM:122:VAL:HB	1.80	0.63
34:B5:524:U:O2'	34:B5:527:A:N7	2.30	0.63
56:AT:108:ARG:O	56:AT:112:ASN:ND2	2.23	0.63
75:Am:88:LYS:HA	75:Am:92:ASP:HB2	1.81	0.63
5:BG:93:LYS:HG2	5:BG:95:LYS:HE3	1.79	0.63
30:Bd:12:ARG:NH2	34:B5:1451:C:OP1	2.32	0.63
33:BM:119:SER:OG	34:B5:1227:A:O2'	2.16	0.63
34:B5:1340:U:C2	34:B5:1378:U:H4'	2.34	0.63
37:AC:18:ASN:ND2	37:AC:252:GLU:OE2	2.32	0.63
38:A1:19:U:H2'	38:A1:20:A:C8	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BG:136:LYS:NZ	5:BG:174:LYS:O	2.31	0.63
26:BT:2:PRO:HG2	34:B5:1361:U:H4'	1.81	0.63
31:Bg:74:THR:HA	31:Bg:115:ILE:HD13	1.80	0.63
34:B5:625:C:H2'	34:B5:626:U:C6	2.33	0.63
10:BN:3:ARG:NH2	34:B5:867:G:OP2	2.28	0.63
14:BX:53:VAL:HA	14:BX:74:VAL:HG12	1.81	0.63
32:Bf:87:THR:O	34:B5:1445:G:N2	2.23	0.63
38:A1:1119:C:H2'	38:A1:1120:A:H8	1.64	0.63
2:BB:142:PHE:HB2	2:BB:208:GLN:HB2	1.81	0.62
34:B5:1656:U:HO2'	38:A1:2292:U:HO2'	1.42	0.62
38:A1:3070:A:OP1	54:AR:62:ARG:NH1	2.31	0.62
38:A1:3215:A:H5''	68:Af:2:ALA:HB2	1.81	0.62
49:AM:60:LEU:HD13	55:AS:152:LEU:HD11	1.80	0.62
30:Bd:15:GLY:HA3	34:B5:1204:A:H61	1.64	0.62
31:Bg:9:LEU:HD12	31:Bg:313:TRP:HE1	1.64	0.62
34:B5:245:U:N3	34:B5:248:U:OP2	2.27	0.62
34:B5:754:A:H5''	34:B5:755:A:H5'	1.81	0.62
38:A1:676:G:HO2'	38:A1:678:G:HO2'	1.44	0.62
2:BB:30:PHE:HE2	2:BB:91:VAL:HG21	1.64	0.62
13:BW:111:MET:HE2	13:BW:116:ALA:CA	2.28	0.62
18:Be:43:ARG:NH2	34:B5:590:C:OP1	2.33	0.62
36:AB:85:VAL:HG22	36:AB:202:THR:HG22	1.81	0.62
38:A1:3231:U:H2'	38:A1:3232:G:H8	1.62	0.62
41:AD:50:ARG:NH1	41:AD:147:ASP:OD2	2.31	0.62
2:BB:26:ARG:O	2:BB:50:LYS:N	2.31	0.62
8:BJ:171:ARG:NH2	34:B5:538:A:OP2	2.31	0.62
14:BX:32:ARG:NH1	34:B5:602:U:OP1	2.33	0.62
34:B5:1297:G:N2	34:B5:1300:A:OP2	2.22	0.62
34:B5:1672:G:H2'	34:B5:1673:G:C8	2.34	0.62
34:B5:1776:A:H2'	34:B5:1777:G:C8	2.34	0.62
38:A1:655:C:H2'	38:A1:656:A:C8	2.34	0.62
38:A1:845:G:H21	38:A1:848:A:H2	1.46	0.62
3:BC:143:TYR:O	13:BW:98:GLN:NE2	2.31	0.62
31:Bg:131:ILE:HD11	31:Bg:151:VAL:HG21	1.82	0.62
38:A1:412:G:OP1	52:AP:62:ARG:NH1	2.33	0.62
46:AI:150:GLU:OE2	46:AI:153:ARG:NH1	2.32	0.62
21:BK:44:LYS:HE2	34:B5:1217:A:H5''	1.82	0.62
39:A3:99:G:H4'	43:AF:128:LYS:HD2	1.81	0.62
43:AF:178:ILE:HG23	43:AF:183:ASP:HB3	1.81	0.62
3:BC:139:ILE:HD13	3:BC:191:ALA:HB1	1.81	0.62
8:BJ:113:VAL:HG11	8:BJ:129:ILE:HD11	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:221:A:OP2	34:B5:832:U:O2'	2.17	0.62
38:A1:627:U:H2'	38:A1:628:A:C8	2.35	0.62
38:A1:952:A:H4'	38:A1:968:G:N2	2.15	0.62
38:A1:3291:G:H2'	38:A1:3292:A:H8	1.65	0.62
50:AN:121:VAL:HG11	50:AN:131:GLU:HG3	1.81	0.62
50:AN:143:ARG:NH2	70:Ah:90:ARG:O	2.33	0.62
4:BE:141:THR:OG1	4:BE:143:ASP:OD1	2.15	0.62
8:BJ:64:GLU:CD	8:BJ:65:LYS:H	2.08	0.62
32:Bf:140:TYR:OH	34:B5:1234:A:O2'	2.13	0.62
38:A1:417:A:H2'	38:A1:418:A:C8	2.35	0.62
38:A1:2611:U:H2'	38:A1:2612:U:C6	2.35	0.62
52:AP:155:GLU:OE1	52:AP:155:GLU:N	2.32	0.62
76:An:1:MET:HE1	76:An:9:ARG:HD3	1.80	0.62
31:Bg:22:SER:OG	31:Bg:69:GLN:O	2.15	0.62
31:Bg:271:VAL:HG23	31:Bg:272:ASP:H	1.65	0.62
34:B5:1584:G:N2	34:B5:1611:A:OP2	2.20	0.62
38:A1:655:C:OP2	67:Ae:27:ARG:NH1	2.30	0.62
38:A1:2213:A:H2'	38:A1:2214:A:H8	1.65	0.62
34:B5:1354:G:O6	34:B5:1369:U:O2	2.18	0.62
38:A1:1667:A:H2'	38:A1:1668:G:H8	1.65	0.62
7:BI:50:GLY:HA2	34:B5:397:A:H4'	1.82	0.61
34:B5:1776:A:H2'	34:B5:1777:G:H8	1.63	0.61
38:A1:1940:G:H21	38:A1:3362:A:H8	1.48	0.61
38:A1:2357:A:H2'	38:A1:2358:A:C8	2.34	0.61
63:Aa:36:GLY:HA3	63:Aa:40:HIS:CE1	2.35	0.61
4:BE:100:ARG:HB3	4:BE:112:HIS:HD2	1.64	0.61
7:BI:47:ARG:NH2	34:B5:398:G:OP2	2.32	0.61
11:BO:83:ILE:HD11	11:BO:102:LEU:HD21	1.82	0.61
31:Bg:26:SER:HB2	31:Bg:29:GLN:HB2	1.82	0.61
34:B5:395:U:H3	34:B5:399:A:H62	1.46	0.61
37:AC:156:LEU:HD12	37:AC:159:ILE:HD12	1.82	0.61
38:A1:674:G:O6	53:AQ:56:LYS:NZ	2.33	0.61
38:A1:2700:G:H5''	56:AT:17:ARG:HG2	1.81	0.61
1:BA:140:ASN:HD22	3:BC:62:PRO:HD3	1.64	0.61
25:BS:115:ARG:HA	25:BS:118:LYS:HE2	1.82	0.61
34:B5:1260:U:H2'	34:B5:1261:G:H8	1.64	0.61
43:AF:102:VAL:HG21	43:AF:129:LEU:HD23	1.82	0.61
11:BO:135:ARG:NH1	34:B5:1007:C:O3'	2.34	0.61
38:A1:289:A:H2'	38:A1:290:G:H8	1.65	0.61
38:A1:542:G:C5	38:A1:543:C:H1'	2.36	0.61
43:AF:98:LYS:HG2	43:AF:129:LEU:HD21	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AN:18:VAL:HG13	50:AN:19:LEU:HD12	1.82	0.61
65:Ac:30:THR:HG23	65:Ac:91:SER:HB2	1.81	0.61
71:Ai:70:ARG:HD3	71:Ai:84:LYS:HG2	1.81	0.61
1:BA:3:LEU:HD21	1:BA:62:ARG:HH12	1.66	0.61
2:BB:222:LYS:HE3	38:A1:2545:C:O2	2.01	0.61
11:BO:17:ALA:HB3	11:BO:81:VAL:HA	1.82	0.61
34:B5:209:U:H2'	34:B5:210:A:O4'	2.01	0.61
34:B5:416:A:O2'	34:B5:418:G:N7	2.32	0.61
34:B5:1393:C:H2'	34:B5:1394:G:H8	1.64	0.61
38:A1:1235:U:O4	38:A1:1254:C:N4	2.26	0.61
1:BA:119:ARG:NH1	3:BC:241:ASP:OD1	2.33	0.61
34:B5:340:U:H2'	34:B5:341:A:H8	1.65	0.61
34:B5:1397:U:O2'	34:B5:1400:A:N6	2.32	0.61
36:AB:19:ARG:NH2	38:A1:3045:G:OP1	2.34	0.61
38:A1:216:G:OP1	61:AY:16:ARG:NH1	2.33	0.61
40:A4:9:A:H2'	40:A4:10:A:C8	2.36	0.61
41:AD:150:LEU:HD12	47:AJ:143:ARG:HG3	1.83	0.61
1:BA:15:GLN:HG2	24:BR:100:LEU:HB2	1.83	0.61
5:BG:23:ARG:HA	5:BG:25:ARG:HH11	1.66	0.61
14:BX:140:LYS:NZ	34:B5:31:C:OP1	2.25	0.61
25:BS:89:GLN:O	34:B5:1547:A:O2'	2.15	0.61
26:BT:47:PRO:HA	34:B5:1477:G:H4'	1.82	0.61
38:A1:2896:A:OP1	75:Am:124:LYS:NZ	2.33	0.61
21:BK:32:HIS:ND1	21:BK:42:VAL:HG11	2.15	0.61
22:BP:39:ALA:N	34:B5:1549:C:OP2	2.33	0.61
34:B5:1222:C:H2'	34:B5:1223:A:H8	1.65	0.61
40:A4:97:A:OP1	70:Ah:67:ARG:NH2	2.31	0.61
54:AR:181:ARG:HA	54:AR:186:LYS:HB2	1.83	0.61
4:BE:100:ARG:HE	4:BE:114:ILE:HG21	1.66	0.61
12:BV:15:ARG:NH1	12:BV:33:GLN:OE1	2.34	0.61
13:BW:41:MET:HG2	13:BW:129:VAL:HG21	1.83	0.61
16:Ba:32:LYS:NZ	34:B5:932:U:O2	2.32	0.61
18:Be:55:ARG:NH2	34:B5:558:U:OP2	2.28	0.61
43:AF:40:LYS:HZ1	43:AF:179:LEU:HB2	1.66	0.61
45:AH:103:ILE:HD11	45:AH:110:LYS:HB3	1.83	0.61
54:AR:151:ARG:HG2	54:AR:151:ARG:HH11	1.66	0.61
13:BW:20:THR:HG23	13:BW:22:LYS:HG2	1.83	0.61
23:BQ:10:PHE:HE1	34:B5:1340:U:H3	1.49	0.61
34:B5:1266:U:H2'	34:B5:1267:G:C8	2.35	0.61
34:B5:1280:4AC:H2'	34:B5:1281:G:C8	2.36	0.61
38:A1:315:C:OP2	71:Ai:28:TYR:OH	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:1388:U:O2'	67:Ae:99:ASN:O	2.19	0.61
42:AE:62:THR:OG1	42:AE:79:VAL:O	2.18	0.61
1:BA:11:PRO:HB3	24:BR:117:LEU:HD22	1.81	0.60
3:BC:52:THR:OG1	3:BC:54:GLU:OE1	2.19	0.60
3:BC:141:ARG:HB3	3:BC:151:PRO:HB2	1.82	0.60
18:Be:39:LEU:HA	18:Be:42:ARG:HG2	1.83	0.60
19:BD:94:ARG:HH22	19:BD:104:SER:HB3	1.66	0.60
26:BT:77:ASN:OD1	26:BT:78:LYS:N	2.34	0.60
37:AC:334:PHE:HA	37:AC:339:LEU:HD13	1.83	0.60
38:A1:2960:C:H2'	38:A1:2961:G:C8	2.36	0.60
1:BA:62:ARG:HH21	12:BV:38:LYS:HA	1.64	0.60
3:BC:88:LYS:HE3	3:BC:95:ARG:HE	1.64	0.60
6:BH:27:LEU:HD12	6:BH:27:LEU:O	2.01	0.60
8:BJ:171:ARG:HG2	8:BJ:175:ARG:HH21	1.65	0.60
33:BM:42:ALA:HB2	33:BM:124:LYS:HE2	1.82	0.60
34:B5:1642:G:H2'	34:B5:1643:U:H6	1.66	0.60
34:B5:1760:G:H1'	34:B5:1781:MA6:H2	1.83	0.60
38:A1:1329:U:OP1	68:Af:17:GLN:NE2	2.34	0.60
44:AG:162:LEU:HD23	50:AN:7:LEU:HD11	1.83	0.60
52:AP:18:ARG:HG2	52:AP:147:GLU:HG2	1.84	0.60
7:BI:178:ARG:NH1	34:B5:258:C:O2	2.34	0.60
26:BT:43:ASN:ND2	34:B5:1477:G:OP1	2.29	0.60
31:Bg:66:HIS:CG	31:Bg:67:ILE:H	2.19	0.60
34:B5:1359:C:H2'	34:B5:1360:A:C8	2.35	0.60
35:AA:36:GLU:OE1	35:AA:163:ARG:NH1	2.33	0.60
36:AB:360:ASP:OD2	36:AB:364:LYS:NZ	2.33	0.60
38:A1:406:G:OP1	38:A1:1415:U:O2'	2.20	0.60
38:A1:2095:G:H2'	38:A1:2096:A:H8	1.65	0.60
38:A1:2305:G:OP2	38:A1:2305:G:N2	2.30	0.60
7:BI:78:ILE:HG21	7:BI:96:LEU:HD11	1.83	0.60
34:B5:116:U:O2'	34:B5:333:A:N3	2.29	0.60
34:B5:384:G:H2'	34:B5:385:A:C8	2.36	0.60
34:B5:1344:A:H61	34:B5:1382:A:H61	1.48	0.60
38:A1:1108:U:H2'	38:A1:1109:U:C6	2.36	0.60
38:A1:1635:G:N2	38:A1:1638:A:OP2	2.25	0.60
45:AH:27:VAL:HG11	45:AH:78:MET:HB3	1.83	0.60
52:AP:122:ALA:HB3	52:AP:143:PRO:HB2	1.83	0.60
1:BA:144:ILE:HG23	1:BA:158:VAL:HB	1.83	0.60
9:BL:148:LYS:HZ3	34:B5:809:A:H4'	1.66	0.60
21:BK:23:ALA:HA	21:BK:32:HIS:HE1	1.66	0.60
34:B5:451:A:N6	34:B5:453:U:O2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:478:A:N1	34:B5:510:G:O6	2.34	0.60
42:AE:51:ARG:NH2	49:AM:114:ASP:OD1	2.33	0.60
42:AE:62:THR:HG21	42:AE:78:ARG:HD2	1.83	0.60
37:AC:3:ARG:HE	37:AC:22:LEU:HB3	1.67	0.60
38:A1:362:U:O4	72:Aj:24:ARG:NH2	2.35	0.60
2:BB:176:VAL:O	2:BB:177:GLN:HG2	2.01	0.60
7:BI:153:GLU:OE1	9:BL:24:LYS:NZ	2.35	0.60
34:B5:1385:G:H2'	34:B5:1386:G:C8	2.37	0.60
38:A1:2697:A:H2'	38:A1:2698:G:C8	2.36	0.60
42:AE:31:ARG:NH1	68:Af:107:ILE:O	2.35	0.60
20:BF:92:ARG:NH2	34:B5:1613:U:OP1	2.34	0.60
30:Bd:17:GLY:N	34:B5:1205:C:O2	2.30	0.60
38:A1:1660:C:H2'	38:A1:1661:G:H8	1.67	0.60
38:A1:1786:G:H2'	38:A1:1787:A:C8	2.37	0.60
38:A1:2697:A:H2'	38:A1:2698:G:H8	1.66	0.60
38:A1:3068:U:OP2	54:AR:62:ARG:NH2	2.31	0.60
47:AJ:75:LYS:O	47:AJ:78:GLU:HG3	2.01	0.60
30:Bd:14:TYR:OH	34:B5:1555:A:N6	2.30	0.60
34:B5:343:C:H2'	34:B5:344:A:H8	1.66	0.60
38:A1:775:A:O2'	38:A1:777:U:OP2	2.19	0.60
38:A1:1799:A:H2'	38:A1:1800:A:H8	1.65	0.60
38:A1:2533:G:H2'	38:A1:2534:G:C8	2.35	0.60
24:BR:10:LYS:NZ	34:B5:1316:G:O2'	2.35	0.60
27:BU:50:LEU:HB3	27:BU:52:LYS:HZ3	1.67	0.60
34:B5:472:U:H2'	34:B5:473:A:H8	1.66	0.60
34:B5:1279:C:H2'	34:B5:1280:4AC:H6	1.83	0.60
38:A1:3050:U:O2'	59:AW:16:GLY:O	2.18	0.60
45:AH:90:MET:HE2	45:AH:179:ILE:HG22	1.84	0.60
1:BA:30:GLN:HE21	1:BA:33:GLN:HG2	1.66	0.59
5:BG:31:ARG:HB3	5:BG:101:ILE:HD13	1.84	0.59
5:BG:84:TYR:OH	5:BG:91:GLU:OE1	2.18	0.59
15:BY:108:ARG:HA	15:BY:111:LYS:HE2	1.84	0.59
25:BS:141:THR:OG1	34:B5:1174:C:OP2	2.19	0.59
34:B5:884:A:H2'	34:B5:885:G:C8	2.36	0.59
34:B5:1187:PSU:H2'	34:B5:1188:G:H8	1.67	0.59
38:A1:1724:U:H1'	38:A1:1725:C:C6	2.37	0.59
47:AJ:90:GLN:NE2	47:AJ:91:LEU:O	2.35	0.59
7:BI:78:ILE:HG23	7:BI:102:VAL:HG11	1.84	0.59
7:BI:137:LYS:HA	7:BI:140:GLU:HB2	1.84	0.59
8:BJ:171:ARG:HD2	34:B5:537:G:C5	2.37	0.59
13:BW:111:MET:HE3	13:BW:115:GLU:OE1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:371:G:N2	34:B5:612:U:O2	2.35	0.59
34:B5:1280:4AC:H2'	34:B5:1281:G:H8	1.67	0.59
38:A1:1616:U:H2'	38:A1:1617:G:C8	2.36	0.59
38:A1:2960:C:H2'	38:A1:2961:G:H8	1.66	0.59
3:BC:147:ASN:HB2	12:BV:3:ASN:HA	1.83	0.59
12:BV:83:TRP:HH2	12:BV:85:TYR:HD1	1.50	0.59
15:BY:55:VAL:HG22	15:BY:75:VAL:HG12	1.85	0.59
34:B5:1546:G:H2'	34:B5:1547:A:C8	2.37	0.59
38:A1:1259:A:H1'	38:A1:1280:C:H4'	1.83	0.59
2:BB:45:LYS:HD2	11:BO:13:VAL:HG13	1.84	0.59
2:BB:131:ASP:OD1	2:BB:180:THR:OG1	2.20	0.59
15:BY:124:ARG:NH1	34:B5:151:G:O6	2.34	0.59
26:BT:117:SER:OG	26:BT:123:ARG:N	2.35	0.59
30:Bd:54:LYS:NZ	34:B5:1420:C:OP1	2.34	0.59
37:AC:317:PRO:C	37:AC:319:LYS:H	2.10	0.59
42:AE:56:LYS:HD2	42:AE:98:VAL:HB	1.83	0.59
47:AJ:92:ARG:HH22	47:AJ:94:ARG:HH11	1.50	0.59
55:AS:125:LYS:HE3	55:AS:127:ALA:HB2	1.84	0.59
1:BA:112:THR:HG22	1:BA:114:SER:H	1.66	0.59
6:BH:44:LYS:HG2	6:BH:63:PRO:HG3	1.84	0.59
14:BX:63:GLN:NE2	34:B5:1755:A:O4'	2.34	0.59
22:BP:43:ARG:NH2	34:B5:1552:U:OP2	2.24	0.59
38:A1:1798:A:H2'	38:A1:1799:A:C8	2.37	0.59
41:AD:77:ALA:O	41:AD:108:ARG:NH1	2.34	0.59
11:BO:16:VAL:HG12	11:BO:18:ARG:HG3	1.84	0.59
34:B5:648:G:O6	34:B5:686:C:N4	2.35	0.59
34:B5:923:A:H2'	34:B5:924:A:C8	2.38	0.59
8:BJ:159:ALA:HB3	8:BJ:162:SER:HB3	1.84	0.59
24:BR:7:LYS:NZ	34:B5:1316:G:OP1	2.23	0.59
38:A1:3295:A:H2'	38:A1:3296:A:C8	2.38	0.59
45:AH:21:LYS:HG3	45:AH:22:SER:H	1.68	0.59
48:AL:157:ARG:NH2	63:Aa:146:GLU:OE2	2.35	0.59
23:BQ:14:LYS:NZ	34:B5:1610:G:O6	2.33	0.59
34:B5:73:U:H2'	34:B5:76:A:H62	1.67	0.59
38:A1:498:A:O2'	38:A1:3273:A:N1	2.35	0.59
38:A1:1110:PSU:H2'	38:A1:1111:U:C6	2.38	0.59
38:A1:2681:U:OP2	47:AJ:51:ARG:NH1	2.35	0.59
55:AS:71:LYS:O	55:AS:73:LYS:NZ	2.36	0.59
11:BO:32:ASP:OD1	11:BO:35:GLY:N	2.34	0.59
14:BX:70:LYS:HB3	14:BX:93:LEU:HD12	1.85	0.59
34:B5:1428:G:H2'	34:B5:1429:G:H8	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:180:LEU:HD21	78:Ap:22:LEU:HB3	1.85	0.59
37:AC:20:LEU:HD11	37:AC:252:GLU:HG3	1.85	0.59
38:A1:583:G:H4'	68:Af:106:ASN:HD22	1.68	0.59
38:A1:3275:U:O2'	68:Af:99:ARG:NH1	2.36	0.59
39:A3:4:U:H2'	39:A3:5:G:C8	2.38	0.59
27:BU:34:LEU:HD21	27:BU:89:ARG:HD3	1.84	0.59
38:A1:2213:A:H2'	38:A1:2214:A:C8	2.38	0.59
38:A1:2880:PSU:OP1	58:AV:47:ASN:ND2	2.31	0.59
62:AZ:103:GLN:OE1	62:AZ:105:SER:OG	2.11	0.59
8:BJ:144:PRO:HD2	34:B5:474:A:H5''	1.84	0.58
14:BX:114:LYS:HD2	34:B5:571:G:H5''	1.84	0.58
23:BQ:41:PRO:HG2	23:BQ:44:LEU:HG	1.84	0.58
24:BR:6:THR:O	24:BR:10:LYS:HG2	2.03	0.58
27:BU:60:THR:HG23	34:B5:1382:A:H5''	1.85	0.58
34:B5:1174:C:O2'	34:B5:1196:A:N6	2.36	0.58
34:B5:1524:A:H2'	34:B5:1525:A:C8	2.38	0.58
38:A1:1078:U:H4'	41:AD:46:THR:HG21	1.84	0.58
52:AP:60:PHE:HB3	52:AP:64:ASN:HB3	1.84	0.58
20:BF:182:ALA:O	20:BF:186:ASN:ND2	2.36	0.58
34:B5:394:C:N4	34:B5:401:A:H62	2.02	0.58
34:B5:486:G:O2'	34:B5:492:A:N6	2.36	0.58
34:B5:891:A:H2'	34:B5:892:A:H8	1.66	0.58
34:B5:1641:C:H2'	34:B5:1642:G:C8	2.37	0.58
36:AB:212:ASN:HD21	36:AB:353:GLU:HG2	1.67	0.58
37:AC:101:ALA:HA	38:A1:800:G:H22	1.67	0.58
38:A1:351:A:N6	74:Al:37:TYR:O	2.34	0.58
38:A1:2683:U:H2'	38:A1:2684:C:C6	2.38	0.58
38:A1:3348:G:N2	38:A1:3357:U:O2	2.30	0.58
40:A4:8:C:H2'	40:A4:9:A:C8	2.38	0.58
44:AG:90:THR:HA	44:AG:214:LEU:HD21	1.85	0.58
22:BP:13:LYS:NZ	47:AJ:85:LYS:O	2.36	0.58
24:BR:106:THR:HA	24:BR:109:LEU:HG	1.86	0.58
26:BT:58:ALA:HB1	26:BT:108:LEU:HD21	1.85	0.58
34:B5:43:A:O2'	34:B5:99:C:OP1	2.15	0.58
34:B5:190:C:OP1	34:B5:196:G:N1	2.34	0.58
34:B5:711:U:O2	34:B5:713:A:N6	2.36	0.58
38:A1:244:G:H3'	38:A1:245:U:H5''	1.86	0.58
38:A1:2228:A:H2'	38:A1:2229:A:H8	1.68	0.58
15:BY:6:THR:O	15:BY:8:ARG:NH1	2.35	0.58
20:BF:80:LYS:HB2	20:BF:83:ARG:HB2	1.85	0.58
23:BQ:99:GLU:HB2	23:BQ:102:LYS:HE3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:507:U:H5''	34:B5:508:U:H5	1.67	0.58
34:B5:525:A:H3'	34:B5:526:A:H8	1.67	0.58
38:A1:292:U:OP2	50:AN:68:ARG:NH2	2.35	0.58
38:A1:1194:G:H2'	38:A1:1195:A:C8	2.38	0.58
38:A1:2848:G:OP1	75:Am:100:TYR:OH	2.17	0.58
39:A3:84:A:H2'	39:A3:85:G:C8	2.38	0.58
52:AP:16:SER:HB3	52:AP:149:VAL:HG22	1.85	0.58
2:BB:150:VAL:HG23	34:B5:1067:C:H5''	1.85	0.58
10:BN:26:PHE:CE2	10:BN:28:LEU:HB2	2.38	0.58
14:BX:62:LYS:HE3	14:BX:118:PRO:HB3	1.86	0.58
17:Bb:67:THR:OG1	17:Bb:70:LYS:O	2.21	0.58
34:B5:51:A:OP2	34:B5:424:C:N4	2.35	0.58
14:BX:28:ASN:OD1	14:BX:32:ARG:NH1	2.36	0.58
38:A1:1831:U:O2'	40:A4:114:G:OP1	2.13	0.58
44:AG:91:PHE:O	44:AG:95:ASN:ND2	2.37	0.58
55:AS:57:GLU:OE1	56:AT:136:ARG:NH2	2.36	0.58
76:An:15:ARG:HG3	76:An:15:ARG:HH11	1.67	0.58
6:BH:56:LYS:HB2	6:BH:88:ARG:NE	2.18	0.58
34:B5:1142:A:H2'	34:B5:1143:A:C8	2.38	0.58
38:A1:1274:A:H3'	38:A1:1275:C:C6	2.39	0.58
44:AG:101:THR:OG1	44:AG:104:GLU:OE1	2.17	0.58
46:AI:76:MET:HE1	46:AI:148:VAL:HA	1.85	0.58
57:AU:38:ILE:HD11	57:AU:56:VAL:HB	1.86	0.58
1:BA:113:ARG:HH21	34:B5:1324:G:H4'	1.69	0.58
25:BS:101:LEU:O	25:BS:105:VAL:HG13	2.04	0.58
34:B5:1546:G:H2'	34:B5:1547:A:H8	1.69	0.58
34:B5:1673:G:O6	34:B5:1728:A:N1	2.36	0.58
38:A1:1477:A:OP1	38:A1:3075:G:O2'	2.20	0.58
34:B5:29:U:H2'	34:B5:30:G:H8	1.69	0.58
34:B5:478:A:H2	34:B5:510:G:H1	1.52	0.58
38:A1:1084:A:H2'	38:A1:1085:A:C8	2.39	0.58
4:BE:6:LYS:NZ	34:B5:95:G:OP1	2.37	0.58
5:BG:195:VAL:HG13	5:BG:199:GLN:HE22	1.69	0.58
15:BY:105:ARG:NH1	34:B5:458:G:OP2	2.36	0.58
34:B5:329:G:H2'	34:B5:330:G:H8	1.69	0.58
51:AO:34[A]:VAL:HG22	51:AO:103[A]:LYS:HB2	1.86	0.58
5:BG:160:ARG:NH2	34:B5:68:A:OP1	2.37	0.57
7:BI:44:HIS:ND1	34:B5:1676:U:OP1	2.37	0.57
15:BY:10:ARG:HH12	34:B5:780:A:H62	1.52	0.57
31:Bg:22:SER:HB2	31:Bg:36:ALA:HB3	1.86	0.57
34:B5:546:U:H2'	34:B5:547:U:C6	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1157:A:O2'	34:B5:1159:C:OP2	2.18	0.57
38:A1:1474:A:OP1	54:AR:53:LYS:NZ	2.33	0.57
50:AN:9:GLU:OE2	50:AN:13:LYS:NZ	2.32	0.57
63:Aa:75:LEU:HB3	63:Aa:118:ILE:HG23	1.86	0.57
2:BB:181:LEU:HA	2:BB:184:LEU:HB3	1.86	0.57
19:BD:113:LEU:HD22	19:BD:118:ALA:HB2	1.87	0.57
38:A1:662:U:H2'	38:A1:663:C:C6	2.39	0.57
47:AJ:48:SER:HB3	47:AJ:66:ALA:HB3	1.85	0.57
4:BE:11:ARG:NH1	4:BE:21:ASP:O	2.33	0.57
5:BG:57:ASP:OD2	5:BG:72:ARG:NH1	2.37	0.57
15:BY:38:ASP:OD1	15:BY:39:GLU:N	2.36	0.57
26:BT:102:ARG:NH2	34:B5:1502:G:N7	2.52	0.57
31:Bg:81:LEU:HD12	31:Bg:91:LEU:HD12	1.86	0.57
34:B5:780:A:H4'	34:B5:781:U:H5''	1.86	0.57
35:AA:79:ASN:ND2	35:AA:166:ILE:O	2.36	0.57
38:A1:1378:U:H2'	38:A1:1379:G:H8	1.69	0.57
38:A1:1551:C:O2'	38:A1:2170:U:O2'	2.16	0.57
62:AZ:54:THR:HG23	62:AZ:56:LYS:H	1.69	0.57
68:Af:6:ARG:NH1	68:Af:8:TYR:O	2.37	0.57
8:BJ:175:ARG:HH12	34:B5:537:G:P	2.27	0.57
11:BO:111:ARG:HH21	11:BO:112:ILE:HB	1.69	0.57
20:BF:189:THR:HB	20:BF:192:GLU:HG3	1.87	0.57
31:Bg:144:LEU:HD11	31:Bg:181:TRP:CZ3	2.40	0.57
34:B5:519:C:H3'	34:B5:520:A:H8	1.68	0.57
34:B5:520:A:H2'	34:B5:521:A:C8	2.40	0.57
38:A1:446:U:H2'	38:A1:448:U:C4	2.39	0.57
53:AQ:62:VAL:HG13	53:AQ:66:ARG:HD2	1.86	0.57
11:BO:78:ALA:HB2	11:BO:111:ARG:HB3	1.87	0.57
19:BD:162:GLN:NE2	19:BD:166:ASP:OD1	2.38	0.57
26:BT:111:ILE:HG23	26:BT:113:ILE:HG12	1.86	0.57
27:BU:62:VAL:HG12	27:BU:85:ARG:HG2	1.86	0.57
27:BU:97:VAL:HA	27:BU:100:VAL:HG22	1.86	0.57
28:BZ:49:ARG:HA	28:BZ:52:LYS:HE2	1.87	0.57
32:Bf:101:ALA:HB2	34:B5:1228:G:H3'	1.87	0.57
34:B5:953:G:H2'	34:B5:954:G:C8	2.38	0.57
34:B5:1163:A:N3	34:B5:1613:U:O2'	2.28	0.57
34:B5:1346:A:O2'	34:B5:1371:A:OP2	2.22	0.57
34:B5:1385:G:H2'	34:B5:1386:G:H8	1.69	0.57
34:B5:1428:G:H2'	34:B5:1429:G:C8	2.39	0.57
38:A1:1493:G:N2	38:A1:1493:G:OP2	2.34	0.57
7:BI:41:LYS:NZ	34:B5:260:U:OP2	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:54:LYS:NZ	34:B5:333:A:OP2	2.29	0.57
7:BI:195:ARG:HG3	7:BI:196:LEU:HD23	1.84	0.57
10:BN:49:GLN:HA	10:BN:52:VAL:HG12	1.87	0.57
16:Ba:92:ARG:HG2	34:B5:1796:C:O2	2.05	0.57
34:B5:1071:U:H2'	34:B5:1072:C:C6	2.40	0.57
34:B5:1692:G:H5''	34:B5:1693:A:N7	2.20	0.57
38:A1:407:A:C2	40:A4:17:A:H1'	2.38	0.57
8:BJ:164:PHE:CE2	34:B5:512:A:H4'	2.40	0.57
10:BN:5:HIS:HD2	34:B5:627:C:H5''	1.69	0.57
10:BN:104:ARG:HH22	34:B5:950:C:H4'	1.69	0.57
14:BX:54:LEU:HD11	14:BX:75:GLN:HB2	1.85	0.57
23:BQ:29:ILE:HG21	23:BQ:36:ILE:HD12	1.86	0.57
25:BS:36:LYS:HB3	25:BS:102:ALA:HA	1.86	0.57
27:BU:50:LEU:HB3	27:BU:52:LYS:NZ	2.19	0.57
31:Bg:123:ILE:HG22	31:Bg:133:VAL:HG22	1.87	0.57
34:B5:973:A:H4'	38:A1:848:A:C8	2.40	0.57
38:A1:1003:A:N1	38:A1:1049:C:O2'	2.36	0.57
2:BB:82:ARG:NH2	2:BB:188:LEU:O	2.28	0.57
9:BL:15:LYS:NZ	9:BL:19:ILE:O	2.26	0.57
18:Be:23:LYS:NZ	34:B5:586:G:OP1	2.35	0.57
34:B5:861:U:O2'	34:B5:862:A:OP1	2.21	0.57
38:A1:501:A:H4'	42:AE:28:GLN:HG3	1.87	0.57
38:A1:938:C:OP2	63:Aa:26:ARG:NH1	2.38	0.57
1:BA:73:VAL:HG13	1:BA:120:LEU:HB3	1.87	0.57
22:BP:30:THR:HG22	22:BP:87:PRO:HD2	1.86	0.57
31:Bg:89:LEU:HD11	31:Bg:110:VAL:HG11	1.87	0.57
34:B5:851:U:N3	34:B5:853:G:N7	2.53	0.57
38:A1:2095:G:H2'	38:A1:2096:A:C8	2.40	0.57
38:A1:2510:U:H2'	38:A1:2511:A:H8	1.70	0.57
38:A1:3182:G:H4'	51:AO:161[A]:LYS:HG2	1.87	0.57
62:AZ:26:VAL:HG11	62:AZ:96:VAL:HB	1.86	0.57
11:BO:111:ARG:HE	11:BO:112:ILE:N	1.91	0.57
34:B5:809:A:H2'	34:B5:810:G:C8	2.40	0.57
35:AA:206:PRO:HG3	35:AA:213:GLY:HA3	1.86	0.57
51:AO:27[A]:LEU:HD23	51:AO:98[A]:ALA:O	2.05	0.57
54:AR:181:ARG:HD2	54:AR:186:LYS:HD2	1.86	0.57
61:AY:118:LEU:HD13	61:AY:121:ARG:HH21	1.69	0.57
2:BB:104:ASP:OD1	2:BB:105:PHE:N	2.38	0.56
7:BI:184:LEU:HB3	7:BI:189:LEU:HB2	1.86	0.56
20:BF:58:LEU:HD12	20:BF:138:THR:HG22	1.86	0.56
28:BZ:77:ARG:NH1	34:B5:1533:C:OP2	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:855:A:C2	34:B5:857:U:H1'	2.40	0.56
35:AA:70:ARG:NH1	38:A1:1580:A:OP1	2.38	0.56
38:A1:2426:U:H2'	38:A1:2427:U:C6	2.40	0.56
38:A1:3233:C:H2'	38:A1:3234:A:C8	2.40	0.56
39:A3:87:G:OP1	43:AF:221:LYS:NZ	2.38	0.56
34:B5:182:A:H2'	34:B5:183:U:C6	2.40	0.56
34:B5:973:A:H4'	38:A1:848:A:H8	1.69	0.56
34:B5:1126:G:OP2	76:An:15:ARG:HD3	2.05	0.56
36:AB:57:VAL:HG22	36:AB:73:VAL:HG22	1.86	0.56
38:A1:1621:A:H2'	38:A1:1622:U:C6	2.40	0.56
41:AD:65:ILE:HG12	41:AD:74:VAL:HG22	1.86	0.56
63:Aa:24:LYS:O	63:Aa:26:ARG:HG2	2.05	0.56
22:BP:123:TYR:OH	25:BS:126:ARG:NH2	2.38	0.56
23:BQ:46:PHE:HA	23:BQ:49:TYR:CD2	2.35	0.56
31:Bg:255:ALA:HB2	31:Bg:292:LEU:HD23	1.87	0.56
34:B5:1175:U:H2'	34:B5:1176:G:C8	2.40	0.56
36:AB:17:LEU:HD21	36:AB:233:TRP:HH2	1.69	0.56
37:AC:35:VAL:HG21	37:AC:244:LEU:HD21	1.86	0.56
38:A1:138:U:H2'	38:A1:139:G:H8	1.70	0.56
38:A1:616:G:H2'	38:A1:617:G:H8	1.70	0.56
38:A1:656:A:H2'	38:A1:657:A:C8	2.40	0.56
38:A1:664:U:H2'	38:A1:665:A:H8	1.68	0.56
6:BH:27:LEU:HD22	6:BH:38:LEU:HD12	1.88	0.56
9:BL:55:ASP:OD1	9:BL:82:ARG:NH2	2.37	0.56
34:B5:513:U:H2'	34:B5:514:G:C8	2.41	0.56
34:B5:1171:A:H2'	34:B5:1172:G:C8	2.41	0.56
38:A1:528:U:H2'	38:A1:529:A:C8	2.40	0.56
38:A1:1350:A:H1'	38:A1:1351:U:H5	1.69	0.56
38:A1:2572:C:H5'	62:AZ:60:LYS:HB3	1.86	0.56
39:A3:45:A:H2'	39:A3:46:A:C8	2.41	0.56
44:AG:78:PHE:O	44:AG:79:GLN:HG3	2.06	0.56
1:BA:177:LEU:O	1:BA:181:VAL:HG23	2.06	0.56
4:BE:3:ARG:HB3	34:B5:93:A:H1'	1.88	0.56
14:BX:48:HIS:HB3	14:BX:103:LEU:HD11	1.87	0.56
15:BY:76:TYR:HE2	15:BY:85:PHE:HB2	1.71	0.56
21:BK:82:LEU:HB2	21:BK:83:PRO:HD2	1.87	0.56
34:B5:129:U:O4'	34:B5:264:G:N1	2.39	0.56
34:B5:947:U:H2'	34:B5:948:G:H8	1.69	0.56
38:A1:1095:U:H3	56:AT:127:GLN:HE22	1.51	0.56
45:AH:34:LEU:HD21	45:AH:149:ASN:HB3	1.86	0.56
5:BG:92:ARG:NH1	34:B5:1674:C:OP1	2.25	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:BQ:134:ALA:O	23:BQ:137:ARG:NH2	2.39	0.56
34:B5:463:U:H2'	34:B5:464:A:H8	1.70	0.56
37:AC:3:ARG:HB3	37:AC:22:LEU:H	1.70	0.56
38:A1:12:A:H2'	38:A1:13:A:C8	2.40	0.56
38:A1:269:G:H5''	50:AN:14:LYS:HE2	1.86	0.56
1:BA:183:ARG:HA	1:BA:188:LEU:HB3	1.88	0.56
2:BB:81:PHE:CD2	2:BB:82:ARG:HG3	2.41	0.56
19:BD:114:ALA:HB3	19:BD:117:ARG:HB2	1.87	0.56
33:BM:35:ALA:HB2	33:BM:123:VAL:HG13	1.88	0.56
34:B5:395:U:O4	34:B5:399:A:N7	2.39	0.56
34:B5:849:C:OP1	54:AR:165:LYS:NZ	2.37	0.56
34:B5:1240:U:O2'	34:B5:1242:A:N7	2.34	0.56
38:A1:2549:G:OP1	38:A1:2549:G:N2	2.39	0.56
8:BJ:48:GLN:O	8:BJ:52:ILE:HD12	2.06	0.56
34:B5:1636:C:O2	34:B5:1765:A:N6	2.38	0.56
38:A1:518:G:OP2	38:A1:518:G:N2	2.30	0.56
38:A1:861:C:OP1	38:A1:2133:PSU:O2'	2.15	0.56
38:A1:2964:G:N2	38:A1:2967:A:OP2	2.35	0.56
49:AM:135:LEU:HD11	51:AO:178[A]:VAL:HG22	1.88	0.56
53:AQ:95:GLU:OE1	53:AQ:95:GLU:N	2.39	0.56
63:Aa:86:LYS:HB3	63:Aa:89:GLN:HE21	1.71	0.56
61:AY:73:VAL:HA	61:AY:80:VAL:HG12	1.88	0.56
5:BG:22:HIS:O	5:BG:25:ARG:NH1	2.39	0.56
8:BJ:35:GLY:HA2	18:Be:36:LYS:HZ1	1.71	0.56
10:BN:26:PHE:HE2	10:BN:28:LEU:HB2	1.71	0.56
22:BP:81:ARG:HH12	22:BP:98:ASN:HA	1.71	0.56
34:B5:896:U:H2'	34:B5:897:C:C6	2.41	0.56
34:B5:1679:G:N2	34:B5:1722:A:H62	2.04	0.56
38:A1:1203:A:H2'	38:A1:1204:A:C8	2.40	0.56
51:AO:125[A]:ARG:HG3	51:AO:129[A]:LEU:HD12	1.88	0.56
61:AY:74:TYR:HD2	61:AY:77:LYS:HG2	1.68	0.56
2:BB:97:LEU:HB3	2:BB:232:HIS:CE1	2.41	0.55
4:BE:108:ARG:NH1	34:B5:789:A:OP1	2.39	0.55
4:BE:150:PRO:HB2	5:BG:208:TYR:CZ	2.41	0.55
20:BF:117:THR:HG21	20:BF:194:LEU:HD22	1.87	0.55
34:B5:461:G:H2'	34:B5:462:G:H8	1.71	0.55
34:B5:939:A:H2'	34:B5:940:A:C8	2.40	0.55
34:B5:1628:U:H2'	34:B5:1629:G:C8	2.41	0.55
38:A1:2930:A:H2'	38:A1:2931:C:C6	2.41	0.55
2:BB:164:ILE:O	2:BB:168:ILE:HG12	2.06	0.55
12:BV:70:ASN:HB3	12:BV:83:TRP:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:219:A:H2'	34:B5:220:A:C8	2.41	0.55
34:B5:1410:A:H2'	34:B5:1411:A:C8	2.41	0.55
38:A1:441:U:H6	38:A1:443:G:H21	1.53	0.55
38:A1:1152:G:OP2	38:A1:1152:G:N2	2.37	0.55
38:A1:2094:C:H2'	38:A1:2095:G:H8	1.71	0.55
41:AD:178:ASN:HA	41:AD:183:TRP:CD2	2.40	0.55
44:AG:115:ALA:O	44:AG:120:LYS:N	2.39	0.55
1:BA:80:THR:HG23	1:BA:81:PHE:HD1	1.71	0.55
3:BC:49:LYS:HB3	3:BC:243:TYR:CD2	2.41	0.55
9:BL:103:ARG:NH1	34:B5:308:C:OP2	2.33	0.55
26:BT:37:VAL:HG21	26:BT:100:ILE:HD11	1.87	0.55
34:B5:58:U:O2'	34:B5:451:A:N3	2.38	0.55
34:B5:120:PSU:HN3	34:B5:297:U:H5	1.55	0.55
36:AB:62:ARG:NH1	38:A1:3039:C:OP1	2.37	0.55
38:A1:148:G:OP2	50:AN:4:TYR:OH	2.18	0.55
43:AF:121:LYS:HB2	56:AT:133:ALA:HB3	1.87	0.55
77:Ao:6:LYS:HG3	77:Ao:94:GLY:HA3	1.87	0.55
1:BA:136:ALA:HB1	1:BA:141:ILE:HB	1.87	0.55
14:BX:6:PRO:HG3	14:BX:14:LYS:HG2	1.88	0.55
20:BF:225:ARG:HD2	29:Bc:58:GLU:HG2	1.88	0.55
26:BT:29:GLU:OE1	26:BT:29:GLU:N	2.40	0.55
34:B5:411:C:H2'	34:B5:412:A:C8	2.42	0.55
34:B5:1041:G:H2'	34:B5:1042:G:C8	2.42	0.55
38:A1:616:G:H2'	38:A1:617:G:C8	2.42	0.55
38:A1:806:A:N3	38:A1:2812:C:O2'	2.38	0.55
38:A1:1597:C:H5'	38:A1:1696:A:H1'	1.89	0.55
38:A1:3064:U:H2'	38:A1:3065:G:H8	1.70	0.55
39:A3:112:G:H2'	39:A3:113:C:C6	2.42	0.55
57:AU:84:LEU:HD22	57:AU:93:ILE:HG21	1.89	0.55
2:BB:144:ARG:HG3	2:BB:208:GLN:OE1	2.07	0.55
26:BT:30:VAL:HG12	26:BT:32:GLY:H	1.70	0.55
34:B5:71:A:O2'	34:B5:72:A:OP1	2.22	0.55
34:B5:207:U:H2'	34:B5:208:U:C6	2.42	0.55
34:B5:272:U:O2'	34:B5:284:G:N2	2.40	0.55
34:B5:1146:G:H2'	34:B5:1147:A:C8	2.41	0.55
34:B5:1474:G:H2'	34:B5:1475:A:C8	2.41	0.55
38:A1:237:G:H2'	38:A1:238:A:H8	1.70	0.55
38:A1:2894:C:H5'	45:AH:168:ARG:NH1	2.21	0.55
38:A1:3006:A:H2'	38:A1:3007:U:O4'	2.07	0.55
38:A1:3191:G:H5''	51:AO:176[A]:LYS:HE2	1.87	0.55
50:AN:8:GLU:HB3	50:AN:50:ARG:HH22	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AU:56:VAL:HG22	57:AU:65:VAL:HG22	1.89	0.55
72:Aj:64:MET:HE3	72:Aj:67:LEU:HD23	1.88	0.55
4:BE:105:VAL:HG21	4:BE:245:LYS:H	1.70	0.55
5:BG:136:LYS:NZ	34:B5:65:A:OP1	2.39	0.55
19:BD:55:THR:HA	19:BD:58:VAL:HG12	1.87	0.55
20:BF:43:PHE:CG	20:BF:115:LYS:HD3	2.41	0.55
21:BK:20:VAL:HG12	21:BK:67:THR:HA	1.88	0.55
24:BR:105:GLN:HG3	24:BR:109:LEU:HD23	1.88	0.55
33:BM:135:MET:O	33:BM:139:HIS:ND1	2.34	0.55
38:A1:428:A:H2'	38:A1:429:U:C6	2.42	0.55
38:A1:900:G:H1'	38:A1:1589:A:N6	2.20	0.55
38:A1:1203:A:H2'	38:A1:1204:A:H8	1.71	0.55
38:A1:1404:G:N2	38:A1:1407:A:OP2	2.28	0.55
38:A1:2883:U:H2'	38:A1:2884:C:C6	2.41	0.55
7:BI:152:ILE:HG13	7:BI:153:GLU:H	1.71	0.55
13:BW:88:LYS:NZ	34:B5:371:G:O3'	2.40	0.55
20:BF:75:GLY:O	23:BQ:122:ARG:NH2	2.39	0.55
34:B5:406:U:H2'	34:B5:407:A:H8	1.71	0.55
38:A1:2250:G:O2'	38:A1:2251:G:OP1	2.23	0.55
38:A1:2568:C:O2'	38:A1:2569:A:O5'	2.23	0.55
45:AH:89:LYS:HG2	45:AH:145:VAL:HG22	1.88	0.55
9:BL:27:THR:HG23	9:BL:30:ARG:H	1.71	0.55
25:BS:39:GLY:H	34:B5:1566:U:H5''	1.70	0.55
26:BT:69:LYS:HG2	34:B5:1367:G:H5''	1.88	0.55
34:B5:891:A:H2'	34:B5:892:A:C8	2.42	0.55
38:A1:2883:U:H2'	38:A1:2884:C:H6	1.72	0.55
3:BC:116:LYS:HG2	3:BC:127:ALA:HB3	1.88	0.55
6:BH:154:LEU:HB2	6:BH:185:ILE:HG12	1.88	0.55
25:BS:41:ARG:HD2	26:BT:46:PRO:HD3	1.88	0.55
31:Bg:45:TRP:HE1	31:Bg:55:GLY:HA3	1.71	0.55
34:B5:1212:G:H2'	34:B5:1213:G:C8	2.42	0.55
34:B5:1725:U:H2'	34:B5:1726:G:C8	2.42	0.55
38:A1:781:G:OP1	53:AQ:151:ARG:HD2	2.07	0.55
38:A1:2193:U:H5''	38:A1:2194:G:H5'	1.88	0.55
38:A1:2881:C:H2'	38:A1:2882:U:C6	2.42	0.55
40:A4:142:C:H2'	40:A4:143:U:C6	2.42	0.55
2:BB:176:VAL:HG12	2:BB:177:GLN:H	1.72	0.55
6:BH:58:LEU:HD23	6:BH:88:ARG:HB3	1.88	0.55
8:BJ:113:VAL:HG21	8:BJ:134:ILE:HG13	1.89	0.55
33:BM:27:ALA:HB3	33:BM:136:ILE:HD11	1.89	0.55
34:B5:980:G:H4'	34:B5:1776:A:H4'	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:AC:9:HIS:HA	37:AC:15:ALA:HA	1.88	0.55
38:A1:1660:C:H2'	38:A1:1661:G:C8	2.42	0.55
6:BH:158:ASP:HB2	6:BH:161:GLN:HE22	1.71	0.54
7:BI:113:PHE:CE2	7:BI:121:LEU:HB2	2.41	0.54
8:BJ:25:ASP:OD1	8:BJ:26:ALA:N	2.40	0.54
8:BJ:94:ASP:OD1	8:BJ:95:TYR:N	2.40	0.54
34:B5:1513:G:H1'	34:B5:1518:C:C2	2.41	0.54
37:AC:81:GLY:O	38:A1:356:C:O2'	2.15	0.54
38:A1:728:G:H5''	53:AQ:43:PRO:HB2	1.89	0.54
38:A1:3291:G:H2'	38:A1:3292:A:C8	2.42	0.54
40:A4:155:A:OP1	44:AG:84:ARG:NH1	2.40	0.54
46:AI:53:VAL:HG21	46:AI:166:ILE:HD12	1.89	0.54
2:BB:144:ARG:HB3	2:BB:206:PRO:HB2	1.88	0.54
6:BH:114:ARG:NH1	34:B5:637:C:O2	2.40	0.54
31:Bg:172:ALA:HB2	31:Bg:202:LEU:HD23	1.88	0.54
34:B5:17:C:H2'	34:B5:18:C:C6	2.42	0.54
34:B5:1086:A:H2'	34:B5:1087:A:C8	2.42	0.54
34:B5:1533:C:H4'	34:B5:1539:G:N1	2.22	0.54
38:A1:490:C:H2'	38:A1:491:A:C8	2.42	0.54
38:A1:797:U:O2	48:AL:12:ASN:ND2	2.40	0.54
38:A1:2727:A:OP2	38:A1:2728:G:N2	2.37	0.54
38:A1:2927:C:H2'	38:A1:2928:C:C6	2.42	0.54
54:AR:105:LEU:HD22	54:AR:135:LYS:HG3	1.88	0.54
56:AT:102:ARG:O	56:AT:106:LEU:HG	2.06	0.54
5:BG:32:ILE:HA	5:BG:52:ILE:HB	1.89	0.54
22:BP:111:MET:HE1	25:BS:119:ILE:HB	1.89	0.54
23:BQ:73:GLY:H	23:BQ:76:SER:HB3	1.71	0.54
29:Bc:12:VAL:HG12	29:Bc:52:ASP:H	1.72	0.54
34:B5:855:A:O2'	34:B5:856:A:H3'	2.07	0.54
41:AD:22:ARG:NE	41:AD:28:THR:OG1	2.35	0.54
4:BE:187:ARG:N	34:B5:753:A:OP1	2.37	0.54
6:BH:21:ALA:HA	6:BH:24:PHE:CE1	2.42	0.54
7:BI:3:ILE:O	7:BI:30:GLY:N	2.36	0.54
12:BV:66:ASP:OD1	12:BV:67:ASP:N	2.40	0.54
19:BD:172:THR:O	19:BD:173:ARG:NH1	2.32	0.54
31:Bg:239:GLU:O	31:Bg:257:ALA:N	2.40	0.54
34:B5:520:A:H2'	34:B5:521:A:H8	1.72	0.54
34:B5:546:U:H2'	34:B5:547:U:H6	1.72	0.54
38:A1:675:C:O2'	38:A1:679:U:OP1	2.25	0.54
49:AM:47:ASP:OD1	49:AM:48:GLY:N	2.39	0.54
4:BE:136:VAL:HG11	4:BE:148:ARG:HH21	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:71:HIS:HB3	6:BH:131:PHE:CZ	2.43	0.54
15:BY:23:PHE:HE2	15:BY:75:VAL:HG22	1.73	0.54
22:BP:80:MET:HB2	22:BP:83:MET:HE3	1.89	0.54
34:B5:1650:U:H2'	34:B5:1651:A:H8	1.71	0.54
38:A1:1671:C:OP1	54:AR:60:LYS:NZ	2.34	0.54
38:A1:3121:U:H1'	38:A1:3122:A:H5''	1.89	0.54
44:AG:183:LYS:HB2	44:AG:194:THR:HG23	1.89	0.54
7:BI:146:ARG:NH2	34:B5:186:C:OP1	2.26	0.54
23:BQ:137:ARG:HB2	34:B5:1580:C:H4'	1.89	0.54
34:B5:156:A:H2'	34:B5:157:A:C8	2.42	0.54
34:B5:1511:U:H2'	34:B5:1512:G:H8	1.72	0.54
38:A1:421:G:O6	38:A1:2383:C:O2'	2.18	0.54
38:A1:1108:U:H2'	38:A1:1109:U:H6	1.70	0.54
38:A1:2999:U:H2'	38:A1:3000:A:H8	1.72	0.54
32:Bf:121:CYS:HB2	32:Bf:130:VAL:HG21	1.89	0.54
34:B5:5:U:H2'	34:B5:6:G:H8	1.73	0.54
38:A1:93:C:OP1	79:A1:3401:SPD:N1	2.39	0.54
38:A1:294:U:P	50:AN:15:GLN:HE22	2.30	0.54
38:A1:2955:U:OP2	38:A1:2977:G:N1	2.36	0.54
40:A4:53:A:OP1	74:Al:19:GLN:NE2	2.33	0.54
48:AL:165:SER:O	48:AL:168:ARG:N	2.41	0.54
52:AP:67:ILE:HD11	52:AP:80:LYS:HB3	1.89	0.54
5:BG:94:ARG:NH2	34:B5:1673:G:OP1	2.36	0.54
25:BS:32:LEU:HD21	25:BS:69:ILE:HG21	1.89	0.54
34:B5:183:U:H2'	34:B5:184:C:C6	2.43	0.54
38:A1:966:PSU:H2'	38:A1:967:A:C8	2.43	0.54
38:A1:2588:U:OP1	44:AG:241:LYS:NZ	2.34	0.54
10:BN:11:ILE:HG13	10:BN:12:SER:N	2.23	0.54
11:BO:91:THR:HG23	11:BO:93:THR:H	1.72	0.54
25:BS:123:ARG:NH1	34:B5:1546:G:OP1	2.33	0.54
26:BT:39:THR:HA	26:BT:100:ILE:HD12	1.90	0.54
33:BM:79:ALA:HA	33:BM:86:VAL:HG23	1.89	0.54
38:A1:501:A:H2'	38:A1:502:U:C6	2.43	0.54
38:A1:943:U:H3'	63:Aa:13:GLY:HA2	1.89	0.54
38:A1:1124:PSU:O2'	38:A1:2635:A:OP1	2.26	0.54
38:A1:2407:C:H2'	38:A1:2408:U:H6	1.73	0.54
38:A1:2946:A:H5''	38:A1:2947:G:H5'	1.90	0.54
30:Bd:32:ARG:NH1	34:B5:1597:A:OP2	2.38	0.54
34:B5:885:G:H2'	34:B5:886:U:C6	2.43	0.54
45:AH:34:LEU:HD11	45:AH:150:SER:HB3	1.90	0.54
47:AJ:125:MET:HE1	47:AJ:127:PHE:HE1	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AU:81:LYS:HG2	57:AU:90:ARG:HH12	1.73	0.54
5:BG:45:PHE:HB3	5:BG:48:TYR:HB2	1.90	0.53
8:BJ:110:GLN:HG3	8:BJ:144:PRO:HB3	1.90	0.53
23:BQ:130:GLY:N	34:B5:1604:U:OP1	2.28	0.53
34:B5:64:U:O2'	34:B5:168:A:N3	2.37	0.53
34:B5:97:C:H2'	34:B5:98:U:C6	2.42	0.53
34:B5:394:C:H42	34:B5:401:A:N6	2.06	0.53
35:AA:28:LYS:HD3	35:AA:123:ARG:HD3	1.90	0.53
38:A1:417:A:H2'	38:A1:418:A:H8	1.72	0.53
38:A1:1019:G:N7	38:A1:1021:G:N2	2.56	0.53
38:A1:1534:A:H2'	38:A1:1535:A:C8	2.43	0.53
56:AT:152:ALA:HB1	56:AT:153:PRO:HD2	1.90	0.53
3:BC:231:ALA:O	12:BV:16:LYS:NZ	2.41	0.53
4:BE:19:LEU:HD22	34:B5:788:A:H2'	1.90	0.53
18:Be:29:LYS:O	18:Be:31:LYS:NZ	2.34	0.53
23:BQ:75:VAL:HB	34:B5:1609:U:H5''	1.89	0.53
25:BS:88:ARG:HD2	25:BS:108:LYS:HD3	1.90	0.53
26:BT:18:TYR:HD1	26:BT:135:ILE:HG13	1.72	0.53
26:BT:40:SER:HB3	26:BT:43:ASN:OD1	2.08	0.53
31:Bg:116:ASP:CG	31:Bg:121:MET:H	2.16	0.53
31:Bg:255:ALA:HA	31:Bg:260:ILE:HD13	1.90	0.53
34:B5:183:U:H2'	34:B5:184:C:H6	1.73	0.53
34:B5:340:U:H2'	34:B5:341:A:C8	2.42	0.53
34:B5:895:G:H1	34:B5:917:U:H3	1.56	0.53
34:B5:1079:U:H2'	34:B5:1080:U:C6	2.44	0.53
34:B5:1170:G:H21	34:B5:1571:C:H4'	1.74	0.53
38:A1:590:G:N2	42:AE:19:LYS:HD3	2.22	0.53
38:A1:1896:A:H61	38:A1:2339:C:H42	1.56	0.53
53:AQ:55:SER:O	53:AQ:59:ARG:HG2	2.09	0.53
4:BE:147:ILE:HG21	4:BE:169:ILE:HG23	1.90	0.53
20:BF:76:ARG:HD2	23:BQ:122:ARG:HH21	1.72	0.53
34:B5:923:A:H2'	34:B5:924:A:H8	1.74	0.53
38:A1:1717:U:H2'	38:A1:1718:G:H8	1.73	0.53
39:A3:23:A:H2'	39:A3:24:A:C8	2.44	0.53
40:A4:150:G:OP1	60:AX:27:ARG:NH2	2.39	0.53
7:BI:21:PHE:CD2	7:BI:22:ARG:HD2	2.43	0.53
15:BY:131:ARG:CZ	34:B5:153:G:H5'	2.39	0.53
25:BS:100:THR:HB	25:BS:105:VAL:HG12	1.89	0.53
31:Bg:220:ILE:HD11	31:Bg:234:LEU:HD22	1.91	0.53
34:B5:208:U:H2'	34:B5:209:U:C6	2.43	0.53
34:B5:896:U:O2'	34:B5:897:C:O5'	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1045:C:H2'	34:B5:1046:G:H8	1.74	0.53
37:AC:114:ASN:HB2	37:AC:117:GLU:HG3	1.90	0.53
38:A1:341:G:O2'	40:A4:22:U:O4	2.26	0.53
38:A1:1290:A:H2'	38:A1:1291:A:C8	2.43	0.53
43:AF:98:LYS:HB3	43:AF:99:PRO:HD3	1.91	0.53
56:AT:106:LEU:HA	56:AT:109:VAL:HG12	1.89	0.53
8:BJ:126:ARG:HD3	18:Be:33:ARG:HD3	1.89	0.53
25:BS:127:HIS:CD2	25:BS:133:VAL:HG11	2.43	0.53
30:Bd:34:TYR:OH	34:B5:1487:A:OP1	2.20	0.53
34:B5:1125:A:O2'	34:B5:1776:A:OP1	2.19	0.53
34:B5:1213:G:O2'	34:B5:1244:A:N7	2.42	0.53
34:B5:1214:U:OP1	34:B5:1246:C:O2'	2.16	0.53
34:B5:1236:A:H2'	34:B5:1237:G:C8	2.42	0.53
37:AC:197:ARG:NH2	38:A1:339:C:OP2	2.41	0.53
38:A1:68:C:OP2	38:A1:301:G:N2	2.41	0.53
47:AJ:87:LYS:NZ	47:AJ:105:GLY:O	2.40	0.53
7:BI:76:THR:HG21	7:BI:104:ILE:HD12	1.90	0.53
20:BF:111:VAL:O	20:BF:114:ILE:HG22	2.08	0.53
27:BU:57:ARG:HA	27:BU:89:ARG:HG3	1.90	0.53
29:Bc:21:SER:OG	29:Bc:22:ARG:NH1	2.42	0.53
32:Bf:85:TYR:HH	34:B5:1445:G:HO2'	1.56	0.53
34:B5:206:A:H1'	34:B5:262:U:O2	2.09	0.53
34:B5:1638:G:O6	34:B5:1767:G:N2	2.41	0.53
38:A1:585:A:H2'	38:A1:586:C:C6	2.43	0.53
38:A1:1039:U:H2'	38:A1:1040:A:C8	2.43	0.53
38:A1:1062:A:O2'	56:AT:108:ARG:NH2	2.41	0.53
46:AI:208:ASN:OD1	46:AI:211:ARG:NH1	2.36	0.53
73:Ak:7:ASP:HB3	73:Ak:10:GLN:HB3	1.89	0.53
15:BY:58:PHE:HB2	15:BY:72:PHE:HB3	1.91	0.53
25:BS:53:ASP:HB3	25:BS:56:LYS:HE2	1.90	0.53
34:B5:5:U:H2'	34:B5:6:G:C8	2.43	0.53
34:B5:1564:U:H2'	34:B5:1565:C:C6	2.43	0.53
36:AB:292:ALA:HB1	36:AB:295:ALA:HB3	1.90	0.53
38:A1:1799:A:H2'	38:A1:1800:A:C8	2.43	0.53
38:A1:2768:U:H2'	38:A1:2769:A:H8	1.74	0.53
38:A1:2999:U:H2'	38:A1:3000:A:C8	2.43	0.53
48:AL:180:ARG:HG3	71:AI:11:LEU:HD11	1.91	0.53
2:BB:224:ASP:OD1	38:A1:2535:A:O2'	2.27	0.53
11:BO:52:ARG:NH1	11:BO:53:ASP:OD1	2.42	0.53
14:BX:90:ASP:OD1	34:B5:567:A:O2'	2.19	0.53
20:BF:109:LYS:HD3	34:B5:1473:U:H4'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:BK:55:VAL:HG22	21:BK:68:LEU:HA	1.90	0.53
24:BR:28:PHE:HB3	24:BR:55:THR:HG21	1.91	0.53
33:BM:51:ALA:HA	33:BM:54:ARG:HG2	1.90	0.53
34:B5:385:A:H2'	34:B5:386:G:C8	2.44	0.53
46:AI:49:CYS:HB3	46:AI:168:SER:HB3	1.91	0.53
48:AL:126:PHE:O	70:Ah:114:ARG:NH2	2.42	0.53
4:BE:94:ALA:O	4:BE:95:THR:OG1	2.23	0.53
11:BO:135:ARG:NH2	34:B5:904:G:OP1	2.42	0.53
21:BK:10:LYS:HB3	21:BK:35:ILE:HD11	1.91	0.53
24:BR:50:ILE:O	24:BR:54:THR:OG1	2.19	0.53
37:AC:159:ILE:HG23	37:AC:164:GLU:HG3	1.91	0.53
38:A1:1340:G:H2'	38:A1:1341:U:C6	2.43	0.53
38:A1:2699:G:H5''	56:AT:16:GLN:NE2	2.24	0.53
1:BA:167:LYS:HD2	1:BA:204:TYR:HB3	1.90	0.53
5:BG:181:PRO:HA	5:BG:184:LEU:HD12	1.90	0.53
7:BI:31:ARG:NH1	34:B5:332:U:OP1	2.39	0.53
16:Ba:41:ILE:O	16:Ba:42:ARG:NE	2.38	0.53
20:BF:46:TRP:HE1	20:BF:122:ASN:CG	2.17	0.53
21:BK:52:LYS:NZ	21:BK:54:TYR:OH	2.42	0.53
34:B5:1012:U:H4'	35:AA:247:ARG:HB3	1.91	0.53
34:B5:1158:C:H5'	34:B5:1161:C:N4	2.21	0.53
34:B5:1466:G:H2'	34:B5:1467:C:C6	2.43	0.53
38:A1:2154:U:H2'	38:A1:2155:G:C8	2.44	0.53
52:AP:60:PHE:O	52:AP:64:ASN:ND2	2.34	0.53
58:AV:10:LYS:HD2	58:AV:13:ILE:HD12	1.90	0.53
10:BN:30:SER:O	10:BN:34:ILE:HG12	2.09	0.52
11:BO:81:VAL:HG11	11:BO:102:LEU:HD11	1.90	0.52
23:BQ:69:VAL:HG11	23:BQ:81:ILE:HD11	1.91	0.52
31:Bg:45:TRP:HD1	31:Bg:47:LEU:HD22	1.73	0.52
33:BM:114:LYS:HD3	34:B5:1226:A:H62	1.75	0.52
34:B5:591:A:H2'	34:B5:592:A:C8	2.44	0.52
34:B5:1592:A:H2'	34:B5:1593:A:C8	2.44	0.52
38:A1:2103:U:H2'	38:A1:2104:A:H8	1.73	0.52
38:A1:2154:U:H2'	38:A1:2155:G:H8	1.74	0.52
38:A1:2389:C:H2'	38:A1:2390:A:H8	1.74	0.52
38:A1:3322:A:H2'	38:A1:3323:A:C8	2.44	0.52
1:BA:195:TRP:CD1	1:BA:196:SER:H	2.28	0.52
8:BJ:64:GLU:O	8:BJ:65:LYS:HG3	2.09	0.52
25:BS:104:ASN:OD1	25:BS:108:LYS:NZ	2.41	0.52
34:B5:408:C:H2'	34:B5:409:C:C6	2.44	0.52
38:A1:673:U:H2'	38:A1:674:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2106:A:H2'	38:A1:2107:A:C8	2.44	0.52
40:A4:78:G:H2'	40:A4:79:A:C8	2.43	0.52
1:BA:23:HIS:O	1:BA:47:VAL:HA	2.09	0.52
3:BC:80:VAL:HA	3:BC:102:VAL:HG12	1.91	0.52
7:BI:38:ILE:HD11	7:BI:81:VAL:HG13	1.89	0.52
15:BY:74:LEU:HD12	15:BY:90:ARG:HH12	1.74	0.52
22:BP:29:SER:OG	22:BP:30:THR:N	2.41	0.52
28:BZ:75:LEU:HD12	28:BZ:78:ILE:HD11	1.90	0.52
31:Bg:195:HIS:CG	31:Bg:199:ILE:HG12	2.45	0.52
34:B5:884:A:H2'	34:B5:885:G:H8	1.71	0.52
38:A1:20:A:H2'	38:A1:21:G:C8	2.43	0.52
38:A1:837:A:OP1	78:Ap:5:THR:OG1	2.24	0.52
38:A1:1696:A:H2'	38:A1:1697:A:C8	2.44	0.52
38:A1:2573:G:OP2	62:AZ:58:GLY:N	2.35	0.52
41:AD:95:TRP:CD1	41:AD:158:ARG:HA	2.45	0.52
44:AG:228:GLU:HA	44:AG:231:LYS:HE3	1.91	0.52
6:BH:163:ASP:OD1	6:BH:164:TYR:N	2.42	0.52
19:BD:97:SER:O	19:BD:101:GLN:NE2	2.43	0.52
22:BP:61:ARG:NH2	22:BP:88:GLU:O	2.42	0.52
29:Bc:10:ALA:HA	29:Bc:32:PHE:HA	1.92	0.52
34:B5:647:G:N2	34:B5:687:G:H1	2.08	0.52
38:A1:1134:G:O2'	38:A1:2642:A:N3	2.34	0.52
38:A1:2116:G:OP1	38:A1:2118:C:N4	2.42	0.52
50:AN:155:VAL:O	50:AN:162:ARG:NH2	2.42	0.52
58:AV:84:SER:HA	58:AV:94:TYR:HB3	1.91	0.52
58:AV:104:ASN:OD1	58:AV:108:GLU:N	2.41	0.52
2:BB:128:LYS:HA	2:BB:134:VAL:HA	1.90	0.52
2:BB:222:LYS:HD3	2:BB:224:ASP:N	2.24	0.52
3:BC:143:TYR:OH	3:BC:149:GLY:O	2.19	0.52
4:BE:11:ARG:NH1	4:BE:21:ASP:OD1	2.42	0.52
10:BN:124:ARG:NH2	34:B5:967:A:OP2	2.43	0.52
11:BO:38:THR:HG21	34:B5:895:G:H21	1.75	0.52
11:BO:72:LYS:O	11:BO:73:GLU:HG3	2.10	0.52
33:BM:63:VAL:HG11	33:BM:94:ALA:HB2	1.90	0.52
34:B5:1171:A:H2'	34:B5:1172:G:H8	1.74	0.52
34:B5:1222:C:H2'	34:B5:1223:A:C8	2.45	0.52
37:AC:141:ARG:NH2	38:A1:1386:A:H5''	2.24	0.52
38:A1:691:A:N1	40:A4:28:C:O2'	2.36	0.52
38:A1:904:A:OP2	72:Aj:30:GLN:NE2	2.41	0.52
38:A1:1615:C:H2'	38:A1:1616:U:C6	2.45	0.52
39:A3:19:C:H2'	39:A3:20:A:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:A4:9:A:H2'	40:A4:10:A:H8	1.73	0.52
5:BG:186:ARG:NH2	34:B5:269:G:N7	2.57	0.52
6:BH:104:ARG:NH2	34:B5:805:U:O4	2.32	0.52
13:BW:27:ILE:HB	13:BW:61:ILE:HB	1.91	0.52
21:BK:30:ALA:HA	21:BK:38:LYS:HB2	1.90	0.52
31:Bg:149:ASP:H	31:Bg:175:ASP:HB3	1.74	0.52
34:B5:900:A:H2'	34:B5:901:G:H8	1.75	0.52
34:B5:1642:G:H2'	34:B5:1643:U:C6	2.43	0.52
35:AA:9:ARG:NH2	38:A1:912:G:OP2	2.35	0.52
38:A1:235:A:H2'	38:A1:236:G:C8	2.45	0.52
38:A1:567:G:H2'	38:A1:568:G:C8	2.45	0.52
38:A1:821:U:H2'	38:A1:822:G:H8	1.73	0.52
38:A1:1643:A:H2'	38:A1:1644:C:C2	2.45	0.52
40:A4:95:G:O2'	72:Aj:81:GLY:O	2.26	0.52
4:BE:129:VAL:HG22	4:BE:139:VAL:HG12	1.92	0.52
8:BJ:163:PRO:HD2	34:B5:513:U:OP1	2.10	0.52
10:BN:107:LYS:NZ	34:B5:1019:A:OP2	2.42	0.52
12:BV:79:LEU:HD23	12:BV:82:VAL:HG21	1.91	0.52
19:BD:33:GLY:HA3	19:BD:53:THR:HG22	1.92	0.52
26:BT:77:ASN:HA	26:BT:96:ALA:HB3	1.91	0.52
32:Bf:129:GLY:HA3	33:BM:50:LYS:HD3	1.92	0.52
34:B5:828:U:H2'	34:B5:829:A:C5	2.45	0.52
34:B5:895:G:H2'	34:B5:896:U:C6	2.44	0.52
37:AC:338:LYS:HE3	37:AC:341:SER:HB2	1.92	0.52
38:A1:2759:U:H5''	38:A1:2760:C:H5'	1.91	0.52
39:A3:64:A:N7	46:AI:209:ASN:ND2	2.58	0.52
4:BE:19:LEU:HD11	4:BE:108:ARG:HD2	1.92	0.52
8:BJ:79:ARG:NH1	34:B5:762:A:OP1	2.43	0.52
17:Bb:54:VAL:HG13	17:Bb:63:LEU:HB3	1.91	0.52
25:BS:11:PHE:CE1	25:BS:59:GLY:HA3	2.45	0.52
34:B5:538:A:O2'	34:B5:539:G:N7	2.37	0.52
34:B5:1229:G:H1'	34:B5:1230:A:H5'	1.92	0.52
34:B5:1469:A:O2'	34:B5:1540:G:N2	2.37	0.52
34:B5:1650:U:H2'	34:B5:1651:A:C8	2.44	0.52
34:B5:1740:A:H2'	34:B5:1741:U:C6	2.45	0.52
38:A1:1149:G:OP2	68:Af:21:ARG:NH2	2.40	0.52
38:A1:1246:G:H22	38:A1:1273:A:H5''	1.74	0.52
38:A1:1644:C:H5''	38:A1:1645:U:H5''	1.90	0.52
47:AJ:45:PRO:HB3	47:AJ:69:VAL:HB	1.91	0.52
63:Aa:82:ILE:HD11	63:Aa:102:ILE:HG12	1.92	0.52
1:BA:195:TRP:HD1	1:BA:196:SER:H	1.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:29:SER:O	10:BN:32:SER:OG	2.25	0.52
25:BS:28:ILE:HD12	25:BS:28:ILE:H	1.75	0.52
34:B5:234:G:H21	34:B5:234:G:P	2.33	0.52
34:B5:1183:A:N3	34:B5:1210:C:O2'	2.40	0.52
34:B5:1606:C:H2'	34:B5:1607:G:C8	2.45	0.52
34:B5:1680:G:O2'	34:B5:1720:G:N2	2.43	0.52
36:AB:95:THR:HG22	38:A1:3243:A:H4'	1.92	0.52
38:A1:47:C:OP2	38:A1:48:A:O2'	2.22	0.52
38:A1:363:G:OP2	72:Aj:56:ARG:NH2	2.39	0.52
38:A1:1498:A:H2'	38:A1:1499:C:C6	2.45	0.52
38:A1:1553:U:H4'	38:A1:1554:U:H5'	1.91	0.52
38:A1:2609:A:H2'	38:A1:2610:G:H8	1.75	0.52
40:A4:57:C:H4'	40:A4:63:G:N7	2.25	0.52
54:AR:159:ALA:O	54:AR:163:ARG:HG2	2.10	0.52
54:AR:170:ARG:HH21	54:AR:173:ARG:HH21	1.58	0.52
61:AY:88:GLU:OE1	61:AY:94:SER:OG	2.26	0.52
3:BC:164:SER:HB3	34:B5:1086:A:H5'	1.92	0.52
4:BE:120:SER:O	4:BE:164:LEU:HB3	2.10	0.52
14:BX:75:GLN:NE2	14:BX:80:GLY:HA2	2.25	0.52
31:Bg:264:SER:HB2	31:Bg:267:PRO:HD2	1.92	0.52
31:Bg:270:LEU:HD11	31:Bg:273:ASP:HB2	1.91	0.52
34:B5:1731:A:H3'	34:B5:1732:A:H5''	1.91	0.52
36:AB:180:GLU:OE2	38:A1:3002:C:O2'	2.26	0.52
38:A1:985:U:H2'	38:A1:986:PSU:H6	1.75	0.52
38:A1:994:G:N2	38:A1:995:U:O4	2.29	0.52
38:A1:1596:C:H2'	38:A1:1597:C:C6	2.45	0.52
39:A3:31:U:H4'	41:AD:218:ARG:NH1	2.25	0.52
2:BB:151:LYS:N	34:B5:1067:C:OP1	2.37	0.51
7:BI:37:LYS:H	7:BI:59:ARG:H	1.58	0.51
27:BU:106:ILE:HG13	27:BU:107:THR:HG23	1.92	0.51
34:B5:384:G:H2'	34:B5:385:A:H8	1.75	0.51
34:B5:956:C:OP1	34:B5:1072:C:O2'	2.29	0.51
34:B5:1458:G:O2'	34:B5:1459:C:OP1	2.24	0.51
34:B5:1475:A:O2'	34:B5:1540:G:OP1	2.28	0.51
37:AC:322:GLN:OE1	38:A1:597:G:N2	2.36	0.51
38:A1:631:U:H2'	38:A1:632:G:H8	1.75	0.51
38:A1:2673:A:OP2	47:AJ:94:ARG:NH2	2.43	0.51
60:AX:63:ILE:HD13	60:AX:86:VAL:HG12	1.92	0.51
4:BE:247:SER:N	4:BE:250:GLU:OE2	2.43	0.51
6:BH:22:GLN:O	6:BH:25:VAL:HG12	2.09	0.51
9:BL:128:CYS:SG	9:BL:131:ILE:HD11	2.49	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:BN:108:ASP:OD1	34:B5:878:G:O2'	2.23	0.51
19:BD:31:GLU:OE1	19:BD:54:ARG:NH2	2.42	0.51
22:BP:40:ARG:NH2	34:B5:1551:U:O4	2.43	0.51
34:B5:1738:U:H2'	34:B5:1739:C:C6	2.45	0.51
34:B5:1758:U:H1'	38:A1:2255:A:N3	2.25	0.51
38:A1:157:A:N7	71:AI:26:ILE:HG12	2.25	0.51
38:A1:307:A:H2'	38:A1:308:A:H8	1.74	0.51
38:A1:307:A:H2'	38:A1:308:A:C8	2.44	0.51
38:A1:1636:U:O2'	62:AZ:79:HIS:ND1	2.38	0.51
38:A1:2208:A:H2'	38:A1:2209:U:C6	2.45	0.51
38:A1:2273:G:O2'	38:A1:2311:G:O6	2.22	0.51
38:A1:2406:C:H2'	38:A1:2407:C:C6	2.45	0.51
38:A1:2675:C:N4	47:AJ:22:SER:OG	2.43	0.51
44:AG:148:ALA:HA	44:AG:201:THR:HG22	1.92	0.51
8:BJ:141:VAL:HG12	8:BJ:143:ILE:H	1.74	0.51
9:BL:59:PRO:HB3	9:BL:66:ILE:HD11	1.92	0.51
34:B5:1269:U:H4'	34:B5:1270:G:H5''	1.92	0.51
34:B5:1484:G:H2'	34:B5:1485:C:C6	2.46	0.51
34:B5:1727:G:H2'	34:B5:1728:A:H8	1.75	0.51
38:A1:67:A:N1	38:A1:300:G:O2'	2.42	0.51
38:A1:631:U:H2'	38:A1:632:G:C8	2.45	0.51
38:A1:2609:A:H2'	38:A1:2610:G:C8	2.46	0.51
5:BG:67:VAL:HG23	5:BG:100:ALA:H	1.73	0.51
5:BG:135:PRO:HB2	5:BG:141:ILE:HG13	1.91	0.51
8:BJ:133:HIS:HE2	34:B5:513:U:H5'	1.75	0.51
17:Bb:81:ARG:HG2	17:Bb:82:LYS:HG2	1.92	0.51
19:BD:23:GLU:HG2	21:BK:61:TRP:HE1	1.75	0.51
22:BP:127:ARG:NH1	34:B5:1181:PSU:H5'	2.24	0.51
25:BS:25:ASN:O	25:BS:57:ARG:NH2	2.43	0.51
31:Bg:185:GLN:HE22	31:Bg:187:GLN:HB3	1.75	0.51
34:B5:925:G:H2'	34:B5:926:A:C8	2.44	0.51
38:A1:19:U:H2'	38:A1:20:A:H8	1.75	0.51
38:A1:177:U:N3	38:A1:241:G:N1	2.45	0.51
38:A1:235:A:H2'	38:A1:236:G:H8	1.76	0.51
38:A1:656:A:H2'	38:A1:657:A:H8	1.76	0.51
38:A1:972:A:H2'	38:A1:973:A:C8	2.46	0.51
42:AE:91:VAL:HG13	42:AE:148:GLU:OE1	2.10	0.51
9:BL:8:GLN:HE22	9:BL:14:GLN:HB2	1.75	0.51
15:BY:117:LYS:NZ	34:B5:159:U:OP2	2.43	0.51
25:BS:39:GLY:N	34:B5:1566:U:H5''	2.26	0.51
34:B5:1619:C:H2'	34:B5:1620:C:H6	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:67:PHE:CE2	58:AV:88:ARG:HB2	2.46	0.51
38:A1:162:G:O6	38:A1:260:C:N4	2.43	0.51
38:A1:249:U:N3	38:A1:250:U:O4	2.44	0.51
38:A1:2103:U:H2'	38:A1:2104:A:C8	2.46	0.51
38:A1:2661:G:H2'	38:A1:2662:G:H8	1.76	0.51
38:A1:2673:A:H5''	47:AJ:95:ASN:OD1	2.11	0.51
38:A1:3176:G:N2	38:A1:3213:A:H1'	2.26	0.51
34:B5:31:C:H2'	34:B5:32:U:C6	2.46	0.51
34:B5:388:G:H2'	34:B5:389:G:C8	2.46	0.51
34:B5:631:G:H2'	34:B5:632:PSU:H6	1.75	0.51
34:B5:948:G:H2'	34:B5:949:C:H6	1.75	0.51
34:B5:979:A:H4'	34:B5:1786:G:N2	2.26	0.51
34:B5:1156:C:H2'	34:B5:1157:A:C8	2.46	0.51
34:B5:1357:A:H2'	34:B5:1358:G:C8	2.46	0.51
36:AB:139:GLN:HG2	36:AB:140:ASP:OD1	2.10	0.51
37:AC:349:THR:HG21	43:AF:67:ARG:HB3	1.92	0.51
38:A1:531:G:H2'	38:A1:532:A:C8	2.46	0.51
38:A1:1192:C:H2'	38:A1:1192:C:O2	2.11	0.51
38:A1:2662:G:H2'	38:A1:2663:G:C8	2.45	0.51
46:AI:110:ARG:HG2	46:AI:111:LEU:HD12	1.92	0.51
47:AJ:26:SER:HA	47:AJ:30:LEU:HB2	1.93	0.51
57:AU:61:THR:HG23	57:AU:62:VAL:HG23	1.92	0.51
1:BA:88:LYS:HE2	1:BA:201:LEU:HB2	1.92	0.51
2:BB:108:ASP:OD1	2:BB:109:LYS:N	2.43	0.51
5:BG:180:THR:HG23	5:BG:183:ARG:H	1.75	0.51
25:BS:58:ALA:HA	25:BS:61:LEU:HD23	1.92	0.51
34:B5:122:U:H2'	34:B5:123:G:C8	2.46	0.51
34:B5:1537:C:O4'	34:B5:1572:G:N2	2.44	0.51
35:AA:28:LYS:HB2	35:AA:123:ARG:HB3	1.93	0.51
35:AA:178:PRO:HG2	78:Ap:26:VAL:HG13	1.92	0.51
36:AB:11:HIS:NE2	38:A1:2881:C:OP1	2.44	0.51
38:A1:799:G:OP2	63:Aa:32:ARG:HD3	2.11	0.51
38:A1:1223:A:H8	38:A1:1223:A:OP2	1.93	0.51
38:A1:1666:G:H2'	38:A1:1667:A:H8	1.74	0.51
40:A4:69:U:H2'	40:A4:70:G:O4'	2.11	0.51
52:AP:25:SER:O	52:AP:29:THR:OG1	2.24	0.51
54:AR:24:LEU:HD23	54:AR:50:ILE:HG12	1.93	0.51
8:BJ:127:VAL:O	8:BJ:131:GLN:HG2	2.11	0.51
14:BX:111:GLY:HA2	14:BX:121:ARG:HD2	1.92	0.51
25:BS:144:ARG:NH2	34:B5:1172:G:OP1	2.37	0.51
31:Bg:167:VAL:O	31:Bg:182:ASN:ND2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:208:U:H2'	34:B5:209:U:H6	1.75	0.51
34:B5:791:A:H2'	34:B5:792:U:C6	2.46	0.51
35:AA:234:LYS:NZ	38:A1:2162:U:OP1	2.35	0.51
38:A1:542:G:N2	38:A1:550:A:N3	2.59	0.51
38:A1:2207:A:N3	38:A1:2208:A:N6	2.58	0.51
38:A1:2427:U:H2'	38:A1:2428:U:C6	2.46	0.51
39:A3:38:U:N3	39:A3:41:G:OP2	2.27	0.51
3:BC:188:LEU:HD13	3:BC:196:VAL:HG11	1.93	0.51
6:BH:8:ILE:HA	6:BH:42:GLN:HG3	1.93	0.51
6:BH:70:PHE:O	6:BH:74:GLN:HG2	2.10	0.51
19:BD:73:VAL:HG23	19:BD:84:ILE:HG12	1.92	0.51
34:B5:17:C:H2'	34:B5:18:C:H6	1.76	0.51
35:AA:40:TYR:HA	35:AA:91:GLY:HA3	1.93	0.51
38:A1:1304:A:H61	38:A1:2860:U:H5''	1.76	0.51
38:A1:3057:U:H5'	38:A1:3086:A:H61	1.76	0.51
41:AD:294:ALA:HB1	46:AI:217:PHE:HB3	1.92	0.51
8:BJ:66:ASP:OD1	8:BJ:67:PRO:HD2	2.11	0.51
11:BO:120:PRO:HB2	34:B5:887:A:H5''	1.92	0.51
19:BD:72:LEU:HD23	19:BD:75:LYS:HD2	1.92	0.51
34:B5:218:A:N1	34:B5:843:U:C4	2.78	0.51
34:B5:321:C:N4	34:B5:1666:U:O3'	2.44	0.51
34:B5:953:G:H2'	34:B5:954:G:H8	1.76	0.51
38:A1:710:A:H2'	38:A1:711:A:C8	2.46	0.51
38:A1:970:A:H2'	38:A1:971:G:H8	1.75	0.51
38:A1:1662:G:H22	38:A1:1787:A:H2	1.57	0.51
39:A3:7:G:OP1	41:AD:33:ARG:NH1	2.44	0.51
39:A3:17:A:P	47:AJ:150:ASN:HD21	2.33	0.51
39:A3:31:U:H4'	41:AD:218:ARG:HH12	1.76	0.51
45:AH:47:LYS:HB2	49:AM:7:VAL:HB	1.93	0.51
54:AR:105:LEU:HD23	54:AR:138:LEU:HD23	1.92	0.51
1:BA:29:VAL:HG13	1:BA:149:LEU:HD12	1.93	0.50
11:BO:131:GLY:O	16:Ba:22:ARG:NH2	2.44	0.50
15:BY:32:ARG:HH22	15:BY:35:VAL:HG12	1.75	0.50
15:BY:124:ARG:HA	15:BY:127:LYS:HE2	1.93	0.50
19:BD:28:GLU:OE1	21:BK:56:LYS:NZ	2.44	0.50
21:BK:13:GLN:HB3	21:BK:80:LEU:HD11	1.93	0.50
24:BR:13:SER:O	24:BR:17:ILE:HG12	2.10	0.50
25:BS:87:ASN:O	34:B5:1546:G:N2	2.43	0.50
34:B5:319:U:H4'	34:B5:323:A:C8	2.45	0.50
34:B5:954:G:H2'	34:B5:955:A:C8	2.46	0.50
34:B5:1151:A:H2'	34:B5:1152:A:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1511:U:H2'	34:B5:1512:G:C8	2.46	0.50
34:B5:1624:C:H2'	34:B5:1625:C:H6	1.75	0.50
34:B5:1752:U:H2'	34:B5:1753:A:C8	2.46	0.50
38:A1:237:G:H2'	38:A1:238:A:C8	2.47	0.50
38:A1:1093:A:OP1	56:AT:120:LYS:NZ	2.38	0.50
38:A1:1472:U:H5''	54:AR:24:LEU:HD12	1.93	0.50
38:A1:1593:A:OP1	69:Ag:60:ARG:NH1	2.39	0.50
38:A1:2389:C:H2'	38:A1:2390:A:C8	2.46	0.50
40:A4:19:C:H2'	40:A4:20:U:C6	2.46	0.50
54:AR:175:GLN:HG2	54:AR:176:ARG:HD2	1.93	0.50
8:BJ:174:ARG:NH1	34:B5:536:C:OP2	2.44	0.50
31:Bg:29:GLN:HB3	31:Bg:32:LEU:HB3	1.93	0.50
34:B5:515:A:H2'	34:B5:516:G:O4'	2.11	0.50
34:B5:1392:U:H2'	34:B5:1393:C:C6	2.45	0.50
34:B5:1673:G:H1	34:B5:1728:A:H2	1.56	0.50
37:AC:181:VAL:O	37:AC:182:LEU:HG	2.11	0.50
38:A1:1460:A:H2'	38:A1:1461:A:H8	1.77	0.50
38:A1:2890:A:O2'	38:A1:2933:A:N3	2.37	0.50
49:AM:112:LEU:HD22	49:AM:116:GLU:HB3	1.93	0.50
63:Aa:19:LYS:HB3	63:Aa:25:HIS:HB2	1.93	0.50
1:BA:64:ILE:HG21	1:BA:181:VAL:HG22	1.92	0.50
2:BB:134:VAL:HG12	2:BB:219:LYS:HG2	1.92	0.50
5:BG:195:VAL:HG22	34:B5:127:G:N2	2.26	0.50
34:B5:339:C:H2'	34:B5:340:U:H6	1.76	0.50
34:B5:1350:U:H2'	34:B5:1351:G:C8	2.46	0.50
34:B5:1580:C:H2'	34:B5:1581:C:C6	2.46	0.50
36:AB:284:ARG:NH1	36:AB:293:ASN:O	2.44	0.50
38:A1:1169:A:H4'	43:AF:219:LYS:HD3	1.91	0.50
38:A1:1654:A:N3	69:Ag:59:PRO:HB3	2.27	0.50
38:A1:1659:U:H2'	38:A1:1660:C:C6	2.46	0.50
38:A1:2106:A:H2'	38:A1:2107:A:H8	1.75	0.50
38:A1:2262:A:C8	38:A1:2262:A:H5''	2.47	0.50
38:A1:2404:A:N7	38:A1:2872:A:N6	2.59	0.50
38:A1:3298:C:C2	38:A1:3299:A:C8	2.98	0.50
2:BB:111:ARG:NH2	34:B5:929:A:N1	2.60	0.50
4:BE:47:PHE:HD2	4:BE:48:LEU:HD12	1.76	0.50
28:BZ:50:ILE:O	28:BZ:54:VAL:HG23	2.12	0.50
31:Bg:214:ALA:HB2	31:Bg:243:LEU:HD11	1.93	0.50
34:B5:1263:G:H2'	34:B5:1264:G:O4'	2.12	0.50
34:B5:1767:G:OP1	34:B5:1770:U:H4'	2.12	0.50
35:AA:37:ARG:NH2	38:A1:2526:C:OP1	2.31	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:819:U:H2'	38:A1:820:A:H8	1.77	0.50
41:AD:60:ILE:HB	41:AD:80:SER:HB2	1.93	0.50
72:Aj:39:TYR:CD1	72:Aj:40:PRO:HA	2.45	0.50
4:BE:199:GLU:HB2	4:BE:207:LEU:HB2	1.93	0.50
26:BT:134:ARG:NH1	34:B5:1360:A:O5'	2.37	0.50
33:BM:59:LEU:HB2	33:BM:123:VAL:HB	1.94	0.50
34:B5:12:U:H2'	34:B5:13:C:C6	2.47	0.50
34:B5:29:U:H2'	34:B5:30:G:C8	2.47	0.50
34:B5:1258:U:H2'	34:B5:1259:U:H6	1.76	0.50
34:B5:1373:C:H2'	34:B5:1374:C:H6	1.77	0.50
34:B5:1642:G:H5'	76:An:1:MET:HB2	1.94	0.50
37:AC:73:ARG:NH1	38:A1:2814:G:OP1	2.27	0.50
38:A1:1555:U:H5'	38:A1:1556:C:OP2	2.12	0.50
38:A1:2835:U:H2'	38:A1:2836:C:O2	2.11	0.50
46:AI:47:PRO:HD2	46:AI:141:LYS:HA	1.93	0.50
49:AM:70:PHE:HE2	49:AM:72:LEU:HD13	1.76	0.50
18:Be:31:LYS:HD3	34:B5:545:A:H2'	1.93	0.50
21:BK:32:HIS:HD2	21:BK:33:GLU:O	1.95	0.50
33:BM:135:MET:HA	33:BM:138:GLU:HG2	1.92	0.50
34:B5:65:A:H2	34:B5:84:A:H62	1.59	0.50
34:B5:333:A:H2'	34:B5:334:G:C8	2.46	0.50
34:B5:696:C:O2	34:B5:697:C:O2'	2.25	0.50
34:B5:1785:U:H2'	34:B5:1786:G:H8	1.77	0.50
38:A1:602:A:O2'	38:A1:603:A:OP1	2.30	0.50
38:A1:860:G:O2'	38:A1:895:A:H4'	2.11	0.50
41:AD:68:THR:OG1	41:AD:71:GLY:O	2.29	0.50
49:AM:103:ILE:O	49:AM:107:GLU:HG3	2.11	0.50
3:BC:82:ASN:HD22	3:BC:207:LEU:HD13	1.77	0.50
4:BE:19:LEU:HD13	34:B5:788:A:C4	2.47	0.50
5:BG:72:ARG:HB3	5:BG:98:ARG:HA	1.92	0.50
6:BH:104:ARG:NH1	34:B5:803:A:N3	2.59	0.50
21:BK:30:ALA:O	21:BK:31:LYS:HE2	2.11	0.50
22:BP:18:ARG:NH1	34:B5:1548:G:OP1	2.39	0.50
25:BS:143:ARG:NH2	34:B5:1462:G:N7	2.56	0.50
31:Bg:238:ASP:HB2	31:Bg:257:ALA:HB3	1.94	0.50
34:B5:472:U:H2'	34:B5:473:A:C8	2.46	0.50
34:B5:1258:U:H2'	34:B5:1259:U:C6	2.46	0.50
34:B5:1587:A:H2'	34:B5:1588:G:H8	1.76	0.50
38:A1:640:U:H2'	38:A1:641:C:C6	2.46	0.50
38:A1:928:C:H2'	38:A1:929:A:C8	2.46	0.50
38:A1:2767:U:H2'	38:A1:2768:U:H6	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:A3:45:A:H2'	39:A3:46:A:H8	1.77	0.50
51:AO:10[A]:ASP:HB2	51:AO:117[A]:ARG:HB3	1.93	0.50
75:Am:78:ILE:HG22	75:Am:83:LYS:HE2	1.93	0.50
75:Am:104:PRO:HG2	75:Am:107:ALA:HB2	1.94	0.50
1:BA:36:TYR:HH	1:BA:56:LYS:NZ	2.09	0.50
3:BC:87:GLN:OE1	34:B5:10:G:O2'	2.22	0.50
4:BE:3:ARG:HG2	34:B5:399:A:H4'	1.93	0.50
5:BG:1:MET:SD	5:BG:2:LYS:N	2.85	0.50
7:BI:64:ASN:ND2	34:B5:257:A:N3	2.60	0.50
21:BK:48:SER:HA	34:B5:1219:A:O2'	2.12	0.50
28:BZ:84:GLU:OE2	28:BZ:85:LYS:HE3	2.12	0.50
31:Bg:83:ALA:HB2	31:Bg:113:VAL:HB	1.94	0.50
31:Bg:181:TRP:CZ3	31:Bg:188:ILE:HB	2.46	0.50
34:B5:463:U:H2'	34:B5:464:A:C8	2.46	0.50
34:B5:1575:G7M:O5'	34:B5:1575:G7M:H8	2.12	0.50
34:B5:1609:U:H2'	34:B5:1610:G:O4'	2.12	0.50
38:A1:4:U:H2'	38:A1:5:G:C8	2.46	0.50
38:A1:40:A:OP1	79:A1:3401:SPD:N10	2.45	0.50
38:A1:970:A:H2'	38:A1:971:G:C8	2.47	0.50
38:A1:1953:G:N1	38:A1:2093:A:N6	2.58	0.50
38:A1:2801:A:O2'	38:A1:2802:A:H2'	2.12	0.50
38:A1:2882:U:H2'	38:A1:2883:U:C6	2.46	0.50
61:AY:70:ILE:HD13	61:AY:82:VAL:HG22	1.94	0.50
7:BI:140:GLU:HA	7:BI:143:TRP:NE1	2.26	0.50
20:BF:45:LYS:HB3	20:BF:46:TRP:CE3	2.46	0.50
21:BK:23:ALA:HA	21:BK:32:HIS:CE1	2.45	0.50
23:BQ:59:LYS:HD3	23:BQ:93:HIS:NE2	2.27	0.50
34:B5:1439:C:H2'	34:B5:1440:C:C6	2.47	0.50
38:A1:999:G:H2'	38:A1:1000:C:C6	2.47	0.50
38:A1:1577:G:O2'	38:A1:1578:C:H6	1.95	0.50
38:A1:2269:U:O2'	38:A1:2270:A:P	2.70	0.50
38:A1:3297:U:H2'	38:A1:3298:C:H6	1.77	0.50
42:AE:60:ASP:OD2	42:AE:78:ARG:NH1	2.45	0.50
49:AM:38:ILE:O	55:AS:95:ARG:NH2	2.35	0.50
1:BA:88:LYS:HD2	1:BA:201:LEU:HD12	1.94	0.49
8:BJ:134:ILE:HG23	8:BJ:156:ILE:HG23	1.94	0.49
13:BW:31:SER:OG	34:B5:636:A:H5''	2.12	0.49
13:BW:44:HIS:NE2	13:BW:112:ASP:OD2	2.36	0.49
26:BT:28:LEU:HD11	26:BT:108:LEU:HD22	1.94	0.49
27:BU:31:VAL:O	27:BU:35:GLU:HG2	2.12	0.49
34:B5:69:G:H2'	34:B5:70:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:108:A:H2'	34:B5:109:G:C8	2.46	0.49
34:B5:1142:A:H2'	34:B5:1143:A:H8	1.77	0.49
38:A1:8:C:H2'	38:A1:9:U:C6	2.47	0.49
38:A1:159:A:H2'	38:A1:160:G:H8	1.76	0.49
38:A1:787:G:H2'	38:A1:788:C:C6	2.47	0.49
38:A1:1480:G:O4'	38:A1:1483:G:N2	2.45	0.49
38:A1:2207:A:H8	38:A1:2207:A:OP2	1.95	0.49
38:A1:2407:C:H2'	38:A1:2408:U:C6	2.47	0.49
55:AS:9:VAL:HG22	55:AS:61:ILE:HD13	1.93	0.49
1:BA:193:GLN:OE1	1:BA:193:GLN:N	2.46	0.49
5:BG:53:SER:OG	34:B5:163:G:O3'	2.30	0.49
6:BH:16:LEU:O	6:BH:19:GLN:NE2	2.45	0.49
8:BJ:130:THR:OG1	34:B5:475:A:OP1	2.25	0.49
11:BO:92:LYS:HZ1	11:BO:122:PRO:HD2	1.77	0.49
25:BS:32:LEU:HB3	25:BS:38:VAL:HG11	1.94	0.49
26:BT:27:LYS:HE2	26:BT:111:ILE:HD11	1.94	0.49
30:Bd:8:PHE:HE1	34:B5:1450:U:H4'	1.77	0.49
31:Bg:16:HIS:HD1	31:Bg:37:SER:HG	1.59	0.49
34:B5:603:U:H2'	34:B5:604:A:C8	2.47	0.49
38:A1:1497:C:H2'	38:A1:1498:A:H8	1.75	0.49
38:A1:2255:A:N6	38:A1:2261:G:H22	2.10	0.49
38:A1:2747:A:H2'	38:A1:2748:A:C8	2.47	0.49
38:A1:2900:A:C8	38:A1:2901:G:C8	3.00	0.49
38:A1:3324:C:OP1	66:Ad:19:ARG:NH1	2.45	0.49
42:AE:70:LYS:HB3	42:AE:146:ILE:HD11	1.94	0.49
10:BN:31:GLU:OE1	10:BN:31:GLU:N	2.45	0.49
14:BX:103:LEU:HD22	14:BX:126:LYS:HD3	1.93	0.49
21:BK:14:TYR:OH	21:BK:34:GLU:OE1	2.30	0.49
21:BK:38:LYS:HG2	21:BK:41:TYR:CD2	2.46	0.49
24:BR:24:LEU:HB2	24:BR:58:MET:HE1	1.93	0.49
34:B5:107:C:H2'	34:B5:108:A:C8	2.47	0.49
34:B5:1484:G:H2'	34:B5:1485:C:H6	1.77	0.49
36:AB:123:TYR:CZ	36:AB:124:LYS:HG3	2.47	0.49
38:A1:36:C:H4'	38:A1:808:A:C2	2.48	0.49
38:A1:95:A:H5''	63:Aa:34:MET:HB3	1.94	0.49
38:A1:314:U:H2'	38:A1:315:C:C6	2.47	0.49
38:A1:874:U:OP2	38:A1:1907:C:O2'	2.28	0.49
38:A1:1688:U:H2'	38:A1:1689:U:C6	2.47	0.49
38:A1:2366:C:H2'	38:A1:2367:A:H8	1.77	0.49
52:AP:41:LEU:HD21	52:AP:99:ALA:HB2	1.93	0.49
71:Ai:59:ASP:OD1	71:Ai:63:ASN:ND2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Ao:4:VAL:O	77:Ao:94:GLY:N	2.44	0.49
1:BA:38:PHE:CD2	1:BA:39:ASN:HB2	2.47	0.49
5:BG:219:ARG:HH11	5:BG:220:LYS:NZ	2.10	0.49
14:BX:75:GLN:NE2	14:BX:76:LEU:O	2.45	0.49
19:BD:141:LYS:HA	19:BD:147:ALA:HA	1.94	0.49
26:BT:83:ALA:HB2	34:B5:1525:A:H4'	1.94	0.49
34:B5:1291:G:H22	34:B5:1324:G:N2	2.10	0.49
38:A1:1498:A:H2'	38:A1:1499:C:H6	1.78	0.49
38:A1:2208:A:O2'	38:A1:2209:U:O4'	2.30	0.49
38:A1:3341:U:H1'	38:A1:3355:U:C4	2.47	0.49
45:AH:163:GLN:O	45:AH:166:ARG:NE	2.44	0.49
71:Ai:5:THR:HG23	71:Ai:12:ASN:HB2	1.94	0.49
11:BO:31:THR:HG22	11:BO:38:THR:HA	1.94	0.49
19:BD:80:ALA:O	19:BD:83:THR:HG22	2.13	0.49
25:BS:15:LEU:O	25:BS:21:ASN:HA	2.12	0.49
29:Bc:18:ARG:HD2	34:B5:1616:G:H4'	1.95	0.49
31:Bg:34:LEU:HD11	31:Bg:42:LEU:HB3	1.93	0.49
32:Bf:106:TYR:HB2	33:BM:74:LEU:HD11	1.93	0.49
34:B5:30:G:H2'	34:B5:31:C:C6	2.47	0.49
34:B5:1647:U:H2'	34:B5:1648:A:C8	2.48	0.49
34:B5:1662:G:H2'	34:B5:1663:G:H8	1.77	0.49
36:AB:274:SER:O	36:AB:275:ARG:NH1	2.42	0.49
38:A1:2152:A:H2'	38:A1:2153:U:H6	1.76	0.49
41:AD:205:SER:HB3	41:AD:236:LEU:HD12	1.94	0.49
46:AI:174:THR:HG23	46:AI:176:LEU:H	1.77	0.49
50:AN:66:VAL:HG21	50:AN:98:LEU:HB3	1.94	0.49
4:BE:35:PRO:HD2	4:BE:83:PRO:HG2	1.95	0.49
5:BG:92:ARG:O	34:B5:405:C:O2'	2.30	0.49
9:BL:65:SER:OG	34:B5:114:C:O2'	2.20	0.49
13:BW:31:SER:H	13:BW:34:ILE:HD12	1.77	0.49
17:Bb:41:LEU:HD23	17:Bb:41:LEU:H	1.78	0.49
20:BF:84:LYS:HE3	20:BF:165:LEU:HD21	1.95	0.49
32:Bf:114:VAL:HG11	33:BM:78:LEU:HD12	1.94	0.49
34:B5:948:G:H2'	34:B5:949:C:C6	2.48	0.49
34:B5:986:G:H2'	34:B5:987:G:O4'	2.12	0.49
34:B5:1328:G:O3'	34:B5:1421:A:O2'	2.30	0.49
37:AC:141:ARG:NH1	38:A1:1385:C:OP1	2.29	0.49
38:A1:987:U:H2'	38:A1:988:U:C6	2.48	0.49
38:A1:2218:G:H2'	38:A1:2219:A:H8	1.76	0.49
38:A1:2406:C:H2'	38:A1:2407:C:H6	1.77	0.49
38:A1:2745:G:N2	38:A1:2748:A:OP2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:3034:C:C2	38:A1:3035:A:C8	3.00	0.49
66:Ad:55:LEU:HB2	66:Ad:95:PRO:HD3	1.94	0.49
73:Ak:15:THR:HG23	73:Ak:16:ARG:HG3	1.95	0.49
4:BE:196:VAL:HB	4:BE:209:HIS:HB2	1.94	0.49
8:BJ:103:ASP:O	8:BJ:107:ARG:HG2	2.13	0.49
10:BN:76:LYS:NZ	34:B5:813:U:OP2	2.42	0.49
25:BS:36:LYS:HG2	25:BS:105:VAL:HG11	1.95	0.49
31:Bg:81:LEU:HD22	31:Bg:113:VAL:HG21	1.95	0.49
34:B5:16:G:H2'	34:B5:17:C:C6	2.47	0.49
34:B5:1230:A:H61	34:B5:1255:G:H1'	1.77	0.49
38:A1:1941:C:H2'	38:A1:1942:U:C6	2.48	0.49
38:A1:3194:C:H2'	38:A1:3195:U:H2'	1.95	0.49
40:A4:143:U:OP1	50:AN:38:ARG:NH2	2.43	0.49
62:AZ:72:ILE:HD11	62:AZ:114:VAL:HG21	1.95	0.49
1:BA:106:SER:OG	1:BA:116:LYS:NZ	2.46	0.49
2:BB:222:LYS:HE3	38:A1:2545:C:C2	2.48	0.49
34:B5:75:U:H5	34:B5:80:A:H61	1.60	0.49
34:B5:416:A:H3'	34:B5:417:A:H8	1.78	0.49
34:B5:522:U:H2'	34:B5:523:G:O4'	2.13	0.49
34:B5:1366:U:H2'	34:B5:1367:G:H8	1.77	0.49
36:AB:139:GLN:HG2	36:AB:140:ASP:N	2.28	0.49
38:A1:627:U:H2'	38:A1:628:A:H8	1.76	0.49
38:A1:1246:G:H1	38:A1:1273:A:H5''	1.77	0.49
38:A1:1323:G:H4'	55:AS:2:ALA:HB2	1.94	0.49
38:A1:1620:U:H2'	38:A1:1621:A:C8	2.47	0.49
38:A1:1896:A:H61	38:A1:2339:C:N4	2.10	0.49
38:A1:3107:U:H2'	38:A1:3108:G:C8	2.47	0.49
39:A3:19:C:H2'	39:A3:20:A:C8	2.48	0.49
47:AJ:92:ARG:HH22	47:AJ:94:ARG:NH1	2.11	0.49
47:AJ:110:ILE:H	47:AJ:110:ILE:HD12	1.78	0.49
48:AL:3:ILE:HG21	63:Aa:45:MET:HE3	1.95	0.49
55:AS:10:ILE:HG13	55:AS:26:ARG:HB2	1.93	0.49
67:Ae:83:GLU:OE2	67:Ae:111:ARG:NE	2.45	0.49
14:BX:3:LYS:HG3	14:BX:7:ARG:NH2	2.27	0.49
24:BR:57:LEU:O	24:BR:61:ILE:HG23	2.13	0.49
32:Bf:133:ALA:N	32:Bf:140:TYR:O	2.46	0.49
34:B5:211:PSU:H3'	34:B5:212:U:H5''	1.94	0.49
34:B5:329:G:H2'	34:B5:330:G:C8	2.47	0.49
34:B5:415:C:O2'	34:B5:418:G:O6	2.23	0.49
34:B5:1056:U:H2'	34:B5:1057:U:O4'	2.12	0.49
35:AA:52:SER:HB3	35:AA:191:LEU:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:236:GLY:N	38:A1:2183:A:O2'	2.36	0.49
38:A1:129:U:H2'	38:A1:130:A:C8	2.48	0.49
38:A1:268:A:N1	38:A1:295:A:H5'	2.28	0.49
38:A1:792:G:H2'	38:A1:793:C:C6	2.47	0.49
38:A1:1460:A:H2'	38:A1:1461:A:C8	2.47	0.49
38:A1:1497:C:O2'	38:A1:1602:A:N3	2.42	0.49
38:A1:3150:A:H2'	38:A1:3151:U:O4'	2.12	0.49
44:AG:75:ILE:HD11	50:AN:18:VAL:HG23	1.95	0.49
62:AZ:100:THR:HA	62:AZ:106:GLN:HG3	1.95	0.49
1:BA:30:GLN:NE2	1:BA:151:SER:O	2.46	0.49
2:BB:64:ARG:CZ	11:BO:36:LYS:HD3	2.43	0.49
7:BI:114:GLU:HA	7:BI:118:GLY:HA2	1.95	0.49
8:BJ:133:HIS:NE2	34:B5:513:U:H5'	2.28	0.49
19:BD:40:ARG:HH22	27:BU:108:ILE:HB	1.77	0.49
20:BF:76:ARG:HH11	23:BQ:122:ARG:HE	1.61	0.49
23:BQ:16:ALA:HB2	23:BQ:72:GLY:HA3	1.94	0.49
23:BQ:41:PRO:HB2	23:BQ:43:ILE:HG22	1.94	0.49
34:B5:1215:C:H2'	34:B5:1216:C:H6	1.78	0.49
38:A1:1733:G:H2'	38:A1:1734:G:H8	1.78	0.49
38:A1:1783:U:H2'	38:A1:1784:G:C8	2.47	0.49
38:A1:1805:C:H2'	38:A1:1806:A:H8	1.78	0.49
38:A1:1874:A:OP2	54:AR:20:ARG:NH1	2.39	0.49
38:A1:2526:C:H2'	38:A1:2527:G:H8	1.77	0.49
38:A1:3089:C:H2'	38:A1:3090:U:O4'	2.13	0.49
38:A1:3165:A:H2'	38:A1:3166:C:C6	2.48	0.49
39:A3:15:C:H2'	39:A3:16:U:C6	2.48	0.49
73:AK:12:LEU:O	73:AK:15:THR:HG22	2.11	0.49
1:BA:7:PHE:HA	1:BA:191:ARG:HH21	1.77	0.48
8:BJ:58:ASP:O	8:BJ:61:THR:HG22	2.13	0.48
9:BL:101:GLU:OE2	9:BL:103:ARG:NE	2.42	0.48
23:BQ:50:GLU:OE1	23:BQ:82:ARG:NH2	2.44	0.48
24:BR:76:GLU:HA	24:BR:79:GLU:HG3	1.94	0.48
34:B5:628:G:H21	34:B5:971:A:H62	1.60	0.48
34:B5:699:U:H2'	34:B5:700:C:C5	2.48	0.48
34:B5:922:G:H2'	34:B5:923:A:H8	1.78	0.48
34:B5:1678:A:H2'	34:B5:1679:G:C8	2.48	0.48
38:A1:266:A:H2'	71:AI:30:LYS:HE3	1.95	0.48
38:A1:1143:A:H5'	38:A1:1368:U:H1'	1.95	0.48
38:A1:2374:C:OP1	38:A1:2823:G:O2'	2.22	0.48
38:A1:2611:U:H2'	38:A1:2612:U:H6	1.77	0.48
38:A1:2828:G:OP2	46:AI:7:ARG:NH2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2916:U:H5	38:A1:2935:U:HO2'	1.61	0.48
38:A1:3116:G:OP1	38:A1:3116:G:N2	2.45	0.48
48:AL:76:THR:HG22	48:AL:101:ARG:HB3	1.95	0.48
4:BE:117:GLU:O	4:BE:120:SER:OG	2.30	0.48
7:BI:141:ARG:NH2	34:B5:196:G:N7	2.60	0.48
15:BY:38:ASP:O	15:BY:42:GLU:OE1	2.31	0.48
18:Be:14:VAL:HA	18:Be:17:GLN:HE21	1.77	0.48
19:BD:68:GLU:HG2	19:BD:69:LEU:HD12	1.95	0.48
20:BF:146:THR:HB	20:BF:157:ARG:HB3	1.94	0.48
23:BQ:37:THR:O	23:BQ:45:ARG:NH1	2.46	0.48
24:BR:71:PHE:CE1	24:BR:73:LEU:HB3	2.48	0.48
26:BT:113:ILE:HD12	26:BT:128:GLY:HA2	1.95	0.48
34:B5:15:U:H2'	34:B5:16:G:O4'	2.13	0.48
34:B5:490:C:H41	34:B5:492:A:H4'	1.78	0.48
34:B5:1078:C:H2'	34:B5:1079:U:C6	2.48	0.48
34:B5:1260:U:H2'	34:B5:1261:G:C8	2.44	0.48
38:A1:86:G:O2'	38:A1:98:G:O6	2.27	0.48
38:A1:640:U:OP1	63:Aa:21:ARG:NH2	2.42	0.48
38:A1:887:G:H2'	38:A1:888:A:C8	2.47	0.48
38:A1:1211:U:H2'	38:A1:1212:A:H8	1.78	0.48
38:A1:2423:U:H2'	38:A1:2424:A:C8	2.48	0.48
78:Ap:29:LEU:HD23	78:Ap:69:TYR:CD2	2.48	0.48
5:BG:121:LEU:HD23	5:BG:124:LEU:HD12	1.95	0.48
9:BL:80:MET:HE3	9:BL:83:THR:HG23	1.96	0.48
11:BO:122:PRO:HB3	34:B5:887:A:C1'	2.43	0.48
34:B5:263:C:H2'	34:B5:264:G:C8	2.48	0.48
34:B5:1391:A:H2'	34:B5:1392:U:C6	2.48	0.48
34:B5:1591:C:H2'	34:B5:1592:A:H8	1.77	0.48
38:A1:3041:U:H2'	38:A1:3042:U:C6	2.48	0.48
40:A4:39:G:O2'	40:A4:105:A:N1	2.43	0.48
62:AZ:54:THR:HG22	62:AZ:57:HIS:CE1	2.48	0.48
73:Ak:32:ASN:HD21	73:Ak:36:LYS:HG2	1.79	0.48
1:BA:11:PRO:O	1:BA:15:GLN:HG3	2.13	0.48
1:BA:16:LEU:HA	1:BA:19:ALA:HB3	1.94	0.48
2:BB:181:LEU:HD12	2:BB:184:LEU:HD23	1.94	0.48
7:BI:61:GLU:OE1	7:BI:61:GLU:N	2.46	0.48
24:BR:10:LYS:HD3	24:BR:53:TYR:HE2	1.78	0.48
25:BS:17:LEU:O	25:BS:20:THR:OG1	2.22	0.48
27:BU:57:ARG:HD2	34:B5:1382:A:N3	2.29	0.48
34:B5:1524:A:N1	34:B5:1607:G:N2	2.62	0.48
34:B5:1735:U:OP1	58:AV:32:ARG:NH1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:126:LYS:NZ	38:A1:3294:A:OP2	2.46	0.48
36:AB:346:THR:HA	36:AB:351:LEU:HD22	1.96	0.48
37:AC:58:HIS:NE2	37:AC:98:ARG:HD3	2.28	0.48
38:A1:1119:C:H2'	38:A1:1120:A:C8	2.48	0.48
38:A1:1724:U:O4	54:AR:125:LYS:NZ	2.44	0.48
38:A1:3217:C:H2'	52:AP:182:ILE:HD11	1.95	0.48
38:A1:3320:A:H2'	38:A1:3321:C:C6	2.49	0.48
45:AH:13:PRO:HG3	45:AH:83:THR:HG21	1.95	0.48
52:AP:19:GLY:HA3	52:AP:22:LEU:HD11	1.95	0.48
68:Af:18:ARG:HA	68:Af:23:ASN:HA	1.94	0.48
5:BG:154:ARG:HB3	34:B5:78:A:H5'	1.95	0.48
7:BI:48:THR:OG1	7:BI:52:ASN:O	2.30	0.48
34:B5:446:A:N6	34:B5:461:G:H21	2.12	0.48
34:B5:954:G:H2'	34:B5:955:A:H8	1.77	0.48
34:B5:1144:U:H2'	34:B5:1145:U:C6	2.48	0.48
34:B5:1525:A:H2'	34:B5:1526:A:C8	2.49	0.48
38:A1:2366:C:H2'	38:A1:2367:A:C8	2.48	0.48
38:A1:2549:G:O2'	44:AG:38:GLN:NE2	2.47	0.48
38:A1:3162:C:H2'	38:A1:3163:A:H8	1.79	0.48
38:A1:3231:U:H2'	38:A1:3232:G:C8	2.47	0.48
58:AV:114:ILE:HB	58:AV:133:SER:HA	1.95	0.48
61:AY:74:TYR:CE2	61:AY:77:LYS:HG2	2.48	0.48
62:AZ:41:ALA:HB2	62:AZ:77:TYR:HE1	1.78	0.48
7:BI:39:GLY:HA2	7:BI:61:GLU:HB3	1.96	0.48
23:BQ:55:VAL:HG21	23:BQ:105:LEU:HG	1.96	0.48
31:Bg:9:LEU:HD12	31:Bg:313:TRP:NE1	2.29	0.48
31:Bg:240:VAL:HG12	31:Bg:256:THR:HA	1.96	0.48
32:Bf:105:TYR:HE2	33:BM:46:ARG:HB2	1.78	0.48
34:B5:227:U:O2	34:B5:834:G:N2	2.46	0.48
34:B5:603:U:H2'	34:B5:604:A:H8	1.79	0.48
34:B5:774:A:N1	34:B5:786:C:N3	2.60	0.48
38:A1:275:U:H2'	38:A1:276:U:C6	2.48	0.48
38:A1:945:C:H2'	38:A1:946:U:C6	2.48	0.48
38:A1:1694:U:H5	38:A1:1752:A:N1	2.11	0.48
38:A1:1791:C:H2'	38:A1:1792:C:C6	2.48	0.48
38:A1:2100:A:H2'	38:A1:2101:C:O4'	2.14	0.48
38:A1:3169:U:H2'	38:A1:3170:A:C8	2.49	0.48
3:BC:140:ARG:HB3	3:BC:221:THR:HB	1.95	0.48
4:BE:252:ARG:HE	4:BE:256:ARG:NH2	2.12	0.48
5:BG:52:ILE:HD13	5:BG:111:LEU:HD21	1.96	0.48
5:BG:133:LEU:HB2	34:B5:66:U:C4	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:104:ILE:HG13	7:BI:105:ASP:N	2.26	0.48
8:BJ:77:ILE:HD13	8:BJ:80:LEU:HD21	1.96	0.48
8:BJ:87:SER:H	8:BJ:90:LYS:NZ	2.11	0.48
34:B5:119:A:H1'	34:B5:397:A:C5	2.49	0.48
34:B5:126:A:N6	34:B5:263:C:HO2'	2.09	0.48
34:B5:609:U:H4'	34:B5:610:G:H5'	1.96	0.48
34:B5:848:C:H2'	34:B5:849:C:H5''	1.95	0.48
34:B5:968:U:H2'	34:B5:969:C:O4'	2.14	0.48
34:B5:1159:C:H41	34:B5:1285:U:H5''	1.78	0.48
34:B5:1290:PSU:H2'	34:B5:1291:G:C8	2.48	0.48
34:B5:1550:A:H2'	34:B5:1551:U:C6	2.49	0.48
38:A1:700:C:H2'	38:A1:701:G:H8	1.79	0.48
38:A1:2218:G:H2'	38:A1:2219:A:C8	2.49	0.48
38:A1:2223:A:H2'	38:A1:2224:A:C8	2.48	0.48
38:A1:2768:U:H2'	38:A1:2769:A:C8	2.49	0.48
4:BE:182:TYR:HE1	4:BE:190:GLY:HA2	1.78	0.48
6:BH:67:LEU:O	6:BH:71:HIS:CD2	2.66	0.48
9:BL:8:GLN:NE2	9:BL:14:GLN:O	2.45	0.48
15:BY:132:ARG:HH22	34:B5:155:U:H5	1.62	0.48
17:Bb:15:GLU:O	17:Bb:29:ARG:NH2	2.47	0.48
31:Bg:54:PHE:CE2	31:Bg:312:VAL:HG11	2.49	0.48
37:AC:303:GLY:H	38:A1:1347:U:H5''	1.79	0.48
38:A1:651:G:O2'	38:A1:1435:A:OP1	2.32	0.48
39:A3:90:U:H2'	39:A3:91:G:O4'	2.14	0.48
70:Ah:31:LEU:HB3	70:Ah:44:ILE:HG22	1.94	0.48
10:BN:13:SER:HB2	17:Bb:21:LEU:HD11	1.96	0.48
15:BY:105:ARG:HB3	34:B5:443:C:OP2	2.13	0.48
20:BF:53:VAL:HG22	20:BF:134:VAL:HG21	1.95	0.48
24:BR:5:ARG:N	34:B5:1402:G:OP1	2.40	0.48
25:BS:126:ARG:HD3	25:BS:132:ARG:O	2.14	0.48
34:B5:909:U:H2'	34:B5:910:C:C6	2.48	0.48
38:A1:29:C:H4'	38:A1:62:A:H4'	1.96	0.48
38:A1:1196:C:OP2	38:A1:1309:U:O2'	2.23	0.48
38:A1:1444:G:H2'	38:A1:1445:U:O4'	2.14	0.48
38:A1:2529:A:OP1	44:AG:248:LYS:NZ	2.43	0.48
38:A1:3094:A:H2'	38:A1:3095:U:C6	2.48	0.48
51:AO:19[A]:LEU:O	51:AO:23[A]:VAL:HG22	2.13	0.48
62:AZ:17:ARG:HD3	69:Ag:73:SER:HB3	1.96	0.48
1:BA:88:LYS:O	1:BA:92:HIS:ND1	2.46	0.48
8:BJ:5:PRO:HG3	34:B5:380:U:C2	2.49	0.48
8:BJ:109:LEU:HB2	8:BJ:146:PHE:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BW:101:TYR:HA	13:BW:113:HIS:CE1	2.49	0.48
14:BX:44:GLY:H	14:BX:78:LYS:NZ	2.12	0.48
16:Ba:15:ARG:HD2	16:Ba:18:VAL:HG22	1.95	0.48
24:BR:110:VAL:HG21	24:BR:117:LEU:HD12	1.94	0.48
31:Bg:90:ARG:HH22	34:B5:1341:A:H4'	1.79	0.48
34:B5:116:U:H2'	34:B5:117:U:C6	2.48	0.48
34:B5:175:G:H1'	34:B5:266:A:N6	2.29	0.48
35:AA:2:GLY:HA2	38:A1:2608:G:OP1	2.14	0.48
38:A1:2185:G:O2'	38:A1:2314:PSU:OP2	2.28	0.48
38:A1:2696:A:H2'	38:A1:2697:A:C8	2.49	0.48
40:A4:78:G:H2'	40:A4:79:A:H8	1.79	0.48
66:Ad:96:VAL:HG12	66:Ad:98:VAL:HG13	1.94	0.48
1:BA:52:LYS:HE3	12:BV:82:VAL:HA	1.96	0.47
1:BA:74:VAL:HG23	1:BA:118:PRO:HB3	1.94	0.47
2:BB:67:GLU:OE2	2:BB:83:LYS:HB2	2.14	0.47
2:BB:109:LYS:HG3	2:BB:113:MET:HE2	1.96	0.47
6:BH:49:ILE:HD11	6:BH:172:VAL:HG12	1.96	0.47
7:BI:165:LEU:HD23	7:BI:183:ILE:HG21	1.95	0.47
12:BV:5:LYS:HE2	12:BV:7:GLN:HE22	1.79	0.47
12:BV:32:VAL:HG22	12:BV:60:ARG:HD2	1.96	0.47
24:BR:9:VAL:HG23	24:BR:50:ILE:HA	1.96	0.47
30:Bd:40:ARG:HD3	34:B5:1199:G:C5	2.49	0.47
31:Bg:266:ASP:HB2	31:Bg:267:PRO:HD3	1.96	0.47
33:BM:61:VAL:HG22	33:BM:89:ILE:HB	1.95	0.47
34:B5:122:U:H2'	34:B5:123:G:H8	1.79	0.47
34:B5:409:C:H2'	34:B5:410:A:C8	2.45	0.47
34:B5:412:A:H2'	34:B5:413:U:O2	2.14	0.47
34:B5:868:G:H1	34:B5:960:U:H3	1.61	0.47
34:B5:922:G:H2'	34:B5:923:A:C8	2.49	0.47
34:B5:1241:G:H2'	34:B5:1242:A:O4'	2.14	0.47
35:AA:140:ASN:OD1	35:AA:147:ARG:NH1	2.47	0.47
36:AB:83:PRO:O	36:AB:165:GLN:NE2	2.47	0.47
38:A1:76:G:H22	38:A1:315:C:H5'	1.77	0.47
38:A1:2986:U:H2'	38:A1:2987:A:H8	1.79	0.47
41:AD:108:ARG:NE	41:AD:253:PHE:HB2	2.29	0.47
42:AE:51:ARG:O	42:AE:72:ASN:ND2	2.47	0.47
60:AX:108:LEU:HD23	60:AX:125:ARG:HD3	1.96	0.47
2:BB:153:HIS:NE2	34:B5:1045:C:OP1	2.30	0.47
5:BG:133:LEU:HD11	34:B5:167:U:H1'	1.96	0.47
6:BH:76:LYS:O	6:BH:79:ARG:HG2	2.14	0.47
7:BI:107:THR:HB	7:BI:108:PRO:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:153:GLU:HG2	7:BI:156:VAL:HG22	1.95	0.47
9:BL:55:ASP:OD2	9:BL:58:CYS:HB2	2.14	0.47
10:BN:61:THR:HB	34:B5:959:U:C6	2.49	0.47
10:BN:99:ARG:NE	10:BN:143:SER:OG	2.47	0.47
18:Be:26:LYS:HE2	34:B5:587:C:H5''	1.96	0.47
20:BF:97:LEU:O	20:BF:103:ASN:ND2	2.47	0.47
20:BF:120:ILE:HA	20:BF:123:VAL:HG22	1.97	0.47
27:BU:51:VAL:O	27:BU:52:LYS:NZ	2.45	0.47
34:B5:556:A:N3	34:B5:590:C:H1'	2.29	0.47
34:B5:968:U:OP1	34:B5:1033:C:O2'	2.31	0.47
34:B5:1580:C:H2'	34:B5:1581:C:H6	1.79	0.47
37:AC:23:PRO:HD2	37:AC:26:PHE:CD2	2.49	0.47
38:A1:676:G:H5''	53:AQ:107:THR:HB	1.96	0.47
38:A1:723:U:O2'	64:Ab:29:TYR:OH	2.22	0.47
38:A1:796:U:H2'	38:A1:797:U:C6	2.49	0.47
38:A1:1211:U:H2'	38:A1:1212:A:C8	2.49	0.47
38:A1:2575:G:H2'	38:A1:2576:G:H8	1.79	0.47
38:A1:3000:A:H2'	38:A1:3001:C:C6	2.49	0.47
38:A1:3047:U:O2'	38:A1:3048:A:H5'	2.13	0.47
51:AO:120[A]:VAL:HG23	51:AO:123[A]:ALA:HB3	1.97	0.47
66:Ad:73:LEU:HD12	66:Ad:93:VAL:CG1	2.44	0.47
73:Ak:16:ARG:NH1	73:Ak:16:ARG:HB2	2.29	0.47
1:BA:66:ALA:HB2	12:BV:37:ALA:HB2	1.95	0.47
3:BC:88:LYS:HD3	3:BC:95:ARG:HH21	1.79	0.47
3:BC:230:TRP:CD2	13:BW:68:ARG:HD2	2.49	0.47
7:BI:194:ARG:HG2	7:BI:199:LYS:HZ1	1.79	0.47
12:BV:4:ASP:N	12:BV:4:ASP:OD1	2.47	0.47
15:BY:60:PHE:H	15:BY:71:GLY:HA3	1.78	0.47
17:Bb:11:THR:HG22	17:Bb:13:ALA:H	1.79	0.47
34:B5:1063:U:C2	34:B5:1064:G:C8	3.02	0.47
35:AA:77:ILE:HD11	35:AA:128:ARG:HE	1.78	0.47
36:AB:48:GLY:HA3	36:AB:81:THR:HG22	1.97	0.47
38:A1:855:U:H2'	38:A1:856:G:C8	2.49	0.47
38:A1:2218:G:OP1	71:Ai:68:ARG:NH2	2.47	0.47
38:A1:2677:G:N3	38:A1:2677:G:H2'	2.30	0.47
40:A4:149:A:H2'	40:A4:150:G:C8	2.49	0.47
44:AG:75:ILE:HG22	44:AG:76:ALA:H	1.79	0.47
67:Ae:3:SER:OG	67:Ae:4:LEU:N	2.46	0.47
7:BI:67:TRP:HE3	7:BI:72:ILE:HD11	1.80	0.47
13:BW:57:ARG:HB3	34:B5:863:A:H4'	1.96	0.47
16:Ba:10:ARG:HH12	34:B5:1790:A:P	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:53:THR:HG23	19:BD:54:ARG:HG3	1.96	0.47
24:BR:10:LYS:O	24:BR:14:LYS:HG2	2.14	0.47
34:B5:947:U:H2'	34:B5:948:G:C8	2.48	0.47
34:B5:1213:G:H1	34:B5:1450:U:H5	1.62	0.47
34:B5:1439:C:H2'	34:B5:1440:C:H6	1.79	0.47
34:B5:1471:A:H2'	34:B5:1471:A:N3	2.29	0.47
36:AB:92:TYR:HB3	36:AB:99:LEU:HG	1.96	0.47
38:A1:170:G:H5'	70:Ah:109:ILE:HD12	1.95	0.47
38:A1:221:A:O2'	38:A1:223:U:OP2	2.32	0.47
38:A1:1167:U:O2'	43:AF:210:PRO:O	2.32	0.47
38:A1:2148:U:H2'	38:A1:2149:A:C8	2.50	0.47
38:A1:2252:A:H61	38:A1:2265:C:H42	1.62	0.47
38:A1:2656:A:C5	38:A1:2658:G:C8	3.03	0.47
38:A1:2881:C:H2'	38:A1:2882:U:H6	1.78	0.47
62:AZ:3:LYS:NZ	65:Ac:36:GLN:O	2.39	0.47
62:AZ:89:VAL:HG12	62:AZ:93:LYS:HB3	1.97	0.47
3:BC:78:ASP:OD2	3:BC:129:ILE:HG12	2.15	0.47
3:BC:194:GLU:OE1	3:BC:194:GLU:N	2.47	0.47
4:BE:98:ASN:ND2	4:BE:116:ASP:OD1	2.48	0.47
8:BJ:132:ARG:HH21	15:BY:65:GLY:HA2	1.78	0.47
14:BX:97:ASP:HB2	14:BX:100:ASP:OD2	2.14	0.47
25:BS:68:ARG:O	25:BS:72:ILE:HG13	2.15	0.47
28:BZ:74:SER:O	28:BZ:78:ILE:HG12	2.14	0.47
34:B5:461:G:H2'	34:B5:462:G:C8	2.49	0.47
35:AA:20:THR:HA	35:AA:23:ARG:HG3	1.96	0.47
35:AA:241:ARG:NH1	38:A1:2155:G:OP1	2.48	0.47
36:AB:259:HIS:CE1	38:A1:2366:C:H5'	2.49	0.47
37:AC:4:PRO:HD2	37:AC:22:LEU:HB2	1.96	0.47
38:A1:975:C:O2'	53:AQ:144:ARG:NH1	2.47	0.47
38:A1:1203:A:N3	38:A1:2855:U:O2'	2.36	0.47
38:A1:1324:U:OP1	55:AS:1:MET:N	2.40	0.47
38:A1:2344:U:H2'	38:A1:2345:A:C8	2.50	0.47
38:A1:2746:A:H5'	41:AD:178:ASN:HD21	1.78	0.47
42:AE:139:LYS:O	42:AE:143:LYS:HG2	2.14	0.47
45:AH:21:LYS:CG	45:AH:22:SER:H	2.28	0.47
49:AM:13:ARG:NH1	49:AM:65:LEU:O	2.47	0.47
54:AR:180:LYS:HA	54:AR:184:LEU:HB3	1.96	0.47
55:AS:90:MET:SD	55:AS:110:MET:HE1	2.55	0.47
62:AZ:15:ARG:HH22	69:Ag:83:ASN:ND2	2.12	0.47
70:Ah:66:VAL:HG13	70:Ah:80:LEU:HD11	1.95	0.47
2:BB:28:GLU:OE1	2:BB:28:GLU:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BC:81:MET:HE1	3:BC:183:ALA:HA	1.96	0.47
4:BE:11:ARG:H	4:BE:27:TYR:HA	1.79	0.47
4:BE:201:HIS:ND1	4:BE:204:GLY:O	2.44	0.47
6:BH:64:VAL:HG11	34:B5:856:A:N3	2.29	0.47
7:BI:193:LEU:HA	7:BI:197:THR:OG1	2.15	0.47
11:BO:42:VAL:HG22	11:BO:67:VAL:HG23	1.95	0.47
19:BD:22:ASN:O	19:BD:26:THR:OG1	2.32	0.47
24:BR:5:ARG:HB3	24:BR:9:VAL:HG11	1.96	0.47
26:BT:45:MET:SD	34:B5:1477:G:H5'	2.54	0.47
26:BT:104:VAL:O	26:BT:108:LEU:HD23	2.15	0.47
31:Bg:38:ARG:HD3	31:Bg:67:ILE:HG23	1.94	0.47
34:B5:78:A:H2'	34:B5:79:C:C6	2.49	0.47
34:B5:1011:G:H2'	34:B5:1012:U:C5	2.50	0.47
34:B5:1236:A:O2'	34:B5:1237:G:OP1	2.33	0.47
38:A1:82:C:H4'	50:AN:204:LYS:HE3	1.97	0.47
38:A1:952:A:N3	38:A1:1114:U:O2'	2.46	0.47
38:A1:1256:G:H2'	38:A1:1257:C:C6	2.50	0.47
38:A1:1622:U:H2'	38:A1:1623:G:C8	2.49	0.47
38:A1:3371:G:H2'	38:A1:3372:A:H8	1.79	0.47
51:AO:61[A]:ALA:HA	51:AO:70[A]:PRO:HD2	1.96	0.47
52:AP:50:GLN:HB3	52:AP:55:GLN:HB2	1.97	0.47
3:BC:239:PRO:HA	3:BC:242:ILE:HG12	1.96	0.47
4:BE:251:GLU:OE1	4:BE:254:ARG:NH1	2.48	0.47
5:BG:65:GLN:HG3	34:B5:1681:A:H8	1.79	0.47
5:BG:68:LEU:HD12	5:BG:68:LEU:O	2.14	0.47
8:BJ:6:ARG:NH1	34:B5:38:C:O3'	2.48	0.47
10:BN:20:ARG:O	10:BN:65:VAL:HG13	2.15	0.47
12:BV:83:TRP:CH2	12:BV:85:TYR:HD1	2.29	0.47
20:BF:143:ARG:HD3	20:BF:143:ARG:H	1.80	0.47
23:BQ:28:LEU:HG	23:BQ:30:LYS:HG2	1.96	0.47
24:BR:34:LEU:O	24:BR:38:ILE:HG12	2.14	0.47
25:BS:143:ARG:HB2	25:BS:144:ARG:NH1	2.30	0.47
27:BU:105:GLN:NE2	27:BU:106:ILE:HG23	2.30	0.47
28:BZ:55:PRO:O	28:BZ:56:THR:OG1	2.28	0.47
29:Bc:16:LEU:HD12	29:Bc:27:GLN:HB3	1.97	0.47
34:B5:751:G:H2'	34:B5:752:A:C8	2.50	0.47
34:B5:821:U:HO2'	34:B5:822:U:P	2.38	0.47
34:B5:994:G:H2'	34:B5:995:A:H8	1.79	0.47
34:B5:1317:C:H2'	34:B5:1318:G:O4'	2.13	0.47
34:B5:1487:A:H2'	34:B5:1488:G:C8	2.49	0.47
34:B5:1515:A:H4'	34:B5:1517:U:H5	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1584:G:O2'	34:B5:1610:G:O6	2.28	0.47
34:B5:1624:C:H2'	34:B5:1625:C:C6	2.49	0.47
34:B5:1708:U:H2'	34:B5:1709:C:H2'	1.97	0.47
35:AA:227:ARG:HG2	35:AA:239:ALA:HB2	1.96	0.47
38:A1:589:A:H1'	38:A1:1337:A:H5''	1.97	0.47
38:A1:1132:C:H2'	38:A1:1133:A:H8	1.80	0.47
38:A1:1220:U:H4'	38:A1:1222:G:O2'	2.13	0.47
38:A1:1241:U:O2'	38:A1:1243:G:OP2	2.32	0.47
38:A1:1282:G:H5'	38:A1:1282:G:N3	2.29	0.47
38:A1:1597:C:H2'	38:A1:1598:G:C8	2.49	0.47
38:A1:2196:C:O2'	38:A1:2270:A:N3	2.42	0.47
38:A1:2232:A:H2'	38:A1:2233:A:C8	2.49	0.47
38:A1:2433:U:H1'	50:AN:125:SER:HB2	1.96	0.47
38:A1:2441:A:N6	38:A1:2507:C:O2	2.48	0.47
38:A1:3157:U:H4'	38:A1:3158:G:H8	1.80	0.47
38:A1:3359:A:H2'	38:A1:3360:C:C6	2.50	0.47
40:A4:79:A:H2'	40:A4:80:A:C8	2.50	0.47
41:AD:83:LEU:HB3	41:AD:88:ILE:HB	1.96	0.47
42:AE:146:ILE:HA	42:AE:149:ILE:HG12	1.97	0.47
45:AH:104:VAL:HG13	45:AH:113:GLU:CD	2.40	0.47
48:AL:3:ILE:HG21	63:Aa:45:MET:CE	2.45	0.47
52:AP:125:GLN:HB2	52:AP:141:SER:HB2	1.96	0.47
54:AR:109:TYR:HB3	54:AR:115:ILE:HG12	1.96	0.47
62:AZ:9:LYS:HB3	62:AZ:25:ILE:HD13	1.96	0.47
67:Ae:3:SER:HB2	67:Ae:71:HIS:CD2	2.49	0.47
2:BB:108:ASP:OD2	16:Ba:65:PRO:HB3	2.15	0.47
8:BJ:89:ASP:O	8:BJ:90:LYS:HG2	2.14	0.47
11:BO:105:LEU:HD11	11:BO:110:LEU:HD23	1.97	0.47
34:B5:447:U:H2'	34:B5:448:C:O4'	2.14	0.47
34:B5:564:G:H1	34:B5:580:A:P	2.37	0.47
34:B5:1180:C:H1'	34:B5:1460:A:H61	1.80	0.47
35:AA:181:LYS:HB2	38:A1:860:G:C5	2.49	0.47
36:AB:10:ARG:NH1	36:AB:11:HIS:O	2.47	0.47
38:A1:77:A:H5'	48:AL:100:ARG:NH1	2.30	0.47
38:A1:195:U:H2'	38:A1:196:G:O4'	2.15	0.47
38:A1:748:U:H2'	38:A1:749:C:C6	2.49	0.47
38:A1:3295:A:H2'	38:A1:3296:A:H8	1.78	0.47
38:A1:3332:U:H2'	38:A1:3333:G:O4'	2.14	0.47
41:AD:45:ASN:OD1	56:AT:33:VAL:HG21	2.15	0.47
46:AI:72:ALA:O	46:AI:76:MET:HG2	2.15	0.47
51:AO:7[A]:VAL:HB	51:AO:33[A]:ILE:HD13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AU:33:TYR:HA	57:AU:83:TYR:CE1	2.49	0.47
66:Ad:73:LEU:HD12	66:Ad:93:VAL:HG12	1.97	0.47
67:Ae:79:VAL:O	67:Ae:83:GLU:HG2	2.15	0.47
5:BG:21:GLU:OE1	5:BG:24:ILE:HD13	2.14	0.47
13:BW:37:PHE:HD1	13:BW:41:MET:HE2	1.80	0.47
13:BW:66:ASN:ND2	13:BW:68:ARG:HE	2.13	0.47
13:BW:94:LEU:HD12	13:BW:100:GLY:HA3	1.97	0.47
33:BM:133:LEU:HD23	33:BM:133:LEU:H	1.79	0.47
34:B5:1639:C:H2'	34:B5:1640:C:O4'	2.15	0.47
37:AC:265:GLU:OE2	37:AC:266:THR:HG23	2.15	0.47
38:A1:872:U:H2'	38:A1:873:C:C6	2.49	0.47
38:A1:1525:G:H5'	38:A1:1830:G:OP2	2.15	0.47
38:A1:1579:C:H2'	38:A1:1580:A:O4'	2.15	0.47
38:A1:2270:A:OP1	38:A1:2270:A:H8	1.98	0.47
38:A1:3013:U:H2'	38:A1:3014:U:C6	2.50	0.47
38:A1:3177:G:O2'	38:A1:3179:U:OP1	2.26	0.47
43:AF:151:ARG:HE	43:AF:244:ASN:HB2	1.79	0.47
44:AG:70:LYS:HB3	44:AG:70:LYS:HE2	1.81	0.47
70:Ah:77:PRO:HD2	70:Ah:80:LEU:HD12	1.97	0.47
71:Ai:27:SER:C	71:Ai:29:LYS:H	2.23	0.47
2:BB:85:LYS:HB3	2:BB:101:HIS:HB3	1.96	0.47
6:BH:27:LEU:CD2	6:BH:38:LEU:HD12	2.45	0.47
7:BI:37:LYS:C	7:BI:59:ARG:HA	2.40	0.47
8:BJ:141:VAL:HG22	34:B5:767:U:H6	1.79	0.47
8:BJ:143:ILE:HG13	34:B5:768:C:C4	2.50	0.47
17:Bb:6:ASP:OD2	17:Bb:9:HIS:N	2.44	0.47
19:BD:94:ARG:HE	19:BD:100:ALA:HB1	1.80	0.47
34:B5:510:G:H2'	34:B5:511:A:O4'	2.15	0.47
34:B5:817:A:H61	34:B5:855:A:N6	2.13	0.47
37:AC:130:ALA:HA	37:AC:148:ILE:HG22	1.97	0.47
38:A1:411:U:H2'	38:A1:412:G:H8	1.80	0.47
38:A1:571:U:H2'	38:A1:572:A:H8	1.80	0.47
38:A1:1289:G:H2'	38:A1:1290:A:H8	1.80	0.47
38:A1:2129:PSU:H2'	38:A1:2130:G:C8	2.50	0.47
38:A1:3358:U:H2'	38:A1:3359:A:C8	2.50	0.47
49:AM:122:VAL:O	49:AM:126:GLN:HG2	2.15	0.47
2:BB:82:ARG:HE	2:BB:103:MET:HE1	1.81	0.46
3:BC:59:HIS:CD2	3:BC:238:SER:HA	2.50	0.46
6:BH:17:GLU:HB2	6:BH:43:PHE:HE1	1.80	0.46
10:BN:22:ALA:HB1	10:BN:23:PRO:HA	1.97	0.46
11:BO:43:THR:O	11:BO:47:LYS:NZ	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:BK:8:ARG:HG3	21:BK:12:HIS:CE1	2.50	0.46
26:BT:57:ARG:NE	34:B5:1479:A:OP1	2.28	0.46
34:B5:925:G:H2'	34:B5:926:A:H8	1.79	0.46
34:B5:1453:G:H2'	34:B5:1454:G:H8	1.80	0.46
35:AA:183:GLY:HA2	38:A1:896:A:H5''	1.97	0.46
35:AA:230:VAL:HG11	38:A1:2424:A:N1	2.30	0.46
38:A1:230:U:H2'	38:A1:231:G:O4'	2.15	0.46
38:A1:1621:A:H2'	38:A1:1622:U:H6	1.79	0.46
38:A1:1687:U:H5''	38:A1:1688:U:H5'	1.97	0.46
38:A1:1914:G:O2'	54:AR:82:LYS:O	2.32	0.46
38:A1:2167:A:H2'	38:A1:2168:A:C8	2.50	0.46
38:A1:3017:A:N1	38:A1:3037:U:H5	2.14	0.46
38:A1:3279:A:N6	68:Af:54:ARG:HD3	2.30	0.46
47:AJ:90:GLN:NE2	47:AJ:173:ASP:HB2	2.30	0.46
63:Aa:134:ALA:O	63:Aa:138:ILE:HD12	2.15	0.46
19:BD:115:ILE:HD13	19:BD:142:LEU:HD22	1.97	0.46
19:BD:141:LYS:HD2	19:BD:179:GLN:CG	2.46	0.46
21:BK:23:ALA:O	21:BK:64:TYR:HB2	2.15	0.46
21:BK:83:PRO:HG2	21:BK:86:ILE:HD11	1.96	0.46
23:BQ:129:PHE:CE2	27:BU:78:THR:HA	2.51	0.46
25:BS:86:LEU:HD12	25:BS:97:ASP:HB3	1.95	0.46
30:Bd:55:PHE:HD2	34:B5:1334:U:H4'	1.79	0.46
31:Bg:205:SER:HB3	31:Bg:210:LEU:HB2	1.97	0.46
31:Bg:248:ASN:ND2	31:Bg:297:ASP:O	2.48	0.46
34:B5:365:G:H5'	34:B5:757:A:H61	1.79	0.46
34:B5:1356:U:H3'	34:B5:1357:A:H5''	1.96	0.46
34:B5:1433:G:H2'	34:B5:1434:U:C6	2.50	0.46
34:B5:1477:G:H2'	34:B5:1478:G:H8	1.80	0.46
35:AA:180:LEU:HD22	78:Ap:18:TYR:HB3	1.98	0.46
38:A1:516:A:H2'	38:A1:517:G:C8	2.51	0.46
38:A1:1226:G:N2	38:A1:1227:C:H41	2.13	0.46
38:A1:3192:U:H2'	38:A1:3193:C:C6	2.50	0.46
50:AN:36:ILE:HG12	50:AN:64:VAL:HG23	1.98	0.46
53:AQ:83:VAL:O	53:AQ:103:ALA:HA	2.15	0.46
54:AR:98:ARG:HD2	54:AR:133:LYS:O	2.16	0.46
78:Ap:59:CYS:C	78:Ap:61:LYS:H	2.23	0.46
1:BA:15:GLN:HG2	24:BR:100:LEU:HD13	1.96	0.46
8:BJ:169:PRO:HG2	8:BJ:174:ARG:HG3	1.97	0.46
10:BN:61:THR:HG22	17:Bb:32:PHE:CZ	2.50	0.46
34:B5:1508:U:H2'	34:B5:1509:C:C6	2.50	0.46
35:AA:65:ASP:HB3	35:AA:68:LYS:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:431:U:H2'	38:A1:432:G:H8	1.81	0.46
38:A1:2767:U:H2'	38:A1:2768:U:C6	2.49	0.46
38:A1:3321:C:H2'	38:A1:3322:A:H8	1.80	0.46
47:AJ:125:MET:HE1	47:AJ:127:PHE:CE1	2.49	0.46
49:AM:76:ALA:HB1	49:AM:80:THR:HG23	1.98	0.46
57:AU:93:ILE:HD11	57:AU:105:LEU:HB3	1.97	0.46
6:BH:49:ILE:HG21	6:BH:175:LYS:HG2	1.96	0.46
24:BR:5:ARG:HE	34:B5:1402:G:P	2.38	0.46
24:BR:71:PHE:CE1	24:BR:74:GLN:HG3	2.50	0.46
26:BT:38:LYS:O	26:BT:39:THR:HG22	2.16	0.46
33:BM:31:VAL:HG22	33:BM:133:LEU:HD12	1.97	0.46
34:B5:52:U:H2'	34:B5:53:G:C8	2.51	0.46
34:B5:304:U:H2'	34:B5:305:C:C6	2.50	0.46
34:B5:1002:G:O6	34:B5:1003:A:N6	2.48	0.46
34:B5:1379:C:H2'	34:B5:1380:U:O2	2.14	0.46
38:A1:671:U:H2'	38:A1:672:A:H8	1.80	0.46
38:A1:1019:G:O6	38:A1:1033:U:H3'	2.14	0.46
38:A1:1054:A:H5''	38:A1:2637:A:H61	1.80	0.46
38:A1:1302:A:N7	38:A1:2857:C:O2'	2.48	0.46
38:A1:1770:G:H2'	38:A1:1771:C:C6	2.50	0.46
38:A1:1828:A:H2'	38:A1:1829:G:C8	2.51	0.46
38:A1:2369:G:H2'	38:A1:2370:G:C8	2.50	0.46
38:A1:2512:C:H2'	38:A1:2513:U:C6	2.51	0.46
38:A1:2724:U:OP2	38:A1:2726:C:N4	2.49	0.46
38:A1:3296:A:H2'	38:A1:3297:U:H6	1.79	0.46
39:A3:31:U:C1'	41:AD:218:ARG:HH22	2.29	0.46
44:AG:63:LYS:O	44:AG:67:ILE:HG12	2.15	0.46
11:BO:29:HIS:HB2	11:BO:41:ARG:HG3	1.97	0.46
20:BF:40:ILE:HG21	20:BF:67:PRO:HB2	1.97	0.46
22:BP:67:ALA:HB2	22:BP:73:PRO:HB3	1.97	0.46
24:BR:71:PHE:HE1	24:BR:73:LEU:HB3	1.80	0.46
27:BU:53:LYS:HD2	27:BU:54:GLY:O	2.15	0.46
31:Bg:294:TRP:CZ2	31:Bg:301:LEU:HD12	2.51	0.46
34:B5:1669:U:H3	34:B5:1732:A:N6	2.12	0.46
35:AA:215:ASN:ND2	38:A1:2969:A:N7	2.64	0.46
38:A1:435:C:H2'	38:A1:436:A:C8	2.50	0.46
38:A1:539:C:H2'	38:A1:540:U:C6	2.50	0.46
38:A1:627:U:H4'	38:A1:1399:A:H1'	1.98	0.46
38:A1:1083:G:H2'	38:A1:1084:A:C8	2.50	0.46
38:A1:1348:U:OP1	53:AQ:39:ARG:NH1	2.49	0.46
40:A4:12:A:P	52:AP:3:ARG:HH21	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:AM:72:LEU:HD21	49:AM:81:VAL:HG22	1.97	0.46
1:BA:23:HIS:HB2	1:BA:47:VAL:HG13	1.97	0.46
4:BE:94:ALA:C	4:BE:96:ASN:H	2.24	0.46
8:BJ:17:ARG:HB3	8:BJ:20:GLU:OE2	2.15	0.46
13:BW:105:THR:HB	13:BW:126:LEU:HD11	1.97	0.46
15:BY:15:ASN:HB2	15:BY:22:GLN:HE22	1.80	0.46
16:Ba:79:ILE:HD13	34:B5:1794:A:H1'	1.98	0.46
25:BS:116:LEU:HA	25:BS:119:ILE:HG12	1.98	0.46
27:BU:101:LYS:HB3	27:BU:101:LYS:HE2	1.69	0.46
31:Bg:242:SER:H	31:Bg:255:ALA:HB3	1.80	0.46
34:B5:887:A:H2'	34:B5:888:U:H6	1.80	0.46
34:B5:1237:G:H2'	34:B5:1238:A:C8	2.46	0.46
36:AB:350:ALA:O	36:AB:351:LEU:HD23	2.16	0.46
38:A1:35:A:H2'	38:A1:36:C:H6	1.80	0.46
38:A1:258:G:H2'	38:A1:259:C:C6	2.51	0.46
38:A1:1174:G:N2	51:AO:87[A]:MET:HE2	2.31	0.46
38:A1:1471:U:H2'	38:A1:1472:U:C6	2.51	0.46
38:A1:1722:U:OP2	54:AR:103:ARG:NH1	2.46	0.46
38:A1:1729:A:N6	78:Ap:42:CYS:HA	2.31	0.46
40:A4:67:U:H5''	72:Aj:85:LYS:O	2.15	0.46
46:AI:206:LEU:O	46:AI:210:ILE:HG12	2.16	0.46
11:BO:50:ALA:C	11:BO:52:ARG:H	2.22	0.46
13:BW:57:ARG:HG2	34:B5:862:A:H4'	1.98	0.46
20:BF:40:ILE:HA	20:BF:69:PHE:CE1	2.50	0.46
23:BQ:47:LYS:HE3	23:BQ:82:ARG:NE	2.31	0.46
25:BS:138:THR:OG1	34:B5:1459:C:H5''	2.16	0.46
34:B5:56:U:H4'	34:B5:57:G:H5'	1.98	0.46
34:B5:206:A:H1'	34:B5:262:U:C2	2.51	0.46
34:B5:708:C:O2'	34:B5:710:U:OP1	2.33	0.46
34:B5:1350:U:H2'	34:B5:1351:G:H8	1.80	0.46
34:B5:1525:A:H2'	34:B5:1526:A:H8	1.81	0.46
36:AB:216:ASP:OD2	36:AB:339:ARG:NH2	2.37	0.46
38:A1:879:U:O2'	52:AP:135:ARG:NH2	2.37	0.46
38:A1:1232:C:N4	38:A1:1262:G:OP2	2.49	0.46
38:A1:1744:G:H2'	38:A1:1745:C:C6	2.50	0.46
38:A1:2683:U:H2'	38:A1:2684:C:H6	1.81	0.46
39:A3:71:G:H2'	39:A3:72:A:C8	2.51	0.46
40:A4:135:G:P	60:AX:56:ARG:HH22	2.39	0.46
47:AJ:35:LYS:O	47:AJ:38:GLU:HG3	2.16	0.46
49:AM:28:SER:HB3	49:AM:31:LYS:HD2	1.98	0.46
58:AV:19:VAL:HG23	58:AV:50:PRO:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:AV:86:ARG:HB2	58:AV:92:PHE:CE1	2.51	0.46
68:Af:16:TYR:OH	68:Af:89:LEU:O	2.21	0.46
4:BE:158:ASP:OD1	4:BE:174:LYS:HD2	2.16	0.46
8:BJ:41:GLU:O	8:BJ:45:ILE:HG13	2.16	0.46
14:BX:75:GLN:HE21	14:BX:80:GLY:HA2	1.79	0.46
31:Bg:164:ASP:N	31:Bg:164:ASP:OD1	2.49	0.46
31:Bg:231:MET:HG3	31:Bg:232:TYR:CD1	2.51	0.46
34:B5:154:G:H2'	34:B5:155:U:C6	2.51	0.46
34:B5:1341:A:C2	34:B5:1342:C:C5	3.03	0.46
34:B5:1358:G:H2'	34:B5:1359:C:C6	2.50	0.46
34:B5:1453:G:H2'	34:B5:1454:G:C8	2.51	0.46
38:A1:173:G:O6	38:A1:245:U:C4	2.69	0.46
45:AH:23:ARG:HB2	45:AH:39:LYS:HG2	1.97	0.46
6:BH:132:PRO:HB2	6:BH:161:GLN:HE21	1.81	0.46
7:BI:81:VAL:HG12	7:BI:102:VAL:HG22	1.97	0.46
9:BL:96:LYS:HG3	34:B5:373:G:H5'	1.96	0.46
14:BX:50:LYS:HB3	14:BX:101:GLU:OE2	2.16	0.46
20:BF:162:VAL:HG13	20:BF:166:ARG:HB3	1.98	0.46
22:BP:126:VAL:HG12	34:B5:1181:PSU:H1'	1.97	0.46
34:B5:21:U:H2'	34:B5:22:A:C8	2.50	0.46
34:B5:467:G:O2'	34:B5:469:C:OP2	2.27	0.46
34:B5:513:U:H2'	34:B5:514:G:H8	1.78	0.46
34:B5:595:G:H2'	34:B5:596:C:C6	2.51	0.46
34:B5:791:A:H2'	34:B5:792:U:H6	1.81	0.46
34:B5:1156:C:H2'	34:B5:1157:A:H8	1.80	0.46
34:B5:1552:U:O2'	34:B5:1597:A:N3	2.36	0.46
38:A1:167:U:H2'	38:A1:168:U:H6	1.81	0.46
38:A1:260:C:H2'	38:A1:261:U:C6	2.51	0.46
38:A1:412:G:H2'	38:A1:413:U:C6	2.51	0.46
38:A1:528:U:H2'	38:A1:529:A:H8	1.80	0.46
38:A1:1072:G:H2'	38:A1:1073:U:C6	2.51	0.46
38:A1:1208:U:O2'	38:A1:3115:C:N4	2.49	0.46
38:A1:1283:C:O2'	38:A1:1284:C:H5''	2.15	0.46
38:A1:1340:G:H2'	38:A1:1341:U:H6	1.79	0.46
38:A1:3254:G:H2'	38:A1:3255:U:O4'	2.16	0.46
39:A3:37:G:H2'	39:A3:38:U:O4'	2.16	0.46
48:AL:106:GLN:HB3	71:AI:18:THR:HB	1.97	0.46
1:BA:35:PRO:O	1:BA:52:LYS:NZ	2.49	0.46
1:BA:189:VAL:HG23	12:BV:44:ARG:HH22	1.81	0.46
2:BB:184:LEU:HD12	2:BB:187:LYS:HD3	1.98	0.46
4:BE:36:HIS:CG	4:BE:85:GLY:HA3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:150:PRO:HG2	5:BG:208:TYR:CG	2.50	0.46
7:BI:60:ILE:HD11	7:BI:179:CYS:HB2	1.98	0.46
7:BI:195:ARG:NH2	9:BL:11:ARG:HG2	2.31	0.46
9:BL:78:THR:HA	9:BL:84:ILE:HG22	1.97	0.46
11:BO:132:ARG:NH2	34:B5:1789:G:N7	2.64	0.46
19:BD:6:SER:HB2	34:B5:1514:U:H1'	1.98	0.46
20:BF:119:ASP:HB3	28:BZ:100:ILE:HD13	1.97	0.46
20:BF:142:PRO:O	20:BF:167:ARG:HG2	2.16	0.46
27:BU:53:LYS:HG2	34:B5:1345:A:O5'	2.16	0.46
27:BU:100:VAL:HA	27:BU:103:ILE:HG22	1.96	0.46
31:Bg:5:GLU:OE1	31:Bg:6:VAL:HG13	2.15	0.46
32:Bf:128:ALA:H	33:BM:54:ARG:NH1	2.14	0.46
35:AA:101:VAL:HG22	35:AA:165:VAL:HG22	1.98	0.46
38:A1:127:G:OP1	50:AN:140:LYS:HG3	2.16	0.46
38:A1:638:C:N4	38:A1:639:G:O6	2.49	0.46
38:A1:875:G:O2'	38:A1:1891:A:OP1	2.33	0.46
38:A1:1144:U:OP1	38:A1:1367:G:O2'	2.27	0.46
38:A1:1622:U:H2'	38:A1:1623:G:H8	1.80	0.46
38:A1:1953:G:N1	38:A1:1954:G:O6	2.49	0.46
38:A1:2376:G:H2'	38:A1:2377:G:C8	2.51	0.46
38:A1:3232:G:H2'	38:A1:3233:C:C6	2.50	0.46
40:A4:141:C:OP1	50:AN:109:ARG:NH2	2.48	0.46
43:AF:96:PRO:HB2	43:AF:99:PRO:HD2	1.98	0.46
48:AL:57:VAL:HB	48:AL:147:ILE:HD12	1.98	0.46
51:AO:186[A]:ALA:O	51:AO:187[A]:GLU:HG2	2.16	0.46
15:BY:56:SER:OG	15:BY:90:ARG:NH1	2.49	0.45
22:BP:29:SER:OG	22:BP:31:GLU:OE1	2.33	0.45
25:BS:41:ARG:HH11	26:BT:46:PRO:HG3	1.81	0.45
34:B5:909:U:H2'	34:B5:910:C:H6	1.81	0.45
34:B5:1151:A:H2'	34:B5:1152:A:C8	2.51	0.45
34:B5:1482:C:P	34:B5:1521:G:H22	2.39	0.45
35:AA:244:GLY:HA3	38:A1:2242:A:H5''	1.98	0.45
37:AC:125:ALA:O	37:AC:129:THR:HG23	2.17	0.45
38:A1:649:A:H2'	38:A1:650:C:C6	2.52	0.45
38:A1:1472:U:H2'	38:A1:1473:G:H8	1.81	0.45
38:A1:2352:A:H5''	52:AP:83:TRP:O	2.14	0.45
38:A1:3051:U:C2	38:A1:3052:G:C8	3.04	0.45
38:A1:3366:G:H2'	38:A1:3367:C:C6	2.51	0.45
39:A3:31:U:H1'	41:AD:218:ARG:HH22	1.81	0.45
41:AD:151:GLN:HG2	41:AD:159:VAL:HG11	1.98	0.45
50:AN:35:VAL:HG12	50:AN:36:ILE:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Ai:96:ALA:HA	71:Ai:99:ARG:HE	1.81	0.45
4:BE:65:LEU:HD13	4:BE:80:THR:HA	1.98	0.45
6:BH:113:PRO:HD3	34:B5:811:A:N6	2.31	0.45
9:BL:72:THR:HB	9:BL:124:THR:HG22	1.98	0.45
10:BN:99:ARG:O	10:BN:103:GLU:HG2	2.16	0.45
18:Be:55:ARG:HH22	34:B5:558:U:P	2.38	0.45
20:BF:193:THR:HA	20:BF:196:GLU:HG2	1.98	0.45
21:BK:59:PHE:CE2	21:BK:62:GLN:HG3	2.51	0.45
28:BZ:39:ALA:O	28:BZ:72:GLY:N	2.44	0.45
33:BM:32:LEU:HB3	33:BM:100:TRP:HH2	1.81	0.45
33:BM:97:LEU:HD11	33:BM:121:VAL:HG21	1.98	0.45
34:B5:330:G:H2'	34:B5:331:A:H8	1.82	0.45
34:B5:339:C:H2'	34:B5:340:U:C6	2.52	0.45
34:B5:772:G:H21	34:B5:774:A:H1'	1.81	0.45
34:B5:1787:C:H2'	34:B5:1788:G:C8	2.51	0.45
36:AB:219:ALA:HB2	36:AB:336:VAL:HG23	1.97	0.45
38:A1:1595:U:OP2	69:Ag:36:LYS:NZ	2.39	0.45
38:A1:1657:C:O2'	38:A1:1797:A:OP2	2.19	0.45
38:A1:1771:C:H2'	38:A1:1772:U:O4'	2.16	0.45
38:A1:2430:A:H2'	38:A1:2431:C:C6	2.51	0.45
38:A1:3095:U:H2'	38:A1:3096:C:C6	2.51	0.45
40:A4:26:U:H2'	40:A4:27:U:C6	2.52	0.45
40:A4:63:G:OP1	40:A4:90:U:H5''	2.15	0.45
41:AD:49:TYR:HB3	41:AD:144:VAL:HG12	1.98	0.45
53:AQ:174:ARG:O	63:Aa:56:VAL:HG21	2.16	0.45
1:BA:51:GLY:H	24:BR:109:LEU:HD22	1.81	0.45
22:BP:122:THR:HG21	34:B5:1454:G:O3'	2.16	0.45
24:BR:102:VAL:O	24:BR:122:ILE:N	2.40	0.45
26:BT:87:GLY:C	34:B5:1542:G:H5''	2.42	0.45
27:BU:58:LEU:HB2	27:BU:88:LYS:O	2.16	0.45
34:B5:523:G:O2'	34:B5:529:A:N6	2.38	0.45
34:B5:950:C:H2'	34:B5:951:A:C8	2.52	0.45
34:B5:1374:C:H2'	34:B5:1375:A:H8	1.81	0.45
34:B5:1502:G:N2	34:B5:1505:A:OP2	2.46	0.45
38:A1:1008:U:O4	38:A1:1043:C:N4	2.49	0.45
38:A1:1066:G:H2'	38:A1:1067:U:C6	2.51	0.45
38:A1:1280:C:H2'	38:A1:1281:G:C8	2.51	0.45
38:A1:1354:G:N2	38:A1:1357:G:H4'	2.32	0.45
38:A1:1677:G:OP2	57:AU:103:TYR:OH	2.31	0.45
38:A1:1679:A:OP1	57:AU:94:ARG:NH1	2.50	0.45
39:A3:64:A:H5'	39:A3:65:G:H5''	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AS:22:PRO:O	56:AT:146:ASN:ND2	2.36	0.45
62:AZ:26:VAL:HA	62:AZ:89:VAL:HG11	1.97	0.45
2:BB:52:THR:H	2:BB:56:SER:CB	2.29	0.45
2:BB:122:GLU:OE2	2:BB:213:ARG:NH2	2.34	0.45
4:BE:100:ARG:NH2	4:BE:118:GLU:O	2.49	0.45
5:BG:32:ILE:HG13	5:BG:52:ILE:O	2.16	0.45
31:Bg:251:TRP:CZ2	31:Bg:271:VAL:HG11	2.52	0.45
34:B5:1279:C:H2'	34:B5:1280:4AC:C6	2.46	0.45
38:A1:167:U:H2'	38:A1:168:U:C6	2.51	0.45
38:A1:487:U:H2'	38:A1:488:U:O4'	2.16	0.45
38:A1:993:G:N3	38:A1:2637:A:H2'	2.31	0.45
38:A1:3358:U:H2'	38:A1:3359:A:H8	1.81	0.45
41:AD:250:ASP:N	41:AD:250:ASP:OD1	2.48	0.45
1:BA:64:ILE:HD13	1:BA:73:VAL:HG11	1.97	0.45
2:BB:123:ALA:HB2	2:BB:165:ARG:HG3	1.97	0.45
2:BB:142:PHE:O	2:BB:208:GLN:N	2.33	0.45
5:BG:57:ASP:HA	5:BG:107:ALA:H	1.81	0.45
8:BJ:32:GLY:HA3	18:Be:40:TYR:CD2	2.52	0.45
11:BO:29:HIS:HD2	11:BO:41:ARG:HB2	1.81	0.45
15:BY:42:GLU:HG3	15:BY:52:LYS:HG3	1.98	0.45
16:Ba:84:VAL:O	34:B5:1797:A:N6	2.46	0.45
23:BQ:58:ASP:N	23:BQ:58:ASP:OD1	2.48	0.45
23:BQ:60:PHE:HA	23:BQ:63:ILE:HG22	1.99	0.45
27:BU:82:TYR:HB3	30:Bd:52:PHE:HB3	1.99	0.45
34:B5:607:G:H21	34:B5:614:C:H5''	1.82	0.45
34:B5:814:A:OP1	54:AR:167:ARG:HD2	2.17	0.45
35:AA:80:GLU:HG2	78:Ap:76:ALA:CB	2.46	0.45
38:A1:1213:G:H4'	55:AS:90:MET:CG	2.40	0.45
38:A1:1761:C:O2'	38:A1:1762:C:O3'	2.33	0.45
38:A1:3024:A:H4'	45:AH:97:PHE:CE2	2.52	0.45
38:A1:3165:A:H2'	38:A1:3166:C:H6	1.82	0.45
40:A4:97:A:O2'	70:Ah:59:ASN:ND2	2.50	0.45
42:AE:132:ALA:HA	42:AE:135:VAL:HG22	1.98	0.45
68:Af:49:ILE:HG12	68:Af:100:ILE:HG13	1.98	0.45
70:Ah:86:ARG:O	70:Ah:90:ARG:HG2	2.16	0.45
4:BE:100:ARG:CZ	4:BE:236:ILE:HD11	2.46	0.45
6:BH:30:SER:HB2	6:BH:33:GLU:HB3	1.97	0.45
7:BI:195:ARG:HH21	9:BL:11:ARG:HG2	1.81	0.45
10:BN:3:ARG:HB3	10:BN:6:SER:HB3	1.97	0.45
15:BY:12:VAL:HA	15:BY:23:PHE:HB3	1.99	0.45
15:BY:15:ASN:OD1	15:BY:17:LEU:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:124:ARG:O	19:BD:128:GLU:HG2	2.16	0.45
19:BD:167:PHE:HD1	19:BD:190:ARG:HG3	1.82	0.45
23:BQ:72:GLY:O	34:B5:1482:C:O2'	2.25	0.45
25:BS:38:VAL:HG22	25:BS:42:TYR:CD2	2.52	0.45
25:BS:75:ASN:HB3	25:BS:78:HIS:ND1	2.32	0.45
30:Bd:46:LYS:O	30:Bd:50:ILE:HG12	2.17	0.45
34:B5:1160:A:H2'	34:B5:1161:C:C6	2.51	0.45
34:B5:1483:A:C2	34:B5:1607:G:H1'	2.52	0.45
38:A1:487:U:HO2'	38:A1:488:U:P	2.40	0.45
38:A1:802:C:H2'	38:A1:803:C:H6	1.82	0.45
38:A1:1238:C:C5	38:A1:1244:A:H3'	2.51	0.45
38:A1:1261:G:H2'	38:A1:1261:G:N3	2.30	0.45
38:A1:1881:A:H2'	38:A1:1882:G:H8	1.82	0.45
38:A1:2367:A:H2'	38:A1:2368:A:C8	2.52	0.45
38:A1:2585:G:H2'	38:A1:2585:G:N3	2.32	0.45
38:A1:2660:G:OP1	38:A1:2750:U:O2'	2.35	0.45
38:A1:3015:G:H2'	38:A1:3016:A:H8	1.82	0.45
38:A1:3322:A:H2'	38:A1:3323:A:H8	1.81	0.45
39:A3:3:U:H2'	39:A3:4:U:C6	2.52	0.45
40:A4:128:U:P	40:A4:129:C:H41	2.38	0.45
48:AL:61:PRO:O	48:AL:62:THR:OG1	2.29	0.45
53:AQ:64:VAL:HA	53:AQ:67:ILE:HD12	1.98	0.45
69:Ag:16:ARG:HG2	69:Ag:37:LYS:HD3	1.98	0.45
6:BH:67:LEU:HD12	6:BH:71:HIS:NE2	2.32	0.45
8:BJ:49:LEU:O	8:BJ:53:ARG:HG2	2.17	0.45
20:BF:98:MET:HG3	20:BF:103:ASN:O	2.17	0.45
21:BK:6:GLU:O	21:BK:10:LYS:HG2	2.17	0.45
31:Bg:209:THR:O	31:Bg:224:ASN:ND2	2.34	0.45
34:B5:683:C:O2'	34:B5:684:A:H8	2.00	0.45
34:B5:821:U:O2'	34:B5:822:U:OP1	2.28	0.45
34:B5:1045:C:H2'	34:B5:1046:G:C8	2.49	0.45
34:B5:1115:U:O2'	76:An:17:ARG:NH1	2.46	0.45
34:B5:1515:A:H4'	34:B5:1517:U:C5	2.51	0.45
35:AA:145:LYS:HD3	35:AA:159:SER:HA	1.99	0.45
38:A1:371:G:N1	38:A1:374:A:OP2	2.37	0.45
38:A1:1094:U:H5''	38:A1:1096:U:OP1	2.16	0.45
38:A1:1176:C:H2'	38:A1:1177:G:N2	2.31	0.45
38:A1:2971:A:H2'	46:AI:110:ARG:NH1	2.32	0.45
40:A4:68:G:H2'	40:A4:69:U:H6	1.80	0.45
40:A4:142:C:H2'	40:A4:143:U:H6	1.80	0.45
43:AF:221:LYS:HB2	43:AF:227:GLY:HA3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AH:132:VAL:HG11	45:AH:157:ASN:HD22	1.80	0.45
48:AL:120:GLN:HA	48:AL:123:ILE:HG22	1.98	0.45
49:AM:105:GLN:OE1	49:AM:109:ARG:NH2	2.50	0.45
54:AR:181:ARG:O	54:AR:181:ARG:NE	2.27	0.45
72:Aj:50:GLY:O	72:Aj:54:LYS:HG3	2.17	0.45
2:BB:69:CYS:HA	2:BB:83:LYS:HA	1.97	0.45
8:BJ:99:LEU:HD21	8:BJ:104:PHE:HE1	1.81	0.45
19:BD:209:ILE:O	24:BR:20:TYR:OH	2.33	0.45
26:BT:78:LYS:NZ	34:B5:1523:G:OP1	2.28	0.45
31:Bg:73:LEU:HD23	31:Bg:80:ALA:HB2	1.97	0.45
34:B5:93:A:H3'	34:B5:94:U:H5'	1.99	0.45
34:B5:521:A:H2'	34:B5:522:U:C6	2.52	0.45
34:B5:1474:G:H2'	34:B5:1475:A:H8	1.81	0.45
34:B5:1619:C:H2'	34:B5:1620:C:C6	2.52	0.45
34:B5:1646:C:H5''	38:A1:2259:A:N6	2.31	0.45
38:A1:40:A:H5''	63:Aa:35:ALA:HB1	1.98	0.45
38:A1:115:A:H8	38:A1:266:A:H5'	1.81	0.45
38:A1:1036:A:H2'	38:A1:1037:C:C6	2.52	0.45
38:A1:2344:U:H2'	38:A1:2345:A:H8	1.82	0.45
38:A1:2762:A:H2'	38:A1:2763:U:H6	1.82	0.45
39:A3:39:C:O2'	47:Aj:43:GLN:HG3	2.17	0.45
51:AO:121[A]:PRO:HA	51:AO:124[A]:LEU:HD12	1.99	0.45
70:Ah:85:THR:HB	70:Ah:88:LEU:HB2	1.97	0.45
2:BB:174:LYS:NZ	2:BB:196:GLU:OE2	2.39	0.45
4:BE:252:ARG:NE	4:BE:256:ARG:HH22	2.13	0.45
8:BJ:175:ARG:NH1	34:B5:537:G:OP2	2.48	0.45
16:Ba:44:ILE:HG23	16:Ba:45:VAL:HG13	1.98	0.45
16:Ba:70:LYS:HD3	34:B5:930:A:H5''	1.97	0.45
19:BD:126:VAL:HG12	19:BD:127:MET:HE2	1.97	0.45
22:BP:30:THR:HG21	22:BP:86:VAL:HB	1.99	0.45
25:BS:65:GLU:O	25:BS:69:ILE:HD12	2.17	0.45
31:Bg:227:ALA:O	31:Bg:229:LYS:HG2	2.16	0.45
34:B5:93:A:H5'	34:B5:94:U:C5	2.52	0.45
34:B5:790:U:H2'	34:B5:791:A:C8	2.52	0.45
34:B5:1488:G:O2'	34:B5:1494:C:O2	2.31	0.45
35:AA:152:SER:OG	38:A1:2157:G:N7	2.47	0.45
38:A1:179:C:H2'	38:A1:180:C:C6	2.52	0.45
38:A1:273:A:H2'	38:A1:274:G:H8	1.82	0.45
38:A1:448:U:O2	38:A1:488:U:O2'	2.30	0.45
38:A1:1497:C:H2'	38:A1:1498:A:C8	2.51	0.45
38:A1:2108:C:H1'	38:A1:3344:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2160:G:H2'	38:A1:2161:G:C8	2.49	0.45
38:A1:3064:U:H2'	38:A1:3065:G:C8	2.50	0.45
38:A1:3072:C:H2'	38:A1:3073:A:O4'	2.17	0.45
38:A1:3110:C:H2'	38:A1:3111:U:C6	2.52	0.45
38:A1:3159:C:H2'	38:A1:3160:U:H6	1.82	0.45
48:AL:53:LEU:HD22	48:AL:94:GLY:HA2	1.99	0.45
52:AP:126:ARG:HD3	52:AP:140:GLU:OE2	2.17	0.45
1:BA:89:PHE:HD1	1:BA:178:ALA:HB2	1.82	0.45
2:BB:72:ASP:CG	11:BO:114:ARG:HE	2.25	0.45
7:BI:195:ARG:HG3	7:BI:196:LEU:CD2	2.47	0.45
15:BY:22:GLN:OE1	15:BY:22:GLN:N	2.50	0.45
34:B5:514:G:O2'	34:B5:515:A:H8	2.00	0.45
34:B5:962:C:H2'	34:B5:963:A:O4'	2.17	0.45
34:B5:1187:PSU:H2'	34:B5:1188:G:C8	2.49	0.45
34:B5:1370:U:OP1	34:B5:1372:U:H3'	2.16	0.45
34:B5:1623:C:H2'	34:B5:1624:C:H6	1.82	0.45
38:A1:71:A:OP1	63:Aa:67:HIS:NE2	2.50	0.45
38:A1:252:U:H4'	38:A1:253:A:O5'	2.16	0.45
38:A1:584:G:H2'	38:A1:585:A:H8	1.81	0.45
38:A1:1107:C:H2'	38:A1:1108:U:O2	2.16	0.45
38:A1:1340:G:OP2	67:Ae:61:LYS:NZ	2.48	0.45
38:A1:2216:G:H22	38:A1:2229:A:H2	1.63	0.45
38:A1:2733:A:H2'	38:A1:2734:A:O4'	2.17	0.45
38:A1:3041:U:H2'	38:A1:3042:U:H6	1.82	0.45
38:A1:3275:U:H5'	68:Af:68:TRP:HZ2	1.82	0.45
51:AO:174[A]:PHE:O	51:AO:177[A]:LYS:HG2	2.16	0.45
69:Ag:10:ARG:HD2	74:Al:4:GLN:NE2	2.32	0.45
2:BB:35:PRO:HA	2:BB:232:HIS:HD2	1.82	0.44
3:BC:76:LEU:HD11	3:BC:133:LYS:HE2	1.97	0.44
3:BC:89:GLN:O	34:B5:1145:U:O2'	2.30	0.44
3:BC:118:ALA:HB3	3:BC:124:ALA:HB2	1.98	0.44
6:BH:13:PRO:HA	6:BH:14:THR:HA	1.67	0.44
10:BN:5:HIS:CD2	34:B5:627:C:H5''	2.51	0.44
10:BN:12:SER:O	10:BN:12:SER:OG	2.31	0.44
12:BV:85:TYR:CD2	17:Bb:6:ASP:HB2	2.52	0.44
19:BD:141:LYS:HD2	19:BD:179:GLN:HG2	1.98	0.44
20:BF:109:LYS:HB2	20:BF:109:LYS:HE2	1.81	0.44
22:BP:83:MET:HB2	22:BP:116:LEU:HD12	2.00	0.44
31:Bg:239:GLU:HB3	31:Bg:257:ALA:HB2	1.98	0.44
34:B5:160:C:H2'	34:B5:161:U:O4'	2.16	0.44
34:B5:1613:U:H2'	34:B5:1614:A:C8	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AA:79:ASN:ND2	35:AA:165:VAL:HG12	2.32	0.44
38:A1:5:G:H2'	38:A1:6:A:O4'	2.17	0.44
38:A1:182:U:H3	38:A1:234:G:H1	1.65	0.44
38:A1:632:G:H2'	38:A1:633:C:C6	2.51	0.44
38:A1:838:G:O6	78:Ap:4:ARG:NH1	2.45	0.44
38:A1:992:A:O2'	38:A1:993:G:H5'	2.17	0.44
38:A1:1213:G:OP1	55:AS:137:ARG:NE	2.49	0.44
40:A4:70:G:OP1	61:AY:121:ARG:NH2	2.50	0.44
41:AD:95:TRP:CE3	41:AD:198:TYR:HD1	2.34	0.44
53:AQ:122:ILE:HG23	53:AQ:126:GLN:HB2	1.98	0.44
57:AU:25:ASN:HB2	57:AU:27:VAL:HG22	1.99	0.44
62:AZ:23:VAL:HG12	62:AZ:45:GLY:HA3	1.99	0.44
2:BB:45:LYS:NZ	11:BO:13:VAL:HA	2.33	0.44
4:BE:103:TYR:O	4:BE:182:TYR:OH	2.36	0.44
6:BH:19:GLN:HA	6:BH:22:GLN:NE2	2.31	0.44
9:BL:131:ILE:HD13	9:BL:135:VAL:HG12	1.98	0.44
11:BO:125:SER:HB3	34:B5:926:A:C2	2.44	0.44
14:BX:112:LYS:NZ	34:B5:18:C:O3'	2.50	0.44
25:BS:36:LYS:HG2	25:BS:105:VAL:HG21	1.98	0.44
31:Bg:16:HIS:ND1	31:Bg:43:ILE:HD13	2.32	0.44
31:Bg:90:ARG:NH2	34:B5:1341:A:H4'	2.32	0.44
34:B5:989:U:H2'	34:B5:990:C:C6	2.52	0.44
36:AB:67:PHE:HA	36:AB:70:ARG:HD3	1.99	0.44
38:A1:127:G:H2'	38:A1:128:G:H8	1.82	0.44
38:A1:2262:A:H5''	38:A1:2262:A:H8	1.81	0.44
38:A1:2283:G:H1'	38:A1:2285:C:N4	2.33	0.44
38:A1:2516:U:OP1	50:AN:31:ARG:NH1	2.50	0.44
38:A1:2864:A:O3'	46:AI:115:MET:HG2	2.17	0.44
39:A3:121:U:H5''	41:AD:260:PHE:HD2	1.82	0.44
48:AL:46:ILE:HD11	48:AL:51:LEU:HA	1.99	0.44
58:AV:87:ARG:HH22	58:AV:137:VAL:HG21	1.82	0.44
59:AW:4:GLU:HB2	59:AW:13:ILE:HB	2.00	0.44
2:BB:228:LEU:HD23	2:BB:228:LEU:H	1.81	0.44
4:BE:30:ARG:HH22	34:B5:299:A:P	2.40	0.44
4:BE:149:TYR:CD2	4:BE:169:ILE:HG12	2.52	0.44
16:Ba:33:ASP:N	16:Ba:33:ASP:OD1	2.49	0.44
18:Be:49:LEU:HG	18:Be:58:PRO:HG2	2.00	0.44
19:BD:179:GLN:HB2	34:B5:579:A:N6	2.32	0.44
23:BQ:35:PRO:HG2	23:BQ:38:LEU:HG	1.98	0.44
26:BT:108:LEU:HD12	26:BT:113:ILE:HG13	1.98	0.44
34:B5:509:G:H2'	34:B5:510:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:593:U:H4'	34:B5:595:G:H4'	1.99	0.44
34:B5:598:U:H2'	34:B5:599:A:H8	1.81	0.44
34:B5:605:A:OP2	34:B5:606:A:O2'	2.32	0.44
34:B5:1213:G:H22	34:B5:1450:U:H5	1.66	0.44
34:B5:1221:A:H2'	34:B5:1222:C:C6	2.52	0.44
34:B5:1413:U:O2'	34:B5:1416:G:OP1	2.34	0.44
36:AB:5:LYS:HE2	38:A1:2878:G:H5''	1.99	0.44
38:A1:837:A:OP2	78:Ap:4:ARG:NE	2.42	0.44
38:A1:1083:G:H2'	38:A1:1084:A:H8	1.82	0.44
38:A1:1221:A:H3'	38:A1:1222:G:C4'	2.45	0.44
38:A1:2651:G:H5''	38:A1:2652:U:O4'	2.16	0.44
38:A1:3294:A:H2'	38:A1:3295:A:O4'	2.18	0.44
38:A1:3348:G:O6	38:A1:3357:U:O4	2.35	0.44
38:A1:3371:G:H2'	38:A1:3372:A:C8	2.52	0.44
39:A3:71:G:H2'	39:A3:72:A:H8	1.82	0.44
40:A4:75:G:H2'	40:A4:76:C:H6	1.82	0.44
51:AO:25[A]:LYS:HA	51:AO:25[A]:LYS:HD3	1.84	0.44
51:AO:58[A]:LEU:HA	51:AO:72[A]:HIS:CD2	2.53	0.44
55:AS:152:LEU:HD12	55:AS:172:TYR:HE2	1.82	0.44
5:BG:27:PHE:HB3	5:BG:102:VAL:HG11	2.00	0.44
27:BU:83:GLU:OE2	30:Bd:56:ARG:NE	2.50	0.44
34:B5:983:A:O2'	78:Ap:28:LYS:NZ	2.46	0.44
34:B5:1739:C:H2'	34:B5:1740:A:C8	2.52	0.44
38:A1:279:U:H2'	38:A1:280:U:C6	2.53	0.44
38:A1:432:G:H2'	38:A1:433:A:H8	1.83	0.44
38:A1:1341:U:H2'	38:A1:1342:C:C6	2.53	0.44
38:A1:1381:A:H2'	38:A1:1382:G:H8	1.82	0.44
38:A1:1675:G:H2'	38:A1:1676:A:H8	1.83	0.44
38:A1:1797:A:H2'	38:A1:1798:A:C8	2.53	0.44
38:A1:2427:U:H2'	38:A1:2428:U:H6	1.82	0.44
38:A1:2813:A:H2'	38:A1:2814:G:O4'	2.18	0.44
38:A1:3029:A:O5'	38:A1:3029:A:H8	2.00	0.44
38:A1:3230:G:H2'	38:A1:3231:U:C6	2.53	0.44
41:AD:95:TRP:HD1	41:AD:158:ARG:HA	1.82	0.44
43:AF:216:VAL:HG12	43:AF:218:ARG:H	1.82	0.44
68:Af:59:VAL:HG12	68:Af:60:ARG:HG2	1.99	0.44
75:Am:97:ARG:HE	75:Am:122:ARG:HB3	1.82	0.44
2:BB:149:GLN:HE21	34:B5:1066:C:H4'	1.82	0.44
2:BB:229:MET:SD	38:A1:2537:U:H5'	2.57	0.44
3:BC:44:LEU:HB3	3:BC:49:LYS:HB2	1.99	0.44
3:BC:157:LYS:HE2	3:BC:170:ILE:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BH:30:SER:O	6:BH:34:LEU:N	2.50	0.44
12:BV:42:GLU:HG2	12:BV:42:GLU:O	2.18	0.44
18:Be:33:ARG:HH12	34:B5:478:A:P	2.40	0.44
26:BT:66:TYR:HD2	26:BT:67:MET:HE2	1.81	0.44
31:Bg:178:VAL:HG23	31:Bg:199:ILE:HD13	1.99	0.44
34:B5:327:U:H2'	34:B5:328:A:C8	2.52	0.44
34:B5:775:G:O6	34:B5:785:U:O2	2.36	0.44
34:B5:1751:C:H2'	34:B5:1752:U:C6	2.53	0.44
38:A1:393:U:H2'	38:A1:394:G:O4'	2.17	0.44
38:A1:873:C:H3'	38:A1:874:U:H4'	1.99	0.44
38:A1:1659:U:H2'	38:A1:1660:C:H6	1.82	0.44
38:A1:1925:U:O2'	38:A1:1927:G:N7	2.49	0.44
47:AJ:45:PRO:HB2	47:AJ:67:VAL:HG22	1.99	0.44
47:AJ:53:THR:HG23	47:AJ:59:ILE:O	2.18	0.44
49:AM:23:ILE:HD13	49:AM:63:VAL:HG12	2.00	0.44
49:AM:102:LYS:HD2	49:AM:102:LYS:HA	1.83	0.44
57:AU:89:LEU:O	57:AU:93:ILE:HG22	2.18	0.44
1:BA:32:HIS:ND1	1:BA:153:SER:OG	2.29	0.44
1:BA:157:ASP:OD1	12:BV:60:ARG:NH2	2.46	0.44
3:BC:63:VAL:HG11	3:BC:69:ILE:HD11	1.98	0.44
5:BG:163:THR:HG22	5:BG:168:THR:HB	2.00	0.44
20:BF:31:GLU:HA	20:BF:34:GLN:HB2	2.00	0.44
22:BP:86:VAL:CG2	22:BP:89:MET:HE3	2.48	0.44
27:BU:53:LYS:HD3	34:B5:1345:A:H4'	1.98	0.44
28:BZ:81:ARG:O	28:BZ:84:GLU:HG3	2.17	0.44
30:Bd:15:GLY:HA3	34:B5:1204:A:N6	2.31	0.44
34:B5:469:C:H2'	34:B5:470:A:O4'	2.17	0.44
34:B5:1321:A:H4'	34:B5:1322:A:O5'	2.17	0.44
34:B5:1357:A:H2'	34:B5:1358:G:H8	1.82	0.44
34:B5:1388:A:N7	34:B5:1411:A:N6	2.64	0.44
38:A1:563:U:H2'	38:A1:564:G:H8	1.81	0.44
38:A1:2908:G:H2'	38:A1:2909:U:C6	2.53	0.44
38:A1:3168:A:H2'	38:A1:3169:U:C6	2.52	0.44
40:A4:6:U:H2'	40:A4:7:U:C6	2.52	0.44
40:A4:37:A:OP2	70:Ah:86:ARG:NH1	2.49	0.44
55:AS:43:TYR:CE1	55:AS:47:LYS:HD2	2.53	0.44
56:AT:150:THR:HG22	56:AT:151:LEU:H	1.83	0.44
58:AV:18:PRO:HA	58:AV:51:ALA:HA	2.00	0.44
62:AZ:14:VAL:HB	69:Ag:86:LYS:HG3	1.99	0.44
62:AZ:115:LYS:HE3	62:AZ:119:GLU:OE2	2.17	0.44
22:BP:50:THR:H	22:BP:52:LYS:NZ	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BR:71:PHE:CZ	24:BR:74:GLN:HG3	2.53	0.44
24:BR:116:LYS:O	24:BR:117:LEU:HD23	2.17	0.44
31:Bg:183:LEU:H	31:Bg:183:LEU:HD23	1.82	0.44
34:B5:74:U:O2	34:B5:76:A:H5''	2.17	0.44
34:B5:182:A:H2'	34:B5:183:U:H6	1.81	0.44
34:B5:877:G:H22	34:B5:951:A:H2	1.65	0.44
34:B5:1357:A:HO2'	34:B5:1358:G:P	2.41	0.44
38:A1:669:U:H1'	38:A1:1110:PSU:H4'	1.99	0.44
38:A1:1292:C:O2'	38:A1:1293:U:OP1	2.31	0.44
38:A1:2439:A:H5'	38:A1:2440:G:OP2	2.18	0.44
42:AE:54:TYR:HA	42:AE:65:ILE:HG13	1.98	0.44
42:AE:94:GLU:OE1	42:AE:94:GLU:N	2.36	0.44
47:AJ:94:ARG:O	47:AJ:95:ASN:HB2	2.18	0.44
54:AR:122:VAL:O	54:AR:126:GLU:HG2	2.18	0.44
6:BH:142:TYR:HE2	6:BH:148:LYS:HE2	1.83	0.44
8:BJ:3:ARG:NH2	34:B5:39:A:OP1	2.50	0.44
8:BJ:13:SER:HB3	8:BJ:47:PHE:CD2	2.53	0.44
10:BN:83:GLU:HG2	10:BN:84:ILE:N	2.33	0.44
11:BO:111:ARG:NE	11:BO:112:ILE:H	1.95	0.44
20:BF:225:ARG:HG3	29:Bc:61:ARG:NH2	2.33	0.44
25:BS:11:PHE:CD1	28:BZ:41:ILE:HD13	2.53	0.44
34:B5:185:U:H2'	34:B5:186:C:H6	1.83	0.44
34:B5:262:U:H2'	34:B5:263:C:C6	2.52	0.44
34:B5:272:U:H1'	34:B5:284:G:H22	1.83	0.44
34:B5:1533:C:H4'	34:B5:1539:G:C6	2.53	0.44
38:A1:179:C:H2'	38:A1:180:C:H6	1.83	0.44
38:A1:550:A:H8	38:A1:551:A:N7	2.16	0.44
38:A1:654:C:H2'	38:A1:655:C:C6	2.53	0.44
38:A1:1290:A:H2'	38:A1:1291:A:H8	1.83	0.44
38:A1:1359:C:H2'	38:A1:1360:C:H6	1.83	0.44
38:A1:1579:C:H42	60:AX:33:ARG:NH2	2.09	0.44
38:A1:3167:A:H2'	38:A1:3168:A:O4'	2.18	0.44
39:A3:18:C:H2'	39:A3:19:C:C6	2.53	0.44
41:AD:40:HIS:CE1	56:AT:69:LYS:HA	2.53	0.44
51:AO:54[A]:TYR:CD1	51:AO:145[A]:VAL:HG21	2.53	0.44
58:AV:40:LYS:HD3	58:AV:59:MET:HE3	1.99	0.44
69:Ag:44:CYS:HB2	69:Ag:81:CYS:HB3	2.00	0.44
8:BJ:13:SER:HB3	8:BJ:47:PHE:HD2	1.82	0.44
20:BF:20:PHE:HD1	20:BF:21:THR:HG23	1.83	0.44
28:BZ:42:LEU:HD21	28:BZ:47:TYR:HD1	1.82	0.44
28:BZ:49:ARG:O	28:BZ:53:GLU:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:188:A:H2'	34:B5:188:A:N3	2.33	0.44
34:B5:333:A:H8	34:B5:333:A:O5'	2.01	0.44
34:B5:617:U:H2'	34:B5:618:U:C6	2.53	0.44
34:B5:1494:C:H2'	34:B5:1495:C:C6	2.53	0.44
34:B5:1541:G:H2'	34:B5:1542:G:C4	2.53	0.44
34:B5:1585:U:H2'	34:B5:1586:A:H8	1.82	0.44
35:AA:33:ASP:O	35:AA:37:ARG:HB2	2.18	0.44
38:A1:153:U:H4'	38:A1:158:G:H4'	1.99	0.44
38:A1:500:C:H2'	38:A1:501:A:C8	2.53	0.44
38:A1:1367:G:N2	38:A1:1368:U:O4	2.50	0.44
38:A1:2094:C:H2'	38:A1:2095:G:C8	2.52	0.44
38:A1:2235:C:C2	38:A1:2236:G:C8	3.06	0.44
38:A1:3191:G:H2'	38:A1:3192:U:C6	2.53	0.44
44:AG:118:GLU:HG2	44:AG:119:GLY:N	2.33	0.44
76:An:2:ARG:HB3	76:An:5:TRP:CD1	2.52	0.44
2:BB:146:GLN:HG2	2:BB:147:ALA:H	1.83	0.43
4:BE:125:LYS:NZ	4:BE:225:VAL:O	2.32	0.43
6:BH:37:GLU:C	6:BH:38:LEU:HD22	2.43	0.43
8:BJ:31:ALA:HA	8:BJ:36:LEU:HD12	1.98	0.43
8:BJ:44:ARG:HD2	34:B5:473:A:OP1	2.18	0.43
12:BV:36:VAL:HG11	12:BV:78:LEU:HD13	2.00	0.43
21:BK:25:LYS:HD2	21:BK:25:LYS:O	2.18	0.43
26:BT:88:VAL:O	34:B5:1467:C:O2'	2.29	0.43
32:Bf:105:TYR:OH	33:BM:46:ARG:NH2	2.44	0.43
34:B5:107:C:H2'	34:B5:108:A:H8	1.83	0.43
34:B5:410:A:OP1	58:AV:28:ASN:HB2	2.18	0.43
34:B5:1107:G:O2'	34:B5:1108:G:H5'	2.18	0.43
38:A1:2526:C:H2'	38:A1:2527:G:C8	2.53	0.43
39:A3:16:U:H2'	39:A3:17:A:H8	1.82	0.43
39:A3:26:C:H2'	39:A3:27:A:O4'	2.18	0.43
47:AJ:32:ARG:HG3	47:AJ:123:PHE:HE2	1.83	0.43
54:AR:171:ASP:OD1	54:AR:175:GLN:NE2	2.32	0.43
77:Ao:14:GLY:C	77:Ao:16:THR:H	2.26	0.43
2:BB:127:VAL:HG23	2:BB:176:VAL:HG11	1.99	0.43
4:BE:45:ILE:HG13	4:BE:61:VAL:HG21	2.00	0.43
5:BG:212:LEU:O	5:BG:216:LEU:HG	2.18	0.43
11:BO:118:VAL:HG12	11:BO:118:VAL:O	2.18	0.43
19:BD:12:VAL:HG21	30:Bd:34:TYR:HB3	1.99	0.43
20:BF:48:PHE:HB2	20:BF:67:PRO:HB3	2.00	0.43
20:BF:225:ARG:C	29:Bc:61:ARG:HH22	2.25	0.43
21:BK:25:LYS:HE3	21:BK:62:GLN:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BZ:49:ARG:O	28:BZ:52:LYS:HG2	2.19	0.43
28:BZ:95:HIS:ND1	28:BZ:96:SER:O	2.47	0.43
34:B5:1483:A:H2	34:B5:1607:G:H1'	1.82	0.43
34:B5:1748:G:H2'	34:B5:1749:A:C8	2.53	0.43
36:AB:232:ARG:HD3	36:AB:233:TRP:NE1	2.33	0.43
38:A1:440:A:H5'	38:A1:441:U:H4'	1.99	0.43
38:A1:786:A:O3'	38:A1:787:G:H8	2.01	0.43
38:A1:802:C:H2'	38:A1:803:C:C6	2.53	0.43
38:A1:821:U:H2'	38:A1:822:G:C8	2.53	0.43
38:A1:991:G:H2'	38:A1:992:A:C8	2.53	0.43
38:A1:1447:G:N7	52:AP:25:SER:OG	2.49	0.43
38:A1:1463:U:H2'	38:A1:1464:G:O4'	2.18	0.43
38:A1:1597:C:H2'	38:A1:1598:G:H8	1.83	0.43
38:A1:1639:C:OP2	69:Ag:74:ARG:NH1	2.42	0.43
38:A1:1666:G:H2'	38:A1:1667:A:C8	2.53	0.43
38:A1:1718:G:H2'	38:A1:1719:G:H8	1.82	0.43
38:A1:2763:U:O2	79:A1:3401:SPD:N1	2.50	0.43
38:A1:3159:C:H2'	38:A1:3160:U:C6	2.52	0.43
40:A4:10:A:H2'	40:A4:11:C:C6	2.53	0.43
41:AD:108:ARG:CZ	41:AD:253:PHE:HB2	2.48	0.43
44:AG:55:TYR:HA	44:AG:58:VAL:HG12	2.00	0.43
45:AH:90:MET:HG2	45:AH:181:VAL:HA	2.00	0.43
46:AI:36:LEU:HD11	46:AI:69:ARG:NE	2.33	0.43
51:AO:181[A]:ALA:O	51:AO:184[A]:THR:OG1	2.34	0.43
57:AU:81:LYS:HG2	57:AU:90:ARG:NH1	2.32	0.43
1:BA:37:VAL:HG21	1:BA:46:HIS:ND1	2.34	0.43
1:BA:155:PHE:O	12:BV:60:ARG:NH2	2.52	0.43
2:BB:48:VAL:HG13	2:BB:49:ASN:N	2.29	0.43
4:BE:155:LYS:N	4:BE:158:ASP:OD2	2.48	0.43
5:BG:161:GLU:OE1	5:BG:161:GLU:N	2.40	0.43
6:BH:139:ARG:HB2	6:BH:151:LYS:HB3	2.00	0.43
34:B5:563:U:H3'	34:B5:564:G:C8	2.53	0.43
34:B5:1582:U:C2	34:B5:1614:A:C6	3.06	0.43
34:B5:1588:G:H1	34:B5:1608:U:H3	1.67	0.43
36:AB:81:THR:O	36:AB:81:THR:OG1	2.36	0.43
36:AB:147:GLU:O	36:AB:151:ILE:HG13	2.17	0.43
36:AB:256:HIS:HA	36:AB:257:PRO:C	2.43	0.43
37:AC:170:LYS:HG2	37:AC:175:HIS:HB2	1.99	0.43
38:A1:629:U:H2'	38:A1:630:A:C8	2.52	0.43
38:A1:1182:A:H2'	38:A1:1183:C:C6	2.54	0.43
38:A1:1953:G:N1	38:A1:2093:A:C6	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2800:G:O6	63:Aa:42:ARG:NH2	2.51	0.43
39:A3:15:C:H2'	39:A3:16:U:H6	1.83	0.43
40:A4:75:G:H2'	40:A4:76:C:C6	2.53	0.43
42:AE:156:LYS:O	42:AE:160:SER:OG	2.32	0.43
50:AN:180:PHE:O	50:AN:184:LYS:HG3	2.17	0.43
57:AU:91:ASP:OD1	57:AU:91:ASP:N	2.51	0.43
5:BG:20:ASP:O	5:BG:22:HIS:N	2.52	0.43
5:BG:159:ARG:HH21	5:BG:170:THR:HG23	1.83	0.43
6:BH:169:PHE:HB2	6:BH:183:PHE:HE2	1.82	0.43
13:BW:25:VAL:HG12	13:BW:63:VAL:HB	2.01	0.43
21:BK:24:LYS:HB2	21:BK:63:TYR:HE1	1.84	0.43
21:BK:56:LYS:NZ	21:BK:58:GLN:OE1	2.52	0.43
33:BM:38:HIS:ND1	33:BM:126:TRP:O	2.51	0.43
34:B5:404:G:H2'	34:B5:405:C:H6	1.83	0.43
34:B5:1552:U:H2'	34:B5:1553:G:C8	2.54	0.43
37:AC:65:TRP:HB3	37:AC:69:ARG:HD3	1.99	0.43
38:A1:39:A:H5''	63:Aa:35:ALA:HB2	2.00	0.43
38:A1:650:C:H2'	38:A1:651:G:C8	2.54	0.43
38:A1:966:PSU:H2'	38:A1:967:A:H8	1.83	0.43
38:A1:1190:A:H2'	38:A1:1190:A:N3	2.34	0.43
38:A1:1549:U:H2'	38:A1:1550:C:C6	2.54	0.43
38:A1:1636:U:O2	38:A1:1710:C:H4'	2.18	0.43
38:A1:2930:A:H2'	38:A1:2931:C:H6	1.82	0.43
46:AI:135:ILE:HG22	46:AI:136:PHE:CD1	2.53	0.43
49:AM:125:LYS:HG2	49:AM:128:ARG:NH2	2.33	0.43
6:BH:114:ARG:HG3	34:B5:860:U:O4'	2.17	0.43
8:BJ:86:LEU:HD23	8:BJ:87:SER:O	2.19	0.43
8:BJ:139:GLN:NE2	15:BY:64:PHE:O	2.40	0.43
8:BJ:143:ILE:HG13	34:B5:768:C:C5	2.53	0.43
13:BW:107:SER:HB2	34:B5:802:G:O2'	2.18	0.43
19:BD:23:GLU:HG2	21:BK:61:TRP:NE1	2.33	0.43
19:BD:156:PHE:CE1	34:B5:1326:A:H4'	2.53	0.43
21:BK:61:TRP:CE3	30:Bd:23:VAL:HG22	2.54	0.43
24:BR:32:LYS:HZ1	34:B5:1389:C:H6	1.65	0.43
31:Bg:66:HIS:CG	31:Bg:67:ILE:N	2.85	0.43
34:B5:300:A:H2'	34:B5:301:A:C8	2.53	0.43
34:B5:331:A:H2'	34:B5:332:U:C6	2.53	0.43
36:AB:236:LYS:HE2	36:AB:236:LYS:HB2	1.87	0.43
38:A1:149:U:OP2	50:AN:49:ARG:NH2	2.51	0.43
38:A1:210:U:C2	38:A1:230:U:H4'	2.54	0.43
38:A1:500:C:H2'	38:A1:501:A:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:759:U:H2'	38:A1:760:G:O4'	2.19	0.43
38:A1:1392:G:H3'	67:Ae:125:ARG:HH12	1.84	0.43
38:A1:1486:G:H21	69:Ag:6:THR:HG22	1.83	0.43
38:A1:1517:G:OP1	74:Al:22:PRO:HG3	2.19	0.43
38:A1:2615:G:H2'	38:A1:2616:C:H6	1.83	0.43
38:A1:2664:C:OP2	47:AJ:142:LYS:NZ	2.46	0.43
38:A1:3174:A:C6	38:A1:3279:A:H1'	2.53	0.43
40:A4:39:G:H1'	40:A4:104:A:N6	2.33	0.43
43:AF:214:TRP:CE2	43:AF:219:LYS:HD2	2.53	0.43
44:AG:73:PRO:HD3	44:AG:233:TRP:CE2	2.54	0.43
51:AO:180[A]:SER:O	51:AO:184[A]:THR:HG23	2.18	0.43
67:Ae:9:ILE:HG12	67:Ae:63:THR:HB	2.00	0.43
7:BI:37:LYS:HB2	7:BI:59:ARG:HB3	2.00	0.43
11:BO:41:ARG:NH1	34:B5:896:U:O2	2.49	0.43
19:BD:163:PRO:HD3	34:B5:1332:C:O2'	2.17	0.43
19:BD:179:GLN:HG3	19:BD:179:GLN:O	2.19	0.43
22:BP:112:LEU:HD23	22:BP:112:LEU:HA	1.85	0.43
34:B5:513:U:H2'	34:B5:513:U:O2	2.19	0.43
34:B5:564:G:N1	34:B5:580:A:OP1	2.39	0.43
34:B5:872:G:N2	34:B5:1047:G:H4'	2.34	0.43
34:B5:1175:U:H2'	34:B5:1176:G:H8	1.82	0.43
34:B5:1296:A:N1	34:B5:1301:U:H5	2.16	0.43
34:B5:1477:G:H2'	34:B5:1478:G:C8	2.53	0.43
34:B5:1589:C:H2'	34:B5:1590:G:C8	2.53	0.43
34:B5:1760:G:H1'	34:B5:1781:MA6:C2	2.47	0.43
37:AC:3:ARG:HA	37:AC:3:ARG:HD2	1.79	0.43
38:A1:741:U:H2'	38:A1:742:G:O4'	2.18	0.43
38:A1:976:U:H2'	38:A1:977:C:O4'	2.19	0.43
38:A1:999:G:N3	38:A1:1002:A:N6	2.66	0.43
38:A1:1066:G:H2'	38:A1:1067:U:H6	1.82	0.43
38:A1:1279:C:C2'	38:A1:1280:C:H5'	2.49	0.43
38:A1:1911:A:H2	38:A1:2122:G:C8	2.36	0.43
38:A1:2840:C:H2'	38:A1:2841:G:O4'	2.19	0.43
46:AI:140:THR:HG21	46:AI:148:VAL:HG11	2.00	0.43
50:AN:193:ARG:O	50:AN:196:THR:HG22	2.19	0.43
53:AQ:50:LYS:HE2	53:AQ:50:LYS:HB3	1.79	0.43
57:AU:84:LEU:HD13	57:AU:93:ILE:HG23	2.01	0.43
4:BE:137:PRO:HG2	4:BE:150:PRO:HA	2.01	0.43
4:BE:162:ILE:HG22	4:BE:163:ASP:H	1.83	0.43
6:BH:81:LEU:HB3	6:BH:90:VAL:HG21	2.00	0.43
11:BO:68:ALA:O	11:BO:72:LYS:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BX:93:LEU:HD21	18:Be:8:LEU:HD21	2.00	0.43
17:Bb:74:SER:O	17:Bb:77:THR:HG22	2.18	0.43
20:BF:185:ARG:HH11	34:B5:1471:A:P	2.42	0.43
27:BU:58:LEU:HD21	27:BU:90:TYR:HD2	1.83	0.43
34:B5:1292:G:H2'	34:B5:1293:U:C6	2.53	0.43
34:B5:1322:A:H2'	34:B5:1323:C:C6	2.54	0.43
34:B5:1462:G:H2'	34:B5:1463:C:C6	2.53	0.43
34:B5:1669:U:H3	34:B5:1732:A:H62	1.66	0.43
35:AA:69:TYR:OH	38:A1:2557:A:OP1	2.29	0.43
35:AA:125:ALA:HB1	38:A1:2177:G:C6	2.54	0.43
36:AB:139:GLN:HG2	36:AB:140:ASP:H	1.82	0.43
37:AC:22:LEU:HA	37:AC:23:PRO:HD3	1.83	0.43
38:A1:594:U:H2'	38:A1:609:G:O6	2.19	0.43
38:A1:852:U:H2'	38:A1:853:G:C8	2.54	0.43
38:A1:1093:A:H5'	56:AT:116:ARG:HH11	1.83	0.43
38:A1:1228:C:N4	38:A1:1282:G:O6	2.51	0.43
38:A1:1658:G:H2'	38:A1:1659:U:C6	2.54	0.43
38:A1:2133:PSU:O2	38:A1:2147:A:H2	2.01	0.43
38:A1:2291:A:H2'	38:A1:2292:U:C6	2.53	0.43
38:A1:2662:G:H2'	38:A1:2663:G:H8	1.82	0.43
44:AG:120:LYS:HD2	44:AG:120:LYS:O	2.19	0.43
65:Ac:41:LEU:HB3	65:Ac:92:ILE:HD11	2.01	0.43
66:Ad:10:ARG:NH1	66:Ad:12:TYR:OH	2.40	0.43
2:BB:53:GLY:C	2:BB:54:LEU:HD23	2.43	0.43
2:BB:157:GLN:C	2:BB:159:SER:H	2.26	0.43
4:BE:35:PRO:HB3	4:BE:143:ASP:O	2.19	0.43
5:BG:218:GLU:HG2	5:BG:219:ARG:N	2.33	0.43
8:BJ:90:LYS:HB2	8:BJ:95:TYR:CD2	2.53	0.43
14:BX:84:THR:O	14:BX:120:VAL:HG23	2.19	0.43
20:BF:76:ARG:HD2	23:BQ:122:ARG:NH2	2.32	0.43
20:BF:160:VAL:HG21	29:Bc:45:LYS:HZ3	1.83	0.43
20:BF:163:SER:HB3	29:Bc:44:VAL:HG11	2.00	0.43
21:BK:92:ILE:HG23	21:BK:96:ASN:HA	2.00	0.43
22:BP:98:ASN:HB3	22:BP:120:SER:HB2	1.99	0.43
26:BT:86:ARG:NH1	34:B5:1601:G:OP1	2.52	0.43
31:Bg:66:HIS:HB3	31:Bg:86:ASP:HB3	2.00	0.43
34:B5:45:U:H2'	34:B5:46:A:H2'	2.01	0.43
34:B5:624:G:H2'	34:B5:625:C:C6	2.54	0.43
34:B5:903:U:O2'	34:B5:905:A:N7	2.38	0.43
34:B5:907:A:H1'	34:B5:997:G:O2'	2.19	0.43
34:B5:1356:U:H5'	34:B5:1357:A:OP2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1381:U:H2'	34:B5:1382:A:C8	2.54	0.43
34:B5:1556:A:H1'	34:B5:1560:U:OP2	2.19	0.43
34:B5:1579:U:H2'	34:B5:1580:C:C6	2.54	0.43
34:B5:1733:C:H2'	34:B5:1734:U:H6	1.83	0.43
36:AB:56:ILE:HD12	36:AB:356:LEU:HD22	2.01	0.43
36:AB:226:PHE:O	38:A1:1886:A:O2'	2.33	0.43
38:A1:38:U:H4'	63:Aa:32:ARG:HD2	2.00	0.43
38:A1:100:A:H2'	38:A1:101:G:N3	2.33	0.43
38:A1:142:C:H2'	38:A1:143:G:O4'	2.18	0.43
38:A1:1289:G:H2'	38:A1:1290:A:C8	2.54	0.43
38:A1:2096:A:H2'	38:A1:2097:U:C6	2.54	0.43
38:A1:2655:U:H4'	38:A1:2656:A:O4'	2.18	0.43
38:A1:2661:G:H2'	38:A1:2662:G:C8	2.54	0.43
38:A1:2836:C:H2'	38:A1:2837:A:O4'	2.19	0.43
38:A1:2961:G:H2'	38:A1:2962:U:C6	2.54	0.43
38:A1:3006:A:C2	38:A1:3141:A:C4	3.07	0.43
40:A4:67:U:H2'	40:A4:68:G:H8	1.84	0.43
47:AJ:106:ILE:HD11	47:AJ:109:HIS:HB2	2.00	0.43
2:BB:116:LYS:HG3	34:B5:931:C:H5''	2.01	0.43
4:BE:149:TYR:HA	4:BE:150:PRO:HD3	1.87	0.43
6:BH:21:ALA:HA	6:BH:24:PHE:HE1	1.83	0.43
7:BI:61:GLU:HG3	7:BI:77:ARG:NH2	2.32	0.43
8:BJ:143:ILE:HG22	8:BJ:145:SER:H	1.83	0.43
9:BL:2:SER:OG	9:BL:3:THR:N	2.41	0.43
19:BD:16:VAL:HG11	30:Bd:22:ARG:CZ	2.48	0.43
22:BP:86:VAL:HG22	22:BP:89:MET:HE3	2.01	0.43
24:BR:16:LEU:HD23	24:BR:16:LEU:HA	1.87	0.43
29:Bc:47:PRO:HB3	34:B5:1615:C:OP1	2.19	0.43
34:B5:236:A:H5''	34:B5:237:C:C5	2.53	0.43
34:B5:852:C:H2'	34:B5:853:G:O4'	2.18	0.43
34:B5:1424:A:H2'	34:B5:1425:A:O4'	2.18	0.43
34:B5:1592:A:H2'	34:B5:1593:A:H8	1.83	0.43
34:B5:1759:C:H2'	34:B5:1760:G:C8	2.54	0.43
37:AC:30:ILE:O	37:AC:32:PRO:HD3	2.18	0.43
38:A1:68:C:O3'	50:AN:177:GLY:HA2	2.17	0.43
38:A1:209:A:H4'	38:A1:211:A:N7	2.33	0.43
38:A1:760:G:N2	38:A1:770:G:N3	2.66	0.43
38:A1:767:U:C2	38:A1:768:C:C6	3.07	0.43
38:A1:2292:U:H2'	38:A1:2293:C:C6	2.54	0.43
38:A1:2631:U:OP1	38:A1:2757:U:O2'	2.34	0.43
38:A1:3110:C:O2'	45:AH:155:SER:OG	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:A3:87:G:H2'	39:A3:88:G:H8	1.84	0.43
39:A3:112:G:H2'	39:A3:113:C:H6	1.82	0.43
41:AD:60:ILE:HD11	41:AD:93:THR:HA	2.01	0.43
44:AG:52:TRP:O	44:AG:57:ARG:NH1	2.51	0.43
51:AO:47[A]:PHE:HE1	51:AO:141[A]:LEU:HA	1.84	0.43
73:Ak:27:ILE:HD12	73:Ak:39:ARG:HH21	1.84	0.43
22:BP:30:THR:O	22:BP:34:VAL:HG23	2.19	0.43
23:BQ:74:HIS:NE2	34:B5:1481:C:O2'	2.32	0.43
31:Bg:20:VAL:HG11	31:Bg:310:ILE:HG12	2.01	0.43
31:Bg:179:LYS:HG2	31:Bg:191:ASP:HB3	2.01	0.43
31:Bg:275:ARG:HE	31:Bg:276:PRO:HD2	1.83	0.43
32:Bf:140:TYR:HE1	32:Bf:145:HIS:HA	1.84	0.43
34:B5:430:G:H2'	34:B5:431:C:H6	1.84	0.43
35:AA:118:GLU:OE1	38:A1:2158:A:O2'	2.31	0.43
35:AA:127:ALA:HB2	35:AA:134:VAL:HG23	2.01	0.43
36:AB:266:ARG:NH2	38:A1:2392:C:H1'	2.34	0.43
37:AC:161:LYS:HB2	37:AC:164:GLU:HG2	2.00	0.43
38:A1:156:G:OP2	71:Ai:25:LYS:HB3	2.19	0.43
38:A1:1494:U:H4'	38:A1:1495:U:O5'	2.19	0.43
38:A1:2429:G:H2'	38:A1:2430:A:H8	1.84	0.43
39:A3:47:C:OP1	41:AD:95:TRP:N	2.44	0.43
39:A3:95:A:N3	55:AS:119:ARG:HD2	2.34	0.43
47:AJ:92:ARG:HG2	47:AJ:174:LYS:HB2	2.00	0.43
47:AJ:96:PHE:HB2	47:AJ:156:LYS:HZ2	1.84	0.43
54:AR:95:TRP:CZ2	54:AR:99:LEU:HD22	2.54	0.43
68:Af:49:ILE:HD11	68:Af:71:VAL:HG22	2.00	0.43
70:Ah:105:ARG:O	70:Ah:109:ILE:HG12	2.19	0.43
1:BA:14:ALA:HA	1:BA:17:LEU:HD12	2.01	0.42
1:BA:148:ASP:OD2	1:BA:165:ARG:NH2	2.52	0.42
3:BC:101:VAL:HG21	3:BC:208:GLU:HG3	2.00	0.42
7:BI:137:LYS:HE2	7:BI:141:ARG:HH21	1.84	0.42
11:BO:82:LYS:HD3	11:BO:118:VAL:HG21	2.02	0.42
14:BX:60:GLU:OE2	18:Be:3:LYS:HB2	2.19	0.42
15:BY:8:ARG:HG2	34:B5:780:A:C4	2.54	0.42
15:BY:26:ASP:OD1	15:BY:26:ASP:N	2.50	0.42
17:Bb:56:CYS:SG	17:Bb:57:GLU:N	2.92	0.42
18:Be:33:ARG:NH2	34:B5:477:A:O2'	2.52	0.42
25:BS:123:ARG:HD2	34:B5:1546:G:OP1	2.19	0.42
27:BU:61:LYS:HE2	27:BU:61:LYS:HB2	1.84	0.42
31:Bg:113:VAL:HG22	31:Bg:122:ILE:HD11	2.01	0.42
31:Bg:223:TRP:NE1	31:Bg:230:ALA:HB2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:1080:U:H2'	34:B5:1081:A:O4'	2.19	0.42
34:B5:1170:G:C2	34:B5:1171:A:C8	3.07	0.42
34:B5:1170:G:N2	34:B5:1571:C:H4'	2.34	0.42
34:B5:1310:U:H2'	34:B5:1311:U:C6	2.54	0.42
34:B5:1429:G:H2'	34:B5:1430:U:C6	2.53	0.42
38:A1:92:G:H5'	38:A1:94:G:N7	2.33	0.42
38:A1:438:A:H2	38:A1:620:U:H5	1.65	0.42
38:A1:1035:G:H3'	38:A1:1036:A:H8	1.83	0.42
38:A1:1762:C:H3'	38:A1:1763:U:C5'	2.49	0.42
38:A1:2419:A:H2'	38:A1:2420:C:C6	2.53	0.42
38:A1:3275:U:H5'	68:Af:68:TRP:CZ2	2.54	0.42
40:A4:68:G:H2'	40:A4:69:U:C6	2.54	0.42
42:AE:60:ASP:OD1	42:AE:60:ASP:N	2.48	0.42
46:AI:205:SER:HB3	46:AI:208:ASN:ND2	2.34	0.42
51:AO:40[A]:GLU:HG3	51:AO:40[A]:GLU:O	2.19	0.42
61:AY:23:PRO:HG2	61:AY:26:GLN:HG2	2.00	0.42
68:Af:75:HIS:HB2	68:Af:82:ARG:HG3	2.01	0.42
77:Ao:53:GLN:NE2	77:Ao:55:LYS:O	2.52	0.42
2:BB:149:GLN:HG3	34:B5:1066:C:O3'	2.18	0.42
4:BE:16:HIS:NE2	34:B5:757:A:OP1	2.52	0.42
4:BE:71:LYS:HA	4:BE:76:VAL:HA	2.01	0.42
4:BE:79:ASP:HB3	4:BE:82:TYR:HB2	2.01	0.42
4:BE:197:HIS:HB3	4:BE:209:HIS:HD2	1.84	0.42
5:BG:64:LYS:O	5:BG:100:ALA:HB2	2.19	0.42
7:BI:56:ARG:NH2	34:B5:332:U:OP1	2.52	0.42
10:BN:55:ARG:HH22	17:Bb:51:GLN:NE2	2.16	0.42
19:BD:5:ILE:HG23	19:BD:10:LYS:HB2	2.00	0.42
21:BK:64:TYR:HB3	21:BK:66:TYR:CE1	2.54	0.42
22:BP:81:ARG:NH1	22:BP:97:TYR:O	2.52	0.42
27:BU:53:LYS:HE3	27:BU:92:ASP:OD1	2.19	0.42
31:Bg:23:LEU:HD22	31:Bg:33:LEU:HD11	2.01	0.42
34:B5:14:C:H2'	34:B5:15:U:C6	2.53	0.42
34:B5:30:G:H2'	34:B5:31:C:H6	1.82	0.42
34:B5:176:C:H2'	34:B5:177:U:C6	2.54	0.42
34:B5:185:U:H2'	34:B5:186:C:C6	2.54	0.42
34:B5:431:C:H2'	34:B5:432:G:H8	1.83	0.42
34:B5:1308:G:H2'	34:B5:1309:C:H6	1.84	0.42
35:AA:3:ARG:HB3	35:AA:207:VAL:HG22	2.01	0.42
35:AA:190:ARG:HG3	35:AA:191:LEU:HD22	2.01	0.42
36:AB:250:ALA:HB1	38:A1:2947:G:N3	2.34	0.42
36:AB:281:LYS:HD2	36:AB:283:TYR:HE1	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:380:MET:SD	36:AB:383:LEU:HD11	2.60	0.42
37:AC:51:ALA:O	40:A4:26:U:O2'	2.37	0.42
38:A1:3:U:C5	40:A4:157:U:H1'	2.53	0.42
38:A1:807:A:H61	38:A1:934:G:H22	1.67	0.42
38:A1:1103:A:O2'	38:A1:1104:G:H5'	2.19	0.42
38:A1:1881:A:H2'	38:A1:1882:G:C8	2.54	0.42
38:A1:2534:G:O6	38:A1:2545:C:N4	2.51	0.42
39:A3:37:G:N2	39:A3:41:G:N3	2.67	0.42
44:AG:106:LYS:O	44:AG:110:THR:HG23	2.18	0.42
44:AG:214:LEU:O	44:AG:218:ILE:HG12	2.20	0.42
47:AJ:52:TYR:CE2	47:AJ:54:VAL:HG22	2.54	0.42
47:AJ:75:LYS:NZ	47:AJ:79:ILE:HD11	2.34	0.42
47:AJ:80:LEU:HD22	47:AJ:129:VAL:HG11	2.01	0.42
76:An:9:ARG:O	76:An:12:ARG:HG2	2.19	0.42
77:Ao:47:GLN:NE2	77:Ao:53:GLN:OE1	2.36	0.42
3:BC:59:HIS:CE1	3:BC:239:PRO:HD3	2.54	0.42
6:BH:111:LYS:O	34:B5:811:A:N6	2.42	0.42
7:BI:36:THR:O	7:BI:96:LEU:N	2.38	0.42
18:Be:23:LYS:HG2	34:B5:586:G:H5''	2.01	0.42
21:BK:54:TYR:HB3	21:BK:72:GLY:HA3	2.01	0.42
23:BQ:59:LYS:HB3	23:BQ:59:LYS:HE2	1.81	0.42
31:Bg:161:LYS:HB3	31:Bg:164:ASP:HB3	2.01	0.42
34:B5:12:U:H2'	34:B5:13:C:H6	1.84	0.42
34:B5:250:C:H2'	34:B5:251:A:C8	2.54	0.42
34:B5:339:C:C2	34:B5:340:U:C5	3.08	0.42
34:B5:566:C:H2'	34:B5:567:A:C8	2.55	0.42
34:B5:1585:U:H2'	34:B5:1586:A:C8	2.54	0.42
38:A1:65:A:H1'	38:A1:77:A:H1'	2.01	0.42
38:A1:287:G:OP1	50:AN:179:LYS:HD3	2.18	0.42
38:A1:1266:G:H2'	38:A1:1267:U:C6	2.54	0.42
50:AN:138:GLN:HA	50:AN:143:ARG:HH11	1.83	0.42
66:Ad:10:ARG:HD3	66:Ad:108:VAL:HG22	2.01	0.42
70:Ah:41:LEU:HD12	70:Ah:41:LEU:HA	1.91	0.42
1:BA:140:ASN:ND2	3:BC:60:SER:O	2.53	0.42
3:BC:44:LEU:O	3:BC:49:LYS:N	2.50	0.42
4:BE:93:ASP:OD1	4:BE:93:ASP:N	2.53	0.42
7:BI:72:ILE:HG21	7:BI:112:TRP:CZ2	2.54	0.42
15:BY:81:GLU:HA	15:BY:84:LYS:HG2	2.01	0.42
19:BD:161:GLY:CA	34:B5:1331:A:H61	2.32	0.42
24:BR:5:ARG:HB3	24:BR:9:VAL:CG1	2.49	0.42
25:BS:114:GLU:O	25:BS:117:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BT:79:LEU:HD13	34:B5:1523:G:C8	2.55	0.42
27:BU:64:LYS:HG3	27:BU:81:THR:HG23	2.00	0.42
31:Bg:45:TRP:CZ3	31:Bg:57:PRO:HD3	2.55	0.42
31:Bg:189:GLU:OE1	31:Bg:189:GLU:N	2.51	0.42
31:Bg:197:SER:OG	31:Bg:216:LYS:N	2.52	0.42
34:B5:36:C:H2'	34:B5:37:U:C6	2.54	0.42
34:B5:244:A:H2'	34:B5:245:U:C6	2.55	0.42
34:B5:825:U:H2'	34:B5:826:U:O4'	2.19	0.42
34:B5:1159:C:N4	34:B5:1285:U:H5''	2.33	0.42
34:B5:1178:G:C6	34:B5:1179:G:C5	3.08	0.42
34:B5:1240:U:H2'	34:B5:1242:A:OP2	2.19	0.42
34:B5:1590:G:H2'	34:B5:1591:C:C6	2.54	0.42
34:B5:1684:U:H2'	34:B5:1685:G:C8	2.54	0.42
34:B5:1780:G:H2'	34:B5:1781:MA6:C8	2.50	0.42
36:AB:250:ALA:HB1	38:A1:2947:G:C2	2.54	0.42
37:AC:104:LYS:NZ	38:A1:800:G:O6	2.39	0.42
38:A1:254:A:H2'	38:A1:255:A:C8	2.55	0.42
38:A1:489:U:H2'	38:A1:490:C:O4'	2.19	0.42
38:A1:916:G:H5'	38:A1:917:A:OP1	2.19	0.42
38:A1:1449:A:H2'	38:A1:1450:G:O4'	2.19	0.42
38:A1:1466:G:N2	38:A1:1510:G:H5''	2.35	0.42
38:A1:1578:C:H2'	38:A1:1579:C:C6	2.54	0.42
38:A1:1733:G:H2'	38:A1:1734:G:C8	2.53	0.42
38:A1:2285:C:OP2	38:A1:2286:U:O2'	2.32	0.42
38:A1:2520:A:H2'	38:A1:2521:U:C6	2.53	0.42
38:A1:3166:C:H2'	38:A1:3167:A:H8	1.83	0.42
38:A1:3271:G:OP2	52:AP:170:SER:OG	2.27	0.42
59:AW:6:ASP:HB3	59:AW:11:ALA:H	1.85	0.42
76:An:9:ARG:HA	76:An:12:ARG:HG2	2.00	0.42
76:An:15:ARG:HG3	76:An:15:ARG:NH1	2.32	0.42
1:BA:27:ARG:NH1	1:BA:43:ASP:O	2.53	0.42
6:BH:99:LEU:HD23	6:BH:99:LEU:HA	1.89	0.42
8:BJ:35:GLY:HA2	18:Be:36:LYS:NZ	2.35	0.42
8:BJ:153:GLU:OE2	8:BJ:154:LYS:NZ	2.40	0.42
9:BL:55:ASP:OD2	9:BL:113:PRO:HD2	2.18	0.42
20:BF:61:TYR:HE2	20:BF:165:LEU:HB2	1.84	0.42
20:BF:140:THR:HA	20:BF:214:LYS:HD3	2.01	0.42
34:B5:1235:C:C2	34:B5:1236:A:C8	3.08	0.42
34:B5:1374:C:H2'	34:B5:1375:A:C8	2.54	0.42
34:B5:1722:A:H2'	34:B5:1723:U:O4'	2.18	0.42
35:AA:80:GLU:HG2	78:Ap:76:ALA:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:AB:250:ALA:HB3	38:A1:2880:PSU:O4	2.19	0.42
38:A1:201:A:H2'	38:A1:202:G:H8	1.85	0.42
38:A1:2985:C:H2'	38:A1:2986:U:C6	2.54	0.42
40:A4:15:G:H2'	40:A4:16:G:C8	2.55	0.42
49:AM:32:LEU:HD11	49:AM:94:TRP:CD1	2.55	0.42
58:AV:104:ASN:HB2	58:AV:105:PRO:HD2	2.02	0.42
76:An:7:LYS:HE2	76:An:11:ARG:HH22	1.85	0.42
3:BC:82:ASN:OD1	3:BC:83:ILE:N	2.53	0.42
7:BI:175:GLN:NE2	34:B5:331:A:OP2	2.45	0.42
10:BN:91:LEU:HB3	10:BN:122:ILE:HG12	2.02	0.42
10:BN:142:GLU:HB2	10:BN:145:THR:HG22	2.01	0.42
14:BX:69:ARG:HA	14:BX:69:ARG:HD3	1.78	0.42
15:BY:44:LEU:HD12	15:BY:48:TYR:CE2	2.55	0.42
15:BY:122:GLY:O	15:BY:125:LEU:HG	2.19	0.42
19:BD:210:GLU:HA	19:BD:211:PRO:HD3	1.91	0.42
20:BF:185:ARG:HD2	34:B5:1471:A:OP1	2.20	0.42
23:BQ:39:VAL:O	23:BQ:45:ARG:NE	2.37	0.42
25:BS:126:ARG:HD2	25:BS:133:VAL:HA	2.01	0.42
27:BU:56:VAL:HG22	34:B5:1345:A:H1'	2.01	0.42
34:B5:103:A:H4'	34:B5:105:A:C8	2.55	0.42
34:B5:586:G:H2'	34:B5:587:C:C6	2.55	0.42
34:B5:1087:A:H2'	34:B5:1088:A:C8	2.54	0.42
34:B5:1215:C:H2'	34:B5:1216:C:C6	2.55	0.42
34:B5:1254:U:H2'	34:B5:1255:G:O4'	2.19	0.42
34:B5:1334:U:H2'	34:B5:1335:U:C6	2.54	0.42
34:B5:1342:C:C2	34:B5:1343:U:C5	3.08	0.42
34:B5:1487:A:H2'	34:B5:1488:G:H8	1.85	0.42
34:B5:1647:U:H2'	34:B5:1648:A:H8	1.83	0.42
35:AA:118:GLU:OE2	38:A1:2177:G:N2	2.50	0.42
36:AB:295:ALA:HB2	36:AB:301:THR:O	2.18	0.42
38:A1:442:G:H2'	38:A1:443:G:H5'	2.01	0.42
38:A1:1095:U:H3	56:AT:127:GLN:NE2	2.17	0.42
38:A1:2282:U:OP1	38:A1:2973:G:O2'	2.24	0.42
38:A1:2533:G:C6	38:A1:2547:A:N6	2.88	0.42
38:A1:2553:U:C4	69:Ag:95:ILE:HD13	2.54	0.42
38:A1:2842:U:O2	38:A1:2842:U:H2'	2.19	0.42
38:A1:3353:G:O2'	38:A1:3356:G:H5''	2.18	0.42
40:A4:145:U:H2'	40:A4:146:U:C6	2.54	0.42
49:AM:35:ILE:HA	49:AM:46:ILE:HG22	2.02	0.42
55:AS:13:ARG:NH1	55:AS:50:LYS:O	2.52	0.42
66:Ad:9:THR:HG23	66:Ad:76:SER:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:81:PHE:CD2	1:BA:167:LYS:HB2	2.55	0.42
2:BB:53:GLY:O	2:BB:54:LEU:HD23	2.19	0.42
6:BH:126:LEU:HD23	6:BH:126:LEU:HA	1.91	0.42
7:BI:39:GLY:O	7:BI:59:ARG:HB2	2.20	0.42
12:BV:46:ILE:HG12	12:BV:49:GLU:OE1	2.20	0.42
22:BP:16:SER:OG	25:BS:93:THR:O	2.24	0.42
31:Bg:122:ILE:HG23	31:Bg:134:TRP:HB2	2.01	0.42
31:Bg:157:VAL:HG12	31:Bg:168:THR:O	2.20	0.42
34:B5:190:C:O2'	34:B5:191:C:O4'	2.37	0.42
34:B5:296:U:H2'	34:B5:297:U:O2	2.20	0.42
34:B5:575:C:H4'	34:B5:582:U:C4	2.54	0.42
34:B5:887:A:H2'	34:B5:888:U:C6	2.54	0.42
38:A1:1575:A:H3'	38:A1:1576:G:H8	1.85	0.42
38:A1:1709:C:H2'	38:A1:1710:C:H6	1.85	0.42
38:A1:2441:A:N1	38:A1:2507:C:H1'	2.34	0.42
38:A1:2722:U:O2'	56:AT:88:ARG:O	2.26	0.42
38:A1:3106:A:H2'	38:A1:3107:U:O4'	2.19	0.42
38:A1:3387:U:H2'	38:A1:3388:C:C6	2.55	0.42
39:A3:6:C:O2'	41:AD:50:ARG:NH2	2.51	0.42
48:AL:67:ARG:HD2	63:Aa:105:LEU:O	2.20	0.42
53:AQ:22:ASP:HA	53:AQ:27:LYS:HE2	2.01	0.42
53:AQ:176:ARG:HA	53:AQ:182:LYS:O	2.20	0.42
61:AY:60:ARG:HB2	61:AY:103:LYS:HB3	2.01	0.42
2:BB:84:ILE:HD11	2:BB:100:PHE:CD1	2.55	0.42
3:BC:242:ILE:HG13	3:BC:243:TYR:N	2.35	0.42
7:BI:49:ARG:HH12	34:B5:399:A:P	2.42	0.42
8:BJ:98:ALA:O	8:BJ:100:LYS:NZ	2.34	0.42
14:BX:103:LEU:HB3	14:BX:126:LYS:HB2	2.02	0.42
15:BY:22:GLN:HA	15:BY:74:LEU:HD23	2.01	0.42
19:BD:158:ILE:HG12	19:BD:189:MET:SD	2.59	0.42
19:BD:177:MET:CE	19:BD:182:LEU:HB2	2.39	0.42
23:BQ:47:LYS:HB3	23:BQ:82:ARG:HD2	2.02	0.42
27:BU:72:ASN:HD21	27:BU:74:GLU:HG2	1.85	0.42
32:Bf:105:TYR:HA	32:Bf:131:PHE:CZ	2.54	0.42
34:B5:1117:U:H2'	34:B5:1118:G:H8	1.84	0.42
34:B5:1117:U:H2'	34:B5:1118:G:C8	2.55	0.42
34:B5:1739:C:H2'	34:B5:1740:A:H8	1.83	0.42
38:A1:835:G:O2'	38:A1:857:G:N2	2.38	0.42
38:A1:929:A:H2'	38:A1:930:U:C6	2.54	0.42
38:A1:1215:U:H2'	38:A1:1216:C:C6	2.55	0.42
38:A1:1723:A:OP1	54:AR:128:LYS:NZ	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2273:G:N2	38:A1:2311:G:H2'	2.35	0.42
38:A1:2332:A:H2'	38:A1:2333:C:O4'	2.20	0.42
38:A1:2533:G:C6	38:A1:2547:A:C6	3.08	0.42
38:A1:3107:U:H2'	38:A1:3108:G:H8	1.84	0.42
38:A1:3198:U:O4	45:AH:26:LYS:HB2	2.18	0.42
38:A1:3215:A:H2	42:AE:157:GLN:HG2	1.85	0.42
40:A4:82:U:H5''	40:A4:84:C:OP1	2.20	0.42
41:AD:52:VAL:HG21	41:AD:65:ILE:HD12	2.02	0.42
41:AD:122:VAL:HG13	41:AD:122:VAL:O	2.20	0.42
42:AE:70:LYS:HA	42:AE:70:LYS:HD2	1.81	0.42
58:AV:54:LEU:HD21	58:AV:119:GLY:HA3	2.02	0.42
69:Ag:46:ASP:HB2	69:Ag:84:CYS:SG	2.60	0.42
1:BA:198:MET:SD	24:BR:88:VAL:O	2.78	0.42
4:BE:105:VAL:HG21	4:BE:245:LYS:N	2.35	0.42
8:BJ:49:LEU:HD11	8:BJ:104:PHE:CE1	2.55	0.42
8:BJ:129:ILE:HG22	8:BJ:142:ASN:HA	2.02	0.42
10:BN:46:THR:HB	10:BN:47:PRO:HD2	2.01	0.42
12:BV:36:VAL:HB	12:BV:51:VAL:HG23	2.02	0.42
20:BF:185:ARG:NH1	34:B5:1471:A:OP2	2.49	0.42
22:BP:37:ALA:HB1	22:BP:41:VAL:HG13	2.02	0.42
23:BQ:136:SER:HA	34:B5:1581:C:H5'	2.02	0.42
27:BU:96:PRO:O	27:BU:100:VAL:HG13	2.20	0.42
34:B5:406:U:H2'	34:B5:407:A:C8	2.52	0.42
34:B5:410:A:H2'	34:B5:411:C:C6	2.55	0.42
34:B5:800:U:H2'	34:B5:801:G:C8	2.54	0.42
34:B5:888:U:H2'	34:B5:889:U:C6	2.55	0.42
34:B5:1173:C:H1'	34:B5:1601:G:H22	1.84	0.42
34:B5:1393:C:H2'	34:B5:1394:G:C8	2.51	0.42
34:B5:1652:C:H2'	34:B5:1653:C:H6	1.84	0.42
38:A1:271:C:O2	71:Ai:82:ARG:NH2	2.34	0.42
38:A1:309:U:H5	38:A1:2780:A:N1	2.18	0.42
38:A1:385:A:H2'	38:A1:386:A:C8	2.55	0.42
38:A1:432:G:H2'	38:A1:433:A:C8	2.54	0.42
38:A1:503:C:H2'	38:A1:504:A:H8	1.85	0.42
38:A1:1295:G:H2'	38:A1:1296:C:C6	2.54	0.42
38:A1:2579:G:OP2	38:A1:2580:A:O2'	2.29	0.42
38:A1:2794:G:O2'	38:A1:2795:U:OP2	2.32	0.42
38:A1:2812:C:H2'	38:A1:2813:A:C8	2.55	0.42
42:AE:43:LEU:HD11	42:AE:85:ILE:HG13	2.01	0.42
43:AF:163:LEU:O	43:AF:165:ASP:N	2.53	0.42
52:AP:47:TYR:OH	52:AP:57:ALA:O	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Ap:8:VAL:O	78:Ap:11:THR:OG1	2.38	0.42
1:BA:9:LEU:HG	1:BA:14:ALA:HB2	2.02	0.42
1:BA:175:TYR:HD1	1:BA:202:TYR:CE1	2.38	0.42
7:BI:113:PHE:CZ	7:BI:119:GLN:HB2	2.55	0.42
11:BO:111:ARG:NH2	16:Ba:57:SER:HA	2.35	0.42
17:Bb:58:SER:OG	17:Bb:59:CYS:N	2.53	0.42
21:BK:29:GLN:HB3	21:BK:39:ASN:OD1	2.19	0.42
34:B5:40:A:H2'	34:B5:41:A:O4'	2.19	0.42
34:B5:58:U:OP1	34:B5:456:A:O2'	2.38	0.42
34:B5:87:C:O2'	34:B5:169:A:N1	2.48	0.42
34:B5:448:C:H2'	34:B5:449:C:H6	1.85	0.42
34:B5:900:A:H2'	34:B5:901:G:C8	2.54	0.42
34:B5:959:U:O2	34:B5:959:U:H2'	2.19	0.42
34:B5:1323:C:H2'	34:B5:1324:G:C8	2.55	0.42
34:B5:1469:A:H2'	34:B5:1470:C:C6	2.55	0.42
36:AB:350:ALA:C	36:AB:351:LEU:HD23	2.45	0.42
38:A1:716:A:C5	63:Aa:117:ARG:HG3	2.54	0.42
38:A1:1482:A:H2'	38:A1:1482:A:N3	2.35	0.42
38:A1:2953:U:H2'	38:A1:2954:U:H2'	2.01	0.42
38:A1:2986:U:C2	38:A1:2987:A:C8	3.08	0.42
39:A3:45:A:OP1	41:AD:151:GLN:NE2	2.52	0.42
42:AE:80:ASN:HB3	42:AE:83:TYR:HD1	1.85	0.42
44:AG:228:GLU:O	44:AG:231:LYS:HG2	2.20	0.42
56:AT:151:LEU:HD12	56:AT:151:LEU:HA	1.87	0.42
63:Aa:98:THR:HG23	63:Aa:98:THR:O	2.20	0.42
1:BA:59:LEU:HB2	12:BV:79:LEU:HD11	2.01	0.41
1:BA:90:ALA:HA	1:BA:95:ALA:HB3	2.02	0.41
2:BB:45:LYS:HZ2	11:BO:13:VAL:HA	1.85	0.41
4:BE:77:ARG:NH2	34:B5:122:U:O3'	2.53	0.41
4:BE:100:ARG:NH2	4:BE:118:GLU:HG2	2.34	0.41
5:BG:98:ARG:NH2	5:BG:105:ASP:OD1	2.50	0.41
5:BG:202:ARG:NH2	34:B5:179:A:H61	2.14	0.41
8:BJ:65:LYS:HD2	8:BJ:65:LYS:O	2.20	0.41
9:BL:3:THR:HG23	9:BL:52:SER:OG	2.20	0.41
13:BW:90:THR:HA	13:BW:94:LEU:HD23	2.02	0.41
14:BX:48:HIS:CD2	14:BX:105:ALA:HB2	2.54	0.41
14:BX:65:ASN:CG	34:B5:575:C:H41	2.28	0.41
26:BT:63:ARG:O	26:BT:67:MET:HG2	2.19	0.41
26:BT:115:GLU:OE2	26:BT:123:ARG:NE	2.53	0.41
31:Bg:47:LEU:HD12	31:Bg:54:PHE:CE2	2.56	0.41
31:Bg:151:VAL:HG11	31:Bg:171:SER:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:263:C:H2'	34:B5:264:G:H8	1.84	0.41
34:B5:1579:U:H2'	34:B5:1580:C:H6	1.85	0.41
34:B5:1648:A:H2'	34:B5:1649:G:C8	2.55	0.41
36:AB:18:PRO:HG2	36:AB:20:LYS:HD2	2.02	0.41
37:AC:93:MET:HB2	38:A1:658:G:N2	2.34	0.41
38:A1:443:G:O6	38:A1:490:C:N4	2.38	0.41
38:A1:551:A:C4	38:A1:552:G:C8	3.08	0.41
38:A1:916:G:H4'	38:A1:917:A:O5'	2.19	0.41
38:A1:945:C:H2'	38:A1:946:U:H6	1.85	0.41
38:A1:1295:G:H1'	55:AS:113:ARG:O	2.20	0.41
38:A1:1661:G:H2'	38:A1:1662:G:H8	1.82	0.41
38:A1:1699:A:C6	38:A1:1747:G:C6	3.08	0.41
38:A1:1855:U:H2'	38:A1:1856:C:H6	1.85	0.41
38:A1:2533:G:O6	38:A1:2547:A:N6	2.53	0.41
38:A1:2597:U:O2	50:AN:125:SER:OG	2.30	0.41
38:A1:2660:G:H1'	38:A1:2744:U:H1'	2.02	0.41
38:A1:2699:G:H5''	56:AT:16:GLN:HE22	1.84	0.41
38:A1:2765:C:H2'	38:A1:2766:U:H6	1.85	0.41
38:A1:3101:G:H2'	38:A1:3102:G:C8	2.55	0.41
38:A1:3232:G:H2'	38:A1:3233:C:H6	1.85	0.41
40:A4:27:U:H2'	40:A4:28:C:C6	2.54	0.41
40:A4:76:C:C2	40:A4:77:A:C8	3.08	0.41
44:AG:64:ILE:O	44:AG:68:ARG:HG2	2.20	0.41
44:AG:82:LEU:HD23	44:AG:82:LEU:HA	1.89	0.41
46:AI:47:PRO:HB3	46:AI:171:TRP:CZ2	2.55	0.41
47:AJ:75:LYS:O	47:AJ:79:ILE:HD12	2.20	0.41
48:AL:27:ASP:OD1	48:AL:27:ASP:N	2.52	0.41
52:AP:13:LYS:HG3	52:AP:154:GLU:OE1	2.20	0.41
60:AX:59:SER:HB3	60:AX:102:LEU:HG	2.02	0.41
62:AZ:10:VAL:O	62:AZ:83:THR:OG1	2.33	0.41
66:Ad:79:ARG:HA	66:Ad:89:LEU:HD23	2.01	0.41
67:Ae:3:SER:HB2	67:Ae:71:HIS:NE2	2.35	0.41
69:Ag:39:ALA:HB3	69:Ag:56:THR:HG22	2.01	0.41
74:Al:44:TRP:CE2	74:Al:45:ARG:HG3	2.54	0.41
11:BO:16:VAL:O	11:BO:30:VAL:HA	2.20	0.41
11:BO:47:LYS:HE3	11:BO:63:ALA:N	2.35	0.41
14:BX:61:SER:OG	14:BX:65:ASN:O	2.27	0.41
17:Bb:50:ALA:O	17:Bb:51:GLN:HG2	2.20	0.41
19:BD:72:LEU:HA	19:BD:75:LYS:HG2	2.01	0.41
19:BD:220:PRO:O	31:Bg:193:ILE:HG13	2.20	0.41
26:BT:105:LEU:HD13	26:BT:122:ARG:HH11	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BU:80:GLU:OE1	30:Bd:54:LYS:HD3	2.20	0.41
34:B5:56:U:O4	34:B5:94:U:N3	2.53	0.41
34:B5:792:U:H2'	34:B5:793:A:C8	2.55	0.41
34:B5:1212:G:H2'	34:B5:1213:G:H8	1.84	0.41
34:B5:1728:A:H2'	34:B5:1729:C:C6	2.55	0.41
36:AB:124:LYS:NZ	38:A1:3297:U:O4	2.53	0.41
37:AC:320:ASN:HD22	38:A1:505:G:P	2.43	0.41
38:A1:426:G:H5'	67:Ae:50:ILE:HG22	2.02	0.41
38:A1:440:A:H5'	38:A1:441:U:C4'	2.50	0.41
38:A1:446:U:H2'	38:A1:448:U:N3	2.34	0.41
38:A1:788:C:H2'	38:A1:789:A:C8	2.55	0.41
38:A1:792:G:H2'	38:A1:793:C:H6	1.85	0.41
38:A1:833:G:OP1	54:AR:86:GLU:HB3	2.20	0.41
38:A1:947:G:H2'	38:A1:948:C:C6	2.55	0.41
38:A1:2676:A:H5'	38:A1:2677:G:C8	2.55	0.41
38:A1:2761:G:N7	77:Ao:63:LYS:NZ	2.57	0.41
38:A1:3041:U:O2'	58:AV:43:GLY:HA3	2.19	0.41
39:A3:56:A:H4'	47:AJ:152:HIS:HB2	2.01	0.41
48:AL:25:HIS:NE2	50:AN:198:SER:OG	2.51	0.41
4:BE:30:ARG:NH2	34:B5:298:C:O3'	2.53	0.41
4:BE:191:ARG:NH2	4:BE:216:ASN:HB3	2.36	0.41
6:BH:104:ARG:HD2	34:B5:803:A:C8	2.55	0.41
7:BI:117:TYR:HE1	7:BI:146:ARG:HB3	1.84	0.41
17:Bb:28:PRO:HB3	34:B5:959:U:O5'	2.21	0.41
20:BF:76:ARG:HH11	23:BQ:122:ARG:HH21	1.68	0.41
34:B5:1344:A:H61	34:B5:1382:A:N6	2.16	0.41
34:B5:1353:U:O2	34:B5:1353:U:H2'	2.20	0.41
34:B5:1662:G:H2'	34:B5:1663:G:C8	2.55	0.41
34:B5:1762:A:H1'	34:B5:1783:C:O5'	2.21	0.41
34:B5:1780:G:H2'	34:B5:1781:MA6:H8	2.01	0.41
38:A1:120:G:N2	44:AG:126:SER:OG	2.54	0.41
38:A1:296:A:H2'	38:A1:297:G:N3	2.36	0.41
38:A1:1184:A:H2'	38:A1:1185:C:C6	2.55	0.41
38:A1:1783:U:H2'	38:A1:1784:G:H8	1.84	0.41
40:A4:27:U:H2'	40:A4:28:C:H6	1.83	0.41
41:AD:8:LYS:HB3	41:AD:12:TYR:CD2	2.55	0.41
44:AG:75:ILE:C	44:AG:77:GLN:H	2.29	0.41
47:AJ:156:LYS:O	47:AJ:160:VAL:HG23	2.21	0.41
53:AQ:158:HIS:H	53:AQ:186:VAL:CG1	2.32	0.41
65:Ac:14:LEU:HD23	65:Ac:14:LEU:HA	1.92	0.41
66:Ad:10:ARG:HB2	66:Ad:12:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BE:94:ALA:HB3	15:BY:17:LEU:HD13	2.01	0.41
4:BE:118:GLU:HA	4:BE:121:TYR:CE2	2.55	0.41
5:BG:87:ARG:NH2	34:B5:160:C:OP1	2.54	0.41
7:BI:88:ASN:OD1	7:BI:89:GLU:N	2.53	0.41
7:BI:200:LYS:HE2	7:BI:200:LYS:HB2	1.89	0.41
10:BN:45:LEU:HB3	10:BN:50:ILE:HG13	2.01	0.41
19:BD:217:ILE:HD11	31:Bg:194:GLY:HA2	2.01	0.41
27:BU:52:LYS:HZ3	27:BU:52:LYS:HG2	1.79	0.41
31:Bg:46:LYS:HE2	31:Bg:58:VAL:HG11	2.02	0.41
34:B5:107:C:H5''	34:B5:383:G:O2'	2.20	0.41
34:B5:179:A:H2'	34:B5:180:A:O4'	2.19	0.41
34:B5:1548:G:N1	34:B5:1564:U:O4	2.54	0.41
38:A1:1170:A:H2'	38:A1:1171:G:O4'	2.20	0.41
38:A1:2180:G:H2'	38:A1:2181:C:C6	2.54	0.41
38:A1:2709:C:H2'	38:A1:2710:C:C6	2.56	0.41
43:AF:189:ILE:HG23	43:AF:190:THR:HG23	2.02	0.41
47:AJ:39:GLN:HE22	47:AJ:114:ILE:HG12	1.85	0.41
54:AR:134:HIS:CD2	54:AR:136:ARG:HB3	2.55	0.41
2:BB:88:VAL:HG13	2:BB:96:LEU:HG	2.02	0.41
2:BB:176:VAL:C	2:BB:178:GLY:H	2.28	0.41
4:BE:126:VAL:HG13	4:BE:139:VAL:HB	2.02	0.41
5:BG:94:ARG:O	5:BG:95:LYS:HE2	2.20	0.41
7:BI:54:LYS:NZ	34:B5:333:A:H5''	2.36	0.41
7:BI:103:GLN:HB3	7:BI:164:ARG:HG3	2.02	0.41
8:BJ:139:GLN:HE22	15:BY:64:PHE:C	2.26	0.41
12:BV:73:ALA:HB1	12:BV:78:LEU:HB2	2.02	0.41
19:BD:74:GLN:HB2	19:BD:79:TYR:HB2	2.02	0.41
21:BK:60:SER:HB3	21:BK:65:TYR:CE1	2.56	0.41
22:BP:114:HIS:ND1	22:BP:118:GLU:OE1	2.54	0.41
34:B5:127:G:N7	34:B5:179:A:C5	2.89	0.41
34:B5:147:A:H2'	34:B5:148:A:O4'	2.21	0.41
34:B5:174:U:H2'	34:B5:175:G:O4'	2.20	0.41
34:B5:984:G:H4'	35:AA:176:ASP:OD2	2.20	0.41
34:B5:1160:A:H2'	34:B5:1161:C:H6	1.86	0.41
34:B5:1230:A:N1	34:B5:1256:A:H5'	2.35	0.41
34:B5:1333:C:H2'	34:B5:1334:U:H6	1.84	0.41
34:B5:1532:U:H2'	34:B5:1533:C:O4'	2.20	0.41
34:B5:1718:G:H2'	34:B5:1719:A:C8	2.55	0.41
36:AB:2:SER:OG	38:A1:2943:G:OP2	2.30	0.41
38:A1:1224:C:C2	38:A1:1225:A:C8	3.08	0.41
38:A1:2115:G:H22	38:A1:2120:A:H1'	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:2269:U:HO2'	38:A1:2270:A:P	2.37	0.41
38:A1:2887:A:N3	38:A1:2887:A:H2'	2.35	0.41
38:A1:2898:G:N7	75:Am:125:LYS:HE2	2.35	0.41
38:A1:2985:C:H2'	38:A1:2986:U:H6	1.85	0.41
38:A1:3018:C:C4	38:A1:3019:U:C4	3.09	0.41
41:AD:117:GLU:HG2	41:AD:118:THR:N	2.36	0.41
42:AE:40:LEU:HD22	42:AE:86:ALA:HA	2.03	0.41
42:AE:76:LEU:HD11	42:AE:141:VAL:HG21	2.02	0.41
46:AI:66:GLU:O	46:AI:70:ILE:HG13	2.21	0.41
78:Ap:36:ARG:HD2	78:Ap:46:THR:HA	2.02	0.41
2:BB:132:ASP:O	2:BB:221:PRO:HD3	2.21	0.41
2:BB:146:GLN:HG2	2:BB:147:ALA:N	2.35	0.41
4:BE:169:ILE:O	4:BE:169:ILE:HG13	2.20	0.41
7:BI:18:ARG:HH21	34:B5:105:A:P	2.43	0.41
7:BI:65:PHE:CD2	7:BI:76:THR:HB	2.55	0.41
8:BJ:56:ALA:O	8:BJ:60:LEU:HG	2.21	0.41
8:BJ:119:ALA:C	8:BJ:121:SER:H	2.29	0.41
16:Ba:88:SER:O	16:Ba:92:ARG:HB2	2.21	0.41
20:BF:142:PRO:HD2	20:BF:167:ARG:HA	2.01	0.41
34:B5:90:C:O2	34:B5:451:A:H4'	2.21	0.41
34:B5:330:G:H2'	34:B5:331:A:C8	2.55	0.41
34:B5:341:A:H2'	34:B5:342:C:C6	2.55	0.41
34:B5:397:A:H2'	34:B5:398:G:O4'	2.21	0.41
34:B5:417:A:H5'	34:B5:418:G:C8	2.56	0.41
34:B5:997:G:C6	34:B5:1008:G:C6	3.08	0.41
34:B5:1591:C:H2'	34:B5:1592:A:C8	2.54	0.41
35:AA:54:ARG:NH2	38:A1:2176:U:OP1	2.36	0.41
38:A1:263:C:H2'	38:A1:264:G:O4'	2.21	0.41
38:A1:842:G:H2'	38:A1:843:A:H8	1.86	0.41
38:A1:879:U:O2	38:A1:2357:A:O2'	2.33	0.41
38:A1:1157:G:H2'	38:A1:1158:A:O4'	2.21	0.41
38:A1:1378:U:H2'	38:A1:1379:G:C8	2.53	0.41
38:A1:1381:A:C2	38:A1:1426:C:C2	3.09	0.41
38:A1:1677:G:OP1	57:AU:97:SER:OG	2.28	0.41
38:A1:1940:G:H2'	38:A1:1941:C:C6	2.56	0.41
38:A1:2328:U:H2'	38:A1:2329:C:H6	1.86	0.41
38:A1:2674:A:N6	47:AJ:124:GLY:O	2.53	0.41
39:A3:74:C:H2'	39:A3:75:G:C8	2.56	0.41
49:AM:49:PRO:HB2	49:AM:82:SER:HB2	2.03	0.41
54:AR:165:LYS:O	54:AR:169:ALA:HB3	2.21	0.41
55:AS:1:MET:HA	55:AS:32:SER:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:38:PHE:CD2	1:BA:39:ASN:N	2.89	0.41
4:BE:105:VAL:HB	4:BE:243:GLY:HA2	2.02	0.41
21:BK:17:GLN:HA	21:BK:90:THR:HG23	2.03	0.41
21:BK:38:LYS:HG3	21:BK:41:TYR:H	1.85	0.41
23:BQ:127:LYS:NZ	23:BQ:131:GLY:O	2.42	0.41
25:BS:126:ARG:CD	25:BS:133:VAL:HA	2.50	0.41
26:BT:65:ILE:HG21	26:BT:114:VAL:HG12	2.02	0.41
31:Bg:144:LEU:HD21	31:Bg:181:TRP:CD2	2.55	0.41
35:AA:241:ARG:HH22	38:A1:2156:C:P	2.44	0.41
36:AB:266:ARG:NH2	38:A1:2392:C:O2'	2.49	0.41
38:A1:756:U:H2'	38:A1:757:C:H6	1.86	0.41
38:A1:1337:A:H2'	38:A1:1338:C:H6	1.85	0.41
38:A1:2206:G:C2'	38:A1:2207:A:H5'	2.50	0.41
38:A1:2225:U:H2'	38:A1:2226:U:C6	2.56	0.41
38:A1:2233:A:H2'	38:A1:2234:G:O4'	2.21	0.41
38:A1:2257:C:H3'	38:A1:2258:PSU:O4'	2.21	0.41
38:A1:3065:G:H2'	38:A1:3066:U:C6	2.56	0.41
40:A4:19:C:H2'	40:A4:20:U:H6	1.84	0.41
40:A4:74:U:C4	61:AY:74:TYR:HD1	2.39	0.41
45:AH:47:LYS:NZ	49:AM:5:SER:O	2.54	0.41
46:AI:49:CYS:SG	46:AI:51:HIS:NE2	2.94	0.41
48:AL:94:GLY:HA3	70:Ah:116:TYR:OH	2.20	0.41
53:AQ:30:VAL:O	53:AQ:34:THR:OG1	2.30	0.41
54:AR:70:LYS:HE2	54:AR:70:LYS:HB3	1.86	0.41
60:AX:57:LEU:HD12	60:AX:57:LEU:HA	1.94	0.41
62:AZ:22:LYS:HE3	62:AZ:134:LEU:HB2	2.03	0.41
69:Ag:41:ARG:NH2	69:Ag:51:LEU:O	2.54	0.41
72:Aj:72:ARG:O	72:Aj:76:ASN:ND2	2.50	0.41
1:BA:29:VAL:HG22	1:BA:149:LEU:HB3	2.02	0.41
2:BB:49:ASN:OD1	2:BB:57:ALA:HB2	2.21	0.41
4:BE:88:ASP:OD1	4:BE:122:LYS:NZ	2.48	0.41
4:BE:162:ILE:HG22	4:BE:163:ASP:N	2.36	0.41
7:BI:84:HIS:ND1	7:BI:86:SER:HB2	2.36	0.41
15:BY:58:PHE:CE1	15:BY:90:ARG:HD3	2.46	0.41
16:Ba:3:LYS:NZ	16:Ba:8:ASN:OD1	2.54	0.41
33:BM:95:LYS:HB3	33:BM:99:GLU:OE2	2.21	0.41
34:B5:69:G:H2'	34:B5:70:C:H6	1.84	0.41
34:B5:81:G:H2'	34:B5:82:U:O4'	2.20	0.41
34:B5:328:A:H2'	34:B5:329:G:C8	2.56	0.41
34:B5:686:C:H3'	34:B5:687:G:C8	2.56	0.41
38:A1:158:G:O2'	38:A1:159:A:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:584:G:H2'	38:A1:585:A:C8	2.56	0.41
38:A1:899:U:H2'	38:A1:900:G:H8	1.86	0.41
38:A1:1265:U:H3'	38:A1:1265:U:OP2	2.21	0.41
38:A1:1342:C:H2'	38:A1:1343:A:C8	2.55	0.41
38:A1:3044:G:H2'	38:A1:3045:G:C8	2.56	0.41
40:A4:133:G:H2'	40:A4:134:G:H8	1.85	0.41
50:AN:68:ARG:HG2	50:AN:128:LYS:HG3	2.03	0.41
56:AT:52:MET:HE2	56:AT:52:MET:HB3	1.94	0.41
1:BA:16:LEU:HD21	24:BR:91:LEU:HA	2.03	0.41
1:BA:38:PHE:CE2	1:BA:39:ASN:HB2	2.56	0.41
1:BA:188:LEU:HD12	1:BA:188:LEU:HA	1.87	0.41
4:BE:131:LEU:HA	4:BE:137:PRO:HA	2.02	0.41
5:BG:15:THR:O	5:BG:16:PHE:HD1	2.04	0.41
6:BH:154:LEU:O	6:BH:186:PRO:HD2	2.21	0.41
7:BI:8:ARG:HH11	7:BI:21:PHE:HB3	1.85	0.41
7:BI:74:LYS:HD3	7:BI:74:LYS:HA	1.89	0.41
7:BI:170:SER:HB3	7:BI:182:TYR:CD1	2.56	0.41
8:BJ:23:ARG:NH1	8:BJ:27:GLU:OE2	2.53	0.41
8:BJ:93:LEU:O	8:BJ:96:VAL:HG12	2.20	0.41
8:BJ:108:ARG:NH1	8:BJ:145:SER:HB3	2.36	0.41
9:BL:79:LYS:HA	9:BL:79:LYS:HD2	1.78	0.41
10:BN:124:ARG:HD2	34:B5:628:G:OP1	2.21	0.41
13:BW:14:ILE:HG12	13:BW:25:VAL:HG11	2.02	0.41
13:BW:56:HIS:O	34:B5:861:U:O2'	2.39	0.41
14:BX:19:ARG:O	14:BX:23:ARG:HG2	2.21	0.41
14:BX:60:GLU:CD	18:Be:3:LYS:HB2	2.46	0.41
15:BY:27:VAL:HG11	15:BY:35:VAL:HG21	2.03	0.41
18:Be:55:ARG:HD2	18:Be:55:ARG:HA	1.88	0.41
19:BD:7:LYS:HE2	27:BU:27:THR:HG21	2.03	0.41
19:BD:76:ARG:HG3	21:BK:63:TYR:CZ	2.56	0.41
22:BP:86:VAL:HG23	22:BP:88:GLU:HG3	2.03	0.41
23:BQ:13:LYS:HG3	23:BQ:14:LYS:N	2.33	0.41
23:BQ:27:GLY:HA2	23:BQ:60:PHE:O	2.20	0.41
23:BQ:69:VAL:HG22	23:BQ:77:GLN:HG2	2.01	0.41
24:BR:41:ILE:HG21	24:BR:47:ARG:HB3	2.03	0.41
25:BS:82:PRO:HB2	25:BS:84:TRP:NE1	2.35	0.41
29:Bc:12:VAL:HG12	29:Bc:52:ASP:N	2.35	0.41
31:Bg:87:LYS:NZ	31:Bg:106:HIS:O	2.46	0.41
31:Bg:102:ARG:HE	31:Bg:102:ARG:HB2	1.64	0.41
31:Bg:211:ILE:HD11	31:Bg:225:LEU:HD13	2.02	0.41
31:Bg:260:ILE:HB	31:Bg:313:TRP:CH2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Bf:138:ARG:O	32:Bf:139:LEU:HD23	2.21	0.41
34:B5:181:A:H2'	34:B5:182:A:C8	2.56	0.41
34:B5:207:U:H2'	34:B5:208:U:H6	1.82	0.41
34:B5:328:A:H2'	34:B5:329:G:H8	1.86	0.41
34:B5:400:A:H4'	34:B5:401:A:H5''	2.02	0.41
34:B5:545:A:O4'	34:B5:594:A:N6	2.54	0.41
34:B5:554:C:H1'	34:B5:555:A:N7	2.35	0.41
34:B5:1682:U:H2'	34:B5:1683:C:C6	2.56	0.41
35:AA:70:ARG:HE	35:AA:72:ARG:NE	2.19	0.41
35:AA:145:LYS:HD3	35:AA:145:LYS:HA	1.83	0.41
36:AB:128:LYS:HG3	38:A1:3294:A:H5'	2.03	0.41
38:A1:163:C:H2'	38:A1:164:A:C8	2.55	0.41
38:A1:525:C:OP2	49:AM:77:ARG:NH2	2.48	0.41
38:A1:640:U:H2'	38:A1:641:C:H6	1.86	0.41
38:A1:728:G:H2'	38:A1:729:C:H6	1.86	0.41
38:A1:791:A:H2'	38:A1:792:G:H8	1.85	0.41
38:A1:816:A:N1	38:A1:919:U:H1'	2.36	0.41
38:A1:987:U:H2'	38:A1:988:U:H6	1.85	0.41
38:A1:991:G:H2'	38:A1:992:A:H8	1.86	0.41
38:A1:1048:A:H2'	46:AI:22:TYR:CZ	2.56	0.41
38:A1:1254:C:N4	38:A1:1263:A:OP1	2.51	0.41
38:A1:1615:C:H2'	38:A1:1616:U:H6	1.84	0.41
38:A1:1744:G:H2'	38:A1:1745:C:H6	1.86	0.41
38:A1:1782:U:H2'	38:A1:1783:U:O4'	2.21	0.41
38:A1:2168:A:H8	38:A1:2168:A:O5'	2.04	0.41
38:A1:2328:U:H2'	38:A1:2329:C:C6	2.55	0.41
38:A1:2926:A:H2'	38:A1:2927:C:C6	2.56	0.41
38:A1:3000:A:H2'	38:A1:3001:C:H6	1.85	0.41
38:A1:3071:U:C4	38:A1:3072:C:C4	3.09	0.41
39:A3:37:G:C2	39:A3:41:G:C2	3.09	0.41
40:A4:40:A:H2'	40:A4:41:A:C8	2.56	0.41
40:A4:70:G:O2'	40:A4:87:G:N2	2.54	0.41
47:AJ:92:ARG:HD3	47:AJ:95:ASN:HD21	1.85	0.41
47:AJ:100:GLY:O	47:AJ:159:THR:HG21	2.21	0.41
54:AR:169:ALA:HB1	54:AR:173:ARG:HH12	1.86	0.41
61:AY:27:ARG:NH1	61:AY:76:LEU:O	2.54	0.41
66:Ad:51:LEU:HG	66:Ad:55:LEU:HD23	2.03	0.41
11:BO:47:LYS:HE2	11:BO:47:LYS:HB2	1.90	0.41
13:BW:82:LYS:NZ	34:B5:748:U:OP1	2.54	0.41
13:BW:90:THR:HG21	13:BW:113:HIS:CD2	2.55	0.41
15:BY:53:ASP:HB3	15:BY:96:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BR:61:ILE:HD12	24:BR:71:PHE:CE2	2.56	0.41
25:BS:42:TYR:O	25:BS:46:VAL:HG22	2.20	0.41
31:Bg:170:ILE:HD13	31:Bg:211:ILE:HG12	2.03	0.41
34:B5:5:U:O2'	34:B5:553:G:H4'	2.21	0.41
34:B5:28:A:H2'	34:B5:29:U:C6	2.55	0.41
34:B5:555:A:H1'	34:B5:590:C:O2'	2.20	0.41
34:B5:560:U:N3	34:B5:561:G:N7	2.69	0.41
34:B5:631:G:H2'	34:B5:632:PSU:C6	2.55	0.41
34:B5:902:G:H2'	34:B5:903:U:C6	2.55	0.41
34:B5:1035:G:H2'	34:B5:1036:A:H8	1.86	0.41
34:B5:1145:U:H2'	34:B5:1146:G:C8	2.56	0.41
34:B5:1175:U:H3	34:B5:1465:C:H42	1.67	0.41
34:B5:1626:U:H2'	34:B5:1627:U:C6	2.55	0.41
37:AC:119:ARG:NH2	38:A1:696:C:OP2	2.54	0.41
37:AC:181:VAL:C	37:AC:183:LYS:H	2.29	0.41
38:A1:946:U:H2'	38:A1:947:G:H8	1.86	0.41
38:A1:1128:U:H2'	38:A1:1129:A:O4'	2.21	0.41
38:A1:1132:C:H2'	38:A1:1133:A:C8	2.56	0.41
38:A1:1138:U:H2'	38:A1:1139:G:C8	2.56	0.41
38:A1:1596:C:H2'	38:A1:1597:C:H6	1.86	0.41
38:A1:2689:A:N3	38:A1:2689:A:H2'	2.35	0.41
39:A3:18:C:H2'	39:A3:19:C:H6	1.86	0.41
40:A4:69:U:H3'	40:A4:70:G:C8	2.56	0.41
52:AP:33:ALA:HB1	52:AP:117:ILE:HG12	2.02	0.41
53:AQ:158:HIS:H	53:AQ:186:VAL:HG11	1.86	0.41
69:Ag:58:ARG:HD2	69:Ag:58:ARG:HA	1.74	0.41
73:Ak:70:PRO:HA	73:Ak:71:PRO:HD3	1.95	0.41
4:BE:199:GLU:OE1	4:BE:209:HIS:NE2	2.54	0.40
5:BG:198:ALA:HB1	34:B5:127:G:C8	2.56	0.40
8:BJ:39:LYS:HG3	34:B5:592:A:OP1	2.21	0.40
8:BJ:167:ALA:HB1	15:BY:31:ASN:HD21	1.86	0.40
9:BL:3:THR:HA	9:BL:52:SER:HB2	2.03	0.40
11:BO:64:ALA:HB3	11:BO:104:ALA:HB3	2.02	0.40
12:BV:62:ARG:HD3	34:B5:1082:C:O2	2.21	0.40
13:BW:37:PHE:CD1	13:BW:41:MET:HE2	2.57	0.40
18:Be:34:ALA:CB	34:B5:477:A:H5'	2.52	0.40
25:BS:145:ARG:NH2	34:B5:1172:G:O3'	2.54	0.40
26:BT:69:LYS:HE3	34:B5:1368:G:OP1	2.21	0.40
26:BT:108:LEU:HA	26:BT:111:ILE:HG22	2.02	0.40
32:Bf:140:TYR:CE1	32:Bf:145:HIS:HA	2.56	0.40
34:B5:19:A:H2'	34:B5:20:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B5:751:G:H2'	34:B5:752:A:H8	1.85	0.40
34:B5:1203:A:C2	34:B5:1556:A:C4	3.09	0.40
34:B5:1267:G:H21	34:B5:1448:G:H5'	1.86	0.40
34:B5:1357:A:O2'	34:B5:1358:G:P	2.79	0.40
34:B5:1625:C:H2'	34:B5:1626:U:C6	2.56	0.40
34:B5:1738:U:H2'	34:B5:1739:C:H6	1.86	0.40
37:AC:315:LYS:NZ	38:A1:608:A:OP1	2.47	0.40
38:A1:8:C:H2'	38:A1:9:U:H6	1.86	0.40
38:A1:792:G:H5''	63:Aa:2:PRO:HD2	2.03	0.40
38:A1:956:U:H2'	38:A1:957:C:C6	2.56	0.40
38:A1:1542:G:H2'	38:A1:1543:G:C8	2.56	0.40
38:A1:1544:G:OP2	50:AN:35:VAL:HG21	2.21	0.40
38:A1:1618:G:O2'	40:A4:126:A:N1	2.54	0.40
38:A1:1807:G:O2'	38:A1:2559:U:O4	2.39	0.40
38:A1:2681:U:O2	47:AJ:20:ASN:ND2	2.54	0.40
38:A1:2765:C:H2'	38:A1:2766:U:C6	2.57	0.40
38:A1:3243:A:C8	51:AO:156[A]:LEU:HD22	2.56	0.40
50:AN:8:GLU:HB3	50:AN:50:ARG:NH2	2.36	0.40
50:AN:99:ARG:NH1	50:AN:118:SER:O	2.54	0.40
56:AT:56:PHE:CZ	56:AT:78:LYS:HG3	2.55	0.40
65:Ac:77:LEU:O	65:Ac:81:VAL:HG22	2.21	0.40
77:Ao:25:VAL:HG22	77:Ao:72:LEU:HD22	2.02	0.40
1:BA:92:HIS:HD2	1:BA:195:TRP:CH2	2.39	0.40
2:BB:136:ARG:CZ	34:B5:884:A:H5''	2.50	0.40
4:BE:51:ARG:HA	4:BE:51:ARG:HD3	1.94	0.40
4:BE:159:THR:OG1	4:BE:227:VAL:HB	2.21	0.40
6:BH:108:GLN:N	34:B5:743:U:OP1	2.53	0.40
7:BI:169:ILE:HG22	7:BI:171:SER:H	1.86	0.40
9:BL:109:VAL:HG21	9:BL:125:VAL:HG11	2.02	0.40
19:BD:113:LEU:HD23	19:BD:114:ALA:N	2.36	0.40
23:BQ:14:LYS:HE2	34:B5:1584:G:N7	2.36	0.40
24:BR:103:ASP:H	24:BR:106:THR:HG22	1.86	0.40
25:BS:17:LEU:HD11	25:BS:66:LEU:HD22	2.03	0.40
31:Bg:218:GLY:HA2	31:Bg:240:VAL:HG22	2.03	0.40
34:B5:240:U:OP1	34:B5:241:U:H3'	2.21	0.40
34:B5:1266:U:H2'	34:B5:1267:G:H8	1.81	0.40
38:A1:245:U:H2'	38:A1:246:U:C6	2.56	0.40
38:A1:291:C:H2'	38:A1:292:U:H6	1.86	0.40
38:A1:595:G:H2'	38:A1:596:C:C6	2.56	0.40
38:A1:671:U:H2'	38:A1:672:A:C8	2.56	0.40
38:A1:744:A:H4'	53:AQ:142:GLY:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:831:G:O2'	38:A1:1864:A:N3	2.47	0.40
38:A1:1047:A:N3	38:A1:2633:U:O2'	2.53	0.40
42:AE:67:GLY:O	42:AE:68:PRO:C	2.64	0.40
43:AF:62:ILE:O	43:AF:66:LYS:HG3	2.22	0.40
45:AH:86:TYR:CE2	45:AH:151:VAL:HB	2.57	0.40
48:AL:128:ARG:CZ	70:Ah:112:PRO:HG3	2.51	0.40
50:AN:63:ARG:HG3	50:AN:131:GLU:HG2	2.03	0.40
55:AS:8:GLN:O	55:AS:8:GLN:HG3	2.21	0.40
56:AT:100:LYS:HA	56:AT:103:GLN:OE1	2.22	0.40
5:BG:27:PHE:CE1	5:BG:36:VAL:HG21	2.56	0.40
6:BH:9:LEU:HD13	6:BH:21:ALA:HB2	2.03	0.40
6:BH:27:LEU:HD22	6:BH:38:LEU:CD1	2.50	0.40
14:BX:103:LEU:HD23	14:BX:125:VAL:HB	2.04	0.40
15:BY:86:GLU:OE2	15:BY:90:ARG:NH1	2.54	0.40
19:BD:135:GLU:HB3	19:BD:187:LYS:HB3	2.03	0.40
20:BF:111:VAL:HA	20:BF:114:ILE:HG22	2.03	0.40
22:BP:25:LEU:HD13	22:BP:28:MET:SD	2.61	0.40
31:Bg:155:ARG:NH1	31:Bg:203:THR:HG23	2.36	0.40
34:B5:501:U:H4'	34:B5:502:U:C5	2.46	0.40
34:B5:1291:G:H22	34:B5:1324:G:H22	1.69	0.40
34:B5:1586:A:N3	34:B5:1611:A:C6	2.90	0.40
34:B5:1729:C:H2'	34:B5:1730:A:O4'	2.20	0.40
38:A1:277:G:H5''	77:Ao:49:GLY:HA2	2.03	0.40
38:A1:422:A:C2	38:A1:2363:A:H4'	2.56	0.40
38:A1:486:A:H2'	38:A1:487:U:C4	2.56	0.40
38:A1:487:U:O2'	38:A1:488:U:OP1	2.33	0.40
38:A1:1120:A:H2'	38:A1:1121:U:H6	1.87	0.40
38:A1:1310:G:O2'	38:A1:2380:U:O2'	2.25	0.40
38:A1:2335:G:N2	38:A1:2339:C:O2'	2.54	0.40
38:A1:2620:G:C4	38:A1:2621:G:C8	3.10	0.40
38:A1:2815:G:N2	38:A1:2818:U:O2	2.53	0.40
39:A3:3:U:H2'	39:A3:4:U:H6	1.86	0.40
46:AI:86:HIS:HB3	46:AI:139:ARG:CG	2.51	0.40
56:AT:112:ASN:HB3	56:AT:128:LEU:HD12	2.03	0.40
64:Ab:14:ARG:O	64:Ab:18:ARG:HG2	2.21	0.40
77:Ao:71:ARG:NH1	77:Ao:80:ARG:HE	2.20	0.40
1:BA:59:LEU:O	1:BA:63:ILE:HG12	2.22	0.40
3:BC:143:TYR:CD1	3:BC:147:ASN:HA	2.57	0.40
5:BG:7:TYR:CE2	5:BG:125:THR:HG23	2.56	0.40
14:BX:14:LYS:NZ	34:B5:1105:C:OP2	2.47	0.40
14:BX:144:ARG:HD3	14:BX:144:ARG:HA	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Bb:18:LYS:O	17:Bb:29:ARG:NH2	2.53	0.40
17:Bb:69:GLY:HA3	34:B5:1048:G:O3'	2.21	0.40
22:BP:57:MET:HE1	22:BP:89:MET:HE1	2.04	0.40
24:BR:48:ASN:HB3	34:B5:1389:C:O4'	2.22	0.40
25:BS:73:MET:HB3	25:BS:101:LEU:HD11	2.03	0.40
27:BU:57:ARG:HH11	27:BU:89:ARG:HE	1.68	0.40
29:Bc:42:ARG:NH2	29:Bc:58:GLU:OE2	2.51	0.40
31:Bg:156:VAL:HG23	31:Bg:169:ILE:HG22	2.02	0.40
33:BM:46:ARG:O	33:BM:50:LYS:HG2	2.21	0.40
34:B5:646:C:H2'	34:B5:647:G:C8	2.56	0.40
34:B5:1308:G:H2'	34:B5:1309:C:C6	2.57	0.40
34:B5:1483:A:H2'	34:B5:1484:G:C8	2.57	0.40
34:B5:1495:C:O2'	34:B5:1519:U:O2	2.27	0.40
34:B5:1663:G:H2'	34:B5:1664:C:C6	2.56	0.40
34:B5:1691:A:N7	34:B5:1707:A:N6	2.69	0.40
36:AB:242:THR:HA	38:A1:2948:C:O2'	2.22	0.40
37:AC:99:MET:HE3	37:AC:99:MET:HB2	1.97	0.40
38:A1:634:C:H5'	68:Af:21:ARG:O	2.21	0.40
38:A1:1541:G:H1'	38:A1:1557:A:C5	2.57	0.40
38:A1:1718:G:H2'	38:A1:1719:G:C8	2.57	0.40
38:A1:2152:A:H2'	38:A1:2153:U:C6	2.56	0.40
39:A3:24:A:H2'	39:A3:25:G:C8	2.57	0.40
39:A3:27:A:H2'	39:A3:28:C:C6	2.57	0.40
56:AT:126:VAL:HG13	56:AT:128:LEU:HD22	2.04	0.40
73:Ak:65:LEU:HD23	73:Ak:65:LEU:HA	1.91	0.40
1:BA:48:ILE:HG13	1:BA:149:LEU:HD21	2.04	0.40
2:BB:100:PHE:HD2	2:BB:181:LEU:HD21	1.86	0.40
9:BL:109:VAL:HG23	9:BL:137:PHE:C	2.46	0.40
19:BD:176:LEU:HD21	34:B5:1437:U:H5''	2.04	0.40
19:BD:203:PRO:C	19:BD:205:ALA:H	2.30	0.40
26:BT:105:LEU:HD13	26:BT:122:ARG:HD3	2.02	0.40
30:Bd:40:ARG:NH2	34:B5:1198:G:O3'	2.51	0.40
31:Bg:13:LEU:HD22	31:Bg:45:TRP:CE2	2.57	0.40
31:Bg:302:PHE:CD1	31:Bg:312:VAL:HG22	2.57	0.40
34:B5:86:A:H2'	34:B5:87:C:H6	1.86	0.40
34:B5:430:G:H2'	34:B5:431:C:C6	2.56	0.40
34:B5:1591:C:C2	34:B5:1592:A:C8	3.10	0.40
36:AB:240:ARG:NH2	38:A1:1907:C:O2	2.53	0.40
37:AC:33:ASP:O	37:AC:37:THR:HG23	2.21	0.40
37:AC:142:VAL:HA	37:AC:145:ILE:HG12	2.02	0.40
37:AC:261:VAL:O	37:AC:269:SER:OG	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A1:37:U:O4	50:AN:83:LYS:NZ	2.55	0.40
38:A1:291:C:H2'	38:A1:292:U:C6	2.57	0.40
38:A1:610:G:N1	38:A1:1337:A:OP1	2.31	0.40
38:A1:1247:U:H5	38:A1:1268:G:C6	2.40	0.40
38:A1:1662:G:H2'	38:A1:1663:C:H6	1.87	0.40
38:A1:1777:U:H2'	38:A1:1778:G:C8	2.57	0.40
38:A1:2295:A:N3	38:A1:2929:C:O2'	2.51	0.40
38:A1:2429:G:H2'	38:A1:2430:A:C8	2.56	0.40
38:A1:3320:A:H2'	38:A1:3321:C:H6	1.86	0.40
41:AD:34:LYS:HA	56:AT:27:LEU:HD11	2.03	0.40
44:AG:81:THR:HG21	44:AG:181:LYS:HG3	2.04	0.40
44:AG:121:SER:OG	44:AG:122:LYS:N	2.52	0.40
45:AH:161:LEU:O	45:AH:164:ILE:HG22	2.21	0.40
48:AL:18:TRP:CD1	48:AL:18:TRP:H	2.40	0.40
53:AQ:123:THR:OG1	53:AQ:126:GLN:OE1	2.37	0.40
56:AT:57:TYR:CD2	56:AT:89:LEU:HD21	2.57	0.40
57:AU:27:VAL:HG21	57:AU:107:PHE:CE1	2.56	0.40
66:Ad:23:VAL:HB	66:Ad:28:ARG:HD3	2.04	0.40
67:Ae:13:HIS:CE1	67:Ae:15:LYS:HB3	2.56	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%)	185 (91%)	19 (9%)	0	100	100
2	BB	212/255 (83%)	176 (83%)	36 (17%)	0	100	100
3	BC	215/254 (85%)	209 (97%)	6 (3%)	0	100	100
4	BE	258/261 (99%)	234 (91%)	24 (9%)	0	100	100
5	BG	224/236 (95%)	210 (94%)	14 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	BH	182/190 (96%)	165 (91%)	16 (9%)	1 (0%)	24	51
7	BI	184/200 (92%)	168 (91%)	16 (9%)	0	100	100
8	BJ	183/197 (93%)	167 (91%)	16 (9%)	0	100	100
9	BL	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
10	BN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
11	BO	125/137 (91%)	110 (88%)	15 (12%)	0	100	100
12	BV	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
13	BW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
14	BX	142/145 (98%)	129 (91%)	13 (9%)	0	100	100
15	BY	132/135 (98%)	127 (96%)	5 (4%)	0	100	100
16	Ba	95/119 (80%)	81 (85%)	14 (15%)	0	100	100
17	Bb	79/82 (96%)	71 (90%)	8 (10%)	0	100	100
18	Be	58/63 (92%)	55 (95%)	3 (5%)	0	100	100
19	BD	221/240 (92%)	204 (92%)	17 (8%)	0	100	100
20	BF	204/225 (91%)	193 (95%)	11 (5%)	0	100	100
21	BK	94/105 (90%)	84 (89%)	10 (11%)	0	100	100
22	BP	122/142 (86%)	115 (94%)	7 (6%)	0	100	100
23	BQ	139/143 (97%)	134 (96%)	5 (4%)	0	100	100
24	BR	117/136 (86%)	110 (94%)	7 (6%)	0	100	100
25	BS	143/146 (98%)	131 (92%)	12 (8%)	0	100	100
26	BT	139/144 (96%)	125 (90%)	14 (10%)	0	100	100
27	BU	105/121 (87%)	100 (95%)	5 (5%)	0	100	100
28	BZ	68/108 (63%)	64 (94%)	4 (6%)	0	100	100
29	Bc	61/67 (91%)	60 (98%)	1 (2%)	0	100	100
30	Bd	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
31	Bg	310/319 (97%)	280 (90%)	30 (10%)	0	100	100
32	Bf	73/152 (48%)	69 (94%)	4 (6%)	0	100	100
33	BM	122/143 (85%)	109 (89%)	13 (11%)	0	100	100
35	AA	245/254 (96%)	233 (95%)	12 (5%)	0	100	100
36	AB	383/387 (99%)	357 (93%)	26 (7%)	0	100	100
37	AC	359/362 (99%)	337 (94%)	22 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	AD	290/297 (98%)	276 (95%)	14 (5%)	0	100	100
42	AE	163/176 (93%)	154 (94%)	9 (6%)	0	100	100
43	AF	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
44	AG	228/256 (89%)	213 (93%)	15 (7%)	0	100	100
45	AH	188/191 (98%)	175 (93%)	13 (7%)	0	100	100
46	AI	215/221 (97%)	204 (95%)	11 (5%)	0	100	100
47	AJ	167/174 (96%)	158 (95%)	9 (5%)	0	100	100
48	AL	191/199 (96%)	183 (96%)	8 (4%)	0	100	100
49	AM	134/138 (97%)	128 (96%)	6 (4%)	0	100	100
50	AN	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
51	AO	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
52	AP	171/184 (93%)	165 (96%)	6 (4%)	0	100	100
53	AQ	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
54	AR	186/189 (98%)	178 (96%)	8 (4%)	0	100	100
55	AS	170/178 (96%)	161 (95%)	9 (5%)	0	100	100
56	AT	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
57	AU	98/121 (81%)	92 (94%)	6 (6%)	0	100	100
58	AV	134/137 (98%)	129 (96%)	5 (4%)	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%)	119 (96%)	5 (4%)	0	100	100
62	AZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
63	Aa	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
64	Ab	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
65	Ac	95/105 (90%)	95 (100%)	0	0	100	100
66	Ad	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
67	Ae	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
68	Af	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
69	Ag	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
70	Ah	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
71	Ai	97/100 (97%)	91 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	Aj	85/88 (97%)	81 (95%)	4 (5%)	0	100	100
73	Ak	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
74	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	Am	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
78	Ap	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
All	All	10920/11886 (92%)	10244 (94%)	675 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	BH	30	SER

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	110 (100%)	0	100	100
14	BX	119/120 (99%)	119 (100%)	0	100	100
15	BY	112/113 (99%)	112 (100%)	0	100	100
16	Ba	83/100 (83%)	83 (100%)	0	100	100
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	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	61/89 (68%)	61 (100%)	0	100	100
29	Bc	56/60 (93%)	56 (100%)	0	100	100
30	Bd	47/49 (96%)	47 (100%)	0	100	100
31	Bg	256/262 (98%)	256 (100%)	0	100	100
32	Bf	66/135 (49%)	66 (100%)	0	100	100
33	BM	100/119 (84%)	100 (100%)	0	100	100
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	321/322 (100%)	321 (100%)	0	100	100
37	AC	288/289 (100%)	288 (100%)	0	100	100
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	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	185/187 (99%)	185 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100
58	AV	104/105 (99%)	104 (100%)	0	100	100
59	AW	55/129 (43%)	55 (100%)	0	100	100
60	AX	105/118 (89%)	105 (100%)	0	100	100
61	AY	109/110 (99%)	109 (100%)	0	100	100
62	AZ	115/116 (99%)	115 (100%)	0	100	100
63	Aa	118/119 (99%)	118 (100%)	0	100	100
64	Ab	46/47 (98%)	46 (100%)	0	100	100
65	Ac	81/88 (92%)	81 (100%)	0	100	100
66	Ad	96/97 (99%)	96 (100%)	0	100	100
67	Ae	109/111 (98%)	109 (100%)	0	100	100
68	Af	90/91 (99%)	90 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	Ap	71/72 (99%)	71 (100%)	0	100	100
All	All	9292/9988 (93%)	9292 (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 (109) such sidechains are listed below:

Mol	Chain	Res	Type
1	BA	15	GLN
1	BA	30	GLN
1	BA	33	GLN
1	BA	140	ASN
2	BB	146	GLN
3	BC	199	GLN
5	BG	65	GLN
6	BH	74	GLN
6	BH	174	ASN
6	BH	180	GLN
8	BJ	131	GLN
8	BJ	139	GLN
9	BL	92	HIS
9	BL	104	HIS
10	BN	49	GLN
10	BN	62	GLN
10	BN	105	ASN
11	BO	12	GLN
12	BV	7	GLN
12	BV	70	ASN
15	BY	29	HIS
17	Bb	5	GLN
18	Be	17	GLN
19	BD	67	ASN
19	BD	179	GLN
20	BF	86	GLN
21	BK	32	HIS
22	BP	15	HIS
22	BP	82	ASN
22	BP	98	ASN
23	BQ	21	HIS
25	BS	21	ASN
25	BS	63	GLN

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Mol	Chain	Res	Type
25	BS	75	ASN
26	BT	16	ASN
28	BZ	82	HIS
30	Bd	27	HIS
30	Bd	53	ASN
31	Bg	268	GLN
31	Bg	308	ASN
32	Bf	135	HIS
33	BM	80	ASN
35	AA	83	HIS
35	AA	97	ASN
35	AA	211	HIS
35	AA	233	GLN
36	AB	121	ASN
36	AB	182	GLN
36	AB	184	ASN
36	AB	293	ASN
41	AD	90	HIS
41	AD	296	GLN
43	AF	61	ASN
43	AF	93	ASN
43	AF	194	HIS
44	AG	38	GLN
44	AG	95	ASN
45	AH	102	ASN
45	AH	163	GLN
46	AI	12	GLN
47	AJ	43	GLN
47	AJ	47	GLN
47	AJ	90	GLN
47	AJ	109	HIS
47	AJ	150	ASN
48	AL	19	GLN
48	AL	99	HIS
48	AL	106	GLN
48	AL	114	GLN
50	AN	15	GLN
50	AN	95	GLN
51	AO	42[A]	ASN
52	AP	50	GLN
52	AP	97	ASN
52	AP	133	HIS

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Mol	Chain	Res	Type
54	AR	3	ASN
55	AS	3	HIS
55	AS	46	GLN
55	AS	49	HIS
55	AS	63	GLN
55	AS	138	GLN
56	AT	5	HIS
56	AT	90	ASN
56	AT	127	GLN
58	AV	24	ASN
58	AV	98	ASN
60	AX	65	GLN
60	AX	85	GLN
61	AY	81	GLN
62	AZ	122	HIS
62	AZ	127	ASN
63	Aa	14	HIS
63	Aa	62	HIS
63	Aa	89	GLN
64	Ab	12	GLN
64	Ab	19	ASN
66	Ad	21	HIS
67	Ae	21	HIS
68	Af	88	ASN
69	Ag	83	ASN
70	Ah	16	GLN
70	Ah	59	ASN
70	Ah	99	GLN
72	Aj	13	ASN
73	Ak	76	ASN
74	Al	4	GLN
74	Al	25	GLN
74	Al	32	ASN
77	Ao	99	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1781/1798 (99%)	476 (26%)	21 (1%)
38	A1	3154/3395 (92%)	582 (18%)	20 (0%)
39	A3	120/121 (99%)	11 (9%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
40	A4	157/158 (99%)	26 (16%)	1 (0%)
All	All	5212/5472 (95%)	1095 (21%)	42 (0%)

All (1095) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	2	A
34	B5	4	C
34	B5	25	C
34	B5	26	A
34	B5	34	G
34	B5	42	G
34	B5	43	A
34	B5	45	U
34	B5	46	A
34	B5	47	A
34	B5	57	G
34	B5	60	U
34	B5	63	G
34	B5	68	A
34	B5	70	C
34	B5	72	A
34	B5	75	U
34	B5	76	A
34	B5	77	U
34	B5	79	C
34	B5	94	U
34	B5	104	A
34	B5	114	C
34	B5	116	U
34	B5	126	A
34	B5	127	G
34	B5	128	U
34	B5	129	U
34	B5	130	C
34	B5	131	C
34	B5	133	U
34	B5	134	U
34	B5	135	A
34	B5	136	C
34	B5	137	U
34	B5	138	A

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Mol	Chain	Res	Type
34	B5	140	A
34	B5	141	U
34	B5	144	U
34	B5	145	A
34	B5	151	G
34	B5	153	G
34	B5	156	A
34	B5	160	C
34	B5	176	C
34	B5	178	U
34	B5	179	A
34	B5	190	C
34	B5	192	U
34	B5	193	U
34	B5	195	G
34	B5	197	A
34	B5	199	G
34	B5	200	A
34	B5	210	A
34	B5	211	PSU
34	B5	212	U
34	B5	213	A
34	B5	217	A
34	B5	221	A
34	B5	224	C
34	B5	225	A
34	B5	226	A
34	B5	229	U
34	B5	231	U
34	B5	233	C
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	243	G
34	B5	246	G
34	B5	257	A
34	B5	260	U
34	B5	261	U
34	B5	276	C

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Mol	Chain	Res	Type
34	B5	278	U
34	B5	280	U
34	B5	281	G
34	B5	285	G
34	B5	287	G
34	B5	299	A
34	B5	309	C
34	B5	314	C
34	B5	316	A
34	B5	321	C
34	B5	322	G
34	B5	324	U
34	B5	333	A
34	B5	337	G
34	B5	338	C
34	B5	352	A
34	B5	359	A
34	B5	360	A
34	B5	361	C
34	B5	365	G
34	B5	380	U
34	B5	390	G
34	B5	396	G
34	B5	400	A
34	B5	401	A
34	B5	402	C
34	B5	417	A
34	B5	423	G
34	B5	424	C
34	B5	425	A
34	B5	426	G
34	B5	434	G
34	B5	435	C
34	B5	437	A
34	B5	439	U
34	B5	444	C
34	B5	445	A
34	B5	453	U
34	B5	460	A
34	B5	461	G
34	B5	468	A
34	B5	475	A

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Mol	Chain	Res	Type
34	B5	476	U
34	B5	477	A
34	B5	481	A
34	B5	482	U
34	B5	483	A
34	B5	484	C
34	B5	485	A
34	B5	486	G
34	B5	487	G
34	B5	490	C
34	B5	491	C
34	B5	492	A
34	B5	494	U
34	B5	496	G
34	B5	497	G
34	B5	498	G
34	B5	499	U
34	B5	500	C
34	B5	501	U
34	B5	504	U
34	B5	506	A
34	B5	508	U
34	B5	515	A
34	B5	517	U
34	B5	518	A
34	B5	519	C
34	B5	524	U
34	B5	525	A
34	B5	527	A
34	B5	534	A
34	B5	538	A
34	B5	539	G
34	B5	541	A
34	B5	542	A
34	B5	544	A
34	B5	555	A
34	B5	557	G
34	B5	558	U
34	B5	559	C
34	B5	564	G
34	B5	565	C
34	B5	568	G

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Mol	Chain	Res	Type
34	B5	577	G
34	B5	578	U
34	B5	579	A
34	B5	585	A
34	B5	594	A
34	B5	595	G
34	B5	606	A
34	B5	608	U
34	B5	610	G
34	B5	611	U
34	B5	619	A
34	B5	620	A
34	B5	621	A
34	B5	622	A
34	B5	623	A
34	B5	624	G
34	B5	635	A
34	B5	638	U
34	B5	639	U
34	B5	643	G
34	B5	645	C
34	B5	648	G
34	B5	650	U
34	B5	651	G
34	B5	652	G
34	B5	654	C
34	B5	655	G
34	B5	656	G
34	B5	657	U
34	B5	658	C
34	B5	677	G
34	B5	679	U
34	B5	681	U
34	B5	683	C
34	B5	684	A
34	B5	688	G
34	B5	694	U
34	B5	696	C
34	B5	697	C
34	B5	698	U
34	B5	699	U
34	B5	702	G

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Mol	Chain	Res	Type
34	B5	704	C
34	B5	705	U
34	B5	706	A
34	B5	707	A
34	B5	708	C
34	B5	711	U
34	B5	712	G
34	B5	714	G
34	B5	715	U
34	B5	716	C
34	B5	717	C
34	B5	718	U
34	B5	719	U
34	B5	720	G
34	B5	721	U
34	B5	727	U
34	B5	728	U
34	B5	730	G
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	765	G
34	B5	766	PSU
34	B5	771	A
34	B5	774	A
34	B5	778	G
34	B5	782	U
34	B5	783	G
34	B5	784	C
34	B5	787	G
34	B5	789	A
34	B5	812	A
34	B5	820	U
34	B5	821	U
34	B5	822	U
34	B5	823	G
34	B5	824	G

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Mol	Chain	Res	Type
34	B5	825	U
34	B5	827	C
34	B5	829	A
34	B5	831	U
34	B5	832	U
34	B5	833	U
34	B5	834	G
34	B5	837	G
34	B5	838	G
34	B5	839	U
34	B5	840	U
34	B5	842	C
34	B5	843	U
34	B5	844	A
34	B5	849	C
34	B5	851	U
34	B5	852	C
34	B5	853	G
34	B5	860	U
34	B5	862	A
34	B5	863	A
34	B5	864	U
34	B5	876	G
34	B5	886	U
34	B5	897	C
34	B5	898	A
34	B5	901	G
34	B5	904	G
34	B5	905	A
34	B5	913	G
34	B5	914	G
34	B5	933	A
34	B5	934	C
34	B5	935	U
34	B5	960	U
34	B5	966	A
34	B5	988	A
34	B5	992	A
34	B5	993	A
34	B5	1003	A
34	B5	1004	U
34	B5	1005	A

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Mol	Chain	Res	Type
34	B5	1020	A
34	B5	1026	A
34	B5	1028	C
34	B5	1031	U
34	B5	1039	A
34	B5	1040	G
34	B5	1052	U
34	B5	1053	G
34	B5	1056	U
34	B5	1058	U
34	B5	1059	U
34	B5	1060	U
34	B5	1061	A
34	B5	1062	A
34	B5	1076	A
34	B5	1081	A
34	B5	1082	C
34	B5	1092	A
34	B5	1093	A
34	B5	1097	U
34	B5	1098	U
34	B5	1100	G
34	B5	1124	A
34	B5	1126	G
34	B5	1138	A
34	B5	1150	G
34	B5	1159	C
34	B5	1167	G
34	B5	1170	G
34	B5	1185	U
34	B5	1186	U
34	B5	1194	A
34	B5	1196	A
34	B5	1199	G
34	B5	1200	G
34	B5	1201	G
34	B5	1202	A
34	B5	1209	C
34	B5	1217	A
34	B5	1218	G
34	B5	1219	A
34	B5	1225	U

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Mol	Chain	Res	Type
34	B5	1228	G
34	B5	1229	G
34	B5	1230	A
34	B5	1234	A
34	B5	1237	G
34	B5	1239	U
34	B5	1240	U
34	B5	1243	G
34	B5	1244	A
34	B5	1245	G
34	B5	1246	C
34	B5	1247	U
34	B5	1248	C
34	B5	1250	U
34	B5	1252	C
34	B5	1253	U
34	B5	1256	A
34	B5	1257	U
34	B5	1263	G
34	B5	1267	G
34	B5	1268	G
34	B5	1269	U
34	B5	1273	G
34	B5	1274	C
34	B5	1276	U
34	B5	1286	U
34	B5	1314	U
34	B5	1315	U
34	B5	1316	G
34	B5	1321	A
34	B5	1338	C
34	B5	1340	U
34	B5	1343	U
34	B5	1344	A
34	B5	1345	A
34	B5	1346	A
34	B5	1353	U
34	B5	1356	U
34	B5	1357	A
34	B5	1358	G
34	B5	1359	C
34	B5	1360	A

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Mol	Chain	Res	Type
34	B5	1361	U
34	B5	1362	U
34	B5	1363	U
34	B5	1364	G
34	B5	1369	U
34	B5	1370	U
34	B5	1371	A
34	B5	1372	U
34	B5	1373	C
34	B5	1375	A
34	B5	1383	G
34	B5	1390	U
34	B5	1398	U
34	B5	1399	C
34	B5	1413	U
34	B5	1414	U
34	B5	1415	PSU
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	1445	G
34	B5	1446	A
34	B5	1450	U
34	B5	1459	C
34	B5	1471	A
34	B5	1472	C
34	B5	1473	U
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	1503	A
34	B5	1507	G
34	B5	1515	A
34	B5	1516	A
34	B5	1521	G

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Mol	Chain	Res	Type
34	B5	1522	U
34	B5	1523	G
34	B5	1524	A
34	B5	1537	C
34	B5	1542	G
34	B5	1554	U
34	B5	1557	U
34	B5	1559	A
34	B5	1570	A
34	B5	1575	G7M
34	B5	1577	A
34	B5	1583	A
34	B5	1584	G
34	B5	1596	C
34	B5	1597	A
34	B5	1601	G
34	B5	1616	G
34	B5	1619	C
34	B5	1622	G
34	B5	1657	U
34	B5	1658	G
34	B5	1663	G
34	B5	1681	A
34	B5	1682	U
34	B5	1683	C
34	B5	1684	U
34	B5	1686	C
34	B5	1687	U
34	B5	1689	A
34	B5	1690	G
34	B5	1692	G
34	B5	1693	A
34	B5	1694	A
34	B5	1695	G
34	B5	1699	G
34	B5	1700	C
34	B5	1702	A
34	B5	1703	C
34	B5	1705	C
34	B5	1709	C
34	B5	1710	U
34	B5	1712	A

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Mol	Chain	Res	Type
34	B5	1713	G
34	B5	1717	G
34	B5	1732	A
34	B5	1751	C
34	B5	1755	A
34	B5	1756[A]	A
34	B5	1757	G
34	B5	1766	A
34	B5	1767	G
34	B5	1769	U
34	B5	1779	U
34	B5	1780	G
34	B5	1782	MA6
34	B5	1792	G
34	B5	1793	G
34	B5	1794	A
34	B5	1795	U
34	B5	1796	C
34	B5	1798	U
34	B5	1799	U
38	A1	6	A
38	A1	14	U
38	A1	26	A
38	A1	30	G
38	A1	40	A
38	A1	43	A
38	A1	49	A
38	A1	59	G
38	A1	60	A
38	A1	65	A
38	A1	66	A
38	A1	71	A
38	A1	92	G
38	A1	93	C
38	A1	99	A
38	A1	109	A
38	A1	110	G
38	A1	111	C
38	A1	116	A
38	A1	122	A
38	A1	133	U
38	A1	134	U

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Mol	Chain	Res	Type
38	A1	135	C
38	A1	136	G
38	A1	146	U
38	A1	148	G
38	A1	156	G
38	A1	157	A
38	A1	161	G
38	A1	162	G
38	A1	165	A
38	A1	166	C
38	A1	170	G
38	A1	172	G
38	A1	173	G
38	A1	177	U
38	A1	187	A
38	A1	190	U
38	A1	191	U
38	A1	200	C
38	A1	210	U
38	A1	219	A
38	A1	222	A
38	A1	239	G
38	A1	241	G
38	A1	242	C
38	A1	244	G
38	A1	245	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	262	U
38	A1	263	C
38	A1	269	G
38	A1	284	A
38	A1	286	U
38	A1	295	A
38	A1	305	U
38	A1	315	C
38	A1	329	U
38	A1	376	G

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Mol	Chain	Res	Type
38	A1	387	A
38	A1	398	A
38	A1	399	A
38	A1	402	A
38	A1	403	C
38	A1	421	G
38	A1	422	A
38	A1	438	A
38	A1	440	A
38	A1	441	U
38	A1	442	G
38	A1	443	G
38	A1	444	U
38	A1	445	G
38	A1	446	U
38	A1	448	U
38	A1	449	U
38	A1	450	G
38	A1	487	U
38	A1	488	U
38	A1	489	U
38	A1	491	A
38	A1	492	C
38	A1	493	U
38	A1	494	G
38	A1	495	G
38	A1	521	A
38	A1	535	G
38	A1	539	C
38	A1	541	U
38	A1	542	G
38	A1	544	C
38	A1	545	U
38	A1	546	C
38	A1	547	G
38	A1	548	G
38	A1	549	U
38	A1	550	A
38	A1	551	A
38	A1	555	U
38	A1	557	A
38	A1	559	A

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Mol	Chain	Res	Type
38	A1	560	G
38	A1	578	A
38	A1	579	G
38	A1	589	A
38	A1	592	A
38	A1	601	U
38	A1	603	A
38	A1	611	A
38	A1	612	U
38	A1	620	U
38	A1	621	A
38	A1	622	A
38	A1	637	C
38	A1	649	A
38	A1	660	A
38	A1	677	A
38	A1	681	U
38	A1	690	A
38	A1	691	A
38	A1	705	A
38	A1	715	A
38	A1	719	U
38	A1	725	G
38	A1	737	G
38	A1	766	U
38	A1	767	U
38	A1	771	A
38	A1	774	G
38	A1	776	PSU
38	A1	777	U
38	A1	780	A
38	A1	781	G
38	A1	785	G
38	A1	786	A
38	A1	799	G
38	A1	806	A
38	A1	817	A
38	A1	830	A
38	A1	844	G
38	A1	849	C
38	A1	861	C
38	A1	865	U

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Mol	Chain	Res	Type
38	A1	869	G
38	A1	874	U
38	A1	879	U
38	A1	896	A
38	A1	907	G
38	A1	908	G
38	A1	909	G
38	A1	914	A
38	A1	916	G
38	A1	917	A
38	A1	921	A
38	A1	923	C
38	A1	924	G
38	A1	925	A
38	A1	937	G
38	A1	944	C
38	A1	959	C
38	A1	960	PSU
38	A1	961	C
38	A1	962	A
38	A1	963	G
38	A1	977	C
38	A1	980	A
38	A1	982	C
38	A1	1010	G
38	A1	1015	U
38	A1	1016	C
38	A1	1018	G
38	A1	1019	G
38	A1	1020	G
38	A1	1021	G
38	A1	1031	C
38	A1	1032	C
38	A1	1034	U
38	A1	1047	A
38	A1	1064	A
38	A1	1072	G
38	A1	1081	U
38	A1	1082	U
38	A1	1087	G
38	A1	1093	A
38	A1	1094	U

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Mol	Chain	Res	Type
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	1117	G
38	A1	1131	G
38	A1	1144	U
38	A1	1159	A
38	A1	1180	A
38	A1	1181	U
38	A1	1182	A
38	A1	1192	C
38	A1	1193	A
38	A1	1196	C
38	A1	1201	C
38	A1	1208	U
38	A1	1219	C
38	A1	1221	A
38	A1	1222	G
38	A1	1223	A
38	A1	1226	G
38	A1	1232	C
38	A1	1235	U
38	A1	1236	G
38	A1	1237	G
38	A1	1238	C
38	A1	1239	C
38	A1	1240	A
38	A1	1241	U
38	A1	1242	G
38	A1	1243	G
38	A1	1245	A
38	A1	1246	G
38	A1	1247	U
38	A1	1249	G
38	A1	1250	G
38	A1	1251	A
38	A1	1252	A
38	A1	1253	U
38	A1	1255	C

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Mol	Chain	Res	Type
38	A1	1256	G
38	A1	1258	U
38	A1	1259	A
38	A1	1260	A
38	A1	1261	G
38	A1	1262	G
38	A1	1263	A
38	A1	1264	G
38	A1	1265	U
38	A1	1266	G
38	A1	1267	U
38	A1	1268	G
38	A1	1270	A
38	A1	1271	A
38	A1	1272	C
38	A1	1273	A
38	A1	1275	C
38	A1	1276	U
38	A1	1277	C
38	A1	1278	A
38	A1	1279	C
38	A1	1280	C
38	A1	1281	G
38	A1	1282	G
38	A1	1284	C
38	A1	1285	G
38	A1	1287	A
38	A1	1293	U
38	A1	1307	G
38	A1	1309	U
38	A1	1316	C
38	A1	1317	A
38	A1	1330	A
38	A1	1331	U
38	A1	1349	G
38	A1	1350	A
38	A1	1351	U
38	A1	1353	U
38	A1	1356	U
38	A1	1357	G
38	A1	1386	A
38	A1	1392	G

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Mol	Chain	Res	Type
38	A1	1399	A
38	A1	1400	G
38	A1	1418	A
38	A1	1419	A
38	A1	1434	G
38	A1	1437	C
38	A1	1446	A
38	A1	1481	A
38	A1	1482	A
38	A1	1483	G
38	A1	1495	U
38	A1	1502	C
38	A1	1503	A
38	A1	1507	G
38	A1	1525	G
38	A1	1539	A
38	A1	1555	U
38	A1	1560	G
38	A1	1562	C
38	A1	1566	A
38	A1	1567	U
38	A1	1568	U
38	A1	1572	U
38	A1	1574	C
38	A1	1576	G
38	A1	1578	C
38	A1	1582	C
38	A1	1589	A
38	A1	1593	A
38	A1	1628	C
38	A1	1629	U
38	A1	1630	U
38	A1	1642	A
38	A1	1643	A
38	A1	1657	C
38	A1	1677	G
38	A1	1715	A
38	A1	1724	U
38	A1	1741	A
38	A1	1750	A
38	A1	1751	G
38	A1	1759	C

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Mol	Chain	Res	Type
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	1796	G
38	A1	1797	A
38	A1	1809	A
38	A1	1813	A
38	A1	1815	U
38	A1	1816	A
38	A1	1817	G
38	A1	1820	U
38	A1	1821	U
38	A1	1842	A
38	A1	1849	C
38	A1	1866	C
38	A1	1878	G
38	A1	1880	U
38	A1	1886	A
38	A1	1893	A
38	A1	1906	G
38	A1	1943	C
38	A1	1953	G
38	A1	1954	G
38	A1	2094	C
38	A1	2097	U
38	A1	2100	A
38	A1	2112	U
38	A1	2114	C
38	A1	2122	G
38	A1	2131	A
38	A1	2140	U
38	A1	2144	A
38	A1	2158	A
38	A1	2169	G
38	A1	2188	A
38	A1	2205	U
38	A1	2206	G
38	A1	2207	A
38	A1	2208	A

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Mol	Chain	Res	Type
38	A1	2225	U
38	A1	2249	G
38	A1	2251	G
38	A1	2252	A
38	A1	2254	U
38	A1	2255	A
38	A1	2256	A
38	A1	2257	C
38	A1	2258	PSU
38	A1	2260	PSU
38	A1	2261	G
38	A1	2262	A
38	A1	2263	C
38	A1	2264	PSU
38	A1	2265	C
38	A1	2266	PSU
38	A1	2269	U
38	A1	2270	A
38	A1	2271	A
38	A1	2272	G
38	A1	2273	G
38	A1	2279	A
38	A1	2280	A
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	2336	U
38	A1	2366	C
38	A1	2373	A
38	A1	2374	C
38	A1	2375	G
38	A1	2383	C
38	A1	2385	G
38	A1	2388	U
38	A1	2391	G
38	A1	2393	G
38	A1	2397	A
38	A1	2402	A
38	A1	2403	G

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Mol	Chain	Res	Type
38	A1	2404	A
38	A1	2411	U
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	2444	C
38	A1	2503	G
38	A1	2507	C
38	A1	2508	U
38	A1	2509	U
38	A1	2514	U
38	A1	2515	A
38	A1	2523	A
38	A1	2524	A
38	A1	2535	A
38	A1	2536	A
38	A1	2537	U
38	A1	2538	U
38	A1	2539	C
38	A1	2540	A
38	A1	2541	U
38	A1	2542	U
38	A1	2543	U
38	A1	2544	U
38	A1	2545	C
38	A1	2546	C
38	A1	2550	U
38	A1	2552	C
38	A1	2559	U
38	A1	2566	C
38	A1	2569	A
38	A1	2570	U
38	A1	2573	G
38	A1	2585	G
38	A1	2593	A
38	A1	2606	G
38	A1	2607	G
38	A1	2614	G
38	A1	2626	A

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Mol	Chain	Res	Type
38	A1	2628	A
38	A1	2629	U
38	A1	2635	A
38	A1	2642	A
38	A1	2651	G
38	A1	2652	U
38	A1	2656	A
38	A1	2674	A
38	A1	2677	G
38	A1	2681	U
38	A1	2689	A
38	A1	2691	A
38	A1	2704	A
38	A1	2714	G
38	A1	2719	U
38	A1	2728	G
38	A1	2729	U
38	A1	2752	U
38	A1	2753	G
38	A1	2755	C
38	A1	2772	C
38	A1	2773	C
38	A1	2777	G
38	A1	2778	G
38	A1	2780	A
38	A1	2796	G
38	A1	2799	A
38	A1	2800	G
38	A1	2801	A
38	A1	2803	A
38	A1	2809	C
38	A1	2810	C
38	A1	2814	G
38	A1	2817	A
38	A1	2821	C
38	A1	2838	A
38	A1	2842	U
38	A1	2845	A
38	A1	2867	C
38	A1	2871	G
38	A1	2875	U
38	A1	2887	A

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Mol	Chain	Res	Type
38	A1	2889	C
38	A1	2898	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	2946	A
38	A1	2947	G
38	A1	2948	C
38	A1	2971	A
38	A1	2972	G
38	A1	2983	C
38	A1	2990	G
38	A1	2997	G
38	A1	3012	A
38	A1	3022	G
38	A1	3032	A
38	A1	3056	U
38	A1	3078	U
38	A1	3080	G
38	A1	3086	A
38	A1	3092	C
38	A1	3094	A
38	A1	3101	G
38	A1	3104	U
38	A1	3113	A
38	A1	3122	A
38	A1	3130	A
38	A1	3131	U
38	A1	3142	A
38	A1	3143	C
38	A1	3144	G
38	A1	3151	U
38	A1	3153	U
38	A1	3154	C
38	A1	3155	U
38	A1	3156	U
38	A1	3165	A
38	A1	3169	U
38	A1	3170	A

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Mol	Chain	Res	Type
38	A1	3173	G
38	A1	3174	A
38	A1	3175	U
38	A1	3176	G
38	A1	3179	U
38	A1	3181	C
38	A1	3187	A
38	A1	3196	U
38	A1	3206	C
38	A1	3207	U
38	A1	3210	A
38	A1	3213	A
38	A1	3214	U
38	A1	3216	G
38	A1	3217	C
38	A1	3218	A
38	A1	3219	G
38	A1	3224	G
38	A1	3231	U
38	A1	3234	A
38	A1	3236	U
38	A1	3238	G
38	A1	3242	G
38	A1	3243	A
38	A1	3244	A
38	A1	3247	G
38	A1	3250	U
38	A1	3259	U
38	A1	3263	G
38	A1	3275	U
38	A1	3276	G
38	A1	3279	A
38	A1	3281	U
38	A1	3289	G
38	A1	3294	A
38	A1	3303	G
38	A1	3304	U
38	A1	3313	U
38	A1	3316	A
38	A1	3317	U
38	A1	3318	G
38	A1	3319	U

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Mol	Chain	Res	Type
38	A1	3320	A
38	A1	3335	A
38	A1	3342	A
38	A1	3345	G
38	A1	3352	U
38	A1	3353	G
38	A1	3354	U
38	A1	3355	U
38	A1	3356	G
38	A1	3358	U
38	A1	3369	G
38	A1	3378	C
38	A1	3382	U
38	A1	3386	G
39	A3	7	G
39	A3	33	U
39	A3	42	A
39	A3	54	U
39	A3	55	A
39	A3	65	G
39	A3	74	C
39	A3	91	G
39	A3	102	A
39	A3	112	G
39	A3	121	U
40	A4	23	U
40	A4	25	G
40	A4	34	U
40	A4	35	C
40	A4	38	U
40	A4	46	G
40	A4	51	G
40	A4	52	A
40	A4	59	A
40	A4	62	C
40	A4	63	G
40	A4	82	U
40	A4	83	C
40	A4	84	C
40	A4	85	G
40	A4	86	U
40	A4	87	G

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Mol	Chain	Res	Type
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	125	U
40	A4	148	G
40	A4	158	U

All (42) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	B5	1	U
34	B5	71	A
34	B5	143	G
34	B5	695	U
34	B5	821	U
34	B5	828	U
34	B5	861	U
34	B5	862	A
34	B5	1055	U
34	B5	1228	G
34	B5	1236	A
34	B5	1239	U
34	B5	1256	A
34	B5	1285	U
34	B5	1344	A
34	B5	1357	A
34	B5	1362	U
34	B5	1426	C
34	B5	1458	G
34	B5	1492	A
34	B5	1755	A
38	A1	251	G
38	A1	252	U
38	A1	487	U
38	A1	602	A
38	A1	843	A
38	A1	873	C
38	A1	916	G
38	A1	1094	U

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Mol	Chain	Res	Type
38	A1	1225	A
38	A1	1249	G
38	A1	1264	G
38	A1	1276	U
38	A1	1292	C
38	A1	1571	A
38	A1	1577	G
38	A1	2250	G
38	A1	2269	U
38	A1	2544	U
38	A1	2772	C
38	A1	3121	U
40	A4	81	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
38	PSU	A1	2266	38	18,21,22	1.45	3 (16%)	21,30,33	2.02	3 (14%)
38	PSU	A1	2340	38	18,21,22	1.41	2 (11%)	21,30,33	2.04	3 (14%)
38	PSU	A1	1052	38	18,21,22	1.37	2 (11%)	21,30,33	2.01	3 (14%)
38	PSU	A1	2264	38	18,21,22	1.41	2 (11%)	21,30,33	1.93	3 (14%)
34	MA6	B5	1782	34	23,26,27	1.50	4 (17%)	33,38,41	2.08	10 (30%)
34	PSU	B5	1187	34	18,21,22	1.35	2 (11%)	21,30,33	2.04	4 (19%)
38	PSU	A1	2923	38	18,21,22	1.38	2 (11%)	21,30,33	2.06	4 (19%)
38	OMG	A1	2922	38	23,26,27	1.18	3 (13%)	32,38,41	1.97	6 (18%)
38	PSU	A1	2133	38	18,21,22	1.45	3 (16%)	21,30,33	2.15	5 (23%)
38	1MA	A1	645	38	21,25,26	1.37	4 (19%)	30,37,40	1.71	5 (16%)
38	UR3	A1	2634	38	19,22,23	0.99	1 (5%)	26,32,35	1.71	3 (11%)
38	PSU	A1	2129	38	18,21,22	1.39	2 (11%)	21,30,33	2.06	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	PSU	A1	2735	38	18,21,22	1.39	2 (11%)	21,30,33	2.06	4 (19%)
34	PSU	B5	632	34	18,21,22	1.34	2 (11%)	21,30,33	2.01	3 (14%)
38	PSU	A1	1004	38	18,21,22	1.38	2 (11%)	21,30,33	2.07	4 (19%)
34	PSU	B5	106	34	18,21,22	1.38	2 (11%)	21,30,33	2.01	4 (19%)
34	MA6	B5	1781	34	23,26,27	1.51	5 (21%)	33,38,41	2.05	10 (30%)
40	PSU	A4	73	40	18,21,22	1.37	2 (11%)	21,30,33	2.03	3 (14%)
38	PSU	A1	2191	38	18,21,22	1.40	2 (11%)	21,30,33	2.09	5 (23%)
38	PSU	A1	1110	38	18,21,22	1.41	2 (11%)	21,30,33	2.07	5 (23%)
34	4AC	B5	1773	34	21,24,25	1.08	1 (4%)	28,34,37	1.24	3 (10%)
38	PSU	A1	986	38	18,21,22	1.37	2 (11%)	21,30,33	1.98	3 (14%)
38	PSU	A1	2826	38	18,21,22	1.34	2 (11%)	21,30,33	2.03	5 (23%)
36	HIC	AB	243	36	10,11,12	1.52	1 (10%)	9,14,16	1.36	2 (22%)
34	PSU	B5	1415	34	18,21,22	1.40	2 (11%)	21,30,33	2.00	3 (14%)
38	PSU	A1	960	38	18,21,22	1.42	3 (16%)	21,30,33	2.07	4 (19%)
38	PSU	A1	2416	38	18,21,22	1.39	2 (11%)	21,30,33	2.04	4 (19%)
34	G7M	B5	1575	34	23,26,27	2.58	7 (30%)	34,39,42	3.04	12 (35%)
34	PSU	B5	120	34	18,21,22	1.39	2 (11%)	21,30,33	1.99	3 (14%)
38	PSU	A1	2975	38	18,21,22	1.36	2 (11%)	21,30,33	2.06	4 (19%)
34	B8N	B5	1191	34	25,29,30	1.39	3 (12%)	28,42,45	2.34	5 (17%)
34	PSU	B5	466	34	18,21,22	1.36	2 (11%)	21,30,33	2.02	4 (19%)
38	PSU	A1	2260	38	18,21,22	1.47	2 (11%)	21,30,33	1.97	4 (19%)
38	PSU	A1	776	38	18,21,22	1.45	2 (11%)	21,30,33	1.98	3 (14%)
34	PSU	B5	759	34	18,21,22	1.37	2 (11%)	21,30,33	2.05	4 (19%)
38	1MA	A1	2142	38	21,25,26	1.36	4 (19%)	30,37,40	1.71	4 (13%)
38	5MC	A1	2278	38	19,22,23	1.68	3 (15%)	26,32,35	1.21	3 (11%)
38	PSU	A1	966	38	18,21,22	1.41	2 (11%)	21,30,33	2.03	3 (14%)
38	PSU	A1	2944	38	18,21,22	1.38	2 (11%)	21,30,33	2.05	4 (19%)
38	PSU	A1	2349	38	18,21,22	1.42	2 (11%)	21,30,33	2.00	3 (14%)
34	PSU	B5	1290	34	18,21,22	1.36	2 (11%)	21,30,33	2.06	4 (19%)
38	PSU	A1	1124	38	18,21,22	1.37	2 (11%)	21,30,33	2.06	4 (19%)
38	PSU	A1	2258	38	18,21,22	1.37	2 (11%)	21,30,33	1.97	3 (14%)
38	PSU	A1	2314	38	18,21,22	1.38	2 (11%)	21,30,33	2.07	4 (19%)
34	PSU	B5	766	34	18,21,22	1.42	2 (11%)	21,30,33	2.05	4 (19%)
34	PSU	B5	1181	34	18,21,22	1.40	2 (11%)	21,30,33	2.03	4 (19%)
38	PSU	A1	2880	38	18,21,22	1.38	2 (11%)	21,30,33	2.03	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	PSU	A1	2351	38	18,21,22	1.39	2 (11%)	21,30,33	2.05	4 (19%)
39	PSU	A3	50	39	18,21,22	1.37	2 (11%)	21,30,33	2.00	3 (14%)
34	PSU	B5	211	34	18,21,22	1.54	3 (16%)	21,30,33	1.97	4 (19%)
38	OMU	A1	2921	38	19,22,23	1.21	2 (10%)	25,31,34	1.79	5 (20%)
38	PSU	A1	1042	38	18,21,22	1.38	2 (11%)	21,30,33	2.06	4 (19%)
34	4AC	B5	1280	34	21,24,25	1.02	1 (4%)	28,34,37	1.17	2 (7%)
38	PSU	A1	990	38	18,21,22	1.38	2 (11%)	21,30,33	2.06	4 (19%)
38	PSU	A1	2865	38	18,21,22	1.42	3 (16%)	21,30,33	2.10	5 (23%)
38	5MC	A1	2870	38	19,22,23	1.61	3 (15%)	26,32,35	1.28	3 (11%)
34	PSU	B5	302	34	18,21,22	1.42	2 (11%)	21,30,33	1.95	3 (14%)
38	PSU	A1	1056	38	18,21,22	1.38	2 (11%)	21,30,33	2.05	4 (19%)
34	PSU	B5	999	34	18,21,22	1.36	2 (11%)	21,30,33	2.02	4 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	PSU	A1	2266	38	-	1/7/25/26	0/2/2/2
38	PSU	A1	2340	38	-	1/7/25/26	0/2/2/2
38	PSU	A1	1052	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2264	38	-	2/7/25/26	0/2/2/2
34	MA6	B5	1782	34	-	4/11/29/30	0/3/3/3
34	PSU	B5	1187	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2923	38	-	3/7/25/26	0/2/2/2
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	PSU	A1	2133	38	-	0/7/25/26	0/2/2/2
38	1MA	A1	645	38	-	2/7/25/26	0/3/3/3
38	UR3	A1	2634	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	2735	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	632	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1004	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	106	34	-	0/7/25/26	0/2/2/2
34	MA6	B5	1781	34	-	3/11/29/30	0/3/3/3
40	PSU	A4	73	40	-	0/7/25/26	0/2/2/2
38	PSU	A1	2191	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	1110	38	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
38	PSU	A1	986	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2826	38	-	0/7/25/26	0/2/2/2
36	HIC	AB	243	36	-	2/5/6/8	0/1/1/1
34	PSU	B5	1415	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	960	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2416	38	-	0/7/25/26	0/2/2/2
34	G7M	B5	1575	34	-	0/7/25/26	0/3/3/3
34	PSU	B5	120	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2975	38	-	0/7/25/26	0/2/2/2
34	B8N	B5	1191	34	-	6/16/34/35	0/2/2/2
34	PSU	B5	466	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2260	38	-	3/7/25/26	0/2/2/2
38	PSU	A1	776	38	-	2/7/25/26	0/2/2/2
34	PSU	B5	759	34	-	0/7/25/26	0/2/2/2
38	1MA	A1	2142	38	-	0/7/25/26	0/3/3/3
38	5MC	A1	2278	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	966	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2944	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2349	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	1124	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2258	38	-	1/7/25/26	0/2/2/2
38	PSU	A1	2314	38	-	1/7/25/26	0/2/2/2
34	PSU	B5	766	34	-	2/7/25/26	0/2/2/2
34	PSU	B5	1181	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	2880	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2351	38	-	0/7/25/26	0/2/2/2
39	PSU	A3	50	39	-	0/7/25/26	0/2/2/2
34	PSU	B5	211	34	-	3/7/25/26	0/2/2/2
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
38	PSU	A1	1042	38	-	0/7/25/26	0/2/2/2
34	4AC	B5	1280	34	-	4/11/29/30	0/2/2/2
38	PSU	A1	990	38	-	0/7/25/26	0/2/2/2
38	PSU	A1	2865	38	-	0/7/25/26	0/2/2/2
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
34	PSU	B5	302	34	-	0/7/25/26	0/2/2/2
38	PSU	A1	1056	38	-	0/7/25/26	0/2/2/2
34	PSU	B5	999	34	-	0/7/25/26	0/2/2/2

All (137) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	C8-N7	7.36	1.45	1.33
38	A1	2278	5MC	C5-C4	6.06	1.48	1.44
38	A1	2870	5MC	C5-C4	5.61	1.48	1.44
34	B5	1575	G7M	C5-N7	-5.31	1.33	1.39
34	B5	1781	MA6	C5-C4	4.78	1.47	1.39
34	B5	1782	MA6	C5-C4	4.74	1.47	1.39
34	B5	1575	G7M	C8-N9	4.04	1.46	1.35
34	B5	1575	G7M	C5-C4	3.90	1.48	1.38
34	B5	1191	B8N	C4-C5	-3.81	1.38	1.47
38	A1	2260	PSU	C6-C5	3.70	1.39	1.35
34	B5	211	PSU	C6-C5	3.68	1.39	1.35
38	A1	2266	PSU	C6-C5	3.61	1.39	1.35
34	B5	1181	PSU	C6-C5	3.56	1.39	1.35
34	B5	1415	PSU	C6-C5	3.55	1.39	1.35
38	A1	966	PSU	C6-C5	3.51	1.39	1.35
34	B5	766	PSU	C6-C5	3.50	1.39	1.35
38	A1	776	PSU	C6-C5	3.50	1.39	1.35
34	B5	120	PSU	C6-C5	3.49	1.39	1.35
34	B5	302	PSU	C6-C5	3.49	1.39	1.35
38	A1	2129	PSU	C6-C5	3.46	1.39	1.35
38	A1	1042	PSU	C6-C5	3.46	1.39	1.35
38	A1	2340	PSU	C6-C5	3.46	1.39	1.35
38	A1	2865	PSU	C6-C5	3.45	1.39	1.35
38	A1	2349	PSU	C6-C5	3.43	1.39	1.35
38	A1	1052	PSU	C6-C5	3.43	1.39	1.35
38	A1	2351	PSU	C6-C5	3.43	1.39	1.35
38	A1	2133	PSU	C6-C5	3.42	1.39	1.35
38	A1	990	PSU	C6-C5	3.42	1.39	1.35
34	B5	759	PSU	C6-C5	3.42	1.39	1.35
38	A1	2416	PSU	C6-C5	3.41	1.39	1.35
34	B5	1290	PSU	C6-C5	3.41	1.39	1.35
34	B5	106	PSU	C6-C5	3.41	1.39	1.35
39	A3	50	PSU	C6-C5	3.41	1.39	1.35
38	A1	2735	PSU	C6-C5	3.41	1.39	1.35
38	A1	2944	PSU	C6-C5	3.40	1.39	1.35
34	B5	999	PSU	C6-C5	3.40	1.39	1.35
38	A1	2880	PSU	C6-C5	3.40	1.39	1.35
34	B5	1187	PSU	C6-C5	3.39	1.39	1.35
38	A1	2314	PSU	C6-C5	3.39	1.39	1.35
38	A1	2258	PSU	C6-C5	3.36	1.39	1.35
34	B5	466	PSU	C6-C5	3.36	1.39	1.35
38	A1	2264	PSU	C6-C5	3.35	1.39	1.35
38	A1	1110	PSU	C6-C5	3.35	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2191	PSU	C6-C5	3.34	1.39	1.35
38	A1	1056	PSU	C6-C5	3.34	1.39	1.35
38	A1	1004	PSU	C6-C5	3.33	1.39	1.35
38	A1	2923	PSU	C6-C5	3.33	1.39	1.35
38	A1	1124	PSU	C6-C5	3.33	1.39	1.35
38	A1	986	PSU	C6-C5	3.33	1.39	1.35
38	A1	2975	PSU	C6-C5	3.33	1.39	1.35
38	A1	960	PSU	C6-C5	3.25	1.38	1.35
40	A4	73	PSU	C6-C5	3.22	1.38	1.35
38	A1	645	1MA	C6-N6	3.21	1.35	1.28
38	A1	2142	1MA	C5-C4	3.14	1.47	1.38
34	B5	1191	B8N	C6-C5	3.13	1.39	1.35
38	A1	645	1MA	C5-C4	3.11	1.47	1.38
34	B5	632	PSU	C6-C5	3.11	1.38	1.35
38	A1	2922	OMG	C5-C4	3.10	1.47	1.38
38	A1	2142	1MA	C6-N6	3.07	1.35	1.28
36	AB	243	HIC	CD2-CG	3.05	1.41	1.36
34	B5	1782	MA6	C5-C6	3.02	1.49	1.41
34	B5	1773	4AC	C4-N4	-2.98	1.35	1.39
38	A1	2133	PSU	C4-N3	-2.98	1.33	1.38
34	B5	1781	MA6	C5-C6	2.92	1.48	1.41
38	A1	2870	5MC	C6-C5	2.87	1.39	1.34
38	A1	2826	PSU	C6-C5	2.84	1.38	1.35
38	A1	2278	5MC	C6-C5	2.79	1.39	1.34
38	A1	1124	PSU	C4-N3	-2.77	1.33	1.38
38	A1	2351	PSU	C4-N3	-2.75	1.33	1.38
38	A1	966	PSU	C4-N3	-2.73	1.33	1.38
38	A1	1110	PSU	C4-N3	-2.72	1.33	1.38
38	A1	1042	PSU	C4-N3	-2.72	1.33	1.38
34	B5	1280	4AC	C4-N4	-2.71	1.35	1.39
38	A1	1004	PSU	C4-N3	-2.71	1.33	1.38
38	A1	776	PSU	C4-N3	-2.71	1.33	1.38
38	A1	2735	PSU	C4-N3	-2.71	1.33	1.38
38	A1	2349	PSU	C4-N3	-2.70	1.33	1.38
38	A1	2129	PSU	C4-N3	-2.69	1.33	1.38
38	A1	1056	PSU	C4-N3	-2.69	1.33	1.38
38	A1	2314	PSU	C4-N3	-2.69	1.33	1.38
38	A1	2340	PSU	C4-N3	-2.69	1.33	1.38
34	B5	632	PSU	C4-N3	-2.68	1.33	1.38
38	A1	2191	PSU	C4-N3	-2.68	1.33	1.38
38	A1	990	PSU	C4-N3	-2.68	1.33	1.38
38	A1	2880	PSU	C4-N3	-2.68	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	120	PSU	C4-N3	-2.68	1.33	1.38
38	A1	2416	PSU	C4-N3	-2.67	1.33	1.38
38	A1	960	PSU	C4-N3	-2.67	1.33	1.38
38	A1	2944	PSU	C4-N3	-2.66	1.33	1.38
38	A1	986	PSU	C4-N3	-2.65	1.33	1.38
34	B5	302	PSU	C4-N3	-2.65	1.33	1.38
34	B5	759	PSU	C4-N3	-2.65	1.33	1.38
38	A1	2921	OMU	C4-N3	-2.65	1.34	1.38
34	B5	766	PSU	C4-N3	-2.64	1.33	1.38
34	B5	106	PSU	C4-N3	-2.64	1.33	1.38
38	A1	2975	PSU	C4-N3	-2.64	1.33	1.38
34	B5	1290	PSU	C4-N3	-2.63	1.33	1.38
38	A1	2826	PSU	C4-N3	-2.63	1.33	1.38
40	A4	73	PSU	C4-N3	-2.63	1.33	1.38
38	A1	2923	PSU	C4-N3	-2.63	1.33	1.38
39	A3	50	PSU	C4-N3	-2.62	1.33	1.38
38	A1	2865	PSU	C4-N3	-2.62	1.33	1.38
38	A1	1052	PSU	C4-N3	-2.61	1.34	1.38
34	B5	466	PSU	C4-N3	-2.61	1.34	1.38
34	B5	211	PSU	C4-N3	-2.60	1.34	1.38
34	B5	1187	PSU	C4-N3	-2.59	1.34	1.38
34	B5	1181	PSU	C4-N3	-2.58	1.34	1.38
38	A1	2264	PSU	C4-N3	-2.58	1.34	1.38
38	A1	2266	PSU	C4-N3	-2.58	1.34	1.38
34	B5	1575	G7M	C2'-C3'	-2.57	1.46	1.53
34	B5	999	PSU	C4-N3	-2.54	1.34	1.38
34	B5	1415	PSU	C4-N3	-2.54	1.34	1.38
38	A1	2260	PSU	C4-N3	-2.54	1.34	1.38
34	B5	1575	G7M	C6-N1	-2.53	1.34	1.38
38	A1	2258	PSU	C4-N3	-2.52	1.34	1.38
38	A1	2922	OMG	C6-N1	-2.45	1.34	1.38
34	B5	1575	G7M	O2'-C2'	-2.41	1.37	1.43
38	A1	2142	1MA	C2-N3	2.40	1.35	1.30
34	B5	211	PSU	O4'-C1'	-2.39	1.40	1.43
38	A1	2278	5MC	C6-N1	-2.33	1.34	1.38
34	B5	1782	MA6	C8-N7	2.29	1.36	1.31
38	A1	2870	5MC	C6-N1	-2.28	1.34	1.38
38	A1	960	PSU	O4'-C1'	-2.25	1.40	1.43
34	B5	1781	MA6	C8-N7	2.24	1.36	1.31
34	B5	1781	MA6	C5-N7	-2.22	1.35	1.39
38	A1	2921	OMU	C2-N3	-2.21	1.34	1.38
34	B5	1191	B8N	CN1-N1	2.20	1.51	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A1	2142	1MA	C5-N7	-2.19	1.34	1.39
38	A1	645	1MA	C2-N3	2.16	1.34	1.30
38	A1	2865	PSU	O4'-C1'	-2.14	1.40	1.43
38	A1	2266	PSU	O4'-C1'	-2.14	1.40	1.43
34	B5	1782	MA6	C5-N7	-2.13	1.35	1.39
38	A1	2133	PSU	C2-N3	-2.11	1.34	1.37
38	A1	2922	OMG	C5-N7	-2.06	1.34	1.39
38	A1	2634	UR3	C2-N1	2.06	1.41	1.38
34	B5	1781	MA6	C4-N9	-2.05	1.33	1.37
38	A1	645	1MA	C5-N7	-2.02	1.35	1.39

All (243) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1191	B8N	C32-C31-N3	8.77	127.48	112.16
34	B5	1575	G7M	CN7-N7-C8	-7.83	112.93	124.79
38	A1	2133	PSU	N1-C2-N3	6.97	122.52	115.17
38	A1	2634	UR3	C4-N3-C2	-6.72	119.17	124.58
38	A1	2735	PSU	N1-C2-N3	6.53	122.06	115.17
38	A1	2191	PSU	N1-C2-N3	6.52	122.05	115.17
38	A1	2129	PSU	N1-C2-N3	6.50	122.03	115.17
38	A1	1004	PSU	N1-C2-N3	6.50	122.02	115.17
38	A1	2923	PSU	N1-C2-N3	6.50	122.02	115.17
38	A1	2865	PSU	N1-C2-N3	6.48	122.01	115.17
38	A1	2314	PSU	N1-C2-N3	6.48	122.00	115.17
38	A1	2944	PSU	N1-C2-N3	6.47	122.00	115.17
38	A1	2340	PSU	N1-C2-N3	6.46	121.98	115.17
38	A1	990	PSU	N1-C2-N3	6.46	121.98	115.17
38	A1	1056	PSU	N1-C2-N3	6.46	121.98	115.17
38	A1	1042	PSU	N1-C2-N3	6.46	121.98	115.17
38	A1	1110	PSU	N1-C2-N3	6.45	121.97	115.17
38	A1	2975	PSU	N1-C2-N3	6.45	121.97	115.17
38	A1	1124	PSU	N1-C2-N3	6.43	121.96	115.17
38	A1	2351	PSU	N1-C2-N3	6.42	121.94	115.17
38	A1	2416	PSU	N1-C2-N3	6.42	121.94	115.17
34	B5	759	PSU	N1-C2-N3	6.41	121.93	115.17
38	A1	960	PSU	N1-C2-N3	6.40	121.92	115.17
34	B5	766	PSU	N1-C2-N3	6.40	121.92	115.17
40	A4	73	PSU	N1-C2-N3	6.39	121.91	115.17
34	B5	1290	PSU	N1-C2-N3	6.39	121.91	115.17
34	B5	1187	PSU	N1-C2-N3	6.39	121.91	115.17
38	A1	966	PSU	N1-C2-N3	6.39	121.90	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2349	PSU	N1-C2-N3	6.38	121.89	115.17
38	A1	2266	PSU	N1-C2-N3	6.37	121.89	115.17
34	B5	106	PSU	N1-C2-N3	6.35	121.87	115.17
34	B5	1575	G7M	N9-C8-N7	-6.34	97.09	112.48
34	B5	1181	PSU	N1-C2-N3	6.34	121.86	115.17
38	A1	2880	PSU	N1-C2-N3	6.33	121.85	115.17
34	B5	632	PSU	N1-C2-N3	6.32	121.84	115.17
38	A1	1052	PSU	N1-C2-N3	6.32	121.83	115.17
34	B5	120	PSU	N1-C2-N3	6.31	121.82	115.17
34	B5	466	PSU	N1-C2-N3	6.30	121.82	115.17
34	B5	999	PSU	N1-C2-N3	6.29	121.80	115.17
34	B5	1575	G7M	C8-N7-C5	6.28	115.64	107.78
38	A1	776	PSU	N1-C2-N3	6.28	121.79	115.17
38	A1	2258	PSU	N1-C2-N3	6.26	121.77	115.17
34	B5	1415	PSU	N1-C2-N3	6.25	121.77	115.17
38	A1	2826	PSU	N1-C2-N3	6.25	121.76	115.17
34	B5	1575	G7M	N9-C4-N3	6.25	138.44	125.95
38	A1	986	PSU	N1-C2-N3	6.23	121.74	115.17
39	A3	50	PSU	N1-C2-N3	6.22	121.73	115.17
34	B5	302	PSU	N1-C2-N3	6.21	121.72	115.17
34	B5	211	PSU	N1-C2-N3	6.18	121.69	115.17
38	A1	2264	PSU	N1-C2-N3	6.10	121.60	115.17
38	A1	2922	OMG	C5-C4-N3	-6.03	118.79	128.39
38	A1	2260	PSU	N1-C2-N3	6.01	121.50	115.17
34	B5	1191	B8N	C4-N3-C2	-5.84	118.44	125.62
34	B5	1575	G7M	C5-C4-N3	-5.61	117.55	128.15
34	B5	1782	MA6	C5-C4-N3	-5.59	119.02	126.72
34	B5	1781	MA6	C5-C4-N3	-5.56	119.06	126.72
38	A1	2142	1MA	C5-C4-N3	-5.54	119.12	127.27
38	A1	645	1MA	C5-C4-N3	-5.33	119.43	127.27
38	A1	2922	OMG	C2-N3-C4	5.00	120.91	112.30
38	A1	2921	OMU	C4-N3-C2	-4.80	120.65	126.61
38	A1	645	1MA	C2-N3-C4	4.62	121.59	112.53
38	A1	2142	1MA	C2-N3-C4	4.58	121.51	112.53
34	B5	1773	4AC	N4-C4-N3	4.46	121.11	113.87
38	A1	2922	OMG	N9-C4-N3	4.40	134.76	125.95
34	B5	1782	MA6	C2-N1-C6	4.27	122.25	111.83
38	A1	2870	5MC	C5-C6-N1	-4.26	118.69	123.31
38	A1	2133	PSU	C4-N3-C2	-4.25	120.52	126.37
38	A1	2921	OMU	N3-C2-N1	4.24	120.42	114.89
34	B5	1781	MA6	C2-N1-C6	4.20	122.09	111.83
34	B5	1181	PSU	C4-N3-C2	-4.20	120.59	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1575	G7M	C2-N3-C4	4.19	119.51	112.30
34	B5	1290	PSU	C4-N3-C2	-4.18	120.61	126.37
38	A1	2314	PSU	C4-N3-C2	-4.18	120.61	126.37
34	B5	1781	MA6	N3-C4-N9	4.17	134.25	127.17
38	A1	1124	PSU	C4-N3-C2	-4.16	120.64	126.37
38	A1	2975	PSU	C4-N3-C2	-4.16	120.64	126.37
38	A1	960	PSU	C4-N3-C2	-4.15	120.65	126.37
38	A1	1042	PSU	C4-N3-C2	-4.15	120.65	126.37
38	A1	2191	PSU	C4-N3-C2	-4.15	120.65	126.37
38	A1	1004	PSU	C4-N3-C2	-4.13	120.69	126.37
38	A1	2129	PSU	C4-N3-C2	-4.12	120.70	126.37
38	A1	2865	PSU	C4-N3-C2	-4.12	120.70	126.37
38	A1	2735	PSU	C4-N3-C2	-4.11	120.70	126.37
38	A1	2923	PSU	C4-N3-C2	-4.11	120.71	126.37
38	A1	990	PSU	C4-N3-C2	-4.11	120.71	126.37
38	A1	1110	PSU	C4-N3-C2	-4.11	120.71	126.37
34	B5	759	PSU	C4-N3-C2	-4.11	120.71	126.37
34	B5	1782	MA6	N3-C4-N9	4.11	134.15	127.17
34	B5	1187	PSU	C4-N3-C2	-4.10	120.72	126.37
38	A1	1056	PSU	C4-N3-C2	-4.10	120.73	126.37
38	A1	2826	PSU	C4-N3-C2	-4.10	120.73	126.37
38	A1	2880	PSU	C4-N3-C2	-4.09	120.74	126.37
38	A1	2351	PSU	C4-N3-C2	-4.08	120.75	126.37
34	B5	1782	MA6	C4-C5-N7	-4.08	105.92	110.58
38	A1	2416	PSU	C4-N3-C2	-4.08	120.76	126.37
34	B5	466	PSU	C4-N3-C2	-4.07	120.77	126.37
34	B5	999	PSU	C4-N3-C2	-4.06	120.78	126.37
38	A1	2944	PSU	C4-N3-C2	-4.06	120.78	126.37
38	A1	1052	PSU	C4-N3-C2	-4.06	120.78	126.37
34	B5	106	PSU	C4-N3-C2	-4.01	120.84	126.37
34	B5	632	PSU	C4-N3-C2	-4.01	120.84	126.37
39	A3	50	PSU	C4-N3-C2	-4.01	120.85	126.37
34	B5	766	PSU	C4-N3-C2	-4.01	120.85	126.37
38	A1	2340	PSU	C4-N3-C2	-4.01	120.85	126.37
40	A4	73	PSU	C4-N3-C2	-4.00	120.86	126.37
38	A1	966	PSU	C4-N3-C2	-3.98	120.89	126.37
38	A1	2266	PSU	C4-N3-C2	-3.95	120.92	126.37
34	B5	120	PSU	C4-N3-C2	-3.93	120.95	126.37
38	A1	2921	OMU	C5-C4-N3	3.90	120.26	114.80
38	A1	986	PSU	C4-N3-C2	-3.89	121.02	126.37
34	B5	1781	MA6	C4-C5-N7	-3.88	106.14	110.58
38	A1	2349	PSU	C4-N3-C2	-3.86	121.05	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1415	PSU	C4-N3-C2	-3.85	121.07	126.37
38	A1	2258	PSU	C4-N3-C2	-3.81	121.13	126.37
34	B5	1575	G7M	C8-N9-C4	3.79	116.47	107.09
34	B5	1280	4AC	N4-C4-N3	3.78	120.00	113.87
38	A1	2260	PSU	C4-N3-C2	-3.77	121.18	126.37
38	A1	776	PSU	C4-N3-C2	-3.75	121.20	126.37
34	B5	1575	G7M	O3'-C3'-C2'	3.74	123.81	111.82
34	B5	302	PSU	C4-N3-C2	-3.73	121.23	126.37
40	A4	73	PSU	O2-C2-N1	-3.73	118.95	122.79
38	A1	2975	PSU	O2-C2-N1	-3.72	118.95	122.79
34	B5	1575	G7M	CN7-N7-C5	3.72	131.43	126.80
38	A1	2340	PSU	O2-C2-N1	-3.71	118.96	122.79
38	A1	1004	PSU	O2-C2-N1	-3.71	118.97	122.79
38	A1	2826	PSU	O2-C2-N1	-3.70	118.97	122.79
38	A1	1110	PSU	O2-C2-N1	-3.70	118.98	122.79
38	A1	2944	PSU	O2-C2-N1	-3.70	118.98	122.79
38	A1	2880	PSU	O2-C2-N1	-3.68	118.99	122.79
38	A1	2142	1MA	N9-C4-N3	3.68	135.28	126.90
38	A1	2266	PSU	O2-C2-N1	-3.67	119.00	122.79
38	A1	2264	PSU	C4-N3-C2	-3.67	121.31	126.37
34	B5	211	PSU	C4-N3-C2	-3.67	121.31	126.37
34	B5	759	PSU	O2-C2-N1	-3.67	119.00	122.79
38	A1	2923	PSU	O2-C2-N1	-3.67	119.00	122.79
34	B5	1782	MA6	C2-N3-C4	3.67	120.78	111.83
38	A1	2264	PSU	O2-C2-N1	-3.65	119.02	122.79
38	A1	2129	PSU	O2-C2-N1	-3.64	119.03	122.79
38	A1	960	PSU	O2-C2-N1	-3.63	119.05	122.79
34	B5	1187	PSU	O2-C2-N1	-3.63	119.05	122.79
38	A1	2191	PSU	O2-C2-N1	-3.63	119.05	122.79
34	B5	1290	PSU	O2-C2-N1	-3.62	119.05	122.79
34	B5	1415	PSU	O2-C2-N1	-3.62	119.05	122.79
34	B5	766	PSU	O2-C2-N1	-3.62	119.06	122.79
38	A1	2865	PSU	O2-C2-N1	-3.62	119.06	122.79
38	A1	990	PSU	O2-C2-N1	-3.61	119.07	122.79
34	B5	211	PSU	O2-C2-N1	-3.60	119.08	122.79
38	A1	2314	PSU	O2-C2-N1	-3.59	119.08	122.79
34	B5	466	PSU	O2-C2-N1	-3.59	119.08	122.79
38	A1	1056	PSU	O2-C2-N1	-3.58	119.10	122.79
38	A1	2351	PSU	O2-C2-N1	-3.58	119.10	122.79
34	B5	999	PSU	O2-C2-N1	-3.57	119.10	122.79
34	B5	1781	MA6	C2-N3-C4	3.57	120.54	111.83
38	A1	2735	PSU	O2-C2-N1	-3.56	119.12	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A1	2258	PSU	O2-C2-N1	-3.55	119.13	122.79
38	A1	2416	PSU	O2-C2-N1	-3.55	119.13	122.79
34	B5	632	PSU	O2-C2-N1	-3.53	119.15	122.79
38	A1	1042	PSU	O2-C2-N1	-3.53	119.15	122.79
39	A3	50	PSU	O2-C2-N1	-3.53	119.15	122.79
34	B5	106	PSU	O2-C2-N1	-3.50	119.18	122.79
38	A1	986	PSU	O2-C2-N1	-3.50	119.18	122.79
38	A1	1052	PSU	O2-C2-N1	-3.47	119.21	122.79
38	A1	966	PSU	O2-C2-N1	-3.47	119.21	122.79
38	A1	2349	PSU	O2-C2-N1	-3.45	119.23	122.79
38	A1	1124	PSU	O2-C2-N1	-3.45	119.23	122.79
38	A1	2278	5MC	C5-C6-N1	-3.44	119.58	123.31
34	B5	302	PSU	O2-C2-N1	-3.43	119.25	122.79
34	B5	1181	PSU	O2-C2-N1	-3.40	119.29	122.79
38	A1	2260	PSU	O2-C2-N1	-3.38	119.31	122.79
38	A1	2634	UR3	C5-C4-N3	3.35	119.45	115.04
34	B5	1191	B8N	C31-N3-C2	3.34	122.57	117.64
38	A1	2922	OMG	C6-C5-N7	3.33	136.34	130.29
34	B5	120	PSU	O2-C2-N1	-3.29	119.39	122.79
34	B5	1782	MA6	N1-C2-N3	-3.27	123.62	128.58
38	A1	776	PSU	O2-C2-N1	-3.26	119.42	122.79
38	A1	645	1MA	N9-C4-N3	3.26	134.32	126.90
34	B5	1191	B8N	N3-C2-N1	3.25	120.69	116.72
38	A1	2133	PSU	O2-C2-N1	-3.24	119.45	122.79
34	B5	1781	MA6	N1-C2-N3	-3.08	123.91	128.58
34	B5	1575	G7M	C1'-N9-C8	-3.08	116.33	126.74
36	AB	243	HIC	NE2-CE1-ND1	-3.02	111.51	112.66
38	A1	2921	OMU	O4-C4-C5	-3.01	119.97	125.16
38	A1	2278	5MC	C5-C4-N3	-2.84	118.84	121.75
38	A1	2260	PSU	C6-C5-C4	-2.83	116.27	118.17
34	B5	1782	MA6	C5-N7-C8	2.80	107.85	103.45
38	A1	2870	5MC	C5-C4-N3	-2.70	118.99	121.75
34	B5	1781	MA6	C5-N7-C8	2.62	107.56	103.45
34	B5	211	PSU	C6-C5-C4	-2.61	116.41	118.17
38	A1	2922	OMG	C4-C5-N7	-2.61	106.54	110.67
38	A1	2278	5MC	O2-C2-N3	-2.58	118.26	122.33
38	A1	645	1MA	C4-C5-N7	-2.54	106.64	110.67
34	B5	1782	MA6	C4-N9-C8	2.53	108.39	105.74
34	B5	1781	MA6	C4-N9-C8	2.48	108.34	105.74
38	A1	2133	PSU	C5-C6-N1	-2.47	118.70	122.14
34	B5	1781	MA6	N1-C6-N6	2.46	119.85	116.86
34	B5	1773	4AC	C5-C4-N4	-2.43	118.85	122.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1773	4AC	C6-C5-C4	2.31	119.78	117.00
38	A1	645	1MA	C6-C5-N7	2.30	136.22	132.16
38	A1	960	PSU	C5-C6-N1	-2.28	118.97	122.14
38	A1	2865	PSU	O4'-C1'-C2'	2.28	108.31	105.15
34	B5	1575	G7M	O6-C6-C5	-2.28	122.92	128.01
34	B5	1782	MA6	C6-C5-N7	2.27	137.06	133.43
38	A1	1124	PSU	C5-C6-N1	-2.26	119.00	122.14
34	B5	1280	4AC	C6-C5-C4	2.20	119.65	117.00
38	A1	2735	PSU	C5-C6-N1	-2.18	119.11	122.14
38	A1	2142	1MA	C4-C5-N7	-2.18	107.22	110.67
38	A1	2314	PSU	C5-C6-N1	-2.16	119.14	122.14
38	A1	1110	PSU	O4'-C1'-C2'	2.16	108.14	105.15
38	A1	2870	5MC	O2-C2-N3	-2.16	118.92	122.33
38	A1	2129	PSU	C5-C6-N1	-2.16	119.14	122.14
34	B5	759	PSU	C5-C6-N1	-2.16	119.15	122.14
38	A1	2133	PSU	O2-C2-N3	-2.16	118.03	121.86
34	B5	1290	PSU	C5-C6-N1	-2.15	119.15	122.14
38	A1	2921	OMU	O2-C2-N1	-2.14	120.00	122.80
38	A1	1004	PSU	C5-C6-N1	-2.14	119.16	122.14
34	B5	1181	PSU	C5-C6-N1	-2.14	119.17	122.14
38	A1	2351	PSU	C5-C6-N1	-2.14	119.17	122.14
38	A1	1042	PSU	C5-C6-N1	-2.14	119.18	122.14
34	B5	766	PSU	O4'-C1'-C2'	2.13	108.10	105.15
38	A1	2826	PSU	O4'-C1'-C2'	2.13	108.09	105.15
38	A1	2944	PSU	C5-C6-N1	-2.12	119.19	122.14
38	A1	2416	PSU	C5-C6-N1	-2.12	119.19	122.14
38	A1	2191	PSU	O4'-C1'-C2'	2.12	108.08	105.15
38	A1	1110	PSU	C5-C6-N1	-2.10	119.23	122.14
38	A1	2191	PSU	C5-C6-N1	-2.09	119.24	122.14
36	AB	243	HIC	CB-CG-CD2	-2.09	124.91	129.96
34	B5	1575	G7M	O2'-C2'-C3'	2.09	118.52	111.82
38	A1	2634	UR3	C3U-N3-C2	2.07	120.94	117.33
38	A1	2923	PSU	C5-C6-N1	-2.07	119.27	122.14
34	B5	1782	MA6	N9-C8-N7	-2.07	111.00	113.94
38	A1	2975	PSU	C5-C6-N1	-2.07	119.27	122.14
38	A1	1056	PSU	C5-C6-N1	-2.06	119.28	122.14
34	B5	1187	PSU	C5-C6-N1	-2.05	119.29	122.14
38	A1	990	PSU	C5-C6-N1	-2.05	119.29	122.14
38	A1	2865	PSU	C5-C6-N1	-2.05	119.29	122.14
38	A1	2922	OMG	O6-C6-C5	-2.05	121.12	126.53
34	B5	1781	MA6	C6-C5-N7	2.04	136.69	133.43
34	B5	106	PSU	C5-C6-N1	-2.04	119.31	122.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	466	PSU	C5-C6-N1	-2.03	119.32	122.14
34	B5	999	PSU	O4'-C1'-C2'	2.03	107.96	105.15
34	B5	1191	B8N	O4'-C1'-C2'	2.01	107.93	105.15
38	A1	2826	PSU	C5-C6-N1	-2.00	119.36	122.14
38	A1	2880	PSU	C5-C6-N1	-2.00	119.36	122.14

There are no chirality outliers.

All (48) 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	1280	4AC	O7-C7-N4-C4
34	B5	1280	4AC	CM7-C7-N4-C4
34	B5	1773	4AC	N3-C4-N4-C7
34	B5	1773	4AC	C5-C4-N4-C7
34	B5	1773	4AC	O7-C7-N4-C4
34	B5	1773	4AC	CM7-C7-N4-C4
34	B5	1781	MA6	C5-C6-N6-C9
34	B5	1782	MA6	O4'-C4'-C5'-O5'
38	A1	776	PSU	O4'-C4'-C5'-O5'
38	A1	2258	PSU	C4'-C5'-O5'-P
38	A1	2264	PSU	O4'-C4'-C5'-O5'
34	B5	211	PSU	C3'-C4'-C5'-O5'
34	B5	211	PSU	O4'-C4'-C5'-O5'
38	A1	2264	PSU	C3'-C4'-C5'-O5'
38	A1	2923	PSU	O4'-C4'-C5'-O5'
34	B5	211	PSU	C4'-C5'-O5'-P
34	B5	1191	B8N	C32-C31-N3-C4
34	B5	1782	MA6	C3'-C4'-C5'-O5'
38	A1	2923	PSU	C3'-C4'-C5'-O5'
38	A1	2266	PSU	C4'-C5'-O5'-P
34	B5	1781	MA6	N1-C6-N6-C9
38	A1	776	PSU	C3'-C4'-C5'-O5'
34	B5	1191	B8N	N34-C33-C34-O36
38	A1	2870	5MC	C2'-C1'-N1-C6
34	B5	766	PSU	C3'-C4'-C5'-O5'
34	B5	1782	MA6	C5-C6-N6-C9
34	B5	1191	B8N	N34-C33-C34-O35
38	A1	2870	5MC	O4'-C1'-N1-C6
38	A1	2870	5MC	C2'-C1'-N1-C2
34	B5	766	PSU	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
34	B5	1191	B8N	C32-C31-N3-C2
38	A1	2260	PSU	C4'-C5'-O5'-P
38	A1	2314	PSU	C4'-C5'-O5'-P
34	B5	1191	B8N	O4'-C1'-C5-C4
38	A1	2870	5MC	O4'-C1'-N1-C2
38	A1	2260	PSU	C3'-C4'-C5'-O5'
36	AB	243	HIC	CA-CB-CG-ND1
34	B5	1781	MA6	C5-C6-N6-C10
38	A1	645	1MA	C2'-C1'-N9-C8
38	A1	2340	PSU	C4'-C5'-O5'-P
36	AB	243	HIC	CA-CB-CG-CD2
38	A1	2923	PSU	C4'-C5'-O5'-P
38	A1	645	1MA	C2'-C1'-N9-C4
34	B5	1191	B8N	C32-C33-C34-O35
34	B5	1782	MA6	C4'-C5'-O5'-P
38	A1	2260	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

21 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2266	PSU	1	0
38	A1	2264	PSU	1	0
34	B5	1187	PSU	2	0
38	A1	2133	PSU	2	0
38	A1	2129	PSU	1	0
34	B5	632	PSU	2	0
34	B5	1781	MA6	4	0
38	A1	1110	PSU	2	0
38	A1	986	PSU	1	0
34	B5	1575	G7M	3	0
34	B5	120	PSU	1	0
38	A1	2260	PSU	2	0
38	A1	966	PSU	2	0
34	B5	1290	PSU	1	0
38	A1	1124	PSU	1	0
38	A1	2258	PSU	1	0
38	A1	2314	PSU	1	0
34	B5	1181	PSU	2	0
38	A1	2880	PSU	2	0
34	B5	211	PSU	1	0
34	B5	1280	4AC	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is 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	$\# Z > 2$
79	SPD	A1	3401	-	9,9,9	0.32	0	8,8,8	0.92	0
80	3HE	A1	3402	-	21,21,21	0.41	0	23,30,30	0.76	1 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
79	SPD	A1	3401	-	-	6/7/7/7	-
80	3HE	A1	3402	-	-	2/8/36/36	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	A1	3402	3HE	C9-C13-C12	-2.71	109.91	114.46

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
80	A1	3402	3HE	C7-C8-C9-C10
79	A1	3401	SPD	N6-C7-C8-C9

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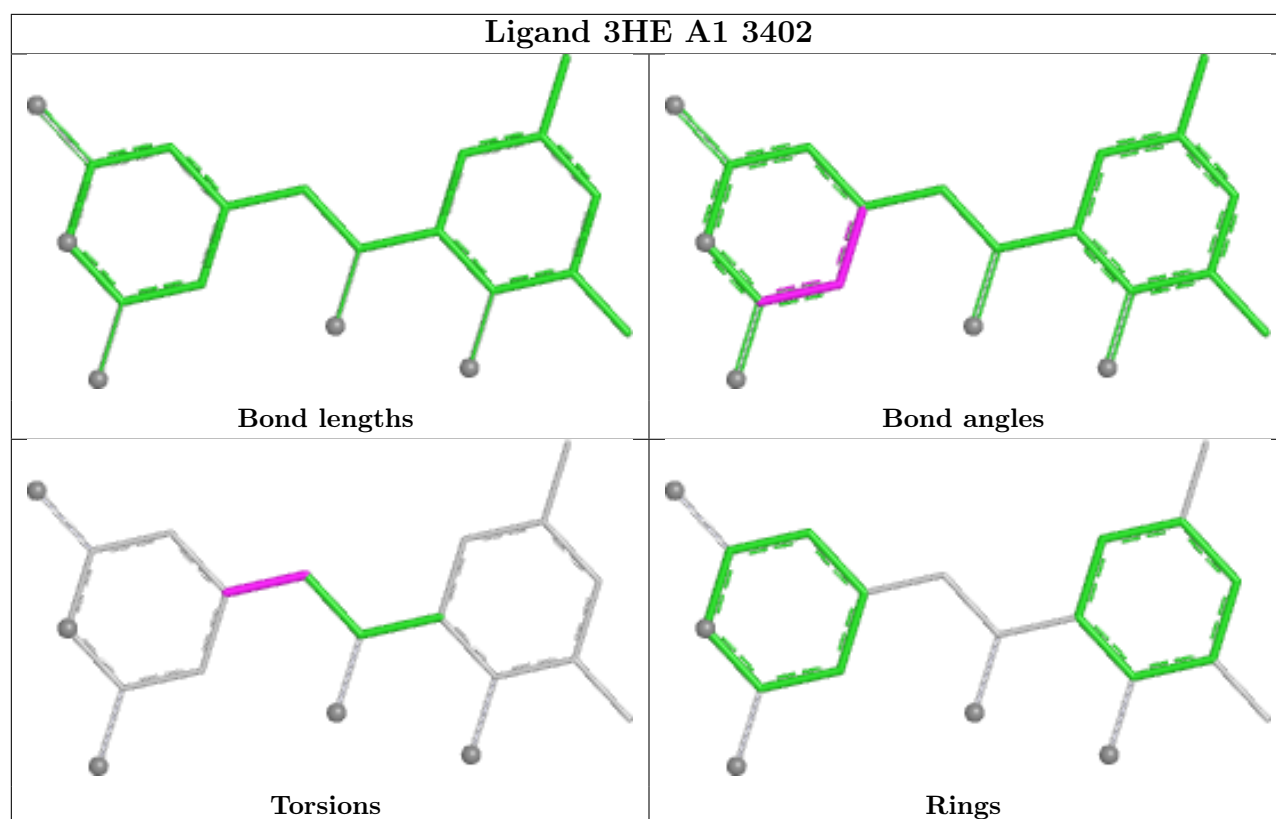
Mol	Chain	Res	Type	Atoms
79	A1	3401	SPD	C3-C4-C5-N6
79	A1	3401	SPD	C2-C3-C4-C5
80	A1	3402	3HE	C7-C8-C9-C13
79	A1	3401	SPD	C4-C5-N6-C7
79	A1	3401	SPD	N1-C2-C3-C4
79	A1	3401	SPD	C7-C8-C9-N10

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
79	A1	3401	SPD	3	0
80	A1	3402	3HE	1	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.

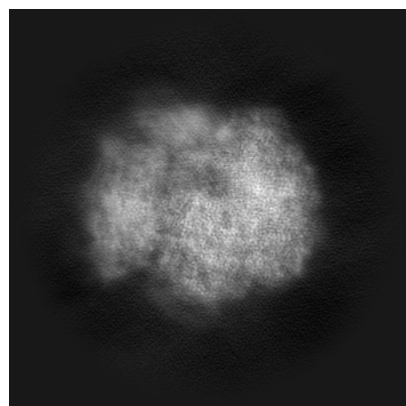
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40993. These allow visual inspection of the internal detail of the map and identification of artifacts.

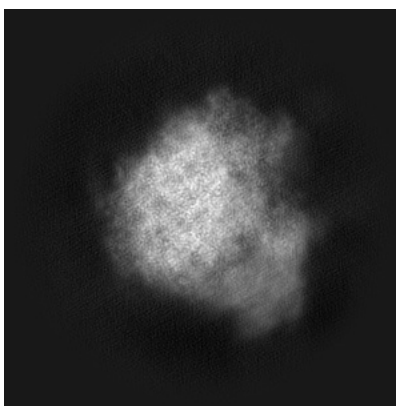
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

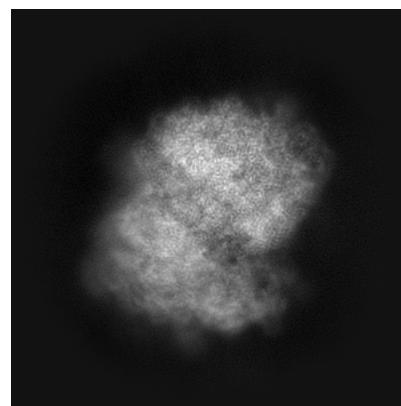
6.1.1 Primary map



X

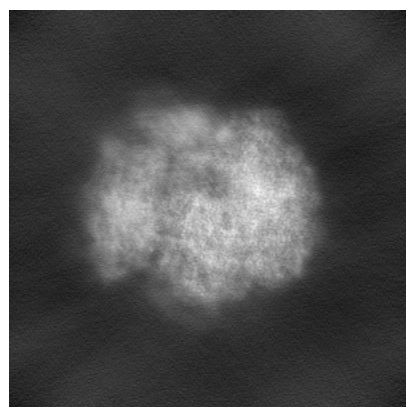


Y

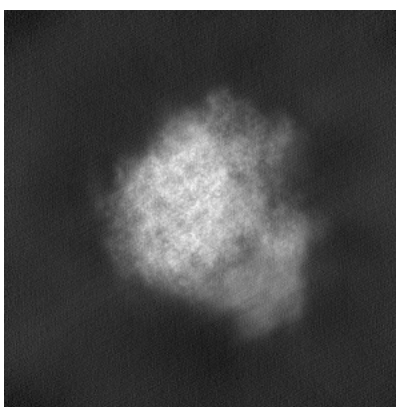


Z

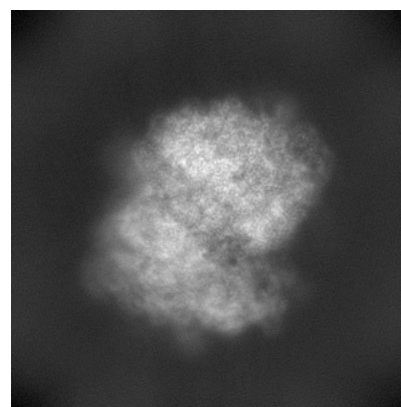
6.1.2 Raw map



X



Y

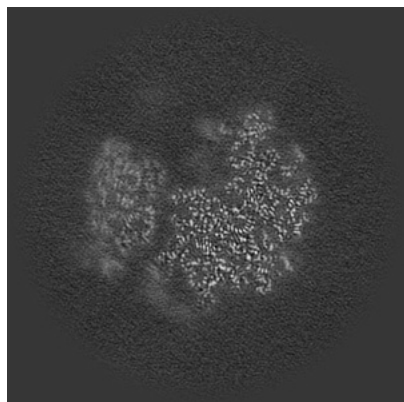


Z

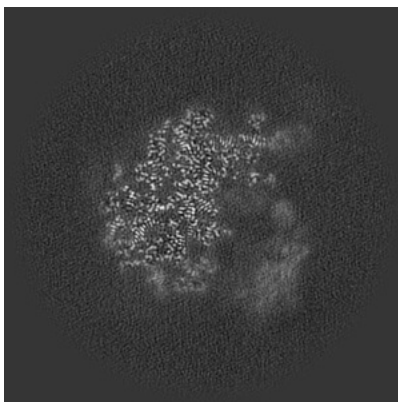
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

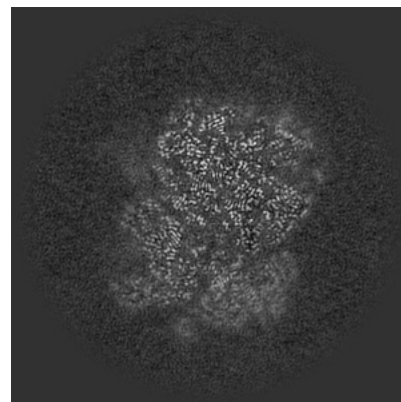
6.2.1 Primary map



X Index: 200

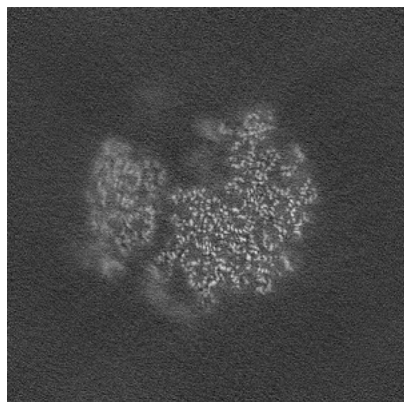


Y Index: 200

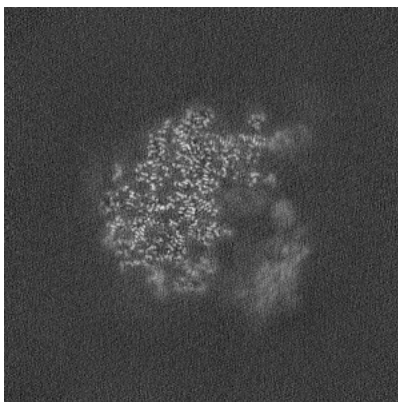


Z Index: 200

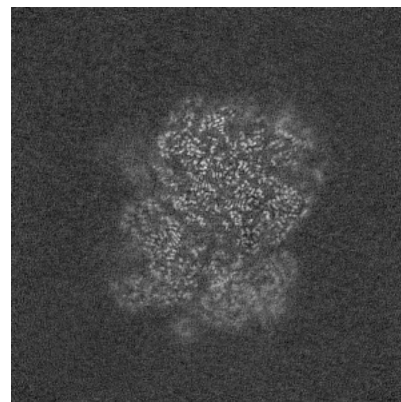
6.2.2 Raw map



X Index: 200



Y Index: 200

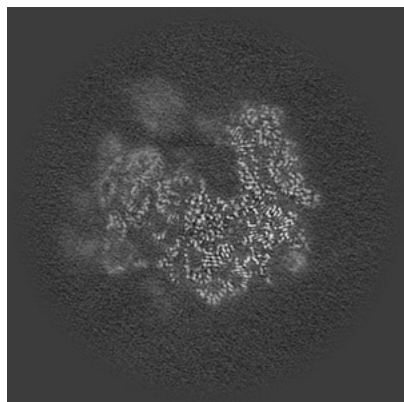


Z Index: 200

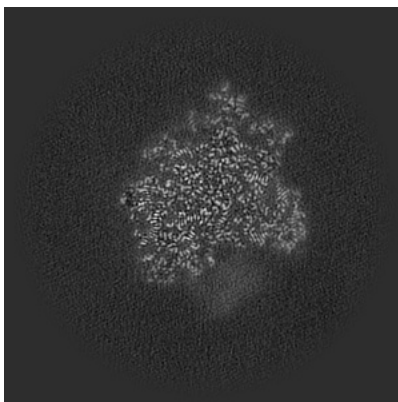
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

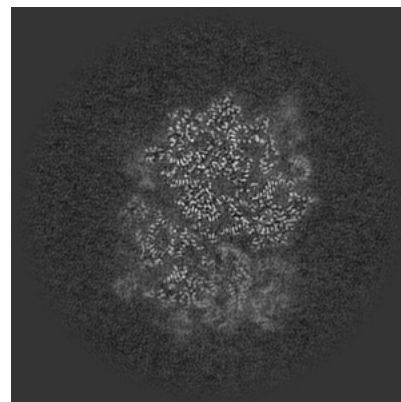
6.3.1 Primary map



X Index: 184

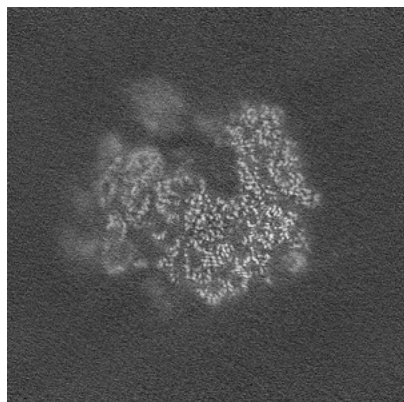


Y Index: 247

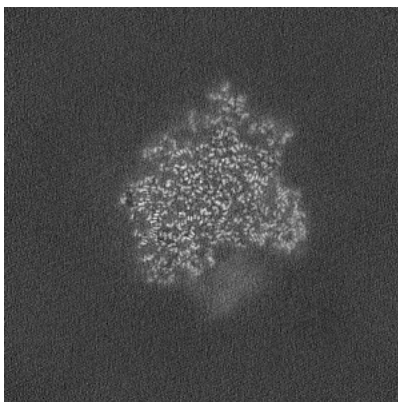


Z Index: 188

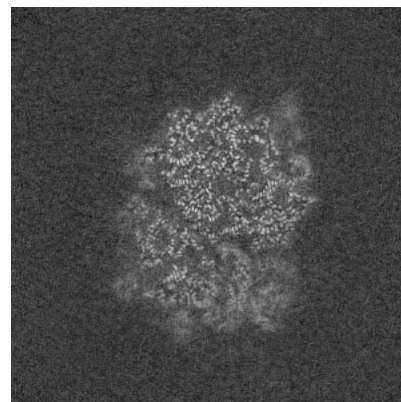
6.3.2 Raw map



X Index: 184



Y Index: 247

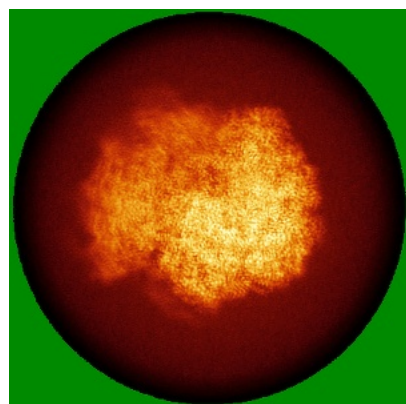


Z Index: 188

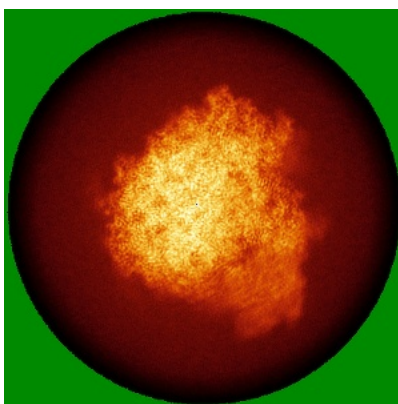
The images above show the largest variance slices of the map in three orthogonal directions.

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

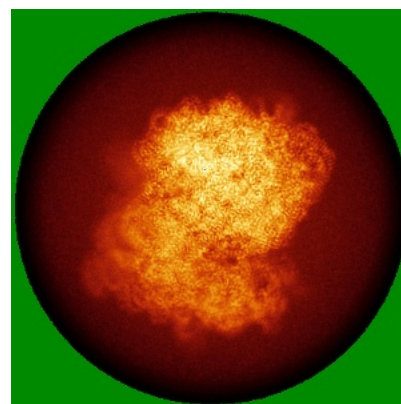
6.4.1 Primary map



X

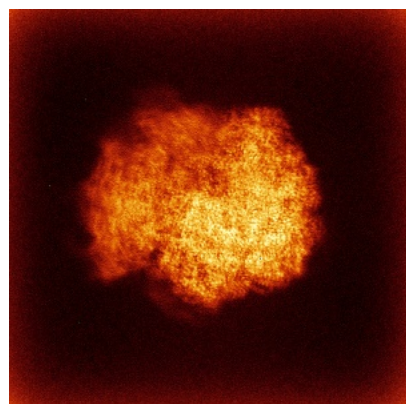


Y

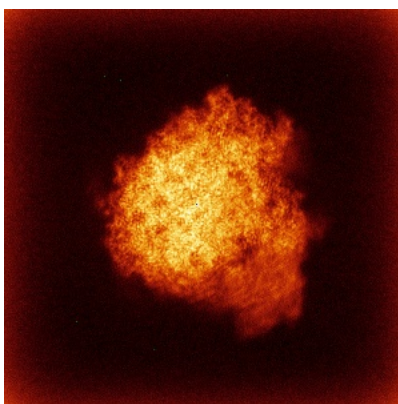


Z

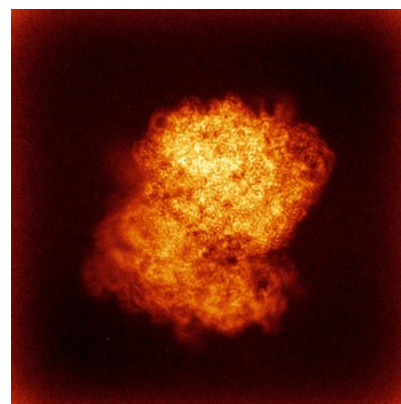
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

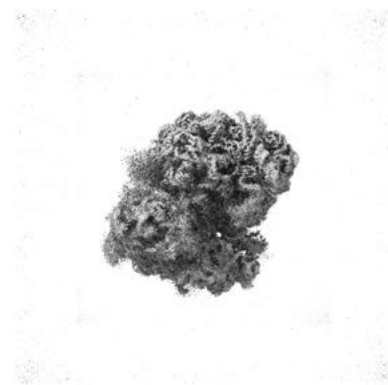
6.5.2 Raw map



X



Y



Z

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

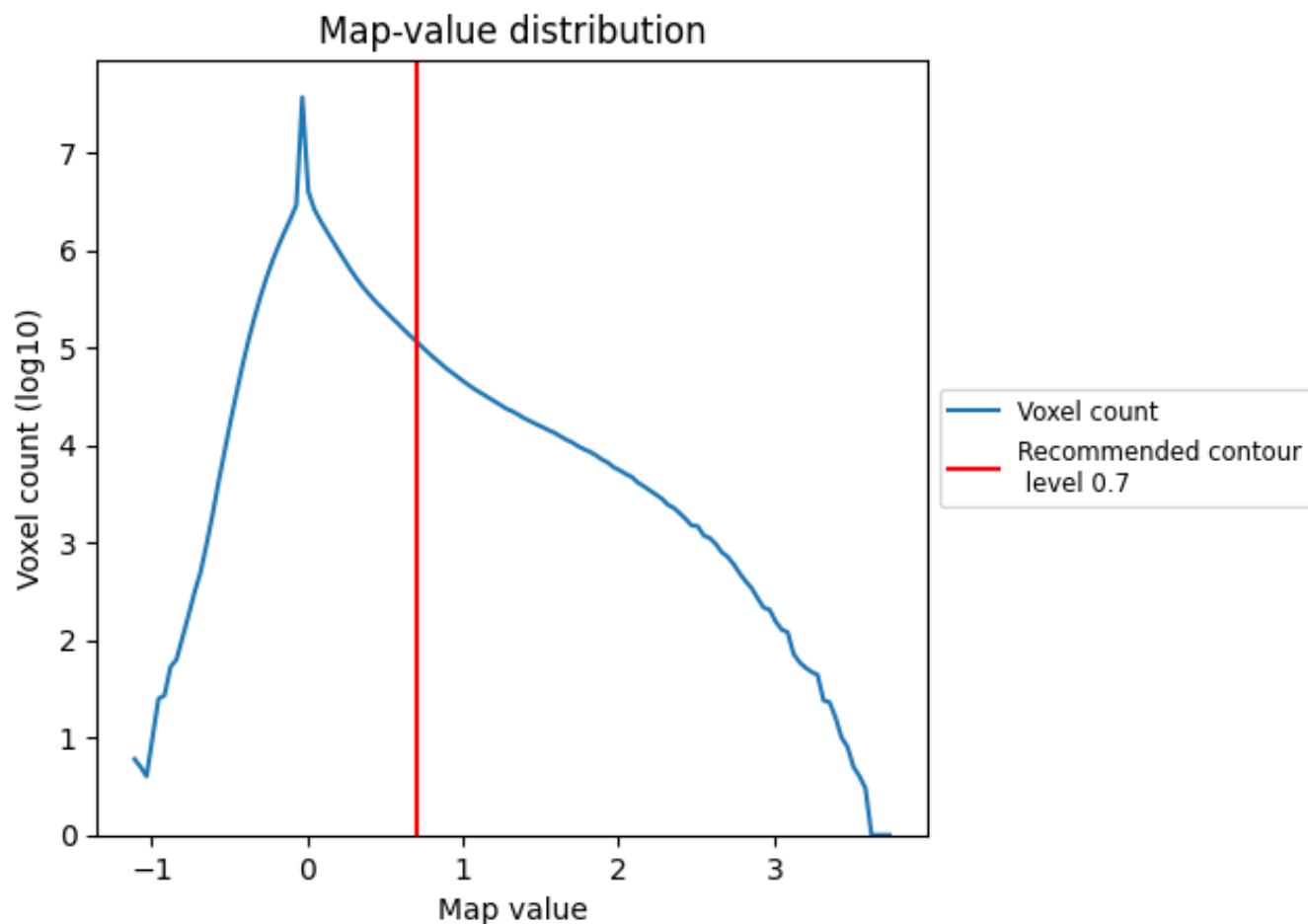
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

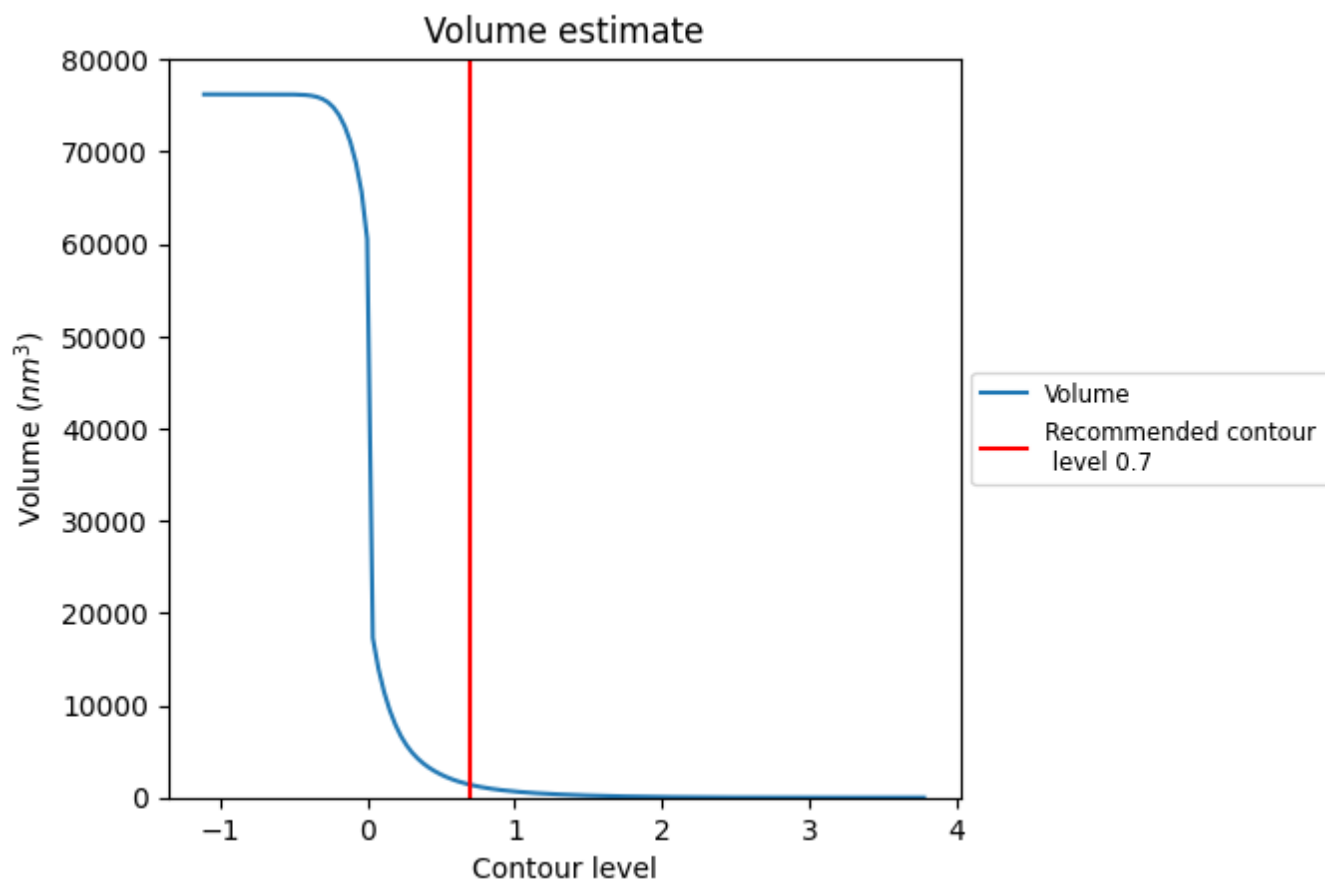
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

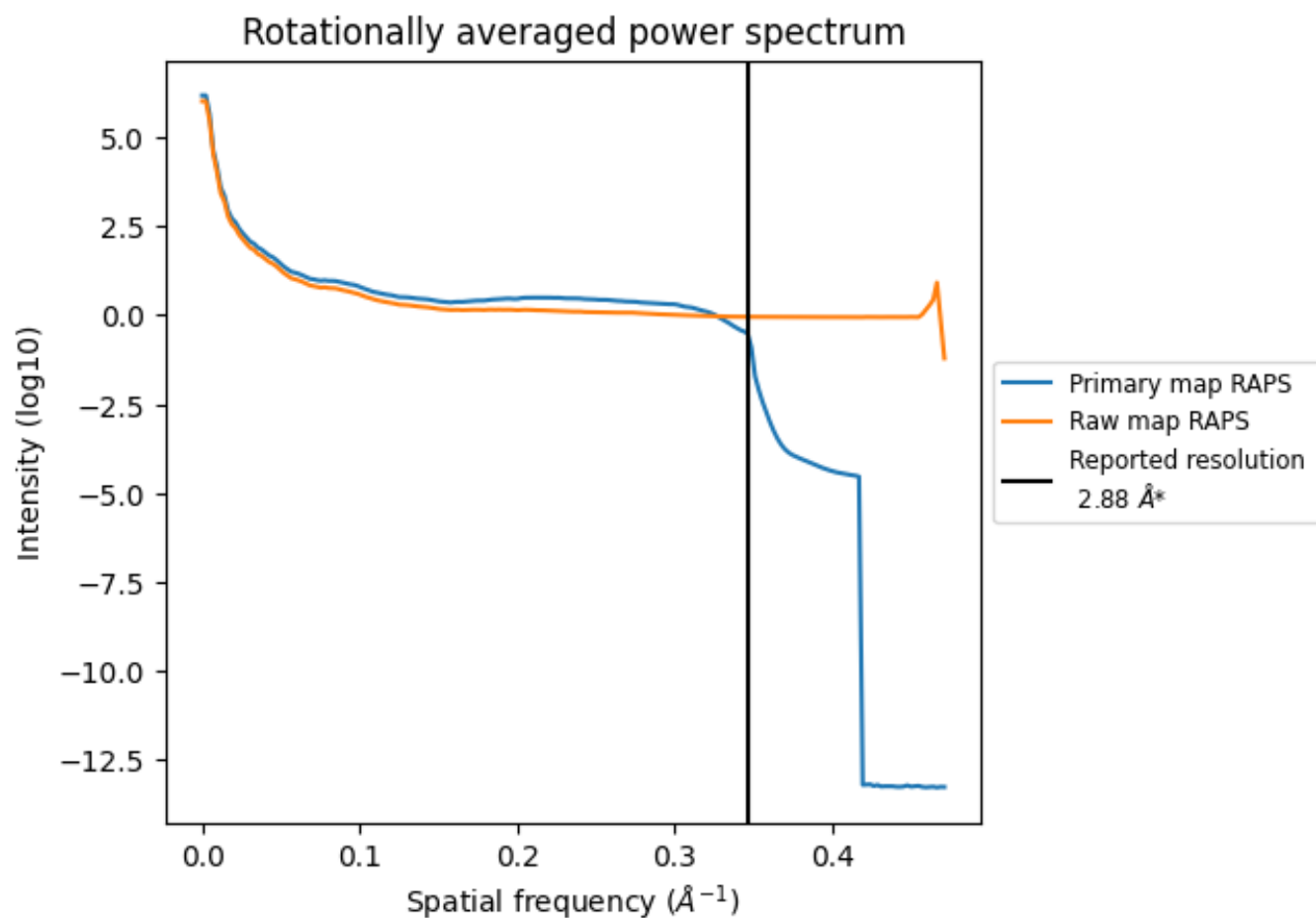
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1381 nm³; this corresponds to an approximate mass of 1247 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 ⓘ

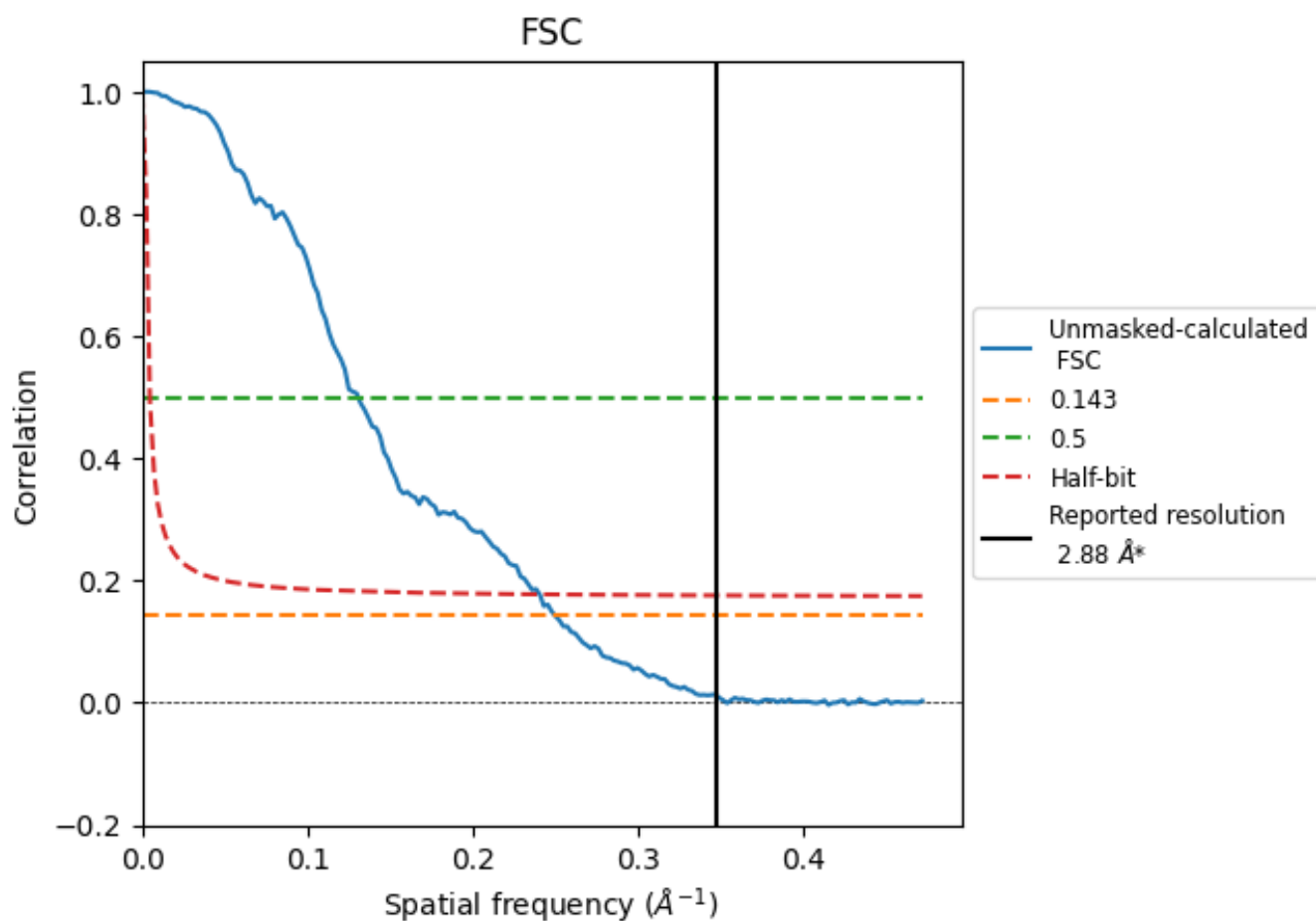


*Reported resolution corresponds to spatial frequency of 0.347 Å⁻¹

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 0.347 Å⁻¹

8.2 Resolution estimates [i](#)

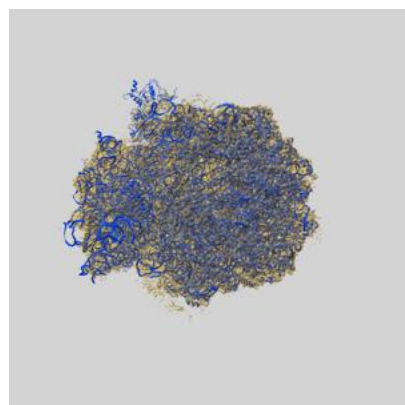
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.88	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.01	7.66	4.16

*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 4.01 differs from the reported value 2.88 by more than 10 %

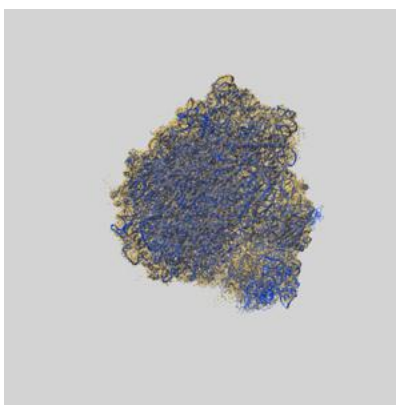
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40993 and PDB model 8T30. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

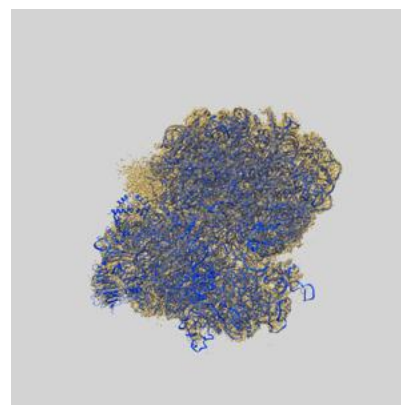
9.1 Map-model overlay [i](#)



X



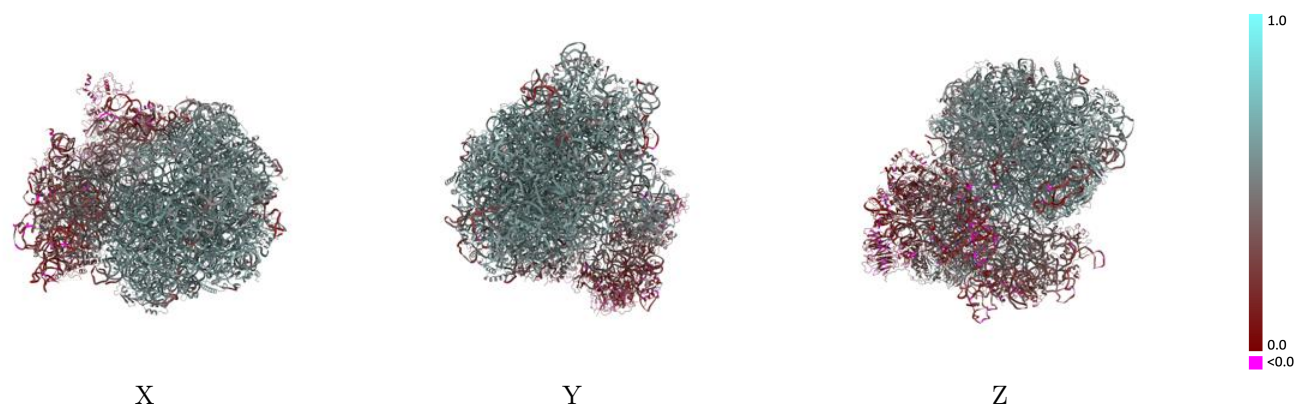
Y



Z

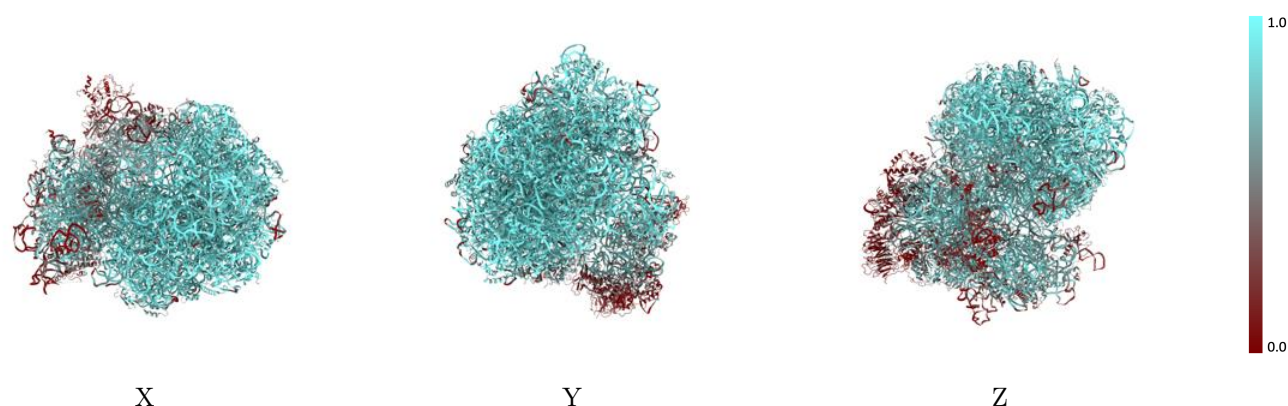
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



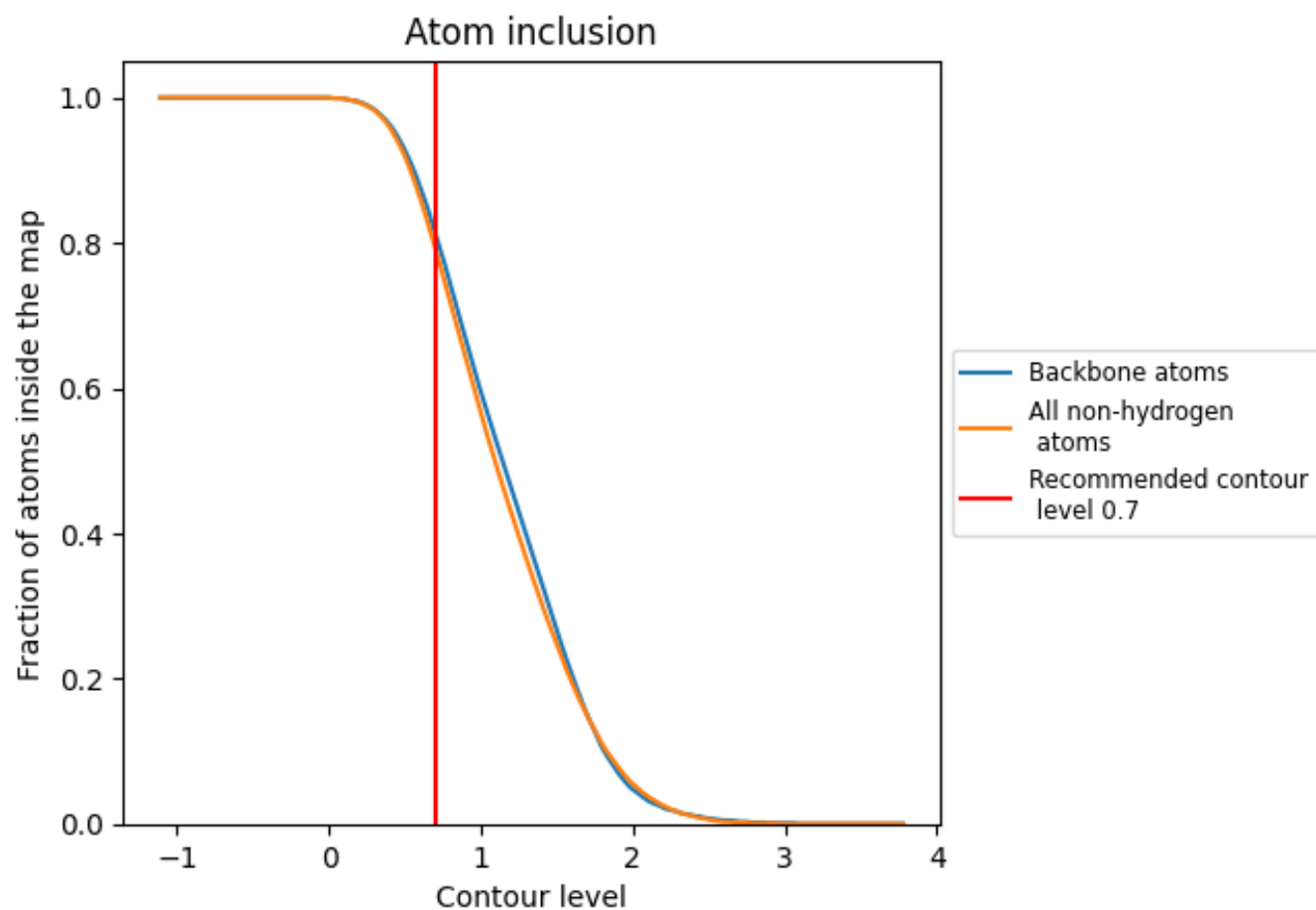
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7920	 0.4770
A1	 0.9290	 0.5520
A3	 0.9710	 0.5580
A4	 0.9690	 0.5780
AA	 0.9330	 0.6000
AB	 0.9140	 0.5810
AC	 0.9150	 0.5730
AD	 0.7930	 0.5080
AE	 0.8240	 0.5270
AF	 0.8900	 0.5670
AG	 0.8490	 0.5430
AH	 0.7940	 0.5410
AI	 0.7780	 0.5280
AJ	 0.7190	 0.4550
AL	 0.8940	 0.5710
AM	 0.8800	 0.5490
AN	 0.9630	 0.6040
AO	 0.9110	 0.5780
AP	 0.9300	 0.5890
AQ	 0.9230	 0.5850
AR	 0.7850	 0.5080
AS	 0.8770	 0.5670
AT	 0.8610	 0.5590
AU	 0.7670	 0.5090
AV	 0.8150	 0.5720
AW	 0.8750	 0.5710
AX	 0.8780	 0.5730
AY	 0.9190	 0.5740
AZ	 0.8390	 0.5560
Aa	 0.9220	 0.5860
Ab	 0.8500	 0.5430
Ac	 0.8700	 0.5550
Ad	 0.8390	 0.5450
Ae	 0.9360	 0.5890
Af	 0.9420	 0.6000



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Chain	Atom inclusion	Q-score
Ag	 0.8980	 0.5850
Ah	 0.8780	 0.5680
Ai	 0.8730	 0.5350
Aj	 0.9560	 0.6010
Ak	 0.7000	 0.5060
Al	 0.9490	 0.5860
Am	 0.8390	 0.5540
An	 0.6890	 0.5090
Ao	 0.8490	 0.5670
Ap	 0.8730	 0.5810
B5	 0.7420	 0.3710
BA	 0.6200	 0.4190
BB	 0.7120	 0.4530
BC	 0.7650	 0.4830
BD	 0.3390	 0.2520
BE	 0.6400	 0.3420
BF	 0.1690	 0.1980
BG	 0.4270	 0.3120
BH	 0.5250	 0.4010
BI	 0.5310	 0.3630
BJ	 0.5650	 0.2880
BK	 0.2580	 0.2120
BL	 0.6090	 0.4180
BM	 0.0090	 0.1480
BN	 0.7750	 0.5100
BO	 0.7380	 0.4660
BP	 0.2730	 0.2220
BQ	 0.2590	 0.2050
BR	 0.2830	 0.2450
BS	 0.3270	 0.2470
BT	 0.3110	 0.2410
BU	 0.2940	 0.2380
BV	 0.7210	 0.4530
BW	 0.8510	 0.5370
BX	 0.6300	 0.4460
BY	 0.5180	 0.2940
BZ	 0.0680	 0.1880
Ba	 0.7900	 0.5040
Bb	 0.7060	 0.4720
Bc	 0.2070	 0.2450
Bd	 0.6450	 0.3280
Be	 0.4750	 0.3260

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Chain	Atom inclusion	Q-score
Bf	 0.0320	 0.1550
Bg	 0.1290	 0.1890