



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 05:13 PM UTC

PDB ID : 9ZRG / pdb_00009zrg
EMDB ID : EMD-74615
Title : Structure of naked mole-rat ribosome (non-rotated)
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.
Deposited on : 2025-12-19
Resolution : 3.10 Å(reported)
Based on initial model : 4V6X

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

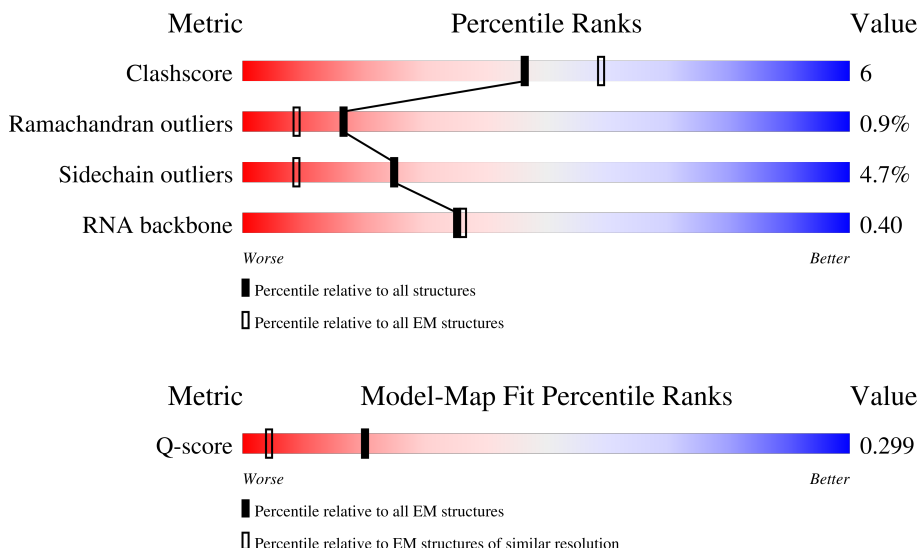
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


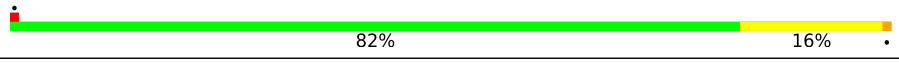

The reported resolution of this entry is 3.10 Å.

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.









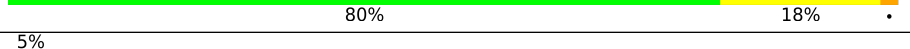
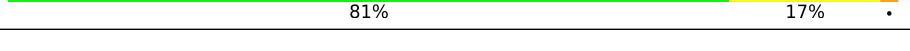
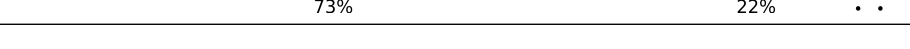
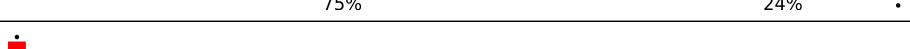
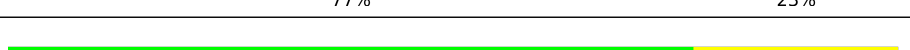

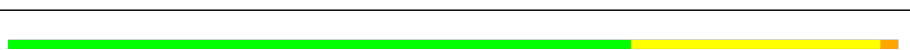

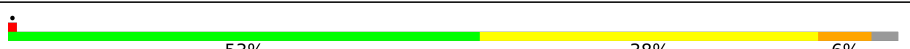





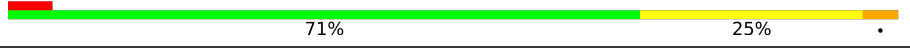
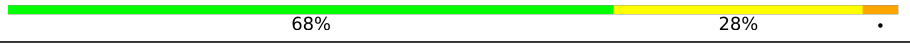



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	AO	136	
2	AX	142	
3	AN	150	










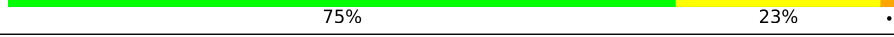

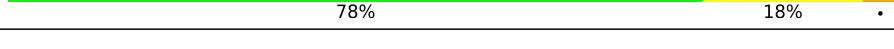
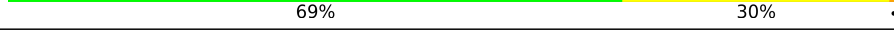
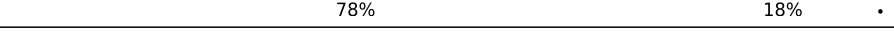
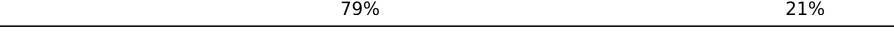


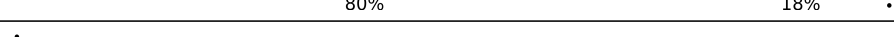




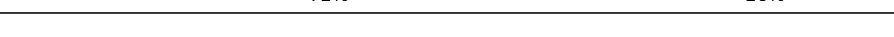
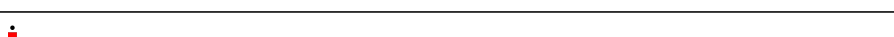
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Mol	Chain	Length	Quality of chain
4	AL	158	
5	AB	215	
6	AA	208	
7	AV	82	
8	AY	126	
9	Aa	107	
10	Ab	84	
11	Ae	59	
12	AJ	182	
13	AE	263	
14	AC	226	
15	AG	237	
16	AH	190	
17	AW	129	
18	AI	206	
19	B2	1861	
20	CR	153	
21	CW	124	
22	Ag	313	
23	AU	104	
24	AK	98	
25	AM	124	
26	AS	137	
27	Ad	53	
28	AR	126	







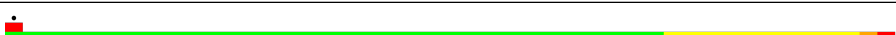
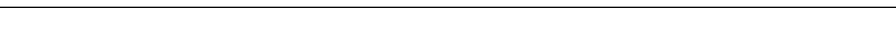
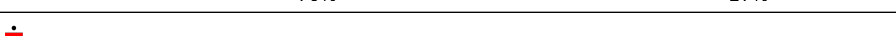
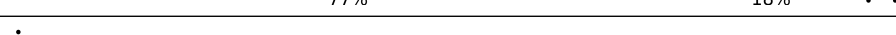
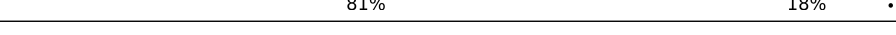
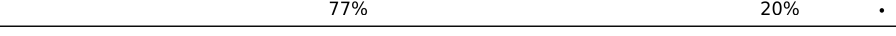













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Mol	Chain	Length	Quality of chain
29	AP	127	
30	AT	141	
31	AZ	75	
32	Ac	64	
33	AD	227	
34	Af	71	
35	AF	191	
36	AQ	141	
37	Cz	217	
38	CO	202	
39	CL	210	
40	CV	133	
41	CM	139	
42	Ca	147	
43	CN	203	
44	CI	213	
45	CD	289	
46	CQ	188	
47	CA	255	
48	CS	175	
49	CT	159	
50	CP	152	
51	CU	112	
52	CX	121	
53	CY	133	


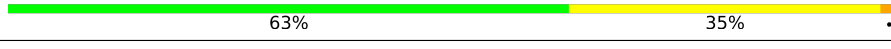
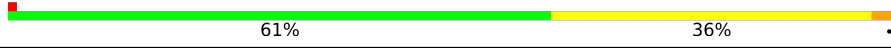

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Mol	Chain	Length	Quality of chain
54	CZ	135	
55	Cr	137	
56	Ch	123	
57	Cb	78	
58	CB	397	
59	CF	229	
60	Cc	100	
61	Cd	113	
62	Ce	133	
63	Cf	109	
64	Cg	114	
65	Ci	103	
66	Cj	90	
67	Ck	69	
68	Cl	50	
69	CC	368	
70	Cm	52	
71	Cn	25	
72	Cp	90	
73	Co	105	
74	CJ	168	
75	CH	191	
76	CE	262	
77	CG	246	
78	A5	3889	

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Mol	Chain	Length	Quality of chain
78	A6	3889	
79	A7	121	
80	A8	157	
81	BC	75	

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 219292 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 S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 2 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AX	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		

- Molecule 3 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 4 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AL	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 5 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AB	215	Total	C	N	O	S	0	0
			1747	1110	313	310	14		

- Molecule 6 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 7 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 8 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 9 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Aa	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 10 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Ab	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 11 is a protein called Ubiquitin-like protein FUBI.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ae	59	Total	C	N	O	S	0	0
			468	290	102	75	1		

- Molecule 12 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AJ	175	Total	C	N	O	S	0	0
			1463	933	292	236	2		

- Molecule 13 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AE	263	Total	C	N	O	S	0	0
			2084	1329	387	359	9		

- Molecule 14 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AC	226	Total	C	N	O	S	0	0
			1751	1130	301	310	10		

- Molecule 15 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 16 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AH	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 18 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 19 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	B2	1799	Total	C	N	O	P	0	0
			37803	16849	6724	12432	1798		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CR	153	Total	C	N	O	S	0	0
			1257	780	265	206	6		

- Molecule 21 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 22 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ag	306	Total	C	N	O	S	0	0
			2387	1506	417	452	12		

- Molecule 23 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AU	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 24 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 25 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AM	124	Total	C	N	O	S	0	0
			960	600	171	181	8		

- Molecule 26 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 27 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ad	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 28 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AR	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 29 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AP	119	Total	C	N	O	S	0	0
			992	631	187	167	7		

- Molecule 30 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AT	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 32 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ac	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 33 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AD	223	Total	C	N	O	S	0	0
			1736	1107	312	310	7		

- Molecule 34 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Af	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 35 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 36 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 37 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Cz	192	Total	C	N	O	S	0	0
			1534	981	274	271	8		

- Molecule 38 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	CO	202	Total	C	N	O	S	0	0
			1655	1066	322	262	5		

- Molecule 39 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	CL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 40 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CV	133	Total	C	N	O	S	0	0
			989	623	186	175	5		

- Molecule 41 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CM	139	Total	C	N	O	S	0	0
			1139	730	218	183	8		

- Molecule 42 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ca	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 43 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 44 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CI	201	Total	C	N	O	S	0	0
			1626	1032	313	268	13		

- Molecule 45 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CD	289	Total	C	N	O	S	0	0
			2353	1483	429	427	14		

- Molecule 46 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CQ	188	Total	C	N	O	S	0	0
			1521	949	315	251	6		

- Molecule 47 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CA	255	Total	C	N	O	S	0	0
			1957	1225	399	327	6		

- Molecule 48 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 49 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 50 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CP	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 51 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CU	112	Total	C	N	O	S	0	0
			921	583	159	177	2		

- Molecule 52 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CX	121	Total	C	N	O	S	0	0
			994	636	187	170	1		

- Molecule 53 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CY	133	Total	C	N	O	S	0	0
			1107	695	225	185	2		

- Molecule 54 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 55 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Cr	137	Total	C	N	O	S	0	0
			1104	682	231	185	6		

- Molecule 56 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ch	123	Total	C	N	O	S	0	0
			1023	646	206	169	2		

- Molecule 57 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Cb	67	Total	C	N	O	S	0	0
			554	341	121	89	3		

- Molecule 58 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CB	392	Total	C	N	O	S	0	0
			3161	2014	593	540	14		

- Molecule 59 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CF	229	Total	C	N	O	S	0	0
			1910	1226	370	305	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cc	100	Total	C	N	O	S	0	0
			776	492	136	141	7		

- Molecule 61 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Cd	113	Total	C	N	O	S	0	0
			931	586	181	162	2		

- Molecule 62 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Ce	133	Total	C	N	O	S	0	0
			1096	691	224	175	6		

- Molecule 63 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Cf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 64 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Cg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 65 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ci	103	Total	C	N	O	S	0	0
			840	526	178	130	6		

- Molecule 66 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cj	90	Total	C	N	O	S	0	0
			733	451	162	115	5		

- Molecule 67 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ck	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 68 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cl	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 69 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	CC	358	Total	C	N	O	S	0	0
			2853	1797	570	473	13		

- Molecule 70 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Cm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 71 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Cn	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 72 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Cp	90	Total	C	N	O	S	0	0
			703	442	135	119	7		

- Molecule 73 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Co	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 74 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	CJ	168	Total	C	N	O	S	0	0
			1349	853	251	239	6		

- Molecule 75 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	CH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 76 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	CE	262	Total	C	N	O	S	0	0
			2113	1357	403	349	4		

- Molecule 77 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	CG	246	Total	C	N	O	S	0	0
			1973	1256	379	334	4		

- Molecule 78 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A5	1720	Total	C	N	O	P	0	0
			36244	16105	6607	11813	1719		
78	A6	2169	Total	C	N	O	P	0	0
			44180	19585	7784	14642	2169		

- Molecule 79 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	A7	121	Total	C	N	O	P	0	0
			2578	1150	458	850	120		

- Molecule 80 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	A8	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

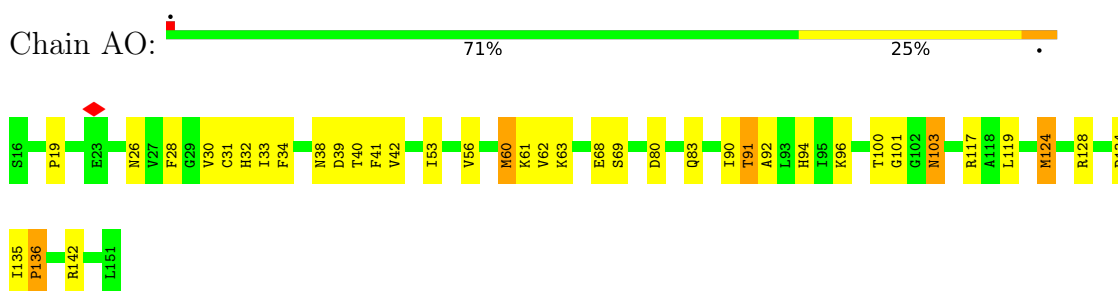
- Molecule 81 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BC	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

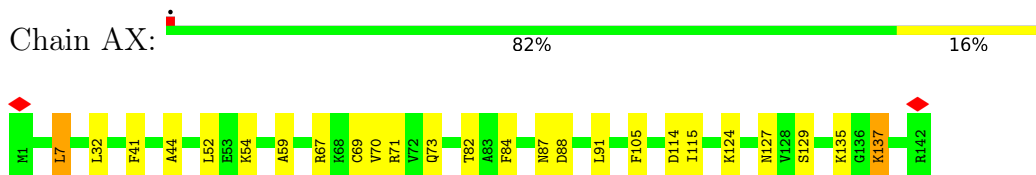
3 Residue-property plots [i](#)

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

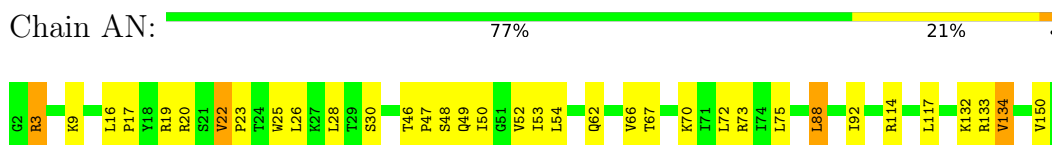
- Molecule 1: 40S ribosomal protein S14



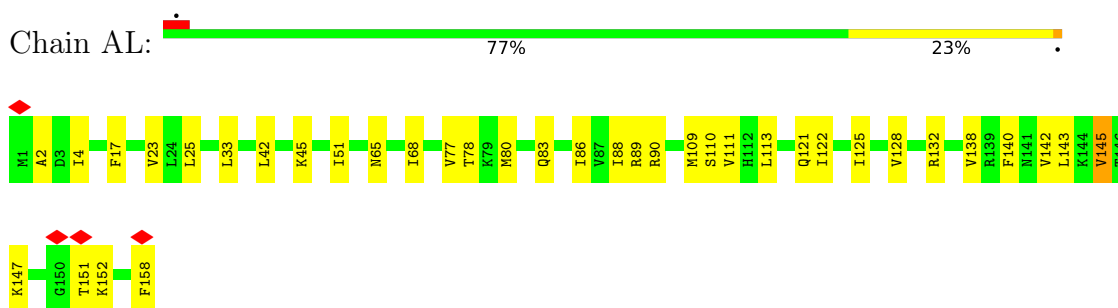
- Molecule 2: Small ribosomal subunit protein uS12




- Molecule 3: Small ribosomal subunit protein uS15

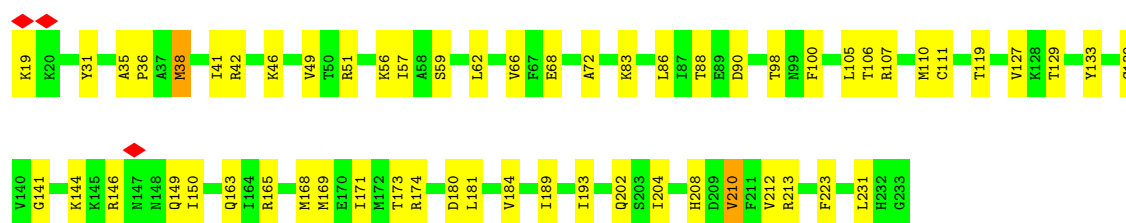


- Molecule 4: Small ribosomal subunit protein uS17




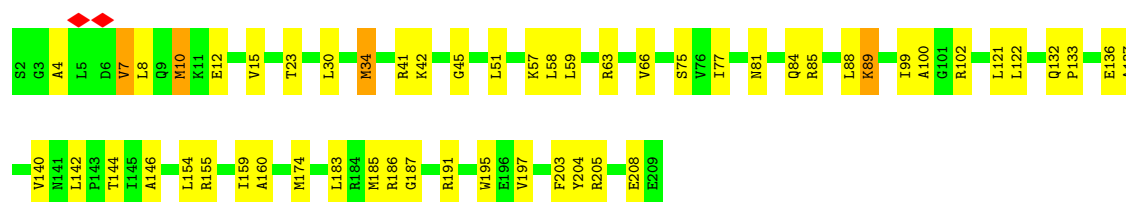
- Molecule 5: Small ribosomal subunit protein eS1

Chain AB:  73% 26%



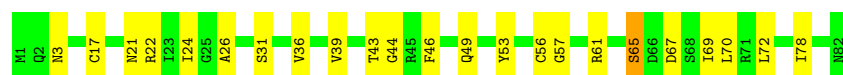
- Molecule 6: Small ribosomal subunit protein uS2

Chain AA:  74% 24%



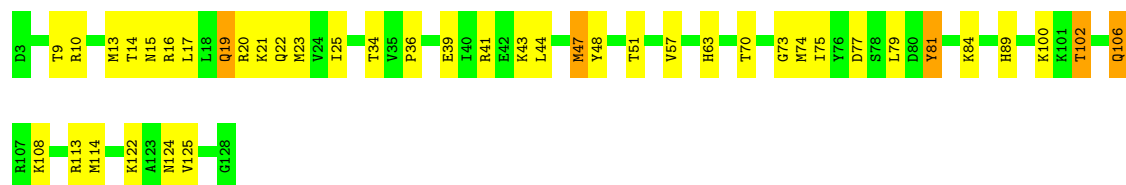
- Molecule 7: 40S ribosomal protein S21

Chain AV:  72% 27%




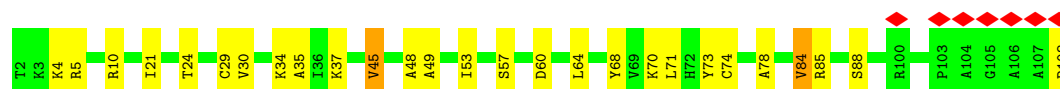
- Molecule 8: 40S ribosomal protein S24

Chain AY:  67% 29%




- Molecule 9: 40S ribosomal protein S26

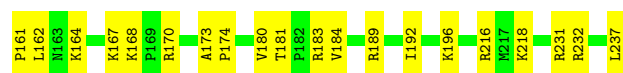
Chain Aa:  7% 75% 23%



- Molecule 10: 40S ribosomal protein S27

Chain Ab:  80% 18%





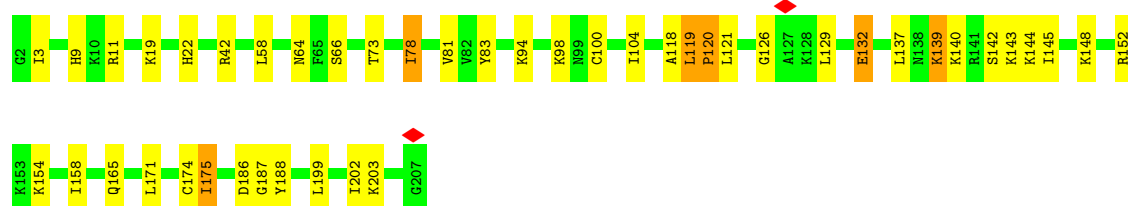
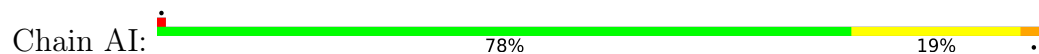
- Molecule 16: 40S ribosomal protein S7



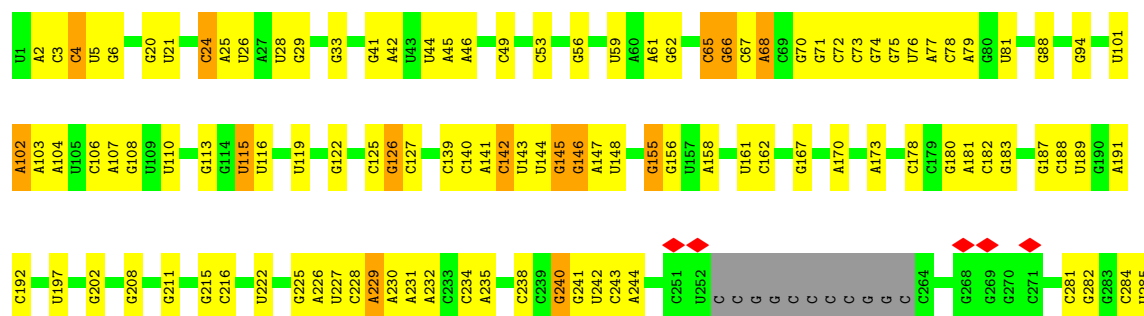
- Molecule 17: Small ribosomal subunit protein uS8



- Molecule 18: 40S ribosomal protein S8



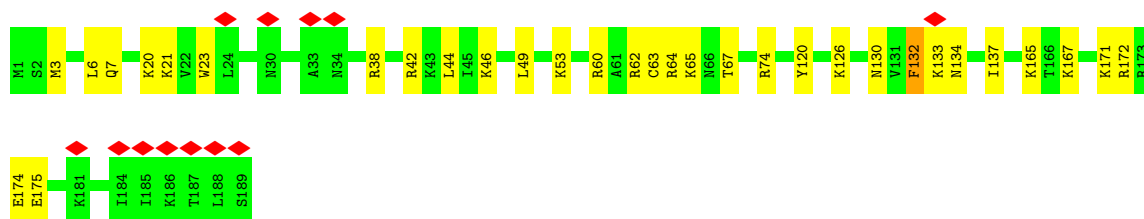
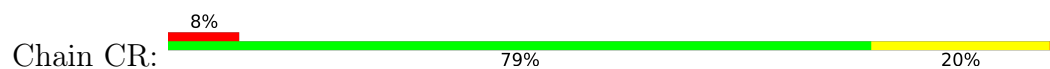
- Molecule 19: 18S ribosomal RNA



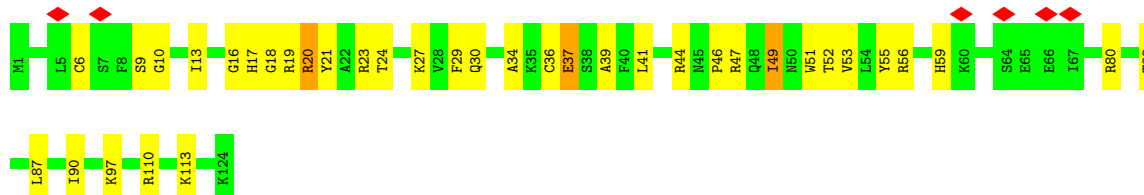
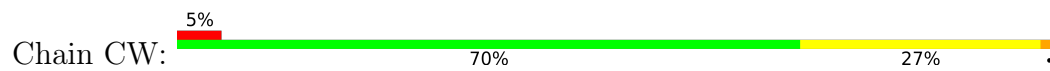
A1561	C1464	G1387	U1307	C1215	U1120	U1017	A920	C840	C753	A679	A590	G504	C382	U286
G1566	A1465	U1392	U1308	C1216	G1121	U1018	G923	G841	C757	G683	U591	G507	G383	U257
G1567	G1466	G1393	C1309	A1217	A1122	U1021	G924	U844	C	G684	C592	A508	U384	G288
G1570	A1474	G1394	G1310	C1218	C1123	A1022	G925	G845	C	A685	C593	A509	G385	G
G1571	A1476	C1395	G1311	G1221	G1125	A1023	A926	G846	U	U686	A594	G510	C386	C293
G1575	U1477	G1397	G1312	G1222	G1126	C1028	G927	A847	C	C687	G600	U511	C381	C295
G1576	A1401	G	A1313	G1223	C1127	U1028	G928	U848	G	U688	G601	A512	A392	A302
G1577	G1490	U1314	U1315	G1224	C1128	G1043	G929	A849	A	G689	G602	G513	C303	C304
U1578	C1403	C1316	C1317	G1225	G1129	U1044	C930	G852	U	C690	C603	C517	C399	U305
U1579	U1404	G1318	G1319	G1226	G1130	U1045	G931	G853	C	A692	A605	G518	U306	C306
A1580	A1405	U1319	G1320	G1229	G1132	U1049	G934	G855	U	G694	G606	A519	G307	G
G1584	U1406	G1320	G1321	U1232	A1133	A1050	U939	A861	C	C695	U607	G	G407	G
U1585	U1407	G	U1322	G1233	U1136	G1051	U940	G867	U	C696	C608	A524	A408	U308
U1586	U1408	G1324	C1325	A1234	U1137	A1052	C941	G872	C	G	U609	U525	A409	G309
U1587	A1409	G1325	G1235	G1235	C1139	C1053	G942	G873	A	G	G610	A526	G410	G
A1588	C1410	U1326	U1239	U1239	C1139	A1060	U943	A869	C	G	G611	G	U428	G312
G1593	G1411	G1327	A1240	A1241	G1140	U1061	A944	A870	U	G	G612	A529	A318	A318
G1597	C1412	U1328	A1242	A1243	A1144	U1062	C948	A871	G	G	G613	U530	C319	C319
G1598	G1416	U1333	U1243	U1244	A1145	A1062	G949	A872	A	C	G614	A531	C322	C322
G1599	C1417	G1337	U1245	U1246	A1148	G1068	U954	G874	G	C	G615	A532	C323	C323
G1600	U1419	G1338	G1245	G1245	A1149	U1069	A955	A875	U	C	G616	A533	C324	C324
A1601	C1420	C1341	A1246	A1247	A1150	A1080	G956	C876	C	C	G617	G534	C325	C325
U1602	G1421	U1342	C1251	C1252	G1151	A1082	A957	C877	C	C	G618	G535	C326	C326
G1605	U1422	G1423	A1251	A1252	U1152	A1083	G961	A882	C	C	A628	G544	G327	U328
G1606	U1426	U1426	A1253	A1254	C1153	A1084	A962	U883	G	A	A629	G547	G329	C483
U1608	G1429	G1430	C1254	G1255	U1154	C1085	U969	C884	C	C	G634	G548	G330	G330
G1610	C1430	C1430	G1256	G1257	U1155	U1090	G971	C885	C	C	A634	C549	G331	G331
G1613	C1435	C1435	A1258	A1259	U1156	G1095	G982	U886	C	C	A640	U551	G332	G332
A1614	U1437	U1437	U1263	U1263	G1170	G1096	A983	U887	C	C	A641	U552	G333	G333
U1615	A1438	A1438	C1264	C1265	U1171	C1097	G989	G894	C	C	A642	U553	G334	G334
U1616	U1441	U1441	A1266	A1266	A1173	G1098	A990	G895	C	C	A643	U554	G335	G335
A1620	U1442	U1442	G1269	G1269	A1183	U1101	A992	C900	C	C	A644	U555	U345	U345
U1621	C1443	U1443	C1270	C1270	G1184	G1102	G999	G901	C	C	A655	A554	C346	C346
A1623	U1444	U1444	C1271	C1271	U1193	C1103	C1000	G902	C	C	A656	A555	G347	G347
U1631	A1445	A1445	C1272	C1272	U1194	G1104	A1001	A903	C	C	G657	U556	A348	A348
G1632	G1447	G1447	C1273	C1273	A1194	G1105	U1004	G904	C	C	C660	U557	A349	A349
A1633	A1448	A1448	G1274	G1274	U1195	C1106	G1005	G905	C	C	U666	G558	C350	C350
G1633	G1449	G1449	G1275	G1275	U1202	G1108	G1006	A908	C	C	U667	G559	G351	G351
A1634	U1450	U1450	A1284	A1284	G1203	C1109	A1008	G909	C	C	U668	A560	C352	C352
A1637	G1451	G1451	G1285	G1285	A1204	G1110	U1009	G910	C	C	U669	A561	G353	G353
G1638	U1452	U1452	G1286	G1286	C1205	U1111	G1010	G911	C	C	A688	U562	A354	A354
U1643	C1453	C1453	A1287	A1287	U1112	U1112	A1011	A913	C	C	A689	A563	U358	U358
U1648	A1454	A1454	U1288	U1288	G1207	U1115	A1012	U914	C	C	A690	A564	C359	C359
U1649	A1455	A1455	A1301	A1301	A1208	C1116	U1013	A915	C	C	A691	C568	G370	G370
	G1456	G1456	A1302	A1302	G1211	C1117	G1014	U916	C	C	A692	A569	A371	A371
	U1462	U1462	G1302	G1302	G1212	C1118	U1015	U917	C	C	A693	U577	U372	U372
	U1463	U1463	C1303	C1303		C1119	U1016	U918	C	C	A694	U582	G373	G373
						A1119		A919	C	C	A695	U583	U374	U374
									C	C	A696	U584	U375	U375
									C	C	A697	U585	A376	A376
									C	C	A698	U586	G377	G377
									C	C	A699	U587	C381	C381



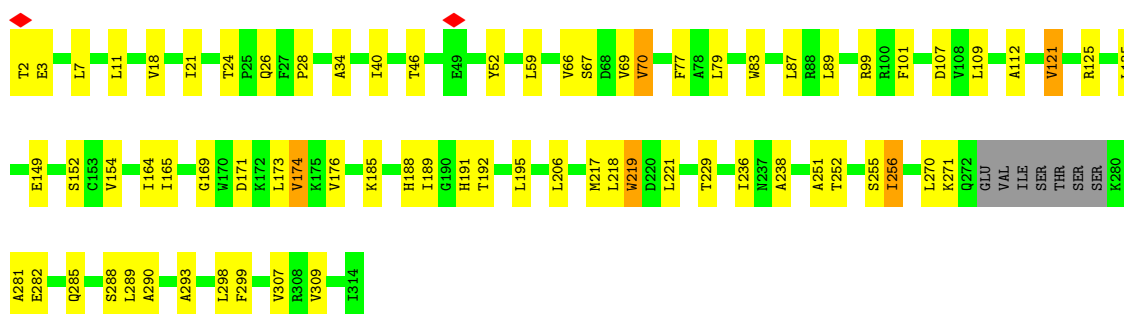
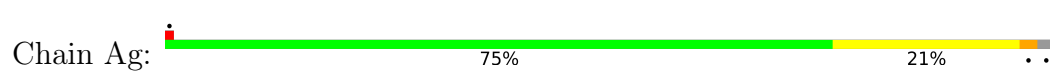
• Molecule 20: 60S ribosomal protein L19



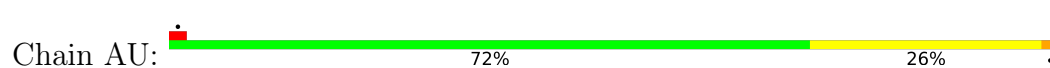
• Molecule 21: Large ribosomal subunit protein eL24



• Molecule 22: Small ribosomal subunit protein RACK1

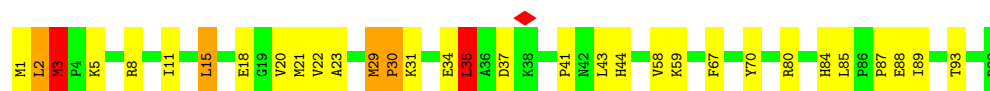


• Molecule 23: 40S ribosomal protein S20

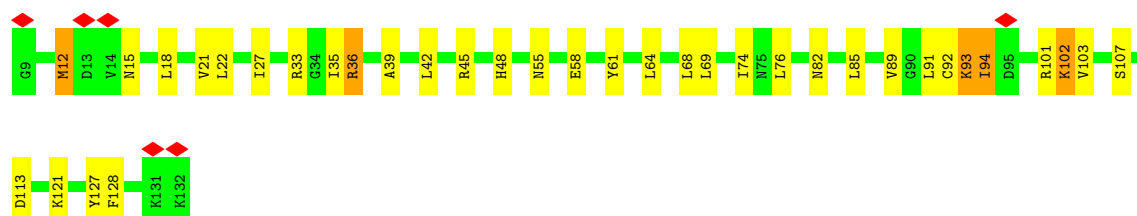
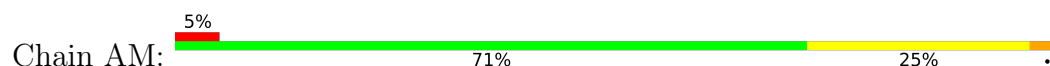




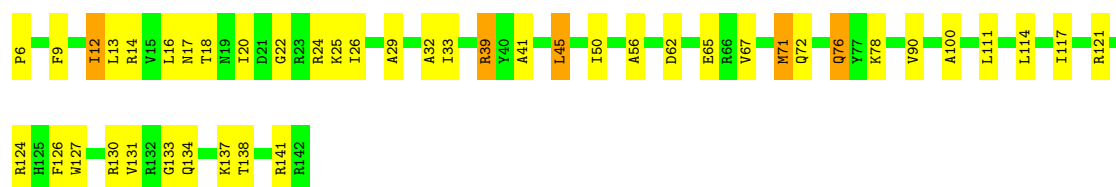
- Molecule 24: Small ribosomal subunit protein eS10



- Molecule 25: 40S ribosomal protein S12



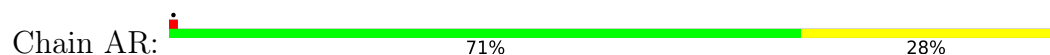
- Molecule 26: Small ribosomal subunit protein uS13



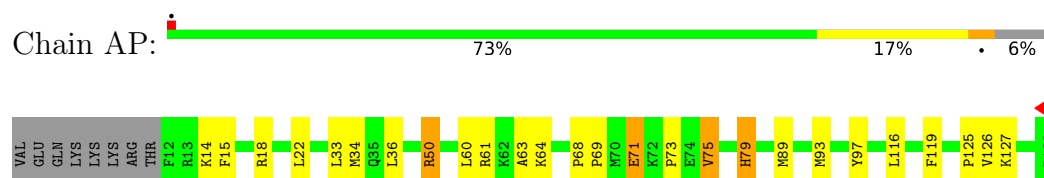
- Molecule 27: Small ribosomal subunit protein uS14



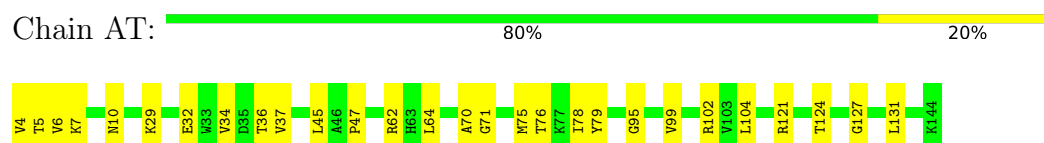
- Molecule 28: Small ribosomal subunit protein eS17



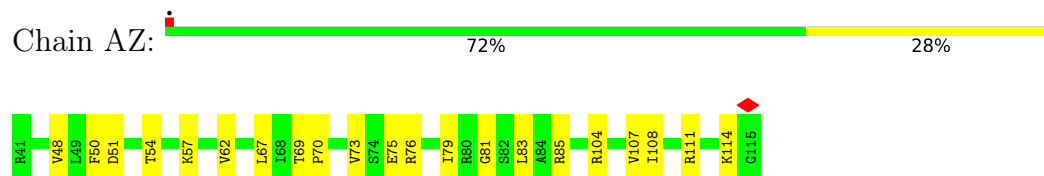
- Molecule 29: 40S ribosomal protein S15



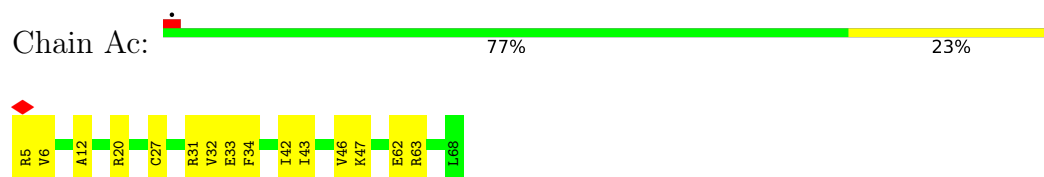
- Molecule 30: Small ribosomal subunit protein eS19



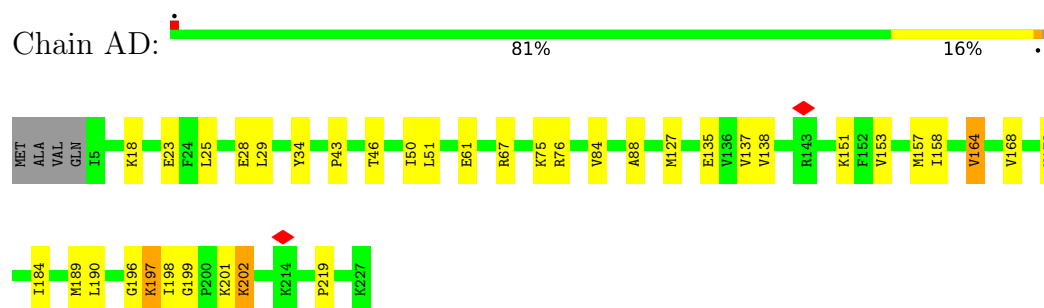
- Molecule 31: 40S ribosomal protein S25



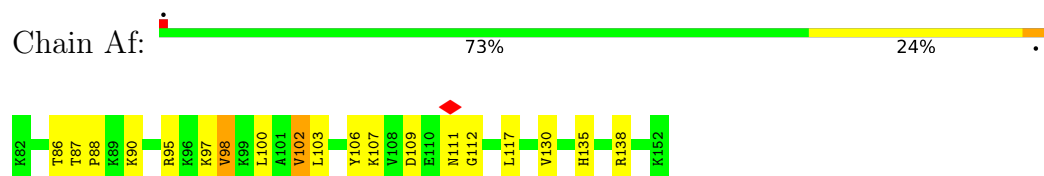
- Molecule 32: 40S ribosomal protein S28




- Molecule 33: 40S ribosomal protein S3

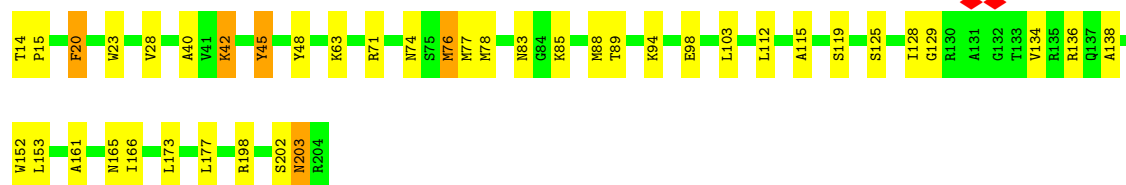


- Molecule 34: Ubiquitin-ribosomal protein eS31 fusion protein




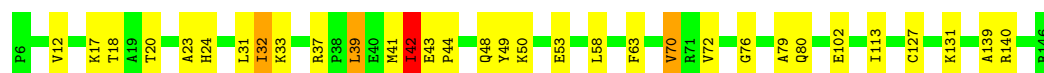
- Molecule 35: Small ribosomal subunit protein uS7

Chain AF:  79% 19%



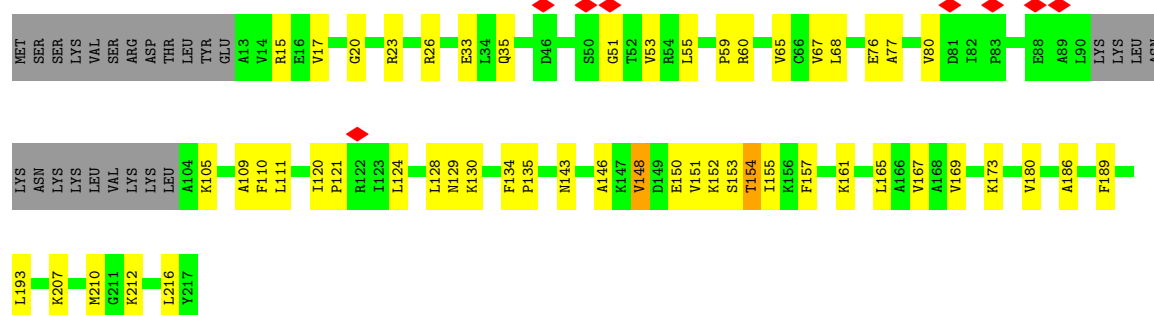
- Molecule 36: Small ribosomal subunit protein uS9

Chain AQ:  77% 20%




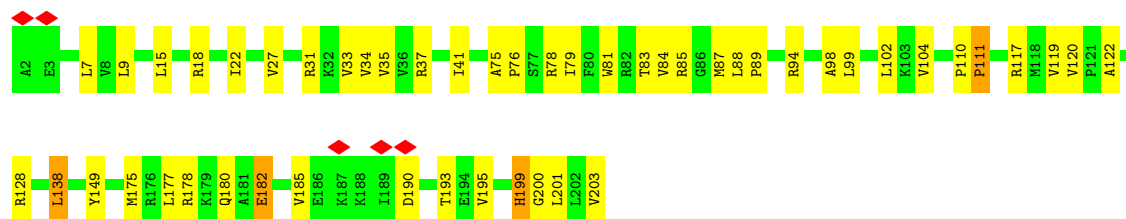
- Molecule 37: 60S ribosomal protein L10a

Chain Cz:  64% 24% 12%




- Molecule 38: 60S ribosomal protein L13a

Chain CO:  75% 23%



- Molecule 39: 60S ribosomal protein L13

Chain CL:  80% 18%





- Molecule 40: Large ribosomal subunit protein uL14

Chain CV: 86% 12%



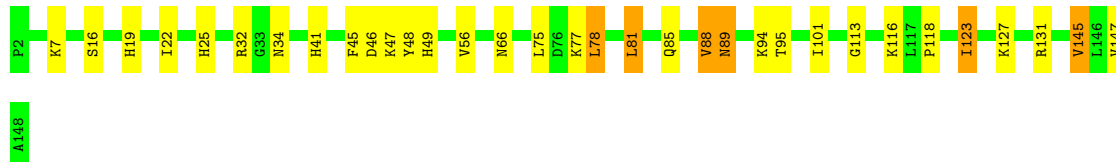
- Molecule 41: 60S ribosomal protein L14

Chain CM: 69% 30%



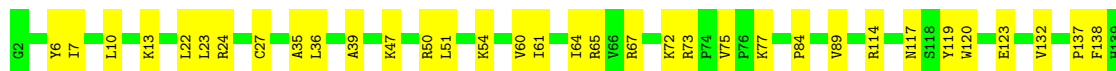
- Molecule 42: 60S ribosomal protein L27a

Chain Ca: 78% 18%



- Molecule 43: Ribosomal protein L15

Chain CN: 79% 21%



- Molecule 44: 60S ribosomal protein L10-like

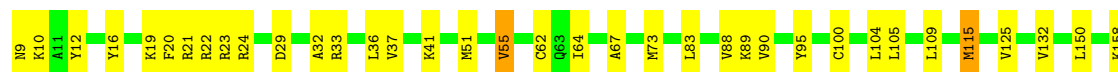
Chain CI: 72% 21% 6%





- Molecule 45: 60S ribosomal protein L5

Chain CD: 78% 21% .



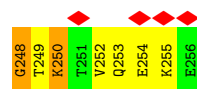
- Molecule 46: 60S ribosomal protein L18

Chain CQ: 80% 18% ..



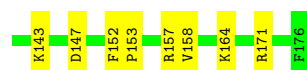
- Molecule 47: Large ribosomal subunit protein uL2

Chain CA: 71% 27% .

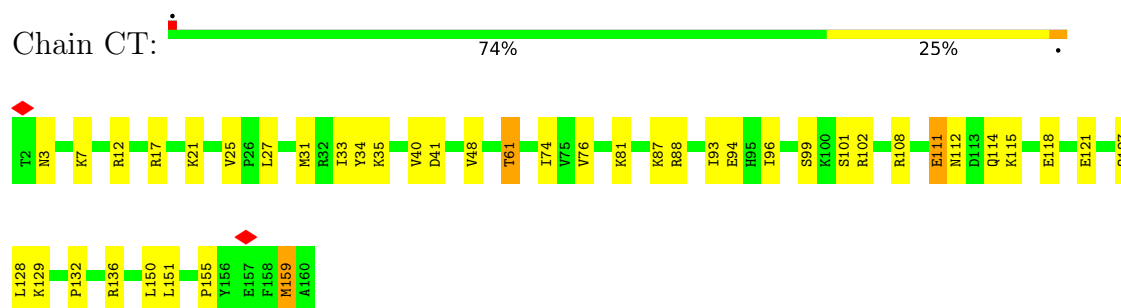


- Molecule 48: 60S ribosomal protein L18a

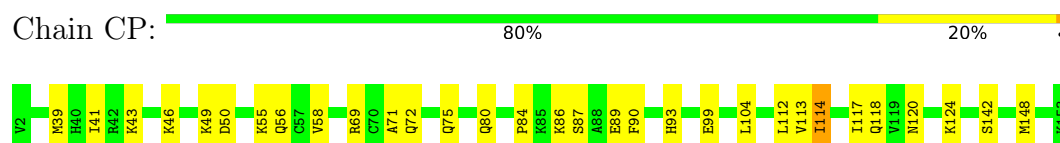
Chain CS: 75% 24% .



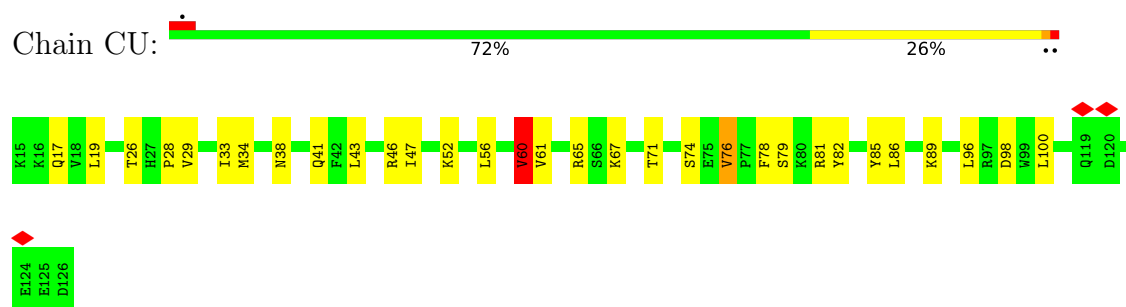
- Molecule 49: Large ribosomal subunit protein eL21



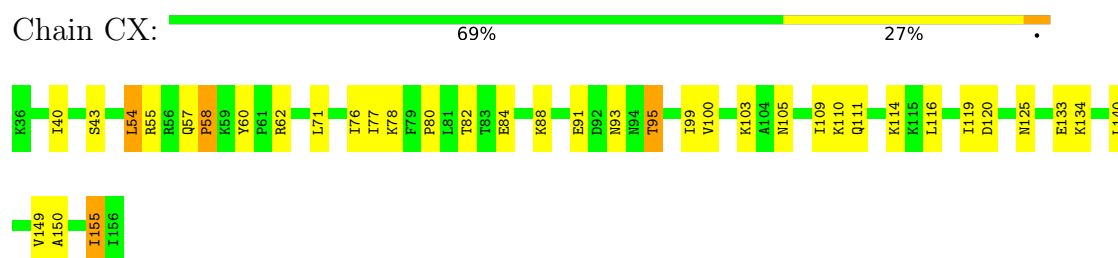
- Molecule 50: 60S ribosomal protein L17



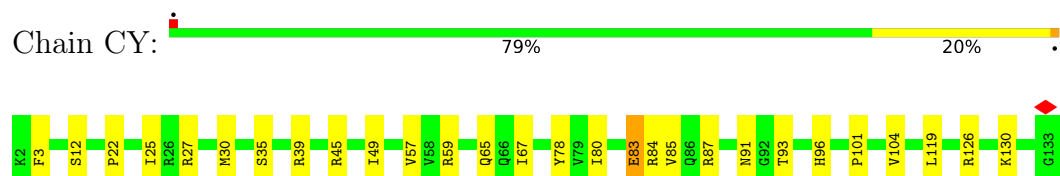
- Molecule 51: Large ribosomal subunit protein eL22



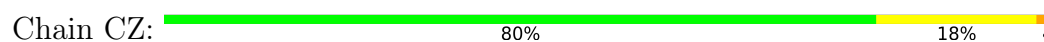
- Molecule 52: Large ribosomal subunit protein uL23

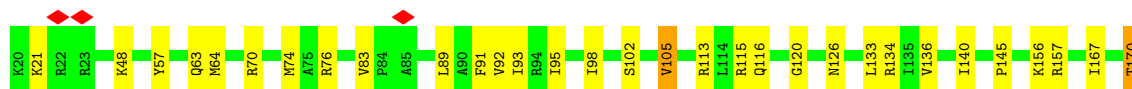


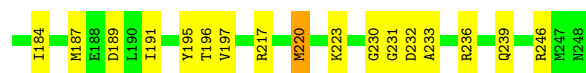
- Molecule 53: 60S ribosomal protein L26



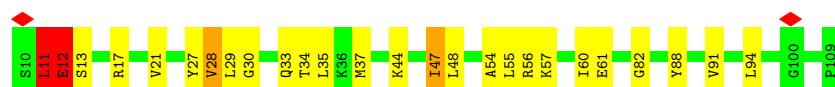
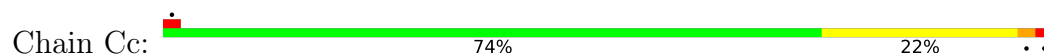
- Molecule 54: 60S ribosomal protein L27







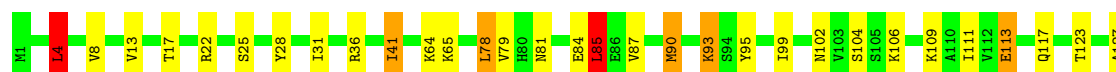
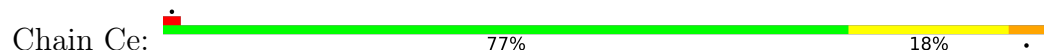
- Molecule 60: 60S ribosomal protein L30



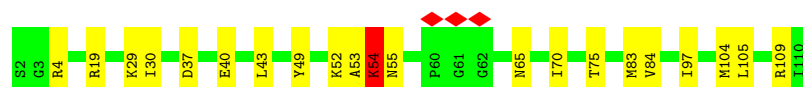
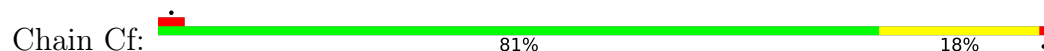
- Molecule 61: Large ribosomal subunit protein eL31



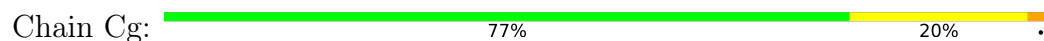
- Molecule 62: 60S ribosomal protein L32



- Molecule 63: 60S ribosomal protein L35a



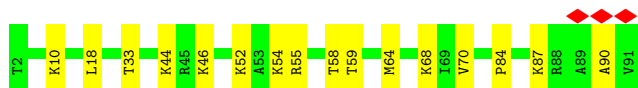
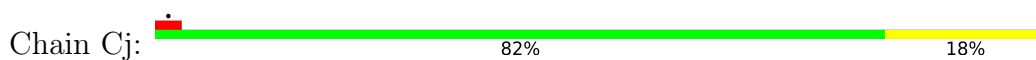
- Molecule 64: Large ribosomal subunit protein eL34



- Molecule 65: 60S ribosomal protein L36



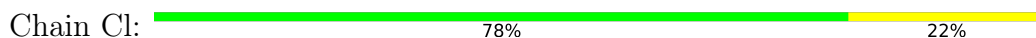
- Molecule 66: Ribosomal protein L37



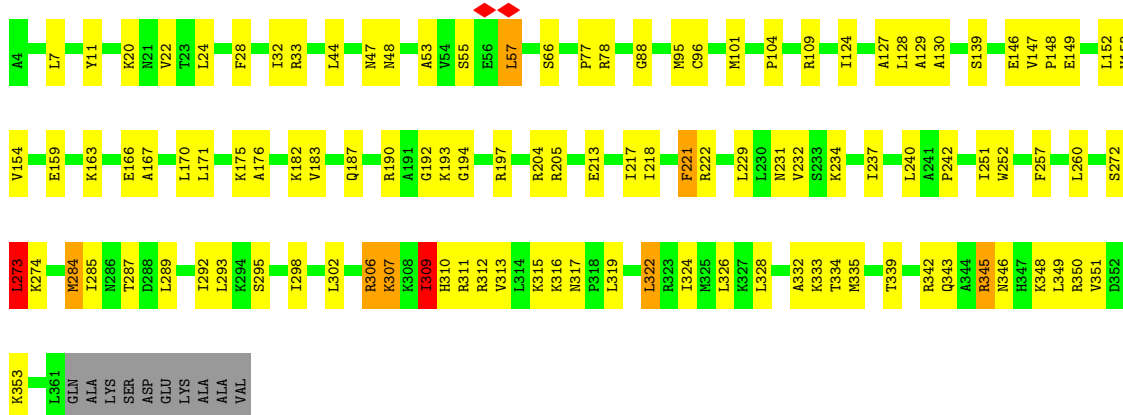
- Molecule 67: Large ribosomal subunit protein eL38



- Molecule 68: Large ribosomal subunit protein eL39



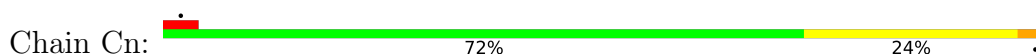
- Molecule 69: 60S ribosomal protein L4



- Molecule 70: Ubiquitin-ribosomal protein eL40 fusion protein

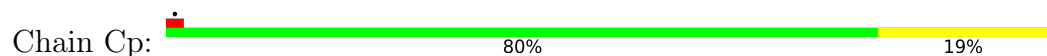


- Molecule 71: 60S ribosomal protein L41

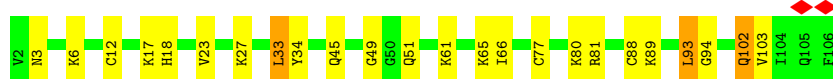
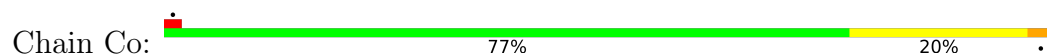




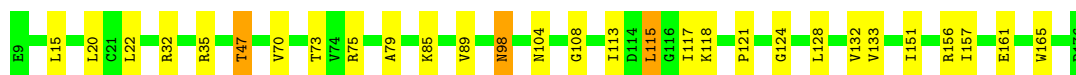
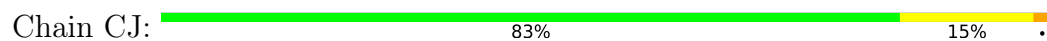
- Molecule 72: Large ribosomal subunit protein eL43



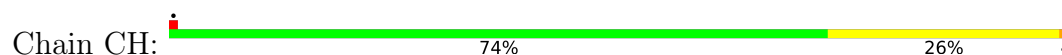
- Molecule 73: 60S ribosomal protein L36a



- Molecule 74: Large ribosomal subunit protein uL5



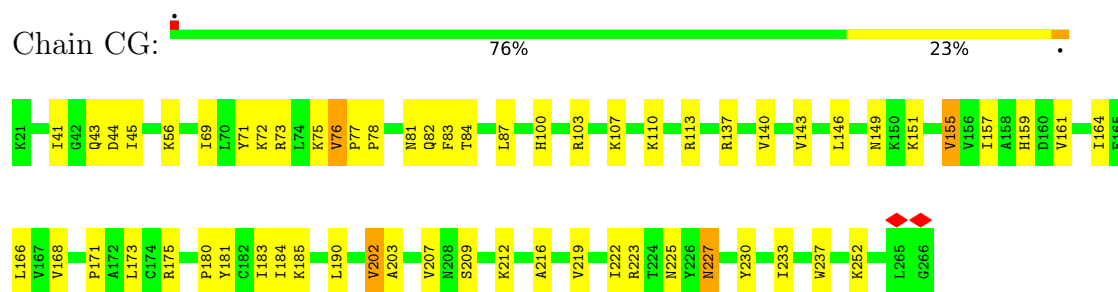
- Molecule 75: 60S ribosomal protein L9



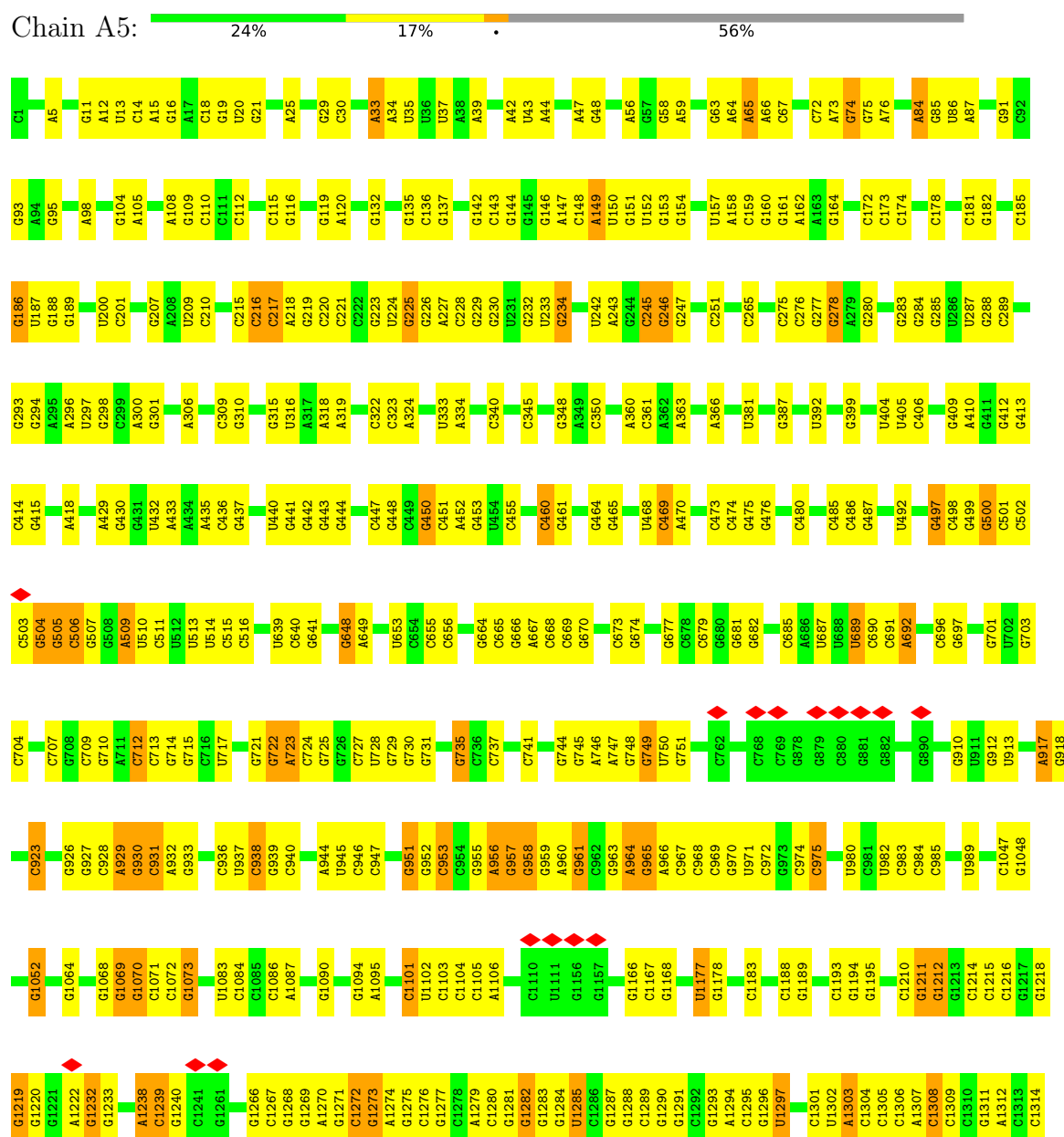
- Molecule 76: 60S ribosomal protein L6



• Molecule 77: 60S ribosomal protein L7a



• Molecule 78: 28S ribosomal RNA




[illegible]



A U U G A A A G U C A G C C C U C G A C A C A A G G G U U U G U U G

• Molecule 78: 28S ribosomal RNA

Chain A6:  32% 20% 44%

C G C G A A C C U C A A G A C A G A C C G C G A A C C C G C G U G A A U U U A A G C C A U U A G U C A G C C A G

A A G A A A C U U A A C C A A G A A U U C C C U C C A G U A A A C G G C G A A G U U A A C A A G A A C C C A A G C C C G A

A U C C C G C C G C C C G

C G C U C G U G G G G G G G G C C C A A G U C C C U U C U G A A U C C C A A G C C C U G G A A C G G U U G U G A G C C C G

G U A G C G G C C C G C C G

G C C C A A A G C C G G G G U G G U A A A C U C C C A A A G G C U U A A A A C C G G A A C C G A G A C C G A U A G U C A A

C A A G U A C C C G U U A A G A A G G A A G U U U G G A A A A A G G C U U U A A A A A G G G C G U G A A A A

C C G U U A A A G A G U A A A C G G A A G

G G G U U C C G C C G C C G

A C C G G U C C C C C C G G A A C C G

C G A C C G

C G G C C G

G G A A U C C C G

G G U C G U G

G G

A G

C G A C C C G G U C C U U G A A A C C A C G G A C C A A G G A A G G U U A A C A C G G G G G G G G G G G G G G G G G G

G A A A G C C G C C C G

C C A G A G C C U C C G G C C G G G A A G

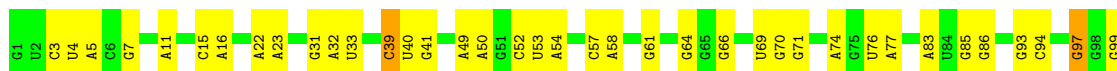
G A G C A C G G A G C C G

C C A G A G G A A A C C G

U G G G U A U A G G G G C C G G A A A G G A C C G G U A A G C C A A G G U C C U A G G U A A C C G G G G G G G G G G G G G

C U C A G C A U A G C C G







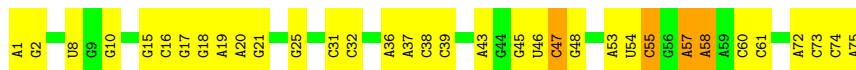
- Molecule 80: 5.8S ribosomal RNA

Chain A8: 61% 36%



- Molecule 81: E-tRNA

Chain BC: 55% 40% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	86927	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	AO	0.30	0/1029	0.81	1/1380 (0.1%)
2	AX	0.32	0/1124	0.76	0/1500
3	AN	0.33	0/1232	0.83	2/1656 (0.1%)
4	AL	0.34	0/1319	0.90	5/1761 (0.3%)
5	AB	0.32	0/1774	0.86	1/2372 (0.0%)
6	AA	0.32	0/1679	0.77	3/2283 (0.1%)
7	AV	0.35	0/631	0.92	1/844 (0.1%)
8	AY	0.32	0/1040	0.89	5/1382 (0.4%)
9	Aa	0.28	0/863	0.80	2/1159 (0.2%)
10	Ab	0.39	0/673	0.94	5/902 (0.6%)
11	Ae	0.32	0/474	0.79	0/623
12	AJ	0.34	0/1487	0.83	3/1985 (0.2%)
13	AE	0.30	0/2126	0.77	3/2859 (0.1%)
14	AC	0.32	0/1788	0.81	5/2414 (0.2%)
15	AG	0.25	0/1946	0.63	1/2590 (0.0%)
16	AH	0.37	0/1553	0.95	9/2079 (0.4%)
17	AW	0.31	0/1051	0.77	1/1406 (0.1%)
18	AI	0.30	0/1715	0.86	8/2287 (0.3%)
19	B2	0.97	13/42229 (0.0%)	0.44	14/65756 (0.0%)
20	CR	0.31	0/1267	0.83	3/1672 (0.2%)
21	CW	0.34	0/1030	0.82	0/1364
22	Ag	0.24	0/2443	0.65	3/3324 (0.1%)
23	AU	0.32	0/832	0.84	1/1117 (0.1%)
24	AK	0.40	0/851	1.10	8/1147 (0.7%)
25	AM	0.34	0/970	0.88	5/1300 (0.4%)
26	AS	0.31	0/1157	0.86	9/1548 (0.6%)
27	Ad	0.23	0/455	0.74	0/603
28	AR	0.39	0/1031	0.96	2/1383 (0.1%)
29	AP	0.35	0/1011	0.95	6/1349 (0.4%)
30	AT	0.27	0/1119	0.66	1/1499 (0.1%)
31	AZ	0.24	0/604	0.66	2/810 (0.2%)
32	Ac	0.27	0/508	0.90	3/680 (0.4%)
33	AD	0.31	0/1764	0.84	10/2375 (0.4%)
34	Af	0.37	0/593	0.90	1/786 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AF	0.33	0/1531	0.83	3/2059 (0.1%)
36	AQ	0.26	0/1142	0.81	3/1528 (0.2%)
37	Cz	0.32	1/1560 (0.1%)	0.70	1/2095 (0.0%)
38	CO	0.35	0/1687	0.82	4/2257 (0.2%)
39	CL	0.29	0/1732	0.72	0/2315
40	CV	0.28	0/1003	0.85	1/1345 (0.1%)
41	CM	0.31	0/1161	0.87	4/1552 (0.3%)
42	Ca	0.30	0/1191	0.82	2/1591 (0.1%)
43	CN	0.30	0/1746	0.73	1/2338 (0.0%)
44	CI	0.34	0/1665	0.76	1/2223 (0.0%)
45	CD	0.28	0/2398	0.76	4/3210 (0.1%)
46	CQ	0.31	0/1545	0.80	4/2062 (0.2%)
47	CA	0.82	1/1995 (0.1%)	0.86	7/2674 (0.3%)
48	CS	0.34	0/1493	0.86	5/2003 (0.2%)
49	CT	0.29	0/1326	0.84	5/1770 (0.3%)
50	CP	0.33	0/1259	0.80	2/1689 (0.1%)
51	CU	0.34	0/935	0.93	3/1253 (0.2%)
52	CX	0.33	0/1011	0.93	4/1356 (0.3%)
53	CY	0.35	0/1124	0.89	4/1494 (0.3%)
54	CZ	0.34	1/1130 (0.1%)	0.79	1/1507 (0.1%)
55	Cr	0.44	0/1120	1.10	8/1497 (0.5%)
56	Ch	0.36	0/1031	0.92	5/1361 (0.4%)
57	Cb	0.42	1/564 (0.2%)	0.90	2/743 (0.3%)
58	CB	0.31	0/3229	0.80	7/4323 (0.2%)
59	CF	0.31	0/1945	0.82	2/2589 (0.1%)
60	Cc	0.39	0/787	0.98	5/1057 (0.5%)
61	Cd	0.31	0/946	0.83	1/1272 (0.1%)
62	Ce	0.38	1/1114 (0.1%)	0.82	5/1485 (0.3%)
63	Cf	0.33	0/895	0.89	2/1198 (0.2%)
64	Cg	0.28	0/916	0.78	0/1220
65	Ci	0.38	0/851	0.95	4/1125 (0.4%)
66	Cj	0.22	0/748	0.60	0/990
67	Ck	0.33	0/575	0.93	5/761 (0.7%)
68	Cl	0.25	0/454	0.65	0/599
69	CC	0.31	0/2907	0.84	6/3905 (0.2%)
70	Cm	0.32	0/435	0.84	1/575 (0.2%)
71	Cn	0.29	0/241	0.79	0/305
72	Cp	0.28	0/713	0.74	0/946
73	Co	0.30	0/877	0.82	1/1156 (0.1%)
74	CJ	0.31	0/1372	0.80	1/1836 (0.1%)
75	CH	0.29	0/1545	0.80	1/2077 (0.0%)
76	CE	0.33	0/2153	0.90	7/2878 (0.2%)
77	CG	0.31	0/2006	0.76	0/2697

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	A5	0.20	0/40489	0.45	12/63083 (0.0%)
78	A6	0.19	0/49259	0.43	10/76579 (0.0%)
79	A7	0.17	0/2880	0.33	0/4489
80	A8	0.18	0/3723	0.40	1/5800 (0.0%)
81	BC	0.16	0/1795	0.35	0/2798
All	All	0.48	18/235572 (0.0%)	0.61	268/345860 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AO	0	1
2	AX	0	1
6	AA	0	1
11	Ae	0	1
12	AJ	0	1
14	AC	0	1
16	AH	0	2
17	AW	0	1
18	AI	0	3
20	CR	0	1
21	CW	0	1
24	AK	0	1
25	AM	0	1
28	AR	0	1
29	AP	0	2
30	AT	0	1
34	Af	0	1
35	AF	0	2
36	AQ	0	1
38	CO	0	2
39	CL	0	1
42	Ca	0	1
44	CI	0	1
45	CD	0	1
46	CQ	0	2
47	CA	0	3
48	CS	0	1
49	CT	0	2
52	CX	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
55	Cr	0	5
58	CB	0	1
60	Cc	0	1
61	Cd	0	1
63	Cf	0	1
69	CC	0	3
73	Co	0	2
75	CH	0	1
76	CE	0	2
77	CG	0	1
All	All	0	57

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	B2	1207	G	C5'-C4'	103.83	3.58	1.51
19	B2	1044	G	C6-N1	60.35	2.60	1.39
19	B2	1044	G	N3-C4	57.34	2.50	1.35
19	B2	1044	G	C2-N3	56.62	2.46	1.32
19	B2	1044	G	N1-C2	56.59	2.50	1.37
19	B2	1044	G	C5-C6	54.23	2.50	1.42
19	B2	1044	G	C5-C4	48.60	2.35	1.38
19	B2	1834	A	C6-N1	41.79	2.19	1.35
19	B2	1834	A	N3-C4	40.28	2.15	1.34
19	B2	1834	A	C2-N3	39.52	2.12	1.33
19	B2	1834	A	N1-C2	39.49	2.13	1.34
19	B2	1834	A	C5-C6	37.52	2.16	1.41
19	B2	1834	A	C5-C4	34.37	2.07	1.38
47	CA	248	GLY	CA-C	33.80	1.99	1.51
37	Cz	152	LYS	CA-CB	6.64	1.70	1.53
62	Ce	93	LYS	CE-NZ	5.95	1.67	1.49
54	CZ	80	LEU	C-N	5.61	1.42	1.33
57	Cb	23	LYS	C-N	5.46	1.38	1.33

All (268) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	CA	248	GLY	O-C-N	-14.20	104.24	122.70
19	B2	1207	G	C5'-C4'-C3'	11.51	139.02	116.00
32	Ac	62	GLU	CA-C-N	9.57	139.81	121.54
32	Ac	62	GLU	C-N-CA	9.57	139.81	121.54
47	CA	248	GLY	N-CA-C	9.20	134.97	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	AY	19	GLN	CA-CB-CG	8.46	131.02	114.10
33	AD	197	LYS	CA-C-N	8.44	136.88	121.70
33	AD	197	LYS	C-N-CA	8.44	136.88	121.70
55	Cr	43	LEU	CA-C-N	8.39	136.80	121.70
55	Cr	43	LEU	C-N-CA	8.39	136.80	121.70
19	B2	1207	G	O5'-C5'-C4'	7.87	126.23	110.50
60	Cc	11	LEU	CA-C-N	7.37	135.62	121.54
60	Cc	11	LEU	C-N-CA	7.37	135.62	121.54
47	CA	250	LYS	CA-C-N	7.33	134.90	121.70
47	CA	250	LYS	C-N-CA	7.33	134.90	121.70
38	CO	190	ASP	CA-C-N	7.33	134.89	121.70
38	CO	190	ASP	C-N-CA	7.33	134.89	121.70
18	AI	142	SER	CA-C-N	7.19	134.64	121.70
18	AI	142	SER	C-N-CA	7.19	134.64	121.70
36	AQ	42	ILE	CA-C-N	7.11	139.15	121.80
36	AQ	42	ILE	C-N-CA	7.11	139.15	121.80
48	CS	147	ASP	CA-C-N	7.11	134.49	121.70
48	CS	147	ASP	C-N-CA	7.11	134.49	121.70
40	CV	128	LEU	CA-CB-CG	7.00	140.79	116.30
47	CA	254	GLU	CA-C-N	6.99	134.28	121.70
47	CA	254	GLU	C-N-CA	6.99	134.28	121.70
29	AP	71	GLU	CA-CB-CG	6.98	128.05	114.10
45	CD	261	VAL	CA-C-N	6.95	134.22	121.70
45	CD	261	VAL	C-N-CA	6.95	134.22	121.70
10	Ab	1	MET	CB-CG-SD	6.95	133.55	112.70
24	AK	3	MET	CA-CB-CG	6.79	127.69	114.10
29	AP	50	ARG	CA-CB-CG	6.76	127.62	114.10
46	CQ	154	LYS	CA-C-N	6.76	133.87	121.70
46	CQ	154	LYS	C-N-CA	6.76	133.87	121.70
18	AI	144	LYS	CA-C-N	6.75	134.12	121.97
18	AI	144	LYS	C-N-CA	6.75	134.12	121.97
10	Ab	81	ARG	CA-C-N	6.62	133.62	121.70
10	Ab	81	ARG	C-N-CA	6.62	133.62	121.70
69	CC	312	ARG	CA-C-N	6.54	133.75	121.97
69	CC	312	ARG	C-N-CA	6.54	133.75	121.97
76	CE	218	LYS	CB-CG-CD	6.43	126.09	111.30
20	CR	167	LYS	CA-CB-CG	6.41	126.92	114.10
19	B2	1044	G	N3-C4-N9	6.40	145.21	126.00
56	Ch	30	GLN	CA-CB-CG	6.40	126.90	114.10
29	AP	125	PRO	CA-C-N	6.40	133.49	121.97
29	AP	125	PRO	C-N-CA	6.40	133.49	121.97
48	CS	21	LYS	CA-C-N	6.38	133.19	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	CS	21	LYS	C-N-CA	6.38	133.19	121.70
8	AY	102	THR	CA-C-N	6.36	133.15	121.70
8	AY	102	THR	C-N-CA	6.36	133.15	121.70
55	Cr	99	LYS	CB-CG-CD	6.36	125.93	111.30
16	AH	159	ASP	CA-C-N	6.36	133.69	121.54
16	AH	159	ASP	C-N-CA	6.36	133.69	121.54
60	Cc	12	GLU	CA-CB-CG	6.28	126.66	114.10
63	Cf	54	LYS	CA-CB-CG	6.28	126.65	114.10
12	AJ	155	LYS	CA-CB-CG	6.26	126.63	114.10
33	AD	201	LYS	CA-C-N	6.26	137.06	121.80
33	AD	201	LYS	C-N-CA	6.26	137.06	121.80
19	B2	1044	G	C4-C5-N7	-6.24	92.08	110.80
52	CX	91	GLU	CA-CB-CG	6.24	126.58	114.10
19	B2	1044	G	N7-C8-N9	6.23	131.78	113.10
24	AK	2	LEU	CA-C-N	6.21	136.97	121.80
24	AK	2	LEU	C-N-CA	6.21	136.97	121.80
45	CD	73	MET	CB-CG-SD	6.20	131.29	112.70
58	CB	325	GLU	CA-C-N	6.11	132.97	121.97
58	CB	325	GLU	C-N-CA	6.11	132.97	121.97
65	Ci	58	MET	CB-CG-SD	6.10	131.01	112.70
55	Cr	28	GLU	CA-CB-CG	6.10	126.30	114.10
4	AL	151	THR	CA-C-N	6.09	133.17	121.54
4	AL	151	THR	C-N-CA	6.09	133.17	121.54
6	AA	88	LEU	CA-CB-CG	6.07	137.55	116.30
55	Cr	94	ARG	CA-CB-CG	6.07	126.23	114.10
4	AL	45	LYS	CB-CG-CD	6.06	125.24	111.30
65	Ci	94	LEU	CA-CB-CG	6.06	137.50	116.30
61	Cd	54	MET	CB-CG-SD	6.05	130.84	112.70
24	AK	34	GLU	CA-CB-CG	6.01	126.13	114.10
26	AS	71	MET	CB-CG-SD	5.99	130.66	112.70
58	CB	199	GLU	CA-CB-CG	5.98	126.07	114.10
76	CE	102	GLY	N-CA-C	5.96	118.89	112.33
65	Ci	56	ARG	CA-CB-CG	5.96	126.02	114.10
52	CX	110	LYS	CA-C-N	-5.95	112.72	122.54
52	CX	110	LYS	C-N-CA	-5.95	112.72	122.54
36	AQ	41	MET	CA-CB-CG	5.95	125.99	114.10
26	AS	78	LYS	CA-CB-CG	5.93	125.97	114.10
30	AT	29	LYS	CA-CB-CG	5.92	125.94	114.10
75	CH	141	LYS	CA-CB-CG	5.90	125.90	114.10
69	CC	273	LEU	CA-CB-CG	5.90	136.94	116.30
22	Ag	281	ALA	CA-C-N	5.89	136.18	121.80
22	Ag	281	ALA	C-N-CA	5.89	136.18	121.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	Af	107	LYS	CB-CG-CD	5.88	124.83	111.30
16	AH	65	PRO	CA-C-N	5.87	132.99	122.13
16	AH	65	PRO	C-N-CA	5.87	132.99	122.13
19	B2	1834	A	N1-C2-N3	-5.87	111.69	129.30
58	CB	158	GLN	CB-CG-CD	5.87	122.57	112.60
76	CE	46	ARG	CA-C-N	5.86	136.09	121.80
76	CE	46	ARG	C-N-CA	5.86	136.09	121.80
26	AS	26	ILE	CB-CG1-CD1	5.84	126.07	113.80
28	AR	4	VAL	N-CA-C	-5.84	107.30	112.90
28	AR	97	GLU	CA-CB-CG	5.81	125.72	114.10
52	CX	111	GLN	CA-CB-CG	5.81	125.72	114.10
25	AM	127	TYR	CA-CB-CG	5.81	124.35	113.90
78	A5	1239	C	P-O3'-C3'	5.80	128.91	120.20
57	Cb	27	GLN	CB-CG-CD	5.80	122.46	112.60
78	A5	2046	G	P-O3'-C3'	5.77	128.86	120.20
49	CT	121	GLU	CA-CB-CG	5.75	125.61	114.10
55	Cr	22	LYS	CB-CG-CD	5.74	124.50	111.30
35	AF	42	LYS	CA-C-O	-5.73	112.32	120.51
49	CT	118	GLU	CA-CB-CG	5.70	125.51	114.10
70	Cm	126	LYS	CB-CG-CD	5.68	124.36	111.30
8	AY	47	MET	CA-CB-CG	5.67	125.43	114.10
78	A5	497	G	P-O3'-C3'	5.66	128.69	120.20
49	CT	111	GLU	CA-CB-CG	5.65	125.40	114.10
53	CY	83	GLU	CA-CB-CG	5.65	125.39	114.10
54	CZ	81	MET	CA-CB-CG	5.64	125.39	114.10
35	AF	76	MET	CA-CB-CG	5.63	125.36	114.10
56	Ch	7	ARG	CG-CD-NE	5.62	124.37	112.00
33	AD	127	MET	CB-CG-SD	5.61	129.53	112.70
8	AY	106	GLN	CB-CG-CD	5.61	122.13	112.60
19	B2	688	U	P-O3'-C3'	5.59	128.58	120.20
13	AE	19	MET	CA-CB-CG	5.57	125.25	114.10
18	AI	132	GLU	CA-C-N	5.57	132.18	121.54
18	AI	132	GLU	C-N-CA	5.57	132.18	121.54
24	AK	88	GLU	CA-CB-CG	5.57	125.23	114.10
19	B2	327	G	P-O3'-C3'	5.56	128.54	120.20
26	AS	26	ILE	CA-CB-CG1	5.56	119.85	110.40
45	CD	115	MET	CA-CB-CG	5.54	125.19	114.10
25	AM	12	MET	CA-CB-CG	5.54	125.17	114.10
74	CJ	115	LEU	CA-CB-CG	5.53	135.66	116.30
53	CY	83	GLU	CB-CG-CD	5.53	122.00	112.60
24	AK	88	GLU	CA-C-N	5.50	131.88	121.97
24	AK	88	GLU	C-N-CA	5.50	131.88	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	CE	72	LYS	CA-C-N	5.50	131.20	122.61
76	CE	72	LYS	C-N-CA	5.50	131.20	122.61
37	Cz	152	LYS	CA-CB-CG	5.50	125.10	114.10
3	AN	134	VAL	CA-C-N	5.49	137.95	122.21
3	AN	134	VAL	C-N-CA	5.49	137.95	122.21
67	Ck	13	LEU	CA-CB-CG	5.49	135.50	116.30
51	CU	52	LYS	CB-CG-CD	5.48	123.91	111.30
47	CA	144	LYS	CA-CB-CG	5.47	125.04	114.10
13	AE	250	GLU	CA-CB-CG	5.47	125.04	114.10
43	CN	77	LYS	CA-CB-CG	5.43	124.96	114.10
78	A6	4889	G	P-O3'-C3'	5.42	128.33	120.20
17	AW	111	MET	CB-CG-SD	5.42	128.95	112.70
19	B2	1823	A	P-O3'-C3'	5.41	128.31	120.20
58	CB	360	LEU	CA-CB-CG	5.41	135.23	116.30
62	Ce	113	GLU	CB-CG-CD	5.41	121.79	112.60
1	AO	124	MET	CB-CG-SD	5.40	128.91	112.70
33	AD	43	PRO	CA-C-N	5.39	130.01	122.08
33	AD	43	PRO	C-N-CA	5.39	130.01	122.08
38	CO	111	PRO	N-CA-C	5.39	123.58	112.47
49	CT	81	LYS	N-CA-C	5.39	122.28	110.80
62	Ce	90	MET	CB-CG-SD	5.39	128.87	112.70
14	AC	175	GLY	CA-C-N	5.37	134.91	121.80
14	AC	175	GLY	C-N-CA	5.37	134.91	121.80
50	CP	75	GLN	CA-CB-CG	5.36	124.83	114.10
67	Ck	6	GLU	CB-CG-CD	5.36	121.71	112.60
63	Cf	109	ARG	CA-CB-CG	5.35	124.80	114.10
56	Ch	27	GLU	CA-CB-CG	5.35	124.80	114.10
16	AH	16	PRO	CA-C-N	5.34	131.75	121.54
16	AH	16	PRO	C-N-CA	5.34	131.75	121.54
41	CM	48	GLN	CB-CG-CD	5.34	121.69	112.60
50	CP	99	GLU	CA-CB-CG	5.34	124.78	114.10
78	A6	3959	U	P-O3'-C3'	5.33	128.20	120.20
19	B2	24	C	P-O3'-C3'	5.33	128.19	120.20
44	CI	183	ASP	CA-CB-CG	5.33	117.93	112.60
78	A5	957	G	P-O3'-C3'	5.33	128.19	120.20
78	A6	2649	G	C2'-C3'-O3'	5.32	121.69	113.70
24	AK	35	LEU	CA-CB-CG	5.32	134.93	116.30
6	AA	10	MET	CB-CG-SD	5.31	128.63	112.70
20	CR	7	GLN	CA-CB-CG	5.31	124.73	114.10
76	CE	218	LYS	CA-CB-CG	5.30	124.69	114.10
12	AJ	21	GLU	CA-CB-CG	5.29	124.68	114.10
78	A6	4738	C	P-O3'-C3'	5.28	128.12	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	AG	218	LYS	CA-CB-CG	5.28	124.65	114.10
69	CC	272	SER	CA-C-N	5.27	135.49	126.32
69	CC	272	SER	C-N-CA	5.27	135.49	126.32
19	B2	1835	A	P-O3'-C3'	5.26	128.09	120.20
38	CO	182	GLU	CA-CB-CG	5.26	124.61	114.10
41	CM	70	GLN	CA-CB-CG	5.25	124.59	114.10
55	Cr	77	TYR	CA-CB-CG	5.25	123.34	113.90
69	CC	284	MET	CA-CB-CG	5.24	124.59	114.10
10	Ab	5	LYS	CB-CG-CD	5.24	123.36	111.30
4	AL	121	GLN	CB-CG-CD	5.24	121.51	112.60
14	AC	261	PHE	CB-CA-C	-5.24	109.55	115.79
19	B2	1830	U	P-O3'-C3'	5.23	128.05	120.20
78	A6	3876	A	P-O3'-C3'	5.23	128.05	120.20
60	Cc	44	LYS	CA-CB-CG	5.23	124.56	114.10
73	Co	33	LEU	CA-CB-CG	5.23	134.59	116.30
78	A5	1358	G	P-O3'-C3'	5.21	128.02	120.20
62	Ce	4	LEU	N-CA-C	5.21	121.89	110.80
19	B2	1834	A	C2-N3-C4	5.20	126.21	110.60
51	CU	17	GLN	CA-CB-CG	5.20	124.51	114.10
62	Ce	113	GLU	CA-CB-CG	5.20	124.50	114.10
12	AJ	107	GLU	CA-CB-CG	5.20	124.50	114.10
59	CF	21	LYS	CA-C-N	5.20	131.06	121.70
59	CF	21	LYS	C-N-CA	5.20	131.06	121.70
60	Cc	44	LYS	CB-CG-CD	5.19	123.23	111.30
46	CQ	98	LEU	CA-CB-CG	5.18	134.45	116.30
78	A5	1841	C	P-O3'-C3'	5.18	127.98	120.20
48	CS	164	LYS	N-CA-C	5.18	112.88	108.22
78	A5	1474	C	C2'-C3'-O3'	5.17	121.46	113.70
13	AE	40	GLU	CA-CB-CG	5.16	124.42	114.10
78	A5	1232	G	P-O3'-C3'	5.16	127.94	120.20
78	A6	4237	C	C2'-C3'-O3'	5.16	121.43	113.70
4	AL	121	GLN	CA-CB-CG	5.15	124.41	114.10
41	CM	136	LEU	CA-CB-CG	5.15	134.33	116.30
55	Cr	94	ARG	CB-CG-CD	5.15	123.15	111.30
22	Ag	171	ASP	CA-C-O	-5.15	110.67	118.91
58	CB	71	GLU	CB-CG-CD	5.15	121.35	112.60
29	AP	34	MET	CA-CB-CG	5.14	124.39	114.10
6	AA	42	LYS	CA-CB-CG	5.14	124.38	114.10
62	Ce	85	LEU	CA-CB-CG	5.14	134.28	116.30
42	Ca	88	VAL	CA-C-N	5.13	131.35	121.54
42	Ca	88	VAL	C-N-CA	5.13	131.35	121.54
65	Ci	88	GLU	CB-CG-CD	5.13	121.33	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	AI	139	LYS	CA-C-N	5.12	131.33	121.54
18	AI	139	LYS	C-N-CA	5.12	131.33	121.54
26	AS	72	GLN	CA-CB-CG	5.12	124.35	114.10
49	CT	159	MET	CB-CG-SD	5.12	128.06	112.70
78	A5	245	C	P-O3'-C3'	5.12	127.88	120.20
80	A8	126	C	P-O3'-C3'	5.12	127.88	120.20
25	AM	93	LYS	CA-C-N	5.12	131.18	121.97
25	AM	93	LYS	C-N-CA	5.12	131.18	121.97
56	Ch	15	GLU	CA-CB-CG	5.12	124.33	114.10
53	CY	65	GLN	CA-C-N	5.11	131.30	121.54
53	CY	65	GLN	C-N-CA	5.11	131.30	121.54
67	Ck	17	ARG	CA-C-N	5.11	131.30	121.54
67	Ck	17	ARG	C-N-CA	5.11	131.30	121.54
33	AD	157	MET	CB-CG-SD	5.10	128.01	112.70
78	A5	917	A	P-O3'-C3'	5.10	127.84	120.20
14	AC	78	LEU	CA-CB-CG	5.10	134.14	116.30
16	AH	75	ILE	CB-CG1-CD1	5.10	124.50	113.80
14	AC	105	GLU	CA-CB-CG	5.09	124.29	114.10
29	AP	34	MET	N-CA-CB	5.09	117.45	110.07
78	A6	4164	C	C2'-C3'-O3'	5.09	121.33	113.70
78	A6	5027	C	P-O3'-C3'	5.09	127.83	120.20
10	Ab	1	MET	CA-CB-CG	5.08	124.26	114.10
26	AS	76	GLN	CA-CB-CG	5.08	124.26	114.10
58	CB	182	GLU	CA-CB-CG	5.08	124.26	114.10
78	A5	186	G	P-O3'-C3'	5.08	127.81	120.20
31	AZ	51	ASP	CA-C-N	5.07	131.22	121.54
31	AZ	51	ASP	C-N-CA	5.07	131.22	121.54
41	CM	70	GLN	CB-CG-CD	5.07	121.22	112.60
51	CU	60	VAL	CA-CB-CG1	5.07	119.01	110.40
78	A6	2526	C	C4'-C3'-O3'	5.07	117.00	109.40
26	AS	72	GLN	CB-CG-CD	5.06	121.20	112.60
67	Ck	6	GLU	CA-CB-CG	5.06	124.21	114.10
33	AD	51	LEU	CA-CB-CG	5.05	133.99	116.30
33	AD	196	GLY	N-CA-C	5.05	125.15	113.18
78	A5	648	G	P-O3'-C3'	5.05	127.78	120.20
20	CR	167	LYS	N-CA-CB	5.05	118.11	110.28
78	A6	3731	C	C2'-C3'-O3'	5.05	121.27	113.70
57	Cb	25	ARG	CB-CG-CD	5.05	122.91	111.30
16	AH	68	GLN	CA-CB-CG	5.04	124.19	114.10
25	AM	45	ARG	CA-CB-CG	5.04	124.19	114.10
32	Ac	33	GLU	CA-CB-CG	5.04	124.18	114.10
5	AB	41	ILE	CA-CB-CG1	5.04	118.96	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	AV	49	GLN	CB-CG-CD	5.04	121.16	112.60
9	Aa	60	ASP	CA-C-N	5.04	131.16	121.54
9	Aa	60	ASP	C-N-CA	5.04	131.16	121.54
19	B2	1637	A	P-O3'-C3'	5.04	127.75	120.20
46	CQ	35	LEU	CA-CB-CG	5.03	133.91	116.30
16	AH	131	GLU	CB-CG-CD	5.03	121.14	112.60
56	Ch	15	GLU	CB-CG-CD	5.02	121.14	112.60
23	AU	45	GLU	CB-CG-CD	5.02	121.13	112.60
26	AS	16	LEU	CA-C-N	5.02	129.46	122.08
26	AS	16	LEU	C-N-CA	5.02	129.46	122.08
35	AF	98	GLU	CA-CB-CG	5.01	124.11	114.10

There are no chirality outliers.

All (57) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	AA	191	ARG	Peptide
14	AC	72	ASP	Peptide
35	AF	198	ARG	Sidechain
35	AF	202	SER	Peptide
16	AH	111	LYS	Peptide
16	AH	17	ASP	Peptide
18	AI	119	LEU	Peptide
18	AI	132	GLU	Peptide
18	AI	143	LYS	Peptide
12	AJ	172	ARG	Sidechain
24	AK	29	MET	Peptide
25	AM	36	ARG	Sidechain
1	AO	136	PRO	Peptide
29	AP	50	ARG	Peptide
29	AP	68	PRO	Peptide
36	AQ	43	GLU	Peptide
28	AR	91	LEU	Peptide
30	AT	62	ARG	Sidechain
17	AW	110	ILE	Peptide
2	AX	87	ASN	Peptide
11	Ae	46	VAL	Peptide
34	Af	87	THR	Peptide
47	CA	220	GLY	Peptide
47	CA	232	GLY	Peptide
47	CA	242	ARG	Sidechain
58	CB	18	PRO	Peptide

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Mol	Chain	Res	Type	Group
69	CC	213	GLU	Peptide
69	CC	273	LEU	Peptide
69	CC	307	LYS	Peptide
45	CD	20	PHE	Peptide
76	CE	131	LYS	Peptide
76	CE	57	TYR	Peptide
77	CG	81	ASN	Peptide
75	CH	140	GLN	Peptide
44	CI	177	ASN	Peptide
39	CL	127	PHE	Peptide
38	CO	110	PRO	Peptide
38	CO	117	ARG	Peptide
46	CQ	152	PHE	Peptide
46	CQ	153	GLY	Peptide
20	CR	132	PHE	Peptide
48	CS	152	PHE	Peptide
49	CT	136	ARG	Peptide
49	CT	151	LEU	Peptide
21	CW	49	ILE	Peptide
52	CX	57	GLN	Peptide
42	Ca	46	ASP	Peptide
60	Cc	11	LEU	Peptide
61	Cd	98	SER	Peptide
63	Cf	53	ALA	Peptide
73	Co	65	LYS	Peptide
73	Co	66	ILE	Peptide
55	Cr	53	PRO	Peptide
55	Cr	55	ALA	Peptide
55	Cr	68	SER	Peptide
55	Cr	70	GLN	Peptide
55	Cr	71	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AO	1016	0	1039	24	0
2	AX	1106	0	1179	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	AN	1208	0	1294	21	0
4	AL	1296	0	1374	16	0
5	AB	1747	0	1829	31	0
6	AA	1642	0	1646	31	0
7	AV	625	0	628	15	0
8	AY	1023	0	1090	26	0
9	Aa	847	0	897	18	0
10	Ab	659	0	683	7	0
11	Ae	468	0	519	7	0
12	AJ	1463	0	1578	19	0
13	AE	2084	0	2189	38	0
14	AC	1751	0	1835	28	0
15	AG	1923	0	2089	41	0
16	AH	1530	0	1627	23	0
17	AW	1034	0	1080	24	0
18	AI	1686	0	1772	19	0
19	B2	37803	0	19015	344	0
20	CR	1257	0	1392	21	0
21	CW	1015	0	1079	26	0
22	Ag	2387	0	2344	41	0
23	AU	822	0	887	16	0
24	AK	827	0	854	15	0
25	AM	960	0	989	16	0
26	AS	1139	0	1191	23	0
27	Ad	445	0	442	4	0
28	AR	1019	0	1075	20	0
29	AP	992	0	1039	9	0
30	AT	1101	0	1135	15	0
31	AZ	598	0	656	10	0
32	Ac	506	0	536	8	0
33	AD	1736	0	1831	23	0
34	Af	581	0	599	10	0
35	AF	1509	0	1563	24	0
36	AQ	1124	0	1193	18	0
37	Cz	1534	0	1609	30	0
38	CO	1655	0	1799	34	0
39	CL	1701	0	1818	30	0
40	CV	989	0	1047	11	0
41	CM	1139	0	1209	24	0
42	Ca	1162	0	1213	22	0
43	CN	1701	0	1749	29	0
44	CI	1626	0	1662	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	CD	2353	0	2372	40	0
46	CQ	1521	0	1640	20	0
47	CA	1957	0	2055	69	0
48	CS	1453	0	1490	26	0
49	CT	1298	0	1366	26	0
50	CP	1233	0	1263	14	0
51	CU	921	0	928	17	0
52	CX	994	0	1079	22	0
53	CY	1107	0	1193	14	0
54	CZ	1107	0	1182	19	0
55	Cr	1104	0	1189	29	0
56	Ch	1023	0	1160	16	0
57	Cb	554	0	585	4	0
58	CB	3161	0	3297	50	0
59	CF	1910	0	2048	29	0
60	Cc	776	0	812	17	0
61	Cd	931	0	980	14	0
62	Ce	1096	0	1189	22	0
63	Cf	876	0	912	11	0
64	Cg	906	0	999	17	0
65	Ci	840	0	929	18	0
66	Cj	733	0	773	10	0
67	Ck	569	0	637	18	0
68	Cl	444	0	483	6	0
69	CC	2853	0	3028	69	0
70	Cm	429	0	469	9	0
71	Cn	240	0	289	5	0
72	Cp	703	0	755	11	0
73	Co	863	0	931	11	0
74	CJ	1349	0	1383	15	0
75	CH	1526	0	1605	28	0
76	CE	2113	0	2320	41	0
77	CG	1973	0	2128	41	0
78	A5	36244	0	18266	281	0
78	A6	44180	0	21937	334	0
79	A7	2578	0	1306	18	0
80	A8	3334	0	1693	18	0
81	BC	1604	0	816	15	0
All	All	219292	0	161761	2305	0

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

All (2305) 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)
19:B2:1834:A:C4	19:B2:1834:A:C5	2.07	1.39
47:CA:248:GLY:CA	47:CA:248:GLY:C	1.99	1.35
19:B2:1834:A:C5	19:B2:1834:A:C6	2.16	1.34
19:B2:1834:A:N3	19:B2:1834:A:C2	2.12	1.17
19:B2:1834:A:C2	19:B2:1834:A:N1	2.13	1.16
19:B2:1834:A:C4	19:B2:1834:A:N3	2.15	1.14
19:B2:1044:G:C4	19:B2:1044:G:C5	2.35	1.13
19:B2:1834:A:C6	19:B2:1834:A:N1	2.19	1.10
19:B2:1288:U:H3	19:B2:1311:C:N4	1.49	1.07
20:CR:126:LYS:O	20:CR:130:ASN:HA	1.58	1.02
78:A6:3946:G:H1	78:A6:4067:U:H3	1.08	1.02
78:A5:1083:U:H3	78:A5:1216:C:N4	1.60	1.00
19:B2:197:U:H3	19:B2:202:G:H1	1.01	1.00
78:A5:989:U:H3	78:A5:1064:G:H1	1.08	0.99
19:B2:1324:G:H1	19:B2:1504:U:H3	0.99	0.99
19:B2:1652:G:H1	19:B2:1672:U:H3	1.01	0.99
19:B2:1044:G:C5	19:B2:1044:G:C6	2.50	0.98
78:A6:2485:U:H3	78:A6:2493:G:H1	0.98	0.98
78:A6:4421:C:H42	78:A6:4475:G:N2	1.64	0.96
78:A6:4272:G:N1	78:A6:4336:A:C2	2.33	0.95
19:B2:1044:G:C4	47:CA:248:GLY:HA3	2.02	0.95
19:B2:191:A:H62	19:B2:208:G:H21	1.07	0.95
78:A6:4272:G:H1	78:A6:4336:A:H2	0.99	0.94
19:B2:1351:G:H1	19:B2:1360:U:H3	1.09	0.93
78:A6:4888:U:H3	78:A6:4931:G:H1	1.14	0.92
19:B2:1757:G:H1	19:B2:1775:U:H3	1.11	0.92
78:A6:4972:U:H3	78:A6:4986:G:H1	1.02	0.91
78:A6:4272:G:N1	78:A6:4336:A:H2	1.69	0.91
78:A5:1724:G:H1	78:A5:1838:A:H2	1.03	0.90
78:A6:4997:G:H1	78:A6:5053:U:H3	1.21	0.89
19:B2:146:G:H1	19:B2:173:A:N6	1.71	0.89
19:B2:116:U:H3	19:B2:347:G:H1	1.18	0.89
19:B2:146:G:H1	19:B2:173:A:H61	0.94	0.89
55:Cr:95:HIS:O	55:Cr:99:LYS:HB3	1.71	0.88
19:B2:1207:G:H4'	19:B2:1834:A:N3	1.91	0.86
78:A5:1761:G:H1	78:A5:1771:U:H3	0.89	0.85
78:A6:3720:G:H1	78:A6:3733:A:H2	1.19	0.84
19:B2:1044:G:C2	19:B2:1044:G:N3	2.46	0.84
19:B2:536:A:H62	19:B2:547:G:N2	1.76	0.83
78:A5:1724:G:N1	78:A5:1838:A:H2	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A6:4745:G:N2	78:A6:4955:A:C6	2.46	0.83
69:CC:298:ILE:O	69:CC:302:LEU:HB2	1.79	0.83
19:B2:924:G:H1	19:B2:1018:U:H3	1.27	0.82
78:A6:4765:G:H1	78:A6:4869:U:H3	1.25	0.82
19:B2:1044:G:C2	47:CA:248:GLY:HA2	2.15	0.82
78:A6:4421:C:H42	78:A6:4475:G:H22	1.28	0.81
19:B2:191:A:H62	19:B2:208:G:N2	1.78	0.80
19:B2:1044:G:C4	19:B2:1044:G:N3	2.50	0.80
78:A5:717:U:H3	78:A5:951:G:H1	1.28	0.80
78:A5:1724:G:N1	78:A5:1838:A:C2	2.45	0.80
78:A5:750:U:H3	78:A5:912:G:H1	1.29	0.79
19:B2:1044:G:C2	19:B2:1044:G:N1	2.50	0.79
81:BC:15:G:H22	81:BC:47:C:H42	1.30	0.79
19:B2:1044:G:C5	47:CA:248:GLY:HA3	2.17	0.79
78:A5:735:G:C2	78:A5:929:A:N6	2.51	0.79
19:B2:110:U:H3	19:B2:351:G:H1	1.31	0.78
19:B2:1044:G:N3	47:CA:248:GLY:HA2	1.98	0.78
19:B2:1044:G:C2	47:CA:248:GLY:CA	2.67	0.78
78:A6:4421:C:N4	78:A6:4475:G:H22	1.82	0.78
66:Cj:54:LYS:O	66:Cj:58:THR:HB	1.83	0.77
19:B2:536:A:H62	19:B2:547:G:H21	1.32	0.77
19:B2:536:A:N6	19:B2:547:G:H21	1.84	0.76
19:B2:1044:G:C4	47:CA:249:THR:N	2.52	0.76
19:B2:1044:G:C4	47:CA:248:GLY:CA	2.69	0.76
78:A6:4321:U:H3	78:A6:4326:G:H1	1.34	0.76
19:B2:1748:G:H1	19:B2:1786:U:H3	1.33	0.76
19:B2:1044:G:C2	47:CA:248:GLY:C	2.65	0.75
39:CL:120:TYR:O	39:CL:124:LEU:HB2	1.86	0.74
19:B2:1044:G:C6	47:CA:248:GLY:C	2.66	0.74
78:A5:1759:G:H1	78:A5:1773:U:H3	1.35	0.74
78:A6:5002:U:H3	78:A6:5045:G:H1	1.35	0.74
78:A6:2550:G:H1	78:A6:2767:U:H3	1.35	0.74
18:AI:64:ASN:O	18:AI:186:ASP:HA	1.86	0.73
53:CY:83:GLU:HG2	53:CY:84:ARG:HD3	1.71	0.73
79:A7:7:G:H1	79:A7:112:U:H3	1.36	0.73
19:B2:1726:G:H1	19:B2:1808:U:H3	1.37	0.73
19:B2:677:G:H21	19:B2:1028:A:H62	1.34	0.73
19:B2:1206:G:H1	19:B2:1694:U:H3	1.38	0.72
78:A6:4460:U:H3	78:A6:4516:G:H1	1.35	0.72
19:B2:1232:U:H3	19:B2:1526:G:H1	1.34	0.72
19:B2:1044:G:C5	47:CA:248:GLY:CA	2.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1409:A:H2'	19:B2:1410:C:H4'	1.72	0.71
20:CR:38:ARG:HD3	52:CX:84:GLU:HG2	1.72	0.71
75:CH:141:LYS:HD3	75:CH:142:ASP:HB2	1.71	0.71
78:A6:4745:G:C2	78:A6:4955:A:N6	2.59	0.71
78:A6:3751:G:H21	78:A6:3775:A:H8	1.39	0.71
20:CR:126:LYS:O	20:CR:130:ASN:CA	2.35	0.70
19:B2:1207:G:H4'	19:B2:1834:A:C2	2.25	0.70
24:AK:15:LEU:HA	24:AK:21:MET:HE3	1.72	0.70
10:Ab:5:LYS:H	17:AW:23:ARG:HH12	1.37	0.70
50:CP:50:ASP:HB3	50:CP:55:LYS:HB2	1.73	0.70
12:AJ:47:LYS:HE2	12:AJ:102:ILE:HD11	1.73	0.70
19:B2:1096:G:H1	19:B2:1136:U:H3	1.37	0.70
22:Ag:152:SER:H	22:Ag:169:GLY:HA2	1.56	0.70
45:CD:12:TYR:O	45:CD:16:TYR:HB2	1.91	0.70
24:AK:23:ALA:O	24:AK:67:PHE:HB2	1.91	0.69
39:CL:188:ASN:O	39:CL:192:PHE:HB2	1.91	0.69
19:B2:1044:G:C6	19:B2:1044:G:N1	2.60	0.69
19:B2:1044:G:C6	47:CA:248:GLY:CA	2.75	0.69
19:B2:1656:G:H1	19:B2:1668:U:H3	1.40	0.69
39:CL:163:LYS:HD3	39:CL:165:LYS:H	1.58	0.69
55:Cr:5:LEU:HB2	69:CC:287:THR:HG21	1.74	0.69
1:AO:34:PHE:HB3	1:AO:41:PHE:HB2	1.75	0.69
19:B2:1095:C:N3	19:B2:1149:A:N1	2.41	0.68
1:AO:101:GLY:HA3	1:AO:134:PRO:HG2	1.74	0.68
16:AH:109:ARG:HG3	16:AH:110:THR:H	1.58	0.68
64:Cg:46:CYS:HB2	64:Cg:49:CYS:H	1.58	0.68
19:B2:1044:G:C5	47:CA:248:GLY:C	2.71	0.68
61:Cd:63:ARG:HH12	61:Cd:104:THR:H	1.40	0.68
78:A5:505:G:O6	78:A5:653:U:C2	2.45	0.68
19:B2:1044:G:N3	47:CA:248:GLY:CA	2.57	0.68
78:A6:2309:G:H1	78:A6:2329:U:H3	1.41	0.68
69:CC:194:GLY:HA2	69:CC:197:ARG:HB2	1.75	0.68
61:Cd:24:GLU:HG2	61:Cd:87:ARG:HB3	1.76	0.68
19:B2:68:A:H61	19:B2:81:U:H3	1.41	0.68
19:B2:1207:G:C5'	19:B2:1834:A:C4	2.76	0.68
78:A6:4745:G:N2	78:A6:4955:A:N6	2.42	0.68
78:A6:2777:G:H5''	78:A6:2778:G:H5'	1.75	0.67
19:B2:1364:U:H3	19:B2:1375:G:H21	1.41	0.67
54:CZ:76:ASN:O	54:CZ:80:LEU:HB3	1.94	0.67
78:A5:450:G:H1	78:A5:1297:U:H3	1.43	0.67
5:AB:150:ILE:H	28:AR:125:GLY:HA3	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:925:G:H1	19:B2:1017:U:H3	1.42	0.67
78:A6:3944:G:H1	78:A6:4069:U:H3	1.42	0.67
15:AG:38:ALA:HA	15:AG:41:LEU:HD13	1.77	0.67
28:AR:22:THR:HG23	28:AR:23:ARG:HD2	1.76	0.67
51:CU:81:ARG:O	51:CU:85:TYR:HB2	1.94	0.67
69:CC:289:LEU:HA	69:CC:292:ILE:HG12	1.77	0.67
16:AH:145:ARG:HB2	16:AH:153:LEU:HB3	1.77	0.67
19:B2:1207:G:C5'	19:B2:1834:A:C6	2.77	0.67
81:BC:15:G:H22	81:BC:47:C:N4	1.93	0.67
42:Ca:123:ILE:HD11	42:Ca:145:VAL:HG22	1.76	0.67
40:CV:62:MET:HE3	40:CV:62:MET:H	1.59	0.66
42:Ca:48:TYR:H	46:CQ:156:PRO:HG2	1.60	0.66
81:BC:15:G:N2	81:BC:47:C:H42	1.93	0.66
21:CW:34:ALA:HA	21:CW:37:GLU:HB2	1.78	0.66
54:CZ:14:LEU:HA	64:Cg:91:ILE:HD11	1.77	0.66
78:A6:2849:A:H62	78:A6:3838:U:H3	1.44	0.66
19:B2:1560:U:H3	19:B2:1575:G:H1	1.42	0.66
19:B2:323:C:N3	19:B2:328:U:O4	2.29	0.66
28:AR:69:ILE:HB	28:AR:71:ILE:HD13	1.78	0.66
19:B2:1044:G:N1	47:CA:248:GLY:O	2.29	0.66
71:Cn:20:MET:O	71:Cn:24:SER:HB3	1.96	0.66
35:AF:85:LYS:HB3	35:AF:88:MET:HG2	1.78	0.66
38:CO:83:THR:O	38:CO:87:MET:HB2	1.95	0.66
50:CP:84:PRO:HB2	50:CP:87:SER:HB3	1.78	0.66
62:Ce:104:SER:HB3	78:A6:2303:C:H5''	1.76	0.65
6:AA:183:LEU:O	6:AA:187:GLY:HA3	1.95	0.65
52:CX:77:ILE:HD11	52:CX:116:LEU:HG	1.77	0.65
77:CG:83:PHE:HA	77:CG:183:ILE:HG21	1.77	0.65
78:A5:1804:A:H61	78:A5:1832:C:H2'	1.60	0.65
59:CF:156:LYS:HG2	59:CF:157:ARG:HD2	1.77	0.65
78:A6:3692:A:H62	78:A6:3823:G:H21	1.44	0.65
19:B2:1244:U:H3	19:B2:1255:G:H1	1.42	0.65
29:AP:63:ALA:HB1	29:AP:73:PRO:HB3	1.79	0.65
50:CP:118:GLN:HE21	50:CP:120:ASN:HD21	1.44	0.65
59:CF:105:VAL:HG23	59:CF:136:VAL:HG23	1.79	0.65
8:AY:122:LYS:HE3	19:B2:66:G:H21	1.62	0.65
78:A5:1083:U:H3	78:A5:1216:C:H42	0.76	0.65
5:AB:107:ARG:HA	5:AB:110:MET:HB2	1.79	0.64
55:Cr:43:LEU:HA	55:Cr:45:HIS:H	1.61	0.64
2:AX:124:LYS:HG2	2:AX:127:ASN:HA	1.79	0.64
4:AL:83:GLN:HE22	19:B2:373:G:H21	1.43	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AW:31:SER:HB3	19:B2:685:A:H5''	1.79	0.64
67:Ck:17:ARG:HD3	67:Ck:19:ASP:HB2	1.79	0.64
78:A6:4454:G:H1	78:A6:4526:U:H3	1.44	0.64
13:AE:26:VAL:HG11	19:B2:509:G:H4'	1.79	0.64
24:AK:22:VAL:HG11	33:AD:76:ARG:HG2	1.78	0.64
13:AE:195:ILE:HG22	13:AE:197:ASN:H	1.63	0.64
22:Ag:87:LEU:HB3	22:Ag:101:PHE:HB2	1.80	0.64
9:Aa:53:ILE:O	9:Aa:57:SER:HB3	1.98	0.64
39:CL:46:ILE:HB	39:CL:49:ARG:HE	1.62	0.64
42:Ca:75:LEU:HD23	42:Ca:113:GLY:HA2	1.78	0.64
19:B2:110:U:O2	19:B2:351:G:N2	2.29	0.63
78:A6:4272:G:O6	78:A6:4336:A:N1	2.31	0.63
56:Ch:9:LEU:HA	56:Ch:12:LYS:HG2	1.81	0.63
13:AE:68:ARG:HA	13:AE:76:VAL:HG21	1.80	0.63
28:AR:17:ILE:HG22	28:AR:71:ILE:HD11	1.80	0.63
45:CD:236:MET:HA	45:CD:239:MET:HG3	1.81	0.63
78:A5:504:G:H1	78:A5:653:U:H3	1.46	0.63
22:Ag:89:LEU:HB3	22:Ag:99:ARG:HB2	1.81	0.63
22:Ag:154:VAL:HB	22:Ag:165:ILE:HD11	1.80	0.63
54:CZ:46:ILE:HA	54:CZ:70:SER:HA	1.81	0.63
4:AL:68:ILE:HG12	4:AL:143:LEU:HD11	1.81	0.63
55:Cr:32:LEU:HD21	55:Cr:110:ALA:HA	1.78	0.63
78:A5:749:G:H1	78:A5:913:U:H3	1.46	0.63
14:AC:207:ALA:HB2	19:B2:4:C:H4'	1.81	0.63
19:B2:1207:G:C5'	19:B2:1834:A:C2	2.82	0.63
44:CI:30:LYS:HG2	44:CI:66:GLU:HG2	1.81	0.63
6:AA:77:ILE:HG21	6:AA:133:PRO:HG3	1.81	0.62
19:B2:1083:A:H62	19:B2:1841:C:H1'	1.64	0.62
78:A6:2439:G:H1	78:A6:2538:U:H3	1.47	0.62
19:B2:1207:G:C5'	19:B2:1834:A:C5	2.83	0.62
37:Cz:143:ASN:H	37:Cz:146:ALA:HB3	1.64	0.62
75:CH:51:LYS:HG2	75:CH:52:LYS:HG2	1.80	0.62
37:Cz:55:LEU:HD11	37:Cz:155:ILE:HG12	1.81	0.62
78:A6:2620:G:H1	78:A6:2636:U:H3	1.47	0.62
14:AC:145:LYS:HE3	19:B2:1348:G:H5'	1.82	0.62
78:A6:4741:C:H2'	78:A6:4742:G:H8	1.63	0.62
61:Cd:90:ARG:HA	61:Cd:103:TYR:O	1.99	0.62
2:AX:7:LEU:HD22	17:AW:77:PRO:HB2	1.82	0.62
5:AB:100:PHE:HB3	5:AB:181:LEU:HD21	1.80	0.62
22:Ag:192:THR:HG22	33:AD:219:PRO:HB3	1.81	0.62
16:AH:98:ARG:HD3	16:AH:125:VAL:HG22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:CD:263:LYS:HG3	45:CD:264:LYS:HG2	1.82	0.62
44:CI:156:LYS:HG3	44:CI:163:GLN:HB2	1.81	0.62
78:A5:1332:C:H2'	78:A5:1333:A:H8	1.64	0.62
19:B2:1044:G:N1	47:CA:248:GLY:CA	2.63	0.61
5:AB:105:LEU:HD21	5:AB:110:MET:HG2	1.82	0.61
34:Af:98:VAL:HG13	34:Af:100:LEU:H	1.64	0.61
36:AQ:131:LYS:HB2	36:AQ:140:ARG:HH22	1.64	0.61
78:A5:1996:C:H42	78:A5:2000:G:N2	1.98	0.61
78:A6:2908:U:H3	78:A6:3586:G:H1	1.46	0.61
19:B2:191:A:N6	19:B2:208:G:H21	1.90	0.61
19:B2:1551:U:N3	19:B2:1577:G:C6	2.67	0.61
6:AA:63:ARG:HA	6:AA:66:VAL:HG22	1.81	0.61
21:CW:47:ARG:HA	21:CW:55:TYR:HE1	1.64	0.61
67:Ck:31:ASN:HD22	67:Ck:33:LYS:HG3	1.65	0.61
78:A6:2395:A:N6	78:A6:2820:C:O2	2.34	0.61
78:A6:2637:U:H5''	78:A6:2638:G:H5'	1.83	0.61
13:AE:38:LEU:HD22	19:B2:346:C:H5''	1.82	0.61
17:AW:86:LEU:HD21	17:AW:117:ARG:HE	1.64	0.61
22:Ag:28:PRO:HG3	22:Ag:293:ALA:HB3	1.83	0.61
28:AR:96:ILE:HG13	28:AR:114:LEU:HB2	1.83	0.61
29:AP:60:LEU:HD13	29:AP:89:MET:HG2	1.81	0.61
33:AD:158:ILE:H	33:AD:189:MET:HE2	1.66	0.61
58:CB:56:ILE:HG22	58:CB:368:ILE:HA	1.82	0.61
11:Ae:15:GLN:HE21	19:B2:612:U:H4'	1.65	0.61
35:AF:136:ARG:HH21	81:BC:31:C:H1'	1.65	0.61
55:Cr:64:ILE:HG23	55:Cr:81:THR:HA	1.82	0.61
2:AX:67:ARG:HG3	2:AX:115:ILE:HG12	1.82	0.61
3:AN:133:ARG:HH22	4:AL:152:LYS:HB3	1.65	0.61
4:AL:111:VAL:HG12	4:AL:140:PHE:HB2	1.82	0.61
21:CW:53:VAL:HA	21:CW:56:ARG:HH21	1.66	0.61
22:Ag:18:VAL:HG21	22:Ag:307:VAL:HG22	1.83	0.61
19:B2:1832:A:H5''	19:B2:1840:U:H5''	1.82	0.60
47:CA:95:GLN:HB2	72:Cp:87:LYS:HE3	1.83	0.60
17:AW:102:ILE:HD13	17:AW:128:PHE:HB3	1.82	0.60
19:B2:1571:G:H5'	19:B2:1615:U:H5''	1.82	0.60
25:AM:93:LYS:HE3	25:AM:102:LYS:HD2	1.83	0.60
78:A5:300:A:H2'	78:A5:301:G:H8	1.65	0.60
18:AI:42:ARG:HB3	18:AI:58:LEU:O	2.00	0.60
70:Cm:99:CYS:HB3	70:Cm:115:CYS:HB3	1.84	0.60
78:A6:3865:A:H61	78:A6:3881:G:H1	1.49	0.60
51:CU:86:LEU:HA	51:CU:89:LYS:HB2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A6:4888:U:O2	78:A6:4931:G:N2	2.33	0.60
15:AG:131:ARG:HD2	21:CW:80:ARG:HH11	1.67	0.60
57:Cb:40:LEU:HB3	57:Cb:44:ARG:HH12	1.67	0.60
59:CF:92:VAL:O	59:CF:120:GLY:HA2	2.01	0.60
19:B2:1207:G:C4'	19:B2:1834:A:C6	2.84	0.60
55:Cr:23:GLN:HE21	62:Ce:95:TYR:HD1	1.47	0.60
61:Cd:29:ILE:HD11	61:Cd:45:ALA:HB1	1.83	0.60
69:CC:324:ILE:O	69:CC:328:LEU:HB3	2.02	0.60
70:Cm:77:ILE:HG23	70:Cm:78:ILE:HG12	1.84	0.60
5:AB:49:VAL:HG21	5:AB:62:LEU:HD23	1.83	0.60
45:CD:115:MET:HE3	45:CD:115:MET:H	1.66	0.60
58:CB:145:GLN:HA	58:CB:148:LYS:HE3	1.83	0.60
77:CG:143:VAL:HG23	77:CG:203:ALA:HB2	1.84	0.60
33:AD:199:GLY:H	33:AD:202:LYS:HE2	1.65	0.60
43:CN:36:LEU:HD13	43:CN:64:ILE:HB	1.83	0.60
77:CG:100:HIS:HA	77:CG:103:ARG:HG3	1.82	0.60
1:AO:31:CYS:HB3	1:AO:96:LYS:H	1.64	0.60
19:B2:1207:G:C4'	19:B2:1834:A:C4	2.85	0.60
38:CO:89:PRO:HD3	78:A5:1914:C:H4'	1.84	0.60
43:CN:60:VAL:HG21	80:A8:141:C:H5''	1.84	0.60
61:Cd:32:ARG:HB3	61:Cd:48:GLU:HG3	1.83	0.60
19:B2:692:G:H2'	19:B2:693:A:H8	1.67	0.60
63:Cf:105:LEU:HD21	76:CE:277:LEU:HD11	1.84	0.60
78:A5:1726:U:H3	78:A5:1836:G:H1	0.80	0.60
81:BC:54:U:O2	81:BC:57:A:N7	2.34	0.60
21:CW:55:TYR:O	21:CW:59:HIS:HB3	2.02	0.59
56:Ch:41:ALA:HA	56:Ch:44:LEU:HB2	1.84	0.59
19:B2:1594:A:H62	31:AZ:104:ARG:HH22	1.50	0.59
21:CW:46:PRO:HB2	21:CW:47:ARG:HD3	1.83	0.59
22:Ag:40:ILE:HB	22:Ag:59:LEU:HB2	1.83	0.59
47:CA:33:ASP:O	47:CA:37:ARG:HB2	2.00	0.59
76:CE:65:ARG:O	76:CE:69:TYR:HB2	2.01	0.59
78:A5:1219:G:H2'	78:A5:1220:G:H8	1.68	0.59
52:CX:80:PRO:HD2	56:Ch:33:VAL:HG22	1.84	0.59
16:AH:51:ILE:HG12	16:AH:179:LYS:HG2	1.84	0.59
39:CL:173:GLU:HA	39:CL:176:PHE:HB3	1.84	0.59
35:AF:129:GLY:HA2	35:AF:134:VAL:HG22	1.83	0.59
38:CO:27:VAL:HG13	38:CO:98:ALA:HB1	1.83	0.59
76:CE:110:ARG:HD2	78:A5:689:U:H4'	1.83	0.59
78:A5:234:G:H22	78:A6:2304:U:H3	1.51	0.59
78:A6:4237:C:H2'	78:A6:4238:G:H8	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AY:15:ASN:HB3	8:AY:20:ARG:HG2	1.84	0.59
19:B2:1326:U:H5'	19:B2:1494:U:H5''	1.84	0.59
49:CT:41:ASP:HB3	49:CT:99:SER:HB2	1.84	0.59
61:CD:63:ARG:HB3	78:A6:2374:A:H5''	1.83	0.59
36:AQ:31:LEU:HD13	36:AQ:33:LYS:HG3	1.84	0.59
15:AG:231:ARG:HH12	19:B2:229:A:H4'	1.67	0.59
24:AK:29:MET:HG2	24:AK:31:LYS:H	1.68	0.59
44:CI:184:MET:HE3	44:CI:190:LEU:HB2	1.85	0.59
69:CC:53:ALA:HB3	80:A8:27:U:H4'	1.83	0.59
78:A5:1841:C:H42	78:A6:2276:A:H1'	1.66	0.59
78:A6:2611:A:H5'	78:A6:2688:G:H4'	1.83	0.59
78:A6:4764:A:N6	78:A6:4870:G:H1	2.00	0.59
47:CA:39:GLY:HA3	77:CG:41:ILE:HG12	1.84	0.59
4:AL:110:SER:HB2	4:AL:138:VAL:HG22	1.85	0.58
16:AH:136:PRO:HG2	16:AH:165:ASN:HD21	1.68	0.58
23:AU:69:PRO:HB3	27:AD:41:GLN:HG2	1.84	0.58
69:CC:78:ARG:HB3	69:CC:88:GLY:HA2	1.84	0.58
69:CC:193:LYS:H	78:A6:2294:G:H5''	1.68	0.58
19:B2:1505:U:H5''	19:B2:1506:A:H5'	1.85	0.58
33:AD:197:LYS:HB2	33:AD:198:ILE:HG12	1.84	0.58
41:CM:105:THR:O	41:CM:109:ARG:HB2	2.04	0.58
46:CQ:81:VAL:O	46:CQ:138:LEU:HA	2.03	0.58
50:CP:69:ARG:HG3	78:A6:4981:G:H1'	1.84	0.58
67:Ck:56:LEU:O	67:Ck:60:LEU:HB2	2.03	0.58
69:CC:171:LEU:HD22	69:CC:176:ALA:HB3	1.85	0.58
48:CS:101:THR:HG23	48:CS:104:GLY:H	1.68	0.58
4:AL:80:MET:HE2	4:AL:122:ILE:HD12	1.85	0.58
19:B2:1207:G:C4'	19:B2:1834:A:C5	2.87	0.58
19:B2:1653:U:O2	19:B2:1671:G:N2	2.33	0.58
19:B2:1756:C:H2'	19:B2:1757:G:H8	1.67	0.58
26:AS:39:ARG:HG2	30:AT:45:LEU:HA	1.85	0.58
38:CO:199:HIS:HE1	38:CO:203:VAL:HG21	1.67	0.58
54:CZ:11:VAL:HG22	54:CZ:82:PRO:HA	1.86	0.58
74:CJ:22:LEU:HB3	74:CJ:128:LEU:HD11	1.86	0.58
78:A5:735:G:N2	78:A5:929:A:N6	2.51	0.58
78:A6:2751:G:H2'	78:A6:2752:G:H8	1.69	0.58
78:A6:3598:C:H2'	78:A6:3599:A:H8	1.68	0.58
38:CO:175:MET:HA	38:CO:178:ARG:HG2	1.86	0.58
65:CI:51:ALA:HB3	65:CI:54:GLU:HG2	1.85	0.58
78:A6:3720:G:N1	78:A6:3733:A:H2	1.97	0.58
19:B2:1207:G:C4'	19:B2:1834:A:C2	2.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1208:A:H8	19:B2:1834:A:H4'	1.68	0.58
53:CY:57:VAL:HA	53:CY:104:VAL:HG12	1.86	0.58
69:CC:153:VAL:HG12	69:CC:252:TRP:HB2	1.85	0.58
78:A5:1996:C:H42	78:A5:2000:G:H22	1.50	0.58
19:B2:642:U:H4'	19:B2:644:G:H4'	1.83	0.58
34:Af:102:VAL:HG22	34:Af:103:LEU:HD12	1.84	0.58
37:Cz:65:VAL:HG22	37:Cz:109:ALA:HB3	1.85	0.58
5:AB:68:GLU:HB2	5:AB:83:LYS:HD2	1.84	0.58
26:AS:22:GLY:HA2	26:AS:56:ALA:HB3	1.85	0.58
47:CA:133:TYR:HB3	47:CA:168:VAL:HG12	1.86	0.58
69:CC:231:ASN:HB3	69:CC:234:LYS:HG2	1.86	0.58
78:A5:65:A:H61	78:A5:75:G:H1'	1.68	0.58
78:A6:4745:G:C2	78:A6:4955:A:C6	2.91	0.58
8:AY:102:THR:HB	8:AY:106:GLN:HE22	1.67	0.58
67:Ck:8:ILE:HD12	67:Ck:56:LEU:HD21	1.86	0.58
78:A5:713:C:H2'	78:A5:714:G:H8	1.69	0.58
14:AC:70:VAL:HG13	14:AC:96:PHE:HD1	1.68	0.58
74:CJ:89:VAL:HG21	74:CJ:115:LEU:HB3	1.86	0.58
76:CE:61:ALA:HA	76:CE:65:ARG:HB3	1.84	0.58
78:A5:1073:G:O6	78:A5:1238:A:N1	2.36	0.58
3:AN:114:ARG:HD3	3:AN:117:LEU:HD11	1.86	0.57
9:Aa:84:VAL:HG23	19:B2:1866:A:H62	1.68	0.57
42:Ca:45:PHE:O	42:Ca:49:HIS:HB2	2.04	0.57
42:Ca:85:GLN:O	42:Ca:89:ASN:HB3	2.04	0.57
69:CC:350:ARG:HA	69:CC:353:LYS:HB2	1.85	0.57
76:CE:153:LEU:HD21	76:CE:195:ILE:HG13	1.86	0.57
9:Aa:10:ARG:HG3	9:Aa:34:LYS:HG3	1.86	0.57
14:AC:149:THR:HA	14:AC:152:ARG:HG2	1.85	0.57
15:AG:181:THR:HG22	15:AG:184:VAL:HG23	1.86	0.57
26:AS:67:VAL:HG22	26:AS:71:MET:HE3	1.85	0.57
38:CO:199:HIS:CE1	38:CO:203:VAL:HB	2.39	0.57
52:CX:58:PRO:HA	78:A5:15:A:H5''	1.87	0.57
19:B2:508:A:H3'	19:B2:509:G:H8	1.69	0.57
19:B2:677:G:N2	19:B2:1028:A:H62	2.02	0.57
20:CR:62:ARG:HA	20:CR:65:LYS:HB3	1.84	0.57
78:A5:469:C:H2'	78:A5:470:A:H8	1.69	0.57
78:A6:2325:C:H2'	78:A6:2326:G:H8	1.70	0.57
2:AX:54:LYS:HD2	2:AX:91:LEU:HD22	1.87	0.57
19:B2:649:U:H2'	19:B2:650:A:H8	1.70	0.57
19:B2:1623:A:H5''	26:AS:133:GLY:H	1.70	0.57
26:AS:6:PRO:HA	31:AZ:50:PHE:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:Cp:9:GLY:HA3	72:Cp:27:LYS:HE2	1.86	0.57
1:AO:32:HIS:H	1:AO:96:LYS:HB3	1.69	0.57
19:B2:1166:G:H1	19:B2:1193:U:H3	1.52	0.57
19:B2:1207:G:C5'	19:B2:1834:A:N1	2.68	0.57
41:CM:90:ARG:HH22	78:A6:4869:U:H5''	1.70	0.57
43:CN:142:ILE:HA	43:CN:145:ASN:HB3	1.85	0.57
44:CI:61:SER:HA	44:CI:126:VAL:HG22	1.87	0.57
19:B2:602:G:H3'	19:B2:603:C:H2'	1.85	0.57
76:CE:219:LYS:HG3	78:A5:1291:G:H5''	1.86	0.57
78:A5:505:G:O6	78:A5:653:U:O2	2.23	0.57
19:B2:1044:G:N1	47:CA:248:GLY:C	2.62	0.57
19:B2:1402:A:N7	19:B2:1441:U:C4	2.73	0.57
19:B2:1044:G:C4	47:CA:248:GLY:C	2.83	0.57
19:B2:1406:G:H21	19:B2:1443:C:H41	1.52	0.57
19:B2:1653:U:H3	19:B2:1671:G:H1	1.50	0.57
21:CW:9:SER:HA	21:CW:52:THR:HB	1.85	0.57
14:AC:92:GLU:HA	14:AC:95:ASP:HB2	1.86	0.57
37:Cz:129:ASN:HA	37:Cz:134:PHE:HB2	1.87	0.57
49:CT:17:ARG:HG2	78:A6:4277:G:H5''	1.85	0.57
15:AG:1:MET:HA	15:AG:107:SER:O	2.05	0.57
19:B2:1044:G:N3	47:CA:248:GLY:C	2.62	0.57
47:CA:40:TYR:HA	47:CA:90:CYS:O	2.04	0.57
62:Ce:25:SER:HA	62:Ce:31:ILE:HB	1.86	0.57
78:A6:2647:A:H62	78:A6:2686:G:H8	1.51	0.57
78:A6:2704:C:H2'	78:A6:2705:G:H8	1.68	0.57
5:AB:146:ARG:HD2	5:AB:149:GLN:HB2	1.86	0.56
9:Aa:35:ALA:HA	9:Aa:73:TYR:O	2.05	0.56
13:AE:11:ARG:HH21	13:AE:20:LEU:HD13	1.70	0.56
15:AG:50:VAL:HG11	15:AG:111:LEU:HD12	1.87	0.56
23:AU:17:ILE:HD11	23:AU:92:HIS:HB3	1.87	0.56
25:AM:93:LYS:HB2	25:AM:101:ARG:HD3	1.87	0.56
58:CB:65:SER:HB3	78:A6:4616:A:H4'	1.86	0.56
8:AY:36:PRO:HG2	8:AY:39:GLU:HB2	1.87	0.56
11:Ae:29:THR:HA	11:Ae:33:LYS:HD2	1.87	0.56
19:B2:1740:C:H42	19:B2:1794:C:H42	1.52	0.56
24:AK:84:HIS:HB2	25:AM:27:ILE:HG22	1.85	0.56
27:Ad:31:ILE:HG13	27:Ad:36:LEU:HD21	1.87	0.56
38:CO:199:HIS:HE1	38:CO:203:VAL:CG2	2.17	0.56
53:CY:3:PHE:HB2	78:A5:243:A:H5''	1.87	0.56
55:Cr:112:ARG:HD2	76:CE:118:THR:HA	1.88	0.56
69:CC:55:SER:HB2	69:CC:57:LEU:HG	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AH:143:ARG:HB3	17:AW:53:ILE:HG22	1.88	0.56
41:CM:124:LYS:HA	41:CM:127:VAL:HG22	1.87	0.56
58:CB:220:ILE:HG12	58:CB:278:THR:HG23	1.87	0.56
19:B2:1207:G:C5'	19:B2:1834:A:N3	2.68	0.56
22:Ag:11:LEU:HD12	22:Ag:307:VAL:HB	1.88	0.56
22:Ag:109:LEU:HD13	22:Ag:152:SER:HA	1.87	0.56
62:Ce:79:VAL:HG13	62:Ce:84:GLU:HG2	1.86	0.56
78:A5:735:G:H21	78:A5:930:G:H1	1.52	0.56
14:AC:70:VAL:HG21	14:AC:93:ILE:HG23	1.88	0.56
30:AT:76:THR:HA	30:AT:79:TYR:HB2	1.88	0.56
55:Cr:50:GLY:O	55:Cr:64:ILE:HB	2.05	0.56
78:A6:3868:G:H22	78:A6:3900:G:H1'	1.71	0.56
69:CC:28:PHE:HA	69:CC:129:ALA:HA	1.88	0.56
75:CH:115:ARG:HE	75:CH:123:ILE:HD12	1.71	0.56
15:AG:136:LYS:HB2	19:B2:65:C:H41	1.71	0.56
1:AO:28:PHE:HA	1:AO:92:ALA:O	2.05	0.56
13:AE:33:THR:HG21	19:B2:119:U:H3	1.71	0.56
55:Cr:44:ILE:HD12	55:Cr:47:LYS:HB3	1.88	0.56
69:CC:146:GLU:HG2	69:CC:175:LYS:HB3	1.87	0.56
76:CE:113:PRO:HA	76:CE:116:TYR:HB3	1.87	0.56
19:B2:870:A:H62	19:B2:915:G:H3'	1.71	0.56
53:CY:45:ARG:HB3	53:CY:126:ARG:HH22	1.71	0.56
55:Cr:108:MET:HG3	55:Cr:112:ARG:HH21	1.71	0.56
15:AG:237:LEU:HD11	19:B2:787:G:H5''	1.88	0.55
24:AK:3:MET:HE1	24:AK:8:ARG:HE	1.71	0.55
40:CV:70:PRO:HA	40:CV:73:ARG:HG3	1.87	0.55
41:CM:7:VAL:HG12	48:CS:153:PRO:HA	1.88	0.55
45:CD:270:LYS:HG2	45:CD:271:MET:HB2	1.87	0.55
48:CS:80:ILE:HD11	48:CS:126:ILE:HG13	1.87	0.55
78:A6:4072:C:H2'	78:A6:4073:A:H8	1.71	0.55
17:AW:48:GLY:HA3	17:AW:64:ASN:O	2.05	0.55
19:B2:1310:U:H5'	34:Af:130:VAL:HG13	1.87	0.55
22:Ag:40:ILE:HG13	22:Ag:66:VAL:HG11	1.88	0.55
23:AU:41:ARG:HA	23:AU:44:LYS:HG2	1.87	0.55
31:AZ:70:PRO:HD3	31:AZ:107:VAL:HG22	1.87	0.55
76:CE:219:LYS:HE2	78:A6:4939:C:H5'	1.89	0.55
24:AK:93:THR:HG22	33:AD:67:ARG:HH12	1.71	0.55
26:AS:138:THR:HA	26:AS:141:ARG:HH21	1.71	0.55
42:Ca:34:ASN:HB2	42:Ca:45:PHE:HZ	1.70	0.55
61:Cd:51:LYS:HA	61:Cd:54:MET:HG2	1.87	0.55
19:B2:1676:U:H5'	35:AF:74:ASN:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:CM:16:SER:HA	41:CM:22:GLY:H	1.71	0.55
45:CD:88:VAL:HG22	45:CD:239:MET:HE1	1.89	0.55
78:A6:3720:G:N1	78:A6:3733:A:C2	2.56	0.55
19:B2:1652:G:O6	19:B2:1672:U:O4	2.24	0.55
28:AR:17:ILE:HG13	28:AR:57:LEU:HD11	1.87	0.55
38:CO:9:LEU:HB2	38:CO:35:VAL:HG22	1.88	0.55
58:CB:160:ILE:HD11	58:CB:193:LYS:HB3	1.89	0.55
14:AC:127:PHE:HA	14:AC:140:GLY:O	2.06	0.55
47:CA:111:THR:HG22	72:Cp:86:LEU:HD13	1.89	0.55
17:AW:12:LYS:HE2	19:B2:1152:U:H2'	1.88	0.55
33:AD:138:VAL:HG22	33:AD:184:ILE:HG22	1.89	0.55
54:CZ:41:ALA:HB3	54:CZ:80:LEU:HD21	1.88	0.55
76:CE:258:LEU:HD12	76:CE:262:LYS:HE2	1.87	0.55
19:B2:1446:A:H5''	23:AU:58:THR:HG23	1.88	0.55
26:AS:114:LEU:HA	26:AS:117:ILE:HG12	1.88	0.55
28:AR:24:LEU:HD22	28:AR:54:VAL:HG11	1.89	0.55
58:CB:9:PRO:HG3	78:A6:4491:G:H5''	1.88	0.55
58:CB:160:ILE:HG21	58:CB:194:LEU:HD21	1.89	0.55
58:CB:305:THR:HG23	58:CB:307:TYR:H	1.71	0.55
76:CE:126:LEU:HD22	76:CE:131:LYS:HD2	1.88	0.55
81:BC:25:G:N1	81:BC:43:A:C2	2.68	0.55
14:AC:102:LEU:HD21	14:AC:130:ILE:HG23	1.89	0.55
14:AC:191:VAL:HG11	14:AC:236:PHE:HA	1.87	0.55
47:CA:83:HIS:HB3	72:Cp:64:VAL:HG12	1.89	0.55
50:CP:46:LYS:HA	50:CP:49:LYS:HG2	1.89	0.55
6:AA:4:ALA:HB3	6:AA:8:LEU:HB2	1.89	0.55
19:B2:1560:U:H2'	19:B2:1561:A:H8	1.72	0.55
30:AT:10:ASN:HA	36:AQ:37:ARG:HH22	1.72	0.55
45:CD:19:LYS:HB2	45:CD:24:ARG:HG3	1.89	0.55
63:Cf:54:LYS:HD3	63:Cf:55:ASN:HB3	1.89	0.55
78:A5:709:C:H2'	78:A5:710:G:H8	1.72	0.55
78:A5:1382:G:H2'	78:A5:1383:G:H8	1.71	0.55
6:AA:75:SER:O	6:AA:122:LEU:HA	2.07	0.54
15:AG:232:ARG:HH22	19:B2:230:A:H5'	1.73	0.54
19:B2:1273:C:O2	19:B2:1508:A:N6	2.40	0.54
43:CN:23:LEU:O	43:CN:27:CYS:HB2	2.08	0.54
65:Cl:25:ARG:HB2	65:Cl:28:ARG:HG2	1.87	0.54
75:CH:69:THR:HA	75:CH:72:THR:HG22	1.89	0.54
24:AK:18:GLU:HG2	33:AD:75:LYS:HE2	1.88	0.54
50:CP:56:GLN:HA	50:CP:72:GLN:HG2	1.88	0.54
53:CY:27:ARG:HH22	80:A8:70:G:H5'	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Cm:80:PRO:HA	70:Cm:83:ARG:HB3	1.89	0.54
6:AA:84:GLN:HG2	6:AA:100:ALA:HB1	1.89	0.54
69:CC:234:LYS:HD2	78:A5:1373:A:H2	1.71	0.54
69:CC:343:GLN:HE21	78:A5:722:G:H21	1.55	0.54
21:CW:36:CYS:HB3	21:CW:51:TRP:HH2	1.73	0.54
46:CQ:3:VAL:HG12	59:CF:116:GLN:HB3	1.88	0.54
65:CI:43:MET:HE3	77:CG:173:LEU:HD23	1.89	0.54
69:CC:48:ASN:HB3	78:A5:1372:A:H4'	1.90	0.54
80:A8:122:G:H21	80:A8:128:C:H5	1.55	0.54
78:A6:4530:U:H2'	78:A6:4531:U:H2'	1.88	0.54
8:AY:17:LEU:HD13	13:AE:64:ILE:HD12	1.89	0.54
29:AP:15:PHE:HD2	29:AP:22:LEU:HB2	1.72	0.54
35:AF:125:SER:HB2	35:AF:136:ARG:HB3	1.88	0.54
43:CN:114:ARG:HE	43:CN:137:PRO:HG3	1.73	0.54
50:CP:114:ILE:HD11	50:CP:117:ILE:HB	1.89	0.54
14:AC:98:LEU:HB3	14:AC:102:LEU:HD12	1.90	0.54
20:CR:60:ARG:HB2	78:A6:2634:C:H5''	1.90	0.54
33:AD:135:GLU:HB2	33:AD:153:VAL:HG13	1.89	0.54
74:CJ:35:ARG:HH21	74:CJ:124:GLY:HA3	1.72	0.54
77:CG:84:THR:H	77:CG:159:HIS:HB2	1.73	0.54
11:Ae:22:GLN:HB2	11:Ae:24:LYS:HZ2	1.72	0.54
19:B2:928:G:H2'	19:B2:929:G:C8	2.43	0.54
33:AD:172:VAL:HG12	33:AD:174:HIS:HE1	1.72	0.54
43:CN:138:PHE:HD2	78:A5:18:C:H4'	1.72	0.54
55:Cr:128:ARG:HH12	62:Ce:113:GLU:HB2	1.72	0.54
58:CB:170:LEU:HD11	58:CB:328:ASN:HB3	1.89	0.54
75:CH:34:LEU:HD21	75:CH:150:ASP:HB2	1.88	0.54
78:A5:104:G:H2'	78:A5:105:A:H8	1.72	0.54
37:Cz:68:LEU:H	37:Cz:111:LEU:HD23	1.73	0.54
63:Cf:40:GLU:HA	63:Cf:43:LEU:HG	1.89	0.54
19:B2:948:C:H2'	19:B2:949:G:H8	1.73	0.54
19:B2:1101:U:H3	19:B2:1131:G:H1	1.55	0.54
29:AP:116:LEU:HD23	29:AP:119:PHE:HD2	1.73	0.54
40:CV:46:LYS:HD3	78:A6:4510:A:H62	1.73	0.54
45:CD:9:ASN:HB2	45:CD:12:TYR:HB3	1.90	0.54
76:CE:188:ARG:HH11	76:CE:217:PHE:HB2	1.73	0.54
78:A5:505:G:C6	78:A5:653:U:O2	2.61	0.54
19:B2:1069:U:H5''	47:CA:247:ARG:HB3	1.89	0.54
19:B2:1745:A:C2	19:B2:1789:G:N2	2.76	0.54
20:CR:133:LYS:HG2	20:CR:137:ILE:HD13	1.89	0.54
22:Ag:256:ILE:HG23	22:Ag:270:LEU:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AU:19:ARG:HB3	23:AU:21:ARG:HH12	1.73	0.54
60:Cc:48:LEU:HD21	60:Cc:57:LYS:HA	1.90	0.54
72:Cp:38:THR:HA	72:Cp:45:THR:HA	1.90	0.54
77:CG:175:ARG:HG3	77:CG:227:ASN:HA	1.89	0.54
19:B2:1206:G:H21	19:B2:1700:C:H41	1.56	0.53
19:B2:1597:C:H5	31:AZ:85:ARG:HH12	1.55	0.53
31:AZ:111:ARG:HB3	31:AZ:114:LYS:HD2	1.89	0.53
44:CI:33:ILE:HD13	44:CI:36:LEU:HD21	1.90	0.53
59:CF:217:ARG:H	59:CF:246:ARG:HB3	1.73	0.53
75:CH:120:GLU:HG2	75:CH:124:ARG:HH12	1.73	0.53
8:AY:19:GLN:HG2	8:AY:77:ASP:HB2	1.90	0.53
12:AJ:18:ARG:HH22	19:B2:4:C:H1'	1.72	0.53
43:CN:24:ARG:HH22	78:A6:3937:C:H5''	1.73	0.53
78:A6:4210:U:O2	78:A6:4222:G:N2	2.38	0.53
78:A6:5022:U:H3	78:A6:5025:C:N4	2.06	0.53
12:AJ:113:GLN:HG2	12:AJ:149:VAL:HG21	1.90	0.53
5:AB:36:PRO:HB3	5:AB:231:LEU:HD13	1.91	0.53
9:Aa:73:TYR:HB3	9:Aa:78:ALA:HB2	1.89	0.53
19:B2:525:A:H62	19:B2:589:G:H22	1.56	0.53
37:Cz:51:GLY:HA3	37:Cz:193:LEU:HG	1.90	0.53
47:CA:225:ILE:HG21	47:CA:234:LYS:HA	1.91	0.53
62:Ce:22:ARG:HG3	62:Ce:36:ARG:H	1.73	0.53
65:CI:82:ARG:HA	65:CI:85:ARG:HG2	1.90	0.53
78:A5:392:U:H3	78:A5:399:G:H1	1.56	0.53
78:A6:2505:C:H41	78:A6:4084:G:H4'	1.72	0.53
19:B2:926:A:H61	19:B2:1015:U:H3	1.57	0.53
45:CD:164:LYS:HG2	45:CD:195:HIS:HE1	1.73	0.53
58:CB:224:LYS:HB3	58:CB:340:THR:HB	1.90	0.53
67:Ck:33:LYS:HA	67:Ck:45:LEU:O	2.09	0.53
69:CC:163:LYS:HB3	69:CC:166:GLU:HG2	1.91	0.53
69:CC:339:THR:H	69:CC:342:ARG:HG2	1.72	0.53
18:AI:165:GLN:HG2	18:AI:171:LEU:HD23	1.91	0.53
51:CU:28:PRO:HB2	51:CU:34:MET:HE1	1.91	0.53
54:CZ:11:VAL:HG11	54:CZ:80:LEU:HD12	1.90	0.53
78:A5:1188:C:H2'	78:A5:1189:G:H8	1.74	0.53
45:CD:104:LEU:HB2	45:CD:247:ILE:HD12	1.91	0.53
60:Cc:28:VAL:HG13	60:Cc:33:GLN:HB3	1.90	0.53
78:A5:1616:U:H2'	78:A5:1617:G:H8	1.74	0.53
78:A6:3720:G:O6	78:A6:3733:A:N1	2.42	0.53
78:A6:4638:U:H3	78:A6:4661:G:H1	1.57	0.53
19:B2:532:C:H2'	19:B2:533:A:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1854:U:H2'	19:B2:1855:G:H8	1.73	0.53
37:Cz:17:VAL:HG21	37:Cz:216:LEU:HB3	1.90	0.53
38:CO:87:MET:HE3	78:A5:1912:G:H21	1.74	0.53
39:CL:47:ALA:HB3	56:Ch:118:LYS:HZ2	1.74	0.53
49:CT:132:PRO:HB2	59:CF:126:ASN:HB3	1.91	0.53
69:CC:339:THR:HG22	69:CC:342:ARG:HH21	1.72	0.53
78:A5:418:A:H4'	78:A6:2311:C:H5'	1.91	0.53
78:A5:1332:C:H2'	78:A5:1333:A:C8	2.43	0.53
19:B2:391:C:H2'	19:B2:392:A:H8	1.74	0.53
28:AR:35:CYS:HA	28:AR:38:ILE:HG22	1.90	0.53
39:CL:91:ALA:HB1	39:CL:96:ILE:HB	1.91	0.53
42:Ca:81:LEU:HB2	78:A5:509:A:H61	1.73	0.53
44:CI:93:PRO:HB2	44:CI:125:THR:HB	1.90	0.53
63:Cf:54:LYS:HG2	78:A6:4747:C:H5''	1.91	0.53
78:A6:4704:C:H2'	78:A6:4705:A:H8	1.74	0.53
19:B2:1539:U:H4'	30:AT:47:PRO:HA	1.90	0.53
59:CF:76:ARG:HH12	78:A5:727:C:H5''	1.74	0.53
66:Cj:52:LYS:HE2	66:Cj:55:ARG:HH12	1.74	0.53
78:A5:1411:C:H2'	78:A5:1412:G:H8	1.73	0.53
78:A6:3917:A:H2'	78:A6:3918:G:H8	1.73	0.53
5:AB:181:LEU:HA	5:AB:184:VAL:HG12	1.91	0.52
9:Aa:108:PRO:HB2	32:Ac:31:ARG:HH22	1.74	0.52
22:Ag:206:LEU:HB3	22:Ag:218:LEU:HD11	1.90	0.52
33:AD:172:VAL:CG1	33:AD:174:HIS:HE1	2.22	0.52
40:CV:107:ASN:HB3	40:CV:113:LYS:HE2	1.92	0.52
41:CM:40:GLY:HA3	41:CM:45:VAL:HB	1.90	0.52
52:CX:60:TYR:HE1	78:A5:16:G:H5''	1.75	0.52
52:CX:77:ILE:HA	52:CX:100:VAL:HG12	1.91	0.52
67:Ck:33:LYS:HG2	67:Ck:46:VAL:HG12	1.91	0.52
75:CH:86:LEU:HD21	75:CH:189:GLN:H	1.73	0.52
77:CG:110:LYS:HA	77:CG:113:ARG:HE	1.74	0.52
78:A5:1306:C:H2'	78:A5:1307:A:H8	1.73	0.52
78:A6:4630:G:H2'	78:A6:4631:G:H8	1.73	0.52
9:Aa:85:ARG:H	19:B2:1866:A:H61	1.57	0.52
12:AJ:24:ARG:O	12:AJ:28:GLU:HB3	2.10	0.52
13:AE:128:LYS:HG2	13:AE:140:VAL:HG12	1.91	0.52
13:AE:151:ASP:HB3	15:AG:216:ARG:HH12	1.74	0.52
38:CO:76:PRO:HA	38:CO:79:ILE:HG12	1.90	0.52
43:CN:13:LYS:HE2	65:CI:45:ARG:HH12	1.73	0.52
60:Cc:11:LEU:H	60:Cc:12:GLU:HG3	1.75	0.52
77:CG:56:LYS:HB2	78:A6:4085:A:H2'	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:CG:180:PRO:HG3	77:CG:223:ARG:HH22	1.75	0.52
38:CO:81:TRP:HB2	38:CO:104:VAL:HG11	1.92	0.52
43:CN:54:LYS:HB3	78:A5:152:U:H5''	1.91	0.52
73:Co:33:LEU:HD12	73:Co:34:TYR:H	1.73	0.52
76:CE:264:ILE:HD12	76:CE:265:PRO:HD2	1.90	0.52
78:A5:1971:C:H2'	78:A5:1972:G:H8	1.74	0.52
78:A6:4492:U:H5''	78:A6:4493:U:H5'	1.91	0.52
78:A6:4745:G:N2	78:A6:4955:A:C5	2.75	0.52
15:AG:6:SER:HB3	15:AG:112:VAL:HG12	1.90	0.52
18:AI:81:VAL:HB	18:AI:94:LYS:HA	1.91	0.52
20:CR:44:LEU:HD22	20:CR:49:LEU:HD11	1.91	0.52
60:Cc:27:TYR:HE1	60:Cc:29:LEU:HG	1.73	0.52
77:CG:137:ARG:HG3	77:CG:146:LEU:HD21	1.91	0.52
78:A5:440:U:H2'	78:A5:441:G:H8	1.75	0.52
78:A6:2711:G:H5''	78:A6:2712:G:H5'	1.91	0.52
1:AO:103:ASN:HB2	1:AO:142:ARG:HB3	1.90	0.52
14:AC:226:ALA:HB1	14:AC:230:THR:HG21	1.91	0.52
22:Ag:238:ALA:HB3	22:Ag:251:ALA:HB3	1.91	0.52
26:AS:130:ARG:HG2	26:AS:134:GLN:HB2	1.91	0.52
67:Ck:23:VAL:HG22	67:Ck:36:VAL:HG12	1.90	0.52
75:CH:114:ILE:HB	75:CH:124:ARG:HB2	1.90	0.52
78:A6:3695:U:H3	78:A6:3820:G:H1	1.58	0.52
78:A6:4972:U:O2	78:A6:4986:G:N2	2.32	0.52
39:CL:62:PRO:HG3	78:A5:74:G:H1'	1.91	0.52
64:Cg:112:GLN:HA	64:Cg:115:LYS:HD2	1.92	0.52
77:CG:69:ILE:HD11	78:A6:4162:C:H1'	1.91	0.52
78:A6:4407:G:H1	78:A6:4435:U:H3	1.56	0.52
8:AY:44:LEU:HA	8:AY:47:MET:HB3	1.91	0.52
12:AJ:149:VAL:HG11	12:AJ:157:ILE:HD11	1.91	0.52
15:AG:135:PRO:HG2	15:AG:144:LEU:HD22	1.91	0.52
19:B2:876:C:H2'	19:B2:878:G:H5'	1.92	0.52
19:B2:1044:G:C6	47:CA:248:GLY:N	2.78	0.52
59:CF:48:LYS:HE2	76:CE:59:ARG:HD2	1.91	0.52
59:CF:220:MET:HG2	59:CF:231:GLY:HA3	1.90	0.52
81:BC:1:A:H2'	81:BC:2:G:H8	1.74	0.52
78:A6:4272:G:C6	78:A6:4336:A:N1	2.77	0.52
3:AN:47:PRO:HG3	3:AN:75:LEU:HD12	1.92	0.52
13:AE:65:CYS:HA	13:AE:70:ILE:HD12	1.90	0.52
19:B2:1402:A:N6	19:B2:1441:U:C2	2.78	0.52
37:Cz:110:PHE:HB3	37:Cz:135:PRO:HB3	1.91	0.52
53:CY:80:ILE:HD13	53:CY:101:PRO:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:CZ:96:VAL:HG23	54:CZ:100:VAL:HG11	1.91	0.52
71:Cn:18:ARG:HA	71:Cn:21:ARG:HB2	1.92	0.52
78:A5:1361:G:H2'	78:A5:1362:G:C8	2.44	0.52
6:AA:85:ARG:HG3	6:AA:89:LYS:HE3	1.91	0.52
14:AC:108:LYS:HG2	14:AC:110:MET:HE3	1.92	0.52
19:B2:943:U:H2'	19:B2:944:A:H8	1.75	0.52
19:B2:1650:A:H5''	36:AQ:139:ALA:HB2	1.92	0.52
24:AK:80:ARG:HD3	24:AK:85:LEU:HB2	1.92	0.52
30:AT:5:THR:HG23	30:AT:7:LYS:H	1.74	0.52
47:CA:20:VAL:HA	47:CA:23:ARG:HG3	1.91	0.52
50:CP:69:ARG:HA	50:CP:80:GLN:HA	1.92	0.52
58:CB:266:VAL:HG13	58:CB:268:ARG:HD3	1.92	0.52
60:Cc:55:LEU:HD21	64:Cg:89:ASP:HB2	1.92	0.52
78:A5:33:A:H5''	78:A5:47:A:H61	1.74	0.52
78:A5:713:C:H2'	78:A5:714:G:C8	2.45	0.52
78:A5:958:G:H1	78:A5:1285:U:H5'	1.74	0.52
19:B2:88:G:H21	19:B2:500:A:H5'	1.74	0.52
19:B2:1207:G:C4'	19:B2:1834:A:N1	2.73	0.52
35:AF:40:ALA:HB1	35:AF:45:TYR:HB2	1.92	0.52
35:AF:63:LYS:HB3	35:AF:71:ARG:HH21	1.75	0.52
42:Ca:19:HIS:HB3	42:Ca:25:HIS:HB2	1.92	0.52
78:A6:4088:C:H2'	78:A6:4089:G:H8	1.74	0.52
78:A6:4992:G:H2'	78:A6:4993:G:H8	1.73	0.52
19:B2:28:U:H2'	19:B2:29:G:H8	1.75	0.51
19:B2:1616:U:H3	19:B2:1620:A:H2	1.58	0.51
25:AM:33:ARG:HG3	25:AM:91:LEU:HD21	1.91	0.51
38:CO:200:GLY:HA2	38:CO:203:VAL:HG12	1.92	0.51
41:CM:46:ARG:HD3	78:A5:938:C:H5'	1.91	0.51
48:CS:16:CYS:HA	48:CS:59:GLY:HA2	1.91	0.51
78:A5:1621:A:H5''	78:A6:2451:A:H5'	1.92	0.51
1:AO:19:PRO:HB2	5:AB:46:LYS:HZ1	1.75	0.51
9:Aa:4:LYS:HG2	9:Aa:5:ARG:HG3	1.93	0.51
11:Ae:34:ARG:HH21	19:B2:642:U:H5	1.58	0.51
19:B2:957:A:H3'	19:B2:958:G:H21	1.75	0.51
26:AS:137:LYS:HG3	26:AS:138:THR:HG23	1.91	0.51
28:AR:78:ARG:HG2	28:AR:79:GLU:HG2	1.92	0.51
30:AT:71:GLY:O	30:AT:75:MET:HB2	2.10	0.51
35:AF:78:MET:HE2	35:AF:152:TRP:HZ3	1.74	0.51
46:CQ:12:LYS:HD2	78:A5:2082:G:H5''	1.91	0.51
51:CU:65:ARG:HG2	51:CU:67:LYS:H	1.75	0.51
67:Ck:7:GLU:HG3	67:Ck:9:LYS:HG3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A5:225:G:H21	78:A5:242:U:H3	1.58	0.51
78:A6:2520:C:H2'	78:A6:2521:G:H8	1.75	0.51
22:Ag:99:ARG:HD3	22:Ag:135:LEU:HA	1.92	0.51
78:A5:1775:A:H3'	78:A5:1776:A:H8	1.75	0.51
78:A6:2677:G:H3'	78:A6:2678:A:H8	1.74	0.51
1:AO:30:VAL:HG12	1:AO:94:HIS:HB2	1.93	0.51
5:AB:163:GLN:HB3	5:AB:204:ILE:HD13	1.92	0.51
5:AB:165:ARG:HA	5:AB:168:MET:HG2	1.93	0.51
19:B2:1337:C:H2'	19:B2:1338:G:H8	1.75	0.51
19:B2:1834:A:N1	19:B2:1837:G:N2	2.58	0.51
22:Ag:164:ILE:HG21	22:Ag:221:LEU:HD11	1.91	0.51
26:AS:17:ASN:HD21	26:AS:100:ALA:HB1	1.75	0.51
31:AZ:54:THR:HA	31:AZ:57:LYS:HG2	1.93	0.51
65:Ci:29:ARG:HH21	65:Ci:32:ARG:HA	1.76	0.51
66:Cj:10:LYS:HB2	78:A5:1535:C:H5''	1.91	0.51
69:CC:152:LEU:HD23	69:CC:251:ILE:HG13	1.91	0.51
78:A6:3701:C:H4'	78:A6:3702:A:H5'	1.93	0.51
78:A6:4523:A:H5''	78:A6:4524:G:H5'	1.92	0.51
11:Ae:42:PHE:HE2	12:AJ:29:LEU:HB3	1.75	0.51
19:B2:920:A:H62	19:B2:1021:U:H3	1.57	0.51
65:Ci:35:LYS:HA	65:Ci:38:LYS:HB2	1.91	0.51
78:A5:323:C:H2'	78:A5:324:A:H8	1.75	0.51
78:A6:3861:A:H2'	78:A6:3862:A:H8	1.75	0.51
3:AN:70:LYS:HG3	3:AN:73:ARG:HB2	1.92	0.51
7:AV:17:CYS:HB2	7:AV:22:ARG:H	1.75	0.51
9:Aa:88:SER:HA	19:B2:1692:U:H5'	1.92	0.51
17:AW:40:VAL:HG11	17:AW:103:VAL:HG21	1.92	0.51
19:B2:1144:A:H5'	19:B2:1356:G:H1	1.76	0.51
19:B2:1609:C:H2'	19:B2:1610:G:H8	1.74	0.51
49:CT:108:ARG:O	49:CT:112:ASN:HB2	2.09	0.51
59:CF:133:LEU:HA	59:CF:136:VAL:HG12	1.93	0.51
78:A5:1593:A:H5''	78:A6:2839:U:H5''	1.93	0.51
78:A6:4237:C:H2'	78:A6:4238:G:C8	2.45	0.51
78:A6:4765:G:O6	78:A6:4869:U:O4	2.29	0.51
19:B2:116:U:O4	19:B2:347:G:O6	2.28	0.51
44:CI:115:MET:HB3	44:CI:118:ALA:HB2	1.93	0.51
49:CT:159:MET:H	49:CT:159:MET:HE2	1.74	0.51
55:Cr:49:VAL:HG11	55:Cr:103:ARG:HE	1.75	0.51
60:Cc:47:ILE:HG23	60:Cc:94:LEU:HB2	1.93	0.51
5:AB:144:LYS:HD2	5:AB:208:HIS:HB3	1.91	0.51
19:B2:373:G:H2'	19:B2:374:G:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:AF:161:ALA:O	35:AF:165:ASN:HB3	2.11	0.51
42:Ca:32:ARG:HG3	78:A5:37:U:H5''	1.92	0.51
46:CQ:67:ILE:HD12	46:CQ:96:PRO:HD2	1.93	0.51
47:CA:29:LEU:H	47:CA:123:ARG:HB3	1.75	0.51
52:CX:78:LYS:HB3	56:Ch:32:ARG:HH12	1.74	0.51
59:CF:236:ARG:HB2	59:CF:239:GLN:HB2	1.91	0.51
74:CJ:15:LEU:HD11	74:CJ:157:ILE:HD13	1.93	0.51
78:A6:4993:G:O6	78:A6:5058:A:N1	2.44	0.51
19:B2:1244:U:H2'	19:B2:1245:G:H8	1.76	0.51
38:CO:119:VAL:HG11	48:CS:171:ARG:HD3	1.92	0.51
50:CP:71:ALA:HB1	78:A6:4970:C:H5''	1.93	0.51
77:CG:164:ILE:O	77:CG:168:VAL:HB	2.11	0.51
78:A6:4764:A:H61	78:A6:4870:G:H1	1.48	0.51
13:AE:68:ARG:HH21	13:AE:76:VAL:HG22	1.76	0.51
19:B2:934:G:H1	19:B2:1008:A:H2	1.53	0.51
19:B2:1010:G:H2'	19:B2:1011:A:H8	1.76	0.51
19:B2:1324:G:O6	19:B2:1504:U:O4	2.29	0.51
24:AK:80:ARG:HD2	24:AK:87:PRO:HA	1.92	0.51
33:AD:172:VAL:HG12	33:AD:174:HIS:CE1	2.45	0.51
41:CM:12:VAL:HA	41:CM:26:ALA:HA	1.93	0.51
64:Cg:95:PHE:HA	64:Cg:98:GLU:HG2	1.92	0.51
69:CC:218:ILE:O	69:CC:222:ARG:HB3	2.11	0.51
70:Cm:114:LYS:HE2	78:A6:4485:C:H4'	1.92	0.51
78:A6:2295:C:H2'	78:A6:2296:G:H8	1.75	0.51
78:A6:4064:C:H2'	78:A6:4065:G:H8	1.76	0.51
19:B2:106:C:H2'	19:B2:107:A:H8	1.75	0.50
36:AQ:42:ILE:HD13	36:AQ:48:GLN:HG2	1.93	0.50
41:CM:111:LYS:HD2	76:CE:266:GLN:HG3	1.93	0.50
53:CY:59:ARG:HD2	78:A5:209:U:H5''	1.92	0.50
55:Cr:113:ARG:HH21	62:Ce:90:MET:HG2	1.76	0.50
63:Cf:19:ARG:HB2	78:A5:1311:G:H5'	1.93	0.50
65:Ci:44:ILE:HA	65:Ci:47:VAL:HG22	1.92	0.50
78:A5:1996:C:N4	78:A5:2000:G:H22	2.07	0.50
8:AY:114:MET:HE1	8:AY:125:VAL:HG12	1.92	0.50
15:AG:181:THR:HG23	15:AG:183:ARG:H	1.76	0.50
19:B2:600:G:H2'	19:B2:601:G:H8	1.76	0.50
48:CS:120:ARG:HH22	78:A5:2060:G:H5''	1.77	0.50
42:Ca:101:ILE:HB	78:A5:509:A:H62	1.76	0.50
45:CD:83:LEU:HB3	45:CD:88:VAL:HB	1.93	0.50
46:CQ:49:LYS:HA	46:CQ:52:PHE:HB2	1.92	0.50
75:CH:171:ASP:HB3	75:CH:174:LYS:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A6:2662:G:H2'	78:A6:2663:G:C8	2.47	0.50
18:AI:175:ILE:HA	18:AI:187:GLY:HA3	1.93	0.50
20:CR:6:LEU:HD22	78:A6:2412:A:H5''	1.94	0.50
28:AR:71:ILE:HG22	28:AR:73:LEU:H	1.76	0.50
40:CV:62:MET:HE2	78:A6:4508:C:H5'	1.93	0.50
61:CD:41:ARG:HD3	61:CD:78:ARG:HA	1.94	0.50
68:CI:22:PRO:HG3	78:A6:2431:A:H5''	1.93	0.50
77:CG:69:ILE:O	77:CG:73:ARG:HB2	2.11	0.50
78:A5:1420:A:H4'	78:A5:1421:G:H5'	1.92	0.50
6:AA:41:ARG:HH21	6:AA:45:GLY:H	1.59	0.50
36:AQ:42:ILE:HG22	36:AQ:44:PRO:HD2	1.93	0.50
69:CC:96:CYS:HA	78:A6:2352:U:H1'	1.94	0.50
69:CC:182:LYS:HE3	69:CC:204:ARG:HG2	1.93	0.50
78:A5:735:G:N3	78:A5:929:A:C6	2.78	0.50
78:A6:4601:U:H2'	78:A6:4602:A:H8	1.76	0.50
1:AO:38:ASN:HA	1:AO:69:SER:HB2	1.94	0.50
6:AA:59:LEU:HD11	7:AV:78:ILE:HD11	1.94	0.50
13:AE:31:PRO:HG3	13:AE:43:PRO:HG3	1.93	0.50
18:AI:83:TYR:HB2	18:AI:202:ILE:HD11	1.94	0.50
19:B2:5:U:H2'	19:B2:6:G:H8	1.76	0.50
19:B2:1538:C:H4'	30:AT:45:LEU:HD21	1.93	0.50
22:Ag:255:SER:HB3	22:Ag:271:LYS:HG3	1.94	0.50
27:Ad:50:ILE:HG23	27:Ad:52:PHE:H	1.76	0.50
35:AF:134:VAL:HB	81:BC:32:C:H4'	1.93	0.50
58:CB:12:GLY:HA3	58:CB:235:TRP:HE3	1.76	0.50
69:CC:274:LYS:HD2	78:A5:1375:C:H5''	1.94	0.50
72:Cp:5:THR:HB	72:Cp:8:VAL:HG12	1.94	0.50
78:A5:1726:U:O4	78:A5:1836:G:O6	2.29	0.50
78:A5:1939:A:H5'	78:A5:1940:G:H4'	1.93	0.50
78:A6:2749:C:H2'	78:A6:2750:G:C8	2.47	0.50
15:AG:189:ARG:HD2	19:B2:331:C:H2'	1.93	0.50
24:AK:1:MET:HG2	24:AK:2:LEU:HD23	1.93	0.50
24:AK:30:PRO:HA	24:AK:41:PRO:HB3	1.92	0.50
38:CO:15:LEU:HB2	38:CO:18:ARG:HB2	1.92	0.50
51:CU:19:LEU:HB2	51:CU:74:SER:HB3	1.93	0.50
75:CH:104:VAL:HG21	75:CH:115:ARG:HH11	1.77	0.50
75:CH:111:LEU:HD23	75:CH:127:ARG:HE	1.75	0.50
78:A6:4867:G:H2'	78:A6:4868:G:H8	1.76	0.50
22:Ag:79:LEU:HG	22:Ag:89:LEU:HD13	1.93	0.50
33:AD:164:VAL:HA	33:AD:168:VAL:HB	1.93	0.50
58:CB:43:LEU:HB2	58:CB:210:VAL:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:CF:223:LYS:HD3	78:A5:1907:A:H4'	1.94	0.50
3:AN:17:PRO:HB2	3:AN:19:ARG:HG2	1.94	0.50
13:AE:198:ARG:HE	13:AE:222:LEU:HD21	1.76	0.50
17:AW:102:ILE:HD12	17:AW:125:ILE:HD11	1.93	0.50
26:AS:12:ILE:HD13	74:CJ:121:PRO:HG3	1.93	0.50
30:AT:6:VAL:HG11	30:AT:131:LEU:HB3	1.93	0.50
39:CL:116:ARG:HH21	39:CL:155:MET:HE2	1.76	0.50
69:CC:284:MET:HE2	69:CC:287:THR:HA	1.94	0.50
78:A6:2330:G:H2'	78:A6:2331:G:C4	2.47	0.50
78:A6:3946:G:O6	78:A6:4067:U:O4	2.30	0.50
31:AZ:67:LEU:HD11	35:AF:103:LEU:HB2	1.94	0.49
57:Cb:58:GLN:HA	57:Cb:61:ASN:HB3	1.94	0.49
78:A5:161:G:H2'	78:A5:162:A:H8	1.76	0.49
78:A6:4730:C:H1'	78:A6:4731:G:H2'	1.94	0.49
78:A6:4877:G:H5''	78:A6:4878:C:H5	1.76	0.49
14:AC:265:PRO:HA	14:AC:268:GLU:HG2	1.93	0.49
30:AT:124:THR:HG23	30:AT:127:GLY:H	1.77	0.49
34:Af:95:ARG:HG3	34:Af:97:LYS:H	1.77	0.49
39:CL:63:THR:HG23	39:CL:65:ARG:H	1.78	0.49
44:CI:36:LEU:HD11	44:CI:69:ARG:HH11	1.77	0.49
45:CD:83:LEU:HD21	45:CD:100:CYS:HB2	1.94	0.49
47:CA:71:LYS:HB2	78:A6:2595:C:H5''	1.94	0.49
47:CA:253:GLN:HB3	47:CA:255:LYS:HD3	1.94	0.49
58:CB:110:ILE:HG21	58:CB:115:LYS:HE2	1.94	0.49
80:A8:55:U:H3	80:A8:62:A:H2	1.60	0.49
78:A6:2749:C:H2'	78:A6:2750:G:H8	1.77	0.49
78:A6:4178:A:H2'	78:A6:4179:G:H8	1.77	0.49
1:AO:117:ARG:HH22	9:Aa:48:ALA:HB3	1.77	0.49
47:CA:51:ASP:HB3	47:CA:54:ARG:HB3	1.95	0.49
47:CA:57:PRO:HG2	47:CA:78:ALA:HB3	1.93	0.49
48:CS:8:ARG:HB3	48:CS:66:GLN:HE22	1.76	0.49
55:Cr:14:SER:HA	69:CC:139:SER:HB2	1.94	0.49
69:CC:128:LEU:HD13	69:CC:260:LEU:HD21	1.93	0.49
69:CC:306:ARG:HD3	69:CC:306:ARG:H	1.77	0.49
78:A5:717:U:O4	78:A5:951:G:O6	2.30	0.49
78:A5:1845:U:H2'	78:A5:1846:G:H8	1.77	0.49
78:A5:1911:C:H1'	78:A5:1917:A:H2'	1.93	0.49
78:A6:2386:U:H2'	78:A6:2387:G:H8	1.77	0.49
78:A6:4755:G:H2'	78:A6:4875:G:H21	1.77	0.49
7:AV:21:ASN:HB3	17:AW:67:GLY:HA3	1.94	0.49
13:AE:147:ILE:HD13	13:AE:167:GLY:HA3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1221:G:H2'	19:B2:1222:G:H8	1.78	0.49
53:CY:30:MET:HE1	53:CY:78:TYR:HA	1.94	0.49
69:CC:342:ARG:HA	69:CC:345:ARG:HE	1.77	0.49
78:A6:2283:G:H2'	78:A6:2284:G:C8	2.47	0.49
78:A6:3855:C:H2'	78:A6:3856:A:H8	1.77	0.49
78:A6:3930:U:H3	78:A6:4180:G:H1	1.60	0.49
9:Aa:88:SER:HB2	19:B2:1691:U:H4'	1.95	0.49
16:AH:95:ILE:HD11	16:AH:129:ILE:HG23	1.94	0.49
19:B2:604:A:H2'	19:B2:605:A:C4	2.47	0.49
24:AK:5:LYS:HZ3	24:AK:8:ARG:HH22	1.60	0.49
41:CM:35:ARG:HA	41:CM:51:PRO:HA	1.95	0.49
47:CA:21:LYS:HE3	78:A6:2743:A:H1'	1.95	0.49
52:CX:76:ILE:HG21	52:CX:109:ILE:HG12	1.95	0.49
55:Cr:84:LYS:HZ1	55:Cr:96:MET:HE2	1.77	0.49
78:A5:735:G:C2	78:A5:929:A:C6	3.01	0.49
78:A5:1047:C:H2'	78:A5:1048:G:H8	1.77	0.49
78:A5:1361:G:H2'	78:A5:1362:G:H8	1.77	0.49
78:A6:4594:U:H2'	78:A6:4595:G:H8	1.77	0.49
5:AB:171:ILE:HA	5:AB:174:ARG:HH12	1.76	0.49
19:B2:1183:A:H2'	19:B2:1184:G:H8	1.76	0.49
25:AM:85:LEU:HD23	25:AM:107:SER:H	1.78	0.49
70:Cm:86:ALA:HB2	75:CH:95:VAL:HG21	1.93	0.49
78:A6:4725:C:H2'	78:A6:4726:G:H8	1.77	0.49
7:AV:67:ASP:HA	7:AV:70:LEU:HB2	1.95	0.49
19:B2:512:A:H5''	19:B2:577:U:H3	1.77	0.49
19:B2:1549:U:O4	19:B2:1584:G:O6	2.30	0.49
45:CD:29:ASP:O	45:CD:33:ARG:HB2	2.13	0.49
46:CQ:184:ARG:HB2	78:A6:4340:U:H5''	1.94	0.49
50:CP:90:PHE:HA	50:CP:93:HIS:CE1	2.47	0.49
52:CX:99:ILE:HG23	52:CX:133:GLU:HG3	1.95	0.49
69:CC:22:VAL:HG11	69:CC:257:PHE:HD2	1.77	0.49
10:Ab:62:VAL:HG12	10:Ab:74:THR:HG21	1.95	0.49
13:AE:48:LEU:HA	13:AE:52:LEU:HB2	1.95	0.49
19:B2:155:G:H2'	19:B2:156:G:H8	1.78	0.49
28:AR:42:PRO:HD2	28:AR:46:LEU:HD23	1.94	0.49
76:CE:218:LYS:HB2	76:CE:220:LYS:HD2	1.95	0.49
78:A5:1523:A:N7	78:A5:1652:U:O2	2.45	0.49
78:A6:3870:C:H2'	78:A6:3871:A:H8	1.78	0.49
6:AA:7:VAL:HG11	7:AV:43:THR:HG23	1.93	0.49
8:AY:10:ARG:HH11	19:B2:833:C:H41	1.59	0.49
14:AC:130:ILE:HG12	14:AC:158:ALA:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AU:21:ARG:HB2	23:AU:115:THR:HG23	1.94	0.49
48:CS:77:ASN:HB2	48:CS:132:ILE:HB	1.95	0.49
78:A5:1533:A:H5''	78:A5:1637:A:H62	1.78	0.49
78:A6:2745:A:H2'	78:A6:2746:A:H8	1.77	0.49
78:A6:4172:A:H3'	78:A6:4173:G:H8	1.77	0.49
9:Aa:24:THR:HG21	9:Aa:71:LEU:HB2	1.93	0.49
22:Ag:24:THR:HG22	22:Ag:26:GLN:H	1.78	0.49
45:CD:272:SER:HB3	45:CD:275:GLN:HB2	1.94	0.49
47:CA:21:LYS:HG2	78:A5:1541:C:H5''	1.94	0.49
75:CH:48:LEU:HD13	75:CH:56:ARG:HD3	1.95	0.49
16:AH:75:ILE:HD12	16:AH:76:GLN:H	1.78	0.48
19:B2:746:C:H2'	19:B2:747:U:H6	1.77	0.48
23:AU:26:SER:HB2	23:AU:32:LEU:HB2	1.93	0.48
26:AS:20:ILE:HG22	26:AS:32:ALA:HB3	1.95	0.48
30:AT:7:LYS:HG2	36:AQ:37:ARG:HG2	1.94	0.48
32:Ac:12:ALA:HB1	32:Ac:32:VAL:HB	1.94	0.48
62:Ce:127:ALA:HB1	78:A6:2326:G:H5''	1.94	0.48
78:A5:1759:G:O6	78:A5:1773:U:O4	2.31	0.48
2:AX:52:LEU:HD23	2:AX:71:ARG:HG3	1.96	0.48
8:AY:57:VAL:HG12	8:AY:73:GLY:HA2	1.94	0.48
19:B2:639:C:H2'	19:B2:640:A:H8	1.77	0.48
19:B2:924:G:N2	19:B2:1018:U:O2	2.39	0.48
19:B2:1499:U:H4'	33:AD:176:LEU:HD11	1.95	0.48
19:B2:1845:A:H2'	19:B2:1846:G:C8	2.48	0.48
20:CR:172:ARG:HA	20:CR:175:GLU:HG3	1.94	0.48
22:Ag:173:LEU:HD12	22:Ag:189:ILE:HA	1.94	0.48
14:AC:65:LYS:HA	14:AC:68:ARG:HD2	1.95	0.48
14:AC:114:LYS:HD2	19:B2:1203:G:H1'	1.96	0.48
15:AG:76:LEU:HD21	15:AG:92:ARG:HD3	1.95	0.48
19:B2:690:G:H22	19:B2:740:C:H42	1.61	0.48
30:AT:34:VAL:H	30:AT:37:VAL:HG22	1.78	0.48
55:Cr:8:MET:HE3	55:Cr:8:MET:HB3	1.76	0.48
62:Ce:4:LEU:HD11	78:A5:703:G:H4'	1.95	0.48
78:A5:440:U:H2'	78:A5:441:G:C8	2.48	0.48
78:A5:964:A:H5'	78:A5:965:G:H3'	1.94	0.48
6:AA:10:MET:HG3	6:AA:12:GLU:HG2	1.94	0.48
23:AU:51:LYS:HG2	23:AU:90:ASP:HB2	1.94	0.48
29:AP:79:HIS:HA	29:AP:97:TYR:HB2	1.95	0.48
43:CN:179:LYS:HB3	78:A5:298:G:H5'	1.95	0.48
49:CT:115:LYS:HZ1	49:CT:127:GLN:HB3	1.77	0.48
54:CZ:42:LEU:HA	54:CZ:74:VAL:HA	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:CB:240:LEU:HB3	58:CB:244:THR:HG21	1.95	0.48
70:Cm:78:ILE:HG22	70:Cm:83:ARG:HB2	1.94	0.48
74:CJ:15:LEU:HD23	74:CJ:165:TRP:HB2	1.95	0.48
78:A5:741:C:H42	78:A5:923:C:H42	1.61	0.48
3:AN:23:PRO:HB3	3:AN:25:TRP:CE2	2.48	0.48
9:Aa:45:VAL:HG11	9:Aa:53:ILE:HG12	1.95	0.48
16:AH:80:VAL:HG22	16:AH:92:VAL:HG13	1.95	0.48
19:B2:1044:G:N1	47:CA:248:GLY:N	2.61	0.48
19:B2:1705:C:H2'	19:B2:1706:G:C8	2.48	0.48
44:CI:48:LEU:HB2	44:CI:142:LEU:HD22	1.94	0.48
59:CF:170:THR:HG22	69:CC:315:LYS:HB3	1.95	0.48
78:A5:146:G:H2'	78:A5:147:A:H8	1.78	0.48
78:A5:724:C:H2'	78:A5:725:G:H8	1.79	0.48
81:BC:54:U:C2	81:BC:57:A:N7	2.82	0.48
78:A6:2723:U:H2'	78:A6:2724:G:C8	2.49	0.48
78:A6:4699:U:H1'	78:A6:4700:A:H5''	1.95	0.48
19:B2:1392:U:H5'	23:AU:83:ARG:HH22	1.79	0.48
22:Ag:34:ALA:HB2	22:Ag:69:VAL:HG13	1.96	0.48
35:AF:136:ARG:HH11	35:AF:203:ASN:HD21	1.62	0.48
66:Cj:46:LYS:HD2	66:Cj:54:LYS:HD3	1.95	0.48
67:Ck:34:PHE:HE1	67:Ck:47:ILE:HD11	1.78	0.48
78:A5:1350:C:H2'	78:A5:1351:G:H8	1.79	0.48
8:AY:21:LYS:HB2	8:AY:75:ILE:HB	1.95	0.48
8:AY:63:HIS:HE1	8:AY:70:THR:HG23	1.78	0.48
12:AJ:136:ARG:HE	12:AJ:161:LEU:H	1.61	0.48
15:AG:131:ARG:HG2	21:CW:80:ARG:HD3	1.96	0.48
23:AU:22:ILE:HG22	23:AU:114:VAL:HG22	1.94	0.48
25:AM:22:LEU:HD22	25:AM:89:VAL:HG22	1.96	0.48
38:CO:84:VAL:HG11	38:CO:102:LEU:HG	1.95	0.48
76:CE:179:LEU:HB3	78:A6:4936:G:H22	1.78	0.48
78:A5:1492:G:H2'	78:A5:1493:G:H8	1.79	0.48
78:A6:3848:U:H2'	78:A6:3849:A:C8	2.48	0.48
16:AH:142:LYS:HE3	17:AW:54:ASP:HB3	1.95	0.48
38:CO:195:VAL:HG11	41:CM:119:ARG:HB2	1.95	0.48
44:CI:50:GLY:HA3	44:CI:148:VAL:HG11	1.96	0.48
47:CA:35:ALA:HA	77:CG:41:ILE:HD11	1.96	0.48
47:CA:250:LYS:HE3	47:CA:252:VAL:HG13	1.96	0.48
51:CU:28:PRO:HB3	51:CU:100:LEU:HD11	1.95	0.48
55:Cr:128:ARG:HH22	62:Ce:113:GLU:HB2	1.78	0.48
58:CB:154:LYS:HG2	58:CB:194:LEU:HD12	1.95	0.48
64:Cg:28:ASN:HD21	78:A6:2698:G:H21	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:CC:218:ILE:HG22	69:CC:222:ARG:HD2	1.95	0.48
78:A5:681:G:H2'	78:A5:682:G:H8	1.78	0.48
16:AH:52:GLU:HG3	16:AH:58:LYS:HE2	1.95	0.48
16:AH:83:LEU:HA	16:AH:86:LYS:HB2	1.95	0.48
32:Ac:63:ARG:HH22	35:AF:138:ALA:HB3	1.79	0.48
42:Ca:75:LEU:HA	42:Ca:78:LEU:HB2	1.95	0.48
45:CD:33:ARG:HH11	45:CD:37:VAL:HG21	1.78	0.48
51:CU:56:LEU:HD13	51:CU:61:VAL:HG23	1.96	0.48
54:CZ:100:VAL:HG13	54:CZ:101:PHE:HD1	1.78	0.48
56:Ch:70:ARG:HB3	56:Ch:83:LEU:HD22	1.94	0.48
60:Cc:11:LEU:N	60:Cc:12:GLU:HG3	2.29	0.48
77:CG:184:ILE:HD11	77:CG:190:LEU:HD21	1.96	0.48
78:A5:1557:C:H2'	78:A5:1558:A:C8	2.49	0.48
78:A5:1994:C:H2'	78:A5:1995:G:H8	1.79	0.48
78:A6:2845:A:H61	78:A6:3843:C:H42	1.61	0.48
78:A6:4892:A:H2	78:A6:4927:G:H1	1.62	0.48
12:AJ:111:GLN:HE21	12:AJ:123:ILE:HG22	1.78	0.48
15:AG:140:ARG:HG3	15:AG:143:LYS:HE2	1.95	0.48
15:AG:159:ARG:HH22	15:AG:161:PRO:HA	1.78	0.48
15:AG:162:LEU:HB3	15:AG:170:ARG:HB2	1.94	0.48
17:AW:24:GLN:HA	17:AW:63:VAL:O	2.14	0.48
18:AI:78:ILE:H	18:AI:78:ILE:HG13	1.49	0.48
36:AQ:17:LYS:HE2	36:AQ:17:LYS:HB3	1.63	0.48
38:CO:75:ALA:HB3	38:CO:78:ARG:HG2	1.95	0.48
41:CM:100:ARG:HA	41:CM:103:LYS:HG2	1.96	0.48
63:Cf:52:LYS:HE3	78:A6:4749:C:H1'	1.96	0.48
76:CE:283:PRO:HA	76:CE:286:LEU:HB2	1.95	0.48
77:CG:82:GLN:HA	77:CG:233:ILE:HD11	1.96	0.48
78:A5:1211:G:H2'	78:A5:1212:G:H8	1.78	0.48
19:B2:1608:U:H3	19:B2:1631:U:H3	1.61	0.47
35:AF:112:LEU:HD13	35:AF:177:LEU:HD21	1.95	0.47
46:CQ:53:MET:HE2	78:A5:1692:C:H5''	1.94	0.47
54:CZ:42:LEU:HB2	54:CZ:74:VAL:HG22	1.95	0.47
59:CF:57:TYR:HE1	59:CF:189:ASP:HA	1.79	0.47
76:CE:206:VAL:HG22	76:CE:209:PRO:HD3	1.96	0.47
77:CG:83:PHE:HZ	77:CG:168:VAL:HA	1.78	0.47
78:A5:1094:G:H2'	78:A5:1095:A:H8	1.79	0.47
78:A6:2312:U:O2	78:A6:2326:G:O6	2.32	0.47
14:AC:253:PRO:HA	17:AW:68:ARG:HH21	1.78	0.47
19:B2:873:G:H2'	19:B2:874:G:H8	1.78	0.47
19:B2:883:U:H3	19:B2:903:A:H62	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1834:A:N1	19:B2:1837:G:C2	2.82	0.47
37:Cz:105:LYS:HB3	78:A6:4041:C:H5''	1.95	0.47
56:Ch:28:LEU:HD23	56:Ch:50:VAL:HG13	1.96	0.47
77:CG:83:PHE:HB3	77:CG:159:HIS:HB2	1.95	0.47
1:AO:119:LEU:HB2	1:AO:124:MET:HB2	1.97	0.47
17:AW:68:ARG:HA	17:AW:68:ARG:HD2	1.70	0.47
22:Ag:188:HIS:HB3	22:Ag:219:TRP:CZ2	2.50	0.47
30:AT:76:THR:HB	30:AT:95:GLY:H	1.79	0.47
37:Cz:150:GLU:HA	37:Cz:154:THR:HB	1.96	0.47
39:CL:56:ARG:HB2	39:CL:72:ALA:HB1	1.95	0.47
39:CL:58:ILE:HG12	39:CL:116:ARG:HD2	1.96	0.47
44:CI:86:HIS:HB3	44:CI:139:ARG:HG3	1.96	0.47
56:Ch:46:LYS:O	56:Ch:50:VAL:HG12	2.15	0.47
74:CJ:151:ILE:HB	74:CJ:156:ARG:HG3	1.97	0.47
80:A8:15:G:H4'	78:A6:2355:G:H4'	1.96	0.47
15:AG:3:LEU:O	15:AG:15:LEU:HA	2.14	0.47
21:CW:6:CYS:HB2	21:CW:10:GLY:H	1.78	0.47
38:CO:195:VAL:HG22	41:CM:118:MET:HE1	1.95	0.47
51:CU:38:ASN:HA	51:CU:41:GLN:HG3	1.96	0.47
55:Cr:75:THR:HA	55:Cr:76:SER:HA	1.56	0.47
78:A5:181:C:H2'	78:A5:182:G:C8	2.49	0.47
78:A6:2521:G:H5'	78:A6:2640:G:H1'	1.97	0.47
6:AA:15:VAL:HG11	28:AR:109:LEU:HD11	1.97	0.47
19:B2:494:C:H41	19:B2:509:G:H21	1.60	0.47
35:AF:14:THR:HG23	35:AF:15:PRO:HD3	1.97	0.47
46:CQ:61:LEU:HD21	46:CQ:139:LEU:HD22	1.97	0.47
54:CZ:76:ASN:O	54:CZ:80:LEU:CB	2.61	0.47
59:CF:64:MET:HE1	59:CF:196:THR:HG22	1.97	0.47
75:CH:52:LYS:HG3	75:CH:53:LYS:HB3	1.96	0.47
78:A6:2604:C:H2'	78:A6:2605:G:H8	1.80	0.47
4:AL:77:VAL:HG12	4:AL:88:ILE:HG22	1.96	0.47
8:AY:114:MET:HA	8:AY:124:ASN:HD22	1.80	0.47
13:AE:48:LEU:HB2	13:AE:54:TYR:HD2	1.78	0.47
38:CO:182:GLU:HA	38:CO:185:VAL:HG22	1.95	0.47
45:CD:67:ALA:HB1	49:CT:31:MET:HE2	1.97	0.47
48:CS:68:PHE:HE1	78:A5:731:G:H1'	1.79	0.47
49:CT:61:THR:HG21	78:A5:1799:G:H21	1.78	0.47
63:Cf:4:ARG:HG2	76:CE:277:LEU:HB2	1.96	0.47
69:CC:346:ASN:HA	69:CC:349:LEU:HD13	1.97	0.47
78:A5:1557:C:H2'	78:A5:1558:A:H8	1.80	0.47
78:A6:2272:C:H2'	78:A6:2273:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A6:4088:C:H2'	78:A6:4089:G:C8	2.49	0.47
1:AO:26:ASN:HD21	1:AO:91:THR:HB	1.80	0.47
1:AO:33:ILE:HA	1:AO:41:PHE:O	2.14	0.47
6:AA:81:ASN:HA	6:AA:84:GLN:HB2	1.96	0.47
7:AV:53:TYR:HB3	7:AV:72:LEU:HD13	1.96	0.47
12:AJ:85:GLY:HA3	12:AJ:108:ARG:HE	1.79	0.47
15:AG:3:LEU:HB3	15:AG:111:LEU:HD21	1.97	0.47
19:B2:5:U:H2'	19:B2:6:G:C8	2.49	0.47
19:B2:1655:C:H2'	19:B2:1656:G:H8	1.79	0.47
20:CR:42:ARG:HD3	20:CR:46:LYS:HB3	1.96	0.47
21:CW:13:ILE:HD11	21:CW:18:GLY:HA3	1.97	0.47
22:Ag:67:SER:HB3	22:Ag:83:TRP:HE1	1.79	0.47
37:Cz:15:ARG:HD2	37:Cz:180:VAL:HG21	1.97	0.47
37:Cz:120:ILE:HG13	37:Cz:121:PRO:HD3	1.97	0.47
37:Cz:212:LYS:HE3	37:Cz:212:LYS:HB3	1.74	0.47
42:Ca:118:PRO:HG3	46:CQ:93:GLN:HG3	1.97	0.47
42:Ca:131:ARG:HH12	78:A5:1489:G:H4'	1.78	0.47
45:CD:22:ARG:HD3	79:A7:7:G:H5''	1.97	0.47
47:CA:64:ARG:HH12	77:CG:43:GLN:HA	1.80	0.47
58:CB:317:LEU:HB3	78:A6:5001:U:H4'	1.96	0.47
69:CC:218:ILE:HA	69:CC:229:LEU:HD13	1.96	0.47
73:Co:45:GLN:HE22	73:Co:51:GLN:HA	1.79	0.47
76:CE:98:GLY:HA2	76:CE:99:ASP:HA	1.62	0.47
77:CG:209:SER:HA	77:CG:212:LYS:HG3	1.96	0.47
77:CG:222:ILE:HA	77:CG:225:ASN:HB3	1.96	0.47
78:A5:318:A:H2'	78:A5:319:A:C8	2.49	0.47
78:A6:3865:A:N6	78:A6:3881:G:H1	2.11	0.47
78:A6:4274:A:H2'	78:A6:4275:G:C8	2.50	0.47
3:AN:50:ILE:O	3:AN:54:LEU:HB2	2.15	0.47
16:AH:91:HIS:HB3	16:AH:169:LYS:HE2	1.96	0.47
18:AI:98:LYS:HB3	19:B2:377:G:H5''	1.95	0.47
19:B2:873:G:H2'	19:B2:874:G:C8	2.50	0.47
19:B2:1096:G:O6	19:B2:1136:U:O4	2.33	0.47
19:B2:1207:G:H5'	19:B2:1834:A:N1	2.30	0.47
20:CR:20:LYS:HE3	20:CR:20:LYS:HB3	1.73	0.47
33:AD:46:THR:HB	33:AD:84:VAL:HG12	1.95	0.47
49:CT:48:VAL:HG11	49:CT:94:GLU:HG3	1.96	0.47
78:A5:1494:U:H2'	78:A5:1495:G:C8	2.50	0.47
78:A6:4650:G:H4'	78:A6:5008:C:H4'	1.96	0.47
1:AO:128:ARG:HH21	5:AB:72:ALA:HB3	1.79	0.47
3:AN:88:LEU:O	3:AN:92:ILE:HD12	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AB:111:CYS:HB3	9:Aa:68:TYR:HB2	1.96	0.47
21:CW:47:ARG:HA	21:CW:55:TYR:CE1	2.48	0.47
41:CM:37:LEU:HD23	48:CS:100:LEU:HD21	1.96	0.47
43:CN:35:ALA:HA	43:CN:65:ARG:HG2	1.97	0.47
43:CN:67:ARG:HG2	78:A6:2458:C:H5'	1.96	0.47
45:CD:21:ARG:HG3	45:CD:22:ARG:HG3	1.96	0.47
45:CD:132:VAL:HG21	45:CD:170:GLY:HA2	1.97	0.47
58:CB:20:LYS:HB3	78:A6:4567:G:H5'	1.96	0.47
58:CB:26:ARG:HH22	78:A6:4580:U:H5''	1.80	0.47
58:CB:240:LEU:HD11	58:CB:252:ALA:HB2	1.95	0.47
58:CB:292:LEU:HG	58:CB:299:ILE:HD11	1.96	0.47
78:A5:161:G:H2'	78:A5:162:A:C8	2.50	0.47
18:AI:66:SER:H	18:AI:188:TYR:HA	1.80	0.47
19:B2:894:G:H2'	19:B2:895:G:H8	1.80	0.47
19:B2:1551:U:C4	19:B2:1577:G:C6	3.03	0.47
39:CL:116:ARG:HE	39:CL:116:ARG:HB2	1.57	0.47
54:CZ:53:VAL:HG21	54:CZ:62:ILE:HG23	1.97	0.47
55:Cr:96:MET:O	55:Cr:99:LYS:HG2	2.14	0.47
78:A6:3927:U:H2'	78:A6:3928:A:H8	1.79	0.47
78:A6:4474:A:H2'	78:A6:4476:C:H5''	1.96	0.47
78:A6:4704:C:H2'	78:A6:4705:A:C8	2.49	0.47
19:B2:240:G:H2'	19:B2:241:G:C8	2.50	0.46
28:AR:111:PHE:HD1	28:AR:112:GLY:H	1.62	0.46
29:AP:75:VAL:HG13	29:AP:93:MET:HE1	1.98	0.46
38:CO:120:VAL:HG12	38:CO:122:ALA:H	1.79	0.46
51:CU:43:LEU:HD13	51:CU:86:LEU:HD12	1.97	0.46
56:Ch:9:LEU:HB2	56:Ch:17:LEU:HD11	1.98	0.46
65:Ci:44:ILE:O	65:Ci:48:CYS:HB3	2.15	0.46
70:Cm:103:LEU:HD21	70:Cm:111:ARG:H	1.79	0.46
78:A5:43:U:H3'	78:A5:44:A:H8	1.80	0.46
78:A5:1933:G:H2'	78:A5:1934:A:C8	2.50	0.46
78:A6:2295:C:H2'	78:A6:2296:G:C8	2.50	0.46
78:A6:4274:A:H2'	78:A6:4275:G:H8	1.80	0.46
78:A6:4764:A:N6	78:A6:4870:G:N1	2.54	0.46
4:AL:86:ILE:HG13	4:AL:113:LEU:HD22	1.98	0.46
12:AJ:91:LYS:HE3	12:AJ:96:TYR:HB3	1.96	0.46
19:B2:691:G:H2'	19:B2:692:G:H8	1.80	0.46
26:AS:25:LYS:O	26:AS:29:ALA:CB	2.63	0.46
38:CO:33:VAL:HG13	38:CO:102:LEU:HD23	1.98	0.46
45:CD:282:GLN:HE22	78:A5:1177:U:H1'	1.80	0.46
46:CQ:147:GLU:HA	46:CQ:150:ARG:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:CY:35:SER:O	53:CY:39:ARG:CB	2.63	0.46
78:A5:436:C:H2'	78:A5:437:G:H8	1.80	0.46
78:A5:1474:C:H2'	78:A5:1475:G:C8	2.49	0.46
1:AO:53:ILE:HD12	1:AO:90:ILE:HG21	1.98	0.46
19:B2:1844:U:H2'	19:B2:1845:A:C8	2.50	0.46
22:Ag:174:VAL:HB	22:Ag:188:HIS:HB2	1.97	0.46
22:Ag:236:ILE:HG12	22:Ag:252:THR:HG22	1.96	0.46
47:CA:27:ALA:HB1	47:CA:77:ILE:HG12	1.97	0.46
58:CB:161:ARG:HB3	58:CB:182:GLU:HB3	1.96	0.46
76:CE:156:ARG:HD2	78:A6:4938:A:H4'	1.97	0.46
77:CG:75:LYS:HE3	78:A6:3940:U:H4'	1.96	0.46
78:A5:148:C:H2'	78:A5:149:A:H8	1.80	0.46
78:A5:1105:C:H2'	78:A5:1106:A:C8	2.50	0.46
78:A6:4736:C:H2'	78:A6:4737:G:H8	1.81	0.46
13:AE:31:PRO:HA	13:AE:81:THR:HB	1.96	0.46
17:AW:18:GLU:HG2	17:AW:69:LEU:HB3	1.97	0.46
19:B2:1384:C:H5''	33:AD:158:ILE:HG22	1.96	0.46
22:Ag:217:MET:HB3	22:Ag:229:THR:HA	1.97	0.46
39:CL:179:PHE:HA	39:CL:182:LEU:HB2	1.97	0.46
43:CN:24:ARG:HD3	43:CN:24:ARG:HA	1.65	0.46
45:CD:10:LYS:HE3	79:A7:66:G:H5'	1.98	0.46
50:CP:41:ILE:HD12	50:CP:112:LEU:HD23	1.96	0.46
78:A5:1101:C:H41	78:A5:1167:C:H1'	1.80	0.46
12:AJ:12:THR:HG23	12:AJ:45:ARG:HG2	1.97	0.46
19:B2:1845:A:H2'	19:B2:1846:G:H8	1.81	0.46
28:AR:102:THR:HA	28:AR:105:MET:HB3	1.97	0.46
33:AD:50:ILE:HG23	33:AD:88:ALA:HA	1.98	0.46
35:AF:115:ALA:O	35:AF:119:SER:HB3	2.16	0.46
38:CO:85:ARG:HB3	38:CO:99:LEU:HD21	1.98	0.46
45:CD:277:LYS:HD3	45:CD:277:LYS:HA	1.75	0.46
47:CA:48:ILE:HG22	72:Cp:54:ILE:HG13	1.97	0.46
52:CX:150:ALA:HB1	52:CX:155:ILE:HG13	1.98	0.46
60:Cc:82:GLY:HA2	60:Cc:91:VAL:HG22	1.98	0.46
61:Cd:22:THR:HA	61:Cd:89:SER:HA	1.96	0.46
78:A5:1918:U:O2	78:A5:2064:G:O6	2.32	0.46
78:A6:4992:G:H2'	78:A6:4993:G:C8	2.50	0.46
2:AX:59:ALA:HB1	2:AX:114:ASP:HB2	1.96	0.46
13:AE:34:GLY:HA3	13:AE:83:PRO:HG2	1.98	0.46
19:B2:900:C:H2'	19:B2:901:G:H8	1.81	0.46
19:B2:1010:G:H2'	19:B2:1011:A:C8	2.50	0.46
19:B2:1419:C:H2'	19:B2:1420:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1475:G:H21	19:B2:1476:A:H1'	1.81	0.46
19:B2:1545:A:H2	19:B2:1671:G:H1'	1.81	0.46
19:B2:1609:C:H2'	19:B2:1610:G:C8	2.50	0.46
19:B2:1786:U:H2'	19:B2:1787:G:H8	1.80	0.46
43:CN:51:LEU:HD12	43:CN:119:TYR:HD2	1.79	0.46
47:CA:189:TYR:HA	47:CA:192:LYS:HG3	1.96	0.46
55:Cr:72:LYS:HD3	55:Cr:72:LYS:HA	1.59	0.46
60:Cc:55:LEU:HD23	64:Cg:93:ARG:HD3	1.97	0.46
78:A5:1360:G:H2'	78:A5:1361:G:C8	2.50	0.46
78:A6:2386:U:H2'	78:A6:2387:G:C8	2.50	0.46
78:A6:3648:A:H1'	78:A6:3785:A:H61	1.79	0.46
5:AB:56:LYS:HE3	5:AB:56:LYS:HB3	1.81	0.46
10:Ab:7:LEU:HA	10:Ab:10:PRO:HG3	1.97	0.46
10:Ab:56:CYS:HB2	10:Ab:63:LEU:HD23	1.98	0.46
14:AC:203:GLY:O	14:AC:221:ASP:HA	2.16	0.46
19:B2:1757:G:O6	19:B2:1775:U:O4	2.33	0.46
48:CS:23:HIS:HA	48:CS:24:THR:HA	1.76	0.46
56:Ch:32:ARG:HG2	56:Ch:47:ILE:HD12	1.98	0.46
76:CE:70:LYS:HD2	78:A5:1071:C:H2'	1.97	0.46
77:CG:72:LYS:HE3	77:CG:73:ARG:HH21	1.81	0.46
78:A5:1523:A:N7	78:A5:1652:U:C2	2.84	0.46
81:BC:55:C:H1'	78:A6:4046:A:H1'	1.98	0.46
78:A6:2375:A:H2'	78:A6:2376:A:H8	1.81	0.46
6:AA:63:ARG:NH2	7:AV:36:VAL:HA	2.30	0.46
8:AY:16:ARG:HA	8:AY:19:GLN:HA	1.97	0.46
13:AE:59:ASP:HA	13:AE:62:LYS:HG2	1.97	0.46
16:AH:99:ARG:HD3	16:AH:101:LEU:HG	1.98	0.46
19:B2:1228:A:H2'	19:B2:1229:G:H8	1.79	0.46
19:B2:1593:C:H2'	19:B2:1594:A:C8	2.51	0.46
44:CI:54:SER:HB3	44:CI:135:ILE:HD11	1.97	0.46
66:Cj:87:LYS:HD3	66:Cj:87:LYS:HA	1.70	0.46
72:Cp:18:TYR:HD1	78:A6:3635:A:H61	1.63	0.46
73:Co:17:LYS:HD2	73:Co:17:LYS:HA	1.77	0.46
74:CJ:85:LYS:HG3	74:CJ:115:LEU:HD12	1.98	0.46
76:CE:79:LYS:H	76:CE:79:LYS:HG2	1.49	0.46
76:CE:279:ASN:H	78:A6:4753:U:H5	1.63	0.46
79:A7:15:C:H2'	79:A7:16:A:H8	1.80	0.46
78:A6:4764:A:N1	78:A6:4870:G:N2	2.64	0.46
3:AN:30:SER:HB3	3:AN:67:THR:HG22	1.98	0.46
19:B2:1004:U:H2'	19:B2:1005:G:H8	1.81	0.46
21:CW:110:ARG:HD3	21:CW:113:LYS:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:CM:41:PRO:HB3	41:CM:70:GLN:HE22	1.81	0.46
46:CQ:39:THR:HG23	69:CC:302:LEU:HD12	1.96	0.46
58:CB:39:LYS:HE2	58:CB:39:LYS:HB2	1.82	0.46
71:Cn:14:LYS:HA	71:Cn:17:ARG:HG2	1.98	0.46
78:A5:975:C:H42	78:A5:1279:A:H61	1.64	0.46
78:A5:1193:C:H2'	78:A5:1194:G:H8	1.81	0.46
78:A6:2362:U:H2'	78:A6:2363:A:H8	1.81	0.46
78:A6:4584:A:H62	78:A6:4718:G:H21	1.63	0.46
6:AA:155:ARG:HH22	19:B2:1137:U:H4'	1.81	0.46
19:B2:610:G:H2'	19:B2:611:G:H8	1.80	0.46
22:Ag:77:PHE:HB3	22:Ag:89:LEU:HD11	1.98	0.46
32:Ac:32:VAL:HG23	32:Ac:42:ILE:HG13	1.98	0.46
42:Ca:94:LYS:HA	42:Ca:95:THR:HA	1.74	0.46
43:CN:50:ARG:HB2	78:A5:278:G:H21	1.80	0.46
46:CQ:69:LYS:HA	46:CQ:72:LEU:HD12	1.96	0.46
51:CU:26:THR:HA	51:CU:29:VAL:HG22	1.98	0.46
69:CC:44:LEU:HA	69:CC:47:ASN:HD22	1.81	0.46
78:A5:1276:C:H2'	78:A5:1277:G:C8	2.51	0.46
78:A5:1538:U:H2'	78:A5:1539:G:H8	1.81	0.46
78:A6:2769:U:O2	78:A6:2770:C:N3	2.49	0.46
4:AL:128:VAL:HG12	4:AL:142:VAL:HA	1.98	0.45
8:AY:89:HIS:HB3	19:B2:574:A:H4'	1.98	0.45
18:AI:148:LYS:HD2	18:AI:152:ARG:HH12	1.81	0.45
19:B2:909:G:H5'	20:CR:172:ARG:HD3	1.97	0.45
19:B2:1348:G:H2'	19:B2:1349:G:H8	1.81	0.45
39:CL:144:LEU:HD21	39:CL:150:LEU:H	1.80	0.45
43:CN:39:ALA:HB3	43:CN:61:ILE:HG22	1.98	0.45
45:CD:95:TYR:HA	45:CD:158:LYS:HG3	1.96	0.45
47:CA:96:LEU:HD13	47:CA:107:MET:HB2	1.97	0.45
49:CT:34:TYR:HE2	49:CT:93:ILE:HG23	1.81	0.45
50:CP:86:LYS:HA	50:CP:89:GLU:HB3	1.98	0.45
51:CU:60:VAL:HG13	51:CU:61:VAL:HG22	1.98	0.45
56:Ch:78:TYR:HB2	56:Ch:84:ARG:HH21	1.80	0.45
69:CC:242:PRO:HB2	78:A6:2297:G:H4'	1.96	0.45
73:Co:80:LYS:HE2	78:A6:4346:U:H5''	1.97	0.45
77:CG:87:LEU:HD23	77:CG:87:LEU:HA	1.81	0.45
78:A6:3731:C:H2'	78:A6:3732:A:H8	1.81	0.45
1:AO:60:MET:HB3	1:AO:61:LYS:HG3	1.98	0.45
19:B2:106:C:H2'	19:B2:107:A:C8	2.50	0.45
19:B2:1351:G:O6	19:B2:1360:U:O4	2.34	0.45
25:AM:48:HIS:HB2	25:AM:113:ASP:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AP:61:ARG:HH12	29:AP:64:LYS:HG3	1.81	0.45
31:AZ:48:VAL:HB	31:AZ:83:LEU:HD13	1.97	0.45
37:Cz:33:GLU:HB2	37:Cz:207:LYS:HB2	1.98	0.45
38:CO:94:ARG:HD2	63:Cf:97:ILE:HG21	1.98	0.45
61:Cd:28:ASN:HA	61:Cd:83:ARG:HD3	1.97	0.45
75:CH:2:LYS:HG3	75:CH:61:TRP:HD1	1.80	0.45
78:A5:2016:C:H2'	78:A5:2017:A:H8	1.79	0.45
15:AG:140:ARG:HA	15:AG:143:LYS:HG2	1.97	0.45
19:B2:382:C:H2'	19:B2:383:G:C8	2.51	0.45
45:CD:263:LYS:HD2	45:CD:263:LYS:HA	1.81	0.45
47:CA:80:GLU:HG3	47:CA:168:VAL:HG23	1.99	0.45
78:A5:1350:C:H2'	78:A5:1351:G:C8	2.51	0.45
78:A6:2654:C:H2'	78:A6:2655:C:H6	1.80	0.45
1:AO:63:LYS:HE2	1:AO:63:LYS:HB2	1.66	0.45
5:AB:129:THR:HB	5:AB:180:ASP:HA	1.98	0.45
19:B2:1455:A:H2'	19:B2:1456:G:H8	1.80	0.45
22:Ag:290:ALA:HB3	22:Ag:299:PHE:HD2	1.81	0.45
78:A5:429:A:H2'	78:A5:430:G:C8	2.52	0.45
78:A5:1327:C:H2'	78:A5:1328:G:C8	2.51	0.45
78:A6:4537:C:H2'	78:A6:4538:G:H8	1.80	0.45
8:AY:108:LYS:HD3	19:B2:53:C:H4'	1.98	0.45
18:AI:126:GLY:HA2	18:AI:129:LEU:HB3	1.98	0.45
19:B2:1337:C:H2'	19:B2:1338:G:C8	2.51	0.45
37:Cz:130:LYS:HD2	37:Cz:130:LYS:HA	1.78	0.45
37:Cz:148:VAL:HA	37:Cz:151:VAL:HG22	1.98	0.45
42:Ca:116:LYS:HA	42:Ca:116:LYS:HD2	1.76	0.45
44:CI:114:GLY:HA2	78:A6:4441:A:H5''	1.99	0.45
50:CP:124:LYS:HE2	50:CP:142:SER:HB3	1.99	0.45
64:Cg:53:LEU:HD22	64:Cg:83:CYS:HB3	1.99	0.45
68:Cl:38:ASN:HB3	68:Cl:41:ARG:HG2	1.97	0.45
78:A5:35:U:H4'	78:A5:1525:A:H2	1.80	0.45
78:A5:1402:C:H2'	78:A5:1403:G:H8	1.82	0.45
78:A5:1509:C:H2'	78:A5:1510:G:H8	1.80	0.45
78:A6:2485:U:H2'	78:A6:2486:G:C8	2.51	0.45
78:A6:2770:C:H2'	78:A6:2771:G:H8	1.81	0.45
78:A6:4563:U:H2'	78:A6:4564:A:H8	1.80	0.45
78:A6:4642:U:H2'	78:A6:4643:G:H8	1.81	0.45
1:AO:80:ASP:HA	1:AO:83:GLN:HG2	1.99	0.45
19:B2:1228:A:H2'	19:B2:1229:G:C8	2.52	0.45
19:B2:1239:U:H3	19:B2:1242:U:H5''	1.80	0.45
19:B2:1362:U:H5''	19:B2:1363:C:H5	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Ag:21:ILE:HG12	22:Ag:288:SER:HB2	1.99	0.45
25:AM:15:ASN:HA	25:AM:18:LEU:HD23	1.98	0.45
41:CM:3:PHE:HE2	41:CM:5:ARG:HE	1.65	0.45
43:CN:84:PRO:HB2	73:Co:49:GLY:HA2	1.99	0.45
44:CI:170:LYS:HA	44:CI:177:ASN:HA	1.98	0.45
45:CD:64:ILE:HG13	45:CD:109:LEU:HD13	1.99	0.45
47:CA:244:GLY:HA3	78:A6:3746:A:H5'	1.98	0.45
61:Cd:46:LEU:HA	61:Cd:49:ILE:HD12	1.99	0.45
75:CH:86:LEU:HD22	75:CH:187:VAL:H	1.81	0.45
78:A6:4186:A:H2'	78:A6:4187:G:C8	2.52	0.45
7:AV:65:SER:O	7:AV:69:ILE:HG12	2.17	0.45
8:AY:41:ARG:HE	8:AY:57:VAL:HG22	1.81	0.45
12:AJ:53:ILE:HD11	12:AJ:81:LEU:HD11	1.97	0.45
19:B2:844:U:H2'	19:B2:845:G:H8	1.82	0.45
19:B2:1101:U:H2'	19:B2:1102:G:H8	1.82	0.45
19:B2:1112:U:O4	19:B2:1121:G:O6	2.34	0.45
19:B2:1419:C:H2'	19:B2:1420:G:C8	2.52	0.45
19:B2:1605:G:H1'	19:B2:1634:A:H61	1.81	0.45
20:CR:120:TYR:HB3	78:A6:2664:G:C8	2.52	0.45
22:Ag:121:VAL:HG21	22:Ag:165:ILE:HD13	1.98	0.45
35:AF:28:VAL:H	35:AF:42:LYS:HE2	1.82	0.45
43:CN:140:LYS:HA	43:CN:143:ARG:HB2	1.99	0.45
46:CQ:91:ARG:HH22	78:A5:1502:G:H5'	1.82	0.45
48:CS:127:MET:HE1	49:CT:155:PRO:HA	1.98	0.45
58:CB:312:LYS:HD3	58:CB:370:THR:HG21	1.98	0.45
60:Cc:28:VAL:HG11	60:Cc:37:MET:HG3	1.99	0.45
69:CC:95:MET:HB2	78:A5:1335:G:N2	2.32	0.45
73:Co:89:LYS:HE2	78:A6:4229:U:H4'	1.98	0.45
78:A5:750:U:O4	78:A5:912:G:O6	2.34	0.45
78:A5:928:C:H2'	78:A5:929:A:C8	2.52	0.45
78:A6:4268:A:H61	78:A6:4281:A:H62	1.65	0.45
19:B2:1285:G:H5'	25:AM:35:ILE:HD13	1.99	0.45
25:AM:42:LEU:HB3	25:AM:68:LEU:HD22	1.99	0.45
36:AQ:50:LYS:HA	36:AQ:53:GLU:HG3	1.99	0.45
43:CN:75:VAL:HG21	43:CN:89:VAL:HG11	1.97	0.45
49:CT:111:GLU:O	49:CT:115:LYS:HB2	2.17	0.45
52:CX:103:LYS:HD3	52:CX:103:LYS:HA	1.80	0.45
54:CZ:72:VAL:HG11	54:CZ:96:VAL:HG21	1.99	0.45
55:Cr:58:LYS:HD3	55:Cr:58:LYS:HA	1.81	0.45
58:CB:99:LEU:HD12	78:A6:4582:C:H4'	1.97	0.45
68:Cl:42:ARG:HG3	68:Cl:47:THR:HB	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:CG:185:LYS:HG3	80:A8:153:C:H4'	1.98	0.45
78:A5:287:U:H2'	78:A5:288:G:C8	2.51	0.45
78:A5:318:A:H2'	78:A5:319:A:H8	1.81	0.45
78:A5:1758:G:H2'	78:A5:1759:G:H8	1.81	0.45
3:AN:47:PRO:HG2	3:AN:72:LEU:HD13	1.99	0.45
13:AE:168:LYS:HD3	13:AE:168:LYS:HA	1.77	0.45
13:AE:197:ASN:HB3	13:AE:209:HIS:HB2	1.99	0.45
19:B2:1609:C:H5''	26:AS:131:VAL:HB	1.97	0.45
19:B2:1756:C:H2'	19:B2:1757:G:C8	2.49	0.45
26:AS:24:ARG:HB3	26:AS:29:ALA:HB2	1.98	0.45
39:CL:129:ARG:HB2	56:Ch:117:ARG:HE	1.81	0.45
41:CM:20:HIS:HB3	41:CM:23:LYS:HD2	1.99	0.45
43:CN:72:LYS:HE2	78:A6:3670:C:H4'	1.99	0.45
47:CA:125:LYS:HB3	78:A6:3681:G:C6	2.52	0.45
48:CS:140:PRO:HA	48:CS:143:LYS:HB3	1.99	0.45
49:CT:111:GLU:HA	49:CT:114:GLN:HG3	1.99	0.45
59:CF:89:LEU:HD22	59:CF:195:TYR:HA	1.98	0.45
74:CJ:108:GLY:HA3	78:A6:4251:A:H5''	1.99	0.45
75:CH:75:SER:HA	75:CH:78:GLN:HG3	1.98	0.45
78:A6:4210:U:H3	78:A6:4222:G:H1	1.63	0.45
1:AO:80:ASP:H	32:Ac:5:ARG:NH2	2.14	0.45
7:AV:31:SER:HB2	7:AV:56:CYS:HA	1.98	0.45
16:AH:61:ILE:HA	16:AH:93:VAL:O	2.16	0.45
18:AI:19:LYS:HD3	19:B2:101:U:H5''	1.99	0.45
19:B2:28:U:H2'	19:B2:29:G:C8	2.50	0.45
19:B2:1095:C:O2	19:B2:1149:A:N6	2.44	0.45
19:B2:1207:G:H5''	19:B2:1834:A:N3	2.32	0.45
41:CM:56:GLN:HA	48:CS:157:ARG:HH12	1.81	0.45
43:CN:22:LEU:HA	43:CN:22:LEU:HD23	1.74	0.45
45:CD:62:CYS:HB3	45:CD:105:LEU:HG	1.99	0.45
59:CF:93:ILE:O	59:CF:140:ILE:HA	2.17	0.45
65:CI:80:HIS:CE1	65:CI:84:LYS:CE	3.00	0.45
66:Cj:64:MET:HB3	66:Cj:68:LYS:HG3	1.99	0.45
69:CC:171:LEU:HD23	69:CC:171:LEU:HA	1.84	0.45
78:A5:181:C:H2'	78:A5:182:G:H8	1.82	0.45
78:A6:2539:C:H2'	78:A6:2540:C:C6	2.52	0.45
78:A6:2922:G:H5''	78:A6:2923:A:H5'	1.99	0.45
78:A6:4765:G:N1	78:A6:4869:U:N3	2.43	0.45
15:AG:131:ARG:HH12	19:B2:167:G:H21	1.65	0.44
16:AH:8:ILE:H	16:AH:8:ILE:HG13	1.59	0.44
16:AH:137:SER:HB2	16:AH:159:ASP:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Ag:70:VAL:HG13	22:Ag:79:LEU:HB2	1.98	0.44
33:AD:25:LEU:HA	33:AD:28:GLU:HB3	1.98	0.44
38:CO:88:LEU:HD11	38:CO:99:LEU:HG	1.99	0.44
47:CA:107:MET:HG3	47:CA:111:THR:HG21	1.99	0.44
64:Cg:87:VAL:HA	64:Cg:90:ARG:HB3	1.99	0.44
66:Cj:70:VAL:HG21	80:A8:35:C:H4'	1.99	0.44
69:CC:32:ILE:HD12	69:CC:130:ALA:HB2	1.98	0.44
77:CG:78:PRO:HG3	77:CG:237:TRP:HA	1.99	0.44
2:AX:137:LYS:H	2:AX:137:LYS:HG3	1.58	0.44
3:AN:16:LEU:HD11	3:AN:62:GLN:HE21	1.82	0.44
6:AA:186:ARG:HD2	7:AV:46:PHE:HB3	1.99	0.44
7:AV:26:ALA:HB1	14:AC:82:TYR:HB2	1.99	0.44
14:AC:196:ILE:HB	14:AC:223:TYR:HB2	1.98	0.44
15:AG:5:ILE:HA	15:AG:111:LEU:O	2.17	0.44
17:AW:26:LEU:HD21	17:AW:60:LYS:HD3	1.99	0.44
35:AF:115:ALA:O	35:AF:119:SER:CB	2.65	0.44
37:Cz:157:PHE:HD2	37:Cz:165:LEU:HD11	1.82	0.44
39:CL:128:PRO:HG3	39:CL:136:LYS:HD2	1.99	0.44
43:CN:6:TYR:O	43:CN:10:LEU:HB2	2.17	0.44
47:CA:41:ILE:HG12	47:CA:63:PHE:HD2	1.81	0.44
48:CS:35:PRO:HD2	48:CS:39:VAL:HG11	1.99	0.44
67:Ck:39:SER:HB2	78:A6:2773:G:H5''	1.99	0.44
68:Cl:5:LYS:HB2	68:Cl:9:ILE:HD11	1.98	0.44
76:CE:77:LYS:HA	76:CE:77:LYS:HD2	1.78	0.44
78:A5:709:C:H2'	78:A5:710:G:C8	2.52	0.44
78:A5:1598:C:H2'	78:A5:1599:A:H8	1.83	0.44
78:A5:1836:G:H2'	78:A5:1837:A:H8	1.82	0.44
78:A6:2283:G:H2'	78:A6:2284:G:H8	1.82	0.44
1:AO:33:ILE:HD12	1:AO:42:VAL:HG22	1.99	0.44
6:AA:174:MET:HE2	6:AA:174:MET:HB2	1.76	0.44
15:AG:180:VAL:HG11	19:B2:142:C:H1'	1.98	0.44
19:B2:375:U:H2'	19:B2:376:A:C8	2.52	0.44
19:B2:549:C:C4	19:B2:550:C:N4	2.86	0.44
19:B2:554:A:H2'	19:B2:555:A:C8	2.53	0.44
19:B2:1317:C:H2'	19:B2:1318:G:H8	1.81	0.44
36:AQ:76:GLY:H	36:AQ:79:ALA:HB3	1.82	0.44
37:Cz:60:ARG:HH22	37:Cz:173:LYS:HB2	1.82	0.44
59:CF:187:MET:O	59:CF:191:ILE:HG13	2.18	0.44
60:Cc:56:ARG:O	60:Cc:60:ILE:HG12	2.17	0.44
63:Cf:29:LYS:HB2	63:Cf:83:MET:HG2	1.98	0.44
68:Cl:40:LYS:HD2	78:A5:366:A:H5'	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A5:246:G:H2'	78:A5:247:G:H8	1.83	0.44
78:A6:2662:G:H2'	78:A6:2663:G:H8	1.83	0.44
3:AN:26:LEU:HD21	3:AN:28:LEU:HD22	2.00	0.44
6:AA:203:PHE:HB3	6:AA:204:TYR:H	1.52	0.44
12:AJ:87:LEU:HD22	12:AJ:91:LYS:HE2	1.98	0.44
14:AC:127:PHE:HD1	14:AC:141:VAL:HG22	1.81	0.44
19:B2:1808:U:H2'	19:B2:1809:A:C8	2.52	0.44
35:AF:20:PHE:HB3	35:AF:23:TRP:HD1	1.83	0.44
37:Cz:59:PRO:HD2	37:Cz:153:SER:HA	2.00	0.44
38:CO:180:GLN:HG3	41:CM:130:LEU:HD11	2.00	0.44
42:Ca:56:VAL:HG12	46:CQ:184:ARG:HD2	1.98	0.44
50:CP:39:MET:HE2	50:CP:43:LYS:HE3	1.99	0.44
76:CE:109:LEU:H	76:CE:114:ARG:HH21	1.65	0.44
80:A8:119:C:H2'	80:A8:120:G:H8	1.83	0.44
78:A6:2272:C:H2'	78:A6:2273:G:C8	2.53	0.44
78:A6:3927:U:H2'	78:A6:3928:A:C8	2.52	0.44
78:A6:4178:A:H2'	78:A6:4179:G:C8	2.53	0.44
78:A6:4519:C:H5''	78:A6:4520:G:H5''	2.00	0.44
13:AE:42:LEU:HB2	13:AE:109:PHE:CE2	2.52	0.44
13:AE:60:GLU:HA	13:AE:63:LYS:HE3	2.00	0.44
20:CR:67:THR:HG21	78:A6:2615:C:H4'	1.99	0.44
39:CL:93:THR:HG21	56:Ch:114:TYR:HB2	1.98	0.44
46:CQ:4:ASP:HB3	59:CF:98:ILE:HG23	2.00	0.44
48:CS:113:MET:HE2	48:CS:113:MET:HB3	1.81	0.44
58:CB:159:VAL:HG13	58:CB:184:GLN:HE22	1.83	0.44
62:Ce:28:TYR:HB2	62:Ce:31:ILE:HG12	2.00	0.44
65:Ci:45:ARG:HE	65:Ci:50:PHE:HE1	1.64	0.44
73:Co:23:VAL:HG12	73:Co:93:LEU:HD21	1.98	0.44
74:CJ:47:THR:HG23	79:A7:39:C:H4'	1.98	0.44
76:CE:124:LYS:HG3	76:CE:126:LEU:HB2	1.98	0.44
78:A6:3932:U:H2'	78:A6:3933:G:C8	2.53	0.44
78:A6:4537:C:H2'	78:A6:4538:G:C8	2.52	0.44
78:A6:4896:G:H2'	78:A6:4897:G:C8	2.53	0.44
3:AN:73:ARG:HD3	19:B2:916:A:C4	2.53	0.44
8:AY:13:MET:HB3	8:AY:22:GLN:HB2	1.98	0.44
9:Aa:21:ILE:O	9:Aa:29:CYS:HA	2.17	0.44
13:AE:122:LYS:HG2	13:AE:162:ILE:HD11	1.98	0.44
14:AC:183:LYS:HE2	17:AW:95:PRO:HA	2.00	0.44
15:AG:27:PHE:HE1	15:AG:36:VAL:HB	1.83	0.44
18:AI:120:PRO:HB2	18:AI:121:LEU:H	1.57	0.44
19:B2:454:U:H2'	19:B2:455:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1098:C:H2'	19:B2:1099:G:C8	2.53	0.44
19:B2:1731:A:H2'	19:B2:1732:G:C8	2.52	0.44
20:CR:38:ARG:HE	52:CX:88:LYS:HD2	1.83	0.44
24:AK:59:LYS:HG3	24:AK:70:TYR:HB3	1.99	0.44
49:CT:87:LYS:HE3	49:CT:87:LYS:HB3	1.83	0.44
54:CZ:36:ARG:HB3	54:CZ:38:TYR:CZ	2.52	0.44
54:CZ:106:LEU:HA	54:CZ:109:LYS:HB2	2.00	0.44
55:Cr:34:ALA:HB2	62:Ce:90:MET:HB2	2.00	0.44
58:CB:272:LYS:HE3	58:CB:272:LYS:HB2	1.86	0.44
62:Ce:106:LYS:HA	62:Ce:109:LYS:HG2	2.00	0.44
69:CC:33:ARG:HA	69:CC:33:ARG:HD2	1.77	0.44
72:Cp:62:LYS:HE2	72:Cp:62:LYS:HB2	1.76	0.44
78:A5:300:A:H2'	78:A5:301:G:C8	2.50	0.44
78:A5:464:G:H2'	78:A5:465:G:C8	2.53	0.44
78:A5:506:C:H2'	78:A5:507:G:H8	1.82	0.44
3:AN:132:LYS:HA	3:AN:132:LYS:HD2	1.86	0.44
5:AB:193:ILE:HD12	5:AB:212:VAL:HG21	1.98	0.44
8:AY:81:TYR:HD2	8:AY:84:LYS:HB3	1.82	0.44
32:Ac:5:ARG:HB3	32:Ac:6:VAL:H	1.56	0.44
47:CA:147:ARG:HH12	47:CA:155:LYS:HB3	1.82	0.44
53:CY:35:SER:O	53:CY:39:ARG:HB2	2.18	0.44
59:CF:70:ARG:HH22	78:A5:1211:G:H5'	1.81	0.44
69:CC:306:ARG:HG2	69:CC:307:LYS:H	1.82	0.44
76:CE:80:VAL:HG22	78:A5:1276:C:H4'	1.98	0.44
78:A6:2605:G:H1	78:A6:2734:U:H3	1.64	0.44
78:A6:3961:G:H21	78:A6:4049:U:H3	1.64	0.44
12:AJ:40:LYS:HD2	19:B2:641:A:H5''	1.99	0.44
19:B2:1004:U:H2'	19:B2:1005:G:C8	2.52	0.44
19:B2:1786:U:H2'	19:B2:1787:G:C8	2.53	0.44
23:AU:107:GLU:HB2	23:AU:108:PRO:HD3	1.99	0.44
33:AD:135:GLU:HG3	33:AD:153:VAL:HG22	2.00	0.44
51:CU:46:ARG:HA	51:CU:46:ARG:HD3	1.83	0.44
62:Ce:65:LYS:H	62:Ce:65:LYS:HG2	1.65	0.44
67:Ck:24:LYS:HB2	67:Ck:24:LYS:HE2	1.71	0.44
75:CH:93:ARG:HG2	75:CH:182:SER:HB3	1.98	0.44
78:A5:20:U:H3'	78:A5:21:G:H8	1.83	0.44
78:A5:450:G:O6	78:A5:1297:U:O4	2.36	0.44
78:A5:1656:U:H2'	78:A5:1657:G:C8	2.53	0.44
81:BC:54:U:N3	81:BC:57:A:C8	2.71	0.44
78:A6:2769:U:H2'	78:A6:2770:C:C2	2.52	0.44
78:A6:3870:C:H2'	78:A6:3871:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A6:4974:C:H2'	78:A6:4975:G:C8	2.53	0.44
4:AL:111:VAL:HG11	4:AL:128:VAL:HG11	2.00	0.44
19:B2:928:G:H1	19:B2:1013:U:H3	1.65	0.44
19:B2:1717:C:H4'	71:Cn:21:ARG:HD3	2.00	0.44
37:Cz:26:ARG:HB3	78:A6:3974:G:H4'	1.99	0.44
44:CI:37:GLY:HA3	44:CI:86:HIS:HA	2.00	0.44
58:CB:51:ALA:HB3	58:CB:78:ILE:HG22	1.99	0.44
67:Ck:8:ILE:HG23	67:Ck:56:LEU:HD11	1.99	0.44
67:Ck:56:LEU:HD13	67:Ck:56:LEU:HA	1.87	0.44
78:A5:441:G:H2'	78:A5:442:G:C8	2.53	0.44
78:A5:1656:U:H2'	78:A5:1657:G:H8	1.82	0.44
78:A6:2447:U:H2'	78:A6:2448:G:H8	1.82	0.44
2:AX:88:ASP:HA	19:B2:617:G:H4'	2.00	0.43
5:AB:139:CYS:HB2	5:AB:168:MET:HE2	1.99	0.43
8:AY:15:ASN:HD22	8:AY:20:ARG:HD3	1.83	0.43
15:AG:189:ARG:HA	15:AG:192:ILE:HG22	2.00	0.43
20:CR:3:MET:HE2	20:CR:6:LEU:HD21	1.99	0.43
22:Ag:2:THR:HG23	22:Ag:3:GLU:HG3	2.00	0.43
37:Cz:124:LEU:HB3	37:Cz:128:LEU:HD12	1.99	0.43
38:CO:84:VAL:O	38:CO:88:LEU:HG	2.18	0.43
44:CI:47:PRO:HB2	44:CI:142:LEU:HD23	1.99	0.43
45:CD:223:PHE:HD2	45:CD:224:SER:H	1.66	0.43
45:CD:283:LYS:HA	45:CD:283:LYS:HD2	1.84	0.43
46:CQ:69:LYS:HB3	46:CQ:75:ARG:HH21	1.83	0.43
55:Cr:47:LYS:HD3	55:Cr:47:LYS:HA	1.79	0.43
59:CF:95:ILE:HD11	59:CF:233:ALA:HB2	1.99	0.43
78:A5:216:C:H2'	78:A5:217:C:H4'	2.00	0.43
78:A5:673:C:H2'	78:A5:674:G:C8	2.52	0.43
78:A5:1101:C:H42	78:A5:1195:G:H21	1.65	0.43
78:A5:1338:G:H4'	78:A5:1339:U:H6	1.83	0.43
78:A6:3847:C:H1'	78:A6:4633:G:H5''	1.99	0.43
78:A6:4055:U:H3'	78:A6:4056:A:H4'	1.98	0.43
8:AY:63:HIS:CE1	8:AY:70:THR:HG23	2.53	0.43
12:AJ:129:LEU:HG	12:AJ:135:ILE:HD11	2.00	0.43
19:B2:1104:G:H2'	19:B2:1105:G:H8	1.84	0.43
22:Ag:112:ALA:HB3	22:Ag:121:VAL:HG23	2.00	0.43
37:Cz:161:LYS:HE2	81:BC:54:U:H4'	2.00	0.43
41:CM:50:MET:HE2	41:CM:50:MET:HB3	1.72	0.43
45:CD:176:SER:HB2	78:A6:4323:A:H4'	1.99	0.43
45:CD:224:SER:HA	45:CD:227:ILE:HD12	2.00	0.43
55:Cr:112:ARG:HA	55:Cr:112:ARG:HD3	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:CB:171:LEU:HD12	58:CB:171:LEU:HA	1.86	0.43
78:A5:1308:C:H2'	78:A5:1309:C:C6	2.53	0.43
78:A5:1645:C:H2'	78:A5:1646:A:C8	2.53	0.43
1:AO:34:PHE:HE1	1:AO:100:THR:HA	1.83	0.43
13:AE:250:GLU:HA	13:AE:253:ASP:HB2	2.00	0.43
15:AG:67:VAL:HA	19:B2:1791:A:H1'	2.01	0.43
16:AH:191:GLU:HG2	16:AH:193:GLN:H	1.84	0.43
19:B2:1144:A:H2'	19:B2:1145:A:C8	2.53	0.43
36:AQ:50:LYS:HA	36:AQ:50:LYS:HD2	1.82	0.43
47:CA:181:LYS:HB2	47:CA:184:ARG:HB2	1.99	0.43
58:CB:13:SER:HB2	78:A6:4622:A:H4'	2.00	0.43
63:Cf:49:TYR:HB3	63:Cf:70:ILE:HG12	1.99	0.43
67:Ck:61:PRO:HA	67:Ck:62:PRO:HD3	1.80	0.43
69:CC:326:LEU:HD11	69:CC:333:LYS:HG2	1.99	0.43
69:CC:348:LYS:HA	69:CC:351:VAL:HG22	1.99	0.43
72:Cp:64:VAL:HG21	72:Cp:71:TYR:HE1	1.83	0.43
78:A5:712:C:H42	78:A5:956:A:H61	1.66	0.43
78:A5:750:U:H2'	78:A5:751:G:H8	1.84	0.43
78:A6:2520:C:H2'	78:A6:2521:G:C8	2.51	0.43
78:A6:3690:U:H5'	78:A6:3818:U:H5''	2.00	0.43
78:A6:4389:C:H2'	78:A6:4390:A:C8	2.53	0.43
78:A6:4866:C:H2'	78:A6:4867:G:C8	2.54	0.43
6:AA:77:ILE:HG13	6:AA:99:ILE:HB	1.99	0.43
14:AC:93:ILE:HD12	14:AC:93:ILE:H	1.83	0.43
18:AI:66:SER:HA	18:AI:73:THR:HA	2.00	0.43
19:B2:1095:C:H42	19:B2:1149:A:H2	1.67	0.43
20:CR:60:ARG:HB3	20:CR:63:CYS:HB3	2.01	0.43
20:CR:165:LYS:HE3	20:CR:165:LYS:HB3	1.81	0.43
21:CW:16:GLY:HA3	58:CB:55:HIS:NE2	2.34	0.43
26:AS:124:ARG:HD3	26:AS:127:TRP:HE3	1.83	0.43
36:AQ:42:ILE:HG21	36:AQ:48:GLN:HA	2.00	0.43
39:CL:80:GLU:HG2	39:CL:110:LEU:HD23	1.99	0.43
39:CL:186:ARG:HE	78:A5:1394:G:H5'	1.84	0.43
45:CD:259:LYS:HE2	45:CD:259:LYS:HB2	1.82	0.43
49:CT:129:LYS:HE3	49:CT:129:LYS:HB2	1.89	0.43
51:CU:60:VAL:HG23	51:CU:76:VAL:HG22	1.99	0.43
58:CB:128:LYS:HB2	58:CB:128:LYS:HE3	1.81	0.43
78:A5:65:A:N6	78:A5:75:G:H1'	2.33	0.43
78:A5:86:U:H2'	78:A5:87:A:C8	2.54	0.43
78:A5:500:G:H2'	78:A5:504:G:C8	2.54	0.43
78:A5:1468:C:H2'	78:A5:1469:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A6:3588:C:H2'	78:A6:3589:G:C8	2.53	0.43
78:A6:4466:C:H2'	78:A6:4467:A:H8	1.83	0.43
5:AB:144:LYS:HB3	5:AB:208:HIS:CG	2.53	0.43
15:AG:14:LYS:HB3	15:AG:14:LYS:HE2	1.82	0.43
15:AG:133:LEU:HB2	19:B2:65:C:C2	2.54	0.43
16:AH:69:LEU:O	16:AH:73:GLN:HG2	2.19	0.43
19:B2:874:G:H2'	19:B2:875:A:C8	2.54	0.43
19:B2:885:U:H2'	19:B2:886:A:H8	1.83	0.43
22:Ag:217:MET:HE1	22:Ag:219:TRP:NE1	2.33	0.43
34:Af:135:HIS:HB2	34:Af:138:ARG:HB3	2.00	0.43
35:AF:48:TYR:CE1	36:AQ:49:TYR:HB3	2.54	0.43
47:CA:80:GLU:HG2	47:CA:170:ALA:HA	1.99	0.43
49:CT:102:ARG:HH11	78:A5:1801:A:H4'	1.84	0.43
54:CZ:73:LYS:HA	54:CZ:101:PHE:HZ	1.83	0.43
58:CB:58:ARG:O	58:CB:71:GLU:HA	2.18	0.43
58:CB:115:LYS:HD3	58:CB:115:LYS:HA	1.79	0.43
69:CC:66:SER:HA	69:CC:77:PRO:HA	2.01	0.43
78:A5:441:G:H2'	78:A5:442:G:H8	1.84	0.43
78:A5:1968:G:H2'	78:A5:1969:G:C8	2.54	0.43
78:A6:4389:C:H2'	78:A6:4390:A:H8	1.82	0.43
4:AL:90:ARG:HD3	4:AL:109:MET:HE3	2.00	0.43
7:AV:39:VAL:HG22	7:AV:44:GLY:HA2	1.99	0.43
19:B2:948:C:H2'	19:B2:949:G:C8	2.53	0.43
19:B2:1507:G:H21	34:Af:86:THR:HG23	1.84	0.43
25:AM:74:ILE:HG13	25:AM:128:PHE:HZ	1.84	0.43
38:CO:41:ILE:HG12	38:CO:138:LEU:HD22	2.01	0.43
41:CM:96:GLU:HG3	41:CM:100:ARG:HE	1.83	0.43
45:CD:89:LYS:HE3	45:CD:90:VAL:HB	2.00	0.43
48:CS:13:VAL:HA	48:CS:28:TYR:O	2.18	0.43
52:CX:100:VAL:HG23	52:CX:134:LYS:HB3	2.00	0.43
76:CE:31:ASN:HB2	78:A5:1052:G:H2'	2.01	0.43
78:A5:691:C:H2'	78:A5:692:A:C8	2.53	0.43
78:A5:1603:C:H2'	78:A5:1604:G:H8	1.83	0.43
2:AX:124:LYS:HA	2:AX:129:SER:HA	2.00	0.43
3:AN:20:ARG:HH12	19:B2:918:U:H4'	1.84	0.43
5:AB:35:ALA:HB3	5:AB:42:ARG:HA	2.00	0.43
10:Ab:13:GLU:O	10:Ab:17:ARG:HB2	2.18	0.43
13:AE:164:LEU:HD23	13:AE:164:LEU:HA	1.85	0.43
16:AH:60:ILE:HD13	16:AH:90:LYS:HE2	1.99	0.43
19:B2:1234:C:H2'	19:B2:1235:G:H8	1.83	0.43
19:B2:1692:U:H2'	19:B2:1693:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Ac:27:CYS:HA	32:Ac:47:LYS:HA	2.01	0.43
33:AD:18:LYS:HE2	33:AD:18:LYS:HB3	1.74	0.43
45:CD:231:VAL:HG13	45:CD:235:MET:HE1	2.00	0.43
60:Cc:17:ARG:HE	60:Cc:17:ARG:HB3	1.59	0.43
70:Cm:96:CYS:HA	70:Cm:121:LEU:HD23	2.01	0.43
75:CH:165:THR:HG21	75:CH:179:ILE:H	1.84	0.43
78:A5:1603:C:H2'	78:A5:1604:G:C8	2.54	0.43
78:A5:2049:G:H2'	78:A5:2050:G:C8	2.53	0.43
78:A6:4153:C:H2'	78:A6:4154:G:C8	2.53	0.43
78:A6:4630:G:H2'	78:A6:4631:G:C8	2.52	0.43
78:A6:4638:U:H2'	78:A6:4639:G:C8	2.54	0.43
2:AX:67:ARG:NH2	19:B2:618:C:H41	2.17	0.43
8:AY:113:ARG:HA	8:AY:113:ARG:HD3	1.87	0.43
18:AI:11:ARG:HD2	19:B2:371:A:H4'	2.01	0.43
19:B2:1104:G:H2'	19:B2:1105:G:C8	2.54	0.43
23:AU:95:SER:HA	23:AU:98:VAL:HG22	2.00	0.43
32:Ac:20:ARG:HA	32:Ac:20:ARG:HD3	1.80	0.43
45:CD:51:MET:HB2	45:CD:51:MET:HE3	1.77	0.43
51:CU:43:LEU:HD12	51:CU:47:ILE:HD11	2.00	0.43
55:Cr:97:ILE:HG23	55:Cr:103:ARG:HH22	1.84	0.43
58:CB:294:LYS:HD2	58:CB:298:LEU:HD22	2.01	0.43
65:Ci:72:PHE:HE1	65:Ci:76:ARG:HE	1.67	0.43
69:CC:167:ALA:HB1	69:CC:221:PHE:HD2	1.83	0.43
75:CH:34:LEU:HD13	75:CH:80:MET:HG2	2.01	0.43
75:CH:80:MET:HE3	75:CH:80:MET:HB2	1.88	0.43
78:A5:86:U:H2'	78:A5:87:A:H8	1.84	0.43
78:A5:1306:C:H2'	78:A5:1307:A:C8	2.53	0.43
78:A5:1514:U:H2'	78:A5:1515:A:C8	2.54	0.43
78:A5:1628:C:H2'	78:A5:1629:G:C8	2.54	0.43
78:A5:1742:A:H2'	78:A5:1743:A:H8	1.82	0.43
80:A8:43:A:H2'	80:A8:44:A:H8	1.84	0.43
78:A6:2413:U:H2'	78:A6:2414:G:C8	2.53	0.43
78:A6:5030:U:H2'	78:A6:5031:G:H8	1.82	0.43
5:AB:88:THR:HG22	5:AB:98:THR:HG22	2.00	0.43
7:AV:24:ILE:HD13	7:AV:56:CYS:HB2	2.01	0.43
19:B2:1375:G:H2'	19:B2:1376:A:C8	2.53	0.43
19:B2:1808:U:H2'	19:B2:1809:A:H8	1.84	0.43
26:AS:12:ILE:HA	26:AS:22:GLY:HA3	2.00	0.43
26:AS:41:ALA:O	26:AS:45:LEU:HD12	2.19	0.43
49:CT:12:ARG:HB2	78:A6:4209:G:H5''	2.01	0.43
56:Ch:46:LYS:HA	56:Ch:46:LYS:HD3	1.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:CB:207:VAL:HA	58:CB:210:VAL:HG12	2.01	0.43
60:Cc:35:LEU:HD13	60:Cc:35:LEU:HA	1.86	0.43
60:Cc:54:ALA:HA	60:Cc:57:LYS:HB3	2.00	0.43
69:CC:147:VAL:HG22	69:CC:152:LEU:HD13	2.00	0.43
71:Cn:15:ARG:NH1	71:Cn:18:ARG:HD2	2.34	0.43
74:CJ:75:ARG:HH11	79:A7:40:U:H3	1.66	0.43
78:A5:1738:A:H2'	78:A5:1739:G:C8	2.54	0.43
13:AE:102:ILE:HG12	13:AE:239:PRO:HD3	2.00	0.43
19:B2:678:U:H2'	19:B2:679:A:H8	1.84	0.43
21:CW:19:ARG:HA	21:CW:19:ARG:HD2	1.72	0.43
23:AU:82:MET:HE3	23:AU:84:ILE:HD11	2.01	0.43
44:CI:49:GLY:HA2	44:CI:138:ILE:O	2.19	0.43
45:CD:41:LYS:HE3	49:CT:33:ILE:HD12	1.99	0.43
55:Cr:33:LYS:HA	62:Ce:90:MET:HG3	2.00	0.43
64:Cg:62:LYS:HD3	78:A6:2516:G:H3'	2.01	0.43
65:Ci:43:MET:SD	65:Ci:44:ILE:HG12	2.59	0.43
66:Cj:84:PRO:HG3	78:A5:251:C:H5'	2.00	0.43
69:CC:109:ARG:HA	78:A5:1341:U:H5'	1.99	0.43
77:CG:216:ALA:HA	77:CG:219:VAL:HG12	2.00	0.43
77:CG:252:LYS:HD3	77:CG:252:LYS:HA	1.74	0.43
78:A5:1333:A:H2'	78:A5:1334:A:C8	2.54	0.43
78:A6:2335:C:H2'	78:A6:2336:G:H8	1.84	0.43
78:A6:4635:A:H2	78:A6:4663:G:H21	1.65	0.43
78:A6:4887:C:N3	78:A6:4932:U:O4	2.52	0.43
1:AO:60:MET:HE3	19:B2:956:G:H4'	2.01	0.42
6:AA:15:VAL:HG23	6:AA:51:LEU:HG	2.01	0.42
12:AJ:78:LEU:HD22	12:AJ:92:MET:HA	2.00	0.42
15:AG:76:LEU:HA	15:AG:94:ARG:HA	2.00	0.42
19:B2:652:U:H2'	19:B2:653:A:C8	2.54	0.42
19:B2:1044:G:C6	47:CA:248:GLY:O	2.71	0.42
28:AR:100:PRO:HG3	28:AR:117:LEU:HD22	2.01	0.42
36:AQ:58:LEU:HB2	36:AQ:63:PHE:HE2	1.85	0.42
37:Cz:35:GLN:HB2	37:Cz:207:LYS:HG3	1.99	0.42
38:CO:22:ILE:HD13	38:CO:120:VAL:HG11	2.01	0.42
42:Ca:127:LYS:HE2	42:Ca:127:LYS:HB2	1.90	0.42
47:CA:150:LEU:HD11	47:CA:156:LYS:HD2	2.01	0.42
55:Cr:76:SER:HA	55:Cr:79:ARG:HD2	2.00	0.42
59:CF:98:ILE:HD11	59:CF:116:GLN:HA	2.01	0.42
65:Ci:80:HIS:CE1	65:Ci:84:LYS:HE3	2.54	0.42
78:A5:1382:G:H2'	78:A5:1383:G:C8	2.53	0.42
78:A5:1492:G:H2'	78:A5:1493:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:A7:83:A:N1	79:A7:93:G:O6	2.52	0.42
80:A8:9:A:H2'	80:A8:10:G:H8	1.84	0.42
4:AL:132:ARG:HD2	19:B2:383:G:H4'	2.00	0.42
19:B2:1359:U:H2'	19:B2:1360:U:H6	1.84	0.42
19:B2:1551:U:C2	19:B2:1577:G:N1	2.87	0.42
20:CR:74:ARG:HA	20:CR:74:ARG:HD3	1.81	0.42
22:Ag:191:HIS:CE1	22:Ag:195:LEU:HD21	2.54	0.42
26:AS:14:ARG:NH2	26:AS:17:ASN:H	2.17	0.42
26:AS:90:VAL:HA	29:AP:18:ARG:HG2	2.01	0.42
28:AR:29:HIS:HA	28:AR:32:LYS:HE3	2.01	0.42
34:Af:111:ASN:HA	34:Af:112:GLY:HA2	1.60	0.42
45:CD:19:LYS:HB3	45:CD:23:ARG:HB3	2.00	0.42
56:Ch:103:LYS:HD3	56:Ch:107:GLN:HB3	1.99	0.42
58:CB:247:GLY:HA3	58:CB:250:LYS:HE2	2.00	0.42
58:CB:324:GLY:HA2	78:A6:5051:C:H4'	2.01	0.42
60:Cc:12:GLU:HA	60:Cc:13:SER:HA	1.71	0.42
61:Cd:59:THR:HA	61:Cd:60:PRO:HD3	1.87	0.42
64:Cg:64:LEU:HA	64:Cg:67:LEU:HD21	2.01	0.42
69:CC:316:LYS:HD2	78:A5:1282:G:H5''	2.01	0.42
78:A5:34:A:H2'	78:A5:35:U:H6	1.85	0.42
78:A5:1876:U:H2'	78:A5:1877:G:C8	2.55	0.42
78:A5:1931:C:H41	78:A5:2040:A:H1'	1.84	0.42
1:AO:135:ILE:HA	1:AO:136:PRO:HD3	1.85	0.42
3:AN:3:ARG:H	19:B2:923:G:H5''	1.83	0.42
19:B2:512:A:H2'	19:B2:513:G:H8	1.84	0.42
19:B2:639:C:H2'	19:B2:640:A:C8	2.54	0.42
21:CW:49:ILE:HD13	78:A6:3615:G:H5''	2.02	0.42
22:Ag:107:ASP:HB3	22:Ag:125:ARG:HD2	2.01	0.42
26:AS:18:THR:HG21	26:AS:33:ILE:HG23	2.01	0.42
37:Cz:20:GLY:HA2	37:Cz:23:ARG:HG3	2.01	0.42
55:Cr:19:LYS:HG3	78:A6:2337:C:H4'	2.02	0.42
57:Cb:41:ARG:HH21	57:Cb:44:ARG:NH2	2.17	0.42
59:CF:91:PHE:HB2	59:CF:145:PRO:HG3	2.01	0.42
69:CC:127:ALA:HB3	69:CC:240:LEU:HD23	2.01	0.42
76:CE:50:LEU:HG	76:CE:54:ILE:HD13	2.02	0.42
76:CE:258:LEU:HA	76:CE:261:ILE:HG22	2.02	0.42
79:A7:4:U:H2'	79:A7:5:A:C8	2.55	0.42
79:A7:57:C:H2'	79:A7:58:A:H8	1.85	0.42
80:A8:133:G:H2'	80:A8:134:G:C8	2.54	0.42
78:A6:2275:G:H2'	78:A6:2276:A:C8	2.54	0.42
78:A6:2372:U:H2'	78:A6:2373:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A6:3783:A:H2	78:A6:3790:U:H3	1.66	0.42
78:A6:3893:C:H2'	78:A6:3894:A:C8	2.55	0.42
78:A6:4151:G:H2'	78:A6:4152:G:H8	1.84	0.42
78:A6:4208:U:H2'	78:A6:4209:G:C8	2.55	0.42
78:A6:4716:C:H2'	78:A6:4717:A:H8	1.84	0.42
13:AE:174:LYS:HD3	13:AE:174:LYS:HA	1.93	0.42
14:AC:207:ALA:HB3	14:AC:210:PRO:HD2	2.00	0.42
19:B2:144:U:H2'	19:B2:145:G:H8	1.84	0.42
19:B2:409:C:H2'	19:B2:410:G:H8	1.85	0.42
19:B2:788:G:H2'	19:B2:789:G:C8	2.55	0.42
19:B2:1051:G:H2'	19:B2:1052:A:H8	1.83	0.42
19:B2:1232:U:H2'	19:B2:1233:G:C8	2.54	0.42
41:CM:31:ILE:HB	41:CM:35:ARG:HB3	2.02	0.42
52:CX:62:ARG:HA	52:CX:62:ARG:HD3	1.81	0.42
58:CB:112:ASP:HA	58:CB:115:LYS:HB2	2.01	0.42
66:Cj:44:LYS:HE2	66:Cj:46:LYS:HB2	2.00	0.42
73:Co:6:LYS:HD3	73:Co:94:GLY:HA2	2.01	0.42
73:Co:27:LYS:HE2	73:Co:27:LYS:HB2	1.74	0.42
74:CJ:113:ILE:HA	74:CJ:113:ILE:HD13	1.84	0.42
75:CH:28:LYS:HE2	75:CH:28:LYS:HB3	1.88	0.42
78:A5:744:G:H2'	78:A5:745:G:C8	2.55	0.42
78:A5:930:G:H8	78:A5:931:C:H5''	1.84	0.42
78:A5:1761:G:N2	78:A5:1771:U:O2	2.33	0.42
79:A7:69:U:H2'	79:A7:70:G:C8	2.54	0.42
78:A6:2608:G:H2'	78:A6:2609:G:H8	1.85	0.42
78:A6:4594:U:H2'	78:A6:4595:G:C8	2.55	0.42
78:A6:4898:G:H2'	78:A6:4899:G:H8	1.84	0.42
1:AO:68:GLU:H	1:AO:68:GLU:HG2	1.56	0.42
5:AB:19:LYS:HD3	5:AB:19:LYS:HA	1.85	0.42
5:AB:105:LEU:HD13	5:AB:213:ARG:HA	2.02	0.42
10:Ab:80:ARG:HB3	10:Ab:82:LYS:HE2	2.02	0.42
12:AJ:66:LYS:HA	12:AJ:66:LYS:HD2	1.82	0.42
14:AC:191:VAL:HG13	14:AC:230:THR:HG22	2.00	0.42
19:B2:1263:U:H5'	27:Ad:27:ARG:HH12	1.83	0.42
47:CA:116:LEU:HD12	47:CA:126:LEU:HD23	2.01	0.42
60:Cc:29:LEU:HD23	60:Cc:29:LEU:HA	1.87	0.42
67:Ck:49:ASP:HB3	67:Ck:52:LYS:HG3	2.01	0.42
73:Co:51:GLN:HB3	78:A6:3925:U:H4'	2.02	0.42
78:A5:246:G:H2'	78:A5:247:G:C8	2.55	0.42
78:A5:443:G:H2'	78:A5:444:G:C8	2.55	0.42
78:A5:744:G:H2'	78:A5:745:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A5:1317:U:H2'	78:A5:1318:C:C6	2.55	0.42
78:A5:1327:C:H2'	78:A5:1328:G:H8	1.84	0.42
78:A5:1950:U:H2'	78:A5:1951:G:C8	2.53	0.42
13:AE:45:ILE:HG13	13:AE:61:VAL:HG21	2.01	0.42
15:AG:159:ARG:HA	15:AG:173:ALA:HA	2.01	0.42
15:AG:164:LYS:HD2	15:AG:164:LYS:HA	1.80	0.42
19:B2:115:U:H2'	19:B2:116:U:C6	2.55	0.42
19:B2:536:A:N6	19:B2:547:G:N2	2.48	0.42
19:B2:808:A:H2	19:B2:855:G:H22	1.66	0.42
19:B2:1408:U:H2'	19:B2:1409:A:C4	2.54	0.42
19:B2:1854:U:H2'	19:B2:1855:G:C8	2.54	0.42
21:CW:39:ALA:HB1	21:CW:44:ARG:HG3	2.00	0.42
25:AM:64:LEU:HD11	34:Af:106:TYR:HB3	2.01	0.42
39:CL:27:ASN:O	39:CL:31:ARG:HB2	2.20	0.42
40:CV:124:GLU:O	40:CV:128:LEU:HD12	2.19	0.42
67:Ck:26:LYS:HD2	67:Ck:26:LYS:HA	1.86	0.42
69:CC:32:ILE:H	69:CC:32:ILE:HG12	1.72	0.42
69:CC:307:LYS:HB3	69:CC:311:ARG:HH12	1.84	0.42
78:A5:18:C:H2'	78:A5:19:G:C8	2.55	0.42
78:A5:475:G:H2'	78:A5:476:G:C8	2.55	0.42
78:A5:500:G:H2'	78:A5:504:G:H8	1.85	0.42
80:A8:8:U:H2'	80:A8:9:A:C8	2.55	0.42
78:A6:3722:G:H2'	78:A6:3723:A:H8	1.85	0.42
78:A6:4642:U:H2'	78:A6:4643:G:C8	2.55	0.42
16:AH:43:LEU:HD22	16:AH:72:PHE:CD2	2.55	0.42
19:B2:603:C:H1'	19:B2:604:A:N7	2.35	0.42
19:B2:695:C:H2'	19:B2:696:G:C8	2.55	0.42
19:B2:1044:G:N3	47:CA:249:THR:N	2.67	0.42
26:AS:62:ASP:HA	26:AS:65:GLU:HG2	2.00	0.42
30:AT:99:VAL:HB	30:AT:102:ARG:HH21	1.84	0.42
46:CQ:84:GLY:H	46:CQ:103:LEU:HB2	1.84	0.42
47:CA:219:ILE:HD11	78:A6:3689:G:H5'	2.01	0.42
48:CS:3:ALA:HB2	59:CF:230:GLY:HA2	2.01	0.42
62:Ce:41:ILE:H	62:Ce:41:ILE:HG12	1.61	0.42
68:Cl:40:LYS:HE2	80:A8:53:G:H4'	2.02	0.42
77:CG:219:VAL:HA	77:CG:222:ILE:HG13	2.01	0.42
78:A5:74:G:H3'	78:A5:75:G:H8	1.85	0.42
78:A5:1509:C:H2'	78:A5:1510:G:C8	2.54	0.42
78:A5:1620:U:H2'	78:A5:1621:A:C8	2.55	0.42
78:A5:1816:C:H2'	78:A5:1817:U:O4'	2.20	0.42
78:A6:4898:G:H2'	78:A6:4899:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AN:46:THR:O	3:AN:50:ILE:HG13	2.20	0.42
14:AC:213:LEU:HA	14:AC:216:MET:HB2	2.01	0.42
19:B2:475:C:H1'	19:B2:507:G:H1'	2.02	0.42
38:CO:18:ARG:HE	38:CO:128:ARG:HE	1.66	0.42
48:CS:38:VAL:HA	48:CS:41:LYS:HG2	2.02	0.42
48:CS:80:ILE:HB	48:CS:129:VAL:HG12	2.02	0.42
60:Cc:30:GLY:O	60:Cc:34:THR:HG23	2.20	0.42
69:CC:20:LYS:H	69:CC:20:LYS:HG2	1.68	0.42
69:CC:350:ARG:HD2	78:A5:723:A:H5''	2.00	0.42
75:CH:41:ILE:HG13	75:CH:73:ILE:HG21	2.02	0.42
78:A5:153:G:H2'	78:A5:154:G:H8	1.85	0.42
78:A5:750:U:H2'	78:A5:751:G:C8	2.55	0.42
78:A5:1167:C:H2'	78:A5:1168:G:H8	1.83	0.42
78:A5:1583:A:H1'	78:A6:2396:A:C6	2.54	0.42
78:A5:1732:C:H2'	78:A5:1733:G:C8	2.55	0.42
81:BC:25:G:O6	81:BC:43:A:N1	2.53	0.42
78:A6:2540:C:H2'	78:A6:2541:G:H8	1.85	0.42
78:A6:3598:C:H2'	78:A6:3599:A:C8	2.51	0.42
78:A6:3731:C:H2'	78:A6:3732:A:C8	2.55	0.42
5:AB:57:ILE:HG13	5:AB:59:SER:H	1.84	0.42
5:AB:66:VAL:HA	5:AB:86:LEU:O	2.20	0.42
12:AJ:46:VAL:HG13	12:AJ:105:PHE:HD2	1.85	0.42
13:AE:44:LEU:HD11	13:AE:72:ILE:HD11	2.02	0.42
13:AE:153:LEU:HD22	15:AG:216:ARG:NH1	2.35	0.42
19:B2:1408:U:H5''	36:AQ:24:HIS:CE1	2.55	0.42
22:Ag:52:TYR:CG	22:Ag:309:VAL:HG21	2.55	0.42
35:AF:76:MET:HG3	35:AF:89:THR:HG22	2.02	0.42
43:CN:47:LYS:HD2	43:CN:47:LYS:HA	1.82	0.42
49:CT:35:LYS:HD2	78:A5:1824:G:H5''	2.02	0.42
62:Ce:64:LYS:HD3	62:Ce:64:LYS:HA	1.84	0.42
62:Ce:79:VAL:HG11	62:Ce:85:LEU:HB3	2.01	0.42
65:Ci:19:LYS:HA	65:Ci:19:LYS:HD2	1.88	0.42
69:CC:11:TYR:CE2	69:CC:148:PRO:HB2	2.55	0.42
77:CG:140:VAL:HA	77:CG:143:VAL:HG12	2.01	0.42
77:CG:149:ASN:HB2	77:CG:151:LYS:HE2	2.01	0.42
78:A5:228:C:H2'	78:A5:229:G:C8	2.55	0.42
78:A5:1750:G:H22	78:A5:1780:A:H2	1.66	0.42
78:A5:2028:C:H2'	78:A5:2029:A:H8	1.85	0.42
79:A7:70:G:H2'	79:A7:71:G:H8	1.85	0.42
79:A7:77:A:H62	79:A7:99:G:H21	1.68	0.42
78:A6:2745:A:H2'	78:A6:2746:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A6:3667:C:H2'	78:A6:3668:C:H6	1.85	0.42
78:A6:4060:U:H2'	78:A6:4061:G:H8	1.83	0.42
78:A6:4493:U:H2'	78:A6:4494:G:C8	2.55	0.42
2:AX:52:LEU:HD21	2:AX:73:GLN:HB2	2.02	0.42
3:AN:75:LEU:HD23	3:AN:75:LEU:HA	1.87	0.42
15:AG:167:LYS:HG3	15:AG:168:LYS:HG3	2.01	0.42
16:AH:57:ARG:HH21	16:AH:172:THR:HG21	1.85	0.42
19:B2:609:U:H2'	19:B2:610:G:C8	2.55	0.42
19:B2:929:G:H2'	19:B2:930:C:O4'	2.20	0.42
21:CW:20:ARG:HH22	40:CV:96:LEU:HD22	1.83	0.42
21:CW:21:TYR:HB3	21:CW:23:ARG:HE	1.85	0.42
31:AZ:73:VAL:HG22	31:AZ:76:ARG:HH21	1.83	0.42
34:Af:88:PRO:HG2	34:Af:90:LYS:HG2	2.01	0.42
38:CO:199:HIS:ND1	38:CO:199:HIS:C	2.77	0.42
44:CI:52:MET:HB2	44:CI:152:LEU:HD13	2.01	0.42
78:A5:722:G:H2'	78:A5:723:A:C8	2.55	0.42
78:A6:2654:C:H2'	78:A6:2655:C:C6	2.55	0.42
78:A6:3720:G:C6	78:A6:3733:A:N1	2.88	0.42
78:A6:3863:C:H4'	78:A6:3903:A:H4'	2.01	0.42
78:A6:4885:U:H2'	78:A6:4886:C:H6	1.85	0.42
11:Ae:27:LYS:HE2	11:Ae:27:LYS:HB2	1.76	0.41
19:B2:518:G:H2'	19:B2:519:A:H8	1.84	0.41
19:B2:1208:A:H5''	19:B2:1835:A:H4'	2.02	0.41
19:B2:1781:A:H2'	19:B2:1782:G:C8	2.55	0.41
21:CW:49:ILE:HD11	78:A6:3615:G:C4	2.55	0.41
25:AM:69:LEU:HD13	25:AM:76:LEU:HB2	2.01	0.41
26:AS:114:LEU:HD23	26:AS:121:ARG:HB3	2.01	0.41
39:CL:5:ARG:HD3	39:CL:5:ARG:HA	1.96	0.41
39:CL:65:ARG:HB3	42:Ca:66:ASN:HB3	2.02	0.41
48:CS:153:PRO:HD2	75:CH:60:TRP:CD2	2.55	0.41
57:Cb:40:LEU:HD23	57:Cb:40:LEU:HA	1.88	0.41
58:CB:216:MET:HG3	58:CB:281:ASN:HA	2.02	0.41
62:Ce:102:ASN:HB3	78:A6:2307:A:H5''	2.02	0.41
63:Cf:75:THR:HA	78:A5:953:C:H4'	2.02	0.41
76:CE:57:TYR:HE2	78:A5:975:C:H5'	1.83	0.41
77:CG:43:GLN:HG3	77:CG:44:ASP:HB2	2.01	0.41
78:A5:1461:C:H2'	78:A5:1462:A:C8	2.55	0.41
78:A5:1839:U:H2'	78:A5:1840:G:C8	2.55	0.41
81:BC:47:C:H2'	81:BC:58:A:H1'	2.02	0.41
78:A6:3664:G:H1	78:A6:3678:G:H1	1.68	0.41
78:A6:4174:U:H2'	78:A6:4175:G:H8	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AA:183:LEU:HD22	6:AA:187:GLY:HA3	2.02	0.41
9:Aa:49:ALA:O	9:Aa:53:ILE:HG13	2.20	0.41
17:AW:83:LEU:HA	17:AW:86:LEU:HD22	2.01	0.41
19:B2:409:C:H2'	19:B2:410:G:C8	2.55	0.41
19:B2:1043:G:C4	47:CA:249:THR:HG22	2.55	0.41
19:B2:1454:A:H4'	19:B2:1455:A:C8	2.54	0.41
21:CW:97:LYS:HE3	21:CW:97:LYS:HB3	1.92	0.41
37:Cz:53:VAL:HG22	37:Cz:189:PHE:HB3	2.02	0.41
40:CV:95:PHE:CE2	78:A6:4629:U:H1'	2.55	0.41
44:CI:160:PRO:HD3	78:A6:4431:U:H5''	2.01	0.41
47:CA:199:VAL:HG21	78:A5:1631:A:C8	2.55	0.41
48:CS:77:ASN:ND2	48:CS:98:ARG:HE	2.18	0.41
48:CS:132:ILE:HG23	48:CS:136:LYS:HB3	2.02	0.41
49:CT:101:SER:HB3	78:A5:1730:U:H1'	2.02	0.41
53:CY:91:ASN:HB2	53:CY:93:THR:HG23	2.01	0.41
54:CZ:109:LYS:HE2	78:A6:2556:G:H4'	2.01	0.41
58:CB:28:LYS:HG3	58:CB:30:LYS:HD3	2.01	0.41
58:CB:114:CYS:HB3	58:CB:165:HIS:CG	2.55	0.41
58:CB:341:LYS:HZ1	78:A6:4626:A:H5''	1.85	0.41
59:CF:134:ARG:HD3	79:A7:97:G:H4'	2.02	0.41
69:CC:205:ARG:HD3	78:A6:2297:G:H5'	2.02	0.41
76:CE:123:ARG:HG3	78:A5:961:G:H4'	2.01	0.41
77:CG:107:LYS:HA	77:CG:110:LYS:HB3	2.02	0.41
78:A5:228:C:H2'	78:A5:229:G:H8	1.86	0.41
78:A5:435:A:H61	78:A5:1312:A:H2	1.67	0.41
78:A5:460:C:H2'	78:A5:461:G:C8	2.55	0.41
78:A5:1523:A:H8	78:A5:1652:U:H3	1.59	0.41
78:A5:1687:U:H2'	78:A5:1688:G:C8	2.55	0.41
78:A6:2521:G:H2'	78:A6:2522:G:C8	2.55	0.41
78:A6:2607:C:H2'	78:A6:2608:G:C8	2.55	0.41
78:A6:4089:G:H2'	78:A6:4090:G:H8	1.85	0.41
78:A6:4188:U:H2'	78:A6:4189:U:C6	2.55	0.41
78:A6:4765:G:N2	78:A6:4869:U:O2	2.41	0.41
3:AN:19:ARG:HB3	3:AN:22:VAL:HB	2.02	0.41
19:B2:234:C:H2'	19:B2:235:A:H8	1.85	0.41
25:AM:21:VAL:HA	25:AM:121:LYS:HD2	2.03	0.41
40:CV:21:PRO:HA	40:CV:54:ALA:HA	2.02	0.41
41:CM:110:PHE:HE2	78:A6:4882:U:H3	1.69	0.41
42:Ca:45:PHE:HD1	42:Ca:45:PHE:HA	1.75	0.41
47:CA:219:ILE:HG22	47:CA:220:GLY:H	1.85	0.41
54:CZ:62:ILE:H	54:CZ:62:ILE:HD12	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Ck:24:LYS:HB2	67:Ck:35:LYS:HG3	2.02	0.41
69:CC:322:LEU:HD13	69:CC:326:LEU:HD23	2.02	0.41
78:A5:229:G:H2'	78:A5:230:G:C8	2.55	0.41
78:A5:713:C:H5''	78:A5:1282:G:OP1	2.20	0.41
80:A8:19:C:H2'	80:A8:20:A:C8	2.55	0.41
80:A8:148:A:H2'	80:A8:149:G:C8	2.55	0.41
81:BC:1:A:H2'	81:BC:2:G:C8	2.54	0.41
78:A6:2360:A:H4'	78:A6:2361:G:H4'	2.02	0.41
78:A6:2713:C:H2'	78:A6:2714:G:H8	1.86	0.41
78:A6:4219:A:H2'	78:A6:4220:A:C8	2.55	0.41
3:AN:48:SER:O	3:AN:52:VAL:HG23	2.19	0.41
10:Ab:14:GLU:HA	10:Ab:17:ARG:HB3	2.03	0.41
17:AW:75:ILE:HD13	17:AW:75:ILE:HA	1.88	0.41
31:AZ:79:ILE:HG23	31:AZ:81:GLY:H	1.85	0.41
38:CO:177:LEU:HB3	41:CM:130:LEU:HD22	2.02	0.41
45:CD:197:LYS:HE3	45:CD:202:GLN:HB2	2.02	0.41
47:CA:250:LYS:HG2	47:CA:252:VAL:HA	2.01	0.41
48:CS:80:ILE:HA	48:CS:128:LYS:O	2.19	0.41
59:CF:74:MET:H	59:CF:74:MET:HG3	1.53	0.41
59:CF:167:ILE:HG22	78:A6:2275:G:H5'	2.03	0.41
62:Ce:78:LEU:HD21	78:A6:2324:C:H4'	2.02	0.41
64:Cg:105:LYS:HD3	64:Cg:105:LYS:HA	1.88	0.41
69:CC:124:ILE:HA	69:CC:237:ILE:HD13	2.02	0.41
70:Cm:90:ASN:HD22	75:CH:176:LEU:HD13	1.86	0.41
75:CH:10:VAL:HG23	75:CH:55:LEU:HB3	2.01	0.41
76:CE:57:TYR:HB2	76:CE:59:ARG:H	1.84	0.41
76:CE:72:LYS:HD2	76:CE:72:LYS:HA	1.58	0.41
76:CE:140:LEU:HD23	76:CE:140:LEU:HA	1.88	0.41
78:A5:14:C:H2'	78:A5:15:A:C8	2.55	0.41
78:A5:1758:G:H2'	78:A5:1759:G:C8	2.55	0.41
78:A6:2521:G:H2'	78:A6:2522:G:H8	1.85	0.41
78:A6:2528:G:H4'	78:A6:2783:A:H4'	2.02	0.41
78:A6:2767:U:H2'	78:A6:2769:U:H6	1.85	0.41
78:A6:4094:G:H2'	78:A6:4095:G:H8	1.85	0.41
78:A6:4760:G:H2'	78:A6:4761:G:C8	2.56	0.41
4:AL:145:VAL:HG22	4:AL:147:LYS:H	1.86	0.41
18:AI:100:CYS:O	18:AI:174:CYS:HA	2.20	0.41
19:B2:1101:U:H2'	19:B2:1102:G:C8	2.55	0.41
19:B2:1726:G:H2'	19:B2:1727:G:C8	2.56	0.41
30:AT:104:LEU:HD11	30:AT:121:ARG:HG3	2.01	0.41
36:AQ:23:ALA:HB2	36:AQ:70:VAL:HG13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Cz:53:VAL:HG11	37:Cz:186:ALA:HA	2.03	0.41
38:CO:7:LEU:HD22	38:CO:31:ARG:HG2	2.02	0.41
38:CO:199:HIS:CE1	38:CO:203:VAL:HG21	2.52	0.41
43:CN:7:ILE:HG21	77:CG:166:LEU:HA	2.03	0.41
45:CD:179:ARG:HA	45:CD:179:ARG:HD2	1.92	0.41
52:CX:105:ASN:O	52:CX:109:ILE:HG13	2.20	0.41
52:CX:114:LYS:HE2	52:CX:114:LYS:HB2	1.78	0.41
52:CX:119:ILE:HD12	52:CX:140:LEU:HD11	2.01	0.41
52:CX:119:ILE:HD13	52:CX:149:VAL:HG21	2.01	0.41
76:CE:248:ILE:HA	76:CE:251:LYS:HE2	2.01	0.41
78:A5:1086:C:H2'	78:A5:1087:A:H8	1.86	0.41
78:A5:1989:G:H2'	78:A5:1990:A:C8	2.55	0.41
79:A7:3:C:H2'	79:A7:4:U:H6	1.86	0.41
78:A6:2362:U:H2'	78:A6:2363:A:C8	2.55	0.41
78:A6:2753:G:H2'	78:A6:2754:G:C4	2.54	0.41
78:A6:4664:A:H3'	78:A6:4665:A:H8	1.85	0.41
5:AB:36:PRO:HB2	5:AB:38:MET:SD	2.60	0.41
6:AA:34:MET:HE3	6:AA:34:MET:HB2	1.73	0.41
6:AA:183:LEU:O	6:AA:187:GLY:CA	2.66	0.41
8:AY:16:ARG:HG3	13:AE:95:THR:HG22	2.03	0.41
11:Ae:51:LYS:HA	11:Ae:51:LYS:HD2	1.88	0.41
13:AE:153:LEU:HD22	15:AG:216:ARG:HH12	1.85	0.41
18:AI:154:LYS:HE2	18:AI:154:LYS:HB2	1.92	0.41
19:B2:144:U:H2'	19:B2:145:G:C8	2.55	0.41
19:B2:1139:C:H3'	19:B2:1140:G:H8	1.85	0.41
19:B2:1593:C:H2'	19:B2:1594:A:H8	1.85	0.41
24:AK:41:PRO:HD2	24:AK:44:HIS:HB2	2.02	0.41
35:AF:153:LEU:HD23	35:AF:153:LEU:HA	1.87	0.41
39:CL:60:ARG:HA	39:CL:60:ARG:HD3	1.83	0.41
42:Ca:81:LEU:H	42:Ca:81:LEU:HG	1.60	0.41
51:CU:33:ILE:HD11	51:CU:96:LEU:HD23	2.03	0.41
53:CY:87:ARG:HE	53:CY:87:ARG:HB3	1.62	0.41
55:Cr:127:LYS:H	55:Cr:130:ARG:HG3	1.86	0.41
61:Cd:33:ILE:HD11	61:Cd:45:ALA:HB2	2.03	0.41
69:CC:190:ARG:HG2	69:CC:192:GLY:H	1.84	0.41
77:CG:72:LYS:HE2	78:A6:4162:C:C4	2.55	0.41
77:CG:110:LYS:HA	77:CG:113:ARG:HH21	1.85	0.41
78:A5:283:G:H2'	78:A5:284:G:H8	1.86	0.41
78:A5:447:C:H2'	78:A5:448:G:H8	1.86	0.41
78:A5:673:C:H2'	78:A5:674:G:H8	1.85	0.41
78:A5:681:G:H2'	78:A5:682:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A5:1812:C:H2'	78:A5:1813:U:C6	2.55	0.41
78:A6:3969:G:H2'	78:A6:3970:G:C8	2.56	0.41
78:A6:3973:G:H2'	78:A6:3974:G:C8	2.56	0.41
78:A6:4577:U:H2'	78:A6:4578:G:C8	2.56	0.41
78:A6:4679:G:H2'	78:A6:4680:G:C8	2.55	0.41
6:AA:208:GLU:HG3	28:AR:81:ARG:HD2	2.02	0.41
13:AE:123:LEU:HD12	13:AE:161:GLN:HG2	2.03	0.41
18:AI:118:ALA:HB1	18:AI:137:LEU:HD12	2.02	0.41
19:B2:939:U:H2'	19:B2:940:U:C6	2.55	0.41
19:B2:1714:U:H2'	19:B2:1715:A:C8	2.55	0.41
22:Ag:289:LEU:HA	22:Ag:299:PHE:O	2.20	0.41
23:AU:99:LYS:HE2	23:AU:99:LYS:HB2	1.85	0.41
37:Cz:155:ILE:HG21	37:Cz:169:VAL:HA	2.01	0.41
47:CA:2:GLY:HA2	47:CA:207:VAL:HG12	2.02	0.41
47:CA:3:ARG:HB2	47:CA:207:VAL:HB	2.03	0.41
58:CB:90:VAL:HG23	58:CB:104:THR:HG22	2.02	0.41
64:Cg:32:TYR:HD1	64:Cg:32:TYR:HA	1.76	0.41
65:Ci:5:TYR:HB2	65:Ci:6:PRO:HD3	2.02	0.41
75:CH:59:LYS:HE3	75:CH:66:GLU:HG3	2.03	0.41
78:A5:288:G:H2'	78:A5:289:C:C6	2.56	0.41
78:A5:447:C:H2'	78:A5:448:G:C8	2.56	0.41
78:A6:4991:U:H2'	78:A6:4992:G:C8	2.55	0.41
19:B2:982:G:H2'	19:B2:983:A:C8	2.56	0.41
19:B2:1259:A:H62	19:B2:1518:C:H3'	1.85	0.41
19:B2:1319:U:H2'	19:B2:1320:G:C8	2.56	0.41
19:B2:1657:G:H2'	19:B2:1658:G:H8	1.86	0.41
21:CW:13:ILE:HD13	21:CW:30:GLN:HG2	2.02	0.41
22:Ag:285:GLN:HE21	22:Ag:285:GLN:HB2	1.61	0.41
25:AM:36:ARG:HG2	25:AM:36:ARG:HH11	1.85	0.41
37:Cz:77:ALA:HA	37:Cz:80:VAL:HG22	2.02	0.41
43:CN:51:LEU:HD13	43:CN:117:ASN:HB3	2.03	0.41
52:CX:55:ARG:HH12	80:A8:117:C:H5'	1.86	0.41
58:CB:56:ILE:O	58:CB:73:VAL:HA	2.20	0.41
59:CF:223:LYS:HA	59:CF:232:ASP:HB2	2.01	0.41
64:Cg:21:ARG:HD2	78:A6:2687:C:H1'	2.03	0.41
64:Cg:90:ARG:HA	64:Cg:93:ARG:HG2	2.02	0.41
77:CG:171:PRO:HB3	77:CG:181:TYR:CZ	2.55	0.41
78:A5:1863:U:H2'	78:A5:1864:G:H8	1.85	0.41
78:A6:3872:A:H2'	78:A6:3873:G:C8	2.56	0.41
4:AL:17:PHE:CG	19:B2:222:U:H5''	2.56	0.41
5:AB:127:VAL:HG11	5:AB:173:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AB:141:GLY:HA2	5:AB:210:VAL:HG22	2.03	0.41
6:AA:102:ARG:HA	6:AA:102:ARG:HD2	1.90	0.41
13:AE:193:GLY:HA3	13:AE:212:ASP:HA	2.03	0.41
14:AC:208:PRO:HA	14:AC:211:LYS:HB2	2.02	0.41
15:AG:130:PRO:HB2	21:CW:83:THR:HG23	2.02	0.41
15:AG:192:ILE:HD11	19:B2:126:G:C2	2.56	0.41
15:AG:196:LYS:HD3	15:AG:196:LYS:HA	1.73	0.41
17:AW:50:PHE:HB3	17:AW:63:VAL:HG13	2.03	0.41
18:AI:199:LEU:O	18:AI:203:LYS:HG3	2.21	0.41
19:B2:102:A:H5'	19:B2:104:A:C4	2.56	0.41
19:B2:107:A:H2'	19:B2:108:G:C8	2.56	0.41
19:B2:941:C:H2'	19:B2:942:G:C8	2.56	0.41
19:B2:1445:U:H4'	23:AU:57:PRO:HG3	2.03	0.41
38:CO:199:HIS:CE1	38:CO:203:VAL:CB	3.03	0.41
39:CL:96:ILE:HD12	39:CL:96:ILE:H	1.86	0.41
39:CL:102:ARG:HA	78:A5:75:G:C6	2.56	0.41
39:CL:189:ALA:HB2	65:CI:10:GLY:HA2	2.03	0.41
40:CV:62:MET:HA	40:CV:78:PRO:HA	2.03	0.41
43:CN:172:ARG:HG2	78:A5:29:G:H5''	2.02	0.41
45:CD:55:VAL:HG11	45:CD:158:LYS:HB2	2.03	0.41
47:CA:145:LYS:HD3	47:CA:145:LYS:HA	1.90	0.41
48:CS:25:PRO:HA	48:CS:26:PRO:HD3	1.92	0.41
49:CT:88:ARG:HB2	78:A6:4299:U:H4'	2.02	0.41
51:CU:79:SER:HB3	78:A6:2619:G:H5''	2.03	0.41
52:CX:93:ASN:HB3	52:CX:95:THR:HG22	2.02	0.41
53:CY:22:PRO:HG2	53:CY:25:ILE:HG12	2.02	0.41
53:CY:130:LYS:HA	53:CY:130:LYS:HD3	1.84	0.41
54:CZ:12:LEU:HD11	54:CZ:81:MET:HE3	2.03	0.41
58:CB:45:ALA:H	58:CB:183:ILE:HG23	1.85	0.41
61:Cd:46:LEU:HD13	61:Cd:64:ILE:HD11	2.03	0.41
62:Ce:111:ILE:HD13	62:Ce:111:ILE:HG21	1.83	0.41
64:Cg:19:LYS:HA	64:Cg:19:LYS:HD2	1.86	0.41
64:Cg:60:ARG:O	64:Cg:64:LEU:HB2	2.21	0.41
67:Ck:67:LYS:HE3	67:Ck:67:LYS:HB3	1.84	0.41
69:CC:159:GLU:HA	69:CC:217:ILE:HD11	2.03	0.41
74:CJ:104:ASN:HB3	74:CJ:133:VAL:HA	2.03	0.41
74:CJ:118:LYS:HD2	74:CJ:118:LYS:HA	1.80	0.41
78:A5:1370:G:H1'	78:A5:1372:A:C5	2.54	0.41
78:A5:1724:G:O6	78:A5:1838:A:N1	2.54	0.41
78:A5:1824:G:H2'	78:A5:1825:A:C8	2.55	0.41
78:A5:2049:G:H2'	78:A5:2050:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:A7:110:G:H2'	79:A7:111:C:C6	2.56	0.41
78:A6:2568:C:H2'	78:A6:2569:G:H8	1.86	0.41
78:A6:2583:C:H2'	78:A6:2584:G:H8	1.85	0.41
78:A6:3875:G:C5	78:A6:3877:A:H5''	2.56	0.41
78:A6:3942:A:H2'	78:A6:3943:A:C8	2.56	0.41
78:A6:4238:G:H2'	78:A6:4239:A:H8	1.86	0.41
78:A6:4493:U:H2'	78:A6:4494:G:H8	1.85	0.41
78:A6:4723:A:H2'	78:A6:4724:A:C8	2.56	0.41
78:A6:4744:A:H2'	78:A6:4745:G:H8	1.84	0.41
6:AA:137:ALA:HB1	6:AA:142:LEU:HB2	2.03	0.41
6:AA:195:TRP:CD1	6:AA:197:VAL:HG12	2.56	0.41
6:AA:205:ARG:HH12	28:AR:81:ARG:HB3	1.86	0.41
7:AV:57:GLY:O	7:AV:61:ARG:HB2	2.20	0.41
8:AY:10:ARG:HB3	19:B2:835:C:H42	1.86	0.41
12:AJ:172:ARG:HA	12:AJ:175:ARG:HG2	2.02	0.41
13:AE:259:LYS:HB2	13:AE:259:LYS:HE2	1.80	0.41
15:AG:142:ARG:HA	15:AG:147:LEU:HD12	2.02	0.41
19:B2:234:C:H2'	19:B2:235:A:C8	2.56	0.41
19:B2:610:G:H2'	19:B2:611:G:C8	2.55	0.41
19:B2:1402:A:N7	19:B2:1441:U:C5	2.89	0.41
21:CW:23:ARG:HB2	21:CW:27:LYS:HB3	2.03	0.41
29:AP:33:LEU:HD12	29:AP:36:LEU:HD22	2.02	0.41
30:AT:64:LEU:HD13	30:AT:70:ALA:HB3	2.03	0.41
46:CQ:13:VAL:HB	78:A5:1691:G:C8	2.56	0.41
46:CQ:125:GLN:HE22	69:CC:285:ILE:HG23	1.86	0.41
49:CT:7:LYS:HD3	78:A6:4334:U:H5''	2.03	0.41
49:CT:21:LYS:HA	49:CT:21:LYS:HD3	1.90	0.41
52:CX:114:LYS:HD3	52:CX:120:ASP:HA	2.03	0.41
77:CG:190:LEU:HD13	77:CG:202:VAL:HG23	2.04	0.41
78:A5:460:C:H2'	78:A5:461:G:H8	1.85	0.41
78:A5:1069:G:H2'	78:A5:1070:G:C8	2.55	0.41
78:A6:2770:C:H2'	78:A6:2771:G:C8	2.56	0.41
78:A6:4080:C:H2'	78:A6:4081:G:C8	2.56	0.41
78:A6:4312:U:H2'	78:A6:4313:A:C8	2.56	0.41
2:AX:54:LYS:HG2	2:AX:70:VAL:HG12	2.02	0.40
2:AX:135:LYS:HB2	2:AX:137:LYS:HD2	2.03	0.40
3:AN:16:LEU:HA	3:AN:17:PRO:HD3	1.94	0.40
4:AL:51:ILE:HD13	4:AL:51:ILE:HA	1.97	0.40
8:AY:43:LYS:HE2	8:AY:43:LYS:HB2	1.92	0.40
14:AC:142:LYS:HG2	14:AC:153:GLY:HA3	2.02	0.40
19:B2:690:G:H1	19:B2:740:C:H42	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:1753:C:H2'	19:B2:1754:G:H8	1.87	0.40
23:AU:94:PRO:HD2	23:AU:97:ILE:HD12	2.04	0.40
28:AR:76:GLU:HA	28:AR:78:ARG:HH11	1.85	0.40
33:AD:61:GLU:H	33:AD:61:GLU:HG3	1.74	0.40
35:AF:166:ILE:H	35:AF:166:ILE:HG12	1.67	0.40
44:CI:170:LYS:HD3	44:CI:177:ASN:HB3	2.03	0.40
47:CA:128:ARG:HB2	78:A6:3681:G:H2'	2.03	0.40
47:CA:136:VAL:HA	47:CA:148:VAL:HG23	2.03	0.40
48:CS:122:HIS:HB2	79:A7:94:C:H4'	2.03	0.40
49:CT:101:SER:HB2	78:A5:1729:A:H2	1.86	0.40
58:CB:190:VAL:HA	58:CB:193:LYS:HB2	2.02	0.40
69:CC:317:ASN:HD21	69:CC:319:LEU:HB2	1.86	0.40
69:CC:332:ALA:HA	69:CC:335:MET:HB2	2.03	0.40
73:Co:102:GLN:HB2	73:Co:103:VAL:H	1.73	0.40
77:CG:76:VAL:HA	77:CG:77:PRO:HD3	1.98	0.40
78:A5:323:C:H2'	78:A5:324:A:C8	2.55	0.40
78:A5:1219:G:H2'	78:A5:1220:G:C8	2.52	0.40
78:A5:1604:G:H2'	78:A5:1605:G:C8	2.56	0.40
78:A5:1733:G:N3	78:A6:4214:A:H2'	2.37	0.40
78:A6:4346:U:H2'	78:A6:4347:G:C8	2.57	0.40
6:AA:146:ALA:HB3	6:AA:160:ALA:HA	2.03	0.40
6:AA:186:ARG:NH1	7:AV:46:PHE:H	2.19	0.40
9:Aa:70:LYS:HE3	9:Aa:70:LYS:HB2	1.89	0.40
16:AH:58:LYS:HE2	16:AH:58:LYS:HB3	1.93	0.40
19:B2:848:U:H2'	19:B2:849:A:H8	1.87	0.40
19:B2:1106:C:H2'	19:B2:1107:G:H8	1.85	0.40
19:B2:1421:A:H3'	19:B2:1422:G:H8	1.86	0.40
20:CR:171:LYS:HA	20:CR:174:GLU:HG3	2.03	0.40
21:CW:87:LEU:HD13	21:CW:90:ILE:HD11	2.03	0.40
25:AM:39:ALA:HB1	34:Af:103:LEU:HD22	2.02	0.40
39:CL:2:ALA:HA	42:Ca:41:HIS:CE1	2.56	0.40
39:CL:116:ARG:HH12	39:CL:157:VAL:HG22	1.87	0.40
45:CD:32:ALA:O	45:CD:36:LEU:HB2	2.21	0.40
47:CA:194:ASN:HB2	78:A5:1539:G:H4'	2.03	0.40
49:CT:40:VAL:HG21	49:CT:96:ILE:HD12	2.02	0.40
49:CT:74:ILE:HG22	49:CT:76:VAL:HB	2.04	0.40
58:CB:103:LYS:HD2	58:CB:149:ASP:HB2	2.03	0.40
69:CC:309:ILE:HB	69:CC:310:HIS:H	1.69	0.40
72:Cp:7:LYS:HE2	78:A6:2875:C:H2'	2.03	0.40
77:CG:155:VAL:O	77:CG:181:TYR:HA	2.21	0.40
78:A5:284:G:H2'	78:A5:285:G:H8	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:A5:1870:C:H2'	78:A5:1871:A:C8	2.56	0.40
78:A5:1882:U:N3	78:A5:1897:A:C8	2.88	0.40
78:A6:2455:G:C2	78:A6:2456:G:H1'	2.57	0.40
78:A6:4238:G:H2'	78:A6:4239:A:C8	2.56	0.40
78:A6:4276:G:H3'	78:A6:4277:G:H8	1.86	0.40
78:A6:4299:U:H2'	78:A6:4300:U:H6	1.85	0.40
6:AA:205:ARG:HD3	28:AR:82:ASP:HB3	2.04	0.40
13:AE:71:LYS:HA	13:AE:76:VAL:HA	2.02	0.40
15:AG:5:ILE:HD11	15:AG:113:ILE:HG23	2.03	0.40
17:AW:26:LEU:HD23	17:AW:62:VAL:HG12	2.03	0.40
19:B2:1103:C:H2'	19:B2:1104:G:C8	2.56	0.40
19:B2:1386:A:H3'	19:B2:1387:G:H8	1.86	0.40
19:B2:1420:G:H2'	19:B2:1421:A:H8	1.86	0.40
19:B2:1453:C:H2'	19:B2:1455:A:C8	2.57	0.40
20:CR:132:PHE:HD1	20:CR:132:PHE:HA	1.78	0.40
21:CW:20:ARG:HA	21:CW:29:PHE:O	2.21	0.40
22:Ag:176:VAL:HG23	22:Ag:185:LYS:HB2	2.03	0.40
36:AQ:32:ILE:HB	36:AQ:39:LEU:HD21	2.02	0.40
42:Ca:147:VAL:HA	65:Ca:6:PRO:HG2	2.01	0.40
43:CN:120:TRP:HZ2	43:CN:123:GLU:HB2	1.86	0.40
52:CX:54:LEU:H	52:CX:54:LEU:HG	1.72	0.40
58:CB:89:ILE:HG22	58:CB:162:VAL:HA	2.03	0.40
58:CB:231:VAL:H	58:CB:231:VAL:HG22	1.63	0.40
62:Ce:117:GLN:H	62:Ce:117:GLN:HG2	1.76	0.40
69:CC:306:ARG:HH22	69:CC:309:ILE:H	1.69	0.40
75:CH:2:LYS:HG3	75:CH:61:TRP:CD1	2.56	0.40
76:CE:95:PRO:HD3	76:CE:105:ARG:HB2	2.03	0.40
78:A5:223:G:H4'	78:A5:225:G:N7	2.36	0.40
78:A5:1346:C:H2'	78:A5:1347:G:C8	2.56	0.40
78:A5:1738:A:H2'	78:A5:1739:G:H8	1.86	0.40
79:A7:85:G:H2'	79:A7:86:G:H8	1.85	0.40
78:A6:2420:A:H5''	78:A6:2421:G:H5''	2.02	0.40
78:A6:3880:G:H2'	78:A6:3881:G:C8	2.56	0.40
78:A6:4246:G:H2'	78:A6:4247:G:H8	1.87	0.40
2:AX:41:PHE:HB3	2:AX:44:ALA:HB3	2.03	0.40
2:AX:69:CYS:HB3	2:AX:84:PHE:HA	2.04	0.40
5:AB:133:TYR:HE2	5:AB:181:LEU:HD22	1.86	0.40
8:AY:9:THR:HB	8:AY:23:MET:HE3	2.04	0.40
13:AE:19:MET:HE3	19:B2:846:G:C5	2.57	0.40
17:AW:47:ILE:HD12	17:AW:47:ILE:HA	1.82	0.40
17:AW:111:MET:HE1	17:AW:116:ALA:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B2:373:G:H2'	19:B2:374:G:C8	2.54	0.40
19:B2:788:G:H2'	19:B2:789:G:H8	1.86	0.40
19:B2:1165:G:H4'	19:B2:1166:G:H5''	2.03	0.40
19:B2:1801:A:H2'	19:B2:1802:C:C6	2.56	0.40
22:Ag:289:LEU:HD13	22:Ag:298:LEU:HD11	2.04	0.40
33:AD:29:LEU:HB2	33:AD:34:TYR:HB2	2.03	0.40
33:AD:137:VAL:HG22	33:AD:151:LYS:HG2	2.04	0.40
36:AQ:72:VAL:HG11	36:AQ:80:GLN:HE21	1.87	0.40
37:Cz:210:MET:HA	78:A6:4052:C:H5'	2.03	0.40
40:CV:30:ASP:HB2	40:CV:31:ASN:H	1.74	0.40
43:CN:51:LEU:HD23	43:CN:51:LEU:HA	1.87	0.40
44:CI:52:MET:HE1	44:CI:159:PHE:HE2	1.86	0.40
59:CF:113:ARG:HA	59:CF:115:ARG:HD3	2.04	0.40
66:Cj:59:THR:HG23	80:A8:41:A:H4'	2.03	0.40
69:CC:289:LEU:O	69:CC:293:LEU:HB2	2.21	0.40
76:CE:221:LYS:HB2	76:CE:221:LYS:HE3	1.84	0.40
76:CE:249:ASP:HA	76:CE:252:ALA:HB3	2.03	0.40
78:A5:84:A:H61	78:A5:98:A:H5''	1.86	0.40
78:A5:132:G:H4'	78:A5:178:C:H4'	2.03	0.40
78:A5:1272:C:H5''	78:A5:1273:G:C2	2.56	0.40
78:A5:1724:G:C2	78:A5:1838:A:H2	2.39	0.40
78:A5:1802:A:H5''	78:A5:1803:G:H5'	2.04	0.40
78:A5:2090:U:C2	78:A6:2259:G:H5'	2.57	0.40
78:A6:2607:C:H2'	78:A6:2608:G:H8	1.87	0.40
78:A6:3732:A:H2'	78:A6:3733:A:C8	2.57	0.40
78:A6:3872:A:H2'	78:A6:3873:G:H8	1.86	0.40
78:A6:4680:G:H2'	78:A6:4681:A:C8	2.56	0.40
78:A6:4745:G:N3	78:A6:4955:A:N1	2.70	0.40
4:AL:78:THR:HG21	4:AL:89:ARG:HD2	2.03	0.40
9:Aa:74:CYS:O	9:Aa:78:ALA:HB2	2.22	0.40
19:B2:328:U:H2'	19:B2:329:G:C8	2.56	0.40
19:B2:345:U:H2'	19:B2:346:C:C6	2.56	0.40
19:B2:1051:G:H2'	19:B2:1052:A:C8	2.56	0.40
19:B2:1217:A:H2'	19:B2:1218:C:C6	2.57	0.40
19:B2:1731:A:H2'	19:B2:1732:G:H8	1.86	0.40
35:AF:94:LYS:HD3	35:AF:94:LYS:HA	1.90	0.40
37:Cz:155:ILE:HD13	37:Cz:169:VAL:HG12	2.04	0.40
39:CL:117:LEU:HD23	39:CL:117:LEU:HA	1.90	0.40
43:CN:73:ARG:HB3	43:CN:89:VAL:HB	2.04	0.40
44:CI:19:LYS:HE3	44:CI:19:LYS:HB2	1.90	0.40
47:CA:180:LEU:HD12	47:CA:180:LEU:HA	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:CU:82:TYR:O	51:CU:86:LEU:HG	2.22	0.40
56:Ch:16:GLU:H	56:Ch:16:GLU:HG3	1.65	0.40
69:CC:101:MET:HE2	69:CC:104:PRO:HA	2.04	0.40
74:CJ:20:LEU:HB3	74:CJ:79:ALA:HB1	2.04	0.40
78:A5:1303:A:H2'	78:A5:1304:C:H6	1.86	0.40
79:A7:31:G:H2'	79:A7:32:A:C8	2.57	0.40
78:A6:3664:G:H2'	78:A6:3665:G:H8	1.87	0.40
78:A6:3937:C:H2'	78:A6:3938:G:N2	2.37	0.40
78:A6:4767:C:H2'	78:A6:4768:G:C8	2.56	0.40
78:A6:4997:G:H2'	78:A6:4998:G:C8	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AO	134/136 (98%)	115 (86%)	18 (13%)	1 (1%)	18	49
2	AX	140/142 (99%)	129 (92%)	11 (8%)	0	100	100
3	AN	148/150 (99%)	136 (92%)	10 (7%)	2 (1%)	9	34
4	AL	156/158 (99%)	130 (83%)	23 (15%)	3 (2%)	6	27
5	AB	213/215 (99%)	193 (91%)	17 (8%)	3 (1%)	9	34
6	AA	206/208 (99%)	175 (85%)	30 (15%)	1 (0%)	24	57
7	AV	80/82 (98%)	70 (88%)	10 (12%)	0	100	100
8	AY	124/126 (98%)	107 (86%)	16 (13%)	1 (1%)	16	47
9	Aa	105/107 (98%)	91 (87%)	14 (13%)	0	100	100
10	Ab	82/84 (98%)	74 (90%)	8 (10%)	0	100	100
11	Ae	57/59 (97%)	46 (81%)	10 (18%)	1 (2%)	6	28
12	AJ	173/182 (95%)	155 (90%)	17 (10%)	1 (1%)	21	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	AE	261/263 (99%)	229 (88%)	29 (11%)	3 (1%)	11	39
14	AC	224/226 (99%)	207 (92%)	16 (7%)	1 (0%)	30	61
15	AG	235/237 (99%)	218 (93%)	16 (7%)	1 (0%)	30	61
16	AH	188/190 (99%)	160 (85%)	23 (12%)	5 (3%)	4	20
17	AW	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
18	AI	204/206 (99%)	173 (85%)	25 (12%)	6 (3%)	3	19
20	CR	149/153 (97%)	136 (91%)	13 (9%)	0	100	100
21	CW	122/124 (98%)	95 (78%)	27 (22%)	0	100	100
22	Ag	302/313 (96%)	270 (89%)	31 (10%)	1 (0%)	36	67
23	AU	102/104 (98%)	90 (88%)	10 (10%)	2 (2%)	6	25
24	AK	96/98 (98%)	71 (74%)	20 (21%)	5 (5%)	1	10
25	AM	122/124 (98%)	94 (77%)	26 (21%)	2 (2%)	7	30
26	AS	135/137 (98%)	119 (88%)	15 (11%)	1 (1%)	18	49
27	Ad	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
28	AR	124/126 (98%)	106 (86%)	16 (13%)	2 (2%)	7	30
29	AP	117/127 (92%)	101 (86%)	11 (9%)	5 (4%)	2	12
30	AT	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
31	AZ	73/75 (97%)	66 (90%)	6 (8%)	1 (1%)	9	34
32	Ac	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
33	AD	221/227 (97%)	198 (90%)	22 (10%)	1 (0%)	24	57
34	Af	69/71 (97%)	57 (83%)	10 (14%)	2 (3%)	3	19
35	AF	189/191 (99%)	164 (87%)	24 (13%)	1 (0%)	24	57
36	AQ	139/141 (99%)	122 (88%)	15 (11%)	2 (1%)	9	34
37	Cz	188/217 (87%)	169 (90%)	19 (10%)	0	100	100
38	CO	200/202 (99%)	191 (96%)	8 (4%)	1 (0%)	24	57
39	CL	208/210 (99%)	192 (92%)	14 (7%)	2 (1%)	12	41
40	CV	131/133 (98%)	121 (92%)	9 (7%)	1 (1%)	16	47
41	CM	137/139 (99%)	121 (88%)	16 (12%)	0	100	100
42	Ca	145/147 (99%)	126 (87%)	17 (12%)	2 (1%)	9	34
43	CN	201/203 (99%)	187 (93%)	14 (7%)	0	100	100
44	CI	197/213 (92%)	173 (88%)	23 (12%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	CD	287/289 (99%)	263 (92%)	23 (8%)	1 (0%)	36	67
46	CQ	186/188 (99%)	163 (88%)	22 (12%)	1 (0%)	24	57
47	CA	253/255 (99%)	231 (91%)	22 (9%)	0	100	100
48	CS	173/175 (99%)	155 (90%)	18 (10%)	0	100	100
49	CT	157/159 (99%)	141 (90%)	16 (10%)	0	100	100
50	CP	150/152 (99%)	142 (95%)	8 (5%)	0	100	100
51	CU	110/112 (98%)	91 (83%)	18 (16%)	1 (1%)	14	44
52	CX	119/121 (98%)	109 (92%)	7 (6%)	3 (2%)	4	21
53	CY	131/133 (98%)	122 (93%)	8 (6%)	1 (1%)	16	47
54	CZ	133/135 (98%)	117 (88%)	15 (11%)	1 (1%)	16	47
55	Cr	135/137 (98%)	107 (79%)	25 (18%)	3 (2%)	5	24
56	Ch	121/123 (98%)	105 (87%)	15 (12%)	1 (1%)	16	47
57	Cb	65/78 (83%)	59 (91%)	4 (6%)	2 (3%)	3	18
58	CB	390/397 (98%)	351 (90%)	35 (9%)	4 (1%)	12	41
59	CF	227/229 (99%)	215 (95%)	9 (4%)	3 (1%)	9	35
60	Cc	98/100 (98%)	92 (94%)	5 (5%)	1 (1%)	12	41
61	Cd	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
62	Ce	131/133 (98%)	122 (93%)	8 (6%)	1 (1%)	16	47
63	Cf	107/109 (98%)	90 (84%)	15 (14%)	2 (2%)	6	27
64	Cg	112/114 (98%)	99 (88%)	13 (12%)	0	100	100
65	Ci	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	41
66	Cj	88/90 (98%)	78 (89%)	9 (10%)	1 (1%)	11	39
67	Ck	67/69 (97%)	58 (87%)	9 (13%)	0	100	100
68	Cl	48/50 (96%)	48 (100%)	0	0	100	100
69	CC	356/368 (97%)	301 (85%)	51 (14%)	4 (1%)	11	39
70	Cm	50/52 (96%)	46 (92%)	3 (6%)	1 (2%)	6	25
71	Cn	23/25 (92%)	23 (100%)	0	0	100	100
72	Cp	88/90 (98%)	82 (93%)	6 (7%)	0	100	100
73	Co	103/105 (98%)	87 (84%)	15 (15%)	1 (1%)	12	41
74	CJ	166/168 (99%)	154 (93%)	10 (6%)	2 (1%)	10	37
75	CH	189/191 (99%)	177 (94%)	11 (6%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	CE	260/262 (99%)	200 (77%)	53 (20%)	7 (3%)	4	20
77	CG	244/246 (99%)	218 (89%)	23 (9%)	3 (1%)	10	37
All	All	11455/11704 (98%)	10164 (89%)	1184 (10%)	107 (1%)	16	44

All (107) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AO	56	VAL
4	AL	23	VAL
13	AE	164	LEU
16	AH	66	VAL
18	AI	120	PRO
18	AI	145	ILE
22	Ag	282	GLU
24	AK	30	PRO
24	AK	43	LEU
24	AK	89	ILE
29	AP	126	VAL
31	AZ	108	ILE
33	AD	202	LYS
34	Af	98	VAL
34	Af	102	VAL
38	CO	111	PRO
39	CL	47	ALA
40	CV	45	ILE
42	Ca	89	ASN
45	CD	125	VAL
52	CX	58	PRO
60	Cc	12	GLU
65	Ci	5	TYR
69	CC	313	VAL
75	CH	107	GLU
76	CE	47	ASN
76	CE	51	VAL
76	CE	94	LYS
76	CE	187	ARG
76	CE	224	LYS
77	CG	230	TYR
16	AH	76	GLN
16	AH	160	LYS
18	AI	22	HIS

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Mol	Chain	Res	Type
18	AI	140	LYS
18	AI	158	ILE
23	AU	50	VAL
25	AM	94	ILE
35	AF	203	ASN
36	AQ	42	ILE
42	Ca	47	LYS
46	CQ	98	LEU
51	CU	60	VAL
55	Cr	44	ILE
55	Cr	70	GLN
58	CB	326	VAL
63	Cf	65	ASN
3	AN	3	ARG
23	AU	107	GLU
24	AK	35	LEU
25	AM	12	MET
26	AS	12	ILE
29	AP	71	GLU
59	CF	197	VAL
66	Cj	90	ALA
73	Co	77	CYS
77	CG	207	VAL
5	AB	106	THR
5	AB	223	PHE
13	AE	171	ASP
16	AH	17	ASP
18	AI	139	LYS
29	AP	14	LYS
29	AP	69	PRO
36	AQ	32	ILE
44	CI	3	ARG
53	CY	67	ILE
55	Cr	78	VAL
57	Cb	25	ARG
69	CC	309	ILE
70	Cm	78	ILE
74	CJ	117	ILE
76	CE	96	VAL
3	AN	22	VAL
5	AB	210	VAL
6	AA	159	ILE

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Mol	Chain	Res	Type
11	Ae	52	LYS
12	AJ	148	ILE
14	AC	176	LYS
15	AG	174	PRO
16	AH	100	ILE
29	AP	75	VAL
39	CL	157	VAL
52	CX	40	ILE
52	CX	43	SER
57	Cb	21	ILE
58	CB	293	ILE
69	CC	295	SER
74	CJ	98	ASN
4	AL	2	ALA
4	AL	25	LEU
28	AR	95	ILE
59	CF	220	MET
62	Ce	4	LEU
63	Cf	54	LYS
76	CE	185	PRO
77	CG	227	ASN
13	AE	90	ILE
24	AK	3	MET
56	Ch	115	PRO
69	CC	24	LEU
8	AY	51	THR
54	CZ	90	PRO
58	CB	40	PRO
59	CF	184	ILE
28	AR	88	VAL
58	CB	18	PRO

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AO	106/106 (100%)	100 (94%)	6 (6%)	18	49
2	AX	114/114 (100%)	109 (96%)	5 (4%)	25	56
3	AN	130/130 (100%)	123 (95%)	7 (5%)	20	50
4	AL	142/142 (100%)	135 (95%)	7 (5%)	22	53
5	AB	196/196 (100%)	188 (96%)	8 (4%)	27	59
6	AA	174/174 (100%)	160 (92%)	14 (8%)	11	37
7	AV	66/66 (100%)	64 (97%)	2 (3%)	36	65
8	AY	108/108 (100%)	100 (93%)	8 (7%)	13	40
9	Aa	90/90 (100%)	85 (94%)	5 (6%)	19	49
10	Ab	76/76 (100%)	72 (95%)	4 (5%)	20	51
11	Ae	48/48 (100%)	47 (98%)	1 (2%)	47	71
12	AJ	156/157 (99%)	149 (96%)	7 (4%)	24	56
13	AE	225/225 (100%)	215 (96%)	10 (4%)	25	56
14	AC	190/190 (100%)	183 (96%)	7 (4%)	30	61
15	AG	207/207 (100%)	201 (97%)	6 (3%)	37	66
16	AH	170/170 (100%)	156 (92%)	14 (8%)	10	36
17	AW	112/112 (100%)	103 (92%)	9 (8%)	11	37
18	AI	178/178 (100%)	172 (97%)	6 (3%)	32	63
20	CR	134/134 (100%)	129 (96%)	5 (4%)	30	61
21	CW	103/103 (100%)	98 (95%)	5 (5%)	22	53
22	Ag	265/272 (97%)	257 (97%)	8 (3%)	36	65
23	AU	94/94 (100%)	92 (98%)	2 (2%)	47	71
24	AK	89/89 (100%)	83 (93%)	6 (7%)	15	43
25	AM	104/104 (100%)	96 (92%)	8 (8%)	12	38
26	AS	119/119 (100%)	111 (93%)	8 (7%)	15	43
27	Ad	47/47 (100%)	47 (100%)	0	100	100
28	AR	114/114 (100%)	112 (98%)	2 (2%)	51	73
29	AP	108/116 (93%)	106 (98%)	2 (2%)	50	73
30	AT	112/112 (100%)	108 (96%)	4 (4%)	31	62
31	AZ	66/66 (100%)	63 (96%)	3 (4%)	24	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	Ac	57/57 (100%)	54 (95%)	3 (5%)	20	51
33	AD	187/190 (98%)	184 (98%)	3 (2%)	55	75
34	Af	64/64 (100%)	62 (97%)	2 (3%)	35	64
35	AF	161/161 (100%)	155 (96%)	6 (4%)	30	61
36	AQ	117/117 (100%)	109 (93%)	8 (7%)	14	42
37	Cz	170/196 (87%)	165 (97%)	5 (3%)	37	66
38	CO	173/173 (100%)	166 (96%)	7 (4%)	28	60
39	CL	176/176 (100%)	172 (98%)	4 (2%)	44	70
40	CV	102/102 (100%)	99 (97%)	3 (3%)	37	66
41	CM	118/118 (100%)	110 (93%)	8 (7%)	14	42
42	Ca	120/120 (100%)	111 (92%)	9 (8%)	12	39
43	CN	171/171 (100%)	167 (98%)	4 (2%)	44	70
44	CI	171/180 (95%)	160 (94%)	11 (6%)	16	44
45	CD	243/243 (100%)	236 (97%)	7 (3%)	37	66
46	CQ	165/165 (100%)	154 (93%)	11 (7%)	15	43
47	CA	197/197 (100%)	188 (95%)	9 (5%)	24	55
48	CS	156/156 (100%)	152 (97%)	4 (3%)	40	68
49	CT	139/139 (100%)	133 (96%)	6 (4%)	26	57
50	CP	133/133 (100%)	128 (96%)	5 (4%)	29	60
51	CU	102/102 (100%)	98 (96%)	4 (4%)	28	60
52	CX	109/109 (100%)	103 (94%)	6 (6%)	19	50
53	CY	123/123 (100%)	118 (96%)	5 (4%)	27	59
54	CZ	117/117 (100%)	113 (97%)	4 (3%)	32	63
55	Cr	121/121 (100%)	108 (89%)	13 (11%)	6	25
56	Ch	110/110 (100%)	105 (96%)	5 (4%)	24	56
57	Cb	58/66 (88%)	55 (95%)	3 (5%)	21	51
58	CB	341/345 (99%)	331 (97%)	10 (3%)	37	66
59	CF	198/198 (100%)	193 (98%)	5 (2%)	42	69
60	Cc	85/85 (100%)	80 (94%)	5 (6%)	18	48
61	Cd	102/102 (100%)	91 (89%)	11 (11%)	6	25
62	Ce	119/119 (100%)	108 (91%)	11 (9%)	8	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	Cf	88/88 (100%)	84 (96%)	4 (4%)	24	56
64	Cg	98/98 (100%)	91 (93%)	7 (7%)	13	41
65	Ci	87/87 (100%)	83 (95%)	4 (5%)	24	55
66	Cj	75/75 (100%)	73 (97%)	2 (3%)	39	67
67	Ck	64/64 (100%)	60 (94%)	4 (6%)	16	45
68	Cl	47/47 (100%)	44 (94%)	3 (6%)	16	44
69	CC	298/305 (98%)	283 (95%)	15 (5%)	22	53
70	Cm	48/48 (100%)	47 (98%)	1 (2%)	47	71
71	Cn	24/24 (100%)	23 (96%)	1 (4%)	26	58
72	Cp	74/74 (100%)	69 (93%)	5 (7%)	14	42
73	Co	93/93 (100%)	85 (91%)	8 (9%)	10	34
74	CJ	142/142 (100%)	135 (95%)	7 (5%)	22	53
75	CH	170/170 (100%)	165 (97%)	5 (3%)	37	66
76	CE	232/232 (100%)	211 (91%)	21 (9%)	9	32
77	CG	209/209 (100%)	202 (97%)	7 (3%)	33	63
All	All	9997/10070 (99%)	9527 (95%)	470 (5%)	25	55

All (470) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AO	39	ASP
1	AO	40	THR
1	AO	60	MET
1	AO	62	VAL
1	AO	91	THR
1	AO	103	ASN
2	AX	7	LEU
2	AX	32	LEU
2	AX	82	THR
2	AX	105	PHE
2	AX	137	LYS
3	AN	9	LYS
3	AN	49	GLN
3	AN	53	ILE
3	AN	66	VAL
3	AN	88	LEU
3	AN	134	VAL

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Mol	Chain	Res	Type
3	AN	150	VAL
4	AL	4	ILE
4	AL	33	LEU
4	AL	42	LEU
4	AL	65	ASN
4	AL	125	ILE
4	AL	145	VAL
4	AL	158	PHE
5	AB	31	TYR
5	AB	38	MET
5	AB	51	ARG
5	AB	90	ASP
5	AB	119	THR
5	AB	169	MET
5	AB	189	ILE
5	AB	202	GLN
6	AA	7	VAL
6	AA	23	THR
6	AA	30	LEU
6	AA	34	MET
6	AA	57	LYS
6	AA	58	LEU
6	AA	89	LYS
6	AA	121	LEU
6	AA	132	GLN
6	AA	136	GLU
6	AA	140	VAL
6	AA	144	THR
6	AA	154	LEU
6	AA	185	MET
7	AV	3	ASN
7	AV	65	SER
8	AY	14	THR
8	AY	25	ILE
8	AY	34	THR
8	AY	48	TYR
8	AY	74	MET
8	AY	79	LEU
8	AY	81	TYR
8	AY	100	LYS
9	Aa	30	VAL
9	Aa	37	LYS

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Mol	Chain	Res	Type
9	Aa	45	VAL
9	Aa	64	LEU
9	Aa	84	VAL
10	Ab	24	LEU
10	Ab	36	LYS
10	Ab	65	GLN
10	Ab	74	THR
11	Ae	15	GLN
12	AJ	7	TRP
12	AJ	34	GLU
12	AJ	66	LYS
12	AJ	93	LYS
12	AJ	101	LYS
12	AJ	140	GLN
12	AJ	142	VAL
13	AE	64	ILE
13	AE	105	THR
13	AE	115	THR
13	AE	160	ILE
13	AE	170	THR
13	AE	199	GLU
13	AE	208	VAL
13	AE	222	LEU
13	AE	233	LYS
13	AE	248	ILE
14	AC	63	VAL
14	AC	70	VAL
14	AC	88	ILE
14	AC	106	VAL
14	AC	151	ILE
14	AC	194	ARG
14	AC	209	VAL
15	AG	24	LEU
15	AG	31	ARG
15	AG	77	LEU
15	AG	83	CYS
15	AG	133	LEU
15	AG	148	SER
16	AH	8	ILE
16	AH	15	LYS
16	AH	17	ASP
16	AH	27	LEU

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Mol	Chain	Res	Type
16	AH	39	GLN
16	AH	40	LEU
16	AH	69	LEU
16	AH	71	SER
16	AH	72	PHE
16	AH	75	ILE
16	AH	80	VAL
16	AH	88	SER
16	AH	92	VAL
16	AH	184	ASP
17	AW	24	GLN
17	AW	26	LEU
17	AW	30	CYS
17	AW	33	VAL
17	AW	42	MET
17	AW	52	ILE
17	AW	70	ASN
17	AW	105	THR
17	AW	120	HIS
18	AI	3	ILE
18	AI	9	HIS
18	AI	78	ILE
18	AI	104	ILE
18	AI	119	LEU
18	AI	175	ILE
20	CR	21	LYS
20	CR	23	TRP
20	CR	53	LYS
20	CR	64	ARG
20	CR	134	ASN
21	CW	17	HIS
21	CW	20	ARG
21	CW	24	THR
21	CW	37	GLU
21	CW	41	LEU
22	Ag	7	LEU
22	Ag	46	THR
22	Ag	70	VAL
22	Ag	121	VAL
22	Ag	149	GLU
22	Ag	174	VAL
22	Ag	219	TRP

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Mol	Chain	Res	Type
22	Ag	256	ILE
23	AU	48	LEU
23	AU	115	THR
24	AK	11	ILE
24	AK	15	LEU
24	AK	20	VAL
24	AK	35	LEU
24	AK	37	ASP
24	AK	58	VAL
25	AM	55	ASN
25	AM	58	GLU
25	AM	61	TYR
25	AM	82	ASN
25	AM	92	CYS
25	AM	94	ILE
25	AM	102	LYS
25	AM	103	VAL
26	AS	9	PHE
26	AS	13	LEU
26	AS	39	ARG
26	AS	45	LEU
26	AS	50	ILE
26	AS	76	GLN
26	AS	111	LEU
26	AS	126	PHE
28	AR	82	ASP
28	AR	115	SER
29	AP	79	HIS
29	AP	127	LYS
30	AT	4	VAL
30	AT	32	GLU
30	AT	36	THR
30	AT	78	ILE
31	AZ	62	VAL
31	AZ	69	THR
31	AZ	75	GLU
32	Ac	34	PHE
32	Ac	43	ILE
32	Ac	46	VAL
33	AD	23	GLU
33	AD	164	VAL
33	AD	190	LEU

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Mol	Chain	Res	Type
34	Af	109	ASP
34	Af	117	LEU
35	AF	20	PHE
35	AF	45	TYR
35	AF	77	MET
35	AF	83	ASN
35	AF	128	ILE
35	AF	173	LEU
36	AQ	12	VAL
36	AQ	18	THR
36	AQ	20	THR
36	AQ	39	LEU
36	AQ	70	VAL
36	AQ	102	GLU
36	AQ	113	ILE
36	AQ	127	CYS
37	Cz	67	VAL
37	Cz	76	GLU
37	Cz	148	VAL
37	Cz	154	THR
37	Cz	167	VAL
38	CO	34	VAL
38	CO	37	ARG
38	CO	138	LEU
38	CO	149	TYR
38	CO	193	THR
38	CO	199	HIS
38	CO	201	LEU
39	CL	65	ARG
39	CL	94	ILE
39	CL	144	LEU
39	CL	173	GLU
40	CV	72	LEU
40	CV	77	HIS
40	CV	96	LEU
41	CM	6	PHE
41	CM	27	ILE
41	CM	29	ASP
41	CM	64	PHE
41	CM	69	HIS
41	CM	74	ARG
41	CM	84	THR

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Mol	Chain	Res	Type
41	CM	108	ASP
42	Ca	7	LYS
42	Ca	16	SER
42	Ca	22	ILE
42	Ca	77	LYS
42	Ca	78	LEU
42	Ca	81	LEU
42	Ca	88	VAL
42	Ca	123	ILE
42	Ca	145	VAL
43	CN	132	VAL
43	CN	171	SER
43	CN	181	HIS
43	CN	197	THR
44	CI	10	ARG
44	CI	59	GLN
44	CI	63	GLU
44	CI	65	LEU
44	CI	134	VAL
44	CI	142	LEU
44	CI	166	HIS
44	CI	167	ILE
44	CI	203	HIS
44	CI	206	LEU
44	CI	208	LYS
45	CD	55	VAL
45	CD	150	LEU
45	CD	223	PHE
45	CD	242	LYS
45	CD	261	VAL
45	CD	268	ARG
45	CD	288	LEU
46	CQ	7	HIS
46	CQ	13	VAL
46	CQ	54	SER
46	CQ	81	VAL
46	CQ	82	VAL
46	CQ	98	LEU
46	CQ	100	VAL
46	CQ	126	LEU
46	CQ	137	VAL
46	CQ	150	ARG

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Mol	Chain	Res	Type
46	CQ	158	THR
47	CA	30	ARG
47	CA	45	VAL
47	CA	62	VAL
47	CA	67	TYR
47	CA	75	LEU
47	CA	101	VAL
47	CA	107	MET
47	CA	165	VAL
47	CA	207	VAL
48	CS	9	GLU
48	CS	24	THR
48	CS	27	LEU
48	CS	158	VAL
49	CT	3	ASN
49	CT	25	VAL
49	CT	27	LEU
49	CT	61	THR
49	CT	128	LEU
49	CT	150	LEU
50	CP	58	VAL
50	CP	104	LEU
50	CP	113	VAL
50	CP	114	ILE
50	CP	148	MET
51	CU	71	THR
51	CU	76	VAL
51	CU	78	PHE
51	CU	98	ASP
52	CX	54	LEU
52	CX	71	LEU
52	CX	82	THR
52	CX	95	THR
52	CX	125	ASN
52	CX	155	ILE
53	CY	12	SER
53	CY	49	ILE
53	CY	85	VAL
53	CY	96	HIS
53	CY	119	LEU
54	CZ	43	VAL
54	CZ	67	LYS

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Mol	Chain	Res	Type
54	CZ	79	HIS
54	CZ	96	VAL
55	Cr	21	ASN
55	Cr	40	TYR
55	Cr	44	ILE
55	Cr	48	THR
55	Cr	49	VAL
55	Cr	63	VAL
55	Cr	64	ILE
55	Cr	80	THR
55	Cr	84	LYS
55	Cr	94	ARG
55	Cr	102	TYR
55	Cr	125	MET
55	Cr	134	THR
56	Ch	19	LYS
56	Ch	47	ILE
56	Ch	104	THR
56	Ch	111	GLU
56	Ch	116	LEU
57	Cb	4	SER
57	Cb	13	SER
57	Cb	54	LEU
58	CB	17	LEU
58	CB	81	THR
58	CB	85	VAL
58	CB	99	LEU
58	CB	231	VAL
58	CB	233	SER
58	CB	240	LEU
58	CB	272	LYS
58	CB	321	VAL
58	CB	344	VAL
59	CF	63	GLN
59	CF	83	VAL
59	CF	102	SER
59	CF	105	VAL
59	CF	170	THR
60	Cc	21	VAL
60	Cc	28	VAL
60	Cc	47	ILE
60	Cc	61	GLU

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Mol	Chain	Res	Type
60	Cc	88	TYR
61	Cd	21	VAL
61	Cd	22	THR
61	Cd	38	PHE
61	Cd	66	THR
61	Cd	68	LEU
61	Cd	88	LEU
61	Cd	103	TYR
61	Cd	105	LEU
61	Cd	107	THR
61	Cd	109	VAL
61	Cd	119	THR
62	Ce	8	VAL
62	Ce	13	VAL
62	Ce	17	THR
62	Ce	41	ILE
62	Ce	78	LEU
62	Ce	81	ASN
62	Ce	85	LEU
62	Ce	87	VAL
62	Ce	93	LYS
62	Ce	99	ILE
62	Ce	123	THR
63	Cf	30	ILE
63	Cf	37	ASP
63	Cf	84	VAL
63	Cf	104	MET
64	Cg	5	LEU
64	Cg	32	TYR
64	Cg	33	LEU
64	Cg	65	MET
64	Cg	67	LEU
64	Cg	91	ILE
64	Cg	104	VAL
65	Ci	4	ARG
65	Ci	37	THR
65	Ci	44	ILE
65	Ci	61	LEU
66	Cj	18	LEU
66	Cj	33	THR
67	Ck	27	LYS
67	Ck	46	VAL

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Mol	Chain	Res	Type
67	Ck	47	ILE
67	Ck	54	GLU
68	Cl	4	HIS
68	Cl	6	THR
68	Cl	17	GLN
69	CC	7	LEU
69	CC	57	LEU
69	CC	149	GLU
69	CC	154	VAL
69	CC	170	LEU
69	CC	183	VAL
69	CC	187	GLN
69	CC	221	PHE
69	CC	232	VAL
69	CC	273	LEU
69	CC	306	ARG
69	CC	309	ILE
69	CC	322	LEU
69	CC	334	THR
69	CC	345	ARG
70	Cm	91	CYS
71	Cn	24	SER
72	Cp	8	VAL
72	Cp	52	VAL
72	Cp	63	THR
72	Cp	70	THR
72	Cp	73	THR
73	Co	3	ASN
73	Co	12	CYS
73	Co	18	HIS
73	Co	61	LYS
73	Co	81	ARG
73	Co	88	CYS
73	Co	93	LEU
73	Co	102	GLN
74	CJ	32	ARG
74	CJ	47	THR
74	CJ	70	VAL
74	CJ	73	THR
74	CJ	98	ASN
74	CJ	132	VAL
74	CJ	161	GLU

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Mol	Chain	Res	Type
75	CH	19	THR
75	CH	21	LYS
75	CH	54	ARG
75	CH	57	VAL
75	CH	110	SER
76	CE	62	MET
76	CE	69	TYR
76	CE	88	VAL
76	CE	89	LEU
76	CE	94	LYS
76	CE	104	THR
76	CE	115	TYR
76	CE	126	LEU
76	CE	145	THR
76	CE	150	LEU
76	CE	153	LEU
76	CE	163	VAL
76	CE	183	ARG
76	CE	189	THR
76	CE	201	ILE
76	CE	207	LYS
76	CE	208	ILE
76	CE	213	THR
76	CE	250	GLN
76	CE	267	LEU
76	CE	274	VAL
77	CG	45	ILE
77	CG	71	TYR
77	CG	76	VAL
77	CG	155	VAL
77	CG	157	ILE
77	CG	161	VAL
77	CG	202	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (130) such sidechains are listed below:

Mol	Chain	Res	Type
1	AO	83	GLN
1	AO	103	ASN
4	AL	5	GLN
4	AL	106	HIS
5	AB	147	ASN

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Mol	Chain	Res	Type
5	AB	149	GLN
6	AA	70	ASN
8	AY	112	ASN
9	Aa	7	ASN
10	Ab	65	GLN
11	Ae	15	GLN
11	Ae	58	ASN
12	AJ	140	GLN
14	AC	120	GLN
15	AG	4	ASN
15	AG	56	ASN
15	AG	155	GLN
15	AG	177	GLN
16	AH	39	GLN
16	AH	162	GLN
16	AH	165	ASN
17	AW	24	GLN
18	AI	111	GLN
18	AI	155	ASN
18	AI	167	GLN
18	AI	168	GLN
20	CR	7	GLN
20	CR	27	ASN
20	CR	121	HIS
22	Ag	20	GLN
22	Ag	187	ASN
22	Ag	191	HIS
22	Ag	226	HIS
22	Ag	285	GLN
22	Ag	305	ASN
22	Ag	311	GLN
23	AU	18	HIS
25	AM	75	ASN
25	AM	82	ASN
26	AS	85	ASN
26	AS	135	HIS
29	AP	104	GLN
30	AT	85	ASN
32	Ac	26	GLN
33	AD	174	HIS
35	AF	101	HIS
35	AF	118	ASN

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Mol	Chain	Res	Type
36	AQ	35	ASN
36	AQ	97	GLN
37	Cz	44	GLN
37	Cz	184	HIS
38	CO	150	GLN
38	CO	199	HIS
39	CL	111	GLN
39	CL	115	GLN
39	CL	205	GLN
40	CV	77	HIS
42	Ca	66	ASN
42	Ca	120	GLN
43	CN	57	GLN
43	CN	201	HIS
44	CI	130	HIS
45	CD	42	ASN
45	CD	63	GLN
45	CD	81	HIS
45	CD	122	GLN
45	CD	198	HIS
45	CD	202	GLN
45	CD	229	ASN
45	CD	250	ASN
45	CD	267	ASN
46	CQ	7	HIS
46	CQ	8	ASN
46	CQ	44	ASN
46	CQ	160	HIS
47	CA	140	ASN
47	CA	217	GLN
47	CA	253	GLN
48	CS	77	ASN
48	CS	91	HIS
48	CS	125	GLN
49	CT	69	GLN
49	CT	127	GLN
50	CP	93	HIS
50	CP	120	ASN
50	CP	133	HIS
52	CX	125	ASN
53	CY	61	HIS
54	CZ	97	ASN

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Mol	Chain	Res	Type
55	Cr	21	ASN
55	Cr	23	GLN
56	Ch	30	GLN
56	Ch	108	GLN
58	CB	109	HIS
58	CB	213	GLN
58	CB	302	ASN
58	CB	315	ASN
59	CF	126	ASN
59	CF	235	ASN
60	Cc	15	ASN
60	Cc	40	GLN
61	Cd	18	ASN
61	Cd	100	ASN
61	Cd	118	GLN
62	Ce	57	ASN
62	Ce	102	ASN
62	Ce	126	ASN
63	Cf	21	GLN
64	Cg	114	GLN
65	Ci	80	HIS
67	Ck	31	ASN
69	CC	21	ASN
69	CC	38	ASN
69	CC	94	ASN
73	Co	102	GLN
73	Co	105	GLN
74	CJ	98	ASN
74	CJ	104	ASN
74	CJ	167	GLN
75	CH	98	HIS
75	CH	102	ASN
75	CH	156	ASN
76	CE	31	ASN
76	CE	191	GLN
76	CE	205	ASN
76	CE	250	GLN
76	CE	256	GLN
76	CE	268	GLN
77	CG	100	HIS
77	CG	112	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
19	B2	1748/1861 (93%)	524 (29%)	37 (2%)
78	A5	1662/3889 (42%)	500 (30%)	58 (3%)
78	A6	1993/3889 (51%)	578 (29%)	45 (2%)
79	A7	120/121 (99%)	21 (17%)	0
80	A8	156/157 (99%)	39 (25%)	3 (1%)
81	BC	74/75 (98%)	26 (35%)	2 (2%)
All	All	5753/9992 (57%)	1688 (29%)	145 (2%)

All (1688) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
19	B2	2	A
19	B2	3	C
19	B2	4	C
19	B2	20	G
19	B2	21	U
19	B2	24	C
19	B2	25	A
19	B2	26	U
19	B2	33	G
19	B2	41	G
19	B2	42	A
19	B2	44	U
19	B2	45	A
19	B2	46	A
19	B2	49	C
19	B2	56	G
19	B2	59	U
19	B2	61	A
19	B2	62	G
19	B2	65	C
19	B2	66	G
19	B2	67	C
19	B2	68	A
19	B2	70	G
19	B2	71	G
19	B2	72	C
19	B2	73	C
19	B2	74	G
19	B2	75	G
19	B2	76	U

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Mol	Chain	Res	Type
19	B2	77	A
19	B2	78	C
19	B2	79	A
19	B2	94	G
19	B2	103	A
19	B2	113	G
19	B2	115	U
19	B2	122	G
19	B2	125	C
19	B2	126	G
19	B2	127	C
19	B2	140	C
19	B2	141	A
19	B2	142	C
19	B2	143	U
19	B2	145	G
19	B2	146	G
19	B2	147	A
19	B2	148	U
19	B2	155	G
19	B2	158	A
19	B2	161	U
19	B2	162	C
19	B2	170	A
19	B2	178	C
19	B2	180	G
19	B2	181	A
19	B2	182	C
19	B2	183	G
19	B2	187	G
19	B2	188	C
19	B2	189	U
19	B2	192	C
19	B2	211	G
19	B2	215	G
19	B2	216	C
19	B2	226	A
19	B2	227	U
19	B2	228	C
19	B2	229	A
19	B2	231	A
19	B2	232	A

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Mol	Chain	Res	Type
19	B2	238	C
19	B2	240	G
19	B2	242	U
19	B2	243	C
19	B2	244	A
19	B2	281	C
19	B2	282	G
19	B2	284	C
19	B2	285	U
19	B2	286	U
19	B2	287	U
19	B2	288	G
19	B2	293	C
19	B2	294	U
19	B2	295	C
19	B2	302	A
19	B2	304	C
19	B2	305	U
19	B2	306	C
19	B2	307	G
19	B2	308	G
19	B2	309	G
19	B2	312	G
19	B2	318	A
19	B2	319	C
19	B2	322	C
19	B2	324	C
19	B2	325	C
19	B2	326	C
19	B2	327	G
19	B2	328	U
19	B2	332	G
19	B2	338	G
19	B2	347	G
19	B2	349	A
19	B2	350	C
19	B2	362	C
19	B2	364	A
19	B2	368	U
19	B2	370	G
19	B2	377	G
19	B2	381	C

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Mol	Chain	Res	Type
19	B2	383	G
19	B2	385	G
19	B2	386	C
19	B2	398	A
19	B2	399	C
19	B2	400	C
19	B2	407	G
19	B2	409	C
19	B2	428	U
19	B2	435	A
19	B2	438	G
19	B2	448	A
19	B2	450	C
19	B2	452	G
19	B2	464	A
19	B2	465	A
19	B2	466	G
19	B2	471	G
19	B2	472	C
19	B2	473	A
19	B2	474	G
19	B2	476	A
19	B2	482	G
19	B2	485	A
19	B2	487	U
19	B2	492	C
19	B2	493	A
19	B2	496	C
19	B2	500	A
19	B2	502	C
19	B2	503	C
19	B2	504	G
19	B2	510	G
19	B2	517	C
19	B2	523	A
19	B2	526	A
19	B2	529	A
19	B2	532	C
19	B2	533	A
19	B2	534	G
19	B2	535	G
19	B2	544	G

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Mol	Chain	Res	Type
19	B2	551	U
19	B2	552	G
19	B2	553	U
19	B2	555	A
19	B2	556	U
19	B2	557	U
19	B2	559	G
19	B2	561	A
19	B2	563	G
19	B2	564	A
19	B2	568	C
19	B2	574	A
19	B2	576	A
19	B2	582	U
19	B2	588	G
19	B2	589	G
19	B2	591	U
19	B2	593	C
19	B2	594	A
19	B2	600	G
19	B2	603	C
19	B2	604	A
19	B2	605	A
19	B2	606	G
19	B2	607	U
19	B2	608	C
19	B2	613	G
19	B2	614	C
19	B2	615	C
19	B2	617	G
19	B2	628	A
19	B2	629	A
19	B2	634	A
19	B2	643	A
19	B2	644	G
19	B2	650	A
19	B2	655	A
19	B2	656	G
19	B2	660	C
19	B2	666	U
19	B2	668	A
19	B2	669	A

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Mol	Chain	Res	Type
19	B2	670	A
19	B2	671	A
19	B2	672	A
19	B2	673	G
19	B2	683	G
19	B2	684	G
19	B2	687	C
19	B2	688	U
19	B2	689	U
19	B2	690	G
19	B2	691	G
19	B2	738	C
19	B2	739	C
19	B2	741	C
19	B2	742	U
19	B2	743	U
19	B2	744	G
19	B2	747	U
19	B2	748	C
19	B2	749	U
19	B2	750	C
19	B2	752	G
19	B2	753	C
19	B2	788	G
19	B2	797	C
19	B2	798	G
19	B2	799	U
19	B2	800	U
19	B2	801	U
19	B2	810	A
19	B2	811	A
19	B2	812	A
19	B2	821	G
19	B2	830	A
19	B2	831	G
19	B2	834	C
19	B2	835	C
19	B2	836	G
19	B2	837	A
19	B2	839	C
19	B2	840	C
19	B2	841	G

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Mol	Chain	Res	Type
19	B2	844	U
19	B2	847	A
19	B2	852	G
19	B2	861	A
19	B2	867	G
19	B2	868	G
19	B2	870	A
19	B2	871	U
19	B2	872	A
19	B2	873	G
19	B2	875	A
19	B2	877	C
19	B2	878	G
19	B2	879	C
19	B2	880	G
19	B2	881	G
19	B2	887	U
19	B2	890	U
19	B2	903	A
19	B2	907	G
19	B2	909	G
19	B2	910	G
19	B2	913	A
19	B2	914	U
19	B2	917	U
19	B2	918	U
19	B2	919	A
19	B2	920	A
19	B2	933	G
19	B2	954	U
19	B2	955	A
19	B2	961	G
19	B2	962	A
19	B2	969	U
19	B2	970	G
19	B2	971	G
19	B2	990	A
19	B2	992	A
19	B2	999	G
19	B2	1001	A
19	B2	1017	U
19	B2	1023	A

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Mol	Chain	Res	Type
19	B2	1045	U
19	B2	1049	A
19	B2	1050	A
19	B2	1053	C
19	B2	1060	A
19	B2	1061	U
19	B2	1062	A
19	B2	1067	C
19	B2	1080	A
19	B2	1082	A
19	B2	1083	A
19	B2	1084	A
19	B2	1085	C
19	B2	1090	C
19	B2	1096	G
19	B2	1097	G
19	B2	1100	A
19	B2	1109	C
19	B2	1110	G
19	B2	1115	U
19	B2	1116	C
19	B2	1117	C
19	B2	1118	C
19	B2	1119	A
19	B2	1120	U
19	B2	1123	C
19	B2	1124	C
19	B2	1126	G
19	B2	1127	C
19	B2	1129	G
19	B2	1133	A
19	B2	1137	U
19	B2	1138	C
19	B2	1148	A
19	B2	1149	A
19	B2	1150	A
19	B2	1153	C
19	B2	1154	U
19	B2	1155	U
19	B2	1157	G
19	B2	1166	G
19	B2	1170	A

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Mol	Chain	Res	Type
19	B2	1172	U
19	B2	1173	A
19	B2	1195	A
19	B2	1202	U
19	B2	1204	A
19	B2	1205	C
19	B2	1206	G
19	B2	1207	G
19	B2	1208	A
19	B2	1211	G
19	B2	1212	G
19	B2	1215	C
19	B2	1216	C
19	B2	1217	A
19	B2	1221	G
19	B2	1223	A
19	B2	1224	G
19	B2	1228	A
19	B2	1240	A
19	B2	1242	U
19	B2	1243	U
19	B2	1247	C
19	B2	1251	A
19	B2	1253	A
19	B2	1254	C
19	B2	1256	G
19	B2	1257	G
19	B2	1259	A
19	B2	1265	A
19	B2	1269	G
19	B2	1271	C
19	B2	1274	G
19	B2	1275	G
19	B2	1284	A
19	B2	1285	G
19	B2	1286	G
19	B2	1301	A
19	B2	1302	G
19	B2	1303	C
19	B2	1307	U
19	B2	1308	U
19	B2	1311	C

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Mol	Chain	Res	Type
19	B2	1313	A
19	B2	1314	U
19	B2	1315	U
19	B2	1324	G
19	B2	1328	G
19	B2	1333	U
19	B2	1341	C
19	B2	1342	U
19	B2	1354	G
19	B2	1355	C
19	B2	1358	U
19	B2	1363	C
19	B2	1364	U
19	B2	1371	U
19	B2	1372	U
19	B2	1378	A
19	B2	1382	A
19	B2	1394	G
19	B2	1395	C
19	B2	1396	A
19	B2	1397	U
19	B2	1401	A
19	B2	1402	A
19	B2	1404	U
19	B2	1410	C
19	B2	1411	G
19	B2	1412	C
19	B2	1416	C
19	B2	1417	C
19	B2	1418	C
19	B2	1419	C
19	B2	1420	G
19	B2	1426	U
19	B2	1430	C
19	B2	1435	C
19	B2	1437	C
19	B2	1438	A
19	B2	1441	U
19	B2	1442	U
19	B2	1444	U
19	B2	1446	A
19	B2	1447	G

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Mol	Chain	Res	Type
19	B2	1449	G
19	B2	1450	G
19	B2	1451	G
19	B2	1452	A
19	B2	1454	A
19	B2	1455	A
19	B2	1456	G
19	B2	1462	U
19	B2	1463	U
19	B2	1464	C
19	B2	1466	G
19	B2	1475	G
19	B2	1476	A
19	B2	1477	U
19	B2	1489	A
19	B2	1490	G
19	B2	1494	U
19	B2	1495	G
19	B2	1498	A
19	B2	1499	U
19	B2	1500	G
19	B2	1507	G
19	B2	1508	A
19	B2	1509	U
19	B2	1520	G
19	B2	1521	C
19	B2	1522	A
19	B2	1523	C
19	B2	1531	A
19	B2	1535	U
19	B2	1536	G
19	B2	1539	U
19	B2	1541	G
19	B2	1542	C
19	B2	1544	C
19	B2	1546	G
19	B2	1550	G
19	B2	1551	U
19	B2	1552	G
19	B2	1553	C
19	B2	1556	A
19	B2	1557	C

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Mol	Chain	Res	Type
19	B2	1560	U
19	B2	1566	G
19	B2	1567	G
19	B2	1570	G
19	B2	1578	U
19	B2	1579	A
19	B2	1580	A
19	B2	1585	U
19	B2	1587	G
19	B2	1588	A
19	B2	1598	G
19	B2	1599	U
19	B2	1600	G
19	B2	1601	A
19	B2	1602	U
19	B2	1605	G
19	B2	1606	G
19	B2	1613	G
19	B2	1621	U
19	B2	1623	A
19	B2	1632	G
19	B2	1637	A
19	B2	1638	G
19	B2	1643	U
19	B2	1648	G
19	B2	1649	U
19	B2	1664	A
19	B2	1665	G
19	B2	1666	C
19	B2	1672	U
19	B2	1675	A
19	B2	1680	G
19	B2	1692	U
19	B2	1695	A
19	B2	1698	C
19	B2	1700	C
19	B2	1701	C
19	B2	1705	C
19	B2	1721	U
19	B2	1722	G
19	B2	1727	G
19	B2	1744	G

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Mol	Chain	Res	Type
19	B2	1745	A
19	B2	1751	C
19	B2	1754	G
19	B2	1757	G
19	B2	1783	C
19	B2	1784	G
19	B2	1785	C
19	B2	1786	U
19	B2	1797	U
19	B2	1805	G
19	B2	1819	A
19	B2	1823	A
19	B2	1824	A
19	B2	1825	A
19	B2	1826	G
19	B2	1829	G
19	B2	1831	A
19	B2	1833	C
19	B2	1834	A
19	B2	1835	A
19	B2	1836	G
19	B2	1837	G
19	B2	1838	U
19	B2	1849	G
19	B2	1851	A
19	B2	1852	C
19	B2	1861	G
19	B2	1862	G
19	B2	1863	A
19	B2	1865	C
19	B2	1866	A
19	B2	1868	U
78	A5	5	A
78	A5	11	G
78	A5	12	A
78	A5	13	U
78	A5	25	A
78	A5	30	C
78	A5	33	A
78	A5	39	A
78	A5	42	A
78	A5	48	G

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Mol	Chain	Res	Type
78	A5	56	A
78	A5	58	G
78	A5	59	A
78	A5	63	G
78	A5	64	A
78	A5	65	A
78	A5	66	A
78	A5	67	C
78	A5	72	C
78	A5	73	A
78	A5	74	G
78	A5	76	A
78	A5	84	A
78	A5	85	G
78	A5	91	G
78	A5	93	G
78	A5	95	G
78	A5	108	A
78	A5	109	G
78	A5	110	C
78	A5	112	C
78	A5	115	C
78	A5	116	G
78	A5	119	G
78	A5	120	A
78	A5	135	G
78	A5	136	C
78	A5	137	G
78	A5	142	G
78	A5	143	C
78	A5	144	G
78	A5	149	A
78	A5	150	U
78	A5	151	G
78	A5	157	U
78	A5	158	A
78	A5	159	C
78	A5	160	G
78	A5	164	G
78	A5	172	C
78	A5	173	C
78	A5	174	C

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Mol	Chain	Res	Type
78	A5	185	C
78	A5	187	U
78	A5	188	G
78	A5	189	G
78	A5	200	U
78	A5	201	C
78	A5	207	G
78	A5	210	C
78	A5	215	C
78	A5	216	C
78	A5	217	C
78	A5	218	A
78	A5	219	G
78	A5	220	C
78	A5	221	C
78	A5	224	U
78	A5	225	G
78	A5	226	G
78	A5	227	A
78	A5	232	G
78	A5	233	U
78	A5	234	G
78	A5	246	G
78	A5	265	C
78	A5	275	C
78	A5	276	C
78	A5	277	G
78	A5	278	G
78	A5	280	G
78	A5	294	G
78	A5	296	A
78	A5	297	U
78	A5	306	A
78	A5	309	C
78	A5	310	G
78	A5	315	G
78	A5	316	U
78	A5	322	C
78	A5	334	A
78	A5	340	C
78	A5	345	C
78	A5	348	G

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Mol	Chain	Res	Type
78	A5	350	C
78	A5	360	A
78	A5	361	C
78	A5	363	A
78	A5	381	U
78	A5	387	G
78	A5	404	U
78	A5	405	U
78	A5	406	C
78	A5	409	G
78	A5	410	A
78	A5	412	G
78	A5	413	G
78	A5	414	C
78	A5	415	G
78	A5	432	U
78	A5	433	A
78	A5	450	G
78	A5	451	C
78	A5	452	A
78	A5	453	G
78	A5	455	C
78	A5	460	C
78	A5	468	U
78	A5	469	C
78	A5	473	C
78	A5	474	C
78	A5	480	C
78	A5	485	C
78	A5	486	C
78	A5	487	G
78	A5	492	U
78	A5	498	C
78	A5	499	G
78	A5	500	G
78	A5	501	C
78	A5	502	C
78	A5	503	C
78	A5	504	G
78	A5	505	G
78	A5	506	C
78	A5	509	A

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Mol	Chain	Res	Type
78	A5	510	U
78	A5	511	C
78	A5	513	U
78	A5	514	U
78	A5	515	C
78	A5	516	C
78	A5	639	U
78	A5	640	C
78	A5	641	G
78	A5	649	A
78	A5	656	C
78	A5	664	G
78	A5	665	C
78	A5	666	G
78	A5	667	A
78	A5	668	C
78	A5	669	C
78	A5	670	G
78	A5	677	G
78	A5	679	C
78	A5	685	C
78	A5	687	U
78	A5	689	U
78	A5	690	C
78	A5	692	A
78	A5	696	C
78	A5	697	G
78	A5	701	G
78	A5	704	C
78	A5	707	C
78	A5	712	C
78	A5	715	G
78	A5	721	G
78	A5	722	G
78	A5	723	A
78	A5	728	U
78	A5	729	G
78	A5	730	G
78	A5	735	G
78	A5	737	C
78	A5	746	A
78	A5	747	A

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Mol	Chain	Res	Type
78	A5	748	G
78	A5	749	G
78	A5	910	G
78	A5	918	G
78	A5	923	C
78	A5	926	G
78	A5	927	G
78	A5	929	A
78	A5	930	G
78	A5	931	C
78	A5	932	A
78	A5	933	G
78	A5	936	C
78	A5	937	U
78	A5	938	C
78	A5	939	G
78	A5	940	C
78	A5	944	A
78	A5	945	U
78	A5	946	C
78	A5	947	C
78	A5	951	G
78	A5	952	G
78	A5	953	C
78	A5	956	A
78	A5	957	G
78	A5	958	G
78	A5	959	G
78	A5	960	A
78	A5	961	G
78	A5	963	G
78	A5	964	A
78	A5	965	G
78	A5	966	A
78	A5	967	C
78	A5	968	C
78	A5	969	C
78	A5	970	G
78	A5	971	U
78	A5	972	C
78	A5	974	C
78	A5	975	C

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Mol	Chain	Res	Type
78	A5	980	U
78	A5	982	U
78	A5	983	C
78	A5	984	C
78	A5	985	C
78	A5	1052	G
78	A5	1068	G
78	A5	1069	G
78	A5	1070	G
78	A5	1072	C
78	A5	1073	G
78	A5	1084	C
78	A5	1090	G
78	A5	1101	C
78	A5	1102	U
78	A5	1103	C
78	A5	1104	C
78	A5	1166	G
78	A5	1177	U
78	A5	1178	G
78	A5	1183	C
78	A5	1210	C
78	A5	1211	G
78	A5	1212	G
78	A5	1214	C
78	A5	1215	C
78	A5	1218	G
78	A5	1219	G
78	A5	1222	A
78	A5	1233	G
78	A5	1238	A
78	A5	1239	C
78	A5	1240	G
78	A5	1266	G
78	A5	1267	C
78	A5	1268	G
78	A5	1269	G
78	A5	1270	A
78	A5	1271	G
78	A5	1272	C
78	A5	1273	G
78	A5	1274	A

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Mol	Chain	Res	Type
78	A5	1275	G
78	A5	1280	C
78	A5	1282	G
78	A5	1283	G
78	A5	1284	G
78	A5	1285	U
78	A5	1287	G
78	A5	1288	G
78	A5	1289	C
78	A5	1290	G
78	A5	1294	A
78	A5	1295	C
78	A5	1296	G
78	A5	1297	U
78	A5	1301	C
78	A5	1302	U
78	A5	1303	A
78	A5	1305	C
78	A5	1308	C
78	A5	1314	C
78	A5	1317	U
78	A5	1319	U
78	A5	1326	A
78	A5	1331	C
78	A5	1344	C
78	A5	1346	C
78	A5	1354	A
78	A5	1357	C
78	A5	1358	G
78	A5	1359	G
78	A5	1360	G
78	A5	1362	G
78	A5	1365	C
78	A5	1366	G
78	A5	1367	C
78	A5	1368	A
78	A5	1369	C
78	A5	1370	G
78	A5	1371	A
78	A5	1377	G
78	A5	1378	C
78	A5	1379	C

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Mol	Chain	Res	Type
78	A5	1387	A
78	A5	1394	G
78	A5	1397	A
78	A5	1398	A
78	A5	1399	G
78	A5	1406	G
78	A5	1407	C
78	A5	1408	G
78	A5	1409	C
78	A5	1410	U
78	A5	1411	C
78	A5	1420	A
78	A5	1421	G
78	A5	1426	G
78	A5	1429	C
78	A5	1432	G
78	A5	1435	G
78	A5	1439	C
78	A5	1449	C
78	A5	1456	C
78	A5	1465	G
78	A5	1475	G
78	A5	1476	C
78	A5	1480	C
78	A5	1482	G
78	A5	1484	G
78	A5	1485	C
78	A5	1498	G
78	A5	1501	C
78	A5	1502	G
78	A5	1511	U
78	A5	1516	G
78	A5	1518	A
78	A5	1523	A
78	A5	1534	A
78	A5	1535	C
78	A5	1543	G
78	A5	1547	A
78	A5	1549	G
78	A5	1553	A
78	A5	1566	C
78	A5	1574	G

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Mol	Chain	Res	Type
78	A5	1575	A
78	A5	1578	U
78	A5	1582	U
78	A5	1591	U
78	A5	1596	U
78	A5	1597	G
78	A5	1601	A
78	A5	1607	C
78	A5	1611	C
78	A5	1612	G
78	A5	1613	A
78	A5	1624	G
78	A5	1625	G
78	A5	1631	A
78	A5	1633	G
78	A5	1634	A
78	A5	1637	A
78	A5	1638	A
78	A5	1640	C
78	A5	1641	G
78	A5	1650	A
78	A5	1654	G
78	A5	1661	C
78	A5	1670	G
78	A5	1676	C
78	A5	1677	U
78	A5	1680	G
78	A5	1681	G
78	A5	1695	U
78	A5	1697	G
78	A5	1698	C
78	A5	1699	A
78	A5	1700	G
78	A5	1724	G
78	A5	1725	U
78	A5	1732	C
78	A5	1733	G
78	A5	1734	G
78	A5	1740	C
78	A5	1741	G
78	A5	1742	A
78	A5	1750	G

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Mol	Chain	Res	Type
78	A5	1751	A
78	A5	1754	U
78	A5	1755	C
78	A5	1756	U
78	A5	1760	G
78	A5	1761	G
78	A5	1762	C
78	A5	1764	G
78	A5	1766	A
78	A5	1769	G
78	A5	1772	C
78	A5	1775	A
78	A5	1776	A
78	A5	1777	C
78	A5	1781	U
78	A5	1785	C
78	A5	1787	A
78	A5	1789	C
78	A5	1797	G
78	A5	1803	G
78	A5	1804	A
78	A5	1805	A
78	A5	1807	C
78	A5	1811	G
78	A5	1812	C
78	A5	1815	G
78	A5	1818	G
78	A5	1819	G
78	A5	1821	G
78	A5	1822	U
78	A5	1833	G
78	A5	1834	U
78	A5	1835	G
78	A5	1836	G
78	A5	1841	C
78	A5	1842	G
78	A5	1850	A
78	A5	1854	G
78	A5	1855	G
78	A5	1869	G
78	A5	1881	C
78	A5	1888	A

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Mol	Chain	Res	Type
78	A5	1890	G
78	A5	1893	C
78	A5	1897	A
78	A5	1898	C
78	A5	1906	U
78	A5	1910	G
78	A5	1912	G
78	A5	1918	U
78	A5	1920	C
78	A5	1921	C
78	A5	1922	G
78	A5	1925	G
78	A5	1930	U
78	A5	1931	C
78	A5	1935	C
78	A5	1938	C
78	A5	1947	U
78	A5	1948	G
78	A5	1951	G
78	A5	1957	U
78	A5	1960	A
78	A5	1961	G
78	A5	1962	A
78	A5	1964	A
78	A5	1966	C
78	A5	1967	A
78	A5	1969	G
78	A5	1973	G
78	A5	1975	G
78	A5	1976	G
78	A5	1979	A
78	A5	1980	U
78	A5	1981	G
78	A5	1982	G
78	A5	1983	A
78	A5	1984	A
78	A5	1985	G
78	A5	1987	C
78	A5	1997	U
78	A5	2001	G
78	A5	2002	A
78	A5	2003	G

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Mol	Chain	Res	Type
78	A5	2004	U
78	A5	2009	A
78	A5	2010	A
78	A5	2011	C
78	A5	2016	C
78	A5	2024	G
78	A5	2025	A
78	A5	2026	A
78	A5	2033	A
78	A5	2034	G
78	A5	2046	G
78	A5	2047	A
78	A5	2048	U
78	A5	2052	G
78	A5	2055	G
78	A5	2056	G
78	A5	2057	A
78	A5	2064	G
78	A5	2068	C
78	A5	2069	A
78	A5	2070	U
78	A5	2076	G
78	A5	2077	C
78	A5	2084	C
78	A5	2085	G
78	A5	2089	G
78	A5	2090	U
78	A5	2091	C
79	A7	11	A
79	A7	22	A
79	A7	23	A
79	A7	33	U
79	A7	39	C
79	A7	41	G
79	A7	49	A
79	A7	50	A
79	A7	52	C
79	A7	53	U
79	A7	54	A
79	A7	61	G
79	A7	64	G
79	A7	74	A

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Mol	Chain	Res	Type
79	A7	76	U
79	A7	97	G
79	A7	100	A
79	A7	110	G
79	A7	114	U
79	A7	115	A
79	A7	121	U
80	A8	22	U
80	A8	23	C
80	A8	25	G
80	A8	34	U
80	A8	35	C
80	A8	39	G
80	A8	47	C
80	A8	51	U
80	A8	59	A
80	A8	61	A
80	A8	62	A
80	A8	63	U
80	A8	70	G
80	A8	71	A
80	A8	75	G
80	A8	81	C
80	A8	82	A
80	A8	83	C
80	A8	84	A
80	A8	85	U
80	A8	86	U
80	A8	93	C
80	A8	94	G
80	A8	96	C
80	A8	103	A
80	A8	105	C
80	A8	107	C
80	A8	110	U
80	A8	111	U
80	A8	114	G
80	A8	125	C
80	A8	126	C
80	A8	127	U
80	A8	128	C
80	A8	147	G

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Mol	Chain	Res	Type
80	A8	150	C
80	A8	153	C
80	A8	154	G
80	A8	157	U
81	BC	8	U
81	BC	10	G
81	BC	16	C
81	BC	17	G
81	BC	18	G
81	BC	19	A
81	BC	20	A
81	BC	21	G
81	BC	36	A
81	BC	37	A
81	BC	38	C
81	BC	39	C
81	BC	45	G
81	BC	46	U
81	BC	47	C
81	BC	48	G
81	BC	53	A
81	BC	55	C
81	BC	57	A
81	BC	58	A
81	BC	60	C
81	BC	61	C
81	BC	72	A
81	BC	73	C
81	BC	74	C
81	BC	75	A
78	A6	2259	G
78	A6	2260	C
78	A6	2261	G
78	A6	2262	G
78	A6	2263	A
78	A6	2264	C
78	A6	2265	G
78	A6	2266	C
78	A6	2267	U
78	A6	2268	A
78	A6	2269	C
78	A6	2270	G

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Mol	Chain	Res	Type
78	A6	2271	C
78	A6	2273	G
78	A6	2280	G
78	A6	2289	C
78	A6	2290	C
78	A6	2297	G
78	A6	2300	A
78	A6	2301	G
78	A6	2305	U
78	A6	2306	G
78	A6	2313	A
78	A6	2314	G
78	A6	2331	G
78	A6	2333	G
78	A6	2338	C
78	A6	2345	G
78	A6	2347	A
78	A6	2348	G
78	A6	2351	C
78	A6	2360	A
78	A6	2366	A
78	A6	2369	U
78	A6	2370	A
78	A6	2382	A
78	A6	2384	U
78	A6	2392	C
78	A6	2395	A
78	A6	2396	A
78	A6	2399	G
78	A6	2410	C
78	A6	2412	A
78	A6	2413	U
78	A6	2417	A
78	A6	2422	C
78	A6	2425	U
78	A6	2434	G
78	A6	2437	C
78	A6	2440	U
78	A6	2441	C
78	A6	2450	G
78	A6	2457	G
78	A6	2461	G

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Mol	Chain	Res	Type
78	A6	2462	C
78	A6	2470	C
78	A6	2473	A
78	A6	2474	G
78	A6	2475	G
78	A6	2476	G
78	A6	2487	G
78	A6	2488	C
78	A6	2489	C
78	A6	2490	U
78	A6	2491	C
78	A6	2503	G
78	A6	2504	C
78	A6	2505	C
78	A6	2511	A
78	A6	2513	A
78	A6	2514	G
78	A6	2517	A
78	A6	2520	C
78	A6	2526	C
78	A6	2527	A
78	A6	2529	A
78	A6	2531	C
78	A6	2532	C
78	A6	2544	G
78	A6	2546	G
78	A6	2547	G
78	A6	2551	A
78	A6	2552	G
78	A6	2554	U
78	A6	2556	G
78	A6	2575	U
78	A6	2582	A
78	A6	2586	G
78	A6	2587	A
78	A6	2589	C
78	A6	2597	G
78	A6	2600	A
78	A6	2601	A
78	A6	2611	A
78	A6	2612	G
78	A6	2617	G

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Mol	Chain	Res	Type
78	A6	2627	C
78	A6	2647	A
78	A6	2648	G
78	A6	2649	G
78	A6	2650	G
78	A6	2652	G
78	A6	2653	C
78	A6	2655	C
78	A6	2658	G
78	A6	2659	A
78	A6	2660	A
78	A6	2661	U
78	A6	2662	G
78	A6	2663	G
78	A6	2664	G
78	A6	2665	U
78	A6	2666	G
78	A6	2667	C
78	A6	2668	G
78	A6	2669	C
78	A6	2670	C
78	A6	2671	C
78	A6	2673	G
78	A6	2674	A
78	A6	2675	G
78	A6	2677	G
78	A6	2678	A
78	A6	2681	G
78	A6	2686	G
78	A6	2687	C
78	A6	2688	G
78	A6	2689	C
78	A6	2694	G
78	A6	2695	A
78	A6	2696	A
78	A6	2700	G
78	A6	2708	U
78	A6	2711	G
78	A6	2716	C
78	A6	2721	G
78	A6	2725	A
78	A6	2726	G

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Mol	Chain	Res	Type
78	A6	2734	U
78	A6	2736	G
78	A6	2738	C
78	A6	2740	U
78	A6	2743	A
78	A6	2750	G
78	A6	2754	G
78	A6	2759	G
78	A6	2760	G
78	A6	2762	G
78	A6	2765	A
78	A6	2766	A
78	A6	2767	U
78	A6	2768	C
78	A6	2769	U
78	A6	2770	C
78	A6	2772	C
78	A6	2783	A
78	A6	2787	A
78	A6	2788	U
78	A6	2789	A
78	A6	2790	U
78	A6	2794	C
78	A6	2796	G
78	A6	2798	A
78	A6	2806	A
78	A6	2813	A
78	A6	2814	C
78	A6	2824	C
78	A6	2825	A
78	A6	2826	U
78	A6	2827	G
78	A6	2829	U
78	A6	2830	G
78	A6	2833	A
78	A6	2839	U
78	A6	2842	G
78	A6	2845	A
78	A6	2848	G
78	A6	2850	A
78	A6	2855	G
78	A6	2863	G

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Mol	Chain	Res	Type
78	A6	2876	G
78	A6	2884	G
78	A6	2894	A
78	A6	2896	G
78	A6	2897	G
78	A6	2900	U
78	A6	2902	G
78	A6	2903	G
78	A6	2904	U
78	A6	2905	C
78	A6	3593	C
78	A6	3594	C
78	A6	3595	U
78	A6	3596	A
78	A6	3597	G
78	A6	3605	C
78	A6	3606	U
78	A6	3611	A
78	A6	3615	G
78	A6	3616	U
78	A6	3617	G
78	A6	3618	C
78	A6	3619	G
78	A6	3625	G
78	A6	3626	G
78	A6	3630	A
78	A6	3635	A
78	A6	3636	C
78	A6	3646	A
78	A6	3650	C
78	A6	3659	G
78	A6	3662	A
78	A6	3664	G
78	A6	3671	G
78	A6	3672	G
78	A6	3673	C
78	A6	3674	G
78	A6	3680	U
78	A6	3688	U
78	A6	3692	A
78	A6	3698	G
78	A6	3699	C

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Mol	Chain	Res	Type
78	A6	3706	C
78	A6	3709	U
78	A6	3710	G
78	A6	3711	A
78	A6	3712	A
78	A6	3713	U
78	A6	3714	G
78	A6	3726	A
78	A6	3727	A
78	A6	3729	U
78	A6	3732	A
78	A6	3748	A
78	A6	3751	G
78	A6	3753	G
78	A6	3759	A
78	A6	3760	A
78	A6	3761	C
78	A6	3776	G
78	A6	3777	G
78	A6	3778	U
78	A6	3786	U
78	A6	3788	C
78	A6	3791	C
78	A6	3807	A
78	A6	3811	G
78	A6	3812	C
78	A6	3814	U
78	A6	3817	A
78	A6	3818	U
78	A6	3819	G
78	A6	3838	U
78	A6	3839	G
78	A6	3840	U
78	A6	3843	C
78	A6	3845	A
78	A6	3851	U
78	A6	3866	C
78	A6	3867	A
78	A6	3869	C
78	A6	3876	A
78	A6	3877	A
78	A6	3878	C

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Mol	Chain	Res	Type
78	A6	3879	G
78	A6	3880	G
78	A6	3886	G
78	A6	3890	A
78	A6	3893	C
78	A6	3897	G
78	A6	3898	G
78	A6	3901	A
78	A6	3906	A
78	A6	3907	G
78	A6	3908	A
78	A6	3915	U
78	A6	3923	A
78	A6	3926	C
78	A6	3939	G
78	A6	3954	A
78	A6	3957	U
78	A6	3958	G
78	A6	3959	U
78	A6	3960	A
78	A6	3962	A
78	A6	3963	A
78	A6	3964	U
78	A6	3965	A
78	A6	3966	A
78	A6	3967	G
78	A6	3969	G
78	A6	3971	G
78	A6	3972	A
78	A6	3973	G
78	A6	3976	C
78	A6	3977	C
78	A6	4040	C
78	A6	4041	C
78	A6	4042	G
78	A6	4043	G
78	A6	4044	U
78	A6	4045	G
78	A6	4046	A
78	A6	4047	A
78	A6	4048	A
78	A6	4049	U

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Mol	Chain	Res	Type
78	A6	4050	A
78	A6	4053	A
78	A6	4056	A
78	A6	4060	U
78	A6	4061	G
78	A6	4062	A
78	A6	4073	A
78	A6	4074	C
78	A6	4076	G
78	A6	4077	A
78	A6	4083	U
78	A6	4085	A
78	A6	4086	G
78	A6	4087	G
78	A6	4088	C
78	A6	4094	G
78	A6	4097	G
78	A6	4104	G
78	A6	4107	G
78	A6	4114	C
78	A6	4115	G
78	A6	4116	C
78	A6	4117	U
78	A6	4118	U
78	A6	4119	C
78	A6	4120	U
78	A6	4121	G
78	A6	4122	G
78	A6	4123	C
78	A6	4125	C
78	A6	4126	C
78	A6	4127	A
78	A6	4133	C
78	A6	4134	C
78	A6	4141	G
78	A6	4143	G
78	A6	4144	C
78	A6	4145	C
78	A6	4162	C
78	A6	4164	C
78	A6	4165	C
78	A6	4170	A

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Mol	Chain	Res	Type
78	A6	4171	C
78	A6	4178	A
78	A6	4183	G
78	A6	4184	G
78	A6	4191	G
78	A6	4205	A
78	A6	4212	A
78	A6	4225	G
78	A6	4228	G
78	A6	4229	U
78	A6	4232	U
78	A6	4233	A
78	A6	4234	A
78	A6	4238	G
78	A6	4240	G
78	A6	4241	C
78	A6	4242	U
78	A6	4243	C
78	A6	4249	G
78	A6	4251	A
78	A6	4254	G
78	A6	4255	A
78	A6	4258	C
78	A6	4266	G
78	A6	4268	A
78	A6	4271	A
78	A6	4273	A
78	A6	4277	G
78	A6	4280	A
78	A6	4282	A
78	A6	4291	G
78	A6	4296	U
78	A6	4303	C
78	A6	4304	A
78	A6	4305	G
78	A6	4314	C
78	A6	4320	G
78	A6	4325	A
78	A6	4326	G
78	A6	4329	G
78	A6	4330	G
78	A6	4332	C

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Mol	Chain	Res	Type
78	A6	4347	G
78	A6	4349	C
78	A6	4350	C
78	A6	4354	U
78	A6	4355	G
78	A6	4364	G
78	A6	4367	G
78	A6	4373	G
78	A6	4376	A
78	A6	4377	G
78	A6	4378	A
78	A6	4380	A
78	A6	4381	A
78	A6	4387	C
78	A6	4393	G
78	A6	4394	A
78	A6	4395	U
78	A6	4396	A
78	A6	4415	A
78	A6	4419	U
78	A6	4422	A
78	A6	4424	A
78	A6	4426	C
78	A6	4432	C
78	A6	4437	U
78	A6	4438	U
78	A6	4444	C
78	A6	4448	G
78	A6	4449	A
78	A6	4463	U
78	A6	4464	A
78	A6	4466	C
78	A6	4471	U
78	A6	4476	C
78	A6	4478	G
78	A6	4488	A
78	A6	4489	G
78	A6	4495	G
78	A6	4500	U
78	A6	4504	C
78	A6	4510	A
78	A6	4512	U

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Mol	Chain	Res	Type
78	A6	4513	A
78	A6	4515	G
78	A6	4519	C
78	A6	4524	G
78	A6	4525	C
78	A6	4528	G
78	A6	4529	G
78	A6	4548	A
78	A6	4560	C
78	A6	4567	G
78	A6	4572	U
78	A6	4574	U
78	A6	4575	G
78	A6	4581	G
78	A6	4590	A
78	A6	4599	A
78	A6	4601	U
78	A6	4608	G
78	A6	4617	G
78	A6	4623	G
78	A6	4627	U
78	A6	4633	G
78	A6	4634	U
78	A6	4636	U
78	A6	4639	G
78	A6	4652	G
78	A6	4656	A
78	A6	4657	U
78	A6	4664	A
78	A6	4670	C
78	A6	4671	C
78	A6	4672	A
78	A6	4677	U
78	A6	4678	G
78	A6	4682	U
78	A6	4687	A
78	A6	4688	C
78	A6	4693	C
78	A6	4694	G
78	A6	4697	U
78	A6	4700	A
78	A6	4708	A

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Mol	Chain	Res	Type
78	A6	4709	U
78	A6	4712	C
78	A6	4714	C
78	A6	4719	G
78	A6	4721	G
78	A6	4730	C
78	A6	4731	G
78	A6	4732	G
78	A6	4734	A
78	A6	4739	C
78	A6	4741	C
78	A6	4748	U
78	A6	4749	C
78	A6	4750	G
78	A6	4751	G
78	A6	4753	U
78	A6	4754	G
78	A6	4756	C
78	A6	4758	U
78	A6	4761	G
78	A6	4764	A
78	A6	4768	G
78	A6	4771	C
78	A6	4870	G
78	A6	4871	C
78	A6	4872	G
78	A6	4873	G
78	A6	4874	A
78	A6	4875	G
78	A6	4876	U
78	A6	4877	G
78	A6	4881	U
78	A6	4882	U
78	A6	4883	C
78	A6	4884	G
78	A6	4885	U
78	A6	4886	C
78	A6	4889	G
78	A6	4890	G
78	A6	4895	C
78	A6	4896	G
78	A6	4900	C

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Mol	Chain	Res	Type
78	A6	4901	G
78	A6	4902	C
78	A6	4910	G
78	A6	4912	G
78	A6	4913	G
78	A6	4914	C
78	A6	4924	C
78	A6	4925	U
78	A6	4927	G
78	A6	4928	C
78	A6	4933	C
78	A6	4936	G
78	A6	4937	C
78	A6	4938	A
78	A6	4939	C
78	A6	4940	C
78	A6	4941	G
78	A6	4944	C
78	A6	4945	G
78	A6	4946	U
78	A6	4947	U
78	A6	4949	G
78	A6	4950	U
78	A6	4952	G
78	A6	4966	A
78	A6	4967	A
78	A6	4974	C
78	A6	4975	G
78	A6	4976	U
78	A6	4978	G
78	A6	4980	C
78	A6	4981	G
78	A6	4985	U
78	A6	4988	U
78	A6	4989	U
78	A6	4991	U
78	A6	4992	G
78	A6	4998	G
78	A6	5002	U
78	A6	5003	U
78	A6	5005	G
78	A6	5006	U

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Mol	Chain	Res	Type
78	A6	5013	C
78	A6	5014	A
78	A6	5017	G
78	A6	5024	C
78	A6	5026	U
78	A6	5027	C
78	A6	5028	G
78	A6	5029	C
78	A6	5035	U
78	A6	5036	C
78	A6	5037	U
78	A6	5038	A
78	A6	5041	G
78	A6	5042	A
78	A6	5047	C
78	A6	5049	G
78	A6	5050	C
78	A6	5054	C
78	A6	5061	A
78	A6	5062	G

All (145) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
19	B2	24	C
19	B2	72	C
19	B2	102	A
19	B2	139	C
19	B2	140	C
19	B2	181	A
19	B2	225	G
19	B2	327	G
19	B2	465	A
19	B2	531	A
19	B2	532	C
19	B2	534	G
19	B2	552	G
19	B2	604	A
19	B2	688	U
19	B2	746	C
19	B2	797	C
19	B2	833	C

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Mol	Chain	Res	Type
19	B2	839	C
19	B2	880	G
19	B2	1108	G
19	B2	1253	A
19	B2	1395	C
19	B2	1396	A
19	B2	1401	A
19	B2	1429	G
19	B2	1474	A
19	B2	1543	U
19	B2	1556	A
19	B2	1601	A
19	B2	1637	A
19	B2	1679	A
19	B2	1756	C
19	B2	1823	A
19	B2	1825	A
19	B2	1830	U
19	B2	1835	A
78	A5	12	A
78	A5	64	A
78	A5	186	G
78	A5	219	G
78	A5	220	C
78	A5	245	C
78	A5	293	G
78	A5	333	U
78	A5	451	C
78	A5	486	C
78	A5	497	G
78	A5	505	G
78	A5	648	G
78	A5	655	C
78	A5	664	G
78	A5	668	C
78	A5	917	A
78	A5	926	G
78	A5	931	C
78	A5	936	C
78	A5	945	U
78	A5	955	G
78	A5	956	A

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Mol	Chain	Res	Type
78	A5	957	G
78	A5	971	U
78	A5	974	C
78	A5	1072	C
78	A5	1211	G
78	A5	1232	G
78	A5	1239	C
78	A5	1269	G
78	A5	1281	G
78	A5	1284	G
78	A5	1288	G
78	A5	1293	G
78	A5	1294	A
78	A5	1296	G
78	A5	1356	U
78	A5	1358	G
78	A5	1359	G
78	A5	1366	G
78	A5	1419	G
78	A5	1428	U
78	A5	1455	G
78	A5	1474	C
78	A5	1481	C
78	A5	1633	G
78	A5	1804	A
78	A5	1832	C
78	A5	1833	G
78	A5	1835	G
78	A5	1841	C
78	A5	1921	C
78	A5	1975	G
78	A5	2046	G
78	A5	2068	C
78	A5	2083	C
78	A5	2089	G
80	A8	109	C
80	A8	124	U
80	A8	126	C
81	BC	17	G
81	BC	37	A
78	A6	2260	C
78	A6	2263	A

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Mol	Chain	Res	Type
78	A6	2266	C
78	A6	2268	A
78	A6	2272	C
78	A6	2313	A
78	A6	2526	C
78	A6	2649	G
78	A6	2661	U
78	A6	2695	A
78	A6	2769	U
78	A6	2812	A
78	A6	3605	C
78	A6	3616	U
78	A6	3731	C
78	A6	3876	A
78	A6	3959	U
78	A6	3965	A
78	A6	3968	U
78	A6	4072	C
78	A6	4082	G
78	A6	4087	G
78	A6	4093	G
78	A6	4144	C
78	A6	4164	C
78	A6	4170	A
78	A6	4232	U
78	A6	4237	C
78	A6	4448	G
78	A6	4656	A
78	A6	4699	U
78	A6	4713	G
78	A6	4738	C
78	A6	4748	U
78	A6	4749	C
78	A6	4871	C
78	A6	4874	A
78	A6	4882	U
78	A6	4885	U
78	A6	4889	G
78	A6	4924	C
78	A6	4951	G
78	A6	4991	U
78	A6	4997	G

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Mol	Chain	Res	Type
78	A6	5027	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
78	A5	11
78	A6	6
19	B2	2
20	CR	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	CR	83:GLY	C	120:TYR	N	39.03
1	A5	1440:U	O3'	1447:C	P	24.44
1	A6	4034:G	O3'	4039:G	P	20.91
1	A6	3292:G	O3'	3572:G	P	20.30
1	A5	1703:C	O3'	1720:C	P	18.79
1	A5	1052:G	O3'	1060:U	P	16.64
1	A6	4797:G	O3'	4834:C	P	15.82
1	A5	1111:U	O3'	1156:G	P	15.44

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Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A5	890:G	O3'	895:C	P	15.20
1	A6	4019:G	O3'	4028:C	P	14.03
1	A5	769:C	O3'	878:G	P	13.56
1	A6	2943:C	O3'	3248:C	P	13.51
1	A5	993:G	O3'	1044:G	P	13.48
1	A6	3993:U	O3'	4007:G	P	11.93
1	A5	524:C	O3'	633:G	P	11.05
1	A5	1222:A	O3'	1232:G	P	9.84
1	B2	1202:U	O3'	1203:G	P	7.12
1	A5	1241:C	O3'	1261:G	P	6.32
1	B2	1690:U	O3'	1691:U	P	4.53
1	A5	1166:G	O3'	1167:C	P	4.35

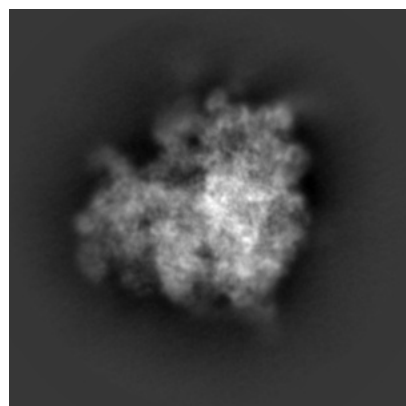
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74615. These allow visual inspection of the internal detail of the map and identification of artifacts.

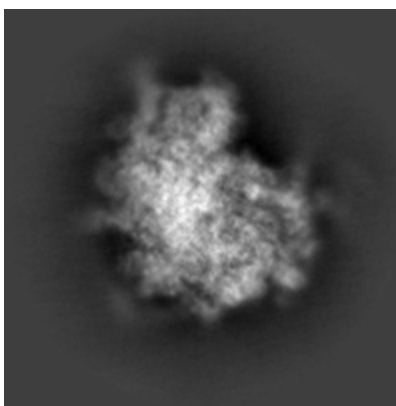
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

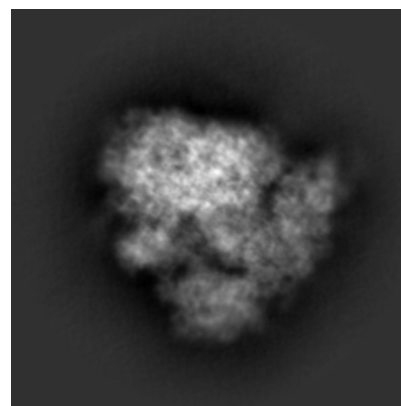
6.1.1 Primary map



X

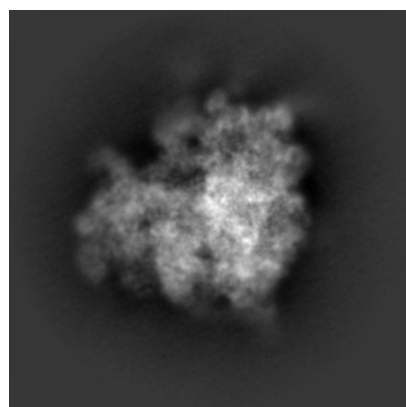


Y

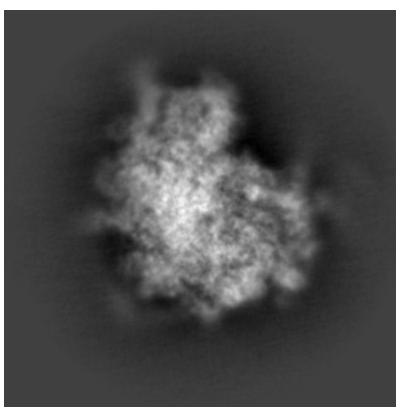


Z

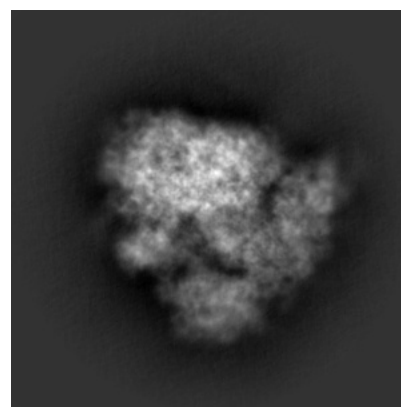
6.1.2 Raw map



X



Y

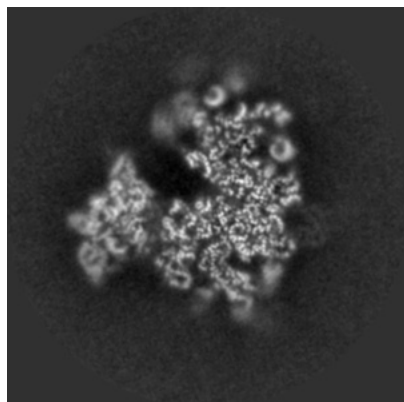


Z

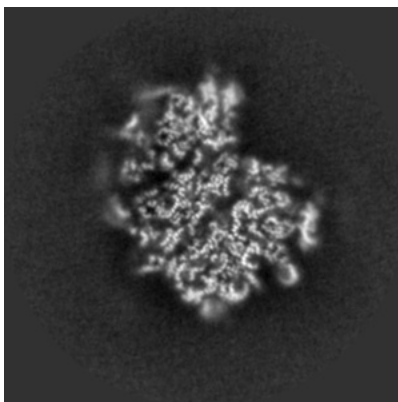
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

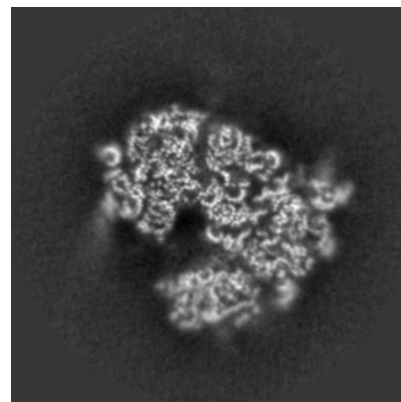
6.2.1 Primary map



X Index: 210

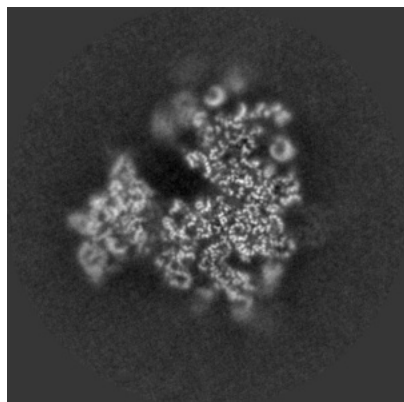


Y Index: 210

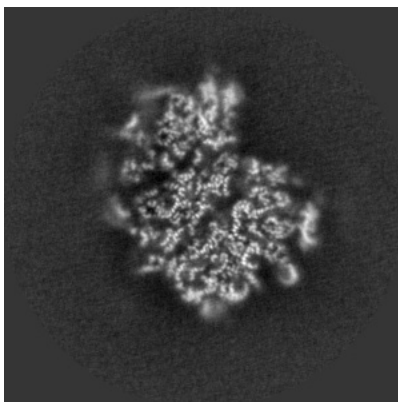


Z Index: 210

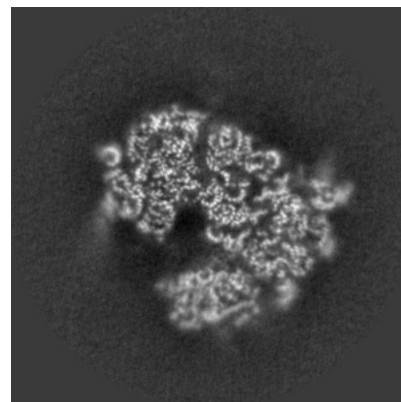
6.2.2 Raw map



X Index: 210



Y Index: 210

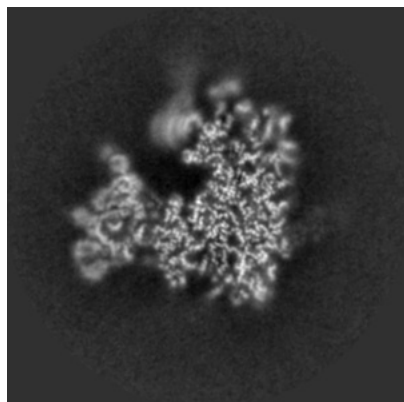


Z Index: 210

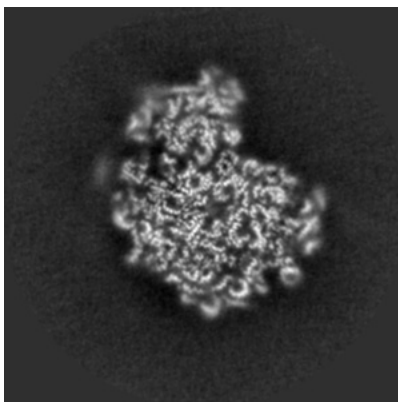
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

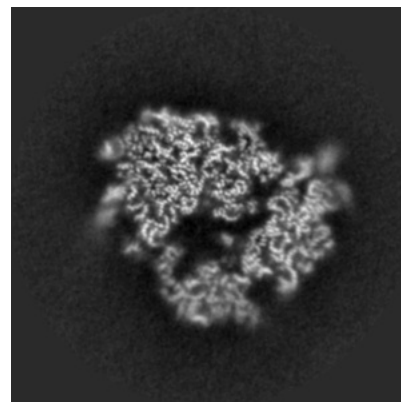
6.3.1 Primary map



X Index: 221

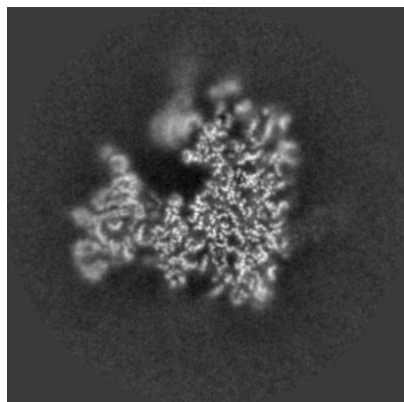


Y Index: 217

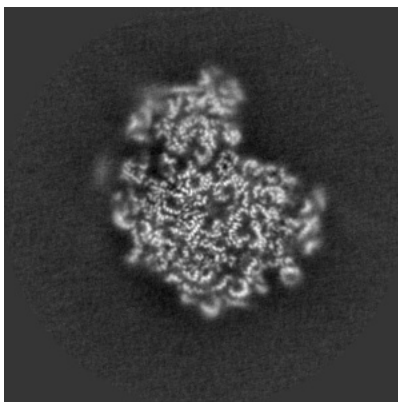


Z Index: 221

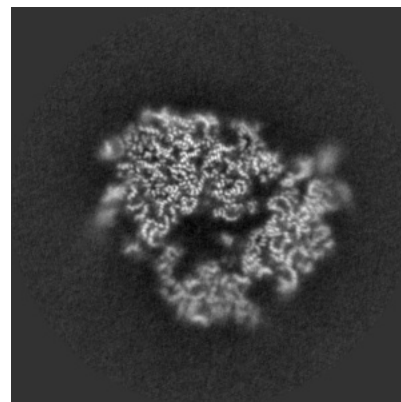
6.3.2 Raw map



X Index: 222



Y Index: 217

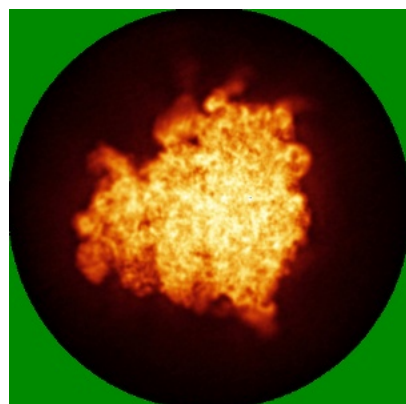


Z Index: 221

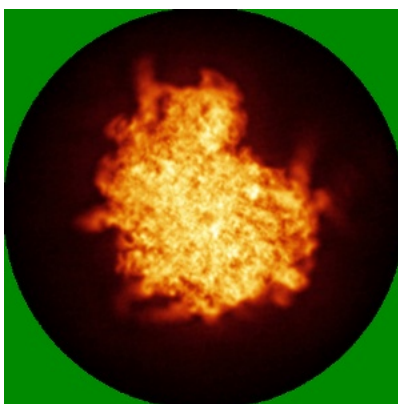
The images above show the largest variance slices of the map in three orthogonal directions.

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

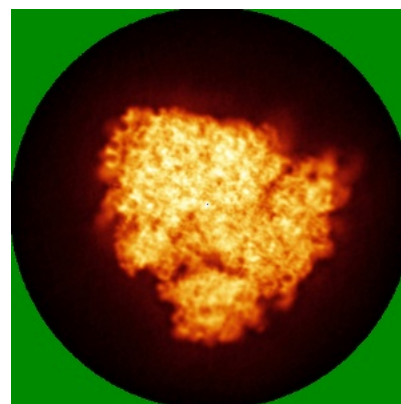
6.4.1 Primary map



X

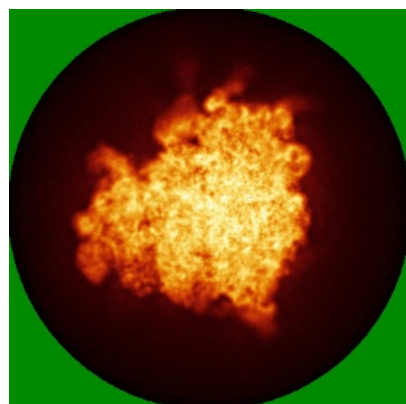


Y

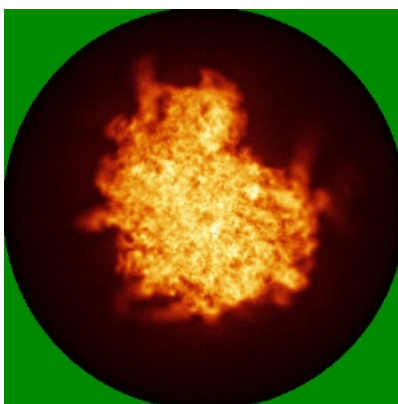


Z

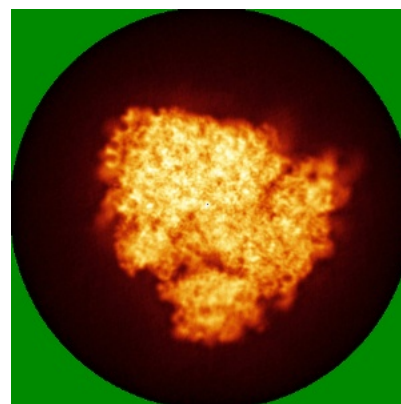
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

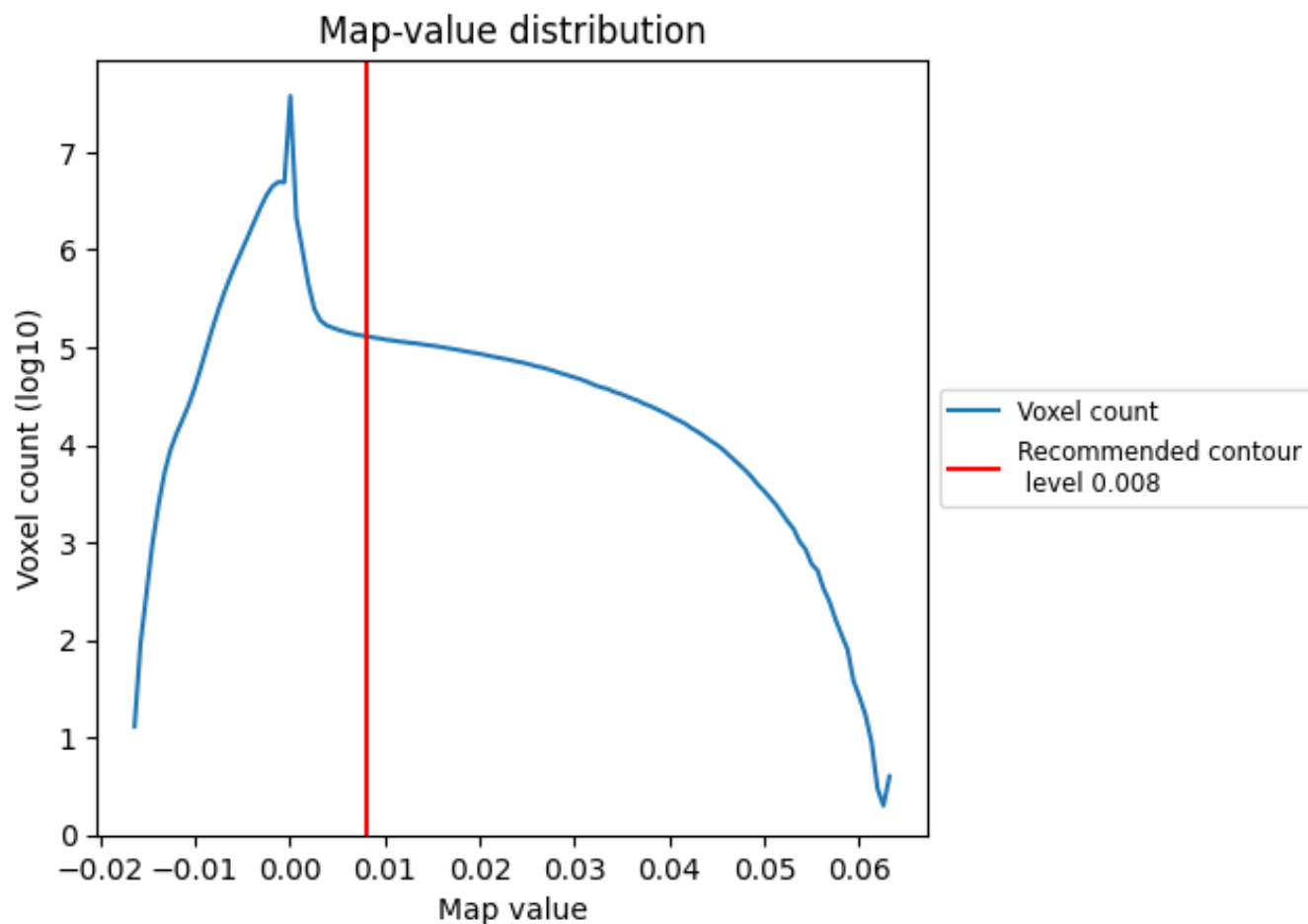
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

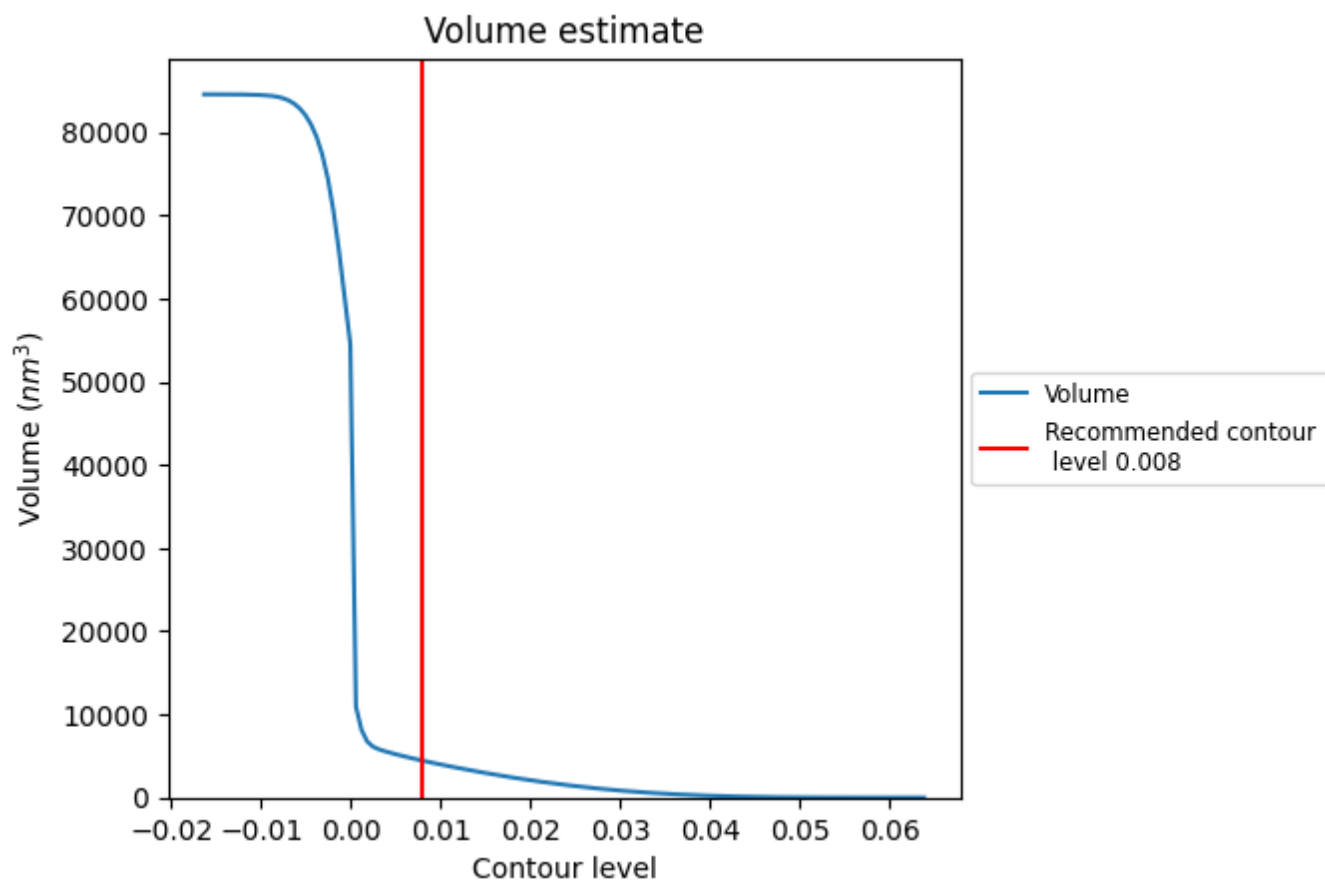
This section contains the results of statistical analysis of the map.

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.

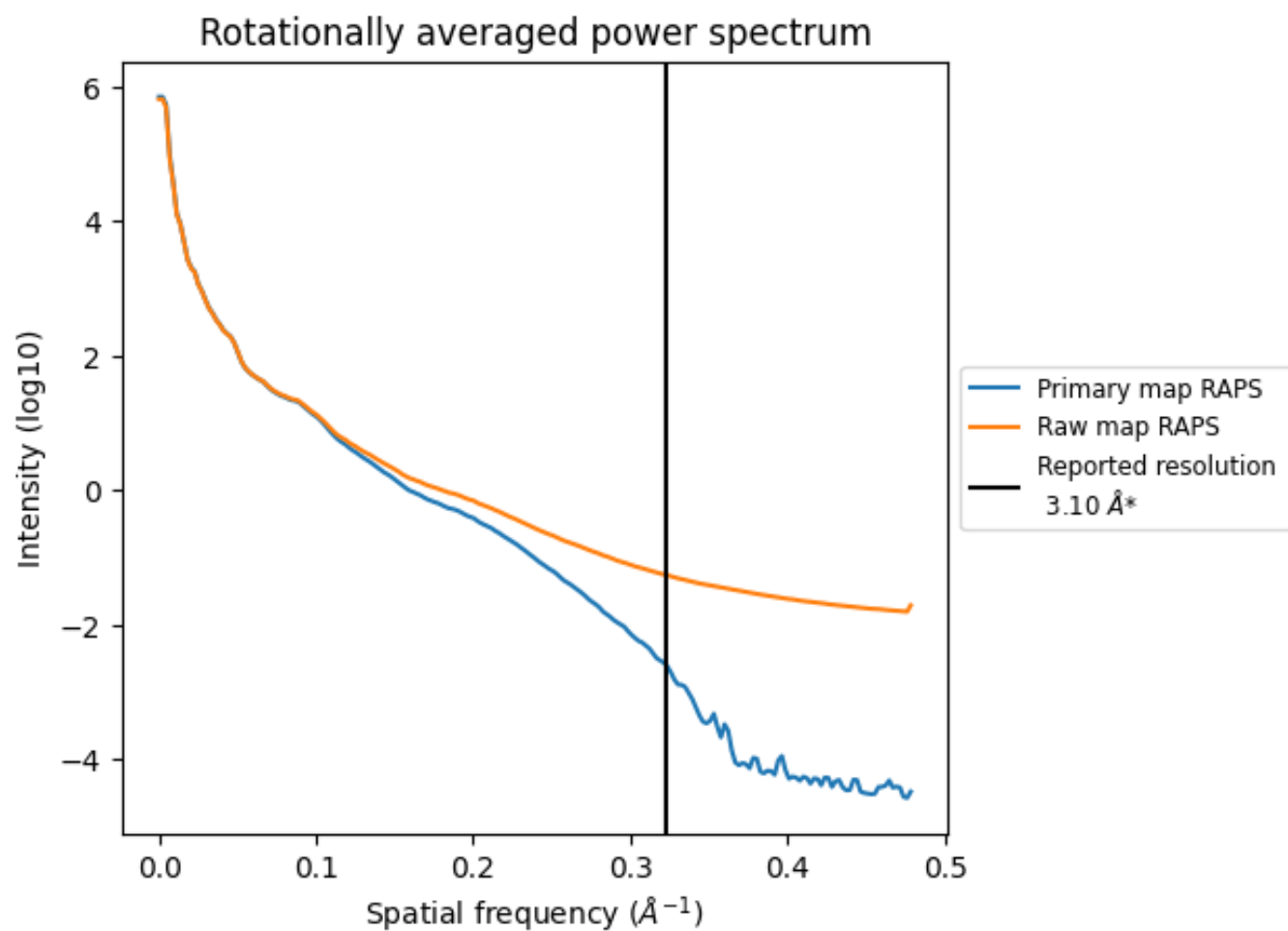
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4431 nm³; this corresponds to an approximate mass of 4002 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 ⓘ

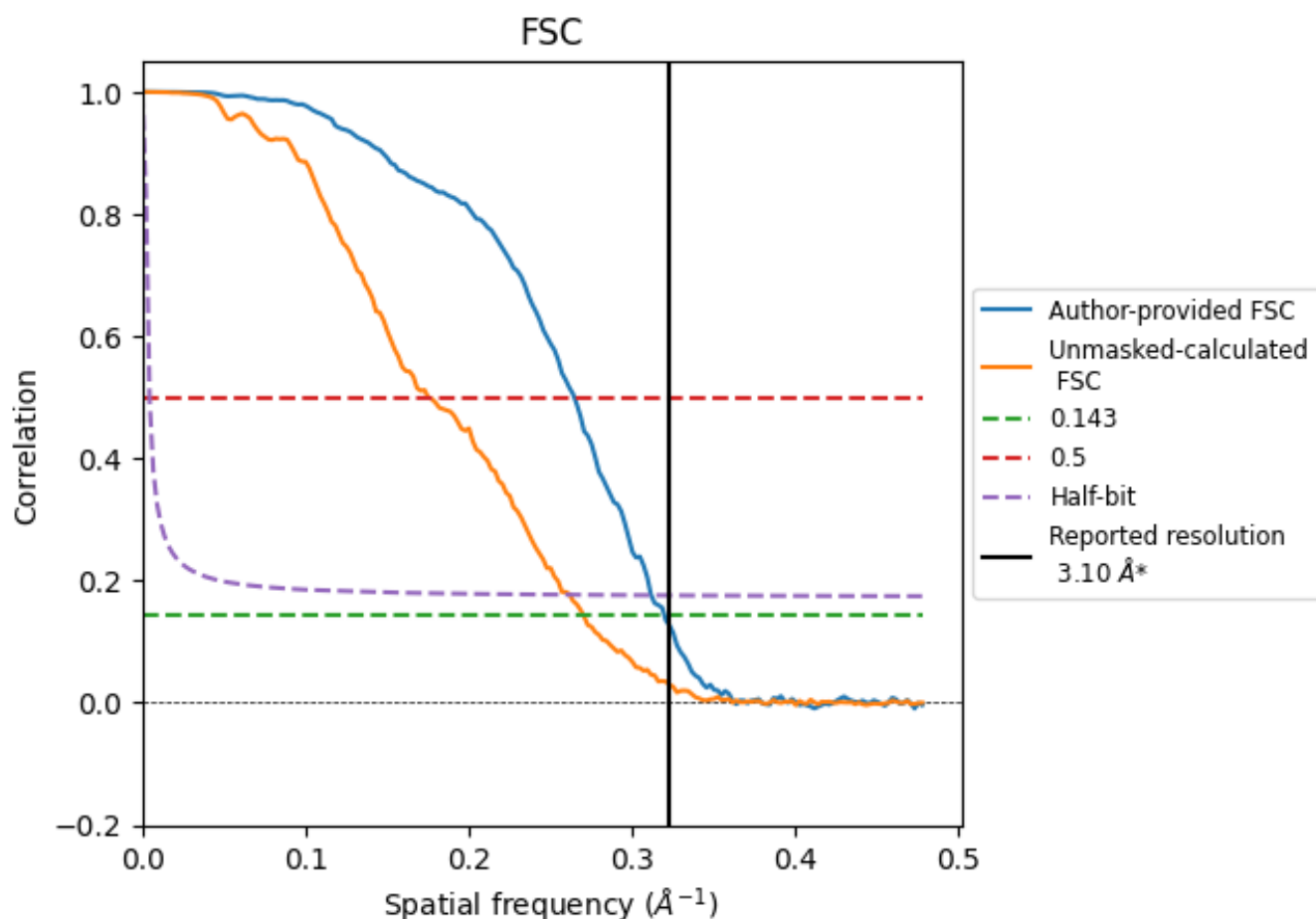


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

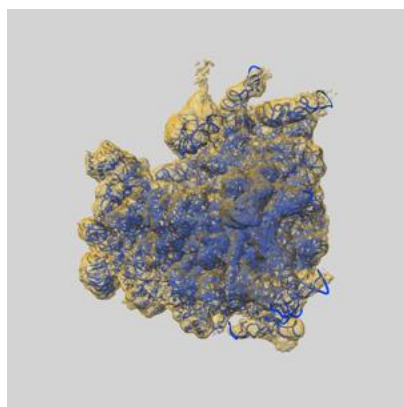
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.77	3.20
Unmasked-calculated*	3.69	5.70	3.81

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.69 differs from the reported value 3.1 by more than 10 %

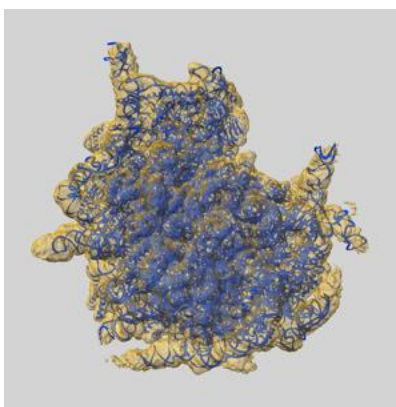
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74615 and PDB model 9ZRG. Per-residue inclusion information can be found in section 3 on page 19.

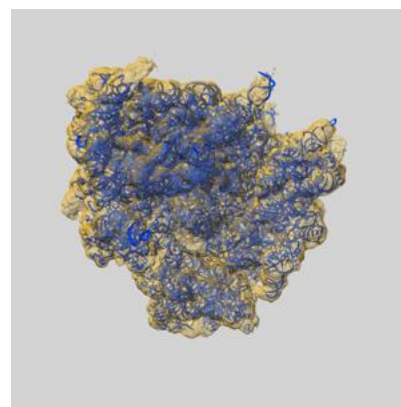
9.1 Map-model overlay [i](#)



X



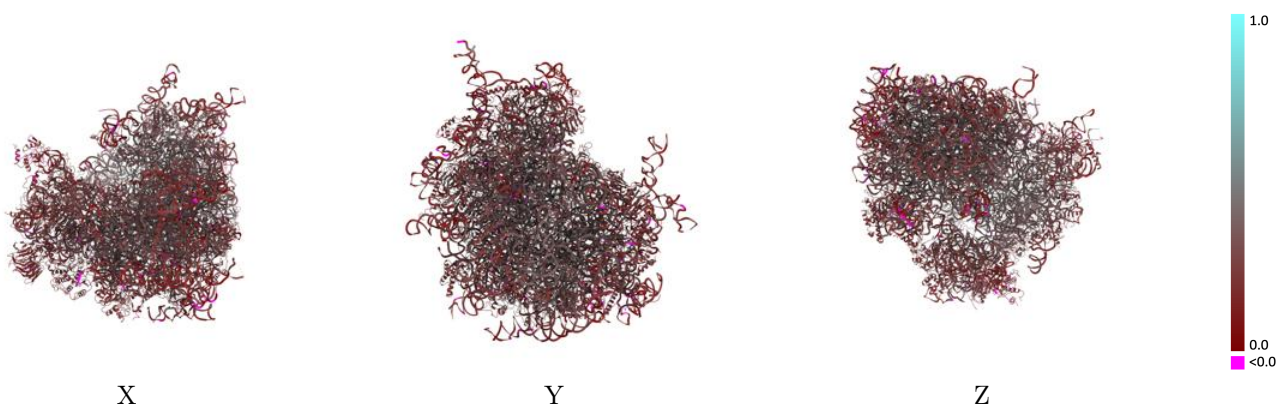
Y



Z

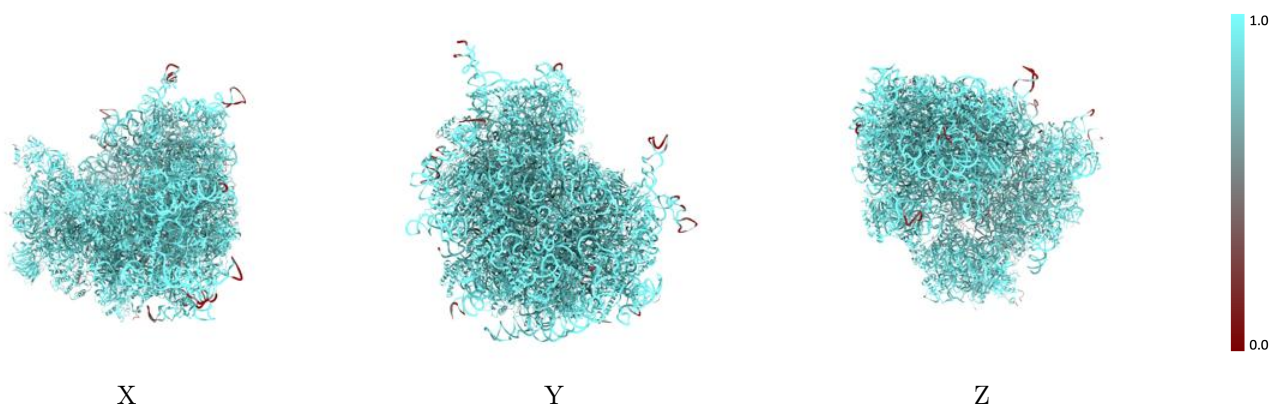
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



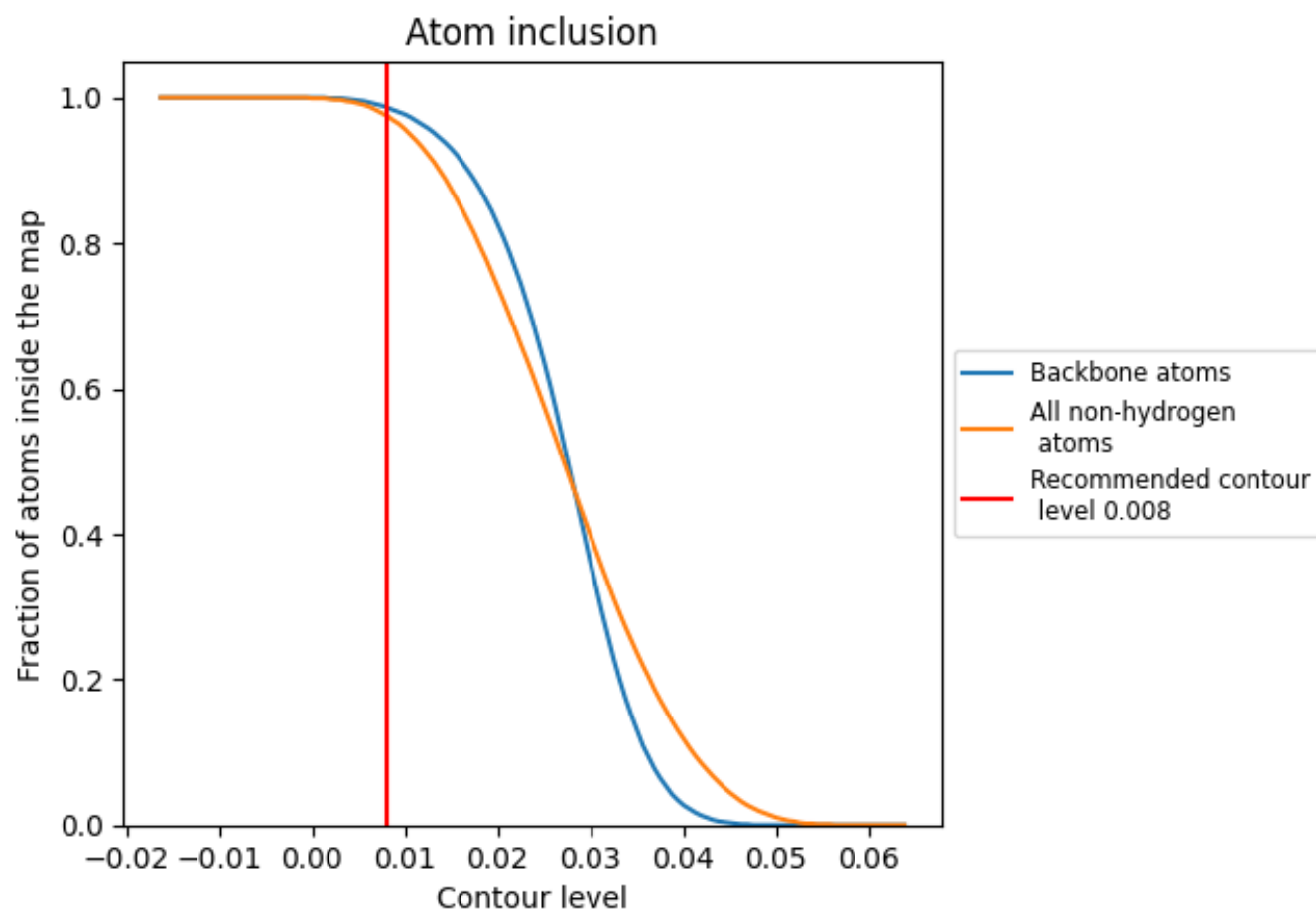
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9750	 0.2990
A5	 0.9860	 0.3110
A6	 0.9870	 0.3360
A7	 0.9960	 0.3370
A8	 0.9930	 0.3320
AA	 0.9680	 0.2540
AB	 0.9520	 0.2780
AC	 0.9460	 0.3020
AD	 0.9600	 0.2340
AE	 0.9810	 0.2850
AF	 0.9720	 0.2190
AG	 0.9810	 0.2330
AH	 0.9500	 0.2420
AI	 0.9610	 0.2760
AJ	 0.9700	 0.2720
AK	 0.9540	 0.2040
AL	 0.8920	 0.3070
AM	 0.9030	 0.1550
AN	 0.9370	 0.2890
AO	 0.9590	 0.2870
AP	 0.9750	 0.1960
AQ	 0.9940	 0.2060
AR	 0.9550	 0.2020
AS	 0.9840	 0.2040
AT	 0.9890	 0.2030
AU	 0.9610	 0.2110
AV	 0.9540	 0.2570
AW	 0.9620	 0.3190
AX	 0.9660	 0.3420
AY	 0.9810	 0.2400
AZ	 0.9780	 0.1950
Aa	 0.9050	 0.2870
Ab	 0.9400	 0.2780
Ac	 0.9200	 0.2430
Ad	 0.9810	 0.2210















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Chain	Atom inclusion	Q-score
Ae	 0.9120	 0.2650
Af	 0.9720	 0.1490
Ag	 0.9840	 0.1960
B2	 0.9920	 0.3010
BC	 0.9810	 0.2310
CA	 0.9260	 0.3620
CB	 0.9720	 0.3290
CC	 0.9600	 0.3290
CD	 0.9860	 0.2600
CE	 0.9700	 0.2250
CF	 0.9490	 0.3180
CG	 0.9560	 0.2650
CH	 0.9660	 0.2960
CI	 0.9590	 0.3370
CJ	 0.9740	 0.2570
CL	 0.9680	 0.3060
CM	 0.9810	 0.2770
CN	 0.9700	 0.3360
CO	 0.9260	 0.3100
CP	 0.9670	 0.3470
CQ	 0.9390	 0.3300
CR	 0.8760	 0.1640
CS	 0.9760	 0.3100
CT	 0.9560	 0.3330
CU	 0.9250	 0.2310
CV	 0.9460	 0.3570
CW	 0.9160	 0.1890
CX	 0.9780	 0.3130
CY	 0.9790	 0.3020
CZ	 0.9790	 0.2840
Ca	 0.9740	 0.3540
Cb	 0.9570	 0.2970
Cc	 0.9310	 0.2850
Cd	 0.9690	 0.3020
Ce	 0.9320	 0.3510
Cf	 0.9480	 0.3350
Cg	 0.9690	 0.3090
Ch	 0.9740	 0.2770
Ci	 0.9540	 0.2620
Cj	 0.9400	 0.3420
Ck	 0.9480	 0.2680
Cl	 0.9650	 0.3260

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Chain	Atom inclusion	Q-score
Cm	 0.9760	 0.3230
Cn	 0.8900	 0.3100
Co	 0.9210	 0.3240
Cp	 0.9060	 0.3460
Cr	 0.9050	 0.2720
Cz	 0.9400	 0.0930