



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 03:01 AM UTC

PDB ID : 8K82 / pdb_00008k82
EMDB ID : EMD-36945
Title : Cryo-EM structure of the yeast 80S ribosome with tigecycline, Not5 and P-site tRNA
Authors : Buschauer, R.; Beckmann, R.; Cheng, J.
Deposited on : 2023-07-28
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

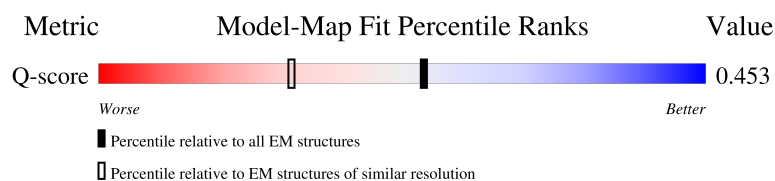
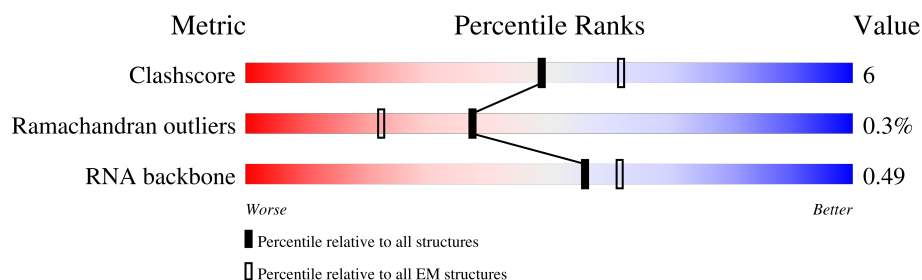
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.



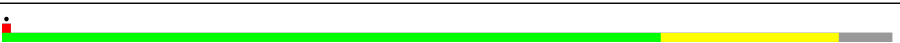
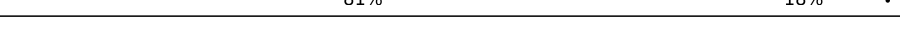
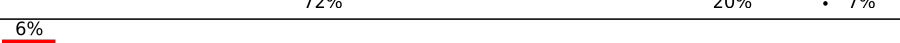
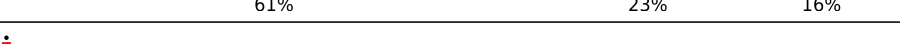
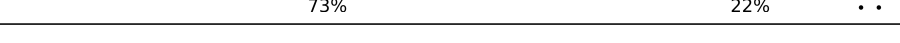
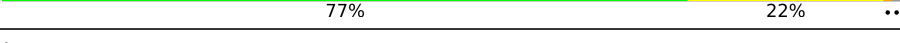
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	C2	1800	
2	C7	3	
3	C5	75	
4	C1	3396	

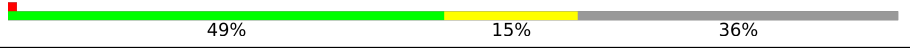
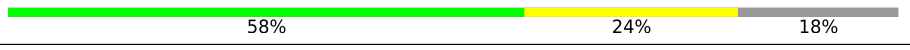
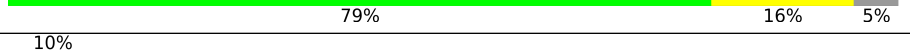
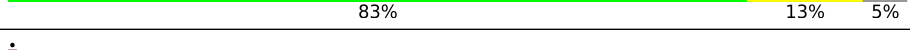
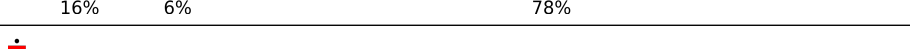
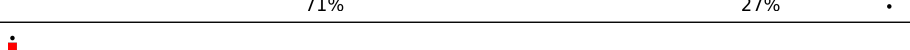
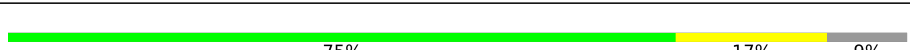
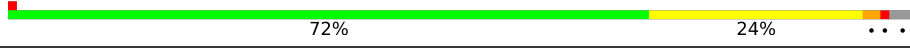
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Mol	Chain	Length	Quality of chain
5	C4	121	
6	C3	158	
7	SA	252	
8	SB	255	
9	SC	254	
10	SD	240	
11	SE	261	
12	SF	225	
13	SG	236	
14	SH	190	
15	SI	200	
16	SJ	197	
17	SK	105	
18	SL	156	
19	SM	143	
20	SN	151	
21	SO	137	
22	SP	142	
23	SQ	143	
24	SR	136	
25	SS	146	
26	ST	144	
27	SU	121	
28	SV	87	
29	SW	130	

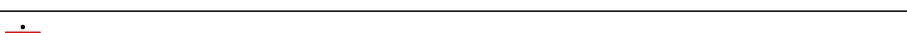
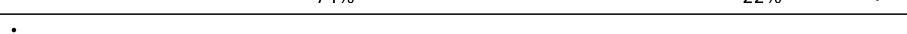
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Mol	Chain	Length	Quality of chain
30	SX	145	
31	SY	135	
32	SZ	108	
33	Sa	119	
34	Sb	82	
35	Sc	67	
36	Sd	56	
37	Se	63	
38	Sf	152	
39	Sg	319	
40	LA	254	
41	LB	387	
42	LC	362	
43	LD	297	
44	LE	176	
45	LF	244	
46	LG	256	
47	LH	191	
48	LI	221	
49	LJ	174	
50	LK	165	
51	LL	199	
52	LM	138	
53	LN	204	
54	LO	199	

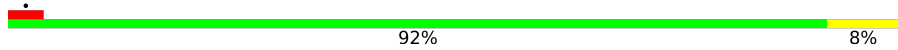
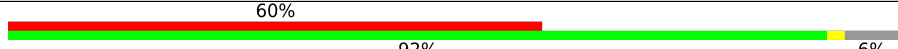
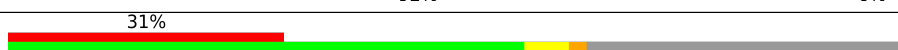
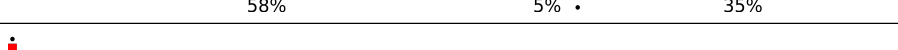
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Mol	Chain	Length	Quality of chain
55	LP	184	
56	LQ	186	
57	LR	189	
58	LS	172	
59	LT	160	
60	LU	121	
61	LV	137	
62	LW	155	
63	LX	142	
64	LY	127	
65	LZ	136	
66	La	149	
67	Lb	59	
68	Lc	105	
69	Ld	113	
70	Le	130	
71	Lf	107	
72	Lg	121	
73	Lh	120	
74	Li	100	
75	Lj	88	
76	Lk	78	
77	Ll	51	
78	Lm	128	
79	L2	25	

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Mol	Chain	Length	Quality of chain
79	Ln	25	
80	Lo	106	
81	Lp	92	
82	L1	217	
83	P0	312	
84	CN	560	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 205122 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 RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 2 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C7	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 3 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C5	75	Total	C	N	O	P	0	0
			1624	728	298	523	75		

- Molecule 4 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C1	3204	Total	C	N	O	P	0	0
			68535	30613	12358	22360	3204		

- Molecule 5 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 6 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 7 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SA	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 8 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SB	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 9 is a protein called 40S ribosomal protein S2.

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

- Molecule 10 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 11 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 13 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SG	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 14 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	SH	185	Total	C	N	O		
			1486	954	266	266	0	0

- Molecule 15 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 16 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 17 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SK	92	Total	C	N	O	S		
			741	478	121	140	2	0	0

- Molecule 18 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SL	146	Total	C	N	O	S		
			1168	747	221	197	3	0	0

- Molecule 19 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SM	124	Total	C	N	O	S		
			890	560	156	172	2	0	0

- Molecule 20 is a protein called 40S ribosomal protein S13.

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

- Molecule 21 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SO	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SP	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

- Molecule 23 is a protein called Small ribosomal subunit protein uS9A.

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

- Molecule 24 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SR	115	Total	C	N	O	S	0	0
			896	557	172	165	2		

- Molecule 25 is a protein called Small ribosomal subunit protein uS13A.

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

- Molecule 26 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 27 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SU	101	Total	C	N	O	S	0	0
			805	512	145	147	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS21A.

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

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SY	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 32 is a protein called Small ribosomal subunit protein eS25A.

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

- Molecule 33 is a protein called Small ribosomal subunit protein eS26B.

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

- Molecule 34 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 35 is a protein called Small ribosomal subunit protein eS28A.

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

- Molecule 36 is a protein called Small ribosomal subunit protein uS14A.

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

- Molecule 37 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 38 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Sf	33	Total	C	N	O	S	0	0
			248	153	46	45	4		

- Molecule 39 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Sg	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

- Molecule 40 is a protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LA	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 41 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 42 is a protein called Large ribosomal subunit protein uL4A.

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

- Molecule 43 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LD	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 44 is a protein called Large ribosomal subunit protein eL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LE	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 45 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LF	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 46 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LG	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 47 is a protein called Large ribosomal subunit protein uL6A.

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

- Molecule 48 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LI	209	Total	C	N	O	S	0	0
			1696	1077	321	293	5		

- Molecule 49 is a protein called Large ribosomal subunit protein uL5A.

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

- Molecule 50 is a protein called Large ribosomal subunit protein uL11A.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	LK	158	Total	C	N	O	0	0
			778	461	158	159		

- Molecule 51 is a protein called Large ribosomal subunit protein eL13A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	LL	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 52 is a protein called Large ribosomal subunit protein eL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 53 is a protein called Large ribosomal subunit protein eL15A.

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

- Molecule 54 is a protein called Large ribosomal subunit protein uL13A.

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

- Molecule 55 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	LP	175	Total	C	N	O	0	0
			1378	856	273	249		

- Molecule 56 is a protein called Large ribosomal subunit protein eL18A.

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

- Molecule 57 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LR	174	Total	C	N	O	S	0	0
			1365	843	286	236			

- Molecule 58 is a protein called Large ribosomal subunit protein eL20A.

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

- Molecule 59 is a protein called Large ribosomal subunit protein eL21A.

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

- Molecule 60 is a protein called Large ribosomal subunit protein eL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LU	98	Total	C	N	O	S	0	0
			778	505	127	146			

- Molecule 61 is a protein called Large ribosomal subunit protein uL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LV	134	Total	C	N	O	S	0	0
			993	623	187	176	7		

- Molecule 62 is a protein called Large ribosomal subunit protein eL24A.

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

- Molecule 63 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LX	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 64 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LY	124	Total	C	N	O		0	0
			976	614	190	172			

- Molecule 65 is a protein called Large ribosomal subunit protein eL27A.

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

- Molecule 66 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 67 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 68 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Lc	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 69 is a protein called Large ribosomal subunit protein eL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Ld	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 70 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 71 is a protein called Large ribosomal subunit protein eL33A.

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

- Molecule 72 is a protein called Large ribosomal subunit protein eL34A.

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

- Molecule 73 is a protein called Large ribosomal subunit protein uL29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Lh	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 74 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Li	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 75 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Lj	82	Total	C	N	O	S	0	0
			650	396	142	107	5		

- Molecule 76 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	Lk	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 77 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	L1	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 78 is a protein called Ubiquitin-ribosomal protein eL40A fusion protein.

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

- Molecule 79 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ln	25	Total	C	N	O	S	0	0
			233	142	63	27	1		
79	L2	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 80 is a protein called Large ribosomal subunit protein eL42A.

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

- Molecule 81 is a protein called Large ribosomal subunit protein eL43A.

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

- Molecule 82 is a protein called Large ribosomal subunit protein uL1A.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	L1	204	Total	C	N	O	0	0
			1010	602	204	204		

- Molecule 83 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	P0	203	Total	C	N	O	0	0
			998	592	203	203		

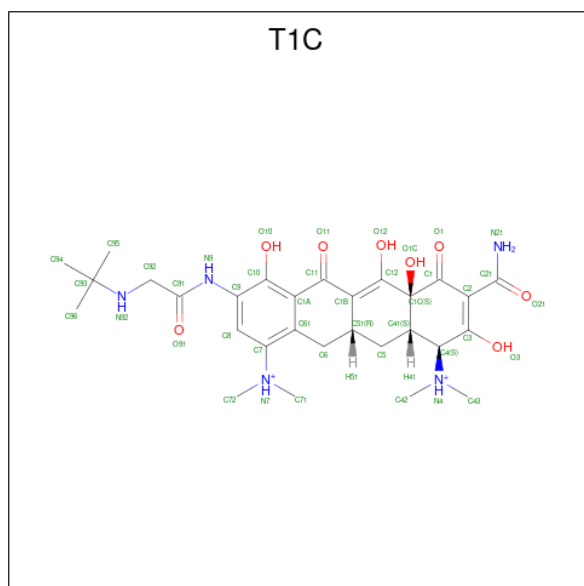
- Molecule 84 is a protein called General negative regulator of transcription subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CN	112	Total	C	N	O	S	0	0
			940	585	170	182	3		

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

Mol	Chain	Residues	Atoms		AltConf
85	C2	89	Total	Mg	0
			89	89	
85	C5	3	Total	Mg	0
			3	3	
85	C1	222	Total	Mg	0
			222	222	
85	C4	1	Total	Mg	0
			1	1	
85	C3	1	Total	Mg	0
			1	1	

- Molecule 86 is TIGECYCLINE (CCD ID: T1C) (formula: C₂₉H₄₁N₅O₈) (labeled as "Ligand of Interest" by depositor).



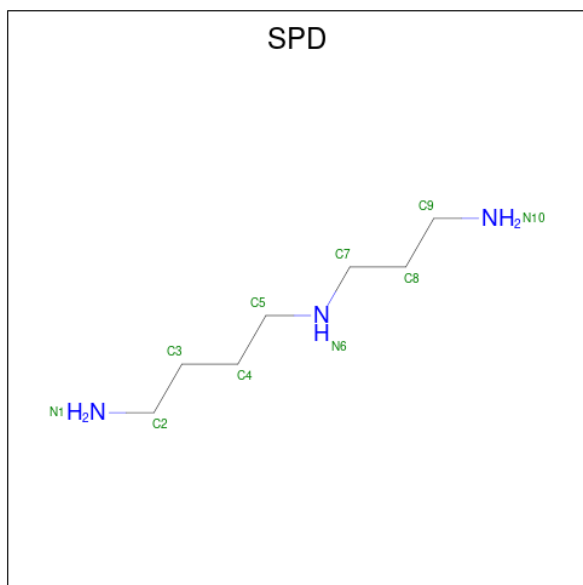
Mol	Chain	Residues	Atoms				AltConf
86	C2	1	Total	C	N	O	0
			42	29	5	8	
86	C1	1	Total	C	N	O	0
			42	29	5	8	
86	C1	1	Total	C	N	O	0
			42	29	5	8	

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Mol	Chain	Residues	Atoms				AltConf
86	C1	1	Total	C	N	O	0
			42	29	5	8	
86	C1	1	Total	C	N	O	0
			42	29	5	8	
86	C1	1	Total	C	N	O	0
			42	29	5	8	

- Molecule 87 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
87	C1	1	Total	C	N	0
			10	7	3	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

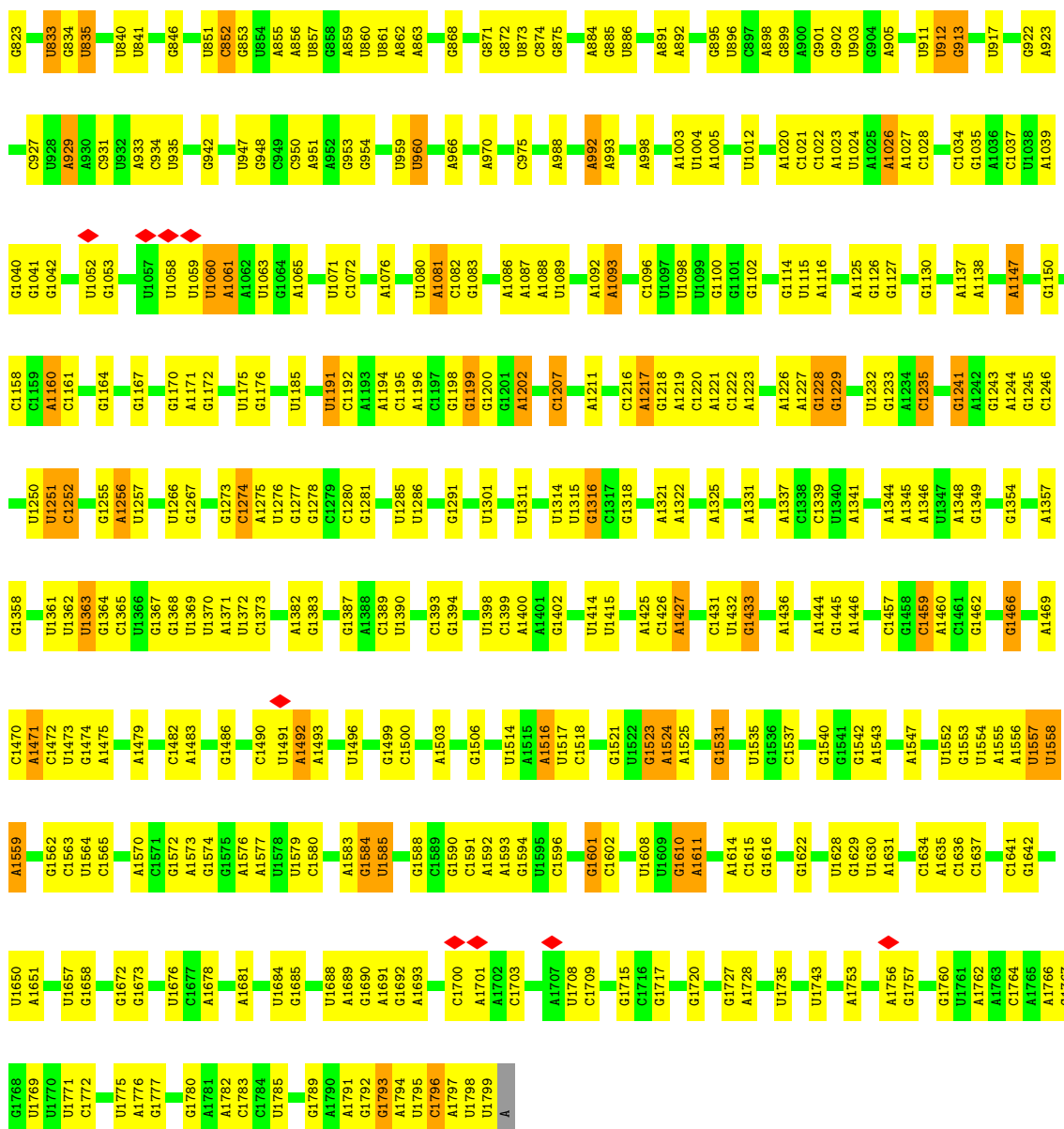
Mol	Chain	Residues	Atoms		AltConf
88	Sa	1	Total	Zn	0
			1	1	
88	Sb	1	Total	Zn	0
			1	1	
88	Sd	1	Total	Zn	0
			1	1	
88	Sf	1	Total	Zn	0
			1	1	
88	Lg	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0





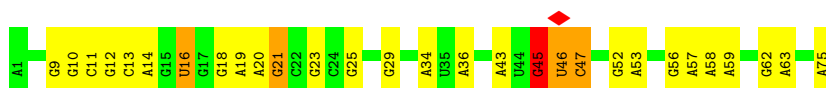
- Molecule 2: mRNA

Chain C7: 100%

There are no outlier residues recorded for this chain.

- Molecule 3: tRNA

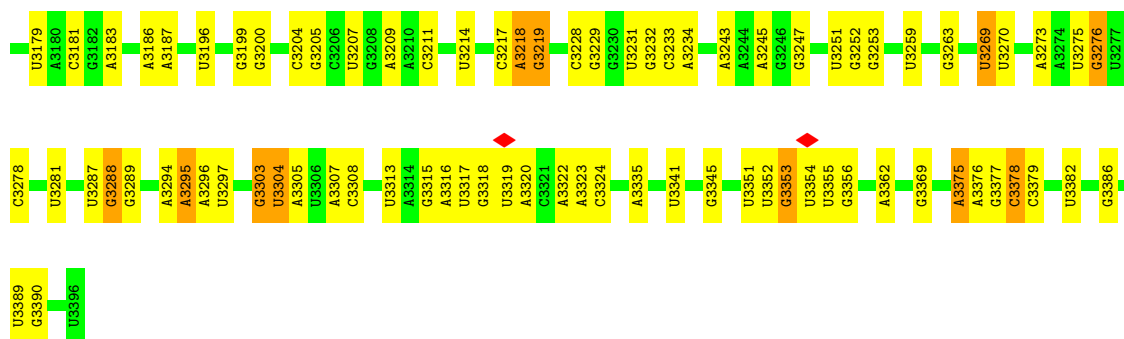
Chain C5: 61% 32% 5%



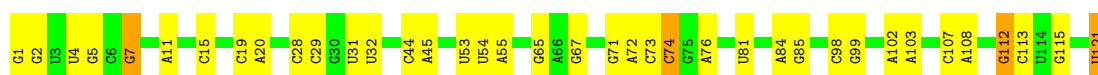
- Molecule 4: 23S rRNA



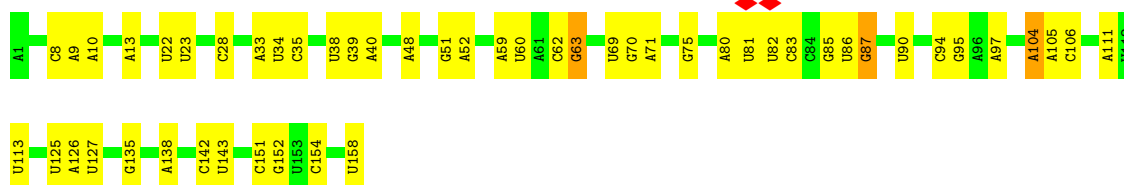




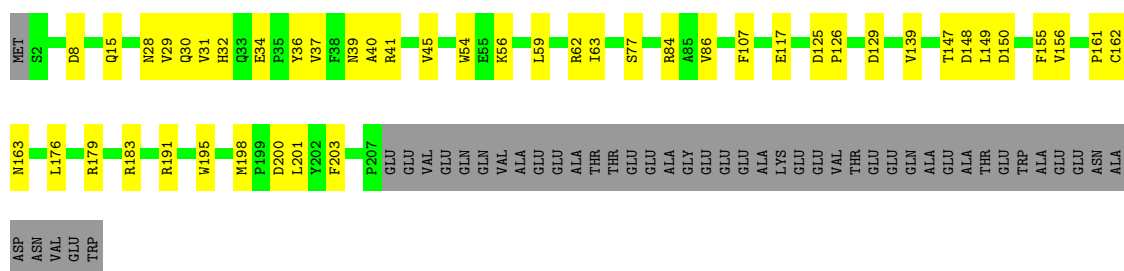
• Molecule 5: 5S rRNA



• Molecule 6: 5.8S rRNA

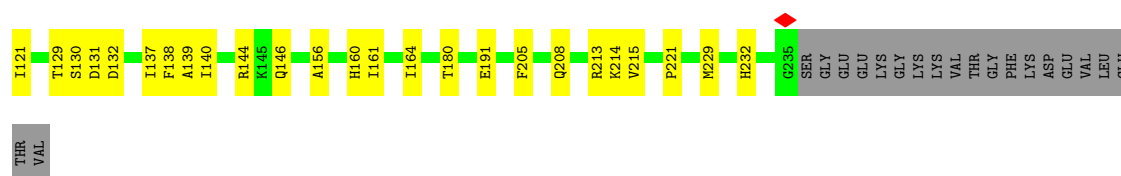


• Molecule 7: Small ribosomal subunit protein uS2A



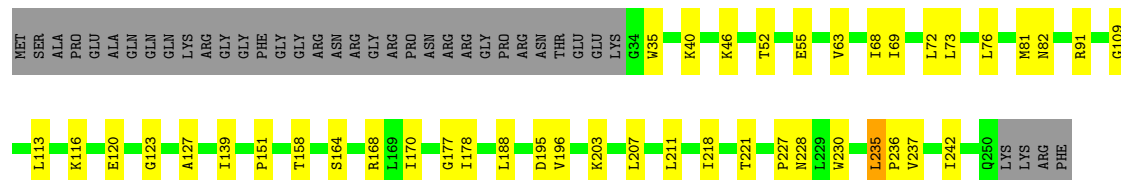
• Molecule 8: 40S ribosomal protein S1-A





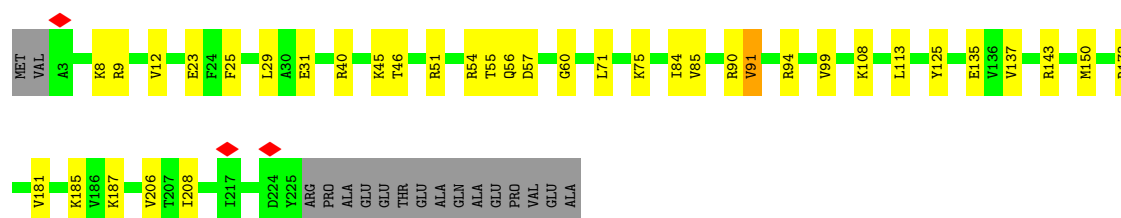
- Molecule 9: 40S ribosomal protein S2

Chain SC: 69% 17% 15%



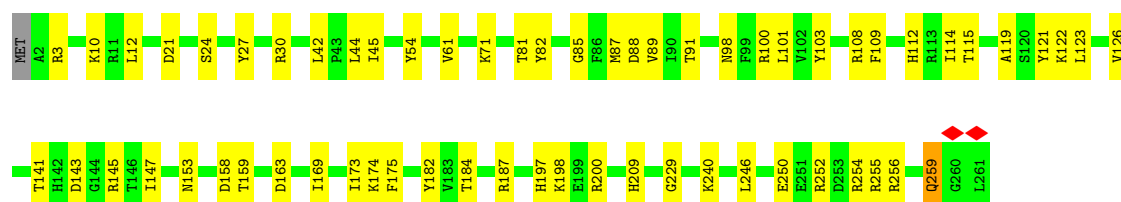
- Molecule 10: Small ribosomal subunit protein uS3

Chain SD: 78% 15% 7%



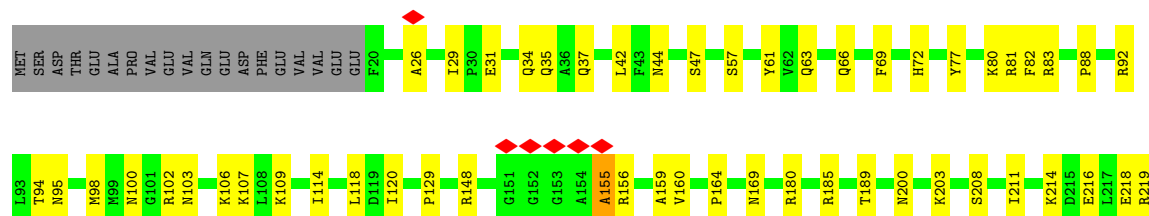
- Molecule 11: 40S ribosomal protein S4-A

Chain SE: 76% 23%



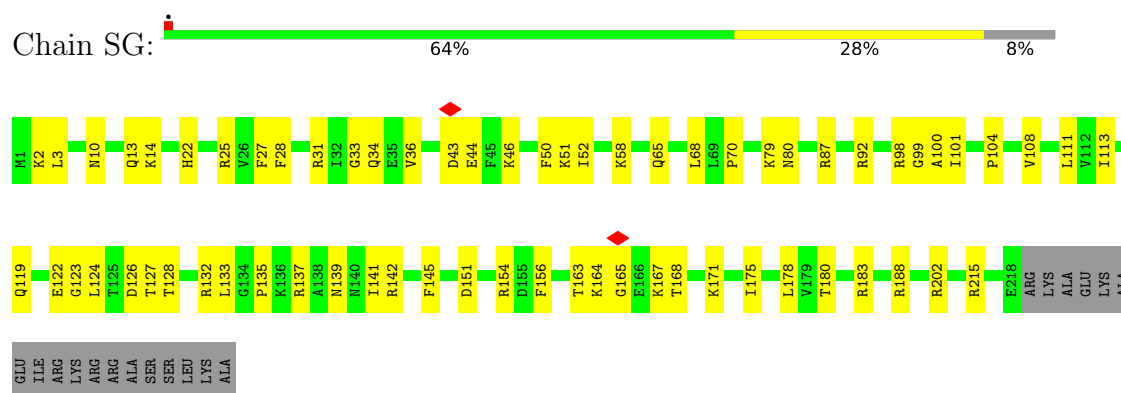
- Molecule 12: Small ribosomal subunit protein uS7

Chain SF: 68% 24% 8%

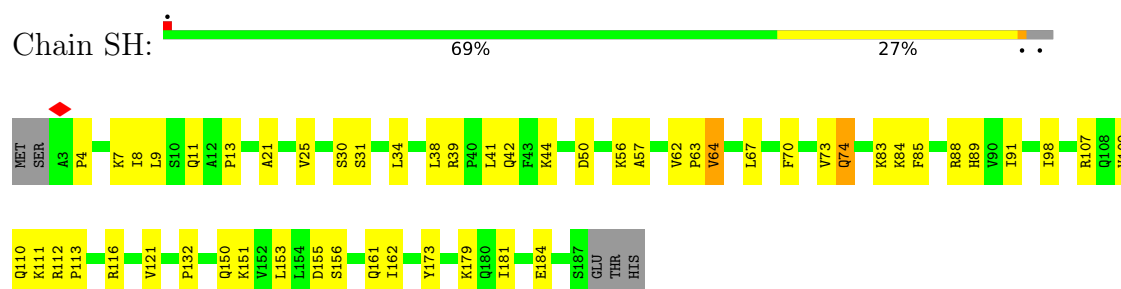




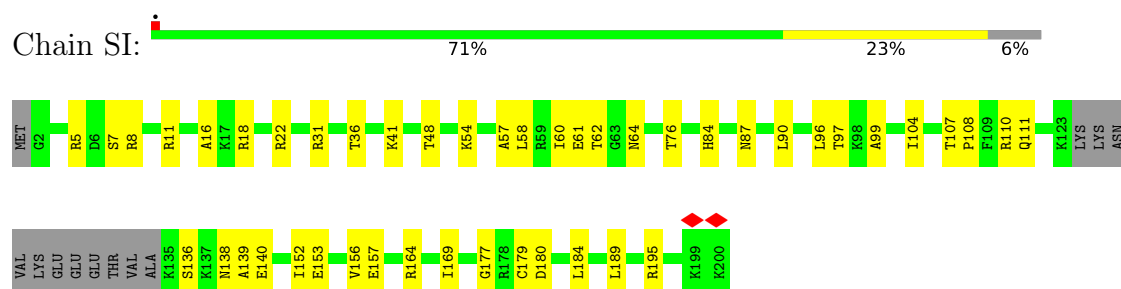
- Molecule 13: 40S ribosomal protein S6-A



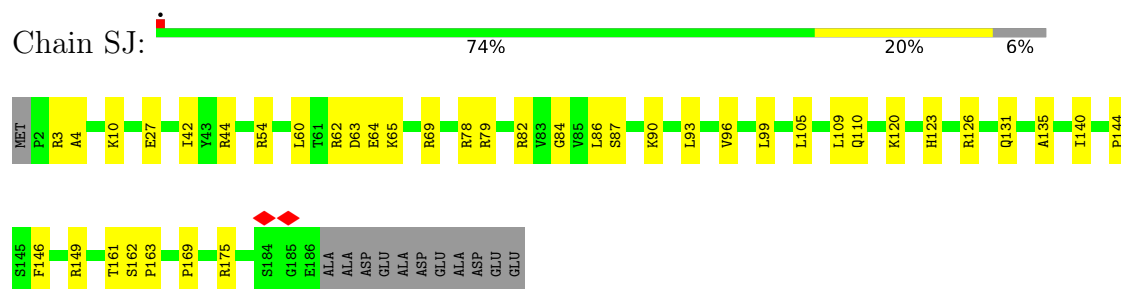
- Molecule 14: 40S ribosomal protein S7-A



- Molecule 15: 40S ribosomal protein S8-A

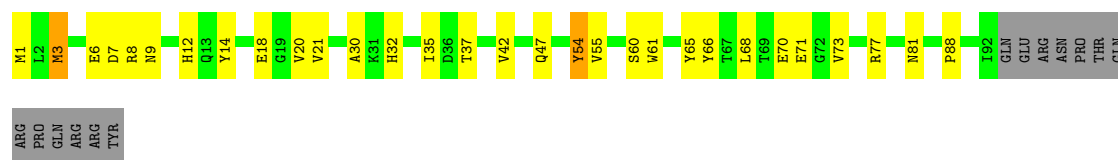


- Molecule 16: 40S ribosomal protein S9-A



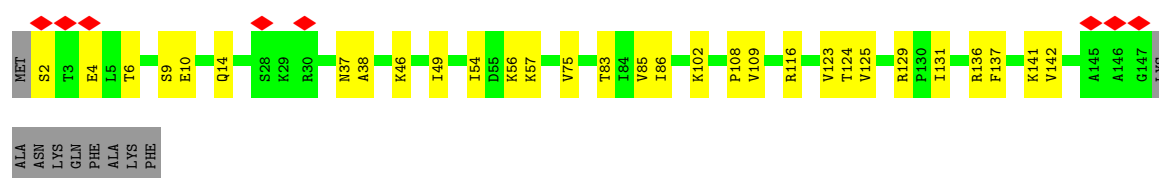
- Molecule 17: Small ribosomal subunit protein eS10A

Chain SK: 



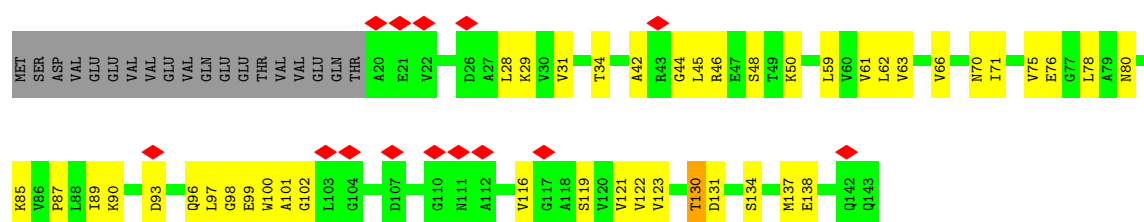
- Molecule 18: Small ribosomal subunit protein uS17A

Chain SL: 



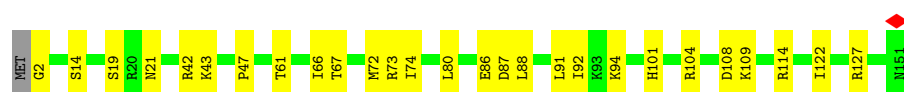
- Molecule 19: Small ribosomal subunit protein eS12

Chain SM: 



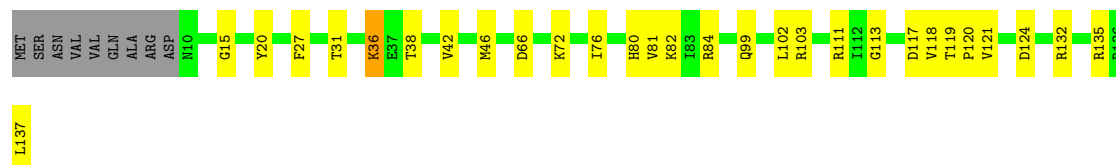
- Molecule 20: 40S ribosomal protein S13

Chain SN: 



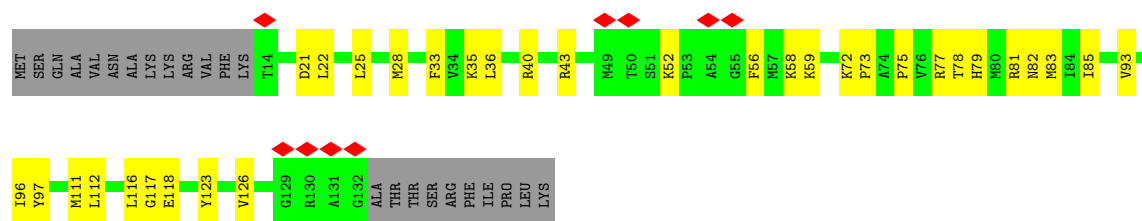
- Molecule 21: 40S ribosomal protein S14-A

Chain SO: 

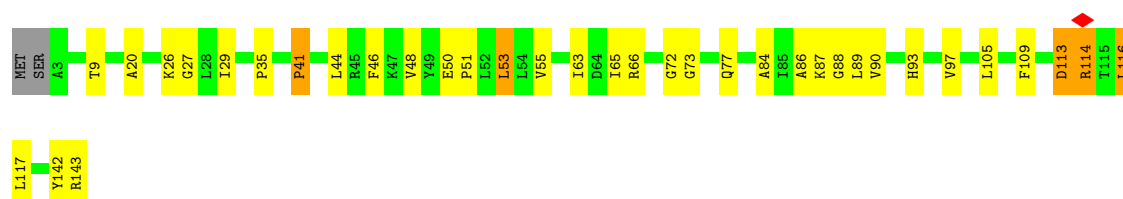
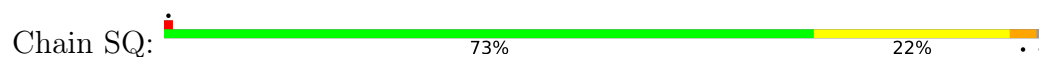


- Molecule 22: Small ribosomal subunit protein uS19

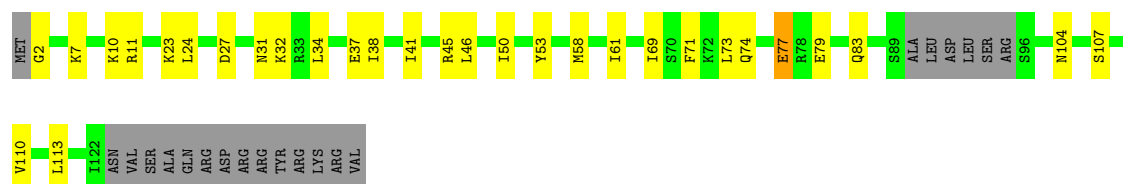
Chain SP: 



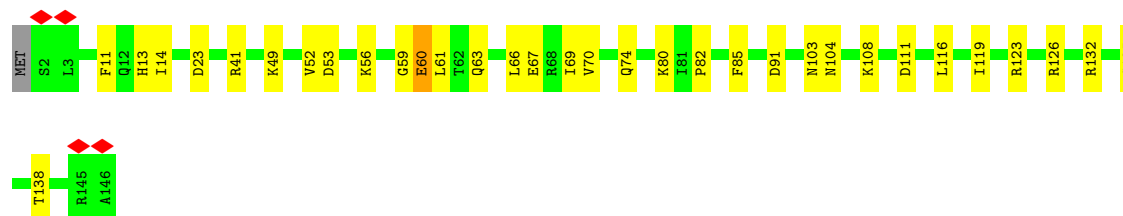
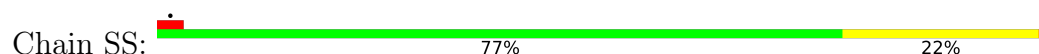
- Molecule 23: Small ribosomal subunit protein uS9A



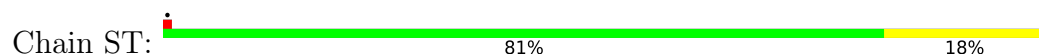
- Molecule 24: Small ribosomal subunit protein eS17A



- Molecule 25: Small ribosomal subunit protein uS13A

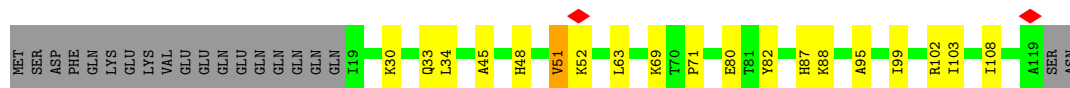


- Molecule 26: Small ribosomal subunit protein eS19A

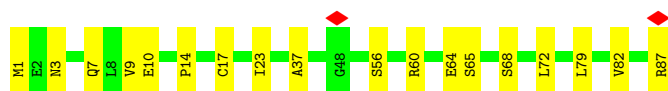
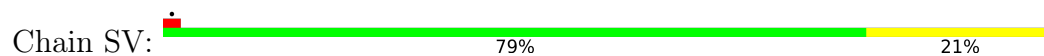


- Molecule 27: Small ribosomal subunit protein uS10

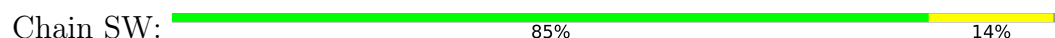




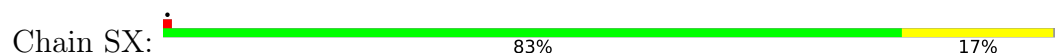
- Molecule 28: Small ribosomal subunit protein eS21A



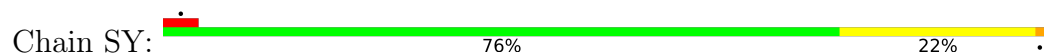
- Molecule 29: 40S ribosomal protein S22-A



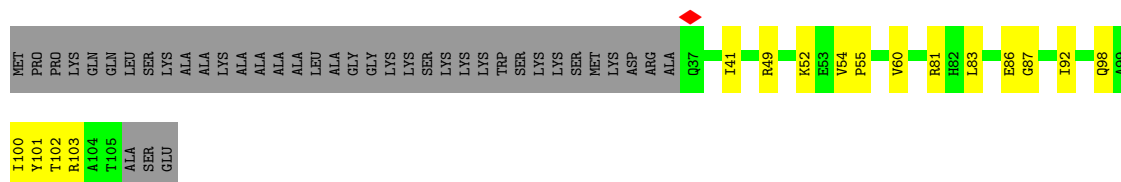
- Molecule 30: 40S ribosomal protein S23-A



- Molecule 31: 40S ribosomal protein S24-A

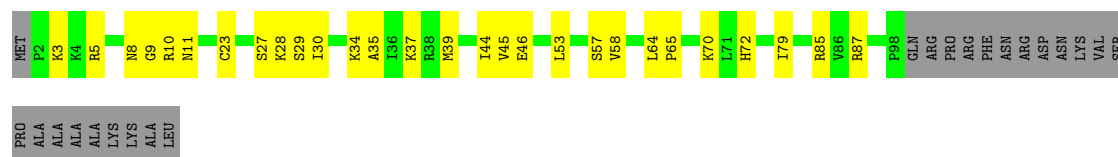


- Molecule 32: Small ribosomal subunit protein eS25A

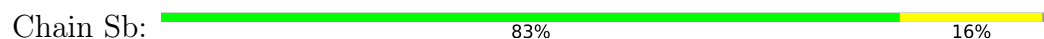


- Molecule 33: Small ribosomal subunit protein eS26B





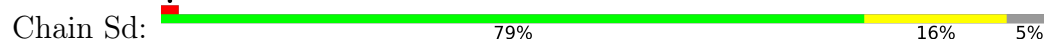
- Molecule 34: 40S ribosomal protein S27-A



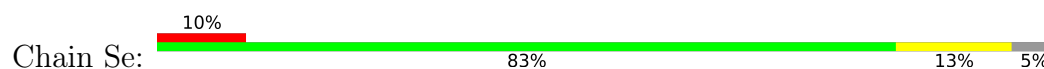
- Molecule 35: Small ribosomal subunit protein eS28A



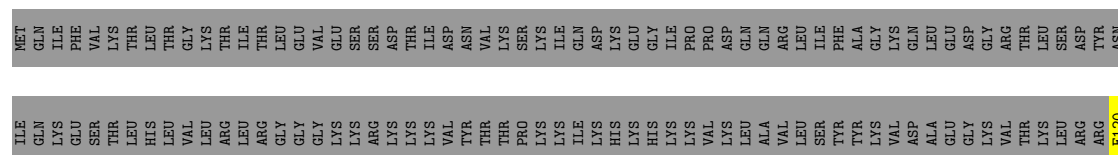
- Molecule 36: Small ribosomal subunit protein uS14A



- Molecule 37: 40S ribosomal protein S30-A

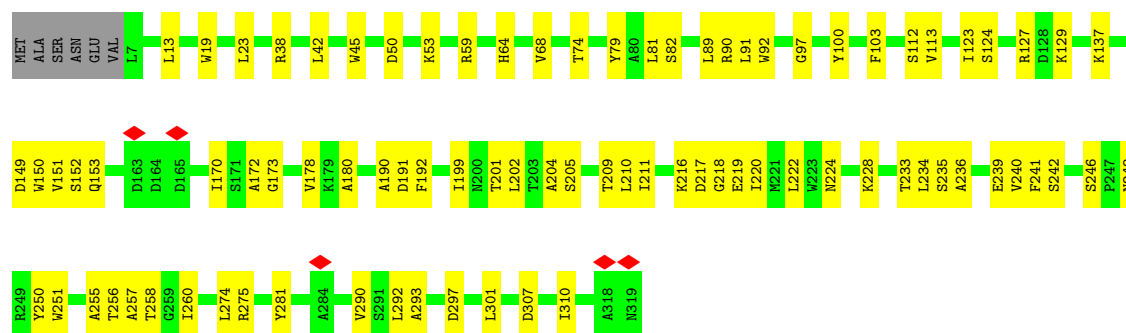


- Molecule 38: Ubiquitin-ribosomal protein eS31 fusion protein



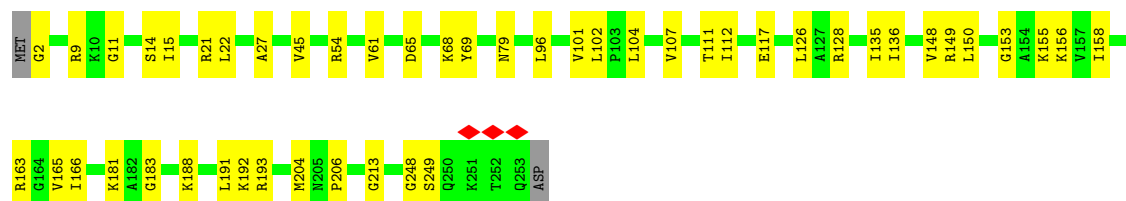
- Molecule 39: Small ribosomal subunit protein RACK1

Chain Sg: 



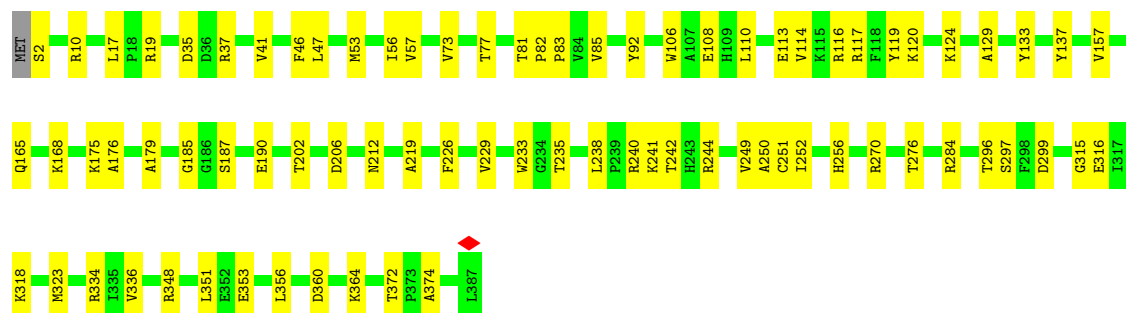
- Molecule 40: Large ribosomal subunit protein uL2A

Chain LA: 



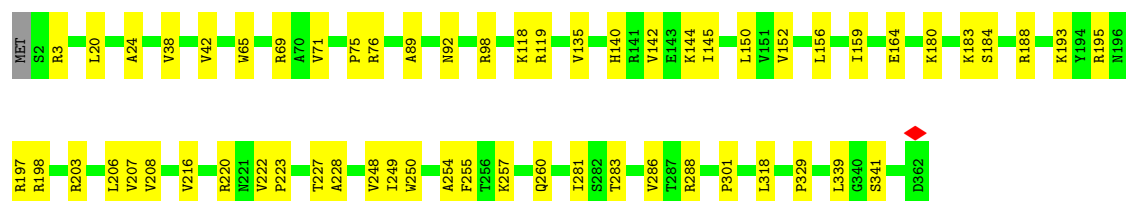
- Molecule 41: Large ribosomal subunit protein uL3

Chain LB: 

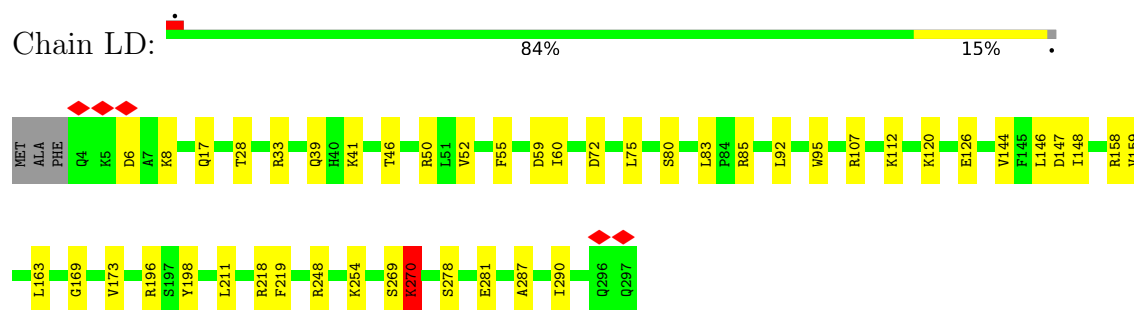


- Molecule 42: Large ribosomal subunit protein uL4A

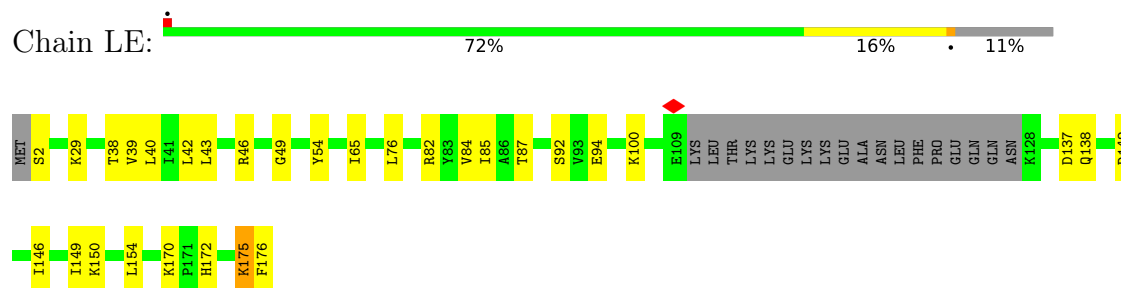
Chain LC: 



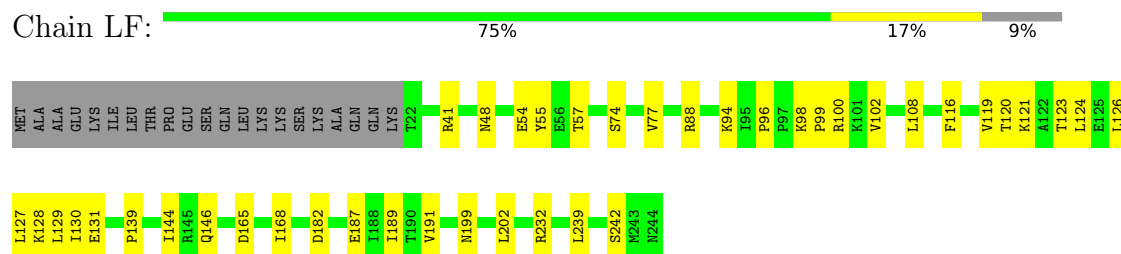
- Molecule 43: Large ribosomal subunit protein uL18



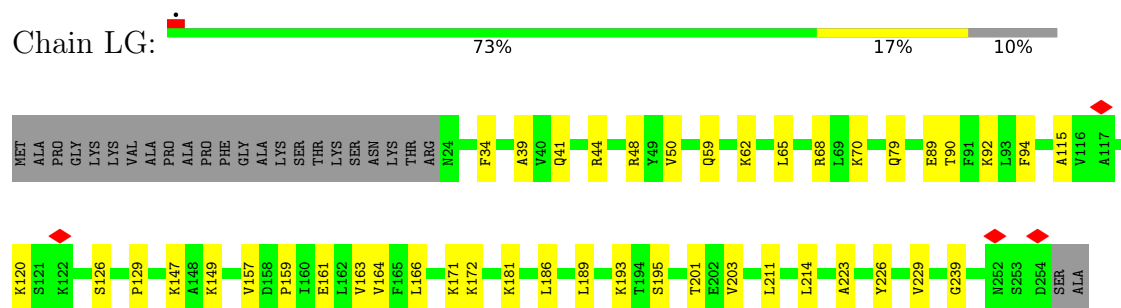
- Molecule 44: Large ribosomal subunit protein eL6A



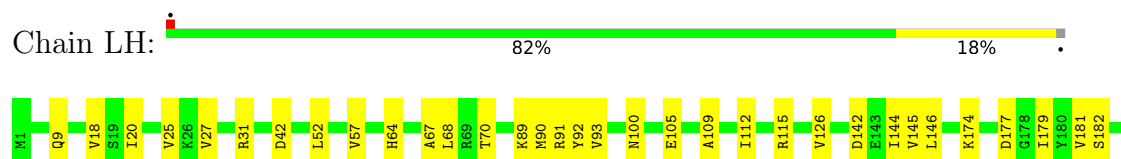
- Molecule 45: Large ribosomal subunit protein uL30A



- Molecule 46: Large ribosomal subunit protein eL8A



- Molecule 47: Large ribosomal subunit protein uL6A





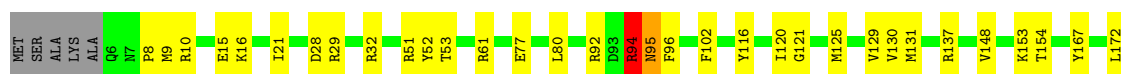
- Molecule 48: Large ribosomal subunit protein uL16

Chain LI: 75% 19% 5%



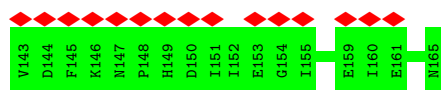
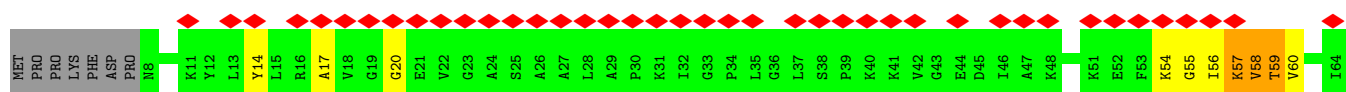
- Molecule 49: Large ribosomal subunit protein uL5A

Chain LJ: 77% 19% ..



- Molecule 50: Large ribosomal subunit protein uL11A

Chain LK: 60% 80% 13% ..



- Molecule 51: Large ribosomal subunit protein eL13A

Chain LL: 72% 24% ..



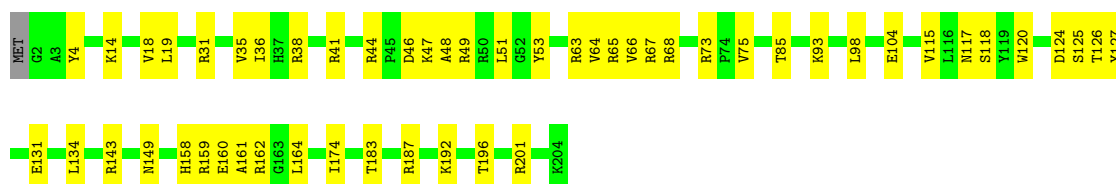
- Molecule 52: Large ribosomal subunit protein eL14A

Chain LM:  88% 11%



- Molecule 53: Large ribosomal subunit protein eL15A

Chain LN:  74% 25%



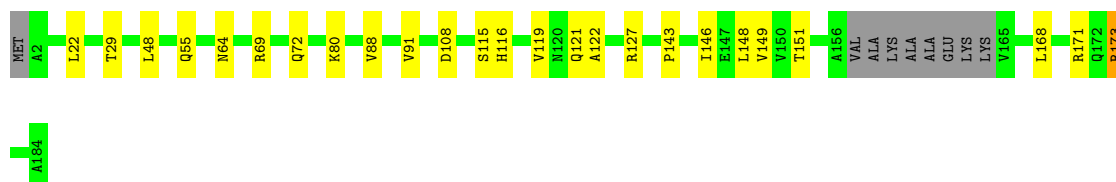
- Molecule 54: Large ribosomal subunit protein uL13A

Chain LO:  84% 15%



- Molecule 55: Large ribosomal subunit protein uL22A

Chain LP:  82% 13% 5%



- Molecule 56: Large ribosomal subunit protein eL18A

Chain LQ:  84% 16%



- Molecule 57: Large ribosomal subunit protein eL19A

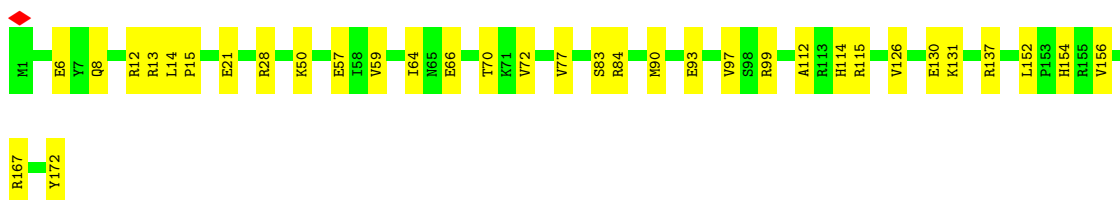
Chain LR:  77% 15% 8%



LYS
ARG
ASP
ALA
LEU
LYS
GLU
ASP
ALA

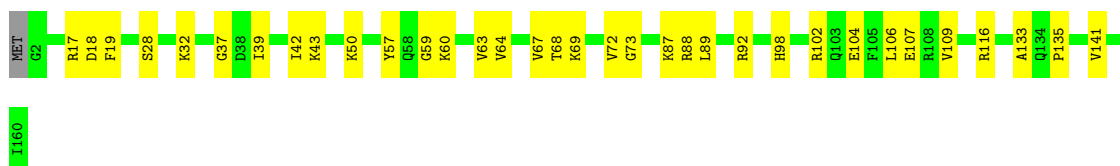
- Molecule 58: Large ribosomal subunit protein eL20A

Chain LS:  80% 20%



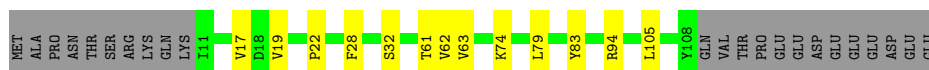
- Molecule 59: Large ribosomal subunit protein eL21A

Chain LT:  78% 21%



- Molecule 60: Large ribosomal subunit protein eL22A

Chain LU:  70% 11% 19%



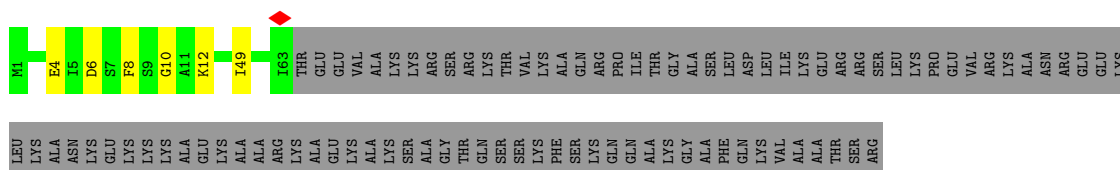
- Molecule 61: Large ribosomal subunit protein uL14A

Chain LV:  76% 22%

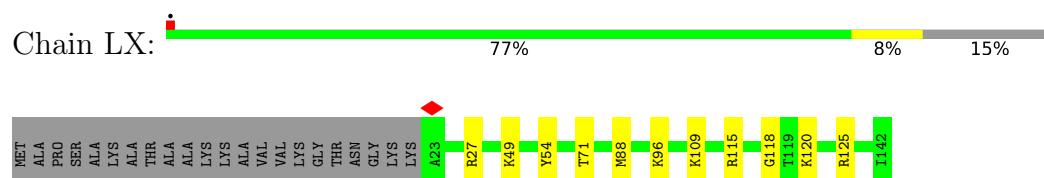


- Molecule 62: Large ribosomal subunit protein eL24A

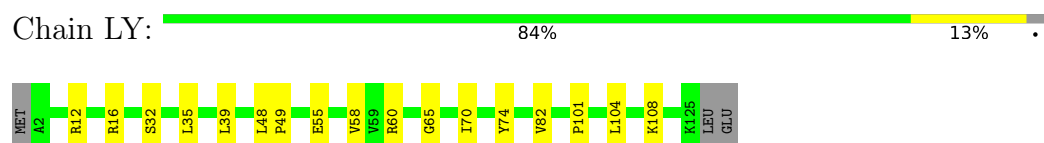
Chain LW:  37% 59%



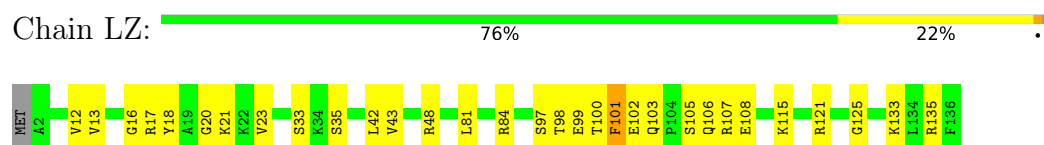
- Molecule 63: Large ribosomal subunit protein uL23



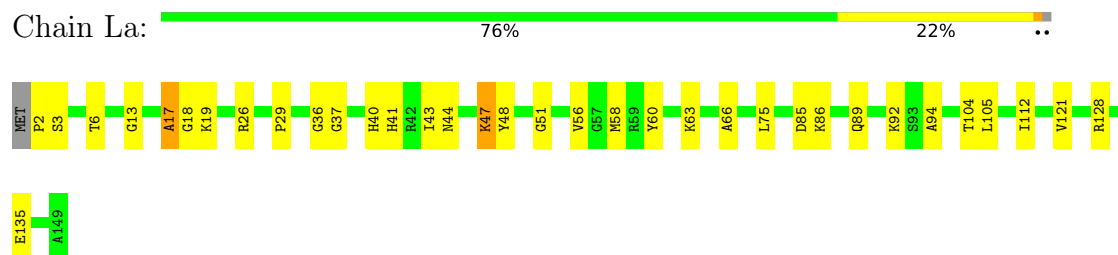
- Molecule 64: Large ribosomal subunit protein uL24A



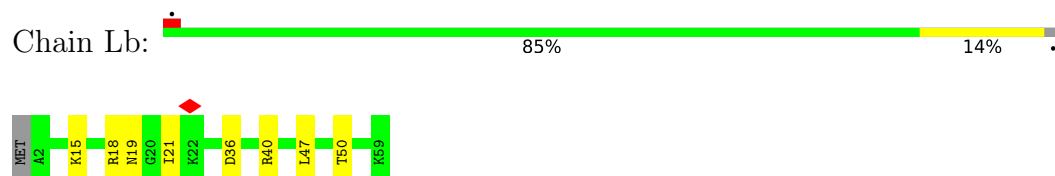
- Molecule 65: Large ribosomal subunit protein eL27A



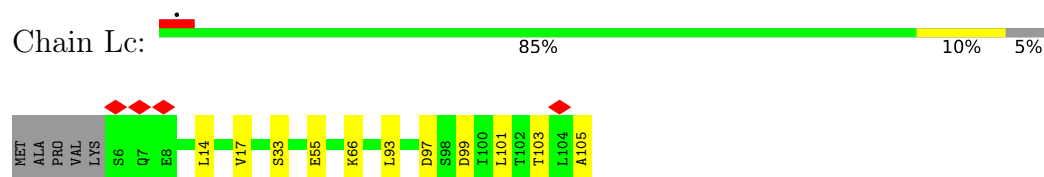
- Molecule 66: Large ribosomal subunit protein uL15



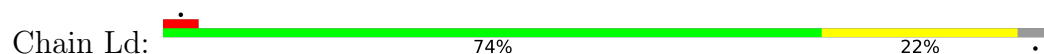
- Molecule 67: Large ribosomal subunit protein eL29



- Molecule 68: Large ribosomal subunit protein eL30

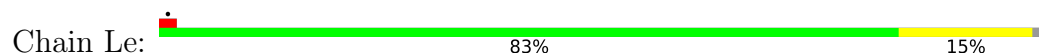


- Molecule 69: Large ribosomal subunit protein eL31A





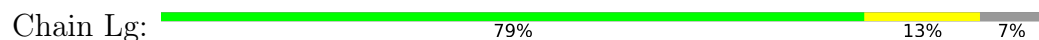
- Molecule 70: Large ribosomal subunit protein eL32



- Molecule 71: Large ribosomal subunit protein eL33A



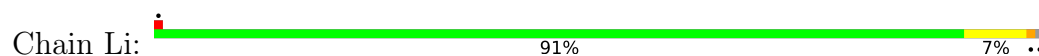
- Molecule 72: Large ribosomal subunit protein eL34A



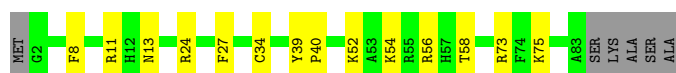
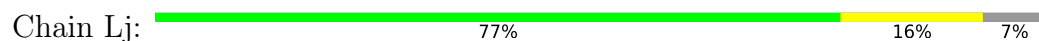
- Molecule 73: Large ribosomal subunit protein uL29A



- Molecule 74: Large ribosomal subunit protein eL36A



- Molecule 75: Large ribosomal subunit protein eL37A



- Molecule 76: Large ribosomal subunit protein eL38

Chain Lk:  76% 22% ..



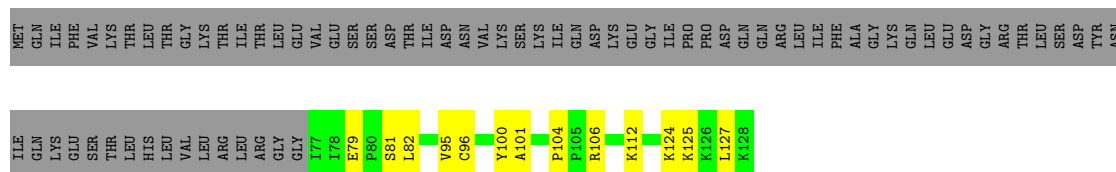
- Molecule 77: Large ribosomal subunit protein eL39

Chain Ll:  84% 14% .

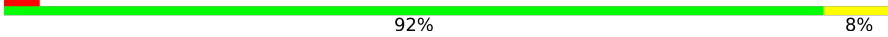


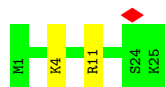
- Molecule 78: Ubiquitin-ribosomal protein eL40A fusion protein

Chain Lm:  30% 10% 59%

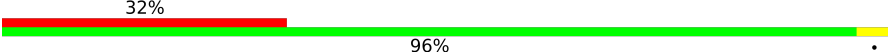


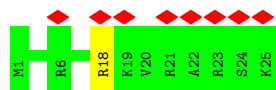
- Molecule 79: Large ribosomal subunit protein eL41A

Chain Ln:  92% 8%



- Molecule 79: Large ribosomal subunit protein eL41A

Chain L2:  32% 96%



- Molecule 80: Large ribosomal subunit protein eL42A

Chain Lo:  79% 20%



- Molecule 81: Large ribosomal subunit protein eL43A

Chain Lp:  79% 20%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	140917	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.362	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	406.56, 406.56, 406.56	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.847, 0.847, 0.847	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: T1C, 5MC, SPD, ZN, 2MG, T6A, 1MG, M2G, 1MA, H2U, MG, 7MG

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	C2	0.24	0/42211	0.42	1/65773 (0.0%)
2	C7	0.20	0/72	0.22	0/110
3	C5	0.22	0/1577	0.33	0/2457
4	C1	0.27	0/76717	0.40	19/119611 (0.0%)
5	C4	0.19	0/2883	0.29	0/4491
6	C3	0.25	0/3746	0.34	0/5832
7	SA	0.31	0/1623	0.74	3/2222 (0.1%)
8	SB	0.25	0/1748	0.60	0/2352
9	SC	0.29	0/1665	0.63	0/2263
10	SD	0.31	0/1759	0.70	2/2368 (0.1%)
11	SE	0.32	0/2109	0.69	3/2839 (0.1%)
12	SF	0.28	0/1629	0.66	0/2202
13	SG	0.21	0/1779	0.50	0/2379
14	SH	0.42	0/1511	0.86	0/2036
15	SI	0.39	0/1514	0.70	3/2021 (0.1%)
16	SJ	0.39	0/1519	0.75	2/2035 (0.1%)
17	SK	0.36	0/757	0.80	0/1022
18	SL	0.28	0/1194	0.55	0/1610
19	SM	0.33	0/898	0.95	2/1220 (0.2%)
20	SN	0.29	0/1215	0.62	0/1638
21	SO	0.24	0/960	0.51	0/1290
22	SP	0.48	1/959 (0.1%)	0.86	2/1288 (0.2%)
23	SQ	0.54	0/1125	0.99	7/1510 (0.5%)
24	SR	0.34	0/904	0.71	1/1210 (0.1%)
25	SS	0.27	0/1211	0.73	2/1628 (0.1%)
26	ST	0.29	0/1130	0.61	0/1517
27	SU	0.27	0/815	0.63	0/1102
28	SV	0.24	0/693	0.64	0/935
29	SW	0.31	0/1038	0.61	0/1395
30	SX	0.24	0/1139	0.59	0/1518
31	SY	0.24	0/1087	0.76	3/1449 (0.2%)
32	SZ	0.37	0/566	0.80	0/761

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sa	0.25	0/782	0.62	0/1047
34	Sb	0.20	0/620	0.66	0/838
35	Sc	0.24	0/499	0.66	1/670 (0.1%)
36	Sd	0.39	0/452	0.65	0/600
37	Se	0.21	0/483	0.63	0/643
38	Sf	0.59	0/253	0.96	0/340
39	Sg	0.31	0/2456	0.75	0/3343
40	LA	0.29	0/1946	0.64	2/2614 (0.1%)
41	LB	0.25	0/3146	0.50	0/4228
42	LC	0.29	0/2800	0.59	0/3790
43	LD	0.25	0/2408	0.55	2/3248 (0.1%)
44	LE	0.28	0/1269	0.63	1/1705 (0.1%)
45	LF	0.27	0/1828	0.57	0/2461
46	LG	0.28	0/1795	0.62	0/2429
47	LH	0.24	0/1531	0.56	0/2062
48	LI	0.27	0/1732	0.63	2/2323 (0.1%)
49	LJ	0.40	0/1374	0.83	0/1842
50	LK	0.85	5/777 (0.6%)	1.20	8/1077 (0.7%)
51	LL	0.30	0/1573	0.68	3/2113 (0.1%)
52	LM	0.24	0/1074	0.46	0/1446
53	LN	0.29	0/1757	0.52	0/2354
54	LO	0.30	0/1585	0.58	0/2128
55	LP	0.31	0/1400	0.56	2/1882 (0.1%)
56	LQ	0.27	0/1465	0.53	0/1965
57	LR	0.27	0/1382	0.57	1/1849 (0.1%)
58	LS	0.26	0/1481	0.52	0/1990
59	LT	0.31	0/1300	0.60	0/1743
60	LU	0.21	0/794	0.47	0/1076
61	LV	0.27	0/1008	0.56	1/1356 (0.1%)
62	LW	0.22	0/533	0.52	0/707
63	LX	0.28	0/974	0.67	0/1314
64	LY	0.23	0/987	0.50	0/1318
65	LZ	0.31	0/1118	0.71	1/1497 (0.1%)
66	La	0.29	0/1204	0.68	2/1612 (0.1%)
67	Lb	0.25	0/473	0.67	0/629
68	Lc	0.22	0/775	0.48	0/1040
69	Ld	0.33	0/897	0.53	0/1205
70	Le	0.25	0/1041	0.60	1/1394 (0.1%)
71	Lf	0.26	0/868	0.53	0/1168
72	Lg	0.44	0/890	0.76	0/1189
73	Lh	0.20	0/974	0.42	0/1297
74	Li	0.25	0/777	0.61	2/1033 (0.2%)
75	Lj	0.31	0/665	0.57	0/882

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Lk	0.25	0/614	0.65	0/822
77	Ll	0.29	0/443	0.59	0/588
78	Lm	0.24	0/423	0.53	0/562
79	L2	0.21	0/234	0.44	0/300
79	Ln	0.24	0/234	0.51	0/300
80	Lo	0.23	0/860	0.55	0/1136
81	Lp	0.29	0/701	0.66	0/934
82	L1	0.31	0/1009	0.83	1/1405 (0.1%)
83	P0	0.54	0/997	1.14	7/1384 (0.5%)
84	CN	0.31	0/950	0.75	5/1260 (0.4%)
All	All	0.28	6/219364 (0.0%)	0.52	92/322222 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	SF	0	1
14	SH	0	1
16	SJ	0	1
19	SM	0	2
21	SO	0	1
23	SQ	0	1
25	SS	0	1
27	SU	0	1
31	SY	0	1
37	Se	0	1
42	LC	0	1
43	LD	0	1
46	LG	0	1
49	LJ	0	1
50	LK	0	5
51	LL	0	2
65	LZ	0	1
66	La	0	2
67	Lb	0	1
74	Li	0	1
81	Lp	0	1
82	L1	0	1
83	P0	0	3
All	All	0	32

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	LK	58	VAL	C-N	9.76	1.48	1.33
50	LK	58	VAL	CA-C	8.17	1.63	1.52
50	LK	59	THR	N-CA	6.87	1.54	1.46
22	SP	52	LYS	C-N	5.67	1.38	1.33
50	LK	57	LYS	C-N	5.63	1.41	1.33
50	LK	58	VAL	N-CA	5.42	1.53	1.46

All (92) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	322	G	C2'-C3'-O3'	9.77	124.16	109.50
4	C1	1307	G	C2'-C3'-O3'	9.48	123.72	109.50
83	P0	41	VAL	CA-C-N	-9.31	108.08	122.60
83	P0	41	VAL	C-N-CA	-9.31	108.08	122.60
66	La	47	LYS	CA-C-N	8.41	137.61	121.54
66	La	47	LYS	C-N-CA	8.41	137.61	121.54
4	C1	1232	C	OP2-P-O3'	-8.31	83.07	108.00
84	CN	34	THR	CA-C-N	7.72	140.63	121.80
84	CN	34	THR	C-N-CA	7.72	140.63	121.80
83	P0	53	MET	N-CA-CB	-7.71	98.98	110.86
4	C1	1239	C	N1-C1'-C2'	7.69	123.54	112.00
31	SY	48	TYR	CA-C-N	7.68	136.21	121.54
31	SY	48	TYR	C-N-CA	7.68	136.21	121.54
4	C1	1240	A	O3'-P-O5'	7.20	114.79	104.00
51	LL	140	SER	CA-C-N	7.17	135.24	121.54
51	LL	140	SER	C-N-CA	7.17	135.24	121.54
22	SP	35	LYS	N-CA-C	-7.03	104.98	113.97
4	C1	1238	C	N1-C1'-C2'	6.85	122.27	112.00
23	SQ	41	PRO	N-CA-C	-6.76	105.20	114.80
50	LK	78	SER	CA-C-N	-6.76	111.38	122.54
50	LK	78	SER	C-N-CA	-6.76	111.38	122.54
48	LI	159	PHE	CA-C-N	6.61	126.57	120.03
48	LI	159	PHE	C-N-CA	6.61	126.57	120.03
4	C1	1241	U	O5'-P-OP1	-6.56	88.32	108.00
4	C1	2505	U	C2'-C3'-O3'	6.55	123.53	113.70
25	SS	91	ASP	CA-C-N	6.50	128.88	120.56
25	SS	91	ASP	C-N-CA	6.50	128.88	120.56
19	SM	102	GLY	N-CA-C	6.49	119.98	110.38
10	SD	150	MET	CA-C-N	-6.46	114.01	123.05
10	SD	150	MET	C-N-CA	-6.46	114.01	123.05
4	C1	1242	G	P-O3'-C3'	6.29	129.63	120.20
23	SQ	53	LEU	N-CA-CB	-6.23	99.97	110.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	LP	173	ARG	CB-CG-CD	6.18	125.52	111.30
44	LE	175	LYS	CD-CE-NZ	-6.14	92.24	111.90
35	Sc	13	ILE	N-CA-C	-6.07	106.82	111.62
50	LK	59	THR	N-CA-C	6.04	119.32	109.24
23	SQ	35	PRO	CB-CA-C	-5.92	103.49	111.12
83	P0	53	MET	CB-CA-C	5.91	118.76	111.43
70	Le	86	THR	N-CA-C	5.91	119.31	111.75
4	C1	1232	C	OP1-P-OP2	-5.90	101.90	119.60
83	P0	59	VAL	N-CA-CB	5.88	116.80	110.62
4	C1	2505	U	C3'-C2'-O2'	5.87	119.51	110.70
51	LL	48	PRO	N-CA-C	5.86	124.53	112.47
57	LR	157	GLU	N-CA-CB	5.76	119.79	110.40
23	SQ	114	ARG	CA-C-N	5.72	132.47	121.54
23	SQ	114	ARG	C-N-CA	5.72	132.47	121.54
82	L1	183	ILE	N-CA-C	-5.71	107.42	112.90
4	C1	1243	G	P-O5'-C5'	5.71	129.46	120.90
4	C1	1233	G	O5'-C5'-C4'	5.68	120.02	111.50
4	C1	1259	A	C1'-C2'-O2'	-5.64	103.34	111.80
40	LA	149	ARG	CA-C-N	5.64	137.32	120.69
40	LA	149	ARG	C-N-CA	5.64	137.32	120.69
74	Li	64	SER	CA-C-N	-5.54	110.54	121.41
74	Li	64	SER	C-N-CA	-5.54	110.54	121.41
22	SP	58	LYS	N-CA-CB	5.53	118.34	110.16
55	LP	173	ARG	CA-CB-CG	5.45	125.00	114.10
4	C1	1229	G	C4'-C3'-C2'	-5.43	97.17	102.60
15	SI	157	GLU	CA-CB-CG	5.43	124.96	114.10
7	SA	15	GLN	N-CA-CB	5.42	119.39	110.39
11	SE	250	GLU	CA-C-N	-5.39	112.11	120.31
11	SE	250	GLU	C-N-CA	-5.39	112.11	120.31
7	SA	161	PRO	CA-C-N	-5.39	116.03	122.44
7	SA	161	PRO	C-N-CA	-5.39	116.03	122.44
50	LK	139	VAL	N-CA-C	-5.38	105.08	110.30
15	SI	157	GLU	N-CA-CB	5.38	118.12	110.16
84	CN	72	VAL	CA-C-N	5.37	131.79	121.54
84	CN	72	VAL	C-N-CA	5.37	131.79	121.54
4	C1	1233	G	O5'-P-OP2	5.33	123.98	108.00
65	LZ	103	GLN	CA-CB-CG	5.32	124.74	114.10
19	SM	138	GLU	N-CA-CB	5.31	118.51	110.28
24	SR	77	GLU	N-CA-CB	5.28	118.42	110.30
43	LD	270	LYS	CG-CD-CE	-5.28	99.17	111.30
61	LV	106	LYS	CB-CG-CD	5.26	123.40	111.30
4	C1	1263	A	C5'-C4'-C3'	-5.25	107.32	115.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	SE	259	GLN	N-CA-CB	5.24	117.86	110.36
4	C1	1242	G	C4-N9-C1'	5.23	142.19	126.50
43	LD	198	TYR	CA-CB-CG	5.22	123.29	113.90
23	SQ	87	LYS	CA-C-N	-5.19	114.22	120.03
23	SQ	87	LYS	C-N-CA	-5.19	114.22	120.03
4	C1	2541	U	P-O3'-C3'	5.18	127.97	120.20
83	P0	84	VAL	CA-C-N	-5.17	116.98	122.67
83	P0	84	VAL	C-N-CA	-5.17	116.98	122.67
16	SJ	84	GLY	CA-C-N	-5.16	112.29	120.55
16	SJ	84	GLY	C-N-CA	-5.16	112.29	120.55
84	CN	14	LEU	CD1-CG-CD2	-5.15	99.46	110.80
31	SY	42	GLU	N-CA-CB	5.15	117.48	110.01
4	C1	282	G	C2'-C3'-O3'	5.14	121.40	113.70
50	LK	79	SER	CA-C-N	-5.10	112.93	120.28
50	LK	79	SER	C-N-CA	-5.10	112.93	120.28
15	SI	140	GLU	CB-CG-CD	5.03	121.15	112.60
50	LK	57	LYS	CA-C-N	5.03	131.01	121.97
50	LK	57	LYS	C-N-CA	5.03	131.01	121.97

There are no chirality outliers.

All (32) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
82	L1	16	LEU	Peptide
42	LC	144	LYS	Peptide
43	LD	270	LYS	Peptide
46	LG	79	GLN	Peptide
49	LJ	94	ARG	Peptide
50	LK	55	GLY	Peptide
50	LK	56	ILE	Peptide
50	LK	74	VAL	Peptide
50	LK	76	SER	Peptide
50	LK	83	THR	Peptide
51	LL	47	ALA	Peptide
51	LL	49	ARG	Peptide
65	LZ	101	PHE	Peptide
66	La	17	ALA	Peptide
66	La	66	ALA	Peptide
67	Lb	21	ILE	Peptide
74	Li	64	SER	Peptide
81	Lp	51	ALA	Peptide
83	P0	42	ARG	Peptide

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Mol	Chain	Res	Type	Group
83	P0	52	LEU	Peptide
83	P0	55	LYS	Peptide
12	SF	155	ALA	Peptide
14	SH	64	VAL	Peptide
16	SJ	105	LEU	Mainchain
19	SM	119	SER	Peptide
19	SM	130	THR	Peptide
21	SO	36	LYS	Peptide
23	SQ	113	ASP	Peptide
25	SS	60	GLU	Peptide
27	SU	51	VAL	Peptide
31	SY	51	GLU	Peptide
37	Se	44	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C2	37739	0	18986	296	0
2	C7	65	0	33	0	0
3	C5	1624	0	841	9	0
4	C1	68535	0	34437	471	0
5	C4	2579	0	1304	27	0
6	C3	3353	0	1695	24	0
7	SA	1583	0	1578	29	0
8	SB	1722	0	1793	29	0
9	SC	1635	0	1723	26	0
10	SD	1734	0	1817	27	0
11	SE	2068	0	2154	51	0
12	SF	1609	0	1675	39	0
13	SG	1755	0	1846	49	0
14	SH	1486	0	1576	34	0
15	SI	1489	0	1525	29	0
16	SJ	1494	0	1573	31	0
17	SK	741	0	691	19	0
18	SL	1168	0	1233	21	0
19	SM	890	0	887	28	0
20	SN	1192	0	1255	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	SO	949	0	985	22	0
22	SP	939	0	968	24	0
23	SQ	1105	0	1166	28	0
24	SR	896	0	902	23	0
25	SS	1192	0	1222	24	0
26	ST	1112	0	1124	21	0
27	SU	805	0	874	14	0
28	SV	684	0	672	17	0
29	SW	1021	0	1060	13	0
30	SX	1121	0	1196	15	0
31	SY	1073	0	1132	24	0
32	SZ	558	0	598	11	0
33	Sa	769	0	815	24	0
34	Sb	610	0	631	9	0
35	Sc	497	0	535	11	0
36	Sd	442	0	428	8	0
37	Se	475	0	525	6	0
38	Sf	248	0	237	7	0
39	Sg	2403	0	2350	60	0
40	LA	1912	0	1976	42	0
41	LB	3075	0	3142	55	0
42	LC	2748	0	2859	42	0
43	LD	2359	0	2311	33	0
44	LE	1248	0	1339	20	0
45	LF	1791	0	1869	31	0
46	LG	1763	0	1819	30	0
47	LH	1510	0	1576	20	0
48	LI	1696	0	1731	26	0
49	LJ	1353	0	1383	26	0
50	LK	778	0	368	24	0
51	LL	1548	0	1613	37	0
52	LM	1059	0	1154	12	0
53	LN	1720	0	1779	37	0
54	LO	1555	0	1659	21	0
55	LP	1378	0	1404	18	0
56	LQ	1441	0	1543	24	0
57	LR	1365	0	1414	24	0
58	LS	1445	0	1487	23	0
59	LT	1276	0	1323	29	0
60	LU	778	0	791	8	0
61	LV	993	0	1040	21	0
62	LW	521	0	551	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	LX	959	0	1023	9	0
64	LY	976	0	1064	12	0
65	LZ	1092	0	1155	23	0
66	La	1173	0	1215	24	0
67	Lb	462	0	491	6	0
68	Lc	767	0	816	7	0
69	Ld	883	0	918	21	0
70	Le	1020	0	1090	12	0
71	Lf	850	0	880	17	0
72	Lg	880	0	942	12	0
73	Lh	965	0	1067	8	0
74	Li	770	0	846	6	0
75	Lj	650	0	650	13	0
76	Lk	608	0	671	15	0
77	Ll	436	0	475	6	0
78	Lm	417	0	455	11	0
79	L2	233	0	284	1	0
79	Ln	233	0	284	3	0
80	Lo	847	0	914	13	0
81	Lp	694	0	734	15	0
82	L1	1010	0	435	1	0
83	P0	998	0	458	18	0
84	CN	940	0	973	16	0
85	C1	222	0	0	0	0
85	C2	89	0	0	0	0
85	C3	1	0	0	0	0
85	C4	1	0	0	0	0
85	C5	3	0	0	0	0
86	C1	210	0	190	7	0
86	C2	42	0	38	0	0
87	C1	10	0	19	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sb	1	0	0	0	0
88	Sd	1	0	0	0	0
88	Sf	1	0	0	0	0
All	All	205122	0	150260	2023	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 (2023) 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)
39:Sg:218:GLY:O	39:Sg:235:SER:HA	1.36	1.25
62:LW:4:GLU:O	62:LW:12:LYS:HA	1.52	1.09
65:LZ:121:ARG:O	65:LZ:125:GLY:HA2	1.55	1.06
81:Lp:53:GLY:HA2	81:Lp:66:GLY:O	1.56	1.05
39:Sg:220:ILE:O	39:Sg:233:THR:HA	1.57	1.04
4:C1:2465:G:H1	4:C1:2491:A:H62	1.12	0.97
4:C1:2465:G:H1	4:C1:2491:A:N6	1.64	0.95
23:SQ:109:PHE:O	23:SQ:113:ASP:HB3	1.71	0.91
4:C1:1239:C:H3'	50:LK:78:SER:HA	1.49	0.90
39:Sg:218:GLY:O	39:Sg:235:SER:CA	2.19	0.90
4:C1:2457:G:N2	4:C1:2486:A:C2	2.39	0.90
48:LI:95:HIS:O	48:LI:125:LEU:HA	1.72	0.89
50:LK:14:TYR:HA	50:LK:60:VAL:O	1.73	0.88
14:SH:70:PHE:O	14:SH:74:GLN:HB2	1.74	0.86
4:C1:1259:A:H2'	83:P0:54:GLY:HA3	1.57	0.83
4:C1:1347:U:H3	4:C1:1357:G:H1	1.25	0.83
1:C2:743:U:H4'	14:SH:107:ARG:HH21	1.44	0.82
1:C2:1588:G:H1	1:C2:1608:U:H3	1.26	0.81
12:SF:37:GLN:HB3	23:SQ:53:LEU:HD21	1.63	0.80
65:LZ:121:ARG:O	65:LZ:125:GLY:CA	2.31	0.78
4:C1:2940:A:N7	41:LB:2:SER:N	2.33	0.77
37:Se:55:ARG:HE	37:Se:56:MET:H	1.33	0.76
49:LJ:8:PRO:HD2	49:LJ:10:ARG:HG2	1.68	0.76
4:C1:1242:G:N7	50:LK:57:LYS:HA	2.01	0.75
1:C2:1086:A:H5'	9:SC:164:SER:HB3	1.67	0.75
11:SE:88:ASP:O	11:SE:100:ARG:HA	1.87	0.75
4:C1:1243:G:O5'	50:LK:59:THR:N	2.20	0.73
4:C1:824:C:H5''	40:LA:21:ARG:HG3	1.70	0.73
1:C2:1775:U:O4	79:Ln:4:LYS:NZ	2.22	0.73
14:SH:150:GLN:HB3	14:SH:181:ILE:HG22	1.71	0.73
4:C1:1566:A:N1	4:C1:1571:A:N6	2.37	0.73
11:SE:100:ARG:HB3	11:SE:112:HIS:HB3	1.71	0.72
54:LO:143:THR:HG21	54:LO:150:GLU:HB2	1.70	0.72
33:Sa:23:CYS:O	33:Sa:27:SER:HA	1.89	0.72
39:Sg:89:LEU:HB2	39:Sg:103:PHE:HB2	1.70	0.72
4:C1:1233:G:H2'	4:C1:1234:G:C8	2.26	0.71
21:SO:80:HIS:HA	21:SO:113:GLY:O	1.91	0.71
39:Sg:260:ILE:HB	39:Sg:274:LEU:HB3	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:SB:61:LEU:HD12	8:SB:96:LEU:HD13	1.72	0.71
12:SF:69:PHE:HZ	23:SQ:53:LEU:HD22	1.55	0.71
4:C1:1639:C:OP2	72:Lg:74:ARG:NH2	2.24	0.70
4:C1:1940:G:H21	4:C1:3362:A:H8	1.39	0.70
1:C2:905:A:H5'	12:SF:156:ARG:HH22	1.57	0.70
4:C1:1245:A:H3'	4:C1:1246:G:H8	1.55	0.70
10:SD:137:VAL:HB	10:SD:185:LYS:HB2	1.74	0.70
19:SM:93:ASP:O	19:SM:97:LEU:HB2	1.91	0.70
72:Lg:20:ILE:HD11	72:Lg:32:ALA:HB1	1.73	0.70
4:C1:829:U:H3	4:C1:895:A:H62	1.40	0.69
4:C1:2231:C:OP1	86:C1:3402:T1C:C42	2.40	0.69
5:C4:76:A:N3	58:LS:50:LYS:NZ	2.39	0.69
4:C1:2794:G:OP1	80:Lo:61:LYS:NZ	2.26	0.69
4:C1:2967:A:H5''	40:LA:213:GLY:HA3	1.74	0.69
10:SD:99:VAL:HG23	10:SD:173:ARG:HH22	1.58	0.69
4:C1:1236:G:N2	4:C1:1272:C:OP1	2.26	0.69
13:SG:33:GLY:N	13:SG:52:ILE:O	2.26	0.68
1:C2:1585:U:H3	1:C2:1611:A:H2	1.40	0.68
4:C1:2193:U:H5'	4:C1:2194:G:H5'	1.75	0.68
1:C2:1610:G:OP1	12:SF:72:HIS:NE2	2.26	0.68
4:C1:1240:A:H61	4:C1:1244:A:H2'	1.56	0.68
6:C3:40:A:N7	6:C3:105:A:N6	2.41	0.67
9:SC:237:VAL:HG13	9:SC:242:ILE:HD11	1.76	0.67
4:C1:1233:G:H5'	83:P0:42:ARG:H	1.59	0.67
51:LL:90:ALA:O	51:LL:93:ILE:O	2.13	0.67
6:C3:63:G:O2'	73:Lh:49:LYS:NZ	2.28	0.67
19:SM:62:LEU:HD23	19:SM:63:VAL:HG12	1.76	0.67
17:SK:73:VAL:O	17:SK:77:ARG:HB2	1.94	0.66
38:Sf:121:CYS:HB3	38:Sf:130:VAL:HG21	1.76	0.66
1:C2:1339:C:O2'	1:C2:1341:A:N7	2.27	0.66
5:C4:76:A:N6	5:C4:103:A:N7	2.42	0.66
1:C2:1331:A:OP1	24:SR:45:ARG:NH2	2.28	0.66
4:C1:361:A:OP1	75:Lj:24:ARG:NH1	2.28	0.66
4:C1:939:U:OP2	66:La:26:ARG:NH2	2.28	0.66
15:SI:99:ALA:N	15:SI:169:ILE:O	2.29	0.66
32:SZ:60:VAL:HB	32:SZ:101:TYR:HB2	1.77	0.66
5:C4:32:U:H5'	43:LD:218:ARG:HH22	1.60	0.66
54:LO:27:LEU:HD21	54:LO:102:LEU:HB2	1.76	0.66
54:LO:65:ASN:HB3	54:LO:68:ARG:HG2	1.78	0.66
4:C1:952:A:OP1	67:Lb:18:ARG:NH2	2.28	0.66
4:C1:2931:C:O2'	61:LV:42:SER:OG	2.13	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:LN:51:LEU:O	53:LN:117:ASN:ND2	2.29	0.66
83:P0:106:ALA:HA	83:P0:182:THR:HA	1.77	0.66
4:C1:1238:C:H2'	50:LK:77:ALA:HB1	1.77	0.66
8:SB:229:MET:O	8:SB:232:HIS:C	2.39	0.66
10:SD:40:ARG:HH12	27:SU:108:ILE:HG13	1.61	0.66
21:SO:20:TYR:HB3	21:SO:27:PHE:HB2	1.76	0.66
39:Sg:220:ILE:H	39:Sg:234:LEU:H	1.43	0.65
67:Lb:15:LYS:HG2	67:Lb:18:ARG:HH21	1.60	0.65
69:Ld:75:ILE:HG12	69:Ld:93:VAL:HG13	1.77	0.65
24:SR:79:GLU:O	24:SR:83:GLN:NE2	2.29	0.65
1:C2:521:A:N3	31:SY:34:ASN:ND2	2.44	0.65
1:C2:246:G:N2	18:SL:38:ALA:O	2.29	0.65
69:Ld:75:ILE:HG23	69:Ld:93:VAL:HG22	1.78	0.65
8:SB:140:ILE:HB	8:SB:213:ARG:HD2	1.77	0.65
9:SC:113:LEU:HD11	9:SC:211:LEU:HB3	1.79	0.65
51:LL:42:ARG:O	51:LL:46:ILE:HB	1.97	0.65
11:SE:153:ASN:O	11:SE:174:LYS:NZ	2.30	0.65
16:SJ:27:GLU:HG2	16:SJ:42:ILE:HG21	1.79	0.65
39:Sg:180:ALA:HB3	39:Sg:190:ALA:HB3	1.76	0.65
11:SE:173:ILE:HG12	11:SE:229:GLY:HA2	1.78	0.65
30:SX:70:LYS:HB3	30:SX:93:LEU:HD22	1.78	0.65
56:LQ:62:VAL:HG23	56:LQ:66:ARG:HD2	1.79	0.65
1:C2:1251:U:H2'	1:C2:1252:C:C6	2.32	0.65
4:C1:1565:G:N2	4:C1:1575:A:N7	2.45	0.65
4:C1:2786:G:N2	66:La:58:MET:SD	2.69	0.65
16:SJ:163:PRO:HB3	16:SJ:169:PRO:HA	1.77	0.64
4:C1:2231:C:OP1	86:C1:3402:T1C:H421	1.96	0.64
14:SH:113:PRO:HG2	14:SH:116:ARG:HD2	1.79	0.64
15:SI:195:ARG:NH2	18:SL:10:GLU:O	2.31	0.64
16:SJ:109:LEU:HD23	16:SJ:144:PRO:HA	1.80	0.64
19:SM:96:GLN:HA	19:SM:99:GLU:HG3	1.79	0.64
39:Sg:178:VAL:HB	39:Sg:192:PHE:HB2	1.80	0.64
45:LF:187:GLU:O	45:LF:191:VAL:HA	1.98	0.64
50:LK:20:GLY:HA3	50:LK:54:LYS:HA	1.79	0.64
1:C2:992:A:O2'	1:C2:1785:U:O2	2.14	0.64
4:C1:1237:G:O5'	50:LK:121:PHE:N	2.25	0.64
39:Sg:239:GLU:HB3	39:Sg:257:ALA:HB2	1.79	0.64
42:LC:180:LYS:O	42:LC:184:SER:HB3	1.98	0.64
4:C1:515:C:O2'	42:LC:341:SER:O	2.15	0.64
4:C1:2728:G:N7	59:LT:87:LYS:NZ	2.45	0.64
83:P0:112:GLY:N	83:P0:165:VAL:O	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:895:G:H1	1:C2:917:U:H3	1.46	0.64
1:C2:895:G:H21	21:SO:38:THR:HG21	1.62	0.64
4:C1:351:A:N6	77:Ll:37:TYR:O	2.31	0.64
24:SR:37:GLU:OE2	39:Sg:150:TRP:NE1	2.31	0.64
25:SS:67:GLU:HA	25:SS:70:VAL:HG12	1.79	0.64
57:LR:105:LEU:HD23	57:LR:138:LEU:HD23	1.79	0.64
4:C1:1412:G:OP1	70:Le:105:ARG:NH2	2.31	0.64
81:Lp:52:ALA:HB1	81:Lp:68:ALA:HA	1.80	0.64
4:C1:2679:A:O2'	49:LJ:52:TYR:OH	2.14	0.64
49:LJ:53:THR:HG22	49:LJ:61:ARG:H	1.63	0.64
1:C2:1065:A:N3	8:SB:146:GLN:NE2	2.46	0.63
4:C1:3269:U:H3'	44:LE:46:ARG:HH12	1.62	0.63
25:SS:41:ARG:NH2	26:ST:36:ILE:O	2.30	0.63
1:C2:522:U:H5''	31:SY:37:LYS:HG3	1.80	0.63
10:SD:206:VAL:HG22	24:SR:41:ILE:HD13	1.80	0.63
41:LB:235:THR:HG21	41:LB:249:VAL:HG22	1.79	0.63
18:SL:102:LYS:O	30:SX:13:ARG:NH2	2.32	0.63
59:LT:28:SER:OG	59:LT:32:LYS:NZ	2.31	0.63
42:LC:208:VAL:HG12	42:LC:228:ALA:HB3	1.81	0.63
4:C1:2948:C:OP1	41:LB:244:ARG:NH2	2.31	0.63
21:SO:99:GLN:NE2	33:Sa:46:GLU:OE1	2.32	0.62
48:LI:43:VAL:O	48:LI:171:TRP:NE1	2.31	0.62
4:C1:364:G:OP2	75:Lj:52:LYS:NZ	2.29	0.62
46:LG:50:VAL:HG21	63:LX:27:ARG:HD2	1.81	0.62
51:LL:16:LYS:O	51:LL:21:ARG:NH2	2.31	0.62
1:C2:334:G:O6	15:SI:5:ARG:NH2	2.32	0.62
1:C2:474:A:OP2	16:SJ:44:ARG:NH1	2.33	0.62
1:C2:647:G:H22	1:C2:687:G:H1	1.46	0.62
1:C2:699:U:H3	1:C2:739:G:H1	1.46	0.62
4:C1:1824:U:O3'	76:Lk:17:ARG:NH2	2.33	0.62
4:C1:1193:A:OP2	54:LO:49:ARG:NH2	2.32	0.62
4:C1:1521:G:O6	77:Ll:17:LYS:NZ	2.31	0.62
83:P0:26:PHE:O	83:P0:86:PHE:HA	2.00	0.62
4:C1:1481:A:HO2'	4:C1:1858:A:HO2'	1.46	0.62
7:SA:183:ARG:NH2	7:SA:191:ARG:O	2.32	0.62
22:SP:28:MET:HE1	22:SP:33:PHE:N	2.14	0.62
1:C2:898:A:H4'	21:SO:46:MET:HE3	1.80	0.62
4:C1:1385:C:HO2'	44:LE:2:SER:N	1.98	0.62
12:SF:159:ALA:O	35:Sc:61:ARG:NH1	2.32	0.62
41:LB:238:LEU:HB3	41:LB:242:THR:HG21	1.81	0.62
1:C2:738:G:OP2	11:SE:200:ARG:NH1	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:1499:G:OP1	26:ST:122:ARG:NH1	2.33	0.62
53:LN:68:ARG:HB3	53:LN:126:THR:O	2.00	0.62
4:C1:1096:U:OP2	59:LT:116:ARG:NH2	2.33	0.61
9:SC:63:VAL:HG13	9:SC:68:ILE:HD11	1.82	0.61
13:SG:163:THR:HG22	13:SG:168:THR:HG22	1.81	0.61
4:C1:719:U:O2'	56:LQ:72:LYS:NZ	2.33	0.61
5:C4:44:C:OP2	49:LJ:137:ARG:NH2	2.34	0.61
34:Sb:20:LYS:HA	34:Sb:29:ARG:HH21	1.65	0.61
4:C1:1757:A:OP1	60:LU:94:ARG:NH2	2.33	0.61
33:Sa:3:LYS:NZ	33:Sa:8:ASN:OD1	2.33	0.61
71:Lf:26:ASN:HA	71:Lf:88:ASN:HD21	1.64	0.61
4:C1:363:G:OP2	75:Lj:56:ARG:NH2	2.33	0.61
38:Sf:121:CYS:SG	38:Sf:122:SER:N	2.73	0.61
51:LL:174:ARG:HG3	74:Li:9:ILE:HD12	1.82	0.61
4:C1:1251:A:OP1	4:C1:1251:A:C4	2.53	0.61
7:SA:156:VAL:O	28:SV:65:SER:OG	2.18	0.61
50:LK:124:THR:O	50:LK:127:SER:N	2.34	0.61
61:LV:10:LYS:NZ	61:LV:56:ASP:OD1	2.32	0.61
1:C2:1610:G:H4'	12:SF:98:MET:HE1	1.83	0.61
4:C1:103:G:OP1	51:LL:70:ARG:NH1	2.34	0.61
19:SM:78:LEU:O	19:SM:85:LYS:NZ	2.33	0.61
9:SC:158:THR:HG21	9:SC:221:THR:HA	1.82	0.61
10:SD:25:PHE:O	10:SD:29:LEU:HB3	2.01	0.61
31:SY:11:LYS:HB2	31:SY:24:VAL:HG22	1.83	0.61
47:LH:100:ASN:HB3	47:LH:115:ARG:HG3	1.83	0.61
4:C1:1603:A:H61	63:LX:71:THR:HG21	1.66	0.61
25:SS:116:LEU:HA	25:SS:119:ILE:HG12	1.81	0.61
9:SC:178:ILE:HG12	9:SC:196:VAL:HG22	1.83	0.60
47:LH:9:GLN:HB3	47:LH:52:LEU:HD11	1.82	0.60
1:C2:142:G:H22	1:C2:173:A:H2	1.46	0.60
16:SJ:135:ALA:HA	16:SJ:140:ILE:HA	1.82	0.60
1:C2:762:A:OP1	16:SJ:79:ARG:NH2	2.34	0.60
1:C2:1034:C:HO2'	29:SW:2:THR:N	1.98	0.60
1:C2:1102:G:OP2	30:SX:7:ARG:NH1	2.33	0.60
4:C1:992:A:H5''	59:LT:43:LYS:HD2	1.81	0.60
48:LI:174:THR:OG1	48:LI:175:ASN:N	2.31	0.60
1:C2:950:C:O2'	20:SN:104:ARG:NH2	2.31	0.60
1:C2:1482:C:O2'	23:SQ:72:GLY:O	2.19	0.60
1:C2:1594:G:OP2	1:C2:1596:C:N4	2.34	0.60
4:C1:1382:G:OP2	42:LC:188:ARG:NH1	2.34	0.60
39:Sg:224:ASN:O	39:Sg:228:LYS:HA	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:LA:21:ARG:HE	40:LA:22:LEU:HG	1.66	0.60
45:LF:88:ARG:HB2	45:LF:108:LEU:HB3	1.84	0.60
49:LJ:92:ARG:HB3	49:LJ:95:ASN:HB2	1.82	0.60
1:C2:278:U:OP2	1:C2:279:G:N2	2.35	0.60
41:LB:219:ALA:HB2	41:LB:336:VAL:HG23	1.83	0.60
7:SA:84:ARG:NH1	7:SA:203:PHE:O	2.31	0.60
31:SY:10:ARG:O	31:SY:11:LYS:C	2.45	0.60
46:LG:203:VAL:HG21	46:LG:211:LEU:HD22	1.83	0.60
52:LM:60:LEU:HD13	58:LS:152:LEU:HD11	1.83	0.60
1:C2:1565:C:OP1	25:SS:41:ARG:NH1	2.33	0.60
4:C1:1386:A:N7	42:LC:183:LYS:NZ	2.46	0.60
60:LU:22:PRO:HB2	60:LU:28:PHE:HB2	1.83	0.60
69:Ld:55:LEU:HB2	69:Ld:95:PRO:HD3	1.83	0.60
44:LE:40:LEU:HD11	44:LE:54:TYR:HB2	1.84	0.60
46:LG:89:GLU:HA	46:LG:92:LYS:HE2	1.84	0.60
1:C2:786:C:OP1	11:SE:240:LYS:NZ	2.35	0.60
4:C1:745:C:H5'	56:LQ:145:ASN:HB2	1.84	0.60
10:SD:51:ARG:HB3	10:SD:91:VAL:HG22	1.84	0.60
15:SI:136:SER:O	15:SI:139:ALA:N	2.34	0.60
4:C1:1155:C:OP2	45:LF:94:LYS:NZ	2.35	0.59
32:SZ:83:LEU:O	32:SZ:87:GLY:HA2	2.02	0.59
33:Sa:23:CYS:O	33:Sa:27:SER:CA	2.50	0.59
1:C2:78:A:OP1	13:SG:154:ARG:NH2	2.35	0.59
1:C2:1171:A:H2'	1:C2:1172:G:C8	2.38	0.59
19:SM:28:LEU:HA	19:SM:31:VAL:HG22	1.83	0.59
4:C1:1864:A:OP1	57:LR:88:ARG:NH2	2.36	0.59
4:C1:2137:U:OP2	4:C1:2142:A:N6	2.34	0.59
54:LO:3:VAL:HG13	54:LO:4:GLU:HG2	1.85	0.59
4:C1:1232:C:OP2	83:P0:38:MET:N	2.35	0.59
4:C1:1258:U:H1'	83:P0:53:MET:H	1.67	0.59
4:C1:1671:C:OP1	57:LR:60:LYS:NZ	2.34	0.59
55:LP:64:ASN:O	55:LP:80:LYS:NZ	2.31	0.59
1:C2:127:G:N7	13:SG:202:ARG:NH2	2.51	0.59
4:C1:1390:A:N6	4:C1:1418:A:O2'	2.36	0.59
4:C1:1592:G:OP1	72:Lg:58:ARG:NH2	2.31	0.59
4:C1:2895:G:O2'	78:Lm:100:TYR:O	2.20	0.59
58:LS:8:GLN:HB3	58:LS:64:ILE:HD11	1.84	0.59
66:La:44:ASN:O	66:La:47:LYS:O	2.19	0.59
84:CN:34:THR:HG23	84:CN:41:HIS:HD2	1.67	0.59
1:C2:68:A:OP1	13:SG:171:LYS:NZ	2.31	0.59
23:SQ:50:GLU:HB3	23:SQ:51:PRO:HD3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Sg:59:ARG:HH22	39:Sg:97:GLY:HA3	1.66	0.59
58:LS:13:ARG:NH1	58:LS:50:LYS:O	2.36	0.59
65:LZ:97:SER:H	65:LZ:100:THR:HG1	1.50	0.59
71:Lf:13:HIS:O	71:Lf:95:GLY:N	2.34	0.59
5:C4:15:C:O2'	43:LD:8:LYS:NZ	2.35	0.59
8:SB:160:HIS:HB3	8:SB:205:PHE:HE2	1.67	0.59
14:SH:161:GLN:HG2	14:SH:162:ILE:HG23	1.85	0.59
18:SL:124:THR:HB	18:SL:141:LYS:HB3	1.85	0.59
27:SU:82:TYR:HB3	36:Sd:52:PHE:HB3	1.84	0.59
29:SW:53:ILE:HD13	34:Sb:24:LEU:HD11	1.83	0.59
53:LN:66:VAL:O	53:LN:127:TYR:HA	2.02	0.59
4:C1:1048:A:HO2'	4:C1:2632:G:HO2'	1.51	0.59
4:C1:1235:U:O2'	50:LK:120:SER:O	2.15	0.59
4:C1:1677:G:N7	60:LU:74:LYS:NZ	2.51	0.59
38:Sf:130:VAL:HG11	38:Sf:141:CYS:HB3	1.84	0.59
40:LA:14:SER:OG	40:LA:15:ILE:N	2.35	0.59
42:LC:329:PRO:HB3	45:LF:41:ARG:HH21	1.68	0.59
1:C2:1:U:O2	16:SJ:54:ARG:NH2	2.36	0.58
44:LE:42:LEU:O	44:LE:49:GLY:N	2.35	0.58
66:La:105:LEU:HD12	66:La:128:ARG:HG3	1.85	0.58
1:C2:25:C:H5'	1:C2:26:A:H5'	1.85	0.58
4:C1:3092:C:O2'	4:C1:3094:A:OP2	2.20	0.58
9:SC:139:ILE:HG13	9:SC:218:ILE:HG23	1.84	0.58
35:Sc:27:GLN:NE2	35:Sc:43:ASN:OD1	2.36	0.58
45:LF:139:PRO:HG2	45:LF:144:ILE:HD11	1.86	0.58
1:C2:1365:C:OP1	23:SQ:66:ARG:NH2	2.36	0.58
1:C2:1483:A:H4'	23:SQ:72:GLY:H	1.68	0.58
4:C1:1348:U:O2	4:C1:1349:G:N2	2.36	0.58
6:C3:143:U:OP1	53:LN:38:ARG:NH2	2.35	0.58
1:C2:17:C:O2'	1:C2:1137:A:N1	2.31	0.58
4:C1:1263:A:N6	50:LK:123:ARG:H	2.02	0.58
49:LJ:92:ARG:HG2	49:LJ:94:ARG:H	1.68	0.58
1:C2:929:A:OP1	1:C2:931:C:N4	2.37	0.58
6:C3:52:A:OP1	77:Ll:21:ARG:NH1	2.36	0.58
65:LZ:97:SER:N	65:LZ:100:THR:OG1	2.32	0.58
1:C2:1531:G:H5''	32:SZ:81:ARG:HH22	1.68	0.58
4:C1:1474:A:O2'	69:Ld:57:GLN:NE2	2.33	0.58
33:Sa:45:VAL:HB	33:Sa:64:LEU:HD11	1.86	0.58
41:LB:360:ASP:OD2	41:LB:364:LYS:NZ	2.37	0.58
52:LM:135:LEU:HD21	54:LO:178:VAL:HA	1.86	0.58
1:C2:385:A:H5''	15:SI:22:ARG:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:804:C:OP1	42:LC:98:ARG:NH2	2.35	0.58
34:Sb:38:PRO:HD3	34:Sb:77:THR:HG22	1.85	0.58
43:LD:107:ARG:NH2	43:LD:169:GLY:O	2.37	0.58
47:LH:112:ILE:HB	47:LH:126:VAL:HB	1.85	0.58
12:SF:200:ASN:O	12:SF:203:LYS:O	2.20	0.58
61:LV:12:ARG:NH1	61:LV:13:ILE:O	2.37	0.58
4:C1:2514:U:OP2	4:C1:2586:G:N2	2.36	0.58
31:SY:57:VAL:O	31:SY:94:TYR:OH	2.22	0.58
39:Sg:218:GLY:O	39:Sg:236:ALA:N	2.36	0.58
65:LZ:13:VAL:O	65:LZ:20:GLY:N	2.36	0.58
1:C2:1387:G:OP1	24:SR:32:LYS:NZ	2.32	0.58
16:SJ:87:SER:HB3	16:SJ:90:LYS:HB2	1.84	0.58
24:SR:41:ILE:HD11	24:SR:46:LEU:HD23	1.86	0.58
55:LP:22:LEU:HD12	55:LP:146:ILE:HD12	1.86	0.58
4:C1:68:C:OP2	4:C1:301:G:N2	2.37	0.57
32:SZ:54:VAL:HG13	32:SZ:55:PRO:HD3	1.86	0.57
43:LD:75:LEU:O	43:LD:112:LYS:NZ	2.34	0.57
76:Lk:5:ILE:HD11	76:Lk:11:PHE:HD1	1.68	0.57
1:C2:354:C:H5''	15:SI:16:ALA:HB2	1.86	0.57
4:C1:3042:U:OP2	4:C1:3092:C:N4	2.35	0.57
8:SB:82:ARG:NH2	8:SB:191:GLU:OE2	2.36	0.57
19:SM:50:LYS:HE3	38:Sf:129:GLY:HA2	1.85	0.57
31:SY:44:LEU:HA	31:SY:47:VAL:HG12	1.85	0.57
44:LE:87:THR:HG22	44:LE:176:PHE:HB3	1.84	0.57
47:LH:31:ARG:HH12	47:LH:187:ILE:HD12	1.69	0.57
56:LQ:70:ALA:HB1	56:LQ:138:LEU:HD21	1.86	0.57
21:SO:103:ARG:NH1	35:Sc:62:GLU:OE2	2.38	0.57
53:LN:31:ARG:NH2	53:LN:124:ASP:OD2	2.36	0.57
8:SB:132:ASP:HB2	8:SB:221:PRO:HB3	1.87	0.57
1:C2:44:U:OP2	1:C2:437:A:N6	2.34	0.57
1:C2:1459:C:OP2	25:SS:138:THR:OG1	2.22	0.57
3:C5:19:A:N3	3:C5:59:A:N6	2.52	0.57
4:C1:687:U:OP2	51:LL:36:ARG:NH1	2.36	0.57
4:C1:912:G:OP2	40:LA:9:ARG:NH2	2.38	0.57
14:SH:8:ILE:HG23	14:SH:9:LEU:HD22	1.86	0.57
26:ST:131:ASP:HA	26:ST:134:ARG:HG2	1.85	0.57
52:LM:40:ASP:OD1	52:LM:41:GLN:N	2.36	0.57
71:Lf:75:HIS:HB2	71:Lf:82:ARG:HG3	1.86	0.57
1:C2:868:G:H1	1:C2:960:U:H3	1.51	0.57
1:C2:1027:A:OP1	1:C2:1789:G:O2'	2.20	0.57
9:SC:82:ASN:HB2	9:SC:207:LEU:HD23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SF:118:LEU:HD22	12:SF:129:PRO:HB2	1.86	0.57
1:C2:1217:A:OP1	17:SK:1:MET:N	2.37	0.57
66:La:60:TYR:HE2	66:La:63:LYS:HA	1.66	0.57
1:C2:141:U:H2'	13:SG:183:ARG:HH22	1.69	0.57
4:C1:1631:C:OP2	65:LZ:48:ARG:NH2	2.37	0.57
4:C1:2700:G:H5''	59:LT:17:ARG:HG2	1.87	0.57
12:SF:63:GLN:HB3	12:SF:88:PRO:HA	1.87	0.57
13:SG:14:LYS:HD2	13:SG:123:GLY:HA3	1.85	0.57
21:SO:99:GLN:NE2	33:Sa:44:ILE:O	2.33	0.57
35:Sc:33:LEU:HD11	35:Sc:53:ILE:HD12	1.87	0.57
42:LC:318:LEU:HD11	45:LF:146:GLN:HG2	1.86	0.57
62:LW:6:ASP:HB3	62:LW:10:GLY:H	1.69	0.57
1:C2:247:A:O2'	18:SL:37:ASN:O	2.21	0.57
4:C1:1793:C:OP2	81:Lp:49:ARG:NH2	2.38	0.57
45:LF:54:GLU:HA	45:LF:57:THR:HG22	1.87	0.57
47:LH:90:MET:HE1	47:LH:146:LEU:HD13	1.87	0.57
49:LJ:148:VAL:HG23	49:LJ:153:LYS:HG2	1.86	0.57
51:LL:192:GLU:O	51:LL:195:ALA:HB3	2.05	0.57
3:C5:34:A:OP1	23:SQ:143:ARG:NH1	2.36	0.56
4:C1:3353:G:OP2	15:SI:164:ARG:NH2	2.38	0.56
7:SA:29:VAL:HG23	7:SA:37:VAL:HG21	1.87	0.56
1:C2:39:A:OP1	16:SJ:3:ARG:NH2	2.38	0.56
1:C2:405:C:O2'	13:SG:92:ARG:O	2.23	0.56
1:C2:479:C:H4'	16:SJ:120:LYS:HD2	1.86	0.56
4:C1:1420:C:OP2	42:LC:193:LYS:NZ	2.35	0.56
48:LI:59:GLN:HE22	48:LI:97:LEU:HD21	1.70	0.56
71:Lf:35:VAL:HG13	71:Lf:40:ASP:HB2	1.86	0.56
1:C2:1127:G:OP1	79:Ln:11:ARG:NH2	2.38	0.56
9:SC:35:TRP:O	9:SC:46:LYS:NZ	2.31	0.56
16:SJ:62:ARG:O	16:SJ:69:ARG:NH1	2.38	0.56
19:SM:29:LYS:HZ1	19:SM:100:TRP:CD1	2.24	0.56
27:SU:99:ILE:HA	27:SU:102:ARG:HG2	1.85	0.56
45:LF:102:VAL:HG12	45:LF:130:ILE:HD12	1.86	0.56
47:LH:93:VAL:HG23	47:LH:177:ASP:HA	1.86	0.56
48:LI:208:ASN:HA	48:LI:211:ARG:HG3	1.87	0.56
53:LN:159:ARG:HB2	53:LN:164:LEU:HB2	1.87	0.56
67:Lb:36:ASP:O	67:Lb:40:ARG:HB2	2.05	0.56
1:C2:1584:G:O2'	1:C2:1610:G:N1	2.39	0.56
1:C2:1615:C:H2'	12:SF:81:ARG:HD3	1.85	0.56
4:C1:1329:U:OP1	71:Lf:17:GLN:NE2	2.38	0.56
4:C1:2803:A:OP1	80:Lo:60:LYS:NZ	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SF:148:ARG:NH1	12:SF:155:ALA:O	2.38	0.56
39:Sg:42:LEU:HD11	39:Sg:68:VAL:HG21	1.87	0.56
41:LB:165:GLN:OE1	41:LB:168:LYS:NZ	2.29	0.56
1:C2:1681:A:N6	1:C2:1720:G:O2'	2.38	0.56
4:C1:98:G:N7	51:LL:13:HIS:NE2	2.52	0.56
22:SP:123:TYR:OH	25:SS:126:ARG:HD3	2.06	0.56
31:SY:53:ASP:HB3	31:SY:96:LEU:HD21	1.87	0.56
34:Sb:40:CYS:SG	34:Sb:41:LEU:N	2.77	0.56
59:LT:32:LYS:HD3	59:LT:98:HIS:HD2	1.70	0.56
1:C2:1022:C:O2'	1:C2:1125:A:N1	2.37	0.56
4:C1:1258:U:H2'	4:C1:1259:A:H3'	1.88	0.56
14:SH:8:ILE:HD12	14:SH:42:GLN:HG3	1.88	0.56
1:C2:129:U:O2'	1:C2:131:C:N4	2.39	0.56
1:C2:1584:G:N2	1:C2:1611:A:OP2	2.29	0.56
4:C1:1268:G:N2	4:C1:1269:U:O4	2.38	0.56
4:C1:3324:C:OP1	69:Ld:19:ARG:NH1	2.39	0.56
7:SA:155:PHE:O	28:SV:60:ARG:NH2	2.39	0.56
12:SF:77:TYR:OH	23:SQ:114:ARG:NH1	2.39	0.56
53:LN:143:ARG:O	53:LN:149:ASN:ND2	2.39	0.56
58:LS:130:GLU:HG2	58:LS:131:LYS:HG2	1.88	0.56
64:LY:35:LEU:HD23	64:LY:39:LEU:HB3	1.87	0.56
72:Lg:22:VAL:HG12	72:Lg:30:LEU:HD12	1.86	0.56
1:C2:793:A:H5''	1:C2:794:U:H5'	1.87	0.56
1:C2:1171:A:H2'	1:C2:1172:G:H8	1.71	0.56
4:C1:1255:C:N4	4:C1:1263:A:OP1	2.39	0.56
4:C1:1386:A:OP2	70:Le:80:LYS:NZ	2.38	0.56
6:C3:154:C:H5''	46:LG:181:LYS:HD3	1.87	0.56
29:SW:81:VAL:O	29:SW:122:SER:OG	2.24	0.56
58:LS:12:ARG:NH1	58:LS:21:GLU:OE1	2.39	0.56
11:SE:246:LEU:HD21	11:SE:254:ARG:HH12	1.71	0.56
13:SG:31:ARG:HB3	13:SG:101:ILE:HD13	1.88	0.56
13:SG:58:LYS:NZ	13:SG:104:PRO:O	2.39	0.56
31:SY:57:VAL:HG12	31:SY:73:GLY:HA3	1.86	0.56
53:LN:63:ARG:HG2	53:LN:131:GLU:HG2	1.86	0.56
4:C1:2737:C:O2'	67:Lb:36:ASP:OD1	2.23	0.56
23:SQ:142:TYR:O	23:SQ:143:ARG:NE	2.39	0.56
48:LI:6:ALA:O	48:LI:10:ARG:HB2	2.06	0.56
71:Lf:48:ARG:HH12	71:Lf:70:LYS:HE2	1.70	0.56
4:C1:1493:G:O6	77:LI:2:ALA:N	2.39	0.55
61:LV:38:ALA:HB3	61:LV:59:MET:HB3	1.88	0.55
4:C1:728:G:H5''	56:LQ:43:PRO:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C3:127:U:O4	79:L2:18:ARG:NH2	2.36	0.55
12:SF:94:THR:HG22	12:SF:114:ILE:HG13	1.87	0.55
17:SK:60:SER:HB3	17:SK:65:TYR:HE1	1.71	0.55
18:SL:109:VAL:HG12	18:SL:137:PHE:HB2	1.89	0.55
19:SM:66:VAL:HG11	19:SM:71:ILE:HD11	1.88	0.55
25:SS:53:ASP:HB3	25:SS:61:LEU:HD21	1.87	0.55
42:LC:207:VAL:O	42:LC:227:THR:HA	2.06	0.55
1:C2:927:C:O2'	21:SO:124:ASP:OD2	2.23	0.55
1:C2:1473:U:O2'	12:SF:102:ARG:NH1	2.40	0.55
4:C1:2722:U:O2'	59:LT:88:ARG:O	2.23	0.55
22:SP:85:ILE:HG22	22:SP:112:LEU:HD13	1.87	0.55
43:LD:41:LYS:NZ	59:LT:32:LYS:O	2.40	0.55
80:Lo:65:THR:O	80:Lo:87:ARG:NH1	2.39	0.55
12:SF:69:PHE:CZ	23:SQ:53:LEU:HD22	2.40	0.55
29:SW:80:ASN:OD1	29:SW:124:LYS:NZ	2.33	0.55
55:LP:29:THR:HG22	55:LP:119:VAL:HG11	1.87	0.55
69:Ld:23:VAL:O	69:Ld:28:ARG:NH1	2.40	0.55
70:Le:22:SER:HA	70:Le:28:VAL:HG23	1.87	0.55
80:Lo:28:TYR:HB3	80:Lo:69:VAL:HG13	1.88	0.55
1:C2:992:A:H2	1:C2:1012:U:H3	1.52	0.55
4:C1:1750:A:OP1	76:Lk:44:LYS:NZ	2.35	0.55
22:SP:96:ILE:HG12	22:SP:116:LEU:HB3	1.89	0.55
51:LL:165:SER:OG	66:La:135:GLU:OE2	2.25	0.55
78:Lm:95:VAL:HA	78:Lm:101:ALA:O	2.05	0.55
1:C2:871:G:H2'	1:C2:872:G:C8	2.42	0.55
4:C1:584:G:OP1	44:LE:82:ARG:NH2	2.40	0.55
4:C1:3276:G:O6	55:LP:171:ARG:NH2	2.39	0.55
6:C3:22:U:H5''	64:LY:16:ARG:HH12	1.72	0.55
16:SJ:161:THR:HG22	16:SJ:162:SER:H	1.72	0.55
47:LH:89:LYS:HG2	47:LH:145:VAL:HG22	1.87	0.55
4:C1:1352:A:H4'	4:C1:1353:U:H5'	1.87	0.55
4:C1:2901:G:O2'	4:C1:3024:A:N1	2.39	0.55
39:Sg:172:ALA:HB1	39:Sg:199:ILE:HD12	1.89	0.55
41:LB:57:VAL:HG22	41:LB:73:VAL:HG12	1.89	0.55
52:LM:13:ARG:HH11	52:LM:67:PRO:HD3	1.70	0.55
70:Le:123:LYS:HA	70:Le:126:LEU:HD12	1.88	0.55
4:C1:2681:U:OP2	49:LJ:51:ARG:NH1	2.38	0.55
8:SB:229:MET:O	8:SB:232:HIS:O	2.25	0.55
12:SF:222:LYS:NZ	35:Sc:58:GLU:OE1	2.39	0.55
26:ST:105:LEU:HD13	26:ST:122:ARG:HD2	1.88	0.55
81:Lp:49:ARG:HH21	81:Lp:52:ALA:HB2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:959:U:H5'	20:SN:14:SER:HB2	1.89	0.55
1:C2:1226:A:H2'	19:SM:116:VAL:HG21	1.89	0.55
1:C2:1229:G:H21	1:C2:1256:A:H62	1.54	0.55
4:C1:120:G:N2	46:LG:126:SER:OG	2.40	0.55
39:Sg:242:SER:OG	39:Sg:290:VAL:O	2.24	0.55
40:LA:112:ILE:HD11	81:Lp:79:VAL:HG22	1.89	0.55
4:C1:2703:A:N6	43:LD:28:THR:O	2.38	0.55
13:SG:122:GLU:HA	13:SG:126:ASP:HB2	1.88	0.55
45:LF:127:LEU:HA	45:LF:130:ILE:HG22	1.89	0.55
14:SH:62:VAL:HG12	14:SH:64:VAL:H	1.73	0.54
15:SI:57:ALA:HB2	15:SI:177:GLY:HA2	1.89	0.54
16:SJ:93:LEU:HA	16:SJ:96:VAL:HG12	1.89	0.54
41:LB:110:LEU:HD12	41:LB:114:VAL:HG11	1.89	0.54
46:LG:65:LEU:O	46:LG:68:ARG:C	2.50	0.54
1:C2:530:C:O2	31:SY:61:ARG:NH1	2.40	0.54
25:SS:108:LYS:HA	25:SS:111:ASP:HB2	1.89	0.54
28:SV:3:ASN:HD21	28:SV:7:GLN:HB2	1.71	0.54
64:LY:55:GLU:HB2	64:LY:108:LYS:HB3	1.88	0.54
10:SD:71:LEU:HB3	17:SK:20:VAL:HG21	1.88	0.54
11:SE:255:ARG:HG3	11:SE:259:GLN:HE22	1.73	0.54
26:ST:6:VAL:HA	26:ST:9:VAL:HG12	1.88	0.54
35:Sc:12:VAL:HG12	35:Sc:30:VAL:HG12	1.89	0.54
39:Sg:81:LEU:HD22	39:Sg:91:LEU:HD13	1.89	0.54
1:C2:1681:A:O2'	13:SG:31:ARG:NH1	2.39	0.54
4:C1:860:G:O4'	40:LA:181:LYS:NZ	2.33	0.54
4:C1:1333:C:OP1	56:LQ:2:GLY:N	2.41	0.54
4:C1:1357:G:H2'	4:C1:1358:C:C6	2.43	0.54
13:SG:43:ASP:HA	13:SG:46:LYS:HE3	1.89	0.54
33:Sa:10:ARG:HD2	33:Sa:34:LYS:HA	1.88	0.54
46:LG:34:PHE:H	46:LG:39:ALA:HB3	1.72	0.54
51:LL:90:ALA:O	51:LL:93:ILE:C	2.50	0.54
4:C1:110:G:OP2	51:LL:73:ARG:NH2	2.41	0.54
4:C1:664:U:H2'	4:C1:665:A:C8	2.43	0.54
4:C1:1383:G:OP1	42:LC:203:ARG:NH1	2.39	0.54
5:C4:121:U:O2	43:LD:269:SER:OG	2.24	0.54
11:SE:45:ILE:HG13	11:SE:61:VAL:HG21	1.89	0.54
24:SR:23:LYS:NZ	39:Sg:149:ASP:OD2	2.39	0.54
64:LY:32:SER:HA	64:LY:49:PRO:HA	1.89	0.54
68:Lc:66:LYS:NZ	68:Lc:101:LEU:O	2.41	0.54
1:C2:1037:C:O2	29:SW:16:ASN:ND2	2.40	0.54
1:C2:1040:G:H5'	7:SA:31:VAL:HG21	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:1273:G:H4'	1:C2:1274:C:H3'	1.89	0.54
4:C1:2555:G:N2	65:LZ:135:ARG:O	2.37	0.54
4:C1:2679:A:HO2'	49:LJ:52:TYR:HH	1.53	0.54
4:C1:3297:U:O4	41:LB:124:LYS:NZ	2.31	0.54
46:LG:163:VAL:HG13	46:LG:166:LEU:HD12	1.88	0.54
49:LJ:15:GLU:HB3	49:LJ:130:VAL:HG23	1.89	0.54
84:CN:66:TRP:HD1	84:CN:70:GLU:HG3	1.72	0.54
1:C2:96:G:OP1	11:SE:10:LYS:NZ	2.40	0.54
4:C1:970:A:OP2	67:Lb:19:ASN:ND2	2.40	0.54
4:C1:3045:G:OP1	41:LB:19:ARG:NH2	2.41	0.54
11:SE:126:VAL:HG12	11:SE:141:THR:HG22	1.90	0.54
1:C2:1553:G:O6	22:SP:43:ARG:NH1	2.40	0.54
4:C1:2468:A:O2'	4:C1:2477:G:N2	2.41	0.54
34:Sb:34:ASP:HB3	34:Sb:43:ILE:HD11	1.88	0.54
48:LI:36:LEU:HD23	48:LI:87:LEU:HD23	1.90	0.54
23:SQ:41:PRO:HB2	23:SQ:44:LEU:HB2	1.89	0.54
26:ST:86:ARG:NH1	26:ST:90:PRO:O	2.41	0.54
39:Sg:209:THR:HG23	39:Sg:210:LEU:HD12	1.88	0.54
44:LE:138:GLN:O	44:LE:142:ASP:HB2	2.07	0.54
45:LF:100:ARG:NH2	56:LQ:4:ASP:OD1	2.41	0.54
4:C1:1255:C:H2'	4:C1:1256:G:C8	2.42	0.54
9:SC:228:ASN:HD22	28:SV:1:MET:HB3	1.73	0.54
16:SJ:82:ARG:HG2	16:SJ:149:ARG:HG2	1.89	0.54
19:SM:75:VAL:HA	19:SM:78:LEU:HG	1.90	0.54
65:LZ:42:LEU:HD22	65:LZ:101:PHE:HE2	1.73	0.54
1:C2:1547:A:OP2	25:SS:123:ARG:NH2	2.41	0.53
4:C1:110:G:OP1	51:LL:91:ARG:NH1	2.40	0.53
4:C1:1047:A:N3	4:C1:2633:U:O2'	2.40	0.53
4:C1:1257:C:H2'	83:P0:52:LEU:CB	2.39	0.53
4:C1:1258:U:H1'	83:P0:53:MET:N	2.23	0.53
10:SD:31:GLU:O	10:SD:54:ARG:NH2	2.41	0.53
17:SK:21:VAL:HB	17:SK:66:TYR:HB2	1.90	0.53
27:SU:71:PRO:O	36:Sd:41:GLN:NE2	2.41	0.53
36:Sd:6:VAL:HG23	36:Sd:7:TRP:HD1	1.72	0.53
40:LA:102:LEU:HD12	40:LA:166:ILE:HD11	1.89	0.53
41:LB:113:GLU:HB2	41:LB:176:ALA:HB2	1.91	0.53
73:Lh:10:ARG:NH1	73:Lh:60:GLU:OE2	2.35	0.53
1:C2:1060:U:H3'	1:C2:1061:A:H5''	1.88	0.53
30:SX:107:PHE:HE2	30:SX:114:LYS:H	1.56	0.53
4:C1:943:U:H3'	66:La:13:GLY:HA2	1.90	0.53
4:C1:2768:U:H2'	4:C1:2769:A:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SG:79:LYS:HD2	13:SG:80:ASN:HB2	1.88	0.53
15:SI:107:THR:HG22	15:SI:110:ARG:HH21	1.73	0.53
31:SY:11:LYS:O	31:SY:23:PHE:HA	2.08	0.53
3:C5:21:G:N7	3:C5:45:7MG:N1	2.43	0.53
9:SC:188:LEU:HD13	9:SC:196:VAL:HG21	1.91	0.53
12:SF:80:LYS:HB2	12:SF:83:ARG:HD3	1.91	0.53
47:LH:92:TYR:HB2	47:LH:142:ASP:OD1	2.08	0.53
52:LM:23:ILE:O	52:LM:30:GLY:N	2.41	0.53
1:C2:447:U:O2'	11:SE:27:TYR:O	2.25	0.53
1:C2:686:C:O3'	29:SW:118:ARG:NH1	2.42	0.53
4:C1:2185:G:O2'	4:C1:2314:U:OP2	2.22	0.53
13:SG:2:LYS:HB3	13:SG:108:VAL:HG22	1.90	0.53
13:SG:70:PRO:HA	13:SG:99:GLY:HA3	1.90	0.53
33:Sa:23:CYS:O	33:Sa:27:SER:N	2.41	0.53
4:C1:2231:C:OP1	86:C1:3402:T1C:H422	2.07	0.53
16:SJ:96:VAL:HA	16:SJ:99:LEU:HD23	1.91	0.53
18:SL:14:GLN:HB3	18:SL:54:ILE:HG13	1.89	0.53
39:Sg:170:ILE:HD11	39:Sg:204:ALA:HB2	1.89	0.53
44:LE:154:LEU:HD23	52:LM:119:GLN:HG2	1.90	0.53
1:C2:164:A:H1'	13:SG:13:GLN:HE21	1.74	0.53
1:C2:1357:A:H2'	1:C2:1358:G:C8	2.44	0.53
4:C1:2557:A:OP1	40:LA:69:TYR:OH	2.23	0.53
11:SE:175:PHE:HE2	11:SE:198:LYS:HD3	1.73	0.53
42:LC:329:PRO:HG3	45:LF:41:ARG:HE	1.73	0.53
48:LI:49:CYS:HB3	48:LI:168:SER:HB3	1.91	0.53
69:Ld:16:LEU:HD23	69:Ld:71:LEU:HD13	1.91	0.53
1:C2:1255:G:N7	19:SM:46:ARG:NH2	2.53	0.53
4:C1:3117:C:O2	78:Lm:106:ARG:NH2	2.41	0.53
9:SC:52:THR:HG23	9:SC:55:GLU:H	1.72	0.53
48:LI:52:LEU:HB2	48:LI:152:LEU:HD13	1.90	0.53
1:C2:325:G:H4'	18:SL:83:THR:HG21	1.91	0.53
4:C1:1244:A:N6	4:C1:1271:A:OP1	2.42	0.53
7:SA:198:MET:HE1	7:SA:200:ASP:HB2	1.91	0.53
57:LR:136:ARG:HA	57:LR:139:VAL:HG22	1.90	0.53
4:C1:1016:C:N4	4:C1:2672:G:OP2	2.42	0.53
4:C1:1240:A:N6	4:C1:1244:A:H2'	2.23	0.53
10:SD:9:ARG:HA	10:SD:12:VAL:HG12	1.91	0.53
40:LA:150:LEU:O	40:LA:153:GLY:N	2.40	0.53
1:C2:209:U:H2'	1:C2:210:A:H8	1.73	0.52
1:C2:1563:C:OP1	26:ST:84:LYS:NZ	2.42	0.52
4:C1:1661:G:H2'	4:C1:1662:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SF:216:GLU:HA	12:SF:219:ARG:HG2	1.90	0.52
17:SK:8:ARG:O	17:SK:12:HIS:ND1	2.42	0.52
19:SM:130:THR:OG1	19:SM:131:ASP:N	2.42	0.52
40:LA:79:ASN:ND2	40:LA:166:ILE:O	2.34	0.52
51:LL:76:THR:O	51:LL:79:GLU:N	2.43	0.52
66:La:60:TYR:CE2	66:La:63:LYS:HA	2.43	0.52
71:Lf:42:GLN:HA	71:Lf:45:LEU:HG	1.91	0.52
83:P0:115:ALA:O	83:P0:162:GLY:N	2.43	0.52
1:C2:332:U:O2'	15:SI:5:ARG:NH1	2.42	0.52
1:C2:1555:A:N6	36:Sd:14:TYR:OH	2.42	0.52
6:C3:60:U:OP1	63:LX:54:TYR:OH	2.27	0.52
14:SH:21:ALA:O	14:SH:25:VAL:HG13	2.09	0.52
14:SH:56:LYS:HB2	14:SH:88:ARG:HD2	1.91	0.52
33:Sa:28:LYS:HG2	33:Sa:30:ILE:HG23	1.91	0.52
53:LN:44:ARG:NH2	53:LN:120:TRP:O	2.40	0.52
65:LZ:101:PHE:O	65:LZ:106:GLN:NE2	2.42	0.52
83:P0:38:MET:O	83:P0:40:GLU:N	2.42	0.52
1:C2:159:U:H5'	31:SY:117:LYS:HG3	1.92	0.52
1:C2:459:G:OP2	31:SY:105:ARG:NH2	2.40	0.52
1:C2:472:U:O2'	1:C2:769:A:N3	2.38	0.52
4:C1:655:C:H2'	4:C1:656:A:H8	1.74	0.52
4:C1:1263:A:H62	50:LK:123:ARG:H	1.57	0.52
34:Sb:40:CYS:SG	34:Sb:58:SER:OG	2.63	0.52
41:LB:47:LEU:HD11	41:LB:179:ALA:HB3	1.91	0.52
4:C1:1277:C:O2'	4:C1:1278:A:O5'	2.24	0.52
4:C1:1786:G:H2'	4:C1:1787:A:C8	2.44	0.52
4:C1:3278:C:OP1	71:Lf:54:ARG:NH2	2.29	0.52
11:SE:252:ARG:HE	11:SE:256:ARG:HH12	1.58	0.52
15:SI:48:THR:HG21	15:SI:54:LYS:HD3	1.90	0.52
1:C2:1368:G:H5''	26:ST:69:LYS:HG2	1.92	0.52
4:C1:655:C:H2'	4:C1:656:A:C8	2.45	0.52
4:C1:1747:G:H21	76:Lk:2:ALA:HB1	1.74	0.52
4:C1:2433:U:H1'	53:LN:125:SER:HB3	1.90	0.52
5:C4:7:G:OP1	43:LD:33:ARG:NH1	2.43	0.52
61:LV:87:ARG:HH22	61:LV:120:LYS:HB3	1.73	0.52
1:C2:1474:G:H2'	1:C2:1475:A:C8	2.44	0.52
4:C1:2478:C:OP2	4:C1:2480:A:N6	2.41	0.52
4:C1:3119:U:H4'	78:Lm:104:PRO:HG2	1.91	0.52
10:SD:55:THR:OG1	10:SD:90:ARG:NH1	2.42	0.52
14:SH:73:VAL:HG23	14:SH:74:GLN:H	1.73	0.52
27:SU:69:LYS:HD3	27:SU:80:GLU:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:LL:46:ILE:HD13	51:LL:51:LEU:HA	1.92	0.52
60:LU:61:THR:HG23	60:LU:62:VAL:HG23	1.91	0.52
3:C5:23:G:O2'	4:C1:2266:U:OP1	2.27	0.52
4:C1:144:A:OP1	46:LG:193:LYS:NZ	2.39	0.52
11:SE:44:LEU:HD23	11:SE:82:TYR:HB3	1.90	0.52
19:SM:59:LEU:HB3	19:SM:123:VAL:HB	1.91	0.52
41:LB:35:ASP:OD2	41:LB:37:ARG:NH1	2.43	0.52
8:SB:160:HIS:HB3	8:SB:205:PHE:CE2	2.45	0.52
16:SJ:64:GLU:HG3	16:SJ:65:LYS:HD2	1.92	0.52
16:SJ:123:HIS:HD2	37:Se:33:ARG:HE	1.58	0.52
25:SS:14:ILE:HG22	25:SS:23:ASP:HA	1.92	0.52
39:Sg:100:TYR:OH	39:Sg:137:LYS:NZ	2.37	0.52
41:LB:372:THR:HG22	41:LB:374:ALA:H	1.75	0.52
43:LD:39:GLN:NE2	43:LD:46:THR:O	2.42	0.52
45:LF:121:LYS:HB2	59:LT:133:ALA:HB3	1.90	0.52
60:LU:19:VAL:HG12	60:LU:105:LEU:HD22	1.92	0.52
1:C2:1793:G:N7	33:Sa:34:LYS:NZ	2.58	0.52
4:C1:1134:G:O2'	4:C1:2642:A:N3	2.38	0.52
4:C1:2163:C:H1'	40:LA:11:GLY:HA3	1.92	0.52
7:SA:36:TYR:OH	7:SA:56:LYS:NZ	2.43	0.52
39:Sg:211:ILE:O	39:Sg:222:LEU:HA	2.09	0.52
42:LC:156:LEU:HA	42:LC:159:ILE:HG12	1.91	0.52
81:Lp:46:THR:OG1	81:Lp:57:CYS:SG	2.68	0.52
4:C1:1480:G:O2'	4:C1:1871:U:O4	2.22	0.52
10:SD:8:LYS:HG3	27:SU:63:LEU:HD11	1.91	0.52
28:SV:79:LEU:HD13	28:SV:82:VAL:HG21	1.91	0.52
54:LO:84:LEU:HD22	54:LO:102:LEU:HD22	1.92	0.52
4:C1:1807:G:OP1	65:LZ:133:LYS:NZ	2.40	0.51
17:SK:55:VAL:HG12	17:SK:68:LEU:HA	1.92	0.51
19:SM:98:GLY:O	19:SM:101:ALA:C	2.52	0.51
4:C1:44:U:H5''	53:LN:85:THR:HG23	1.92	0.51
30:SX:61:SER:HB2	30:SX:116:ASP:HB2	1.90	0.51
39:Sg:82:SER:HB3	39:Sg:92:TRP:HZ3	1.75	0.51
42:LC:193:LYS:HA	42:LC:198:ARG:HA	1.92	0.51
54:LO:126:VAL:O	58:LS:154:HIS:NE2	2.43	0.51
69:Ld:13:THR:HA	69:Ld:71:LEU:O	2.10	0.51
1:C2:388:G:OP1	1:C2:423:G:O2'	2.27	0.51
13:SG:68:LEU:HD23	13:SG:100:ALA:HB3	1.92	0.51
7:SA:107:PHE:HB3	7:SA:139:VAL:HG11	1.91	0.51
13:SG:145:PHE:HD2	13:SG:156:PHE:HD2	1.57	0.51
23:SQ:48:VAL:O	23:SQ:51:PRO:HD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:LA:156:LYS:HG2	40:LA:158:ILE:HG23	1.92	0.51
44:LE:92:SER:OG	44:LE:94:GLU:OE1	2.29	0.51
1:C2:144:U:H5	13:SG:137:ARG:HH22	1.58	0.51
4:C1:982:C:H2'	4:C1:983:A:H8	1.76	0.51
4:C1:1613:A:OP1	76:Lk:2:ALA:N	2.43	0.51
4:C1:1799:A:H2'	4:C1:1800:A:C8	2.46	0.51
7:SA:117:GLU:HG3	9:SC:40:LYS:HE2	1.91	0.51
47:LH:93:VAL:HG12	78:Lm:82:LEU:HD13	1.92	0.51
64:LY:58:VAL:O	64:LY:65:GLY:N	2.43	0.51
1:C2:1081:A:O2'	1:C2:1083:G:N7	2.42	0.51
4:C1:200:C:OP1	64:LY:60:ARG:NH1	2.43	0.51
4:C1:1263:A:N7	50:LK:122:GLY:HA2	2.26	0.51
4:C1:3375:A:O2'	4:C1:3378:C:OP2	2.23	0.51
4:C1:3379:C:H4'	41:LB:315:GLY:HA2	1.92	0.51
42:LC:142:VAL:HA	42:LC:145:ILE:HG13	1.92	0.51
43:LD:120:LYS:O	43:LD:248:ARG:NH1	2.44	0.51
48:LI:146:ASP:OD1	48:LI:147:VAL:N	2.43	0.51
49:LJ:32:ARG:NE	49:LJ:120:ILE:O	2.43	0.51
78:Lm:79:GLU:OE2	78:Lm:81:SER:OG	2.27	0.51
9:SC:116:LYS:HG2	9:SC:127:ALA:HB3	1.92	0.51
10:SD:45:LYS:HE2	10:SD:85:VAL:HB	1.93	0.51
36:Sd:36:LEU:HB3	36:Sd:38:ILE:HG12	1.92	0.51
45:LF:232:ARG:HH12	45:LF:239:LEU:HD13	1.76	0.51
81:Lp:75:ALA:O	81:Lp:79:VAL:HG23	2.10	0.51
1:C2:1426:C:H3'	1:C2:1427:A:H4'	1.92	0.51
4:C1:3137:C:H5''	41:LB:276:THR:HG21	1.93	0.51
47:LH:20:ILE:HG12	47:LH:25:VAL:HG13	1.92	0.51
49:LJ:172:LEU:HG	49:LJ:173:ASP:H	1.75	0.51
1:C2:159:U:H1'	13:SG:87:ARG:HH12	1.76	0.51
1:C2:912:U:OP1	1:C2:913:G:O2'	2.25	0.51
9:SC:168:ARG:HD3	9:SC:170:ILE:HD11	1.93	0.51
13:SG:135:PRO:HG2	13:SG:141:ILE:HD13	1.91	0.51
42:LC:20:LEU:HD12	42:LC:255:PHE:HD2	1.76	0.51
43:LD:211:LEU:HB3	43:LD:219:PHE:HB2	1.93	0.51
4:C1:75:G:H5''	51:LL:58:VAL:HG13	1.92	0.51
39:Sg:19:TRP:HB2	39:Sg:38:ARG:HG3	1.93	0.51
39:Sg:112:SER:O	39:Sg:124:SER:HA	2.11	0.51
46:LG:147:LYS:O	46:LG:201:THR:OG1	2.24	0.51
58:LS:6:GLU:OE1	58:LS:99:ARG:NH1	2.44	0.51
66:La:85:ASP:N	66:La:85:ASP:OD1	2.42	0.51
81:Lp:50:GLY:O	81:Lp:54:ILE:HB	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:284:G:O6	13:SG:188:ARG:NH2	2.38	0.50
49:LJ:32:ARG:HG2	49:LJ:120:ILE:HA	1.93	0.50
51:LL:93:ILE:HG22	51:LL:94:GLY:H	1.75	0.50
52:LM:55:ARG:NH1	58:LS:70:THR:O	2.44	0.50
54:LO:127:LEU:HD22	58:LS:156:VAL:HG13	1.92	0.50
1:C2:29:U:H2'	1:C2:30:G:H8	1.75	0.50
1:C2:959:U:O2	34:Sb:30:SER:OG	2.30	0.50
1:C2:1474:G:H2'	1:C2:1475:A:H8	1.76	0.50
4:C1:1242:G:N3	50:LK:17:ALA:N	2.59	0.50
11:SE:126:VAL:HA	11:SE:141:THR:HA	1.92	0.50
26:ST:18:TYR:HD1	26:ST:135:ILE:HD13	1.76	0.50
1:C2:800:U:H2'	1:C2:801:G:C8	2.46	0.50
1:C2:1278:G:H5''	10:SD:185:LYS:HE3	1.92	0.50
4:C1:62:A:OP1	53:LN:162:ARG:NH2	2.44	0.50
8:SB:22:ASP:OD2	8:SB:25:THR:OG1	2.29	0.50
18:SL:56:LYS:HG3	18:SL:57:LYS:HG3	1.94	0.50
23:SQ:27:GLY:HA2	23:SQ:63:ILE:O	2.11	0.50
45:LF:48:ASN:ND2	45:LF:182:ASP:OD2	2.35	0.50
59:LT:32:LYS:HD3	59:LT:98:HIS:CD2	2.47	0.50
65:LZ:100:THR:HA	65:LZ:106:GLN:OE1	2.12	0.50
4:C1:681:U:O4	42:LC:118:LYS:NZ	2.32	0.50
4:C1:2160:G:H2'	4:C1:2161:G:H8	1.76	0.50
4:C1:2207:A:H2'	4:C1:2208:A:H4'	1.92	0.50
4:C1:3016:A:H2'	4:C1:3017:A:H8	1.76	0.50
30:SX:95:PHE:O	30:SX:142:LYS:NZ	2.44	0.50
42:LC:159:ILE:HD12	42:LC:164:GLU:HG3	1.94	0.50
46:LG:186:LEU:HB3	46:LG:195:SER:HB2	1.92	0.50
60:LU:17:VAL:HB	60:LU:63:VAL:HB	1.94	0.50
1:C2:1466:G:O2'	1:C2:1602:C:OP1	2.28	0.50
4:C1:297:G:O2'	74:Li:32:ALA:O	2.29	0.50
4:C1:860:G:O5'	40:LA:181:LYS:NZ	2.45	0.50
4:C1:1054:A:H5''	4:C1:2637:A:H61	1.75	0.50
4:C1:1345:G:H2'	4:C1:1346:G:H8	1.77	0.50
4:C1:2727:A:OP2	4:C1:2728:G:N2	2.41	0.50
8:SB:139:ALA:HA	8:SB:213:ARG:H	1.75	0.50
11:SE:103:TYR:HB2	11:SE:182:TYR:OH	2.11	0.50
22:SP:81:ARG:NH2	22:SP:117:GLY:O	2.45	0.50
38:Sf:120:GLU:N	38:Sf:132:LEU:H	2.08	0.50
40:LA:206:PRO:HD3	40:LA:213:GLY:HA2	1.93	0.50
71:Lf:16:TYR:OH	71:Lf:89:LEU:O	2.23	0.50
1:C2:209:U:H2'	1:C2:210:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:752:A:O5'	11:SE:187:ARG:NH2	2.45	0.50
4:C1:582:G:OP1	44:LE:29:LYS:NZ	2.36	0.50
4:C1:1508:C:OP1	55:LP:127:ARG:NH2	2.45	0.50
4:C1:1597:C:H5'	4:C1:1696:A:H1'	1.94	0.50
4:C1:3231:U:H2'	4:C1:3232:G:H8	1.77	0.50
13:SG:180:THR:HG23	13:SG:183:ARG:H	1.77	0.50
15:SI:31:ARG:HH12	15:SI:48:THR:HG22	1.76	0.50
43:LD:55:PHE:HE2	43:LD:159:VAL:HB	1.76	0.50
51:LL:83:ALA:O	51:LL:117:LYS:NZ	2.31	0.50
53:LN:66:VAL:HG21	53:LN:98:LEU:HB3	1.93	0.50
1:C2:121:U:H2'	1:C2:122:U:C6	2.46	0.50
4:C1:215:G:H5''	64:LY:12:ARG:HG3	1.94	0.50
4:C1:1196:C:OP1	4:C1:1309:U:O2'	2.29	0.50
4:C1:1236:G:O2'	4:C1:1237:G:OP1	2.28	0.50
5:C4:99:G:H4'	45:LF:128:LYS:HD3	1.94	0.50
12:SF:208:SER:HB2	12:SF:211:ILE:HG12	1.94	0.50
19:SM:70:ASN:OD1	19:SM:71:ILE:N	2.45	0.50
23:SQ:109:PHE:HD2	23:SQ:117:LEU:HD11	1.77	0.50
41:LB:108:GLU:HA	41:LB:137:TYR:CD2	2.47	0.50
71:Lf:38:PRO:HB3	71:Lf:74:THR:HG21	1.94	0.50
1:C2:1690:G:H2'	1:C2:1691:A:C8	2.47	0.50
4:C1:2842:U:OP1	4:C1:2844:C:N4	2.41	0.50
10:SD:54:ARG:HB3	10:SD:57:ASP:HB3	1.91	0.50
11:SE:21:ASP:N	11:SE:21:ASP:OD1	2.44	0.50
41:LB:46:PHE:CE2	41:LB:81:THR:HG23	2.47	0.50
44:LE:65:ILE:O	44:LE:76:LEU:HA	2.11	0.50
4:C1:1203:A:H2'	4:C1:1204:A:C8	2.47	0.50
4:C1:2568:C:O2'	4:C1:2569:A:O4'	2.28	0.50
4:C1:2697:A:H2'	4:C1:2698:G:C8	2.47	0.50
13:SG:3:LEU:HD21	13:SG:111:LEU:HD12	1.94	0.50
14:SH:41:LEU:HD13	14:SH:70:PHE:HE1	1.77	0.50
22:SP:83:MET:HB3	22:SP:116:LEU:HD13	1.93	0.50
28:SV:9:VAL:HG12	28:SV:10:GLU:H	1.77	0.50
32:SZ:83:LEU:O	32:SZ:86:GLU:O	2.30	0.50
33:Sa:64:LEU:HD12	33:Sa:65:PRO:HD2	1.94	0.50
55:LP:48:LEU:HD22	55:LP:88:VAL:HG13	1.94	0.50
59:LT:104:GLU:HA	59:LT:107:GLU:HG2	1.94	0.50
4:C1:157:A:C8	74:Li:26:ILE:HD13	2.47	0.49
4:C1:825:U:OP2	40:LA:21:ARG:NH1	2.45	0.49
4:C1:874:U:OP2	41:LB:240:ARG:NH2	2.44	0.49
16:SJ:110:GLN:NE2	16:SJ:126:ARG:HB2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30: SX:56: LYS: HG2	30: SX:72: VAL: HG12	1.93	0.49
30: SX:130: VAL: HG23	30: SX:131: SER: H	1.77	0.49
56: LQ:38: ARG: HE	56: LQ:39: ARG: HG3	1.77	0.49
1: C2:1797: A: N6	33: Sa:85: ARG: O	2.44	0.49
4: C1:1727: G: OP1	81: Lp:44: LYS: NZ	2.45	0.49
5: C4:32: U: H5'	43: LD:218: ARG: NH2	2.27	0.49
15: SI:108: PRO: HA	15: SI:111: GLN: HG2	1.93	0.49
21: SO:132: ARG: HD2	33: Sa:29: SER: HB3	1.94	0.49
54: LO:12: LYS: O	58: LS:167: ARG: NH2	2.38	0.49
1: C2:371: G: O3'	29: SW:88: LYS: NZ	2.45	0.49
1: C2:1559: A: H5''	25: SS:135: GLY: HA3	1.95	0.49
12: SF:42: LEU: HD22	12: SF:47: SER: HA	1.94	0.49
13: SG:163: THR: HA	13: SG:167: LYS: O	2.12	0.49
39: Sg:191: ASP: OD1	39: Sg:191: ASP: N	2.45	0.49
46: LG:90: THR: HG22	46: LG:214: LEU: HD21	1.95	0.49
51: LL:141: ALA: HA	51: LL:144: THR: HB	1.94	0.49
53: LN:35: VAL: HA	53: LN:65: ARG: HE	1.77	0.49
59: LT:42: ILE: O	59: LT:59: GLY: N	2.45	0.49
60: LU:32: SER: OG	60: LU:83: TYR: OH	2.27	0.49
4: C1:63: A: H5''	53: LN:174: ILE: HG21	1.94	0.49
4: C1:1717: U: H2'	4: C1:1718: G: C8	2.48	0.49
4: C1:3252: G: H2'	4: C1:3253: G: C8	2.47	0.49
5: C4:31: U: O2'	43: LD:218: ARG: NH2	2.45	0.49
6: C3:8: C: H2'	6: C3:9: A: C8	2.47	0.49
11: SE:103: TYR: HE2	11: SE:184: THR: HG23	1.78	0.49
16: SJ:123: HIS: CD2	37: Se:33: ARG: HE	2.30	0.49
19: SM:89: ILE: HG13	19: SM:90: LYS: H	1.77	0.49
24: SR:107: SER: HA	24: SR:110: VAL: HG12	1.94	0.49
44: LE:43: LEU: HD11	44: LE:85: ILE: HG13	1.94	0.49
48: LI:52: LEU: HB3	48: LI:136: PHE: HB2	1.95	0.49
56: LQ:19: PRO: HG3	56: LQ:30: VAL: HG21	1.93	0.49
65: LZ:99: GLU: O	65: LZ:106: GLN: NE2	2.46	0.49
1: C2:1516: A: OP1	27: SU:88: LYS: NZ	2.39	0.49
11: SE:54: TYR: O	31: SY:15: ASN: ND2	2.44	0.49
22: SP:111: MET: HG2	25: SS:119: ILE: HB	1.94	0.49
25: SS:11: PHE: CD2	25: SS:59: GLY: HA3	2.48	0.49
47: LH:90: MET: HE2	47: LH:144: ILE: HG23	1.94	0.49
48: LI:44: ASP: HA	48: LI:185: ARG: HH22	1.77	0.49
69: Ld:14: ILE: HD13	69: Ld:36: ILE: HD13	1.95	0.49
70: Le:6: HIS: ND1	70: Le:6: HIS: O	2.45	0.49
1: C2:859: A: C5	20: SN:73: ARG: HD3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:3108:G:OP2	78:Lm:112:LYS:NZ	2.46	0.49
11:SE:89:VAL:HG22	11:SE:100:ARG:HE	1.76	0.49
13:SG:22:HIS:HA	13:SG:25:ARG:HB3	1.93	0.49
13:SG:25:ARG:HA	13:SG:28:PHE:HD2	1.76	0.49
19:SM:61:VAL:HB	19:SM:121:VAL:HB	1.94	0.49
39:Sg:23:LEU:HD21	39:Sg:310:ILE:HD13	1.93	0.49
43:LD:85:ARG:HH12	43:LD:254:LYS:HB2	1.77	0.49
66:La:3:SER:O	66:La:6:THR:OG1	2.24	0.49
1:C2:523:G:H21	1:C2:528:U:H5	1.59	0.49
1:C2:1241:G:O4'	22:SP:79:HIS:ND1	2.46	0.49
4:C1:1236:G:H5'	50:LK:119:LYS:HA	1.95	0.49
4:C1:3315:G:OP1	41:LB:116:ARG:NH2	2.45	0.49
7:SA:162:CYS:SG	7:SA:163:ASN:N	2.85	0.49
18:SL:4:GLU:OE1	18:SL:116:ARG:NH2	2.46	0.49
25:SS:56:LYS:HZ1	25:SS:60:GLU:C	2.21	0.49
31:SY:103:ALA:O	31:SY:108:ARG:NH2	2.44	0.49
39:Sg:64:HIS:CE1	39:Sg:90:ARG:HD2	2.48	0.49
41:LB:53:MET:HG2	41:LB:77:THR:HG22	1.93	0.49
41:LB:85:VAL:HG12	41:LB:202:THR:HA	1.93	0.49
41:LB:296:THR:HG23	41:LB:299:ASP:H	1.78	0.49
45:LF:96:PRO:HB2	45:LF:99:PRO:HD2	1.94	0.49
72:Lg:66:SER:OG	72:Lg:67:LYS:N	2.44	0.49
1:C2:1219:A:H1'	17:SK:47:GLN:HE22	1.77	0.49
4:C1:394:G:N1	4:C1:397:A:OP2	2.46	0.49
7:SA:198:MET:SD	7:SA:201:LEU:N	2.85	0.49
19:SM:63:VAL:HG21	19:SM:66:VAL:HG13	1.95	0.49
40:LA:117:GLU:OE2	40:LA:163:ARG:NH2	2.43	0.49
43:LD:126:GLU:HA	43:LD:196:ARG:HD3	1.95	0.49
1:C2:477:A:H2'	1:C2:478:A:H8	1.78	0.49
1:C2:1727:G:H2'	1:C2:1728:A:C8	2.48	0.49
4:C1:591:G:N2	4:C1:612:U:OP1	2.41	0.49
4:C1:925:A:N6	40:LA:2:GLY:O	2.41	0.49
4:C1:1342:C:H5''	56:LQ:12:ARG:HG2	1.95	0.49
4:C1:1629:U:O3'	65:LZ:115:LYS:NZ	2.43	0.49
4:C1:1646:G:O2'	4:C1:1808:G:N2	2.37	0.49
4:C1:3386:G:OP1	69:Ld:10:ARG:NH2	2.46	0.49
8:SB:86:LEU:HB3	8:SB:98:THR:HB	1.95	0.49
11:SE:85:GLY:N	11:SE:88:ASP:OD2	2.46	0.49
42:LC:206:LEU:HB3	42:LC:248:VAL:HG22	1.95	0.49
48:LI:95:HIS:O	48:LI:125:LEU:CA	2.52	0.49
83:P0:42:ARG:HA	83:P0:45:LEU:H	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:163:G:OP2	1:C2:163:G:N2	2.38	0.49
6:C3:9:A:H2'	6:C3:10:A:C8	2.47	0.49
43:LD:148:ILE:HG22	43:LD:159:VAL:HG21	1.95	0.49
71:Lf:49:ILE:HG12	71:Lf:100:ILE:HG12	1.94	0.49
84:CN:6:LEU:O	84:CN:10:ILE:HG12	2.13	0.49
1:C2:737:A:H5''	11:SE:200:ARG:HH12	1.78	0.48
4:C1:2898:G:N7	78:Lm:125:LYS:NZ	2.59	0.48
12:SF:81:ARG:HG3	12:SF:82:PHE:CD1	2.48	0.48
19:SM:44:GLY:O	19:SM:48:SER:HB2	2.13	0.48
53:LN:73:ARG:HG2	53:LN:75:VAL:HG23	1.95	0.48
59:LT:67:VAL:HG12	59:LT:72:VAL:HG12	1.95	0.48
1:C2:1220:C:H2'	1:C2:1221:A:H8	1.78	0.48
7:SA:62:ARG:NH2	28:SV:37:ALA:O	2.38	0.48
40:LA:136:ILE:HD13	40:LA:148:VAL:HG12	1.95	0.48
43:LD:60:ILE:HB	43:LD:80:SER:HB2	1.95	0.48
48:LI:53:VAL:HG12	48:LI:134:ILE:HD13	1.95	0.48
53:LN:14:LYS:HA	53:LN:19:LEU:HD22	1.95	0.48
4:C1:307:A:H2'	4:C1:308:A:C8	2.48	0.48
4:C1:691:A:N1	6:C3:28:C:O2'	2.42	0.48
4:C1:1261:G:H3'	4:C1:1261:G:N3	2.28	0.48
4:C1:2176:U:OP1	40:LA:54:ARG:NH2	2.46	0.48
4:C1:2724:U:OP2	4:C1:2726:C:N4	2.46	0.48
13:SG:31:ARG:HG3	13:SG:34:GLN:HG3	1.95	0.48
16:SJ:63:ASP:OD1	16:SJ:64:GLU:N	2.46	0.48
26:ST:22:LEU:HB3	26:ST:55:TYR:HD2	1.79	0.48
32:SZ:92:ILE:HD13	32:SZ:100:ILE:HG22	1.94	0.48
39:Sg:205:SER:HB3	39:Sg:210:LEU:HB2	1.94	0.48
8:SB:71:ALA:HB2	8:SB:80:SER:HA	1.94	0.48
23:SQ:20:ALA:HB2	23:SQ:84:ALA:HB1	1.95	0.48
45:LF:77:VAL:HG12	58:LS:59:VAL:HA	1.95	0.48
51:LL:140:SER:OG	51:LL:141:ALA:N	2.45	0.48
54:LO:35:VAL:HB	54:LO:104:VAL:HG13	1.95	0.48
55:LP:122:ALA:HB3	55:LP:143:PRO:HB2	1.96	0.48
1:C2:590:C:H2'	1:C2:591:A:C8	2.48	0.48
1:C2:1202:A:N6	1:C2:1457:C:O5'	2.47	0.48
1:C2:1232:U:H2'	1:C2:1233:G:C8	2.49	0.48
4:C1:744:A:H1'	56:LQ:141:ARG:HE	1.78	0.48
4:C1:3090:U:OP1	41:LB:270:ARG:NH2	2.39	0.48
33:Sa:70:LYS:HE2	33:Sa:72:HIS:CE1	2.47	0.48
42:LC:3:ARG:HH12	42:LC:24:ALA:HB2	1.79	0.48
53:LN:18:VAL:HG23	53:LN:19:LEU:HD12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:LY:101:PRO:HA	64:LY:104:LEU:HB2	1.96	0.48
1:C2:5:U:H2'	1:C2:6:G:H8	1.78	0.48
1:C2:751:G:H2'	1:C2:752:A:H8	1.79	0.48
4:C1:1497:C:H2'	4:C1:1498:A:H8	1.78	0.48
15:SI:84:HIS:NE2	15:SI:97:THR:OG1	2.31	0.48
46:LG:65:LEU:O	46:LG:68:ARG:O	2.32	0.48
57:LR:25:ASP:HB3	57:LR:28:GLU:HB2	1.95	0.48
58:LS:77:VAL:HG22	58:LS:126:VAL:HG23	1.95	0.48
80:Lo:8:ARG:HG2	80:Lo:10:THR:HG23	1.96	0.48
4:C1:1794:G:H4'	40:LA:191:LEU:HD12	1.96	0.48
4:C1:2129:U:H2'	4:C1:2130:G:C8	2.49	0.48
4:C1:3304:U:O2'	41:LB:334:ARG:NH2	2.46	0.48
13:SG:31:ARG:NH2	13:SG:65:GLN:OE1	2.46	0.48
14:SH:70:PHE:O	14:SH:74:GLN:CB	2.53	0.48
15:SI:36:THR:OG1	15:SI:96:LEU:O	2.27	0.48
22:SP:75:PRO:HA	22:SP:93:VAL:HG13	1.95	0.48
28:SV:14:PRO:HB2	28:SV:23:ILE:HD12	1.96	0.48
39:Sg:113:VAL:HA	39:Sg:123:ILE:O	2.13	0.48
45:LF:144:ILE:HD13	45:LF:189:ILE:HG22	1.95	0.48
65:LZ:98:THR:HA	65:LZ:101:PHE:HB2	1.95	0.48
69:Ld:20:LEU:HD11	69:Ld:32:ALA:HB2	1.95	0.48
72:Lg:57:LEU:HB3	72:Lg:61:GLN:HB2	1.95	0.48
1:C2:1220:C:H2'	1:C2:1221:A:C8	2.49	0.48
4:C1:2357:A:H2'	4:C1:2358:A:C8	2.49	0.48
39:Sg:255:ALA:HB2	39:Sg:292:LEU:HG	1.95	0.48
49:LJ:28:ASP:OD1	49:LJ:29:ARG:N	2.46	0.48
51:LL:122:LYS:HG3	73:Lh:118:ILE:HG23	1.95	0.48
58:LS:6:GLU:OE2	58:LS:28:ARG:NE	2.46	0.48
1:C2:704:C:H42	1:C2:734:A:H61	1.60	0.48
4:C1:289:A:H2'	4:C1:290:G:H8	1.79	0.48
4:C1:1657:C:O2'	4:C1:1797:A:OP2	2.28	0.48
4:C1:2880:U:OP1	61:LV:47:ASN:ND2	2.39	0.48
11:SE:147:ILE:HG21	11:SE:169:ILE:HG12	1.96	0.48
13:SG:113:ILE:HD11	13:SG:124:LEU:HD13	1.96	0.48
14:SH:4:PRO:HA	14:SH:7:LYS:HG3	1.96	0.48
41:LB:212:ASN:HD21	41:LB:353:GLU:HA	1.78	0.48
71:Lf:12:LYS:HA	71:Lf:96:ALA:O	2.14	0.48
74:Li:84:LYS:O	74:Li:88:GLU:HG2	2.13	0.48
1:C2:487:G:H2'	1:C2:488:G:C8	2.48	0.48
4:C1:86:G:O2'	4:C1:98:G:O6	2.31	0.48
4:C1:528:U:H2'	4:C1:529:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:671:U:H2'	4:C1:672:A:H8	1.79	0.48
8:SB:34:ALA:O	8:SB:41:ARG:NH1	2.46	0.48
11:SE:71:LYS:HB2	11:SE:91:THR:HB	1.96	0.48
11:SE:141:THR:OG1	11:SE:143:ASP:OD1	2.25	0.48
39:Sg:246:SER:O	39:Sg:250:TYR:N	2.47	0.48
61:LV:18:PRO:HA	61:LV:51:ALA:HA	1.96	0.48
1:C2:76:A:N3	1:C2:80:A:N6	2.62	0.47
1:C2:1601:G:OP1	26:ST:86:ARG:NH2	2.38	0.47
1:C2:1672:G:H2'	1:C2:1673:G:C8	2.49	0.47
4:C1:627:U:H2'	4:C1:628:A:C8	2.49	0.47
4:C1:3016:A:H2'	4:C1:3017:A:C8	2.49	0.47
11:SE:88:ASP:HB2	11:SE:101:LEU:HB2	1.96	0.47
20:SN:47:PRO:HD2	20:SN:86:GLU:HG3	1.96	0.47
22:SP:22:LEU:HA	22:SP:25:LEU:HD12	1.95	0.47
23:SQ:55:VAL:HB	23:SQ:105:LEU:HD22	1.96	0.47
24:SR:46:LEU:O	24:SR:50:ILE:HG12	2.14	0.47
42:LC:75:PRO:HB2	42:LC:89:ALA:HB3	1.95	0.47
42:LC:250:TRP:HE3	42:LC:254:ALA:HB1	1.79	0.47
48:LI:189:GLU:HB2	48:LI:200:LEU:HB3	1.95	0.47
75:Lj:8:PHE:HA	75:Lj:11:ARG:HE	1.79	0.47
4:C1:121:A:N6	46:LG:126:SER:OG	2.46	0.47
4:C1:743:C:N3	56:LQ:141:ARG:NH2	2.62	0.47
33:Sa:35:ALA:O	33:Sa:37:LYS:HG3	2.14	0.47
54:LO:54:TYR:CD1	54:LO:145:VAL:HG21	2.49	0.47
65:LZ:33:SER:OG	65:LZ:35:SER:O	2.28	0.47
1:C2:174:U:H3	1:C2:266:A:H62	1.61	0.47
1:C2:800:U:H2'	1:C2:801:G:H8	1.77	0.47
4:C1:982:C:H2'	4:C1:983:A:C8	2.48	0.47
5:C4:84:A:H2'	5:C4:85:G:C8	2.49	0.47
12:SF:26:ALA:H	23:SQ:26:LYS:HZ3	1.62	0.47
18:SL:2:SER:O	18:SL:116:ARG:NH1	2.47	0.47
53:LN:46:ASP:OD1	53:LN:47:LYS:N	2.46	0.47
69:Ld:11:GLU:OE2	69:Ld:74:ARG:NH1	2.48	0.47
76:Lk:14:LEU:HD11	76:Lk:52:TYR:CG	2.49	0.47
83:P0:56:ASN:HA	83:P0:59:VAL:H	1.79	0.47
84:CN:83:ARG:O	84:CN:87:GLU:HG3	2.14	0.47
1:C2:139:C:O2'	1:C2:177:U:O2	2.32	0.47
1:C2:1357:A:H2'	1:C2:1358:G:H8	1.79	0.47
1:C2:1591:C:H2'	1:C2:1592:A:H8	1.78	0.47
4:C1:515:C:H2'	4:C1:516:A:H8	1.78	0.47
4:C1:1805:C:H2'	4:C1:1806:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:2960:C:H2'	4:C1:2961:G:C8	2.48	0.47
30:SX:142:LYS:O	30:SX:144:ARG:NH1	2.47	0.47
39:Sg:258:THR:HG22	39:Sg:275:ARG:NH1	2.29	0.47
49:LJ:102:PHE:CD1	49:LJ:131:MET:HE1	2.50	0.47
76:Lk:26:LYS:NZ	76:Lk:28:ASN:OD1	2.46	0.47
3:C5:11:C:H2'	3:C5:12:G:C8	2.49	0.47
4:C1:2307:G:O2'	4:C1:2310:U:OP2	2.30	0.47
4:C1:2896:A:OP1	78:Lm:124:LYS:NZ	2.38	0.47
15:SI:7:SER:O	15:SI:18:ARG:NH2	2.47	0.47
15:SI:60:ILE:HD12	15:SI:179:CYS:HB2	1.96	0.47
31:SY:124:ARG:HG3	31:SY:127:LYS:HE2	1.95	0.47
35:Sc:19:THR:HG21	35:Sc:27:GLN:HE21	1.79	0.47
39:Sg:13:LEU:HB3	39:Sg:45:TRP:CZ3	2.49	0.47
41:LB:348:ARG:HA	41:LB:351:LEU:HB2	1.96	0.47
61:LV:129:VAL:O	61:LV:133:SER:OG	2.27	0.47
68:Lc:33:SER:HB2	68:Lc:93:LEU:HD21	1.96	0.47
68:Lc:55:GLU:OE2	72:Lg:90:ILE:HG23	2.14	0.47
1:C2:578:U:H4'	1:C2:579:A:H5'	1.95	0.47
4:C1:901:G:OP1	75:Lj:13:ASN:ND2	2.35	0.47
4:C1:1233:G:H5''	83:P0:38:MET:C	2.40	0.47
4:C1:3233:C:H2'	4:C1:3234:A:C8	2.48	0.47
4:C1:3308:C:O2'	55:LP:69:ARG:O	2.25	0.47
9:SC:69:ILE:HA	9:SC:72:LEU:HB3	1.97	0.47
9:SC:73:LEU:HD13	9:SC:76:LEU:HD13	1.95	0.47
25:SS:13:HIS:CG	25:SS:14:ILE:H	2.33	0.47
30:SX:59:ILE:HD12	30:SX:118:PRO:HD2	1.95	0.47
41:LB:56:ILE:HG21	41:LB:356:LEU:HD22	1.95	0.47
48:LI:44:ASP:OD1	48:LI:185:ARG:NH2	2.47	0.47
53:LN:158:HIS:HB3	53:LN:161:ALA:HB3	1.97	0.47
58:LS:83:SER:OG	58:LS:84:ARG:N	2.48	0.47
66:La:26:ARG:HB2	66:La:29:PRO:HG3	1.96	0.47
66:La:36:GLY:HA3	66:La:40:HIS:CE1	2.50	0.47
69:Ld:78:LYS:HE3	69:Ld:90:PHE:HD2	1.78	0.47
76:Lk:61:LYS:HA	76:Lk:64:LYS:HG2	1.97	0.47
1:C2:753:A:OP2	11:SE:187:ARG:NH1	2.48	0.47
1:C2:1473:U:O4	12:SF:180:ARG:NE	2.47	0.47
4:C1:215:G:OP1	64:LY:12:ARG:NH1	2.42	0.47
4:C1:650:C:H2'	4:C1:651:G:C8	2.50	0.47
4:C1:1203:A:H2'	4:C1:1204:A:H8	1.80	0.47
4:C1:1243:G:O4'	50:LK:59:THR:N	2.47	0.47
4:C1:2897:A:H2'	4:C1:2899:C:H5''	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:3121:U:H1'	4:C1:3122:A:H5''	1.97	0.47
8:SB:87:ARG:HG3	8:SB:101:HIS:HB2	1.95	0.47
8:SB:121:ILE:O	8:SB:140:ILE:HA	2.15	0.47
14:SH:38:LEU:HA	14:SH:41:LEU:HD12	1.97	0.47
14:SH:50:ASP:HA	14:SH:56:LYS:HD2	1.94	0.47
14:SH:57:ALA:HA	14:SH:89:HIS:O	2.14	0.47
46:LG:171:LYS:NZ	46:LG:223:ALA:O	2.47	0.47
58:LS:66:GLU:OE2	58:LS:99:ARG:N	2.38	0.47
61:LV:87:ARG:O	61:LV:90:GLY:N	2.42	0.47
66:La:104:THR:HG21	66:La:112:ILE:HD11	1.96	0.47
84:CN:53:ILE:O	84:CN:57:GLN:HG2	2.14	0.47
1:C2:538:A:OP2	16:SJ:175:ARG:NH1	2.48	0.47
1:C2:1222:C:H2'	1:C2:1223:A:H8	1.80	0.47
4:C1:1241:U:OP1	50:LK:57:LYS:N	2.47	0.47
4:C1:2476:C:N4	4:C1:2477:G:O6	2.48	0.47
12:SF:98:MET:HE3	12:SF:107:LYS:HB3	1.97	0.47
23:SQ:114:ARG:HA	23:SQ:114:ARG:HD3	1.74	0.47
24:SR:34:LEU:O	24:SR:38:ILE:HG12	2.13	0.47
49:LJ:21:ILE:HG12	49:LJ:125:MET:HB3	1.96	0.47
53:LN:68:ARG:CB	53:LN:126:THR:O	2.63	0.47
54:LO:106:GLU:HG2	54:LO:147:TRP:CZ2	2.50	0.47
80:Lo:28:TYR:HD1	80:Lo:71:ARG:HH21	1.62	0.47
1:C2:975:C:H5''	20:SN:109:LYS:HD2	1.97	0.47
4:C1:2510:U:H2'	4:C1:2511:A:H8	1.80	0.47
4:C1:2772:C:H4'	4:C1:2773:C:H5'	1.96	0.47
4:C1:2988:C:OP1	54:LO:65:ASN:ND2	2.48	0.47
4:C1:3322:A:H2'	4:C1:3323:A:C8	2.50	0.47
9:SC:81:MET:HG3	9:SC:211:LEU:HD11	1.97	0.47
13:SG:132:ARG:HG3	13:SG:133:LEU:HD12	1.97	0.47
51:LL:74:GLY:HA3	51:LL:98:ASP:HB2	1.96	0.47
54:LO:62:THR:HG22	54:LO:65:ASN:H	1.80	0.47
55:LP:88:VAL:HA	55:LP:91:VAL:HG12	1.96	0.47
56:LQ:123:THR:OG1	56:LQ:126:GLN:OE1	2.23	0.47
4:C1:94:G:H2'	4:C1:95:A:C8	2.50	0.47
4:C1:1899:G:O2'	4:C1:2334:U:O4	2.27	0.47
7:SA:56:LYS:HD3	28:SV:82:VAL:HG11	1.96	0.47
19:SM:42:ALA:HB3	19:SM:122:VAL:HB	1.97	0.47
20:SN:61:THR:H	20:SN:66:ILE:HD11	1.79	0.47
20:SN:101:HIS:NE2	20:SN:108:ASP:OD2	2.48	0.47
24:SR:71:PHE:HE2	24:SR:73:LEU:HB3	1.80	0.47
55:LP:119:VAL:HG12	55:LP:146:ILE:HG23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Lf:56:SER:O	71:Lf:63:LYS:NZ	2.40	0.47
80:Lo:2:VAL:N	80:Lo:90:HIS:O	2.48	0.47
1:C2:231:U:O2	1:C2:235:G:N2	2.47	0.46
4:C1:716:A:OP1	4:C1:752:C:O2'	2.33	0.46
4:C1:1666:G:H2'	4:C1:1667:A:C8	2.50	0.46
45:LF:98:LYS:HG2	45:LF:129:LEU:HD21	1.97	0.46
47:LH:105:GLU:OE2	47:LH:109:ALA:N	2.41	0.46
54:LO:189:ASP:OD1	54:LO:190:VAL:N	2.47	0.46
61:LV:54:LEU:HB2	61:LV:81:GLN:HE21	1.80	0.46
61:LV:54:LEU:HD11	61:LV:79:VAL:C	2.40	0.46
1:C2:513:U:H2'	1:C2:514:G:C8	2.51	0.46
1:C2:1115:U:H2'	1:C2:1116:A:H8	1.80	0.46
4:C1:19:U:H2'	4:C1:20:A:C8	2.50	0.46
4:C1:1255:C:H2'	4:C1:1256:G:H8	1.78	0.46
4:C1:1802:C:O2'	72:Lg:59:PRO:O	2.33	0.46
4:C1:3015:G:H2'	4:C1:3016:A:H8	1.80	0.46
20:SN:42:ARG:HD3	20:SN:80:LEU:HD21	1.96	0.46
21:SO:117:ASP:OD1	21:SO:119:THR:OG1	2.32	0.46
39:Sg:307:ASP:OD1	39:Sg:307:ASP:N	2.48	0.46
47:LH:90:MET:HG3	47:LH:181:VAL:HA	1.97	0.46
70:Le:63:THR:HA	70:Le:66:LEU:HD12	1.97	0.46
1:C2:237:C:O2'	1:C2:238:U:O4'	2.32	0.46
1:C2:1228:G:H5'	19:SM:45:LEU:HG	1.98	0.46
1:C2:1490:C:H5'	1:C2:1492:A:H1'	1.96	0.46
4:C1:2284:C:N4	4:C1:2308:C:OP2	2.46	0.46
25:SS:63:GLN:O	25:SS:66:LEU:N	2.49	0.46
39:Sg:50:ASP:HB3	39:Sg:53:LYS:O	2.16	0.46
43:LD:146:LEU:HD22	43:LD:163:LEU:HD13	1.96	0.46
46:LG:161:GLU:HA	46:LG:164:VAL:HG22	1.97	0.46
47:LH:57:VAL:HG22	47:LH:68:LEU:HD22	1.96	0.46
1:C2:1444:A:H4'	1:C2:1445:G:H5'	1.97	0.46
4:C1:1546:A:O2'	53:LN:104:GLU:OE2	2.30	0.46
9:SC:109:GLY:HA2	9:SC:139:ILE:HG22	1.97	0.46
9:SC:235:LEU:HD12	9:SC:236:PRO:HD2	1.97	0.46
31:SY:38:ASP:OD1	31:SY:39:GLU:N	2.47	0.46
32:SZ:49:ARG:O	32:SZ:52:LYS:N	2.47	0.46
65:LZ:18:TYR:HA	65:LZ:21:LYS:HD2	1.97	0.46
68:Lc:14:LEU:HA	68:Lc:17:VAL:HG12	1.97	0.46
70:Le:25:TYR:HB2	70:Le:28:VAL:HG22	1.97	0.46
1:C2:78:A:H2'	1:C2:79:C:C6	2.50	0.46
1:C2:1211:A:N3	22:SP:97:TYR:OH	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:1524:A:H2'	1:C2:1525:A:C8	2.51	0.46
4:C1:792:G:H5''	66:La:2:PRO:HD2	1.97	0.46
4:C1:1778:G:O2'	4:C1:1780:G:OP2	2.32	0.46
4:C1:2413:A:H2'	4:C1:2414:G:H8	1.81	0.46
4:C1:2457:G:C2	4:C1:2486:A:N1	2.84	0.46
5:C4:4:U:H2'	5:C4:5:G:H8	1.81	0.46
18:SL:10:GLU:OE2	18:SL:14:GLN:HG2	2.16	0.46
75:Lj:8:PHE:HD1	75:Lj:11:ARG:HE	1.63	0.46
1:C2:852:C:H2'	1:C2:853:G:C8	2.51	0.46
4:C1:307:A:H2'	4:C1:308:A:H8	1.80	0.46
4:C1:1194:G:H2'	4:C1:1195:A:C8	2.51	0.46
4:C1:2103:U:H2'	4:C1:2104:A:C8	2.51	0.46
4:C1:2423:U:H2'	4:C1:2424:A:C8	2.50	0.46
4:C1:2540:A:N3	4:C1:2541:U:N3	2.63	0.46
4:C1:3070:A:OP1	57:LR:62:ARG:NH1	2.44	0.46
13:SG:34:GLN:O	13:SG:51:LYS:HA	2.16	0.46
29:SW:25:VAL:HG22	29:SW:63:VAL:HB	1.98	0.46
39:Sg:258:THR:HG22	39:Sg:275:ARG:HH12	1.81	0.46
43:LD:287:ALA:HA	43:LD:290:ILE:HD12	1.97	0.46
76:Lk:2:ALA:N	76:Lk:51:LEU:O	2.49	0.46
80:Lo:46:LYS:HE2	80:Lo:54:THR:HB	1.97	0.46
1:C2:31:C:O2'	1:C2:547:U:OP1	2.34	0.46
1:C2:1735:U:OP1	61:LV:32:ARG:NH1	2.43	0.46
4:C1:1672:U:OP1	57:LR:64:ARG:NH1	2.49	0.46
5:C4:44:C:H2'	5:C4:45:A:H8	1.81	0.46
5:C4:72:A:O2'	5:C4:74:C:OP1	2.29	0.46
7:SA:148:ASP:OD1	7:SA:149:LEU:N	2.46	0.46
16:SJ:135:ALA:HB2	16:SJ:140:ILE:HG22	1.98	0.46
42:LC:286:VAL:HG11	56:LQ:31:LYS:HD2	1.98	0.46
1:C2:1556:A:O5'	22:SP:40:ARG:NH2	2.48	0.46
4:C1:831:G:O2'	4:C1:1864:A:N3	2.40	0.46
4:C1:1635:G:N2	4:C1:1638:A:OP2	2.39	0.46
4:C1:1724:U:H1'	4:C1:1725:C:C6	2.51	0.46
7:SA:125:ASP:O	7:SA:129:ASP:HB2	2.16	0.46
9:SC:120:GLU:OE1	9:SC:123:GLY:N	2.37	0.46
10:SD:206:VAL:HG12	10:SD:208:ILE:HD11	1.98	0.46
11:SE:197:HIS:HB3	11:SE:209:HIS:HB2	1.97	0.46
12:SF:160:VAL:HA	35:Sc:61:ARG:HH12	1.81	0.46
20:SN:87:ASP:OD1	20:SN:87:ASP:N	2.47	0.46
28:SV:87:ARG:HH12	34:Sb:2:VAL:HG23	1.80	0.46
43:LD:278:SER:OG	43:LD:281:GLU:OE1	2.22	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:LG:172:LYS:HD2	74:Li:39:PHE:HE1	1.79	0.46
61:LV:10:LYS:HB2	61:LV:125:LEU:HD21	1.98	0.46
61:LV:15:LEU:HD13	61:LV:51:ALA:HB3	1.96	0.46
1:C2:1556:A:H8	22:SP:40:ARG:HH21	1.64	0.46
4:C1:240:U:H4'	4:C1:241:G:H5'	1.98	0.46
4:C1:1258:U:H2'	4:C1:1259:A:H2'	1.97	0.46
12:SF:57:SER:HA	35:Sc:53:ILE:HB	1.98	0.46
14:SH:109:VAL:HG23	14:SH:110:GLN:HG2	1.98	0.46
45:LF:74:SER:OG	59:LT:141:VAL:O	2.25	0.46
46:LG:41:GLN:OE1	46:LG:44:ARG:NH1	2.43	0.46
47:LH:91:ARG:HG2	47:LH:182:SER:HB3	1.98	0.46
70:Le:100:ILE:O	70:Le:105:ARG:NH1	2.49	0.46
1:C2:107:C:H2'	1:C2:108:A:C8	2.51	0.46
4:C1:3163:A:N6	4:C1:3288:G:O6	2.49	0.46
17:SK:32:HIS:CE1	17:SK:42:VAL:HG11	2.51	0.46
21:SO:135:ARG:HH21	21:SO:137:LEU:HD11	1.81	0.46
23:SQ:9:THR:HG21	23:SQ:88:GLY:HA2	1.98	0.46
30:SX:53:VAL:HA	30:SX:74:VAL:HG12	1.97	0.46
59:LT:18:ASP:OD1	59:LT:19:PHE:N	2.48	0.46
68:Lc:99:ASP:OD1	68:Lc:99:ASP:N	2.49	0.46
80:Lo:74:CYS:HB3	80:Lo:79:THR:HG22	1.97	0.46
1:C2:61:A:O2'	1:C2:62:A:O4'	2.34	0.45
1:C2:953:G:H2'	1:C2:954:G:C8	2.52	0.45
1:C2:959:U:H6	20:SN:61:THR:HG23	1.81	0.45
4:C1:121:A:C2	46:LG:129:PRO:HB3	2.51	0.45
4:C1:1242:G:H1'	50:LK:17:ALA:H	1.80	0.45
86:C1:3403:T1C:H722	75:Lj:75:LYS:HB2	1.98	0.45
11:SE:21:ASP:OD2	11:SE:24:SER:OG	2.32	0.45
19:SM:76:GLU:OE1	19:SM:80:ASN:ND2	2.50	0.45
37:Se:29:LYS:O	37:Se:31:LYS:NZ	2.44	0.45
58:LS:90:MET:HE1	58:LS:114:HIS:CE1	2.51	0.45
83:P0:38:MET:O	83:P0:39:HIS:C	2.59	0.45
84:CN:10:ILE:O	84:CN:14:LEU:HD23	2.16	0.45
1:C2:32:U:O2'	1:C2:594:A:N1	2.46	0.45
1:C2:199:G:H2'	1:C2:200:A:C8	2.50	0.45
1:C2:1471:A:OP1	12:SF:185:ARG:NH1	2.45	0.45
1:C2:1555:A:O2'	22:SP:82:ASN:ND2	2.38	0.45
4:C1:1239:C:H5''	50:LK:77:ALA:HB1	1.98	0.45
4:C1:3214:U:C4	52:LM:121:MET:HG3	2.51	0.45
5:C4:31:U:O3'	43:LD:218:ARG:NH2	2.48	0.45
11:SE:87:MET:HE2	11:SE:123:LEU:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SG:44:GLU:O	13:SG:119:GLN:NE2	2.49	0.45
15:SI:64:ASN:O	15:SI:180:ASP:HA	2.16	0.45
26:ST:134:ARG:O	26:ST:138:GLN:OE1	2.35	0.45
1:C2:67:A:N6	1:C2:83:G:O2'	2.50	0.45
1:C2:194:U:H2'	1:C2:195:G:H4'	1.98	0.45
1:C2:1041:G:H2'	1:C2:1042:G:C8	2.51	0.45
4:C1:297:G:OP2	4:C1:297:G:N2	2.35	0.45
4:C1:340:C:OP2	42:LC:195:ARG:NH1	2.38	0.45
4:C1:370:U:H4'	4:C1:404:G:H5'	1.98	0.45
4:C1:914:A:C2	40:LA:204:MET:HG2	2.51	0.45
9:SC:227:PRO:HA	9:SC:230:TRP:CG	2.51	0.45
11:SE:30:ARG:O	11:SE:81:THR:OG1	2.34	0.45
11:SE:121:TYR:HA	11:SE:163:ASP:HA	1.98	0.45
13:SG:10:ASN:HD22	13:SG:128:THR:HG22	1.78	0.45
26:ST:109:GLU:OE2	26:ST:122:ARG:NE	2.35	0.45
39:Sg:152:SER:N	39:Sg:172:ALA:O	2.48	0.45
39:Sg:209:THR:OG1	39:Sg:224:ASN:OD1	2.32	0.45
41:LB:92:TYR:HB2	41:LB:157:VAL:HB	1.98	0.45
44:LE:146:ILE:HG23	44:LE:150:LYS:HE2	1.98	0.45
51:LL:18:TRP:O	51:LL:21:ARG:C	2.59	0.45
1:C2:884:A:H2'	1:C2:885:G:C8	2.50	0.45
1:C2:1795:U:H5'	33:Sa:79:ILE:HD11	1.98	0.45
4:C1:673:U:H2'	4:C1:674:G:C8	2.52	0.45
4:C1:874:U:OP2	41:LB:241:LYS:NZ	2.47	0.45
4:C1:1241:U:H5''	50:LK:79:SER:N	2.32	0.45
4:C1:1666:G:H2'	4:C1:1667:A:H8	1.81	0.45
4:C1:1675:G:H2'	4:C1:1676:A:H8	1.81	0.45
4:C1:2376:G:H2'	4:C1:2377:G:C8	2.52	0.45
12:SF:120:ILE:HD11	32:SZ:98:GLN:HE22	1.81	0.45
27:SU:30:LYS:HB2	27:SU:33:GLN:HG2	1.98	0.45
44:LE:175:LYS:NZ	52:LM:111:ALA:HA	2.31	0.45
48:LI:212:GLU:HG3	48:LI:213:PHE:CD2	2.51	0.45
49:LJ:131:MET:HB2	49:LJ:131:MET:HE3	1.53	0.45
1:C2:1369:U:OP2	26:ST:69:LYS:NZ	2.48	0.45
1:C2:1611:A:O2'	12:SF:95:ASN:O	2.34	0.45
4:C1:649:A:OP2	4:C1:2868:U:O2'	2.33	0.45
4:C1:1637:A:H5''	65:LZ:16:GLY:HA3	1.97	0.45
4:C1:1740:U:H4'	4:C1:1741:A:H5'	1.98	0.45
4:C1:1921:A:H2'	4:C1:1922:A:C8	2.51	0.45
4:C1:2683:U:H2'	4:C1:2684:C:C6	2.52	0.45
8:SB:30:PHE:HB3	8:SB:96:LEU:HD22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SF:103:ASN:HA	12:SF:106:LYS:HE2	1.98	0.45
16:SJ:86:LEU:HG	16:SJ:90:LYS:HB3	1.98	0.45
25:SS:52:VAL:HG13	25:SS:61:LEU:HD22	1.99	0.45
26:ST:65:ILE:HG21	26:ST:114:VAL:HG12	1.98	0.45
39:Sg:246:SER:HB3	39:Sg:251:TRP:H	1.81	0.45
41:LB:187:SER:O	41:LB:190:GLU:N	2.49	0.45
45:LF:120:THR:H	45:LF:123:THR:HG1	1.62	0.45
57:LR:91:SER:HA	57:LR:94:VAL:HG12	1.97	0.45
81:Lp:36:ARG:HG2	81:Lp:48:LYS:HD3	1.97	0.45
1:C2:304:U:H5''	18:SL:136:ARG:HD3	1.99	0.45
1:C2:513:U:H4'	16:SJ:131:GLN:HB3	1.99	0.45
4:C1:1497:C:H2'	4:C1:1498:A:C8	2.52	0.45
11:SE:42:LEU:HB2	11:SE:109:PHE:CE2	2.51	0.45
14:SH:98:ILE:HG12	14:SH:121:VAL:HG11	1.97	0.45
21:SO:42:VAL:HG21	21:SO:66:ASP:HB3	1.98	0.45
56:LQ:170:ARG:NH1	66:La:56:VAL:O	2.38	0.45
1:C2:399:A:N3	11:SE:3:ARG:NH1	2.65	0.45
4:C1:1015:U:O2'	4:C1:1017:C:OP2	2.31	0.45
4:C1:2688:U:N3	43:LD:17:GLN:O	2.41	0.45
4:C1:3183:A:OP1	54:LO:37:ARG:NH2	2.48	0.45
18:SL:123:VAL:HG22	18:SL:142:VAL:HG22	1.99	0.45
21:SO:81:VAL:HG11	21:SO:102:LEU:HD13	1.98	0.45
30:SX:42:PRO:HG3	30:SX:121:ARG:HE	1.82	0.45
36:Sd:6:VAL:HG23	36:Sd:7:TRP:CD1	2.51	0.45
80:Lo:73:GLU:HA	80:Lo:79:THR:O	2.17	0.45
1:C2:167:U:H5''	13:SG:135:PRO:HA	1.99	0.45
4:C1:120:G:N2	46:LG:126:SER:O	2.48	0.45
4:C1:149:U:P	53:LN:49:ARG:HH12	2.40	0.45
4:C1:835:G:O2'	4:C1:857:G:N2	2.37	0.45
4:C1:3295:A:H2'	4:C1:3296:A:C8	2.51	0.45
6:C3:135:G:H5''	63:LX:49:LYS:HD2	1.99	0.45
14:SH:31:SER:HB3	14:SH:34:LEU:HB2	1.99	0.45
47:LH:92:TYR:CD1	47:LH:179:ILE:HG12	2.51	0.45
47:LH:174:LYS:HE3	78:Lm:127:LEU:HD21	1.98	0.45
51:LL:172:LEU:O	51:LL:176:GLU:HG3	2.16	0.45
55:LP:116:HIS:HB3	55:LP:149:VAL:HG22	1.98	0.45
56:LQ:38:ARG:NE	56:LQ:39:ARG:HG3	2.32	0.45
63:LX:88:MET:HE1	77:Ll:7:PHE:CE1	2.52	0.45
1:C2:135:A:H4'	1:C2:136:C:H5'	1.99	0.45
1:C2:329:G:H2'	1:C2:330:G:H8	1.81	0.45
1:C2:861:U:H2'	1:C2:862:A:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:348:A:N3	4:C1:352:A:O2'	2.50	0.45
4:C1:439:C:O2'	4:C1:494:G:N2	2.36	0.45
4:C1:1258:U:H2'	4:C1:1259:A:C3'	2.47	0.45
7:SA:77:SER:HB2	7:SA:86:VAL:HG11	1.99	0.45
10:SD:25:PHE:O	10:SD:29:LEU:CB	2.65	0.45
12:SF:44:ASN:HA	23:SQ:46:PHE:HE2	1.81	0.45
21:SO:84:ARG:HG3	21:SO:119:THR:HA	1.98	0.45
27:SU:51:VAL:HG23	27:SU:52:LYS:H	1.82	0.45
39:Sg:216:LYS:HG3	39:Sg:239:GLU:OE1	2.16	0.45
42:LC:150:LEU:HB3	42:LC:249:ILE:HG22	1.99	0.45
75:Lj:27:PHE:HA	75:Lj:34:CYS:HA	1.98	0.45
84:CN:64:LYS:HG2	84:CN:83:ARG:HH22	1.82	0.45
1:C2:107:C:H2'	1:C2:108:A:H8	1.81	0.45
1:C2:1393:C:H2'	1:C2:1394:G:H8	1.82	0.45
1:C2:1564:U:OP1	26:ST:38:LYS:NZ	2.35	0.45
4:C1:571:U:H2'	4:C1:572:A:H8	1.82	0.45
4:C1:994:G:N2	4:C1:995:U:O4	2.39	0.45
7:SA:41:ARG:N	7:SA:45:VAL:O	2.34	0.45
13:SG:50:PHE:HB3	13:SG:111:LEU:HD22	1.98	0.45
15:SI:61:GLU:HG3	15:SI:62:THR:HG22	1.99	0.45
15:SI:153:GLU:N	15:SI:153:GLU:OE1	2.49	0.45
30:SX:42:PRO:HG3	30:SX:121:ARG:HH21	1.82	0.45
51:LL:75:PHE:H	51:LL:97:VAL:HA	1.81	0.45
58:LS:72:VAL:HA	58:LS:97:VAL:HA	1.98	0.45
1:C2:5:U:H2'	1:C2:6:G:C8	2.52	0.44
4:C1:531:G:H2'	4:C1:532:A:C8	2.52	0.44
4:C1:1236:G:H3'	50:LK:120:SER:CA	2.47	0.44
6:C3:13:A:O2'	55:LP:121:GLN:O	2.34	0.44
31:SY:32:ARG:HB3	31:SY:33:ALA:H	1.59	0.44
37:Se:23:LYS:HE2	37:Se:23:LYS:HB2	1.69	0.44
42:LC:152:VAL:HG21	42:LC:156:LEU:HD23	1.99	0.44
73:Lh:31:LEU:HB3	73:Lh:44:ILE:HG22	1.99	0.44
1:C2:142:G:H5''	13:SG:139:ASN:HD21	1.82	0.44
1:C2:1691:A:H2'	1:C2:1692:G:C8	2.53	0.44
4:C1:3295:A:H5'	41:LB:119:TYR:HE1	1.83	0.44
4:C1:3303:G:O2'	4:C1:3305:A:N6	2.48	0.44
10:SD:135:GLU:HG2	10:SD:187:LYS:HB3	1.99	0.44
23:SQ:93:HIS:HA	23:SQ:97:VAL:HG22	2.00	0.44
40:LA:112:ILE:HG22	40:LA:135:ILE:HG12	1.99	0.44
42:LC:180:LYS:O	42:LC:184:SER:CB	2.65	0.44
44:LE:38:THR:OG1	44:LE:39:VAL:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:LV:84:SER:HA	61:LV:94:TYR:HB3	1.99	0.44
69:Ld:16:LEU:HA	69:Ld:19:ARG:HB2	1.98	0.44
84:CN:35:ASP:O	84:CN:37:SER:N	2.50	0.44
1:C2:540:G:N2	1:C2:542:A:N7	2.65	0.44
1:C2:1202:A:H1'	1:C2:1207:C:N4	2.33	0.44
4:C1:696:C:OP2	42:LC:119:ARG:NH2	2.50	0.44
4:C1:2097:U:H2'	4:C1:2098:C:C6	2.52	0.44
4:C1:3116:G:OP1	4:C1:3116:G:N2	2.49	0.44
12:SF:61:TYR:CD2	12:SF:164:PRO:HB2	2.52	0.44
12:SF:63:GLN:HE22	12:SF:66:GLN:HB2	1.83	0.44
15:SI:76:THR:HG21	15:SI:104:ILE:HD12	2.00	0.44
23:SQ:86:ALA:O	23:SQ:90:VAL:HG23	2.18	0.44
23:SQ:116:LEU:HB3	23:SQ:117:LEU:H	1.72	0.44
45:LF:124:LEU:HD23	45:LF:124:LEU:HA	1.87	0.44
80:Lo:71:ARG:HD2	80:Lo:80:ARG:HD3	1.98	0.44
81:Lp:46:THR:O	81:Lp:57:CYS:HA	2.17	0.44
1:C2:798:C:H2'	1:C2:799:A:H8	1.83	0.44
1:C2:1433:G:N2	36:Sd:45:GLU:OE2	2.43	0.44
1:C2:1641:C:H2'	1:C2:1642:G:C8	2.53	0.44
4:C1:1886:A:O2'	41:LB:226:PHE:O	2.33	0.44
6:C3:142:C:H2'	6:C3:143:U:C6	2.53	0.44
8:SB:82:ARG:HG2	8:SB:105:PHE:CE1	2.53	0.44
11:SE:42:LEU:HD22	11:SE:109:PHE:HD2	1.82	0.44
11:SE:158:ASP:OD1	11:SE:159:THR:N	2.46	0.44
14:SH:132:PRO:HB2	14:SH:161:GLN:HE21	1.82	0.44
14:SH:153:LEU:HD23	14:SH:184:GLU:HB2	1.98	0.44
18:SL:75:VAL:HG12	18:SL:86:ILE:HG12	1.99	0.44
19:SM:50:LYS:HE3	38:Sf:129:GLY:CA	2.47	0.44
41:LB:284:ARG:HB3	41:LB:323:MET:HB3	1.98	0.44
48:LI:38:LYS:HG2	48:LI:41:ALA:HB2	1.98	0.44
53:LN:36:ILE:HG12	53:LN:64:VAL:HG23	1.99	0.44
1:C2:273:G:H1	1:C2:283:U:H3	1.64	0.44
1:C2:1462:G:O2'	3:C5:29:G:OP1	2.36	0.44
3:C5:43:A:OP2	84:CN:107:LYS:NZ	2.42	0.44
4:C1:1477:A:OP1	4:C1:3075:G:O2'	2.28	0.44
4:C1:1832:C:OP1	63:LX:120:LYS:NZ	2.39	0.44
5:C4:115:G:N2	43:LD:72:ASP:O	2.44	0.44
11:SE:98:ASN:HB2	11:SE:114:ILE:HG13	2.00	0.44
14:SH:151:LYS:NZ	14:SH:184:GLU:HG3	2.33	0.44
21:SO:84:ARG:HD2	21:SO:120:PRO:HD3	1.98	0.44
28:SV:3:ASN:OD1	28:SV:7:GLN:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LB:41:VAL:HG12	41:LB:185:GLY:HA3	1.99	0.44
44:LE:170:LYS:HB3	44:LE:172:HIS:CE1	2.51	0.44
46:LG:157:VAL:HG21	46:LG:163:VAL:HG21	2.00	0.44
49:LJ:9:MET:HE2	49:LJ:9:MET:HB2	1.72	0.44
51:LL:45:LYS:HB3	51:LL:45:LYS:HE2	1.76	0.44
66:La:17:ALA:O	66:La:19:LYS:N	2.51	0.44
4:C1:1562:C:H2'	4:C1:1563:C:C6	2.53	0.44
4:C1:2106:A:H2'	4:C1:2107:A:C8	2.53	0.44
4:C1:2131:A:N1	81:Lp:17:ARG:HB2	2.33	0.44
4:C1:2218:G:H2'	4:C1:2219:A:H8	1.82	0.44
4:C1:2768:U:H2'	4:C1:2769:A:C8	2.51	0.44
21:SO:36:LYS:HA	21:SO:36:LYS:HD2	1.80	0.44
25:SS:49:LYS:NZ	25:SS:80:LYS:O	2.50	0.44
27:SU:45:ALA:O	27:SU:48:HIS:O	2.36	0.44
49:LJ:77:GLU:OE2	49:LJ:167:TYR:OH	2.26	0.44
62:LW:8:PHE:HZ	62:LW:49:ILE:HG13	1.83	0.44
4:C1:341:G:O2'	6:C3:22:U:O4	2.26	0.44
4:C1:629:U:H2'	4:C1:630:A:C8	2.52	0.44
4:C1:1119:C:H2'	4:C1:1120:A:H8	1.82	0.44
4:C1:2266:U:H2'	4:C1:2267:C:C6	2.52	0.44
4:C1:2473:C:OP2	4:C1:2474:G:N2	2.51	0.44
4:C1:2482:U:H2'	4:C1:2483:G:C8	2.52	0.44
7:SA:59:LEU:O	7:SA:63:ILE:HG12	2.17	0.44
14:SH:39:ARG:HD2	14:SH:39:ARG:HA	1.70	0.44
32:SZ:92:ILE:HD11	32:SZ:102:THR:HG22	2.00	0.44
43:LD:50:ARG:NH2	43:LD:72:ASP:OD2	2.51	0.44
45:LF:165:ASP:HB3	45:LF:168:ILE:HG12	1.98	0.44
48:LI:65:LEU:HD23	48:LI:159:PHE:CE1	2.53	0.44
49:LJ:80:LEU:HD12	49:LJ:129:VAL:HG11	2.00	0.44
51:LL:48:PRO:HB3	51:LL:137:GLN:HB2	2.00	0.44
53:LN:192:LYS:O	53:LN:196:THR:HG23	2.18	0.44
58:LS:93:GLU:HG2	58:LS:137:ARG:HG2	2.00	0.44
58:LS:152:LEU:HB2	58:LS:172:TYR:CZ	2.53	0.44
59:LT:39:ILE:HD12	59:LT:102:ARG:HH21	1.82	0.44
76:Lk:46:ARG:HH11	76:Lk:51:LEU:HB2	1.83	0.44
80:Lo:36:PHE:O	80:Lo:41:ARG:NH1	2.50	0.44
1:C2:1500:C:P	26:ST:122:ARG:HH22	2.40	0.44
4:C1:154:U:OP2	73:Lh:103:LYS:NZ	2.38	0.44
4:C1:1096:U:N3	86:C1:3404:T1C:H51	2.32	0.44
4:C1:2344:U:H2'	4:C1:2345:A:C8	2.53	0.44
11:SE:143:ASP:OD1	11:SE:143:ASP:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:SI:184:LEU:HD23	15:SI:189:LEU:HA	1.99	0.44
22:SP:56:PHE:CE1	22:SP:78:THR:HB	2.53	0.44
31:SY:59:GLY:O	31:SY:71:GLY:CA	2.66	0.44
31:SY:59:GLY:O	31:SY:71:GLY:HA2	2.17	0.44
33:Sa:11:ASN:OD1	33:Sa:11:ASN:N	2.49	0.44
33:Sa:39:MET:HE1	33:Sa:70:LYS:HD3	1.99	0.44
39:Sg:248:ASN:ND2	39:Sg:297:ASP:OD1	2.51	0.44
45:LF:119:VAL:HG23	59:LT:135:PRO:HG3	2.00	0.44
47:LH:67:ALA:HA	47:LH:70:THR:HG22	1.99	0.44
57:LR:98:ARG:NH2	57:LR:132:PHE:O	2.51	0.44
58:LS:14:LEU:HA	58:LS:15:PRO:HD3	1.88	0.44
1:C2:609:U:O2	30:SX:19:ARG:NH1	2.50	0.44
1:C2:959:U:C6	20:SN:61:THR:HG23	2.53	0.44
4:C1:3149:G:O2'	41:LB:129:ALA:O	2.28	0.44
7:SA:39:ASN:OD1	7:SA:40:ALA:N	2.50	0.44
14:SH:155:ASP:OD1	14:SH:156:SER:N	2.48	0.44
21:SO:15:GLY:HA3	21:SO:76:ILE:HD11	2.00	0.44
25:SS:126:ARG:NH2	25:SS:132:ARG:O	2.51	0.44
40:LA:79:ASN:ND2	40:LA:165:VAL:HG12	2.33	0.44
41:LB:229:VAL:HG21	41:LB:249:VAL:HG23	2.00	0.44
48:LI:28:ASP:OD1	48:LI:29:SER:N	2.51	0.44
51:LL:131:LYS:HD2	51:LL:131:LYS:HA	1.75	0.44
59:LT:37:GLY:N	59:LT:64:VAL:O	2.45	0.44
1:C2:186:C:H2'	1:C2:187:G:O4'	2.18	0.43
1:C2:428:A:N3	1:C2:440:U:O2'	2.41	0.43
1:C2:1195:C:N4	23:SQ:143:ARG:O	2.43	0.43
4:C1:158:G:H2'	4:C1:159:A:H8	1.82	0.43
4:C1:951:A:H5''	4:C1:1143:A:N1	2.33	0.43
4:C1:2305:G:OP2	4:C1:2305:G:N2	2.38	0.43
4:C1:3214:U:O4	52:LM:124:ARG:NH1	2.51	0.43
5:C4:11:A:N1	5:C4:67:G:O2'	2.49	0.43
5:C4:107:C:H2'	5:C4:108:A:H8	1.82	0.43
10:SD:94:ARG:NH1	10:SD:125:TYR:OH	2.51	0.43
13:SG:98:ARG:NH1	13:SG:99:GLY:O	2.50	0.43
16:SJ:109:LEU:HB2	16:SJ:146:PHE:HB3	1.98	0.43
19:SM:44:GLY:O	19:SM:48:SER:CB	2.66	0.43
22:SP:56:PHE:CD2	22:SP:83:MET:HE1	2.53	0.43
27:SU:45:ALA:O	27:SU:48:HIS:C	2.61	0.43
28:SV:68:SER:O	28:SV:72:LEU:HG	2.18	0.43
39:Sg:218:GLY:O	39:Sg:235:SER:C	2.61	0.43
44:LE:43:LEU:HD21	44:LE:85:ILE:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:LG:59:GLN:HA	46:LG:62:LYS:HE3	1.99	0.43
48:LI:5:PRO:HB2	48:LI:7:ARG:HG2	2.00	0.43
51:LL:27:ASP:OD1	51:LL:27:ASP:N	2.44	0.43
69:Ld:80:ASN:ND2	69:Ld:87:ASN:O	2.47	0.43
76:Lk:12:LEU:HB3	76:Lk:16:ARG:HH12	1.83	0.43
1:C2:115:G:H5'	18:SL:129:ARG:HG3	2.00	0.43
1:C2:250:C:H2'	1:C2:251:A:H8	1.82	0.43
1:C2:834:G:H2'	1:C2:835:U:C6	2.53	0.43
1:C2:1229:G:N2	1:C2:1256:A:H62	2.15	0.43
1:C2:1316:G:OP1	24:SR:7:LYS:N	2.51	0.43
4:C1:671:U:H2'	4:C1:672:A:C8	2.52	0.43
4:C1:796:U:H2'	4:C1:797:U:C6	2.53	0.43
4:C1:1721:U:OP2	57:LR:124:TYR:OH	2.32	0.43
4:C1:2374:C:N4	4:C1:2941:A:O4'	2.51	0.43
4:C1:3211:C:P	52:LM:109:ARG:HH12	2.41	0.43
12:SF:92:ARG:NH2	12:SF:169:ASN:OD1	2.51	0.43
15:SI:152:ILE:HD12	15:SI:156:VAL:HG13	2.00	0.43
16:SJ:60:LEU:HD23	16:SJ:60:LEU:HA	1.83	0.43
42:LC:188:ARG:NE	42:LC:197:ARG:O	2.38	0.43
42:LC:283:THR:HB	42:LC:288:ARG:HH22	1.82	0.43
57:LR:7:GLN:HE21	57:LR:36:ASN:HB3	1.82	0.43
59:LT:106:LEU:HA	59:LT:109:VAL:HG12	2.00	0.43
65:LZ:17:ARG:H	72:Lg:74:ARG:HG3	1.83	0.43
4:C1:3068:U:OP2	57:LR:62:ARG:NH2	2.45	0.43
4:C1:3376:A:H5'	4:C1:3377:G:H5''	2.00	0.43
13:SG:25:ARG:HA	13:SG:28:PHE:CD2	2.54	0.43
13:SG:33:GLY:CA	13:SG:52:ILE:O	2.66	0.43
22:SP:21:ASP:O	22:SP:25:LEU:HG	2.18	0.43
43:LD:95:TRP:HD1	43:LD:158:ARG:HA	1.82	0.43
56:LQ:176:ARG:H	66:La:51:GLY:HA2	1.84	0.43
65:LZ:84:ARG:HH21	72:Lg:100:ILE:HD12	1.84	0.43
65:LZ:102:GLU:HA	65:LZ:107:ARG:HE	1.82	0.43
66:La:94:ALA:HA	66:La:121:VAL:HG13	1.99	0.43
70:Le:82:LEU:HD11	70:Le:108:ILE:HG23	2.00	0.43
1:C2:444:C:OP2	31:SY:108:ARG:NH1	2.47	0.43
1:C2:1684:U:H2'	1:C2:1685:G:H8	1.82	0.43
4:C1:860:G:C5	40:LA:181:LYS:HB2	2.53	0.43
4:C1:860:G:OP1	81:Lp:17:ARG:NH2	2.51	0.43
4:C1:896:A:H5'	40:LA:183:GLY:HA2	2.01	0.43
4:C1:904:A:H2	40:LA:15:ILE:HD11	1.84	0.43
4:C1:989:A:O2'	59:LT:104:GLU:OE1	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:2112:U:H4'	4:C1:2113:A:H5'	2.00	0.43
7:SA:41:ARG:HH21	7:SA:45:VAL:HG21	1.83	0.43
8:SB:111:ARG:HA	8:SB:114:VAL:HG12	2.00	0.43
13:SG:164:LYS:HG3	13:SG:165:GLY:H	1.83	0.43
39:Sg:151:VAL:HA	39:Sg:173:GLY:HA2	2.00	0.43
46:LG:94:PHE:HB3	46:LG:189:LEU:HD21	2.00	0.43
51:LL:64:LYS:HD2	51:LL:65:TYR:CZ	2.54	0.43
55:LP:108:ASP:OD1	55:LP:108:ASP:N	2.51	0.43
68:Lc:103:THR:HG23	68:Lc:105:ALA:H	1.83	0.43
1:C2:1235:C:H4'	38:Sf:147:VAL:HG12	2.00	0.43
1:C2:1592:A:H2'	1:C2:1593:A:C8	2.53	0.43
4:C1:900:G:H1'	4:C1:1589:A:N6	2.33	0.43
4:C1:1259:A:H1'	83:P0:59:VAL:N	2.34	0.43
5:C4:19:C:H2'	5:C4:20:A:H8	1.83	0.43
8:SB:164:ILE:HD11	8:SB:205:PHE:CD2	2.54	0.43
12:SF:31:GLU:OE2	12:SF:35:GLN:NE2	2.49	0.43
15:SI:87:ASN:HB3	15:SI:90:LEU:HD13	2.01	0.43
31:SY:15:ASN:O	31:SY:19:ALA:N	2.52	0.43
57:LR:89:LEU:HD11	57:LR:97:ARG:HH22	1.84	0.43
61:LV:54:LEU:HD12	61:LV:54:LEU:HA	1.63	0.43
1:C2:58:U:O2'	1:C2:451:A:N3	2.50	0.43
1:C2:591:A:H2'	1:C2:592:A:C8	2.54	0.43
1:C2:1160:A:H2'	1:C2:1161:C:C6	2.54	0.43
4:C1:1237:G:C8	4:C1:1263:A:H1'	2.54	0.43
4:C1:2213:A:H2'	4:C1:2214:A:C8	2.53	0.43
4:C1:2393:G:H4'	41:LB:252:ILE:HG13	1.99	0.43
7:SA:126:PRO:HG3	7:SA:147:THR:HG22	2.01	0.43
13:SG:142:ARG:NE	13:SG:151:ASP:OD1	2.51	0.43
17:SK:18:GLU:HG2	17:SK:20:VAL:H	1.84	0.43
18:SL:6:THR:HG23	18:SL:9:SER:HB3	2.00	0.43
19:SM:59:LEU:HA	19:SM:87:PRO:HB2	1.99	0.43
29:SW:11:LEU:HD23	29:SW:11:LEU:HA	1.80	0.43
66:La:37:GLY:HA2	66:La:41:HIS:HB2	2.00	0.43
84:CN:25:ASP:OD1	84:CN:92:ARG:NH2	2.52	0.43
1:C2:56:U:H5''	1:C2:403:G:H22	1.83	0.43
4:C1:129:U:H2'	4:C1:130:A:C8	2.54	0.43
4:C1:1347:U:O4	4:C1:1357:G:O6	2.37	0.43
4:C1:1616:U:H2'	4:C1:1617:G:C8	2.53	0.43
4:C1:2413:A:H2'	4:C1:2414:G:C8	2.54	0.43
4:C1:2526:C:H2'	4:C1:2527:G:H8	1.84	0.43
4:C1:2631:U:H2'	4:C1:2632:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:2882:U:O3'	41:LB:10:ARG:NH1	2.52	0.43
6:C3:71:A:N6	6:C3:87:G:N3	2.67	0.43
7:SA:59:LEU:HD22	28:SV:79:LEU:HD11	2.00	0.43
14:SH:44:LYS:HB2	14:SH:63:PRO:HD3	2.01	0.43
24:SR:27:ASP:O	24:SR:31:ASN:ND2	2.51	0.43
24:SR:61:ILE:HD11	24:SR:69:ILE:HD11	2.00	0.43
54:LO:27:LEU:HD12	54:LO:33:ILE:HD12	1.99	0.43
67:Lb:47:LEU:HA	67:Lb:50:THR:HG22	2.00	0.43
76:Lk:46:ARG:HA	76:Lk:46:ARG:HD2	1.91	0.43
84:CN:103:LYS:HB2	84:CN:106:SER:HB2	2.00	0.43
1:C2:821:U:O4	1:C2:852:C:N3	2.52	0.43
1:C2:833:U:H5'	1:C2:834:G:H5''	2.01	0.43
4:C1:655:C:H5''	70:Le:26:HIS:HB3	2.00	0.43
4:C1:1261:G:O6	83:P0:52:LEU:HA	2.19	0.43
4:C1:1783:U:H2'	4:C1:1784:G:C8	2.54	0.43
4:C1:2898:G:H5''	4:C1:2899:C:H5'	2.01	0.43
4:C1:2940:A:O2'	41:LB:256:HIS:O	2.35	0.43
9:SC:177:GLY:O	9:SC:195:ASP:HA	2.18	0.43
19:SM:134:SER:HA	19:SM:137:MET:HE2	2.01	0.43
20:SN:114:ARG:HA	20:SN:114:ARG:HD3	1.87	0.43
26:ST:97:SER:HB3	26:ST:100:ILE:HG12	1.99	0.43
29:SW:11:LEU:HD21	29:SW:37:PHE:HE2	1.83	0.43
39:Sg:127:ARG:HD2	39:Sg:150:TRP:CE2	2.53	0.43
39:Sg:240:VAL:HA	39:Sg:256:THR:HA	2.00	0.43
41:LB:206:ASP:OD1	41:LB:206:ASP:N	2.52	0.43
51:LL:192:GLU:O	51:LL:195:ALA:N	2.51	0.43
59:LT:57:TYR:CG	59:LT:89:LEU:HD21	2.53	0.43
1:C2:146:U:H2'	1:C2:147:A:H8	1.84	0.43
1:C2:1071:U:H2'	1:C2:1072:C:C6	2.54	0.43
1:C2:1592:A:H2'	1:C2:1593:A:H8	1.84	0.43
1:C2:1628:U:H2'	1:C2:1629:G:C8	2.53	0.43
3:C5:19:A:N1	3:C5:56:G:N2	2.66	0.43
4:C1:75:G:O3'	51:LL:70:ARG:NH2	2.51	0.43
4:C1:1354:G:N1	4:C1:1357:G:O2'	2.52	0.43
4:C1:3204:C:H2'	4:C1:3205:G:C8	2.53	0.43
6:C3:39:G:O2'	6:C3:105:A:N1	2.49	0.43
8:SB:129:THR:OG1	8:SB:130:SER:N	2.50	0.43
8:SB:156:ALA:HB3	8:SB:161:ILE:HD11	2.01	0.43
11:SE:122:LYS:NZ	11:SE:143:ASP:OD2	2.43	0.43
12:SF:29:ILE:O	12:SF:34:GLN:NE2	2.42	0.43
18:SL:46:LYS:O	18:SL:49:ILE:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:SP:36:LEU:H	22:SP:36:LEU:HG	1.75	0.43
23:SQ:73:GLY:O	23:SQ:77:GLN:HG2	2.17	0.43
26:ST:77:ASN:HB3	26:ST:95:ASP:HB3	2.01	0.43
41:LB:56:ILE:O	41:LB:73:VAL:HA	2.18	0.43
51:LL:5:LYS:HE2	51:LL:5:LYS:HB2	1.88	0.43
61:LV:104:ASN:HD21	61:LV:108:GLU:HB3	1.83	0.43
66:La:94:ALA:HB2	66:La:121:VAL:HG22	2.00	0.43
5:C4:112:G:H2'	5:C4:113:C:C6	2.54	0.43
13:SG:175:ILE:HD11	13:SG:178:LEU:HD22	2.01	0.43
14:SH:91:ILE:HD12	14:SH:91:ILE:HA	1.89	0.43
20:SN:67:THR:HG21	20:SN:74:ILE:HD11	2.00	0.43
20:SN:94:LYS:HE2	20:SN:94:LYS:HB2	1.77	0.43
21:SO:82:LYS:HE3	21:SO:118:VAL:HG11	2.01	0.43
40:LA:45:VAL:HA	40:LA:61:VAL:HA	2.00	0.43
42:LC:216:VAL:O	42:LC:220:ARG:HB3	2.18	0.43
44:LE:100:LYS:NZ	44:LE:137:ASP:OD2	2.52	0.43
46:LG:68:ARG:HH22	46:LG:239:GLY:HA3	1.84	0.43
1:C2:1591:C:H2'	1:C2:1592:A:C8	2.53	0.42
4:C1:1234:G:H8	4:C1:1234:G:O5'	2.01	0.42
4:C1:1378:U:H2'	4:C1:1379:G:H8	1.84	0.42
4:C1:1827:C:H2'	4:C1:1828:A:C8	2.54	0.42
4:C1:2526:C:H2'	4:C1:2527:G:C8	2.54	0.42
4:C1:3000:A:H5''	41:LB:120:LYS:HE2	2.01	0.42
4:C1:3067:C:H3'	57:LR:62:ARG:HH22	1.83	0.42
13:SG:27:PHE:HE1	13:SG:36:VAL:HG21	1.82	0.42
19:SM:31:VAL:HA	19:SM:34:THR:HG22	2.00	0.42
20:SN:43:LYS:HA	68:Lc:97:ASP:OD2	2.18	0.42
24:SR:71:PHE:CE2	24:SR:73:LEU:HB3	2.54	0.42
41:LB:106:TRP:HB2	41:LB:133:TYR:HE2	1.84	0.42
45:LF:116:PHE:O	45:LF:199:ASN:ND2	2.51	0.42
55:LP:115:SER:HB3	55:LP:151:THR:HG22	2.01	0.42
61:LV:15:LEU:HA	61:LV:53:SER:HB3	2.01	0.42
69:Ld:112:ASP:N	69:Ld:112:ASP:OD1	2.52	0.42
71:Lf:14:LEU:HD11	71:Lf:31:LYS:HB2	2.01	0.42
75:Lj:54:LYS:O	75:Lj:58:THR:HG23	2.18	0.42
76:Lk:27:ILE:HD12	76:Lk:39:ARG:HH21	1.84	0.42
1:C2:187:G:H3'	15:SI:138:ASN:HD21	1.84	0.42
1:C2:763:G:H5''	16:SJ:78:ARG:HH22	1.85	0.42
1:C2:896:U:OP1	8:SB:26:ARG:NH2	2.52	0.42
1:C2:1089:U:O2'	1:C2:1093:A:N1	2.50	0.42
1:C2:1147:A:H5''	9:SC:91:ARG:HD2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:1237:G:H1'	4:C1:1263:A:C5	2.54	0.42
13:SG:171:LYS:HB3	13:SG:171:LYS:HE2	1.80	0.42
17:SK:6:GLU:HA	17:SK:9:ASN:HD22	1.84	0.42
28:SV:17:CYS:HB2	28:SV:56:SER:HB3	2.01	0.42
41:LB:17:LEU:HD21	41:LB:233:TRP:HH2	1.84	0.42
42:LC:281:ILE:HD12	56:LQ:29:LEU:HG	2.00	0.42
43:LD:144:VAL:HG23	43:LD:173:VAL:HG22	2.01	0.42
54:LO:43:ILE:HD11	54:LO:138:LEU:HD13	2.01	0.42
55:LP:168:LEU:O	55:LP:173:ARG:NH1	2.52	0.42
57:LR:134:HIS:CD2	57:LR:136:ARG:HG2	2.54	0.42
1:C2:898:A:N1	1:C2:911:U:O2'	2.42	0.42
1:C2:1311:U:O3'	24:SR:2:GLY:N	2.51	0.42
1:C2:1776:A:H2'	1:C2:1777:G:C8	2.55	0.42
4:C1:656:A:H2'	4:C1:657:A:C8	2.54	0.42
4:C1:1129:A:H2'	4:C1:1130:A:C8	2.53	0.42
4:C1:1643:A:H2'	4:C1:1644:C:C2	2.55	0.42
16:SJ:86:LEU:HD13	16:SJ:99:LEU:HD21	2.01	0.42
29:SW:14:ILE:HG12	29:SW:25:VAL:HG21	2.01	0.42
39:Sg:172:ALA:HB2	39:Sg:202:LEU:HD23	1.99	0.42
41:LB:117:ARG:HA	41:LB:175:LYS:HG3	2.02	0.42
43:LD:80:SER:OG	43:LD:92:LEU:O	2.25	0.42
45:LF:102:VAL:HG21	45:LF:129:LEU:HD23	2.01	0.42
47:LH:42:ASP:HB3	47:LH:64:HIS:HE2	1.84	0.42
49:LJ:116:TYR:OH	49:LJ:121:GLY:HA2	2.20	0.42
53:LN:67:ARG:C	53:LN:126:THR:O	2.62	0.42
57:LR:134:HIS:HD2	57:LR:136:ARG:HG2	1.83	0.42
63:LX:115:ARG:O	63:LX:118:GLY:N	2.37	0.42
65:LZ:23:VAL:HB	65:LZ:43:VAL:HB	2.00	0.42
75:Lj:39:TYR:CD1	75:Lj:40:PRO:HA	2.54	0.42
1:C2:123:G:H4'	11:SE:145:ARG:HD2	2.02	0.42
1:C2:891:A:H2'	1:C2:892:A:H8	1.84	0.42
4:C1:1263:A:H61	50:LK:127:SER:CB	2.33	0.42
4:C1:1362:G:H2'	4:C1:1363:A:C8	2.54	0.42
4:C1:2160:G:H2'	4:C1:2161:G:C8	2.54	0.42
7:SA:8:ASP:O	7:SA:54:TRP:NE1	2.53	0.42
11:SE:115:THR:O	11:SE:119:ALA:HB2	2.19	0.42
31:SY:10:ARG:HB2	31:SY:24:VAL:HG23	2.02	0.42
39:Sg:201:THR:OG1	39:Sg:241:PHE:O	2.30	0.42
39:Sg:217:ASP:OD1	39:Sg:217:ASP:N	2.48	0.42
42:LC:257:LYS:HA	42:LC:260:GLN:HG2	2.01	0.42
52:LM:123:LEU:HD13	54:LO:193:GLN:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:26:A:N3	4:C1:328:U:O2'	2.46	0.42
4:C1:494:G:H2'	4:C1:495:G:H8	1.84	0.42
4:C1:1234:G:H3'	4:C1:1235:U:H2'	2.02	0.42
4:C1:1621:A:H2'	4:C1:1622:U:C6	2.54	0.42
4:C1:1783:U:H2'	4:C1:1784:G:H8	1.84	0.42
4:C1:1913:A:N3	4:C1:2120:A:H2'	2.34	0.42
4:C1:2443:A:H61	4:C1:2504:U:H3	1.67	0.42
4:C1:2588:U:OP1	46:LG:48:ARG:NH2	2.47	0.42
4:C1:2943:G:N2	41:LB:251:CYS:SG	2.92	0.42
29:SW:89:TRP:O	29:SW:93:LEU:HD23	2.19	0.42
45:LF:55:TYR:CE1	45:LF:189:ILE:HD11	2.55	0.42
49:LJ:94:ARG:O	49:LJ:96:PHE:N	2.35	0.42
51:LL:188:ARG:O	51:LL:189:GLU:C	2.63	0.42
53:LN:115:VAL:HG21	53:LN:160:GLU:HG2	2.01	0.42
1:C2:623:A:O2'	1:C2:624:G:OP1	2.31	0.42
1:C2:886:U:O2'	21:SO:121:VAL:O	2.37	0.42
1:C2:1241:G:OP2	22:SP:77:ARG:NH2	2.43	0.42
4:C1:1009:A:H2'	4:C1:1010:G:C8	2.54	0.42
4:C1:1149:G:OP2	71:Lf:21:ARG:NH2	2.52	0.42
5:C4:28:C:H5''	49:LJ:137:ARG:HB3	2.01	0.42
34:Sb:18:LYS:HB3	34:Sb:18:LYS:HE3	1.90	0.42
40:LA:27:ALA:HB3	40:LA:128:ARG:HH21	1.84	0.42
42:LC:65:TRP:HB3	42:LC:69:ARG:HD3	2.02	0.42
61:LV:109:MET:HE2	61:LV:109:MET:HB3	1.89	0.42
72:Lg:85:VAL:HG12	72:Lg:89:ILE:HD11	2.01	0.42
73:Lh:31:LEU:HD22	73:Lh:41:LEU:HD21	2.02	0.42
1:C2:590:C:H5''	37:Se:43:ARG:HH22	1.85	0.42
4:C1:59:G:H2'	6:C3:33:A:H2'	2.01	0.42
4:C1:67:A:O2'	4:C1:315:C:O2	2.36	0.42
4:C1:91:G:OP2	4:C1:93:C:N4	2.41	0.42
4:C1:201:A:H2'	4:C1:202:G:H8	1.84	0.42
4:C1:411:U:H2'	4:C1:412:G:H8	1.84	0.42
4:C1:417:A:H2'	4:C1:418:A:C8	2.55	0.42
4:C1:1596:C:H2'	4:C1:1597:C:C6	2.55	0.42
4:C1:3251:U:H2'	4:C1:3252:G:C8	2.54	0.42
10:SD:46:THR:OG1	10:SD:84:ILE:HG22	2.20	0.42
13:SG:123:GLY:O	13:SG:127:THR:OG1	2.37	0.42
39:Sg:246:SER:O	39:Sg:250:TYR:HA	2.20	0.42
40:LA:104:LEU:HD22	40:LA:136:ILE:HD11	2.02	0.42
41:LB:316:GLU:OE1	41:LB:318:LYS:HG2	2.20	0.42
43:LD:80:SER:HA	43:LD:83:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:269:G:H5''	53:LN:14:LYS:HE2	2.01	0.42
4:C1:616:G:H2'	4:C1:617:G:C8	2.55	0.42
4:C1:1237:G:H5'	4:C1:1238:C:OP2	2.20	0.42
4:C1:1238:C:H41	4:C1:1244:A:H3'	1.85	0.42
7:SA:34:GLU:OE2	28:SV:87:ARG:NH1	2.52	0.42
8:SB:103:MET:HB3	8:SB:215:VAL:HG22	2.02	0.42
9:SC:151:PRO:HG2	28:SV:9:VAL:HG11	2.00	0.42
11:SE:147:ILE:HG13	11:SE:169:ILE:HD11	2.01	0.42
16:SJ:10:LYS:HE2	16:SJ:10:LYS:HB2	1.88	0.42
17:SK:3:MET:HE2	17:SK:8:ARG:HG2	2.00	0.42
43:LD:52:VAL:HA	43:LD:147:ASP:HB3	2.01	0.42
44:LE:146:ILE:HA	44:LE:149:ILE:HG12	2.02	0.42
51:LL:51:LEU:HD13	51:LL:139:LEU:HD12	2.02	0.42
51:LL:106:GLN:NE2	51:LL:110:ASP:OD1	2.51	0.42
73:Lh:101:THR:HG23	73:Lh:104:GLN:H	1.84	0.42
84:CN:75:LYS:HB3	84:CN:78:VAL:HG22	2.02	0.42
1:C2:1198:G:OP1	1:C2:1199:G:O2'	2.25	0.42
1:C2:1558:U:OP2	1:C2:1559:A:O2'	2.25	0.42
19:SM:93:ASP:OD1	19:SM:93:ASP:N	2.52	0.42
20:SN:47:PRO:HG2	20:SN:72:MET:HG2	2.01	0.42
23:SQ:29:ILE:HG23	23:SQ:65:ILE:HD11	2.00	0.42
24:SR:7:LYS:O	24:SR:11:ARG:HB2	2.20	0.42
39:Sg:219:GLU:HB2	39:Sg:233:THR:OG1	2.20	0.42
51:LL:64:LYS:O	51:LL:67:ARG:NH1	2.52	0.42
73:Lh:83:LYS:O	75:Lj:73:ARG:NH1	2.52	0.42
1:C2:385:A:H2'	1:C2:386:G:C8	2.55	0.42
1:C2:451:A:N6	1:C2:453:U:O2	2.53	0.42
1:C2:1280:C:H2'	1:C2:1281:G:H8	1.85	0.42
1:C2:1552:U:OP2	22:SP:43:ARG:NH2	2.53	0.42
1:C2:1579:U:H2'	1:C2:1580:C:C6	2.55	0.42
4:C1:1269:U:C2	4:C1:1271:A:H5''	2.55	0.42
4:C1:2218:G:H2'	4:C1:2219:A:C8	2.54	0.42
4:C1:2600:C:OP1	53:LN:93:LYS:NZ	2.42	0.42
4:C1:2960:C:H2'	4:C1:2961:G:H8	1.85	0.42
4:C1:3199:G:H2'	4:C1:3200:G:H8	1.85	0.42
8:SB:137:ILE:HG13	8:SB:215:VAL:HG12	2.01	0.42
17:SK:7:ASP:CG	17:SK:37:THR:HG21	2.45	0.42
21:SO:111:ARG:HB3	33:Sa:58:VAL:HG13	2.01	0.42
31:SY:51:GLU:O	31:SY:53:ASP:N	2.53	0.42
40:LA:101:VAL:HB	40:LA:165:VAL:HG22	2.02	0.42
46:LG:226:TYR:HA	46:LG:229:VAL:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:LJ:16:LYS:HG2	49:LJ:130:VAL:CG2	2.49	0.42
69:Ld:47:ASP:HB2	69:Ld:87:ASN:ND2	2.35	0.42
81:Lp:54:ILE:HG23	81:Lp:63:THR:HG23	2.02	0.42
1:C2:107:C:OP1	1:C2:383:G:O2'	2.32	0.41
4:C1:63:A:N3	4:C1:78:U:O2'	2.44	0.41
4:C1:87:U:H2'	4:C1:88:A:C8	2.55	0.41
4:C1:147:U:O2'	53:LN:41:ARG:NH1	2.53	0.41
4:C1:1108:U:H2'	4:C1:1109:U:C6	2.55	0.41
4:C1:1448:U:H2'	4:C1:1449:A:H8	1.85	0.41
4:C1:1667:A:H2'	4:C1:1668:G:C8	2.55	0.41
4:C1:2152:A:H2'	4:C1:2153:U:H6	1.85	0.41
4:C1:2751:G:OP1	59:LT:50:LYS:NZ	2.43	0.41
4:C1:3218:A:H5''	4:C1:3219:G:C5	2.55	0.41
40:LA:248:GLY:HA2	40:LA:249:SER:HA	1.81	0.41
55:LP:168:LEU:HD12	55:LP:173:ARG:HD3	2.02	0.41
59:LT:39:ILE:HG12	59:LT:63:VAL:HG22	2.02	0.41
64:LY:48:LEU:HD12	64:LY:49:PRO:HD2	2.02	0.41
70:Le:96:ILE:H	70:Le:121:ASN:HD21	1.66	0.41
82:L1:180:VAL:O	82:L1:184:LEU:CB	2.68	0.41
1:C2:106:U:OP1	15:SI:8:ARG:NH2	2.53	0.41
1:C2:1126:G:H5'	79:Ln:11:ARG:HD2	2.01	0.41
4:C1:981:U:H2'	4:C1:982:C:C6	2.55	0.41
4:C1:1230:G:H2'	4:C1:1231:A:C5	2.56	0.41
10:SD:23:GLU:HG2	17:SK:61:TRP:CD1	2.55	0.41
10:SD:143:ARG:H	10:SD:143:ARG:HG2	1.61	0.41
13:SG:50:PHE:CE1	13:SG:113:ILE:HG12	2.55	0.41
14:SH:11:GLN:NE2	14:SH:13:PRO:HD2	2.35	0.41
35:Sc:31:GLU:HB3	35:Sc:39:THR:HG22	2.02	0.41
39:Sg:152:SER:OG	39:Sg:153:GLN:N	2.53	0.41
42:LC:92:ASN:OD1	42:LC:92:ASN:N	2.53	0.41
45:LF:126:LEU:HD23	45:LF:126:LEU:HA	1.84	0.41
45:LF:202:LEU:HD23	45:LF:202:LEU:HA	1.94	0.41
53:LN:115:VAL:HA	53:LN:134:LEU:HD23	2.01	0.41
66:La:92:LYS:HD2	66:La:92:LYS:HA	1.84	0.41
70:Le:103:LYS:O	70:Le:107:VAL:HG23	2.19	0.41
1:C2:496:G:H2'	1:C2:497:G:C8	2.55	0.41
1:C2:788:A:OP2	11:SE:108:ARG:NH1	2.47	0.41
1:C2:1393:C:H4'	39:Sg:281:TYR:HE1	1.84	0.41
1:C2:1691:A:H2'	1:C2:1692:G:H8	1.84	0.41
4:C1:93:C:OP2	4:C1:2764:C:O2'	2.27	0.41
4:C1:745:C:H2'	4:C1:746:A:H8	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:1233:G:H5'	83:P0:42:ARG:N	2.30	0.41
4:C1:1616:U:H2'	4:C1:1617:G:H8	1.85	0.41
10:SD:8:LYS:HE3	10:SD:8:LYS:HB2	1.89	0.41
22:SP:72:LYS:HA	22:SP:73:PRO:HD3	1.87	0.41
23:SQ:89:LEU:HD12	23:SQ:89:LEU:HA	1.77	0.41
42:LC:71:VAL:HB	42:LC:76:ARG:HH21	1.83	0.41
43:LD:6:ASP:OD1	43:LD:6:ASP:N	2.49	0.41
48:LI:206:LEU:HD23	48:LI:206:LEU:HA	1.96	0.41
49:LJ:174:LYS:HD3	49:LJ:174:LYS:HA	1.77	0.41
59:LT:73:GLY:HA2	59:LT:89:LEU:O	2.20	0.41
74:Li:38:LYS:HB3	74:Li:38:LYS:HE3	1.76	0.41
76:Lk:12:LEU:HB3	76:Lk:16:ARG:NH1	2.34	0.41
84:CN:98:LYS:HA	84:CN:101:LYS:HD3	2.01	0.41
1:C2:29:U:H2'	1:C2:30:G:C8	2.53	0.41
1:C2:895:G:H2'	1:C2:896:U:C6	2.55	0.41
1:C2:922:G:H2'	1:C2:923:A:C8	2.55	0.41
1:C2:1199:G:N2	36:Sd:30:LEU:O	2.46	0.41
1:C2:1473:U:H4'	12:SF:109:LYS:HE3	2.03	0.41
1:C2:1689:A:H2'	1:C2:1690:G:C8	2.55	0.41
4:C1:649:A:H2'	4:C1:650:C:C6	2.55	0.41
4:C1:1063:G:C6	59:LT:109:VAL:HG23	2.55	0.41
4:C1:1345:G:H2'	4:C1:1346:G:C8	2.56	0.41
4:C1:1659:U:H2'	4:C1:1660:C:C6	2.56	0.41
4:C1:1696:A:H2'	4:C1:1697:A:C8	2.55	0.41
4:C1:1798:A:H2'	4:C1:1799:A:C8	2.55	0.41
4:C1:2727:A:C2	66:La:43:ILE:HG23	2.55	0.41
7:SA:176:LEU:O	7:SA:179:ARG:N	2.54	0.41
17:SK:70:GLU:O	17:SK:73:VAL:HG12	2.19	0.41
21:SO:31:THR:HG22	21:SO:38:THR:HG22	2.02	0.41
25:SS:52:VAL:HG21	25:SS:69:ILE:HD11	2.02	0.41
26:ST:42:GLY:HA2	26:ST:84:LYS:HD3	2.02	0.41
27:SU:34:LEU:HD13	27:SU:87:HIS:HB2	2.02	0.41
33:Sa:53:LEU:O	33:Sa:57:SER:CB	2.68	0.41
41:LB:212:ASN:ND2	41:LB:353:GLU:HA	2.35	0.41
42:LC:301:PRO:O	56:LQ:39:ARG:NH2	2.53	0.41
44:LE:40:LEU:HB3	44:LE:84:VAL:HG13	2.02	0.41
49:LJ:153:LYS:O	49:LJ:154:THR:C	2.63	0.41
53:LN:183:THR:HB	53:LN:187:ARG:HB2	2.01	0.41
63:LX:109:LYS:HG2	63:LX:125:ARG:HB3	2.02	0.41
1:C2:1175:U:H2'	1:C2:1176:G:H8	1.85	0.41
1:C2:1796:C:H5''	33:Sa:87:ARG:HH21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:20:A:H2'	4:C1:21:G:C8	2.55	0.41
4:C1:87:U:H2'	4:C1:88:A:H8	1.85	0.41
4:C1:1240:A:H8	50:LK:78:SER:CB	2.33	0.41
4:C1:1242:G:H2'	50:LK:59:THR:HA	2.03	0.41
4:C1:1249:G:C5	4:C1:1250:G:H1'	2.56	0.41
4:C1:1263:A:H62	50:LK:123:ARG:N	2.18	0.41
8:SB:35:PRO:O	8:SB:41:ARG:NH2	2.41	0.41
8:SB:131:ASP:OD1	8:SB:180:THR:OG1	2.35	0.41
14:SH:64:VAL:HG23	14:SH:67:LEU:HD23	2.02	0.41
24:SR:74:GLN:HA	24:SR:77:GLU:OE1	2.21	0.41
25:SS:11:PHE:CG	32:SZ:41:ILE:HD13	2.55	0.41
32:SZ:102:THR:OG1	32:SZ:103:ARG:N	2.52	0.41
39:Sg:13:LEU:HB3	39:Sg:45:TRP:HZ3	1.85	0.41
39:Sg:224:ASN:O	39:Sg:228:LYS:CA	2.67	0.41
40:LA:27:ALA:O	40:LA:128:ARG:NH2	2.54	0.41
40:LA:155:LYS:HA	40:LA:155:LYS:HD2	1.92	0.41
42:LC:38:VAL:O	42:LC:42:VAL:HG23	2.20	0.41
46:LG:149:LYS:HB2	46:LG:149:LYS:HE2	1.84	0.41
47:LH:18:VAL:HG12	47:LH:27:VAL:HG22	2.02	0.41
53:LN:66:VAL:HB	53:LN:98:LEU:HD22	2.03	0.41
57:LR:105:LEU:HD22	57:LR:135:LYS:HG3	2.01	0.41
57:LR:122:VAL:O	57:LR:126:GLU:HG3	2.21	0.41
63:LX:96:LYS:HB2	63:LX:96:LYS:HE2	1.93	0.41
1:C2:329:G:H2'	1:C2:330:G:C8	2.55	0.41
1:C2:629:U:H5''	20:SN:127:ARG:HH12	1.84	0.41
4:C1:904:A:C2	40:LA:15:ILE:HD11	2.56	0.41
4:C1:1577:G:H2'	4:C1:1578:C:H6	1.86	0.41
4:C1:2882:U:H2'	4:C1:2883:U:C6	2.55	0.41
5:C4:19:C:H2'	5:C4:20:A:C8	2.55	0.41
6:C3:69:U:H2'	6:C3:70:G:O4'	2.21	0.41
10:SD:108:LYS:HD2	10:SD:113:LEU:HD22	2.02	0.41
12:SF:214:LYS:O	12:SF:218:GLU:HG2	2.20	0.41
15:SI:41:LYS:HB3	15:SI:41:LYS:HE2	1.77	0.41
18:SL:57:LYS:HD2	18:SL:131:ILE:HG23	2.02	0.41
18:SL:85:VAL:HA	18:SL:108:PRO:HA	2.03	0.41
20:SN:19:SER:C	20:SN:21:ASN:H	2.29	0.41
20:SN:91:LEU:HB3	20:SN:122:ILE:HG12	2.02	0.41
24:SR:37:GLU:OE1	39:Sg:129:LYS:NZ	2.52	0.41
24:SR:110:VAL:HA	24:SR:113:LEU:HG	2.02	0.41
27:SU:95:ALA:HB1	27:SU:99:ILE:HG23	2.02	0.41
29:SW:19:LYS:NZ	29:SW:70:ASN:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Sg:45:TRP:CH2	39:Sg:310:ILE:HD12	2.55	0.41
39:Sg:220:ILE:O	39:Sg:233:THR:CA	2.47	0.41
41:LB:296:THR:OG1	41:LB:297:SER:N	2.53	0.41
53:LN:48:ALA:HB1	53:LN:53:TYR:HB3	2.03	0.41
59:LT:68:THR:OG1	59:LT:69:LYS:N	2.52	0.41
71:Lf:60:ARG:HA	71:Lf:60:ARG:HD3	1.87	0.41
72:Lg:36:LYS:HB3	72:Lg:36:LYS:HE3	1.86	0.41
4:C1:1055:A:N3	5:C4:81:U:O2'	2.53	0.41
4:C1:1128:U:O4'	48:Li:4:ARG:NH2	2.54	0.41
4:C1:2103:U:H2'	4:C1:2104:A:H8	1.85	0.41
4:C1:2880:U:H1'	41:LB:250:ALA:HB3	2.03	0.41
4:C1:3275:U:O2'	71:Lf:99:ARG:NH1	2.53	0.41
4:C1:3324:C:H4'	69:Ld:13:THR:HG23	2.02	0.41
10:SD:75:LYS:HE2	17:SK:20:VAL:HG23	2.03	0.41
17:SK:54:TYR:CD1	17:SK:71:GLU:HG3	2.55	0.41
24:SR:104:ASN:O	24:SR:107:SER:OG	2.25	0.41
39:Sg:293:ALA:O	39:Sg:301:LEU:HA	2.20	0.41
40:LA:107:VAL:HG22	40:LA:111:THR:HG21	2.03	0.41
65:LZ:12:VAL:HG23	65:LZ:81:LEU:HB3	2.03	0.41
80:Lo:70:LEU:HD21	80:Lo:91:PHE:HZ	1.85	0.41
1:C2:1216:C:H2'	1:C2:1444:A:N1	2.36	0.41
1:C2:1277:G:H1'	10:SD:181:VAL:HG13	2.03	0.41
1:C2:1523:G:OP2	1:C2:1523:G:N2	2.40	0.41
1:C2:1650:U:H2'	1:C2:1651:A:C8	2.55	0.41
4:C1:860:G:C6	40:LA:181:LYS:HB2	2.55	0.41
4:C1:1116:G:N2	4:C1:2817:A:O4'	2.54	0.41
4:C1:1829:G:H5''	4:C1:1830:G:H5'	2.01	0.41
7:SA:28:ASN:HB2	7:SA:150:ASP:HB3	2.03	0.41
11:SE:103:TYR:CE1	11:SE:109:PHE:HE1	2.39	0.41
24:SR:24:LEU:HB3	24:SR:58:MET:HE3	2.02	0.41
43:LD:270:LYS:HZ2	43:LD:270:LYS:HG3	1.49	0.41
46:LG:70:LYS:HE2	46:LG:70:LYS:HB3	1.85	0.41
55:LP:116:HIS:O	55:LP:148:LEU:HA	2.21	0.41
59:LT:28:SER:O	59:LT:32:LYS:HG3	2.20	0.41
60:LU:79:LEU:HD23	60:LU:79:LEU:HA	1.90	0.41
1:C2:207:U:H2'	1:C2:208:U:C6	2.55	0.41
1:C2:931:C:OP2	33:Sa:70:LYS:NZ	2.54	0.41
1:C2:1191:U:H2'	1:C2:1192:C:C6	2.56	0.41
1:C2:1557:U:H1'	22:SP:118:GLU:HB3	2.03	0.41
1:C2:1562:G:OP1	26:ST:89:ARG:NH1	2.40	0.41
1:C2:1795:U:O2	33:Sa:10:ARG:NE	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C1:1034:U:H2'	4:C1:1035:G:H8	1.86	0.41
4:C1:1229:G:H2'	4:C1:1230:G:O4'	2.21	0.41
4:C1:1785:U:H2'	4:C1:1786:G:C8	2.56	0.41
4:C1:1927:G:P	81:Lp:6:LYS:H	2.44	0.41
4:C1:2504:U:H2'	4:C1:2505:U:C6	2.56	0.41
4:C1:2736:A:OP1	59:LT:92:ARG:NH2	2.54	0.41
5:C4:98:C:O2'	45:LF:131:GLU:OE1	2.34	0.41
6:C3:75:G:OP2	64:LY:74:TYR:OH	2.27	0.41
6:C3:94:C:OP1	75:Lj:75:LYS:NZ	2.50	0.41
8:SB:138:PHE:CD1	8:SB:214:LYS:HB3	2.56	0.41
8:SB:144:ARG:HD3	8:SB:208:GLN:HB3	2.02	0.41
14:SH:111:LYS:HG3	14:SH:112:ARG:H	1.85	0.41
14:SH:173:TYR:HE2	14:SH:179:LYS:HB2	1.84	0.41
17:SK:14:TYR:CD2	17:SK:35:ILE:HD11	2.56	0.41
24:SR:10:LYS:HG2	24:SR:53:TYR:CE2	2.56	0.41
27:SU:99:ILE:O	27:SU:103:ILE:HG12	2.20	0.41
40:LA:188:LYS:O	40:LA:192:LYS:HG2	2.20	0.41
41:LB:2:SER:O	41:LB:2:SER:OG	2.23	0.41
42:LC:135:VAL:HG12	42:LC:140:HIS:HB2	2.02	0.41
46:LG:159:PRO:HB2	46:LG:161:GLU:HG3	2.01	0.41
55:LP:55:GLN:O	55:LP:72:GLN:NE2	2.52	0.41
56:LQ:148:GLU:O	56:LQ:151:ARG:HG2	2.21	0.41
66:La:86:LYS:O	66:La:89:GLN:HG2	2.21	0.41
69:Ld:14:ILE:HG12	69:Ld:16:LEU:HD22	2.03	0.41
69:Ld:32:ALA:O	69:Ld:36:ILE:HG12	2.21	0.41
69:Ld:44:MET:HE3	69:Ld:44:MET:HB2	1.73	0.41
76:Lk:65:LEU:HD12	76:Lk:65:LEU:HA	1.96	0.41
77:Ll:26:TRP:HA	77:Ll:29:LEU:HG	2.03	0.41
78:Lm:96:CYS:HB3	78:Lm:101:ALA:HB3	2.03	0.41
1:C2:625:C:H2'	1:C2:626:U:C6	2.56	0.41
1:C2:1087:A:H2'	1:C2:1088:A:C8	2.56	0.41
1:C2:1114:G:O2'	1:C2:1130:G:O6	2.35	0.41
1:C2:1266:U:H2'	1:C2:1267:G:C8	2.56	0.41
4:C1:148:G:OP2	53:LN:4:TYR:OH	2.24	0.41
4:C1:692:A:OP1	53:LN:201:ARG:NH2	2.35	0.41
4:C1:1001:G:O2'	4:C1:1041:U:OP2	2.32	0.41
4:C1:2150:G:O2'	4:C1:2189:U:OP1	2.37	0.41
4:C1:2676:A:H5'	4:C1:2677:G:C8	2.56	0.41
4:C1:2812:C:H2'	4:C1:2813:A:C8	2.56	0.41
4:C1:3165:A:H2'	4:C1:3166:C:C6	2.56	0.41
11:SE:240:LYS:HE3	11:SE:240:LYS:HB2	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:SJ:126:ARG:NE	16:SJ:144:PRO:HG2	2.36	0.41
31:SY:10:ARG:O	31:SY:11:LYS:O	2.38	0.41
40:LA:96:LEU:HD11	40:LA:107:VAL:HG23	2.03	0.41
40:LA:192:LYS:HE3	40:LA:193:ARG:HH22	1.86	0.41
41:LB:106:TRP:HB2	41:LB:133:TYR:CE2	2.56	0.41
42:LC:222:VAL:HA	42:LC:223:PRO:HD3	1.87	0.41
53:LN:118:SER:HA	53:LN:131:GLU:O	2.21	0.41
54:LO:37:ARG:HD2	54:LO:108:ILE:HD11	2.03	0.41
57:LR:105:LEU:HD13	57:LR:135:LYS:HE3	2.02	0.41
65:LZ:105:SER:O	65:LZ:108:GLU:HB3	2.20	0.41
1:C2:874:C:H2'	1:C2:875:G:C8	2.57	0.40
1:C2:947:U:H2'	1:C2:948:G:C8	2.56	0.40
1:C2:1026:A:N7	1:C2:1772:C:O2'	2.51	0.40
4:C1:515:C:H2'	4:C1:516:A:C8	2.56	0.40
4:C1:597:G:H2'	4:C1:598:A:H8	1.86	0.40
4:C1:1233:G:H2'	4:C1:1234:G:N7	2.35	0.40
4:C1:2429:G:H2'	4:C1:2430:A:C8	2.56	0.40
4:C1:2525:G:O2'	4:C1:2526:C:OP2	2.35	0.40
5:C4:107:C:H2'	5:C4:108:A:C8	2.56	0.40
6:C3:8:C:H2'	6:C3:9:A:H8	1.86	0.40
6:C3:63:G:H22	6:C3:97:A:H2	1.69	0.40
7:SA:179:ARG:HG2	7:SA:195:TRP:CE3	2.56	0.40
10:SD:56:GLN:O	10:SD:60:GLY:HA2	2.21	0.40
21:SO:72:LYS:HD3	21:SO:72:LYS:HA	1.89	0.40
22:SP:59:LYS:HE2	22:SP:59:LYS:HB3	1.89	0.40
25:SS:70:VAL:HG22	25:SS:74:GLN:HE22	1.86	0.40
25:SS:103:ASN:OD1	25:SS:104:ASN:N	2.54	0.40
30:SX:52:ILE:HG12	30:SX:77:ILE:HD11	2.03	0.40
35:Sc:12:VAL:HG22	35:Sc:52:ASP:H	1.86	0.40
41:LB:82:PRO:HA	41:LB:83:PRO:HD3	1.93	0.40
57:LR:10:LEU:HD23	57:LR:10:LEU:HA	1.93	0.40
61:LV:19:VAL:HG23	61:LV:50:PRO:O	2.21	0.40
1:C2:241:U:H2'	1:C2:242:U:C6	2.55	0.40
1:C2:1250:U:H2'	1:C2:1251:U:C1'	2.51	0.40
4:C1:640:U:H2'	4:C1:641:C:C6	2.57	0.40
4:C1:1799:A:H2'	4:C1:1800:A:H8	1.84	0.40
4:C1:1874:A:N7	57:LR:20:ARG:NH1	2.69	0.40
5:C4:71:G:H2'	5:C4:72:A:C8	2.57	0.40
14:SH:84:LYS:HD2	14:SH:85:PHE:HB2	2.03	0.40
18:SL:109:VAL:HG11	18:SL:125:VAL:HG11	2.01	0.40
33:Sa:5:ARG:HD2	33:Sa:9:GLY:HA2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:LR:136:ARG:O	57:LR:140:GLU:HG2	2.21	0.40
1:C2:323:A:OP1	15:SI:11:ARG:HG2	2.21	0.40
3:C5:52:G:H2'	3:C5:53:A:H8	1.87	0.40
86:C1:3403:T1C:C1A	75:Lj:75:LYS:HD3	2.50	0.40
6:C3:39:G:H1'	6:C3:104:A:N6	2.36	0.40
40:LA:65:ASP:HB3	40:LA:68:LYS:O	2.21	0.40
42:LC:188:ARG:NE	42:LC:197:ARG:HB3	2.36	0.40
48:LI:47:PRO:HD2	48:LI:141:LYS:HA	2.04	0.40
48:LI:65:LEU:HD23	48:LI:159:PHE:CZ	2.57	0.40
51:LL:18:TRP:O	51:LL:22:VAL:HG23	2.21	0.40
56:LQ:41:ASP:OD1	56:LQ:41:ASP:N	2.53	0.40
57:LR:139:VAL:O	57:LR:143:ILE:HG12	2.20	0.40
61:LV:10:LYS:HB2	61:LV:125:LEU:HD11	2.03	0.40
64:LY:70:ILE:HA	64:LY:82:VAL:HG12	2.01	0.40
66:La:75:LEU:HD23	66:La:75:LEU:HA	1.94	0.40
84:CN:76:GLN:OE1	84:CN:76:GLN:N	2.54	0.40
1:C2:16:G:O6	9:SC:203:LYS:NZ	2.54	0.40
1:C2:110:U:OP1	1:C2:753:A:O2'	2.33	0.40
1:C2:816:G:O2'	14:SH:110:GLN:NE2	2.54	0.40
1:C2:1035:G:OP1	20:SN:2:GLY:N	2.54	0.40
1:C2:1229:G:H21	1:C2:1256:A:N6	2.18	0.40
1:C2:1250:U:H2'	1:C2:1251:U:H1'	2.03	0.40
1:C2:1676:U:H5'	15:SI:58:LEU:HD21	2.02	0.40
4:C1:985:U:H2'	4:C1:986:U:H6	1.86	0.40
4:C1:1254:C:H41	4:C1:1263:A:H5''	1.86	0.40
4:C1:1631:C:H5''	4:C1:1632:A:H5''	2.02	0.40
4:C1:1719:G:OP1	57:LR:110:ARG:NH1	2.52	0.40
4:C1:2961:G:H2'	4:C1:2962:U:C6	2.57	0.40
7:SA:32:HIS:NE2	28:SV:64:GLU:OE2	2.34	0.40
11:SE:12:LEU:HD11	16:SJ:4:ALA:HB2	2.04	0.40
11:SE:24:SER:OG	11:SE:24:SER:O	2.37	0.40
11:SE:153:ASN:OD1	13:SG:215:ARG:NH1	2.42	0.40
25:SS:82:PRO:HG2	25:SS:85:PHE:HB2	2.03	0.40
40:LA:126:LEU:HD22	40:LA:150:LEU:HD11	2.03	0.40
43:LD:59:ASP:OD1	43:LD:60:ILE:N	2.54	0.40
45:LF:239:LEU:O	45:LF:242:SER:OG	2.35	0.40
46:LG:115:ALA:O	46:LG:120:LYS:N	2.51	0.40
48:LI:46:PHE:HB2	48:LI:139:ARG:NH1	2.37	0.40
56:LQ:42:ALA:HB1	56:LQ:45:ASN:HB2	2.03	0.40
58:LS:12:ARG:HE	58:LS:57:GLU:CD	2.30	0.40
59:LT:57:TYR:HA	59:LT:60:LYS:HG3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C2:1362:U:O2'	1:C2:1363:U:O2	2.25	0.40
1:C2:1473:U:OP2	12:SF:189:THR:OG1	2.26	0.40
1:C2:1630:U:O2'	1:C2:1764:C:O2'	2.35	0.40
4:C1:333:G:H5'	86:C1:3403:T1C:H51	2.03	0.40
4:C1:1258:U:H3'	4:C1:1259:A:H5''	2.03	0.40
4:C1:2742:C:H2'	4:C1:2743:A:H8	1.87	0.40
5:C4:1:G:H2'	5:C4:2:G:H8	1.87	0.40
10:SD:75:LYS:NZ	17:SK:18:GLU:OE2	2.54	0.40
11:SE:115:THR:O	11:SE:119:ALA:CB	2.69	0.40
14:SH:83:LYS:HA	14:SH:83:LYS:HD3	1.84	0.40
20:SN:88:LEU:O	20:SN:92:ILE:HG12	2.21	0.40
39:Sg:74:THR:HG22	39:Sg:79:TYR:H	1.86	0.40
42:LC:286:VAL:HG23	56:LQ:32:LEU:HB2	2.03	0.40
56:LQ:37:ALA:HB1	56:LQ:46:LYS:HD3	2.03	0.40
58:LS:112:ALA:O	58:LS:115:ARG:NH1	2.54	0.40
84:CN:34:THR:HG23	84:CN:41:HIS:CD2	2.53	0.40
84:CN:100:MET:HB2	84:CN:100:MET:HE3	1.68	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	
7	SA	204/252 (81%)	179 (88%)	24 (12%)	1 (0%)	24	60
8	SB	214/255 (84%)	200 (94%)	14 (6%)	0	100	100
9	SC	215/254 (85%)	205 (95%)	9 (4%)	1 (0%)	24	60
10	SD	221/240 (92%)	196 (89%)	24 (11%)	1 (0%)	24	60
11	SE	258/261 (99%)	234 (91%)	24 (9%)	0	100	100
12	SF	204/225 (91%)	181 (89%)	22 (11%)	1 (0%)	24	60
13	SG	216/236 (92%)	204 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	SH	183/190 (96%)	157 (86%)	24 (13%)	2 (1%)	11	43
15	SI	184/200 (92%)	176 (96%)	8 (4%)	0	100	100
16	SJ	183/197 (93%)	168 (92%)	15 (8%)	0	100	100
17	SK	90/105 (86%)	78 (87%)	7 (8%)	5 (6%)	1	8
18	SL	144/156 (92%)	133 (92%)	11 (8%)	0	100	100
19	SM	122/143 (85%)	86 (70%)	36 (30%)	0	100	100
20	SN	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
21	SO	126/137 (92%)	107 (85%)	19 (15%)	0	100	100
22	SP	117/142 (82%)	99 (85%)	17 (14%)	1 (1%)	14	48
23	SQ	139/143 (97%)	119 (86%)	19 (14%)	1 (1%)	18	53
24	SR	111/136 (82%)	100 (90%)	11 (10%)	0	100	100
25	SS	143/146 (98%)	127 (89%)	16 (11%)	0	100	100
26	ST	141/144 (98%)	134 (95%)	7 (5%)	0	100	100
27	SU	99/121 (82%)	92 (93%)	7 (7%)	0	100	100
28	SV	85/87 (98%)	76 (89%)	9 (11%)	0	100	100
29	SW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
30	SX	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
31	SY	132/135 (98%)	117 (89%)	13 (10%)	2 (2%)	8	35
32	SZ	67/108 (62%)	63 (94%)	4 (6%)	0	100	100
33	Sa	95/119 (80%)	81 (85%)	14 (15%)	0	100	100
34	Sb	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
35	Sc	61/67 (91%)	59 (97%)	2 (3%)	0	100	100
36	Sd	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
37	Se	58/63 (92%)	52 (90%)	6 (10%)	0	100	100
38	Sf	31/152 (20%)	25 (81%)	5 (16%)	1 (3%)	3	18
39	Sg	311/319 (98%)	277 (89%)	34 (11%)	0	100	100
40	LA	250/254 (98%)	224 (90%)	26 (10%)	0	100	100
41	LB	384/387 (99%)	367 (96%)	17 (4%)	0	100	100
42	LC	359/362 (99%)	325 (90%)	33 (9%)	1 (0%)	36	70
43	LD	292/297 (98%)	276 (94%)	16 (6%)	0	100	100
44	LE	153/176 (87%)	139 (91%)	14 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	LF	221/244 (91%)	217 (98%)	4 (2%)	0	100	100
46	LG	229/256 (90%)	206 (90%)	23 (10%)	0	100	100
47	LH	188/191 (98%)	179 (95%)	9 (5%)	0	100	100
48	LI	205/221 (93%)	194 (95%)	11 (5%)	0	100	100
49	LJ	167/174 (96%)	147 (88%)	18 (11%)	2 (1%)	10	40
50	LK	156/165 (94%)	137 (88%)	16 (10%)	3 (2%)	6	30
51	LL	192/199 (96%)	173 (90%)	15 (8%)	4 (2%)	5	27
52	LM	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
53	LN	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
54	LO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
55	LP	171/184 (93%)	167 (98%)	4 (2%)	0	100	100
56	LQ	183/186 (98%)	175 (96%)	8 (4%)	0	100	100
57	LR	172/189 (91%)	167 (97%)	5 (3%)	0	100	100
58	LS	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
59	LT	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
60	LU	96/121 (79%)	93 (97%)	3 (3%)	0	100	100
61	LV	132/137 (96%)	129 (98%)	3 (2%)	0	100	100
62	LW	61/155 (39%)	59 (97%)	2 (3%)	0	100	100
63	LX	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
64	LY	122/127 (96%)	119 (98%)	3 (2%)	0	100	100
65	LZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
66	La	146/149 (98%)	125 (86%)	19 (13%)	2 (1%)	9	36
67	Lb	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
68	Lc	98/105 (93%)	94 (96%)	4 (4%)	0	100	100
69	Ld	107/113 (95%)	101 (94%)	6 (6%)	0	100	100
70	Le	125/130 (96%)	118 (94%)	7 (6%)	0	100	100
71	Lf	104/107 (97%)	97 (93%)	7 (7%)	0	100	100
72	Lg	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
73	Lh	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
74	Li	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
75	Lj	80/88 (91%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	Lk	75/78 (96%)	71 (95%)	3 (4%)	1 (1%)	9	38
77	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
78	Lm	50/128 (39%)	50 (100%)	0	0	100	100
79	L2	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
79	Ln	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
80	Lo	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
81	Lp	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
82	L1	202/217 (93%)	149 (74%)	53 (26%)	0	100	100
83	P0	201/312 (64%)	184 (92%)	16 (8%)	1 (0%)	24	60
84	CN	110/560 (20%)	104 (94%)	6 (6%)	0	100	100
All	All	11507/13159 (87%)	10583 (92%)	894 (8%)	30 (0%)	37	70

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	SK	81	ASN
31	SY	32	ARG
49	LJ	95	ASN
51	LL	48	PRO
14	SH	30	SER
17	SK	88	PRO
22	SP	126	VAL
23	SQ	116	LEU
31	SY	52	LYS
50	LK	58	VAL
66	La	48	TYR
38	Sf	135	HIS
49	LJ	94	ARG
51	LL	76	THR
51	LL	77	LEU
7	SA	30	GLN
14	SH	74	GLN
17	SK	54	TYR
50	LK	134	GLY
10	SD	91	VAL
17	SK	3	MET
51	LL	47	ALA
83	P0	38	MET

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Mol	Chain	Res	Type
12	SF	100	ASN
17	SK	30	ALA
42	LC	339	LEU
76	Lk	17	ARG
9	SC	235	LEU
50	LK	140	GLY
66	La	18	GLY

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1768/1800 (98%)	472 (26%)	0
2	C7	2/3 (66%)	0	0
3	C5	74/75 (98%)	13 (17%)	0
4	C1	3201/3396 (94%)	632 (19%)	0
5	C4	120/121 (99%)	11 (9%)	0
6	C3	157/158 (99%)	28 (17%)	0
All	All	5322/5553 (95%)	1156 (21%)	0

All (1156) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	4	C
1	C2	17	C
1	C2	25	C
1	C2	26	A
1	C2	34	G
1	C2	42	G
1	C2	43	A
1	C2	45	U
1	C2	47	A
1	C2	56	U
1	C2	57	G
1	C2	61	A
1	C2	62	A
1	C2	63	G

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Mol	Chain	Res	Type
1	C2	65	A
1	C2	67	A
1	C2	68	A
1	C2	69	G
1	C2	71	A
1	C2	73	U
1	C2	74	U
1	C2	75	U
1	C2	76	A
1	C2	78	A
1	C2	79	C
1	C2	81	G
1	C2	100	A
1	C2	104	A
1	C2	114	C
1	C2	115	G
1	C2	116	U
1	C2	126	A
1	C2	127	G
1	C2	129	U
1	C2	130	C
1	C2	131	C
1	C2	133	U
1	C2	134	U
1	C2	135	A
1	C2	138	A
1	C2	140	A
1	C2	141	U
1	C2	142	G
1	C2	145	A
1	C2	155	U
1	C2	159	U
1	C2	168	A
1	C2	171	A
1	C2	176	C
1	C2	178	U
1	C2	179	A
1	C2	180	A
1	C2	188	A
1	C2	191	C
1	C2	192	U
1	C2	193	U

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Mol	Chain	Res	Type
1	C2	194	U
1	C2	195	G
1	C2	198	A
1	C2	216	U
1	C2	217	A
1	C2	218	A
1	C2	223	U
1	C2	224	C
1	C2	225	A
1	C2	227	U
1	C2	228	G
1	C2	230	C
1	C2	232	U
1	C2	233	C
1	C2	234	G
1	C2	235	G
1	C2	236	A
1	C2	240	U
1	C2	241	U
1	C2	249	U
1	C2	250	C
1	C2	257	A
1	C2	260	U
1	C2	265	A
1	C2	272	U
1	C2	274	G
1	C2	276	C
1	C2	277	U
1	C2	278	U
1	C2	279	G
1	C2	280	U
1	C2	281	G
1	C2	287	G
1	C2	299	A
1	C2	314	C
1	C2	316	A
1	C2	321	C
1	C2	322	G
1	C2	323	A
1	C2	330	G
1	C2	333	A
1	C2	337	G

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Mol	Chain	Res	Type
1	C2	338	C
1	C2	352	A
1	C2	353	A
1	C2	359	A
1	C2	361	C
1	C2	370	A
1	C2	373	G
1	C2	388	G
1	C2	390	G
1	C2	400	A
1	C2	401	A
1	C2	402	C
1	C2	404	G
1	C2	416	A
1	C2	417	A
1	C2	419	G
1	C2	422	G
1	C2	423	G
1	C2	424	C
1	C2	425	A
1	C2	426	G
1	C2	434	G
1	C2	436	A
1	C2	439	U
1	C2	444	C
1	C2	446	A
1	C2	448	C
1	C2	452	A
1	C2	454	U
1	C2	460	A
1	C2	468	A
1	C2	471	A
1	C2	477	A
1	C2	482	U
1	C2	483	A
1	C2	485	A
1	C2	487	G
1	C2	489	C
1	C2	491	C
1	C2	492	A
1	C2	493	U
1	C2	494	U

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Mol	Chain	Res	Type
1	C2	496	G
1	C2	498	G
1	C2	499	U
1	C2	500	C
1	C2	502	U
1	C2	505	A
1	C2	506	A
1	C2	507	U
1	C2	510	G
1	C2	511	A
1	C2	517	U
1	C2	527	A
1	C2	534	A
1	C2	538	A
1	C2	539	G
1	C2	540	G
1	C2	541	A
1	C2	542	A
1	C2	544	A
1	C2	555	A
1	C2	556	A
1	C2	557	G
1	C2	558	U
1	C2	565	C
1	C2	568	G
1	C2	572	C
1	C2	579	A
1	C2	580	A
1	C2	582	U
1	C2	594	A
1	C2	595	G
1	C2	606	A
1	C2	610	G
1	C2	611	U
1	C2	617	U
1	C2	619	A
1	C2	620	A
1	C2	621	A
1	C2	622	A
1	C2	623	A
1	C2	624	G
1	C2	638	U

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Mol	Chain	Res	Type
1	C2	639	U
1	C2	640	U
1	C2	641	G
1	C2	643	G
1	C2	648	G
1	C2	653	C
1	C2	654	C
1	C2	655	G
1	C2	678	A
1	C2	680	U
1	C2	681	U
1	C2	682	C
1	C2	683	C
1	C2	687	G
1	C2	693	U
1	C2	694	U
1	C2	696	C
1	C2	698	U
1	C2	700	C
1	C2	702	G
1	C2	703	G
1	C2	704	C
1	C2	705	U
1	C2	706	A
1	C2	707	A
1	C2	708	C
1	C2	709	C
1	C2	710	U
1	C2	711	U
1	C2	712	G
1	C2	713	A
1	C2	714	G
1	C2	728	U
1	C2	729	G
1	C2	730	G
1	C2	731	C
1	C2	732	G
1	C2	733	A
1	C2	734	A
1	C2	736	C
1	C2	737	A
1	C2	738	G

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Mol	Chain	Res	Type
1	C2	739	G
1	C2	741	C
1	C2	742	U
1	C2	743	U
1	C2	745	U
1	C2	756	A
1	C2	765	G
1	C2	766	U
1	C2	767	U
1	C2	774	A
1	C2	775	G
1	C2	778	G
1	C2	779	U
1	C2	780	A
1	C2	781	U
1	C2	782	U
1	C2	783	G
1	C2	787	G
1	C2	789	A
1	C2	812	A
1	C2	813	U
1	C2	814	A
1	C2	815	G
1	C2	819	G
1	C2	820	U
1	C2	821	U
1	C2	823	G
1	C2	833	U
1	C2	835	U
1	C2	840	U
1	C2	841	U
1	C2	846	G
1	C2	851	U
1	C2	852	C
1	C2	855	A
1	C2	856	A
1	C2	857	U
1	C2	860	U
1	C2	863	A
1	C2	873	U
1	C2	899	G
1	C2	901	G

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Mol	Chain	Res	Type
1	C2	902	G
1	C2	903	U
1	C2	912	U
1	C2	913	G
1	C2	929	A
1	C2	933	A
1	C2	934	C
1	C2	935	U
1	C2	942	G
1	C2	951	A
1	C2	960	U
1	C2	966	A
1	C2	970	A
1	C2	988	A
1	C2	992	A
1	C2	993	A
1	C2	998	A
1	C2	1003	A
1	C2	1004	U
1	C2	1005	A
1	C2	1020	A
1	C2	1021	C
1	C2	1023	A
1	C2	1024	U
1	C2	1026	A
1	C2	1028	C
1	C2	1039	A
1	C2	1052	U
1	C2	1053	G
1	C2	1058	U
1	C2	1059	U
1	C2	1060	U
1	C2	1061	A
1	C2	1063	U
1	C2	1076	A
1	C2	1080	U
1	C2	1081	A
1	C2	1082	C
1	C2	1092	A
1	C2	1093	A
1	C2	1096	C
1	C2	1098	U

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Mol	Chain	Res	Type
1	C2	1100	G
1	C2	1138	A
1	C2	1147	A
1	C2	1150	G
1	C2	1158	C
1	C2	1160	A
1	C2	1164	G
1	C2	1167	G
1	C2	1170	G
1	C2	1185	U
1	C2	1191	U
1	C2	1194	A
1	C2	1196	A
1	C2	1199	G
1	C2	1200	G
1	C2	1202	A
1	C2	1207	C
1	C2	1217	A
1	C2	1218	G
1	C2	1227	A
1	C2	1228	G
1	C2	1229	G
1	C2	1235	C
1	C2	1241	G
1	C2	1243	G
1	C2	1244	A
1	C2	1245	G
1	C2	1246	C
1	C2	1251	U
1	C2	1252	C
1	C2	1256	A
1	C2	1257	U
1	C2	1274	C
1	C2	1275	A
1	C2	1276	U
1	C2	1285	U
1	C2	1286	U
1	C2	1291	G
1	C2	1301	U
1	C2	1314	U
1	C2	1315	U
1	C2	1316	G

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Mol	Chain	Res	Type
1	C2	1318	G
1	C2	1321	A
1	C2	1322	A
1	C2	1325	A
1	C2	1337	A
1	C2	1344	A
1	C2	1345	A
1	C2	1346	A
1	C2	1348	A
1	C2	1349	G
1	C2	1354	G
1	C2	1361	U
1	C2	1363	U
1	C2	1364	G
1	C2	1367	G
1	C2	1370	U
1	C2	1371	A
1	C2	1372	U
1	C2	1373	C
1	C2	1382	A
1	C2	1383	G
1	C2	1389	C
1	C2	1390	U
1	C2	1398	U
1	C2	1399	C
1	C2	1400	A
1	C2	1402	G
1	C2	1414	U
1	C2	1415	U
1	C2	1425	A
1	C2	1427	A
1	C2	1431	C
1	C2	1432	U
1	C2	1433	G
1	C2	1436	A
1	C2	1446	A
1	C2	1459	C
1	C2	1460	A
1	C2	1466	G
1	C2	1469	A
1	C2	1470	C
1	C2	1471	A

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Mol	Chain	Res	Type
1	C2	1472	C
1	C2	1479	A
1	C2	1486	G
1	C2	1491	U
1	C2	1492	A
1	C2	1493	A
1	C2	1496	U
1	C2	1503	A
1	C2	1506	G
1	C2	1514	U
1	C2	1516	A
1	C2	1517	U
1	C2	1518	C
1	C2	1521	G
1	C2	1523	G
1	C2	1524	A
1	C2	1531	G
1	C2	1535	U
1	C2	1537	C
1	C2	1540	G
1	C2	1542	G
1	C2	1543	A
1	C2	1554	U
1	C2	1557	U
1	C2	1558	U
1	C2	1559	A
1	C2	1570	A
1	C2	1572	G
1	C2	1573	A
1	C2	1574	G
1	C2	1576	A
1	C2	1577	A
1	C2	1583	A
1	C2	1584	G
1	C2	1585	U
1	C2	1590	G
1	C2	1601	G
1	C2	1610	G
1	C2	1611	A
1	C2	1614	A
1	C2	1616	G
1	C2	1622	G

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Mol	Chain	Res	Type
1	C2	1631	A
1	C2	1634	C
1	C2	1635	A
1	C2	1636	C
1	C2	1637	C
1	C2	1657	U
1	C2	1658	G
1	C2	1678	A
1	C2	1688	U
1	C2	1693	A
1	C2	1700	C
1	C2	1701	A
1	C2	1703	C
1	C2	1708	U
1	C2	1709	C
1	C2	1715	G
1	C2	1717	G
1	C2	1743	U
1	C2	1753	A
1	C2	1756	A
1	C2	1757	G
1	C2	1760	G
1	C2	1762	A
1	C2	1766	A
1	C2	1767	G
1	C2	1769	U
1	C2	1771	U
1	C2	1780	G
1	C2	1782	A
1	C2	1783	C
1	C2	1791	A
1	C2	1792	G
1	C2	1793	G
1	C2	1794	A
1	C2	1796	C
1	C2	1798	U
1	C2	1799	U
3	C5	13	C
3	C5	14	A
3	C5	16	H2U
3	C5	18	G
3	C5	20	A

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Mol	Chain	Res	Type
3	C5	21	G
3	C5	45	7MG
3	C5	46	H2U
3	C5	47	5MC
3	C5	58	A
3	C5	62	G
3	C5	63	A
3	C5	75	A
4	C1	6	A
4	C1	13	A
4	C1	14	U
4	C1	26	A
4	C1	40	A
4	C1	43	A
4	C1	49	A
4	C1	59	G
4	C1	60	A
4	C1	65	A
4	C1	66	A
4	C1	67	A
4	C1	92	G
4	C1	109	A
4	C1	110	G
4	C1	111	C
4	C1	116	A
4	C1	120	G
4	C1	121	A
4	C1	122	A
4	C1	133	U
4	C1	134	U
4	C1	135	C
4	C1	136	G
4	C1	150	A
4	C1	156	G
4	C1	157	A
4	C1	165	A
4	C1	166	C
4	C1	172	G
4	C1	173	G
4	C1	187	A
4	C1	190	U
4	C1	191	U

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Mol	Chain	Res	Type
4	C1	200	C
4	C1	206	G
4	C1	210	U
4	C1	213	A
4	C1	218	G
4	C1	219	A
4	C1	234	G
4	C1	240	U
4	C1	241	G
4	C1	242	C
4	C1	243	G
4	C1	245	U
4	C1	249	U
4	C1	252	U
4	C1	269	G
4	C1	283	G
4	C1	286	U
4	C1	295	A
4	C1	305	U
4	C1	323	A
4	C1	329	U
4	C1	337	G
4	C1	339	C
4	C1	350	C
4	C1	374	A
4	C1	376	G
4	C1	390	G
4	C1	398	A
4	C1	399	A
4	C1	401	U
4	C1	402	A
4	C1	403	C
4	C1	421	G
4	C1	422	A
4	C1	439	C
4	C1	440	A
4	C1	503	C
4	C1	517	G
4	C1	518	G
4	C1	521	A
4	C1	523	A
4	C1	535	G

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Mol	Chain	Res	Type
4	C1	543	C
4	C1	544	C
4	C1	546	C
4	C1	547	G
4	C1	548	G
4	C1	551	A
4	C1	552	G
4	C1	555	U
4	C1	557	A
4	C1	558	U
4	C1	559	A
4	C1	578	A
4	C1	579	G
4	C1	589	A
4	C1	597	G
4	C1	600	G
4	C1	604	G
4	C1	609	G
4	C1	611	A
4	C1	620	U
4	C1	621	A
4	C1	622	A
4	C1	637	C
4	C1	638	C
4	C1	649	A
4	C1	660	A
4	C1	662	U
4	C1	667	C
4	C1	677	A
4	C1	681	U
4	C1	690	A
4	C1	705	A
4	C1	712	G
4	C1	715	A
4	C1	716	A
4	C1	719	U
4	C1	738	A
4	C1	758	C
4	C1	763	G
4	C1	764	U
4	C1	765	C
4	C1	766	U

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Mol	Chain	Res	Type
4	C1	767	U
4	C1	776	U
4	C1	777	U
4	C1	780	A
4	C1	781	G
4	C1	785	G
4	C1	786	A
4	C1	798	G
4	C1	801	A
4	C1	806	A
4	C1	808	A
4	C1	817	A
4	C1	830	A
4	C1	848	A
4	C1	849	C
4	C1	850	U
4	C1	861	C
4	C1	865	U
4	C1	874	U
4	C1	879	U
4	C1	896	A
4	C1	907	G
4	C1	908	G
4	C1	909	G
4	C1	914	A
4	C1	916	G
4	C1	917	A
4	C1	921	A
4	C1	923	C
4	C1	924	G
4	C1	925	A
4	C1	933	A
4	C1	937	G
4	C1	944	C
4	C1	959	C
4	C1	960	U
4	C1	974	G
4	C1	979	U
4	C1	984	G
4	C1	991	G
4	C1	1000	C
4	C1	1001	G

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Mol	Chain	Res	Type
4	C1	1002	A
4	C1	1010	G
4	C1	1013	G
4	C1	1015	U
4	C1	1017	C
4	C1	1018	G
4	C1	1020	G
4	C1	1024	G
4	C1	1028	U
4	C1	1029	G
4	C1	1036	A
4	C1	1037	C
4	C1	1041	U
4	C1	1047	A
4	C1	1049	C
4	C1	1063	G
4	C1	1064	A
4	C1	1065	A
4	C1	1072	G
4	C1	1081	U
4	C1	1083	G
4	C1	1087	G
4	C1	1093	A
4	C1	1094	U
4	C1	1095	U
4	C1	1096	U
4	C1	1097	G
4	C1	1098	A
4	C1	1103	A
4	C1	1104	G
4	C1	1117	G
4	C1	1131	G
4	C1	1143	A
4	C1	1144	U
4	C1	1153	A
4	C1	1155	C
4	C1	1159	A
4	C1	1178	G
4	C1	1180	A
4	C1	1181	U
4	C1	1192	C
4	C1	1193	A

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Mol	Chain	Res	Type
4	C1	1196	C
4	C1	1197	A
4	C1	1201	C
4	C1	1202	A
4	C1	1208	U
4	C1	1217	A
4	C1	1222	G
4	C1	1223	A
4	C1	1227	C
4	C1	1230	G
4	C1	1231	A
4	C1	1232	C
4	C1	1233	G
4	C1	1234	G
4	C1	1236	G
4	C1	1237	G
4	C1	1238	C
4	C1	1240	A
4	C1	1241	U
4	C1	1242	G
4	C1	1244	A
4	C1	1245	A
4	C1	1246	G
4	C1	1248	C
4	C1	1251	A
4	C1	1252	A
4	C1	1253	U
4	C1	1254	C
4	C1	1256	G
4	C1	1257	C
4	C1	1258	U
4	C1	1259	A
4	C1	1260	A
4	C1	1261	G
4	C1	1262	G
4	C1	1263	A
4	C1	1264	G
4	C1	1267	U
4	C1	1269	U
4	C1	1270	A
4	C1	1271	A
4	C1	1272	C

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Mol	Chain	Res	Type
4	C1	1273	A
4	C1	1274	A
4	C1	1275	C
4	C1	1278	A
4	C1	1279	C
4	C1	1280	C
4	C1	1282	G
4	C1	1283	C
4	C1	1285	G
4	C1	1286	A
4	C1	1287	A
4	C1	1305	U
4	C1	1307	G
4	C1	1308	A
4	C1	1309	U
4	C1	1313	G
4	C1	1325	U
4	C1	1330	A
4	C1	1332	A
4	C1	1348	U
4	C1	1349	G
4	C1	1351	U
4	C1	1352	A
4	C1	1355	A
4	C1	1356	U
4	C1	1357	G
4	C1	1386	A
4	C1	1392	G
4	C1	1399	A
4	C1	1400	G
4	C1	1418	A
4	C1	1419	A
4	C1	1434	G
4	C1	1435	A
4	C1	1437	C
4	C1	1443	G
4	C1	1446	A
4	C1	1450	G
4	C1	1477	A
4	C1	1481	A
4	C1	1483	G
4	C1	1487	G

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Mol	Chain	Res	Type
4	C1	1488	G
4	C1	1496	C
4	C1	1502	C
4	C1	1508	C
4	C1	1536	G
4	C1	1539	A
4	C1	1555	U
4	C1	1556	C
4	C1	1557	A
4	C1	1560	G
4	C1	1562	C
4	C1	1563	C
4	C1	1566	A
4	C1	1568	U
4	C1	1569	U
4	C1	1572	U
4	C1	1573	G
4	C1	1575	A
4	C1	1576	G
4	C1	1580	A
4	C1	1581	C
4	C1	1582	C
4	C1	1583	A
4	C1	1587	A
4	C1	1590	G
4	C1	1593	A
4	C1	1605	A
4	C1	1607	U
4	C1	1619	A
4	C1	1620	U
4	C1	1629	U
4	C1	1639	C
4	C1	1642	A
4	C1	1643	A
4	C1	1645	U
4	C1	1657	C
4	C1	1683	A
4	C1	1716	U
4	C1	1717	U
4	C1	1724	U
4	C1	1725	C
4	C1	1736	G

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Mol	Chain	Res	Type
4	C1	1741	A
4	C1	1750	A
4	C1	1751	G
4	C1	1760	A
4	C1	1761	C
4	C1	1765	U
4	C1	1766	G
4	C1	1770	G
4	C1	1775	G
4	C1	1778	G
4	C1	1780	G
4	C1	1794	G
4	C1	1797	A
4	C1	1808	G
4	C1	1814	A
4	C1	1816	A
4	C1	1819	U
4	C1	1820	U
4	C1	1821	U
4	C1	1835	A
4	C1	1839	A
4	C1	1840	U
4	C1	1841	A
4	C1	1842	A
4	C1	1846	C
4	C1	1849	C
4	C1	1866	C
4	C1	1867	A
4	C1	1879	A
4	C1	1880	U
4	C1	1881	A
4	C1	1893	A
4	C1	1906	G
4	C1	1952	G
4	C1	1953	G
4	C1	1954	G
4	C1	2094	C
4	C1	2102	U
4	C1	2111	G
4	C1	2112	U
4	C1	2113	A
4	C1	2114	C

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Mol	Chain	Res	Type
4	C1	2121	G
4	C1	2122	G
4	C1	2131	A
4	C1	2140	U
4	C1	2144	A
4	C1	2158	A
4	C1	2169	G
4	C1	2171	G
4	C1	2176	U
4	C1	2188	A
4	C1	2201	G
4	C1	2205	U
4	C1	2206	G
4	C1	2207	A
4	C1	2208	A
4	C1	2209	U
4	C1	2210	G
4	C1	2223	A
4	C1	2225	U
4	C1	2228	A
4	C1	2235	C
4	C1	2249	G
4	C1	2250	G
4	C1	2255	A
4	C1	2256	A
4	C1	2257	C
4	C1	2272	G
4	C1	2273	G
4	C1	2281	A
4	C1	2282	U
4	C1	2288	G
4	C1	2307	G
4	C1	2310	U
4	C1	2313	A
4	C1	2314	U
4	C1	2315	G
4	C1	2334	U
4	C1	2335	G
4	C1	2336	U
4	C1	2372	A
4	C1	2373	A
4	C1	2374	C

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Mol	Chain	Res	Type
4	C1	2375	G
4	C1	2385	G
4	C1	2388	U
4	C1	2393	G
4	C1	2397	A
4	C1	2398	A
4	C1	2402	A
4	C1	2403	G
4	C1	2404	A
4	C1	2411	U
4	C1	2419	A
4	C1	2435	G
4	C1	2437	G
4	C1	2439	A
4	C1	2443	A
4	C1	2445	A
4	C1	2450	G
4	C1	2453	U
4	C1	2454	G
4	C1	2455	U
4	C1	2456	A
4	C1	2457	G
4	C1	2458	A
4	C1	2459	A
4	C1	2460	U
4	C1	2461	A
4	C1	2463	G
4	C1	2467	G
4	C1	2468	A
4	C1	2472	U
4	C1	2474	G
4	C1	2475	G
4	C1	2477	G
4	C1	2479	C
4	C1	2480	A
4	C1	2486	A
4	C1	2487	U
4	C1	2490	C
4	C1	2491	A
4	C1	2493	U
4	C1	2495	C
4	C1	2497	U

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Mol	Chain	Res	Type
4	C1	2498	U
4	C1	2499	U
4	C1	2501	U
4	C1	2503	G
4	C1	2505	U
4	C1	2506	U
4	C1	2514	U
4	C1	2515	A
4	C1	2526	C
4	C1	2530	G
4	C1	2537	U
4	C1	2538	U
4	C1	2539	C
4	C1	2540	A
4	C1	2541	U
4	C1	2542	U
4	C1	2543	U
4	C1	2544	U
4	C1	2547	A
4	C1	2548	C
4	C1	2549	G
4	C1	2552	C
4	C1	2554	A
4	C1	2555	G
4	C1	2561	A
4	C1	2569	A
4	C1	2570	U
4	C1	2571	U
4	C1	2572	C
4	C1	2573	G
4	C1	2585	G
4	C1	2586	G
4	C1	2593	A
4	C1	2594	C
4	C1	2606	G
4	C1	2607	G
4	C1	2614	G
4	C1	2629	U
4	C1	2651	G
4	C1	2652	U
4	C1	2656	A
4	C1	2674	A

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Mol	Chain	Res	Type
4	C1	2677	G
4	C1	2678	A
4	C1	2689	A
4	C1	2691	A
4	C1	2694	A
4	C1	2696	A
4	C1	2704	A
4	C1	2714	G
4	C1	2719	U
4	C1	2728	G
4	C1	2737	C
4	C1	2752	U
4	C1	2753	G
4	C1	2755	C
4	C1	2772	C
4	C1	2777	G
4	C1	2778	G
4	C1	2788	C
4	C1	2791	G
4	C1	2796	G
4	C1	2800	G
4	C1	2801	A
4	C1	2803	A
4	C1	2810	C
4	C1	2814	G
4	C1	2816	G
4	C1	2817	A
4	C1	2818	U
4	C1	2821	C
4	C1	2842	U
4	C1	2844	C
4	C1	2845	A
4	C1	2849	C
4	C1	2859	U
4	C1	2860	U
4	C1	2867	C
4	C1	2871	G
4	C1	2872	A
4	C1	2875	U
4	C1	2876	C
4	C1	2887	A
4	C1	2898	G

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Mol	Chain	Res	Type
4	C1	2899	C
4	C1	2911	A
4	C1	2923	U
4	C1	2933	A
4	C1	2935	U
4	C1	2936	A
4	C1	2942	C
4	C1	2947	G
4	C1	2957	G
4	C1	2971	A
4	C1	2981	U
4	C1	2983	C
4	C1	2984	C
4	C1	2996	U
4	C1	2997	G
4	C1	3003	G
4	C1	3012	A
4	C1	3056	U
4	C1	3059	G
4	C1	3078	U
4	C1	3079	U
4	C1	3086	A
4	C1	3092	C
4	C1	3101	G
4	C1	3104	U
4	C1	3109	G
4	C1	3119	U
4	C1	3122	A
4	C1	3130	A
4	C1	3131	U
4	C1	3142	A
4	C1	3143	C
4	C1	3151	U
4	C1	3154	C
4	C1	3155	U
4	C1	3156	U
4	C1	3157	U
4	C1	3165	A
4	C1	3170	A
4	C1	3173	G
4	C1	3174	A
4	C1	3175	U

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Mol	Chain	Res	Type
4	C1	3176	G
4	C1	3179	U
4	C1	3181	C
4	C1	3186	A
4	C1	3187	A
4	C1	3196	U
4	C1	3207	U
4	C1	3209	A
4	C1	3217	C
4	C1	3218	A
4	C1	3219	G
4	C1	3228	C
4	C1	3229	G
4	C1	3243	A
4	C1	3245	A
4	C1	3247	G
4	C1	3259	U
4	C1	3263	G
4	C1	3269	U
4	C1	3270	U
4	C1	3273	A
4	C1	3276	G
4	C1	3281	U
4	C1	3287	U
4	C1	3288	G
4	C1	3289	G
4	C1	3294	A
4	C1	3295	A
4	C1	3303	G
4	C1	3304	U
4	C1	3307	A
4	C1	3313	U
4	C1	3316	A
4	C1	3317	U
4	C1	3318	G
4	C1	3319	U
4	C1	3320	A
4	C1	3335	A
4	C1	3341	U
4	C1	3345	G
4	C1	3351	U
4	C1	3352	U

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Mol	Chain	Res	Type
4	C1	3353	G
4	C1	3354	U
4	C1	3355	U
4	C1	3356	G
4	C1	3369	G
4	C1	3375	A
4	C1	3378	C
4	C1	3382	U
4	C1	3389	U
4	C1	3390	G
5	C4	7	G
5	C4	29	C
5	C4	53	U
5	C4	54	U
5	C4	55	A
5	C4	65	G
5	C4	73	C
5	C4	74	C
5	C4	102	A
5	C4	112	G
5	C4	121	U
6	C3	23	U
6	C3	34	U
6	C3	35	C
6	C3	38	U
6	C3	48	A
6	C3	51	G
6	C3	59	A
6	C3	62	C
6	C3	63	G
6	C3	80	A
6	C3	81	U
6	C3	82	U
6	C3	83	C
6	C3	85	G
6	C3	86	U
6	C3	87	G
6	C3	90	U
6	C3	95	G
6	C3	104	A
6	C3	106	C
6	C3	111	A

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Mol	Chain	Res	Type
6	C3	113	U
6	C3	125	U
6	C3	126	A
6	C3	138	A
6	C3	151	C
6	C3	152	G
6	C3	158	U

There are no RNA pucker outliers to report.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	H2U	C5	16	3	18,21,22	3.07	5 (27%)	19,30,33	1.49	4 (21%)
3	1MG	C5	9	3	23,26,27	2.91	8 (34%)	33,39,42	1.73	7 (21%)
3	1MA	C5	57	3	21,25,26	2.87	5 (23%)	30,37,40	2.78	8 (26%)
3	2MG	C5	10	3	23,26,27	2.68	9 (39%)	33,38,41	2.44	13 (39%)
3	7MG	C5	45	3	23,26,27	3.49	10 (43%)	27,39,42	2.09	9 (33%)
3	H2U	C5	46	3	18,21,22	3.16	5 (27%)	19,30,33	1.48	4 (21%)
3	5MC	C5	47	3	19,22,23	3.78	8 (42%)	26,32,35	0.99	2 (7%)
3	T6A	C5	36	3,85	31,34,35	2.03	10 (32%)	43,49,52	2.26	10 (23%)
3	M2G	C5	25	3	24,27,28	2.68	9 (37%)	33,40,43	2.09	9 (27%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	H2U	C5	16	3	-	0/7/38/39	0/2/2/2
3	1MG	C5	9	3	-	2/7/25/26	0/3/3/3
3	1MA	C5	57	3	-	0/7/25/26	0/3/3/3
3	2MG	C5	10	3	-	0/9/27/28	0/3/3/3
3	7MG	C5	45	3	-	0/7/37/38	0/3/3/3
3	H2U	C5	46	3	-	6/7/38/39	0/2/2/2
3	5MC	C5	47	3	-	2/7/25/26	0/2/2/2
3	T6A	C5	36	3,85	-	1/23/41/42	0/3/3/3
3	M2G	C5	25	3	-	0/11/29/30	0/3/3/3

All (69) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C5	46	H2U	C2-N1	9.77	1.49	1.35
3	C5	16	H2U	C2-N1	9.39	1.48	1.35
3	C5	47	5MC	C6-C5	9.08	1.49	1.34
3	C5	57	1MA	C2-N3	8.90	1.46	1.30
3	C5	45	7MG	C8-N9	8.09	1.51	1.45
3	C5	9	1MG	C2-N3	7.93	1.46	1.33
3	C5	10	2MG	C2-N3	7.53	1.46	1.32
3	C5	45	7MG	C5-N7	7.20	1.44	1.35
3	C5	57	1MA	C4-N3	6.87	1.49	1.35
3	C5	47	5MC	C4-N3	6.78	1.45	1.34
3	C5	25	M2G	C4-N3	6.77	1.49	1.34
3	C5	46	H2U	C2-N3	6.70	1.49	1.38
3	C5	16	H2U	C2-N3	6.55	1.49	1.38
3	C5	9	1MG	C4-N3	6.50	1.49	1.34
3	C5	9	1MG	C2-N2	6.40	1.45	1.34
3	C5	47	5MC	C5-C4	6.32	1.48	1.44
3	C5	25	M2G	C2-N2	6.13	1.46	1.35
3	C5	47	5MC	C2-N3	6.12	1.48	1.36
3	C5	45	7MG	C4-N3	5.69	1.47	1.34
3	C5	45	7MG	C2-N3	5.67	1.46	1.33
3	C5	10	2MG	C2-N2	5.59	1.45	1.33
3	C5	10	2MG	C4-N3	5.40	1.46	1.34
3	C5	16	H2U	C4-N3	5.17	1.46	1.37
3	C5	46	H2U	C4-N3	5.16	1.46	1.37
3	C5	36	T6A	C10-N6	5.01	1.48	1.37
3	C5	25	M2G	C2-N3	4.98	1.44	1.32
3	C5	45	7MG	C4-N9	4.76	1.43	1.37
3	C5	45	7MG	C2-N2	4.73	1.45	1.34
3	C5	47	5MC	C6-N1	4.51	1.45	1.38
3	C5	47	5MC	C4-N4	4.42	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C5	36	T6A	C10-N11	4.29	1.47	1.35
3	C5	47	5MC	C2-N1	4.16	1.48	1.40
3	C5	57	1MA	C2-N1	4.08	1.44	1.35
3	C5	57	1MA	C5-C6	3.94	1.54	1.43
3	C5	9	1MG	C2-N1	3.87	1.44	1.37
3	C5	45	7MG	C2-N1	3.80	1.46	1.37
3	C5	36	T6A	C6-N6	3.68	1.47	1.39
3	C5	45	7MG	C5-C6	3.66	1.52	1.43
3	C5	25	M2G	O6-C6	-3.64	1.16	1.23
3	C5	36	T6A	ODA-C13	3.46	1.32	1.22
3	C5	10	2MG	C2-N1	3.46	1.42	1.36
3	C5	36	T6A	C12-N11	3.45	1.53	1.45
3	C5	25	M2G	C2-N1	3.44	1.44	1.36
3	C5	25	M2G	C5-N7	-3.33	1.32	1.39
3	C5	45	7MG	C6-N1	3.29	1.45	1.38
3	C5	25	M2G	C4-N9	-3.13	1.30	1.38
3	C5	9	1MG	C5-C6	3.11	1.53	1.45
3	C5	9	1MG	C5-N7	-2.90	1.33	1.39
3	C5	36	T6A	O10-C10	-2.77	1.17	1.23
3	C5	25	M2G	C6-N1	2.75	1.44	1.38
3	C5	36	T6A	C12-C13	-2.74	1.47	1.52
3	C5	47	5MC	O2-C2	-2.69	1.18	1.23
3	C5	57	1MA	C5-N7	-2.66	1.33	1.39
3	C5	10	2MG	C5-N7	-2.66	1.33	1.39
3	C5	10	2MG	O6-C6	-2.60	1.18	1.23
3	C5	36	T6A	C5-C4	-2.56	1.34	1.39
3	C5	45	7MG	O6-C6	-2.53	1.18	1.23
3	C5	10	2MG	CM2-N2	2.52	1.50	1.45
3	C5	36	T6A	C5-C6	-2.49	1.35	1.41
3	C5	10	2MG	C6-N1	2.38	1.43	1.38
3	C5	16	H2U	O2-C2	-2.29	1.19	1.23
3	C5	46	H2U	O2-C2	-2.26	1.19	1.23
3	C5	10	2MG	C4-N9	-2.23	1.32	1.38
3	C5	9	1MG	O6-C6	-2.21	1.18	1.23
3	C5	25	M2G	C5-C6	2.17	1.52	1.44
3	C5	16	H2U	O4-C4	-2.13	1.19	1.23
3	C5	9	1MG	C4-N9	-2.12	1.32	1.38
3	C5	46	H2U	O4-C4	-2.04	1.19	1.23
3	C5	36	T6A	C8-N7	2.02	1.35	1.31

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C5	57	1MA	C1'-N9-C8	-8.83	101.64	126.73
3	C5	57	1MA	C1'-N9-C4	8.11	150.46	126.49
3	C5	10	2MG	C2-N3-C4	6.58	120.23	112.00
3	C5	36	T6A	N6-C10-N11	6.24	122.35	113.77
3	C5	25	M2G	C1'-N9-C8	-5.64	110.70	126.73
3	C5	36	T6A	N3-C2-N1	-5.55	120.17	128.58
3	C5	36	T6A	C5-C4-N3	-5.49	119.16	126.72
3	C5	10	2MG	C5-C4-N3	-5.17	120.16	128.39
3	C5	45	7MG	C5-C6-N1	4.95	119.66	110.94
3	C5	36	T6A	C4-C5-C6	4.94	120.89	116.78
3	C5	9	1MG	C5-C4-N3	-4.86	120.66	128.39
3	C5	57	1MA	C5-C4-N3	-4.83	120.15	127.27
3	C5	57	1MA	N1-C2-N3	-4.73	120.37	126.00
3	C5	25	M2G	C5-C4-N3	-4.59	121.09	128.39
3	C5	25	M2G	C1'-N9-C4	4.57	140.00	126.49
3	C5	45	7MG	C2-N3-C4	4.50	120.06	112.30
3	C5	10	2MG	C1'-N9-C8	-4.49	113.96	126.73
3	C5	10	2MG	C2-N1-C6	-4.28	119.38	124.55
3	C5	46	H2U	N3-C2-N1	4.03	120.70	116.65
3	C5	25	M2G	C2-N3-C4	4.01	119.93	112.51
3	C5	10	2MG	N1-C2-N2	3.84	120.48	116.56
3	C5	45	7MG	C5-C4-N3	-3.78	121.04	128.13
3	C5	57	1MA	C2-N3-C4	3.77	119.92	112.53
3	C5	36	T6A	N9-C8-N7	-3.74	108.63	113.94
3	C5	10	2MG	C1'-N9-C4	3.71	137.44	126.49
3	C5	25	M2G	N9-C8-N7	-3.55	106.81	113.40
3	C5	45	7MG	C4-C5-N7	3.54	109.56	105.38
3	C5	36	T6A	N3-C4-N9	3.54	133.19	127.17
3	C5	16	H2U	N3-C2-N1	3.48	120.14	116.65
3	C5	36	T6A	C2-N3-C4	3.42	120.19	111.83
3	C5	9	1MG	C2-N3-C4	3.42	119.67	111.98
3	C5	47	5MC	C5-C6-N1	-3.30	119.73	123.31
3	C5	9	1MG	N9-C8-N7	-3.28	107.32	113.40
3	C5	45	7MG	C5-C4-N9	3.22	110.46	106.33
3	C5	10	2MG	N9-C8-N7	-3.22	107.43	113.40
3	C5	16	H2U	C5-C4-N3	3.12	120.01	116.69
3	C5	46	H2U	C5-C6-N1	3.10	120.89	111.52
3	C5	10	2MG	N9-C4-N3	3.03	132.02	125.95
3	C5	36	T6A	O10-C10-N6	-2.92	118.46	123.64
3	C5	57	1MA	N9-C8-N7	-2.85	108.11	113.40
3	C5	9	1MG	N9-C4-N3	2.81	131.57	125.95
3	C5	16	H2U	C5-C6-N1	2.77	119.90	111.52
3	C5	10	2MG	C5-C6-N1	2.68	120.06	113.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C5	25	M2G	C5-C6-N1	2.66	120.02	113.25
3	C5	16	H2U	O2-C2-N1	-2.65	119.92	123.10
3	C5	36	T6A	C5-N7-C8	2.63	107.58	103.45
3	C5	9	1MG	C5-C6-N1	2.59	119.80	115.02
3	C5	25	M2G	N9-C4-N3	2.58	131.12	125.95
3	C5	45	7MG	C2-N1-C6	-2.58	120.43	125.11
3	C5	9	1MG	C1'-N9-C8	-2.56	119.47	126.73
3	C5	36	T6A	N6-C6-N1	2.51	124.04	117.54
3	C5	25	M2G	O6-C6-C5	-2.47	120.02	126.53
3	C5	10	2MG	O6-C6-C5	-2.46	120.03	126.53
3	C5	45	7MG	O6-C6-C5	-2.46	121.59	127.62
3	C5	46	H2U	C5-C4-N3	2.43	119.27	116.69
3	C5	25	M2G	C8-N7-C5	2.32	108.40	104.26
3	C5	10	2MG	C8-N7-C5	2.31	108.37	104.26
3	C5	9	1MG	C8-N7-C5	2.27	108.31	104.26
3	C5	45	7MG	N9-C8-N7	2.25	106.56	103.37
3	C5	57	1MA	N9-C4-N3	2.14	131.77	126.90
3	C5	46	H2U	O2-C2-N1	-2.13	120.54	123.10
3	C5	57	1MA	C8-N7-C5	2.11	108.01	104.26
3	C5	10	2MG	CM2-N2-C2	-2.10	119.14	123.65
3	C5	45	7MG	N9-C4-N3	2.08	128.50	125.46
3	C5	10	2MG	N1-C2-N3	-2.02	120.27	123.68
3	C5	47	5MC	CM5-C5-C6	-2.02	120.11	122.85

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C5	46	H2U	O4'-C4'-C5'-O5'
3	C5	46	H2U	O4'-C1'-N1-C6
3	C5	46	H2U	C2'-C1'-N1-C2
3	C5	46	H2U	C2'-C1'-N1-C6
3	C5	47	5MC	O4'-C4'-C5'-O5'
3	C5	46	H2U	C3'-C4'-C5'-O5'
3	C5	47	5MC	C3'-C4'-C5'-O5'
3	C5	36	T6A	C3'-C4'-C5'-O5'
3	C5	46	H2U	O4'-C1'-N1-C2
3	C5	9	1MG	C2'-C1'-N9-C8
3	C5	9	1MG	C2'-C1'-N9-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C5	45	7MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 332 ligands modelled in this entry, 325 are monoatomic - leaving 7 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
86	T1C	C1	3402	-	45,45,45	1.17	4 (8%)	56,72,72	1.14	4 (7%)
86	T1C	C1	3404	85	45,45,45	1.16	4 (8%)	56,72,72	1.02	3 (5%)
86	T1C	C1	3405	85	45,45,45	1.14	4 (8%)	56,72,72	1.33	6 (10%)
86	T1C	C2	1990	-	45,45,45	1.17	4 (8%)	56,72,72	0.93	2 (3%)
87	SPD	C1	3628	-	9,9,9	0.30	0	8,8,8	0.97	0
86	T1C	C1	3401	-	45,45,45	1.15	4 (8%)	56,72,72	1.44	9 (16%)
86	T1C	C1	3403	85	45,45,45	1.18	4 (8%)	56,72,72	1.06	4 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	T1C	C1	3402	-	-	13/22/80/80	0/4/4/4
86	T1C	C1	3404	85	-	7/22/80/80	0/4/4/4
86	T1C	C1	3405	85	-	11/22/80/80	0/4/4/4
86	T1C	C2	1990	-	-	9/22/80/80	0/4/4/4
87	SPD	C1	3628	-	-	5/7/7/7	-
86	T1C	C1	3401	-	-	11/22/80/80	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	T1C	C1	3403	85	-	13/22/80/80	0/4/4/4

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	C1	3402	T1C	C21-N21	5.09	1.48	1.33
86	C2	1990	T1C	C21-N21	5.08	1.48	1.33
86	C1	3401	T1C	C21-N21	5.04	1.48	1.33
86	C1	3403	T1C	C21-N21	5.04	1.48	1.33
86	C1	3404	T1C	C21-N21	5.01	1.47	1.33
86	C1	3405	T1C	C21-N21	4.96	1.47	1.33
86	C1	3402	T1C	C4-N4	2.53	1.52	1.47
86	C1	3404	T1C	C4-N4	2.51	1.52	1.47
86	C2	1990	T1C	C4-N4	2.28	1.52	1.47
86	C1	3405	T1C	O11-C11	2.28	1.28	1.23
86	C2	1990	T1C	O11-C11	2.26	1.28	1.23
86	C1	3402	T1C	O11-C11	2.25	1.28	1.23
86	C1	3401	T1C	O11-C11	2.24	1.27	1.23
86	C1	3404	T1C	O11-C11	2.23	1.27	1.23
86	C1	3403	T1C	O11-C11	2.21	1.27	1.23
86	C1	3405	T1C	C4-N4	2.20	1.52	1.47
86	C1	3401	T1C	C7-N7	2.17	1.48	1.42
86	C1	3403	T1C	C4-N4	2.15	1.51	1.47
86	C1	3401	T1C	C4-N4	2.14	1.51	1.47
86	C1	3402	T1C	C7-N7	2.12	1.48	1.42
86	C1	3403	T1C	C7-N7	2.11	1.48	1.42
86	C2	1990	T1C	C7-N7	2.08	1.48	1.42
86	C1	3405	T1C	C7-N7	2.04	1.47	1.42
86	C1	3404	T1C	C7-N7	2.03	1.47	1.42

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	C1	3401	T1C	C11-C1B-C12	4.63	122.47	118.80
86	C1	3405	T1C	C1-C1C-C12	4.47	115.12	109.88
86	C1	3402	T1C	C1C-C1-C2	4.39	122.72	115.75
86	C1	3401	T1C	C1C-C1-C2	4.23	122.47	115.75
86	C1	3405	T1C	C11-C1B-C12	4.09	122.03	118.80
86	C1	3405	T1C	O1C-C1C-C12	-3.97	103.79	110.14
86	C1	3401	T1C	C1C-C41-C4	3.86	116.91	111.64
86	C1	3403	T1C	C11-C1B-C12	3.74	121.76	118.80
86	C2	1990	T1C	C1-C1C-C12	3.34	113.80	109.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	C1	3402	T1C	C11-C1B-C12	2.99	121.17	118.80
86	C1	3405	T1C	C21-C2-C1	2.97	124.48	120.97
86	C1	3401	T1C	C61-C6-C51	2.94	117.01	113.12
86	C1	3405	T1C	C1C-C41-C4	2.91	115.62	111.64
86	C1	3401	T1C	O1C-C1C-C12	-2.67	105.87	110.14
86	C1	3403	T1C	C51-C5-C41	-2.63	105.90	110.38
86	C1	3404	T1C	C11-C1B-C12	2.62	120.87	118.80
86	C1	3401	T1C	C51-C5-C41	-2.62	105.92	110.38
86	C1	3401	T1C	C5-C51-C1B	-2.61	104.62	110.28
86	C1	3401	T1C	C1-C1C-C12	2.60	112.94	109.88
86	C1	3405	T1C	C5-C41-C4	-2.50	110.12	113.73
86	C2	1990	T1C	C11-C1B-C12	2.44	120.73	118.80
86	C1	3402	T1C	C61-C6-C51	2.37	116.26	113.12
86	C1	3402	T1C	O1C-C1C-C12	-2.35	106.39	110.14
86	C1	3403	T1C	C1-C1C-C12	2.30	112.58	109.88
86	C1	3404	T1C	C61-C6-C51	2.29	116.16	113.12
86	C1	3401	T1C	C72-N7-C71	-2.06	109.56	116.18
86	C1	3404	T1C	C8-C9-C10	-2.05	118.54	120.53
86	C1	3403	T1C	C1C-C41-C4	2.00	114.37	111.64

There are no chirality outliers.

All (69) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	C2	1990	T1C	C92-C91-N9-C9
86	C2	1990	T1C	C3-C2-C21-O21
86	C2	1990	T1C	C3-C2-C21-N21
86	C2	1990	T1C	C1-C2-C21-O21
86	C2	1990	T1C	C1-C2-C21-N21
86	C1	3401	T1C	C94-C93-N92-C92
86	C1	3401	T1C	C95-C93-N92-C92
86	C1	3401	T1C	C96-C93-N92-C92
86	C1	3401	T1C	C41-C4-N4-C43
86	C1	3401	T1C	C1-C2-C21-O21
86	C1	3401	T1C	C1-C2-C21-N21
86	C1	3402	T1C	C92-C91-N9-C9
86	C1	3402	T1C	C1-C2-C21-O21
86	C1	3402	T1C	C1-C2-C21-N21
86	C1	3403	T1C	C92-C91-N9-C9
86	C1	3403	T1C	C3-C4-N4-C43
86	C1	3403	T1C	C3-C2-C21-O21
86	C1	3404	T1C	C91-C92-N92-C93

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Mol	Chain	Res	Type	Atoms
86	C1	3404	T1C	C1-C2-C21-O21
86	C1	3404	T1C	C1-C2-C21-N21
86	C1	3405	T1C	C92-C91-N9-C9
86	C1	3405	T1C	C3-C2-C21-O21
86	C1	3405	T1C	C3-C2-C21-N21
86	C1	3405	T1C	C1-C2-C21-O21
86	C1	3405	T1C	C1-C2-C21-N21
86	C2	1990	T1C	O91-C91-N9-C9
86	C1	3405	T1C	O91-C91-N9-C9
87	C1	3628	SPD	C3-C4-C5-N6
86	C1	3402	T1C	O91-C91-N9-C9
86	C1	3403	T1C	O91-C91-N9-C9
87	C1	3628	SPD	N6-C7-C8-C9
87	C1	3628	SPD	C4-C5-N6-C7
86	C1	3405	T1C	O91-C91-C92-N92
86	C1	3405	T1C	N9-C91-C92-N92
86	C1	3401	T1C	C10-C9-N9-C91
86	C1	3403	T1C	O91-C91-C92-N92
86	C1	3401	T1C	C8-C9-N9-C91
86	C1	3404	T1C	O91-C91-N9-C9
86	C1	3403	T1C	N9-C91-C92-N92
86	C1	3402	T1C	N9-C91-C92-N92
86	C1	3402	T1C	O91-C91-C92-N92
86	C1	3401	T1C	C3-C2-C21-N21
86	C1	3403	T1C	C41-C4-N4-C43
86	C1	3403	T1C	C41-C4-N4-C42
86	C1	3403	T1C	C3-C4-N4-C42
86	C1	3403	T1C	C3-C2-C21-N21
86	C1	3401	T1C	C3-C2-C21-O21
86	C1	3402	T1C	C3-C2-C21-O21
86	C2	1990	T1C	C91-C92-N92-C93
86	C1	3401	T1C	C91-C92-N92-C93
86	C1	3402	T1C	C91-C92-N92-C93
86	C1	3405	T1C	C91-C92-N92-C93
86	C1	3403	T1C	C1-C2-C21-N21
86	C1	3404	T1C	C92-C91-N9-C9
87	C1	3628	SPD	C2-C3-C4-C5
86	C1	3402	T1C	C95-C93-N92-C92
86	C1	3403	T1C	C10-C9-N9-C91
86	C1	3402	T1C	C96-C93-N92-C92
87	C1	3628	SPD	C8-C7-N6-C5
86	C1	3405	T1C	C61-C7-N7-C71

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Mol	Chain	Res	Type	Atoms
86	C1	3402	T1C	C61-C7-N7-C71
86	C1	3402	T1C	C61-C7-N7-C72
86	C1	3405	T1C	C61-C7-N7-C72
86	C1	3402	T1C	C3-C2-C21-N21
86	C1	3404	T1C	C3-C2-C21-N21
86	C2	1990	T1C	C61-C7-N7-C71
86	C1	3404	T1C	C95-C93-N92-C92
86	C1	3403	T1C	C1-C2-C21-O21
86	C2	1990	T1C	C61-C7-N7-C72

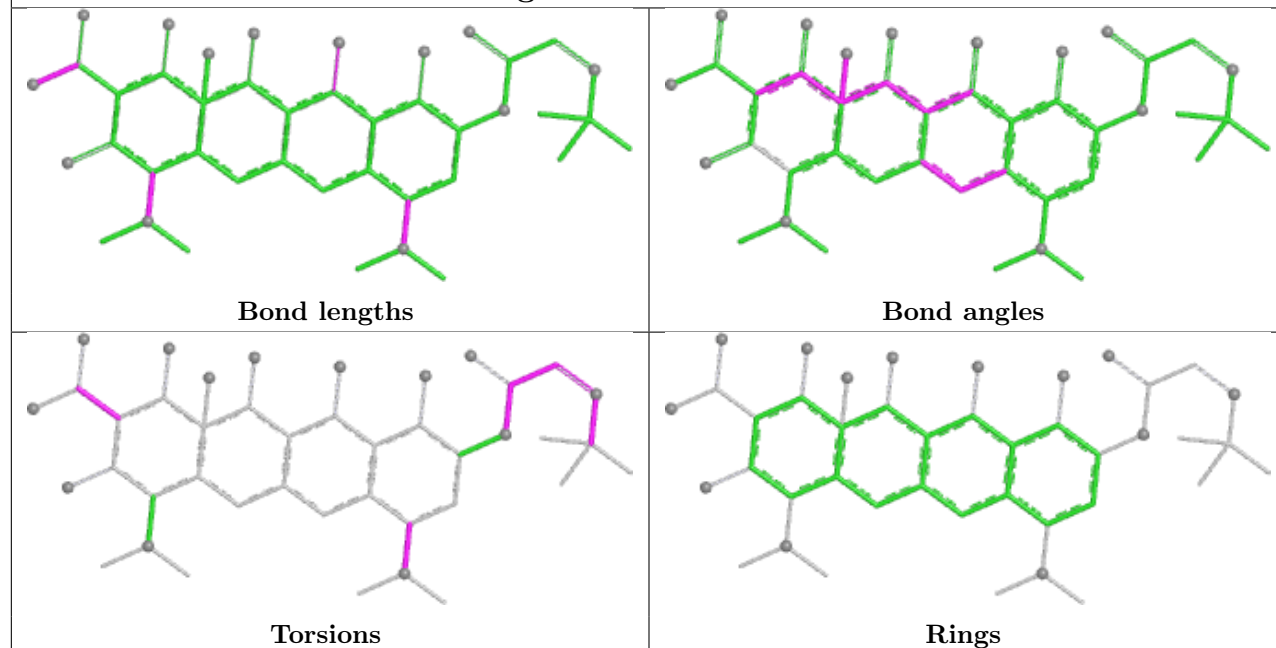
There are no ring outliers.

3 monomers are involved in 7 short contacts:

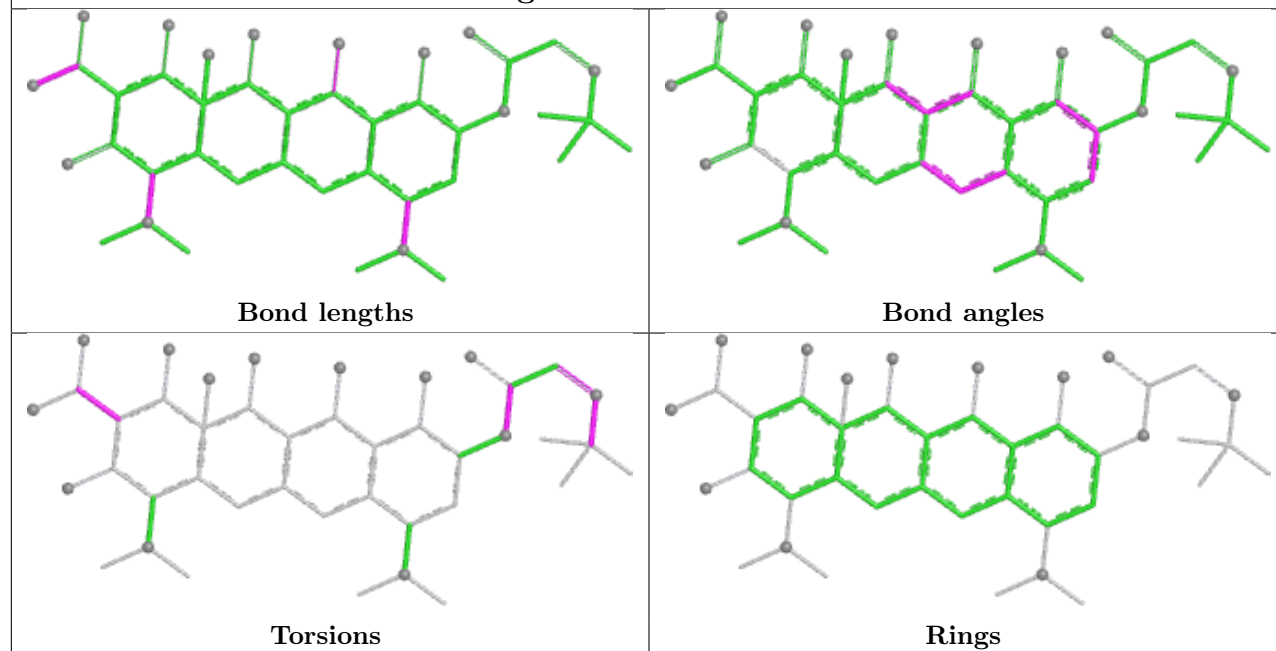
Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	C1	3402	T1C	3	0
86	C1	3404	T1C	1	0
86	C1	3403	T1C	3	0

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

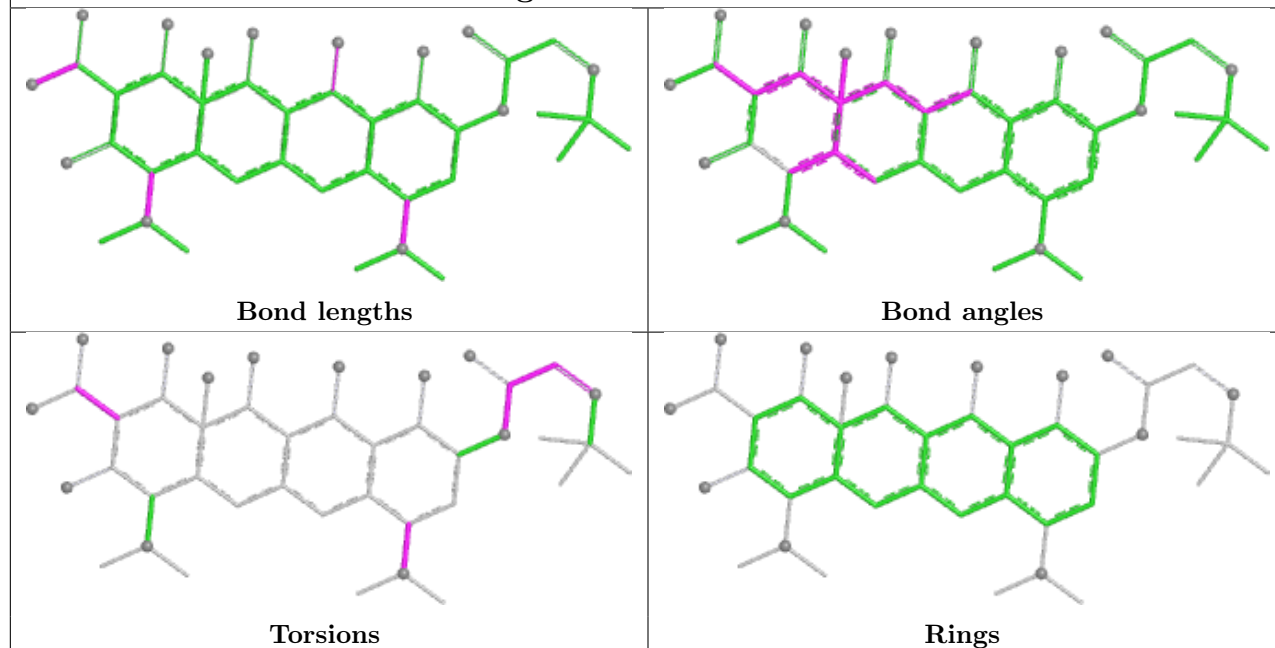
Ligand T1C C1 3402



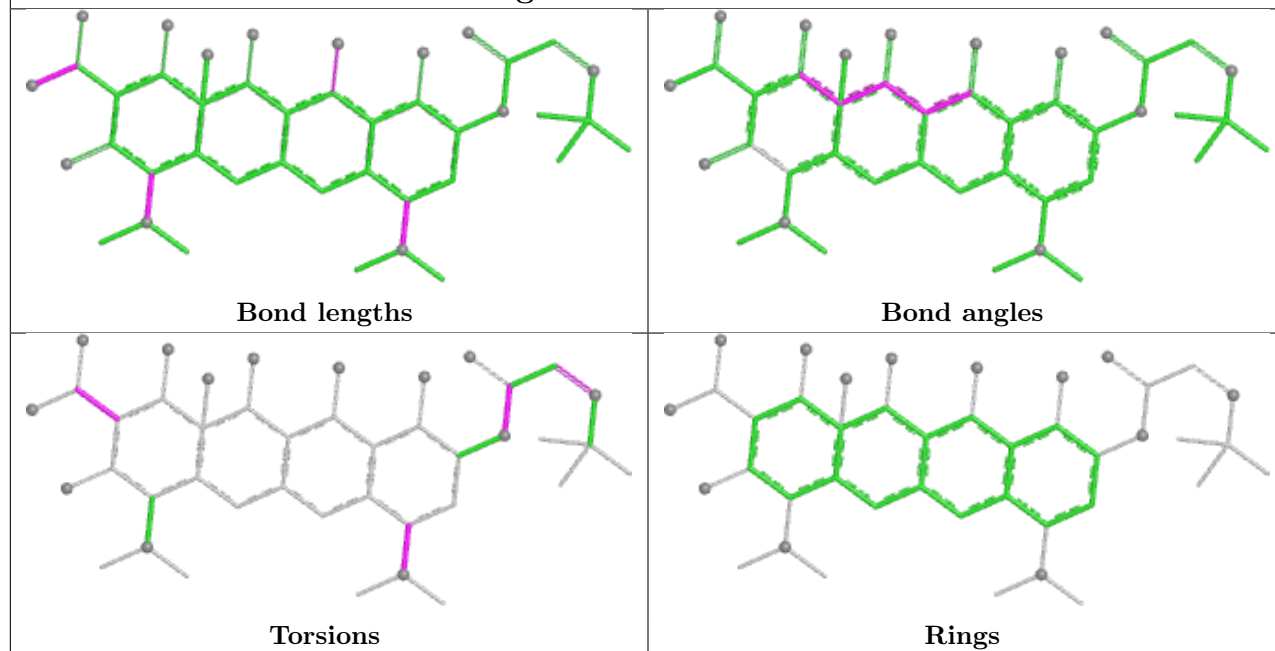
Ligand T1C C1 3404

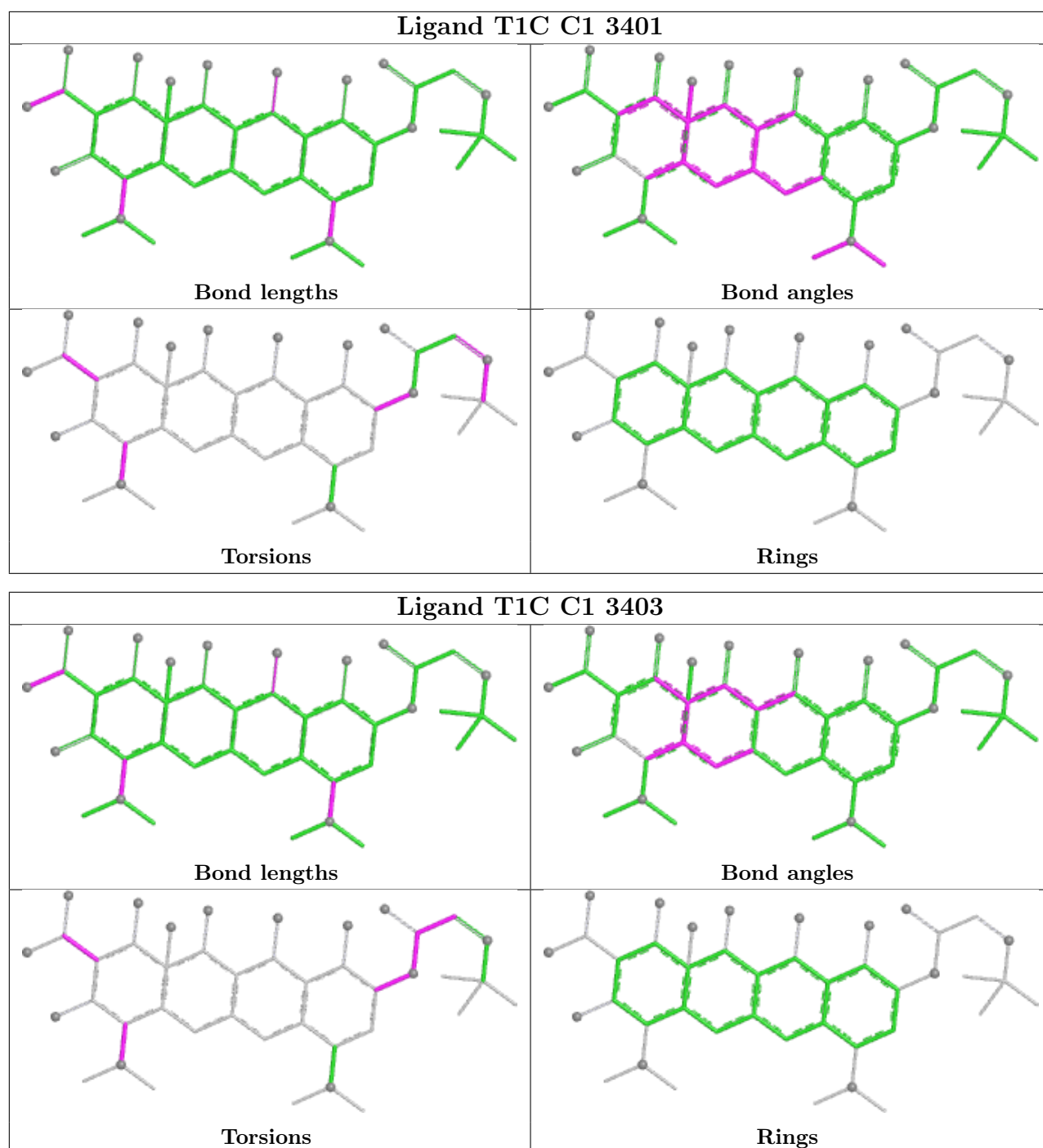


Ligand T1C C1 3405



Ligand T1C C2 1990





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

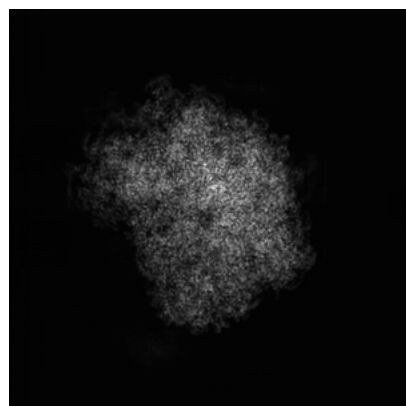
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36945. These allow visual inspection of the internal detail of the map and identification of artifacts.

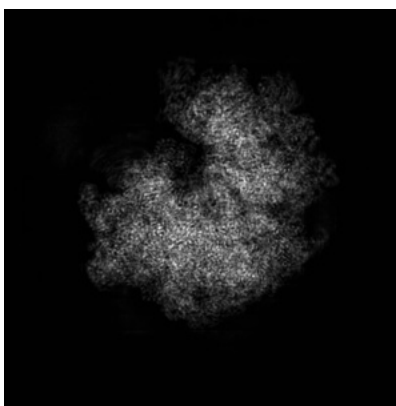
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

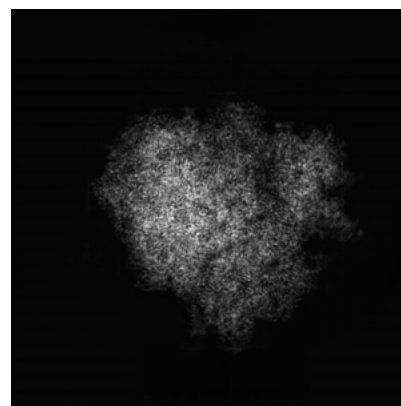
6.1.1 Primary map



X

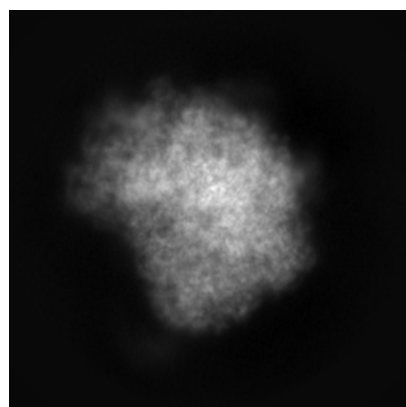


Y

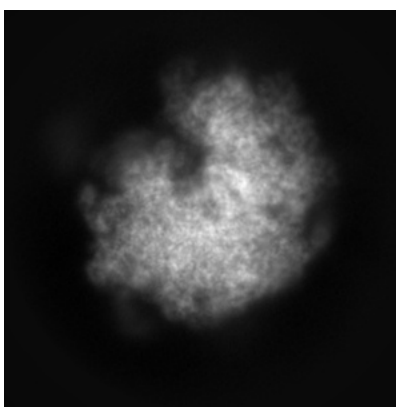


Z

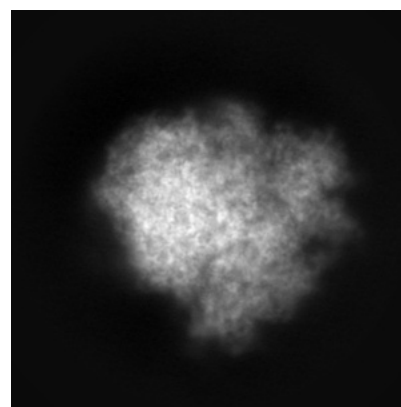
6.1.2 Raw map



X



Y



Z

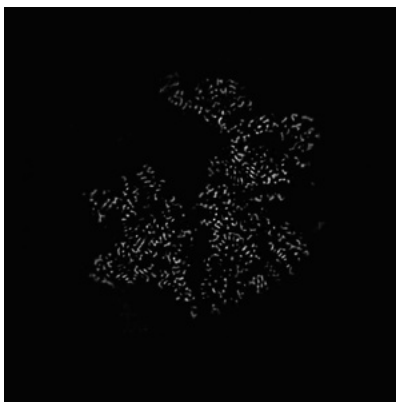
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240

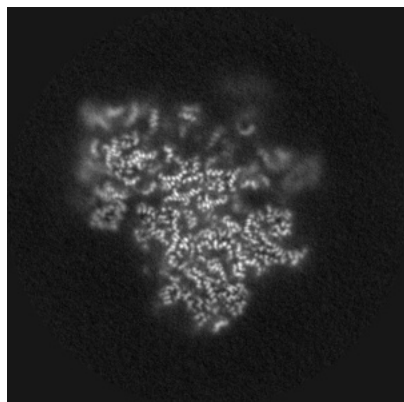


Y Index: 240

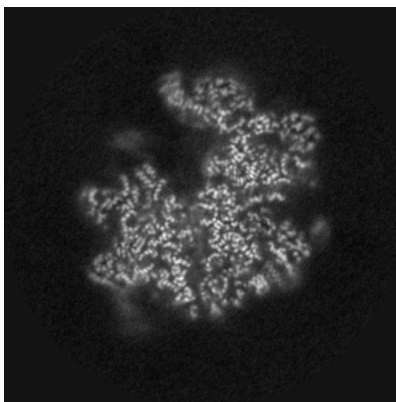


Z Index: 240

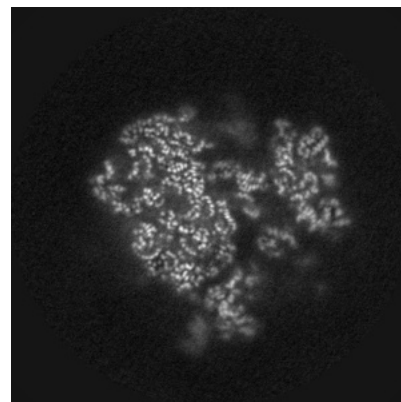
6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

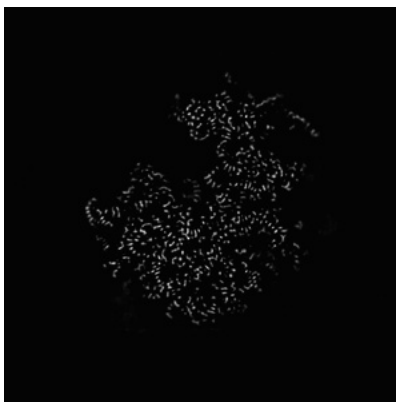
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

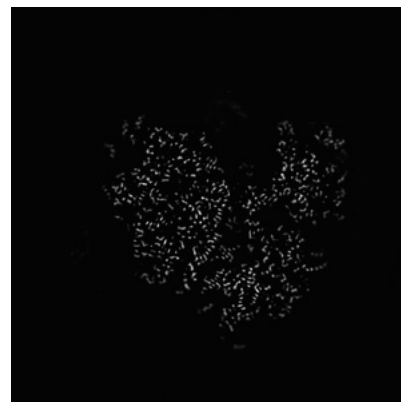
6.3.1 Primary map



X Index: 213

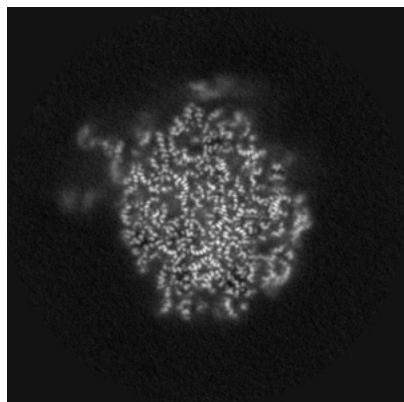


Y Index: 256

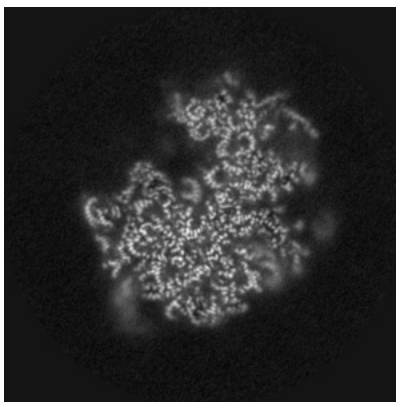


Z Index: 268

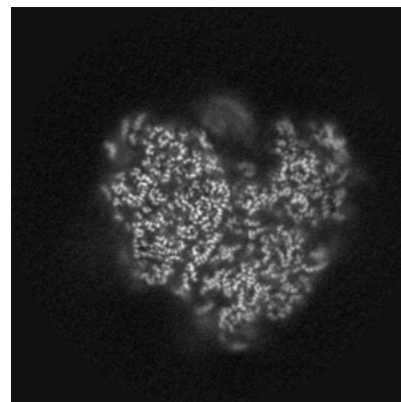
6.3.2 Raw map



X Index: 213



Y Index: 256

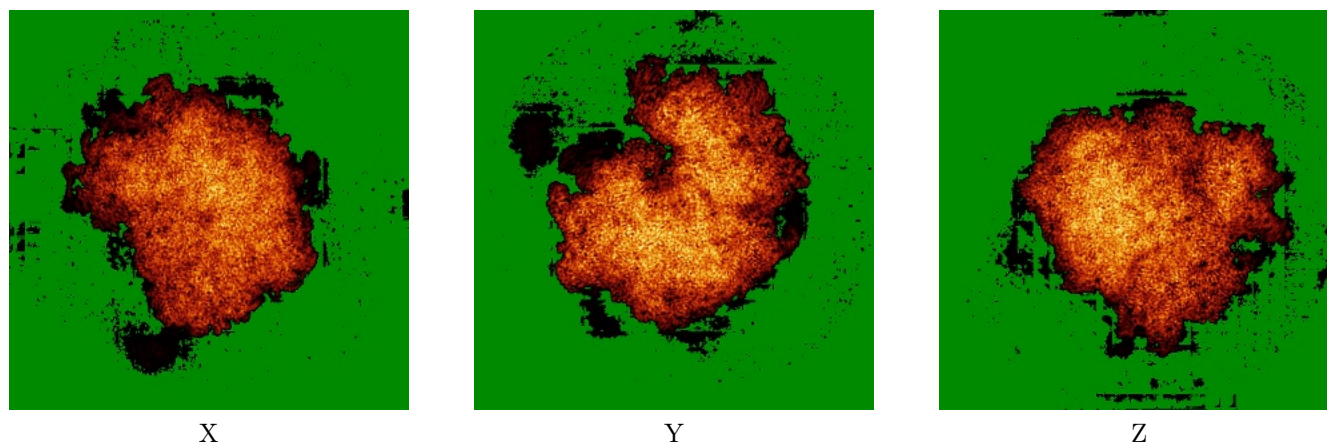


Z Index: 268

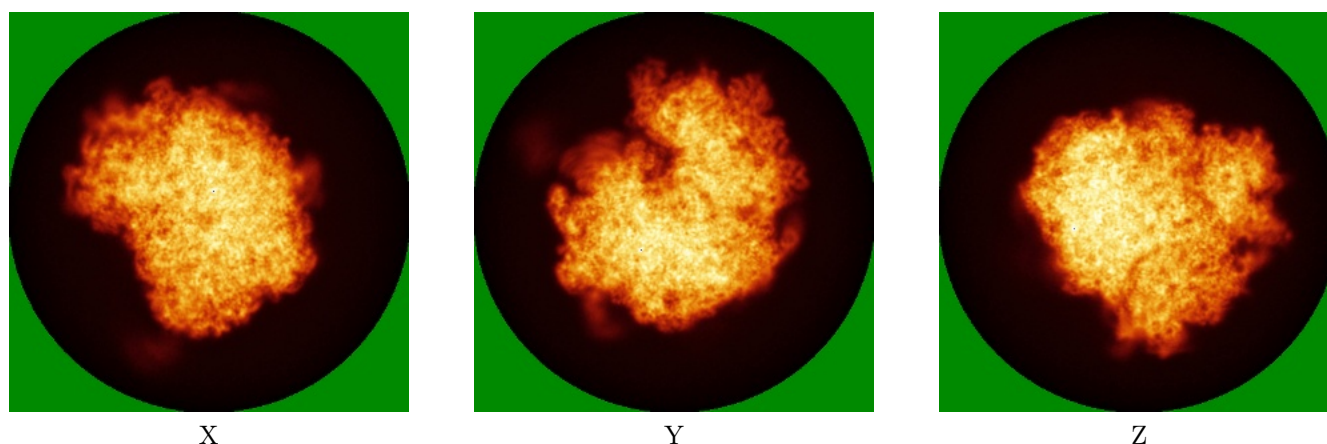
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

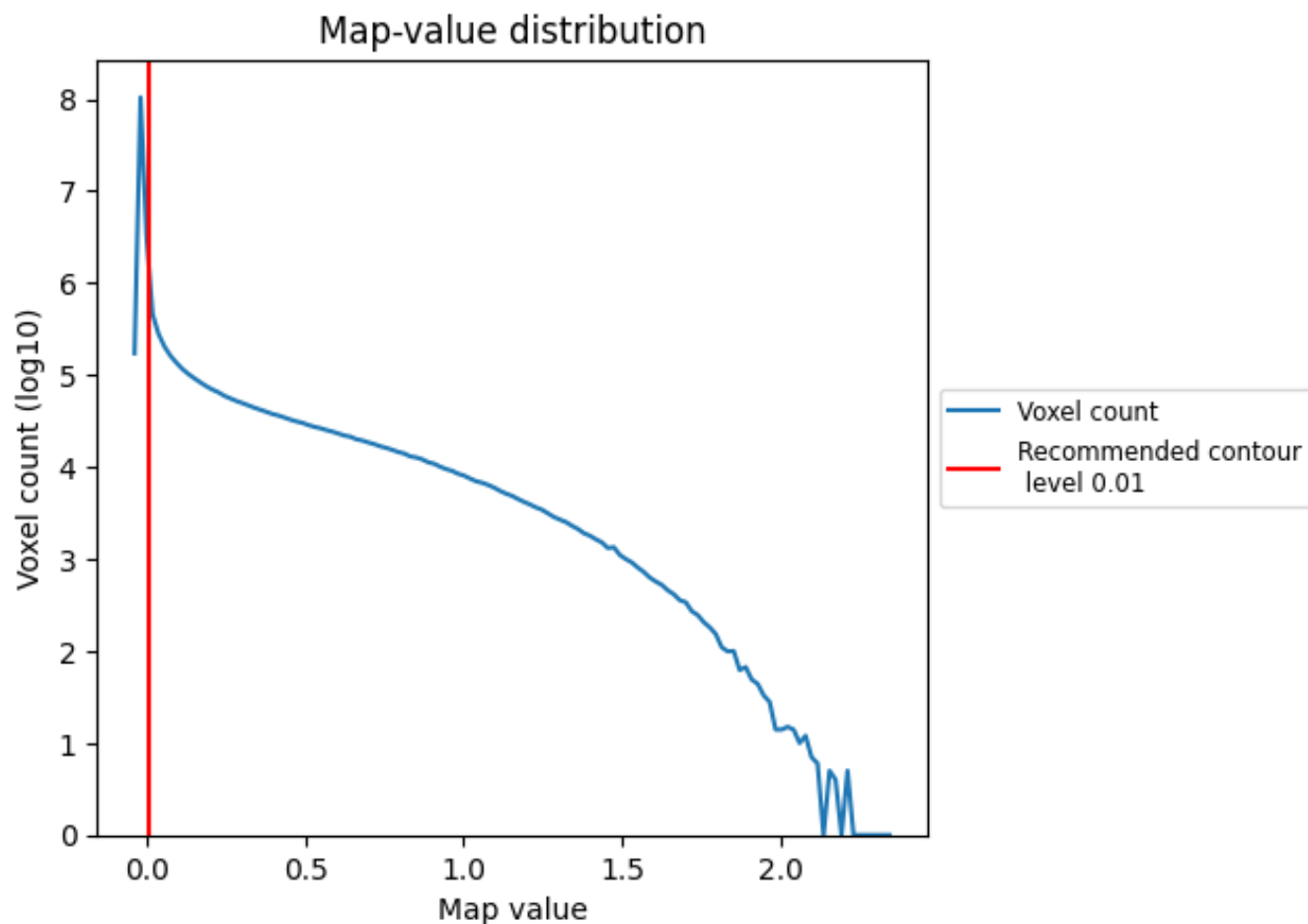
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

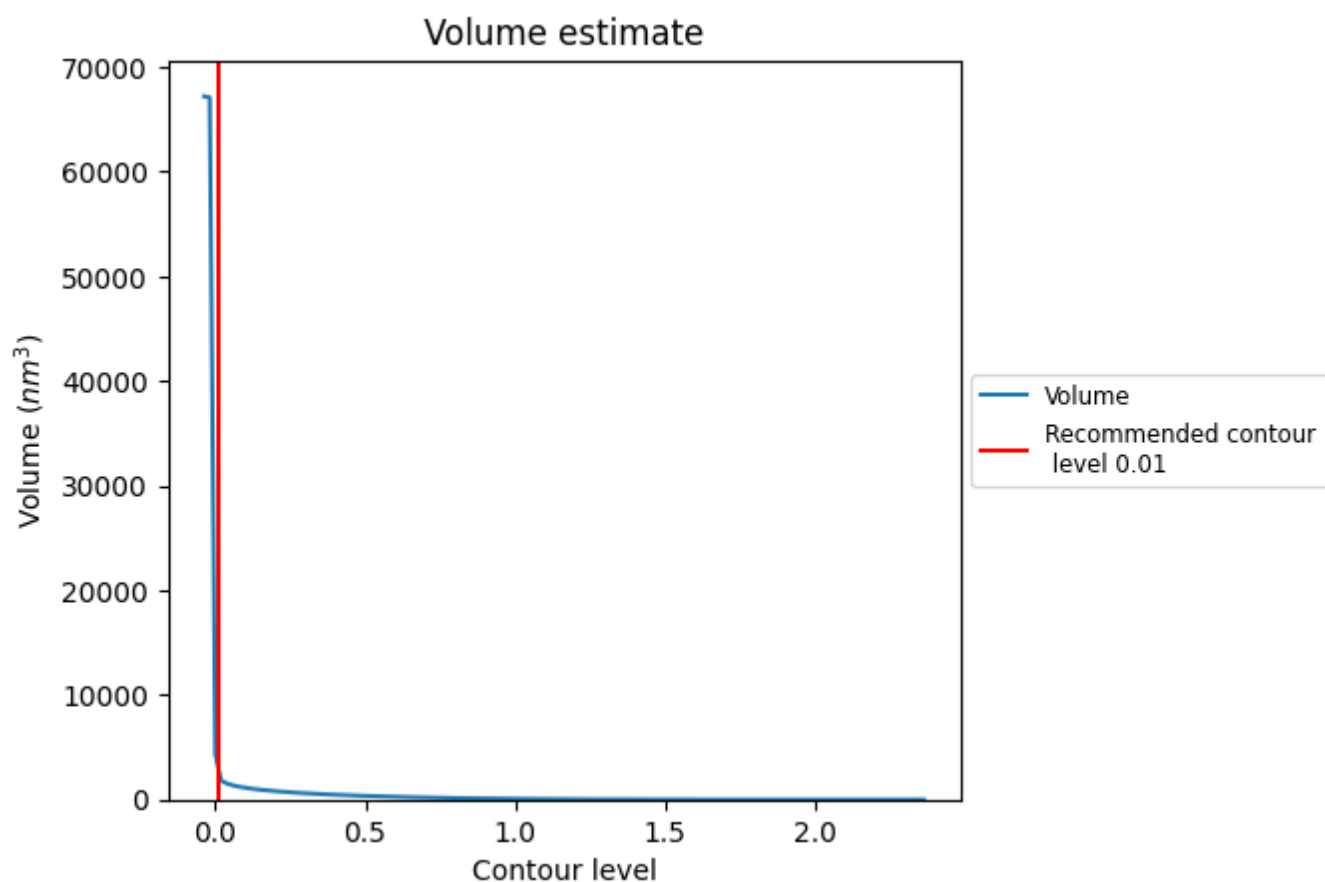
This section contains the results of statistical analysis of the map.

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.

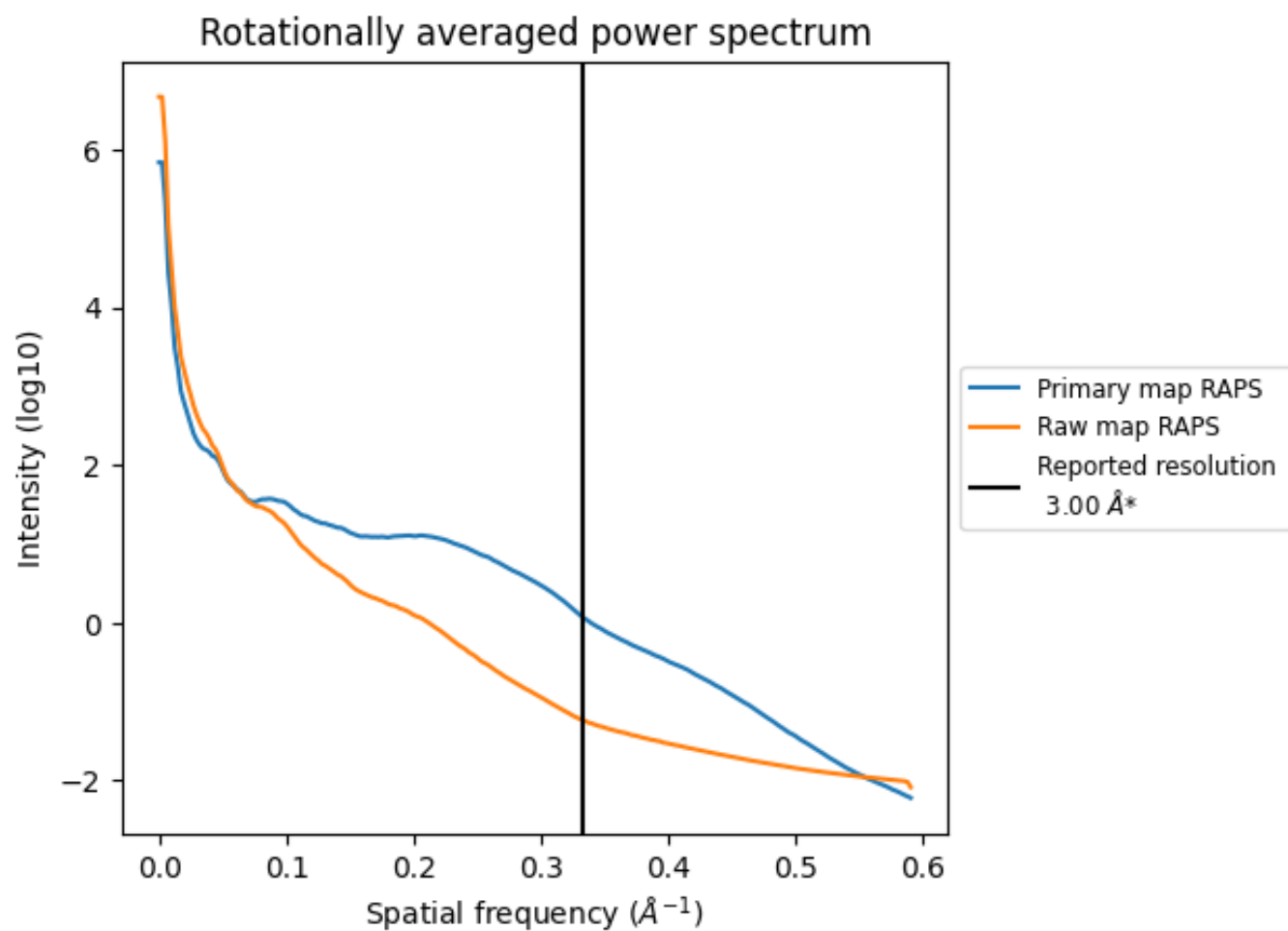
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3065 nm³; this corresponds to an approximate mass of 2769 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 ⓘ

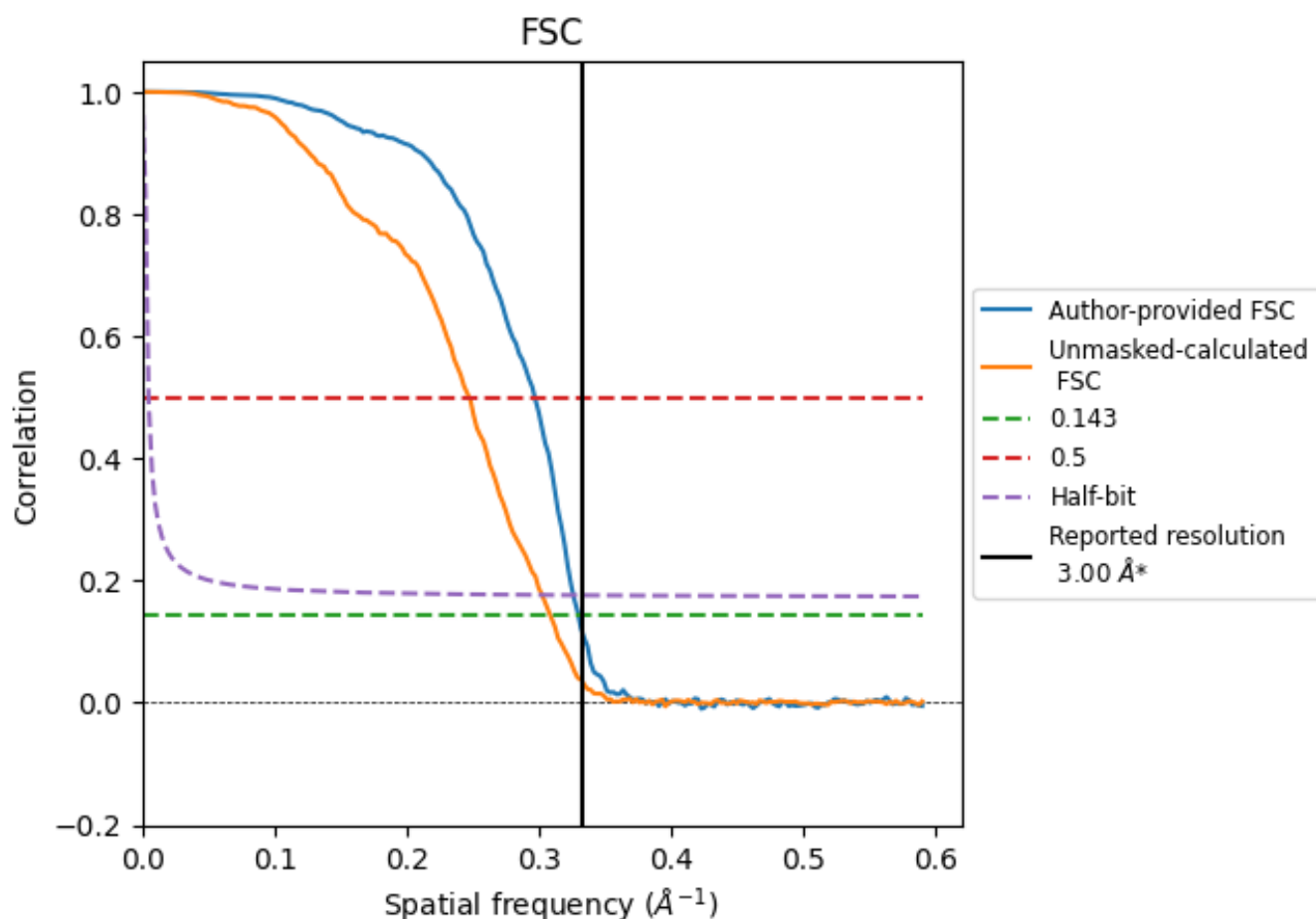


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

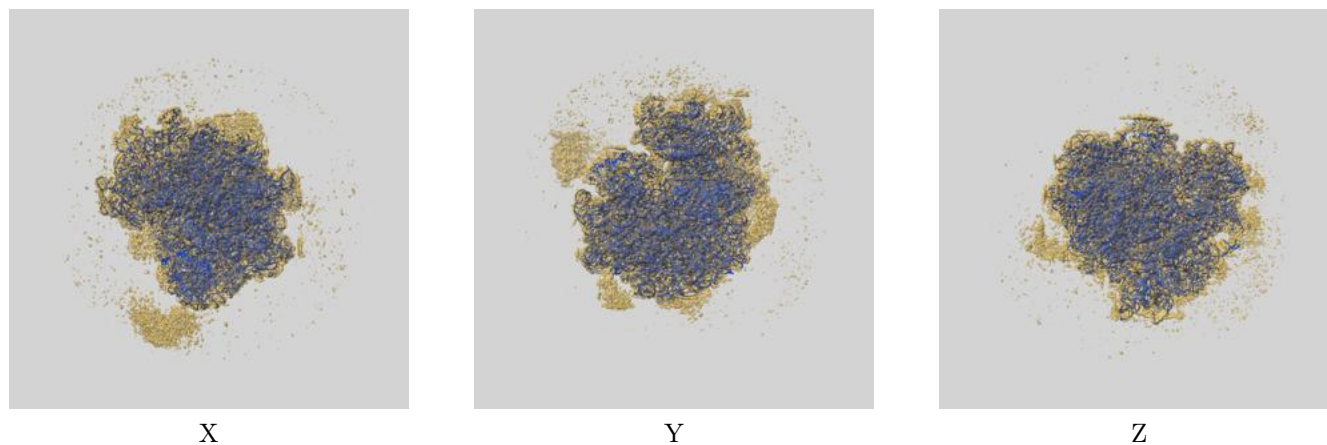
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.03	3.37	3.06
Unmasked-calculated*	3.24	4.04	3.30

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

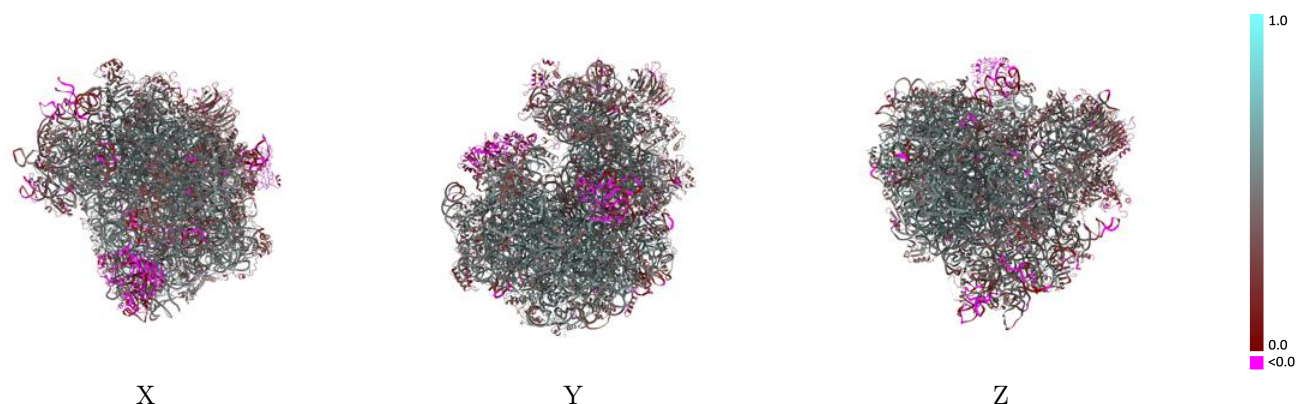
This section contains information regarding the fit between EMDB map EMD-36945 and PDB model 8K82. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



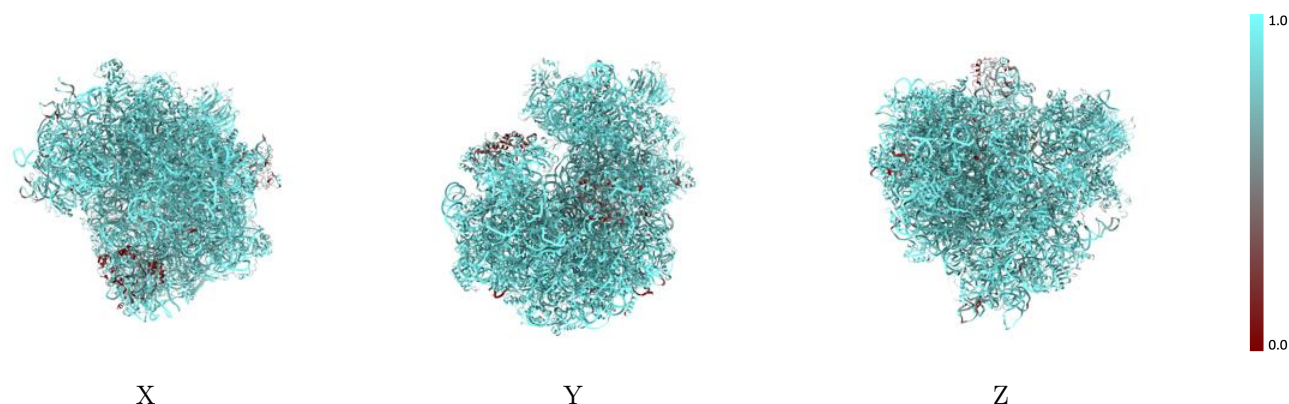
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



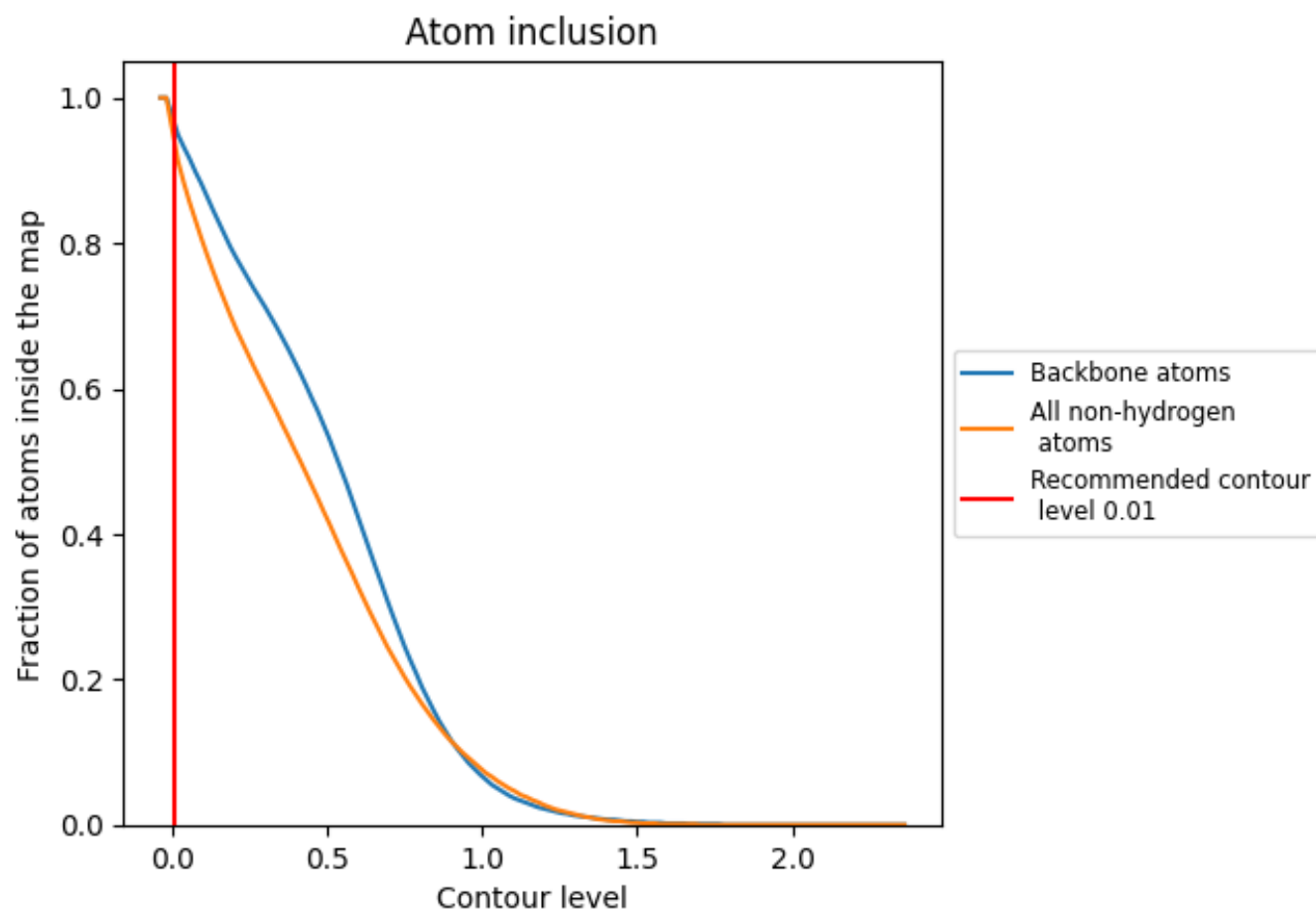
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9330	 0.4530
C1	 0.9650	 0.5090
C2	 0.9580	 0.4620
C3	 0.9820	 0.5350
C4	 0.9920	 0.5310
C5	 0.9480	 0.4580
C7	 1.0000	 0.5590
CN	 0.7270	 0.2950
L1	 0.3790	 -0.0680
L2	 0.6130	 0.2870
LA	 0.9440	 0.5020
LB	 0.9350	 0.4740
LC	 0.9380	 0.4510
LD	 0.8690	 0.3370
LE	 0.9050	 0.3950
LF	 0.9460	 0.4710
LG	 0.9160	 0.4020
LH	 0.9180	 0.4230
LI	 0.9020	 0.4290
LJ	 0.9120	 0.4070
LK	 0.3750	 -0.0300
LL	 0.9300	 0.4450
LM	 0.9250	 0.4390
LN	 0.9590	 0.5190
LO	 0.9550	 0.4860
LP	 0.9350	 0.4850
LQ	 0.9420	 0.4720
LR	 0.9380	 0.4810
LS	 0.9310	 0.4710
LT	 0.9290	 0.4650
LU	 0.9170	 0.4060
LV	 0.9080	 0.4630
LW	 0.9170	 0.4710
LX	 0.9250	 0.4630
LY	 0.9220	 0.4320



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Chain	Atom inclusion	Q-score
LZ	 0.9130	 0.4250
La	 0.9540	 0.4870
Lb	 0.8830	 0.4080
Lc	 0.9020	 0.4380
Ld	 0.8840	 0.4360
Le	 0.9300	 0.4780
Lf	 0.9570	 0.5090
Lg	 0.9320	 0.4900
Lh	 0.9050	 0.4340
Li	 0.9020	 0.4010
Lj	 0.9730	 0.5400
Lk	 0.8990	 0.3960
Ll	 0.9470	 0.4730
Lm	 0.9310	 0.4650
Ln	 0.8910	 0.4330
Lo	 0.9230	 0.4630
Lp	 0.9060	 0.4620
P0	 0.5110	 0.0120
SA	 0.9340	 0.4020
SB	 0.9050	 0.3940
SC	 0.9280	 0.4420
SD	 0.8720	 0.3340
SE	 0.9070	 0.3970
SF	 0.8830	 0.3540
SG	 0.8670	 0.3200
SH	 0.8770	 0.3190
SI	 0.9180	 0.4380
SJ	 0.8970	 0.3920
SK	 0.8860	 0.3090
SL	 0.9110	 0.4550
SM	 0.7640	 0.0910
SN	 0.9200	 0.4400
SO	 0.9260	 0.4350
SP	 0.8630	 0.3220
SQ	 0.9040	 0.3890
SR	 0.9020	 0.3690
SS	 0.8710	 0.3250
ST	 0.8920	 0.3610
SU	 0.8600	 0.3220
SV	 0.9010	 0.3780
SW	 0.9480	 0.4860
SX	 0.8990	 0.4400

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Chain	Atom inclusion	Q-score
SY	 0.8620	 0.3510
SZ	 0.8760	 0.3060
Sa	 0.9260	 0.4570
Sb	 0.9370	 0.4190
Sc	 0.8550	 0.3490
Sd	 0.9340	 0.4670
Se	 0.8040	 0.3400
Sf	 0.7590	 0.0760
Sg	 0.8800	 0.2950