



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:04 PM UTC

PDB ID : 7ZW0 / pdb_00007zw0
EMDB ID : EMD-14990
Title : FAP-80S Complex - Rotated state
Authors : Ikeuchi, K.; Buschauer, R.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2022-05-17
Resolution : 2.40 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:

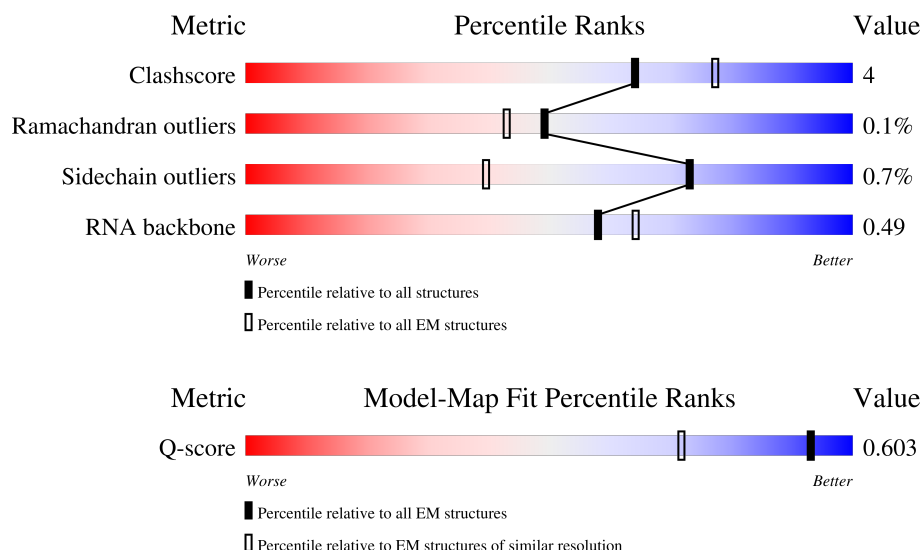
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5628 (1.90 - 2.90)

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	LA	3396	
2	LB	217	
3	2	1800	

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Mol	Chain	Length	Quality of chain
4	sP	252	
5	sQ	255	
6	sE	142	
7	sR	254	
8	sA	240	
9	sS	261	
10	sB	225	
11	sT	236	
12	sU	190	
13	sV	200	
14	sW	197	
15	sC	105	
16	sX	156	
17	sD	143	
18	sY	151	
19	sZ	137	
20	sF	143	
21	sG	136	
22	sH	146	
23	sI	144	
24	sJ	121	
25	sa	87	
26	sb	130	
27	sc	145	
28	sd	135	

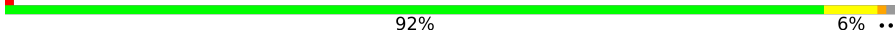
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Mol	Chain	Length	Quality of chain
29	sK	108	
30	se	119	
31	sf	82	
32	sM	56	
33	sg	63	
34	sN	76	
35	sO	319	
36	sL	67	
37	sj	235	
38	sk	114	
39	sm	29	
40	sl	76	
40	sn	76	
41	LC	121	
42	LD	158	
43	LE	254	
44	LF	387	
45	LG	362	
46	LH	297	
47	LI	176	
48	LJ	244	
49	LK	256	
50	LL	191	
51	LM	221	
52	LN	174	

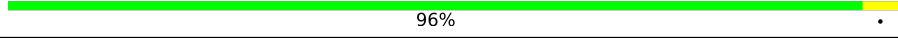
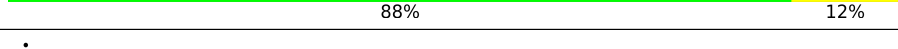
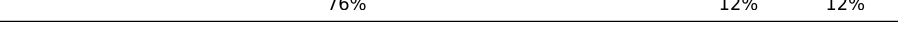
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Mol	Chain	Length	Quality of chain
53	LO	199	
54	LP	138	
55	LQ	204	
56	LR	199	
57	LS	184	
58	LT	186	
59	LU	189	
60	LV	172	
61	LW	160	
62	LX	121	
63	LY	137	
64	LZ	155	
65	La	142	
66	Lb	127	
67	Lc	136	
68	Ld	149	
69	Le	59	
70	Lf	105	
71	Lg	113	
72	Lh	130	
73	Li	107	
74	Lj	121	
75	Lk	120	
76	Ll	100	
77	Lm	88	

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Mol	Chain	Length	Quality of chain
78	Ln	78	
79	Lo	51	
80	Lp	52	
81	Lq	25	
81	Lt	25	
82	Lr	106	
83	Ls	92	
84	sh	965	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	ZN	sh	1004	-	-	X	-
87	ZN	sh	1015	-	-	X	-

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 214001 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 25S ribosomal RNA (RDN25-1).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	3217	Total	C	N	O	P	0	0
			68809	30735	12400	22457	3217		

- Molecule 2 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 3 is a RNA chain called 18S ribosomal RNA (RDN18-1).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	1765	Total	C	N	O	P	0	0
			37614	16816	6663	12370	1765		

- Molecule 4 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	sP	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 5 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	sQ	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 6 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	sE	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 7 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	sR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 8 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	sA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 9 is a protein called 40S ribosomal protein S4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	sS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 10 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	sB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 11 is a protein called 40S ribosomal protein S6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	sT	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 12 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	sU	184	Total	C	N	O	0	0
			1473	946	263	264		

- Molecule 13 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	sV	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 14 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	sW	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 15 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	sC	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 16 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	sX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 17 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	sD	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 18 is a protein called 40S ribosomal protein S13.

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

- Molecule 19 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	sZ	127	Total	C	N	O	S	0	0
			923	568	185	167	3		

- Molecule 20 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	sG	125	Total	C	N	O	S	0	0
			979	613	187	177	2		

- Molecule 22 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	sH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 23 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	sJ	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 25 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	sa	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 26 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 28 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	sK	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 30 is a protein called 40S ribosomal protein S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	se	97	Total	C	N	O	S	0	0
			765	473	160	127	5		

- Molecule 31 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 32 is a protein called RPS29A isoform 1.

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

- Molecule 33 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	sg	58	Total	C	N	O	S	0	0
			451	284	92	74	1		

- Molecule 34 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	sN	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 35 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	sO	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 36 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	sL	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 37 is a protein called Uncharacterized protein YIL161W.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	sj	135	Total	C	N	O	S	0	0
			1128	725	190	208	5		

- Molecule 38 is a protein called FK506-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	sk	114	Total	C	N	O	S	0	0
			858	548	144	164	2		

- Molecule 39 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	sm	29	Total	C	N	O	P	0	0
			632	286	135	182	29		

- Molecule 40 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	sl	76	Total	C	N	O	P	0	0
			1622	721	285	540	76		
40	sn	76	Total	C	N	O	P	0	0
			1622	721	285	540	76		

- Molecule 41 is a RNA chain called 5S ribosomal RNA (RDN5-1).

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

- Molecule 42 is a RNA chain called 5.8S ribosomal RNA (RDN58-1).

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

- Molecule 43 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LE	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 44 is a protein called 60S ribosomal protein L3.

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

- Molecule 45 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LH	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 47 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	LI	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 48 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LK	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 50 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LL	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 51 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LM	211	Total	C	N	O	S	0	0
			1719	1093	324	296	6		

- Molecule 52 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LN	172	Total	C	N	O	S	0	0
			1365	855	256	250	4		

- Molecule 53 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LO	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 54 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LS	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 58 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L19-A.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LV	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 61 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LW	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 62 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LX	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 63 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 64 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LZ	126	Total	C	N	O	S	0	0
			869	547	174	147	1		

- Molecule 65 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	La	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 66 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Lb	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 67 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Lc	135	Total	C	N	O		0	0
			1080	701	199	180			

- Molecule 68 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ld	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 69 is a protein called 60S ribosomal protein L29.

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

- Molecule 70 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Lf	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 71 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lg	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 72 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Lh	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 73 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 74 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 75 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 76 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ll	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 77 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Lm	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 78 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Ln	77	Total	C	N	O	S	0	0
			612	391	115	106			

- Molecule 79 is a protein called 60S ribosomal protein L39.

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

- Molecule 80 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Lp	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 81 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Lq	25	Total	C	N	O	S	0	0
			229	139	62	27	1		
81	Lt	22	Total	C	N	O	S	0	0
			207	127	56	23	1		

- Molecule 82 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Lr	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 83 is a protein called 60S ribosomal protein L43-A.

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

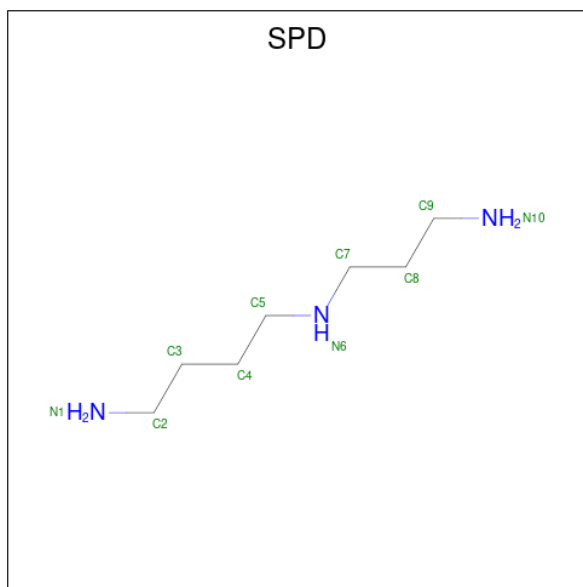
- Molecule 84 is a protein called FAP1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	sh	776	Total	C	N	O	S	0	0
			6024	3719	1092	1108	105		

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

Mol	Chain	Residues	Atoms		AltConf
85	LA	220	Total	Mg	0
			220	220	
85	2	87	Total	Mg	0
			87	87	
85	sS	1	Total	Mg	0
			1	1	
85	sB	1	Total	Mg	0
			1	1	
85	sc	1	Total	Mg	0
			1	1	
85	sm	1	Total	Mg	0
			1	1	
85	LC	1	Total	Mg	0
			1	1	
85	LE	2	Total	Mg	0
			2	2	
85	LF	1	Total	Mg	0
			1	1	
85	LQ	1	Total	Mg	0
			1	1	
85	LS	1	Total	Mg	0
			1	1	
85	LU	2	Total	Mg	0
			2	2	
85	LW	1	Total	Mg	0
			1	1	
85	LY	1	Total	Mg	0
			1	1	
85	Lh	1	Total	Mg	0
			1	1	
85	Lj	1	Total	Mg	0
			1	1	
85	Lm	1	Total	Mg	0
			1	1	

- Molecule 86 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
86	LA	1	Total	C	N	0
			10	7	3	

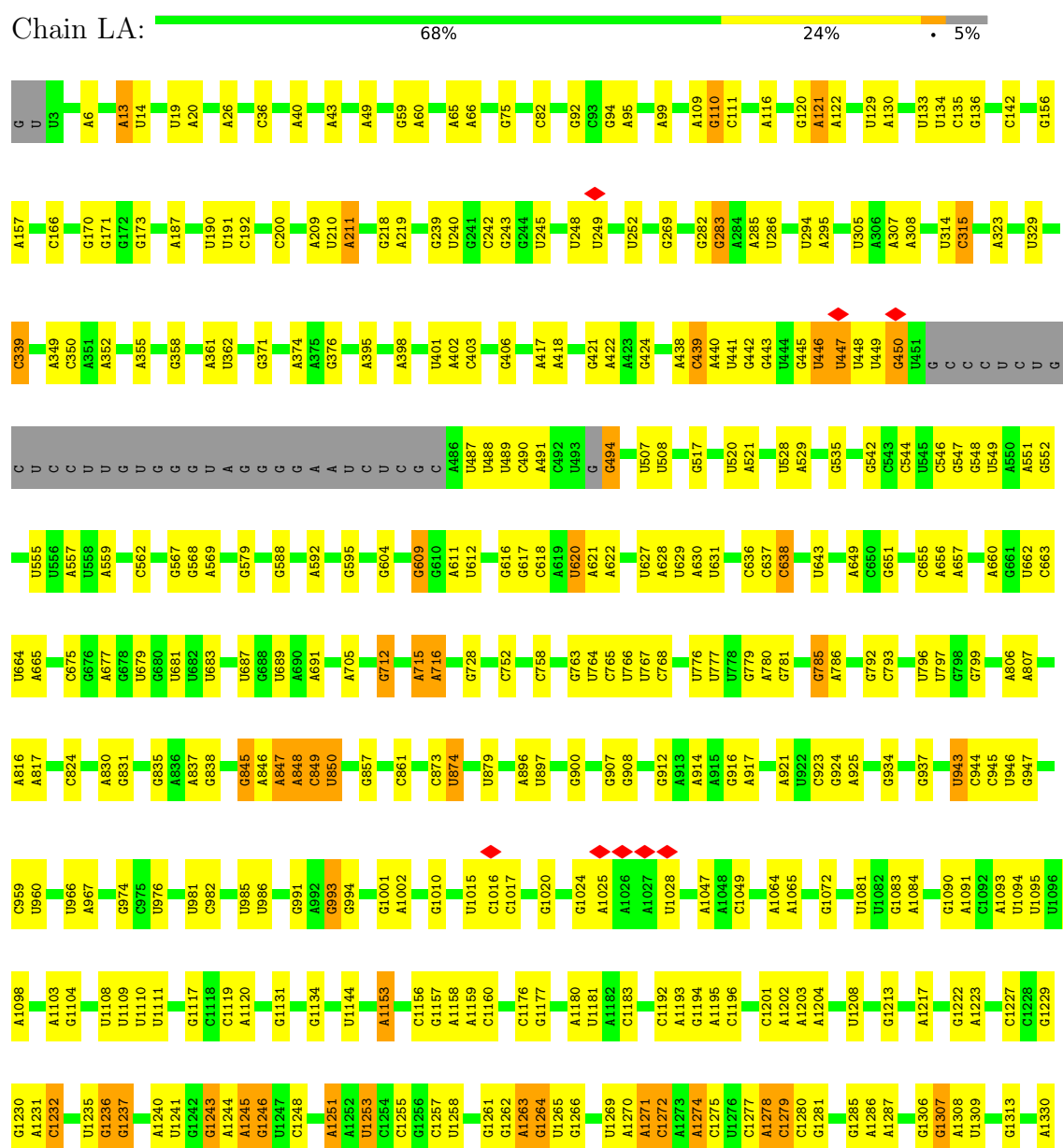
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	sM	1	Total	Zn	0
			1	1	
87	sN	1	Total	Zn	0
			1	1	
87	Lj	1	Total	Zn	0
			1	1	
87	Lm	1	Total	Zn	0
			1	1	
87	Lp	1	Total	Zn	0
			1	1	
87	Lr	1	Total	Zn	0
			1	1	
87	Ls	1	Total	Zn	0
			1	1	
87	sh	27	Total	Zn	0
			27	27	

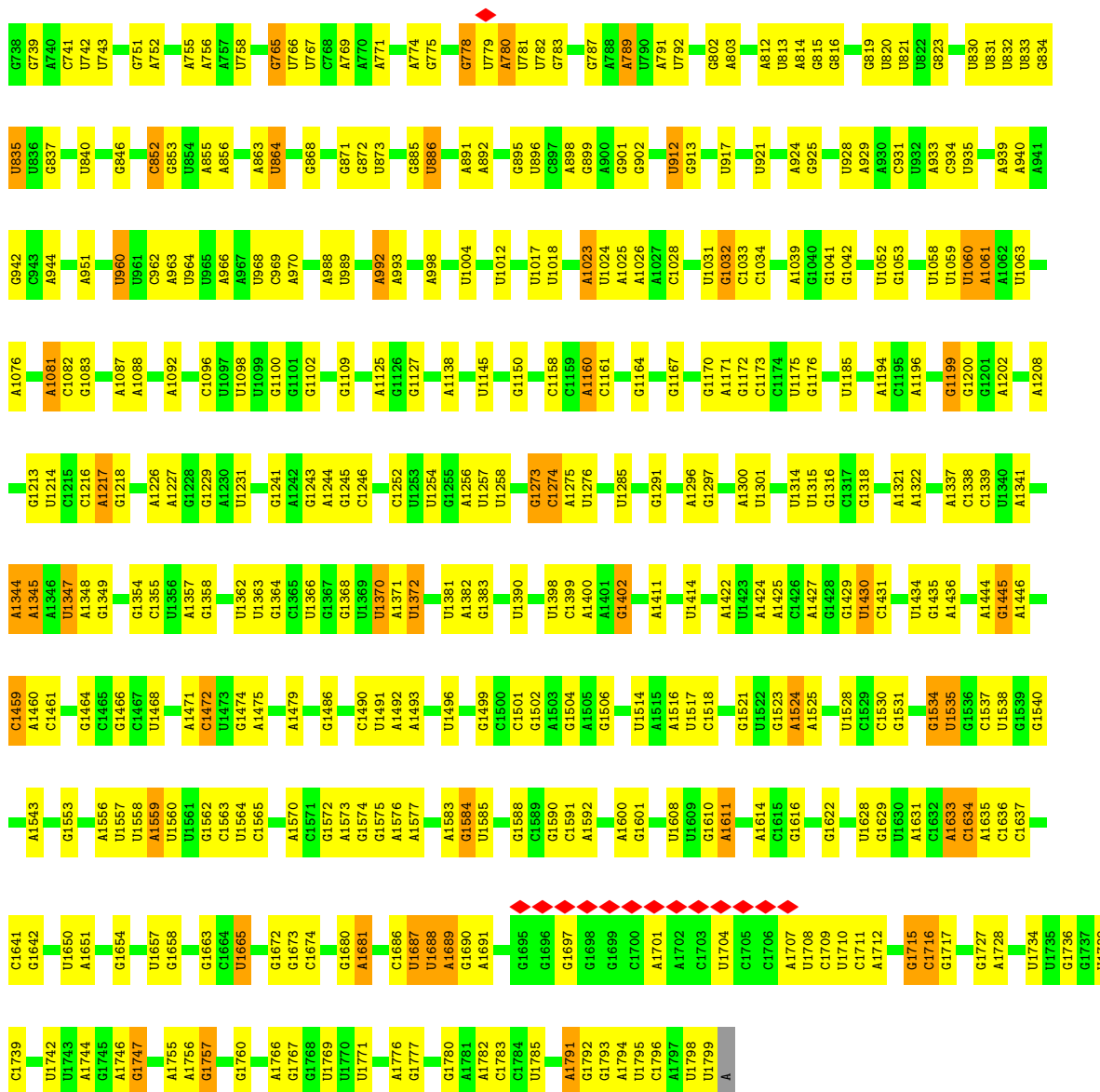
3 Residue-property plots

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

- Molecule 1: 25S ribosomal RNA (RDN25-1)

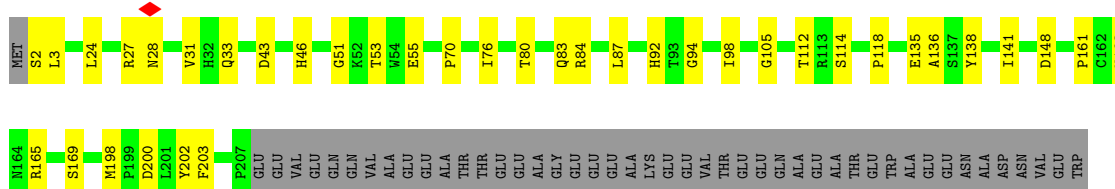


U3068	G2898	U2768	A2637	G2503	C2420	G2273	A2158	U1955	G1952	A1797	G1646	U1554
U3078	C2899	A2769	A2642	U2504	U2426	C2277	U2159	G1953	G1954	A1798	C1657	U1555
U3079	A2900	G2777	U2506	U2505	U2427	C2281	G2160	A1800	A1800	A1799	C1658	C1556
A3086	A2911	G2778	C2507	C2507	U2428	U2282	G2161	A1805	A1805	A1800	U1659	A1557
C3092	G2914	C2788	U2514	U2515	U2433	U2288	G2169	A1806	A1806	A1800	G1660	G1560
C3096	U2923	G2796	A2515	A2515	A2439	G2288	U2170	A1807	A1807	A1800	G1661	G1561
C3097	G2923	G2799	A2522	A2522	A2447	A2303	G2177	A1808	A1808	A1800	G1662	C1562
U3104	A2930	A2799	A2524	A2524	G2450	G2307	G2180	A1814	A1814	A1805	U1666	G1563
U3121	C2931	G2800	G2525	G2525	U2450	C2308	G2181	U1815	U1815	A1806	U1667	U1564
U3122	U2935	A2802	C2526	C2526	U2453	A2309	G2185	A1816	A1816	A1807	G1668	A1566
A3129	A2936	C2810	G2534	G2534	G2454	U2310	U2189	U1816	U1816	A1808	U1675	U1567
A3130	A2942	G2814	A2535	A2535	U2455	U2313	U2193	U1817	U1817	A1809	A1676	U1568
A3131	C2942	U2817	A2536	A2536	U2456	U2314	G2199	U1818	U1818	U1810	U1572	U1569
U3139	G2947	A2678	U	U	G2457	G2315	U2199	A1835	A1835	U1811	A1574	A1570
C3120	U2953	U2680	C	C	U2458	U2334	U2194	G1838	G1838	U1812	C1574	A1571
A3121	U2954	U2682	A	A	U2459	U2335	G2199	U1839	U1839	U1813	A1575	A1572
A3122	U2954	U2683	U	U	U2460	U2336	U2199	U1840	U1840	U1814	G1576	A1573
A3129	G2957	C2684	U	U	A2461	U2336	G2201	A1841	A1841	U1717	U1716	A1580
A3130	C2960	A2689	U2543	U2543	U2462	U2344	G2204	A1842	A1842	G1718	G1718	C1581
U3131	G2961	G2690	C2546	C2546	U2463	A2345	U2205	G1845	G1845	U1722	U1722	C1582
A3139	U2969	A2691	U2549	U2549	G2465	C2354	G2207	A1846	A1846	A1723	A1723	A1583
C2970	C2970	A2694	U2550	U2550	A2468	U2355	A2207	U1724	U1724	U1724	U1724	A1589
A2971	U2972	U2695	U2551	U2551	U2469	A2356	A2208	C1725	C1725	U1725	U1725	G1590
U3151	G2972	A2696	U2552	U2552	C2470	U2373	U2209	G1726	G1726	G1727	G1727	G1591
U3153	C2973	A2697	U2553	U2553	U2471	C2374	G2211	A1863	A1863	G1728	G1728	G1592
C2983	U2983	G2698	C2554	C2554	G2475	G2375	G2212	A1864	A1864	A1729	A1729	A1593
G2990	G2990	A2704	U2555	U2555	U2476	G2385	A2214	A1865	A1865	G1730	G1730	C1596
U2996	U2996	U2711	A2556	A2556	G2477	U2388	G2218	A1867	A1867	G1736	G1736	C1597
G2997	G2997	G2714	U2557	U2557	U2480	C2389	A2219	U1877	U1877	A1741	A1741	G1598
A3012	U3012	U2723	C2561	C2561	U2481	A2390	A2223	A1878	A1878	A1605	A1605	C1469
U3013	U3013	U2724	U2568	U2568	U2482	G2391	A2224	U1879	U1879	U1606	U1606	U1470
U3014	G3015	G2728	U2570	U2570	U2483	C2392	U2225	A1880	A1880	U1607	U1607	U1471
A3016	A3016	U2729	U2571	U2571	U2484	G2393	A2228	A1881	A1881	G1615	G1615	A1474
A3017	U3017	U2744	C2572	C2572	U2485	A2397	A2229	A1883	A1883	U1616	U1616	A1481
A3024	A3024	G2745	G2573	G2573	U2486	U2397	A2236	U1894	U1894	A1760	A1760	A1482
U3041	U3041	U2748	U2585	U2585	U2487	A2402	G2237	A1895	A1895	U1765	U1765	G1483
U3050	U3050	G2752	C2589	C2589	U2488	A2403	A2244	G1899	G1899	G1766	G1766	G1488
G3053	G3053	U2753	A2594	A2594	U2489	A2404	A2245	G1906	G1906	U1629	U1629	U1495
U3056	U3056	G2754	C2594	C2594	U2490	C2407	A2252	A1913	A1913	U1630	U1630	U1630
G3059	G3059	U2755	G2606	G2606	U2491	U2411	A2256	G1914	G1914	C1631	C1631	C1508
U3179	U3179	U2762	G2607	G2607	U2492	U2412	A2257	A1915	A1915	G1634	G1634	A1534
A3160	A3160	U2767	U2611	U2611	U2493	G2413	A2270	U1916	U1916	C1639	C1639	A1535
C3181	C3181	U2767	U2612	U2612	U2494	G2414	A2271	C1917	C1917	A1643	A1643	G1536
A3187	A3187	U2767	U2613	U2613	U2495	U2418	G2272	G1940	G1940	G1644	G1644	A1539
U3192	U3192	U2767	G2614	G2614	U2500	A2419		G1949	G1949	U1645	U1645	U1553
C3193	C3193	U2767	G2614	G2614	A2502							



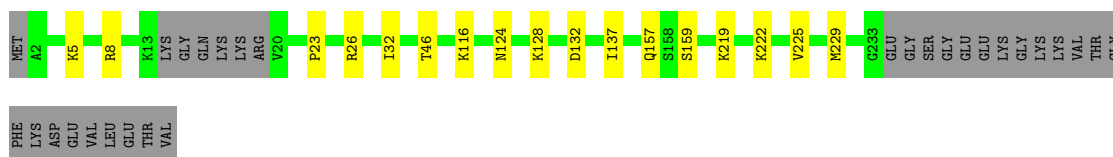
- Molecule 4: 40S ribosomal protein S0-A

Chain sP: 67% 15% 18%



- Molecule 5: 40S ribosomal protein S1-A

Chain sQ: 82% 7% 11%



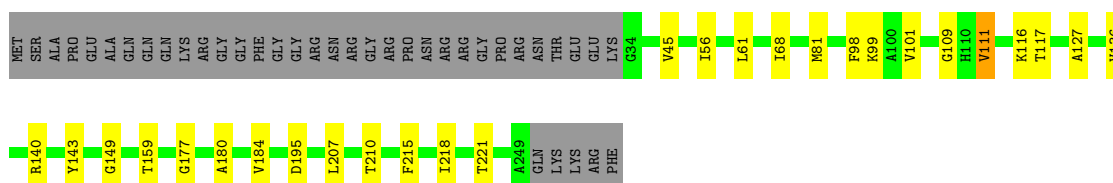
- Molecule 6: RPS15 isoform 1

Chain sE: 74% 8% 18%



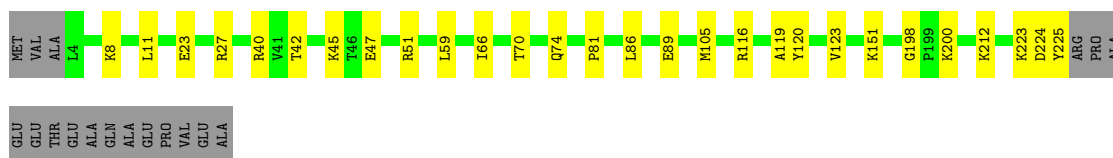
- Molecule 7: 40S ribosomal protein S2

Chain sR: 74% 10% 15%



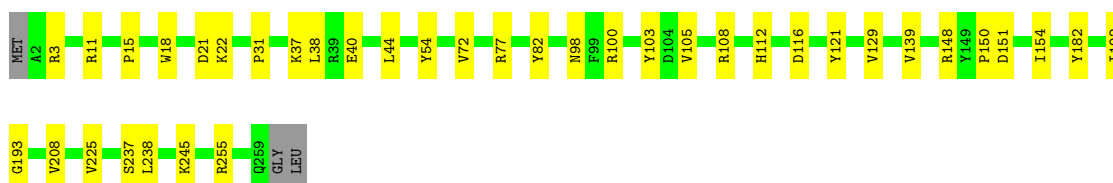
- Molecule 8: 40S ribosomal protein S3

Chain sA: 81% 12% 8%



- Molecule 9: 40S ribosomal protein S4-B

Chain sS: 84% 15% 1%



- Molecule 10: 40S ribosomal protein S5

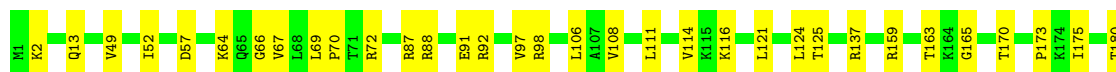
Chain sB: 80% 11% 8%





- Molecule 11: 40S ribosomal protein S6-B

Chain sT: 80% 17% .



- Molecule 12: 40S ribosomal protein S7-A

Chain sU: 78% 18% . .



- Molecule 13: 40S ribosomal protein S8-A

Chain sV: 74% 20% 6%



- Molecule 14: 40S ribosomal protein S9-A

Chain sW: 83% 10% 7%



- Molecule 15: 40S ribosomal protein S10-A

Chain sC: 65% 23% 12%



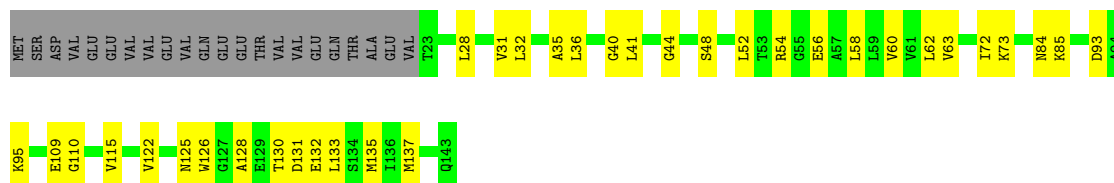
- Molecule 16: 40S ribosomal protein S11-A

Chain sX: 



- Molecule 17: 40S ribosomal protein S12

Chain sD: 



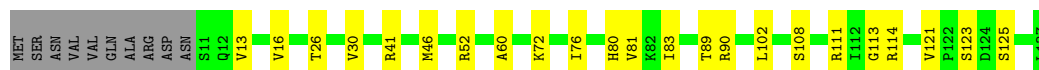
- Molecule 18: 40S ribosomal protein S13

Chain sY: 



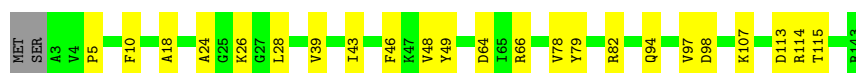
- Molecule 19: 40S ribosomal protein S14-A

Chain sZ: 



- Molecule 20: 40S ribosomal protein S16-A

Chain sF: 



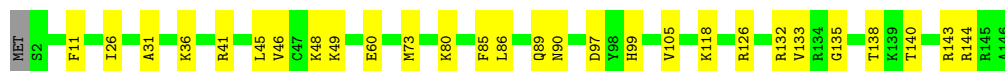
- Molecule 21: 40S ribosomal protein S17-A

Chain sG: 



- Molecule 22: 40S ribosomal protein S18-A

Chain sH: 



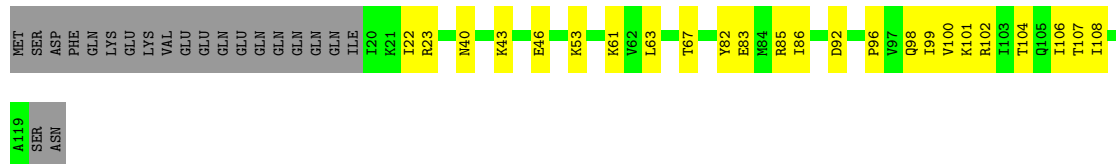
- Molecule 23: 40S ribosomal protein S19-A

Chain sI:  83% 17% .

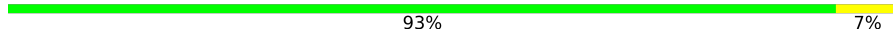


- Molecule 24: 40S ribosomal protein S20

Chain sJ:  63% 20% 17%



- Molecule 25: 40S ribosomal protein S21-A

Chain sa:  93% 7%



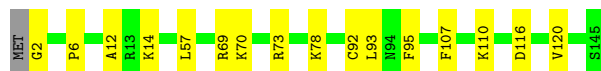
- Molecule 26: 40S ribosomal protein S22-A

Chain sb:  87% 12% .



- Molecule 27: 40S ribosomal protein S23-A

Chain sc:  88% 11% .



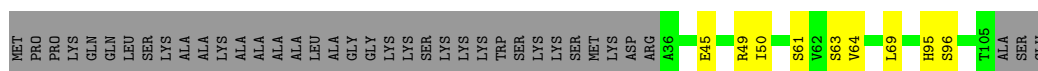
- Molecule 28: 40S ribosomal protein S24-A

Chain sd:  87% 13% .



- Molecule 29: 40S ribosomal protein S25-A

Chain sK:  56% 8% 35%



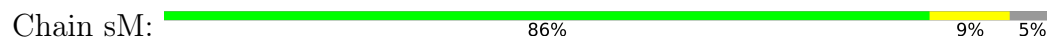
- Molecule 30: 40S ribosomal protein S26-A



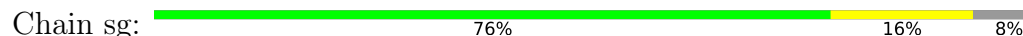
- Molecule 31: 40S ribosomal protein S27-A



- Molecule 32: RPS29A isoform 1



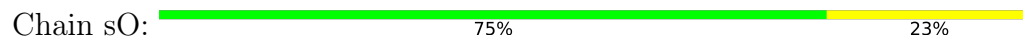
- Molecule 33: 40S ribosomal protein S30-A



- Molecule 34: 40S ribosomal protein S31



- Molecule 35: Guanine nucleotide-binding protein subunit beta-like protein





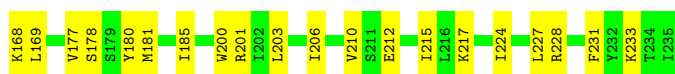
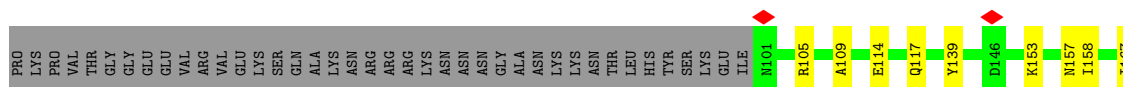
- Molecule 36: 40S ribosomal protein S28-A

Chain sL: 81% 13% 6%



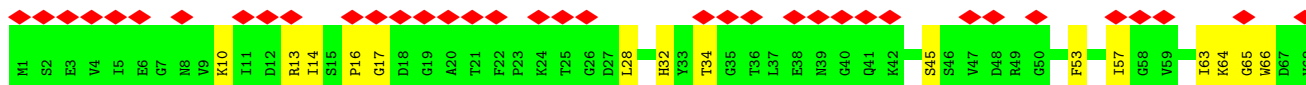
- Molecule 37: Uncharacterized protein YIL161W

Chain sj: 45% 12% 43%



- Molecule 38: FK506-binding protein 1

Chain sk: 39% 77% 23%



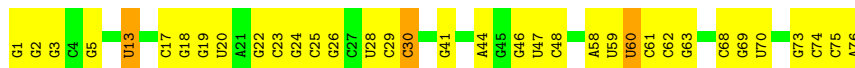
- Molecule 39: mRNA

Chain sm: 41% 48% 10%



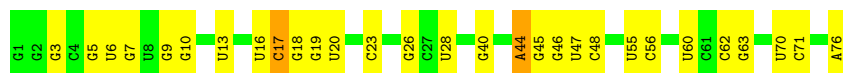
- Molecule 40: tRNA

Chain sl: 54% 42% 4%



- Molecule 40: tRNA

Chain sn:  62% 36% .



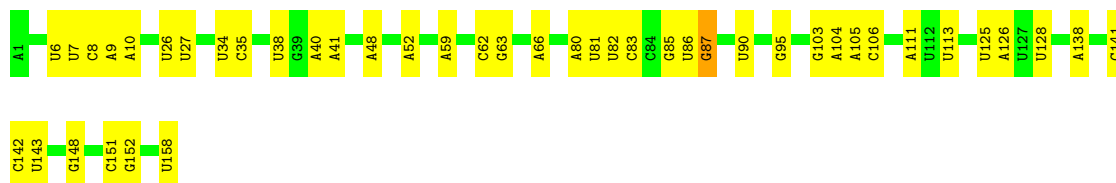
- Molecule 41: 5S ribosomal RNA (RDN5-1)

Chain LC:  85% 14% .



- Molecule 42: 5.8S ribosomal RNA (RDN58-1)

Chain LD:  72% 27% .

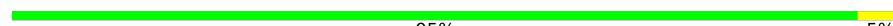


- Molecule 43: 60S ribosomal protein L2-A

Chain LE:  90% 9% .



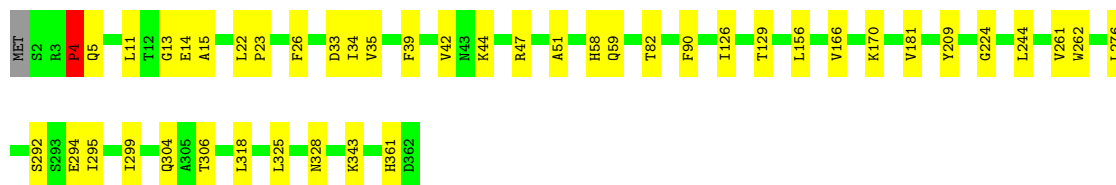
- Molecule 44: 60S ribosomal protein L3

Chain LF:  95% 5% .



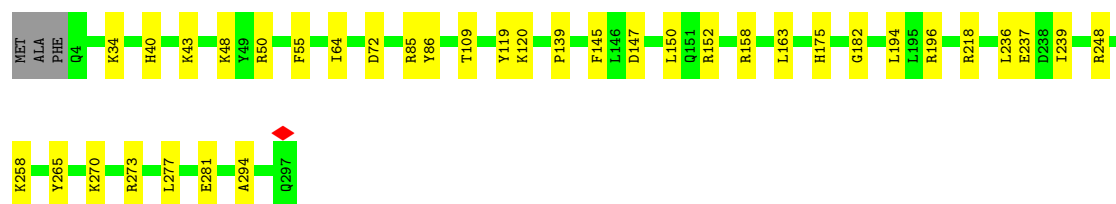
- Molecule 45: 60S ribosomal protein L4-A

Chain LG:  88% 12% .



- Molecule 46: 60S ribosomal protein L5

Chain LH:  87% 12%



- Molecule 47: 60S ribosomal protein L6-B

Chain LI:  84% 11% 5%



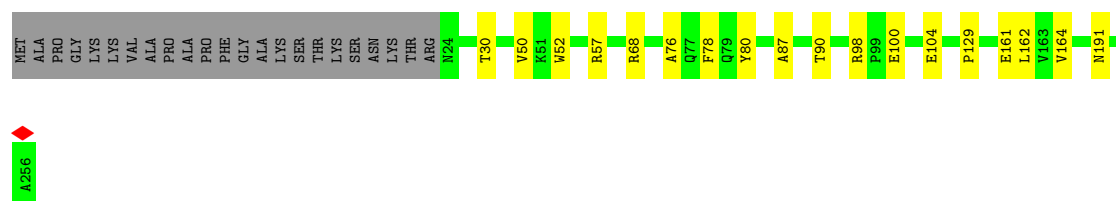
- Molecule 48: 60S ribosomal protein L7-A

Chain LJ:  84% 7% 9%



- Molecule 49: 60S ribosomal protein L8-A

Chain LK:  84% 7% 9%



- Molecule 50: 60S ribosomal protein L9-A

Chain LL:  91% 9%



- Molecule 51: 60S ribosomal protein L10

Chain LM:  85% 10% 5%



- Molecule 52: 60S ribosomal protein L11-A

Chain LN:  91% 8%

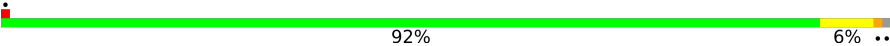


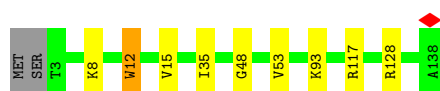
- Molecule 53: 60S ribosomal protein L13-A

Chain LO:  86% 11%



- Molecule 54: 60S ribosomal protein L14-A

Chain LP:  92% 6%



- Molecule 55: 60S ribosomal protein L15-A

Chain LQ:  90% 9%



- Molecule 56: 60S ribosomal protein L16-A

Chain LR:  89% 10%



- Molecule 57: 60S ribosomal protein L17-A

Chain LS:  90% 9%

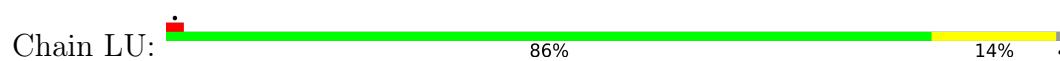


- Molecule 58: 60S ribosomal protein L18-A

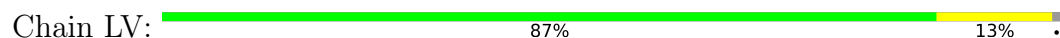
Chain LT:  90% 9%



- Molecule 59: 60S ribosomal protein L19-A



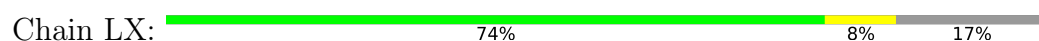
- Molecule 60: 60S ribosomal protein L20-A



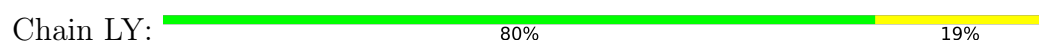
- Molecule 61: 60S ribosomal protein L21-A



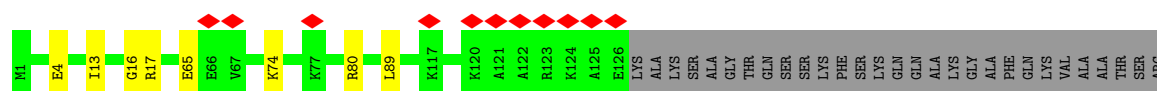
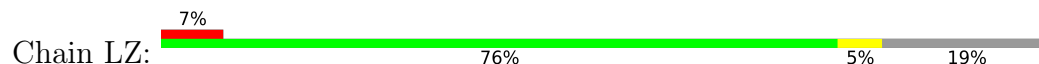
- Molecule 62: 60S ribosomal protein L22-A



- Molecule 63: 60S ribosomal protein L23-A



- Molecule 64: 60S ribosomal protein L24-A

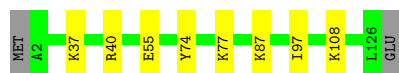


- Molecule 65: 60S ribosomal protein L25



- Molecule 66: 60S ribosomal protein L26-A

Chain Lb:  92% 6% .



- Molecule 67: 60S ribosomal protein L27-A

Chain Lc:  82% 17% .



- Molecule 68: 60S ribosomal protein L28

Chain Ld:  91% 8% .



- Molecule 69: 60S ribosomal protein L29

Chain Le:  83% 14% . .



- Molecule 70: 60S ribosomal protein L30

Chain Lf:  78% 13% 9%



- Molecule 71: 60S ribosomal protein L31-A

Chain Lg:  81% 15% .



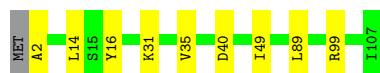
- Molecule 72: 60S ribosomal protein L32

Chain Lh:  92% 6% .



- Molecule 73: 60S ribosomal protein L33-A

Chain Li:  91% 8%



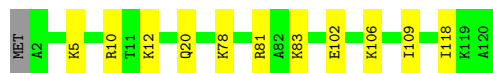
- Molecule 74: 60S ribosomal protein L34-A

Chain Lj:  84% 8% 7%



- Molecule 75: 60S ribosomal protein L35-A

Chain Lk:  90% 9%



- Molecule 76: 60S ribosomal protein L36-A

Chain Ll:  91% 8%



- Molecule 77: 60S ribosomal protein L37-A

Chain Lm:  84% 8% 8%



- Molecule 78: 60S ribosomal protein L38

Chain Ln:  88% 10%

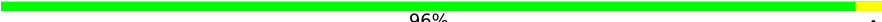


- Molecule 79: 60S ribosomal protein L39

Chain Lo:  88% 10%



- Molecule 80: 60S ribosomal protein L40-A

Chain Lp:  96% .



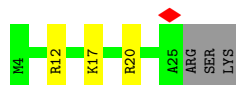
- Molecule 81: 60S ribosomal protein L41-A

Chain Lq:  88% 12%



- Molecule 81: 60S ribosomal protein L41-A

Chain Lt:  76% 12% 12%



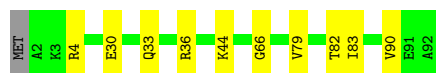
- Molecule 82: 60S ribosomal protein L42-A

Chain Lr:  87% 10% .



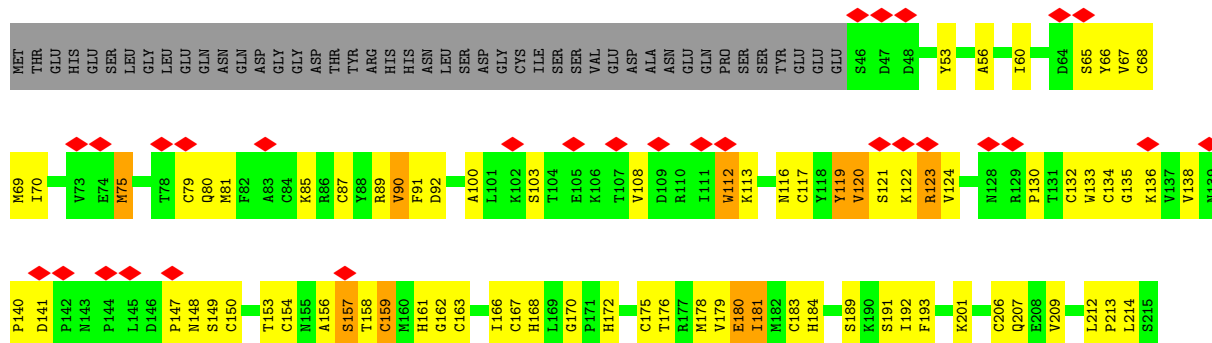
- Molecule 83: 60S ribosomal protein L43-A

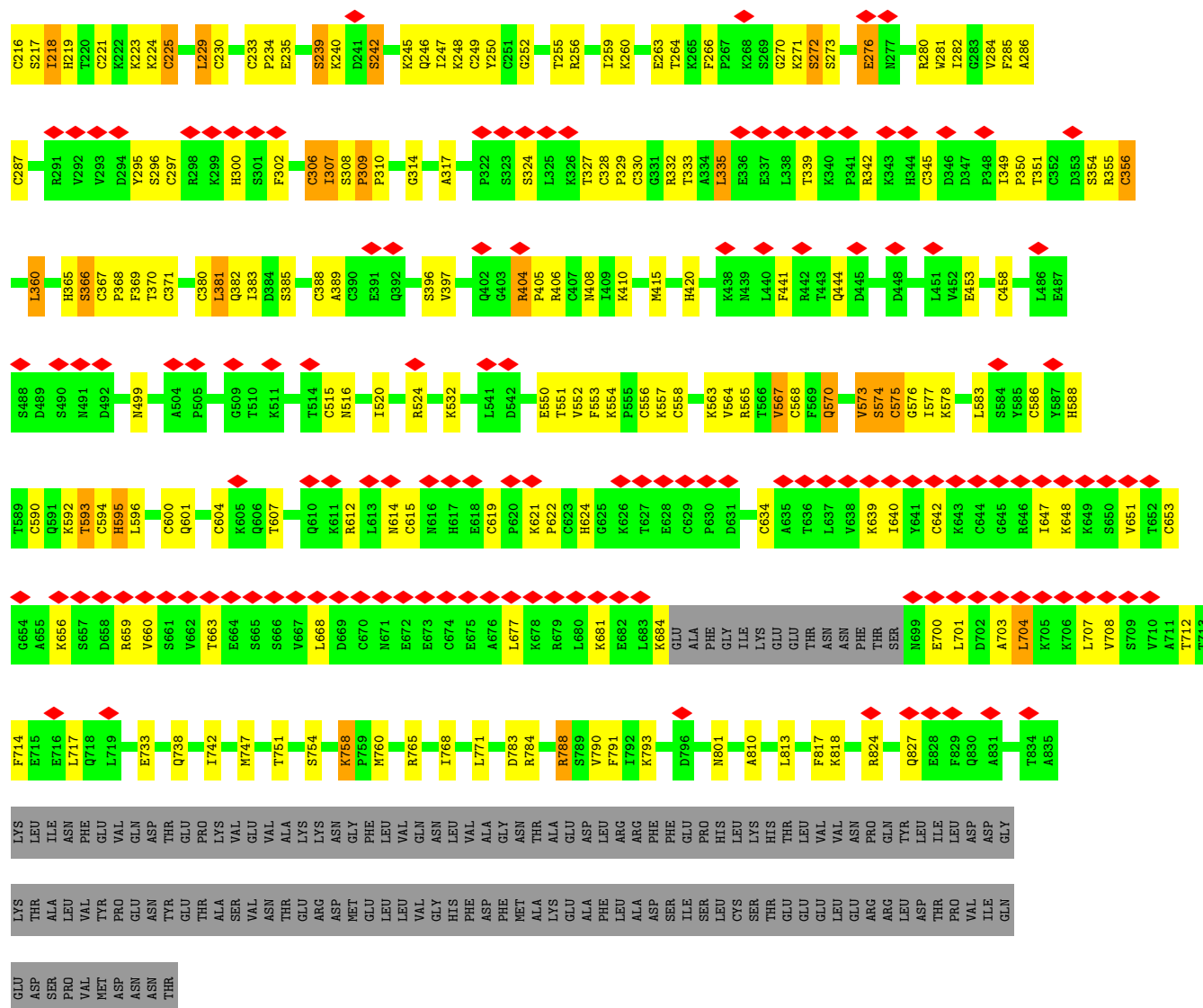
Chain Ls:  88% 11% .



- Molecule 84: FAP1 isoform 1

Chain sh:  17% 52% 24% . 20%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	114964	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	47.687	Depositor
Minimum map value	-8.227	Depositor
Average map value	0.005	Depositor
Map value standard deviation	1.107	Depositor
Recommended contour level	2	Depositor
Map size (Å)	501.59998, 501.59998, 501.59998	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SPD, ZN

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	LA	0.36	0/77021	0.42	2/120082 (0.0%)
2	LB	0.26	0/1634	0.69	1/2195 (0.0%)
3	2	0.38	0/42071	0.46	5/65553 (0.0%)
4	sP	0.29	0/1644	0.49	0/2249
5	sQ	0.30	0/1823	0.54	0/2447
6	sE	0.32	0/936	0.61	0/1259
7	sR	0.41	0/1656	0.68	1/2251 (0.0%)
8	sA	0.30	0/1754	0.57	0/2361
9	sS	0.35	0/2097	0.62	1/2823 (0.0%)
10	sB	0.32	0/1625	0.55	2/2197 (0.1%)
11	sT	0.26	0/1839	0.50	0/2460
12	sU	0.30	0/1498	0.64	1/2019 (0.0%)
13	sV	0.32	0/1501	0.53	0/2006
14	sW	0.31	0/1504	0.58	1/2016 (0.0%)
15	sC	0.35	0/769	0.72	0/1039
16	sX	0.35	0/1168	0.52	0/1575
17	sD	0.31	0/883	0.92	0/1199
18	sY	0.35	0/1215	0.64	0/1638
19	sZ	0.35	0/934	0.63	0/1257
20	sF	0.33	0/1125	0.52	0/1510
21	sG	0.36	0/989	0.69	1/1327 (0.1%)
22	sH	0.37	0/1207	0.59	0/1623
23	sI	0.35	0/1130	0.70	4/1517 (0.3%)
24	sJ	0.34	0/807	0.70	0/1091
25	sa	0.31	0/682	0.57	0/921
26	sb	0.37	0/1038	0.63	0/1395
27	sc	0.33	0/1139	0.54	2/1518 (0.1%)
28	sd	0.30	0/1087	0.54	0/1449
29	sK	0.30	0/571	0.61	0/768
30	se	0.37	0/778	0.66	1/1042 (0.1%)
31	sf	0.32	0/620	0.54	0/838
32	sM	0.47	0/452	0.57	0/600

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	sg	0.29	0/458	0.62	0/610
34	sN	0.28	0/567	0.83	0/764
35	sO	0.32	0/2436	0.65	2/3318 (0.1%)
36	sL	0.33	0/493	0.57	0/663
37	sj	0.17	0/1149	0.55	0/1541
38	sk	0.18	0/878	0.51	0/1192
39	sm	0.24	0/714	0.41	0/1111
40	sl	0.18	0/1810	0.37	0/2821
40	sn	0.26	0/1810	0.38	0/2821
41	LC	0.33	0/2883	0.34	0/4491
42	LD	0.37	0/3746	0.38	0/5832
43	LE	0.36	0/1933	0.56	0/2598
44	LF	0.33	0/3146	0.52	0/4228
45	LG	0.32	0/2800	0.57	2/3790 (0.1%)
46	LH	0.28	0/2400	0.50	0/3239
47	LI	0.29	0/1329	0.55	0/1794
48	LJ	0.33	0/1821	0.56	0/2451
49	LK	0.29	0/1836	0.55	0/2481
50	LL	0.30	0/1529	0.53	0/2060
51	LM	0.33	0/1755	0.50	0/2353
52	LN	0.26	0/1386	0.53	0/1859
53	LO	0.28	0/1568	0.57	0/2106
54	LP	0.33	0/1068	0.51	0/1438
55	LQ	0.33	0/1757	0.52	1/2354 (0.0%)
56	LR	0.34	0/1585	0.53	0/2128
57	LS	0.32	0/1439	0.54	0/1938
58	LT	0.32	0/1465	0.56	0/1965
59	LU	0.42	0/1538	0.56	0/2050
60	LV	0.37	0/1473	0.54	0/1980
61	LW	0.30	0/1296	0.52	0/1739
62	LX	0.26	0/812	0.57	2/1099 (0.2%)
63	LY	0.30	0/1018	0.51	0/1369
64	LZ	0.41	0/883	0.74	1/1193 (0.1%)
65	La	0.45	0/979	0.64	2/1321 (0.2%)
66	Lb	0.29	0/995	0.50	0/1329
67	Lc	0.29	0/1106	0.50	0/1485
68	Ld	0.41	0/1200	0.59	1/1607 (0.1%)
69	Le	0.27	0/473	0.64	2/629 (0.3%)
70	Lf	0.25	0/745	0.45	0/1001
71	Lg	0.31	0/890	0.53	0/1196
72	Lh	0.33	0/1034	0.48	0/1385
73	Li	0.35	0/868	0.54	0/1168
74	Lj	0.31	0/890	0.54	0/1189

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Lk	0.27	0/978	0.48	0/1301
76	Ll	0.28	0/772	0.51	0/1026
77	Lm	0.36	0/660	0.62	0/875
78	Ln	0.27	0/618	0.42	0/826
79	Lo	0.34	0/443	0.56	0/588
80	Lp	0.27	0/416	0.52	0/553
81	Lq	0.26	0/230	0.41	0/296
81	Lt	0.17	0/208	0.41	0/267
82	Lr	0.29	0/836	0.54	0/1104
83	Ls	0.26	0/701	0.49	0/934
84	sh	0.52	0/6154	1.04	44/8290 (0.5%)
All	All	0.35	0/229174	0.51	79/335971 (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	sU	0	1
17	sD	0	2
19	sZ	0	1
20	sF	0	1
26	sb	0	1
35	sO	0	2
44	LF	0	1
45	LG	0	2
49	LK	0	2
50	LL	0	1
54	LP	0	1
64	LZ	0	1
69	Le	0	1
75	Lk	0	1
All	All	0	18

There are no bond length outliers.

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	sh	122	LYS	N-CA-C	10.15	122.34	111.28
84	sh	159	CYS	N-CA-C	-9.47	97.15	110.50
84	sh	158	THR	N-CA-C	-9.14	97.57	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	sR	109	GLY	N-CA-C	8.45	124.74	114.69
45	LG	4	PRO	CA-C-N	7.99	136.79	121.54
45	LG	4	PRO	C-N-CA	7.99	136.79	121.54
84	sh	516	ASN	N-CA-C	-7.94	103.57	113.18
14	sW	19	TYR	N-CA-C	7.82	119.57	108.54
84	sh	70	ILE	N-CA-C	7.56	117.68	110.42
84	sh	248	LYS	N-CA-C	7.42	119.32	108.86
84	sh	701	LEU	N-CA-C	7.39	119.13	111.14
84	sh	123	ARG	N-CA-C	7.20	120.39	109.23
84	sh	135	GLY	N-CA-C	-7.16	106.56	115.08
21	sG	97	ASN	N-CA-C	6.97	121.15	111.74
84	sh	381	LEU	N-CA-C	-6.84	103.83	111.28
9	sS	193	GLY	N-CA-C	6.74	129.15	113.18
84	sh	588	HIS	N-CA-C	6.70	119.37	110.53
23	sI	34	VAL	CA-C-N	6.63	135.39	124.31
23	sI	34	VAL	C-N-CA	6.63	135.39	124.31
3	2	555	A	C2'-C3'-O3'	6.61	123.61	113.70
84	sh	574	SER	N-CA-C	6.55	119.09	108.34
84	sh	157	SER	N-CA-C	6.50	119.42	107.99
68	Ld	66	ALA	N-CA-C	-6.46	106.36	114.56
10	sB	99	MET	CA-C-N	6.08	131.30	122.36
10	sB	99	MET	C-N-CA	6.08	131.30	122.36
84	sh	751	THR	N-CA-C	6.05	117.87	111.28
69	Le	22	LYS	CA-C-N	5.89	129.63	120.68
69	Le	22	LYS	C-N-CA	5.89	129.63	120.68
62	LX	51	GLY	CA-C-N	5.85	135.32	125.02
62	LX	51	GLY	C-N-CA	5.85	135.32	125.02
84	sh	218	ILE	N-CA-C	-5.83	107.06	112.83
84	sh	532	LYS	CA-C-N	-5.74	113.78	119.92
84	sh	532	LYS	C-N-CA	-5.74	113.78	119.92
2	LB	183	ILE	N-CA-C	-5.68	107.44	112.90
84	sh	65	SER	N-CA-C	5.68	119.79	112.41
84	sh	150	CYS	N-CA-C	-5.64	105.22	111.36
84	sh	712	THR	N-CA-C	5.63	117.50	111.36
84	sh	596	LEU	N-CA-C	-5.59	102.54	109.64
30	se	42	ARG	CB-CG-CD	5.54	124.03	111.30
84	sh	156	ALA	N-CA-C	-5.51	101.69	109.96
1	LA	406	G	O4'-C1'-N9	5.45	116.37	108.20
65	La	85	GLN	N-CA-C	-5.44	100.37	109.24
84	sh	170	GLY	CA-C-N	-5.41	115.17	120.52
84	sh	170	GLY	C-N-CA	-5.41	115.17	120.52
55	LQ	177	GLY	N-CA-C	5.39	117.83	111.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	sh	306	CYS	N-CA-C	-5.36	102.45	110.23
84	sh	397	VAL	CA-C-N	-5.35	114.19	119.92
84	sh	397	VAL	C-N-CA	-5.35	114.19	119.92
84	sh	141	ASP	CA-C-N	-5.35	114.29	119.90
84	sh	141	ASP	C-N-CA	-5.35	114.29	119.90
84	sh	53	TYR	N-CA-C	5.34	117.10	111.28
84	sh	619	CYS	CA-C-N	-5.34	114.28	120.04
84	sh	619	CYS	C-N-CA	-5.34	114.28	120.04
65	La	87	SER	N-CA-C	5.30	117.56	110.35
3	2	1600	A	C4'-C3'-O3'	-5.30	101.46	109.40
84	sh	758	LYS	CA-C-N	-5.28	114.32	119.76
84	sh	758	LYS	C-N-CA	-5.28	114.32	119.76
84	sh	69	MET	N-CA-C	5.24	117.07	111.36
3	2	1791	A	C2'-C3'-O3'	5.23	117.34	109.50
27	sc	116	ASP	CA-C-N	-5.21	118.84	122.59
27	sc	116	ASP	C-N-CA	-5.21	118.84	122.59
84	sh	615	CYS	N-CA-C	5.21	117.74	109.50
23	sI	52	GLY	CA-C-N	5.21	131.49	121.54
23	sI	52	GLY	C-N-CA	5.21	131.49	121.54
84	sh	108	VAL	N-CA-C	-5.18	104.57	111.05
64	LZ	74	LYS	N-CA-C	5.18	116.85	108.41
84	sh	79	CYS	N-CA-C	5.17	117.39	110.35
3	2	1023	A	C4'-C3'-O3'	5.15	117.13	109.40
1	LA	1307	G	P-O3'-C3'	5.14	127.92	120.20
3	2	1791	A	P-O3'-C3'	5.13	127.89	120.20
35	sO	29	GLN	CA-C-N	-5.12	114.77	120.45
35	sO	29	GLN	C-N-CA	-5.12	114.77	120.45
84	sh	596	LEU	CA-C-N	-5.12	114.31	119.83
84	sh	596	LEU	C-N-CA	-5.12	114.31	119.83
84	sh	212	LEU	CA-C-N	-5.04	114.39	119.83
84	sh	212	LEU	C-N-CA	-5.04	114.39	119.83
84	sh	229	LEU	N-CA-C	5.01	117.31	110.55
12	sU	38	LEU	N-CA-C	-5.01	106.76	112.92
84	sh	404	ARG	N-CA-C	-5.01	102.76	110.32

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
44	LF	141	GLY	Peptide
45	LG	13	GLY	Peptide
45	LG	318	LEU	Peptide

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Mol	Chain	Res	Type	Group
49	LK	30	THR	Peptide
49	LK	76	ALA	Peptide
50	LL	21	LYS	Peptide
54	LP	12	TRP	Peptide
64	LZ	65	GLU	Peptide
69	Le	20	GLY	Peptide
75	Lk	83	LYS	Peptide
17	sD	110	GLY	Peptide
17	sD	84	ASN	Peptide
20	sF	39	VAL	Peptide
35	sO	147	HIS	Peptide
35	sO	97	GLY	Peptide
12	sU	64	VAL	Peptide
19	sZ	90	ARG	Peptide
26	sb	54	ASP	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	68809	0	34575	330	0
2	LB	1609	0	1701	39	0
3	2	37614	0	18925	201	0
4	sP	1603	0	1610	22	0
5	sQ	1798	0	1890	11	0
6	sE	916	0	941	8	0
7	sR	1626	0	1715	15	0
8	sA	1729	0	1812	20	0
9	sS	2056	0	2140	24	0
10	sB	1605	0	1668	15	0
11	sT	1815	0	1894	28	0
12	sU	1473	0	1555	28	0
13	sV	1476	0	1501	25	0
14	sW	1479	0	1556	14	0
15	sC	752	0	719	15	0
16	sX	1142	0	1209	11	0
17	sD	875	0	878	20	0
18	sY	1192	0	1255	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	sZ	923	0	948	16	0
20	sF	1105	0	1166	14	0
21	sG	979	0	1025	8	0
22	sH	1188	0	1218	20	0
23	sI	1112	0	1124	17	0
24	sJ	797	0	863	17	0
25	sa	673	0	662	4	0
26	sb	1021	0	1060	9	0
27	sc	1121	0	1195	11	0
28	sd	1073	0	1132	11	0
29	sK	563	0	603	5	0
30	se	765	0	814	8	0
31	sf	610	0	633	6	0
32	sM	442	0	428	4	0
33	sg	451	0	491	6	0
34	sN	556	0	546	20	0
35	sO	2383	0	2332	47	0
36	sL	491	0	524	10	0
37	sj	1128	0	1161	41	0
38	sk	858	0	863	16	0
39	sm	632	0	318	9	0
40	sl	1622	0	820	11	0
40	sn	1622	0	820	10	0
41	LC	2579	0	1304	6	0
42	LD	3353	0	1695	14	0
43	LE	1899	0	1957	18	0
44	LF	3075	0	3142	12	0
45	LG	2748	0	2859	27	0
46	LH	2351	0	2294	21	0
47	LI	1307	0	1377	12	0
48	LJ	1784	0	1862	12	0
49	LK	1804	0	1877	10	0
50	LL	1508	0	1572	12	0
51	LM	1719	0	1763	15	0
52	LN	1365	0	1393	9	0
53	LO	1543	0	1608	17	0
54	LP	1053	0	1149	7	0
55	LQ	1720	0	1779	14	0
56	LR	1555	0	1659	11	0
57	LS	1416	0	1433	12	0
58	LT	1441	0	1543	12	0
59	LU	1521	0	1617	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	LV	1437	0	1475	17	0
61	LW	1272	0	1312	9	0
62	LX	796	0	812	6	0
63	LY	1003	0	1048	15	0
64	LZ	869	0	783	4	0
65	La	964	0	1025	10	0
66	Lb	984	0	1075	4	0
67	Lc	1080	0	1122	12	0
68	Ld	1169	0	1211	10	0
69	Le	462	0	491	6	0
70	Lf	737	0	792	10	0
71	Lg	876	0	912	10	0
72	Lh	1013	0	1077	6	0
73	Li	850	0	880	6	0
74	Lj	880	0	942	10	0
75	Lk	969	0	1078	7	0
76	Ll	766	0	844	6	0
77	Lm	645	0	645	6	0
78	Ln	612	0	682	5	0
79	Lo	436	0	475	3	0
80	Lp	410	0	442	2	0
81	Lq	229	0	273	3	0
81	Lt	207	0	250	3	0
82	Lr	824	0	888	6	0
83	Ls	694	0	734	10	0
84	sh	6024	0	5965	211	0
85	2	87	0	0	0	0
85	LA	220	0	0	0	0
85	LC	1	0	0	0	0
85	LE	2	0	0	0	0
85	LF	1	0	0	0	0
85	LQ	1	0	0	0	0
85	LS	1	0	0	0	0
85	LU	2	0	0	0	0
85	LW	1	0	0	0	0
85	LY	1	0	0	0	0
85	Lh	1	0	0	0	0
85	Lj	1	0	0	0	0
85	Lm	1	0	0	0	0
85	sB	1	0	0	0	0
85	sS	1	0	0	0	0
85	sc	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	sm	1	0	0	0	0
86	LA	10	0	19	0	0
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Lr	1	0	0	0	0
87	Ls	1	0	0	0	0
87	sM	1	0	0	0	0
87	sN	1	0	0	0	0
87	sh	27	0	0	4	0
All	All	214001	0	159425	1503	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 4.

All (1503) 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)
84:sh:249:CYS:SG	84:sh:286:ALA:HA	1.58	1.42
84:sh:219:HIS:CD2	84:sh:235:GLU:HG3	1.61	1.34
39:sm:7:A:H5'	84:sh:788:ARG:NH2	1.65	1.12
37:sj:228:ARG:NE	84:sh:266:PHE:CD1	2.20	1.09
84:sh:249:CYS:SG	84:sh:286:ALA:CA	2.39	1.09
39:sm:7:A:C5'	84:sh:788:ARG:HH22	1.69	1.05
69:Le:16:ALA:O	69:Le:20:GLY:HA3	1.57	1.03
37:sj:228:ARG:CZ	84:sh:266:PHE:HB3	1.88	1.03
84:sh:219:HIS:CD2	84:sh:235:GLU:CG	2.39	1.03
84:sh:604:CYS:HG	87:sh:1004:ZN:ZN	0.72	1.00
1:LA:2465:G:H1	1:LA:2491:A:N6	1.60	0.99
37:sj:228:ARG:NE	84:sh:266:PHE:CG	2.32	0.96
39:sm:7:A:C5'	84:sh:788:ARG:NH2	2.29	0.96
37:sj:200:TRP:CZ3	84:sh:213:PRO:HB2	1.99	0.95
1:LA:2465:G:H1	1:LA:2491:A:H62	1.11	0.94
3:2:868:G:H1	3:2:960:U:H3	1.14	0.94
35:sO:299:GLN:HG3	84:sh:576:GLY:HA3	1.50	0.91
34:sN:121:CYS:HB3	34:sN:126:CYS:SG	2.14	0.87
3:2:1665:U:H3	3:2:1736:G:H1	1.23	0.85
37:sj:228:ARG:CZ	84:sh:266:PHE:CB	2.53	0.85
37:sj:231:PHE:CD2	84:sh:266:PHE:HE1	1.94	0.84
59:LU:159:ALA:HB1	59:LU:163:ARG:NH1	1.93	0.83
12:sU:39:ARG:HH21	59:LU:188:ASP:CB	1.90	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:sl:3:G:H1	40:sl:70:U:H3	1.26	0.83
12:sU:39:ARG:NH2	59:LU:188:ASP:HB3	1.94	0.82
84:sh:153:THR:HA	84:sh:166:ILE:HA	1.60	0.82
84:sh:575:CYS:SG	84:sh:577:ILE:HG13	2.19	0.82
12:sU:39:ARG:HH21	59:LU:188:ASP:HB3	1.45	0.81
3:2:895:G:H1	3:2:917:U:H3	1.27	0.81
69:Le:23:LYS:HE3	69:Le:24:PRO:HD2	1.61	0.80
1:LA:2677:G:H1	1:LA:2680:A:H2	1.30	0.79
84:sh:219:HIS:HD2	84:sh:235:GLU:HG3	1.39	0.79
37:sj:200:TRP:HZ3	84:sh:213:PRO:HB2	1.46	0.78
37:sj:228:ARG:CZ	84:sh:266:PHE:CG	2.67	0.77
37:sj:228:ARG:CZ	84:sh:266:PHE:CD1	2.68	0.77
84:sh:219:HIS:CD2	84:sh:235:GLU:CB	2.67	0.77
69:Le:16:ALA:O	69:Le:20:GLY:CA	2.32	0.77
84:sh:219:HIS:NE2	84:sh:235:GLU:CB	2.48	0.76
84:sh:250:TYR:HB3	84:sh:308:SER:HA	1.66	0.76
33:sg:6:GLY:HA2	33:sg:10:ARG:HH22	1.51	0.76
36:sL:14:LYS:NZ	84:sh:783:ASP:OD2	2.20	0.75
84:sh:553:PHE:HB3	84:sh:563:LYS:HB3	1.67	0.75
84:sh:760:MET:HG3	84:sh:765:ARG:HG3	1.66	0.75
1:LA:3348:G:H1	1:LA:3357:U:H3	1.32	0.75
84:sh:240:LYS:HB2	84:sh:245:LYS:HD3	1.68	0.75
1:LA:2205:U:O4	1:LA:2237:C:N4	2.20	0.74
37:sj:231:PHE:CD2	84:sh:266:PHE:CE1	2.74	0.74
3:2:165:G:H4'	64:LZ:80:ARG:HH22	1.53	0.74
84:sh:634:CYS:HB3	84:sh:653:CYS:HB3	1.71	0.73
1:LA:1639:C:OP2	74:Lj:74:ARG:NH2	2.21	0.72
84:sh:219:HIS:CE1	84:sh:235:GLU:HB2	2.24	0.72
37:sj:227:LEU:HD22	84:sh:270:GLY:O	1.90	0.71
84:sh:209:VAL:HA	84:sh:224:LYS:HA	1.73	0.71
3:2:1102:G:N7	27:sc:2:GLY:N	2.38	0.71
37:sj:200:TRP:CZ3	84:sh:213:PRO:CB	2.72	0.71
84:sh:578:LYS:HA	84:sh:593:THR:HA	1.72	0.71
12:sU:39:ARG:NH2	59:LU:188:ASP:CB	2.51	0.71
66:Lb:55:GLU:HB2	66:Lb:108:LYS:HB3	1.73	0.71
2:LB:181:ASN:HB3	2:LB:185:MET:HE1	1.72	0.71
29:sK:95:HIS:ND1	29:sK:96:SER:O	2.24	0.71
1:LA:542:G:H1	1:LA:549:U:H3	1.40	0.70
12:sU:150:GLN:HB3	12:sU:181:ILE:HG22	1.74	0.69
3:2:1585:U:H3	3:2:1611:A:H2	1.38	0.69
28:sd:82:ALA:O	28:sd:86:GLU:HB2	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:sZ:16:VAL:HG12	19:sZ:80:HIS:HB2	1.74	0.69
40:sn:26:G:O6	40:sn:44:A:N1	2.26	0.69
35:sO:118:LYS:NZ	84:sh:550:GLU:OE1	2.25	0.69
38:sk:85:GLY:O	38:sk:88:ALA:C	2.35	0.69
84:sh:219:HIS:NE2	84:sh:235:GLU:HB3	2.07	0.69
84:sh:272:SER:HB2	84:sh:280:ARG:HB3	1.74	0.69
84:sh:183:CYS:HB2	84:sh:206:CYS:H	1.56	0.68
1:LA:1257:C:N4	1:LA:1261:G:N2	2.40	0.68
1:LA:824:C:H5''	43:LE:21:ARG:HD3	1.76	0.68
3:2:486:G:H1	3:2:501:U:H3	1.39	0.68
8:sA:42:THR:HB	8:sA:45:LYS:O	1.94	0.68
84:sh:132:CYS:SG	87:sh:1015:ZN:ZN	1.82	0.68
3:2:1459:C:OP2	22:sH:138:THR:OG1	2.10	0.68
4:sP:53:THR:HG22	4:sP:161:PRO:HG2	1.76	0.67
84:sh:604:CYS:SG	87:sh:1004:ZN:ZN	1.80	0.67
2:LB:68:PHE:O	2:LB:86:SER:HB3	1.95	0.67
3:2:1588:G:H1	3:2:1608:U:H3	1.43	0.67
37:sj:228:ARG:NH1	84:sh:266:PHE:HB3	2.09	0.67
3:2:530:C:O2	28:sd:61:ARG:NH1	2.28	0.67
17:sD:133:LEU:HG	17:sD:137:MET:HE1	1.76	0.67
35:sO:180:ALA:HB3	35:sO:190:ALA:HB3	1.77	0.67
84:sh:388:CYS:HA	84:sh:405:PRO:HG2	1.76	0.67
37:sj:178:SER:H	37:sj:181:MET:HE2	1.59	0.67
8:sA:223:LYS:HB3	35:sO:191:ASP:HB3	1.76	0.66
24:sJ:106:ILE:HG23	24:sJ:107:THR:HG23	1.78	0.66
1:LA:2193:U:H5'	1:LA:2194:G:H5'	1.77	0.66
28:sd:60:PHE:H	28:sd:71:GLY:HA2	1.60	0.66
3:2:388:G:OP1	3:2:423:G:O2'	2.14	0.66
1:LA:2677:G:N1	1:LA:2680:A:C2	2.57	0.66
2:LB:58:CYS:SG	2:LB:152:ARG:NH2	2.69	0.66
84:sh:134:CYS:HB3	84:sh:167:CYS:HB3	1.78	0.66
3:2:1339:C:O2'	3:2:1341:A:N7	2.29	0.65
1:LA:2205:U:O4	1:LA:2237:C:N3	2.29	0.65
1:LA:1940:G:H21	1:LA:3362:A:H8	1.44	0.65
13:sV:37:LYS:HE2	13:sV:95:THR:HG22	1.79	0.65
35:sO:297:ASP:HB3	84:sh:574:SER:OG	1.96	0.65
1:LA:838:G:O6	83:Ls:4:ARG:NH2	2.30	0.65
3:2:992:A:H2	3:2:1012:U:H3	1.42	0.65
51:LM:189:GLU:HB2	51:LM:200:LEU:HB3	1.78	0.65
1:LA:1257:C:N3	1:LA:1261:G:N1	2.45	0.65
11:sT:2:LYS:HB3	11:sT:108:VAL:HG22	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Lc:27:LYS:HB2	67:Lc:42:LEU:HB2	1.79	0.65
36:sL:37:SER:HB2	84:sh:793:LYS:HD3	1.78	0.65
1:LA:562:C:H5''	60:LV:71:LYS:HD2	1.79	0.64
37:sj:228:ARG:NH2	84:sh:266:PHE:HB3	2.12	0.64
30:se:44:ILE:HG23	30:se:45:VAL:HG13	1.79	0.64
84:sh:575:CYS:SG	84:sh:577:ILE:CG1	2.85	0.64
3:2:1171:A:H2'	3:2:1172:G:C8	2.31	0.64
1:LA:3329:U:H5''	44:LF:308:MET:HE2	1.79	0.64
9:sS:100:ARG:NH2	9:sS:121:TYR:O	2.31	0.64
38:sk:53:PHE:CE1	84:sh:383:ILE:HG21	2.33	0.64
1:LA:1348:U:O2	1:LA:1349:G:N2	2.31	0.63
9:sS:37:LYS:HB2	9:sS:40:GLU:HG2	1.79	0.63
1:LA:3214:U:OP2	54:LP:128:ARG:NH2	2.32	0.63
12:sU:39:ARG:HH21	59:LU:188:ASP:HB2	1.61	0.63
46:LH:50:ARG:NH1	46:LH:147:ASP:OD2	2.32	0.63
84:sh:264:THR:HB	84:sh:284:VAL:HB	1.79	0.63
13:sV:48:THR:OG1	13:sV:52:ASN:O	2.16	0.63
37:sj:158:ILE:HG12	37:sj:167:ILE:HD12	1.79	0.63
84:sh:714:PHE:HA	84:sh:717:LEU:HG	1.80	0.63
36:sL:14:LYS:HD2	84:sh:783:ASP:OD2	1.98	0.62
3:2:1173:C:OP1	22:sH:132:ARG:NH2	2.31	0.62
3:2:1559:A:H5''	22:sH:135:GLY:HA3	1.80	0.62
59:LU:159:ALA:CB	59:LU:163:ARG:NH1	2.62	0.62
73:Li:35:VAL:HG23	73:Li:40:ASP:HB2	1.81	0.62
35:sO:109:ASP:HB2	35:sO:127:ARG:HD2	1.81	0.62
1:LA:2245:C:O2'	43:LE:220:GLY:O	2.18	0.62
34:sN:141:CYS:SG	34:sN:144:CYS:N	2.65	0.62
35:sO:185:GLN:HG2	35:sO:187:GLN:HG2	1.80	0.62
1:LA:1722:U:OP1	59:LU:100:ARG:NH1	2.33	0.62
3:2:647:G:H22	3:2:687:G:H1	1.46	0.62
37:sj:200:TRP:HZ2	84:sh:217:SER:HG	1.46	0.62
3:2:1502:G:N7	23:sI:102:ARG:NH2	2.48	0.62
3:2:1565:C:OP1	22:sH:41:ARG:NH1	2.33	0.61
84:sh:681:LYS:HA	84:sh:684:LYS:HD2	1.81	0.61
35:sO:295:SER:OG	35:sO:300:THR:OG1	2.18	0.61
1:LA:2836:C:H5	1:LA:2852:C:H42	1.48	0.61
11:sT:57:ASP:HA	11:sT:106:LEU:HA	1.82	0.61
59:LU:13:SER:OG	59:LU:38:ARG:NH2	2.33	0.61
3:2:1444:A:H4'	3:2:1445:G:H5'	1.83	0.61
13:sV:57:ALA:HB2	13:sV:177:GLY:HA2	1.83	0.61
37:sj:228:ARG:CD	84:sh:266:PHE:CG	2.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:LH:64:ILE:HG13	46:LH:109:THR:HG21	1.82	0.61
1:LA:847:A:H2'	1:LA:848:A:C8	2.35	0.61
35:sO:126:SER:OG	35:sO:128:ASP:OD1	2.16	0.61
3:2:1217:A:H5''	15:sC:1:MET:HG3	1.82	0.61
43:LE:27:ALA:O	43:LE:128:ARG:NH2	2.33	0.61
43:LE:111:THR:HB	43:LE:136:ILE:HD13	1.82	0.61
52:LN:108:GLU:O	52:LN:109:HIS:ND1	2.34	0.61
84:sh:380:CYS:HB3	84:sh:382:GLN:HG3	1.83	0.61
84:sh:583:LEU:HD21	84:sh:590:CYS:HB3	1.82	0.61
39:sm:9:A:OP1	84:sh:784:ARG:NH1	2.34	0.60
43:LE:32:LEU:HD13	43:LE:163:ARG:HD3	1.83	0.60
10:sB:157:ARG:HB2	10:sB:224:ASN:HD22	1.65	0.60
46:LH:50:ARG:NH2	46:LH:72:ASP:OD2	2.34	0.60
34:sN:148:TYR:H	34:sN:149:LYS:HZ3	1.49	0.60
84:sh:183:CYS:HB2	84:sh:206:CYS:N	2.15	0.60
54:LP:48:GLY:HA3	54:LP:53:VAL:HB	1.84	0.60
66:Lb:37:LYS:HD2	66:Lb:40:ARG:HH21	1.67	0.60
84:sh:219:HIS:CG	84:sh:235:GLU:HG3	2.29	0.60
24:sJ:99:ILE:HA	24:sJ:102:ARG:HG2	1.84	0.60
52:LN:15:GLU:OE2	52:LN:132:ASN:ND2	2.35	0.60
84:sh:360:LEU:HD23	84:sh:366:SER:O	2.02	0.60
84:sh:369:PHE:HE1	84:sh:381:LEU:HD12	1.67	0.60
12:sU:70:PHE:O	12:sU:74:GLN:HB2	2.01	0.60
1:LA:439:C:O2'	1:LA:494:G:N2	2.26	0.60
1:LA:3041:U:OP1	63:LY:12:ARG:NH1	2.33	0.60
47:LI:175:LYS:O	54:LP:117:ARG:NH2	2.35	0.60
62:LX:56:VAL:HG12	62:LX:65:VAL:HG22	1.83	0.60
1:LA:3050:U:O2'	64:LZ:16:GLY:O	2.20	0.60
61:LW:84:TYR:HB2	69:Le:24:PRO:HD3	1.84	0.60
36:sL:19:THR:HG23	36:sL:25:VAL:HG23	1.84	0.59
1:LA:3268:A:OP1	47:LI:46:ARG:NH2	2.36	0.59
3:2:477:A:H62	3:2:540:G:H1	1.49	0.59
5:sQ:128:LYS:NZ	5:sQ:132:ASP:OD1	2.35	0.59
21:sG:26:LEU:HD21	21:sG:62:GLN:HG3	1.84	0.59
1:LA:1231:A:H5''	1:LA:1232:C:H5'	1.83	0.59
4:sP:70:PRO:HB2	4:sP:94:GLY:HA3	1.84	0.59
22:sH:36:LYS:HG2	22:sH:105:VAL:HG21	1.84	0.59
60:LV:77:VAL:HG11	60:LV:106:LEU:HD22	1.84	0.59
3:2:540:G:N2	3:2:542:A:N7	2.43	0.59
44:LF:57:VAL:HG22	44:LF:73:VAL:HG12	1.84	0.59
84:sh:335:LEU:HD11	84:sh:350:PRO:HD2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:912:G:OP2	43:LE:9:ARG:NH2	2.34	0.59
63:LY:33:ASN:HD21	63:LY:64:LYS:HD3	1.68	0.59
3:2:1411:A:OP1	20:sF:114:ARG:NH2	2.35	0.59
35:sO:127:ARG:HA	35:sO:150:TRP:HB2	1.85	0.59
1:LA:2969:A:N7	43:LE:215:ASN:ND2	2.48	0.59
1:LA:1237:G:H1	1:LA:1251:A:H61	1.51	0.59
2:LB:14:LYS:HD2	2:LB:201:VAL:HG13	1.84	0.59
3:2:1534:G:O2'	3:2:1535:U:O2	2.19	0.59
12:sU:98:ILE:HG12	12:sU:121:VAL:HG21	1.85	0.59
13:sV:138:ASN:OD1	13:sV:141:ARG:NH2	2.36	0.59
1:LA:837:A:OP2	83:Ls:4:ARG:NH1	2.36	0.59
1:LA:2307:G:O2'	1:LA:2310:U:OP2	2.20	0.59
17:sD:132:GLU:HA	17:sD:135:MET:HG3	1.84	0.59
56:LR:61[A]:ALA:HA	56:LR:70[A]:PRO:HD2	1.85	0.58
1:LA:1257:C:N4	1:LA:1261:G:H22	2.01	0.58
40:sn:3:G:H22	40:sn:70:U:H3	1.50	0.58
84:sh:133:TRP:CD1	84:sh:149:SER:HB2	2.38	0.58
84:sh:558:CYS:HB3	84:sh:594:CYS:HA	1.85	0.58
39:sm:7:A:O5'	84:sh:788:ARG:NH2	2.31	0.58
14:sW:59:LEU:HD22	14:sW:69:ARG:HA	1.85	0.58
16:sX:109:VAL:HG12	16:sX:137:PHE:HB2	1.84	0.58
40:sl:13:U:H3	40:sl:22:G:H1	1.51	0.58
40:sl:58:A:O2'	40:sl:60:U:OP2	2.20	0.58
70:Lf:17:VAL:HG11	70:Lf:92:ILE:HD12	1.84	0.58
2:LB:177:ASP:HA	2:LB:180:VAL:HG12	1.84	0.58
50:LL:93:VAL:HG13	80:Lp:78:ILE:HG21	1.86	0.58
1:LA:1661:G:H2'	1:LA:1662:G:C8	2.39	0.58
63:LY:15:LEU:HD23	63:LY:53:SER:HB3	1.84	0.58
1:LA:687:U:OP2	53:LO:36:ARG:NH2	2.36	0.58
3:2:144:U:O4	11:sT:137:ARG:NH2	2.36	0.58
5:sQ:32:ILE:HD11	5:sQ:46:THR:HG23	1.86	0.58
63:LY:14:SER:O	63:LY:81:GLN:NE2	2.37	0.58
84:sh:132:CYS:HG	87:sh:1015:ZN:ZN	1.16	0.58
2:LB:193:LEU:HG	2:LB:195:LYS:H	1.68	0.58
51:LM:18:PRO:O	51:LM:23:ASN:ND2	2.37	0.58
51:LM:61:SER:OG	51:LM:63:GLU:OE1	2.22	0.58
2:LB:66:CYS:SG	2:LB:67:ILE:N	2.77	0.58
2:LB:180:VAL:O	2:LB:184:LEU:HB2	2.03	0.58
2:LB:193:LEU:O	2:LB:196:LYS:NZ	2.37	0.58
38:sk:10:LYS:HG3	38:sk:82:THR:HB	1.85	0.58
53:LO:31:LYS:HG2	53:LO:35:ARG:HH21	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LB:34:LEU:HD11	2:LB:210:MET:HE2	1.86	0.57
67:Lc:95:VAL:HG21	67:Lc:113:VAL:HG11	1.85	0.57
1:LA:2767:U:O2'	82:Lr:30:ALA:O	2.19	0.57
84:sh:554:LYS:HB2	84:sh:573:VAL:HG11	1.85	0.57
3:2:1034:C:HO2'	26:sb:2:THR:N	2.02	0.57
1:LA:728:G:H5''	58:LT:43:PRO:HB2	1.86	0.57
3:2:1672:G:H2'	3:2:1673:G:C8	2.39	0.57
10:sB:42:LEU:HD21	10:sB:90:ILE:HG21	1.86	0.57
51:LM:43:VAL:HG21	51:LM:197:VAL:HB	1.86	0.57
65:La:59:SER:HA	65:La:62:VAL:HG22	1.85	0.57
3:2:787:G:OP1	9:sS:255:ARG:NH2	2.36	0.57
34:sN:126:CYS:HB2	34:sN:130:VAL:HG11	1.86	0.57
60:LV:8:GLN:HB3	60:LV:64:ILE:HD11	1.86	0.57
17:sD:95:LYS:NZ	17:sD:115:VAL:O	2.37	0.57
38:sk:14:ILE:HB	38:sk:78:LYS:HG3	1.86	0.57
1:LA:2457:G:H1'	1:LA:2486:A:H61	1.69	0.57
7:sR:180:ALA:HB1	7:sR:184:VAL:HG23	1.87	0.57
34:sN:141:CYS:HB3	34:sN:144:CYS:HB3	1.86	0.57
3:2:151:G:N3	11:sT:13:GLN:NE2	2.53	0.57
46:LH:120:LYS:O	46:LH:248:ARG:NH2	2.37	0.57
56:LR:7[A]:VAL:HB	56:LR:33[A]:ILE:HD13	1.86	0.57
9:sS:129:VAL:HG22	9:sS:139:VAL:HG12	1.86	0.57
40:sl:26:G:O6	40:sl:44:A:N1	2.37	0.57
46:LH:236:LEU:HA	46:LH:239:ILE:HG12	1.86	0.57
2:LB:48:ARG:HH22	2:LB:159:LEU:HD22	1.70	0.57
2:LB:185:MET:HG2	2:LB:201:VAL:HG11	1.85	0.57
70:Lf:30:THR:HG23	70:Lf:91:SER:HB2	1.87	0.57
1:LA:715:A:H5''	68:Ld:115:LYS:HA	1.87	0.56
53:LO:145:PHE:HE2	75:Lk:118:ILE:HD11	1.70	0.56
1:LA:2392:C:O2'	44:LF:266:ARG:NH2	2.38	0.56
1:LA:3375:A:O2'	1:LA:3378:C:OP2	2.22	0.56
10:sB:156:ARG:HD3	19:sZ:52:ARG:CZ	2.35	0.56
30:se:46:GLU:HA	39:sm:7:A:H62	1.70	0.56
34:sN:124:PRO:HG2	37:sj:177:VAL:HG12	1.87	0.56
84:sh:592:LYS:HB2	84:sh:595:HIS:CE1	2.41	0.56
1:LA:1682:U:O4	62:LX:90:ARG:NH1	2.37	0.56
8:sA:120:TYR:HA	8:sA:123:VAL:HG12	1.86	0.56
35:sO:216:LYS:HA	35:sO:239:GLU:HG3	1.87	0.56
6:sE:86:VAL:HG22	6:sE:89:MET:HE3	1.88	0.56
47:LI:92:SER:OG	47:LI:94:GLU:OE1	2.23	0.56
53:LO:2:ALA:HB3	68:Ld:41:HIS:CE1	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:2484:A:H1'	40:sn:56:C:C6	2.40	0.56
1:LA:2522:G:O6	43:LE:70:ARG:NH2	2.31	0.56
1:LA:2818:U:H6	1:LA:2818:U:H5'	1.70	0.56
49:LK:161:GLU:HA	49:LK:164:VAL:HG22	1.86	0.56
70:Lf:22:LYS:HB2	70:Lf:94:GLU:HB2	1.86	0.56
76:Ll:66:GLU:OE1	76:Ll:91:ASN:ND2	2.32	0.56
84:sh:639:LYS:HB3	84:sh:648:LYS:HB2	1.88	0.56
1:LA:2677:G:H2'	1:LA:2679:A:H2	1.70	0.56
1:LA:2895:G:O2'	80:Lp:100:TYR:O	2.24	0.56
24:sJ:40:ASN:HA	24:sJ:43:LYS:HG2	1.88	0.56
63:LY:30:GLY:HA3	63:LY:66:LYS:HD3	1.88	0.56
7:sR:56:ILE:HG23	7:sR:61:LEU:HB2	1.87	0.56
54:LP:15:VAL:HG23	54:LP:35:ILE:HD13	1.88	0.56
84:sh:614:ASN:HB3	84:sh:656:LYS:HA	1.86	0.56
84:sh:717:LEU:HD11	84:sh:817:PHE:HB2	1.87	0.56
1:LA:2356:A:H61	1:LA:2983:C:H5	1.54	0.56
1:LA:2842:U:OP1	1:LA:2844:C:N4	2.38	0.56
2:LB:62:ASN:HB2	2:LB:150:ASP:HA	1.88	0.56
1:LA:2897:A:H2'	1:LA:2899:C:H5''	1.88	0.55
65:La:57:LEU:HG	65:La:62:VAL:HG12	1.88	0.55
1:LA:424:G:O2'	72:Lh:23:ASP:OD2	2.20	0.55
1:LA:2568:C:O2'	1:LA:2569:A:O4'	2.21	0.55
3:2:1199:G:O6	24:sJ:67:THR:HG22	2.06	0.55
36:sL:37:SER:CB	84:sh:793:LYS:HD3	2.37	0.55
59:LU:159:ALA:HB1	59:LU:163:ARG:HH11	1.69	0.55
71:Lg:77:ARG:HD2	71:Lg:89:LEU:HD13	1.88	0.55
1:LA:2205:U:O4	1:LA:2237:C:C4	2.59	0.55
18:sY:23:PRO:HD2	18:sY:26:PHE:HB3	1.87	0.55
37:sj:180:TYR:HB2	37:sj:217:LYS:HB2	1.87	0.55
40:sn:62:C:H2'	40:sn:63:G:H8	1.71	0.55
45:LG:126:ILE:O	45:LG:129:THR:OG1	2.24	0.55
46:LH:163:LEU:HD21	46:LH:175:HIS:CG	2.41	0.55
50:LL:89:LYS:HG2	50:LL:145:VAL:HG22	1.87	0.55
1:LA:2213:A:H2'	1:LA:2214:A:C8	2.42	0.55
3:2:538:A:OP2	14:sW:175:ARG:NH2	2.39	0.55
3:2:1553:G:O2'	32:sM:14:TYR:OH	2.24	0.55
15:sC:31:LYS:NZ	15:sC:36:ASP:O	2.38	0.55
49:LK:52:TRP:O	49:LK:57:ARG:NH1	2.39	0.55
79:Lo:25:GLN:OE1	79:Lo:28:ARG:NH2	2.40	0.55
84:sh:307:ILE:O	84:sh:310:PRO:HD3	2.07	0.55
3:2:1081:A:O2'	3:2:1083:G:N7	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:sP:31:VAL:HG12	4:sP:33:GLN:H	1.70	0.55
6:sE:25:LEU:HA	6:sE:28:MET:HG2	1.87	0.55
20:sF:94:GLN:NE2	35:sO:60:SER:OG	2.37	0.55
51:LM:30:LYS:HG3	51:LM:63:GLU:HG3	1.88	0.55
84:sh:68:CYS:HB2	84:sh:92:ASP:H	1.71	0.55
1:LA:520:U:OP2	48:LJ:70:LYS:NZ	2.38	0.55
1:LA:2677:G:N1	1:LA:2680:A:H2	2.01	0.55
37:sj:200:TRP:CZ3	84:sh:213:PRO:CG	2.89	0.55
3:2:61:A:O2'	3:2:62:A:O4'	2.25	0.55
3:2:135:A:H4'	3:2:136:C:H5'	1.89	0.55
31:sf:59:CYS:HG	31:sf:61:THR:HG1	1.53	0.55
61:LW:17:ARG:NH2	61:LW:23:GLY:O	2.39	0.55
1:LA:618:C:OP1	57:LS:173:ARG:NH2	2.39	0.55
1:LA:1646:G:H5''	81:Lt:12:ARG:HH22	1.71	0.55
1:LA:3373:U:OP2	71:Lg:102:LYS:NZ	2.36	0.55
84:sh:272:SER:H	84:sh:280:ARG:HH21	1.53	0.55
1:LA:1243:G:HO2'	1:LA:1271:A:HO2'	1.52	0.55
1:LA:1778:G:O2'	1:LA:1780:G:OP2	2.25	0.55
38:sk:64:LYS:HE2	38:sk:87:TYR:HA	1.88	0.55
3:2:1060:U:H3'	3:2:1061:A:H5''	1.87	0.55
5:sQ:23:PRO:HB3	5:sQ:26:ARG:HH21	1.72	0.55
12:sU:17:GLU:HA	12:sU:20:VAL:HG22	1.88	0.55
35:sO:12:THR:HG22	35:sO:311:ARG:HG2	1.89	0.55
37:sj:228:ARG:CD	84:sh:266:PHE:CD2	2.90	0.55
1:LA:1348:U:OP2	58:LT:38:ARG:NH2	2.40	0.54
1:LA:3153:U:H3	1:LA:3293:U:H3	1.54	0.54
10:sB:216:GLU:OE2	10:sB:219:ARG:NH2	2.39	0.54
84:sh:219:HIS:CG	84:sh:235:GLU:CG	2.89	0.54
1:LA:170:G:H1	1:LA:248:U:H3	1.55	0.54
1:LA:3379:C:H4'	44:LF:315:GLY:HA2	1.90	0.54
27:sc:6:PRO:HG3	27:sc:14:LYS:HG2	1.89	0.54
27:sc:107:PHE:HE2	27:sc:120:VAL:HG12	1.72	0.54
37:sj:228:ARG:NH2	84:sh:266:PHE:CD1	2.76	0.54
42:LD:66:A:OP1	75:Lk:10:ARG:NH2	2.40	0.54
84:sh:708:VAL:HG11	84:sh:813:LEU:O	2.06	0.54
3:2:1688:U:H2'	3:2:1689:A:O4'	2.08	0.54
19:sZ:111:ARG:NH2	30:se:57:SER:O	2.40	0.54
84:sh:103:SER:HB2	84:sh:112:TRP:HA	1.90	0.54
1:LA:2150:G:O2'	1:LA:2189:U:OP1	2.24	0.54
7:sR:45:VAL:HG21	7:sR:68:ILE:HG23	1.89	0.54
62:LX:38:ILE:HD11	62:LX:56:VAL:HG22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LC:44:C:H4'	46:LH:152:ARG:HG3	1.89	0.54
84:sh:87:CYS:HB2	84:sh:116:ASN:HD22	1.73	0.54
84:sh:754:SER:HB2	84:sh:791:PHE:HE1	1.72	0.54
24:sJ:82:TYR:HB3	32:sM:52:PHE:HB3	1.89	0.54
71:Lg:9:THR:HG23	71:Lg:109:VAL:HG23	1.89	0.54
84:sh:157:SER:HA	84:sh:162:GLY:HA2	1.88	0.54
1:LA:779:G:OP1	58:LT:185:LYS:NZ	2.40	0.54
9:sS:11:ARG:NH1	9:sS:21:ASP:O	2.39	0.54
22:sH:126:ARG:HB3	22:sH:133:VAL:HG12	1.89	0.54
1:LA:2557:A:OP1	43:LE:69:TYR:OH	2.26	0.54
17:sD:63:VAL:HG23	17:sD:93:ASP:HA	1.90	0.54
60:LV:22:PRO:O	61:LW:146:ASN:ND2	2.39	0.54
84:sh:708:VAL:HG21	84:sh:813:LEU:HB3	1.89	0.54
1:LA:110:G:OP2	53:LO:73:ARG:NH2	2.39	0.54
1:LA:1229:G:H2'	1:LA:1230:G:C8	2.43	0.54
1:LA:1352:A:H4'	1:LA:1353:U:H5'	1.90	0.54
1:LA:3243:A:H4'	44:LF:95:THR:HG22	1.88	0.54
42:LD:128:U:O4	81:Lt:17:LYS:NZ	2.40	0.54
49:LK:98:ARG:NH2	49:LK:191:ASN:OD1	2.40	0.54
3:2:194:U:H2'	3:2:195:G:H4'	1.90	0.53
43:LE:104:LEU:HD12	43:LE:158:ILE:HD11	1.89	0.53
84:sh:249:CYS:SG	84:sh:250:TYR:N	2.81	0.53
1:LA:1565:G:H22	1:LA:1574:C:H42	1.56	0.53
1:LA:1631:C:OP2	67:Lc:48:ARG:NH2	2.41	0.53
3:2:246:G:N2	16:sX:38:ALA:O	2.40	0.53
4:sP:28:ASN:HA	4:sP:46:HIS:HE2	1.73	0.53
9:sS:112:HIS:NE2	9:sS:237:SER:O	2.41	0.53
27:sc:70:LYS:HB3	27:sc:93:LEU:HD22	1.89	0.53
55:LQ:96:ARG:NH2	55:LQ:104:GLU:OE1	2.42	0.53
71:Lg:51:LEU:HB3	71:Lg:55:LEU:HD23	1.89	0.53
1:LA:1553:U:H4'	1:LA:1554:U:H5'	1.89	0.53
1:LA:1657:C:O2'	1:LA:1797:A:OP2	2.22	0.53
2:LB:145:TYR:O	2:LB:149:THR:OG1	2.21	0.53
2:LB:158:GLN:HG3	2:LB:160:LYS:H	1.74	0.53
15:sC:20:VAL:HG12	15:sC:67:THR:HG22	1.90	0.53
28:sd:14:SER:OG	28:sd:21:LYS:NZ	2.40	0.53
35:sO:247:PRO:O	84:sh:565:ARG:NH1	2.42	0.53
47:LI:56:LYS:NZ	47:LI:101:PHE:O	2.40	0.53
84:sh:80:GLN:HB3	84:sh:130:PRO:HB3	1.91	0.53
84:sh:184:HIS:HB2	84:sh:225:CYS:SG	2.48	0.53
1:LA:13:A:H5''	1:LA:13:A:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:2555:G:N7	74:Lj:95:ILE:HD11	2.23	0.53
4:sP:27:ARG:NH1	4:sP:43:ASP:O	2.42	0.53
43:LE:142:ASP:OD1	43:LE:142:ASP:N	2.41	0.53
59:LU:21:LYS:HE3	59:LU:55:VAL:HA	1.89	0.53
16:sX:27:THR:OG1	16:sX:28:SER:N	2.41	0.53
40:sl:62:C:H2'	40:sl:63:G:H8	1.73	0.53
1:LA:2553:U:C4	74:Lj:95:ILE:HG22	2.43	0.53
2:LB:141:ASN:OD1	2:LB:145:TYR:OH	2.27	0.53
12:sU:50:ASP:HA	12:sU:56:LYS:HG2	1.90	0.53
22:sH:46:VAL:HG11	22:sH:73:MET:HG3	1.89	0.53
84:sh:180:GLU:HG2	84:sh:189:SER:HB2	1.90	0.53
84:sh:575:CYS:SG	84:sh:577:ILE:N	2.81	0.53
1:LA:1236:G:N2	1:LA:1272:C:OP1	2.41	0.53
2:LB:60:ARG:NH2	2:LB:166:ALA:O	2.38	0.53
50:LL:31:ARG:NH1	50:LL:149:ASN:OD1	2.42	0.53
3:2:1355:C:H4'	84:sh:420:HIS:CD2	2.44	0.53
11:sT:121:LEU:HD13	11:sT:124:LEU:HD12	1.91	0.53
33:sg:41:THR:HA	33:sg:45:VAL:HG22	1.91	0.53
1:LA:655:C:H2'	1:LA:656:A:C8	2.44	0.53
1:LA:2854:U:OP2	51:LM:3:ARG:NH2	2.42	0.53
84:sh:307:ILE:HG13	84:sh:310:PRO:HB3	1.91	0.53
84:sh:558:CYS:SG	84:sh:575:CYS:SG	3.07	0.53
7:sR:81:MET:HB2	7:sR:101:VAL:HG13	1.90	0.52
13:sV:4:SER:OG	13:sV:6:ASP:OD2	2.27	0.52
45:LG:292:SER:OG	45:LG:294:GLU:OE1	2.26	0.52
44:LF:215:ILE:HD12	44:LF:338:LEU:HD12	1.89	0.52
82:Lr:34:SER:OG	82:Lr:35:LEU:O	2.22	0.52
84:sh:583:LEU:HD11	84:sh:601:GLN:HE21	1.75	0.52
10:sB:80:LYS:HB2	10:sB:83:ARG:HG3	1.91	0.52
33:sg:50:VAL:HG23	33:sg:54:ARG:H	1.73	0.52
1:LA:2514:U:H5'	49:LK:68:ARG:HG3	1.90	0.52
1:LA:3344:A:C2	1:LA:3361:G:N2	2.69	0.52
14:sW:66:ASP:HB3	14:sW:69:ARG:HB3	1.92	0.52
21:sG:36:ASP:HB3	21:sG:47:ARG:HD2	1.92	0.52
26:sb:31:SER:H	26:sb:34:ILE:HD12	1.74	0.52
2:LB:122:ARG:HG3	2:LB:123:LEU:HD12	1.90	0.52
4:sP:92:HIS:ND1	4:sP:202:TYR:OH	2.37	0.52
84:sh:355:ARG:HD3	84:sh:368:PRO:HA	1.92	0.52
1:LA:2206:G:H21	1:LA:2207:A:N6	2.08	0.52
1:LA:2457:G:H2'	1:LA:2458:A:H2'	1.92	0.52
3:2:1145:U:H5	3:2:1633:A:N1	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:sE:18:ARG:NH1	22:sH:90:ASN:O	2.42	0.52
35:sO:89:LEU:HB2	35:sO:103:PHE:HB2	1.91	0.52
84:sh:239:SER:HB2	84:sh:246:GLN:HA	1.90	0.52
3:2:1474:G:H2'	3:2:1475:A:C8	2.44	0.52
20:sF:46:PHE:HA	20:sF:49:TYR:HB2	1.91	0.52
7:sR:140:ARG:HB3	7:sR:221:THR:HB	1.92	0.52
13:sV:4:SER:HB2	13:sV:24:LYS:HD3	1.92	0.52
19:sZ:72:LYS:NZ	19:sZ:108:SER:O	2.42	0.52
37:sj:200:TRP:HZ2	84:sh:217:SER:OG	1.93	0.52
49:LK:162:LEU:HA	55:LQ:7:LEU:HD11	1.90	0.52
56:LR:54[A]:TYR:CD1	56:LR:145[A]:VAL:HG21	2.45	0.52
59:LU:105:LEU:HD23	59:LU:138:LEU:HD23	1.91	0.52
84:sh:56:ALA:O	84:sh:60:ILE:HG13	2.10	0.52
2:LB:54:LYS:HD2	2:LB:187:VAL:HB	1.91	0.52
4:sP:136:ALA:HB1	4:sP:141:ILE:HB	1.91	0.52
1:LA:638:C:OP1	72:Lh:21:HIS:NE2	2.25	0.52
1:LA:664:U:H2'	1:LA:665:A:C8	2.45	0.52
2:LB:42:ASP:OD1	2:LB:200:ASN:ND2	2.43	0.52
9:sS:98:ASN:ND2	9:sS:116:ASP:OD1	2.42	0.52
12:sU:115:SER:OG	12:sU:116:ARG:NH1	2.43	0.52
13:sV:20:GLN:NE2	13:sV:22:ARG:O	2.43	0.52
45:LG:35:VAL:HG21	45:LG:244:LEU:HD21	1.91	0.51
57:LS:16:SER:HB3	57:LS:149:VAL:HG22	1.92	0.51
58:LT:99:THR:O	58:LT:119:GLY:HA3	2.10	0.51
84:sh:590:CYS:HB3	84:sh:601:GLN:HG2	1.92	0.51
3:2:127:G:O6	11:sT:202:ARG:NH2	2.41	0.51
3:2:233:C:O2'	3:2:234:G:N2	2.40	0.51
3:2:591:A:H2'	3:2:592:A:C8	2.45	0.51
3:2:1347:U:OP2	24:sJ:23:ARG:NH2	2.33	0.51
11:sT:159:ARG:HB3	11:sT:170:THR:HB	1.91	0.51
14:sW:109:LEU:HB2	14:sW:146:PHE:HB3	1.92	0.51
83:Ls:30:GLU:HA	83:Ls:33:GLN:HG2	1.92	0.51
1:LA:1237:G:H1	1:LA:1251:A:N6	2.07	0.51
1:LA:1794:G:H4'	43:LE:191:LEU:HD12	1.92	0.51
1:LA:2108:C:OP1	13:sV:92:ARG:NH2	2.44	0.51
1:LA:2406:C:H2'	1:LA:2407:C:C6	2.46	0.51
1:LA:2960:C:H2'	1:LA:2961:G:C8	2.46	0.51
1:LA:3115:C:OP1	50:LL:62:ARG:NH2	2.43	0.51
3:2:123:G:OP1	9:sS:77:ARG:NH2	2.42	0.51
4:sP:84:ARG:NH1	4:sP:203:PHE:O	2.39	0.51
24:sJ:43:LYS:HA	24:sJ:46:GLU:HG3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:LO:163:GLY:HA2	68:Ld:139:ARG:HH12	1.75	0.51
84:sh:556:CYS:SG	84:sh:557:LYS:N	2.83	0.51
1:LA:595:G:H1	1:LA:609:G:H5''	1.75	0.51
1:LA:2138:A:HO2'	77:Lm:2:GLY:N	2.08	0.51
3:2:1300:A:OP1	7:sR:99:LYS:NZ	2.42	0.51
35:sO:7:LEU:HG	35:sO:315:VAL:HG12	1.92	0.51
3:2:566:C:OP1	33:sg:4:VAL:N	2.44	0.51
24:sJ:22:ILE:HD13	24:sJ:100:VAL:HG22	1.91	0.51
37:sj:200:TRP:CH2	84:sh:213:PRO:HB2	2.44	0.51
40:sl:3:G:O6	40:sl:70:U:O4	2.28	0.51
47:LI:31:ARG:NH2	47:LI:81:ALA:O	2.44	0.51
1:LA:2413:A:H2'	1:LA:2414:G:H8	1.74	0.51
2:LB:108:ASN:HB2	2:LB:136:THR:HB	1.93	0.51
3:2:1584:G:O2'	3:2:1610:G:N1	2.39	0.51
7:sR:116:LYS:HG2	7:sR:127:ALA:HB3	1.93	0.51
8:sA:8:LYS:HE2	24:sJ:61:LYS:HD3	1.92	0.51
65:La:63:ILE:HD12	65:La:102:LEU:HD12	1.92	0.51
73:Li:14:LEU:HD11	73:Li:31:LYS:HB2	1.91	0.51
84:sh:133:TRP:HA	84:sh:133:TRP:CE3	2.46	0.51
84:sh:327:THR:HA	84:sh:335:LEU:H	1.76	0.51
1:LA:655:C:H2'	1:LA:656:A:H8	1.74	0.51
15:sC:23:ALA:O	15:sC:64:TYR:HB2	2.11	0.51
1:LA:1786:G:H2'	1:LA:1787:A:C8	2.45	0.51
19:sZ:83:ILE:HG21	30:se:44:ILE:HD11	1.92	0.51
24:sJ:98:GLN:HG2	24:sJ:99:ILE:HD12	1.93	0.51
46:LH:85:ARG:NH2	46:LH:86:TYR:OH	2.43	0.51
65:La:105:VAL:HG11	65:La:135:ILE:HD13	1.93	0.51
84:sh:810:ALA:HA	84:sh:813:LEU:HD12	1.93	0.51
1:LA:1696:A:H2'	1:LA:1697:A:C8	2.46	0.51
1:LA:2864:A:H5''	51:LM:114:GLY:HA2	1.92	0.51
1:LA:3016:A:H2'	1:LA:3017:A:H8	1.76	0.51
3:2:898:A:H4'	19:sZ:46:MET:HE3	1.92	0.51
17:sD:62:LEU:HD21	17:sD:72:ILE:HG23	1.93	0.51
17:sD:128:ALA:HB1	17:sD:130:THR:HG23	1.93	0.51
74:Lj:22:VAL:HG12	74:Lj:30:LEU:HD22	1.93	0.51
84:sh:81:MET:HE1	84:sh:147:PRO:HB3	1.93	0.51
84:sh:367:CYS:HB2	84:sh:369:PHE:HD2	1.76	0.51
1:LA:1245:A:H3'	1:LA:1246:G:H8	1.76	0.51
4:sP:92:HIS:HD1	4:sP:202:TYR:HH	1.55	0.51
24:sJ:63:LEU:O	24:sJ:83:GLU:HA	2.11	0.51
35:sO:205:SER:HB2	35:sO:210:LEU:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:sk:63:ILE:HG13	38:sk:66:TRP:H	1.75	0.51
45:LG:44:LYS:HB3	45:LG:47:ARG:HH11	1.76	0.51
46:LH:294:ALA:HB1	51:LM:217:PHE:HB3	1.92	0.51
68:Ld:36:GLY:HA3	68:Ld:40:HIS:CE1	2.46	0.51
84:sh:356:CYS:SG	84:sh:371:CYS:HA	2.51	0.51
1:LA:627:U:H2'	1:LA:628:A:C8	2.46	0.50
1:LA:1255:C:N4	1:LA:1263:A:OP1	2.44	0.50
3:2:186:C:OP1	13:sV:146:ARG:NH2	2.44	0.50
3:2:1231:U:HO2'	3:2:1258:U:HO2'	1.59	0.50
3:2:1697:G:H1	3:2:1704:U:H3	1.59	0.50
10:sB:118:LEU:HD22	10:sB:129:PRO:HB2	1.93	0.50
10:sB:160:VAL:HG11	36:sL:25:VAL:HG11	1.93	0.50
1:LA:2177:G:OP2	43:LE:128:ARG:NH1	2.44	0.50
13:sV:152:ILE:HG13	13:sV:153:GLU:H	1.76	0.50
30:se:36:ILE:HB	30:se:73:TYR:HB2	1.92	0.50
38:sk:53:PHE:HE1	84:sh:383:ILE:HG21	1.73	0.50
49:LK:100:GLU:HB2	49:LK:104:GLU:HG3	1.93	0.50
53:LO:62:THR:HG23	53:LO:64:LYS:H	1.76	0.50
84:sh:260:LYS:HB3	84:sh:263:GLU:HB2	1.93	0.50
1:LA:2270:A:H2'	1:LA:2271:A:C8	2.45	0.50
4:sP:105:GLY:N	4:sP:135:GLU:OE1	2.35	0.50
46:LH:277:LEU:HG	46:LH:281:GLU:HG3	1.93	0.50
53:LO:2:ALA:HB3	68:Ld:41:HIS:HE1	1.76	0.50
63:LY:2:SER:OG	63:LY:3:GLY:N	2.39	0.50
84:sh:704:LEU:HB3	84:sh:813:LEU:HD22	1.94	0.50
1:LA:1717:U:H2'	1:LA:1718:G:C8	2.47	0.50
3:2:1087:A:H2'	3:2:1088:A:C8	2.47	0.50
3:2:1650:U:H2'	3:2:1651:A:C8	2.45	0.50
28:sd:92:VAL:HG21	28:sd:99:LYS:HB2	1.92	0.50
84:sh:56:ALA:HB1	84:sh:66:TYR:CE1	2.47	0.50
84:sh:112:TRP:NE1	84:sh:121:SER:HB3	2.27	0.50
84:sh:621:LYS:HB2	84:sh:624:HIS:CE1	2.46	0.50
84:sh:704:LEU:HD13	84:sh:813:LEU:HD13	1.93	0.50
1:LA:417:A:H2'	1:LA:418:A:C8	2.47	0.50
1:LA:2107:A:H2	1:LA:3344:A:H8	1.59	0.50
1:LA:3215:A:H5''	73:Li:2:ALA:HB2	1.93	0.50
1:LA:3322:A:H2'	1:LA:3323:A:C8	2.46	0.50
33:sg:49:LEU:HD22	33:sg:58:PRO:HG3	1.93	0.50
37:sj:228:ARG:NH1	84:sh:266:PHE:CB	2.72	0.50
39:sm:7:A:H5'	84:sh:788:ARG:HH22	1.34	0.50
71:Lg:4:LEU:O	71:Lg:79:ARG:NH2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:sh:247:ILE:HD13	84:sh:259:ILE:HG22	1.93	0.50
1:LA:2555:G:C5	74:Lj:95:ILE:HD11	2.46	0.50
3:2:687:G:H5'	26:sb:119:LYS:HG2	1.93	0.50
6:sE:75:PRO:HA	6:sE:93:VAL:HG23	1.94	0.50
9:sS:44:LEU:HD13	9:sS:82:TYR:HB3	1.92	0.50
38:sk:112:LYS:HE2	84:sh:408:ASN:OD1	2.12	0.50
55:LQ:9:GLU:HG3	76:Ll:44:VAL:HG11	1.94	0.50
67:Lc:5:LEU:HD11	70:Lf:35:ARG:HD2	1.94	0.50
3:2:298:C:H5''	9:sS:38:LEU:HD23	1.93	0.50
3:2:1697:G:H22	3:2:1704:U:H3	1.59	0.50
22:sH:48:LYS:HD3	23:sI:35:ASP:HB2	1.94	0.50
23:sI:105:LEU:HD13	23:sI:122:ARG:HD3	1.93	0.50
26:sb:81:VAL:O	26:sb:122:SER:OG	2.28	0.50
84:sh:100:ALA:HB3	84:sh:124:VAL:HG13	1.94	0.50
35:sO:83:ALA:HB2	35:sO:113:VAL:HB	1.94	0.50
63:LY:54:LEU:HD21	63:LY:119:GLY:HA3	1.94	0.50
1:LA:1845:G:H5'	1:LA:1846:C:H5'	1.93	0.49
1:LA:1863:G:H4'	59:LU:82:LYS:HD3	1.94	0.49
1:LA:2697:A:H2'	1:LA:2698:G:C8	2.47	0.49
34:sN:100:LEU:HD12	34:sN:103:LEU:HD21	1.94	0.49
45:LG:295:ILE:O	45:LG:299:ILE:HG12	2.12	0.49
46:LH:119:TYR:OH	46:LH:139:PRO:O	2.25	0.49
46:LH:258:LYS:O	46:LH:265:TYR:OH	2.23	0.49
78:Ln:26:LYS:HD3	78:Ln:78:LEU:HD12	1.94	0.49
84:sh:56:ALA:HB1	84:sh:66:TYR:HE1	1.76	0.49
84:sh:219:HIS:NE2	84:sh:235:GLU:HB2	2.23	0.49
84:sh:404:ARG:HD2	84:sh:406:ARG:HH22	1.76	0.49
13:sV:87:ASN:HB3	13:sV:90:LEU:HG	1.94	0.49
52:LN:21:ILE:HD11	52:LN:125:MET:HE2	1.94	0.49
56:LR:3[A]:VAL:HG13	56:LR:4[A]:GLU:HG3	1.94	0.49
1:LA:3354:U:H3	13:sV:162:ALA:HA	1.77	0.49
13:sV:107:THR:O	13:sV:111:GLN:HG3	2.13	0.49
17:sD:54:ARG:HG3	17:sD:56:GLU:H	1.78	0.49
35:sO:117:LYS:O	35:sO:118:LYS:HB2	2.13	0.49
50:LL:57:VAL:HG12	50:LL:68:LEU:HD22	1.93	0.49
50:LL:112:ILE:HD11	50:LL:134:ILE:HG12	1.94	0.49
68:Ld:112:ILE:HB	68:Ld:130:VAL:HG12	1.94	0.49
70:Lf:57:GLU:OE1	70:Lf:69:TYR:OH	2.29	0.49
67:Lc:50:PRO:HD3	67:Lc:68:ILE:HG12	1.93	0.49
84:sh:765:ARG:HG2	84:sh:790:VAL:HG23	1.93	0.49
1:LA:2471:U:O2	1:LA:2475:G:O6	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:3275:U:O2'	73:Li:99:ARG:NH1	2.44	0.49
3:2:207:U:O2	13:sV:178:ARG:NH2	2.35	0.49
3:2:789:A:OP1	9:sS:108:ARG:NH1	2.45	0.49
43:LE:14:SER:OG	43:LE:15:ILE:N	2.46	0.49
61:LW:91:LEU:HD12	61:LW:96:ILE:HD11	1.94	0.49
71:Lg:46:THR:HG21	71:Lg:90:PHE:HA	1.94	0.49
1:LA:1805:C:H2'	1:LA:1806:A:H8	1.77	0.49
43:LE:80:GLU:HG3	83:Ls:66:GLY:HA2	1.94	0.49
44:LF:35:ASP:OD2	44:LF:37:ARG:NH1	2.46	0.49
51:LM:54:SER:OG	51:LM:130:ASP:O	2.31	0.49
3:2:330:G:OP2	13:sV:172:ARG:NH1	2.45	0.49
3:2:1296:A:OP1	4:sP:138:TYR:OH	2.28	0.49
11:sT:180:THR:HG23	11:sT:183:ARG:H	1.78	0.49
12:sU:41:LEU:HD21	12:sU:73:VAL:HG21	1.95	0.49
12:sU:56:LYS:HB2	12:sU:88:ARG:HE	1.77	0.49
20:sF:113:ASP:OD1	20:sF:115:THR:OG1	2.29	0.49
31:sf:59:CYS:SG	31:sf:61:THR:OG1	2.67	0.49
53:LO:174:ARG:HB2	76:Ll:9:ILE:HD12	1.95	0.49
1:LA:3016:A:H2'	1:LA:3017:A:C8	2.48	0.49
3:2:1098:U:OP1	7:sR:159:THR:OG1	2.30	0.49
9:sS:103:TYR:O	9:sS:182:TYR:OH	2.31	0.49
37:sj:206:ILE:HG13	84:sh:229:LEU:HD21	1.93	0.49
40:sn:17:C:H42	40:sn:55:U:H1'	1.78	0.49
42:LD:141:C:OP1	55:LQ:109:ARG:NH2	2.46	0.49
52:LN:48:SER:HB2	52:LN:66:ALA:HB3	1.95	0.49
82:Lr:10:THR:HA	82:Lr:20:HIS:HD2	1.78	0.49
84:sh:590:CYS:HB2	84:sh:595:HIS:HE1	1.77	0.49
1:LA:900:G:H1'	1:LA:1589:A:N6	2.28	0.49
1:LA:3233:C:H2'	1:LA:3234:A:C8	2.48	0.49
3:2:992:A:O2'	3:2:1785:U:O2	2.28	0.49
9:sS:208:VAL:HG11	9:sS:225:VAL:HG21	1.95	0.49
12:sU:13:PRO:HB3	12:sU:18:LEU:HD21	1.93	0.49
16:sX:125:VAL:HG12	16:sX:139:VAL:HA	1.94	0.49
1:LA:1596:C:H2'	1:LA:1597:C:C6	2.47	0.49
13:sV:26:LYS:HG2	13:sV:29:LEU:HD23	1.95	0.49
35:sO:17:ASN:HA	35:sO:308:ASN:HD22	1.78	0.49
35:sO:42:LEU:HB2	35:sO:61:PHE:HB2	1.94	0.49
35:sO:274:LEU:HD13	35:sO:313:TRP:CZ2	2.48	0.49
84:sh:567:VAL:HG23	84:sh:570:GLN:HB2	1.95	0.49
1:LA:129:U:H2'	1:LA:130:A:C8	2.48	0.48
1:LA:528:U:H2'	1:LA:529:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:620:U:OP1	57:LS:167:ARG:NH2	2.46	0.48
3:2:1445:G:N2	34:sN:88:PRO:O	2.46	0.48
84:sh:132:CYS:SG	84:sh:133:TRP:N	2.86	0.48
84:sh:216:CYS:SG	84:sh:218:ILE:HG13	2.53	0.48
1:LA:595:G:OP2	48:LJ:30:ARG:NH1	2.47	0.48
1:LA:1279:C:H2'	1:LA:1280:C:C6	2.49	0.48
1:LA:2303:A:O2'	3:2:1747:G:O2'	2.22	0.48
3:2:12:U:H2'	3:2:13:C:C6	2.47	0.48
8:sA:51:ARG:HD2	8:sA:89:GLU:HB3	1.95	0.48
12:sU:159:VAL:O	12:sU:163:ASP:HB3	2.13	0.48
36:sL:14:LYS:CD	84:sh:783:ASP:OD2	2.61	0.48
45:LG:11:LEU:HD21	45:LG:156:LEU:HB2	1.95	0.48
1:LA:170:G:H5''	75:Lk:109:ILE:HD12	1.96	0.48
1:LA:3198:U:O2	50:LL:21:LYS:N	2.44	0.48
1:LA:3343:G:H21	1:LA:3362:A:H2	1.61	0.48
2:LB:80:CYS:O	2:LB:84:ALA:HB3	2.13	0.48
6:sE:28:MET:HG3	6:sE:29:SER:H	1.78	0.48
40:sl:23:C:H2'	40:sl:24:G:H8	1.78	0.48
60:LV:77:VAL:HG22	60:LV:126:VAL:HG23	1.95	0.48
3:2:886:U:O2'	19:sZ:121:VAL:O	2.30	0.48
3:2:1524:A:H2'	3:2:1525:A:C8	2.48	0.48
45:LG:59:GLN:O	77:Lm:52:LYS:NZ	2.42	0.48
84:sh:595:HIS:CE1	84:sh:600:CYS:HA	2.48	0.48
1:LA:1799:A:H2'	1:LA:1800:A:C8	2.48	0.48
1:LA:2468:A:O2'	1:LA:2477:G:N2	2.47	0.48
2:LB:21:ASN:OD1	2:LB:22:GLU:N	2.47	0.48
23:sI:9:VAL:HG22	23:sI:140:LEU:HD13	1.94	0.48
50:LL:41:ILE:HD13	50:LL:71:VAL:HB	1.96	0.48
78:Ln:14:LEU:HD21	78:Ln:52:TYR:CG	2.49	0.48
84:sh:271:LYS:HA	84:sh:280:ARG:NH2	2.29	0.48
84:sh:771:LEU:HD12	84:sh:771:LEU:HA	1.72	0.48
9:sS:105:VAL:HG21	9:sS:245:LYS:H	1.78	0.48
34:sN:107:LYS:HD3	34:sN:115:THR:H	1.79	0.48
53:LO:76:THR:HG22	53:LO:78:ALA:H	1.79	0.48
1:LA:651:G:O2'	1:LA:1435:A:OP1	2.29	0.48
1:LA:1257:C:H42	1:LA:1261:G:N2	2.07	0.48
3:2:1591:C:H2'	3:2:1592:A:C8	2.49	0.48
3:2:1629:G:OP1	30:se:89:ARG:NH2	2.46	0.48
9:sS:148:ARG:NH2	11:sT:201:GLN:OE1	2.47	0.48
17:sD:131:ASP:OD1	17:sD:131:ASP:N	2.46	0.48
26:sb:15:ASN:ND2	26:sb:72:CYS:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:sO:217:ASP:N	35:sO:217:ASP:OD1	2.45	0.48
38:sk:13:ARG:HH21	38:sk:16:PRO:HA	1.79	0.48
3:2:912:U:OP2	5:sQ:8:ARG:NH1	2.46	0.48
8:sA:70:THR:O	8:sA:74:GLN:HB2	2.13	0.48
16:sX:73:GLY:HA3	16:sX:86:ILE:HD12	1.95	0.48
37:sj:203:LEU:HA	37:sj:206:ILE:HG12	1.95	0.48
45:LG:304:GLN:NE2	45:LG:306:THR:O	2.42	0.48
84:sh:595:HIS:NE2	84:sh:600:CYS:HA	2.28	0.48
3:2:1628:U:H2'	3:2:1629:G:C8	2.48	0.48
3:2:1665:U:O2	3:2:1736:G:N2	2.37	0.48
4:sP:118:PRO:HG2	4:sP:141:ILE:HD13	1.96	0.48
6:sE:57:MET:O	6:sE:61:ARG:HG3	2.14	0.48
46:LH:48:LYS:HG2	46:LH:145:PHE:HE2	1.78	0.48
75:Lk:12:LYS:NZ	75:Lk:20:GLN:OE1	2.46	0.48
1:LA:2103:U:H2'	1:LA:2104:A:H8	1.79	0.48
1:LA:3231:U:H2'	1:LA:3232:G:H8	1.79	0.48
3:2:871:G:H2'	3:2:872:G:C8	2.48	0.48
3:2:1368:G:OP1	23:sI:69:LYS:NZ	2.47	0.48
8:sA:40:ARG:NH1	8:sA:47:GLU:OE2	2.42	0.48
17:sD:35:ALA:O	17:sD:40:GLY:N	2.44	0.48
46:LH:34:LYS:HA	61:LW:27:LEU:HD11	1.94	0.48
55:LQ:155:VAL:O	55:LQ:162:ARG:NH2	2.39	0.48
56:LR:121[A]:PRO:HA	56:LR:124[A]:LEU:HD12	1.96	0.48
2:LB:55:LEU:HD12	2:LB:154:THR:HG21	1.95	0.47
6:sE:22:LEU:HA	6:sE:25:LEU:HG	1.96	0.47
15:sC:11:ILE:HG12	15:sC:42:VAL:HG12	1.96	0.47
27:sc:57:LEU:HD11	27:sc:73:ARG:HB2	1.95	0.47
57:LS:118:GLN:HG2	57:LS:147:GLU:HG2	1.95	0.47
84:sh:282:ILE:HD12	84:sh:282:ILE:H	1.79	0.47
84:sh:621:LYS:HB2	84:sh:624:HIS:HE1	1.78	0.47
1:LA:1634:G:N7	67:Lc:17:ARG:NH1	2.62	0.47
3:2:129:U:H4'	3:2:131:C:H42	1.79	0.47
3:2:1727:G:H2'	3:2:1728:A:C8	2.49	0.47
22:sH:11:PHE:HD1	22:sH:60:GLU:HB3	1.79	0.47
34:sN:141:CYS:CB	34:sN:144:CYS:HB3	2.44	0.47
58:LT:19:PRO:HB3	58:LT:53:PHE:HA	1.95	0.47
1:LA:768:C:OP1	53:LO:186:ARG:NH2	2.40	0.47
1:LA:1474:A:O2'	71:Lg:57:GLN:NE2	2.47	0.47
1:LA:1495:U:H5	1:LA:1835:A:N1	2.13	0.47
3:2:765:G:O6	14:sW:152:SER:OG	2.29	0.47
29:sK:50:ILE:HG22	29:sK:69:LEU:HD13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:sk:28:LEU:HB3	38:sk:114:ASN:HB2	1.95	0.47
43:LE:150:LEU:HD11	43:LE:156:LYS:HD2	1.96	0.47
84:sh:367:CYS:HA	84:sh:368:PRO:HD3	1.79	0.47
3:2:1366:U:OP2	20:sF:66:ARG:NH1	2.47	0.47
79:Lo:5:LYS:HE2	79:Lo:13:MET:HE1	1.95	0.47
1:LA:36:C:OP2	55:LQ:83:LYS:NZ	2.43	0.47
1:LA:446:U:H4'	1:LA:447:U:H5	1.80	0.47
1:LA:943:U:H3'	68:Ld:13:GLY:HA2	1.96	0.47
1:LA:2901:G:O2'	1:LA:3024:A:N1	2.46	0.47
2:LB:36:VAL:HG11	2:LB:206:VAL:HG23	1.96	0.47
19:sZ:16:VAL:O	19:sZ:30:VAL:HA	2.15	0.47
48:LJ:156:ILE:HD11	48:LJ:168:ILE:HG23	1.96	0.47
1:LA:94:G:H2'	1:LA:95:A:C8	2.50	0.47
1:LA:873:C:H3'	1:LA:874:U:H4'	1.97	0.47
1:LA:1016:C:N3	52:LN:94:ARG:NH1	2.63	0.47
1:LA:1727:G:OP1	83:Ls:44:LYS:NZ	2.42	0.47
1:LA:2129:U:H2'	1:LA:2130:G:C8	2.50	0.47
3:2:1461:C:OP1	22:sH:144:ARG:NH2	2.38	0.47
3:2:1776:A:H2'	3:2:1777:G:C8	2.49	0.47
17:sD:44:GLY:O	17:sD:48:SER:HB3	2.14	0.47
23:sI:109:GLU:HG3	23:sI:114:VAL:HG23	1.95	0.47
52:LN:92:ARG:HH21	52:LN:94:ARG:HE	1.63	0.47
84:sh:684:LYS:NZ	84:sh:700:GLU:HA	2.29	0.47
1:LA:1390:A:N6	1:LA:1418:A:O2'	2.48	0.47
1:LA:2093:A:N1	59:LU:114:LYS:NZ	2.58	0.47
1:LA:2768:U:H2'	1:LA:2769:A:H8	1.79	0.47
2:LB:100:ILE:HD11	2:LB:103:LEU:HD12	1.96	0.47
3:2:284:G:N7	11:sT:188:ARG:NH1	2.61	0.47
3:2:1634:C:H1'	39:sm:23:A:N6	2.30	0.47
12:sU:10:SER:OG	12:sU:11:GLN:N	2.47	0.47
17:sD:28:LEU:HA	17:sD:31:VAL:HG12	1.97	0.47
19:sZ:80:HIS:HA	19:sZ:113:GLY:O	2.14	0.47
35:sO:37:SER:OG	35:sO:38:ARG:N	2.47	0.47
46:LH:40:HIS:HB3	46:LH:43:LYS:HG3	1.96	0.47
56:LR:74[A]:ARG:HG3	56:LR:145[A]:VAL:HG13	1.97	0.47
67:Lc:119:GLU:O	67:Lc:123:GLN:HG2	2.15	0.47
73:Li:16:TYR:OH	73:Li:89:LEU:O	2.31	0.47
3:2:532:U:O2'	28:sd:33:ALA:O	2.33	0.47
3:2:896:U:O2	19:sZ:41:ARG:NH1	2.48	0.47
3:2:1175:U:H2'	3:2:1176:G:C8	2.50	0.47
3:2:1424:A:OP2	8:sA:151:LYS:NZ	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:1504:G:OP1	23:sI:97:SER:OG	2.28	0.47
29:sK:61:SER:H	29:sK:64:VAL:HB	1.80	0.47
37:sj:210:VAL:HG11	84:sh:229:LEU:HD13	1.95	0.47
84:sh:90:VAL:HG21	84:sh:133:TRP:HH2	1.79	0.47
84:sh:607:THR:HA	84:sh:622:PRO:HA	1.97	0.47
1:LA:2185:G:O2'	1:LA:2314:U:OP2	2.26	0.47
3:2:144:U:H2'	3:2:145:A:O4'	2.15	0.47
3:2:791:A:H2'	3:2:792:U:H6	1.80	0.47
8:sA:59:LEU:HA	8:sA:66:ILE:HG12	1.96	0.47
34:sN:104:SER:HA	34:sN:131:PHE:HE2	1.78	0.47
35:sO:211:ILE:HD11	35:sO:225:LEU:HD13	1.96	0.47
44:LF:292:ALA:HB1	44:LF:295:ALA:HB3	1.97	0.47
61:LW:29:THR:HA	61:LW:32:LYS:HD2	1.97	0.47
77:Lm:64:MET:HE3	77:Lm:67:LEU:HD23	1.97	0.47
84:sh:388:CYS:SG	84:sh:389:ALA:N	2.88	0.47
84:sh:453:GLU:CD	84:sh:453:GLU:H	2.22	0.47
1:LA:1729:A:O4'	70:Lf:52:ARG:NH1	2.42	0.47
3:2:732:G:O2'	3:2:735:C:N4	2.47	0.47
17:sD:73:LYS:HZ2	34:sN:109:ASP:H	1.61	0.47
24:sJ:83:GLU:OE2	24:sJ:85:ARG:NH2	2.36	0.47
47:LI:43:LEU:HD11	47:LI:85:ILE:HG13	1.97	0.47
47:LI:146:LEU:HA	47:LI:149:ILE:HB	1.96	0.47
9:sS:54:TYR:O	28:sd:15:ASN:ND2	2.46	0.46
36:sL:44:VAL:HG22	36:sL:54:LEU:HD21	1.97	0.46
38:sk:85:GLY:O	38:sk:88:ALA:O	2.33	0.46
1:LA:170:G:N2	1:LA:248:U:O2	2.43	0.46
1:LA:307:A:H2'	1:LA:308:A:C8	2.50	0.46
1:LA:567:G:H2'	1:LA:568:G:C8	2.50	0.46
3:2:499:U:H5'	3:2:500:C:H5''	1.96	0.46
3:2:1556:A:O2'	3:2:1560:U:OP2	2.24	0.46
34:sN:133:ALA:HB3	34:sN:140:TYR:HB3	1.96	0.46
63:LY:59:MET:HE3	63:LY:73:VAL:HG12	1.97	0.46
63:LY:80:ARG:HB2	63:LY:99:ALA:HB3	1.97	0.46
65:La:67:ILE:HD12	65:La:121:LYS:HG3	1.97	0.46
84:sh:183:CYS:SG	84:sh:206:CYS:HB3	2.54	0.46
84:sh:295:TYR:HE1	84:sh:302:PHE:HB3	1.79	0.46
1:LA:19:U:H2'	1:LA:20:A:C8	2.50	0.46
1:LA:1591:G:OP1	74:Lj:37:LYS:NZ	2.46	0.46
1:LA:3295:A:H2'	1:LA:3296:A:C8	2.50	0.46
3:2:511:A:N6	3:2:539:G:O6	2.43	0.46
38:sk:80:ARG:HH21	38:sk:107:ASP:HB3	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:Ll:66:GLU:OE2	76:Ll:70:ARG:NH2	2.49	0.46
1:LA:1447:G:OP1	57:LS:65:SER:OG	2.28	0.46
1:LA:1593:A:OP1	74:Lj:60:ARG:NH1	2.48	0.46
1:LA:1724:U:H1'	1:LA:1725:C:C6	2.50	0.46
1:LA:2711:C:O2'	1:LA:2744:U:OP1	2.34	0.46
3:2:751:G:H2'	3:2:752:A:H8	1.81	0.46
3:2:1434:U:H4'	32:sM:24:CYS:HB2	1.97	0.46
14:sW:119:ALA:HB1	14:sW:124:HIS:HB3	1.96	0.46
42:LD:6:U:H2'	42:LD:7:U:C6	2.51	0.46
45:LG:14:GLU:HG2	45:LG:15:ALA:H	1.79	0.46
71:Lg:55:LEU:HB2	71:Lg:95:PRO:HD3	1.97	0.46
84:sh:221:CYS:SG	84:sh:223:LYS:HB2	2.55	0.46
1:LA:2219:A:OP2	76:Ll:68:ARG:NH2	2.49	0.46
3:2:924:A:H2'	3:2:925:G:C8	2.50	0.46
7:sR:143:TYR:OH	7:sR:149:GLY:O	2.30	0.46
15:sC:77:ARG:HD3	15:sC:84:GLU:HA	1.98	0.46
18:sY:100:LYS:HE3	18:sY:104:ARG:HH12	1.81	0.46
49:LK:87:ALA:HA	49:LK:90:THR:HG22	1.97	0.46
53:LO:43:ALA:O	53:LO:47:ALA:HA	2.16	0.46
84:sh:308:SER:O	84:sh:309:PRO:C	2.58	0.46
1:LA:1213:G:OP1	60:LV:139:TYR:OH	2.33	0.46
3:2:1681:A:H1'	11:sT:66:GLY:HA2	1.97	0.46
11:sT:88:ARG:HB3	11:sT:91:GLU:HB2	1.98	0.46
14:sW:92:LYS:HB2	14:sW:95:TYR:CE2	2.51	0.46
45:LG:4:PRO:O	45:LG:5:GLN:HG2	2.16	0.46
45:LG:325:LEU:O	48:LJ:41:ARG:NH2	2.46	0.46
48:LJ:86:VAL:O	48:LJ:114:GLY:HA2	2.15	0.46
3:2:319:U:H4'	3:2:323:A:C8	2.50	0.46
3:2:1436:A:OP2	8:sA:27:ARG:NH2	2.46	0.46
3:2:1472:C:OP1	10:sB:102:ARG:NH1	2.45	0.46
9:sS:31:PRO:HG2	9:sS:38:LEU:HB2	1.97	0.46
12:sU:59:ALA:HA	12:sU:91:ILE:HG13	1.98	0.46
12:sU:150:GLN:O	12:sU:181:ILE:HA	2.15	0.46
18:sY:119:GLU:O	18:sY:123:HIS:ND1	2.49	0.46
26:sb:30:SER:HB2	26:sb:61:ILE:HG13	1.98	0.46
78:Ln:2:ALA:N	78:Ln:51:LEU:O	2.48	0.46
84:sh:656:LYS:HE3	84:sh:659:ARG:HB3	1.97	0.46
3:2:864:U:OP1	31:sf:26:GLN:NE2	2.49	0.46
4:sP:76:ILE:HD13	4:sP:98:ILE:HB	1.97	0.46
21:sG:107:SER:O	21:sG:111:LYS:HG3	2.15	0.46
28:sd:12:VAL:HG22	28:sd:23:PHE:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:LH:196:ARG:NH2	46:LH:237:GLU:OE1	2.38	0.46
84:sh:415:MET:HB3	84:sh:458:CYS:HB2	1.98	0.46
5:sQ:225:VAL:O	5:sQ:229:MET:HG2	2.16	0.46
16:sX:21:ASN:O	16:sX:21:ASN:ND2	2.45	0.46
35:sO:299:GLN:CG	84:sh:576:GLY:HA3	2.33	0.46
40:sn:6:U:H2'	40:sn:7:G:C8	2.50	0.46
40:sn:26:G:H1	40:sn:44:A:H2	1.63	0.46
1:LA:507:U:H2'	1:LA:508:U:C6	2.51	0.46
1:LA:1108:U:H2'	1:LA:1109:U:C6	2.50	0.46
1:LA:2768:U:H2'	1:LA:2769:A:C8	2.51	0.46
3:2:93:A:H1'	9:sS:3:ARG:HB3	1.98	0.46
4:sP:198:MET:HG2	4:sP:200:ASP:H	1.81	0.46
35:sO:88:THR:HG22	35:sO:104:VAL:HG12	1.98	0.46
35:sO:266:ASP:CG	35:sO:267:PRO:HD3	2.41	0.46
37:sj:114:GLU:HA	37:sj:201:ARG:HH21	1.80	0.46
45:LG:328:ASN:OD1	48:LJ:48:ASN:ND2	2.49	0.46
84:sh:214:LEU:HD12	84:sh:219:HIS:HB3	1.98	0.46
84:sh:272:SER:CB	84:sh:280:ARG:HB3	2.44	0.46
1:LA:1760:A:H61	59:LU:46:LYS:NZ	2.14	0.45
1:LA:2501:U:H2'	1:LA:2502:A:C4	2.51	0.45
3:2:354:C:H5''	13:sV:16:ALA:HB2	1.97	0.45
3:2:802:G:H21	26:sb:107:SER:HB2	1.81	0.45
16:sX:46:LYS:O	16:sX:50:GLU:HG2	2.16	0.45
30:se:51:ARG:O	30:se:55:GLU:HG3	2.16	0.45
59:LU:15:VAL:HG11	59:LU:52:LYS:HB2	1.98	0.45
1:LA:362:U:O4	77:Lm:24:ARG:NH2	2.48	0.45
3:2:126:A:OP1	11:sT:201:GLN:HG3	2.15	0.45
3:2:771:A:OP1	14:sW:9:SER:OG	2.31	0.45
3:2:1125:A:O2'	3:2:1776:A:OP1	2.29	0.45
25:sa:4:ASP:N	25:sa:4:ASP:OD1	2.49	0.45
46:LH:270:LYS:HA	46:LH:273:ARG:HG2	1.97	0.45
57:LS:33:ALA:HB1	57:LS:117:ILE:HG12	1.98	0.45
1:LA:1243:G:O2'	1:LA:1271:A:O2'	2.25	0.45
1:LA:2256:A:C5	3:2:1757:G:H5'	2.51	0.45
37:sj:228:ARG:NH2	84:sh:266:PHE:HD1	2.12	0.45
1:LA:629:U:H2'	1:LA:630:A:C8	2.50	0.45
1:LA:1280:C:H2'	1:LA:1281:G:C8	2.51	0.45
1:LA:1621:A:H2'	1:LA:1622:U:C6	2.51	0.45
1:LA:1750:A:H4'	78:Ln:26:LYS:HZ1	1.81	0.45
1:LA:2413:A:H2'	1:LA:2414:G:C8	2.51	0.45
3:2:625:C:H2'	3:2:626:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:sP:2:SER:OG	4:sP:3:LEU:N	2.46	0.45
13:sV:172:ARG:HE	13:sV:175:GLN:HG3	1.82	0.45
16:sX:99:ARG:HG3	27:sc:12:ALA:HB2	1.98	0.45
32:sM:4:GLU:HB3	32:sM:6:VAL:HG12	1.99	0.45
45:LG:343:LYS:HB3	45:LG:343:LYS:HE3	1.80	0.45
1:LA:1764:U:P	59:LU:43:LYS:HZ2	2.39	0.45
1:LA:2880:U:H1'	44:LF:250:ALA:HB3	1.98	0.45
3:2:853:G:H3'	59:LU:173:ARG:HH12	1.81	0.45
3:2:962:C:H2'	3:2:963:A:O4'	2.16	0.45
3:2:1474:G:H2'	3:2:1475:A:H8	1.81	0.45
3:2:1738:U:H2'	3:2:1739:C:C6	2.51	0.45
8:sA:42:THR:HG23	24:sJ:108:ILE:HD13	1.98	0.45
10:sB:26:ALA:HB2	20:sF:26:LYS:HG3	1.97	0.45
12:sU:45:SER:OG	12:sU:46:ILE:N	2.50	0.45
12:sU:85:PHE:CE1	12:sU:88:ARG:HG3	2.52	0.45
12:sU:85:PHE:HE1	12:sU:88:ARG:HG3	1.82	0.45
15:sC:13:GLN:O	15:sC:17:GLN:HG3	2.16	0.45
19:sZ:89:THR:HG22	19:sZ:125:SER:HB2	1.99	0.45
31:sf:62:ILE:H	31:sf:62:ILE:HD12	1.82	0.45
35:sO:211:ILE:HG13	35:sO:225:LEU:HD22	1.99	0.45
41:LC:4:U:H2'	41:LC:5:G:H8	1.82	0.45
59:LU:105:LEU:HD22	59:LU:135:LYS:HG3	1.98	0.45
1:LA:438:A:OP1	72:Lh:118:LYS:NZ	2.45	0.45
1:LA:689:U:O4	45:LG:209:TYR:OH	2.33	0.45
1:LA:1899:G:O2'	1:LA:2334:U:O4	2.30	0.45
1:LA:2389:C:H2'	1:LA:2390:A:C8	2.52	0.45
3:2:751:G:H2'	3:2:752:A:C8	2.52	0.45
4:sP:148:ASP:OD2	4:sP:165:ARG:NH1	2.49	0.45
9:sS:139:VAL:HG13	9:sS:150:PRO:HG3	1.99	0.45
44:LF:166:ILE:HD11	44:LF:171:LEU:HD12	1.99	0.45
45:LG:361:HIS:O	60:LV:28:ARG:NH1	2.48	0.45
52:LN:49:LYS:HB2	52:LN:62:ASN:HA	1.98	0.45
84:sh:117:CYS:SG	84:sh:119:TYR:HB3	2.57	0.45
1:LA:355:A:N1	45:LG:82:THR:HG23	2.31	0.45
1:LA:2211:U:HO2'	40:sn:71:C:HO2'	1.64	0.45
3:2:1490:C:H5'	3:2:1492:A:H1'	1.98	0.45
8:sA:224:ASP:OD1	8:sA:225:TYR:N	2.50	0.45
20:sF:28:LEU:HG	20:sF:64:ASP:HB2	1.99	0.45
45:LG:59:GLN:OE1	77:Lm:55:ARG:NH2	2.49	0.45
75:Lk:102:GLU:HG2	75:Lk:106:LYS:HE3	1.99	0.45
84:sh:89:ARG:HG3	84:sh:90:VAL:N	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:sh:385:SER:HA	84:sh:396:SER:HA	1.98	0.45
1:LA:1083:G:H2'	1:LA:1084:A:C8	2.51	0.45
1:LA:3252:G:H2'	1:LA:3253:G:C8	2.51	0.45
1:LA:3348:G:O6	1:LA:3357:U:O4	2.35	0.45
3:2:190:C:N4	3:2:191:C:O2	2.50	0.45
11:sT:70:PRO:HA	11:sT:98:ARG:HH12	1.82	0.45
20:sF:97:VAL:HG12	20:sF:98:ASP:H	1.80	0.45
26:sb:10:ALA:HB1	26:sb:27:ILE:HD13	1.98	0.45
67:Lc:23:VAL:HG12	67:Lc:45:GLY:HA3	1.99	0.45
75:Lk:78:LYS:HA	75:Lk:81:ARG:HG2	1.98	0.45
82:Lr:23:HIS:HA	82:Lr:73:GLU:O	2.17	0.45
81:Lt:17:LYS:HA	81:Lt:20:ARG:HG2	1.98	0.45
84:sh:684:LYS:HD3	84:sh:703:ALA:HB3	1.98	0.45
1:LA:2160:G:H2'	1:LA:2161:G:C8	2.52	0.45
1:LA:2389:C:H2'	1:LA:2390:A:H8	1.82	0.45
3:2:78:A:H1'	11:sT:175:ILE:HG12	1.97	0.45
3:2:393:C:H2'	3:2:394:C:C6	2.52	0.45
4:sP:80:THR:HA	4:sP:83:GLN:HG3	1.97	0.45
12:sU:49:ILE:HD12	12:sU:172:VAL:HG23	1.98	0.45
17:sD:126:TRP:HD1	17:sD:133:LEU:HD11	1.82	0.45
22:sH:86:LEU:HD22	22:sH:99:HIS:HB2	1.98	0.45
36:sL:21:SER:OG	36:sL:22:ARG:NH1	2.50	0.45
46:LH:150:LEU:HD12	52:LN:143:ARG:HG3	1.99	0.45
74:Lj:95:ILE:HG21	74:Lj:95:ILE:HD13	1.66	0.45
84:sh:90:VAL:HG21	84:sh:133:TRP:CH2	2.52	0.45
84:sh:242:SER:HB3	84:sh:245:LYS:HB2	1.99	0.45
84:sh:738:GLN:O	84:sh:742:ILE:HG13	2.17	0.45
1:LA:209:A:O2'	1:LA:211:A:OP2	2.30	0.45
3:2:1297:G:N2	3:2:1300:A:OP2	2.43	0.45
3:2:1357:A:H2'	3:2:1358:G:C8	2.52	0.45
4:sP:112:THR:HG22	4:sP:114:SER:H	1.82	0.45
17:sD:126:TRP:CD1	17:sD:133:LEU:HD11	2.52	0.45
76:Ll:5:THR:HG23	76:Ll:12:ASN:HB2	1.99	0.45
1:LA:976:U:OP1	58:LT:144:ARG:NH2	2.44	0.44
1:LA:2180:G:H2'	1:LA:2181:C:C6	2.52	0.44
1:LA:2228:A:H2'	1:LA:2229:A:C8	2.51	0.44
1:LA:3309:G:H1'	57:LS:69:ARG:HH11	1.82	0.44
3:2:647:G:N2	3:2:687:G:H22	2.14	0.44
15:sC:70:GLU:HA	15:sC:73:VAL:HG12	1.99	0.44
46:LH:55:PHE:CZ	46:LH:158:ARG:HG3	2.52	0.44
63:LY:38:ALA:HB3	63:LY:59:MET:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:sh:553:PHE:HB3	84:sh:563:LYS:CB	2.44	0.44
1:LA:82:C:H4'	55:LQ:204:LYS:HE2	1.99	0.44
1:LA:1203:A:H2'	1:LA:1204:A:C8	2.53	0.44
3:2:939:A:H2'	3:2:940:A:C8	2.52	0.44
3:2:1563:C:OP1	23:sI:84:LYS:NZ	2.45	0.44
8:sA:74:GLN:NE2	8:sA:81:PRO:HA	2.33	0.44
11:sT:163:THR:OG1	11:sT:165:GLY:O	2.35	0.44
35:sO:299:GLN:HG3	84:sh:576:GLY:CA	2.35	0.44
60:LV:40:ARG:HA	60:LV:40:ARG:HD2	1.78	0.44
66:Lb:74:TYR:HB3	66:Lb:77:LYS:HB2	1.98	0.44
68:Ld:63:LYS:HD3	68:Ld:65:GLN:HE22	1.82	0.44
1:LA:1119:C:H2'	1:LA:1120:A:H8	1.82	0.44
1:LA:3013:U:H2'	1:LA:3014:U:C6	2.52	0.44
7:sR:177:GLY:O	7:sR:195:ASP:HA	2.18	0.44
18:sY:115:LEU:O	18:sY:119:GLU:HG3	2.17	0.44
22:sH:89:GLN:HA	22:sH:97:ASP:HA	1.99	0.44
38:sk:34:THR:HA	38:sk:45:SER:HA	2.00	0.44
42:LD:142:C:OP1	55:LQ:38:ARG:NH1	2.49	0.44
56:LR:8[A]:VAL:HG13	56:LR:34[A]:VAL:HG13	1.99	0.44
57:LS:60:PHE:HB3	57:LS:64:ASN:HB3	1.99	0.44
77:Lm:64:MET:O	77:Lm:68:LYS:HG2	2.16	0.44
1:LA:712:G:OP1	53:LO:174:ARG:NH1	2.51	0.44
1:LA:1666:G:H2'	1:LA:1667:A:H8	1.83	0.44
11:sT:121:LEU:N	11:sT:125:THR:OG1	2.50	0.44
27:sc:70:LYS:HE2	33:sg:11:ALA:HB2	1.99	0.44
35:sO:68:VAL:HA	35:sO:84:SER:HA	1.99	0.44
41:LC:31:U:O3'	46:LH:218:ARG:NH2	2.51	0.44
42:LD:52:A:H62	79:Lo:27:ILE:HD13	1.82	0.44
45:LG:261:VAL:HG23	45:LG:262:TRP:CD1	2.52	0.44
84:sh:499:ASN:HB3	84:sh:515:CYS:SG	2.57	0.44
1:LA:2882:U:H2'	1:LA:2883:U:C6	2.52	0.44
3:2:66:U:H5''	11:sT:173:PRO:HA	1.98	0.44
3:2:78:A:O2'	11:sT:173:PRO:O	2.33	0.44
3:2:142:G:H22	3:2:173:A:H2	1.65	0.44
3:2:1654:G:H4'	81:Lq:24:SER:HB2	1.98	0.44
12:sU:64:VAL:HB	12:sU:94:ALA:HB1	1.99	0.44
22:sH:140:THR:HA	22:sH:143:ARG:HH21	1.81	0.44
34:sN:113:LYS:HA	34:sN:113:LYS:HD3	1.69	0.44
36:sL:64:ARG:HD2	36:sL:64:ARG:HA	1.85	0.44
48:LJ:38:LYS:HE3	48:LJ:38:LYS:HB3	1.85	0.44
51:LM:76:MET:HE1	51:LM:87:LEU:HD12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:La:47:ALA:HB3	65:La:50:ALA:HB2	1.98	0.44
84:sh:75:MET:HE1	84:sh:81:MET:HG2	1.98	0.44
1:LA:1597:C:H2'	1:LA:1598:G:C8	2.52	0.44
1:LA:1666:G:H2'	1:LA:1667:A:C8	2.52	0.44
2:LB:78:LYS:HA	2:LB:78:LYS:HD3	1.86	0.44
3:2:555:A:H2'	3:2:556:A:C8	2.53	0.44
4:sP:51:GLY:O	4:sP:55:GLU:HG3	2.18	0.44
5:sQ:124:ASN:HA	5:sQ:137:ILE:O	2.18	0.44
22:sH:49:LYS:NZ	22:sH:80:LYS:O	2.50	0.44
35:sO:69:GLN:N	35:sO:83:ALA:O	2.47	0.44
35:sO:260:ILE:HD12	35:sO:274:LEU:HD11	2.00	0.44
37:sj:117:GLN:HB3	37:sj:201:ARG:NH2	2.32	0.44
51:LM:54:SER:HB3	51:LM:135:ILE:HD11	1.99	0.44
60:LV:152:LEU:HB2	60:LV:172:TYR:CE2	2.52	0.44
62:LX:36:TYR:O	62:LX:40:HIS:HB2	2.17	0.44
84:sh:642:CYS:HA	84:sh:668:LEU:HB2	1.98	0.44
1:LA:121:A:C2	49:LK:129:PRO:HB3	2.53	0.44
1:LA:1176:C:H2'	1:LA:1177:G:N2	2.32	0.44
1:LA:2482:U:H2'	1:LA:2483:G:C8	2.52	0.44
1:LA:2611:U:H2'	1:LA:2612:U:C6	2.53	0.44
1:LA:2930:A:H2'	1:LA:2931:C:C6	2.52	0.44
1:LA:3356:G:H2'	1:LA:3357:U:C6	2.53	0.44
3:2:1674:C:OP1	11:sT:92:ARG:NH1	2.37	0.44
8:sA:105:MET:HE1	8:sA:119:ALA:HB2	2.00	0.44
23:sI:66:TYR:HD2	23:sI:124:ILE:HD13	1.83	0.44
43:LE:177:LYS:NZ	83:Ls:33:GLN:OE1	2.48	0.44
48:LJ:120:THR:HB	61:LW:132:PRO:HB2	2.00	0.44
56:LR:27[A]:LEU:HD12	56:LR:101[A]:ARG:HB2	1.99	0.44
56:LR:51[A]:LYS:HE2	56:LR:144[A]:SER:HB2	2.00	0.44
60:LV:109:ASP:OD1	60:LV:113:ARG:NH1	2.42	0.44
84:sh:132:CYS:HA	84:sh:140:PRO:HB3	1.99	0.44
84:sh:758:LYS:H	84:sh:758:LYS:HD3	1.83	0.44
2:LB:174:MET:HG3	2:LB:177:ASP:HB2	1.99	0.44
11:sT:49:VAL:HG13	11:sT:114:VAL:HG23	1.99	0.44
12:sU:14:THR:N	12:sU:17:GLU:OE2	2.51	0.44
12:sU:38:LEU:HB2	12:sU:41:LEU:HD22	1.98	0.44
37:sj:200:TRP:CZ3	84:sh:213:PRO:HG2	2.53	0.44
42:LD:9:A:H2'	42:LD:10:A:C8	2.53	0.44
84:sh:181:ILE:HD13	84:sh:201:LYS:HA	2.00	0.44
84:sh:308:SER:HB3	84:sh:309:PRO:HD2	1.99	0.44
1:LA:75:G:H5''	53:LO:58:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:662:U:H2'	1:LA:663:C:C6	2.53	0.44
3:2:1435:G:O6	15:sC:64:TYR:OH	2.25	0.44
10:sB:133:VAL:HG22	10:sB:198:LEU:HD13	1.99	0.44
84:sh:575:CYS:SG	84:sh:577:ILE:CB	3.06	0.44
1:LA:656:A:H2'	1:LA:657:A:C8	2.53	0.43
1:LA:1253:U:N3	1:LA:1264:G:OP1	2.51	0.43
1:LA:1306:G:C6	56:LR:62[A]:THR:HA	2.53	0.43
1:LA:2282:U:OP1	1:LA:2973:G:O2'	2.36	0.43
21:sG:35:CYS:HA	21:sG:38:ILE:HG22	2.00	0.43
51:LM:19:LYS:HA	51:LM:23:ASN:HD22	1.83	0.43
1:LA:1565:G:H22	1:LA:1574:C:N4	2.14	0.43
1:LA:3068:U:OP2	59:LU:62:ARG:NH2	2.40	0.43
2:LB:48:ARG:HH12	2:LB:159:LEU:HA	1.83	0.43
2:LB:54:LYS:HG2	2:LB:190:PHE:HE1	1.84	0.43
3:2:1429:G:H2'	3:2:1430:U:C6	2.52	0.43
8:sA:212:LYS:HB3	8:sA:212:LYS:HE3	1.83	0.43
11:sT:211:LEU:HD11	11:sT:215:ARG:HH21	1.84	0.43
19:sZ:26:THR:HG21	19:sZ:60:ALA:HB2	1.99	0.43
20:sF:5:PRO:HG2	20:sF:24:ALA:HB2	2.00	0.43
20:sF:48:VAL:HG13	20:sF:78:VAL:HG13	2.00	0.43
35:sO:210:LEU:HD13	35:sO:231:MET:HE1	2.01	0.43
35:sO:302:PHE:HD1	35:sO:312:VAL:HG12	1.83	0.43
37:sj:233:LYS:HA	37:sj:233:LYS:HD3	1.75	0.43
53:LO:57:VAL:HG23	53:LO:147:ILE:HG23	2.00	0.43
70:Lf:20:SER:OG	70:Lf:96:GLY:O	2.35	0.43
84:sh:818:LYS:HA	84:sh:818:LYS:HD3	1.74	0.43
1:LA:792:G:H2'	1:LA:793:C:C6	2.53	0.43
1:LA:985:U:H2'	1:LA:986:U:H6	1.83	0.43
1:LA:1119:C:H2'	1:LA:1120:A:C8	2.53	0.43
1:LA:1134:G:O2'	1:LA:2642:A:N3	2.42	0.43
1:LA:1798:A:H2'	1:LA:1799:A:C8	2.53	0.43
1:LA:2218:G:H2'	1:LA:2219:A:H8	1.83	0.43
1:LA:2525:G:O2'	1:LA:2526:C:OP2	2.36	0.43
3:2:885:G:H2'	3:2:886:U:C6	2.53	0.43
3:2:1690:G:H2'	3:2:1691:A:H8	1.83	0.43
7:sR:98:PHE:O	7:sR:117:THR:HA	2.19	0.43
12:sU:38:LEU:HA	12:sU:41:LEU:HD13	2.00	0.43
12:sU:80:GLU:HA	12:sU:83:LYS:HG2	1.99	0.43
18:sY:142:GLU:O	18:sY:146:ALA:HB2	2.18	0.43
34:sN:103:LEU:HB3	34:sN:104:SER:H	1.72	0.43
37:sj:105:ARG:HH12	37:sj:109:ALA:HB2	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:sk:65:GLY:HA3	38:sk:83:ILE:HD13	2.00	0.43
41:LC:112:G:H2'	41:LC:113:C:C6	2.54	0.43
45:LG:166:VAL:O	45:LG:170:LYS:HG2	2.18	0.43
67:Lc:24:VAL:HG21	67:Lc:87:LEU:HB3	2.00	0.43
84:sh:824:ARG:HA	84:sh:827:GLN:HB2	2.01	0.43
1:LA:2683:U:H2'	1:LA:2684:C:C6	2.54	0.43
1:LA:3121:U:H1'	1:LA:3122:A:H5''	1.99	0.43
3:2:17:C:H2'	3:2:18:C:C6	2.53	0.43
3:2:1565:C:O2'	22:sH:85:PHE:O	2.26	0.43
6:sE:53:PRO:O	6:sE:57:MET:HG2	2.18	0.43
45:LG:181:VAL:HG11	45:LG:224:GLY:HA3	2.00	0.43
66:Lb:87:LYS:HB2	66:Lb:97:ILE:HD11	1.99	0.43
67:Lc:25:ILE:HG23	67:Lc:41:ALA:HB1	2.00	0.43
1:LA:170:G:H2'	1:LA:171:G:C8	2.53	0.43
1:LA:314:U:H2'	1:LA:315:C:C6	2.53	0.43
1:LA:1534:A:H2'	1:LA:1535:A:C8	2.53	0.43
1:LA:2878:G:H5''	44:LF:5:LYS:HE2	2.00	0.43
3:2:159:U:O2'	11:sT:87:ARG:NH1	2.52	0.43
3:2:601:A:OP2	27:sc:110:LYS:HD2	2.18	0.43
3:2:803:A:O2'	12:sU:104:ARG:NH2	2.52	0.43
3:2:1564:U:H2'	3:2:1565:C:C6	2.53	0.43
17:sD:73:LYS:NZ	34:sN:109:ASP:H	2.17	0.43
38:sk:13:ARG:HH21	38:sk:17:GLY:H	1.66	0.43
42:LD:26:U:H2'	42:LD:27:U:C6	2.54	0.43
3:2:337:G:H3'	16:sX:133:LYS:HB2	2.00	0.43
3:2:407:A:H2'	3:2:408:C:C6	2.53	0.43
5:sQ:157:GLN:O	5:sQ:159:SER:N	2.47	0.43
7:sR:140:ARG:HE	25:sa:10:GLU:CD	2.25	0.43
9:sS:72:VAL:HG12	9:sS:77:ARG:HG3	2.00	0.43
10:sB:192:GLU:OE1	29:sK:63:SER:OG	2.30	0.43
35:sO:14:GLU:HG2	35:sO:309:VAL:HG12	1.99	0.43
37:sj:212:GLU:HB2	37:sj:215:ILE:HG22	2.01	0.43
60:LV:93:GLU:HG3	60:LV:140:VAL:HG11	1.99	0.43
84:sh:207:GLN:HB3	84:sh:224:LYS:HD3	1.99	0.43
1:LA:2103:U:H2'	1:LA:2104:A:C8	2.53	0.43
1:LA:2426:U:H2'	1:LA:2427:U:C6	2.53	0.43
1:LA:2745:G:N2	1:LA:2748:A:OP2	2.49	0.43
3:2:1370:U:O2'	3:2:1372:U:OP1	2.30	0.43
3:2:1686:C:H2'	3:2:1687:U:C5	2.53	0.43
10:sB:57:SER:OG	10:sB:167:ARG:NH2	2.52	0.43
18:sY:91:LEU:HD12	18:sY:125:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:LO:141:ALA:HA	53:LO:144:THR:HG22	2.00	0.43
84:sh:75:MET:HE3	84:sh:75:MET:HB2	1.92	0.43
84:sh:360:LEU:HD13	84:sh:360:LEU:HA	1.89	0.43
1:LA:2427:U:H2'	1:LA:2428:U:C6	2.54	0.43
13:sV:171:SER:HB3	13:sV:180:ASP:H	1.84	0.43
14:sW:92:LYS:HE2	14:sW:92:LYS:HB3	1.85	0.43
63:LY:18:PRO:HA	63:LY:51:ALA:HA	2.00	0.43
84:sh:214:LEU:HD13	84:sh:233:CYS:HA	1.99	0.43
84:sh:813:LEU:H	84:sh:813:LEU:HG	1.56	0.43
1:LA:807:A:H61	1:LA:934:G:H22	1.67	0.43
1:LA:2115:G:H22	1:LA:2120:A:H1'	1.83	0.43
1:LA:2160:G:H2'	1:LA:2161:G:H8	1.84	0.43
17:sD:48:SER:O	17:sD:52:LEU:HB2	2.18	0.43
57:LS:126:ARG:NH1	57:LS:140:GLU:OE2	2.52	0.43
84:sh:175:CYS:SG	84:sh:176:THR:N	2.92	0.43
1:LA:966:U:H2'	1:LA:967:A:C8	2.54	0.43
1:LA:1675:G:H2'	1:LA:1676:A:H8	1.83	0.43
1:LA:2679:A:O2'	52:LN:52:TYR:OH	2.32	0.43
1:LA:2828:G:OP2	51:LM:7:ARG:NH2	2.51	0.43
3:2:758:U:OP1	9:sS:22:LYS:NZ	2.52	0.43
3:2:1499:G:OP1	23:sI:122:ARG:NH1	2.49	0.43
10:sB:58:LEU:HD12	10:sB:138:THR:HA	2.00	0.43
14:sW:112:GLN:HG3	14:sW:148:VAL:HG21	2.00	0.43
17:sD:36:LEU:HB3	17:sD:41:LEU:HD13	2.01	0.43
22:sH:45:LEU:HD11	23:sI:36:ILE:HD13	2.01	0.43
40:sl:1:G:H2'	40:sl:2:G:C8	2.54	0.43
1:LA:339:C:OP1	1:LA:1380:G:O2'	2.35	0.42
1:LA:683:U:OP1	55:LQ:204:LYS:NZ	2.52	0.42
23:sI:101:ASN:HA	23:sI:104:VAL:HG12	2.00	0.42
24:sJ:101:LYS:HA	24:sJ:104:THR:HG22	2.00	0.42
74:Lj:58:ARG:HB2	74:Lj:61:GLN:HG3	2.01	0.42
1:LA:283:G:OP2	1:LA:285:A:H4'	2.19	0.42
1:LA:371:G:N1	1:LA:374:A:OP2	2.48	0.42
1:LA:831:G:O2'	1:LA:1864:A:N3	2.45	0.42
1:LA:1659:U:H2'	1:LA:1660:C:C6	2.54	0.42
2:LB:89:ASP:O	2:LB:92:LYS:NZ	2.51	0.42
3:2:424:C:O2'	3:2:426:G:OP1	2.33	0.42
3:2:830:U:H2'	3:2:831:U:C6	2.54	0.42
3:2:852:C:H2'	3:2:853:G:C8	2.54	0.42
7:sR:111:VAL:O	7:sR:136:VAL:HA	2.19	0.42
9:sS:15:PRO:HG2	9:sS:18:TRP:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:sC:14:TYR:CZ	15:sC:18:GLU:HG3	2.54	0.42
21:sG:54:THR:O	21:sG:58:MET:HG2	2.19	0.42
38:sk:57:ILE:HG12	38:sk:70:ILE:HB	2.01	0.42
45:LG:22:LEU:HA	45:LG:23:PRO:HD3	1.85	0.42
45:LG:39:PHE:HA	45:LG:42:VAL:HG12	1.99	0.42
54:LP:12:TRP:HB2	60:LV:172:TYR:O	2.19	0.42
58:LT:80:THR:HG23	58:LT:100:THR:HG23	2.01	0.42
63:LY:74:MET:HE2	63:LY:74:MET:HB3	1.95	0.42
84:sh:214:LEU:HB3	84:sh:233:CYS:HB2	2.01	0.42
84:sh:242:SER:HB3	84:sh:245:LYS:HD2	2.02	0.42
1:LA:643:U:O2'	1:LA:1153:A:N1	2.49	0.42
1:LA:947:G:H5''	72:Lh:55:ILE:HB	2.01	0.42
1:LA:2205:U:H2'	1:LA:2206:G:C8	2.54	0.42
1:LA:2662:G:H2'	1:LA:2663:G:C8	2.53	0.42
3:2:520:A:H2'	3:2:521:A:C8	2.54	0.42
4:sP:163:ASN:O	4:sP:169:SER:OG	2.25	0.42
13:sV:34:ALA:HB2	13:sV:56:ARG:HD2	1.99	0.42
22:sH:118:LYS:HB2	22:sH:118:LYS:HE2	1.74	0.42
42:LD:26:U:O2'	45:LG:51:ALA:O	2.37	0.42
1:LA:1471:U:H5''	59:LU:5:ARG:HG3	2.01	0.42
1:LA:1615:C:H2'	1:LA:1616:U:C6	2.54	0.42
1:LA:2218:G:H2'	1:LA:2219:A:C8	2.54	0.42
3:2:1041:G:H2'	3:2:1042:G:C8	2.54	0.42
11:sT:52:ILE:HA	11:sT:111:LEU:HD23	2.01	0.42
24:sJ:53:LYS:HB2	24:sJ:92:ASP:HB2	2.01	0.42
41:LC:4:U:H2'	41:LC:5:G:C8	2.54	0.42
72:Lh:32:TRP:CZ2	72:Lh:53:PRO:HD2	2.55	0.42
72:Lh:96:ILE:HG21	72:Lh:105:ARG:HG2	2.01	0.42
84:sh:219:HIS:CE1	84:sh:235:GLU:CB	2.92	0.42
1:LA:785:G:N7	68:Ld:77:LYS:NZ	2.59	0.42
1:LA:1016:C:N4	1:LA:2672:G:OP2	2.53	0.42
1:LA:2277:C:OP1	81:Lq:23:ARG:HD2	2.19	0.42
8:sA:23:GLU:OE2	8:sA:27:ARG:NE	2.52	0.42
14:sW:115:LYS:HD3	14:sW:115:LYS:HA	1.82	0.42
21:sG:76:GLU:HA	21:sG:79:GLU:HG2	2.01	0.42
23:sI:27:LYS:HE2	23:sI:111:ILE:HG22	2.01	0.42
37:sj:169:LEU:HB2	37:sj:185:ILE:HG23	2.01	0.42
50:LL:22:SER:OG	50:LL:23:ARG:N	2.52	0.42
74:Lj:59:PRO:HA	74:Lj:62:TYR:HD2	1.85	0.42
84:sh:250:TYR:CD2	84:sh:286:ALA:HB2	2.53	0.42
84:sh:317:ALA:HB1	84:sh:324:SER:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:1838:G:H5''	1:LA:1839:A:H5'	2.02	0.42
1:LA:2546:C:O3'	5:sQ:222:LYS:NZ	2.37	0.42
3:2:393:C:N4	3:2:401:A:OP2	2.53	0.42
3:2:778:G:OP2	3:2:780:A:N6	2.53	0.42
3:2:1171:A:H2'	3:2:1172:G:H8	1.80	0.42
3:2:1358:G:O2'	23:sI:133:ASP:OD2	2.29	0.42
3:2:1734:U:H5''	63:LY:32:ARG:HD3	2.02	0.42
15:sC:3:MET:HE1	15:sC:45:ALA:HB2	2.02	0.42
15:sC:55:VAL:HA	15:sC:68:LEU:HA	2.02	0.42
16:sX:78:THR:HA	16:sX:84:ILE:HG22	2.01	0.42
34:sN:148:TYR:H	34:sN:149:LYS:NZ	2.18	0.42
65:La:62:VAL:HG21	65:La:98:ALA:HB2	2.02	0.42
83:Ls:79:VAL:HA	83:Ls:82:THR:HG22	2.02	0.42
1:LA:1597:C:H2'	1:LA:1598:G:H8	1.83	0.42
1:LA:2506:U:H2'	1:LA:2507:C:H6	1.85	0.42
2:LB:83:ASP:HB3	2:LB:145:TYR:CD2	2.54	0.42
3:2:592:A:O2'	3:2:596:C:OP1	2.38	0.42
3:2:1127:G:OP1	81:Lq:11:ARG:NH2	2.53	0.42
3:2:1213:G:OP1	34:sN:87:THR:OG1	2.29	0.42
3:2:1273:G:H4'	3:2:1274:C:H3'	2.01	0.42
9:sS:151:ASP:HB3	9:sS:154:ILE:HG13	2.01	0.42
20:sF:10:PHE:HA	20:sF:18:ALA:O	2.20	0.42
20:sF:107:LYS:HB3	20:sF:107:LYS:HE2	1.73	0.42
35:sO:270:LEU:HD21	35:sO:273:ASP:HB2	2.01	0.42
35:sO:300:THR:HG22	35:sO:314:GLN:HE21	1.85	0.42
37:sj:224:ILE:O	37:sj:228:ARG:HG2	2.20	0.42
48:LJ:178:ILE:HG23	48:LJ:183:ASP:HB3	2.02	0.42
58:LT:22:ASP:HA	58:LT:27:LYS:HE3	2.02	0.42
84:sh:252:GLY:HA3	84:sh:281:TRP:HZ2	1.84	0.42
84:sh:329:PRO:HG3	84:sh:349:ILE:HD12	2.01	0.42
1:LA:294:U:OP2	55:LQ:15:GLN:NE2	2.51	0.42
1:LA:616:G:H2'	1:LA:617:G:C8	2.55	0.42
1:LA:3294:A:H2'	1:LA:3295:A:O4'	2.20	0.42
2:LB:158:GLN:NE2	2:LB:161:LYS:O	2.53	0.42
3:2:1459:C:OP1	22:sH:126:ARG:NH2	2.53	0.42
11:sT:64:LYS:HB2	11:sT:97:VAL:HG21	2.02	0.42
35:sO:177:MET:SD	35:sO:193:ILE:HG13	2.60	0.42
70:Lf:99:ASP:OD1	70:Lf:99:ASP:N	2.52	0.42
78:Ln:7:ASP:HB3	78:Ln:10:GLN:HB3	2.02	0.42
1:LA:1090:G:H2'	1:LA:1091:A:C8	2.54	0.42
3:2:188:A:H62	3:2:197:A:H8	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:622:A:O2'	3:2:1032:G:H5'	2.19	0.42
3:2:700:C:H2'	3:2:701:U:C6	2.55	0.42
11:sT:67:VAL:HG12	11:sT:69:LEU:HG	2.02	0.42
13:sV:110:ARG:O	13:sV:114:GLU:HG2	2.20	0.42
34:sN:106:TYR:HD2	34:sN:116:LYS:HG2	1.85	0.42
42:LD:40:A:H2'	42:LD:41:A:C8	2.55	0.42
47:LI:14:ASP:N	47:LI:14:ASP:OD1	2.44	0.42
50:LL:21:LYS:HG3	54:LP:8:LYS:HG3	2.01	0.42
55:LQ:73:ARG:HA	55:LQ:74:PRO:HD3	1.90	0.42
1:LA:449:U:O2'	1:LA:450:G:N2	2.53	0.42
1:LA:1915:A:H2'	1:LA:1916:U:C6	2.55	0.42
2:LB:41:TYR:CD1	2:LB:161:LYS:HE2	2.55	0.42
2:LB:89:ASP:OD2	2:LB:91:LYS:NZ	2.52	0.42
3:2:260:U:O2	13:sV:41:LYS:NZ	2.41	0.42
7:sR:207:LEU:HA	7:sR:210:THR:HG22	2.02	0.42
15:sC:44:LYS:HA	15:sC:44:LYS:HD3	1.71	0.42
25:sa:32:VAL:HG22	25:sa:60:ARG:HD2	2.02	0.42
35:sO:28:GLY:HA2	84:sh:570:GLN:CG	2.49	0.42
40:sl:29:C:H2'	40:sl:30:C:O4'	2.19	0.42
49:LK:50:VAL:HG21	65:La:27:ARG:HD3	2.01	0.42
82:Lr:25:VAL:HG22	82:Lr:72:LEU:HD22	2.02	0.42
1:LA:1183:C:OP1	60:LV:158:LYS:NZ	2.53	0.41
1:LA:1605:A:O2'	1:LA:1607:U:OP2	2.32	0.41
1:LA:1667:A:H2'	1:LA:1668:G:C8	2.55	0.41
1:LA:2344:U:H2'	1:LA:2345:A:C8	2.55	0.41
3:2:931:C:H5''	5:sQ:116:LYS:HG2	2.01	0.41
3:2:968:U:H2'	3:2:969:C:O4'	2.20	0.41
22:sH:26:ILE:HG13	22:sH:31:ALA:HB2	2.01	0.41
28:sd:89:TYR:OH	28:sd:90:ARG:NH2	2.53	0.41
35:sO:17:ASN:HA	35:sO:308:ASN:ND2	2.35	0.41
37:sj:139:TYR:N	37:sj:153:LYS:HD2	2.35	0.41
59:LU:24:LEU:HD23	59:LU:32:ILE:HG21	2.01	0.41
62:LX:89:LEU:HB3	62:LX:93:ILE:HD12	2.02	0.41
68:Ld:63:LYS:HD3	68:Ld:65:GLN:NE2	2.35	0.41
84:sh:113:LYS:HA	84:sh:120:VAL:HA	2.02	0.41
84:sh:700:GLU:O	84:sh:704:LEU:HB2	2.19	0.41
1:LA:1261:G:H4'	1:LA:1278:A:N1	2.35	0.41
1:LA:2152:A:H2'	1:LA:2153:U:H6	1.84	0.41
3:2:156:A:H2'	3:2:157:A:O4'	2.20	0.41
3:2:419:G:H5'	11:sT:72:ARG:HH21	1.83	0.41
3:2:736:C:H2'	3:2:737:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:sD:60:VAL:HG23	17:sD:122:VAL:HG22	2.01	0.41
18:sY:6:SER:OG	18:sY:7:ALA:N	2.54	0.41
31:sf:36:LYS:HG3	31:sf:43:ILE:HD13	2.02	0.41
43:LE:179:LEU:HD23	43:LE:179:LEU:HA	1.91	0.41
84:sh:247:ILE:HB	84:sh:256:ARG:O	2.19	0.41
84:sh:249:CYS:HA	84:sh:285:PHE:O	2.20	0.41
84:sh:276:GLU:H	84:sh:276:GLU:HG3	1.60	0.41
1:LA:716:A:OP1	1:LA:752:C:O2'	2.39	0.41
1:LA:993:G:N3	1:LA:2637:A:H2'	2.35	0.41
1:LA:1257:C:C4	1:LA:1261:G:N2	2.83	0.41
1:LA:1917:C:OP1	59:LU:85:ARG:NH2	2.52	0.41
3:2:57:G:OP1	28:sd:112:LYS:NZ	2.42	0.41
3:2:1584:G:O2'	3:2:1585:U:OP2	2.38	0.41
17:sD:58:LEU:HD21	17:sD:125:ASN:H	1.85	0.41
40:sl:23:C:H2'	40:sl:24:G:C8	2.54	0.41
44:LF:218:ILE:HG12	44:LF:276:THR:HG23	2.01	0.41
50:LL:90:MET:HE2	50:LL:179:ILE:HG22	2.02	0.41
53:LO:10:LEU:HD23	58:LT:166:LEU:HD11	2.02	0.41
57:LS:111:LYS:HB3	57:LS:153:LYS:HB3	2.02	0.41
71:Lg:60:TRP:CZ3	71:Lg:64:VAL:HG22	2.54	0.41
84:sh:550:GLU:HB2	84:sh:568:CYS:SG	2.60	0.41
1:LA:1110:U:H2'	1:LA:1111:U:C6	2.55	0.41
1:LA:1194:G:H2'	1:LA:1195:A:C8	2.56	0.41
1:LA:1725:C:H5''	83:Ls:36:ARG:HH12	1.84	0.41
1:LA:1895:A:O2'	1:LA:3053:G:H4'	2.21	0.41
1:LA:1913:A:N3	1:LA:2120:A:H2'	2.35	0.41
3:2:434:G:H5'	27:sc:78:LYS:HB3	2.03	0.41
3:2:1344:A:H2'	3:2:1345:A:C8	2.55	0.41
21:sG:93:LEU:HA	21:sG:93:LEU:HD23	1.84	0.41
35:sO:36:ALA:HB1	35:sO:68:VAL:HG13	2.03	0.41
35:sO:156:VAL:HG12	35:sO:169:ILE:HG22	2.03	0.41
60:LV:71:LYS:HE3	60:LV:73:LYS:HD2	2.03	0.41
84:sh:163:CYS:SG	84:sh:172:HIS:HB3	2.60	0.41
84:sh:747:MET:HE2	84:sh:801:ASN:HA	2.01	0.41
2:LB:205:VAL:HG13	2:LB:213:ALA:HA	2.02	0.41
3:2:478:A:O2'	14:sW:124:HIS:ND1	2.49	0.41
7:sR:215:PHE:HA	7:sR:218:ILE:HG12	2.02	0.41
14:sW:110:GLN:NE2	14:sW:126:ARG:HB2	2.36	0.41
40:sl:68:C:H2'	40:sl:69:G:C8	2.56	0.41
47:LI:132:THR:O	47:LI:136:GLU:HG2	2.20	0.41
55:LQ:159:ARG:HB3	55:LQ:164:LEU:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:LS:153:LYS:HE2	57:LS:153:LYS:HB2	1.89	0.41
58:LT:122:ILE:HG23	58:LT:126:GLN:HB2	2.01	0.41
63:LY:109:MET:SD	63:LY:132:ASN:ND2	2.82	0.41
71:Lg:20:LEU:HD11	71:Lg:32:ALA:HB2	2.03	0.41
84:sh:81:MET:SD	84:sh:148:ASN:HB2	2.60	0.41
84:sh:332:ARG:HD2	84:sh:354:SER:HB3	2.01	0.41
1:LA:630:A:H2'	1:LA:631:U:C6	2.55	0.41
1:LA:1280:C:H2'	1:LA:1281:G:H8	1.84	0.41
1:LA:2433:U:H1'	55:LQ:125:SER:HB3	2.03	0.41
3:2:1562:G:OP1	23:sI:89:ARG:NH2	2.54	0.41
8:sA:116:ARG:HH22	39:sm:25:A:H2	1.67	0.41
9:sS:192:ILE:HD13	9:sS:238:LEU:HD13	2.03	0.41
10:sB:92:ARG:NH2	10:sB:169:ASN:OD1	2.54	0.41
13:sV:159:GLN:HB3	13:sV:165:LEU:HD23	2.03	0.41
17:sD:32:LEU:HD22	17:sD:41:LEU:HD21	2.02	0.41
31:sf:55:THR:HG22	31:sf:62:ILE:HG13	2.02	0.41
37:sj:157:ASN:HB2	37:sj:168:LYS:HB2	2.02	0.41
45:LG:276:LEU:HD23	45:LG:276:LEU:HA	1.94	0.41
47:LI:170:LYS:HB3	47:LI:172:HIS:CE1	2.56	0.41
1:LA:1156:C:OP2	48:LJ:94:LYS:NZ	2.51	0.41
1:LA:1264:G:N2	1:LA:1265:U:O4	2.53	0.41
1:LA:1274:A:H2'	1:LA:1275:C:C6	2.56	0.41
1:LA:1277:C:O2'	1:LA:1278:A:O5'	2.37	0.41
1:LA:2723:U:H2'	1:LA:2724:U:C6	2.55	0.41
1:LA:2953:U:H2'	1:LA:2954:U:H2'	2.00	0.41
2:LB:26:ARG:HH22	2:LB:212:PRO:HG3	1.85	0.41
3:2:224:C:H2'	3:2:225:A:C8	2.56	0.41
3:2:1017:U:H2'	3:2:1018:U:C6	2.56	0.41
3:2:1641:C:H2'	3:2:1642:G:C8	2.55	0.41
8:sA:70:THR:HG22	8:sA:86:LEU:HD13	2.03	0.41
14:sW:70:LEU:O	14:sW:74:ASN:ND2	2.34	0.41
19:sZ:81:VAL:HG11	19:sZ:102:LEU:HD13	2.03	0.41
19:sZ:114:ARG:HD3	19:sZ:114:ARG:HA	1.90	0.41
47:LI:132:THR:HA	47:LI:135:VAL:HG12	2.03	0.41
61:LW:100:LYS:O	61:LW:103:GLN:HG3	2.21	0.41
65:La:82:LEU:HD11	65:La:135:ILE:HD11	2.01	0.41
84:sh:296:SER:HA	84:sh:314:GLY:O	2.21	0.41
1:LA:1274:A:H2'	1:LA:1275:C:H6	1.85	0.41
1:LA:2236:G:HO2'	40:sn:70:U:HO2'	1.68	0.41
1:LA:2697:A:H2'	1:LA:2698:G:H8	1.86	0.41
3:2:116:U:H2'	3:2:117:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:209:U:H2'	3:2:210:A:C8	2.55	0.41
3:2:1715:G:H2'	3:2:1716:C:C6	2.55	0.41
30:se:32:LYS:O	30:se:37:LYS:NZ	2.45	0.41
35:sO:278:PHE:CE1	35:sO:287:PRO:HG2	2.55	0.41
82:Lr:70:LEU:HD12	82:Lr:83:LEU:HD11	2.03	0.41
1:LA:845:G:N2	1:LA:847:A:O5'	2.53	0.41
1:LA:847:A:H2'	1:LA:848:A:H8	1.81	0.41
1:LA:974:G:H5'	58:LT:16:ARG:HB2	2.02	0.41
1:LA:1565:G:H2'	1:LA:1566:A:C8	2.55	0.41
1:LA:1759:C:H2'	1:LA:1760:A:O4'	2.21	0.41
1:LA:1877:U:H5''	1:LA:1878:G:O4'	2.21	0.41
1:LA:1949:G:OP2	59:LU:135:LYS:NZ	2.47	0.41
1:LA:2354:C:OP1	57:LS:86:LYS:NZ	2.48	0.41
4:sP:87:LEU:HD23	4:sP:87:LEU:HA	1.92	0.41
15:sC:31:LYS:HD3	15:sC:31:LYS:HA	1.89	0.41
35:sO:192:PHE:HB3	35:sO:223:TRP:CZ3	2.55	0.41
42:LD:8:C:H2'	42:LD:9:A:C8	2.56	0.41
48:LJ:34:LYS:O	48:LJ:38:LYS:HG3	2.20	0.41
67:Lc:9:LYS:HD2	67:Lc:83:THR:O	2.21	0.41
69:Le:25:LYS:HE2	69:Le:25:LYS:HB2	1.92	0.41
73:Li:49:ILE:HD13	73:Li:49:ILE:HG21	1.89	0.41
84:sh:221:CYS:HB2	84:sh:230:CYS:HB3	2.02	0.41
84:sh:295:TYR:HB2	84:sh:297:CYS:SG	2.61	0.41
84:sh:330:CYS:CB	84:sh:356:CYS:HA	2.51	0.41
84:sh:520:ILE:HG12	84:sh:524:ARG:HE	1.85	0.41
1:LA:358:G:N2	1:LA:361:A:OP2	2.48	0.41
1:LA:1562:C:H2'	1:LA:1563:C:C6	2.56	0.41
3:2:472:U:O2'	3:2:769:A:N3	2.43	0.41
4:sP:24:LEU:O	4:sP:163:ASN:ND2	2.54	0.41
8:sA:198:GLY:O	8:sA:200:LYS:NZ	2.52	0.41
10:sB:111:VAL:HG23	20:sF:43:ILE:HG12	2.04	0.41
13:sV:21:PHE:CD2	13:sV:22:ARG:HB2	2.56	0.41
16:sX:123:VAL:HG12	16:sX:142:VAL:HG22	2.02	0.41
35:sO:154:VAL:O	35:sO:155:ARG:NH1	2.54	0.41
35:sO:248:ASN:OD1	35:sO:248:ASN:N	2.54	0.41
45:LG:33:ASP:OD1	45:LG:34:ILE:N	2.54	0.41
47:LI:76:LEU:N	47:LI:138:GLN:OE1	2.54	0.41
55:LQ:68:ARG:HA	55:LQ:98:LEU:HD21	2.02	0.41
59:LU:149:ALA:O	59:LU:152:GLU:HG3	2.21	0.41
1:LA:796:U:H2'	1:LA:797:U:C6	2.55	0.40
1:LA:849:C:O2'	1:LA:850:U:O5'	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LA:1805:C:H2'	1:LA:1806:A:C8	2.55	0.40
1:LA:3218:A:H5''	1:LA:3219:G:C5	2.55	0.40
3:2:1160:A:H2'	3:2:1161:C:C6	2.56	0.40
3:2:1501:C:OP2	23:sI:102:ARG:NH1	2.54	0.40
5:sQ:5:LYS:HE2	5:sQ:5:LYS:HB3	1.81	0.40
23:sI:117:SER:HB2	23:sI:123:ARG:HG2	2.02	0.40
25:sa:15:ARG:NH1	25:sa:33:GLN:OE1	2.52	0.40
27:sc:69:ARG:HD3	27:sc:69:ARG:HA	1.76	0.40
29:sK:45:GLU:O	29:sK:49:ARG:HB2	2.21	0.40
37:sj:231:PHE:CE2	84:sh:266:PHE:CE1	3.08	0.40
42:LD:103:G:OP2	42:LD:105:A:O2'	2.31	0.40
46:LH:182:GLY:HA2	46:LH:194:LEU:HD23	2.02	0.40
54:LP:93:LYS:HB2	54:LP:93:LYS:HE3	1.82	0.40
60:LV:90:MET:HE1	60:LV:114:HIS:CE1	2.57	0.40
62:LX:35:LYS:HA	62:LX:35:LYS:HD2	1.91	0.40
84:sh:178:MET:HA	84:sh:193:PHE:HA	2.03	0.40
84:sh:553:PHE:HA	84:sh:564:VAL:O	2.21	0.40
84:sh:684:LYS:HZ3	84:sh:700:GLU:HA	1.87	0.40
3:2:513:U:H2'	3:2:514:G:C8	2.56	0.40
3:2:891:A:H2'	3:2:892:A:C8	2.56	0.40
3:2:1709:C:H2'	3:2:1710:U:C6	2.56	0.40
34:sN:143:LYS:HD3	34:sN:143:LYS:HA	1.93	0.40
42:LD:87:G:OP2	75:Lk:5:LYS:NZ	2.54	0.40
42:LD:142:C:H2'	42:LD:143:U:C6	2.56	0.40
45:LG:58:HIS:HA	45:LG:90:PHE:HE1	1.86	0.40
56:LR:23[A]:VAL:O	56:LR:27[A]:LEU:HD23	2.21	0.40
63:LY:104:ASN:OD1	63:LY:108:GLU:N	2.54	0.40
83:Ls:83:ILE:HD13	83:Ls:83:ILE:HA	1.92	0.40
84:sh:134:CYS:SG	84:sh:136:LYS:HB2	2.60	0.40
84:sh:351:THR:HB	84:sh:371:CYS:O	2.21	0.40
1:LA:848:A:N6	1:LA:849:C:H1'	2.36	0.40
1:LA:945:C:H2'	1:LA:946:U:C6	2.56	0.40
1:LA:2419:A:H2'	1:LA:2420:C:C6	2.57	0.40
1:LA:3096:C:H2'	1:LA:3097:C:C6	2.56	0.40
1:LA:3291:G:H2'	1:LA:3292:A:H8	1.85	0.40
3:2:15:U:H2'	3:2:16:G:O4'	2.21	0.40
3:2:195:G:N7	13:sV:137:LYS:NZ	2.68	0.40
3:2:522:U:H5''	28:sd:37:LYS:HG3	2.03	0.40
11:sT:116:LYS:HE2	11:sT:116:LYS:HB3	1.89	0.40
26:sb:89:TRP:O	26:sb:93:LEU:HD23	2.20	0.40
27:sc:92:CYS:HA	27:sc:95:PHE:HD2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LC:89:G:H4'	60:LV:84:ARG:HD3	2.04	0.40
45:LG:23:PRO:HD2	45:LG:26:PHE:CE2	2.56	0.40
58:LT:161:LYS:HA	58:LT:161:LYS:HD3	1.81	0.40
61:LW:115:LYS:HB2	61:LW:115:LYS:HE3	1.72	0.40
64:LZ:4:GLU:HB2	64:LZ:13:ILE:HB	2.02	0.40
64:LZ:17:ARG:HA	64:LZ:17:ARG:HD3	1.82	0.40
69:Le:55:ALA:O	69:Le:59:LYS:HB3	2.21	0.40
84:sh:221:CYS:SG	84:sh:230:CYS:HB3	2.62	0.40
1:LA:675:C:O2'	1:LA:679:U:OP1	2.35	0.40
1:LA:2677:G:H22	1:LA:2680:A:H2	1.69	0.40
1:LA:3192:U:H2'	1:LA:3193:C:C6	2.56	0.40
1:LA:3203:U:H2'	1:LA:3204:C:C6	2.57	0.40
2:LB:115:VAL:HB	2:LB:118:LYS:HE3	2.04	0.40
3:2:140:A:OP2	3:2:140:A:H4'	2.21	0.40
3:2:834:G:H2'	3:2:835:U:C6	2.55	0.40
3:2:968:U:OP1	3:2:1033:C:O2'	2.36	0.40
5:sQ:219:LYS:NZ	83:Ls:90:VAL:O	2.46	0.40
8:sA:11:LEU:HD12	24:sJ:86:ILE:HG12	2.03	0.40
15:sC:59:PHE:CZ	15:sC:62:GLN:HA	2.56	0.40
19:sZ:13:VAL:HG13	19:sZ:76:ILE:HA	2.03	0.40
20:sF:79:TYR:O	20:sF:82:ARG:HG2	2.21	0.40
24:sJ:96:PRO:HG2	24:sJ:99:ILE:HD13	2.02	0.40
48:LJ:136:TYR:CZ	48:LJ:231:ASN:HB2	2.56	0.40
49:LK:78:PHE:C	49:LK:80:TYR:H	2.29	0.40
65:La:56:ARG:O	65:La:61:LYS:HD2	2.22	0.40
67:Lc:70:PRO:HG3	67:Lc:115:LYS:HB2	2.04	0.40
84:sh:551:THR:HB	84:sh:565:ARG:HG3	2.03	0.40
1:LA:835:G:O2'	1:LA:857:G:N2	2.39	0.40
1:LA:1157:G:H2'	1:LA:1158:A:O4'	2.21	0.40
1:LA:1213:G:H5'	60:LV:137:ARG:HH21	1.87	0.40
1:LA:1373:A:H2'	1:LA:1374:G:C8	2.57	0.40
1:LA:2801:A:O2'	1:LA:2802:A:H2'	2.21	0.40
1:LA:3296:A:H2'	1:LA:3297:U:H6	1.86	0.40
2:LB:41:TYR:HD1	2:LB:161:LYS:HE2	1.86	0.40
3:2:138:A:H62	3:2:266:A:H61	1.70	0.40
3:2:885:G:N2	19:sZ:123:SER:O	2.54	0.40
3:2:1231:U:H3	3:2:1254:U:H3	1.70	0.40
3:2:1402:G:OP2	21:sG:5:ARG:NH1	2.55	0.40
18:sY:96:VAL:HG21	18:sY:150:VAL:HG21	2.03	0.40
40:sn:62:C:H2'	40:sn:63:G:C8	2.55	0.40
50:LL:2:LYS:HA	50:LL:2:LYS:HD3	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:LM:48:LEU:O	51:LM:139:ARG:HA	2.21	0.40
51:LM:184:LYS:HG2	51:LM:190:VAL:HG23	2.04	0.40
70:Lf:22:LYS:HD3	70:Lf:22:LYS:HA	1.85	0.40
70:Lf:83:LYS:HA	70:Lf:83:LYS:HD3	1.91	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	
2	LB	202/217 (93%)	158 (78%)	44 (22%)	0	100	100
4	sP	204/252 (81%)	189 (93%)	15 (7%)	0	100	100
5	sQ	222/255 (87%)	217 (98%)	5 (2%)	0	100	100
6	sE	115/142 (81%)	106 (92%)	9 (8%)	0	100	100
7	sR	214/254 (84%)	198 (92%)	16 (8%)	0	100	100
8	sA	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
9	sS	256/261 (98%)	239 (93%)	17 (7%)	0	100	100
10	sB	204/225 (91%)	198 (97%)	6 (3%)	0	100	100
11	sT	226/236 (96%)	212 (94%)	14 (6%)	0	100	100
12	sU	182/190 (96%)	172 (94%)	10 (6%)	0	100	100
13	sV	183/200 (92%)	172 (94%)	11 (6%)	0	100	100
14	sW	182/197 (92%)	170 (93%)	12 (7%)	0	100	100
15	sC	90/105 (86%)	75 (83%)	15 (17%)	0	100	100
16	sX	140/156 (90%)	131 (94%)	9 (6%)	0	100	100
17	sD	119/143 (83%)	90 (76%)	27 (23%)	2 (2%)	7	10
18	sY	148/151 (98%)	140 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	sZ	125/137 (91%)	114 (91%)	11 (9%)	0	100	100
20	sF	139/143 (97%)	134 (96%)	5 (4%)	0	100	100
21	sG	123/136 (90%)	122 (99%)	1 (1%)	0	100	100
22	sH	143/146 (98%)	135 (94%)	8 (6%)	0	100	100
23	sI	141/144 (98%)	136 (96%)	5 (4%)	0	100	100
24	sJ	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
25	sa	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
26	sb	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
27	sc	142/145 (98%)	140 (99%)	2 (1%)	0	100	100
28	sd	132/135 (98%)	126 (96%)	6 (4%)	0	100	100
29	sK	68/108 (63%)	63 (93%)	5 (7%)	0	100	100
30	se	95/119 (80%)	88 (93%)	7 (7%)	0	100	100
31	sf	79/82 (96%)	71 (90%)	8 (10%)	0	100	100
32	sM	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
33	sg	56/63 (89%)	53 (95%)	3 (5%)	0	100	100
34	sN	71/76 (93%)	48 (68%)	22 (31%)	1 (1%)	9	13
35	sO	310/319 (97%)	284 (92%)	26 (8%)	0	100	100
36	sL	61/67 (91%)	59 (97%)	2 (3%)	0	100	100
37	sj	133/235 (57%)	130 (98%)	3 (2%)	0	100	100
38	sk	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
43	LE	249/254 (98%)	233 (94%)	16 (6%)	0	100	100
44	LF	384/387 (99%)	360 (94%)	24 (6%)	0	100	100
45	LG	359/362 (99%)	332 (92%)	26 (7%)	1 (0%)	36	50
46	LH	292/297 (98%)	282 (97%)	10 (3%)	0	100	100
47	LI	163/176 (93%)	156 (96%)	7 (4%)	0	100	100
48	LJ	220/244 (90%)	209 (95%)	11 (5%)	0	100	100
49	LK	231/256 (90%)	219 (95%)	12 (5%)	0	100	100
50	LL	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
51	LM	207/221 (94%)	198 (96%)	9 (4%)	0	100	100
52	LN	170/174 (98%)	166 (98%)	4 (2%)	0	100	100
53	LO	191/199 (96%)	172 (90%)	18 (9%)	1 (0%)	24	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	LP	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
55	LQ	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
56	LR	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
57	LS	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
58	LT	183/186 (98%)	173 (94%)	10 (6%)	0	100	100
59	LU	186/189 (98%)	182 (98%)	4 (2%)	0	100	100
60	LV	169/172 (98%)	164 (97%)	5 (3%)	0	100	100
61	LW	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
62	LX	98/121 (81%)	94 (96%)	4 (4%)	0	100	100
63	LY	134/137 (98%)	131 (98%)	3 (2%)	0	100	100
64	LZ	124/155 (80%)	123 (99%)	1 (1%)	0	100	100
65	La	119/142 (84%)	114 (96%)	5 (4%)	0	100	100
66	Lb	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
67	Lc	133/136 (98%)	128 (96%)	4 (3%)	1 (1%)	16	25
68	Ld	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
69	Le	56/59 (95%)	53 (95%)	2 (4%)	1 (2%)	6	9
70	Lf	94/105 (90%)	94 (100%)	0	0	100	100
71	Lg	107/113 (95%)	98 (92%)	9 (8%)	0	100	100
72	Lh	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
73	Li	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
74	Lj	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
75	Lk	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
76	Ll	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
77	Lm	79/88 (90%)	77 (98%)	2 (2%)	0	100	100
78	Ln	75/78 (96%)	75 (100%)	0	0	100	100
79	Lo	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
80	Lp	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
81	Lq	23/25 (92%)	23 (100%)	0	0	100	100
81	Lt	20/25 (80%)	20 (100%)	0	0	100	100
82	Lr	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
83	Ls	89/92 (97%)	85 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
84	sh	772/965 (80%)	748 (97%)	21 (3%)	3 (0%)	30	43
All	All	12203/13284 (92%)	11518 (94%)	675 (6%)	10 (0%)	49	64

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	sD	85	LYS
34	sN	145	HIS
84	sh	309	PRO
67	Lc	59	ALA
84	sh	366	SER
45	LG	4	PRO
17	sD	109	GLU
84	sh	234	PRO
53	LO	61	PRO
69	Le	21	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	LB	185/198 (93%)	185 (100%)	0	100	100
4	sP	170/210 (81%)	170 (100%)	0	100	100
5	sQ	200/224 (89%)	200 (100%)	0	100	100
6	sE	95/118 (80%)	95 (100%)	0	100	100
7	sR	175/205 (85%)	174 (99%)	1 (1%)	78	89
8	sA	182/195 (93%)	182 (100%)	0	100	100
9	sS	220/222 (99%)	220 (100%)	0	100	100
10	sB	172/191 (90%)	172 (100%)	0	100	100
11	sT	189/201 (94%)	189 (100%)	0	100	100
12	sU	163/170 (96%)	163 (100%)	0	100	100
13	sV	148/161 (92%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	sW	156/166 (94%)	156 (100%)	0	100	100
15	sC	77/98 (79%)	77 (100%)	0	100	100
16	sX	126/137 (92%)	125 (99%)	1 (1%)	73	86
17	sD	88/119 (74%)	88 (100%)	0	100	100
18	sY	127/128 (99%)	127 (100%)	0	100	100
19	sZ	90/105 (86%)	90 (100%)	0	100	100
20	sF	117/119 (98%)	117 (100%)	0	100	100
21	sG	105/124 (85%)	102 (97%)	3 (3%)	37	60
22	sH	127/129 (98%)	127 (100%)	0	100	100
23	sI	115/116 (99%)	115 (100%)	0	100	100
24	sJ	93/114 (82%)	93 (100%)	0	100	100
25	sa	71/74 (96%)	71 (100%)	0	100	100
26	sb	110/111 (99%)	110 (100%)	0	100	100
27	sc	119/120 (99%)	119 (100%)	0	100	100
28	sd	112/113 (99%)	112 (100%)	0	100	100
29	sK	61/89 (68%)	61 (100%)	0	100	100
30	se	82/101 (81%)	82 (100%)	0	100	100
31	sf	70/71 (99%)	70 (100%)	0	100	100
32	sM	47/49 (96%)	47 (100%)	0	100	100
33	sg	47/54 (87%)	47 (100%)	0	100	100
34	sN	56/66 (85%)	56 (100%)	0	100	100
35	sO	250/262 (95%)	250 (100%)	0	100	100
36	sL	55/60 (92%)	55 (100%)	0	100	100
37	sj	128/213 (60%)	128 (100%)	0	100	100
38	sk	95/95 (100%)	94 (99%)	1 (1%)	65	82
43	LE	190/196 (97%)	190 (100%)	0	100	100
44	LF	319/323 (99%)	319 (100%)	0	100	100
45	LG	288/289 (100%)	288 (100%)	0	100	100
46	LH	241/245 (98%)	241 (100%)	0	100	100
47	LI	139/155 (90%)	139 (100%)	0	100	100
48	LJ	186/205 (91%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	LK	187/208 (90%)	187 (100%)	0	100	100
50	LL	168/171 (98%)	168 (100%)	0	100	100
51	LM	181/187 (97%)	181 (100%)	0	100	100
52	LN	146/150 (97%)	146 (100%)	0	100	100
53	LO	154/159 (97%)	154 (100%)	0	100	100
54	LP	107/109 (98%)	107 (100%)	0	100	100
55	LQ	175/176 (99%)	175 (100%)	0	100	100
56	LR	160/162 (99%)	160 (100%)	0	100	100
57	LS	138/146 (94%)	138 (100%)	0	100	100
58	LT	150/151 (99%)	150 (100%)	0	100	100
59	LU	153/154 (99%)	152 (99%)	1 (1%)	76	88
60	LV	155/156 (99%)	155 (100%)	0	100	100
61	LW	135/137 (98%)	135 (100%)	0	100	100
62	LX	87/107 (81%)	87 (100%)	0	100	100
63	LY	104/105 (99%)	104 (100%)	0	100	100
64	LZ	65/129 (50%)	64 (98%)	1 (2%)	57	77
65	La	104/118 (88%)	102 (98%)	2 (2%)	50	71
66	Lb	108/110 (98%)	108 (100%)	0	100	100
67	Lc	112/116 (97%)	111 (99%)	1 (1%)	70	85
68	Ld	117/119 (98%)	117 (100%)	0	100	100
69	Le	46/47 (98%)	46 (100%)	0	100	100
70	Lf	81/88 (92%)	81 (100%)	0	100	100
71	Lg	92/97 (95%)	92 (100%)	0	100	100
72	Lh	107/111 (96%)	107 (100%)	0	100	100
73	Li	90/91 (99%)	90 (100%)	0	100	100
74	Lj	95/103 (92%)	95 (100%)	0	100	100
75	Lk	104/105 (99%)	104 (100%)	0	100	100
76	Ll	80/82 (98%)	80 (100%)	0	100	100
77	Lm	67/71 (94%)	67 (100%)	0	100	100
78	Ln	68/69 (99%)	68 (100%)	0	100	100
79	Lo	45/46 (98%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	Lp	45/47 (96%)	45 (100%)	0	100	100
81	Lq	22/23 (96%)	22 (100%)	0	100	100
81	Lt	20/23 (87%)	20 (100%)	0	100	100
82	Lr	87/91 (96%)	87 (100%)	0	100	100
83	Ls	71/72 (99%)	71 (100%)	0	100	100
84	sh	709/879 (81%)	646 (91%)	63 (9%)	9	15
All	All	10321/11256 (92%)	10247 (99%)	74 (1%)	73	88

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	sR	111	VAL
16	sX	21	ASN
21	sG	88	VAL
21	sG	99	VAL
21	sG	100	LEU
38	sk	32	HIS
59	LU	130	ASN
64	LZ	89	LEU
65	La	64	GLU
65	La	86	VAL
67	Lc	106	GLN
84	sh	67	VAL
84	sh	75	MET
84	sh	85	LYS
84	sh	90	VAL
84	sh	91	PHE
84	sh	112	TRP
84	sh	119	TYR
84	sh	120	VAL
84	sh	123	ARG
84	sh	138	VAL
84	sh	154	CYS
84	sh	159	CYS
84	sh	161	HIS
84	sh	168	HIS
84	sh	179	VAL
84	sh	180	GLU
84	sh	181	ILE
84	sh	191	SER

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Mol	Chain	Res	Type
84	sh	192	ILE
84	sh	225	CYS
84	sh	239	SER
84	sh	242	SER
84	sh	255	THR
84	sh	272	SER
84	sh	273	SER
84	sh	276	GLU
84	sh	287	CYS
84	sh	300	HIS
84	sh	306	CYS
84	sh	307	ILE
84	sh	328	CYS
84	sh	333	THR
84	sh	335	LEU
84	sh	339	THR
84	sh	342	ARG
84	sh	345	CYS
84	sh	356	CYS
84	sh	360	LEU
84	sh	365	HIS
84	sh	370	THR
84	sh	410	LYS
84	sh	441	PHE
84	sh	444	GLN
84	sh	552	VAL
84	sh	567	VAL
84	sh	570	GLN
84	sh	573	VAL
84	sh	575	CYS
84	sh	586	CYS
84	sh	593	THR
84	sh	595	HIS
84	sh	612	ARG
84	sh	640	ILE
84	sh	647	ILE
84	sh	651	VAL
84	sh	660	VAL
84	sh	663	THR
84	sh	677	LEU
84	sh	704	LEU
84	sh	707	LEU

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Mol	Chain	Res	Type
84	sh	733	GLU
84	sh	768	ILE
84	sh	788	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (110) such sidechains are listed below:

Mol	Chain	Res	Type
4	sP	32	HIS
4	sP	49	ASN
4	sP	163	ASN
5	sQ	146	GLN
5	sQ	232	HIS
6	sE	103	ASN
8	sA	67	ASN
9	sS	17	HIS
9	sS	36	HIS
9	sS	57	ASN
9	sS	67	GLN
9	sS	98	ASN
10	sB	79	ASN
10	sB	224	ASN
11	sT	56	ASN
11	sT	176	GLN
11	sT	182	GLN
12	sU	11	GLN
12	sU	22	GLN
12	sU	42	GLN
13	sV	64	ASN
13	sV	116	HIS
16	sX	21	ASN
16	sX	138	ASN
17	sD	80	ASN
18	sY	78	ASN
18	sY	105	ASN
19	sZ	24	ASN
21	sG	42	GLN
21	sG	62	GLN
22	sH	6	GLN
22	sH	25	ASN
22	sH	75	ASN
23	sI	64	HIS
26	sb	12	ASN

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Mol	Chain	Res	Type
26	sb	42	GLN
26	sb	56	HIS
28	sd	63	GLN
28	sd	107	GLN
28	sd	113	ASN
31	sf	26	GLN
32	sM	37	ASN
35	sO	224	ASN
35	sO	308	ASN
35	sO	314	GLN
37	sj	117	GLN
37	sj	120	HIS
38	sk	101	ASN
43	LE	24	GLN
44	LF	109	HIS
44	LF	139	GLN
44	LF	182	GLN
45	LG	5	GLN
45	LG	213	ASN
46	LH	32	GLN
48	LJ	64	GLN
48	LJ	244	ASN
49	LK	61	GLN
49	LK	95	ASN
50	LL	58	HIS
50	LL	100	ASN
50	LL	163	GLN
50	LL	169	ASN
50	LL	183	HIS
51	LM	23	ASN
51	LM	73	ASN
51	LM	92	HIS
52	LN	101	ASN
54	LP	119	GLN
55	LQ	95	GLN
55	LQ	181	ASN
57	LS	45	GLN
57	LS	54	HIS
57	LS	133	HIS
58	LT	9	GLN
62	LX	101	ASN
63	LY	33	ASN

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Mol	Chain	Res	Type
66	Lb	4	GLN
67	Lc	103	GLN
67	Lc	127	ASN
68	Ld	14	HIS
68	Ld	44	ASN
68	Ld	65	GLN
69	Le	19	ASN
70	Lf	36	GLN
70	Lf	71	GLN
71	Lg	15	ASN
71	Lg	21	HIS
71	Lg	57	GLN
72	Lh	13	HIS
72	Lh	26	HIS
72	Lh	49	ASN
73	Li	17	GLN
73	Li	24	ASN
73	Li	26	ASN
73	Li	88	ASN
75	Lk	16	GLN
75	Lk	99	GLN
77	Lm	12	HIS
79	Lo	33	ASN
84	sh	116	ASN
84	sh	152	GLN
84	sh	184	HIS
84	sh	258	ASN
84	sh	290	ASN
84	sh	392	GLN
84	sh	478	HIS
84	sh	601	GLN
84	sh	606	GLN
84	sh	610	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	LA	3213/3396 (94%)	562 (17%)	39 (1%)
3	2	1761/1800 (97%)	436 (24%)	37 (2%)
39	sm	28/29 (96%)	16 (57%)	0
40	sl	75/76 (98%)	20 (26%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
40	sn	75/76 (98%)	19 (25%)	0
41	LC	120/121 (99%)	11 (9%)	1 (0%)
42	LD	157/158 (99%)	27 (17%)	1 (0%)
All	All	5429/5656 (95%)	1091 (20%)	78 (1%)

All (1091) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	LA	6	A
1	LA	13	A
1	LA	14	U
1	LA	26	A
1	LA	40	A
1	LA	43	A
1	LA	49	A
1	LA	59	G
1	LA	60	A
1	LA	65	A
1	LA	66	A
1	LA	92	G
1	LA	99	A
1	LA	109	A
1	LA	110	G
1	LA	111	C
1	LA	116	A
1	LA	120	G
1	LA	121	A
1	LA	122	A
1	LA	133	U
1	LA	134	U
1	LA	135	C
1	LA	136	G
1	LA	142	C
1	LA	156	G
1	LA	157	A
1	LA	166	C
1	LA	173	G
1	LA	187	A
1	LA	190	U
1	LA	191	U
1	LA	192	C
1	LA	200	C

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Mol	Chain	Res	Type
1	LA	210	U
1	LA	211	A
1	LA	218	G
1	LA	219	A
1	LA	240	U
1	LA	242	C
1	LA	243	G
1	LA	245	U
1	LA	249	U
1	LA	252	U
1	LA	269	G
1	LA	283	G
1	LA	286	U
1	LA	295	A
1	LA	305	U
1	LA	315	C
1	LA	323	A
1	LA	329	U
1	LA	339	C
1	LA	349	A
1	LA	350	C
1	LA	352	A
1	LA	376	G
1	LA	395	A
1	LA	398	A
1	LA	401	U
1	LA	402	A
1	LA	403	C
1	LA	421	G
1	LA	422	A
1	LA	439	C
1	LA	440	A
1	LA	441	U
1	LA	442	G
1	LA	443	G
1	LA	445	G
1	LA	446	U
1	LA	447	U
1	LA	448	U
1	LA	450	G
1	LA	487	U
1	LA	488	U

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Mol	Chain	Res	Type
1	LA	489	U
1	LA	490	C
1	LA	491	A
1	LA	494	G
1	LA	517	G
1	LA	521	A
1	LA	535	G
1	LA	544	C
1	LA	546	C
1	LA	547	G
1	LA	548	G
1	LA	551	A
1	LA	552	G
1	LA	555	U
1	LA	557	A
1	LA	559	A
1	LA	569	A
1	LA	579	G
1	LA	592	A
1	LA	604	G
1	LA	609	G
1	LA	611	A
1	LA	612	U
1	LA	620	U
1	LA	621	A
1	LA	622	A
1	LA	636	C
1	LA	637	C
1	LA	638	C
1	LA	649	A
1	LA	660	A
1	LA	677	A
1	LA	681	U
1	LA	691	A
1	LA	705	A
1	LA	712	G
1	LA	715	A
1	LA	716	A
1	LA	758	C
1	LA	764	U
1	LA	765	C
1	LA	766	U

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Mol	Chain	Res	Type
1	LA	767	U
1	LA	776	U
1	LA	777	U
1	LA	780	A
1	LA	781	G
1	LA	785	G
1	LA	786	A
1	LA	799	G
1	LA	806	A
1	LA	817	A
1	LA	830	A
1	LA	845	G
1	LA	846	A
1	LA	847	A
1	LA	848	A
1	LA	849	C
1	LA	850	U
1	LA	861	C
1	LA	874	U
1	LA	879	U
1	LA	896	A
1	LA	897	U
1	LA	907	G
1	LA	908	G
1	LA	914	A
1	LA	916	G
1	LA	917	A
1	LA	921	A
1	LA	923	C
1	LA	924	G
1	LA	925	A
1	LA	937	G
1	LA	943	U
1	LA	944	C
1	LA	959	C
1	LA	960	U
1	LA	981	U
1	LA	982	C
1	LA	991	G
1	LA	994	G
1	LA	1001	G
1	LA	1002	A

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Mol	Chain	Res	Type
1	LA	1010	G
1	LA	1015	U
1	LA	1017	C
1	LA	1020	G
1	LA	1024	G
1	LA	1025	A
1	LA	1028	U
1	LA	1047	A
1	LA	1049	C
1	LA	1064	A
1	LA	1065	A
1	LA	1072	G
1	LA	1081	U
1	LA	1093	A
1	LA	1094	U
1	LA	1095	U
1	LA	1097	G
1	LA	1098	A
1	LA	1103	A
1	LA	1104	G
1	LA	1117	G
1	LA	1131	G
1	LA	1144	U
1	LA	1153	A
1	LA	1159	A
1	LA	1160	C
1	LA	1180	A
1	LA	1181	U
1	LA	1192	C
1	LA	1193	A
1	LA	1196	C
1	LA	1201	C
1	LA	1202	A
1	LA	1208	U
1	LA	1217	A
1	LA	1222	G
1	LA	1223	A
1	LA	1227	C
1	LA	1232	C
1	LA	1235	U
1	LA	1236	G
1	LA	1237	G

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Mol	Chain	Res	Type
1	LA	1240	A
1	LA	1241	U
1	LA	1243	G
1	LA	1244	A
1	LA	1245	A
1	LA	1246	G
1	LA	1248	C
1	LA	1251	A
1	LA	1253	U
1	LA	1258	U
1	LA	1262	G
1	LA	1263	A
1	LA	1264	G
1	LA	1266	G
1	LA	1269	U
1	LA	1270	A
1	LA	1271	A
1	LA	1272	C
1	LA	1274	A
1	LA	1278	A
1	LA	1279	C
1	LA	1285	G
1	LA	1286	A
1	LA	1287	A
1	LA	1307	G
1	LA	1308	A
1	LA	1309	U
1	LA	1313	G
1	LA	1330	A
1	LA	1348	U
1	LA	1349	G
1	LA	1351	U
1	LA	1352	A
1	LA	1355	A
1	LA	1356	U
1	LA	1357	G
1	LA	1386	A
1	LA	1399	A
1	LA	1400	G
1	LA	1419	A
1	LA	1434	G
1	LA	1437	C

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Mol	Chain	Res	Type
1	LA	1446	A
1	LA	1450	G
1	LA	1469	C
1	LA	1481	A
1	LA	1482	A
1	LA	1483	G
1	LA	1488	G
1	LA	1508	C
1	LA	1536	G
1	LA	1539	A
1	LA	1555	U
1	LA	1556	C
1	LA	1557	A
1	LA	1560	G
1	LA	1562	C
1	LA	1563	C
1	LA	1566	A
1	LA	1568	U
1	LA	1569	U
1	LA	1572	U
1	LA	1575	A
1	LA	1576	G
1	LA	1580	A
1	LA	1581	C
1	LA	1582	C
1	LA	1583	A
1	LA	1589	A
1	LA	1593	A
1	LA	1605	A
1	LA	1607	U
1	LA	1620	U
1	LA	1629	U
1	LA	1639	C
1	LA	1643	A
1	LA	1645	U
1	LA	1657	C
1	LA	1683	A
1	LA	1716	U
1	LA	1717	U
1	LA	1724	U
1	LA	1725	C
1	LA	1730	G

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Mol	Chain	Res	Type
1	LA	1736	G
1	LA	1741	A
1	LA	1750	A
1	LA	1751	G
1	LA	1760	A
1	LA	1764	U
1	LA	1765	U
1	LA	1766	G
1	LA	1770	G
1	LA	1778	G
1	LA	1780	G
1	LA	1797	A
1	LA	1808	G
1	LA	1814	A
1	LA	1816	A
1	LA	1821	U
1	LA	1835	A
1	LA	1839	A
1	LA	1840	U
1	LA	1841	A
1	LA	1842	A
1	LA	1846	C
1	LA	1849	C
1	LA	1866	C
1	LA	1867	A
1	LA	1880	U
1	LA	1881	A
1	LA	1893	A
1	LA	1906	G
1	LA	1952	G
1	LA	1953	G
1	LA	1954	G
1	LA	2094	C
1	LA	2100	A
1	LA	2101	C
1	LA	2102	U
1	LA	2110	G
1	LA	2111	G
1	LA	2112	U
1	LA	2113	A
1	LA	2114	C
1	LA	2121	G

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Mol	Chain	Res	Type
1	LA	2122	G
1	LA	2131	A
1	LA	2140	U
1	LA	2144	A
1	LA	2158	A
1	LA	2169	G
1	LA	2170	U
1	LA	2171	G
1	LA	2192	C
1	LA	2201	G
1	LA	2204	C
1	LA	2205	U
1	LA	2206	G
1	LA	2208	A
1	LA	2209	U
1	LA	2210	G
1	LA	2223	A
1	LA	2225	U
1	LA	2244	A
1	LA	2252	A
1	LA	2255	A
1	LA	2270	A
1	LA	2272	G
1	LA	2273	G
1	LA	2281	A
1	LA	2282	U
1	LA	2288	G
1	LA	2307	G
1	LA	2308	C
1	LA	2310	U
1	LA	2313	A
1	LA	2314	U
1	LA	2315	G
1	LA	2334	U
1	LA	2335	G
1	LA	2336	U
1	LA	2373	A
1	LA	2374	C
1	LA	2375	G
1	LA	2385	G
1	LA	2388	U
1	LA	2393	G

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Mol	Chain	Res	Type
1	LA	2397	A
1	LA	2402	A
1	LA	2403	G
1	LA	2404	A
1	LA	2411	U
1	LA	2418	G
1	LA	2419	A
1	LA	2439	A
1	LA	2447	A
1	LA	2450	G
1	LA	2453	U
1	LA	2454	G
1	LA	2455	U
1	LA	2456	A
1	LA	2459	A
1	LA	2460	U
1	LA	2461	A
1	LA	2463	G
1	LA	2468	A
1	LA	2470	C
1	LA	2471	U
1	LA	2474	G
1	LA	2477	G
1	LA	2480	A
1	LA	2485	A
1	LA	2486	A
1	LA	2487	U
1	LA	2488	A
1	LA	2491	A
1	LA	2492	C
1	LA	2493	U
1	LA	2495	C
1	LA	2497	U
1	LA	2498	U
1	LA	2499	U
1	LA	2501	U
1	LA	2505	U
1	LA	2506	U
1	LA	2514	U
1	LA	2515	A
1	LA	2522	G
1	LA	2523	A

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Mol	Chain	Res	Type
1	LA	2526	C
1	LA	2534	G
1	LA	2549	G
1	LA	2550	U
1	LA	2552	C
1	LA	2555	G
1	LA	2561	A
1	LA	2569	A
1	LA	2570	U
1	LA	2571	U
1	LA	2572	C
1	LA	2573	G
1	LA	2585	G
1	LA	2593	A
1	LA	2594	C
1	LA	2606	G
1	LA	2607	G
1	LA	2614	G
1	LA	2651	G
1	LA	2652	U
1	LA	2656	A
1	LA	2672	G
1	LA	2674	A
1	LA	2677	G
1	LA	2678	A
1	LA	2681	U
1	LA	2689	A
1	LA	2691	A
1	LA	2694	A
1	LA	2696	A
1	LA	2704	A
1	LA	2714	G
1	LA	2728	G
1	LA	2729	U
1	LA	2752	U
1	LA	2753	G
1	LA	2755	C
1	LA	2762	A
1	LA	2777	G
1	LA	2778	G
1	LA	2788	C
1	LA	2796	G

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Mol	Chain	Res	Type
1	LA	2799	A
1	LA	2800	G
1	LA	2801	A
1	LA	2802	A
1	LA	2810	C
1	LA	2814	G
1	LA	2817	A
1	LA	2818	U
1	LA	2819	A
1	LA	2821	C
1	LA	2834	G
1	LA	2842	U
1	LA	2844	C
1	LA	2845	A
1	LA	2871	G
1	LA	2872	A
1	LA	2875	U
1	LA	2876	C
1	LA	2887	A
1	LA	2899	C
1	LA	2911	A
1	LA	2914	G
1	LA	2923	U
1	LA	2935	U
1	LA	2936	A
1	LA	2942	C
1	LA	2947	G
1	LA	2957	G
1	LA	2971	A
1	LA	2983	C
1	LA	2990	G
1	LA	2996	U
1	LA	2997	G
1	LA	3012	A
1	LA	3056	U
1	LA	3059	G
1	LA	3078	U
1	LA	3079	U
1	LA	3086	A
1	LA	3092	C
1	LA	3104	U
1	LA	3113	A

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Mol	Chain	Res	Type
1	LA	3119	U
1	LA	3122	A
1	LA	3129	A
1	LA	3130	A
1	LA	3131	U
1	LA	3139	A
1	LA	3142	A
1	LA	3143	C
1	LA	3151	U
1	LA	3154	C
1	LA	3155	U
1	LA	3156	U
1	LA	3157	U
1	LA	3165	A
1	LA	3170	A
1	LA	3171	U
1	LA	3173	G
1	LA	3174	A
1	LA	3176	G
1	LA	3179	U
1	LA	3181	C
1	LA	3187	A
1	LA	3196	U
1	LA	3207	U
1	LA	3209	A
1	LA	3217	C
1	LA	3218	A
1	LA	3219	G
1	LA	3229	G
1	LA	3243	A
1	LA	3245	A
1	LA	3247	G
1	LA	3259	U
1	LA	3263	G
1	LA	3270	U
1	LA	3273	A
1	LA	3276	G
1	LA	3281	U
1	LA	3287	U
1	LA	3288	G
1	LA	3289	G
1	LA	3294	A

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Mol	Chain	Res	Type
1	LA	3295	A
1	LA	3303	G
1	LA	3304	U
1	LA	3316	A
1	LA	3317	U
1	LA	3318	G
1	LA	3319	U
1	LA	3320	A
1	LA	3341	U
1	LA	3342	A
1	LA	3345	G
1	LA	3351	U
1	LA	3352	U
1	LA	3353	G
1	LA	3354	U
1	LA	3355	U
1	LA	3369	G
1	LA	3375	A
1	LA	3376	A
1	LA	3378	C
1	LA	3382	U
1	LA	3386	G
1	LA	3389	U
1	LA	3396	U
3	2	2	A
3	2	4	C
3	2	17	C
3	2	25	C
3	2	26	A
3	2	34	G
3	2	47	A
3	2	56	U
3	2	57	G
3	2	61	A
3	2	62	A
3	2	63	G
3	2	65	A
3	2	68	A
3	2	69	G
3	2	73	U
3	2	74	U
3	2	75	U

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Mol	Chain	Res	Type
3	2	76	A
3	2	78	A
3	2	79	C
3	2	81	G
3	2	104	A
3	2	114	C
3	2	115	G
3	2	121	U
3	2	127	G
3	2	128	U
3	2	129	U
3	2	130	C
3	2	131	C
3	2	133	U
3	2	134	U
3	2	135	A
3	2	136	C
3	2	138	A
3	2	140	A
3	2	141	U
3	2	142	G
3	2	153	G
3	2	155	U
3	2	158	U
3	2	171	A
3	2	172	C
3	2	176	C
3	2	178	U
3	2	179	A
3	2	180	A
3	2	185	U
3	2	186	C
3	2	188	A
3	2	191	C
3	2	192	U
3	2	193	U
3	2	194	U
3	2	195	G
3	2	217	A
3	2	218	A
3	2	223	U
3	2	227	U

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Mol	Chain	Res	Type
3	2	228	G
3	2	230	C
3	2	232	U
3	2	233	C
3	2	234	G
3	2	235	G
3	2	236	A
3	2	238	U
3	2	240	U
3	2	241	U
3	2	249	U
3	2	250	C
3	2	257	A
3	2	260	U
3	2	261	U
3	2	265	A
3	2	272	U
3	2	274	G
3	2	279	G
3	2	280	U
3	2	281	G
3	2	287	G
3	2	299	A
3	2	314	C
3	2	316	A
3	2	330	G
3	2	333	A
3	2	337	G
3	2	338	C
3	2	352	A
3	2	353	A
3	2	359	A
3	2	361	C
3	2	373	G
3	2	388	G
3	2	390	G
3	2	400	A
3	2	401	A
3	2	402	C
3	2	404	G
3	2	405	C
3	2	415	C

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Mol	Chain	Res	Type
3	2	416	A
3	2	417	A
3	2	419	G
3	2	422	G
3	2	423	G
3	2	424	C
3	2	425	A
3	2	426	G
3	2	428	A
3	2	434	G
3	2	436	A
3	2	437	A
3	2	439	U
3	2	444	C
3	2	448	C
3	2	452	A
3	2	468	A
3	2	471	A
3	2	477	A
3	2	483	A
3	2	486	G
3	2	488	G
3	2	499	U
3	2	500	C
3	2	503	G
3	2	506	A
3	2	510	G
3	2	511	A
3	2	514	G
3	2	519	C
3	2	534	A
3	2	538	A
3	2	540	G
3	2	541	A
3	2	542	A
3	2	544	A
3	2	548	G
3	2	549	G
3	2	555	A
3	2	556	A
3	2	557	G
3	2	558	U

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Mol	Chain	Res	Type
3	2	565	C
3	2	578	U
3	2	580	A
3	2	582	U
3	2	583	C
3	2	594	A
3	2	595	G
3	2	609	U
3	2	610	G
3	2	611	U
3	2	619	A
3	2	620	A
3	2	621	A
3	2	622	A
3	2	623	A
3	2	624	G
3	2	638	U
3	2	639	U
3	2	640	U
3	2	641	G
3	2	643	G
3	2	653	C
3	2	654	C
3	2	655	G
3	2	678	A
3	2	681	U
3	2	694	U
3	2	696	C
3	2	698	U
3	2	700	C
3	2	702	G
3	2	703	G
3	2	704	C
3	2	705	U
3	2	706	A
3	2	707	A
3	2	708	C
3	2	709	C
3	2	710	U
3	2	711	U
3	2	712	G
3	2	713	A

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Mol	Chain	Res	Type
3	2	714	G
3	2	728	U
3	2	729	G
3	2	730	G
3	2	732	G
3	2	733	A
3	2	734	A
3	2	736	C
3	2	739	G
3	2	741	C
3	2	742	U
3	2	743	U
3	2	756	A
3	2	765	G
3	2	766	U
3	2	767	U
3	2	774	A
3	2	775	G
3	2	778	G
3	2	779	U
3	2	780	A
3	2	781	U
3	2	782	U
3	2	783	G
3	2	789	A
3	2	812	A
3	2	813	U
3	2	814	A
3	2	815	G
3	2	816	G
3	2	819	G
3	2	820	U
3	2	821	U
3	2	823	G
3	2	832	U
3	2	833	U
3	2	835	U
3	2	837	G
3	2	840	U
3	2	846	G
3	2	852	C
3	2	855	A

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Mol	Chain	Res	Type
3	2	856	A
3	2	863	A
3	2	864	U
3	2	873	U
3	2	886	U
3	2	899	G
3	2	901	G
3	2	902	G
3	2	912	U
3	2	913	G
3	2	921	U
3	2	929	A
3	2	933	A
3	2	934	C
3	2	935	U
3	2	942	G
3	2	944	A
3	2	951	A
3	2	960	U
3	2	964	U
3	2	966	A
3	2	970	A
3	2	988	A
3	2	989	U
3	2	992	A
3	2	993	A
3	2	998	A
3	2	1004	U
3	2	1024	U
3	2	1025	A
3	2	1026	A
3	2	1028	C
3	2	1031	U
3	2	1032	G
3	2	1039	A
3	2	1052	U
3	2	1053	G
3	2	1058	U
3	2	1059	U
3	2	1060	U
3	2	1061	A
3	2	1063	U

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Mol	Chain	Res	Type
3	2	1076	A
3	2	1081	A
3	2	1082	C
3	2	1092	A
3	2	1096	C
3	2	1100	G
3	2	1109	G
3	2	1138	A
3	2	1150	G
3	2	1158	C
3	2	1160	A
3	2	1164	G
3	2	1167	G
3	2	1170	G
3	2	1185	U
3	2	1194	A
3	2	1196	A
3	2	1199	G
3	2	1200	G
3	2	1202	A
3	2	1208	A
3	2	1214	U
3	2	1216	C
3	2	1217	A
3	2	1218	G
3	2	1227	A
3	2	1229	G
3	2	1241	G
3	2	1243	G
3	2	1244	A
3	2	1245	G
3	2	1246	C
3	2	1252	C
3	2	1256	A
3	2	1257	U
3	2	1274	C
3	2	1275	A
3	2	1276	U
3	2	1285	U
3	2	1291	G
3	2	1301	U
3	2	1314	U

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Mol	Chain	Res	Type
3	2	1315	U
3	2	1316	G
3	2	1318	G
3	2	1321	A
3	2	1322	A
3	2	1337	A
3	2	1338	C
3	2	1344	A
3	2	1345	A
3	2	1347	U
3	2	1348	A
3	2	1349	G
3	2	1354	G
3	2	1362	U
3	2	1363	U
3	2	1364	G
3	2	1370	U
3	2	1371	A
3	2	1372	U
3	2	1381	U
3	2	1382	A
3	2	1383	G
3	2	1390	U
3	2	1398	U
3	2	1399	C
3	2	1400	A
3	2	1402	G
3	2	1414	U
3	2	1422	A
3	2	1425	A
3	2	1427	A
3	2	1431	C
3	2	1445	G
3	2	1446	A
3	2	1459	C
3	2	1460	A
3	2	1464	G
3	2	1466	G
3	2	1468	U
3	2	1471	A
3	2	1472	C
3	2	1479	A

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Mol	Chain	Res	Type
3	2	1486	G
3	2	1491	U
3	2	1493	A
3	2	1496	U
3	2	1506	G
3	2	1514	U
3	2	1516	A
3	2	1517	U
3	2	1518	C
3	2	1521	G
3	2	1523	G
3	2	1524	A
3	2	1528	U
3	2	1530	C
3	2	1531	G
3	2	1535	U
3	2	1537	C
3	2	1538	U
3	2	1540	G
3	2	1543	A
3	2	1557	U
3	2	1558	U
3	2	1559	A
3	2	1570	A
3	2	1572	G
3	2	1573	A
3	2	1574	G
3	2	1575	G
3	2	1576	A
3	2	1577	A
3	2	1583	A
3	2	1584	G
3	2	1590	G
3	2	1601	G
3	2	1611	A
3	2	1614	A
3	2	1616	G
3	2	1622	G
3	2	1631	A
3	2	1634	C
3	2	1635	A
3	2	1637	C

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Mol	Chain	Res	Type
3	2	1657	U
3	2	1658	G
3	2	1663	G
3	2	1665	U
3	2	1680	G
3	2	1681	A
3	2	1687	U
3	2	1688	U
3	2	1689	A
3	2	1701	A
3	2	1707	A
3	2	1708	U
3	2	1711	C
3	2	1712	A
3	2	1715	G
3	2	1716	C
3	2	1717	G
3	2	1742	U
3	2	1744	A
3	2	1746	A
3	2	1747	G
3	2	1755	A
3	2	1756	A
3	2	1757	G
3	2	1760	G
3	2	1766	A
3	2	1767	G
3	2	1769	U
3	2	1771	U
3	2	1780	G
3	2	1782	A
3	2	1783	C
3	2	1791	A
3	2	1792	G
3	2	1793	G
3	2	1794	A
3	2	1795	U
3	2	1796	C
3	2	1798	U
3	2	1799	U
39	sm	6	A
39	sm	7	A

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Mol	Chain	Res	Type
39	sm	8	A
39	sm	11	A
39	sm	12	A
39	sm	13	A
39	sm	23	A
39	sm	24	A
39	sm	25	A
39	sm	26	A
39	sm	28	A
39	sm	29	A
39	sm	30	A
39	sm	31	A
39	sm	32	A
39	sm	33	A
40	sl	5	G
40	sl	13	U
40	sl	17	C
40	sl	18	G
40	sl	19	G
40	sl	20	U
40	sl	25	C
40	sl	28	U
40	sl	30	C
40	sl	41	G
40	sl	46	G
40	sl	47	U
40	sl	48	C
40	sl	59	U
40	sl	60	U
40	sl	61	C
40	sl	73	G
40	sl	74	C
40	sl	75	C
40	sl	76	A
40	sn	5	G
40	sn	9	G
40	sn	10	G
40	sn	13	U
40	sn	16	U
40	sn	17	C
40	sn	18	G
40	sn	19	G

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Mol	Chain	Res	Type
40	sn	20	U
40	sn	23	C
40	sn	28	U
40	sn	40	G
40	sn	44	A
40	sn	45	G
40	sn	46	G
40	sn	47	U
40	sn	48	C
40	sn	60	U
40	sn	76	A
41	LC	42	A
41	LC	53	U
41	LC	54	U
41	LC	55	A
41	LC	65	G
41	LC	73	C
41	LC	76	A
41	LC	95	A
41	LC	102	A
41	LC	112	G
41	LC	121	U
42	LD	34	U
42	LD	35	C
42	LD	38	U
42	LD	48	A
42	LD	59	A
42	LD	62	C
42	LD	63	G
42	LD	80	A
42	LD	81	U
42	LD	82	U
42	LD	83	C
42	LD	85	G
42	LD	86	U
42	LD	87	G
42	LD	90	U
42	LD	95	G
42	LD	104	A
42	LD	106	C
42	LD	111	A
42	LD	113	U

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Mol	Chain	Res	Type
42	LD	125	U
42	LD	126	A
42	LD	138	A
42	LD	148	G
42	LD	151	C
42	LD	152	G
42	LD	158	U

All (78) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	LA	13	A
1	LA	239	G
1	LA	282	G
1	LA	439	C
1	LA	588	G
1	LA	637	C
1	LA	715	A
1	LA	763	G
1	LA	816	A
1	LA	849	C
1	LA	896	A
1	LA	916	G
1	LA	993	G
1	LA	1064	A
1	LA	1097	G
1	LA	1307	G
1	LA	1355	A
1	LA	1554	U
1	LA	1562	C
1	LA	1716	U
1	LA	1815	U
1	LA	1820	U
1	LA	2101	C
1	LA	2112	U
1	LA	2504	U
1	LA	2505	U
1	LA	2525	G
1	LA	2585	G
1	LA	2677	G
1	LA	2801	A
1	LA	2818	U

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Mol	Chain	Res	Type
1	LA	3121	U
1	LA	3218	A
1	LA	3228	C
1	LA	3269	U
1	LA	3316	A
1	LA	3319	U
1	LA	3350	C
1	LA	3375	A
3	2	68	A
3	2	77	U
3	2	139	C
3	2	278	U
3	2	280	U
3	2	352	A
3	2	387	A
3	2	400	A
3	2	539	G
3	2	541	A
3	2	555	A
3	2	609	U
3	2	639	U
3	2	640	U
3	2	705	U
3	2	711	U
3	2	755	A
3	2	819	G
3	2	863	A
3	2	912	U
3	2	928	U
3	2	1023	A
3	2	1216	C
3	2	1226	A
3	2	1245	G
3	2	1256	A
3	2	1273	G
3	2	1274	C
3	2	1344	A
3	2	1382	A
3	2	1430	U
3	2	1471	A
3	2	1534	G
3	2	1573	A

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Mol	Chain	Res	Type
3	2	1633	A
3	2	1636	C
3	2	1791	A
41	LC	52	G
42	LD	85	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 359 ligands modelled in this entry, 358 are monoatomic - leaving 1 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	SPD	LA	3618	-	9,9,9	0.40	0	8,8,8	1.00	0

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	SPD	LA	3618	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	LA	3618	SPD	N6-C7-C8-C9
86	LA	3618	SPD	C3-C4-C5-N6
86	LA	3618	SPD	C2-C3-C4-C5
86	LA	3618	SPD	C4-C5-N6-C7
86	LA	3618	SPD	C8-C7-N6-C5

There are no ring outliers.

No monomer is involved in short contacts.

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.

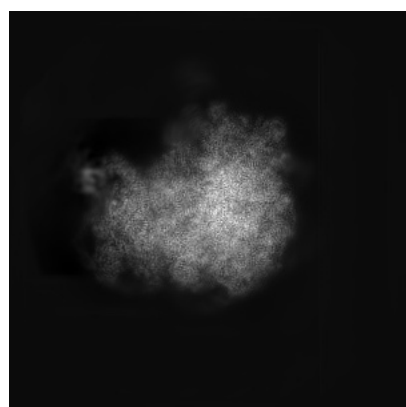
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14990. These allow visual inspection of the internal detail of the map and identification of artifacts.

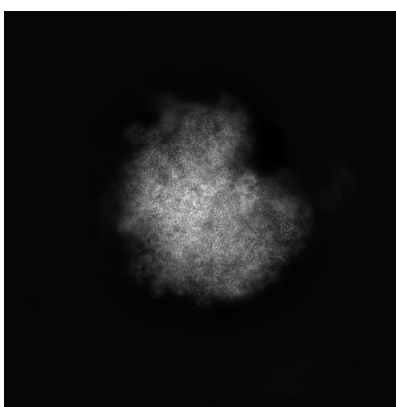
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

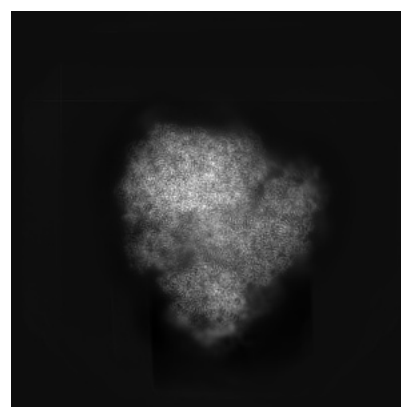
6.1.1 Primary map



X



Y

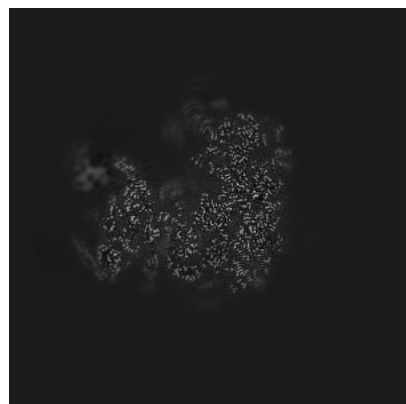


Z

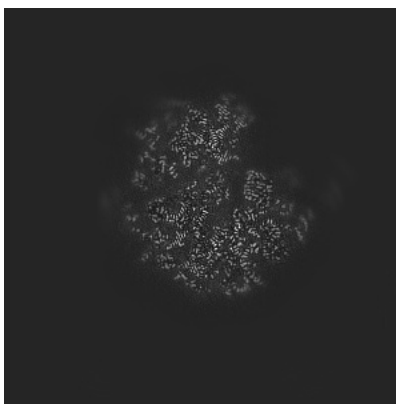
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

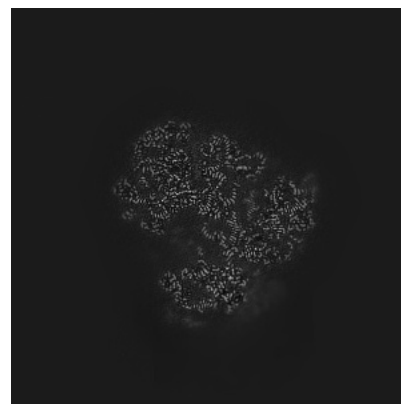
6.2.1 Primary map



X Index: 240



Y Index: 240

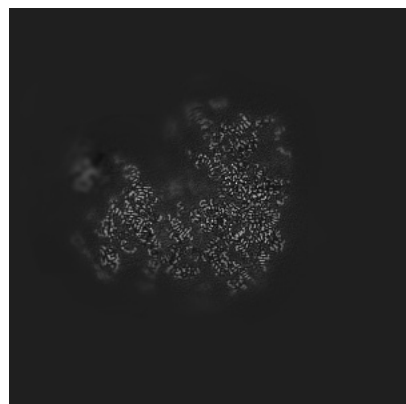


Z Index: 240

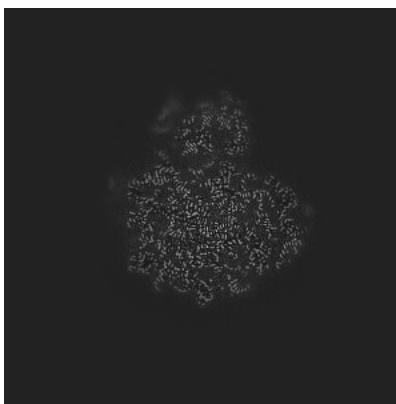
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 236



Y Index: 260

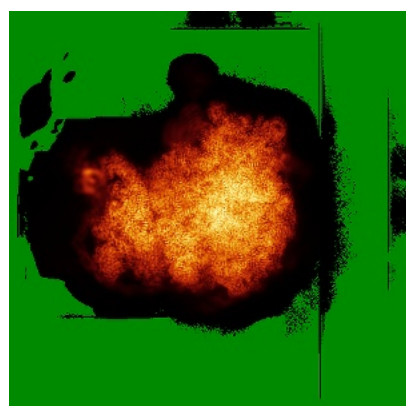


Z Index: 253

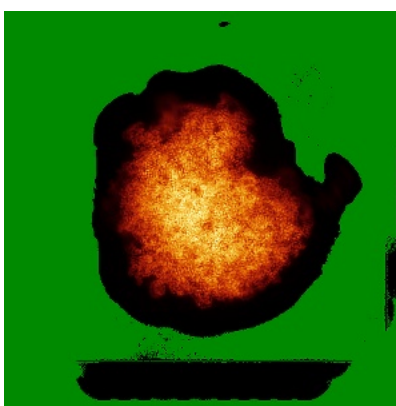
The images above show the largest variance slices of the map in three orthogonal directions.

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

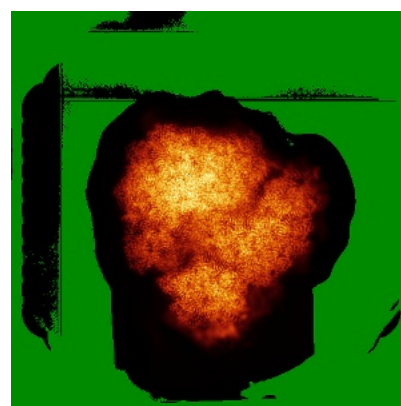
6.4.1 Primary map



X



Y

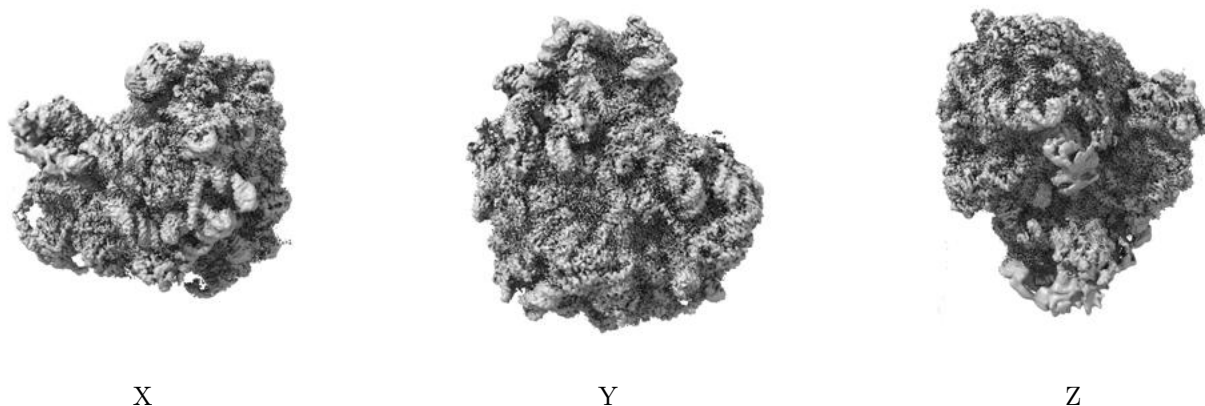


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

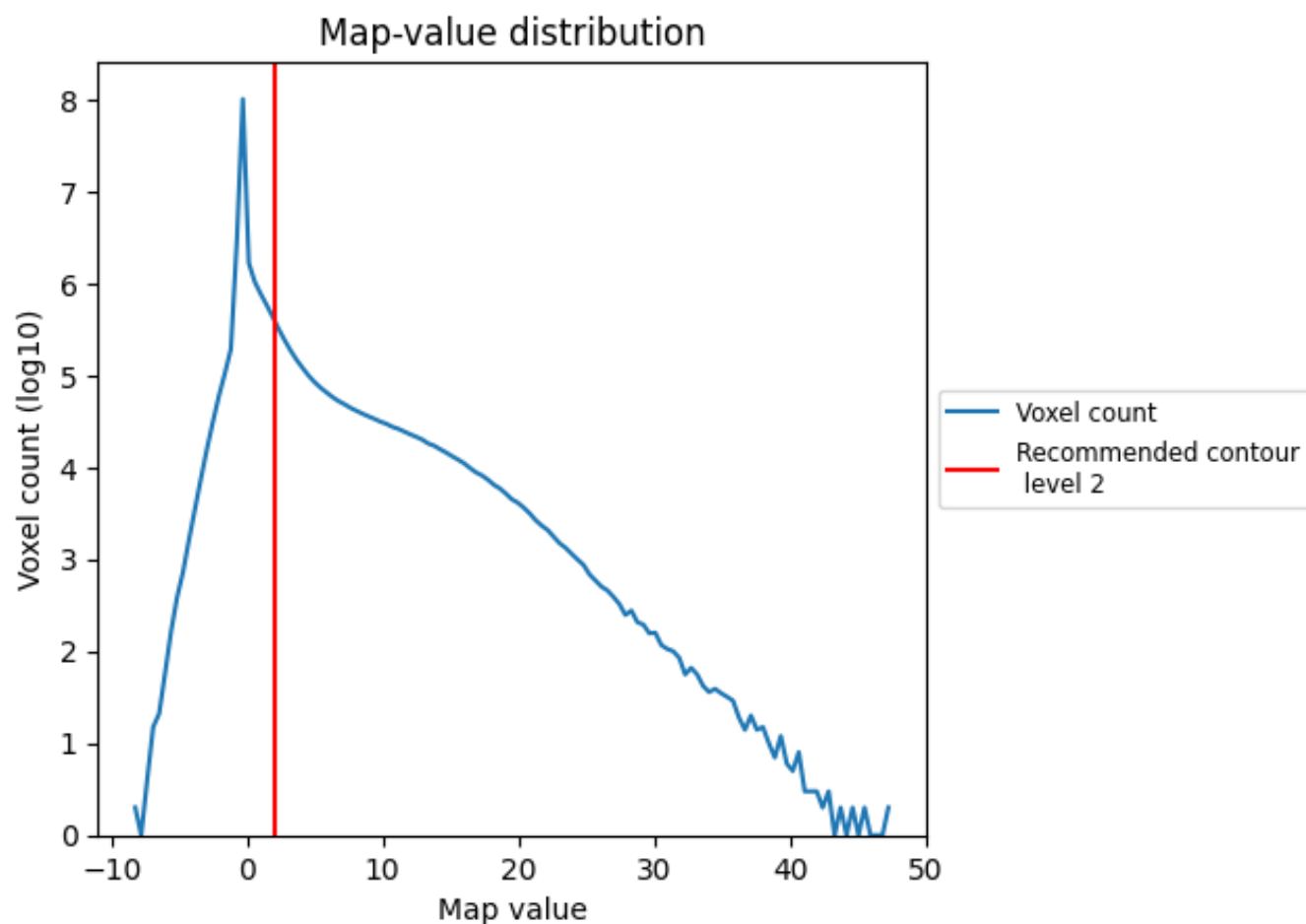
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

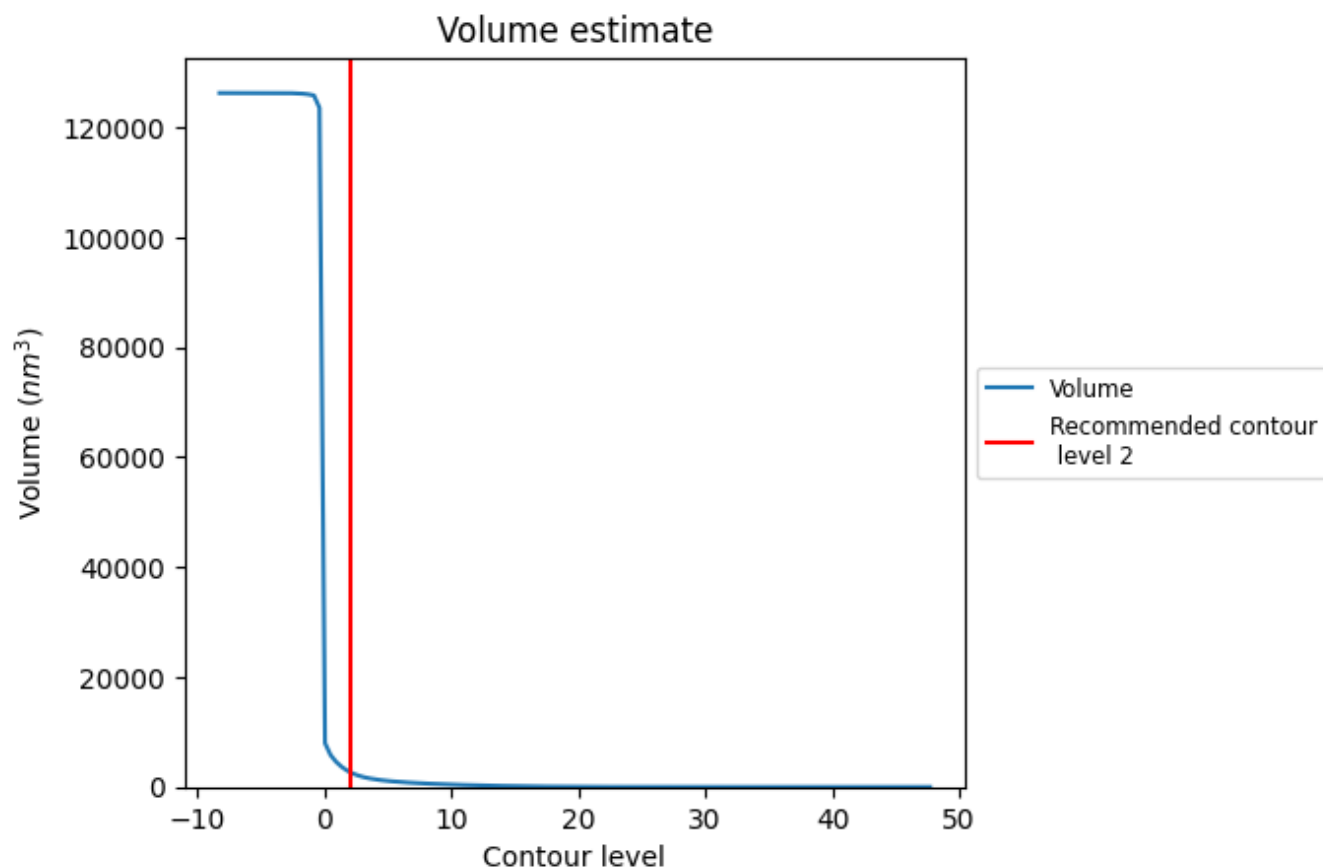
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

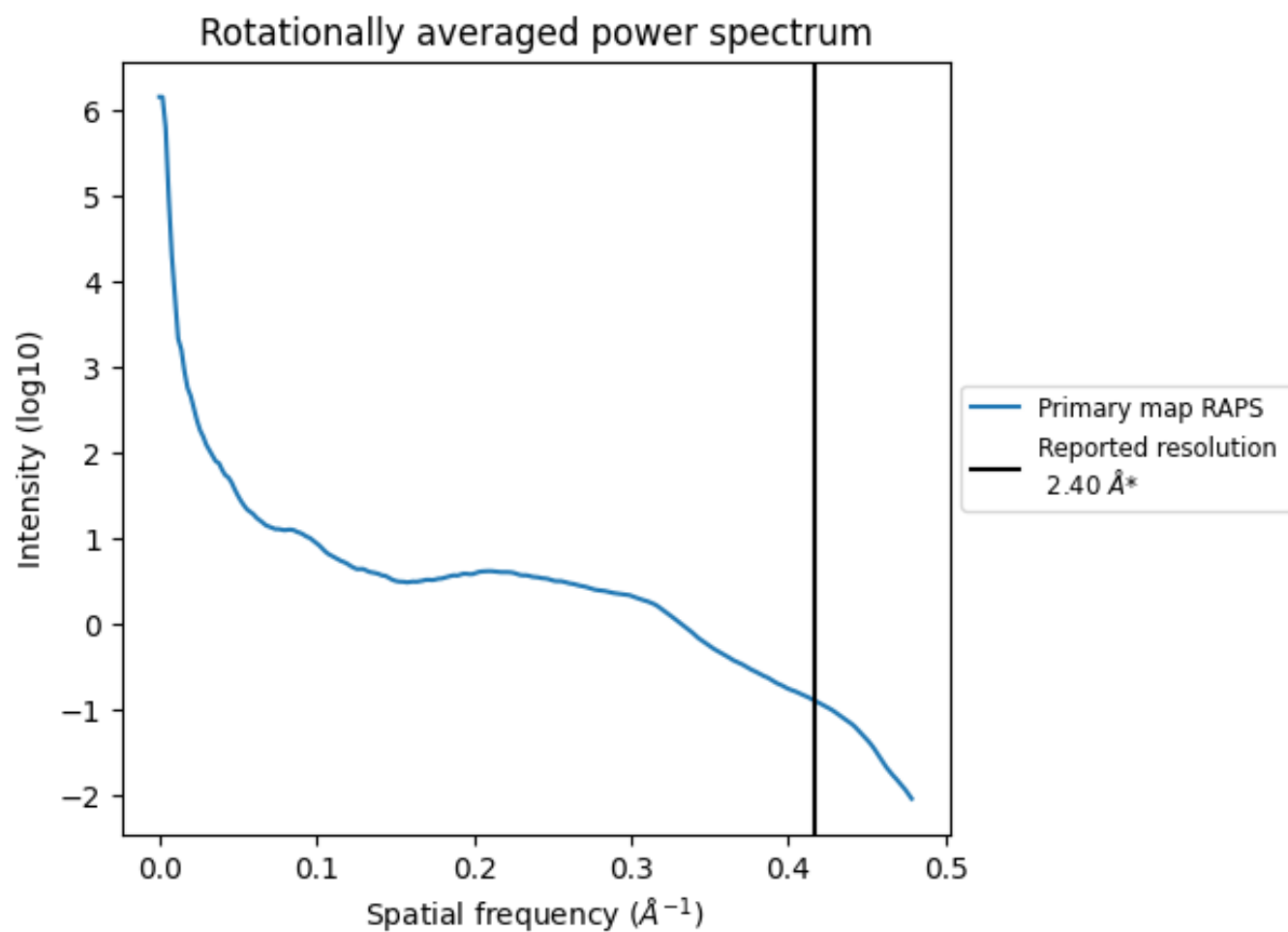
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2756 nm^3 ; this corresponds to an approximate mass of 2490 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 0.417 Å⁻¹

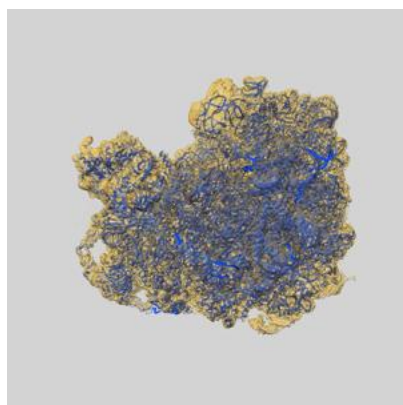
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

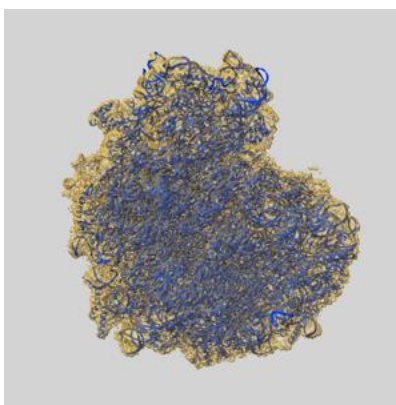
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14990 and PDB model 7ZW0. Per-residue inclusion information can be found in section 3 on page 21.

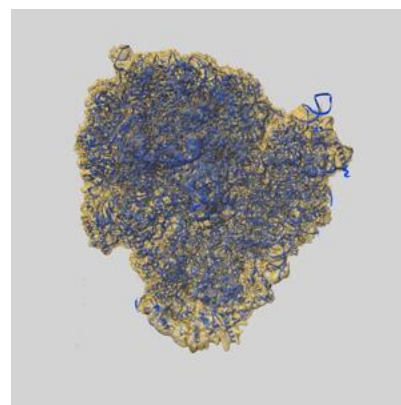
9.1 Map-model overlay [i](#)



X



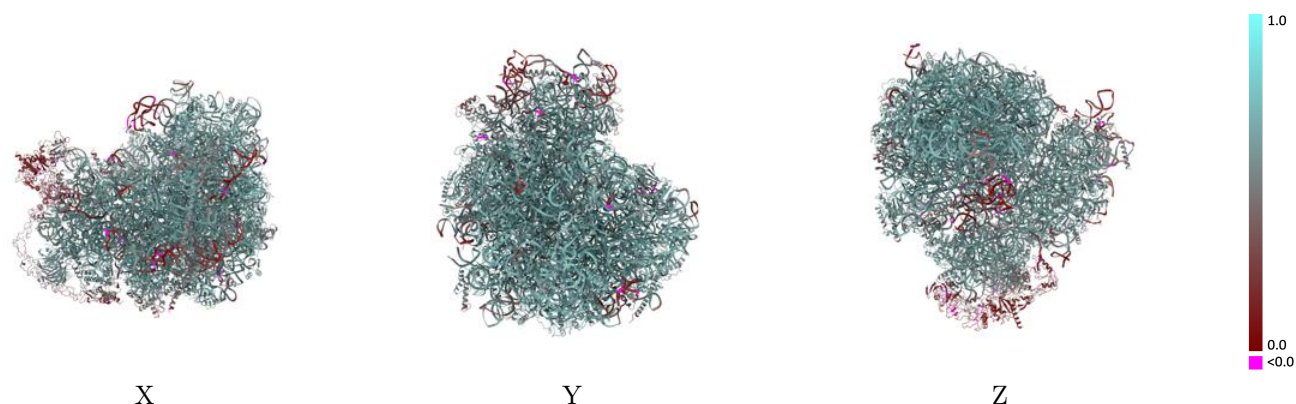
Y



Z

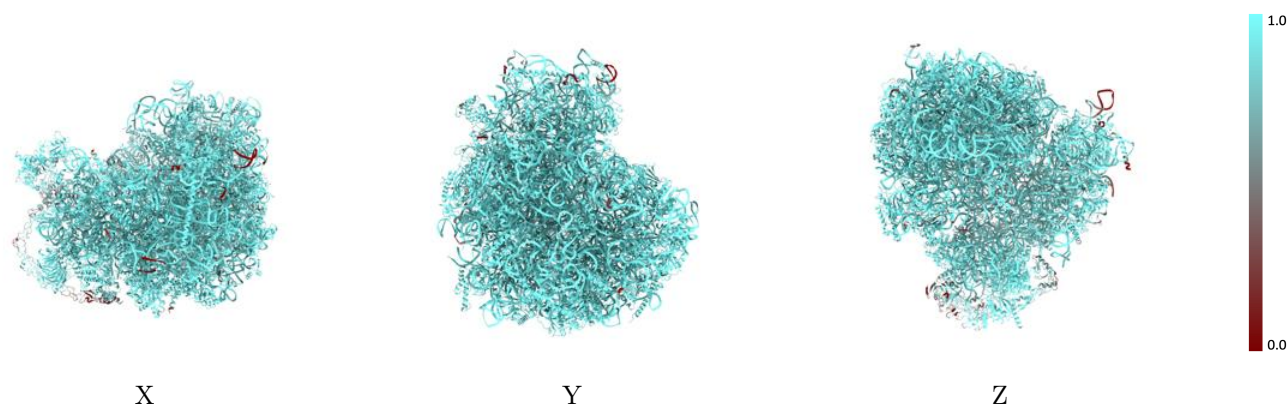
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



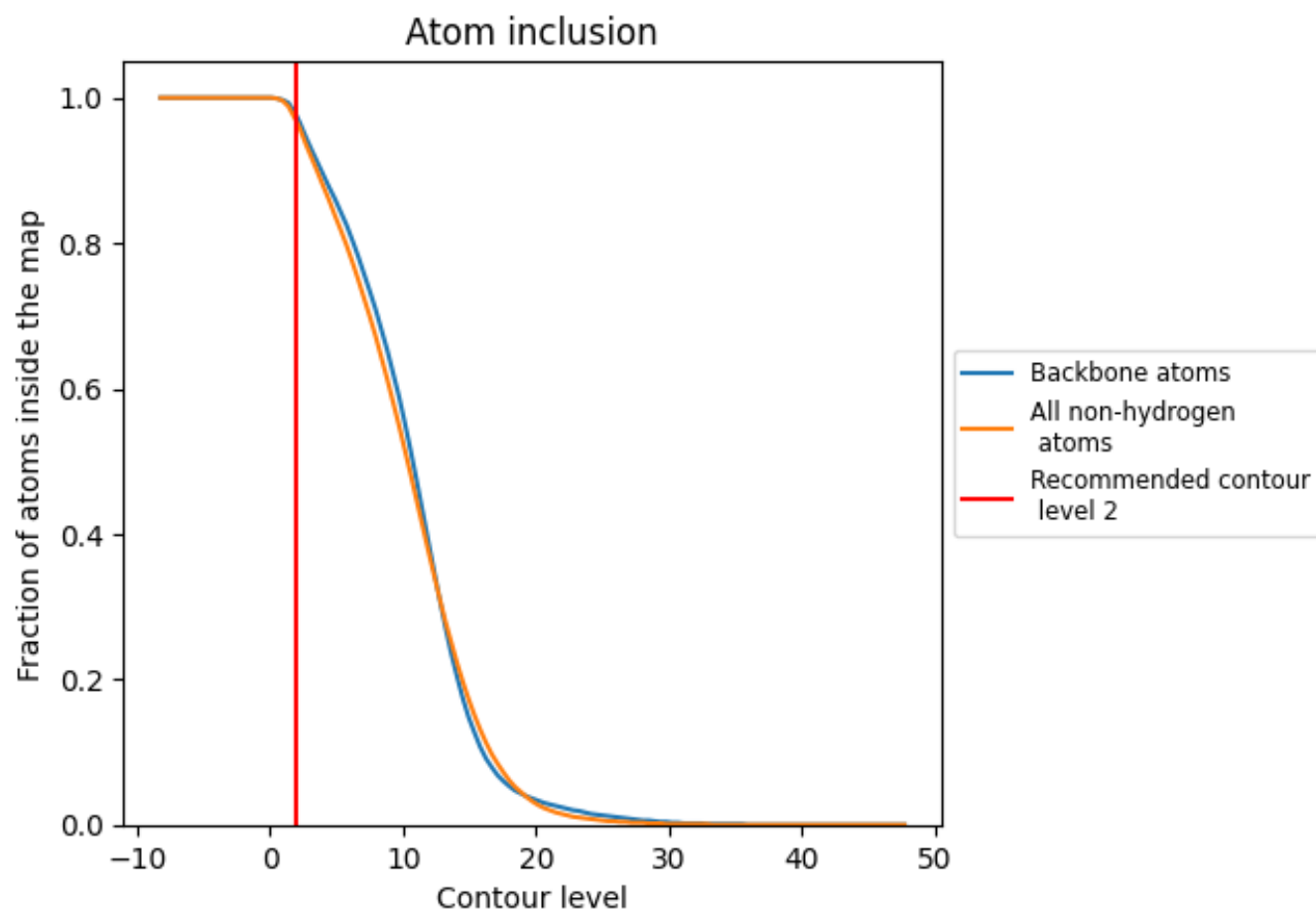
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9670	 0.6030
2	 0.9700	 0.6030
LA	 0.9870	 0.6360
LB	 0.4740	 0.1140
LC	 0.9980	 0.6570
LD	 0.9950	 0.6700
LE	 0.9940	 0.6940
LF	 0.9890	 0.6680
LG	 0.9870	 0.6630
LH	 0.9650	 0.5970
LI	 0.9780	 0.6140
LJ	 0.9870	 0.6590
LK	 0.9700	 0.6010
LL	 0.9870	 0.6360
LM	 0.9850	 0.6560
LN	 0.9740	 0.5860
LO	 0.9760	 0.6420
LP	 0.9830	 0.6480
LQ	 0.9990	 0.7010
LR	 0.9890	 0.6830
LS	 0.9850	 0.6810
LT	 0.9890	 0.6700
LU	 0.9600	 0.5990
LV	 0.9910	 0.6790
LW	 0.9880	 0.6430
LX	 0.9670	 0.5570
LY	 0.9890	 0.6700
LZ	 0.9140	 0.5770
La	 0.9890	 0.6660
Lb	 0.9890	 0.6460
Lc	 0.9870	 0.6280
Ld	 0.9870	 0.6840
Le	 0.9740	 0.6170
Lf	 0.9950	 0.6300
Lg	 0.9590	 0.6270



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Chain	Atom inclusion	Q-score
Lh	 0.9980	 0.7010
Li	 0.9960	 0.7090
Lj	 0.9910	 0.6620
Lk	 0.9880	 0.6450
Ll	 0.9800	 0.6170
Lm	 0.9980	 0.7120
Ln	 0.9570	 0.5920
Lo	 0.9950	 0.6940
Lp	 0.9850	 0.6650
Lq	 1.0000	 0.6730
Lr	 0.9830	 0.6600
Ls	 0.9960	 0.6740
Lt	 0.8460	 0.5180
sA	 0.9850	 0.5740
sB	 0.9940	 0.6390
sC	 0.9860	 0.5550
sD	 0.9670	 0.3550
sE	 0.9840	 0.5990
sF	 0.9950	 0.6590
sG	 0.9720	 0.5770
sH	 0.9890	 0.6200
sI	 0.9820	 0.6300
sJ	 0.9800	 0.5640
sK	 0.9870	 0.5950
sL	 0.9890	 0.6140
sM	 0.9980	 0.6630
sN	 0.9360	 0.3470
sO	 0.9850	 0.5620
sP	 0.9860	 0.5990
sQ	 0.9930	 0.6270
sR	 0.9930	 0.6500
sS	 0.9940	 0.6240
sT	 0.9730	 0.5500
sU	 0.9460	 0.5260
sV	 0.9900	 0.6220
sW	 0.9710	 0.5680
sX	 0.9780	 0.6410
sY	 0.9910	 0.6320
sZ	 0.9910	 0.6410
sa	 0.9890	 0.6260
sb	 0.9930	 0.6760
sc	 0.9900	 0.6810

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Chain	Atom inclusion	Q-score
sd	 0.9650	 0.5890
se	 0.9930	 0.6690
sf	 0.9750	 0.6210
sg	 0.9890	 0.5770
sh	 0.6700	 0.2320
sj	 0.9450	 0.1420
sk	 0.5530	 0.1880
sl	 0.9240	 0.2800
sm	 0.9810	 0.3350
sn	 0.9900	 0.5100