



Full wwPDB EM Validation Report ⓘ

Dec 8, 2025 – 02:09 PM JST

PDB ID : 9KZU / pdb_00009kzu
EMDB ID : EMD-62671
Title : Cryo-EM structure of the HCV IRES-dependently initiated CMV-stalled 80S ribosome (non-rotated state) in complexed with eIF3
Authors : Iwasaki, W.; Kashiwagi, K.; Sakamoto, A.; Nishimoto, M.; Takahashi, M.; Machida, K.; Imataka, H.; Matsumoto, A.; Shichino, Y.; Iwasaki, S.; Imami, K.; Ito, T.
Deposited on : 2024-12-11
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.47

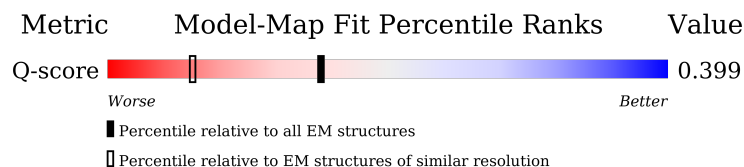
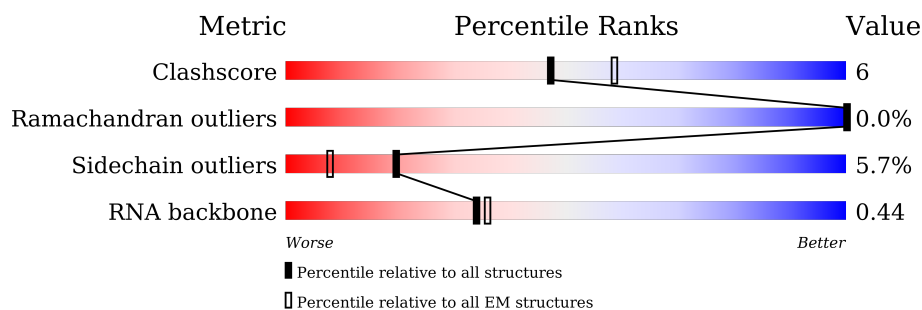
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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




























Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L5	5070	
2	L7	120	
3	L8	156	


























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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

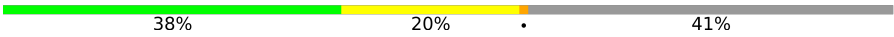









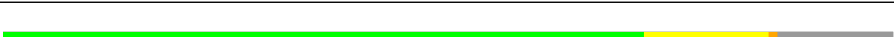


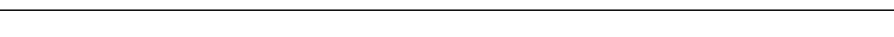
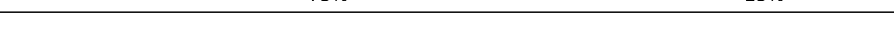
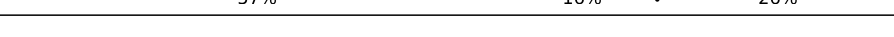



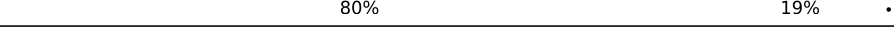





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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1869	
47	SA	295	
48	SB	264	
49	SD	243	
50	SE	263	
51	SF	204	
52	SH	194	
53	SI	208	


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Mol	Chain	Length	Quality of chain
54	SK	165	
55	SL	158	
56	SP	145	
57	SQ	146	
58	SR	135	
59	SS	152	
60	ST	145	
61	SU	119	
62	SV	83	
63	SX	143	
64	Sa	115	
65	Sc	69	
66	Sd	56	
67	Sg	317	
68	SC	293	
69	SG	249	
70	SJ	194	
71	Sf	132	
72	SN	151	
73	SO	151	
74	SW	130	
75	SY	133	
76	SZ	125	
77	Sb	84	
78	Se	59	

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Mol	Chain	Length	Quality of chain
79	sh	156	
80	zv	19	
81	zx	31	
82	zy	75	
83	zz	332	
84	3m	374	
85	3f	357	
86	3a	1382	
87	3e	445	
88	3c	913	
89	3h	352	
90	3d	548	
91	3k	218	
92	3l	564	

2 Entry composition

There are 94 unique types of molecules in this entry. The entry contains 245916 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3663	Total	C	N	O	P	0	0
			78531	34970	14374	25525	3662		

- Molecule 2 is a RNA chain called 5S_ribosomal_RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S_ribosomal_RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	399	Total	C	N	O	S	0	0
			3220	2050	605	551	14		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	366	Total	C	N	O	S	0	0
			2914	1832	581	487	14		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	226	Total	C	N	O	S	0	0
			1818	1169	345	300	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			1866	1200	358	299	9		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	239	Total	C	N	O	S	0	0
			1914	1220	369	321	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1510	952	282	270	6		

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

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

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

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

- Molecule 22 is a protein called 60S ribosomal protein L21.

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

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

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

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	119	Total	C	N	O	S	0	0
			976	625	184	166	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	112	Total	C	N	O	S	0	0
			886	554	181	145	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1741	Total	C	N	O	P	0	0
			36887	16454	6590	12103	1740		

- Molecule 47 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 50 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SF	189	Total	C	N	O	S	0	0
			1483	926	282	268	7		

- Molecule 52 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	186	Total	C	N	O	S	0	0
			1494	953	273	267	1		

- Molecule 53 is a protein called 40S ribosomal protein S8.

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

- Molecule 54 is a protein called 40S ribosomal protein S10.

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

- Molecule 55 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SL	142	Total	C	N	O	S	0	0
			1162	740	218	198	6		

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SP	128	Total	C	N	O	S	0	0
			1050	666	198	179	7		

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 58 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SR	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 59 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 60 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 61 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SU	103	Total	C	N	O	S	0	0
			817	511	155	147	4		

- Molecule 62 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 63 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 64 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Sa	100	Total	C	N	O	S	0	0
			803	501	166	131	5		

- Molecule 65 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Sc	64	Total	C	N	O	S	0	0
			500	305	99	94	2		

- Molecule 66 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 67 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SC	217	Total	C	N	O	S	0	0
			1683	1090	288	295	10		

- Molecule 69 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SG	236	Total	C	N	O	S	0	0
			1915	1194	386	328	7		

- Molecule 70 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 71 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Sf	122	Total	C	N	O	S	0	0
			933	584	163	177	9		

- Molecule 72 is a protein called 40S ribosomal protein S13.

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

- Molecule 73 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SO	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 74 is a protein called 40S ribosomal protein S15a.

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

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 76 is a protein called 40S ribosomal protein S25.

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

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	sh	63	Total	C	N	O	S	0	0
			515	324	98	86	7		

- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	zv	13	Total	C	N	O	P	0	0
			267	120	42	92	13		

- Molecule 81 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	zx	21	Total	C	N	O	S	0	0
			160	107	25	27	1		

- Molecule 82 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	zy	75	Total	C	N	O	P	0	0
			1599	713	284	528	74		

- Molecule 83 is a RNA chain called HCV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	zz	210	Total	C	N	O	P	0	0
			4481	1995	796	1480	210		

- Molecule 84 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	3m	363	Total	C	N	O	S	0	0
			2639	1666	450	511	12		

- Molecule 85 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	3f	269	Total	C	N	O	S	0	0
			2063	1303	354	394	12		

- Molecule 86 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	3a	592	Total	C	N	O	S	0	0
			4497	2849	805	822	21		

- Molecule 87 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	3e	429	Total	C	N	O	S	0	0
			3218	2050	560	592	16		

- Molecule 88 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	3c	652	Total	C	N	O	S	0	0
			4822	3030	881	885	26		

- Molecule 89 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	3h	315	Total	C	N	O	S	0	0
			2499	1585	427	472	15		

- Molecule 90 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	3d	55	Total	C	N	O	S	0	0
			347	222	65	59	1		

- Molecule 91 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	3k	215	Total	C	N	O	S	0	0
			1475	932	251	282	10		

- Molecule 92 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	3l	520	Total	C	N	O	S	0	0
			4335	2808	715	793	19		

- Molecule 93 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
93	L5	70	Total	Mg	0
			70	70	
93	L8	1	Total	Mg	0
			1	1	
93	S2	10	Total	Mg	0
			10	10	

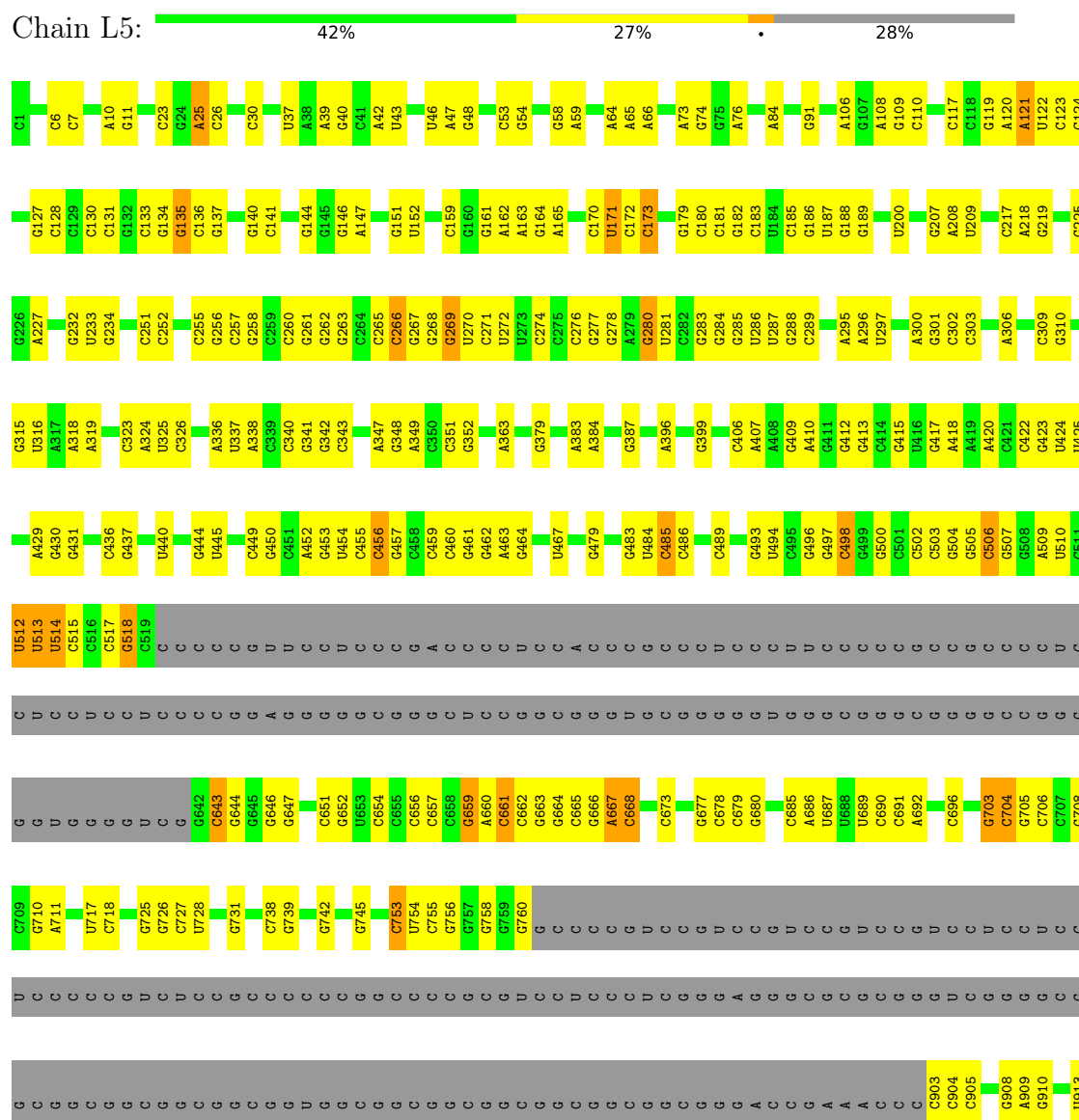
- Molecule 94 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
94	Lg	1	Total	Zn	0
			1	1	
94	Lj	1	Total	Zn	0
			1	1	
94	Lm	1	Total	Zn	0
			1	1	
94	Lo	1	Total	Zn	0
			1	1	
94	Lp	1	Total	Zn	0
			1	1	
94	Sa	1	Total	Zn	0
			1	1	
94	sh	1	Total	Zn	0
			1	1	

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: 28S ribosomal RNA





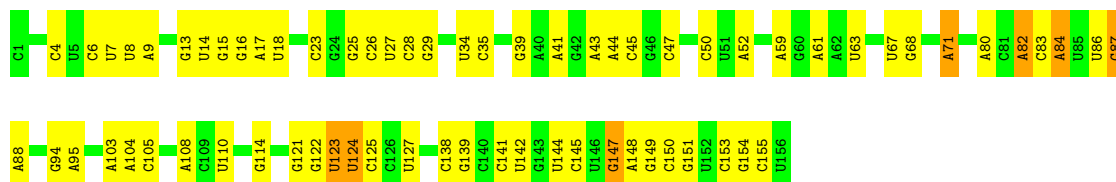


U4981	U4985	U4988	C	G4761	U4685	C4582	U4493	U4353	A4251	C4140	U	C9931	U3932	U3851
U4989	U4991	G4889	G	A4762	G4686	A4583	G4494	U4354	C4252	G4140	A	C	U3932	C3855
U4992	U4993	G4891	G	U4763	A4687	A4584	G4495	U4355	C4253	G4141	C	C	G3933	A3856
U4994	U4995	U4888	C	A4764	C4688	U4585	A4496	C4365	G4254	C4142	C	C	U3934	
U4996	U4997	A4893	G	G4765	U4689	G4586			A4255	A4143	C	C	C3937	A3861
U4998	U4999	U4890	G		G4690	A4589	G4499	G4377	U4256	C4144	U4060	C	G3938	A3862
U5000	U5001	A4691	G		A4691	A4590	U4500	A4378	A4257	C4145	A4061	C	G3939	
U5002	U5003	U4770	A	U4770	A4591	A4591	U4501	A4379	C4258		A4062	G		A3867
U5004	U5005	C4771	G	C4771	C4592	A4592	A4507	A4380	U4259	G4151	U4063	A		A3868
U5006	U5007	C4772	G	C4772	C4593	A4593	A4508	A4381	U4260		C4064	G	G3944	C3869
U5008	U5009	C4773	G	C4773	U4594	A4594	U4509	C4387	C4261	C4160	C4065	G	G3945	C3870
U5010	U5011	U4699	G	C4774	G4595	A4510	A4510	A4388	C4262	G4161	U4066	G	G3946	A3871
U5012	U5013	A4700	G	C4775	A4599	A4511	A4511	A4389	G4264	U4163	U4068	C	C3947	A3872
U5014	U5015	C4704	C		G4600	A4512	A4512	A4390			U4069	C	A3949	G3873
U5016	U5017	A4705	G		U4601	A4513	A4513	A4391	A4273	G4168	U4070	C	U3950	G3874
U5018	U5019	G4706	U			C4514	C4514	A4392	A4274	G4169	U4071	G	A3951	A3877
U5020	U5021	A4707	C		G4617	A4518		G4393	G4275	A4170	C4072	G	A3952	C3878
U5022	U5023	U4708	C		C4621	A4523	A4523	U4394	A4280	G4173		G	A3877	C3879
U5024	U5025	U4709	C		A4622	C4524	U4532	U4395	A4281	A4178		G	U3953	G3880
U5026	U5027	C4712	C				U4533	U4396	A4282		C4080	G		G3881
U5028	U5029	C4713	C		A4626	G4528	C4530	A4397		G4179	G4081	G		
U5030	U5031	A4717	G		U4627	U4628	U4531	G4405	G4287	G4183		G		G3885
U5032	U5033	C4719	C		U4629	U4630	U4532	U4420	G4288		G4084	U		G3888
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U5036	U5037	A4723	C			U4637	U4534	A4422	U4299	G4185	G4086	C	A	A3890
U5038	U5039	U4724	C		A4635	U4638	C4537	A4430	U4300	G4187	G4087	C	C	A3891
U5040	U5041	A4730	G		U4636	U4639	C4538	G4433	U4301	U4189	G4088	C	U	U3892
U5042	U5043	C4731	C		U4637	U4640	G4543	G4434	G4305	U4190	G4095	C	A	C3893
U5044	U5045	C4732	C		U4638	U4641	G4544	C4444	U4306	G4191	G4096	G	A	A3894
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U5050	U5051	C4735	C		A4648	U4643	U4556	A4449	C4314	A4203	C4103	U	G	A3901
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U5068	U5069	C4746	C		U4657	U4652	U4567	U4465	C4330	A4234	U4112	C	C	U3912
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U5124	U5125	C4774	C		U4708	U4680	C4596		U4369					
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U5128	U5129	C4776	C		C4710	U4682	C4598		U4371					
U5130	U5131	C4777	C		A4711	U4683	C4599		U4372					
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U5156	U5157	C4790	C		U4724	U4696	C4612		U4385					
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U5160	U5161	C4792	C		U4726	U4698	C4614		U4387					
U5162	U5163	C4793	C		U4727	U4699	C4615		U4388					
U5164	U5165	C4794	C		U4728	U4700	C4616		U4389					
U5166	U5167	C4795	C		U4729	U4701	C4617		U4390					
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U5170	U5171	C4797	C		U4731	U4703	C4619		U4392					
U5172	U5173	C4798	C		U4732	U4704	C4620		U4393					
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U5192	U5193	C4808	C		U4742	U4714	C4630		U4403					
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U5196	U													



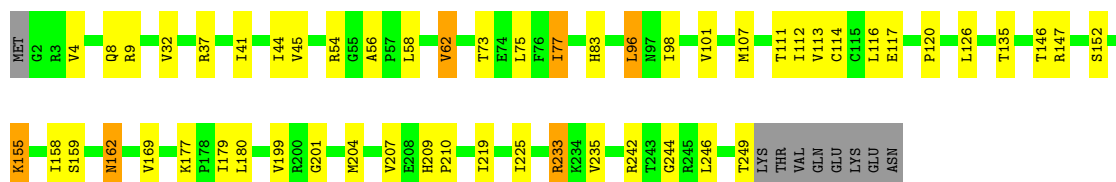
• Molecule 3: 5.8S_ribosomal_RNA

Chain L8: 56% 39% .



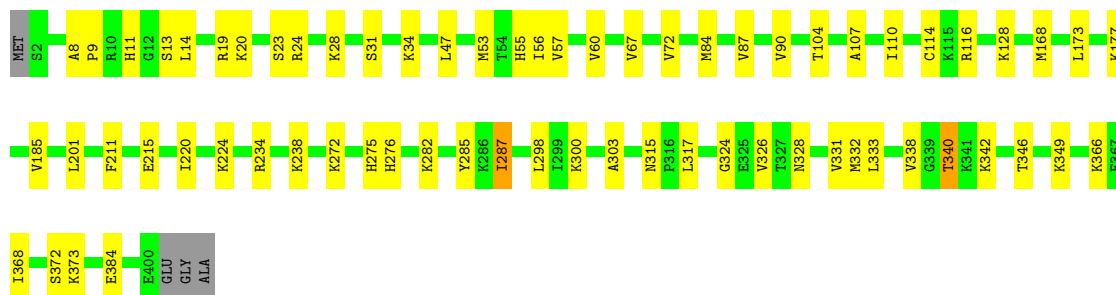
• Molecule 4: 60S ribosomal protein L8

Chain LA: 75% 19% . .



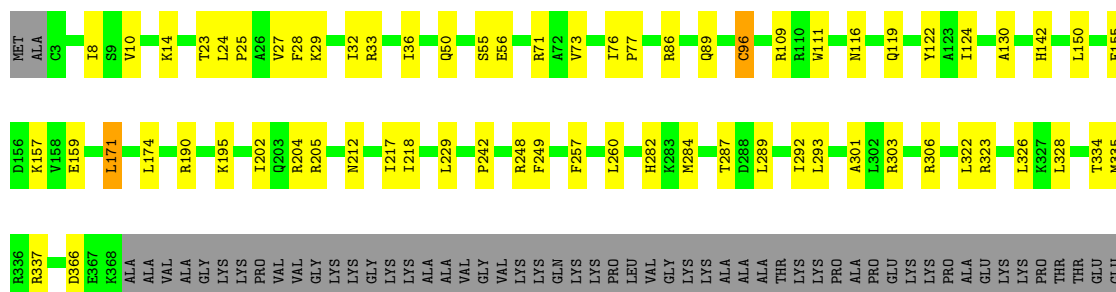
• Molecule 5: 60S ribosomal protein L3

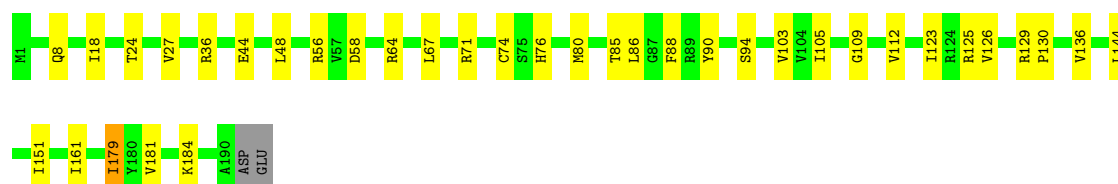
Chain LB: 82% 16% .



• Molecule 6: 60S ribosomal protein L4

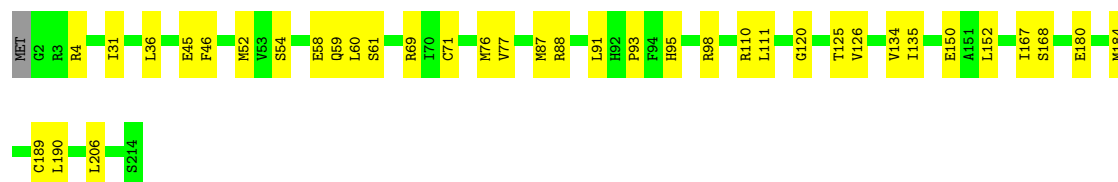
Chain LC: 70% 15% 14%





- Molecule 12: 60S ribosomal protein L10-like

Chain LI: 82% 17%



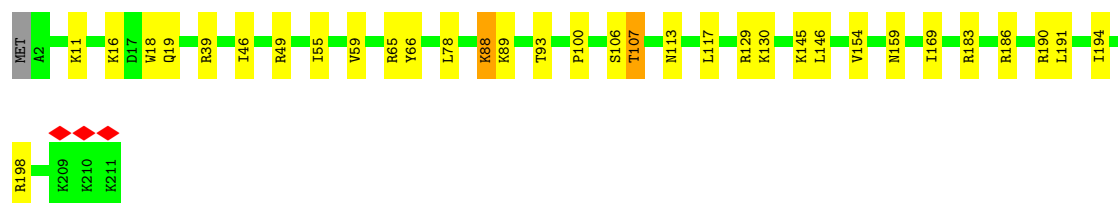
- Molecule 13: 60S ribosomal protein L11

Chain LJ: 84% 14% ..



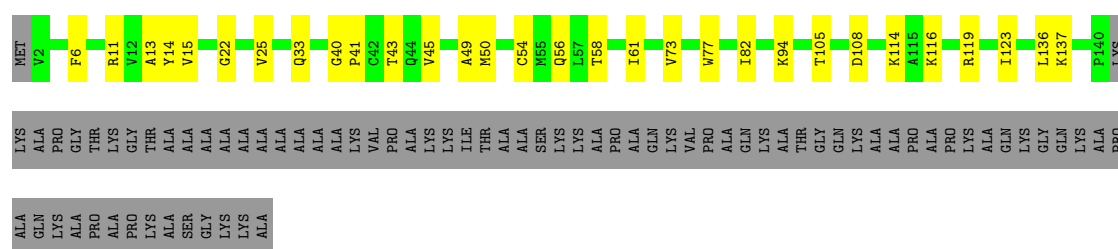
- Molecule 14: 60S ribosomal protein L13

Chain LL: 84% 15% .



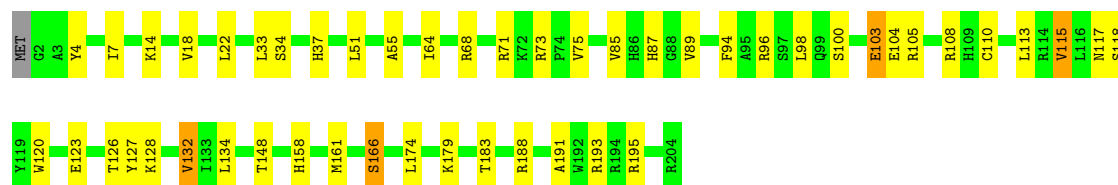
- Molecule 15: 60S ribosomal protein L14

Chain LM: 51% 14% 35%



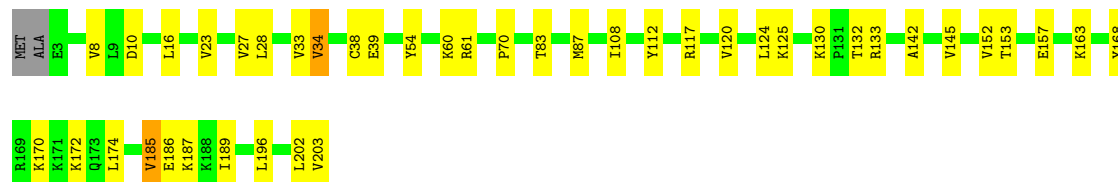
- Molecule 16: 60S ribosomal protein L15

Chain LN: 75% 22% .



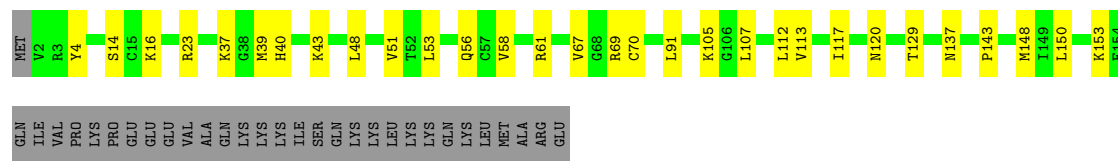
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 78% 20% ..



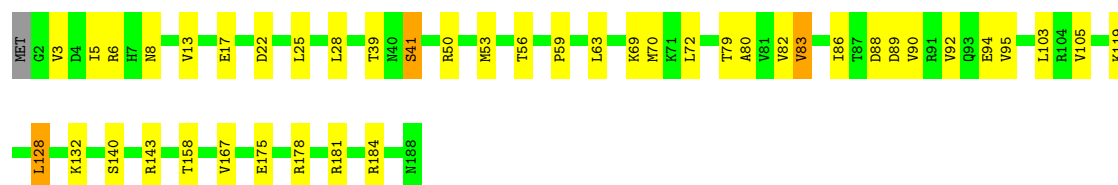
- Molecule 18: 60S ribosomal protein L17

Chain LP: 67% 16% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ: 77% 21% ..



- Molecule 20: 60S ribosomal protein L19

Chain LR: 83% 11% 5%



- Molecule 21: 60S ribosomal protein L18a

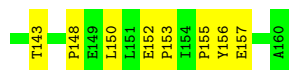
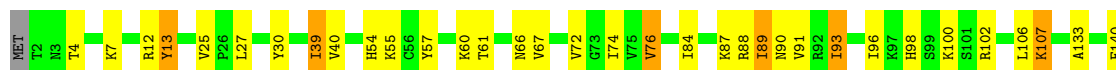
Chain LS: 72% 27% ..





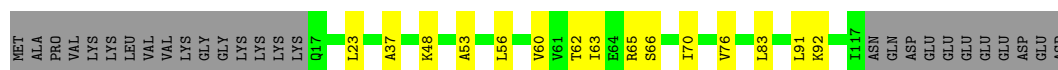
- Molecule 22: 60S ribosomal protein L21

Chain LT: 73% 22%



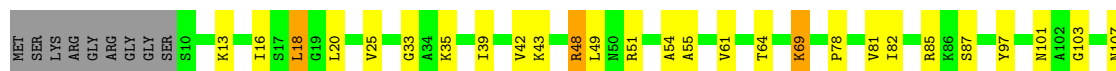
- Molecule 23: 60S ribosomal protein L22

Chain LU: 67% 12% 21%



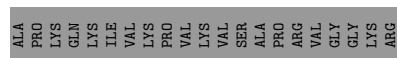
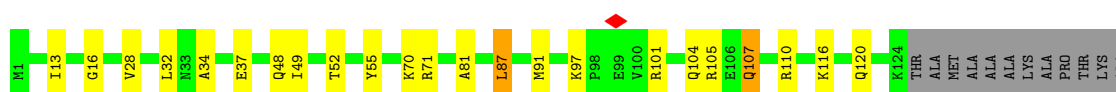
- Molecule 24: 60S ribosomal protein L23

Chain LV: 72% 19% 6%



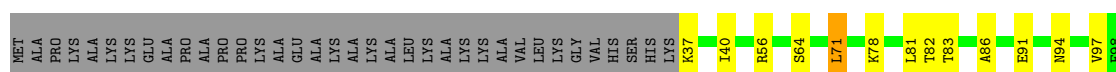
- Molecule 25: 60S ribosomal protein L24

Chain LW: 64% 13% 21%



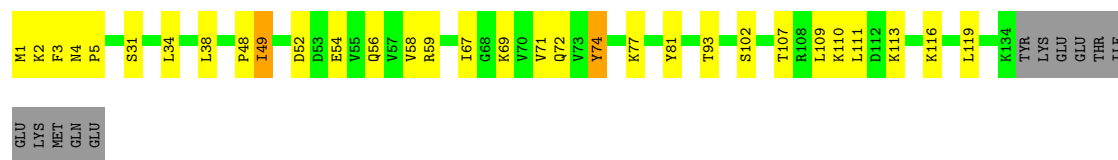
- Molecule 26: 60S ribosomal protein L23a

Chain LX: 60% 14% 24%




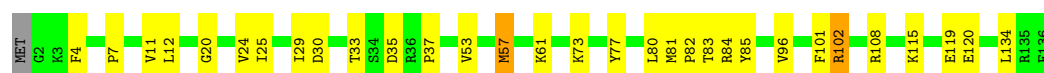
- Molecule 27: 60S ribosomal protein L26

Chain LY:  71% 20% 8%



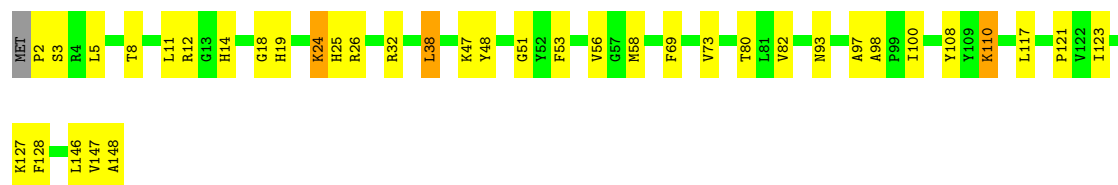
- Molecule 28: 60S ribosomal protein L27

Chain LZ:  76% 21% ..



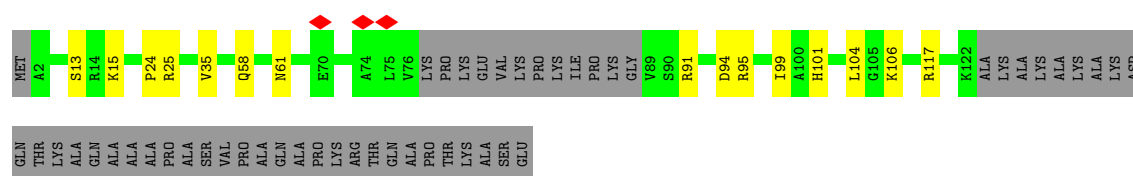
- Molecule 29: 60S ribosomal protein L27a

Chain La:  74% 24% ..



- Molecule 30: 60S ribosomal protein L29

Chain Lb:  59% 9% 31%



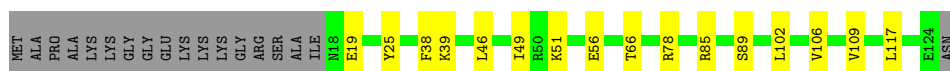
- Molecule 31: 60S ribosomal protein L30

Chain Lc:  53% 29% 15%



- Molecule 32: 60S ribosomal protein L31

Chain Ld:  73% 13% 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le: 81% 13% 5%



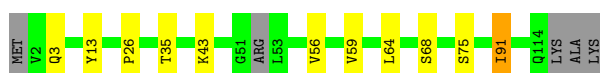
- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 85% 14% ..



- Molecule 35: 60S ribosomal protein L34

Chain Lg: 86% 9% ..



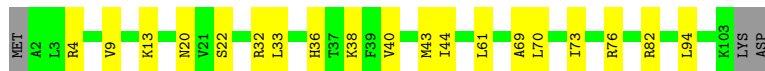
- Molecule 36: 60S ribosomal protein L35

Chain Lh: 85% 13% ..



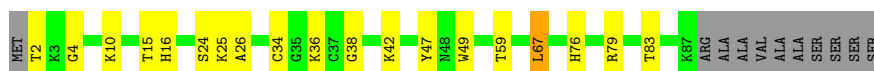
- Molecule 37: 60S ribosomal protein L36

Chain Li: 79% 18% .



- Molecule 38: 60S ribosomal protein L37

Chain Lj: 69% 19% . 11%

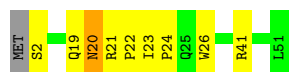
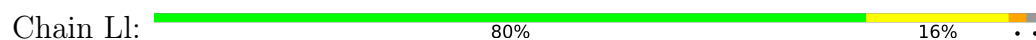


- Molecule 39: 60S ribosomal protein L38

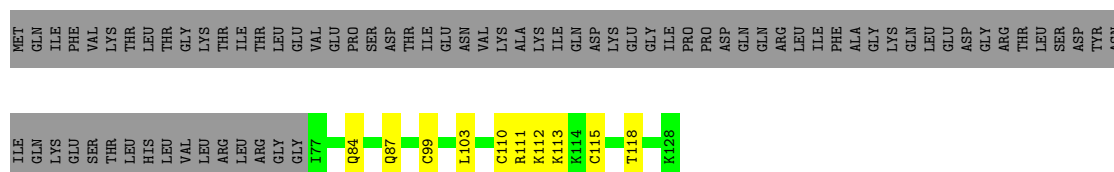
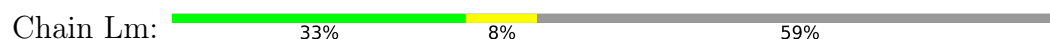
Chain Lk: 77% 17% ..



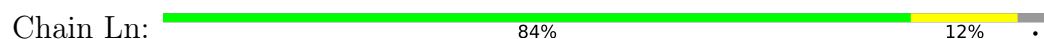
- Molecule 40: 60S ribosomal protein L39



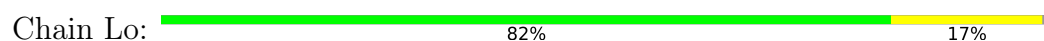
- Molecule 41: Ubiquitin-60S ribosomal protein L40



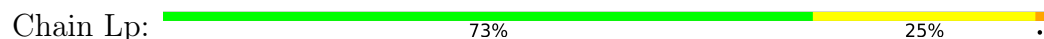
- Molecule 42: 60S ribosomal protein L41



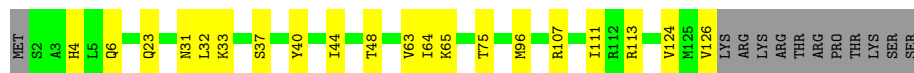
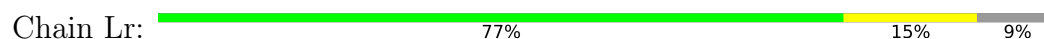
- Molecule 43: 60S ribosomal protein L36a



- Molecule 44: 60S ribosomal protein L37a




- Molecule 45: 60S ribosomal protein L28

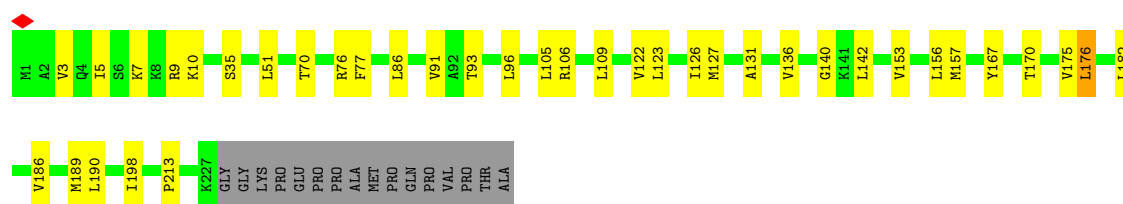


- Molecule 46: 18S ribosomal RNA


Response	Percentage
Yes	49%
No	37%
Don't know	7%
Refuse to answer	7%

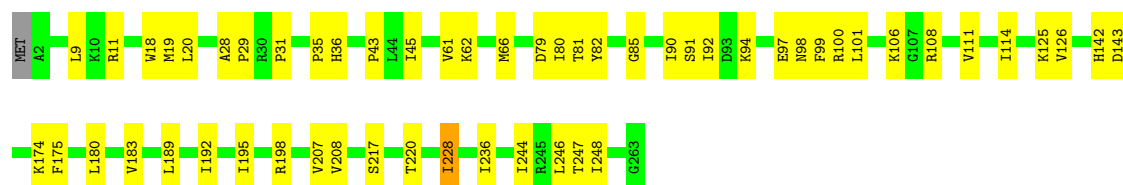


Chain SD:  78% 15% 7%



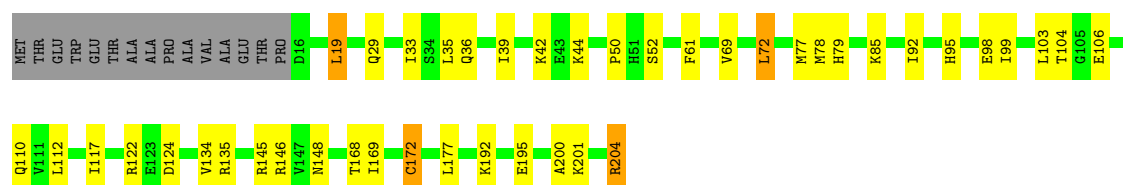
- Molecule 50: 40S ribosomal protein S4, X isoform

Chain SE:  79% 21%




- Molecule 51: 40S ribosomal protein S5

Chain SF:  72% 19% 7%



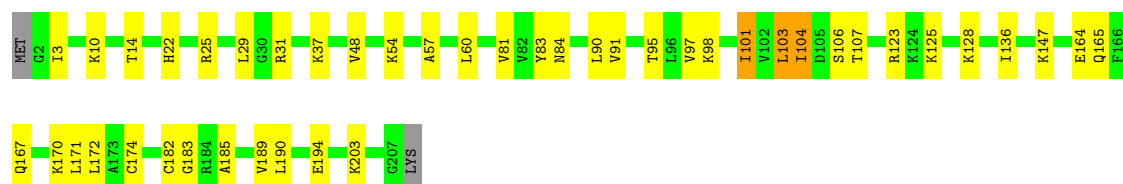
- Molecule 52: 40S ribosomal protein S7

Chain SH:  76% 20%

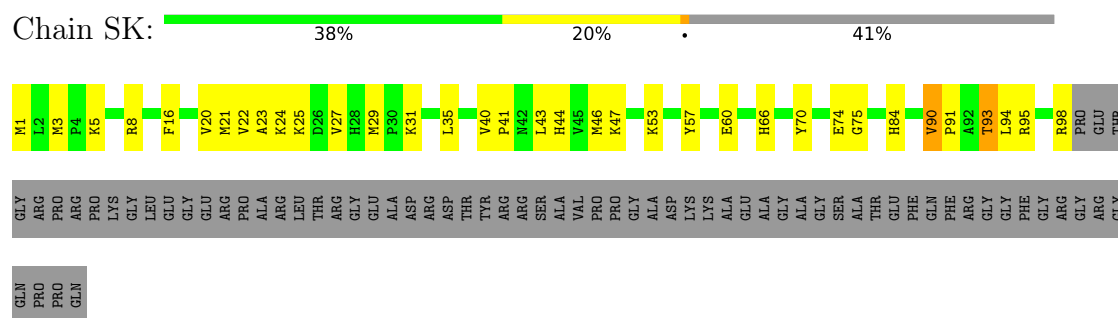


- Molecule 53: 40S ribosomal protein S8

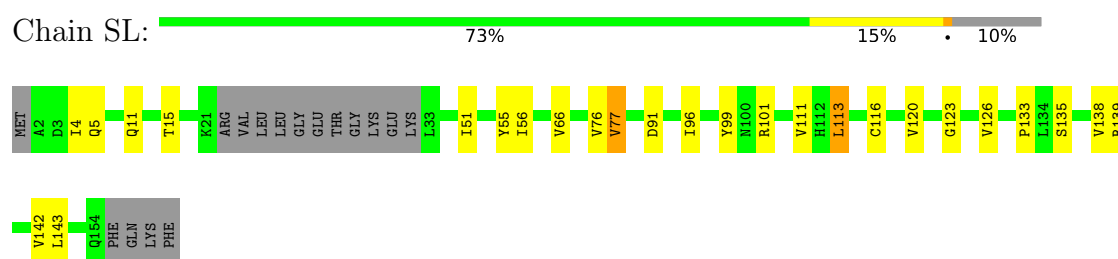
Chain SI:  78% 20%



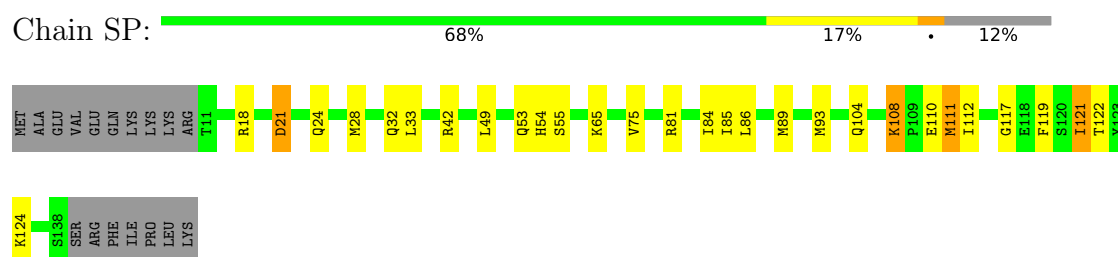
- Molecule 54: 40S ribosomal protein S10



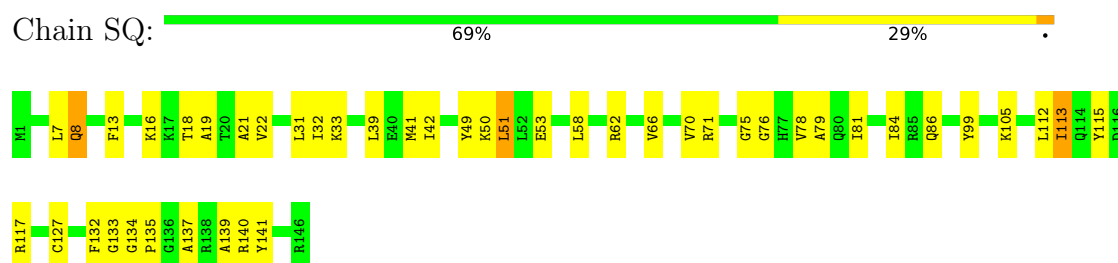
- Molecule 55: 40S ribosomal protein S11



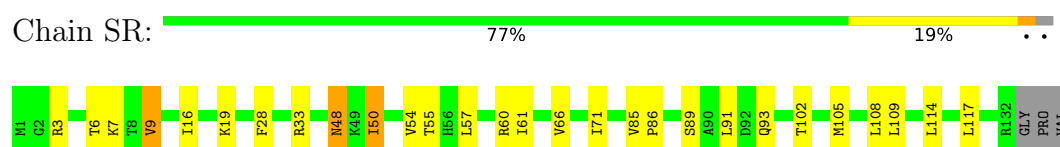
- Molecule 56: 40S ribosomal protein S15



- Molecule 57: 40S ribosomal protein S16




- Molecule 58: 40S ribosomal protein S17



• Molecule 59: 40S ribosomal protein S18

Chain SS:  74% 20% 5%


• Molecule 60: 40S ribosomal protein S19

Chain ST:  83% 14% ..


• Molecule 61: 40S ribosomal protein S20

Chain SU:  68% 18% 13%

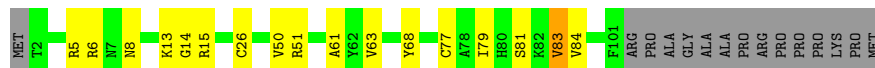
• Molecule 62: 40S ribosomal protein S21

Chain SV:  76% 24%

• Molecule 63: 40S ribosomal protein S23

Chain SX:  81% 17% ..


• Molecule 64: 40S ribosomal protein S26

Chain Sa:  72% 14% 13%

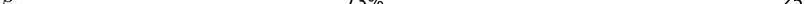
• Molecule 65: 40S ribosomal protein S28

Chain Sc:  72% 19% 7%

- Molecule 66: 40S ribosomal protein S29

Chain Sd:  86% 9% 5%

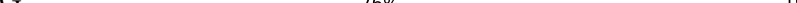
- Molecule 67: Receptor of activated protein C kinase 1

Chain Sg:  73% 25% ..

- Molecule 68: 40S ribosomal protein S2

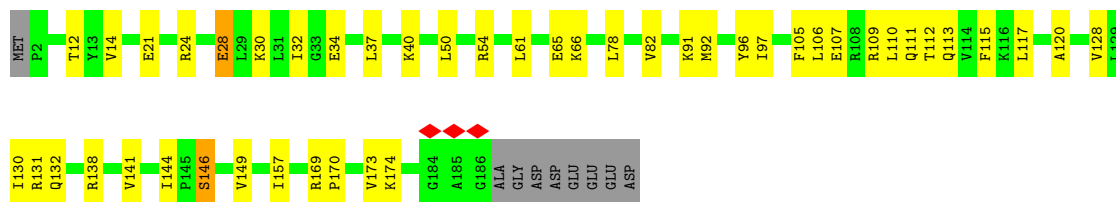
Chain SC:  57% 16% 26%

- Molecule 69: 40S ribosomal protein S6

Chain SG:  76% 19% 5%

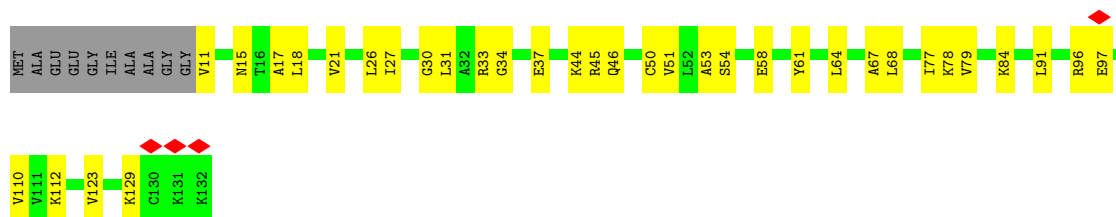
- Molecule 70: 40S ribosomal protein S9

Chain SJ:  72% 23% 5%




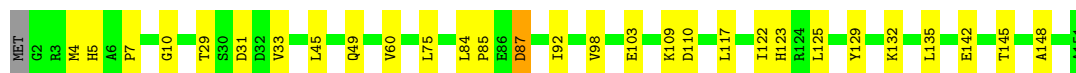
- Molecule 71: 40S ribosomal protein S12

Chain Sf:  66% 27% 8%



- Molecule 72: 40S ribosomal protein S13

Chain SN:  80% 19% ..




- Molecule 73: 40S ribosomal protein S14

Chain SO:  68% 19% 11%




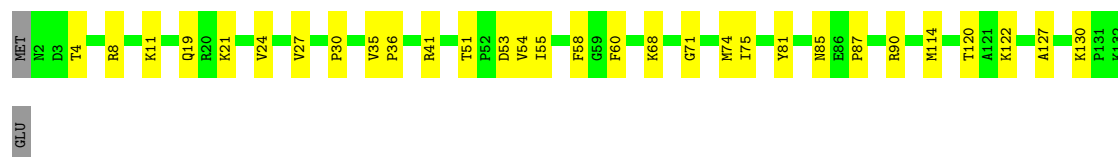
- Molecule 74: 40S ribosomal protein S15a

Chain SW:  76% 21% ..

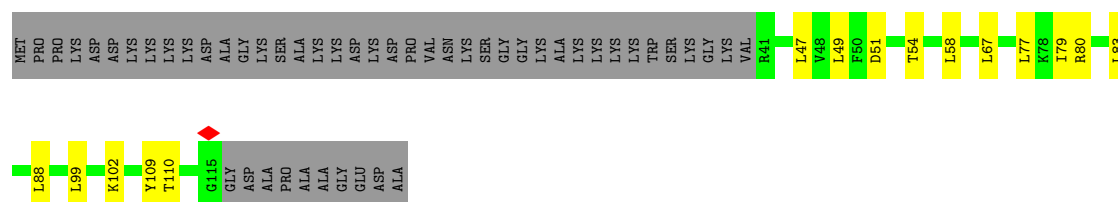


- Molecule 75: 40S ribosomal protein S24

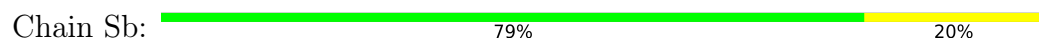
Chain SY:  76% 23% .



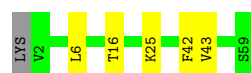
- Molecule 76: 40S ribosomal protein S25



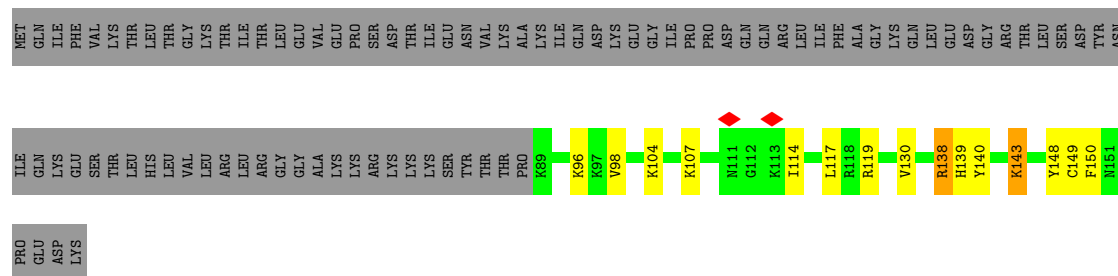
- Molecule 77: 40S ribosomal protein S27



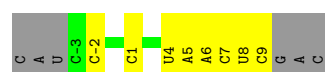
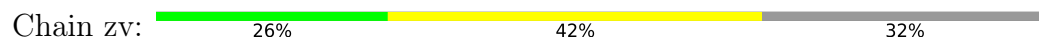
- Molecule 78: 40S ribosomal protein S30



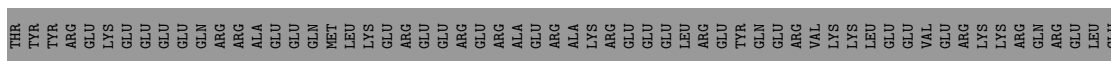
- Molecule 79: Ubiquitin-40S ribosomal protein S27a



- Molecule 80: mRNA

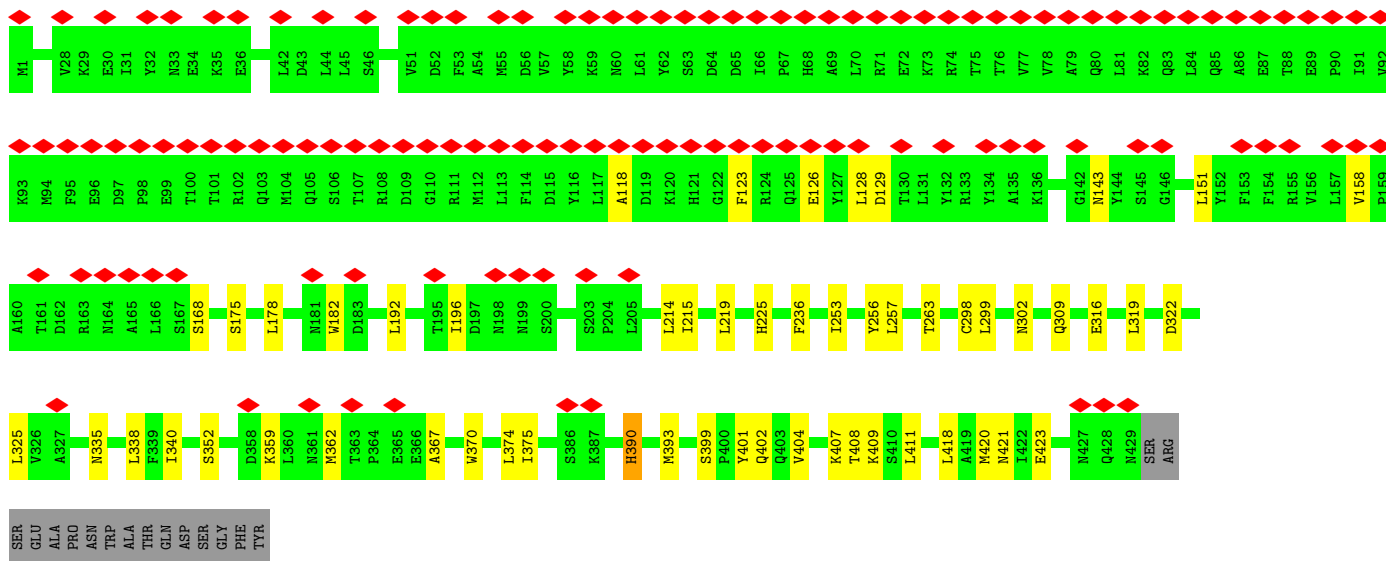
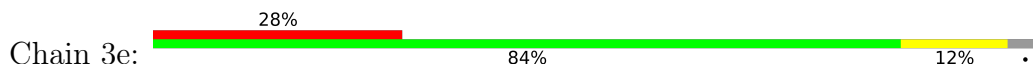


- | Year | Number of Publications |
|------|------------------------|
| 2023 | 239 |
| 2024 | 242 |
| 2025 | 243 |
| 2026 | 244 |
| 2027 | 245 |
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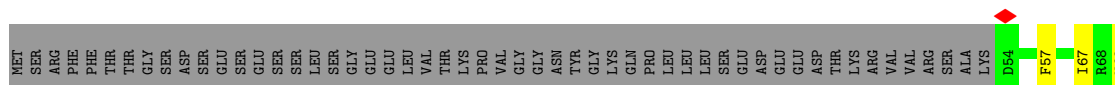


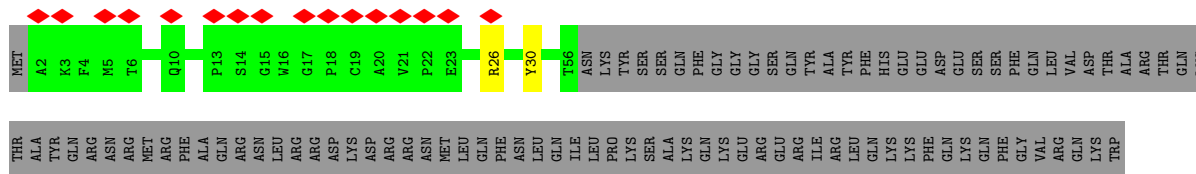
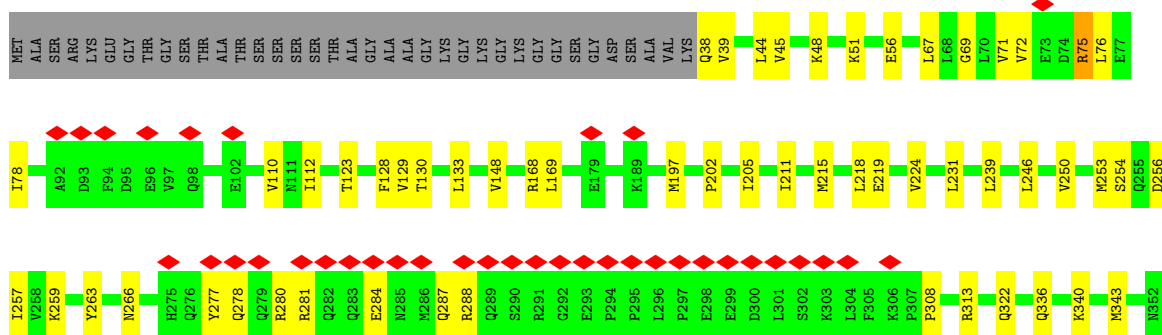
[illegible]

- Molecule 87: Eukaryotic translation initiation factor 3 subunit E



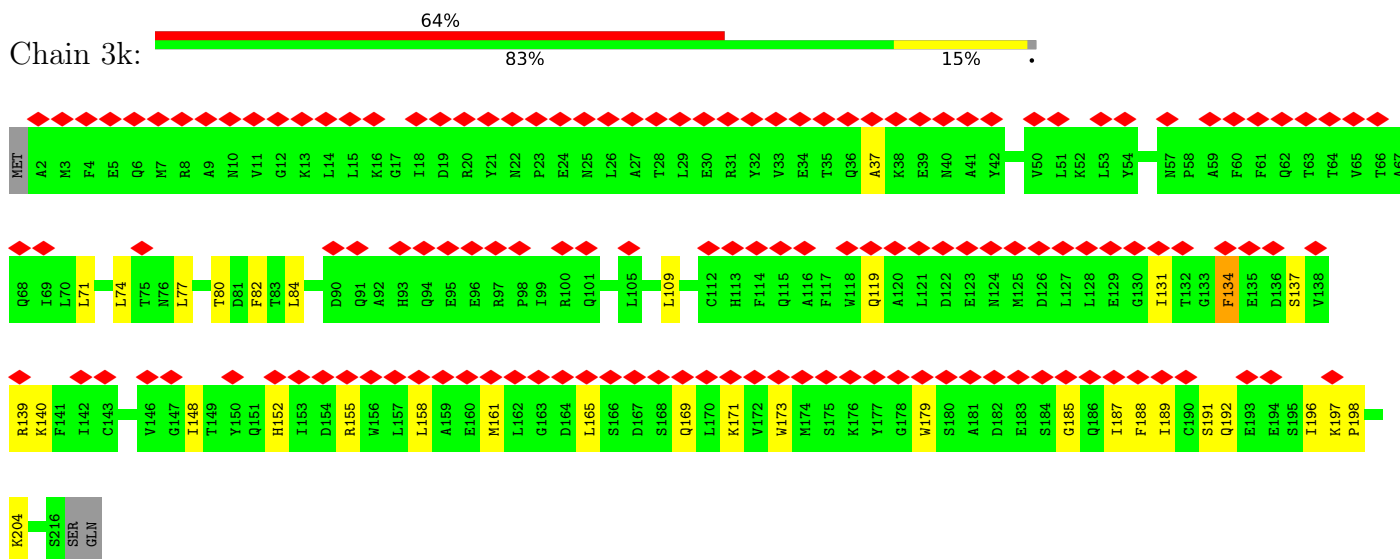
- Molecule 88: Eukaryotic translation initiation factor 3 subunit C



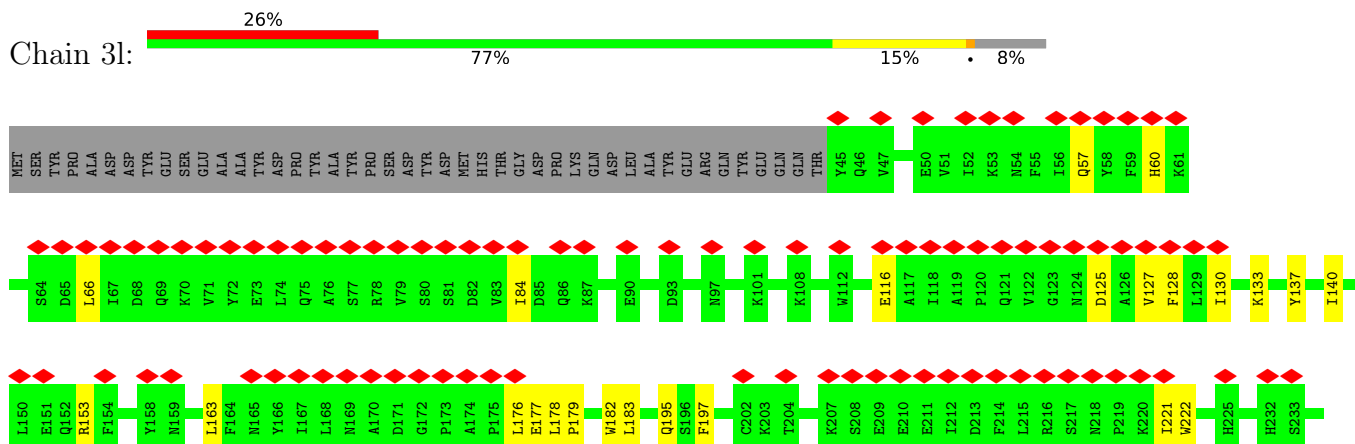


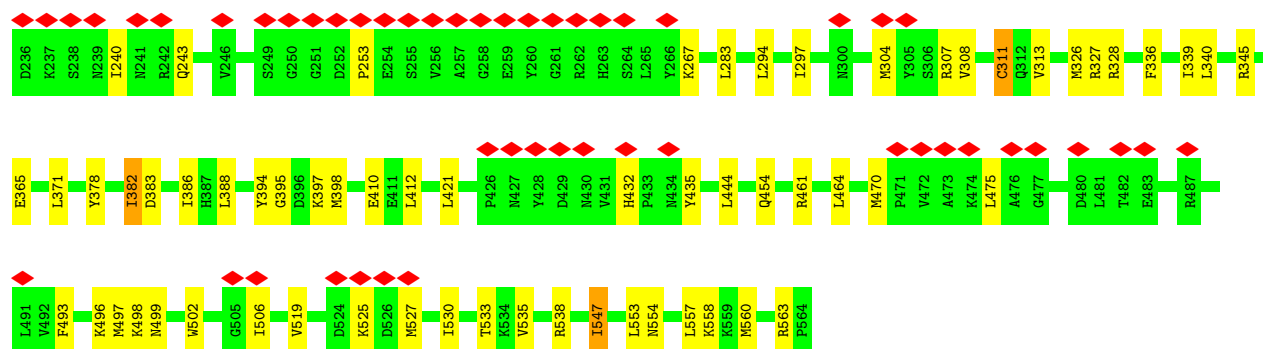
[illegible]

- Molecule 91: Eukaryotic translation initiation factor 3 subunit K



- Molecule 92: Eukaryotic translation initiation factor 3 subunit L





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63366	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.174	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (\AA)	742.0, 742.0, 742.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.484, 1.484, 1.484	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, 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	L5	0.26	0/87848	0.34	0/137041
2	L7	0.24	0/2858	0.30	0/4455
3	L8	0.26	0/3701	0.34	0/5766
4	LA	0.29	0/1936	0.49	0/2596
5	LB	0.25	0/3288	0.42	0/4400
6	LC	0.27	0/2968	0.49	0/3985
7	LD	0.21	0/2428	0.42	0/3252
8	LE	0.24	0/1852	0.52	1/2484 (0.0%)
9	LF	0.27	0/1901	0.43	0/2534
10	LG	0.23	0/1947	0.46	0/2621
11	LH	0.24	0/1529	0.48	0/2056
12	LI	0.26	0/1751	0.50	0/2340
13	LJ	0.20	0/1433	0.42	0/1915
14	LL	0.22	0/1732	0.39	0/2315
15	LM	0.21	0/1161	0.38	0/1554
16	LN	0.30	0/1746	0.46	0/2338
17	LO	0.27	0/1682	0.41	0/2250
18	LP	0.28	0/1268	0.50	0/1701
19	LQ	0.27	0/1537	0.50	1/2052 (0.0%)
20	LR	0.23	0/1582	0.45	0/2091
21	LS	0.28	0/1493	0.50	0/2003
22	LT	0.26	0/1326	0.46	0/1770
23	LU	0.26	0/839	0.67	2/1126 (0.2%)
24	LV	0.27	0/993	0.56	1/1332 (0.1%)
25	LW	0.23	0/1030	0.48	0/1364
26	LX	0.25	0/992	0.53	0/1330
27	LY	0.24	0/1132	0.45	0/1504
28	LZ	0.24	0/1130	0.49	1/1507 (0.1%)
29	La	0.28	0/1191	0.45	0/1591
30	Lb	0.21	0/889	0.41	0/1175
31	Lc	0.26	0/774	0.48	0/1038
32	Ld	0.24	0/903	0.44	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.25	0/1071	0.42	0/1429
34	Lf	0.28	0/895	0.48	0/1198
35	Lg	0.25	0/895	0.41	0/1192
36	Lh	0.23	0/1023	0.47	0/1351
37	Li	0.20	0/843	0.41	0/1115
38	Lj	0.27	0/720	0.47	0/952
39	Lk	0.24	0/575	0.56	0/761
40	Ll	0.27	0/454	0.48	0/599
41	Lm	0.26	0/435	0.56	0/575
42	Ln	0.21	0/231	0.34	0/294
43	Lo	0.25	0/876	0.47	0/1156
44	Lp	0.27	0/718	0.43	0/953
45	Lr	0.24	0/1017	0.44	0/1364
46	S2	0.23	0/41229	0.34	0/64235
47	SA	0.26	0/1784	0.51	0/2424
48	SB	0.24	0/1765	0.54	0/2362
49	SD	0.19	0/1793	0.46	0/2414
50	SE	0.21	0/2118	0.44	0/2849
51	SF	0.22	0/1504	0.48	0/2024
52	SH	0.20	0/1516	0.51	2/2030 (0.1%)
53	SI	0.25	0/1715	0.48	0/2287
54	SK	0.26	0/851	0.56	0/1147
55	SL	0.25	0/1182	0.46	0/1581
56	SP	0.21	0/1071	0.54	0/1432
57	SQ	0.22	0/1177	0.54	0/1575
58	SR	0.23	0/1086	0.57	0/1457
59	SS	0.21	0/1216	0.53	0/1628
60	ST	0.18	0/1131	0.44	0/1515
61	SU	0.19	0/827	0.48	0/1110
62	SV	0.23	0/643	0.48	0/860
63	SX	0.25	0/1116	0.55	1/1490 (0.1%)
64	Sa	0.26	0/817	0.47	0/1095
65	Sc	0.20	0/502	0.55	0/673
66	Sd	0.27	0/470	0.67	1/623 (0.2%)
67	Sg	0.17	0/2493	0.41	0/3394
68	SC	0.26	0/1719	0.47	0/2322
69	SG	0.18	0/1938	0.43	0/2579
70	SJ	0.22	0/1550	0.51	0/2069
71	Sf	0.16	0/943	0.52	0/1267
72	SN	0.24	0/1232	0.49	0/1656
73	SO	0.27	0/1023	0.51	0/1372
74	SW	0.29	0/1051	0.60	0/1406
75	SY	0.21	0/1083	0.52	0/1438

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SZ	0.23	0/604	0.44	0/810
77	Sb	0.22	0/665	0.51	0/891
78	Se	0.17	0/465	0.41	0/612
79	sh	0.16	0/525	0.46	0/695
80	zv	0.19	0/295	0.45	0/455
81	zx	0.21	0/163	0.68	0/221
82	zy	0.18	0/1786	0.28	0/2784
83	zz	0.14	0/5005	0.29	0/7803
84	3m	0.13	0/2676	0.37	0/3635
85	3f	0.11	0/2099	0.32	0/2856
86	3a	0.12	0/4583	0.34	0/6237
87	3e	0.10	0/3282	0.29	0/4467
88	3c	0.12	0/4900	0.35	1/6641 (0.0%)
89	3h	0.12	0/2550	0.35	0/3456
90	3d	0.10	0/358	0.29	0/493
91	3k	0.21	0/1502	0.52	0/2052
92	3l	0.11	0/4446	0.32	0/6013
All	All	0.24	0/263042	0.39	11/384076 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	SH	65	PRO	CA-C-N	6.95	124.62	120.24
52	SH	65	PRO	C-N-CA	6.95	124.62	120.24
24	LV	111	GLU	CA-CB-CG	6.75	127.60	114.10
8	LE	279	ASN	N-CA-CB	-6.07	107.25	114.17
19	LQ	94	GLU	CA-CB-CG	5.72	125.53	114.10
63	SX	108	LYS	CB-CA-C	-5.52	110.19	116.54
88	3c	328	VAL	N-CA-C	-5.31	108.32	113.53
66	Sd	13	LYS	CA-CB-CG	5.29	124.67	114.10
28	LZ	102	ARG	CA-CB-CG	5.17	124.44	114.10
23	LU	66	SER	CA-C-N	5.05	131.18	121.54
23	LU	66	SER	C-N-CA	5.05	131.18	121.54

There are no chirality outliers.

There are no planarity outliers.

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	L5	78531	0	39682	651	0
2	L7	2558	0	1296	13	0
3	L8	3314	0	1683	35	0
4	LA	1898	0	1993	30	0
5	LB	3220	0	3362	35	0
6	LC	2914	0	3087	43	0
7	LD	2382	0	2410	22	0
8	LE	1818	0	1979	31	0
9	LF	1866	0	1992	28	0
10	LG	1914	0	2060	25	0
11	LH	1510	0	1589	19	0
12	LI	1711	0	1749	20	0
13	LJ	1410	0	1441	16	0
14	LL	1701	0	1818	22	0
15	LM	1138	0	1204	16	0
16	LN	1701	0	1749	27	0
17	LO	1650	0	1794	23	0
18	LP	1242	0	1269	16	0
19	LQ	1513	0	1628	24	0
20	LR	1566	0	1729	14	0
21	LS	1453	0	1490	29	0
22	LT	1298	0	1366	29	0
23	LU	825	0	850	6	0
24	LV	979	0	1039	13	0
25	LW	1015	0	1079	17	0
26	LX	976	0	1059	13	0
27	LY	1115	0	1205	15	0
28	LZ	1107	0	1182	19	0
29	La	1162	0	1213	27	0
30	Lb	876	0	948	12	0
31	Lc	764	0	804	20	0
32	Ld	888	0	930	9	0
33	Le	1053	0	1147	11	0
34	Lf	876	0	912	7	0
35	Lg	886	0	971	6	0
36	Lh	1015	0	1148	11	0
37	Li	832	0	917	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lj	705	0	737	12	0
39	Lk	569	0	637	6	0
40	Ll	444	0	483	6	0
41	Lm	429	0	465	6	0
42	Ln	230	0	276	3	0
43	Lo	862	0	930	7	0
44	Lp	708	0	757	15	0
45	Lr	1002	0	1068	9	0
46	S2	36887	0	18594	362	0
47	SA	1747	0	1751	34	0
48	SB	1738	0	1809	25	0
49	SD	1765	0	1865	19	0
50	SE	2076	0	2177	28	0
51	SF	1483	0	1523	27	0
52	SH	1494	0	1582	22	0
53	SI	1686	0	1772	22	0
54	SK	827	0	854	21	0
55	SL	1162	0	1227	12	0
56	SP	1050	0	1094	22	0
57	SQ	1158	0	1232	28	0
58	SR	1072	0	1130	14	0
59	SS	1198	0	1261	19	0
60	ST	1112	0	1146	13	0
61	SU	817	0	882	14	0
62	SV	636	0	637	15	0
63	SX	1098	0	1167	11	0
64	Sa	803	0	850	9	0
65	Sc	500	0	525	6	0
66	Sd	459	0	452	7	0
67	Sg	2436	0	2393	46	0
68	SC	1683	0	1770	31	0
69	SG	1915	0	2078	34	0
70	SJ	1525	0	1640	24	0
71	Sf	933	0	945	20	0
72	SN	1208	0	1294	18	0
73	SO	1010	0	1034	20	0
74	SW	1034	0	1080	14	0
75	SY	1065	0	1142	16	0
76	SZ	598	0	656	9	0
77	Sb	651	0	672	3	0
78	Se	459	0	503	2	0
79	sh	515	0	522	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	zv	267	0	141	0	0
81	zx	160	0	183	6	0
82	zy	1599	0	810	5	0
83	zz	4481	0	2267	53	0
84	3m	2639	0	2442	40	0
85	3f	2063	0	2054	39	0
86	3a	4497	0	4224	42	0
87	3e	3218	0	2920	31	0
88	3c	4822	0	4415	52	0
89	3h	2499	0	2418	34	0
90	3d	347	0	259	1	0
91	3k	1475	0	1239	21	0
92	3l	4335	0	4272	52	0
93	L5	70	0	0	0	0
93	L8	1	0	0	0	0
93	S2	10	0	0	0	0
94	Lg	1	0	0	0	0
94	Lj	1	0	0	0	0
94	Lm	1	0	0	0	0
94	Lo	1	0	0	0	0
94	Lp	1	0	0	0	0
94	Sa	1	0	0	0	0
94	sh	1	0	0	0	0
All	All	245916	0	186030	2513	0

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

All (2513) 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)
46:S2:1302:G:O6	46:S2:1307:U:C4	2.18	0.97
1:L5:1177:U:H3	1:L5:1183:C:N4	1.64	0.95
1:L5:2845:A:H61	1:L5:3843:C:N4	1.63	0.95
83:zz:145:G:H1	83:zz:248:U:H3	1.10	0.94
1:L5:2845:A:N6	1:L5:3843:C:H42	1.65	0.93
1:L5:3946:G:H1	1:L5:4067:U:H3	0.95	0.90
1:L5:2557:G:H1	1:L5:2570:U:H3	0.89	0.86
46:S2:1743:G:H21	46:S2:1791:A:H62	1.27	0.82
46:S2:383:G:H21	55:SL:133:PRO:HG2	1.43	0.81
1:L5:3692:A:H62	1:L5:3823:G:H21	1.28	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:71:A:H62	3:L8:87:G:H21	1.25	0.81
1:L5:1177:U:H3	1:L5:1183:C:H42	0.84	0.80
1:L5:2845:A:H61	1:L5:3843:C:H42	0.85	0.80
3:L8:71:A:H62	3:L8:87:G:N2	1.81	0.79
1:L5:1442:C:H41	1:L5:2104:G:H21	1.31	0.78
1:L5:4885:U:N3	1:L5:4936:G:N1	2.31	0.78
87:3e:362:MET:HE1	87:3e:370:TRP:HE1	1.49	0.77
1:L5:4745:G:H22	1:L5:4954:G:H1	1.33	0.76
4:LA:58:LEU:HD23	4:LA:75:LEU:HD12	1.67	0.76
23:LU:37:ALA:HA	23:LU:65:ARG:HH12	1.51	0.76
46:S2:1043:G:H21	46:S2:1073:U:H3	1.32	0.75
46:S2:1144:A:H5'	46:S2:1355:C:H41	1.51	0.74
74:SW:106:THR:HG23	74:SW:108:ALA:H	1.52	0.74
48:SB:38:MET:HE3	48:SB:38:MET:H	1.53	0.73
46:S2:1598:G:H5'	76:SZ:80:ARG:HH11	1.53	0.73
6:LC:33:ARG:HD2	6:LC:122:TYR:HE2	1.53	0.73
46:S2:150:A:H62	46:S2:168:C:N4	1.85	0.73
1:L5:4885:U:H3	1:L5:4936:G:H1	1.29	0.73
27:LY:56:GLN:HB2	27:LY:67:ILE:HG22	1.72	0.72
46:S2:150:A:N6	46:S2:168:C:C4	2.58	0.72
67:Sg:196:ASN:HD21	67:Sg:237:ASN:HA	1.55	0.72
53:SI:165:GLN:HE22	53:SI:172:LEU:HD23	1.56	0.71
46:S2:677:G:H21	46:S2:1028:A:H62	1.39	0.71
11:LH:103:VAL:HG11	11:LH:144:LEU:HD11	1.71	0.71
46:S2:1349:G:H21	47:SA:112:ILE:HD11	1.55	0.70
53:SI:190:LEU:HD23	53:SI:194:GLU:HB3	1.71	0.70
66:Sd:13:LYS:HD3	66:Sd:14:PHE:H	1.56	0.70
83:zz:186:C:N4	83:zz:212:U:C4	2.57	0.70
1:L5:4313:A:H1'	22:LT:90:ASN:HD22	1.56	0.70
46:S2:533:A:H61	46:S2:550:C:H42	1.40	0.70
6:LC:76:ILE:HD12	6:LC:77:PRO:HD2	1.73	0.70
48:SB:87:ILE:HG12	48:SB:101:HIS:HB2	1.74	0.69
10:LG:148:GLU:HA	10:LG:177:MET:HE1	1.72	0.69
46:S2:1550:G:H3'	46:S2:1579:A:H61	1.57	0.69
1:L5:25:A:H61	1:L5:58:G:H1	1.40	0.69
54:SK:31:LYS:HA	54:SK:41:PRO:HA	1.73	0.69
4:LA:242:ARG:HH22	4:LA:246:LEU:HA	1.57	0.69
26:LX:81:LEU:HD21	26:LX:99:ILE:HD13	1.75	0.68
54:SK:84:HIS:HD2	71:Sf:27:ILE:HG22	1.59	0.68
48:SB:39:PHE:HD2	48:SB:74:LEU:HD22	1.57	0.68
85:3f:242:TYR:HB2	85:3f:245:GLU:HB2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:3e:399:SER:HB3	87:3e:402:GLN:HG2	1.76	0.68
1:L5:2780:C:H2'	1:L5:2781:G:H8	1.57	0.68
51:SF:29:GLN:H	51:SF:110:GLN:HE22	1.41	0.68
1:L5:2020:U:H2'	1:L5:2021:G:H8	1.59	0.68
50:SE:92:ILE:HG22	50:SE:94:LYS:H	1.58	0.68
1:L5:2034:G:H5'	21:LS:87:ARG:HH21	1.58	0.67
51:SF:201:LYS:HA	51:SF:204:ARG:HE	1.59	0.67
1:L5:1332:C:H2'	1:L5:1333:A:H8	1.59	0.67
1:L5:2822:G:H5'	20:LR:18:GLY:HA3	1.76	0.67
67:Sg:32:LEU:HD21	67:Sg:92:LEU:HD21	1.77	0.67
1:L5:3944:G:H1	1:L5:4069:U:H3	1.42	0.67
46:S2:924:G:H1	46:S2:1018:U:H3	1.43	0.67
74:SW:94:LEU:HD13	74:SW:95:PRO:HD2	1.76	0.67
6:LC:303:ARG:HH21	6:LC:306:ARG:HG3	1.59	0.67
83:zz:141:U:H2'	83:zz:142:A:H8	1.60	0.67
46:S2:64:A:H2	46:S2:83:A:H62	1.42	0.66
73:SO:42:VAL:HG11	73:SO:81:VAL:HG11	1.76	0.66
1:L5:2112:G:H4'	1:L5:2251:G:H1	1.59	0.66
16:LN:110:CYS:HB3	16:LN:113:LEU:HD13	1.77	0.66
39:Lk:10:ASP:HA	39:Lk:13:LEU:HD13	1.77	0.66
13:LJ:24:ILE:HD11	13:LJ:36:ALA:HB1	1.78	0.66
68:SC:262:THR:HG23	68:SC:264:SER:H	1.60	0.66
86:3a:59:VAL:HG21	86:3a:96:MET:HE1	1.78	0.66
1:L5:515:C:H41	1:L5:647:G:H21	1.43	0.66
84:3m:259:ASN:HB2	84:3m:262:PHE:HB3	1.77	0.66
9:LF:110:GLN:HG3	9:LF:115:ARG:HE	1.61	0.66
31:Lc:34:THR:HG23	31:Lc:95:ALA:HB2	1.78	0.66
57:SQ:31:LEU:HD11	57:SQ:33:LYS:HG2	1.78	0.66
69:SG:118:GLU:HG2	69:SG:119:LYS:HG3	1.78	0.66
47:SA:189:ILE:HG12	47:SA:195:TRP:HD1	1.61	0.66
84:3m:119:VAL:HG13	84:3m:120:ARG:HE	1.59	0.66
51:SF:52:SER:HB2	57:SQ:117:ARG:HH21	1.60	0.65
1:L5:2562:G:H1'	1:L5:2566:G:H1	1.60	0.65
75:SY:21:LYS:HB2	75:SY:75:ILE:HB	1.77	0.65
1:L5:4885:U:O2	1:L5:4936:G:N2	2.29	0.65
5:LB:224:LYS:HG3	5:LB:340:THR:HG22	1.77	0.65
1:L5:300:A:H2'	1:L5:301:G:H8	1.60	0.65
46:S2:639:C:H2'	46:S2:640:A:H8	1.61	0.65
1:L5:512:U:H3	1:L5:647:G:H1	1.44	0.65
1:L5:4765:G:H22	1:L5:4869:U:H3	1.43	0.65
16:LN:68:ARG:HD2	16:LN:128:LYS:HG3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LR:24:LEU:HA	20:LR:50:ILE:HG22	1.79	0.65
1:L5:964:A:H2'	1:L5:965:G:H4'	1.78	0.65
86:3a:164:LEU:HB3	86:3a:174:TYR:HB2	1.78	0.65
46:S2:178:C:H3'	46:S2:313:A:H61	1.62	0.64
83:zz:186:C:N4	83:zz:212:U:N3	2.44	0.64
6:LC:27:VAL:HG11	6:LC:260:LEU:HD12	1.78	0.64
14:LL:89:LYS:HB2	36:Lh:114:TYR:HE2	1.62	0.64
1:L5:1870:C:H2'	1:L5:1871:A:H8	1.63	0.64
1:L5:3610:A:H2'	1:L5:3611:A:H8	1.62	0.64
89:3h:281:ARG:HA	89:3h:284:GLU:HB2	1.79	0.64
62:SV:43:THR:HG23	62:SV:45:ARG:H	1.62	0.64
67:Sg:87:LEU:HD11	67:Sg:111:VAL:HG11	1.79	0.64
10:LG:34:LYS:HG2	10:LG:36:PRO:HD3	1.79	0.64
46:S2:508:A:H3'	46:S2:509:G:H8	1.63	0.64
56:SP:108:LYS:HG3	56:SP:110:GLU:H	1.62	0.64
68:SC:65:LYS:HG2	68:SC:273:LEU:HD11	1.80	0.64
5:LB:57:VAL:HG23	5:LB:366:LYS:HB2	1.80	0.63
46:S2:902:G:N1	46:S2:904:A:N6	2.45	0.63
92:3l:195:GLN:HG2	92:3l:421:LEU:HD11	1.79	0.63
14:LL:186:ARG:HH21	37:Li:9:VAL:HG11	1.63	0.63
58:SR:60:ARG:HH11	58:SR:66:VAL:HG11	1.63	0.63
62:SV:15:ARG:HH12	68:SC:84:PHE:HA	1.62	0.63
65:Sc:12:ALA:HB1	65:Sc:32:VAL:HG13	1.80	0.63
46:S2:851:C:H5''	46:S2:852:G:H5'	1.81	0.63
46:S2:1620:A:C5	46:S2:1624:U:H1'	2.34	0.63
19:LQ:50:ARG:HH12	19:LQ:140:SER:HB2	1.62	0.63
50:SE:18:TRP:HB3	50:SE:20:LEU:HD23	1.79	0.63
67:Sg:36:ARG:HG2	67:Sg:65:PHE:CD2	2.33	0.63
50:SE:80:ILE:HG23	50:SE:81:THR:HG23	1.81	0.63
68:SC:202:THR:HG22	68:SC:221:ASP:HB3	1.80	0.63
8:LE:179:LEU:HB2	8:LE:250:GLN:HE21	1.62	0.63
46:S2:95:G:H21	46:S2:474:G:H5'	1.63	0.63
46:S2:1302:G:O6	46:S2:1307:U:C5	2.51	0.63
1:L5:106:A:H1'	1:L5:336:A:H8	1.64	0.63
87:3e:409:LYS:HG2	92:3l:388:LEU:HD11	1.80	0.63
89:3h:211:ILE:HG13	89:3h:215:MET:HE1	1.80	0.63
1:L5:1906:U:H2'	1:L5:1907:A:H8	1.63	0.63
46:S2:925:G:H1	46:S2:1017:U:H3	1.47	0.63
46:S2:1109:C:HO2'	46:S2:1110:G:H8	1.45	0.63
51:SF:19:LEU:HD21	51:SF:69:VAL:HG11	1.81	0.63
59:SS:24:ARG:HB2	59:SS:29:ALA:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SS:141:ARG:HA	59:SS:144:ARG:HD2	1.81	0.63
71:Sf:54:SER:HB3	71:Sf:78:LYS:HE3	1.81	0.63
52:SH:60:ILE:HB	52:SH:92:VAL:HG12	1.81	0.62
84:3m:69:SER:HA	84:3m:72:LEU:HD12	1.80	0.62
84:3m:249:LEU:HB2	84:3m:278:ARG:HH22	1.63	0.62
31:Lc:28:VAL:HG21	31:Lc:37:MET:HG3	1.81	0.62
46:S2:1755:C:C4	46:S2:1756:C:N4	2.67	0.62
92:3l:470:MET:HG2	92:3l:475:LEU:HD22	1.80	0.62
86:3a:51:MET:HA	86:3a:54:TYR:HB3	1.81	0.62
1:L5:283:G:H1'	37:Li:82:ARG:HH22	1.65	0.62
21:LS:76:LYS:HG3	21:LS:78:PHE:HE2	1.64	0.62
91:3k:74:LEU:HA	91:3k:77:LEU:HD12	1.82	0.62
1:L5:1503:A:H4'	1:L5:1504:G:H5'	1.81	0.62
46:S2:902:G:H1	46:S2:904:A:N6	1.98	0.62
74:SW:7:LEU:HA	74:SW:34:ILE:HD11	1.81	0.62
19:LQ:70:MET:HE2	19:LQ:80:ALA:HB2	1.82	0.62
46:S2:1860:A:H3'	64:Sa:8:ASN:HB3	1.82	0.62
92:3l:432:HIS:HB3	92:3l:435:TYR:HB2	1.81	0.62
1:L5:958:G:H21	8:LE:125:LEU:H	1.46	0.62
67:Sg:254:PRO:HB2	67:Sg:271:LYS:HE2	1.82	0.62
1:L5:2461:G:H4'	16:LN:108:ARG:HH22	1.64	0.62
1:L5:3946:G:N2	1:L5:4067:U:O2	2.27	0.62
1:L5:4301:U:H4'	22:LT:54:HIS:HD1	1.65	0.62
67:Sg:42:MET:HE2	67:Sg:92:LEU:HD23	1.82	0.62
50:SE:91:SER:HA	50:SE:98:ASN:HA	1.81	0.61
69:SG:2:LYS:HB3	69:SG:15:LEU:HD11	1.82	0.61
83:zz:248:U:H2'	83:zz:249:G:H8	1.65	0.61
84:3m:126:SER:HA	84:3m:129:LYS:HD2	1.81	0.61
91:3k:71:LEU:HB3	91:3k:134:PHE:HZ	1.64	0.61
16:LN:98:LEU:HD23	16:LN:128:LYS:HD2	1.82	0.61
29:La:11:LEU:HD21	29:La:18:GLY:H	1.64	0.61
46:S2:872:A:HO2'	46:S2:873:G:H8	1.48	0.61
46:S2:1516:G:H4'	56:SP:122:THR:HG21	1.81	0.61
83:zz:306:U:H3	83:zz:329:U:H3	1.45	0.61
1:L5:1095:A:H61	1:L5:1200:G:H1	1.49	0.61
1:L5:2350:U:H5''	1:L5:2351:C:H5''	1.82	0.61
53:SI:164:GLU:HA	53:SI:167:GLN:HG2	1.82	0.61
83:zz:319:G:H2'	83:zz:320:G:H8	1.64	0.61
1:L5:951:G:H2'	1:L5:952:G:H8	1.65	0.61
9:LF:163:ASN:HB2	9:LF:164:LYS:HE3	1.81	0.61
59:SS:5:ILE:HG22	59:SS:7:GLU:H	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lf:18:LEU:HD23	34:Lf:19:ARG:HG3	1.81	0.61
46:S2:980:A:H2'	46:S2:981:A:C8	2.36	0.61
85:3f:311:LEU:HG	86:3a:526:MET:HE1	1.82	0.61
3:L8:71:A:N6	3:L8:87:G:H21	1.98	0.61
46:S2:563:G:H1	46:S2:592:C:H5	1.47	0.61
46:S2:570:C:H4'	75:SY:36:PRO:HG3	1.82	0.61
1:L5:4491:G:H5'	5:LB:9:PRO:HG3	1.82	0.61
46:S2:1101:U:H2'	46:S2:1102:G:H8	1.65	0.61
72:SN:29:THR:HG23	72:SN:31:ASP:H	1.66	0.61
91:3k:198:PRO:HB3	92:3l:533:THR:HG23	1.82	0.61
70:SJ:65:GLU:HG3	70:SJ:66:LYS:HG3	1.82	0.61
74:SW:27:ILE:HB	74:SW:61:ILE:HB	1.81	0.61
1:L5:3861:A:H2'	1:L5:3862:A:H8	1.66	0.61
8:LE:245:GLN:HA	8:LE:248:ILE:HD12	1.83	0.61
21:LS:34:ALA:HB1	21:LS:39:VAL:HG13	1.83	0.61
5:LB:116:ARG:HB3	5:LB:177:LYS:HG2	1.81	0.60
9:LF:113:ARG:HH12	9:LF:206:ASN:HA	1.64	0.60
12:LI:93:PRO:HB2	12:LI:125:THR:HB	1.83	0.60
69:SG:32:MET:HE3	69:SG:33:ALA:H	1.65	0.60
85:3f:206:LEU:HD21	86:3a:554:VAL:HG22	1.83	0.60
13:LJ:22:LEU:HB2	13:LJ:128:LEU:HD11	1.83	0.60
47:SA:51:LEU:H	58:SR:105:MET:HE1	1.65	0.60
87:3e:299:LEU:HD13	87:3e:340:ILE:HD13	1.82	0.60
88:3c:573:ILE:HG23	88:3c:585:ALA:HB1	1.83	0.60
52:SH:8:ILE:HG12	52:SH:20:GLU:HB3	1.83	0.60
91:3k:37:ALA:HB1	91:3k:131:ILE:HG12	1.83	0.60
76:SZ:99:LEU:HD21	76:SZ:102:LYS:HB2	1.83	0.60
83:zz:262:U:O2	83:zz:271:G:O6	2.19	0.60
1:L5:1333:A:H2'	1:L5:1334:A:H8	1.67	0.60
1:L5:4929:C:H5'	15:LM:114:LYS:HD2	1.81	0.60
21:LS:101:THR:HG23	21:LS:104:GLY:H	1.67	0.60
44:Lp:57:CYS:CB	44:Lp:60:CYS:SG	2.89	0.60
69:SG:31:ARG:HG2	69:SG:101:ILE:HG22	1.84	0.60
85:3f:115:ARG:HH22	85:3f:183:SER:HB3	1.65	0.60
86:3a:190:ARG:HB2	86:3a:193:GLU:HB2	1.84	0.60
89:3h:278:GLN:HA	89:3h:281:ARG:HE	1.67	0.60
1:L5:2411:C:H2'	1:L5:2412:A:H8	1.66	0.60
20:LR:38:ARG:HA	20:LR:41:ILE:HG22	1.83	0.60
46:S2:150:A:N6	46:S2:168:C:N4	2.50	0.60
69:SG:159:ARG:HG2	69:SG:173:ALA:HB2	1.84	0.60
31:Lc:83:THR:HG22	72:SN:148:ALA:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SK:84:HIS:CD2	71:Sf:27:ILE:HG22	2.37	0.60
1:L5:4103:C:O2	1:L5:4107:G:O6	2.19	0.60
67:Sg:5:MET:HB2	67:Sg:270:LEU:HD21	1.84	0.60
85:3f:336:MET:HE2	87:3e:401:TYR:HD1	1.67	0.60
1:L5:3953:G:H22	1:L5:4060:U:H4'	1.67	0.59
46:S2:634:A:H2'	46:S2:635:G:H8	1.67	0.59
83:zz:184:G:H2'	83:zz:214:A:H61	1.66	0.59
88:3c:695:ILE:HA	88:3c:698:MET:HG2	1.83	0.59
1:L5:1997:U:H2'	1:L5:1998:A:H3'	1.85	0.59
1:L5:2745:A:H2'	1:L5:2746:A:H8	1.67	0.59
46:S2:1259:A:H62	46:S2:1518:C:H3'	1.67	0.59
52:SH:25:GLN:HA	52:SH:28:LEU:HG	1.84	0.59
1:L5:3607:U:H2'	1:L5:3608:A:H8	1.67	0.59
1:L5:2611:A:H5'	1:L5:2688:G:H4'	1.84	0.59
1:L5:4991:U:H2'	1:L5:4992:G:H8	1.68	0.59
1:L5:1341:U:H2'	1:L5:1342:A:H8	1.68	0.59
4:LA:180:LEU:HD11	44:Lp:26:VAL:HG21	1.83	0.59
1:L5:512:U:O4	1:L5:647:G:O6	2.21	0.59
46:S2:1499:U:H4'	49:SD:176:LEU:HD11	1.85	0.59
49:SD:76:ARG:HB2	54:SK:22:VAL:HG11	1.83	0.59
51:SF:33:ILE:HA	51:SF:36:GLN:HG3	1.85	0.59
91:3k:152:HIS:HB3	91:3k:188:PHE:HD1	1.67	0.59
1:L5:1802:A:H5''	1:L5:1803:G:H5'	1.85	0.59
1:L5:4981:G:H1'	18:LP:69:ARG:HD2	1.84	0.59
5:LB:173:LEU:HD11	5:LB:342:LYS:HB3	1.85	0.59
58:SR:28:PHE:HA	58:SR:55:THR:HG21	1.84	0.59
84:3m:14:GLN:HE22	85:3f:226:ARG:HG3	1.68	0.59
1:L5:3755:G:H21	82:zy:12:C:H4'	1.68	0.59
7:LD:155:THR:H	7:LD:179:ARG:HD2	1.68	0.59
18:LP:23:ARG:HA	18:LP:143:PRO:HB3	1.85	0.59
21:LS:78:PHE:HE1	21:LS:102:THR:HA	1.67	0.59
29:La:47:LYS:HE2	29:La:48:TYR:HE2	1.67	0.59
41:Lm:84:GLN:HA	41:Lm:87:GLN:HB2	1.83	0.59
46:S2:525:A:H2'	46:S2:526:A:H8	1.67	0.59
46:S2:617:G:H4'	63:SX:88:ASP:HB3	1.83	0.59
54:SK:57:TYR:HB3	54:SK:75:GLY:HA2	1.85	0.59
57:SQ:58:LEU:HB3	57:SQ:62:ARG:HD2	1.85	0.59
1:L5:4910:G:H1	17:LO:108:ILE:H	1.50	0.59
87:3e:215:ILE:HD12	87:3e:236:PHE:HE1	1.68	0.59
1:L5:1270:A:H8	1:L5:2106:G:H21	1.49	0.58
1:L5:4712:C:H2'	1:L5:4713:G:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SB:36:PRO:HB2	48:SB:38:MET:HE1	1.84	0.58
48:SB:40:ASN:HB2	48:SB:75:GLN:HG2	1.85	0.58
49:SD:93:THR:HG21	49:SD:198:ILE:HG22	1.84	0.58
9:LF:108:VAL:HG11	9:LF:135:ILE:HD11	1.85	0.58
46:S2:981:A:H2'	46:S2:982:G:C8	2.37	0.58
61:SU:61:LEU:HB2	61:SU:82:MET:HB3	1.83	0.58
68:SC:270:THR:HA	68:SC:273:LEU:HB3	1.85	0.58
46:S2:902:G:N1	46:S2:904:A:C6	2.71	0.58
48:SB:62:LEU:HA	48:SB:65:ARG:HE	1.68	0.58
84:3m:249:LEU:HD13	84:3m:278:ARG:HH12	1.67	0.58
85:3f:97:VAL:HG21	89:3h:51:LYS:HD2	1.86	0.58
1:L5:4274:A:H2'	1:L5:4275:G:H8	1.69	0.58
3:L8:8:U:H2'	3:L8:9:A:H8	1.68	0.58
14:LL:107:THR:HG22	37:Li:20:ASN:HB2	1.85	0.58
46:S2:28:U:H2'	46:S2:29:G:H8	1.67	0.58
46:S2:306:C:H5''	46:S2:307:G:C5	2.38	0.58
1:L5:4537:C:H2'	1:L5:4538:G:H8	1.68	0.58
1:L5:4992:G:H2'	1:L5:4993:G:C8	2.39	0.58
46:S2:948:C:H2'	46:S2:949:G:H8	1.69	0.58
1:L5:1175:A:H2	1:L5:1185:G:H22	1.52	0.58
6:LC:334:THR:HG22	6:LC:337:ARG:HH21	1.67	0.58
8:LE:66:LYS:HD3	8:LE:68:MET:HE2	1.86	0.58
10:LG:95:LEU:HD12	10:LG:218:LEU:HD13	1.84	0.58
10:LG:158:ALA:HB2	10:LG:190:LEU:HD12	1.85	0.58
46:S2:671:A:H4'	46:S2:672:A:H5''	1.84	0.58
46:S2:1302:G:C6	46:S2:1307:U:O4	2.56	0.58
46:S2:1418:C:H2'	46:S2:1419:C:H2'	1.85	0.58
49:SD:106:ARG:HG2	49:SD:175:VAL:HG22	1.86	0.58
73:SO:27:VAL:HG23	73:SO:90:ILE:HD12	1.86	0.58
1:L5:2283:G:H2'	1:L5:2284:G:H8	1.68	0.58
72:SN:5:HIS:HD2	72:SN:117:LEU:HB3	1.68	0.58
83:zz:327:C:H2'	83:zz:328:G:C8	2.38	0.58
36:Lh:91:MET:HB3	36:Lh:94:ARG:HH21	1.68	0.57
46:S2:126:G:H22	69:SG:196:LYS:HD2	1.69	0.57
46:S2:1542:C:H5''	60:ST:62:ARG:HH22	1.69	0.57
70:SJ:21:GLU:HG3	70:SJ:24:ARG:H	1.68	0.57
1:L5:1442:C:H2'	1:L5:1443:A:H8	1.68	0.57
17:LO:16:LEU:HD21	17:LO:83:THR:HG21	1.86	0.57
25:LW:13:ILE:HD11	25:LW:32:LEU:HA	1.84	0.57
41:Lm:99:CYS:HB3	41:Lm:115:CYS:HB3	1.87	0.57
50:SE:175:PHE:HE2	50:SE:198:ARG:HD2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SQ:76:GLY:H	57:SQ:79:ALA:HB3	1.68	0.57
68:SC:107:LEU:HD12	68:SC:127:PHE:HB3	1.87	0.57
75:SY:114:MET:HG3	75:SY:122:LYS:HD3	1.85	0.57
92:3l:328:ARG:HH12	92:3l:502:TRP:HB2	1.70	0.57
1:L5:4594:U:H2'	1:L5:4595:G:H8	1.70	0.57
46:S2:1228:A:H2'	46:S2:1229:G:C8	2.39	0.57
50:SE:100:ARG:HB3	50:SE:114:ILE:HG13	1.86	0.57
56:SP:111:MET:HG3	56:SP:119:PHE:HE2	1.68	0.57
88:3c:733:MET:HE1	88:3c:765:VAL:HB	1.86	0.57
1:L5:1207:C:H2'	1:L5:1208:G:H8	1.69	0.57
22:LT:57:TYR:HE1	22:LT:89:ILE:HG21	1.70	0.57
51:SF:78:MET:HE3	51:SF:79:HIS:H	1.68	0.57
56:SP:21:ASP:H	56:SP:24:GLN:HE21	1.51	0.57
1:L5:3921:U:H1'	1:L5:4543:G:H21	1.70	0.57
55:SL:113:LEU:HD12	55:SL:142:VAL:HG21	1.86	0.57
83:zz:145:G:N2	83:zz:248:U:O2	2.32	0.57
1:L5:1598:C:H2'	1:L5:1599:A:H8	1.68	0.57
5:LB:19:ARG:HB3	5:LB:234:ARG:HH21	1.70	0.57
16:LN:120:TRP:HE1	16:LN:123:GLU:HG2	1.70	0.57
46:S2:599:A:H2'	46:S2:606:G:H21	1.69	0.57
46:S2:848:U:H2'	46:S2:849:A:H8	1.69	0.57
50:SE:106:LYS:HG3	50:SE:108:ARG:HH21	1.69	0.57
1:L5:1332:C:H2'	1:L5:1333:A:C8	2.40	0.57
1:L5:2375:A:H2'	1:L5:2376:A:H8	1.70	0.57
1:L5:2521:G:H2'	1:L5:2522:G:H8	1.70	0.57
56:SP:93:MET:HE2	56:SP:104:GLN:HE22	1.69	0.57
1:L5:667:A:H5''	1:L5:668:C:H5''	1.86	0.56
19:LQ:6:ARG:NH2	19:LQ:8:ASN:HD21	2.02	0.56
46:S2:1756:C:H2'	46:S2:1757:G:C5	2.40	0.56
60:ST:141:ALA:HA	60:ST:144:LYS:HE3	1.86	0.56
4:LA:107:MET:HE1	4:LA:113:VAL:HG11	1.87	0.56
31:Lc:47:ILE:HG22	31:Lc:72:HIS:HB3	1.88	0.56
51:SF:122:ARG:HG3	51:SF:146:ARG:HH21	1.70	0.56
85:3f:314:GLN:HG3	86:3a:529:VAL:HG21	1.87	0.56
1:L5:181:C:H2'	1:L5:182:G:H8	1.70	0.56
4:LA:147:ARG:HH22	4:LA:155:LYS:HD3	1.70	0.56
5:LB:287:ILE:HG22	5:LB:331:VAL:HG22	1.86	0.56
5:LB:317:LEU:HB2	5:LB:372:SER:HB2	1.87	0.56
46:S2:1130:G:H4'	72:SN:10:GLY:HA2	1.87	0.56
84:3m:165:LEU:HD12	84:3m:188:LEU:HD12	1.85	0.56
85:3f:244:THR:HA	85:3f:247:ILE:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3848:U:H2'	1:L5:3849:A:H8	1.70	0.56
1:L5:4991:U:H2'	1:L5:4992:G:C8	2.41	0.56
16:LN:73:ARG:HB3	16:LN:89:VAL:HG23	1.86	0.56
24:LV:82:ILE:HG12	24:LV:103:GLY:HA2	1.87	0.56
1:L5:1273:G:C8	30:Lb:117:ARG:HD2	2.41	0.56
1:L5:1845:U:H5'	30:Lb:25:ARG:HH12	1.71	0.56
1:L5:1976:G:O6	1:L5:1990:A:N1	2.38	0.56
91:3k:165:LEU:HD22	91:3k:169:GLN:HE22	1.71	0.56
29:La:24:LYS:HE2	29:La:26:ARG:NH2	2.21	0.56
46:S2:616:A:H62	46:S2:625:G:H21	1.54	0.56
11:LH:129:ARG:HD3	11:LH:130:PRO:HD2	1.86	0.56
5:LB:90:VAL:HG13	5:LB:104:THR:HG22	1.88	0.56
46:S2:159:A:H2	46:S2:467:G:H21	1.53	0.56
46:S2:527:C:H2'	46:S2:528:A:H8	1.71	0.56
12:LI:54:SER:HB3	12:LI:135:ILE:HD11	1.88	0.56
34:Lf:33:VAL:HG23	34:Lf:38:GLU:HG3	1.88	0.56
87:3e:126:GLU:HA	87:3e:129:ASP:HB2	1.87	0.56
46:S2:1144:A:H2'	46:S2:1145:A:C8	2.41	0.56
1:L5:1333:A:H2'	1:L5:1334:A:C8	2.41	0.55
6:LC:33:ARG:HD2	6:LC:122:TYR:CE2	2.38	0.55
24:LV:48:ARG:HG3	24:LV:49:LEU:H	1.71	0.55
28:LZ:101:PHE:C	28:LZ:102:ARG:HD3	2.31	0.55
46:S2:1050:A:H62	46:S2:1068:G:H21	1.54	0.55
1:L5:2298:U:H5''	6:LC:204:ARG:HH21	1.70	0.55
1:L5:4088:C:H2'	1:L5:4089:G:H8	1.71	0.55
46:S2:1743:G:N2	46:S2:1791:A:H62	1.99	0.55
47:SA:68:ILE:HG23	47:SA:120:ARG:HH21	1.71	0.55
52:SH:22:GLY:HA2	52:SH:25:GLN:HE22	1.71	0.55
62:SV:1:MET:HA	62:SV:9:VAL:HG22	1.87	0.55
89:3h:254:SER:HA	89:3h:257:ILE:HD12	1.88	0.55
1:L5:679:C:H2'	1:L5:680:G:H8	1.71	0.55
1:L5:2555:G:H4'	28:LZ:108:ARG:HH12	1.72	0.55
87:3e:196:ILE:HD12	87:3e:214:LEU:HD12	1.88	0.55
1:L5:760:G:H1	1:L5:903:C:H1'	1.70	0.55
1:L5:2670:C:N4	1:L5:2671:C:N4	2.54	0.55
2:L7:57:C:H2'	2:L7:58:A:H8	1.71	0.55
15:LM:15:VAL:HG22	15:LM:50:MET:HE1	1.88	0.55
31:Lc:74:TYR:HD2	31:Lc:81:LEU:HG	1.71	0.55
71:Sf:46:GLN:HE21	71:Sf:112:LYS:HG3	1.71	0.55
83:zz:144:U:O2	83:zz:249:G:O6	2.25	0.55
84:3m:196:ASN:O	84:3m:196:ASN:ND2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1193:C:H2'	1:L5:1194:G:H8	1.70	0.55
46:S2:388:U:H2'	46:S2:389:A:H8	1.72	0.55
46:S2:639:C:H2'	46:S2:640:A:C8	2.40	0.55
81:zx:7:SER:HB2	81:zx:9:LYS:HE2	1.88	0.55
1:L5:10:A:H2'	1:L5:11:G:H8	1.72	0.55
1:L5:1094:G:O6	1:L5:1201:U:O2	2.24	0.55
1:L5:1730:U:H4'	22:LT:100:LYS:HB3	1.87	0.55
22:LT:40:VAL:HG21	22:LT:96:ILE:HD12	1.87	0.55
1:L5:4548:A:H8	12:LI:110:ARG:HH12	1.55	0.55
46:S2:1228:A:H2'	46:S2:1229:G:H8	1.71	0.55
83:zz:294:U:H2'	83:zz:295:G:H2'	1.88	0.55
91:3k:158:LEU:HA	91:3k:161:MET:HB3	1.88	0.55
3:L8:121:G:H2'	3:L8:122:G:C8	2.42	0.55
13:LJ:20:LEU:HD13	13:LJ:132:VAL:HG12	1.89	0.55
16:LN:117:ASN:HD21	16:LN:166:SER:HB3	1.72	0.55
22:LT:54:HIS:HD2	22:LT:55:LYS:HG2	1.71	0.55
46:S2:928:G:H2'	46:S2:929:G:C8	2.41	0.55
48:SB:83:LYS:HE3	48:SB:106:THR:HG22	1.89	0.55
60:ST:126:GLN:HB2	60:ST:129:ARG:HH21	1.72	0.55
87:3e:182:TRP:HB3	87:3e:225:HIS:CE1	2.41	0.55
89:3h:215:MET:HA	89:3h:218:LEU:HB2	1.87	0.55
46:S2:1736:G:H2'	46:S2:1737:G:H8	1.72	0.55
12:LI:61:SER:HA	12:LI:126:VAL:HG23	1.89	0.55
49:SD:136:VAL:HG22	49:SD:186:VAL:HG12	1.89	0.55
71:Sf:33:ARG:HE	71:Sf:91:LEU:HD11	1.72	0.55
1:L5:1759:G:H1	1:L5:1773:U:H3	1.54	0.54
6:LC:159:GLU:HA	6:LC:217:ILE:HD11	1.88	0.54
9:LF:116:GLN:HB3	19:LQ:3:VAL:HG12	1.88	0.54
46:S2:28:U:H2'	46:S2:29:G:C8	2.42	0.54
46:S2:106:C:H2'	46:S2:107:A:H8	1.72	0.54
48:SB:105:LEU:HD13	48:SB:213:ARG:HA	1.88	0.54
49:SD:105:LEU:HD22	49:SD:122:VAL:HG11	1.89	0.54
55:SL:5:GLN:HE22	55:SL:11:GLN:H	1.55	0.54
87:3e:175:SER:HA	87:3e:178:LEU:HD12	1.87	0.54
15:LM:40:GLY:HA3	15:LM:45:VAL:HB	1.89	0.54
28:LZ:11:VAL:HG11	28:LZ:80:LEU:HG	1.88	0.54
47:SA:50:ASN:HB3	47:SA:53:ARG:HB2	1.89	0.54
52:SH:73:GLN:HB3	52:SH:135:PHE:CE2	2.42	0.54
67:Sg:220:ASP:HB2	67:Sg:225:LYS:H	1.73	0.54
75:SY:87:PRO:HG2	75:SY:90:ARG:HE	1.71	0.54
1:L5:3873:G:H2'	1:L5:3874:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LP:153:LYS:HE3	18:LP:153:LYS:HA	1.89	0.54
26:LX:86:ALA:HB1	26:LX:97:VAL:HG21	1.87	0.54
1:L5:4492:U:H5''	1:L5:4493:U:H5'	1.89	0.54
28:LZ:12:LEU:HB2	28:LZ:81:MET:HB3	1.89	0.54
46:S2:996:A:H2'	46:S2:997:A:C8	2.42	0.54
1:L5:1558:A:H2'	1:L5:1559:G:H8	1.73	0.54
1:L5:4237:C:H2'	1:L5:4238:G:H8	1.72	0.54
4:LA:32:VAL:HG12	4:LA:37:ARG:HH21	1.72	0.54
28:LZ:20:GLY:HA2	35:Lg:91:ILE:HD12	1.89	0.54
38:Lj:34:CYS:HB3	38:Lj:38:GLY:H	1.71	0.54
50:SE:35:PRO:HB2	50:SE:143:ASP:HB2	1.90	0.54
9:LF:154:ILE:HD11	9:LF:208:LEU:HD11	1.90	0.54
18:LP:40:HIS:HA	18:LP:113:VAL:HG12	1.89	0.54
25:LW:107:GLN:HA	25:LW:110:ARG:HB3	1.89	0.54
89:3h:231:LEU:HD22	89:3h:343:MET:HE1	1.90	0.54
56:SP:111:MET:HA	59:SS:117:ILE:HD11	1.90	0.54
68:SC:66:LEU:HD11	68:SC:81:ILE:HD12	1.89	0.54
89:3h:69:GLY:HA3	89:3h:78:ILE:HD13	1.89	0.54
1:L5:4239:A:H2'	1:L5:4240:G:H8	1.73	0.54
1:L5:4299:U:H2'	1:L5:4300:U:H6	1.73	0.54
6:LC:24:LEU:HD12	6:LC:25:PRO:HD2	1.88	0.54
46:S2:877:C:H5'	46:S2:878:G:H5''	1.88	0.54
46:S2:1475:G:H21	58:SR:3:ARG:HH12	1.55	0.54
46:S2:1858:G:H2'	46:S2:1859:A:H8	1.73	0.54
83:zz:213:C:H2'	83:zz:214:A:C8	2.43	0.54
1:L5:337:U:H2'	1:L5:338:A:H8	1.73	0.54
1:L5:4252:C:H5''	1:L5:4253:A:H2'	1.89	0.54
2:L7:92:C:H2'	2:L7:93:G:H8	1.73	0.54
9:LF:94:ARG:HA	9:LF:140:ILE:HG22	1.90	0.54
16:LN:158:HIS:HB3	16:LN:161:MET:HG2	1.90	0.54
54:SK:5:LYS:HA	54:SK:8:ARG:HB3	1.89	0.54
67:Sg:251:ALA:HB2	67:Sg:289:LEU:HD22	1.89	0.54
88:3c:574:TYR:HB2	88:3c:612:THR:HG22	1.89	0.54
1:L5:2482:C:H41	1:L5:2483:G:H21	1.55	0.54
52:SH:19:PHE:HE2	52:SH:50:GLU:HB2	1.72	0.54
82:zy:21:U:H2'	82:zy:22:G:H8	1.71	0.54
83:zz:319:G:H2'	83:zz:320:G:C8	2.42	0.54
1:L5:1511:U:H2'	1:L5:1512:G:H8	1.73	0.53
1:L5:2011:C:H3'	1:L5:2012:A:H8	1.73	0.53
1:L5:4237:C:H2'	1:L5:4238:G:C8	2.42	0.53
19:LQ:3:VAL:HG23	19:LQ:5:ILE:HG12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lr:32:LEU:HD12	45:Lr:113:ARG:HD3	1.88	0.53
46:S2:1759:G:H2'	46:S2:1760:G:C8	2.43	0.53
47:SA:61:ALA:HB2	47:SA:159:ILE:HG21	1.90	0.53
56:SP:28:MET:HE1	56:SP:33:LEU:HD22	1.89	0.53
84:3m:148:ARG:HE	84:3m:187:GLU:HG2	1.74	0.53
88:3c:627:LYS:HA	88:3c:693:LEU:HD21	1.90	0.53
1:L5:459:C:H5'	8:LE:110:ARG:HA	1.90	0.53
1:L5:3611:A:H2	1:L5:5016:A:H8	1.55	0.53
46:S2:1030:A:H2'	46:S2:1031:A:H8	1.73	0.53
47:SA:76:VAL:HA	47:SA:123:VAL:HG23	1.90	0.53
24:LV:13:LYS:HB2	24:LV:128:LEU:HD21	1.91	0.53
46:S2:640:A:H2'	46:S2:641:A:C8	2.43	0.53
46:S2:888:U:H2'	46:S2:898:U:H3	1.73	0.53
62:SV:14:PRO:HG2	62:SV:23:ILE:HD12	1.90	0.53
64:Sa:51:ARG:HH22	65:Sc:39:SER:HB2	1.72	0.53
88:3c:573:ILE:HD11	88:3c:588:LEU:HB3	1.90	0.53
89:3h:38:GLN:HG2	89:3h:202:PRO:HG2	1.89	0.53
1:L5:1382:G:H2'	1:L5:1383:G:H8	1.72	0.53
7:LD:223:PHE:HB3	7:LD:226:TYR:HB2	1.90	0.53
40:Ll:21:ARG:HD3	40:Ll:22:PRO:HD2	1.89	0.53
46:S2:1302:G:C6	46:S2:1307:U:C4	2.94	0.53
46:S2:1320:G:C2	46:S2:1321:G:H1'	2.44	0.53
46:S2:1536:G:H2'	46:S2:1537:A:C8	2.43	0.53
71:Sf:96:ARG:H	71:Sf:96:ARG:HD3	1.73	0.53
1:L5:1338:G:H3'	29:La:8:THR:HG21	1.91	0.53
1:L5:4747:C:H5''	34:Lf:54:LYS:HE3	1.89	0.53
31:Lc:21:VAL:HG12	31:Lc:22:MET:HE2	1.90	0.53
46:S2:1562:C:H2'	46:S2:1563:G:H8	1.74	0.53
83:zz:285:G:H2'	83:zz:286:G:C8	2.43	0.53
85:3f:184:VAL:HG13	85:3f:228:MET:HE1	1.91	0.53
1:L5:121:A:H2	1:L5:152:U:H3	1.56	0.53
1:L5:2903:G:H4'	1:L5:3591:C:H42	1.72	0.53
1:L5:3901:A:H5'	1:L5:3902:A:H5'	1.90	0.53
1:L5:4537:C:H2'	1:L5:4538:G:C8	2.43	0.53
46:S2:873:G:H2'	46:S2:874:G:H8	1.74	0.53
46:S2:1010:G:H2'	46:S2:1011:A:H8	1.74	0.53
53:SI:83:TYR:HB3	53:SI:101:ILE:HD11	1.91	0.53
1:L5:2647:A:H62	1:L5:2686:G:H8	1.56	0.53
1:L5:2710:C:H5'	20:LR:39:GLN:HE21	1.74	0.53
1:L5:3717:A:H2'	1:L5:3718:A:H8	1.72	0.53
6:LC:32:ILE:HD12	6:LC:130:ALA:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lp:37:TYR:HD2	44:Lp:71:TYR:HB2	1.74	0.53
46:S2:1272:C:H5''	46:S2:1273:C:H5	1.74	0.53
92:3l:383:ASP:HB2	92:3l:386:ILE:HD12	1.91	0.53
92:3l:557:LEU:HA	92:3l:560:MET:HE2	1.91	0.53
1:L5:10:A:H2'	1:L5:11:G:C8	2.44	0.53
1:L5:3933:G:H2'	1:L5:3934:G:H8	1.74	0.53
46:S2:4:C:H5'	68:SC:230:THR:HG21	1.91	0.53
46:S2:1457:U:H2'	46:S2:1458:G:H8	1.73	0.53
71:Sf:58:GLU:HG3	71:Sf:61:TYR:HB3	1.91	0.53
1:L5:1308:C:H2'	1:L5:1309:C:C6	2.44	0.53
3:L8:8:U:H2'	3:L8:9:A:C8	2.43	0.53
6:LC:36:ILE:HG21	6:LC:122:TYR:HD2	1.73	0.53
46:S2:1845:A:H2'	46:S2:1846:G:H8	1.74	0.53
52:SH:178:LYS:HD2	52:SH:182:GLY:HA2	1.90	0.53
87:3e:420:MET:HA	87:3e:423:GLU:HB2	1.90	0.53
92:3l:464:LEU:HB3	92:3l:530:ILE:HG12	1.90	0.53
1:L5:496:G:H2'	1:L5:498:C:H5''	1.91	0.53
1:L5:1912:G:H21	17:LO:87:MET:HE2	1.74	0.53
67:Sg:24:THR:HG22	67:Sg:71:ILE:HG21	1.91	0.53
72:SN:92:ILE:HD13	72:SN:122:ILE:HD13	1.91	0.53
83:zz:145:G:H2'	83:zz:146:G:H8	1.74	0.53
1:L5:2670:C:C4	1:L5:2671:C:N4	2.77	0.52
21:LS:8:ARG:HD3	21:LS:66:GLN:NE2	2.24	0.52
22:LT:39:ILE:HD13	22:LT:102:ARG:HD3	1.91	0.52
46:S2:528:A:H2'	46:S2:529:A:H8	1.74	0.52
46:S2:952:G:H21	73:SO:52:THR:HG21	1.74	0.52
83:zz:193:C:H42	83:zz:202:A:H61	1.56	0.52
85:3f:92:VAL:HG23	85:3f:129:VAL:HG13	1.90	0.52
85:3f:253:MET:HE2	89:3h:219:GLU:HG2	1.91	0.52
88:3c:514:PHE:HE1	88:3c:519:HIS:HB2	1.73	0.52
1:L5:2386:U:H2'	1:L5:2387:G:H8	1.75	0.52
1:L5:3870:C:H2'	1:L5:3871:A:H8	1.74	0.52
7:LD:111:ASN:HD21	7:LD:252:VAL:HG22	1.73	0.52
46:S2:1244:U:H2'	46:S2:1245:G:H8	1.73	0.52
64:Sa:83:VAL:HG13	64:Sa:84:VAL:HG23	1.91	0.52
3:L8:47:C:H1'	3:L8:61:A:H2'	1.92	0.52
6:LC:142:HIS:CE1	6:LC:249:PHE:H	2.28	0.52
10:LG:80:ILE:HD11	16:LN:18:VAL:HG23	1.91	0.52
46:S2:750:C:H3'	46:S2:751:G:H4'	1.92	0.52
46:S2:1281:G:H2'	46:S2:1282:A:C8	2.44	0.52
53:SI:84:ASN:HD22	53:SI:90:LEU:HB2	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SL:135:SER:HB3	55:SL:138:VAL:HG12	1.90	0.52
1:L5:3585:G:H2'	1:L5:3586:G:C8	2.44	0.52
1:L5:3727:A:H2'	1:L5:3728:A:C8	2.44	0.52
7:LD:38:ILE:HD13	22:LT:30:TYR:HD2	1.73	0.52
8:LE:179:LEU:HB2	8:LE:250:GLN:NE2	2.24	0.52
14:LL:89:LYS:HB2	36:Lh:114:TYR:CE2	2.44	0.52
48:SB:175:GLU:OE2	48:SB:187:LYS:HD2	2.09	0.52
56:SP:49:LEU:HD12	56:SP:53:GLN:HG3	1.92	0.52
57:SQ:132:PHE:HE2	61:SU:76:THR:HA	1.73	0.52
72:SN:87:ASP:HB2	72:SN:125:LEU:HD21	1.90	0.52
88:3c:507:ILE:HA	88:3c:510:THR:HG22	1.91	0.52
1:L5:2295:C:H2'	1:L5:2296:G:H8	1.74	0.52
1:L5:3658:C:H2'	1:L5:3659:G:H8	1.74	0.52
6:LC:171:LEU:HA	6:LC:174:LEU:HB2	1.90	0.52
69:SG:21:GLU:HB2	69:SG:25:ARG:HH21	1.75	0.52
1:L5:2079:G:H2'	1:L5:2080:U:C6	2.45	0.52
46:S2:1004:U:H2'	46:S2:1005:G:H8	1.75	0.52
46:S2:1473:G:H22	46:S2:1475:G:H5''	1.74	0.52
47:SA:143:PRO:HB3	62:SV:32:ILE:HD12	1.92	0.52
79:sh:107:LYS:HE3	79:sh:117:LEU:HD22	1.92	0.52
83:zz:154:A:H61	83:zz:173:A:H1'	1.75	0.52
1:L5:1617:G:H2'	1:L5:1618:G:H8	1.75	0.52
1:L5:3717:A:H2'	1:L5:3718:A:C8	2.45	0.52
17:LO:10:ASP:HB2	17:LO:117:ARG:HG2	1.92	0.52
33:Le:75:ARG:HB2	33:Le:95:TYR:HD1	1.74	0.52
47:SA:141:ASN:HD21	68:SC:86:LEU:HD13	1.75	0.52
71:Sf:18:LEU:HA	71:Sf:21:VAL:HG12	1.91	0.52
73:SO:113:GLN:CA	73:SO:113:GLN:HE21	2.22	0.52
88:3c:80:LEU:HD13	88:3c:141:LEU:HB2	1.91	0.52
1:L5:268:G:H2'	1:L5:269:G:H8	1.74	0.52
1:L5:2906:G:H1	1:L5:3588:C:H42	1.58	0.52
4:LA:120:PRO:HA	4:LA:162:ASN:HB3	1.90	0.52
14:LL:65:ARG:HG2	14:LL:66:TYR:CE2	2.45	0.52
46:S2:24:C:HO2'	46:S2:25:A:H8	1.58	0.52
1:L5:1341:U:H2'	1:L5:1342:A:C8	2.44	0.52
1:L5:1514:U:H2'	1:L5:1515:A:C8	2.45	0.52
1:L5:3917:A:H2'	1:L5:3918:G:H8	1.75	0.52
19:LQ:178:ARG:H	29:La:51:GLY:HA2	1.75	0.52
46:S2:1154:U:H1'	68:SC:194:ARG:HE	1.75	0.52
50:SE:9:LEU:HB3	50:SE:28:ALA:HB3	1.92	0.52
1:L5:1350:C:H2'	1:L5:1351:G:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4508:C:H5''	24:LV:43:LYS:HD3	1.92	0.52
9:LF:144:TYR:HE2	9:LF:237:GLU:HG3	1.75	0.52
10:LG:175:ARG:HG2	10:LG:230:TYR:CD2	2.45	0.52
11:LH:85:THR:HG23	11:LH:86:LEU:HG	1.92	0.52
46:S2:151:C:H2'	46:S2:152:U:C6	2.44	0.52
46:S2:958:G:H2'	46:S2:959:G:C8	2.45	0.52
74:SW:115:GLU:HA	74:SW:118:ARG:HB2	1.92	0.52
1:L5:3661:G:H4'	1:L5:3662:A:H5'	1.92	0.51
11:LH:44:GLU:HB3	11:LH:58:ASP:HB2	1.92	0.51
16:LN:103:GLU:HG2	16:LN:115:VAL:HG21	1.91	0.51
21:LS:84:TYR:HE1	21:LS:86:SER:HB2	1.75	0.51
92:3l:57:GLN:HA	92:3l:60:HIS:CE1	2.45	0.51
1:L5:323:C:H2'	1:L5:324:A:H8	1.74	0.51
1:L5:4080:C:H2'	1:L5:4081:G:H8	1.74	0.51
5:LB:47:LEU:HD12	5:LB:84:MET:HE1	1.91	0.51
8:LE:56:ARG:HG3	8:LE:57:TYR:HD1	1.75	0.51
22:LT:54:HIS:CD2	22:LT:55:LYS:HG2	2.45	0.51
23:LU:23:LEU:HD23	23:LU:83:LEU:HD12	1.93	0.51
32:Ld:46:LEU:HA	32:Ld:49:ILE:HD12	1.92	0.51
46:S2:145:G:H2'	46:S2:146:G:C8	2.45	0.51
46:S2:1779:G:H2'	46:S2:1780:G:C8	2.44	0.51
89:3h:123:THR:HG21	89:3h:128:PHE:HB3	1.92	0.51
92:3l:327:ARG:HG2	92:3l:499:ASN:HD21	1.74	0.51
1:L5:43:U:H1'	43:Lo:52:THR:HG23	1.92	0.51
1:L5:181:C:H2'	1:L5:182:G:C8	2.45	0.51
1:L5:267:G:H2'	1:L5:268:G:H8	1.75	0.51
1:L5:2906:G:H22	1:L5:3588:C:H42	1.58	0.51
1:L5:4301:U:H4'	22:LT:54:HIS:ND1	2.25	0.51
17:LO:185:VAL:HG12	17:LO:189:ILE:HG12	1.91	0.51
70:SJ:144:ILE:HG22	70:SJ:146:SER:H	1.75	0.51
85:3f:108:ARG:HH21	89:3h:112:ILE:HA	1.75	0.51
86:3a:403:LEU:HA	86:3a:406:ARG:HE	1.74	0.51
5:LB:285:TYR:HB2	5:LB:332:MET:HG2	1.93	0.51
46:S2:1357:A:H5''	68:SC:112:VAL:HG21	1.93	0.51
68:SC:167:ARG:HB3	68:SC:177:PRO:HB2	1.91	0.51
1:L5:4379:A:C8	43:Lo:54:PRO:HB3	2.45	0.51
46:S2:17:C:H2'	46:S2:18:C:C6	2.46	0.51
46:S2:377:G:H5'	53:SI:98:LYS:HB3	1.91	0.51
46:S2:1199:A:H2'	46:S2:1200:A:C8	2.46	0.51
69:SG:121:ILE:HB	69:SG:124:LEU:HB2	1.92	0.51
69:SG:159:ARG:HB3	69:SG:171:THR:HB	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SJ:91:LYS:HB3	70:SJ:96:TYR:CD1	2.45	0.51
84:3m:138:GLN:H	84:3m:138:GLN:CD	2.19	0.51
84:3m:189:LEU:HB3	84:3m:226:LEU:HB3	1.93	0.51
86:3a:497:LEU:HD11	86:3a:515:PRO:HB2	1.93	0.51
1:L5:1095:A:N6	1:L5:1200:G:H1	2.09	0.51
1:L5:1824:G:H2'	1:L5:1825:A:C8	2.45	0.51
6:LC:301:ALA:HB1	19:LQ:132:LYS:HD3	1.92	0.51
8:LE:176:THR:HB	8:LE:186:LEU:HA	1.93	0.51
46:S2:1849:G:H1'	46:S2:1850:A:H5'	1.93	0.51
50:SE:125:LYS:HG2	50:SE:142:HIS:HB3	1.92	0.51
1:L5:25:A:H2'	1:L5:26:C:H6	1.75	0.51
1:L5:1458:C:H5''	19:LQ:69:LYS:HE3	1.91	0.51
1:L5:4103:C:N3	1:L5:4107:G:N1	2.59	0.51
1:L5:4734:A:H2'	1:L5:4735:G:H8	1.76	0.51
2:L7:60:G:H2'	2:L7:61:G:H8	1.76	0.51
67:Sg:256:ILE:HB	67:Sg:270:LEU:HB2	1.92	0.51
1:L5:152:U:H5'	16:LN:55:ALA:HB3	1.93	0.51
1:L5:2743:A:H2'	1:L5:2744:A:C8	2.44	0.51
1:L5:4642:U:H2'	1:L5:4643:G:H8	1.74	0.51
14:LL:65:ARG:HG2	14:LL:66:TYR:CD2	2.46	0.51
46:S2:1670:C:H2'	46:S2:1671:G:C8	2.46	0.51
46:S2:1845:A:H2'	46:S2:1846:G:C8	2.45	0.51
47:SA:49:ILE:HD12	47:SA:49:ILE:H	1.76	0.51
86:3a:191:LYS:HE3	86:3a:243:MET:HB2	1.93	0.51
10:LG:105:GLU:HB2	10:LG:109:GLU:HG3	1.93	0.51
32:Ld:38:PHE:HB3	32:Ld:78:ARG:HD2	1.92	0.51
46:S2:16:G:H21	46:S2:1195:A:H62	1.59	0.51
46:S2:941:C:H2'	46:S2:942:G:H8	1.76	0.51
46:S2:1319:U:H2'	46:S2:1320:G:H8	1.76	0.51
89:3h:45:VAL:HG21	89:3h:78:ILE:HG22	1.91	0.51
89:3h:256:ASP:HA	89:3h:259:LYS:HG2	1.93	0.51
1:L5:1351:G:H2'	1:L5:1352:C:C6	2.46	0.51
1:L5:3848:U:H2'	1:L5:3849:A:C8	2.45	0.51
1:L5:4734:A:H2'	1:L5:4735:G:C8	2.45	0.51
5:LB:315:ASN:HD21	5:LB:326:VAL:HB	1.75	0.51
32:Ld:25:TYR:CE1	32:Ld:56:GLU:HG2	2.46	0.51
47:SA:74:VAL:HG12	47:SA:121:LEU:HB3	1.93	0.51
48:SB:67:PHE:HB3	73:SO:48:SER:HA	1.93	0.51
75:SY:58:PHE:HE1	75:SY:74:MET:HE2	1.75	0.51
79:sh:117:LEU:HD23	79:sh:117:LEU:H	1.75	0.51
84:3m:219:LEU:HB3	85:3f:306:ARG:HH12	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:3f:304:VAL:HG11	86:3a:537:ILE:HD13	1.93	0.51
1:L5:4324:A:H2'	1:L5:4325:A:C8	2.46	0.50
28:LZ:83:THR:HG22	28:LZ:85:TYR:H	1.76	0.50
71:Sf:11:VAL:HG13	71:Sf:15:ASN:HD22	1.75	0.50
73:SO:113:GLN:HA	73:SO:113:GLN:NE2	2.26	0.50
1:L5:518:G:H1	1:L5:643:C:H2'	1.76	0.50
1:L5:2749:C:H2'	1:L5:2750:G:H8	1.76	0.50
1:L5:3844:U:H2'	1:L5:3845:A:H8	1.76	0.50
1:L5:3916:G:H2'	1:L5:3917:A:H8	1.76	0.50
3:L8:28:C:H2'	3:L8:29:G:H8	1.75	0.50
15:LM:6:PHE:H	15:LM:11:ARG:HH21	1.59	0.50
26:LX:116:LEU:HD23	26:LX:117:TYR:CD2	2.47	0.50
49:SD:127:MET:HE2	49:SD:127:MET:HA	1.93	0.50
67:Sg:14:HIS:CE1	67:Sg:35:SER:HB2	2.47	0.50
71:Sf:64:LEU:O	71:Sf:68:LEU:HD22	2.11	0.50
83:zz:220:U:H2'	83:zz:221:G:C8	2.47	0.50
1:L5:3610:A:H2'	1:L5:3611:A:C8	2.44	0.50
1:L5:4186:A:H2'	1:L5:4187:G:C8	2.46	0.50
46:S2:71:G:H1	69:SG:170:ARG:HG2	1.77	0.50
46:S2:455:A:H5'	69:SG:94:ARG:HH21	1.77	0.50
46:S2:1511:U:HO2'	46:S2:1512:C:H6	1.58	0.50
46:S2:1665:G:C6	60:ST:88:MET:HE1	2.47	0.50
51:SF:35:LEU:HD12	51:SF:117:ILE:HG12	1.93	0.50
51:SF:134:VAL:HG12	51:SF:135:ARG:HD3	1.93	0.50
52:SH:30:LEU:HB3	52:SH:36:LEU:HD12	1.94	0.50
67:Sg:120:ILE:HB	67:Sg:132:TRP:HB2	1.94	0.50
76:SZ:79:ILE:HD12	76:SZ:83:LEU:HB3	1.92	0.50
1:L5:1700:G:P	6:LC:306:ARG:HH12	2.34	0.50
1:L5:3700:C:H2'	1:L5:3746:A:H61	1.76	0.50
1:L5:4352:U:H1'	29:La:58:MET:HE1	1.94	0.50
1:L5:4885:U:O4	1:L5:4936:G:O6	2.29	0.50
5:LB:8:ALA:HB2	24:LV:49:LEU:HD13	1.93	0.50
46:S2:113:G:N2	46:S2:292:A:H1'	2.27	0.50
46:S2:300:U:H2'	46:S2:301:A:H8	1.77	0.50
46:S2:1097:G:H4'	47:SA:32:PHE:CD2	2.47	0.50
47:SA:176:TRP:CD2	47:SA:199:PRO:HB3	2.46	0.50
73:SO:40:THR:HG21	73:SO:111:GLY:HA3	1.92	0.50
75:SY:41:ARG:HA	75:SY:55:ILE:HG21	1.93	0.50
84:3m:354:LEU:HA	84:3m:357:TRP:CE2	2.46	0.50
85:3f:202:VAL:HG22	85:3f:213:ILE:HG23	1.93	0.50
1:L5:287:U:H2'	1:L5:288:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LF:75:ALA:HB2	22:LT:140:PHE:HE1	1.77	0.50
21:LS:97:TYR:HE2	21:LS:109:CYS:HB2	1.77	0.50
25:LW:52:THR:HG23	25:LW:55:TYR:H	1.76	0.50
46:S2:201:C:H5''	46:S2:202:G:C8	2.47	0.50
46:S2:687:C:H1'	52:SH:116:ARG:HH21	1.76	0.50
46:S2:837:A:H62	75:SY:8:ARG:HE	1.60	0.50
53:SI:3:ILE:H	53:SI:3:ILE:HD12	1.76	0.50
62:SV:73:ALA:HB1	62:SV:78:ILE:HB	1.94	0.50
70:SJ:28:GLU:HG3	70:SJ:40:LYS:HD3	1.93	0.50
70:SJ:50:LEU:HD23	70:SJ:105:PHE:HD2	1.76	0.50
1:L5:663:G:H2'	1:L5:664:G:C8	2.46	0.50
1:L5:1645:C:H2'	1:L5:1646:A:C8	2.46	0.50
1:L5:3606:U:H2'	1:L5:3607:U:C6	2.47	0.50
8:LE:148:THR:HG22	8:LE:200:LYS:HG2	1.94	0.50
19:LQ:63:LEU:HB2	19:LQ:88:ASP:HA	1.93	0.50
27:LY:111:LEU:HD13	27:LY:116:LYS:HG3	1.93	0.50
57:SQ:13:PHE:HA	57:SQ:22:VAL:HA	1.91	0.50
67:Sg:36:ARG:HG2	67:Sg:65:PHE:CE2	2.46	0.50
1:L5:651:C:H2'	1:L5:652:G:C8	2.47	0.50
1:L5:1478:C:H2'	1:L5:1479:G:H8	1.76	0.50
1:L5:1989:G:H2'	1:L5:1990:A:C8	2.47	0.50
4:LA:225:ILE:HD11	4:LA:235:VAL:O	2.12	0.50
10:LG:166:LEU:HB3	16:LN:7:ILE:HD11	1.93	0.50
11:LH:126:VAL:HG11	11:LH:161:ILE:HG22	1.93	0.50
16:LN:71:ARG:HD2	16:LN:94:PHE:HD1	1.76	0.50
23:LU:48:LYS:HG2	23:LU:53:ALA:HB2	1.94	0.50
29:La:19:HIS:HB3	29:La:25:HIS:HB2	1.93	0.50
46:S2:429:C:H2'	46:S2:430:C:H6	1.76	0.50
46:S2:941:C:H2'	46:S2:942:G:C8	2.47	0.50
46:S2:1289:U:H2'	46:S2:1290:G:C8	2.47	0.50
58:SR:57:LEU:O	58:SR:61:ILE:HG22	2.12	0.50
68:SC:183:LYS:HB3	68:SC:196:ILE:HG22	1.93	0.50
71:Sf:67:ALA:HB1	79:sh:114:ILE:HD11	1.93	0.50
86:3a:47:HIS:HA	86:3a:50:ILE:HD12	1.94	0.50
1:L5:4239:A:H2'	1:L5:4240:G:C8	2.47	0.50
16:LN:118:SER:HB3	16:LN:132:VAL:HB	1.93	0.50
46:S2:406:U:H2'	46:S2:408:A:H8	1.77	0.50
60:ST:10:ASN:HD21	60:ST:13:GLU:HB2	1.76	0.50
87:3e:151:LEU:HD22	87:3e:168:SER:HB2	1.94	0.50
87:3e:319:LEU:HD23	87:3e:325:LEU:HD13	1.93	0.50
88:3c:69:ASN:HA	88:3c:72:LYS:HD3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4699:U:H1'	1:L5:4700:A:H5''	1.93	0.50
4:LA:117:GLU:HB2	4:LA:162:ASN:HB2	1.94	0.50
42:Ln:7:LYS:HE3	42:Ln:11:ARG:HH12	1.77	0.50
44:Lp:57:CYS:HB3	44:Lp:60:CYS:SG	2.49	0.50
46:S2:1413:G:H2'	46:S2:1414:A:H8	1.77	0.50
81:zx:20:ILE:HG13	81:zx:21:PRO:HD3	1.93	0.50
83:zz:220:U:H2'	83:zz:221:G:H8	1.77	0.50
89:3h:39:VAL:HG22	89:3h:76:LEU:HD23	1.94	0.50
1:L5:2743:A:H2'	1:L5:2744:A:H8	1.77	0.49
1:L5:3707:U:H2'	1:L5:3708:C:C6	2.46	0.49
1:L5:5006:U:H4'	1:L5:5007:A:H5'	1.93	0.49
11:LH:36:ARG:HH22	11:LH:76:HIS:CE1	2.30	0.49
46:S2:16:G:H2'	46:S2:17:C:C6	2.47	0.49
54:SK:24:LYS:HG3	54:SK:66:HIS:CE1	2.47	0.49
74:SW:8:ALA:HA	74:SW:74:VAL:HG11	1.94	0.49
1:L5:25:A:N6	1:L5:58:G:H1	2.07	0.49
1:L5:1847:C:H2'	1:L5:1848:C:C6	2.47	0.49
1:L5:3950:U:H3'	1:L5:3951:G:H8	1.77	0.49
4:LA:204:MET:HG3	4:LA:209:HIS:HB2	1.94	0.49
32:Ld:85:ARG:HG3	32:Ld:109:VAL:HG23	1.93	0.49
46:S2:17:C:H2'	46:S2:18:C:H6	1.77	0.49
46:S2:1570:G:H2'	46:S2:1571:G:H8	1.77	0.49
59:SS:117:ILE:HG23	59:SS:119:ALA:H	1.77	0.49
63:SX:46:HIS:HB3	63:SX:101:LEU:HD21	1.93	0.49
1:L5:1346:C:H2'	1:L5:1347:G:H8	1.77	0.49
1:L5:1950:U:H2'	1:L5:1951:G:H8	1.76	0.49
1:L5:3893:C:H2'	1:L5:3894:A:H8	1.76	0.49
1:L5:4892:A:H61	1:L5:4928:C:H42	1.60	0.49
10:LG:194:VAL:HG13	10:LG:196:ARG:HG2	1.94	0.49
28:LZ:7:PRO:HA	28:LZ:25:ILE:HG22	1.95	0.49
46:S2:493:A:H61	46:S2:510:G:H1'	1.77	0.49
46:S2:1777:G:H2'	46:S2:1778:C:O4'	2.12	0.49
67:Sg:87:LEU:HB2	67:Sg:101:PHE:HB2	1.95	0.49
92:3l:378:TYR:HE1	92:3l:497:MET:HA	1.77	0.49
1:L5:1683:U:H2'	1:L5:1684:A:H8	1.78	0.49
1:L5:1933:G:H2'	1:L5:1934:A:C8	2.47	0.49
1:L5:3861:A:H2'	1:L5:3862:A:C8	2.46	0.49
1:L5:3911:C:H2'	1:L5:3912:U:H6	1.78	0.49
3:L8:67:U:H2'	3:L8:68:G:H8	1.77	0.49
4:LA:44:ILE:HG23	4:LA:62:VAL:HG13	1.94	0.49
5:LB:56:ILE:HG22	5:LB:368:ILE:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LX:64:SER:HB2	36:Lh:69:LEU:HD23	1.95	0.49
29:La:127:LYS:HD3	29:La:148:ALA:HA	1.93	0.49
30:Lb:58:GLN:HA	30:Lb:61:ASN:HB2	1.94	0.49
31:Lc:102:SER:HB3	31:Lc:105:ILE:HD11	1.94	0.49
46:S2:151:C:H2'	46:S2:152:U:H6	1.78	0.49
85:3f:222:GLY:HA3	85:3f:226:ARG:HD2	1.94	0.49
87:3e:418:LEU:HA	87:3e:421:ASN:HB2	1.94	0.49
1:L5:318:A:H2'	1:L5:319:A:H8	1.76	0.49
1:L5:4274:A:H2'	1:L5:4275:G:C8	2.46	0.49
1:L5:4680:G:H2'	1:L5:4681:A:C8	2.47	0.49
12:LI:45:GLU:HG2	12:LI:46:PHE:HD1	1.78	0.49
14:LL:78:LEU:HD11	14:LL:88:LYS:HD3	1.92	0.49
24:LV:39:ILE:HD12	24:LV:61:VAL:HG11	1.95	0.49
28:LZ:37:PRO:HB3	88:3c:72:LYS:HE3	1.94	0.49
46:S2:375:U:H2'	46:S2:376:A:C8	2.47	0.49
46:S2:1218:C:H2'	46:S2:1219:C:H6	1.76	0.49
46:S2:1536:G:H2'	46:S2:1537:A:H8	1.78	0.49
52:SH:69:LEU:HD22	52:SH:96:ALA:HB2	1.94	0.49
72:SN:4:MET:HE2	72:SN:5:HIS:CE1	2.47	0.49
1:L5:513:U:H3'	1:L5:514:U:H4'	1.94	0.49
1:L5:908:G:H2'	1:L5:909:A:H8	1.78	0.49
46:S2:527:C:H2'	46:S2:528:A:C8	2.48	0.49
46:S2:1649:U:H5''	57:SQ:137:ALA:HB3	1.94	0.49
48:SB:71:LEU:HD23	48:SB:82:ARG:HB3	1.94	0.49
50:SE:11:ARG:CZ	50:SE:20:LEU:HD12	2.42	0.49
67:Sg:247:TRP:HB3	67:Sg:258:ILE:HD11	1.94	0.49
83:zz:205:A:H2'	83:zz:206:A:C8	2.47	0.49
1:L5:25:A:C8	1:L5:341:G:C8	3.00	0.49
1:L5:1468:C:H2'	1:L5:1469:C:H6	1.77	0.49
1:L5:1735:U:H2'	1:L5:1736:A:H8	1.78	0.49
1:L5:3832:U:H2'	1:L5:3833:C:H6	1.78	0.49
17:LO:186:GLU:HA	17:LO:189:ILE:HG13	1.95	0.49
27:LY:58:VAL:HG12	27:LY:59:ARG:HG2	1.94	0.49
28:LZ:4:PHE:HE1	31:Lc:39:ARG:HA	1.77	0.49
33:Le:75:ARG:HB2	33:Le:95:TYR:CD1	2.48	0.49
46:S2:106:C:H2'	46:S2:107:A:C8	2.48	0.49
46:S2:158:A:H2'	46:S2:159:A:O4'	2.13	0.49
85:3f:95:HIS:HB2	85:3f:98:ILE:HG12	1.94	0.49
87:3e:263:THR:HG23	87:3e:335:ASN:HD21	1.78	0.49
8:LE:222:LEU:HG	8:LE:237:LYS:HD3	1.95	0.49
14:LL:46:ILE:HG12	14:LL:49:ARG:HD2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LY:52:ASP:HB2	27:LY:110:LYS:HD2	1.93	0.49
41:Lm:103:LEU:HD21	41:Lm:110:CYS:HA	1.93	0.49
46:S2:49:C:H2'	46:S2:472:C:H41	1.77	0.49
46:S2:979:C:H2'	46:S2:980:A:H8	1.77	0.49
54:SK:93:THR:HG23	54:SK:94:LEU:HD23	1.95	0.49
56:SP:86:LEU:HB2	56:SP:89:MET:HE1	1.95	0.49
58:SR:9:VAL:HG23	58:SR:50:ILE:HG22	1.94	0.49
67:Sg:45:LEU:HB3	67:Sg:47:ARG:HE	1.78	0.49
70:SJ:97:ILE:HD12	70:SJ:97:ILE:H	1.76	0.49
83:zz:166:C:H41	83:zz:231:G:H5'	1.77	0.49
1:L5:1069:G:O2'	1:L5:1070:G:H5''	2.13	0.49
1:L5:1912:G:N2	17:LO:87:MET:HE2	2.27	0.49
7:LD:164:LYS:HG2	7:LD:195:HIS:HE1	1.78	0.49
17:LO:61:ARG:HA	17:LO:70:PRO:HD2	1.95	0.49
46:S2:538:U:H1'	46:S2:544:G:H1	1.78	0.49
47:SA:137:ALA:HB1	47:SA:142:LEU:HB3	1.95	0.49
64:Sa:26:CYS:HB3	64:Sa:77:CYS:SG	2.53	0.49
83:zz:270:C:H2'	83:zz:271:G:H8	1.78	0.49
1:L5:1194:G:H2'	1:L5:1195:G:C8	2.47	0.49
27:LY:71:VAL:HG12	27:LY:72:GLN:HG2	1.95	0.49
46:S2:1294:G:H2'	46:S2:1295:A:C8	2.48	0.49
46:S2:1405:A:H2'	46:S2:1406:G:O4'	2.13	0.49
48:SB:144:LYS:HB2	48:SB:208:HIS:HB3	1.95	0.49
57:SQ:32:ILE:HG21	57:SQ:39:LEU:HD22	1.94	0.49
84:3m:69:SER:HB2	85:3f:230:VAL:HG11	1.94	0.49
86:3a:465:PHE:HB3	88:3c:810:MET:HE1	1.95	0.49
88:3c:804:MET:HE2	88:3c:822:ILE:HD13	1.95	0.49
89:3h:168:ARG:HE	89:3h:169:LEU:N	2.11	0.49
1:L5:6:C:H5''	10:LG:197:LYS:HG2	1.95	0.48
1:L5:161:G:H2'	1:L5:162:A:H8	1.78	0.48
1:L5:659:G:H2'	1:L5:660:A:C8	2.48	0.48
1:L5:703:G:H2'	1:L5:704:C:H4'	1.94	0.48
1:L5:1604:G:H2'	1:L5:1605:G:C8	2.48	0.48
1:L5:2832:A:H2'	1:L5:2833:A:H8	1.78	0.48
1:L5:4186:A:H2'	1:L5:4187:G:H8	1.78	0.48
1:L5:4478:G:H2'	1:L5:4479:A:H8	1.78	0.48
21:LS:27:LEU:HD12	22:LT:148:PRO:HG3	1.94	0.48
44:Lp:8:VAL:HG23	44:Lp:11:VAL:HG23	1.95	0.48
46:S2:145:G:H2'	46:S2:146:G:H8	1.78	0.48
46:S2:731:G:H8	46:S2:733:C:H41	1.61	0.48
46:S2:1797:U:H2'	46:S2:1798:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
91:3k:80:THR:HA	91:3k:82:PHE:CE2	2.48	0.48
1:L5:3723:A:H2'	1:L5:3724:A:H8	1.77	0.48
1:L5:4626:A:H5'	5:LB:53:MET:HE1	1.94	0.48
3:L8:141:C:H2'	3:L8:142:U:C6	2.48	0.48
46:S2:1546:G:H21	46:S2:1670:C:H1'	1.78	0.48
59:SS:71:MET:HE3	59:SS:99:LEU:HG	1.94	0.48
72:SN:142:GLU:HB2	72:SN:145:THR:HG22	1.95	0.48
86:3a:401:LEU:HA	86:3a:458:LEU:HD11	1.94	0.48
1:L5:1824:G:H2'	1:L5:1825:A:H8	1.77	0.48
1:L5:4252:C:H3'	1:L5:4253:A:H8	1.78	0.48
1:L5:4744:A:H61	1:L5:4955:A:H61	1.62	0.48
10:LG:209:SER:HA	10:LG:212:LYS:HE3	1.95	0.48
22:LT:12:ARG:HD3	22:LT:13:TYR:HE2	1.78	0.48
46:S2:197:U:H3	46:S2:202:G:H1	1.60	0.48
46:S2:388:U:H2'	46:S2:389:A:C8	2.49	0.48
46:S2:505:G:H2'	46:S2:506:G:H8	1.78	0.48
46:S2:906:U:H2'	46:S2:907:G:H8	1.78	0.48
46:S2:1446:A:H1'	61:SU:55:ARG:HG3	1.93	0.48
46:S2:1457:U:H2'	46:S2:1458:G:C8	2.48	0.48
1:L5:106:A:H1'	1:L5:336:A:C8	2.46	0.48
1:L5:3633:C:H2'	1:L5:3634:G:C8	2.48	0.48
1:L5:3697:U:H5''	1:L5:3698:G:H5'	1.96	0.48
1:L5:4704:C:H2'	1:L5:4705:A:C8	2.49	0.48
21:LS:127:MET:HE1	22:LT:155:PRO:HA	1.95	0.48
24:LV:18:LEU:HD23	24:LV:54:ALA:HB3	1.95	0.48
46:S2:1128:C:H2'	46:S2:1129:G:C8	2.48	0.48
46:S2:1798:C:H2'	46:S2:1799:G:O4'	2.14	0.48
47:SA:145:ILE:HG12	47:SA:159:ILE:HB	1.95	0.48
50:SE:92:ILE:HG13	50:SE:97:GLU:HB2	1.95	0.48
53:SI:106:SER:HB3	53:SI:171:LEU:HG	1.94	0.48
73:SO:129:ILE:H	73:SO:129:ILE:HD12	1.78	0.48
76:SZ:51:ASP:HB2	76:SZ:54:THR:HG23	1.95	0.48
83:zz:310:A:H2'	83:zz:311:G:H8	1.78	0.48
1:L5:3916:G:H2'	1:L5:3917:A:C8	2.49	0.48
5:LB:24:ARG:HH21	5:LB:28:LYS:HE2	1.79	0.48
19:LQ:86:ILE:HB	19:LQ:105:VAL:HG22	1.95	0.48
24:LV:87:SER:HB3	24:LV:97:TYR:HB3	1.95	0.48
46:S2:442:C:H42	46:S2:449:A:H62	1.61	0.48
54:SK:5:LYS:H	54:SK:5:LYS:HG2	1.50	0.48
77:Sb:36:LYS:HE3	77:Sb:80:ARG:HH21	1.79	0.48
87:3e:316:GLU:HA	87:3e:319:LEU:HD12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LF:127:LYS:HB2	22:LT:133:ALA:HB3	1.94	0.48
19:LQ:181:ARG:NE	29:La:56:VAL:HG21	2.29	0.48
38:Lj:76:HIS:CG	38:Lj:79:ARG:HH21	2.32	0.48
83:zz:244:A:H2'	83:zz:245:G:C8	2.49	0.48
86:3a:386:GLU:HG2	86:3a:413:TRP:CG	2.49	0.48
87:3e:118:ALA:HA	87:3e:123:PHE:H	1.77	0.48
1:L5:659:G:H2'	1:L5:660:A:H8	1.78	0.48
1:L5:981:C:C4	8:LE:73:TYR:HE2	2.31	0.48
1:L5:1692:C:H5''	19:LQ:53:MET:HE2	1.95	0.48
1:L5:2402:G:H21	35:Lg:13:TYR:HE1	1.60	0.48
1:L5:2664:G:H5''	20:LR:110:ARG:HH12	1.79	0.48
1:L5:2902:G:N2	1:L5:3597:G:H22	2.11	0.48
1:L5:3746:A:H5''	4:LA:244:GLY:HA3	1.96	0.48
1:L5:3855:C:H2'	1:L5:3856:A:H8	1.78	0.48
1:L5:4745:G:N2	1:L5:4954:G:H22	2.12	0.48
6:LC:109:ARG:HD3	6:LC:111:TRP:CZ2	2.49	0.48
10:LG:32:PHE:HE1	28:LZ:53:VAL:HG12	1.77	0.48
13:LJ:75:ARG:HD3	13:LJ:75:ARG:HA	1.68	0.48
38:Lj:16:HIS:HD2	38:Lj:26:ALA:HA	1.79	0.48
46:S2:1310:U:H5'	79:sh:143:LYS:HG2	1.94	0.48
46:S2:1552:G:H2'	49:SD:3:VAL:HG13	1.95	0.48
46:S2:1553:C:H5''	49:SD:9:ARG:HH21	1.78	0.48
86:3a:336:THR:HG22	86:3a:338:ILE:H	1.78	0.48
1:L5:284:G:H2'	1:L5:285:G:H8	1.79	0.48
1:L5:1199:G:H2'	1:L5:1200:G:C8	2.48	0.48
1:L5:1511:U:H2'	1:L5:1512:G:C8	2.47	0.48
1:L5:1870:C:H2'	1:L5:1871:A:C8	2.48	0.48
1:L5:2634:C:H2'	1:L5:2635:U:H6	1.79	0.48
1:L5:3715:U:H5	1:L5:3738:G:H1	1.61	0.48
1:L5:4578:G:H2'	1:L5:4579:U:H6	1.79	0.48
6:LC:86:ARG:HA	6:LC:89:GLN:NE2	2.28	0.48
8:LE:152:ILE:HD11	8:LE:157:HIS:HB2	1.95	0.48
17:LO:202:LEU:HD12	17:LO:202:LEU:HA	1.76	0.48
68:SC:170:TRP:H	68:SC:178:HIS:HE1	1.60	0.48
83:zz:240:C:H2'	83:zz:241:G:C8	2.49	0.48
88:3c:671:VAL:HG23	88:3c:675:LEU:HD23	1.96	0.48
92:3l:221:ILE:HG12	92:3l:222:TRP:CD2	2.48	0.48
92:3l:535:VAL:HG12	92:3l:538:ARG:H	1.79	0.48
1:L5:1989:G:H2'	1:L5:1990:A:H8	1.79	0.48
1:L5:2283:G:H2'	1:L5:2284:G:C8	2.48	0.48
1:L5:2352:U:H1'	6:LC:96:CYS:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2756:G:H2'	1:L5:2757:A:C8	2.49	0.48
1:L5:3607:U:H2'	1:L5:3608:A:C8	2.48	0.48
1:L5:3684:G:H2'	1:L5:3685:C:C6	2.49	0.48
45:Lr:6:GLN:HB2	45:Lr:44:ILE:HD11	1.96	0.48
46:S2:1743:G:H21	46:S2:1791:A:N6	2.06	0.48
88:3c:744:MET:HE2	88:3c:744:MET:N	2.29	0.48
1:L5:4594:U:H2'	1:L5:4595:G:C8	2.49	0.48
18:LP:48:LEU:HD21	18:LP:91:LEU:HB3	1.96	0.48
25:LW:81:ALA:HB2	25:LW:87:LEU:HD23	1.94	0.48
46:S2:1413:G:H2'	46:S2:1414:A:C8	2.49	0.48
46:S2:1736:G:H2'	46:S2:1737:G:C8	2.48	0.48
48:SB:111:CYS:SG	64:Sa:68:TYR:HB2	2.53	0.48
49:SD:5:ILE:HG23	49:SD:9:ARG:HB2	1.95	0.48
49:SD:70:THR:HG22	49:SD:86:LEU:HG	1.95	0.48
85:3f:337:VAL:HG11	89:3h:239:LEU:HD11	1.96	0.48
1:L5:262:G:H2'	1:L5:263:G:C8	2.49	0.47
1:L5:710:G:H2'	1:L5:711:A:H8	1.78	0.47
1:L5:980:U:H2'	1:L5:981:C:C6	2.48	0.47
1:L5:4953:G:H2'	1:L5:4954:G:H8	1.79	0.47
3:L8:148:A:H2'	3:L8:149:G:C8	2.49	0.47
8:LE:168:LEU:HD11	8:LE:174:LEU:HB2	1.95	0.47
10:LG:150:LYS:HE2	10:LG:150:LYS:HB2	1.61	0.47
21:LS:10:TYR:HE2	21:LS:37:HIS:HA	1.78	0.47
33:Le:45:VAL:HG21	33:Le:53:ILE:HB	1.96	0.47
47:SA:70:ASN:HB3	47:SA:73:ASP:HB2	1.95	0.47
47:SA:189:ILE:HG12	47:SA:195:TRP:CD1	2.46	0.47
57:SQ:78:VAL:HA	57:SQ:81:ILE:HG22	1.95	0.47
74:SW:105:THR:HB	74:SW:110:ILE:HD13	1.95	0.47
1:L5:1996:C:H2'	1:L5:1997:U:C2	2.49	0.47
1:L5:2611:A:H2'	1:L5:2612:G:C8	2.49	0.47
1:L5:2679:G:H21	88:3c:73:ILE:HD11	1.78	0.47
1:L5:4260:U:H2'	1:L5:4261:C:H6	1.79	0.47
1:L5:4578:G:H2'	1:L5:4579:U:C6	2.49	0.47
7:LD:41:LYS:HG3	22:LT:93:ILE:HD11	1.96	0.47
9:LF:220:MET:O	9:LF:221:LYS:HG2	2.14	0.47
12:LI:52:MET:HB3	12:LI:152:LEU:HD13	1.95	0.47
12:LI:98:ARG:HB3	12:LI:120:GLY:HA3	1.96	0.47
21:LS:76:LYS:HG3	21:LS:78:PHE:CE2	2.47	0.47
37:Li:69:ALA:O	37:Li:73:ILE:HD12	2.14	0.47
46:S2:1403:C:H2'	46:S2:1433:C:H42	1.79	0.47
46:S2:1505:U:H5'	46:S2:1506:A:H5'	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1756:C:H2'	46:S2:1757:G:C4	2.49	0.47
68:SC:253:PRO:HA	68:SC:256:TRP:CD1	2.49	0.47
73:SO:43:HIS:HA	73:SO:55:ARG:HB2	1.96	0.47
88:3c:705:ALA:HB2	88:3c:858:GLN:HB3	1.96	0.47
1:L5:429:A:H2'	1:L5:430:G:C8	2.50	0.47
1:L5:3705:G:H2'	1:L5:3706:C:H6	1.79	0.47
1:L5:4510:A:H2'	1:L5:4511:A:C8	2.49	0.47
1:L5:4622:A:H4'	5:LB:13:SER:HB2	1.96	0.47
3:L8:28:C:H2'	3:L8:29:G:C8	2.50	0.47
9:LF:50:ILE:HG12	9:LF:186:CYS:HB3	1.96	0.47
12:LI:91:LEU:HD12	12:LI:91:LEU:HA	1.74	0.47
38:Lj:2:THR:HG22	38:Lj:4:GLY:H	1.78	0.47
46:S2:70:G:H21	46:S2:79:A:H62	1.63	0.47
58:SR:33:ARG:HG3	67:Sg:83:TRP:HZ3	1.79	0.47
66:Sd:31:ILE:HD11	66:Sd:33:LYS:HB2	1.96	0.47
67:Sg:149:GLU:OE1	67:Sg:170:TRP:HB2	2.14	0.47
1:L5:2019:C:H2'	1:L5:2020:U:C6	2.49	0.47
1:L5:4088:C:H2'	1:L5:4089:G:C8	2.49	0.47
1:L5:4691:A:H4'	11:LH:71:ARG:HG2	1.96	0.47
39:Lk:40:ARG:HH21	39:Lk:41:TYR:HE2	1.62	0.47
46:S2:298:G:H2'	46:S2:299:A:H8	1.79	0.47
46:S2:1805:G:H2'	46:S2:1806:A:H8	1.80	0.47
54:SK:53:LYS:HZ1	54:SK:60:GLU:HG2	1.79	0.47
58:SR:16:ILE:HD11	58:SR:54:VAL:HG21	1.96	0.47
70:SJ:37:LEU:HD11	70:SJ:106:LEU:HD11	1.96	0.47
1:L5:1530:G:H4'	38:Lj:47:TYR:HE1	1.79	0.47
1:L5:2732:G:H2'	1:L5:2733:C:H6	1.80	0.47
1:L5:3893:C:H1'	18:LP:69:ARG:HH21	1.79	0.47
6:LC:142:HIS:HD2	6:LC:204:ARG:HH12	1.61	0.47
6:LC:218:ILE:HD13	6:LC:229:LEU:HD12	1.95	0.47
50:SE:180:LEU:HB3	50:SE:192:ILE:HD11	1.96	0.47
57:SQ:113:ILE:HA	57:SQ:113:ILE:HD13	1.81	0.47
67:Sg:109:LEU:HD11	67:Sg:125:ARG:HG3	1.96	0.47
81:zx:15:LEU:HD12	81:zx:18:LYS:HG3	1.97	0.47
92:3l:179:PRO:HD2	92:3l:182:TRP:HE3	1.78	0.47
1:L5:1461:C:H2'	1:L5:1462:A:H8	1.79	0.47
1:L5:3789:C:H2'	1:L5:3790:U:C5	2.50	0.47
1:L5:4478:G:H2'	1:L5:4479:A:C8	2.49	0.47
8:LE:278:THR:H	8:LE:281:ILE:HD11	1.79	0.47
46:S2:560:A:H5'	70:SJ:174:LYS:HB2	1.96	0.47
46:S2:1661:A:C8	66:Sd:14:PHE:HD1	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SH:28:LEU:HA	52:SH:31:GLU:HB2	1.96	0.47
60:ST:44:GLU:HB3	60:ST:45:LEU:HD23	1.96	0.47
81:zx:9:LYS:HD3	81:zx:9:LYS:HA	1.65	0.47
88:3c:625:LEU:HD21	88:3c:628:ASP:H	1.80	0.47
88:3c:679:LEU:HD13	88:3c:682:LEU:HD23	1.96	0.47
1:L5:691:C:H2'	1:L5:692:A:C8	2.50	0.47
1:L5:979:C:H4'	8:LE:43:HIS:HB2	1.96	0.47
1:L5:1392:A:H2'	1:L5:1393:G:C8	2.50	0.47
1:L5:2411:C:H2'	1:L5:2412:A:C8	2.47	0.47
1:L5:2521:G:H2'	1:L5:2522:G:C8	2.47	0.47
1:L5:3932:U:H2'	1:L5:3933:G:H8	1.79	0.47
1:L5:4704:C:H2'	1:L5:4705:A:H8	1.79	0.47
1:L5:5024:C:N4	1:L5:5028:G:H21	2.13	0.47
4:LA:96:LEU:HD23	44:Lp:83:ILE:HG23	1.96	0.47
8:LE:151:ILE:HG13	8:LE:195:ILE:HB	1.95	0.47
11:LH:18:ILE:HG22	11:LH:27:VAL:HG22	1.97	0.47
16:LN:51:LEU:HD12	16:LN:117:ASN:HB3	1.96	0.47
19:LQ:22:ASP:HB3	19:LQ:25:LEU:HB2	1.96	0.47
20:LR:38:ARG:C	20:LR:40:GLN:H	2.22	0.47
26:LX:78:LYS:HB2	26:LX:99:ILE:HG22	1.96	0.47
31:Lc:38:ILE:HG21	31:Lc:63:TYR:HB3	1.95	0.47
43:Lo:25:GLN:HG3	43:Lo:66:ILE:HD11	1.97	0.47
46:S2:528:A:H2'	46:S2:529:A:C8	2.50	0.47
46:S2:982:G:H2'	46:S2:983:A:H8	1.80	0.47
46:S2:1589:A:H2'	46:S2:1590:C:C6	2.49	0.47
46:S2:1778:C:H2'	46:S2:1779:G:O4'	2.14	0.47
47:SA:116:PHE:HE2	68:SC:64:THR:HG22	1.79	0.47
48:SB:128:LYS:HA	48:SB:134:LEU:HA	1.96	0.47
54:SK:95:ARG:HH12	54:SK:98:ARG:HA	1.80	0.47
61:SU:22:ILE:HG13	61:SU:89:ILE:HB	1.96	0.47
61:SU:56:MET:HG3	61:SU:86:LYS:NZ	2.30	0.47
69:SG:70:HIS:HA	69:SG:101:ILE:HD11	1.96	0.47
87:3e:322:ASP:HB3	87:3e:325:LEU:HB2	1.96	0.47
88:3c:749:TRP:HE1	88:3c:783:ILE:HG23	1.80	0.47
89:3h:130:THR:HG23	89:3h:133:LEU:H	1.80	0.47
91:3k:188:PHE:HZ	91:3k:191:SER:HB2	1.79	0.47
92:3l:382:ILE:HG22	92:3l:383:ASP:H	1.79	0.47
1:L5:1558:A:H2'	1:L5:1559:G:C8	2.49	0.47
1:L5:2333:G:H5''	6:LC:195:LYS:HE2	1.95	0.47
1:L5:4364:G:H2'	1:L5:4365:C:H6	1.80	0.47
3:L8:82:A:H62	3:L8:84:A:H3'	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:147:G:H2'	3:L8:148:A:H8	1.78	0.47
12:LI:180:GLU:O	12:LI:184:MET:HG3	2.14	0.47
49:SD:96:LEU:HD11	49:SD:131:ALA:HB2	1.96	0.47
60:ST:22:LEU:HD12	60:ST:28:LEU:HD21	1.96	0.47
69:SG:137:ARG:HD3	69:SG:178:ARG:HD2	1.97	0.47
86:3a:222:ASN:HD21	86:3a:225:SER:HB3	1.80	0.47
88:3c:430:ASN:HD21	88:3c:438:LEU:HA	1.80	0.47
91:3k:139:ARG:HH22	91:3k:173:TRP:CD1	2.32	0.47
1:L5:1699:A:H2'	1:L5:1700:G:N3	2.30	0.47
1:L5:2634:C:H2'	1:L5:2635:U:C6	2.49	0.47
1:L5:4523:A:H5''	1:L5:4524:G:H5'	1.96	0.47
1:L5:4621:C:H2'	1:L5:4622:A:H8	1.79	0.47
15:LM:77:TRP:CD2	15:LM:82:ILE:HD12	2.49	0.47
39:Lk:37:ARG:HD2	39:Lk:37:ARG:HA	1.77	0.47
46:S2:19:A:H5'	63:SX:107:ARG:HH11	1.80	0.47
46:S2:391:C:H2'	46:S2:392:A:H8	1.79	0.47
50:SE:31:PRO:HB3	50:SE:43:PRO:HB3	1.97	0.47
51:SF:112:LEU:HD12	51:SF:177:LEU:HD21	1.96	0.47
68:SC:166:ARG:HG2	68:SC:181:PRO:HG3	1.95	0.47
75:SY:127:ALA:HA	75:SY:130:LYS:HE3	1.97	0.47
91:3k:139:ARG:HH22	91:3k:173:TRP:CG	2.33	0.47
1:L5:251:C:H2'	1:L5:252:C:C6	2.50	0.47
1:L5:3664:G:H2'	1:L5:3665:G:H8	1.80	0.47
1:L5:4188:U:H2'	1:L5:4189:U:C6	2.50	0.47
11:LH:123:ILE:HG21	11:LH:125:ARG:HH21	1.80	0.47
14:LL:130:LYS:HD2	14:LL:130:LYS:HA	1.71	0.47
15:LM:77:TRP:CE2	15:LM:82:ILE:HD12	2.50	0.47
46:S2:677:G:N2	46:S2:1028:A:H62	2.08	0.47
46:S2:794:A:H2'	46:S2:795:A:H4'	1.97	0.47
46:S2:1114:U:H2'	46:S2:1115:U:C6	2.50	0.47
49:SD:35:SER:HB2	49:SD:51:LEU:HB2	1.98	0.47
59:SS:45:LEU:HD12	59:SS:50:ILE:HB	1.97	0.47
89:3h:253:MET:O	89:3h:253:MET:HE3	2.14	0.47
92:3l:394:TYR:HB3	92:3l:397:LYS:HB2	1.96	0.47
1:L5:1298:C:H2'	1:L5:1299:G:C8	2.50	0.46
1:L5:3910:C:H2'	1:L5:3911:C:C6	2.50	0.46
1:L5:4066:U:H2'	1:L5:4067:U:C6	2.49	0.46
1:L5:4761:G:H2'	1:L5:4762:A:C4	2.51	0.46
9:LF:161:LYS:HB2	9:LF:209:TRP:HE3	1.80	0.46
15:LM:13:ALA:HA	15:LM:58:THR:HG23	1.95	0.46
46:S2:1562:C:H2'	46:S2:1563:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SN:132:LYS:HD3	72:SN:132:LYS:HA	1.73	0.46
83:zz:320:G:H2'	83:zz:321:A:C8	2.49	0.46
88:3c:803:SER:HA	88:3c:841:THR:HG22	1.97	0.46
92:3l:395:GLY:HA2	92:3l:398:MET:HE2	1.97	0.46
1:L5:287:U:H2'	1:L5:288:G:H8	1.79	0.46
1:L5:2566:G:H2'	1:L5:2567:G:C8	2.50	0.46
1:L5:3950:U:H3'	1:L5:3951:G:C8	2.50	0.46
6:LC:116:ASN:HB2	6:LC:119:GLN:HG2	1.97	0.46
18:LP:148:MET:HE2	18:LP:150:LEU:HD11	1.97	0.46
25:LW:49:ILE:HD12	25:LW:49:ILE:HA	1.78	0.46
26:LX:91:GLU:HB3	26:LX:147:LEU:HD21	1.97	0.46
46:S2:331:C:H5	69:SG:189:ARG:HD2	1.80	0.46
46:S2:921:G:C6	74:SW:28:ARG:HD3	2.50	0.46
53:SI:203:LYS:HD3	53:SI:203:LYS:HA	1.72	0.46
57:SQ:8:GLN:HG2	57:SQ:99:TYR:CZ	2.50	0.46
67:Sg:210:GLY:HA3	67:Sg:236:ILE:HG21	1.98	0.46
69:SG:32:MET:HE3	69:SG:33:ALA:N	2.30	0.46
71:Sf:53:ALA:HA	71:Sf:79:VAL:HG12	1.97	0.46
83:zz:258:G:H22	83:zz:273:G:H2'	1.80	0.46
89:3h:266:ASN:HB3	89:3h:308:PRO:HG3	1.97	0.46
1:L5:2745:A:H2'	1:L5:2746:A:C8	2.47	0.46
1:L5:3867:A:H2'	1:L5:3868:G:C8	2.50	0.46
1:L5:4642:U:H2'	1:L5:4643:G:C8	2.51	0.46
1:L5:4960:G:H2'	1:L5:4961:G:C8	2.49	0.46
12:LI:95:HIS:O	12:LI:126:VAL:HG12	2.16	0.46
16:LN:183:THR:HG22	16:LN:188:ARG:N	2.30	0.46
21:LS:92:ASN:HD21	22:LT:156:TYR:N	2.14	0.46
29:La:93:ASN:ND2	29:La:97:ALA:HB3	2.31	0.46
57:SQ:50:LYS:HB2	57:SQ:50:LYS:HE2	1.77	0.46
70:SJ:131:ARG:HA	70:SJ:131:ARG:HD2	1.75	0.46
1:L5:164:G:H2'	1:L5:165:A:H8	1.79	0.46
1:L5:207:G:H2'	1:L5:208:A:C8	2.50	0.46
1:L5:512:U:H2'	1:L5:513:U:H4'	1.97	0.46
1:L5:1334:A:H2'	1:L5:1335:G:H8	1.79	0.46
1:L5:1346:C:H2'	1:L5:1347:G:C8	2.51	0.46
1:L5:1839:U:H2'	1:L5:1840:G:C8	2.49	0.46
1:L5:4273:A:H2'	1:L5:4274:A:C8	2.51	0.46
6:LC:289:LEU:HB2	45:Lr:4:HIS:CE1	2.49	0.46
10:LG:190:LEU:HD23	10:LG:190:LEU:HA	1.76	0.46
34:Lf:104:MET:HE3	34:Lf:104:MET:HB3	1.78	0.46
46:S2:1348:G:H2'	46:S2:1349:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1453:C:H5'	58:SR:48:ASN:HB3	1.97	0.46
46:S2:1680:G:H2'	46:S2:1681:U:C6	2.50	0.46
68:SC:170:TRP:CE2	68:SC:199:PRO:HG3	2.51	0.46
68:SC:180:VAL:HG22	68:SC:181:PRO:HD2	1.98	0.46
83:zz:320:G:H2'	83:zz:321:A:H8	1.79	0.46
89:3h:67:LEU:HD23	89:3h:78:ILE:HG21	1.96	0.46
1:L5:436:C:H2'	1:L5:437:G:H8	1.81	0.46
1:L5:663:G:H2'	1:L5:664:G:H8	1.81	0.46
1:L5:710:G:H2'	1:L5:711:A:C8	2.50	0.46
1:L5:1577:G:H5'	1:L5:1578:U:H5''	1.97	0.46
1:L5:2775:C:H2'	1:L5:2776:G:C8	2.50	0.46
1:L5:3633:C:H2'	1:L5:3634:G:H8	1.80	0.46
1:L5:3722:G:H2'	1:L5:3723:A:H8	1.80	0.46
1:L5:3767:C:H2'	1:L5:3768:U:C6	2.51	0.46
6:LC:150:LEU:HD12	6:LC:150:LEU:HA	1.74	0.46
13:LJ:173:ILE:HD12	13:LJ:173:ILE:H	1.81	0.46
36:Lh:50:VAL:O	36:Lh:54:ILE:HG13	2.15	0.46
48:SB:171:ILE:HD12	48:SB:174:ARG:HE	1.80	0.46
51:SF:104:THR:HG23	51:SF:106:GLU:H	1.80	0.46
89:3h:129:VAL:HB	89:3h:322:GLN:HG3	1.97	0.46
1:L5:123:C:H2'	1:L5:124:C:H6	1.81	0.46
1:L5:164:G:H2'	1:L5:165:A:C8	2.51	0.46
1:L5:1646:A:H1'	38:Lj:49:TRP:CZ3	2.51	0.46
1:L5:4238:G:H2'	1:L5:4239:A:H8	1.80	0.46
8:LE:62:MET:HE1	8:LE:65:ARG:HD3	1.98	0.46
18:LP:51:VAL:HG23	18:LP:56:GLN:O	2.15	0.46
46:S2:1092:G:H2'	46:S2:1093:A:H8	1.81	0.46
46:S2:1462:U:H2'	46:S2:1464:C:C4	2.51	0.46
46:S2:1675:A:H1'	51:SF:77:MET:HG2	1.98	0.46
46:S2:1681:U:H2'	46:S2:1682:C:C6	2.51	0.46
47:SA:30:LEU:HD22	47:SA:47:TYR:HE2	1.81	0.46
61:SU:56:MET:HG3	61:SU:86:LYS:HZ2	1.80	0.46
64:Sa:13:LYS:HD2	64:Sa:13:LYS:HA	1.71	0.46
67:Sg:17:TRP:HB2	67:Sg:36:ARG:HD2	1.98	0.46
68:SC:69:LEU:HD21	68:SC:273:LEU:HD12	1.98	0.46
84:3m:129:LYS:HG3	84:3m:167:LEU:HD13	1.98	0.46
1:L5:37:U:H4'	29:La:32:ARG:HD2	1.98	0.46
1:L5:1086:C:H2'	1:L5:1087:A:H8	1.80	0.46
1:L5:2285:A:H2'	1:L5:2286:G:H8	1.81	0.46
1:L5:3707:U:H2'	1:L5:3708:C:H6	1.81	0.46
4:LA:114:CYS:SG	4:LA:169:VAL:HB	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LD:228:LYS:HB2	7:LD:228:LYS:HE2	1.74	0.46
10:LG:141:ASN:HD21	16:LN:4:TYR:HE1	1.64	0.46
15:LM:137:LYS:HE3	15:LM:137:LYS:HB3	1.73	0.46
16:LN:33:LEU:HD13	16:LN:37:HIS:ND1	2.30	0.46
16:LN:94:PHE:HE2	16:LN:96:ARG:HB2	1.81	0.46
17:LO:142:ALA:HA	17:LO:145:VAL:HG12	1.98	0.46
46:S2:432:G:H2'	46:S2:433:A:H8	1.80	0.46
48:SB:56:LYS:HE2	48:SB:56:LYS:HB2	1.69	0.46
69:SG:217:MET:HE2	69:SG:217:MET:HB2	1.86	0.46
85:3f:335:LEU:HB3	92:3l:547:ILE:HG21	1.98	0.46
87:3e:236:PHE:HD2	87:3e:257:LEU:HD13	1.81	0.46
88:3c:855:LEU:HA	88:3c:858:GLN:HE21	1.80	0.46
1:L5:257:C:H2'	1:L5:258:G:C8	2.51	0.46
1:L5:1577:G:O2'	1:L5:1612:G:H4'	2.15	0.46
1:L5:4562:C:H2'	1:L5:4563:U:C6	2.51	0.46
5:LB:211:PHE:HE1	5:LB:349:LYS:HG3	1.80	0.46
8:LE:264:ILE:HB	8:LE:267:LEU:HD12	1.98	0.46
12:LI:87:MET:HE3	12:LI:88:ARG:N	2.30	0.46
29:La:73:VAL:HB	29:La:108:TYR:CD1	2.51	0.46
44:Lp:47:MET:HG2	44:Lp:71:TYR:HE1	1.79	0.46
76:SZ:88:LEU:HB3	76:SZ:109:TYR:HE2	1.80	0.46
84:3m:162:HIS:HB3	84:3m:166:ARG:HH22	1.81	0.46
86:3a:312:GLN:H	86:3a:312:GLN:HG3	1.61	0.46
88:3c:678:ASN:HB3	88:3c:681:LEU:HB3	1.97	0.46
1:L5:1177:U:C4	1:L5:1183:C:N4	2.82	0.46
1:L5:1951:G:H5'	21:LS:116:ARG:HH11	1.81	0.46
1:L5:2513:A:C4	35:Lg:13:TYR:HD2	2.34	0.46
1:L5:2633:U:H2'	1:L5:2634:C:H6	1.80	0.46
1:L5:3732:A:H2'	1:L5:3733:A:C8	2.51	0.46
3:L8:13:G:H2'	3:L8:14:U:C6	2.51	0.46
16:LN:191:ALA:O	16:LN:195:ARG:HG3	2.16	0.46
25:LW:34:ALA:HA	25:LW:37:GLU:HB2	1.97	0.46
29:La:93:ASN:HD21	29:La:97:ALA:HB3	1.81	0.46
44:Lp:37:TYR:CD2	44:Lp:71:TYR:HB2	2.50	0.46
50:SE:192:ILE:HD13	50:SE:228:ILE:HD11	1.98	0.46
59:SS:64:VAL:O	59:SS:68:ILE:HG12	2.16	0.46
70:SJ:107:GLU:HA	70:SJ:112:THR:HG21	1.97	0.46
75:SY:4:THR:HB	75:SY:30:PRO:HD2	1.98	0.46
84:3m:193:THR:HG22	84:3m:196:ASN:HB3	1.97	0.46
85:3f:99:LEU:HD12	85:3f:102:ILE:HD12	1.98	0.46
92:3l:243:GLN:HB3	92:3l:253:PRO:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:266:C:H1'	1:L5:267:G:C8	2.50	0.46
1:L5:280:G:H5''	16:LN:14:LYS:NZ	2.31	0.46
1:L5:1848:C:H2'	1:L5:1849:U:O4'	2.16	0.46
1:L5:2540:C:H2'	1:L5:2541:G:H8	1.81	0.46
1:L5:3710:G:H2'	1:L5:3712:A:C6	2.50	0.46
1:L5:3768:U:H2'	1:L5:3769:C:H6	1.80	0.46
1:L5:3805:U:H2'	1:L5:3806:G:H8	1.81	0.46
1:L5:5001:U:H4'	5:LB:317:LEU:HB3	1.98	0.46
26:LX:100:VAL:HG23	26:LX:134:LYS:HB2	1.98	0.46
46:S2:96:C:H2'	46:S2:97:U:C6	2.51	0.46
46:S2:982:G:H2'	46:S2:983:A:C8	2.50	0.46
46:S2:1416:C:H2'	46:S2:1417:C:C6	2.51	0.46
63:SX:41:PHE:HZ	63:SX:102:VAL:HG12	1.81	0.46
68:SC:73:MET:HE2	68:SC:73:MET:HB3	1.75	0.46
68:SC:145:LYS:HB3	68:SC:145:LYS:HE2	1.63	0.46
69:SG:221:LYS:HD2	69:SG:224:ARG:HH12	1.81	0.46
71:Sf:129:LYS:HD3	71:Sf:129:LYS:HA	1.75	0.46
73:SO:46:ASP:OD2	73:SO:51:GLU:HB2	2.16	0.46
85:3f:354:LEU:HD21	88:3c:874:PHE:HB2	1.98	0.46
86:3a:330:PRO:HA	86:3a:434:ASN:HD21	1.81	0.46
86:3a:450:ILE:HG21	86:3a:455:LEU:HD13	1.97	0.46
88:3c:117:LEU:HD11	88:3c:141:LEU:HD23	1.97	0.46
92:3l:125:ASP:HB3	92:3l:128:PHE:HB3	1.98	0.46
1:L5:1193:C:H2'	1:L5:1194:G:C8	2.50	0.45
1:L5:1994:C:H2'	1:L5:1995:G:C8	2.51	0.45
1:L5:2557:G:O6	1:L5:2570:U:O4	2.33	0.45
1:L5:4563:U:H2'	1:L5:4564:A:H8	1.81	0.45
3:L8:44:A:H2'	3:L8:45:C:C6	2.51	0.45
12:LI:152:LEU:HD23	12:LI:152:LEU:HA	1.79	0.45
22:LT:66:ASN:ND2	30:Lb:35:VAL:HA	2.31	0.45
46:S2:520:A:H5''	70:SJ:12:THR:HG22	1.97	0.45
46:S2:1217:A:H2'	46:S2:1218:C:C6	2.51	0.45
46:S2:1401:A:H4'	61:SU:52:GLY:HA3	1.98	0.45
51:SF:169:ILE:HA	51:SF:172:CYS:HB2	1.98	0.45
68:SC:77:SER:O	68:SC:80:GLU:HG3	2.15	0.45
74:SW:115:GLU:HB3	74:SW:118:ARG:NH2	2.32	0.45
85:3f:100:ALA:HB1	89:3h:44:LEU:HG	1.97	0.45
92:3l:283:LEU:HB3	92:3l:421:LEU:HD13	1.97	0.45
1:L5:1970:A:H5''	1:L5:1971:C:H5'	1.97	0.45
1:L5:2413:U:H2'	1:L5:2414:G:H8	1.81	0.45
1:L5:3723:A:H2'	1:L5:3724:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:153:C:H2'	3:L8:154:G:H8	1.81	0.45
5:LB:238:LYS:HE2	5:LB:238:LYS:HB2	1.69	0.45
34:Lf:63:LYS:HD3	34:Lf:63:LYS:HA	1.57	0.45
45:Lr:33:LYS:HE2	45:Lr:40:TYR:HE2	1.80	0.45
46:S2:1103:C:H2'	46:S2:1104:G:H8	1.81	0.45
46:S2:1421:A:H2'	46:S2:1422:G:C2	2.51	0.45
46:S2:1606:G:H22	46:S2:1632:G:H2'	1.82	0.45
66:Sd:13:LYS:CD	66:Sd:14:PHE:H	2.27	0.45
82:zy:30:C:H2'	82:zy:31:U:H6	1.80	0.45
84:3m:244:PHE:HZ	84:3m:276:LYS:HD2	1.79	0.45
1:L5:1296:G:H2'	1:L5:1297:U:C6	2.51	0.45
1:L5:2018:C:H2'	1:L5:2019:C:C6	2.52	0.45
1:L5:3615:G:H5'	25:LW:48:GLN:HG2	1.99	0.45
1:L5:3946:G:O6	1:L5:4067:U:O4	2.34	0.45
21:LS:84:TYR:HB2	21:LS:124:ILE:HG22	1.98	0.45
46:S2:115:U:H2'	46:S2:116:U:C6	2.51	0.45
46:S2:349:A:H2'	46:S2:350:C:C6	2.51	0.45
46:S2:979:C:H2'	46:S2:980:A:C8	2.52	0.45
46:S2:1781:A:H2'	46:S2:1783:C:C2	2.51	0.45
47:SA:118:GLU:HA	47:SA:119:PRO:HD3	1.83	0.45
51:SF:61:PHE:CE1	65:Sc:49:PRO:HB2	2.51	0.45
52:SH:130:LEU:HD23	52:SH:130:LEU:HA	1.81	0.45
59:SS:48:ALA:HB2	59:SS:70:ILE:HD12	1.97	0.45
60:ST:56:ARG:O	60:ST:60:THR:HG22	2.17	0.45
66:Sd:13:LYS:HD3	66:Sd:14:PHE:N	2.28	0.45
70:SJ:113:GLN:HG3	70:SJ:149:VAL:HG21	1.99	0.45
83:zz:181:G:H2'	83:zz:182:A:C8	2.52	0.45
89:3h:313:ARG:HD2	89:3h:313:ARG:HA	1.82	0.45
92:3l:66:LEU:HD21	92:3l:177:GLU:HB2	1.98	0.45
1:L5:462:G:H2'	1:L5:463:A:C8	2.52	0.45
12:LI:91:LEU:HD22	12:LI:135:ILE:HG23	1.98	0.45
18:LP:37:LYS:HB3	18:LP:37:LYS:HE3	1.68	0.45
44:Lp:29:ILE:HD11	44:Lp:69:TRP:CD2	2.51	0.45
45:Lr:48:THR:HG22	45:Lr:65:LYS:HD2	1.98	0.45
46:S2:5:U:H2'	46:S2:6:G:H8	1.81	0.45
46:S2:122:G:H2'	46:S2:123:G:C8	2.52	0.45
46:S2:643:A:H4'	46:S2:644:G:H5'	1.97	0.45
50:SE:62:LYS:O	50:SE:66:MET:HG2	2.16	0.45
51:SF:103:LEU:HD12	76:SZ:67:LEU:HD12	1.98	0.45
70:SJ:30:LYS:HB2	78:Se:42:PHE:HE1	1.81	0.45
70:SJ:32:ILE:HG13	70:SJ:37:LEU:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
89:3h:246:LEU:O	89:3h:250:VAL:HG23	2.17	0.45
1:L5:2095:A:H4'	1:L5:2096:G:C5	2.51	0.45
1:L5:3911:C:H2'	1:L5:3912:U:C6	2.52	0.45
31:Lc:48:LEU:HD21	31:Lc:60:ILE:HG21	1.99	0.45
43:Lo:66:ILE:HD12	43:Lo:67:VAL:H	1.81	0.45
46:S2:306:C:H2'	46:S2:307:G:C2	2.51	0.45
46:S2:842:C:H2'	46:S2:843:C:C6	2.51	0.45
46:S2:1286:G:H2'	46:S2:1312:G:N2	2.32	0.45
67:Sg:217:MET:HG3	67:Sg:219:TRP:NE1	2.32	0.45
70:SJ:78:LEU:HD21	70:SJ:97:ILE:HD11	1.99	0.45
71:Sf:96:ARG:HG2	71:Sf:97:GLU:H	1.80	0.45
86:3a:407:VAL:HG12	86:3a:411:LEU:HD23	1.98	0.45
1:L5:1415:G:H2'	1:L5:1416:G:H8	1.82	0.45
1:L5:1514:U:H2'	1:L5:1515:A:H8	1.81	0.45
1:L5:1876:U:H2'	1:L5:1877:G:H8	1.81	0.45
1:L5:3872:A:H2'	1:L5:3873:G:H8	1.81	0.45
1:L5:3893:C:H2'	1:L5:3894:A:C8	2.51	0.45
1:L5:4260:U:H2'	1:L5:4261:C:C6	2.52	0.45
1:L5:4736:C:H2'	1:L5:4737:G:H8	1.81	0.45
6:LC:155:GLU:HG2	6:LC:157:LYS:H	1.81	0.45
21:LS:11:LYS:HE3	21:LS:29:ARG:HD2	1.98	0.45
46:S2:67:C:H2'	69:SG:162:LEU:HD11	1.97	0.45
46:S2:1438:A:H2'	46:S2:1439:A:C8	2.51	0.45
46:S2:1610:G:H2'	46:S2:1611:G:C8	2.52	0.45
48:SB:85:LYS:HB2	48:SB:101:HIS:HB3	1.99	0.45
61:SU:40:ILE:HD12	61:SU:40:ILE:HA	1.83	0.45
83:zz:223:A:O2'	83:zz:224:G:H8	2.00	0.45
83:zz:277:G:H2'	83:zz:278:G:H8	1.80	0.45
87:3e:219:LEU:HD21	87:3e:253:ILE:HG23	1.99	0.45
88:3c:745:LYS:HA	88:3c:745:LYS:HD2	1.61	0.45
91:3k:171:LYS:HA	91:3k:171:LYS:HD3	1.69	0.45
1:L5:2358:G:H2'	1:L5:2359:U:O4'	2.17	0.45
4:LA:177:LYS:HB2	44:Lp:29:ILE:HD13	1.98	0.45
5:LB:366:LYS:HE2	5:LB:366:LYS:HB3	1.77	0.45
9:LF:232:ASP:HB2	9:LF:236:ARG:NH2	2.32	0.45
12:LI:36:LEU:HD11	12:LI:69:ARG:HD2	1.99	0.45
15:LM:94:LYS:HE3	15:LM:94:LYS:HB2	1.62	0.45
21:LS:31:ARG:HH22	21:LS:129:VAL:HB	1.81	0.45
27:LY:72:GLN:HG3	27:LY:81:TYR:HD2	1.82	0.45
30:Lb:91:ARG:HB3	30:Lb:94:ASP:HB3	1.99	0.45
46:S2:65:C:C4	69:SG:133:LEU:HG	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:107:A:H2'	46:S2:108:G:C8	2.52	0.45
46:S2:1103:C:H2'	46:S2:1104:G:C8	2.51	0.45
48:SB:160:GLN:O	48:SB:164:ILE:HG13	2.17	0.45
53:SI:31:ARG:HH12	53:SI:48:VAL:HG12	1.81	0.45
55:SL:99:TYR:CE2	63:SX:13:LEU:HB3	2.51	0.45
63:SX:53:GLU:HB3	63:SX:71:ARG:HB3	1.99	0.45
63:SX:101:LEU:HD12	63:SX:124:LYS:HD2	1.99	0.45
69:SG:51:ARG:HB3	69:SG:112:VAL:HG13	1.99	0.45
73:SO:113:GLN:CA	73:SO:113:GLN:NE2	2.80	0.45
83:zz:172:A:H2'	83:zz:173:A:C8	2.52	0.45
90:3d:26:ARG:HA	90:3d:30:TYR:HE2	1.81	0.45
1:L5:173:C:H5'	14:LL:129:ARG:HH21	1.80	0.45
1:L5:1519:C:H2'	1:L5:1520:C:H6	1.82	0.45
1:L5:1617:G:H2'	1:L5:1618:G:C8	2.52	0.45
1:L5:3880:G:H2'	1:L5:3881:G:C8	2.52	0.45
3:L8:13:G:H1'	18:LP:120:ASN:HD22	1.81	0.45
7:LD:111:ASN:ND2	7:LD:252:VAL:HG22	2.30	0.45
19:LQ:89:ASP:HB3	19:LQ:92:VAL:HG12	1.99	0.45
23:LU:37:ALA:N	23:LU:65:ARG:HH22	2.15	0.45
24:LV:85:ARG:HD2	24:LV:85:ARG:HA	1.79	0.45
30:Lb:101:HIS:ND1	30:Lb:104:LEU:HG	2.31	0.45
68:SC:209:VAL:HG11	68:SC:233:LEU:HD11	1.98	0.45
92:3l:326:MET:HE1	92:3l:328:ARG:HD3	1.99	0.45
1:L5:146:G:H2'	1:L5:147:A:H8	1.82	0.45
1:L5:725:G:H2'	1:L5:726:G:H8	1.82	0.45
1:L5:1391:A:P	19:LQ:181:ARG:HH22	2.40	0.45
1:L5:2375:A:H2'	1:L5:2376:A:C8	2.49	0.45
3:L8:153:C:H5'	10:LG:185:LYS:HD3	1.98	0.45
13:LJ:151:ILE:HD12	13:LJ:151:ILE:HA	1.84	0.45
24:LV:35:LYS:HA	24:LV:35:LYS:HD3	1.76	0.45
33:Le:8:VAL:HG23	33:Le:10:PRO:HD3	1.97	0.45
33:Le:70:LEU:HD11	33:Le:76:LYS:HB3	1.97	0.45
38:Lj:67:LEU:HD23	38:Lj:67:LEU:HA	1.74	0.45
46:S2:84:A:H1'	75:SY:120:THR:HG22	1.99	0.45
46:S2:122:G:H2'	46:S2:123:G:H8	1.82	0.45
46:S2:352:U:H2'	46:S2:353:C:C6	2.51	0.45
46:S2:454:U:H2'	46:S2:455:A:H8	1.80	0.45
46:S2:1101:U:H2'	46:S2:1102:G:C8	2.49	0.45
50:SE:183:VAL:HG12	50:SE:189:LEU:HA	1.99	0.45
53:SI:10:LYS:HE3	53:SI:10:LYS:HB3	1.72	0.45
53:SI:57:ALA:HB2	53:SI:183:GLY:HA2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SV:15:ARG:NH1	68:SC:84:PHE:HA	2.31	0.45
67:Sg:189:ILE:HD12	67:Sg:189:ILE:HA	1.88	0.45
83:zz:224:G:H2'	83:zz:225:A:C8	2.52	0.45
86:3a:384:VAL:HG12	86:3a:386:GLU:H	1.82	0.45
92:3l:137:TYR:HA	92:3l:140:ILE:HD12	1.98	0.45
1:L5:351:C:H2'	1:L5:352:G:C8	2.52	0.45
1:L5:1685:G:H21	30:Lb:15:LYS:NZ	2.14	0.45
1:L5:2060:G:H2'	1:L5:2061:U:C6	2.52	0.45
1:L5:2080:U:H2'	1:L5:2081:C:C6	2.52	0.45
1:L5:2540:C:H2'	1:L5:2541:G:C8	2.52	0.45
1:L5:4103:C:O2	1:L5:4107:G:C6	2.70	0.45
2:L7:22:A:H61	7:LD:266:TRP:NE1	2.15	0.45
6:LC:71:ARG:HB3	6:LC:73:VAL:HG22	1.99	0.45
8:LE:271:LEU:HD12	8:LE:271:LEU:HA	1.80	0.45
10:LG:121:LYS:HA	10:LG:126:GLY:H	1.80	0.45
28:LZ:11:VAL:HG22	28:LZ:82:PRO:HA	1.99	0.45
46:S2:844:U:H2'	46:S2:845:G:C8	2.52	0.45
46:S2:1665:G:C5	60:ST:88:MET:HE1	2.52	0.45
47:SA:198:MET:HE1	58:SR:89:SER:HB2	1.99	0.45
1:L5:53:C:H2'	1:L5:54:G:H8	1.80	0.44
1:L5:1328:G:H2'	1:L5:1329:G:C8	2.52	0.44
1:L5:1759:G:H22	1:L5:1773:U:H3	1.64	0.44
1:L5:1846:G:H2'	1:L5:1847:C:C6	2.53	0.44
1:L5:1951:G:H5'	21:LS:116:ARG:NH1	2.31	0.44
1:L5:2067:C:H2'	1:L5:2068:C:C6	2.52	0.44
1:L5:3585:G:C6	1:L5:3586:G:O6	2.70	0.44
7:LD:241:LYS:HE2	7:LD:241:LYS:HB3	1.79	0.44
9:LF:144:TYR:CE2	9:LF:237:GLU:HA	2.52	0.44
21:LS:8:ARG:HG3	21:LS:10:TYR:CE1	2.53	0.44
46:S2:874:G:H2'	46:S2:875:A:C8	2.51	0.44
46:S2:1264:C:H4'	46:S2:1265:A:H5'	1.99	0.44
46:S2:1418:C:H42	46:S2:1420:G:H5''	1.80	0.44
46:S2:1625:U:H2'	46:S2:1626:C:H6	1.82	0.44
47:SA:110:ASN:HD22	47:SA:113:GLN:HB2	1.82	0.44
52:SH:69:LEU:O	52:SH:73:GLN:HG2	2.16	0.44
60:ST:85:ASN:HB2	60:ST:88:MET:HB2	1.98	0.44
83:zz:126:C:H2'	83:zz:127:U:C6	2.52	0.44
83:zz:145:G:H2'	83:zz:146:G:C8	2.51	0.44
84:3m:64:MET:HB3	84:3m:105:LEU:HD21	1.98	0.44
1:L5:271:C:H2'	1:L5:272:U:H6	1.82	0.44
1:L5:1509:C:H2'	1:L5:1510:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1726:U:H2'	1:L5:1727:U:H6	1.82	0.44
1:L5:2732:G:H2'	1:L5:2733:C:C6	2.52	0.44
4:LA:107:MET:HB2	4:LA:111:THR:HG21	1.99	0.44
7:LD:55:VAL:HG11	7:LD:158:LYS:HZ3	1.81	0.44
10:LG:176:LYS:HE2	37:Li:43:MET:HE1	1.99	0.44
22:LT:152:GLU:OE2	22:LT:153:PRO:HD2	2.16	0.44
28:LZ:84:ARG:HH21	28:LZ:85:TYR:HE2	1.66	0.44
39:Lk:23:VAL:HG22	39:Lk:36:VAL:HG22	1.99	0.44
46:S2:557:U:H2'	46:S2:558:G:C8	2.53	0.44
46:S2:1680:G:H4'	65:Sc:20:ARG:HG2	2.00	0.44
46:S2:1805:G:H2'	46:S2:1806:A:C8	2.52	0.44
53:SI:104:ILE:HG23	53:SI:171:LEU:HB2	1.99	0.44
54:SK:1:MET:HE2	54:SK:1:MET:HA	1.98	0.44
54:SK:24:LYS:HG3	54:SK:66:HIS:NE2	2.32	0.44
67:Sg:59:LEU:HB3	67:Sg:90:TRP:CZ3	2.52	0.44
67:Sg:185:LYS:HB3	67:Sg:185:LYS:HE2	1.80	0.44
68:SC:265:PRO:HD2	68:SC:266:TYR:CZ	2.52	0.44
73:SO:63:LYS:HD3	73:SO:63:LYS:HA	1.65	0.44
77:Sb:16:LYS:HB3	77:Sb:16:LYS:HE2	1.72	0.44
84:3m:172:LEU:HD22	84:3m:177:LYS:HD2	1.98	0.44
1:L5:1772:C:H2'	1:L5:1773:U:H6	1.82	0.44
1:L5:4324:A:H4'	7:LD:174:PRO:HB2	1.98	0.44
1:L5:4591:U:H2'	1:L5:4592:C:C6	2.52	0.44
17:LO:187:LYS:HD3	17:LO:187:LYS:HA	1.69	0.44
22:LT:84:ILE:HG22	30:Lb:24:PRO:HD3	2.00	0.44
46:S2:432:G:H2'	46:S2:433:A:C8	2.53	0.44
46:S2:1644:C:H4'	57:SQ:140:ARG:HB2	1.98	0.44
55:SL:96:ILE:HG22	55:SL:99:TYR:H	1.82	0.44
75:SY:19:GLN:HE21	75:SY:85:ASN:HD21	1.65	0.44
78:Se:25:LYS:H	78:Se:25:LYS:HG3	1.55	0.44
92:3l:493:PHE:O	92:3l:497:MET:HG3	2.17	0.44
1:L5:1509:C:H5''	29:La:2:PRO:HG3	1.99	0.44
1:L5:2482:C:N4	1:L5:2483:G:H21	2.14	0.44
1:L5:2749:C:H2'	1:L5:2750:G:C8	2.52	0.44
1:L5:4585:U:H2'	1:L5:4586:G:C8	2.52	0.44
1:L5:4941:G:H4'	8:LE:187:ARG:HH21	1.83	0.44
6:LC:190:ARG:HG3	6:LC:202:ILE:HD13	1.98	0.44
9:LF:164:LYS:HB2	9:LF:165:LYS:HG2	1.99	0.44
15:LM:116:LYS:HG3	17:LO:196:LEU:HD11	1.99	0.44
25:LW:116:LYS:O	25:LW:120:GLN:HG2	2.17	0.44
32:Ld:19:GLU:H	32:Ld:19:GLU:CD	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:375:U:H2'	46:S2:376:A:H8	1.81	0.44
55:SL:77:VAL:HG22	55:SL:123:GLY:H	1.83	0.44
64:Sa:14:GLY:H	64:Sa:15:ARG:NH1	2.16	0.44
79:sh:138:ARG:H	79:sh:150:PHE:HB2	1.82	0.44
92:3l:558:LYS:HA	92:3l:558:LYS:HD2	1.84	0.44
1:L5:1327:C:H2'	1:L5:1328:G:C8	2.53	0.44
1:L5:2539:C:H2'	1:L5:2540:C:C6	2.52	0.44
1:L5:3920:U:H2'	1:L5:3921:U:C6	2.53	0.44
5:LB:60:VAL:HG11	5:LB:67:VAL:HG23	2.00	0.44
18:LP:39:MET:SD	18:LP:43:LYS:HE2	2.58	0.44
29:La:12:ARG:HD3	29:La:12:ARG:HA	1.79	0.44
30:Lb:106:LYS:HE3	30:Lb:106:LYS:HB2	1.79	0.44
40:Ll:21:ARG:C	40:Ll:41:ARG:HH12	2.25	0.44
46:S2:804:U:H2'	46:S2:805:U:C6	2.53	0.44
46:S2:1205:C:H2'	46:S2:1206:G:H8	1.82	0.44
47:SA:148:CYS:SG	47:SA:160:ALA:HB1	2.57	0.44
51:SF:42:LYS:HB2	51:SF:42:LYS:HE3	1.73	0.44
53:SI:54:LYS:HE3	53:SI:54:LYS:HB3	1.81	0.44
53:SI:147:LYS:HE3	53:SI:147:LYS:HB3	1.89	0.44
56:SP:28:MET:SD	56:SP:32:GLN:HG2	2.58	0.44
72:SN:84:LEU:HD23	72:SN:84:LEU:HA	1.82	0.44
79:sh:96:LYS:HA	79:sh:96:LYS:HD2	1.80	0.44
83:zz:180:G:H2'	83:zz:181:G:C8	2.52	0.44
89:3h:169:LEU:HD12	89:3h:169:LEU:HA	1.83	0.44
1:L5:679:C:H2'	1:L5:680:G:C8	2.50	0.44
1:L5:1070:G:O2'	1:L5:1071:C:H5'	2.18	0.44
1:L5:1188:C:H2'	1:L5:1189:G:H8	1.82	0.44
1:L5:1418:C:H2'	1:L5:1419:G:C8	2.52	0.44
1:L5:1749:A:H2'	1:L5:1750:G:C8	2.52	0.44
1:L5:2376:A:H2'	1:L5:2377:C:C6	2.51	0.44
1:L5:4103:C:H42	1:L5:4107:G:H22	1.65	0.44
5:LB:55:HIS:NE2	25:LW:16:GLY:HA3	2.33	0.44
6:LC:218:ILE:H	6:LC:218:ILE:HG12	1.62	0.44
19:LQ:69:LYS:HA	19:LQ:69:LYS:HD2	1.87	0.44
20:LR:7:GLN:HG2	20:LR:32:ILE:HG22	1.98	0.44
20:LR:63:CYS:O	20:LR:67:THR:HG23	2.17	0.44
40:Ll:20:ASN:HD22	40:Ll:41:ARG:NH2	2.16	0.44
44:Lp:33:GLN:HG2	44:Lp:34:HIS:CD2	2.53	0.44
46:S2:943:U:H2'	46:S2:944:A:H8	1.83	0.44
59:SS:132:ARG:HA	59:SS:132:ARG:HD2	1.72	0.44
69:SG:53:SER:HB2	69:SG:112:VAL:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Sf:17:ALA:HB1	71:Sf:123:VAL:HG22	2.00	0.44
83:zz:243:G:H2'	83:zz:244:A:C8	2.52	0.44
84:3m:110:PHE:HA	84:3m:120:ARG:NH1	2.33	0.44
87:3e:128:LEU:HD23	87:3e:158:VAL:HG23	2.00	0.44
88:3c:146:ARG:HE	88:3c:146:ARG:HB2	1.66	0.44
92:3l:133:LYS:HD2	92:3l:133:LYS:HA	1.81	0.44
1:L5:40:G:H21	1:L5:4380:A:H62	1.66	0.44
1:L5:424:U:H2'	1:L5:425:U:C6	2.52	0.44
1:L5:2567:G:H2'	1:L5:2568:C:C6	2.53	0.44
1:L5:2671:C:H2'	1:L5:2672:C:C6	2.53	0.44
1:L5:2695:A:H4'	1:L5:2696:A:O5'	2.18	0.44
1:L5:4126:C:H5''	1:L5:4127:A:H5''	1.99	0.44
8:LE:223:ARG:HG2	8:LE:236:GLU:HB2	1.98	0.44
13:LJ:12:MET:HB2	13:LJ:137:PRO:HG2	2.00	0.44
14:LL:145:LYS:HG3	14:LL:146:LEU:HG	1.99	0.44
18:LP:105:LYS:HB3	18:LP:107:LEU:HD23	1.99	0.44
25:LW:97:LYS:HA	25:LW:101:ARG:HB2	2.00	0.44
27:LY:54:GLU:HA	27:LY:69:LYS:HA	2.00	0.44
28:LZ:57:MET:HG3	28:LZ:61:LYS:HB3	2.00	0.44
33:Le:118:LEU:HD23	33:Le:118:LEU:HA	1.83	0.44
52:SH:158:LEU:HD21	52:SH:187:PHE:HD2	1.83	0.44
61:SU:19:ARG:H	61:SU:117:ALA:HB2	1.83	0.44
83:zz:158:G:H2'	83:zz:159:G:H8	1.83	0.44
84:3m:22:LEU:HD23	84:3m:22:LEU:HA	1.89	0.44
84:3m:189:LEU:HA	84:3m:192:TYR:HB2	1.98	0.44
84:3m:201:ARG:HA	84:3m:232:LEU:HD11	1.99	0.44
1:L5:1761:G:N2	1:L5:1762:C:H42	2.15	0.44
1:L5:2297:G:H4'	6:LC:242:PRO:HB2	1.99	0.44
1:L5:3668:C:H5'	4:LA:8:GLN:O	2.18	0.44
1:L5:3754:G:H2'	1:L5:3755:G:C8	2.53	0.44
1:L5:3930:U:H2'	1:L5:3931:C:C6	2.53	0.44
3:L8:26:C:H2'	3:L8:27:U:C6	2.53	0.44
5:LB:220:ILE:HB	5:LB:346:THR:OG1	2.18	0.44
12:LI:98:ARG:HH11	12:LI:98:ARG:HB2	1.83	0.44
28:LZ:120:GLU:H	28:LZ:120:GLU:HG3	1.65	0.44
29:La:11:LEU:HD21	29:La:18:GLY:N	2.33	0.44
50:SE:236:ILE:HD12	50:SE:236:ILE:HA	1.87	0.44
56:SP:65:LYS:HB3	56:SP:65:LYS:HE2	1.68	0.44
60:ST:66:LEU:HA	60:ST:66:LEU:HD23	1.88	0.44
73:SO:124:MET:HA	73:SO:124:MET:HE3	2.00	0.44
85:3f:109:ARG:HH11	85:3f:114:ALA:HA	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
91:3k:71:LEU:HD23	91:3k:74:LEU:HD22	1.99	0.44
1:L5:518:G:H22	1:L5:643:C:H2'	1.81	0.44
1:L5:2079:G:H2'	1:L5:2080:U:H6	1.82	0.44
7:LD:276:LYS:HE3	7:LD:276:LYS:HB2	1.69	0.44
10:LG:136:LEU:HD12	10:LG:136:LEU:HA	1.87	0.44
11:LH:8:GLN:HG2	11:LH:74:CYS:SG	2.57	0.44
16:LN:126:THR:HG22	16:LN:127:TYR:CD1	2.53	0.44
46:S2:12:U:H2'	46:S2:13:C:C6	2.53	0.44
46:S2:928:G:H2'	46:S2:929:G:H8	1.82	0.44
46:S2:955:A:H61	46:S2:971:G:H1'	1.82	0.44
46:S2:1683:C:H2'	46:S2:1684:C:H6	1.83	0.44
70:SJ:115:PHE:HA	70:SJ:120:ALA:HB3	1.99	0.44
88:3c:602:ASP:HB2	88:3c:604:PRO:HD2	1.99	0.44
89:3h:336:GLN:HG2	89:3h:340:LYS:HE2	1.99	0.44
1:L5:318:A:H2'	1:L5:319:A:C8	2.53	0.43
1:L5:4095:G:H1	1:L5:4113:U:H3	1.66	0.43
1:L5:4378:A:O2'	1:L5:4379:A:H2'	2.18	0.43
14:LL:194:ILE:HD11	14:LL:198:ARG:HH21	1.83	0.43
46:S2:538:U:H5''	46:S2:546:G:C6	2.52	0.43
46:S2:1393:G:H2'	46:S2:1394:G:C8	2.52	0.43
46:S2:1589:A:H2'	46:S2:1590:C:H6	1.83	0.43
46:S2:1601:A:H1'	46:S2:1604:G:O6	2.17	0.43
47:SA:180:ARG:HD2	47:SA:184:ARG:NH2	2.32	0.43
50:SE:36:HIS:CE1	50:SE:85:GLY:HA3	2.53	0.43
52:SH:20:GLU:HA	52:SH:23:ILE:HD12	2.00	0.43
74:SW:23:ARG:HG3	77:Sb:4:ALA:HB1	1.99	0.43
83:zz:186:C:N3	83:zz:212:U:C2	2.86	0.43
84:3m:218:PHE:HE1	84:3m:280:LEU:HD22	1.82	0.43
1:L5:2689:C:H2'	1:L5:2690:C:C6	2.54	0.43
1:L5:2871:A:H62	1:L5:2878:G:H21	1.64	0.43
4:LA:4:VAL:HG13	4:LA:8:GLN:HB3	2.00	0.43
5:LB:272:LYS:HB2	5:LB:272:LYS:HE3	1.82	0.43
8:LE:56:ARG:HG3	8:LE:57:TYR:CD1	2.53	0.43
10:LG:159:HIS:CE1	10:LG:185:LYS:HG2	2.54	0.43
15:LM:41:PRO:HG3	15:LM:73:VAL:HG13	2.00	0.43
17:LO:54:TYR:HE2	17:LO:145:VAL:HG11	1.83	0.43
20:LR:110:ARG:HE	20:LR:110:ARG:HB3	1.63	0.43
20:LR:180:LYS:HE2	20:LR:180:LYS:HB3	1.93	0.43
46:S2:26:U:H2'	46:S2:27:A:H8	1.84	0.43
46:S2:328:U:H2'	46:S2:329:G:C8	2.53	0.43
46:S2:811:A:H2'	46:S2:812:A:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SP:111:MET:HG3	56:SP:119:PHE:CE2	2.52	0.43
70:SJ:50:LEU:HD13	70:SJ:54:ARG:HD3	2.00	0.43
71:Sf:26:LEU:HD12	71:Sf:30:GLY:HA2	1.99	0.43
71:Sf:51:VAL:HG22	71:Sf:77:ILE:HB	1.99	0.43
74:SW:90:GLN:HE21	74:SW:113:HIS:CD2	2.36	0.43
84:3m:183:LYS:HD3	84:3m:183:LYS:HA	1.79	0.43
92:3l:340:LEU:HD23	92:3l:386:ILE:HG12	1.99	0.43
92:3l:412:LEU:HD12	92:3l:412:LEU:HA	1.88	0.43
1:L5:1309:C:H2'	1:L5:1310:C:C6	2.53	0.43
1:L5:1317:U:H2'	1:L5:1318:C:C6	2.54	0.43
1:L5:1504:G:H2'	1:L5:1505:C:C6	2.53	0.43
1:L5:1751:A:H2'	1:L5:1752:G:C8	2.53	0.43
1:L5:1751:A:H2'	1:L5:1752:G:H8	1.83	0.43
1:L5:1876:U:H2'	1:L5:1877:G:C8	2.53	0.43
1:L5:4688:C:H2'	1:L5:4689:U:C6	2.54	0.43
1:L5:4953:G:H2'	1:L5:4954:G:C8	2.53	0.43
10:LG:219:VAL:HA	10:LG:222:ILE:HG22	2.01	0.43
45:Lr:107:ARG:O	45:Lr:111:ILE:HG12	2.19	0.43
47:SA:166:LYS:HE2	47:SA:166:LYS:HB2	1.80	0.43
62:SV:1:MET:HG2	62:SV:2:GLN:HG2	2.00	0.43
69:SG:52:ILE:HD13	69:SG:52:ILE:HA	1.94	0.43
83:zz:281:U:H5	83:zz:283:G:H21	1.67	0.43
85:3f:92:VAL:HG12	85:3f:237:VAL:HA	2.00	0.43
88:3c:121:TRP:HE3	88:3c:142:ARG:HD3	1.84	0.43
88:3c:619:CYS:HA	88:3c:622:ARG:HG2	1.99	0.43
1:L5:271:C:H2'	1:L5:272:U:C6	2.53	0.43
1:L5:420:A:H61	3:L8:15:G:H1'	1.83	0.43
1:L5:2046:G:C4	17:LO:60:LYS:HD3	2.53	0.43
1:L5:2277:C:H2'	1:L5:2278:G:C8	2.53	0.43
1:L5:3764:U:H4'	1:L5:3765:G:H5'	2.00	0.43
1:L5:4493:U:H2'	1:L5:4494:G:H8	1.83	0.43
5:LB:300:LYS:HE3	5:LB:300:LYS:HB3	1.70	0.43
6:LC:292:ILE:HG22	6:LC:293:LEU:HD23	1.99	0.43
7:LD:264:LYS:HB3	7:LD:264:LYS:HE2	1.75	0.43
11:LH:64:ARG:HA	11:LH:67:LEU:HB2	2.00	0.43
15:LM:123:ILE:HD13	15:LM:123:ILE:HA	1.91	0.43
29:La:38:LEU:HD22	29:La:53:PHE:CE2	2.53	0.43
33:Le:77:PHE:HD1	45:Lr:23:GLN:HE21	1.65	0.43
46:S2:1024:A:H2'	46:S2:1025:U:C6	2.53	0.43
46:S2:1055:A:H2'	46:S2:1056:U:C6	2.53	0.43
49:SD:140:GLY:HA3	49:SD:182:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SH:43:LEU:HD12	52:SH:72:PHE:CE2	2.53	0.43
62:SV:23:ILE:HD11	68:SC:255:LEU:HD23	2.00	0.43
69:SG:149:LYS:HB3	69:SG:149:LYS:HE2	1.86	0.43
88:3c:780:VAL:HA	88:3c:783:ILE:HG22	2.00	0.43
1:L5:689:U:H2'	1:L5:690:C:C6	2.53	0.43
1:L5:1981:G:H5''	1:L5:1982:G:C8	2.53	0.43
1:L5:2074:C:H2'	1:L5:2075:G:H8	1.84	0.43
1:L5:2832:A:H2'	1:L5:2833:A:C8	2.54	0.43
13:LJ:88:LYS:HE2	13:LJ:88:LYS:HB2	1.93	0.43
17:LO:130:LYS:HB2	17:LO:133:ARG:HG3	2.01	0.43
31:Lc:74:TYR:CD2	31:Lc:81:LEU:HG	2.53	0.43
46:S2:1004:U:H2'	46:S2:1005:G:C8	2.53	0.43
46:S2:1124:C:H5''	48:SB:150:ILE:HG12	2.01	0.43
46:S2:1220:A:H4'	51:SF:145:ARG:HH22	1.82	0.43
46:S2:1491:G:H2'	46:S2:1492:U:C6	2.53	0.43
46:S2:1511:U:O2'	46:S2:1512:C:H5'	2.19	0.43
49:SD:76:ARG:HG3	49:SD:77:PHE:CD1	2.54	0.43
51:SF:50:PRO:HB3	51:SF:69:VAL:HB	2.00	0.43
52:SH:37:LYS:HA	52:SH:37:LYS:HE3	2.00	0.43
54:SK:43:LEU:O	54:SK:47:LYS:HG2	2.19	0.43
55:SL:101:ARG:HB2	63:SX:10:ALA:HB2	2.00	0.43
59:SS:22:GLY:HA2	59:SS:56:ALA:HB3	2.00	0.43
68:SC:102:LEU:HB3	68:SC:130:ILE:HD11	2.00	0.43
84:3m:221:ASP:HB3	85:3f:306:ARG:HH22	1.84	0.43
87:3e:404:VAL:HA	87:3e:407:LYS:HE3	2.01	0.43
88:3c:832:MET:HE1	88:3c:846:ARG:H	1.83	0.43
92:3l:304:MET:O	92:3l:304:MET:HE3	2.19	0.43
1:L5:1509:C:H2'	1:L5:1510:G:C8	2.54	0.43
1:L5:2559:G:H1	1:L5:2568:C:N4	2.16	0.43
1:L5:2909:C:H2'	1:L5:2910:G:C8	2.54	0.43
1:L5:4466:C:H2'	1:L5:4467:A:H8	1.84	0.43
1:L5:4493:U:H2'	1:L5:4494:G:C8	2.54	0.43
26:LX:117:TYR:CE1	26:LX:153:ILE:HD12	2.53	0.43
27:LY:34:LEU:HD21	27:LY:109:LEU:HD21	2.00	0.43
31:Lc:77:ASN:OD1	31:Lc:79:ILE:HG22	2.18	0.43
46:S2:327:G:H1'	46:S2:328:U:C2	2.54	0.43
46:S2:1189:A:H2'	46:S2:1190:A:H8	1.84	0.43
46:S2:1347:U:H2'	46:S2:1348:G:C8	2.54	0.43
46:S2:1671:G:H2'	46:S2:1672:U:C6	2.53	0.43
46:S2:1808:U:H2'	46:S2:1809:A:H8	1.82	0.43
47:SA:39:TYR:CD2	47:SA:40:LYS:HG2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SI:103:LEU:HD12	53:SI:170:LYS:HE3	1.99	0.43
53:SI:125:LYS:HA	53:SI:125:LYS:HD3	1.80	0.43
59:SS:54:LYS:HA	59:SS:54:LYS:HD2	1.80	0.43
69:SG:172:LYS:HB3	69:SG:172:LYS:HE2	1.82	0.43
1:L5:1199:G:H2'	1:L5:1200:G:H8	1.82	0.43
1:L5:1461:C:H2'	1:L5:1462:A:C8	2.54	0.43
1:L5:1739:G:H2'	1:L5:1740:C:C6	2.54	0.43
1:L5:3905:A:C4	81:zx:15:LEU:HD21	2.54	0.43
1:L5:4255:A:H2'	1:L5:4256:A:O4'	2.18	0.43
4:LA:147:ARG:NH2	4:LA:155:LYS:HD3	2.33	0.43
14:LL:78:LEU:HD23	14:LL:100:PRO:HA	2.01	0.43
20:LR:123:LEU:HD23	20:LR:123:LEU:HA	1.85	0.43
20:LR:152:LYS:HD2	20:LR:152:LYS:HA	1.84	0.43
25:LW:105:ARG:HD2	25:LW:105:ARG:HA	1.81	0.43
46:S2:97:U:H2'	46:S2:98:C:C6	2.53	0.43
46:S2:748:C:H1'	46:S2:794:A:H61	1.83	0.43
46:S2:1010:G:H2'	46:S2:1011:A:C8	2.52	0.43
46:S2:1203:G:H2'	46:S2:1204:A:N3	2.33	0.43
46:S2:1657:G:H1	46:S2:1667:U:H3	1.66	0.43
48:SB:38:MET:H	48:SB:38:MET:CE	2.28	0.43
51:SF:61:PHE:HE1	65:Sc:49:PRO:HB2	1.83	0.43
52:SH:104:PRO:HD3	52:SH:116:ARG:HD3	2.00	0.43
67:Sg:49:GLU:HG3	67:Sg:50:THR:HG23	2.00	0.43
73:SO:56:VAL:HA	73:SO:60:MET:HE2	1.99	0.43
86:3a:95:LYS:HE3	86:3a:95:LYS:HB3	1.87	0.43
86:3a:269:PRO:HB2	86:3a:306:MET:HE2	2.01	0.43
1:L5:286:U:H2'	1:L5:287:U:C6	2.54	0.43
1:L5:705:G:H2'	1:L5:706:C:C6	2.54	0.43
1:L5:1759:G:H3'	1:L5:1760:G:C8	2.54	0.43
1:L5:1840:G:H1'	9:LF:111:LEU:HD13	2.01	0.43
1:L5:4184:G:H5'	4:LA:233:ARG:HG2	2.00	0.43
1:L5:4421:C:O2'	1:L5:4422:A:H5'	2.19	0.43
6:LC:328:LEU:HD23	6:LC:328:LEU:HA	1.81	0.43
11:LH:67:LEU:HD23	11:LH:67:LEU:HA	1.83	0.43
21:LS:92:ASN:HD21	22:LT:156:TYR:H	1.66	0.43
24:LV:78:PRO:HG2	24:LV:107:ASN:HA	2.00	0.43
25:LW:107:GLN:HB2	25:LW:110:ARG:HE	1.84	0.43
34:Lf:22:ARG:HG2	34:Lf:24:HIS:CE1	2.54	0.43
46:S2:1183:A:H2'	46:S2:1184:G:H8	1.84	0.43
46:S2:1292:C:H5''	79:sh:140:TYR:CE2	2.53	0.43
46:S2:1392:U:H2'	46:S2:1393:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SF:124:ASP:HA	51:SF:200:ALA:HB2	2.00	0.43
52:SH:107:LYS:HA	52:SH:107:LYS:HD2	1.74	0.43
56:SP:18:ARG:HB3	59:SS:93:GLY:HA3	2.00	0.43
57:SQ:135:PRO:HD3	57:SQ:141:TYR:CE1	2.53	0.43
69:SG:133:LEU:HD12	69:SG:133:LEU:HA	1.89	0.43
73:SO:95:ILE:HG13	73:SO:116:LEU:HD11	2.00	0.43
79:sh:119:ARG:HH12	79:sh:139:HIS:HB3	1.82	0.43
86:3a:177:ILE:HD12	86:3a:177:ILE:HA	1.91	0.43
92:3l:294:LEU:HD22	92:3l:297:ILE:HD12	2.00	0.43
92:3l:345:ARG:HA	92:3l:553:LEU:HD21	2.01	0.43
92:3l:470:MET:HE3	92:3l:475:LEU:HD13	2.01	0.43
1:L5:727:C:H2'	1:L5:728:U:C6	2.53	0.43
1:L5:753:C:H41	1:L5:910:G:H1	1.66	0.43
1:L5:1274:A:O2'	1:L5:1275:G:H8	2.02	0.43
1:L5:1415:G:H2'	1:L5:1416:G:C8	2.52	0.43
1:L5:1683:U:H2'	1:L5:1684:A:C8	2.53	0.43
1:L5:2091:C:H4'	1:L5:2092:G:H5'	2.00	0.43
1:L5:3684:G:H2'	1:L5:3685:C:H6	1.83	0.43
1:L5:4143:G:N3	1:L5:4145:C:H4'	2.34	0.43
1:L5:4627:U:H2'	1:L5:4628:U:C6	2.54	0.43
1:L5:4629:U:H2'	1:L5:4630:G:H8	1.83	0.43
10:LG:157:ILE:HD11	10:LG:170:LEU:HB3	2.00	0.43
16:LN:113:LEU:HB3	16:LN:134:LEU:HD12	2.01	0.43
19:LQ:119:LYS:HD2	19:LQ:119:LYS:HA	1.84	0.43
24:LV:33:GLY:HA3	24:LV:69:LYS:HE2	1.99	0.43
29:La:110:LYS:HG2	29:La:128:PHE:HB2	2.00	0.43
38:Lj:15:THR:HG23	38:Lj:16:HIS:ND1	2.33	0.43
41:Lm:112:LYS:HA	41:Lm:112:LYS:HD2	1.76	0.43
46:S2:1553:C:H4'	46:S2:1554:C:H5	1.84	0.43
50:SE:79:ASP:HB3	50:SE:82:TYR:HB2	2.01	0.43
53:SI:22:HIS:HB2	53:SI:25:ARG:HH12	1.84	0.43
59:SS:14:ARG:HD2	59:SS:19:ASN:HB3	2.00	0.43
62:SV:55:ILE:HD11	62:SV:69:ILE:HD11	2.00	0.43
76:SZ:49:LEU:HD12	76:SZ:49:LEU:HA	1.83	0.43
1:L5:690:C:H2'	1:L5:691:C:H6	1.84	0.43
1:L5:1298:C:H2'	1:L5:1299:G:H8	1.83	0.43
1:L5:1857:C:H2'	1:L5:1858:A:C8	2.54	0.43
1:L5:1950:U:H2'	1:L5:1951:G:C8	2.53	0.43
1:L5:1992:U:H5''	1:L5:1993:C:H5'	2.00	0.43
1:L5:2073:C:H4'	9:LF:157:ARG:HH21	1.84	0.43
1:L5:2538:U:H2'	1:L5:2539:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2633:U:H2'	1:L5:2634:C:C6	2.53	0.43
1:L5:3671:G:H2'	1:L5:3672:G:C8	2.53	0.43
1:L5:3796:U:H2'	1:L5:3797:C:C6	2.54	0.43
1:L5:4723:A:H2'	1:L5:4724:A:C8	2.53	0.43
3:L8:123:U:H3'	3:L8:124:U:O4'	2.19	0.43
5:LB:24:ARG:HD2	5:LB:276:HIS:CD2	2.54	0.43
13:LJ:145:LYS:HA	13:LJ:145:LYS:HD2	1.74	0.43
21:LS:69:GLU:HB2	21:LS:72:PRO:HB3	2.00	0.43
23:LU:63:ILE:HD11	23:LU:70:ILE:HG23	2.00	0.43
29:La:146:LEU:HD23	29:La:146:LEU:HA	1.90	0.43
31:Lc:28:VAL:HB	31:Lc:33:GLN:HG2	2.01	0.43
36:Lh:16:GLU:HA	36:Lh:19:LYS:HB3	2.00	0.43
36:Lh:113:LEU:C	36:Lh:114:TYR:HD1	2.27	0.43
43:Lo:104:ILE:HD12	43:Lo:104:ILE:HA	1.89	0.43
46:S2:1239:U:H5''	56:SP:124:LYS:HE3	1.99	0.43
46:S2:1402:A:H5'	61:SU:51:LYS:HE3	2.00	0.43
46:S2:1623:A:H5'	59:SS:133:GLY:HA3	2.00	0.43
46:S2:1630:A:H5''	59:SS:37:GLY:N	2.33	0.43
52:SH:73:GLN:HB3	52:SH:135:PHE:HE2	1.82	0.43
84:3m:160:LYS:HD2	84:3m:160:LYS:HA	1.83	0.43
85:3f:251:LEU:HD22	89:3h:205:ILE:HD12	1.99	0.43
86:3a:191:LYS:HA	86:3a:191:LYS:HD3	1.70	0.43
86:3a:446:ILE:HB	86:3a:511:LEU:HD22	2.01	0.43
89:3h:48:LYS:HA	89:3h:51:LYS:HG2	2.01	0.43
92:3l:127:VAL:HG11	92:3l:176:LEU:HD21	2.01	0.43
1:L5:677:G:H2'	1:L5:678:C:C6	2.53	0.42
1:L5:3650:C:H2'	1:L5:3651:A:C8	2.54	0.42
1:L5:3736:A:H2'	1:L5:3737:A:C8	2.54	0.42
1:L5:3893:C:H1'	18:LP:69:ARG:NH2	2.34	0.42
1:L5:4593:C:H2'	1:L5:4594:U:H6	1.83	0.42
1:L5:4635:A:H2	1:L5:4663:G:H21	1.66	0.42
2:L7:92:C:H2'	2:L7:93:G:C8	2.52	0.42
3:L8:144:U:H2'	3:L8:145:C:C6	2.53	0.42
9:LF:96:ARG:HD2	9:LF:139:TYR:CE2	2.54	0.42
17:LO:23:VAL:O	17:LO:27:VAL:HG12	2.18	0.42
42:Ln:10:MET:HE2	42:Ln:10:MET:HB2	1.91	0.42
54:SK:25:LYS:HA	54:SK:46:MET:HE1	2.01	0.42
55:SL:11:GLN:HB3	55:SL:56:ILE:HG21	2.00	0.42
63:SX:76:LYS:HG3	63:SX:77:ASN:HD22	1.83	0.42
66:Sd:30:LEU:HD23	66:Sd:30:LEU:HA	1.80	0.42
82:zy:49:C:H2'	82:zy:50:G:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:zz:180:G:H2'	83:zz:181:G:H8	1.84	0.42
84:3m:60:VAL:HG11	84:3m:101:LEU:HD23	2.01	0.42
86:3a:403:LEU:HD23	86:3a:439:LEU:HB3	2.00	0.42
91:3k:196:ILE:HG23	91:3k:197:LYS:HD2	2.01	0.42
1:L5:347:A:H2'	1:L5:348:G:C8	2.54	0.42
1:L5:1507:C:H2'	1:L5:1508:A:H8	1.83	0.42
1:L5:2520:C:H2'	1:L5:2521:G:H8	1.83	0.42
1:L5:2570:U:H2'	1:L5:2571:C:C6	2.54	0.42
1:L5:4585:U:H2'	1:L5:4586:G:H8	1.83	0.42
1:L5:4967:A:H2'	1:L5:4968:A:C8	2.55	0.42
6:LC:205:ARG:HB3	6:LC:248:ARG:HH12	1.83	0.42
13:LJ:56:THR:HA	13:LJ:63:ARG:HA	2.01	0.42
17:LO:34:VAL:HG21	17:LO:112:TYR:CE2	2.54	0.42
19:LQ:50:ARG:HB3	19:LQ:83:VAL:HG11	2.00	0.42
22:LT:84:ILE:HD13	22:LT:84:ILE:HA	1.86	0.42
28:LZ:77:TYR:HD2	31:Lc:39:ARG:HD3	1.85	0.42
32:Ld:39:LYS:HA	32:Ld:39:LYS:HD2	1.73	0.42
41:Lm:113:LYS:HE2	41:Lm:113:LYS:HB2	1.84	0.42
44:Lp:47:MET:HG2	44:Lp:71:TYR:CE1	2.54	0.42
45:Lr:124:VAL:HG22	45:Lr:126:VAL:H	1.84	0.42
46:S2:178:C:H3'	46:S2:313:A:N6	2.32	0.42
46:S2:1278:A:H2'	46:S2:1279:C:C6	2.54	0.42
47:SA:210:ILE:HD13	47:SA:210:ILE:HA	1.89	0.42
51:SF:92:ILE:HD12	51:SF:169:ILE:HG23	2.00	0.42
67:Sg:164:ILE:HD11	67:Sg:221:LEU:HD13	2.02	0.42
68:SC:209:VAL:HG21	68:SC:233:LEU:HD11	2.01	0.42
70:SJ:109:ARG:HG2	70:SJ:112:THR:HG22	2.01	0.42
74:SW:14:ILE:HD13	74:SW:14:ILE:HA	1.90	0.42
85:3f:119:THR:HG21	85:3f:157:TYR:HE1	1.83	0.42
88:3c:450:ARG:HD2	88:3c:450:ARG:HA	1.93	0.42
91:3k:137:SER:HA	91:3k:140:LYS:HZ3	1.83	0.42
1:L5:302:C:H2'	1:L5:303:C:H6	1.83	0.42
1:L5:342:G:H2'	1:L5:343:C:C6	2.54	0.42
1:L5:963:G:H2'	1:L5:964:A:C4	2.55	0.42
1:L5:1069:G:HO2'	1:L5:1070:G:H8	1.67	0.42
1:L5:1942:A:H2'	1:L5:1943:A:C8	2.54	0.42
1:L5:2496:G:H2'	1:L5:2497:C:C6	2.54	0.42
1:L5:4659:G:H2'	1:L5:4660:G:C8	2.54	0.42
3:L8:4:C:H5'	18:LP:61:ARG:HB3	2.00	0.42
3:L8:7:U:H2'	3:L8:8:U:C6	2.54	0.42
7:LD:48:LYS:HE2	7:LD:145:TYR:HE2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:La:14:HIS:CE1	33:Le:39:ARG:HH12	2.37	0.42
34:Lf:101:ILE:HD13	34:Lf:101:ILE:HA	1.84	0.42
35:Lg:43:LYS:HB3	35:Lg:43:LYS:HE3	1.74	0.42
46:S2:223:C:H2'	46:S2:224:A:C8	2.54	0.42
46:S2:398:A:H4'	46:S2:399:C:H5''	2.02	0.42
46:S2:599:A:H2'	46:S2:606:G:N2	2.31	0.42
46:S2:839:C:H6	46:S2:839:C:H2'	1.53	0.42
46:S2:844:U:H2'	46:S2:845:G:H8	1.84	0.42
46:S2:1449:G:H1'	46:S2:1450:G:H5'	2.00	0.42
46:S2:1518:C:H5''	46:S2:1519:U:H5''	2.00	0.42
50:SE:99:PHE:HA	50:SE:114:ILE:HB	2.00	0.42
56:SP:21:ASP:H	56:SP:24:GLN:NE2	2.15	0.42
57:SQ:19:ALA:HB2	57:SQ:75:GLY:HA3	2.00	0.42
67:Sg:296:GLN:HB3	67:Sg:311:GLN:HE22	1.84	0.42
69:SG:32:MET:HE1	69:SG:53:SER:C	2.45	0.42
83:zz:292:C:H2'	83:zz:293:C:H6	1.84	0.42
86:3a:535:GLU:HB3	89:3h:224:VAL:HG21	2.00	0.42
88:3c:624:GLY:H	88:3c:778:MET:HE2	1.85	0.42
92:3l:313:VAL:HG22	92:3l:339:ILE:HD11	2.01	0.42
1:L5:6:C:H2'	1:L5:7:C:H6	1.84	0.42
1:L5:943:A:H62	9:LF:151:ASN:HD21	1.67	0.42
1:L5:2762:G:H1'	1:L5:2763:U:O4'	2.20	0.42
1:L5:4318:C:H4'	43:Lo:17:LYS:HA	2.01	0.42
4:LA:158:ILE:HD12	4:LA:159:SER:H	1.84	0.42
5:LB:107:ALA:HB2	5:LB:201:LEU:HD11	2.01	0.42
14:LL:190:ARG:HG2	14:LL:191:LEU:HD12	2.02	0.42
18:LP:51:VAL:HG21	18:LP:58:VAL:HG23	2.02	0.42
19:LQ:167:VAL:HG12	19:LQ:175:GLU:HG3	2.01	0.42
27:LY:2:LYS:HE3	27:LY:2:LYS:HB3	1.73	0.42
46:S2:634:A:H2'	46:S2:635:G:C8	2.50	0.42
46:S2:901:G:C2	46:S2:902:G:H1'	2.54	0.42
46:S2:906:U:H2'	46:S2:907:G:C8	2.54	0.42
46:S2:940:U:H3	46:S2:1002:U:H3	1.67	0.42
46:S2:980:A:H2'	46:S2:981:A:H8	1.81	0.42
46:S2:1259:A:N6	46:S2:1518:C:H3'	2.34	0.42
46:S2:1444:U:H2'	46:S2:1445:U:C6	2.54	0.42
46:S2:1711:U:H2'	46:S2:1712:A:H8	1.83	0.42
47:SA:10:MET:HA	47:SA:10:MET:HE3	2.02	0.42
47:SA:84:GLN:HG3	47:SA:100:ALA:HB1	2.01	0.42
72:SN:129:TYR:HB3	72:SN:135:LEU:HD22	2.02	0.42
73:SO:95:ILE:HB	73:SO:129:ILE:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:zz:258:G:N2	83:zz:273:G:H2'	2.34	0.42
84:3m:148:ARG:NE	84:3m:187:GLU:HG2	2.33	0.42
85:3f:216:TYR:HA	85:3f:234:PRO:HA	2.00	0.42
88:3c:810:MET:HA	88:3c:810:MET:HE3	2.00	0.42
92:3l:308:VAL:HG12	92:3l:311:CYS:H	1.83	0.42
92:3l:554:ASN:HA	92:3l:557:LEU:HD12	2.01	0.42
1:L5:717:U:H2'	1:L5:718:C:C6	2.55	0.42
1:L5:1097:C:H2'	1:L5:1098:G:H8	1.84	0.42
1:L5:1631:A:C5	4:LA:204:MET:HE1	2.53	0.42
1:L5:4244:A:H2'	1:L5:4245:G:O4'	2.19	0.42
1:L5:4495:G:H2'	1:L5:4496:A:H8	1.84	0.42
1:L5:4568:A:P	5:LB:20:LYS:HB2	2.60	0.42
1:L5:5024:C:H41	1:L5:5028:G:H21	1.68	0.42
6:LC:335:MET:HE3	6:LC:335:MET:HB3	1.91	0.42
7:LD:104:LEU:HB2	7:LD:247:ILE:HD12	2.01	0.42
8:LE:96:VAL:HG11	8:LE:105:ARG:HE	1.85	0.42
8:LE:162:VAL:HG11	8:LE:184:VAL:HG11	2.01	0.42
14:LL:117:LEU:HD12	14:LL:117:LEU:HA	1.89	0.42
17:LO:196:LEU:HA	17:LO:196:LEU:HD23	1.85	0.42
26:LX:114:LYS:HA	26:LX:119:ILE:O	2.18	0.42
29:La:100:ILE:HA	29:La:123:ILE:HB	2.01	0.42
33:Le:65:LYS:HE3	33:Le:65:LYS:HB2	1.87	0.42
46:S2:1136:U:H2'	46:S2:1137:U:C6	2.54	0.42
46:S2:1232:U:H2'	46:S2:1233:G:H8	1.84	0.42
47:SA:83:GLY:O	47:SA:87:VAL:HG22	2.18	0.42
48:SB:89:GLU:HB3	48:SB:223:PHE:CE2	2.54	0.42
48:SB:108:ASP:O	48:SB:112:SER:HB3	2.20	0.42
51:SF:72:LEU:HD23	51:SF:72:LEU:HA	1.89	0.42
52:SH:58:LYS:HA	52:SH:58:LYS:HD2	1.87	0.42
53:SI:60:LEU:HD12	53:SI:185:ALA:HB2	2.00	0.42
58:SR:102:THR:O	58:SR:105:MET:HG3	2.19	0.42
62:SV:54:ALA:C	62:SV:55:ILE:HD13	2.44	0.42
69:SG:7:PHE:CE2	69:SG:9:ALA:HB3	2.55	0.42
83:zz:262:U:O2	83:zz:271:G:C6	2.72	0.42
84:3m:192:TYR:CE2	84:3m:197:ALA:HA	2.55	0.42
87:3e:309:GLN:HE22	87:3e:359:LYS:HB2	1.85	0.42
87:3e:362:MET:HE1	87:3e:370:TRP:NE1	2.28	0.42
88:3c:778:MET:SD	88:3c:782:LYS:HD2	2.59	0.42
1:L5:135:G:N7	36:Lh:97:LYS:HB2	2.34	0.42
1:L5:1086:C:H2'	1:L5:1087:A:C8	2.55	0.42
1:L5:1374:G:H2'	1:L5:1375:C:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1837:A:H2'	1:L5:1838:A:H8	1.85	0.42
1:L5:2112:G:H4'	1:L5:2251:G:N1	2.32	0.42
1:L5:2459:G:C6	16:LN:105:ARG:HD2	2.55	0.42
1:L5:2464:C:O2'	1:L5:2465:C:H6	2.03	0.42
1:L5:2641:A:H62	1:L5:2693:G:H21	1.67	0.42
1:L5:3729:U:H2'	1:L5:3730:U:C6	2.54	0.42
3:L8:67:U:H2'	3:L8:68:G:C8	2.54	0.42
3:L8:84:A:C2	27:LY:113:LYS:HD2	2.54	0.42
4:LA:83:HIS:HB3	44:Lp:64:VAL:HG22	2.02	0.42
6:LC:36:ILE:HD13	6:LC:36:ILE:HA	1.75	0.42
9:LF:157:ARG:HA	9:LF:157:ARG:HD2	1.95	0.42
11:LH:94:SER:HA	11:LH:179:ILE:HA	2.01	0.42
15:LM:49:ALA:HB2	21:LS:100:LEU:HD11	2.02	0.42
46:S2:26:U:H2'	46:S2:27:A:C8	2.55	0.42
46:S2:152:U:C2	46:S2:167:G:N2	2.88	0.42
46:S2:806:U:H2'	46:S2:807:G:H8	1.84	0.42
46:S2:1058:A:H2'	46:S2:1059:G:C8	2.55	0.42
57:SQ:49:TYR:O	57:SQ:53:GLU:HG3	2.20	0.42
84:3m:196:ASN:ND2	84:3m:196:ASN:C	2.78	0.42
88:3c:127:LYS:HB3	88:3c:127:LYS:HE2	1.77	0.42
88:3c:687:LEU:HD22	88:3c:737:VAL:HG11	2.02	0.42
89:3h:277:TYR:HA	89:3h:280:ARG:HG2	2.02	0.42
1:L5:975:C:P	9:LF:43:ARG:HH22	2.43	0.42
1:L5:1306:C:H2'	1:L5:1307:A:C8	2.55	0.42
1:L5:4630:G:H2'	1:L5:4631:G:H8	1.85	0.42
2:L7:51:G:H21	13:LJ:12:MET:HE1	1.85	0.42
3:L8:43:A:H2'	3:L8:44:A:H8	1.84	0.42
12:LI:167:ILE:HD13	12:LI:167:ILE:HA	1.85	0.42
16:LN:64:ILE:HD13	16:LN:64:ILE:HA	1.87	0.42
17:LO:170:LYS:HE3	17:LO:170:LYS:HB2	1.82	0.42
19:LQ:90:VAL:HB	29:La:80:THR:HG21	2.01	0.42
19:LQ:128:LEU:HD12	19:LQ:128:LEU:HA	1.90	0.42
41:Lm:111:ARG:HG3	41:Lm:112:LYS:HD3	2.02	0.42
48:SB:181:LEU:HD23	48:SB:181:LEU:HA	1.85	0.42
50:SE:9:LEU:HD12	50:SE:9:LEU:HA	1.88	0.42
58:SR:57:LEU:HD23	58:SR:57:LEU:HA	1.82	0.42
61:SU:99:LYS:HA	61:SU:99:LYS:HD3	1.65	0.42
70:SJ:169:ARG:HD2	70:SJ:170:PRO:HD2	2.02	0.42
83:zz:172:A:H2'	83:zz:173:A:H8	1.85	0.42
85:3f:183:SER:HA	85:3f:186:ILE:HD12	2.02	0.42
86:3a:32:TYR:CZ	86:3a:36:LYS:HE2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
89:3h:197:MET:O	89:3h:197:MET:HE3	2.18	0.42
92:3l:66:LEU:HD11	92:3l:84:ILE:HG23	2.02	0.42
1:L5:506:C:H2'	1:L5:507:G:H8	1.84	0.42
1:L5:1350:C:H2'	1:L5:1351:G:H8	1.83	0.42
1:L5:1662:C:H2'	1:L5:1663:C:C6	2.55	0.42
1:L5:1662:C:H2'	1:L5:1663:C:H6	1.84	0.42
1:L5:1705:G:H21	9:LF:46:ARG:HH21	1.67	0.42
1:L5:2102:G:H1'	1:L5:2103:G:C8	2.54	0.42
3:L8:27:U:H2'	3:L8:28:C:C6	2.54	0.42
22:LT:7:LYS:HE2	22:LT:7:LYS:HB3	1.80	0.42
26:LX:102:VAL:HA	26:LX:134:LYS:HD2	2.00	0.42
29:La:26:ARG:HA	29:La:26:ARG:HD3	1.82	0.42
46:S2:110:U:H2'	46:S2:111:A:C8	2.55	0.42
46:S2:562:U:H2'	46:S2:563:G:C8	2.55	0.42
46:S2:1410:C:H2'	46:S2:1411:G:C8	2.55	0.42
46:S2:1447:G:H2'	46:S2:1448:A:C8	2.55	0.42
46:S2:1650:A:H5''	57:SQ:139:ALA:HB2	2.02	0.42
46:S2:1801:A:H2'	46:S2:1802:C:C6	2.55	0.42
50:SE:66:MET:HE3	50:SE:66:MET:HA	2.02	0.42
63:SX:50:ILE:HD13	63:SX:50:ILE:HA	1.82	0.42
67:Sg:23:THR:HG22	67:Sg:31:ILE:HG22	2.01	0.42
67:Sg:179:LEU:HD23	67:Sg:179:LEU:H	1.83	0.42
71:Sf:44:LYS:HD2	71:Sf:44:LYS:HA	1.89	0.42
73:SO:91:THR:HA	73:SO:124:MET:HE1	2.02	0.42
92:3l:398:MET:H	92:3l:398:MET:HG3	1.63	0.42
92:3l:410:GLU:HG2	92:3l:444:LEU:HD11	2.01	0.42
1:L5:909:A:H2'	1:L5:910:G:H8	1.85	0.42
1:L5:1374:G:H2'	1:L5:1375:C:C6	2.54	0.42
1:L5:4674:C:H2'	1:L5:4675:U:C6	2.54	0.42
1:L5:4871:C:C4	15:LM:56:GLN:HG2	2.55	0.42
1:L5:4964:C:H2'	1:L5:4965:U:C6	2.55	0.42
6:LC:29:LYS:HA	6:LC:29:LYS:HD2	1.74	0.42
6:LC:323:ARG:HA	6:LC:326:LEU:HD12	2.01	0.42
8:LE:178:PRO:HB3	8:LE:258:LEU:HD21	2.01	0.42
11:LH:76:HIS:O	11:LH:80:MET:HG3	2.20	0.42
31:Lc:94:LEU:HD12	31:Lc:95:ALA:N	2.35	0.42
46:S2:331:C:H41	69:SG:186:GLN:HG3	1.84	0.42
46:S2:1650:A:H2'	46:S2:1651:A:O4'	2.19	0.42
57:SQ:132:PHE:CE2	61:SU:76:THR:HA	2.55	0.42
59:SS:118:ARG:HE	59:SS:123:LEU:HD11	1.84	0.42
67:Sg:165:ILE:HG13	67:Sg:177:TRP:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:3m:227:LYS:HE3	84:3m:227:LYS:HB3	1.91	0.42
85:3f:267:SER:HB3	85:3f:270:GLN:HG2	2.02	0.42
88:3c:762:ASN:HA	88:3c:766:TRP:HD1	1.84	0.42
1:L5:325:U:H2'	1:L5:326:C:C6	2.54	0.42
1:L5:1248:C:H2'	1:L5:1249:C:C6	2.55	0.42
1:L5:2851:G:H2'	1:L5:2852:U:O4'	2.20	0.42
1:L5:3705:G:H2'	1:L5:3706:C:C6	2.54	0.42
1:L5:4178:A:H2'	1:L5:4179:G:H8	1.85	0.42
1:L5:4566:U:H2'	1:L5:4567:G:O4'	2.20	0.42
8:LE:138:ARG:HE	8:LE:170:SER:C	2.27	0.42
44:Lp:29:ILE:HD11	44:Lp:69:TRP:CE3	2.55	0.42
44:Lp:46:LYS:HD2	44:Lp:46:LYS:HA	1.73	0.42
46:S2:454:U:H2'	46:S2:455:A:C8	2.55	0.42
46:S2:496:C:H2'	46:S2:497:C:C6	2.55	0.42
46:S2:666:U:H2'	46:S2:667:U:C6	2.55	0.42
46:S2:885:U:H1'	46:S2:901:G:H21	1.85	0.42
46:S2:1628:C:H2'	46:S2:1629:C:H6	1.85	0.42
46:S2:1667:U:H2'	46:S2:1668:U:C6	2.55	0.42
46:S2:1711:U:H2'	46:S2:1712:A:C8	2.55	0.42
51:SF:145:ARG:HA	51:SF:148:ASN:HB2	2.02	0.42
72:SN:5:HIS:CD2	72:SN:117:LEU:HB3	2.52	0.42
84:3m:277:MET:HA	84:3m:280:LEU:HB2	2.01	0.42
92:3l:153:ARG:HD2	92:3l:197:PHE:CD2	2.55	0.42
1:L5:1308:C:H2'	1:L5:1309:C:H6	1.85	0.41
1:L5:1340:C:H2'	1:L5:1341:U:C6	2.55	0.41
1:L5:2277:C:H2'	1:L5:2278:G:H8	1.85	0.41
1:L5:3736:A:H2'	1:L5:3737:A:H8	1.85	0.41
1:L5:4507:A:H2'	1:L5:4508:C:C6	2.54	0.41
5:LB:34:LYS:HD3	5:LB:34:LYS:HA	1.90	0.41
5:LB:282:LYS:HB3	5:LB:333:LEU:HD23	2.02	0.41
6:LC:284:MET:HE3	6:LC:287:THR:HA	2.02	0.41
9:LF:226:HIS:ND1	9:LF:228:VAL:HG23	2.35	0.41
18:LP:4:TYR:CZ	18:LP:16:LYS:HB2	2.55	0.41
46:S2:71:G:N1	69:SG:170:ARG:HG2	2.35	0.41
46:S2:353:C:H2'	46:S2:354:U:C6	2.54	0.41
46:S2:496:C:H5'	50:SE:29:PRO:HA	2.01	0.41
46:S2:1093:A:H2'	46:S2:1094:C:C6	2.54	0.41
46:S2:1189:A:H2'	46:S2:1190:A:C8	2.55	0.41
46:S2:1319:U:H2'	46:S2:1320:G:C8	2.55	0.41
57:SQ:31:LEU:C	57:SQ:32:ILE:HD13	2.45	0.41
62:SV:1:MET:HE1	68:SC:255:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Sg:158:PRO:HD3	67:Sg:200:VAL:HG21	2.02	0.41
86:3a:243:MET:HE3	86:3a:243:MET:HB3	1.94	0.41
1:L5:288:G:H2'	1:L5:289:C:C6	2.55	0.41
1:L5:661:C:H2'	1:L5:662:C:C6	2.55	0.41
1:L5:2414:G:H2'	1:L5:2415:U:H6	1.85	0.41
1:L5:2639:U:H1'	35:Lg:26:PRO:HG3	2.02	0.41
1:L5:3832:U:H2'	1:L5:3833:C:C6	2.53	0.41
1:L5:4653:C:H2'	1:L5:4654:C:C6	2.55	0.41
2:L7:60:G:H5''	7:LD:270:LYS:HG2	2.02	0.41
9:LF:50:ILE:HD13	9:LF:172:ASN:HD22	1.85	0.41
9:LF:130:ILE:HD13	9:LF:130:ILE:HA	1.87	0.41
12:LI:59:GLN:HG3	12:LI:126:VAL:HG21	2.02	0.41
14:LL:183:ARG:HD2	14:LL:183:ARG:HA	1.82	0.41
17:LO:168:TYR:CE2	17:LO:172:LYS:HD3	2.55	0.41
25:LW:87:LEU:HD13	25:LW:91:MET:HG2	2.01	0.41
28:LZ:33:THR:HG22	28:LZ:35:ASP:H	1.85	0.41
29:La:117:LEU:HD12	29:La:117:LEU:HA	1.87	0.41
32:Ld:46:LEU:HA	32:Ld:46:LEU:HD12	1.80	0.41
40:Ll:22:PRO:HD3	40:Ll:41:ARG:NH2	2.35	0.41
46:S2:600:G:H2'	46:S2:601:G:H8	1.84	0.41
46:S2:847:A:H2	50:SE:248:ILE:HG12	1.85	0.41
47:SA:155:ARG:HG3	47:SA:156:TYR:CD1	2.55	0.41
73:SO:141:ARG:HE	73:SO:141:ARG:HB3	1.60	0.41
75:SY:68:LYS:HB3	75:SY:68:LYS:HE3	1.84	0.41
81:zx:21:PRO:HA	81:zx:22:PRO:HD3	1.93	0.41
85:3f:347:GLN:HB3	88:3c:866:LEU:HD23	2.01	0.41
86:3a:251:LYS:HB2	86:3a:251:LYS:HE2	1.87	0.41
86:3a:338:ILE:HD11	88:3c:745:LYS:HB2	2.02	0.41
91:3k:155:ARG:HG3	91:3k:187:ILE:HD11	2.03	0.41
92:3l:461:ARG:HB2	92:3l:519:VAL:HG21	2.01	0.41
1:L5:319:A:H1'	1:L5:3726:A:H8	1.84	0.41
1:L5:431:G:H21	1:L5:3888:G:H3'	1.85	0.41
1:L5:1468:C:H2'	1:L5:1469:C:C6	2.54	0.41
1:L5:2670:C:N4	1:L5:2671:C:H41	2.17	0.41
1:L5:2775:C:H2'	1:L5:2776:G:H8	1.83	0.41
1:L5:3870:C:H2'	1:L5:3871:A:C8	2.54	0.41
1:L5:4263:C:H2'	1:L5:4264:G:O4'	2.21	0.41
1:L5:4627:U:H4'	5:LB:373:LYS:NZ	2.35	0.41
1:L5:4716:C:H2'	1:L5:4717:A:H8	1.85	0.41
3:L8:154:G:H2'	3:L8:155:C:C6	2.56	0.41
6:LC:142:HIS:CD2	6:LC:204:ARG:HH12	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LH:105:ILE:HG13	11:LH:109:GLY:HA2	2.01	0.41
14:LL:18:TRP:CD1	14:LL:18:TRP:H	2.38	0.41
15:LM:14:TYR:HE1	15:LM:22:GLY:HA2	1.85	0.41
19:LQ:59:PRO:HG3	19:LQ:143:ARG:HA	2.03	0.41
25:LW:71:ARG:HD3	25:LW:71:ARG:HA	1.88	0.41
46:S2:465:A:H5'	46:S2:466:G:C5	2.54	0.41
46:S2:835:C:H2'	46:S2:837:A:C4	2.56	0.41
46:S2:1217:A:H2'	46:S2:1218:C:H6	1.86	0.41
46:S2:1279:C:H2'	46:S2:1280:G:C8	2.55	0.41
46:S2:1606:G:H1'	46:S2:1633:A:N6	2.35	0.41
48:SB:91:VAL:HG12	48:SB:96:CYS:HB2	2.02	0.41
56:SP:84:ILE:HD12	56:SP:85:ILE:H	1.85	0.41
60:ST:11:GLN:HB3	60:ST:62:ARG:HH12	1.85	0.41
72:SN:84:LEU:HA	72:SN:85:PRO:HD3	1.90	0.41
83:zz:216:U:N3	86:3a:69:GLU:HB3	2.35	0.41
85:3f:171:GLY:HA3	85:3f:198:ILE:H	1.86	0.41
85:3f:220:LEU:HD12	85:3f:220:LEU:HA	1.91	0.41
88:3c:797:SER:HA	88:3c:846:ARG:HH12	1.85	0.41
91:3k:155:ARG:HB2	91:3k:185:GLY:O	2.21	0.41
1:L5:302:C:H2'	1:L5:303:C:C6	2.55	0.41
1:L5:1327:C:H2'	1:L5:1328:G:H8	1.85	0.41
1:L5:1381:U:H2'	1:L5:1382:G:O4'	2.20	0.41
1:L5:2810:U:H5''	20:LR:70:ARG:HH22	1.85	0.41
1:L5:2877:G:H2'	1:L5:2878:G:O4'	2.21	0.41
1:L5:4745:G:H22	1:L5:4954:G:H22	1.67	0.41
2:L7:114:U:H2'	2:L7:115:A:H8	1.85	0.41
3:L8:50:C:H2'	40:Ll:26:TRP:CZ3	2.56	0.41
4:LA:54:ARG:HG3	4:LA:56:ALA:H	1.84	0.41
6:LC:76:ILE:HD12	6:LC:76:ILE:HA	1.89	0.41
12:LI:45:GLU:HG2	12:LI:46:PHE:CD1	2.55	0.41
13:LJ:7:GLU:H	13:LJ:7:GLU:HG3	1.65	0.41
21:LS:7:LEU:HB3	21:LS:107:THR:OG1	2.21	0.41
26:LX:40:ILE:HD12	26:LX:40:ILE:HA	1.79	0.41
27:LY:1:MET:HB3	27:LY:3:PHE:HE1	1.85	0.41
28:LZ:29:ILE:HG22	28:LZ:30:ASP:O	2.20	0.41
40:Ll:23:ILE:HD12	40:Ll:24:PRO:HD2	2.02	0.41
46:S2:429:C:H2'	46:S2:430:C:C6	2.54	0.41
46:S2:644:G:H2'	46:S2:645:C:H6	1.86	0.41
46:S2:654:A:C8	46:S2:655:A:H2'	2.55	0.41
46:S2:846:G:H2'	50:SE:19:MET:HE2	2.02	0.41
46:S2:1760:G:H22	46:S2:1772:C:H3'	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SB:84:PHE:CE1	48:SB:103:MET:HG3	2.55	0.41
56:SP:81:ARG:HB3	56:SP:117:GLY:HA3	2.02	0.41
62:SV:70:LEU:HD12	62:SV:70:LEU:HA	1.85	0.41
67:Sg:17:TRP:CE2	67:Sg:303:THR:HB	2.55	0.41
67:Sg:239:LEU:HD22	67:Sg:248:LEU:HD11	2.02	0.41
68:SC:183:LYS:HE2	68:SC:196:ILE:HG22	2.03	0.41
83:zz:210:G:N2	83:zz:212:U:H1'	2.35	0.41
86:3a:450:ILE:HD12	86:3a:450:ILE:HA	1.85	0.41
1:L5:423:G:H2'	1:L5:424:U:C6	2.56	0.41
1:L5:978:G:H2'	1:L5:979:C:C6	2.56	0.41
1:L5:1238:A:H5''	8:LE:60:SER:HB3	2.02	0.41
1:L5:1464:C:H2'	1:L5:1465:G:O4'	2.20	0.41
1:L5:1478:C:H2'	1:L5:1479:G:C8	2.55	0.41
1:L5:1631:A:C8	4:LA:199:VAL:HG11	2.55	0.41
1:L5:1750:G:H22	1:L5:1780:A:H2	1.68	0.41
1:L5:1779:U:H2'	1:L5:1780:A:C8	2.55	0.41
1:L5:2611:A:H2'	1:L5:2612:G:H8	1.85	0.41
1:L5:2793:G:H3'	1:L5:2794:C:H5'	2.03	0.41
2:L7:58:A:H2'	2:L7:59:G:H8	1.85	0.41
6:LC:322:LEU:O	6:LC:326:LEU:HD12	2.20	0.41
7:LD:128:ASP:HA	7:LD:190:PHE:HE2	1.85	0.41
11:LH:94:SER:HB3	11:LH:179:ILE:HG23	2.02	0.41
13:LJ:141:ILE:HD13	13:LJ:141:ILE:HA	1.83	0.41
31:Lc:78:ASN:HD22	31:Lc:90:ARG:HB2	1.85	0.41
38:Lj:36:LYS:HE2	38:Lj:36:LYS:HB3	1.89	0.41
42:Ln:7:LYS:HE3	42:Ln:11:ARG:NH1	2.35	0.41
46:S2:804:U:H2'	46:S2:805:U:H6	1.85	0.41
46:S2:1760:G:H2'	46:S2:1761:U:C6	2.56	0.41
46:S2:1864:U:H3'	64:Sa:5:ARG:HH21	1.85	0.41
47:SA:124:VAL:HG12	47:SA:126:ASP:H	1.85	0.41
54:SK:20:VAL:HG12	54:SK:70:TYR:HA	2.02	0.41
75:SY:41:ARG:HH21	75:SY:53:ASP:HA	1.84	0.41
88:3c:859:LEU:HD13	88:3c:859:LEU:HA	1.94	0.41
91:3k:148:ILE:HD12	92:3l:498:LYS:HG3	2.01	0.41
1:L5:455:C:O2'	1:L5:456:C:H5'	2.21	0.41
1:L5:952:G:H2'	1:L5:953:C:H6	1.86	0.41
1:L5:1645:C:H2'	1:L5:1646:A:H8	1.85	0.41
1:L5:3658:C:H2'	1:L5:3659:G:C8	2.54	0.41
1:L5:3722:G:H2'	1:L5:3723:A:C8	2.56	0.41
1:L5:3920:U:H2'	1:L5:3921:U:H6	1.85	0.41
1:L5:4238:G:H2'	1:L5:4239:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4344:U:H2'	1:L5:4345:C:C6	2.56	0.41
1:L5:4405:G:H4'	12:LI:4:ARG:HD3	2.03	0.41
1:L5:4577:U:H2'	1:L5:4578:G:H8	1.86	0.41
1:L5:4685:U:H2'	1:L5:4686:G:C8	2.56	0.41
1:L5:4876:U:H5'	21:LS:170:LYS:NZ	2.35	0.41
4:LA:210:PRO:HD2	4:LA:235:VAL:HG11	2.02	0.41
6:LC:25:PRO:HG2	6:LC:28:PHE:CD2	2.56	0.41
8:LE:286:LEU:HD23	8:LE:286:LEU:HA	1.89	0.41
25:LW:104:GLN:HB3	25:LW:107:GLN:HE22	1.85	0.41
28:LZ:115:LYS:O	28:LZ:119:GLU:HG2	2.21	0.41
36:Lh:94:ARG:HG2	36:Lh:95:LEU:N	2.34	0.41
51:SF:85:LYS:H	51:SF:85:LYS:HG2	1.52	0.41
53:SI:172:LEU:HB3	53:SI:190:LEU:HD13	2.02	0.41
57:SQ:51:LEU:HD13	57:SQ:81:ILE:HD11	2.03	0.41
60:ST:75:MET:HE2	60:ST:75:MET:HA	2.03	0.41
67:Sg:270:LEU:HD23	67:Sg:270:LEU:HA	1.84	0.41
86:3a:296:LEU:HD21	86:3a:321:ARG:HG3	2.03	0.41
88:3c:589:MET:HE1	88:3c:594:LEU:HD12	2.03	0.41
91:3k:204:LYS:HD2	91:3k:204:LYS:HA	1.83	0.41
1:L5:163:A:H2'	1:L5:164:G:H8	1.86	0.41
1:L5:270:U:H2'	1:L5:271:C:C6	2.55	0.41
1:L5:1266:G:C8	30:Lb:95:ARG:HG3	2.55	0.41
1:L5:1845:U:H5''	30:Lb:25:ARG:HH22	1.86	0.41
1:L5:2776:G:H2'	1:L5:2777:G:H8	1.85	0.41
1:L5:3910:C:H2'	1:L5:3911:C:H6	1.85	0.41
1:L5:4582:C:H2'	1:L5:4583:C:O4'	2.21	0.41
6:LC:14:LYS:HD3	6:LC:14:LYS:HA	1.69	0.41
6:LC:205:ARG:HA	6:LC:205:ARG:HD2	1.88	0.41
12:LI:76:MET:HE2	12:LI:76:MET:HB3	1.97	0.41
14:LL:65:ARG:HD2	29:La:69:PHE:HB2	2.03	0.41
16:LN:94:PHE:CE2	16:LN:96:ARG:HB2	2.56	0.41
31:Lc:36:LYS:HE2	31:Lc:36:LYS:HB2	1.88	0.41
38:Lj:25:LYS:HE3	38:Lj:25:LYS:HB2	1.80	0.41
43:Lo:13:LYS:HB2	43:Lo:13:LYS:HE3	1.87	0.41
46:S2:12:U:H2'	46:S2:13:C:H6	1.85	0.41
46:S2:54:A:H3'	46:S2:451:G:H22	1.85	0.41
62:SV:72:LEU:HD23	62:SV:72:LEU:HA	1.79	0.41
67:Sg:17:TRP:H	67:Sg:36:ARG:HB2	1.85	0.41
67:Sg:239:LEU:HD23	67:Sg:239:LEU:HA	1.89	0.41
67:Sg:271:LYS:HA	67:Sg:271:LYS:HD2	1.78	0.41
85:3f:98:ILE:HG13	85:3f:131:VAL:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:3a:523:LEU:HD12	86:3a:523:LEU:H	1.85	0.41
87:3e:335:ASN:HA	87:3e:338:LEU:HB3	2.02	0.41
88:3c:671:VAL:HG13	88:3c:676:HIS:CE1	2.56	0.41
92:3l:498:LYS:HA	92:3l:498:LYS:HD2	1.86	0.41
1:L5:170:C:H4'	1:L5:171:U:O4'	2.21	0.41
1:L5:678:C:H2'	1:L5:679:C:C6	2.56	0.41
1:L5:1481:C:H42	37:Li:4:ARG:NH1	2.19	0.41
1:L5:1968:G:H2'	1:L5:1969:G:H8	1.85	0.41
1:L5:2374:A:H2'	1:L5:2375:A:H8	1.86	0.41
1:L5:4860:G:H2'	1:L5:4861:G:O4'	2.21	0.41
1:L5:4926:C:H2'	1:L5:4927:G:O4'	2.20	0.41
1:L5:5004:C:H2'	1:L5:5005:G:O4'	2.21	0.41
2:L7:1:G:H21	7:LD:266:TRP:HZ2	1.68	0.41
2:L7:3:C:H2'	2:L7:4:U:H6	1.86	0.41
4:LA:246:LEU:HA	4:LA:246:LEU:HD12	1.81	0.41
11:LH:88:PHE:CE2	11:LH:151:ILE:HB	2.56	0.41
15:LM:61:ILE:HD13	15:LM:61:ILE:HA	1.90	0.41
20:LR:44:LEU:HD12	20:LR:49:LEU:HB2	2.02	0.41
27:LY:31:SER:HA	27:LY:48:PRO:HA	2.02	0.41
31:Lc:99:PRO:HG3	31:Lc:104:ILE:HG12	2.02	0.41
46:S2:1225:U:H2'	46:S2:1226:G:H8	1.85	0.41
46:S2:1628:C:H2'	46:S2:1629:C:C6	2.56	0.41
47:SA:90:PHE:HD1	47:SA:179:ALA:HB2	1.86	0.41
50:SE:183:VAL:HG21	50:SE:220:THR:HG21	2.02	0.41
55:SL:55:TYR:OH	55:SL:116:CYS:HB3	2.21	0.41
57:SQ:133:GLY:HA3	57:SQ:140:ARG:NH1	2.36	0.41
57:SQ:135:PRO:HD3	57:SQ:141:TYR:CZ	2.55	0.41
62:SV:24:ILE:HD13	62:SV:24:ILE:HA	1.86	0.41
67:Sg:36:ARG:HG2	67:Sg:65:PHE:HD2	1.83	0.41
83:zz:207:C:H2'	83:zz:208:C:C5	2.55	0.41
87:3e:374:LEU:HD12	87:3e:375:ILE:HG13	2.03	0.41
89:3h:75:ARG:HD2	89:3h:75:ARG:HA	1.75	0.41
89:3h:287:GLN:HG2	89:3h:288:ARG:HE	1.85	0.41
1:L5:46:U:H5''	14:LL:16:LYS:HG3	2.02	0.41
1:L5:309:C:H5''	1:L5:310:G:O4'	2.21	0.41
1:L5:429:A:H2'	1:L5:430:G:H8	1.84	0.41
1:L5:460:C:H2'	1:L5:461:G:H8	1.85	0.41
1:L5:1296:G:H2'	1:L5:1297:U:H6	1.86	0.41
1:L5:1318:C:H2'	1:L5:1319:U:O4'	2.21	0.41
1:L5:2285:A:H2'	1:L5:2286:G:C8	2.56	0.41
1:L5:2784:C:H2'	1:L5:2785:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2878:G:H5''	1:L5:2879:A:H2'	2.03	0.41
1:L5:3599:A:H2'	1:L5:3600:G:H8	1.86	0.41
1:L5:3608:A:H2'	1:L5:3609:G:H8	1.86	0.41
1:L5:4071:U:H2'	1:L5:4072:C:C6	2.56	0.41
1:L5:4769:G:H2'	1:L5:4770:U:H5''	2.03	0.41
1:L5:4889:G:N2	1:L5:4931:G:H1	2.18	0.41
1:L5:4934:A:H2'	1:L5:4935:C:C6	2.56	0.41
3:L8:17:A:H2'	3:L8:18:U:H6	1.86	0.41
7:LD:33:ARG:HE	7:LD:37:VAL:HG21	1.85	0.41
8:LE:51:VAL:H	8:LE:54:ILE:HG22	1.86	0.41
11:LH:90:TYR:CE1	11:LH:184:LYS:HB3	2.56	0.41
13:LJ:20:LEU:HB3	13:LJ:74:VAL:HG13	2.02	0.41
14:LL:11:LYS:HE2	14:LL:11:LYS:HB3	1.91	0.41
17:LO:153:THR:O	17:LO:157:GLU:HG2	2.21	0.41
17:LO:163:LYS:HE3	17:LO:163:LYS:HB2	1.81	0.41
19:LQ:39:THR:HG22	19:LQ:41:SER:H	1.86	0.41
21:LS:41:LYS:HE2	21:LS:41:LYS:HB3	1.92	0.41
21:LS:78:PHE:CE1	21:LS:102:THR:HA	2.50	0.41
21:LS:127:MET:HA	22:LT:152:GLU:OE1	2.21	0.41
22:LT:74:ILE:HG22	22:LT:76:VAL:HG22	2.02	0.41
23:LU:70:ILE:HD13	23:LU:70:ILE:HA	1.83	0.41
29:La:14:HIS:CG	33:Le:39:ARG:HH12	2.38	0.41
36:Lh:4:ILE:HD13	36:Lh:4:ILE:HA	1.87	0.41
37:Li:13:LYS:HB2	37:Li:13:LYS:HE2	1.92	0.41
37:Li:32:ARG:HD2	37:Li:32:ARG:HA	1.84	0.41
38:Lj:10:LYS:HB2	38:Lj:10:LYS:HE2	1.81	0.41
39:Lk:26:LYS:HB2	39:Lk:69:LEU:HD22	2.03	0.41
46:S2:5:U:H2'	46:S2:6:G:C8	2.55	0.41
46:S2:71:G:H2'	46:S2:73:C:H41	1.85	0.41
46:S2:318:A:H2'	46:S2:319:C:C6	2.56	0.41
46:S2:431:G:H2'	46:S2:432:G:H8	1.86	0.41
46:S2:687:C:H4'	52:SH:121:THR:OG1	2.21	0.41
46:S2:1407:U:H2'	46:S2:1408:U:C6	2.55	0.41
46:S2:1661:A:N7	66:Sd:14:PHE:HD1	2.19	0.41
46:S2:1808:U:H2'	46:S2:1809:A:C8	2.56	0.41
47:SA:49:ILE:HG21	47:SA:162:PRO:HB2	2.02	0.41
49:SD:213:PRO:HD3	58:SR:19:LYS:HE2	2.02	0.41
51:SF:192:LYS:HA	51:SF:195:GLU:HB3	2.03	0.41
61:SU:104:ILE:HD12	61:SU:105:SER:HB3	2.02	0.41
65:Sc:10:LYS:HA	65:Sc:10:LYS:HD3	1.83	0.41
67:Sg:38:LYS:HE3	67:Sg:38:LYS:HB2	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SJ:92:MET:HE2	70:SJ:92:MET:HA	2.02	0.41
71:Sf:84:LYS:HD3	71:Sf:84:LYS:HA	1.84	0.41
74:SW:31:SER:OG	74:SW:33:VAL:HG12	2.20	0.41
83:zz:166:C:H2'	83:zz:167:A:C8	2.55	0.41
84:3m:106:LEU:HD12	84:3m:106:LEU:HA	1.90	0.41
85:3f:117:ILE:HA	85:3f:172:TRP:HZ3	1.85	0.41
86:3a:62:ARG:NH2	86:3a:148:PRO:HB2	2.35	0.41
87:3e:298:CYS:HA	87:3e:302:ASN:HB2	2.03	0.41
87:3e:367:ALA:HA	87:3e:370:TRP:NE1	2.36	0.41
88:3c:80:LEU:HA	88:3c:141:LEU:HD12	2.02	0.41
1:L5:106:A:OP1	14:LL:39:ARG:HD3	2.21	0.41
1:L5:1895:G:H2'	1:L5:1896:A:O4'	2.21	0.41
1:L5:2085:G:H2'	1:L5:2086:G:H8	1.86	0.41
1:L5:3726:A:H2'	1:L5:3727:A:C8	2.56	0.41
1:L5:4600:G:H4'	1:L5:4601:U:O5'	2.21	0.41
3:L8:41:A:O2'	38:Lj:59:THR:HG22	2.20	0.41
4:LA:77:ILE:H	4:LA:77:ILE:HG12	1.67	0.41
16:LN:14:LYS:HE2	16:LN:14:LYS:HB3	1.69	0.41
25:LW:13:ILE:HD13	25:LW:13:ILE:HA	1.84	0.41
26:LX:71:LEU:HD12	26:LX:71:LEU:HA	1.83	0.41
32:Ld:117:LEU:HD23	32:Ld:117:LEU:HA	1.87	0.41
37:Li:76:ARG:HD3	37:Li:76:ARG:HA	1.85	0.41
46:S2:873:G:H2'	46:S2:874:G:C8	2.55	0.41
46:S2:996:A:H5''	72:SN:7:PRO:HD3	2.02	0.41
46:S2:1030:A:H2'	46:S2:1031:A:C8	2.54	0.41
46:S2:1198:G:H2'	46:S2:1199:A:H8	1.86	0.41
46:S2:1501:C:H2'	46:S2:1502:C:H6	1.86	0.41
46:S2:1804:U:H2'	46:S2:1805:G:H8	1.86	0.41
53:SI:123:ARG:HB3	53:SI:128:LYS:HE2	2.02	0.41
57:SQ:39:LEU:HD12	57:SQ:39:LEU:HA	1.81	0.41
58:SR:85:VAL:HA	58:SR:86:PRO:HD3	1.96	0.41
69:SG:30:LYS:HD3	69:SG:36:VAL:HG11	2.02	0.41
75:SY:60:PHE:CE1	75:SY:71:GLY:HA3	2.55	0.41
76:SZ:77:LEU:HB2	76:SZ:79:ILE:HG23	2.02	0.41
83:zz:308:C:H2'	83:zz:309:G:C8	2.56	0.41
84:3m:45:ILE:HD13	84:3m:67:VAL:HG22	2.03	0.41
85:3f:320:PRO:HA	85:3f:323:PHE:HB3	2.02	0.41
91:3k:179:TRP:NE1	91:3k:189:ILE:HG23	2.36	0.41
92:3l:525:LYS:HE2	92:3l:525:LYS:HB2	1.85	0.41
1:L5:2078:C:H2'	1:L5:2079:G:C8	2.56	0.40
1:L5:4070:U:H2'	1:L5:4071:U:H6	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4389:C:H2'	1:L5:4390:A:H8	1.85	0.40
1:L5:5051:C:H4'	5:LB:324:GLY:HA2	2.02	0.40
3:L8:138:C:H2'	3:L8:139:G:H8	1.86	0.40
10:LG:77:PRO:HA	10:LG:78:PRO:HD3	1.95	0.40
14:LL:19:GLN:H	14:LL:19:GLN:HG2	1.57	0.40
17:LO:125:LYS:HE2	17:LO:125:LYS:HB2	1.78	0.40
19:LQ:28:LEU:HA	19:LQ:28:LEU:HD23	1.75	0.40
22:LT:107:LYS:HE2	22:LT:107:LYS:HB2	1.96	0.40
30:Lb:99:ILE:H	30:Lb:99:ILE:HG13	1.72	0.40
33:Le:20:PHE:HD1	33:Le:20:PHE:HA	1.77	0.40
39:Lk:37:ARG:HD2	39:Lk:42:LEU:HB2	2.03	0.40
46:S2:843:C:H2'	46:S2:844:U:C6	2.56	0.40
46:S2:902:G:C6	46:S2:904:A:N6	2.89	0.40
49:SD:156:LEU:HD12	49:SD:157:MET:H	1.86	0.40
50:SE:174:LYS:HE3	50:SE:174:LYS:HB3	1.84	0.40
54:SK:3:MET:HB3	54:SK:44:HIS:CD2	2.56	0.40
54:SK:90:VAL:HG22	54:SK:91:PRO:HD2	2.03	0.40
56:SP:85:ILE:HG21	56:SP:111:MET:O	2.20	0.40
57:SQ:21:ALA:HB1	57:SQ:84:ILE:HG22	2.04	0.40
59:SS:125:HIS:CD2	59:SS:131:VAL:HG11	2.56	0.40
67:Sg:58:ALA:HB3	67:Sg:60:ARG:HH22	1.87	0.40
67:Sg:104:HIS:CE1	67:Sg:124:SER:HB3	2.56	0.40
70:SJ:110:LEU:HG	70:SJ:130:ILE:HD11	2.02	0.40
74:SW:94:LEU:HD21	74:SW:102:ILE:HG13	2.02	0.40
75:SY:11:LYS:HB2	75:SY:24:VAL:HG12	2.02	0.40
75:SY:51:THR:HB	75:SY:54:VAL:HG23	2.01	0.40
84:3m:162:HIS:HB3	84:3m:166:ARG:NH2	2.36	0.40
86:3a:383:VAL:HG23	86:3a:388:LYS:HG2	2.03	0.40
88:3c:57:PHE:HZ	88:3c:96:ILE:HG21	1.86	0.40
1:L5:920:C:H2'	1:L5:921:C:C6	2.56	0.40
1:L5:1392:A:H2'	1:L5:1393:G:H8	1.86	0.40
1:L5:4111:U:H2'	1:L5:4112:C:C6	2.55	0.40
2:L7:107:G:H5''	7:LD:273:LEU:HD11	2.04	0.40
9:LF:174:LEU:HD23	9:LF:174:LEU:HA	1.90	0.40
22:LT:57:TYR:CE1	22:LT:89:ILE:HG21	2.52	0.40
31:Lc:65:MET:HE3	31:Lc:66:LEU:HD22	2.03	0.40
32:Ld:51:LYS:HE3	32:Ld:51:LYS:HB2	1.72	0.40
37:Li:36:HIS:O	37:Li:40:VAL:HG23	2.21	0.40
37:Li:61:LEU:HD23	37:Li:61:LEU:HA	1.86	0.40
45:Lr:63:VAL:C	45:Lr:64:ILE:HD13	2.46	0.40
46:S2:107:A:H2'	46:S2:108:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:877:C:H5''	46:S2:879:C:OP2	2.22	0.40
46:S2:946:U:H2'	46:S2:947:G:C8	2.56	0.40
46:S2:1102:G:H22	46:S2:1130:G:N2	2.18	0.40
46:S2:1447:G:H2'	46:S2:1448:A:H8	1.86	0.40
46:S2:1809:A:H2'	46:S2:1810:U:C6	2.56	0.40
49:SD:156:LEU:HG	49:SD:189:MET:HE3	2.02	0.40
51:SF:95:HIS:O	51:SF:99:ILE:HG23	2.22	0.40
54:SK:21:MET:HE1	54:SK:23:ALA:HB2	2.03	0.40
55:SL:101:ARG:HH12	63:SX:5:ARG:HA	1.86	0.40
56:SP:86:LEU:H	56:SP:89:MET:HE1	1.85	0.40
67:Sg:194:TYR:CE2	67:Sg:212:LYS:HB3	2.55	0.40
69:SG:1:MET:HE2	69:SG:1:MET:HB2	1.83	0.40
69:SG:136:LYS:HE2	69:SG:136:LYS:HB3	1.85	0.40
69:SG:175:LYS:HB3	69:SG:175:LYS:HE3	1.81	0.40
70:SJ:37:LEU:HD23	70:SJ:111:GLN:HE22	1.86	0.40
73:SO:75:MET:HG2	73:SO:118:ALA:HB2	2.03	0.40
82:zy:22:G:H2'	82:zy:23:A:C8	2.56	0.40
84:3m:14:GLN:NE2	85:3f:226:ARG:HG3	2.36	0.40
86:3a:302:LEU:O	86:3a:306:MET:HG3	2.21	0.40
88:3c:118:ASN:HA	88:3c:142:ARG:HH12	1.86	0.40
92:3l:178:LEU:HD12	92:3l:183:LEU:HD12	2.03	0.40
92:3l:454:GLN:CD	92:3l:496:LYS:HG3	2.46	0.40
1:L5:444:G:H2'	1:L5:445:U:C6	2.56	0.40
1:L5:660:A:H2'	1:L5:661:C:C6	2.56	0.40
1:L5:690:C:H2'	1:L5:691:C:C6	2.56	0.40
1:L5:755:C:H2'	1:L5:756:G:C8	2.56	0.40
1:L5:1888:A:P	1:L5:1888:A:H8	2.44	0.40
1:L5:3598:C:H2'	1:L5:3599:A:H8	1.86	0.40
1:L5:4312:U:H2'	1:L5:4313:A:C8	2.57	0.40
1:L5:4513:A:H2'	1:L5:4514:G:H8	1.87	0.40
1:L5:4741:C:H2'	1:L5:4742:G:C8	2.56	0.40
5:LB:19:ARG:HB3	5:LB:234:ARG:NH2	2.34	0.40
5:LB:19:ARG:HG3	5:LB:275:HIS:CE1	2.56	0.40
7:LD:153:THR:HB	7:LD:160:PHE:HE1	1.86	0.40
8:LE:62:MET:O	8:LE:66:LYS:HB3	2.20	0.40
8:LE:124:LYS:HA	8:LE:124:LYS:HD2	2.00	0.40
21:LS:43:ARG:HA	21:LS:43:ARG:HD2	1.92	0.40
22:LT:57:TYR:OH	22:LT:87:LYS:HD3	2.21	0.40
24:LV:20:LEU:HB2	24:LV:55:ALA:O	2.21	0.40
25:LW:70:LYS:HD3	25:LW:70:LYS:HA	1.88	0.40
27:LY:49:ILE:HD12	27:LY:49:ILE:HA	1.81	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LY:74:TYR:CD2	27:LY:77:LYS:HE2	2.56	0.40
28:LZ:57:MET:HB2	28:LZ:61:LYS:HD3	2.03	0.40
36:Lh:14:LYS:HE2	36:Lh:14:LYS:HB3	1.86	0.40
46:S2:1407:U:H4'	57:SQ:71:ARG:NH2	2.36	0.40
51:SF:44:LYS:HA	51:SF:44:LYS:HD2	1.85	0.40
53:SI:101:ILE:HG22	53:SI:174:CYS:HB2	2.03	0.40
54:SK:35:LEU:HD23	54:SK:35:LEU:HA	1.82	0.40
56:SP:85:ILE:HG12	56:SP:111:MET:HB3	2.04	0.40
57:SQ:134:GLY:HA2	57:SQ:141:TYR:CD2	2.56	0.40
67:Sg:64:HIS:ND1	67:Sg:65:PHE:HD1	2.20	0.40
76:SZ:102:LYS:HD2	76:SZ:102:LYS:HA	1.82	0.40
79:sh:138:ARG:HB3	79:sh:149:CYS:HA	2.03	0.40
83:zz:206:A:H1'	83:zz:207:C:O4'	2.22	0.40
86:3a:183:LYS:HA	86:3a:183:LYS:HD2	1.90	0.40
87:3e:253:ILE:HA	87:3e:256:TYR:HD2	1.87	0.40
87:3e:408:THR:HA	87:3e:411:LEU:HG	2.03	0.40
88:3c:67:ILE:O	88:3c:71:MET:HG3	2.21	0.40
91:3k:109:LEU:HD23	91:3k:109:LEU:HA	1.94	0.40
92:3l:240:ILE:HG13	92:3l:267:LYS:HD3	2.03	0.40
1:L5:162:A:H2'	1:L5:163:A:H8	1.86	0.40
1:L5:260:C:H2'	1:L5:261:G:H8	1.86	0.40
1:L5:483:G:N7	1:L5:485:C:H5''	2.36	0.40
1:L5:2804:C:H2'	1:L5:2805:C:C6	2.56	0.40
1:L5:3923:A:H2'	1:L5:3924:C:C6	2.57	0.40
1:L5:4080:C:H2'	1:L5:4081:G:C8	2.55	0.40
1:L5:4178:A:H2'	1:L5:4179:G:C8	2.56	0.40
1:L5:4499:G:C2	1:L5:4529:G:H1'	2.55	0.40
3:L8:6:C:H2'	3:L8:7:U:C6	2.57	0.40
9:LF:36:LYS:HE2	9:LF:36:LYS:HB3	1.73	0.40
10:LG:120:LYS:HA	10:LG:120:LYS:HD3	1.65	0.40
11:LH:48:LEU:HD21	11:LH:56:ARG:HE	1.87	0.40
21:LS:2:LYS:HA	21:LS:2:LYS:HD2	1.60	0.40
26:LX:37:LYS:HD2	26:LX:37:LYS:HA	1.86	0.40
27:LY:4:ASN:HA	27:LY:5:PRO:HD3	1.94	0.40
31:Lc:44:LYS:HD3	31:Lc:44:LYS:HA	1.89	0.40
35:Lg:59:VAL:HG23	35:Lg:64:LEU:HB2	2.03	0.40
46:S2:352:U:H5''	55:SL:139:ARG:HG3	2.03	0.40
46:S2:694:G:H2'	46:S2:695:C:C6	2.56	0.40
46:S2:1284:A:C2	71:Sf:34:GLY:HA2	2.56	0.40
46:S2:1410:C:H2'	46:S2:1411:G:H8	1.87	0.40
46:S2:1693:G:H2'	46:S2:1694:U:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1834:A:H2	46:S2:1837:G:H22	1.70	0.40
49:SD:7:LYS:HA	49:SD:10:LYS:HZ3	1.86	0.40
54:SK:74:GLU:CD	54:SK:74:GLU:H	2.29	0.40
61:SU:66:ARG:NH1	61:SU:75:LYS:HA	2.36	0.40
64:Sa:79:ILE:H	64:Sa:79:ILE:HG13	1.52	0.40
67:Sg:155:ARG:HD3	67:Sg:155:ARG:HA	1.89	0.40
69:SG:147:LEU:HD12	69:SG:151:ASP:HB3	2.04	0.40
72:SN:4:MET:HE2	72:SN:5:HIS:HE1	1.85	0.40
72:SN:45:LEU:HD12	72:SN:49:GLN:HB3	2.02	0.40
84:3m:109:LEU:HD23	84:3m:123:VAL:HG13	2.03	0.40
87:3e:352:SER:HB3	87:3e:390:HIS:CE1	2.56	0.40
88:3c:105:PHE:HA	88:3c:108:ARG:HG2	2.03	0.40
92:3l:130:ILE:HG21	92:3l:163:LEU:HB2	2.02	0.40
92:3l:336:PHE:HB3	92:3l:371:LEU:HD13	2.03	0.40
92:3l:527:MET:HE2	92:3l:527:MET:HA	2.03	0.40
1:L5:6:C:H2'	1:L5:7:C:C6	2.57	0.40
1:L5:1948:G:H2'	1:L5:1949:U:C6	2.57	0.40
1:L5:1977:C:H2'	1:L5:1978:C:O4'	2.21	0.40
1:L5:2776:G:H2'	1:L5:2777:G:C8	2.57	0.40
1:L5:3702:A:C5	1:L5:3703:G:C8	3.10	0.40
1:L5:4110:C:H2'	1:L5:4111:U:C6	2.56	0.40
1:L5:4251:A:C2	13:LJ:127:GLY:HA3	2.57	0.40
1:L5:4466:C:H2'	1:L5:4467:A:C8	2.57	0.40
1:L5:4577:U:H2'	1:L5:4578:G:C8	2.56	0.40
2:L7:46:C:H2'	2:L7:47:G:C8	2.57	0.40
4:LA:41:ILE:HD12	4:LA:41:ILE:HA	1.93	0.40
4:LA:201:GLY:O	4:LA:204:MET:HB2	2.22	0.40
10:LG:212:LYS:HE3	10:LG:212:LYS:HB2	1.94	0.40
13:LJ:118:LYS:HE2	13:LJ:118:LYS:HB2	1.90	0.40
22:LT:54:HIS:CD2	22:LT:55:LYS:H	2.40	0.40
29:La:98:ALA:HB2	29:La:121:PRO:HB2	2.02	0.40
37:Li:33:LEU:HD11	37:Li:38:LYS:HB2	2.02	0.40
46:S2:1739:C:H2'	46:S2:1740:C:H6	1.87	0.40
56:SP:110:GLU:HB3	59:SS:117:ILE:HD12	2.03	0.40
56:SP:121:ILE:HD12	56:SP:121:ILE:HA	1.89	0.40
57:SQ:16:LYS:HZ2	57:SQ:16:LYS:HG3	1.61	0.40
57:SQ:41:MET:HE2	57:SQ:41:MET:N	2.37	0.40
70:SJ:128:VAL:HG12	70:SJ:132:GLN:NE2	2.36	0.40
72:SN:4:MET:HG3	72:SN:5:HIS:ND1	2.36	0.40
72:SN:29:THR:HG23	72:SN:31:ASP:N	2.34	0.40
73:SO:77:ALA:O	73:SO:81:VAL:HG12	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:3a:24:LYS:HB2	86:3a:57:LEU:HD22	2.04	0.40
88:3c:73:ILE:HA	88:3c:73:ILE:HD12	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/257 (96%)	224 (91%)	22 (9%)	0	100	100
5	LB	397/403 (98%)	366 (92%)	30 (8%)	1 (0%)	37	70
6	LC	364/427 (85%)	345 (95%)	19 (5%)	0	100	100
7	LD	291/297 (98%)	259 (89%)	31 (11%)	1 (0%)	37	70
8	LE	220/288 (76%)	191 (87%)	29 (13%)	0	100	100
9	LF	223/248 (90%)	215 (96%)	8 (4%)	0	100	100
10	LG	237/266 (89%)	218 (92%)	19 (8%)	0	100	100
11	LH	188/192 (98%)	171 (91%)	17 (9%)	0	100	100
12	LI	211/214 (99%)	192 (91%)	19 (9%)	0	100	100
13	LJ	174/178 (98%)	166 (95%)	8 (5%)	0	100	100
14	LL	208/211 (99%)	194 (93%)	14 (7%)	0	100	100
15	LM	137/215 (64%)	131 (96%)	6 (4%)	0	100	100
16	LN	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
17	LO	199/203 (98%)	196 (98%)	3 (2%)	0	100	100
18	LP	151/184 (82%)	142 (94%)	9 (6%)	0	100	100
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	185/196 (94%)	183 (99%)	2 (1%)	0	100	100
21	LS	173/176 (98%)	157 (91%)	16 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	LT	157/160 (98%)	143 (91%)	14 (9%)	0	100	100
23	LU	99/128 (77%)	89 (90%)	10 (10%)	0	100	100
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/157 (78%)	117 (96%)	5 (4%)	0	100	100
26	LX	115/156 (74%)	110 (96%)	5 (4%)	0	100	100
27	LY	132/145 (91%)	127 (96%)	5 (4%)	0	100	100
28	LZ	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
30	Lb	105/159 (66%)	96 (91%)	9 (9%)	0	100	100
31	Lc	96/115 (84%)	93 (97%)	3 (3%)	0	100	100
32	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
33	Le	126/135 (93%)	122 (97%)	4 (3%)	0	100	100
34	Lf	107/110 (97%)	99 (92%)	8 (8%)	0	100	100
35	Lg	108/117 (92%)	101 (94%)	7 (6%)	0	100	100
36	Lh	120/123 (98%)	112 (93%)	8 (7%)	0	100	100
37	Li	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
38	Lj	84/97 (87%)	77 (92%)	7 (8%)	0	100	100
39	Lk	67/70 (96%)	61 (91%)	6 (9%)	0	100	100
40	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	Lm	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
44	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	Lr	123/137 (90%)	112 (91%)	11 (9%)	0	100	100
47	SA	220/295 (75%)	210 (96%)	10 (4%)	0	100	100
48	SB	212/264 (80%)	199 (94%)	13 (6%)	0	100	100
49	SD	225/243 (93%)	222 (99%)	3 (1%)	0	100	100
50	SE	260/263 (99%)	243 (94%)	17 (6%)	0	100	100
51	SF	187/204 (92%)	177 (95%)	10 (5%)	0	100	100
52	SH	182/194 (94%)	170 (93%)	12 (7%)	0	100	100
53	SI	204/208 (98%)	191 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	SK	96/165 (58%)	91 (95%)	5 (5%)	0	100	100
55	SL	138/158 (87%)	127 (92%)	11 (8%)	0	100	100
56	SP	126/145 (87%)	120 (95%)	6 (5%)	0	100	100
57	SQ	144/146 (99%)	129 (90%)	14 (10%)	1 (1%)	19	54
58	SR	130/135 (96%)	125 (96%)	5 (4%)	0	100	100
59	SS	143/152 (94%)	132 (92%)	11 (8%)	0	100	100
60	ST	141/145 (97%)	139 (99%)	2 (1%)	0	100	100
61	SU	101/119 (85%)	96 (95%)	5 (5%)	0	100	100
62	SV	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
63	SX	139/143 (97%)	125 (90%)	14 (10%)	0	100	100
64	Sa	98/115 (85%)	93 (95%)	4 (4%)	1 (1%)	13	46
65	Sc	62/69 (90%)	53 (86%)	9 (14%)	0	100	100
66	Sd	53/56 (95%)	47 (89%)	6 (11%)	0	100	100
67	Sg	311/317 (98%)	292 (94%)	19 (6%)	0	100	100
68	SC	215/293 (73%)	199 (93%)	16 (7%)	0	100	100
69	SG	234/249 (94%)	228 (97%)	6 (3%)	0	100	100
70	SJ	183/194 (94%)	171 (93%)	12 (7%)	0	100	100
71	Sf	120/132 (91%)	108 (90%)	12 (10%)	0	100	100
72	SN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
73	SO	133/151 (88%)	121 (91%)	12 (9%)	0	100	100
74	SW	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
75	SY	129/133 (97%)	124 (96%)	5 (4%)	0	100	100
76	SZ	73/125 (58%)	68 (93%)	5 (7%)	0	100	100
77	Sb	81/84 (96%)	75 (93%)	6 (7%)	0	100	100
78	Se	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
79	sh	61/156 (39%)	55 (90%)	5 (8%)	1 (2%)	8	34
81	zx	19/31 (61%)	12 (63%)	7 (37%)	0	100	100
84	3m	361/374 (96%)	350 (97%)	11 (3%)	0	100	100
85	3f	267/357 (75%)	263 (98%)	4 (2%)	0	100	100
86	3a	590/1382 (43%)	578 (98%)	12 (2%)	0	100	100
87	3e	427/445 (96%)	417 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
88	3c	644/913 (70%)	633 (98%)	11 (2%)	0	100	100
89	3h	313/352 (89%)	305 (97%)	8 (3%)	0	100	100
90	3d	53/548 (10%)	53 (100%)	0	0	100	100
91	3k	213/218 (98%)	204 (96%)	9 (4%)	0	100	100
92	3l	518/564 (92%)	507 (98%)	11 (2%)	0	100	100
All	All	14693/17872 (82%)	13878 (94%)	810 (6%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	LB	303	ALA
7	LD	126	THR
64	Sa	61	ALA
79	sh	138	ARG
57	SQ	42	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	
4	LA	190/199 (96%)	169 (89%)	21 (11%)	5	21
5	LB	347/349 (99%)	329 (95%)	18 (5%)	19	52
6	LC	305/348 (88%)	292 (96%)	13 (4%)	25	58
7	LD	246/250 (98%)	237 (96%)	9 (4%)	29	63
8	LE	200/252 (79%)	188 (94%)	12 (6%)	16	47
9	LF	193/215 (90%)	179 (93%)	14 (7%)	11	39
10	LG	202/223 (91%)	192 (95%)	10 (5%)	20	53
11	LH	167/171 (98%)	162 (97%)	5 (3%)	36	69
12	LI	180/181 (99%)	168 (93%)	12 (7%)	13	43
13	LJ	148/149 (99%)	141 (95%)	7 (5%)	22	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	LL	176/177 (99%)	166 (94%)	10 (6%)	17	49
15	LM	118/161 (73%)	110 (93%)	8 (7%)	13	42
16	LN	171/172 (99%)	156 (91%)	15 (9%)	8	31
17	LO	173/174 (99%)	160 (92%)	13 (8%)	11	38
18	LP	134/163 (82%)	126 (94%)	8 (6%)	16	47
19	LQ	164/165 (99%)	151 (92%)	13 (8%)	10	35
20	LR	166/175 (95%)	156 (94%)	10 (6%)	16	47
21	LS	156/157 (99%)	141 (90%)	15 (10%)	7	27
22	LT	139/140 (99%)	119 (86%)	20 (14%)	2	13
23	LU	91/115 (79%)	85 (93%)	6 (7%)	14	43
24	LV	101/107 (94%)	90 (89%)	11 (11%)	5	22
25	LW	103/126 (82%)	100 (97%)	3 (3%)	37	70
26	LX	107/133 (80%)	96 (90%)	11 (10%)	6	24
27	LY	124/135 (92%)	117 (94%)	7 (6%)	17	49
28	LZ	117/118 (99%)	112 (96%)	5 (4%)	25	58
29	La	120/121 (99%)	113 (94%)	7 (6%)	17	48
30	Lb	88/126 (70%)	87 (99%)	1 (1%)	70	87
31	Lc	83/97 (86%)	72 (87%)	11 (13%)	3	15
32	Ld	98/110 (89%)	94 (96%)	4 (4%)	26	60
33	Le	114/121 (94%)	109 (96%)	5 (4%)	24	58
34	Lf	88/89 (99%)	81 (92%)	7 (8%)	10	35
35	Lg	96/100 (96%)	90 (94%)	6 (6%)	15	45
36	Lh	109/110 (99%)	102 (94%)	7 (6%)	14	44
37	Li	86/89 (97%)	82 (95%)	4 (5%)	22	56
38	Lj	73/80 (91%)	69 (94%)	4 (6%)	18	50
39	Lk	64/65 (98%)	56 (88%)	8 (12%)	3	17
40	Ll	47/48 (98%)	44 (94%)	3 (6%)	14	44
41	Lm	48/116 (41%)	47 (98%)	1 (2%)	48	77
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	83 (89%)	10 (11%)	5	22
44	Lp	74/75 (99%)	64 (86%)	10 (14%)	3	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	Lr	109/121 (90%)	105 (96%)	4 (4%)	29	63
47	SA	184/243 (76%)	173 (94%)	11 (6%)	16	47
48	SB	195/231 (84%)	179 (92%)	16 (8%)	9	34
49	SD	190/202 (94%)	180 (95%)	10 (5%)	19	51
50	SE	224/225 (100%)	210 (94%)	14 (6%)	15	45
51	SF	156/170 (92%)	149 (96%)	7 (4%)	23	57
52	SH	166/174 (95%)	159 (96%)	7 (4%)	25	59
53	SI	178/180 (99%)	164 (92%)	14 (8%)	10	35
54	SK	89/136 (65%)	83 (93%)	6 (7%)	13	43
55	SL	128/142 (90%)	116 (91%)	12 (9%)	7	28
56	SP	114/130 (88%)	105 (92%)	9 (8%)	10	35
57	SQ	121/121 (100%)	109 (90%)	12 (10%)	6	26
58	SR	120/122 (98%)	108 (90%)	12 (10%)	6	25
59	SS	126/132 (96%)	122 (97%)	4 (3%)	34	67
60	ST	113/115 (98%)	108 (96%)	5 (4%)	24	58
61	SU	94/107 (88%)	89 (95%)	5 (5%)	19	51
62	SV	67/67 (100%)	64 (96%)	3 (4%)	23	57
63	SX	113/115 (98%)	103 (91%)	10 (9%)	8	31
64	Sa	87/98 (89%)	82 (94%)	5 (6%)	17	49
65	Sc	56/62 (90%)	47 (84%)	9 (16%)	2	10
66	Sd	48/49 (98%)	45 (94%)	3 (6%)	15	45
67	Sg	272/275 (99%)	257 (94%)	15 (6%)	18	50
68	SC	183/225 (81%)	170 (93%)	13 (7%)	12	40
69	SG	206/218 (94%)	200 (97%)	6 (3%)	37	70
70	SJ	161/168 (96%)	150 (93%)	11 (7%)	13	42
71	Sf	100/108 (93%)	95 (95%)	5 (5%)	20	53
72	SN	130/131 (99%)	121 (93%)	9 (7%)	13	42
73	SO	105/119 (88%)	95 (90%)	10 (10%)	7	28
74	SW	112/113 (99%)	101 (90%)	11 (10%)	6	26
75	SY	113/115 (98%)	110 (97%)	3 (3%)	40	71
76	SZ	66/103 (64%)	63 (96%)	3 (4%)	23	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
77	Sb	75/76 (99%)	62 (83%)	13 (17%)	1	8
78	Se	47/48 (98%)	44 (94%)	3 (6%)	14	44
79	sh	56/140 (40%)	51 (91%)	5 (9%)	8	31
81	zx	20/29 (69%)	19 (95%)	1 (5%)	20	53
84	3m	252/335 (75%)	245 (97%)	7 (3%)	38	70
85	3f	229/289 (79%)	221 (96%)	8 (4%)	31	65
86	3a	439/1259 (35%)	431 (98%)	8 (2%)	54	80
87	3e	301/406 (74%)	297 (99%)	4 (1%)	65	85
88	3c	442/811 (54%)	433 (98%)	9 (2%)	50	78
89	3h	270/310 (87%)	263 (97%)	7 (3%)	41	72
90	3d	20/494 (4%)	20 (100%)	0	100	100
91	3k	121/193 (63%)	117 (97%)	4 (3%)	33	67
92	3l	475/515 (92%)	467 (98%)	8 (2%)	56	81
All	All	12395/15442 (80%)	11690 (94%)	705 (6%)	20	49

All (705) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	9	ARG
4	LA	45	VAL
4	LA	62	VAL
4	LA	73	THR
4	LA	77	ILE
4	LA	96	LEU
4	LA	98	ILE
4	LA	101	VAL
4	LA	112	ILE
4	LA	116	LEU
4	LA	126	LEU
4	LA	135	THR
4	LA	146	THR
4	LA	152	SER
4	LA	155	LYS
4	LA	162	ASN
4	LA	179	ILE
4	LA	207	VAL
4	LA	219	ILE

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Mol	Chain	Res	Type
4	LA	233	ARG
4	LA	249	THR
5	LB	11	HIS
5	LB	14	LEU
5	LB	23	SER
5	LB	31	SER
5	LB	72	VAL
5	LB	87	VAL
5	LB	110	ILE
5	LB	114	CYS
5	LB	128	LYS
5	LB	168	MET
5	LB	185	VAL
5	LB	215	GLU
5	LB	287	ILE
5	LB	298	LEU
5	LB	328	ASN
5	LB	338	VAL
5	LB	340	THR
5	LB	384	GLU
6	LC	8	ILE
6	LC	10	VAL
6	LC	23	THR
6	LC	50	GLN
6	LC	55	SER
6	LC	56	GLU
6	LC	96	CYS
6	LC	124	ILE
6	LC	171	LEU
6	LC	212	ASN
6	LC	257	PHE
6	LC	282	HIS
6	LC	366	ASP
7	LD	37	VAL
7	LD	62	CYS
7	LD	72	ASP
7	LD	126	THR
7	LD	132	VAL
7	LD	144	CYS
7	LD	150	LEU
7	LD	256	LYS
7	LD	266	TRP

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Mol	Chain	Res	Type
8	LE	54	ILE
8	LE	62	MET
8	LE	106	VAL
8	LE	128	HIS
8	LE	137	VAL
8	LE	150	LEU
8	LE	151	ILE
8	LE	154	THR
8	LE	174	LEU
8	LE	176	THR
8	LE	191	GLN
8	LE	212	LEU
9	LF	89	LEU
9	LF	108	VAL
9	LF	111	LEU
9	LF	112	LEU
9	LF	125	LEU
9	LF	126	ASN
9	LF	129	SER
9	LF	153	LEU
9	LF	154	ILE
9	LF	167	ILE
9	LF	196	THR
9	LF	197	VAL
9	LF	214	SER
9	LF	225	THR
10	LG	33	GLU
10	LG	55	VAL
10	LG	70	LEU
10	LG	107	LYS
10	LG	154	LEU
10	LG	168	VAL
10	LG	199	CYS
10	LG	201	THR
10	LG	228	ASP
10	LG	263	THR
11	LH	24	THR
11	LH	112	VAL
11	LH	136	VAL
11	LH	179	ILE
11	LH	181	VAL
12	LI	31	ILE

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Mol	Chain	Res	Type
12	LI	58	GLU
12	LI	60	LEU
12	LI	71	CYS
12	LI	77	VAL
12	LI	111	LEU
12	LI	134	VAL
12	LI	150	GLU
12	LI	168	SER
12	LI	189	CYS
12	LI	190	LEU
12	LI	206	LEU
13	LJ	18	ARG
13	LJ	74	VAL
13	LJ	83	LEU
13	LJ	115	LEU
13	LJ	117	ILE
13	LJ	134	LEU
13	LJ	155	HIS
14	LL	55	ILE
14	LL	59	VAL
14	LL	88	LYS
14	LL	93	THR
14	LL	106	SER
14	LL	107	THR
14	LL	113	ASN
14	LL	154	VAL
14	LL	159	ASN
14	LL	169	ILE
15	LM	25	VAL
15	LM	33	GLN
15	LM	43	THR
15	LM	54	CYS
15	LM	105	THR
15	LM	108	ASP
15	LM	119	ARG
15	LM	136	LEU
16	LN	22	LEU
16	LN	34	SER
16	LN	75	VAL
16	LN	85	VAL
16	LN	87	HIS
16	LN	100	SER

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Mol	Chain	Res	Type
16	LN	103	GLU
16	LN	104	GLU
16	LN	115	VAL
16	LN	132	VAL
16	LN	148	THR
16	LN	166	SER
16	LN	174	LEU
16	LN	179	LYS
16	LN	193	ARG
17	LO	8	VAL
17	LO	28	LEU
17	LO	33	VAL
17	LO	34	VAL
17	LO	38	CYS
17	LO	39	GLU
17	LO	120	VAL
17	LO	124	LEU
17	LO	132	THR
17	LO	152	VAL
17	LO	174	LEU
17	LO	185	VAL
17	LO	203	VAL
18	LP	14	SER
18	LP	53	LEU
18	LP	67	VAL
18	LP	70	CYS
18	LP	112	LEU
18	LP	117	ILE
18	LP	129	THR
18	LP	137	ASN
19	LQ	13	VAL
19	LQ	17	GLU
19	LQ	41	SER
19	LQ	56	THR
19	LQ	72	LEU
19	LQ	79	THR
19	LQ	82	VAL
19	LQ	83	VAL
19	LQ	95	VAL
19	LQ	103	LEU
19	LQ	128	LEU
19	LQ	158	THR

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Mol	Chain	Res	Type
19	LQ	184	ARG
20	LR	44	LEU
20	LR	49	LEU
20	LR	52	ARG
20	LR	63	CYS
20	LR	65	LYS
20	LR	99	MET
20	LR	112	SER
20	LR	145	LEU
20	LR	176	ARG
20	LR	177	LEU
21	LS	2	LYS
21	LS	19	THR
21	LS	64	CYS
21	LS	67	VAL
21	LS	113	MET
21	LS	123	SER
21	LS	144	GLN
21	LS	148	SER
21	LS	150	ILE
21	LS	158	VAL
21	LS	159	LEU
21	LS	166	ARG
21	LS	168	THR
21	LS	169	THR
21	LS	174	THR
22	LT	4	THR
22	LT	13	TYR
22	LT	25	VAL
22	LT	27	LEU
22	LT	39	ILE
22	LT	60	LYS
22	LT	61	THR
22	LT	67	VAL
22	LT	72	VAL
22	LT	76	VAL
22	LT	88	ARG
22	LT	89	ILE
22	LT	91	VAL
22	LT	93	ILE
22	LT	98	HIS
22	LT	106	LEU

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Mol	Chain	Res	Type
22	LT	107	LYS
22	LT	143	THR
22	LT	150	LEU
22	LT	157	GLU
23	LU	56	LEU
23	LU	60	VAL
23	LU	62	THR
23	LU	76	VAL
23	LU	91	LEU
23	LU	92	LYS
24	LV	16	ILE
24	LV	18	LEU
24	LV	25	VAL
24	LV	42	VAL
24	LV	48	ARG
24	LV	51	ARG
24	LV	64	THR
24	LV	69	LYS
24	LV	81	VAL
24	LV	101	ASN
24	LV	118	THR
25	LW	28	VAL
25	LW	87	LEU
25	LW	107	GLN
26	LX	56	ARG
26	LX	71	LEU
26	LX	82	THR
26	LX	83	THR
26	LX	94	ASN
26	LX	99	ILE
26	LX	116	LEU
26	LX	121	VAL
26	LX	124	VAL
26	LX	127	LEU
26	LX	147	LEU
27	LY	38	LEU
27	LY	49	ILE
27	LY	74	TYR
27	LY	93	THR
27	LY	102	SER
27	LY	107	THR
27	LY	119	LEU

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Mol	Chain	Res	Type
28	LZ	24	VAL
28	LZ	57	MET
28	LZ	73	LYS
28	LZ	96	VAL
28	LZ	134	LEU
29	La	3	SER
29	La	5	LEU
29	La	24	LYS
29	La	38	LEU
29	La	82	VAL
29	La	110	LYS
29	La	147	VAL
30	Lb	13	SER
31	Lc	13	SER
31	Lc	17	ARG
31	Lc	23	LYS
31	Lc	35	LEU
31	Lc	45	LEU
31	Lc	48	LEU
31	Lc	66	LEU
31	Lc	69	THR
31	Lc	71	VAL
31	Lc	81	LEU
31	Lc	105	ILE
32	Ld	66	THR
32	Ld	89	SER
32	Ld	102	LEU
32	Ld	106	VAL
33	Le	13	VAL
33	Le	55	MET
33	Le	79	VAL
33	Le	103	VAL
33	Le	111	ILE
34	Lf	28	LEU
34	Lf	33	VAL
34	Lf	73	LYS
34	Lf	74	VAL
34	Lf	100	ARG
34	Lf	103	VAL
34	Lf	105	LEU
35	Lg	3	GLN
35	Lg	35	THR

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Mol	Chain	Res	Type
35	Lg	56	VAL
35	Lg	68	SER
35	Lg	75	SER
35	Lg	91	ILE
36	Lh	9	LEU
36	Lh	16	GLU
36	Lh	37	THR
36	Lh	45	SER
36	Lh	95	LEU
36	Lh	104	THR
36	Lh	107	GLN
37	Li	22	SER
37	Li	44	ILE
37	Li	70	LEU
37	Li	94	LEU
38	Lj	24	SER
38	Lj	42	LYS
38	Lj	67	LEU
38	Lj	83	THR
39	Lk	12	LEU
39	Lk	19	ASP
39	Lk	23	VAL
39	Lk	37	ARG
39	Lk	42	LEU
39	Lk	47	ILE
39	Lk	48	THR
39	Lk	66	VAL
40	Ll	2	SER
40	Ll	19	GLN
40	Ll	20	ASN
41	Lm	118	THR
43	Lo	2	VAL
43	Lo	23	VAL
43	Lo	24	THR
43	Lo	55	ILE
43	Lo	59	LYS
43	Lo	62	THR
43	Lo	68	LEU
43	Lo	70	LEU
43	Lo	79	SER
43	Lo	106	PHE
44	Lp	6	LYS

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Mol	Chain	Res	Type
44	Lp	8	VAL
44	Lp	10	ILE
44	Lp	13	LYS
44	Lp	18	TYR
44	Lp	21	SER
44	Lp	32	SER
44	Lp	40	SER
44	Lp	70	THR
44	Lp	73	THR
45	Lr	31	ASN
45	Lr	37	SER
45	Lr	75	THR
45	Lr	96	MET
47	SA	13	GLU
47	SA	38	ILE
47	SA	69	GLU
47	SA	122	LEU
47	SA	123	VAL
47	SA	144	THR
47	SA	154	LEU
47	SA	164	ASN
47	SA	171	VAL
47	SA	190	SER
47	SA	212	LYS
48	SB	48	LEU
48	SB	49	VAL
48	SB	55	THR
48	SB	67	PHE
48	SB	69	VAL
48	SB	71	LEU
48	SB	82	ARG
48	SB	88	THR
48	SB	119	THR
48	SB	153	THR
48	SB	178	THR
48	SB	183	GLU
48	SB	186	ASN
48	SB	192	SER
48	SB	203	SER
48	SB	231	LEU
49	SD	91	VAL
49	SD	109	LEU

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Mol	Chain	Res	Type
49	SD	123	LEU
49	SD	126	ILE
49	SD	142	LEU
49	SD	153	VAL
49	SD	167	TYR
49	SD	170	THR
49	SD	176	LEU
49	SD	190	LEU
50	SE	45	ILE
50	SE	61	VAL
50	SE	90	ILE
50	SE	101	LEU
50	SE	111	VAL
50	SE	126	VAL
50	SE	195	ILE
50	SE	207	VAL
50	SE	208	VAL
50	SE	217	SER
50	SE	228	ILE
50	SE	244	ILE
50	SE	246	LEU
50	SE	247	THR
51	SF	19	LEU
51	SF	39	ILE
51	SF	72	LEU
51	SF	98	GLU
51	SF	168	THR
51	SF	172	CYS
51	SF	204	ARG
52	SH	61	ILE
52	SH	66	VAL
52	SH	114	GLN
52	SH	119	SER
52	SH	134	VAL
52	SH	153	LEU
52	SH	185	VAL
53	SI	14	THR
53	SI	29	LEU
53	SI	37	LYS
53	SI	81	VAL
53	SI	91	VAL
53	SI	95	THR

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Mol	Chain	Res	Type
53	SI	97	VAL
53	SI	101	ILE
53	SI	103	LEU
53	SI	104	ILE
53	SI	107	THR
53	SI	136	ILE
53	SI	182	CYS
53	SI	189	VAL
54	SK	16	PHE
54	SK	27	VAL
54	SK	29	MET
54	SK	40	VAL
54	SK	90	VAL
54	SK	93	THR
55	SL	4	ILE
55	SL	15	THR
55	SL	51	ILE
55	SL	66	VAL
55	SL	76	VAL
55	SL	77	VAL
55	SL	91	ASP
55	SL	111	VAL
55	SL	113	LEU
55	SL	120	VAL
55	SL	126	VAL
55	SL	143	LEU
56	SP	21	ASP
56	SP	42	ARG
56	SP	54	HIS
56	SP	55	SER
56	SP	75	VAL
56	SP	108	LYS
56	SP	111	MET
56	SP	112	ILE
56	SP	121	ILE
57	SQ	7	LEU
57	SQ	8	GLN
57	SQ	18	THR
57	SQ	51	LEU
57	SQ	66	VAL
57	SQ	70	VAL
57	SQ	86	GLN

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Mol	Chain	Res	Type
57	SQ	105	LYS
57	SQ	112	LEU
57	SQ	113	ILE
57	SQ	115	TYR
57	SQ	127	CYS
58	SR	6	THR
58	SR	7	LYS
58	SR	9	VAL
58	SR	48	ASN
58	SR	50	ILE
58	SR	71	ILE
58	SR	91	LEU
58	SR	93	GLN
58	SR	108	LEU
58	SR	109	LEU
58	SR	114	LEU
58	SR	117	LEU
59	SS	60	THR
59	SS	73	ASN
59	SS	96	SER
59	SS	144	ARG
60	ST	9	VAL
60	ST	15	VAL
60	ST	45	LEU
60	ST	99	VAL
60	ST	104	LEU
61	SU	22	ILE
61	SU	26	SER
61	SU	68	THR
61	SU	85	HIS
61	SU	95	SER
62	SV	10	ASP
62	SV	20	SER
62	SV	56	CYS
63	SX	52	LEU
63	SX	82	THR
63	SX	85	VAL
63	SX	91	LEU
63	SX	92	ASN
63	SX	94	ILE
63	SX	107	ARG
63	SX	112	VAL

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Mol	Chain	Res	Type
63	SX	115	ILE
63	SX	122	VAL
64	Sa	6	ARG
64	Sa	50	VAL
64	Sa	63	VAL
64	Sa	81	SER
64	Sa	83	VAL
65	Sc	18	LEU
65	Sc	26	GLN
65	Sc	28	THR
65	Sc	32	VAL
65	Sc	34	PHE
65	Sc	38	THR
65	Sc	55	VAL
65	Sc	58	LEU
65	Sc	66	ARG
66	Sd	25	SER
66	Sd	31	ILE
66	Sd	50	ILE
67	Sg	6	THR
67	Sg	10	THR
67	Sg	27	PHE
67	Sg	107	ASP
67	Sg	111	VAL
67	Sg	126	ASP
67	Sg	134	THR
67	Sg	135	LEU
67	Sg	151	VAL
67	Sg	164	ILE
67	Sg	218	LEU
67	Sg	246	TYR
67	Sg	274	VAL
67	Sg	277	THR
67	Sg	287	THR
68	SC	80	GLU
68	SC	81	ILE
68	SC	112	VAL
68	SC	122	THR
68	SC	137	VAL
68	SC	143	CYS
68	SC	147	VAL
68	SC	157	LEU

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Mol	Chain	Res	Type
68	SC	163	VAL
68	SC	214	LEU
68	SC	232	THR
68	SC	244	ILE
68	SC	266	TYR
69	SG	29	GLU
69	SG	49	VAL
69	SG	97	VAL
69	SG	109	LEU
69	SG	112	VAL
69	SG	129	VAL
70	SJ	14	VAL
70	SJ	28	GLU
70	SJ	34	GLU
70	SJ	61	LEU
70	SJ	82	VAL
70	SJ	117	LEU
70	SJ	138	ARG
70	SJ	141	VAL
70	SJ	146	SER
70	SJ	157	ILE
70	SJ	173	VAL
71	Sf	31	LEU
71	Sf	37	GLU
71	Sf	45	ARG
71	Sf	50	CYS
71	Sf	110	VAL
72	SN	33	VAL
72	SN	60	VAL
72	SN	75	LEU
72	SN	87	ASP
72	SN	98	VAL
72	SN	103	GLU
72	SN	109	LYS
72	SN	110	ASP
72	SN	123	HIS
73	SO	33	ILE
73	SO	56	VAL
73	SO	57	THR
73	SO	76	LEU
73	SO	88	LEU
73	SO	90	ILE

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Mol	Chain	Res	Type
73	SO	113	GLN
73	SO	119	LEU
73	SO	133	THR
73	SO	135	ILE
74	SW	11	LEU
74	SW	15	ASN
74	SW	25	VAL
74	SW	34	ILE
74	SW	42	MET
74	SW	43	LYS
74	SW	57	ARG
74	SW	65	LEU
74	SW	74	VAL
74	SW	105	THR
74	SW	126	LEU
75	SY	27	VAL
75	SY	35	VAL
75	SY	81	TYR
76	SZ	47	LEU
76	SZ	58	LEU
76	SZ	110	THR
77	Sb	13	GLU
77	Sb	17	ARG
77	Sb	25	VAL
77	Sb	37	CYS
77	Sb	45	THR
77	Sb	51	GLN
77	Sb	52	THR
77	Sb	53	VAL
77	Sb	54	VAL
77	Sb	55	LEU
77	Sb	57	VAL
77	Sb	63	LEU
77	Sb	72	ARG
78	Se	6	LEU
78	Se	16	THR
78	Se	43	VAL
79	sh	98	VAL
79	sh	104	LYS
79	sh	130	VAL
79	sh	143	LYS
79	sh	148	TYR

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Mol	Chain	Res	Type
81	zx	20	ILE
84	3m	61	GLU
84	3m	63	VAL
84	3m	84	GLU
84	3m	185	MET
84	3m	192	TYR
84	3m	196	ASN
84	3m	280	LEU
85	3f	127	HIS
85	3f	129	VAL
85	3f	183	SER
85	3f	223	VAL
85	3f	232	PHE
85	3f	262	VAL
85	3f	281	ASP
85	3f	319	VAL
86	3a	58	CYS
86	3a	99	GLU
86	3a	243	MET
86	3a	359	LEU
86	3a	501	THR
86	3a	514	MET
86	3a	523	LEU
86	3a	524	THR
87	3e	143	ASN
87	3e	192	LEU
87	3e	390	HIS
87	3e	393	MET
88	3c	86	LEU
88	3c	110	LEU
88	3c	120	LEU
88	3c	671	VAL
88	3c	677	ILE
88	3c	695	ILE
88	3c	751	THR
88	3c	807	LEU
88	3c	857	LEU
89	3h	56	GLU
89	3h	71	VAL
89	3h	72	VAL
89	3h	75	ARG
89	3h	110	VAL

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Mol	Chain	Res	Type
89	3h	148	VAL
89	3h	263	TYR
91	3k	84	LEU
91	3k	119	GLN
91	3k	134	PHE
91	3k	192	GLN
92	3l	116	GLU
92	3l	307	ARG
92	3l	311	CYS
92	3l	365	GLU
92	3l	382	ILE
92	3l	506	ILE
92	3l	547	ILE
92	3l	563	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (121) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	95	GLN
5	LB	208	ASN
5	LB	315	ASN
5	LB	322	HIS
6	LC	41	HIS
6	LC	60	HIS
6	LC	142	HIS
7	LD	111	ASN
7	LD	175	HIS
7	LD	195	HIS
7	LD	229	ASN
9	LF	63	GLN
9	LF	131	ASN
9	LF	206	ASN
11	LH	116	ASN
11	LH	140	GLN
12	LI	144	ASN
12	LI	213	HIS
13	LJ	71	HIS
14	LL	115	GLN
15	LM	125	ASN
16	LN	57	GLN
16	LN	117	ASN
16	LN	149	GLN

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Mol	Chain	Res	Type
16	LN	196	ASN
18	LP	97	ASN
19	LQ	45	GLN
20	LR	158	GLN
21	LS	91	HIS
21	LS	92	ASN
22	LT	79	GLN
22	LT	90	ASN
22	LT	127	GLN
23	LU	38	ASN
24	LV	27	ASN
25	LW	63	GLN
26	LX	125	ASN
27	LY	91	ASN
32	Ld	79	ASN
35	Lg	73	HIS
36	Lh	108	GLN
37	Li	20	ASN
40	Ll	20	ASN
47	SA	110	ASN
47	SA	132	GLN
47	SA	193	HIS
49	SD	159	HIS
51	SF	36	GLN
51	SF	110	GLN
51	SF	186	ASN
51	SF	203	ASN
52	SH	163	GLN
53	SI	44	HIS
53	SI	146	GLN
53	SI	165	GLN
54	SK	44	HIS
55	SL	94	HIS
55	SL	154	GLN
56	SP	24	GLN
56	SP	104	GLN
57	SQ	142	GLN
60	ST	142	ASN
65	Sc	26	GLN
67	Sg	4	GLN
67	Sg	76	GLN
67	Sg	117	ASN

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Mol	Chain	Res	Type
67	Sg	196	ASN
67	Sg	215	GLN
67	Sg	285	GLN
67	Sg	296	GLN
67	Sg	311	GLN
68	SC	178	HIS
71	Sf	15	ASN
71	Sf	73	GLN
71	Sf	75	ASN
72	SN	5	HIS
72	SN	62	GLN
73	SO	43	HIS
73	SO	113	GLN
75	SY	29	HIS
75	SY	85	ASN
77	Sb	51	GLN
78	Se	37	GLN
81	zx	2	GLN
84	3m	14	GLN
84	3m	146	GLN
84	3m	259	ASN
85	3f	356	ASN
86	3a	73	GLN
86	3a	180	GLN
86	3a	288	ASN
86	3a	309	ASN
86	3a	352	GLN
86	3a	434	ASN
86	3a	441	GLN
86	3a	448	GLN
86	3a	518	GLN
87	3e	143	ASN
87	3e	283	GLN
87	3e	335	ASN
88	3c	149	ASN
88	3c	465	HIS
88	3c	519	HIS
88	3c	630	HIS
88	3c	676	HIS
89	3h	38	GLN
89	3h	287	GLN
91	3k	186	GLN

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Mol	Chain	Res	Type
92	3l	60	HIS
92	3l	92	GLN
92	3l	180	ASN
92	3l	223	ASN
92	3l	243	GLN
92	3l	363	GLN
92	3l	364	ASN
92	3l	432	HIS
92	3l	452	GLN
92	3l	489	GLN
92	3l	495	HIS
92	3l	514	GLN
92	3l	546	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3652/5070 (72%)	876 (23%)	19 (0%)
2	L7	119/120 (99%)	17 (14%)	0
3	L8	155/156 (99%)	31 (20%)	2 (1%)
46	S2	1714/1869 (91%)	496 (28%)	8 (0%)
80	zv	12/19 (63%)	8 (66%)	0
82	zy	74/75 (98%)	13 (17%)	0
83	zz	209/332 (62%)	76 (36%)	0
All	All	5935/7641 (77%)	1517 (25%)	29 (0%)

All (1517) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	23	C
1	L5	25	A
1	L5	30	C
1	L5	39	A
1	L5	42	A
1	L5	47	A
1	L5	48	G
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	66	A
1	L5	73	A

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Mol	Chain	Res	Type
1	L5	74	G
1	L5	76	A
1	L5	84	A
1	L5	91	G
1	L5	108	A
1	L5	109	G
1	L5	110	C
1	L5	117	C
1	L5	119	G
1	L5	120	A
1	L5	121	A
1	L5	122	U
1	L5	127	G
1	L5	128	C
1	L5	130	C
1	L5	131	C
1	L5	133	C
1	L5	134	G
1	L5	135	G
1	L5	136	C
1	L5	137	G
1	L5	140	G
1	L5	141	C
1	L5	144	G
1	L5	151	G
1	L5	159	C
1	L5	171	U
1	L5	172	C
1	L5	173	C
1	L5	179	G
1	L5	180	C
1	L5	183	C
1	L5	185	C
1	L5	186	G
1	L5	187	U
1	L5	188	G
1	L5	189	G
1	L5	200	U
1	L5	209	U
1	L5	217	C
1	L5	218	A
1	L5	219	G

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Mol	Chain	Res	Type
1	L5	225	G
1	L5	227	A
1	L5	232	G
1	L5	233	U
1	L5	234	G
1	L5	255	C
1	L5	256	G
1	L5	265	C
1	L5	266	C
1	L5	269	G
1	L5	274	C
1	L5	276	C
1	L5	277	G
1	L5	278	G
1	L5	280	G
1	L5	281	U
1	L5	295	A
1	L5	296	A
1	L5	297	U
1	L5	306	A
1	L5	315	G
1	L5	316	U
1	L5	340	C
1	L5	349	A
1	L5	363	A
1	L5	379	G
1	L5	383	A
1	L5	384	A
1	L5	387	G
1	L5	396	A
1	L5	399	G
1	L5	407	A
1	L5	409	G
1	L5	410	A
1	L5	412	G
1	L5	413	G
1	L5	415	G
1	L5	418	A
1	L5	422	C
1	L5	440	U
1	L5	449	C
1	L5	450	G

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Mol	Chain	Res	Type
1	L5	452	A
1	L5	453	G
1	L5	454	U
1	L5	456	C
1	L5	457	G
1	L5	464	G
1	L5	467	U
1	L5	479	G
1	L5	484	U
1	L5	485	C
1	L5	486	C
1	L5	489	C
1	L5	493	G
1	L5	494	U
1	L5	497	G
1	L5	498	C
1	L5	500	G
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	505	G
1	L5	506	C
1	L5	509	A
1	L5	510	U
1	L5	512	U
1	L5	513	U
1	L5	514	U
1	L5	517	C
1	L5	518	G
1	L5	643	C
1	L5	644	G
1	L5	646	G
1	L5	654	C
1	L5	656	C
1	L5	657	C
1	L5	659	G
1	L5	661	C
1	L5	665	C
1	L5	666	G
1	L5	667	A
1	L5	668	C
1	L5	673	C

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Mol	Chain	Res	Type
1	L5	685	C
1	L5	686	A
1	L5	687	U
1	L5	696	C
1	L5	703	G
1	L5	704	C
1	L5	708	G
1	L5	731	G
1	L5	738	C
1	L5	739	G
1	L5	742	G
1	L5	745	G
1	L5	753	C
1	L5	754	U
1	L5	758	G
1	L5	904	C
1	L5	905	C
1	L5	913	U
1	L5	914	U
1	L5	915	A
1	L5	916	C
1	L5	917	A
1	L5	918	G
1	L5	923	C
1	L5	924	C
1	L5	926	G
1	L5	932	A
1	L5	933	G
1	L5	934	C
1	L5	935	A
1	L5	936	C
1	L5	943	A
1	L5	944	A
1	L5	945	U
1	L5	946	C
1	L5	959	G
1	L5	960	A
1	L5	961	G
1	L5	962	C
1	L5	965	G
1	L5	966	A
1	L5	970	G

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Mol	Chain	Res	Type
1	L5	971	U
1	L5	977	C
1	L5	982	U
1	L5	984	C
1	L5	985	C
1	L5	986	C
1	L5	987	C
1	L5	988	C
1	L5	991	C
1	L5	992	C
1	L5	993	G
1	L5	995	C
1	L5	1049	C
1	L5	1051	G
1	L5	1065	G
1	L5	1066	G
1	L5	1067	G
1	L5	1068	G
1	L5	1069	G
1	L5	1070	G
1	L5	1071	C
1	L5	1075	G
1	L5	1082	C
1	L5	1083	U
1	L5	1095	A
1	L5	1097	C
1	L5	1168	G
1	L5	1169	G
1	L5	1170	G
1	L5	1171	G
1	L5	1173	G
1	L5	1179	U
1	L5	1180	C
1	L5	1181	C
1	L5	1182	C
1	L5	1183	C
1	L5	1187	G
1	L5	1200	G
1	L5	1201	U
1	L5	1202	C
1	L5	1203	G
1	L5	1204	C

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Mol	Chain	Res	Type
1	L5	1211	G
1	L5	1214	C
1	L5	1215	C
1	L5	1216	C
1	L5	1217	G
1	L5	1218	G
1	L5	1219	G
1	L5	1222	A
1	L5	1235	G
1	L5	1241	C
1	L5	1251	C
1	L5	1254	A
1	L5	1255	A
1	L5	1257	A
1	L5	1258	G
1	L5	1260	G
1	L5	1261	G
1	L5	1262	G
1	L5	1266	G
1	L5	1269	G
1	L5	1270	A
1	L5	1271	G
1	L5	1272	C
1	L5	1273	G
1	L5	1275	G
1	L5	1280	C
1	L5	1284	G
1	L5	1287	G
1	L5	1293	G
1	L5	1294	A
1	L5	1295	C
1	L5	1296	G
1	L5	1301	C
1	L5	1302	U
1	L5	1303	A
1	L5	1320	U
1	L5	1326	A
1	L5	1338	G
1	L5	1344	C
1	L5	1354	A
1	L5	1358	G
1	L5	1365	C

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Mol	Chain	Res	Type
1	L5	1367	C
1	L5	1370	G
1	L5	1379	C
1	L5	1381	U
1	L5	1387	A
1	L5	1394	G
1	L5	1399	G
1	L5	1407	C
1	L5	1408	G
1	L5	1409	C
1	L5	1410	U
1	L5	1415	G
1	L5	1416	G
1	L5	1420	A
1	L5	1435	G
1	L5	1437	C
1	L5	1439	C
1	L5	1441	C
1	L5	1442	C
1	L5	1443	A
1	L5	1444	G
1	L5	1465	G
1	L5	1482	G
1	L5	1483	C
1	L5	1497	A
1	L5	1498	G
1	L5	1502	G
1	L5	1513	U
1	L5	1518	A
1	L5	1523	A
1	L5	1525	A
1	L5	1534	A
1	L5	1547	A
1	L5	1564	A
1	L5	1566	C
1	L5	1577	G
1	L5	1578	U
1	L5	1591	U
1	L5	1596	U
1	L5	1597	G
1	L5	1613	A
1	L5	1624	G

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Mol	Chain	Res	Type
1	L5	1625	G
1	L5	1631	A
1	L5	1632	A
1	L5	1633	G
1	L5	1634	A
1	L5	1640	C
1	L5	1641	G
1	L5	1654	G
1	L5	1660	U
1	L5	1661	C
1	L5	1676	C
1	L5	1677	U
1	L5	1678	C
1	L5	1691	G
1	L5	1694	C
1	L5	1696	C
1	L5	1697	G
1	L5	1699	A
1	L5	1700	G
1	L5	1701	A
1	L5	1703	C
1	L5	1704	C
1	L5	1705	G
1	L5	1707	C
1	L5	1719	A
1	L5	1724	G
1	L5	1734	G
1	L5	1742	A
1	L5	1750	G
1	L5	1756	U
1	L5	1757	U
1	L5	1758	G
1	L5	1760	G
1	L5	1761	G
1	L5	1762	C
1	L5	1763	C
1	L5	1764	G
1	L5	1765	A
1	L5	1766	A
1	L5	1767	A
1	L5	1768	C
1	L5	1770	A

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Mol	Chain	Res	Type
1	L5	1775	A
1	L5	1781	U
1	L5	1787	A
1	L5	1803	G
1	L5	1804	A
1	L5	1806	G
1	L5	1810	G
1	L5	1821	G
1	L5	1822	U
1	L5	1833	G
1	L5	1836	G
1	L5	1837	A
1	L5	1842	G
1	L5	1855	G
1	L5	1869	G
1	L5	1882	U
1	L5	1897	A
1	L5	1918	U
1	L5	1919	G
1	L5	1920	C
1	L5	1921	C
1	L5	1922	G
1	L5	1925	G
1	L5	1931	C
1	L5	1932	A
1	L5	1936	C
1	L5	1940	G
1	L5	1948	G
1	L5	1961	G
1	L5	1974	U
1	L5	1975	G
1	L5	1980	U
1	L5	1981	G
1	L5	1982	G
1	L5	1984	A
1	L5	1985	G
1	L5	1987	C
1	L5	1998	A
1	L5	1999	A
1	L5	2001	G
1	L5	2002	A
1	L5	2003	G

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Mol	Chain	Res	Type
1	L5	2004	U
1	L5	2026	A
1	L5	2034	G
1	L5	2044	U
1	L5	2045	G
1	L5	2046	G
1	L5	2048	U
1	L5	2055	G
1	L5	2056	G
1	L5	2069	A
1	L5	2084	C
1	L5	2085	G
1	L5	2089	G
1	L5	2092	G
1	L5	2093	A
1	L5	2094	G
1	L5	2095	A
1	L5	2096	G
1	L5	2097	U
1	L5	2098	G
1	L5	2101	C
1	L5	2102	G
1	L5	2105	A
1	L5	2106	G
1	L5	2108	G
1	L5	2111	G
1	L5	2112	G
1	L5	2252	G
1	L5	2253	A
1	L5	2254	G
1	L5	2255	C
1	L5	2256	C
1	L5	2258	C
1	L5	2259	G
1	L5	2268	A
1	L5	2269	C
1	L5	2286	G
1	L5	2288	G
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2306	G

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Mol	Chain	Res	Type
1	L5	2313	A
1	L5	2322	G
1	L5	2327	G
1	L5	2328	G
1	L5	2331	G
1	L5	2333	G
1	L5	2351	C
1	L5	2360	A
1	L5	2370	A
1	L5	2382	A
1	L5	2395	A
1	L5	2398	U
1	L5	2402	G
1	L5	2409	U
1	L5	2410	C
1	L5	2417	A
1	L5	2421	G
1	L5	2426	U
1	L5	2441	C
1	L5	2442	G
1	L5	2465	C
1	L5	2469	C
1	L5	2471	G
1	L5	2474	G
1	L5	2475	G
1	L5	2483	G
1	L5	2484	A
1	L5	2485	U
1	L5	2487	G
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2493	G
1	L5	2495	U
1	L5	2496	G
1	L5	2498	C
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2507	A
1	L5	2513	A
1	L5	2514	G

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Mol	Chain	Res	Type
1	L5	2529	A
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2553	A
1	L5	2554	U
1	L5	2555	G
1	L5	2556	G
1	L5	2563	C
1	L5	2564	G
1	L5	2566	G
1	L5	2567	G
1	L5	2569	G
1	L5	2583	C
1	L5	2587	A
1	L5	2588	C
1	L5	2589	C
1	L5	2600	A
1	L5	2601	A
1	L5	2602	G
1	L5	2607	C
1	L5	2618	G
1	L5	2627	C
1	L5	2638	G
1	L5	2653	C
1	L5	2662	G
1	L5	2669	C
1	L5	2670	C
1	L5	2675	G
1	L5	2686	G
1	L5	2687	U
1	L5	2694	G
1	L5	2696	A
1	L5	2705	G
1	L5	2707	U
1	L5	2708	U
1	L5	2710	C
1	L5	2711	G
1	L5	2712	G
1	L5	2721	G
1	L5	2724	G
1	L5	2726	G

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Mol	Chain	Res	Type
1	L5	2739	C
1	L5	2743	A
1	L5	2744	A
1	L5	2754	G
1	L5	2761	U
1	L5	2762	G
1	L5	2763	U
1	L5	2767	U
1	L5	2768	C
1	L5	2769	U
1	L5	2770	C
1	L5	2772	C
1	L5	2776	G
1	L5	2787	A
1	L5	2788	U
1	L5	2791	C
1	L5	2793	G
1	L5	2794	C
1	L5	2795	A
1	L5	2796	G
1	L5	2798	A
1	L5	2802	C
1	L5	2814	C
1	L5	2826	U
1	L5	2827	G
1	L5	2828	U
1	L5	2829	U
1	L5	2835	A
1	L5	2842	G
1	L5	2855	G
1	L5	2856	C
1	L5	2860	C
1	L5	2870	A
1	L5	2875	C
1	L5	2877	G
1	L5	2879	A
1	L5	2892	C
1	L5	2902	G
1	L5	2903	G
1	L5	2904	U
1	L5	2905	C
1	L5	3586	G

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Mol	Chain	Res	Type
1	L5	3589	G
1	L5	3590	G
1	L5	3592	G
1	L5	3593	C
1	L5	3595	U
1	L5	3596	A
1	L5	3597	G
1	L5	3605	C
1	L5	3615	G
1	L5	3616	U
1	L5	3617	G
1	L5	3620	G
1	L5	3626	G
1	L5	3635	A
1	L5	3646	A
1	L5	3662	A
1	L5	3664	G
1	L5	3670	C
1	L5	3671	G
1	L5	3673	C
1	L5	3678	G
1	L5	3696	C
1	L5	3709	U
1	L5	3711	A
1	L5	3712	A
1	L5	3713	U
1	L5	3727	A
1	L5	3728	A
1	L5	3750	G
1	L5	3753	G
1	L5	3757	G
1	L5	3760	A
1	L5	3761	C
1	L5	3762	U
1	L5	3763	A
1	L5	3766	A
1	L5	3767	C
1	L5	3768	U
1	L5	3773	U
1	L5	3774	A
1	L5	3776	G
1	L5	3777	G

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Mol	Chain	Res	Type
1	L5	3778	U
1	L5	3784	A
1	L5	3785	A
1	L5	3786	U
1	L5	3787	G
1	L5	3788	C
1	L5	3789	C
1	L5	3811	G
1	L5	3814	U
1	L5	3817	A
1	L5	3818	U
1	L5	3819	G
1	L5	3838	U
1	L5	3839	G
1	L5	3851	U
1	L5	3867	A
1	L5	3869	C
1	L5	3877	A
1	L5	3878	C
1	L5	3879	G
1	L5	3885	G
1	L5	3889	G
1	L5	3890	A
1	L5	3892	U
1	L5	3895	G
1	L5	3897	G
1	L5	3901	A
1	L5	3906	A
1	L5	3907	G
1	L5	3908	A
1	L5	3909	C
1	L5	3915	U
1	L5	3916	G
1	L5	3937	C
1	L5	3938	G
1	L5	3939	G
1	L5	3947	A
1	L5	3948	C
1	L5	3951	G
1	L5	3952	A
1	L5	4061	G
1	L5	4062	A

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Mol	Chain	Res	Type
1	L5	4063	U
1	L5	4064	C
1	L5	4065	G
1	L5	4068	U
1	L5	4076	G
1	L5	4084	G
1	L5	4085	A
1	L5	4086	G
1	L5	4088	C
1	L5	4097	G
1	L5	4100	C
1	L5	4103	C
1	L5	4104	G
1	L5	4105	A
1	L5	4108	G
1	L5	4110	C
1	L5	4115	G
1	L5	4119	C
1	L5	4120	U
1	L5	4121	G
1	L5	4127	A
1	L5	4128	A
1	L5	4135	G
1	L5	4140	C
1	L5	4141	G
1	L5	4142	C
1	L5	4143	G
1	L5	4144	C
1	L5	4145	C
1	L5	4151	G
1	L5	4160	C
1	L5	4162	C
1	L5	4163	U
1	L5	4168	G
1	L5	4170	A
1	L5	4173	G
1	L5	4183	G
1	L5	4184	G
1	L5	4191	G
1	L5	4201	G
1	L5	4203	A
1	L5	4204	C

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Mol	Chain	Res	Type
1	L5	4212	A
1	L5	4213	A
1	L5	4214	A
1	L5	4228	G
1	L5	4229	U
1	L5	4233	A
1	L5	4234	A
1	L5	4243	C
1	L5	4249	G
1	L5	4250	G
1	L5	4251	A
1	L5	4252	C
1	L5	4253	A
1	L5	4254	G
1	L5	4256	A
1	L5	4258	C
1	L5	4262	C
1	L5	4273	A
1	L5	4280	A
1	L5	4281	A
1	L5	4282	A
1	L5	4287	G
1	L5	4288	C
1	L5	4291	G
1	L5	4305	G
1	L5	4306	U
1	L5	4313	A
1	L5	4314	C
1	L5	4317	A
1	L5	4326	G
1	L5	4329	G
1	L5	4330	G
1	L5	4338	G
1	L5	4339	A
1	L5	4343	U
1	L5	4349	C
1	L5	4350	C
1	L5	4354	U
1	L5	4377	G
1	L5	4378	A
1	L5	4380	A
1	L5	4381	A

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Mol	Chain	Res	Type
1	L5	4387	C
1	L5	4393	G
1	L5	4394	A
1	L5	4396	A
1	L5	4398	C
1	L5	4420	U
1	L5	4421	C
1	L5	4422	A
1	L5	4430	G
1	L5	4433	G
1	L5	4444	C
1	L5	4448	G
1	L5	4449	A
1	L5	4450	U
1	L5	4452	U
1	L5	4453	C
1	L5	4459	U
1	L5	4460	U
1	L5	4464	A
1	L5	4466	C
1	L5	4471	U
1	L5	4476	C
1	L5	4477	A
1	L5	4479	A
1	L5	4500	U
1	L5	4501	U
1	L5	4512	U
1	L5	4513	A
1	L5	4518	A
1	L5	4524	G
1	L5	4528	G
1	L5	4531	U
1	L5	4532	U
1	L5	4548	A
1	L5	4555	U
1	L5	4556	U
1	L5	4560	C
1	L5	4565	C
1	L5	4567	G
1	L5	4569	U
1	L5	4570	G
1	L5	4573	G

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Mol	Chain	Res	Type
1	L5	4575	G
1	L5	4581	G
1	L5	4589	A
1	L5	4590	A
1	L5	4599	A
1	L5	4601	U
1	L5	4617	G
1	L5	4636	U
1	L5	4637	G
1	L5	4639	G
1	L5	4648	A
1	L5	4652	G
1	L5	4658	G
1	L5	4670	C
1	L5	4672	A
1	L5	4694	G
1	L5	4695	C
1	L5	4700	A
1	L5	4707	A
1	L5	4708	A
1	L5	4709	U
1	L5	4719	G
1	L5	4722	G
1	L5	4730	C
1	L5	4731	G
1	L5	4732	G
1	L5	4740	G
1	L5	4743	G
1	L5	4744	A
1	L5	4750	G
1	L5	4751	G
1	L5	4753	U
1	L5	4756	C
1	L5	4757	C
1	L5	4758	U
1	L5	4762	A
1	L5	4764	A
1	L5	4770	U
1	L5	4771	C
1	L5	4772	C
1	L5	4773	C
1	L5	4774	C

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Mol	Chain	Res	Type
1	L5	4775	C
1	L5	4776	G
1	L5	4860	G
1	L5	4861	G
1	L5	4862	G
1	L5	4863	G
1	L5	4869	U
1	L5	4871	C
1	L5	4872	G
1	L5	4873	G
1	L5	4874	A
1	L5	4875	G
1	L5	4876	U
1	L5	4877	G
1	L5	4878	C
1	L5	4882	U
1	L5	4883	C
1	L5	4884	G
1	L5	4887	C
1	L5	4888	U
1	L5	4890	G
1	L5	4894	A
1	L5	4895	C
1	L5	4897	G
1	L5	4900	C
1	L5	4901	G
1	L5	4910	G
1	L5	4912	G
1	L5	4914	C
1	L5	4925	U
1	L5	4926	C
1	L5	4928	C
1	L5	4929	C
1	L5	4937	C
1	L5	4940	C
1	L5	4941	G
1	L5	4943	A
1	L5	4944	C
1	L5	4947	U
1	L5	4951	G
1	L5	4960	G
1	L5	4963	G

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Mol	Chain	Res	Type
1	L5	4966	A
1	L5	4975	G
1	L5	4976	U
1	L5	4985	U
1	L5	4988	U
1	L5	4989	U
1	L5	4990	C
1	L5	4991	U
1	L5	5006	U
1	L5	5014	A
1	L5	5017	G
1	L5	5022	U
1	L5	5023	C
1	L5	5024	C
1	L5	5030	U
1	L5	5031	G
1	L5	5034	A
1	L5	5041	G
1	L5	5047	C
1	L5	5050	C
1	L5	5054	C
1	L5	5055	G
1	L5	5061	A
1	L5	5069	U
2	L7	7	G
2	L7	22	A
2	L7	23	A
2	L7	27	G
2	L7	31	G
2	L7	33	U
2	L7	39	C
2	L7	40	U
2	L7	49	A
2	L7	53	U
2	L7	54	A
2	L7	63	C
2	L7	64	G
2	L7	97	G
2	L7	100	A
2	L7	102	U
2	L7	120	U
3	L8	16	G

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Mol	Chain	Res	Type
3	L8	23	C
3	L8	25	G
3	L8	34	U
3	L8	35	C
3	L8	39	G
3	L8	52	A
3	L8	59	A
3	L8	63	U
3	L8	71	A
3	L8	80	A
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	87	G
3	L8	88	A
3	L8	94	G
3	L8	95	A
3	L8	103	A
3	L8	104	A
3	L8	105	C
3	L8	108	A
3	L8	110	U
3	L8	114	G
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	127	U
3	L8	147	G
3	L8	150	C
3	L8	151	G
46	S2	25	A
46	S2	33	G
46	S2	37	C
46	S2	42	A
46	S2	44	U
46	S2	45	A
46	S2	46	A
46	S2	56	G
46	S2	61	A
46	S2	62	G
46	S2	65	C
46	S2	66	G

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Mol	Chain	Res	Type
46	S2	67	C
46	S2	68	A
46	S2	72	C
46	S2	73	C
46	S2	75	G
46	S2	76	U
46	S2	78	C
46	S2	79	A
46	S2	80	G
46	S2	99	A
46	S2	103	A
46	S2	113	G
46	S2	114	G
46	S2	115	U
46	S2	124	U
46	S2	125	C
46	S2	126	G
46	S2	127	C
46	S2	140	U
46	S2	141	A
46	S2	143	U
46	S2	148	U
46	S2	154	U
46	S2	160	U
46	S2	161	U
46	S2	162	C
46	S2	168	C
46	S2	175	A
46	S2	180	G
46	S2	183	G
46	S2	184	G
46	S2	198	U
46	S2	199	C
46	S2	201	C
46	S2	202	G
46	S2	211	G
46	S2	214	U
46	S2	215	G
46	S2	286	U
46	S2	287	U
46	S2	291	G
46	S2	292	A

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Mol	Chain	Res	Type
46	S2	293	C
46	S2	302	A
46	S2	304	C
46	S2	305	U
46	S2	306	C
46	S2	307	G
46	S2	309	G
46	S2	312	G
46	S2	313	A
46	S2	314	U
46	S2	323	C
46	S2	324	C
46	S2	326	C
46	S2	327	G
46	S2	331	C
46	S2	332	G
46	S2	338	G
46	S2	339	A
46	S2	340	C
46	S2	347	G
46	S2	356	C
46	S2	362	C
46	S2	364	A
46	S2	368	U
46	S2	369	C
46	S2	370	G
46	S2	380	G
46	S2	381	C
46	S2	383	G
46	S2	385	G
46	S2	386	C
46	S2	399	C
46	S2	400	C
46	S2	407	G
46	S2	408	A
46	S2	409	C
46	S2	417	C
46	S2	418	A
46	S2	419	G
46	S2	438	G
46	S2	447	A
46	S2	448	A

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Mol	Chain	Res	Type
46	S2	449	A
46	S2	450	C
46	S2	452	G
46	S2	463	C
46	S2	464	A
46	S2	465	A
46	S2	466	G
46	S2	467	G
46	S2	471	G
46	S2	472	C
46	S2	473	A
46	S2	482	G
46	S2	485	A
46	S2	487	U
46	S2	488	U
46	S2	489	A
46	S2	492	C
46	S2	493	A
46	S2	502	C
46	S2	503	C
46	S2	504	G
46	S2	507	G
46	S2	517	C
46	S2	530	U
46	S2	531	A
46	S2	532	C
46	S2	534	G
46	S2	536	A
46	S2	537	C
46	S2	538	U
46	S2	539	C
46	S2	540	U
46	S2	541	U
46	S2	542	U
46	S2	543	C
46	S2	544	G
46	S2	545	A
46	S2	546	G
46	S2	549	C
46	S2	551	U
46	S2	553	U
46	S2	556	U

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Mol	Chain	Res	Type
46	S2	557	U
46	S2	559	G
46	S2	562	U
46	S2	563	G
46	S2	575	A
46	S2	576	A
46	S2	582	U
46	S2	583	A
46	S2	587	A
46	S2	589	G
46	S2	591	U
46	S2	592	C
46	S2	593	C
46	S2	595	U
46	S2	596	U
46	S2	604	A
46	S2	605	A
46	S2	606	G
46	S2	608	C
46	S2	614	C
46	S2	617	G
46	S2	627	U
46	S2	629	A
46	S2	638	C
46	S2	643	A
46	S2	644	G
46	S2	649	U
46	S2	655	A
46	S2	656	G
46	S2	660	C
46	S2	663	C
46	S2	668	A
46	S2	669	A
46	S2	670	A
46	S2	671	A
46	S2	672	A
46	S2	673	G
46	S2	683	G
46	S2	684	G
46	S2	688	U
46	S2	689	U
46	S2	690	G

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Mol	Chain	Res	Type
46	S2	692	G
46	S2	694	G
46	S2	695	C
46	S2	696	G
46	S2	697	G
46	S2	698	G
46	S2	732	U
46	S2	733	C
46	S2	734	C
46	S2	735	C
46	S2	738	C
46	S2	739	C
46	S2	747	U
46	S2	748	C
46	S2	749	U
46	S2	751	G
46	S2	752	G
46	S2	753	C
46	S2	789	G
46	S2	790	C
46	S2	791	C
46	S2	794	A
46	S2	795	A
46	S2	796	G
46	S2	797	C
46	S2	798	G
46	S2	799	U
46	S2	810	A
46	S2	811	A
46	S2	812	A
46	S2	813	A
46	S2	818	A
46	S2	821	G
46	S2	830	A
46	S2	834	C
46	S2	835	C
46	S2	836	G
46	S2	837	A
46	S2	838	G
46	S2	839	C
46	S2	840	C
46	S2	841	G

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Mol	Chain	Res	Type
46	S2	842	C
46	S2	847	A
46	S2	865	A
46	S2	869	A
46	S2	870	A
46	S2	872	A
46	S2	873	G
46	S2	874	G
46	S2	877	C
46	S2	879	C
46	S2	883	U
46	S2	885	U
46	S2	888	U
46	S2	889	U
46	S2	890	U
46	S2	891	G
46	S2	893	U
46	S2	894	G
46	S2	895	G
46	S2	896	U
46	S2	897	U
46	S2	898	U
46	S2	899	U
46	S2	900	C
46	S2	901	G
46	S2	902	G
46	S2	913	A
46	S2	914	U
46	S2	920	A
46	S2	933	G
46	S2	934	G
46	S2	958	G
46	S2	970	G
46	S2	971	G
46	S2	990	A
46	S2	992	A
46	S2	999	G
46	S2	1001	A
46	S2	1002	U
46	S2	1023	A
46	S2	1027	A
46	S2	1042	A

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Mol	Chain	Res	Type
46	S2	1045	U
46	S2	1060	A
46	S2	1061	U
46	S2	1062	A
46	S2	1078	C
46	S2	1083	A
46	S2	1085	C
46	S2	1086	G
46	S2	1109	C
46	S2	1110	G
46	S2	1114	U
46	S2	1116	C
46	S2	1119	A
46	S2	1121	G
46	S2	1126	G
46	S2	1133	A
46	S2	1149	A
46	S2	1150	A
46	S2	1153	C
46	S2	1154	U
46	S2	1155	U
46	S2	1157	G
46	S2	1168	G
46	S2	1170	A
46	S2	1181	A
46	S2	1183	A
46	S2	1195	A
46	S2	1207	G
46	S2	1208	A
46	S2	1212	G
46	S2	1215	C
46	S2	1216	C
46	S2	1217	A
46	S2	1221	G
46	S2	1224	G
46	S2	1242	U
46	S2	1243	U
46	S2	1251	A
46	S2	1253	A
46	S2	1256	G
46	S2	1257	G
46	S2	1265	A

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Mol	Chain	Res	Type
46	S2	1269	G
46	S2	1270	G
46	S2	1272	C
46	S2	1273	C
46	S2	1274	G
46	S2	1275	G
46	S2	1281	G
46	S2	1282	A
46	S2	1283	C
46	S2	1284	A
46	S2	1285	G
46	S2	1286	G
46	S2	1288	U
46	S2	1289	U
46	S2	1291	A
46	S2	1292	C
46	S2	1294	G
46	S2	1295	A
46	S2	1296	U
46	S2	1297	U
46	S2	1298	G
46	S2	1299	A
46	S2	1302	G
46	S2	1303	C
46	S2	1306	U
46	S2	1307	U
46	S2	1308	U
46	S2	1310	U
46	S2	1311	C
46	S2	1312	G
46	S2	1314	U
46	S2	1315	U
46	S2	1316	C
46	S2	1317	C
46	S2	1318	G
46	S2	1326	U
46	S2	1327	G
46	S2	1330	G
46	S2	1331	C
46	S2	1332	A
46	S2	1333	U
46	S2	1342	U

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Mol	Chain	Res	Type
46	S2	1358	U
46	S2	1371	U
46	S2	1372	U
46	S2	1373	C
46	S2	1378	A
46	S2	1393	G
46	S2	1396	A
46	S2	1397	U
46	S2	1402	A
46	S2	1404	U
46	S2	1418	C
46	S2	1419	C
46	S2	1421	A
46	S2	1422	G
46	S2	1423	C
46	S2	1424	G
46	S2	1428	G
46	S2	1431	G
46	S2	1433	C
46	S2	1435	C
46	S2	1436	C
46	S2	1437	C
46	S2	1438	A
46	S2	1439	A
46	S2	1442	U
46	S2	1449	G
46	S2	1450	G
46	S2	1454	A
46	S2	1462	U
46	S2	1463	U
46	S2	1475	G
46	S2	1476	A
46	S2	1477	U
46	S2	1482	C
46	S2	1487	A
46	S2	1488	C
46	S2	1489	A
46	S2	1490	G
46	S2	1495	G
46	S2	1497	G
46	S2	1498	A
46	S2	1505	U

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Mol	Chain	Res	Type
46	S2	1508	A
46	S2	1509	U
46	S2	1510	G
46	S2	1511	U
46	S2	1512	C
46	S2	1514	G
46	S2	1517	G
46	S2	1520	G
46	S2	1521	C
46	S2	1522	A
46	S2	1524	G
46	S2	1527	C
46	S2	1528	G
46	S2	1531	A
46	S2	1533	A
46	S2	1534	C
46	S2	1535	U
46	S2	1539	U
46	S2	1540	G
46	S2	1543	U
46	S2	1544	C
46	S2	1548	G
46	S2	1552	G
46	S2	1553	C
46	S2	1555	U
46	S2	1560	U
46	S2	1567	G
46	S2	1568	C
46	S2	1570	G
46	S2	1573	G
46	S2	1575	G
46	S2	1578	U
46	S2	1579	A
46	S2	1580	A
46	S2	1582	C
46	S2	1585	U
46	S2	1586	U
46	S2	1587	G
46	S2	1588	A
46	S2	1589	A
46	S2	1594	A
46	S2	1598	G

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Mol	Chain	Res	Type
46	S2	1599	U
46	S2	1601	A
46	S2	1602	U
46	S2	1621	U
46	S2	1623	A
46	S2	1624	U
46	S2	1632	G
46	S2	1634	A
46	S2	1639	G
46	S2	1640	A
46	S2	1643	U
46	S2	1644	C
46	S2	1646	C
46	S2	1648	G
46	S2	1654	G
46	S2	1661	A
46	S2	1663	A
46	S2	1664	A
46	S2	1665	G
46	S2	1672	U
46	S2	1683	C
46	S2	1695	A
46	S2	1698	C
46	S2	1699	A
46	S2	1719	A
46	S2	1721	U
46	S2	1722	G
46	S2	1743	G
46	S2	1744	G
46	S2	1745	A
46	S2	1746	U
46	S2	1748	G
46	S2	1752	C
46	S2	1754	G
46	S2	1755	C
46	S2	1756	C
46	S2	1757	G
46	S2	1772	C
46	S2	1773	C
46	S2	1774	C
46	S2	1775	U
46	S2	1778	C

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Mol	Chain	Res	Type
46	S2	1781	A
46	S2	1782	G
46	S2	1783	C
46	S2	1784	G
46	S2	1813	A
46	S2	1814	G
46	S2	1819	A
46	S2	1823	A
46	S2	1825	A
46	S2	1829	G
46	S2	1835	A
46	S2	1838	U
46	S2	1839	U
46	S2	1849	G
46	S2	1850	A
46	S2	1852	C
46	S2	1855	G
46	S2	1861	G
46	S2	1862	G
46	S2	1863	A
46	S2	1865	C
46	S2	1869	A
80	zv	-2	C
80	zv	1	C
80	zv	4	U
80	zv	5	A
80	zv	6	A
80	zv	7	C
80	zv	8	U
80	zv	9	C
82	zy	9	G
82	zy	13	U
82	zy	16	G
82	zy	17	G
82	zy	18	G
82	zy	19	U
82	zy	36	G
82	zy	47	C
82	zy	48	C
82	zy	57	A
82	zy	73	C
82	zy	74	C

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Mol	Chain	Res	Type
82	zy	75	A
83	zz	134	A
83	zz	135	G
83	zz	136	A
83	zz	137	G
83	zz	141	U
83	zz	143	G
83	zz	150	G
83	zz	154	A
83	zz	156	C
83	zz	157	C
83	zz	161	G
83	zz	162	A
83	zz	163	G
83	zz	164	U
83	zz	165	A
83	zz	166	C
83	zz	167	A
83	zz	169	C
83	zz	175	U
83	zz	176	G
83	zz	177	C
83	zz	185	A
83	zz	186	C
83	zz	188	G
83	zz	189	G
83	zz	190	G
83	zz	191	U
83	zz	196	U
83	zz	197	C
83	zz	198	U
83	zz	202	A
83	zz	204	C
83	zz	206	A
83	zz	207	C
83	zz	208	C
83	zz	209	C
83	zz	210	G
83	zz	211	C
83	zz	213	C
83	zz	216	U
83	zz	217	G

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Mol	Chain	Res	Type
83	zz	223	A
83	zz	224	G
83	zz	225	A
83	zz	229	G
83	zz	233	G
83	zz	234	U
83	zz	237	C
83	zz	245	G
83	zz	253	G
83	zz	257	A
83	zz	258	G
83	zz	259	U
83	zz	260	A
83	zz	265	U
83	zz	266	G
83	zz	268	G
83	zz	270	C
83	zz	271	G
83	zz	280	C
83	zz	281	U
83	zz	282	U
83	zz	284	U
83	zz	288	A
83	zz	291	G
83	zz	292	C
83	zz	295	G
83	zz	296	A
83	zz	297	U
83	zz	301	G
83	zz	304	C
83	zz	306	U
83	zz	323	G
83	zz	324	U
83	zz	325	C
83	zz	328	G

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	406	C
1	L5	417	G
1	L5	914	U

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Mol	Chain	Res	Type
1	L5	1082	C
1	L5	2002	A
1	L5	2033	A
1	L5	2695	A
1	L5	2760	G
1	L5	2775	C
1	L5	3585	G
1	L5	3614	G
1	L5	3767	C
1	L5	3888	G
1	L5	3908	A
1	L5	4452	U
1	L5	4600	G
1	L5	4699	U
1	L5	4731	G
1	L5	4913	G
3	L8	86	U
3	L8	87	G
46	S2	213	G
46	S2	339	A
46	S2	465	A
46	S2	604	A
46	S2	688	U
46	S2	1434	C
46	S2	1849	G
46	S2	1860	A

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 88 ligands modelled in this entry, 88 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

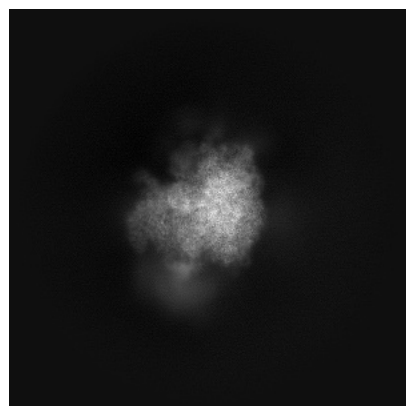
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62671. These allow visual inspection of the internal detail of the map and identification of artifacts.

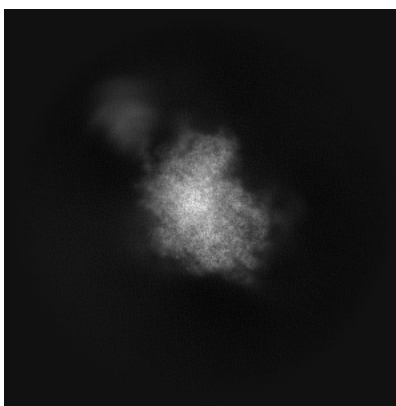
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

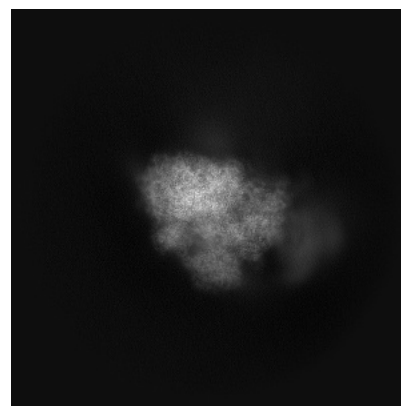
6.1.1 Primary map



X

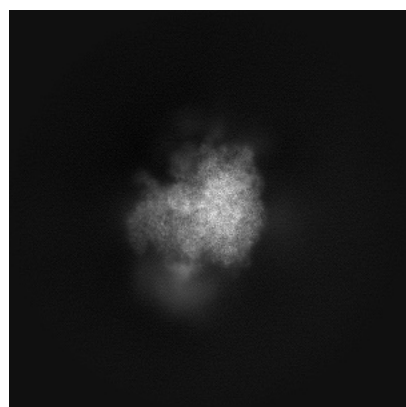


Y

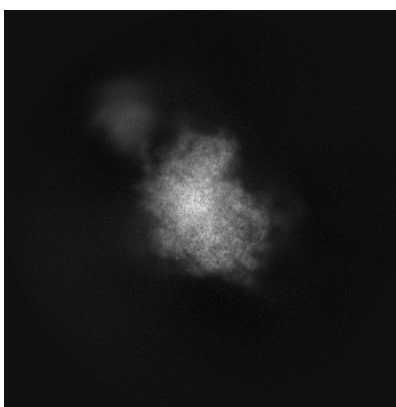


Z

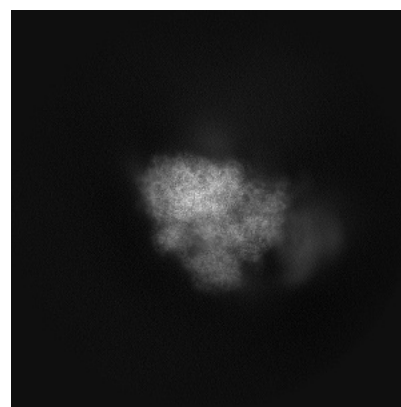
6.1.2 Raw map



X



Y

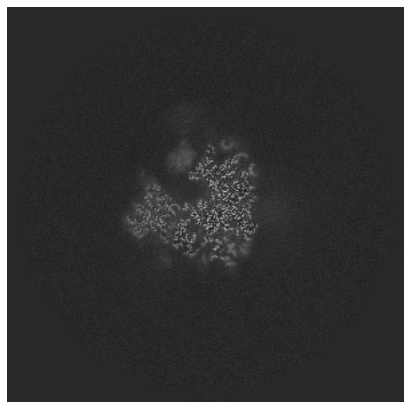


Z

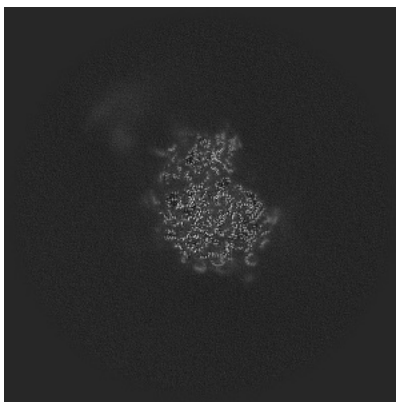
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

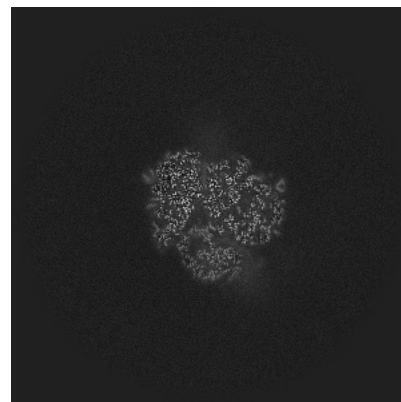
6.2.1 Primary map



X Index: 250

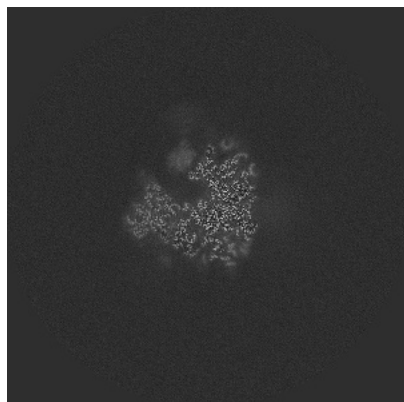


Y Index: 250

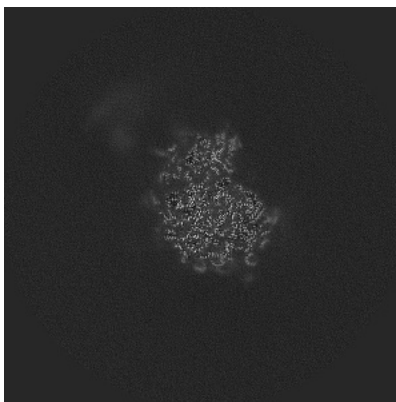


Z Index: 250

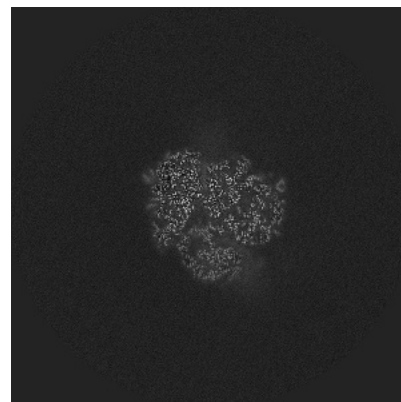
6.2.2 Raw map



X Index: 250



Y Index: 250

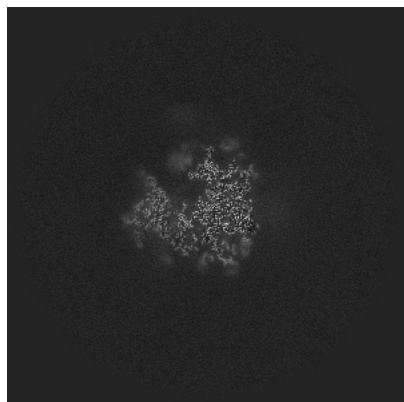


Z Index: 250

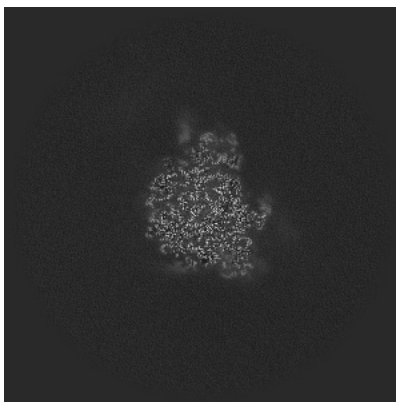
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

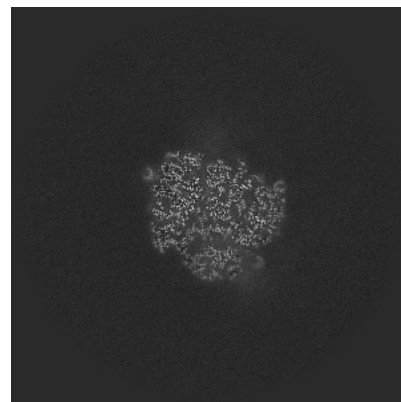
6.3.1 Primary map



X Index: 253

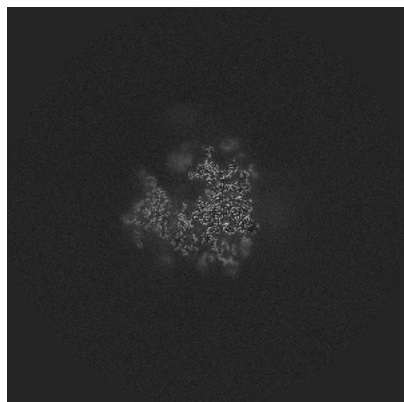


Y Index: 271

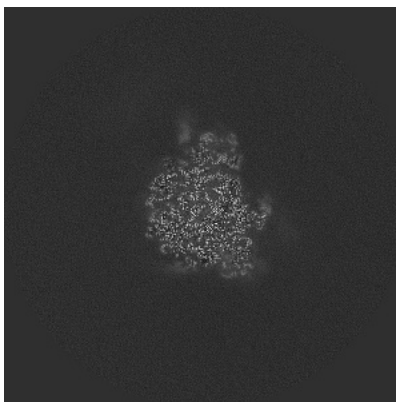


Z Index: 253

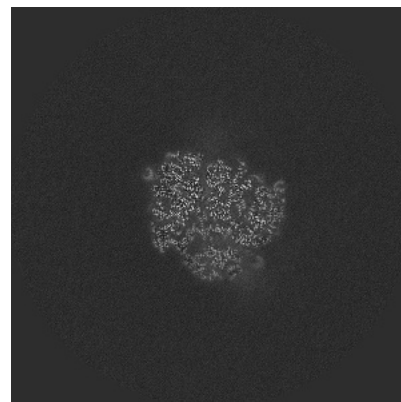
6.3.2 Raw map



X Index: 253



Y Index: 271

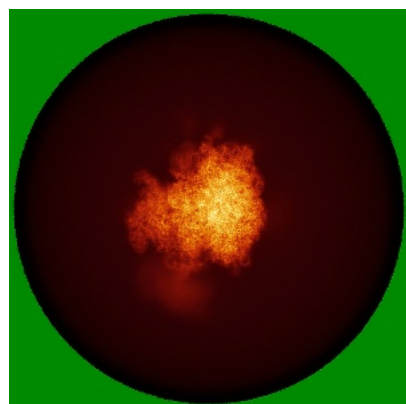


Z Index: 253

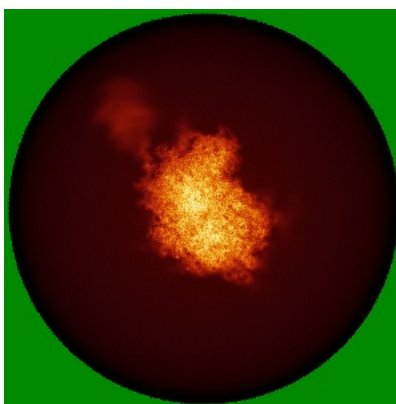
The images above show the largest variance slices of the map in three orthogonal directions.

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

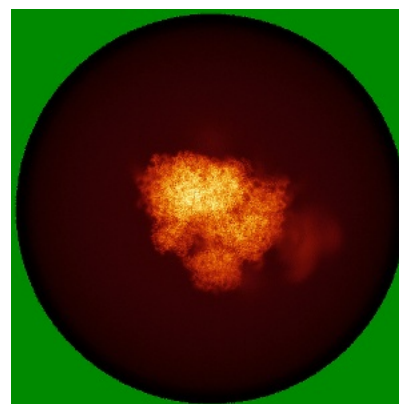
6.4.1 Primary map



X

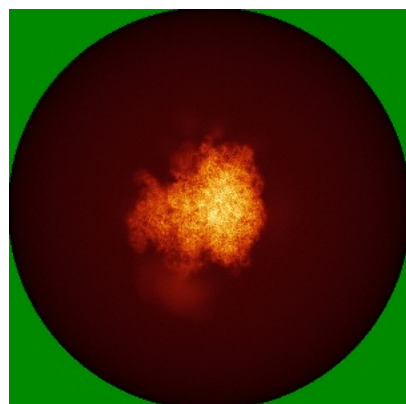


Y

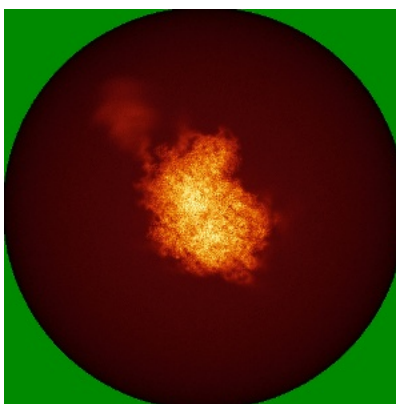


Z

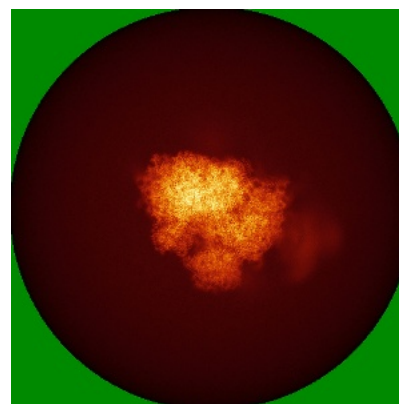
6.4.2 Raw map



X



Y

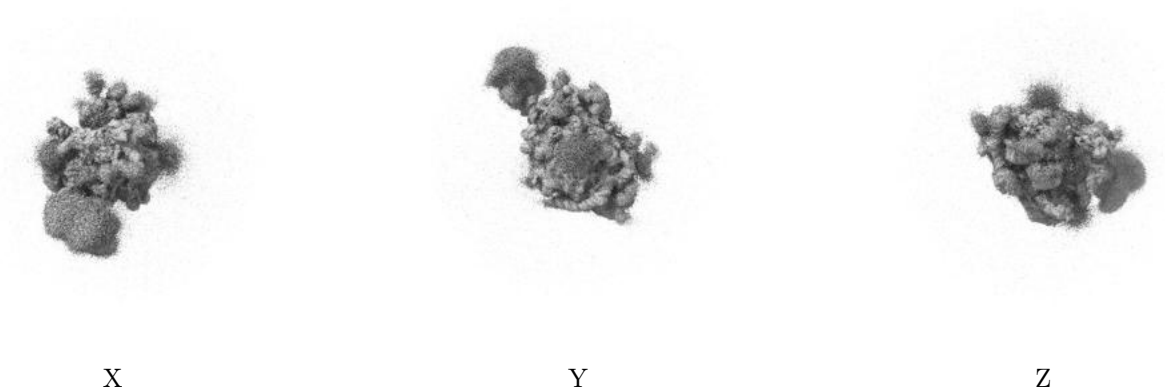


Z

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

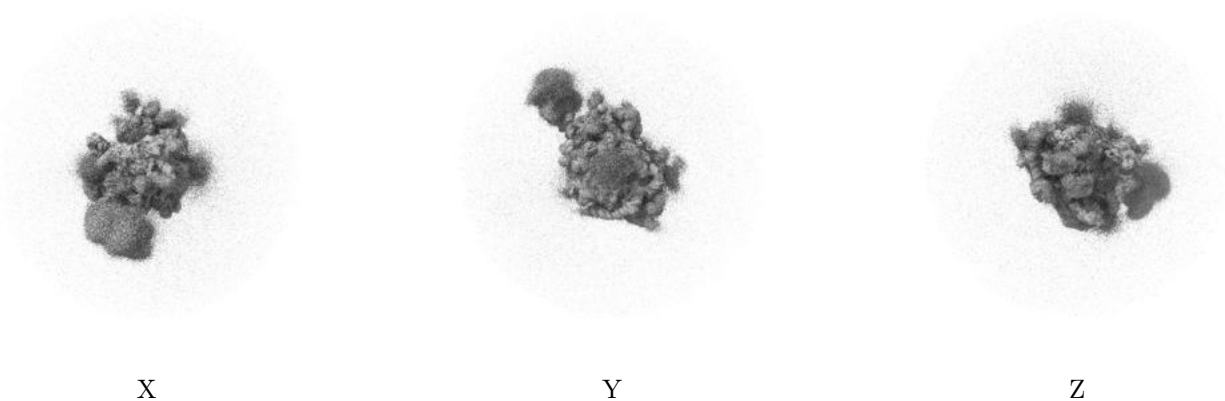
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

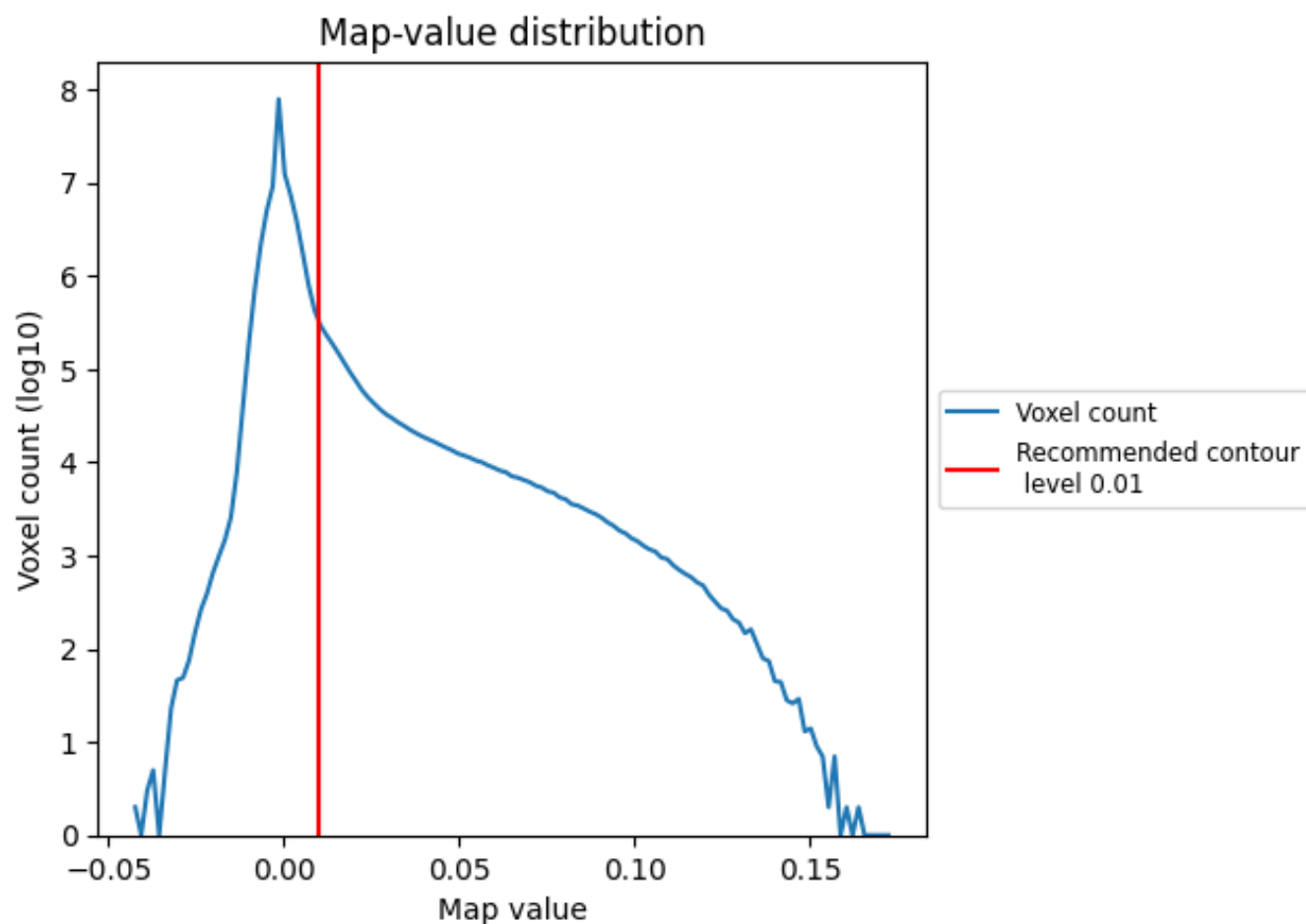
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

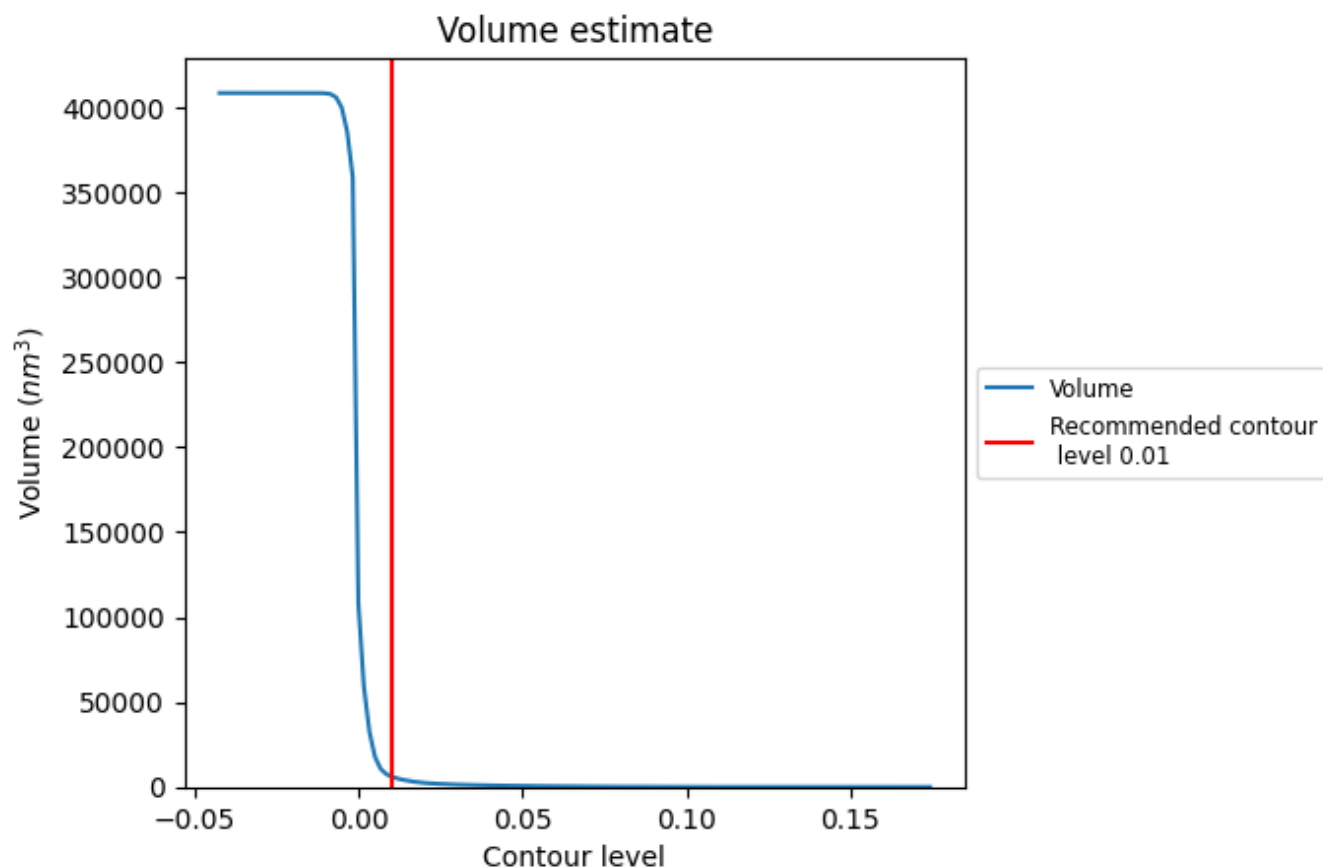
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

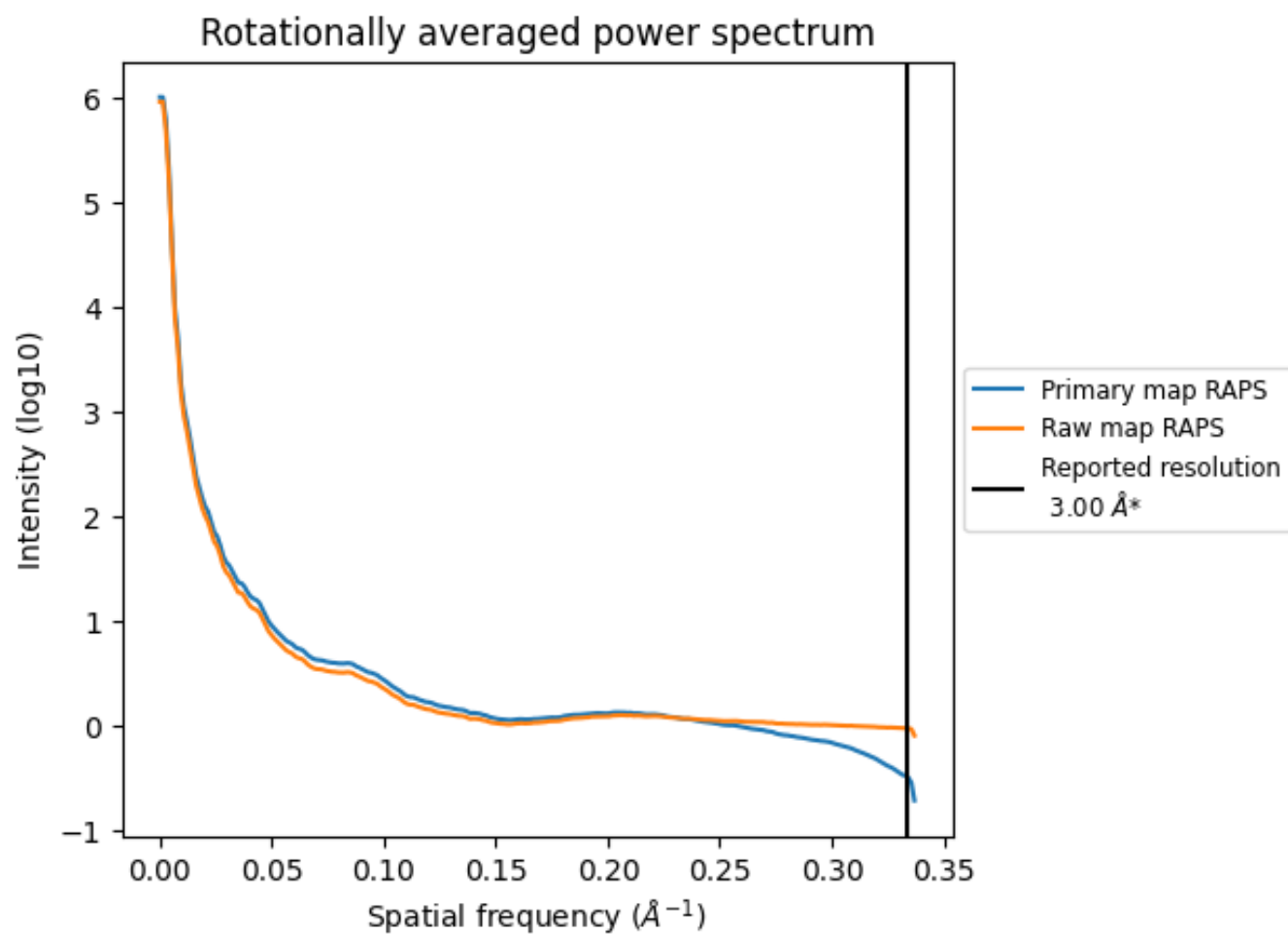
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6223 nm^3 ; this corresponds to an approximate mass of 5622 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

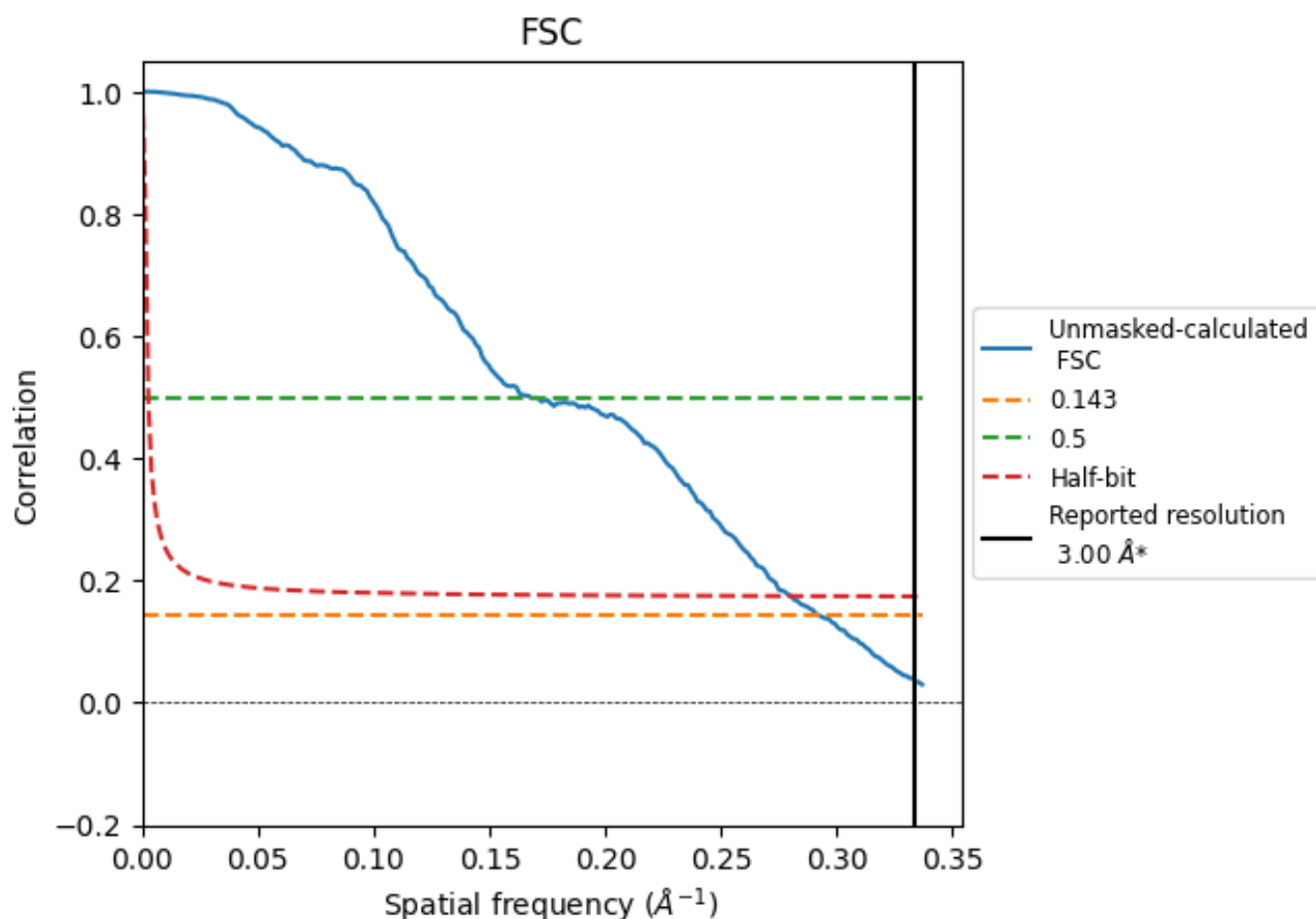


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

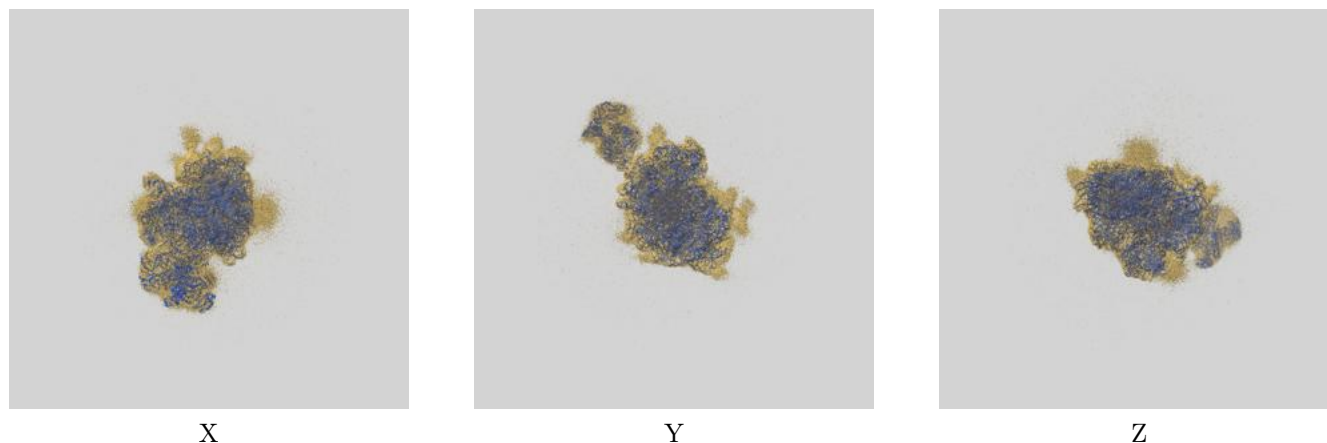
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.42	5.96	3.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.42 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

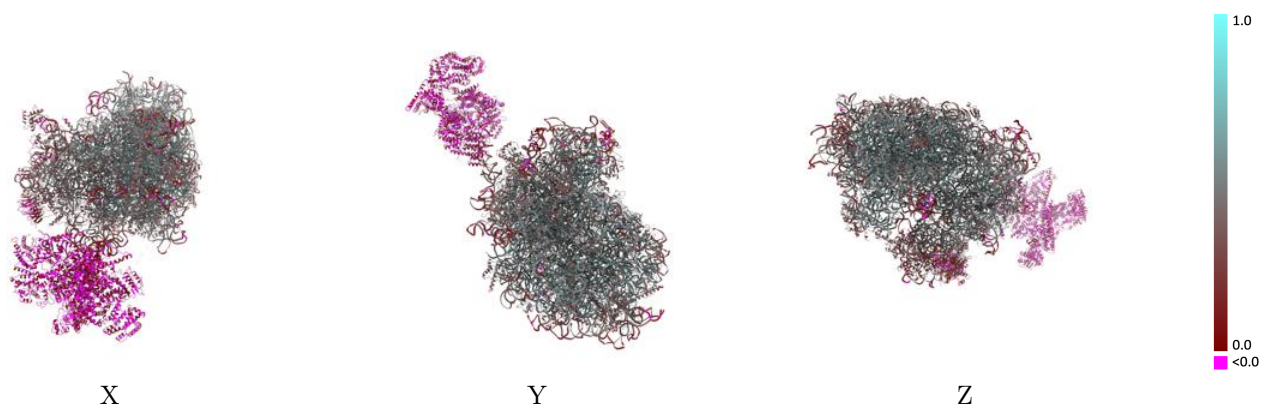
This section contains information regarding the fit between EMDB map EMD-62671 and PDB model 9KZU. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



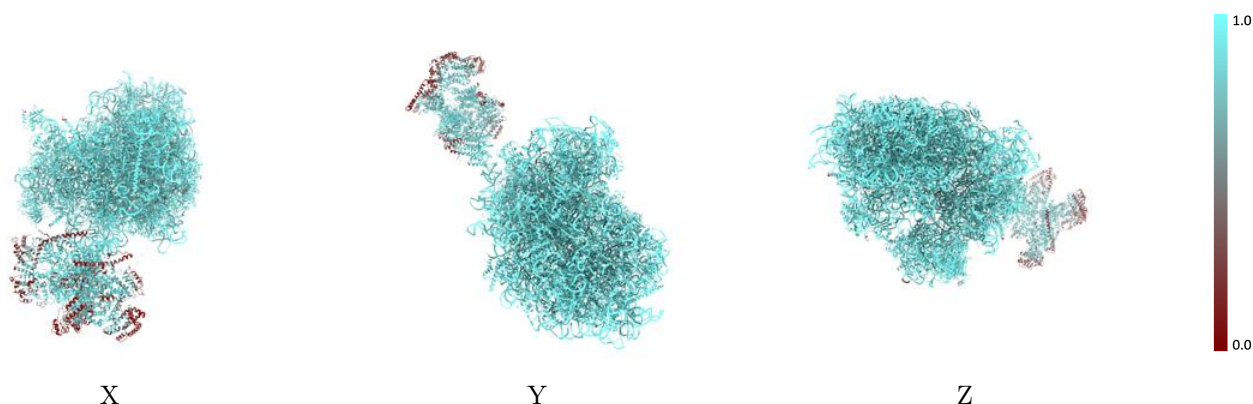
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



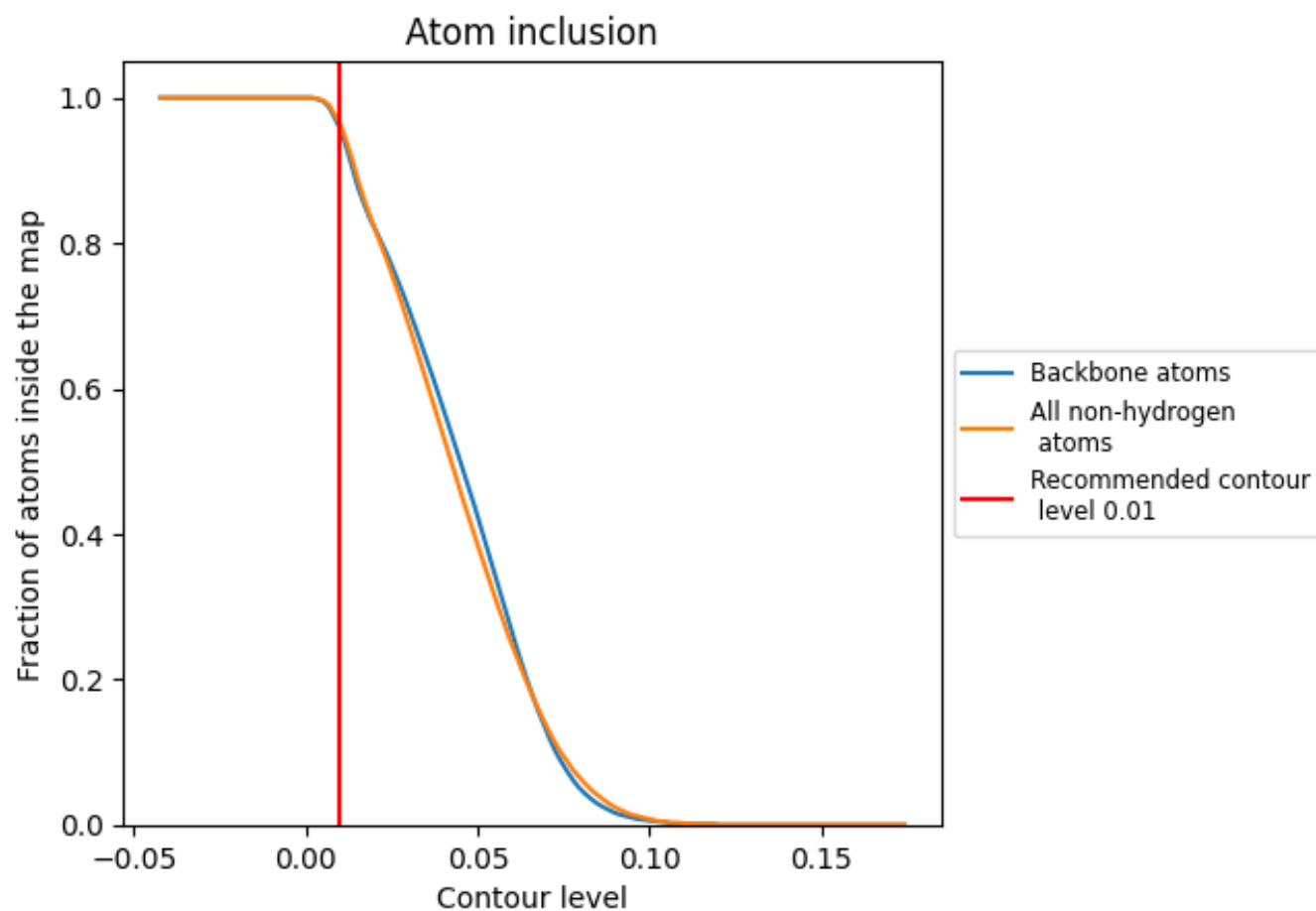
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.3990
3a	 0.8530	 0.0400
3c	 0.8570	 0.0900
3d	 0.6770	 0.0280
3e	 0.6950	 0.0250
3f	 0.8210	 0.0330
3h	 0.8250	 0.0060
3k	 0.3450	 0.0190
3l	 0.6430	 0.0240
3m	 0.5320	 0.0400
L5	 0.9980	 0.4730
L7	 1.0000	 0.5110
L8	 0.9940	 0.4930
LA	 0.9970	 0.5170
LB	 0.9920	 0.4940
LC	 0.9940	 0.4860
LD	 0.9810	 0.4320
LE	 0.9900	 0.4290
LF	 0.9970	 0.5030
LG	 0.9800	 0.4330
LH	 0.9920	 0.4630
LI	 0.9950	 0.4900
LJ	 0.9760	 0.4370
LL	 0.9700	 0.4760
LM	 0.9970	 0.5020
LN	 0.9990	 0.5360
LO	 0.9940	 0.5020
LP	 0.9900	 0.4730
LQ	 0.9980	 0.5060
LR	 0.9910	 0.4550
LS	 0.9960	 0.5170
LT	 0.9950	 0.4730
LU	 0.9550	 0.3270
LV	 0.9950	 0.5010
LW	 0.9810	 0.3640



































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Chain	Atom inclusion	Q-score
LX	 0.9870	 0.4660
LY	 0.9910	 0.4600
LZ	 0.9880	 0.4110
La	 0.9900	 0.4860
Lb	 0.9680	 0.4120
Lc	 0.9870	 0.4700
Ld	 0.9810	 0.4470
Le	 0.9980	 0.5280
Lf	 0.9950	 0.5310
Lg	 0.9950	 0.4840
Lh	 0.9910	 0.4720
Li	 0.9940	 0.4780
Lj	 1.0000	 0.5160
Lk	 0.9620	 0.3710
Ll	 1.0000	 0.4880
Lm	 0.9900	 0.4820
Ln	 1.0000	 0.5030
Lo	 0.9950	 0.5140
Lp	 0.9970	 0.5100
Lr	 0.9960	 0.4800
S2	 0.9970	 0.4260
SA	 0.9680	 0.3950
SB	 0.9920	 0.4380
SC	 0.9740	 0.3830
SD	 0.9780	 0.3520
SE	 0.9880	 0.4460
SF	 0.9830	 0.2980
SG	 0.9940	 0.4010
SH	 0.9770	 0.3910
SI	 0.9930	 0.4570
SJ	 0.9750	 0.4350
SK	 0.9740	 0.3000
SL	 0.9960	 0.4900
SN	 0.9970	 0.4850
SO	 0.9900	 0.4570
SP	 0.9750	 0.3510
SQ	 0.9830	 0.2580
SR	 0.9750	 0.3600
SS	 0.9790	 0.3460
ST	 0.9660	 0.2460
SU	 0.9850	 0.3290
SV	 0.9660	 0.3550

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Chain	Atom inclusion	Q-score
SW	 0.9860	 0.4020
SX	 0.9940	 0.4600
SY	 0.9870	 0.4210
SZ	 0.9620	 0.2610
Sa	 0.9970	 0.4720
Sb	 0.9830	 0.4130
Sc	 0.9940	 0.3920
Sd	 0.9980	 0.3720
Se	 0.9960	 0.3880
Sf	 0.8840	 0.2150
Sg	 0.9440	 0.1500
sh	 0.9460	 0.2260
zv	 1.0000	 0.3530
zx	 1.0000	 0.2170
zy	 1.0000	 0.4800
zz	 0.9760	 0.2000