



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 04:34 AM UTC

PDB ID : 9S3B / pdb_00009s3b
EMDB ID : EMD-54528
Title : NMT1-NAC bound human RNC with 58 amino acid ARF1-linker - State 1
Authors : Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-07-24
Resolution : 2.38 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

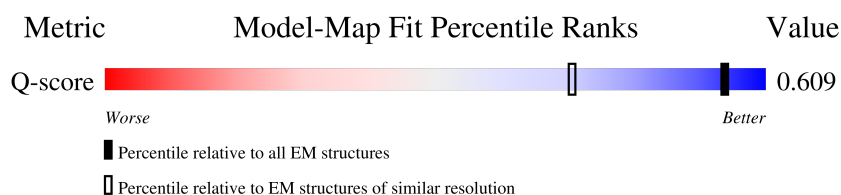
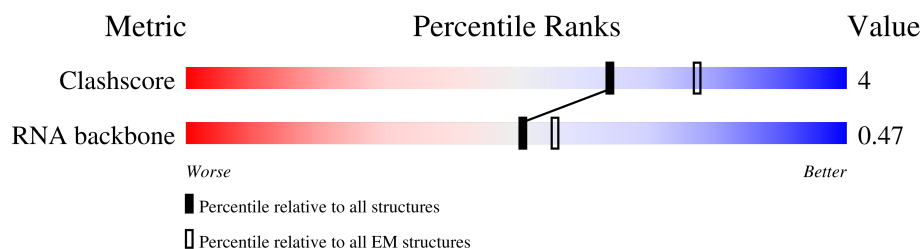
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.38 Å.

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



















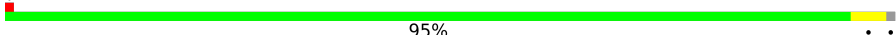








Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
RNA backbone	8273	3508	-
Q-score	-	25397	4811 (1.88 - 2.88)

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	CM	586	 98%
2	CP	75	 64% 36%
3	CR	437	 85% 10% 5%
4	L5	5070	 49% 20% 28%
5	L7	121	 79% 19%


























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Mol	Chain	Length	Quality of chain
6	L8	157	
7	LA	257	
8	LB	403	
9	LC	427	
10	LD	297	
11	LE	288	
12	LF	248	
13	LG	266	
14	LH	192	
15	LI	214	
16	LJ	178	
17	LL	211	
18	LM	215	
19	LN	204	
20	LO	203	
21	LP	184	
22	LQ	188	
23	LR	196	
24	LS	176	
25	LT	160	
26	LU	128	
27	LV	140	
28	LW	157	
29	LX	156	
30	LY	145	

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Mol	Chain	Length	Quality of chain
31	LZ	136	
32	La	148	
33	Lb	159	
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	Ls	317	
50	Lt	165	
51	S2	1869	
52	SA	295	
53	SB	264	
54	SC	293	
55	SD	243	









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Mol	Chain	Length	Quality of chain
56	SE	263	
57	SF	204	
58	SG	249	
59	SH	194	
60	SI	208	
61	SJ	194	
62	SK	165	
63	SL	158	
64	SM	132	
65	SN	151	
66	SO	151	
67	SP	145	
68	SQ	146	
69	SR	135	
70	SS	152	
71	ST	145	
72	SU	119	
73	SV	83	
74	SW	130	
75	SX	143	
76	SY	133	
77	SZ	125	
78	Sa	115	
79	Sb	84	
80	Sc	69	

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Mol	Chain	Length	Quality of chain
81	Sd	56	 79%16%5%
82	Se	133	 38%59%
83	Sf	156	 35%5%60%
84	Sg	317	 85%12%
85	NA	215	 6%20%11%69%
86	NB	162	 9%61%15%23%
87	NM	496	 63%16%21%
88	CZ	95	 32%79%17%

2 Entry composition [i](#)

There are 91 unique types of molecules in this entry. The entry contains 222378 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 58 amino acid ARF1-linker - V5 peptide - hCMV staller mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CM	12	Total	C	N	O	P	0	0
			247	111	37	87	12		

- Molecule 2 is a RNA chain called prolyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CP	75	Total	C	N	O	P	0	0
			1602	713	284	530	75		

- Molecule 3 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CR	414	Total	C	N	O	S	0	0
			3269	2080	557	621	11		

- Molecule 4 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L5	3648	Total	C	N	O	P	0	0
			78199	34823	14307	25422	3647		

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

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

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

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

- Molecule 7 is a protein called 60S ribosomal protein L8.

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

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LB	395	Total	C	N	O	S	0	0
			3183	2027	597	545	14		

- Molecule 9 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LC	364	Total	C	N	O	S	0	0
			2884	1814	576	479	15		

- Molecule 10 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LD	293	Total	C	N	O	S	0	0
			2361	1496	430	421	14		

- Molecule 11 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	219	Total	C	N	O	S	0	0
			1754	1129	334	287	4		

- Molecule 12 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	229	Total	C	N	O	S	0	0
			1818	1157	351	306	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 15 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	207	Total	C	N	O	S	0	0
			1666	1059	323	270	14		

- Molecule 16 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	169	Total	C	N	O	S	0	0
			1329	841	250	232	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LL	205	Total	C	N	O	S	0	0
			1630	1020	340	266	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LM	139	Total	C	N	O	S	0	0
			1122	720	216	179	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	200	Total	C	N	O	S	0	0
			1633	1053	318	257	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	153	Total	C	N	O	S	0	0
			1234	771	240	214	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LQ	187	Total	C	N	O	S	0	0
			1502	939	313	245	5		

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	176	Total	C	N	O	S	0	0
			1452	898	318	227	9		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LS	175	Total	C	N	O	S	0	0
			1452	925	283	234	10		

- Molecule 25 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LT	159	Total	C	N	O	S	0	0
			1282	813	250	213	6		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LU	101	Total	C	N	O	S	0	0
			806	520	141	143	2		

- Molecule 27 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	131	Total	C	N	O	S	0	0
			971	613	183	170	5		

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LW	115	Total	C	N	O	S	0	0
			808	506	160	139	3		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	120	Total	C	N	O	S	0	0
			981	627	184	169	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LY	134	Total	C	N	O	S	0	0
			1111	697	225	186	3		

- Molecule 31 is a protein called 60S ribosomal protein L27.

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

- Molecule 32 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	La	147	Total	C	N	O	S	0	0
			1154	731	236	184	3		

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lb	75	Total	C	N	O	S	0	0
			590	367	123	97	3		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lc	97	Total	C	N	O	S	0	0
			742	473	130	133	6		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ld	107	Total	C	N	O	S	0	0
			874	554	171	147	2		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Le	128	Total	C	N	O	S	0	0
			1049	664	215	165	5		

- Molecule 37 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 38 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lg	114	Total	C	N	O	S	0	0
			889	557	184	142	6		

- Molecule 39 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		

- Molecule 40 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Li	102	Total	C	N	O	S	0	0
			813	510	176	123	4		

- Molecule 41 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lk	69	Total	C	N	O	S	0	0
			542	350	100	91	1		

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lm	52	Total	C	N	O	S	0	0
			425	264	90	65	6		

- Molecule 45 is a protein called 60S ribosomal protein L41.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a.

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

- Molecule 47 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lp	91	Total	C	N	O	S	0	0
			696	440	135	114	7		

- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	125	Total	C	N	O	S	0	0
			997	618	207	168	4		

- Molecule 49 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ls	212	Total	C	N	O	S	0	0
			1640	1042	284	305	9		

- Molecule 50 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lt	160	Total	C	N	O	S	0	0
			1208	749	226	229	4		

- Molecule 51 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S2	1713	Total	C	N	O	P	0	0
			36562	16320	6564	11966	1712		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SA	216	Total	C	N	O	S	0	0
			1671	1068	297	298	8		

- Molecule 53 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SB	213	Total	C	N	O	S	0	0
			1718	1092	308	304	14		

- Molecule 54 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SC	219	Total	C	N	O	S	0	0
			1661	1076	284	291	10		

- Molecule 55 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SD	223	Total	C	N	O	S	0	0
			1594	1023	291	273	7		

- Molecule 56 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SE	262	Total	C	N	O	S	0	0
			1972	1270	370	324	8		

- Molecule 57 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SF	181	Total	C	N	O	S	0	0
			1403	879	269	248	7		

- Molecule 58 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SG	231	Total	C	N	O	S	0	0
			1634	1026	332	269	7		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SH	183	Total	C	N	O		0	0
			1274	819	242	213			

- Molecule 60 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SI	206	Total	C	N	O	S	0	0
			1574	989	308	272	5		

- Molecule 61 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SJ	179	Total	C	N	O	S	0	0
			1431	915	290	224	2		

- Molecule 62 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SK	96	Total	C	N	O	S	0	0
			726	479	127	115	5		

- Molecule 63 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SL	144	Total	C	N	O	S	0	0
			1143	730	213	194	6		

- Molecule 64 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SM	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- Molecule 65 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SN	150	Total	C	N	O	S	0	0
			1182	758	226	197	1		

- Molecule 66 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	6		

- Molecule 67 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SP	129	Total	C	N	O	S	0	0
			990	626	190	168	6		

- Molecule 68 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SQ	142	Total	C	N	O	S	0	0
			1075	689	204	179	3		

- Molecule 69 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SR	131	Total	C	N	O	S	0	0
			942	600	179	159	4		

- Molecule 70 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SS	141	Total	C	N	O	S	0	0
			1130	712	232	185	1		

- Molecule 71 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	ST	143	Total	C	N	O	S	0	0
			1081	679	210	189	3		

- Molecule 72 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SU	101	Total	C	N	O	S	0	0
			713	447	137	125	4		

- Molecule 73 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SV	83	Total	C	N	O	S	0	0
			618	385	115	113	5		

- 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
			1026	655	193	172	6		

- Molecule 75 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SX	141	Total	C	N	O	S	0	0
			1078	682	212	181	3		

- Molecule 76 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SY	123	Total	C	N	O	S	0	0
			927	588	183	152	4		

- Molecule 77 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SZ	75	Total	C	N	O	S	0	0
			559	361	105	92	1		

- Molecule 78 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sa	99	Total	C	N	O	S	0	0
			781	487	165	124	5		

- Molecule 79 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sb	83	Total	C	N	O	S	0	0
			618	386	118	107	7		

- Molecule 80 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sc	63	Total	C	N	O	S	0	0
			472	289	92	89	2		

- Molecule 81 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sd	53	Total	C	N	O	S	0	0
			433	271	87	70	5		

- Molecule 82 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Se	55	Total	C	N	O	S	0	0
			416	254	93	68	1		

- Molecule 83 is a protein called Ubiquitin.

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

- Molecule 84 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sg	308	Total	C	N	O	S	0	0
			2180	1393	381	395	11		

- Molecule 85 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	NA	67	Total	C	N	O	S	0	0
			531	335	97	98	1		

- Molecule 86 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	NB	124	Total	C	N	O	S	0	0
			963	597	175	188	3		

- Molecule 87 is a protein called Glycylpeptide N-tetradecanoyltransferase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	NM	393	Total	C	N	O	S	3	0
			3209	2075	544	573	17		

- Molecule 88 is a protein called nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	CZ	79	Total	C	N	O	S	0	0
			455	283	83	87	2		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	CM	1	Total	Mg	0
			1	1	
89	L5	126	Total	Mg	0
			126	126	
89	L7	3	Total	Mg	0
			3	3	
89	L8	3	Total	Mg	0
			3	3	
89	LA	1	Total	Mg	0
			1	1	
89	LC	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
89	LI	1	Total 1	Mg 1	0
89	LN	1	Total 1	Mg 1	0
89	LP	1	Total 1	Mg 1	0
89	LV	1	Total 1	Mg 1	0
89	S2	51	Total 51	Mg 51	0
89	ST	1	Total 1	Mg 1	0

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
90	Lg	1	Total 1	Zn 1	0
90	Lj	1	Total 1	Zn 1	0
90	Lm	1	Total 1	Zn 1	0
90	Lo	1	Total 1	Zn 1	0
90	Lp	1	Total 1	Zn 1	0
90	Sa	1	Total 1	Zn 1	0
90	Sd	1	Total 1	Zn 1	0
90	Sf	1	Total 1	Zn 1	0

- Molecule 91 is water.

Mol	Chain	Residues	Atoms		AltConf
91	L5	4	Total 4	O 4	0
91	L7	1	Total 1	O 1	0
91	LI	1	Total 1	O 1	0

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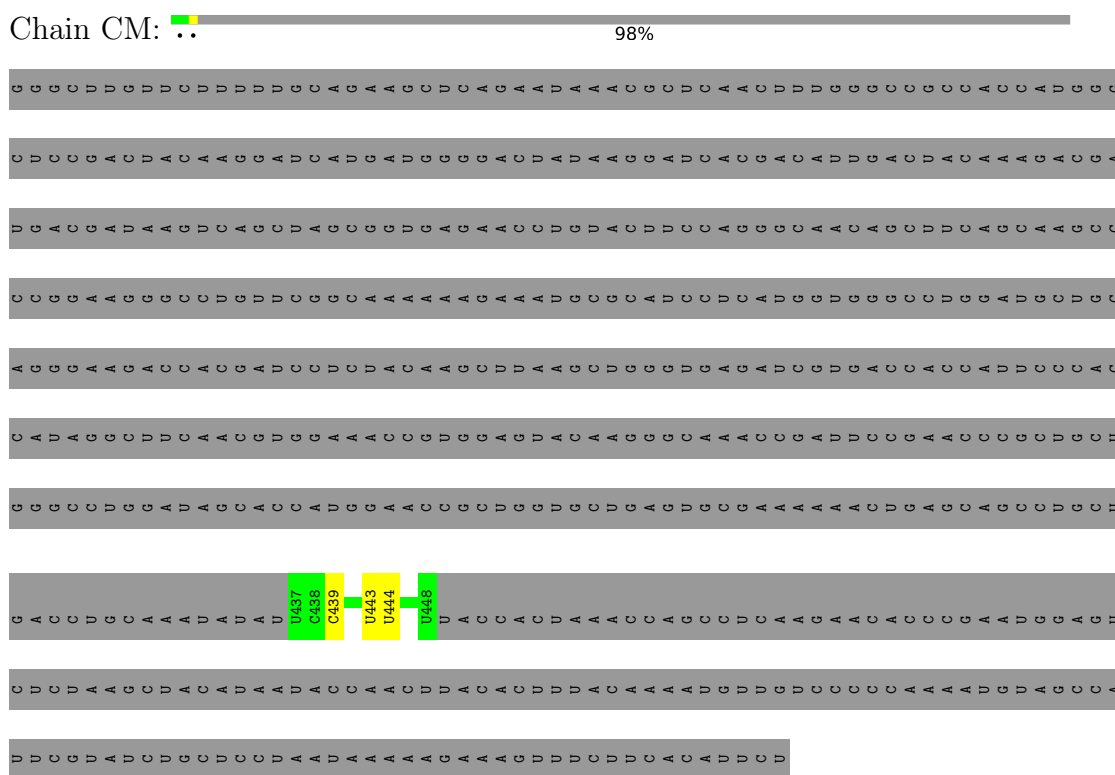
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Mol	Chain	Residues	Atoms		AltConf
91	LN	1	Total 1	O 1	0
91	La	1	Total 1	O 1	0
91	S2	3	Total 3	O 3	0

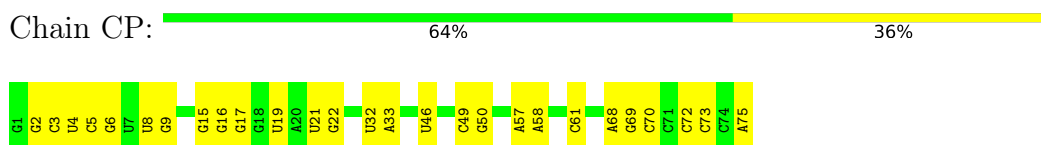
3 Residue-property plots

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.

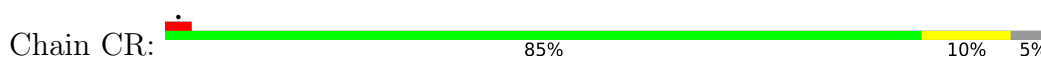
- Molecule 1: 58 amino acid ARF1-linker - V5 peptide - hCMV staller mRNA



- Molecule 2: prolyl-tRNA

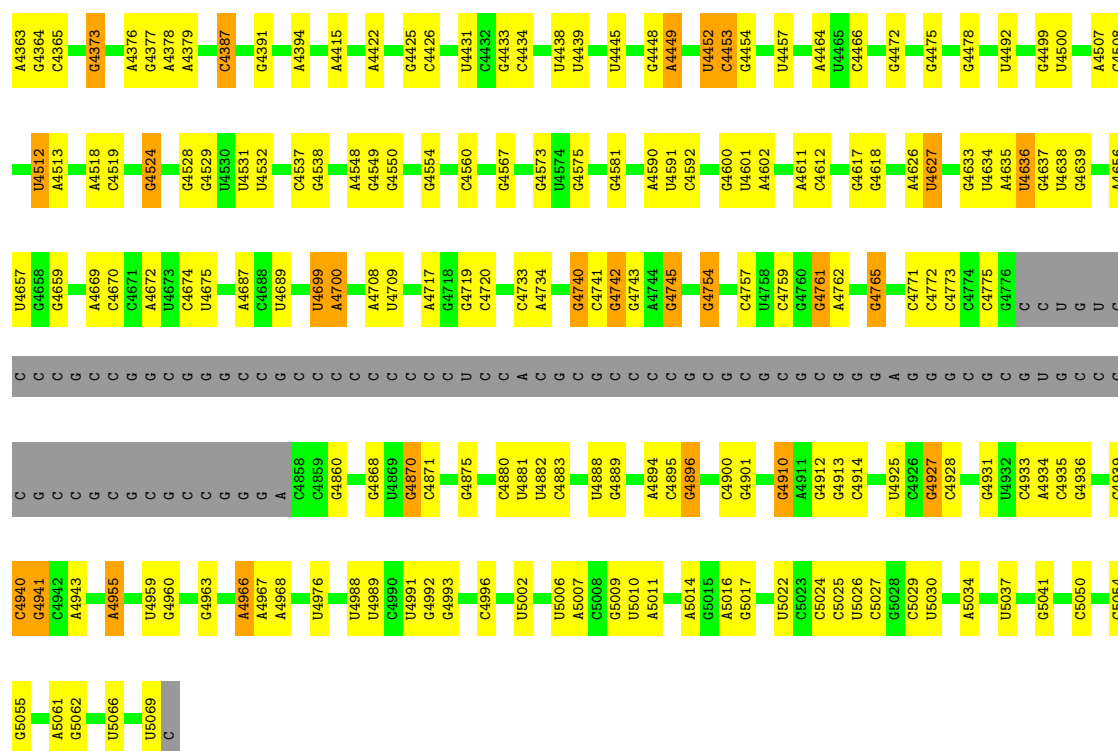


- Molecule 3: Eukaryotic peptide chain release factor subunit 1

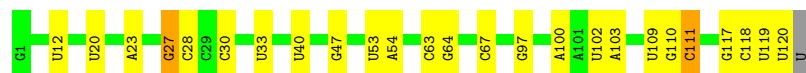


WORLDWIDE
PDB
PROTEIN DATA BANK



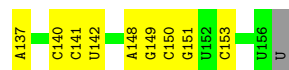
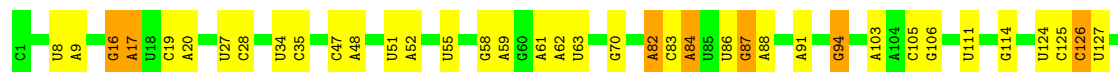


Chain L7: 79% 19% ..



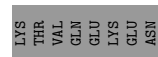
• Molecule 6: 5.8S rRNA

Chain L8: 69% 25% . .



• Molecule 7: 60S ribosomal protein L8

Chain LA: 85% 12% .



• Molecule 8: 60S ribosomal protein L3

D306	Y307	Y323	Y337	T340	D369	T370	S371	K373	R378	K385	R396	ILE	ALA	LYS	GLU	GLY	ALA															
MET	S2	K30	V41	I56	V73	T77	E80	Y92	L99	A107	K132	K135	D139	E140	M153	H165	M168	L180	G187	L194	R198	L201	K224	G247	K252	C253	T254	G255	H258	V266	K300	T305

[illegible]

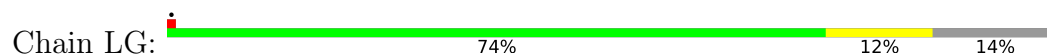
ALA	GLU	SER	MET
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			R33
			K41
			I60
			G62
			T93
			L104
			L105
			A106
			R107
			K117
			E120
			R152
			T153
			T154
			R179
			K197
			Q202
			M208
			R209
			Y210
			L211
			M212
			Y219
			F223
			Y226
			P233
			D234
			M235
			M236
			M239
			I247
			K256
			V261
			S286
			L293

GLY	GLU	ILE	PHE	ASP	THR	K237	E244	K247	I248	K251	L271	M279	F288	VAL	LEU	ALA	T91	V92	D99	K100	N101	R105	L109	R110	K111	M112	R123	K124	L125	L126	I149	R161	L165	T176	G177	N182	R183	R187	R188	T189	H190	F193	S198	N205	I208	P209	K210	K219	K220	K221	LEU	ARG	LYS	PRO	ARG	HIS	GLN	GLU
MET	ALA	GLY	GLU	LYS	VAL	GLU	GLU	ASP	THR	LYS	GLU	LYS	LYS	PRO	ALA	LYS	GLU	ASP	VAL	ASP	ASP	THR	LYS	GLU	LYS	LYS	PRO	GLU	ALA	LYS	LYS	GLY	ASP	ALA	ASN	LEU	LYS	LYS	LYS	PRO	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	VAL	LYS	SER	LYS	GLU	LYS	LYS	LYS	LYS	GLU

Met	GLU	GLY	VAL	GLU	LYS	LYS	VAL	PRO	ALA	VAL	PRO	GLU	LEU	LYS	LYS	ARG	ARG	R24	R32	R43	E52	R66	R76	K88	V105	A128	M132	V136	K148	E152	I162	M163	K164	I167	Y182	T196	P200
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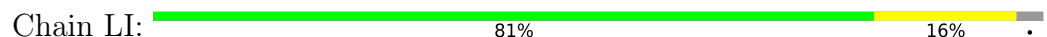
- Molecule 13: 60S ribosomal protein L7a



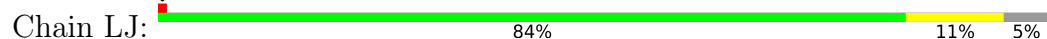
- Molecule 14: 60S ribosomal protein L9



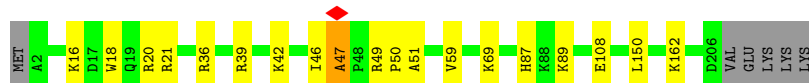
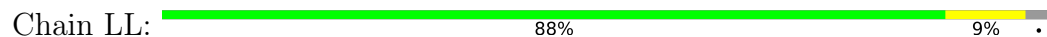
- Molecule 15: Ribosomal protein uL16-like



- Molecule 16: 60S ribosomal protein L11



- Molecule 17: 60S ribosomal protein L13

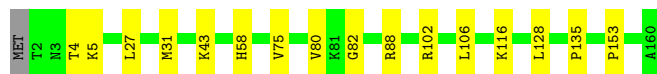


- Molecule 18: 60S ribosomal protein L14



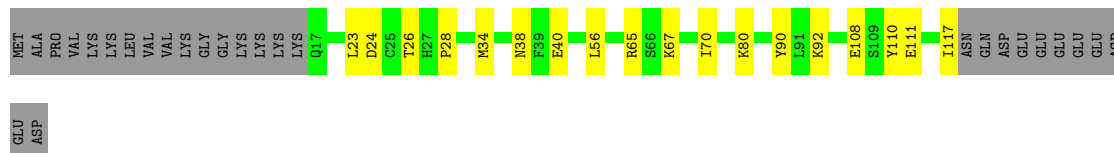
- Molecule 25: 60S ribosomal protein L21

Chain LT:  89% 10%




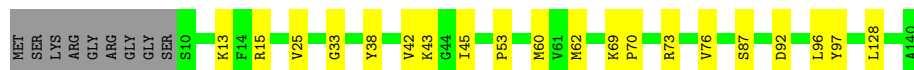
- Molecule 26: 60S ribosomal protein L22

Chain LU:  65% 14% 21%



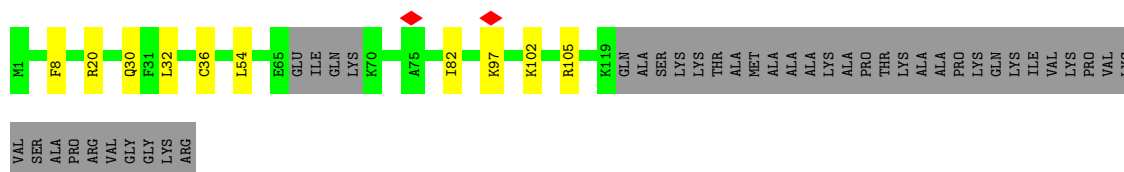
- Molecule 27: 60S ribosomal protein L23

Chain LV:  79% 14% 6%



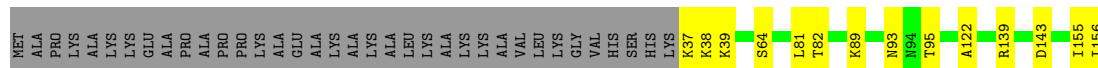
- Molecule 28: 60S ribosomal protein L24

Chain LW:  67% 6% 27%




- Molecule 29: 60S ribosomal protein L23a

Chain LX:  68% 9% 23%




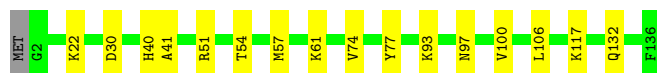
- Molecule 30: 60S ribosomal protein L26

Chain LY:  77% 15% 8%




- Molecule 31: 60S ribosomal protein L27

Chain LZ:  88% 12%



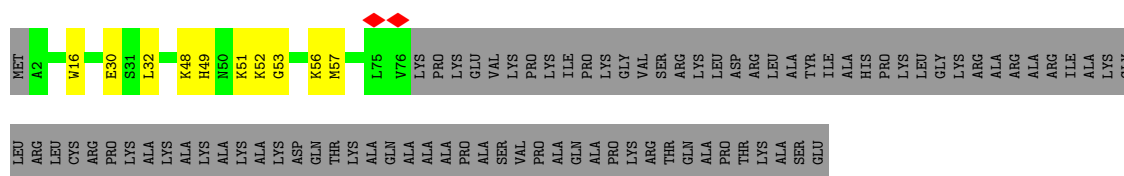
- Molecule 32: 60S ribosomal protein L27a

Chain La:  87% 12%



- Molecule 33: 60S ribosomal protein L29

Chain Lb:  41% 6% 53%



- Molecule 34: 60S ribosomal protein L30

Chain Lc:  70% 15% 16%




- Molecule 35: 60S ribosomal protein L31

Chain Ld:  75% 10% 14%




- Molecule 36: 60S ribosomal protein L32

Chain Le:  88% 7% 5%




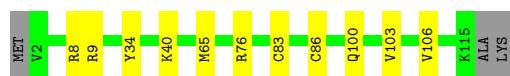
- Molecule 37: 60S ribosomal protein L35a

Chain Lf:  90% 9%



- Molecule 38: 60S ribosomal protein L34

Chain Lg:  88% 9%



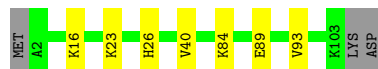
- Molecule 39: 60S ribosomal protein L35

Chain Lh:  92% 7%




- Molecule 40: 60S ribosomal protein L36

Chain Li:  90% 7%




- Molecule 41: Large ribosomal subunit protein eL37

Chain Lj:  75% 13% 11%




- Molecule 42: 60S ribosomal protein L38

Chain Lk:  86% 13%



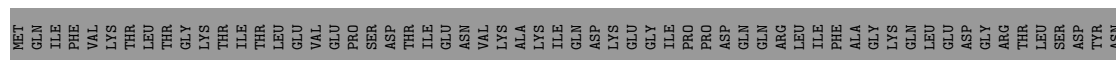
- Molecule 43: 60S ribosomal protein L39

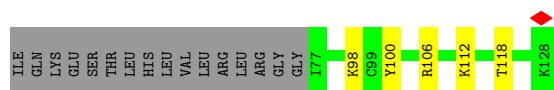
Chain Ll:  76% 22%



- Molecule 44: Ubiquitin-60S ribosomal protein L40

Chain Lm:  37% 59%





- Molecule 45: 60S ribosomal protein L41

Chain Ln: 92%



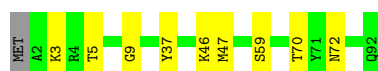
- Molecule 46: 60S ribosomal protein L36a

Chain Lo: 88% 11%



- Molecule 47: 60S ribosomal protein L37a

Chain Lp: 89% 10%



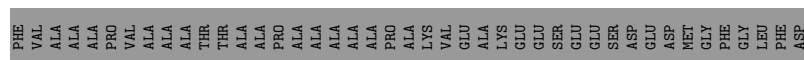
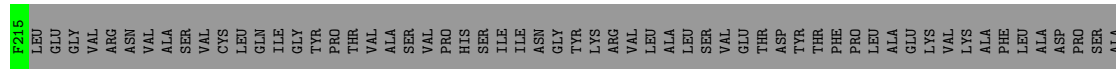
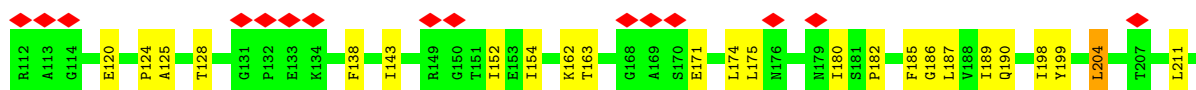
- Molecule 48: 60S ribosomal protein L28

Chain Lr: 81% 10% 9%



- Molecule 49: 60S acidic ribosomal protein P0

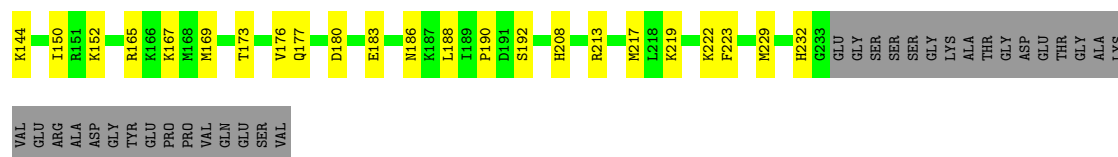
Chain Ls: 5% 49% 18% 33%



- Molecule 50: Large ribosomal subunit protein uL11

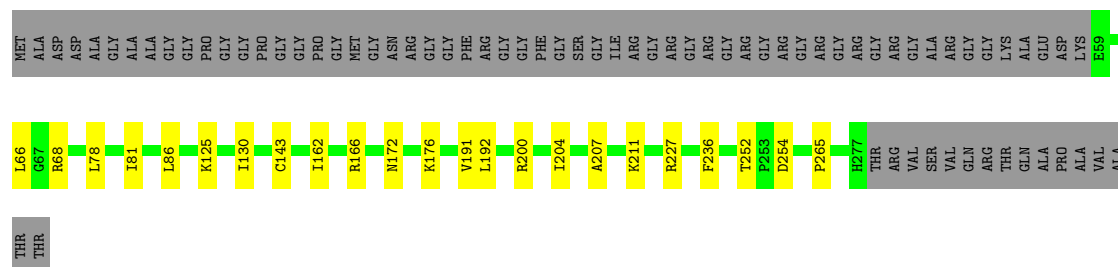
M11	M12	M13	M14	M15	M16	M17	M18	M19	M20	M21	M22	M23	M24	M25	M26	M27	M28	M29	M30	M31	M32	M33	M34	M35	M36	M37	M38	M39	M40	M41	M42	M43	M44	M45	M46	M47	M48	M49	M50	M51	M52	M53	M54	M55	M56	M57	M58	M59	M60	M61	M62	M63	M64	M65	M66	M67	M68	M69	M70	M71	M72	M73	M74	M75	M76	M77	M78	M79	M80	M81	M82	M83	M84	M85	M86	M87	M88	M89	M90	M91	M92	M93	M94	M95	M96	M97	M98	M99	M100	M101	M102	M103	M104	M105	M106	M107	M108	M109	M110	M111	M112	M113	M114	M115	M116	M117	M118	M119	M120	M121	M122	M123	M124	M125	M126	M127	M128	M129	M130	M131	M132	M133	M134	M135	M136	M137	M138	M139	M140	M141	M142	M143	M144	M145	M146	M147	M148	M149	M150	M151	M152	M153	M154	M155	M156	M157	M158	M159	M160	M161	M162	M163	M164	M165	M166	M167	M168	M169	M170	M171	M172	M173	M174	M175	M176	M177	M178	M179	M180	M181	M182	M183	M184	M185	M186	M187	M188	M189	M190	M191	M192	M193	M194	M195	M196	M197	M198	M199	M200	M201	M202	M203	M204	M205	M206	M207	M208	M209	M210	M211	M212	M213	M214	M215	M216	M217	M218	M219	M220	M221	M222	M223	M224	M225	M226	M227	M228	M229	M230	M231	M232	M233	M234	M235	M236	M237	M238	M239	M240	M241	M242	M243	M244	M245	M246	M247	M248	M249	M250	M251	M252	M253	M254	M255	M256	M257	M258	M259	M260	M261	M262	M263	M264	M265	M266	M267	M268	M269	M270	M271	M272	M273	M274	M275	M276	M277	M278	M279	M280	M281	M282	M283	M284	M285	M286	M287	M288	M289	M290	M291	M292	M293	M294	M295	M296	M297	M298	M299	M300	M301	M302	M303	M304	M305	M306	M307	M308	M309	M310	M311	M312	M313	M314	M315	M316	M317	M318	M319	M320	M321	M322	M323	M324	M325	M326	M327	M328	M329	M330	M331	M332	M333	M334	M335	M336	M337	M338	M339	M340	M341	M342	M343	M344	M345	M346	M347	M348	M349	M350	M351	M352	M353	M354	M355	M356	M357	M358	M359	M360	M361	M362	M363	M364	M365	M366	M367	M368	M369	M370	M371	M372	M373	M374	M375	M376	M377	M378	M379	M380	M381	M382	M383	M384	M385	M386	M387	M388	M389	M390	M391	M392	M393	M394	M395	M396	M397	M398	M399	M400	M401	M402	M403	M404	M405	M406	M407	M408	M409	M410	M411	M412	M413	M414	M415	M416	M417	M418	M419	M420	M421	M422	M423	M424	M425	M426	M427	M428	M429	M430	M431	M432	M433	M434	M435	M436	M437	M438	M439	M440	M441	M442	M443	M444	M445	M446	M447	M448	M449	M450	M451	M452	M453	M454	M455	M456	M457	M458	M459	M460	M461	M462	M463	M464	M465	M466	M467	M468	M469	M470	M471	M472	M473	M474	M475	M476	M477	M478	M479	M480	M481	M482	M483	M484	M485	M486	M487	M488	M489	M490	M491	M492	M493	M494	M495	M496	M497	M498	M499	M500	M501	M502	M503	M504	M505	M506	M507	M508	M509	M510	M511	M512	M513	M514	M515	M516	M517	M518	M519	M520	M521	M522	M523	M524	M525	M526	M527	M528	M529	M530	M531	M532	M533
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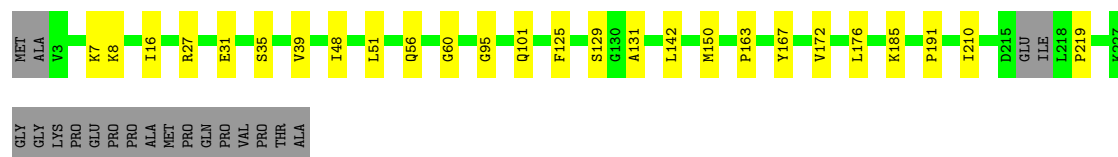
- Molecule 54: 40S ribosomal protein S2

Chain SC: 67% 8% 25%



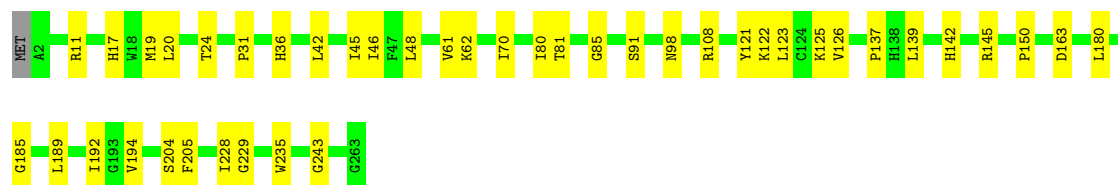
- Molecule 55: 40S ribosomal protein S3

Chain SD: 81% 11% 8%



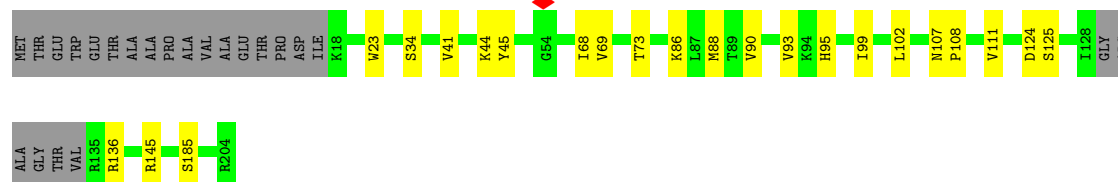
- Molecule 56: Small ribosomal subunit protein eS4, X isoform

Chain SE: 84% 16%




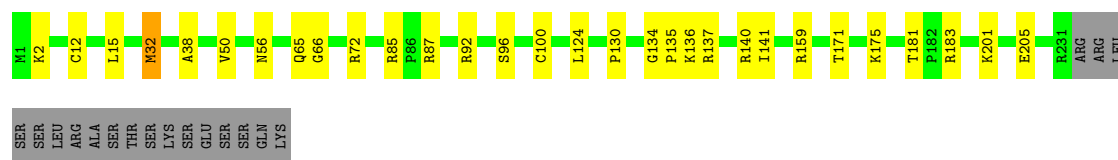
- Molecule 57: 40S ribosomal protein S5

Chain SF: 77% 11% 11%




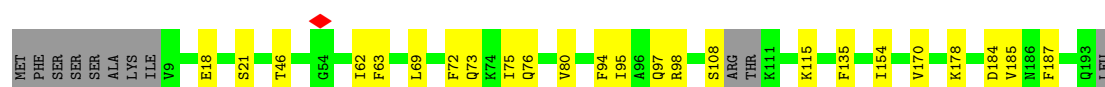
- Molecule 58: 40S ribosomal protein S6

Chain SG:  81% 12% 7%




- Molecule 59: 40S ribosomal protein S7

Chain SH:  82% 12% 6%




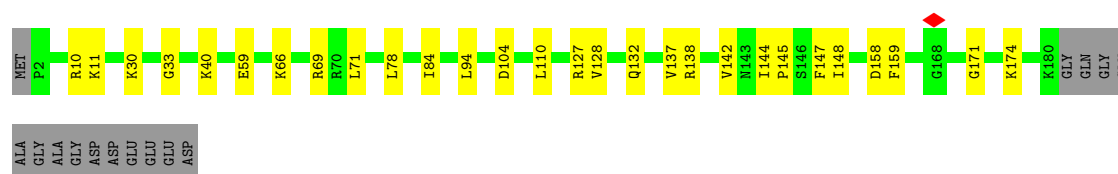
- Molecule 60: 40S ribosomal protein S8

Chain SI:  88% 12% 0%



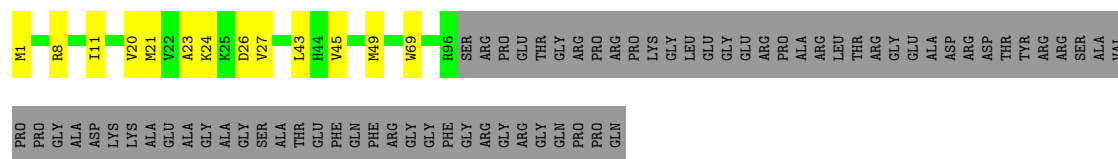
- Molecule 61: 40S ribosomal protein S9

Chain SJ:  78% 14% 8%




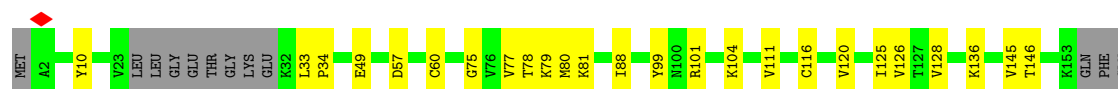
- Molecule 62: 40S ribosomal protein S10

Chain SK:  50% 8% 42%



- Molecule 63: 40S ribosomal protein S11

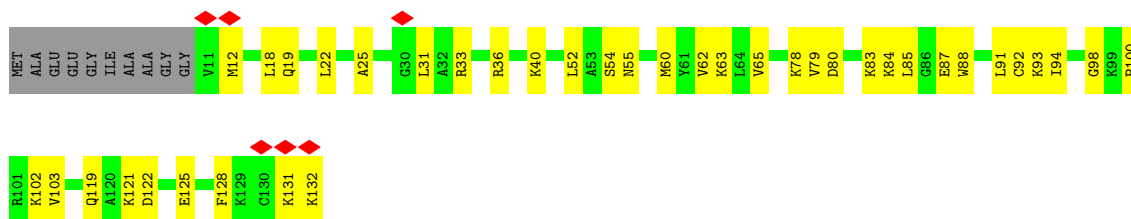
Chain SL:  75% 16% 9%



LYS
PHE

- Molecule 64: 40S ribosomal protein S12

Chain SM: 




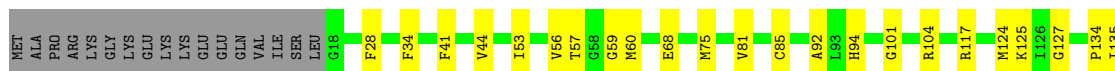
- Molecule 65: 40S ribosomal protein S13

Chain SN: 




- Molecule 66: 40S ribosomal protein S14

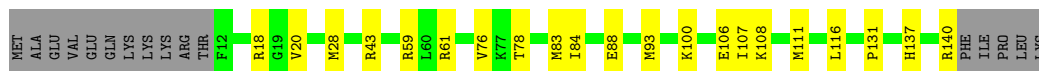
Chain SO: 




L151

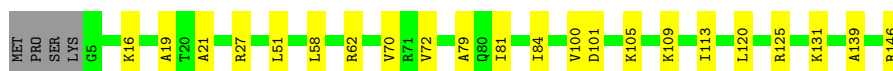
- Molecule 67: 40S ribosomal protein S15

Chain SP: 




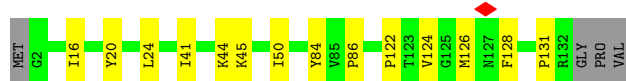
- Molecule 68: 40S ribosomal protein S16

Chain SQ: 



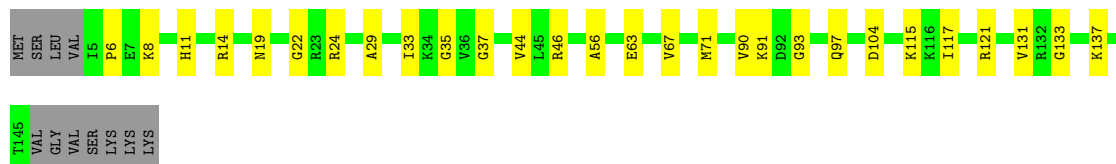
- Molecule 69: 40S ribosomal protein S17

Chain SR: 



- Molecule 70: 40S ribosomal protein S18

Chain SS: 74% 18% 7%



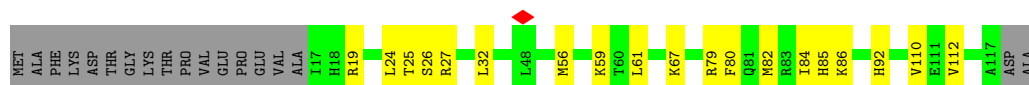
- Molecule 71: 40S ribosomal protein S19

Chain ST: 82% 17% .



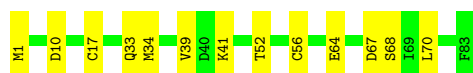
- Molecule 72: 40S ribosomal protein S20

Chain SU: 69% 16% 15%



- Molecule 73: 40S ribosomal protein S21

Chain SV: 84% 16%



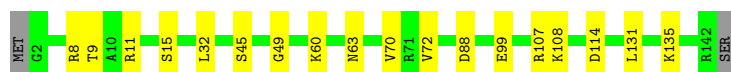
- Molecule 74: 40S ribosomal protein S15a

Chain SW: 88% 11% .




- Molecule 75: 40S ribosomal protein S23

Chain SX: 86% 13% .



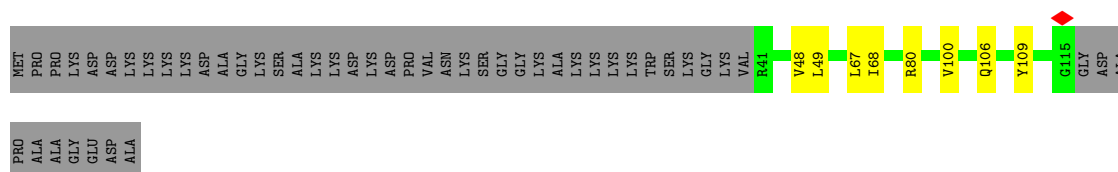
- Molecule 76: 40S ribosomal protein S24

Chain SY:  74% 18% 8%




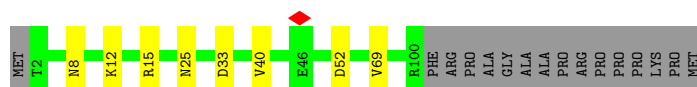
- Molecule 77: 40S ribosomal protein S25

Chain SZ:  54% 6% 40%




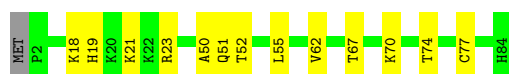
- Molecule 78: 40S ribosomal protein S26

Chain Sa:  79% 7% 14%




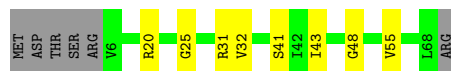
- Molecule 79: 40S ribosomal protein S27

Chain Sb:  83% 15% 2%




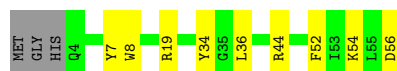
- Molecule 80: 40S ribosomal protein S28

Chain Sc:  80% 12% 9%



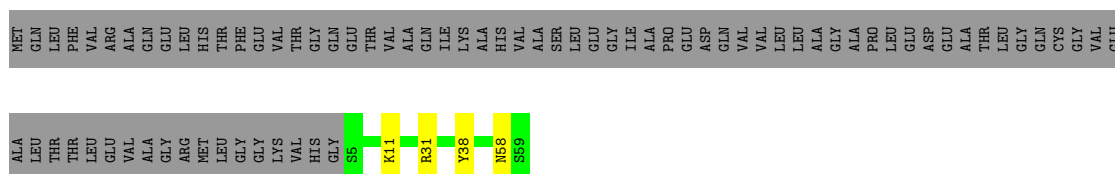
- Molecule 81: 40S ribosomal protein S29

Chain Sd:  79% 16% 5%

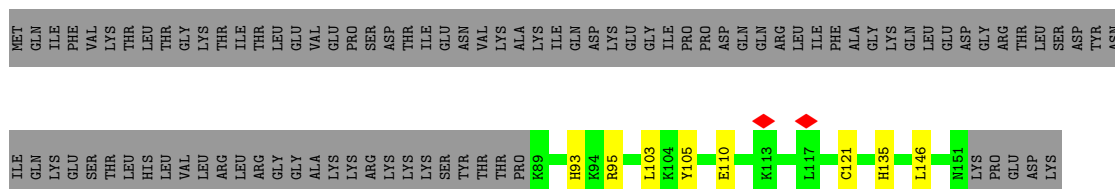
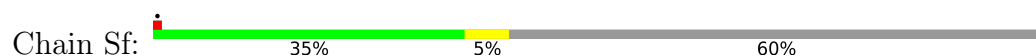


- Molecule 82: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

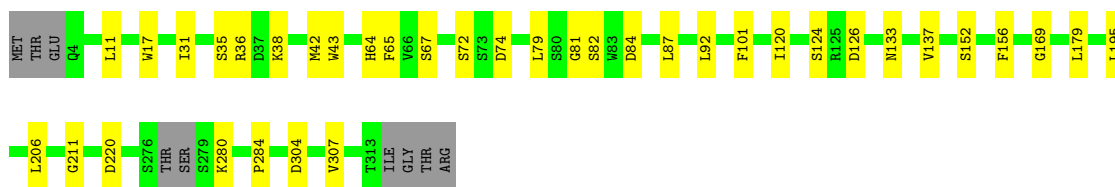
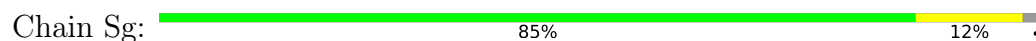
Chain Se:  38% 59%



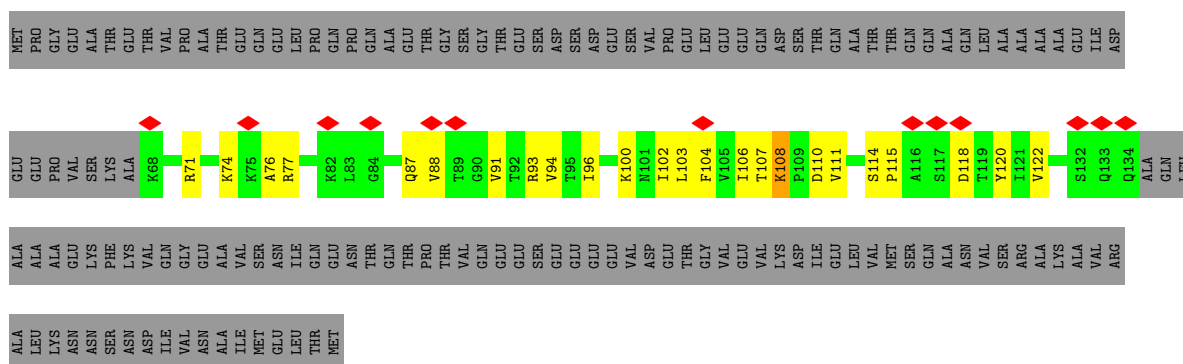
- Molecule 83: Ubiquitin



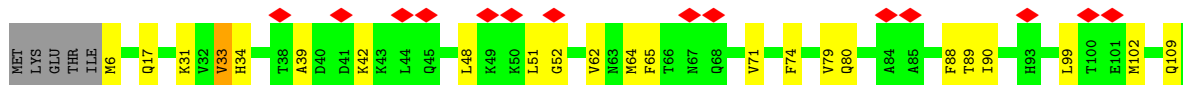
- Molecule 84: Receptor of activated protein C kinase 1



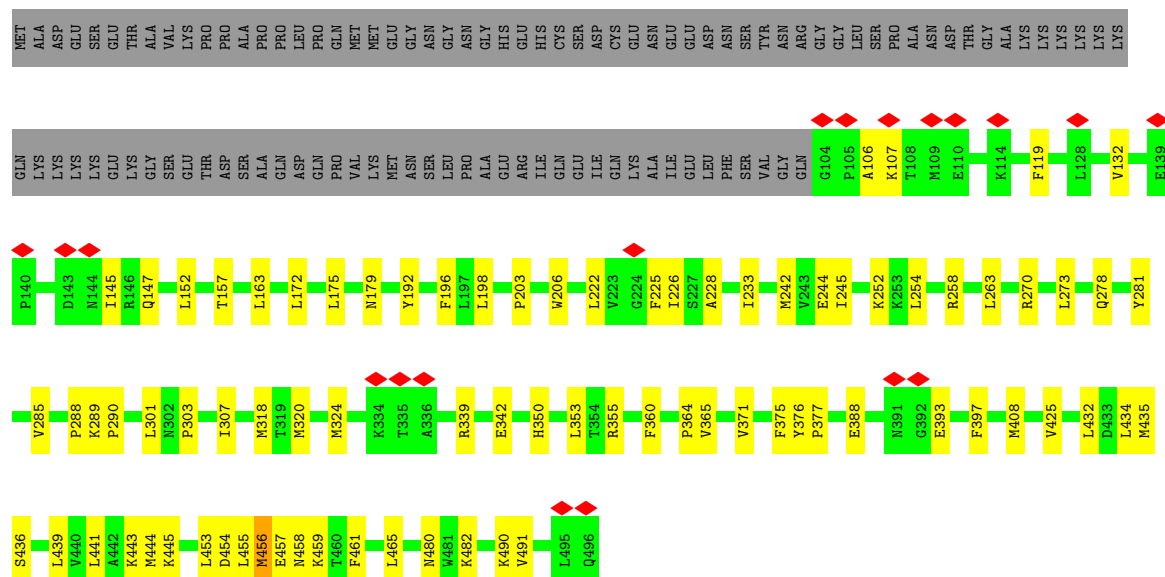
- Molecule 85: Nascent polypeptide-associated complex subunit alpha



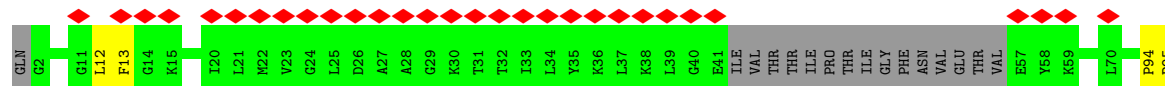
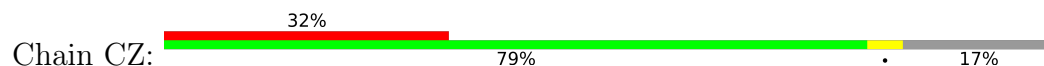
- Molecule 86: Isoform 2 of Transcription factor BTF3



- Molecule 87: Glycylpeptide N-tetradecanoyltransferase 1



- Molecule 88: nascent chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	60443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	5.209	Depositor
Minimum map value	-2.009	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.116	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	465.28, 465.28, 465.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality

5.1 Standard geometry

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

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	CM	0.36	0/273	0.48	0/421
2	CP	0.31	0/1789	0.47	0/2788
3	CR	0.27	0/3311	0.54	2/4452 (0.0%)
4	L5	0.36	0/87471	0.41	1/136443 (0.0%)
5	L7	0.35	0/2858	0.36	0/4455
6	L8	0.36	0/3701	0.38	0/5766
7	LA	0.36	0/1936	0.61	0/2596
8	LB	0.33	0/3251	0.55	1/4352 (0.0%)
9	LC	0.32	0/2938	0.56	2/3947 (0.1%)
10	LD	0.28	0/2407	0.52	0/3227
11	LE	0.31	0/1788	0.62	2/2399 (0.1%)
12	LF	0.33	0/1905	0.55	0/2539
13	LG	0.30	0/1849	0.60	1/2496 (0.0%)
14	LH	0.31	0/1529	0.55	0/2058
15	LI	0.31	0/1705	0.53	0/2277
16	LJ	0.30	0/1352	0.57	0/1813
17	LL	0.30	0/1661	0.53	0/2229
18	LM	0.28	0/1145	0.51	0/1536
19	LN	0.33	0/1746	0.48	0/2338
20	LO	0.35	0/1665	0.57	1/2229 (0.0%)
21	LP	0.32	0/1260	0.53	0/1692
22	LQ	0.33	0/1526	0.55	0/2038
23	LR	0.29	0/1468	0.54	0/1945
24	LS	0.33	0/1492	0.51	0/2003
25	LT	0.30	0/1310	0.60	0/1752
26	LU	0.27	0/820	0.65	0/1102
27	LV	0.31	0/985	0.58	0/1323
28	LW	0.29	0/820	0.56	0/1104
29	LX	0.29	0/998	0.50	0/1341
30	LY	0.34	0/1128	0.61	0/1500
31	LZ	0.30	0/1130	0.50	0/1507
32	La	0.32	0/1183	0.50	0/1582

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lb	0.29	0/600	0.53	0/796
34	Lc	0.32	0/752	0.53	0/1011
35	Ld	0.31	0/889	0.48	0/1198
36	Le	0.33	0/1067	0.55	0/1425
37	Lf	0.35	0/891	0.59	0/1194
38	Lg	0.30	0/899	0.52	0/1200
39	Lh	0.28	0/1014	0.52	0/1340
40	Li	0.24	0/824	0.45	0/1093
41	Lj	0.34	0/720	0.57	0/952
42	Lk	0.30	0/548	0.62	0/730
43	Ll	0.33	0/454	0.48	0/599
44	Lm	0.27	0/431	0.42	0/570
45	Ln	0.34	0/231	0.41	0/294
46	Lo	0.33	0/876	0.53	0/1156
47	Lp	0.31	0/706	0.54	0/939
48	Lr	0.32	0/1012	0.55	0/1358
49	Ls	0.33	0/1666	0.78	2/2250 (0.1%)
50	Lt	0.32	0/1224	0.87	3/1651 (0.2%)
51	S2	0.35	0/40882	0.44	1/63715 (0.0%)
52	SA	0.32	0/1708	0.57	0/2324
53	SB	0.28	0/1745	0.51	0/2337
54	SC	0.31	0/1697	0.56	0/2301
55	SD	0.44	2/1620 (0.1%)	0.67	4/2198 (0.2%)
56	SE	0.28	0/2014	0.52	0/2726
57	SF	0.31	0/1423	0.61	3/1913 (0.2%)
58	SG	0.24	0/1657	0.54	0/2247
59	SH	0.24	0/1295	0.50	0/1763
60	SI	0.29	0/1603	0.52	0/2161
61	SJ	0.28	0/1456	0.53	1/1957 (0.1%)
62	SK	0.27	0/750	0.56	0/1026
63	SL	0.35	0/1163	0.51	0/1562
64	SM	0.35	0/960	0.91	3/1286 (0.2%)
65	SN	0.28	0/1206	0.45	0/1626
66	SO	0.32	0/982	0.62	0/1320
67	SP	0.25	0/1010	0.48	0/1362
68	SQ	0.27	0/1093	0.61	0/1470
69	SR	0.31	0/955	0.67	1/1294 (0.1%)
70	SS	0.30	0/1148	0.69	2/1542 (0.1%)
71	ST	0.26	0/1100	0.44	0/1479
72	SU	0.27	0/722	0.59	0/983
73	SV	0.31	0/625	0.55	0/837
74	SW	0.31	0/1043	0.51	0/1396
75	SX	0.33	0/1096	0.63	0/1467

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SY	0.34	1/944 (0.1%)	0.70	2/1271 (0.2%)
77	SZ	0.26	0/565	0.56	0/764
78	Sa	0.35	0/794	0.64	0/1065
79	Sb	0.32	0/632	0.68	0/851
80	Sc	0.27	0/474	0.61	0/638
81	Sd	0.31	0/443	0.52	0/589
82	Se	0.26	0/420	0.54	0/554
83	Sf	0.30	0/525	0.73	1/695 (0.1%)
84	Sg	0.26	0/2235	0.63	0/3068
85	NA	0.43	0/536	1.03	6/715 (0.8%)
86	NB	0.32	0/972	0.71	1/1304 (0.1%)
87	NM	0.25	0/3299	0.69	7/4483 (0.2%)
88	CZ	0.24	0/459	0.45	0/629
All	All	0.34	3/238455 (0.0%)	0.49	47/349924 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	LE	0	1
17	LL	0	1
25	LT	0	1
58	SG	0	1
68	SQ	0	1
70	SS	0	1
86	NB	0	2
87	NM	0	1
All	All	0	9

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	SD	219	PRO	CG-CD	-10.58	1.14	1.50
55	SD	219	PRO	N-CD	6.77	1.57	1.47
76	SY	52	PRO	CG-CD	-5.21	1.33	1.50

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	SY	52	PRO	CA-N-CD	-13.23	93.47	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	SD	219	PRO	CA-N-CD	-12.40	94.64	112.00
55	SD	219	PRO	N-CD-CG	-12.01	85.18	103.20
49	Ls	124	PRO	CA-N-CD	-10.16	97.78	112.00
87	NM	456	MET	CB-CG-SD	8.74	138.91	112.70
13	LG	165	GLU	N-CA-C	-8.54	97.15	108.34
76	SY	52	PRO	N-CD-CG	-7.97	91.25	103.20
87	NM	456	MET	CA-CB-CG	7.30	128.70	114.10
64	SM	100	PRO	CA-N-CD	-6.37	103.08	112.00
55	SD	219	PRO	N-CA-CB	-6.34	96.60	103.25
61	SJ	30	LYS	CA-CB-CG	6.25	126.60	114.10
11	LE	100	LYS	CA-CB-CG	6.12	126.34	114.10
9	LC	109	ARG	CA-C-N	6.11	133.21	121.54
9	LC	109	ARG	C-N-CA	6.11	133.21	121.54
55	SD	219	PRO	CA-CB-CG	-6.10	92.92	104.50
11	LE	177	GLY	N-CA-C	-6.09	99.92	112.34
85	NA	108	LYS	CB-CG-CD	6.04	125.20	111.30
85	NA	77	ARG	CB-CG-CD	6.02	125.15	111.30
69	SR	122	PRO	CA-N-CD	-5.88	103.76	112.00
8	LB	255	GLY	N-CA-C	5.87	120.08	112.68
64	SM	119	GLN	CA-CB-CG	5.87	125.84	114.10
87	NM	254	LEU	CA-CB-CG	5.76	136.44	116.30
57	SF	88	MET	CA-CB-CG	5.72	125.54	114.10
86	NB	33	VAL	N-CA-C	-5.66	107.98	113.53
49	Ls	204	LEU	CA-CB-CG	5.65	136.07	116.30
87	NM	107	LYS	CB-CG-CD	5.61	124.21	111.30
85	NA	118	ASP	CB-CA-C	5.54	118.56	110.26
57	SF	44	LYS	CA-CB-CG	5.49	125.09	114.10
83	Sf	110	GLU	CA-CB-CG	5.42	124.94	114.10
3	CR	329	MET	CB-CG-SD	5.40	128.91	112.70
51	S2	1860	A	C2'-C3'-O3'	5.39	117.58	109.50
87	NM	353	LEU	CA-CB-CG	5.38	135.13	116.30
70	SS	8	LYS	CA-C-N	5.32	131.70	121.54
70	SS	8	LYS	C-N-CA	5.32	131.70	121.54
3	CR	309	LEU	CA-CB-CG	5.30	134.86	116.30
50	Lt	73	VAL	CA-C-N	-5.29	118.78	122.59
50	Lt	73	VAL	C-N-CA	-5.29	118.78	122.59
57	SF	88	MET	CG-SD-CE	-5.29	89.26	100.90
20	LO	110	PRO	N-CA-C	5.27	117.13	110.70
85	NA	77	ARG	CA-CB-CG	5.24	124.57	114.10
4	L5	417	G	O4'-C1'-N9	5.17	115.95	108.20
87	NM	434	LEU	CA-C-N	-5.16	112.11	121.14
87	NM	434	LEU	C-N-CA	-5.16	112.11	121.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	Lt	87	GLU	CA-CB-CG	5.09	124.29	114.10
64	SM	12	MET	CB-CG-SD	5.09	127.97	112.70
85	NA	76	ALA	CA-C-N	-5.04	112.78	121.66
85	NA	76	ALA	C-N-CA	-5.04	112.78	121.66

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	LE	176	THR	Peptide
17	LL	47	ALA	Peptide
25	LT	135	PRO	Peptide
86	NB	52	GLY	Peptide
86	NB	99	LEU	Peptide
87	NM	365	VAL	Peptide
58	SG	32	MET	Peptide
68	SQ	27	ARG	Sidechain
70	SS	11	HIS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CM	247	0	128	1	0
2	CP	1602	0	809	2	0
3	CR	3269	0	3312	28	0
4	L5	78199	0	39525	374	0
5	L7	2558	0	1296	9	0
6	L8	3314	0	1683	17	0
7	LA	1898	0	1993	21	0
8	LB	3183	0	3316	28	0
9	LC	2884	0	3050	19	0
10	LD	2361	0	2378	21	0
11	LE	1754	0	1899	32	0
12	LF	1870	0	1996	17	0
13	LG	1818	0	1911	23	0
14	LH	1510	0	1579	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	LI	1666	0	1711	21	0
16	LJ	1329	0	1348	12	0
17	LL	1630	0	1715	15	0
18	LM	1122	0	1174	14	0
19	LN	1701	0	1749	20	0
20	LO	1633	0	1771	13	0
21	LP	1234	0	1254	13	0
22	LQ	1502	0	1616	6	0
23	LR	1452	0	1580	13	0
24	LS	1452	0	1490	12	0
25	LT	1282	0	1336	13	0
26	LU	806	0	826	14	0
27	LV	971	0	1023	12	0
28	LW	808	0	726	8	0
29	LX	981	0	1055	14	0
30	LY	1111	0	1194	16	0
31	LZ	1107	0	1182	11	0
32	La	1154	0	1198	12	0
33	Lb	590	0	613	9	0
34	Lc	742	0	774	10	0
35	Ld	874	0	918	9	0
36	Le	1049	0	1136	7	0
37	Lf	872	0	901	7	0
38	Lg	889	0	968	8	0
39	Lh	1006	0	1132	6	0
40	Li	813	0	887	6	0
41	Lj	705	0	737	10	0
42	Lk	542	0	590	7	0
43	Ll	444	0	483	8	0
44	Lm	425	0	461	5	0
45	Ln	230	0	276	1	0
46	Lo	862	0	929	8	0
47	Lp	696	0	744	8	0
48	Lr	997	0	1054	10	0
49	Ls	1640	0	1687	41	0
50	Lt	1208	0	1257	26	0
51	S2	36562	0	18472	257	0
52	SA	1671	0	1672	27	0
53	SB	1718	0	1786	29	0
54	SC	1661	0	1710	15	0
55	SD	1594	0	1568	19	0
56	SE	1972	0	2012	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	SF	1403	0	1421	15	0
58	SG	1634	0	1568	21	0
59	SH	1274	0	1196	17	0
60	SI	1574	0	1540	16	0
61	SJ	1431	0	1497	21	0
62	SK	726	0	674	9	0
63	SL	1143	0	1177	16	0
64	SM	950	0	987	21	0
65	SN	1182	0	1249	11	0
66	SO	969	0	982	16	0
67	SP	990	0	974	16	0
68	SQ	1075	0	1110	15	0
69	SR	942	0	913	12	0
70	SS	1130	0	1167	19	0
71	ST	1081	0	1093	19	0
72	SU	713	0	692	14	0
73	SV	618	0	617	9	0
74	SW	1026	0	1072	12	0
75	SX	1078	0	1130	16	0
76	SY	927	0	914	17	0
77	SZ	559	0	594	7	0
78	Sa	781	0	831	6	0
79	Sb	618	0	604	8	0
80	Sc	472	0	484	5	0
81	Sd	433	0	415	11	0
82	Se	416	0	439	4	0
83	Sf	515	0	521	5	0
84	Sg	2180	0	1968	22	0
85	NA	531	0	573	15	0
86	NB	963	0	982	18	0
87	NM	3209	0	3185	47	0
88	CZ	455	0	338	3	0
89	CM	1	0	0	0	0
89	L5	126	0	0	0	0
89	L7	3	0	0	0	0
89	L8	3	0	0	0	0
89	LA	1	0	0	0	0
89	LC	1	0	0	0	0
89	LI	1	0	0	0	0
89	LN	1	0	0	0	0
89	LP	1	0	0	0	0
89	LV	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
89	S2	51	0	0	0	0
89	ST	1	0	0	0	0
90	Lg	1	0	0	0	0
90	Lj	1	0	0	0	0
90	Lm	1	0	0	0	0
90	Lo	1	0	0	0	0
90	Lp	1	0	0	0	0
90	Sa	1	0	0	0	0
90	Sd	1	0	0	0	0
90	Sf	1	0	0	0	0
91	L5	4	0	0	0	0
91	L7	1	0	0	0	0
91	LI	1	0	0	0	0
91	LN	1	0	0	0	0
91	La	1	0	0	0	0
91	S2	3	0	0	0	0
All	All	222378	0	164497	1563	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (1563) 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)
51:S2:1748:G:H1	51:S2:1786:U:H3	1.14	0.89
4:L5:3751:G:H21	4:L5:3775:A:H8	1.18	0.88
1:CM:443:U:H3	2:CP:33:A:H61	1.26	0.84
51:S2:1098:C:H5	51:S2:1134:G:H1	1.30	0.80
51:S2:1142:G:H21	51:S2:1145:A:H2	1.30	0.80
51:S2:1649:U:H3	51:S2:1675:A:H2	1.29	0.79
51:S2:925:G:H1	51:S2:1017:U:H3	1.30	0.78
4:L5:1443:A:N6	4:L5:2104:G:C2	2.52	0.78
15:LI:87:MET:HG2	15:LI:138:ILE:HG12	1.66	0.77
51:S2:1107:G:H1	51:S2:1125:C:H5	1.33	0.77
51:S2:1348:G:H1	51:S2:1381:G:H22	1.32	0.77
4:L5:2557:G:H1	4:L5:2570:U:H3	1.32	0.76
27:LV:33:GLY:HA3	27:LV:69:LYS:HD2	1.66	0.76
4:L5:2838:G:H5'	8:LB:247:GLY:HA2	1.67	0.76
6:L8:55:U:H3	6:L8:62:A:H2	1.34	0.76
51:S2:1396:A:O2'	51:S2:1398:G:N7	2.19	0.75
3:CR:286:LEU:HD21	3:CR:390:GLU:HG3	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2611:A:H5'	4:L5:2688:G:H4'	1.70	0.73
51:S2:1276:A:H62	51:S2:1321:G:H8	1.36	0.73
51:S2:1488:C:O2'	51:S2:1490:G:OP2	2.05	0.73
25:LT:43:LYS:O	25:LT:58:HIS:ND1	2.21	0.73
27:LV:13:LYS:HD2	27:LV:128:LEU:HD11	1.71	0.73
42:Lk:54:GLU:O	42:Lk:58:GLN:NE2	2.22	0.73
84:Sg:87:LEU:HB2	84:Sg:101:PHE:HB2	1.69	0.73
4:L5:1443:A:N6	4:L5:2103:G:C6	2.56	0.72
4:L5:4745:G:H1	4:L5:4955:A:H61	1.37	0.72
43:Ll:21:ARG:O	43:Ll:38:ASN:ND2	2.22	0.72
4:L5:4415:A:OP1	15:LI:154:ARG:NH1	2.23	0.72
49:Ls:40:MET:HE3	49:Ls:55:MET:HE3	1.69	0.72
51:S2:1616:U:H3	51:S2:1620:A:H2	1.38	0.71
87:Nm:456:MET:HE2	87:Nm:457:GLU:H	1.54	0.70
86:NB:39:ALA:HA	86:NB:42:LYS:HE3	1.74	0.70
4:L5:1443:A:N6	4:L5:2103:G:N1	2.39	0.70
51:S2:923:G:H1	51:S2:1019:C:H5	1.40	0.70
7:LA:117:GLU:HB2	7:LA:162:ASN:HB2	1.74	0.70
51:S2:1544:C:N4	51:S2:1588:A:O2'	2.24	0.69
4:L5:2262:G:OP2	48:Lr:98:ARG:NH1	2.25	0.69
51:S2:928:G:H1	51:S2:1013:U:H3	1.41	0.69
86:NB:79:VAL:HG12	86:NB:90:ILE:HD13	1.73	0.69
31:LZ:57:MET:HB3	31:LZ:61:LYS:HD3	1.73	0.69
51:S2:360:A:N6	51:S2:400:C:O2'	2.25	0.69
64:SM:36:ARG:HH12	64:SM:40:LYS:HE3	1.57	0.69
4:L5:4626:A:H62	4:L5:4669:A:H2	1.41	0.69
4:L5:1267:C:OP2	4:L5:2121:C:N4	2.25	0.68
4:L5:3946:G:H21	4:L5:3947:A:H62	1.40	0.68
53:SB:152:LYS:HB2	69:SR:131:PRO:HB3	1.76	0.68
85:NA:110:ASP:O	85:NA:122:VAL:HA	1.93	0.68
63:SL:104:LYS:HZ3	75:SX:8:ARG:HH12	1.42	0.68
56:SE:185:GLY:H	56:SE:189:LEU:HD13	1.59	0.67
21:LP:42:ARG:NH2	21:LP:99:GLU:OE2	2.27	0.67
55:SD:163:PRO:O	55:SD:167:TYR:HB2	1.95	0.67
51:S2:927:C:O2	79:Sb:51:GLN:NE2	2.28	0.67
51:S2:1745:A:H1'	58:SG:66:GLY:HA2	1.76	0.67
57:SF:102:LEU:HD11	77:SZ:100:VAL:HG21	1.77	0.67
87:Nm:278:GLN:HG3	87:Nm:480:ASN:HB3	1.77	0.67
4:L5:2469:C:H5	4:L5:2471:G:H1	1.43	0.66
51:S2:921:G:H3'	74:SW:28:ARG:HH21	1.60	0.66
53:SB:34:LYS:O	53:SB:98:THR:HB	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4258:C:OP2	16:LJ:54:ARG:NH1	2.28	0.66
10:LD:208:MET:HE2	10:LD:233:PRO:HD3	1.76	0.66
54:SC:192:LEU:HB3	54:SC:227:ARG:HB3	1.77	0.66
51:S2:1265:A:H2	51:S2:1517:G:H22	1.42	0.66
52:SA:184:ARG:HD3	52:SA:191:ARG:HD3	1.78	0.66
25:LT:88:ARG:NH1	33:Lb:30:GLU:OE1	2.29	0.66
51:S2:151:C:OP1	76:SY:120:THR:OG1	2.14	0.65
8:LB:305:THR:HG23	8:LB:307:TYR:H	1.62	0.65
52:SA:108:PHE:HB2	52:SA:136:GLU:HG2	1.78	0.65
55:SD:35:SER:OG	55:SD:51:LEU:O	2.13	0.65
51:S2:1451:G:N7	69:SR:44:LYS:NZ	2.45	0.65
51:S2:563:G:H1	51:S2:592:C:H5	1.44	0.65
87:Nm:228:ALA:HA	87:Nm:244:GLU:O	1.97	0.64
4:L5:4128:A:H2	4:L5:4156:G:H21	1.44	0.64
50:Lt:65:GLN:O	50:Lt:68:GLN:NE2	2.30	0.64
51:S2:672:A:N6	51:S2:1027:A:OP1	2.28	0.64
51:S2:1228:A:H2'	51:S2:1229:G:C8	2.32	0.64
43:Ll:43:HIS:HB3	43:Ll:46:ARG:HG2	1.79	0.64
3:CR:372:MET:HE1	3:CR:377:TRP:HB2	1.80	0.64
51:S2:66:G:H21	51:S2:82:G:H21	1.45	0.64
4:L5:194:C:O2	30:LY:121:ARG:NH1	2.31	0.64
4:L5:952:G:H5''	37:Lf:73:LYS:HD2	1.80	0.64
4:L5:1238:A:O2'	12:LF:52:GLU:OE1	2.16	0.64
22:LQ:154:LYS:NZ	22:LQ:159:PRO:O	2.31	0.64
76:SY:91:LEU:HB3	76:SY:96:LEU:HD22	1.80	0.64
2:CP:32:U:OP2	68:SQ:146:ARG:NH2	2.31	0.63
4:L5:1998:A:N3	4:L5:2019:C:O2'	2.28	0.63
31:LZ:54:THR:H	31:LZ:57:MET:HE3	1.63	0.63
51:S2:1512:C:O2'	81:Sd:7:TYR:O	2.15	0.63
87:Nm:461:PHE:HB2	87:Nm:465:LEU:HD23	1.79	0.63
4:L5:2389:A:H4'	35:Ld:70:LYS:HD2	1.80	0.63
15:LI:48:LEU:O	15:LI:139:ARG:HA	1.98	0.63
52:SA:137:ALA:HB1	52:SA:142:LEU:HB3	1.81	0.63
5:L7:30:C:H5	5:L7:47:G:H1	1.46	0.63
86:NB:80:GLN:O	86:NB:88:PHE:HA	1.98	0.63
4:L5:966:A:H5''	4:L5:2092:G:H22	1.63	0.62
4:L5:1351:G:OP1	9:LC:33:ARG:NH1	2.32	0.62
31:LZ:30:ASP:OD2	31:LZ:30:ASP:N	2.32	0.62
55:SD:16:ILE:HD11	81:Sd:36:LEU:HD23	1.80	0.62
4:L5:74:G:H5''	17:LL:59:VAL:HB	1.80	0.62
7:LA:120:PRO:HA	7:LA:162:ASN:HB3	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LS:99:ASP:OD2	24:LS:108:GLN:NE2	2.32	0.62
56:SE:11:ARG:HE	56:SE:20:LEU:HB3	1.63	0.62
38:Lg:83:CYS:SG	38:Lg:86:CYS:HB2	2.39	0.62
4:L5:3663:A:N6	4:L5:4168:G:O2'	2.33	0.62
50:Lt:104:ILE:HB	50:Lt:143:VAL:HG12	1.81	0.62
4:L5:4941:G:OP2	11:LE:188:ARG:NH2	2.33	0.62
29:LX:93:ASN:HB3	29:LX:95:THR:HG23	1.80	0.62
51:S2:1298:G:O2'	51:S2:1299:A:O4'	2.16	0.62
24:LS:19:THR:HG23	24:LS:22:CYS:H	1.64	0.62
51:S2:1347:U:H2'	51:S2:1348:G:C8	2.34	0.62
84:Sg:124:SER:OG	84:Sg:126:ASP:OD1	2.17	0.62
17:LL:47:ALA:O	17:LL:49:ARG:N	2.31	0.62
50:Lt:111:ASN:HA	50:Lt:114:ARG:HB2	1.82	0.62
87:Nm:203:PRO:HD2	87:Nm:206:TRP:HB3	1.82	0.62
4:L5:103:G:OP1	17:LL:69:LYS:NZ	2.32	0.62
4:L5:3689:G:O2'	4:L5:3818:U:OP2	2.16	0.62
4:L5:4302:U:H4'	25:LT:5:LYS:HD3	1.80	0.62
51:S2:155:G:N2	58:SG:56:ASN:OD1	2.33	0.62
52:SA:134:LEU:HD21	52:SA:144:THR:HG21	1.82	0.62
13:LG:187:LYS:HG3	13:LG:198:THR:HA	1.81	0.61
85:NA:96:ILE:HG23	85:NA:104:PHE:HB2	1.82	0.61
64:SM:122:ASP:HA	64:SM:125:GLU:HG3	1.81	0.61
12:LF:222:LYS:HB3	12:LF:231:GLY:HA2	1.83	0.61
87:Nm:453:LEU:O	87:Nm:458:ASN:ND2	2.31	0.61
52:SA:50:ASN:HD21	52:SA:53:ARG:HD2	1.64	0.61
64:SM:19:GLN:OE1	64:SM:88:TRP:NE1	2.24	0.61
78:Sa:12:LYS:HG3	78:Sa:15:ARG:HB2	1.82	0.61
79:Sb:74:THR:OG1	79:Sb:77:CYS:SG	2.57	0.61
4:L5:4537:C:H2'	4:L5:4538:G:C8	2.35	0.61
4:L5:137:G:H2'	4:L5:138:G:H8	1.64	0.61
8:LB:56:ILE:O	8:LB:73:VAL:HA	2.00	0.61
31:LZ:93:LYS:O	31:LZ:97:ASN:ND2	2.32	0.61
51:S2:617:G:H4'	75:SX:88:ASP:HB3	1.82	0.61
86:NB:65:PHE:HB3	86:NB:71:VAL:HG23	1.82	0.61
4:L5:5011:A:H62	4:L5:5037:U:H3	1.49	0.61
30:LY:35:SER:O	30:LY:39:ARG:HB2	2.01	0.61
49:Ls:96:THR:HA	49:Ls:99:ARG:HD3	1.81	0.61
51:S2:562:U:H4'	61:SJ:132:GLN:HB3	1.83	0.61
84:Sg:195:LEU:HA	84:Sg:211:GLY:HA3	1.83	0.61
83:Sf:103:LEU:HD23	83:Sf:105:TYR:H	1.66	0.61
4:L5:435:A:O2'	36:Le:26:ASP:OD1	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2601:A:OP1	38:Lg:40:LYS:NZ	2.34	0.60
34:Lc:20:LEU:O	34:Lc:24:SER:OG	2.19	0.60
14:LH:106:GLN:NE2	14:LH:113:GLU:OE2	2.34	0.60
85:NA:71:ARG:HA	85:NA:74:LYS:HD2	1.82	0.60
4:L5:518:G:H1	4:L5:643:C:H2'	1.64	0.60
52:SA:81:ASN:HA	52:SA:84:GLN:HG3	1.83	0.60
68:SQ:58:LEU:HB3	68:SQ:62:ARG:HD2	1.82	0.60
72:SU:24:LEU:HD13	72:SU:112:VAL:HG12	1.83	0.60
11:LE:112:MET:O	48:Lr:87:ARG:NH1	2.34	0.60
51:S2:1091:C:HO2'	74:SW:2:VAL:N	2.00	0.60
30:LY:52:ASP:HB2	30:LY:110:LYS:HD2	1.83	0.60
51:S2:696:G:N2	51:S2:737:G:O6	2.35	0.60
51:S2:1060:A:O2'	51:S2:1062:A:N7	2.28	0.60
78:Sa:33:ASP:OD2	78:Sa:33:ASP:N	2.34	0.60
51:S2:114:G:O2'	51:S2:382:C:O2'	2.18	0.60
4:L5:4293:U:O2'	46:Lo:81:ARG:NH2	2.35	0.60
63:SL:77:VAL:HG11	63:SL:80:MET:HE3	1.84	0.60
10:LD:197:LYS:HG3	10:LD:202:GLN:HB2	1.84	0.60
52:SA:77:ILE:HD13	52:SA:99:ILE:HB	1.84	0.60
34:Lc:34:THR:HG23	34:Lc:95:ALA:HB2	1.83	0.59
64:SM:80:ASP:OD2	64:SM:80:ASP:N	2.35	0.59
69:SR:126:MET:HE2	69:SR:128:PHE:HE2	1.67	0.59
72:SU:26:SER:HB2	72:SU:110:VAL:HA	1.84	0.59
3:CR:34:MET:HE3	3:CR:100:ILE:HG22	1.84	0.59
15:LI:141:LYS:HD3	15:LI:143:GLN:HE22	1.68	0.59
51:S2:192:C:H41	51:S2:207:G:H21	1.49	0.59
51:S2:1454:A:N1	51:S2:1476:A:O2'	2.31	0.59
4:L5:2601:A:N6	4:L5:2744:A:OP2	2.32	0.59
24:LS:101:THR:HG22	24:LS:104:GLY:H	1.67	0.59
51:S2:1016:U:H5''	65:SN:14:SER:HB3	1.83	0.59
11:LE:149:ILE:HD12	11:LE:271:LEU:HD21	1.84	0.59
51:S2:1568:C:OP1	71:ST:96:SER:OG	2.20	0.59
53:SB:57:ILE:HG22	53:SB:59:SER:H	1.67	0.59
4:L5:1443:A:H62	4:L5:2104:G:N2	2.00	0.59
51:S2:433:A:H5''	60:SI:22:HIS:HB3	1.85	0.59
63:SL:126:VAL:HG12	63:SL:145:VAL:HG22	1.85	0.59
3:CR:317:VAL:HA	3:CR:413:LEU:HA	1.84	0.59
30:LY:30:MET:HB3	30:LY:101:PRO:HG2	1.85	0.59
64:SM:84:LYS:O	64:SM:88:TRP:HB2	2.03	0.59
50:Lt:44:ASP:OD1	50:Lt:44:ASP:N	2.34	0.59
55:SD:142:LEU:HD13	55:SD:150:MET:HE3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SM:62:VAL:HA	64:SM:65:VAL:HG12	1.84	0.59
4:L5:3811:G:O2'	4:L5:3814:U:OP2	2.20	0.59
51:S2:1776:G:OP2	51:S2:1776:G:N2	2.36	0.59
4:L5:2695:A:OP1	42:Lk:35:LYS:NZ	2.34	0.58
10:LD:209:ARG:HH12	10:LD:234:ASP:HB3	1.68	0.58
49:Ls:100:ASP:OD2	49:Ls:100:ASP:N	2.32	0.58
53:SB:124:HIS:HA	53:SB:137:LEU:O	2.04	0.58
4:L5:2487:G:H22	4:L5:2492:C:H1'	1.69	0.58
53:SB:129:THR:HB	53:SB:180:ASP:HA	1.84	0.58
61:SJ:127:ARG:HD2	82:Se:31:ARG:HD3	1.83	0.58
67:SP:18:ARG:HD3	70:SS:90:VAL:HA	1.86	0.58
51:S2:190:G:O2'	51:S2:209:A:N6	2.34	0.58
21:LP:42:ARG:NH1	21:LP:110:ASP:OD2	2.37	0.58
29:LX:156:ILE:HG21	87:NM:318:MET:HE2	1.84	0.58
49:Ls:48:ARG:O	49:Ls:50:LYS:NZ	2.36	0.58
51:S2:913:A:N6	59:SH:98:ARG:O	2.36	0.58
59:SH:154:ILE:HB	59:SH:185:VAL:HG22	1.85	0.58
76:SY:23:MET:HE1	76:SY:75:ILE:HG12	1.84	0.58
4:L5:4531:U:H4'	88:CZ:94:PRO:HD2	1.85	0.58
4:L5:4910:G:N2	20:LO:106:ASP:O	2.37	0.58
51:S2:506:G:OP1	76:SY:108:LYS:NZ	2.34	0.58
70:SS:35:GLY:O	70:SS:97:GLN:NE2	2.35	0.58
84:Sg:38:LYS:HG2	84:Sg:65:PHE:H	1.68	0.58
16:LJ:85:LYS:HB3	16:LJ:115:LEU:HB2	1.85	0.58
21:LP:14:SER:O	21:LP:105:LYS:NZ	2.32	0.58
50:Lt:32:ILE:HG23	50:Lt:37:LEU:HB2	1.86	0.58
51:S2:1482:C:OP1	81:Sd:54:LYS:NZ	2.37	0.58
55:SD:7:LYS:HE2	72:SU:25:THR:HG21	1.84	0.58
50:Lt:28:LEU:O	50:Lt:32:ILE:HB	2.03	0.58
56:SE:180:LEU:HA	56:SE:194:VAL:HA	1.86	0.58
71:ST:96:SER:HB3	71:ST:99:VAL:HB	1.85	0.58
51:S2:94:G:HO2'	51:S2:508:A:HO2'	1.51	0.58
51:S2:1536:G:H2'	51:S2:1537:A:C8	2.38	0.58
51:S2:1550:G:H3'	51:S2:1579:A:H61	1.69	0.58
52:SA:22:GLY:O	52:SA:24:HIS:ND1	2.36	0.58
66:SO:59:GLY:HA2	66:SO:68:GLU:HG2	1.85	0.58
86:NB:62:VAL:HG22	86:NB:74:PHE:HB2	1.85	0.58
7:LA:137:ILE:HD11	7:LA:149:LYS:HB2	1.84	0.57
4:L5:703:G:H2'	4:L5:704:C:H4'	1.86	0.57
50:Lt:110:VAL:HG11	50:Lt:163:PRO:HG2	1.86	0.57
51:S2:1598:G:O2'	77:SZ:80:ARG:O	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:S2:957:A:OP1	66:SO:57:THR:OG1	2.21	0.57
4:L5:2554:U:O2	4:L5:2764:A:N7	2.37	0.57
12:LF:162:ILE:HD13	12:LF:167:ILE:HB	1.86	0.57
33:Lb:53:GLY:O	33:Lb:57:MET:HB2	2.04	0.57
8:LB:41:VAL:HA	8:LB:187:GLY:HA3	1.86	0.57
21:LP:36:ILE:HA	21:LP:39:MET:HE3	1.86	0.57
67:SP:18:ARG:O	70:SS:93:GLY:N	2.35	0.57
24:LS:84:TYR:HB2	24:LS:124:ILE:HG22	1.87	0.57
77:SZ:68:ILE:HB	77:SZ:109:TYR:HB2	1.86	0.57
4:L5:468:U:H3	4:L5:688:U:H3	1.53	0.57
4:L5:5066:U:OP1	21:LP:43:LYS:NZ	2.36	0.57
51:S2:957:A:O2'	51:S2:958:G:N3	2.35	0.57
61:SJ:128:VAL:O	61:SJ:132:GLN:HG2	2.04	0.57
72:SU:26:SER:OG	72:SU:27:ARG:N	2.36	0.57
4:L5:1697:G:N2	4:L5:2084:C:OP1	2.38	0.57
4:L5:4305:G:H1	25:LT:80:VAL:HG21	1.70	0.57
51:S2:587:A:H5'	51:S2:592:C:H42	1.70	0.57
77:SZ:48:VAL:HG23	77:SZ:80:ARG:HD2	1.87	0.57
56:SE:45:ILE:HA	56:SE:61:VAL:HG11	1.87	0.57
85:NA:96:ILE:HD13	86:NB:62:VAL:HG12	1.87	0.57
32:La:37:GLY:H	32:La:41:HIS:HB2	1.70	0.56
4:L5:469:C:N3	11:LE:105:ARG:NH1	2.52	0.56
4:L5:4274:A:H2'	4:L5:4275:G:C8	2.40	0.56
4:L5:4457:U:H1'	8:LB:252:ALA:HB3	1.87	0.56
6:L8:82:A:H62	6:L8:84:A:H3'	1.70	0.56
27:LV:45:ILE:HG21	27:LV:53:PRO:HB3	1.87	0.56
50:Lt:11:LYS:O	50:Lt:63:THR:HA	2.06	0.56
51:S2:1616:U:OP2	67:SP:43:ARG:NH2	2.38	0.56
72:SU:67:LYS:HA	81:Sd:44:ARG:HD2	1.88	0.56
3:CR:322:VAL:O	3:CR:391:ILE:HA	2.05	0.56
4:L5:4139:G:H4'	4:L5:4146:G:H22	1.70	0.56
51:S2:1422:G:O2'	51:S2:1424:G:OP2	2.22	0.56
61:SJ:158:ASP:OD1	61:SJ:159:PHE:N	2.31	0.56
84:Sg:65:PHE:O	84:Sg:82:SER:OG	2.22	0.56
3:CR:38:ILE:HG12	3:CR:94:VAL:HG13	1.88	0.56
72:SU:56:MET:HB2	72:SU:86:LYS:HB3	1.87	0.56
11:LE:190:HIS:HB3	11:LE:193:PHE:HD2	1.71	0.56
63:SL:99:TYR:O	63:SL:101:ARG:N	2.39	0.56
85:NA:107:THR:HG22	85:NA:108:LYS:HD2	1.88	0.56
46:Lo:71:GLU:HG3	46:Lo:80:LYS:HG2	1.87	0.56
59:SH:63:PHE:HA	59:SH:95:ILE:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SO:34:PHE:HB3	66:SO:41:PHE:HB2	1.88	0.56
4:L5:2658:G:N2	4:L5:2676:A:OP2	2.39	0.56
35:Ld:64:ILE:HG23	35:Ld:68:LEU:HD23	1.88	0.56
7:LA:28:ARG:HB2	7:LA:123:ARG:HG3	1.87	0.56
18:LM:50:MET:HB3	18:LM:55:MET:HE2	1.87	0.56
51:S2:922:A:OP1	74:SW:28:ARG:NH2	2.38	0.56
11:LE:244:GLU:O	11:LE:248:ILE:HD12	2.06	0.55
26:LU:65:ARG:HH21	26:LU:67:LYS:HA	1.71	0.55
73:SV:64:GLU:O	73:SV:68:SER:OG	2.23	0.55
4:L5:1281:G:OP1	9:LC:316:LYS:NZ	2.38	0.55
8:LB:254:ILE:HG23	8:LB:266:VAL:HG11	1.89	0.55
29:LX:82:THR:HG22	29:LX:155:ILE:HG23	1.88	0.55
55:SD:172:VAL:HG22	55:SD:185:LYS:HG3	1.88	0.55
87:NM:456:MET:HE2	87:NM:457:GLU:N	2.21	0.55
4:L5:2711:G:OP2	23:LR:39:GLN:NE2	2.38	0.55
4:L5:3788:C:N4	4:L5:3812:C:OP2	2.38	0.55
13:LG:244:PRO:HA	13:LG:247:VAL:HG22	1.88	0.55
50:Lt:154:ASP:HB2	50:Lt:159:ALA:HB3	1.89	0.55
4:L5:4431:U:OP2	15:LI:3:ARG:NH2	2.39	0.55
4:L5:4472:G:O2'	44:Lm:100:TYR:O	2.23	0.55
4:L5:4745:G:H1	4:L5:4955:A:N6	2.05	0.55
37:Lf:36:ARG:O	37:Lf:39:THR:OG1	2.24	0.55
56:SE:62:LYS:HA	56:SE:80:ILE:HD11	1.89	0.55
63:SL:75:GLY:HA3	63:SL:88:ILE:HD12	1.89	0.55
87:NM:175:LEU:HD22	87:NM:222:LEU:HG	1.89	0.55
3:CR:118:LYS:NZ	3:CR:142:ASP:O	2.39	0.55
3:CR:373:PRO:HD2	3:CR:376:GLU:HG3	1.88	0.55
47:Lp:5:THR:HG21	47:Lp:9:GLY:H	1.72	0.55
51:S2:640:A:H2'	51:S2:641:A:C8	2.41	0.55
57:SF:95:HIS:HD2	77:SZ:106:GLN:HB3	1.71	0.55
63:SL:57:ASP:HB3	63:SL:60:CYS:HB2	1.89	0.55
87:NM:454:ASP:O	87:NM:459:LYS:NZ	2.40	0.55
53:SB:82:ARG:HD3	53:SB:103:MET:HE2	1.89	0.55
54:SC:204:ILE:HB	54:SC:211:LYS:HD3	1.89	0.55
56:SE:42:LEU:HD11	56:SE:46:ILE:HD11	1.89	0.55
73:SV:41:LYS:HE2	73:SV:41:LYS:H	1.71	0.55
56:SE:31:PRO:HA	56:SE:81:THR:HB	1.89	0.55
51:S2:562:U:H2'	51:S2:563:G:C8	2.42	0.54
51:S2:895:G:H8	51:S2:896:U:H4'	1.72	0.54
52:SA:143:PRO:HB3	73:SV:34:MET:HE3	1.88	0.54
49:Ls:138:PHE:HB2	49:Ls:143:ILE:HB	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SB:183:GLU:HA	53:SB:186:ASN:HB2	1.88	0.54
72:SU:59:LYS:HB2	72:SU:84:ILE:HB	1.89	0.54
4:L5:1942:A:H2'	4:L5:1943:A:C8	2.42	0.54
12:LF:182:TYR:HB3	12:LF:200:ARG:HG3	1.89	0.54
78:Sa:40:VAL:HB	78:Sa:69:VAL:HG12	1.89	0.54
84:Sg:31:ILE:HG13	84:Sg:43:TRP:HB2	1.89	0.54
86:NB:155:GLU:O	86:NB:158:LYS:NZ	2.39	0.54
4:L5:3717:A:H2'	4:L5:3718:A:C8	2.43	0.54
4:L5:4992:G:H2'	4:L5:4993:G:C8	2.42	0.54
10:LD:60:ILE:HD11	10:LD:93:THR:HA	1.89	0.54
37:Lf:33:VAL:HG13	37:Lf:38:GLU:HG3	1.89	0.54
51:S2:959:G:OP1	66:SO:104:ARG:NH2	2.41	0.54
4:L5:1328:G:O2'	4:L5:2349:A:OP1	2.26	0.54
20:LO:61:ARG:HA	20:LO:70:PRO:HD2	1.88	0.54
51:S2:687:C:OP2	74:SW:32:LYS:NZ	2.38	0.54
63:SL:104:LYS:HZ3	75:SX:8:ARG:NH1	2.06	0.54
68:SQ:16:LYS:H	68:SQ:19:ALA:HB3	1.73	0.54
4:L5:1553:A:N6	4:L5:1574:G:H1'	2.22	0.54
4:L5:1994:C:H2'	4:L5:1995:G:H8	1.72	0.54
4:L5:4699:U:H1'	4:L5:4700:A:H5''	1.90	0.54
13:LG:62:ARG:O	13:LG:66:GLN:HG3	2.08	0.54
51:S2:528:A:H2'	51:S2:529:A:C8	2.43	0.54
52:SA:36:GLN:NE2	73:SV:67:ASP:OD2	2.40	0.54
52:SA:84:GLN:HB3	52:SA:100:ALA:HB1	1.90	0.54
65:SN:87:ASP:OD1	65:SN:87:ASP:N	2.38	0.54
3:CR:312:LEU:HD11	3:CR:320:LEU:HD11	1.88	0.54
4:L5:3619:G:H22	4:L5:3624:A:H1'	1.73	0.54
17:LL:16:LYS:O	17:LL:21:ARG:NH2	2.35	0.54
55:SD:31:GLU:OE2	55:SD:31:GLU:N	2.38	0.54
16:LJ:13:ARG:NH1	16:LJ:154:LYS:O	2.32	0.54
16:LJ:120:ASP:OD2	16:LJ:122:SER:OG	2.25	0.54
17:LL:108:GLU:N	17:LL:108:GLU:OE2	2.40	0.54
26:LU:28:PRO:HB2	26:LU:34:MET:HG2	1.90	0.54
46:Lo:33:LEU:HA	46:Lo:38:LYS:HG2	1.90	0.54
51:S2:65:C:N4	58:SG:134:GLY:O	2.40	0.54
51:S2:1753:C:H4'	51:S2:1780:G:H1	1.72	0.54
52:SA:8:LEU:HD11	73:SV:39:VAL:HG11	1.90	0.54
63:SL:80:MET:HE2	63:SL:120:VAL:HG23	1.90	0.54
73:SV:1:MET:N	73:SV:10:ASP:OD1	2.32	0.54
84:Sg:11:LEU:HB2	84:Sg:307:VAL:HB	1.89	0.54
85:NA:94:VAL:HB	85:NA:106:ILE:HG23	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2306:G:OP1	36:Le:128:ARG:NH1	2.41	0.54
4:L5:4740:G:O6	4:L5:4959:U:O2	2.25	0.54
49:Ls:99:ARG:HD2	49:Ls:204:LEU:HD11	1.89	0.54
51:S2:1315:U:OP1	62:SK:1:MET:N	2.40	0.54
11:LE:165:LEU:HD11	11:LE:176:THR:HG22	1.91	0.53
8:LB:132:LYS:HA	8:LB:135:LYS:HE2	1.91	0.53
19:LN:158:HIS:HB3	19:LN:161:MET:HG3	1.91	0.53
54:SC:78:LEU:HD12	54:SC:81:ILE:HD11	1.90	0.53
55:SD:125:PHE:O	55:SD:129:SER:OG	2.25	0.53
73:SV:33:GLN:HE21	73:SV:52:THR:HG21	1.73	0.53
4:L5:280:G:OP1	19:LN:47:LYS:NZ	2.41	0.53
4:L5:418:A:N6	6:L8:16:G:H1'	2.22	0.53
4:L5:1362:G:OP1	17:LL:39:ARG:NH2	2.42	0.53
4:L5:4220:A:H2'	4:L5:4222:G:H5''	1.89	0.53
7:LA:117:GLU:OE2	7:LA:163:ARG:NH2	2.39	0.53
15:LI:31:ILE:HG22	15:LI:62:SER:HB2	1.90	0.53
55:SD:131:ALA:HA	55:SD:191:PRO:HD3	1.89	0.53
58:SG:85:ARG:O	58:SG:87:ARG:NH1	2.41	0.53
49:Ls:18:ILE:HG23	49:Ls:68:HIS:CE1	2.43	0.53
87:Nm:441:LEU:HA	87:Nm:444:MET:HE1	1.90	0.53
4:L5:3906:A:H2'	9:LC:69:THR:HG23	1.91	0.53
4:L5:4387:C:OP2	4:L5:4532:U:O2'	2.25	0.53
72:SU:79:ARG:NH1	81:Sd:56:ASP:O	2.42	0.53
59:SH:72:PHE:O	59:SH:75:ILE:O	2.27	0.53
4:L5:2020:U:H2'	4:L5:2021:G:H8	1.71	0.53
30:LY:38:LEU:HA	30:LY:41:LYS:HB3	1.91	0.53
10:LD:223:PHE:HB3	10:LD:226:TYR:HB2	1.91	0.53
52:SA:50:ASN:HD21	52:SA:53:ARG:HH11	1.57	0.53
53:SB:222:LYS:NZ	53:SB:223:PHE:O	2.42	0.53
87:Nm:163:LEU:HD12	87:Nm:198:LEU:HD22	1.89	0.53
5:L7:118:C:OP1	10:LD:256:LYS:NZ	2.38	0.53
11:LE:101:ASN:OD1	11:LE:105:ARG:NH2	2.41	0.53
79:Sb:50:ALA:O	79:Sb:52:THR:N	2.42	0.53
84:Sg:133:ASN:HD21	84:Sg:137:VAL:HB	1.74	0.53
85:NA:120:TYR:HD1	86:NB:90:ILE:HG23	1.74	0.53
4:L5:2123:C:H1'	11:LE:72:LYS:HD2	1.91	0.53
54:SC:130:ILE:HG23	54:SC:162:ILE:HD11	1.91	0.53
75:SX:49:GLY:O	75:SX:99:GLU:HA	2.09	0.53
4:L5:1812:C:H5''	33:Lb:56:LYS:HD2	1.91	0.52
4:L5:2324:C:O2'	36:Le:98:GLU:OE2	2.22	0.52
6:L8:141:C:H5''	19:LN:60:VAL:HG11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LP:27:LYS:HG2	21:LP:63:TYR:CG	2.45	0.52
26:LU:38:ASN:OD1	26:LU:90:TYR:OH	2.27	0.52
70:SS:46:ARG:HG2	71:ST:35:ASP:HB2	1.91	0.52
4:L5:452:A:H4'	4:L5:453:G:H5'	1.91	0.52
4:L5:2894:A:H62	4:L5:3607:U:H3	1.56	0.52
9:LC:152:LEU:HD23	9:LC:251:ILE:HG12	1.91	0.52
12:LF:236:ARG:HB3	12:LF:239:GLN:HB2	1.90	0.52
20:LO:9:LEU:HD23	20:LO:118:MET:HB3	1.91	0.52
50:Lt:121:LEU:O	50:Lt:123:ARG:NH1	2.42	0.52
51:S2:1109:C:C5	69:SR:124:VAL:HG23	2.44	0.52
87:NM:245:ILE:HB	87:NM:281:TYR:HB3	1.89	0.52
4:L5:1468:C:OP1	32:La:132:ARG:NH2	2.42	0.52
25:LT:82:GLY:HA3	33:Lb:16:TRP:HB2	1.91	0.52
75:SX:108:LYS:HD3	75:SX:108:LYS:H	1.74	0.52
4:L5:407:A:O2'	4:L5:410:A:OP1	2.24	0.52
4:L5:1998:A:N7	49:Ls:55:MET:HE2	2.24	0.52
34:Lc:38:ILE:HD11	34:Lc:46:VAL:HG21	1.92	0.52
49:Ls:109:ALA:HB3	49:Ls:185:PHE:HE1	1.74	0.52
51:S2:530:U:H2'	51:S2:531:A:H8	1.73	0.52
51:S2:1129:G:H5'	79:Sb:19:HIS:HB2	1.91	0.52
53:SB:128:LYS:HZ3	53:SB:132:GLY:HA2	1.73	0.52
68:SQ:70:VAL:HG11	68:SQ:84:ILE:HG23	1.91	0.52
4:L5:513:U:N3	4:L5:516:C:OP2	2.28	0.52
12:LF:105:VAL:HG13	12:LF:136:VAL:HG12	1.92	0.52
29:LX:64:SER:HB2	39:Lh:69:LEU:HD13	1.92	0.52
50:Lt:106:PHE:O	50:Lt:110:VAL:HG23	2.09	0.52
51:S2:1473:G:O2'	51:S2:1475:G:N2	2.43	0.52
51:S2:1860:A:H3'	78:Sa:8:ASN:HB3	1.89	0.52
87:NM:339:ARG:NH2	87:NM:388:GLU:OE1	2.43	0.52
4:L5:1380:G:N2	4:L5:1381:U:O4	2.37	0.52
4:L5:3641:U:H5	4:L5:3646:A:N7	2.08	0.52
4:L5:4260:U:H2'	4:L5:4261:C:C6	2.44	0.52
34:Lc:38:ILE:HG21	34:Lc:63:TYR:HB3	1.91	0.52
51:S2:1606:G:H1'	51:S2:1633:A:N6	2.24	0.52
84:Sg:72:SER:OG	84:Sg:74:ASP:O	2.25	0.52
3:CR:108:LYS:NZ	67:SP:140:ARG:O	2.43	0.52
10:LD:209:ARG:HA	10:LD:212:MET:HE2	1.91	0.52
24:LS:127:MET:HB3	25:LT:153:PRO:HG2	1.92	0.52
87:NM:233:ILE:HA	87:NM:364:PRO:HA	1.92	0.52
4:L5:480:C:OP1	48:Lr:67:ARG:NH1	2.37	0.52
51:S2:377:G:H5'	60:SI:98:LYS:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:NM:179:ASN:HA	87:NM:252:LYS:HD3	1.91	0.52
87:NM:226:ILE:HG21	87:NM:263:LEU:HB3	1.92	0.52
51:S2:72:C:H1'	51:S2:73:C:H2'	1.92	0.52
51:S2:455:A:H2'	51:S2:456:C:C6	2.45	0.52
51:S2:1101:U:H2'	51:S2:1102:G:C8	2.45	0.52
10:LD:152:ARG:HG3	10:LD:154:THR:HG23	1.92	0.52
26:LU:24:ASP:HB3	26:LU:111:GLU:HA	1.92	0.52
51:S2:1308:U:H1'	83:Sf:135:HIS:HE1	1.75	0.52
70:SS:63:GLU:O	70:SS:67:VAL:HG23	2.10	0.52
4:L5:184:U:H1'	4:L5:254:G:H22	1.75	0.51
4:L5:1503:A:H4'	4:L5:1504:G:H5'	1.92	0.51
4:L5:2474:G:N2	4:L5:2502:G:O2'	2.43	0.51
8:LB:80:GLU:OE1	8:LB:323:TYR:OH	2.25	0.51
4:L5:28:C:OP2	19:LN:189:ARG:NH1	2.42	0.51
4:L5:1801:A:H4'	25:LT:102:ARG:HH21	1.74	0.51
30:LY:13:LYS:O	30:LY:17:ARG:HG2	2.10	0.51
51:S2:326:C:O2	51:S2:327:G:N2	2.44	0.51
58:SG:159:ARG:HD2	58:SG:171:THR:HB	1.92	0.51
84:Sg:42:MET:HE2	84:Sg:92:LEU:HD23	1.92	0.51
4:L5:4618:G:H5''	27:LV:15:ARG:HB3	1.93	0.51
5:L7:117:G:H5'	10:LD:256:LYS:HD3	1.91	0.51
33:Lb:49:HIS:HB3	33:Lb:52:LYS:HE2	1.92	0.51
51:S2:466:G:O2'	58:SG:72:ARG:NH2	2.43	0.51
64:SM:93:LYS:NZ	64:SM:102:LYS:O	2.44	0.51
87:NM:301:LEU:O	87:NM:443:LYS:NZ	2.37	0.51
4:L5:3594:C:O2	4:L5:3597:G:N2	2.43	0.51
4:L5:3710:G:N3	4:L5:3711:A:N6	2.58	0.51
60:SI:194:GLU:HG3	63:SL:10:TYR:CD1	2.45	0.51
64:SM:60:MET:HA	64:SM:63:LYS:HB3	1.92	0.51
76:SY:11:LYS:HB2	76:SY:24:VAL:HG12	1.91	0.51
4:L5:3717:A:OP2	4:L5:3735:G:N2	2.36	0.51
13:LG:106:THR:OG1	13:LG:107:LYS:N	2.36	0.51
51:S2:429:C:O2'	51:S2:811:A:N1	2.39	0.51
41:Lj:54:LYS:O	41:Lj:58:THR:HB	2.11	0.51
86:NB:48:LEU:HA	86:NB:51:LEU:HB2	1.91	0.51
51:S2:107:A:H2'	51:S2:108:G:C8	2.46	0.51
51:S2:940:U:H3	51:S2:1002:U:H3	1.59	0.51
79:Sb:67:THR:OG1	79:Sb:70:LYS:O	2.29	0.51
4:L5:5027:C:H42	60:SI:170:LYS:HE3	1.74	0.51
14:LH:89:ARG:NH1	14:LH:147:GLU:OE2	2.44	0.51
26:LU:117:ILE:HG21	86:NB:17:GLN:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Ls:28:PHE:HB3	49:Ls:89:VAL:HB	1.92	0.51
51:S2:846:G:H2'	56:SE:19:MET:HG2	1.92	0.51
51:S2:996:A:H2'	51:S2:997:A:C8	2.46	0.51
69:SR:126:MET:HE2	69:SR:128:PHE:CE2	2.46	0.51
3:CR:305:VAL:O	3:CR:309:LEU:HD12	2.11	0.51
4:L5:3868:G:H22	4:L5:3900:G:H1'	1.76	0.51
4:L5:4940:C:OP2	11:LE:219:LYS:NZ	2.35	0.51
71:ST:39:LEU:O	71:ST:96:SER:HB2	2.11	0.51
87:NM:152:LEU:HD13	87:NM:157:THR:HA	1.92	0.51
4:L5:6:C:H5''	13:LG:197:LYS:HB3	1.93	0.51
4:L5:2758:G:O2'	4:L5:2765:A:N3	2.36	0.51
7:LA:101:VAL:HG22	7:LA:165:VAL:HG22	1.93	0.51
13:LG:165:GLU:HA	13:LG:168:VAL:HG22	1.93	0.51
24:LS:13:VAL:HG22	24:LS:29:ARG:HB2	1.92	0.51
4:L5:4093:G:H2'	4:L5:4094:G:C8	2.46	0.50
37:Lf:6:TRP:CE2	37:Lf:102:ARG:HD3	2.46	0.50
50:Lt:15:LEU:HD11	50:Lt:28:LEU:HB3	1.92	0.50
50:Lt:90:ARG:NH2	50:Lt:95:GLN:O	2.45	0.50
51:S2:379:C:O2	60:SI:5:ARG:NE	2.43	0.50
66:SO:85:CYS:HB3	66:SO:124:MET:HE1	1.92	0.50
4:L5:496:G:H2'	4:L5:498:C:H5''	1.93	0.50
4:L5:4363:A:H5''	46:Lo:36:GLN:HG2	1.93	0.50
11:LE:198:SER:OG	11:LE:288:PHE:OXT	2.27	0.50
25:LT:75:VAL:HG22	25:LT:88:ARG:HD2	1.93	0.50
56:SE:229:GLY:HA2	56:SE:235:TRP:CD1	2.46	0.50
4:L5:1952:G:H4'	24:LS:93:MET:HG2	1.93	0.50
51:S2:874:G:H2'	51:S2:875:A:H8	1.76	0.50
51:S2:928:G:H2'	51:S2:929:G:C8	2.45	0.50
51:S2:1740:C:OP1	60:SI:44:HIS:ND1	2.45	0.50
68:SQ:51:LEU:HD13	68:SQ:81:ILE:HG23	1.93	0.50
69:SR:41:ILE:HD13	69:SR:50:ILE:HD12	1.93	0.50
4:L5:1308:C:H2'	4:L5:1309:C:C6	2.47	0.50
4:L5:4478:G:O2'	4:L5:4602:A:N1	2.42	0.50
27:LV:92:ASP:OD1	27:LV:92:ASP:N	2.40	0.50
30:LY:47:MET:HE3	30:LY:48:PRO:HD2	1.93	0.50
51:S2:1748:G:O6	51:S2:1786:U:O4	2.30	0.50
53:SB:77:ASP:OD1	53:SB:77:ASP:N	2.42	0.50
4:L5:4927:G:H5'	4:L5:4928:C:H5	1.77	0.50
11:LE:279:ASN:H	37:Lf:4:ARG:HH12	1.59	0.50
19:LN:138:PHE:HA	19:LN:143:ARG:HD2	1.94	0.50
35:Ld:26:THR:HG22	35:Ld:85:ARG:HH11	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:S2:527:C:H2'	51:S2:528:A:H8	1.77	0.50
51:S2:1536:G:H2'	51:S2:1537:A:H8	1.74	0.50
54:SC:191:VAL:HG11	54:SC:236:PHE:HA	1.94	0.50
84:Sg:38:LYS:HD3	84:Sg:64:HIS:H	1.76	0.50
4:L5:2705:G:H1	4:L5:2710:C:H5	1.60	0.50
64:SM:128:PHE:HA	64:SM:131:LYS:HE3	1.94	0.50
3:CR:24:LEU:HD21	3:CR:112:ILE:HD13	1.94	0.50
4:L5:150:U:OP2	13:LG:200:THR:OG1	2.30	0.50
4:L5:2640:G:H2'	4:L5:2641:A:C8	2.46	0.50
6:L8:58:G:O6	41:Lj:63:ARG:NH1	2.44	0.50
49:Ls:171:GLU:HA	49:Ls:174:LEU:HG	1.92	0.50
50:Lt:130:LYS:HG2	50:Lt:152:ILE:HD13	1.94	0.50
59:SH:69:LEU:O	59:SH:73:GLN:HG2	2.12	0.50
4:L5:4537:C:H2'	4:L5:4538:G:H8	1.77	0.50
47:Lp:70:THR:OG1	47:Lp:72:ASN:O	2.25	0.50
62:SK:11:ILE:HG21	62:SK:45:VAL:HG22	1.94	0.50
10:LD:62:CYS:HB3	10:LD:105:LEU:HD22	1.94	0.50
51:S2:560:A:H5'	61:SJ:174:LYS:HG2	1.94	0.50
54:SC:166:ARG:HH12	54:SC:252:THR:HG21	1.76	0.50
60:SI:134:GLU:OE2	60:SI:134:GLU:N	2.34	0.50
4:L5:3664:G:H2'	4:L5:3665:G:H8	1.77	0.49
28:LW:102:LYS:HD3	28:LW:105:ARG:HH22	1.77	0.49
43:Ll:28:ARG:HA	43:Ll:33:ASN:HD22	1.77	0.49
61:SJ:33:GLY:HA3	82:Se:38:TYR:CG	2.47	0.49
84:Sg:17:TRP:HB2	84:Sg:36:ARG:HD2	1.94	0.49
4:L5:496:G:N2	4:L5:658:C:O2	2.40	0.49
4:L5:4765:G:OP1	14:LH:23:ARG:NE	2.45	0.49
19:LN:178:HIS:HA	19:LN:181:HIS:CE1	2.48	0.49
49:Ls:180:ILE:HG22	49:Ls:182:PRO:HD3	1.93	0.49
51:S2:615:C:O2	82:Se:11:LYS:NZ	2.45	0.49
52:SA:123:VAL:HG12	52:SA:145:ILE:HB	1.94	0.49
53:SB:134:LEU:HB3	53:SB:219:LYS:HB2	1.94	0.49
57:SF:145:ARG:HB2	80:Sc:48:GLY:HA3	1.93	0.49
87:Nm:371:VAL:HG23	87:Nm:375:PHE:HD2	1.77	0.49
87:Nm:441:LEU:O	87:Nm:445:LYS:NZ	2.39	0.49
4:L5:210:C:OP1	30:LY:59:ARG:NE	2.45	0.49
4:L5:1994:C:H2'	4:L5:1995:G:C8	2.47	0.49
4:L5:2493:G:H21	6:L8:126:C:H5''	1.77	0.49
48:Lr:90:LEU:HG	48:Lr:111:ILE:HG23	1.93	0.49
59:SH:178:LYS:NZ	59:SH:184:ASP:OD1	2.46	0.49
66:SO:56:VAL:HG12	66:SO:81:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:S2:414:A:OP1	51:S2:814:U:O2'	2.31	0.49
51:S2:1801:A:H2'	51:S2:1802:C:C6	2.47	0.49
4:L5:1332:C:H2'	4:L5:1333:A:H8	1.76	0.49
4:L5:4499:G:C2	4:L5:4529:G:H1'	2.47	0.49
18:LM:81:ASP:OD1	18:LM:81:ASP:N	2.45	0.49
51:S2:1845:A:H2'	51:S2:1846:G:C8	2.48	0.49
13:LG:207:VAL:O	13:LG:212:LYS:NZ	2.41	0.49
16:LJ:19:LYS:HG2	16:LJ:133:VAL:HB	1.95	0.49
42:Lk:36:VAL:HG13	42:Lk:43:TYR:HB2	1.95	0.49
51:S2:641:A:OP1	61:SJ:40:LYS:NZ	2.32	0.49
51:S2:1752:C:H42	51:S2:1781:A:H2	1.59	0.49
87:Nm:106:ALA:H	87:Nm:285:VAL:HG23	1.76	0.49
4:L5:1175:A:H2	4:L5:1185:G:H22	1.60	0.49
5:L7:119:U:H2'	10:LD:261:VAL:HG11	1.93	0.49
32:La:35:ALA:O	32:La:41:HIS:ND1	2.45	0.49
51:S2:943:U:O2'	66:SO:135:ILE:O	2.30	0.49
51:S2:1506:A:O2'	51:S2:1508:A:OP2	2.31	0.49
55:SD:56:GLN:O	55:SD:60:GLY:CA	2.60	0.49
56:SE:17:HIS:HB2	56:SE:108:ARG:HA	1.94	0.49
4:L5:2748:C:H4'	38:Lg:65:MET:HE2	1.93	0.49
5:L7:12:U:OP2	5:L7:67:C:O2'	2.29	0.49
6:L8:16:G:HO2'	6:L8:17:A:H8	1.60	0.49
32:La:119:LYS:HA	32:La:140:VAL:HG22	1.93	0.49
51:S2:51:U:H2'	51:S2:52:G:C8	2.48	0.49
74:SW:24:GLN:NE2	74:SW:64:ASN:OD1	2.46	0.49
3:CR:330:ARG:NH1	3:CR:344:LEU:O	2.46	0.49
4:L5:5006:U:H4'	4:L5:5007:A:H5'	1.95	0.49
8:LB:224:LYS:HG2	8:LB:340:THR:HG22	1.93	0.49
51:S2:1240:A:C8	67:SP:100:LYS:HD2	2.47	0.49
55:SD:210:ILE:HD13	69:SR:16:ILE:HG13	1.95	0.49
4:L5:1704:C:OP1	12:LF:43:ARG:NH1	2.46	0.49
4:L5:2382:A:N1	4:L5:2829:U:O2'	2.45	0.49
4:L5:5002:U:OP2	8:LB:385:LYS:NZ	2.44	0.49
19:LN:116:LEU:HD22	19:LN:135:ILE:HD11	1.95	0.49
49:Ls:125:ALA:HA	49:Ls:154:ILE:HG23	1.95	0.49
51:S2:86:C:OP2	51:S2:149:A:O2'	2.28	0.49
51:S2:1563:G:H5''	71:ST:121:ARG:HH21	1.78	0.49
56:SE:192:ILE:HD12	56:SE:243:GLY:HA3	1.95	0.49
4:L5:654:C:N3	4:L5:655:C:N4	2.60	0.48
4:L5:1333:A:H2'	4:L5:1334:A:C8	2.48	0.48
4:L5:4754:G:N7	11:LE:279:ASN:HB2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LO:194:GLU:O	20:LO:198:THR:HG23	2.13	0.48
72:SU:80:PHE:HB3	81:Sd:52:PHE:HB3	1.94	0.48
48:Lr:28:GLU:HG2	48:Lr:31:ASN:HB2	1.94	0.48
51:S2:606:G:H8	82:Se:58:ASN:HD21	1.60	0.48
59:SH:18:GLU:O	59:SH:21:SER:OG	2.26	0.48
85:NA:93:ARG:NH2	85:NA:107:THR:OG1	2.45	0.48
87:NM:119:PHE:HB2	87:NM:258:ARG:HH22	1.78	0.48
87:NM:192:TYR:HD1	87:NM:196:PHE:HE2	1.60	0.48
4:L5:68:U:OP1	19:LN:178:HIS:ND1	2.35	0.48
4:L5:1210:C:H41	12:LF:66:ARG:NH1	2.11	0.48
4:L5:5011:A:N6	4:L5:5037:U:H3	2.11	0.48
25:LT:27:LEU:O	25:LT:31:MET:HG3	2.13	0.48
51:S2:868:G:C5	59:SH:115:LYS:HG3	2.48	0.48
51:S2:1597:C:H4'	51:S2:1603:G:C6	2.48	0.48
57:SF:41:VAL:HG11	57:SF:68:ILE:HG22	1.94	0.48
3:CR:87:LYS:HB3	3:CR:87:LYS:HE3	1.61	0.48
4:L5:1339:U:H2'	4:L5:1340:C:C6	2.48	0.48
8:LB:369:ASP:OD2	8:LB:371:THR:OG1	2.31	0.48
19:LN:63:ARG:NH1	19:LN:131:GLU:OE1	2.45	0.48
35:Ld:24:GLU:OE2	35:Ld:87:ARG:NH2	2.38	0.48
58:SG:137:ARG:HB3	58:SG:140:ARG:HG3	1.93	0.48
87:NM:350:HIS:HB2	87:NM:371:VAL:HG11	1.94	0.48
4:L5:717:U:H2'	4:L5:718:C:C6	2.49	0.48
49:Ls:65:ILE:HG21	49:Ls:79:LEU:HD21	1.96	0.48
51:S2:150:A:N6	51:S2:168:C:C2	2.82	0.48
51:S2:1024:A:OP2	65:SN:124:ARG:NH2	2.41	0.48
65:SN:64:ARG:HD3	65:SN:70:LYS:HD3	1.95	0.48
71:ST:42:HIS:HB2	71:ST:83:GLN:HA	1.96	0.48
4:L5:1604:G:H2'	4:L5:1605:G:C8	2.48	0.48
4:L5:4128:A:H1'	13:LG:35:ARG:HG3	1.96	0.48
9:LC:163:LYS:HB2	9:LC:166:GLU:HG2	1.95	0.48
11:LE:161:ARG:O	11:LE:182:ASN:ND2	2.47	0.48
13:LG:90:GLN:OE1	13:LG:90:GLN:N	2.36	0.48
17:LL:18:TRP:CD1	17:LL:18:TRP:H	2.32	0.48
29:LX:143:ASP:OD1	29:LX:143:ASP:N	2.35	0.48
34:Lc:37:MET:HG3	34:Lc:97:ILE:HD11	1.94	0.48
51:S2:527:C:H2'	51:S2:528:A:C8	2.48	0.48
51:S2:1650:A:H5''	68:SQ:139:ALA:HB2	1.96	0.48
53:SB:165:ARG:HG2	53:SB:169:MET:HE2	1.95	0.48
70:SS:67:VAL:O	70:SS:71:MET:HG3	2.14	0.48
15:LI:36:LEU:HD11	15:LI:69:ARG:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LX:38:LYS:HA	29:LX:38:LYS:HD2	1.67	0.48
29:LX:82:THR:HG21	39:Lh:37:THR:HG22	1.95	0.48
31:LZ:40:HIS:HD1	31:LZ:74:VAL:HG13	1.78	0.48
50:Lt:10:ILE:HD13	50:Lt:65:GLN:HG3	1.95	0.48
51:S2:468:A:OP1	58:SG:96:SER:OG	2.28	0.48
51:S2:1228:A:H2'	51:S2:1229:G:H8	1.75	0.48
51:S2:1232:U:H2'	51:S2:1233:G:H8	1.77	0.48
69:SR:84:TYR:HD1	69:SR:86:PRO:HD2	1.79	0.48
78:Sa:25:ASN:OD1	78:Sa:25:ASN:N	2.44	0.48
84:Sg:284:PRO:HB3	84:Sg:304:ASP:HB3	1.95	0.48
12:LF:128:ALA:O	12:LF:132:MET:HG3	2.12	0.48
15:LI:103:LEU:HD12	15:LI:111:LEU:HD21	1.94	0.48
16:LJ:167:GLN:HA	16:LJ:172:GLY:H	1.79	0.48
24:LS:15:ARG:HD2	24:LS:25:PRO:HG2	1.96	0.48
50:Lt:42:VAL:O	50:Lt:46:ILE:HG12	2.13	0.48
51:S2:1232:U:H2'	51:S2:1233:G:C8	2.49	0.48
51:S2:1255:G:OP1	51:S2:1256:G:O2'	2.29	0.48
58:SG:136:LYS:NZ	58:SG:175:LYS:O	2.44	0.48
62:SK:23:ALA:HB3	62:SK:69:TRP:HZ3	1.79	0.48
70:SS:22:GLY:HA2	70:SS:56:ALA:HB3	1.95	0.48
86:NB:80:GLN:HB3	86:NB:89:THR:HG22	1.96	0.48
4:L5:433:A:C2	4:L5:3867:A:H4'	2.49	0.48
4:L5:500:G:H1'	4:L5:504:G:H3'	1.95	0.48
4:L5:1097:C:H2'	4:L5:1098:G:H8	1.77	0.48
4:L5:1332:C:H2'	4:L5:1333:A:C8	2.49	0.48
4:L5:1998:A:H62	49:Ls:55:MET:HE2	1.79	0.48
8:LB:168:MET:HB3	8:LB:168:MET:HE3	1.80	0.48
23:LR:42:ARG:HA	23:LR:45:ILE:HD12	1.96	0.48
43:Ll:38:ASN:HB3	43:Ll:41:ARG:HG2	1.95	0.48
66:SO:56:VAL:HG23	66:SO:60:MET:HE2	1.96	0.48
4:L5:2280:G:OP1	36:Le:48:ARG:NH2	2.46	0.48
4:L5:3707:U:H2'	4:L5:3708:C:C6	2.49	0.48
5:L7:12:U:O3'	5:L7:109:U:O2'	2.26	0.48
15:LI:73:ASN:HB2	15:LI:87:MET:HE1	1.95	0.48
43:Ll:20:ASN:ND2	43:Ll:42:ARG:O	2.33	0.48
51:S2:66:G:N2	51:S2:82:G:H21	2.11	0.48
52:SA:10:MET:HG2	52:SA:15:VAL:HG23	1.95	0.48
55:SD:8:LYS:HG2	72:SU:61:LEU:HD21	1.96	0.48
4:L5:4128:A:H8	13:LG:35:ARG:H	1.62	0.47
49:Ls:77:LYS:HD3	49:Ls:198:ILE:HG12	1.95	0.47
50:Lt:78:SER:O	50:Lt:82:ILE:HG13	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:S2:367:U:H4'	51:S2:371:A:C8	2.49	0.47
51:S2:385:G:H3'	63:SL:136:LYS:HB2	1.96	0.47
51:S2:508:A:H3'	51:S2:509:G:H8	1.79	0.47
54:SC:86:LEU:HD11	54:SC:265:PRO:HG2	1.96	0.47
60:SI:174:CYS:HB2	60:SI:190:LEU:HD21	1.97	0.47
66:SO:117:ARG:NH2	78:Sa:52:ASP:OD1	2.47	0.47
4:L5:320:C:OP1	40:Li:84:LYS:NZ	2.34	0.47
4:L5:1706:A:N6	4:L5:2118:G:O4'	2.46	0.47
4:L5:2394:G:O2'	4:L5:2819:U:O4	2.32	0.47
4:L5:2568:C:H2'	4:L5:2569:G:H8	1.78	0.47
4:L5:2724:G:O2'	4:L5:2726:G:OP2	2.31	0.47
9:LC:156:ASP:OD2	9:LC:255:SER:OG	2.30	0.47
44:Lm:98:LYS:HD2	44:Lm:118:THR:HG21	1.95	0.47
49:Ls:47:LEU:HD12	49:Ls:51:ALA:HB3	1.95	0.47
51:S2:981:A:H2'	51:S2:982:G:C8	2.49	0.47
87:NM:145:ILE:O	87:NM:147:GLN:NE2	2.45	0.47
4:L5:459:C:H5'	11:LE:110:ARG:HB3	1.96	0.47
4:L5:3910:C:H2'	4:L5:3911:C:C6	2.49	0.47
8:LB:194:LEU:O	8:LB:198:ARG:HG3	2.14	0.47
9:LC:291:ARG:NH1	9:LC:291:ARG:HB2	2.29	0.47
12:LF:148:LYS:O	12:LF:152:GLU:HG2	2.13	0.47
20:LO:34:VAL:HG22	20:LO:103:LYS:HB2	1.96	0.47
48:Lr:2:SER:O	48:Lr:6:GLN:HG3	2.14	0.47
51:S2:5:U:H2'	51:S2:6:G:H8	1.78	0.47
51:S2:921:G:O6	74:SW:60:LYS:NZ	2.47	0.47
51:S2:1451:G:OP1	84:Sg:64:HIS:NE2	2.45	0.47
74:SW:14:ILE:HG13	74:SW:27:ILE:HD11	1.96	0.47
4:L5:3923:A:H2'	4:L5:3924:C:C6	2.49	0.47
13:LG:81:ASN:O	13:LG:84:THR:OG1	2.31	0.47
21:LP:39:MET:HB2	21:LP:43:LYS:HD3	1.95	0.47
49:Ls:28:PHE:HE1	49:Ls:189:ILE:HG23	1.79	0.47
51:S2:1568:C:O2	51:S2:1627:C:O2'	2.31	0.47
59:SH:76:GLN:O	59:SH:80:VAL:HG23	2.14	0.47
61:SJ:110:LEU:HB2	61:SJ:147:PHE:HB3	1.96	0.47
67:SP:61:ARG:NH1	67:SP:88:GLU:OE2	2.47	0.47
80:Sc:32:VAL:O	80:Sc:41:SER:HA	2.14	0.47
86:NB:64:MET:HE3	86:NB:65:PHE:H	1.79	0.47
3:CR:106:LYS:HA	3:CR:106:LYS:HD3	1.70	0.47
4:L5:93:G:H2'	4:L5:94:A:C8	2.49	0.47
4:L5:239:C:OP1	30:LY:46:SER:OG	2.33	0.47
4:L5:691:C:H2'	4:L5:692:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:958:G:O2'	11:LE:123:ARG:O	2.26	0.47
4:L5:2755:A:OP2	31:LZ:51:ARG:NH1	2.47	0.47
9:LC:317:ASN:ND2	9:LC:318:PRO:O	2.47	0.47
15:LI:44:ASP:OD1	15:LI:44:ASP:N	2.43	0.47
51:S2:319:C:H2'	51:S2:320:G:H8	1.80	0.47
75:SX:70:VAL:HG13	75:SX:72:VAL:HG23	1.96	0.47
4:L5:1401:C:OP2	33:Lb:51:LYS:NZ	2.48	0.47
20:LO:113:ASP:OD1	20:LO:113:ASP:N	2.46	0.47
56:SE:91:SER:OG	56:SE:98:ASN:OD1	2.26	0.47
57:SF:185:SER:O	57:SF:185:SER:OG	2.28	0.47
87:NM:342:GLU:N	87:NM:342:GLU:OE1	2.47	0.47
4:L5:160:G:C5	40:Li:26:HIS:CE1	3.02	0.47
4:L5:711:A:H2'	4:L5:712:C:C6	2.50	0.47
4:L5:3917:A:H2'	4:L5:3918:G:H8	1.79	0.47
9:LC:110:ARG:O	9:LC:112:HIS:N	2.48	0.47
15:LI:38:ARG:HG2	15:LI:41:ALA:HB2	1.97	0.47
15:LI:55:ASP:HA	15:LI:131:ILE:HG23	1.97	0.47
21:LP:54:GLN:HA	21:LP:83:TRP:CD1	2.50	0.47
29:LX:122:ALA:HB3	29:LX:139:ARG:HG2	1.97	0.47
46:Lo:68:LEU:HD12	46:Lo:83:LEU:HB3	1.95	0.47
51:S2:649:U:H1'	75:SX:45:SER:HB3	1.97	0.47
51:S2:956:G:H4'	66:SO:60:MET:HG2	1.97	0.47
51:S2:1037:G:H4'	51:S2:1845:A:H4'	1.96	0.47
53:SB:103:MET:HE3	53:SB:188:LEU:HD22	1.97	0.47
53:SB:123:ALA:HB2	53:SB:165:ARG:HG3	1.96	0.47
61:SJ:59:GLU:OE2	61:SJ:69:ARG:NH2	2.42	0.47
67:SP:108:LYS:H	67:SP:111:MET:HE2	1.78	0.47
72:SU:26:SER:HB3	72:SU:32:LEU:HD13	1.95	0.47
4:L5:1307:A:H2'	4:L5:1308:C:C6	2.50	0.47
10:LD:33:ARG:HE	25:LT:27:LEU:HD12	1.80	0.47
43:Ll:34:LYS:HE3	43:Ll:34:LYS:HB2	1.67	0.47
48:Lr:63:VAL:HG22	48:Lr:79:ARG:HG2	1.96	0.47
51:S2:24:C:OP1	61:SJ:11:LYS:NZ	2.48	0.47
60:SI:163:GLU:HA	60:SI:166:PHE:HB2	1.96	0.47
64:SM:79:VAL:HG11	64:SM:85:LEU:HB2	1.96	0.47
7:LA:29:LEU:O	7:LA:123:ARG:NH1	2.43	0.47
40:Li:23:LYS:H	40:Li:23:LYS:HG3	1.54	0.47
49:Ls:128:THR:OG1	49:Ls:152:ILE:O	2.29	0.47
50:Lt:107:ASP:OD1	50:Lt:108:GLU:N	2.48	0.47
51:S2:955:A:N6	51:S2:971:G:H1'	2.30	0.47
55:SD:95:GLY:HA2	55:SD:101:GLN:NE2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:NM:432:LEU:O	87:NM:436[B]:SER:OG	2.25	0.47
4:L5:1811:G:H21	33:Lb:57:MET:HE3	1.80	0.47
4:L5:4627:U:H4'	8:LB:373:LYS:HE2	1.96	0.47
6:L8:8:U:H2'	6:L8:9:A:C8	2.50	0.47
46:Lo:2:VAL:N	46:Lo:90:HIS:O	2.47	0.47
51:S2:54:A:OP1	76:SY:111:LYS:NZ	2.41	0.47
51:S2:932:G:O2'	51:S2:934:G:OP2	2.28	0.47
73:SV:17:CYS:HB2	73:SV:56:CYS:HB3	1.97	0.47
76:SY:20:ARG:HE	76:SY:22:GLN:HE21	1.62	0.47
4:L5:1692:C:O2'	22:LQ:143:ARG:NH2	2.48	0.46
4:L5:3684:G:H2'	4:L5:3685:C:C6	2.50	0.46
49:Ls:162:LYS:HA	49:Ls:162:LYS:HD2	1.75	0.46
59:SH:72:PHE:O	59:SH:76:GLN:HB2	2.15	0.46
4:L5:97:G:OP1	17:LL:16:LYS:NZ	2.48	0.46
4:L5:2284:G:OP1	32:La:7:LYS:NZ	2.46	0.46
11:LE:92:VAL:HG13	11:LE:109:LEU:HD21	1.97	0.46
36:Le:82:VAL:O	36:Le:86:GLU:HG2	2.16	0.46
49:Ls:31:GLY:HA3	49:Ls:190:GLN:HE22	1.80	0.46
49:Ls:174:LEU:HD12	49:Ls:175:LEU:HG	1.97	0.46
76:SY:26:ASP:OD1	76:SY:26:ASP:N	2.48	0.46
8:LB:92:TYR:HB3	8:LB:99:LEU:HD22	1.97	0.46
8:LB:378:ARG:HG2	28:LW:32:LEU:HD21	1.97	0.46
18:LM:116:LYS:HB2	20:LO:196:LEU:HD21	1.97	0.46
27:LV:96:LEU:HD13	28:LW:20:ARG:HG2	1.97	0.46
51:S2:115:U:H2'	51:S2:116:U:C6	2.51	0.46
51:S2:804:U:H5	51:S2:859:G:H1	1.63	0.46
51:S2:1351:G:H4'	52:SA:110:ASN:HA	1.97	0.46
51:S2:1356:G:H2'	51:S2:1357:A:C8	2.50	0.46
51:S2:1623:A:O5'	70:SS:133:GLY:HA3	2.15	0.46
61:SJ:78:LEU:HD11	61:SJ:94:LEU:HB3	1.98	0.46
88:CZ:12:LEU:HA	88:CZ:13:PHE:HA	1.67	0.46
4:L5:99:A:H4'	19:LN:181:HIS:CE1	2.51	0.46
4:L5:1553:A:O2'	47:Lp:9:GLY:O	2.27	0.46
4:L5:2121:C:H2'	4:L5:2122:G:C8	2.51	0.46
4:L5:2532:C:O2'	29:LX:93:ASN:OD1	2.33	0.46
4:L5:2864:A:H2'	4:L5:2865:U:C6	2.50	0.46
4:L5:3938:G:OP2	19:LN:24:ARG:HD3	2.15	0.46
32:La:131:ARG:O	32:La:135:GLU:HG3	2.16	0.46
51:S2:94:G:O2'	51:S2:508:A:O2'	2.29	0.46
51:S2:561:A:H5'	61:SJ:171:GLY:HA3	1.97	0.46
51:S2:1839:U:H2'	51:S2:1840:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SS:33:ILE:HD13	70:SS:71:MET:HE1	1.97	0.46
84:Sg:152:SER:H	84:Sg:169:GLY:HA2	1.81	0.46
4:L5:1662:C:H2'	4:L5:1663:C:C6	2.50	0.46
4:L5:3736:A:H2'	4:L5:3737:A:C8	2.51	0.46
4:L5:3908:A:H2	4:L5:4449:A:H61	1.63	0.46
51:S2:522:A:H5''	61:SJ:145:PRO:HD2	1.98	0.46
51:S2:839:C:H41	76:SY:10:ARG:HA	1.79	0.46
56:SE:137:PRO:HB2	56:SE:150:PRO:HD2	1.98	0.46
59:SH:73:GLN:HB3	59:SH:135:PHE:CE1	2.50	0.46
62:SK:24:LYS:HD3	62:SK:26:ASP:HB2	1.96	0.46
4:L5:1326:A:OP2	4:L5:4445:U:O2'	2.31	0.46
4:L5:1443:A:N1	4:L5:2103:G:C2	2.84	0.46
4:L5:3664:G:H2'	4:L5:3665:G:C8	2.51	0.46
19:LN:63:ARG:HG3	19:LN:131:GLU:HG3	1.98	0.46
51:S2:164:A:H3'	51:S2:165:G:H21	1.80	0.46
51:S2:1305:C:OP2	83:Sf:95:ARG:NH1	2.44	0.46
58:SG:32:MET:HB2	58:SG:100:CYS:HB2	1.98	0.46
64:SM:131:LYS:HD2	64:SM:132:LYS:HB2	1.98	0.46
74:SW:42:MET:HE2	74:SW:42:MET:HB3	1.71	0.46
3:CR:84:LEU:HD13	67:SP:131:PRO:HA	1.98	0.46
3:CR:330:ARG:HH12	3:CR:344:LEU:H	1.63	0.46
4:L5:517:C:N4	4:L5:646:G:O2'	2.43	0.46
4:L5:1558:A:H2'	4:L5:1559:G:C8	2.51	0.46
23:LR:105:LEU:HD22	23:LR:135:LYS:HG2	1.98	0.46
34:Lc:47:ILE:HB	34:Lc:94:LEU:HG	1.98	0.46
49:Ls:199:TYR:CE1	49:Ls:204:LEU:HB2	2.51	0.46
51:S2:30:C:O2'	51:S2:596:U:OP1	2.28	0.46
51:S2:681:U:H4'	75:SX:9:THR:HG22	1.97	0.46
51:S2:1217:A:H2'	51:S2:1218:C:C6	2.50	0.46
60:SI:76:THR:HG22	60:SI:108:PRO:HG2	1.97	0.46
64:SM:94:ILE:HD11	64:SM:98:GLY:HA2	1.96	0.46
72:SU:61:LEU:HB2	72:SU:82:MET:HB3	1.97	0.46
87:Nm:172:LEU:HD23	87:Nm:172:LEU:HA	1.77	0.46
87:Nm:435:MET:O	87:Nm:439:LEU:HD12	2.15	0.46
7:LA:248:GLY:HA2	51:S2:1044:G:C6	2.51	0.46
15:LI:61:SER:HA	15:LI:126:VAL:HG12	1.97	0.46
22:LQ:49:LYS:HB3	22:LQ:49:LYS:HE2	1.70	0.46
51:S2:1354:G:N2	51:S2:1357:A:OP2	2.41	0.46
57:SF:86:LYS:O	57:SF:90:VAL:HG13	2.16	0.46
84:Sg:280:LYS:HE2	84:Sg:280:LYS:N	2.31	0.46
15:LI:54:SER:O	15:LI:132:GLY:N	2.37	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Ls:120:GLU:OE2	49:Ls:163:THR:OG1	2.33	0.46
51:S2:824:C:H1'	61:SJ:144:ILE:HG21	1.98	0.46
54:SC:66:LEU:HD11	54:SC:81:ILE:HG21	1.98	0.46
64:SM:55:ASN:OD1	64:SM:55:ASN:N	2.49	0.46
75:SX:9:THR:O	75:SX:11:ARG:N	2.46	0.46
76:SY:18:LEU:O	76:SY:85:ASN:ND2	2.49	0.46
3:CR:319:ILE:HB	3:CR:412:ILE:HB	1.97	0.46
4:L5:257:C:H2'	4:L5:258:G:C8	2.51	0.46
38:Lg:9:ARG:HD2	38:Lg:34:TYR:CZ	2.50	0.46
53:SB:126:ASP:OD1	53:SB:136:ARG:NE	2.48	0.46
70:SS:44:VAL:HG11	70:SS:71:MET:HG2	1.98	0.46
41:Lj:20:ARG:NH2	41:Lj:39:TYR:OH	2.49	0.45
50:Lt:40:LYS:O	50:Lt:40:LYS:NZ	2.42	0.45
51:S2:1705:C:H2'	51:S2:1706:G:C8	2.51	0.45
53:SB:229:MET:HE3	53:SB:229:MET:HA	1.98	0.45
67:SP:20:VAL:HG21	67:SP:28:MET:HE1	1.98	0.45
4:L5:1548:G:O2'	4:L5:2812:A:N3	2.42	0.45
4:L5:2591:A:N6	4:L5:2754:G:O2'	2.50	0.45
30:LY:2:LYS:HB3	30:LY:2:LYS:HE3	1.70	0.45
60:SI:62:VAL:HA	60:SI:77:ARG:HA	1.97	0.45
61:SJ:142:VAL:HG12	61:SJ:144:ILE:H	1.82	0.45
66:SO:92:ALA:HB2	66:SO:125:LYS:HB2	1.98	0.45
68:SQ:105:LYS:O	68:SQ:109:LYS:HB2	2.16	0.45
71:ST:32:GLU:H	71:ST:32:GLU:CD	2.25	0.45
4:L5:1846:G:H2'	4:L5:1847:C:C6	2.50	0.45
4:L5:4258:C:H2'	4:L5:4259:C:H6	1.80	0.45
42:Lk:70:LYS:HA	42:Lk:70:LYS:HD3	1.76	0.45
48:Lr:101:LYS:HE3	48:Lr:101:LYS:HB3	1.74	0.45
49:Ls:48:ARG:CZ	50:Lt:123:ARG:HH21	2.29	0.45
50:Lt:44:ASP:C	50:Lt:48:LYS:HZ2	2.25	0.45
51:S2:857:U:H2'	51:S2:858:A:C8	2.51	0.45
51:S2:1499:U:H4'	55:SD:176:LEU:HD11	1.97	0.45
51:S2:1661:A:OP1	81:Sd:19:ARG:NH2	2.46	0.45
52:SA:77:ILE:HB	52:SA:124:VAL:HG12	1.98	0.45
60:SI:87:ASN:HB3	60:SI:90:LEU:HG	1.99	0.45
69:SR:20:TYR:O	69:SR:24:LEU:HD22	2.17	0.45
70:SS:24:ARG:HB2	70:SS:29:ALA:HB2	1.99	0.45
87:Nm:288:PRO:HA	87:Nm:289:LYS:HA	1.74	0.45
4:L5:3612:C:H1'	4:L5:5016:A:C8	2.51	0.45
4:L5:3861:A:H2'	4:L5:3862:A:C8	2.51	0.45
5:L7:27:G:H2'	5:L7:28:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LA:41:ILE:HG12	7:LA:63:PHE:HD2	1.82	0.45
39:Lh:6:ALA:O	39:Lh:10:ARG:HG2	2.17	0.45
49:Ls:101:MET:HA	49:Ls:104:ALA:HB3	1.98	0.45
51:S2:1215:C:O2'	51:S2:1645:C:OP2	2.33	0.45
60:SI:103:LEU:HD22	60:SI:170:LYS:HB3	1.97	0.45
67:SP:107:ILE:HA	67:SP:111:MET:HE2	1.98	0.45
4:L5:1785:C:OP1	15:LI:133:GLN:NE2	2.47	0.45
4:L5:4162:C:O2	13:LG:73:ARG:NH2	2.40	0.45
26:LU:80:LYS:HE2	26:LU:110:TYR:CZ	2.51	0.45
26:LU:117:ILE:HG23	86:NB:31:LYS:HB3	1.99	0.45
30:LY:121:ARG:HG3	30:LY:124:LYS:HE3	1.98	0.45
31:LZ:22:LYS:NZ	31:LZ:132:GLN:O	2.38	0.45
51:S2:1521:C:N4	70:SS:137:LYS:HD3	2.32	0.45
75:SX:131:LEU:HD21	75:SX:135:LYS:HE2	1.99	0.45
85:NA:111:VAL:HG12	85:NA:122:VAL:HB	1.98	0.45
4:L5:2411:C:H2'	4:L5:2412:A:C8	2.52	0.45
9:LC:137:VAL:HG21	9:LC:150:LEU:HD21	1.99	0.45
51:S2:17:C:H2'	51:S2:18:C:C6	2.52	0.45
51:S2:1544:C:H2'	51:S2:1545:A:H5''	1.98	0.45
54:SC:172:ASN:OD1	54:SC:172:ASN:N	2.49	0.45
56:SE:125:LYS:HG2	56:SE:142:HIS:HB3	1.98	0.45
57:SF:69:VAL:O	57:SF:73:THR:HG23	2.16	0.45
64:SM:33:ARG:HH11	64:SM:91:LEU:HD23	1.81	0.45
71:ST:107:LEU:HD22	71:ST:112:MET:HE2	1.98	0.45
4:L5:3668:C:H5'	7:LA:8:GLN:O	2.16	0.45
4:L5:4208:U:OP2	25:LT:4:THR:OG1	2.29	0.45
4:L5:4258:C:H5'	16:LJ:68:ILE:HD11	1.98	0.45
19:LN:159:ARG:HB3	19:LN:164:LEU:HB2	1.98	0.45
56:SE:48:LEU:HD11	56:SE:70:ILE:HG13	1.98	0.45
68:SQ:21:ALA:HB2	68:SQ:72:VAL:HG23	1.98	0.45
70:SS:6:PRO:HD3	77:SZ:49:LEU:HB3	1.99	0.45
75:SX:63:ASN:ND2	75:SX:114:ASP:OD1	2.44	0.45
85:NA:93:ARG:NH1	85:NA:94:VAL:O	2.49	0.45
4:L5:4281:A:O2'	4:L5:4282:A:H2'	2.17	0.45
20:LO:90:HIS:O	20:LO:96:GLN:NE2	2.50	0.45
35:Ld:36:VAL:HG21	35:Ld:44:ARG:HG2	1.98	0.45
50:Lt:18:THR:HA	50:Lt:57:ARG:HA	1.98	0.45
51:S2:1447:G:OP1	72:SU:85:HIS:ND1	2.43	0.45
68:SQ:100:VAL:HG12	68:SQ:101:ASP:H	1.81	0.45
71:ST:56:ARG:HG3	71:ST:103:VAL:HG21	1.98	0.45
71:ST:133:ARG:O	71:ST:137:GLN:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1317:U:H2'	4:L5:1318:C:C6	2.52	0.45
51:S2:848:U:H2'	51:S2:849:A:H8	1.82	0.45
51:S2:1217:A:H2'	51:S2:1218:C:H6	1.82	0.45
51:S2:1839:U:H1'	51:S2:1863:A:H2	1.82	0.45
55:SD:142:LEU:HD23	55:SD:142:LEU:HA	1.85	0.45
74:SW:111:MET:HB2	74:SW:115:GLU:OE2	2.16	0.45
87:NM:303:PRO:O	87:NM:307:ILE:HD12	2.17	0.45
4:L5:268:G:H2'	4:L5:269:G:H8	1.82	0.45
4:L5:960:A:C8	11:LE:126:LEU:HD12	2.51	0.45
4:L5:2527:A:OP2	23:LR:38:ARG:NH1	2.35	0.45
4:L5:3786:U:O2	4:L5:3814:U:H4'	2.16	0.45
9:LC:221:PHE:HB3	9:LC:227:ILE:HG21	1.99	0.45
11:LE:247:LYS:O	11:LE:251:LYS:HG3	2.17	0.45
30:LY:47:MET:HG2	30:LY:109:LEU:HD21	1.98	0.45
51:S2:656:G:H5'	51:S2:662:G:N2	2.32	0.45
51:S2:1350:U:H1'	52:SA:112:ILE:HD13	1.99	0.45
53:SB:27:LYS:HE2	53:SB:27:LYS:HB2	1.76	0.45
6:L8:141:C:H2'	6:L8:142:U:C6	2.52	0.44
18:LM:113:MET:HE3	18:LM:113:MET:HB3	1.88	0.44
24:LS:7:LEU:O	24:LS:103:ALA:HB1	2.16	0.44
51:S2:96:C:H1'	51:S2:474:G:H5'	1.98	0.44
55:SD:56:GLN:O	55:SD:60:GLY:HA3	2.17	0.44
56:SE:121:TYR:HA	56:SE:163:ASP:HA	1.98	0.44
67:SP:59:ARG:HH21	67:SP:76:VAL:HG13	1.82	0.44
3:CR:377:TRP:CD1	3:CR:381:ASN:HD21	2.35	0.44
4:L5:99:A:H5''	19:LN:184:ILE:HD13	1.99	0.44
4:L5:1574:G:OP2	23:LR:92:LYS:NZ	2.41	0.44
4:L5:4742:G:H2'	4:L5:4743:G:H8	1.82	0.44
10:LD:117:LYS:HB2	10:LD:117:LYS:HE2	1.69	0.44
10:LD:179:ARG:HA	10:LD:179:ARG:HD3	1.80	0.44
26:LU:23:LEU:HB2	26:LU:70:ILE:HB	2.00	0.44
41:Lj:25:LYS:HB3	41:Lj:25:LYS:HE3	1.76	0.44
58:SG:181:THR:HG22	58:SG:183:ARG:H	1.81	0.44
4:L5:729:G:H5''	12:LF:76:ARG:HD2	1.98	0.44
4:L5:1915:C:OP2	20:LO:94:ARG:NH2	2.50	0.44
4:L5:2017:A:O2'	4:L5:2018:C:O5'	2.33	0.44
4:L5:3654:G:O2'	4:L5:3693:U:OP1	2.29	0.44
4:L5:4689:U:H5	4:L5:4699:U:O4	2.00	0.44
12:LF:196:THR:O	12:LF:196:THR:OG1	2.35	0.44
51:S2:639:C:H2'	51:S2:640:A:C8	2.52	0.44
51:S2:803:C:H5	51:S2:860:G:H22	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SB:135:LEU:HD11	53:SB:176:VAL:HG11	1.99	0.44
63:SL:111:VAL:HG11	63:SL:128:VAL:HG11	1.99	0.44
70:SS:115:LYS:C	70:SS:117:ILE:H	2.26	0.44
72:SU:19:ARG:HA	72:SU:92:HIS:HA	1.99	0.44
86:NB:102:MET:HE2	86:NB:102:MET:HA	1.99	0.44
4:L5:226:G:N7	9:LC:184:TYR:OH	2.48	0.44
4:L5:1097:C:H2'	4:L5:1098:G:C8	2.52	0.44
4:L5:2265:G:OP1	48:Lr:35:ARG:NH2	2.40	0.44
4:L5:2809:G:OP1	23:LR:60:ARG:NH2	2.50	0.44
4:L5:4130:C:H5	4:L5:4154:G:H1	1.66	0.44
10:LD:107:ARG:HH12	10:LD:120:GLU:HA	1.80	0.44
15:LI:91:LEU:HD21	15:LI:129:VAL:HB	1.99	0.44
16:LJ:18:ARG:H	16:LJ:134:LEU:HA	1.82	0.44
18:LM:53:LYS:H	18:LM:53:LYS:HG2	1.57	0.44
18:LM:104:MET:HG2	18:LM:108:ASP:HB2	1.98	0.44
32:La:7:LYS:HB3	32:La:7:LYS:HE2	1.81	0.44
51:S2:691:G:H4'	59:SH:178:LYS:HE3	1.99	0.44
51:S2:1512:C:H5''	81:Sd:8:TRP:HZ3	1.82	0.44
53:SB:217:MET:HE2	53:SB:217:MET:HB2	1.82	0.44
56:SE:61:VAL:HG12	56:SE:80:ILE:HD12	1.99	0.44
57:SF:34:SER:HA	80:Sc:55:VAL:HB	2.00	0.44
79:Sb:18:LYS:HB2	79:Sb:23:ARG:HG3	1.99	0.44
4:L5:1590:C:H4'	4:L5:2857:A:H5'	2.00	0.44
4:L5:4967:A:H2'	4:L5:4968:A:C8	2.52	0.44
26:LU:40:GLU:OE2	26:LU:65:ARG:NH1	2.51	0.44
51:S2:1562:C:H2'	51:S2:1563:G:H8	1.83	0.44
52:SA:123:VAL:HA	52:SA:145:ILE:O	2.18	0.44
59:SH:46:THR:HG21	59:SH:97:GLN:HG3	2.00	0.44
76:SY:62:THR:HA	76:SY:69:THR:HA	2.00	0.44
87:Nm:408:MET:HE3	87:Nm:408:MET:H	1.83	0.44
4:L5:4935:C:H2'	4:L5:4936:G:C8	2.51	0.44
20:LO:186:GLU:HA	20:LO:189:ILE:HG22	2.00	0.44
35:Ld:54:MET:HG2	35:Ld:60:PRO:HA	1.98	0.44
51:S2:860:G:N2	74:SW:107:SER:OG	2.50	0.44
51:S2:1298:G:H4'	67:SP:78:THR:HA	2.00	0.44
51:S2:1407:U:H2'	51:S2:1408:U:C6	2.53	0.44
56:SE:122:LYS:HE2	56:SE:145:ARG:HH21	1.82	0.44
60:SI:48:VAL:HG11	60:SI:54:LYS:HD2	1.99	0.44
62:SK:21:MET:HE2	62:SK:49:MET:HE1	2.00	0.44
70:SS:91:LYS:HE2	70:SS:91:LYS:HB2	1.85	0.44
4:L5:963:G:P	12:LF:32:ARG:HH21	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1441:C:O2	4:L5:2108:G:O2'	2.35	0.44
4:L5:1460:C:H5''	22:LQ:144:LYS:HG3	2.00	0.44
4:L5:2434:G:O2'	4:L5:2527:A:N1	2.51	0.44
4:L5:2745:A:H2'	4:L5:2746:A:C8	2.53	0.44
4:L5:4492:U:O2'	4:L5:4512:U:O2	2.25	0.44
4:L5:4927:G:H5'	4:L5:4928:C:C5	2.52	0.44
9:LC:116:ASN:HB2	9:LC:119:GLN:HG3	1.99	0.44
21:LP:8:PRO:HD3	21:LP:149:ILE:HD13	1.99	0.44
51:S2:920:A:O2'	51:S2:922:A:O5'	2.36	0.44
51:S2:1314:U:O2'	62:SK:8:ARG:NH2	2.51	0.44
51:S2:1588:A:OP1	71:ST:77:LYS:HG2	2.17	0.44
56:SE:204:SER:OG	56:SE:205:PHE:N	2.51	0.44
60:SI:117:TYR:CD1	60:SI:156:ALA:HB2	2.53	0.44
68:SQ:105:LYS:HB3	68:SQ:105:LYS:HE3	1.73	0.44
84:Sg:206:LEU:HA	84:Sg:220:ASP:HA	1.99	0.44
85:NA:91:VAL:HG21	85:NA:111:VAL:HG21	2.00	0.44
4:L5:1327:C:H2'	4:L5:1328:G:C8	2.53	0.44
4:L5:2765:A:H2'	4:L5:2766:A:C8	2.52	0.44
4:L5:4238:G:H2'	4:L5:4239:A:C8	2.53	0.44
26:LU:80:LYS:HD2	26:LU:108:GLU:HA	2.00	0.44
51:S2:1365:G:H2'	51:S2:1366:G:C8	2.53	0.44
56:SE:11:ARG:NH1	56:SE:24:THR:O	2.50	0.44
61:SJ:104:ASP:OD1	61:SJ:104:ASP:N	2.47	0.44
63:SL:49:GLU:HG3	63:SL:116:CYS:HA	2.00	0.44
4:L5:2664:G:H4'	4:L5:2677:G:H4'	2.00	0.44
4:L5:2730:U:H2'	4:L5:2731:C:C6	2.53	0.44
4:L5:4169:G:H4'	4:L5:4171:C:C2	2.52	0.44
8:LB:77:THR:HG21	8:LB:337:VAL:HG22	2.00	0.44
48:Lr:33:LYS:HE2	48:Lr:33:LYS:HB3	1.86	0.44
51:S2:803:C:H5	51:S2:860:G:H1	1.65	0.44
51:S2:1281:G:H3'	51:S2:1282:A:H8	1.81	0.44
51:S2:1348:G:H22	51:S2:1381:G:N2	2.15	0.44
51:S2:1775:U:H2'	51:S2:1776:G:C4	2.53	0.44
52:SA:77:ILE:HG13	52:SA:122:LEU:HD11	1.99	0.44
58:SG:38:ALA:HB2	58:SG:50:VAL:HG22	2.00	0.44
87:Nm:393:GLU:OE2	87:Nm:393:GLU:N	2.50	0.44
87:Nm:455:LEU:HB2	87:Nm:491:VAL:HB	2.00	0.44
4:L5:935:A:O2'	18:LM:46:ARG:NH1	2.51	0.43
4:L5:2021:G:P	49:Ls:57:LYS:HG2	2.58	0.43
4:L5:2652:G:N2	47:Lp:59:SER:O	2.51	0.43
4:L5:3871:A:H2'	4:L5:3872:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LG:171:PRO:HB3	13:LG:181:TYR:CE1	2.53	0.43
16:LJ:23:ASN:HB3	16:LJ:129:ASP:OD2	2.18	0.43
17:LL:87:HIS:HE1	17:LL:89:LYS:HD2	1.83	0.43
19:LN:201:HIS:O	19:LN:204:ARG:HD3	2.18	0.43
28:LW:97:LYS:O	28:LW:102:LYS:NZ	2.51	0.43
50:Lt:15:LEU:HD22	50:Lt:17:CYS:HB2	2.00	0.43
51:S2:1667:U:H2'	51:S2:1668:U:C6	2.53	0.43
54:SC:125:LYS:HG3	54:SC:143:CYS:HB2	2.00	0.43
76:SY:102:THR:HG23	76:SY:107:ARG:HH11	1.82	0.43
86:NB:33:VAL:O	86:NB:34:HIS:ND1	2.51	0.43
4:L5:4192:A:H2'	4:L5:4193:C:H6	1.83	0.43
8:LB:165:HIS:HB3	8:LB:180:LEU:HD13	1.99	0.43
24:LS:113:MET:HE3	24:LS:113:MET:HB3	1.88	0.43
27:LV:70:PRO:HA	27:LV:73:ARG:HG3	1.99	0.43
32:La:110:LYS:HG3	32:La:128:PHE:HB2	1.99	0.43
36:Le:20:PHE:CG	36:Le:56:PRO:HG3	2.54	0.43
39:Lh:94:ARG:HE	39:Lh:94:ARG:HB2	1.59	0.43
43:Ll:28:ARG:HA	43:Ll:33:ASN:ND2	2.34	0.43
51:S2:441:C:H2'	51:S2:442:C:C6	2.53	0.43
51:S2:1153:C:OP2	74:SW:71:LYS:NZ	2.34	0.43
51:S2:1274:G:C2	62:SK:27:VAL:HG11	2.53	0.43
57:SF:23:TRP:CH2	57:SF:108:PRO:HG2	2.54	0.43
4:L5:1:C:O2'	29:LX:38:LYS:NZ	2.51	0.43
4:L5:258:G:H2'	4:L5:259:C:C6	2.52	0.43
4:L5:1199:G:H2'	4:L5:1200:G:C8	2.53	0.43
4:L5:3947:A:H61	4:L5:4068:U:H1'	1.83	0.43
4:L5:4438:U:H2'	4:L5:4439:U:O4'	2.18	0.43
9:LC:291:ARG:HB2	9:LC:291:ARG:HH11	1.82	0.43
51:S2:493:A:H1'	51:S2:574:A:H5'	2.01	0.43
51:S2:1692:U:H2'	51:S2:1693:G:C8	2.53	0.43
54:SC:176:LYS:O	54:SC:200:ARG:NH2	2.44	0.43
63:SL:33:LEU:HD12	63:SL:34:PRO:HD2	2.00	0.43
67:SP:83:MET:HE3	67:SP:84:ILE:H	1.83	0.43
67:SP:93:MET:SD	67:SP:106:GLU:HG2	2.58	0.43
70:SS:104:ASP:OD1	70:SS:104:ASP:N	2.51	0.43
76:SY:29:HIS:NE2	76:SY:69:THR:OG1	2.34	0.43
87:NM:172:LEU:HD21	87:NM:225:PHE:CD1	2.53	0.43
4:L5:279:A:OP2	19:LN:8:GLN:NE2	2.50	0.43
18:LM:106:ASP:OD2	18:LM:109:ARG:NH1	2.52	0.43
23:LR:11:ALA:HA	23:LR:41:ILE:HD13	2.00	0.43
42:Lk:10:ASP:HA	42:Lk:13:LEU:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SE:126:VAL:HG12	56:SE:139:LEU:HD21	2.00	0.43
87:NM:355:ARG:O	87:NM:355:ARG:NE	2.50	0.43
4:L5:4591:U:H2'	4:L5:4592:C:C6	2.53	0.43
10:LD:211:LEU:HB3	10:LD:219:TYR:HB2	1.99	0.43
26:LU:56:LEU:HD13	26:LU:56:LEU:HA	1.86	0.43
27:LV:62:MET:HE3	27:LV:76:VAL:HG12	2.00	0.43
47:Lp:37:TYR:HB2	47:Lp:47:MET:HB3	2.01	0.43
51:S2:150:A:N6	51:S2:168:C:O2	2.52	0.43
4:L5:85:G:O2'	4:L5:97:G:O6	2.34	0.43
7:LA:122:ASP:N	7:LA:122:ASP:OD1	2.50	0.43
29:LX:39:LYS:HB2	29:LX:39:LYS:HE2	1.76	0.43
34:Lc:48:LEU:HD21	34:Lc:60:ILE:HG21	1.99	0.43
51:S2:4:C:H4'	54:SC:207:ALA:HB2	1.99	0.43
51:S2:118:C:H1'	51:S2:445:A:C5	2.53	0.43
51:S2:453:C:O2'	58:SG:92:ARG:O	2.30	0.43
51:S2:916:A:C5	65:SN:73:ARG:HD3	2.53	0.43
51:S2:1543:U:OP2	71:ST:62:ARG:NH2	2.43	0.43
57:SF:107:ASN:O	57:SF:111:VAL:HG12	2.19	0.43
61:SJ:66:LYS:HA	61:SJ:71:LEU:HD11	2.01	0.43
4:L5:325:U:H2'	4:L5:326:C:C6	2.54	0.43
4:L5:1570:G:N7	47:Lp:3:LYS:NZ	2.66	0.43
4:L5:1788:A:H2'	15:LI:22:PHE:CZ	2.52	0.43
4:L5:2017:A:O2'	4:L5:2018:C:H6	2.02	0.43
4:L5:2029:A:H2'	4:L5:2030:A:C8	2.54	0.43
4:L5:2461:G:H2'	4:L5:2462:C:C6	2.54	0.43
4:L5:2744:A:H2'	4:L5:2745:A:C8	2.54	0.43
4:L5:4274:A:H2'	4:L5:4275:G:H8	1.82	0.43
6:L8:27:U:H2'	6:L8:28:C:C6	2.53	0.43
7:LA:20:VAL:HA	7:LA:23:ARG:HG3	2.01	0.43
8:LB:99:LEU:HD23	8:LB:99:LEU:HA	1.91	0.43
18:LM:81:ASP:OD2	18:LM:84:THR:OG1	2.34	0.43
19:LN:5:LYS:HG2	40:Li:40:VAL:HG11	2.01	0.43
19:LN:84:PRO:HA	19:LN:87:HIS:CG	2.54	0.43
23:LR:105:LEU:HD23	23:LR:138:LEU:HD23	1.99	0.43
51:S2:1628:C:H2'	51:S2:1629:C:C6	2.54	0.43
57:SF:90:VAL:HA	57:SF:93:VAL:HG22	2.01	0.43
79:Sb:21:LYS:O	79:Sb:23:ARG:N	2.52	0.43
4:L5:1504:G:H2'	4:L5:1505:C:C6	2.54	0.43
4:L5:4717:A:OP2	8:LB:30:LYS:NZ	2.41	0.43
7:LA:54:ARG:HG2	7:LA:56:ALA:H	1.84	0.43
7:LA:208:GLU:H	7:LA:208:GLU:HG2	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LF:243:LEU:O	12:LF:247:MET:HB2	2.18	0.43
51:S2:1745:A:H8	58:SG:65:GLN:HG3	1.82	0.43
51:S2:1797:U:H2'	51:S2:1798:C:C6	2.53	0.43
52:SA:119:PRO:HG2	52:SA:142:LEU:HD21	2.00	0.43
52:SA:196:GLU:H	52:SA:196:GLU:CD	2.26	0.43
80:Sc:20:ARG:NH1	80:Sc:25:GLY:O	2.52	0.43
4:L5:424:U:H2'	4:L5:425:U:C6	2.54	0.43
4:L5:2020:U:H5''	49:Ls:57:LYS:HG3	2.00	0.43
4:L5:2626:U:C6	26:LU:92:LYS:HG2	2.53	0.43
4:L5:3880:G:H2'	4:L5:3881:G:C8	2.54	0.43
7:LA:5:ILE:HG12	7:LA:8:GLN:HB2	2.01	0.43
11:LE:183:ARG:HA	11:LE:183:ARG:HD2	1.78	0.43
13:LG:138:ALA:HB2	13:LG:194:VAL:HG11	2.01	0.43
20:LO:39:GLU:HB2	20:LO:139:GLY:HA3	2.01	0.43
24:LS:110:TYR:CZ	24:LS:124:ILE:HD11	2.54	0.43
51:S2:830:A:OP2	51:S2:846:G:N2	2.52	0.43
52:SA:198:MET:HE3	69:SR:84:TYR:CE1	2.53	0.43
53:SB:85:LYS:HD3	53:SB:85:LYS:HA	1.92	0.43
53:SB:150:ILE:HD12	69:SR:128:PHE:HB2	2.01	0.43
55:SD:39:VAL:HG22	55:SD:48:ILE:HG12	2.00	0.43
56:SE:123:LEU:HD11	56:SE:228:ILE:HG22	2.01	0.43
59:SH:170:VAL:HG13	59:SH:187:PHE:HB2	2.01	0.43
3:CR:91:ASN:HB2	3:CR:115:GLU:HG3	2.00	0.43
4:L5:1617:G:H1'	4:L5:2513:A:N6	2.34	0.43
4:L5:2448:G:H2'	4:L5:2449:A:C8	2.54	0.43
4:L5:3726:A:H2'	4:L5:3727:A:C8	2.54	0.43
6:L8:94:G:C5	41:Lj:84:PRO:HG3	2.54	0.43
9:LC:284:MET:HE3	22:LQ:28:LEU:HD23	2.01	0.43
41:Lj:64:MET:HE3	41:Lj:64:MET:HB3	1.90	0.43
51:S2:5:U:H2'	51:S2:6:G:C8	2.54	0.43
51:S2:165:G:OP2	51:S2:165:G:N2	2.43	0.43
51:S2:1082:A:H2'	51:S2:1084:A:H5''	2.00	0.43
51:S2:1648:G:H5''	68:SQ:125:ARG:HB2	2.00	0.43
63:SL:125:ILE:HB	63:SL:146:THR:HG23	2.00	0.43
4:L5:1279:A:O2'	4:L5:1281:G:N7	2.47	0.42
4:L5:4260:U:H2'	4:L5:4261:C:H6	1.83	0.42
6:L8:148:A:H2'	6:L8:149:G:C8	2.54	0.42
12:LF:164:LYS:HD2	12:LF:164:LYS:HA	1.91	0.42
30:LY:52:ASP:OD2	30:LY:69:LYS:NZ	2.44	0.42
36:Le:64:LYS:HE2	36:Le:64:LYS:HB2	1.80	0.42
47:Lp:3:LYS:HE3	47:Lp:3:LYS:HB2	1.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Ls:39:GLN:HE22	49:Ls:107:VAL:H	1.66	0.42
51:S2:674:C:H2'	51:S2:675:U:C6	2.54	0.42
51:S2:816:A:OP2	61:SJ:10:ARG:NH2	2.41	0.42
51:S2:957:A:H2'	51:S2:958:G:H21	1.83	0.42
51:S2:1284:A:OP1	51:S2:1285:G:O2'	2.30	0.42
85:NA:87:GLN:NE2	85:NA:88:VAL:O	2.52	0.42
87:NM:289:LYS:HA	87:NM:290:PRO:HD3	1.93	0.42
4:L5:136:C:N4	39:Lh:79:LYS:HE3	2.34	0.42
4:L5:960:A:H8	11:LE:126:LEU:HD12	1.83	0.42
4:L5:1558:A:H2'	4:L5:1559:G:H8	1.82	0.42
4:L5:4870:G:C6	18:LM:56:GLN:HG2	2.54	0.42
9:LC:230:LEU:HD23	9:LC:230:LEU:HA	1.94	0.42
18:LM:24:LEU:HB2	18:LM:43:THR:HG21	2.01	0.42
23:LR:105:LEU:HD13	23:LR:135:LYS:HE3	2.01	0.42
25:LT:102:ARG:O	25:LT:106:LEU:HD22	2.18	0.42
38:Lg:8:ARG:HB2	38:Lg:34:TYR:HE1	1.84	0.42
87:NM:459:LYS:HB2	87:NM:459:LYS:HE2	1.85	0.42
88:CZ:94:PRO:HA	88:CZ:95:PRO:HD3	1.74	0.42
4:L5:10:A:H2'	4:L5:11:G:C8	2.54	0.42
4:L5:267:G:H2'	4:L5:268:G:H8	1.83	0.42
4:L5:1946:G:O2'	4:L5:1948:G:OP2	2.34	0.42
4:L5:2483:G:H2'	4:L5:2484:A:C8	2.54	0.42
4:L5:3652:A:H2'	4:L5:3653:A:C5	2.54	0.42
4:L5:3848:U:H2'	4:L5:3849:A:C8	2.54	0.42
4:L5:3946:G:H22	4:L5:4067:U:H3	1.67	0.42
7:LA:80:GLU:HB2	7:LA:170:ALA:HA	2.01	0.42
9:LC:60:HIS:HA	9:LC:92:PHE:HE1	1.84	0.42
13:LG:108:GLN:O	13:LG:112:GLN:HG2	2.19	0.42
22:LQ:27:LEU:HD23	22:LQ:30:LYS:HD2	2.02	0.42
31:LZ:117:LYS:HA	31:LZ:117:LYS:HD3	1.86	0.42
46:Lo:78:ARG:O	46:Lo:80:LYS:NZ	2.51	0.42
51:S2:15:U:H2'	51:S2:16:G:O4'	2.19	0.42
51:S2:85:A:O2'	51:S2:86:C:O5'	2.30	0.42
51:S2:1092:G:OP1	65:SN:2:GLY:N	2.52	0.42
51:S2:1683:C:H2'	51:S2:1684:C:H6	1.85	0.42
53:SB:94:LYS:HD2	53:SB:94:LYS:HA	1.76	0.42
56:SE:36:HIS:CG	56:SE:85:GLY:HA3	2.54	0.42
64:SM:25:ALA:HB1	64:SM:31:LEU:HD21	2.01	0.42
70:SS:14:ARG:NH1	70:SS:19:ASN:OD1	2.45	0.42
87:NM:132:VAL:HG22	87:NM:482:LYS:HE3	2.01	0.42
4:L5:1238:A:C8	11:LE:59:ARG:HD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LI:171:TRP:O	15:LI:174:THR:OG1	2.30	0.42
27:LV:42:VAL:HB	27:LV:45:ILE:HG13	2.00	0.42
30:LY:103:LYS:HA	30:LY:103:LYS:HD3	1.87	0.42
34:Lc:36:LYS:HB2	34:Lc:36:LYS:HE3	1.90	0.42
52:SA:50:ASN:ND2	52:SA:53:ARG:HH11	2.17	0.42
71:ST:129:ARG:HD3	71:ST:133:ARG:HH21	1.84	0.42
85:NA:100:LYS:HE2	85:NA:102:ILE:HD12	2.01	0.42
85:NA:114:SER:HA	85:NA:115:PRO:HD3	1.91	0.42
4:L5:684:G:O3'	11:LE:101:ASN:HB2	2.20	0.42
4:L5:2411:C:O2'	4:L5:2526:C:O2	2.38	0.42
4:L5:2520:C:O2	4:L5:2640:G:N2	2.53	0.42
4:L5:2583:C:OP2	38:Lg:76:ARG:NH1	2.51	0.42
4:L5:4453:C:H2'	4:L5:4454:G:O4'	2.19	0.42
28:LW:20:ARG:NE	28:LW:30:GLN:HE21	2.18	0.42
49:Ls:106:LYS:HE2	49:Ls:187:LEU:H	1.84	0.42
51:S2:86:C:P	51:S2:149:A:HO2'	2.43	0.42
51:S2:1305:C:OP1	83:Sf:93:HIS:NE2	2.52	0.42
61:SJ:78:LEU:HD21	61:SJ:94:LEU:HA	2.01	0.42
66:SO:94:HIS:HA	66:SO:127:GLY:O	2.19	0.42
74:SW:49:GLU:O	74:SW:64:ASN:ND2	2.52	0.42
84:Sg:79:LEU:HD21	84:Sg:120:ILE:HG23	2.02	0.42
4:L5:61:A:H5''	19:LN:164:LEU:HD21	2.02	0.42
4:L5:501:C:H42	4:L5:506:C:H41	1.67	0.42
4:L5:1079:C:H2'	4:L5:1080:C:C6	2.55	0.42
4:L5:1884:C:H4'	4:L5:2070:U:C4	2.54	0.42
4:L5:1940:G:H22	4:L5:4434:C:H5''	1.84	0.42
4:L5:2520:C:H2'	4:L5:2521:G:C8	2.55	0.42
4:L5:2732:G:H2'	4:L5:2733:C:C6	2.54	0.42
8:LB:139:ASP:OD2	8:LB:140:GLU:N	2.53	0.42
12:LF:226:HIS:ND1	12:LF:228:VAL:HG22	2.35	0.42
13:LG:209:SER:HA	13:LG:212:LYS:HG3	2.00	0.42
14:LH:115:ARG:HD3	14:LH:115:ARG:HA	1.94	0.42
15:LI:48:LEU:HD21	15:LI:145:GLU:HA	2.01	0.42
16:LJ:88:LYS:HB2	16:LJ:88:LYS:HE3	1.75	0.42
20:LO:126:VAL:HG13	20:LO:127:VAL:HG13	2.01	0.42
26:LU:67:LYS:HB2	26:LU:67:LYS:HE2	1.77	0.42
33:Lb:32:LEU:HD23	33:Lb:32:LEU:HA	1.90	0.42
51:S2:1425:G:H21	71:ST:5:THR:HG21	1.85	0.42
83:Sf:121:CYS:HB2	83:Sf:146:LEU:HD11	2.01	0.42
87:Nm:320:MET:O	87:Nm:324:MET:HG2	2.19	0.42
3:CR:86:ASN:OD1	3:CR:86:ASN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1590:C:H3'	4:L5:1591:U:H4'	2.02	0.42
4:L5:1646:A:O2'	41:Lj:49:TRP:O	2.34	0.42
4:L5:4237:C:O3'	4:L5:4326:G:N2	2.53	0.42
4:L5:4518:A:P	8:LB:258:HIS:HB2	2.60	0.42
6:L8:70:G:H22	6:L8:87:G:H1'	1.83	0.42
37:Lf:36:ARG:NH1	37:Lf:79:GLY:O	2.41	0.42
44:Lm:106:ARG:HE	44:Lm:106:ARG:HB3	1.57	0.42
49:Ls:199:TYR:HE1	49:Ls:204:LEU:HB2	1.85	0.42
51:S2:146:G:N2	51:S2:175:A:H1'	2.35	0.42
53:SB:190:PRO:O	53:SB:192:SER:N	2.50	0.42
58:SG:12:CYS:HB3	58:SG:124:LEU:HA	2.02	0.42
68:SQ:51:LEU:HD12	68:SQ:51:LEU:HA	1.85	0.42
3:CR:131:PHE:HD2	3:CR:131:PHE:HA	1.72	0.42
4:L5:1345:A:H2'	4:L5:1346:C:C6	2.54	0.42
4:L5:2412:A:H2'	4:L5:2413:U:C6	2.55	0.42
4:L5:4291:G:H5'	4:L5:4293:U:C6	2.55	0.42
9:LC:138:MET:HB3	9:LC:138:MET:HE3	1.74	0.42
15:LI:95:HIS:CD2	15:LI:128:ARG:HH11	2.38	0.42
21:LP:94:MET:HB3	21:LP:148:MET:HE3	2.01	0.42
41:Lj:21:ARG:O	41:Lj:23:GLY:N	2.50	0.42
45:Ln:1:MET:HB2	51:S2:1706:G:H5'	2.02	0.42
49:Ls:57:LYS:O	49:Ls:61:MET:HG2	2.19	0.42
51:S2:1396:A:H4'	51:S2:1396:A:OP1	2.19	0.42
4:L5:443:G:H5''	37:Lf:54:LYS:HG2	2.02	0.42
4:L5:968:C:H5''	11:LE:110:ARG:HH12	1.85	0.42
4:L5:1733:G:N3	4:L5:4214:A:H2'	2.35	0.42
14:LH:187:VAL:HG12	14:LH:188:GLN:H	1.85	0.42
29:LX:89:LYS:HA	29:LX:89:LYS:HD2	1.92	0.42
51:S2:1238:U:O2	51:S2:1242:U:H5	2.02	0.42
51:S2:1798:C:H2'	51:S2:1799:G:O4'	2.20	0.42
71:ST:24:LYS:HE2	71:ST:24:LYS:HB3	1.95	0.42
84:Sg:156:PHE:HE1	84:Sg:179:LEU:HD11	1.85	0.42
4:L5:958:G:H21	11:LE:125:LEU:H	1.68	0.42
4:L5:1177:U:O2'	10:LD:286:SER:OG	2.28	0.42
4:L5:1552:G:O2'	4:L5:1574:G:N2	2.40	0.42
4:L5:3859:G:N7	21:LP:25:HIS:HE1	2.17	0.42
4:L5:3932:U:H2'	4:L5:3933:G:C8	2.54	0.42
17:LL:46:ILE:HD11	17:LL:51:ALA:HA	2.00	0.42
17:LL:162:LYS:HD2	17:LL:162:LYS:HA	1.80	0.42
30:LY:109:LEU:HD23	30:LY:109:LEU:HA	1.85	0.42
34:Lc:21:VAL:HG11	34:Lc:96:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Lk:27:LYS:HE3	42:Lk:27:LYS:HB2	1.90	0.42
47:Lp:46:LYS:HE3	47:Lp:46:LYS:HB3	1.78	0.42
51:S2:888:U:O2'	51:S2:890:U:OP1	2.27	0.42
51:S2:1498:A:OP2	55:SD:27:ARG:NH2	2.53	0.42
51:S2:1549:U:OP1	81:Sd:34:TYR:OH	2.36	0.42
66:SO:28:PHE:HA	66:SO:92:ALA:O	2.19	0.42
3:CR:325:ASN:OD1	3:CR:325:ASN:N	2.48	0.41
4:L5:318:A:H2'	4:L5:319:A:C8	2.55	0.41
4:L5:1992:U:H1'	4:L5:2002:A:H5''	2.01	0.41
4:L5:4373:G:N7	46:Lo:61:LYS:NZ	2.65	0.41
4:L5:4635:A:H3'	4:L5:4636:U:H4'	2.02	0.41
49:Ls:190:GLN:OE1	49:Ls:190:GLN:N	2.52	0.41
51:S2:16:G:H2'	51:S2:17:C:C6	2.55	0.41
51:S2:1007:C:H2'	51:S2:1008:A:C8	2.54	0.41
51:S2:1017:U:H5'	65:SN:55:ARG:HD3	2.01	0.41
61:SJ:137:VAL:HG12	61:SJ:138:ARG:H	1.84	0.41
66:SO:75:MET:HE2	66:SO:75:MET:HB3	1.88	0.41
67:SP:116:LEU:HD23	67:SP:116:LEU:HA	1.90	0.41
67:SP:137:HIS:O	67:SP:137:HIS:ND1	2.53	0.41
4:L5:979:C:OP2	11:LE:66:LYS:HE2	2.20	0.41
4:L5:1445:U:H2'	4:L5:1446:C:C6	2.55	0.41
4:L5:2621:A:H2'	4:L5:2622:G:C8	2.55	0.41
4:L5:4119:C:H5	38:Lg:100:GLN:HG2	1.82	0.41
8:LB:300:LYS:HE3	8:LB:300:LYS:HB3	1.69	0.41
13:LG:228:ASP:N	13:LG:228:ASP:OD1	2.36	0.41
17:LL:50:PRO:HB3	17:LL:150:LEU:HB3	2.01	0.41
28:LW:54:LEU:HD23	28:LW:54:LEU:HA	1.92	0.41
28:LW:82:ILE:O	58:SG:130:PRO:HB2	2.20	0.41
30:LY:54:GLU:HB2	30:LY:108:ARG:HB3	2.01	0.41
31:LZ:41:ALA:HB2	31:LZ:77:TYR:HE1	1.85	0.41
40:Li:16:LYS:HA	40:Li:16:LYS:HD3	1.68	0.41
49:Ls:77:LYS:HB3	49:Ls:77:LYS:HE2	1.62	0.41
51:S2:96:C:O2	51:S2:473:A:O2'	2.39	0.41
51:S2:349:A:H2'	51:S2:350:C:C6	2.55	0.41
51:S2:503:C:H3'	51:S2:504:G:H8	1.85	0.41
51:S2:1546:G:N2	51:S2:1670:C:O2	2.53	0.41
66:SO:101:GLY:HA3	66:SO:134:PRO:HG2	2.02	0.41
87:NM:242:MET:HE3	87:NM:242:MET:HA	2.02	0.41
4:L5:4130:C:H41	4:L5:4154:G:H1	1.68	0.41
4:L5:4154:G:OP1	29:LX:37:LYS:N	2.53	0.41
4:L5:4761:G:H2'	4:L5:4762:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4967:A:H2'	4:L5:4968:A:H8	1.85	0.41
31:LZ:100:VAL:HG22	31:LZ:106:LEU:HB3	2.03	0.41
32:La:85:GLN:HA	32:La:88:VAL:HG22	2.02	0.41
51:S2:329:G:H2'	51:S2:330:G:C8	2.55	0.41
51:S2:1759:G:H1'	51:S2:1774:C:N3	2.36	0.41
60:SI:57:ALA:HB2	60:SI:183:GLY:HA2	2.02	0.41
64:SM:87:GLU:OE2	64:SM:92:CYS:HB3	2.20	0.41
75:SX:60:LYS:H	75:SX:114:ASP:HB2	1.84	0.41
75:SX:88:ASP:N	75:SX:88:ASP:OD1	2.53	0.41
76:SY:23:MET:HE2	76:SY:23:MET:HB3	1.85	0.41
84:Sg:84:ASP:OD2	84:Sg:84:ASP:N	2.52	0.41
4:L5:1631:A:N7	7:LA:199:VAL:HG21	2.35	0.41
4:L5:3786:U:OP1	4:L5:4550:G:O2'	2.35	0.41
4:L5:4075:U:OP1	13:LG:246:SER:OG	2.34	0.41
4:L5:4219:A:H2'	4:L5:4220:A:C8	2.55	0.41
15:LI:74:LYS:HE3	15:LI:74:LYS:HB2	1.61	0.41
51:S2:942:G:H2'	51:S2:943:U:C6	2.54	0.41
51:S2:1617:G:N1	51:S2:1620:A:OP2	2.53	0.41
53:SB:144:LYS:HD3	53:SB:208:HIS:HB3	2.02	0.41
54:SC:252:THR:HG23	54:SC:254:ASP:OD2	2.21	0.41
64:SM:52:LEU:HD21	64:SM:65:VAL:HG21	2.01	0.41
75:SX:32:LEU:HD12	75:SX:32:LEU:HA	1.89	0.41
87:NM:360:PHE:HB3	87:NM:490:LYS:O	2.20	0.41
87:NM:432:LEU:HD13	87:NM:432:LEU:HA	1.94	0.41
4:L5:52:G:H4'	4:L5:1529:G:H4'	2.03	0.41
4:L5:1971:C:H5	4:L5:2000:G:H2'	1.86	0.41
4:L5:2520:C:H2'	4:L5:2521:G:H8	1.86	0.41
4:L5:2568:C:H2'	4:L5:2569:G:C8	2.54	0.41
4:L5:3883:U:H2'	4:L5:3884:U:C6	2.56	0.41
4:L5:4093:G:OP2	4:L5:4093:G:N2	2.43	0.41
4:L5:4581:G:HO2'	8:LB:92:TYR:HH	1.61	0.41
6:L8:106:G:H4'	6:L8:137:A:H5'	2.02	0.41
11:LE:205:ASN:OD1	11:LE:205:ASN:N	2.43	0.41
14:LH:10:VAL:HG22	14:LH:55:LEU:HB3	2.02	0.41
40:Li:89:GLU:O	40:Li:93:VAL:HG13	2.20	0.41
51:S2:145:G:H1	51:S2:175:A:H2	1.67	0.41
57:SF:99:ILE:HG23	77:SZ:67:LEU:HD13	2.02	0.41
59:SH:62:ILE:HD11	59:SH:94:PHE:CE2	2.55	0.41
61:SJ:84:ILE:HD11	61:SJ:148:ILE:HG22	2.02	0.41
75:SX:107:ARG:HE	75:SX:107:ARG:HB3	1.75	0.41
87:NM:376:TYR:HA	87:NM:377:PRO:HD3	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1577:G:O2'	4:L5:1612:G:H4'	2.20	0.41
4:L5:2676:A:OP2	4:L5:2676:A:H8	2.03	0.41
4:L5:3612:C:H1'	4:L5:5016:A:H8	1.85	0.41
4:L5:4364:G:H2'	4:L5:4365:C:H6	1.84	0.41
10:LD:41:LYS:HD3	10:LD:41:LYS:HA	1.89	0.41
20:LO:181:ALA:O	20:LO:185:VAL:HG22	2.20	0.41
23:LR:76:MET:HE2	23:LR:76:MET:HB3	1.98	0.41
51:S2:798:G:H1'	59:SH:108:SER:H	1.85	0.41
51:S2:1480:A:O2'	81:Sd:56:ASP:O	2.35	0.41
52:SA:57:LYS:HD3	73:SV:70:LEU:HD13	2.01	0.41
52:SA:183:LEU:HB3	52:SA:189:ILE:HG12	2.01	0.41
54:SC:68:ARG:HE	54:SC:68:ARG:HB2	1.67	0.41
58:SG:135:PRO:HG2	58:SG:141:ILE:HD13	2.03	0.41
68:SQ:16:LYS:HG2	68:SQ:79:ALA:HA	2.03	0.41
70:SS:121:ARG:HG3	70:SS:131:VAL:HB	2.02	0.41
71:ST:94:ARG:H	71:ST:94:ARG:HG2	1.67	0.41
84:Sg:67:SER:N	84:Sg:81:GLY:O	2.52	0.41
4:L5:515:C:H41	4:L5:647:G:H21	1.68	0.41
4:L5:1461:C:H2'	4:L5:1462:A:C8	2.56	0.41
4:L5:1751:A:H2'	4:L5:1752:G:C8	2.56	0.41
4:L5:2008:U:H1'	4:L5:2011:C:H5	1.86	0.41
4:L5:4674:C:H2'	4:L5:4675:U:C6	2.56	0.41
4:L5:4996:C:OP1	35:Ld:32:ARG:NH1	2.33	0.41
6:L8:19:C:H2'	6:L8:20:A:C8	2.55	0.41
6:L8:47:C:H1'	6:L8:61:A:H2'	2.02	0.41
7:LA:145:LYS:HA	7:LA:145:LYS:HD3	1.87	0.41
9:LC:150:LEU:HD12	9:LC:150:LEU:HA	1.81	0.41
13:LG:166:LEU:HA	19:LN:7:ILE:HD11	2.02	0.41
13:LG:253:LEU:HD23	13:LG:253:LEU:HA	1.89	0.41
16:LJ:101:ASP:HA	16:LJ:159:LYS:HB3	2.03	0.41
27:LV:25:VAL:HG22	27:LV:38:TYR:HB2	2.03	0.41
32:La:16:SER:OG	32:La:17:HIS:N	2.53	0.41
42:Lk:35:LYS:HA	42:Lk:43:TYR:O	2.20	0.41
49:Ls:45:MET:HE2	49:Ls:45:MET:HA	2.01	0.41
51:S2:629:A:O2'	51:S2:631:U:OP1	2.39	0.41
51:S2:1229:G:H21	71:ST:87:VAL:HG22	1.85	0.41
51:S2:1512:C:H5''	81:Sd:8:TRP:CZ3	2.56	0.41
58:SG:2:LYS:HB3	58:SG:15:LEU:HD11	2.02	0.41
64:SM:121:LYS:HE2	64:SM:121:LYS:HB2	1.81	0.41
3:CR:16:LYS:HA	3:CR:16:LYS:HD3	1.75	0.41
4:L5:107:G:OP1	17:LL:42:LYS:NZ	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1443:A:N6	4:L5:2104:G:N2	2.66	0.41
4:L5:4452:U:H6	4:L5:4452:U:H2'	1.53	0.41
4:L5:4966:A:H2'	4:L5:4967:A:O4'	2.21	0.41
5:L7:40:U:O2'	16:LJ:75:ARG:HG2	2.21	0.41
6:L8:140:C:H2'	6:L8:141:C:C6	2.55	0.41
8:LB:107:ALA:HB2	8:LB:201:LEU:HD22	2.03	0.41
12:LF:88:LYS:H	12:LF:88:LYS:HG2	1.66	0.41
24:LS:28:TYR:CZ	24:LS:52:LYS:HE3	2.56	0.41
25:LT:116:LYS:HD3	25:LT:128:LEU:HD11	2.03	0.41
35:Ld:24:GLU:HG2	35:Ld:87:ARG:HB2	2.01	0.41
49:Ls:17:ILE:HD12	49:Ls:54:LEU:HD11	2.03	0.41
51:S2:495:U:H2'	51:S2:496:C:O4'	2.20	0.41
51:S2:1480:A:O5'	68:SQ:131:LYS:HE2	2.21	0.41
52:SA:110:ASN:HB3	52:SA:113:GLN:HG3	2.02	0.41
53:SB:138:PHE:O	53:SB:213:ARG:N	2.54	0.41
57:SF:125:SER:HB3	57:SF:136:ARG:HB3	2.03	0.41
59:SH:154:ILE:O	59:SH:185:VAL:HA	2.20	0.41
62:SK:20:VAL:HA	62:SK:69:TRP:O	2.20	0.41
63:SL:81:LYS:HB3	63:SL:81:LYS:HE3	1.73	0.41
87:Nm:270:ARG:HA	87:Nm:273:LEU:HD12	2.03	0.41
3:CR:226:LEU:O	3:CR:253:LEU:HA	2.21	0.41
4:L5:50:C:OP1	17:LL:20:ARG:NH2	2.47	0.41
4:L5:504:G:H1	4:L5:656:C:H1'	1.86	0.41
4:L5:968:C:P	11:LE:110:ARG:HH22	2.43	0.41
4:L5:1961:G:OP2	49:Ls:59:THR:OG1	2.24	0.41
4:L5:2045:G:O6	4:L5:3870:C:O2'	2.39	0.41
4:L5:3775:A:H5'	4:L5:3776:G:OP2	2.21	0.41
4:L5:4425:G:OP1	44:Lm:100:TYR:OH	2.26	0.41
4:L5:4507:A:H2'	4:L5:4508:C:C6	2.56	0.41
4:L5:4581:G:O2'	8:LB:92:TYR:OH	2.33	0.41
4:L5:4611:A:H2'	4:L5:4612:C:H6	1.86	0.41
4:L5:4896:G:N2	4:L5:4927:G:O6	2.54	0.41
7:LA:173:GLY:O	7:LA:176:ASP:HB2	2.20	0.41
8:LB:153:MET:HB3	8:LB:194:LEU:HD11	2.03	0.41
13:LG:53:ARG:HG2	13:LG:54:PHE:CE1	2.56	0.41
14:LH:92:MET:O	14:LH:143:GLU:HA	2.20	0.41
28:LW:8:PHE:HB3	28:LW:36:CYS:HB3	2.03	0.41
32:La:17:HIS:O	32:La:19:HIS:N	2.50	0.41
44:Lm:112:LYS:HD3	44:Lm:112:LYS:HA	1.86	0.41
49:Ls:37:SER:O	49:Ls:41:GLN:HG2	2.20	0.41
49:Ls:106:LYS:HE2	49:Ls:186:GLY:HA3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:S2:804:U:H2'	51:S2:805:U:C6	2.56	0.41
51:S2:1745:A:N6	51:S2:1789:G:O2'	2.54	0.41
53:SB:167:LYS:HA	53:SB:167:LYS:HD3	1.87	0.41
55:SD:176:LEU:HA	55:SD:176:LEU:HD13	1.89	0.41
57:SF:124:ASP:OD1	57:SF:125:SER:N	2.48	0.41
58:SG:2:LYS:HD3	58:SG:15:LEU:HD21	2.01	0.41
64:SM:54:SER:HB3	64:SM:78:LYS:HD2	2.03	0.41
65:SN:40:LEU:HB3	65:SN:45:LEU:HD12	2.02	0.41
65:SN:110:ASP:O	65:SN:114:ARG:HG2	2.21	0.41
75:SX:11:ARG:O	75:SX:15:SER:OG	2.29	0.41
76:SY:40:ILE:HD13	76:SY:40:ILE:HA	1.87	0.41
85:NA:103:LEU:HD21	86:NB:109:GLN:NE2	2.36	0.41
87:NM:397:PHE:HD1	87:NM:425:VAL:HG22	1.86	0.41
3:CR:81:ARG:HD3	3:CR:84:LEU:HD12	2.03	0.41
4:L5:2261:G:H4'	11:LE:112:MET:HE1	2.03	0.41
4:L5:2539:C:H2'	4:L5:2540:C:C6	2.56	0.41
4:L5:2756:G:O6	31:LZ:51:ARG:NH2	2.37	0.41
4:L5:3642:A:C4	41:Lj:3:LYS:HB3	2.55	0.41
4:L5:3707:U:H2'	4:L5:3708:C:H6	1.86	0.41
4:L5:4239:A:H2'	4:L5:4240:G:C8	2.56	0.41
4:L5:4524:G:C2	8:LB:252:ALA:HB1	2.56	0.41
5:L7:110:G:H2'	5:L7:111:C:C6	2.56	0.41
26:LU:24:ASP:OD2	26:LU:26:THR:HG23	2.21	0.41
29:LX:81:LEU:HD12	29:LX:81:LEU:HA	1.97	0.41
49:Ls:29:ILE:HD11	49:Ls:78:LEU:HD23	2.03	0.41
50:Lt:143:VAL:HG22	50:Lt:148:PRO:HG3	2.03	0.41
51:S2:344:U:H2'	51:S2:345:U:C6	2.56	0.41
51:S2:1201:U:H2'	51:S2:1202:U:C6	2.55	0.41
51:S2:1630:A:H5''	70:SS:37:GLY:H	1.86	0.41
54:SC:254:ASP:OD2	54:SC:254:ASP:N	2.51	0.41
63:SL:78:THR:HG22	63:SL:79:LYS:HG3	2.03	0.41
66:SO:44:VAL:HG12	66:SO:53:ILE:HB	2.02	0.41
69:SR:45:LYS:HE2	69:SR:45:LYS:HB2	1.72	0.41
3:CR:123:SER:OG	4:L5:3762:U:OP1	2.31	0.40
4:L5:158:A:H5''	4:L5:159:C:H2'	2.03	0.40
4:L5:3599:A:H2'	4:L5:3600:G:C8	2.56	0.40
13:LG:252:LYS:HE3	13:LG:252:LYS:HB2	1.85	0.40
14:LH:92:MET:HB3	14:LH:179:ILE:HG22	2.03	0.40
18:LM:79:LYS:HE3	18:LM:79:LYS:HB3	1.92	0.40
21:LP:103:GLU:HG2	21:LP:109:VAL:HG11	2.03	0.40
27:LV:87:SER:HA	27:LV:97:TYR:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Lg:103:VAL:HA	38:Lg:106:VAL:HG22	2.03	0.40
51:S2:147:A:N6	51:S2:173:A:H61	2.18	0.40
51:S2:639:C:H2'	51:S2:640:A:H8	1.87	0.40
51:S2:846:G:OP2	56:SE:108:ARG:NH1	2.48	0.40
53:SB:36:PRO:HD3	53:SB:98:THR:HG22	2.03	0.40
53:SB:98:THR:O	53:SB:232:HIS:NE2	2.53	0.40
64:SM:18:LEU:O	64:SM:22:LEU:HG	2.21	0.40
79:Sb:55:LEU:HB3	79:Sb:62:VAL:HA	2.03	0.40
4:L5:1755:C:H1'	10:LD:2:GLY:HA3	2.03	0.40
4:L5:2465:C:H2'	4:L5:2466:G:O4'	2.21	0.40
4:L5:4188:U:H2'	4:L5:4189:U:C6	2.56	0.40
10:LD:104:LEU:HB2	10:LD:247:ILE:HD13	2.03	0.40
18:LM:52:PHE:HA	18:LM:55:MET:HE3	2.01	0.40
21:LP:20:SER:O	21:LP:22:LEU:N	2.54	0.40
33:Lb:48:LYS:HE2	33:Lb:49:HIS:CE1	2.56	0.40
39:Lh:60:VAL:O	39:Lh:64:THR:HG22	2.20	0.40
51:S2:12:U:H2'	51:S2:13:C:C6	2.56	0.40
51:S2:28:U:H2'	51:S2:29:G:H8	1.85	0.40
51:S2:924:G:OP1	65:SN:4:MET:N	2.51	0.40
51:S2:1274:G:OP2	51:S2:1275:G:H5'	2.21	0.40
51:S2:1531:A:H4'	51:S2:1605:G:H4'	2.02	0.40
51:S2:1597:C:O2'	51:S2:1598:G:O4'	2.38	0.40
57:SF:41:VAL:HA	57:SF:45:TYR:HB2	2.02	0.40
71:ST:60:THR:HG23	71:ST:75:MET:HE2	2.03	0.40
80:Sc:31:ARG:NH2	80:Sc:43:ILE:HD11	2.36	0.40
86:NB:64:MET:HE3	86:NB:65:PHE:N	2.35	0.40
3:CR:362:THR:HG23	3:CR:364:GLN:H	1.86	0.40
4:L5:1364:U:OP2	17:LL:36:ARG:NH1	2.49	0.40
4:L5:2862:G:N3	4:L5:3624:A:H2'	2.37	0.40
4:L5:4939:C:OP1	11:LE:187:ARG:NH1	2.52	0.40
7:LA:181:LYS:HB2	7:LA:184:ARG:HG3	2.03	0.40
34:Lc:65:MET:HE3	34:Lc:65:MET:HB3	1.99	0.40
35:Ld:25:TYR:O	35:Ld:85:ARG:HD2	2.21	0.40
51:S2:1046:U:H2'	51:S2:1047:C:O4'	2.21	0.40
51:S2:1845:A:H2'	51:S2:1846:G:H8	1.86	0.40
58:SG:201:LYS:O	58:SG:205:GLU:HG3	2.22	0.40
64:SM:83:LYS:HD3	64:SM:103:VAL:HG11	2.03	0.40
65:SN:114:ARG:HA	65:SN:114:ARG:HD3	1.96	0.40
76:SY:41:ARG:HA	76:SY:55:ILE:HG21	2.03	0.40
86:NB:6:MET:HE3	86:NB:6:MET:HB3	1.87	0.40
4:L5:123:C:H2'	4:L5:124:C:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1645:C:H2'	4:L5:1646:A:C8	2.56	0.40
4:L5:2411:C:H2'	4:L5:2412:A:H8	1.87	0.40
4:L5:3928:A:H2'	4:L5:3929:G:O4'	2.20	0.40
10:LD:236:MET:HA	10:LD:239:MET:HE2	2.03	0.40
11:LE:208:ILE:HG22	11:LE:210:LYS:H	1.86	0.40
23:LR:19:LYS:HB2	23:LR:19:LYS:HE2	1.88	0.40
23:LR:80:LYS:HD2	23:LR:80:LYS:HA	1.89	0.40
27:LV:43:LYS:HG3	27:LV:60:MET:HG2	2.02	0.40
32:La:3:SER:HA	32:La:6:ARG:HG3	2.02	0.40
43:Ll:9:ILE:HD13	43:Ll:9:ILE:HA	1.92	0.40
49:Ls:211:LEU:HD23	49:Ls:211:LEU:HA	1.96	0.40
50:Lt:92:ARG:HA	50:Lt:92:ARG:HD2	1.78	0.40
51:S2:170:A:OP1	58:SG:136:LYS:N	2.42	0.40
51:S2:1822:A:H2'	51:S2:1823:A:C8	2.57	0.40
53:SB:173:THR:O	53:SB:177:GLN:HG2	2.21	0.40
56:SE:45:ILE:HB	56:SE:80:ILE:HG23	2.03	0.40
71:ST:102:ARG:HA	71:ST:102:ARG:HD3	1.82	0.40
76:SY:41:ARG:HG2	76:SY:55:ILE:HG22	2.03	0.40
84:Sg:35:SER:OG	84:Sg:36:ARG:N	2.54	0.40
4:L5:1174:G:H1	4:L5:1186:U:H3	1.69	0.40
4:L5:1972:G:N2	50:Lt:131:GLU:OE1	2.55	0.40
7:LA:123:ARG:HD3	7:LA:123:ARG:HA	1.85	0.40
11:LE:99:ASP:OD1	11:LE:99:ASP:N	2.53	0.40
18:LM:28:VAL:HG11	18:LM:47:ARG:NH1	2.37	0.40
23:LR:95:TRP:CH2	23:LR:99:MET:HE3	2.56	0.40
41:Lj:67:LEU:HD23	41:Lj:67:LEU:HA	1.91	0.40
51:S2:186:C:H2'	51:S2:187:G:C8	2.57	0.40
62:SK:27:VAL:HG13	62:SK:43:LEU:HG	2.02	0.40
68:SQ:113:ILE:HG12	68:SQ:120:LEU:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CM	11/586 (1%)	2 (18%)	0
2	CP	74/75 (98%)	23 (31%)	2 (2%)
4	L5	3633/5070 (71%)	750 (20%)	21 (0%)
5	L7	119/121 (98%)	14 (11%)	0
51	S2	1704/1869 (91%)	458 (26%)	18 (1%)
6	L8	155/157 (98%)	27 (17%)	3 (1%)
All	All	5696/7878 (72%)	1274 (22%)	44 (0%)

All (1274) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CM	439	C
1	CM	444	U
2	CP	2	G
2	CP	4	U
2	CP	5	C
2	CP	6	G
2	CP	8	U
2	CP	9	G
2	CP	15	G
2	CP	16	G
2	CP	17	G
2	CP	19	U
2	CP	22	G
2	CP	46	U
2	CP	49	C
2	CP	50	G
2	CP	57	A
2	CP	58	A
2	CP	61	C
2	CP	68	A
2	CP	69	G
2	CP	70	C
2	CP	72	C
2	CP	73	C
2	CP	75	A
4	L5	17	A
4	L5	21	G
4	L5	30	C
4	L5	39	A
4	L5	42	A

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Mol	Chain	Res	Type
4	L5	48	G
4	L5	56	A
4	L5	59	A
4	L5	64	A
4	L5	65	A
4	L5	69	A
4	L5	73	A
4	L5	91	G
4	L5	98	A
4	L5	104	G
4	L5	108	A
4	L5	109	G
4	L5	110	C
4	L5	116	G
4	L5	117	C
4	L5	119	G
4	L5	120	A
4	L5	133	C
4	L5	134	G
4	L5	135	G
4	L5	136	C
4	L5	137	G
4	L5	143	C
4	L5	144	G
4	L5	152	U
4	L5	159	C
4	L5	165	A
4	L5	172	C
4	L5	180	C
4	L5	183	C
4	L5	184	U
4	L5	185	C
4	L5	188	G
4	L5	189	G
4	L5	200	U
4	L5	210	C
4	L5	216	C
4	L5	217	C
4	L5	218	A
4	L5	220	C
4	L5	233	U
4	L5	234	G

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Mol	Chain	Res	Type
4	L5	255	C
4	L5	261	G
4	L5	266	C
4	L5	267	G
4	L5	269	G
4	L5	276	C
4	L5	280	G
4	L5	297	U
4	L5	306	A
4	L5	315	G
4	L5	316	U
4	L5	340	C
4	L5	349	A
4	L5	350	C
4	L5	387	G
4	L5	388	A
4	L5	399	G
4	L5	401	G
4	L5	407	A
4	L5	409	G
4	L5	410	A
4	L5	411	G
4	L5	412	G
4	L5	449	C
4	L5	450	G
4	L5	452	A
4	L5	453	G
4	L5	454	U
4	L5	456	C
4	L5	457	G
4	L5	461	G
4	L5	467	U
4	L5	474	C
4	L5	485	C
4	L5	486	C
4	L5	489	C
4	L5	493	G
4	L5	494	U
4	L5	497	G
4	L5	498	C
4	L5	500	G
4	L5	501	C

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Mol	Chain	Res	Type
4	L5	502	C
4	L5	503	C
4	L5	504	G
4	L5	505	G
4	L5	509	A
4	L5	510	U
4	L5	512	U
4	L5	513	U
4	L5	514	U
4	L5	517	C
4	L5	518	G
4	L5	643	C
4	L5	644	G
4	L5	646	G
4	L5	655	C
4	L5	656	C
4	L5	657	C
4	L5	658	C
4	L5	660	A
4	L5	666	G
4	L5	667	A
4	L5	668	C
4	L5	669	C
4	L5	673	C
4	L5	674	G
4	L5	675	C
4	L5	676	C
4	L5	686	A
4	L5	687	U
4	L5	688	U
4	L5	689	U
4	L5	692	A
4	L5	696	C
4	L5	697	G
4	L5	703	G
4	L5	704	C
4	L5	708	G
4	L5	730	G
4	L5	731	G
4	L5	738	C
4	L5	739	G
4	L5	742	G

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Mol	Chain	Res	Type
4	L5	746	A
4	L5	753	C
4	L5	758	G
4	L5	759	G
4	L5	904	C
4	L5	912	G
4	L5	913	U
4	L5	914	U
4	L5	915	A
4	L5	917	A
4	L5	918	G
4	L5	923	C
4	L5	924	C
4	L5	926	G
4	L5	932	A
4	L5	933	G
4	L5	941	C
4	L5	944	A
4	L5	945	U
4	L5	946	C
4	L5	959	G
4	L5	960	A
4	L5	961	G
4	L5	962	C
4	L5	965	G
4	L5	966	A
4	L5	967	C
4	L5	968	C
4	L5	970	G
4	L5	972	C
4	L5	977	C
4	L5	984	C
4	L5	988	C
4	L5	989	U
4	L5	990	C
4	L5	991	C
4	L5	992	C
4	L5	993	G
4	L5	1066	G
4	L5	1069	G
4	L5	1070	G
4	L5	1075	G

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Mol	Chain	Res	Type
4	L5	1083	U
4	L5	1168	G
4	L5	1171	G
4	L5	1173	G
4	L5	1178	G
4	L5	1179	U
4	L5	1180	C
4	L5	1181	C
4	L5	1182	C
4	L5	1183	C
4	L5	1184	A
4	L5	1187	G
4	L5	1193	C
4	L5	1202	C
4	L5	1203	G
4	L5	1209	U
4	L5	1211	G
4	L5	1214	C
4	L5	1215	C
4	L5	1235	G
4	L5	1238	A
4	L5	1241	C
4	L5	1253	G
4	L5	1259	G
4	L5	1260	G
4	L5	1261	G
4	L5	1266	G
4	L5	1269	G
4	L5	1270	A
4	L5	1271	G
4	L5	1272	C
4	L5	1273	G
4	L5	1274	A
4	L5	1275	G
4	L5	1277	G
4	L5	1280	C
4	L5	1284	G
4	L5	1285	U
4	L5	1287	G
4	L5	1293	G
4	L5	1294	A
4	L5	1295	C

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Mol	Chain	Res	Type
4	L5	1296	G
4	L5	1301	C
4	L5	1303	A
4	L5	1304	C
4	L5	1312	A
4	L5	1324	A
4	L5	1326	A
4	L5	1337	A
4	L5	1344	C
4	L5	1354	A
4	L5	1358	G
4	L5	1359	G
4	L5	1365	C
4	L5	1366	G
4	L5	1378	C
4	L5	1379	C
4	L5	1387	A
4	L5	1393	G
4	L5	1394	G
4	L5	1397	A
4	L5	1398	A
4	L5	1402	C
4	L5	1403	G
4	L5	1404	G
4	L5	1405	C
4	L5	1408	G
4	L5	1410	U
4	L5	1411	C
4	L5	1420	A
4	L5	1425	G
4	L5	1435	G
4	L5	1437	C
4	L5	1439	C
4	L5	1441	C
4	L5	1442	C
4	L5	1443	A
4	L5	1444	G
4	L5	1447	C
4	L5	1454	G
4	L5	1457	G
4	L5	1480	C
4	L5	1483	C

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Mol	Chain	Res	Type
4	L5	1493	G
4	L5	1497	A
4	L5	1498	G
4	L5	1502	G
4	L5	1514	U
4	L5	1525	A
4	L5	1534	A
4	L5	1547	A
4	L5	1566	C
4	L5	1578	U
4	L5	1591	U
4	L5	1596	U
4	L5	1624	G
4	L5	1625	G
4	L5	1631	A
4	L5	1633	G
4	L5	1634	A
4	L5	1640	C
4	L5	1641	G
4	L5	1642	A
4	L5	1654	G
4	L5	1656	U
4	L5	1661	C
4	L5	1663	C
4	L5	1676	C
4	L5	1677	U
4	L5	1684	A
4	L5	1685	G
4	L5	1697	G
4	L5	1699	A
4	L5	1700	G
4	L5	1704	C
4	L5	1705	G
4	L5	1707	C
4	L5	1726	U
4	L5	1734	G
4	L5	1742	A
4	L5	1750	G
4	L5	1753	G
4	L5	1756	U
4	L5	1758	G
4	L5	1760	G

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Mol	Chain	Res	Type
4	L5	1765	A
4	L5	1767	A
4	L5	1781	U
4	L5	1787	A
4	L5	1797	G
4	L5	1803	G
4	L5	1804	A
4	L5	1806	G
4	L5	1810	G
4	L5	1815	G
4	L5	1820	C
4	L5	1821	G
4	L5	1822	U
4	L5	1834	U
4	L5	1836	G
4	L5	1837	A
4	L5	1842	G
4	L5	1855	G
4	L5	1869	G
4	L5	1882	U
4	L5	1891	A
4	L5	1897	A
4	L5	1912	G
4	L5	1918	U
4	L5	1919	G
4	L5	1920	C
4	L5	1921	C
4	L5	1922	G
4	L5	1924	C
4	L5	1931	C
4	L5	1932	A
4	L5	1936	C
4	L5	1940	G
4	L5	1948	G
4	L5	1961	G
4	L5	1962	A
4	L5	1965	G
4	L5	1976	G
4	L5	1980	U
4	L5	1981	G
4	L5	1983	A
4	L5	1984	A

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Mol	Chain	Res	Type
4	L5	1985	G
4	L5	1986	U
4	L5	1987	C
4	L5	1997	U
4	L5	1999	A
4	L5	2001	G
4	L5	2002	A
4	L5	2004	U
4	L5	2007	G
4	L5	2016	C
4	L5	2017	A
4	L5	2018	C
4	L5	2024	G
4	L5	2025	A
4	L5	2026	A
4	L5	2046	G
4	L5	2048	U
4	L5	2052	G
4	L5	2055	G
4	L5	2056	G
4	L5	2069	A
4	L5	2084	C
4	L5	2092	G
4	L5	2094	G
4	L5	2095	A
4	L5	2098	G
4	L5	2101	C
4	L5	2102	G
4	L5	2103	G
4	L5	2106	G
4	L5	2107	C
4	L5	2108	G
4	L5	2116	C
4	L5	2117	G
4	L5	2118	G
4	L5	2119	C
4	L5	2120	G
4	L5	2121	C
4	L5	2123	C
4	L5	2250	C
4	L5	2252	G
4	L5	2253	A

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Mol	Chain	Res	Type
4	L5	2254	G
4	L5	2255	C
4	L5	2256	C
4	L5	2258	C
4	L5	2269	C
4	L5	2289	C
4	L5	2300	A
4	L5	2301	G
4	L5	2313	A
4	L5	2316	G
4	L5	2333	G
4	L5	2348	G
4	L5	2351	C
4	L5	2360	A
4	L5	2395	A
4	L5	2397	G
4	L5	2417	A
4	L5	2421	G
4	L5	2422	C
4	L5	2424	G
4	L5	2425	U
4	L5	2441	C
4	L5	2447	U
4	L5	2450	G
4	L5	2453	A
4	L5	2463	G
4	L5	2464	C
4	L5	2465	C
4	L5	2475	G
4	L5	2483	G
4	L5	2484	A
4	L5	2487	G
4	L5	2488	C
4	L5	2489	C
4	L5	2490	U
4	L5	2491	C
4	L5	2493	G
4	L5	2503	G
4	L5	2504	C
4	L5	2505	C
4	L5	2506	G
4	L5	2513	A

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Mol	Chain	Res	Type
4	L5	2519	U
4	L5	2520	C
4	L5	2537	A
4	L5	2544	G
4	L5	2545	U
4	L5	2546	G
4	L5	2547	G
4	L5	2554	U
4	L5	2555	G
4	L5	2567	G
4	L5	2573	A
4	L5	2583	C
4	L5	2587	A
4	L5	2589	C
4	L5	2601	A
4	L5	2611	A
4	L5	2618	G
4	L5	2627	C
4	L5	2653	C
4	L5	2662	G
4	L5	2669	C
4	L5	2676	A
4	L5	2687	U
4	L5	2694	G
4	L5	2695	A
4	L5	2696	A
4	L5	2703	G
4	L5	2710	C
4	L5	2711	G
4	L5	2721	G
4	L5	2724	G
4	L5	2726	G
4	L5	2739	C
4	L5	2742	G
4	L5	2743	A
4	L5	2746	A
4	L5	2754	G
4	L5	2761	U
4	L5	2763	U
4	L5	2764	A
4	L5	2769	U
4	L5	2770	C

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Mol	Chain	Res	Type
4	L5	2788	U
4	L5	2790	U
4	L5	2814	C
4	L5	2815	A
4	L5	2826	U
4	L5	2827	G
4	L5	2838	G
4	L5	2842	G
4	L5	2848	G
4	L5	2855	G
4	L5	2856	C
4	L5	2867	C
4	L5	2877	G
4	L5	2889	G
4	L5	2891	U
4	L5	2892	C
4	L5	2894	A
4	L5	2896	G
4	L5	2897	G
4	L5	2900	U
4	L5	2902	G
4	L5	2903	G
4	L5	2904	U
4	L5	2905	C
4	L5	2906	G
4	L5	2907	G
4	L5	2908	U
4	L5	3585	G
4	L5	3586	G
4	L5	3588	C
4	L5	3591	C
4	L5	3593	C
4	L5	3594	C
4	L5	3595	U
4	L5	3596	A
4	L5	3597	G
4	L5	3604	A
4	L5	3605	C
4	L5	3606	U
4	L5	3615	G
4	L5	3618	C
4	L5	3626	G

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Mol	Chain	Res	Type
4	L5	3630	A
4	L5	3635	A
4	L5	3644	U
4	L5	3646	A
4	L5	3648	A
4	L5	3662	A
4	L5	3664	G
4	L5	3673	C
4	L5	3674	G
4	L5	3685	C
4	L5	3705	G
4	L5	3711	A
4	L5	3713	U
4	L5	3735	G
4	L5	3736	A
4	L5	3748	A
4	L5	3750	G
4	L5	3753	G
4	L5	3760	A
4	L5	3761	C
4	L5	3771	C
4	L5	3775	A
4	L5	3776	G
4	L5	3777	G
4	L5	3784	A
4	L5	3785	A
4	L5	3786	U
4	L5	3810	C
4	L5	3812	C
4	L5	3814	U
4	L5	3817	A
4	L5	3818	U
4	L5	3819	G
4	L5	3823	G
4	L5	3838	U
4	L5	3839	G
4	L5	3840	U
4	L5	3841	C
4	L5	3851	U
4	L5	3867	A
4	L5	3876	A
4	L5	3877	A

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Mol	Chain	Res	Type
4	L5	3878	C
4	L5	3879	G
4	L5	3885	G
4	L5	3892	U
4	L5	3897	G
4	L5	3901	A
4	L5	3905	A
4	L5	3906	A
4	L5	3907	G
4	L5	3908	A
4	L5	3915	U
4	L5	3916	G
4	L5	3926	C
4	L5	3930	U
4	L5	3939	G
4	L5	3942	A
4	L5	3943	A
4	L5	3947	A
4	L5	3949	A
4	L5	4064	C
4	L5	4065	G
4	L5	4076	G
4	L5	4099	G
4	L5	4102	C
4	L5	4104	G
4	L5	4107	G
4	L5	4111	U
4	L5	4113	U
4	L5	4114	C
4	L5	4115	G
4	L5	4116	C
4	L5	4119	C
4	L5	4122	G
4	L5	4128	A
4	L5	4131	G
4	L5	4137	C
4	L5	4138	C
4	L5	4140	C
4	L5	4141	G
4	L5	4142	C
4	L5	4143	G
4	L5	4145	C

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Mol	Chain	Res	Type
4	L5	4150	G
4	L5	4154	G
4	L5	4155	C
4	L5	4160	C
4	L5	4162	C
4	L5	4163	U
4	L5	4170	A
4	L5	4177	C
4	L5	4183	G
4	L5	4184	G
4	L5	4191	G
4	L5	4201	G
4	L5	4203	A
4	L5	4222	G
4	L5	4225	G
4	L5	4229	U
4	L5	4233	A
4	L5	4249	G
4	L5	4251	A
4	L5	4254	G
4	L5	4258	C
4	L5	4268	A
4	L5	4273	A
4	L5	4281	A
4	L5	4291	G
4	L5	4296	U
4	L5	4304	A
4	L5	4305	G
4	L5	4306	U
4	L5	4314	C
4	L5	4319	C
4	L5	4329	G
4	L5	4330	G
4	L5	4332	C
4	L5	4339	A
4	L5	4349	C
4	L5	4373	G
4	L5	4376	A
4	L5	4377	G
4	L5	4378	A
4	L5	4379	A
4	L5	4387	C

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Mol	Chain	Res	Type
4	L5	4391	G
4	L5	4394	A
4	L5	4422	A
4	L5	4426	C
4	L5	4433	G
4	L5	4448	G
4	L5	4449	A
4	L5	4452	U
4	L5	4453	C
4	L5	4464	A
4	L5	4466	C
4	L5	4475	G
4	L5	4500	U
4	L5	4512	U
4	L5	4513	A
4	L5	4519	C
4	L5	4524	G
4	L5	4528	G
4	L5	4548	A
4	L5	4549	G
4	L5	4554	G
4	L5	4560	C
4	L5	4567	G
4	L5	4573	G
4	L5	4575	G
4	L5	4590	A
4	L5	4600	G
4	L5	4601	U
4	L5	4617	G
4	L5	4627	U
4	L5	4633	G
4	L5	4634	U
4	L5	4636	U
4	L5	4637	G
4	L5	4638	U
4	L5	4639	G
4	L5	4656	A
4	L5	4657	U
4	L5	4659	G
4	L5	4670	C
4	L5	4672	A
4	L5	4687	A

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Mol	Chain	Res	Type
4	L5	4700	A
4	L5	4708	A
4	L5	4709	U
4	L5	4719	G
4	L5	4720	C
4	L5	4733	C
4	L5	4734	A
4	L5	4740	G
4	L5	4741	C
4	L5	4742	G
4	L5	4745	G
4	L5	4754	G
4	L5	4757	C
4	L5	4759	C
4	L5	4761	G
4	L5	4765	G
4	L5	4771	C
4	L5	4772	C
4	L5	4773	C
4	L5	4775	C
4	L5	4860	G
4	L5	4868	G
4	L5	4870	G
4	L5	4871	C
4	L5	4875	G
4	L5	4880	C
4	L5	4881	U
4	L5	4882	U
4	L5	4883	C
4	L5	4888	U
4	L5	4889	G
4	L5	4894	A
4	L5	4895	C
4	L5	4896	G
4	L5	4900	C
4	L5	4901	G
4	L5	4910	G
4	L5	4912	G
4	L5	4914	C
4	L5	4925	U
4	L5	4927	G
4	L5	4931	G

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Mol	Chain	Res	Type
4	L5	4933	C
4	L5	4934	A
4	L5	4940	C
4	L5	4941	G
4	L5	4943	A
4	L5	4955	A
4	L5	4960	G
4	L5	4963	G
4	L5	4966	A
4	L5	4976	U
4	L5	4988	U
4	L5	4989	U
4	L5	4991	U
4	L5	5009	G
4	L5	5010	U
4	L5	5014	A
4	L5	5017	G
4	L5	5022	U
4	L5	5024	C
4	L5	5025	C
4	L5	5026	U
4	L5	5029	C
4	L5	5030	U
4	L5	5034	A
4	L5	5041	G
4	L5	5050	C
4	L5	5054	C
4	L5	5055	G
4	L5	5061	A
4	L5	5062	G
4	L5	5069	U
5	L7	20	U
5	L7	23	A
5	L7	27	G
5	L7	33	U
5	L7	53	U
5	L7	54	A
5	L7	63	C
5	L7	64	G
5	L7	97	G
5	L7	100	A
5	L7	102	U

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Mol	Chain	Res	Type
5	L7	103	A
5	L7	111	C
5	L7	120	U
6	L8	16	G
6	L8	17	A
6	L8	34	U
6	L8	35	C
6	L8	48	A
6	L8	52	A
6	L8	59	A
6	L8	63	U
6	L8	82	A
6	L8	83	C
6	L8	84	A
6	L8	86	U
6	L8	87	G
6	L8	88	A
6	L8	91	A
6	L8	94	G
6	L8	103	A
6	L8	105	C
6	L8	111	U
6	L8	114	G
6	L8	124	U
6	L8	125	C
6	L8	126	C
6	L8	127	U
6	L8	150	C
6	L8	151	G
6	L8	153	C
51	S2	7	G
51	S2	27	A
51	S2	33	G
51	S2	44	U
51	S2	46	A
51	S2	56	G
51	S2	58	C
51	S2	59	U
51	S2	62	G
51	S2	66	G
51	S2	67	C
51	S2	68	A

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Mol	Chain	Res	Type
51	S2	70	G
51	S2	71	G
51	S2	72	C
51	S2	73	C
51	S2	75	G
51	S2	76	U
51	S2	84	A
51	S2	86	C
51	S2	96	C
51	S2	101	U
51	S2	103	A
51	S2	113	G
51	S2	114	G
51	S2	121	U
51	S2	126	G
51	S2	127	C
51	S2	128	U
51	S2	130	G
51	S2	143	U
51	S2	144	U
51	S2	145	G
51	S2	149	A
51	S2	152	U
51	S2	155	G
51	S2	161	U
51	S2	162	C
51	S2	163	U
51	S2	167	G
51	S2	168	C
51	S2	170	A
51	S2	179	C
51	S2	182	C
51	S2	184	G
51	S2	198	U
51	S2	202	G
51	S2	207	G
51	S2	210	U
51	S2	211	G
51	S2	214	U
51	S2	219	U
51	S2	290	U
51	S2	293	C

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Mol	Chain	Res	Type
51	S2	295	C
51	S2	302	A
51	S2	306	C
51	S2	308	G
51	S2	309	G
51	S2	310	C
51	S2	311	C
51	S2	312	G
51	S2	313	A
51	S2	319	C
51	S2	322	C
51	S2	323	C
51	S2	324	C
51	S2	325	C
51	S2	326	C
51	S2	328	U
51	S2	329	G
51	S2	332	G
51	S2	339	A
51	S2	340	C
51	S2	347	G
51	S2	360	A
51	S2	362	C
51	S2	364	A
51	S2	368	U
51	S2	370	G
51	S2	380	G
51	S2	381	C
51	S2	385	G
51	S2	386	C
51	S2	398	A
51	S2	400	C
51	S2	409	C
51	S2	413	G
51	S2	438	G
51	S2	448	A
51	S2	450	C
51	S2	452	G
51	S2	462	C
51	S2	464	A
51	S2	465	A
51	S2	466	G

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Mol	Chain	Res	Type
51	S2	471	G
51	S2	472	C
51	S2	473	A
51	S2	474	G
51	S2	482	G
51	S2	487	U
51	S2	488	U
51	S2	489	A
51	S2	492	C
51	S2	493	A
51	S2	500	A
51	S2	502	C
51	S2	503	C
51	S2	525	A
51	S2	531	A
51	S2	532	C
51	S2	536	A
51	S2	537	C
51	S2	539	C
51	S2	540	U
51	S2	541	U
51	S2	542	U
51	S2	543	C
51	S2	544	G
51	S2	545	A
51	S2	547	G
51	S2	551	U
51	S2	554	A
51	S2	555	A
51	S2	556	U
51	S2	559	G
51	S2	561	A
51	S2	563	G
51	S2	566	U
51	S2	567	C
51	S2	575	A
51	S2	576	A
51	S2	582	U
51	S2	583	A
51	S2	587	A
51	S2	590	A
51	S2	591	U

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Mol	Chain	Res	Type
51	S2	593	C
51	S2	595	U
51	S2	596	U
51	S2	604	A
51	S2	605	A
51	S2	606	G
51	S2	607	U
51	S2	608	C
51	S2	613	G
51	S2	614	C
51	S2	617	G
51	S2	628	A
51	S2	631	U
51	S2	632	C
51	S2	643	A
51	S2	650	A
51	S2	651	U
51	S2	652	U
51	S2	655	A
51	S2	660	C
51	S2	664	A
51	S2	668	A
51	S2	669	A
51	S2	671	A
51	S2	672	A
51	S2	688	U
51	S2	689	U
51	S2	690	G
51	S2	692	G
51	S2	693	A
51	S2	694	G
51	S2	696	G
51	S2	697	G
51	S2	698	G
51	S2	732	U
51	S2	733	C
51	S2	734	C
51	S2	735	C
51	S2	736	C
51	S2	738	C
51	S2	739	C
51	S2	746	C

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Mol	Chain	Res	Type
51	S2	747	U
51	S2	748	C
51	S2	749	U
51	S2	751	G
51	S2	752	G
51	S2	753	C
51	S2	790	C
51	S2	791	C
51	S2	795	A
51	S2	796	G
51	S2	797	C
51	S2	799	U
51	S2	801	U
51	S2	807	G
51	S2	808	A
51	S2	809	A
51	S2	810	A
51	S2	811	A
51	S2	812	A
51	S2	813	A
51	S2	818	A
51	S2	821	G
51	S2	822	U
51	S2	830	A
51	S2	834	C
51	S2	835	C
51	S2	836	G
51	S2	837	A
51	S2	838	G
51	S2	839	C
51	S2	840	C
51	S2	841	G
51	S2	842	C
51	S2	847	A
51	S2	856	C
51	S2	858	A
51	S2	859	G
51	S2	860	G
51	S2	861	A
51	S2	869	A
51	S2	870	A
51	S2	872	A

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Mol	Chain	Res	Type
51	S2	873	G
51	S2	874	G
51	S2	878	G
51	S2	879	C
51	S2	880	G
51	S2	883	U
51	S2	884	C
51	S2	888	U
51	S2	889	U
51	S2	890	U
51	S2	891	G
51	S2	892	U
51	S2	893	U
51	S2	894	G
51	S2	895	G
51	S2	896	U
51	S2	898	U
51	S2	900	C
51	S2	901	G
51	S2	903	A
51	S2	904	A
51	S2	909	G
51	S2	913	A
51	S2	917	U
51	S2	919	A
51	S2	920	A
51	S2	924	G
51	S2	926	A
51	S2	930	C
51	S2	933	G
51	S2	934	G
51	S2	958	G
51	S2	963	A
51	S2	970	G
51	S2	971	G
51	S2	972	A
51	S2	990	A
51	S2	992	A
51	S2	1001	A
51	S2	1017	U
51	S2	1019	C
51	S2	1021	U

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Mol	Chain	Res	Type
51	S2	1023	A
51	S2	1027	A
51	S2	1055	A
51	S2	1060	A
51	S2	1061	U
51	S2	1062	A
51	S2	1083	A
51	S2	1085	C
51	S2	1089	G
51	S2	1096	G
51	S2	1100	A
51	S2	1101	U
51	S2	1105	G
51	S2	1108	G
51	S2	1112	U
51	S2	1114	U
51	S2	1116	C
51	S2	1120	U
51	S2	1121	G
51	S2	1126	G
51	S2	1131	G
51	S2	1133	A
51	S2	1134	G
51	S2	1140	G
51	S2	1142	G
51	S2	1143	A
51	S2	1144	A
51	S2	1146	C
51	S2	1147	C
51	S2	1149	A
51	S2	1153	C
51	S2	1154	U
51	S2	1155	U
51	S2	1157	G
51	S2	1168	G
51	S2	1181	A
51	S2	1183	A
51	S2	1195	A
51	S2	1207	G
51	S2	1212	G
51	S2	1215	C
51	S2	1217	A

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Mol	Chain	Res	Type
51	S2	1221	G
51	S2	1224	G
51	S2	1242	U
51	S2	1243	U
51	S2	1251	A
51	S2	1253	A
51	S2	1256	G
51	S2	1257	G
51	S2	1259	A
51	S2	1260	A
51	S2	1265	A
51	S2	1268	C
51	S2	1271	C
51	S2	1272	C
51	S2	1273	C
51	S2	1274	G
51	S2	1275	G
51	S2	1276	A
51	S2	1281	G
51	S2	1282	A
51	S2	1284	A
51	S2	1285	G
51	S2	1286	G
51	S2	1297	U
51	S2	1298	G
51	S2	1299	A
51	S2	1301	A
51	S2	1302	G
51	S2	1303	C
51	S2	1308	U
51	S2	1313	A
51	S2	1314	U
51	S2	1321	G
51	S2	1326	U
51	S2	1332	A
51	S2	1342	U
51	S2	1348	G
51	S2	1371	U
51	S2	1372	U
51	S2	1378	A
51	S2	1384	C
51	S2	1396	A

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Mol	Chain	Res	Type
51	S2	1397	U
51	S2	1402	A
51	S2	1404	U
51	S2	1415	C
51	S2	1419	C
51	S2	1420	G
51	S2	1421	A
51	S2	1422	G
51	S2	1423	C
51	S2	1438	A
51	S2	1449	G
51	S2	1450	G
51	S2	1452	A
51	S2	1454	A
51	S2	1462	U
51	S2	1463	U
51	S2	1473	G
51	S2	1475	G
51	S2	1476	A
51	S2	1477	U
51	S2	1487	A
51	S2	1489	A
51	S2	1490	G
51	S2	1494	U
51	S2	1498	A
51	S2	1505	U
51	S2	1506	A
51	S2	1507	G
51	S2	1508	A
51	S2	1510	G
51	S2	1519	U
51	S2	1520	G
51	S2	1521	C
51	S2	1522	A
51	S2	1526	G
51	S2	1527	C
51	S2	1533	A
51	S2	1544	C
51	S2	1546	G
51	S2	1548	G
51	S2	1552	G
51	S2	1553	C

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Mol	Chain	Res	Type
51	S2	1556	A
51	S2	1563	G
51	S2	1567	G
51	S2	1569	A
51	S2	1570	G
51	S2	1578	U
51	S2	1580	A
51	S2	1585	U
51	S2	1586	U
51	S2	1587	G
51	S2	1588	A
51	S2	1589	A
51	S2	1599	U
51	S2	1601	A
51	S2	1602	U
51	S2	1613	G
51	S2	1614	A
51	S2	1621	U
51	S2	1623	A
51	S2	1624	U
51	S2	1639	G
51	S2	1644	C
51	S2	1648	G
51	S2	1654	G
51	S2	1661	A
51	S2	1663	A
51	S2	1664	A
51	S2	1665	G
51	S2	1671	G
51	S2	1678	A
51	S2	1694	U
51	S2	1695	A
51	S2	1719	A
51	S2	1721	U
51	S2	1722	G
51	S2	1742	C
51	S2	1743	G
51	S2	1744	G
51	S2	1745	A
51	S2	1748	G
51	S2	1749	G
51	S2	1753	C

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Mol	Chain	Res	Type
51	S2	1754	G
51	S2	1755	C
51	S2	1773	C
51	S2	1775	U
51	S2	1781	A
51	S2	1782	G
51	S2	1783	C
51	S2	1784	G
51	S2	1786	U
51	S2	1813	A
51	S2	1824	A
51	S2	1825	A
51	S2	1829	G
51	S2	1831	A
51	S2	1835	A
51	S2	1838	U
51	S2	1849	G
51	S2	1850	A
51	S2	1851	A
51	S2	1852	C
51	S2	1860	A
51	S2	1861	G
51	S2	1862	G
51	S2	1863	A
51	S2	1865	C
51	S2	1868	U

All (44) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	CP	3	C
2	CP	21	U
4	L5	278	G
4	L5	406	C
4	L5	504	G
4	L5	914	U
4	L5	955	G
4	L5	1082	C
4	L5	1633	G
4	L5	2117	G
4	L5	2416	G
4	L5	2428	A

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Mol	Chain	Res	Type
4	L5	2675	G
4	L5	2760	G
4	L5	3614	G
4	L5	3673	C
4	L5	3784	A
4	L5	3876	A
4	L5	4305	G
4	L5	4600	G
4	L5	4633	G
4	L5	4699	U
4	L5	4913	G
6	L8	16	G
6	L8	51	U
6	L8	87	G
51	S2	85	A
51	S2	144	U
51	S2	213	G
51	S2	465	A
51	S2	604	A
51	S2	688	U
51	S2	912	C
51	S2	971	G
51	S2	1120	U
51	S2	1273	C
51	S2	1326	U
51	S2	1395	C
51	S2	1519	U
51	S2	1585	U
51	S2	1597	C
51	S2	1601	A
51	S2	1664	A
51	S2	1860	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	LYO	CR	63	3	7,9,10	0.80	0	7,10,12	1.15	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LYO	CR	63	3	-	2/8/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	CR	63	LYO	N-CA-CB-CG
3	CR	63	LYO	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 199 ligands modelled in this entry, 199 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.

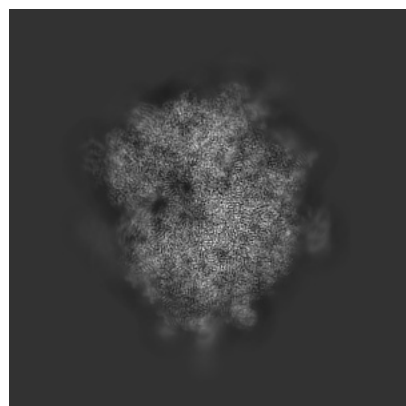
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54528. These allow visual inspection of the internal detail of the map and identification of artifacts.

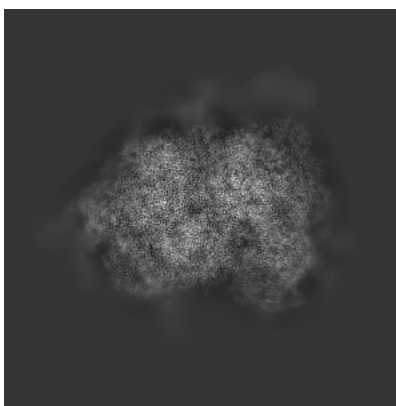
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

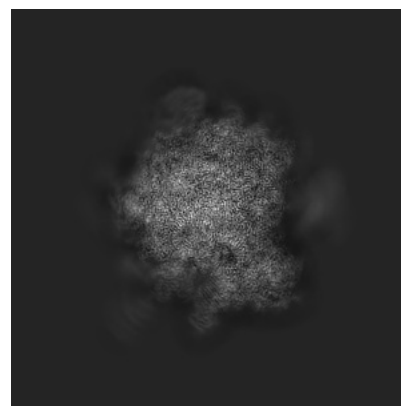
6.1.1 Primary map



X

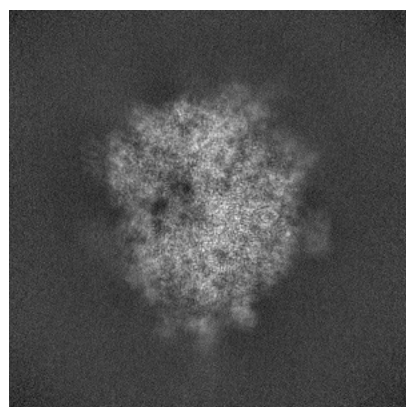


Y

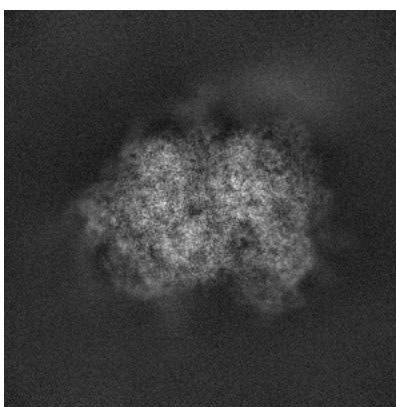


Z

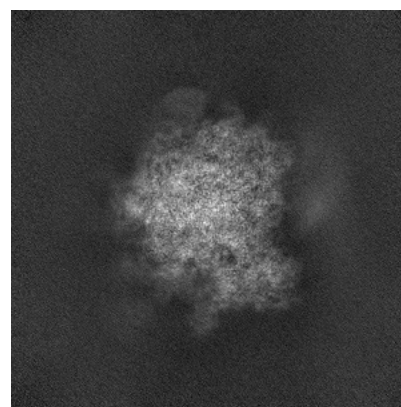
6.1.2 Raw map



X



Y

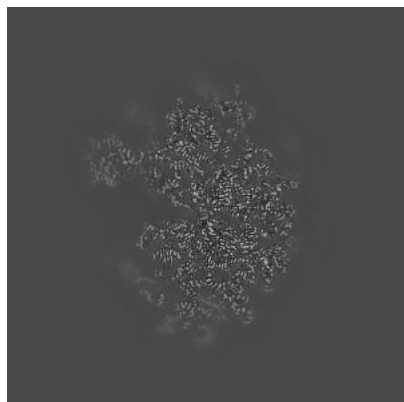


Z

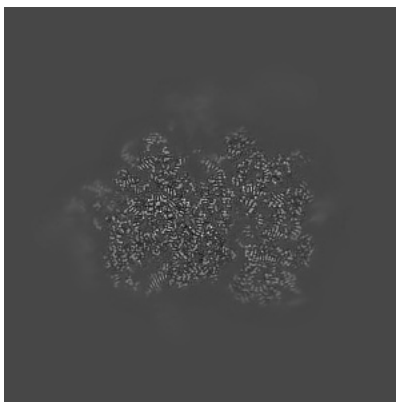
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

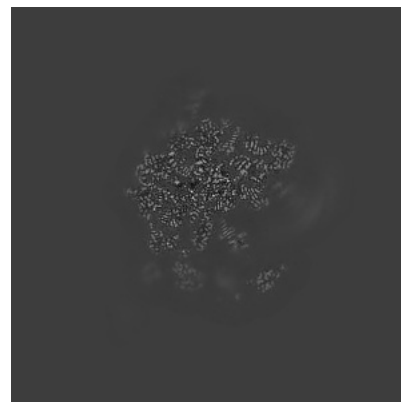
6.2.1 Primary map



X Index: 320

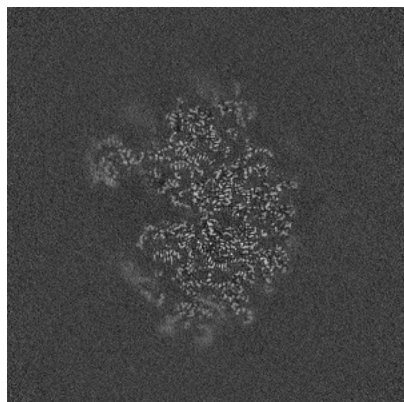


Y Index: 320

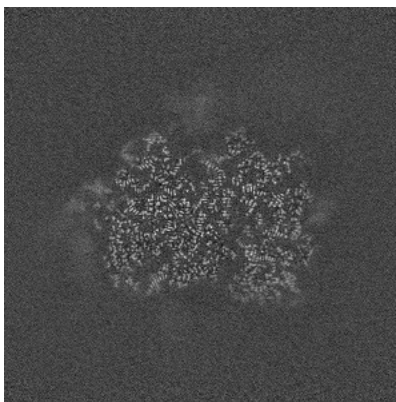


Z Index: 320

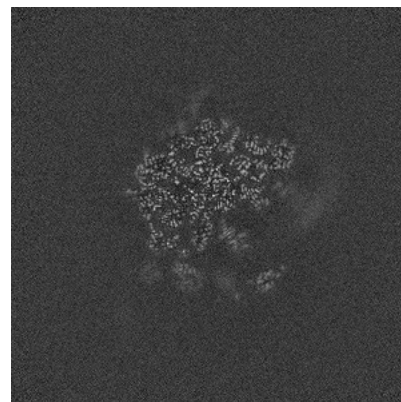
6.2.2 Raw map



X Index: 320



Y Index: 320

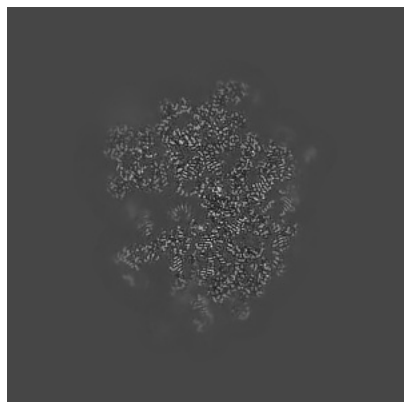


Z Index: 320

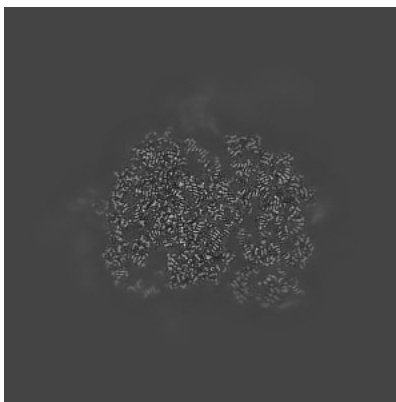
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

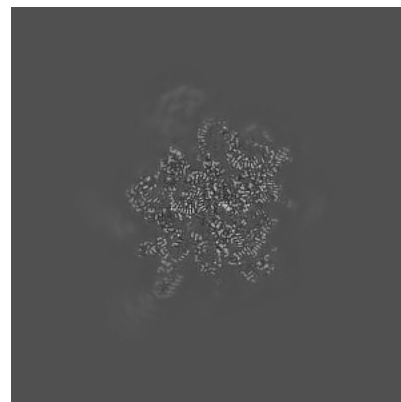
6.3.1 Primary map



X Index: 344

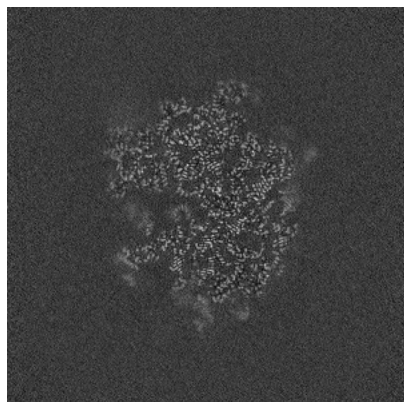


Y Index: 329

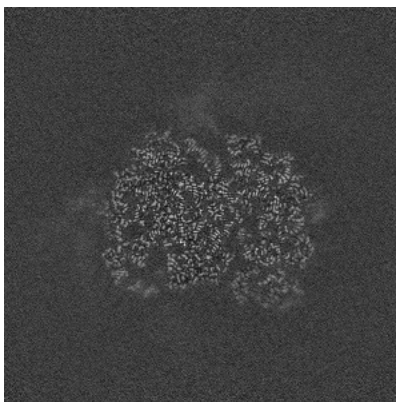


Z Index: 267

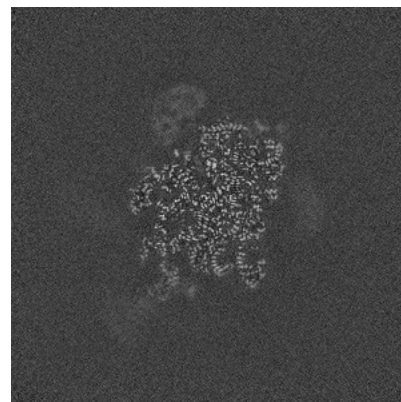
6.3.2 Raw map



X Index: 344



Y Index: 329

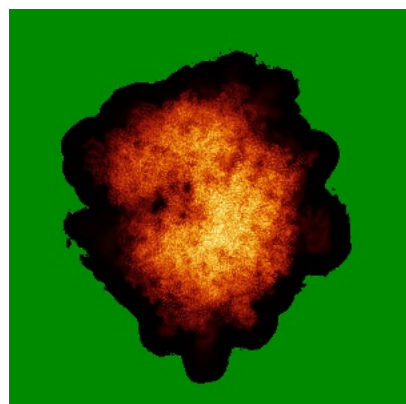


Z Index: 282

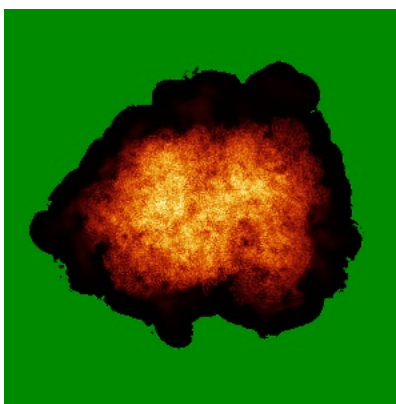
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

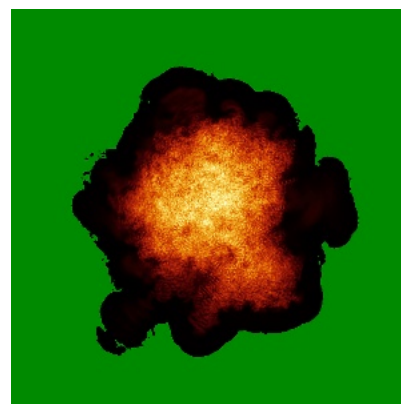
6.4.1 Primary map



X

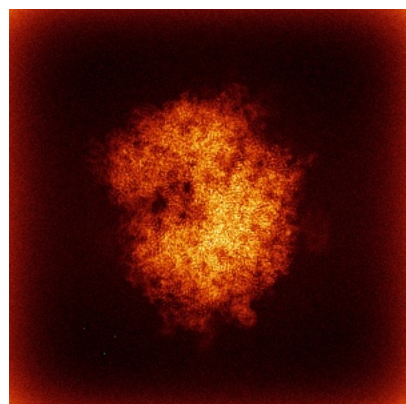


Y

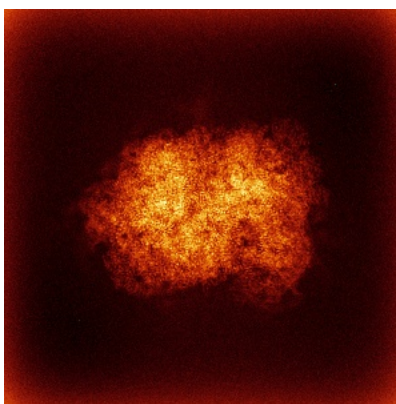


Z

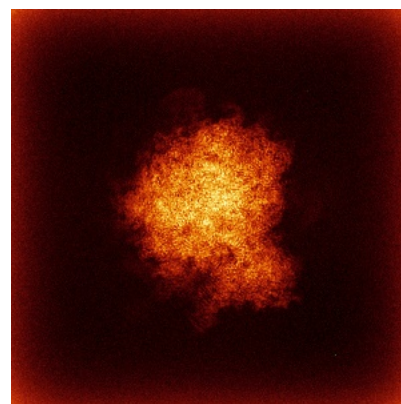
6.4.2 Raw map



X



Y

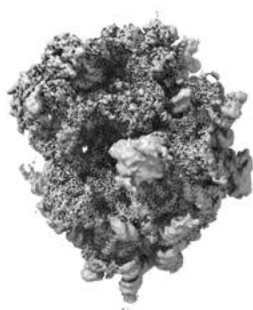


Z

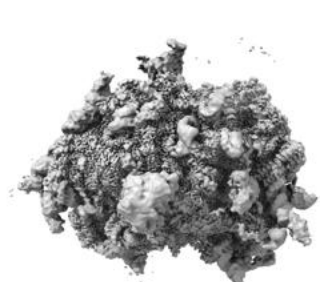
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



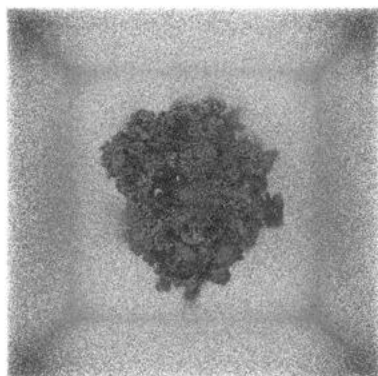
Y



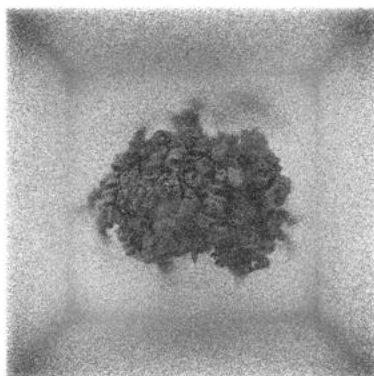
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

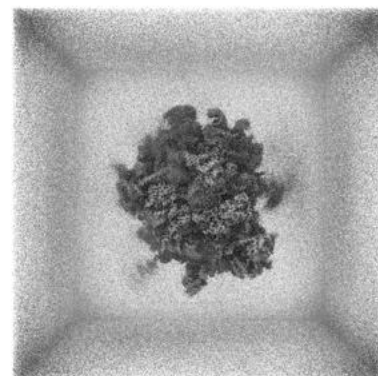
6.5.2 Raw map



X



Y



Z

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

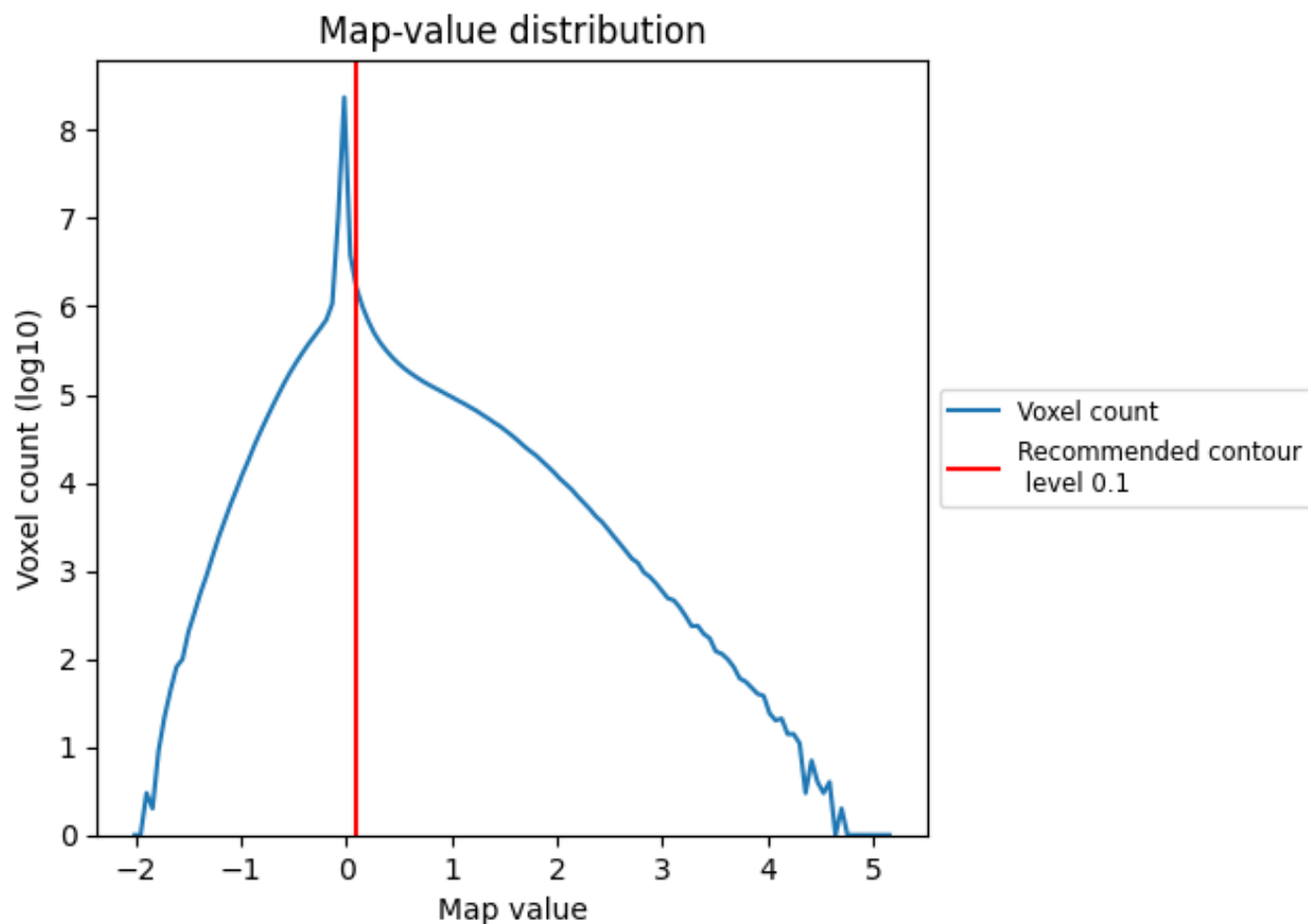
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

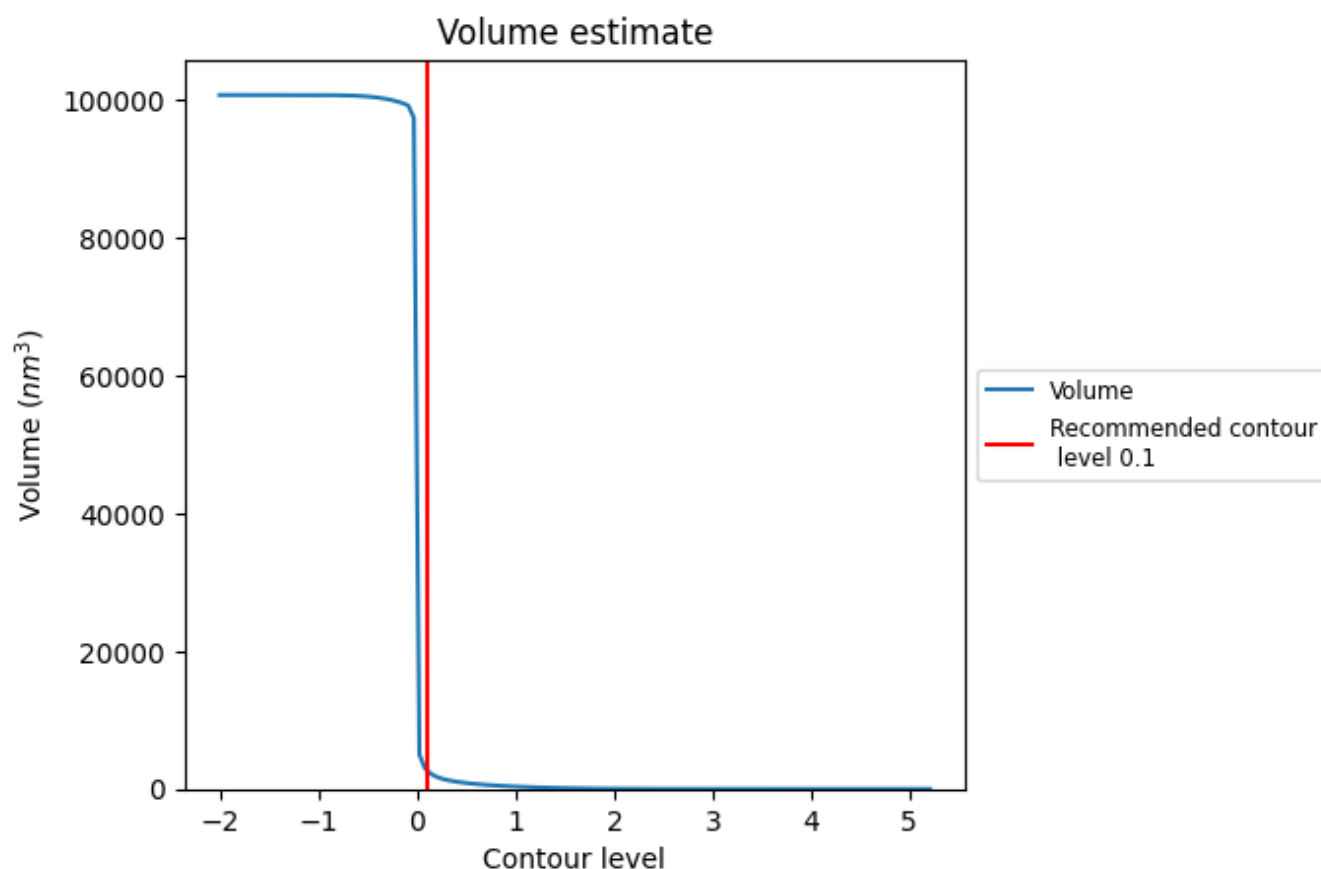
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

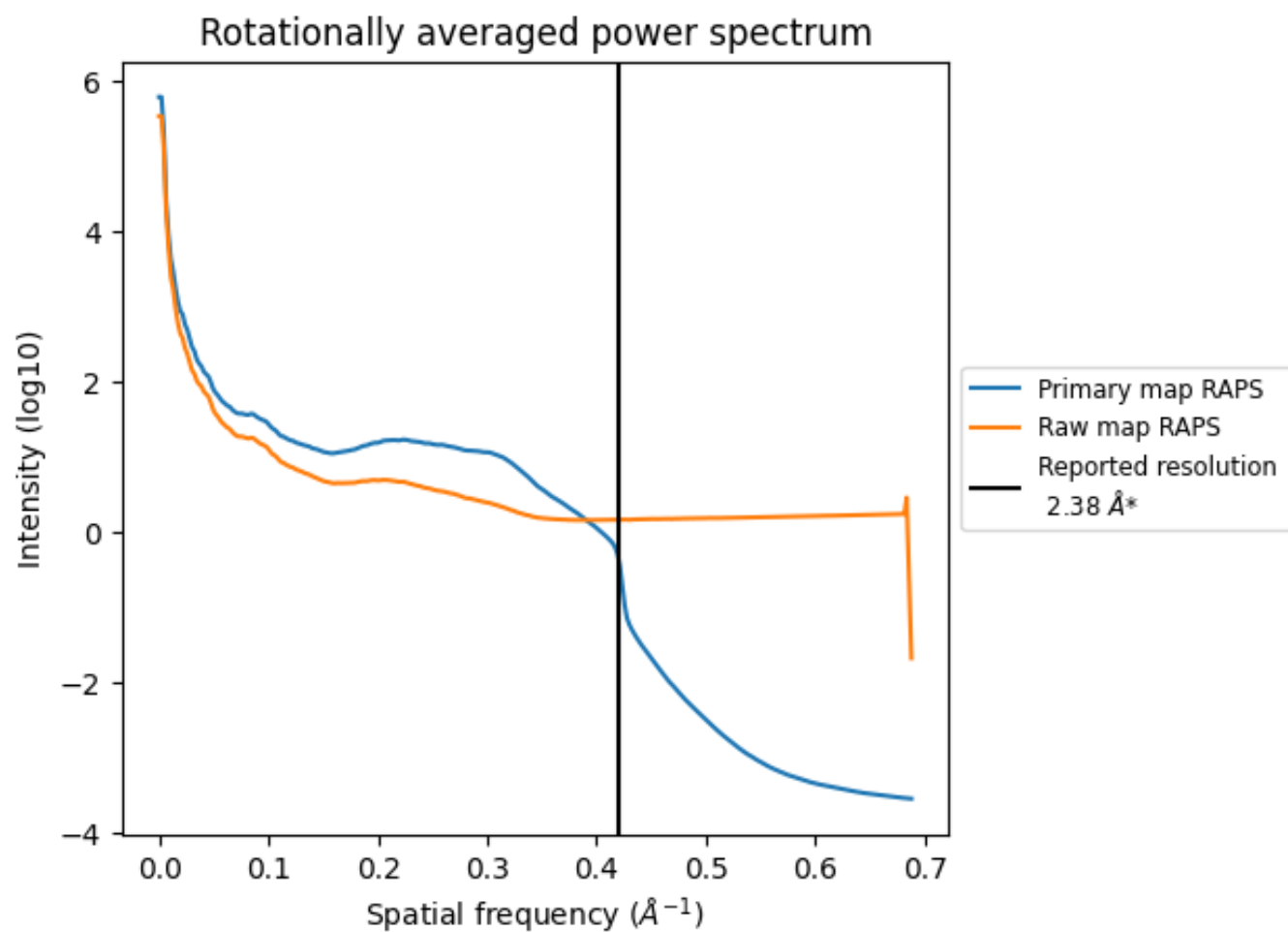
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2692 nm^3 ; this corresponds to an approximate mass of 2432 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 ⓘ

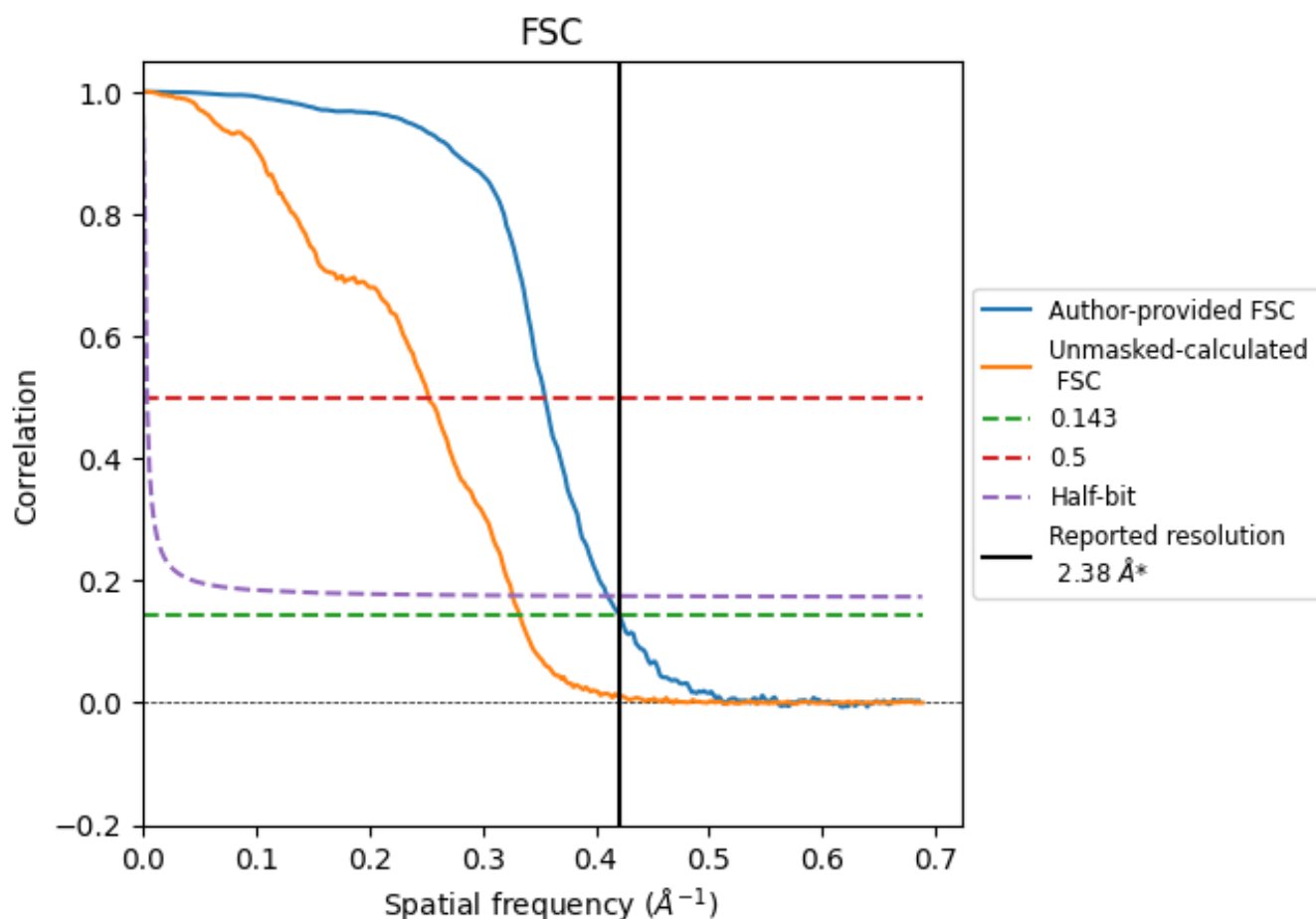


*Reported resolution corresponds to spatial frequency of 0.420 \AA^{-1}

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 0.420 \AA^{-1}

8.2 Resolution estimates [i](#)

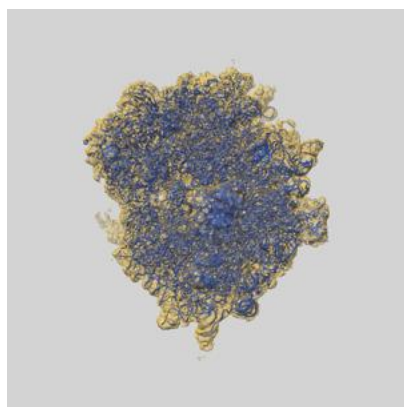
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.38	-	-
Author-provided FSC curve	2.38	2.82	2.44
Unmasked-calculated*	3.00	3.96	3.06

*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 3.00 differs from the reported value 2.38 by more than 10 %

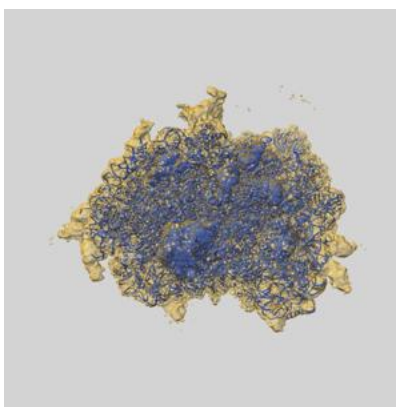
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-54528 and PDB model 9S3B. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

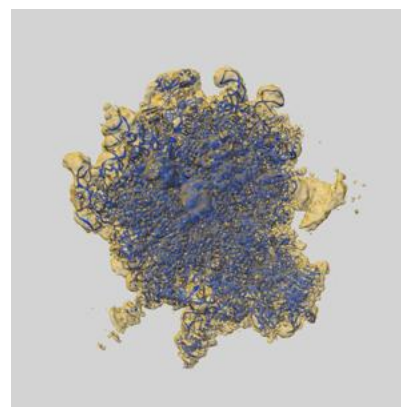
9.1 Map-model overlay [i](#)



X



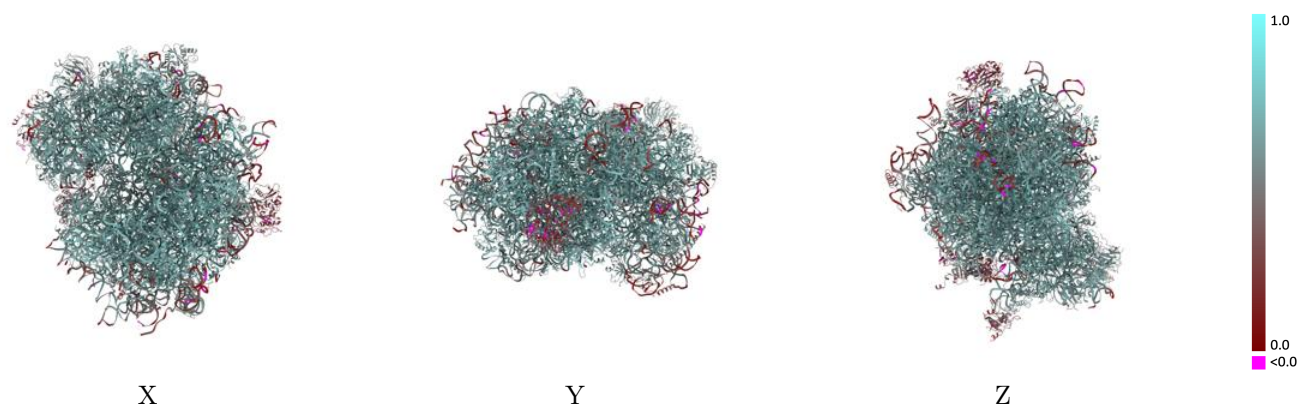
Y



Z

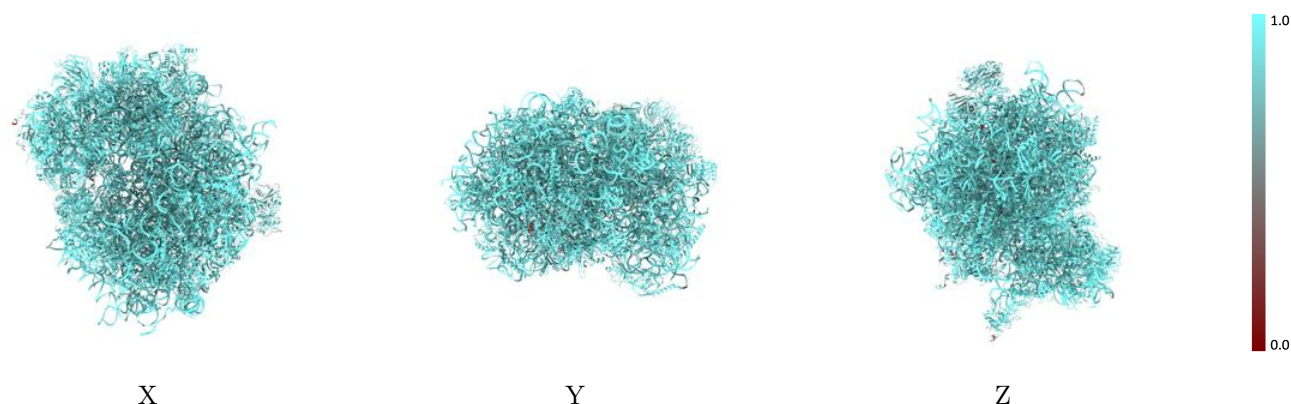
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



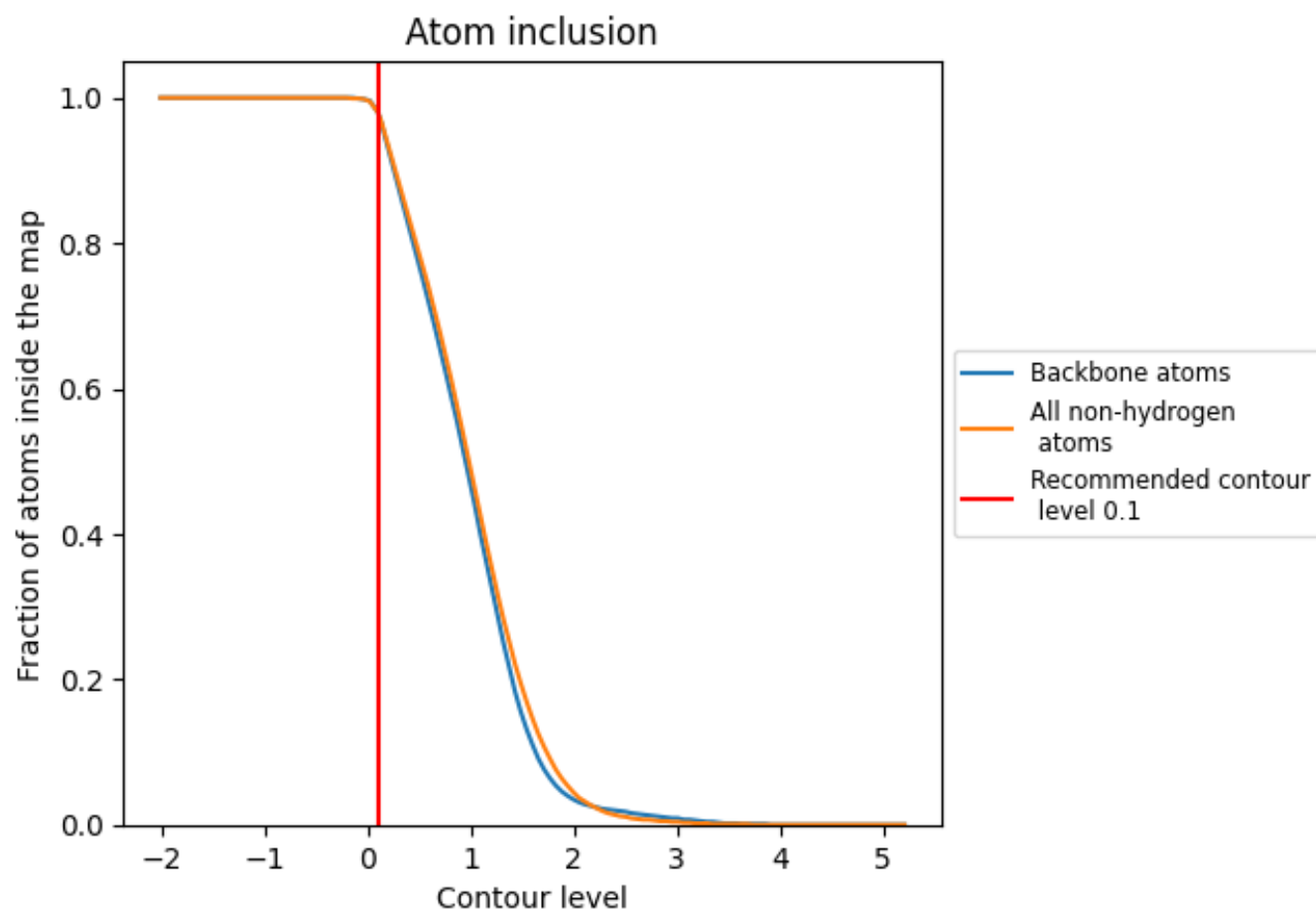
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9800	 0.6090
CM	 0.9880	 0.6080
CP	 0.9890	 0.5940
CR	 0.9230	 0.5290
CZ	 0.6670	 0.3350
L5	 0.9890	 0.6200
L7	 0.9950	 0.6690
L8	 0.9860	 0.6360
LA	 0.9940	 0.6970
LB	 0.9920	 0.6760
LC	 0.9890	 0.6720
LD	 0.9870	 0.6300
LE	 0.9860	 0.6200
LF	 0.9860	 0.6730
LG	 0.9770	 0.6140
LH	 0.9900	 0.6430
LI	 0.9850	 0.6490
LJ	 0.9810	 0.6120
LL	 0.9800	 0.6420
LM	 0.9960	 0.6510
LN	 0.9960	 0.7030
LO	 0.9940	 0.6860
LP	 0.9880	 0.6830
LQ	 0.9940	 0.6880
LR	 0.9880	 0.6610
LS	 0.9960	 0.6800
LT	 0.9820	 0.6410
LU	 0.9820	 0.5780
LV	 0.9930	 0.6860
LW	 0.9590	 0.5280
LX	 0.9790	 0.6560
LY	 0.9900	 0.6500
LZ	 0.9880	 0.6470
La	 0.9910	 0.6880
Lb	 0.9710	 0.5960



























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Chain	Atom inclusion	Q-score
Lc	 0.9840	 0.6610
Ld	 0.9890	 0.6610
Le	 0.9970	 0.6950
Lf	 0.9880	 0.6870
Lg	 0.9800	 0.6650
Lh	 0.9900	 0.6520
Li	 0.9950	 0.6490
Lj	 0.9910	 0.6880
Lk	 0.9510	 0.5770
Ll	 0.9880	 0.6640
Lm	 0.9760	 0.6660
Ln	 0.9950	 0.6940
Lo	 0.9920	 0.6680
Lp	 0.9960	 0.6920
Lr	 0.9950	 0.6690
Ls	 0.8520	 0.3050
Lt	 0.9390	 0.3680
NA	 0.6760	 0.1570
NB	 0.8010	 0.2540
NM	 0.8720	 0.2240
S2	 0.9850	 0.6000
SA	 0.9900	 0.6440
SB	 0.9860	 0.6340
SC	 0.9910	 0.6550
SD	 0.9860	 0.6020
SE	 0.9910	 0.6230
SF	 0.9750	 0.6080
SG	 0.9880	 0.5440
SH	 0.9890	 0.5770
SI	 0.9900	 0.6270
SJ	 0.9920	 0.6250
SK	 0.9870	 0.5870
SL	 0.9890	 0.6570
SM	 0.8710	 0.3010
SN	 0.9940	 0.6670
SO	 0.9920	 0.6550
SP	 0.9840	 0.5970
SQ	 0.9790	 0.6210
SR	 0.9620	 0.5660
SS	 0.9760	 0.5980
ST	 0.9870	 0.6230
SU	 0.9780	 0.5630

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Chain	Atom inclusion	Q-score
SV	 0.9880	 0.6390
SW	 0.9940	 0.6760
SX	 0.9840	 0.6480
SY	 0.9910	 0.5910
SZ	 0.9760	 0.5800
Sa	 0.9870	 0.6480
Sb	 0.9800	 0.6000
Sc	 0.9340	 0.5500
Sd	 0.9900	 0.6480
Se	 0.9900	 0.5960
Sf	 0.8490	 0.3210
Sg	 0.9770	 0.5450