



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 12:29 PM UTC

PDB ID : 9S3C / pdb_00009s3c
EMDB ID : EMD-54529
Title : NMT1-NAC bound human RNC with 58 amino acid ARF1-linker - State 2
Authors : Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-07-24
Resolution : 2.42 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

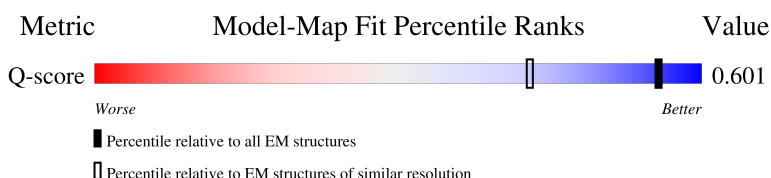
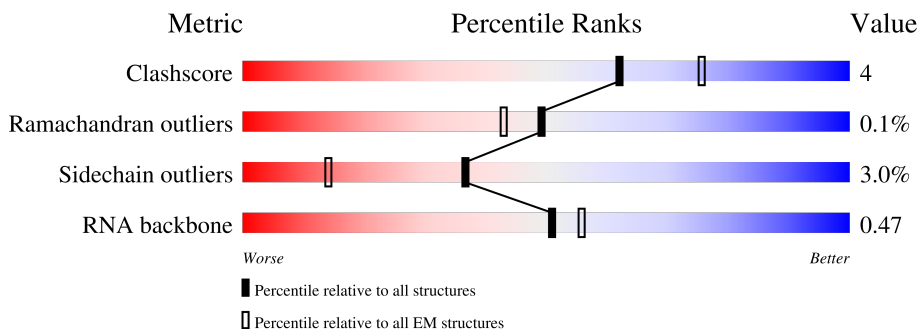
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.42 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5729 (1.92 - 2.92)

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	59% 41%
3	CR	437	82% 12% 5%



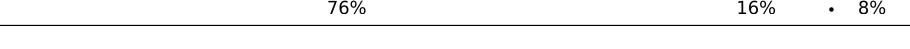
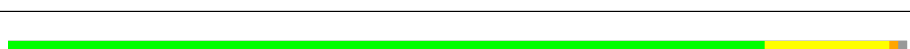



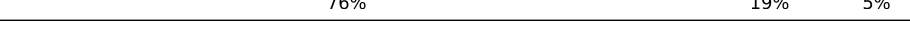


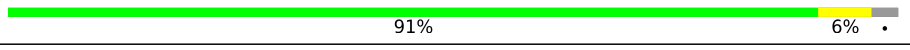
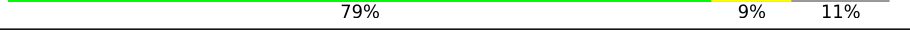




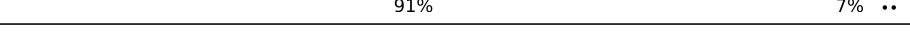







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Mol	Chain	Length	Quality of chain
4	CZ	95	
5	L5	5070	
6	L7	121	
7	L8	157	
8	LA	257	
9	LB	403	
10	LC	427	
11	LD	297	
12	LE	288	
13	LF	248	
14	LG	266	
15	LH	192	
16	LI	214	
17	LJ	178	
18	LL	211	
19	LM	215	
20	LN	204	
21	LO	203	
22	LP	184	
23	LQ	188	
24	LR	196	
25	LS	176	
26	LT	160	
27	LU	128	
28	LV	140	

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Mol	Chain	Length	Quality of chain
29	LW	157	
30	LX	156	
31	LY	145	
32	LZ	136	
33	La	148	
34	Lb	159	
35	Lc	115	
36	Ld	125	
37	Le	135	
38	Lf	110	
39	Lg	117	
40	Lh	123	
41	Li	105	
42	Lj	97	
43	Lk	70	
44	Ll	51	
45	Lm	128	
46	Ln	25	
47	Lo	106	
48	Lp	92	
49	Lr	137	
50	Ls	317	
51	Lt	165	
52	NA	215	
53	NB	162	



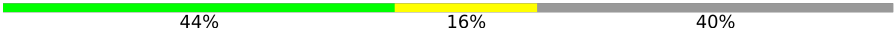






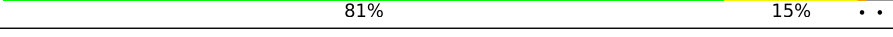
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Mol	Chain	Length	Quality of chain
54	NM	496	
55	S2	1869	
56	SA	295	
57	SB	264	
58	SC	293	
59	SD	243	
60	SE	263	
61	SF	204	
62	SG	249	
63	SH	194	
64	SI	208	
65	SJ	194	
66	SK	165	
67	SL	158	
68	SM	132	
69	SN	151	
70	SO	151	
71	SP	145	
72	SQ	146	
73	SR	135	
74	SS	152	
75	ST	145	
76	SU	119	
77	SV	83	
78	SW	130	

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Mol	Chain	Length	Quality of chain
79	SX	143	 84%14%..
80	SY	133	 75%15%•8%
81	SZ	125	 44%16%40%
82	Sa	115	 72%13%•14%
83	Sb	84	 89%10%•
84	Sc	69	 67%23%•9%
85	Sd	56	 79%16%5%
86	Se	133	 38%59%•
87	Sf	156	 33%8%60%
88	Sg	317	 81%15%••

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 222376 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 protein called nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CZ	80	Total	C	N	O	S	0	0
			461	287	84	88	2		

- Molecule 5 is a RNA chain called 28S rRNA.

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

- Molecule 6 is a RNA chain called 5S rRNA.

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

- Molecule 7 is a RNA chain called 5.8S rRNA.

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

- Molecule 8 is a protein called 60S ribosomal protein L8.

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

- Molecule 9 is a protein called 60S ribosomal protein L3.

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

- Molecule 10 is a protein called 60S ribosomal protein L4.

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

- Molecule 11 is a protein called 60S ribosomal protein L5.

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

- Molecule 12 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 14 is a protein called 60S ribosomal protein L7a.

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

- Molecule 15 is a protein called 60S ribosomal protein L9.

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

- Molecule 16 is a protein called Ribosomal protein uL16-like.

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

- Molecule 17 is a protein called 60S ribosomal protein L11.

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

- Molecule 18 is a protein called 60S ribosomal protein L13.

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

- Molecule 19 is a protein called 60S ribosomal protein L14.

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

- Molecule 20 is a protein called 60S ribosomal protein L15.

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

- Molecule 21 is a protein called 60S ribosomal protein L13a.

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

- Molecule 22 is a protein called 60S ribosomal protein L17.

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

- Molecule 23 is a protein called 60S ribosomal protein L18.

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

- Molecule 24 is a protein called 60S ribosomal protein L19.

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

- Molecule 25 is a protein called 60S ribosomal protein L18a.

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

- Molecule 26 is a protein called 60S ribosomal protein L21.

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

- Molecule 27 is a protein called 60S ribosomal protein L22.

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

- Molecule 28 is a protein called 60S ribosomal protein L23.

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

- Molecule 29 is a protein called 60S ribosomal protein L24.

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

- Molecule 30 is a protein called 60S ribosomal protein L23a.

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

- Molecule 31 is a protein called 60S ribosomal protein L26.

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

- Molecule 32 is a protein called 60S ribosomal protein L27.

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

- Molecule 33 is a protein called 60S ribosomal protein L27a.

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

- Molecule 34 is a protein called 60S ribosomal protein L29.

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

- Molecule 35 is a protein called 60S ribosomal protein L30.

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

- Molecule 36 is a protein called 60S ribosomal protein L31.

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

- Molecule 37 is a protein called 60S ribosomal protein L32.

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

- Molecule 38 is a protein called 60S ribosomal protein L35a.

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

- Molecule 39 is a protein called 60S ribosomal protein L34.

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

- Molecule 40 is a protein called 60S ribosomal protein L35.

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

- Molecule 41 is a protein called 60S ribosomal protein L36.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 43 is a protein called 60S ribosomal protein L38.

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

- Molecule 44 is a protein called 60S ribosomal protein L39.

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

- Molecule 45 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 46 is a protein called 60S ribosomal protein L41.

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

- Molecule 47 is a protein called 60S ribosomal protein L36a.

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

- Molecule 48 is a protein called 60S ribosomal protein L37a.

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

- Molecule 49 is a protein called 60S ribosomal protein L28.

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

- Molecule 50 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 51 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 52 is a protein called Nascent polypeptide-associated complex subunit alpha.

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

- Molecule 53 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	NB	124	Total	C	N	O	S	0	0
			955	593	172	187	3		

- Molecule 54 is a protein called Glycylpeptide N-tetradecanoyltransferase 1.

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

- Molecule 55 is a RNA chain called 18S rRNA.

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

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

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

- Molecule 57 is a protein called 40S ribosomal protein S3a.

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

- Molecule 58 is a protein called 40S ribosomal protein S2.

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

- Molecule 59 is a protein called 40S ribosomal protein S3.

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

- Molecule 60 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 61 is a protein called 40S ribosomal protein S5.

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

- Molecule 62 is a protein called 40S ribosomal protein S6.

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

- Molecule 63 is a protein called 40S ribosomal protein S7.

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

- Molecule 64 is a protein called 40S ribosomal protein S8.

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

- Molecule 65 is a protein called 40S ribosomal protein S9.

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

- Molecule 66 is a protein called 40S ribosomal protein S10.

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

- Molecule 67 is a protein called 40S ribosomal protein S11.

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

- Molecule 68 is a protein called 40S ribosomal protein S12.

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

- Molecule 69 is a protein called 40S ribosomal protein S13.

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

- Molecule 70 is a protein called 40S ribosomal protein S14.

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

- Molecule 71 is a protein called 40S ribosomal protein S15.

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

- Molecule 72 is a protein called 40S ribosomal protein S16.

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

- Molecule 73 is a protein called 40S ribosomal protein S17.

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

- Molecule 74 is a protein called 40S ribosomal protein S18.

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

- Molecule 75 is a protein called 40S ribosomal protein S19.

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

- Molecule 76 is a protein called 40S ribosomal protein S20.

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

- Molecule 77 is a protein called 40S ribosomal protein S21.

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

- Molecule 78 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SW	129	Total	C	N	O	S	0	0
			1026	655	193	172	6		

- Molecule 79 is a protein called 40S ribosomal protein S23.

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

- Molecule 80 is a protein called 40S ribosomal protein S24.

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

- Molecule 81 is a protein called 40S ribosomal protein S25.

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

- Molecule 82 is a protein called 40S ribosomal protein S26.

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

- Molecule 83 is a protein called 40S ribosomal protein S27.

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

- Molecule 84 is a protein called 40S ribosomal protein S28.

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

- Molecule 85 is a protein called 40S ribosomal protein S29.

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

- Molecule 86 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

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

- Molecule 87 is a protein called Ubiquitin.

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

- Molecule 88 is a protein called Receptor of activated protein C kinase 1.

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

- 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	125	Total	Mg	0
			125	125	
89	L7	3	Total	Mg	0
			3	3	
89	L8	3	Total	Mg	0
			3	3	
89	LA	2	Total	Mg	0
			2	2	
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	50	Total 50	Mg 50	0
89	ST	1	Total 1	Mg 1	0
89	Sa	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

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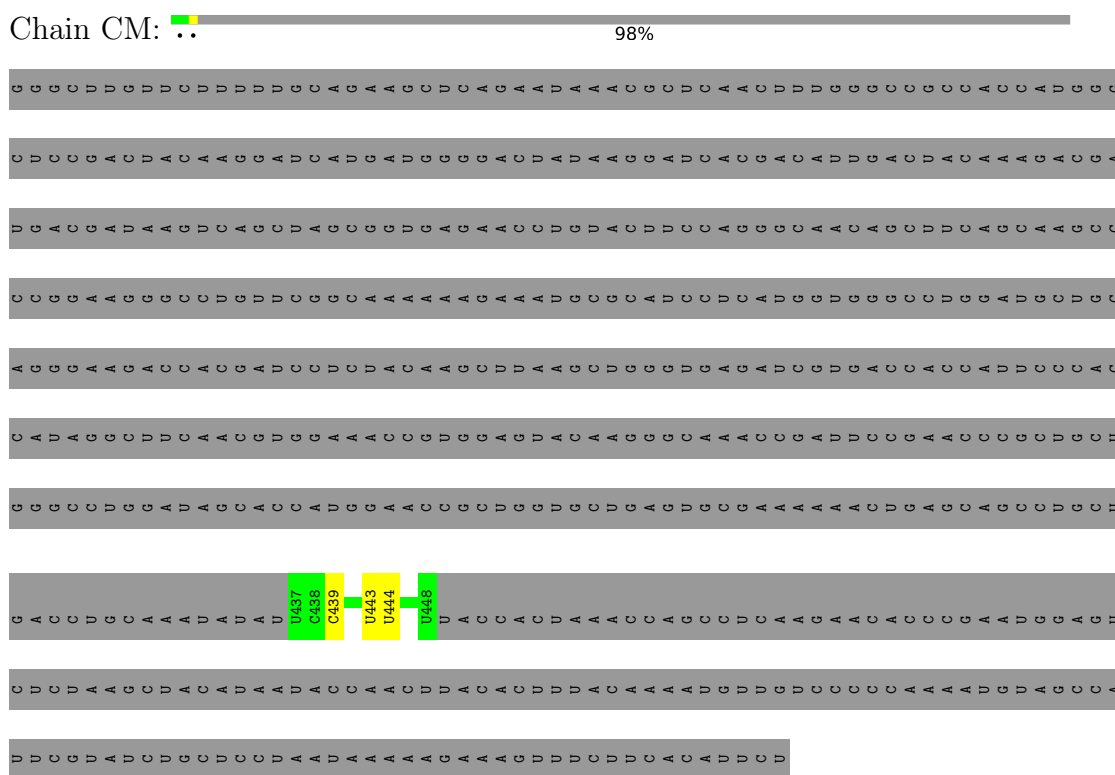
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Mol	Chain	Residues	Atoms		AltConf
91	LI	1	Total 1	O 1	0
91	LN	1	Total 1	O 1	0
91	La	1	Total 1	O 1	0
91	S2	3	Total 3	O 3	0

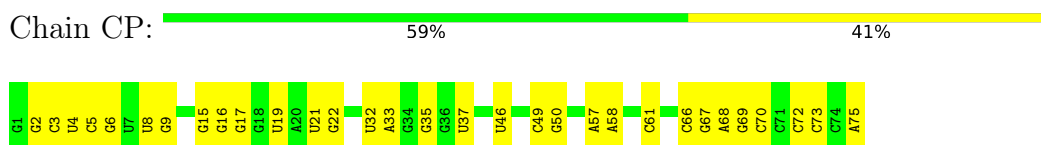
3 Residue-property plots

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.

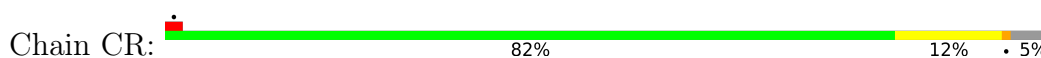
- Molecule 1: 58 amino acid ARF1-linker - V5 peptide - hCMV staller mRNA



- Molecule 2: prolyl-tRNA



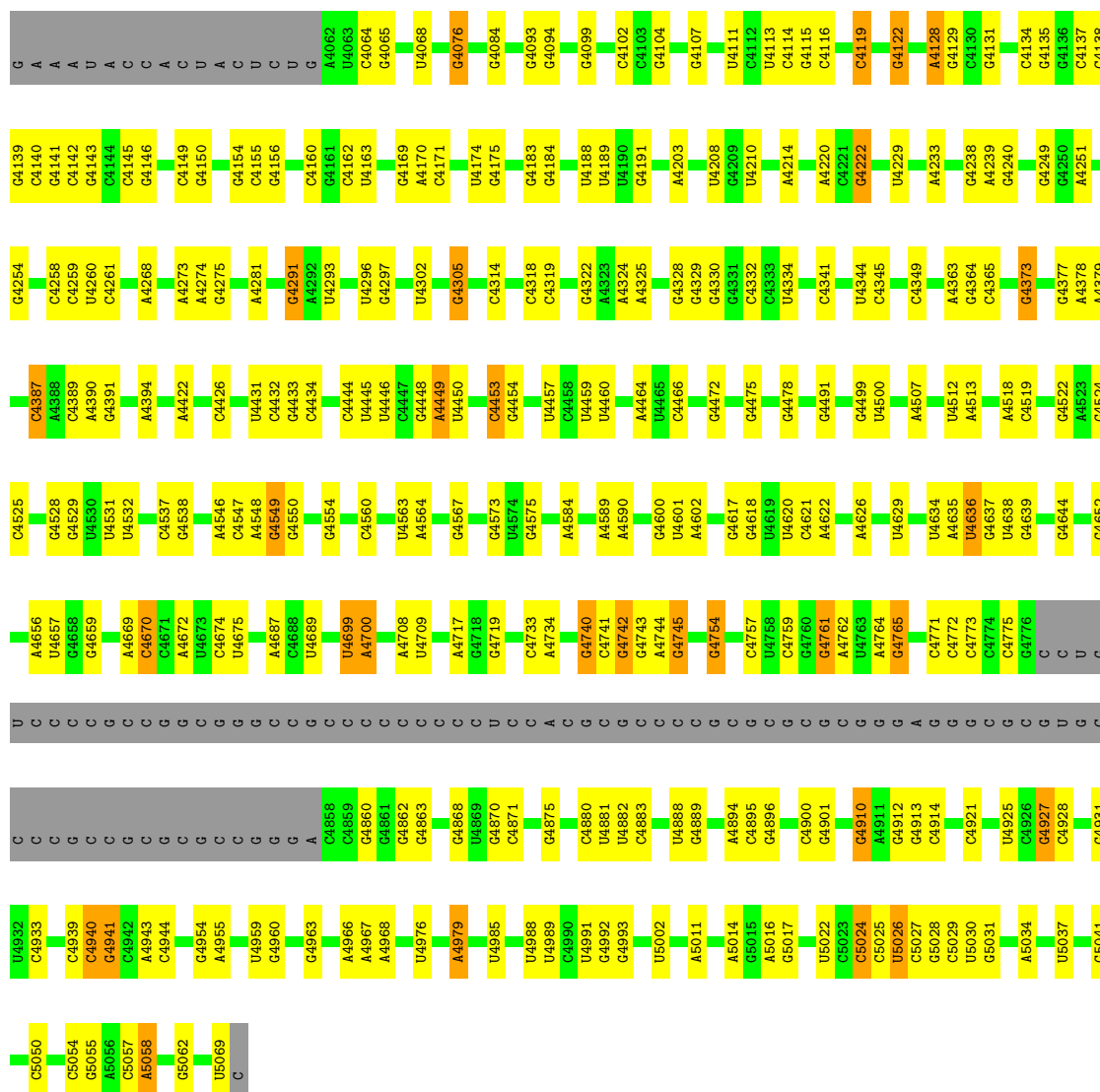
- Molecule 3: Eukaryotic peptide chain release factor subunit 1





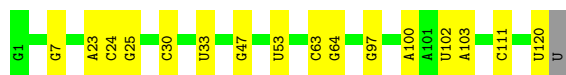






● Molecule 6: 5S rRNA

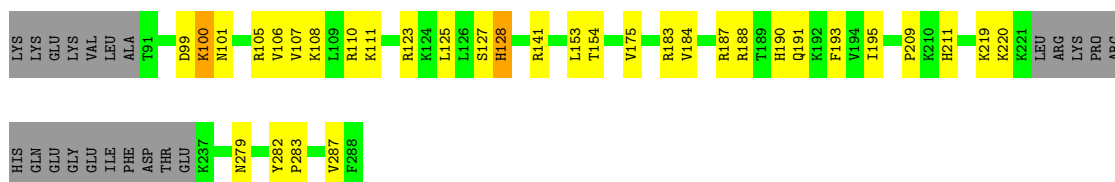
Chain L7: 86% 13%



● Molecule 7: 5.8S rRNA

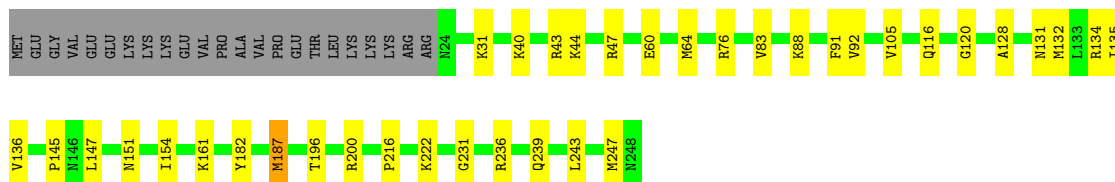
Chain L8: 73% 25%





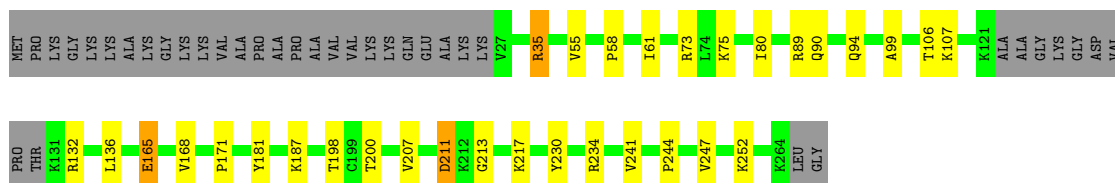
- Molecule 13: Large ribosomal subunit protein uL30

Chain LF: 76% 15% 9%



- Molecule 14: 60S ribosomal protein L7a

Chain LG: 74% 11% 14%



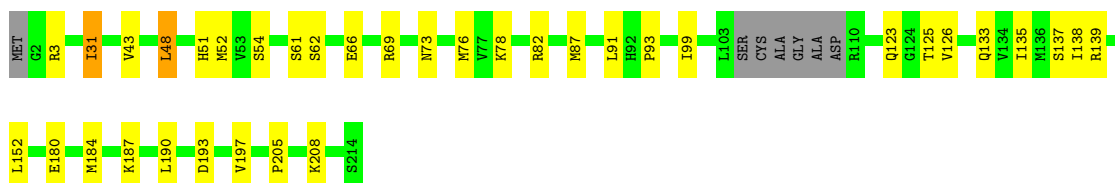
- Molecule 15: 60S ribosomal protein L9

Chain LH: 84% 15% 1%



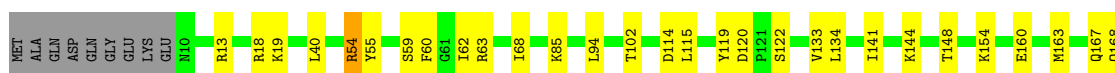
- Molecule 16: Ribosomal protein uL16-like

Chain LI: 80% 16% 4%



- Molecule 17: 60S ribosomal protein L11

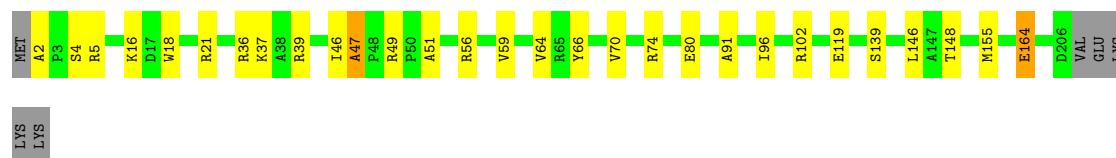
Chain LJ: 78% 17% 5%





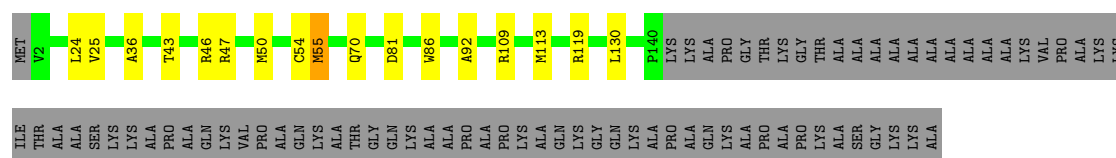
- Molecule 18: 60S ribosomal protein L13

Chain LL: 83% 13% ..



- Molecule 19: 60S ribosomal protein L14

Chain LM: 57% 7% 35%



- Molecule 20: 60S ribosomal protein L15

Chain LN: 82% 17%



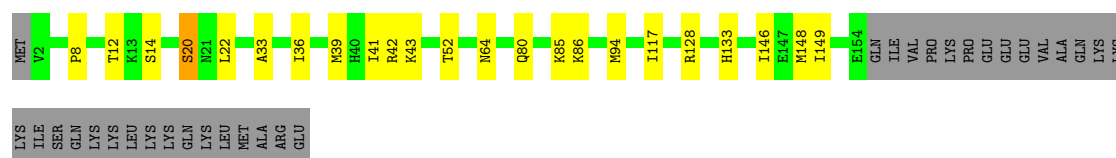
- Molecule 21: 60S ribosomal protein L13a

Chain LO: 87% 10% ..




- Molecule 22: 60S ribosomal protein L17

Chain LP: 71% 12% 17%




- Molecule 23: 60S ribosomal protein L18

Chain LQ:  89% 10% .




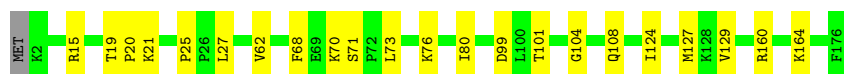
- Molecule 24: 60S ribosomal protein L19

Chain LR:  79% 10% • 10%




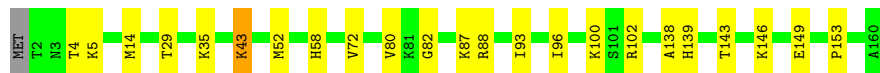
- Molecule 25: 60S ribosomal protein L18a

Chain LS:  87% 13% .



- Molecule 26: 60S ribosomal protein L21

Chain LT:  85% 14% ..




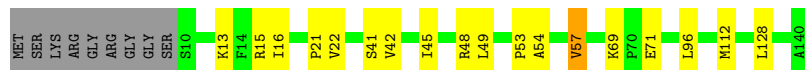
- Molecule 27: 60S ribosomal protein L22

Chain LU:  65% 14% 21%



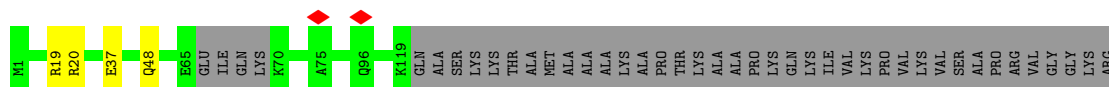
- Molecule 28: 60S ribosomal protein L23


Chain LV:  81% 12% • 6%



- Molecule 29: 60S ribosomal protein L24


Chain LW:  71% 27%



Chain Ld:  75% 10% 14%



- Molecule 37: 60S ribosomal protein L32

Chain Le:  76% 19% 5%



- Molecule 38: 60S ribosomal protein L35a

Chain Lf:  89% 10%




- Molecule 39: 60S ribosomal protein L34

Chain Lg:  86% 10%



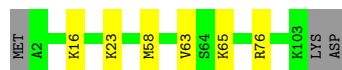
- Molecule 40: 60S ribosomal protein L35

Chain Lh:  85% 13%




- Molecule 41: 60S ribosomal protein L36

Chain Li:  91% 6%




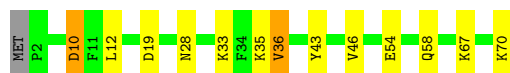
- Molecule 42: Large ribosomal subunit protein eL37

Chain Lj:  79% 9% 11%



- Molecule 43: 60S ribosomal protein L38

Chain Lk:  80% 16% ..



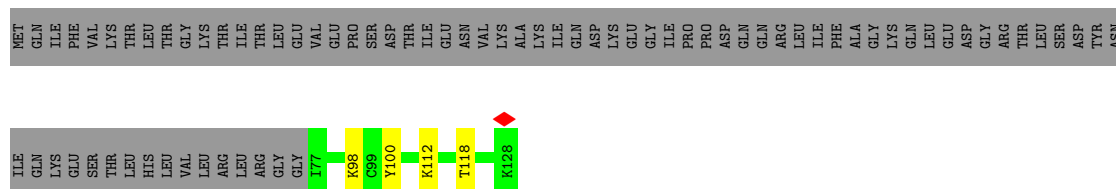
- Molecule 44: 60S ribosomal protein L39

Chain Ll:  73% 25% .




- Molecule 45: Ubiquitin-60S ribosomal protein L40

Chain Lm:  38% . 59%




- Molecule 46: 60S ribosomal protein L41

Chain Ln:  80% 16% .



- Molecule 47: 60S ribosomal protein L36a

Chain Lo:  82% 17% .




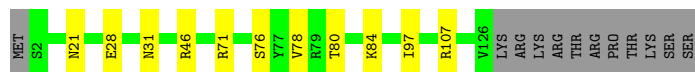
- Molecule 48: 60S ribosomal protein L37a

Chain Lp:  91% 7% ..

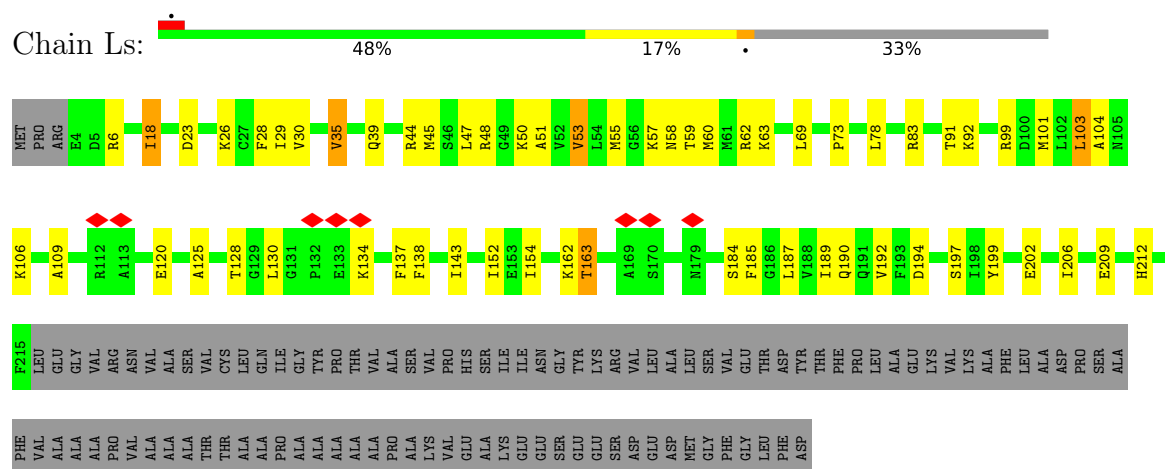


- Molecule 49: 60S ribosomal protein L28

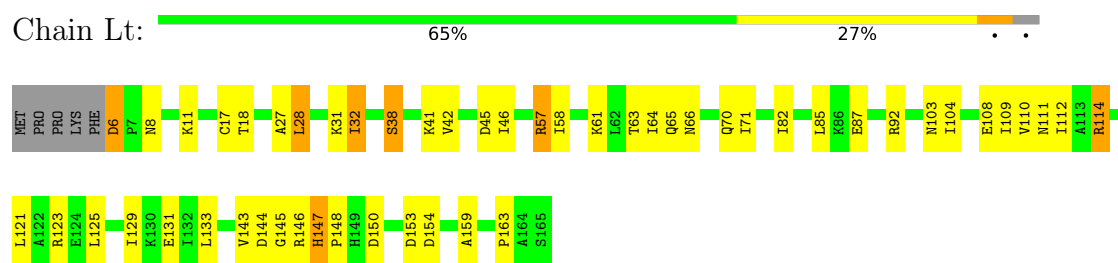
Chain Lr:  83% 8% 9%



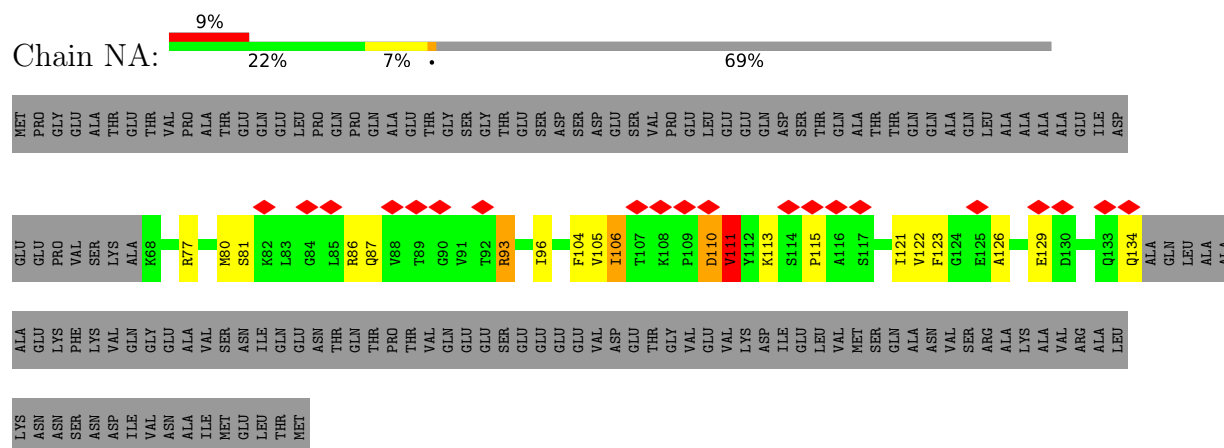
- Molecule 50: 60S acidic ribosomal protein P0



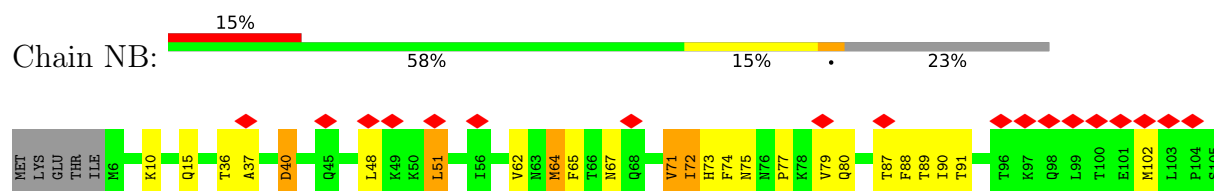
- Molecule 51: Large ribosomal subunit protein uL11

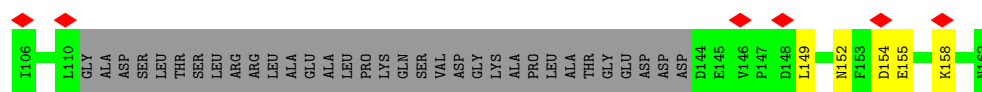


- Molecule 52: Nascent polypeptide-associated complex subunit alpha

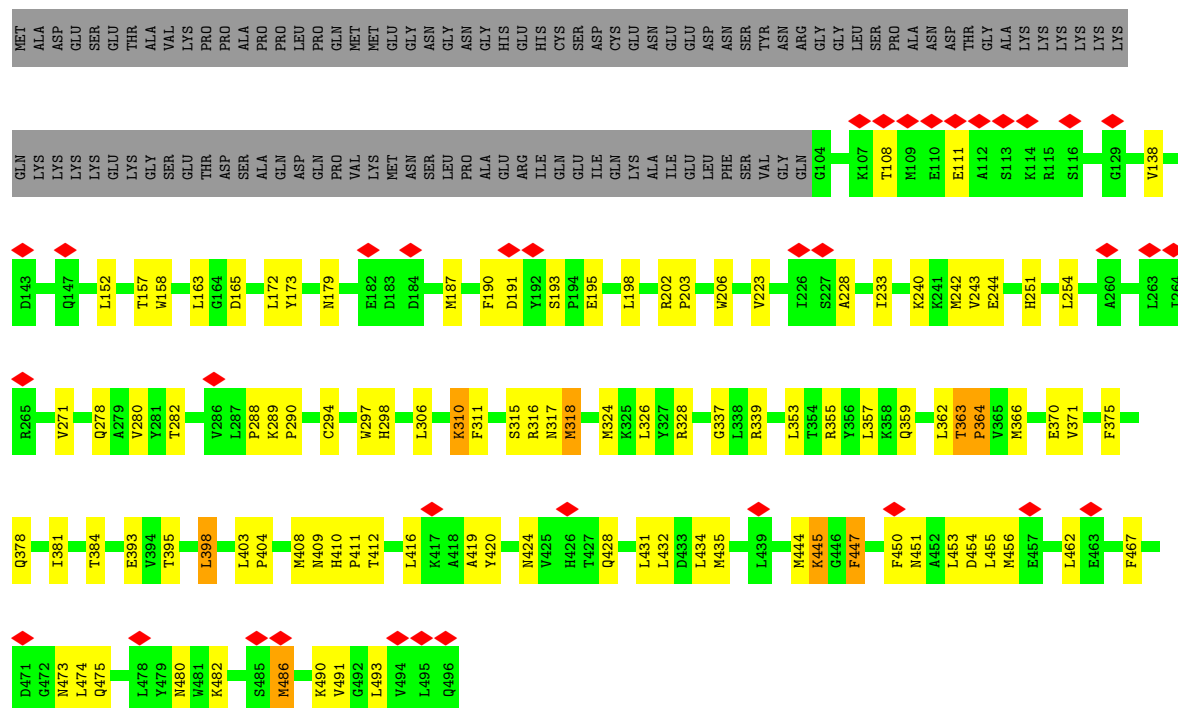


- Molecule 53: Isoform 2 of Transcription factor BTF3

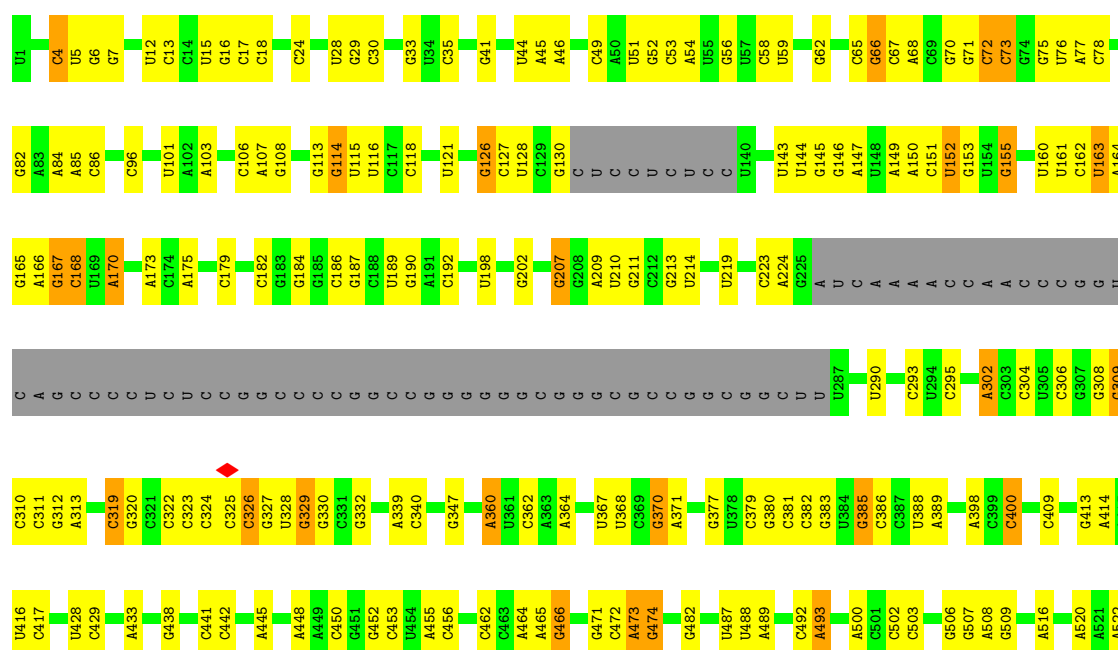


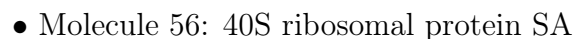


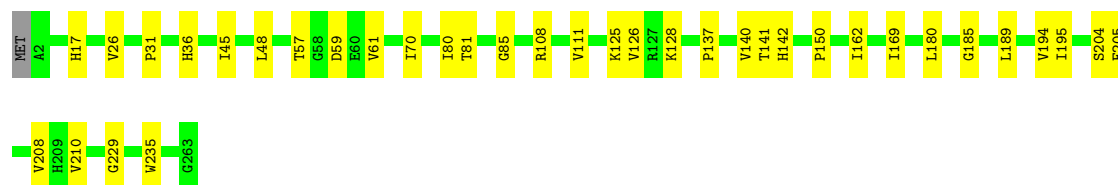
• Molecule 54: Glycylpeptide N-tetradecanoyltransferase 1



• Molecule 55: 18S rRNA

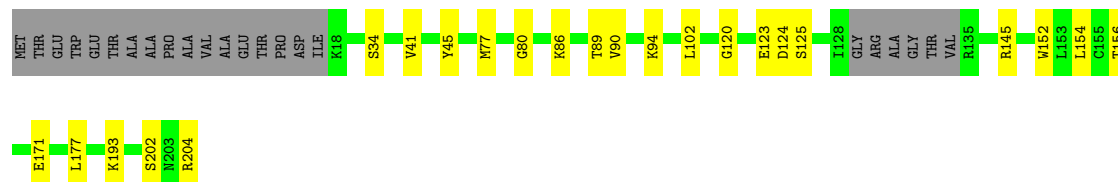






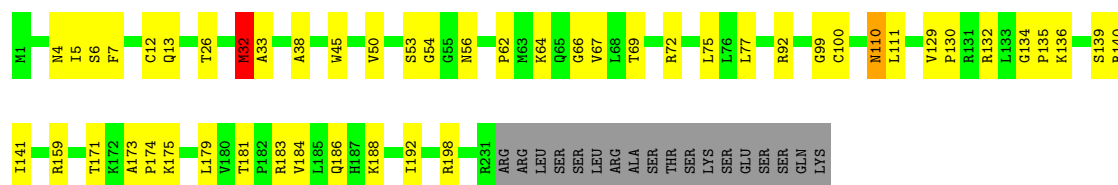
- Molecule 61: 40S ribosomal protein S5

Chain SF: 77% 11% 11%



- Molecule 62: 40S ribosomal protein S6

Chain SG: 73% 19% 7%



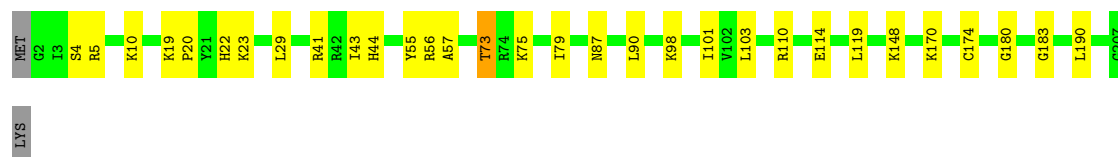
- Molecule 63: 40S ribosomal protein S7

Chain SH: 83% 11% 6%



- Molecule 64: 40S ribosomal protein S8

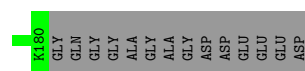
Chain SI: 84% 14% 2%



- Molecule 65: 40S ribosomal protein S9

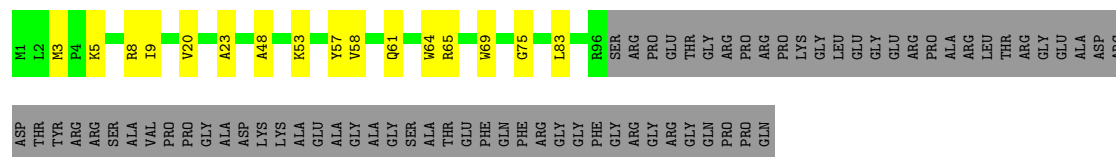
Chain SJ: 76% 15% 8%





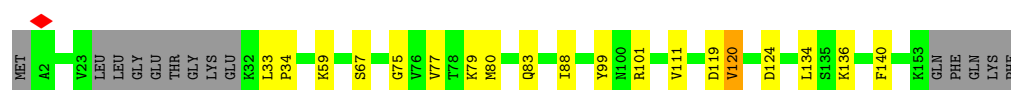
- Molecule 66: 40S ribosomal protein S10

Chain SK: 48% 10% 42%



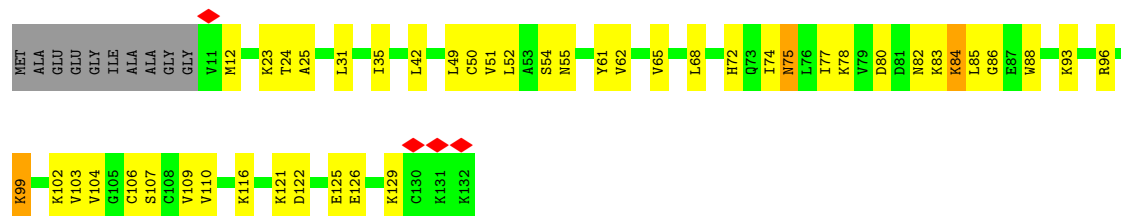
- Molecule 67: 40S ribosomal protein S11

Chain SL: 79% 11% 9%



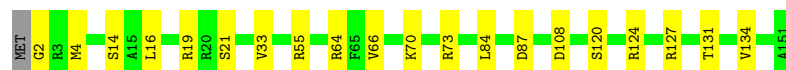
- Molecule 68: 40S ribosomal protein S12

Chain SM: 58% 32% 8%



- Molecule 69: 40S ribosomal protein S13

Chain SN: 86% 13%



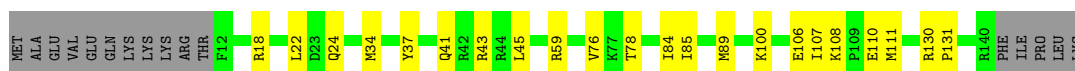
- Molecule 70: 40S ribosomal protein S14

Chain SO: 75% 11% 11%

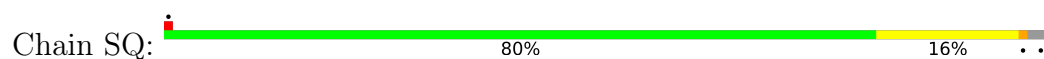


- Molecule 71: 40S ribosomal protein S15

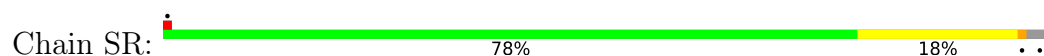
Chain SP: 74% 15% 11%



- Molecule 72: 40S ribosomal protein S16



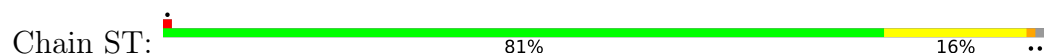
- Molecule 73: 40S ribosomal protein S17



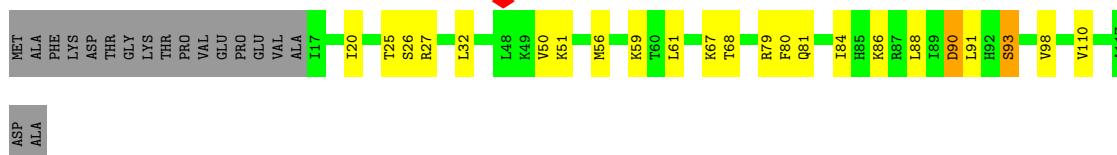
- Molecule 74: 40S ribosomal protein S18



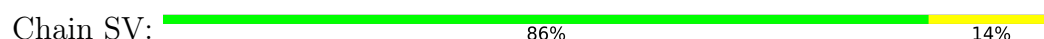
- Molecule 75: 40S ribosomal protein S19



- Molecule 76: 40S ribosomal protein S20



- Molecule 77: 40S ribosomal protein S21





- Molecule 78: 40S ribosomal protein S15a

Chain SW: 82% 18%



- Molecule 79: 40S ribosomal protein S23

Chain SX: 84% 14%



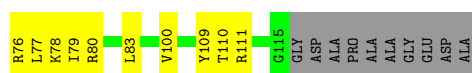
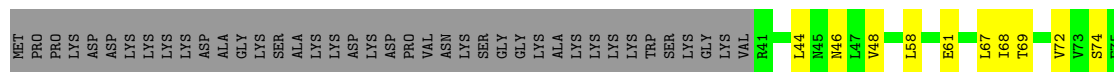
- Molecule 80: 40S ribosomal protein S24

Chain SY: 75% 15% 8%



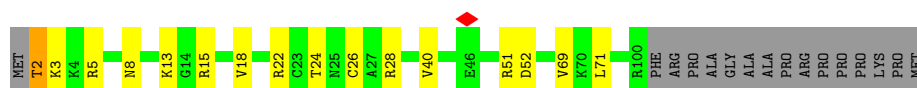
- Molecule 81: 40S ribosomal protein S25

Chain SZ: 44% 16% 40%



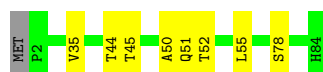
- Molecule 82: 40S ribosomal protein S26

Chain Sa: 72% 13% 14%



- Molecule 83: 40S ribosomal protein S27

Chain Sb: 89% 10%



- Molecule 84: 40S ribosomal protein S28

MET	ASP	THR	SER	ARG	V6	T15	K16	V17	L18	Q29	V30	R31	V32	S39	R40	S41	I42	I43	G48	P49	V50	V55	L56	T57	R66	R67	L68	ARG
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- MET
GLY
HIS
Q4
Y7
W8
C21
R22
V23
L30
M38
C39
R40
R44
F52
D56

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | GLN | LEU | PHE | VAL | ARG | ALA | GLN | LEU | HIS | THR | PHE | GLU | VAL | THR | GLY | GLN | GLU | THR | VAL | ALA | ALA | ILE | LYS | ALA | HIS | ALA | VAL | VAL | SER | LEU | GLU | GLY | ILE | ALA | PRO | ASP | GLN | VAL | VAL | LEU | LEU | ALA | GLY | ALA | ALA | PRO | ASP | GLU | THR | LEU | GLY | CYS | GLN | VAL |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

ALA	LEU	THR	THR	LEU	GLU	VAL	ALA	GLY	ARG	MET	LEU	GLY	GLY	LYS	VAL	HIS	GLY	S5	K11	R31	R35	Y38	S59
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	-----	-----	-----	-----	-----

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | GLN | ILE | PHE | VAL | LYS | THR | LEU | THR | GLY | LYS | THR | ILE | THR | LEU | GLU | VAL | GLU | PRO | SER | ASP | THR | ILE | GLU | ASN | GLN | ILE | LYS | LYS | LYS | ILE | GLN | ASP | LYS | GLY | GLY | PRO | PRO | ASP | ASP | GLN | GLN | ARG | LEU | ILE | PHE | ALA | ALA | GLY | LYS | GLN | GLN | LEU | LEU | SER | TYR | ASN |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TLE	GLN	LYS	GLU	SER	THR	LEU	HIS	LEU	VAL	LEU	ARG	LEU	ARG	GLY	GLY	ALA	LYS	LYS	ARG	LYS	LYS	LYS	SER	TYR	THR	THR	PRO	K89	Y98	K107	K113	I114	C121	A128	M132	H135	Y140	C144	C145	L146	C149	F150	M151	LYS	PRO	GLU	ASP
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|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|
| MET | THR | GLU | Q4 | L11 | K12 | W17 | V18 | T24 | F27 | I31 | S36 | R36 | W43 | K44 | L45 | H64 | S67 | S72 | S73 | D74 | G81 | D84 | L87 | F101 | T105 | S114 | Q119 | S122 | G123 | S124 | R125 | D126 | N133 | V137 | S152 | P163 |
|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|

V166	S167	C168	G169	V170	D171	V174	L179	T186	H191	T192	L195	S201	S209	G210	G211	L239	G240	F241	S242	P243	W244	R245	S276	THR	SER	S279	S288	W291	A300	L306	V307	T313	ILE	GLY	THR	SEC
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	------	------	------	------	------	------	------	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	49105	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	5.017	Depositor
Minimum map value	-2.474	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.119	Depositor
Recommended contour level	0.075	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: MG, LYO, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CM	0.26	0/273	0.42	0/421
2	CP	0.24	0/1789	0.44	0/2788
3	CR	0.22	0/3311	0.52	1/4452 (0.0%)
4	CZ	0.19	0/465	0.44	0/638
5	L5	0.27	0/87471	0.36	0/136443
6	L7	0.26	0/2858	0.33	0/4455
7	L8	0.26	0/3701	0.34	0/5766
8	LA	0.26	0/1936	0.56	2/2596 (0.1%)
9	LB	0.25	0/3251	0.50	0/4352
10	LC	0.23	0/2938	0.50	3/3947 (0.1%)
11	LD	0.21	0/2407	0.47	0/3227
12	LE	0.25	0/1788	0.58	1/2399 (0.0%)
13	LF	0.25	0/1905	0.48	0/2539
14	LG	0.24	0/1849	0.53	1/2496 (0.0%)
15	LH	0.24	0/1529	0.47	0/2058
16	LI	0.23	0/1705	0.48	0/2277
17	LJ	0.24	0/1352	0.52	1/1813 (0.1%)
18	LL	0.23	0/1661	0.49	0/2229
19	LM	0.21	0/1145	0.44	0/1536
20	LN	0.25	0/1746	0.44	0/2338
21	LO	0.25	0/1665	0.50	1/2229 (0.0%)
22	LP	0.23	0/1260	0.46	0/1692
23	LQ	0.24	0/1526	0.48	0/2038
24	LR	0.25	0/1468	0.47	0/1945
25	LS	0.31	1/1492 (0.1%)	0.55	2/2003 (0.1%)
26	LT	0.23	0/1310	0.51	0/1752
27	LU	0.23	0/820	0.62	0/1102
28	LV	0.23	0/985	0.49	0/1323
29	LW	0.23	0/820	0.49	0/1104
30	LX	0.26	0/998	0.49	0/1341
31	LY	0.24	0/1128	0.48	0/1500
32	LZ	0.26	0/1130	0.47	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	La	0.24	0/1183	0.44	0/1582
34	Lb	0.26	0/600	0.54	0/796
35	Lc	0.22	0/752	0.47	0/1011
36	Ld	0.23	0/889	0.43	0/1198
37	Le	0.24	0/1067	0.47	0/1425
38	Lf	0.27	0/891	0.53	0/1194
39	Lg	0.23	0/899	0.46	0/1200
40	Lh	0.21	0/1014	0.46	0/1340
41	Li	0.20	0/824	0.43	0/1093
42	Lj	0.25	0/720	0.46	0/952
43	Lk	0.29	0/548	0.61	0/730
44	Ll	0.22	0/454	0.40	0/599
45	Lm	0.20	0/431	0.35	0/570
46	Ln	0.24	0/231	0.36	0/294
47	Lo	0.22	0/876	0.46	0/1156
48	Lp	0.22	0/706	0.47	0/939
49	Lr	0.23	0/1012	0.45	0/1358
50	Ls	0.32	0/1666	0.75	2/2250 (0.1%)
51	Lt	0.33	0/1224	0.82	0/1651
52	NA	0.42	0/536	0.91	2/715 (0.3%)
53	NB	0.42	0/963	0.82	3/1292 (0.2%)
54	NM	0.68	6/3299 (0.2%)	1.00	14/4483 (0.3%)
55	S2	0.26	0/40882	0.39	0/63715
56	SA	0.26	0/1708	0.53	0/2324
57	SB	0.21	0/1745	0.45	0/2337
58	SC	0.23	0/1697	0.47	0/2301
59	SD	0.22	0/1620	0.50	0/2198
60	SE	0.22	0/2014	0.47	0/2726
61	SF	0.25	0/1423	0.55	0/1913
62	SG	0.24	0/1657	0.51	0/2247
63	SH	0.20	0/1295	0.46	0/1763
64	SI	0.22	0/1603	0.47	0/2161
65	SJ	0.22	0/1456	0.51	0/1957
66	SK	0.34	0/750	0.59	0/1026
67	SL	0.24	0/1163	0.44	0/1562
68	SM	0.36	0/960	0.96	6/1286 (0.5%)
69	SN	0.21	0/1206	0.45	0/1626
70	SO	0.26	0/982	0.60	1/1320 (0.1%)
71	SP	0.22	0/1010	0.45	0/1362
72	SQ	0.22	0/1093	0.51	0/1470
73	SR	0.29	0/955	0.66	1/1294 (0.1%)
74	SS	0.27	0/1148	0.67	2/1542 (0.1%)
75	ST	0.21	0/1100	0.40	0/1479

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SU	0.23	0/722	0.55	0/983
77	SV	0.22	0/625	0.41	0/837
78	SW	0.25	0/1043	0.49	0/1396
79	SX	0.25	0/1096	0.52	0/1467
80	SY	0.24	0/944	0.57	1/1271 (0.1%)
81	SZ	0.29	0/565	0.67	2/764 (0.3%)
82	Sa	0.27	0/794	0.52	0/1065
83	Sb	0.26	0/632	0.63	0/851
84	Sc	0.25	0/474	0.69	0/638
85	Sd	0.23	0/443	0.51	0/589
86	Se	0.17	0/420	0.41	0/554
87	Sf	0.30	0/525	0.70	0/695
88	Sg	0.21	0/2235	0.57	0/3068
All	All	0.27	7/238452 (0.0%)	0.45	46/349921 (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
18	LL	0	1
23	LQ	0	1
39	Lg	0	1
51	Lt	0	1
52	NA	0	1
57	SB	0	1
62	SG	0	1
65	SJ	0	1
74	SS	0	1
All	All	0	9

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	NM	364	PRO	CB-CG	20.43	2.51	1.49
54	NM	364	PRO	CG-CD	-17.53	0.91	1.50
54	NM	364	PRO	N-CD	11.46	1.63	1.47
54	NM	364	PRO	N-CA	-9.92	1.35	1.47
54	NM	364	PRO	CA-CB	-6.16	1.45	1.53
54	NM	363	THR	C-N	5.96	1.40	1.33
25	LS	20	PRO	CG-CD	-5.78	1.31	1.50

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	NM	364	PRO	CB-CG-CD	-33.15	0.04	106.10
54	NM	364	PRO	CA-N-CD	-17.85	87.01	112.00
54	NM	364	PRO	N-CA-CB	-10.86	91.98	103.38
73	SR	122	PRO	CA-N-CD	-10.44	97.39	112.00
54	NM	364	PRO	CA-CB-CG	-10.33	84.88	104.50
80	SY	52	PRO	CA-N-CD	-10.25	97.65	112.00
25	LS	20	PRO	CA-N-CD	-9.88	98.17	112.00
54	NM	445	LYS	CD-CE-NZ	-9.33	82.05	111.90
54	NM	493	LEU	CB-CG-CD2	-9.16	83.23	110.70
25	LS	20	PRO	N-CD-CG	-7.30	92.25	103.20
54	NM	362	LEU	CA-CB-CG	7.08	141.09	116.30
54	NM	364	PRO	N-CA-C	6.93	121.81	111.41
12	LE	100	LYS	CA-CB-CG	6.89	127.89	114.10
50	Ls	73	PRO	CA-N-CD	-6.89	102.36	112.00
68	SM	84	LYS	CA-CB-CG	6.83	127.75	114.10
54	NM	493	LEU	CD1-CG-CD2	-6.81	95.83	110.80
14	LG	165	GLU	N-CA-C	-6.72	99.53	108.34
10	LC	268	ARG	CG-CD-NE	6.58	126.48	112.00
54	NM	363	THR	C-N-CD	6.29	150.77	125.00
54	NM	310	LYS	CA-CB-CG	6.13	126.36	114.10
53	NB	72	ILE	CB-CG1-CD1	5.92	126.24	113.80
21	LO	110	PRO	N-CA-C	5.83	117.81	110.70
53	NB	64	MET	N-CA-C	-5.69	100.77	109.41
81	SZ	61	GLU	CA-C-N	5.59	123.76	120.24
81	SZ	61	GLU	C-N-CA	5.59	123.76	120.24
10	LC	109	ARG	CA-C-N	5.58	132.20	121.54
10	LC	109	ARG	C-N-CA	5.58	132.20	121.54
3	CR	372	MET	CB-CG-SD	5.55	129.35	112.70
54	NM	318	MET	CB-CG-SD	5.45	129.06	112.70
68	SM	12	MET	CB-CG-SD	5.33	128.70	112.70
54	NM	364	PRO	CB-CA-C	5.31	117.91	110.95
54	NM	486	MET	CA-CB-CG	5.30	124.70	114.10
8	LA	171	GLY	CA-C-N	5.26	131.72	121.41
8	LA	171	GLY	C-N-CA	5.26	131.72	121.41
74	SS	8	LYS	CA-C-N	5.24	131.55	121.54
74	SS	8	LYS	C-N-CA	5.24	131.55	121.54
53	NB	72	ILE	CA-CB-CG1	5.22	119.28	110.40
68	SM	84	LYS	CA-C-N	-5.22	112.38	120.31
68	SM	84	LYS	C-N-CA	-5.22	112.38	120.31
70	SO	92	ALA	N-CA-C	5.15	117.56	110.35
52	NA	80	MET	CB-CG-SD	5.12	128.07	112.70
52	NA	111	VAL	CA-CB-CG1	5.12	119.11	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	Ls	18	ILE	CG1-CB-CG2	5.12	126.05	110.70
68	SM	99	LYS	CB-CG-CD	5.09	123.01	111.30
17	LJ	168	GLN	CB-CG-CD	5.02	121.13	112.60
68	SM	96	ARG	CG-CD-NE	5.01	123.03	112.00

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	LL	47	ALA	Peptide
23	LQ	94	GLU	Peptide
39	Lg	52	ARG	Peptide
51	Lt	57	ARG	Sidechain
52	NA	110	ASP	Peptide
57	SB	189	ILE	Peptide
62	SG	32	MET	Peptide
65	SJ	137	VAL	Peptide
74	SS	11	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CM	247	0	128	1	0
2	CP	1602	0	809	4	0
3	CR	3269	0	3312	30	0
4	CZ	461	0	338	4	0
5	L5	78199	0	39524	400	0
6	L7	2558	0	1296	3	0
7	L8	3314	0	1683	15	0
8	LA	1898	0	1993	21	0
9	LB	3183	0	3316	26	0
10	LC	2884	0	3050	19	0
11	LD	2361	0	2378	25	0
12	LE	1754	0	1899	26	0
13	LF	1870	0	1996	21	0
14	LG	1818	0	1911	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	LH	1510	0	1579	15	0
16	LI	1666	0	1711	22	0
17	LJ	1329	0	1348	17	0
18	LL	1630	0	1715	20	0
19	LM	1122	0	1174	11	0
20	LN	1701	0	1749	26	0
21	LO	1633	0	1771	13	0
22	LP	1234	0	1254	13	0
23	LQ	1502	0	1616	11	0
24	LR	1452	0	1580	14	0
25	LS	1452	0	1490	13	0
26	LT	1282	0	1336	17	0
27	LU	806	0	826	11	0
28	LV	971	0	1024	12	0
29	LW	808	0	726	2	0
30	LX	981	0	1055	18	0
31	LY	1111	0	1194	14	0
32	LZ	1107	0	1182	13	0
33	La	1154	0	1198	11	0
34	Lb	590	0	613	9	0
35	Lc	742	0	774	8	0
36	Ld	874	0	918	6	0
37	Le	1049	0	1136	14	0
38	Lf	872	0	901	6	0
39	Lg	889	0	968	8	0
40	Lh	1006	0	1132	14	0
41	Li	813	0	887	4	0
42	Lj	705	0	737	7	0
43	Lk	542	0	590	8	0
44	Ll	444	0	483	7	0
45	Lm	425	0	461	3	0
46	Ln	230	0	276	3	0
47	Lo	862	0	929	10	0
48	Lp	696	0	744	5	0
49	Lr	997	0	1054	5	0
50	Ls	1640	0	1687	36	0
51	Lt	1208	0	1257	33	0
52	NA	531	0	573	10	0
53	NB	955	0	973	19	0
54	NM	3209	0	3185	77	0
55	S2	36562	0	18472	268	0
56	SA	1671	0	1672	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	SB	1718	0	1786	25	0
58	SC	1661	0	1710	21	0
59	SD	1594	0	1568	19	0
60	SE	1972	0	2012	18	0
61	SF	1403	0	1421	12	0
62	SG	1634	0	1568	32	0
63	SH	1274	0	1196	16	0
64	SI	1574	0	1540	22	0
65	SJ	1431	0	1497	22	0
66	SK	726	0	674	10	0
67	SL	1143	0	1177	10	0
68	SM	950	0	987	26	0
69	SN	1182	0	1249	15	0
70	SO	969	0	982	13	0
71	SP	990	0	974	16	0
72	SQ	1075	0	1110	14	0
73	SR	942	0	913	16	0
74	SS	1130	0	1167	19	0
75	ST	1081	0	1093	16	0
76	SU	713	0	692	17	0
77	SV	618	0	617	8	0
78	SW	1026	0	1072	17	0
79	SX	1078	0	1130	12	0
80	SY	927	0	914	12	0
81	SZ	559	0	594	12	0
82	Sa	781	0	831	13	0
83	Sb	618	0	604	4	0
84	Sc	472	0	484	9	0
85	Sd	433	0	415	7	0
86	Se	416	0	439	4	0
87	Sf	515	0	521	6	0
88	Sg	2180	0	1968	28	0
89	CM	1	0	0	0	0
89	L5	125	0	0	0	0
89	L7	3	0	0	0	0
89	L8	3	0	0	0	0
89	LA	2	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	50	0	0	0	0
89	ST	1	0	0	0	0
89	Sa	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	222376	0	164488	1651	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 (1651) 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)
54:NM:364:PRO:CG	54:NM:364:PRO:N	2.04	1.18
54:NM:364:PRO:CD	54:NM:364:PRO:HG3	1.68	1.17
54:NM:364:PRO:CD	54:NM:364:PRO:HG2	1.68	1.10
54:NM:364:PRO:CG	54:NM:364:PRO:HD2	1.55	1.05
54:NM:364:PRO:CG	54:NM:364:PRO:HD3	1.55	1.02
55:S2:1748:G:H1	55:S2:1786:U:H3	1.16	0.91
54:NM:364:PRO:CG	54:NM:364:PRO:CD	0.91	0.91
5:L5:1443:A:N6	5:L5:2104:G:C2	2.46	0.84
30:LX:114:LYS:HD3	30:LX:120:ASP:HA	1.60	0.82
55:S2:167:G:H21	62:SG:132:ARG:HD3	1.46	0.80
52:NA:86:ARG:HE	52:NA:113:LYS:HE2	1.49	0.78
5:L5:3751:G:H21	5:L5:3775:A:H8	1.30	0.78
55:S2:925:G:H1	55:S2:1017:U:H3	1.31	0.78
55:S2:1348:G:H1	55:S2:1381:G:H22	1.29	0.75
55:S2:1142:G:H21	55:S2:1145:A:H2	1.34	0.75
8:LA:117:GLU:HB2	8:LA:162:ASN:HB2	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:NA:96:ILE:HB	52:NA:104:PHE:HB3	1.69	0.74
55:S2:1396:A:O2'	55:S2:1398:G:N7	2.21	0.74
16:LI:48:LEU:O	16:LI:139:ARG:HA	1.88	0.73
1:CM:443:U:H3	2:CP:33:A:H61	1.35	0.73
5:L5:5027:C:H42	64:SI:170:LYS:HE3	1.53	0.72
88:Sg:87:LEU:HB2	88:Sg:101:PHE:HB2	1.71	0.72
54:NM:195:GLU:HG2	54:NM:381:ILE:HD11	1.71	0.72
34:Lb:55:LYS:HE2	34:Lb:55:LYS:H	1.56	0.71
60:SE:45:ILE:HA	60:SE:61:VAL:HG11	1.73	0.70
5:L5:1443:A:N6	5:L5:2103:G:C6	2.59	0.70
5:L5:2611:A:H5'	5:L5:2688:G:H4'	1.74	0.70
5:L5:1443:A:H62	5:L5:2104:G:N2	1.89	0.70
53:NB:79:VAL:HG22	53:NB:90:ILE:HG22	1.74	0.69
54:NM:228:ALA:HA	54:NM:244:GLU:O	1.91	0.69
55:S2:1649:U:H3	55:S2:1675:A:H2	1.38	0.69
5:L5:74:G:H5''	18:LL:59:VAL:HB	1.75	0.69
57:SB:152:LYS:HB2	73:SR:131:PRO:HB3	1.75	0.69
7:L8:55:U:H3	7:L8:62:A:H2	1.41	0.69
54:NM:294:CYS:HB3	54:NM:453:LEU:HD21	1.75	0.68
5:L5:2838:G:H5'	9:LB:247:GLY:HA2	1.73	0.68
54:NM:398:LEU:HD11	54:NM:434:LEU:HB3	1.74	0.68
26:LT:88:ARG:NH2	34:Lb:30:GLU:OE1	2.26	0.68
55:S2:1107:G:H1	55:S2:1125:C:H5	1.42	0.68
68:SM:122:ASP:HA	68:SM:125:GLU:HG3	1.76	0.68
63:SH:63:PHE:HA	63:SH:95:ILE:O	1.94	0.68
44:LI:21:ARG:O	44:LI:38:ASN:ND2	2.27	0.67
30:LX:151:ASN:HD21	54:NM:326:LEU:HD21	1.57	0.67
59:SD:163:PRO:O	59:SD:167:TYR:HB2	1.94	0.67
5:L5:1267:C:OP2	5:L5:2121:C:N4	2.27	0.67
53:NB:62:VAL:HG23	53:NB:74:PHE:HB3	1.77	0.67
57:SB:36:PRO:HD3	57:SB:98:THR:HG22	1.77	0.67
5:L5:1443:A:N6	5:L5:2103:G:N1	2.42	0.67
79:SX:49:GLY:O	79:SX:99:GLU:HA	1.95	0.66
53:NB:64:MET:SD	53:NB:72:ILE:HB	2.35	0.66
60:SE:185:GLY:H	60:SE:189:LEU:HD13	1.59	0.66
71:SP:41:GLN:HG3	71:SP:84:ILE:HD12	1.78	0.66
54:NM:316:ARG:HH11	54:NM:317:ASN:HB3	1.61	0.66
55:S2:617:G:H4'	79:SX:88:ASP:HB3	1.77	0.65
61:SF:102:LEU:HD11	81:SZ:100:VAL:HG21	1.77	0.65
42:Lj:54:LYS:O	42:Lj:58:THR:HB	1.97	0.65
8:LA:29:LEU:O	8:LA:123:ARG:NH1	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LT:43:LYS:O	26:LT:58:HIS:ND1	2.30	0.65
54:NM:191:ASP:HB3	54:NM:404:PRO:HB2	1.78	0.65
51:Lt:104:ILE:HB	51:Lt:143:VAL:HG23	1.77	0.65
28:LV:69:LYS:NZ	28:LV:71:GLU:OE2	2.31	0.64
55:S2:1544:C:N4	55:S2:1588:A:O2'	2.30	0.64
55:S2:1745:A:H1'	62:SG:66:GLY:HA2	1.80	0.64
55:S2:360:A:N6	55:S2:400:C:O2'	2.31	0.64
53:NB:80:GLN:O	53:NB:88:PHE:HA	1.98	0.64
5:L5:2557:G:H1	5:L5:2570:U:H3	1.45	0.64
5:L5:3759:A:HO2'	55:S2:1826:G:HO2'	1.44	0.64
57:SB:124:HIS:HA	57:SB:137:LEU:O	1.97	0.64
5:L5:2658:G:N2	5:L5:2676:A:OP2	2.31	0.64
5:L5:1396:G:HO2'	5:L5:1468:C:HO2'	1.42	0.63
74:SS:34:LYS:HG2	74:SS:103:LEU:HD23	1.79	0.63
5:L5:1919:G:N3	25:LS:164:LYS:NZ	2.46	0.63
5:L5:4122:G:H4'	39:Lg:90:ARG:HD2	1.80	0.63
5:L5:4910:G:N2	21:LO:106:ASP:O	2.31	0.63
55:S2:151:C:OP1	80:SY:120:THR:OG1	2.17	0.63
55:S2:1616:U:H3	55:S2:1620:A:H2	1.47	0.63
5:L5:435:A:O2'	37:Le:26:ASP:OD1	2.15	0.63
5:L5:966:A:H5''	5:L5:2092:G:H22	1.62	0.63
13:LF:222:LYS:HB3	13:LF:231:GLY:HA2	1.80	0.63
5:L5:518:G:H1	5:L5:643:C:H2'	1.63	0.63
55:S2:1228:A:H2'	55:S2:1229:G:C8	2.34	0.63
47:Lo:33:LEU:HA	47:Lo:38:LYS:HG2	1.81	0.63
51:Lt:28:LEU:O	51:Lt:32:ILE:HB	1.98	0.63
5:L5:3946:G:H21	5:L5:3947:A:H62	1.47	0.62
55:S2:114:G:O2'	55:S2:382:C:O2'	2.17	0.62
88:Sg:152:SER:H	88:Sg:169:GLY:HA2	1.65	0.62
55:S2:1488:C:O2'	55:S2:1490:G:OP2	2.13	0.62
5:L5:1785:C:OP1	16:LI:133:GLN:NE2	2.33	0.62
54:NM:297:TRP:CZ3	54:NM:454:ASP:HB3	2.35	0.62
31:LY:30:MET:HB3	31:LY:101:PRO:HG2	1.82	0.62
76:SU:50:VAL:HG23	76:SU:91:LEU:HB3	1.82	0.62
5:L5:2469:C:H5	5:L5:2471:G:H1	1.47	0.61
7:L8:82:A:H62	7:L8:84:A:H3'	1.64	0.61
51:Lt:18:THR:HA	51:Lt:57:ARG:HA	1.81	0.61
53:NB:73:HIS:HB2	53:NB:102:MET:HE1	1.82	0.61
58:SC:86:LEU:HD11	58:SC:265:PRO:HG2	1.81	0.61
61:SF:77:MET:HG2	61:SF:89:THR:HG21	1.81	0.61
68:SM:24:THR:HG21	68:SM:116:LYS:HE3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:4258:C:OP2	17:LJ:54:ARG:NH1	2.33	0.61
3:CR:317:VAL:HA	3:CR:413:LEU:HA	1.81	0.61
76:SU:68:THR:O	85:Sd:40:ARG:NH2	2.34	0.61
5:L5:137:G:H2'	5:L5:138:G:H8	1.64	0.61
5:L5:2695:A:OP1	43:Lk:35:LYS:NZ	2.33	0.61
5:L5:5011:A:H62	5:L5:5037:U:H3	1.48	0.61
39:Lg:83:CYS:SG	39:Lg:86:CYS:HB2	2.40	0.61
51:Lt:11:LYS:O	51:Lt:63:THR:HA	2.01	0.61
55:S2:164:A:H3'	55:S2:165:G:H21	1.65	0.61
12:LE:128:HIS:O	12:LE:128:HIS:ND1	2.32	0.61
18:LL:47:ALA:O	18:LL:49:ARG:N	2.31	0.61
56:SA:77:ILE:HB	56:SA:124:VAL:HG12	1.83	0.61
5:L5:1824:G:OP1	26:LT:35:LYS:NZ	2.34	0.60
19:LM:119:ARG:HG3	21:LO:189:ILE:HD12	1.83	0.60
81:SZ:79:ILE:HG13	81:SZ:83:LEU:HD23	1.82	0.60
48:Lp:5:THR:HG21	48:Lp:9:GLY:H	1.66	0.60
54:Nm:486:MET:SD	54:Nm:490:LYS:HB2	2.41	0.60
75:ST:96:SER:HB3	75:ST:99:VAL:HB	1.83	0.60
5:L5:684:G:H4'	12:LE:100:LYS:HE3	1.84	0.60
5:L5:4128:A:H2	5:L5:4156:G:H21	1.50	0.60
55:S2:1098:C:H5	55:S2:1134:G:H1	1.46	0.60
2:CP:32:U:OP2	72:SQ:146:ARG:NH1	2.26	0.60
5:L5:958:G:H21	12:LE:125:LEU:H	1.49	0.60
44:Ll:20:ASN:ND2	44:Ll:42:ARG:O	2.32	0.60
54:Nm:419:ALA:HB3	54:Nm:450:PHE:HA	1.83	0.60
57:SB:183:GLU:HA	57:SB:186:ASN:HB2	1.82	0.60
5:L5:4626:A:H62	5:L5:4669:A:H2	1.49	0.60
8:LA:247:ARG:HD3	55:S2:1069:U:H4'	1.84	0.60
22:LP:36:ILE:HA	22:LP:39:MET:HE3	1.84	0.60
72:SQ:6:PRO:O	72:SQ:27:ARG:NH2	2.35	0.60
88:Sg:163:PRO:HB2	88:Sg:179:LEU:HD12	1.84	0.60
3:CR:322:VAL:O	3:CR:391:ILE:HA	2.02	0.59
5:L5:703:G:H2'	5:L5:704:C:H4'	1.83	0.59
59:SD:35:SER:OG	59:SD:51:LEU:O	2.19	0.59
53:NB:48:LEU:HA	53:NB:51:LEU:HB2	1.84	0.59
35:Lc:38:ILE:HG21	35:Lc:63:TYR:HB3	1.84	0.59
55:S2:696:G:N2	55:S2:737:G:O6	2.35	0.59
76:SU:91:LEU:HD13	76:SU:93:SER:HB3	1.84	0.59
87:Sf:121:CYS:HB3	87:Sf:132:MET:HE1	1.82	0.59
5:L5:1362:G:OP1	18:LL:39:ARG:NH2	2.35	0.59
58:SC:176:LYS:O	58:SC:200:ARG:NH2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:2894:A:H62	5:L5:3607:U:H3	1.50	0.59
50:Ls:26:LYS:HZ1	50:Ls:92:LYS:HE2	1.66	0.59
53:NB:62:VAL:HG22	53:NB:77:PRO:HG3	1.84	0.59
55:S2:1776:G:OP2	55:S2:1776:G:N2	2.36	0.59
57:SB:29:ASP:OD1	57:SB:51:ARG:NH1	2.35	0.59
3:CR:289:ARG:HH12	3:CR:319:ILE:HD12	1.67	0.59
5:L5:1351:G:OP1	10:LC:33:ARG:NH1	2.35	0.59
16:LI:66:GLU:OE1	16:LI:69:ARG:NH1	2.35	0.59
24:LR:105:LEU:HD22	24:LR:135:LYS:HG2	1.83	0.59
55:S2:170:A:OP2	62:SG:140:ARG:NH1	2.36	0.59
55:S2:1091:C:HO2'	78:SW:2:VAL:N	2.00	0.59
13:LF:105:VAL:HG13	13:LF:136:VAL:HG12	1.84	0.59
53:NB:149:LEU:HG	54:NM:254:LEU:HD11	1.84	0.59
5:L5:1732:C:H5''	26:LT:43:LYS:HE3	1.84	0.59
6:L7:30:C:H5	6:L7:47:G:H1	1.49	0.59
22:LP:94:MET:HG2	22:LP:148:MET:HE3	1.84	0.59
55:S2:1550:G:H3'	55:S2:1579:A:H61	1.67	0.59
5:L5:3689:G:O2'	5:L5:3818:U:OP2	2.20	0.59
5:L5:3868:G:H22	5:L5:3900:G:H1'	1.68	0.59
40:Lh:99:GLU:HA	40:Lh:102:LEU:HD12	1.85	0.59
55:S2:927:C:O2	83:Sb:51:GLN:NE2	2.36	0.59
57:SB:129:THR:HB	57:SB:180:ASP:HA	1.83	0.59
68:SM:35:ILE:HD11	68:SM:61:TYR:CE1	2.37	0.59
5:L5:2487:G:H22	5:L5:2492:C:H1'	1.68	0.58
47:Lo:11:PHE:O	47:Lo:81:ARG:NH2	2.36	0.58
72:SQ:16:LYS:H	72:SQ:19:ALA:HB3	1.68	0.58
5:L5:758:G:O3'	15:LH:50:LYS:NZ	2.35	0.58
55:S2:1347:U:H2'	55:S2:1348:G:C8	2.38	0.58
55:S2:433:A:H5''	64:SI:22:HIS:HB3	1.85	0.58
68:SM:80:ASP:OD2	68:SM:80:ASP:N	2.36	0.58
5:L5:1704:C:OP1	13:LF:43:ARG:NH1	2.37	0.58
68:SM:61:TYR:HH	68:SM:107:SER:HG	1.51	0.58
8:LA:120:PRO:HA	8:LA:162:ASN:HB3	1.84	0.58
8:LA:137:ILE:HD11	8:LA:149:LYS:HB2	1.85	0.58
9:LB:168:MET:HG3	9:LB:178:ALA:HA	1.85	0.58
52:NA:87:GLN:NE2	52:NA:110:ASP:OD2	2.36	0.58
54:NM:419:ALA:HB2	54:NM:447:PHE:HE2	1.69	0.58
76:SU:26:SER:HB2	76:SU:110:VAL:HA	1.86	0.58
55:S2:672:A:N6	55:S2:1027:A:OP1	2.36	0.58
73:SR:65:PRO:HB3	73:SR:73:LEU:HD11	1.86	0.58
5:L5:2899:C:OP1	24:LR:108:ARG:NH2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CR:376:GLU:OE2	3:CR:380:ASN:ND2	2.36	0.58
72:SQ:58:LEU:HB3	72:SQ:62:ARG:HD2	1.86	0.58
50:Ls:99:ARG:HE	50:Ls:103:LEU:HD22	1.69	0.58
55:S2:563:G:H1	55:S2:592:C:H5	1.50	0.58
33:La:131:ARG:NH1	33:La:135:GLU:OE2	2.37	0.57
51:Lt:85:LEU:HD23	51:Lt:87:GLU:HB2	1.85	0.57
55:S2:190:G:O2'	55:S2:209:A:N6	2.36	0.57
68:SM:54:SER:HB3	68:SM:78:LYS:HD2	1.84	0.57
16:LI:87:MET:HG2	16:LI:138:ILE:HG12	1.86	0.57
55:S2:429:C:O2'	55:S2:811:A:N1	2.36	0.57
58:SC:199:PRO:HG2	65:SJ:58:ARG:HD3	1.84	0.57
11:LD:209:ARG:HH12	11:LD:234:ASP:HB3	1.68	0.57
71:SP:18:ARG:O	74:SS:93:GLY:N	2.35	0.57
8:LA:101:VAL:HG22	8:LA:165:VAL:HG22	1.85	0.57
51:Lt:110:VAL:HG11	51:Lt:163:PRO:HG2	1.85	0.57
56:SA:69:GLU:N	56:SA:69:GLU:OE1	2.36	0.57
56:SA:128:ARG:NH2	56:SA:151:ASP:O	2.38	0.57
81:SZ:68:ILE:HB	81:SZ:109:TYR:HB2	1.87	0.57
13:LF:154:ILE:HG22	13:LF:187:MET:HE3	1.86	0.57
69:SN:19:ARG:NH1	69:SN:21:SER:OG	2.37	0.57
5:L5:4618:G:H5''	28:LV:15:ARG:HB3	1.85	0.57
15:LH:113:GLU:OE1	15:LH:115:ARG:NH1	2.37	0.57
60:SE:31:PRO:HA	60:SE:81:THR:HB	1.87	0.57
5:L5:2601:A:N6	5:L5:2744:A:OP2	2.36	0.57
12:LE:99:ASP:N	12:LE:99:ASP:OD1	2.34	0.57
50:Ls:26:LYS:HG3	50:Ls:91:THR:HG23	1.86	0.57
51:Lt:121:LEU:O	51:Lt:123:ARG:NH1	2.37	0.57
73:SR:24:LEU:HB2	73:SR:58:MET:HE3	1.86	0.57
25:LS:99:ASP:OD1	25:LS:108:GLN:NE2	2.36	0.57
50:Ls:35:VAL:HG23	50:Ls:39:GLN:HB3	1.86	0.57
5:L5:468:U:H3	5:L5:688:U:H3	1.53	0.57
55:S2:1536:G:H2'	55:S2:1537:A:C8	2.39	0.57
62:SG:4:ASN:HB3	62:SG:110:ASN:HB3	1.87	0.57
9:LB:168:MET:HA	9:LB:171:LEU:HD12	1.86	0.56
58:SC:130:ILE:HG23	58:SC:162:ILE:HD11	1.86	0.56
43:Lk:54:GLU:O	43:Lk:58:GLN:NE2	2.28	0.56
55:S2:659:G:HO2'	55:S2:662:G:HO2'	1.51	0.56
55:S2:1265:A:H2	55:S2:1517:G:H22	1.50	0.56
5:L5:4941:G:OP2	12:LE:188:ARG:NH2	2.37	0.56
55:S2:956:G:H4'	70:SO:60:MET:HG2	1.87	0.56
57:SB:52:THR:HG23	57:SB:57:ILE:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SP:18:ARG:HD3	74:SS:90:VAL:HA	1.87	0.56
5:L5:2554:U:O2	5:L5:2764:A:N7	2.39	0.56
44:LI:43:HIS:HB3	44:LI:46:ARG:HG2	1.87	0.56
55:S2:78:C:H1'	62:SG:175:LYS:HB2	1.85	0.56
55:S2:165:G:H4'	62:SG:53:SER:HB3	1.86	0.56
5:L5:654:C:N3	5:L5:655:C:N4	2.54	0.56
19:LM:50:MET:HB3	19:LM:55:MET:HE2	1.87	0.56
55:S2:1598:G:O2'	81:SZ:80:ARG:O	2.22	0.56
71:SP:59:ARG:HH21	71:SP:76:VAL:HG13	1.70	0.56
5:L5:2758:G:O2'	5:L5:2765:A:N3	2.36	0.56
55:S2:1092:G:OP1	69:SN:2:GLY:N	2.38	0.56
63:SH:79:LEU:HD11	63:SH:94:PHE:HZ	1.69	0.56
5:L5:1332:C:H2'	5:L5:1333:A:H8	1.70	0.56
43:LK:10:ASP:OD1	43:LK:10:ASP:N	2.33	0.56
54:NM:278:GLN:HG3	54:NM:480:ASN:HB3	1.87	0.56
5:L5:2123:C:H1'	12:LE:72:LYS:HD2	1.88	0.56
26:LT:82:GLY:HA3	34:Lb:16:TRP:HB2	1.88	0.56
52:NA:106:ILE:HB	52:NA:126:ALA:HB2	1.88	0.56
56:SA:8:LEU:HD11	77:SV:39:VAL:HG11	1.88	0.56
65:SJ:127:ARG:HD2	86:Se:31:ARG:HD3	1.88	0.56
80:SY:91:LEU:HB3	80:SY:96:LEU:HD22	1.87	0.56
88:Sg:195:LEU:HA	88:Sg:211:GLY:HA3	1.87	0.56
50:Ls:29:ILE:HD11	50:Ls:78:LEU:HD23	1.87	0.56
55:S2:377:G:H5'	64:SI:98:LYS:HB3	1.87	0.56
5:L5:1801:A:H4'	26:LT:102:ARG:HH21	1.71	0.55
5:L5:2520:C:O2	5:L5:2640:G:N2	2.39	0.55
30:LX:120:ASP:OD2	30:LX:120:ASP:N	2.35	0.55
81:SZ:110:THR:OG1	81:SZ:111:ARG:N	2.39	0.55
16:LI:190:LEU:HB3	16:LI:197:VAL:HG22	1.87	0.55
19:LM:130:LEU:HD23	21:LO:177:LEU:HD22	1.88	0.55
81:SZ:48:VAL:HG23	81:SZ:80:ARG:HD2	1.88	0.55
20:LN:96:ARG:NH1	20:LN:100:SER:OG	2.38	0.55
55:S2:1124:C:H5''	57:SB:150:ILE:HG12	1.89	0.55
50:Ls:138:PHE:HB2	50:Ls:143:ILE:HB	1.88	0.55
55:S2:923:G:H1	55:S2:1019:C:H5	1.55	0.55
5:L5:1994:C:H2'	5:L5:1995:G:H8	1.72	0.55
9:LB:297:LYS:HE3	9:LB:299:ILE:HG23	1.88	0.55
57:SB:222:LYS:NZ	57:SB:223:PHE:O	2.39	0.55
25:LS:127:MET:HB3	26:LT:153:PRO:HG2	1.88	0.55
55:S2:1298:G:O2'	55:S2:1299:A:O4'	2.24	0.55
59:SD:132:LYS:HB3	59:SD:156:LEU:HD12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SE:180:LEU:HA	60:SE:194:VAL:HA	1.89	0.55
65:SJ:113:GLN:OE1	65:SJ:154:GLN:NE2	2.39	0.55
8:LA:14:SER:H	8:LA:17:ARG:HG3	1.71	0.55
55:S2:587:A:H5'	55:S2:592:C:H42	1.71	0.55
55:S2:943:U:O2'	70:SO:135:ILE:O	2.24	0.55
76:SU:56:MET:HB2	76:SU:86:LYS:HB3	1.88	0.55
5:L5:4507:A:O2'	28:LV:41:SER:OG	2.24	0.55
15:LH:106:GLN:NE2	15:LH:113:GLU:OE2	2.40	0.55
18:LL:16:LYS:O	18:LL:21:ARG:NH2	2.37	0.55
51:Lt:27:ALA:O	51:Lt:31:LYS:NZ	2.40	0.55
55:S2:1753:C:H4'	55:S2:1780:G:H1	1.71	0.55
59:SD:7:LYS:HD2	76:SU:25:THR:HG21	1.89	0.55
5:L5:1070:G:OP2	12:LE:65:ARG:NH1	2.40	0.55
32:LZ:30:ASP:OD1	32:LZ:30:ASP:N	2.35	0.55
55:S2:66:G:H21	55:S2:82:G:H21	1.53	0.55
55:S2:1648:G:H5''	72:SQ:125:ARG:HB2	1.89	0.55
64:SI:103:LEU:HD22	64:SI:170:LYS:HB3	1.89	0.55
68:SM:83:LYS:HD3	68:SM:103:VAL:HG11	1.88	0.55
5:L5:2755:A:OP2	32:LZ:51:ARG:NH1	2.39	0.54
5:L5:3788:C:N4	5:L5:3812:C:OP2	2.39	0.54
67:SL:75:GLY:HA3	67:SL:88:ILE:HD12	1.89	0.54
24:LR:25:ASP:HB3	24:LR:28:GLU:HB2	1.88	0.54
35:Lc:34:THR:HG23	35:Lc:95:ALA:HB2	1.89	0.54
51:Lt:85:LEU:HD12	51:Lt:104:ILE:HD11	1.88	0.54
53:NB:75:ASN:HD22	54:NM:409:ASN:HA	1.71	0.54
55:S2:1276:A:H62	55:S2:1321:G:H8	1.55	0.54
31:LY:48:PRO:O	31:LY:115:ARG:NH1	2.41	0.54
39:Lg:41:ALA:O	39:Lg:52:ARG:NH1	2.39	0.54
55:S2:820:U:P	65:SJ:79:ARG:HH22	2.31	0.54
5:L5:4139:G:H4'	5:L5:4146:G:H22	1.72	0.54
69:SN:87:ASP:OD1	69:SN:87:ASP:N	2.38	0.54
71:SP:110:GLU:N	71:SP:110:GLU:OE2	2.40	0.54
76:SU:90:ASP:OD1	76:SU:90:ASP:N	2.37	0.54
5:L5:1443:A:N6	5:L5:2104:G:N2	2.53	0.54
12:LE:279:ASN:H	38:Lf:4:ARG:HH12	1.55	0.54
73:SR:61:ILE:HD12	73:SR:71:ILE:HG13	1.89	0.54
76:SU:80:PHE:HB3	85:Sd:52:PHE:HB3	1.88	0.54
5:L5:4699:U:H1'	5:L5:4700:A:H5''	1.88	0.54
18:LL:46:ILE:HD11	18:LL:51:ALA:HA	1.89	0.54
11:LD:223:PHE:HB3	11:LD:226:TYR:HB2	1.89	0.54
25:LS:15:ARG:HB3	25:LS:27:LEU:HD23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:528:A:H2'	55:S2:529:A:C8	2.43	0.54
68:SM:85:LEU:HD11	68:SM:109:VAL:HG23	1.89	0.54
23:LQ:119:LYS:HD3	23:LQ:121:LEU:HD21	1.88	0.54
33:La:72:THR:HG22	33:La:110:LYS:HB3	1.89	0.54
51:Lt:153:ASP:OD1	51:Lt:153:ASP:N	2.38	0.54
55:S2:895:G:H8	55:S2:896:U:H4'	1.72	0.54
56:SA:123:VAL:HA	56:SA:145:ILE:O	2.07	0.54
68:SM:126:GLU:OE1	68:SM:129:LYS:NZ	2.34	0.54
77:SV:74:LYS:HG3	77:SV:79:VAL:HG13	1.90	0.54
55:S2:860:G:N2	78:SW:107:SER:OG	2.39	0.53
30:LX:89:LYS:HB3	30:LX:95:THR:HG23	1.90	0.53
51:Lt:65:GLN:NE2	51:Lt:66:ASN:OD1	2.41	0.53
51:Lt:154:ASP:HB2	51:Lt:159:ALA:HB3	1.89	0.53
52:NA:93:ARG:HG3	53:NB:65:PHE:HE1	1.73	0.53
55:S2:5:U:H2'	55:S2:6:G:H8	1.73	0.53
55:S2:804:U:H5	55:S2:859:G:H1	1.55	0.53
55:S2:1536:G:H2'	55:S2:1537:A:H8	1.72	0.53
74:SS:45:LEU:HD22	74:SS:50:ILE:HD11	1.89	0.53
88:Sg:124:SER:OG	88:Sg:126:ASP:OD1	2.20	0.53
34:Lb:53:GLY:O	34:Lb:57:MET:HB2	2.08	0.53
55:S2:508:A:H3'	55:S2:509:G:H8	1.73	0.53
64:SI:87:ASN:HB3	64:SI:90:LEU:HG	1.90	0.53
5:L5:280:G:OP1	20:LN:47:LYS:NZ	2.41	0.53
5:L5:3717:A:H2'	5:L5:3718:A:C8	2.44	0.53
8:LA:158:ILE:HB	8:LA:162:ASN:HD21	1.74	0.53
52:NA:77:ARG:NH2	52:NA:81:SER:OG	2.42	0.53
60:SE:80:ILE:HG23	60:SE:81:THR:HG23	1.89	0.53
5:L5:1326:A:OP2	5:L5:4445:U:O2'	2.27	0.53
55:S2:527:C:H2'	55:S2:528:A:H8	1.74	0.53
55:S2:615:C:O2	86:Se:11:LYS:NZ	2.41	0.53
62:SG:181:THR:HB	62:SG:184:VAL:HG23	1.91	0.53
5:L5:1998:A:N3	5:L5:2019:C:O2'	2.39	0.53
35:Lc:47:ILE:HD12	35:Lc:94:LEU:HD11	1.91	0.53
56:SA:137:ALA:HB1	56:SA:142:LEU:HB3	1.90	0.53
59:SD:131:ALA:HA	59:SD:191:PRO:HD3	1.90	0.53
5:L5:4363:A:H5''	47:Lo:36:GLN:HG2	1.90	0.53
51:Lt:133:LEU:HD22	51:Lt:143:VAL:HG11	1.90	0.53
55:S2:561:A:H5'	65:SJ:171:GLY:HA3	1.90	0.53
55:S2:1512:C:O2'	85:Sd:7:TYR:O	2.22	0.53
56:SA:77:ILE:HD13	56:SA:99:ILE:HB	1.90	0.53
59:SD:32:ASP:OD2	59:SD:65:ARG:NH1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
88:Sg:133:ASN:HD21	88:Sg:137:VAL:HB	1.73	0.53
88:Sg:171:ASP:OD1	88:Sg:171:ASP:N	2.39	0.53
3:CR:38:ILE:HG12	3:CR:94:VAL:HG13	1.90	0.53
5:L5:1731:C:OP1	26:LT:100:LYS:NZ	2.42	0.53
19:LM:81:ASP:OD1	19:LM:81:ASP:N	2.41	0.53
51:Lt:147:HIS:HE1	51:Lt:150:ASP:HB2	1.74	0.53
54:NM:163:LEU:HD11	54:NM:202:ARG:HG3	1.90	0.53
54:NM:297:TRP:CH2	54:NM:454:ASP:HB3	2.44	0.53
82:Sa:3:LYS:NZ	82:Sa:8:ASN:OD1	2.42	0.53
5:L5:2493:G:H21	7:L8:126:C:H5'	1.74	0.53
55:S2:1402:A:H5'	76:SU:51:LYS:HE3	1.91	0.53
60:SE:204:SER:OG	60:SE:205:PHE:N	2.41	0.53
5:L5:759:G:OP1	15:LH:51:LYS:NZ	2.42	0.52
55:S2:54:A:OP1	80:SY:111:LYS:NZ	2.39	0.52
59:SD:8:LYS:HG2	76:SU:61:LEU:HD21	1.91	0.52
66:SK:3:MET:HE1	66:SK:48:ALA:HB2	1.90	0.52
5:L5:4992:G:H2'	5:L5:4993:G:C8	2.43	0.52
21:LO:61:ARG:HA	21:LO:70:PRO:HD2	1.92	0.52
59:SD:56:GLN:O	59:SD:60:GLY:CA	2.57	0.52
84:Sc:18:LEU:HD12	84:Sc:29:GLN:HB3	1.91	0.52
13:LF:131:ASN:OD1	13:LF:134:ARG:NH1	2.42	0.52
20:LN:185:GLY:HA3	20:LN:194:ARG:HH12	1.75	0.52
5:L5:1702:C:H4'	10:LC:308:LYS:HD2	1.90	0.52
24:LR:136:ARG:O	24:LR:140:GLU:HG3	2.10	0.52
55:S2:640:A:H2'	55:S2:641:A:C8	2.45	0.52
55:S2:957:A:H2'	55:S2:958:G:H21	1.74	0.52
55:S2:1422:G:O2'	55:S2:1424:G:OP2	2.25	0.52
5:L5:420:A:H61	7:L8:15:G:H1'	1.74	0.52
11:LD:62:CYS:HB3	11:LD:105:LEU:HD22	1.92	0.52
22:LP:52:THR:HG23	22:LP:85:LYS:HG3	1.92	0.52
55:S2:155:G:N2	62:SG:56:ASN:OD1	2.42	0.52
71:SP:85:ILE:HA	71:SP:89:MET:HE2	1.91	0.52
62:SG:159:ARG:HD2	62:SG:171:THR:HB	1.90	0.52
9:LB:36:ASP:OD1	9:LB:38:SER:OG	2.27	0.52
37:Le:82:VAL:HG13	37:Le:114:ARG:HG2	1.91	0.52
5:L5:3786:U:OP1	5:L5:4550:G:O2'	2.27	0.52
9:LB:56:ILE:O	9:LB:73:VAL:HA	2.09	0.52
55:S2:466:G:O2'	62:SG:72:ARG:NH2	2.42	0.52
59:SD:39:VAL:HG22	59:SD:48:ILE:HG12	1.92	0.52
5:L5:513:U:N3	5:L5:516:C:OP2	2.30	0.52
5:L5:4305:G:H1	26:LT:80:VAL:HG21	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LG:58:PRO:HG2	14:LG:61:ILE:HD12	1.92	0.52
15:LH:8:GLN:HE22	15:LH:71:ARG:HG3	1.74	0.52
55:S2:922:A:OP1	78:SW:28:ARG:NH2	2.43	0.52
55:S2:1743:G:H21	55:S2:1791:A:H62	1.56	0.52
79:SX:88:ASP:N	79:SX:88:ASP:OD1	2.43	0.52
84:Sc:29:GLN:NE2	84:Sc:66:ARG:O	2.43	0.52
5:L5:1328:G:O2'	5:L5:2349:A:OP1	2.28	0.52
5:L5:1994:C:H2'	5:L5:1995:G:C8	2.45	0.52
5:L5:4274:A:H2'	5:L5:4275:G:C8	2.45	0.52
25:LS:15:ARG:HD2	25:LS:25:PRO:HG2	1.92	0.52
25:LS:71:SER:O	25:LS:76:LYS:NZ	2.42	0.52
70:SO:27:VAL:N	70:SO:91:THR:OG1	2.43	0.52
74:SS:35:GLY:O	74:SS:97:GLN:NE2	2.43	0.52
76:SU:56:MET:HE3	76:SU:88:LEU:HD22	1.91	0.52
83:Sb:50:ALA:O	83:Sb:52:THR:N	2.42	0.52
88:Sg:17:TRP:HB2	88:Sg:36:ARG:HD2	1.92	0.52
5:L5:62:A:N3	5:L5:77:U:O2'	2.40	0.51
5:L5:1940:G:H22	5:L5:4434:C:H5''	1.74	0.51
5:L5:2705:G:O6	24:LR:46:LYS:NZ	2.43	0.51
5:L5:4537:C:H2'	5:L5:4538:G:C8	2.45	0.51
28:LV:45:ILE:HG21	28:LV:53:PRO:HB3	1.92	0.51
54:NM:455:LEU:HG	54:NM:456:MET:HG3	1.92	0.51
63:SH:46:THR:HG21	63:SH:97:GLN:HG3	1.92	0.51
5:L5:68:U:OP1	20:LN:178:HIS:ND1	2.36	0.51
13:LF:91:PHE:HB2	13:LF:145:PRO:HG3	1.93	0.51
16:LI:73:ASN:HB2	16:LI:87:MET:HE1	1.91	0.51
54:NM:473:ASN:OD1	54:NM:475:GLN:NE2	2.43	0.51
56:SA:22:GLY:O	56:SA:24:HIS:ND1	2.41	0.51
51:Lt:111:ASN:HA	51:Lt:114:ARG:HB2	1.93	0.51
55:S2:1060:A:O2'	55:S2:1062:A:N7	2.35	0.51
60:SE:162:ILE:HG22	60:SE:169:ILE:HA	1.92	0.51
77:SV:32:ILE:O	77:SV:54:ALA:HA	2.11	0.51
3:CR:84:LEU:HD13	71:SP:131:PRO:HA	1.91	0.51
5:L5:669:C:OP1	49:Lr:71:ARG:NH1	2.42	0.51
54:NM:395:THR:HG21	54:NM:428:GLN:HG2	1.93	0.51
54:NM:419:ALA:HB2	54:NM:447:PHE:CE2	2.46	0.51
80:SY:26:ASP:N	80:SY:26:ASP:OD1	2.42	0.51
5:L5:1332:C:H2'	5:L5:1333:A:C8	2.46	0.51
5:L5:1697:G:N2	5:L5:2084:C:OP1	2.41	0.51
47:Lo:68:LEU:HD12	47:Lo:83:LEU:HB3	1.92	0.51
55:S2:72:C:H1'	55:S2:73:C:H2'	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:192:C:H41	55:S2:207:G:H21	1.57	0.51
74:SS:33:ILE:HD13	74:SS:71:MET:HE1	1.91	0.51
78:SW:90:GLN:OE1	78:SW:117:ARG:NH2	2.40	0.51
80:SY:117:VAL:O	80:SY:122:LYS:NZ	2.43	0.51
5:L5:3664:G:H2'	5:L5:3665:G:H8	1.75	0.51
30:LX:93:ASN:HB3	30:LX:95:THR:HG22	1.93	0.51
50:Ls:28:PHE:HE1	50:Ls:189:ILE:HG23	1.76	0.51
55:S2:506:G:OP1	80:SY:108:LYS:NZ	2.36	0.51
54:NM:152:LEU:HD13	54:NM:157:THR:HA	1.92	0.51
55:S2:1454:A:H5''	73:SR:3:ARG:HD2	1.91	0.51
79:SX:109:GLY:O	79:SX:119:ARG:NH1	2.44	0.51
5:L5:210:C:OP1	31:LY:59:ARG:NE	2.41	0.51
55:S2:1033:G:N1	55:S2:1080:A:O2'	2.38	0.51
55:S2:1748:G:O6	55:S2:1786:U:O4	2.29	0.51
5:L5:1563:A:N6	55:S2:1028:A:N1	2.58	0.51
5:L5:2020:U:H2'	5:L5:2021:G:H8	1.75	0.51
11:LD:60:ILE:HD11	11:LD:93:THR:HA	1.92	0.51
30:LX:82:THR:HG21	40:Lh:37:THR:HG22	1.93	0.51
31:LY:54:GLU:HB2	31:LY:108:ARG:HB3	1.92	0.51
51:Lt:8:ASN:HA	51:Lt:65:GLN:HE21	1.76	0.51
58:SC:187:ARG:HD3	58:SC:192:LEU:HD12	1.93	0.51
63:SH:148:LEU:HA	78:SW:42:MET:HE3	1.93	0.51
76:SU:26:SER:OG	76:SU:27:ARG:N	2.42	0.51
32:LZ:125:GLY:O	32:LZ:128:LYS:NZ	2.38	0.50
55:S2:530:U:H2'	55:S2:531:A:H8	1.74	0.50
55:S2:562:U:H2'	55:S2:563:G:C8	2.45	0.50
55:S2:928:G:H1	55:S2:1013:U:H3	1.57	0.50
69:SN:64:ARG:HD3	69:SN:70:LYS:HD3	1.93	0.50
47:Lo:2:VAL:N	47:Lo:90:HIS:O	2.44	0.50
55:S2:65:C:N4	62:SG:134:GLY:O	2.43	0.50
55:S2:527:C:H2'	55:S2:528:A:C8	2.46	0.50
5:L5:4174:U:H2'	5:L5:4175:G:H8	1.77	0.50
18:LL:164:GLU:HG2	33:La:100:ILE:HG13	1.92	0.50
31:LY:120:GLU:O	31:LY:124:LYS:HE2	2.12	0.50
48:Lp:36:LYS:HZ1	48:Lp:48:LYS:HD2	1.75	0.50
55:S2:1199:A:OP1	82:Sa:2:THR:N	2.44	0.50
61:SF:34:SER:HA	84:Sc:55:VAL:HB	1.94	0.50
73:SR:27:ASP:OD1	73:SR:30:THR:OG1	2.25	0.50
88:Sg:11:LEU:HB2	88:Sg:307:VAL:HB	1.92	0.50
5:L5:496:G:N2	5:L5:658:C:O2	2.40	0.50
5:L5:1468:C:OP1	33:La:132:ARG:NH2	2.38	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:1961:G:OP2	50:Ls:59:THR:OG1	2.20	0.50
5:L5:4589:A:N1	5:L5:4621:C:O2'	2.40	0.50
55:S2:1752:C:H42	55:S2:1781:A:H2	1.60	0.50
55:S2:1860:A:H3'	82:Sa:8:ASN:HB3	1.93	0.50
5:L5:452:A:H4'	5:L5:453:G:H5'	1.94	0.50
24:LR:23:TRP:HB3	24:LR:51:ILE:HG13	1.93	0.50
52:NA:113:LYS:NZ	52:NA:115:PRO:HA	2.27	0.50
55:S2:152:U:H2'	55:S2:153:G:H8	1.76	0.50
55:S2:803:C:H5	55:S2:860:G:H22	1.59	0.50
57:SB:125:VAL:HG22	57:SB:172:MET:HE3	1.93	0.50
5:L5:4258:C:H5'	17:LJ:68:ILE:HD11	1.93	0.50
14:LG:230:TYR:CE2	14:LG:234:ARG:HD3	2.47	0.50
25:LS:68:PHE:O	25:LS:70:LYS:NZ	2.45	0.50
29:LW:19:ARG:NH2	29:LW:37:GLU:OE2	2.41	0.50
50:Ls:125:ALA:HA	50:Ls:154:ILE:HG23	1.94	0.50
55:S2:319:C:H2'	55:S2:320:G:H8	1.77	0.50
55:S2:1232:U:H2'	55:S2:1233:G:H8	1.75	0.50
55:S2:1568:C:OP1	75:ST:96:SER:OG	2.26	0.50
63:SH:51:ILE:HG12	63:SH:61:ILE:HD11	1.92	0.50
66:SK:9:ILE:HG23	66:SK:83:LEU:HD22	1.92	0.50
5:L5:1914:C:H4'	21:LO:89:PRO:HD3	1.93	0.50
21:LO:34:VAL:HG22	21:LO:103:LYS:HB2	1.94	0.50
53:NB:40:ASP:OD2	53:NB:40:ASP:N	2.42	0.50
55:S2:28:U:H2'	55:S2:29:G:H8	1.76	0.50
55:S2:1109:C:C5	73:SR:124:VAL:HG23	2.47	0.50
55:S2:1616:U:OP2	71:SP:43:ARG:NH2	2.43	0.50
80:SY:27:VAL:HG21	80:SY:35:VAL:HG11	1.94	0.50
88:Sg:31:ILE:HG13	88:Sg:43:TRP:HB2	1.94	0.50
5:L5:4387:C:OP2	5:L5:4532:U:O2'	2.28	0.50
11:LD:65:ALA:HB2	11:LD:74:ILE:HD13	1.93	0.50
55:S2:1024:A:OP2	69:SN:124:ARG:NH2	2.39	0.50
78:SW:32:LYS:O	78:SW:36:ARG:HG2	2.12	0.50
3:CR:317:VAL:O	3:CR:414:ARG:NH2	2.44	0.50
20:LN:178:HIS:HA	20:LN:181:HIS:CE1	2.47	0.50
50:Ls:190:GLN:OE1	50:Ls:190:GLN:N	2.45	0.50
55:S2:370:G:O2'	64:SI:10:LYS:NZ	2.45	0.50
5:L5:2764:A:H2'	5:L5:2765:A:H8	1.77	0.49
51:Lt:17:CYS:SG	51:Lt:18:THR:N	2.85	0.49
55:S2:981:A:H2'	55:S2:982:G:C8	2.47	0.49
59:SD:109:LEU:HD12	59:SD:184:ILE:HD11	1.94	0.49
60:SE:137:PRO:HB2	60:SE:150:PRO:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SO:34:PHE:HB3	70:SO:41:PHE:HB2	1.94	0.49
75:ST:5:THR:OG1	75:ST:6:VAL:N	2.40	0.49
88:Sg:84:ASP:OD2	88:Sg:84:ASP:N	2.45	0.49
5:L5:4472:G:O2'	45:Lm:100:TYR:O	2.27	0.49
7:L8:58:G:O6	42:Lj:63:ARG:NH1	2.44	0.49
9:LB:254:ILE:HG23	9:LB:266:VAL:HG11	1.95	0.49
54:Nm:315:SER:OG	54:Nm:316:ARG:N	2.44	0.49
55:S2:382:C:H2'	55:S2:383:G:H8	1.77	0.49
56:SA:184:ARG:HD3	56:SA:191:ARG:HD3	1.94	0.49
58:SC:259:THR:HG21	77:SV:16:LYS:H	1.77	0.49
62:SG:32:MET:HE3	62:SG:54:GLY:HA3	1.93	0.49
75:ST:76:THR:HG21	75:ST:97:LYS:HG3	1.93	0.49
5:L5:2745:A:H2'	5:L5:2746:A:C8	2.47	0.49
27:LU:24:ASP:HB3	27:LU:111:GLU:HA	1.94	0.49
36:Ld:64:ILE:HG23	36:Ld:68:LEU:HD23	1.94	0.49
54:Nm:290:PRO:HB3	54:Nm:475:GLN:HB3	1.94	0.49
54:Nm:364:PRO:N	54:Nm:364:PRO:HG3	2.10	0.49
68:SM:72:HIS:HE1	68:SM:74:ILE:HD13	1.77	0.49
55:S2:1606:G:H1'	55:S2:1633:A:N6	2.27	0.49
12:LE:153:LEU:HD11	12:LE:195:ILE:HG13	1.94	0.49
22:LP:41:ILE:HG23	22:LP:42:ARG:HD2	1.93	0.49
55:S2:1568:C:O2	55:S2:1627:C:O2'	2.30	0.49
68:SM:84:LYS:O	68:SM:88:TRP:CD1	2.66	0.49
3:CR:157:LEU:HD12	3:CR:171:LYS:HE3	1.95	0.49
5:L5:1590:C:H4'	5:L5:2857:A:H5'	1.94	0.49
5:L5:4239:A:H2'	5:L5:4240:G:C8	2.47	0.49
5:L5:4499:G:C2	5:L5:4529:G:H1'	2.48	0.49
55:S2:150:A:N6	55:S2:168:C:C2	2.81	0.49
55:S2:1425:G:O3'	72:SQ:33:LYS:NZ	2.46	0.49
68:SM:51:VAL:HG22	68:SM:77:ILE:HB	1.94	0.49
3:CR:398:GLU:HA	3:CR:401:GLN:HG2	1.95	0.49
5:L5:1503:A:H4'	5:L5:1504:G:H5'	1.95	0.49
5:L5:4260:U:H2'	5:L5:4261:C:C6	2.48	0.49
20:LN:120:TRP:HZ2	20:LN:123:GLU:HB2	1.78	0.49
55:S2:874:G:H2'	55:S2:875:A:H8	1.77	0.49
82:Sa:51:ARG:HH12	84:Sc:39:SER:HB2	1.78	0.49
5:L5:2082:G:H5''	23:LQ:12:LYS:HE3	1.94	0.49
5:L5:4765:G:OP1	15:LH:23:ARG:NE	2.44	0.49
51:Lt:11:LYS:HG2	51:Lt:64:ILE:HB	1.95	0.49
55:S2:414:A:OP1	55:S2:814:U:O2'	2.31	0.49
55:S2:683:G:H4'	78:SW:4:MET:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:1308:U:H1'	87:Sf:135:HIS:HE1	1.77	0.49
57:SB:77:ASP:OD1	57:SB:77:ASP:N	2.45	0.49
62:SG:5:ILE:HG21	62:SG:45:TRP:HH2	1.78	0.49
5:L5:119:G:OP1	14:LG:132:ARG:NH2	2.45	0.49
5:L5:302:C:OP1	20:LN:68:ARG:NE	2.43	0.49
5:L5:3947:A:H61	5:L5:4068:U:H1'	1.78	0.49
12:LE:190:HIS:HB3	12:LE:193:PHE:HD2	1.78	0.49
21:LO:113:ASP:OD2	21:LO:113:ASP:N	2.40	0.49
54:NM:328:ARG:CZ	54:NM:328:ARG:HA	2.43	0.49
55:S2:163:U:H2'	55:S2:164:A:H8	1.78	0.49
55:S2:888:U:O2'	55:S2:890:U:OP1	2.28	0.49
78:SW:14:ILE:HG13	78:SW:27:ILE:HD11	1.93	0.49
5:L5:1176:C:H42	5:L5:1184:A:H61	1.61	0.49
5:L5:1514:U:OP1	18:LL:2:ALA:N	2.46	0.49
10:LC:107:THR:O	10:LC:111:TRP:NE1	2.43	0.49
11:LD:152:ARG:HG3	11:LD:154:THR:HG23	1.95	0.49
88:Sg:31:ILE:HG12	88:Sg:45:LEU:HD11	1.95	0.49
5:L5:37:U:H5''	33:La:32:ARG:HD3	1.94	0.48
5:L5:1942:A:H2'	5:L5:1943:A:C8	2.48	0.48
68:SM:62:VAL:HA	68:SM:65:VAL:HG12	1.95	0.48
73:SR:126:MET:HE2	73:SR:128:PHE:HE1	1.78	0.48
17:LJ:120:ASP:OD2	17:LJ:122:SER:OG	2.23	0.48
55:S2:17:C:H2'	55:S2:18:C:C6	2.49	0.48
55:S2:53:C:O2'	55:S2:507:G:N7	2.43	0.48
5:L5:4076:G:OP1	14:LG:73:ARG:NE	2.33	0.48
17:LJ:60:PHE:HB2	17:LJ:62:ILE:HG12	1.96	0.48
55:S2:857:U:H2'	55:S2:858:A:C8	2.49	0.48
55:S2:913:A:N6	63:SH:98:ARG:O	2.37	0.48
55:S2:928:G:H2'	55:S2:929:G:C8	2.48	0.48
80:SY:18:LEU:O	80:SY:85:ASN:ND2	2.47	0.48
4:CZ:94:PRO:HD2	5:L5:4531:U:H4'	1.94	0.48
5:L5:1364:U:OP2	18:LL:36:ARG:NH2	2.38	0.48
15:LH:37:ASP:OD2	15:LH:39:ASN:ND2	2.45	0.48
43:Lk:36:VAL:HG13	43:Lk:43:TYR:HB2	1.96	0.48
55:S2:153:G:N2	62:SG:13:GLN:OE1	2.41	0.48
81:SZ:72:VAL:HG22	81:SZ:76:ARG:HH12	1.78	0.48
88:Sg:72:SER:OG	88:Sg:74:ASP:O	2.29	0.48
5:L5:691:C:H2'	5:L5:692:A:C8	2.49	0.48
5:L5:1175:A:H2	5:L5:1185:G:H22	1.61	0.48
14:LG:106:THR:OG1	14:LG:107:LYS:N	2.40	0.48
17:LJ:18:ARG:H	17:LJ:134:LEU:HA	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LM:47:ARG:HD2	25:LS:73:LEU:HD13	1.95	0.48
26:LT:138:ALA:O	26:LT:139:HIS:ND1	2.45	0.48
45:Lm:98:LYS:HG3	45:Lm:118:THR:HG21	1.95	0.48
48:Lp:37:TYR:HB2	48:Lp:47:MET:HB3	1.95	0.48
53:NB:152:ASN:N	53:NB:155:GLU:OE2	2.42	0.48
62:SG:32:MET:HB2	62:SG:100:CYS:HB2	1.94	0.48
68:SM:55:ASN:ND2	68:SM:82:ASN:H	2.11	0.48
5:L5:150:U:OP2	14:LG:200:THR:OG1	2.26	0.48
5:L5:2711:G:OP2	24:LR:39:GLN:NE2	2.42	0.48
52:NA:111:VAL:HG23	52:NA:122:VAL:HG13	1.95	0.48
55:S2:96:C:O2	55:S2:473:A:O2'	2.31	0.48
55:S2:189:U:OP1	64:SI:148:LYS:NZ	2.45	0.48
59:SD:132:LYS:HE2	59:SD:189:MET:HE2	1.95	0.48
5:L5:1558:A:H2'	5:L5:1559:G:C8	2.49	0.48
5:L5:4740:G:O6	5:L5:4959:U:O2	2.31	0.48
11:LD:51:MET:HE3	11:LD:105:LEU:HD23	1.94	0.48
50:Ls:194:ASP:O	50:Ls:197:SER:OG	2.29	0.48
55:S2:379:C:O2	64:SI:5:ARG:NE	2.47	0.48
55:S2:803:C:H41	55:S2:860:G:H1	1.61	0.48
88:Sg:12:LYS:HA	88:Sg:306:LEU:HD12	1.95	0.48
5:L5:709:C:OP1	38:Lf:89:ARG:NH2	2.47	0.48
5:L5:1380:G:N2	5:L5:1381:U:O4	2.41	0.48
5:L5:2626:U:O4	27:LU:97:ARG:NH1	2.45	0.48
32:LZ:60:LYS:H	32:LZ:60:LYS:HD2	1.78	0.48
72:SQ:134:GLY:HA3	72:SQ:140:ARG:HA	1.95	0.48
5:L5:1441:C:O2	5:L5:2108:G:O2'	2.31	0.48
5:L5:1553:A:N6	5:L5:1574:G:H1'	2.29	0.48
5:L5:3937:C:H1'	20:LN:125:SER:HB3	1.95	0.48
10:LC:262:GLU:OE2	10:LC:272:SER:OG	2.28	0.48
17:LJ:85:LYS:HB3	17:LJ:115:LEU:HB2	1.95	0.48
17:LJ:114:ASP:OD2	17:LJ:114:ASP:N	2.46	0.48
17:LJ:160:GLU:HA	17:LJ:163:MET:HE2	1.95	0.48
35:Lc:48:LEU:HD21	35:Lc:60:ILE:HG21	1.96	0.48
51:Lt:103:ASN:HD21	51:Lt:145:GLY:HA2	1.78	0.48
55:S2:304:C:OP1	64:SI:75:LYS:NZ	2.44	0.48
55:S2:957:A:O2'	55:S2:958:G:N3	2.43	0.48
55:S2:1845:A:H2'	55:S2:1846:G:C8	2.49	0.48
67:SL:99:TYR:O	67:SL:101:ARG:N	2.46	0.48
77:SV:58:ALA:O	77:SV:62:MET:HG3	2.14	0.48
10:LC:221:PHE:HB3	10:LC:227:ILE:HG21	1.96	0.48
53:NB:65:PHE:HB3	53:NB:71:VAL:HG23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:NM:203:PRO:HD2	54:NM:206:TRP:HB3	1.96	0.48
54:NM:282:THR:HB	54:NM:474:LEU:HD11	1.95	0.48
67:SL:80:MET:HE1	67:SL:120:VAL:HG13	1.96	0.48
72:SQ:89:SER:HB3	72:SQ:112:LEU:HD13	1.95	0.48
3:CR:393:THR:HG22	3:CR:395:LYS:HG3	1.96	0.47
5:L5:267:G:H2'	5:L5:268:G:H8	1.78	0.47
5:L5:2407:G:O6	44:LI:2:SER:N	2.47	0.47
5:L5:4305:G:O6	26:LT:87:LYS:NZ	2.47	0.47
5:L5:4547:C:O2'	5:L5:4549:G:OP1	2.28	0.47
41:LI:63:VAL:HG23	41:LI:65:LYS:HG3	1.94	0.47
54:NM:378:GLN:HG2	54:NM:381:ILE:HD12	1.95	0.47
55:S2:581:U:OP1	65:SJ:133:ARG:NH1	2.42	0.47
55:S2:1016:U:H5''	69:SN:14:SER:HB3	1.95	0.47
75:ST:39:LEU:O	75:ST:96:SER:HB2	2.14	0.47
5:L5:239:C:OP1	31:LY:46:SER:OG	2.32	0.47
5:L5:1558:A:H2'	5:L5:1559:G:H8	1.79	0.47
5:L5:2520:C:H2'	5:L5:2521:G:H8	1.79	0.47
43:LK:19:ASP:OD1	43:LK:19:ASP:N	2.39	0.47
55:S2:1589:A:N3	55:S2:1653:U:O2'	2.39	0.47
84:SC:32:VAL:O	84:SC:41:SER:HA	2.13	0.47
5:L5:1097:C:H2'	5:L5:1098:G:H8	1.78	0.47
24:LR:42:ARG:HA	24:LR:45:ILE:HD12	1.96	0.47
65:SJ:59:GLU:OE1	65:SJ:69:ARG:NH2	2.47	0.47
74:SS:20:ILE:HD11	74:SS:33:ILE:HG13	1.96	0.47
5:L5:2348:G:OP1	5:L5:2351:C:N4	2.47	0.47
52:NA:129:GLU:HG2	52:NA:134:GLN:HE22	1.79	0.47
54:NM:179:ASN:HB3	54:NM:251:HIS:HA	1.96	0.47
54:NM:410:HIS:NE2	54:NM:412:THR:OG1	2.47	0.47
55:S2:921:G:H3'	78:SW:28:ARG:HH21	1.78	0.47
55:S2:955:A:N6	55:S2:971:G:H1'	2.30	0.47
59:SD:211:VAL:O	73:SR:20:TYR:OH	2.31	0.47
60:SE:17:HIS:HB2	60:SE:108:ARG:HA	1.95	0.47
64:SI:101:ILE:HD12	64:SI:190:LEU:HD11	1.96	0.47
67:SL:77:VAL:HG11	67:SL:80:MET:HE3	1.97	0.47
74:SS:15:VAL:HB	74:SS:68:ILE:HD11	1.96	0.47
5:L5:496:G:H2'	5:L5:498:C:H5''	1.96	0.47
5:L5:2520:C:H2'	5:L5:2521:G:C8	2.49	0.47
5:L5:4491:G:H5''	9:LB:9:PRO:HG3	1.95	0.47
5:L5:5002:U:OP2	9:LB:385:LYS:NZ	2.45	0.47
5:L5:2705:G:H1	5:L5:2710:C:H5	1.62	0.47
5:L5:2809:G:O2'	5:L5:4644:G:OP1	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:5026:U:H1'	5:L5:5027:C:H5	1.79	0.47
27:LU:38:ASN:OD1	27:LU:90:TYR:OH	2.32	0.47
54:NM:223:VAL:HB	54:NM:251:HIS:CE1	2.49	0.47
78:SW:49:GLU:O	78:SW:64:ASN:ND2	2.47	0.47
3:CR:333:LEU:HD23	3:CR:342:LYS:HB2	1.96	0.47
5:L5:153:G:H2'	5:L5:154:G:H8	1.78	0.47
5:L5:303:C:OP2	20:LN:68:ARG:NH2	2.44	0.47
5:L5:1339:U:H2'	5:L5:1340:C:C6	2.50	0.47
5:L5:1662:C:H2'	5:L5:1663:C:C6	2.50	0.47
5:L5:4208:U:OP2	26:LT:4:THR:OG1	2.30	0.47
5:L5:4373:G:N7	47:Lo:61:LYS:NZ	2.62	0.47
5:L5:4629:U:H3	5:L5:4669:A:H62	1.61	0.47
10:LC:138:MET:HB3	10:LC:138:MET:HE3	1.70	0.47
15:LH:92:MET:HG2	15:LH:181:VAL:HA	1.97	0.47
26:LT:143:THR:OG1	26:LT:146:LYS:O	2.33	0.47
50:Ls:47:LEU:HD12	50:Ls:51:ALA:HB3	1.96	0.47
50:Ls:134:LYS:HB3	50:Ls:137:PHE:HZ	1.80	0.47
54:NM:357:LEU:HD22	54:NM:363:THR:HB	1.97	0.47
54:NM:384:THR:HA	54:NM:398:LEU:O	2.14	0.47
55:S2:24:C:OP1	65:SJ:11:LYS:NZ	2.47	0.47
55:S2:522:A:H5''	65:SJ:145:PRO:HD2	1.96	0.47
57:SB:150:ILE:HD12	73:SR:128:PHE:HB2	1.96	0.47
58:SC:191:VAL:HG11	58:SC:236:PHE:HA	1.97	0.47
62:SG:136:LYS:NZ	62:SG:175:LYS:O	2.48	0.47
63:SH:165:ASN:N	63:SH:165:ASN:OD1	2.48	0.47
73:SR:126:MET:HE2	73:SR:128:PHE:CE1	2.49	0.47
74:SS:24:ARG:HB2	74:SS:29:ALA:HB2	1.96	0.47
83:Sb:35:VAL:HA	83:Sb:78:SER:O	2.14	0.47
84:Sc:15:THR:HG22	84:Sc:16:LYS:H	1.80	0.47
84:Sc:17:VAL:HG22	84:Sc:30:VAL:HG12	1.96	0.47
5:L5:4128:A:H1'	14:LG:35:ARG:HG3	1.96	0.47
5:L5:4546:A:N7	8:LA:215:ASN:ND2	2.60	0.47
30:LX:38:LYS:HA	30:LX:38:LYS:HD2	1.67	0.47
61:SF:120:GLY:O	61:SF:193:LYS:NZ	2.48	0.47
65:SJ:114:VAL:HG12	65:SJ:157:ILE:HG21	1.96	0.47
5:L5:109:G:OP2	18:LL:74:ARG:NH2	2.41	0.47
5:L5:2275:G:H2'	5:L5:2276:A:C8	2.50	0.47
6:L7:7:G:OP1	11:LD:33:ARG:NH1	2.43	0.47
11:LD:59:ASP:OD1	11:LD:81:HIS:NE2	2.48	0.47
11:LD:208:MET:HG2	11:LD:219:TYR:HE1	1.80	0.47
12:LE:46:ARG:HB2	12:LE:62:MET:HE1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LO:194:GLU:O	21:LO:198:THR:HG23	2.15	0.47
55:S2:5:U:H2'	55:S2:6:G:C8	2.50	0.47
55:S2:326:C:O2	55:S2:327:G:N2	2.48	0.47
62:SG:67:VAL:HG12	62:SG:69:THR:HG22	1.96	0.47
4:CZ:69:GLY:O	22:LP:128:ARG:NH2	2.48	0.47
5:L5:4220:A:H2'	5:L5:4222:G:H5''	1.96	0.47
11:LD:56:THR:OG1	11:LD:58:ARG:O	2.31	0.47
11:LD:209:ARG:HA	11:LD:212:MET:HE2	1.97	0.47
19:LM:36:ALA:HB3	19:LM:55:MET:HE1	1.97	0.47
27:LU:80:LYS:HE2	27:LU:110:TYR:CZ	2.50	0.47
59:SD:219:PRO:HD2	88:Sg:192:THR:HG22	1.97	0.47
63:SH:58:LYS:HE3	63:SH:58:LYS:HB3	1.69	0.47
68:SM:75:ASN:OD1	68:SM:75:ASN:N	2.48	0.47
5:L5:97:G:OP1	18:LL:16:LYS:NZ	2.46	0.46
5:L5:2280:G:OP1	37:Le:48:ARG:NH2	2.48	0.46
5:L5:4093:G:H2'	5:L5:4094:G:C8	2.50	0.46
5:L5:4431:U:OP2	16:LI:3:ARG:NH2	2.45	0.46
7:L8:106:G:H4'	7:L8:137:A:H5'	1.96	0.46
14:LG:230:TYR:O	14:LG:234:ARG:HG3	2.15	0.46
15:LH:44:GLU:HB3	15:LH:58:ASP:HB2	1.97	0.46
23:LQ:159:PRO:HA	23:LQ:160:HIS:HA	1.73	0.46
30:LX:122:ALA:HB3	30:LX:139:ARG:HG2	1.97	0.46
50:Ls:26:LYS:HZ3	50:Ls:92:LYS:HA	1.80	0.46
50:Ls:106:LYS:HG2	50:Ls:184:SER:HB2	1.98	0.46
54:NM:190:PHE:HD1	54:NM:403:LEU:HD21	1.80	0.46
55:S2:1047:C:H5''	70:SO:143:LYS:HB2	1.97	0.46
55:S2:1217:A:H2'	55:S2:1218:C:H6	1.80	0.46
5:L5:759:G:P	15:LH:50:LYS:HZ1	2.38	0.46
13:LF:40:LYS:HB3	13:LF:40:LYS:HE3	1.71	0.46
24:LR:160:GLU:OE2	24:LR:163:ARG:NH2	2.41	0.46
60:SE:195:ILE:HA	60:SE:210:VAL:HG22	1.98	0.46
80:SY:44:LEU:HD22	80:SY:75:ILE:HD11	1.97	0.46
5:L5:1604:G:H2'	5:L5:1605:G:C8	2.51	0.46
5:L5:4238:G:H2'	5:L5:4239:A:C8	2.51	0.46
16:LI:180:GLU:O	16:LI:184:MET:HG3	2.15	0.46
51:Lt:63:THR:HG23	51:Lt:70:GLN:HE22	1.81	0.46
54:NM:310:LYS:HE2	54:NM:310:LYS:N	2.30	0.46
55:S2:1599:U:H5''	81:SZ:44:LEU:HD12	1.97	0.46
58:SC:110:MET:HG2	58:SC:127:PHE:HE1	1.80	0.46
3:CR:312:LEU:HD23	3:CR:317:VAL:HG11	1.97	0.46
5:L5:1726:U:H5'	13:LF:135:ILE:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LD:220:LYS:O	11:LD:224:SER:HB3	2.16	0.46
13:LF:216:PRO:HD3	13:LF:247:MET:HE3	1.97	0.46
20:LN:63:ARG:HG3	20:LN:131:GLU:HG3	1.97	0.46
54:NM:378:GLN:OE1	54:NM:378:GLN:N	2.48	0.46
54:NM:393:GLU:OE1	54:NM:395:THR:HG23	2.15	0.46
55:S2:1228:A:H2'	55:S2:1229:G:H8	1.78	0.46
58:SC:146:GLU:OE1	59:SD:120:TYR:OH	2.33	0.46
78:SW:39:THR:O	78:SW:43:LYS:HG2	2.15	0.46
3:CR:151:ILE:HD12	3:CR:205:VAL:HG11	1.98	0.46
5:L5:418:A:N6	7:L8:16:G:H1'	2.30	0.46
5:L5:1419:G:O2'	33:La:116:LYS:NZ	2.48	0.46
5:L5:2411:C:H2'	5:L5:2412:A:C8	2.51	0.46
14:LG:90:GLN:O	14:LG:94:GLN:HG3	2.15	0.46
28:LV:96:LEU:HD13	29:LW:20:ARG:HG2	1.98	0.46
32:LZ:41:ALA:HB2	32:LZ:77:TYR:HE1	1.80	0.46
44:Ll:12:PHE:O	44:Ll:16:LYS:HG2	2.15	0.46
55:S2:1007:C:H2'	55:S2:1008:A:C8	2.51	0.46
62:SG:50:VAL:HB	62:SG:111:LEU:HB3	1.96	0.46
5:L5:2532:C:O2'	30:LX:93:ASN:OD1	2.31	0.46
5:L5:2613:C:H4'	39:Lg:2:VAL:HG23	1.97	0.46
5:L5:2744:A:H2'	5:L5:2745:A:C8	2.50	0.46
5:L5:4635:A:H3'	5:L5:4636:U:H4'	1.98	0.46
16:LI:31:ILE:HG22	16:LI:62:SER:HB2	1.98	0.46
31:LY:116:LYS:O	31:LY:120:GLU:HG2	2.16	0.46
55:S2:677:G:OP1	69:SN:120:SER:OG	2.33	0.46
55:S2:940:U:H3	55:S2:1002:U:H3	1.64	0.46
58:SC:110:MET:HG3	58:SC:125:LYS:HB3	1.97	0.46
13:LF:128:ALA:O	13:LF:132:MET:HG3	2.16	0.46
16:LI:61:SER:HA	16:LI:126:VAL:HG12	1.97	0.46
20:LN:138:PHE:HA	20:LN:143:ARG:HD2	1.98	0.46
24:LR:105:LEU:HD23	24:LR:138:LEU:HD23	1.98	0.46
50:Ls:48:ARG:O	50:Ls:50:LYS:NZ	2.38	0.46
54:NM:298:HIS:ND1	54:NM:451:ASN:OD1	2.47	0.46
55:S2:824:C:H1'	65:SJ:144:ILE:HG21	1.98	0.46
55:S2:1232:U:H2'	55:S2:1233:G:C8	2.51	0.46
55:S2:1665:G:H5''	75:ST:89:PRO:HD2	1.98	0.46
62:SG:64:LYS:HE2	62:SG:77:LEU:HD21	1.98	0.46
68:SM:93:LYS:NZ	68:SM:102:LYS:O	2.49	0.46
73:SR:16:ILE:HD11	73:SR:54:VAL:HG21	1.97	0.46
76:SU:59:LYS:HB2	76:SU:84:ILE:HB	1.96	0.46
5:L5:188:G:O2'	5:L5:190:G:OP2	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:1306:C:H2'	5:L5:1307:A:H8	1.81	0.46
5:L5:1548:G:O2'	5:L5:2812:A:N3	2.41	0.46
5:L5:2745:A:H2'	5:L5:2746:A:H8	1.80	0.46
5:L5:5057:C:H2'	5:L5:5058:A:C8	2.51	0.46
70:SO:28:PHE:HA	70:SO:92:ALA:O	2.16	0.46
75:ST:56:ARG:HG3	75:ST:103:VAL:HG21	1.97	0.46
88:Sg:168:CYS:HB2	88:Sg:195:LEU:HG	1.97	0.46
88:Sg:201:SER:HB3	88:Sg:241:PHE:CZ	2.51	0.46
5:L5:153:G:OP1	20:LN:56:LYS:NZ	2.49	0.46
10:LC:175:LYS:HB3	10:LC:175:LYS:HE3	1.77	0.46
11:LD:271:MET:HE2	11:LD:276:LYS:HG3	1.98	0.46
33:La:16:SER:OG	33:La:17:HIS:N	2.49	0.46
55:S2:666:U:H3	55:S2:1145:A:H62	1.63	0.46
55:S2:1736:G:H2'	55:S2:1737:G:C8	2.51	0.46
64:SI:79:ILE:HG21	64:SI:170:LYS:HE2	1.97	0.46
68:SM:35:ILE:HD11	68:SM:61:TYR:HE1	1.79	0.46
5:L5:4743:G:H2'	5:L5:4744:A:C8	2.51	0.46
5:L5:4967:A:H2'	5:L5:4968:A:C8	2.51	0.46
12:LE:101:ASN:OD1	12:LE:105:ARG:NH2	2.47	0.46
17:LJ:19:LYS:HG2	17:LJ:133:VAL:HB	1.98	0.46
35:Lc:38:ILE:HD11	35:Lc:46:VAL:HG21	1.97	0.46
47:Lo:74:GLU:HB3	47:Lo:77:CYS:HB3	1.97	0.46
60:SE:48:LEU:HD11	60:SE:70:ILE:HG13	1.97	0.46
68:SM:99:LYS:HE2	68:SM:99:LYS:N	2.31	0.46
70:SO:93:LEU:HG	70:SO:124:MET:HE2	1.98	0.46
88:Sg:105:THR:N	88:Sg:126:ASP:OD2	2.48	0.46
12:LE:183:ARG:HA	12:LE:183:ARG:HD2	1.78	0.45
13:LF:243:LEU:O	13:LF:247:MET:HB2	2.16	0.45
16:LI:78:LYS:HE3	16:LI:78:LYS:HB3	1.67	0.45
20:LN:145:ASN:O	20:LN:148:THR:HG22	2.16	0.45
27:LU:98:ASP:HB3	53:NB:15:GLN:HG2	1.97	0.45
31:LY:47:MET:HE1	31:LY:118:ILE:HG13	1.97	0.45
55:S2:96:C:H1'	55:S2:474:G:H5'	1.97	0.45
55:S2:106:C:H2'	55:S2:107:A:H8	1.81	0.45
56:SA:81:ASN:HB2	56:SA:204:TYR:CE1	2.51	0.45
57:SB:138:PHE:O	57:SB:213:ARG:N	2.50	0.45
61:SF:152:TRP:O	61:SF:156:THR:HG23	2.15	0.45
62:SG:7:PHE:HB3	62:SG:12:CYS:HB2	1.97	0.45
51:Lt:38:SER:H	51:Lt:41:LYS:NZ	2.15	0.45
55:S2:126:G:OP2	62:SG:198:ARG:NH1	2.50	0.45
58:SC:204:ILE:HB	58:SC:211:LYS:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SJ:47:LYS:HE3	65:SJ:47:LYS:HB3	1.71	0.45
72:SQ:34:VAL:HG22	72:SQ:70:VAL:HB	1.98	0.45
72:SQ:41:MET:HE2	72:SQ:41:MET:HB2	1.85	0.45
5:L5:4258:C:H2'	5:L5:4259:C:H6	1.81	0.45
14:LG:165:GLU:HA	14:LG:168:VAL:HG22	1.99	0.45
30:LX:81:LEU:HG	30:LX:83:THR:HG23	1.97	0.45
50:Ls:194:ASP:HB2	50:Ls:199:TYR:HE2	1.81	0.45
55:S2:570:C:O2'	80:SY:34:THR:O	2.24	0.45
55:S2:1512:C:H5''	85:Sd:8:TRP:HZ3	1.82	0.45
60:SE:229:GLY:HA2	60:SE:235:TRP:CD1	2.51	0.45
71:SP:107:ILE:HA	71:SP:111:MET:HE2	1.98	0.45
5:L5:10:A:H2'	5:L5:11:G:C8	2.52	0.45
5:L5:2008:U:H1'	5:L5:2011:C:H5	1.82	0.45
5:L5:4967:A:H2'	5:L5:4968:A:H8	1.82	0.45
12:LE:108:LYS:HZ2	12:LE:111:LYS:HA	1.82	0.45
13:LF:43:ARG:HH21	13:LF:47:ARG:HD3	1.82	0.45
15:LH:55:LEU:HD23	15:LH:77:VAL:HG11	1.98	0.45
42:Lj:48:ASN:HA	42:Lj:54:LYS:HE2	1.97	0.45
55:S2:639:C:H2'	55:S2:640:A:C8	2.51	0.45
62:SG:159:ARG:HD3	62:SG:173:ALA:HB2	1.98	0.45
77:SV:32:ILE:HD13	77:SV:32:ILE:HA	1.79	0.45
5:L5:67:C:OP2	5:L5:312:G:N2	2.49	0.45
5:L5:1283:G:N1	5:L5:2076:G:OP1	2.37	0.45
7:L8:141:C:H5''	20:LN:60:VAL:HG11	1.98	0.45
9:LB:77:THR:HG21	9:LB:337:VAL:HG22	1.98	0.45
35:Lc:47:ILE:HB	35:Lc:94:LEU:HG	1.99	0.45
40:Lh:87:LYS:HB3	40:Lh:91:MET:HE2	1.99	0.45
43:Lk:70:LYS:HD3	43:Lk:70:LYS:HA	1.82	0.45
50:Ls:128:THR:OG1	50:Ls:152:ILE:O	2.32	0.45
60:SE:36:HIS:CG	60:SE:85:GLY:HA3	2.52	0.45
66:SK:5:LYS:O	66:SK:9:ILE:HD12	2.17	0.45
68:SM:23:LYS:HA	68:SM:23:LYS:HD3	1.81	0.45
82:Sa:24:THR:HG21	82:Sa:71:LEU:HD22	1.99	0.45
87:Sf:121:CYS:HB2	87:Sf:146:LEU:HD11	1.97	0.45
9:LB:224:LYS:HG2	9:LB:340:THR:HG22	1.98	0.45
17:LJ:54:ARG:NH2	17:LJ:55:TYR:OH	2.50	0.45
17:LJ:94:LEU:O	17:LJ:174:ILE:HA	2.16	0.45
24:LR:173:ARG:HD2	24:LR:173:ARG:HA	1.75	0.45
40:Lh:6:ALA:O	40:Lh:10:ARG:HG2	2.17	0.45
64:SI:56:ARG:NH2	64:SI:180:GLY:O	2.48	0.45
68:SM:42:LEU:HD11	68:SM:110:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SS:105:ASN:OD1	74:SS:108:ARG:NH2	2.50	0.45
78:SW:38:LEU:O	78:SW:42:MET:HB2	2.16	0.45
5:L5:4188:U:H2'	5:L5:4189:U:C6	2.52	0.45
23:LQ:157:GLY:O	23:LQ:188:ASN:ND2	2.50	0.45
25:LS:19:THR:HG23	25:LS:21:LYS:H	1.81	0.45
27:LU:80:LYS:HD2	27:LU:108:GLU:HA	1.99	0.45
50:Ls:26:LYS:NZ	50:Ls:92:LYS:HE2	2.31	0.45
51:Lt:129:ILE:O	51:Lt:133:LEU:HG	2.16	0.45
55:S2:520:A:O2'	55:S2:825:A:N3	2.45	0.45
75:ST:51:ASN:HB3	75:ST:54:TYR:HD2	1.82	0.45
84:Sc:31:ARG:HE	84:Sc:43:ILE:HD11	1.82	0.45
3:CR:85:TYR:OH	3:CR:113:ASP:OD2	2.30	0.45
5:L5:717:U:H2'	5:L5:718:C:C6	2.52	0.45
5:L5:2017:A:O2'	5:L5:2018:C:O5'	2.29	0.45
7:L8:90:C:H1'	31:LY:24:HIS:HB3	1.99	0.45
13:LF:60:GLU:O	13:LF:64:MET:HG3	2.17	0.45
18:LL:91:ALA:HB1	18:LL:96:ILE:HB	1.97	0.45
30:LX:109:ILE:O	30:LX:113:VAL:HG23	2.17	0.45
50:Ls:83:ARG:HE	50:Ls:83:ARG:HA	1.82	0.45
55:S2:1628:C:H2'	55:S2:1629:C:C6	2.52	0.45
55:S2:1692:U:H2'	55:S2:1693:G:C8	2.51	0.45
58:SC:192:LEU:HB3	58:SC:227:ARG:HB3	1.97	0.45
66:SK:57:TYR:HB3	66:SK:75:GLY:HA2	1.99	0.45
5:L5:99:A:H5''	20:LN:184:ILE:HD13	1.98	0.45
5:L5:257:C:H2'	5:L5:258:G:C8	2.52	0.45
5:L5:1308:C:H2'	5:L5:1309:C:C6	2.52	0.45
5:L5:1706:A:N6	5:L5:2118:G:O4'	2.49	0.45
5:L5:1811:G:H21	34:Lb:57:MET:HE3	1.81	0.45
5:L5:4174:U:H2'	5:L5:4175:G:C8	2.52	0.45
28:LV:112:MET:HE2	28:LV:112:MET:HB3	1.87	0.45
52:NA:121:ILE:HG13	52:NA:123:PHE:CE2	2.52	0.45
54:Nm:297:TRP:CE2	54:Nm:462:LEU:HD13	2.52	0.45
5:L5:958:G:O2'	12:LE:123:ARG:O	2.30	0.45
5:L5:2835:A:O2'	9:LB:228:TYR:O	2.25	0.45
5:L5:3932:U:H2'	5:L5:3933:G:C8	2.52	0.45
7:L8:8:U:H2'	7:L8:9:A:C8	2.52	0.45
30:LX:64:SER:HB2	40:Lh:69:LEU:HD13	1.98	0.45
49:Lr:97:ILE:HD13	49:Lr:107:ARG:HA	1.99	0.45
50:Ls:57:LYS:HB3	50:Ls:60:MET:HG2	1.98	0.45
53:NB:152:ASN:HB3	53:NB:155:GLU:HG3	1.98	0.45
55:S2:1275:G:H5''	55:S2:1506:A:H61	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:1281:G:H3'	55:S2:1282:A:H8	1.81	0.45
55:S2:1348:G:H5'	58:SC:145:LYS:HE3	1.97	0.45
65:SJ:32:ILE:HD11	65:SJ:40:LYS:HA	1.99	0.45
73:SR:6:THR:HG22	73:SR:9:VAL:HG23	1.99	0.45
80:SY:62:THR:HA	80:SY:69:THR:HA	1.99	0.45
5:L5:1366:G:N7	18:LL:37:LYS:NZ	2.48	0.44
5:L5:2539:C:H2'	5:L5:2540:C:C6	2.51	0.44
5:L5:2856:C:O2	9:LB:242:ARG:NH2	2.47	0.44
5:L5:3855:C:H2'	5:L5:3856:A:H8	1.82	0.44
11:LD:217:ASP:OD2	11:LD:217:ASP:N	2.50	0.44
12:LE:141:ARG:N	12:LE:191:GLN:OE1	2.50	0.44
31:LY:22:PRO:O	31:LY:26:ARG:HB2	2.17	0.44
37:Le:88:LEU:HB2	37:Le:120:ILE:HD13	1.99	0.44
39:Lg:100:GLN:HA	39:Lg:103:VAL:HG22	1.99	0.44
55:S2:107:A:H2'	55:S2:108:G:C8	2.51	0.44
55:S2:878:G:O6	55:S2:908:A:N1	2.50	0.44
55:S2:1240:A:C8	71:SP:100:LYS:HD2	2.51	0.44
55:S2:1627:C:H5''	75:ST:41:LYS:HD2	1.98	0.44
58:SC:163:VAL:HG22	58:SC:164:PRO:HD2	1.99	0.44
59:SD:56:GLN:O	59:SD:60:GLY:HA3	2.17	0.44
59:SD:105:LEU:HB2	59:SD:122:VAL:HG21	1.99	0.44
66:SK:65:ARG:NH1	85:Sd:21:CYS:O	2.50	0.44
5:L5:313:U:H5''	20:LN:179:LYS:HE2	2.00	0.44
5:L5:3726:A:H2'	5:L5:3727:A:C8	2.52	0.44
5:L5:4291:G:H8	5:L5:4328:G:H2'	1.82	0.44
5:L5:4717:A:OP2	9:LB:30:LYS:NZ	2.42	0.44
23:LQ:70:MET:HE3	23:LQ:70:MET:HB3	1.86	0.44
41:Li:16:LYS:HA	41:Li:16:LYS:HD3	1.68	0.44
46:Ln:10:MET:HE1	46:Ln:17:ARG:HH12	1.81	0.44
55:S2:453:C:O2'	62:SG:92:ARG:O	2.29	0.44
55:S2:1199:A:H5''	82:Sa:2:THR:HB	1.98	0.44
69:SN:127:ARG:O	69:SN:131:THR:HG23	2.17	0.44
82:Sa:40:VAL:HB	82:Sa:69:VAL:HG22	1.98	0.44
88:Sg:24:THR:HG23	88:Sg:27:PHE:H	1.81	0.44
3:CR:279:LYS:HD2	3:CR:279:LYS:C	2.42	0.44
5:L5:262:G:H2'	5:L5:263:G:H8	1.82	0.44
5:L5:1097:C:H2'	5:L5:1098:G:C8	2.52	0.44
5:L5:2296:G:O2'	10:LC:242:PRO:O	2.30	0.44
5:L5:2708:U:H4'	5:L5:2709:C:H5''	1.98	0.44
37:Le:23:HIS:HA	37:Le:53:ILE:HD13	2.00	0.44
54:NM:190:PHE:CD1	54:NM:403:LEU:HD21	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:302:A:H1'	64:SI:73:THR:HG23	1.99	0.44
55:S2:866:U:H2'	55:S2:867:G:C8	2.52	0.44
55:S2:913:A:OP1	63:SH:99:ARG:NH1	2.51	0.44
55:S2:916:A:C5	69:SN:73:ARG:HD3	2.52	0.44
55:S2:1037:G:H4'	55:S2:1845:A:H4'	1.99	0.44
56:SA:183:LEU:HB3	56:SA:189:ILE:HG12	1.99	0.44
61:SF:86:LYS:O	61:SF:90:VAL:HG13	2.18	0.44
75:ST:76:THR:HB	75:ST:94:ARG:HB3	1.99	0.44
5:L5:300:A:H2'	5:L5:301:G:H8	1.82	0.44
5:L5:679:C:H2'	5:L5:680:G:C8	2.53	0.44
5:L5:1443:A:N1	5:L5:2103:G:C2	2.86	0.44
5:L5:2017:A:O2'	5:L5:2018:C:H6	2.00	0.44
14:LG:252:LYS:HB2	14:LG:252:LYS:HE3	1.62	0.44
37:Le:66:THR:HA	37:Le:69:MET:HE3	1.99	0.44
51:Lt:108:GLU:O	51:Lt:112:ILE:HG12	2.18	0.44
61:SF:123:GLU:OE2	61:SF:204:ARG:NH1	2.50	0.44
65:SJ:33:GLY:HA3	86:Se:38:TYR:CG	2.53	0.44
82:Sa:15:ARG:HG2	82:Sa:18:VAL:HG22	1.98	0.44
5:L5:935:A:O2'	19:LM:46:ARG:NH1	2.51	0.44
5:L5:4754:G:N7	12:LE:279:ASN:HB2	2.33	0.44
18:LL:47:ALA:HB1	40:Lh:118:LYS:HE3	1.99	0.44
21:LO:76:PRO:HB3	21:LO:138:LEU:HG	2.00	0.44
41:Li:76:ARG:HD3	41:Li:76:ARG:HA	1.86	0.44
55:S2:51:U:H2'	55:S2:52:G:C8	2.53	0.44
65:SJ:131:ARG:HA	65:SJ:131:ARG:HD2	1.77	0.44
70:SO:91:THR:HB	70:SO:92:ALA:H	1.65	0.44
81:SZ:46:ASN:HB3	81:SZ:80:ARG:HA	2.00	0.44
5:L5:268:G:H2'	5:L5:269:G:H8	1.81	0.44
5:L5:3736:A:H2'	5:L5:3737:A:C8	2.53	0.44
5:L5:4862:G:H2'	5:L5:4863:G:C8	2.53	0.44
5:L5:4939:C:OP1	12:LE:187:ARG:NH1	2.51	0.44
7:L8:67:U:H2'	7:L8:68:G:H8	1.81	0.44
10:LC:210:ILE:HA	10:LC:230:LEU:O	2.18	0.44
21:LO:9:LEU:HD23	21:LO:118:MET:HB3	1.99	0.44
31:LY:49:ILE:H	31:LY:49:ILE:HG12	1.62	0.44
38:Lf:36:ARG:O	38:Lf:39:THR:OG1	2.30	0.44
46:Ln:1:MET:HB2	55:S2:1706:G:H5'	1.99	0.44
49:Lr:84:LYS:HB3	49:Lr:84:LYS:HE2	1.72	0.44
50:Ls:202:GLU:O	50:Ls:206:ILE:HG23	2.18	0.44
55:S2:921:G:O6	78:SW:60:LYS:NZ	2.51	0.44
65:SJ:131:ARG:NH1	65:SJ:143:ASN:O	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CR:306:GLU:OE1	3:CR:306:GLU:N	2.37	0.44
5:L5:111:C:OP1	40:Lh:110:LYS:NZ	2.49	0.44
5:L5:407:A:O2'	5:L5:410:A:OP1	2.27	0.44
5:L5:517:C:N4	5:L5:646:G:O2'	2.44	0.44
5:L5:3784:A:O2'	5:L5:3785:A:H3'	2.18	0.44
5:L5:4459:U:H2'	5:L5:4460:U:C6	2.52	0.44
15:LH:140:GLN:HB3	15:LH:143:GLU:HG2	1.99	0.44
53:NB:80:GLN:HB3	53:NB:89:THR:HG22	1.99	0.44
55:S2:28:U:H2'	55:S2:29:G:C8	2.52	0.44
55:S2:1562:C:H2'	55:S2:1563:G:H8	1.82	0.44
60:SE:57:THR:OG1	60:SE:59:ASP:OD1	2.36	0.44
74:SS:44:VAL:HG11	74:SS:71:MET:HG3	1.99	0.44
77:SV:17:CYS:HB2	77:SV:56:CYS:HB3	2.00	0.44
88:Sg:114:SER:HB2	88:Sg:119:GLN:HB2	1.99	0.44
5:L5:724:C:OP1	10:LC:350:ARG:HD2	2.18	0.44
5:L5:1333:A:H2'	5:L5:1334:A:C8	2.52	0.44
5:L5:2730:U:H2'	5:L5:2731:C:C6	2.53	0.44
5:L5:3917:A:H2'	5:L5:3918:G:H8	1.82	0.44
5:L5:4742:G:H2'	5:L5:4743:G:H8	1.83	0.44
7:L8:141:C:H2'	7:L8:142:U:C6	2.53	0.44
8:LA:10:LYS:HA	8:LA:16:PHE:CD2	2.52	0.44
36:Ld:26:THR:HG22	36:Ld:85:ARG:HH11	1.83	0.44
40:Lh:110:LYS:HB2	40:Lh:110:LYS:HE2	1.92	0.44
54:Nm:297:TRP:HB3	54:Nm:467:PHE:HB3	1.99	0.44
55:S2:367:U:H4'	55:S2:371:A:C8	2.53	0.44
55:S2:609:U:H2'	55:S2:610:G:H8	1.82	0.44
55:S2:661:U:OP2	79:SX:3:LYS:NZ	2.41	0.44
5:L5:1686:C:O2'	34:Lb:18:ARG:NH1	2.50	0.44
5:L5:4119:C:H5	39:Lg:100:GLN:HG2	1.82	0.44
5:L5:4324:A:H2'	5:L5:4325:A:C8	2.53	0.44
5:L5:4745:G:H1	5:L5:4955:A:H61	1.65	0.44
51:Lt:133:LEU:HB3	51:Lt:148:PRO:HB3	1.99	0.44
53:NB:74:PHE:CZ	53:NB:77:PRO:HB3	2.53	0.44
55:S2:166:A:O2'	62:SG:6:SER:OG	2.29	0.44
55:S2:1283:C:H2'	68:SM:104:VAL:HG21	1.99	0.44
65:SJ:107:GLU:O	65:SJ:113:GLN:NE2	2.51	0.44
5:L5:1077:C:H4'	5:L5:1215:C:C4	2.53	0.43
5:L5:2765:A:H2'	5:L5:2766:A:C8	2.52	0.43
5:L5:3707:U:H2'	5:L5:3708:C:C6	2.53	0.43
5:L5:4093:G:OP2	5:L5:4093:G:N2	2.39	0.43
5:L5:4169:G:H4'	5:L5:4171:C:C2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:4446:U:O2'	5:L5:4450:U:OP1	2.35	0.43
5:L5:4761:G:H2'	5:L5:4762:A:C8	2.52	0.43
19:LM:113:MET:HE3	19:LM:113:MET:HB3	1.79	0.43
37:Le:98:GLU:OE2	37:Le:123:THR:OG1	2.31	0.43
37:Le:106:LYS:HE2	37:Le:106:LYS:HB3	1.63	0.43
42:Lj:25:LYS:HB3	42:Lj:25:LYS:HE3	1.74	0.43
54:Nm:410:HIS:HA	54:Nm:411:PRO:HD3	1.90	0.43
55:S2:996:A:H2'	55:S2:997:A:C8	2.53	0.43
65:SJ:93:LYS:HE2	65:SJ:96:TYR:HE1	1.83	0.43
68:SM:25:ALA:HB1	68:SM:31:LEU:HD21	1.99	0.43
5:L5:163:A:H2'	5:L5:164:G:H8	1.84	0.43
5:L5:1478:C:H2'	5:L5:1479:G:H8	1.83	0.43
5:L5:2019:C:OP1	50:Ls:6:ARG:NH2	2.51	0.43
5:L5:2568:C:H2'	5:L5:2569:G:H8	1.83	0.43
5:L5:2764:A:H2'	5:L5:2765:A:C8	2.53	0.43
5:L5:3848:U:H2'	5:L5:3849:A:H8	1.83	0.43
17:LJ:119:TYR:HD1	74:SS:11:HIS:HB3	1.82	0.43
30:LX:82:THR:HG22	30:LX:155:ILE:HG23	2.00	0.43
50:Ls:109:ALA:HB3	50:Ls:185:PHE:HE1	1.83	0.43
54:Nm:172:LEU:HD23	54:Nm:172:LEU:HA	1.87	0.43
55:S2:993:G:OP1	55:S2:1131:G:N2	2.38	0.43
55:S2:1775:U:H2'	55:S2:1776:G:C4	2.53	0.43
56:SA:207:PRO:HA	56:SA:210:ILE:HB	1.98	0.43
59:SD:123:LEU:HD22	59:SD:134:CYS:SG	2.58	0.43
61:SF:41:VAL:HA	61:SF:45:TYR:HB2	1.99	0.43
71:SP:18:ARG:H	71:SP:18:ARG:HG2	1.53	0.43
72:SQ:31:LEU:HD21	72:SQ:33:LYS:HE3	1.98	0.43
5:L5:1327:C:H2'	5:L5:1328:G:C8	2.53	0.43
5:L5:1918:U:O2'	5:L5:1920:C:OP2	2.37	0.43
5:L5:4620:U:OP2	5:L5:4670:C:N4	2.45	0.43
9:LB:300:LYS:HB3	9:LB:300:LYS:HE3	1.71	0.43
16:LI:99:ILE:HG22	16:LI:123:GLN:HB2	2.00	0.43
24:LR:151:ARG:NH2	67:SL:119:ASP:OD2	2.39	0.43
38:Lf:36:ARG:HB2	38:Lf:80:ASN:HA	1.99	0.43
50:Ls:162:LYS:HD2	50:Ls:162:LYS:HA	1.81	0.43
51:Lt:46:ILE:HD13	51:Lt:71:ILE:HG12	2.00	0.43
54:Nm:187:MET:HA	54:Nm:187:MET:HE3	2.00	0.43
55:S2:309:G:OP2	64:SI:55:TYR:OH	2.23	0.43
61:SF:94:LYS:HD2	61:SF:94:LYS:HA	1.83	0.43
70:SO:92:ALA:HB2	70:SO:125:LYS:HB2	2.00	0.43
74:SS:142:ARG:HD2	74:SS:142:ARG:HA	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
88:Sg:191:HIS:NE2	88:Sg:209:SER:OG	2.48	0.43
5:L5:1553:A:O2'	48:Lp:9:GLY:O	2.26	0.43
5:L5:2029:A:H2'	5:L5:2030:A:C8	2.53	0.43
5:L5:3906:A:H2'	10:LC:69:THR:HG23	2.00	0.43
11:LD:125:VAL:HG12	11:LD:127:GLY:H	1.83	0.43
22:LP:8:PRO:HD3	22:LP:149:ILE:HD13	2.00	0.43
31:LY:2:LYS:HB3	31:LY:2:LYS:HE3	1.77	0.43
33:La:3:SER:HA	33:La:6:ARG:HG3	2.00	0.43
47:Lo:22:LYS:HB3	47:Lo:22:LYS:HE3	1.84	0.43
50:Ls:106:LYS:HE2	50:Ls:106:LYS:HB2	1.64	0.43
54:Nm:198:LEU:O	54:Nm:202:ARG:HB2	2.18	0.43
54:Nm:355:ARG:NH2	54:Nm:359:GLN:OE1	2.51	0.43
55:S2:15:U:H2'	55:S2:16:G:O4'	2.19	0.43
55:S2:1017:U:H5'	69:SN:55:ARG:HD3	2.00	0.43
71:SP:34:MET:HE2	71:SP:45:LEU:HB3	2.00	0.43
74:SS:22:GLY:HA2	74:SS:56:ALA:HB3	2.00	0.43
5:L5:99:A:H4'	20:LN:181:HIS:CE1	2.54	0.43
5:L5:433:A:C2	5:L5:3867:A:H4'	2.53	0.43
5:L5:2579:G:N2	5:L5:2582:A:OP2	2.41	0.43
5:L5:2848:G:O2'	5:L5:3838:U:O4	2.31	0.43
5:L5:4128:A:H8	14:LG:35:ARG:H	1.66	0.43
14:LG:187:LYS:HG3	14:LG:198:THR:HA	1.99	0.43
18:LL:18:TRP:CD1	18:LL:18:TRP:H	2.36	0.43
27:LU:63:ILE:HG13	27:LU:72:VAL:HG22	2.01	0.43
28:LV:13:LYS:HD3	28:LV:128:LEU:HD11	2.00	0.43
50:Ls:44:ARG:NH1	50:Ls:53:VAL:O	2.51	0.43
50:Ls:120:GLU:OE2	50:Ls:163:THR:OG1	2.36	0.43
54:Nm:138:VAL:HG22	54:Nm:482:LYS:HG3	2.00	0.43
55:S2:118:C:H1'	55:S2:445:A:C5	2.53	0.43
55:S2:147:A:H61	55:S2:173:A:H61	1.65	0.43
55:S2:319:C:H2'	55:S2:320:G:C8	2.54	0.43
55:S2:656:G:H5'	55:S2:662:G:N2	2.34	0.43
57:SB:191:ASP:HB3	57:SB:195:LYS:HZ1	1.84	0.43
72:SQ:113:ILE:HD13	72:SQ:113:ILE:HA	1.89	0.43
81:SZ:74:SER:HA	81:SZ:79:ILE:HG23	1.99	0.43
5:L5:1280:C:O2'	10:LC:321:ASN:OD1	2.30	0.43
5:L5:1539:G:H4'	8:LA:194:ASN:HB2	2.00	0.43
5:L5:1802:A:H5''	5:L5:1803:G:H5'	2.01	0.43
5:L5:4621:C:OP1	28:LV:48:ARG:HD2	2.18	0.43
10:LC:152:LEU:HD23	10:LC:251:ILE:HG12	2.00	0.43
13:LF:182:TYR:CD1	13:LF:200:ARG:HD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LJ:13:ARG:NH1	17:LJ:154:LYS:O	2.41	0.43
38:Lf:33:VAL:HG13	38:Lf:38:GLU:HB2	2.00	0.43
55:S2:12:U:H2'	55:S2:13:C:C6	2.54	0.43
55:S2:799:U:H3	55:S2:866:U:H5	1.67	0.43
55:S2:1298:G:H4'	71:SP:78:THR:HA	1.99	0.43
57:SB:135:LEU:HD11	57:SB:176:VAL:HG11	2.00	0.43
57:SB:191:ASP:HB3	57:SB:195:LYS:NZ	2.33	0.43
64:SI:56:ARG:HA	64:SI:180:GLY:HA2	2.00	0.43
70:SO:94:HIS:HA	70:SO:127:GLY:O	2.17	0.43
3:CR:324:GLU:HG3	3:CR:391:ILE:HG22	2.00	0.43
5:L5:88:A:N7	23:LQ:173:LYS:NZ	2.67	0.43
5:L5:258:G:H2'	5:L5:259:C:C6	2.53	0.43
5:L5:3641:U:OP2	5:L5:3646:A:N6	2.49	0.43
5:L5:3717:A:H2'	5:L5:3718:A:H8	1.84	0.43
5:L5:3923:A:H2'	5:L5:3924:C:C6	2.54	0.43
8:LA:242:ARG:NH2	8:LA:243:THR:O	2.52	0.43
14:LG:99:ALA:HB1	14:LG:136:LEU:HD11	2.00	0.43
20:LN:143:ARG:NH2	40:Lh:93:ARG:O	2.52	0.43
40:Lh:94:ARG:HE	40:Lh:94:ARG:HB3	1.61	0.43
55:S2:1623:A:O5'	74:SS:133:GLY:HA3	2.19	0.43
65:SJ:124:HIS:CE1	86:Se:35:ARG:HB2	2.54	0.43
79:SX:128:VAL:HG13	79:SX:133:LEU:HD11	2.01	0.43
82:Sa:52:ASP:OD1	82:Sa:52:ASP:N	2.52	0.43
5:L5:160:G:OP2	41:Li:23:LYS:NZ	2.50	0.43
5:L5:162:A:H2'	5:L5:163:A:C8	2.54	0.43
5:L5:1351:G:O6	23:LQ:55:ARG:NH1	2.45	0.43
5:L5:3848:U:H2'	5:L5:3849:A:C8	2.53	0.43
5:L5:3880:G:H2'	5:L5:3881:G:C8	2.54	0.43
5:L5:3932:U:H2'	5:L5:3933:G:H8	1.83	0.43
5:L5:4134:C:H2'	5:L5:4135:G:C8	2.54	0.43
5:L5:4274:A:H2'	5:L5:4275:G:H8	1.84	0.43
5:L5:4322:G:N2	5:L5:4325:A:OP2	2.48	0.43
54:NM:152:LEU:HD11	54:NM:158:TRP:CD1	2.54	0.43
54:NM:408:MET:HE3	54:NM:408:MET:H	1.82	0.43
55:S2:441:C:H2'	55:S2:442:C:C6	2.54	0.43
55:S2:629:A:O2'	55:S2:631:U:OP1	2.37	0.43
55:S2:1348:G:H22	55:S2:1381:G:N2	2.16	0.43
55:S2:1606:G:H5''	75:ST:86:GLY:C	2.44	0.43
67:SL:33:LEU:HD12	67:SL:34:PRO:HD2	2.01	0.43
81:SZ:77:LEU:HB2	81:SZ:79:ILE:HG22	2.01	0.43
5:L5:92:C:OP2	5:L5:4341:C:O2'	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:1346:C:H2'	5:L5:1347:G:H8	1.83	0.43
5:L5:2411:C:H2'	5:L5:2412:A:H8	1.84	0.43
5:L5:2675:G:N7	35:Lc:32:LYS:HG3	2.34	0.43
5:L5:2693:G:OP2	43:Lk:33:LYS:NZ	2.41	0.43
5:L5:4622:A:H4'	9:LB:13:SER:HB2	2.00	0.43
5:L5:4689:U:H5	5:L5:4699:U:O4	2.02	0.43
11:LD:238:GLU:O	11:LD:242:LYS:HG3	2.19	0.43
12:LE:287:VAL:O	19:LM:109:ARG:NH2	2.52	0.43
16:LI:91:LEU:HD12	16:LI:91:LEU:HA	1.91	0.43
17:LJ:141:ILE:HA	17:LJ:144:LYS:HD3	2.01	0.43
21:LO:158:GLU:O	21:LO:162:GLU:HG3	2.18	0.43
55:S2:1243:U:OP2	55:S2:1518:C:O2'	2.29	0.43
55:S2:1597:C:H4'	55:S2:1603:G:C6	2.53	0.43
58:SC:68:ARG:HE	58:SC:68:ARG:HB2	1.74	0.43
66:SK:23:ALA:HB3	66:SK:69:TRP:HZ3	1.84	0.43
68:SM:50:CYS:HB2	68:SM:110:VAL:HG22	2.00	0.43
69:SN:16:LEU:HD12	69:SN:16:LEU:HA	1.90	0.43
5:L5:325:U:H2'	5:L5:326:C:C6	2.54	0.43
5:L5:1946:G:O2'	5:L5:1948:G:OP2	2.35	0.43
5:L5:4260:U:H2'	5:L5:4261:C:H6	1.83	0.43
16:LI:193:ASP:OD1	16:LI:193:ASP:N	2.51	0.43
26:LT:52:MET:HE2	26:LT:52:MET:HB3	1.98	0.43
51:Lt:6:ASP:OD1	51:Lt:6:ASP:N	2.51	0.43
55:S2:30:C:O2'	55:S2:596:U:OP1	2.27	0.43
55:S2:455:A:H2'	55:S2:456:C:C6	2.54	0.43
55:S2:1740:C:OP1	64:SI:44:HIS:ND1	2.40	0.43
60:SE:125:LYS:HG2	60:SE:142:HIS:HB3	2.00	0.43
64:SI:174:CYS:HB2	64:SI:190:LEU:HD21	1.99	0.43
66:SK:53:LYS:HE3	66:SK:53:LYS:HB3	1.88	0.43
73:SR:57:LEU:O	73:SR:61:ILE:HG23	2.19	0.43
79:SX:22:TRP:HE3	79:SX:28:LYS:HG3	1.83	0.43
3:CR:372:MET:HA	3:CR:373:PRO:HD3	1.77	0.42
4:CZ:94:PRO:HA	4:CZ:95:PRO:HD3	1.75	0.42
5:L5:1199:G:H2'	5:L5:1200:G:C8	2.54	0.42
5:L5:1346:C:H2'	5:L5:1347:G:C8	2.54	0.42
5:L5:2647:A:H3'	5:L5:2648:G:H8	1.83	0.42
5:L5:4457:U:H1'	9:LB:252:ALA:HB3	2.00	0.42
9:LB:136:LYS:HB3	9:LB:136:LYS:HE2	1.82	0.42
14:LG:211:ASP:N	14:LG:211:ASP:OD1	2.51	0.42
25:LS:101:THR:HG22	25:LS:104:GLY:H	1.83	0.42
28:LV:21:PRO:HA	28:LV:54:ALA:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Lo:10:THR:HG21	47:Lo:70:LEU:HD13	2.00	0.42
48:Lp:46:LYS:HE3	48:Lp:46:LYS:HB3	1.80	0.42
49:Lr:28:GLU:HG2	49:Lr:31:ASN:HB2	2.00	0.42
55:S2:1351:G:H4'	56:SA:110:ASN:HA	2.01	0.42
55:S2:1736:G:H2'	55:S2:1737:G:H8	1.82	0.42
55:S2:1797:U:H2'	55:S2:1798:C:C6	2.54	0.42
56:SA:84:GLN:HG2	56:SA:100:ALA:HB1	2.01	0.42
62:SG:181:THR:HG22	62:SG:183:ARG:H	1.83	0.42
63:SH:104:PRO:HD3	63:SH:116:ARG:HD3	2.01	0.42
64:SI:19:LYS:HA	64:SI:20:PRO:HD3	1.90	0.42
68:SM:121:LYS:HE2	68:SM:121:LYS:HB2	1.78	0.42
71:SP:108:LYS:H	71:SP:111:MET:HE2	1.83	0.42
82:Sa:13:LYS:HD3	82:Sa:13:LYS:HA	1.85	0.42
5:L5:279:A:C4	20:LN:12:ARG:HG2	2.54	0.42
5:L5:493:G:N2	5:L5:661:C:O2	2.52	0.42
5:L5:501:C:H42	5:L5:506:C:H41	1.66	0.42
5:L5:2483:G:H2'	5:L5:2484:A:C8	2.54	0.42
10:LC:230:LEU:HD23	10:LC:230:LEU:HA	1.91	0.42
32:LZ:109:LYS:HB2	32:LZ:109:LYS:HE2	1.74	0.42
36:Ld:54:MET:HG2	36:Ld:60:PRO:HA	2.00	0.42
51:Lt:45:ASP:OD1	51:Lt:45:ASP:N	2.43	0.42
51:Lt:82:ILE:HA	51:Lt:85:LEU:HB2	2.01	0.42
54:Nm:108:THR:HG23	54:Nm:111:GLU:H	1.84	0.42
55:S2:1759:G:H1'	55:S2:1774:C:N3	2.34	0.42
62:SG:38:ALA:HB2	62:SG:50:VAL:HG22	2.00	0.42
3:CR:152:ASP:OD2	3:CR:154:SER:OG	2.33	0.42
5:L5:1577:G:O2'	5:L5:1612:G:H4'	2.19	0.42
5:L5:1734:G:N2	5:L5:1735:U:O4	2.41	0.42
5:L5:2045:G:O6	5:L5:3870:C:O2'	2.37	0.42
5:L5:2474:G:N2	5:L5:2502:G:O2'	2.52	0.42
5:L5:4537:C:H2'	5:L5:4538:G:H8	1.84	0.42
11:LD:88:VAL:HG13	11:LD:239:MET:HE3	2.01	0.42
30:LX:39:LYS:HE2	30:LX:39:LYS:HB2	1.76	0.42
32:LZ:60:LYS:HD2	32:LZ:60:LYS:N	2.34	0.42
55:S2:115:U:H2'	55:S2:116:U:C6	2.54	0.42
55:S2:167:G:H21	62:SG:132:ARG:CD	2.22	0.42
55:S2:1217:A:H2'	55:S2:1218:C:C6	2.54	0.42
55:S2:1798:C:H2'	55:S2:1799:G:O4'	2.20	0.42
61:SF:124:ASP:OD2	61:SF:125:SER:N	2.47	0.42
75:ST:113:VAL:HG12	75:ST:123:LEU:HD23	2.01	0.42
5:L5:318:A:H2'	5:L5:319:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:323:C:H2'	5:L5:324:A:H8	1.84	0.42
5:L5:1281:G:H5'	10:LC:323:ARG:HB2	2.00	0.42
5:L5:3605:C:OP2	24:LR:71:ARG:NH1	2.52	0.42
8:LA:41:ILE:HG12	8:LA:63:PHE:HD2	1.85	0.42
8:LA:107:MET:O	8:LA:139:HIS:NE2	2.53	0.42
16:LI:54:SER:HB2	16:LI:135:ILE:HD11	2.01	0.42
18:LL:80:GLU:OE2	18:LL:102:ARG:NH2	2.52	0.42
25:LS:160:ARG:HA	25:LS:160:ARG:HD3	1.80	0.42
32:LZ:27:LYS:HD3	32:LZ:29:ILE:HD11	2.02	0.42
40:Lh:7:ARG:H	40:Lh:7:ARG:HG3	1.59	0.42
55:S2:1705:C:H2'	55:S2:1706:G:C8	2.54	0.42
62:SG:135:PRO:HB2	62:SG:141:ILE:HG13	2.02	0.42
63:SH:50:GLU:OE2	63:SH:90:LYS:HE2	2.20	0.42
64:SI:41:ARG:HD3	64:SI:43:ILE:HD12	2.01	0.42
76:SU:26:SER:HB3	76:SU:32:LEU:HD13	2.01	0.42
81:SZ:78:LYS:HA	81:SZ:78:LYS:HD3	1.77	0.42
5:L5:1392:A:H2'	5:L5:1393:G:C8	2.54	0.42
5:L5:1867:A:H2'	5:L5:1868:A:C8	2.55	0.42
5:L5:3607:U:H2'	5:L5:3608:A:C8	2.54	0.42
5:L5:3720:G:H22	5:L5:3733:A:H2	1.67	0.42
5:L5:4478:G:O2'	5:L5:4602:A:N1	2.48	0.42
7:L8:148:A:H2'	7:L8:149:G:C8	2.54	0.42
10:LC:5:ARG:HH21	10:LC:25:PRO:HA	1.84	0.42
14:LG:213:GLY:O	14:LG:217:LYS:HG3	2.19	0.42
16:LI:187:LYS:HB3	16:LI:187:LYS:HE3	1.81	0.42
18:LL:4:SER:OG	18:LL:5:ARG:N	2.52	0.42
20:LN:146:PRO:HA	20:LN:149:GLN:HG2	2.02	0.42
22:LP:39:MET:HB2	22:LP:43:LYS:HD3	2.01	0.42
26:LT:93:ILE:HA	26:LT:96:ILE:HG12	2.02	0.42
32:LZ:50:PRO:HD3	32:LZ:68:ILE:HG12	2.01	0.42
54:NM:233:ILE:HB	54:NM:242:MET:HG2	2.01	0.42
54:NM:444:MET:SD	54:NM:444:MET:N	2.93	0.42
55:S2:66:G:N2	55:S2:82:G:H21	2.16	0.42
55:S2:77:A:O2'	62:SG:174:PRO:O	2.31	0.42
55:S2:681:U:H4'	79:SX:9:THR:HG22	2.01	0.42
5:L5:1:C:O2'	30:LX:38:LYS:NZ	2.53	0.42
5:L5:2622:G:O6	27:LU:81:ARG:NH2	2.53	0.42
5:L5:3717:A:OP2	5:L5:3735:G:N2	2.43	0.42
7:L8:67:U:H2'	7:L8:68:G:C8	2.55	0.42
13:LF:92:VAL:O	13:LF:120:GLY:HA2	2.20	0.42
16:LI:205:PRO:HG2	16:LI:208:LYS:HD3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LJ:59:SER:OG	17:LJ:60:PHE:N	2.53	0.42
42:Lj:67:LEU:HD23	42:Lj:67:LEU:HA	1.86	0.42
55:S2:1669:G:OP1	76:SU:79:ARG:NH2	2.47	0.42
56:SA:122:LEU:O	56:SA:144:THR:HA	2.19	0.42
63:SH:72:PHE:O	63:SH:76:GLN:HB2	2.19	0.42
64:SI:110:ARG:O	64:SI:114:GLU:HG2	2.19	0.42
5:L5:667:A:OP1	49:Lr:46:ARG:NH2	2.53	0.42
5:L5:746:A:H2'	5:L5:747:A:C8	2.55	0.42
5:L5:2640:G:H2'	5:L5:2641:A:C8	2.54	0.42
5:L5:3908:A:H2	5:L5:4449:A:H61	1.67	0.42
11:LD:55:VAL:HG13	11:LD:60:ILE:HG12	2.00	0.42
11:LD:119:TYR:OH	11:LD:139:PRO:O	2.34	0.42
14:LG:171:PRO:HB3	14:LG:181:TYR:CE1	2.55	0.42
15:LH:126:VAL:HG11	15:LH:161:ILE:HG22	2.00	0.42
20:LN:16:SER:O	20:LN:20:ARG:HB2	2.19	0.42
31:LY:21:ALA:O	31:LY:26:ARG:NH1	2.46	0.42
50:Ls:69:LEU:HD23	50:Ls:69:LEU:HA	1.82	0.42
54:NM:306:LEU:HD22	54:NM:311:PHE:HB3	2.01	0.42
54:NM:455:LEU:HB2	54:NM:491:VAL:HB	2.01	0.42
55:S2:150:A:N6	55:S2:168:C:O2	2.53	0.42
55:S2:1801:A:H2'	55:S2:1802:C:C6	2.55	0.42
57:SB:34:LYS:O	57:SB:98:THR:HB	2.19	0.42
59:SD:101:GLN:HE21	59:SD:122:VAL:HG13	1.83	0.42
63:SH:79:LEU:HD11	63:SH:94:PHE:CZ	2.53	0.42
63:SH:144:ILE:HB	78:SW:52:ILE:HB	2.02	0.42
70:SO:26:ASN:OD1	70:SO:26:ASN:N	2.49	0.42
78:SW:3:ARG:HD2	78:SW:6:VAL:HG12	2.02	0.42
5:L5:3619:G:H22	5:L5:3624:A:H1'	1.83	0.42
5:L5:3710:G:N3	5:L5:3711:A:N6	2.68	0.42
5:L5:3893:C:O2'	5:L5:4979:A:N1	2.51	0.42
5:L5:4302:U:H4'	26:LT:5:LYS:HD3	2.01	0.42
14:LG:244:PRO:HA	14:LG:247:VAL:HG22	2.02	0.42
18:LL:146:LEU:HB2	18:LL:148:THR:HG23	2.02	0.42
31:LY:66:GLN:CD	31:LY:66:GLN:H	2.28	0.42
37:Le:38:PRO:HG2	37:Le:46:ARG:HB3	2.01	0.42
50:Ls:101:MET:HA	50:Ls:104:ALA:HB3	2.02	0.42
55:S2:681:U:O2'	55:S2:1160:U:OP1	2.36	0.42
55:S2:1004:U:H2'	55:S2:1005:G:C8	2.55	0.42
64:SI:57:ALA:HB2	64:SI:183:GLY:HA2	2.02	0.42
67:SL:59:LYS:HB3	67:SL:134:LEU:HD13	2.01	0.42
72:SQ:51:LEU:HD12	72:SQ:51:LEU:HA	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SS:12:ILE:HD13	74:SS:19:ASN:HB3	2.01	0.42
75:ST:42:HIS:HB2	75:ST:83:GLN:HA	2.01	0.42
88:Sg:67:SER:N	88:Sg:81:GLY:O	2.49	0.42
5:L5:1086:C:H2'	5:L5:1087:A:H8	1.85	0.42
5:L5:1692:C:O2'	23:LQ:143:ARG:NH2	2.52	0.42
5:L5:1751:A:H2'	5:L5:1752:G:C8	2.55	0.42
5:L5:1877:G:O6	34:Lb:10:HIS:NE2	2.47	0.42
5:L5:4453:C:H2'	5:L5:4454:G:O4'	2.20	0.42
5:L5:4954:G:H2'	5:L5:4955:A:C8	2.55	0.42
8:LA:234:LYS:HG2	8:LA:238:ILE:HG12	2.01	0.42
9:LB:107:ALA:HB2	9:LB:201:LEU:HD22	2.02	0.42
12:LE:220:LYS:HB3	12:LE:220:LYS:HE3	1.79	0.42
33:La:89:ASN:O	33:La:93:ASN:HB2	2.20	0.42
54:NM:288:PRO:HA	54:NM:289:LYS:HA	1.72	0.42
55:S2:146:G:H22	55:S2:175:A:H1'	1.85	0.42
55:S2:851:C:H5''	55:S2:852:G:H5'	2.02	0.42
55:S2:962:A:H5''	70:SO:66:ARG:HB3	2.01	0.42
55:S2:980:A:H2'	55:S2:981:A:C8	2.55	0.42
55:S2:1506:A:O2'	55:S2:1508:A:OP2	2.35	0.42
55:S2:1513:C:H2'	55:S2:1514:G:H8	1.85	0.42
57:SB:68:GLU:HG2	57:SB:85:LYS:HD3	2.02	0.42
60:SE:128:LYS:HG2	60:SE:140:VAL:HB	2.01	0.42
62:SG:67:VAL:HB	62:SG:99:GLY:HA2	2.02	0.42
65:SJ:66:LYS:HA	65:SJ:71:LEU:HD11	2.02	0.42
78:SW:12:LYS:HA	78:SW:12:LYS:HD3	1.83	0.42
5:L5:459:C:H5'	12:LE:110:ARG:HB3	2.02	0.42
5:L5:758:G:H5'	15:LH:51:LYS:HZ3	1.84	0.42
5:L5:2521:G:H5'	5:L5:2640:G:H1'	2.02	0.42
5:L5:3612:C:H1'	5:L5:5016:A:C8	2.55	0.42
9:LB:34:LYS:HB2	9:LB:34:LYS:HE2	1.90	0.42
11:LD:179:ARG:HD3	11:LD:179:ARG:HA	1.80	0.42
19:LM:24:LEU:HB2	19:LM:43:THR:HG21	2.02	0.42
20:LN:47:LYS:HA	20:LN:47:LYS:HD2	1.89	0.42
34:Lb:13:SER:HA	34:Lb:16:TRP:NE1	2.35	0.42
37:Le:20:PHE:CG	37:Le:56:PRO:HG3	2.55	0.42
53:NB:36:THR:OG1	53:NB:37:ALA:N	2.53	0.42
54:NM:353:LEU:HD11	54:NM:366:MET:CG	2.49	0.42
56:SA:17:LYS:HG2	73:SR:91:LEU:HD12	2.02	0.42
65:SJ:110:LEU:HB2	65:SJ:147:PHE:HB3	2.01	0.42
67:SL:124:ASP:OD1	67:SL:124:ASP:N	2.51	0.42
87:Sf:107:LYS:HE2	87:Sf:107:LYS:HB2	1.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L5:121:A:H62	5:L5:152:U:H3	1.68	0.41
5:L5:1646:A:O2'	42:Lj:49:TRP:O	2.32	0.41
5:L5:2000:G:N2	5:L5:2000:G:OP2	2.52	0.41
5:L5:2725:A:N6	24:LR:88:ARG:O	2.52	0.41
5:L5:3807:A:OP1	46:Ln:23:ARG:NE	2.53	0.41
18:LL:56:ARG:NH1	18:LL:74:ARG:O	2.41	0.41
20:LN:159:ARG:HB3	20:LN:164:LEU:HB2	2.02	0.41
51:Lt:42:VAL:O	51:Lt:46:ILE:HG12	2.20	0.41
54:NM:431:LEU:HA	54:NM:434:LEU:HD23	2.02	0.41
55:S2:16:G:H2'	55:S2:17:C:C6	2.55	0.41
55:S2:862:A:C8	78:SW:107:SER:HA	2.55	0.41
55:S2:924:G:OP1	69:SN:4:MET:N	2.53	0.41
55:S2:1314:U:O2'	66:SK:8:ARG:NH2	2.45	0.41
57:SB:137:LEU:HD23	57:SB:172:MET:HG2	2.02	0.41
62:SG:56:ASN:HD22	62:SG:62:PRO:HA	1.84	0.41
88:Sg:18:VAL:HA	88:Sg:35:SER:HA	2.02	0.41
5:L5:1921:C:H1'	25:LS:160:ARG:HB3	2.01	0.41
5:L5:1942:A:N3	5:L5:4432:C:O2'	2.47	0.41
5:L5:2789:A:H1'	44:Ll:45:ARG:HH22	1.85	0.41
9:LB:220:ILE:HG12	9:LB:278:THR:HG23	2.02	0.41
10:LC:137:VAL:HG21	10:LC:150:LEU:HD21	2.02	0.41
16:LI:52:MET:HB2	16:LI:152:LEU:HD22	2.01	0.41
17:LJ:167:GLN:HA	17:LJ:172:GLY:H	1.85	0.41
22:LP:22:LEU:HD12	22:LP:146:ILE:HD12	2.01	0.41
28:LV:16:ILE:HD11	28:LV:57:VAL:H	1.85	0.41
37:Le:19:LYS:HE3	37:Le:19:LYS:HB3	1.86	0.41
50:Ls:45:MET:HE2	50:Ls:45:MET:HA	2.01	0.41
50:Ls:63:LYS:HA	50:Ls:63:LYS:HD3	1.80	0.41
54:NM:173:TYR:HE1	54:NM:193:SER:HA	1.85	0.41
55:S2:927:C:H1'	83:Sb:51:GLN:HE21	1.85	0.41
55:S2:1457:U:H2'	55:S2:1458:G:H8	1.85	0.41
55:S2:1839:U:H2'	55:S2:1840:U:C6	2.55	0.41
73:SR:21:TYR:CE2	73:SR:61:ILE:HD11	2.55	0.41
76:SU:20:ILE:HD11	76:SU:98:VAL:HG11	2.01	0.41
3:CR:314:MET:HE1	3:CR:417:VAL:HG11	2.02	0.41
3:CR:377:TRP:HE1	3:CR:381:ASN:HD21	1.67	0.41
5:L5:1382:G:OP1	18:LL:66:TYR:OH	2.35	0.41
5:L5:1719:A:H2'	5:L5:1720:C:C6	2.55	0.41
5:L5:4927:G:H5'	5:L5:4928:C:H5	1.84	0.41
7:L8:60:G:OP1	30:LX:68:ARG:NH2	2.50	0.41
9:LB:201:LEU:HD23	9:LB:201:LEU:HA	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LD:53:VAL:HG11	11:LD:159:VAL:HA	2.02	0.41
13:LF:88:LYS:H	13:LF:88:LYS:HG2	1.65	0.41
13:LF:236:ARG:HB3	13:LF:239:GLN:HB2	2.01	0.41
27:LU:42:PHE:O	27:LU:46:ARG:HB2	2.20	0.41
40:Lh:82:ASP:OD1	40:Lh:82:ASP:N	2.52	0.41
51:Lt:109:ILE:HD13	51:Lt:133:LEU:HD21	2.01	0.41
54:Nm:240:LYS:HG2	54:Nm:242:MET:SD	2.60	0.41
54:Nm:403:LEU:HB3	54:Nm:420:TYR:CE2	2.55	0.41
55:S2:106:C:H2'	55:S2:107:A:C8	2.55	0.41
57:SB:123:ALA:HB2	57:SB:165:ARG:HG3	2.02	0.41
79:SX:28:LYS:O	79:SX:32:LEU:HB2	2.20	0.41
3:CR:198:ARG:NH2	5:L5:3790:U:OP2	2.53	0.41
5:L5:968:C:P	12:LE:110:ARG:HH22	2.43	0.41
5:L5:1979:A:OP1	51:Lt:92:ARG:NH1	2.53	0.41
5:L5:4291:G:H5'	5:L5:4293:U:C6	2.55	0.41
22:LP:20:SER:O	22:LP:22:LEU:HG	2.20	0.41
45:Lm:112:LYS:HA	45:Lm:112:LYS:HD3	1.89	0.41
54:Nm:431:LEU:HD22	54:Nm:435:MET:HE1	2.03	0.41
55:S2:1123:C:OP1	57:SB:151:ARG:NH1	2.50	0.41
55:S2:1356:G:H2'	55:S2:1357:A:C8	2.54	0.41
55:S2:1405:A:H2'	55:S2:1406:G:O4'	2.21	0.41
62:SG:188:LYS:O	62:SG:192:ILE:HG12	2.19	0.41
70:SO:56:VAL:HG23	70:SO:60:MET:HE2	2.03	0.41
80:SY:32:LYS:HE3	80:SY:32:LYS:HB3	1.84	0.41
88:Sg:35:SER:OG	88:Sg:36:ARG:N	2.53	0.41
5:L5:1846:G:H2'	5:L5:1847:C:C6	2.55	0.41
5:L5:4149:C:OP1	32:LZ:60:LYS:NZ	2.39	0.41
5:L5:4563:U:H2'	5:L5:4564:A:H8	1.85	0.41
14:LG:80:ILE:HD11	20:LN:18:VAL:HG23	2.03	0.41
15:LH:43:VAL:HG12	15:LH:59:LYS:HD3	2.02	0.41
26:LT:14:MET:HE2	26:LT:14:MET:HB2	1.90	0.41
50:Ls:134:LYS:HB3	50:Ls:137:PHE:CZ	2.55	0.41
55:S2:17:C:O2'	55:S2:1194:A:N1	2.43	0.41
55:S2:416:U:H2'	55:S2:417:C:O4'	2.21	0.41
55:S2:493:A:H1'	55:S2:574:A:H5'	2.02	0.41
55:S2:1653:U:H2'	55:S2:1654:G:C8	2.55	0.41
55:S2:1864:U:H3'	82:Sa:5:ARG:HH21	1.86	0.41
79:SX:70:VAL:HG13	79:SX:72:VAL:HG23	2.02	0.41
5:L5:4318:C:H4'	47:Lo:17:LYS:HA	2.03	0.41
5:L5:4674:C:H2'	5:L5:4675:U:C6	2.56	0.41
5:L5:4927:G:H5'	5:L5:4928:C:C5	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LA:122:ASP:OD1	8:LA:122:ASP:N	2.52	0.41
55:S2:1010:G:H2'	55:S2:1011:A:C8	2.55	0.41
55:S2:1448:A:O2'	55:S2:1449:G:O4'	2.38	0.41
57:SB:32:ASP:OD1	57:SB:46:LYS:NZ	2.41	0.41
57:SB:94:LYS:HD2	57:SB:94:LYS:HA	1.75	0.41
59:SD:35:SER:HA	59:SD:99:ILE:HG13	2.02	0.41
71:SP:130:ARG:HA	71:SP:131:PRO:HD3	1.91	0.41
72:SQ:100:VAL:HG12	72:SQ:101:ASP:H	1.85	0.41
74:SS:51:ASP:HB3	74:SS:54:LYS:HG3	2.03	0.41
79:SX:100:VAL:HG12	79:SX:125:VAL:HA	2.03	0.41
88:Sg:244:ASN:OD1	88:Sg:245:ARG:N	2.54	0.41
5:L5:136:C:N4	40:Lh:79:LYS:HE3	2.36	0.41
5:L5:3599:A:H2'	5:L5:3600:G:C8	2.56	0.41
5:L5:3910:C:H2'	5:L5:3911:C:C6	2.55	0.41
11:LD:117:LYS:HA	11:LD:117:LYS:HD3	1.81	0.41
30:LX:156:ILE:HA	54:NM:316:ARG:HH12	1.85	0.41
32:LZ:121:ARG:HH11	32:LZ:127:ASN:ND2	2.19	0.41
54:NM:424:ASN:OD1	54:NM:424:ASN:N	2.53	0.41
55:S2:1507:G:N3	87:Sf:89:LYS:NZ	2.68	0.41
60:SE:126:VAL:HA	60:SE:141:THR:HA	2.02	0.41
4:CZ:78:VAL:HG21	22:LP:133:HIS:HB3	2.02	0.41
5:L5:85:G:O2'	5:L5:97:G:O6	2.29	0.41
5:L5:422:C:H2'	5:L5:423:G:H8	1.86	0.41
5:L5:1578:U:H2'	5:L5:1579:C:C6	2.56	0.41
5:L5:3940:U:H5''	14:LG:75:LYS:HD2	2.02	0.41
5:L5:4389:C:H2'	5:L5:4390:A:C8	2.56	0.41
8:LA:206:PRO:HG3	8:LA:213:GLY:HA3	2.03	0.41
9:LB:50:LYS:HB2	9:LB:345:LEU:HD11	2.02	0.41
13:LF:161:LYS:HB3	13:LF:161:LYS:HE3	1.98	0.41
18:LL:119:GLU:HG2	18:LL:155:MET:HE3	2.03	0.41
20:LN:22:LEU:HD23	20:LN:22:LEU:HA	1.84	0.41
23:LQ:59:PRO:HG3	23:LQ:143:ARG:HA	2.03	0.41
23:LQ:69:LYS:HD3	23:LQ:69:LYS:HA	1.83	0.41
28:LV:42:VAL:HB	28:LV:45:ILE:HG13	2.03	0.41
39:Lg:8:ARG:HB2	39:Lg:34:TYR:HE1	1.86	0.41
39:Lg:105:LYS:HE3	39:Lg:105:LYS:HB3	1.89	0.41
55:S2:329:G:H2'	55:S2:330:G:C8	2.55	0.41
55:S2:688:U:OP1	63:SH:116:ARG:NH2	2.49	0.41
55:S2:1628:C:H2'	55:S2:1629:C:H6	1.86	0.41
88:Sg:288:SER:O	88:Sg:300:ALA:HA	2.21	0.41
2:CP:66:C:H2'	2:CP:67:G:H8	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CR:226:LEU:O	3:CR:253:LEU:HA	2.21	0.41
3:CR:395:LYS:HD2	3:CR:396:SER:N	2.35	0.41
5:L5:184:U:H1'	5:L5:254:G:H22	1.86	0.41
5:L5:267:G:H2'	5:L5:268:G:C8	2.56	0.41
5:L5:347:A:H2'	5:L5:348:G:C8	2.55	0.41
5:L5:959:G:C5	12:LE:123:ARG:HG3	2.55	0.41
5:L5:1538:U:H2'	5:L5:1539:G:H8	1.86	0.41
5:L5:1617:G:H1'	5:L5:2513:A:N6	2.36	0.41
5:L5:1961:G:N2	5:L5:2024:G:O2'	2.54	0.41
5:L5:2318:G:N2	5:L5:2321:G:OP2	2.40	0.41
5:L5:2412:A:H2'	5:L5:2413:U:C6	2.56	0.41
5:L5:2864:A:H2'	5:L5:2865:U:C6	2.55	0.41
5:L5:3680:U:OP1	8:LA:54:ARG:NH2	2.37	0.41
5:L5:4364:G:H2'	5:L5:4365:C:H6	1.85	0.41
5:L5:4522:G:O2'	5:L5:4525:C:OP2	2.30	0.41
8:LA:245:ARG:H	8:LA:245:ARG:HG3	1.67	0.41
9:LB:56:ILE:HD13	9:LB:365:LEU:HD22	2.03	0.41
9:LB:80:GLU:OE1	9:LB:323:TYR:OH	2.37	0.41
12:LE:209:PRO:HB2	12:LE:211:HIS:CE1	2.55	0.41
16:LI:76:MET:HE2	16:LI:138:ILE:HG21	2.02	0.41
19:LM:86:TRP:CE2	19:LM:92:ALA:HB2	2.55	0.41
32:LZ:92:ASP:HB3	32:LZ:95:VAL:HG12	2.03	0.41
33:La:75:LEU:HD23	33:La:75:LEU:HA	1.91	0.41
36:Ld:32:ARG:HB3	36:Ld:48:GLU:HG3	2.03	0.41
43:Lk:35:LYS:HA	43:Lk:43:TYR:O	2.20	0.41
44:Ll:38:ASN:HB3	44:Ll:41:ARG:HG2	2.03	0.41
50:Ls:58:ASN:HB3	50:Ls:62:ARG:HH12	1.86	0.41
53:NB:154:ASP:O	53:NB:158:LYS:HB2	2.19	0.41
54:Nm:165:ASP:OD1	54:Nm:165:ASP:N	2.53	0.41
54:Nm:315:SER:HB3	54:Nm:318:MET:HG3	2.02	0.41
54:Nm:337:GLY:HA2	54:Nm:339:ARG:HH21	1.86	0.41
55:S2:35:C:H5''	55:S2:579:C:H5''	2.02	0.41
55:S2:186:C:H2'	55:S2:187:G:C8	2.56	0.41
55:S2:634:A:H2'	55:S2:635:G:H8	1.85	0.41
55:S2:634:A:H2'	55:S2:635:G:C8	2.56	0.41
55:S2:689:U:H2'	55:S2:690:G:O4'	2.20	0.41
55:S2:833:C:H2'	55:S2:834:C:C6	2.56	0.41
55:S2:1627:C:H2'	55:S2:1628:C:H6	1.86	0.41
56:SA:76:VAL:HG23	56:SA:98:PRO:HA	2.03	0.41
61:SF:145:ARG:HB2	84:Sc:48:GLY:HA3	2.03	0.41
61:SF:154:LEU:HD22	61:SF:177:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SH:72:PHE:O	63:SH:75:ILE:O	2.38	0.41
64:SI:119:LEU:HD23	64:SI:119:LEU:HA	1.89	0.41
68:SM:52:LEU:HD23	68:SM:65:VAL:HG21	2.03	0.41
68:SM:86:GLY:HA2	68:SM:106:CYS:HB3	2.02	0.41
69:SN:33:VAL:HG21	69:SN:66:VAL:HG11	2.03	0.41
74:SS:115:LYS:C	74:SS:117:ILE:H	2.29	0.41
79:SX:9:THR:O	79:SX:11:ARG:N	2.53	0.41
82:Sa:26:CYS:SG	82:Sa:28:ARG:HB2	2.61	0.41
87:Sf:114:ILE:HD12	87:Sf:114:ILE:HA	1.89	0.41
88:Sg:87:LEU:HD11	88:Sg:122:SER:HB3	2.02	0.41
5:L5:1828:C:H1'	34:Lb:57:MET:HE2	2.03	0.41
13:LF:147:LEU:O	13:LF:151:ASN:ND2	2.50	0.41
20:LN:84:PRO:HA	20:LN:87:HIS:CG	2.55	0.41
25:LS:80:ILE:HG12	25:LS:129:VAL:HG13	2.03	0.41
30:LX:129:ARG:HD2	30:LX:135:LYS:HE2	2.03	0.41
37:Le:105:SER:HA	37:Le:108:ARG:HG2	2.02	0.41
38:Lf:43:LEU:HD12	38:Lf:43:LEU:HA	1.88	0.41
50:Ls:30:VAL:HG21	50:Ls:187:LEU:HG	2.02	0.41
50:Ls:209:GLU:HA	50:Ls:212:HIS:CD2	2.56	0.41
54:NM:324:MET:O	54:NM:328:ARG:HG2	2.21	0.41
55:S2:388:U:H2'	55:S2:389:A:C8	2.55	0.41
58:SC:66:LEU:HD11	58:SC:81:ILE:HG21	2.03	0.41
58:SC:196:ILE:HB	58:SC:223:TYR:HB2	2.02	0.41
67:SL:111:VAL:HG12	67:SL:140:PHE:HB2	2.03	0.41
75:ST:116:ASP:OD1	75:ST:116:ASP:N	2.54	0.41
3:CR:316:ALA:O	3:CR:414:ARG:N	2.46	0.40
5:L5:153:G:H2'	5:L5:154:G:C8	2.57	0.40
5:L5:369:G:N2	5:L5:372:A:OP2	2.46	0.40
5:L5:729:G:H5''	13:LF:76:ARG:HD2	2.03	0.40
5:L5:1552:G:O2'	5:L5:1574:G:N2	2.41	0.40
5:L5:1733:G:N3	5:L5:4214:A:H2'	2.36	0.40
5:L5:3642:A:C4	42:Lj:3:LYS:HB3	2.56	0.40
5:L5:4128:A:H3'	5:L5:4129:G:H8	1.85	0.40
6:L7:24:C:H2'	6:L7:25:G:O4'	2.21	0.40
9:LB:103:LYS:HD2	9:LB:103:LYS:HA	1.93	0.40
16:LI:51:HIS:ND1	16:LI:137:SER:OG	2.50	0.40
16:LI:93:PRO:HB2	16:LI:125:THR:HB	2.02	0.40
21:LO:174:LEU:HA	21:LO:174:LEU:HD12	1.87	0.40
22:LP:64:ASN:ND2	22:LP:80:GLN:OE1	2.39	0.40
35:Lc:26:LYS:HB2	35:Lc:26:LYS:HE2	1.85	0.40
55:S2:4:C:H4'	58:SC:207:ALA:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:S2:935:G:O2'	69:SN:108:ASP:OD1	2.36	0.40
55:S2:948:C:H2'	55:S2:949:G:H8	1.87	0.40
55:S2:1454:A:N1	55:S2:1476:A:O2'	2.35	0.40
57:SB:198:GLU:HG2	57:SB:210:VAL:HB	2.03	0.40
58:SC:176:LYS:HD2	58:SC:176:LYS:HA	1.75	0.40
66:SK:20:VAL:HA	66:SK:69:TRP:O	2.21	0.40
5:L5:684:G:H5''	5:L5:685:C:C5	2.56	0.40
5:L5:1307:A:H2'	5:L5:1308:C:C6	2.55	0.40
5:L5:1397:A:N1	5:L5:1498:G:O2'	2.53	0.40
5:L5:3775:A:H5'	5:L5:3776:G:OP2	2.21	0.40
5:L5:4208:U:OP1	5:L5:4334:U:O2'	2.32	0.40
5:L5:4344:U:H2'	5:L5:4345:C:C6	2.57	0.40
10:LC:60:HIS:HA	10:LC:92:PHE:HE1	1.86	0.40
12:LE:282:TYR:HA	12:LE:283:PRO:HD3	1.95	0.40
16:LI:82:ARG:H	16:LI:82:ARG:HG3	1.66	0.40
27:LU:67:LYS:HE2	27:LU:67:LYS:HB2	1.78	0.40
33:La:28:HIS:CD2	33:La:32:ARG:HG3	2.56	0.40
37:Le:5:ARG:HH11	37:Le:5:ARG:HG3	1.87	0.40
51:Lt:144:ASP:O	51:Lt:146:ARG:NE	2.50	0.40
54:NM:371:VAL:HA	54:NM:375:PHE:CE1	2.56	0.40
55:S2:223:C:H2'	55:S2:224:A:C8	2.56	0.40
55:S2:1010:G:H2'	55:S2:1011:A:H8	1.87	0.40
55:S2:1355:C:O3'	58:SC:238:LYS:NZ	2.55	0.40
55:S2:1606:G:H5''	75:ST:87:VAL:N	2.36	0.40
58:SC:172:ASN:OD1	58:SC:172:ASN:N	2.54	0.40
69:SN:84:LEU:HD12	69:SN:84:LEU:HA	1.90	0.40
82:Sa:22:ARG:HA	82:Sa:22:ARG:HD2	1.90	0.40
88:Sg:242:SER:HB2	88:Sg:291:TRP:CE2	2.56	0.40
3:CR:87:LYS:HE3	3:CR:87:LYS:HB3	1.60	0.40
3:CR:106:LYS:HA	3:CR:106:LYS:HD3	1.70	0.40
3:CR:330:ARG:HD2	3:CR:330:ARG:HA	1.79	0.40
5:L5:2099:G:P	13:LF:31:LYS:HZ1	2.43	0.40
5:L5:2543:A:H2	5:L5:2773:G:H22	1.70	0.40
5:L5:2621:A:OP1	27:LU:80:LYS:NZ	2.50	0.40
5:L5:2664:G:H4'	5:L5:2677:G:H4'	2.03	0.40
5:L5:4940:C:OP2	12:LE:219:LYS:NZ	2.36	0.40
10:LC:150:LEU:HD12	10:LC:150:LEU:HA	1.85	0.40
11:LD:216:GLU:O	11:LD:220:LYS:HG2	2.21	0.40
22:LP:33:ALA:HB1	22:LP:117:ILE:HG12	2.04	0.40
28:LV:48:ARG:HG3	28:LV:49:LEU:H	1.85	0.40
36:Ld:36:VAL:HG21	36:Ld:44:ARG:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:NM:445:LYS:H	54:NM:445:LYS:HD3	1.85	0.40
55:S2:929:G:H2'	55:S2:930:C:O4'	2.21	0.40
65:SJ:137:VAL:HG12	65:SJ:138:ARG:H	1.85	0.40
66:SK:64:TRP:CD1	85:Sd:23:VAL:HG13	2.56	0.40
74:SS:60:THR:O	74:SS:64:VAL:HG23	2.20	0.40
75:ST:64:LEU:HD23	75:ST:64:LEU:HA	1.84	0.40
77:SV:73:ALA:HB1	77:SV:78:ILE:HB	2.02	0.40
3:CR:362:THR:HG23	3:CR:364:GLN:H	1.86	0.40
5:L5:19:G:P	40:Lh:93:ARG:HE	2.45	0.40
5:L5:1725:U:H2'	5:L5:1726:U:H6	1.85	0.40
5:L5:1933:G:H2'	5:L5:1934:A:C8	2.56	0.40
5:L5:5024:C:N4	5:L5:5028:G:H21	2.19	0.40
8:LA:30:ARG:HG2	8:LA:74:GLU:HG3	2.04	0.40
8:LA:248:GLY:HA2	55:S2:1044:G:C6	2.57	0.40
11:LD:182:GLY:HA2	11:LD:194:VAL:HB	2.03	0.40
17:LJ:40:LEU:HD23	17:LJ:40:LEU:HA	1.97	0.40
21:LO:179:LYS:HA	21:LO:179:LYS:HD3	1.78	0.40
23:LQ:43:PHE:CD2	23:LQ:133:GLY:HA3	2.57	0.40
32:LZ:103:ASP:HA	32:LZ:104:PRO:HD3	1.91	0.40
54:NM:366:MET:HE1	54:NM:370:GLU:HB3	2.03	0.40
55:S2:385:G:H3'	67:SL:136:LYS:HB2	2.03	0.40
55:S2:639:C:H2'	55:S2:640:A:H8	1.86	0.40
55:S2:846:G:OP2	60:SE:108:ARG:NH1	2.46	0.40
76:SU:67:LYS:HA	85:Sd:44:ARG:HD2	2.03	0.40
2:CP:37:U:O2'	55:S2:1058:A:OP1	2.36	0.40
3:CR:330:ARG:NH1	3:CR:344:LEU:H	2.19	0.40
5:L5:1787:A:N3	5:L5:4210:U:O2'	2.53	0.40
5:L5:3857:G:H5''	22:LP:86:LYS:HB2	2.04	0.40
5:L5:3861:A:H2'	5:L5:3862:A:C8	2.56	0.40
36:Ld:22:THR:HG22	36:Ld:122:VAL:HB	2.03	0.40
37:Le:109:LYS:HB2	37:Le:109:LYS:HE2	1.80	0.40
51:Lt:147:HIS:HA	51:Lt:148:PRO:HD3	1.88	0.40
54:NM:243:VAL:HG11	54:NM:271:VAL:HG21	2.03	0.40
55:S2:1101:U:H2'	55:S2:1102:G:C8	2.56	0.40
57:SB:217:MET:HE2	57:SB:217:MET:HB2	1.79	0.40
71:SP:24:GLN:H	71:SP:24:GLN:HG2	1.65	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CR	411/437 (94%)	403 (98%)	8 (2%)	0	100	100
4	CZ	76/95 (80%)	67 (88%)	8 (10%)	1 (1%)	9	13
8	LA	246/257 (96%)	230 (94%)	16 (6%)	0	100	100
9	LB	393/403 (98%)	373 (95%)	20 (5%)	0	100	100
10	LC	362/427 (85%)	342 (94%)	19 (5%)	1 (0%)	36	49
11	LD	291/297 (98%)	270 (93%)	21 (7%)	0	100	100
12	LE	213/288 (74%)	191 (90%)	22 (10%)	0	100	100
13	LF	223/248 (90%)	213 (96%)	10 (4%)	0	100	100
14	LG	225/266 (85%)	212 (94%)	13 (6%)	0	100	100
15	LH	188/192 (98%)	177 (94%)	11 (6%)	0	100	100
16	LI	203/214 (95%)	193 (95%)	10 (5%)	0	100	100
17	LJ	167/178 (94%)	164 (98%)	3 (2%)	0	100	100
18	LL	203/211 (96%)	191 (94%)	12 (6%)	0	100	100
19	LM	137/215 (64%)	132 (96%)	5 (4%)	0	100	100
20	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
21	LO	198/203 (98%)	194 (98%)	4 (2%)	0	100	100
22	LP	151/184 (82%)	142 (94%)	9 (6%)	0	100	100
23	LQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
24	LR	174/196 (89%)	173 (99%)	1 (1%)	0	100	100
25	LS	173/176 (98%)	165 (95%)	8 (5%)	0	100	100
26	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
27	LU	99/128 (77%)	94 (95%)	5 (5%)	0	100	100
28	LV	129/140 (92%)	119 (92%)	10 (8%)	0	100	100
29	LW	111/157 (71%)	101 (91%)	10 (9%)	0	100	100
30	LX	118/156 (76%)	115 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	LY	132/145 (91%)	128 (97%)	4 (3%)	0	100	100
32	LZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
33	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
34	Lb	73/159 (46%)	70 (96%)	3 (4%)	0	100	100
35	Lc	95/115 (83%)	92 (97%)	3 (3%)	0	100	100
36	Ld	105/125 (84%)	103 (98%)	2 (2%)	0	100	100
37	Le	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
38	Lf	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
39	Lg	112/117 (96%)	104 (93%)	8 (7%)	0	100	100
40	Lh	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
41	Li	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
42	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
43	Lk	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
44	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
45	Lm	50/128 (39%)	50 (100%)	0	0	100	100
46	Ln	22/25 (88%)	22 (100%)	0	0	100	100
47	Lo	103/106 (97%)	100 (97%)	3 (3%)	0	100	100
48	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
49	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
50	Ls	210/317 (66%)	204 (97%)	6 (3%)	0	100	100
51	Lt	158/165 (96%)	156 (99%)	2 (1%)	0	100	100
52	NA	65/215 (30%)	57 (88%)	8 (12%)	0	100	100
53	NB	120/162 (74%)	107 (89%)	13 (11%)	0	100	100
54	NM	394/496 (79%)	378 (96%)	16 (4%)	0	100	100
56	SA	214/295 (72%)	202 (94%)	12 (6%)	0	100	100
57	SB	211/264 (80%)	202 (96%)	9 (4%)	0	100	100
58	SC	217/293 (74%)	207 (95%)	10 (5%)	0	100	100
59	SD	219/243 (90%)	207 (94%)	12 (6%)	0	100	100
60	SE	260/263 (99%)	252 (97%)	8 (3%)	0	100	100
61	SF	177/204 (87%)	167 (94%)	9 (5%)	1 (1%)	21	30
62	SG	229/249 (92%)	213 (93%)	14 (6%)	2 (1%)	14	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	SH	179/194 (92%)	168 (94%)	11 (6%)	0	100	100
64	SI	204/208 (98%)	197 (97%)	7 (3%)	0	100	100
65	SJ	177/194 (91%)	173 (98%)	4 (2%)	0	100	100
66	SK	94/165 (57%)	88 (94%)	6 (6%)	0	100	100
67	SL	140/158 (89%)	130 (93%)	10 (7%)	0	100	100
68	SM	120/132 (91%)	112 (93%)	8 (7%)	0	100	100
69	SN	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
70	SO	132/151 (87%)	118 (89%)	14 (11%)	0	100	100
71	SP	127/145 (88%)	122 (96%)	5 (4%)	0	100	100
72	SQ	140/146 (96%)	131 (94%)	9 (6%)	0	100	100
73	SR	129/135 (96%)	115 (89%)	14 (11%)	0	100	100
74	SS	139/152 (91%)	118 (85%)	21 (15%)	0	100	100
75	ST	141/145 (97%)	136 (96%)	5 (4%)	0	100	100
76	SU	99/119 (83%)	91 (92%)	8 (8%)	0	100	100
77	SV	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
78	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
79	SX	139/143 (97%)	130 (94%)	8 (6%)	1 (1%)	18	27
80	SY	121/133 (91%)	116 (96%)	5 (4%)	0	100	100
81	SZ	73/125 (58%)	68 (93%)	5 (7%)	0	100	100
82	Sa	97/115 (84%)	91 (94%)	6 (6%)	0	100	100
83	Sb	81/84 (96%)	72 (89%)	9 (11%)	0	100	100
84	Sc	61/69 (88%)	54 (88%)	7 (12%)	0	100	100
85	Sd	51/56 (91%)	51 (100%)	0	0	100	100
86	Se	53/133 (40%)	51 (96%)	2 (4%)	0	100	100
87	Sf	61/156 (39%)	55 (90%)	5 (8%)	1 (2%)	7	10
88	Sg	304/317 (96%)	276 (91%)	28 (9%)	0	100	100
All	All	12559/14649 (86%)	11898 (95%)	654 (5%)	7 (0%)	49	63

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CZ	48	THR
10	LC	111	TRP

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Mol	Chain	Res	Type
61	SF	80	GLY
79	SX	10	ALA
87	Sf	128	ALA
62	SG	33	ALA
62	SG	130	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CR	356/375 (95%)	347 (98%)	9 (2%)	42	62
4	CZ	25/83 (30%)	24 (96%)	1 (4%)	28	45
8	LA	190/199 (96%)	182 (96%)	8 (4%)	26	43
9	LB	343/349 (98%)	337 (98%)	6 (2%)	53	73
10	LC	299/348 (86%)	294 (98%)	5 (2%)	53	73
11	LD	241/250 (96%)	235 (98%)	6 (2%)	42	62
12	LE	191/252 (76%)	183 (96%)	8 (4%)	26	43
13	LF	194/215 (90%)	189 (97%)	5 (3%)	40	61
14	LG	188/223 (84%)	182 (97%)	6 (3%)	34	54
15	LH	167/171 (98%)	159 (95%)	8 (5%)	23	38
16	LI	174/181 (96%)	171 (98%)	3 (2%)	53	73
17	LJ	136/149 (91%)	132 (97%)	4 (3%)	37	57
18	LL	164/177 (93%)	160 (98%)	4 (2%)	43	63
19	LM	114/161 (71%)	110 (96%)	4 (4%)	32	51
20	LN	171/172 (99%)	167 (98%)	4 (2%)	44	64
21	LO	170/174 (98%)	165 (97%)	5 (3%)	37	57
22	LP	132/163 (81%)	129 (98%)	3 (2%)	44	64
23	LQ	161/165 (98%)	158 (98%)	3 (2%)	50	70
24	LR	150/175 (86%)	148 (99%)	2 (1%)	61	78
25	LS	156/157 (99%)	154 (99%)	2 (1%)	61	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	LT	135/140 (96%)	131 (97%)	4 (3%)	36	56
27	LU	86/115 (75%)	83 (96%)	3 (4%)	32	51
28	LV	99/107 (92%)	97 (98%)	2 (2%)	48	68
29	LW	61/126 (48%)	60 (98%)	1 (2%)	55	74
30	LX	107/133 (80%)	106 (99%)	1 (1%)	70	84
31	LY	123/135 (91%)	118 (96%)	5 (4%)	27	44
32	LZ	117/118 (99%)	112 (96%)	5 (4%)	26	42
33	La	118/121 (98%)	112 (95%)	6 (5%)	21	35
34	Lb	59/126 (47%)	59 (100%)	0	100	100
35	Lc	79/97 (81%)	77 (98%)	2 (2%)	42	62
36	Ld	94/110 (86%)	92 (98%)	2 (2%)	47	67
37	Le	113/121 (93%)	110 (97%)	3 (3%)	39	60
38	Lf	87/89 (98%)	84 (97%)	3 (3%)	32	52
39	Lg	93/100 (93%)	91 (98%)	2 (2%)	45	66
40	Lh	108/110 (98%)	107 (99%)	1 (1%)	70	84
41	Li	81/89 (91%)	80 (99%)	1 (1%)	63	79
42	Lj	73/80 (91%)	72 (99%)	1 (1%)	59	77
43	Lk	57/65 (88%)	51 (90%)	6 (10%)	6	9
44	Ll	47/48 (98%)	45 (96%)	2 (4%)	26	42
45	Lm	47/116 (40%)	47 (100%)	0	100	100
46	Ln	23/24 (96%)	23 (100%)	0	100	100
47	Lo	93/94 (99%)	91 (98%)	2 (2%)	45	66
48	Lp	71/75 (95%)	70 (99%)	1 (1%)	59	77
49	Lr	107/121 (88%)	103 (96%)	4 (4%)	30	49
50	Ls	180/258 (70%)	171 (95%)	9 (5%)	22	36
51	Lt	132/137 (96%)	122 (92%)	10 (8%)	12	19
52	NA	60/183 (33%)	56 (93%)	4 (7%)	15	24
53	NB	104/136 (76%)	97 (93%)	7 (7%)	15	24
54	NM	353/443 (80%)	348 (99%)	5 (1%)	59	77
56	SA	170/243 (70%)	162 (95%)	8 (5%)	23	39
57	SB	191/231 (83%)	188 (98%)	3 (2%)	55	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	SC	175/225 (78%)	171 (98%)	4 (2%)	44	64
59	SD	148/202 (73%)	145 (98%)	3 (2%)	48	68
60	SE	196/225 (87%)	193 (98%)	3 (2%)	57	75
61	SF	142/170 (84%)	140 (99%)	2 (1%)	59	77
62	SG	138/218 (63%)	130 (94%)	8 (6%)	18	30
63	SH	109/174 (63%)	107 (98%)	2 (2%)	51	71
64	SI	149/180 (83%)	145 (97%)	4 (3%)	39	60
65	SJ	143/168 (85%)	142 (99%)	1 (1%)	76	87
66	SK	65/136 (48%)	63 (97%)	2 (3%)	35	55
67	SL	121/142 (85%)	117 (97%)	4 (3%)	33	53
68	SM	104/108 (96%)	101 (97%)	3 (3%)	37	57
69	SN	123/131 (94%)	122 (99%)	1 (1%)	73	85
70	SO	95/119 (80%)	90 (95%)	5 (5%)	20	34
71	SP	98/130 (75%)	95 (97%)	3 (3%)	35	55
72	SQ	103/121 (85%)	98 (95%)	5 (5%)	22	37
73	SR	84/122 (69%)	78 (93%)	6 (7%)	13	22
74	SS	112/132 (85%)	110 (98%)	2 (2%)	51	71
75	ST	105/115 (91%)	100 (95%)	5 (5%)	23	38
76	SU	68/107 (64%)	65 (96%)	3 (4%)	25	41
77	SV	62/67 (92%)	62 (100%)	0	100	100
78	SW	110/113 (97%)	108 (98%)	2 (2%)	51	71
79	SX	109/115 (95%)	105 (96%)	4 (4%)	30	49
80	SY	86/115 (75%)	79 (92%)	7 (8%)	11	17
81	SZ	56/103 (54%)	53 (95%)	3 (5%)	20	33
82	Sa	83/98 (85%)	82 (99%)	1 (1%)	63	79
83	Sb	65/76 (86%)	62 (95%)	3 (5%)	24	39
84	Sc	51/62 (82%)	47 (92%)	4 (8%)	11	18
85	Sd	44/49 (90%)	42 (96%)	2 (4%)	24	40
86	Se	39/104 (38%)	38 (97%)	1 (3%)	40	61
87	Sf	56/140 (40%)	52 (93%)	4 (7%)	13	22
88	Sg	201/275 (73%)	193 (96%)	8 (4%)	28	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	10230/12472 (82%)	9926 (97%)	304 (3%)	37 56

All (304) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	CR	54	ASP
3	CR	77	SER
3	CR	120	ILE
3	CR	154	SER
3	CR	308	THR
3	CR	328	ILE
3	CR	389	LEU
3	CR	395	LYS
3	CR	409	ILE
4	CZ	88	LEU
8	LA	15	VAL
8	LA	32	VAL
8	LA	36	GLU
8	LA	102	LEU
8	LA	123	ARG
8	LA	128	ARG
8	LA	207	VAL
8	LA	208	GLU
9	LB	38	SER
9	LB	73	VAL
9	LB	159	VAL
9	LB	231	VAL
9	LB	384	GLU
9	LB	392	LEU
10	LC	170	LEU
10	LC	232	VAL
10	LC	255	SER
10	LC	319	LEU
10	LC	334	THR
11	LD	4	VAL
11	LD	59	ASP
11	LD	75	VAL
11	LD	81	HIS
11	LD	118	ILE
11	LD	136	ASP
12	LE	43	HIS
12	LE	106	VAL

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Mol	Chain	Res	Type
12	LE	107	VAL
12	LE	127	SER
12	LE	128	HIS
12	LE	154	THR
12	LE	175	VAL
12	LE	184	VAL
13	LF	44	LYS
13	LF	83	VAL
13	LF	116	GLN
13	LF	187	MET
13	LF	196	THR
14	LG	35	ARG
14	LG	55	VAL
14	LG	89	ARG
14	LG	207	VAL
14	LG	211	ASP
14	LG	241	VAL
15	LH	16	VAL
15	LH	19	THR
15	LH	47	LEU
15	LH	48	LEU
15	LH	111	LEU
15	LH	161	ILE
15	LH	182	SER
15	LH	187	VAL
16	LI	31	ILE
16	LI	43	VAL
16	LI	48	LEU
17	LJ	54	ARG
17	LJ	63	ARG
17	LJ	102	THR
17	LJ	148	THR
18	LL	64	VAL
18	LL	70	VAL
18	LL	139	SER
18	LL	164	GLU
19	LM	25	VAL
19	LM	54	CYS
19	LM	55	MET
19	LM	70	GLN
20	LN	18	VAL
20	LN	89	VAL

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Mol	Chain	Res	Type
20	LN	126	THR
20	LN	151	ILE
21	LO	36	VAL
21	LO	118	MET
21	LO	119	VAL
21	LO	127	VAL
21	LO	189	ILE
22	LP	12	THR
22	LP	14	SER
22	LP	20	SER
23	LQ	5	ILE
23	LQ	10	ASP
23	LQ	14	ARG
24	LR	2	SER
24	LR	51	ILE
25	LS	62	VAL
25	LS	124	ILE
26	LT	29	THR
26	LT	43	LYS
26	LT	72	VAL
26	LT	149	GLU
27	LU	62	THR
27	LU	73	THR
27	LU	96	LEU
28	LV	22	VAL
28	LV	57	VAL
29	LW	48	GLN
30	LX	93	ASN
31	LY	9	SER
31	LY	43	ASN
31	LY	120	GLU
31	LY	125	SER
31	LY	127	GLN
32	LZ	26	VAL
32	LZ	53	VAL
32	LZ	60	LYS
32	LZ	66	SER
32	LZ	100	VAL
33	La	17	HIS
33	La	56	VAL
33	La	78	LEU
33	La	120	GLN

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Mol	Chain	Res	Type
33	La	134	GLU
33	La	140	VAL
35	Lc	28	VAL
35	Lc	93	THR
36	Ld	26	THR
36	Ld	46	LEU
37	Le	21	ILE
37	Le	86	GLU
37	Le	117	GLN
38	Lf	24	HIS
38	Lf	67	THR
38	Lf	105	LEU
39	Lg	38	VAL
39	Lg	53	LEU
40	Lh	74	LYS
41	Li	58	MET
42	Lj	22	CYS
43	Lk	10	ASP
43	Lk	12	LEU
43	Lk	28	ASN
43	Lk	36	VAL
43	Lk	46	VAL
43	Lk	67	LYS
44	Ll	29	MET
44	Ll	51	LEU
47	Lo	8	ARG
47	Lo	43	ARG
48	Lp	5	THR
49	Lr	21	ASN
49	Lr	76	SER
49	Lr	78	VAL
49	Lr	80	THR
50	Ls	18	ILE
50	Ls	23	ASP
50	Ls	35	VAL
50	Ls	53	VAL
50	Ls	55	MET
50	Ls	103	LEU
50	Ls	130	LEU
50	Ls	163	THR
50	Ls	192	VAL
51	Lt	6	ASP

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Mol	Chain	Res	Type
51	Lt	28	LEU
51	Lt	32	ILE
51	Lt	38	SER
51	Lt	58	ILE
51	Lt	61	LYS
51	Lt	114	ARG
51	Lt	125	LEU
51	Lt	131	GLU
51	Lt	147	HIS
52	NA	93	ARG
52	NA	105	VAL
52	NA	106	ILE
52	NA	111	VAL
53	NB	10	LYS
53	NB	40	ASP
53	NB	51	LEU
53	NB	67	ASN
53	NB	71	VAL
53	NB	87	THR
53	NB	91	THR
54	NM	280	VAL
54	NM	398	LEU
54	NM	416	LEU
54	NM	432	LEU
54	NM	447	PHE
56	SA	76	VAL
56	SA	104	THR
56	SA	112	ILE
56	SA	113	GLN
56	SA	123	VAL
56	SA	134	LEU
56	SA	157	VAL
56	SA	197	VAL
57	SB	88	THR
57	SB	91	VAL
57	SB	98	THR
58	SC	128	VAL
58	SC	163	VAL
58	SC	206	SER
58	SC	248	TYR
59	SD	84	VAL
59	SD	108	LYS

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Mol	Chain	Res	Type
59	SD	190	LEU
60	SE	26	VAL
60	SE	111	VAL
60	SE	208	VAL
61	SF	171	GLU
61	SF	202	SER
62	SG	26	THR
62	SG	32	MET
62	SG	75	LEU
62	SG	110	ASN
62	SG	129	VAL
62	SG	139	SER
62	SG	179	LEU
62	SG	186	GLN
63	SH	21	SER
63	SH	79	LEU
64	SI	4	SER
64	SI	23	LYS
64	SI	29	LEU
64	SI	73	THR
65	SJ	102	ILE
66	SK	58	VAL
66	SK	61	GLN
67	SL	67	SER
67	SL	79	LYS
67	SL	83	GLN
67	SL	120	VAL
68	SM	49	LEU
68	SM	68	LEU
68	SM	75	ASN
69	SN	134	VAL
70	SO	27	VAL
70	SO	56	VAL
70	SO	81	VAL
70	SO	88	LEU
70	SO	90	ILE
71	SP	22	LEU
71	SP	37	TYR
71	SP	106	GLU
72	SQ	48	GLN
72	SQ	89	SER
72	SQ	111	ILE

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Mol	Chain	Res	Type
72	SQ	119	LEU
72	SQ	120	LEU
73	SR	8	THR
73	SR	16	ILE
73	SR	24	LEU
73	SR	62	GLN
73	SR	102	THR
73	SR	108	LEU
74	SS	99	LEU
74	SS	131	VAL
75	ST	4	VAL
75	ST	5	THR
75	ST	34	VAL
75	ST	87	VAL
75	ST	88	MET
76	SU	81	GLN
76	SU	90	ASP
76	SU	93	SER
78	SW	74	VAL
78	SW	106	THR
79	SX	71	ARG
79	SX	77	ASN
79	SX	123	VAL
79	SX	125	VAL
80	SY	5	VAL
80	SY	9	THR
80	SY	24	VAL
80	SY	26	ASP
80	SY	35	VAL
80	SY	44	LEU
80	SY	50	THR
81	SZ	58	LEU
81	SZ	67	LEU
81	SZ	69	THR
82	Sa	2	THR
83	Sb	44	THR
83	Sb	45	THR
83	Sb	55	LEU
84	Sc	18	LEU
84	Sc	50	VAL
84	Sc	56	LEU
84	Sc	57	THR

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Mol	Chain	Res	Type
85	Sd	30	LEU
85	Sd	38	MET
86	Se	5	SER
87	Sf	98	VAL
87	Sf	140	TYR
87	Sf	144	CYS
87	Sf	149	CYS
88	Sg	18	VAL
88	Sg	64	HIS
88	Sg	166	VAL
88	Sg	174	VAL
88	Sg	186	THR
88	Sg	239	LEU
88	Sg	241	PHE
88	Sg	306	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
3	CR	79	GLN
3	CR	381	ASN
4	CZ	65	ASN
8	LA	22	HIS
8	LA	95	GLN
8	LA	194	ASN
8	LA	205	ASN
9	LB	68	ASN
9	LB	109	HIS
9	LB	121	ASN
9	LB	184	GLN
9	LB	203	GLN
9	LB	213	GLN
9	LB	376	HIS
10	LC	21	ASN
10	LC	61	GLN
10	LC	310	HIS
10	LC	329	ASN
11	LD	131	ASN
11	LD	202	GLN
11	LD	229	ASN
11	LD	282	GLN
13	LF	192	HIS

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Mol	Chain	Res	Type
13	LF	239	GLN
14	LG	100	HIS
14	LG	112	GLN
15	LH	8	GLN
15	LH	98	HIS
15	LH	116	ASN
15	LH	138	GLN
16	LI	123	GLN
18	LL	111	GLN
19	LM	78	GLN
19	LM	131	GLN
20	LN	32	GLN
20	LN	149	GLN
21	LO	50	ASN
21	LO	167	HIS
21	LO	180	GLN
22	LP	75	GLN
23	LQ	44	ASN
25	LS	173	ASN
26	LT	3	ASN
28	LV	27	ASN
28	LV	50	ASN
30	LX	125	ASN
30	LX	151	ASN
31	LY	14	ASN
31	LY	56	GLN
31	LY	66	GLN
31	LY	72	GLN
32	LZ	127	ASN
32	LZ	132	GLN
34	Lb	6	ASN
35	Lc	15	ASN
36	Ld	79	ASN
36	Ld	100	ASN
37	Le	117	GLN
42	Lj	30	GLN
44	Ll	4	HIS
44	Ll	17	GLN
44	Ll	25	GLN
47	Lo	105	GLN
49	Lr	36	ASN
50	Ls	68	HIS

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Mol	Chain	Res	Type
50	Ls	159	GLN
50	Ls	191	GLN
51	Lt	65	GLN
52	NA	87	GLN
52	NA	134	GLN
53	NB	7	ASN
53	NB	67	ASN
53	NB	108	ASN
54	NM	135	HIS
54	NM	147	GLN
54	NM	380	ASN
56	SA	29	ASN
56	SA	33	GLN
56	SA	84	GLN
56	SA	110	ASN
56	SA	113	GLN
57	SB	159	GLN
57	SB	177	GLN
58	SC	113	GLN
58	SC	115	GLN
59	SD	101	GLN
61	SF	82	ASN
61	SF	118	ASN
62	SG	177	GLN
62	SG	186	GLN
64	SI	52	ASN
64	SI	165	GLN
65	SJ	113	GLN
65	SJ	154	GLN
67	SL	19	ASN
67	SL	94	HIS
68	SM	55	ASN
68	SM	72	HIS
68	SM	82	ASN
69	SN	62	GLN
69	SN	69	ASN
71	SP	103	ASN
72	SQ	11	GLN
74	SS	87	GLN
75	ST	85	ASN
79	SX	77	ASN
79	SX	127	ASN

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Mol	Chain	Res	Type
80	SY	15	ASN
80	SY	22	GLN
80	SY	89	HIS
83	Sb	51	GLN
84	Sc	7	GLN
84	Sc	29	GLN
86	Se	37	GLN
88	Sg	237	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CM	11/586 (1%)	2 (18%)	0
2	CP	74/75 (98%)	24 (32%)	2 (2%)
5	L5	3633/5070 (71%)	741 (20%)	14 (0%)
55	S2	1704/1869 (91%)	467 (27%)	16 (0%)
6	L7	119/121 (98%)	11 (9%)	0
7	L8	155/157 (98%)	25 (16%)	1 (0%)
All	All	5696/7878 (72%)	1270 (22%)	33 (0%)

All (1270) 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	35	G
2	CP	46	U
2	CP	49	C
2	CP	50	G
2	CP	57	A

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Mol	Chain	Res	Type
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
5	L5	17	A
5	L5	21	G
5	L5	25	A
5	L5	30	C
5	L5	39	A
5	L5	42	A
5	L5	48	G
5	L5	56	A
5	L5	59	A
5	L5	64	A
5	L5	65	A
5	L5	69	A
5	L5	72	C
5	L5	73	A
5	L5	91	G
5	L5	98	A
5	L5	104	G
5	L5	108	A
5	L5	109	G
5	L5	110	C
5	L5	116	G
5	L5	117	C
5	L5	119	G
5	L5	120	A
5	L5	133	C
5	L5	134	G
5	L5	135	G
5	L5	136	C
5	L5	137	G
5	L5	144	G
5	L5	152	U
5	L5	159	C
5	L5	165	A
5	L5	172	C

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Mol	Chain	Res	Type
5	L5	180	C
5	L5	183	C
5	L5	184	U
5	L5	185	C
5	L5	188	G
5	L5	189	G
5	L5	200	U
5	L5	210	C
5	L5	216	C
5	L5	217	C
5	L5	218	A
5	L5	233	U
5	L5	234	G
5	L5	254	G
5	L5	255	C
5	L5	261	G
5	L5	266	C
5	L5	267	G
5	L5	269	G
5	L5	280	G
5	L5	297	U
5	L5	306	A
5	L5	315	G
5	L5	316	U
5	L5	340	C
5	L5	349	A
5	L5	350	C
5	L5	387	G
5	L5	388	A
5	L5	399	G
5	L5	407	A
5	L5	409	G
5	L5	410	A
5	L5	411	G
5	L5	412	G
5	L5	449	C
5	L5	450	G
5	L5	452	A
5	L5	453	G
5	L5	454	U
5	L5	456	C
5	L5	457	G

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Mol	Chain	Res	Type
5	L5	461	G
5	L5	467	U
5	L5	474	C
5	L5	485	C
5	L5	486	C
5	L5	489	C
5	L5	493	G
5	L5	494	U
5	L5	497	G
5	L5	498	C
5	L5	500	G
5	L5	501	C
5	L5	502	C
5	L5	503	C
5	L5	504	G
5	L5	505	G
5	L5	509	A
5	L5	510	U
5	L5	511	C
5	L5	512	U
5	L5	513	U
5	L5	514	U
5	L5	517	C
5	L5	518	G
5	L5	643	C
5	L5	644	G
5	L5	646	G
5	L5	654	C
5	L5	655	C
5	L5	656	C
5	L5	657	C
5	L5	658	C
5	L5	660	A
5	L5	666	G
5	L5	667	A
5	L5	668	C
5	L5	669	C
5	L5	673	C
5	L5	674	G
5	L5	675	C
5	L5	676	C
5	L5	684	G

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Mol	Chain	Res	Type
5	L5	685	C
5	L5	686	A
5	L5	687	U
5	L5	688	U
5	L5	692	A
5	L5	696	C
5	L5	697	G
5	L5	703	G
5	L5	704	C
5	L5	708	G
5	L5	730	G
5	L5	731	G
5	L5	738	C
5	L5	739	G
5	L5	740	G
5	L5	742	G
5	L5	746	A
5	L5	747	A
5	L5	758	G
5	L5	759	G
5	L5	904	C
5	L5	907	C
5	L5	912	G
5	L5	913	U
5	L5	914	U
5	L5	915	A
5	L5	916	C
5	L5	917	A
5	L5	918	G
5	L5	923	C
5	L5	924	C
5	L5	926	G
5	L5	929	A
5	L5	932	A
5	L5	933	G
5	L5	936	C
5	L5	945	U
5	L5	946	C
5	L5	956	A
5	L5	958	G
5	L5	959	G
5	L5	960	A

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Mol	Chain	Res	Type
5	L5	961	G
5	L5	962	C
5	L5	965	G
5	L5	966	A
5	L5	967	C
5	L5	968	C
5	L5	970	G
5	L5	972	C
5	L5	977	C
5	L5	984	C
5	L5	985	C
5	L5	988	C
5	L5	989	U
5	L5	990	C
5	L5	991	C
5	L5	992	C
5	L5	993	G
5	L5	1069	G
5	L5	1070	G
5	L5	1075	G
5	L5	1083	U
5	L5	1168	G
5	L5	1171	G
5	L5	1173	G
5	L5	1178	G
5	L5	1179	U
5	L5	1180	C
5	L5	1181	C
5	L5	1182	C
5	L5	1183	C
5	L5	1184	A
5	L5	1187	G
5	L5	1193	C
5	L5	1196	G
5	L5	1202	C
5	L5	1203	G
5	L5	1209	U
5	L5	1211	G
5	L5	1214	C
5	L5	1215	C
5	L5	1235	G
5	L5	1238	A

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Mol	Chain	Res	Type
5	L5	1241	C
5	L5	1253	G
5	L5	1259	G
5	L5	1260	G
5	L5	1261	G
5	L5	1266	G
5	L5	1269	G
5	L5	1270	A
5	L5	1271	G
5	L5	1272	C
5	L5	1273	G
5	L5	1274	A
5	L5	1275	G
5	L5	1277	G
5	L5	1280	C
5	L5	1284	G
5	L5	1285	U
5	L5	1287	G
5	L5	1293	G
5	L5	1294	A
5	L5	1295	C
5	L5	1301	C
5	L5	1302	U
5	L5	1303	A
5	L5	1304	C
5	L5	1312	A
5	L5	1326	A
5	L5	1337	A
5	L5	1344	C
5	L5	1354	A
5	L5	1358	G
5	L5	1359	G
5	L5	1365	C
5	L5	1366	G
5	L5	1378	C
5	L5	1379	C
5	L5	1387	A
5	L5	1393	G
5	L5	1394	G
5	L5	1397	A
5	L5	1398	A
5	L5	1403	G

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Mol	Chain	Res	Type
5	L5	1404	G
5	L5	1405	C
5	L5	1408	G
5	L5	1410	U
5	L5	1420	A
5	L5	1425	G
5	L5	1435	G
5	L5	1437	C
5	L5	1439	C
5	L5	1441	C
5	L5	1442	C
5	L5	1443	A
5	L5	1444	G
5	L5	1447	C
5	L5	1454	G
5	L5	1457	G
5	L5	1480	C
5	L5	1482	G
5	L5	1483	C
5	L5	1497	A
5	L5	1498	G
5	L5	1502	G
5	L5	1534	A
5	L5	1547	A
5	L5	1564	A
5	L5	1566	C
5	L5	1578	U
5	L5	1591	U
5	L5	1596	U
5	L5	1624	G
5	L5	1625	G
5	L5	1631	A
5	L5	1633	G
5	L5	1634	A
5	L5	1640	C
5	L5	1641	G
5	L5	1642	A
5	L5	1654	G
5	L5	1656	U
5	L5	1661	C
5	L5	1663	C
5	L5	1676	C

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Mol	Chain	Res	Type
5	L5	1677	U
5	L5	1685	G
5	L5	1691	G
5	L5	1694	C
5	L5	1697	G
5	L5	1699	A
5	L5	1700	G
5	L5	1704	C
5	L5	1705	G
5	L5	1707	C
5	L5	1731	C
5	L5	1734	G
5	L5	1735	U
5	L5	1742	A
5	L5	1750	G
5	L5	1753	G
5	L5	1756	U
5	L5	1758	G
5	L5	1760	G
5	L5	1765	A
5	L5	1767	A
5	L5	1785	C
5	L5	1787	A
5	L5	1803	G
5	L5	1804	A
5	L5	1806	G
5	L5	1810	G
5	L5	1815	G
5	L5	1820	C
5	L5	1821	G
5	L5	1822	U
5	L5	1834	U
5	L5	1836	G
5	L5	1837	A
5	L5	1842	G
5	L5	1843	A
5	L5	1855	G
5	L5	1869	G
5	L5	1882	U
5	L5	1891	A
5	L5	1897	A
5	L5	1898	C

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Mol	Chain	Res	Type
5	L5	1912	G
5	L5	1918	U
5	L5	1919	G
5	L5	1920	C
5	L5	1921	C
5	L5	1922	G
5	L5	1924	C
5	L5	1931	C
5	L5	1932	A
5	L5	1936	C
5	L5	1940	G
5	L5	1948	G
5	L5	1949	U
5	L5	1962	A
5	L5	1965	G
5	L5	1976	G
5	L5	1980	U
5	L5	1981	G
5	L5	1983	A
5	L5	1984	A
5	L5	1985	G
5	L5	1986	U
5	L5	1987	C
5	L5	1997	U
5	L5	2001	G
5	L5	2002	A
5	L5	2004	U
5	L5	2007	G
5	L5	2016	C
5	L5	2017	A
5	L5	2018	C
5	L5	2024	G
5	L5	2025	A
5	L5	2026	A
5	L5	2046	G
5	L5	2048	U
5	L5	2055	G
5	L5	2056	G
5	L5	2069	A
5	L5	2084	C
5	L5	2085	G
5	L5	2092	G

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Mol	Chain	Res	Type
5	L5	2094	G
5	L5	2095	A
5	L5	2098	G
5	L5	2101	C
5	L5	2102	G
5	L5	2103	G
5	L5	2106	G
5	L5	2107	C
5	L5	2108	G
5	L5	2116	C
5	L5	2117	G
5	L5	2118	G
5	L5	2119	C
5	L5	2120	G
5	L5	2121	C
5	L5	2123	C
5	L5	2250	C
5	L5	2252	G
5	L5	2253	A
5	L5	2254	G
5	L5	2255	C
5	L5	2256	C
5	L5	2257	C
5	L5	2258	C
5	L5	2269	C
5	L5	2289	C
5	L5	2300	A
5	L5	2301	G
5	L5	2313	A
5	L5	2316	G
5	L5	2333	G
5	L5	2348	G
5	L5	2351	C
5	L5	2360	A
5	L5	2395	A
5	L5	2397	G
5	L5	2417	A
5	L5	2421	G
5	L5	2422	C
5	L5	2424	G
5	L5	2425	U
5	L5	2441	C

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Mol	Chain	Res	Type
5	L5	2453	A
5	L5	2464	C
5	L5	2465	C
5	L5	2475	G
5	L5	2483	G
5	L5	2484	A
5	L5	2487	G
5	L5	2488	C
5	L5	2489	C
5	L5	2490	U
5	L5	2491	C
5	L5	2493	G
5	L5	2503	G
5	L5	2504	C
5	L5	2505	C
5	L5	2506	G
5	L5	2513	A
5	L5	2519	U
5	L5	2520	C
5	L5	2529	A
5	L5	2537	A
5	L5	2544	G
5	L5	2545	U
5	L5	2546	G
5	L5	2547	G
5	L5	2554	U
5	L5	2555	G
5	L5	2567	G
5	L5	2573	A
5	L5	2583	C
5	L5	2587	A
5	L5	2589	C
5	L5	2601	A
5	L5	2618	G
5	L5	2627	C
5	L5	2638	G
5	L5	2653	C
5	L5	2662	G
5	L5	2669	C
5	L5	2676	A
5	L5	2686	G
5	L5	2687	U

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Mol	Chain	Res	Type
5	L5	2694	G
5	L5	2695	A
5	L5	2696	A
5	L5	2703	G
5	L5	2710	C
5	L5	2711	G
5	L5	2721	G
5	L5	2724	G
5	L5	2726	G
5	L5	2739	C
5	L5	2742	G
5	L5	2743	A
5	L5	2746	A
5	L5	2754	G
5	L5	2761	U
5	L5	2763	U
5	L5	2764	A
5	L5	2770	C
5	L5	2788	U
5	L5	2790	U
5	L5	2814	C
5	L5	2815	A
5	L5	2826	U
5	L5	2827	G
5	L5	2838	G
5	L5	2842	G
5	L5	2848	G
5	L5	2855	G
5	L5	2856	C
5	L5	2877	G
5	L5	2890	C
5	L5	2891	U
5	L5	2892	C
5	L5	2894	A
5	L5	2897	G
5	L5	2900	U
5	L5	2902	G
5	L5	2903	G
5	L5	2904	U
5	L5	2905	C
5	L5	2906	G
5	L5	2907	G

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Mol	Chain	Res	Type
5	L5	2908	U
5	L5	3585	G
5	L5	3586	G
5	L5	3588	C
5	L5	3591	C
5	L5	3593	C
5	L5	3594	C
5	L5	3595	U
5	L5	3596	A
5	L5	3597	G
5	L5	3604	A
5	L5	3605	C
5	L5	3606	U
5	L5	3615	G
5	L5	3618	C
5	L5	3626	G
5	L5	3630	A
5	L5	3635	A
5	L5	3644	U
5	L5	3646	A
5	L5	3662	A
5	L5	3664	G
5	L5	3673	C
5	L5	3674	G
5	L5	3711	A
5	L5	3713	U
5	L5	3727	A
5	L5	3735	G
5	L5	3736	A
5	L5	3748	A
5	L5	3750	G
5	L5	3753	G
5	L5	3761	C
5	L5	3771	C
5	L5	3775	A
5	L5	3776	G
5	L5	3777	G
5	L5	3784	A
5	L5	3786	U
5	L5	3810	C
5	L5	3812	C
5	L5	3814	U

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Mol	Chain	Res	Type
5	L5	3817	A
5	L5	3818	U
5	L5	3819	G
5	L5	3823	G
5	L5	3838	U
5	L5	3839	G
5	L5	3840	U
5	L5	3841	C
5	L5	3851	U
5	L5	3867	A
5	L5	3877	A
5	L5	3878	C
5	L5	3879	G
5	L5	3885	G
5	L5	3892	U
5	L5	3897	G
5	L5	3901	A
5	L5	3905	A
5	L5	3906	A
5	L5	3907	G
5	L5	3908	A
5	L5	3915	U
5	L5	3926	C
5	L5	3942	A
5	L5	3943	A
5	L5	3947	A
5	L5	3949	A
5	L5	4064	C
5	L5	4065	G
5	L5	4076	G
5	L5	4084	G
5	L5	4099	G
5	L5	4102	C
5	L5	4104	G
5	L5	4107	G
5	L5	4111	U
5	L5	4113	U
5	L5	4114	C
5	L5	4115	G
5	L5	4116	C
5	L5	4119	C
5	L5	4122	G

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Mol	Chain	Res	Type
5	L5	4128	A
5	L5	4131	G
5	L5	4137	C
5	L5	4138	C
5	L5	4140	C
5	L5	4141	G
5	L5	4142	C
5	L5	4143	G
5	L5	4145	C
5	L5	4150	G
5	L5	4154	G
5	L5	4155	C
5	L5	4160	C
5	L5	4162	C
5	L5	4163	U
5	L5	4170	A
5	L5	4183	G
5	L5	4184	G
5	L5	4191	G
5	L5	4203	A
5	L5	4222	G
5	L5	4229	U
5	L5	4233	A
5	L5	4249	G
5	L5	4251	A
5	L5	4254	G
5	L5	4268	A
5	L5	4273	A
5	L5	4281	A
5	L5	4291	G
5	L5	4296	U
5	L5	4297	G
5	L5	4305	G
5	L5	4314	C
5	L5	4319	C
5	L5	4329	G
5	L5	4330	G
5	L5	4332	C
5	L5	4349	C
5	L5	4373	G
5	L5	4377	G
5	L5	4378	A

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Mol	Chain	Res	Type
5	L5	4379	A
5	L5	4387	C
5	L5	4391	G
5	L5	4394	A
5	L5	4422	A
5	L5	4426	C
5	L5	4433	G
5	L5	4444	C
5	L5	4448	G
5	L5	4449	A
5	L5	4453	C
5	L5	4464	A
5	L5	4466	C
5	L5	4475	G
5	L5	4500	U
5	L5	4512	U
5	L5	4513	A
5	L5	4518	A
5	L5	4519	C
5	L5	4524	G
5	L5	4528	G
5	L5	4548	A
5	L5	4549	G
5	L5	4554	G
5	L5	4560	C
5	L5	4567	G
5	L5	4573	G
5	L5	4575	G
5	L5	4584	A
5	L5	4590	A
5	L5	4600	G
5	L5	4601	U
5	L5	4617	G
5	L5	4634	U
5	L5	4636	U
5	L5	4637	G
5	L5	4638	U
5	L5	4639	G
5	L5	4652	G
5	L5	4656	A
5	L5	4657	U
5	L5	4659	G

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Mol	Chain	Res	Type
5	L5	4670	C
5	L5	4672	A
5	L5	4687	A
5	L5	4700	A
5	L5	4708	A
5	L5	4709	U
5	L5	4719	G
5	L5	4733	C
5	L5	4734	A
5	L5	4740	G
5	L5	4741	C
5	L5	4742	G
5	L5	4745	G
5	L5	4754	G
5	L5	4757	C
5	L5	4759	C
5	L5	4761	G
5	L5	4764	A
5	L5	4765	G
5	L5	4771	C
5	L5	4772	C
5	L5	4773	C
5	L5	4775	C
5	L5	4860	G
5	L5	4868	G
5	L5	4870	G
5	L5	4871	C
5	L5	4875	G
5	L5	4880	C
5	L5	4881	U
5	L5	4882	U
5	L5	4883	C
5	L5	4888	U
5	L5	4889	G
5	L5	4894	A
5	L5	4895	C
5	L5	4896	G
5	L5	4900	C
5	L5	4901	G
5	L5	4910	G
5	L5	4912	G
5	L5	4914	C

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Mol	Chain	Res	Type
5	L5	4921	C
5	L5	4925	U
5	L5	4927	G
5	L5	4931	G
5	L5	4933	C
5	L5	4940	C
5	L5	4941	G
5	L5	4943	A
5	L5	4944	C
5	L5	4960	G
5	L5	4963	G
5	L5	4966	A
5	L5	4976	U
5	L5	4979	A
5	L5	4985	U
5	L5	4988	U
5	L5	4989	U
5	L5	4991	U
5	L5	5014	A
5	L5	5017	G
5	L5	5022	U
5	L5	5024	C
5	L5	5025	C
5	L5	5026	U
5	L5	5029	C
5	L5	5030	U
5	L5	5031	G
5	L5	5034	A
5	L5	5041	G
5	L5	5050	C
5	L5	5054	C
5	L5	5055	G
5	L5	5058	A
5	L5	5062	G
5	L5	5069	U
6	L7	23	A
6	L7	33	U
6	L7	53	U
6	L7	63	C
6	L7	64	G
6	L7	97	G
6	L7	100	A

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Mol	Chain	Res	Type
6	L7	102	U
6	L7	103	A
6	L7	111	C
6	L7	120	U
7	L8	23	C
7	L8	34	U
7	L8	35	C
7	L8	48	A
7	L8	59	A
7	L8	63	U
7	L8	82	A
7	L8	83	C
7	L8	84	A
7	L8	86	U
7	L8	87	G
7	L8	88	A
7	L8	94	G
7	L8	103	A
7	L8	105	C
7	L8	110	U
7	L8	111	U
7	L8	112	G
7	L8	114	G
7	L8	124	U
7	L8	125	C
7	L8	126	C
7	L8	127	U
7	L8	150	C
7	L8	151	G
55	S2	4	C
55	S2	7	G
55	S2	33	G
55	S2	41	G
55	S2	44	U
55	S2	45	A
55	S2	46	A
55	S2	49	C
55	S2	56	G
55	S2	58	C
55	S2	59	U
55	S2	62	G
55	S2	66	G

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Mol	Chain	Res	Type
55	S2	67	C
55	S2	68	A
55	S2	70	G
55	S2	71	G
55	S2	72	C
55	S2	73	C
55	S2	75	G
55	S2	76	U
55	S2	84	A
55	S2	86	C
55	S2	101	U
55	S2	103	A
55	S2	113	G
55	S2	114	G
55	S2	121	U
55	S2	126	G
55	S2	127	C
55	S2	128	U
55	S2	130	G
55	S2	143	U
55	S2	144	U
55	S2	145	G
55	S2	149	A
55	S2	152	U
55	S2	155	G
55	S2	160	U
55	S2	161	U
55	S2	162	C
55	S2	163	U
55	S2	167	G
55	S2	168	C
55	S2	170	A
55	S2	179	C
55	S2	182	C
55	S2	184	G
55	S2	198	U
55	S2	202	G
55	S2	207	G
55	S2	210	U
55	S2	211	G
55	S2	214	U
55	S2	219	U

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Mol	Chain	Res	Type
55	S2	290	U
55	S2	293	C
55	S2	295	C
55	S2	302	A
55	S2	306	C
55	S2	308	G
55	S2	309	G
55	S2	310	C
55	S2	311	C
55	S2	312	G
55	S2	313	A
55	S2	319	C
55	S2	322	C
55	S2	323	C
55	S2	324	C
55	S2	325	C
55	S2	326	C
55	S2	328	U
55	S2	329	G
55	S2	332	G
55	S2	339	A
55	S2	340	C
55	S2	347	G
55	S2	360	A
55	S2	362	C
55	S2	364	A
55	S2	368	U
55	S2	370	G
55	S2	380	G
55	S2	381	C
55	S2	385	G
55	S2	386	C
55	S2	398	A
55	S2	400	C
55	S2	409	C
55	S2	413	G
55	S2	428	U
55	S2	438	G
55	S2	448	A
55	S2	450	C
55	S2	452	G
55	S2	462	C

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Mol	Chain	Res	Type
55	S2	464	A
55	S2	465	A
55	S2	466	G
55	S2	471	G
55	S2	472	C
55	S2	473	A
55	S2	474	G
55	S2	482	G
55	S2	487	U
55	S2	488	U
55	S2	489	A
55	S2	492	C
55	S2	493	A
55	S2	500	A
55	S2	502	C
55	S2	503	C
55	S2	516	A
55	S2	525	A
55	S2	530	U
55	S2	531	A
55	S2	532	C
55	S2	536	A
55	S2	537	C
55	S2	539	C
55	S2	540	U
55	S2	541	U
55	S2	542	U
55	S2	543	C
55	S2	544	G
55	S2	545	A
55	S2	547	G
55	S2	551	U
55	S2	554	A
55	S2	555	A
55	S2	556	U
55	S2	559	G
55	S2	561	A
55	S2	563	G
55	S2	566	U
55	S2	567	C
55	S2	575	A
55	S2	576	A

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Mol	Chain	Res	Type
55	S2	582	U
55	S2	583	A
55	S2	587	A
55	S2	590	A
55	S2	591	U
55	S2	593	C
55	S2	595	U
55	S2	596	U
55	S2	604	A
55	S2	605	A
55	S2	606	G
55	S2	607	U
55	S2	608	C
55	S2	613	G
55	S2	614	C
55	S2	617	G
55	S2	628	A
55	S2	631	U
55	S2	643	A
55	S2	648	A
55	S2	650	A
55	S2	652	U
55	S2	655	A
55	S2	660	C
55	S2	668	A
55	S2	669	A
55	S2	671	A
55	S2	672	A
55	S2	673	G
55	S2	688	U
55	S2	689	U
55	S2	690	G
55	S2	692	G
55	S2	693	A
55	S2	694	G
55	S2	696	G
55	S2	697	G
55	S2	698	G
55	S2	732	U
55	S2	733	C
55	S2	734	C
55	S2	735	C

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Mol	Chain	Res	Type
55	S2	736	C
55	S2	738	C
55	S2	739	C
55	S2	746	C
55	S2	747	U
55	S2	748	C
55	S2	749	U
55	S2	751	G
55	S2	752	G
55	S2	753	C
55	S2	790	C
55	S2	791	C
55	S2	795	A
55	S2	796	G
55	S2	797	C
55	S2	798	G
55	S2	799	U
55	S2	807	G
55	S2	808	A
55	S2	809	A
55	S2	810	A
55	S2	811	A
55	S2	812	A
55	S2	813	A
55	S2	818	A
55	S2	821	G
55	S2	822	U
55	S2	830	A
55	S2	834	C
55	S2	835	C
55	S2	836	G
55	S2	837	A
55	S2	838	G
55	S2	839	C
55	S2	840	C
55	S2	841	G
55	S2	842	C
55	S2	847	A
55	S2	856	C
55	S2	858	A
55	S2	859	G
55	S2	860	G

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Mol	Chain	Res	Type
55	S2	861	A
55	S2	868	G
55	S2	869	A
55	S2	870	A
55	S2	872	A
55	S2	873	G
55	S2	874	G
55	S2	878	G
55	S2	879	C
55	S2	880	G
55	S2	883	U
55	S2	884	C
55	S2	888	U
55	S2	889	U
55	S2	890	U
55	S2	891	G
55	S2	892	U
55	S2	893	U
55	S2	894	G
55	S2	895	G
55	S2	896	U
55	S2	898	U
55	S2	900	C
55	S2	901	G
55	S2	903	A
55	S2	904	A
55	S2	905	C
55	S2	909	G
55	S2	913	A
55	S2	920	A
55	S2	922	A
55	S2	924	G
55	S2	926	A
55	S2	930	C
55	S2	933	G
55	S2	934	G
55	S2	958	G
55	S2	963	A
55	S2	970	G
55	S2	971	G
55	S2	972	A
55	S2	990	A

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Mol	Chain	Res	Type
55	S2	992	A
55	S2	1001	A
55	S2	1017	U
55	S2	1019	C
55	S2	1021	U
55	S2	1023	A
55	S2	1027	A
55	S2	1028	A
55	S2	1060	A
55	S2	1061	U
55	S2	1062	A
55	S2	1083	A
55	S2	1085	C
55	S2	1089	G
55	S2	1090	C
55	S2	1096	G
55	S2	1099	G
55	S2	1100	A
55	S2	1101	U
55	S2	1105	G
55	S2	1108	G
55	S2	1110	G
55	S2	1112	U
55	S2	1114	U
55	S2	1116	C
55	S2	1120	U
55	S2	1121	G
55	S2	1126	G
55	S2	1131	G
55	S2	1133	A
55	S2	1140	G
55	S2	1142	G
55	S2	1143	A
55	S2	1144	A
55	S2	1146	C
55	S2	1147	C
55	S2	1149	A
55	S2	1153	C
55	S2	1154	U
55	S2	1155	U
55	S2	1157	G
55	S2	1168	G

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Mol	Chain	Res	Type
55	S2	1181	A
55	S2	1183	A
55	S2	1195	A
55	S2	1207	G
55	S2	1212	G
55	S2	1215	C
55	S2	1217	A
55	S2	1221	G
55	S2	1224	G
55	S2	1242	U
55	S2	1243	U
55	S2	1251	A
55	S2	1253	A
55	S2	1256	G
55	S2	1257	G
55	S2	1259	A
55	S2	1265	A
55	S2	1268	C
55	S2	1271	C
55	S2	1272	C
55	S2	1273	C
55	S2	1274	G
55	S2	1275	G
55	S2	1276	A
55	S2	1281	G
55	S2	1282	A
55	S2	1284	A
55	S2	1285	G
55	S2	1286	G
55	S2	1297	U
55	S2	1298	G
55	S2	1299	A
55	S2	1301	A
55	S2	1302	G
55	S2	1303	C
55	S2	1308	U
55	S2	1313	A
55	S2	1314	U
55	S2	1321	G
55	S2	1326	U
55	S2	1332	A
55	S2	1333	U

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Mol	Chain	Res	Type
55	S2	1342	U
55	S2	1363	C
55	S2	1371	U
55	S2	1372	U
55	S2	1378	A
55	S2	1396	A
55	S2	1397	U
55	S2	1402	A
55	S2	1414	A
55	S2	1415	C
55	S2	1419	C
55	S2	1420	G
55	S2	1421	A
55	S2	1422	G
55	S2	1423	C
55	S2	1429	G
55	S2	1438	A
55	S2	1449	G
55	S2	1450	G
55	S2	1452	A
55	S2	1454	A
55	S2	1462	U
55	S2	1463	U
55	S2	1473	G
55	S2	1475	G
55	S2	1477	U
55	S2	1487	A
55	S2	1489	A
55	S2	1490	G
55	S2	1498	A
55	S2	1505	U
55	S2	1506	A
55	S2	1507	G
55	S2	1510	G
55	S2	1519	U
55	S2	1520	G
55	S2	1521	C
55	S2	1522	A
55	S2	1527	C
55	S2	1528	G
55	S2	1533	A
55	S2	1544	C

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Mol	Chain	Res	Type
55	S2	1546	G
55	S2	1548	G
55	S2	1552	G
55	S2	1553	C
55	S2	1556	A
55	S2	1560	U
55	S2	1563	G
55	S2	1567	G
55	S2	1569	A
55	S2	1570	G
55	S2	1574	C
55	S2	1578	U
55	S2	1580	A
55	S2	1585	U
55	S2	1586	U
55	S2	1587	G
55	S2	1588	A
55	S2	1589	A
55	S2	1599	U
55	S2	1601	A
55	S2	1602	U
55	S2	1613	G
55	S2	1614	A
55	S2	1621	U
55	S2	1623	A
55	S2	1624	U
55	S2	1634	A
55	S2	1639	G
55	S2	1644	C
55	S2	1648	G
55	S2	1654	G
55	S2	1661	A
55	S2	1663	A
55	S2	1664	A
55	S2	1665	G
55	S2	1671	G
55	S2	1678	A
55	S2	1694	U
55	S2	1695	A
55	S2	1719	A
55	S2	1721	U
55	S2	1722	G

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Mol	Chain	Res	Type
55	S2	1742	C
55	S2	1743	G
55	S2	1744	G
55	S2	1745	A
55	S2	1748	G
55	S2	1749	G
55	S2	1753	C
55	S2	1754	G
55	S2	1755	C
55	S2	1773	C
55	S2	1775	U
55	S2	1781	A
55	S2	1782	G
55	S2	1783	C
55	S2	1784	G
55	S2	1786	U
55	S2	1813	A
55	S2	1823	A
55	S2	1824	A
55	S2	1825	A
55	S2	1829	G
55	S2	1831	A
55	S2	1835	A
55	S2	1838	U
55	S2	1849	G
55	S2	1850	A
55	S2	1851	A
55	S2	1852	C
55	S2	1860	A
55	S2	1861	G
55	S2	1862	G
55	S2	1863	A
55	S2	1865	C
55	S2	1868	U

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	CP	3	C
2	CP	21	U
5	L5	406	C
5	L5	504	G

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Mol	Chain	Res	Type
5	L5	914	U
5	L5	1082	C
5	L5	1633	G
5	L5	2117	G
5	L5	2416	G
5	L5	2675	G
5	L5	2760	G
5	L5	3614	G
5	L5	3673	C
5	L5	4600	G
5	L5	4699	U
5	L5	4913	G
7	L8	87	G
55	S2	85	A
55	S2	144	U
55	S2	213	G
55	S2	465	A
55	S2	604	A
55	S2	688	U
55	S2	912	C
55	S2	971	G
55	S2	1120	U
55	S2	1273	C
55	S2	1395	C
55	S2	1519	U
55	S2	1585	U
55	S2	1597	C
55	S2	1664	A
55	S2	1860	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	0.81	0	7,10,12	1.07	1 (14%)

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.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	CR	63	LYO	CE-CD-CG	-2.12	109.00	113.47

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.

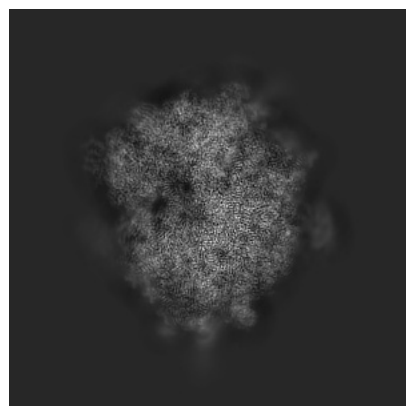
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54529. These allow visual inspection of the internal detail of the map and identification of artifacts.

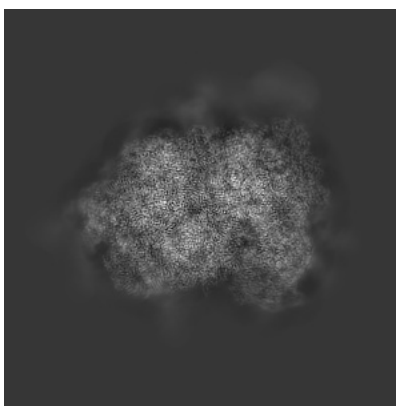
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

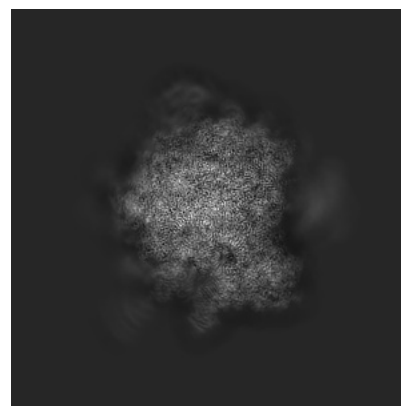
6.1.1 Primary map



X

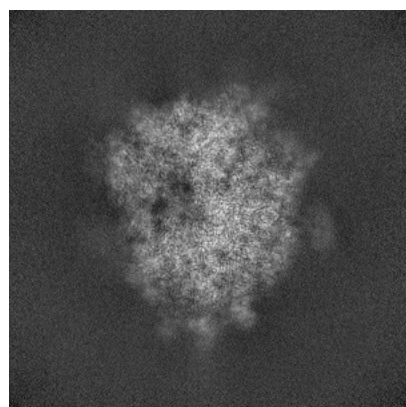


Y

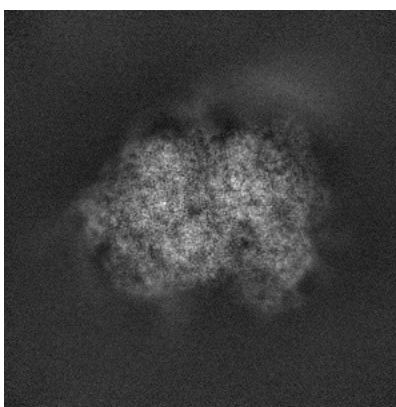


Z

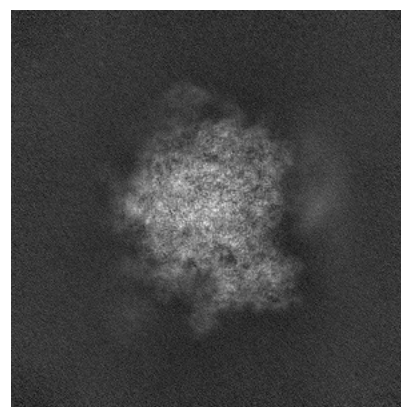
6.1.2 Raw map



X



Y

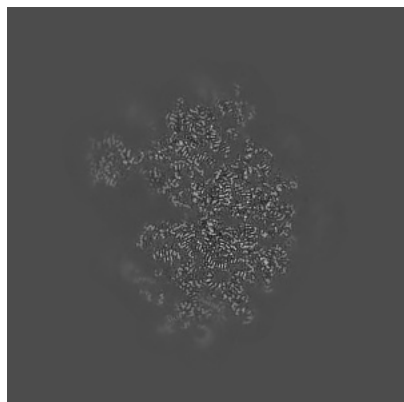


Z

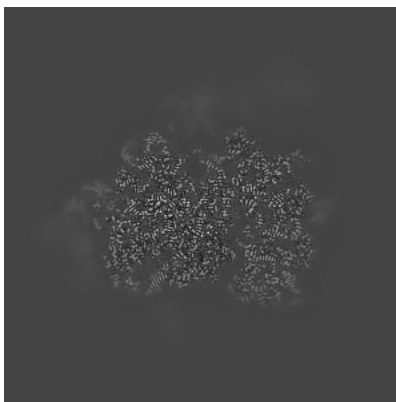
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

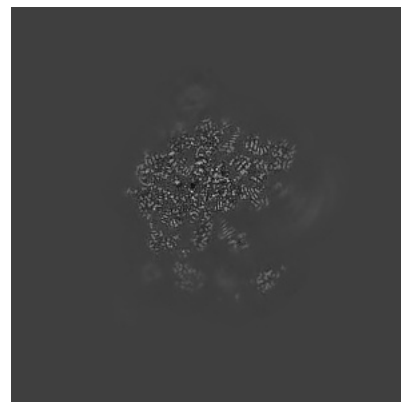
6.2.1 Primary map



X Index: 320

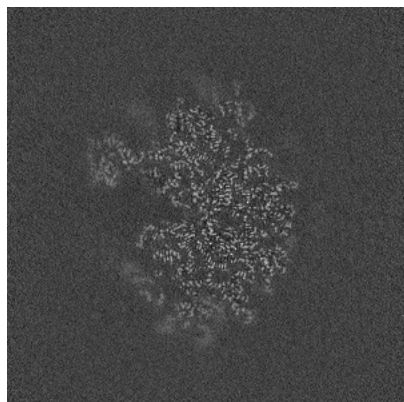


Y Index: 320

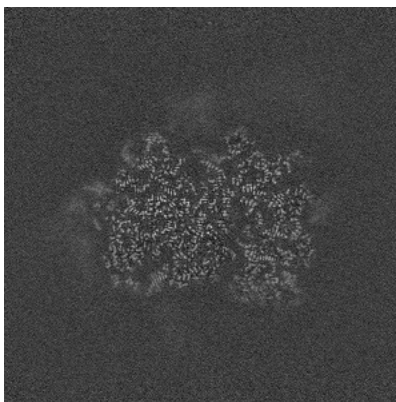


Z Index: 320

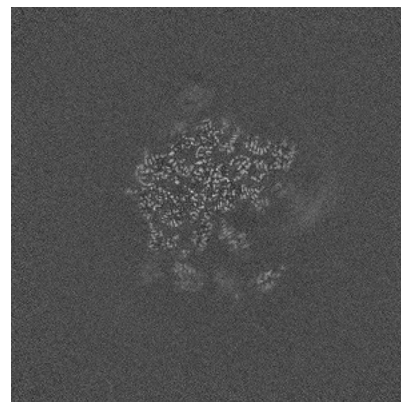
6.2.2 Raw map



X Index: 320



Y Index: 320

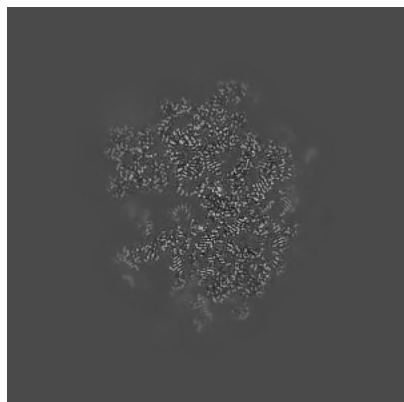


Z Index: 320

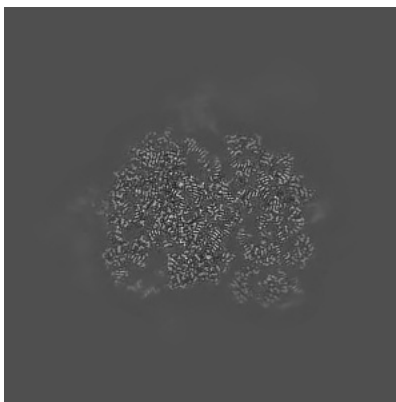
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

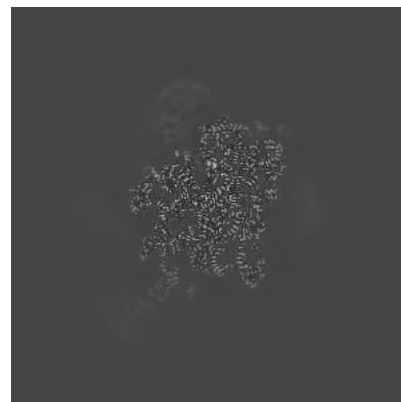
6.3.1 Primary map



X Index: 344

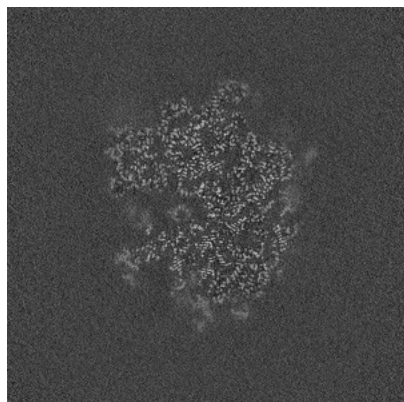


Y Index: 329

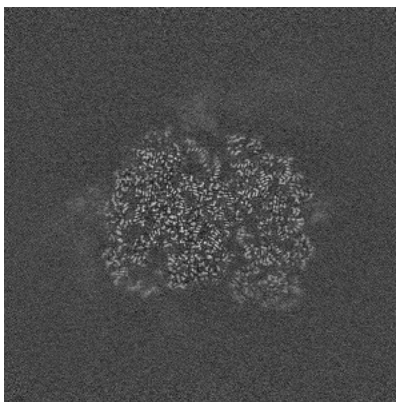


Z Index: 282

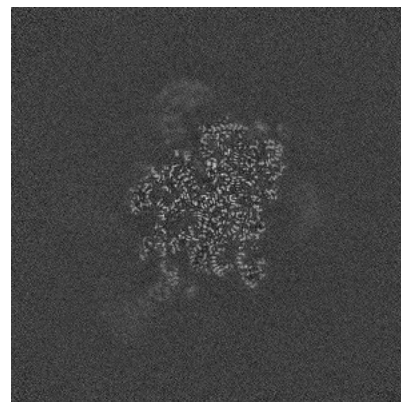
6.3.2 Raw map



X Index: 345



Y Index: 328

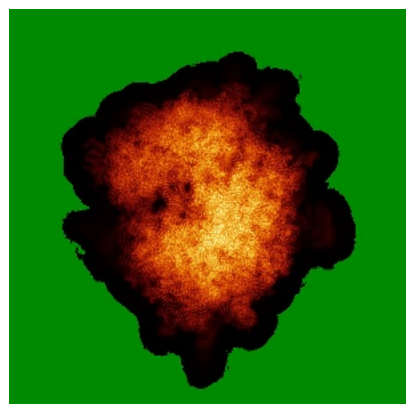


Z Index: 282

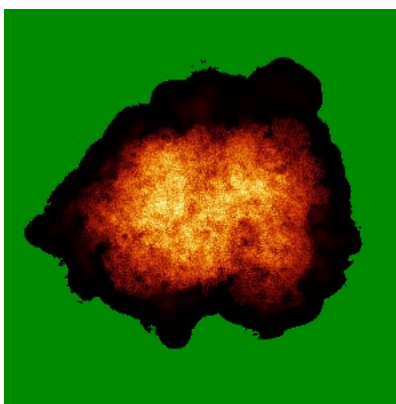
The images above show the largest variance slices of the map in three orthogonal directions.

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

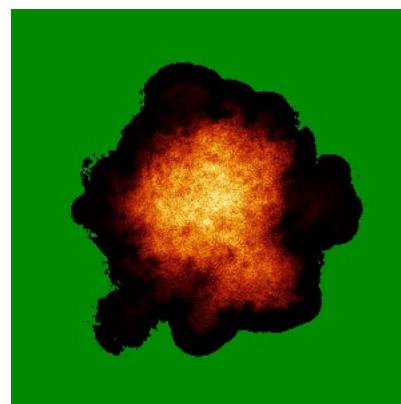
6.4.1 Primary map



X

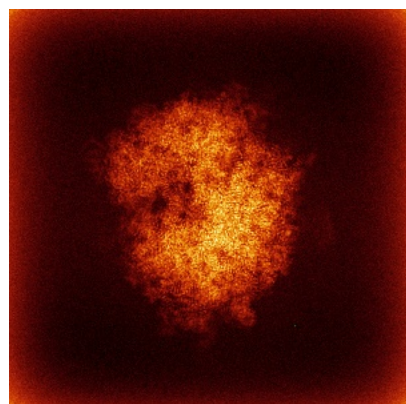


Y

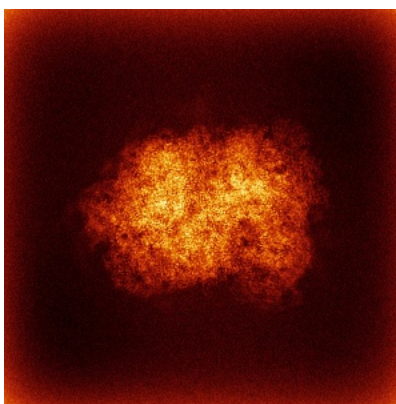


Z

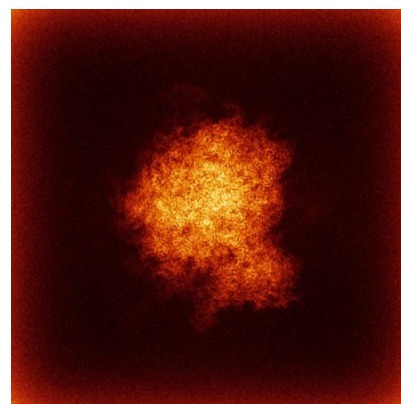
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

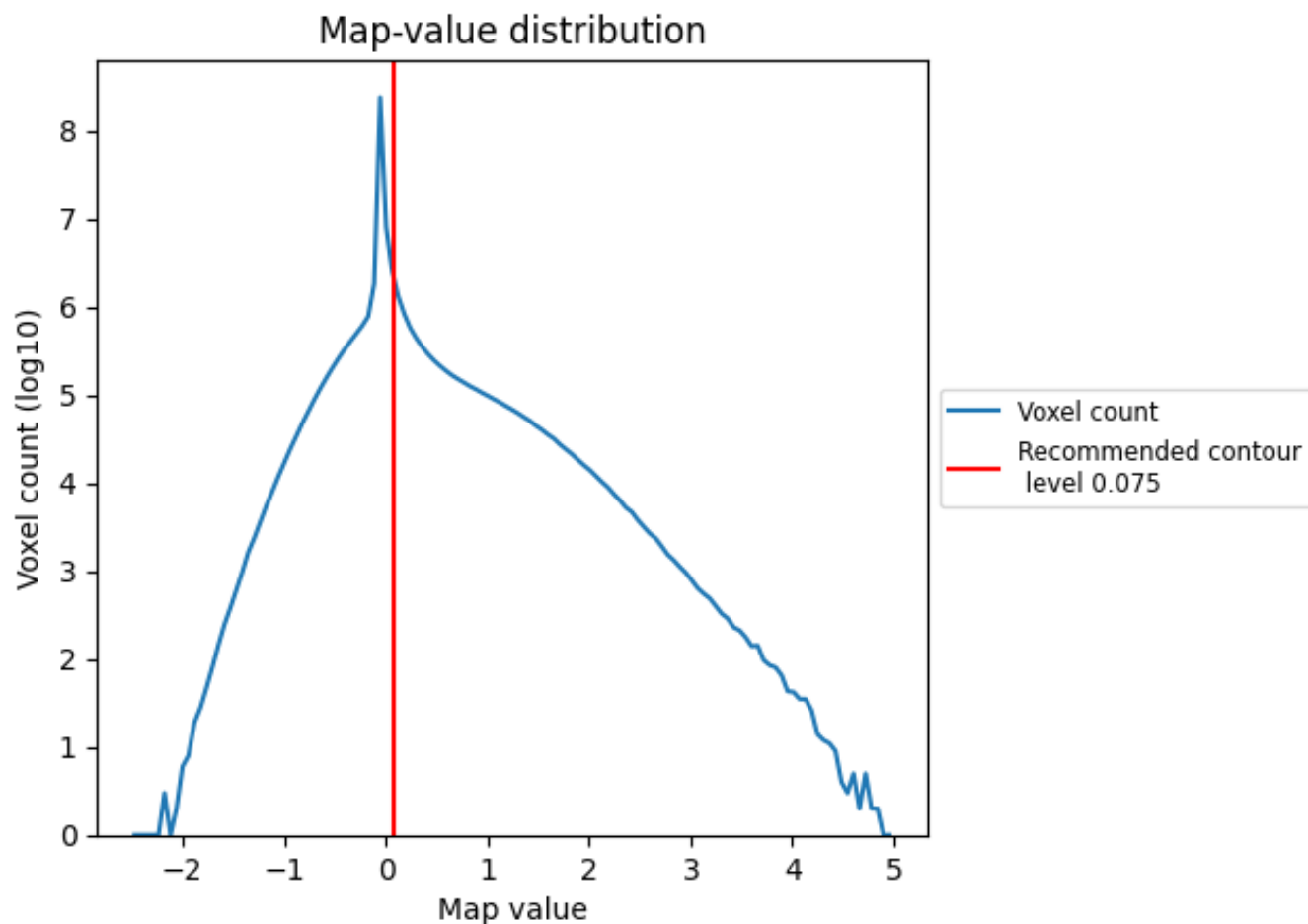
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

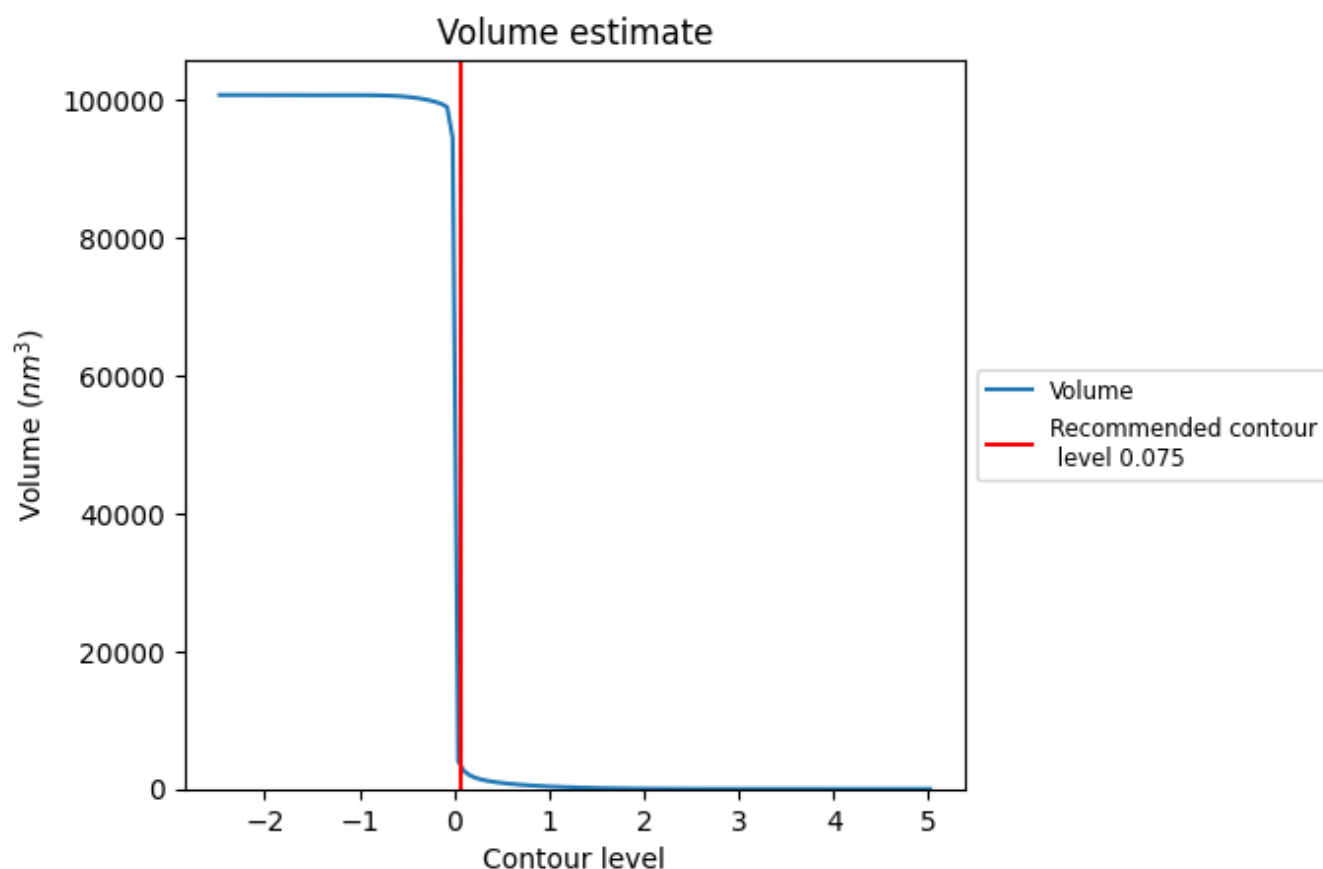
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

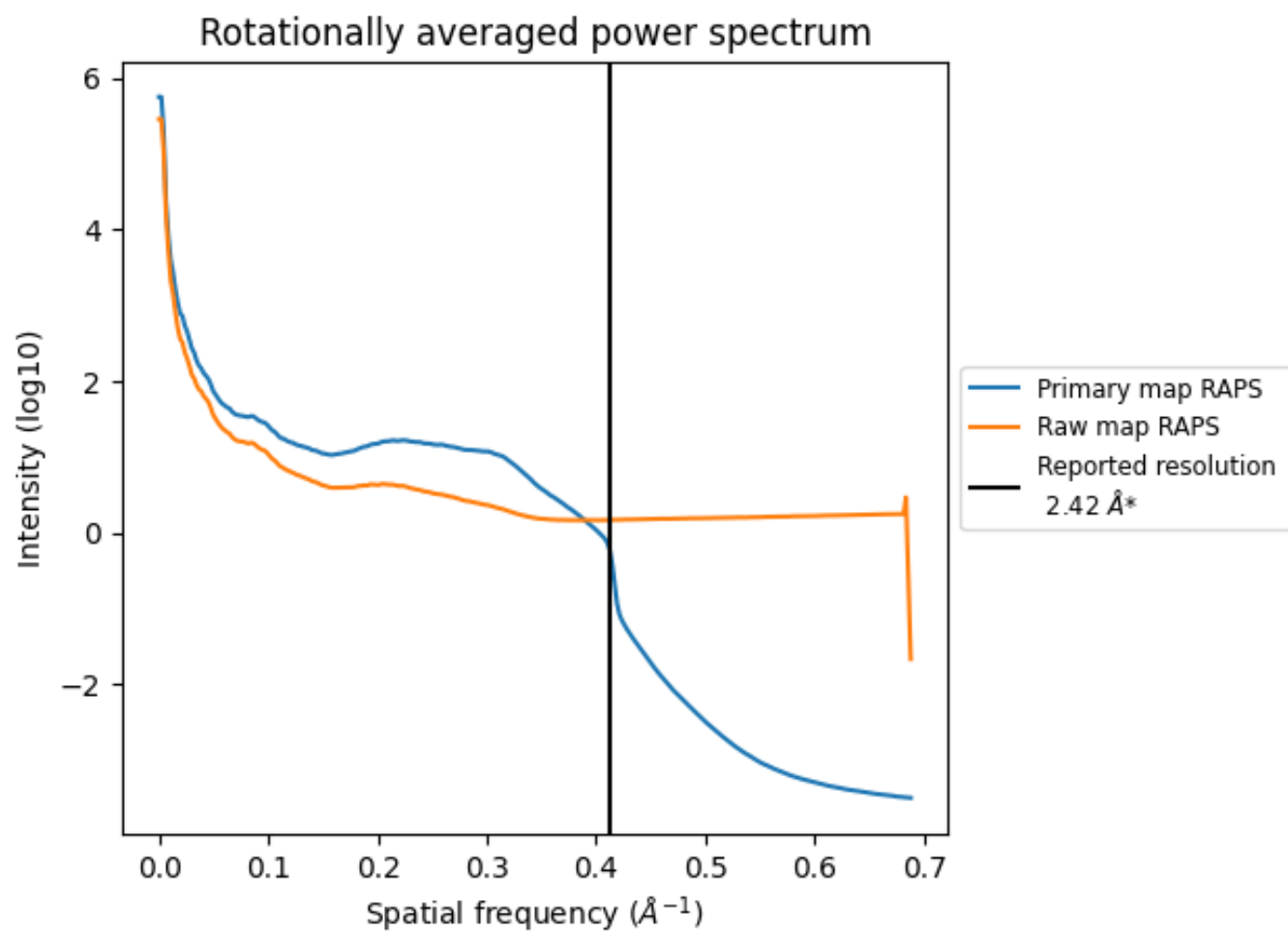
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3243 nm^3 ; this corresponds to an approximate mass of 2929 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 ⓘ

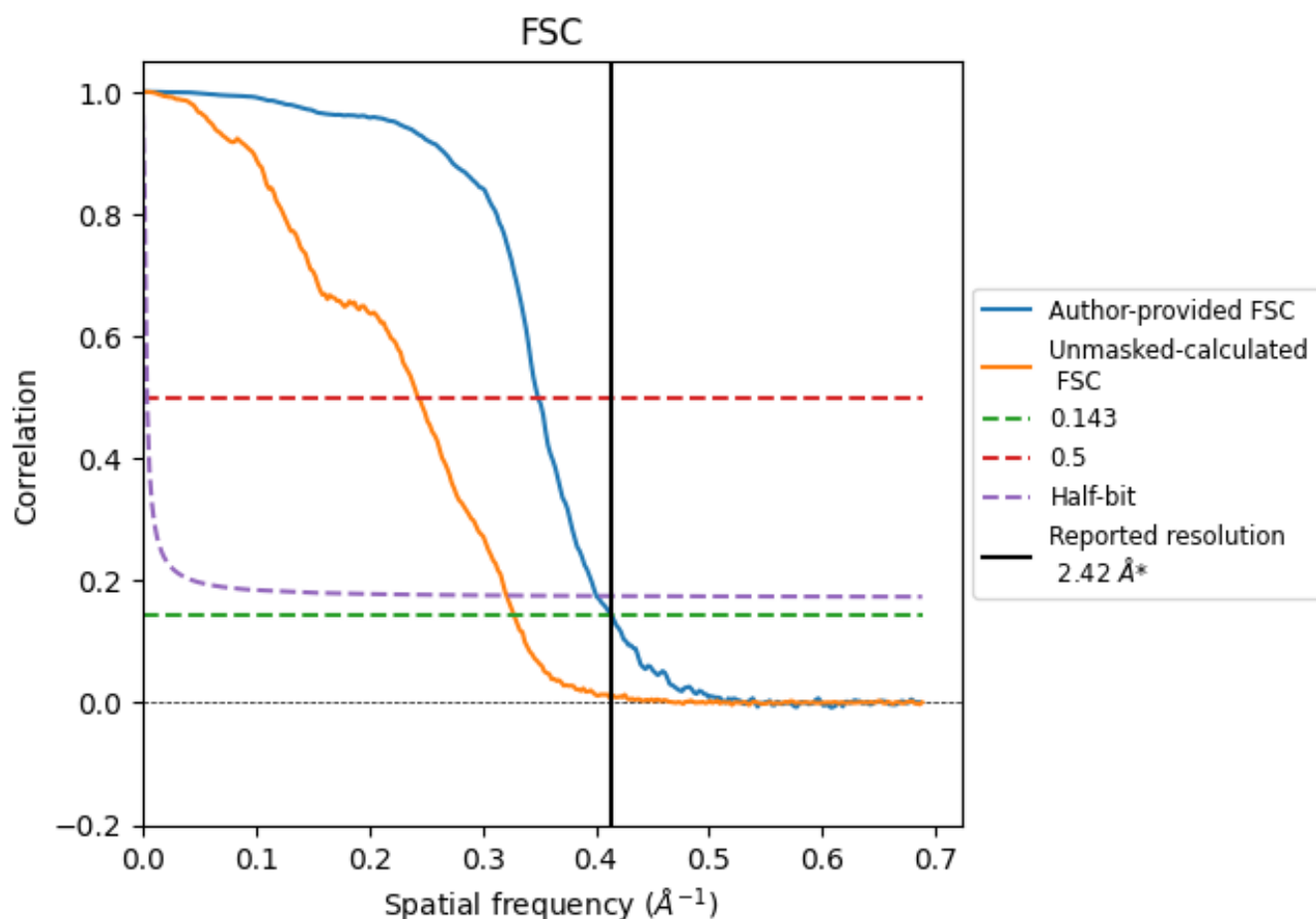


*Reported resolution corresponds to spatial frequency of 0.413 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.413 Å⁻¹

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.42	-	-
Author-provided FSC curve	2.42	2.87	2.50
Unmasked-calculated*	3.05	4.12	3.11

*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 3.05 differs from the reported value 2.42 by more than 10 %

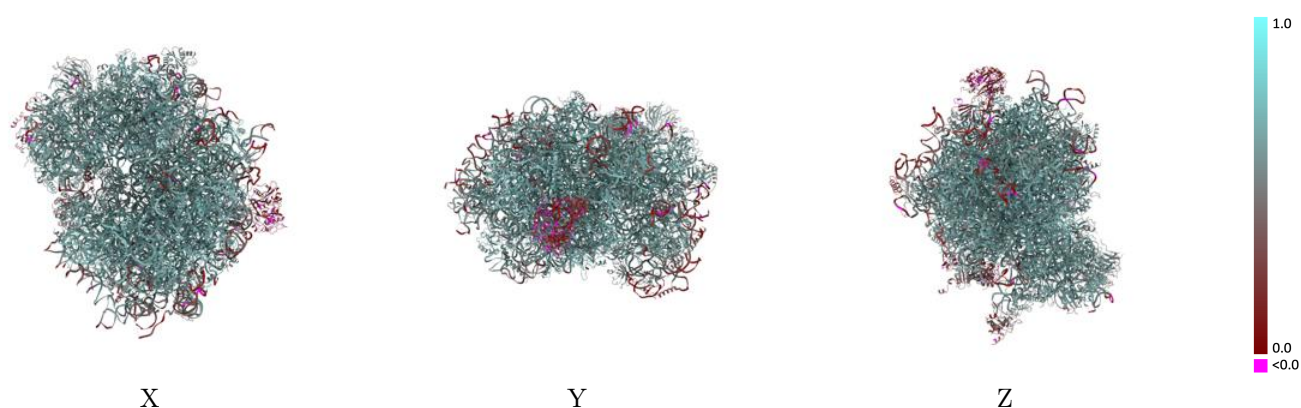
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-54529 and PDB model 9S3C. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)

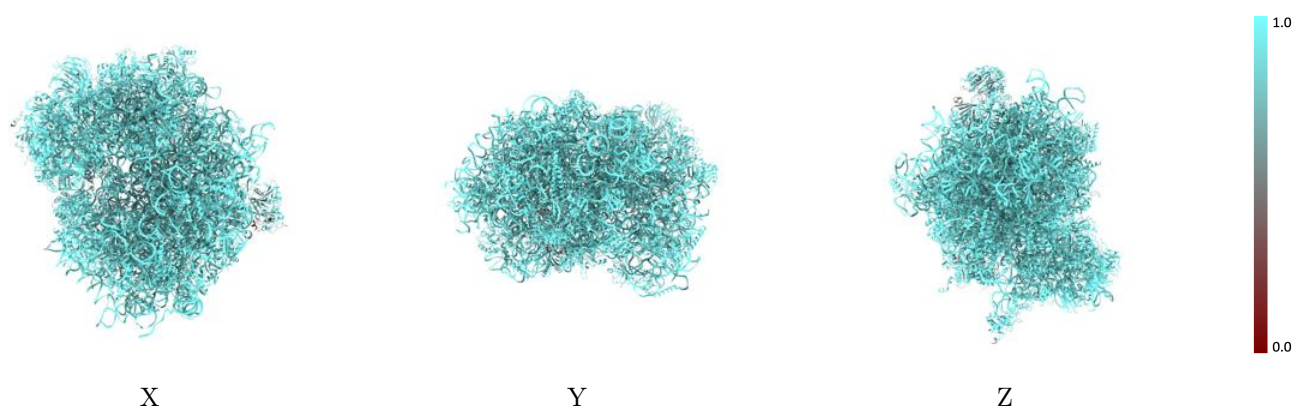
This section was not generated.

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



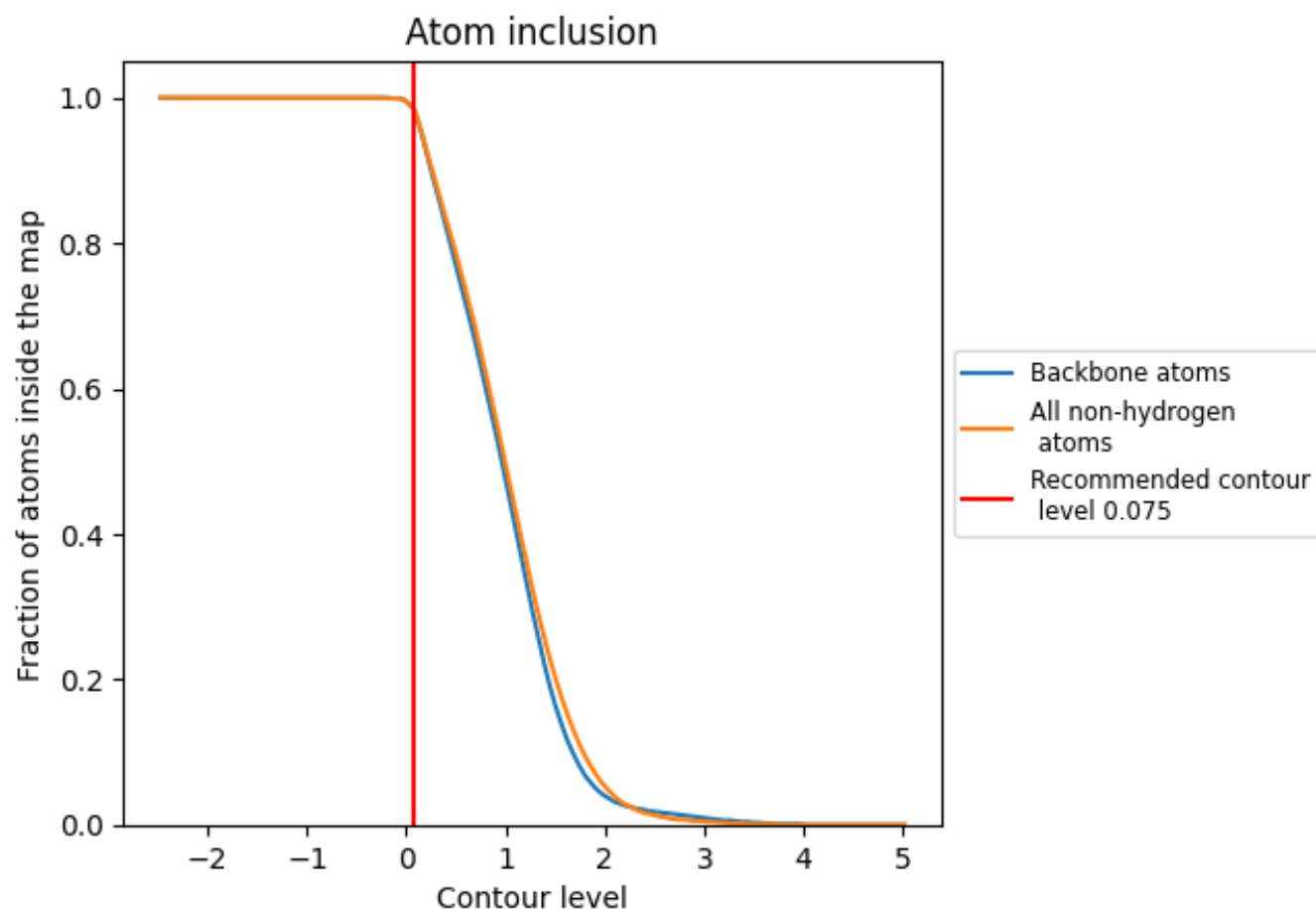
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.075).







































































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 (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9850	 0.6010
CM	 0.9880	 0.5930
CP	 0.9880	 0.5870
CR	 0.9390	 0.5180
CZ	 0.8300	 0.3920
L5	 0.9920	 0.6110
L7	 0.9980	 0.6610
L8	 0.9870	 0.6260
LA	 0.9920	 0.6870
LB	 0.9920	 0.6730
LC	 0.9890	 0.6680
LD	 0.9930	 0.6240
LE	 0.9880	 0.6120
LF	 0.9920	 0.6720
LG	 0.9810	 0.6070
LH	 0.9930	 0.6330
LI	 0.9880	 0.6460
LJ	 0.9830	 0.6030
LL	 0.9860	 0.6400
LM	 0.9940	 0.6450
LN	 0.9950	 0.6960
LO	 0.9910	 0.6790
LP	 0.9930	 0.6790
LQ	 0.9920	 0.6800
LR	 0.9940	 0.6590
LS	 0.9940	 0.6750
LT	 0.9830	 0.6340
LU	 0.9840	 0.5710
LV	 0.9970	 0.6760
LW	 0.9760	 0.5270
LX	 0.9850	 0.6450
LY	 0.9940	 0.6480
LZ	 0.9870	 0.6400
La	 0.9950	 0.6820
Lb	 0.9690	 0.5890



























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Chain	Atom inclusion	Q-score
Lc	 0.9890	 0.6580
Ld	 0.9930	 0.6520
Le	 0.9970	 0.6860
Lf	 0.9870	 0.6790
Lg	 0.9880	 0.6610
Lh	 0.9930	 0.6400
Li	 0.9950	 0.6360
Lj	 0.9930	 0.6800
Lk	 0.9790	 0.5800
Ll	 0.9930	 0.6550
Lm	 0.9760	 0.6570
Ln	 1.0000	 0.6850
Lo	 0.9950	 0.6640
Lp	 0.9960	 0.6850
Lr	 0.9970	 0.6650
Ls	 0.9200	 0.3060
Lt	 0.9740	 0.3720
NA	 0.6820	 0.1220
NB	 0.7660	 0.2050
NM	 0.8470	 0.1490
S2	 0.9890	 0.5920
SA	 0.9930	 0.6360
SB	 0.9890	 0.6320
SC	 0.9920	 0.6460
SD	 0.9920	 0.5950
SE	 0.9920	 0.6190
SF	 0.9800	 0.6050
SG	 0.9930	 0.5420
SH	 0.9860	 0.5680
SI	 0.9950	 0.6250
SJ	 0.9950	 0.6240
SK	 0.9830	 0.5790
SL	 0.9910	 0.6560
SM	 0.9200	 0.3100
SN	 0.9900	 0.6640
SO	 0.9920	 0.6470
SP	 0.9900	 0.5940
SQ	 0.9790	 0.6120
SR	 0.9680	 0.5590
SS	 0.9910	 0.5990
ST	 0.9900	 0.6140
SU	 0.9840	 0.5590

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Chain	Atom inclusion	Q-score
SV	 0.9900	 0.6300
SW	 0.9940	 0.6700
SX	 0.9890	 0.6460
SY	 0.9930	 0.5860
SZ	 0.9910	 0.5820
Sa	 0.9810	 0.6390
Sb	 0.9820	 0.5940
Sc	 0.9720	 0.5540
Sd	 0.9880	 0.6410
Se	 0.9980	 0.6010
Sf	 0.9120	 0.3480
Sg	 0.9880	 0.5440