



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 10:30 AM UTC

PDB ID : 8PV4 / pdb_00008pv4
EMDB ID : EMD-17953
Title : Chaetomium thermophilum pre-60S State 2 - pre-5S rotation with Rix1 complex - composite structure
Authors : Thoms, M.; Cheng, J.; Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2023-07-17
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

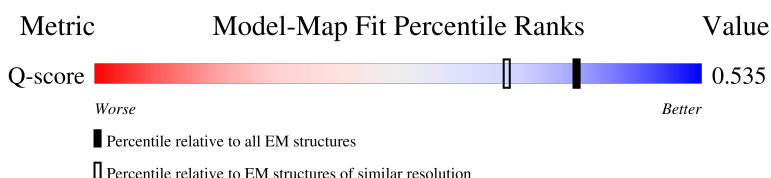
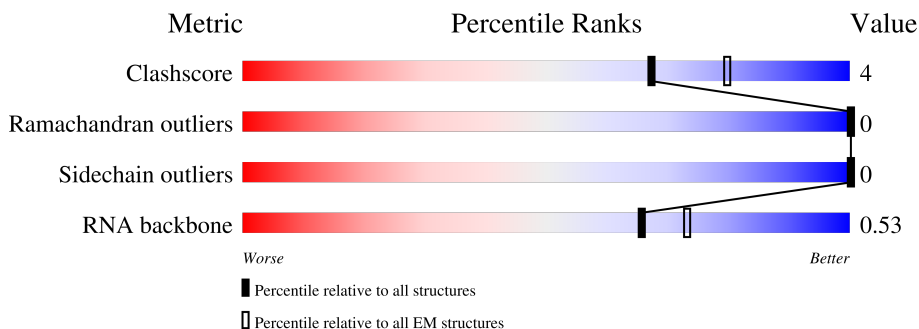
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



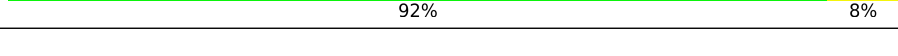
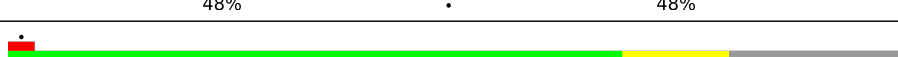
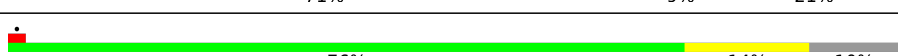
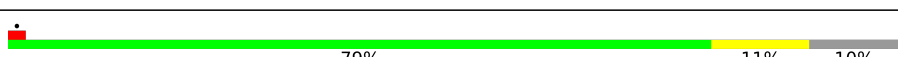
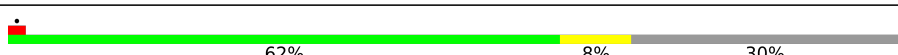
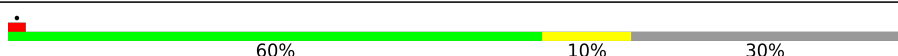
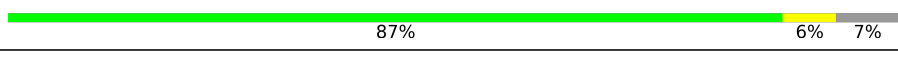
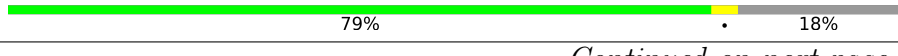
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	C1	3342	
2	C2	156	
3	C3	162	

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Mol	Chain	Length	Quality of chain
4	C4	119	
5	CB	391	
6	CF	270	
7	CH	661	
8	CI	414	
9	CJ	679	
10	CK	261	
11	CL	558	
12	CM	249	
12	LF	249	
13	CN	246	
14	CO	120	
15	CQ	225	
16	CS	338	
17	CT	437	
17	CU	437	
18	CV	781	
18	CW	781	
19	Cb	117	
20	Cd	627	
21	Ce	443	
22	Cf	350	
23	Cg	202	
24	Ch	517	
25	Cz	123	

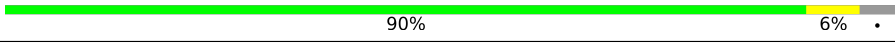
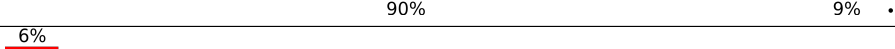
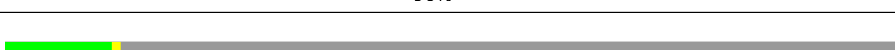
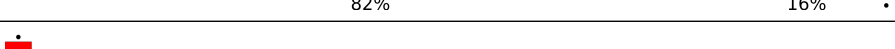
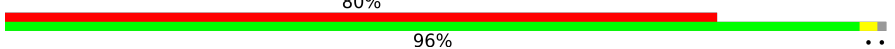
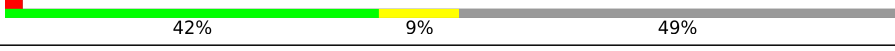
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Mol	Chain	Length	Quality of chain
26	LA	254	
27	LB	392	
28	LC	365	
29	LD	304	
30	LE	200	
31	LG	262	
32	LH	229	
33	LJ	173	
34	LK	165	
35	LL	213	
36	LM	142	
37	LN	203	
38	LO	204	
39	LP	187	
40	LQ	213	
41	LR	2898	
42	LS	174	
43	LT	160	
44	LU	127	
45	LV	139	
46	LX	156	
47	LY	138	
48	LZ	135	
49	La	149	
50	Lc	108	

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Mol	Chain	Length	Quality of chain
51	Ld	120	
52	Le	131	
53	Lf	109	
54	Lg	119	
55	Lh	935	
56	Li	110	
57	Lj	95	
58	Lk	94	
59	Ll	51	
60	Lp	92	
61	Lq	147	
62	Lr	217	
63	CR	767	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 178878 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 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	3136	Total	C	N	O	P	0	0
			67131	29984	12153	21858	3136		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	156	Total	C	N	O	P	0	0
			3319	1484	589	1090	156		

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	82	Total	C	N	O	P	0	0
			1754	780	316	576	82		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C4	119	Total	C	N	O	P	0	0
			2536	1131	453	833	119		

- Molecule 5 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CB	265	Total	C	N	O	S	0	0
			2107	1351	371	382	3		

- Molecule 6 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CF	245	Total	C	N	O	S	0	0
			1934	1215	350	360	9		

- Molecule 7 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CH	627	Total	C	N	O	S	0	0
			5063	3181	924	939	19		

- Molecule 8 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CI	152	Total	C	N	O	S	0	0
			1234	791	230	208	5		

- Molecule 9 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CJ	382	Total	C	N	O	S	0	0
			3116	2008	548	550	10		

- Molecule 10 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CK	237	Total	C	N	O	S	0	0
			1903	1198	368	333	4		

- Molecule 11 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CL	79	Total	C	N	O	S	0	0
			622	389	125	108			

- Molecule 12 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CM	217	Total	C	N	O	S	0	0
			1773	1144	329	297	3		
12	LF	248	Total	C	N	O	S	0	0
			2023	1297	377	346	3		

- Molecule 13 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CN	246	Total	C	N	O	S	0	0
			1853	1156	322	368	7		

- Molecule 14 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CO	62	Total	C	N	O	S	0	0
			468	290	94	82	2		

- Molecule 15 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CQ	183	Total	C	N	O	S	0	0
			1480	925	304	241	10		

- Molecule 16 is a protein called Pre-rRNA-processing protein IPI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CS	268	Total	C	N	O	S	0	0
			2063	1312	363	381	7		

- Molecule 17 is a protein called Pre-rRNA-processing protein IPI3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CT	395	Total	C	N	O	S	0	0
			2953	1873	494	568	18		
17	CU	395	Total	C	N	O	S	0	0
			2965	1881	496	570	18		

- Molecule 18 is a protein called Pre-rRNA-processing protein RIX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CV	550	Total	C	N	O	S	0	0
			4217	2691	735	777	14		
18	CW	550	Total	C	N	O	S	0	0
			4204	2685	729	776	14		

- Molecule 19 is a protein called Zinc finger domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Cb	101	Total	C	N	O	S	0	0
			830	517	161	148	4		

- Molecule 20 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cd	462	Total	C	N	O	S	0	0
			3691	2350	671	659	11		

- Molecule 21 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ce	262	Total	C	N	O	S	0	0
			2148	1337	413	394	4		

- Molecule 22 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Cf	285	Total	C	N	O	S	0	0
			2282	1443	417	401	21		

- Molecule 23 is a protein called Ribosome biogenesis regulatory protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Cg	188	Total	C	N	O	S	0	0
			1478	924	283	270	1		

- Molecule 24 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ch	485	Total	C	N	O	S	0	0
			3809	2394	696	709	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ch	117	ASP	GLU	engineered mutation	UNP G0SC29

- Molecule 25 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Cz	101	Total	C	N	O	S	0	0
			869	541	180	144	4		

- Molecule 26 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LA	191	Total	C	N	O	S	0	0
			1454	917	278	256	3		

- Molecule 27 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LB	389	Total	C	N	O	S	0	0
			3104	1973	579	539	13		

- Molecule 28 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LC	363	Total	C	N	O	S	0	0
			2751	1737	527	478	9		

- Molecule 29 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LD	286	Total	C	N	O	S	0	0
			2266	1434	407	422	3		

- Molecule 30 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LE	191	Total	C	N	O	S	0	0
			1477	944	267	263	3		

- Molecule 31 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LG	235	Total	C	N	O	S	0	0
			1889	1210	350	324	5		

- Molecule 32 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LH	190	Total	C	N	O	S	0	0
			1495	949	268	272	6		

- Molecule 33 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LJ	169	Total	C	N	O	S	0	0
			1357	850	266	235	6		

- Molecule 34 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LK	158	Total	C	N	O	S	0	0
			1184	743	215	224	2		

- Molecule 35 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LL	203	Total	C	N	O	S	0	0
			1587	989	325	271	2		

- Molecule 36 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LM	141	Total	C	N	O	S	0	0
			1126	714	216	195	1		

- Molecule 37 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LN	202	Total	C	N	O	S	0	0
			1704	1062	360	278	4		

- Molecule 38 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LO	203	Total	C	N	O	S	0	0
			1611	1034	305	267	5		

- Molecule 39 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LP	171	Total	C	N	O	S	0	0
			1345	836	274	232	3		

- Molecule 40 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LQ	150	Total	C	N	O	S	0	0
			1200	759	239	200	2		

- Molecule 41 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LR	155	Total	C	N	O	S	0	0
			1241	772	262	203	4		

- Molecule 42 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LS	174	Total	C	N	O	S	0	0
			1426	917	266	238	5		

- Molecule 43 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LT	129	Total	C	N	O	S	0	0
			1021	647	194	178	2		

- Molecule 44 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LU	105	Total	C	N	O	S	0	0
			846	548	146	151	1		

- Molecule 45 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LV	135	Total	C	N	O	S	0	0
			991	630	184	170	7		

- Molecule 46 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	LX	145	Total	C	N	O	0	0
			1133	723	211	199		

- Molecule 47 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LY	133	Total	C	N	O	S	0	0
			1056	658	213	183	2		

- Molecule 48 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LZ	135	Total	C	N	O	S	0	0
			1112	713	207	188	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	La	108	Total	C	N	O	S	0	0
			872	556	168	147	1		

- Molecule 50 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lc	95	Total	C	N	O	S	0	0
			705	449	122	129	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ld	110	Total	C	N	O	S	0	0
			875	555	171	148	1		

- Molecule 52 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Le	126	Total	C	N	O	S	0	0
			1017	640	208	163	6		

- Molecule 53 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 54 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Lg	118	Total	C	N	O	S	0	0
			914	567	186	157	4		

- Molecule 55 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Lh	122	Total	C	N	O		0	0
			1003	637	198	168			

- Molecule 56 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Li	101	Total	C	N	O	S	0	0
			827	509	181	136	1		

- Molecule 57 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Lj	88	Total	C	N	O	S	0	0
			698	427	154	112	5		

- Molecule 58 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Lk	76	Total	C	N	O	S	0	0
			632	400	121	109	2		

- Molecule 59 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	Ll	50	Total	C	N	O	0	0
			436	275	97	64		

- Molecule 60 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Lp	91	Total	C	N	O	S	0	0
			698	430	138	124	6		

- Molecule 61 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	Lq	139	Total	C	N	O	0	0
			1073	672	213	188		

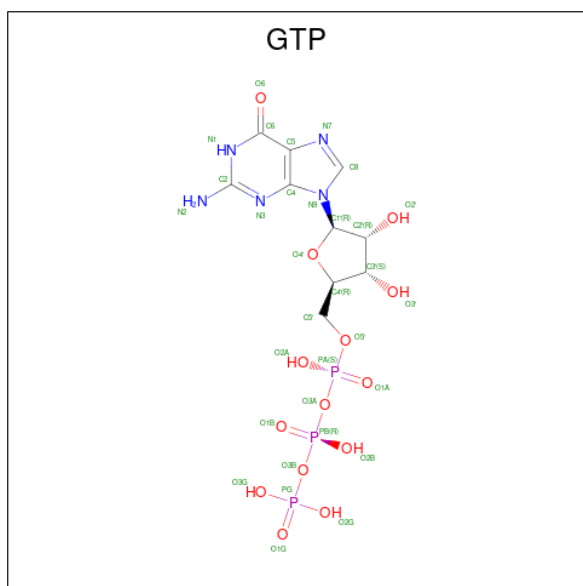
- Molecule 62 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	Lr	214	Total	C	N	O	0	0
			1056	628	214	214		

- Molecule 63 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CR	390	Total	C	N	O	S	0	0
			2934	1879	517	526	12		

- Molecule 64 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
64	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	
64	Cd	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 65 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
65	CH	1	Total 1	Mg 1	0
65	Cd	2	Total 2	Mg 2	0

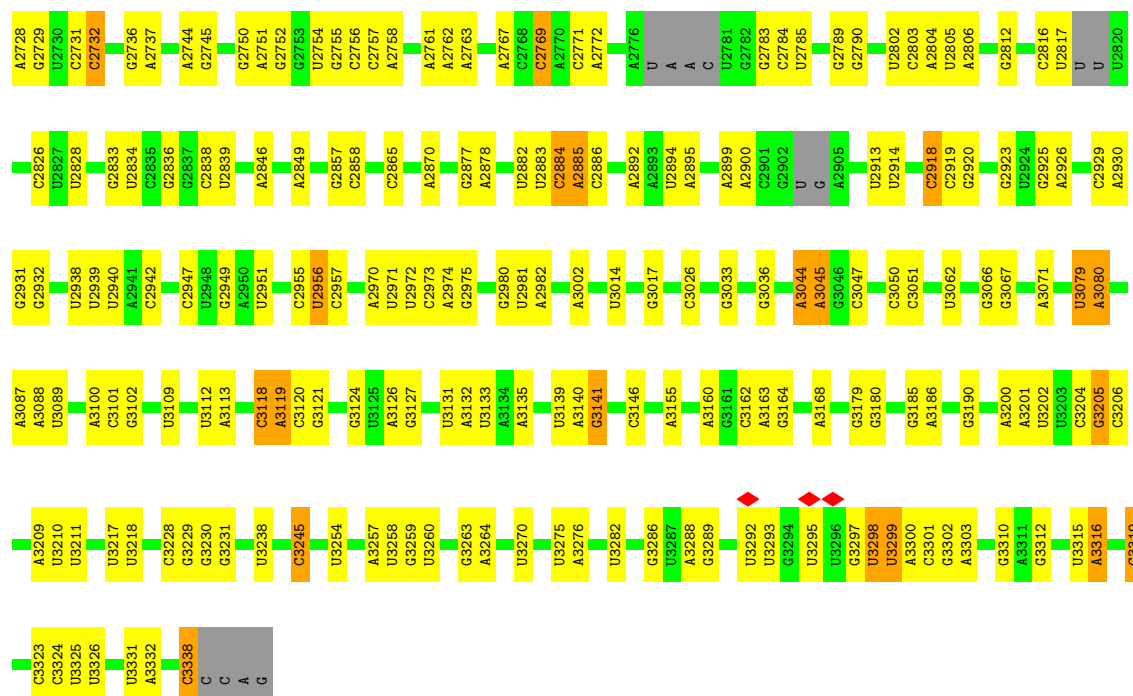
- Molecule 66 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
66	CQ	1	Total 1	Zn 1	0
66	Cb	1	Total 1	Zn 1	0
66	Lg	1	Total 1	Zn 1	0
66	Lj	1	Total 1	Zn 1	0
66	Lp	1	Total 1	Zn 1	0

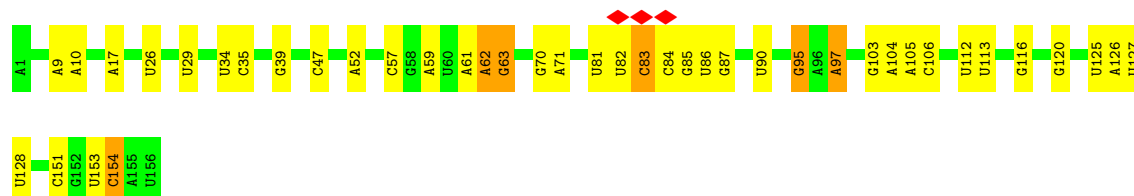
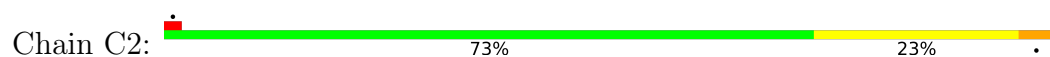
- Molecule 67 is water.

Mol	Chain	Residues	Atoms		AltConf
67	CH	1	Total 1	O 1	0
67	Cd	2	Total 2	O 2	0

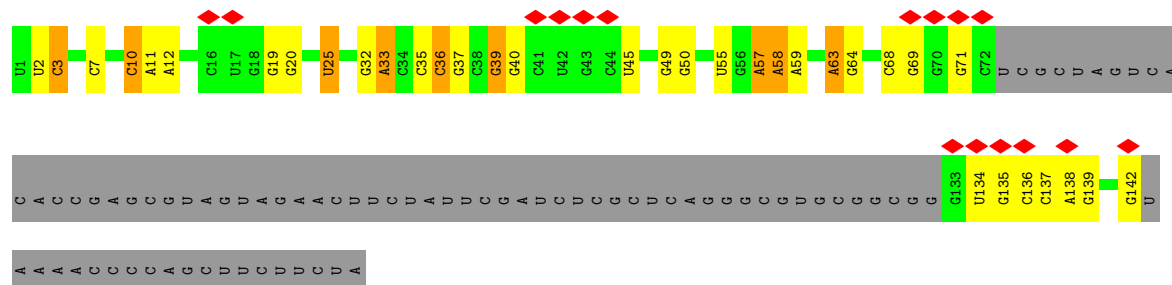
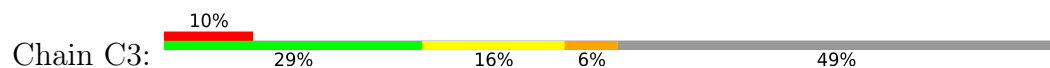
U	C2513	U2418	A2320	A2243	G2150	A1793	U1625	G1493	A1382	C1260	C1159
A	U2514	A2419	A2321	A	A2151	A1794	G1626	U1505	G1383	A1261	G1160
A	G2515	G2420	G2327	G	U2156	U1795	G1638	U1506	G1387	C1262	G1161
C	A2421	A2421	G2327	G	G2157	A1796	A1639	U1536	U1390	C1263	A1162
C	G2516	G2420	G2327	C	G2158	U1799	C1640	U1537	A1390	U1264	G1163
C	A2422	A2422	A2330	C	C2159	C1800	G1641	U1538	U1393	G1265	U1164
U	U2423	U2423	A2331	U	C2160	U1801	G1642	U1539	C1393	C1266	G1165
U	A2424	A2424	A2331	C	C2161	G1809	G1643	C1539	C1394	C1267	C1175
C	G2425	G2425	G2340	G	A2161	G1810	G1644	A1541	G1395	U1269	A1176
C	U2427	U2427	G2340	C	G2167	G1811	G1645	A1542	U1400	A1270	A1177
U	G2428	G2428	A2348	U	C2168	C1812	G1658	A1543	G1401	G1278	A1178
U	G2429	G2429	A2348	A	U2169	C1813	G1659	G1543	A1401	G1278	C1179
U	A2431	A2431	C2352	U	G2170	U1814	C1663	G1543	G1404	G1283	C1182
U	G2432	G2432	A2353	C	A2171	A1815	A1676	A1548	G1405	U1287	A1185
U	A2433	A2433	G2354	U	U2172	C1816	A1677	C1549	G1405	A1288	A1186
U	U2435	U2435	G2355	A	A2176	A1822	U1685	U1550	G1414	G1289	G1190
U	C2436	C2436	G2356	U	G2179	C1823	C1697	G1552	G1417	G1290	U1193
U	G2437	G2437	G2359	U	G2179	C1824	C1698	U1553	A1418	A1291	U1194
U	G2438	G2438	A2362	G	U2180	G1825	A1698	G1554	U1419	U1292	U1194
U	C2439	C2439	G2363	U	A2182	C1826	G1699	C1555	C1420	U1292	U1194
U	G2440	G2440	A2364	G	A2185	C1829	U1704	G1559	U1421	G1296	U1197
U	C2441	C2441	A2364	C	A2186	A1830	U1721	U1560	G1429	G1303	A1198
U	C2442	C2442	C2368	G	A2186	C1836	U1722	G1561	G1430	U1305	G1205
U	G2446	G2446	U2373	C	A2192	U1856	U1751	G1576	U1453	A1331	A1214
U	A2447	A2447	U2374	C	G2197	U1857	U1752	C1577	U1454	G1332	C1215
U	G2448	G2448	G2375	C	G2197	G1858	U1752	G1578	U1455	A1333	G1216
U	A2449	A2449	A2376	A	G2203	A1859	G1758	G1585	G1458	A1334	G1219
U	U2450	U2450	G2377	U	G2204	U1860	G1759	U1586	G1459	C1336	G1209
U	C2453	C2453	U2380	A	U2205	A1866	C1760	U1586	A1460	G1337	A1223
U	A2454	A2454	A2381	U	A2206	U1867	G1766	U1596	G1463	U1339	A1227
U	C2458	C2458	A2382	G	G2210	U1868	A1767	U1596	A1464	A1228	G1229
U	G2458	G2458	U2384	C	G2211	U1869	G1776	U1609	U1467	G1345	C1240
U	U2465	U2465	U2389	U	G2212	G1878	A1777	G1610	U1477	A1346	U1241
U	G2466	G2466	U2390	U	G2213	G1879	A1778	G1611	U1478	A1242	A1243
U	U2473	U2473	U2391	C	G2216	C1886	A1780	G1614	G1476	U1361	G1244
U	A2474	A2474	G2392	C	U2217	C1887	G1783	G1615	U1477	G1362	G1245
U	U2477	U2477	A2393	U	U2218	A1888	G1784	A1617	U1478	A1246	C1247
U	C2489	C2489	A2401	U	A2219	A1889	G1785	A1618	A1481	G1370	U1248
U	U2495	U2495	G2405	U	A2220	A1890	G1786	G1619	G1485	A1373	A1254
U	G2496	G2496	A2406	U	A2221	U1901	G1787	A1622	C1491	G1374	C1255
U	G2497	G2497	C2407	U	U2222	A1902	G1788	C1624	G1492	G1375	
U	A2498	A2498	U2307	U	A2223						
U	G2500	G2500	A2308	U	G2224						
U	U2501	U2501	G2411	U	A2225						
U	G2502	G2502	G2415	U	U2231						
U	C2503	C2503	U2416	U	U						
U	G2506	G2506	G2417	U	A						
U	C2507	C2507		U	G						
U	A2508	A2508		C	U2237						
U	C2604	C2604									
U	A2605	A2605									
U	G2615	G2615									
U	G2621	G2621									
U	G2622	G2622									
U	G2628	G2628									
U	A2629	A2629									
U	G2630	G2630									
U	A2632	A2632									
U	G2633	G2633									
U	G2634	G2634									
U	A2635	A2635									
U	G2636	G2636									
U	A2647	A2647									
U	A2648	A2648									
U	G2649	G2649									
U	A2651	A2651									
U	A2656	A2656									
U	G2657	G2657									
U	A2663	A2663									
U	A2664	A2664									
U	G2672	G2672									
U	A2674	A2674									
U	G2675	G2675									
U	U2676	U2676									
U	A2680	A2680									
U	U2683	U2683									
U	G2688	G2688									
U	G2689	G2689									
U	G2690	G2690									
U	G2691	G2691									
U	A2705	A2705									
U	G2710	G2710									
U	G2711	G2711									
U	G2712	G2712									
U	G2713	G2713									
U	A2717	A2717									



• Molecule 2: 5.8S rRNA

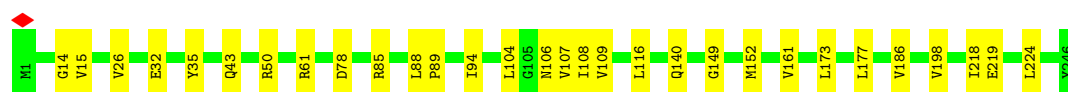


• Molecule 3: ITS2

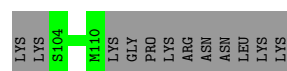
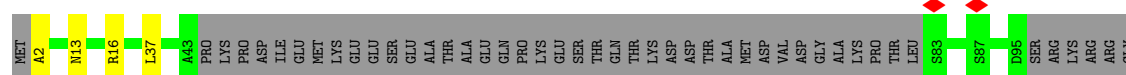


• Molecule 4: 5S rRNA

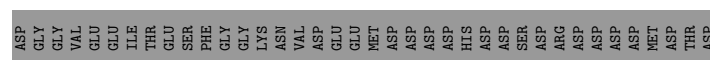
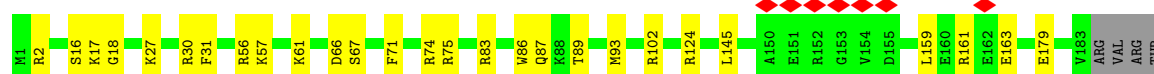




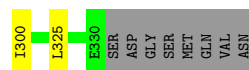
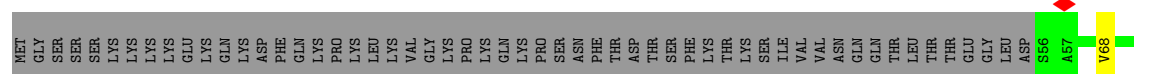
- Molecule 14: DUF2423 domain-containing protein



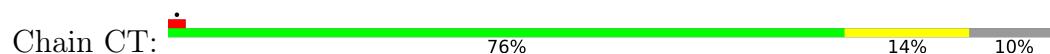
- Molecule 15: Ribosome biogenesis protein RLP24

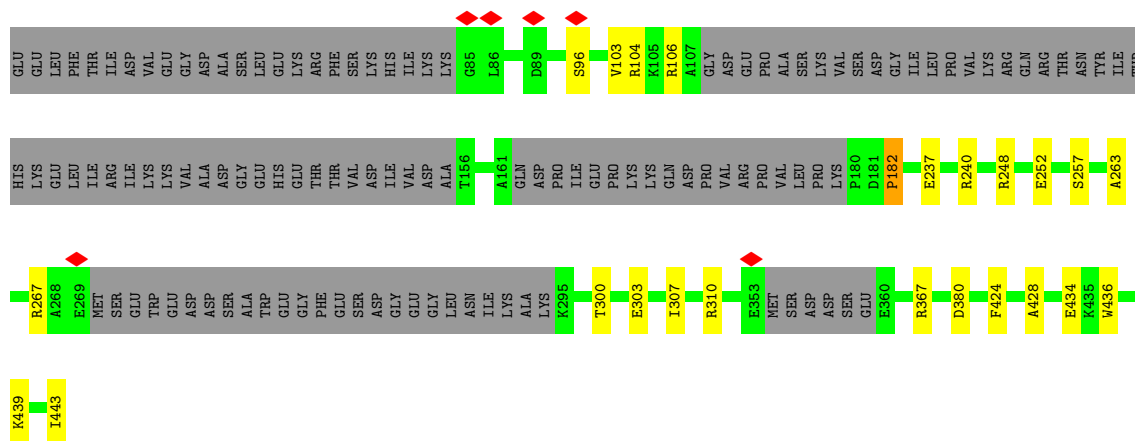


- Molecule 16: Pre-rRNA-processing protein IPI1



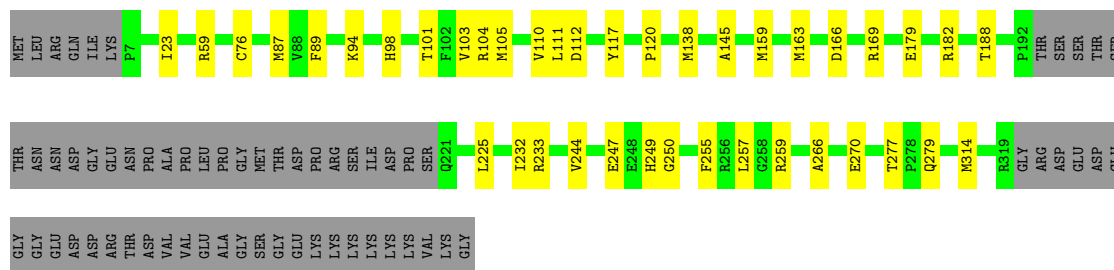
- Molecule 17: Pre-rRNA-processing protein IPI3





- Molecule 22: Ribosome production factor 2 homolog

Chain Cf: 70% 11% 19%



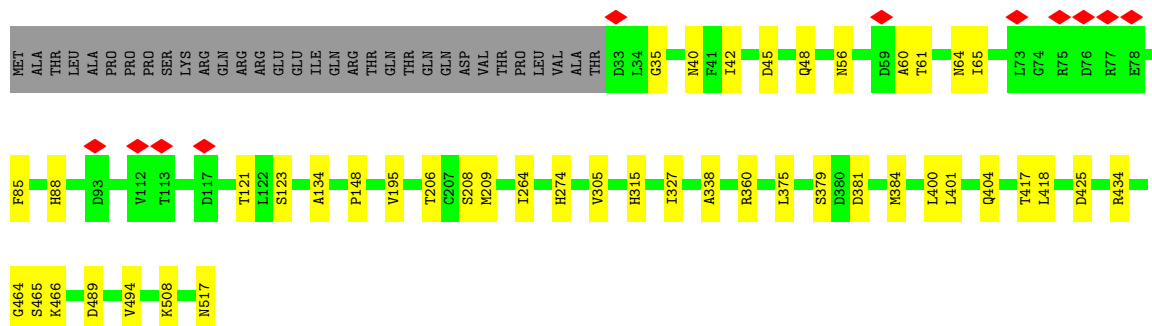
- Molecule 23: Ribosome biogenesis regulatory protein

Chain Cg: 87% 6% 7%



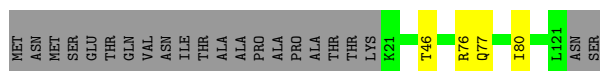
- Molecule 24: Ribosome assembly protein 4

Chain Ch: 85% 9% 6%



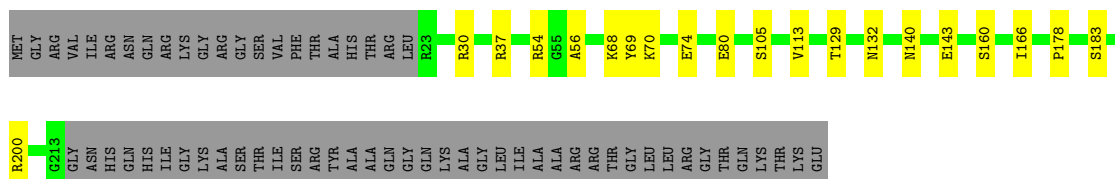
- Molecule 25: rRNA-processing protein

Chain Cz:  79% 18%



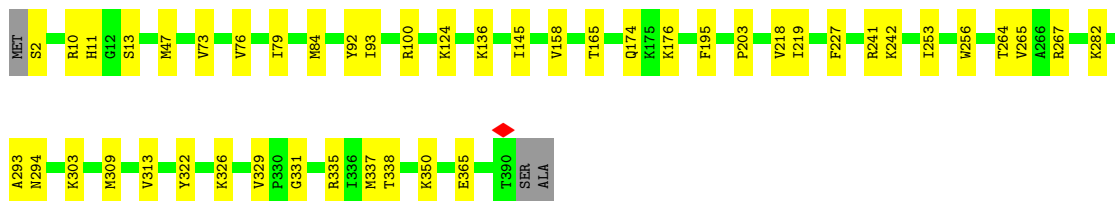
- Molecule 26: 60S ribosomal protein L2-like protein

Chain LA:  67% 8% 25%

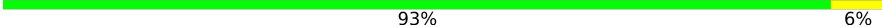


- Molecule 27: 60S ribosomal protein L3-like protein

Chain LB:  88% 12%



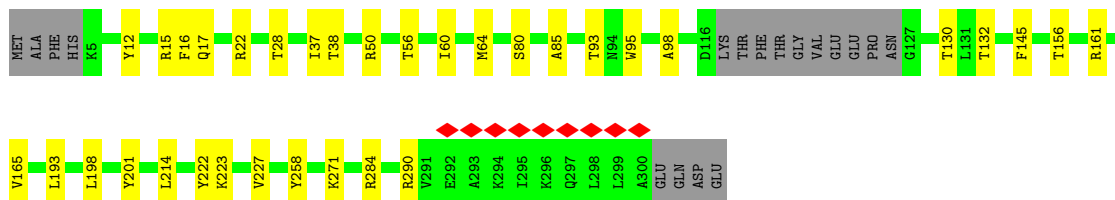
- Molecule 28: 60S ribosomal protein L4-like protein

Chain LC:  93% 6%



- Molecule 29: 60S ribosomal protein L5-like protein

Chain LD:  83% 11% 6%



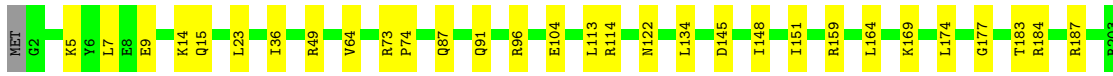
- Molecule 30: 60S ribosomal protein L6

Chain LE:  86% 9%



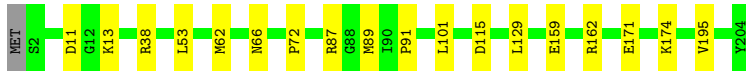
- Molecule 37: Ribosomal protein L15

Chain LN: 



- Molecule 38: 60S ribosomal protein L16-like protein

Chain LO: 91% 9%



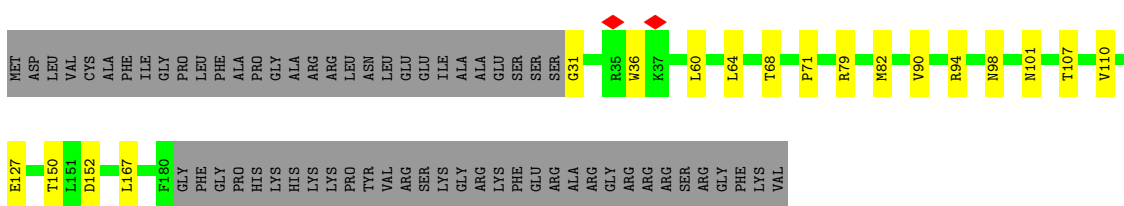
- Molecule 39: 60S ribosomal protein l17-like protein

Chain LP: 86% 6% 9%

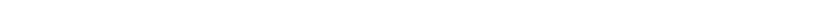


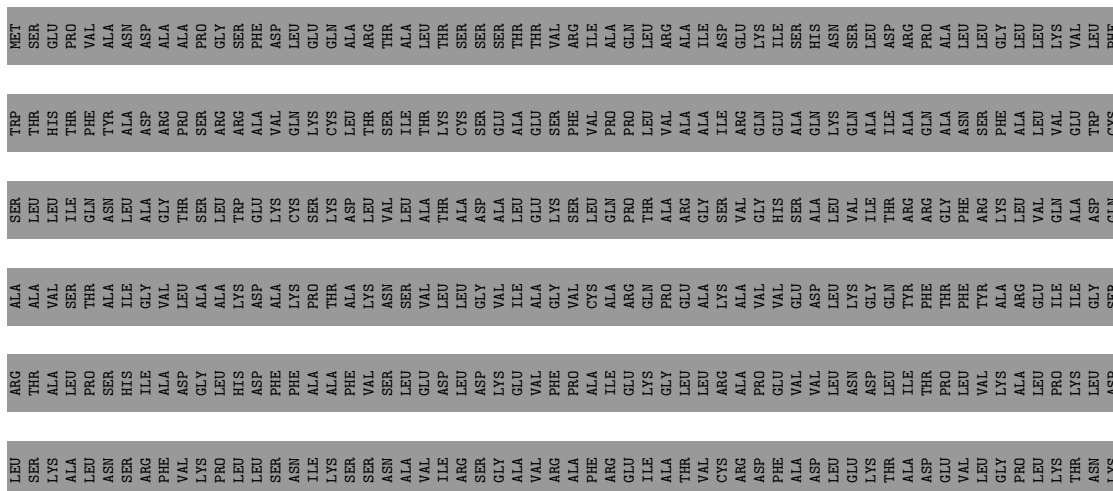
- Molecule 40: Ribosomal protein L18-like protein

Chain LQ: 62% 8% 30%



- Molecule 41: Ribosomal protein L19

Chain LR:  5% . 95%





[illegible]

GLU
ARG
GLN
ALA
ALA
LYS
ARG
ARG
ASN
ALA
LEU
LEU
GLY
GLU
GLU
GLU
SER
LYS

- Molecule 42: 60S ribosomal protein L20

Chain LS:  84% 16%

M1 Q8 R12 L24 S60 V61 N62 V63 I64 L70 K71 V72 K73 N89 T97 V100 E104 M110 R115 A116 R117 F118 L124 K125 V126 V127 P138 K141 H154 R155 R169 P170 S171 T172 F173 S174

- Molecule 43: 60S ribosomal protein l21-like protein

Chain LT:  71% 9% 19%

MET GLY HIS ALA ALA GLY LEU ARG SER THR ARG TYR ALA PHE SER ARG GLY PHE ARG LYS HIS GLY ILE PRO LEU SER THR LEU R32 I42 Q49 M52 K55 V74 R108 V109 K116 K120 A121 E122 G123 V124 R130 K147 P148 V154

A155 T158 T159 I160

- Molecule 44: 60S ribosomal protein L22-like protein

Chain LU:  77% 6% 17%

MET ALA PRO VAL LYS LYS SER GLY ALA LYS GLY LYS GLY PRO K16 I22 V59 I60 B81 R101 S106 V109 D120 ALA GLU GLU GLU ASP

- Molecule 45: 60S ribosomal protein l23-like protein

Chain LV:  88% 9% 3%

MET ALA LYS GLN R5 R6 M15 M25 M49 V56 P77 G102 V105 N106 P107 E110 M111 A135 M139

- Molecule 46: 60S ribosomal protein L25-like protein

Chain LX:  87% 6% 7%

MET ALA PRO LYS ASP VAL LYS LYS GLY ALA S12 K16 G17 K21 K36 K68 H78 P79 F97 I148 K152 V156

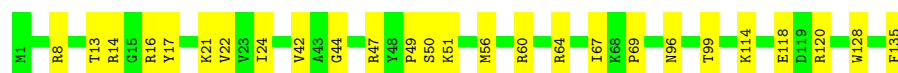
- Molecule 47: 60S ribosomal protein L26-like protein

Chain LY:  88% 9% 3%

M1 R15 M30 S46 Y73 K76 R86 T90 I96 P100 R120 R125 V128 G133 LYS LYS THR ALA ALA

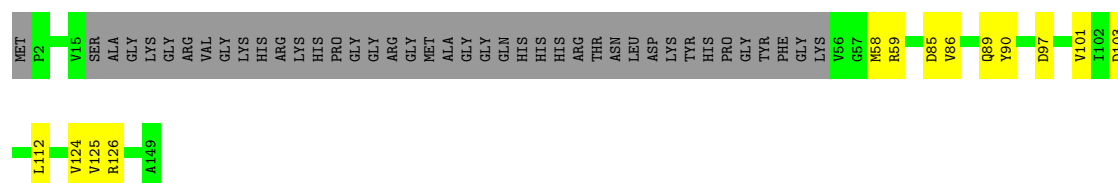
- Molecule 48: 60S ribosomal protein L27

Chain LZ:  81% 19%



- Molecule 49: 60S ribosomal protein L28-like protein

Chain La:  64% 9% 28%



- Molecule 50: 60S ribosomal protein l30-like protein

Chain Lc:  70% 18% 12%



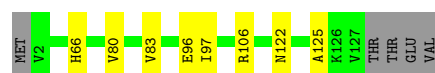
- Molecule 51: Putative 60S ribosomal protein

Chain Ld:  85% 7% 8%



- Molecule 52: 60S ribosomal protein L32-like protein

Chain Le:  90% 6% .

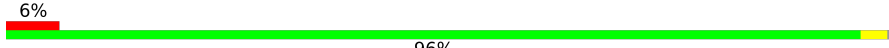


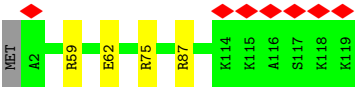
- Molecule 53: 60S ribosomal protein l33-like protein

Chain Lf:  90% 9% .

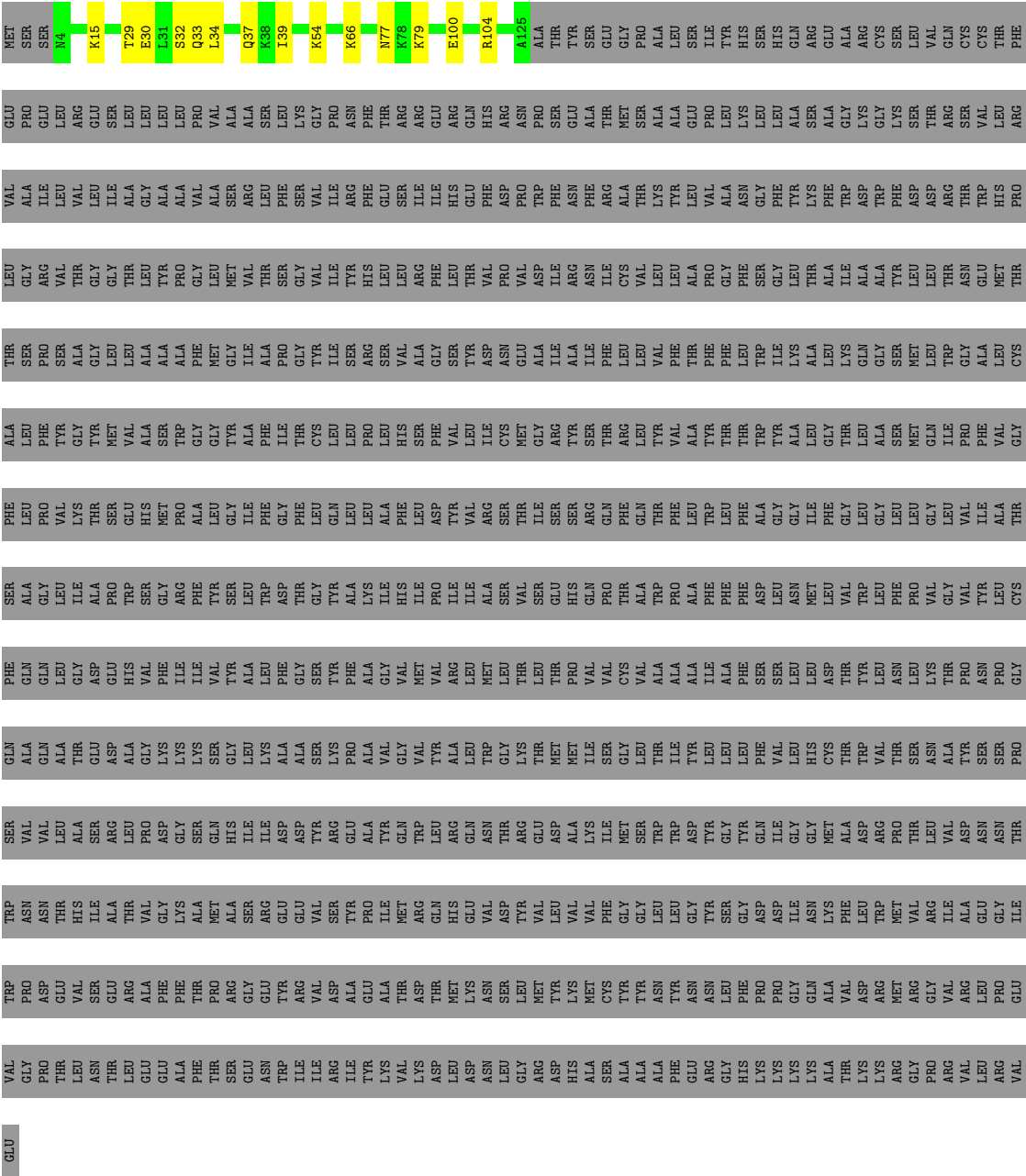


- Molecule 54: Ribosomal protein l34-like protein

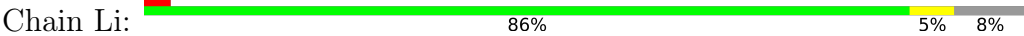
Chain Lg:  6% 96% . .



• Molecule 55: dolichyl-diphosphooligosaccharide--protein glycotransferase

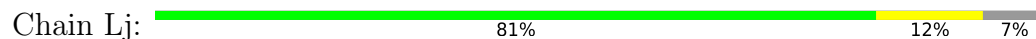


• Molecule 56: 60S ribosomal protein L36

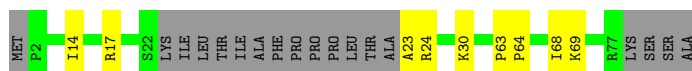




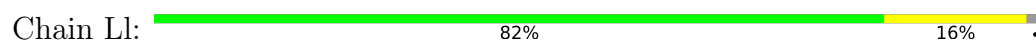
- Molecule 57: Ribosomal protein L37



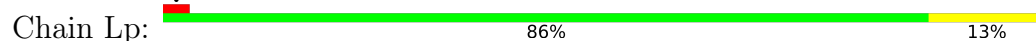
- Molecule 58: 60S ribosomal protein L38-like protein



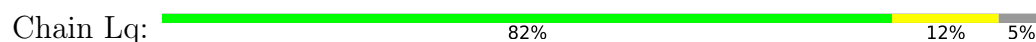
- Molecule 59: Ribosomal protein eL39



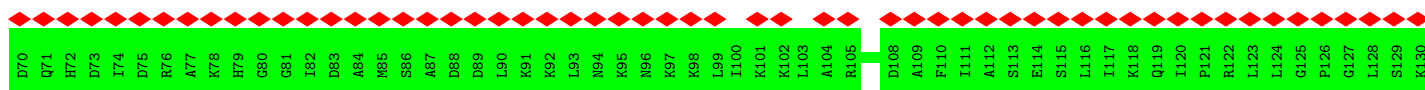
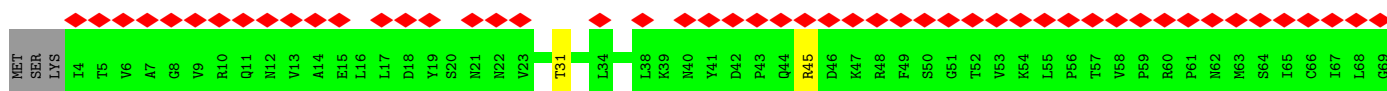
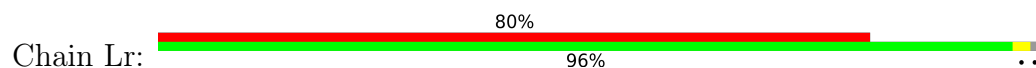
- Molecule 60: 60S ribosomal protein L43-like protein



- Molecule 61: Putative 60S ribosomal protein



- Molecule 62: Ribosomal protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25363	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.938	Depositor
Minimum map value	0.000	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.153	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	522.5, 522.5, 522.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, OMG, A2M, OMU, GTP, ZN, OMC

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	C1	0.15	1/74274 (0.0%)	0.31	0/115802
2	C2	0.14	0/3710	0.29	0/5778
3	C3	0.14	0/1958	0.32	0/3050
4	C4	0.15	0/2833	0.32	0/4414
5	CB	0.20	0/2153	0.51	0/2926
6	CF	0.16	0/1972	0.38	0/2660
7	CH	0.15	0/5147	0.38	0/6926
8	CI	0.19	0/1265	0.53	0/1702
9	CJ	0.16	0/3196	0.37	0/4319
10	CK	0.14	0/1939	0.34	0/2608
11	CL	0.18	0/631	0.39	0/843
12	CM	0.18	0/1805	0.46	0/2417
12	LF	0.19	0/2061	0.43	0/2765
13	CN	0.16	0/1878	0.42	0/2555
14	CO	0.15	0/470	0.37	0/619
15	CQ	0.21	0/1504	0.49	1/2000 (0.1%)
16	CS	0.23	1/2109 (0.0%)	0.46	0/2871
17	CT	0.17	0/3022	0.46	0/4132
17	CU	0.18	0/3034	0.51	0/4147
18	CV	0.22	0/4312	0.51	4/5897 (0.1%)
18	CW	0.19	0/4299	0.46	2/5882 (0.0%)
19	Cb	0.18	0/845	0.47	0/1128
20	Cd	0.15	0/3770	0.36	0/5082
21	Ce	0.16	0/2173	0.38	1/2890 (0.0%)
22	Cf	0.14	0/2326	0.37	0/3113
23	Cg	0.16	0/1508	0.39	0/2051
24	Ch	0.16	0/3908	0.44	0/5311
25	Cz	0.20	0/877	0.43	0/1148
26	LA	0.17	0/1488	0.44	0/2009
27	LB	0.16	0/3172	0.41	0/4260
28	LC	0.15	0/2808	0.36	0/3785
29	LD	0.15	0/2308	0.37	0/3105

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	LE	0.16	0/1504	0.37	0/2027
31	LG	0.17	0/1918	0.40	0/2565
32	LH	0.14	0/1515	0.37	0/2037
33	LJ	0.17	0/1379	0.44	0/1844
34	LK	0.18	0/1198	0.48	0/1611
35	LL	0.15	0/1614	0.36	0/2168
36	LM	0.18	0/1145	0.41	0/1539
37	LN	0.15	0/1741	0.36	0/2332
38	LO	0.17	0/1645	0.39	0/2205
39	LP	0.15	0/1367	0.38	0/1840
40	LQ	0.15	0/1218	0.39	0/1639
41	LR	0.14	0/1260	0.32	0/1683
42	LS	0.16	0/1461	0.39	0/1966
43	LT	0.18	0/1040	0.47	0/1401
44	LU	0.15	0/859	0.41	0/1151
45	LV	0.14	0/1009	0.36	0/1357
46	LX	0.19	0/1151	0.45	0/1547
47	LY	0.16	0/1070	0.43	0/1432
48	LZ	0.15	0/1135	0.37	0/1519
49	La	0.15	0/892	0.33	0/1200
50	Lc	0.16	0/714	0.45	0/960
51	Ld	0.15	0/889	0.36	0/1192
52	Le	0.14	0/1035	0.38	0/1379
53	Lf	0.15	0/883	0.37	0/1187
54	Lg	0.16	0/927	0.38	0/1244
55	Lh	0.19	0/1014	0.45	0/1349
56	Li	0.14	0/834	0.37	0/1099
57	Lj	0.17	0/712	0.44	0/944
58	Lk	0.19	0/640	0.48	0/850
59	Ll	0.14	0/446	0.30	0/593
60	Lp	0.19	0/706	0.54	0/940
61	Lq	0.15	0/1091	0.44	2/1468 (0.1%)
62	Lr	0.13	0/1055	0.36	0/1467
63	CR	0.20	0/2990	0.51	0/4073
All	All	0.16	2/188812 (0.0%)	0.37	10/272003 (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
17	CT	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	CS	126	THR	C-N	6.14	1.42	1.33
1	C1	1847	A2M	O3'-P	5.11	1.61	1.56

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	CV	351	PRO	CA-N-CD	-9.73	98.37	112.00
21	Ce	182	PRO	CA-N-CD	-7.02	102.18	112.00
15	CQ	161	ARG	CB-CG-CD	6.59	126.46	111.30
18	CW	451	LEU	CA-C-N	6.21	124.15	120.24
18	CW	451	LEU	C-N-CA	6.21	124.15	120.24
18	CV	400	ALA	CA-C-N	6.12	124.09	120.24
18	CV	400	ALA	C-N-CA	6.12	124.09	120.24
61	Lq	127	PRO	CA-C-N	5.65	128.51	120.49
61	Lq	127	PRO	C-N-CA	5.65	128.51	120.49
18	CV	351	PRO	N-CD-CG	-5.24	95.35	103.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	CT	42	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C1	67131	0	33866	411	0
2	C2	3319	0	1678	23	0
3	C3	1754	0	890	19	0
4	C4	2536	0	1286	18	0
5	CB	2107	0	2161	22	0
6	CF	1934	0	1945	13	0
7	CH	5063	0	5157	38	0
8	CI	1234	0	1245	17	0
9	CJ	3116	0	3122	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	CK	1903	0	1990	15	0
11	CL	622	0	641	7	0
12	CM	1773	0	1879	13	0
12	LF	2023	0	2132	12	0
13	CN	1853	0	1852	17	0
14	CO	468	0	503	3	0
15	CQ	1480	0	1523	19	0
16	CS	2063	0	2048	16	0
17	CT	2953	0	2886	39	0
17	CU	2965	0	2915	27	0
18	CV	4217	0	4334	36	0
18	CW	4204	0	4309	49	0
19	Cb	830	0	838	11	0
20	Cd	3691	0	3817	37	0
21	Ce	2148	0	2250	19	0
22	Cf	2282	0	2347	26	0
23	Cg	1478	0	1517	9	0
24	Ch	3809	0	3710	25	0
25	Cz	869	0	956	3	0
26	LA	1454	0	1490	15	0
27	LB	3104	0	3221	30	0
28	LC	2751	0	2875	15	0
29	LD	2266	0	2219	22	0
30	LE	1477	0	1567	13	0
31	LG	1889	0	2043	19	0
32	LH	1495	0	1573	11	0
33	LJ	1357	0	1385	14	0
34	LK	1184	0	1249	8	0
35	LL	1587	0	1655	15	0
36	LM	1126	0	1198	13	0
37	LN	1704	0	1767	19	0
38	LO	1611	0	1702	13	0
39	LP	1345	0	1375	9	0
40	LQ	1200	0	1296	13	0
41	LR	1241	0	1298	12	0
42	LS	1426	0	1481	22	0
43	LT	1021	0	1063	12	0
44	LU	846	0	883	5	0
45	LV	991	0	1044	8	0
46	LX	1133	0	1234	7	0
47	LY	1056	0	1143	9	0
48	LZ	1112	0	1181	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	La	872	0	903	12	0
50	Lc	705	0	751	10	0
51	Ld	875	0	918	7	0
52	Le	1017	0	1092	6	0
53	Lf	862	0	891	6	0
54	Lg	914	0	960	5	0
55	Lh	1003	0	1116	10	0
56	Li	827	0	906	5	0
57	Lj	698	0	726	11	0
58	Lk	632	0	693	5	0
59	Ll	436	0	473	8	0
60	Lp	698	0	737	7	0
61	Lq	1073	0	1130	11	0
62	Lr	1056	0	473	4	0
63	CR	2934	0	2855	39	0
64	CH	32	0	12	1	0
64	Cd	32	0	12	0	0
65	CH	1	0	0	0	0
65	Cd	2	0	0	0	0
66	CQ	1	0	0	0	0
66	Cb	1	0	0	0	0
66	Lg	1	0	0	0	0
66	Lj	1	0	0	0	0
66	Lp	1	0	0	0	0
67	CH	1	0	0	0	0
67	Cd	2	0	0	0	0
All	All	178878	0	144387	1179	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 (1179) 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)
3:C3:40:G:H1	3:C3:45:U:H3	1.12	0.95
1:C1:1809:G:HO2'	9:CJ:2:GLY:N	1.69	0.90
1:C1:1054:U:H3	1:C1:1070:G:H1	0.87	0.87
19:Cb:68:HIS:HE1	19:Cb:74:HIS:ND1	1.82	0.78
1:C1:2421:A:H62	1:C1:2442:C:H41	1.37	0.72
19:Cb:68:HIS:CE1	19:Cb:74:HIS:ND1	2.58	0.71
18:CW:157:LEU:O	18:CW:161:LYS:HB2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LB:136:LYS:HG3	27:LB:145:ILE:HD11	1.74	0.68
5:CB:183:VAL:O	5:CB:215:ARG:NH2	2.27	0.68
5:CB:215:ARG:NH1	5:CB:219:GLU:OE1	2.27	0.68
1:C1:2899:A:H2'	27:LB:256:TRP:HB3	1.75	0.68
17:CT:232:SER:HB2	18:CW:595:ARG:HD3	1.76	0.68
1:C1:2101:A:HO2'	57:Lj:2:THR:N	1.92	0.68
19:Cb:52:CYS:SG	19:Cb:74:HIS:HE1	2.16	0.67
18:CW:30:ILE:HD11	18:CW:83:CYS:HB3	1.78	0.66
1:C1:3289:G:H1	1:C1:3298:U:H3	1.40	0.66
46:LX:78:HIS:HB2	55:Lh:39:ILE:HD13	1.77	0.66
1:C1:448:C:H41	30:LE:15:ARG:HH21	1.42	0.66
17:CU:27:ILE:HB	17:CU:42:PHE:HB2	1.77	0.66
17:CT:90:ARG:HG2	17:CT:104:THR:HG22	1.78	0.65
1:C1:3:G:H1'	46:LX:36:LYS:HE2	1.78	0.65
1:C1:2197:G:HO2'	20:Cd:2:GLY:N	1.95	0.65
1:C1:1207:C:O2'	6:CF:8:ARG:NH2	2.30	0.65
63:CR:344:VAL:HG12	63:CR:347:LEU:H	1.62	0.65
27:LB:331:GLY:HA3	27:LB:337:MET:HE1	1.79	0.65
1:C1:3204:C:H2'	1:C1:3205:G:H8	1.62	0.64
20:Cd:285:ILE:HD11	20:Cd:296:ALA:HB2	1.80	0.63
61:Lq:31:ASP:HB3	61:Lq:34:ASN:HB2	1.80	0.63
29:LD:37:ILE:HG13	29:LD:38:THR:HG23	1.81	0.63
26:LA:105:SER:HB3	26:LA:160:SER:HB3	1.80	0.63
22:Cf:145:ALA:HB3	22:Cf:188:THR:HG22	1.81	0.62
24:Ch:35:GLY:O	24:Ch:56:ASN:ND2	2.32	0.62
16:CS:117:ARG:NH1	16:CS:157:ASP:OD2	2.32	0.62
63:CR:357:PRO:HD3	63:CR:392:GLU:HB3	1.82	0.62
1:C1:1431:U:H2'	1:C1:1432:A2M:H8	1.80	0.62
17:CU:303:GLN:OE1	17:CU:320:ASN:ND2	2.32	0.62
14:CO:13:ASN:OD1	14:CO:16:ARG:NH2	2.32	0.62
1:C1:2932:G:N7	10:CK:140:LYS:NZ	2.42	0.61
20:Cd:428:GLU:HB2	20:Cd:445:LYS:HZ1	1.65	0.61
28:LC:185:VAL:HG11	28:LC:231:GLY:HA3	1.82	0.61
8:CI:240:VAL:HG21	46:LX:16:LYS:HZ2	1.65	0.61
18:CW:349:VAL:HG12	18:CW:378:LEU:HD21	1.83	0.61
7:CH:186:VAL:HG23	7:CH:187:THR:HG23	1.82	0.61
24:Ch:195:VAL:HG12	24:Ch:206:THR:HG22	1.82	0.61
8:CI:246:ARG:NH2	21:Ce:443:ILE:OXT	2.34	0.61
1:C1:984:A:N1	1:C1:1033:U:O2'	2.34	0.61
2:C2:112:U:OP2	59:Ll:8:ARG:NH1	2.33	0.61
7:CH:628:ASN:O	39:LP:125:GLN:NE2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CT:385:LEU:HD11	18:CV:30:ILE:HD11	1.83	0.60
1:C1:2223:U:H2'	1:C1:2224:G:H4'	1.83	0.60
13:CN:116:LEU:HD11	13:CN:177:LEU:HD21	1.82	0.60
18:CV:177:ASP:OD1	18:CV:226:ASN:ND2	2.34	0.60
18:CV:301:PRO:O	18:CV:312:ARG:NH2	2.34	0.60
20:Cd:181:GLU:OE2	20:Cd:182:LYS:NZ	2.32	0.60
55:Lh:15:LYS:O	55:Lh:66:LYS:NZ	2.35	0.60
1:C1:52:A:H5'	35:LL:20:ARG:HH12	1.67	0.60
1:C1:1619:C:OP2	54:Lg:75:ARG:NH1	2.30	0.60
10:CK:163:ARG:HH22	20:Cd:228:LYS:HG2	1.66	0.60
7:CH:644:MET:HE3	28:LC:72:VAL:HG11	1.84	0.60
63:CR:342:LEU:O	63:CR:374:HIS:NE2	2.30	0.60
1:C1:949:A:H62	1:C1:1098:G:H8	1.48	0.60
1:C1:1929:G:OP2	41:LR:135:LYS:NZ	2.34	0.60
26:LA:140:ASN:ND2	26:LA:143:GLU:OE2	2.35	0.60
18:CV:368:ARG:HH21	18:CW:8:ARG:HH22	1.48	0.60
18:CV:140:LEU:HA	18:CV:143:GLU:HG2	1.84	0.60
37:LN:159:ARG:HB3	37:LN:164:LEU:HB2	1.83	0.59
18:CW:396:LEU:HB3	18:CW:399:ASN:HB2	1.83	0.59
1:C1:643:C:H2'	1:C1:644:A:H8	1.67	0.59
9:CJ:263:ASP:OD1	12:CM:146:ASN:ND2	2.36	0.59
13:CN:107:VAL:HG23	13:CN:108:ILE:HG13	1.83	0.59
3:C3:71:G:H1	3:C3:134:U:H3	1.50	0.59
5:CB:103:ASP:O	5:CB:206:ARG:NH1	2.36	0.59
16:CS:242:GLU:O	18:CV:570:ARG:NH2	2.35	0.59
1:C1:706:G:OP2	1:C1:706:G:N2	2.34	0.59
1:C1:1240:C:O2	6:CF:54:LYS:NZ	2.36	0.59
18:CV:78:ARG:HD2	18:CV:110:VAL:HG22	1.84	0.59
11:CL:5:ILE:HD13	38:LO:53:LEU:HD12	1.84	0.59
1:C1:2544:G:H5'	21:Ce:436:TRP:HE1	1.68	0.59
17:CU:338:LYS:HD2	17:CU:339:PRO:HD2	1.84	0.59
1:C1:1912:A:N1	20:Cd:448:ARG:NH2	2.49	0.59
18:CV:121:GLU:HG3	18:CV:178:THR:HG21	1.85	0.59
22:Cf:104:ARG:NH1	22:Cf:166:ASP:OD2	2.33	0.59
1:C1:1614:G:N7	48:LZ:16:ARG:NH1	2.51	0.58
4:C4:100:G:OP1	22:Cf:259:ARG:NH2	2.35	0.58
17:CU:196:SER:O	17:CU:203:CYS:HA	2.03	0.58
1:C1:1264:U:H2'	1:C1:1265:G:H8	1.68	0.58
4:C4:26:C:H5'	29:LD:56:THR:HB	1.85	0.58
26:LA:129:THR:HG1	26:LA:132:ASN:HD22	1.48	0.58
1:C1:1159:C:H4'	38:LO:91:PRO:HD3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:Lh:33:GLN:O	55:Lh:37:GLN:NE2	2.36	0.58
28:LC:319:PRO:HB2	28:LC:326:MET:HE2	1.86	0.58
1:C1:2079:G:OP1	1:C1:2081:C:N4	2.37	0.58
16:CS:144:ARG:NH2	16:CS:183:THR:OG1	2.37	0.58
18:CV:306:LEU:HD21	18:CV:374:LEU:HB2	1.85	0.58
21:Ce:307:ILE:HG12	21:Ce:310:ARG:HH21	1.69	0.58
37:LN:96:ARG:NH2	37:LN:104:GLU:OE2	2.36	0.58
1:C1:1211:A:H5''	6:CF:203:SER:HB3	1.85	0.58
1:C1:2419:A:N6	1:C1:2424:A:N7	2.50	0.58
63:CR:412:GLU:OE1	63:CR:416:ARG:NH1	2.36	0.58
13:CN:109:VAL:HB	13:CN:149:GLY:HA2	1.86	0.57
22:Cf:233:ARG:HH21	22:Cf:247:GLU:HG2	1.68	0.57
3:C3:3:C:N4	31:LG:88:ASN:OD1	2.37	0.57
3:C3:25:U:OP2	12:CM:73:ARG:NH1	2.37	0.57
17:CT:339:PRO:HA	17:CT:364:MET:HE1	1.86	0.57
22:Cf:105:MET:HG2	22:Cf:110:VAL:HA	1.86	0.57
7:CH:174:PHE:HE2	7:CH:266:GLN:HA	1.69	0.57
13:CN:152:MET:HG3	13:CN:161:VAL:HG12	1.85	0.57
17:CU:126:VAL:HG23	17:CU:127:GLN:HG3	1.86	0.57
37:LN:87:GLN:OE1	37:LN:91:GLN:NE2	2.37	0.57
1:C1:702:G:HO2'	1:C1:735:C:HO2'	1.51	0.57
48:LZ:49:PRO:HD3	48:LZ:67:ILE:HG12	1.86	0.57
56:Li:65:ARG:NH1	56:Li:68:GLU:OE2	2.38	0.57
1:C1:1438:U:OP1	1:C1:1859:A:N6	2.37	0.57
1:C1:1812:OMC:H2'	1:C1:1813:G:H8	1.69	0.57
1:C1:2429:G:N2	62:Lr:209:THR:O	2.36	0.57
8:CI:225:GLY:HA3	8:CI:282:VAL:HG12	1.86	0.57
33:LJ:94:ARG:HG2	33:LJ:157:ARG:HH21	1.70	0.57
41:LR:98:ARG:NH1	41:LR:130:ASN:OD1	2.37	0.57
1:C1:1081:A:OP2	43:LT:130:ARG:NH1	2.37	0.57
13:CN:106:ASN:ND2	45:LV:135:ALA:O	2.36	0.57
17:CT:135:THR:HG22	17:CT:183:VAL:HG11	1.85	0.57
20:Cd:411:ILE:HG13	20:Cd:439:LEU:HD11	1.87	0.57
7:CH:242:LEU:O	7:CH:280:LYS:NZ	2.37	0.57
24:Ch:40:ASN:OD1	24:Ch:48:GLN:NE2	2.37	0.57
1:C1:2087:G:O2'	20:Cd:448:ARG:NH1	2.38	0.57
1:C1:3209:A:OP2	30:LE:151:LYS:NZ	2.38	0.57
7:CH:86:ASP:OD2	7:CH:89:HIS:ND1	2.38	0.57
17:CT:89:ILE:HG21	17:CT:92:LEU:HD23	1.87	0.57
1:C1:243:U:O4	35:LL:132:LYS:NZ	2.37	0.57
2:C2:83:C:OP1	2:C2:85:G:N2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CW:78:ARG:HD2	18:CW:110:VAL:HG22	1.86	0.57
21:Ce:263:ALA:HB1	21:Ce:267:ARG:HH12	1.69	0.57
22:Cf:76:CYS:HA	22:Cf:105:MET:HE1	1.86	0.57
1:C1:2833:G:OP2	1:C1:2833:G:N2	2.35	0.57
27:LB:10:ARG:NH1	27:LB:11:HIS:O	2.38	0.56
1:C1:69:C:OP2	1:C1:294:G:N2	2.37	0.56
1:C1:582:G:O2'	30:LE:35:GLN:O	2.23	0.56
18:CW:267:ARG:NH1	18:CW:370:GLU:OE2	2.38	0.56
20:Cd:95:MET:HE2	20:Cd:118:ARG:HG2	1.86	0.56
29:LD:130:THR:HG22	29:LD:132:THR:H	1.70	0.56
37:LN:23:LEU:O	37:LN:122:ASN:ND2	2.36	0.56
1:C1:1476:G:OP2	1:C1:1476:G:N2	2.36	0.56
4:C4:53:U:O2'	4:C4:55:A:N7	2.38	0.56
15:CQ:179:GLU:OE1	51:Ld:86:ARG:NH1	2.39	0.56
17:CT:280:VAL:HG13	17:CT:303:GLN:HE21	1.71	0.56
18:CV:104:ILE:HG12	18:CV:130:LEU:HD13	1.87	0.56
22:Cf:89:PHE:HB3	22:Cf:101:THR:HB	1.87	0.56
31:LG:165:LEU:HA	37:LN:7:LEU:HD11	1.86	0.56
47:LY:86:ARG:HB3	47:LY:96:ILE:HD11	1.88	0.56
7:CH:497:GLU:HG3	51:Ld:107:LYS:HD2	1.88	0.56
15:CQ:57:LYS:HD3	19:Cb:94:ALA:HA	1.87	0.56
9:CJ:75:GLU:HG3	9:CJ:77:LEU:H	1.69	0.56
10:CK:202:LYS:NZ	20:Cd:71:GLU:OE1	2.37	0.56
51:Ld:28:LEU:HD11	51:Ld:40:ALA:HB2	1.86	0.56
1:C1:1337:G:N2	1:C1:1339:U:O2'	2.35	0.56
1:C1:1559:G:OP2	1:C1:1559:G:N2	2.35	0.56
5:CB:73:HIS:HD1	5:CB:75:SER:H	1.51	0.56
18:CV:267:ARG:O	18:CV:363:ASN:ND2	2.38	0.56
20:Cd:238:HIS:HD1	20:Cd:332:ILE:HG13	1.70	0.56
1:C1:1242:A:N3	1:C1:1263:C:O2'	2.38	0.56
1:C1:2160:C:N3	1:C1:2210:G:N2	2.54	0.56
1:C1:2767:A:N6	1:C1:2913:U:O2'	2.38	0.56
30:LE:24:ALA:O	61:Lq:88:ARG:NH1	2.38	0.56
57:Lj:21:ARG:NH2	57:Lj:41:ALA:O	2.30	0.56
1:C1:2892:A:OP2	45:LV:6:ARG:NH1	2.35	0.56
16:CS:73:ASP:OD1	16:CS:76:ARG:NH2	2.34	0.56
17:CT:192:ASN:HD21	17:CT:209:GLN:HG3	1.71	0.56
1:C1:563:U:H2'	1:C1:564:A:H8	1.70	0.56
18:CV:263:ASP:OD1	18:CV:345:ARG:NH2	2.35	0.56
35:LL:115:ARG:NH2	35:LL:155:PHE:O	2.37	0.56
1:C1:1420:OMC:HM22	1:C1:1421:U:H5'	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2878:A:H61	1:C1:2886:C:H42	1.54	0.56
9:CJ:380:ARG:NH1	9:CJ:401:LEU:O	2.39	0.56
1:C1:1260:C:H2'	1:C1:1261:A:H8	1.70	0.55
17:CT:374:LEU:HD23	17:CT:381:PRO:HD2	1.87	0.55
18:CW:268:ALA:HA	18:CW:366:ILE:HG13	1.87	0.55
1:C1:346:G:O6	57:Lj:55:ARG:NH2	2.39	0.55
1:C1:948:U:H2'	1:C1:949:A:H8	1.71	0.55
16:CS:144:ARG:HE	16:CS:182:LYS:HG2	1.71	0.55
20:Cd:235:VAL:O	20:Cd:329:VAL:HA	2.06	0.55
1:C1:64:A:H5''	37:LN:174:LEU:HD13	1.88	0.55
1:C1:782:G:H22	28:LC:102:ALA:HA	1.71	0.55
1:C1:2157:G:O6	20:Cd:315:ARG:NH2	2.39	0.55
2:C2:63:G:O2'	55:Lh:54:LYS:NZ	2.38	0.55
18:CW:322:ALA:O	18:CW:326:ASN:ND2	2.40	0.55
38:LO:13:LYS:O	42:LS:169:ARG:NH2	2.40	0.55
1:C1:1737:G:OP1	44:LU:101:ARG:NH2	2.34	0.55
1:C1:3002:A:H4'	27:LB:13:SER:HB2	1.88	0.55
17:CU:2:LEU:HD12	17:CU:333:PRO:HB2	1.89	0.55
2:C2:71:A:O2'	2:C2:83:C:N4	2.39	0.55
22:Cf:277:THR:HG22	22:Cf:279:GLN:H	1.72	0.55
1:C1:2923:G:O2'	20:Cd:30:ARG:NH2	2.38	0.55
4:C4:23:A:N3	4:C4:119:U:O2'	2.39	0.55
5:CB:282:TYR:OH	8:CI:316:ARG:NH1	2.39	0.55
7:CH:544:ILE:O	7:CH:549:ARG:NH1	2.40	0.55
18:CW:398:ALA:HA	18:CW:438:LEU:HD11	1.89	0.55
61:Lq:7:ASP:OD1	61:Lq:41:ARG:NH1	2.38	0.55
5:CB:24:LEU:HB2	5:CB:28:LYS:HZ3	1.71	0.55
13:CN:219:GLU:HA	13:CN:224:LEU:HD12	1.89	0.55
17:CT:230:PRO:HG3	18:CW:583:ARG:HE	1.72	0.54
61:Lq:139:ARG:O	61:Lq:140:ARG:NE	2.40	0.54
1:C1:1685:U:O2	1:C1:1766:G:O2'	2.25	0.54
1:C1:3270:U:H5''	27:LB:309:MET:HE2	1.89	0.54
29:LD:85:ALA:HB2	29:LD:258:TYR:HB2	1.89	0.54
62:Lr:45:ARG:O	63:CR:341:LYS:NZ	2.40	0.54
1:C1:1611:C:OP2	48:LZ:47:ARG:NH2	2.40	0.54
2:C2:103:G:OP2	2:C2:105:A:O2'	2.24	0.54
7:CH:183:VAL:HG21	7:CH:219:ASP:HB2	1.89	0.54
18:CW:293:GLY:HA3	18:CW:302:PRO:HA	1.88	0.54
22:Cf:87:MET:HB2	22:Cf:103:VAL:HB	1.90	0.54
2:C2:154:C:H5'	31:LG:184:LYS:HD3	1.90	0.54
7:CH:315:GLU:OE2	7:CH:337:ARG:NH1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:LM:54:ARG:HG2	42:LS:70:LEU:HD22	1.90	0.54
1:C1:151:G:H5''	1:C1:152:G:H2'	1.90	0.54
1:C1:258:A:OP1	56:Li:38:ARG:NH1	2.41	0.54
1:C1:1658:G:O6	44:LU:81:ARG:NH2	2.39	0.54
1:C1:2112:A:N6	1:C1:2150:G:O2'	2.39	0.54
63:CR:303:GLN:NE2	63:CR:307:GLU:OE2	2.41	0.54
17:CU:231:SER:HA	18:CV:582:VAL:HG11	1.90	0.54
32:LH:10:ILE:HG12	32:LH:109:ARG:HG2	1.90	0.54
39:LP:125:GLN:HB3	39:LP:141:SER:HB2	1.90	0.54
4:C4:44:C:OP2	33:LJ:138:ARG:NH2	2.40	0.54
24:Ch:264:ILE:HD12	24:Ch:274:HIS:HB2	1.89	0.54
28:LC:236:PRO:HG2	28:LC:239:ALA:HB3	1.89	0.54
1:C1:282:U:H2'	1:C1:283:G:H8	1.72	0.54
1:C1:341:C:O2	1:C1:345:A:O2'	2.26	0.54
33:LJ:38:LEU:HD13	33:LJ:70:VAL:HG23	1.89	0.54
3:C3:64:G:O6	8:CI:278:ARG:NH1	2.40	0.54
25:Cz:76:ARG:NH1	25:Cz:77:GLN:OE1	2.41	0.54
32:LH:146:THR:HG23	32:LH:148:CYS:H	1.73	0.54
17:CT:192:ASN:O	17:CT:207:ASN:ND2	2.41	0.53
17:CU:9:ALA:HB3	17:CU:327:ASN:HB2	1.91	0.53
18:CV:252:ARG:NH1	18:CV:338:GLU:OE2	2.41	0.53
18:CW:209:ILE:HD11	18:CW:231:LEU:HD12	1.89	0.53
18:CW:420:GLN:HG2	18:CW:421:LEU:HD12	1.89	0.53
1:C1:259:C:OP1	37:LN:5:LYS:NZ	2.37	0.53
1:C1:1373:A:N6	1:C1:1401:A:O2'	2.42	0.53
1:C1:2389:U:H3	1:C1:2562:G:H1	1.57	0.53
1:C1:2453:C:O2'	62:Lr:211:SER:O	2.27	0.53
18:CV:24:ARG:NH1	18:CW:216:ASN:OD1	2.41	0.53
24:Ch:327:ILE:HB	24:Ch:375:LEU:HD11	1.90	0.53
1:C1:129:G:H5''	46:LX:58:LYS:HE3	1.90	0.53
1:C1:1228:A:N7	1:C1:1254:A:O2'	2.41	0.53
1:C1:2632:A:OP1	33:LJ:96:ASN:ND2	2.42	0.53
16:CS:275:ARG:NH1	16:CS:281:MET:SD	2.81	0.53
18:CW:322:ALA:HA	18:CW:325:ASN:HB2	1.90	0.53
34:LK:10:ILE:HG12	34:LK:65:GLN:HB2	1.90	0.53
1:C1:2314:U:H2'	1:C1:2315:A:H8	1.73	0.53
3:C3:55:U:O2'	3:C3:58:A:N7	2.35	0.53
1:C1:278:A:H8	1:C1:297:G:H1'	1.73	0.53
18:CV:420:GLN:HG2	18:CV:421:LEU:HD12	1.89	0.53
18:CW:301:PRO:O	18:CW:312:ARG:NH2	2.42	0.53
1:C1:842:G:H8	26:LA:183:SER:HB3	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2920:G:O2'	20:Cd:366:TYR:O	2.27	0.53
63:CR:116:ARG:NH2	63:CR:155:GLU:OE2	2.42	0.53
1:C1:210:G:OP1	47:LY:15:ARG:NH1	2.41	0.53
1:C1:813:G:O2'	1:C1:1844:A:N3	2.39	0.53
1:C1:1095:A:H2'	1:C1:1096:G:C8	2.43	0.53
12:CM:21:LYS:O	12:CM:25:GLN:OE1	2.27	0.53
18:CV:393:ILE:HG21	18:CV:434:GLU:HB3	1.90	0.53
28:LC:114:ILE:HB	28:LC:119:LYS:HE3	1.90	0.53
60:Lp:51:ALA:HB3	60:Lp:54:ILE:HD12	1.90	0.53
1:C1:64:A:N3	1:C1:79:U:O2'	2.40	0.53
1:C1:1879:G:O2'	1:C1:2297:U:O4	2.26	0.53
18:CW:205:LEU:HD11	18:CW:230:LEU:HD23	1.90	0.53
21:Ce:248:ARG:NH2	21:Ce:252:GLU:OE2	2.42	0.53
1:C1:1824:C:O2'	57:Lj:11:ARG:NH1	2.42	0.52
9:CJ:36:LEU:HD11	9:CJ:75:GLU:HG2	1.91	0.52
20:Cd:364:TRP:HA	20:Cd:377:ASP:O	2.09	0.52
1:C1:639:G:O2'	1:C1:1418:A:OP1	2.27	0.52
1:C1:2591:G:H21	1:C1:2605:C:H41	1.57	0.52
1:C1:2789:G:H2'	1:C1:2790:G:C8	2.44	0.52
9:CJ:379:PRO:HB2	9:CJ:382:PRO:HG2	1.90	0.52
27:LB:282:LYS:NZ	27:LB:350:LYS:O	2.37	0.52
42:LS:12:ARG:HB3	42:LS:24:LEU:HD23	1.90	0.52
47:LY:30:MET:HB3	47:LY:100:PRO:HG2	1.91	0.52
13:CN:85:ARG:NH2	13:CN:89:PRO:O	2.42	0.52
29:LD:214:LEU:HB3	29:LD:222:TYR:HB2	1.92	0.52
41:LR:99:GLN:HE22	41:LR:128:LYS:HA	1.75	0.52
40:LQ:107:THR:HG23	40:LQ:127:GLU:HG2	1.92	0.52
1:C1:118:U:O2'	21:Ce:106:ARG:NH2	2.42	0.52
1:C1:1460:A:OP1	1:C1:3033:G:O2'	2.26	0.52
2:C2:86:U:O2	57:Lj:87:ARG:NH1	2.42	0.52
2:C2:153:U:OP1	31:LG:66:LYS:NZ	2.41	0.52
35:LL:191:ASP:OD1	35:LL:198:ARG:NH1	2.35	0.52
1:C1:262:G:H5''	37:LN:14:LYS:HE2	1.91	0.52
9:CJ:25:LYS:HE3	9:CJ:73:LEU:HD11	1.90	0.52
10:CK:241:ARG:NH1	20:Cd:79:ASN:OD1	2.42	0.52
17:CT:179:THR:N	17:CT:197:ALA:O	2.41	0.52
24:Ch:417:THR:HG23	24:Ch:418:LEU:HG	1.92	0.52
27:LB:253:ILE:HB	27:LB:265:VAL:HG11	1.91	0.52
33:LJ:85:LEU:HD21	33:LJ:164:PHE:HE1	1.75	0.52
1:C1:1316:C:OP1	40:LQ:31:GLY:N	2.43	0.52
1:C1:1361:U:H2'	1:C1:1362:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2900:A:N7	27:LB:2:SER:N	2.58	0.52
1:C1:2919:C:H2'	1:C1:2920:G:H8	1.75	0.52
18:CV:210:ALA:O	18:CV:312:ARG:NH1	2.43	0.52
63:CR:134:ILE:HD11	63:CR:185:LYS:HB3	1.92	0.52
13:CN:140:GLN:HG2	13:CN:173:LEU:HD21	1.92	0.52
40:LQ:94:ARG:O	40:LQ:98:ASN:ND2	2.43	0.52
1:C1:2713:G:OP2	23:Cg:119:ARG:NH2	2.42	0.52
12:CM:102:PRO:HB2	12:CM:105:PRO:HD2	1.92	0.52
17:CU:143:SER:OG	17:CU:144:ASP:N	2.42	0.52
20:Cd:427:TYR:O	20:Cd:445:LYS:NZ	2.40	0.52
12:LF:67:GLU:OE1	12:LF:70:ARG:NH2	2.43	0.52
40:LQ:150:THR:OG1	40:LQ:152:ASP:OD1	2.27	0.52
1:C1:1560:U:OP1	26:LA:68:LYS:NZ	2.41	0.51
15:CQ:16:SER:HB3	27:LB:73:VAL:HG11	1.91	0.51
16:CS:146:GLY:HA3	16:CS:158:THR:HG21	1.92	0.51
17:CU:97:ASP:OD2	17:CU:97:ASP:N	2.42	0.51
17:CU:117:ARG:NH2	17:CU:158:GLU:O	2.43	0.51
18:CV:3:ALA:HA	18:CV:55:THR:HG22	1.91	0.51
1:C1:2103:U:OP2	7:CH:657:LYS:NZ	2.41	0.51
1:C1:2355:C:O2'	27:LB:267:ARG:NH1	2.36	0.51
3:C3:49:G:H4'	5:CB:238:SER:HB2	1.91	0.51
20:Cd:160:THR:OG1	20:Cd:162:ASP:OD1	2.24	0.51
12:LF:23:LYS:HA	12:LF:26:GLU:HG2	1.91	0.51
48:LZ:24:ILE:HA	48:LZ:42:VAL:HG12	1.91	0.51
1:C1:344:A:N6	59:LI:37:TYR:O	2.39	0.51
1:C1:1641:G:H2'	1:C1:1642:G:C8	2.45	0.51
5:CB:73:HIS:ND1	5:CB:75:SER:O	2.43	0.51
49:La:97:ASP:OD1	49:La:97:ASP:N	2.43	0.51
4:C4:16:C:N3	4:C4:64:A:N6	2.58	0.51
17:CU:85:LEU:HB2	17:CU:89:ILE:HD11	1.92	0.51
17:CU:195:VAL:HG22	17:CU:205:ILE:HG12	1.91	0.51
1:C1:333:C:OP2	28:LC:199:ARG:NH1	2.37	0.51
1:C1:3299:U:H2'	1:C1:3300:A:H8	1.75	0.51
12:CM:103:PRO:HA	12:CM:106:ARG:HG2	1.91	0.51
63:CR:181:ARG:HB3	63:CR:218:ASP:H	1.75	0.51
1:C1:1067:A:H2'	1:C1:1068:A:C8	2.46	0.51
13:CN:186:VAL:HG12	13:CN:218:ILE:HD11	1.93	0.51
48:LZ:50:SER:HB2	48:LZ:64:ARG:HB3	1.92	0.51
1:C1:877:A:O2'	1:C1:879:U:OP2	2.27	0.51
1:C1:2745:G:N2	49:La:58:MET:SD	2.76	0.51
17:CU:71:VAL:HB	17:CU:81:ALA:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:Ce:434:GLU:HB3	21:Ce:439:LYS:HE3	1.93	0.51
24:Ch:379:SER:OG	24:Ch:381:ASP:OD1	2.29	0.51
27:LB:84:MET:O	27:LB:203:PRO:HA	2.11	0.51
1:C1:382:A:H5''	39:LP:16:ARG:HG3	1.91	0.51
3:C3:7:C:OP1	5:CB:162:ARG:NH1	2.44	0.51
3:C3:12:A:OP2	5:CB:188:ARG:NH2	2.43	0.51
48:LZ:16:ARG:NH2	48:LZ:17:TYR:OH	2.44	0.51
49:La:112:LEU:HD22	49:La:125:VAL:HG11	1.93	0.51
1:C1:643:C:H2'	1:C1:644:A:C8	2.44	0.51
1:C1:1766:G:H2'	1:C1:1767:A:C8	2.46	0.51
2:C2:26:U:O2'	28:LC:52:ALA:O	2.28	0.51
63:CR:178:THR:HA	63:CR:181:ARG:HE	1.75	0.51
1:C1:1219:G:N2	1:C1:1227:A:OP1	2.43	0.51
1:C1:1758:G:O2'	1:C1:1760:G:OP2	2.29	0.51
1:C1:2865:C:OP1	7:CH:23:ARG:NH2	2.44	0.51
2:C2:126:A:O2'	2:C2:128:U:OP2	2.27	0.51
23:Cg:43:ASP:HB3	23:Cg:46:VAL:HG12	1.93	0.51
49:La:85:ASP:O	49:La:89:GLN:OE1	2.29	0.51
49:La:103:ASP:OD1	49:La:126:ARG:NH1	2.44	0.51
61:Lq:9:ILE:HG22	61:Lq:47:VAL:HG22	1.91	0.51
1:C1:450:U:O4	1:C1:468:G:N2	2.44	0.50
1:C1:523:G:H2'	1:C1:524:A:C8	2.46	0.50
1:C1:2425:G:H3'	1:C1:2426:G:H8	1.76	0.50
17:CT:27:ILE:HB	17:CT:42:PHE:HB2	1.92	0.50
43:LT:42:ILE:HD11	43:LT:74:VAL:HG11	1.92	0.50
45:LV:106:ASN:OD1	45:LV:110:GLU:N	2.44	0.50
63:CR:355:LEU:HD13	63:CR:389:ILE:HG13	1.92	0.50
1:C1:3139:U:O2'	42:LS:172:THR:OG1	2.29	0.50
4:C4:75:A:O2'	22:Cf:94:LYS:NZ	2.43	0.50
18:CV:35:ARG:NH1	18:CW:376:SER:O	2.43	0.50
1:C1:1572:G:OP1	54:Lg:59:ARG:NH2	2.41	0.50
7:CH:248:ALA:HB2	7:CH:338:LEU:HD21	1.91	0.50
17:CU:303:GLN:HB3	17:CU:305:MET:HE3	1.93	0.50
48:LZ:8:ARG:HB3	48:LZ:24:ILE:HD12	1.93	0.50
1:C1:1103:A:OP1	11:CL:26:LYS:NZ	2.40	0.50
1:C1:1404:G:H2'	1:C1:1405:G:H8	1.76	0.50
17:CT:90:ARG:HG3	17:CT:128:ALA:HB1	1.93	0.50
18:CW:3:ALA:HA	18:CW:55:THR:HG22	1.94	0.50
1:C1:2769:C:OP2	1:C1:2914:U:O2'	2.28	0.50
7:CH:267:ILE:HG22	7:CH:271:LYS:HE2	1.92	0.50
23:Cg:150:ASP:O	23:Cg:170:ARG:NH1	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:CR:435:SER:OG	63:CR:436:LYS:N	2.45	0.50
1:C1:51:U:H2'	1:C1:52:A:H8	1.76	0.50
1:C1:2392:G:H2'	1:C1:2393:A:H8	1.76	0.50
4:C4:62:U:H4'	29:LD:290:ARG:HH12	1.77	0.50
20:CD:213:ILE:HD12	20:CD:403:ASN:HB2	1.92	0.50
35:LL:167:GLU:OE1	49:LA:90:TYR:OH	2.23	0.50
36:LM:67:ILE:HG21	36:LM:90:VAL:HG13	1.93	0.50
7:CH:85:TYR:O	7:CH:148:TYR:OH	2.24	0.50
1:C1:2092:U:H2'	1:C1:2093:G:C8	2.47	0.50
1:C1:2648:A:P	29:LD:15:ARG:HH12	2.33	0.50
17:CT:197:ALA:HB1	17:CT:223:PRO:HB2	1.93	0.50
18:CV:352:PRO:HD3	18:CV:375:TRP:HE3	1.77	0.50
18:CV:572:ARG:HH21	18:CV:573:TYR:HD1	1.60	0.50
34:LK:28:LEU:HB3	34:LK:32:ILE:HD13	1.93	0.50
37:LN:9:GLU:HB2	56:LI:53:ILE:HG13	1.93	0.50
50:Lc:47:ILE:HG21	50:Lc:56:LYS:HG3	1.94	0.50
50:Lc:76:THR:OG1	50:Lc:79:GLU:OE1	2.24	0.50
1:C1:1624:C:H5'	1:C1:1625:U:H5''	1.93	0.50
9:CJ:42:ILE:HG13	9:CJ:72:LEU:HD11	1.92	0.50
27:LB:293:ALA:HB2	27:LB:303:LYS:HD2	1.94	0.50
29:LD:64:MET:HE3	29:LD:145:PHE:HE1	1.76	0.50
12:LF:110:GLN:OE1	40:LQ:36:TRP:NE1	2.45	0.50
35:LL:160:PRO:HB2	35:LL:161:LEU:HD12	1.94	0.50
50:Lc:20:VAL:HG11	50:Lc:95:ILE:HG12	1.93	0.50
1:C1:1077:U:O2'	1:C1:1078:U:O2	2.27	0.49
1:C1:1555:C:H5''	21:CE:428:ALA:HB2	1.94	0.49
1:C1:1785:C:H2'	1:C1:1786:G:H8	1.76	0.49
1:C1:2368:C:H4'	10:CK:142:THR:HG21	1.94	0.49
1:C1:2647:U:N3	29:LD:17:GLN:O	2.43	0.49
5:CB:265:GLU:HA	5:CB:268:GLU:HG2	1.94	0.49
17:CT:305:MET:HE3	17:CT:315:PRO:HB2	1.94	0.49
17:CU:65:GLU:HA	17:CU:88:ARG:HH21	1.77	0.49
18:CV:273:TRP:NE1	18:CV:341:ASP:OD1	2.43	0.49
1:C1:300:A:H2'	1:C1:301:A:C8	2.48	0.49
1:C1:967:U:H2'	1:C1:968:U:H6	1.77	0.49
37:LN:36:ILE:HG12	37:LN:64:VAL:HG23	1.94	0.49
61:Lq:10:TRP:O	61:Lq:14:ARG:HB3	2.13	0.49
1:C1:231:A:H2'	1:C1:232:A:C8	2.47	0.49
1:C1:405:G:OP1	39:LP:62:ARG:NH1	2.45	0.49
1:C1:3315:U:OP1	51:Ld:23:HIS:NE2	2.35	0.49
15:CQ:56:ARG:HE	15:CQ:61:LYS:HB2	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:287:A:OP2	37:LN:15:GLN:NE2	2.42	0.49
21:Ce:300:THR:HB	21:Ce:303:GLU:HG3	1.95	0.49
12:LF:92:VAL:O	12:LF:120:GLY:HA2	2.12	0.49
41:LR:89:MET:HE3	41:LR:90:PRO:HD2	1.94	0.49
1:C1:76:G:H5'	35:LL:58:VAL:HB	1.94	0.49
1:C1:289:A:N3	1:C1:292:G:O2'	2.44	0.49
1:C1:1826:C:OP1	1:C1:1829:C:N4	2.44	0.49
11:CL:70:GLU:HA	11:CL:73:ARG:HG2	1.95	0.49
24:Ch:384:MET:HB2	24:Ch:400:LEU:HB2	1.94	0.49
24:Ch:464:GLY:HA3	24:Ch:494:VAL:HG21	1.95	0.49
1:C1:788:A:N3	1:C1:2771:C:O2'	2.43	0.49
3:C3:36:C:H2'	3:C3:37:G:C8	2.48	0.49
17:CT:75:LEU:HD12	17:CT:76:ARG:HG3	1.95	0.49
31:LG:208:SER:HA	31:LG:211:LYS:HG2	1.94	0.49
1:C1:118:U:O2'	1:C1:120:U:OP2	2.29	0.49
3:C3:57:A:OP2	5:CB:144:ARG:NH2	2.45	0.49
17:CT:295:LEU:HB2	17:CT:309:ILE:HD11	1.95	0.49
37:LN:183:THR:HG22	37:LN:187:ARG:HB2	1.94	0.49
63:CR:212:LYS:HD2	63:CR:299:ILE:HD11	1.94	0.49
10:CK:149:ARG:HH22	20:Cd:44:GLY:HA2	1.77	0.49
13:CN:88:LEU:HD12	13:CN:94:ILE:HD11	1.95	0.49
24:Ch:338:ALA:O	24:Ch:360:ARG:NH1	2.39	0.49
1:C1:21:A:H2'	1:C1:22:G:C8	2.48	0.48
1:C1:1626:G:O2'	1:C1:1788:G:N2	2.39	0.48
1:C1:1779:A:H2'	1:C1:1780:A:H8	1.78	0.48
1:C1:3238:U:O4	27:LB:124:LYS:NZ	2.47	0.48
24:Ch:61:THR:OG1	24:Ch:64:ASN:OD1	2.31	0.48
28:LC:34:ASP:OD1	28:LC:34:ASP:N	2.46	0.48
31:LG:136:LYS:HD2	31:LG:141:HIS:HE1	1.78	0.48
36:LM:54:ARG:NH2	36:LM:76:ALA:O	2.46	0.48
1:C1:1920:G:H21	1:C1:3303:A:H8	1.60	0.48
1:C1:2181:G:H2'	1:C1:2182:A:H8	1.78	0.48
1:C1:2947:C:OP1	38:LO:66:ASN:ND2	2.42	0.48
1:C1:3179:G:H2'	1:C1:3180:G:H8	1.78	0.48
7:CH:168:THR:HA	7:CH:216:GLN:O	2.13	0.48
33:LJ:11:ARG:NH2	33:LJ:152:SER:O	2.47	0.48
1:C1:1476:G:H2'	59:LL:13:LEU:HD22	1.95	0.48
1:C1:2420:G:H2'	1:C1:2422:A:N1	2.28	0.48
3:C3:40:G:O6	3:C3:45:U:O4	2.30	0.48
20:Cd:336:ASN:ND2	20:Cd:356:PRO:O	2.43	0.48
24:Ch:42:ILE:O	24:Ch:123:SER:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Ch:134:ALA:O	24:Ch:517:ASN:ND2	2.47	0.48
63:CR:115:ARG:NH1	63:CR:122:SER:OG	2.46	0.48
1:C1:464:C:H2'	1:C1:465:G:H8	1.77	0.48
1:C1:2176:A:N3	1:C1:2560:A:O2'	2.45	0.48
1:C1:2518:G:OP1	26:LA:69:TYR:OH	2.28	0.48
36:LM:56:ILE:HD11	42:LS:97:THR:HG21	1.94	0.48
63:CR:313:HIS:O	63:CR:326:ARG:NH2	2.47	0.48
1:C1:56:G:OP1	57:Lj:43:LYS:NZ	2.47	0.48
1:C1:2427:U:H2'	1:C1:2428:G:C8	2.48	0.48
12:CM:220:PHE:HD2	12:CM:223:ARG:HG2	1.78	0.48
17:CU:236:PHE:HD2	17:CU:246:VAL:HG12	1.77	0.48
19:Cb:30:ARG:HH12	19:Cb:34:GLN:HB3	1.79	0.48
24:Ch:489:ASP:HB3	24:Ch:508:LYS:HB3	1.94	0.48
26:LA:30:ARG:HG2	26:LA:74:GLU:HG3	1.96	0.48
1:C1:3160:A:N6	1:C1:3202:U:OP2	2.46	0.48
7:CH:250:LEU:HD11	7:CH:334:VAL:HG11	1.95	0.48
39:LP:122:ALA:HB3	39:LP:143:PRO:HG2	1.95	0.48
1:C1:180:U:H1'	47:LY:128:VAL:HG11	1.94	0.48
1:C1:404:U:H2'	1:C1:405:G:H8	1.78	0.48
1:C1:976:G:H4'	1:C1:977:U:H5'	1.95	0.48
1:C1:1698:A:H4'	41:LR:117:LYS:HD2	1.96	0.48
1:C1:2489:C:OP1	26:LA:37:ARG:NH1	2.39	0.48
1:C1:2981:U:H2'	1:C1:2982:A:H8	1.79	0.48
6:CF:176:LYS:NZ	6:CF:184:GLU:OE1	2.46	0.48
8:CI:271:ASP:HA	8:CI:274:LYS:NZ	2.29	0.48
10:CK:165:PRO:HG2	20:Cd:326:GLN:HE21	1.78	0.48
27:LB:313:VAL:HG23	27:LB:365:GLU:HG3	1.96	0.48
33:LJ:33:ARG:HD3	33:LJ:121:ILE:HA	1.95	0.48
37:LN:114:ARG:NH1	37:LN:151:ILE:O	2.47	0.48
48:LZ:13:THR:HB	54:Lg:87:ARG:HG3	1.94	0.48
1:C1:230:G:H2'	1:C1:231:A:C8	2.49	0.48
1:C1:2391:U:H2'	1:C1:2392:G:H8	1.78	0.48
1:C1:3026:C:OP2	41:LR:62:ARG:NH2	2.46	0.48
1:C1:3179:G:H2'	1:C1:3180:G:C8	2.49	0.48
7:CH:632:ARG:HB3	7:CH:637:ASP:HB3	1.95	0.48
9:CJ:141:LEU:HD11	9:CJ:241:VAL:HG11	1.94	0.48
18:CW:313:LEU:HD23	18:CW:381:ILE:HD13	1.94	0.48
1:C1:464:C:H2'	1:C1:465:G:C8	2.49	0.48
1:C1:1452:C:H3'	1:C1:1492:G:H22	1.78	0.48
1:C1:3202:U:OP1	36:LM:122:ARG:NH2	2.44	0.48
24:Ch:208:SER:OG	24:Ch:209:MET:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:LZ:114:LYS:NZ	48:LZ:118:GLU:OE1	2.38	0.48
1:C1:129:G:OP2	55:Lh:79:LYS:NZ	2.46	0.48
1:C1:3109:U:H3	1:C1:3338:C:H42	1.61	0.48
1:C1:3139:U:HO2'	42:LS:172:THR:HG1	1.62	0.48
1:C1:1186:A:H62	1:C1:1283:G:H21	1.62	0.47
7:CH:635:GLU:OE2	59:Ll:41:ARG:NH1	2.43	0.47
17:CT:230:PRO:HB2	18:CW:579:PRO:HB3	1.96	0.47
20:Cd:121:PRO:HG2	24:Ch:404:GLN:HE21	1.78	0.47
32:LH:138:VAL:HG11	32:LH:183:LEU:HD11	1.95	0.47
35:LL:59:ARG:NH1	35:LL:66:ASN:O	2.39	0.47
45:LV:25:MET:HE3	45:LV:102:GLY:HA3	1.96	0.47
62:Lr:31:THR:HA	62:Lr:171:ASN:HA	1.96	0.47
1:C1:696:G:N2	1:C1:699:A:OP2	2.38	0.47
1:C1:1216:G:N2	34:LK:131:GLU:OE2	2.44	0.47
1:C1:2123:G:H2'	1:C1:2124:G:H8	1.78	0.47
1:C1:2320:A:H2'	1:C1:2321:A:H8	1.79	0.47
1:C1:2518:G:N2	31:LG:41:GLN:O	2.47	0.47
2:C2:47:C:H1'	2:C2:61:A:H2'	1.96	0.47
18:CW:294:GLY:N	18:CW:299:GLU:OE1	2.47	0.47
1:C1:848:A2M:HM'2	1:C1:849:G:H5'	1.95	0.47
1:C1:1698:A:H2'	1:C1:1699:G:C8	2.50	0.47
1:C1:2212:G:H4'	20:Cd:315:ARG:HD2	1.95	0.47
1:C1:2308:A:H5''	51:Ld:32:THR:HG23	1.97	0.47
1:C1:2376:A:H2'	1:C1:2377:G:H8	1.78	0.47
4:C4:10:C:OP2	22:Cf:59:ARG:NH1	2.47	0.47
36:LM:123:LEU:HD22	38:LO:195:VAL:HG22	1.96	0.47
1:C1:2169:G:H2'	1:C1:2170:A:H8	1.78	0.47
1:C1:3326:U:H1'	51:Ld:113:LEU:HD23	1.96	0.47
5:CB:129:ASP:OD1	5:CB:129:ASP:N	2.43	0.47
63:CR:337:VAL:HA	63:CR:342:LEU:HB2	1.96	0.47
1:C1:243:U:O2'	1:C1:244:G:O5'	2.30	0.47
1:C1:575:G:H2'	1:C1:576:A:C8	2.50	0.47
1:C1:2523:G:H2'	1:C1:2524:G:H8	1.79	0.47
15:CQ:145:LEU:HD21	15:CQ:163:GLU:HG3	1.97	0.47
18:CW:369:ASP:OD2	18:CW:370:GLU:N	2.47	0.47
1:C1:1395:G:H5''	52:Le:125:ALA:HB2	1.97	0.47
1:C1:2330:A:H2'	1:C1:2331:A:C8	2.49	0.47
32:LH:75:LEU:HD13	32:LH:108:VAL:HG13	1.97	0.47
63:CR:85:PRO:HG3	63:CR:114:LEU:HD13	1.97	0.47
1:C1:1866:A:O2'	27:LB:227:PHE:O	2.28	0.47
1:C1:2495:U:H2'	1:C1:2496:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CK:132:MET:HG2	10:CK:209:TYR:CE1	2.50	0.47
12:CM:99:ASN:OD1	12:CM:100:LYS:N	2.48	0.47
12:CM:151:ARG:NH2	12:CM:188:GLU:OE1	2.48	0.47
13:CN:14:GLY:HA2	13:CN:198:VAL:HG13	1.96	0.47
13:CN:32:GLU:OE1	13:CN:50:ARG:NH1	2.48	0.47
17:CT:250:PHE:HE1	17:CT:256:LEU:HB2	1.80	0.47
18:CV:135:GLN:HG2	18:CV:189:LEU:HD22	1.96	0.47
18:CW:104:ILE:HG12	18:CW:130:LEU:HD13	1.96	0.47
18:CW:352:PRO:HD3	18:CW:375:TRP:CE3	2.50	0.47
20:Cd:47:ILE:HB	20:Cd:56:LYS:HB3	1.96	0.47
21:Ce:103:VAL:HG22	56:Li:45:ARG:HD2	1.96	0.47
27:LB:79:ILE:HD12	27:LB:337:MET:HG3	1.96	0.47
30:LE:98:ASN:HB3	30:LE:101:TYR:HD1	1.80	0.47
63:CR:115:ARG:O	63:CR:115:ARG:NE	2.48	0.47
63:CR:366:LEU:HA	63:CR:369:LEU:HG	1.96	0.47
1:C1:88:U:H2'	1:C1:89:A:H8	1.80	0.47
1:C1:1135:G:OP2	1:C1:1135:G:N2	2.37	0.47
1:C1:2446:G:H22	1:C1:2449:A:H5'	1.79	0.47
1:C1:2973:C:OP2	14:CO:2:ALA:N	2.48	0.47
3:C3:39:G:H5''	8:CI:305:LYS:NZ	2.29	0.47
10:CK:165:PRO:HG2	20:Cd:326:GLN:NE2	2.30	0.47
36:LM:20:LEU:HD21	36:LM:30:ILE:HD11	1.96	0.47
1:C1:582:G:H1'	30:LE:37:LYS:HG3	1.97	0.47
1:C1:3275:U:H4'	1:C1:3276:A:H5'	1.96	0.47
2:C2:120:G:H5'	21:Ce:182:PRO:HB3	1.97	0.47
40:LQ:79:ARG:HA	40:LQ:82:MET:HE2	1.97	0.47
48:LZ:13:THR:OG1	54:Lg:87:ARG:NH1	2.48	0.47
49:La:101:VAL:HG22	49:La:124:VAL:HB	1.97	0.47
63:CR:421:MET:HG2	63:CR:425:LEU:HD23	1.96	0.47
1:C1:604:G:H2'	1:C1:605:G:C8	2.49	0.47
1:C1:920:C:O2	1:C1:2772:A:O2'	2.33	0.47
1:C1:1877:G:OP2	19:Cb:11:LYS:NZ	2.38	0.47
1:C1:2751:A:H2'	1:C1:2752:G:H8	1.80	0.47
1:C1:3044:A:H3'	1:C1:3045:A:H8	1.80	0.47
36:LM:59:LEU:O	42:LS:155:ARG:NH2	2.48	0.47
1:C1:1193:U:H5	6:CF:3:LYS:HB2	1.80	0.46
5:CB:115:GLU:HG3	5:CB:217:ILE:HG21	1.96	0.46
10:CK:219:THR:HB	10:CK:245:ILE:HD12	1.98	0.46
17:CU:83:VAL:HG12	17:CU:347:LYS:HG2	1.96	0.46
29:LD:98:ALA:HB1	29:LD:165:VAL:HG23	1.96	0.46
34:LK:92:ARG:HH22	34:LK:98:ILE:HD13	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:Lh:29:THR:O	55:Lh:32:SER:OG	2.30	0.46
1:C1:525:A:O2'	1:C1:527:G:OP2	2.30	0.46
11:CL:27:ARG:HA	11:CL:30:GLU:HG2	1.97	0.46
16:CS:68:VAL:HG11	16:CS:104:LYS:HB3	1.98	0.46
50:Lc:78:ILE:HG13	50:Lc:89:ARG:HG2	1.98	0.46
8:CI:255:GLY:O	31:LG:216:LYS:NZ	2.38	0.46
9:CJ:70:GLN:HA	9:CJ:73:LEU:HD12	1.96	0.46
16:CS:293:ASP:OD1	16:CS:297:ARG:NH2	2.44	0.46
18:CV:449:ASP:HA	18:CV:452:ILE:HD12	1.96	0.46
1:C1:390:A:H4'	1:C1:391:U:H3'	1.98	0.46
1:C1:422:U:O2'	53:Lf:90:PRO:O	2.28	0.46
1:C1:494:C:H2'	1:C1:495:G:H8	1.80	0.46
1:C1:979:A:N6	1:C1:1033:U:O4	2.48	0.46
2:C2:95:G:OP1	57:Lj:76:ASN:ND2	2.48	0.46
13:CN:15:VAL:HA	13:CN:61:ARG:HG2	1.97	0.46
18:CW:210:ALA:O	18:CW:312:ARG:NH1	2.49	0.46
24:Ch:148:PRO:HB3	24:Ch:508:LYS:HA	1.98	0.46
37:LN:145:ASP:HB3	37:LN:148:ILE:HG22	1.96	0.46
54:Lg:59:ARG:HB2	54:Lg:62:GLU:HG3	1.97	0.46
1:C1:575:G:H2'	1:C1:576:A:H8	1.80	0.46
1:C1:2120:G:N2	1:C1:2140:G:O2'	2.49	0.46
18:CV:269:VAL:HG12	18:CV:362:THR:HG22	1.98	0.46
26:LA:129:THR:OG1	26:LA:132:ASN:ND2	2.39	0.46
27:LB:294:ASN:O	27:LB:322:TYR:OH	2.33	0.46
33:LJ:8:ASN:HB3	33:LJ:11:ARG:HG3	1.97	0.46
41:LR:105:LEU:HD23	41:LR:138:LEU:HD23	1.98	0.46
46:LX:17:GLY:O	46:LX:21:LYS:HG2	2.15	0.46
1:C1:1345:G:H2'	1:C1:1346:A:C8	2.51	0.46
1:C1:2384:OMU:HM23	1:C1:2384:OMU:H1'	1.69	0.46
12:CM:149:SER:HG	12:CM:246:ARG:HH12	1.61	0.46
18:CV:156:CYS:HB3	18:CV:179:VAL:HG13	1.98	0.46
31:LG:31:GLU:HB2	31:LG:33:ARG:HH11	1.81	0.46
1:C1:2100:U:OP2	1:C1:2105:A:N6	2.39	0.46
1:C1:2427:U:H2'	1:C1:2428:G:H8	1.80	0.46
7:CH:174:PHE:O	7:CH:179:LYS:NZ	2.47	0.46
35:LL:114:GLN:NE2	35:LL:118:ASP:OD2	2.48	0.46
35:LL:164:GLY:HA2	49:La:103:ASP:HB3	1.97	0.46
1:C1:91:C:OP1	49:La:59:ARG:NH1	2.48	0.46
1:C1:633:A:O5'	1:C1:1125:G:O2'	2.34	0.46
5:CB:31:LEU:HD12	5:CB:252:PRO:HG3	1.97	0.46
17:CT:306:ARG:HB2	17:CT:318:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CW:231:LEU:HD23	18:CW:234:LEU:HD12	1.98	0.46
20:Cd:119:ASP:OD1	20:Cd:119:ASP:N	2.48	0.46
44:LU:106:SER:HB3	44:LU:109:VAL:HB	1.98	0.46
1:C1:576:A:H4'	53:Lf:74:THR:HG22	1.98	0.46
1:C1:3079:U:H1'	1:C1:3080:A:H5''	1.98	0.46
4:C4:11:A:N1	4:C4:67:G:O2'	2.40	0.46
15:CQ:83:ARG:O	15:CQ:87:GLN:HG2	2.15	0.46
17:CT:378:THR:HG23	18:CV:90:ASP:HB3	1.98	0.46
17:CU:205:ILE:O	17:CU:214:LEU:N	2.47	0.46
58:Lk:14:ILE:HA	58:Lk:17:ARG:HD3	1.98	0.46
63:CR:99:LEU:HD22	63:CR:103:LEU:HD22	1.97	0.46
1:C1:117:A:C4	21:Ce:104:ARG:HD3	2.51	0.46
1:C1:716:G:H5''	40:LQ:71:PRO:HB2	1.98	0.46
9:CJ:170:ARG:HG3	9:CJ:271:PHE:HZ	1.81	0.46
24:Ch:45:ASP:HA	24:Ch:434:ARG:HH12	1.80	0.46
12:LF:102:PRO:HB2	12:LF:105:PRO:HD2	1.97	0.46
31:LG:101:ARG:NH2	31:LG:191:THR:O	2.49	0.46
34:LK:37:LEU:HD21	34:LK:42:VAL:HG21	1.97	0.46
43:LT:52:MET:HB2	43:LT:55:LYS:HE2	1.98	0.46
52:Le:97:ILE:HG21	52:Le:106:ARG:HG2	1.98	0.46
63:CR:194:ARG:HD2	63:CR:229:PHE:HD1	1.80	0.46
1:C1:1623:A:H5''	1:C1:1624:C:C5	2.52	0.45
3:C3:63:A:N6	8:CI:218:VAL:O	2.43	0.45
7:CH:131:ALA:O	7:CH:135:MET:HG3	2.16	0.45
8:CI:213:ILE:HG21	8:CI:216:LEU:HD23	1.98	0.45
20:Cd:318:SER:OG	20:Cd:372:ARG:NH1	2.48	0.45
22:Cf:179:GLU:OE2	29:LD:132:THR:OG1	2.28	0.45
46:LX:79:PRO:HA	46:LX:97:PHE:HA	1.98	0.45
47:LY:73:TYR:HE2	47:LY:76:LYS:HG3	1.81	0.45
63:CR:211:MET:HE3	63:CR:226:GLY:HA2	1.98	0.45
1:C1:630:U:H2'	1:C1:631:U:C2	2.52	0.45
1:C1:2169:G:H2'	1:C1:2170:A:C8	2.51	0.45
1:C1:2974:A:H2'	1:C1:2975:G:H8	1.81	0.45
7:CH:645:PRO:HG2	7:CH:648:LEU:HD12	1.98	0.45
23:Cg:36:VAL:HG13	23:Cg:54:VAL:HG21	1.98	0.45
27:LB:219:ILE:HB	27:LB:338:THR:HB	1.97	0.45
31:LG:85:LEU:HD22	31:LG:89:LEU:HD23	1.98	0.45
60:Lp:81:SER:OG	60:Lp:85:ARG:NH2	2.49	0.45
1:C1:2179:G:H22	1:C1:2192:A:H2	1.64	0.45
7:CH:465:GLU:OE2	15:CQ:102:ARG:NH2	2.45	0.45
11:CL:54:GLY:O	42:LS:89:ASN:ND2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LA:113:VAL:HG12	26:LA:166:ILE:HD13	1.97	0.45
31:LG:152:SER:N	31:LG:203:ILE:O	2.45	0.45
36:LM:120:VAL:HG12	36:LM:124:LYS:HE2	1.98	0.45
1:C1:1080:G:O6	43:LT:116:LYS:NZ	2.49	0.45
1:C1:1480:C:H2'	1:C1:1481:A:H8	1.81	0.45
1:C1:2121:A:H4'	1:C1:2122:U:H5'	1.97	0.45
1:C1:2222:A:H5''	1:C1:2223:U:H5	1.80	0.45
3:C3:36:C:H2'	3:C3:37:G:H8	1.81	0.45
21:Ce:263:ALA:HB1	21:Ce:267:ARG:NH1	2.31	0.45
39:LP:41:LEU:HD21	39:LP:99:GLU:HB2	1.98	0.45
42:LS:8:GLN:HB2	42:LS:64:ILE:HD11	1.99	0.45
1:C1:20:U:H2'	1:C1:21:A:C8	2.52	0.45
1:C1:652:A:H2'	1:C1:653:A:C8	2.51	0.45
1:C1:736:G:H2'	1:C1:737:A:H8	1.81	0.45
1:C1:1345:G:H2'	1:C1:1346:A:H8	1.81	0.45
1:C1:2405:G:H2'	1:C1:2406:A:H8	1.81	0.45
1:C1:2683:OMU:HM23	1:C1:2683:OMU:H1'	1.62	0.45
1:C1:2849:A:O2'	1:C1:2892:A:N3	2.42	0.45
15:CQ:17:LYS:O	15:CQ:30:ARG:NH2	2.44	0.45
29:LD:22:ARG:NE	29:LD:28:THR:OG1	2.37	0.45
33:LJ:11:ARG:O	33:LJ:134:ARG:NH1	2.47	0.45
63:CR:131:PRO:HA	63:CR:134:ILE:HG22	1.99	0.45
1:C1:1640:C:H2'	1:C1:1641:G:H8	1.80	0.45
1:C1:2711:U:H2'	1:C1:2712:G:C8	2.52	0.45
5:CB:225:ARG:HA	5:CB:228:ILE:HG22	1.99	0.45
15:CQ:27:LYS:HE3	15:CQ:27:LYS:HB2	1.83	0.45
17:CT:217:LEU:HD22	17:CT:269:ILE:HD11	1.99	0.45
18:CW:303:TRP:CD1	18:CW:312:ARG:HE	2.34	0.45
22:Cf:169:ARG:HG2	23:Cg:27:LEU:HD22	1.99	0.45
37:LN:169:LYS:HG2	37:LN:174:LEU:HD12	1.97	0.45
60:Lp:86:LEU:HA	60:Lp:89:ILE:HB	1.98	0.45
1:C1:364:G:O2'	1:C1:389:A2M:N6	2.47	0.45
1:C1:957:C:H2'	1:C1:958:G:C8	2.51	0.45
1:C1:1752:U:OP2	58:Lk:30:LYS:NZ	2.46	0.45
18:CW:298:ASP:OD2	18:CW:298:ASP:N	2.50	0.45
1:C1:663:C:O2'	1:C1:667:U:OP1	2.33	0.45
1:C1:735:C:H2'	1:C1:736:G:H8	1.82	0.45
1:C1:2318:G:OP1	39:LP:141:SER:OG	2.27	0.45
10:CK:132:MET:HE1	10:CK:214:VAL:HG11	1.98	0.45
12:CM:108:ILE:HG23	12:CM:132:MET:HE2	1.98	0.45
17:CU:106:GLY:HA2	17:CU:129:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:CU:148:ILE:HD13	17:CU:181:LEU:HD21	1.99	0.45
18:CV:268:ALA:HA	18:CV:366:ILE:HD12	1.97	0.45
33:LJ:126:MET:HE2	33:LJ:128:PHE:HE1	1.81	0.45
44:LU:59:VAL:HG12	44:LU:60:ILE:HG13	1.98	0.45
1:C1:391:U:H5'	39:LP:3:ARG:HD3	1.98	0.45
1:C1:524:A:H2'	1:C1:525:A:C8	2.52	0.45
1:C1:957:C:H2'	1:C1:958:G:H8	1.82	0.45
1:C1:2392:G:H2'	1:C1:2393:A:C8	2.52	0.45
7:CH:46:THR:HG23	7:CH:112:VAL:HG22	1.98	0.45
17:CT:152:SER:HB2	17:CT:168:LEU:HD11	1.99	0.45
22:Cf:138:MET:HE1	22:Cf:182:ARG:HH21	1.82	0.45
33:LJ:94:ARG:O	33:LJ:157:ARG:NH2	2.50	0.45
1:C1:911:A:O2'	57:Lj:49:TRP:O	2.33	0.45
18:CW:19:VAL:HA	18:CW:22:LEU:HD12	1.99	0.45
31:LG:249:GLU:OE1	31:LG:252:ARG:NH1	2.50	0.45
32:LH:154:ARG:HG2	32:LH:162:VAL:HG22	1.97	0.45
35:LL:165:PHE:HZ	49:La:86:VAL:HG11	1.82	0.45
1:C1:619:A:H2'	1:C1:620:G:C8	2.52	0.44
5:CB:120:LEU:HD12	5:CB:221:VAL:HG13	1.99	0.44
21:Ce:257:SER:O	48:LZ:120:ARG:NH1	2.49	0.44
28:LC:4:ARG:NH2	28:LC:23:LEU:O	2.47	0.44
1:C1:980:A:H2'	1:C1:981:G:C8	2.51	0.44
1:C1:1812:OMC:H2'	1:C1:1813:G:C8	2.50	0.44
17:CT:71:VAL:HB	17:CT:81:ALA:HB3	1.99	0.44
17:CT:383:ASP:OD1	17:CT:384:ALA:N	2.51	0.44
50:Lc:17:LEU:O	50:Lc:21:ILE:HG12	2.17	0.44
1:C1:1054:U:O2	1:C1:1070:G:N2	2.39	0.44
1:C1:1638:G:H2'	1:C1:1639:A:C8	2.53	0.44
1:C1:1814:U:OP2	59:Ll:10:LYS:NZ	2.46	0.44
1:C1:2516:G:O2'	48:LZ:135:PHE:OXT	2.36	0.44
1:C1:3066:G:H21	32:LH:202:GLN:HE22	1.66	0.44
6:CF:224:LEU:HD11	6:CF:243:ARG:HH11	1.83	0.44
17:CT:228:LEU:HD23	17:CT:235:ILE:HG12	1.99	0.44
18:CW:267:ARG:HD3	18:CW:290:PRO:HB3	1.99	0.44
18:CW:307:GLN:NE2	18:CW:311:GLU:OE2	2.44	0.44
24:Ch:60:ALA:HA	24:Ch:65:ILE:HD11	1.98	0.44
60:Lp:73:THR:HG22	60:Lp:75:ALA:H	1.83	0.44
1:C1:774:A:H2'	1:C1:775:A:H8	1.82	0.44
1:C1:1698:A:H2'	1:C1:1699:G:H8	1.83	0.44
3:C3:142:G:N2	8:CI:288:MET:HE1	2.33	0.44
4:C4:6:C:O3'	29:LD:50:ARG:NH2	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:44:SER:OG	6:CF:222:SER:OG	2.34	0.44
17:CT:229:ASP:OD1	17:CT:233:ARG:N	2.49	0.44
21:Ce:237:GLU:HA	21:Ce:240:ARG:HG2	1.99	0.44
44:LU:22:ILE:HB	44:LU:109:VAL:HG22	2.00	0.44
48:LZ:96:ASN:ND2	48:LZ:99:THR:OG1	2.50	0.44
53:Lf:16:LEU:HD11	53:Lf:33:LYS:HB2	2.00	0.44
4:C4:78:A:H3'	4:C4:79:G:H8	1.82	0.44
7:CH:294:PHE:O	7:CH:302:GLN:NE2	2.50	0.44
9:CJ:409:ASP:OD1	9:CJ:409:ASP:N	2.51	0.44
22:Cf:117:TYR:O	22:Cf:255:PHE:HA	2.17	0.44
30:LE:86:PRO:HD2	30:LE:89:ILE:HD12	1.99	0.44
43:LT:155:ALA:O	43:LT:158:THR:OG1	2.29	0.44
58:Lk:24:ARG:HA	58:Lk:69:LYS:O	2.18	0.44
61:Lq:11:GLU:HA	61:Lq:14:ARG:HD2	1.99	0.44
1:C1:410:A:H2'	1:C1:411:A:C8	2.53	0.44
1:C1:1577:C:H5'	1:C1:1676:A:H1'	2.00	0.44
1:C1:3315:U:H2'	1:C1:3319:C:H41	1.82	0.44
2:C2:95:G:O2'	57:Lj:81:GLY:O	2.32	0.44
16:CS:128:PRO:HB2	16:CS:131:GLU:HG3	1.99	0.44
16:CS:295:LYS:HB3	16:CS:296:TRP:CD1	2.53	0.44
17:CU:152:SER:HB2	17:CU:168:LEU:HD11	2.00	0.44
19:Cb:18:ASP:OD1	19:Cb:19:LEU:N	2.51	0.44
20:Cd:358:PRO:HD2	20:Cd:400:ARG:HG2	1.98	0.44
1:C1:404:U:H2'	1:C1:405:G:C8	2.53	0.44
1:C1:425:G:H2'	1:C1:426:A:C8	2.53	0.44
1:C1:2069:A:H2'	1:C1:2070:A:C8	2.53	0.44
2:C2:9:A:H2'	2:C2:10:A:C8	2.53	0.44
6:CF:121:GLN:NE2	6:CF:122:VAL:O	2.51	0.44
7:CH:365:MET:HA	7:CH:368:ILE:HG12	2.00	0.44
18:CW:205:LEU:HD13	18:CW:227:SER:HA	2.00	0.44
32:LH:127:MET:HG2	32:LH:220:VAL:HA	1.99	0.44
37:LN:177:GLY:O	37:LN:184:ARG:NH1	2.51	0.44
63:CR:112:VAL:HG21	63:CR:148:LYS:HD2	2.00	0.44
1:C1:371:A:H4'	47:LY:90:THR:HG22	1.99	0.44
6:CF:131:ALA:HB2	6:CF:201:LEU:HD21	2.00	0.44
12:CM:241:ILE:HD12	12:CM:244:LEU:HD12	1.98	0.44
17:CU:197:ALA:HB2	17:CU:226:MET:HE3	1.98	0.44
30:LE:58:LEU:HD11	30:LE:72:LEU:HB2	1.99	0.44
45:LV:105:VAL:HG12	45:LV:111:MET:HA	2.00	0.44
1:C1:159:U:H2'	1:C1:160:G:C8	2.53	0.44
1:C1:293:G:H2'	1:C1:294:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1779:A:H2'	1:C1:1780:A:C8	2.52	0.44
1:C1:2074:G:C6	19:Cb:76:ARG:HD3	2.53	0.44
1:C1:2409:U:H2'	1:C1:2410:A:C8	2.53	0.44
1:C1:2580:G:H4'	23:Cg:180:ARG:HD2	2.00	0.44
7:CH:616:ALA:HB1	59:Ll:25:GLN:HB3	1.99	0.44
15:CQ:145:LEU:HD11	15:CQ:163:GLU:HG3	1.99	0.44
17:CT:143:SER:OG	17:CT:144:ASP:N	2.50	0.44
26:LA:80:GLU:HG3	60:Lp:66:GLY:HA2	2.00	0.44
32:LH:7:GLU:HA	32:LH:92:LEU:O	2.17	0.44
52:Le:80:VAL:HA	52:Le:83:VAL:HG12	2.00	0.44
1:C1:1046:G:C6	43:LT:109:VAL:HG22	2.53	0.43
1:C1:1140:G:O2'	1:C1:1152:A:N3	2.47	0.43
2:C2:52:A:OP1	59:Ll:21:ARG:NH1	2.42	0.43
7:CH:41:ILE:HD13	7:CH:121:LEU:HB2	1.99	0.43
16:CS:128:PRO:HA	16:CS:129:PRO:HD3	1.91	0.43
52:Le:122:ASN:OD1	52:Le:122:ASN:N	2.51	0.43
55:Lh:30:GLU:HB3	55:Lh:34:LEU:HD13	1.98	0.43
63:CR:428:ASP:HA	63:CR:431:LEU:HG	1.99	0.43
63:CR:451:TYR:OH	63:CR:458:MET:HB3	2.16	0.43
1:C1:1615:G:N2	1:C1:1618:A:OP2	2.41	0.43
1:C1:2556:U:H2'	1:C1:2557:G:H8	1.83	0.43
20:Cd:60:PHE:O	20:Cd:61:GLN:NE2	2.47	0.43
41:LR:44:LEU:HD22	41:LR:49:LEU:HD22	2.00	0.43
48:LZ:21:LYS:NZ	48:LZ:128:TRP:O	2.38	0.43
50:Lc:19:LEU:HD22	50:Lc:101:SER:HB2	2.00	0.43
1:C1:351:G:N2	1:C1:354:A:OP2	2.37	0.43
1:C1:1303:C:O2	42:LS:115:ARG:NH2	2.52	0.43
1:C1:1887:C:O2	27:LB:241:ARG:NH2	2.46	0.43
1:C1:3120:C:H2'	1:C1:3121:G:H8	1.84	0.43
1:C1:3316:A:O2'	1:C1:3319:C:OP2	2.31	0.43
16:CS:129:PRO:HB3	16:CS:168:VAL:HB	2.00	0.43
28:LC:211:ILE:HG13	28:LC:256:VAL:HB	2.00	0.43
50:Lc:30:TYR:OH	50:Lc:58:GLU:OE1	2.29	0.43
50:Lc:33:THR:HG23	50:Lc:94:ALA:HB2	2.00	0.43
1:C1:670:U:H5''	1:C1:671:U:H5	1.83	0.43
1:C1:774:A:H2'	1:C1:775:A:C8	2.53	0.43
1:C1:2409:U:H2'	1:C1:2410:A:H8	1.83	0.43
1:C1:2877:G:H2'	1:C1:2878:A:H8	1.82	0.43
9:CJ:384:GLU:HG3	9:CJ:388:ARG:HH21	1.83	0.43
12:CM:92:VAL:O	12:CM:120:GLY:HA2	2.18	0.43
15:CQ:71:PHE:O	15:CQ:75:ARG:NH2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CV:138:GLN:HB2	18:CV:142:ARG:HH12	1.82	0.43
27:LB:10:ARG:NH2	27:LB:264:THR:O	2.48	0.43
42:LS:110:MET:HE3	42:LS:110:MET:HB3	1.90	0.43
1:C1:73:C:OP2	56:Li:22:LYS:NZ	2.51	0.43
1:C1:644:A:H2'	1:C1:645:A:C8	2.52	0.43
1:C1:1783:C:H2'	1:C1:1784:G:C8	2.54	0.43
1:C1:2327:G:H22	1:C1:2359:G:H1'	1.83	0.43
2:C2:29:U:H5''	35:LL:27:ASP:HB3	2.01	0.43
2:C2:70:G:OP1	47:LY:120:ARG:NH2	2.39	0.43
16:CS:268:LEU:HB3	16:CS:270:LEU:HG	1.99	0.43
31:LG:85:LEU:HD12	31:LG:183:ILE:HD12	2.01	0.43
37:LN:113:LEU:HB2	37:LN:134:LEU:HD23	2.01	0.43
41:LR:108:LYS:HB3	41:LR:108:LYS:HE2	1.75	0.43
42:LS:1:MET:HG3	42:LS:118:PHE:HD2	1.83	0.43
1:C1:2352:C:H2'	1:C1:2353:A:H8	1.83	0.43
1:C1:2677:U:O2'	20:Cd:80:THR:O	2.37	0.43
3:C3:35:C:O2'	5:CB:288:THR:O	2.37	0.43
4:C4:108:G:OP1	29:LD:284:ARG:NH2	2.43	0.43
15:CQ:145:LEU:HD22	15:CQ:159:LEU:HB3	2.00	0.43
18:CW:95:GLU:OE2	18:CW:99:SER:OG	2.36	0.43
18:CW:306:LEU:HD21	18:CW:374:LEU:HB2	2.01	0.43
22:Cf:249:HIS:ND1	22:Cf:250:GLY:O	2.51	0.43
25:Cz:46:THR:HG22	42:LS:141:LYS:HE2	2.00	0.43
42:LS:124:LEU:HD22	43:LT:154:VAL:HG22	2.01	0.43
42:LS:125:LYS:HG2	42:LS:127:VAL:HG13	1.99	0.43
58:Lk:23:ALA:O	58:Lk:68:ILE:HA	2.18	0.43
1:C1:219:C:OP1	47:LY:46:SER:OG	2.36	0.43
1:C1:2728:A:H2'	1:C1:2729:G:C8	2.53	0.43
1:C1:2925:G:H2'	1:C1:2926:A:C8	2.54	0.43
1:C1:2956:U:H2'	1:C1:2957:C:C6	2.54	0.43
9:CJ:141:LEU:HD23	9:CJ:141:LEU:HA	1.90	0.43
11:CL:55:ILE:HB	11:CL:62:LYS:HE3	2.01	0.43
22:Cf:232:ILE:HG23	22:Cf:244:VAL:HG13	2.01	0.43
42:LS:71:LYS:O	42:LS:73:LYS:NZ	2.52	0.43
1:C1:363:U:H4'	1:C1:397:G:H5'	2.01	0.43
1:C1:882:G:H1'	1:C1:1569:A:N6	2.33	0.43
1:C1:2069:A:H2'	1:C1:2070:A:H8	1.84	0.43
1:C1:2277:OMU:H1'	1:C1:2277:OMU:HM23	1.76	0.43
1:C1:2884:C:H2'	1:C1:2885:A:C4	2.53	0.43
5:CB:135:ALA:HB1	31:LG:209:GLU:HG2	2.01	0.43
9:CJ:156:SER:HB2	9:CJ:162:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LE:194:LYS:HB3	30:LE:196:HIS:CE1	2.53	0.43
42:LS:60:SER:OG	42:LS:62:ASN:OD1	2.35	0.43
1:C1:803:U:H2'	1:C1:804:G:H8	1.84	0.43
1:C1:1157:G:N2	38:LO:89:MET:SD	2.92	0.43
1:C1:1463:G:O2'	1:C1:1851:U:O4	2.26	0.43
1:C1:2729:G:H2'	1:C1:2732:C:H5	1.84	0.43
6:CF:94:ARG:HD2	6:CF:245:LYS:HD3	2.01	0.43
7:CH:307:ASP:HA	7:CH:310:LYS:HG3	2.00	0.43
16:CS:234:LEU:HD13	16:CS:325:LEU:HD21	2.00	0.43
17:CU:229:ASP:OD1	17:CU:233:ARG:N	2.52	0.43
22:Cf:23:ILE:HD13	23:Cg:97:PRO:HD2	2.00	0.43
30:LE:86:PRO:HB3	30:LE:166:ASP:HB2	2.01	0.43
40:LQ:110:VAL:HG22	40:LQ:167:LEU:HB2	2.00	0.43
1:C1:181:G:OP1	47:LY:125:ARG:NE	2.50	0.43
1:C1:1454:U:H2'	1:C1:1455:G:C8	2.54	0.43
1:C1:2110:A:OP2	26:LA:200:ARG:NH2	2.49	0.43
4:C4:17:A:H2'	4:C4:18:G:H8	1.84	0.43
6:CF:43:PHE:HB3	6:CF:223:LEU:HD23	2.01	0.43
7:CH:174:PHE:CE2	7:CH:266:GLN:HA	2.51	0.43
8:CI:299:GLU:HA	8:CI:302:TRP:HE3	1.84	0.43
9:CJ:46:GLU:OE2	21:Ce:367:ARG:NH2	2.48	0.43
17:CT:380:PHE:HB2	17:CT:385:LEU:HG	2.00	0.43
17:CU:188:SER:O	17:CU:192:ASN:ND2	2.49	0.43
22:Cf:98:HIS:CD2	22:Cf:120:PRO:HG3	2.54	0.43
24:Ch:88:HIS:HB2	24:Ch:121:THR:HB	2.01	0.43
25:Cz:76:ARG:O	25:Cz:80:ILE:HG12	2.19	0.43
39:LP:126:ARG:HA	39:LP:140:MET:HG2	2.01	0.43
40:LQ:64:LEU:O	40:LQ:68:THR:OG1	2.23	0.43
63:CR:123:VAL:HG22	63:CR:165:LEU:HD13	2.01	0.43
1:C1:1197:U:H2'	1:C1:1198:A:C8	2.54	0.42
1:C1:1643:C:H5''	41:LR:96:MET:HE1	2.00	0.42
1:C1:2648:A:O2'	1:C1:2650:A:N7	2.46	0.42
7:CH:504:ASN:ND2	51:Ld:106:VAL:O	2.52	0.42
21:Ce:380:ASP:OD2	21:Ce:380:ASP:N	2.51	0.42
1:C1:2067:A:OP2	41:LR:81:ARG:NH2	2.40	0.42
3:C3:32:G:H2'	3:C3:33:A:C8	2.55	0.42
15:CQ:86:TRP:HA	15:CQ:89:THR:HG22	2.00	0.42
18:CV:322:ALA:O	18:CV:326:ASN:ND2	2.51	0.42
20:Cd:334:TYR:HE1	20:Cd:383:PRO:HD2	1.84	0.42
29:LD:93:THR:O	29:LD:161:ARG:NH1	2.46	0.42
42:LS:100:VAL:O	42:LS:104:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:LZ:56:MET:HG2	48:LZ:60:ARG:HD3	2.01	0.42
53:Lf:73:ILE:HD13	53:Lf:85:ALA:HB2	2.00	0.42
60:Lp:10:ILE:HG22	60:Lp:27:LYS:HG3	2.01	0.42
63:CR:374:HIS:CE1	63:CR:376:LEU:HB2	2.54	0.42
1:C1:251:U:OP1	35:LL:81:LYS:NZ	2.44	0.42
1:C1:726:A:OP1	40:LQ:94:ARG:NH1	2.50	0.42
1:C1:2185:A:H2'	1:C1:2186:A:C8	2.55	0.42
1:C1:2577:G:H21	1:C1:2578:OMG:HM23	1.83	0.42
27:LB:47:MET:HE3	27:LB:165:THR:HG23	1.99	0.42
38:LO:11:ASP:OD2	38:LO:38:ARG:NH2	2.38	0.42
38:LO:115:ASP:OD1	38:LO:115:ASP:N	2.52	0.42
1:C1:1159:C:OP2	1:C1:1160:G:O2'	2.35	0.42
1:C1:1480:C:H2'	1:C1:1481:A:C8	2.55	0.42
1:C1:1778:A:H2'	1:C1:1779:A:C8	2.55	0.42
1:C1:1816:C:O2'	1:C1:1822:A:N1	2.42	0.42
4:C4:77:U:H2'	4:C4:78:A:H8	1.84	0.42
27:LB:93:ILE:HD11	27:LB:100:ARG:HE	1.84	0.42
28:LC:287:LEU:HD11	40:LQ:60:LEU:HB2	2.02	0.42
49:La:85:ASP:OD1	49:La:86:VAL:N	2.52	0.42
1:C1:92:G:N2	1:C1:95:G:O2'	2.52	0.42
1:C1:1243:A:H2'	1:C1:1244:G:C4	2.54	0.42
1:C1:1576:C:H2'	1:C1:1577:C:C6	2.54	0.42
1:C1:1697:C:H2'	1:C1:1698:A:C8	2.54	0.42
1:C1:2918:OMC:HM23	1:C1:2918:OMC:H1'	1.86	0.42
1:C1:3288:A:H2'	1:C1:3289:G:H8	1.83	0.42
4:C4:17:A:H2'	4:C4:18:G:C8	2.55	0.42
7:CH:317:LEU:HB3	7:CH:330:VAL:HG22	2.01	0.42
15:CQ:18:GLY:HA3	15:CQ:31:PHE:O	2.19	0.42
18:CV:443:LEU:HD22	18:CV:447:THR:HG21	2.02	0.42
27:LB:242:LYS:HD2	27:LB:242:LYS:HA	1.84	0.42
34:LK:90:ARG:HB2	34:LK:92:ARG:HH21	1.84	0.42
43:LT:49:GLN:HA	43:LT:52:MET:HG2	2.00	0.42
57:Lj:32:LYS:HD3	57:Lj:32:LYS:HA	1.88	0.42
63:CR:136:SER:HB3	63:CR:142:ARG:HE	1.83	0.42
1:C1:644:A:H2'	1:C1:645:A:H8	1.85	0.42
1:C1:1929:G:OP1	41:LR:104:ARG:NH1	2.45	0.42
38:LO:129:LEU:HD11	42:LS:170:PRO:HG2	2.02	0.42
63:CR:92:LEU:O	63:CR:96:HIS:HB3	2.19	0.42
63:CR:227:CYS:O	63:CR:231:LEU:HB2	2.20	0.42
1:C1:42:G:H21	1:C1:2571:U:H4'	1.84	0.42
1:C1:3245:C:O3'	27:LB:335:ARG:NH2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CK:174:PRO:HG2	10:CK:177:LEU:HD12	2.00	0.42
30:LE:57:VAL:O	30:LE:105:THR:OG1	2.32	0.42
38:LO:171:GLU:OE1	38:LO:174:LYS:NZ	2.45	0.42
40:LQ:90:VAL:HG13	40:LQ:94:ARG:HD2	2.02	0.42
1:C1:2181:G:H2'	1:C1:2182:A:C8	2.55	0.42
18:CW:206:ARG:HG2	18:CW:301:PRO:HD3	2.02	0.42
18:CW:559:LEU:HD23	18:CW:581:LEU:HD21	2.02	0.42
20:Cd:448:ARG:HB3	20:Cd:456:ASP:HB3	2.02	0.42
27:LB:218:VAL:HG11	27:LB:329:VAL:HB	2.01	0.42
29:LD:12:TYR:O	29:LD:16:PHE:HB2	2.19	0.42
46:LX:148:ILE:HG23	46:LX:152:LYS:HD2	2.02	0.42
53:Lf:59:LYS:O	53:Lf:67:ARG:NH2	2.53	0.42
1:C1:803:U:H2'	1:C1:804:G:C8	2.55	0.42
1:C1:2551:G:H4'	1:C1:2553:C:C2	2.55	0.42
1:C1:3141:G:C8	36:LM:9:THR:HG22	2.54	0.42
1:C1:3204:C:H2'	1:C1:3205:G:C8	2.49	0.42
5:CB:154:LEU:HD23	5:CB:182:VAL:HG11	2.00	0.42
11:CL:55:ILE:HD13	11:CL:65:LEU:HD23	2.02	0.42
17:CT:226:MET:HA	17:CT:236:PHE:O	2.20	0.42
17:CU:383:ASP:OD1	17:CU:384:ALA:N	2.52	0.42
22:Cf:105:MET:HA	22:Cf:111:LEU:H	1.85	0.42
63:CR:119:VAL:HG23	63:CR:120:ILE:HG23	2.01	0.42
1:C1:1548:A:O2'	1:C1:1550:U:OP2	2.30	0.42
1:C1:1676:A:H2'	1:C1:1677:A:C8	2.55	0.42
4:C4:80:U:H3	4:C4:98:G:H1	1.67	0.42
9:CJ:262:ASP:OD2	12:CM:148:LYS:NZ	2.47	0.42
17:CT:71:VAL:HG11	17:CT:345:ILE:HD13	2.02	0.42
17:CT:148:ILE:HD13	17:CT:181:LEU:HD21	2.01	0.42
17:CU:11:CYS:SG	17:CU:46:SER:OG	2.68	0.42
38:LO:87:ARG:HG3	38:LO:101:LEU:HD11	2.01	0.42
1:C1:400:A:C2	2:C2:17:A:H1'	2.54	0.41
1:C1:1337:G:OP1	1:C1:1340:G:O2'	2.27	0.41
2:C2:57:C:H4'	2:C2:63:G:N7	2.34	0.41
9:CJ:28:LEU:HD21	9:CJ:78:LEU:HD22	2.02	0.41
22:Cf:314:MET:HE3	22:Cf:314:MET:HB2	1.95	0.41
34:LK:40:LYS:HE2	34:LK:40:LYS:HB3	1.89	0.41
35:LL:124:ILE:HG23	35:LL:138:THR:HG21	2.01	0.41
38:LO:62:MET:HA	38:LO:72:PRO:HD2	2.01	0.41
38:LO:159:GLU:OE2	38:LO:162:ARG:NH1	2.52	0.41
1:C1:1045:A:O2'	43:LT:108:ARG:NH2	2.53	0.41
1:C1:1177:G:H2'	1:C1:1178:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1449:G:N2	1:C1:1493:G:H5''	2.34	0.41
1:C1:1595:C:H2'	1:C1:1596:U:C6	2.55	0.41
1:C1:2307:U:H2'	1:C1:2308:A:C8	2.55	0.41
8:CI:219:VAL:HG12	8:CI:228:ARG:HD2	2.01	0.41
10:CK:154:PRO:HG2	10:CK:249:PRO:HB2	2.01	0.41
17:CT:199:LYS:HA	17:CT:222:TYR:HB2	2.00	0.41
18:CV:340:LEU:HD23	18:CV:340:LEU:HA	1.96	0.41
22:Cf:112:ASP:OD1	22:Cf:112:ASP:N	2.52	0.41
1:C1:37:C:H4'	1:C1:790:A:H2	1.85	0.41
1:C1:2839:U:OP1	45:LV:49:ASN:ND2	2.51	0.41
19:Cb:30:ARG:NH1	19:Cb:34:GLN:HB3	2.36	0.41
1:C1:3263:G:H2'	1:C1:3264:A:H8	1.85	0.41
2:C2:63:G:H22	2:C2:97:A:H2	1.66	0.41
6:CF:86:ALA:H	6:CF:89:LEU:HD12	1.85	0.41
7:CH:484:GLU:OE2	15:CQ:124:ARG:NH1	2.50	0.41
18:CV:134:LEU:HD22	18:CV:140:LEU:HB3	2.02	0.41
18:CW:219:VAL:HG13	18:CW:223:LEU:HD23	2.02	0.41
27:LB:174:GLN:NE2	27:LB:176:LYS:O	2.54	0.41
31:LG:188:ARG:O	31:LG:191:THR:OG1	2.38	0.41
50:Lc:45:ILE:HD11	50:Lc:70:VAL:HG22	2.03	0.41
63:CR:433:GLN:NE2	63:CR:448:GLN:OE1	2.50	0.41
1:C1:88:U:H2'	1:C1:89:A:C8	2.55	0.41
1:C1:661:C:H2'	1:C1:662:G:C8	2.55	0.41
1:C1:2495:U:H2'	1:C1:2496:G:H8	1.86	0.41
1:C1:2581:C:H5''	23:Cg:177:ILE:HG23	2.01	0.41
1:C1:3140:A:OP1	42:LS:154:HIS:ND1	2.44	0.41
17:CT:111:TRP:CD1	17:CT:348:PRO:HG3	2.56	0.41
18:CW:389:HIS:O	18:CW:393:ILE:HG12	2.21	0.41
26:LA:54:ARG:HG2	26:LA:56:ALA:H	1.85	0.41
50:Lc:65:MET:HE3	50:Lc:65:MET:HB3	1.89	0.41
1:C1:724:G:OP1	40:LQ:101:ASN:ND2	2.49	0.41
1:C1:967:U:H2'	1:C1:968:U:C6	2.54	0.41
1:C1:1214:A:H5''	1:C1:1215:C:H5'	2.03	0.41
1:C1:1393:C:O2'	52:Le:96:GLU:OE2	2.38	0.41
1:C1:2405:G:H2'	1:C1:2406:A:C8	2.55	0.41
1:C1:2621:G:H2'	1:C1:2622:G:H8	1.85	0.41
3:C3:10:C:H2'	3:C3:11:A:H8	1.84	0.41
9:CJ:147:MET:HG2	9:CJ:234:TYR:HD2	1.85	0.41
13:CN:26:VAL:HG21	13:CN:35:TYR:HD2	1.86	0.41
22:Cf:104:ARG:HB3	22:Cf:112:ASP:OD1	2.21	0.41
57:Lj:43:LYS:HB2	57:Lj:43:LYS:HE3	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:410:A:H2'	1:C1:411:A:H8	1.85	0.41
1:C1:817:G:O2'	1:C1:839:G:N2	2.40	0.41
1:C1:1316:C:O2'	12:LF:213:LEU:O	2.35	0.41
1:C1:2171:A:OP2	63:CR:148:LYS:NZ	2.49	0.41
2:C2:47:C:O2'	2:C2:62:A:OP2	2.35	0.41
7:CH:6:ASP:OD1	7:CH:6:ASP:N	2.54	0.41
10:CK:133:PHE:HB3	10:CK:149:ARG:HB3	2.01	0.41
18:CW:443:LEU:HD22	18:CW:447:THR:HG21	2.03	0.41
18:CW:584:ARG:HA	18:CW:584:ARG:HD2	1.89	0.41
20:Cd:481:GLU:HA	20:Cd:482:PRO:HD3	1.96	0.41
24:Ch:465:SER:OG	24:Ch:466:LYS:N	2.54	0.41
12:LF:114:LEU:HD21	12:LF:121:VAL:HG22	2.02	0.41
33:LJ:54:THR:HG23	33:LJ:61:ARG:HA	2.02	0.41
37:LN:73:ARG:HA	37:LN:74:PRO:HD3	1.89	0.41
45:LV:15:MET:HE1	45:LV:56:VAL:HB	2.03	0.41
63:CR:374:HIS:CE1	63:CR:377:VAL:HG13	2.56	0.41
1:C1:665:A:N1	1:C1:691:G:O2'	2.43	0.41
1:C1:859:C:N4	1:C1:860:G:O6	2.54	0.41
1:C1:1577:C:H2'	1:C1:1578:G:C8	2.56	0.41
1:C1:1889:A:H2'	1:C1:1890:A:C8	2.56	0.41
1:C1:3289:G:O6	1:C1:3298:U:O4	2.38	0.41
8:CI:191:ILE:HA	8:CI:259:THR:O	2.21	0.41
8:CI:206:TYR:CE2	8:CI:248:MET:HE2	2.56	0.41
13:CN:104:LEU:HA	13:CN:107:VAL:HG22	2.03	0.41
14:CO:37:LEU:HG	27:LB:195:PHE:HZ	1.86	0.41
15:CQ:74:ARG:HB2	19:Cb:97:TYR:HE2	1.85	0.41
24:Ch:425:ASP:OD1	24:Ch:425:ASP:N	2.47	0.41
27:LB:76:VAL:HG12	27:LB:326:LYS:HA	2.03	0.41
29:LD:60:ILE:HB	29:LD:80:SER:HB3	2.02	0.41
36:LM:107:GLU:HA	36:LM:110:GLN:HG2	2.03	0.41
43:LT:147:LYS:HA	43:LT:148:PRO:HD3	1.96	0.41
48:LZ:69:PRO:HG3	48:LZ:114:LYS:HB2	2.02	0.41
55:Lh:77:ASN:OD1	55:Lh:77:ASN:N	2.54	0.41
1:C1:145:U:OP2	37:LN:49:ARG:NH1	2.53	0.41
1:C1:278:A:C8	1:C1:297:G:H1'	2.54	0.41
1:C1:425:G:H2'	1:C1:426:A:H8	1.85	0.41
1:C1:656:U:H2'	1:C1:657:U:C6	2.56	0.41
1:C1:672:G:OP2	35:LL:28:GLN:NE2	2.49	0.41
1:C1:1054:U:O4	1:C1:1070:G:O6	2.39	0.41
1:C1:1387:G:N2	1:C1:1390:A:OP2	2.33	0.41
1:C1:1623:A:H2'	1:C1:1624:C:C2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1793:A:O2'	1:C1:1796:A:N3	2.52	0.41
1:C1:1901:A:H2'	1:C1:1902:A:C8	2.56	0.41
1:C1:2157:G:C6	20:Cd:311:ILE:HG21	2.56	0.41
1:C1:2159:C:H2'	1:C1:2160:C:C6	2.56	0.41
1:C1:2751:A:H2'	1:C1:2752:G:C8	2.56	0.41
1:C1:3118:C:O2'	1:C1:3119:A:H8	2.04	0.41
4:C4:1:A:C8	29:LD:271:LYS:HG2	2.55	0.41
5:CB:19:ASP:OD1	5:CB:19:ASP:N	2.49	0.41
7:CH:267:ILE:HG23	7:CH:308:LEU:HD21	2.02	0.41
7:CH:391:LYS:O	13:CN:43:GLN:NE2	2.39	0.41
10:CK:61:MET:O	10:CK:65:ILE:HG12	2.21	0.41
17:CT:217:LEU:HA	17:CT:267:VAL:O	2.21	0.41
18:CV:81:ALA:O	18:CV:85:ILE:HD12	2.20	0.41
18:CW:138:GLN:HA	18:CW:141:ILE:HD12	2.02	0.41
18:CW:393:ILE:HG21	18:CW:434:GLU:HB3	2.03	0.41
22:Cf:159:MET:O	22:Cf:163:MET:HG3	2.21	0.41
22:Cf:225:LEU:HD22	22:Cf:257:LEU:HD21	2.03	0.41
22:Cf:266:ALA:O	22:Cf:270:GLU:HG2	2.21	0.41
26:LA:68:LYS:HE3	26:LA:70:LYS:HB3	2.03	0.41
26:LA:178:PRO:HD2	60:Lp:26:VAL:HG12	2.03	0.41
29:LD:193:LEU:HD21	29:LD:198:LEU:HD22	2.02	0.41
12:LF:92:VAL:HG13	12:LF:142:TYR:HB3	2.03	0.41
12:LF:190:LEU:HD21	12:LF:208:LEU:HD21	2.01	0.41
31:LG:33:ARG:NH2	48:LZ:51:LYS:HD2	2.36	0.41
32:LH:75:LEU:HD23	32:LH:75:LEU:HA	1.96	0.41
33:LJ:165:LYS:HZ3	33:LJ:172:VAL:HG23	1.86	0.41
36:LM:112:LEU:HD22	36:LM:116:ASP:HB3	2.02	0.41
52:Le:66:HIS:HB3	61:Lq:25:THR:HG22	2.02	0.41
55:Lh:54:LYS:HA	55:Lh:54:LYS:HD3	1.90	0.41
58:Lk:63:PRO:HA	58:Lk:64:PRO:HD3	1.88	0.41
61:Lq:54:ILE:HG12	61:Lq:63:VAL:HG22	2.02	0.41
61:Lq:136:ALA:O	61:Lq:139:ARG:NH1	2.53	0.41
63:CR:215:CYS:HB3	63:CR:309:LEU:HD21	2.03	0.41
1:C1:230:G:H2'	1:C1:231:A:H8	1.85	0.41
1:C1:580:A:H1'	1:C1:1320:G:H5''	2.01	0.41
1:C1:1617:A:H4'	48:LZ:14:ARG:HB3	2.04	0.41
1:C1:1917:OMU:HM23	1:C1:1917:OMU:H1'	1.65	0.41
1:C1:2383:C:H2'	1:C1:2384:OMU:H6	2.03	0.41
1:C1:2885:A:H2'	1:C1:2886:C:C6	2.56	0.41
5:CB:267:VAL:HG11	5:CB:275:TRP:CE2	2.56	0.41
7:CH:331:LYS:HE2	7:CH:331:LYS:HB3	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CN:78:ASP:OD2	15:CQ:2:ARG:NH1	2.54	0.41
17:CT:130:SER:H	17:CT:143:SER:HA	1.86	0.41
17:CT:250:PHE:HB2	18:CW:599:VAL:HG12	2.02	0.41
23:Cg:66:LEU:O	23:Cg:70:THR:OG1	2.32	0.41
27:LB:92:TYR:HB2	27:LB:158:VAL:HB	2.03	0.41
29:LD:95:TRP:CE3	29:LD:201:TYR:HB3	2.56	0.41
32:LH:15:ASN:OD1	32:LH:15:ASN:N	2.50	0.41
42:LS:138:PRO:HA	42:LS:141:LYS:HB2	2.03	0.41
1:C1:203:A:H4'	1:C1:205:A:N7	2.36	0.40
1:C1:804:G:H2'	1:C1:805:C:H6	1.86	0.40
1:C1:1077:U:H5	43:LT:120:LYS:HA	1.86	0.40
1:C1:1305:U:OP1	42:LS:117:ARG:NH2	2.41	0.40
1:C1:2971:U:H2'	1:C1:2972:U:C6	2.56	0.40
2:C2:153:U:O2'	31:LG:159:ASP:OD1	2.35	0.40
8:CI:215:ARG:HA	8:CI:277:ASN:HD21	1.86	0.40
8:CI:283:VAL:HG13	8:CI:288:MET:HE2	2.02	0.40
19:Cb:20:ASP:OD1	19:Cb:21:GLN:N	2.54	0.40
32:LH:127:MET:HE2	32:LH:218:ILE:HG22	2.02	0.40
33:LJ:47:VAL:O	33:LJ:68:VAL:HA	2.20	0.40
53:Lf:17:SER:OG	53:Lf:18:TYR:N	2.52	0.40
1:C1:300:A:H2'	1:C1:301:A:H8	1.82	0.40
1:C1:2305:U:OP1	1:C1:3047:C:O2'	2.40	0.40
1:C1:2628:G:H2'	1:C1:2629:G:H8	1.85	0.40
15:CQ:66:ASP:OD1	15:CQ:67:SER:N	2.54	0.40
17:CT:375:LEU:HD11	18:CV:132:ILE:HD12	2.03	0.40
28:LC:284:GLN:HB3	28:LC:290:LEU:HD21	2.03	0.40
30:LE:30:ALA:HA	61:Lq:113:ALA:HB1	2.02	0.40
30:LE:199:LYS:NZ	36:LM:110:GLN:O	2.51	0.40
12:LF:132:MET:O	12:LF:136:VAL:HG22	2.21	0.40
63:CR:382:ILE:HG22	63:CR:386:VAL:HG23	2.03	0.40
1:C1:698:A:H2'	1:C1:699:A:C8	2.57	0.40
16:CS:292:PHE:HZ	16:CS:300:ILE:HD11	1.85	0.40
18:CW:301:PRO:HA	18:CW:302:PRO:HD3	1.90	0.40
28:LC:273:LYS:HE2	28:LC:273:LYS:HB2	1.86	0.40
28:LC:301:ARG:HH12	28:LC:304:LYS:HE2	1.85	0.40
34:LK:114:ARG:HG2	34:LK:125:LEU:HD11	2.04	0.40
1:C1:508:G:OP1	12:LF:73:ARG:NH2	2.45	0.40
1:C1:1045:A:N3	43:LT:130:ARG:NH2	2.69	0.40
1:C1:2391:U:H2'	1:C1:2392:G:C8	2.55	0.40
1:C1:2533:G:O2'	21:Ce:424:PHE:O	2.31	0.40
1:C1:2705:A:C6	29:LD:156:THR:HG21	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CH:288:LYS:HG2	64:CH:701:GTP:C6	2.57	0.40
18:CW:140:LEU:O	18:CW:144:MET:HB3	2.21	0.40
24:Ch:85:PHE:HA	24:Ch:123:SER:O	2.21	0.40
24:Ch:305:VAL:HB	24:Ch:315:HIS:HB2	2.03	0.40
29:LD:223:LYS:O	29:LD:227:VAL:HB	2.21	0.40
45:LV:77:PRO:HG2	45:LV:107:PRO:HD3	2.04	0.40
48:LZ:22:VAL:HG12	48:LZ:44:GLY:HA3	2.02	0.40
49:La:58:MET:HE3	49:La:58:MET:HB2	1.92	0.40
1:C1:282:U:H2'	1:C1:283:G:C8	2.55	0.40
1:C1:424:U:H2'	1:C1:425:G:C8	2.57	0.40
1:C1:551:C:H2'	1:C1:552:C:H6	1.87	0.40
1:C1:629:C:H2'	1:C1:630:U:C6	2.56	0.40
1:C1:1823:C:OP1	59:Ll:48:ARG:NH2	2.54	0.40
1:C1:2628:G:H2'	1:C1:2629:G:C8	2.57	0.40
1:C1:2710:G:H2'	1:C1:2711:U:C6	2.57	0.40
1:C1:2744:A:H2'	1:C1:2745:G:H8	1.86	0.40
6:CF:227:TRP:HB2	6:CF:234:VAL:HG22	2.02	0.40
15:CQ:89:THR:O	15:CQ:93:MET:HG3	2.21	0.40
18:CW:188:VAL:HG13	18:CW:189:LEU:HG	2.04	0.40
20:Cd:123:LEU:HD21	24:Ch:401:LEU:HB3	2.03	0.40
21:Ce:96:SER:HB3	31:LG:177:GLY:HA3	2.04	0.40
12:LF:242:ASN:O	12:LF:246:ARG:HG2	2.22	0.40
55:Lh:100:GLU:O	55:Lh:104:ARG:HG3	2.22	0.40
63:CR:202:TRP:HB3	63:CR:207:PRO:HG2	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
5	CB	259/391 (66%)	255 (98%)	4 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	CF	243/270 (90%)	240 (99%)	3 (1%)	0	100	100
7	CH	621/661 (94%)	615 (99%)	6 (1%)	0	100	100
8	CI	150/414 (36%)	147 (98%)	3 (2%)	0	100	100
9	CJ	376/679 (55%)	373 (99%)	3 (1%)	0	100	100
10	CK	231/261 (88%)	226 (98%)	5 (2%)	0	100	100
11	CL	77/558 (14%)	76 (99%)	1 (1%)	0	100	100
12	CM	211/249 (85%)	206 (98%)	5 (2%)	0	100	100
12	LF	246/249 (99%)	240 (98%)	6 (2%)	0	100	100
13	CN	244/246 (99%)	236 (97%)	8 (3%)	0	100	100
14	CO	56/120 (47%)	56 (100%)	0	0	100	100
15	CQ	181/225 (80%)	180 (99%)	1 (1%)	0	100	100
16	CS	264/338 (78%)	262 (99%)	2 (1%)	0	100	100
17	CT	393/437 (90%)	383 (98%)	10 (2%)	0	100	100
17	CU	393/437 (90%)	382 (97%)	11 (3%)	0	100	100
18	CV	544/781 (70%)	535 (98%)	9 (2%)	0	100	100
18	CW	544/781 (70%)	536 (98%)	8 (2%)	0	100	100
19	Cb	99/117 (85%)	98 (99%)	1 (1%)	0	100	100
20	Cd	458/627 (73%)	449 (98%)	9 (2%)	0	100	100
21	Ce	252/443 (57%)	250 (99%)	2 (1%)	0	100	100
22	Cf	281/350 (80%)	279 (99%)	2 (1%)	0	100	100
23	Cg	186/202 (92%)	185 (100%)	1 (0%)	0	100	100
24	Ch	483/517 (93%)	469 (97%)	14 (3%)	0	100	100
25	Cz	99/123 (80%)	98 (99%)	1 (1%)	0	100	100
26	LA	189/254 (74%)	183 (97%)	6 (3%)	0	100	100
27	LB	387/392 (99%)	380 (98%)	7 (2%)	0	100	100
28	LC	361/365 (99%)	357 (99%)	4 (1%)	0	100	100
29	LD	282/304 (93%)	280 (99%)	2 (1%)	0	100	100
30	LE	187/200 (94%)	183 (98%)	4 (2%)	0	100	100
31	LG	233/262 (89%)	230 (99%)	3 (1%)	0	100	100
32	LH	188/229 (82%)	185 (98%)	3 (2%)	0	100	100
33	LJ	167/173 (96%)	166 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	LK	156/165 (94%)	156 (100%)	0	0	100	100
35	LL	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
36	LM	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
37	LN	200/203 (98%)	194 (97%)	6 (3%)	0	100	100
38	LO	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
39	LP	167/187 (89%)	164 (98%)	3 (2%)	0	100	100
40	LQ	148/213 (70%)	145 (98%)	3 (2%)	0	100	100
41	LR	153/2898 (5%)	152 (99%)	1 (1%)	0	100	100
42	LS	172/174 (99%)	169 (98%)	3 (2%)	0	100	100
43	LT	127/160 (79%)	126 (99%)	1 (1%)	0	100	100
44	LU	103/127 (81%)	102 (99%)	1 (1%)	0	100	100
45	LV	133/139 (96%)	132 (99%)	1 (1%)	0	100	100
46	LX	143/156 (92%)	139 (97%)	4 (3%)	0	100	100
47	LY	131/138 (95%)	128 (98%)	3 (2%)	0	100	100
48	LZ	133/135 (98%)	131 (98%)	2 (2%)	0	100	100
49	La	104/149 (70%)	104 (100%)	0	0	100	100
50	Lc	93/108 (86%)	93 (100%)	0	0	100	100
51	Ld	108/120 (90%)	107 (99%)	1 (1%)	0	100	100
52	Le	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
53	Lf	106/109 (97%)	106 (100%)	0	0	100	100
54	Lg	116/119 (98%)	114 (98%)	2 (2%)	0	100	100
55	Lh	120/935 (13%)	116 (97%)	4 (3%)	0	100	100
56	Li	99/110 (90%)	98 (99%)	1 (1%)	0	100	100
57	Lj	86/95 (90%)	84 (98%)	2 (2%)	0	100	100
58	Lk	74/94 (79%)	73 (99%)	1 (1%)	0	100	100
59	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
60	Lp	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
61	Lq	137/147 (93%)	132 (96%)	5 (4%)	0	100	100
62	Lr	212/217 (98%)	207 (98%)	5 (2%)	0	100	100
63	CR	386/767 (50%)	379 (98%)	7 (2%)	0	100	100
All	All	13094/20153 (65%)	12881 (98%)	213 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
5	CB	227/329 (69%)	227 (100%)	0	100	100
6	CF	212/236 (90%)	212 (100%)	0	100	100
7	CH	549/575 (96%)	549 (100%)	0	100	100
8	CI	124/336 (37%)	124 (100%)	0	100	100
9	CJ	331/579 (57%)	331 (100%)	0	100	100
10	CK	206/225 (92%)	206 (100%)	0	100	100
11	CL	61/458 (13%)	61 (100%)	0	100	100
12	CM	185/215 (86%)	185 (100%)	0	100	100
12	LF	213/215 (99%)	213 (100%)	0	100	100
13	CN	205/206 (100%)	205 (100%)	0	100	100
14	CO	48/99 (48%)	48 (100%)	0	100	100
15	CQ	144/192 (75%)	144 (100%)	0	100	100
16	CS	216/291 (74%)	216 (100%)	0	100	100
17	CT	324/376 (86%)	324 (100%)	0	100	100
17	CU	328/376 (87%)	328 (100%)	0	100	100
18	CV	472/675 (70%)	472 (100%)	0	100	100
18	CW	469/675 (70%)	469 (100%)	0	100	100
19	Cb	85/101 (84%)	85 (100%)	0	100	100
20	Cd	403/541 (74%)	403 (100%)	0	100	100
21	Ce	223/383 (58%)	223 (100%)	0	100	100
22	Cf	250/310 (81%)	250 (100%)	0	100	100
23	Cg	158/176 (90%)	158 (100%)	0	100	100
24	Ch	407/436 (93%)	407 (100%)	0	100	100
25	Cz	89/107 (83%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	LA	150/198 (76%)	150 (100%)	0	100	100
27	LB	329/331 (99%)	329 (100%)	0	100	100
28	LC	282/285 (99%)	282 (100%)	0	100	100
29	LD	221/253 (87%)	221 (100%)	0	100	100
30	LE	157/166 (95%)	157 (100%)	0	100	100
31	LG	200/222 (90%)	200 (100%)	0	100	100
32	LH	167/200 (84%)	167 (100%)	0	100	100
33	LJ	140/150 (93%)	140 (100%)	0	100	100
34	LK	127/136 (93%)	127 (100%)	0	100	100
35	LL	158/176 (90%)	158 (100%)	0	100	100
36	LM	116/117 (99%)	116 (100%)	0	100	100
37	LN	179/180 (99%)	179 (100%)	0	100	100
38	LO	162/163 (99%)	162 (100%)	0	100	100
39	LP	134/152 (88%)	134 (100%)	0	100	100
40	LQ	128/178 (72%)	128 (100%)	0	100	100
41	LR	125/2396 (5%)	125 (100%)	0	100	100
42	LS	152/154 (99%)	152 (100%)	0	100	100
43	LT	108/135 (80%)	108 (100%)	0	100	100
44	LU	92/108 (85%)	92 (100%)	0	100	100
45	LV	98/102 (96%)	98 (100%)	0	100	100
46	LX	122/129 (95%)	122 (100%)	0	100	100
47	LY	116/119 (98%)	116 (100%)	0	100	100
48	LZ	121/121 (100%)	121 (100%)	0	100	100
49	La	93/122 (76%)	93 (100%)	0	100	100
50	Lc	76/88 (86%)	76 (100%)	0	100	100
51	Ld	90/105 (86%)	90 (100%)	0	100	100
52	Le	109/114 (96%)	109 (100%)	0	100	100
53	Lf	89/90 (99%)	89 (100%)	0	100	100
54	Lg	95/102 (93%)	95 (100%)	0	100	100
55	Lh	109/781 (14%)	109 (100%)	0	100	100
56	Li	85/93 (91%)	85 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	Lj	72/78 (92%)	72 (100%)	0	100	100
58	Lk	73/88 (83%)	73 (100%)	0	100	100
59	Ll	45/46 (98%)	45 (100%)	0	100	100
60	Lp	73/74 (99%)	73 (100%)	0	100	100
61	Lq	109/112 (97%)	109 (100%)	0	100	100
63	CR	293/663 (44%)	293 (100%)	0	100	100
All	All	10924/16839 (65%)	10924 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (89) such sidechains are listed below:

Mol	Chain	Res	Type
5	CB	150	HIS
5	CB	187	GLN
6	CF	50	ASN
6	CF	153	HIS
7	CH	14	GLN
7	CH	82	ASN
7	CH	226	HIS
7	CH	266	GLN
7	CH	287	ASN
7	CH	499	HIS
7	CH	536	GLN
7	CH	608	GLN
7	CH	619	GLN
9	CJ	481	GLN
10	CK	33	HIS
10	CK	95	ASN
10	CK	190	ASN
14	CO	20	ASN
15	CQ	5	ASN
15	CQ	82	ASN
15	CQ	87	GLN
16	CS	75	GLN
16	CS	152	ASN
17	CT	207	ASN
17	CT	360	GLN
17	CT	376	ASN
17	CU	30	HIS

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Mol	Chain	Res	Type
17	CU	165	HIS
18	CV	280	HIS
18	CV	456	GLN
18	CV	553	HIS
18	CW	65	HIS
18	CW	554	ASN
19	Cb	33	GLN
19	Cb	68	HIS
20	Cd	9	ASN
20	Cd	22	HIS
20	Cd	99	GLN
20	Cd	271	ASN
20	Cd	292	HIS
20	Cd	463	GLN
21	Ce	329	GLN
22	Cf	40	GLN
23	Cg	31	ASN
24	Ch	114	ASN
24	Ch	326	HIS
24	Ch	340	HIS
24	Ch	411	GLN
26	LA	205	ASN
27	LB	257	HIS
27	LB	346	HIS
28	LC	324	GLN
28	LC	330	ASN
29	LD	90	HIS
30	LE	124	GLN
12	LF	77	GLN
12	LF	165	GLN
31	LG	36	ASN
31	LG	92	GLN
32	LH	5	HIS
32	LH	95	HIS
32	LH	133	HIS
32	LH	179	GLN
32	LH	225	ASN
35	LL	13	HIS
35	LL	99	HIS
37	LN	86	ASN
37	LN	91	GLN
38	LO	56	HIS

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Mol	Chain	Res	Type
39	LP	121	GLN
44	LU	27	GLN
46	LX	92	GLN
46	LX	110	GLN
48	LZ	126	ASN
49	La	11	HIS
51	Ld	62	GLN
51	Ld	64	ASN
52	Le	21	HIS
53	Lf	7	HIS
55	Lh	37	GLN
56	Li	21	ASN
57	Lj	13	ASN
57	Lj	76	ASN
63	CR	95	HIS
63	CR	96	HIS
63	CR	297	HIS
63	CR	315	GLN
63	CR	391	ASN
63	CR	417	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3127/3342 (93%)	587 (18%)	23 (0%)
2	C2	155/156 (99%)	22 (14%)	0
3	C3	80/162 (49%)	21 (26%)	0
4	C4	118/119 (99%)	24 (20%)	1 (0%)
All	All	3480/3779 (92%)	654 (18%)	24 (0%)

All (654) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	4	U
1	C1	6	G
1	C1	27	A
1	C1	44	A
1	C1	50	A
1	C1	60	G
1	C1	61	A
1	C1	66	A

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Mol	Chain	Res	Type
1	C1	67	A
1	C1	68	A
1	C1	78	A
1	C1	94	C
1	C1	95	G
1	C1	96	A
1	C1	110	A
1	C1	111	G
1	C1	112	C
1	C1	116	A
1	C1	117	A
1	C1	123	A
1	C1	132	U
1	C1	134	G
1	C1	135	G
1	C1	139	G
1	C1	144	G
1	C1	152	G
1	C1	153	A
1	C1	156	G
1	C1	157	G
1	C1	181	G
1	C1	184	U
1	C1	185	U
1	C1	194	C
1	C1	200	G
1	C1	204	C
1	C1	213	A
1	C1	214	G
1	C1	225	A
1	C1	241	U
1	C1	244	G
1	C1	247	A
1	C1	258	A
1	C1	262	G
1	C1	276	G
1	C1	277	A
1	C1	278	A
1	C1	288	A
1	C1	291	U
1	C1	298	U
1	C1	308	C

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Mol	Chain	Res	Type
1	C1	316	A
1	C1	322	C
1	C1	323	G
1	C1	331	A
1	C1	332	C
1	C1	343	C
1	C1	344	A
1	C1	369	G
1	C1	388	A
1	C1	389	A2M
1	C1	391	U
1	C1	394	C
1	C1	395	A
1	C1	396	C
1	C1	414	G
1	C1	415	A
1	C1	422	U
1	C1	434	U
1	C1	435	G
1	C1	443	C
1	C1	446	A
1	C1	447	U
1	C1	448	C
1	C1	458	U
1	C1	459	C
1	C1	460	U
1	C1	469	C
1	C1	470	A
1	C1	471	C
1	C1	472	U
1	C1	479	G
1	C1	512	A
1	C1	514	A
1	C1	527	G
1	C1	535	U
1	C1	536	C
1	C1	537	C
1	C1	545	U
1	C1	547	A
1	C1	548	U
1	C1	549	A
1	C1	570	G

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Mol	Chain	Res	Type
1	C1	580	A
1	C1	583	A
1	C1	588	G
1	C1	592	U
1	C1	593	G
1	C1	595	A
1	C1	597	G
1	C1	599	A
1	C1	608	U
1	C1	609	A
1	C1	610	A
1	C1	624	C
1	C1	632	G
1	C1	634	A
1	C1	648	A
1	C1	665	A
1	C1	669	U
1	C1	693	A
1	C1	700	G
1	C1	703	A
1	C1	704	A
1	C1	719	U
1	C1	720	C
1	C1	721	G
1	C1	724	G
1	C1	747	A
1	C1	748	U
1	C1	755	G
1	C1	756	G
1	C1	757	A
1	C1	759	U
1	C1	761	G
1	C1	762	A
1	C1	763	G
1	C1	767	G
1	C1	782	G
1	C1	790	A
1	C1	799	A
1	C1	812	A
1	C1	830	A
1	C1	843	C
1	C1	856	U

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Mol	Chain	Res	Type
1	C1	857	G
1	C1	862	G
1	C1	877	A
1	C1	878	A
1	C1	879	U
1	C1	889	G
1	C1	890	G
1	C1	896	A
1	C1	898	G
1	C1	899	A
1	C1	903	A
1	C1	905	C
1	C1	906	G
1	C1	919	G
1	C1	926	A
1	C1	931	C
1	C1	933	A
1	C1	934	A
1	C1	935	G
1	C1	937	U
1	C1	940	C
1	C1	941	C
1	C1	944	A
1	C1	945	G
1	C1	947	A
1	C1	955	G
1	C1	956	U
1	C1	963	U
1	C1	964	C
1	C1	976	G
1	C1	977	U
1	C1	983	G
1	C1	984	A
1	C1	1032	C
1	C1	1034	U
1	C1	1040	A
1	C1	1047	A
1	C1	1048	A
1	C1	1049	G
1	C1	1051	C
1	C1	1055	G
1	C1	1058	A

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Mol	Chain	Res	Type
1	C1	1064	C
1	C1	1065	U
1	C1	1066	G
1	C1	1070	G
1	C1	1075	C
1	C1	1076	A
1	C1	1077	U
1	C1	1078	U
1	C1	1079	C
1	C1	1080	G
1	C1	1081	A
1	C1	1086	A
1	C1	1099	G
1	C1	1110	G
1	C1	1115	C
1	C1	1118	A
1	C1	1127	U
1	C1	1132	G
1	C1	1136	A
1	C1	1143	C
1	C1	1161	G
1	C1	1163	G
1	C1	1164	U
1	C1	1165	G
1	C1	1175	C
1	C1	1176	A
1	C1	1179	C
1	C1	1182	C
1	C1	1185	A
1	C1	1190	G
1	C1	1194	U
1	C1	1205	G
1	C1	1209	G
1	C1	1228	A
1	C1	1229	G
1	C1	1241	U
1	C1	1246	A
1	C1	1248	U
1	C1	1255	C
1	C1	1268	G
1	C1	1269	A
1	C1	1270	A

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Mol	Chain	Res	Type
1	C1	1278	G
1	C1	1287	A
1	C1	1288	U
1	C1	1290	G
1	C1	1292	U
1	C1	1296	G
1	C1	1313	A
1	C1	1331	A
1	C1	1332	G
1	C1	1333	A
1	C1	1334	A
1	C1	1335	A
1	C1	1336	C
1	C1	1337	G
1	C1	1338	A
1	C1	1349	A
1	C1	1370	G
1	C1	1375	G
1	C1	1382	A
1	C1	1383	G
1	C1	1400	G
1	C1	1401	A
1	C1	1414	G
1	C1	1417	G
1	C1	1420	OMC
1	C1	1429	A
1	C1	1433	OMG
1	C1	1438	U
1	C1	1458	G
1	C1	1464	A
1	C1	1467	U
1	C1	1477	U
1	C1	1479	C
1	C1	1485	G
1	C1	1491	OMC
1	C1	1505	U
1	C1	1506	U
1	C1	1536	U
1	C1	1538	U
1	C1	1539	C
1	C1	1540	A
1	C1	1542	A

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Mol	Chain	Res	Type
1	C1	1543	G
1	C1	1549	C
1	C1	1550	U
1	C1	1552	G
1	C1	1554	G
1	C1	1560	U
1	C1	1561	G
1	C1	1563	G
1	C1	1567	A
1	C1	1568	A
1	C1	1569	A
1	C1	1573	A
1	C1	1585	A
1	C1	1586	U
1	C1	1609	U
1	C1	1619	C
1	C1	1622	A
1	C1	1623	A
1	C1	1624	C
1	C1	1638	G
1	C1	1663	C
1	C1	1685	U
1	C1	1697	C
1	C1	1704	U
1	C1	1721	A
1	C1	1722	U
1	C1	1730	A
1	C1	1731	G
1	C1	1745	U
1	C1	1746	G
1	C1	1751	G
1	C1	1760	G
1	C1	1776	G
1	C1	1777	A
1	C1	1792	G
1	C1	1793	A
1	C1	1794	A
1	C1	1795	U
1	C1	1796	A
1	C1	1799	U
1	C1	1800	C
1	C1	1801	U

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Mol	Chain	Res	Type
1	C1	1822	A
1	C1	1826	C
1	C1	1829	C
1	C1	1830	A
1	C1	1846	C
1	C1	1847	A2M
1	C1	1856	U
1	C1	1858	G
1	C1	1860	U
1	C1	1866	A
1	C1	1873	A
1	C1	1886	G
1	C1	1887	C
1	C1	1917	OMU
1	C1	1923	C
1	C1	1933	G
1	C1	1934	G
1	C1	1935	C
1	C1	1937	C
1	C1	2046	C
1	C1	2048	U
1	C1	2050	C
1	C1	2052	G
1	C1	2056	A
1	C1	2076	A
1	C1	2084	G
1	C1	2085	G
1	C1	2089	A
1	C1	2094	A
1	C1	2103	U
1	C1	2121	A
1	C1	2122	U
1	C1	2126	C
1	C1	2132	G
1	C1	2151	A
1	C1	2156	U
1	C1	2157	G
1	C1	2158	C
1	C1	2160	C
1	C1	2161	A
1	C1	2167	C
1	C1	2168	U

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Mol	Chain	Res	Type
1	C1	2171	A
1	C1	2172	U
1	C1	2185	A
1	C1	2186	A
1	C1	2192	A
1	C1	2203	G
1	C1	2205	A
1	C1	2206	A
1	C1	2212	G
1	C1	2213	G
1	C1	2216	G
1	C1	2218	A
1	C1	2220	C
1	C1	2221	U
1	C1	2222	A
1	C1	2223	U
1	C1	2224	G
1	C1	2225	A
1	C1	2231	U
1	C1	2237	U
1	C1	2279	G
1	C1	2281	U
1	C1	2282	U
1	C1	2284	A
1	C1	2297	U
1	C1	2298	G
1	C1	2299	U
1	C1	2340	G
1	C1	2348	A
1	C1	2351	U
1	C1	2355	C
1	C1	2356	G
1	C1	2362	A
1	C1	2364	A
1	C1	2373	U
1	C1	2374	U
1	C1	2381	G
1	C1	2382	A
1	C1	2398	G
1	C1	2401	A
1	C1	2407	C
1	C1	2409	U

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Mol	Chain	Res	Type
1	C1	2410	A
1	C1	2411	G
1	C1	2415	G
1	C1	2416	U
1	C1	2421	A
1	C1	2422	A
1	C1	2423	U
1	C1	2425	G
1	C1	2426	G
1	C1	2431	A
1	C1	2432	G
1	C1	2435	U
1	C1	2436	C
1	C1	2437	G
1	C1	2438	G
1	C1	2440	G
1	C1	2441	C
1	C1	2446	G
1	C1	2450	U
1	C1	2454	A
1	C1	2458	C
1	C1	2465	U
1	C1	2466	G
1	C1	2473	U
1	C1	2474	A
1	C1	2477	U
1	C1	2489	C
1	C1	2498	A
1	C1	2499	C
1	C1	2500	U
1	C1	2501	U
1	C1	2502	G
1	C1	2503	C
1	C1	2506	C
1	C1	2507	C
1	C1	2508	A
1	C1	2513	C
1	C1	2515	G
1	C1	2521	A
1	C1	2527	C
1	C1	2533	G
1	C1	2544	G

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Mol	Chain	Res	Type
1	C1	2545	G
1	C1	2552	A
1	C1	2565	G
1	C1	2566	G
1	C1	2569	G
1	C1	2573	G
1	C1	2575	C
1	C1	2576	U
1	C1	2577	G
1	C1	2578	OMG
1	C1	2582	G
1	C1	2584	C
1	C1	2585	A
1	C1	2592	U
1	C1	2606	A
1	C1	2615	A
1	C1	2631	G
1	C1	2633	A
1	C1	2635	A
1	C1	2636	G
1	C1	2647	U
1	C1	2651	A
1	C1	2656	A
1	C1	2657	G
1	C1	2663	A
1	C1	2664	A
1	C1	2672	U
1	C1	2673	G
1	C1	2674	A
1	C1	2675	U
1	C1	2680	A
1	C1	2689	G
1	C1	2690	OMU
1	C1	2691	G
1	C1	2713	G
1	C1	2717	A
1	C1	2731	C
1	C1	2732	C
1	C1	2736	G
1	C1	2737	A
1	C1	2750	G
1	C1	2754	U

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Mol	Chain	Res	Type
1	C1	2755	G
1	C1	2756	C
1	C1	2757	C
1	C1	2758	A
1	C1	2761	A
1	C1	2762	A
1	C1	2763	A
1	C1	2769	C
1	C1	2783	G
1	C1	2784	C
1	C1	2785	U
1	C1	2802	U
1	C1	2803	C
1	C1	2804	A
1	C1	2805	U
1	C1	2806	A
1	C1	2812	G
1	C1	2816	C
1	C1	2817	U
1	C1	2826	C
1	C1	2828	U
1	C1	2834	U
1	C1	2836	G
1	C1	2846	A
1	C1	2857	G
1	C1	2858	C
1	C1	2870	A
1	C1	2882	U
1	C1	2883	U
1	C1	2884	C
1	C1	2885	A
1	C1	2894	U
1	C1	2895	A
1	C1	2929	C
1	C1	2930	A
1	C1	2931	G
1	C1	2938	U
1	C1	2939	U
1	C1	2940	U
1	C1	2942	C
1	C1	2949	G
1	C1	2951	U

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Mol	Chain	Res	Type
1	C1	2955	C
1	C1	2956	U
1	C1	2970	A
1	C1	2980	G
1	C1	3014	U
1	C1	3017	G
1	C1	3036	G
1	C1	3044	A
1	C1	3045	A
1	C1	3050	C
1	C1	3051	C
1	C1	3062	U
1	C1	3067	G
1	C1	3071	A
1	C1	3080	A
1	C1	3087	A
1	C1	3088	A
1	C1	3089	U
1	C1	3100	A
1	C1	3101	C
1	C1	3102	G
1	C1	3112	U
1	C1	3113	A
1	C1	3118	C
1	C1	3119	A
1	C1	3124	G
1	C1	3126	A
1	C1	3127	G
1	C1	3131	U
1	C1	3133	U
1	C1	3135	A
1	C1	3141	G
1	C1	3146	C
1	C1	3155	A
1	C1	3162	C
1	C1	3163	A
1	C1	3164	G
1	C1	3168	A
1	C1	3185	G
1	C1	3186	A
1	C1	3190	G
1	C1	3200	A

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Mol	Chain	Res	Type
1	C1	3201	A
1	C1	3206	C
1	C1	3210	U
1	C1	3211	U
1	C1	3217	U
1	C1	3218	U
1	C1	3228	C
1	C1	3229	G
1	C1	3231	G
1	C1	3245	C
1	C1	3254	U
1	C1	3257	A
1	C1	3258	U
1	C1	3259	G
1	C1	3260	U
1	C1	3282	U
1	C1	3286	G
1	C1	3292	U
1	C1	3293	U
1	C1	3295	U
1	C1	3297	G
1	C1	3299	U
1	C1	3302	G
1	C1	3310	G
1	C1	3312	G
1	C1	3316	A
1	C1	3319	C
1	C1	3323	C
1	C1	3324	C
1	C1	3325	U
1	C1	3331	U
1	C1	3332	A
1	C1	3338	C
2	C2	34	U
2	C2	35	C
2	C2	39	G
2	C2	59	A
2	C2	62	A
2	C2	63	G
2	C2	81	U
2	C2	82	U
2	C2	83	C

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Mol	Chain	Res	Type
2	C2	84	C
2	C2	87	G
2	C2	90	U
2	C2	95	G
2	C2	97	A
2	C2	104	A
2	C2	106	C
2	C2	113	U
2	C2	116	G
2	C2	125	U
2	C2	127	U
2	C2	151	C
2	C2	154	C
3	C3	2	U
3	C3	3	C
3	C3	10	C
3	C3	19	G
3	C3	20	G
3	C3	25	U
3	C3	33	A
3	C3	36	C
3	C3	39	G
3	C3	50	G
3	C3	57	A
3	C3	58	A
3	C3	59	A
3	C3	63	A
3	C3	68	C
3	C3	69	G
3	C3	135	G
3	C3	136	C
3	C3	137	C
3	C3	138	A
3	C3	139	G
4	C4	7	G
4	C4	9	C
4	C4	22	A
4	C4	29	G
4	C4	54	U
4	C4	55	A
4	C4	64	A
4	C4	66	G

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Mol	Chain	Res	Type
4	C4	75	A
4	C4	76	G
4	C4	77	U
4	C4	81	U
4	C4	82	G
4	C4	83	G
4	C4	84	G
4	C4	87	G
4	C4	90	G
4	C4	91	A
4	C4	93	G
4	C4	97	A
4	C4	99	C
4	C4	100	G
4	C4	101	A
4	C4	111	G

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	151	G
1	C1	243	U
1	C1	898	G
1	C1	1047	A
1	C1	1064	C
1	C1	1077	U
1	C1	1267	C
1	C1	1537	U
1	C1	2157	G
1	C1	2160	C
1	C1	2280	A
1	C1	2409	U
1	C1	2575	C
1	C1	2883	U
1	C1	3079	U
1	C1	3132	A
1	C1	3205	G
1	C1	3210	U
1	C1	3230	G
1	C1	3258	U
1	C1	3298	U
1	C1	3301	C

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Mol	Chain	Res	Type
1	C1	3324	C
4	C4	90	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	OMC	C1	2918	1	19,22,23	0.55	0	25,31,34	0.82	1 (4%)
1	OMC	C1	2300	1	19,22,23	0.51	0	25,31,34	0.74	1 (4%)
1	A2M	C1	389	1	22,25,26	3.98	11 (50%)	30,36,39	3.36	14 (46%)
1	OMC	C1	1491	1	19,22,23	0.53	0	25,31,34	0.80	1 (4%)
1	A2M	C1	1432	1	22,25,26	3.99	12 (54%)	30,36,39	3.36	13 (43%)
1	OMU	C1	1917	1	19,22,23	3.14	6 (31%)	25,31,34	1.84	5 (20%)
1	A2M	C1	1223	1	22,25,26	3.97	11 (50%)	30,36,39	3.36	13 (43%)
1	OMU	C1	2690	1	19,22,23	3.10	6 (31%)	25,31,34	1.79	5 (20%)
1	OMC	C1	1836	1	19,22,23	0.55	0	25,31,34	0.82	1 (4%)
1	OMG	C1	2876	1	23,26,27	0.45	0	32,38,41	0.50	0
1	OMC	C1	2838	1	19,22,23	0.67	0	25,31,34	1.55	4 (16%)
1	OMU	C1	2384	1	19,22,23	3.11	6 (31%)	25,31,34	1.77	5 (20%)
1	OMU	C1	2380	1	19,22,23	3.11	6 (31%)	25,31,34	1.80	5 (20%)
1	OMG	C1	1433	1	23,26,27	0.48	0	32,38,41	0.49	0
1	OMG	C1	385	1	23,26,27	0.48	0	32,38,41	0.61	0
1	A2M	C1	1847	1	22,25,26	4.00	12 (54%)	30,36,39	3.51	15 (50%)
1	OMU	C1	2683	1	19,22,23	3.08	6 (31%)	25,31,34	1.72	5 (20%)
1	OMG	C1	2578	1	23,26,27	0.47	0	32,38,41	0.57	0
1	OMG	C1	646	1	23,26,27	0.46	0	32,38,41	0.49	0
1	OMU	C1	1868	1	19,22,23	3.14	6 (31%)	25,31,34	1.84	5 (20%)
1	A2M	C1	848	1	22,25,26	3.99	12 (54%)	30,36,39	3.41	14 (46%)
1	A2M	C1	2289	1	22,25,26	4.01	11 (50%)	30,36,39	3.33	14 (46%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	C1	2774	1	23,26,27	0.47	0	32,38,41	0.51	0
1	OMC	C1	1812	1	19,22,23	0.54	0	25,31,34	1.11	2 (8%)
1	OMG	C1	2358	1	23,26,27	0.48	0	32,38,41	0.49	0
1	OMU	C1	2688	1	19,22,23	3.13	6 (31%)	25,31,34	1.78	5 (20%)
1	OMU	C1	2277	1	19,22,23	3.12	6 (31%)	25,31,34	1.75	4 (16%)
1	OMC	C1	778	1	19,22,23	0.56	0	25,31,34	0.96	1 (4%)
1	OMC	C1	1420	1	19,22,23	0.61	0	25,31,34	1.47	4 (16%)
1	OMG	C1	2881	1	23,26,27	0.45	0	32,38,41	0.47	0
1	A2M	C1	637	1	22,25,26	3.98	11 (50%)	30,36,39	3.41	13 (43%)
1	OMG	C1	627	1	23,26,27	0.47	0	32,38,41	0.50	0
1	OMG	C1	787	1	23,26,27	0.48	0	32,38,41	0.57	0
1	A2M	C1	858	1	22,25,26	4.01	12 (54%)	30,36,39	3.38	12 (40%)

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
1	OMC	C1	2918	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	2300	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	389	1	-	3/9/27/28	0/3/3/3
1	OMC	C1	1491	1	-	1/9/27/28	0/2/2/2
1	A2M	C1	1432	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	1917	1	-	3/9/27/28	0/2/2/2
1	A2M	C1	1223	1	-	1/9/27/28	0/3/3/3
1	OMU	C1	2690	1	-	2/9/27/28	0/2/2/2
1	OMC	C1	1836	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	2876	1	-	1/9/27/28	0/3/3/3
1	OMC	C1	2838	1	-	2/9/27/28	0/2/2/2
1	OMU	C1	2384	1	-	1/9/27/28	0/2/2/2
1	OMU	C1	2380	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	1433	1	-	2/9/27/28	0/3/3/3
1	OMG	C1	385	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	1847	1	-	3/9/27/28	0/3/3/3
1	OMU	C1	2683	1	-	1/9/27/28	0/2/2/2
1	OMG	C1	2578	1	-	3/9/27/28	0/3/3/3
1	OMG	C1	646	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	1868	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	C1	848	1	-	1/9/27/28	0/3/3/3
1	A2M	C1	2289	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	2774	1	-	0/9/27/28	0/3/3/3
1	OMC	C1	1812	1	-	1/9/27/28	0/2/2/2
1	OMG	C1	2358	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2688	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2277	1	-	1/9/27/28	0/2/2/2
1	OMC	C1	778	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1420	1	-	2/9/27/28	0/2/2/2
1	OMG	C1	2881	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	637	1	-	1/9/27/28	0/3/3/3
1	OMG	C1	627	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	787	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	858	1	-	0/9/27/28	0/3/3/3

All (140) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	858	A2M	C3'-C2'	-13.08	1.24	1.53
1	C1	2289	A2M	C3'-C2'	-13.07	1.24	1.53
1	C1	848	A2M	C3'-C2'	-12.98	1.24	1.53
1	C1	1432	A2M	C3'-C2'	-12.96	1.24	1.53
1	C1	1847	A2M	C3'-C2'	-12.94	1.24	1.53
1	C1	1223	A2M	C3'-C2'	-12.92	1.24	1.53
1	C1	637	A2M	C3'-C2'	-12.92	1.24	1.53
1	C1	389	A2M	C3'-C2'	-12.83	1.24	1.53
1	C1	1917	OMU	C2-N1	7.64	1.50	1.38
1	C1	1868	OMU	C2-N1	7.52	1.50	1.38
1	C1	2384	OMU	C2-N1	7.49	1.50	1.38
1	C1	2277	OMU	C2-N1	7.47	1.50	1.38
1	C1	2688	OMU	C2-N1	7.43	1.50	1.38
1	C1	2380	OMU	C2-N1	7.37	1.50	1.38
1	C1	2690	OMU	C2-N1	7.34	1.50	1.38
1	C1	2380	OMU	C2-N3	7.31	1.50	1.38
1	C1	2384	OMU	C2-N3	7.31	1.50	1.38
1	C1	2688	OMU	C2-N3	7.30	1.50	1.38
1	C1	1868	OMU	C2-N3	7.28	1.50	1.38
1	C1	2277	OMU	C2-N3	7.28	1.50	1.38
1	C1	2683	OMU	C2-N1	7.27	1.49	1.38
1	C1	1917	OMU	C2-N3	7.27	1.50	1.38
1	C1	2690	OMU	C2-N3	7.26	1.50	1.38
1	C1	2683	OMU	C2-N3	7.23	1.50	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	389	A2M	O4'-C4'	-6.58	1.30	1.45
1	C1	637	A2M	O4'-C4'	-6.56	1.30	1.45
1	C1	1223	A2M	O4'-C4'	-6.54	1.30	1.45
1	C1	1847	A2M	O4'-C4'	-6.49	1.30	1.45
1	C1	1432	A2M	O4'-C4'	-6.49	1.30	1.45
1	C1	858	A2M	O4'-C4'	-6.45	1.30	1.45
1	C1	2289	A2M	O4'-C4'	-6.39	1.30	1.45
1	C1	848	A2M	O4'-C4'	-6.37	1.30	1.45
1	C1	2688	OMU	C6-C5	6.25	1.49	1.35
1	C1	1868	OMU	C6-C5	6.24	1.49	1.35
1	C1	2277	OMU	C6-C5	6.23	1.49	1.35
1	C1	2380	OMU	C6-C5	6.22	1.49	1.35
1	C1	2690	OMU	C6-C5	6.21	1.49	1.35
1	C1	2683	OMU	C6-C5	6.20	1.49	1.35
1	C1	2384	OMU	C6-C5	6.18	1.49	1.35
1	C1	1917	OMU	C6-C5	6.17	1.49	1.35
1	C1	2289	A2M	C3'-C4'	5.36	1.66	1.53
1	C1	1432	A2M	C3'-C4'	5.35	1.66	1.53
1	C1	858	A2M	C3'-C4'	5.31	1.66	1.53
1	C1	848	A2M	C3'-C4'	5.27	1.66	1.53
1	C1	1223	A2M	C3'-C4'	5.23	1.66	1.53
1	C1	389	A2M	C3'-C4'	5.18	1.66	1.53
1	C1	637	A2M	C3'-C4'	5.12	1.66	1.53
1	C1	1847	A2M	C3'-C4'	5.11	1.66	1.53
1	C1	1847	A2M	O4'-C1'	4.50	1.52	1.42
1	C1	1847	A2M	C1'-N9	-4.50	1.33	1.46
1	C1	858	A2M	O4'-C1'	4.48	1.52	1.42
1	C1	1432	A2M	O4'-C1'	4.47	1.52	1.42
1	C1	2289	A2M	O4'-C1'	4.46	1.52	1.42
1	C1	1223	A2M	C6-N6	4.46	1.45	1.34
1	C1	848	A2M	O4'-C1'	4.45	1.52	1.42
1	C1	848	A2M	C6-N6	4.45	1.45	1.34
1	C1	858	A2M	C6-N6	4.44	1.45	1.34
1	C1	2380	OMU	C4-N3	4.44	1.46	1.38
1	C1	1847	A2M	C6-N6	4.44	1.45	1.34
1	C1	389	A2M	C6-N6	4.43	1.45	1.34
1	C1	637	A2M	O4'-C1'	4.42	1.52	1.42
1	C1	2277	OMU	C4-N3	4.41	1.46	1.38
1	C1	2688	OMU	C4-N3	4.41	1.46	1.38
1	C1	2289	A2M	C1'-N9	-4.41	1.34	1.46
1	C1	848	A2M	C1'-N9	-4.40	1.34	1.46
1	C1	637	A2M	C6-N6	4.40	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	1432	A2M	C6-N6	4.39	1.45	1.34
1	C1	2690	OMU	C4-N3	4.39	1.46	1.38
1	C1	2289	A2M	C6-N6	4.38	1.45	1.34
1	C1	1868	OMU	C4-N3	4.38	1.46	1.38
1	C1	1917	OMU	C4-N3	4.37	1.46	1.38
1	C1	389	A2M	O4'-C1'	4.36	1.52	1.42
1	C1	2683	OMU	C4-N3	4.33	1.46	1.38
1	C1	2384	OMU	C4-N3	4.33	1.46	1.38
1	C1	858	A2M	C1'-N9	-4.31	1.34	1.46
1	C1	637	A2M	C1'-N9	-4.29	1.34	1.46
1	C1	1223	A2M	O4'-C1'	4.27	1.51	1.42
1	C1	1223	A2M	C1'-N9	-4.27	1.34	1.46
1	C1	389	A2M	C1'-N9	-4.24	1.34	1.46
1	C1	1432	A2M	C1'-N9	-4.21	1.34	1.46
1	C1	389	A2M	O2'-C2'	3.83	1.52	1.42
1	C1	637	A2M	O2'-C2'	3.64	1.51	1.42
1	C1	1223	A2M	O2'-C2'	3.63	1.51	1.42
1	C1	2289	A2M	O2'-C2'	3.59	1.51	1.42
1	C1	1847	A2M	O2'-C2'	3.56	1.51	1.42
1	C1	848	A2M	O2'-C2'	3.56	1.51	1.42
1	C1	858	A2M	O2'-C2'	3.56	1.51	1.42
1	C1	1432	A2M	O2'-C2'	3.55	1.51	1.42
1	C1	389	A2M	C2'-C1'	3.30	1.61	1.53
1	C1	1847	A2M	C2'-C1'	3.10	1.60	1.53
1	C1	848	A2M	C2'-C1'	3.08	1.60	1.53
1	C1	2289	A2M	C5-C4	-3.02	1.33	1.39
1	C1	858	A2M	C5-C4	-3.01	1.33	1.39
1	C1	2289	A2M	C2'-C1'	3.00	1.60	1.53
1	C1	637	A2M	C2'-C1'	2.99	1.60	1.53
1	C1	1223	A2M	C2'-C1'	2.98	1.60	1.53
1	C1	1847	A2M	C5-C4	-2.97	1.33	1.39
1	C1	1432	A2M	C5-C4	-2.95	1.33	1.39
1	C1	848	A2M	C5-C4	-2.94	1.33	1.39
1	C1	1432	A2M	C2'-C1'	2.93	1.60	1.53
1	C1	389	A2M	C5-C4	-2.91	1.33	1.39
1	C1	637	A2M	C5-C4	-2.86	1.34	1.39
1	C1	1223	A2M	C5-C4	-2.86	1.34	1.39
1	C1	858	A2M	C2'-C1'	2.84	1.60	1.53
1	C1	2688	OMU	C6-N1	2.75	1.44	1.38
1	C1	1868	OMU	C6-N1	2.73	1.44	1.38
1	C1	2690	OMU	C6-N1	2.70	1.44	1.38
1	C1	1917	OMU	C6-N1	2.70	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2277	OMU	C6-N1	2.69	1.44	1.38
1	C1	2683	OMU	C6-N1	2.68	1.44	1.38
1	C1	389	A2M	C5-N7	-2.66	1.34	1.39
1	C1	2380	OMU	C6-N1	2.66	1.44	1.38
1	C1	2384	OMU	C6-N1	2.63	1.44	1.38
1	C1	637	A2M	C5-N7	-2.62	1.34	1.39
1	C1	858	A2M	C5-N7	-2.59	1.34	1.39
1	C1	1432	A2M	C5-N7	-2.58	1.34	1.39
1	C1	2289	A2M	C5-N7	-2.55	1.34	1.39
1	C1	1223	A2M	C5-N7	-2.53	1.34	1.39
1	C1	1847	A2M	C5-N7	-2.50	1.34	1.39
1	C1	848	A2M	C5-N7	-2.47	1.34	1.39
1	C1	1868	OMU	C5-C4	2.37	1.48	1.43
1	C1	2690	OMU	C5-C4	2.30	1.48	1.43
1	C1	2688	OMU	C5-C4	2.29	1.48	1.43
1	C1	1917	OMU	C5-C4	2.27	1.48	1.43
1	C1	2277	OMU	C5-C4	2.26	1.48	1.43
1	C1	2380	OMU	C5-C4	2.25	1.48	1.43
1	C1	2683	OMU	C5-C4	2.24	1.48	1.43
1	C1	1847	A2M	C8-N9	-2.22	1.33	1.37
1	C1	637	A2M	C8-N9	-2.20	1.33	1.37
1	C1	2384	OMU	C5-C4	2.14	1.48	1.43
1	C1	858	A2M	C8-N9	-2.14	1.33	1.37
1	C1	1432	A2M	C8-N9	-2.11	1.34	1.37
1	C1	1847	A2M	O3'-C3'	2.11	1.48	1.43
1	C1	848	A2M	C8-N9	-2.09	1.34	1.37
1	C1	1432	A2M	O3'-C3'	2.06	1.48	1.43
1	C1	848	A2M	O3'-C3'	2.05	1.48	1.43
1	C1	858	A2M	O3'-C3'	2.04	1.48	1.43
1	C1	1223	A2M	C8-N9	-2.02	1.34	1.37
1	C1	2289	A2M	O3'-C3'	2.00	1.47	1.43
1	C1	389	A2M	C8-N9	-2.00	1.34	1.37

All (162) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1847	A2M	C1'-N9-C8	-9.69	105.58	127.09
1	C1	637	A2M	C1'-N9-C8	-9.37	106.30	127.09
1	C1	858	A2M	C1'-N9-C8	-9.23	106.61	127.09
1	C1	1432	A2M	C1'-N9-C8	-9.10	106.91	127.09
1	C1	389	A2M	C1'-N9-C8	-9.09	106.92	127.09
1	C1	848	A2M	C1'-N9-C8	-9.07	106.96	127.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1223	A2M	C1'-N9-C8	-9.07	106.97	127.09
1	C1	2289	A2M	C1'-N9-C8	-8.75	107.68	127.09
1	C1	1847	A2M	C4-N9-C1'	8.21	145.83	126.63
1	C1	637	A2M	C4-N9-C1'	8.10	145.57	126.63
1	C1	1432	A2M	C4-N9-C1'	7.91	145.12	126.63
1	C1	858	A2M	C4-N9-C1'	7.89	145.09	126.63
1	C1	1223	A2M	C4-N9-C1'	7.82	144.91	126.63
1	C1	389	A2M	C4-N9-C1'	7.80	144.88	126.63
1	C1	848	A2M	C4-N9-C1'	7.68	144.59	126.63
1	C1	2289	A2M	C4-N9-C1'	7.41	143.96	126.63
1	C1	858	A2M	N3-C2-N1	-5.89	119.67	128.58
1	C1	2289	A2M	N3-C2-N1	-5.85	119.73	128.58
1	C1	1847	A2M	N3-C2-N1	-5.82	119.78	128.58
1	C1	848	A2M	N3-C2-N1	-5.81	119.78	128.58
1	C1	389	A2M	N3-C2-N1	-5.77	119.86	128.58
1	C1	637	A2M	N3-C2-N1	-5.76	119.87	128.58
1	C1	1432	A2M	N3-C2-N1	-5.72	119.92	128.58
1	C1	1223	A2M	N3-C2-N1	-5.69	119.97	128.58
1	C1	1868	OMU	C4-N3-C2	-5.67	119.58	126.61
1	C1	1847	A2M	N6-C6-N1	-5.58	105.95	118.38
1	C1	2380	OMU	C4-N3-C2	-5.55	119.72	126.61
1	C1	2688	OMU	C4-N3-C2	-5.53	119.75	126.61
1	C1	2690	OMU	C4-N3-C2	-5.52	119.76	126.61
1	C1	637	A2M	N6-C6-N1	-5.51	106.11	118.38
1	C1	1223	A2M	N6-C6-N1	-5.49	106.15	118.38
1	C1	1432	A2M	N6-C6-N1	-5.47	106.18	118.38
1	C1	2289	A2M	N6-C6-N1	-5.47	106.19	118.38
1	C1	848	A2M	N6-C6-N1	-5.47	106.19	118.38
1	C1	858	A2M	N6-C6-N1	-5.45	106.25	118.38
1	C1	1917	OMU	C4-N3-C2	-5.41	119.89	126.61
1	C1	389	A2M	N6-C6-N1	-5.38	106.40	118.38
1	C1	2277	OMU	C4-N3-C2	-5.34	119.98	126.61
1	C1	2384	OMU	C4-N3-C2	-5.26	120.08	126.61
1	C1	2683	OMU	C4-N3-C2	-5.20	120.16	126.61
1	C1	637	A2M	C5-C4-N3	-4.98	119.87	126.72
1	C1	1847	A2M	C5-C4-N3	-4.90	119.97	126.72
1	C1	1432	A2M	C5-C4-N3	-4.89	119.99	126.72
1	C1	389	A2M	C5-C4-N3	-4.85	120.03	126.72
1	C1	1223	A2M	C5-C4-N3	-4.85	120.04	126.72
1	C1	848	A2M	C5-C4-N3	-4.76	120.16	126.72
1	C1	858	A2M	C5-C4-N3	-4.76	120.16	126.72
1	C1	2838	OMC	C1'-N1-C2	4.73	128.88	118.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	2289	A2M	C5-C4-N3	-4.55	120.45	126.72
1	C1	1847	A2M	N9-C8-N7	-4.52	107.52	113.94
1	C1	2289	A2M	N9-C8-N7	-4.37	107.73	113.94
1	C1	848	A2M	N9-C8-N7	-4.37	107.73	113.94
1	C1	1420	OMC	C1'-N1-C2	4.37	128.10	118.44
1	C1	2289	A2M	C5-C6-N6	4.34	134.04	123.29
1	C1	1847	A2M	C5-C6-N6	4.31	133.95	123.29
1	C1	858	A2M	C5-C6-N6	4.30	133.92	123.29
1	C1	1223	A2M	C5-C6-N6	4.29	133.92	123.29
1	C1	637	A2M	C5-C6-N6	4.26	133.84	123.29
1	C1	389	A2M	N9-C8-N7	-4.26	107.89	113.94
1	C1	1432	A2M	C5-C6-N6	4.24	133.77	123.29
1	C1	848	A2M	C5-C6-N6	4.22	133.74	123.29
1	C1	858	A2M	N9-C8-N7	-4.21	107.96	113.94
1	C1	389	A2M	C5-C6-N6	4.17	133.62	123.29
1	C1	1223	A2M	N9-C8-N7	-4.17	108.03	113.94
1	C1	637	A2M	N9-C8-N7	-4.10	108.11	113.94
1	C1	848	A2M	O4'-C1'-N9	4.06	115.89	108.09
1	C1	1432	A2M	N9-C8-N7	-4.04	108.20	113.94
1	C1	2289	A2M	O4'-C1'-N9	4.04	115.85	108.09
1	C1	858	A2M	O4'-C1'-N9	3.94	115.66	108.09
1	C1	1868	OMU	N3-C2-N1	3.93	120.01	114.89
1	C1	1432	A2M	O4'-C1'-N9	3.93	115.64	108.09
1	C1	2380	OMU	N3-C2-N1	3.91	119.98	114.89
1	C1	2690	OMU	N3-C2-N1	3.90	119.96	114.89
1	C1	2384	OMU	N3-C2-N1	3.84	119.89	114.89
1	C1	1223	A2M	O4'-C1'-N9	3.83	115.44	108.09
1	C1	2688	OMU	N3-C2-N1	3.83	119.87	114.89
1	C1	1917	OMU	N3-C2-N1	3.80	119.84	114.89
1	C1	2683	OMU	N3-C2-N1	3.77	119.80	114.89
1	C1	1812	OMC	CM2-O2'-C2'	3.76	124.12	114.47
1	C1	2277	OMU	N3-C2-N1	3.74	119.76	114.89
1	C1	389	A2M	O4'-C1'-N9	3.71	115.21	108.09
1	C1	637	A2M	O4'-C1'-N9	3.64	115.08	108.09
1	C1	1868	OMU	C5-C4-N3	3.58	119.82	114.80
1	C1	2688	OMU	C5-C4-N3	3.57	119.81	114.80
1	C1	2380	OMU	C5-C4-N3	3.53	119.75	114.80
1	C1	1917	OMU	C5-C4-N3	3.53	119.74	114.80
1	C1	2690	OMU	C5-C4-N3	3.52	119.73	114.80
1	C1	2838	OMC	C1'-N1-C6	-3.52	113.27	120.78
1	C1	2277	OMU	C5-C4-N3	3.50	119.70	114.80
1	C1	1847	A2M	C2-N3-C4	3.46	120.27	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	637	A2M	C2-N3-C4	3.45	120.27	111.83
1	C1	2384	OMU	C5-C4-N3	3.42	119.58	114.80
1	C1	389	A2M	C2-N3-C4	3.39	120.12	111.83
1	C1	858	A2M	C2-N3-C4	3.38	120.10	111.83
1	C1	848	A2M	C2-N3-C4	3.38	120.10	111.83
1	C1	1432	A2M	C2-N3-C4	3.38	120.09	111.83
1	C1	2683	OMU	C5-C4-N3	3.38	119.53	114.80
1	C1	1223	A2M	C2-N3-C4	3.36	120.04	111.83
1	C1	2289	A2M	C2-N3-C4	3.30	119.89	111.83
1	C1	1847	A2M	O4'-C1'-N9	3.16	114.16	108.09
1	C1	1420	OMC	C1'-N1-C6	-3.13	114.10	120.78
1	C1	848	A2M	C2'-C1'-N9	-3.11	108.64	113.75
1	C1	637	A2M	N3-C4-N9	3.09	132.43	127.17
1	C1	1847	A2M	C5-N7-C8	3.06	108.26	103.45
1	C1	389	A2M	N3-C4-N9	3.06	132.36	127.17
1	C1	1847	A2M	N3-C4-N9	3.04	132.34	127.17
1	C1	858	A2M	N3-C4-N9	3.00	132.28	127.17
1	C1	848	A2M	N3-C4-N9	2.98	132.24	127.17
1	C1	1223	A2M	N3-C4-N9	2.96	132.19	127.17
1	C1	1432	A2M	N3-C4-N9	2.95	132.18	127.17
1	C1	2380	OMU	O4-C4-C5	-2.92	120.12	125.16
1	C1	389	A2M	C5-N7-C8	2.92	108.04	103.45
1	C1	2688	OMU	O4-C4-C5	-2.92	120.13	125.16
1	C1	848	A2M	C5-N7-C8	2.92	108.03	103.45
1	C1	1917	OMU	O4-C4-C5	-2.92	120.13	125.16
1	C1	2384	OMU	O4-C4-C5	-2.91	120.14	125.16
1	C1	1868	OMU	O4-C4-C5	-2.91	120.15	125.16
1	C1	1847	A2M	C2'-C1'-N9	-2.87	109.03	113.75
1	C1	1223	A2M	C5-N7-C8	2.86	107.94	103.45
1	C1	637	A2M	C5-N7-C8	2.86	107.94	103.45
1	C1	2289	A2M	C5-N7-C8	2.85	107.93	103.45
1	C1	2277	OMU	O4-C4-C5	-2.85	120.25	125.16
1	C1	2690	OMU	O4-C4-C5	-2.83	120.29	125.16
1	C1	858	A2M	C5-N7-C8	2.79	107.83	103.45
1	C1	2683	OMU	O4-C4-C5	-2.77	120.38	125.16
1	C1	1432	A2M	C5-N7-C8	2.75	107.78	103.45
1	C1	2838	OMC	O2-C2-N3	-2.73	118.02	122.33
1	C1	778	OMC	C1'-N1-C2	2.73	124.47	118.44
1	C1	2289	A2M	N3-C4-N9	2.72	131.80	127.17
1	C1	1847	A2M	C4-N9-C8	2.71	108.58	105.74
1	C1	2289	A2M	C2'-C1'-N9	-2.63	109.42	113.75
1	C1	848	A2M	C4-N9-C8	2.58	108.45	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1420	OMC	O2-C2-N1	2.53	123.86	118.90
1	C1	2289	A2M	C4-N9-C8	2.50	108.36	105.74
1	C1	1420	OMC	O2-C2-N3	-2.46	118.45	122.33
1	C1	858	A2M	C4-N9-C8	2.43	108.29	105.74
1	C1	1917	OMU	C1'-N1-C2	2.42	121.95	117.59
1	C1	1836	OMC	C1'-N1-C2	2.40	123.73	118.44
1	C1	2838	OMC	O2-C2-N1	2.39	123.58	118.90
1	C1	389	A2M	C4-N9-C8	2.34	108.19	105.74
1	C1	2380	OMU	O2-C2-N1	-2.33	119.77	122.80
1	C1	1847	A2M	C4-C5-N7	-2.31	107.94	110.58
1	C1	1223	A2M	C4-N9-C8	2.27	108.12	105.74
1	C1	637	A2M	C4-N9-C8	2.26	108.11	105.74
1	C1	1868	OMU	O2-C2-N1	-2.23	119.89	122.80
1	C1	2688	OMU	O2-C2-N1	-2.20	119.93	122.80
1	C1	2690	OMU	O2-C2-N1	-2.19	119.95	122.80
1	C1	1491	OMC	C1'-N1-C2	2.19	123.27	118.44
1	C1	2918	OMC	C1'-N1-C2	2.14	123.17	118.44
1	C1	637	A2M	C4-C5-N7	-2.14	108.14	110.58
1	C1	1223	A2M	C4-C5-N7	-2.13	108.15	110.58
1	C1	1432	A2M	C4-N9-C8	2.13	107.97	105.74
1	C1	389	A2M	C4'-O4'-C1'	-2.11	104.81	109.47
1	C1	2300	OMC	C1'-N1-C2	2.10	123.08	118.44
1	C1	2683	OMU	O2-C2-N1	-2.10	120.06	122.80
1	C1	848	A2M	C4-C5-N7	-2.10	108.18	110.58
1	C1	1812	OMC	C2'-C1'-N1	-2.08	110.30	114.24
1	C1	1432	A2M	C4-C5-N7	-2.07	108.22	110.58
1	C1	2289	A2M	C4-C5-N7	-2.06	108.23	110.58
1	C1	2384	OMU	C1'-N1-C2	2.03	121.24	117.59
1	C1	1847	A2M	C4'-O4'-C1'	-2.03	104.99	109.47
1	C1	389	A2M	C4-C5-N7	-2.02	108.27	110.58

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	389	A2M	O4'-C4'-C5'-O5'
1	C1	389	A2M	C1'-C2'-O2'-CM'
1	C1	637	A2M	C1'-C2'-O2'-CM'
1	C1	1433	OMG	O4'-C4'-C5'-O5'
1	C1	1812	OMC	C1'-C2'-O2'-CM2
1	C1	1917	OMU	C1'-C2'-O2'-CM2
1	C1	1917	OMU	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
1	C1	2384	OMU	C1'-C2'-O2'-CM2
1	C1	2578	OMG	O4'-C4'-C5'-O5'
1	C1	2683	OMU	C1'-C2'-O2'-CM2
1	C1	2838	OMC	O4'-C1'-N1-C2
1	C1	2838	OMC	O4'-C1'-N1-C6
1	C1	2578	OMG	C3'-C4'-C5'-O5'
1	C1	2690	OMU	C3'-C4'-C5'-O5'
1	C1	2690	OMU	O4'-C4'-C5'-O5'
1	C1	1847	A2M	C3'-C4'-C5'-O5'
1	C1	389	A2M	C3'-C4'-C5'-O5'
1	C1	1433	OMG	C3'-C4'-C5'-O5'
1	C1	1917	OMU	C3'-C4'-C5'-O5'
1	C1	1847	A2M	O4'-C4'-C5'-O5'
1	C1	1223	A2M	O4'-C4'-C5'-O5'
1	C1	2277	OMU	C1'-C2'-O2'-CM2
1	C1	1491	OMC	O4'-C4'-C5'-O5'
1	C1	1847	A2M	C4'-C5'-O5'-P
1	C1	2578	OMG	C4'-C5'-O5'-P
1	C1	2876	OMG	C3'-C2'-O2'-CM2
1	C1	848	A2M	O4'-C4'-C5'-O5'
1	C1	1420	OMC	C2'-C1'-N1-C6
1	C1	1420	OMC	C2'-C1'-N1-C2

There are no ring outliers.

11 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C1	2918	OMC	1	0
1	C1	389	A2M	1	0
1	C1	1432	A2M	1	0
1	C1	1917	OMU	1	0
1	C1	2384	OMU	2	0
1	C1	2683	OMU	1	0
1	C1	2578	OMG	1	0
1	C1	848	A2M	1	0
1	C1	1812	OMC	2	0
1	C1	2277	OMU	1	0
1	C1	1420	OMC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
64	GTP	Cd	1000	65	33,34,34	0.97	2 (6%)	50,54,54	1.60	9 (18%)
64	GTP	CH	701	65	33,34,34	0.92	1 (3%)	50,54,54	1.59	9 (18%)

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
64	GTP	Cd	1000	65	-	3/22/38/38	0/3/3/3
64	GTP	CH	701	65	-	4/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	CH	701	GTP	C2-N3	2.16	1.38	1.33
64	Cd	1000	GTP	C2-N3	2.09	1.38	1.33
64	Cd	1000	GTP	PA-O3A	2.02	1.61	1.59

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	CH	701	GTP	C5-C4-N3	-5.04	120.37	128.39
64	Cd	1000	GTP	C5-C4-N3	-4.98	120.46	128.39
64	CH	701	GTP	C2-N3-C4	4.59	120.21	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	Cd	1000	GTP	C2-N3-C4	4.57	120.18	112.30
64	CH	701	GTP	N9-C4-N3	3.24	132.44	125.95
64	Cd	1000	GTP	N9-C4-N3	3.18	132.32	125.95
64	CH	701	GTP	C2-N1-C6	-2.92	119.82	125.11
64	Cd	1000	GTP	C2-N1-C6	-2.90	119.85	125.11
64	Cd	1000	GTP	N9-C8-N7	-2.65	108.49	113.40
64	CH	701	GTP	N9-C8-N7	-2.60	108.57	113.40
64	CH	701	GTP	C5-C6-N1	2.51	119.63	113.25
64	Cd	1000	GTP	C5-C6-N1	2.50	119.63	113.25
64	CH	701	GTP	C8-N7-C5	2.49	108.69	104.26
64	Cd	1000	GTP	C8-N7-C5	2.48	108.68	104.26
64	Cd	1000	GTP	O6-C6-C5	-2.46	120.04	126.53
64	CH	701	GTP	O6-C6-C5	-2.41	120.17	126.53
64	CH	701	GTP	C3'-C2'-C1'	2.28	105.77	101.46
64	Cd	1000	GTP	C3'-C2'-C1'	2.19	105.61	101.46

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
64	Cd	1000	GTP	C5'-O5'-PA-O1A
64	Cd	1000	GTP	C3'-C4'-C5'-O5'
64	Cd	1000	GTP	O4'-C4'-C5'-O5'
64	CH	701	GTP	C3'-C4'-C5'-O5'
64	CH	701	GTP	PB-O3A-PA-O2A
64	CH	701	GTP	O4'-C4'-C5'-O5'
64	CH	701	GTP	PB-O3A-PA-O1A

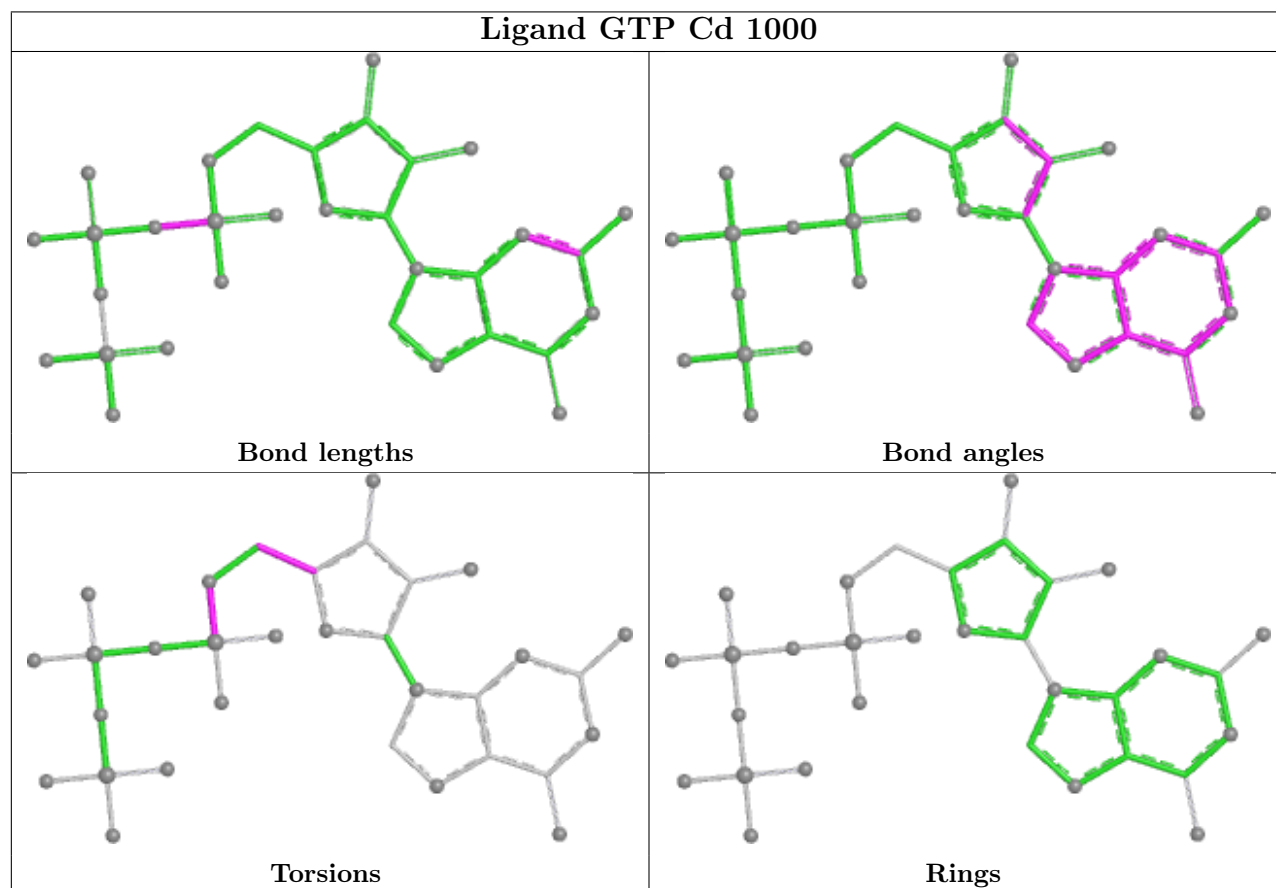
There are no ring outliers.

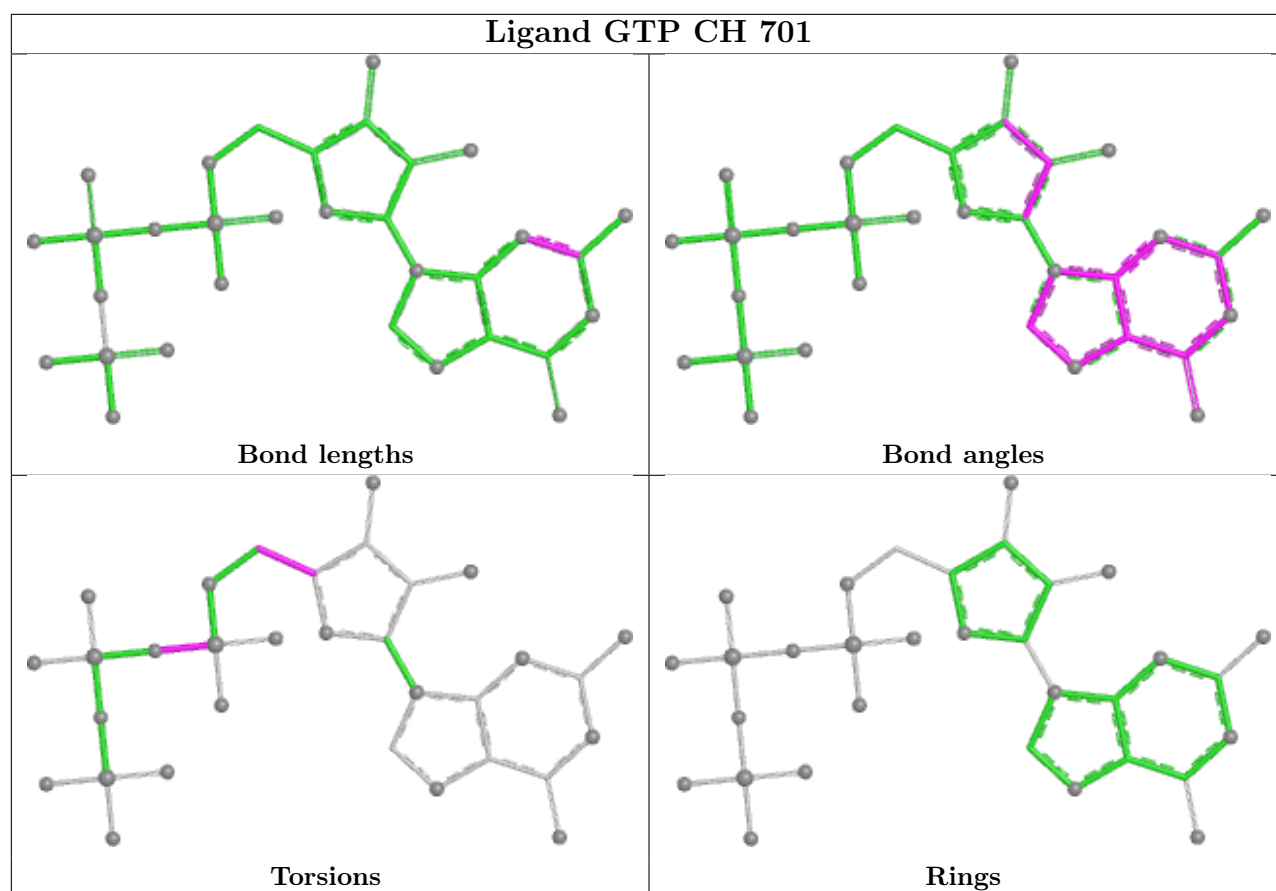
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
64	CH	701	GTP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

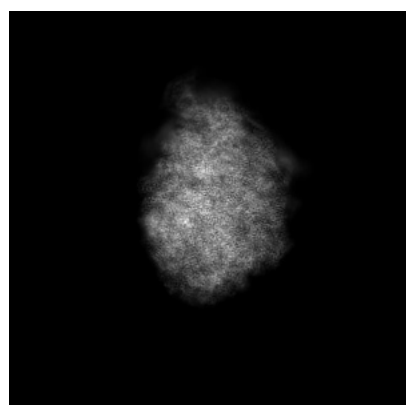
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17953. These allow visual inspection of the internal detail of the map and identification of artifacts.

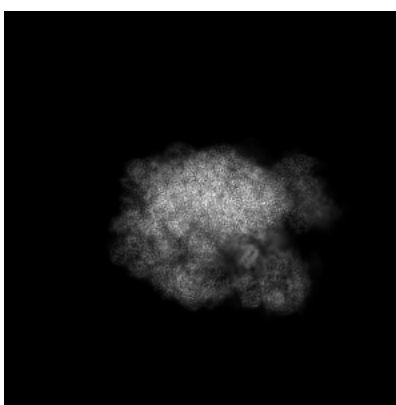
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

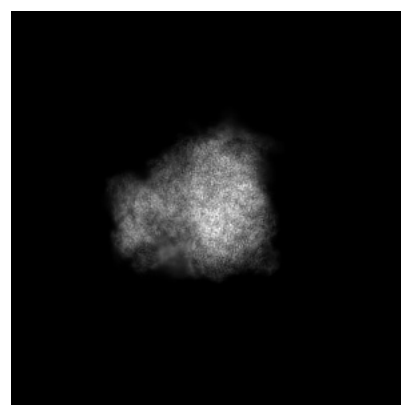
6.1.1 Primary map



X



Y

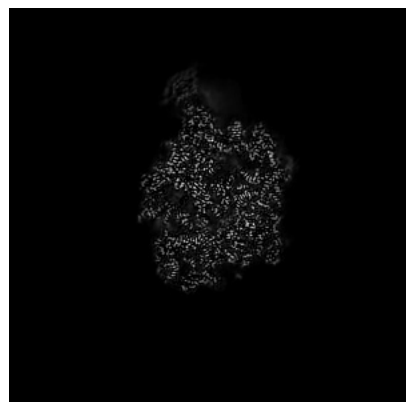


Z

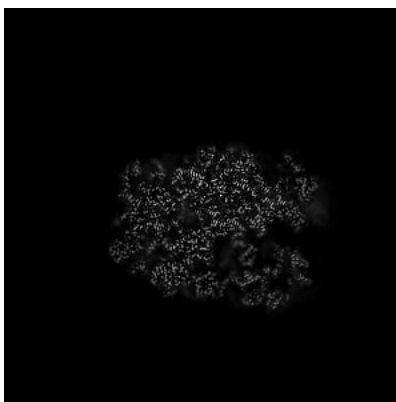
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

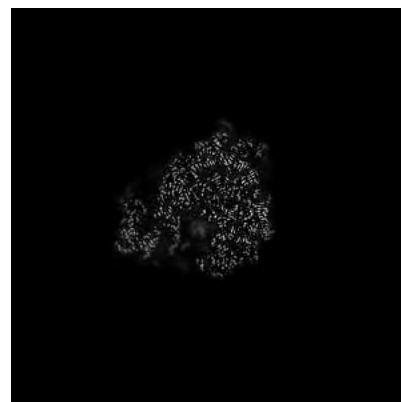
6.2.1 Primary map



X Index: 250



Y Index: 250

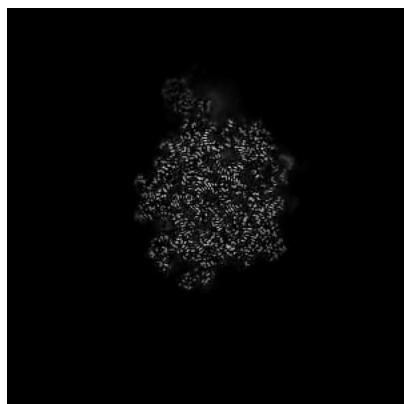


Z Index: 250

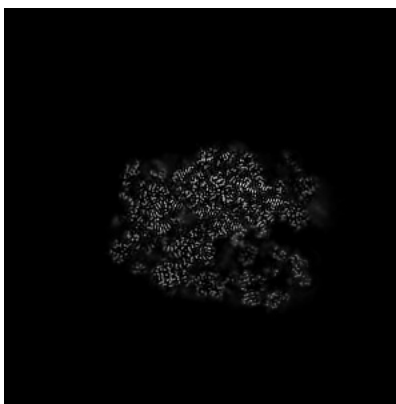
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

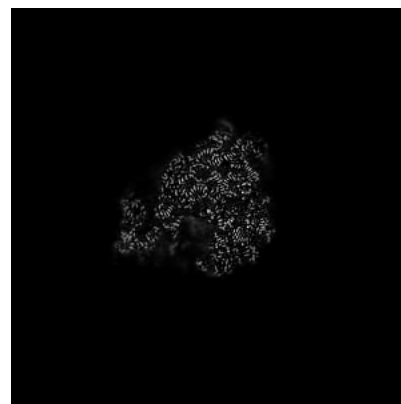
6.3.1 Primary map



X Index: 259



Y Index: 248

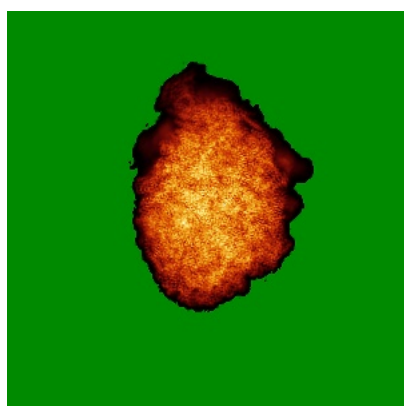


Z Index: 252

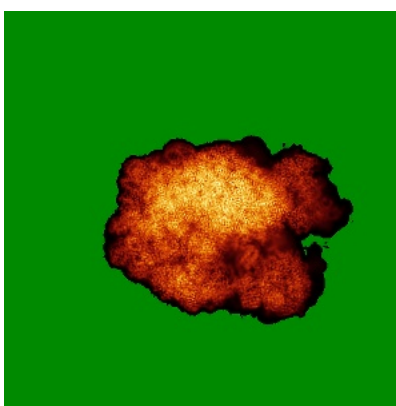
The images above show the largest variance slices of the map in three orthogonal directions.

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

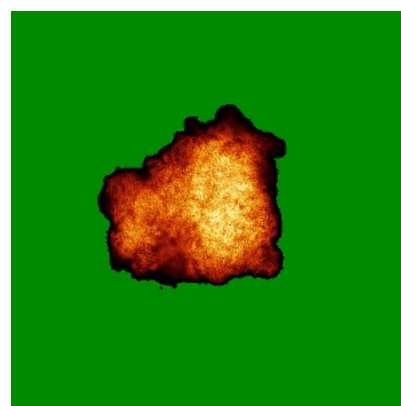
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

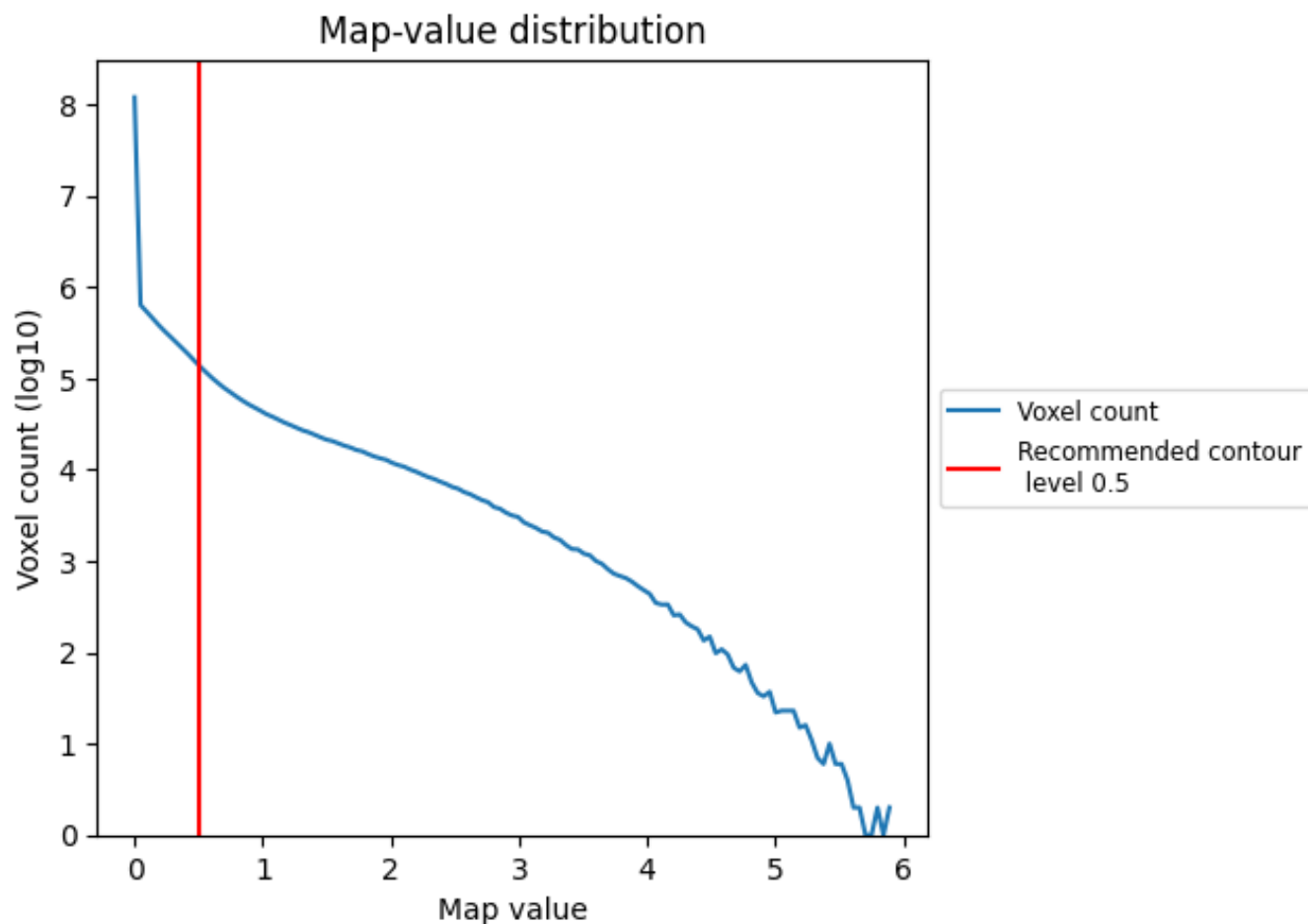
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

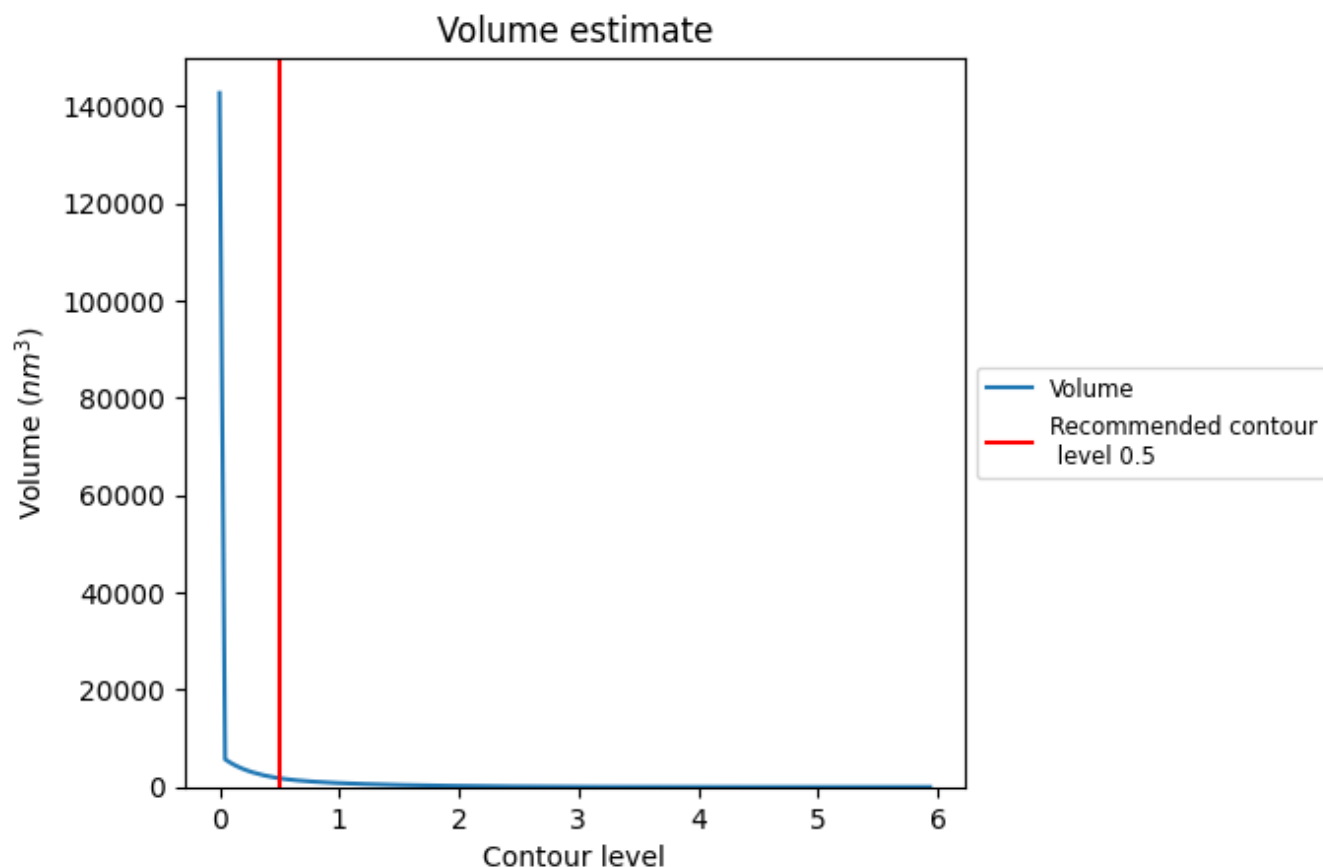
This section contains the results of statistical analysis of the map.

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.

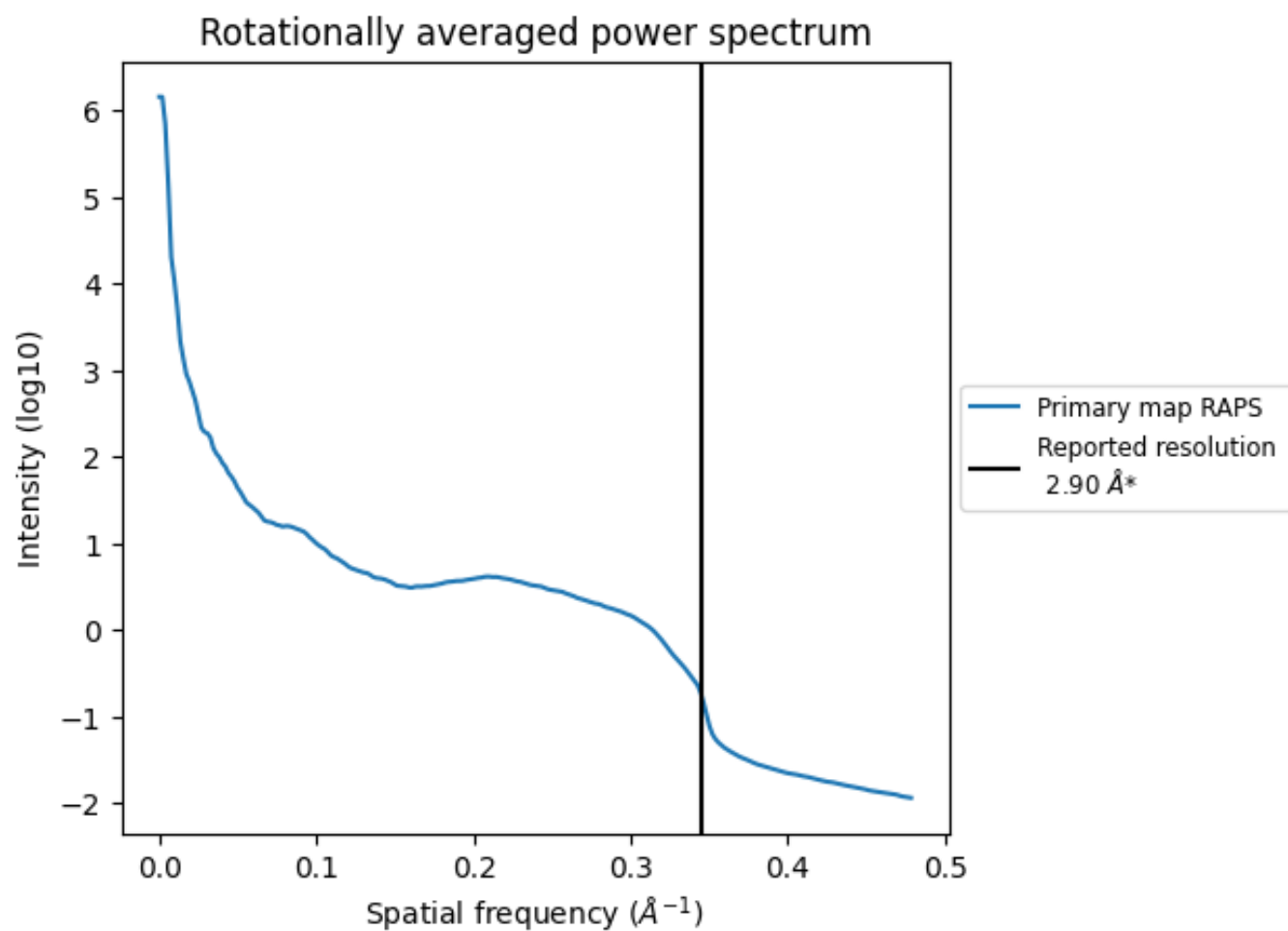
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1795 nm^3 ; this corresponds to an approximate mass of 1622 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 0.345 Å⁻¹

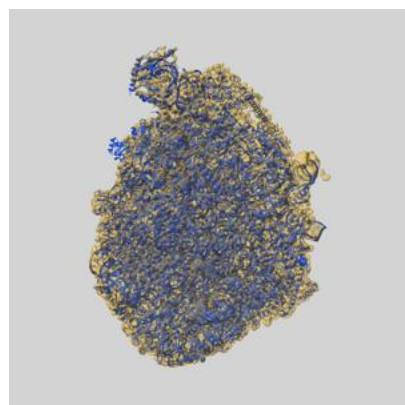
8 Fourier-Shell correlation

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

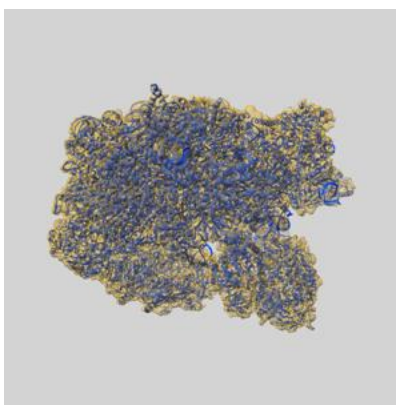
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17953 and PDB model 8PV4. Per-residue inclusion information can be found in section 3 on page 17.

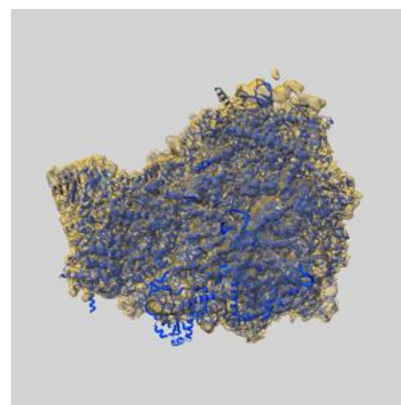
9.1 Map-model overlay [i](#)



X



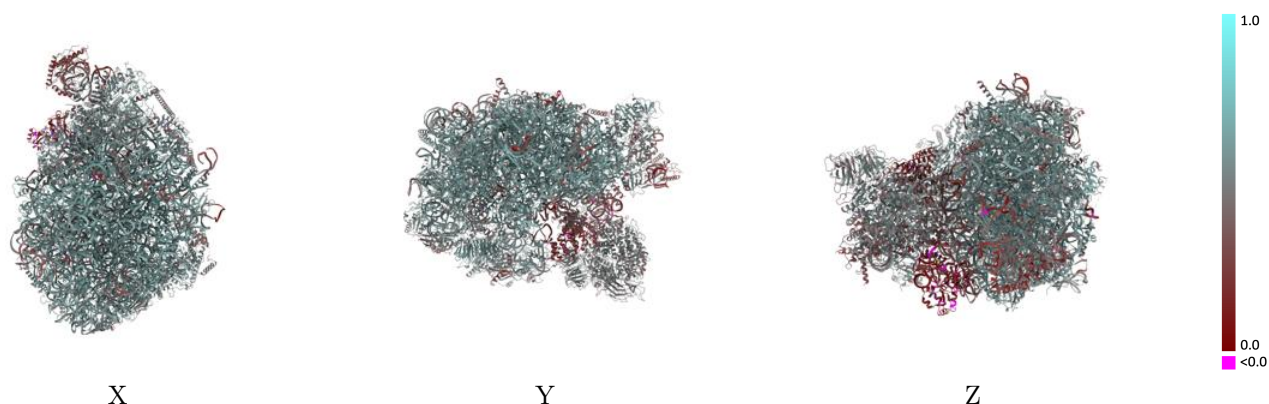
Y



Z

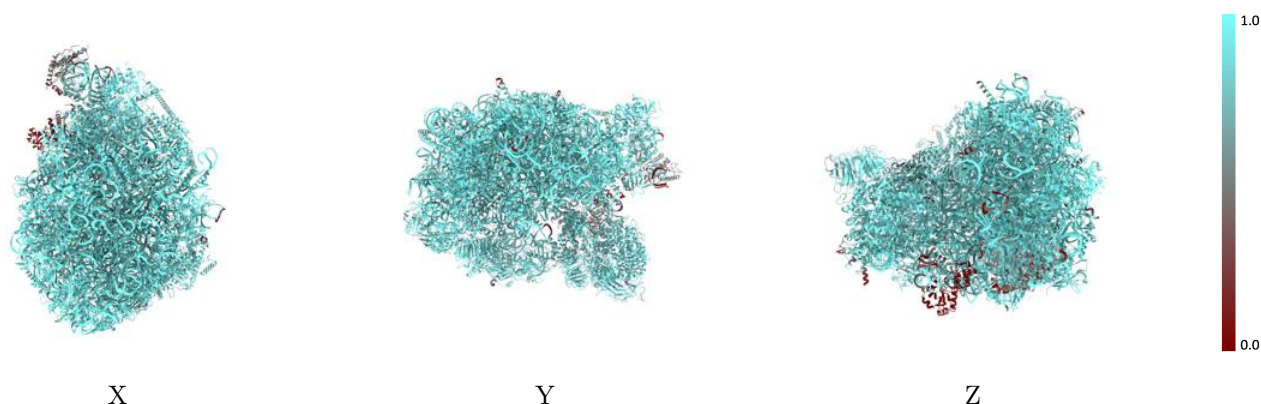
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



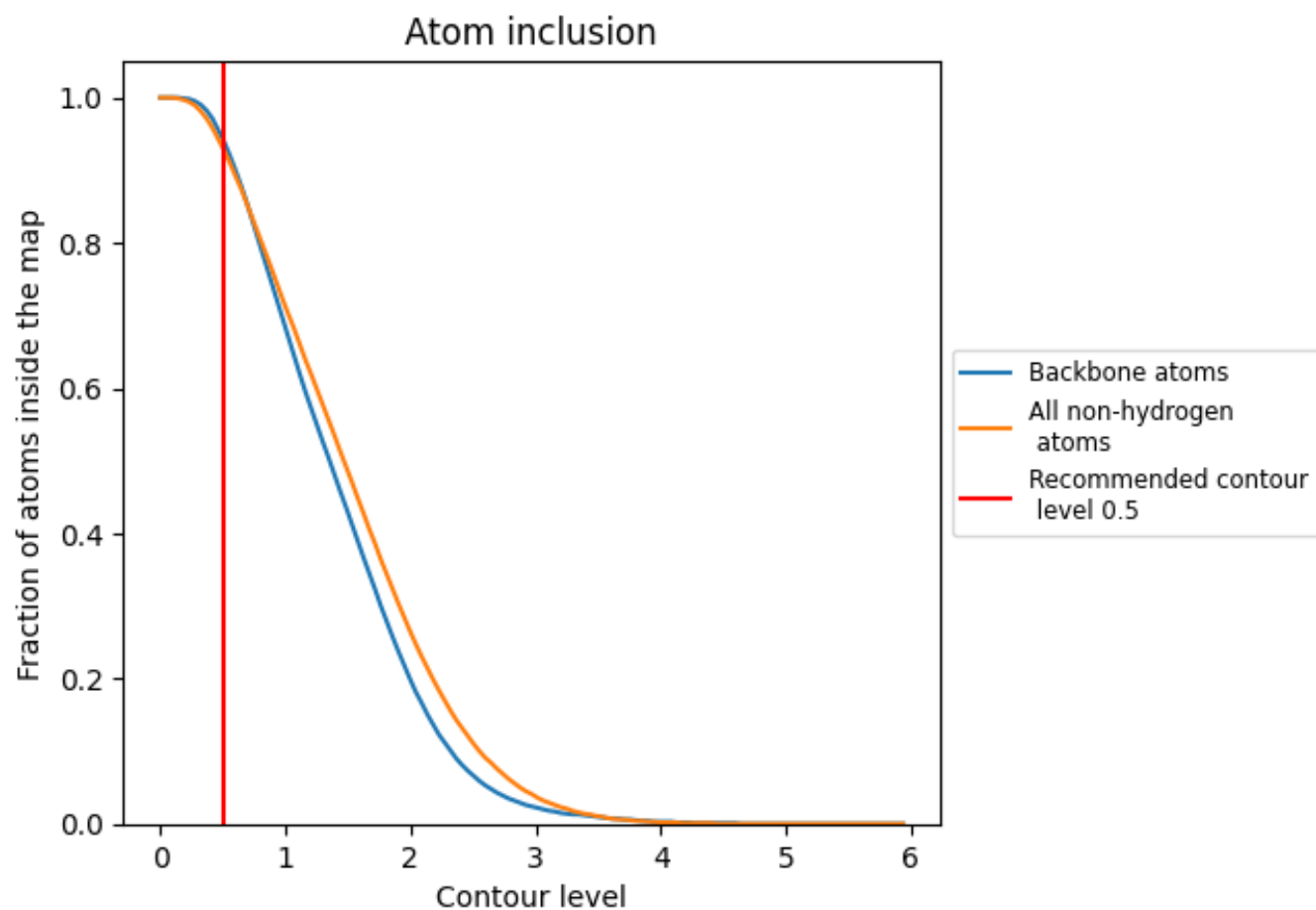
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9310	 0.5350
C1	 0.9750	 0.5590
C2	 0.9770	 0.5980
C3	 0.7060	 0.3310
C4	 0.9720	 0.5060
CB	 0.5850	 0.3470
CF	 0.9140	 0.5230
CH	 0.9130	 0.5410
CI	 0.7490	 0.4200
CJ	 0.9590	 0.5600
CK	 0.9700	 0.5960
CL	 0.9170	 0.5060
CM	 0.8960	 0.4900
CN	 0.9460	 0.5630
CO	 0.9010	 0.5510
CQ	 0.8990	 0.5410
CR	 0.7680	 0.2830
CS	 0.7710	 0.2640
CT	 0.8610	 0.4660
CU	 0.9010	 0.4720
CV	 0.8630	 0.4530
CW	 0.8840	 0.4640
Cb	 0.9530	 0.5560
Cd	 0.9540	 0.5690
Ce	 0.8550	 0.4760
Cf	 0.9500	 0.5510
Cg	 0.9320	 0.5280
Ch	 0.9180	 0.5350
Cz	 0.8370	 0.4620
LA	 0.9820	 0.5900
LB	 0.9720	 0.6040
LC	 0.9650	 0.5970
LD	 0.9260	 0.5320
LE	 0.9320	 0.5540
LF	 0.9410	 0.5710



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Chain	Atom inclusion	Q-score
LG	 0.9560	 0.5670
LH	 0.9450	 0.5740
LJ	 0.9120	 0.4830
LK	 0.8650	 0.4690
LL	 0.9430	 0.5680
LM	 0.9470	 0.5740
LN	 0.9900	 0.6170
LO	 0.9760	 0.6050
LP	 0.9780	 0.6040
LQ	 0.9360	 0.5680
LR	 0.9710	 0.5860
LS	 0.9640	 0.5840
LT	 0.8910	 0.4810
LU	 0.9160	 0.5320
LV	 0.9770	 0.6000
LX	 0.9510	 0.5660
LY	 0.9480	 0.5750
LZ	 0.9660	 0.5760
La	 0.9590	 0.5830
Lc	 0.9380	 0.5520
Ld	 0.9560	 0.5960
Le	 0.9730	 0.6050
Lf	 0.9860	 0.6210
Lg	 0.9200	 0.5770
Lh	 0.9470	 0.5430
Li	 0.9440	 0.5300
Lj	 0.9900	 0.6260
Lk	 0.9210	 0.5400
Ll	 0.9930	 0.6360
Lp	 0.9350	 0.5460
Lq	 0.9590	 0.5760
Lr	 0.1740	 0.1330