



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 03:36 AM UTC

PDB ID : 6RZZ / pdb_00006rzz
EMDB ID : EMD-10068
Title : Cryo-EM structures of Lsg1-TAP pre-60S ribosomal particles
Authors : Kargas, V.; Warren, A.J.
Deposited on : 2019-06-13
Resolution : 3.20 Å(reported)
Based on initial model : 4V88

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:

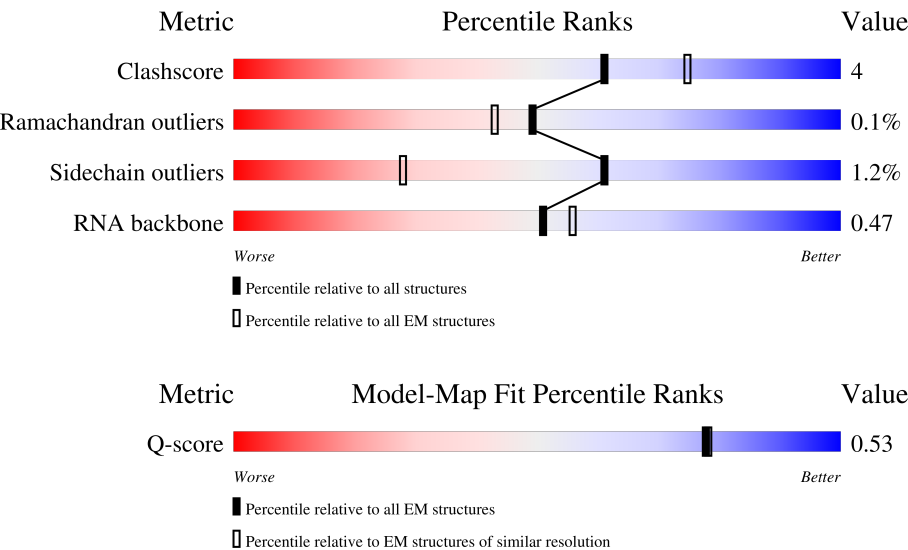
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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.



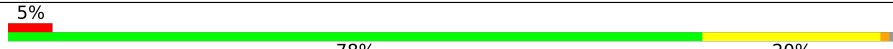
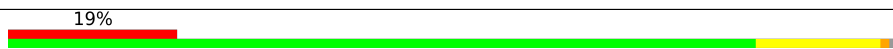
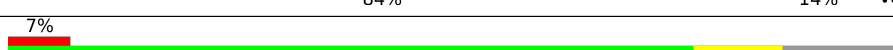
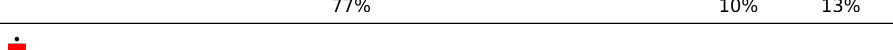
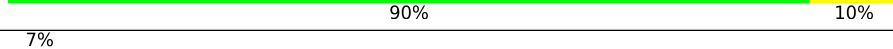
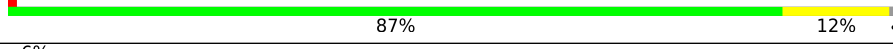
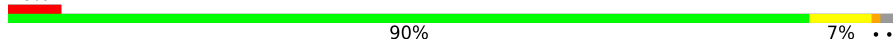
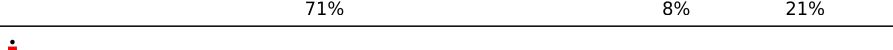
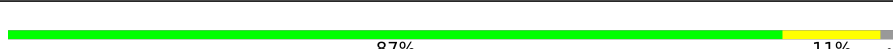
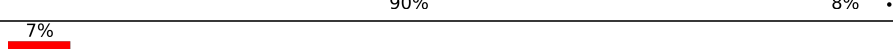
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	A	3396	
2	B	254	
3	C	387	

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Mol	Chain	Length	Quality of chain
4	D	362	
5	E	174	
6	F	191	
7	G	176	
8	H	256	
9	J	198	
10	K	199	
11	L	137	
12	M	138	
13	N	149	
14	O	204	
15	P	297	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	184	
21	V	121	
22	W	142	
23	X	127	
24	Y	136	
25	Z	120	
26	a	59	
27	b	244	
28	c	105	

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Mol	Chain	Length	Quality of chain
29	d	113	
30	e	130	
31	f	107	
32	g	121	
33	h	100	
34	i	88	
35	j	78	
36	k	51	
37	l	106	
38	m	92	
39	n	245	
40	o	640	
41	p	210	
42	r	593	
43	s	364	
44	u	393	
45	v	155	
46	w	518	
47	x	121	
48	y	158	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 134359 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3146	Total	C	N	O	P	0	0
			67292	30062	12142	21944	3144		

- Molecule 2 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	381	Total	C	N	O	S	0	0
			3039	1928	577	526	8		

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	361	Total	C	N	O	S	0	0
			2748	1730	522	493	3		

- Molecule 5 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	169	Total	C	N	O	S	0	0
			1352	847	253	248	4		

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	189	Total	C	N	O	S	0	0
			1502	953	272	273	4		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1399	902	251	245	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	223	Total	C	N	O	S	0	0
			1742	1117	309	313	3		

- Molecule 9 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	197	Total	C	N	O	S	0	0
			1563	1005	292	265	1		

- Molecule 10 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	K	186	Total	C	N	O	0	0
			1486	929	304	253		

- Molecule 11 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	136	Total	C	N	O	S	0	0
			1002	628	189	178	7		

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	135	Total	C	N	O	S	0	0
			1045	669	197	177	2		

- Molecule 13 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	148	Total	C	N	O	S	0	0
			1172	749	231	189	3		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	203	Total	C	N	O	S	0	0
			1719	1077	361	280	1		

- Molecule 15 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	269	Total	C	N	O	S	0	0
			2176	1378	375	421	2		

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	185	Total	C	N	O	S	0	0
			1440	908	290	240	2		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	150	Total	C	N	O		0	0
			1209	752	257	200			

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	171	Total	C	N	O	S	0	0
			1436	925	266	242	3		

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1275	805	246	220	4		

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	154	Total	C	N	O		0	0
			1222	761	237	224			

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	99	Total	C	N	O	0	0
			786	510	129	147		

- Molecule 22 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	120	Total	C	N	O	S	0	0
			958	617	168	171	2		

- Molecule 23 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Y	135	Total	C	N	O	0	0
			1091	710	202	179		

- Molecule 25 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	118	Total	C	N	O	S	0	0
			963	612	185	165	1		

- Molecule 26 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	a	52	Total	C	N	O	0	0
			415	259	90	66		

- Molecule 27 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	219	Total	C	N	O	S	0	0
			1760	1138	320	301	1		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	97	Total	C	N	O	S	0	0
			741	479	124	137	1		

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			872	553	165	153	1		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	127	Total	C	N	O	S	0	0
			1020	646	205	167	2		

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	106	Total	C	N	O	S	0	0
			849	540	165	143	1		

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	103	Total	C	N	O	S	0	0
			812	504	167	137	4		

- Molecule 33 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	98	Total	C	N	O	S	0	0
			763	477	155	129	2		

- Molecule 34 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 35 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	j	77	Total	C	N	O	0	0
			611	391	115	105		

- Molecule 36 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	50	Total	C	N	O	S	0	0
			435	272	97	64	2		

- Molecule 37 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	94	Total	C	N	O	S	0	0
			756	476	153	122	5		

- Molecule 38 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	89	Total	C	N	O	S	0	0
			680	421	136	117	6		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	224	Total	C	N	O	S	0	0
			1691	1051	293	340	7		

- Molecule 40 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	320	Total	C	N	O	S	0	0
			2574	1648	444	475	7		

- Molecule 41 is a protein called uL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	p	210	Total	C	N	O	0	0
			1050	630	210	210		

- Molecule 42 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	516	Total	C	N	O	S	0	0
			3999	2530	688	766	15		

- Molecule 43 is a protein called Tyrosine-protein phosphatase YVH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	128	Total	C	N	O	S	0	0
			991	625	179	179	8		

- Molecule 44 is a protein called Cytoplasmic 60S subunit biogenesis factor REI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	211	Total	C	N	O	S	0	0
			1724	1095	307	314	8		

- Molecule 45 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	60	Total	C	N	O	S	0	0
			500	322	98	79	1		

- Molecule 46 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	w	389	Total	C	N	O	S	0	0
			3076	1955	530	571	20		

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	121	Total	C	N	O	P	0	0
			2576	1152	461	843	120		

- Molecule 48 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	156	Total	C	N	O	P	0	0
			3310	1482	582	1091	155		

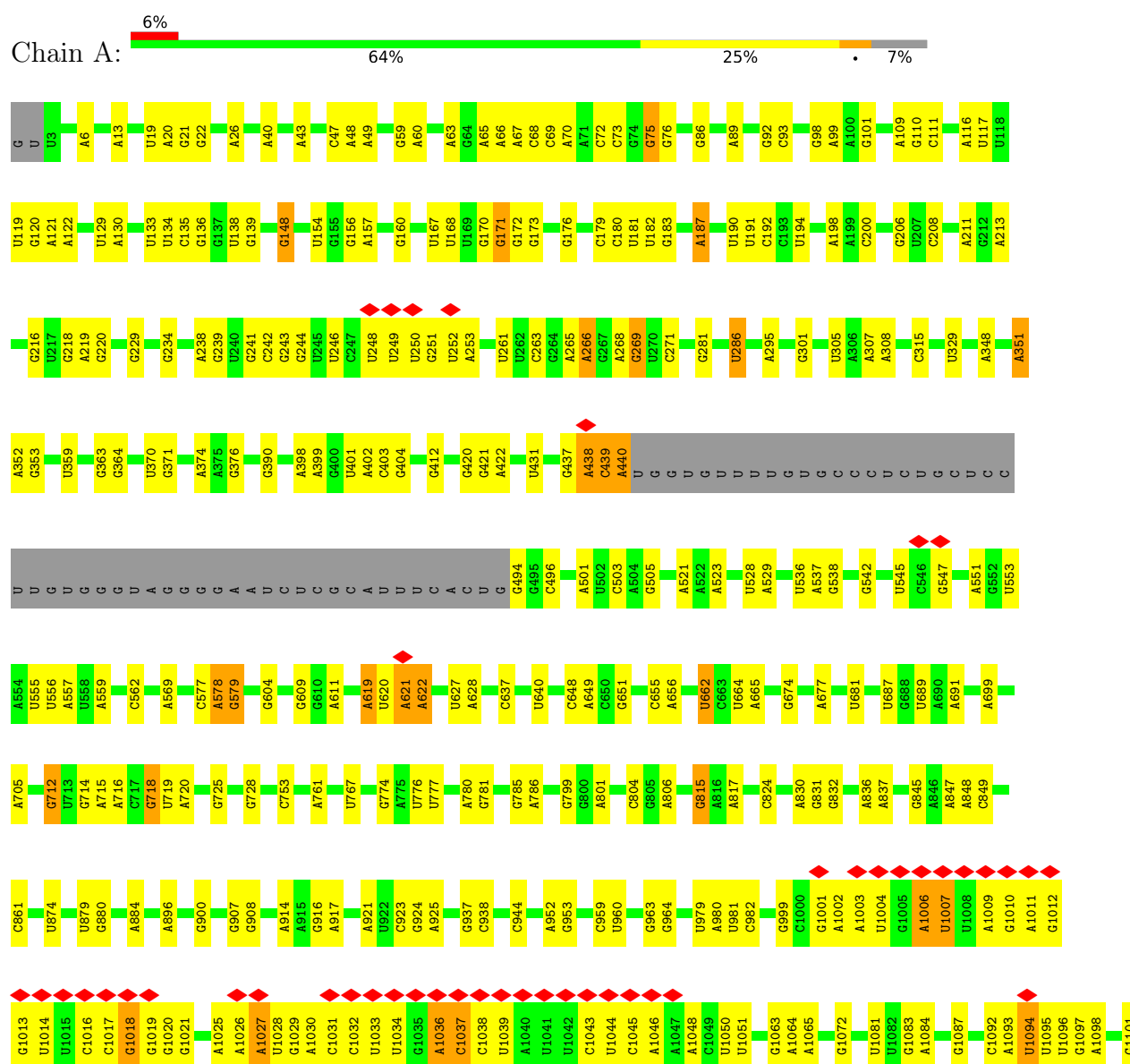
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	g	1	Total 1	Zn 1	0
49	i	1	Total 1	Zn 1	0
49	l	1	Total 1	Zn 1	0
49	m	1	Total 1	Zn 1	0
49	s	2	Total 2	Zn 2	0
49	u	2	Total 2	Zn 2	0
49	w	2	Total 2	Zn 2	0

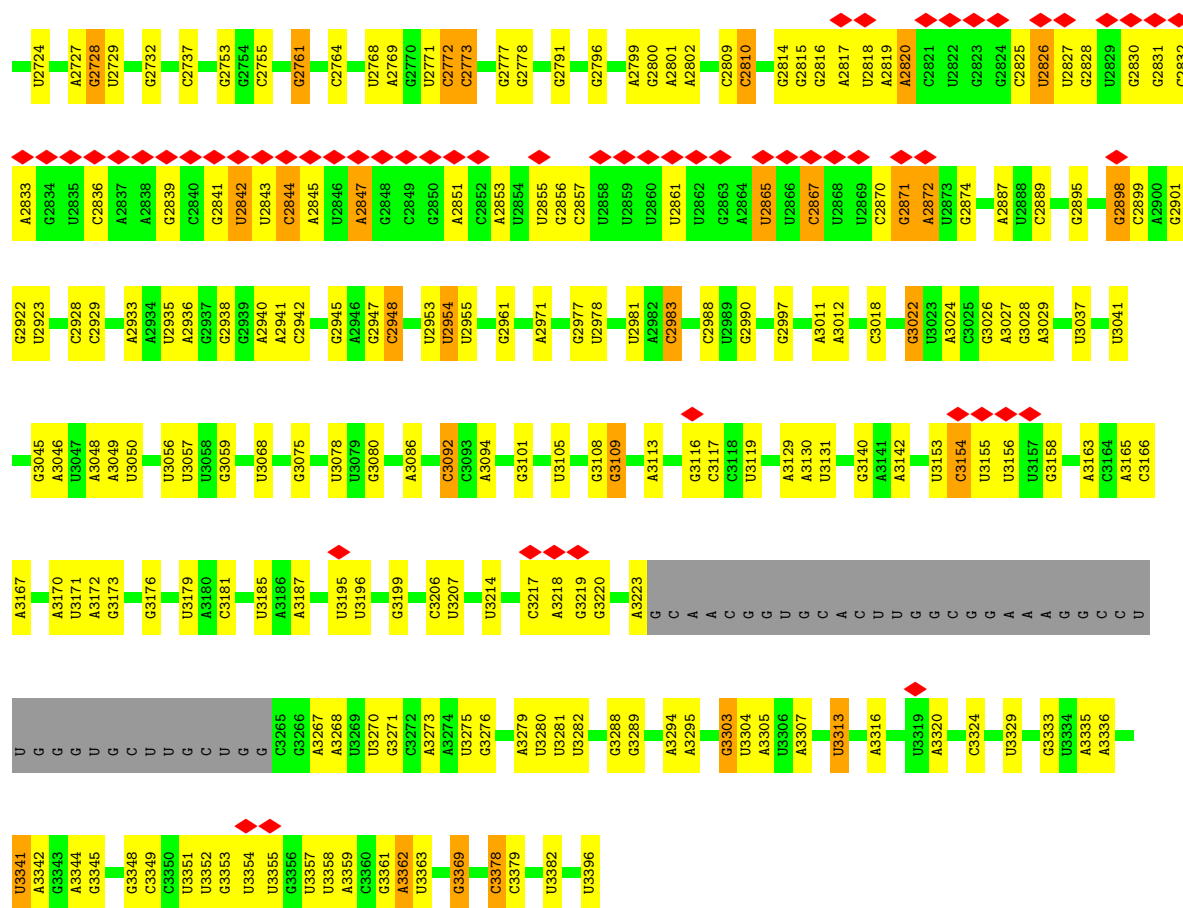
3 Residue-property plots

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

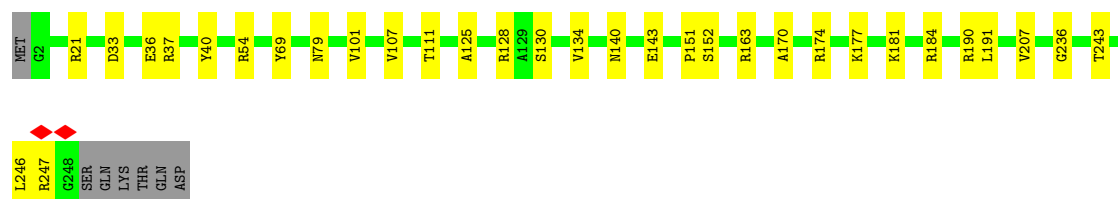
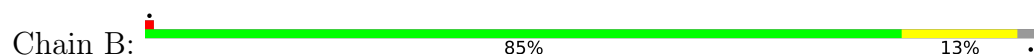
• Molecule 1: 25S ribosomal RNA



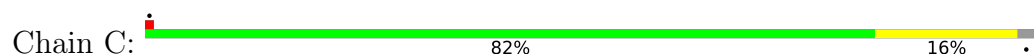
U2570	A2488	G2403	A2289	A2142	A1907	C1761	A1587	G1450	G1289	G1229	A1102
U2571	C2489	A2404	U2260	A2143	A1908	C1762	A1588	U1455	A1301	G1230	A1103
C2572	A2490	C2405	G2261	A2144	G1914	U1763	A1589	U1456	A1302	A1231	G1104
G2573	C2492	U2411	A2262	A2145	G1914	U1764	G1590	A1467	A1303	C1232	U1110
U2493	U2493	G2418	U2266	A2149	A1930	U1765	A1593	A1475	A1304	G1233	G1115
A2494	C2495	A2419	U2267	G2150	G1940	G1775	U1601	G1476	U1305	G1234	G1116
C2495	C2496	A2424	U2268	G2155	G1949	C1779	U1950	A1477	G1306	U1235	G1117
G2584	U2497	A2437	U2269	G2156	G1950	G1780	G1604	U1950	G1307	G1236	C1118
G2585	U2498	G2437	A2271	G2157	C1951	U1785	U1950	A1481	A1308	G1237	C1119
U2499	U2499	G2437	G2272	A2158	G1952	G1786	G1618	A1482	U1309	G1238	A1120
A2500	U2501	G2440	G2273	A2168	G1953	U1797	A1619	A1493	G1313	C1239	U1128
A2502	A2502	A2441	U2281	G2169	G1954	G1796	U1620	U1494	U1325	A1240	A1129
A2503	G2442	G2442	U2282	C2176	U1955	A1797	C1628	U1494	U1325	A1241	A1130
U2504	A2445	A2445	A2295	U2176	A	A1807	U1628	G1493	A1330	G1242	G1131
U2505	U2446	U2446	A2296	G2180	G	G1808	U1629	U1494	U1331	G1243	A1130
U2506	U2447	U2447	U2298	G2183	G	U1813	U1630	U1494	A1332	A1244	U1144
A2511	G2448	G2448	U2299	A2183	G	A1814	U1631	U1494	C1333	A1245	A1153
U2514	A2449	G2450	G2307	U2184	G	U1815	U1632	U1494	U1348	G1246	A1154
A2515	G2450	G2450	G2308	G2185	G	A1816	A1642	U1494	G1349	U1247	C1155
U2516	G2451	G2451	A2309	U2186	G	A1816	A1643	U1494	A1350	G1248	G1156
U2526	G2452	G2452	U2310	G2187	C	U1820	G1644	U1494	U1351	G1249	G1157
C2526	U2453	U2453	A2313	A2188	C	U1821	G1645	U1494	A1352	G1250	A1158
G2530	G2454	G2454	U2314	U2189	U	A1835	U1646	U1494	U1353	A1251	A1159
C	U2455	U2455	G2315	U2193	A	A1839	G1657	U1494	A1354	A1252	A1169
G	U2456	U2456	G2315	G2194	A	A1842	G1658	U1494	A1355	U1253	A1179
G	G2457	G2457	U2334	A2198	G	C1843	G1661	U1494	U1356	C1254	A1180
A	A2458	A2458	G2335	U2205	G	A1849	G1662	U1494	A1381	G1255	U1181
U	A2459	A2459	U2336	G2206	C	C1850	G1677	U1494	A1386	G1256	A1190
U	U2460	U2460	U2344	U2206	C	A1850	G1681	U1494	G1389	C1257	U1191
U	A2461	A2461	A2345	G2210	C	A1859	A1696	U1494	A1390	U1258	C1192
C	G2462	G2462	A2356	G2210	C	A1859	A1697	U1494	G1391	A1259	A1193
U	U2463	U2463	G2359	A2213	C	G1863	A1715	U1494	G1392	A1260	A1195
U	U2464	U2464	U2364	A2214	C	A1864	U1716	U1494	G1411	G1261	C1196
U	G2465	G2465	G2364	A2219	C	A1866	U1717	U1494	G1412	G1262	C1201
U	G2466	G2466	A2372	A2220	C	U1871	U1718	U1494	A1418	A1263	A1202
U	U2467	U2467	G2373	A2228	C	U1874	U1721	U1494	A1419	G1264	A1203
U	G2468	G2468	A2374	A2229	C	A1874	U1724	U1494	C1411	U1265	U1208
U	G2469	G2469	G2375	A2232	C	G1878	C1725	U1494	G1412	G1266	G1209
U	C2470	C2470	G2375	A2232	C	U1879	U1740	U1494	A1418	U1267	A1217
U	U2471	U2471	G2375	A2232	C	U1880	A1741	U1494	A1419	G1268	U1218
U	U2472	U2472	U2388	A2232	C	A1886	U1742	U1494	C1432	U1269	G1219
U	C2473	C2473	G2389	A2232	C	A1886	U1749	U1494	G1433	A1270	A1221
U	G2474	G2474	U2389	A2232	C	A1886	A1750	U1494	G1434	A1271	A1221
U	G2475	G2475	G2392	A2232	C	A1886	G1751	U1494	A1435	C1272	G1222
U	G2476	G2476	G2393	A2232	C	A1886	A1760	U1494	U1436	A1273	A1225
U	G2477	G2477	A2401	A2255	C	A1886	A1760	U1494	C1437	A1274	A1225
U	G2478	G2478	A2402	A2256	C	A1886	A1760	U1494	A1446	C1275	G1226
U	G2479	G2479	A2402	U2258	C	A1886	A1760	U1494	A1446	U1276	C1227
U	G2480	G2480	A2402	U2258	C	A1886	A1760	U1494	A1446	C1277	G1228
U	G2481	G2481	A2402	U2258	C	A1886	A1760	U1494	A1446	A1278	A1286
U	U2482	U2482	A2402	U2258	C	A1886	A1760	U1494	A1446	C1279	A1287
U	G2483	G2483	A2402	U2258	C	A1886	A1760	U1494	A1446	U1280	G1281
U	A2484	A2484	A2402	U2258	C	A1886	A1760	U1494	A1446	G1282	C1283
U	A2485	A2485	A2402	U2258	C	A1886	A1760	U1494	A1446	C1284	G1285
U	A2486	A2486	A2402	U2258	C	A1886	A1760	U1494	A1446	G1286	A1287
U	A2487	A2487	A2402	U2258	C	A1886	A1760	U1494	A1446	U1288	A1288



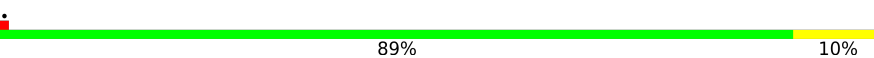
• Molecule 2: 60S ribosomal protein L2-A



• Molecule 3: 60S ribosomal protein L3



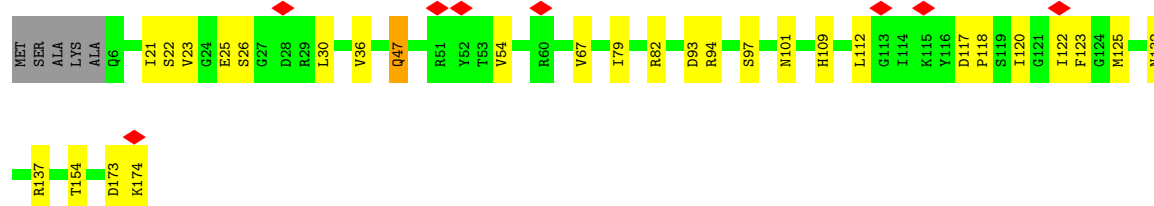
- Molecule 4: 60S ribosomal protein L4-A

Chain D:  89% 10%



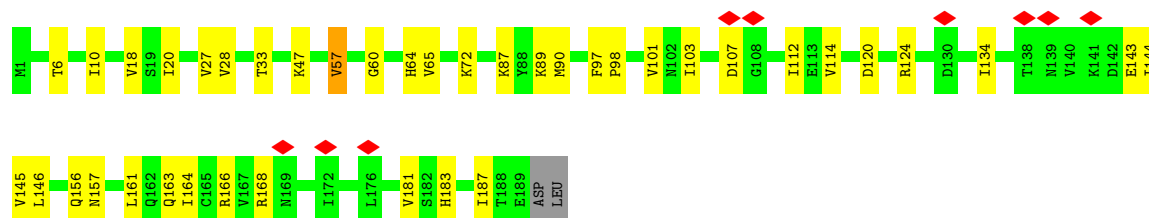
- Molecule 5: 60S ribosomal protein L11-A

Chain E:  80% 16% 5%



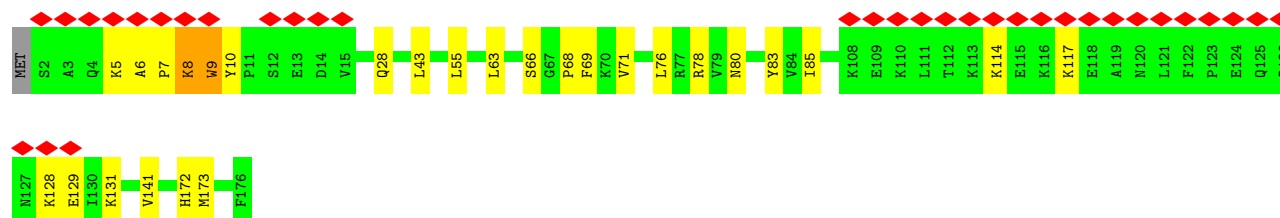
- Molecule 6: 60S ribosomal protein L9-A

Chain F:  78% 20% 5%



- Molecule 7: 60S ribosomal protein L6-A

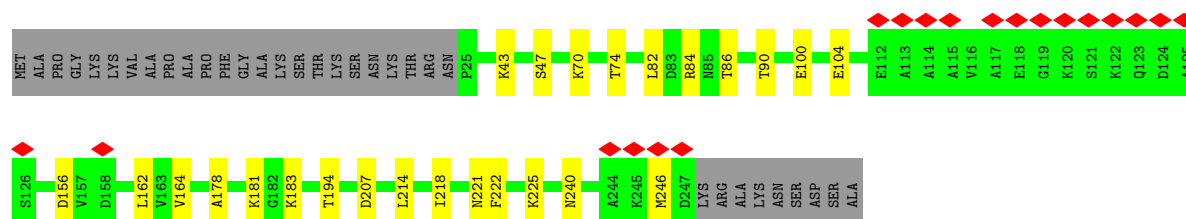
Chain G:  84% 14% 19%



- Molecule 8: 60S ribosomal protein L8-A

Chain H:  77% 10% 13%

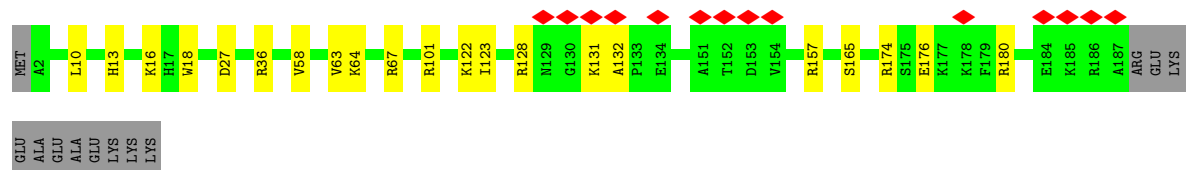
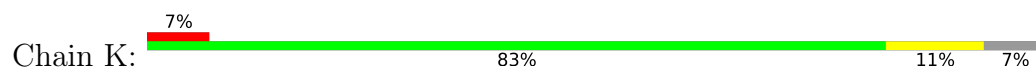




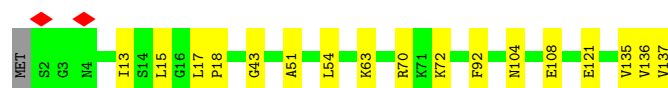
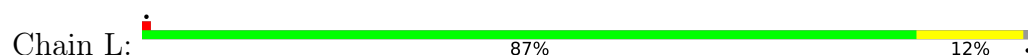
- Molecule 9: 60S ribosomal protein L16-B



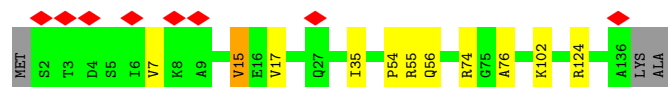
- Molecule 10: 60S ribosomal protein L13-A



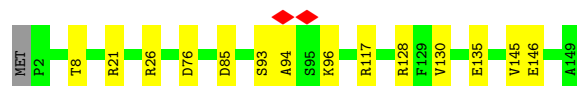
- Molecule 11: 60S ribosomal protein L23-A



- Molecule 12: 60S ribosomal protein L14-A



- Molecule 13: 60S ribosomal protein L28



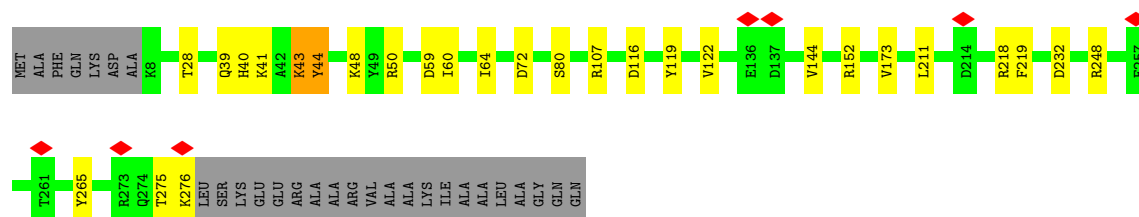
- Molecule 14: 60S ribosomal protein L15-A

Chain O:  84% 15%



- Molecule 15: 60S ribosomal protein L5

Chain P:  81% 9% 9%



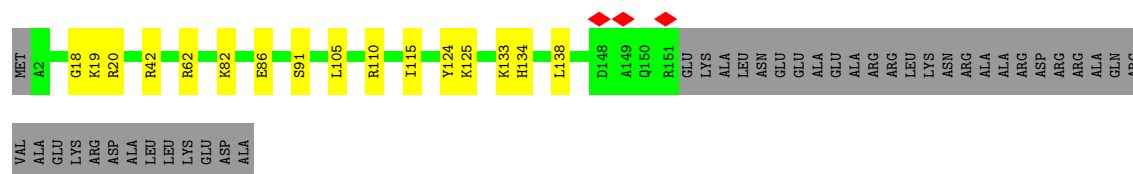
- Molecule 16: 60S ribosomal protein L18-A

Chain Q:  85% 14%



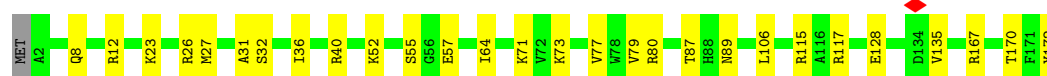
- Molecule 17: 60S ribosomal protein L19-A

Chain R:  71% 8% 21%



- Molecule 18: 60S ribosomal protein L20-A

Chain S:  83% 16%

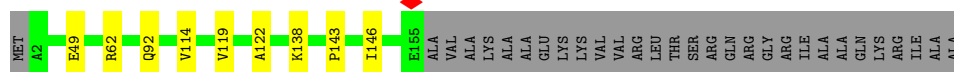
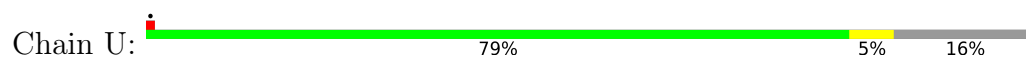


- Molecule 19: 60S ribosomal protein L21-A

Chain T:  86% 13%



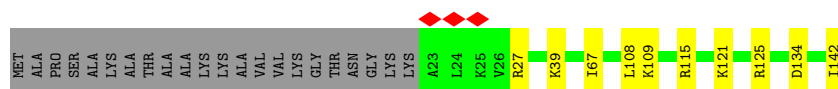
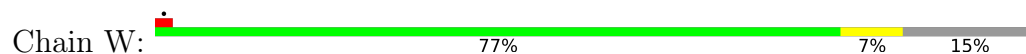
- Molecule 20: 60S ribosomal protein L17-A



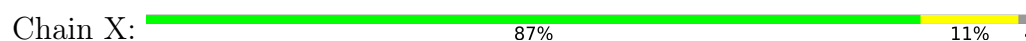
- Molecule 21: 60S ribosomal protein L22-A



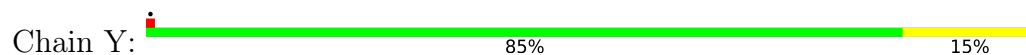
- Molecule 22: 60S ribosomal protein L25



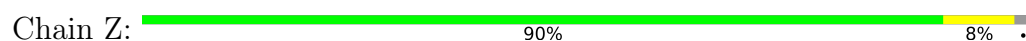
- Molecule 23: 60S ribosomal protein L26-A



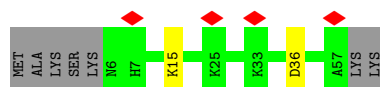
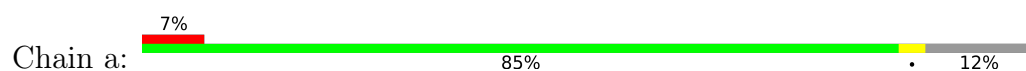
- Molecule 24: 60S ribosomal protein L27-A



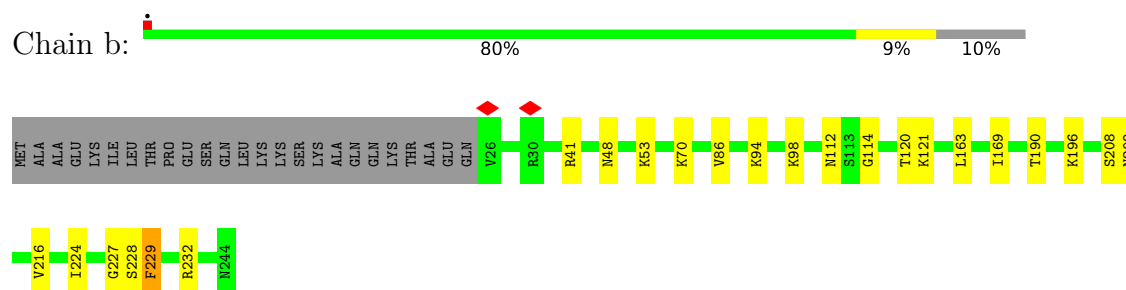
- Molecule 25: 60S ribosomal protein L35-A



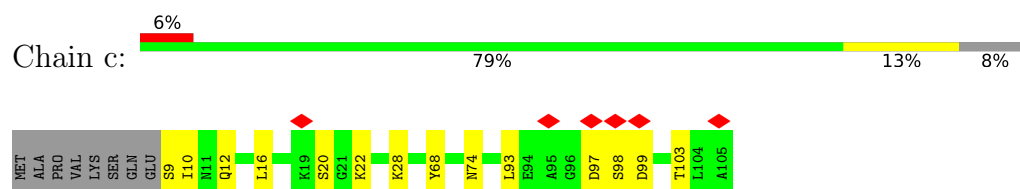
- Molecule 26: 60S ribosomal protein L29



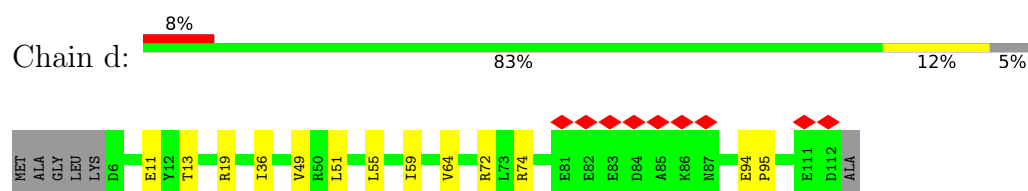
- Molecule 27: 60S ribosomal protein L7-A



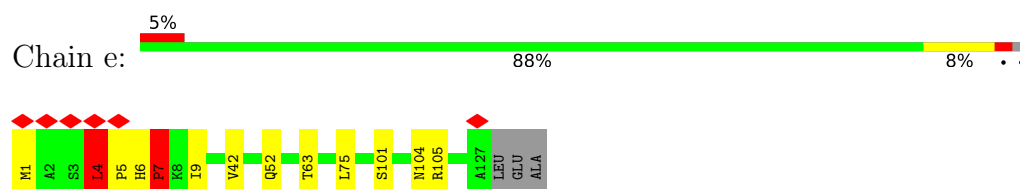
- Molecule 28: 60S ribosomal protein L30



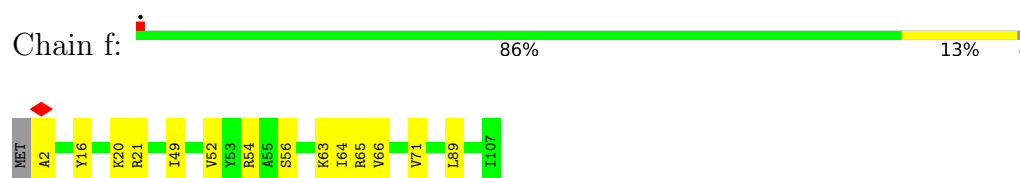
- Molecule 29: 60S ribosomal protein L31-A



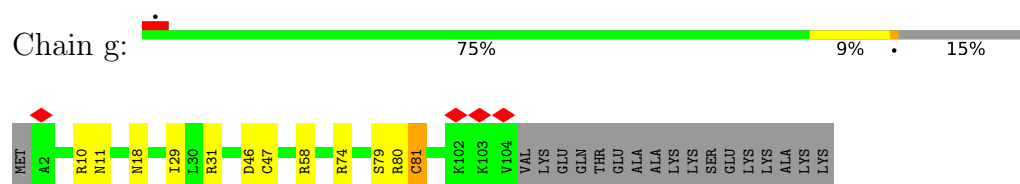
- Molecule 30: 60S ribosomal protein L32



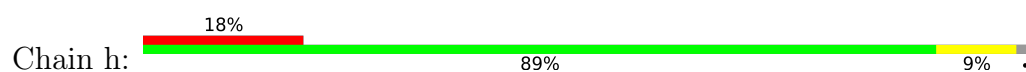
- Molecule 31: 60S ribosomal protein L33-A



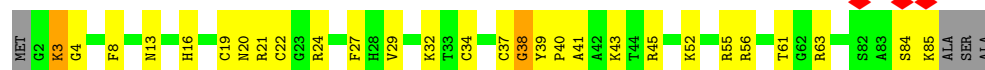
- Molecule 32: 60S ribosomal protein L34-A



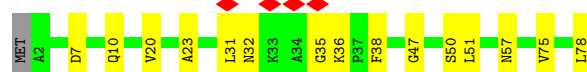
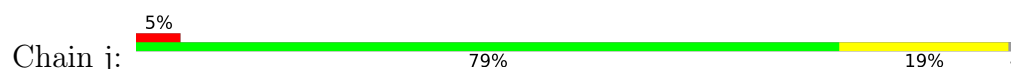
- Molecule 33: 60S ribosomal protein L36-A



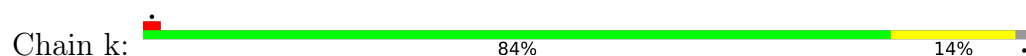
- Molecule 34: 60S ribosomal protein L37-A



- Molecule 35: 60S ribosomal protein L38



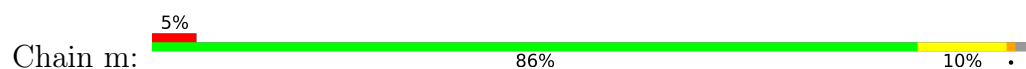
- Molecule 36: 60S ribosomal protein L39



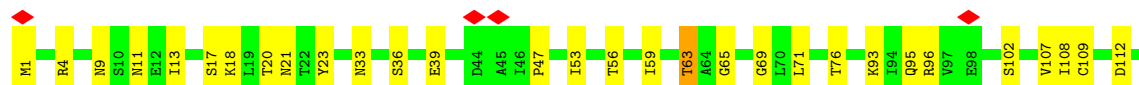
- Molecule 37: 60S ribosomal protein L42-A

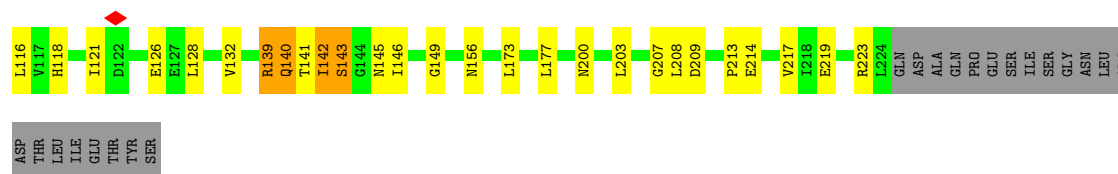


- Molecule 38: 60S ribosomal protein L43-A

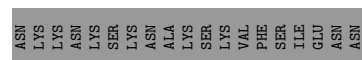
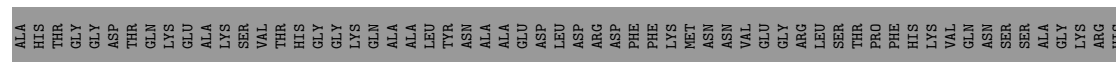
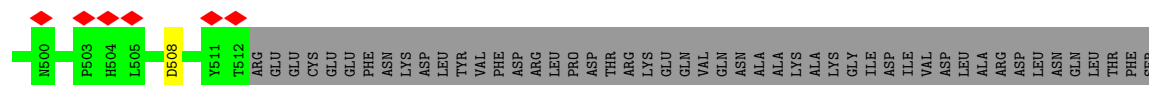
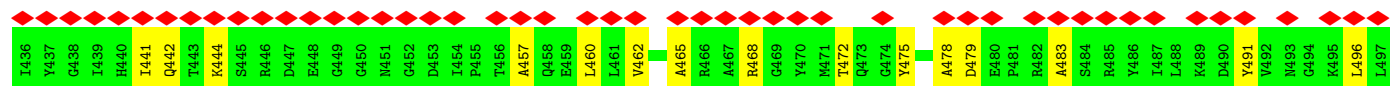
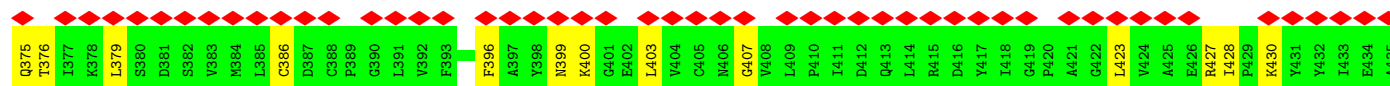
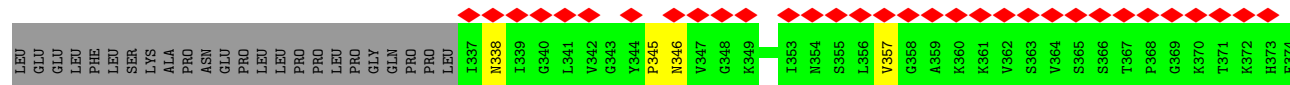
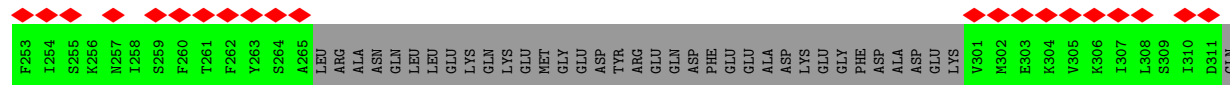
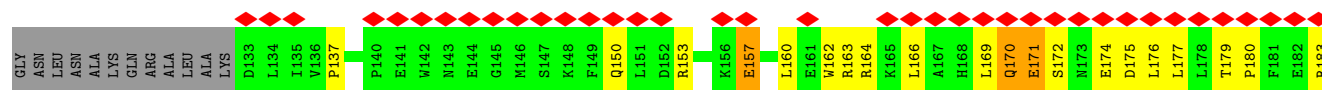
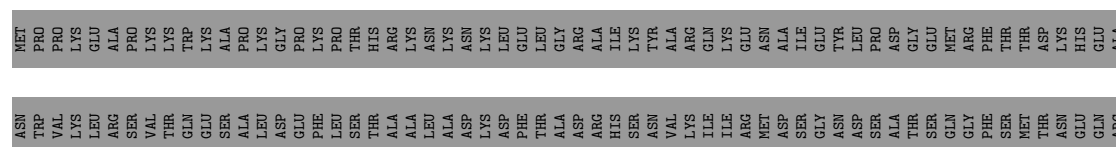
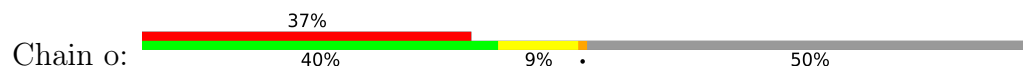


- Molecule 39: Eukaryotic translation initiation factor 6



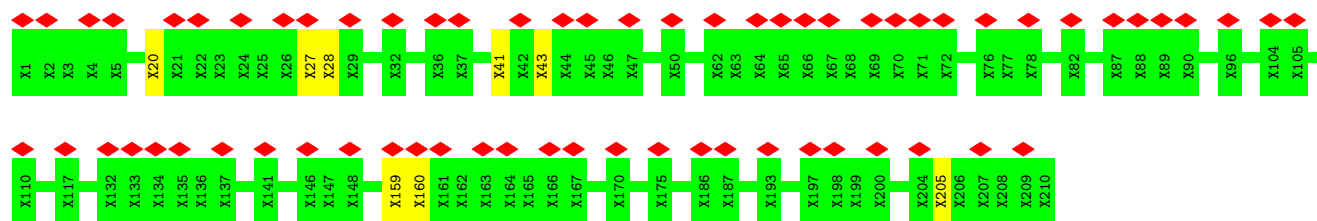


• Molecule 40: Large subunit GTPase 1

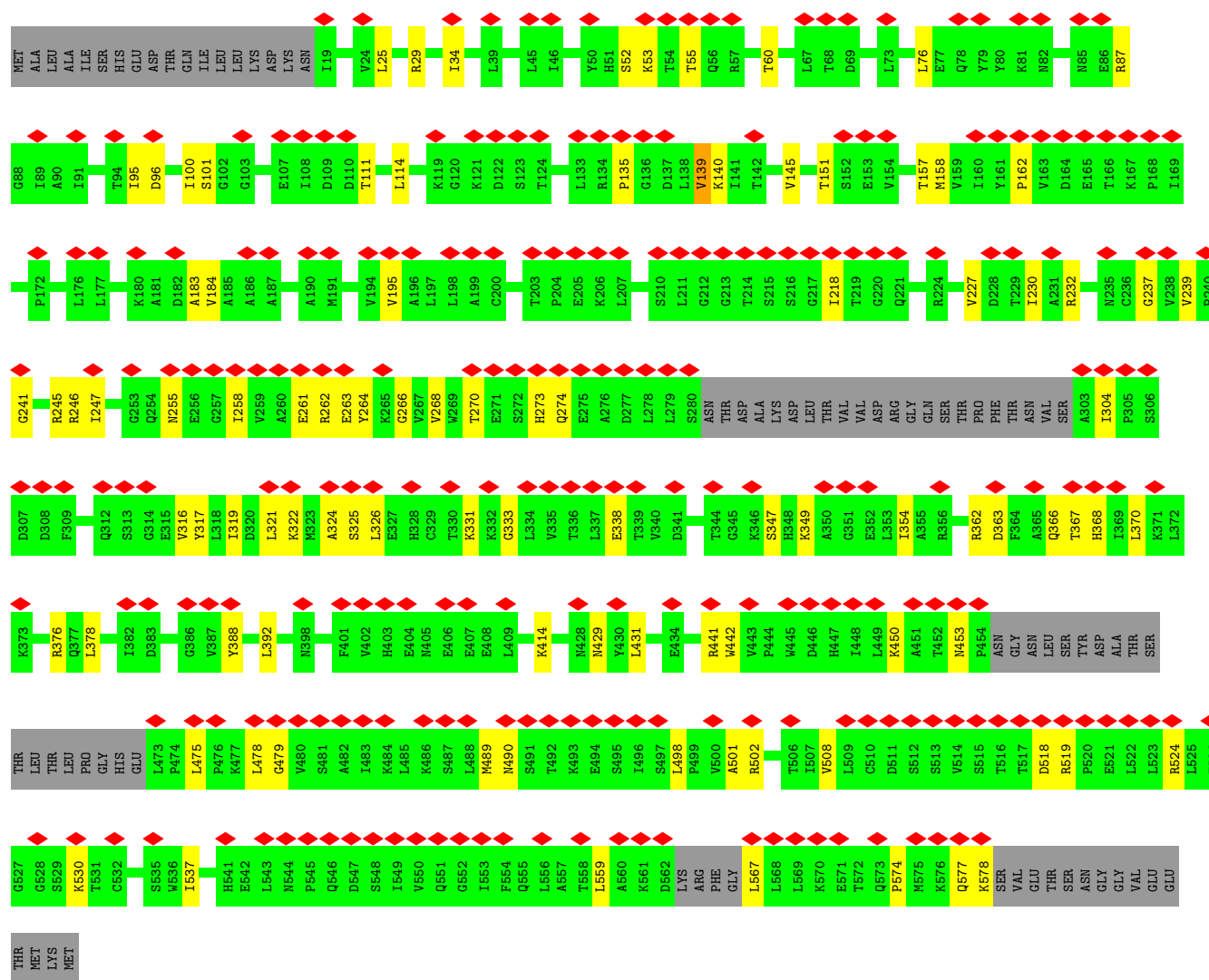


• Molecule 41: uL1





• Molecule 42: Probable metalloprotease ARX1

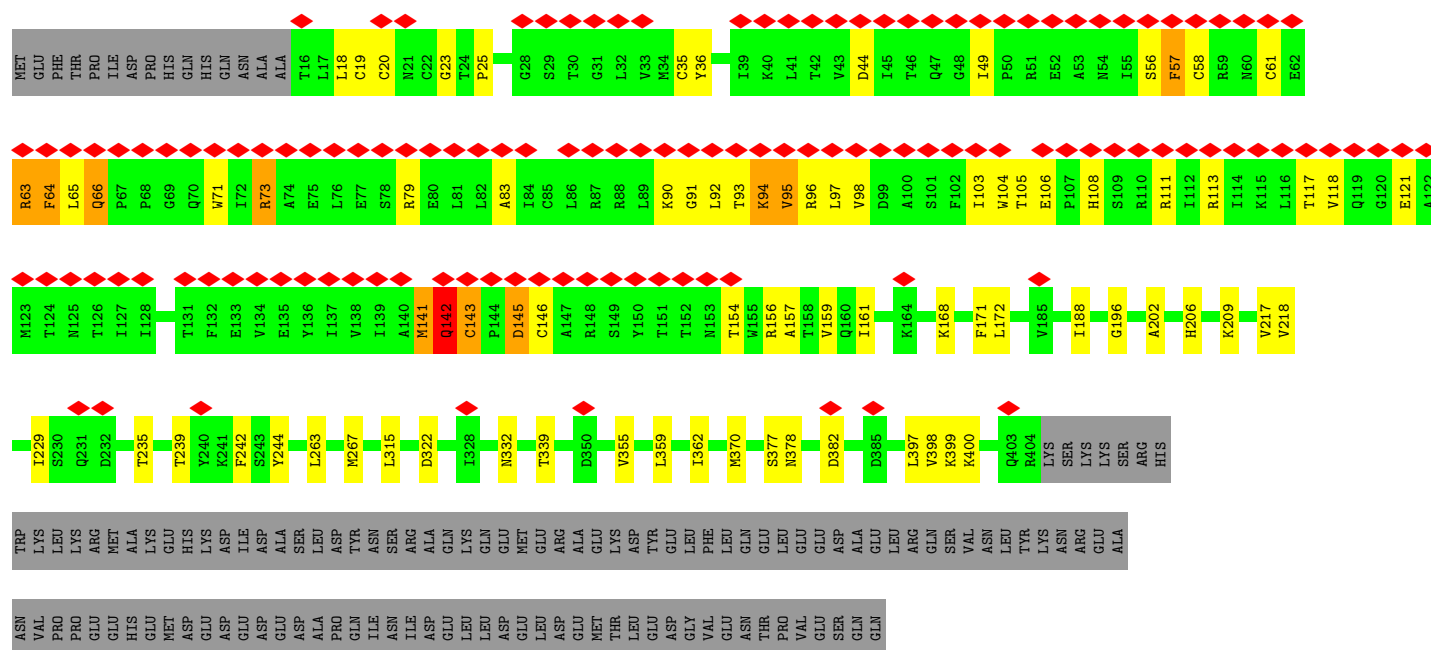


• Molecule 43: Tyrosine-protein phosphatase YVH1

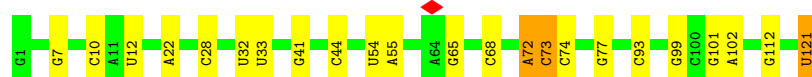
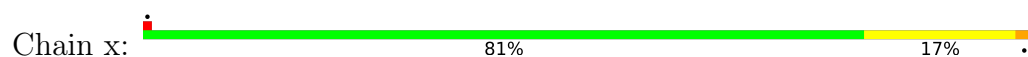


THR	VAL	LYS	LYS	ALA	GLN	ARG	PRO	ILE	THR	GLY	ALA	SER	LEU	ASP	LEU	ILE	LYS	LYS	GLU	ARG	ANG	ARG	SER	SER	LEU	LYS	PRO	GLU	VAL	ARG	LYS	LYS	ASN	ARG	GLU	GLU	LYS	LYS	LEU	LYS	ALA	ALA	ASN	LYS	GLU	LYS	LYS	ALA	GLU	LYS	ALA	ALA	ARG	LYS	ALA	GLY	THR	GLN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
SER	SER	LYS	PHE	THR	SER	LYS	GLN	GLN	GLN	ALA	ALA	GLY	ALA	PHE	GLN	LYS	VAL	ALA	ALA	THR	THR	SER	SER	ARG																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								

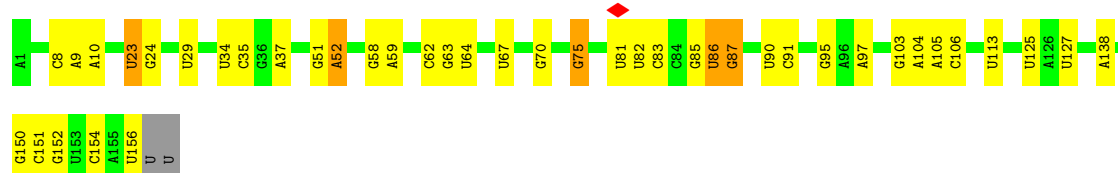
• Molecule 46: 60S ribosomal export protein NMD3



• Molecule 47: 5S ribosomal RNA



• Molecule 48: 5.8S ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	216403	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	63	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.638	Depositor
Minimum map value	-0.372	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	383.40002, 383.40002, 383.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.065, 1.065, 1.065	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A	0.39	1/75327 (0.0%)	0.41	3/117440 (0.0%)
2	B	0.41	0/1912	0.59	0/2569
3	C	0.41	0/3110	0.64	3/4184 (0.1%)
4	D	0.40	0/2800	0.53	0/3791
5	E	0.24	0/1373	0.50	0/1841
6	F	0.26	0/1523	0.50	0/2051
7	G	0.32	0/1423	0.57	0/1911
8	H	0.30	0/1774	0.52	0/2395
9	J	0.37	0/1593	0.51	0/2137
10	K	0.35	0/1511	0.51	0/2031
11	L	0.40	0/1017	0.58	0/1368
12	M	0.29	0/1060	0.48	0/1428
13	N	0.42	0/1203	0.52	0/1611
14	O	0.43	0/1756	0.61	2/2353 (0.1%)
15	P	0.30	0/2225	0.54	1/3004 (0.0%)
16	Q	0.38	0/1464	0.51	0/1964
17	R	0.35	0/1226	0.48	0/1637
18	S	0.36	0/1472	0.49	0/1979
19	T	0.36	0/1299	0.50	0/1742
20	U	0.42	0/1245	0.55	0/1676
21	V	0.27	0/802	0.51	0/1087
22	W	0.37	0/973	0.58	0/1313
23	X	0.37	0/995	0.54	0/1329
24	Y	0.27	0/1117	0.53	0/1496
25	Z	0.32	0/972	0.47	0/1293
26	a	0.29	0/426	0.49	0/570
27	b	0.40	0/1797	0.58	0/2419
28	c	0.25	0/749	0.46	0/1007
29	d	0.39	0/886	0.59	0/1190
30	e	0.41	0/1041	0.57	1/1393 (0.1%)
31	f	0.41	0/867	0.63	0/1167
32	g	0.43	0/822	0.58	0/1099

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.26	0/770	0.48	0/1023
34	i	0.53	0/680	0.67	0/901
35	j	0.29	0/617	0.47	0/825
36	k	0.40	0/442	0.46	0/587
37	l	0.42	0/768	0.56	0/1016
38	m	0.42	0/687	0.67	0/915
39	n	0.30	0/1712	0.54	0/2330
40	o	0.37	0/2628	0.76	6/3557 (0.2%)
42	r	0.21	0/4069	0.56	2/5520 (0.0%)
43	s	0.29	0/1016	0.67	0/1368
44	u	0.27	0/1759	0.59	3/2363 (0.1%)
45	v	0.21	0/512	0.46	0/680
46	w	0.36	0/3135	0.65	1/4255 (0.0%)
47	x	0.32	0/2880	0.36	0/4487
48	y	0.41	0/3699	0.41	0/5760
All	All	0.37	1/143134 (0.0%)	0.48	22/210062 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2258	U	C1'-N1	6.15	1.57	1.48

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	18	PRO	CA-N-CD	-9.60	98.57	112.00
40	o	171	GLU	CA-C-N	9.15	139.02	121.54
40	o	171	GLU	C-N-CA	9.15	139.02	121.54
3	C	18	PRO	CB-CA-C	8.90	126.25	111.56
42	r	55	THR	CA-C-N	6.38	133.74	121.54
42	r	55	THR	C-N-CA	6.38	133.74	121.54
44	u	220	CYS	CA-C-N	6.28	133.54	121.54
44	u	220	CYS	C-N-CA	6.28	133.54	121.54
14	O	125	SER	CA-C-N	6.11	133.20	121.54
14	O	125	SER	C-N-CA	6.11	133.20	121.54
40	o	345	PRO	CA-C-N	6.01	130.91	122.08
40	o	345	PRO	C-N-CA	6.01	130.91	122.08
30	e	7	PRO	N-CA-CB	-5.92	97.04	103.25
15	P	44	TYR	N-CA-C	5.85	117.45	111.14
46	w	235	THR	N-CA-C	-5.75	108.06	114.62
40	o	198	SER	CA-C-N	5.68	130.42	122.08
40	o	198	SER	C-N-CA	5.68	130.42	122.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	u	220	CYS	O-C-N	5.48	129.87	122.59
3	C	256	HIS	N-CA-C	5.44	121.83	109.81
1	A	1815	U	P-O3'-C3'	5.31	128.16	120.20
1	A	621	A	P-O3'-C3'	5.15	127.93	120.20
1	A	2112	U	P-O3'-C3'	5.10	127.85	120.20

There are no chirality outliers.

There are no planarity outliers.

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	A	67292	0	33821	335	0
2	B	1878	0	1946	21	0
3	C	3039	0	3113	46	0
4	D	2748	0	2863	27	0
5	E	1352	0	1383	17	0
6	F	1502	0	1572	26	0
7	G	1399	0	1501	26	0
8	H	1742	0	1834	18	0
9	J	1563	0	1665	12	0
10	K	1486	0	1554	18	0
11	L	1002	0	1048	14	0
12	M	1045	0	1136	8	0
13	N	1172	0	1215	12	0
14	O	1719	0	1779	24	0
15	P	2176	0	2116	19	0
16	Q	1440	0	1543	17	0
17	R	1209	0	1295	12	0
18	S	1436	0	1475	19	0
19	T	1275	0	1323	16	0
20	U	1222	0	1231	5	0
21	V	786	0	799	8	0
22	W	958	0	1023	8	0
23	X	984	0	1075	11	0
24	Y	1091	0	1155	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	Z	963	0	1073	9	0
26	a	415	0	429	2	0
27	b	1760	0	1843	20	0
28	c	741	0	797	10	0
29	d	872	0	914	7	0
30	e	1020	0	1091	12	0
31	f	849	0	880	11	0
32	g	812	0	874	7	0
33	h	763	0	842	7	0
34	i	665	0	668	26	0
35	j	611	0	682	7	0
36	k	435	0	475	7	0
37	l	756	0	817	9	0
38	m	680	0	723	9	0
39	n	1691	0	1689	43	0
40	o	2574	0	2601	65	0
41	p	1050	0	246	5	0
42	r	3999	0	4088	61	0
43	s	991	0	985	20	0
44	u	1724	0	1682	24	0
45	v	500	0	524	6	0
46	w	3076	0	3104	81	0
47	x	2576	0	1305	9	0
48	y	3310	0	1676	17	0
49	g	1	0	0	0	0
49	i	1	0	0	0	0
49	l	1	0	0	0	0
49	m	1	0	0	0	0
49	s	2	0	0	0	0
49	u	2	0	0	0	0
49	w	2	0	0	0	0
All	All	134359	0	99473	990	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 (990) 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)
40:o:163:ARG:HD3	40:o:183:ARG:CZ	1.56	1.34
46:w:63:ARG:HG2	46:w:71:TRP:CB	1.64	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:o:163:ARG:CD	40:o:183:ARG:NH1	2.02	1.22
40:o:163:ARG:HD2	40:o:183:ARG:NH1	1.55	1.21
46:w:63:ARG:HG2	46:w:71:TRP:HB3	1.20	1.18
46:w:63:ARG:CG	46:w:71:TRP:HB3	1.74	1.14
46:w:91:GLY:HA2	46:w:94:LYS:HE3	1.16	1.12
46:w:56:SER:OG	46:w:141:MET:HG3	1.51	1.11
3:C:17:LEU:HB3	3:C:18:PRO:HD2	1.32	1.09
46:w:91:GLY:O	46:w:95:VAL:HG13	1.55	1.04
40:o:163:ARG:HG2	46:w:104:TRP:CD1	1.91	1.04
1:A:1003:A:H62	1:A:1046:A:N6	1.57	1.03
40:o:163:ARG:CD	40:o:183:ARG:CZ	2.34	1.02
46:w:143:CYS:HB3	46:w:146:CYS:SG	1.99	1.02
7:G:7:PRO:HD3	7:G:10:TYR:OH	1.58	0.99
44:u:219:VAL:HG12	44:u:243:PRO:HD3	1.45	0.99
44:u:219:VAL:CG1	44:u:243:PRO:HD3	1.94	0.97
39:n:140:GLN:OE1	39:n:173:LEU:CD2	2.16	0.94
1:A:1003:A:N6	1:A:1046:A:H61	1.67	0.92
34:i:37:CYS:SG	34:i:37:CYS:O	2.28	0.92
46:w:96:ARG:NH1	46:w:121:GLU:OE2	2.03	0.92
46:w:91:GLY:CA	46:w:94:LYS:HE3	2.00	0.92
1:A:2467:G:H21	1:A:2488:A:N6	1.69	0.91
46:w:91:GLY:HA2	46:w:94:LYS:CE	1.99	0.91
40:o:163:ARG:CG	46:w:104:TRP:CD1	2.55	0.90
1:A:160:G:H1	1:A:261:U:H3	1.13	0.90
34:i:21:ARG:NH2	34:i:41:ALA:O	2.06	0.89
46:w:63:ARG:HG2	46:w:71:TRP:HB2	1.55	0.88
1:A:1003:A:H62	1:A:1046:A:H61	0.87	0.86
39:n:116:LEU:HD23	39:n:142:ILE:HD11	1.57	0.86
46:w:95:VAL:CG2	46:w:118:VAL:HG11	2.07	0.85
34:i:4:GLY:O	34:i:8:PHE:CD2	2.30	0.84
39:n:140:GLN:OE1	39:n:173:LEU:HD21	1.80	0.81
40:o:164:ARG:NE	46:w:104:TRP:CZ2	2.49	0.80
46:w:63:ARG:HG3	46:w:71:TRP:HB3	1.61	0.79
1:A:2467:G:H21	1:A:2488:A:H62	1.27	0.78
3:C:17:LEU:HB3	3:C:18:PRO:CD	2.13	0.78
40:o:164:ARG:HE	46:w:104:TRP:HZ2	1.32	0.78
1:A:2467:G:N2	1:A:2488:A:H62	1.79	0.78
27:b:216:VAL:HG11	27:b:227:GLY:HA3	1.66	0.77
39:n:140:GLN:OE1	39:n:173:LEU:HD23	1.82	0.77
46:w:95:VAL:HG23	46:w:118:VAL:HB	1.68	0.76
30:e:4:LEU:HD23	30:e:4:LEU:O	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:e:4:LEU:N	30:e:5:PRO:HD3	2.03	0.74
40:o:163:ARG:HD3	40:o:183:ARG:NH2	2.04	0.73
40:o:169:LEU:O	40:o:169:LEU:HD23	1.89	0.73
24:Y:61:LYS:O	24:Y:65:ARG:HB3	1.88	0.72
46:w:63:ARG:CG	46:w:71:TRP:CB	2.47	0.72
34:i:22:CYS:SG	34:i:24:ARG:HG2	2.30	0.71
44:u:219:VAL:HG12	44:u:243:PRO:CD	2.20	0.70
32:g:74:ARG:NH2	32:g:81:CYS:O	2.25	0.70
1:A:3214:U:HO2'	31:f:2:ALA:N	1.88	0.70
7:G:68:PRO:HB2	7:G:71:VAL:HG23	1.72	0.70
46:w:56:SER:OG	46:w:141:MET:CG	2.36	0.68
1:A:2816:G:O6	1:A:2820:A:C5	2.45	0.68
46:w:57:PHE:O	46:w:141:MET:HB2	1.94	0.68
27:b:228:SER:HA	27:b:232:ARG:HH21	1.57	0.67
15:P:40:HIS:HB3	15:P:43:LYS:HG3	1.77	0.66
43:s:323:ARG:HG3	43:s:327:GLY:HA2	1.77	0.66
46:w:63:ARG:HE	46:w:73:ARG:HG2	1.59	0.66
1:A:2816:G:O6	1:A:2820:A:C6	2.49	0.65
46:w:95:VAL:HG23	46:w:118:VAL:CB	2.25	0.65
1:A:2816:G:O6	1:A:2820:A:N7	2.30	0.65
1:A:2258:U:H5	40:o:193:ARG:HE	1.43	0.65
1:A:837:A:OP2	38:m:4:ARG:NE	2.28	0.64
34:i:37:CYS:O	34:i:38:GLY:C	2.40	0.64
40:o:163:ARG:HG2	46:w:104:TRP:NE1	2.12	0.64
40:o:163:ARG:CG	46:w:104:TRP:HD1	2.09	0.64
46:w:95:VAL:HG21	46:w:118:VAL:HG11	1.78	0.64
2:B:190:ARG:HH21	2:B:191:LEU:HD11	1.63	0.64
43:s:324:CYS:HB2	43:s:327:GLY:H	1.64	0.63
46:w:71:TRP:HE3	46:w:71:TRP:H	1.46	0.63
46:w:161:ILE:O	46:w:196:GLY:HA3	1.99	0.63
40:o:157:GLU:OE1	40:o:157:GLU:HA	1.98	0.63
4:D:188:ARG:HB3	4:D:193:LYS:HB3	1.80	0.63
22:W:108:LEU:HD12	22:W:109:LYS:HB2	1.80	0.63
30:e:4:LEU:N	30:e:5:PRO:CD	2.62	0.62
46:w:91:GLY:O	46:w:95:VAL:CG1	2.41	0.62
1:A:47:C:H5''	10:K:16:LYS:HG2	1.81	0.62
1:A:2255:A:OP1	1:A:2259:A:N6	2.33	0.62
16:Q:8:LYS:HB3	16:Q:11:LYS:HE2	1.82	0.62
29:d:11:GLU:HG2	29:d:74:ARG:HB3	1.81	0.62
1:A:1246:G:N2	1:A:1266:G:OP2	2.33	0.62
39:n:4:ARG:HB3	39:n:208:LEU:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:o:169:LEU:HD23	40:o:169:LEU:C	2.24	0.62
40:o:179:THR:HG22	40:o:396:PHE:HA	1.82	0.62
7:G:8:LYS:O	7:G:9:TRP:CD1	2.53	0.62
1:A:1560:G:N2	1:A:1580:A:N1	2.48	0.62
1:A:2198:A:HO2'	1:A:2269:U:HO2'	1.47	0.61
1:A:3041:U:O2'	11:L:43:GLY:HA3	1.99	0.61
40:o:179:THR:HA	40:o:399:ASN:ND2	2.16	0.61
1:A:1002:A:N6	1:A:1044:U:O4	2.33	0.61
46:w:95:VAL:CG2	46:w:118:VAL:CG1	2.77	0.61
1:A:687:U:OP2	10:K:36:ARG:NH2	2.33	0.61
1:A:2356:A:H5'	20:U:138:LYS:HZ2	1.65	0.61
40:o:163:ARG:HD2	40:o:183:ARG:HH11	1.61	0.61
1:A:1203:A:H1'	1:A:2856:G:H5'	1.83	0.61
40:o:163:ARG:HD3	40:o:183:ARG:NH1	1.75	0.61
40:o:164:ARG:NE	46:w:104:TRP:HZ2	1.94	0.61
6:F:47:LYS:HB2	12:M:7:VAL:HB	1.83	0.61
4:D:325:LEU:O	27:b:41:ARG:NH2	2.34	0.60
40:o:163:ARG:HD2	40:o:183:ARG:HH12	1.60	0.60
1:A:89:A:N7	16:Q:171:LYS:NZ	2.48	0.60
1:A:609:G:N7	4:D:308:LYS:NZ	2.49	0.60
6:F:89:LYS:HG2	6:F:145:VAL:HG12	1.83	0.60
39:n:116:LEU:CD2	39:n:142:ILE:HD11	2.31	0.60
1:A:2392:C:O2'	3:C:266:ARG:NH2	2.33	0.60
46:w:95:VAL:HG23	46:w:118:VAL:CG1	2.31	0.60
46:w:58:CYS:SG	46:w:143:CYS:HB2	2.42	0.60
1:A:440:A:H61	7:G:117:LYS:HE2	1.66	0.60
1:A:438:A:H5'	1:A:440:A:H2'	1.84	0.59
1:A:1807:G:OP1	24:Y:133:LYS:NZ	2.35	0.59
40:o:170:GLN:HE21	40:o:170:GLN:HA	1.67	0.59
40:o:198:SER:HA	40:o:338:ASN:HB3	1.82	0.59
4:D:148:ILE:HG23	4:D:149:PRO:HD3	1.83	0.59
22:W:115:ARG:HD3	22:W:121:LYS:HE3	1.83	0.59
1:A:1301:A:H4'	1:A:1302:A:H5''	1.82	0.59
34:i:84:SER:HB3	48:y:67:U:H4'	1.85	0.59
44:u:219:VAL:HG23	44:u:219:VAL:O	2.02	0.59
40:o:170:GLN:HA	40:o:170:GLN:NE2	2.18	0.59
32:g:11:ASN:O	32:g:18:ASN:ND2	2.35	0.59
40:o:177:LEU:HG	40:o:399:ASN:HB2	1.83	0.59
3:C:10:ARG:NH1	3:C:11:HIS:O	2.36	0.59
16:Q:122:ILE:HG23	16:Q:126:GLN:HB2	1.85	0.59
30:e:42:VAL:O	30:e:52:GLN:NE2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:s:310:CYS:SG	43:s:311:SER:N	2.76	0.59
1:A:1092:C:H4'	19:T:120:LYS:HE2	1.85	0.58
1:A:1575:A:H5''	1:A:1576:G:H2'	1.84	0.58
1:A:674:G:OP1	4:D:31:ARG:NH1	2.36	0.58
11:L:18:PRO:HA	11:L:51:ALA:HA	1.85	0.58
30:e:9:ILE:HG12	30:e:63:THR:HB	1.85	0.58
43:s:283:PHE:HB2	43:s:336:LEU:HB3	1.84	0.58
1:A:3108:G:O2'	6:F:166:ARG:NH2	2.37	0.58
3:C:106:TRP:O	3:C:137:TYR:OH	2.21	0.58
1:A:2841:G:N2	1:A:2847:A:H62	2.01	0.58
3:C:57:VAL:HG22	3:C:73:VAL:HG22	1.86	0.58
1:A:3026:G:N2	1:A:3029:A:OP2	2.37	0.58
46:w:145:ASP:OD1	46:w:145:ASP:N	2.32	0.58
38:m:38:ASP:HA	38:m:45:LYS:HA	1.84	0.58
39:n:121:ILE:O	39:n:139:ARG:NH2	2.36	0.58
1:A:216:G:OP1	23:X:16:ARG:NH1	2.37	0.58
1:A:2832:C:H42	1:A:2856:G:H22	1.52	0.58
1:A:3045:G:OP1	3:C:19:ARG:NH2	2.33	0.58
6:F:6:THR:HG21	6:F:65:VAL:HG13	1.86	0.58
23:X:16:ARG:NE	48:y:23:U:OP2	2.37	0.58
40:o:176:LEU:HB3	40:o:400:LYS:HZ3	1.69	0.58
1:A:2482:U:O4	1:A:2486:A:N6	2.36	0.57
19:T:18:ASP:HB2	19:T:21:LYS:HG3	1.85	0.57
40:o:174:GLU:O	40:o:175:ASP:OD1	2.22	0.57
16:Q:147:ARG:HB2	16:Q:150:VAL:HG23	1.87	0.57
39:n:214:GLU:HG3	46:w:20:CYS:HB2	1.86	0.57
42:r:441:ARG:NH2	42:r:489:MET:O	2.38	0.57
1:A:824:C:H5''	2:B:21:ARG:HD3	1.87	0.57
6:F:120:ASP:OD2	6:F:124:ARG:NH2	2.37	0.57
6:F:163:GLN:OE1	6:F:166:ARG:NH2	2.37	0.57
1:A:1027:A:OP2	46:w:400:LYS:NZ	2.37	0.57
1:A:2842:U:OP1	1:A:2844:C:N4	2.37	0.57
3:C:284:ARG:NH2	3:C:295:ALA:O	2.38	0.57
1:A:244:G:N7	10:K:131:LYS:NZ	2.52	0.57
1:A:1264:G:N2	1:A:1265:U:O4	2.38	0.57
34:i:4:GLY:O	34:i:8:PHE:CE2	2.56	0.57
40:o:427:ARG:HG3	40:o:428:ILE:HD12	1.86	0.57
42:r:255:ASN:O	44:u:345:ARG:NH2	2.38	0.57
1:A:1628:C:O2'	1:A:1813:A:N6	2.38	0.57
13:N:76:ASP:HB3	16:Q:92:ARG:HG2	1.87	0.57
24:Y:51:LEU:HB2	24:Y:65:ARG:HG3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:w:35:CYS:SG	46:w:36:TYR:N	2.77	0.57
1:A:1481:A:N3	1:A:1858:A:O2'	2.38	0.57
1:A:2258:U:H5	40:o:193:ARG:NE	2.01	0.57
1:A:2901:G:O2'	1:A:3024:A:N1	2.38	0.57
46:w:168:LYS:HB2	46:w:171:PHE:HB3	1.86	0.57
24:Y:100:THR:HG22	24:Y:106:GLN:HB3	1.87	0.56
1:A:2727:A:OP2	1:A:2728:G:N2	2.37	0.56
43:s:288:LEU:HG	43:s:290:TRP:H	1.69	0.56
46:w:90:LYS:HB2	46:w:92:LEU:HD22	1.87	0.56
1:A:68:C:OP2	1:A:301:G:N2	2.38	0.56
1:A:1390:A:N6	1:A:1418:A:O2'	2.38	0.56
1:A:2442:G:H1	1:A:2505:U:H3	1.51	0.56
1:A:2476:C:H2'	1:A:2477:G:H8	1.70	0.56
4:D:203:ARG:NH1	4:D:226:GLU:OE2	2.37	0.56
34:i:19:CYS:SG	34:i:39:TYR:HB2	2.45	0.56
39:n:112:ASP:OD2	39:n:156:ASN:ND2	2.38	0.56
15:P:122:VAL:O	15:P:248:ARG:NH2	2.39	0.56
21:V:58:GLU:HG2	21:V:63:VAL:HG22	1.87	0.56
1:A:804:C:OP1	4:D:98:ARG:NH2	2.33	0.56
1:A:2898:G:H1'	43:s:271:ILE:HG12	1.88	0.56
1:A:2185:G:O2'	1:A:2314:U:OP2	2.23	0.56
4:D:328:ASN:OD1	27:b:48:ASN:ND2	2.38	0.56
7:G:8:LYS:O	7:G:9:TRP:CG	2.59	0.56
25:Z:67:ARG:NH2	48:y:97:A:OP1	2.38	0.56
1:A:1907:C:O2	3:C:240:ARG:NH2	2.37	0.56
18:S:32:SER:H	18:S:36:ILE:HD11	1.69	0.56
1:A:2841:G:N2	1:A:2847:A:N6	2.54	0.56
1:A:3185:U:HO2'	18:S:170:THR:HG1	1.50	0.56
7:G:68:PRO:HB2	7:G:71:VAL:CG2	2.35	0.56
18:S:8:GLN:HE21	18:S:26:ARG:HE	1.54	0.56
1:A:2401:A:N6	44:u:382:ASN:O	2.38	0.55
1:A:3378:C:O2'	3:C:312:VAL:O	2.19	0.55
39:n:36:SER:HA	39:n:39:GLU:HG2	1.87	0.55
40:o:163:ARG:HH11	46:w:104:TRP:HD1	1.53	0.55
1:A:2948:C:OP1	3:C:244:ARG:NH1	2.39	0.55
1:A:268:A:OP1	14:O:50:ARG:NH1	2.39	0.55
29:d:55:LEU:HB2	29:d:95:PRO:HD3	1.87	0.55
1:A:718:G:OP1	13:N:117:ARG:NH2	2.40	0.55
1:A:3324:C:OP1	29:d:19:ARG:NH1	2.34	0.55
32:g:29:ILE:HD11	32:g:31:ARG:HH21	1.70	0.55
39:n:219:GLU:OE2	43:s:236:ARG:NH1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:A:N3	1:A:352:A:O2'	2.39	0.55
21:V:51:GLY:O	44:u:185:ARG:NH2	2.39	0.55
42:r:347:SER:HB2	42:r:349:LYS:HG2	1.87	0.55
46:w:71:TRP:N	46:w:71:TRP:CE3	2.73	0.55
1:A:728:G:H5''	16:Q:43:PRO:HB2	1.89	0.55
1:A:2258:U:C5	40:o:193:ARG:NE	2.71	0.55
6:F:20:ILE:HB	12:M:7:VAL:HG13	1.89	0.55
1:A:1874:A:N7	17:R:20:ARG:NH1	2.55	0.55
1:A:2157:G:N7	2:B:152:SER:OG	2.40	0.55
32:g:79:SER:OG	32:g:80:ARG:NH1	2.39	0.55
39:n:11:ASN:ND2	39:n:209:ASP:OD2	2.40	0.55
45:v:46:PRO:HB2	45:v:54:LEU:HD22	1.89	0.55
28:c:16:LEU:HD11	28:c:97:ASP:HB3	1.89	0.55
1:A:1940:G:H21	1:A:3362:A:H8	1.54	0.54
1:A:1348:U:OP2	16:Q:38:ARG:NH2	2.36	0.54
1:A:799:G:O2'	10:K:18:TRP:NE1	2.30	0.54
1:A:938:C:OP2	13:N:26:ARG:NH1	2.41	0.54
21:V:98:THR:OG1	21:V:104:ARG:NH1	2.40	0.54
27:b:229:PHE:CD1	27:b:229:PHE:C	2.86	0.54
6:F:134:ILE:HG12	6:F:146:LEU:HD23	1.90	0.54
37:l:36:PHE:O	37:l:41:ARG:NH1	2.40	0.54
3:C:53:MET:HG2	3:C:77:THR:HG22	1.89	0.54
39:n:95:GLN:HG2	39:n:128:LEU:HD11	1.89	0.54
42:r:363:ASP:HB2	42:r:366:GLN:HE22	1.72	0.54
5:E:137:ARG:NH2	47:x:44:C:OP2	2.40	0.54
18:S:77:VAL:HG11	18:S:106:LEU:HD22	1.90	0.54
1:A:2988:C:O2	3:C:266:ARG:NH1	2.41	0.54
14:O:68:ARG:NH1	14:O:124:ASP:O	2.41	0.54
10:K:64:LYS:O	10:K:67:ARG:NH1	2.40	0.54
15:P:116:ASP:OD1	15:P:116:ASP:N	2.39	0.54
1:A:439:C:O3'	1:A:494:G:N2	2.41	0.54
1:A:1006:A:H2'	1:A:1007:U:H4'	1.90	0.54
46:w:64:PHE:CD1	46:w:64:PHE:N	2.72	0.54
1:A:1721:U:OP2	17:R:124:TYR:OH	2.25	0.54
1:A:266:A:N6	33:h:29:LYS:O	2.41	0.53
1:A:1348:U:H4'	1:A:1349:G:H21	1.73	0.53
1:A:1765:U:OP2	42:r:376:ARG:NH2	2.41	0.53
15:P:152:ARG:HD3	47:x:44:C:H4'	1.90	0.53
39:n:71:LEU:HD21	39:n:132:VAL:HG11	1.90	0.53
40:o:179:THR:HA	40:o:399:ASN:HD21	1.72	0.53
1:A:1563:C:N3	1:A:1577:G:N2	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:l:38:GLN:OE1	37:l:41:ARG:NH2	2.41	0.53
39:n:213:PRO:HB2	46:w:20:CYS:HA	1.90	0.53
40:o:163:ARG:HH11	46:w:104:TRP:CD1	2.26	0.53
40:o:479:ASP:OD1	40:o:479:ASP:N	2.38	0.53
6:F:87:LYS:HB2	6:F:187:ILE:HG23	1.89	0.53
8:H:162:LEU:HD23	14:O:7:LEU:HD11	1.91	0.53
31:f:56:SER:O	31:f:63:LYS:NZ	2.41	0.53
34:i:29:VAL:O	34:i:32:LYS:NZ	2.41	0.53
35:j:23:ALA:HB3	35:j:75:VAL:HG22	1.91	0.53
45:v:45:ASN:HB3	45:v:48:ARG:HG2	1.90	0.53
1:A:2198:A:O2'	1:A:2269:U:O2'	2.19	0.53
3:C:41:VAL:HA	3:C:185:GLY:HA3	1.90	0.53
24:Y:115:LYS:NZ	24:Y:119:GLU:OE2	2.42	0.53
40:o:375:GLN:NE2	40:o:376:THR:O	2.41	0.53
1:A:2424:A:OP1	14:O:90:ASN:ND2	2.41	0.53
19:T:136:ARG:HD2	19:T:139:ARG:HH12	1.73	0.53
1:A:1119:C:H2'	1:A:1120:A:H8	1.73	0.53
46:w:105:THR:HG21	46:w:111:ARG:HB2	1.91	0.53
1:A:2470:C:OP1	41:p:20:UNK:N	2.41	0.53
42:r:237:GLY:H	42:r:326:LEU:HD23	1.73	0.53
1:A:86:G:O2'	1:A:98:G:O6	2.24	0.53
15:P:211:LEU:HB3	15:P:219:PHE:HB2	1.90	0.53
40:o:169:LEU:O	40:o:172:SER:HB2	2.09	0.53
1:A:1018:G:H2'	1:A:1019:G:H8	1.73	0.52
1:A:1779:C:N4	1:A:2102:U:OP2	2.42	0.52
1:A:1835:A:OP1	32:g:10:ARG:NH2	2.42	0.52
1:A:2307:G:O2'	1:A:2310:U:OP2	2.27	0.52
5:E:137:ARG:NH1	47:x:28:C:OP1	2.41	0.52
10:K:27:ASP:HB3	48:y:29:U:H5''	1.91	0.52
39:n:116:LEU:CD2	39:n:142:ILE:CD1	2.88	0.52
42:r:324:ALA:HB1	42:r:498:LEU:HB3	1.91	0.52
1:A:168:U:O2'	10:K:128:ARG:NH1	2.42	0.52
7:G:43:LEU:HD11	7:G:85:ILE:HG13	1.91	0.52
31:f:54:ARG:HD3	31:f:64:ILE:HG22	1.91	0.52
1:A:1307:G:OP1	9:J:59:LYS:NZ	2.42	0.52
1:A:364:G:OP2	34:i:52:LYS:NZ	2.35	0.52
29:d:51:LEU:HB3	29:d:55:LEU:HD23	1.92	0.52
46:w:98:VAL:O	46:w:117:THR:OG1	2.27	0.52
46:w:217:VAL:HG23	46:w:218:VAL:HG23	1.90	0.52
1:A:1874:A:H5''	17:R:18:GLY:HA3	1.91	0.52
2:B:184:ARG:NH2	38:m:14:TYR:OH	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:28:VAL:HG22	6:F:33:THR:HG23	1.92	0.52
14:O:96:ARG:NH1	14:O:104:GLU:OE1	2.39	0.52
1:A:3348:G:O6	1:A:3357:U:O2	2.26	0.52
35:j:32:ASN:OD1	35:j:36:LYS:N	2.43	0.52
1:A:286:U:O2'	14:O:179:LYS:O	2.27	0.52
1:A:1436:U:H5''	1:A:1437:C:H5''	1.92	0.52
44:u:359:GLN:HA	44:u:362:VAL:HG12	1.91	0.52
1:A:1229:G:H2'	1:A:1230:G:H8	1.75	0.52
1:A:2557:A:OP1	2:B:69:TYR:OH	2.28	0.52
1:A:3018:C:OP1	39:n:9:ASN:ND2	2.38	0.52
6:F:124:ARG:NH1	6:F:164:ILE:O	2.42	0.52
38:m:38:ASP:N	38:m:38:ASP:OD1	2.43	0.52
42:r:52:SER:OG	42:r:53:LYS:N	2.42	0.52
42:r:316:VAL:HG22	42:r:508:VAL:HG22	1.92	0.52
46:w:65:LEU:HD13	46:w:71:TRP:CZ2	2.45	0.52
1:A:148:G:OP2	14:O:4:TYR:OH	2.27	0.52
1:A:1101:G:OP2	27:b:196:LYS:NZ	2.42	0.52
1:A:2180:G:OP1	2:B:174:ARG:NH2	2.43	0.52
3:C:150:ARG:NH1	3:C:154:TYR:OH	2.42	0.52
4:D:220:ARG:NH1	23:X:4:GLN:OE1	2.43	0.52
14:O:5:LYS:NZ	14:O:8:GLU:OE2	2.42	0.52
7:G:114:LYS:O	7:G:117:LYS:NZ	2.38	0.52
40:o:205:VAL:HG23	40:o:235:VAL:HG13	1.91	0.52
42:r:25:LEU:HB3	42:r:29:ARG:HH11	1.75	0.52
44:u:230:VAL:O	44:u:234:MET:HG2	2.09	0.52
1:A:1381:A:OP1	4:D:188:ARG:NH1	2.43	0.51
4:D:237:GLN:O	4:D:246:ARG:NH1	2.42	0.51
40:o:465:ALA:HB3	40:o:478:ALA:HB1	1.92	0.51
42:r:378:LEU:HD21	42:r:392:LEU:HD22	1.92	0.51
47:x:72:A:O2'	47:x:74:C:OP2	2.28	0.51
1:A:964:G:OP2	1:A:1115:G:N1	2.42	0.51
1:A:836:A:P	38:m:4:ARG:HD2	2.51	0.51
1:A:2449:A:N6	1:A:2496:C:O2'	2.44	0.51
6:F:18:VAL:HG22	6:F:27:VAL:HG22	1.91	0.51
39:n:116:LEU:HD23	39:n:142:ILE:CD1	2.33	0.51
1:A:714:G:HO2'	1:A:753:C:HO2'	1.56	0.51
20:U:122:ALA:HB3	20:U:143:PRO:HB2	1.92	0.51
40:o:222:VAL:HG21	40:o:231:ASN:HB3	1.92	0.51
42:r:183:ALA:HB2	42:r:325:SER:HB3	1.91	0.51
42:r:475:LEU:HD12	42:r:478:LEU:HD13	1.92	0.51
2:B:246:LEU:HD23	2:B:247:ARG:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:178:ALA:HB2	8:H:218:ILE:HD12	1.93	0.51
42:r:270:THR:O	42:r:274:GLN:HB2	2.10	0.51
1:A:640:U:OP1	13:N:21:ARG:NH1	2.33	0.51
1:A:1203:A:N3	1:A:2855:U:O2'	2.41	0.51
1:A:2981:U:OP2	3:C:244:ARG:NH2	2.44	0.51
1:A:3037:U:H5''	3:C:349:LYS:HE3	1.93	0.51
23:X:87:LYS:HB2	23:X:97:ILE:HD11	1.92	0.51
35:j:20:VAL:HG12	35:j:47:GLY:HA2	1.93	0.51
1:A:431:U:OP1	31:f:65:ARG:NH1	2.43	0.51
1:A:1239:C:O2	1:A:1250:G:N2	2.38	0.51
1:A:2548:C:O2'	1:A:2549:G:N2	2.44	0.51
1:A:3267:A:N7	7:G:69:PHE:HE1	2.09	0.51
3:C:115:LYS:NZ	3:C:129:ALA:O	2.42	0.51
8:H:207:ASP:OD1	8:H:207:ASP:N	2.41	0.51
1:A:2116:G:OP1	1:A:2118:C:N4	2.43	0.51
8:H:156:ASP:HB2	8:H:183:LYS:HG3	1.93	0.51
15:P:107:ARG:NH2	15:P:119:TYR:O	2.43	0.51
19:T:68:THR:OG1	19:T:69:LYS:N	2.44	0.51
42:r:76:LEU:HG	42:r:87:ARG:HD3	1.93	0.51
1:A:2484:A:O2'	1:A:2485:A:O4'	2.29	0.51
14:O:110:ALA:HB1	14:O:113:LEU:HD12	1.92	0.51
2:B:36:GLU:OE2	2:B:163:ARG:NH1	2.44	0.51
3:C:36:ASP:OD2	3:C:39:LYS:NZ	2.44	0.51
9:J:33:VAL:HG12	9:J:102:LYS:HB2	1.92	0.51
18:S:31:ALA:HB1	18:S:36:ILE:HG13	1.92	0.51
30:e:7:PRO:HD2	30:e:63:THR:HG22	1.93	0.51
31:f:52:VAL:HG22	31:f:66:VAL:HG22	1.93	0.51
1:A:1268:G:O2'	1:A:1269:U:O2	2.29	0.50
1:A:2359:C:H4'	1:A:2399:A:H4'	1.92	0.50
1:A:2675:C:N4	5:E:22:SER:OG	2.44	0.50
2:B:130:SER:OG	2:B:174:ARG:NH1	2.45	0.50
34:i:39:TYR:CD1	34:i:39:TYR:C	2.87	0.50
2:B:107:VAL:HB	2:B:111:THR:HG21	1.94	0.50
1:A:2953:U:H2'	1:A:2954:U:H2'	1.93	0.50
18:S:115:ARG:O	18:S:117:ARG:NH2	2.44	0.50
42:r:268:VAL:O	42:r:273:HIS:NE2	2.37	0.50
1:A:1231:A:H5''	1:A:1232:C:H5'	1.92	0.50
15:P:218:ARG:NH1	47:x:32:U:O5'	2.45	0.50
1:A:1257:C:H42	1:A:1261:G:H22	1.59	0.50
6:F:103:ILE:HG23	6:F:112:ILE:HG22	1.93	0.50
16:Q:83:VAL:HG12	16:Q:85:GLY:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:74:ARG:HG3	29:d:94:GLU:HG3	1.94	0.50
34:i:13:ASN:OD1	34:i:13:ASN:N	2.45	0.50
1:A:3214:U:O4	12:M:124:ARG:NH1	2.44	0.50
3:C:18:PRO:O	3:C:20:LYS:HG2	2.10	0.50
9:J:40:LEU:HD11	9:J:79:LEU:HD22	1.93	0.50
11:L:72:LYS:NZ	46:w:121:GLU:OE2	2.45	0.50
13:N:130:VAL:HG21	13:N:145:VAL:HG11	1.92	0.50
42:r:333:GLY:H	42:r:442:TRP:HE1	1.59	0.50
42:r:338:GLU:HG3	42:r:441:ARG:HD3	1.94	0.50
9:J:42:ILE:HG23	9:J:135:THR:HB	1.92	0.50
9:J:188:ASP:OD1	9:J:188:ASP:N	2.44	0.50
10:K:157:ARG:NH1	13:N:146:GLU:OE1	2.41	0.50
11:L:63:LYS:HD2	40:o:475:TYR:HB2	1.94	0.50
1:A:268:A:O2'	14:O:14:LYS:NZ	2.45	0.49
1:A:2499:U:H2'	1:A:2500:A:C8	2.47	0.49
1:A:2832:C:H2'	1:A:2833:A:H8	1.76	0.49
2:B:177:LYS:HE3	38:m:26:VAL:HG13	1.94	0.49
40:o:403:LEU:HA	40:o:423:LEU:HD21	1.93	0.49
1:A:2137:U:OP2	1:A:2142:A:N6	2.36	0.49
1:A:3092:C:O2'	1:A:3094:A:OP2	2.26	0.49
16:Q:120:GLU:OE2	16:Q:130:ARG:NH1	2.43	0.49
40:o:508:ASP:OD1	40:o:508:ASP:N	2.45	0.49
1:A:1094:U:OP2	19:T:116:ARG:NH2	2.43	0.49
1:A:3109:G:N2	6:F:156:GLN:OE1	2.45	0.49
19:T:112:ASN:HA	19:T:115:LYS:HG2	1.95	0.49
23:X:84:LYS:HZ1	42:r:450:LYS:HG2	1.78	0.49
40:o:462:VAL:HG23	40:o:478:ALA:HB3	1.94	0.49
42:r:101:SER:O	42:r:502:ARG:NH1	2.45	0.49
1:A:651:G:O2'	1:A:1435:A:OP1	2.29	0.49
13:N:93:SER:OG	13:N:96:LYS:NZ	2.45	0.49
40:o:150:GLN:HA	40:o:153:ARG:HB2	1.94	0.49
44:u:197:LEU:HD21	44:u:200:LYS:HD2	1.95	0.49
1:A:2816:G:C6	1:A:2820:A:N7	2.81	0.49
3:C:348:ARG:HA	3:C:351:LEU:HB2	1.93	0.49
1:A:824:C:O2'	1:A:1534:A:N3	2.43	0.49
5:E:97:SER:OG	5:E:101:ASN:OD1	2.25	0.49
42:r:157:THR:HG21	42:r:501:ALA:HB1	1.95	0.49
42:r:530:LYS:HB3	42:r:574:PRO:HG3	1.95	0.49
1:A:2526:C:OP1	2:B:37:ARG:NH1	2.42	0.49
2:B:140:ASN:ND2	2:B:143:GLU:OE2	2.45	0.49
1:A:268:A:N7	14:O:12:ARG:NH1	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1477:A:OP1	1:A:3075:G:O2'	2.27	0.49
1:A:2978:U:O4	44:u:388:ARG:NH2	2.45	0.49
1:A:3214:U:O2'	31:f:2:ALA:N	2.45	0.49
40:o:169:LEU:C	40:o:169:LEU:CD2	2.85	0.49
1:A:242:C:OP1	25:Z:115:LYS:NZ	2.44	0.49
1:A:1129:A:N3	1:A:2826:U:O2'	2.46	0.49
18:S:8:GLN:HB2	18:S:64:ILE:HD11	1.95	0.49
42:r:577:GLN:HG2	42:r:578:LYS:HE3	1.94	0.49
46:w:49:ILE:HG22	46:w:91:GLY:H	1.78	0.49
1:A:1255:C:H2'	1:A:1256:G:H8	1.77	0.49
1:A:1604:G:H4'	1:A:1835:A:H4'	1.95	0.49
7:G:55:LEU:HD11	7:G:66:SER:HB3	1.94	0.49
9:J:124:ARG:HG3	9:J:128:LEU:HD12	1.95	0.49
10:K:165:SER:OG	13:N:135:GLU:OE1	2.27	0.49
42:r:322:LYS:HE3	42:r:502:ARG:HD3	1.93	0.49
2:B:33:ASP:OD1	2:B:33:ASP:N	2.40	0.48
2:B:125:ALA:HA	2:B:128:ARG:HD2	1.95	0.48
18:S:12:ARG:NH1	18:S:57:GLU:OE2	2.44	0.48
34:i:4:GLY:O	34:i:8:PHE:CG	2.65	0.48
40:o:472:THR:OG1	40:o:475:TYR:O	2.31	0.48
1:A:1899:G:O2'	1:A:2334:U:O4	2.27	0.48
1:A:2442:G:N2	1:A:2505:U:O2	2.37	0.48
1:A:3050:U:O2'	45:v:16:GLY:O	2.30	0.48
3:C:10:ARG:HH21	3:C:14:LEU:HD21	1.77	0.48
13:N:93:SER:OG	13:N:94:ALA:N	2.43	0.48
34:i:84:SER:OG	34:i:85:LYS:N	2.44	0.48
1:A:160:G:O6	1:A:261:U:O4	2.31	0.48
1:A:3349:C:O2'	44:u:168:GLU:OE1	2.31	0.48
6:F:90:MET:HG2	6:F:181:VAL:HA	1.95	0.48
19:T:133:ALA:HB3	27:b:121:LYS:HB2	1.95	0.48
8:H:84:ARG:NH1	48:y:156:U:OP2	2.47	0.48
12:M:54:PRO:HG2	12:M:56:GLN:HE21	1.77	0.48
14:O:5:LYS:HG3	33:h:40:VAL:HG11	1.96	0.48
19:T:112:ASN:HB2	19:T:128:LEU:HD22	1.95	0.48
42:r:95:ILE:HG23	42:r:139:VAL:HG23	1.95	0.48
1:A:138:U:H2'	1:A:139:G:H8	1.79	0.48
1:A:1036:A:H2'	1:A:1037:C:H4'	1.95	0.48
23:X:31:LEU:HB3	23:X:101:PRO:HG2	1.94	0.48
1:A:1566:A:N7	1:A:1567:U:O2'	2.44	0.48
1:A:2566:C:N4	1:A:2576:G:O6	2.46	0.48
18:S:89:ASN:HD21	19:T:156:TYR:H	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:229:PHE:C	27:b:229:PHE:HD1	2.21	0.48
37:l:4:VAL:CG1	37:l:5:PRO:HD2	2.44	0.48
7:G:7:PRO:HD3	7:G:10:TYR:HH	1.74	0.48
38:m:7:LYS:O	38:m:8:VAL:C	2.57	0.48
43:s:301:LEU:HD21	43:s:320:LYS:HD3	1.95	0.48
1:A:712:G:H5'	10:K:174:ARG:HE	1.79	0.48
1:A:2193:U:H5''	1:A:2194:G:H5'	1.95	0.48
6:F:57:VAL:HG21	6:F:64:HIS:HB3	1.96	0.48
7:G:6:ALA:HB1	7:G:7:PRO:CD	2.43	0.48
23:X:55:GLU:HB3	23:X:108:LYS:HB3	1.96	0.48
42:r:368:HIS:HB2	42:r:431:LEU:HD21	1.96	0.48
46:w:157:ALA:HA	46:w:242:PHE:O	2.13	0.48
1:A:1949:G:N2	1:A:2097:U:O2	2.47	0.48
1:A:2732:G:H5'	1:A:2761:G:H5''	1.96	0.48
27:b:86:VAL:O	27:b:114:GLY:HA2	2.13	0.48
40:o:163:ARG:CD	46:w:104:TRP:HD1	2.25	0.48
46:w:79:ARG:HH12	46:w:83:ALA:HB2	1.79	0.48
46:w:322:ASP:HB3	46:w:339:THR:HB	1.96	0.48
1:A:1130:A:O2'	1:A:2825:C:O2'	2.28	0.47
1:A:1632:A:OP1	24:Y:48:ARG:NH2	2.47	0.47
3:C:159:ARG:HG2	3:C:182:GLN:HA	1.96	0.47
33:h:12:ASN:OD1	33:h:12:ASN:N	2.45	0.47
43:s:285:ILE:HD13	43:s:336:LEU:HD22	1.95	0.47
1:A:3329:U:H5''	3:C:308:MET:HE2	1.96	0.47
5:E:79:ILE:HA	5:E:82:ARG:HG2	1.96	0.47
14:O:192:LYS:O	14:O:196:THR:OG1	2.32	0.47
39:n:76:THR:O	39:n:96:ARG:NH2	2.47	0.47
18:S:80:ARG:HH11	18:S:87:THR:HG21	1.79	0.47
1:A:182:U:H2'	1:A:183:G:H8	1.79	0.47
8:H:100:GLU:HB2	8:H:104:GLU:HB2	1.96	0.47
39:n:118:HIS:HE1	39:n:146:ILE:HD12	1.78	0.47
1:A:2568:C:O3'	1:A:2573:G:N2	2.48	0.47
1:A:3333:G:N2	1:A:3369:G:O2'	2.47	0.47
3:C:236:LYS:HB2	3:C:236:LYS:HE2	1.75	0.47
39:n:53:ILE:O	39:n:56:THR:OG1	2.32	0.47
44:u:205:LYS:HD2	44:u:205:LYS:HA	1.76	0.47
46:w:355:VAL:HG21	46:w:397:LEU:HD13	1.97	0.47
1:A:1717:U:H2'	1:A:1718:G:C8	2.49	0.47
2:B:134:VAL:HG12	2:B:151:PRO:HD3	1.97	0.47
5:E:93:ASP:HB2	5:E:173:ASP:HA	1.97	0.47
5:E:132:ASN:HA	5:E:154:THR:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:22:PRO:HB2	21:V:28:PHE:HB2	1.97	0.47
31:f:20:LYS:HG2	31:f:21:ARG:HG3	1.97	0.47
40:o:465:ALA:HB2	40:o:483:ALA:HB2	1.96	0.47
42:r:370:LEU:HD23	42:r:429:ASN:HD22	1.79	0.47
1:A:172:G:H2'	1:A:173:G:H8	1.80	0.47
1:A:655:C:H2'	1:A:656:A:C8	2.50	0.47
1:A:2373:A:N1	1:A:2867:C:O2'	2.35	0.47
1:A:2458:A:H3'	1:A:2459:A:H8	1.80	0.47
1:A:3068:U:OP2	17:R:62:ARG:NH2	2.41	0.47
3:C:10:ARG:NH2	3:C:263:SER:O	2.48	0.47
5:E:21:ILE:HD11	5:E:125:MET:HE2	1.97	0.47
14:O:35:VAL:O	14:O:64:VAL:HA	2.14	0.47
22:W:27:ARG:NH2	48:y:150:G:OP1	2.48	0.47
42:r:151:THR:HG1	42:r:388:TYR:HH	1.62	0.47
46:w:93:THR:HG23	46:w:94:LYS:HG3	1.96	0.47
1:A:63:A:H5''	14:O:174:ILE:HG21	1.97	0.47
1:A:815:G:OP1	34:i:16:HIS:NE2	2.45	0.47
1:A:1110:U:OP1	16:Q:164:ARG:NH2	2.39	0.47
1:A:1420:C:OP2	4:D:193:LYS:NZ	2.40	0.47
39:n:59:ILE:O	39:n:63:THR:OG1	2.32	0.47
39:n:107:VAL:HG23	39:n:108:ILE:HG13	1.97	0.47
1:A:1389:G:OP1	30:e:104:ASN:ND2	2.47	0.47
1:A:1661:G:H2'	1:A:1662:G:C8	2.49	0.47
1:A:2403:G:H22	1:A:2874:G:H1'	1.80	0.47
3:C:86:VAL:HG22	3:C:162:VAL:HG12	1.97	0.47
4:D:292:SER:OG	4:D:293:SER:N	2.47	0.47
29:d:36:ILE:HD12	29:d:59:ILE:HD11	1.97	0.47
34:i:20:ASN:OD1	36:k:8:ARG:NH1	2.47	0.47
44:u:220:CYS:HB3	44:u:222:TYR:H	1.79	0.47
44:u:247:GLU:HA	44:u:250:ARG:HB2	1.97	0.47
1:A:2295:A:N3	1:A:2929:C:O2'	2.45	0.47
1:A:3140:G:N7	3:C:28:ARG:NH2	2.63	0.47
5:E:23:VAL:HG12	5:E:25:GLU:HG3	1.96	0.47
15:P:39:GLN:HG3	15:P:48:LYS:HD2	1.96	0.47
16:Q:66:ARG:HH22	16:Q:143:PRO:HD3	1.80	0.47
48:y:70:G:O2'	48:y:87:G:N2	2.48	0.47
1:A:370:U:H4'	1:A:404:G:H5'	1.97	0.46
1:A:1155:C:OP2	27:b:94:LYS:NZ	2.48	0.46
1:A:1493:G:O6	36:k:2:ALA:N	2.48	0.46
1:A:2454:G:N2	1:A:2456:A:N3	2.62	0.46
1:A:2841:G:H21	1:A:2847:A:N6	2.12	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:41:ASP:OD1	16:Q:41:ASP:N	2.46	0.46
40:o:211:LEU:HD23	40:o:249:TRP:HH2	1.80	0.46
46:w:96:ARG:O	46:w:97:LEU:HG	2.14	0.46
1:A:170:G:N2	1:A:171:G:N3	2.63	0.46
9:J:11:LYS:HD3	9:J:36:ARG:HH11	1.80	0.46
37:l:25:VAL:HG12	37:l:72:LEU:HG	1.97	0.46
1:A:2455:U:O4	1:A:2482:U:O2'	2.33	0.46
1:A:2468:A:N6	1:A:2477:G:O2'	2.48	0.46
1:A:2487:U:H3'	1:A:2489:C:H41	1.80	0.46
3:C:17:LEU:HD23	3:C:17:LEU:HA	1.67	0.46
34:i:39:TYR:CD1	34:i:39:TYR:O	2.68	0.46
35:j:31:LEU:HB2	35:j:35:GLY:HA2	1.97	0.46
1:A:3313:U:H4'	3:C:173:GLN:HG3	1.97	0.46
4:D:269:SER:OG	4:D:274:TYR:O	2.33	0.46
8:H:181:LYS:HD3	48:y:154:C:H5''	1.97	0.46
41:p:28:UNK:O	41:p:159:UNK:N	2.48	0.46
3:C:360:ASP:OD2	3:C:364:LYS:NZ	2.48	0.46
4:D:3:ARG:NH2	4:D:23:PRO:O	2.48	0.46
10:K:122:LYS:HD3	25:Z:120:ALA:HB2	1.98	0.46
1:A:67:A:N6	1:A:271:C:O2'	2.48	0.46
1:A:187:A:N3	1:A:208:C:O2'	2.41	0.46
1:A:578:A:O2'	4:D:331:ALA:O	2.33	0.46
1:A:1724:U:O4	17:R:125:LYS:NZ	2.49	0.46
1:A:2389:C:O2'	1:A:3307:A:N1	2.45	0.46
1:A:2703:A:N6	15:P:28:THR:O	2.48	0.46
3:C:59:ASP:HA	3:C:71:GLU:HA	1.96	0.46
9:J:157:ASP:OD1	9:J:157:ASP:N	2.48	0.46
23:X:101:PRO:HA	23:X:104:LEU:HD12	1.98	0.46
40:o:338:ASN:HD21	40:o:386:CYS:HB3	1.80	0.46
44:u:215:ASN:O	44:u:223:GLN:NE2	2.49	0.46
1:A:1578:C:OP1	8:H:43:LYS:NZ	2.38	0.46
1:A:2268:U:O4	1:A:2272:G:O6	2.34	0.46
5:E:47:GLN:HG3	5:E:67:VAL:HG22	1.98	0.46
7:G:172:HIS:CD2	7:G:173:MET:HG3	2.51	0.46
11:L:136:VAL:H	39:n:102:SER:HB3	1.80	0.46
21:V:25:ASN:HD22	21:V:107:PHE:HE2	1.63	0.46
21:V:94:ARG:HD2	21:V:108:TYR:HE1	1.81	0.46
39:n:140:GLN:HE21	39:n:140:GLN:HB2	1.45	0.46
41:p:27:UNK:HA	41:p:160:UNK:HA	1.97	0.46
42:r:262:ARG:NH2	44:u:338:THR:O	2.46	0.46
1:A:1229:G:H2'	1:A:1230:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1349:G:N2	1:A:1350:A:N3	2.64	0.46
1:A:1481:A:O2'	1:A:1859:A:OP2	2.33	0.46
1:A:3341:U:H1'	44:u:225:ARG:HH22	1.81	0.46
6:F:90:MET:O	6:F:143:GLU:HA	2.16	0.46
38:m:7:LYS:O	38:m:9:GLY:N	2.49	0.46
42:r:262:ARG:HD3	44:u:342:ALA:HB3	1.97	0.46
39:n:69:GLY:HA2	39:n:93:LYS:H	1.81	0.46
1:A:1119:C:H2'	1:A:1120:A:C8	2.50	0.46
6:F:112:ILE:HD11	6:F:161:LEU:HD11	1.98	0.46
11:L:54:LEU:HD23	11:L:121:GLU:HB2	1.98	0.46
15:P:64:ILE:HD12	15:P:144:VAL:HG11	1.97	0.46
16:Q:123:THR:OG1	16:Q:125:ASP:OD1	2.30	0.46
34:i:3:LYS:H	34:i:3:LYS:HG3	1.62	0.46
1:A:2815:G:N7	1:A:2870:C:O2'	2.45	0.45
1:A:3267:A:N6	7:G:69:PHE:O	2.49	0.45
3:C:211:GLN:NE2	3:C:283:TYR:O	2.50	0.45
35:j:7:ASP:OD2	35:j:10:GLN:N	2.46	0.45
39:n:116:LEU:HD13	39:n:177:LEU:HD21	1.98	0.45
1:A:1646:G:O2'	1:A:1808:G:N2	2.38	0.45
4:D:112:LYS:HE2	4:D:112:LYS:HB3	1.81	0.45
7:G:66:SER:HB2	7:G:76:LEU:HD23	1.98	0.45
15:P:265:TYR:OH	47:x:121:U:OP2	2.29	0.45
28:c:16:LEU:HD21	28:c:97:ASP:H	1.81	0.45
43:s:244:SER:OG	43:s:245:PHE:N	2.50	0.45
1:A:269:G:OP2	14:O:44:ARG:NH2	2.35	0.45
1:A:538:G:H1	1:A:553:U:H3	1.65	0.45
1:A:2768:U:H2'	1:A:2769:A:H8	1.82	0.45
40:o:357:VAL:HB	40:o:379:LEU:HD22	1.97	0.45
1:A:129:U:H2'	1:A:130:A:C8	2.51	0.45
4:D:113:VAL:HB	4:D:118:LYS:HD2	1.98	0.45
12:M:55:ARG:NH2	12:M:76:ALA:O	2.47	0.45
14:O:203:ARG:HA	14:O:203:ARG:HD3	1.83	0.45
42:r:232:ARG:HA	42:r:232:ARG:HD2	1.71	0.45
1:A:1235:U:H4'	1:A:1236:G:H5'	1.98	0.45
1:A:2585:G:O6	8:H:47:SER:OG	2.33	0.45
1:A:2830:G:H2'	1:A:2831:G:H8	1.82	0.45
1:A:3048:A:OP2	3:C:222:LYS:NZ	2.45	0.45
15:P:60:ILE:HB	15:P:80:SER:HB3	1.97	0.45
30:e:6:HIS:ND1	30:e:6:HIS:C	2.73	0.45
1:A:412:G:OP1	20:U:62:ARG:NH1	2.48	0.45
1:A:655:C:H2'	1:A:656:A:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2815:G:H21	1:A:2818:U:H3	1.64	0.45
18:S:170:THR:O	18:S:170:THR:OG1	2.34	0.45
24:Y:25:ILE:HA	24:Y:43:VAL:HG23	1.99	0.45
39:n:140:GLN:O	39:n:140:GLN:HG3	2.15	0.45
42:r:135:PRO:HB3	42:r:162:PRO:HD3	1.98	0.45
42:r:139:VAL:HG13	42:r:158:MET:HG3	1.99	0.45
43:s:281:SER:O	43:s:281:SER:OG	2.31	0.45
1:A:2945:G:O2'	1:A:2948:C:OP2	2.27	0.45
1:A:3303:G:O2'	1:A:3305:A:N6	2.50	0.45
4:D:99:MET:HE2	4:D:102:PRO:HA	1.98	0.45
6:F:107:ASP:OD1	6:F:107:ASP:N	2.49	0.45
42:r:362:ARG:NH2	42:r:363:ASP:O	2.49	0.45
42:r:453:ASN:ND2	42:r:479:GLY:O	2.49	0.45
1:A:2176:U:OP1	2:B:54:ARG:NH2	2.41	0.45
15:P:144:VAL:HG23	15:P:173:VAL:HG22	1.98	0.45
20:U:49:GLU:HG2	20:U:92:GLN:HE22	1.82	0.45
1:A:1521:G:O6	36:k:17:LYS:NZ	2.49	0.45
1:A:2856:G:N2	1:A:2857:C:N3	2.65	0.45
15:P:50:ARG:NH2	15:P:72:ASP:OD2	2.49	0.45
18:S:27:MET:HE3	18:S:27:MET:HB3	1.89	0.45
27:b:163:LEU:HB3	27:b:169:ILE:HD11	1.99	0.45
43:s:304:LYS:HA	43:s:316:GLY:HA2	1.98	0.45
1:A:307:A:H2'	1:A:308:A:C8	2.52	0.45
1:A:1333:C:OP1	16:Q:2:GLY:N	2.50	0.45
3:C:80:ASP:OD2	3:C:314:TYR:OH	2.34	0.45
28:c:22:LYS:HB3	28:c:93:LEU:HD12	1.97	0.45
40:o:491:TYR:HA	40:o:496:LEU:HB2	1.99	0.45
46:w:229:ILE:HB	46:w:239:THR:HG23	1.98	0.45
1:A:371:G:N1	1:A:374:A:OP2	2.48	0.44
1:A:1914:G:O2'	17:R:82:LYS:O	2.28	0.44
1:A:3379:C:H4'	3:C:315:GLY:HA2	1.99	0.44
8:H:86:THR:O	8:H:90:THR:OG1	2.32	0.44
9:J:36:ARG:HH21	9:J:159:ARG:HH22	1.64	0.44
14:O:155:VAL:O	14:O:162:ARG:NH2	2.49	0.44
37:l:72:LEU:O	37:l:80:ARG:HA	2.16	0.44
40:o:468:ARG:HA	40:o:468:ARG:HD3	1.79	0.44
43:s:306:SER:HA	43:s:314:VAL:HG23	1.99	0.44
1:A:98:G:N7	10:K:13:HIS:NE2	2.65	0.44
1:A:3358:U:H2'	1:A:3359:A:H8	1.82	0.44
14:O:135:VAL:HG21	14:O:151:ILE:HG21	1.98	0.44
17:R:86:GLU:OE2	17:R:91:SER:OG	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:190:THR:O	27:b:190:THR:OG1	2.32	0.44
1:A:1194:G:H2'	1:A:1195:A:C8	2.51	0.44
20:U:119:VAL:HG12	20:U:146:ILE:HG23	1.98	0.44
34:i:39:TYR:N	34:i:40:PRO:CD	2.79	0.44
42:r:111:THR:HA	42:r:114:LEU:HB2	1.99	0.44
42:r:239:VAL:HB	42:r:322:LYS:HB2	2.00	0.44
42:r:246:ARG:HA	42:r:317:TYR:HA	1.99	0.44
42:r:331:LYS:HD3	42:r:331:LYS:HA	1.76	0.44
46:w:377:SER:OG	46:w:378:ASN:N	2.50	0.44
1:A:13:A:H4'	22:W:39:LYS:HG3	1.99	0.44
1:A:2344:U:H2'	1:A:2345:A:C8	2.53	0.44
1:A:2832:C:H2'	1:A:2833:A:C8	2.52	0.44
1:A:3154:C:H4'	1:A:3155:U:H5'	2.00	0.44
6:F:60:GLY:HA3	6:F:64:HIS:HB2	1.99	0.44
19:T:67:VAL:HG13	19:T:72:VAL:HG12	1.99	0.44
25:Z:77:PRO:HD2	25:Z:80:LEU:HD12	1.99	0.44
1:A:76:G:N7	10:K:101:ARG:HB3	2.33	0.44
1:A:2574:G:H2'	1:A:2575:G:C8	2.53	0.44
1:A:2724:U:OP1	19:T:78:LYS:NZ	2.51	0.44
33:h:16:LYS:H	33:h:16:LYS:HG2	1.64	0.44
1:A:353:G:O6	34:i:55:ARG:NH2	2.51	0.44
4:D:61:SER:O	4:D:61:SER:OG	2.35	0.44
4:D:82:THR:HG23	4:D:84:ARG:H	1.82	0.44
39:n:53:ILE:HD13	39:n:63:THR:HG23	1.99	0.44
44:u:327:LYS:HD2	44:u:327:LYS:HA	1.82	0.44
46:w:44:ASP:OD1	46:w:44:ASP:N	2.51	0.44
1:A:1601:U:OP2	17:R:42:ARG:NH2	2.51	0.44
1:A:2356:A:H61	1:A:2983:C:H5	1.65	0.44
1:A:2810:C:OP2	1:A:2955:U:O2'	2.35	0.44
23:X:74:TYR:OH	48:y:75:G:OP2	2.35	0.44
25:Z:49:LYS:HD2	48:y:64:U:H5'	2.00	0.44
37:l:61:LYS:HB3	37:l:61:LYS:HE2	1.78	0.44
39:n:143:SER:C	39:n:145:ASN:H	2.25	0.44
40:o:164:ARG:CD	46:w:104:TRP:CZ2	3.01	0.44
1:A:22:G:H5''	34:i:43:LYS:HG2	2.00	0.44
1:A:1863:G:N1	1:A:1866:C:OP2	2.32	0.44
42:r:519:ARG:HH12	42:r:567:LEU:HA	1.82	0.44
44:u:180:LEU:HD21	44:u:204:VAL:HG11	2.00	0.44
1:A:69:C:OP1	14:O:178:HIS:ND1	2.35	0.44
1:A:3049:A:H4'	3:C:364:LYS:HD2	1.99	0.44
1:A:3344:A:N6	1:A:3361:G:O2'	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:105:LEU:HD23	17:R:138:LEU:HD23	1.99	0.44
24:Y:33:SER:OG	24:Y:34:LYS:N	2.51	0.44
33:h:66:GLU:OE2	33:h:91:ASN:ND2	2.37	0.44
38:m:36:ARG:HG2	38:m:48:LYS:HD3	2.00	0.44
40:o:179:THR:CG2	40:o:396:PHE:HA	2.47	0.44
46:w:66:GLN:HE21	46:w:66:GLN:HB2	1.55	0.44
1:A:2149:A:N6	1:A:2187:G:O2'	2.46	0.43
16:Q:54:LEU:HB3	16:Q:58:ASN:HB2	2.01	0.43
18:S:52:LYS:H	18:S:55:SER:HB2	1.83	0.43
27:b:112:ASN:ND2	27:b:209:ASN:OD1	2.50	0.43
37:l:28:TYR:HB3	37:l:69:VAL:HB	1.99	0.43
39:n:11:ASN:HB3	39:n:207:GLY:HA3	1.99	0.43
39:n:20:THR:OG1	39:n:21:ASN:N	2.50	0.43
46:w:154:THR:HG23	46:w:156:ARG:HH22	1.83	0.43
1:A:179:C:H2'	1:A:180:C:H6	1.83	0.43
1:A:229:G:H5''	23:X:4:GLN:HG2	2.00	0.43
1:A:1696:A:H2'	1:A:1697:A:C8	2.53	0.43
5:E:109:HIS:HE1	5:E:122:ILE:HA	1.83	0.43
10:K:132:ALA:HB3	25:Z:115:LYS:HD3	2.00	0.43
18:S:23:LYS:HE2	47:x:73:C:H42	1.82	0.43
41:p:41:UNK:O	41:p:43:UNK:N	2.52	0.43
42:r:366:GLN:HE21	42:r:431:LEU:HA	1.83	0.43
1:A:627:U:H2'	1:A:628:A:C8	2.52	0.43
1:A:2150:G:O2'	1:A:2189:U:OP1	2.30	0.43
11:L:135:VAL:HG11	45:v:26:SER:HB3	2.00	0.43
29:d:13:THR:OG1	29:d:72:ARG:NH2	2.46	0.43
42:r:34:ILE:HD12	42:r:145:VAL:HG11	2.00	0.43
44:u:217:CYS:SG	44:u:220:CYS:HB2	2.58	0.43
1:A:3279:A:N6	31:f:54:ARG:HE	2.16	0.43
7:G:128:LYS:HE3	7:G:128:LYS:HB3	1.91	0.43
12:M:15:VAL:HG23	12:M:35:ILE:HD13	2.00	0.43
46:w:159:VAL:HG12	46:w:244:TYR:HB2	2.00	0.43
46:w:188:ILE:HD11	46:w:202:ALA:HB2	1.99	0.43
1:A:664:U:H5'	4:D:107:ARG:HA	1.99	0.43
1:A:1018:G:H2'	1:A:1019:G:C8	2.52	0.43
7:G:129:GLU:HB3	7:G:131:LYS:HE2	2.00	0.43
39:n:13:ILE:O	39:n:17:SER:OG	2.33	0.43
46:w:315:LEU:HB3	46:w:370:MET:HG2	1.99	0.43
47:x:12:U:OP2	47:x:68:C:O2'	2.35	0.43
1:A:2516:U:OP1	14:O:31:ARG:NH1	2.52	0.43
2:B:181:LYS:HB2	2:B:184:ARG:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:10:ILE:HG13	6:F:72:LYS:HG2	2.00	0.43
15:P:275:THR:OG1	15:P:276:LYS:N	2.52	0.43
42:r:195:VAL:HG21	42:r:524:ARG:HD2	2.00	0.43
43:s:306:SER:OG	43:s:307:CYS:N	2.52	0.43
43:s:338:THR:HA	43:s:341:VAL:HB	2.00	0.43
1:A:831:G:O2'	1:A:1864:A:N3	2.47	0.43
8:H:90:THR:HG23	8:H:214:LEU:HD21	2.00	0.43
18:S:40:ARG:HD2	18:S:40:ARG:HA	1.72	0.43
30:e:1:MET:HE2	30:e:1:MET:HB3	1.92	0.43
40:o:137:PRO:HD3	40:o:162:TRP:CH2	2.54	0.43
42:r:264:TYR:HD2	42:r:304:ILE:HD12	1.83	0.43
46:w:359:LEU:HB3	46:w:362:ILE:HG22	2.01	0.43
9:J:12:ASP:HB2	18:S:167:ARG:HH12	1.82	0.43
10:K:63:VAL:HG22	13:N:128:ARG:HH12	1.84	0.43
27:b:208:SER:OG	27:b:209:ASN:N	2.51	0.43
40:o:163:ARG:NE	40:o:183:ARG:HD3	2.34	0.43
1:A:69:C:HO2'	1:A:101:G:HO2'	1.59	0.43
1:A:1273:A:H3'	1:A:1274:A:H8	1.84	0.43
1:A:1493:G:OP2	1:A:1493:G:N2	2.48	0.43
1:A:2458:A:H3'	1:A:2459:A:C8	2.53	0.43
1:A:2895:G:OP2	6:F:168:ARG:NH1	2.42	0.43
4:D:34:ILE:HD11	4:D:120:TYR:CD1	2.54	0.43
10:K:176:GLU:O	10:K:180:ARG:HB2	2.19	0.43
33:h:35:ASN:OD1	33:h:35:ASN:N	2.52	0.43
35:j:50:SER:OG	35:j:51:LEU:N	2.51	0.43
48:y:85:G:O2'	48:y:86:U:O5'	2.32	0.43
1:A:1190:A:H2'	9:J:48:ARG:HH12	1.82	0.43
1:A:2485:A:N7	1:A:2486:A:N6	2.67	0.43
1:A:3022:G:OP2	39:n:33:ASN:ND2	2.52	0.43
3:C:53:MET:HE2	3:C:53:MET:HB3	1.86	0.43
14:O:146:ALA:HB3	25:Z:101:THR:HG23	2.00	0.43
17:R:110:ARG:HB3	17:R:115:ILE:HG13	2.01	0.43
18:S:73:LYS:HD2	18:S:128:GLU:HG3	2.01	0.43
19:T:132:PRO:HB2	27:b:120:THR:HB	2.01	0.43
33:h:89:GLU:HG2	33:h:90:MET:HE2	2.01	0.43
36:k:21:ARG:HD3	48:y:52:A:H5'	2.01	0.43
39:n:118:HIS:CE1	39:n:146:ILE:HD12	2.54	0.43
48:y:8:C:H2'	48:y:9:A:C8	2.54	0.43
1:A:1639:C:OP2	32:g:74:ARG:NH1	2.44	0.42
1:A:2697:A:H2'	1:A:2698:G:C8	2.54	0.42
12:M:17:VAL:HG11	12:M:74:ARG:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:232:ASP:OD1	15:P:232:ASP:N	2.42	0.42
17:R:19:LYS:HB2	17:R:19:LYS:HE3	1.79	0.42
39:n:126:GLU:OE2	39:n:139:ARG:NH1	2.52	0.42
42:r:245:ARG:HA	42:r:266:GLY:HA2	2.01	0.42
44:u:219:VAL:HG12	44:u:243:PRO:CG	2.48	0.42
46:w:141:MET:HB3	46:w:142:GLN:H	1.56	0.42
1:A:952:A:H5''	26:a:15:LYS:HD2	2.00	0.42
1:A:1432:C:O2'	1:A:1434:G:OP2	2.37	0.42
1:A:2183:A:O2'	2:B:236:GLY:N	2.45	0.42
2:B:79:ASN:HA	2:B:170:ALA:H	1.84	0.42
4:D:357:GLU:O	4:D:361:HIS:HB2	2.20	0.42
11:L:15:LEU:HD13	11:L:51:ALA:HB3	2.00	0.42
19:T:102:ARG:HD2	19:T:102:ARG:HA	1.89	0.42
24:Y:61:LYS:O	24:Y:65:ARG:CB	2.63	0.42
28:c:98:SER:OG	28:c:99:ASP:N	2.52	0.42
1:A:2772:C:H4'	1:A:2773:C:H5'	2.01	0.42
7:G:76:LEU:HD11	7:G:141:VAL:HG21	2.01	0.42
8:H:74:THR:HG22	8:H:164:VAL:HG22	2.01	0.42
11:L:17:LEU:HA	11:L:18:PRO:HD2	1.96	0.42
39:n:217:VAL:HG11	46:w:18:LEU:HD13	2.02	0.42
42:r:321:LEU:O	42:r:502:ARG:HA	2.20	0.42
42:r:349:LYS:NZ	42:r:490:ASN:OD1	2.46	0.42
46:w:19:CYS:HB3	46:w:23:GLY:H	1.84	0.42
46:w:63:ARG:NE	46:w:73:ARG:HG2	2.30	0.42
46:w:267:MET:HE2	46:w:267:MET:HB3	1.89	0.42
46:w:398:VAL:HG23	46:w:399:LYS:HG2	2.00	0.42
1:A:2213:A:H2'	1:A:2214:A:C8	2.54	0.42
3:C:87:VAL:O	3:C:107:ALA:N	2.53	0.42
16:Q:102:ALA:HA	16:Q:122:ILE:O	2.19	0.42
34:i:27:PHE:HA	34:i:34:CYS:HA	2.01	0.42
46:w:19:CYS:HB2	46:w:25:PRO:HD2	2.01	0.42
1:A:351:A:N6	36:k:37:TYR:O	2.44	0.42
1:A:2418:G:OP2	1:A:2606:G:N2	2.41	0.42
42:r:96:ASP:HB2	42:r:140:LYS:HB2	2.01	0.42
46:w:94:LYS:HG3	46:w:94:LYS:H	1.52	0.42
1:A:69:C:O2'	1:A:101:G:O2'	2.31	0.42
1:A:1497:C:H2'	1:A:1498:A:C8	2.54	0.42
7:G:80:ASN:HD22	7:G:83:TYR:HE2	1.67	0.42
11:L:72:LYS:HZ2	46:w:96:ARG:HH11	1.68	0.42
14:O:36:ILE:HG12	14:O:64:VAL:HG23	2.02	0.42
15:P:44:TYR:CD1	15:P:44:TYR:N	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:108:ARG:O	19:T:112:ASN:OD1	2.36	0.42
34:i:21:ARG:HG3	48:y:103:G:H4'	2.02	0.42
40:o:346:ASN:HD21	40:o:407:GLY:HA2	1.84	0.42
1:A:93:C:OP2	1:A:2764:C:O2'	2.33	0.42
1:A:2737:C:O2'	26:a:36:ASP:OD1	2.36	0.42
5:E:117:ASP:HB3	5:E:120:ILE:HG12	2.02	0.42
8:H:82:LEU:HD13	8:H:222:PHE:HE2	1.84	0.42
37:l:15:LYS:HE2	37:l:15:LYS:HB2	1.89	0.42
42:r:518:ASP:OD1	42:r:518:ASP:N	2.52	0.42
1:A:19:U:H2'	1:A:20:A:C8	2.55	0.42
1:A:537:A:H3'	1:A:538:G:H8	1.85	0.42
31:f:20:LYS:HB3	31:f:20:LYS:HE2	1.89	0.42
34:i:63:ARG:NH2	48:y:58:G:O6	2.53	0.42
1:A:1020:G:H2'	1:A:1021:G:H8	1.85	0.42
1:A:1785:U:H2'	1:A:1786:G:C8	2.55	0.42
1:A:2476:C:H2'	1:A:2477:G:C8	2.52	0.42
3:C:163:HIS:ND1	3:C:164:THR:O	2.52	0.42
3:C:222:LYS:HB3	3:C:222:LYS:HE2	1.77	0.42
40:o:430:LYS:HG3	40:o:441:ILE:HD11	2.01	0.42
46:w:172:LEU:HD23	46:w:172:LEU:HA	1.90	0.42
1:A:1157:G:O2'	1:A:1169:A:N3	2.44	0.42
23:X:27:ARG:NH1	23:X:75:ARG:O	2.42	0.42
24:Y:23:VAL:HB	24:Y:43:VAL:HG22	2.02	0.42
27:b:228:SER:HA	27:b:232:ARG:NH2	2.31	0.42
28:c:68:TYR:HD1	28:c:103:THR:HB	1.85	0.42
1:A:1020:G:H2'	1:A:1021:G:C8	2.55	0.41
1:A:2228:A:H2'	1:A:2229:A:C8	2.55	0.41
5:E:36:VAL:HG21	5:E:123:PHE:HZ	1.84	0.41
22:W:134:ASP:OD2	42:r:414:LYS:NZ	2.53	0.41
24:Y:46:ILE:HG23	24:Y:68:ILE:HG23	2.01	0.41
39:n:23:TYR:HA	39:n:47:PRO:HD2	2.01	0.41
1:A:662:U:OP1	13:N:8:THR:OG1	2.34	0.41
1:A:1018:G:O6	1:A:1034:U:C2	2.73	0.41
1:A:1083:G:H2'	1:A:1084:A:C8	2.55	0.41
1:A:1244:A:O2'	1:A:1247:U:OP1	2.32	0.41
1:A:1268:G:N2	1:A:1269:U:O4	2.53	0.41
10:K:123:ILE:HG22	25:Z:118:ILE:HG12	2.02	0.41
11:L:104:ASN:OD1	11:L:108:GLU:N	2.53	0.41
27:b:98:LYS:HB2	27:b:98:LYS:HE2	1.93	0.41
40:o:137:PRO:HB3	40:o:162:TRP:CE3	2.55	0.41
42:r:239:VAL:HG12	42:r:241:GLY:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:G:OP2	34:i:56:ARG:NH2	2.48	0.41
1:A:2673:A:OP1	5:E:94:ARG:NE	2.52	0.41
28:c:9:SER:HB3	28:c:12:GLN:HG3	2.02	0.41
1:A:900:G:H1'	1:A:1589:A:N6	2.35	0.41
1:A:2219:A:H2'	1:A:2220:A:C8	2.56	0.41
6:F:90:MET:HB2	6:F:144:ILE:HG23	2.02	0.41
7:G:63:LEU:O	7:G:78:ARG:HA	2.19	0.41
11:L:92:PHE:O	45:v:20:LEU:N	2.51	0.41
28:c:74:ASN:OD1	28:c:74:ASN:N	2.54	0.41
31:f:49:ILE:HD11	31:f:71:VAL:HG22	2.02	0.41
40:o:242:THR:HG23	40:o:245:GLN:HE21	1.85	0.41
40:o:457:ALA:HA	40:o:460:LEU:HB3	2.03	0.41
1:A:505:G:OP1	4:D:320:ASN:ND2	2.54	0.41
1:A:1480:G:O2'	1:A:1871:U:O4	2.33	0.41
3:C:47:LEU:HD12	3:C:335:ILE:HD11	2.02	0.41
9:J:9:ASP:HB2	9:J:116:ARG:HB3	2.02	0.41
27:b:53:LYS:HA	27:b:53:LYS:HD3	1.87	0.41
39:n:18:LYS:HE3	39:n:65:GLY:H	1.86	0.41
40:o:180:PRO:HD3	40:o:399:ASN:OD1	2.21	0.41
42:r:96:ASP:HB3	42:r:100:ILE:HG13	2.03	0.41
1:A:20:A:H2'	1:A:21:G:C8	2.56	0.41
1:A:1236:G:N2	1:A:1272:C:OP1	2.53	0.41
1:A:2551:U:O2	2:B:40:TYR:OH	2.28	0.41
1:A:2584:G:O2'	8:H:240:ASN:OD1	2.39	0.41
1:A:2841:G:C2	1:A:2847:A:N6	2.89	0.41
8:H:246:MET:HE2	8:H:246:MET:HB3	1.85	0.41
19:T:110:LYS:HB3	19:T:110:LYS:HE2	1.88	0.41
42:r:227:VAL:HA	42:r:230:ILE:HG22	2.03	0.41
42:r:247:ILE:N	42:r:316:VAL:O	2.48	0.41
1:A:1354:G:H1'	7:G:9:TRP:HZ3	1.85	0.41
5:E:26:SER:HA	5:E:30:LEU:HD22	2.02	0.41
6:F:101:VAL:HG22	6:F:114:VAL:HG12	2.02	0.41
22:W:39:LYS:HE3	22:W:39:LYS:HB2	1.77	0.41
31:f:16:TYR:OH	31:f:89:LEU:O	2.33	0.41
32:g:58:ARG:HD2	32:g:58:ARG:HA	1.83	0.41
46:w:382:ASP:OD1	46:w:382:ASP:N	2.54	0.41
1:A:1354:G:H21	7:G:9:TRP:HE3	1.69	0.41
7:G:5:LYS:HB3	7:G:5:LYS:HE3	1.86	0.41
21:V:30:PRO:HA	21:V:33:TYR:HB3	2.03	0.41
21:V:91:ASP:HA	44:u:316:ARG:HG2	2.03	0.41
35:j:38:PHE:HE2	35:j:57:ASN:HB3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:x:77:G:O2'	47:x:101:G:O6	2.37	0.41
1:A:501:A:H4'	7:G:28:GLN:HG3	2.02	0.41
1:A:528:U:H2'	1:A:529:A:C8	2.56	0.41
1:A:577:C:O2'	1:A:579:G:OP1	2.33	0.41
1:A:1410:U:H4'	30:e:75:LEU:HD11	2.03	0.41
1:A:1412:G:OP1	30:e:105:ARG:NH1	2.49	0.41
1:A:2486:A:H4'	1:A:2487:U:H5'	2.03	0.41
1:A:3267:A:C8	7:G:69:PHE:HE1	2.38	0.41
4:D:108:LYS:HB3	4:D:108:LYS:HE2	1.88	0.41
5:E:82:ARG:HD3	5:E:112:LEU:HB3	2.02	0.41
5:E:117:ASP:HA	5:E:118:PRO:HD3	1.92	0.41
8:H:183:LYS:HB3	8:H:194:THR:HG23	2.02	0.41
13:N:85:ASP:N	13:N:85:ASP:OD1	2.54	0.41
14:O:5:LYS:HD2	14:O:5:LYS:HA	1.86	0.41
15:P:59:ASP:OD1	15:P:80:SER:OG	2.32	0.41
16:Q:178:ARG:HA	16:Q:178:ARG:HD3	1.79	0.41
24:Y:57:HIS:HB3	24:Y:61:LYS:HB2	2.03	0.41
34:i:37:CYS:HA	34:i:45:ARG:HB2	2.03	0.41
42:r:184:VAL:HB	42:r:537:ILE:HG21	2.01	0.41
43:s:313:LYS:HB2	43:s:313:LYS:HE2	1.76	0.41
48:y:9:A:H2'	48:y:10:A:C8	2.56	0.41
1:A:619:A:H3'	7:G:117:LYS:HD3	2.03	0.41
1:A:1569:U:H3	1:A:1571:A:H1'	1.86	0.41
1:A:2871:G:H5'	1:A:2872:A:H5''	2.03	0.41
11:L:13:ILE:HD13	11:L:54:LEU:HB3	2.03	0.41
22:W:108:LEU:HD11	22:W:125:ARG:HD3	2.02	0.41
42:r:262:ARG:HG3	42:r:263:GLU:HG2	2.03	0.41
46:w:206:HIS:CD2	46:w:209:LYS:HD3	2.56	0.41
1:A:1260:A:O2'	1:A:1279:C:O2	2.38	0.40
1:A:1389:G:H5''	30:e:101:SER:HB3	2.02	0.40
1:A:1494:U:OP1	36:k:42:ARG:NH2	2.48	0.40
1:A:1843:C:OP1	36:k:48:LYS:NZ	2.50	0.40
1:A:2618:G:H1'	1:A:2865:U:H5'	2.03	0.40
3:C:313:HIS:HB2	3:C:332:ARG:HG3	2.02	0.40
8:H:221:ASN:HA	8:H:225:LYS:HE3	2.02	0.40
15:P:41:LYS:HD2	19:T:93:VAL:HG21	2.02	0.40
17:R:133:LYS:HE3	17:R:134:HIS:HE2	1.86	0.40
28:c:28:LYS:HB3	28:c:28:LYS:HE2	1.89	0.40
39:n:1:MET:H2	39:n:203:LEU:HD12	1.85	0.40
42:r:559:LEU:HD22	42:r:567:LEU:HD13	2.02	0.40
1:A:648:C:O2	1:A:2374:C:O2'	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2111:G:H1'	45:v:44:LYS:HD2	2.02	0.40
1:A:2467:G:N2	1:A:2488:A:N6	2.43	0.40
6:F:89:LYS:HE2	6:F:183:HIS:CD2	2.56	0.40
37:l:40:LYS:NZ	37:l:44:ASP:OD2	2.53	0.40
42:r:218:ILE:HD13	42:r:218:ILE:HA	1.98	0.40
42:r:258:ILE:HA	42:r:261:GLU:HG3	2.03	0.40
42:r:367:THR:HA	42:r:431:LEU:HD22	2.02	0.40
43:s:283:PHE:O	43:s:336:LEU:N	2.53	0.40
43:s:285:ILE:HG13	43:s:334:ILE:HG23	2.03	0.40
1:A:75:G:H5'	10:K:58:VAL:HB	2.04	0.40
1:A:437:G:H22	1:A:622:A:H62	1.69	0.40
1:A:664:U:H2'	1:A:665:A:C8	2.55	0.40
1:A:1026:A:H4'	1:A:1027:A:C8	2.56	0.40
1:A:1740:U:H4'	1:A:1741:A:H5'	2.02	0.40
1:A:2461:A:P	1:A:2461:A:H8	2.45	0.40
1:A:2491:A:OP2	41:p:205:UNK:N	2.54	0.40
4:D:351:PRO:HB3	27:b:70:LYS:HG2	2.03	0.40
8:H:70:LYS:HD2	8:H:70:LYS:HA	1.90	0.40
11:L:70:ARG:H	11:L:70:ARG:HG2	1.74	0.40
12:M:102:LYS:HE2	12:M:102:LYS:HB3	1.97	0.40
28:c:9:SER:OG	28:c:10:ILE:N	2.54	0.40
43:s:277:GLN:NE2	43:s:279:ASN:OD1	2.43	0.40
1:A:562:C:H5''	18:S:71:LYS:HE2	2.03	0.40
1:A:2463:G:H2'	1:A:2464:U:H4'	2.04	0.40
1:A:3358:U:H2'	1:A:3359:A:C8	2.57	0.40
3:C:139:GLN:H	3:C:139:GLN:HG3	1.73	0.40
3:C:287:LYS:HB2	3:C:290:ASP:HB2	2.02	0.40
3:C:361:THR:OG1	3:C:371:GLN:O	2.39	0.40
18:S:36:ILE:HG22	27:b:224:ILE:HA	2.03	0.40
22:W:67:ILE:HD12	22:W:121:LYS:HG3	2.02	0.40
24:Y:66:THR:O	24:Y:66:THR:OG1	2.40	0.40
28:c:20:SER:O	28:c:20:SER:OG	2.37	0.40
39:n:109:CYS:HB2	39:n:149:GLY:HA2	2.02	0.40
39:n:223:ARG:HH21	43:s:236:ARG:HH12	1.70	0.40
40:o:442:GLN:HG3	40:o:444:LYS:H	1.86	0.40
46:w:103:ILE:HB	46:w:113:ARG:HG2	2.03	0.40
46:w:263:LEU:O	46:w:267:MET:HG2	2.22	0.40
1:A:2309:A:N3	1:A:2961:G:O2'	2.52	0.40
1:A:3057:U:H5'	1:A:3086:A:H61	1.87	0.40
1:A:3163:A:N6	1:A:3288:G:O6	2.55	0.40
6:F:97:PHE:HA	6:F:98:PRO:HD3	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z:86:ARG:HD2	48:y:37:A:OP2	2.22	0.40
39:n:200:ASN:N	39:n:203:LEU:O	2.53	0.40
40:o:198:SER:OG	40:o:200:LEU:O	2.34	0.40
42:r:414:LYS:HA	42:r:414:LYS:HD2	1.86	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	
2	B	245/254 (96%)	224 (91%)	21 (9%)	0	100	100
3	C	379/387 (98%)	352 (93%)	26 (7%)	1 (0%)	36	68
4	D	359/362 (99%)	342 (95%)	17 (5%)	0	100	100
5	E	167/174 (96%)	154 (92%)	13 (8%)	0	100	100
6	F	187/191 (98%)	178 (95%)	9 (5%)	0	100	100
7	G	173/176 (98%)	159 (92%)	13 (8%)	1 (1%)	21	56
8	H	221/256 (86%)	210 (95%)	11 (5%)	0	100	100
9	J	195/198 (98%)	193 (99%)	2 (1%)	0	100	100
10	K	184/199 (92%)	174 (95%)	10 (5%)	0	100	100
11	L	134/137 (98%)	125 (93%)	9 (7%)	0	100	100
12	M	133/138 (96%)	128 (96%)	5 (4%)	0	100	100
13	N	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
14	O	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
15	P	267/297 (90%)	253 (95%)	14 (5%)	0	100	100
16	Q	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
17	R	148/189 (78%)	147 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	S	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
19	T	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
20	U	152/184 (83%)	144 (95%)	8 (5%)	0	100	100
21	V	97/121 (80%)	91 (94%)	6 (6%)	0	100	100
22	W	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
23	X	123/127 (97%)	118 (96%)	5 (4%)	0	100	100
24	Y	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
25	Z	116/120 (97%)	114 (98%)	2 (2%)	0	100	100
26	a	50/59 (85%)	45 (90%)	5 (10%)	0	100	100
27	b	217/244 (89%)	209 (96%)	8 (4%)	0	100	100
28	c	95/105 (90%)	93 (98%)	2 (2%)	0	100	100
29	d	105/113 (93%)	92 (88%)	13 (12%)	0	100	100
30	e	125/130 (96%)	118 (94%)	5 (4%)	2 (2%)	7	36
31	f	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
32	g	101/121 (84%)	92 (91%)	8 (8%)	1 (1%)	12	45
33	h	96/100 (96%)	95 (99%)	1 (1%)	0	100	100
34	i	82/88 (93%)	74 (90%)	7 (8%)	1 (1%)	10	42
35	j	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
36	k	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
37	l	92/106 (87%)	89 (97%)	3 (3%)	0	100	100
38	m	87/92 (95%)	80 (92%)	6 (7%)	1 (1%)	11	43
39	n	222/245 (91%)	208 (94%)	14 (6%)	0	100	100
40	o	314/640 (49%)	265 (84%)	48 (15%)	1 (0%)	36	68
42	r	508/593 (86%)	475 (94%)	33 (6%)	0	100	100
43	s	126/364 (35%)	105 (83%)	21 (17%)	0	100	100
44	u	207/393 (53%)	193 (93%)	13 (6%)	1 (0%)	24	59
45	v	58/155 (37%)	58 (100%)	0	0	100	100
46	w	387/518 (75%)	348 (90%)	38 (10%)	1 (0%)	36	68
All	All	7486/8961 (84%)	7006 (94%)	470 (6%)	10 (0%)	49	79

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	18	PRO
32	g	81	CYS
30	e	7	PRO
44	u	221	ASN
7	G	9	TRP
46	w	142	GLN
40	o	231	ASN
30	e	4	LEU
34	i	38	GLY
38	m	8	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	189/196 (96%)	186 (98%)	3 (2%)	55	75
3	C	317/323 (98%)	314 (99%)	3 (1%)	70	81
4	D	288/289 (100%)	287 (100%)	1 (0%)	86	88
5	E	147/150 (98%)	144 (98%)	3 (2%)	48	72
6	F	169/171 (99%)	167 (99%)	2 (1%)	63	79
7	G	152/153 (99%)	151 (99%)	1 (1%)	76	83
8	H	183/208 (88%)	183 (100%)	0	100	100
9	J	163/164 (99%)	162 (99%)	1 (1%)	78	84
10	K	149/159 (94%)	148 (99%)	1 (1%)	76	83
11	L	104/105 (99%)	103 (99%)	1 (1%)	68	80
12	M	107/109 (98%)	106 (99%)	1 (1%)	70	81
13	N	118/119 (99%)	118 (100%)	0	100	100
14	O	175/176 (99%)	175 (100%)	0	100	100
15	P	227/245 (93%)	226 (100%)	1 (0%)	84	86
16	Q	150/151 (99%)	149 (99%)	1 (1%)	76	83
17	R	124/154 (80%)	124 (100%)	0	100	100
18	S	155/156 (99%)	152 (98%)	3 (2%)	50	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	T	136/137 (99%)	134 (98%)	2 (2%)	57	76
20	U	125/146 (86%)	124 (99%)	1 (1%)	73	82
21	V	86/107 (80%)	86 (100%)	0	100	100
22	W	104/118 (88%)	103 (99%)	1 (1%)	68	80
23	X	108/110 (98%)	107 (99%)	1 (1%)	70	81
24	Y	115/116 (99%)	113 (98%)	2 (2%)	53	75
25	Z	104/105 (99%)	103 (99%)	1 (1%)	68	80
26	a	41/47 (87%)	41 (100%)	0	100	100
27	b	184/205 (90%)	183 (100%)	1 (0%)	81	85
28	c	81/88 (92%)	81 (100%)	0	100	100
29	d	94/97 (97%)	92 (98%)	2 (2%)	47	71
30	e	109/111 (98%)	107 (98%)	2 (2%)	51	74
31	f	90/91 (99%)	90 (100%)	0	100	100
32	g	88/103 (85%)	86 (98%)	2 (2%)	44	70
33	h	80/82 (98%)	80 (100%)	0	100	100
34	i	69/71 (97%)	67 (97%)	2 (3%)	37	67
35	j	68/69 (99%)	67 (98%)	1 (2%)	57	76
36	k	45/46 (98%)	45 (100%)	0	100	100
37	l	81/91 (89%)	78 (96%)	3 (4%)	30	63
38	m	70/72 (97%)	70 (100%)	0	100	100
39	n	192/211 (91%)	186 (97%)	6 (3%)	35	66
40	o	282/555 (51%)	277 (98%)	5 (2%)	51	74
42	r	453/520 (87%)	449 (99%)	4 (1%)	70	81
43	s	110/323 (34%)	109 (99%)	1 (1%)	70	81
44	u	181/359 (50%)	179 (99%)	2 (1%)	65	79
45	v	53/129 (41%)	53 (100%)	0	100	100
46	w	348/467 (74%)	333 (96%)	15 (4%)	26	59
All	All	6414/7604 (84%)	6338 (99%)	76 (1%)	61	79

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	101	VAL

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Mol	Chain	Res	Type
2	B	207	VAL
2	B	243	THR
3	C	17	LEU
3	C	18	PRO
3	C	85	VAL
4	D	230	VAL
5	E	47	GLN
5	E	54	VAL
5	E	174	LYS
6	F	57	VAL
6	F	157	ASN
7	G	8	LYS
9	J	26	VAL
10	K	10	LEU
11	L	137	VAL
12	M	15	VAL
15	P	43	LYS
16	Q	186	VAL
18	S	79	VAL
18	S	135	VAL
18	S	172	TYR
19	T	112	ASN
19	T	160	ILE
20	U	114	VAL
22	W	142	ILE
23	X	56	VAL
24	Y	53	VAL
24	Y	127	ASN
25	Z	93	THR
27	b	229	PHE
29	d	49	VAL
29	d	64	VAL
30	e	4	LEU
30	e	7	PRO
32	g	46	ASP
32	g	47	CYS
34	i	3	LYS
34	i	61	THR
35	j	78	LEU
37	l	2	VAL
37	l	3	ASN
37	l	25	VAL

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Mol	Chain	Res	Type
39	n	63	THR
39	n	139	ARG
39	n	140	GLN
39	n	141	THR
39	n	142	ILE
39	n	143	SER
40	o	157	GLU
40	o	160	LEU
40	o	166	LEU
40	o	170	GLN
40	o	171	GLU
42	r	60	THR
42	r	139	VAL
42	r	319	ILE
42	r	354	ILE
43	s	314	VAL
44	u	220	CYS
44	u	253	ILE
46	w	57	PHE
46	w	61	CYS
46	w	63	ARG
46	w	64	PHE
46	w	66	GLN
46	w	73	ARG
46	w	94	LYS
46	w	95	VAL
46	w	106	GLU
46	w	108	HIS
46	w	141	MET
46	w	142	GLN
46	w	143	CYS
46	w	145	ASP
46	w	332	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (74) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	83	HIS
2	B	140	ASN
3	C	13	HIS
3	C	121	ASN
3	C	165	GLN

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Mol	Chain	Res	Type
3	C	182	GLN
3	C	371	GLN
4	D	296	GLN
4	D	316	ASN
6	F	50	ASN
6	F	100	ASN
6	F	183	HIS
8	H	59	GLN
8	H	221	ASN
10	K	28	GLN
10	K	114	GLN
12	M	56	GLN
13	N	40	HIS
14	O	86	ASN
14	O	87	GLN
16	Q	126	GLN
17	R	66	HIS
17	R	68	GLN
18	S	68	HIS
19	T	77	ASN
20	U	92	GLN
20	U	125	GLN
20	U	137	ASN
21	V	40	HIS
24	Y	29	HIS
24	Y	127	ASN
25	Z	68	GLN
25	Z	113	GLN
26	a	6	ASN
26	a	17	HIS
27	b	81	HIS
27	b	166	ASN
29	d	15	ASN
29	d	87	ASN
30	e	21	HIS
30	e	31	ASN
31	f	24	ASN
31	f	88	ASN
33	h	63	ASN
36	k	4	GLN
37	l	53	GLN
37	l	90	HIS

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Mol	Chain	Res	Type
39	n	21	ASN
39	n	75	GLN
39	n	95	GLN
39	n	170	GLN
40	o	170	GLN
40	o	203	GLN
40	o	209	ASN
40	o	245	GLN
40	o	257	ASN
40	o	346	ASN
40	o	458	GLN
42	r	26	ASN
42	r	58	GLN
42	r	116	ASN
42	r	366	GLN
42	r	394	HIS
42	r	410	GLN
42	r	447	HIS
42	r	577	GLN
43	s	274	GLN
44	u	170	ASN
44	u	179	ASN
44	u	221	ASN
45	v	32	GLN
46	w	181	HIS
46	w	182	ASN
46	w	205	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3141/3396 (92%)	678 (21%)	15 (0%)
47	x	120/121 (99%)	15 (12%)	0
48	y	155/158 (98%)	27 (17%)	0
All	All	3416/3675 (92%)	720 (21%)	15 (0%)

All (720) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	A
1	A	26	A

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Mol	Chain	Res	Type
1	A	40	A
1	A	43	A
1	A	48	A
1	A	49	A
1	A	59	G
1	A	60	A
1	A	65	A
1	A	66	A
1	A	70	A
1	A	72	C
1	A	73	C
1	A	75	G
1	A	92	G
1	A	99	A
1	A	109	A
1	A	110	G
1	A	111	C
1	A	116	A
1	A	117	U
1	A	119	U
1	A	120	G
1	A	121	A
1	A	122	A
1	A	133	U
1	A	134	U
1	A	135	C
1	A	136	G
1	A	148	G
1	A	154	U
1	A	156	G
1	A	157	A
1	A	167	U
1	A	171	G
1	A	176	G
1	A	181	U
1	A	187	A
1	A	190	U
1	A	191	U
1	A	192	C
1	A	194	U
1	A	198	A
1	A	200	C

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Mol	Chain	Res	Type
1	A	206	G
1	A	211	A
1	A	213	A
1	A	218	G
1	A	219	A
1	A	220	G
1	A	234	G
1	A	238	A
1	A	239	G
1	A	241	G
1	A	243	G
1	A	246	U
1	A	248	U
1	A	249	U
1	A	250	U
1	A	251	G
1	A	252	U
1	A	253	A
1	A	263	C
1	A	265	A
1	A	266	A
1	A	269	G
1	A	281	G
1	A	286	U
1	A	295	A
1	A	305	U
1	A	315	C
1	A	329	U
1	A	351	A
1	A	359	U
1	A	376	G
1	A	390	G
1	A	398	A
1	A	399	A
1	A	401	U
1	A	402	A
1	A	403	C
1	A	420	G
1	A	421	G
1	A	422	A
1	A	438	A
1	A	439	C

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Mol	Chain	Res	Type
1	A	440	A
1	A	496	C
1	A	503	C
1	A	521	A
1	A	523	A
1	A	536	U
1	A	542	G
1	A	545	U
1	A	547	G
1	A	551	A
1	A	555	U
1	A	556	U
1	A	557	A
1	A	559	A
1	A	569	A
1	A	578	A
1	A	579	G
1	A	604	G
1	A	611	A
1	A	619	A
1	A	620	U
1	A	621	A
1	A	622	A
1	A	637	C
1	A	649	A
1	A	662	U
1	A	677	A
1	A	681	U
1	A	689	U
1	A	691	A
1	A	699	A
1	A	705	A
1	A	712	G
1	A	715	A
1	A	716	A
1	A	718	G
1	A	719	U
1	A	720	A
1	A	725	G
1	A	761	A
1	A	767	U
1	A	774	G

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Mol	Chain	Res	Type
1	A	776	U
1	A	777	U
1	A	780	A
1	A	781	G
1	A	785	G
1	A	786	A
1	A	801	A
1	A	806	A
1	A	815	G
1	A	817	A
1	A	830	A
1	A	832	G
1	A	845	G
1	A	847	A
1	A	848	A
1	A	849	C
1	A	861	C
1	A	874	U
1	A	879	U
1	A	880	G
1	A	884	A
1	A	896	A
1	A	907	G
1	A	908	G
1	A	914	A
1	A	916	G
1	A	917	A
1	A	921	A
1	A	923	C
1	A	924	G
1	A	925	A
1	A	937	G
1	A	944	C
1	A	953	G
1	A	959	C
1	A	960	U
1	A	963	G
1	A	979	U
1	A	980	A
1	A	981	U
1	A	982	C
1	A	999	G

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Mol	Chain	Res	Type
1	A	1001	G
1	A	1004	U
1	A	1006	A
1	A	1007	U
1	A	1009	A
1	A	1010	G
1	A	1011	A
1	A	1012	G
1	A	1013	G
1	A	1014	U
1	A	1016	C
1	A	1017	C
1	A	1018	G
1	A	1025	A
1	A	1027	A
1	A	1028	U
1	A	1029	G
1	A	1030	A
1	A	1031	C
1	A	1032	C
1	A	1033	U
1	A	1036	A
1	A	1037	C
1	A	1038	C
1	A	1039	U
1	A	1043	C
1	A	1045	C
1	A	1048	A
1	A	1050	U
1	A	1051	U
1	A	1063	G
1	A	1064	A
1	A	1065	A
1	A	1072	G
1	A	1081	U
1	A	1087	G
1	A	1093	A
1	A	1094	U
1	A	1095	U
1	A	1096	U
1	A	1097	G
1	A	1098	A

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Mol	Chain	Res	Type
1	A	1103	A
1	A	1104	G
1	A	1116	G
1	A	1117	G
1	A	1118	C
1	A	1130	A
1	A	1131	G
1	A	1144	U
1	A	1153	A
1	A	1159	A
1	A	1179	A
1	A	1180	A
1	A	1181	U
1	A	1190	A
1	A	1192	C
1	A	1193	A
1	A	1195	A
1	A	1196	C
1	A	1201	C
1	A	1209	G
1	A	1218	U
1	A	1220	U
1	A	1222	G
1	A	1235	U
1	A	1236	G
1	A	1238	C
1	A	1240	A
1	A	1241	U
1	A	1242	G
1	A	1243	G
1	A	1245	A
1	A	1246	G
1	A	1247	U
1	A	1248	C
1	A	1249	G
1	A	1252	A
1	A	1253	U
1	A	1254	C
1	A	1258	U
1	A	1260	A
1	A	1262	G
1	A	1263	A

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Mol	Chain	Res	Type
1	A	1265	U
1	A	1266	G
1	A	1270	A
1	A	1271	A
1	A	1272	C
1	A	1273	A
1	A	1274	A
1	A	1277	C
1	A	1278	A
1	A	1279	C
1	A	1280	C
1	A	1285	G
1	A	1287	A
1	A	1289	G
1	A	1302	A
1	A	1303	A
1	A	1305	U
1	A	1307	G
1	A	1309	U
1	A	1313	G
1	A	1325	U
1	A	1330	A
1	A	1331	U
1	A	1332	A
1	A	1348	U
1	A	1349	G
1	A	1350	A
1	A	1352	A
1	A	1353	U
1	A	1354	G
1	A	1355	A
1	A	1356	U
1	A	1386	A
1	A	1392	G
1	A	1399	A
1	A	1400	G
1	A	1418	A
1	A	1419	A
1	A	1434	G
1	A	1436	U
1	A	1437	C
1	A	1446	A

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Mol	Chain	Res	Type
1	A	1450	G
1	A	1455	U
1	A	1467	A
1	A	1475	A
1	A	1481	A
1	A	1482	A
1	A	1494	U
1	A	1508	C
1	A	1523	U
1	A	1527	C
1	A	1533	U
1	A	1546	A
1	A	1555	U
1	A	1556	C
1	A	1562	C
1	A	1563	C
1	A	1565	G
1	A	1566	A
1	A	1567	U
1	A	1568	U
1	A	1569	U
1	A	1570	U
1	A	1572	U
1	A	1573	G
1	A	1574	C
1	A	1576	G
1	A	1578	C
1	A	1583	A
1	A	1587	A
1	A	1589	A
1	A	1590	G
1	A	1593	A
1	A	1618	G
1	A	1619	A
1	A	1620	U
1	A	1629	U
1	A	1630	U
1	A	1631	C
1	A	1642	A
1	A	1643	A
1	A	1645	U
1	A	1657	C

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Mol	Chain	Res	Type
1	A	1658	G
1	A	1677	G
1	A	1715	A
1	A	1724	U
1	A	1725	C
1	A	1741	A
1	A	1742	U
1	A	1749	A
1	A	1750	A
1	A	1751	G
1	A	1760	A
1	A	1762	C
1	A	1763	U
1	A	1765	U
1	A	1775	G
1	A	1780	G
1	A	1797	A
1	A	1813	A
1	A	1814	A
1	A	1815	U
1	A	1816	A
1	A	1820	U
1	A	1821	U
1	A	1835	A
1	A	1839	A
1	A	1842	A
1	A	1849	C
1	A	1850	A
1	A	1866	C
1	A	1878	G
1	A	1880	U
1	A	1886	A
1	A	1893	A
1	A	1906	G
1	A	1907	C
1	A	1908	A
1	A	1930	A
1	A	1951	C
1	A	1952	G
1	A	1953	G
1	A	1954	G
1	A	2095	G

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Mol	Chain	Res	Type
1	A	2096	A
1	A	2100	A
1	A	2101	C
1	A	2102	U
1	A	2111	G
1	A	2113	A
1	A	2121	G
1	A	2122	G
1	A	2131	A
1	A	2140	U
1	A	2144	A
1	A	2145	A
1	A	2155	G
1	A	2158	A
1	A	2168	A
1	A	2169	G
1	A	2176	U
1	A	2187	G
1	A	2188	A
1	A	2195	C
1	A	2205	U
1	A	2206	G
1	A	2210	G
1	A	2232	A
1	A	2244	A
1	A	2249	G
1	A	2252	A
1	A	2255	A
1	A	2257	C
1	A	2259	A
1	A	2260	U
1	A	2261	G
1	A	2262	A
1	A	2266	U
1	A	2268	U
1	A	2269	U
1	A	2270	A
1	A	2273	G
1	A	2281	A
1	A	2282	U
1	A	2295	A
1	A	2298	U

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Mol	Chain	Res	Type
1	A	2307	G
1	A	2308	C
1	A	2309	A
1	A	2310	U
1	A	2313	A
1	A	2314	U
1	A	2315	G
1	A	2334	U
1	A	2335	G
1	A	2336	U
1	A	2364	G
1	A	2372	A
1	A	2373	A
1	A	2374	C
1	A	2375	G
1	A	2388	U
1	A	2393	G
1	A	2397	A
1	A	2401	A
1	A	2402	A
1	A	2404	A
1	A	2405	C
1	A	2411	U
1	A	2419	A
1	A	2437	G
1	A	2440	G
1	A	2442	G
1	A	2445	A
1	A	2446	U
1	A	2448	G
1	A	2449	A
1	A	2450	G
1	A	2454	G
1	A	2455	U
1	A	2458	A
1	A	2459	A
1	A	2460	U
1	A	2461	A
1	A	2462	A
1	A	2463	G
1	A	2464	U
1	A	2465	G

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Mol	Chain	Res	Type
1	A	2466	G
1	A	2467	G
1	A	2468	A
1	A	2470	C
1	A	2471	U
1	A	2472	U
1	A	2473	C
1	A	2474	G
1	A	2475	G
1	A	2479	C
1	A	2481	G
1	A	2483	G
1	A	2484	A
1	A	2485	A
1	A	2486	A
1	A	2488	A
1	A	2489	C
1	A	2490	C
1	A	2492	C
1	A	2493	U
1	A	2494	A
1	A	2495	C
1	A	2496	C
1	A	2497	U
1	A	2498	U
1	A	2501	U
1	A	2502	A
1	A	2503	G
1	A	2505	U
1	A	2506	U
1	A	2511	A
1	A	2514	U
1	A	2515	A
1	A	2549	G
1	A	2550	U
1	A	2551	U
1	A	2560	C
1	A	2561	A
1	A	2566	C
1	A	2568	C
1	A	2569	A
1	A	2571	U

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Mol	Chain	Res	Type
1	A	2572	C
1	A	2573	G
1	A	2585	G
1	A	2593	A
1	A	2594	C
1	A	2606	G
1	A	2607	G
1	A	2614	G
1	A	2618	G
1	A	2626	A
1	A	2628	A
1	A	2629	U
1	A	2635	A
1	A	2651	G
1	A	2652	U
1	A	2656	A
1	A	2672	G
1	A	2674	A
1	A	2677	G
1	A	2678	A
1	A	2679	A
1	A	2680	A
1	A	2681	U
1	A	2689	A
1	A	2691	A
1	A	2694	A
1	A	2705	A
1	A	2714	G
1	A	2719	U
1	A	2728	G
1	A	2729	U
1	A	2753	G
1	A	2755	C
1	A	2761	G
1	A	2771	U
1	A	2772	C
1	A	2773	C
1	A	2777	G
1	A	2778	G
1	A	2791	G
1	A	2796	G
1	A	2799	A

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Mol	Chain	Res	Type
1	A	2800	G
1	A	2801	A
1	A	2802	A
1	A	2809	C
1	A	2810	C
1	A	2814	G
1	A	2817	A
1	A	2819	A
1	A	2820	A
1	A	2826	U
1	A	2827	U
1	A	2828	G
1	A	2836	C
1	A	2839	G
1	A	2842	U
1	A	2843	U
1	A	2844	C
1	A	2845	A
1	A	2847	A
1	A	2851	A
1	A	2853	A
1	A	2861	U
1	A	2865	U
1	A	2867	C
1	A	2871	G
1	A	2872	A
1	A	2887	A
1	A	2889	C
1	A	2898	G
1	A	2899	C
1	A	2911	A
1	A	2914	G
1	A	2918	G
1	A	2922	G
1	A	2923	U
1	A	2928	C
1	A	2933	A
1	A	2935	U
1	A	2936	A
1	A	2938	G
1	A	2940	A
1	A	2941	A

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Mol	Chain	Res	Type
1	A	2942	C
1	A	2947	G
1	A	2948	C
1	A	2954	U
1	A	2971	A
1	A	2977	G
1	A	2983	C
1	A	2990	G
1	A	2997	G
1	A	3011	A
1	A	3012	A
1	A	3022	G
1	A	3027	A
1	A	3028	G
1	A	3046	A
1	A	3056	U
1	A	3059	G
1	A	3078	U
1	A	3080	G
1	A	3092	C
1	A	3101	G
1	A	3105	U
1	A	3109	G
1	A	3113	A
1	A	3116	G
1	A	3117	C
1	A	3119	U
1	A	3129	A
1	A	3130	A
1	A	3131	U
1	A	3142	A
1	A	3153	U
1	A	3154	C
1	A	3156	U
1	A	3158	G
1	A	3165	A
1	A	3166	C
1	A	3167	A
1	A	3170	A
1	A	3171	U
1	A	3172	A
1	A	3173	G

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Mol	Chain	Res	Type
1	A	3176	G
1	A	3179	U
1	A	3181	C
1	A	3187	A
1	A	3195	U
1	A	3196	U
1	A	3199	G
1	A	3207	U
1	A	3217	C
1	A	3218	A
1	A	3219	G
1	A	3220	G
1	A	3223	A
1	A	3268	A
1	A	3270	U
1	A	3271	G
1	A	3273	A
1	A	3275	U
1	A	3276	G
1	A	3280	U
1	A	3281	U
1	A	3282	U
1	A	3289	G
1	A	3294	A
1	A	3295	A
1	A	3303	G
1	A	3304	U
1	A	3313	U
1	A	3316	A
1	A	3320	A
1	A	3335	A
1	A	3336	A
1	A	3341	U
1	A	3342	A
1	A	3345	G
1	A	3351	U
1	A	3352	U
1	A	3353	G
1	A	3354	U
1	A	3355	U
1	A	3362	A
1	A	3363	U

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Mol	Chain	Res	Type
1	A	3369	G
1	A	3378	C
1	A	3382	U
1	A	3396	U
47	x	7	G
47	x	10	C
47	x	22	A
47	x	33	U
47	x	41	G
47	x	54	U
47	x	55	A
47	x	65	G
47	x	72	A
47	x	73	C
47	x	93	C
47	x	99	G
47	x	102	A
47	x	112	G
47	x	121	U
48	y	23	U
48	y	24	G
48	y	34	U
48	y	35	C
48	y	51	G
48	y	52	A
48	y	59	A
48	y	62	C
48	y	63	G
48	y	75	G
48	y	81	U
48	y	82	U
48	y	83	C
48	y	86	U
48	y	87	G
48	y	90	U
48	y	91	C
48	y	95	G
48	y	104	A
48	y	105	A
48	y	106	C
48	y	113	U
48	y	125	U

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Mol	Chain	Res	Type
48	y	127	U
48	y	138	A
48	y	151	C
48	y	152	G

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	621	A
1	A	916	G
1	A	1064	A
1	A	1217	A
1	A	1355	A
1	A	1569	U
1	A	1629	U
1	A	1815	U
1	A	2101	C
1	A	2112	U
1	A	2400	G
1	A	2404	A
1	A	2459	A
1	A	3027	A
1	A	3206	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

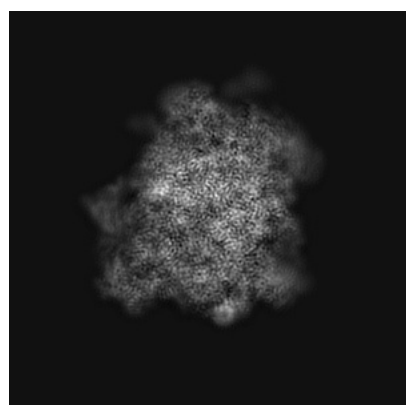
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10068. These allow visual inspection of the internal detail of the map and identification of artifacts.

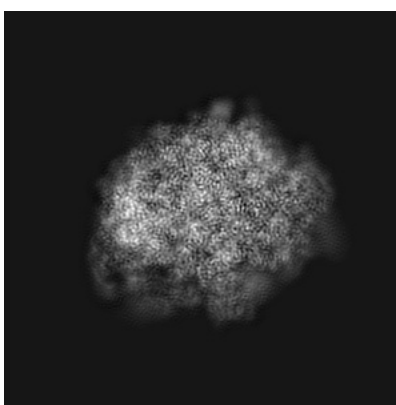
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

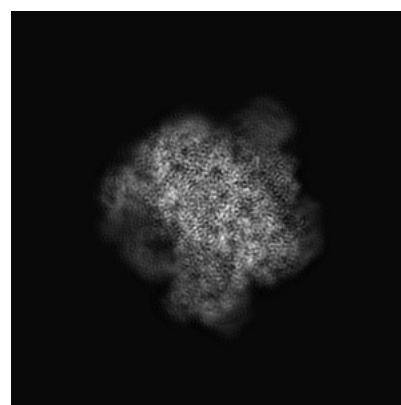
6.1.1 Primary map



X



Y

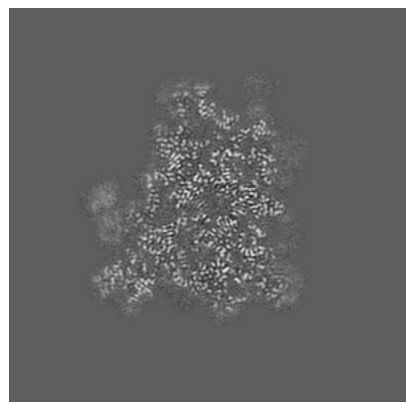


Z

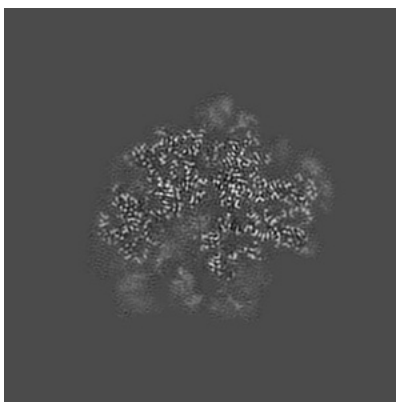
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

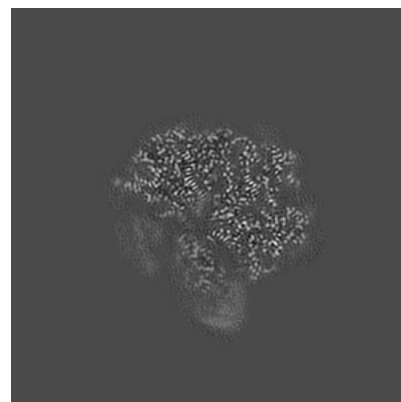
6.2.1 Primary map



X Index: 180



Y Index: 180

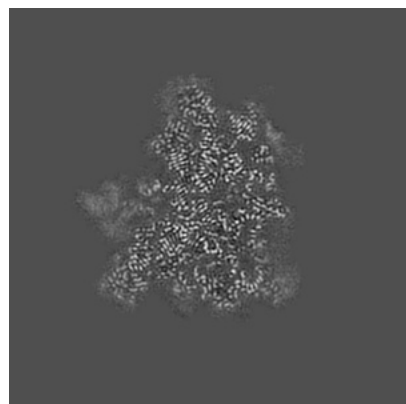


Z Index: 180

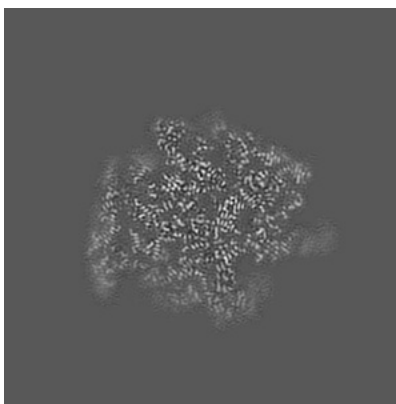
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

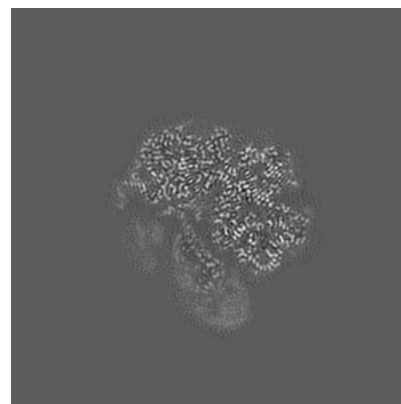
6.3.1 Primary map



X Index: 189



Y Index: 196

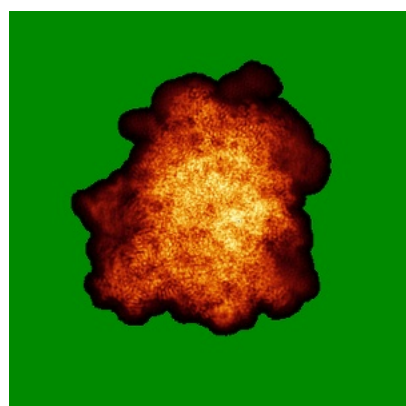


Z Index: 177

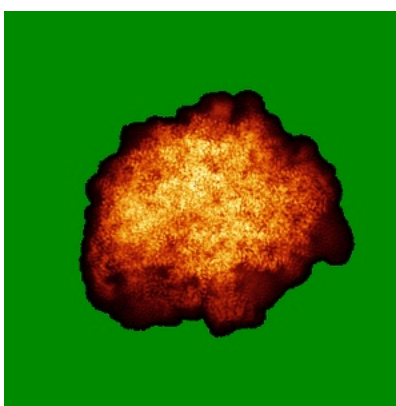
The images above show the largest variance slices of the map in three orthogonal directions.

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

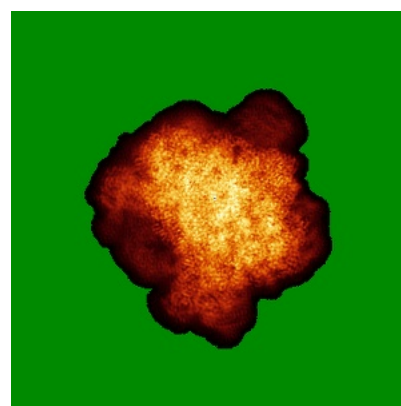
6.4.1 Primary map



X



Y

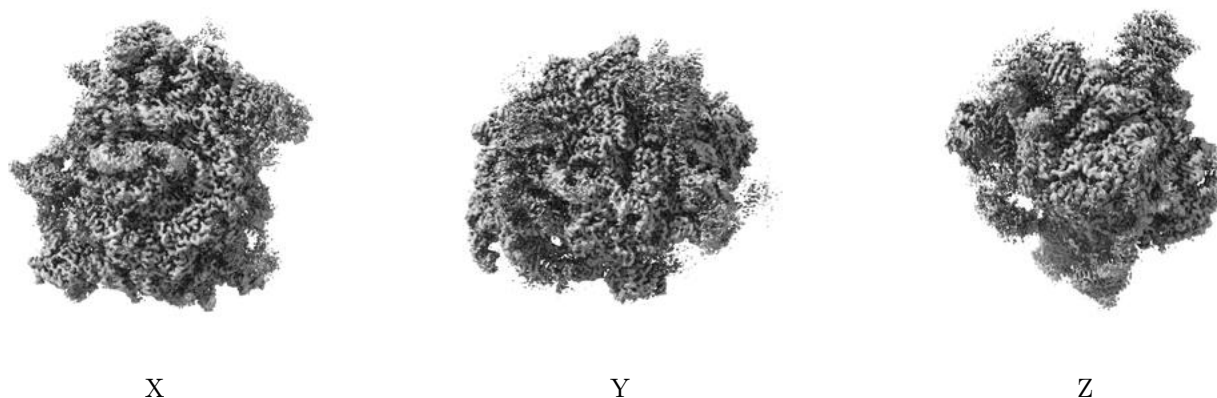


Z

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 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

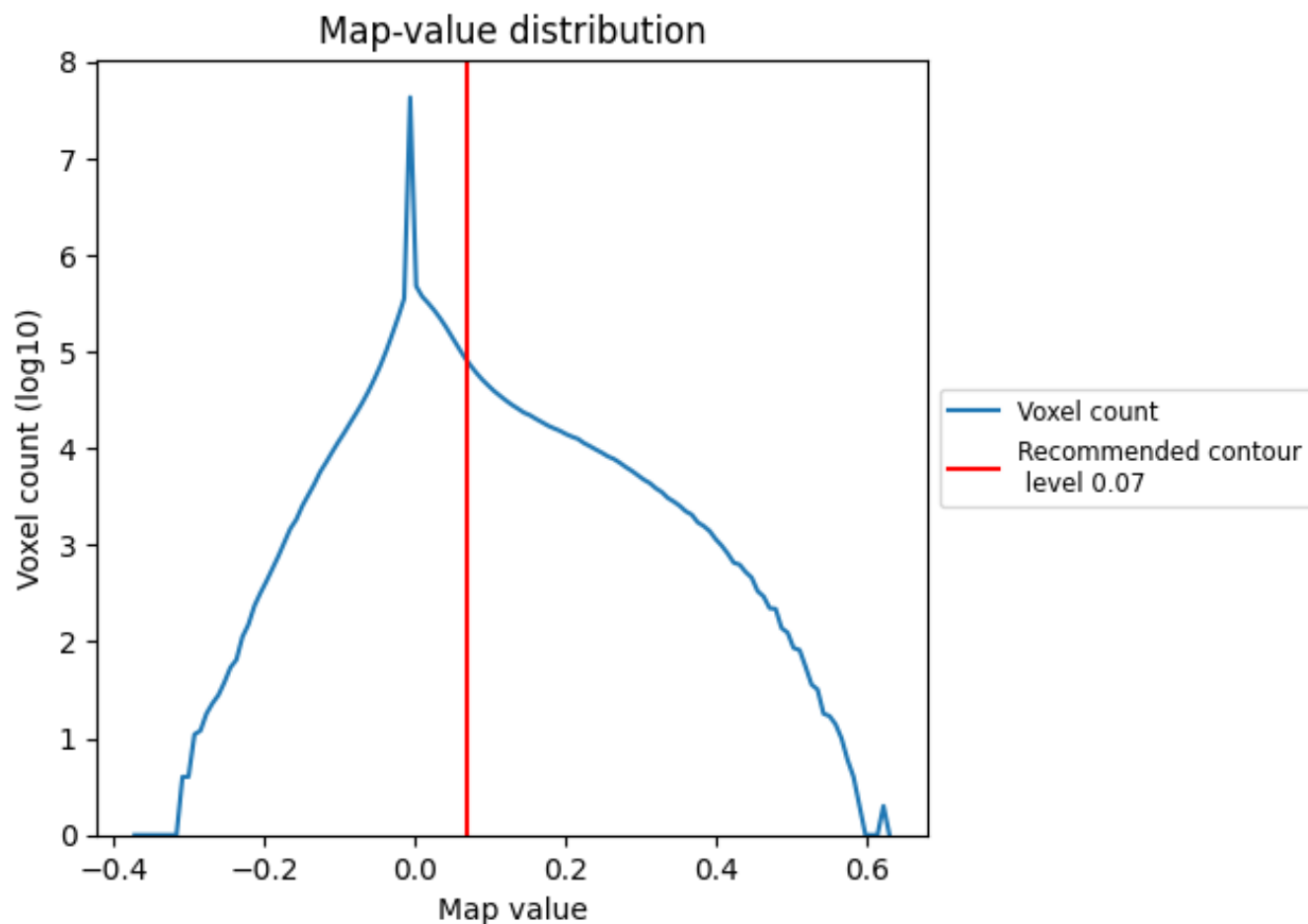
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

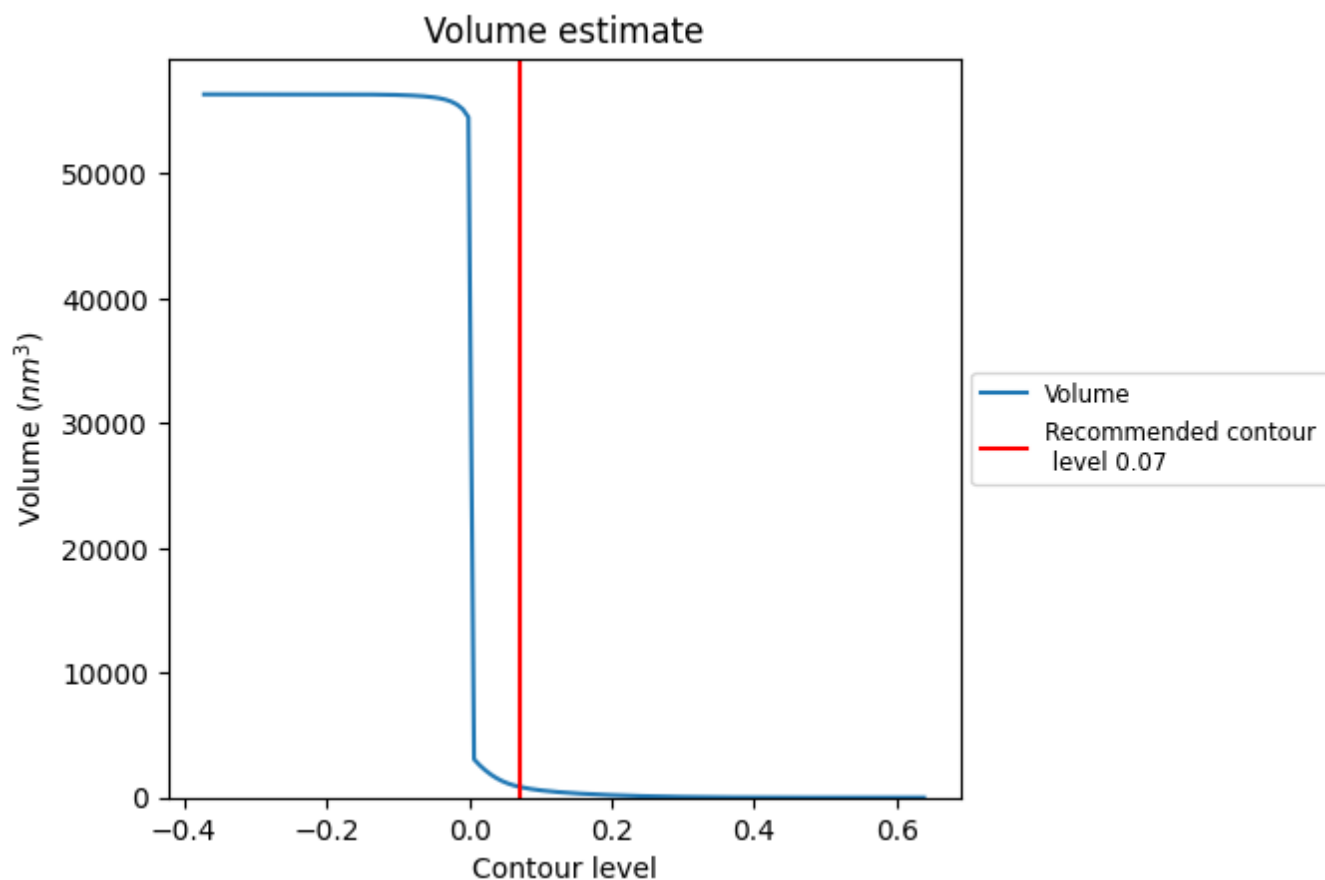
This section contains the results of statistical analysis of the map.

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.

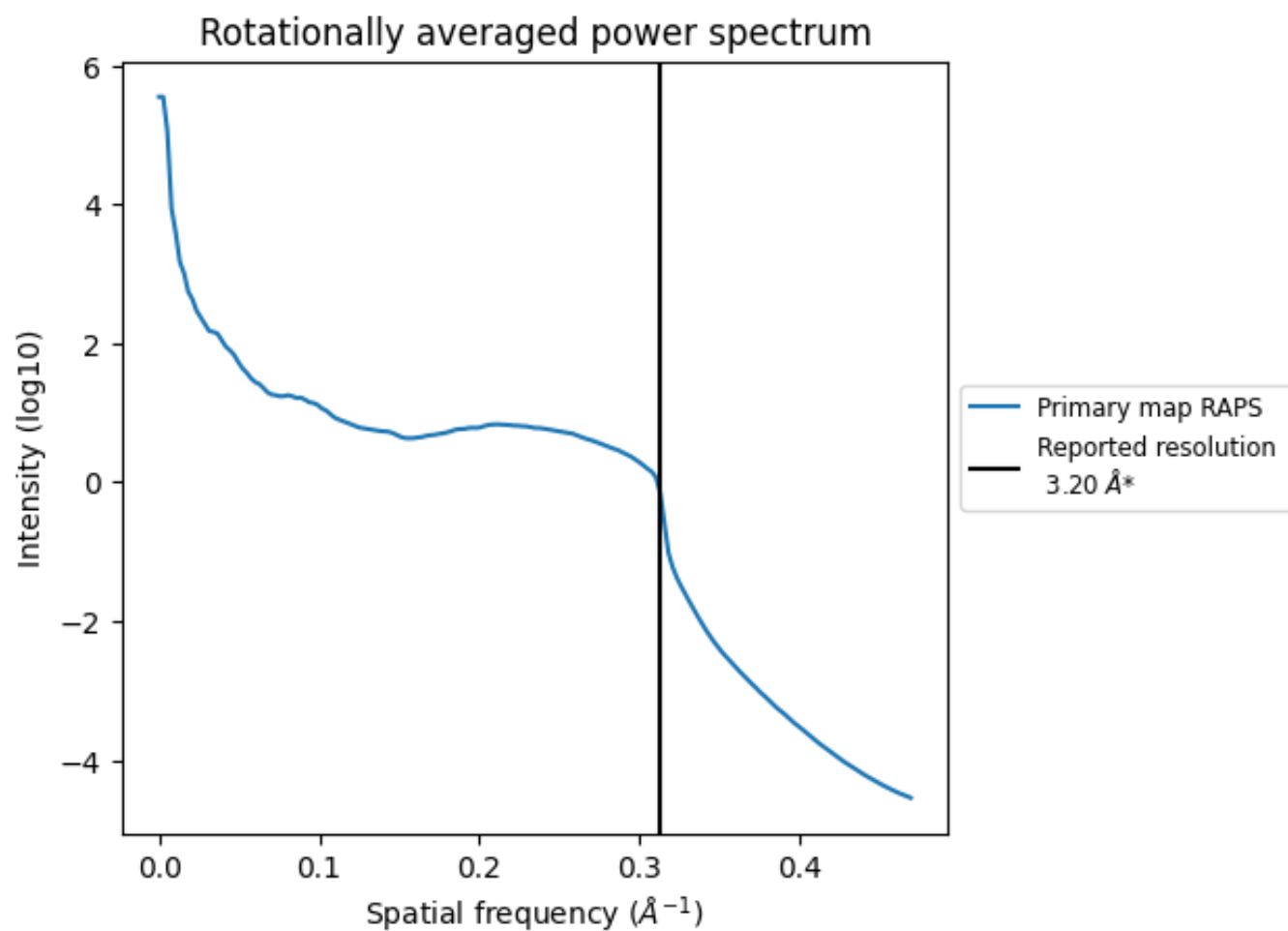
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 871 nm³; this corresponds to an approximate mass of 787 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 0.312 Å⁻¹

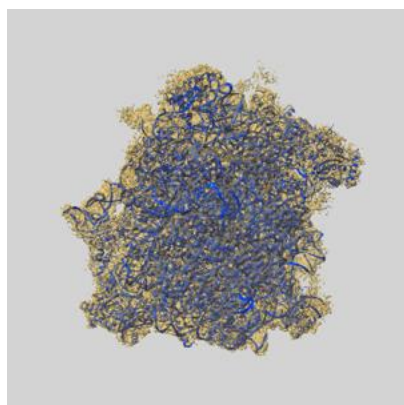
8 Fourier-Shell correlation

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

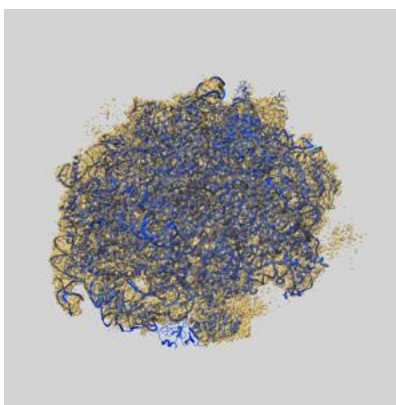
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10068 and PDB model 6RZZ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

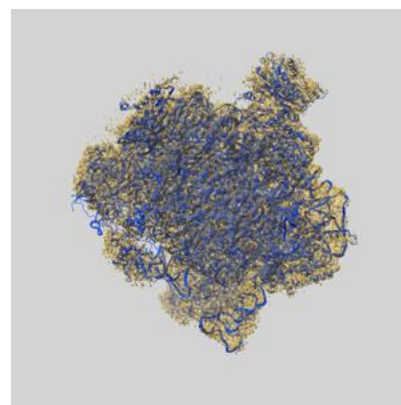
9.1 Map-model overlay [i](#)



X



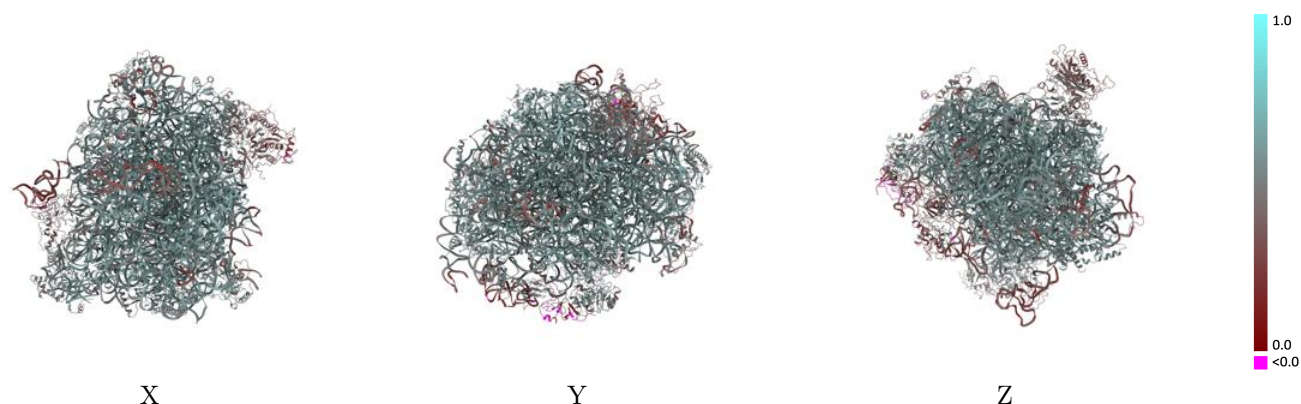
Y



Z

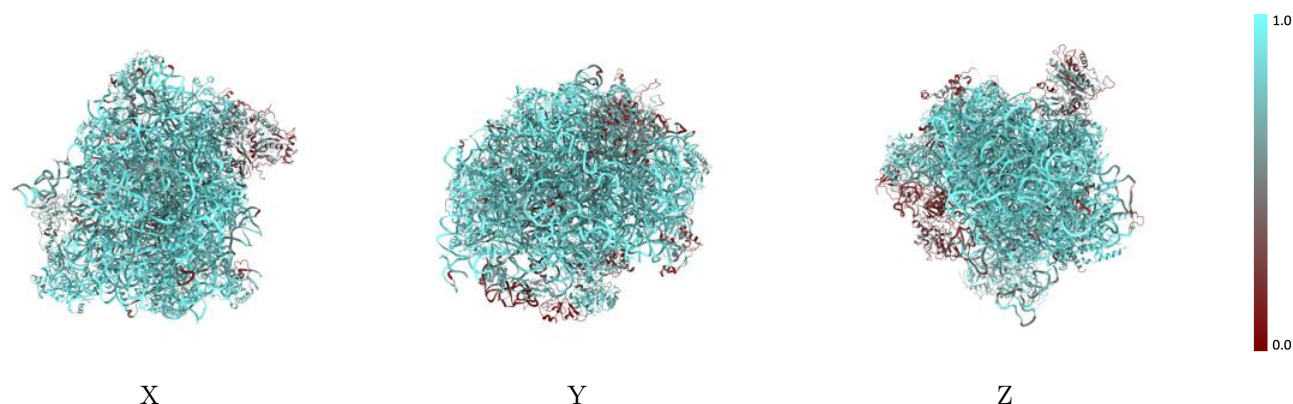
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



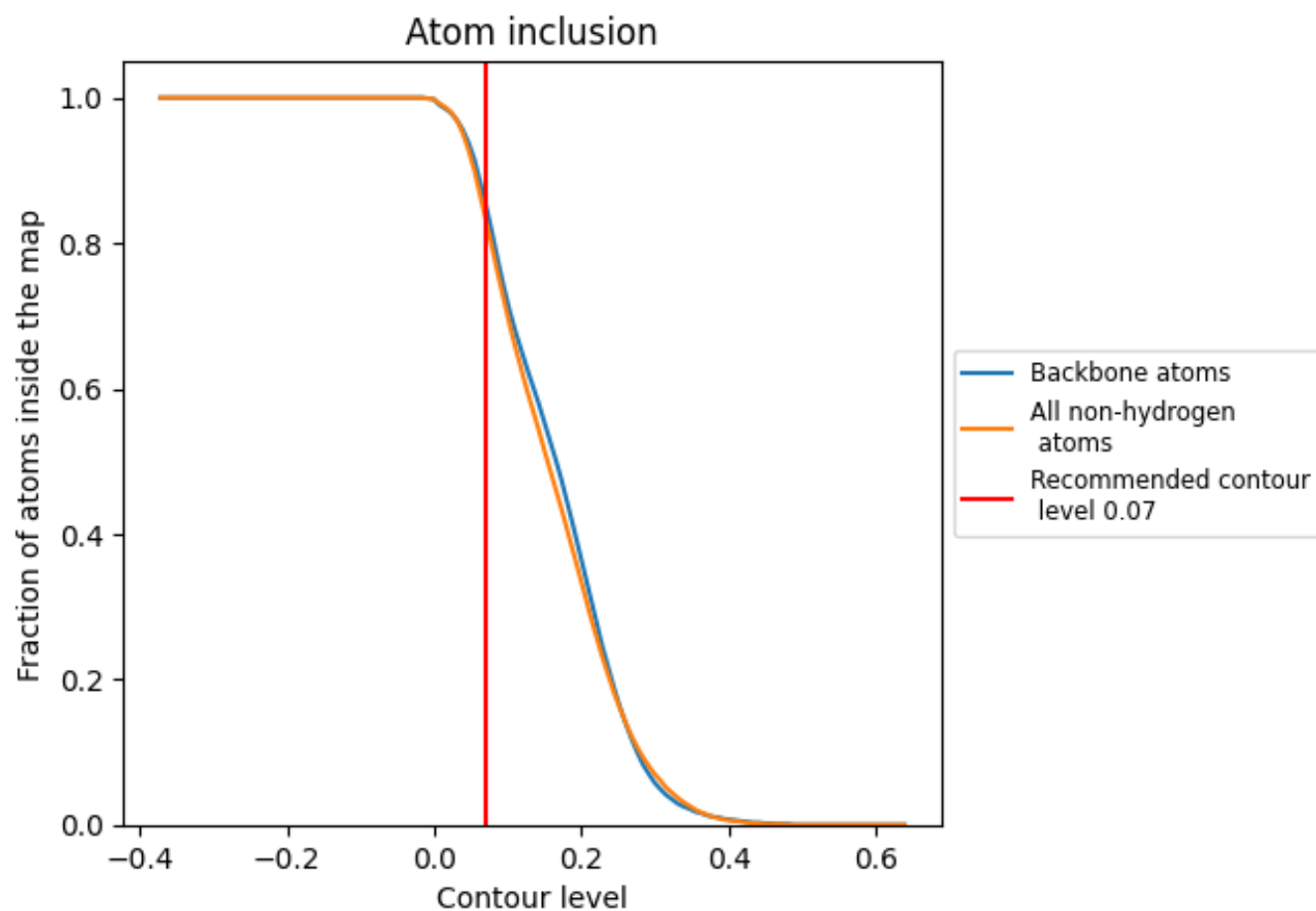
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 83% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8320	 0.5300
A	 0.8910	 0.5350
B	 0.8990	 0.5870
C	 0.8930	 0.5770
D	 0.8980	 0.5820
E	 0.7620	 0.4720
F	 0.7440	 0.5210
G	 0.7010	 0.4950
H	 0.8180	 0.5400
J	 0.8840	 0.5770
K	 0.8550	 0.5680
L	 0.8790	 0.5830
M	 0.8390	 0.5480
N	 0.9120	 0.5870
O	 0.9080	 0.5990
P	 0.8560	 0.5380
Q	 0.9250	 0.5930
R	 0.8790	 0.5690
S	 0.8950	 0.5770
T	 0.8480	 0.5610
U	 0.9060	 0.5900
V	 0.8430	 0.5390
W	 0.8470	 0.5700
X	 0.8900	 0.5840
Y	 0.8240	 0.5210
Z	 0.8710	 0.5690
a	 0.8070	 0.5630
b	 0.9050	 0.5810
c	 0.8080	 0.5110
d	 0.8310	 0.5690
e	 0.8700	 0.5790
f	 0.9050	 0.5900
g	 0.8780	 0.5820
h	 0.7030	 0.5210
i	 0.9170	 0.6030



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Chain	Atom inclusion	Q-score
j	 0.8280	 0.5320
k	 0.8620	 0.5950
l	 0.8930	 0.5930
m	 0.8430	 0.5700
n	 0.7920	 0.4990
o	 0.2820	 0.3550
p	 0.6140	 0.3850
r	 0.4140	 0.3880
s	 0.0040	 0.1110
u	 0.4260	 0.4540
v	 0.4440	 0.5140
w	 0.5320	 0.4450
x	 0.9740	 0.5520
y	 0.9610	 0.5760