



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 11:38 AM UTC

PDB ID : 6QIK / pdb_00006qik
EMDB ID : EMD-4560
Title : Cryo-EM structures of Lsg1-TAP pre-60S ribosomal particles
Authors : Kargas, V.; Warren, A.J.
Deposited on : 2019-01-20
Resolution : 3.10 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:

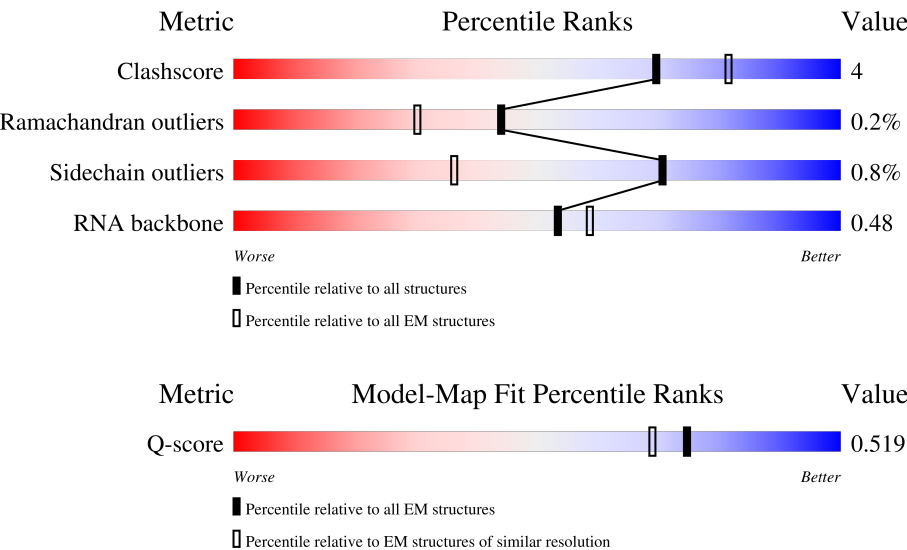
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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	14724 (2.60 - 3.60)

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	154	
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	z	432	
41	w	518	
42	v	155	
43	o	640	
44	p	210	
45	t	128	
46	x	121	
47	y	158	

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 128569 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	S	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		
			611	391	115	105	0	0

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

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

- 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		
			756	476	153	122	5	0	0

- 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		
			680	421	136	117	6	0	0

- 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		
			1691	1051	293	340	7	0	0

- Molecule 40 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	z	58	Total	C	N	O	S		
			491	301	100	87	3	0	0

- Molecule 41 is a protein called 60S ribosomal export protein NMD3.

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

- Molecule 42 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 43 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	322	Total	C	N	O	S	0	0
			2593	1660	449	477	7		

- Molecule 44 is a protein called uL1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 46 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 47 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
48	g	1	Total	Zn	0
			1	1	
48	i	1	Total	Zn	0
			1	1	
48	l	1	Total	Zn	0
			1	1	

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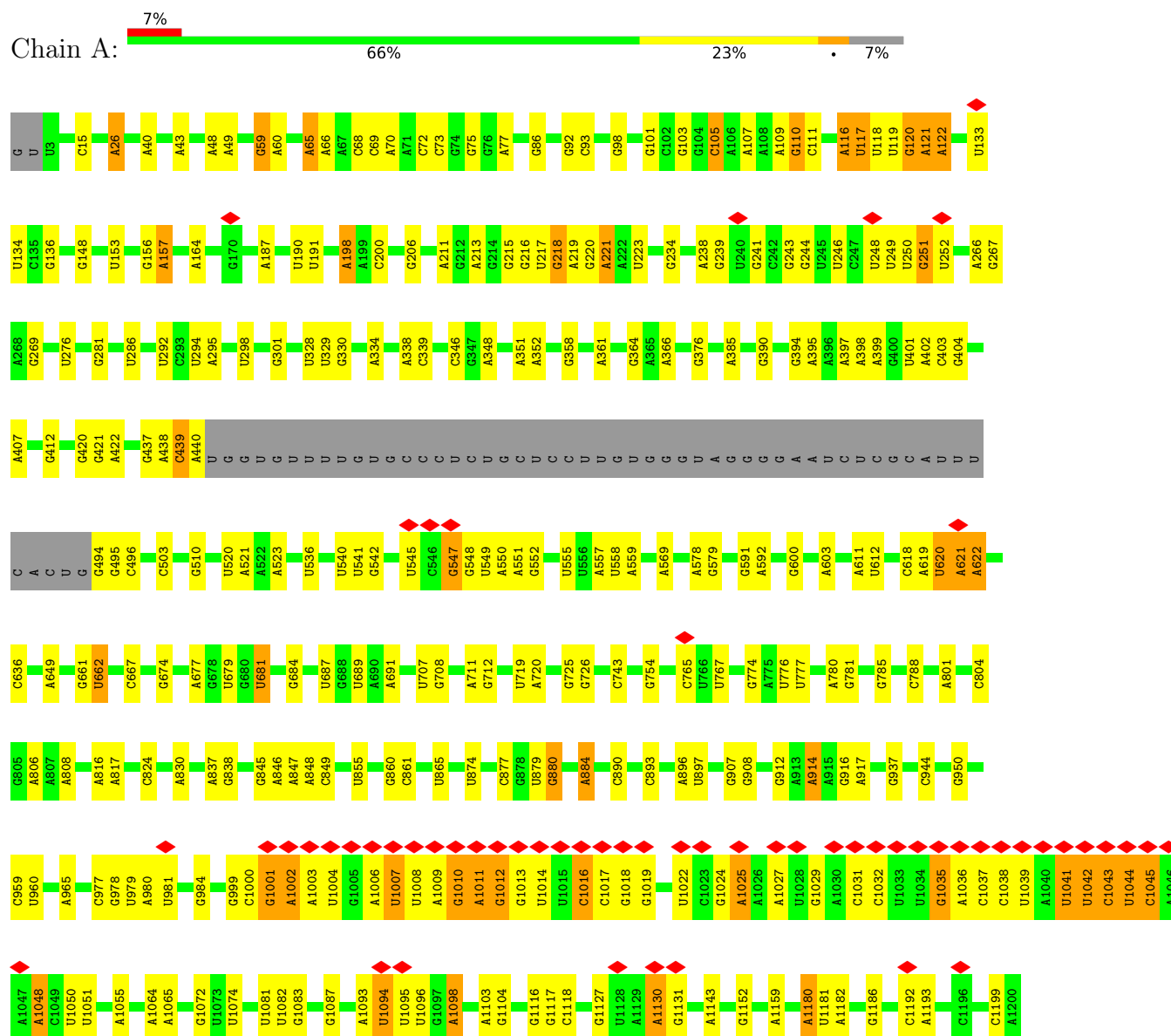
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Mol	Chain	Residues	Atoms		AltConf
48	m	1	Total 1	Zn 1	0
48	w	2	Total 2	Zn 2	0
48	t	1	Total 1	Zn 1	0

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



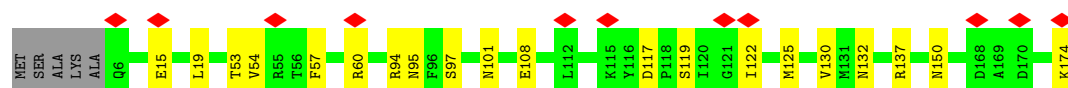
A2626	G2454	U2310	U2184	U1955	A1813	U1830	G1517	C1385	A1270	C1201
A2635	U2455	G2311	G2185	A	A1814	C1631	G1517	A1386	A1271	G1207
G2648	A2456	A2312	U2186	G	U1815	C1632	U1523	G1389	C1272	U1208
U2652	G2457	A2313	G2187	U	A1816	G1633	G1525	G1392	A1273	G1209
A2656	A2458	G2314	G2188	G	U1820	G1635	U1526	G1399	A1274	U1210
A2657	U2460	G2315	C2196	A	U1821	A1838	A1534	G1400	C1275	A1217
G2672	A2461	G2323	C2197	G	G1833	C1639	G1542	G1404	U1218	U1219
A2673	G2462	A2324	U2205	C	U1834	A1642	G1547	U1405	C1277	C1218
A2674	C2463	G2325	G2206	A	A1835	A1643	G1547	U1406	A1278	U1220
G2677	U2464	C2330	A2207	C	U1839	U1645	C1551	A1407	C1279	U1221
A2678	G2465	U2334	U2208	A	A1841	G1646	U1555	G1417	C1280	G1222
A2680	U2466	G2335	U2209	C	A1842	C1657	C1556	A1418	G1281	A1223
U2681	C2470	C2350	G2221	U	U1849	G1677	C1562	A1419	C1282	C1224
G2677	A2547	A2356	A2224	C	A1850	U1689	C1563	A1428	C1283	A1225
A2678	C2548	A2372	C2245	G	A1858	U1705	U1564	G1434	C1284	G1226
A2679	U2550	A2373	G2251	C	A1859	U1715	U1565	A1435	G1285	C1227
A2691	G2551	C2374	A2252	A	G1863	U1721	A1566	U1436	A1287	C1228
A2694	C2555	G2375	U2253	C	C1866	U1724	U1567	C1437	U1288	G1230
A2703	A2557	U2377	A2254	U	U1871	U1725	U1569	G1443	G1289	A1231
A2704	C2560	G2382	C2255	G	G1872	C1725	U1570	A1444	G1295	C1232
A2705	A2561	U2388	U2256	U	U1873	U1729	U1571	U1445	A1302	G1233
A2708	A2562	G2393	A2257	C	A1874	U1737	G1573	A1450	A1303	G1234
U2712	C2566	C2394	U2260	A	G1878	U1741	C1574	A1451	A1304	U1235
U2713	G2567	G2397	A2261	G	U1879	U1750	C1574	A1452	G1307	G1236
G2714	A2569	A2397	U2262	C	U1880	G1751	U1579	U1455	A1308	G1237
U2719	U2493	A2401	C2263	U	A1886	U1761	C1582	U1458	U1309	C1238
U2722	C2495	A2402	U2264	C	A1893	C1762	A1583	U1458	G1313	C1239
C2572	C2496	G2403	C2265	C	A1900	C1762	A1583	G1466	A1240	U1241
G2728	U2497	A2404	U2266	U	G1906	U1764	A1588	A1467	C1316	G1242
U2737	U2498	C2405	A2270	C	C1907	U1765	A1588	U1476	A1317	A1244
A2740	U2501	U2411	A2271	G	A1921	G1775	A1593	A1477	A1330	G1245
G2753	U2502	G2412	G2272	U	A1930	G1778	A1602	A1481	U1331	U1247
C2755	G2503	G2435	U2273	C	G1940	G1779	A1603	G1487	A1332	C1248
C2764	U2504	U2436	A2274	U	U1942	U1780	A1604	U1494	A1333	G1250
A2771	A2511	A2444	U2279	C	C1943	C1788	U1606	G1493	U1348	A1251
C2772	U2514	A2445	A2281	U	U1950	G1794	A1613	C1497	A1349	A1252
C2773	U2515	U2446	U2282	C	C1951	U1950	A1618	G1507	A1350	U1253
G2777	U2516	U2447	A2295	U	G1952	U1951	A1619	A1355	U1351	C1254
	G2522	G2448	U2298	A	G1953	U1952	U1620	G1508	A1352	C1255
	A2523	A2449	G2307	C	U1954	G1954	U1620	G1507	U1353	G1256
	A2524	U2452	C2308	A				G1507	A1357	U1257
		U2453	G2180	C				G1508	G1357	G1258
										U1269

Chain D:  92% 8%

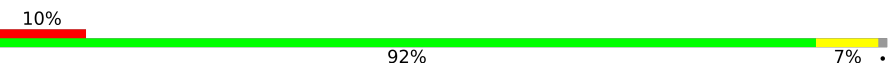


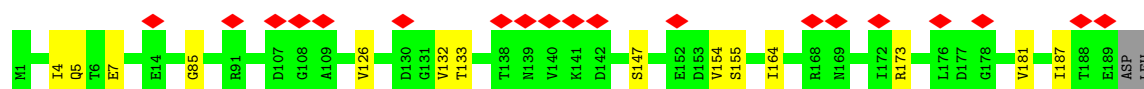
- Molecule 5: 60S ribosomal protein L11-A

Chain E:  6% 86% 11%

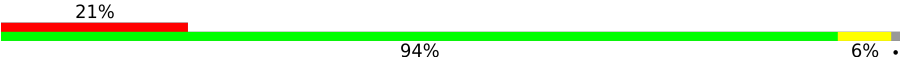


- Molecule 6: 60S ribosomal protein L9-A

Chain F:  10% 92% 7%



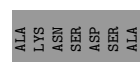
- Molecule 7: 60S ribosomal protein L6-A

Chain G:  21% 94% 6%



- Molecule 8: 60S ribosomal protein L8-A

Chain H:  7% 84% 13%



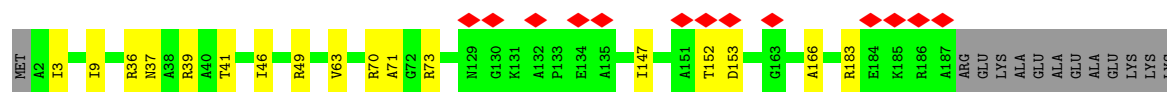
- Molecule 9: 60S ribosomal protein L16-B

Chain J:  91% 8%



- Molecule 10: 60S ribosomal protein L13-A

Chain K:  7% 85% 9% 7%



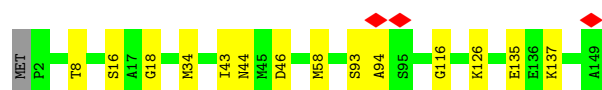
- Molecule 11: 60S ribosomal protein L23-A



- Molecule 12: 60S ribosomal protein L14-A



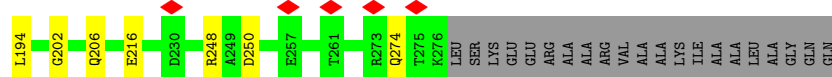
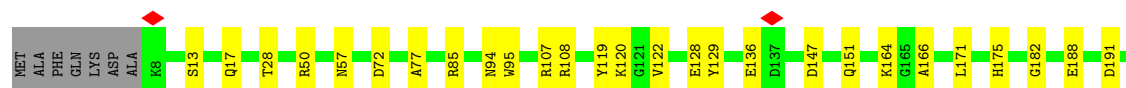
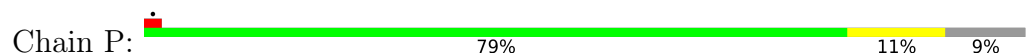
- Molecule 13: 60S ribosomal protein L28



- Molecule 14: 60S ribosomal protein L15-A



- Molecule 15: 60S ribosomal protein L5

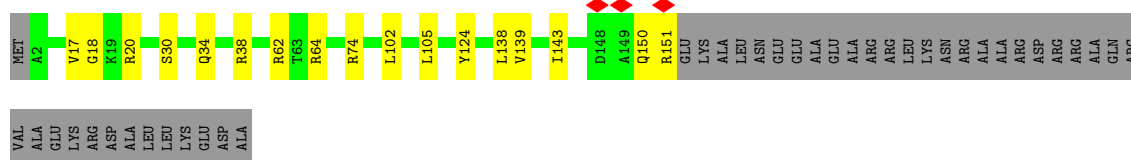


- Molecule 16: 60S ribosomal protein L18-A

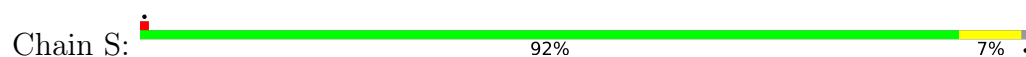




- Molecule 17: 60S ribosomal protein L19-A



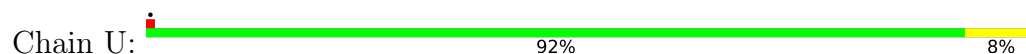
- Molecule 18: 60S ribosomal protein L20-A



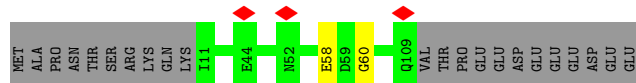
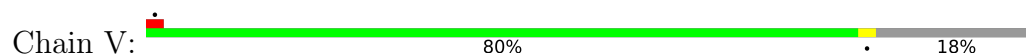
- Molecule 19: 60S ribosomal protein L21-A



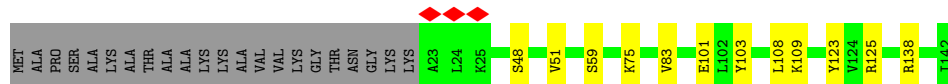
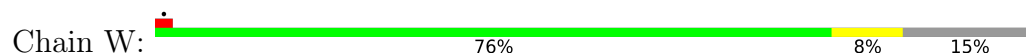
- Molecule 20: 60S ribosomal protein L17-A



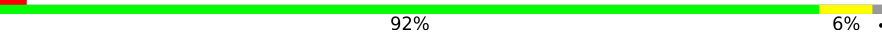
- Molecule 21: 60S ribosomal protein L22-A



- Molecule 22: 60S ribosomal protein L25

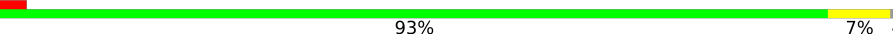


- Molecule 23: 60S ribosomal protein L26-A

Chain X:  92% 6%



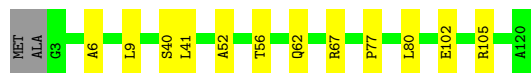
- Molecule 24: 60S ribosomal protein L27-A

Chain Y:  93% 7%



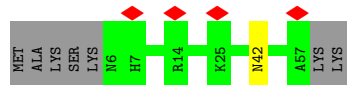
- Molecule 25: 60S ribosomal protein L35-A

Chain Z:  88% 10%



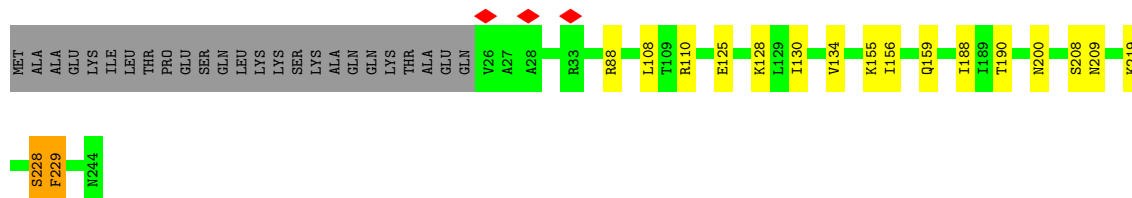
- Molecule 26: 60S ribosomal protein L29

Chain a:  86% 12%



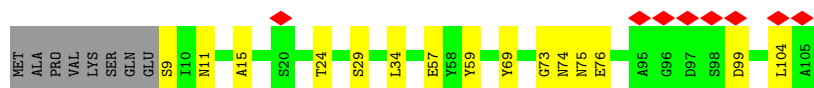
- Molecule 27: 60S ribosomal protein L7-A

Chain b:  82% 7% 10%

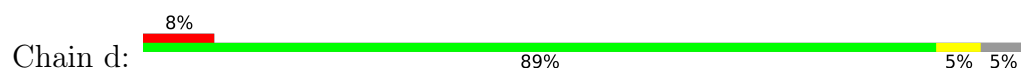


- Molecule 28: 60S ribosomal protein L30

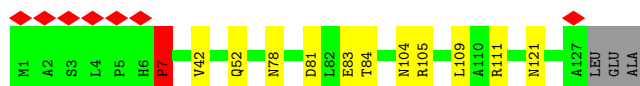
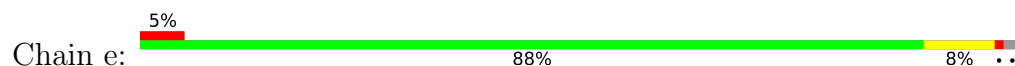
Chain c:  78% 14% 8%



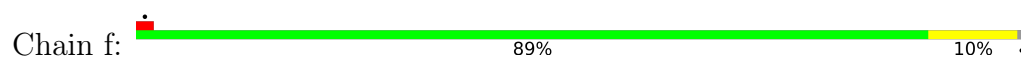
- Molecule 29: 60S ribosomal protein L31-A



- Molecule 30: 60S ribosomal protein L32



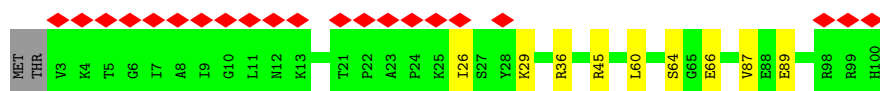
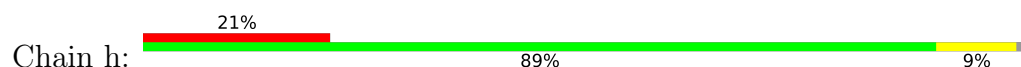
- Molecule 31: 60S ribosomal protein L33-A



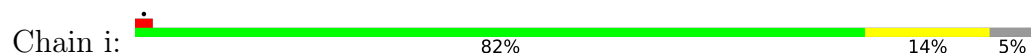
- Molecule 32: 60S ribosomal protein L34-A



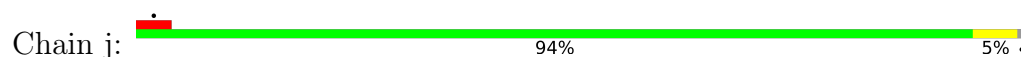
- Molecule 33: 60S ribosomal protein L36-A

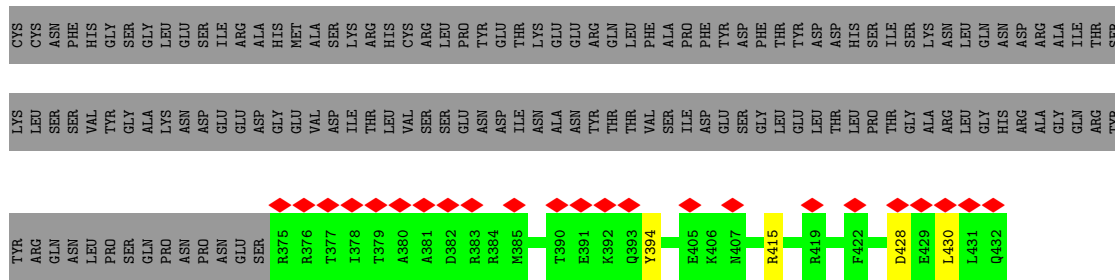


- Molecule 34: 60S ribosomal protein L37-A

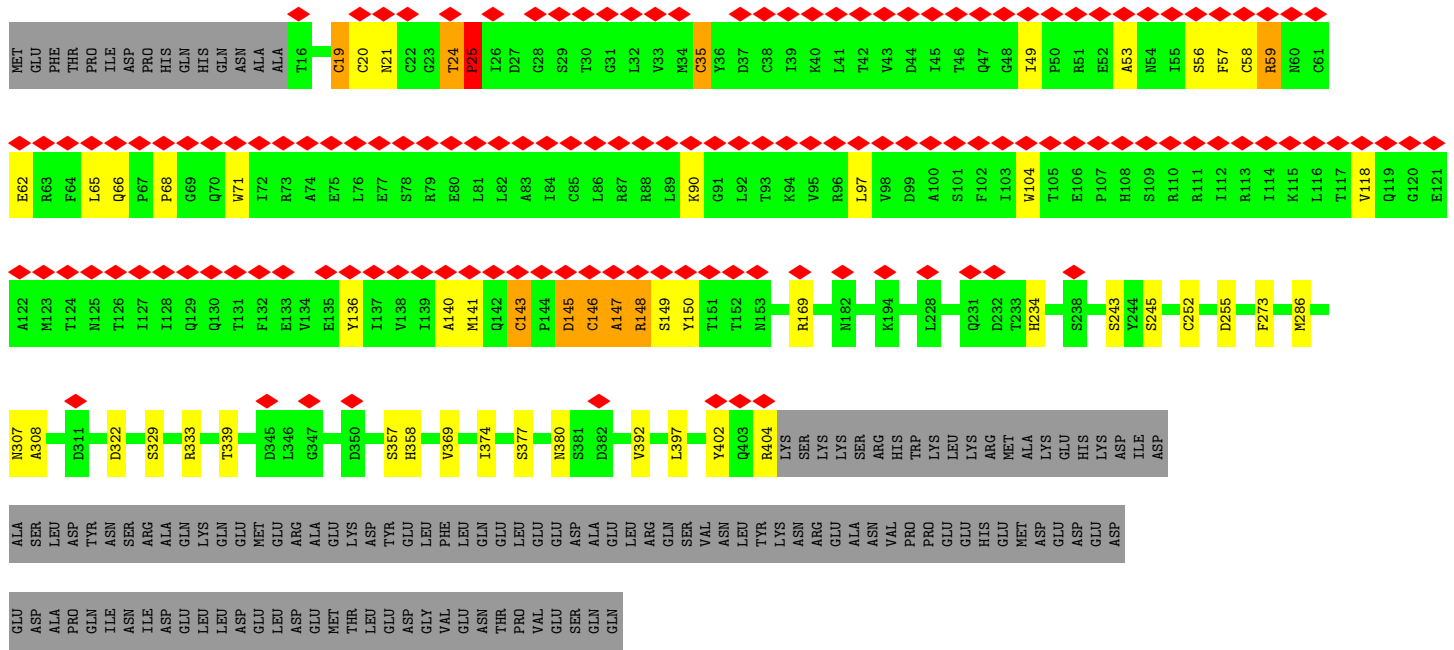


- Molecule 35: 60S ribosomal protein L38

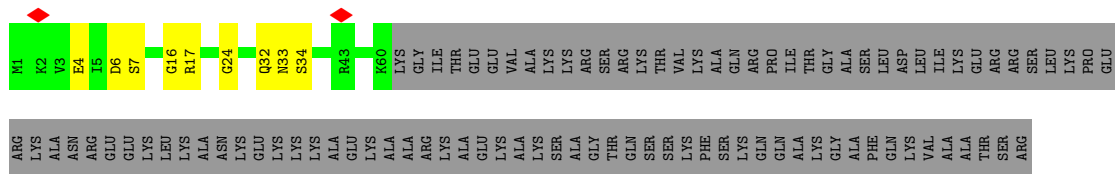




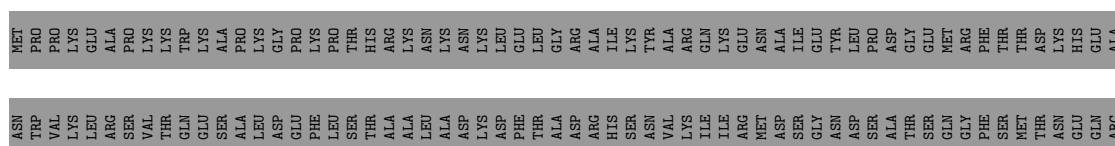
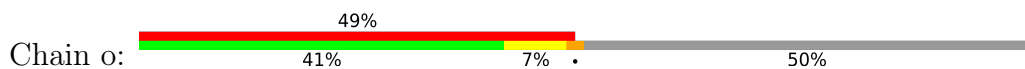
- Molecule 41: 60S ribosomal export protein NMD3

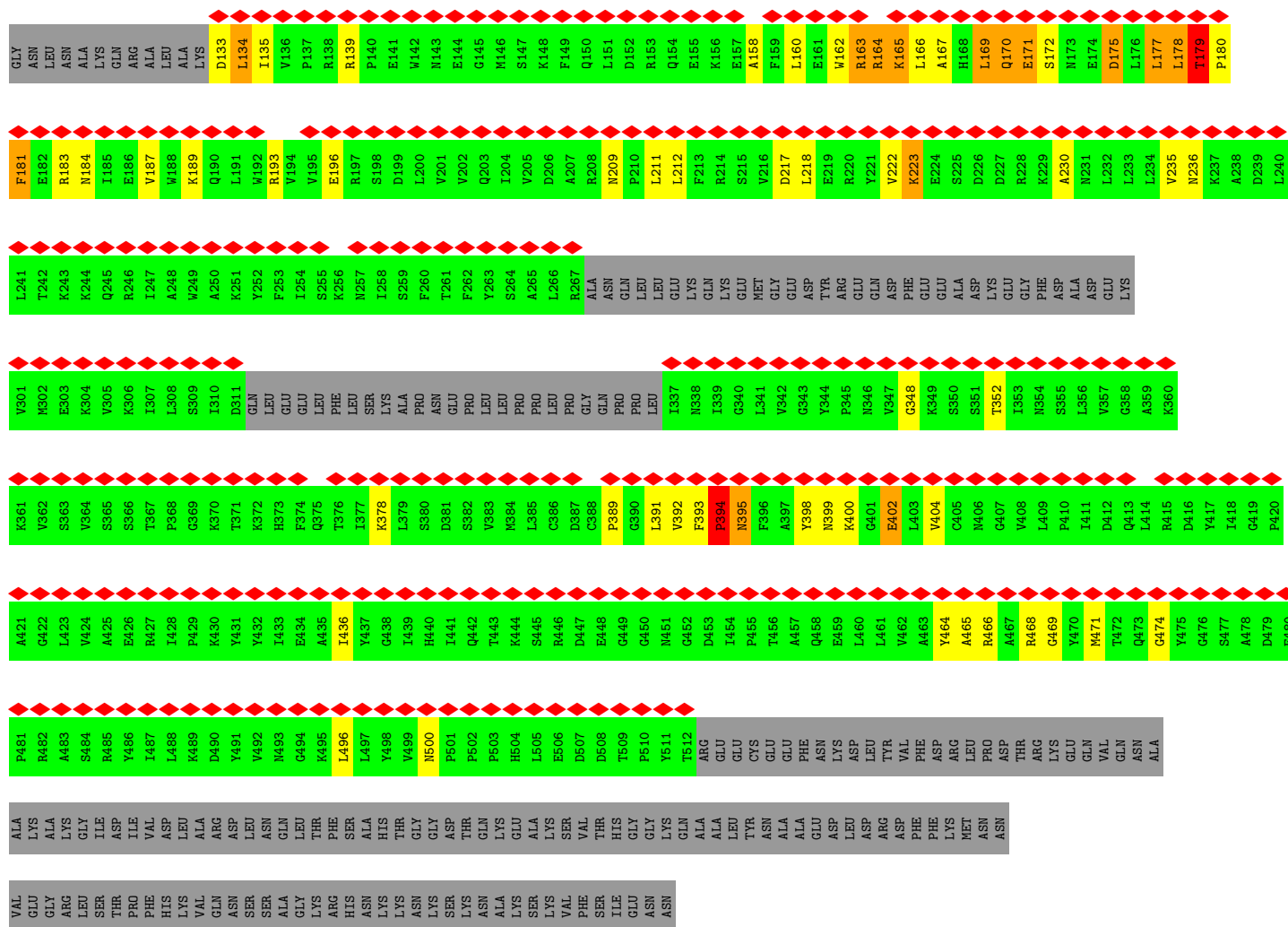


- Molecule 42: 60S ribosomal protein L24-A

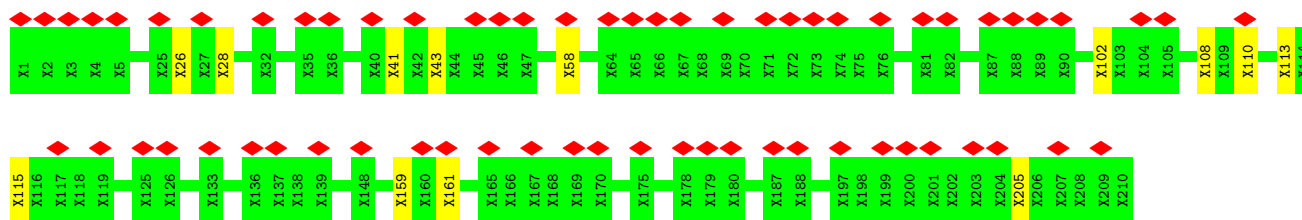


- Molecule 43: Large subunit GTPase 1

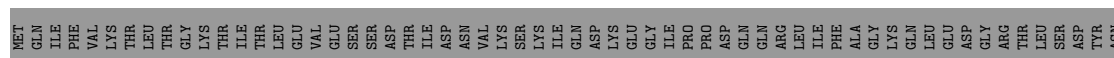
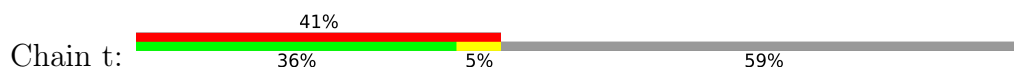


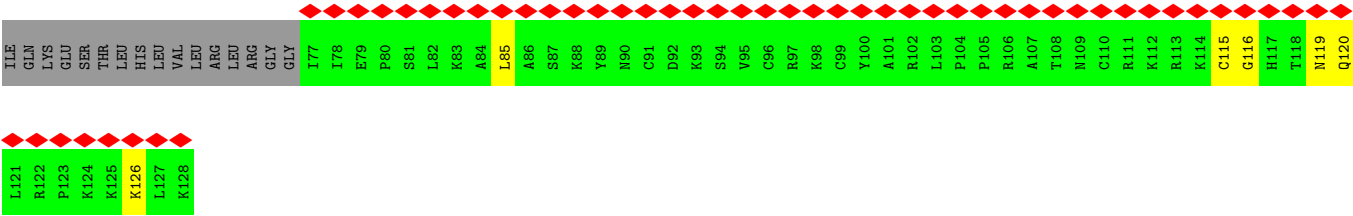


• Molecule 44: uL1

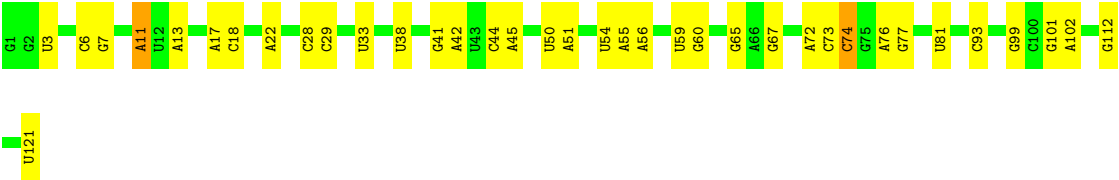


• Molecule 45: Ubiquitin-60S ribosomal protein L40

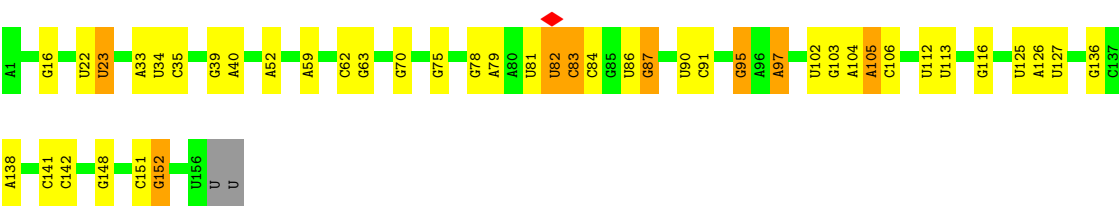




• Molecule 46: 5S ribosomal RNA



• Molecule 47: 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	260853	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	0.560	Depositor
Minimum map value	-0.287	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.022	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	0.58	1/75327 (0.0%)	0.47	0/117440
2	B	0.86	0/1912	0.69	0/2569
3	C	0.81	0/3110	0.72	4/4184 (0.1%)
4	D	0.82	0/2800	0.58	0/3791
5	E	0.40	0/1373	0.52	0/1841
6	F	0.37	0/1523	0.51	0/2051
7	G	0.52	0/1423	0.51	0/1911
8	H	0.61	0/1774	0.54	0/2395
9	J	0.82	0/1593	0.59	0/2137
10	K	0.78	0/1511	0.72	0/2031
11	L	0.78	0/1017	0.60	0/1368
12	M	0.58	0/1060	0.52	0/1428
13	N	0.85	0/1203	0.56	0/1611
14	O	0.90	0/1756	0.64	0/2353
15	P	0.60	0/2225	0.53	0/3004
16	Q	0.83	0/1464	0.60	0/1964
17	R	0.81	0/1226	0.60	0/1637
18	S	0.66	0/1472	0.53	0/1979
19	T	0.70	0/1299	0.55	0/1742
20	U	0.90	0/1245	0.63	0/1676
21	V	0.51	0/802	0.52	0/1087
22	W	0.70	0/973	0.56	0/1313
23	X	0.76	0/995	0.60	0/1329
24	Y	0.50	0/1117	0.56	0/1496
25	Z	0.72	0/972	0.60	0/1293
26	a	0.59	0/426	0.54	0/570
27	b	0.83	0/1797	0.65	1/2419 (0.0%)
28	c	0.60	0/749	0.57	0/1007
29	d	0.74	0/886	0.63	0/1190
30	e	0.77	0/1041	0.63	2/1393 (0.1%)
31	f	0.83	0/867	0.68	0/1167
32	g	0.83	0/822	0.73	0/1099

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.56	0/770	0.57	0/1023
34	i	0.87	0/680	0.72	0/901
35	j	0.56	0/617	0.52	0/825
36	k	0.88	0/442	0.56	0/587
37	l	0.75	0/768	0.75	0/1016
38	m	0.74	0/687	0.69	0/915
39	n	0.44	0/1712	0.51	0/2330
40	z	0.37	0/494	0.60	0/654
41	w	0.63	2/3135 (0.1%)	0.72	3/4255 (0.1%)
42	v	0.51	0/512	0.52	0/680
43	o	0.55	3/2647 (0.1%)	0.87	5/3582 (0.1%)
45	t	0.24	0/423	0.44	0/562
46	x	0.50	0/2880	0.41	0/4487
47	y	0.65	0/3699	0.50	0/5760
All	All	0.63	6/137226 (0.0%)	0.53	15/202052 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	w	25	PRO	N-CA	18.79	1.71	1.47
43	o	394	PRO	N-CA	17.92	1.70	1.47
41	w	19	CYS	C-O	-8.30	1.13	1.24
43	o	179	THR	C-N	7.15	1.50	1.33
1	A	2258	U	C1'-N1	6.14	1.57	1.48
43	o	393	PHE	C-N	5.02	1.45	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	18	PRO	CA-N-CD	-16.35	89.11	112.00
43	o	393	PHE	CA-C-N	16.11	139.97	119.84
43	o	393	PHE	C-N-CA	16.11	139.97	119.84
41	w	24	THR	CA-C-N	14.42	137.86	119.84
41	w	24	THR	C-N-CA	14.42	137.86	119.84
43	o	179	THR	CA-C-N	13.53	136.75	119.84
43	o	179	THR	C-N-CA	13.53	136.75	119.84
43	o	394	PRO	CA-N-CD	-8.64	99.91	112.00
3	C	18	PRO	CB-CA-C	8.08	124.89	111.56
41	w	25	PRO	CA-N-CD	-7.53	101.46	112.00
30	e	7	PRO	N-CA-CB	-6.05	96.89	103.25
3	C	17	LEU	CA-C-N	6.01	127.36	119.84
3	C	17	LEU	C-N-CA	6.01	127.36	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	b	228	SER	N-CA-CB	-5.94	108.16	114.10
30	e	7	PRO	N-CA-C	5.06	122.90	112.47

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	67292	0	33821	304	0
2	B	1878	0	1946	33	0
3	C	3039	0	3113	35	0
4	D	2748	0	2863	20	0
5	E	1352	0	1383	14	0
6	F	1502	0	1572	9	0
7	G	1399	0	1501	7	0
8	H	1742	0	1834	8	0
9	J	1563	0	1665	10	0
10	K	1486	0	1554	13	0
11	L	1002	0	1048	6	0
12	M	1045	0	1136	5	0
13	N	1172	0	1215	12	0
14	O	1719	0	1779	20	0
15	P	2176	0	2116	25	0
16	Q	1440	0	1543	10	0
17	R	1209	0	1295	12	0
18	S	1436	0	1475	7	0
19	T	1275	0	1323	10	0
20	U	1222	0	1231	9	0
21	V	786	0	799	1	0
22	W	958	0	1023	8	0
23	X	984	0	1075	8	0
24	Y	1091	0	1155	7	0
25	Z	963	0	1073	7	0
26	a	415	0	429	1	0
27	b	1760	0	1843	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	c	741	0	797	10	0
29	d	872	0	914	7	0
30	e	1020	0	1091	7	0
31	f	849	0	880	9	0
32	g	812	0	873	8	0
33	h	763	0	842	6	0
34	i	665	0	668	7	0
35	j	611	0	682	2	0
36	k	435	0	475	7	0
37	l	756	0	818	6	0
38	m	680	0	724	10	0
39	n	1691	0	1689	37	0
40	z	491	0	518	3	0
41	w	3076	0	3105	54	0
42	v	500	0	524	7	0
43	o	2593	0	2625	83	0
44	p	1050	0	249	7	0
45	t	417	0	458	5	0
46	x	2576	0	1305	16	0
47	y	3310	0	1676	15	0
48	g	1	0	0	0	0
48	i	1	0	0	0	0
48	l	1	0	0	0	0
48	m	1	0	0	0	0
48	t	1	0	0	0	0
48	w	2	0	0	0	0
All	All	128569	0	93723	752	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 (752) 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)
2:B:125:ALA:CB	2:B:128:ARG:HD2	1.33	1.57
41:w:25:PRO:N	41:w:25:PRO:CA	1.71	1.46
43:o:394:PRO:N	43:o:394:PRO:CA	1.70	1.42
2:B:125:ALA:CB	2:B:128:ARG:CD	2.02	1.34
39:n:140:GLN:O	39:n:141:THR:HG22	1.22	1.29
39:n:140:GLN:O	39:n:141:THR:CG2	1.92	1.17
43:o:163:ARG:HA	43:o:166:LEU:HD23	1.17	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:o:162:TRP:O	43:o:165:LYS:HD3	1.46	1.13
43:o:162:TRP:HA	43:o:165:LYS:HE2	1.23	1.10
43:o:162:TRP:O	43:o:165:LYS:CD	2.00	1.08
43:o:162:TRP:CA	43:o:165:LYS:HE2	1.84	1.08
41:w:65:LEU:HG	41:w:66:GLN:O	1.53	1.08
41:w:147:ALA:O	41:w:149:SER:N	1.87	1.08
2:B:125:ALA:HB2	2:B:128:ARG:CD	1.72	1.06
2:B:125:ALA:HB1	2:B:128:ARG:CD	1.85	1.05
41:w:58:CYS:HB2	41:w:143:CYS:SG	2.06	0.96
1:A:2819:A:N6	1:A:2870:C:N3	2.16	0.94
43:o:402:GLU:OE1	43:o:404:VAL:HG22	1.67	0.94
43:o:163:ARG:CA	43:o:166:LEU:HD23	1.98	0.93
43:o:162:TRP:HA	43:o:165:LYS:CE	1.97	0.93
37:l:77:CYS:HG	37:l:79:THR:HG1	1.10	0.93
2:B:125:ALA:CB	2:B:128:ARG:HD3	1.99	0.91
34:i:37:CYS:SG	34:i:37:CYS:O	2.29	0.91
39:n:140:GLN:C	39:n:141:THR:CG2	2.41	0.89
41:w:59:ARG:HD3	41:w:140:ALA:CB	2.07	0.85
41:w:59:ARG:HD3	41:w:140:ALA:HB1	1.58	0.84
1:A:3068:U:OP2	17:R:62:ARG:NH2	2.11	0.84
41:w:59:ARG:HB2	41:w:59:ARG:CZ	2.07	0.84
37:l:77:CYS:SG	37:l:79:THR:OG1	2.32	0.84
43:o:166:LEU:H	43:o:166:LEU:HD22	1.43	0.83
43:o:133:ASP:O	43:o:217:ASP:OD1	1.97	0.82
1:A:1508:C:OP1	20:U:127:ARG:NH2	2.12	0.82
41:w:59:ARG:CD	41:w:140:ALA:HB1	2.10	0.82
43:o:165:LYS:HG2	43:o:166:LEU:HD22	1.61	0.81
1:A:2514:U:OP1	8:H:68:ARG:NH1	2.14	0.80
39:n:142:ILE:HG22	39:n:162:HIS:HE1	1.47	0.80
1:A:2282:U:OP1	1:A:2973:G:O2'	2.00	0.80
14:O:192:LYS:O	14:O:196:THR:OG1	1.99	0.79
3:C:10:ARG:NH1	3:C:11:HIS:O	2.16	0.79
1:A:687:U:OP2	10:K:36:ARG:NH2	2.16	0.78
1:A:69:C:HO2'	1:A:101:G:HO2'	1.17	0.78
32:g:11:ASN:O	32:g:18:ASN:ND2	2.15	0.78
1:A:1493:G:O6	36:k:2:ALA:N	2.16	0.78
1:A:221:A:O2'	1:A:223:U:OP2	2.02	0.78
1:A:2455:U:O4	1:A:2482:U:O2'	2.01	0.77
41:w:19:CYS:O	41:w:19:CYS:SG	2.43	0.77
43:o:163:ARG:HD3	43:o:183:ARG:CD	2.15	0.77
1:A:2948:C:OP1	3:C:244:ARG:NH2	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:w:147:ALA:O	41:w:150:TYR:N	2.17	0.77
43:o:398:TYR:HB3	43:o:402:GLU:HB3	1.66	0.77
1:A:110:G:OP2	10:K:73:ARG:NH2	2.18	0.76
1:A:2557:A:OP1	2:B:69:TYR:OH	2.02	0.76
1:A:2819:A:N6	1:A:2870:C:C2	2.53	0.76
39:n:140:GLN:C	39:n:141:THR:HG23	2.09	0.75
2:B:125:ALA:HB2	2:B:128:ARG:HD2	0.77	0.75
39:n:53:ILE:O	39:n:56:THR:OG1	2.05	0.75
1:A:2459:A:O2'	1:A:2460:U:OP1	2.04	0.75
3:C:205:VAL:HG21	3:C:322:ILE:HD11	1.67	0.75
43:o:162:TRP:O	43:o:165:LYS:CE	2.33	0.75
1:A:3042:U:OP2	1:A:3092:C:N4	2.19	0.75
1:A:1217:A:O2'	1:A:1218:U:OP1	2.04	0.75
1:A:2208:A:O2'	1:A:2209:U:O2	2.05	0.75
5:E:137:ARG:NH1	46:x:28:C:OP1	2.20	0.74
1:A:1834:U:OP2	36:k:10:LYS:NZ	2.20	0.74
43:o:163:ARG:HD3	43:o:183:ARG:HD3	1.69	0.74
1:A:1873:U:OP2	17:R:20:ARG:NH2	2.20	0.74
1:A:2522:G:O2'	1:A:2524:A:OP2	2.05	0.74
14:O:8:GLU:OE1	14:O:50:ARG:NH2	2.20	0.74
43:o:178:LEU:HD23	43:o:178:LEU:O	1.86	0.74
19:T:70:SER:OG	19:T:92:ARG:NH1	2.20	0.74
1:A:1364:C:OP1	27:b:110:ARG:NH2	2.19	0.74
1:A:1007:U:O4	1:A:1043:C:N3	2.21	0.74
1:A:1098:A:OP2	19:T:130:ARG:NE	2.21	0.74
1:A:1094:U:OP2	19:T:116:ARG:NH2	2.22	0.73
6:F:173:ARG:NH1	45:t:126:LYS:O	2.21	0.73
3:C:90:VAL:HG12	3:C:104:THR:HG23	1.70	0.73
17:R:150:GLN:OE1	17:R:151:ARG:NH1	2.21	0.73
1:A:2255:A:OP1	1:A:2259:A:N6	2.21	0.73
1:A:2492:C:O2	1:A:2494:A:N6	2.22	0.73
1:A:116:A:OP1	14:O:2:GLY:N	2.22	0.72
43:o:163:ARG:HA	43:o:166:LEU:CD2	2.09	0.72
15:P:85:ARG:NH2	15:P:250:ASP:OD2	2.22	0.72
1:A:1348:U:OP2	16:Q:38:ARG:NH2	2.23	0.72
1:A:217:U:O2	23:X:103:LYS:NZ	2.19	0.72
1:A:1494:U:OP1	36:k:42:ARG:NH2	2.22	0.72
1:A:2474:G:N7	1:A:2476:C:N4	2.36	0.72
1:A:2945:G:O2'	1:A:2948:C:OP2	2.05	0.72
1:A:2323:G:O2'	1:A:2325:G:OP2	2.07	0.72
1:A:3280:U:O2'	1:A:3281:U:O5'	2.08	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2485:A:N7	1:A:2486:A:N6	2.37	0.72
29:d:51:LEU:HD23	29:d:93:VAL:HB	1.70	0.72
1:A:2262:A:N3	43:o:378:LYS:NZ	2.37	0.72
28:c:24:THR:HG1	28:c:29:SER:HG	1.28	0.71
43:o:189:LYS:O	43:o:193:ARG:NH1	2.23	0.71
1:A:2505:U:O2'	1:A:2506:U:O2	2.06	0.71
31:f:37:THR:OG1	31:f:39:GLN:O	2.05	0.71
39:n:142:ILE:CG2	39:n:162:HIS:CE1	2.73	0.71
20:U:138:LYS:NZ	20:U:140:GLU:OE2	2.19	0.71
1:A:1778:G:O2'	1:A:1780:G:OP2	2.08	0.71
1:A:3026:G:O2'	1:A:3028:G:O6	2.09	0.71
1:A:3042:U:OP1	11:L:48:ARG:NH1	2.24	0.71
22:W:59:SER:OG	22:W:101:GLU:OE1	2.08	0.71
31:f:6:ARG:NH1	31:f:8:TYR:O	2.23	0.71
43:o:162:TRP:C	43:o:165:LYS:HE2	2.16	0.71
43:o:162:TRP:C	43:o:165:LYS:HD3	2.14	0.71
45:t:119:ASN:OD1	45:t:120:GLN:NE2	2.24	0.71
1:A:148:G:OP2	14:O:4:TYR:OH	2.08	0.71
1:A:1025:A:N6	41:w:329:SER:OG	2.23	0.71
1:A:2492:C:O2'	1:A:2494:A:N7	2.23	0.70
1:A:591:G:N2	1:A:612:U:OP1	2.23	0.70
1:A:1207:G:O2'	1:A:1209:G:OP1	2.07	0.70
1:A:1551:C:O2'	1:A:2170:U:O2'	2.08	0.70
1:A:439:C:O2'	1:A:494:G:N2	2.24	0.70
25:Z:67:ARG:NH2	47:y:97:A:OP1	2.24	0.70
1:A:2468:A:N6	1:A:2477:G:O2'	2.25	0.70
1:A:2469:G:O6	1:A:2476:C:N4	2.19	0.70
47:y:39:G:O2'	47:y:105:A:N1	2.25	0.70
1:A:1907:C:O2	3:C:240:ARG:NH2	2.24	0.70
2:B:79:ASN:ND2	2:B:166:ILE:O	2.24	0.70
15:P:13:SER:O	46:x:11:A:N6	2.22	0.69
1:A:1007:U:C4	1:A:1043:C:N3	2.60	0.69
1:A:1386:A:O4'	4:D:141:ARG:NH2	2.25	0.69
1:A:2722:U:O2'	19:T:88:ARG:O	2.10	0.69
41:w:147:ALA:O	41:w:148:ARG:C	2.35	0.69
1:A:1044:U:O2	1:A:1045:C:O2'	2.07	0.69
14:O:43:THR:OG1	14:O:131:GLU:OE2	2.07	0.69
39:n:85:ARG:NH2	39:n:89:PRO:O	2.26	0.69
1:A:1477:A:OP1	1:A:3075:G:O2'	2.10	0.69
1:A:2185:G:O2'	1:A:2314:U:OP2	2.11	0.69
39:n:142:ILE:HG22	39:n:162:HIS:CE1	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:865:U:OP2	1:A:893:C:N4	2.26	0.68
43:o:180:PRO:O	43:o:392:VAL:HG23	1.93	0.68
1:A:1327:C:O2'	31:f:76:GLY:HA3	1.94	0.68
1:A:1689:U:OP1	17:R:64:ARG:NH1	2.26	0.68
1:A:1729:A:N6	38:m:41:PHE:O	2.27	0.68
1:A:2491:A:OP2	44:p:205:UNK:N	2.25	0.68
1:A:3170:A:OP2	31:f:56:SER:OG	2.03	0.68
5:E:97:SER:OG	5:E:101:ASN:OD1	2.11	0.68
1:A:2815:G:N7	1:A:2870:C:O2'	2.27	0.68
43:o:222:VAL:O	43:o:223:LYS:HE2	1.94	0.68
1:A:1523:U:O4	22:W:75:LYS:NZ	2.26	0.68
1:A:2786:G:N2	13:N:58:MET:SD	2.65	0.68
1:A:1632:A:OP1	24:Y:48:ARG:NH2	2.25	0.67
27:b:219:LYS:O	27:b:228:SER:HB2	1.93	0.67
1:A:1333:C:OP1	16:Q:2:GLY:N	2.28	0.67
15:P:50:ARG:NH2	15:P:72:ASP:OD2	2.27	0.67
20:U:118:GLN:NE2	20:U:147:GLU:OE2	2.28	0.67
1:A:86:G:O2'	1:A:98:G:O6	2.10	0.67
1:A:3330:A:OP2	3:C:376:LYS:NZ	2.25	0.67
43:o:134:LEU:HD13	43:o:165:LYS:HB2	1.77	0.67
44:p:28:UNK:O	44:p:159:UNK:N	2.25	0.67
1:A:1152:G:OP2	1:A:1152:G:N2	2.27	0.67
1:A:2307:G:O2'	1:A:2310:U:OP2	2.13	0.67
41:w:59:ARG:NE	41:w:140:ALA:HB1	2.09	0.67
1:A:855:U:O4	38:m:4:ARG:NH1	2.28	0.66
1:A:1288:U:O2'	1:A:1289:G:OP1	2.12	0.66
10:K:153:ASP:OD2	13:N:126:LYS:NZ	2.28	0.66
1:A:1044:U:O2'	1:A:1045:C:O4'	2.12	0.66
43:o:223:LYS:HZ1	43:o:230:ALA:HA	1.60	0.66
15:P:77:ALA:O	15:P:108:ARG:NH1	2.27	0.66
1:A:3140:G:N7	3:C:28:ARG:NH2	2.42	0.66
2:B:80:GLU:OE1	38:m:76:ALA:HB2	1.95	0.66
3:C:139:GLN:NE2	3:C:140:ASP:O	2.28	0.66
1:A:266:A:OP1	14:O:5:LYS:NZ	2.22	0.66
1:A:412:G:OP1	20:U:62:ARG:NH1	2.28	0.66
1:A:681:U:O4	4:D:118:LYS:NZ	2.28	0.66
1:A:1547:G:OP1	14:O:108:ARG:NH2	2.28	0.66
1:A:2794:G:OP1	41:w:380:ASN:ND2	2.28	0.66
20:U:18:ARG:NH1	20:U:147:GLU:OE1	2.28	0.65
32:g:46:ASP:OD2	32:g:88:ARG:NH2	2.27	0.65
39:n:187:ASN:OD1	39:n:210:THR:OG1	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1355:A:OP1	16:Q:27:LYS:NZ	2.29	0.65
1:A:2622:C:HO2'	41:w:245:SER:HG	1.41	0.65
1:A:1392:G:HO2'	1:A:1417:G:H1	1.43	0.65
43:o:162:TRP:O	43:o:165:LYS:HE2	1.97	0.65
1:A:877:C:HO2'	1:A:880:G:HO2'	1.40	0.65
1:A:1954:G:N7	1:A:2094:C:N4	2.44	0.65
1:A:1629:U:O2'	1:A:1630:U:OP1	2.13	0.65
23:X:16:ARG:NE	47:y:23:U:OP2	2.28	0.65
41:w:402:TYR:O	41:w:404:ARG:NH2	2.30	0.65
1:A:1385:C:O2	7:G:2:SER:OG	2.13	0.65
3:C:46:PHE:CE2	3:C:81:THR:HG23	2.31	0.65
16:Q:123:THR:OG1	16:Q:125:ASP:OD1	2.10	0.64
43:o:177:LEU:HD22	43:o:399:ASN:HB2	1.80	0.64
1:A:884:A:OP1	34:i:5:THR:OG1	2.11	0.64
34:i:22:CYS:SG	34:i:24:ARG:HG2	2.37	0.64
4:D:226:GLU:OE1	4:D:237:GLN:NE2	2.31	0.64
28:c:73:GLY:N	28:c:76:GLU:OE1	2.30	0.64
1:A:1481:A:O2'	1:A:1859:A:OP2	2.16	0.64
43:o:171:GLU:HG2	43:o:171:GLU:O	1.96	0.64
43:o:395:ASN:N	43:o:395:ASN:HD22	1.96	0.64
1:A:912:G:N7	2:B:9:ARG:NH1	2.45	0.64
43:o:166:LEU:H	43:o:166:LEU:CD2	2.11	0.63
15:P:107:ARG:NH2	15:P:119:TYR:O	2.31	0.63
24:Y:17:ARG:NH2	24:Y:18:TYR:OH	2.31	0.63
1:A:3045:G:O3'	3:C:275:ARG:NH2	2.31	0.63
30:e:81:ASP:O	30:e:84:THR:OG1	2.17	0.63
1:A:860:G:OP1	38:m:17:ARG:NH2	2.32	0.63
43:o:166:LEU:HD22	43:o:166:LEU:N	2.12	0.63
2:B:112:ILE:HD13	2:B:135:ILE:HG22	1.79	0.63
41:w:147:ALA:C	41:w:149:SER:N	2.54	0.62
1:A:1245:A:N6	1:A:1272:C:O2'	2.31	0.62
1:A:1942:U:OP2	17:R:74:ARG:NE	2.28	0.62
1:A:3353:G:O2'	1:A:3354:U:OP1	2.14	0.62
1:A:1517:G:O2'	40:z:394:TYR:OH	2.17	0.62
1:A:877:C:O2'	1:A:880:G:O2'	2.12	0.62
1:A:2273:G:O2'	1:A:2311:G:O6	2.15	0.62
1:A:837:A:OP2	38:m:4:ARG:NE	2.32	0.62
41:w:57:PHE:CZ	41:w:62:GLU:HA	2.35	0.62
1:A:1568:U:O2'	1:A:1570:U:O5'	2.17	0.61
43:o:398:TYR:HB3	43:o:402:GLU:CB	2.30	0.61
1:A:121:A:O2'	1:A:122:A:OP1	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1389:G:OP1	30:e:104:ASN:ND2	2.33	0.61
43:o:180:PRO:O	43:o:392:VAL:CG2	2.49	0.61
6:F:181:VAL:O	45:t:85:LEU:HD11	1.99	0.61
43:o:218:LEU:O	43:o:222:VAL:HG12	1.99	0.61
15:P:216:GLU:N	15:P:216:GLU:OE1	2.33	0.61
28:c:9:SER:HA	28:c:104:LEU:HD11	1.83	0.61
1:A:1243:G:N2	1:A:1244:A:N7	2.48	0.61
27:b:208:SER:OG	27:b:209:ASN:N	2.32	0.61
31:f:3:GLU:N	31:f:3:GLU:OE1	2.33	0.61
37:l:2:VAL:N	37:l:90:HIS:O	2.34	0.61
1:A:2451:G:O4'	1:A:2497:U:N3	2.33	0.61
1:A:3313:U:O5'	3:C:173:GLN:NE2	2.33	0.61
1:A:2272:G:OP2	1:A:2272:G:N2	2.26	0.60
22:W:103:TYR:O	22:W:138:ARG:NH1	2.32	0.60
36:k:5:LYS:HE2	36:k:13:MET:HE1	1.82	0.60
14:O:112:ASN:ND2	47:y:141:C:O2	2.34	0.60
1:A:1646:G:O2'	1:A:1808:G:N2	2.21	0.60
1:A:2818:U:O2'	1:A:2870:C:N4	2.34	0.60
1:A:3114:A:H62	1:A:3118:C:H42	1.47	0.60
4:D:156:LEU:HD12	4:D:159:ILE:HD12	1.84	0.60
43:o:179:THR:OG1	43:o:180:PRO:HD2	2.02	0.60
1:A:3003:G:O2'	3:C:92:TYR:OH	2.12	0.60
1:A:3022:G:O2'	1:A:3031:G:O6	2.18	0.60
41:w:59:ARG:HD3	41:w:140:ALA:HB2	1.84	0.60
15:P:122:VAL:O	15:P:248:ARG:NH2	2.35	0.60
1:A:2943:G:N2	3:C:251:CYS:SG	2.75	0.60
43:o:160:LEU:O	43:o:164:ARG:HD3	2.02	0.60
1:A:2712:U:HO2'	1:A:2743:A:HO2'	1.48	0.59
4:D:229:ASN:OD1	4:D:230:VAL:N	2.35	0.59
1:A:2673:A:OP1	5:E:94:ARG:NE	2.34	0.59
43:o:348:GLY:O	43:o:352:THR:HG23	2.01	0.59
1:A:351:A:N6	36:k:37:TYR:O	2.36	0.59
1:A:1523:U:OP2	1:A:1604:G:O2'	2.20	0.59
1:A:2101:C:O2'	1:A:2102:U:O5'	2.19	0.59
1:A:1634:G:N7	24:Y:17:ARG:NH1	2.51	0.59
1:A:978:G:N2	1:A:979:U:O4	2.33	0.59
1:A:1603:A:OP1	17:R:38:ARG:NH2	2.36	0.59
24:Y:76:ASN:OD1	24:Y:77:TYR:N	2.36	0.59
1:A:366:A:O2'	40:z:415:ARG:NH1	2.36	0.58
1:A:1016:C:O2	1:A:1035:G:N1	2.36	0.58
1:A:3050:U:O2'	42:v:16:GLY:O	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:621:A:O2'	1:A:622:A:OP2	2.17	0.58
1:A:2832:C:H42	1:A:2856:G:H22	1.51	0.58
1:A:2931:C:O2'	11:L:39:VAL:O	2.22	0.58
15:P:57:ASN:ND2	46:x:28:C:OP2	2.33	0.58
37:l:25:VAL:HG12	37:l:72:LEU:HG	1.86	0.58
41:w:56:SER:OG	41:w:141:MET:SD	2.59	0.58
1:A:2888:U:O4'	1:A:2911:A:N6	2.37	0.58
2:B:33:ASP:OD1	2:B:33:ASP:N	2.35	0.58
1:A:266:A:N6	33:h:29:LYS:O	2.37	0.58
1:A:765:C:N3	10:K:183:ARG:NH2	2.50	0.58
1:A:2456:A:N6	1:A:2460:U:O5'	2.36	0.58
1:A:3002:C:O2'	3:C:180:GLU:OE2	2.19	0.58
1:A:1010:G:O2'	1:A:1011:A:OP1	2.19	0.58
1:A:1350:A:N6	1:A:1353:U:O3'	2.36	0.58
2:B:125:ALA:HB1	2:B:128:ARG:CG	2.34	0.58
1:A:2257:C:C5	1:A:2258:U:C4	2.92	0.57
3:C:221:THR:O	3:C:334:ARG:NH1	2.36	0.57
4:D:265:GLU:OE1	4:D:265:GLU:N	2.37	0.57
43:o:162:TRP:O	43:o:165:LYS:CG	2.51	0.57
39:n:168:GLN:OE1	39:n:168:GLN:N	2.37	0.57
25:Z:52:ALA:O	25:Z:56:THR:OG1	2.23	0.57
1:A:1639:C:OP2	32:g:74:ARG:NH1	2.37	0.57
38:m:46:THR:OG1	38:m:57:CYS:SG	2.62	0.57
43:o:222:VAL:C	43:o:223:LYS:HG2	2.30	0.57
1:A:1460:A:H5'	29:d:51:LEU:O	2.05	0.57
1:A:2137:U:OP2	1:A:2142:A:N6	2.34	0.57
27:b:88:ARG:NH1	27:b:108:LEU:O	2.37	0.57
41:w:143:CYS:HB2	41:w:146:CYS:HB2	1.86	0.57
1:A:3085:G:OP1	42:v:34:SER:OG	2.14	0.56
4:D:292:SER:OG	4:D:294:GLU:OE1	2.22	0.56
34:i:2:GLY:O	34:i:7:SER:OG	2.20	0.56
1:A:691:A:OP1	4:D:46:LYS:NZ	2.38	0.56
1:A:2450:G:N1	1:A:2498:U:OP1	2.38	0.56
10:K:37:ASN:O	10:K:41:THR:HG23	2.06	0.56
41:w:286:MET:SD	41:w:333:ARG:NH2	2.79	0.56
18:S:112:ALA:O	18:S:115:ARG:NH1	2.39	0.56
39:n:142:ILE:HG21	39:n:162:HIS:CE1	2.40	0.56
1:A:838:G:O6	38:m:4:ARG:NH1	2.37	0.56
1:A:1737:U:O2	32:g:52:GLN:NE2	2.39	0.56
1:A:2819:A:OP2	1:A:2866:U:O2'	2.11	0.56
1:A:1007:U:O4	1:A:1043:C:C4	2.58	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:h:45:ARG:NH1	33:h:89:GLU:OE2	2.37	0.55
1:A:1566:A:O2'	1:A:1569:U:O4	2.24	0.55
4:D:237:GLN:O	4:D:246:ARG:NH1	2.39	0.55
1:A:914:A:O2'	2:B:203:ALA:O	2.23	0.55
1:A:1863:G:N1	1:A:1866:C:OP2	2.36	0.55
1:A:2981:U:OP2	3:C:244:ARG:NH1	2.37	0.55
43:o:163:ARG:HD3	43:o:183:ARG:HD2	1.86	0.55
10:K:166:ALA:N	13:N:135:GLU:OE2	2.39	0.55
20:U:47:TYR:O	20:U:51:VAL:HG23	2.06	0.55
22:W:48:SER:OG	47:y:136:G:OP1	2.23	0.55
1:A:1000:C:N3	1:A:1001:G:N2	2.54	0.55
2:B:125:ALA:HB3	2:B:128:ARG:HD3	1.87	0.55
1:A:2466:G:N2	1:A:2491:A:O4'	2.40	0.55
2:B:146:THR:OG1	2:B:160:SER:OG	2.21	0.55
5:E:19:LEU:HD23	5:E:125:MET:SD	2.47	0.55
9:J:53:TYR:OH	9:J:72:PHE:O	2.25	0.55
39:n:66:ASN:ND2	39:n:111:ASN:O	2.40	0.55
1:A:394:G:N1	1:A:397:A:OP2	2.39	0.54
1:A:838:G:N7	38:m:4:ARG:NH2	2.55	0.54
31:f:19:SER:OG	31:f:20:LYS:N	2.39	0.54
43:o:212:LEU:O	43:o:395:ASN:OD1	2.23	0.54
17:R:105:LEU:HD23	17:R:138:LEU:HD23	1.89	0.54
2:B:125:ALA:HB3	2:B:128:ARG:CD	2.24	0.54
1:A:2158:A:O2'	2:B:118:GLU:OE2	2.23	0.54
27:b:155:LYS:NZ	27:b:200:ASN:OD1	2.39	0.54
28:c:57:GLU:OE2	28:c:69:TYR:OH	2.23	0.54
1:A:2483:G:N3	1:A:2486:A:N6	2.56	0.54
15:P:17:GLN:NE2	19:T:22:HIS:O	2.39	0.54
41:w:357:SER:OG	41:w:358:HIS:N	2.39	0.54
44:p:58:UNK:O	44:p:102:UNK:N	2.41	0.54
2:B:7:ASN:OD1	2:B:8:GLN:N	2.41	0.54
43:o:177:LEU:HD13	43:o:399:ASN:HB2	1.90	0.54
45:t:115:CYS:SG	45:t:116:GLY:N	2.80	0.54
1:A:2180:G:OP1	2:B:174:ARG:NH2	2.40	0.54
1:A:2621:G:N2	41:w:243:SER:OG	2.41	0.54
1:A:3280:U:HO2'	1:A:3281:U:P	2.31	0.54
37:l:21:THR:OG1	37:l:74:CYS:SG	2.58	0.54
43:o:169:LEU:HA	43:o:172:SER:HB3	1.90	0.54
22:W:108:LEU:HD11	22:W:125:ARG:HD3	1.90	0.54
41:w:53:ALA:HB3	41:w:136:TYR:CD1	2.43	0.54
43:o:223:LYS:NZ	43:o:230:ALA:HA	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2465:G:N2	1:A:2466:G:O6	2.38	0.53
25:Z:102:GLU:OE1	25:Z:105:ARG:NH1	2.42	0.53
43:o:222:VAL:O	43:o:223:LYS:CE	2.56	0.53
15:P:136:GLU:N	15:P:136:GLU:OE1	2.42	0.53
21:V:58:GLU:OE2	21:V:60:GLY:N	2.41	0.53
1:A:2672:G:O2'	5:E:95:ASN:O	2.27	0.53
16:Q:120:GLU:OE2	16:Q:130:ARG:NH1	2.41	0.53
10:K:9:ILE:HD12	13:N:34:MET:SD	2.49	0.53
16:Q:89:ASP:OD1	16:Q:90:ASP:N	2.42	0.53
1:A:3324:C:OP1	29:d:19:ARG:NH1	2.42	0.53
5:E:15:GLU:OE2	5:E:132:ASN:ND2	2.38	0.53
3:C:74:GLU:OE1	3:C:283:TYR:OH	2.25	0.53
15:P:128:GLU:O	15:P:164:LYS:NZ	2.28	0.53
43:o:398:TYR:C	43:o:402:GLU:HB3	2.33	0.53
1:A:3306:U:OP1	3:C:269:GLN:NE2	2.39	0.53
5:E:150:ASN:ND2	46:x:17:A:OP1	2.41	0.53
39:n:115:ALA:HB2	39:n:135:VAL:HG11	1.90	0.53
43:o:167:ALA:HA	43:o:170:GLN:HB2	1.89	0.53
1:A:1208:U:O2'	1:A:1210:U:OP2	2.27	0.52
41:w:104:TRP:CH2	43:o:164:ARG:NH2	2.75	0.52
1:A:2754:G:O2'	1:A:2755:C:OP1	2.27	0.52
1:A:3214:U:HO2'	31:f:2:ALA:N	2.08	0.52
14:O:68:ARG:NH1	14:O:124:ASP:O	2.41	0.52
46:x:72:A:O2'	46:x:74:C:OP2	2.14	0.52
11:L:54:LEU:N	11:L:81:GLN:OE1	2.43	0.52
23:X:112:ASP:OD1	23:X:113:LYS:N	2.42	0.52
8:H:207:ASP:OD1	8:H:207:ASP:N	2.38	0.52
39:n:140:GLN:HG3	39:n:141:THR:H	1.75	0.52
1:A:2109:U:HO2'	1:A:3363:U:HO2'	1.56	0.52
14:O:155:VAL:O	14:O:162:ARG:NH2	2.43	0.52
46:x:13:A:OP2	46:x:67:G:N2	2.43	0.52
3:C:291:GLU:N	3:C:291:GLU:OE1	2.40	0.52
1:A:3270:U:O2'	1:A:3271:G:OP1	2.27	0.52
3:C:212:ASN:O	3:C:281:LYS:NZ	2.42	0.52
3:C:284:ARG:NH2	3:C:295:ALA:O	2.43	0.52
15:P:166:ALA:HB1	15:P:171:LEU:HD21	1.91	0.52
32:g:61:GLN:O	32:g:64:THR:OG1	2.19	0.52
1:A:215:G:OP1	23:X:12:ARG:NH1	2.41	0.52
1:A:3110:C:HO2'	6:F:155:SER:HG	1.51	0.52
17:R:17:VAL:HG22	17:R:18:GLY:H	1.75	0.52
39:n:30:GLY:O	39:n:31:SER:OG	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:A:OP2	47:y:16:G:N2	2.43	0.51
1:A:1507:G:N7	20:U:129:THR:OG1	2.36	0.51
13:N:93:SER:OG	13:N:94:ALA:N	2.43	0.51
15:P:188:GLU:N	15:P:188:GLU:OE1	2.42	0.51
1:A:439:C:H1'	1:A:494:G:H21	1.75	0.51
37:l:36:PHE:O	37:l:41:ARG:NH1	2.43	0.51
11:L:104:ASN:OD1	11:L:108:GLU:N	2.43	0.51
1:A:105:C:HO2'	1:A:684:G:HO2'	1.53	0.51
11:L:128:ARG:NE	39:n:12:GLU:OE2	2.41	0.51
1:A:494:G:H22	1:A:619:A:H2	1.59	0.51
1:A:674:G:OP1	4:D:31:ARG:NH1	2.44	0.51
1:A:1074:U:O2	26:a:42:ASN:ND2	2.42	0.51
6:F:5:GLN:OE1	6:F:7:GLU:OE2	2.28	0.51
8:H:124:ASP:OD1	8:H:124:ASP:N	2.42	0.51
32:g:6:THR:OG1	32:g:7:PHE:O	2.25	0.51
1:A:1721:U:OP2	17:R:124:TYR:OH	2.29	0.51
1:A:2116:G:OP1	1:A:2118:C:N4	2.43	0.51
1:A:1807:G:OP1	24:Y:133:LYS:NZ	2.43	0.51
3:C:44:THR:OG1	3:C:182:GLN:O	2.21	0.51
30:e:78:ASN:N	30:e:78:ASN:OD1	2.44	0.51
43:o:135:ILE:HG23	43:o:394:PRO:HD2	1.93	0.51
7:G:31:ARG:NH2	7:G:81:ALA:O	2.43	0.51
12:M:119:GLN:O	12:M:123:LEU:HD23	2.11	0.51
41:w:59:ARG:CD	41:w:140:ALA:CB	2.79	0.51
1:A:348:A:N3	1:A:352:A:O2'	2.44	0.50
8:H:202:GLU:N	8:H:202:GLU:OE1	2.43	0.50
10:K:3:ILE:HG22	13:N:44:ASN:ND2	2.26	0.50
16:Q:84:VAL:HG12	16:Q:84:VAL:O	2.11	0.50
43:o:165:LYS:CD	43:o:165:LYS:H	2.24	0.50
1:A:2703:A:N6	15:P:28:THR:O	2.43	0.50
9:J:157:ASP:OD1	9:J:158:LYS:N	2.45	0.50
1:A:2991:A:O2'	1:A:3309:G:N7	2.45	0.50
4:D:282:SER:OG	16:Q:125:ASP:OD2	2.19	0.50
1:A:1180:A:OP1	31:f:76:GLY:O	2.29	0.50
44:p:113:UNK:O	44:p:115:UNK:N	2.45	0.50
1:A:339:C:OP2	4:D:197:ARG:NH2	2.44	0.50
15:P:182:GLY:HA2	15:P:194:LEU:HD23	1.94	0.50
1:A:965:A:C2	13:N:43:ILE:HD11	2.46	0.50
1:A:1605:A:O2'	1:A:1607:U:OP2	2.26	0.50
1:A:3027:A:O2'	1:A:3028:G:OP1	2.25	0.50
7:G:66:SER:HB2	7:G:76:LEU:HD23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:96:GLU:OE1	42:v:24:GLY:N	2.42	0.50
1:A:2393:G:O2'	1:A:2394:G:OP2	2.29	0.50
14:O:122:ASN:OD1	14:O:123:GLN:N	2.42	0.50
17:R:102:LEU:HD22	17:R:138:LEU:HD22	1.94	0.50
41:w:57:PHE:CD2	41:w:58:CYS:O	2.65	0.50
43:o:395:ASN:N	43:o:395:ASN:ND2	2.60	0.50
1:A:250:U:N3	1:A:251:G:N7	2.59	0.49
1:A:2555:G:O6	32:g:95:ILE:HG21	2.12	0.49
1:A:2901:G:O2'	1:A:3024:A:N1	2.45	0.49
27:b:229:PHE:CD1	27:b:229:PHE:C	2.90	0.49
41:w:369:VAL:HG21	41:w:397:LEU:CD2	2.42	0.49
43:o:436:ILE:HD12	43:o:496:LEU:HD21	1.94	0.49
47:y:82:U:O2'	47:y:83:C:OP1	2.30	0.49
1:A:540:U:OP2	1:A:547:G:N1	2.44	0.49
1:A:2196:C:O2'	1:A:2270:A:N3	2.45	0.49
1:A:2712:U:O2'	1:A:2743:A:O2'	2.19	0.49
1:A:2941:A:OP2	3:C:256:HIS:N	2.44	0.49
43:o:139:ARG:NH1	43:o:196:GLU:OE1	2.44	0.49
1:A:3306:U:O2'	1:A:3308:C:OP2	2.19	0.49
39:n:142:ILE:HD11	39:n:152:CYS:HB2	1.93	0.49
1:A:1042:U:O2'	1:A:1043:C:O4'	2.24	0.49
1:A:1566:A:N7	1:A:1567:U:O2'	2.43	0.49
1:A:2897:A:OP2	1:A:2899:C:N4	2.45	0.49
3:C:163:HIS:ND1	3:C:164:THR:O	2.43	0.49
1:A:1458:U:O2	29:d:56:ASN:ND2	2.42	0.49
2:B:114:SER:N	2:B:165:VAL:O	2.46	0.49
18:S:73:LYS:NZ	18:S:97:VAL:O	2.30	0.49
1:A:618:C:HO2'	1:A:620:U:H3	1.56	0.49
1:A:1186:G:O3'	18:S:113:ARG:NH2	2.46	0.49
1:A:3184:A:N3	1:A:3187:A:O2'	2.39	0.49
23:X:88:GLU:N	23:X:88:GLU:OE1	2.45	0.49
28:c:24:THR:OG1	28:c:29:SER:OG	2.07	0.49
43:o:184:ASN:HB3	43:o:187:VAL:HG12	1.95	0.49
1:A:1041:U:O2'	1:A:1042:U:O4'	2.31	0.49
17:R:139:VAL:HG12	17:R:143:ILE:HD12	1.95	0.49
20:U:155:GLU:N	20:U:155:GLU:OE1	2.46	0.49
28:c:74:ASN:OD1	28:c:75:ASN:N	2.46	0.49
43:o:209:ASN:OD1	43:o:500:ASN:ND2	2.45	0.49
3:C:189:SER:OG	3:C:190:GLU:OE2	2.30	0.49
17:R:30:SER:O	17:R:34:GLN:NE2	2.45	0.48
41:w:97:LEU:HD23	41:w:118:VAL:CG1	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:v:17:ARG:NH2	42:v:32:GLN:OE1	2.46	0.48
41:w:24:THR:OG1	41:w:25:PRO:HD3	2.13	0.48
41:w:369:VAL:HG21	41:w:397:LEU:HD23	1.96	0.48
1:A:2516:U:OP1	14:O:31:ARG:NH1	2.45	0.48
1:A:2847:A:HO2'	1:A:2897:A:HO2'	1.34	0.48
6:F:133:THR:OG1	6:F:147:SER:OG	2.30	0.48
12:M:19:ARG:NH2	12:M:66:THR:O	2.45	0.48
4:D:148:ILE:O	4:D:150:LEU:N	2.47	0.48
13:N:16:SER:O	13:N:18:GLY:N	2.47	0.48
24:Y:128:GLN:OE1	24:Y:128:GLN:N	2.43	0.48
39:n:13:ILE:O	39:n:17:SER:OG	2.27	0.48
43:o:134:LEU:H	43:o:134:LEU:HG	1.39	0.48
1:A:1273:A:O2'	1:A:1274:A:OP1	2.30	0.48
2:B:112:ILE:CD1	2:B:135:ILE:HG22	2.44	0.48
15:P:129:TYR:OH	15:P:175:HIS:O	2.24	0.48
18:S:170:THR:O	18:S:170:THR:OG1	2.32	0.48
27:b:125:GLU:OE2	27:b:128:LYS:NZ	2.37	0.48
19:T:101:CYS:SG	19:T:102:ARG:N	2.87	0.48
25:Z:77:PRO:HD2	25:Z:80:LEU:HD12	1.96	0.48
43:o:163:ARG:CD	43:o:183:ARG:HD2	2.44	0.48
43:o:465:ALA:O	43:o:469:GLY:N	2.46	0.48
1:A:804:C:OP1	4:D:98:ARG:NH2	2.41	0.47
3:C:212:ASN:ND2	3:C:353:GLU:OE1	2.47	0.47
4:D:264:SER:OG	4:D:265:GLU:N	2.47	0.47
10:K:152:THR:HG22	10:K:153:ASP:H	1.79	0.47
46:x:77:G:O2'	46:x:101:G:O6	2.30	0.47
1:A:26:A:N3	1:A:328:U:O2'	2.46	0.47
1:A:1635:G:N2	1:A:1638:A:OP2	2.39	0.47
1:A:1761:C:O2'	1:A:1762:C:O5'	2.31	0.47
1:A:3216:G:O2'	1:A:3220:G:OP2	2.26	0.47
29:d:51:LEU:CD2	29:d:93:VAL:HB	2.43	0.47
1:A:1579:C:O2'	1:A:1580:A:O4'	2.32	0.47
1:A:2808:A:O2'	1:A:2969:A:OP1	2.14	0.47
2:B:6:ARG:NH2	2:B:199:THR:O	2.47	0.47
12:M:2:SER:OG	12:M:3:THR:N	2.44	0.47
32:g:44:CYS:SG	32:g:47:CYS:N	2.85	0.47
1:A:1481:A:N3	1:A:1858:A:O2'	2.47	0.47
15:P:147:ASP:OD1	15:P:147:ASP:N	2.45	0.47
1:A:93:C:OP2	1:A:2764:C:O2'	2.19	0.47
1:A:1921:A:OP2	1:A:1930:A:N6	2.45	0.47
15:P:202:GLY:O	15:P:206:GLN:OE1	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:112:ASN:OD1	19:T:113:ALA:N	2.48	0.47
39:n:11:ASN:O	39:n:187:ASN:ND2	2.48	0.47
39:n:46:ILE:HD12	39:n:202:TYR:OH	2.15	0.47
1:A:2597:U:O2	14:O:125:SER:OG	2.30	0.47
1:A:3184:A:OP2	9:J:11:LYS:NZ	2.45	0.47
7:G:59:GLU:OE2	7:G:59:GLU:N	2.47	0.47
15:P:94:ASN:OD1	15:P:95:TRP:N	2.45	0.47
9:J:192:GLN:O	9:J:195:SER:OG	2.33	0.47
41:w:141:MET:HE2	41:w:143:CYS:HA	1.96	0.47
9:J:53:TYR:HE1	9:J:57:LEU:HD21	1.80	0.47
39:n:142:ILE:HG22	39:n:143:SER:N	2.30	0.46
39:n:20:THR:O	39:n:200:ASN:ND2	2.48	0.46
1:A:2176:U:OP1	2:B:54:ARG:NH2	2.46	0.46
1:A:1011:A:N6	1:A:1012:G:N3	2.63	0.46
42:v:33:ASN:OD1	42:v:33:ASN:N	2.48	0.46
43:o:158:ALA:O	43:o:162:TRP:N	2.48	0.46
1:A:292:U:OP2	14:O:68:ARG:NH2	2.49	0.46
3:C:348:ARG:NH2	3:C:351:LEU:O	2.43	0.46
14:O:136:ASP:OD2	47:y:142:C:O2'	2.34	0.46
18:S:77:VAL:HG11	18:S:106:LEU:HD13	1.97	0.46
24:Y:33:SER:OG	24:Y:34:LYS:N	2.49	0.46
25:Z:40:SER:O	25:Z:41:LEU:HD22	2.15	0.46
1:A:103:G:OP1	10:K:70:ARG:NH2	2.49	0.46
6:F:132:VAL:HG12	6:F:154:VAL:HG22	1.98	0.46
20:U:51:VAL:HG22	20:U:56:ARG:O	2.15	0.46
46:x:29:C:H2'	46:x:51:A:H61	1.81	0.46
47:y:70:G:O2'	47:y:87:G:N2	2.48	0.46
12:M:14:LEU:O	12:M:19:ARG:NE	2.49	0.46
1:A:2728:G:N7	19:T:87:LYS:NZ	2.62	0.46
22:W:83:VAL:HG22	22:W:123:TYR:CD1	2.50	0.46
43:o:162:TRP:O	43:o:166:LEU:CD2	2.64	0.46
1:A:2490:C:O2'	1:A:2491:A:N7	2.48	0.46
10:K:71:ALA:HB2	10:K:147:ILE:HD12	1.97	0.46
1:A:2568:C:O3'	1:A:2573:G:N2	2.49	0.46
43:o:165:LYS:HD3	43:o:165:LYS:H	1.81	0.46
1:A:2466:G:H22	1:A:2491:A:C4'	2.29	0.45
3:C:150:ARG:NH2	3:C:154:TYR:OH	2.49	0.45
1:A:65:A:N1	1:A:109:A:O2'	2.48	0.45
1:A:2356:A:H61	1:A:2983:C:H5	1.63	0.45
1:A:2588:U:OP1	8:H:48:ARG:NH2	2.49	0.45
39:n:28:VAL:O	39:n:28:VAL:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:w:147:ALA:C	41:w:149:SER:H	2.20	0.45
1:A:662:U:OP1	13:N:8:THR:OG1	2.33	0.45
15:P:151:GLN:NE2	46:x:45:A:OP1	2.46	0.45
43:o:398:TYR:CB	43:o:402:GLU:HB3	2.42	0.45
1:A:157:A:N7	33:h:26:ILE:HD13	2.32	0.45
1:A:1940:G:H21	1:A:3362:A:H8	1.64	0.45
1:A:2330:C:OP1	43:o:474:GLY:N	2.50	0.45
22:W:51:VAL:HG21	25:Z:62:GLN:HB3	1.99	0.45
28:c:104:LEU:HD12	28:c:104:LEU:O	2.16	0.45
43:o:162:TRP:O	43:o:165:LYS:HG2	2.16	0.45
1:A:1349:G:N2	1:A:1350:A:N3	2.65	0.45
5:E:54:VAL:HG21	5:E:57:PHE:HD2	1.81	0.45
39:n:140:GLN:O	39:n:141:THR:HG23	1.98	0.45
39:n:142:ILE:HG21	39:n:162:HIS:ND1	2.32	0.45
43:o:163:ARG:HG2	43:o:181:PHE:CZ	2.51	0.45
1:A:120:G:N2	8:H:126:SER:OG	2.50	0.45
1:A:1524:A:O2'	1:A:1526:U:OP2	2.22	0.45
14:O:125:SER:O	14:O:126:THR:HG22	2.16	0.45
15:P:182:GLY:O	15:P:191:ASP:N	2.48	0.45
19:T:94:GLU:OE2	19:T:94:GLU:N	2.45	0.45
43:o:177:LEU:HD13	43:o:399:ASN:ND2	2.32	0.45
43:o:211:LEU:HD22	43:o:500:ASN:HD21	1.82	0.45
1:A:1348:U:O4	1:A:1355:A:O2'	2.21	0.45
1:A:2922:G:N1	41:w:234:HIS:O	2.46	0.45
36:k:6:SER:OG	36:k:9:ILE:HD12	2.17	0.45
1:A:2221:G:N2	1:A:2224:A:OP2	2.46	0.45
1:A:1523:U:OP1	1:A:1607:U:N3	2.40	0.45
1:A:2875:U:OP2	1:A:2945:G:N1	2.47	0.45
1:A:3009:G:N2	3:C:15:GLY:O	2.48	0.45
3:C:136:LYS:HG3	3:C:144:ILE:HD11	1.99	0.45
5:E:117:ASP:OD1	5:E:119:SER:N	2.48	0.45
38:m:78:THR:O	38:m:82:THR:OG1	2.28	0.45
41:w:322:ASP:HB2	41:w:339:THR:HG22	1.99	0.45
1:A:1201:C:H42	1:A:2857:C:H5''	1.81	0.44
27:b:130:ILE:O	27:b:134:VAL:HG22	2.16	0.44
29:d:82:GLU:OE2	29:d:82:GLU:N	2.44	0.44
10:K:46:ILE:O	10:K:49:ARG:N	2.47	0.44
15:P:171:LEU:HD23	15:P:171:LEU:H	1.81	0.44
43:o:181:PHE:O	43:o:181:PHE:CG	2.70	0.44
44:p:26:UNK:O	44:p:161:UNK:N	2.50	0.44
1:A:3395:G:O2'	1:A:3396:U:OP2	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2468:A:O2'	1:A:2477:G:N2	2.50	0.44
9:J:47:PHE:O	9:J:51:LEU:HD23	2.18	0.44
23:X:51:ARG:NH2	47:y:83:C:O2	2.45	0.44
28:c:11:ASN:O	28:c:15:ALA:HB3	2.17	0.44
39:n:172:GLU:O	39:n:175:SER:OG	2.29	0.44
43:o:163:ARG:C	43:o:166:LEU:HD23	2.42	0.44
1:A:1348:U:H4'	1:A:1349:G:H21	1.83	0.44
1:A:2945:G:P	1:A:2945:G:H21	2.41	0.44
30:e:42:VAL:O	30:e:52:GLN:NE2	2.50	0.44
1:A:2375:G:O2'	1:A:2377:G:OP2	2.26	0.44
1:A:2463:G:N2	1:A:2494:A:O3'	2.51	0.44
5:E:53:THR:HG22	5:E:60:ARG:HA	2.00	0.44
5:E:137:ARG:NH2	46:x:44:C:OP2	2.49	0.44
41:w:143:CYS:CB	41:w:146:CYS:HB2	2.47	0.44
1:A:1222:G:O2'	1:A:1285:G:N2	2.44	0.44
1:A:1497:C:O2'	1:A:1602:A:O2'	2.30	0.44
1:A:2549:G:HO2'	1:A:2550:U:H4'	1.83	0.44
39:n:22:THR:HG23	39:n:23:TYR:HD2	1.82	0.44
42:v:6:ASP:OD1	42:v:7:SER:N	2.51	0.44
46:x:38:U:O2'	46:x:42:A:N6	2.51	0.44
1:A:824:C:O2'	1:A:1534:A:N3	2.42	0.44
1:A:2456:A:H62	1:A:2460:U:P	2.40	0.44
1:A:2548:C:O2'	1:A:2549:G:N2	2.50	0.44
4:D:230:VAL:CG1	4:D:254:ALA:HB1	2.48	0.44
1:A:216:G:OP1	23:X:16:ARG:NH1	2.47	0.43
1:A:358:G:N2	1:A:361:A:OP2	2.48	0.43
30:e:83:GLU:OE2	30:e:111:ARG:NE	2.50	0.43
30:e:105:ARG:O	30:e:109:LEU:HD23	2.18	0.43
39:n:4:ARG:HD3	39:n:215:LEU:HD11	1.99	0.43
9:J:112:ASP:OD1	9:J:113:LYS:N	2.51	0.43
34:i:58:THR:O	34:i:61:THR:OG1	2.26	0.43
41:w:104:TRP:CD1	43:o:163:ARG:NH2	2.85	0.43
1:A:1055:A:N3	46:x:81:U:O2'	2.51	0.43
1:A:1127:G:N2	1:A:1130:A:OP2	2.51	0.43
4:D:300:ARG:NH1	4:D:301:PRO:O	2.51	0.43
39:n:142:ILE:CD1	39:n:152:CYS:HB2	2.48	0.43
41:w:65:LEU:HD13	41:w:71:TRP:CE2	2.53	0.43
1:A:708:G:N2	1:A:711:A:OP2	2.46	0.43
15:P:120:LYS:O	15:P:248:ARG:NH1	2.47	0.43
22:W:108:LEU:HD12	22:W:109:LYS:HB2	2.00	0.43
39:n:122:ASP:OD1	39:n:123:ARG:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:o:179:THR:CB	43:o:180:PRO:HD2	2.48	0.43
2:B:130:SER:OG	2:B:174:ARG:NH1	2.52	0.43
44:p:41:UNK:O	44:p:43:UNK:N	2.52	0.43
1:A:364:G:OP2	34:i:52:LYS:NZ	2.22	0.43
41:w:57:PHE:CE2	41:w:58:CYS:O	2.72	0.43
1:A:198:A:N3	1:A:218:G:O2'	2.48	0.43
1:A:1207:G:OP1	45:t:119:ASN:ND2	2.52	0.43
27:b:156:ILE:O	27:b:159:GLN:N	2.45	0.43
27:b:190:THR:O	27:b:190:THR:OG1	2.35	0.43
39:n:155:SER:OG	39:n:156:ASN:N	2.50	0.43
1:A:1613:A:OP1	35:j:51:LEU:N	2.45	0.43
1:A:2402:A:N6	1:A:2403:G:O6	2.51	0.43
2:B:146:THR:HG1	2:B:160:SER:HG	1.51	0.43
9:J:53:TYR:CE1	9:J:57:LEU:HD21	2.54	0.43
23:X:73:VAL:O	23:X:73:VAL:HG23	2.18	0.43
8:H:60:ARG:NE	47:y:152:G:OP1	2.51	0.43
29:d:51:LEU:HD23	29:d:93:VAL:CB	2.44	0.43
41:w:19:CYS:O	41:w:21:ASN:N	2.51	0.43
1:A:520:U:H3	4:D:347:THR:HG1	1.67	0.43
8:H:144:GLU:OE2	33:h:36:ARG:NH1	2.52	0.43
30:e:121:ASN:OD1	30:e:121:ASN:N	2.50	0.43
43:o:163:ARG:HG2	43:o:181:PHE:CE1	2.54	0.43
43:o:222:VAL:O	43:o:222:VAL:HG13	2.19	0.43
1:A:2259:A:O2'	1:A:2262:A:N6	2.48	0.42
1:A:3378:C:O2'	3:C:312:VAL:O	2.24	0.42
41:w:374:ILE:O	41:w:377:SER:OG	2.35	0.42
1:A:2382:G:N7	9:J:90:LYS:NZ	2.65	0.42
2:B:125:ALA:HB1	2:B:128:ARG:HG3	2.01	0.42
16:Q:100:THR:HG23	16:Q:120:GLU:HG3	2.01	0.42
44:p:108:UNK:O	44:p:110:UNK:N	2.52	0.42
1:A:59:G:H2'	47:y:33:A:H2'	2.02	0.42
1:A:1643:A:O2'	1:A:1644:C:O4'	2.32	0.42
3:C:17:LEU:HD23	3:C:17:LEU:HA	1.79	0.42
6:F:4:ILE:HD11	18:S:143:PHE:CE1	2.55	0.42
6:F:126:VAL:HG23	6:F:164:ILE:HD13	2.02	0.42
34:i:72:ARG:NE	47:y:95:G:OP2	2.48	0.42
1:A:2469:G:N1	1:A:2475:G:O6	2.52	0.42
5:E:108:GLU:OE1	5:E:122:ILE:HG23	2.19	0.42
43:o:163:ARG:CD	43:o:183:ARG:CD	2.94	0.42
3:C:113:GLU:O	3:C:176:ALA:N	2.49	0.42
3:C:205:VAL:CG2	3:C:322:ILE:HD11	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1833:G:O2'	36:k:3:ALA:O	2.37	0.42
41:w:141:MET:CE	41:w:143:CYS:HA	2.49	0.42
1:A:2162:U:OP1	2:B:227:ARG:NH1	2.52	0.42
2:B:5:ILE:HG22	2:B:6:ARG:N	2.34	0.42
13:N:46:ASP:OD2	16:Q:176:ARG:NH1	2.53	0.42
40:z:428:ASP:O	40:z:430:LEU:N	2.52	0.42
43:o:163:ARG:CG	43:o:181:PHE:CZ	3.03	0.42
1:A:1618:G:O2'	47:y:126:A:N1	2.51	0.42
2:B:125:ALA:HB1	2:B:128:ARG:HD3	1.73	0.42
5:E:15:GLU:HB3	5:E:130:VAL:HG23	2.01	0.42
5:E:54:VAL:HG21	5:E:57:PHE:CD2	2.54	0.42
39:n:119:PRO:O	39:n:139:ARG:NH2	2.53	0.42
43:o:162:TRP:C	43:o:165:LYS:CD	2.85	0.42
43:o:235:VAL:HG12	43:o:236:ASN:H	1.85	0.42
1:A:950:G:N1	1:A:1368:U:OP2	2.45	0.42
1:A:2874:G:N2	1:A:2875:U:O4	2.45	0.42
39:n:5:THR:OG1	39:n:6:GLN:N	2.53	0.42
41:w:307:ASN:OD1	41:w:308:ALA:N	2.52	0.42
1:A:294:U:OP2	14:O:15:GLN:NE2	2.50	0.41
39:n:186:VAL:O	39:n:190:SER:OG	2.22	0.41
1:A:600:G:N2	1:A:603:A:OP2	2.34	0.41
1:A:965:A:H2	13:N:43:ILE:HD11	1.83	0.41
1:A:2705:A:N6	19:T:47:SER:O	2.53	0.41
14:O:112:ASN:OD1	14:O:112:ASN:N	2.52	0.41
18:S:13:ARG:NH1	18:S:50:LYS:O	2.53	0.41
1:A:68:C:OP2	1:A:301:G:N2	2.51	0.41
1:A:107:A:OP1	10:K:39:ARG:NH1	2.49	0.41
1:A:707:U:O2'	1:A:754:G:N3	2.53	0.41
7:G:12:SER:OG	7:G:14:ASP:OD2	2.20	0.41
1:A:1001:G:O6	1:A:1045:C:N4	2.53	0.41
9:J:76:SER:OG	9:J:105:GLU:OE2	2.31	0.41
41:w:59:ARG:CZ	41:w:59:ARG:CB	2.89	0.41
41:w:145:ASP:O	41:w:149:SER:OG	2.30	0.41
1:A:105:C:O2'	1:A:684:G:O2'	2.26	0.41
1:A:726:G:N1	1:A:743:C:OP2	2.45	0.41
14:O:64:VAL:HG11	14:O:102:ALA:HB1	2.03	0.41
35:j:12:LEU:O	35:j:15:THR:OG1	2.37	0.41
39:n:22:THR:HG23	39:n:23:TYR:CD2	2.55	0.41
41:w:59:ARG:HB2	41:w:59:ARG:NH1	2.34	0.41
1:A:1180:A:P	31:f:76:GLY:O	2.78	0.41
1:A:1900:A:O2'	1:A:1906:G:N7	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2847:A:O2'	1:A:2897:A:O2'	2.11	0.41
3:C:361:THR:OG1	3:C:371:GLN:O	2.34	0.41
12:M:22:LEU:O	12:M:64:VAL:N	2.54	0.41
13:N:116:GLY:O	13:N:137:LYS:NZ	2.45	0.41
28:c:34:LEU:HD13	28:c:59:TYR:HB3	2.03	0.41
41:w:58:CYS:CB	41:w:143:CYS:SG	2.93	0.41
41:w:252:CYS:N	41:w:255:ASP:OD2	2.51	0.41
46:x:29:C:C2'	46:x:51:A:H61	2.33	0.41
4:D:42:VAL:HG12	4:D:236:LEU:HD21	2.02	0.41
6:F:85:GLY:HA3	6:F:187:ILE:HD12	2.02	0.41
1:A:1002:A:N7	1:A:1003:A:N6	2.67	0.41
33:h:66:GLU:OE2	33:h:87:VAL:HG11	2.21	0.41
41:w:59:ARG:HE	41:w:140:ALA:HB1	1.85	0.41
43:o:222:VAL:O	43:o:223:LYS:HG2	2.21	0.41
43:o:389:PRO:O	43:o:391:LEU:HD12	2.21	0.41
1:A:117:U:O2'	1:A:118:U:O5'	2.35	0.41
1:A:541:U:O2	1:A:550:A:N6	2.44	0.41
1:A:2458:A:O2'	1:A:2459:A:OP1	2.33	0.41
1:A:3335:A:OP2	1:A:3368:U:N3	2.50	0.41
15:P:50:ARG:NH2	46:x:6:C:O2'	2.54	0.41
15:P:274:GLN:OE1	46:x:60:G:N2	2.42	0.41
25:Z:6:ALA:O	25:Z:9:LEU:N	2.53	0.41
43:o:466:ARG:HG3	43:o:471:MET:HE1	2.02	0.41
1:A:1404:G:N2	1:A:1407:A:OP2	2.46	0.41
1:A:3289:G:O2'	1:A:3290:G:O5'	2.38	0.41
7:G:2:SER:OG	7:G:2:SER:O	2.38	0.41
33:h:60:LEU:O	33:h:64:SER:N	2.54	0.41
39:n:28:VAL:HG12	39:n:52:THR:HG23	2.03	0.41
41:w:19:CYS:SG	41:w:35:CYS:HB3	2.61	0.41
43:o:464:TYR:O	43:o:468:ARG:N	2.54	0.41
1:A:1001:G:H22	1:A:1048:A:N6	2.19	0.40
1:A:1022:U:OP2	41:w:169:ARG:NH2	2.47	0.40
4:D:188:ARG:HE	4:D:200:THR:CG2	2.35	0.40
42:v:4:GLU:N	42:v:4:GLU:OE1	2.54	0.40
43:o:196:GLU:OE1	43:o:196:GLU:N	2.49	0.40
46:x:3:U:OP1	46:x:59:U:O2'	2.28	0.40
1:A:276:U:O2'	14:O:91:GLU:OE1	2.39	0.40
1:A:679:U:O2'	1:A:788:C:O2	2.39	0.40
1:A:2245:C:O2'	2:B:220:GLY:O	2.39	0.40
1:A:2890:A:H61	1:A:2913:C:H42	1.69	0.40
7:G:30:LEU:HD22	7:G:34:LEU:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:m:37:TYR:O	38:m:47:VAL:HG22	2.21	0.40
41:w:273:PHE:CE2	41:w:392:VAL:HG13	2.56	0.40
2:B:117:GLU:OE2	2:B:163:ARG:NH2	2.52	0.40
2:B:135:ILE:HD11	2:B:149:ARG:HE	1.86	0.40
28:c:99:ASP:OD1	28:c:99:ASP:N	2.51	0.40
41:w:49:ILE:HG22	41:w:90:LYS:HB3	2.02	0.40
47:y:40:A:OP2	47:y:103:G:N1	2.52	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%)	221 (90%)	24 (10%)	0	100	100
3	C	379/387 (98%)	347 (92%)	31 (8%)	1 (0%)	36	67
4	D	359/362 (99%)	332 (92%)	27 (8%)	0	100	100
5	E	167/174 (96%)	158 (95%)	9 (5%)	0	100	100
6	F	187/191 (98%)	175 (94%)	12 (6%)	0	100	100
7	G	173/176 (98%)	156 (90%)	17 (10%)	0	100	100
8	H	221/256 (86%)	204 (92%)	17 (8%)	0	100	100
9	J	195/198 (98%)	187 (96%)	8 (4%)	0	100	100
10	K	184/199 (92%)	173 (94%)	11 (6%)	0	100	100
11	L	134/137 (98%)	126 (94%)	8 (6%)	0	100	100
12	M	133/138 (96%)	123 (92%)	9 (7%)	1 (1%)	16	47
13	N	146/149 (98%)	123 (84%)	23 (16%)	0	100	100
14	O	201/204 (98%)	184 (92%)	17 (8%)	0	100	100
15	P	267/297 (90%)	253 (95%)	14 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	Q	183/186 (98%)	173 (94%)	10 (6%)	0	100	100
17	R	148/189 (78%)	146 (99%)	2 (1%)	0	100	100
18	S	169/172 (98%)	162 (96%)	7 (4%)	0	100	100
19	T	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
20	U	152/154 (99%)	142 (93%)	10 (7%)	0	100	100
21	V	97/121 (80%)	88 (91%)	9 (9%)	0	100	100
22	W	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
23	X	123/127 (97%)	114 (93%)	9 (7%)	0	100	100
24	Y	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
25	Z	116/120 (97%)	113 (97%)	3 (3%)	0	100	100
26	a	50/59 (85%)	43 (86%)	7 (14%)	0	100	100
27	b	217/244 (89%)	200 (92%)	17 (8%)	0	100	100
28	c	95/105 (90%)	90 (95%)	5 (5%)	0	100	100
29	d	105/113 (93%)	91 (87%)	14 (13%)	0	100	100
30	e	125/130 (96%)	110 (88%)	14 (11%)	1 (1%)	16	47
31	f	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
32	g	101/121 (84%)	88 (87%)	13 (13%)	0	100	100
33	h	96/100 (96%)	88 (92%)	8 (8%)	0	100	100
34	i	82/88 (93%)	70 (85%)	11 (13%)	1 (1%)	10	37
35	j	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
36	k	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
37	l	92/106 (87%)	85 (92%)	6 (6%)	1 (1%)	11	39
38	m	87/92 (95%)	81 (93%)	6 (7%)	0	100	100
39	n	222/245 (91%)	199 (90%)	22 (10%)	1 (0%)	24	57
40	z	56/432 (13%)	48 (86%)	8 (14%)	0	100	100
41	w	387/518 (75%)	340 (88%)	41 (11%)	6 (2%)	7	30
42	v	58/155 (37%)	57 (98%)	1 (2%)	0	100	100
43	o	316/640 (49%)	246 (78%)	68 (22%)	2 (1%)	21	52
45	t	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
All	All	6753/8141 (83%)	6178 (92%)	561 (8%)	14 (0%)	44	73

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	18	PRO
41	w	148	ARG
41	w	20	CYS
41	w	68	PRO
30	e	7	PRO
39	n	141	THR
34	i	38	GLY
41	w	147	ALA
43	o	175	ASP
41	w	25	PRO
43	o	394	PRO
41	w	143	CYS
37	l	51	GLY
12	M	49	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	189/196 (96%)	187 (99%)	2 (1%)	65	78
3	C	317/323 (98%)	312 (98%)	5 (2%)	55	75
4	D	288/289 (100%)	288 (100%)	0	100	100
5	E	147/150 (98%)	146 (99%)	1 (1%)	76	82
6	F	169/171 (99%)	169 (100%)	0	100	100
7	G	152/153 (99%)	152 (100%)	0	100	100
8	H	183/208 (88%)	183 (100%)	0	100	100
9	J	163/164 (99%)	162 (99%)	1 (1%)	78	83
10	K	149/159 (94%)	148 (99%)	1 (1%)	76	82
11	L	104/105 (99%)	103 (99%)	1 (1%)	68	79
12	M	107/109 (98%)	107 (100%)	0	100	100
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%)	227 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	Q	150/151 (99%)	149 (99%)	1 (1%)	76	82
17	R	124/154 (80%)	124 (100%)	0	100	100
18	S	155/156 (99%)	154 (99%)	1 (1%)	78	83
19	T	136/137 (99%)	136 (100%)	0	100	100
20	U	125/125 (100%)	125 (100%)	0	100	100
21	V	86/107 (80%)	86 (100%)	0	100	100
22	W	104/118 (88%)	104 (100%)	0	100	100
23	X	108/110 (98%)	108 (100%)	0	100	100
24	Y	115/116 (99%)	115 (100%)	0	100	100
25	Z	104/105 (99%)	104 (100%)	0	100	100
26	a	41/47 (87%)	41 (100%)	0	100	100
27	b	184/205 (90%)	182 (99%)	2 (1%)	65	78
28	c	81/88 (92%)	81 (100%)	0	100	100
29	d	94/97 (97%)	93 (99%)	1 (1%)	65	78
30	e	109/111 (98%)	108 (99%)	1 (1%)	70	80
31	f	90/91 (99%)	89 (99%)	1 (1%)	65	78
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%)	68 (99%)	1 (1%)	59	76
35	j	68/69 (99%)	67 (98%)	1 (2%)	57	75
36	k	45/46 (98%)	45 (100%)	0	100	100
37	l	81/91 (89%)	81 (100%)	0	100	100
38	m	70/72 (97%)	68 (97%)	2 (3%)	37	66
39	n	192/211 (91%)	190 (99%)	2 (1%)	68	79
40	z	53/392 (14%)	53 (100%)	0	100	100
41	w	348/467 (74%)	344 (99%)	4 (1%)	65	78
42	v	53/129 (41%)	53 (100%)	0	100	100
43	o	284/555 (51%)	268 (94%)	16 (6%)	19	49
45	t	47/116 (40%)	47 (100%)	0	100	100
All	All	5772/6889 (84%)	5726 (99%)	46 (1%)	70	81

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	123	ARG
2	B	134	VAL
3	C	17	LEU
3	C	18	PRO
3	C	19	ARG
3	C	44	THR
3	C	256	HIS
5	E	174	LYS
9	J	26	VAL
10	K	63	VAL
11	L	137	VAL
16	Q	186	VAL
18	S	172	TYR
27	b	188	ILE
27	b	229	PHE
29	d	105	GLN
30	e	7	PRO
31	f	75	HIS
32	g	44	CYS
32	g	49	SER
34	i	21	ARG
35	j	78	LEU
38	m	60	CYS
38	m	64	VAL
39	n	141	THR
39	n	142	ILE
41	w	35	CYS
41	w	59	ARG
41	w	145	ASP
41	w	146	CYS
43	o	134	LEU
43	o	163	ARG
43	o	164	ARG
43	o	165	LYS
43	o	169	LEU
43	o	170	GLN
43	o	171	GLU
43	o	175	ASP
43	o	177	LEU
43	o	178	LEU
43	o	179	THR
43	o	181	PHE
43	o	223	LYS

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Mol	Chain	Res	Type
43	o	395	ASN
43	o	400	LYS
43	o	402	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	194	ASN
3	C	182	GLN
4	D	48	GLN
4	D	296	GLN
5	E	43	GLN
5	E	62	ASN
6	F	116	ASN
7	G	97	ASN
7	G	126	GLN
8	H	123	GLN
14	O	86	ASN
16	Q	9	GLN
17	R	141	HIS
18	S	62	ASN
18	S	68	HIS
19	T	98	HIS
19	T	131	GLN
20	U	45	GLN
20	U	121	GLN
20	U	145	HIS
23	X	4	GLN
23	X	81	GLN
23	X	98	ASN
30	e	49	ASN
31	f	88	ASN
32	g	14	ASN
37	l	82	GLN
39	n	82	GLN
39	n	83	HIS
40	z	402	GLN
41	w	163	GLN
41	w	182	ASN
41	w	272	GLN
43	o	395	ASN
43	o	399	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3141/3396 (92%)	664 (21%)	22 (0%)
46	x	120/121 (99%)	19 (15%)	0
47	y	155/158 (98%)	34 (21%)	0
All	All	3416/3675 (92%)	717 (20%)	22 (0%)

All (717) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	15	C
1	A	26	A
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	77	A
1	A	92	G
1	A	105	C
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	136	G
1	A	153	U
1	A	156	G
1	A	157	A
1	A	164	A
1	A	187	A

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Mol	Chain	Res	Type
1	A	190	U
1	A	191	U
1	A	198	A
1	A	200	C
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	221	A
1	A	234	G
1	A	238	A
1	A	239	G
1	A	241	G
1	A	243	G
1	A	244	G
1	A	246	U
1	A	248	U
1	A	249	U
1	A	251	G
1	A	252	U
1	A	267	G
1	A	269	G
1	A	281	G
1	A	286	U
1	A	295	A
1	A	298	U
1	A	329	U
1	A	330	G
1	A	334	A
1	A	338	A
1	A	346	C
1	A	376	G
1	A	385	A
1	A	390	G
1	A	395	A
1	A	398	A
1	A	399	A
1	A	401	U
1	A	402	A
1	A	403	C

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Mol	Chain	Res	Type
1	A	404	G
1	A	420	G
1	A	421	G
1	A	422	A
1	A	437	G
1	A	438	A
1	A	439	C
1	A	440	A
1	A	495	G
1	A	496	C
1	A	503	C
1	A	510	G
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	548	G
1	A	549	U
1	A	551	A
1	A	552	G
1	A	555	U
1	A	557	A
1	A	558	U
1	A	559	A
1	A	569	A
1	A	578	A
1	A	579	G
1	A	592	A
1	A	611	A
1	A	620	U
1	A	621	A
1	A	622	A
1	A	636	C
1	A	649	A
1	A	661	G
1	A	662	U
1	A	667	C
1	A	677	A
1	A	681	U
1	A	689	U

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Mol	Chain	Res	Type
1	A	712	G
1	A	719	U
1	A	720	A
1	A	725	G
1	A	767	U
1	A	774	G
1	A	776	U
1	A	777	U
1	A	780	A
1	A	781	G
1	A	785	G
1	A	801	A
1	A	806	A
1	A	808	A
1	A	816	A
1	A	817	A
1	A	830	A
1	A	845	G
1	A	846	A
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	890	C
1	A	896	A
1	A	897	U
1	A	907	G
1	A	908	G
1	A	914	A
1	A	916	G
1	A	917	A
1	A	937	G
1	A	944	C
1	A	959	C
1	A	960	U
1	A	977	C
1	A	980	A
1	A	981	U

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Mol	Chain	Res	Type
1	A	984	G
1	A	999	G
1	A	1001	G
1	A	1002	A
1	A	1004	U
1	A	1006	A
1	A	1007	U
1	A	1008	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	1019	G
1	A	1024	G
1	A	1025	A
1	A	1027	A
1	A	1029	G
1	A	1031	C
1	A	1032	C
1	A	1035	G
1	A	1036	A
1	A	1037	C
1	A	1038	C
1	A	1039	U
1	A	1041	U
1	A	1042	U
1	A	1043	C
1	A	1044	U
1	A	1045	C
1	A	1048	A
1	A	1050	U
1	A	1051	U
1	A	1064	A
1	A	1065	A
1	A	1072	G
1	A	1081	U
1	A	1082	U

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Mol	Chain	Res	Type
1	A	1083	G
1	A	1087	G
1	A	1093	A
1	A	1094	U
1	A	1095	U
1	A	1096	U
1	A	1098	A
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	1143	A
1	A	1159	A
1	A	1180	A
1	A	1181	U
1	A	1182	A
1	A	1192	C
1	A	1193	A
1	A	1199	C
1	A	1201	C
1	A	1208	U
1	A	1217	A
1	A	1218	U
1	A	1222	G
1	A	1227	C
1	A	1236	G
1	A	1239	C
1	A	1240	A
1	A	1242	G
1	A	1243	G
1	A	1245	A
1	A	1246	G
1	A	1248	C
1	A	1251	A
1	A	1258	U
1	A	1262	G
1	A	1263	A
1	A	1264	G
1	A	1269	U

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Mol	Chain	Res	Type
1	A	1270	A
1	A	1271	A
1	A	1274	A
1	A	1278	A
1	A	1279	C
1	A	1285	G
1	A	1287	A
1	A	1288	U
1	A	1289	G
1	A	1295	G
1	A	1302	A
1	A	1304	A
1	A	1307	G
1	A	1309	U
1	A	1313	G
1	A	1316	C
1	A	1317	A
1	A	1325	U
1	A	1330	A
1	A	1332	A
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	1357	G
1	A	1386	A
1	A	1399	A
1	A	1400	G
1	A	1405	U
1	A	1418	A
1	A	1419	A
1	A	1428	A
1	A	1434	G
1	A	1436	U
1	A	1437	C
1	A	1443	G
1	A	1445	U
1	A	1446	A
1	A	1450	G

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Mol	Chain	Res	Type
1	A	1452	A
1	A	1455	U
1	A	1465	A
1	A	1467	A
1	A	1475	A
1	A	1481	A
1	A	1487	G
1	A	1508	C
1	A	1542	G
1	A	1547	G
1	A	1555	U
1	A	1556	C
1	A	1562	C
1	A	1563	C
1	A	1564	U
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	1571	A
1	A	1572	U
1	A	1573	G
1	A	1574	C
1	A	1575	A
1	A	1578	C
1	A	1579	C
1	A	1583	A
1	A	1588	A
1	A	1589	A
1	A	1593	A
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	1646	G
1	A	1657	C

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Mol	Chain	Res	Type
1	A	1677	G
1	A	1705	U
1	A	1715	A
1	A	1724	U
1	A	1725	C
1	A	1741	A
1	A	1750	A
1	A	1751	G
1	A	1762	C
1	A	1763	U
1	A	1764	U
1	A	1765	U
1	A	1775	G
1	A	1788	C
1	A	1794	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	1840	U
1	A	1842	A
1	A	1849	C
1	A	1850	A
1	A	1871	U
1	A	1874	A
1	A	1878	G
1	A	1880	U
1	A	1886	A
1	A	1893	A
1	A	1906	G
1	A	1930	A
1	A	1943	C
1	A	1950	U
1	A	1951	C
1	A	1952	G
1	A	1954	G
1	A	2096	A

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Mol	Chain	Res	Type
1	A	2100	A
1	A	2101	C
1	A	2102	U
1	A	2111	G
1	A	2112	U
1	A	2113	A
1	A	2114	C
1	A	2121	G
1	A	2122	G
1	A	2126	A
1	A	2131	A
1	A	2142	A
1	A	2158	A
1	A	2168	A
1	A	2169	G
1	A	2184	U
1	A	2187	G
1	A	2188	A
1	A	2197	C
1	A	2205	U
1	A	2206	G
1	A	2209	U
1	A	2251	G
1	A	2252	A
1	A	2254	U
1	A	2256	A
1	A	2257	C
1	A	2258	U
1	A	2259	A
1	A	2260	U
1	A	2261	G
1	A	2262	A
1	A	2264	U
1	A	2266	U
1	A	2268	U
1	A	2269	U
1	A	2270	A
1	A	2273	G
1	A	2274	U
1	A	2279	A
1	A	2281	A
1	A	2282	U

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Mol	Chain	Res	Type
1	A	2294	U
1	A	2295	A
1	A	2298	U
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	2350	C
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	2403	G
1	A	2404	A
1	A	2405	C
1	A	2411	U
1	A	2412	G
1	A	2435	G
1	A	2437	G
1	A	2444	C
1	A	2445	A
1	A	2446	U
1	A	2448	G
1	A	2449	A
1	A	2454	G
1	A	2455	U
1	A	2456	A
1	A	2457	G
1	A	2458	A
1	A	2459	A
1	A	2460	U

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Mol	Chain	Res	Type
1	A	2461	A
1	A	2462	A
1	A	2464	U
1	A	2465	G
1	A	2466	G
1	A	2468	A
1	A	2470	C
1	A	2471	U
1	A	2474	G
1	A	2476	C
1	A	2479	C
1	A	2481	G
1	A	2482	U
1	A	2483	G
1	A	2484	A
1	A	2486	A
1	A	2490	C
1	A	2492	C
1	A	2493	U
1	A	2495	C
1	A	2496	C
1	A	2497	U
1	A	2498	U
1	A	2499	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	2524	A
1	A	2530	G
1	A	2549	G
1	A	2550	U
1	A	2551	U
1	A	2561	A
1	A	2562	A
1	A	2566	C
1	A	2568	C
1	A	2569	A

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Mol	Chain	Res	Type
1	A	2571	U
1	A	2572	C
1	A	2573	G
1	A	2585	G
1	A	2593	A
1	A	2606	G
1	A	2607	G
1	A	2614	G
1	A	2618	G
1	A	2619	G
1	A	2626	A
1	A	2635	A
1	A	2648	G
1	A	2652	U
1	A	2656	A
1	A	2657	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	2690	G
1	A	2691	A
1	A	2694	A
1	A	2703	A
1	A	2704	A
1	A	2708	C
1	A	2714	G
1	A	2719	U
1	A	2728	G
1	A	2737	C
1	A	2740	A
1	A	2753	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

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Mol	Chain	Res	Type
1	A	2796	G
1	A	2800	G
1	A	2801	A
1	A	2803	A
1	A	2810	C
1	A	2817	A
1	A	2818	U
1	A	2819	A
1	A	2820	A
1	A	2823	G
1	A	2842	U
1	A	2843	U
1	A	2844	C
1	A	2845	A
1	A	2846	U
1	A	2850	G
1	A	2851	A
1	A	2853	A
1	A	2860	U
1	A	2867	C
1	A	2871	G
1	A	2875	U
1	A	2887	A
1	A	2889	C
1	A	2898	G
1	A	2899	C
1	A	2900	A
1	A	2916	U
1	A	2923	U
1	A	2935	U
1	A	2936	A
1	A	2938	G
1	A	2940	A
1	A	2941	A
1	A	2942	C
1	A	2947	G
1	A	2951	G
1	A	2971	A
1	A	2977	G
1	A	2983	C
1	A	2990	G
1	A	2997	G

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Mol	Chain	Res	Type
1	A	3011	A
1	A	3012	A
1	A	3016	A
1	A	3022	G
1	A	3027	A
1	A	3028	G
1	A	3038	U
1	A	3056	U
1	A	3059	G
1	A	3078	U
1	A	3080	G
1	A	3092	C
1	A	3094	A
1	A	3101	G
1	A	3103	A
1	A	3105	U
1	A	3109	G
1	A	3116	G
1	A	3117	C
1	A	3118	C
1	A	3122	A
1	A	3129	A
1	A	3130	A
1	A	3131	U
1	A	3134	A
1	A	3142	A
1	A	3148	U
1	A	3153	U
1	A	3154	C
1	A	3155	U
1	A	3156	U
1	A	3157	U
1	A	3158	G
1	A	3165	A
1	A	3167	A
1	A	3170	A
1	A	3171	U
1	A	3173	G
1	A	3174	A
1	A	3176	G
1	A	3179	U
1	A	3180	A

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Mol	Chain	Res	Type
1	A	3181	C
1	A	3187	A
1	A	3197	G
1	A	3199	G
1	A	3206	C
1	A	3207	U
1	A	3213	A
1	A	3217	C
1	A	3218	A
1	A	3219	G
1	A	3221	C
1	A	3222	U
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	3278	C
1	A	3279	A
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	3304	U
1	A	3313	U
1	A	3316	A
1	A	3334	U
1	A	3335	A
1	A	3341	U
1	A	3351	U
1	A	3352	U
1	A	3353	G
1	A	3354	U
1	A	3355	U
1	A	3358	U
1	A	3369	G
1	A	3378	C
1	A	3382	U
1	A	3386	G

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Mol	Chain	Res	Type
1	A	3396	U
46	x	7	G
46	x	11	A
46	x	18	C
46	x	22	A
46	x	33	U
46	x	41	G
46	x	50	U
46	x	54	U
46	x	55	A
46	x	56	A
46	x	65	G
46	x	73	C
46	x	74	C
46	x	76	A
46	x	93	C
46	x	99	G
46	x	102	A
46	x	112	G
46	x	121	U
47	y	22	U
47	y	23	U
47	y	34	U
47	y	35	C
47	y	52	A
47	y	59	A
47	y	62	C
47	y	63	G
47	y	75	G
47	y	78	G
47	y	79	A
47	y	81	U
47	y	82	U
47	y	83	C
47	y	84	C
47	y	86	U
47	y	87	G
47	y	90	U
47	y	91	C
47	y	95	G
47	y	97	A
47	y	102	U

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Mol	Chain	Res	Type
47	y	104	A
47	y	105	A
47	y	106	C
47	y	112	U
47	y	113	U
47	y	116	G
47	y	125	U
47	y	127	U
47	y	138	A
47	y	148	G
47	y	151	C
47	y	152	G

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	621	A
1	A	916	G
1	A	1010	G
1	A	1064	A
1	A	1217	A
1	A	1273	A
1	A	1287	A
1	A	1288	U
1	A	1355	A
1	A	1629	U
1	A	1815	U
1	A	2101	C
1	A	2112	U
1	A	2261	G
1	A	2404	A
1	A	2458	A
1	A	2459	A
1	A	2497	U
1	A	3027	A
1	A	3055	U
1	A	3206	C
1	A	3353	G

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

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 7 ligands modelled in this entry, 7 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

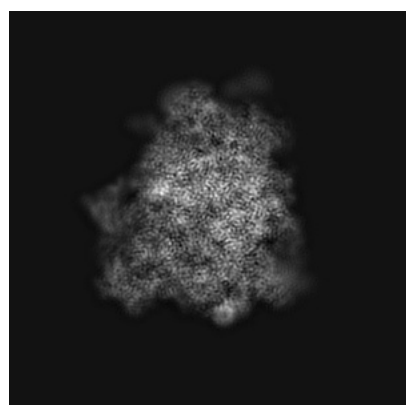
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4560. These allow visual inspection of the internal detail of the map and identification of artifacts.

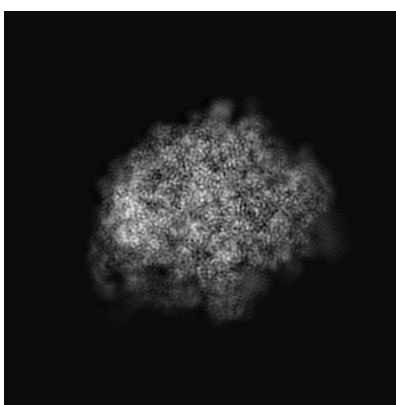
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

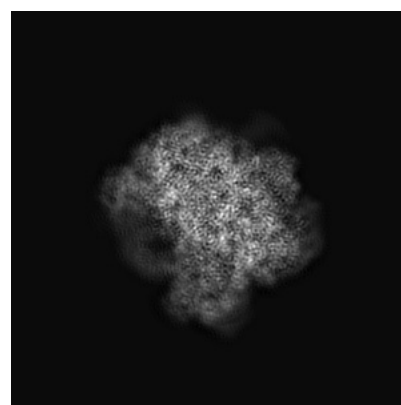
6.1.1 Primary map



X



Y

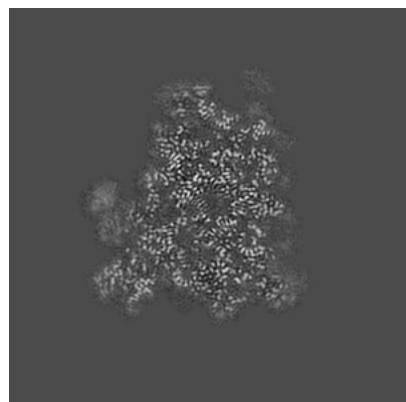


Z

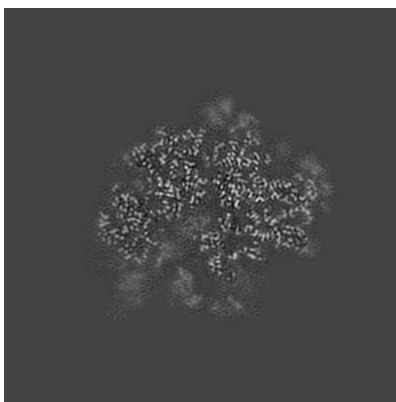
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

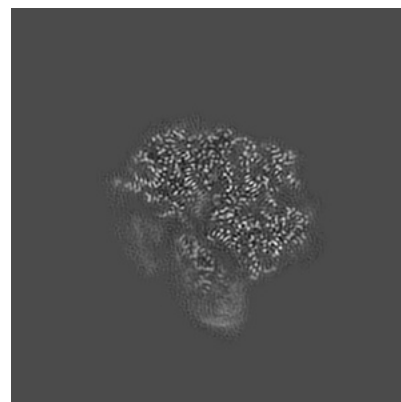
6.2.1 Primary map



X Index: 180



Y Index: 180

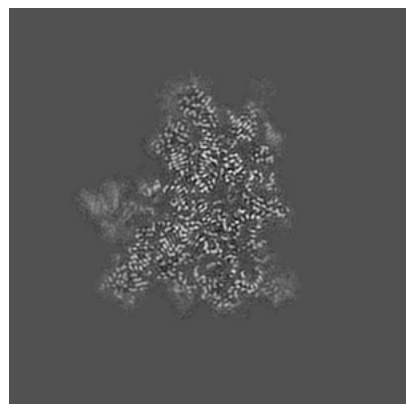


Z Index: 180

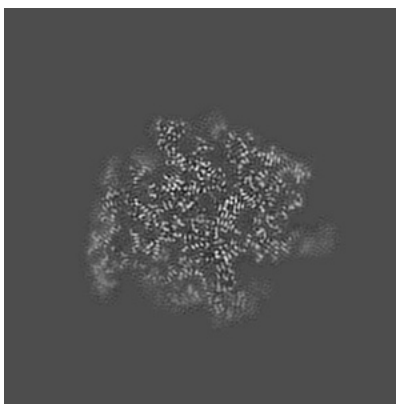
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

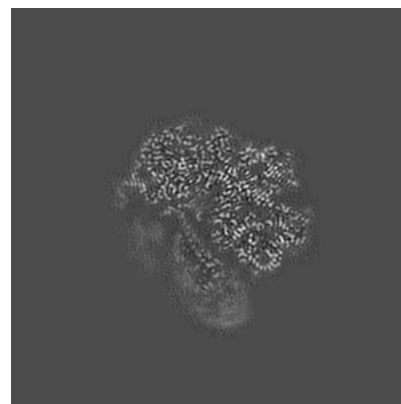
6.3.1 Primary map



X Index: 189



Y Index: 196

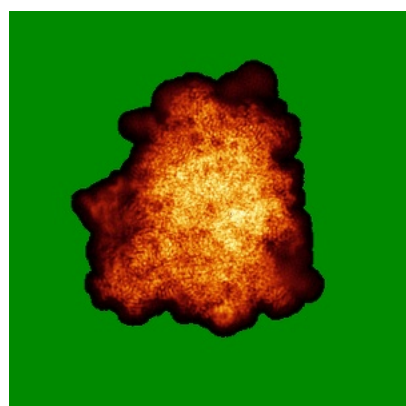


Z Index: 177

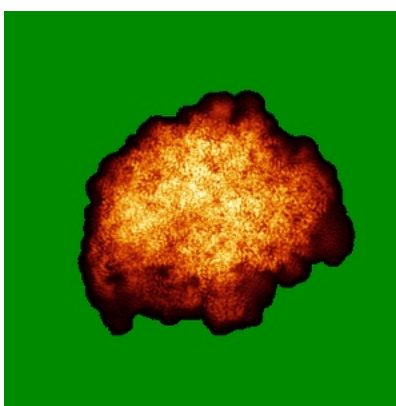
The images above show the largest variance slices of the map in three orthogonal directions.

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

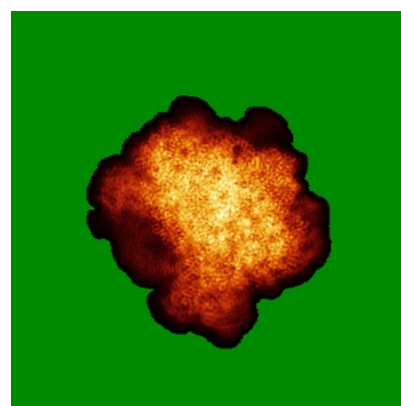
6.4.1 Primary map



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

This section was not generated.

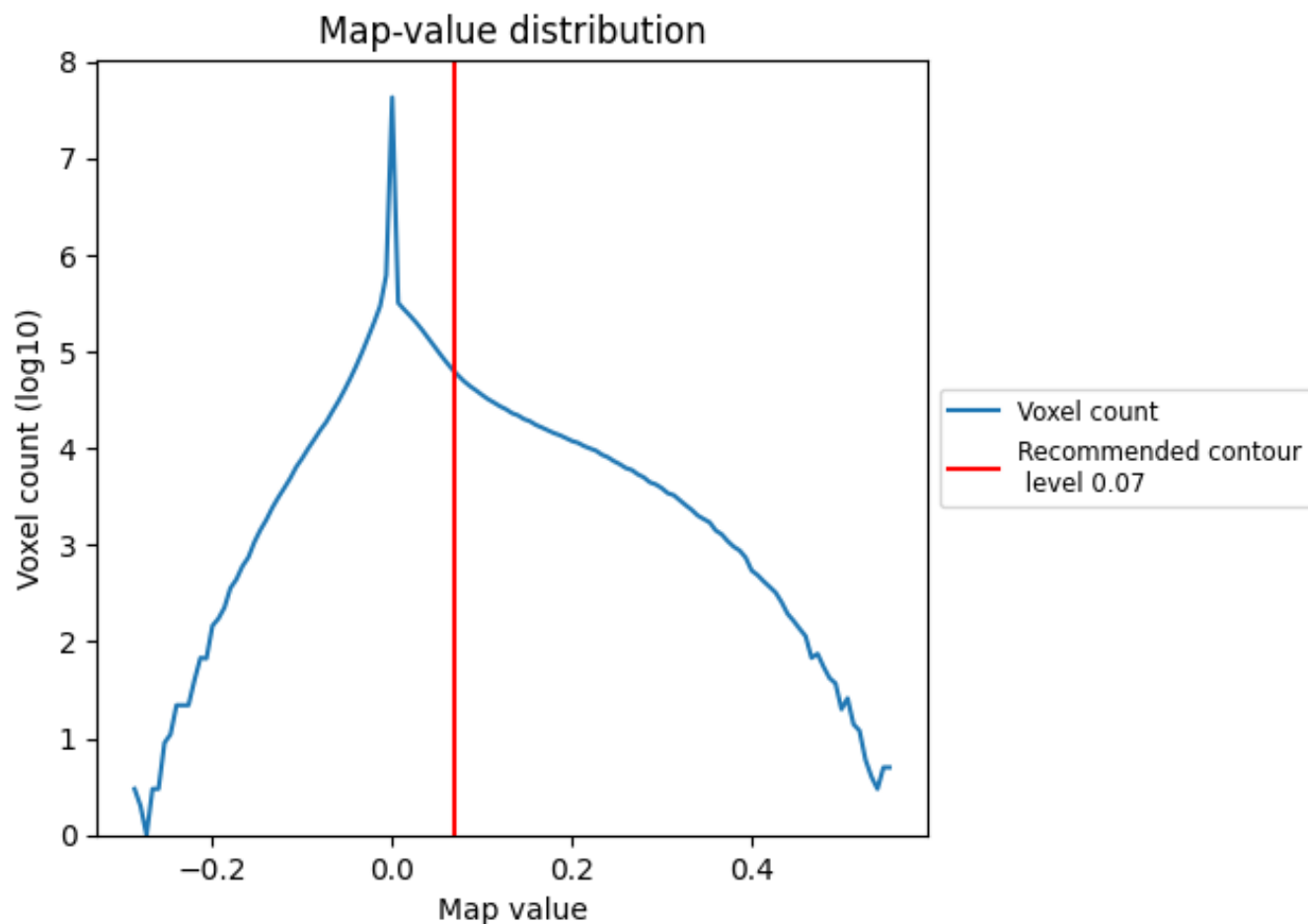
6.6 Mask visualisation

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

7 Map analysis [i](#)

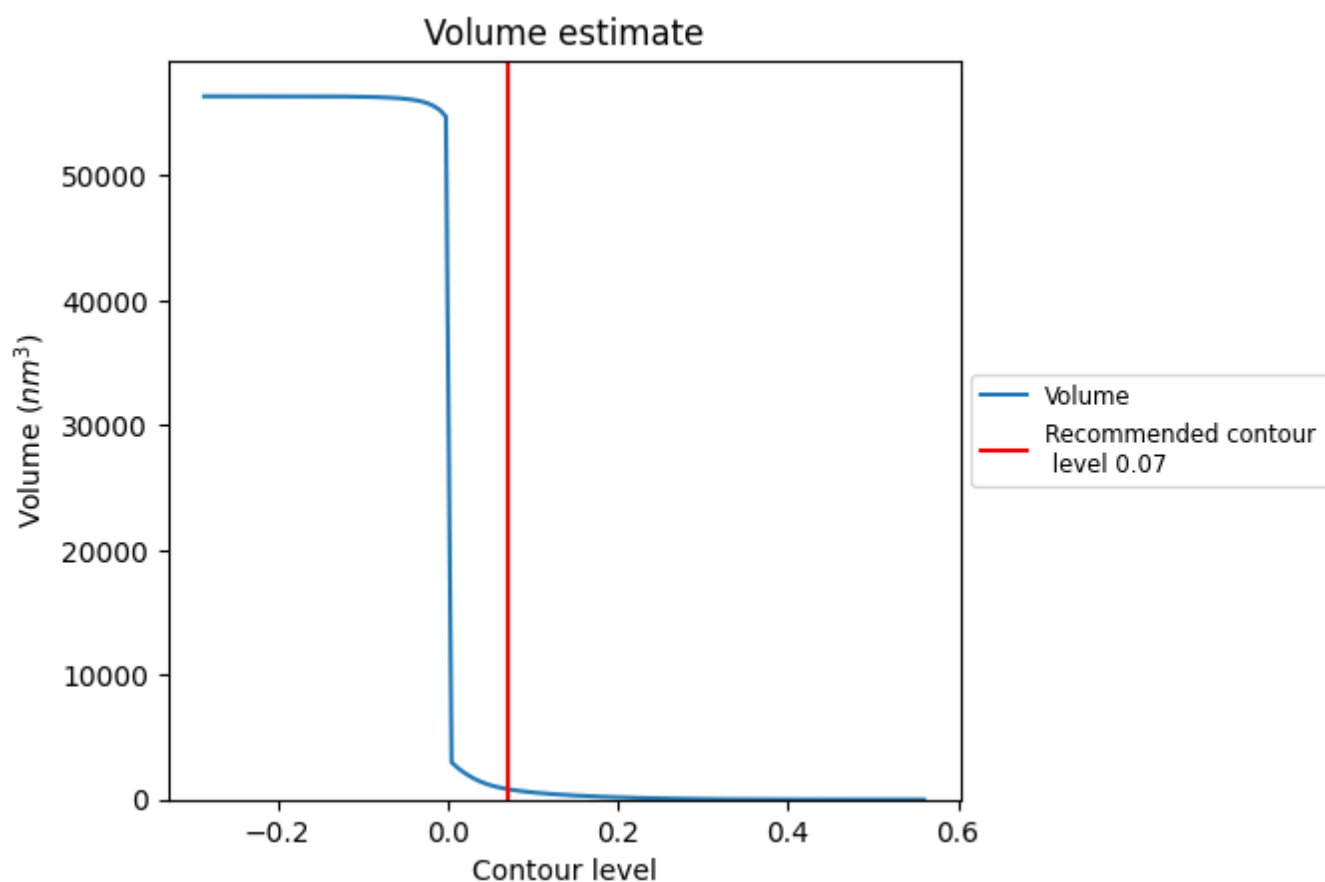
This section contains the results of statistical analysis of the map.

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.

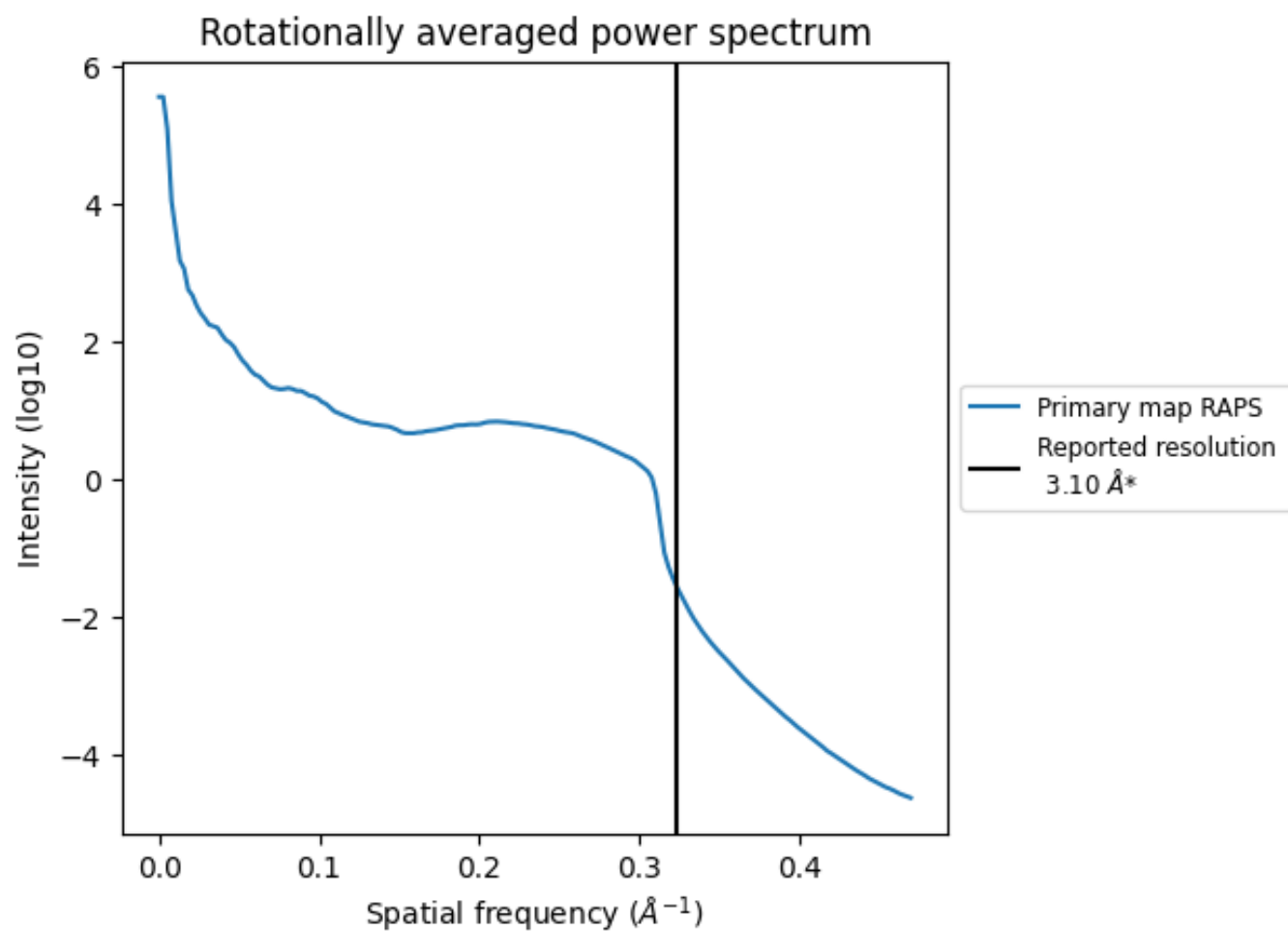
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 838 nm³; this corresponds to an approximate mass of 757 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 0.323 Å⁻¹

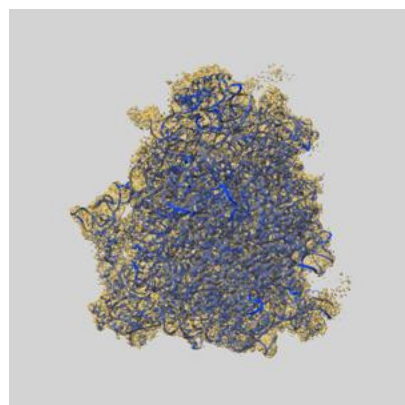
8 Fourier-Shell correlation ⓘ

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

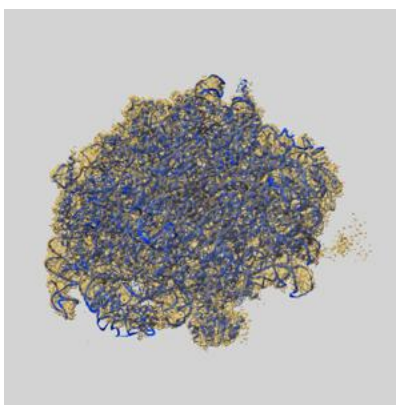
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4560 and PDB model 6QIK. Per-residue inclusion information can be found in section [3](#) on page [13](#).

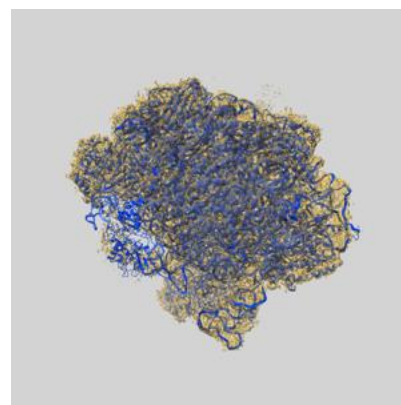
9.1 Map-model overlay [i](#)



X



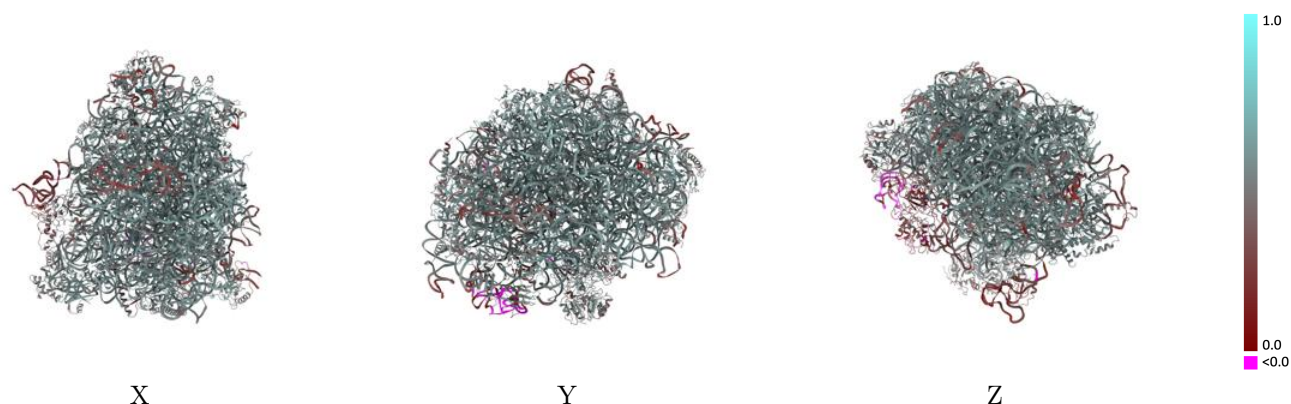
Y



Z

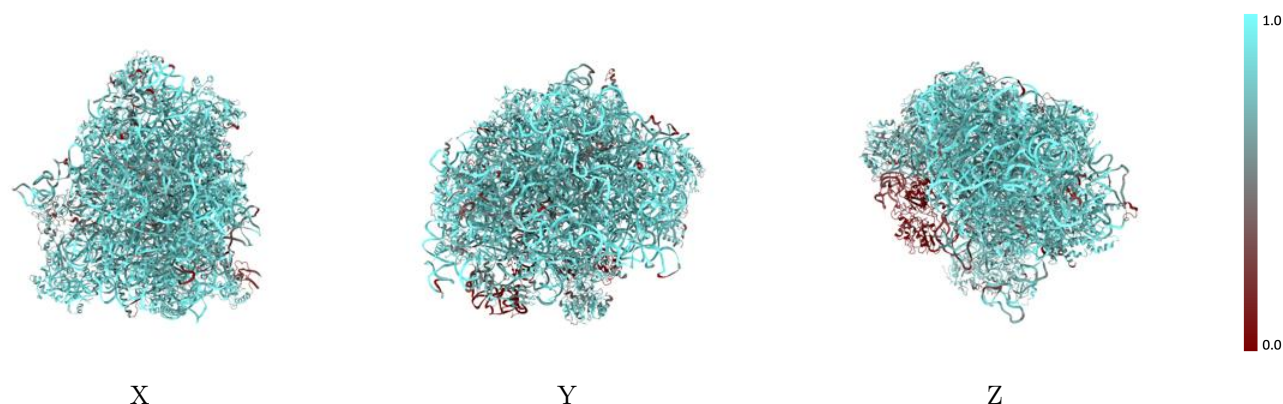
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



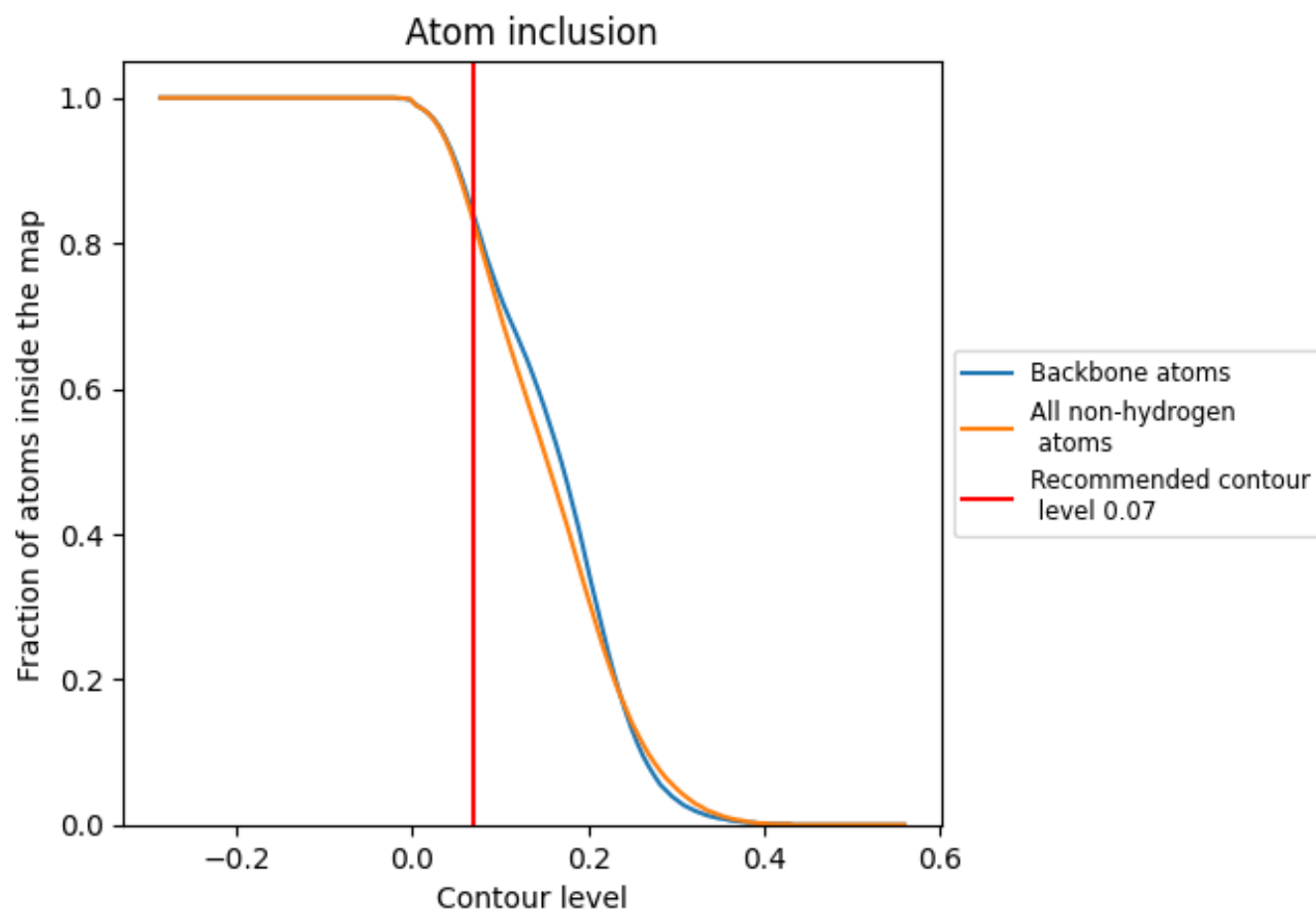
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 84% 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	 0.8280	 0.5190
A	 0.8780	 0.5150
B	 0.8610	 0.5770
C	 0.8640	 0.5630
D	 0.8520	 0.5690
E	 0.7490	 0.4610
F	 0.6790	 0.4980
G	 0.6780	 0.4830
H	 0.7840	 0.5170
J	 0.8340	 0.5540
K	 0.8030	 0.5460
L	 0.8290	 0.5690
M	 0.7970	 0.5290
N	 0.8760	 0.5670
O	 0.8800	 0.5860
P	 0.8360	 0.5290
Q	 0.8720	 0.5780
R	 0.8350	 0.5530
S	 0.8440	 0.5580
T	 0.8040	 0.5440
U	 0.8590	 0.5720
V	 0.8070	 0.5060
W	 0.8330	 0.5540
X	 0.8430	 0.5640
Y	 0.8160	 0.5130
Z	 0.8340	 0.5500
a	 0.7800	 0.5470
b	 0.8530	 0.5570
c	 0.7800	 0.5000
d	 0.7920	 0.5430
e	 0.8120	 0.5700
f	 0.8450	 0.5750
g	 0.8430	 0.5660
h	 0.6470	 0.5110
i	 0.8690	 0.5840



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Chain	Atom inclusion	Q-score
j	 0.7980	 0.5120
k	 0.8500	 0.5830
l	 0.8550	 0.5810
m	 0.8200	 0.5570
n	 0.7450	 0.4860
o	 0.0670	 0.2950
p	 0.6140	 0.3640
t	 0.0030	 0.3180
v	 0.7340	 0.5290
w	 0.4820	 0.4100
x	 0.9690	 0.5410
y	 0.9680	 0.5680
z	 0.4610	 0.5160