



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 05:20 PM UTC

PDB ID : 6SZS / pdb_00006szs
EMDB ID : EMD-10353
Title : Release factor-dependent ribosome rescue by BrfA in the Gram-positive bacterium *Bacillus subtilis*
Authors : Muller, C.; Beckert, B.; Wilson, D.N.
Deposited on : 2019-10-02
Resolution : 3.06 Å(reported)
Based on initial model : 5MGP

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

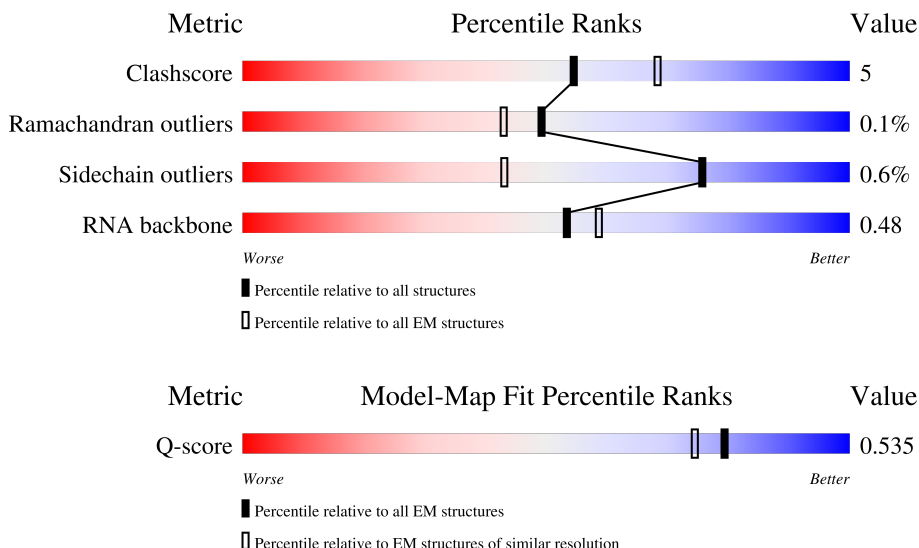
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.06 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	13976 (2.56 - 3.56)

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	0	57	9% 81% 16% .
2	1	55	18% 62% 29% 9%
3	2	46	. 89% 11%

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Mol	Chain	Length	Quality of chain
4	3	65	
5	4	38	
6	5	70	
7	A	2903	
8	B	120	
9	C	273	
10	D	209	
11	E	201	
12	F	179	
13	G	177	
14	H	149	
15	J	142	
16	K	123	
17	L	144	
18	M	136	
19	N	127	
20	O	117	
21	P	115	
22	Q	118	
23	R	103	
24	S	110	
25	T	100	
26	U	104	
27	V	94	
28	W	85	

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Mol	Chain	Length	Quality of chain
29	X	78	
30	Y	63	
31	Z	59	
32	a	1540	
33	b	241	
34	c	233	
35	d	206	
36	e	167	
37	f	135	
38	g	179	
39	h	130	
40	i	130	
41	j	103	
42	k	129	
43	l	124	
44	m	118	
45	n	101	
46	o	89	
47	p	82	
48	q	84	
49	r	75	
50	s	92	
51	t	87	
52	u	71	
53	v	6	

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Mol	Chain	Length	Quality of chain
54	x	77	10% 64% 30% 6%
55	y	71	25% 63% 13% 24%
56	z	362	57% 77% 23%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 147361 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 protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	65	Total	C	N	O	S	0	0
			514	317	98	93	6		

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	174	Total	C	N	O	S	0	0
			1304	820	239	243	2		

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	89	Total	C	N	O	S	0	0
			709	449	133	125	2		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 32 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1540	Total	C	N	O	P	0	0
			33037	14735	6057	10705	1540		

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	99	Total	C	N	O	S	0	0
			811	512	147	146	6		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 45 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	66	Total	C	N	O	S	0	0
			545	344	102	98	1		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 52 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	6	Total	C	N	O	P	0	0
			126	56	22	42	6		

- Molecule 54 is a RNA chain called P-site tRNA-Pro(CGG).

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

- Molecule 55 is a protein called Uncharacterized protein YqkK.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	54	Total	C	N	O	S	0	0
			434	264	95	74	1		

- Molecule 56 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	362	Total	C	N	O	S	0	0
			2742	1701	495	534	12		

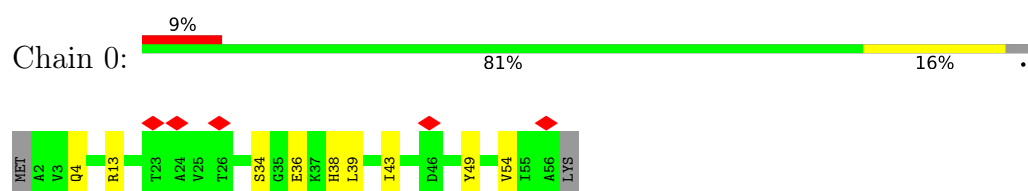
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	251	PRO	GLN	engineered mutation	UNP P28367

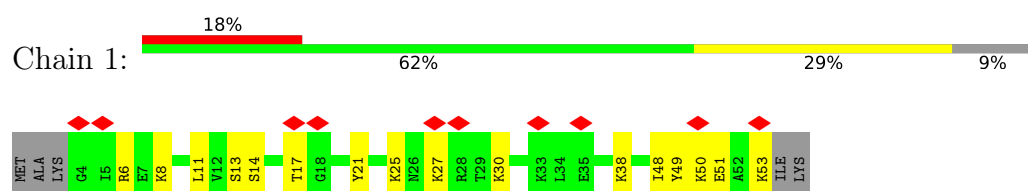
3 Residue-property plots [i](#)

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.

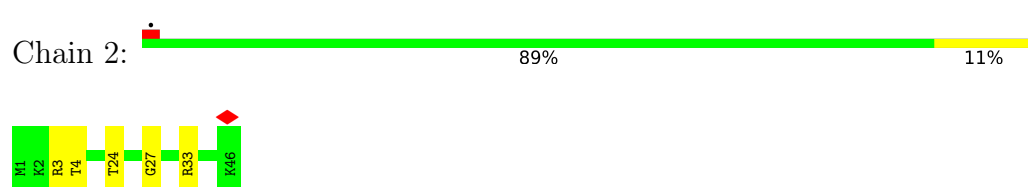
- Molecule 1: 50S ribosomal protein L32



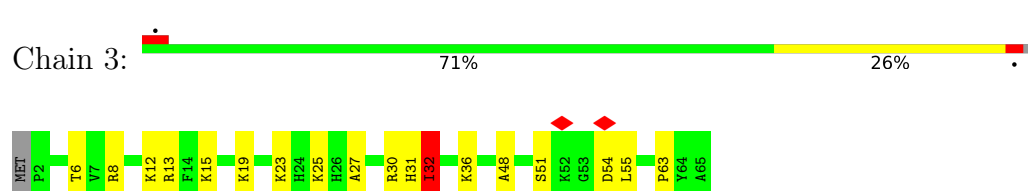
- Molecule 2: 50S ribosomal protein L33



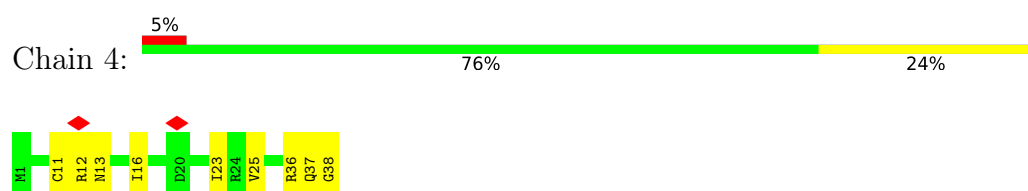
- Molecule 3: 50S ribosomal protein L34



- Molecule 4: 50S ribosomal protein L35



- Molecule 5: 50S ribosomal protein L36



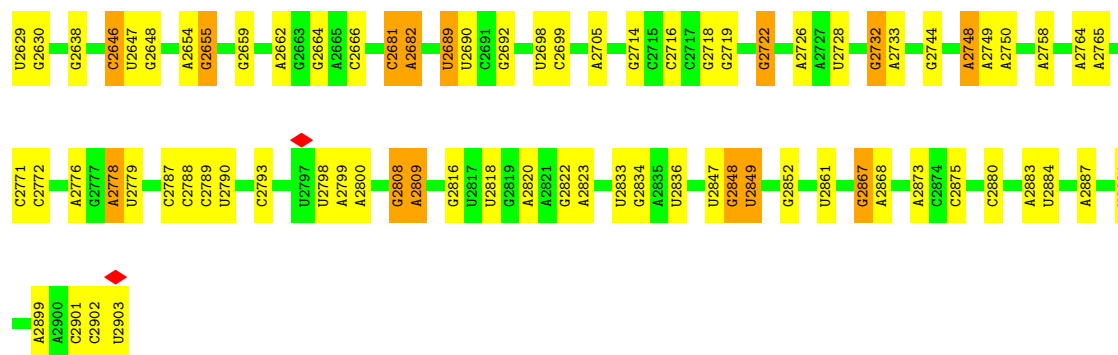
Chain 5:

Amino Acid Type	Segment 1 (29%)	Segment 2 (74%)	Segment 3 (17%)	Segment 4 (7%)
M1				
K2				
K3				
D4				
K8				
E11				
S15				
C18				
G19				
N20				
K23				
S26				
T27				
V28				
G29				
H30				
D31				
L32				
N33				
L34				
D35				
V36				
C37				
S38				
K47				
Q48				
R49				
D50				
V51				
A52				
T53				
G54				
D58				
R63				
F64				
M65				
I66				
PRO				
GLY				
SER				
YS				

Chain A:

The figure displays a large grid of colored squares (yellow and green) representing a sequence or data set. The grid is organized into 10 columns and 100 rows. The colors of the squares correspond to the 65% green and 31% yellow distribution shown in the Chain A bar chart. Red diamonds are placed on specific squares, likely indicating a specific path or state.

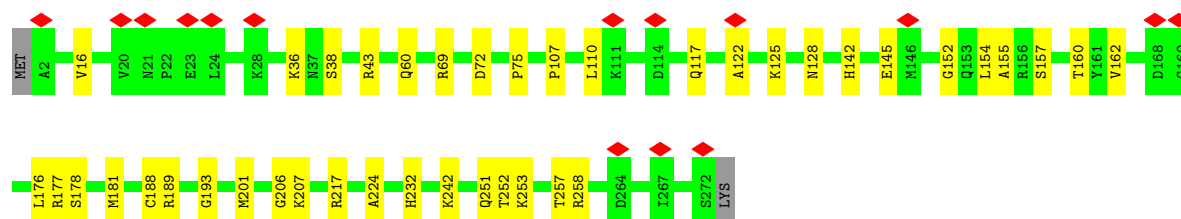
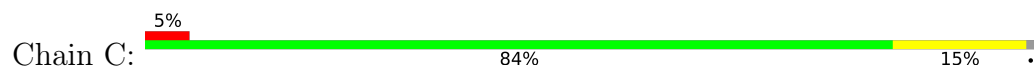
G2505	G2391	C2283	A2169	A2108	G2012	A1889	C1764	A1630	G1522	C1414	C1305	C1178
U2506	G2392	G2286	A2170	U2109	A2013	A1890	C1765	G1631	U1523	U1415	C1306	G1179
C2507	U2393	A2287	A2171	G2110	A2020	G1891	U1769	A1632	G1524	G1416	G1310	U1180
A2513	G2396	A2288	A2172	U2111	C2021	G1896	A1773	C1638	G1529	G1418	U1312	G1182
U2514	U2402	U2291	C2174	G2112	U2022	A1900	G1776	G1645	G1533	G1419	C1321	G1186
C2515	C2403	U2292	C2175	U2113	C2023	A1901	U1779	C1646	U1534	A1420	U1326	U1187
A2516	C2406	G2304	A2176	A2114	A2030	G1906	A1784	U1647	U1535	G1421	G1316	U1188
U2518	U2305	G2306	C2177	G2115	A2031	A1912	A1785	U1648	C1536	G1427	U1317	A1189
U2519	G2307	G2308	C2178	G2116	A2032	A1913	A1786	U1649	U1537	C1428	A1321	G1190
C2520	G2309	G2309	U2180	U2117	G2035	C1914	U1787	G1659	G1538	G1432	U1326	U1203
C2521	A2119	A2119	U2181	U2118	C2036	U1915	A1788	G1667	U1539	A1433	A1327	A1204
G2529	C2310	C2310	U2182	U2119	A2037	A1916	A1789	U1668	U1540	G1434	U1327	C1211
A2530	U2311	U2311	U2183	G2120	G2038	U1917	A1791	A1669	G1543	G1435	G1332	G1212
G2535	U2312	U2312	A2184	G2121	C2043	A1927	A1794	G1674	A1544	C1437	U1340	A1213
A2542	G2315	G2315	U2185	U2122	A2080	A1928	U1795	U1688	U1554	G1441	G1341	A1214
G2544	G2316	G2316	U2186	G2123	G2061	G1929	U1796	U1689	G1555	U1442	G1342	U1219
G2319	G2319	G2319	G2187	G2124	C2055	U1930	G1797	A1690	U1556	C1447	G1343	G1220
G2325	G2325	G2325	U2188	G2125	G2056	U1931	U1798	C1558	U1559	G1450	G1345	U1222
C2326	G2326	G2326	U2189	A2126	A2080	G1935	G1799	U1693	U1580	G1451	U1352	G1223
A2327	A2327	A2327	G2190	G2127	G2062	A1936	C1800	G1694	A1586	G1452	G1358	U1234
A2328	U2328	U2328	G2191	U2128	A2062	A1937	A1801	G1695	U1587	A1453	G1359	G1235
U2329	U2329	U2329	U2192	C2129	C2063	U1940	A1802	A1700	A1588	G1454	G1360	G1236
A2333	A2333	A2333	U2193	U2130	G2069	C1941	G1807	G1715	U1589	G1455	G1361	A1247
U2334	U2334	U2334	U2194	U2131	G2072	U1943	A1808	G1721	U1578	U1457	G1364	A1248
A2335	A2335	A2335	U2195	U2132	C2072	U1955	A1815	U1729	A1579	U1458	A1365	G1280
G2345	G2345	G2345	U2210	G2133	U2075	C1958	C1816	G1724	U1580	U1459	A1366	A1283
A2346	A2346	A2346	A2212	U2136	A2076	C1962	U1817	U1725	G1581	U1460	A1367	A1284
C2347	C2347	C2347	U2213	U2137	A2077	U1963	U1818	C1726	C1582	C1461	G1368	U1254
C2350	C2350	C2350	U2219	G2138	U2081	U1964	A1819	U1584	A1583	U1468	A1373	U1255
C2354	C2354	C2354	A2225	U2139	A2082	G1965	U1820	U1585	U1584	A1469	U1378	G1256
G2357	G2357	G2357	G2230	G2140	U2086	C1966	U1825	C1586	U1586	A1470	G1379	A1262
A2358	A2358	A2358	U2233	G2141	G2087	C1967	U1826	G1731	G1587	U1476	G1380	G1266
C2359	C2359	C2359	G2234	A2142	A2088	C1967	U1827	G1732	A1590	A1477	A1383	G1271
G2360	G2360	G2360	G2235	G2143	U2092	A1970	G1828	G1733	A1591	G1482	A1384	A1272
G2361	G2361	G2361	G2236	C2144	G2093	U1971	A1829	U1734	A1597	G1483	A1385	U1273
C2364	C2364	C2364	G2238	C2145	G2093	G1972	C1833	U1736	A1598	A1490	A1387	A1274
U2372	U2372	U2372	G2239	C2146	C2096	A1981	A1847	G1737	C1607	A1503	A1392	A1275
G2373	G2373	G2373	G2240	A2147	A2097	U1982	A1848	A1739	A1608	A1504	A1392	C1278
C2381	C2381	C2381	U2245	G2148	U2098	U1991	A1868	A1744	A1609	A1505	C1399	G1279
A2381	A2381	A2381	G2246	C2150	G2100	U1992	U1869	A1745	A1610	U1506	G1403	G1283
C2382	C2382	C2382	A2247	U2151	A2101	U1993	C1870	U1747	C1611	C1507	A1403	A1286
G2383	G2383	G2383	G2250	G2152	G2102	C1996	U1880	G1753	C1612	A1508	U1405	G1404
U2384	U2384	U2384	A2266	C2153	C2104	C1997	A1884	A1754	A1509	G1510	U1406	U1405
C2385	C2385	C2385	G2273	U2155	U2106	C2006	G1884	G1756	G1622	A1515	U1412	G1300
G2385	G2385	G2385	A2278	G2156	G2107			A1757	G1627	G1516	A1413	A1301
			G2279	A2158					G1628			
				G2159								
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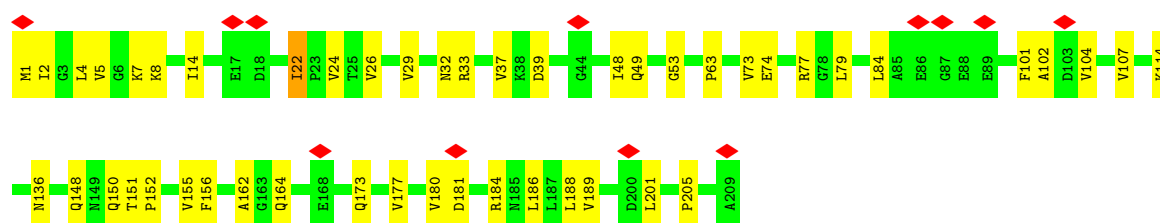
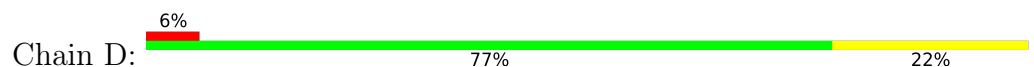
• Molecule 8: 5S ribosomal RNA



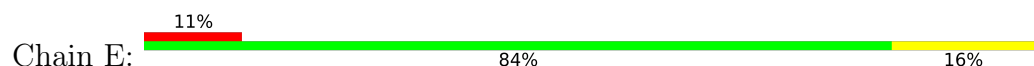
• Molecule 9: 50S ribosomal protein L2

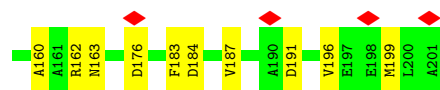


• Molecule 10: 50S ribosomal protein L3

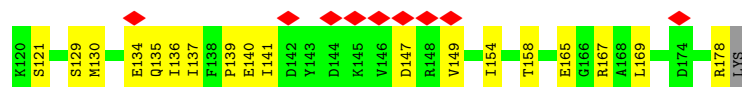
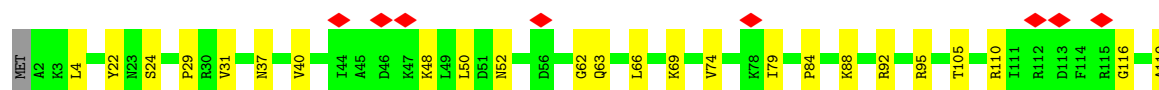
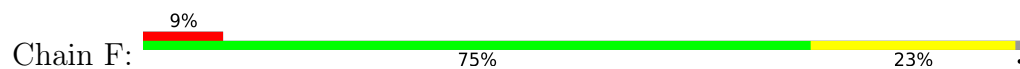


• Molecule 11: 50S ribosomal protein L4

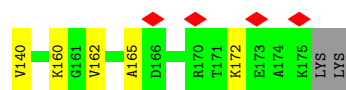
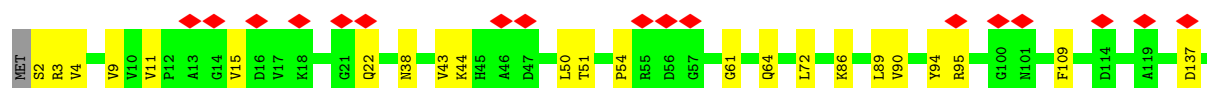
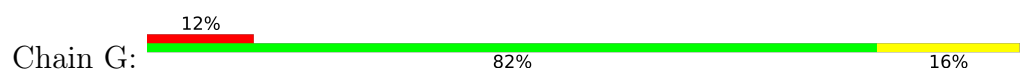




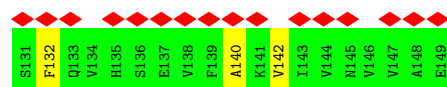
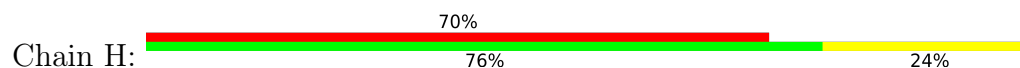
- Molecule 12: 50S ribosomal protein L5



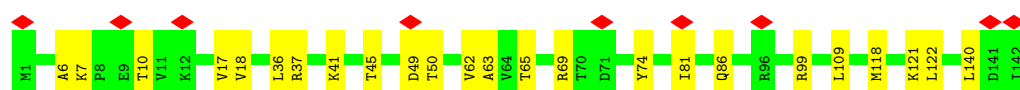
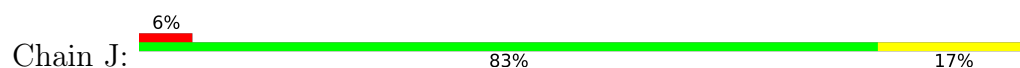
- Molecule 13: 50S ribosomal protein L6



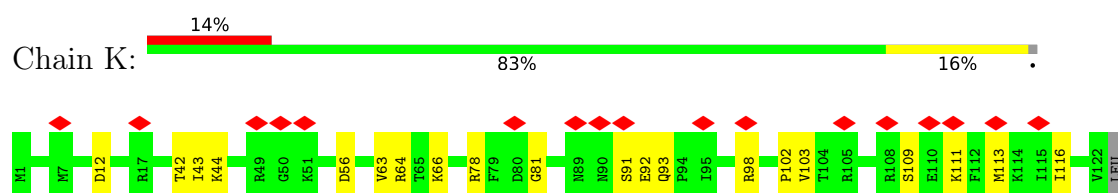
- Molecule 14: 50S ribosomal protein L9



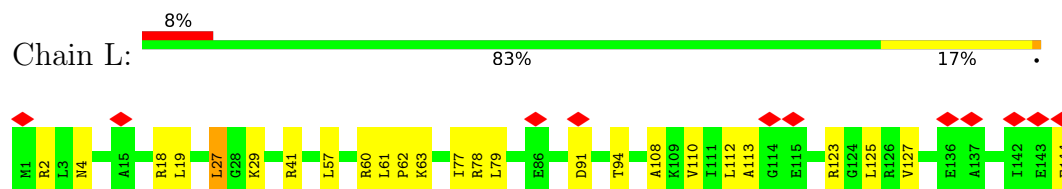
- Molecule 15: 50S ribosomal protein L13



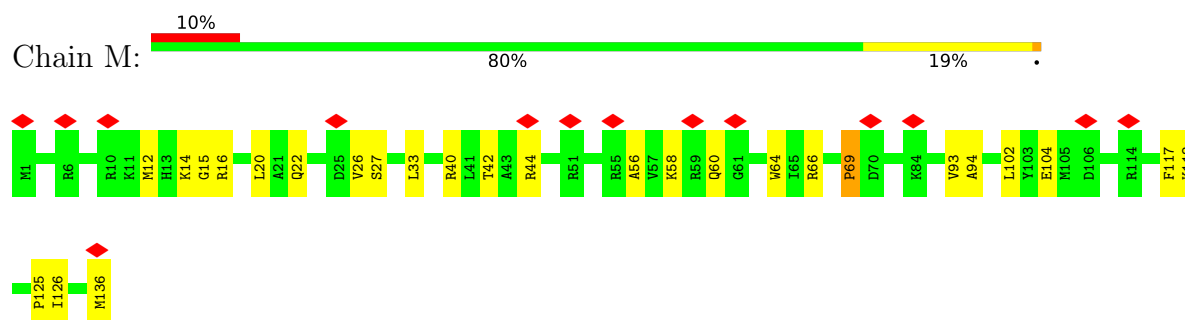
- Molecule 16: 50S ribosomal protein L14



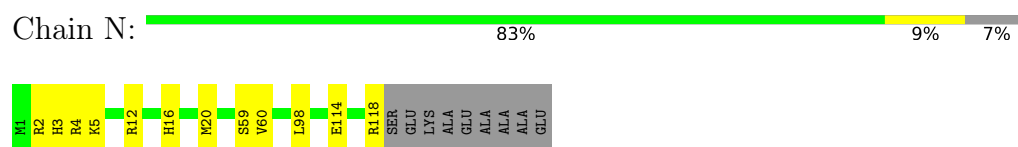
- Molecule 17: 50S ribosomal protein L15



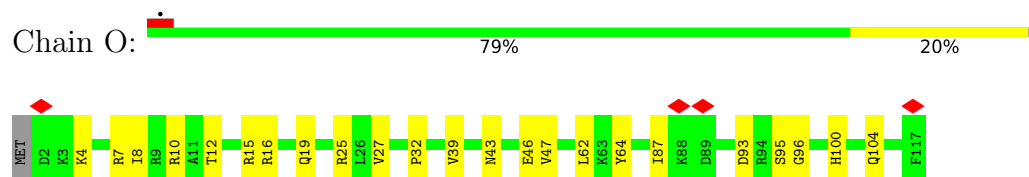
- Molecule 18: 50S ribosomal protein L16



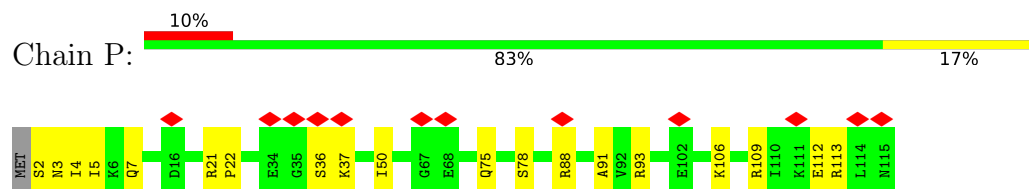
- Molecule 19: 50S ribosomal protein L17



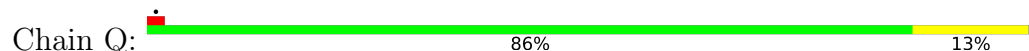
- Molecule 20: 50S ribosomal protein L18



- Molecule 21: 50S ribosomal protein L19

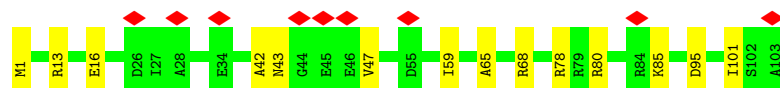
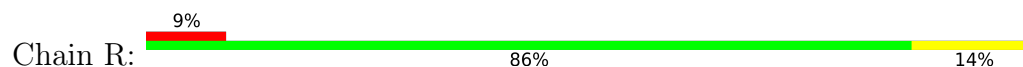


- Molecule 22: 50S ribosomal protein L20

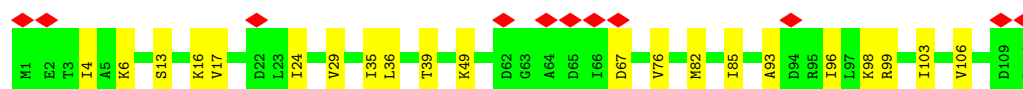
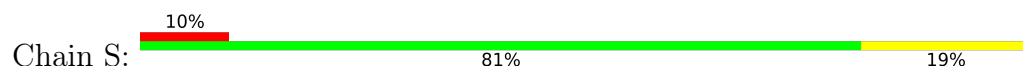




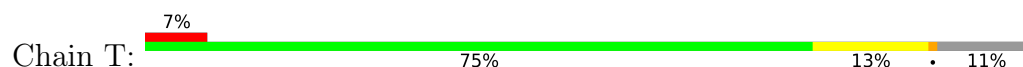
- Molecule 23: 50S ribosomal protein L21



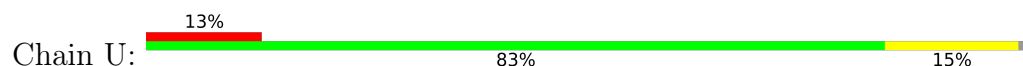
- Molecule 24: 50S ribosomal protein L22



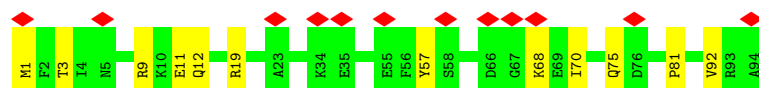
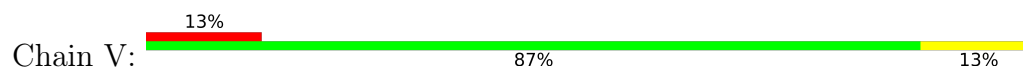
- Molecule 25: 50S ribosomal protein L23



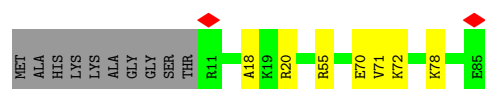
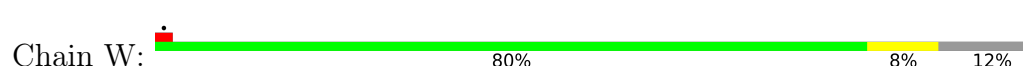
- Molecule 26: 50S ribosomal protein L24



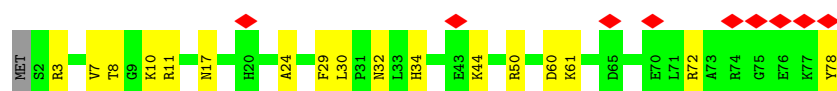
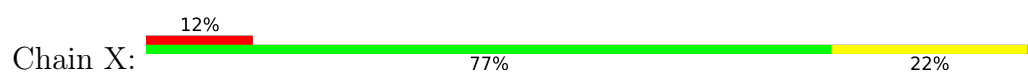
- Molecule 27: 50S ribosomal protein L25



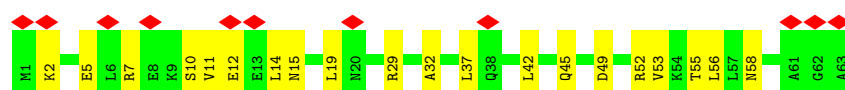
- Molecule 28: 50S ribosomal protein L27



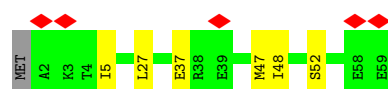
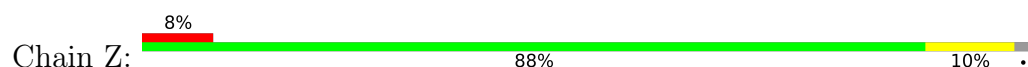
- Molecule 29: 50S ribosomal protein L28



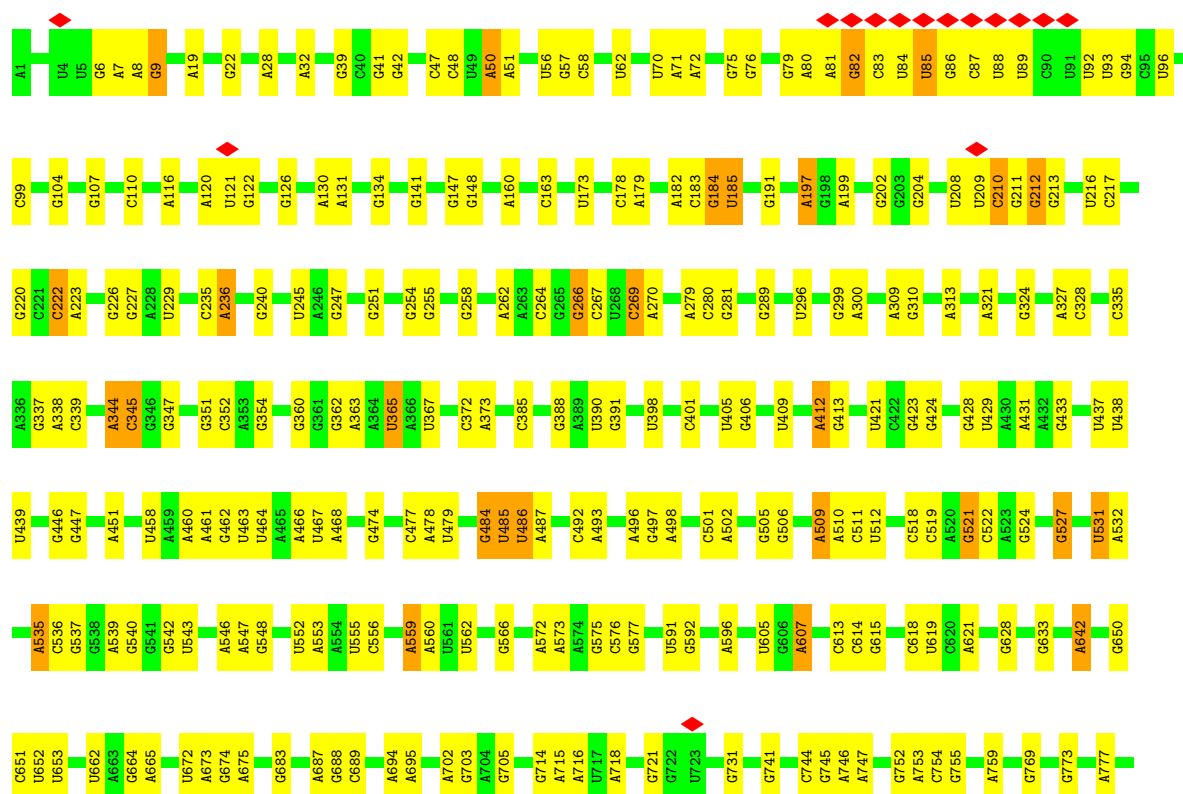
- Molecule 30: 50S ribosomal protein L29

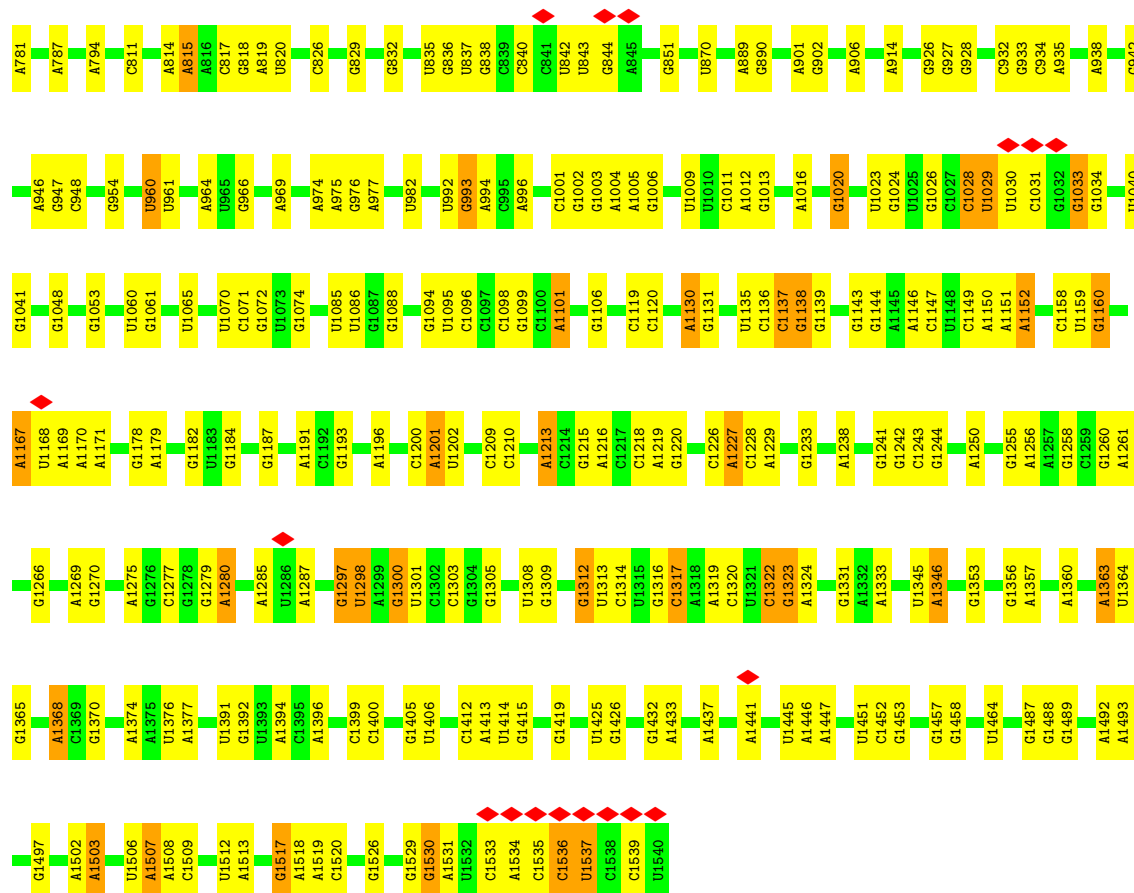


- Molecule 31: 50S ribosomal protein L30

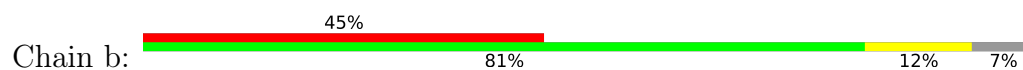


- Molecule 32: 16S ribosomal RNA

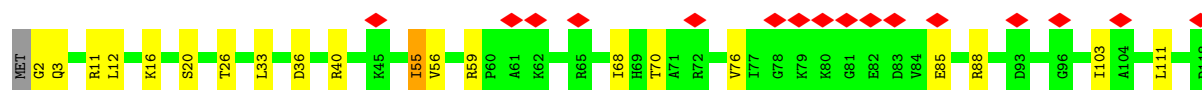
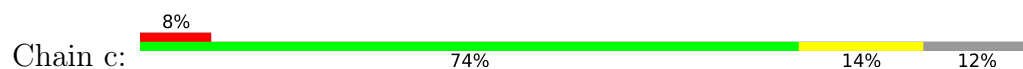


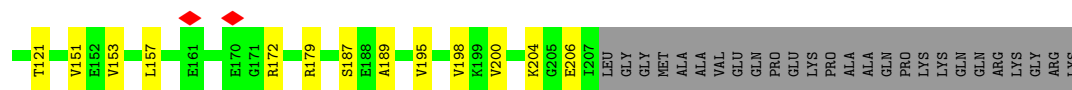


• Molecule 33: 30S ribosomal protein S2

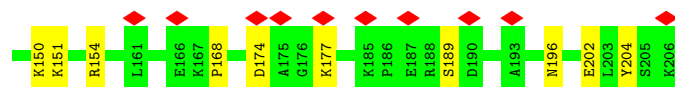
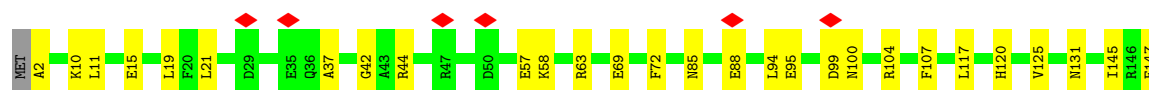
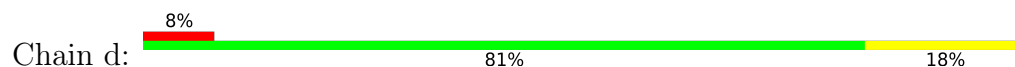


• Molecule 34: 30S ribosomal protein S3

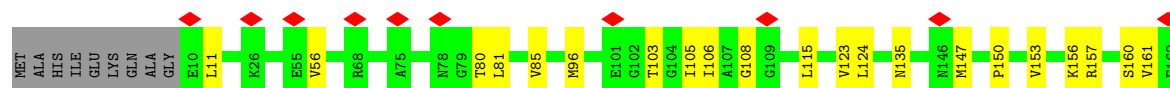
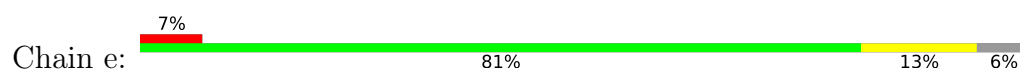




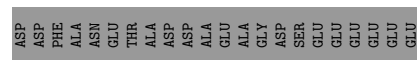
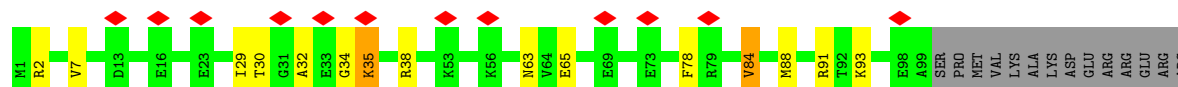
- Molecule 35: 30S ribosomal protein S4



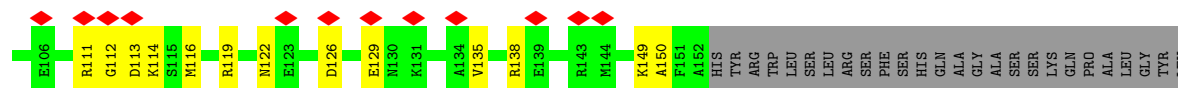
- Molecule 36: 30S ribosomal protein S5



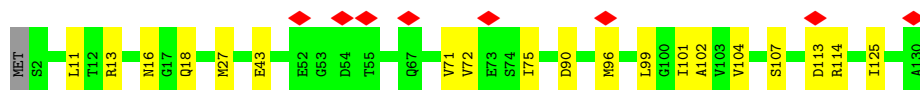
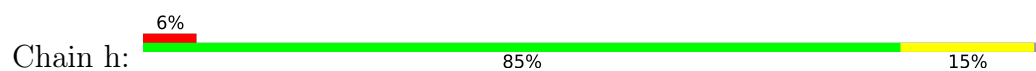
- Molecule 37: 30S ribosomal protein S6



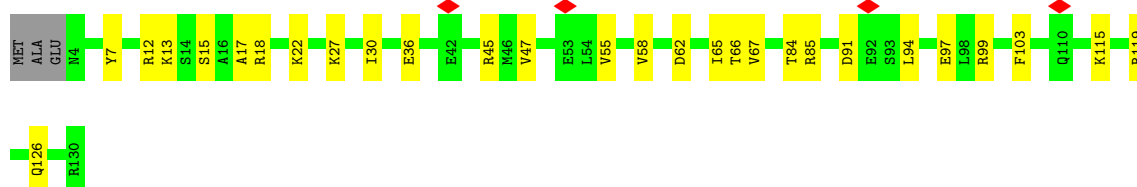
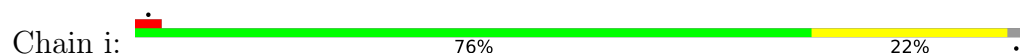
- Molecule 38: 30S ribosomal protein S7



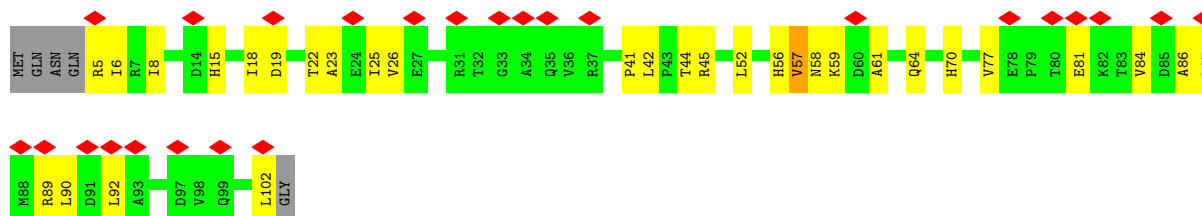
- Molecule 39: 30S ribosomal protein S8



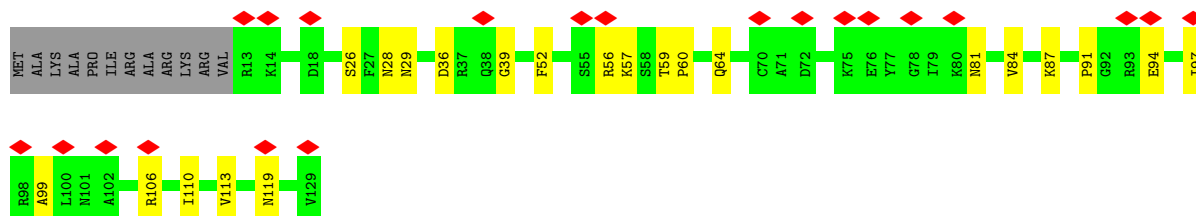
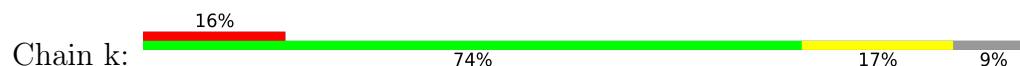
- Molecule 40: 30S ribosomal protein S9



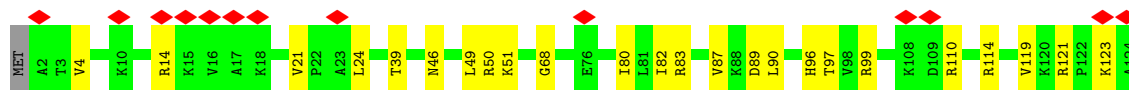
- Molecule 41: 30S ribosomal protein S10



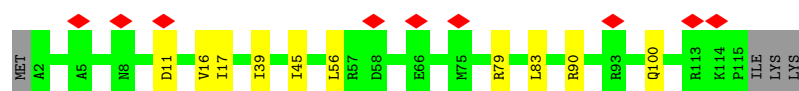
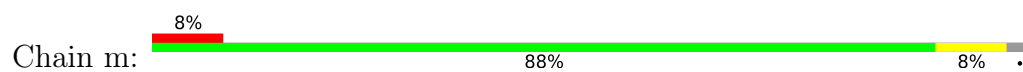
- Molecule 42: 30S ribosomal protein S11



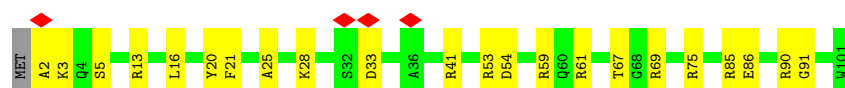
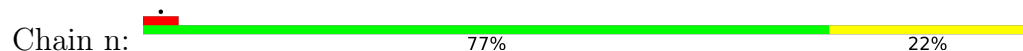
- Molecule 43: 30S ribosomal protein S12



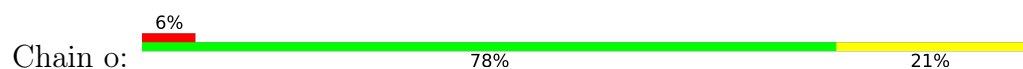
- Molecule 44: 30S ribosomal protein S13



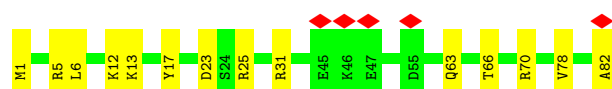
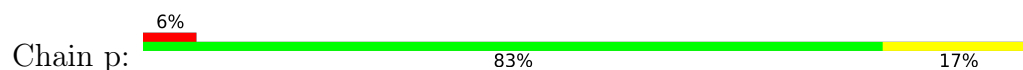
- Molecule 45: 30S ribosomal protein S14



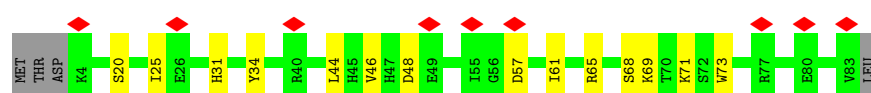
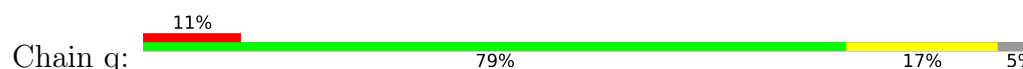
- Molecule 46: 30S ribosomal protein S15



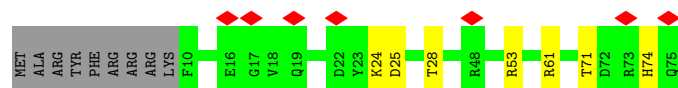
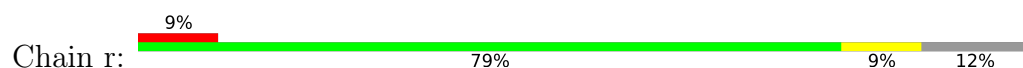
- Molecule 47: 30S ribosomal protein S16



- Molecule 48: 30S ribosomal protein S17



- Molecule 49: 30S ribosomal protein S18

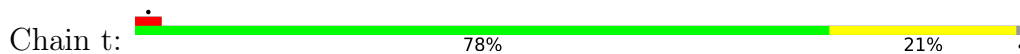


- Molecule 50: 30S ribosomal protein S19

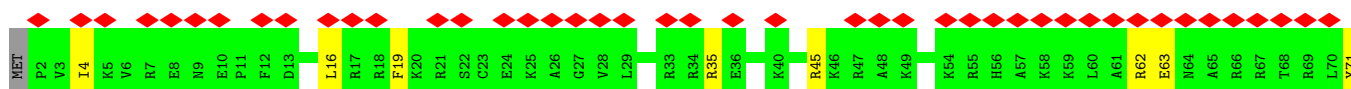
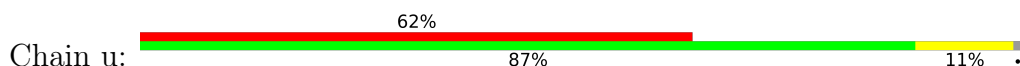




- Molecule 51: 30S ribosomal protein S20



- Molecule 52: 30S ribosomal protein S21

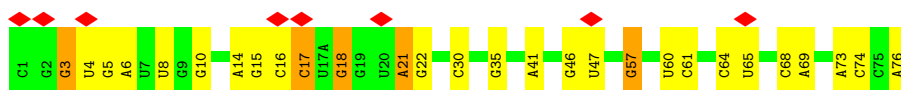


- Molecule 53: mRNA

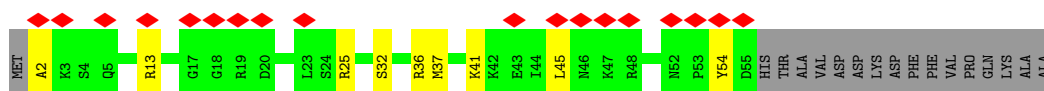


There are no outlier residues recorded for this chain.

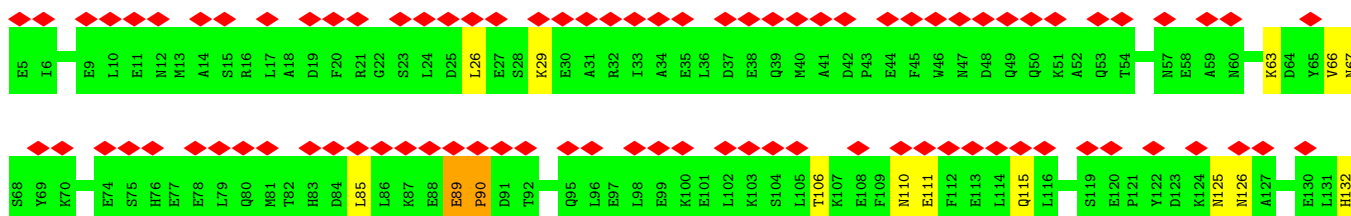
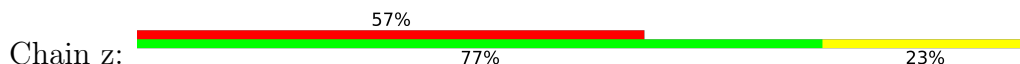
- Molecule 54: P-site tRNA-Pro(CGG)

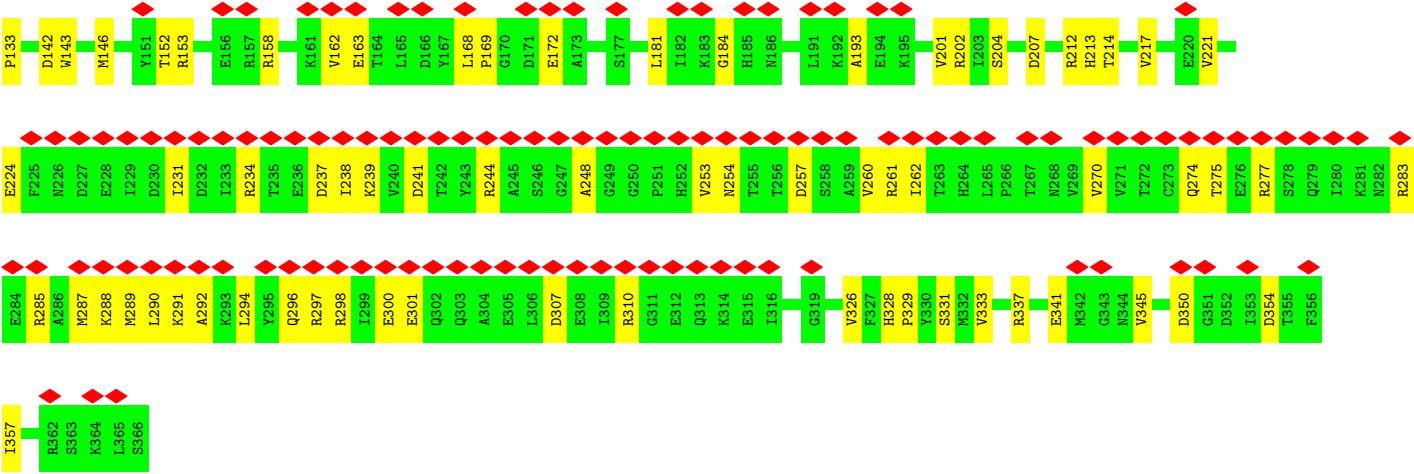


- Molecule 55: Uncharacterized protein YqkK



- Molecule 56: Peptide chain release factor 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	154405	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	83.0	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	0.187	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0387	Depositor
Map size (Å)	391.92, 391.92, 391.92	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0	0.38	0/440	0.51	0/588
2	1	0.38	0/416	0.54	0/554
3	2	0.43	0/380	0.52	0/498
4	3	0.47	0/513	0.58	0/676
5	4	0.41	0/303	0.50	0/397
6	5	0.30	0/523	0.61	0/698
7	A	0.44	0/69800	0.45	4/108892 (0.0%)
8	B	0.38	0/2873	0.44	0/4478
9	C	0.43	0/2121	0.57	0/2852
10	D	0.42	0/1586	0.57	0/2134
11	E	0.38	0/1571	0.50	0/2113
12	F	0.33	0/1434	0.58	0/1926
13	G	0.30	0/1324	0.53	0/1794
14	H	0.29	0/1122	0.68	2/1515 (0.1%)
15	J	0.37	0/1152	0.48	0/1551
16	K	0.41	0/947	0.59	0/1268
17	L	0.40	0/1062	0.61	0/1413
18	M	0.38	0/1093	0.54	0/1460
19	N	0.43	0/958	0.61	0/1281
20	O	0.34	0/902	0.55	0/1209
21	P	0.38	0/929	0.50	0/1242
22	Q	0.42	0/960	0.54	0/1278
23	R	0.37	0/829	0.50	0/1107
24	S	0.36	0/864	0.53	0/1156
25	T	0.30	0/715	0.54	0/955
26	U	0.34	0/787	0.53	0/1051
27	V	0.35	0/766	0.54	0/1025
28	W	0.40	0/582	0.50	0/769
29	X	0.40	0/635	0.54	0/848
30	Y	0.31	0/510	0.48	0/677
31	Z	0.36	0/453	0.48	0/605
32	a	0.44	0/36991	0.44	1/57705 (0.0%)
33	b	0.30	0/1784	0.57	0/2403
34	c	0.38	0/1651	0.61	0/2225

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	d	0.37	0/1665	0.57	0/2227
36	e	0.39	0/1169	0.58	0/1573
37	f	0.40	0/829	0.61	0/1120
38	g	0.33	0/1195	0.60	0/1602
39	h	0.37	0/989	0.46	0/1326
40	i	0.38	0/1034	0.63	0/1375
41	j	0.41	0/796	0.66	2/1077 (0.2%)
42	k	0.35	0/893	0.55	0/1205
43	l	0.41	0/969	0.62	0/1300
44	m	0.36	0/892	0.66	0/1193
45	n	0.39	0/817	0.59	0/1088
46	o	0.34	0/722	0.62	0/964
47	p	0.40	0/659	0.59	0/884
48	q	0.36	0/657	0.61	0/881
49	r	0.35	0/554	0.51	0/743
50	s	0.36	0/680	0.50	0/915
51	t	0.35	0/676	0.48	0/895
52	u	0.27	0/598	0.49	0/792
53	v	0.35	0/139	0.37	0/214
54	x	0.35	0/1839	0.49	1/2866 (0.0%)
55	y	0.34	0/440	0.61	0/579
56	z	0.33	0/2786	0.60	1/3764 (0.0%)
All	All	0.42	0/159974	0.48	11/238926 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	z	90	PRO	N-CA-CB	7.81	111.45	103.25
14	H	50	ARG	CA-C-N	5.63	132.29	121.54
14	H	50	ARG	C-N-CA	5.63	132.29	121.54
41	j	57	VAL	CA-C-N	5.44	131.93	121.54
41	j	57	VAL	C-N-CA	5.44	131.93	121.54
7	A	1930	G	P-O3'-C3'	5.16	127.94	120.20
32	a	960	U	P-O3'-C3'	5.16	127.93	120.20
7	A	1420	A	P-O3'-C3'	5.06	127.78	120.20
7	A	242	G	P-O3'-C3'	5.05	127.77	120.20
7	A	1022	G	P-O3'-C3'	5.04	127.76	120.20
54	x	3	G	P-O3'-C3'	5.01	127.71	120.20

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	0	434	0	445	7	0
2	1	409	0	440	11	0
3	2	377	0	418	4	0
4	3	504	0	572	16	0
5	4	302	0	343	5	0
6	5	514	0	513	10	0
7	A	62321	0	31344	358	0
8	B	2570	0	1301	14	0
9	C	2082	0	2154	32	0
10	D	1565	0	1616	34	0
11	E	1552	0	1619	23	0
12	F	1410	0	1444	26	0
13	G	1304	0	1345	19	0
14	H	1111	0	1148	23	0
15	J	1129	0	1162	17	0
16	K	938	0	1012	12	0
17	L	1053	0	1129	20	0
18	M	1074	0	1157	21	0
19	N	945	0	989	9	0
20	O	892	0	923	16	0
21	P	917	0	962	13	0
22	Q	947	0	1019	13	0
23	R	816	0	839	10	0
24	S	857	0	922	13	0
25	T	709	0	779	9	0
26	U	779	0	831	9	0
27	V	753	0	780	8	0
28	W	575	0	592	4	0
29	X	625	0	652	13	0
30	Y	509	0	543	14	0
31	Z	449	0	488	3	0
32	a	33037	0	16628	234	0
33	b	1753	0	1780	17	0
34	c	1624	0	1696	19	0
35	d	1643	0	1707	27	0
36	e	1156	0	1199	16	0
37	f	811	0	803	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	g	1181	0	1238	28	0
39	h	979	0	1031	13	0
40	i	1022	0	1070	20	0
41	j	786	0	828	21	0
42	k	877	0	887	16	0
43	l	955	0	1016	19	0
44	m	883	0	941	7	0
45	n	805	0	844	16	0
46	o	714	0	734	11	0
47	p	649	0	666	12	0
48	q	648	0	691	12	0
49	r	545	0	560	5	0
50	s	663	0	688	15	0
51	t	670	0	719	13	0
52	u	590	0	629	8	0
53	v	126	0	67	0	0
54	x	1646	0	832	10	0
55	y	434	0	462	8	0
56	z	2742	0	2539	55	0
All	All	147361	0	99736	1171	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 5.

All (1171) 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)
7:A:1042:G:H1	7:A:1113:U:H3	1.00	0.97
32:a:458:U:H3	32:a:474:G:H1	0.96	0.95
32:a:1006:G:H1	32:a:1023:U:H3	1.09	0.91
7:A:1036:G:H1	7:A:1119:U:H3	1.16	0.90
32:a:1009:U:H3	32:a:1020:G:H1	1.12	0.90
32:a:1088:G:N2	32:a:1167:A:H61	1.69	0.89
32:a:1088:G:H21	32:a:1167:A:H61	1.25	0.83
32:a:1088:G:H21	32:a:1167:A:N6	1.80	0.78
7:A:1724:G:H1	7:A:1736:U:H3	1.33	0.76
7:A:2099:U:H3	7:A:2190:G:H1	1.37	0.72
32:a:664:G:H22	32:a:741:G:H1	1.39	0.70
32:a:437:U:HO2'	35:d:120:HIS:HD1	1.38	0.69
7:A:279:A:H62	7:A:361:G:H8	1.40	0.69
10:D:5:VAL:H	10:D:32:ASN:HD21	1.38	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:i:84:THR:HG21	40:i:103:PHE:HB3	1.75	0.69
32:a:107:G:N7	51:t:10:ARG:NH2	2.41	0.69
7:A:285:G:O6	7:A:355:U:C2	2.46	0.69
7:A:1051:G:H1	7:A:1108:U:H3	1.39	0.69
13:G:90:VAL:O	13:G:160:LYS:HA	1.93	0.68
47:p:78:VAL:O	47:p:82:ALA:HB3	1.93	0.68
2:1:6:ARG:NH2	7:A:2286:G:OP2	2.27	0.68
38:g:112:GLY:HA2	38:g:119:ARG:HD3	1.74	0.68
14:H:54:LEU:HA	14:H:57:LYS:HG2	1.76	0.67
7:A:2514:U:H5''	15:J:81:ILE:HD12	1.77	0.66
7:A:1721:G:O2'	7:A:1739:A:N6	2.28	0.66
38:g:111:ARG:HH22	38:g:122:ASN:HB3	1.61	0.66
32:a:1200:C:H5''	32:a:1201:A:H3'	1.76	0.66
38:g:5:ARG:HE	38:g:7:ILE:HG23	1.59	0.66
56:z:262:ILE:O	56:z:270:VAL:HA	1.95	0.66
35:d:19:LEU:HB2	35:d:21:LEU:HD22	1.79	0.65
7:A:2848:G:O2'	7:A:2867:G:N2	2.24	0.64
9:C:145:GLU:HB2	9:C:188:CYS:HB2	1.80	0.64
18:M:20:LEU:HD13	27:V:81:PRO:HG2	1.79	0.64
13:G:137:ASP:HB3	13:G:140:VAL:HG22	1.79	0.63
4:3:23:LYS:HA	4:3:48:ALA:O	1.98	0.63
1:0:13:ARG:NH2	7:A:517:C:OP1	2.32	0.63
7:A:1607:C:N4	7:A:1622:G:OP2	2.32	0.63
38:g:75:VAL:HG13	38:g:86:GLN:HB3	1.81	0.63
24:S:82:MET:HB2	24:S:98:LYS:HB2	1.82	0.62
9:C:155:ALA:HB2	9:C:162:VAL:HG23	1.80	0.62
10:D:181:ASP:HB3	10:D:186:LEU:HB2	1.80	0.62
14:H:5:LEU:HD13	14:H:13:GLY:HA2	1.81	0.62
7:A:2573:C:N4	56:z:254:ASN:O	2.32	0.62
19:N:2:ARG:HA	19:N:5:LYS:HD2	1.82	0.62
7:A:1084:A:N3	7:A:1105:U:O2'	2.32	0.62
20:O:7:ARG:NH1	20:O:95:SER:O	2.33	0.62
50:s:19:VAL:HG21	50:s:44:MET:HG2	1.82	0.62
2:1:11:LEU:HA	2:1:50:LYS:O	2.00	0.62
7:A:1779:U:OP2	7:A:1784:A:N6	2.33	0.62
7:A:990:A:N1	23:R:78:ARG:NH1	2.48	0.61
32:a:1233:G:OP1	40:i:119:ARG:NH1	2.33	0.61
32:a:1445:U:H3	32:a:1457:G:H1	1.46	0.61
32:a:826:C:O2	39:h:16:ASN:ND2	2.33	0.61
37:f:2:ARG:HG2	37:f:91:ARG:HH11	1.65	0.61
6:5:18:CYS:SG	6:5:20:ASN:ND2	2.73	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2530:A:N7	13:G:172:LYS:NZ	2.47	0.61
34:c:12:LEU:HD11	45:n:91:GLY:HA2	1.83	0.61
14:H:48:GLU:HA	14:H:52:ALA:HB2	1.82	0.61
44:m:11:ASP:HA	44:m:45:ILE:HB	1.83	0.60
7:A:1558:C:H4'	7:A:1559:U:H5'	1.83	0.60
56:z:106:THR:O	56:z:110:ASN:ND2	2.34	0.60
10:D:1:MET:HE3	10:D:2:ILE:H	1.66	0.60
7:A:1089:A:O2'	7:A:1090:A:N7	2.35	0.60
7:A:1310:G:H1'	7:A:1611:C:H5''	1.82	0.60
26:U:72:ILE:HG21	26:U:83:VAL:HG13	1.82	0.60
36:e:106:ILE:HD11	36:e:124:LEU:HD23	1.83	0.60
33:b:126:PHE:HB2	33:b:128:LYS:HG3	1.83	0.59
10:D:7:LYS:HE3	10:D:77:ARG:HH11	1.66	0.59
32:a:1106:G:H5''	34:c:172:ARG:HB3	1.84	0.59
7:A:27:G:N2	7:A:512:G:O2'	2.35	0.59
7:A:658:U:O2'	11:E:95:LYS:NZ	2.35	0.59
32:a:1297:G:N2	38:g:114:LYS:O	2.36	0.59
4:3:8:ARG:NH1	7:A:243:U:OP1	2.36	0.59
7:A:1936:A:H2	7:A:1943:U:H3	1.50	0.59
16:K:109:SER:O	16:K:113:MET:N	2.35	0.59
7:A:1007:C:OP1	15:J:37:ARG:NH2	2.36	0.59
35:d:104:ARG:HG3	35:d:168:PRO:HG3	1.84	0.59
41:j:86:ALA:O	41:j:89:ARG:NH1	2.36	0.59
47:p:6:LEU:HB3	47:p:17:TYR:HB3	1.85	0.59
56:z:26:LEU:HA	56:z:29:LYS:HD3	1.85	0.59
7:A:1154:G:OP2	22:Q:58:ARG:NH1	2.36	0.58
7:A:2128:G:N2	7:A:2173:A:N3	2.51	0.58
14:H:39:ALA:HA	14:H:43:ASN:HD22	1.68	0.58
14:H:88:GLY:HA2	14:H:125:THR:H	1.68	0.58
32:a:264:C:H4'	48:q:65:ARG:HD2	1.84	0.58
4:3:23:LYS:NZ	7:A:631:A:OP2	2.35	0.58
7:A:994:C:OP1	22:Q:53:ARG:NH2	2.35	0.58
56:z:262:ILE:HG21	56:z:290:LEU:HD11	1.86	0.58
7:A:1891:G:HO2'	7:A:2235:G:HO2'	1.52	0.58
2:1:25:LYS:NZ	2:1:30:LYS:O	2.36	0.58
39:h:104:VAL:HG22	39:h:125:ILE:HG12	1.83	0.58
5:4:11:CYS:SG	5:4:12:ARG:N	2.76	0.58
9:C:72:ASP:OD2	9:C:189:ARG:NH2	2.33	0.58
32:a:694:A:N1	32:a:787:A:O2'	2.37	0.58
7:A:2032:G:N2	10:D:151:THR:OG1	2.37	0.58
32:a:683:G:N2	42:k:39:GLY:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:1061:G:N7	34:c:2:GLY:N	2.52	0.58
7:A:1826:G:O2'	7:A:1971:U:OP2	2.21	0.57
32:a:1029:U:O2	32:a:1033:G:N1	2.37	0.57
14:H:76:GLU:HG2	14:H:142:VAL:HG22	1.85	0.57
35:d:15:GLU:OE2	35:d:63:ARG:NH1	2.37	0.57
56:z:63:LYS:O	56:z:67:ASN:ND2	2.37	0.57
7:A:560:C:O2'	22:Q:48:ARG:NH2	2.37	0.57
7:A:1825:U:O2	9:C:253:LYS:NZ	2.37	0.57
35:d:117:LEU:HD13	35:d:154:ARG:HH21	1.68	0.57
55:y:32:SER:O	55:y:36:ARG:NH2	2.37	0.57
7:A:1437:C:HO2'	7:A:1516:G:HO2'	1.48	0.57
50:s:11:ILE:HG13	50:s:38:SER:HB3	1.87	0.57
52:u:62:ARG:NH1	52:u:63:GLU:OE1	2.38	0.57
56:z:133:PRO:HA	56:z:217:VAL:HG22	1.85	0.57
7:A:247:G:OP2	7:A:249:C:N4	2.38	0.57
7:A:629:G:N3	7:A:639:U:O2'	2.37	0.57
7:A:77:G:O2'	30:Y:7:ARG:NH2	2.37	0.57
7:A:881:G:O6	7:A:895:U:O2	2.22	0.57
7:A:1066:U:N3	7:A:1069:A:OP2	2.37	0.57
32:a:531:U:OP1	56:z:212:ARG:NH2	2.37	0.57
34:c:189:ALA:O	34:c:195:VAL:HA	2.04	0.57
56:z:193:ALA:O	56:z:337:ARG:NH2	2.31	0.57
5:4:11:CYS:SG	5:4:13:ASN:ND2	2.78	0.57
7:A:2507:C:O2'	56:z:244:ARG:NH2	2.37	0.57
7:A:574:A:N6	7:A:2034:U:OP1	2.38	0.57
7:A:2139:U:O2	7:A:2152:G:O6	2.23	0.57
9:C:232:HIS:HA	9:C:242:LYS:HE3	1.86	0.57
16:K:43:ILE:HD12	16:K:56:ASP:HB2	1.86	0.57
32:a:76:G:H1	32:a:93:U:H3	1.53	0.57
32:a:1241:G:OP1	38:g:35:LYS:NZ	2.37	0.57
7:A:2638:G:O2'	7:A:2778:A:N6	2.38	0.57
32:a:1003:G:H21	32:a:1005:A:H5'	1.70	0.57
56:z:158:ARG:NH2	56:z:354:ASP:OD1	2.38	0.57
32:a:993:G:O2'	32:a:994:A:N7	2.37	0.56
7:A:910:A:H62	18:M:12:MET:HA	1.70	0.56
32:a:1300:G:O2'	32:a:1303:C:N4	2.38	0.56
3:2:24:THR:HG23	3:2:27:GLY:H	1.69	0.56
11:E:117:ARG:NH2	11:E:183:PHE:O	2.36	0.56
17:L:108:ALA:HB3	17:L:125:LEU:HD22	1.87	0.56
25:T:34:VAL:HG11	25:T:43:ILE:HG12	1.86	0.56
25:T:61:LEU:HD11	25:T:82:LYS:HE2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:g:28:ASN:OD1	38:g:36:LYS:NZ	2.38	0.56
11:E:119:ILE:O	11:E:187:VAL:HA	2.05	0.56
18:M:56:ALA:O	18:M:58:LYS:NZ	2.39	0.56
32:a:1179:A:OP2	40:i:99:ARG:NH1	2.38	0.56
56:z:285:ARG:HA	56:z:288:LYS:HD3	1.87	0.56
32:a:134:G:O6	47:p:25:ARG:NH2	2.38	0.56
34:c:153:VAL:HG23	34:c:198:VAL:HG22	1.86	0.56
56:z:126:ASN:HD22	56:z:184:GLY:H	1.54	0.56
56:z:326:VAL:O	56:z:331:SER:HA	2.05	0.56
2:1:11:LEU:HB3	2:1:49:TYR:HB3	1.88	0.56
7:A:304:U:H3	7:A:313:G:H1	1.53	0.56
7:A:2484:G:OP1	18:M:44:ARG:NH2	2.38	0.56
13:G:89:LEU:HD23	13:G:94:TYR:HB3	1.87	0.56
14:H:132:PHE:H	14:H:140:ALA:HB3	1.71	0.56
34:c:20:SER:OG	34:c:40:ARG:NH2	2.39	0.56
7:A:1069:A:O2'	7:A:1073:A:N6	2.39	0.56
11:E:191:ASP:OD1	11:E:191:ASP:N	2.38	0.56
21:P:2:SER:OG	21:P:3:ASN:N	2.38	0.56
32:a:310:G:H5''	47:p:31:ARG:HB2	1.88	0.56
7:A:373:U:O2	7:A:401:A:N7	2.39	0.56
7:A:2304:G:H22	7:A:2312:U:H3	1.54	0.56
25:T:69:ARG:HH11	25:T:74:ILE:HD13	1.70	0.56
7:A:1223:G:OP1	23:R:68:ARG:NH2	2.39	0.56
7:A:1283:G:N1	7:A:1286:A:OP2	2.39	0.56
15:J:18:VAL:HG22	15:J:140:LEU:HB3	1.88	0.56
50:s:28:LYS:NZ	50:s:46:GLY:O	2.38	0.56
7:A:2075:U:OP2	7:A:2238:G:O2'	2.24	0.55
11:E:119:ILE:HB	11:E:187:VAL:HG22	1.86	0.55
12:F:31:VAL:HA	12:F:158:THR:HA	1.87	0.55
25:T:8:LEU:O	30:Y:29:ARG:NH1	2.39	0.55
12:F:69:LYS:HA	12:F:84:PRO:HA	1.87	0.55
56:z:201:VAL:HG22	56:z:214:THR:HG23	1.88	0.55
7:A:221:A:N1	7:A:265:A:O2'	2.39	0.55
12:F:63:GLN:HE21	12:F:95:ARG:HD3	1.72	0.55
34:c:179:ARG:HG2	34:c:206:GLU:HB3	1.88	0.55
38:g:53:ARG:NH2	38:g:122:ASN:OD1	2.40	0.55
20:O:7:ARG:HA	20:O:10:ARG:HE	1.71	0.55
56:z:260:VAL:HG21	56:z:283:ARG:HG2	1.88	0.55
12:F:130:MET:HE2	12:F:154:ILE:HD12	1.88	0.55
18:M:58:LYS:O	18:M:60:GLN:NE2	2.38	0.55
46:o:32:LEU:HD22	46:o:59:MET:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:8:LYS:NZ	2:1:53:LYS:O	2.40	0.55
7:A:781:A:OP1	9:C:217:ARG:NH2	2.40	0.55
32:a:255:G:OP1	48:q:71:LYS:NZ	2.40	0.55
56:z:237:ASP:O	56:z:239:LYS:NZ	2.40	0.55
7:A:69:C:O2	7:A:73:A:O2'	2.23	0.55
20:O:27:VAL:HA	20:O:93:ASP:HB3	1.89	0.55
32:a:405:U:O4	35:d:2:ALA:N	2.40	0.55
32:a:519:C:OP1	55:y:36:ARG:NH1	2.39	0.55
32:a:1280:A:H5'	41:j:42:LEU:HD12	1.88	0.55
42:k:84:VAL:HB	42:k:110:ILE:HG23	1.89	0.55
7:A:958:U:OP1	18:M:40:ARG:NH1	2.40	0.54
16:K:64:ARG:NH1	16:K:102:PRO:O	2.40	0.54
45:n:33:ASP:O	45:n:41:ARG:NH1	2.38	0.54
7:A:864:G:OP2	18:M:22:GLN:NE2	2.41	0.54
10:D:186:LEU:HD21	21:P:4:ILE:HG12	1.88	0.54
16:K:98:ARG:NH1	32:a:339:C:OP2	2.40	0.54
32:a:8:A:N6	35:d:202:GLU:O	2.36	0.54
7:A:2553:G:H1	56:z:253:VAL:HG21	1.70	0.54
15:J:41:LYS:HD2	15:J:50:THR:HG22	1.88	0.54
37:f:35:LYS:HG3	37:f:65:GLU:HB3	1.88	0.54
38:g:49:THR:HG22	38:g:53:ARG:HD2	1.90	0.54
36:e:115:LEU:HD13	36:e:123:VAL:HG11	1.90	0.54
4:3:54:ASP:OD2	7:A:2359:C:O2'	2.25	0.54
13:G:9:VAL:HB	13:G:50:LEU:HB2	1.90	0.54
13:G:86:LYS:HB2	13:G:165:ALA:HB2	1.90	0.54
14:H:59:ALA:HA	14:H:62:LEU:HD12	1.90	0.54
32:a:1072:G:H21	33:b:106:THR:HG21	1.71	0.54
32:a:1130:A:H2'	32:a:1131:G:H8	1.73	0.54
56:z:307:ASP:HA	56:z:310:ARG:HG2	1.89	0.54
7:A:572:A:OP2	23:R:80:ARG:NH2	2.39	0.54
14:H:76:GLU:HA	14:H:142:VAL:HG13	1.90	0.54
7:A:413:C:HO2'	7:A:1880:U:HO2'	1.52	0.54
7:A:491:G:O6	24:S:49:LYS:NZ	2.40	0.54
32:a:202:G:H21	32:a:466:A:H61	1.55	0.54
56:z:142:ASP:OD2	56:z:202:ARG:NH2	2.40	0.54
7:A:275:C:O2'	7:A:362:A:N6	2.40	0.54
9:C:251:GLN:NE2	9:C:252:THR:O	2.41	0.54
32:a:552:U:O2'	43:l:83:ARG:O	2.24	0.54
51:t:67:ILE:HB	51:t:71:LYS:HD3	1.90	0.54
56:z:244:ARG:HG3	56:z:257:ASP:HB3	1.90	0.54
7:A:370:G:O2'	7:A:424:G:OP1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:8:C:O3'	20:O:25:ARG:NH2	2.41	0.54
32:a:1316:G:N1	32:a:1319:A:OP2	2.41	0.53
35:d:57:GLU:OE2	35:d:196:ASN:ND2	2.41	0.53
5:4:16:ILE:HG12	5:4:25:VAL:HG22	1.91	0.53
7:A:1278:C:H2'	7:A:1279:G:H8	1.73	0.53
7:A:1799:G:N2	7:A:1818:U:O2'	2.41	0.53
18:M:40:ARG:HD2	18:M:93:VAL:HG21	1.89	0.53
32:a:1086:U:H3	32:a:1099:G:H22	1.56	0.53
36:e:157:ARG:NH1	39:h:43:GLU:OE1	2.41	0.53
11:E:58:LYS:HG2	11:E:71:GLY:HA2	1.91	0.53
32:a:1006:G:N2	32:a:1023:U:O2	2.31	0.53
56:z:231:ILE:O	56:z:291:LYS:NZ	2.40	0.53
18:M:64:TRP:HB2	18:M:104:GLU:HB2	1.90	0.53
30:Y:2:LYS:HB2	30:Y:5:GLU:HG2	1.90	0.53
32:a:107:G:H1	51:t:6:SER:HG	1.57	0.53
38:g:51:ALA:HB2	38:g:58:GLU:HG3	1.90	0.53
54:x:8:U:O2'	54:x:21:A:N1	2.33	0.53
43:l:46:ASN:ND2	43:l:89:ASP:OD2	2.40	0.53
4:3:12:LYS:NZ	7:A:249:C:O2	2.42	0.53
10:D:39:ASP:N	10:D:39:ASP:OD1	2.40	0.53
13:G:22:GLN:NE2	13:G:38:ASN:O	2.41	0.53
32:a:556:C:OP1	43:l:14:ARG:NH1	2.42	0.53
11:E:52:VAL:HG21	11:E:82:GLY:H	1.73	0.53
11:E:154:ASP:OD1	11:E:154:ASP:N	2.40	0.53
12:F:40:VAL:HG21	12:F:50:LEU:HD13	1.91	0.53
12:F:74:VAL:H	12:F:79:ILE:HG13	1.73	0.53
13:G:11:VAL:HG11	13:G:15:VAL:HG13	1.90	0.53
13:G:44:LYS:HG2	13:G:51:THR:HB	1.90	0.53
32:a:401:C:O2'	32:a:621:A:N3	2.36	0.53
7:A:2666:C:N4	13:G:109:PHE:O	2.41	0.53
32:a:362:G:N2	32:a:365:U:OP2	2.37	0.53
32:a:484:G:H4'	32:a:485:U:H5'	1.89	0.53
4:3:32:ILE:O	4:3:36:LYS:NZ	2.35	0.53
7:A:1753:G:N1	7:A:1756:G:OP2	2.39	0.53
7:A:1799:G:OP1	9:C:258:ARG:NH1	2.40	0.53
20:O:16:ARG:NH2	20:O:19:GLN:OE1	2.42	0.53
32:a:1193:G:O6	34:c:3:GLN:NE2	2.42	0.53
32:a:1425:U:H2'	32:a:1426:G:H8	1.74	0.53
45:n:86:GLU:OE2	45:n:90:ARG:NH1	2.41	0.53
7:A:2123:G:N2	7:A:2171:A:O5'	2.39	0.53
32:a:553:A:H5''	43:l:21:VAL:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:s:36:ARG:NH2	50:s:75:ALA:O	2.42	0.53
7:A:1434:A:H2'	7:A:1435:G:H8	1.73	0.52
7:A:1962:C:O2'	7:A:1964:G:OP2	2.27	0.52
7:A:2312:U:O2	12:F:37:ASN:ND2	2.32	0.52
12:F:135:GLN:HG3	12:F:141:ILE:HG21	1.90	0.52
19:N:114:GLU:OE1	19:N:118:ARG:NH2	2.37	0.52
34:c:11:ARG:O	34:c:16:LYS:N	2.42	0.52
38:g:69:VAL:HB	38:g:135:VAL:HG12	1.91	0.52
46:o:23:GLY:O	46:o:28:GLN:NE2	2.41	0.52
11:E:21:ARG:O	11:E:114:ARG:NH2	2.40	0.52
30:Y:10:SER:OG	30:Y:11:VAL:N	2.42	0.52
43:l:39:THR:HG22	43:l:51:LYS:HG3	1.89	0.52
22:Q:49:ASP:HA	22:Q:52:GLN:HB2	1.91	0.52
32:a:409:U:H3	32:a:433:G:H1	1.56	0.52
32:a:619:U:H3	35:d:131:ASN:HB3	1.74	0.52
33:b:88:ASP:O	33:b:89:GLN:NE2	2.42	0.52
35:d:69:GLU:OE2	35:d:204:TYR:OH	2.26	0.52
10:D:8:LYS:HB2	10:D:201:LEU:HD11	1.90	0.52
11:E:145:ASP:HB3	11:E:184:ASP:H	1.75	0.52
22:Q:72:ASN:HB3	22:Q:110:VAL:HG11	1.91	0.52
32:a:28:A:O2'	32:a:296:U:OP1	2.24	0.52
32:a:1071:C:H2'	32:a:1072:G:H8	1.75	0.52
7:A:1582:C:O2'	7:A:1585:C:N3	2.39	0.52
10:D:33:ARG:NH2	10:D:74:GLU:O	2.39	0.52
32:a:1061:G:H5'	41:j:61:ALA:HB2	1.91	0.52
34:c:85:GLU:OE2	34:c:88:ARG:NH2	2.43	0.52
7:A:627:A:OP1	17:L:78:ARG:NH1	2.34	0.52
7:A:1262:A:OP1	24:S:99:ARG:NH1	2.38	0.52
7:A:2137:U:H2'	7:A:2138:G:H8	1.74	0.52
12:F:116:GLY:HA3	12:F:178:ARG:HB3	1.91	0.52
14:H:51:ARG:HG3	14:H:54:LEU:HB2	1.92	0.52
35:d:99:ASP:OD1	35:d:99:ASP:N	2.42	0.52
5:4:36:ARG:HD3	5:4:37:GLN:HB2	1.91	0.52
7:A:1769:U:O2'	7:A:1958:C:OP1	2.27	0.52
7:A:2816:G:N3	7:A:2883:A:O2'	2.39	0.52
29:X:32:ASN:OD1	29:X:34:HIS:NE2	2.42	0.52
56:z:234:ARG:NE	56:z:234:ARG:O	2.43	0.52
4:3:6:THR:HG22	4:3:63:PRO:HD2	1.91	0.52
7:A:1071:G:H1'	7:A:1089:A:H2'	1.91	0.52
7:A:1250:G:N7	17:L:18:ARG:NH2	2.54	0.52
11:E:48:THR:HG23	11:E:50:ALA:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:e:105:ILE:HG22	36:e:123:VAL:HG12	1.90	0.52
42:k:119:ASN:OD1	52:u:35:ARG:NH1	2.43	0.52
7:A:1900:A:H1'	7:A:1970:A:H2'	1.92	0.52
12:F:48:LYS:O	12:F:52:ASN:ND2	2.43	0.52
12:F:62:GLY:HA3	12:F:95:ARG:HH21	1.75	0.52
32:a:942:G:H21	40:i:126:GLN:HE22	1.58	0.52
41:j:6:ILE:HG22	41:j:102:LEU:HG	1.91	0.52
7:A:2013:A:H4'	24:S:96:ILE:HG22	1.92	0.52
32:a:837:U:H2'	32:a:838:G:H8	1.75	0.52
24:S:35:ILE:O	24:S:39:THR:OG1	2.26	0.51
32:a:344:A:H5''	32:a:345:C:H5	1.75	0.51
32:a:1040:U:H2'	32:a:1041:G:C8	2.46	0.51
45:n:2:ALA:N	45:n:67:THR:O	2.44	0.51
7:A:1819:A:H4'	7:A:1820:U:H5''	1.93	0.51
51:t:28:MET:HG3	51:t:58:VAL:HG12	1.93	0.51
7:A:30:G:O2'	7:A:1214:A:N3	2.39	0.51
9:C:16:VAL:HG22	9:C:206:GLY:HA3	1.93	0.51
32:a:116:A:H61	32:a:313:A:H1'	1.75	0.51
32:a:447:G:N1	32:a:486:U:OP2	2.40	0.51
32:a:458:U:O4	32:a:474:G:O6	2.28	0.51
32:a:542:G:OP1	35:d:10:LYS:NZ	2.40	0.51
32:a:835:U:OP1	49:r:53:ARG:NH2	2.41	0.51
32:a:946:A:H2'	32:a:947:G:C8	2.46	0.51
6:5:32:LEU:HD11	12:F:139:PRO:HB2	1.93	0.51
7:A:476:G:N1	7:A:479:A:OP2	2.36	0.51
7:A:1028:A:N3	7:A:2486:C:O2'	2.39	0.51
7:A:1415:U:O2	7:A:1587:G:N2	2.40	0.51
9:C:160:THR:HG23	9:C:177:ARG:HG2	1.91	0.51
10:D:4:LEU:HD23	10:D:29:VAL:HG11	1.92	0.51
21:P:109:ARG:NH1	32:a:1464:U:OP2	2.43	0.51
32:a:82:G:N2	32:a:84:U:O4	2.42	0.51
32:a:1119:C:OP1	40:i:85:ARG:NH1	2.42	0.51
32:a:1137:C:O2'	32:a:1138:G:N2	2.43	0.51
32:a:50:A:O2'	32:a:360:G:N2	2.43	0.51
7:A:371:A:N3	29:X:61:LYS:NZ	2.58	0.51
7:A:566:U:H5''	17:L:29:LYS:HE3	1.93	0.51
18:M:14:LYS:HD2	18:M:16:ARG:HH12	1.75	0.51
27:V:1:MET:HG3	27:V:3:THR:HG23	1.93	0.51
42:k:94:GLU:HG2	52:u:16:LEU:HD11	1.93	0.51
7:A:815:C:OP2	23:R:85:LYS:NZ	2.42	0.51
7:A:1364:G:OP2	29:X:50:ARG:NH1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:P:36:SER:OG	21:P:37:LYS:NZ	2.43	0.51
42:k:36:ASP:OD1	42:k:36:ASP:N	2.43	0.51
48:q:20:SER:HA	48:q:48:ASP:H	1.75	0.51
7:A:1667:G:O2'	7:A:1991:U:O4	2.26	0.51
18:M:27:SER:OG	18:M:66:ARG:NH1	2.44	0.51
32:a:1040:U:H2'	32:a:1041:G:H8	1.75	0.51
32:a:1377:A:OP1	38:g:92:ARG:NH2	2.44	0.51
56:z:85:LEU:O	56:z:89:GLU:N	2.43	0.51
7:A:1326:U:H2'	7:A:1327:A:H8	1.76	0.51
7:A:1529:G:O6	7:A:1542:U:O4	2.28	0.51
7:A:2109:U:N3	7:A:2110:G:O6	2.44	0.51
7:A:2579:C:O2'	10:D:136:ASN:ND2	2.44	0.51
9:C:142:HIS:ND1	9:C:193:GLY:O	2.35	0.51
10:D:14:ILE:HG13	10:D:22:ILE:HG13	1.93	0.51
32:a:1098:C:O2'	52:u:71:TYR:O	2.28	0.51
32:a:1360:A:OP2	45:n:75:ARG:NH2	2.44	0.51
38:g:8:GLY:O	38:g:9:GLN:NE2	2.44	0.51
43:l:114:ARG:HB3	43:l:119:VAL:HB	1.92	0.51
6:5:63:ARG:NH2	32:a:1312:G:OP2	2.44	0.51
42:k:26:SER:OG	42:k:29:ASN:O	2.29	0.51
7:A:788:A:OP1	7:A:791:C:N4	2.35	0.50
7:A:1057:A:OP2	7:A:1089:A:N6	2.44	0.50
7:A:1275:A:OP2	7:A:1646:C:N4	2.38	0.50
8:B:55:U:HO2'	12:F:24:SER:HG	1.56	0.50
17:L:123:ARG:NH1	17:L:144:GLU:OXT	2.44	0.50
32:a:210:C:O2'	32:a:211:G:N2	2.44	0.50
56:z:294:LEU:HD13	56:z:297:ARG:HE	1.74	0.50
7:A:526:A:O2'	7:A:2043:C:O2	2.29	0.50
7:A:740:C:H5'	7:A:1784:A:H3'	1.93	0.50
10:D:104:VAL:HG21	10:D:205:PRO:HB3	1.92	0.50
26:U:86:ARG:HH12	26:U:100:SER:HB3	1.76	0.50
32:a:1255:G:OP2	41:j:45:ARG:NH2	2.43	0.50
7:A:320:A:N3	11:E:163:ASN:ND2	2.59	0.50
9:C:154:LEU:HD13	9:C:176:LEU:HD21	1.93	0.50
13:G:43:VAL:HA	13:G:51:THR:O	2.12	0.50
32:a:227:G:O2'	47:p:63:GLN:NE2	2.40	0.50
7:A:690:G:H21	9:C:43:ARG:HH12	1.59	0.50
38:g:69:VAL:HG23	38:g:138:ARG:HB2	1.93	0.50
7:A:807:U:OP2	17:L:41:ARG:NH1	2.44	0.50
13:G:2:SER:OG	13:G:3:ARG:N	2.45	0.50
13:G:94:TYR:O	13:G:95:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:R:42:ALA:HB2	23:R:47:VAL:HG13	1.93	0.50
28:W:18:ALA:O	28:W:20:ARG:NH1	2.44	0.50
32:a:1160:G:OP1	33:b:132:LYS:NZ	2.37	0.50
33:b:173:ILE:HG23	33:b:183:VAL:HG11	1.93	0.50
40:i:30:ILE:HG12	40:i:65:ILE:HD12	1.93	0.50
41:j:5:ARG:HB2	41:j:77:VAL:HA	1.94	0.50
42:k:87:LYS:NZ	42:k:113:VAL:O	2.45	0.50
7:A:33:C:N4	7:A:446:G:O2'	2.40	0.50
9:C:107:PRO:HD2	9:C:110:LEU:HD22	1.93	0.50
14:H:1:MET:SD	14:H:1:MET:N	2.77	0.50
32:a:1356:G:H2'	32:a:1357:A:C8	2.46	0.50
40:i:55:VAL:HG21	40:i:94:LEU:HD13	1.94	0.50
41:j:5:ARG:NH1	41:j:102:LEU:O	2.37	0.50
7:A:1754:A:N1	7:A:2716:C:O2'	2.42	0.50
7:A:2875:C:OP1	19:N:4:ARG:NH2	2.45	0.50
16:K:91:SER:O	16:K:93:GLN:NE2	2.44	0.50
32:a:974:A:OP1	45:n:69:ARG:NH1	2.37	0.50
7:A:589:U:H2'	7:A:590:A:C8	2.47	0.49
10:D:184:ARG:HH22	21:P:7:GLN:HB3	1.77	0.49
14:H:39:ALA:HB1	14:H:44:ILE:HG12	1.93	0.49
25:T:4:GLU:OE2	25:T:49:LYS:NZ	2.44	0.49
17:L:91:ASP:OD1	17:L:91:ASP:N	2.45	0.49
19:N:59:SER:OG	19:N:60:VAL:N	2.45	0.49
26:U:27:ASN:HB3	26:U:35:ILE:HD12	1.94	0.49
39:h:43:GLU:HG3	39:h:101:ILE:HD13	1.93	0.49
40:i:18:ARG:NE	40:i:66:THR:OG1	2.42	0.49
40:i:36:GLU:O	40:i:45:ARG:NH1	2.45	0.49
6:5:1:MET:SD	12:F:95:ARG:NH1	2.86	0.49
7:A:81:G:O2'	7:A:295:G:O2'	2.29	0.49
7:A:488:G:O2'	7:A:491:G:O6	2.30	0.49
56:z:63:LYS:HA	56:z:66:VAL:HG22	1.93	0.49
7:A:674:G:H1'	11:E:69:ARG:HD3	1.95	0.49
7:A:698:C:O2'	7:A:734:A:N6	2.42	0.49
7:A:2112:G:OP1	7:A:2119:A:N6	2.36	0.49
9:C:36:LYS:NZ	9:C:38:SER:OG	2.45	0.49
14:H:43:ASN:HA	14:H:46:PHE:HB3	1.94	0.49
32:a:1526:G:OP1	52:u:45:ARG:NH1	2.45	0.49
34:c:151:VAL:HG22	34:c:200:VAL:HG22	1.94	0.49
7:A:2848:G:HO2'	7:A:2867:G:H22	1.53	0.49
36:e:156:LYS:HG2	39:h:71:VAL:HG13	1.94	0.49
40:i:94:LEU:HA	40:i:97:GLU:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:l:121:ARG:HD3	43:l:123:LYS:HZ2	1.77	0.49
1:o:54:VAL:HG21	19:N:98:LEU:HD22	1.95	0.49
2:1:13:SER:OG	2:1:14:SER:N	2.45	0.49
7:A:302:C:H2'	7:A:303:G:H8	1.78	0.49
9:C:252:THR:OG1	9:C:253:LYS:N	2.45	0.49
24:S:4:ILE:HG13	24:S:106:VAL:HG22	1.94	0.49
32:a:662:U:OP1	37:f:93:LYS:NZ	2.46	0.49
32:a:673:A:H2'	32:a:674:G:C8	2.47	0.49
32:a:946:A:O2'	32:a:1333:A:N3	2.40	0.49
56:z:241:ASP:OD1	56:z:261:ARG:NH2	2.46	0.49
7:A:286:U:H2'	7:A:287:G:H8	1.76	0.49
7:A:2308:G:H2'	7:A:2310:C:H5	1.78	0.49
7:A:2787:C:H1'	10:D:63:PRO:HG3	1.95	0.49
14:H:17:ASP:OD1	14:H:17:ASP:N	2.44	0.49
20:O:8:ILE:O	20:O:12:THR:OG1	2.28	0.49
32:a:815:A:N7	32:a:1509:C:O2'	2.41	0.49
32:a:1005:A:OP2	32:a:1024:G:N2	2.43	0.49
7:A:878:A:N6	7:A:899:A:O2'	2.45	0.49
14:H:30:LEU:HB3	14:H:36:ALA:HB3	1.95	0.49
15:J:62:VAL:O	15:J:69:ARG:NH2	2.43	0.49
54:x:17:C:OP1	54:x:60:U:O2'	2.30	0.49
56:z:168:LEU:HD12	56:z:169:PRO:HD2	1.95	0.49
32:a:62:U:OP1	32:a:385:C:O2'	2.31	0.49
6:5:11:GLU:HB3	6:5:23:LYS:HE3	1.95	0.49
7:A:1028:A:H2'	7:A:1029:A:C8	2.47	0.49
7:A:1315:C:O2'	7:A:1392:A:N3	2.40	0.49
7:A:1744:A:H3'	7:A:1745:A:H8	1.76	0.49
8:B:52:A:N7	20:O:64:TYR:OH	2.35	0.49
39:h:90:ASP:OD1	39:h:90:ASP:N	2.40	0.49
48:q:46:VAL:HG11	48:q:61:ILE:HG12	1.95	0.49
6:5:38:SER:HB3	12:F:105:THR:HA	1.94	0.48
11:E:34:ALA:HA	11:E:94:GLN:HE21	1.78	0.48
32:a:126:G:OP1	32:a:605:U:O2'	2.28	0.48
32:a:522:C:H41	43:l:50:ARG:HH12	1.61	0.48
32:a:1297:G:N2	32:a:1298:U:O4	2.46	0.48
32:a:1314:C:OP1	50:s:6:LYS:NZ	2.37	0.48
32:a:1322:C:OP1	50:s:78:ARG:NH2	2.46	0.48
35:d:95:GLU:OE2	35:d:104:ARG:NH2	2.46	0.48
56:z:244:ARG:NH2	56:z:253:VAL:O	2.46	0.48
4:3:30:ARG:NH1	17:L:63:LYS:O	2.45	0.48
7:A:111:A:O3'	30:Y:58:ASN:ND2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1469:A:H2'	7:A:1470:A:C8	2.48	0.48
7:A:1914:C:OP2	55:y:25:ARG:NH1	2.38	0.48
7:A:2391:G:H2'	7:A:2424:C:H41	1.78	0.48
7:A:2469:A:N6	7:A:2481:G:O2'	2.45	0.48
7:A:2659:G:N2	7:A:2662:A:OP2	2.39	0.48
7:A:397:U:OP2	29:X:10:LYS:NZ	2.38	0.48
7:A:2771:C:O2'	10:D:173:GLN:NE2	2.41	0.48
32:a:309:A:H2'	32:a:310:G:H8	1.78	0.48
7:A:340:A:O2'	11:E:162:ARG:NH1	2.46	0.48
7:A:964:C:O2'	7:A:2273:A:N3	2.44	0.48
7:A:1168:G:H1	7:A:1181:U:H3	1.61	0.48
42:k:81:ASN:HB3	42:k:106:ARG:HH11	1.79	0.48
56:z:152:THR:HG22	56:z:162:VAL:HG11	1.94	0.48
7:A:299:A:N3	7:A:319:G:O2'	2.38	0.48
7:A:992:C:OP1	22:Q:47:TYR:OH	2.24	0.48
7:A:1358:G:O2'	7:A:1373:A:N6	2.47	0.48
32:a:1028:C:N4	32:a:1033:G:O6	2.47	0.48
7:A:243:U:OP2	7:A:254:G:N1	2.38	0.48
7:A:373:U:H2'	7:A:374:A:H8	1.79	0.48
7:A:1178:C:H2'	7:A:1179:G:C8	2.49	0.48
14:H:9:VAL:HG22	14:H:35:LYS:HE2	1.96	0.48
25:T:47:VAL:O	25:T:51:PHE:HB2	2.14	0.48
32:a:110:C:O2'	47:p:25:ARG:O	2.23	0.48
32:a:1437:A:OP1	51:t:29:ARG:NH2	2.47	0.48
7:A:1332:G:N7	7:A:1609:A:O2'	2.40	0.48
32:a:1151:A:H1'	41:j:41:PRO:HB2	1.96	0.48
40:i:22:LYS:HG2	40:i:62:ASP:HB2	1.96	0.48
3:2:33:ARG:NE	7:A:467:G:OP1	2.46	0.48
6:5:28:VAL:HG21	6:5:32:LEU:HD13	1.95	0.48
7:A:931:U:O2	7:A:1167:C:O2'	2.31	0.48
7:A:1450:G:H21	7:A:1452:G:H1	1.61	0.48
7:A:2458:G:O2'	7:A:2460:U:O4	2.31	0.48
38:g:74:GLU:O	38:g:88:PRO:HA	2.14	0.48
47:p:1:MET:HE2	47:p:66:THR:HG21	1.96	0.48
2:1:13:SER:HB3	2:1:17:THR:HA	1.95	0.48
7:A:45:G:H5''	7:A:46:G:H5'	1.96	0.48
7:A:270:A:N1	7:A:369:U:O2'	2.38	0.48
32:a:178:C:H2'	32:a:179:A:H8	1.78	0.48
32:a:1130:A:H61	32:a:1144:G:H1'	1.78	0.48
37:f:38:ARG:HH21	37:f:63:ASN:HD22	1.62	0.48
40:i:17:ALA:HB2	40:i:67:VAL:HG23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2682:A:H61	7:A:2728:U:H1'	1.78	0.48
32:a:1187:G:H5'	40:i:115:LYS:HE2	1.96	0.48
55:y:41:LYS:O	55:y:45:LEU:HB2	2.13	0.48
56:z:257:ASP:OD1	56:z:257:ASP:N	2.45	0.48
7:A:2077:A:OP1	7:A:2238:G:N2	2.44	0.47
16:K:66:LYS:HG2	16:K:81:GLY:H	1.78	0.47
35:d:147:GLU:OE2	35:d:151:LYS:NZ	2.43	0.47
7:A:184:C:O2'	7:A:217:A:N3	2.42	0.47
7:A:219:A:N3	7:A:234:U:O2'	2.42	0.47
7:A:805:G:N2	7:A:829:A:OP1	2.47	0.47
7:A:1386:C:H2'	7:A:1387:A:C8	2.49	0.47
12:F:121:SER:OG	12:F:129:SER:O	2.29	0.47
32:a:1209:C:H2'	32:a:1210:C:H6	1.79	0.47
33:b:18:HIS:ND1	33:b:188:ASP:OD2	2.40	0.47
56:z:333:VAL:HG23	56:z:345:VAL:HG12	1.95	0.47
7:A:832:U:H2'	7:A:833:A:H8	1.79	0.47
7:A:1141:U:OP2	15:J:65:THR:OG1	2.30	0.47
7:A:2689:U:OP1	7:A:2719:G:N1	2.36	0.47
37:f:29:ILE:HG22	37:f:34:GLY:HA3	1.96	0.47
3:2:3:ARG:HA	3:2:3:ARG:HD3	1.72	0.47
31:Z:48:ILE:O	31:Z:52:SER:HB3	2.13	0.47
32:a:652:U:O4	32:a:752:G:O2'	2.27	0.47
32:a:1009:U:O4	32:a:1020:G:O6	2.32	0.47
32:a:1218:C:H2'	32:a:1219:A:C8	2.49	0.47
46:o:18:ASP:OD1	46:o:18:ASP:N	2.46	0.47
14:H:130:VAL:HG23	14:H:142:VAL:HB	1.96	0.47
33:b:117:LEU:HD12	33:b:120:GLN:HE21	1.79	0.47
45:n:54:ASP:HA	45:n:59:ARG:HD3	1.97	0.47
56:z:207:ASP:OD2	56:z:213:HIS:NE2	2.37	0.47
7:A:848:C:H2'	7:A:849:A:H8	1.78	0.47
7:A:864:G:O2'	7:A:914:G:O6	2.33	0.47
7:A:2134:A:C4	7:A:2158:A:H4'	2.49	0.47
7:A:2345:G:H5'	7:A:2347:C:H5'	1.97	0.47
7:A:2521:C:O2'	7:A:2564:A:N3	2.44	0.47
56:z:153:ARG:NH1	56:z:350:ASP:OD2	2.38	0.47
1:0:38:HIS:ND1	1:0:39:LEU:O	2.47	0.47
2:1:27:LYS:NZ	2:1:51:GLU:OE2	2.48	0.47
4:3:27:ALA:HB2	17:L:61:LEU:HA	1.96	0.47
7:A:285:G:O6	7:A:355:U:O2	2.32	0.47
7:A:2092:U:OP1	7:A:2199:A:O2'	2.31	0.47
32:a:147:G:H2'	32:a:148:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:254:G:OP1	48:q:68:SER:OG	2.28	0.47
32:a:1363:A:O2'	32:a:1365:G:N7	2.43	0.47
39:h:102:ALA:HB3	39:h:113:ASP:HB3	1.96	0.47
52:u:4:ILE:HG21	52:u:19:PHE:HB2	1.95	0.47
7:A:494:G:H4'	24:S:6:LYS:HB2	1.96	0.47
7:A:2646:C:OP2	7:A:2732:G:O2'	2.33	0.47
10:D:101:PHE:HA	10:D:104:VAL:HG12	1.97	0.47
32:a:9:G:H5'	36:e:108:GLY:HA3	1.96	0.47
32:a:412:A:H62	32:a:431:A:H61	1.63	0.47
4:3:25:LYS:HB3	17:L:62:PRO:HG2	1.96	0.47
7:A:576:U:H2'	7:A:577:G:C8	2.50	0.47
7:A:2250:G:O2'	7:A:2496:C:OP1	2.30	0.47
9:C:117:GLN:H	9:C:128:ASN:ND2	2.13	0.47
17:L:78:ARG:HB3	17:L:113:ALA:HB3	1.96	0.47
27:V:9:ARG:NH2	27:V:11:GLU:O	2.48	0.47
32:a:938:A:N3	32:a:1376:U:O2'	2.39	0.47
32:a:1178:G:N7	40:i:99:ARG:NH2	2.62	0.47
35:d:174:ASP:OD1	35:d:177:LYS:N	2.46	0.47
7:A:184:C:H2'	7:A:185:G:H8	1.79	0.47
7:A:2849:U:O4	21:P:21:ARG:NH2	2.38	0.47
24:S:24:ILE:HD13	24:S:36:LEU:HD11	1.95	0.47
32:a:674:G:H2'	32:a:675:A:H8	1.80	0.47
32:a:769:G:H4'	32:a:1513:A:H4'	1.97	0.47
32:a:1406:U:O2	32:a:1517:G:N2	2.42	0.47
38:g:126:ASP:HA	38:g:129:GLU:HB3	1.97	0.47
48:q:61:ILE:HG22	48:q:73:TRP:HE3	1.80	0.47
54:x:18:G:O2'	54:x:57:G:N2	2.33	0.47
6:5:35:ASP:OD1	6:5:35:ASP:N	2.43	0.46
7:A:1278:C:H2'	7:A:1279:G:C8	2.49	0.46
17:L:110:VAL:HB	17:L:127:VAL:HG13	1.96	0.46
30:Y:14:LEU:HD22	30:Y:53:VAL:HG13	1.96	0.46
51:t:55:GLN:HG3	51:t:76:LYS:HD3	1.96	0.46
4:3:13:ARG:NH1	7:A:2393:U:O2'	2.47	0.46
7:A:1042:G:O6	7:A:1113:U:O4	2.33	0.46
7:A:1266:G:O2'	7:A:2012:G:O6	2.29	0.46
8:B:5:U:OP1	8:B:61:G:O2'	2.32	0.46
32:a:460:A:H2'	32:a:461:A:H8	1.80	0.46
48:q:31:HIS:HD2	48:q:34:TYR:H	1.62	0.46
7:A:832:U:H2'	7:A:833:A:C8	2.51	0.46
7:A:1434:A:H2'	7:A:1435:G:C8	2.50	0.46
7:A:1799:G:N7	9:C:178:SER:OG	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:S:67:ASP:OD1	24:S:67:ASP:N	2.45	0.46
32:a:591:U:H2'	32:a:592:G:H8	1.81	0.46
32:a:890:G:O2'	32:a:906:A:N6	2.48	0.46
10:D:49:GLN:HE21	10:D:79:LEU:HB3	1.80	0.46
12:F:119:ALA:HB1	12:F:167:ARG:HE	1.79	0.46
18:M:15:GLY:O	18:M:16:ARG:NH1	2.48	0.46
32:a:104:G:OP1	51:t:16:LYS:NZ	2.37	0.46
32:a:324:G:N1	32:a:327:A:OP2	2.47	0.46
32:a:714:G:H2'	32:a:715:A:C8	2.51	0.46
41:j:81:GLU:HA	41:j:84:VAL:HB	1.98	0.46
46:o:74:ASP:OD1	46:o:77:ARG:NH1	2.48	0.46
7:A:820:A:H4'	7:A:836:G:H22	1.81	0.46
7:A:2748:A:H5'	13:G:4:VAL:HG21	1.97	0.46
20:O:43:ASN:HD21	20:O:46:GLU:HG2	1.81	0.46
32:a:486:U:H2'	32:a:487:A:H8	1.80	0.46
32:a:689:C:OP1	42:k:29:ASN:ND2	2.46	0.46
32:a:1149:C:H2'	32:a:1150:A:C8	2.50	0.46
33:b:94:HIS:ND1	33:b:146:ASN:O	2.44	0.46
7:A:184:C:H2'	7:A:185:G:C8	2.51	0.46
7:A:782:A:O2'	9:C:224:ALA:O	2.33	0.46
7:A:1791:A:N6	7:A:1828:G:O2'	2.42	0.46
7:A:2722:G:O2'	19:N:3:HIS:O	2.27	0.46
32:a:309:A:O2'	32:a:607:A:N1	2.43	0.46
7:A:1013:C:H2'	7:A:1014:A:H8	1.80	0.46
7:A:1340:U:OP1	25:T:84:TYR:OH	2.27	0.46
8:B:1:U:H2'	8:B:2:G:H8	1.80	0.46
8:B:40:U:N3	8:B:44:G:OP2	2.39	0.46
32:a:1216:A:OP1	45:n:5:SER:OG	2.28	0.46
35:d:147:GLU:HA	35:d:150:LYS:HB2	1.96	0.46
36:e:153:VAL:HG23	36:e:156:LYS:HE2	1.98	0.46
41:j:56:HIS:CD2	41:j:57:VAL:HG23	2.50	0.46
54:x:15:G:N2	54:x:21:A:N3	2.63	0.46
7:A:801:G:O6	11:E:48:THR:OG1	2.34	0.46
7:A:1800:C:H5	7:A:1819:A:H62	1.64	0.46
12:F:29:PRO:HB2	12:F:169:LEU:HD22	1.98	0.46
18:M:118:LYS:HE3	18:M:118:LYS:HB2	1.77	0.46
32:a:216:U:H4'	32:a:464:U:H4'	1.98	0.46
41:j:44:THR:HG22	41:j:70:HIS:HA	1.98	0.46
7:A:764:A:OP1	9:C:207:LYS:NZ	2.42	0.46
7:A:1412:U:H2'	7:A:1413:A:C8	2.50	0.46
32:a:1270:G:HO2'	32:a:1313:U:HO2'	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2230:G:H5''	29:X:30:LEU:HD12	1.99	0.45
10:D:148:GLN:HB2	10:D:152:PRO:HG2	1.97	0.45
18:M:33:LEU:HD13	18:M:117:PHE:HB3	1.98	0.45
21:P:106:LYS:O	21:P:109:ARG:NH2	2.44	0.45
32:a:1530:G:H2'	32:a:1531:A:C8	2.51	0.45
32:a:1536:C:H5'	32:a:1537:U:H5	1.81	0.45
50:s:39:THR:HA	50:s:70:LYS:HA	1.98	0.45
7:A:59:U:O2'	7:A:74:A:OP2	2.30	0.45
7:A:577:G:O2'	7:A:1254:A:OP1	2.34	0.45
7:A:1012:U:OP2	22:Q:70:ARG:NH1	2.44	0.45
7:A:1724:G:N2	7:A:1736:U:O2	2.37	0.45
7:A:1794:A:H2'	7:A:1795:C:C6	2.51	0.45
11:E:131:THR:HG22	11:E:160:ALA:HA	1.99	0.45
14:H:84:ALA:HA	14:H:91:PHE:H	1.81	0.45
32:a:811:C:O2'	32:a:901:A:N1	2.49	0.45
32:a:1391:U:H2'	32:a:1392:G:C8	2.51	0.45
7:A:2144:G:H1'	7:A:2147:A:H61	1.81	0.45
8:B:75:G:H5''	27:V:12:GLN:HG2	1.98	0.45
14:H:41:LYS:HA	14:H:44:ILE:HB	1.98	0.45
15:J:118:MET:HA	15:J:121:LYS:HE2	1.98	0.45
29:X:17:ASN:O	29:X:24:ALA:HA	2.16	0.45
32:a:546:A:O2'	32:a:548:G:O2'	2.27	0.45
32:a:674:G:H2'	32:a:675:A:C8	2.51	0.45
34:c:121:THR:OG1	34:c:187:SER:OG	2.33	0.45
35:d:150:LYS:HB3	35:d:151:LYS:HZ2	1.82	0.45
3:2:4:THR:HG22	7:A:687:C:H1'	1.97	0.45
7:A:1645:G:H5''	7:A:1646:C:H5'	1.98	0.45
14:H:27:ARG:NH1	29:X:60:ASP:OD2	2.50	0.45
18:M:42:THR:HG22	18:M:93:VAL:HG12	1.98	0.45
43:l:50:ARG:HG3	43:l:90:LEU:HD21	1.99	0.45
44:m:16:VAL:HG23	44:m:17:ILE:HG12	1.98	0.45
46:o:46:HIS:O	46:o:48:LYS:N	2.49	0.45
7:A:523:C:O2	7:A:554:U:O2'	2.35	0.45
7:A:1038:G:H2'	7:A:1039:A:C8	2.51	0.45
7:A:1529:G:O6	7:A:1542:U:C4	2.70	0.45
32:a:672:U:H2'	32:a:673:A:C8	2.52	0.45
32:a:1013:G:N2	32:a:1016:A:OP2	2.38	0.45
34:c:70:THR:HG21	34:c:76:VAL:HG21	1.99	0.45
36:e:11:LEU:HD23	36:e:11:LEU:HA	1.85	0.45
39:h:43:GLU:OE2	39:h:114:ARG:NH2	2.41	0.45
1:0:4:GLN:HA	7:A:2615:U:C2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:443:A:N6	11:E:36:ALA:O	2.49	0.45
7:A:581:C:H2'	7:A:582:A:C8	2.52	0.45
7:A:691:C:OP1	9:C:217:ARG:NH1	2.50	0.45
7:A:1203:U:O2'	17:L:4:ASN:OD1	2.33	0.45
7:A:1568:G:H5'	9:C:60:GLN:HA	1.98	0.45
7:A:2822:G:H5''	10:D:164:GLN:HE22	1.82	0.45
19:N:2:ARG:NH1	19:N:5:LYS:O	2.49	0.45
20:O:7:ARG:HG2	20:O:96:GLY:HA3	1.99	0.45
26:U:74:ASN:HD22	26:U:77:THR:H	1.63	0.45
32:a:229:U:O2'	47:p:23:ASP:OD1	2.34	0.45
32:a:744:C:H2'	32:a:745:G:C8	2.52	0.45
32:a:1060:U:OP1	45:n:85:ARG:NH2	2.49	0.45
35:d:189:SER:O	35:d:189:SER:OG	2.30	0.45
41:j:89:ARG:NH1	41:j:90:LEU:HB3	2.32	0.45
1:0:43:ILE:HG22	1:0:49:TYR:HB2	1.99	0.45
7:A:673:C:OP1	11:E:49:ARG:NH2	2.49	0.45
7:A:1378:A:O2'	7:A:1380:G:N7	2.43	0.45
7:A:2647:U:H2'	7:A:2648:G:H8	1.82	0.45
10:D:177:VAL:HG12	10:D:189:VAL:HG12	1.98	0.45
22:Q:94:ILE:HD12	23:R:13:ARG:HB2	1.98	0.45
26:U:99:ASN:OD1	26:U:99:ASN:N	2.49	0.45
32:a:651:C:N4	32:a:753:A:OP2	2.50	0.45
32:a:928:G:O2'	32:a:1533:C:OP1	2.34	0.45
38:g:74:GLU:OE2	38:g:95:ARG:NH2	2.50	0.45
47:p:66:THR:O	47:p:66:THR:OG1	2.35	0.45
49:r:25:ASP:OD2	49:r:28:THR:OG1	2.27	0.45
50:s:31:LEU:HD21	50:s:47:LEU:HD13	1.98	0.45
55:y:37:MET:HA	56:z:212:ARG:O	2.16	0.45
56:z:143:TRP:HA	56:z:146:MET:HE3	1.99	0.45
7:A:630:G:N2	7:A:633:A:OP2	2.38	0.45
7:A:1590:A:H2'	7:A:1591:A:C8	2.52	0.45
7:A:2081:U:H2'	7:A:2082:A:H8	1.82	0.45
7:A:2372:U:H2'	7:A:2373:G:H8	1.81	0.45
17:L:91:ASP:H	17:L:94:THR:HG1	1.64	0.45
18:M:136:MET:HE2	27:V:57:TYR:HB3	1.97	0.45
38:g:79:ARG:HG2	38:g:84:THR:H	1.82	0.45
46:o:43:PHE:HE1	46:o:49:ASP:HB3	1.82	0.45
7:A:511:U:H4'	7:A:1235:G:H4'	1.98	0.45
7:A:1417:C:O2'	7:A:1587:G:O2'	2.34	0.45
7:A:1447:C:O2'	7:A:1544:A:N3	2.40	0.45
7:A:2450:A:N6	7:A:2501:C:C2	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:1412:C:H2'	32:a:1413:A:C8	2.51	0.45
40:i:91:ASP:N	40:i:91:ASP:OD1	2.49	0.45
7:A:2291:U:OP1	7:A:2380:C:O2'	2.31	0.45
7:A:2749:A:OP1	13:G:2:SER:OG	2.32	0.45
12:F:66:LEU:HB3	12:F:88:LYS:HG2	1.99	0.45
29:X:72:ARG:NH2	29:X:78:TYR:OH	2.49	0.45
32:a:6:G:H22	36:e:103:THR:HG21	1.81	0.45
32:a:131:A:O2'	32:a:262:A:N3	2.46	0.45
32:a:505:G:H2'	32:a:506:G:C8	2.52	0.45
35:d:107:PHE:HB3	35:d:145:ILE:HD11	1.99	0.45
4:3:54:ASP:HB3	17:L:57:LEU:HD22	1.99	0.44
7:A:1733:G:H2'	7:A:1734:G:H8	1.82	0.44
32:a:642:A:C5	39:h:107:SER:HA	2.51	0.44
32:a:715:A:H2'	32:a:716:A:C8	2.52	0.44
7:A:2564:A:OP1	7:A:2648:G:O2'	2.30	0.44
7:A:2758:A:H1'	13:G:64:GLN:HE22	1.83	0.44
8:B:1:U:H2'	8:B:2:G:C8	2.51	0.44
15:J:74:TYR:O	15:J:86:GLN:HA	2.17	0.44
16:K:12:ASP:OD1	16:K:12:ASP:N	2.50	0.44
18:M:69:PRO:HA	18:M:94:ALA:HB2	1.98	0.44
21:P:75:GLN:HB2	21:P:78:SER:HB2	1.98	0.44
32:a:837:U:H2'	32:a:838:G:C8	2.52	0.44
32:a:1308:U:OP2	44:m:100:GLN:NE2	2.41	0.44
7:A:116:C:O2'	7:A:126:A:N3	2.39	0.44
7:A:1079:C:H2'	7:A:1080:A:C8	2.52	0.44
7:A:1688:U:O2'	7:A:1700:A:N7	2.43	0.44
10:D:37:VAL:HG22	10:D:48:ILE:HG22	1.98	0.44
23:R:59:ILE:HG12	23:R:101:ILE:HG23	2.00	0.44
32:a:222:C:H2'	32:a:223:A:H8	1.83	0.44
56:z:333:VAL:O	56:z:341:GLU:HA	2.17	0.44
7:A:558:U:H2'	7:A:559:G:C8	2.53	0.44
7:A:2705:A:O2'	7:A:2852:G:OP1	2.32	0.44
7:A:2808:G:O2'	7:A:2809:A:O5'	2.34	0.44
12:F:22:TYR:OH	12:F:165:GLU:OE2	2.29	0.44
20:O:100:HIS:HA	20:O:104:GLN:HE21	1.83	0.44
30:Y:12:GLU:HA	30:Y:15:ASN:HD22	1.82	0.44
32:a:335:C:O2'	32:a:1433:A:N3	2.42	0.44
54:x:73:A:H5''	54:x:74:C:H5'	2.00	0.44
4:3:19:LYS:HG3	7:A:651:G:H5'	2.00	0.44
7:A:807:U:O2'	7:A:2060:A:N1	2.45	0.44
7:A:833:A:H2'	7:A:834:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1476:U:H2'	7:A:1477:A:H8	1.82	0.44
7:A:1917:U:OP1	55:y:13:ARG:NH1	2.49	0.44
7:A:2104:C:N4	7:A:2185:U:O4	2.50	0.44
7:A:2291:U:H2'	7:A:2292:U:C6	2.52	0.44
29:X:7:VAL:HG23	29:X:8:THR:HG23	1.99	0.44
32:a:511:C:H5'	35:d:44:ARG:HH22	1.81	0.44
41:j:57:VAL:HG12	41:j:58:ASN:H	1.81	0.44
1:0:34:SER:OG	1:0:36:GLU:OE1	2.35	0.44
7:A:1178:C:H2'	7:A:1179:G:H8	1.82	0.44
7:A:1935:G:N2	7:A:1962:C:O2'	2.51	0.44
12:F:134:GLU:HB3	12:F:136:ILE:HG12	2.00	0.44
14:H:37:VAL:HG12	14:H:39:ALA:HB2	2.00	0.44
23:R:16:GLU:OE2	23:R:101:ILE:N	2.48	0.44
32:a:19:A:OP1	36:e:135:ASN:ND2	2.48	0.44
41:j:19:ASP:HA	41:j:22:THR:HG22	2.00	0.44
7:A:1036:G:N2	7:A:1119:U:O2	2.43	0.44
7:A:1365:A:OP1	29:X:3:ARG:NH1	2.44	0.44
7:A:1432:G:H2'	7:A:1433:A:C8	2.53	0.44
7:A:2446:G:N2	7:A:2449:U:O2	2.44	0.44
8:B:52:A:N6	20:O:32:PRO:O	2.50	0.44
8:B:94:A:OP1	27:V:19:ARG:NH1	2.47	0.44
9:C:177:ARG:HD2	9:C:177:ARG:HA	1.84	0.44
15:J:6:ALA:H	15:J:45:THR:HG21	1.83	0.44
32:a:1308:U:H2'	32:a:1309:G:H8	1.81	0.44
35:d:72:PHE:HE1	35:d:94:LEU:HD11	1.83	0.44
35:d:95:GLU:O	35:d:100:ASN:ND2	2.51	0.44
40:i:12:ARG:HD3	40:i:13:LYS:HB2	2.00	0.44
7:A:818:G:N1	7:A:1188:U:OP2	2.33	0.44
7:A:2233:U:H2'	7:A:2234:G:C8	2.52	0.44
7:A:2345:G:N2	7:A:2382:G:OP2	2.40	0.44
32:a:56:U:H2'	32:a:57:G:C8	2.52	0.44
32:a:1096:C:O2	32:a:1170:A:O2'	2.36	0.44
32:a:1151:A:H2'	32:a:1152:A:C8	2.53	0.44
33:b:153:ASP:OD1	33:b:153:ASP:N	2.50	0.44
56:z:163:GLU:HB2	56:z:181:LEU:HB3	2.00	0.44
7:A:1026:G:H2'	7:A:1027:A:H8	1.82	0.44
7:A:1509:A:H2'	7:A:1510:G:C8	2.53	0.44
7:A:2584:U:H5'	56:z:248:ALA:HB1	1.99	0.44
8:B:7:G:OP1	20:O:4:LYS:NZ	2.50	0.44
9:C:125:LYS:HE3	9:C:125:LYS:HB3	1.84	0.44
10:D:102:ALA:HA	10:D:180:VAL:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:g:5:ARG:HB3	38:g:7:ILE:HG12	1.99	0.44
40:i:12:ARG:O	40:i:15:SER:OG	2.31	0.44
46:o:2:SER:O	46:o:2:SER:OG	2.27	0.44
51:t:79:LEU:HD23	51:t:79:LEU:HA	1.86	0.44
2:1:14:SER:OG	2:1:48:ILE:O	2.31	0.43
2:1:38:LYS:HE3	2:1:38:LYS:HB3	1.82	0.43
7:A:1:G:H2'	7:A:2:G:C8	2.53	0.43
7:A:1433:A:H2'	7:A:1434:A:C8	2.52	0.43
7:A:2581:G:OP2	7:A:2581:G:N2	2.46	0.43
9:C:181:MET:HB3	9:C:181:MET:HE3	1.78	0.43
16:K:92:GLU:OE1	16:K:111:LYS:NZ	2.42	0.43
20:O:100:HIS:HA	20:O:104:GLN:HB2	2.00	0.43
28:W:70:GLU:HG3	28:W:72:LYS:HG3	1.98	0.43
36:e:85:VAL:HG11	36:e:147:MET:HB2	1.99	0.43
7:A:28:A:H61	7:A:512:G:H1'	1.82	0.43
7:A:1638:C:O2	7:A:2698:U:O2'	2.34	0.43
7:A:1818:U:H5'	9:C:157:SER:HB2	2.00	0.43
10:D:33:ARG:NH1	10:D:53:GLY:O	2.51	0.43
25:T:9:LYS:HB3	25:T:9:LYS:HE2	1.85	0.43
30:Y:32:ALA:HB2	30:Y:37:LEU:HD23	2.00	0.43
32:a:1048:G:H5''	45:n:3:LYS:HD2	2.00	0.43
39:h:11:LEU:HD22	39:h:75:ILE:HD11	1.99	0.43
42:k:28:ASN:O	42:k:57:LYS:NZ	2.48	0.43
43:l:110:ARG:HB3	43:l:119:VAL:HG21	2.00	0.43
45:n:21:PHE:O	45:n:25:ALA:HB2	2.18	0.43
17:L:79:LEU:HD12	17:L:112:LEU:HA	2.00	0.43
21:P:91:ALA:HB2	21:P:113:ARG:HA	2.00	0.43
32:a:559:A:H4'	32:a:560:A:H3'	2.00	0.43
32:a:932:C:H2'	32:a:933:G:C8	2.53	0.43
33:b:90:PHE:HB3	33:b:151:ILE:HG22	2.00	0.43
38:g:116:MET:HA	38:g:119:ARG:HE	1.82	0.43
43:l:68:GLY:O	43:l:99:ARG:NH1	2.51	0.43
45:n:13:ARG:HG2	45:n:54:ASP:HB3	2.00	0.43
56:z:234:ARG:HD2	56:z:238:ILE:HD12	1.99	0.43
7:A:1181:U:H2'	7:A:1182:G:C8	2.53	0.43
7:A:1579:A:H2'	7:A:1580:A:C8	2.53	0.43
7:A:1800:C:HO2'	7:A:1818:U:H3	1.66	0.43
32:a:178:C:OP2	51:t:60:ARG:NH1	2.51	0.43
32:a:745:G:H2'	32:a:746:A:C8	2.53	0.43
32:a:964:A:H1'	41:j:57:VAL:HG21	2.00	0.43
32:a:1074:G:O2'	32:a:1101:A:N1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:1137:C:H5'	32:a:1138:G:H5'	2.00	0.43
32:a:1226:C:OP2	44:m:90:ARG:NH2	2.43	0.43
32:a:1266:G:N2	32:a:1269:A:OP2	2.38	0.43
7:A:151:C:H2'	7:A:152:A:C8	2.53	0.43
7:A:483:A:H5''	26:U:47:LYS:HG2	1.99	0.43
7:A:514:A:N3	7:A:581:C:O2'	2.41	0.43
7:A:700:G:O2'	7:A:1632:A:N3	2.42	0.43
7:A:783:A:O2'	7:A:1779:U:O2	2.33	0.43
7:A:1405:U:H2'	7:A:1406:U:C6	2.54	0.43
30:Y:49:ASP:OD1	30:Y:52:ARG:NH2	2.47	0.43
30:Y:56:LEU:HA	30:Y:56:LEU:HD13	1.80	0.43
32:a:197:A:N1	32:a:220:G:O2'	2.48	0.43
32:a:266:G:H3'	48:q:69:LYS:HB2	2.00	0.43
32:a:337:G:H2'	32:a:338:A:C8	2.53	0.43
7:A:265:A:N1	7:A:427:U:O2'	2.48	0.43
7:A:563:A:H4'	22:Q:41:LYS:HE3	1.99	0.43
7:A:1889:A:N3	7:A:2086:U:O2'	2.43	0.43
10:D:26:VAL:HG22	10:D:188:LEU:HD22	2.01	0.43
28:W:71:VAL:HG22	28:W:78:LYS:HD2	2.00	0.43
32:a:451:A:OP2	47:p:70:ARG:NH2	2.44	0.43
32:a:591:U:H2'	32:a:592:G:C8	2.54	0.43
33:b:165:ASP:HB3	33:b:168:HIS:HB3	2.00	0.43
34:c:55:ILE:HG22	34:c:68:ILE:HG12	2.00	0.43
42:k:81:ASN:N	42:k:81:ASN:OD1	2.51	0.43
44:m:39:ILE:HG13	44:m:56:LEU:HD21	2.00	0.43
7:A:83:A:OP1	26:U:2:ALA:N	2.51	0.43
7:A:1597:A:H5''	7:A:1598:A:H5'	2.00	0.43
14:H:24:GLY:O	14:H:28:ASN:ND2	2.51	0.43
23:R:65:ALA:HB3	23:R:95:ASP:HB2	2.01	0.43
24:S:17:VAL:HB	24:S:76:VAL:HG11	2.01	0.43
32:a:1227:A:OP1	50:s:80:TYR:OH	2.35	0.43
51:t:5:LYS:HA	51:t:8:LYS:HD2	2.00	0.43
4:3:31:HIS:NE2	7:A:2392:A:OP2	2.50	0.43
7:A:1629:U:O4	7:A:1630:A:N6	2.51	0.43
7:A:2032:G:O2'	10:D:150:GLN:NE2	2.52	0.43
16:K:113:MET:HA	16:K:116:ILE:HG22	2.01	0.43
33:b:214:LEU:HA	33:b:217:VAL:HG22	1.99	0.43
36:e:56:VAL:HG21	55:y:54:TYR:HB3	2.01	0.43
38:g:13:LEU:HD21	40:i:47:VAL:HG22	2.00	0.43
42:k:60:PRO:HD3	42:k:91:PRO:HB2	1.99	0.43
44:m:79:ARG:NH1	50:s:65:GLU:OE1	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:n:16:LEU:HD22	45:n:20:TYR:HE2	1.84	0.43
49:r:71:THR:H	49:r:74:HIS:CE1	2.37	0.43
56:z:193:ALA:HB3	56:z:357:ILE:HG12	2.01	0.43
7:A:1579:A:H2'	7:A:1580:A:H8	1.83	0.43
7:A:2328:A:H2'	7:A:2329:U:C6	2.53	0.43
10:D:84:LEU:HD23	10:D:84:LEU:HA	1.89	0.43
18:M:26:VAL:HG13	18:M:104:GLU:HG2	2.01	0.43
32:a:269:C:H2'	32:a:270:A:C8	2.54	0.43
32:a:299:G:H2'	32:a:300:A:C8	2.54	0.43
32:a:555:U:H2'	32:a:556:C:C6	2.54	0.43
32:a:1368:A:OP1	41:j:64:GLN:NE2	2.47	0.43
32:a:1458:G:OP1	51:t:30:THR:OG1	2.31	0.43
56:z:204:SER:HB3	56:z:207:ASP:HB2	2.01	0.43
7:A:155:A:H2'	7:A:156:A:C8	2.54	0.43
7:A:223:A:N1	7:A:407:G:O2'	2.43	0.43
7:A:512:G:OP1	7:A:1234:U:O2'	2.30	0.43
7:A:602:A:O2'	7:A:604:G:O2'	2.32	0.43
7:A:1027:A:C2	7:A:2488:G:H5'	2.54	0.43
7:A:1093:G:H21	7:A:1098:A:H62	1.66	0.43
12:F:4:LEU:HD23	12:F:4:LEU:HA	1.87	0.43
30:Y:42:LEU:HA	30:Y:45:GLN:HG2	2.00	0.43
31:Z:5:ILE:O	31:Z:37:GLU:HA	2.18	0.43
32:a:1487:G:N7	55:y:2:ALA:N	2.67	0.43
33:b:93:ASN:OD1	33:b:93:ASN:N	2.47	0.43
15:J:45:THR:HG22	22:Q:64:ARG:HH21	1.84	0.42
32:a:41:G:H2'	32:a:42:G:H8	1.84	0.42
32:a:521:G:N7	43:l:50:ARG:NH2	2.67	0.42
32:a:744:C:H2'	32:a:745:G:H8	1.84	0.42
34:c:76:VAL:HG11	34:c:103:ILE:HD11	2.01	0.42
35:d:58:LYS:NZ	35:d:69:GLU:OE1	2.44	0.42
19:N:20:MET:HE2	19:N:20:MET:HB3	1.83	0.42
21:P:2:SER:HB3	21:P:5:ILE:HB	2.01	0.42
32:a:492:C:H2'	32:a:493:A:C8	2.54	0.42
33:b:8:ASP:OD1	33:b:8:ASP:N	2.52	0.42
35:d:37:ALA:HB3	35:d:42:GLY:HA2	2.01	0.42
41:j:52:LEU:HD11	41:j:59:LYS:HD2	2.01	0.42
47:p:12:LYS:HG2	47:p:13:LYS:HG2	2.01	0.42
7:A:60:G:O2'	7:A:62:U:OP2	2.34	0.42
7:A:558:U:H2'	7:A:559:G:H8	1.84	0.42
7:A:1476:U:H2'	7:A:1477:A:C8	2.54	0.42
37:f:30:THR:C	37:f:32:ALA:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:g:2:PRO:HB2	38:g:3:ARG:H	1.69	0.42
39:h:13:ARG:HD2	39:h:27:MET:HE2	2.01	0.42
39:h:96:MET:HE3	39:h:99:LEU:HB2	2.01	0.42
43:l:82:ILE:HA	43:l:96:HIS:O	2.19	0.42
47:p:5:ARG:NH2	47:p:23:ASP:O	2.52	0.42
7:A:1506:U:H2'	7:A:1507:C:C6	2.55	0.42
7:A:1797:G:O2'	9:C:257:THR:OG1	2.26	0.42
7:A:2315:G:H2'	7:A:2316:G:C8	2.54	0.42
7:A:2772:C:H5'	10:D:173:GLN:HE21	1.84	0.42
9:C:201:MET:HE3	32:a:773:G:H4'	2.01	0.42
15:J:99:ARG:HD2	15:J:99:ARG:HA	1.88	0.42
22:Q:91:ASP:OD1	22:Q:91:ASP:N	2.40	0.42
32:a:390:U:H2'	32:a:391:G:C8	2.54	0.42
32:a:527:G:O2'	32:a:535:A:N1	2.50	0.42
7:A:373:U:H2'	7:A:374:A:C8	2.54	0.42
7:A:1042:G:N2	7:A:1113:U:O2	2.33	0.42
7:A:2620:C:O2'	10:D:162:ALA:O	2.32	0.42
10:D:24:VAL:HG21	10:D:188:LEU:HD13	2.00	0.42
11:E:113:VAL:HB	11:E:118:LEU:HD23	2.01	0.42
12:F:110:ARG:NE	12:F:137:ILE:O	2.53	0.42
23:R:1:MET:HA	23:R:43:ASN:HB3	2.02	0.42
30:Y:19:LEU:HD23	30:Y:19:LEU:HA	1.86	0.42
43:l:24:LEU:HD23	43:l:24:LEU:HA	1.91	0.42
46:o:10:LYS:HA	46:o:10:LYS:HD2	1.88	0.42
50:s:37:ARG:O	50:s:70:LYS:NZ	2.41	0.42
54:x:73:A:H2'	56:z:277:ARG:HH11	1.84	0.42
6:5:26:SER:OG	6:5:27:THR:N	2.53	0.42
7:A:2:G:H2'	7:A:3:U:C6	2.55	0.42
7:A:2450:A:N6	7:A:2501:C:O2	2.52	0.42
7:A:2515:C:H2'	7:A:2516:A:H8	1.84	0.42
7:A:2618:G:H21	10:D:155:VAL:HG21	1.85	0.42
7:A:2681:C:OP2	10:D:114:LYS:NZ	2.34	0.42
8:B:8:C:OP1	20:O:15:ARG:NH2	2.53	0.42
32:a:212:G:H2'	32:a:213:G:H8	1.84	0.42
32:a:1011:C:H2'	32:a:1012:A:C8	2.53	0.42
38:g:70:ARG:HD3	38:g:100:ALA:HB2	2.02	0.42
38:g:150:ALA:HB2	42:k:52:PHE:HE1	1.85	0.42
40:i:27:LYS:HE3	40:i:27:LYS:HB2	1.93	0.42
43:l:80:ILE:HD12	43:l:97:THR:HG22	2.01	0.42
7:A:2245:U:H5''	7:A:2246:G:H5'	2.01	0.42
7:A:2315:G:H2'	7:A:2316:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:48:U:H4'	20:O:100:HIS:CE1	2.54	0.42
26:U:3:ALA:O	26:U:6:ARG:NH2	2.35	0.42
31:Z:27:LEU:HG	31:Z:47:MET:HE2	2.00	0.42
32:a:927:G:O2'	32:a:1503:A:N7	2.42	0.42
32:a:1308:U:H2'	32:a:1309:G:C8	2.54	0.42
46:o:80:GLN:O	46:o:84:ARG:HB2	2.20	0.42
7:A:396:G:H1'	29:X:29:PHE:HB3	2.01	0.42
7:A:848:C:H2'	7:A:849:A:C8	2.54	0.42
7:A:1847:A:O2'	7:A:1848:A:N7	2.48	0.42
18:M:12:MET:HE3	18:M:12:MET:HB2	1.83	0.42
32:a:539:A:H2'	32:a:540:G:C8	2.54	0.42
32:a:672:U:H2'	32:a:673:A:H8	1.85	0.42
32:a:689:C:O2'	32:a:705:G:O2'	2.38	0.42
32:a:1243:C:H2'	32:a:1244:G:H8	1.85	0.42
32:a:1277:C:H2'	32:a:1279:G:H21	1.84	0.42
34:c:33:LEU:HD23	34:c:33:LEU:HA	1.90	0.42
39:h:18:GLN:HE21	39:h:72:VAL:HB	1.85	0.42
50:s:33:THR:HG23	50:s:51:VAL:HG23	2.02	0.42
56:z:274:GLN:HG3	56:z:275:THR:HG23	2.02	0.42
7:A:1939:U:OP1	7:A:2604:U:O2'	2.30	0.42
7:A:1992:G:N2	7:A:1996:C:O2'	2.52	0.42
7:A:2655:G:O2'	7:A:2664:G:N1	2.32	0.42
21:P:93:ARG:HE	21:P:93:ARG:HB2	1.65	0.42
32:a:477:C:H2'	32:a:478:A:C8	2.55	0.42
32:a:1149:C:H2'	32:a:1150:A:H8	1.84	0.42
7:A:76:C:H1'	30:Y:55:THR:HG21	2.01	0.42
7:A:742:A:H2'	7:A:743:A:C8	2.55	0.42
7:A:1115:G:H2'	7:A:1116:G:H8	1.84	0.42
9:C:117:GLN:HG3	9:C:122:ALA:HB1	2.01	0.42
11:E:196:VAL:HA	11:E:199:MET:HE2	2.01	0.42
15:J:49:ASP:OD1	15:J:121:LYS:NZ	2.43	0.42
16:K:42:THR:HG23	16:K:44:LYS:HD3	2.02	0.42
18:M:102:LEU:HD11	18:M:126:ILE:HD11	2.01	0.42
32:a:509:A:N3	32:a:543:U:O2'	2.47	0.42
37:f:88:MET:HE1	49:r:61:ARG:HG2	2.01	0.42
43:l:4:VAL:HG13	48:q:34:TYR:HB3	2.01	0.42
51:t:85:LYS:HE3	51:t:85:LYS:HB3	1.89	0.42
54:x:35:G:O2'	56:z:172:GLU:OE2	2.37	0.42
7:A:1:G:H2'	7:A:2:G:H8	1.85	0.41
7:A:320:A:H4'	7:A:322:A:C8	2.55	0.41
7:A:1802:A:H2'	7:A:1803:A:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1914:C:H1'	56:z:132:HIS:CE1	2.55	0.41
10:D:33:ARG:HB3	10:D:73:VAL:HG11	2.02	0.41
10:D:156:PHE:HB3	15:J:81:ILE:HG22	2.02	0.41
16:K:63:VAL:HB	16:K:103:VAL:HG12	2.01	0.41
32:a:1119:C:H2'	32:a:1120:C:H6	1.85	0.41
32:a:1220:G:P	45:n:53:ARG:HH22	2.42	0.41
32:a:1405:G:H21	32:a:1518:A:H8	1.67	0.41
44:m:83:LEU:HD11	50:s:66:MET:HG2	2.01	0.41
13:G:50:LEU:HD23	13:G:50:LEU:HA	1.92	0.41
24:S:17:VAL:HG11	24:S:103:ILE:HG12	2.02	0.41
32:a:501:C:OP1	43:l:114:ARG:NH2	2.39	0.41
32:a:511:C:O2'	32:a:512:U:O4'	2.37	0.41
34:c:157:LEU:HA	34:c:157:LEU:HD23	1.85	0.41
48:q:25:ILE:HD12	48:q:44:LEU:HD12	2.01	0.41
15:J:7:LYS:HB2	15:J:10:THR:HG22	2.00	0.41
17:L:19:LEU:HA	17:L:27:LEU:HD13	2.02	0.41
24:S:85:ILE:HG23	24:S:93:ALA:HB1	2.02	0.41
32:a:184:G:H2'	32:a:185:U:C6	2.55	0.41
32:a:746:A:H2'	32:a:747:A:C8	2.55	0.41
32:a:1512:U:H2'	32:a:1513:A:C8	2.55	0.41
33:b:149:GLY:HA2	33:b:152:LYS:HB3	2.02	0.41
56:z:26:LEU:HD13	56:z:29:LYS:HD3	2.02	0.41
5:4:23:ILE:HB	5:4:38:GLY:HA3	2.01	0.41
21:P:22:PRO:HD3	21:P:50:ILE:HD12	2.02	0.41
48:q:57:ASP:OD1	48:q:57:ASP:N	2.50	0.41
7:A:1136:G:O2'	7:A:2038:G:O2'	2.28	0.41
7:A:1590:A:H2'	7:A:1591:A:H8	1.86	0.41
15:J:109:LEU:HD13	15:J:118:MET:HG3	2.02	0.41
32:a:718:A:O2'	52:u:35:ARG:NH2	2.53	0.41
32:a:1229:A:O2'	54:x:30:C:OP1	2.38	0.41
38:g:88:PRO:HG3	38:g:149:LYS:HA	2.02	0.41
7:A:863:A:H2'	7:A:864:G:H8	1.85	0.41
7:A:871:U:H2'	7:A:872:U:C6	2.55	0.41
7:A:1028:A:N6	7:A:1125:G:H2'	2.36	0.41
7:A:1689:A:H2'	7:A:1690:A:C8	2.56	0.41
7:A:2364:C:OP1	28:W:55:ARG:NH1	2.52	0.41
11:E:176:ASP:OD1	11:E:176:ASP:N	2.47	0.41
27:V:68:LYS:HZ2	27:V:70:ILE:HG12	1.86	0.41
27:V:75:GLN:HB2	27:V:92:VAL:HG23	2.01	0.41
29:X:44:LYS:HD2	29:X:44:LYS:HA	1.85	0.41
32:a:1135:U:O2'	32:a:1138:G:O6	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:1241:G:H2'	32:a:1242:G:H8	1.85	0.41
32:a:1488:G:H2'	32:a:1489:G:H8	1.85	0.41
33:b:7:ARG:H	33:b:7:ARG:HG2	1.68	0.41
41:j:15:HIS:HA	41:j:18:ILE:HG22	2.02	0.41
43:l:49:LEU:HD23	43:l:49:LEU:HA	1.93	0.41
46:o:39:LEU:HA	46:o:39:LEU:HD23	1.86	0.41
56:z:326:VAL:HG13	56:z:329:PRO:HD2	2.02	0.41
7:A:743:A:O2'	7:A:1659:G:OP1	2.36	0.41
7:A:1019:U:O2'	7:A:1021:A:N7	2.51	0.41
42:k:56:ARG:O	42:k:59:THR:OG1	2.39	0.41
6:5:28:VAL:HG22	12:F:140:GLU:HA	2.03	0.41
7:A:151:C:H2'	7:A:152:A:H8	1.85	0.41
7:A:366:C:H2'	7:A:367:G:C8	2.56	0.41
7:A:1086:A:O2'	7:A:1087:G:N7	2.52	0.41
7:A:2087:G:H2'	7:A:2088:A:C8	2.56	0.41
7:A:2124:G:N7	7:A:2125:G:O2'	2.45	0.41
8:B:45:A:O4'	12:F:92:ARG:NH2	2.54	0.41
9:C:75:PRO:HA	9:C:117:GLN:HB3	2.02	0.41
12:F:147:ASP:OD1	12:F:147:ASP:N	2.46	0.41
14:H:12:LEU:HD22	14:H:19:VAL:HG11	2.03	0.41
24:S:13:SER:HB3	24:S:16:LYS:HD2	2.03	0.41
32:a:83:C:O2'	32:a:85:U:OP2	2.32	0.41
33:b:20:THR:HG22	33:b:39:HIS:CE1	2.56	0.41
34:c:36:ASP:OD1	34:c:59:ARG:NH2	2.51	0.41
37:f:78:PHE:HA	37:f:84:VAL:HG11	2.03	0.41
1:0:49:TYR:OH	7:A:2883:A:OP1	2.35	0.41
4:3:51:SER:O	4:3:55:LEU:N	2.48	0.41
7:A:414:C:H2'	7:A:415:A:C8	2.55	0.41
7:A:1009:A:N3	7:A:1153:C:O2'	2.45	0.41
7:A:1316:U:H2'	7:A:1317:G:H8	1.86	0.41
7:A:1441:G:H2'	7:A:1442:U:C6	2.56	0.41
7:A:1746:A:H2'	7:A:1747:U:C6	2.56	0.41
7:A:2104:C:H2'	7:A:2105:U:H5	1.86	0.41
7:A:2210:U:H4'	7:A:2211:A:H5'	2.03	0.41
7:A:2808:G:O2'	7:A:2809:A:H8	2.03	0.41
9:C:145:GLU:HA	9:C:152:GLY:HA2	2.02	0.41
11:E:5:LEU:HB2	11:E:10:SER:H	1.85	0.41
32:a:6:G:N2	36:e:103:THR:HG21	2.36	0.41
32:a:993:G:N7	32:a:1213:A:N6	2.69	0.41
32:a:1011:C:H2'	32:a:1012:A:H8	1.86	0.41
32:a:1323:G:H2'	32:a:1324:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:1346:A:N1	32:a:1374:A:H5''	2.35	0.41
32:a:1507:A:H2'	32:a:1508:A:C8	2.56	0.41
35:d:85:ASN:HB3	35:d:88:GLU:HG2	2.02	0.41
35:d:177:LYS:HE3	35:d:177:LYS:HB2	1.87	0.41
38:g:113:ASP:OD1	38:g:119:ARG:HG3	2.21	0.41
42:k:64:GLN:HG3	42:k:99:ALA:HB2	2.02	0.41
49:r:24:LYS:HE2	49:r:24:LYS:HB2	1.95	0.41
54:x:68:C:H2'	54:x:69:A:C8	2.56	0.41
56:z:298:ARG:NH1	56:z:301:GLU:OE2	2.54	0.41
7:A:286:U:H2'	7:A:287:G:C8	2.54	0.41
7:A:1035:U:H2'	7:A:1036:G:H8	1.85	0.41
7:A:1796:U:H2'	7:A:1797:G:H8	1.85	0.41
7:A:2360:G:H1'	17:L:60:ARG:HD2	2.03	0.41
7:A:2692:G:H1'	7:A:2847:U:H1'	2.03	0.41
9:C:69:ARG:O	9:C:189:ARG:NH1	2.54	0.41
19:N:12:ARG:HG2	19:N:16:HIS:ND1	2.36	0.41
25:T:68:LYS:HA	25:T:68:LYS:HD3	1.89	0.41
32:a:210:C:H4'	32:a:211:G:C2	2.55	0.41
32:a:235:C:H2'	32:a:236:A:C8	2.56	0.41
42:k:97:ILE:HD11	52:u:16:LEU:HD13	2.03	0.41
56:z:296:GLN:O	56:z:300:GLU:HG2	2.21	0.41
7:A:181:A:H2'	7:A:182:A:C8	2.56	0.40
7:A:2006:C:O2'	7:A:2823:A:N3	2.53	0.40
7:A:2246:G:H2'	7:A:2247:A:C8	2.56	0.40
17:L:2:ARG:HD3	17:L:2:ARG:HA	1.81	0.40
30:Y:37:LEU:HD11	30:Y:42:LEU:HD12	2.03	0.40
32:a:41:G:H2'	32:a:42:G:C8	2.56	0.40
32:a:1001:C:H2'	32:a:1002:G:H8	1.86	0.40
36:e:150:PRO:HA	36:e:153:VAL:HG12	2.03	0.40
41:j:23:ALA:HA	41:j:26:VAL:HG12	2.04	0.40
41:j:25:ILE:HG13	41:j:87:LEU:HD11	2.03	0.40
45:n:61:ARG:HD2	45:n:61:ARG:HA	1.86	0.40
46:o:64:ARG:O	46:o:64:ARG:NH1	2.54	0.40
56:z:111:GLU:O	56:z:115:GLN:HG3	2.21	0.40
56:z:287:MET:HE3	56:z:291:LYS:HG2	2.03	0.40
7:A:639:U:H2'	7:A:640:C:C6	2.56	0.40
7:A:872:U:H2'	7:A:873:C:C6	2.56	0.40
7:A:1222:U:H2'	7:A:1223:G:H8	1.87	0.40
7:A:1366:A:H5'	29:X:11:ARG:HH22	1.85	0.40
32:a:216:U:H2'	32:a:217:C:C6	2.57	0.40
32:a:501:C:H2'	32:a:502:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:613:C:H2'	32:a:614:C:C6	2.57	0.40
32:a:1071:C:H2'	32:a:1072:G:C8	2.55	0.40
34:c:111:LEU:O	34:c:204:LYS:NZ	2.39	0.40
35:d:11:LEU:HD13	35:d:63:ARG:HG2	2.03	0.40
36:e:160:SER:OG	36:e:161:VAL:N	2.54	0.40
41:j:8:ILE:HG21	41:j:25:ILE:HD13	2.03	0.40
48:q:31:HIS:CD2	48:q:34:TYR:H	2.40	0.40
51:t:39:ILE:HD11	51:t:83:ILE:HG13	2.03	0.40
4:3:15:LYS:HB2	4:3:23:LYS:HE3	2.03	0.40
7:A:172:A:H2'	7:A:173:A:C8	2.56	0.40
7:A:181:A:H2'	7:A:182:A:H8	1.85	0.40
7:A:1222:U:H2'	7:A:1223:G:C8	2.55	0.40
13:G:72:LEU:HD23	13:G:72:LEU:HA	1.91	0.40
17:L:77:ILE:HG23	17:L:110:VAL:HA	2.03	0.40
18:M:125:PRO:HG2	18:M:126:ILE:HG23	2.04	0.40
26:U:9:ASP:O	26:U:24:LYS:HG3	2.22	0.40
32:a:510:A:O2'	32:a:542:G:O2'	2.39	0.40
32:a:1147:C:O2'	40:i:7:TYR:OH	2.25	0.40
32:a:1213:A:O2'	32:a:1215:G:N7	2.51	0.40
32:a:1414:U:H2'	32:a:1415:G:H8	1.85	0.40
38:g:13:LEU:HD12	38:g:14:PRO:HD2	2.03	0.40
56:z:125:ASN:ND2	56:z:224:GLU:O	2.43	0.40
2:1:21:TYR:OH	7:A:2347:C:O2'	2.36	0.40
7:A:589:U:H2'	7:A:590:A:H8	1.86	0.40
7:A:2698:U:H2'	7:A:2699:C:C6	2.56	0.40
13:G:54:PRO:HB3	13:G:61:GLY:HA3	2.03	0.40
15:J:36:LEU:HD11	15:J:122:LEU:HB2	2.03	0.40
15:J:63:ALA:HA	15:J:69:ARG:HH21	1.86	0.40
20:O:39:VAL:HG11	20:O:87:ILE:HG21	2.03	0.40
22:Q:11:ARG:HE	22:Q:11:ARG:HB2	1.65	0.40
50:s:35:SER:OG	50:s:38:SER:OG	2.37	0.40
54:x:16:C:OP2	54:x:17:C:N4	2.54	0.40
56:z:289:MET:HA	56:z:292:ALA:HB3	2.02	0.40
7:A:240:C:H3'	7:A:241:A:H2'	2.04	0.40
7:A:1093:G:N2	7:A:1098:A:H62	2.20	0.40
7:A:1219:U:H2'	7:A:1220:G:C8	2.56	0.40
7:A:1858:A:H2'	7:A:1859:U:O4'	2.21	0.40
7:A:2543:G:H2'	7:A:2544:G:C8	2.56	0.40
16:K:78:ARG:HH11	16:K:78:ARG:HD3	1.77	0.40
21:P:88:ARG:HE	21:P:112:GLU:HG2	1.87	0.40
22:Q:103:LYS:HE2	22:Q:103:LYS:HB2	1.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:82:G:H2'	32:a:83:C:C6	2.57	0.40
32:a:460:A:H2'	32:a:461:A:C8	2.56	0.40
32:a:1317:C:OP2	45:n:28:LYS:NZ	2.40	0.40
32:a:1488:G:H2'	32:a:1489:G:C8	2.56	0.40
36:e:81:LEU:HD21	36:e:96:MET:HE3	2.04	0.40
38:g:27:VAL:HG12	38:g:43:VAL:HG11	2.03	0.40
43:l:90:LEU:HD23	43:l:90:LEU:HA	1.96	0.40
50:s:17:LYS:HE3	50:s:17:LYS:HB3	1.93	0.40
56:z:212:ARG:HD3	56:z:328:HIS:ND1	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	53/57 (93%)	50 (94%)	3 (6%)	0	100	100
2	1	48/55 (87%)	43 (90%)	5 (10%)	0	100	100
3	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
4	3	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	7	26
5	4	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
6	5	63/70 (90%)	54 (86%)	9 (14%)	0	100	100
9	C	269/273 (98%)	247 (92%)	22 (8%)	0	100	100
10	D	207/209 (99%)	188 (91%)	19 (9%)	0	100	100
11	E	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
12	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
13	G	172/177 (97%)	153 (89%)	19 (11%)	0	100	100
14	H	147/149 (99%)	121 (82%)	26 (18%)	0	100	100
15	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	K	120/123 (98%)	110 (92%)	10 (8%)	0	100	100
17	L	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
18	M	134/136 (98%)	129 (96%)	4 (3%)	1 (1%)	18	45
19	N	116/127 (91%)	105 (90%)	11 (10%)	0	100	100
20	O	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
21	P	112/115 (97%)	104 (93%)	8 (7%)	0	100	100
22	Q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
23	R	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
24	S	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
25	T	87/100 (87%)	81 (93%)	6 (7%)	0	100	100
26	U	100/104 (96%)	86 (86%)	14 (14%)	0	100	100
27	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
28	W	73/85 (86%)	70 (96%)	3 (4%)	0	100	100
29	X	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
30	Y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
31	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
33	b	222/241 (92%)	203 (91%)	19 (9%)	0	100	100
34	c	204/233 (88%)	191 (94%)	13 (6%)	0	100	100
35	d	203/206 (98%)	190 (94%)	13 (6%)	0	100	100
36	e	155/167 (93%)	142 (92%)	13 (8%)	0	100	100
37	f	97/135 (72%)	92 (95%)	5 (5%)	0	100	100
38	g	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
39	h	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
40	i	125/130 (96%)	112 (90%)	13 (10%)	0	100	100
41	j	96/103 (93%)	86 (90%)	10 (10%)	0	100	100
42	k	115/129 (89%)	105 (91%)	10 (9%)	0	100	100
43	l	121/124 (98%)	108 (89%)	13 (11%)	0	100	100
44	m	112/118 (95%)	97 (87%)	15 (13%)	0	100	100
45	n	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
46	o	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	10	32
47	p	80/82 (98%)	71 (89%)	9 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	q	78/84 (93%)	68 (87%)	10 (13%)	0	100	100
49	r	64/75 (85%)	64 (100%)	0	0	100	100
50	s	81/92 (88%)	79 (98%)	2 (2%)	0	100	100
51	t	84/87 (97%)	82 (98%)	2 (2%)	0	100	100
52	u	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
55	y	52/71 (73%)	46 (88%)	6 (12%)	0	100	100
56	z	360/362 (99%)	324 (90%)	34 (9%)	2 (1%)	21	48
All	All	5998/6346 (94%)	5546 (92%)	447 (8%)	5 (0%)	49	75

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
56	z	90	PRO
46	o	47	LYS
56	z	89	GLU
18	M	69	PRO
4	3	32	ILE

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	
1	0	46/48 (96%)	46 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	50 (98%)	1 (2%)	48	69
5	4	34/34 (100%)	34 (100%)	0	100	100
6	5	58/62 (94%)	56 (97%)	2 (3%)	32	59
9	C	216/218 (99%)	216 (100%)	0	100	100
10	D	164/164 (100%)	162 (99%)	2 (1%)	63	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	E	165/165 (100%)	165 (100%)	0	100	100
12	F	148/150 (99%)	147 (99%)	1 (1%)	76	80
13	G	135/138 (98%)	134 (99%)	1 (1%)	76	80
14	H	114/114 (100%)	114 (100%)	0	100	100
15	J	116/116 (100%)	115 (99%)	1 (1%)	70	78
16	K	103/104 (99%)	103 (100%)	0	100	100
17	L	103/103 (100%)	102 (99%)	1 (1%)	68	77
18	M	109/109 (100%)	109 (100%)	0	100	100
19	N	98/103 (95%)	98 (100%)	0	100	100
20	O	86/87 (99%)	84 (98%)	2 (2%)	44	66
21	P	99/100 (99%)	99 (100%)	0	100	100
22	Q	89/90 (99%)	89 (100%)	0	100	100
23	R	84/84 (100%)	84 (100%)	0	100	100
24	S	93/93 (100%)	92 (99%)	1 (1%)	65	76
25	T	77/84 (92%)	76 (99%)	1 (1%)	61	74
26	U	83/85 (98%)	82 (99%)	1 (1%)	63	75
27	V	78/78 (100%)	78 (100%)	0	100	100
28	W	57/63 (90%)	57 (100%)	0	100	100
29	X	67/68 (98%)	67 (100%)	0	100	100
30	Y	55/55 (100%)	55 (100%)	0	100	100
31	Z	48/49 (98%)	48 (100%)	0	100	100
33	b	186/199 (94%)	185 (100%)	1 (0%)	81	82
34	c	170/190 (90%)	167 (98%)	3 (2%)	51	70
35	d	172/173 (99%)	171 (99%)	1 (1%)	78	81
36	e	119/126 (94%)	118 (99%)	1 (1%)	73	79
37	f	86/116 (74%)	83 (96%)	3 (4%)	32	59
38	g	124/147 (84%)	124 (100%)	0	100	100
39	h	104/105 (99%)	104 (100%)	0	100	100
40	i	105/107 (98%)	104 (99%)	1 (1%)	68	77
41	j	86/90 (96%)	85 (99%)	1 (1%)	63	75
42	k	90/99 (91%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	l	103/104 (99%)	102 (99%)	1 (1%)	68	77
44	m	92/96 (96%)	92 (100%)	0	100	100
45	n	83/84 (99%)	83 (100%)	0	100	100
46	o	76/77 (99%)	75 (99%)	1 (1%)	61	74
47	p	65/65 (100%)	65 (100%)	0	100	100
48	q	74/78 (95%)	74 (100%)	0	100	100
49	r	57/65 (88%)	57 (100%)	0	100	100
50	s	72/79 (91%)	72 (100%)	0	100	100
51	t	65/66 (98%)	65 (100%)	0	100	100
52	u	60/61 (98%)	60 (100%)	0	100	100
55	y	47/61 (77%)	47 (100%)	0	100	100
56	z	267/319 (84%)	266 (100%)	1 (0%)	84	84
All	All	4962/5210 (95%)	4934 (99%)	28 (1%)	76	81

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	3	32	ILE
6	5	27	THR
6	5	37	CYS
10	D	22	ILE
10	D	107	VAL
12	F	149	VAL
13	G	162	VAL
15	J	17	VAL
17	L	27	LEU
20	O	47	VAL
20	O	62	LEU
24	S	29	VAL
25	T	34	VAL
26	U	49	VAL
33	b	163	VAL
34	c	26	THR
34	c	55	ILE
34	c	56	VAL
35	d	125	VAL
36	e	80	THR
37	f	7	VAL

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Mol	Chain	Res	Type
37	f	35	LYS
37	f	84	VAL
40	i	58	VAL
41	j	92	LEU
43	l	87	VAL
46	o	87	LEU
56	z	221	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	6	ASN
2	1	45	GLN
3	2	29	GLN
4	3	43	HIS
5	4	33	HIS
6	5	20	ASN
6	5	30	HIS
9	C	25	HIS
9	C	86	ASN
9	C	128	ASN
9	C	243	HIS
10	D	32	ASN
10	D	49	GLN
10	D	67	HIS
10	D	130	GLN
10	D	150	GLN
10	D	164	GLN
10	D	173	GLN
11	E	41	GLN
11	E	92	HIS
12	F	52	ASN
12	F	63	GLN
13	G	22	GLN
13	G	45	HIS
13	G	48	ASN
13	G	64	GLN
13	G	73	ASN
14	H	20	ASN
14	H	28	ASN
14	H	128	HIS
14	H	133	GLN

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Mol	Chain	Res	Type
14	H	145	ASN
16	K	9	ASN
18	M	13	HIS
18	M	22	GLN
20	O	100	HIS
20	O	104	GLN
21	P	10	GLN
21	P	41	GLN
21	P	52	ASN
22	Q	20	GLN
23	R	11	GLN
25	T	59	ASN
26	U	27	ASN
26	U	54	GLN
26	U	69	ASN
26	U	74	ASN
28	W	76	ASN
30	Y	15	ASN
30	Y	20	ASN
30	Y	31	GLN
30	Y	36	GLN
33	b	120	GLN
33	b	146	ASN
34	c	102	ASN
35	d	36	GLN
35	d	100	ASN
35	d	140	ASN
36	e	146	ASN
37	f	63	ASN
37	f	81	ASN
38	g	9	GLN
38	g	52	GLN
38	g	97	ASN
39	h	18	GLN
39	h	38	ASN
40	i	5	GLN
40	i	50	GLN
40	i	110	GLN
40	i	126	GLN
42	k	24	HIS
42	k	118	HIS
46	o	35	GLN

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Mol	Chain	Res	Type
47	p	26	ASN
47	p	40	ASN
47	p	59	HIS
47	p	63	GLN
48	q	31	HIS
49	r	75	GLN
50	s	14	HIS
50	s	43	ASN
52	u	64	ASN
55	y	12	HIS
56	z	115	GLN
56	z	126	ASN
56	z	141	GLN
56	z	186	ASN
56	z	252	HIS
56	z	254	ASN
56	z	303	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	a	1539/1540 (99%)	272 (17%)	0
53	v	5/6 (83%)	0	0
54	x	76/77 (98%)	18 (23%)	0
7	A	2902/2903 (99%)	622 (21%)	28 (0%)
8	B	119/120 (99%)	19 (15%)	3 (2%)
All	All	4641/4646 (99%)	931 (20%)	31 (0%)

All (931) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	3	U
7	A	10	A
7	A	13	A
7	A	15	G
7	A	23	G
7	A	36	G
7	A	46	G
7	A	50	U
7	A	51	G
7	A	55	G

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Mol	Chain	Res	Type
7	A	60	G
7	A	61	C
7	A	62	U
7	A	63	A
7	A	71	A
7	A	74	A
7	A	75	G
7	A	76	C
7	A	84	A
7	A	91	A
7	A	96	C
7	A	98	G
7	A	102	U
7	A	103	A
7	A	110	G
7	A	118	A
7	A	119	A
7	A	120	U
7	A	135	U
7	A	137	U
7	A	138	U
7	A	140	C
7	A	141	G
7	A	157	C
7	A	160	A
7	A	163	C
7	A	166	U
7	A	181	A
7	A	196	A
7	A	199	A
7	A	204	A
7	A	215	G
7	A	216	A
7	A	218	A
7	A	222	A
7	A	228	C
7	A	233	A
7	A	241	A
7	A	242	G
7	A	243	U
7	A	244	A
7	A	245	G

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Mol	Chain	Res	Type
7	A	248	G
7	A	249	C
7	A	250	G
7	A	255	A
7	A	265	A
7	A	267	C
7	A	274	C
7	A	275	C
7	A	277	G
7	A	278	A
7	A	279	A
7	A	281	C
7	A	285	G
7	A	294	A
7	A	311	A
7	A	323	C
7	A	329	G
7	A	330	A
7	A	350	G
7	A	352	A
7	A	353	C
7	A	356	G
7	A	358	U
7	A	359	G
7	A	361	G
7	A	371	A
7	A	372	G
7	A	386	G
7	A	387	U
7	A	391	A
7	A	396	G
7	A	403	U
7	A	404	A
7	A	405	U
7	A	406	G
7	A	411	G
7	A	424	G
7	A	435	C
7	A	447	A
7	A	456	C
7	A	457	A
7	A	467	G

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Mol	Chain	Res	Type
7	A	471	A
7	A	480	A
7	A	481	G
7	A	489	G
7	A	491	G
7	A	496	G
7	A	505	A
7	A	508	A
7	A	510	C
7	A	512	G
7	A	518	G
7	A	527	C
7	A	531	C
7	A	532	A
7	A	546	U
7	A	547	A
7	A	548	G
7	A	556	A
7	A	563	A
7	A	573	U
7	A	575	A
7	A	586	A
7	A	603	A
7	A	613	A
7	A	614	A
7	A	615	U
7	A	616	A
7	A	622	G
7	A	627	A
7	A	634	C
7	A	637	A
7	A	643	A
7	A	645	C
7	A	646	U
7	A	647	G
7	A	654	A
7	A	668	A
7	A	669	G
7	A	670	A
7	A	684	G
7	A	686	U
7	A	693	A

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Mol	Chain	Res	Type
7	A	694	U
7	A	695	G
7	A	714	U
7	A	717	C
7	A	726	G
7	A	728	G
7	A	730	A
7	A	738	G
7	A	740	C
7	A	745	G
7	A	746	U
7	A	747	U
7	A	748	G
7	A	749	A
7	A	753	A
7	A	764	A
7	A	775	G
7	A	776	G
7	A	782	A
7	A	784	G
7	A	785	G
7	A	789	A
7	A	790	U
7	A	792	A
7	A	793	A
7	A	794	A
7	A	799	G
7	A	805	G
7	A	806	C
7	A	811	U
7	A	812	C
7	A	819	A
7	A	827	U
7	A	828	U
7	A	830	G
7	A	845	A
7	A	846	U
7	A	847	U
7	A	858	G
7	A	860	U
7	A	869	G
7	A	878	A

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Mol	Chain	Res	Type
7	A	881	G
7	A	882	G
7	A	883	G
7	A	884	U
7	A	887	U
7	A	888	C
7	A	889	C
7	A	890	C
7	A	891	G
7	A	892	A
7	A	893	C
7	A	897	C
7	A	899	A
7	A	906	U
7	A	907	G
7	A	910	A
7	A	914	G
7	A	927	A
7	A	941	A
7	A	945	A
7	A	946	C
7	A	953	G
7	A	961	C
7	A	973	A
7	A	974	G
7	A	975	A
7	A	982	C
7	A	983	A
7	A	989	G
7	A	996	A
7	A	1005	C
7	A	1006	C
7	A	1011	G
7	A	1012	U
7	A	1013	C
7	A	1018	U
7	A	1020	A
7	A	1021	A
7	A	1022	G
7	A	1023	U
7	A	1025	G
7	A	1026	G

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Mol	Chain	Res	Type
7	A	1033	U
7	A	1046	A
7	A	1047	G
7	A	1048	A
7	A	1052	C
7	A	1055	G
7	A	1057	A
7	A	1058	U
7	A	1059	G
7	A	1060	U
7	A	1061	U
7	A	1062	G
7	A	1063	G
7	A	1066	U
7	A	1067	A
7	A	1068	G
7	A	1070	A
7	A	1071	G
7	A	1072	C
7	A	1074	G
7	A	1075	C
7	A	1076	C
7	A	1077	A
7	A	1078	U
7	A	1079	C
7	A	1080	A
7	A	1081	U
7	A	1083	U
7	A	1085	A
7	A	1088	A
7	A	1089	A
7	A	1090	A
7	A	1101	U
7	A	1103	A
7	A	1104	C
7	A	1111	A
7	A	1112	G
7	A	1113	U
7	A	1114	C
7	A	1119	U
7	A	1130	U
7	A	1131	G

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Mol	Chain	Res	Type
7	A	1132	U
7	A	1133	A
7	A	1134	A
7	A	1135	C
7	A	1139	G
7	A	1142	A
7	A	1157	G
7	A	1171	G
7	A	1172	C
7	A	1173	U
7	A	1174	U
7	A	1175	A
7	A	1176	U
7	A	1177	G
7	A	1178	C
7	A	1180	U
7	A	1186	G
7	A	1204	A
7	A	1211	C
7	A	1212	G
7	A	1236	G
7	A	1247	A
7	A	1250	G
7	A	1253	A
7	A	1255	U
7	A	1256	G
7	A	1271	G
7	A	1272	A
7	A	1273	U
7	A	1289	C
7	A	1300	G
7	A	1301	A
7	A	1305	C
7	A	1312	U
7	A	1321	A
7	A	1340	U
7	A	1341	G
7	A	1342	A
7	A	1343	G
7	A	1345	C
7	A	1352	U
7	A	1359	A

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Mol	Chain	Res	Type
7	A	1360	G
7	A	1365	A
7	A	1368	G
7	A	1378	A
7	A	1379	U
7	A	1383	A
7	A	1385	A
7	A	1386	C
7	A	1403	A
7	A	1414	C
7	A	1416	G
7	A	1419	A
7	A	1421	G
7	A	1427	A
7	A	1428	C
7	A	1437	C
7	A	1454	C
7	A	1456	G
7	A	1458	U
7	A	1459	G
7	A	1460	U
7	A	1461	C
7	A	1468	U
7	A	1482	G
7	A	1483	G
7	A	1490	A
7	A	1503	A
7	A	1504	A
7	A	1508	A
7	A	1509	A
7	A	1515	A
7	A	1522	A
7	A	1524	G
7	A	1529	G
7	A	1533	C
7	A	1534	U
7	A	1535	A
7	A	1536	C
7	A	1542	U
7	A	1544	A
7	A	1554	U
7	A	1555	G

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Mol	Chain	Res	Type
7	A	1558	C
7	A	1559	U
7	A	1560	G
7	A	1566	A
7	A	1569	A
7	A	1578	U
7	A	1581	G
7	A	1584	U
7	A	1585	C
7	A	1587	G
7	A	1607	C
7	A	1608	A
7	A	1610	A
7	A	1611	C
7	A	1613	G
7	A	1622	G
7	A	1627	G
7	A	1647	U
7	A	1648	U
7	A	1649	G
7	A	1669	A
7	A	1674	G
7	A	1693	U
7	A	1695	G
7	A	1715	G
7	A	1725	U
7	A	1726	C
7	A	1729	U
7	A	1730	C
7	A	1732	C
7	A	1735	A
7	A	1738	G
7	A	1757	A
7	A	1764	C
7	A	1773	A
7	A	1776	G
7	A	1780	A
7	A	1784	A
7	A	1786	A
7	A	1787	A
7	A	1800	C
7	A	1801	A

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Mol	Chain	Res	Type
7	A	1807	G
7	A	1808	A
7	A	1815	A
7	A	1816	C
7	A	1817	G
7	A	1820	U
7	A	1829	A
7	A	1833	C
7	A	1848	A
7	A	1858	A
7	A	1870	C
7	A	1884	G
7	A	1896	G
7	A	1900	A
7	A	1901	A
7	A	1906	G
7	A	1912	A
7	A	1913	A
7	A	1914	C
7	A	1915	U
7	A	1927	A
7	A	1929	G
7	A	1930	G
7	A	1931	U
7	A	1941	C
7	A	1955	U
7	A	1966	A
7	A	1967	C
7	A	1970	A
7	A	1971	U
7	A	1972	G
7	A	1981	A
7	A	1982	U
7	A	1991	U
7	A	1992	G
7	A	1993	U
7	A	1996	C
7	A	1997	C
7	A	2020	A
7	A	2022	U
7	A	2023	C
7	A	2030	A

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Mol	Chain	Res	Type
7	A	2031	A
7	A	2033	A
7	A	2035	G
7	A	2036	C
7	A	2043	C
7	A	2052	A
7	A	2055	C
7	A	2056	G
7	A	2060	A
7	A	2061	G
7	A	2062	A
7	A	2063	C
7	A	2069	G
7	A	2072	C
7	A	2093	G
7	A	2096	C
7	A	2098	U
7	A	2101	A
7	A	2102	G
7	A	2105	U
7	A	2106	U
7	A	2111	U
7	A	2112	G
7	A	2113	U
7	A	2114	A
7	A	2115	G
7	A	2116	G
7	A	2117	A
7	A	2118	U
7	A	2125	G
7	A	2130	U
7	A	2131	U
7	A	2132	U
7	A	2133	G
7	A	2134	A
7	A	2135	A
7	A	2136	G
7	A	2137	U
7	A	2138	G
7	A	2145	C
7	A	2146	C
7	A	2147	A

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Mol	Chain	Res	Type
7	A	2150	C
7	A	2152	G
7	A	2158	A
7	A	2159	G
7	A	2161	C
7	A	2165	C
7	A	2166	U
7	A	2167	U
7	A	2169	A
7	A	2170	A
7	A	2171	A
7	A	2172	U
7	A	2174	C
7	A	2179	C
7	A	2180	U
7	A	2181	U
7	A	2182	U
7	A	2188	U
7	A	2198	A
7	A	2203	U
7	A	2204	G
7	A	2211	A
7	A	2212	A
7	A	2219	U
7	A	2225	A
7	A	2238	G
7	A	2239	G
7	A	2250	G
7	A	2266	A
7	A	2278	A
7	A	2279	G
7	A	2283	C
7	A	2287	A
7	A	2288	A
7	A	2305	U
7	A	2307	G
7	A	2309	A
7	A	2319	G
7	A	2325	G
7	A	2326	C
7	A	2327	A
7	A	2333	A

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Mol	Chain	Res	Type
7	A	2334	U
7	A	2336	A
7	A	2345	G
7	A	2350	C
7	A	2354	C
7	A	2357	G
7	A	2361	G
7	A	2383	G
7	A	2384	U
7	A	2385	C
7	A	2391	G
7	A	2392	A
7	A	2396	G
7	A	2402	U
7	A	2403	C
7	A	2406	A
7	A	2423	U
7	A	2429	G
7	A	2430	A
7	A	2435	A
7	A	2441	U
7	A	2445	G
7	A	2447	G
7	A	2448	A
7	A	2465	C
7	A	2468	A
7	A	2476	A
7	A	2478	A
7	A	2484	G
7	A	2491	U
7	A	2498	C
7	A	2502	G
7	A	2503	A
7	A	2504	U
7	A	2505	G
7	A	2506	U
7	A	2513	A
7	A	2518	A
7	A	2519	U
7	A	2520	C
7	A	2529	G
7	A	2535	G

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Mol	Chain	Res	Type
7	A	2542	A
7	A	2547	A
7	A	2554	U
7	A	2566	A
7	A	2567	G
7	A	2572	A
7	A	2573	C
7	A	2585	U
7	A	2586	U
7	A	2592	G
7	A	2602	A
7	A	2603	G
7	A	2609	U
7	A	2613	U
7	A	2614	A
7	A	2615	U
7	A	2629	U
7	A	2630	G
7	A	2646	C
7	A	2654	A
7	A	2655	G
7	A	2681	C
7	A	2682	A
7	A	2689	U
7	A	2690	U
7	A	2714	G
7	A	2718	G
7	A	2722	G
7	A	2726	A
7	A	2732	G
7	A	2733	A
7	A	2744	G
7	A	2748	A
7	A	2750	A
7	A	2764	A
7	A	2765	A
7	A	2776	A
7	A	2778	A
7	A	2779	U
7	A	2788	C
7	A	2789	C
7	A	2790	U

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Mol	Chain	Res	Type
7	A	2793	C
7	A	2798	U
7	A	2799	A
7	A	2800	A
7	A	2808	G
7	A	2809	A
7	A	2818	U
7	A	2820	A
7	A	2833	U
7	A	2834	G
7	A	2836	U
7	A	2848	G
7	A	2849	U
7	A	2861	U
7	A	2867	G
7	A	2868	A
7	A	2873	A
7	A	2880	C
7	A	2884	U
7	A	2887	A
7	A	2891	U
7	A	2899	A
7	A	2902	C
7	A	2903	U
8	B	4	C
8	B	9	G
8	B	13	G
8	B	24	G
8	B	25	U
8	B	26	C
8	B	30	C
8	B	35	C
8	B	41	G
8	B	44	G
8	B	56	G
8	B	67	G
8	B	87	U
8	B	88	C
8	B	89	U
8	B	91	C
8	B	105	G
8	B	108	A

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Mol	Chain	Res	Type
8	B	109	A
32	a	7	A
32	a	9	G
32	a	22	G
32	a	32	A
32	a	39	G
32	a	47	C
32	a	48	C
32	a	50	A
32	a	51	A
32	a	58	C
32	a	70	U
32	a	71	A
32	a	72	A
32	a	75	G
32	a	79	G
32	a	80	A
32	a	81	A
32	a	82	G
32	a	85	U
32	a	86	G
32	a	87	C
32	a	88	U
32	a	89	U
32	a	92	U
32	a	94	G
32	a	96	U
32	a	99	C
32	a	120	A
32	a	121	U
32	a	122	G
32	a	130	A
32	a	141	G
32	a	160	A
32	a	163	C
32	a	173	U
32	a	182	A
32	a	183	C
32	a	184	G
32	a	185	U
32	a	191	G
32	a	197	A

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Mol	Chain	Res	Type
32	a	199	A
32	a	204	G
32	a	208	U
32	a	209	U
32	a	210	C
32	a	212	G
32	a	222	C
32	a	226	G
32	a	236	A
32	a	240	G
32	a	245	U
32	a	247	G
32	a	251	G
32	a	258	G
32	a	266	G
32	a	267	C
32	a	269	C
32	a	279	A
32	a	280	C
32	a	281	G
32	a	289	G
32	a	321	A
32	a	328	C
32	a	344	A
32	a	345	C
32	a	347	G
32	a	351	G
32	a	352	C
32	a	354	G
32	a	363	A
32	a	365	U
32	a	367	U
32	a	372	C
32	a	373	A
32	a	388	G
32	a	398	U
32	a	406	G
32	a	412	A
32	a	413	G
32	a	421	U
32	a	423	G
32	a	424	G

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Mol	Chain	Res	Type
32	a	428	G
32	a	429	U
32	a	438	U
32	a	439	U
32	a	446	G
32	a	462	G
32	a	463	U
32	a	467	U
32	a	468	A
32	a	479	U
32	a	484	G
32	a	485	U
32	a	486	U
32	a	496	A
32	a	497	G
32	a	498	A
32	a	509	A
32	a	518	C
32	a	521	G
32	a	524	G
32	a	527	G
32	a	531	U
32	a	532	A
32	a	535	A
32	a	536	C
32	a	537	G
32	a	547	A
32	a	559	A
32	a	562	U
32	a	566	G
32	a	572	A
32	a	573	A
32	a	575	G
32	a	576	C
32	a	577	G
32	a	596	A
32	a	607	A
32	a	615	G
32	a	618	C
32	a	628	G
32	a	633	G
32	a	642	A

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Mol	Chain	Res	Type
32	a	650	G
32	a	653	U
32	a	665	A
32	a	687	A
32	a	688	G
32	a	695	A
32	a	702	A
32	a	703	G
32	a	721	G
32	a	731	G
32	a	754	C
32	a	755	G
32	a	759	A
32	a	777	A
32	a	781	A
32	a	794	A
32	a	814	A
32	a	815	A
32	a	817	C
32	a	818	G
32	a	819	A
32	a	820	U
32	a	829	G
32	a	832	G
32	a	836	G
32	a	840	C
32	a	842	U
32	a	843	U
32	a	844	G
32	a	851	G
32	a	870	U
32	a	889	A
32	a	902	G
32	a	914	A
32	a	926	G
32	a	934	C
32	a	935	A
32	a	948	C
32	a	954	G
32	a	960	U
32	a	961	U
32	a	966	G

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Mol	Chain	Res	Type
32	a	969	A
32	a	975	A
32	a	976	G
32	a	977	A
32	a	982	U
32	a	992	U
32	a	993	G
32	a	996	A
32	a	1004	A
32	a	1020	G
32	a	1026	G
32	a	1028	C
32	a	1029	U
32	a	1030	U
32	a	1031	C
32	a	1033	G
32	a	1034	G
32	a	1053	G
32	a	1065	U
32	a	1070	U
32	a	1085	U
32	a	1094	G
32	a	1095	U
32	a	1101	A
32	a	1130	A
32	a	1136	C
32	a	1137	C
32	a	1138	G
32	a	1139	G
32	a	1143	G
32	a	1146	A
32	a	1152	A
32	a	1158	C
32	a	1159	U
32	a	1160	G
32	a	1167	A
32	a	1168	U
32	a	1169	A
32	a	1171	A
32	a	1182	G
32	a	1184	G
32	a	1191	A

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Mol	Chain	Res	Type
32	a	1196	A
32	a	1201	A
32	a	1202	U
32	a	1213	A
32	a	1227	A
32	a	1228	C
32	a	1238	A
32	a	1250	A
32	a	1256	A
32	a	1258	G
32	a	1260	G
32	a	1261	A
32	a	1275	A
32	a	1280	A
32	a	1285	A
32	a	1287	A
32	a	1297	G
32	a	1298	U
32	a	1300	G
32	a	1301	U
32	a	1305	G
32	a	1312	G
32	a	1317	C
32	a	1320	C
32	a	1322	C
32	a	1323	G
32	a	1331	G
32	a	1345	U
32	a	1346	A
32	a	1353	G
32	a	1363	A
32	a	1364	U
32	a	1368	A
32	a	1370	G
32	a	1394	A
32	a	1396	A
32	a	1399	C
32	a	1400	C
32	a	1419	G
32	a	1432	G
32	a	1441	A
32	a	1446	A

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Mol	Chain	Res	Type
32	a	1447	A
32	a	1451	U
32	a	1452	C
32	a	1453	G
32	a	1492	A
32	a	1493	A
32	a	1497	G
32	a	1502	A
32	a	1503	A
32	a	1506	U
32	a	1507	A
32	a	1517	G
32	a	1519	A
32	a	1520	C
32	a	1529	G
32	a	1530	G
32	a	1534	A
32	a	1535	C
32	a	1536	C
32	a	1537	U
32	a	1539	C
54	x	3	G
54	x	4	U
54	x	5	G
54	x	6	A
54	x	10	G
54	x	14	A
54	x	17	C
54	x	18	G
54	x	21	A
54	x	22	G
54	x	41	A
54	x	46	G
54	x	47	U
54	x	57	G
54	x	61	C
54	x	64	C
54	x	65	U
54	x	76	A

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	134	G
7	A	227	A
7	A	242	G
7	A	479	A
7	A	490	C
7	A	555	G
7	A	748	G
7	A	784	G
7	A	827	U
7	A	859	G
7	A	1020	A
7	A	1022	G
7	A	1060	U
7	A	1062	G
7	A	1111	A
7	A	1173	U
7	A	1179	G
7	A	1190	G
7	A	1300	G
7	A	1399	C
7	A	1420	A
7	A	1930	G
7	A	1940	U
7	A	2097	A
7	A	2326	C
7	A	2391	G
7	A	2808	G
7	A	2901	C
8	B	66	A
8	B	86	G
8	B	88	C

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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.

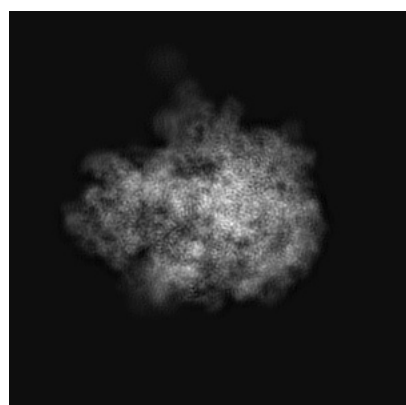
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10353. These allow visual inspection of the internal detail of the map and identification of artifacts.

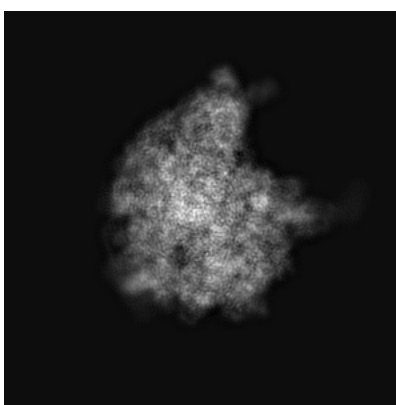
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

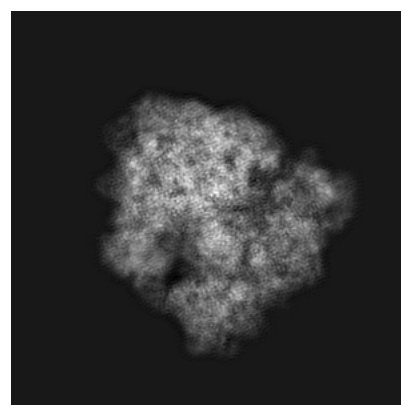
6.1.1 Primary map



X



Y

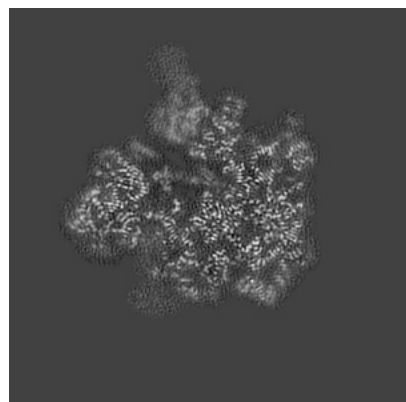


Z

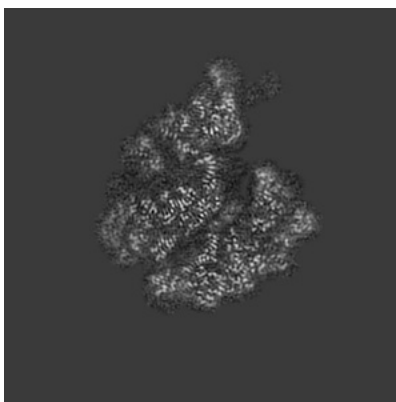
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

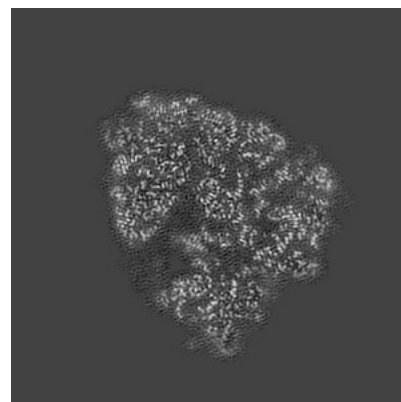
6.2.1 Primary map



X Index: 184



Y Index: 184

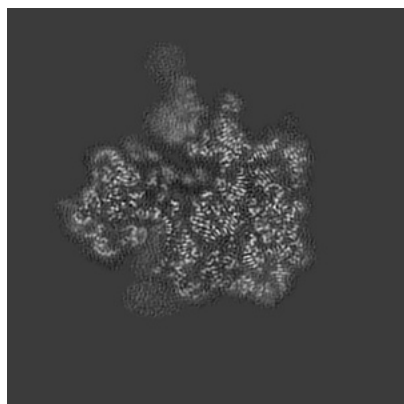


Z Index: 184

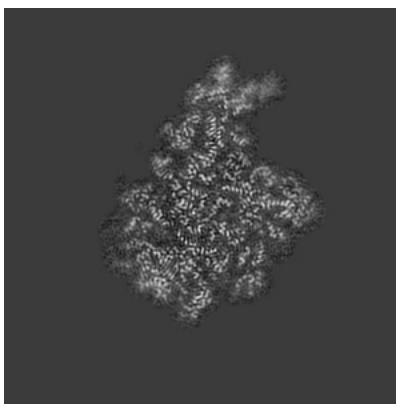
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

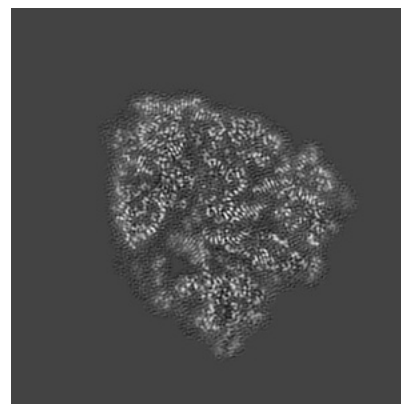
6.3.1 Primary map



X Index: 188



Y Index: 200

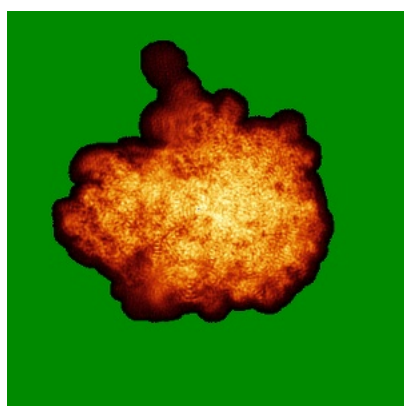


Z Index: 188

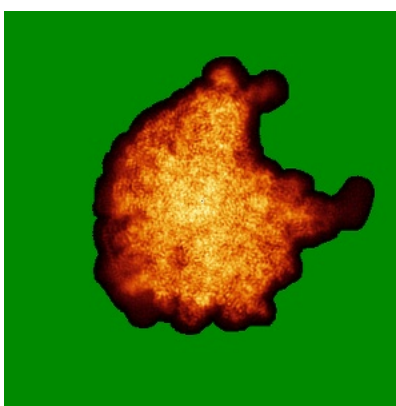
The images above show the largest variance slices of the map in three orthogonal directions.

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

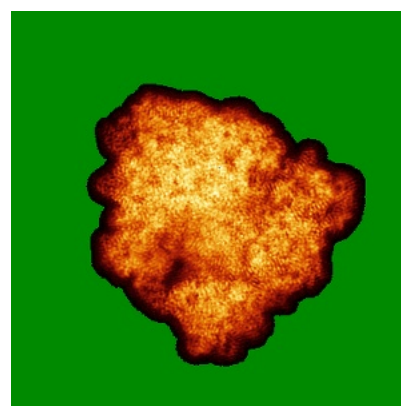
6.4.1 Primary map



X



Y

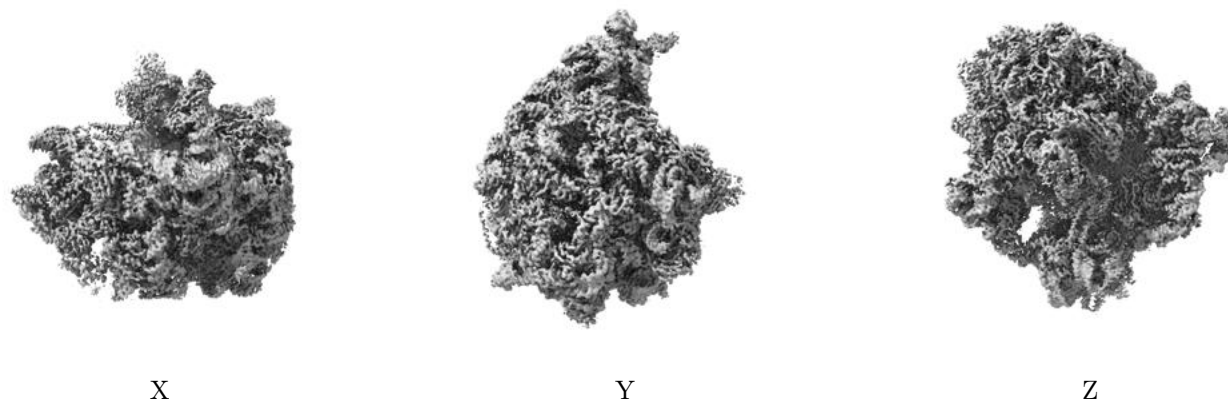


Z

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 0.0387. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

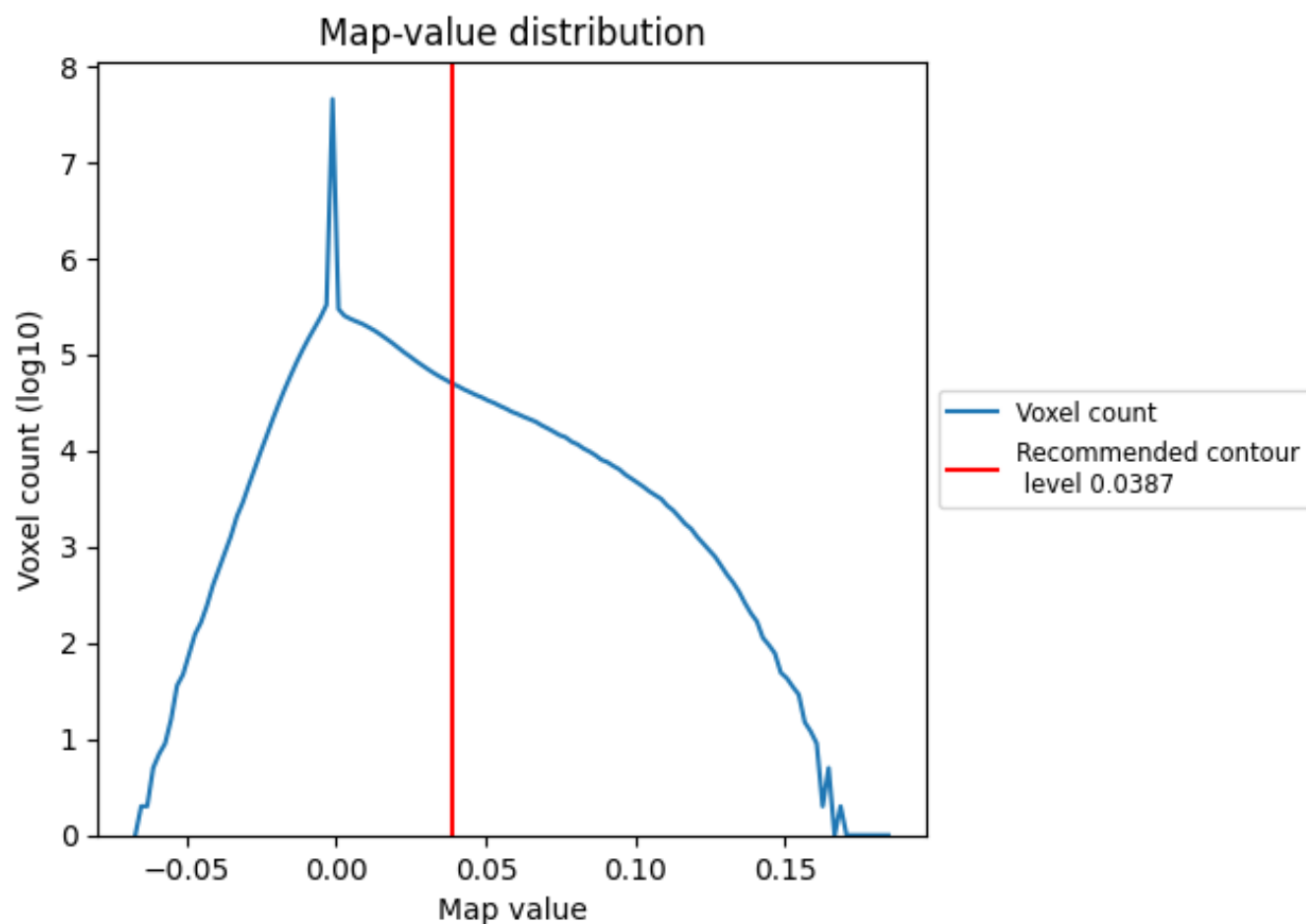
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

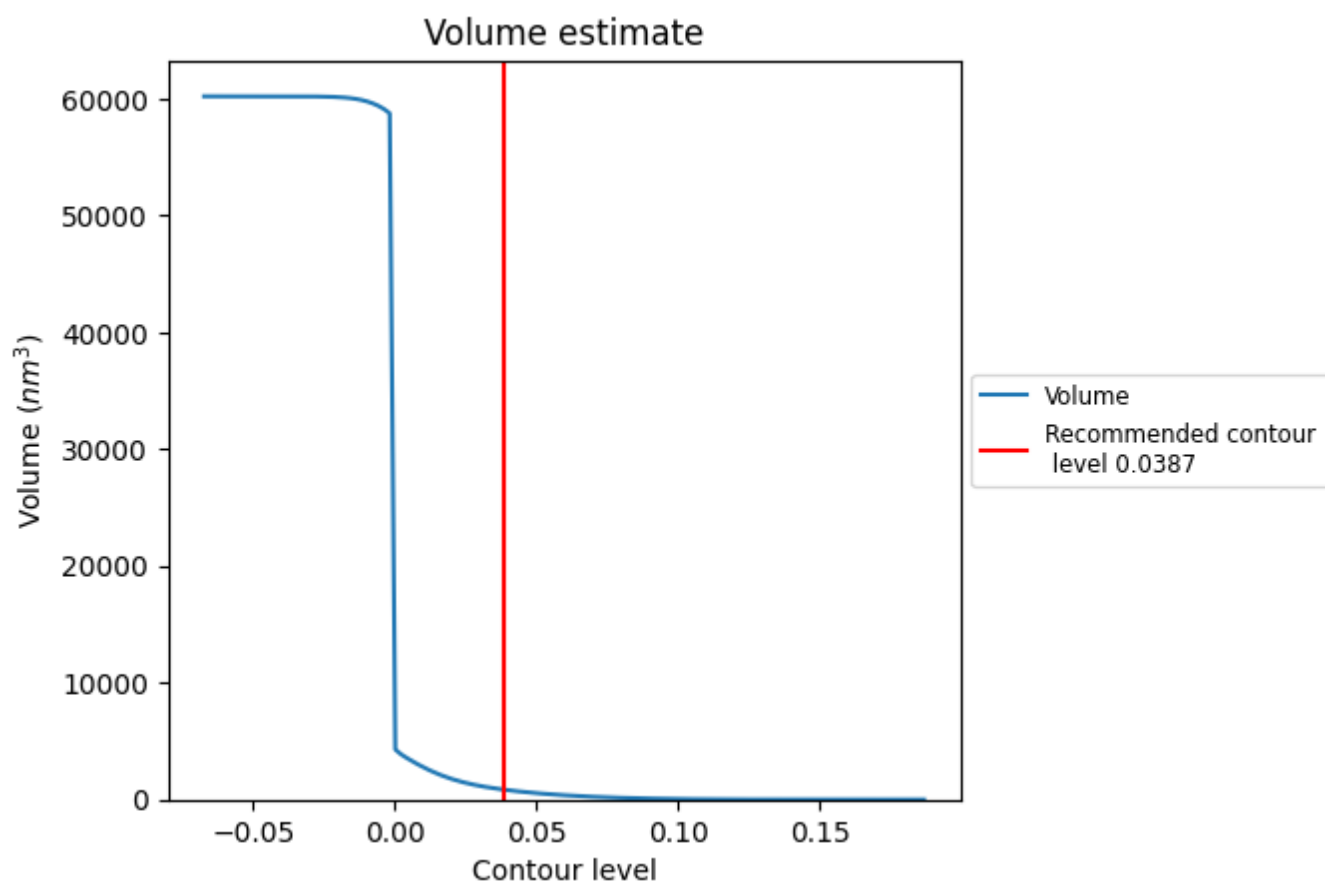
This section contains the results of statistical analysis of the map.

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.

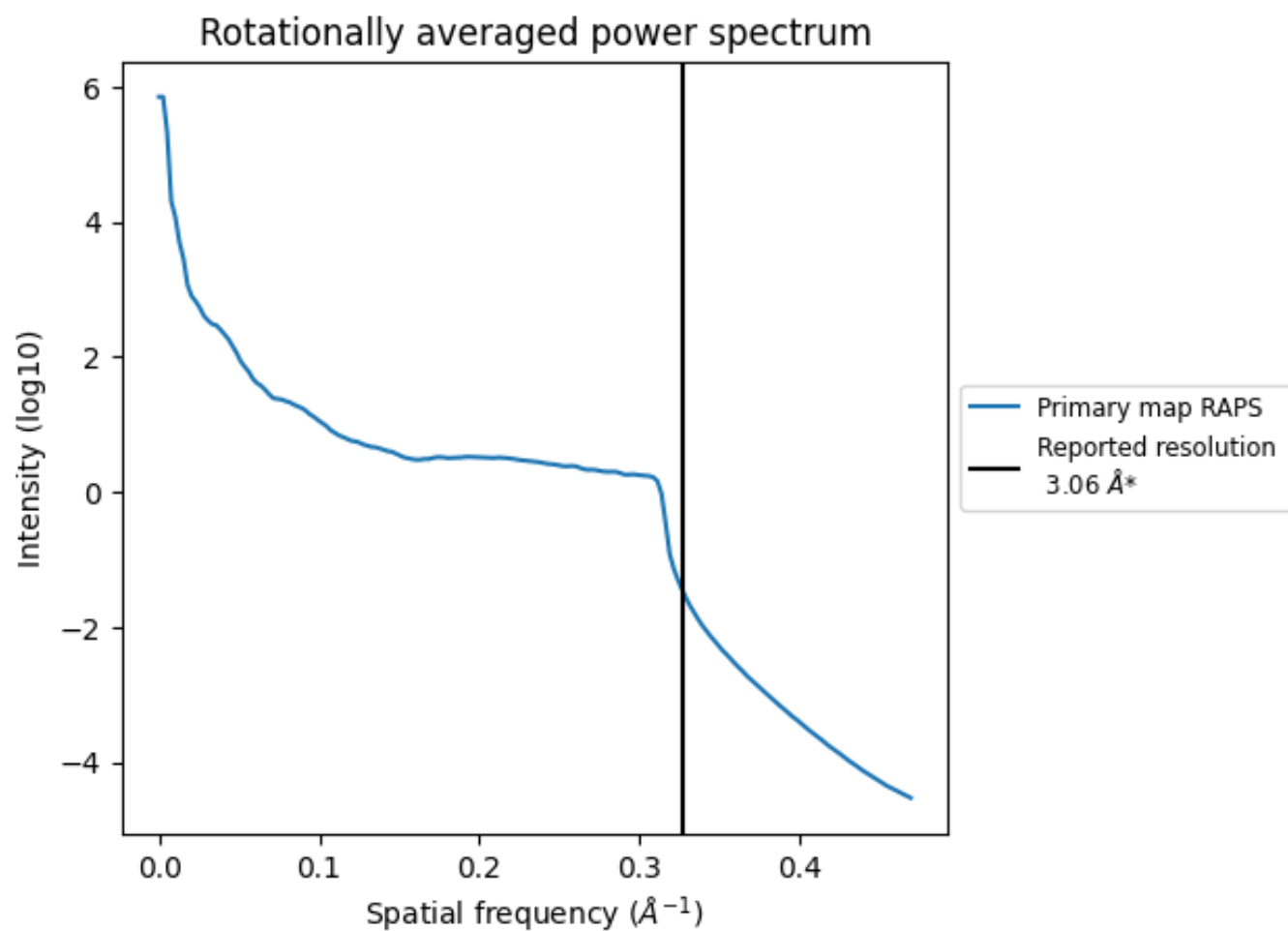
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 842 nm³; this corresponds to an approximate mass of 760 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 ⓘ

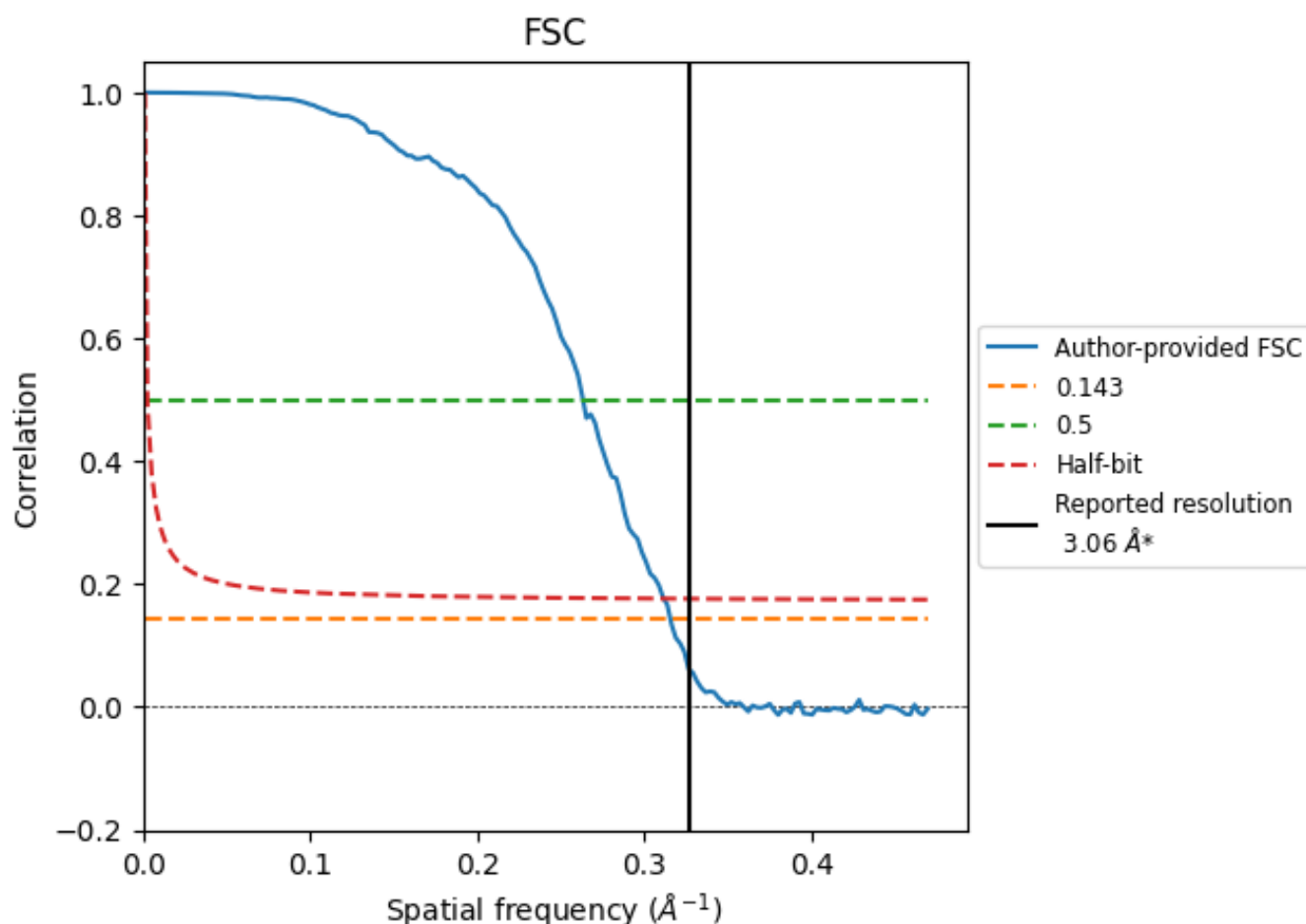


*Reported resolution corresponds to spatial frequency of 0.327 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.327 Å⁻¹

8.2 Resolution estimates [i](#)

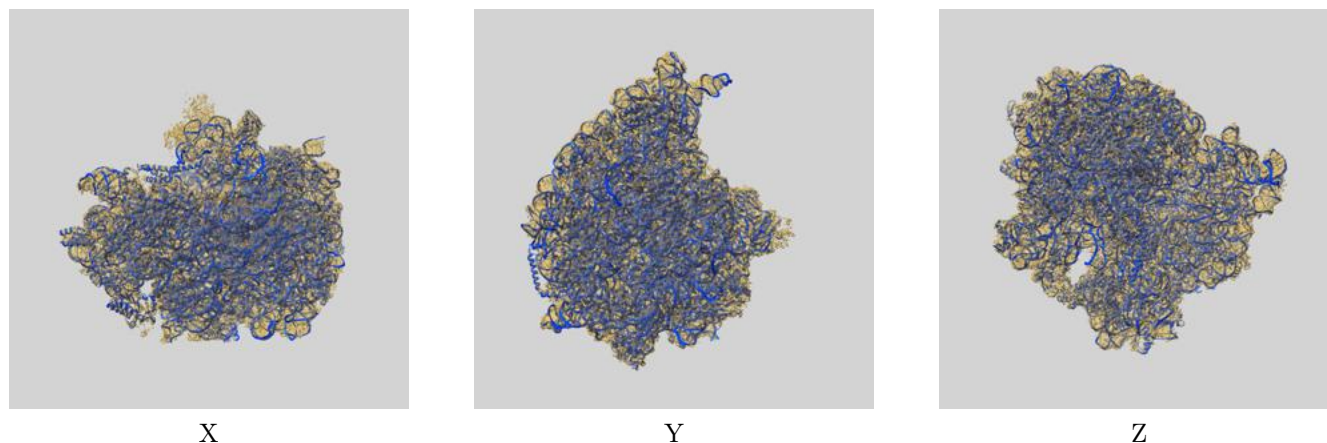
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.06	-	-
Author-provided FSC curve	3.17	3.80	3.21
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

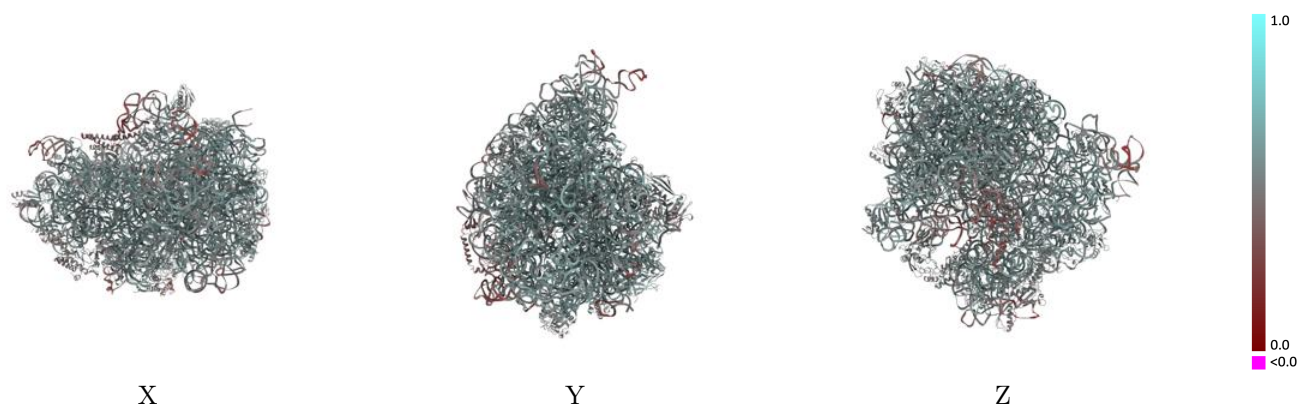
This section contains information regarding the fit between EMDB map EMD-10353 and PDB model 6SZS. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



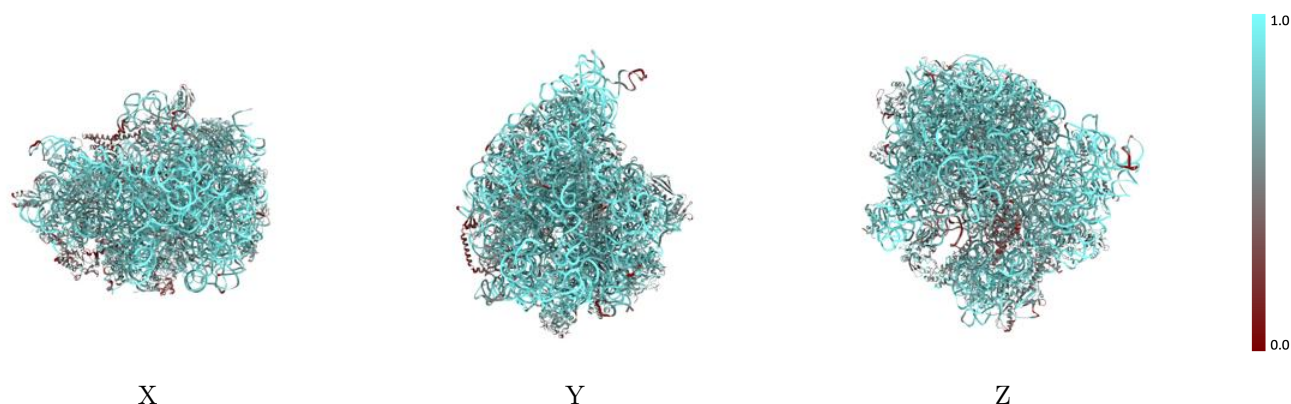
The images above show the 3D surface view of the map at the recommended contour level 0.0387 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



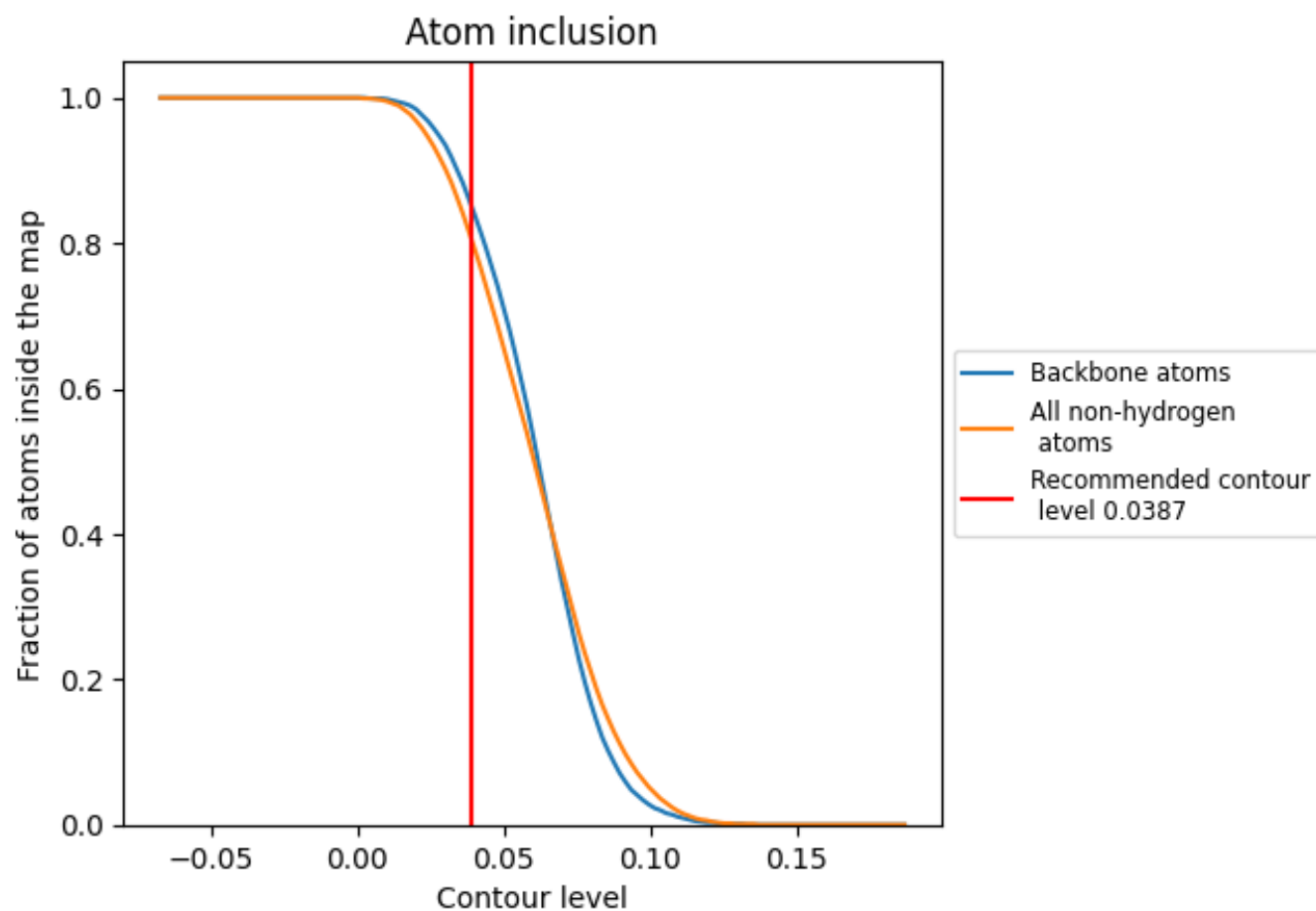
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0387).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 81% 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 (0.0387) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8080	 0.5350
0	 0.7200	 0.5610
1	 0.6760	 0.5510
2	 0.7440	 0.5870
3	 0.7800	 0.5850
4	 0.7020	 0.5650
5	 0.5610	 0.4760
A	 0.8820	 0.5380
B	 0.9150	 0.5320
C	 0.6880	 0.5710
D	 0.6980	 0.5650
E	 0.6490	 0.5340
F	 0.6350	 0.5060
G	 0.6070	 0.5000
H	 0.2930	 0.4060
J	 0.7440	 0.5570
K	 0.6300	 0.5610
L	 0.6890	 0.5490
M	 0.6340	 0.5600
N	 0.7820	 0.5700
O	 0.7380	 0.5340
P	 0.6620	 0.5620
Q	 0.7570	 0.5600
R	 0.6840	 0.5590
S	 0.6580	 0.5520
T	 0.6160	 0.5410
U	 0.6230	 0.5160
V	 0.6760	 0.5400
W	 0.7140	 0.5780
X	 0.7120	 0.5540
Y	 0.6180	 0.5030
Z	 0.6730	 0.5530
a	 0.9070	 0.5390
b	 0.4060	 0.4690
c	 0.6740	 0.5350



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Chain	Atom inclusion	Q-score
d	 0.7110	 0.5320
e	 0.6820	 0.5460
f	 0.6530	 0.5180
g	 0.5680	 0.5020
h	 0.7120	 0.5520
i	 0.7290	 0.5250
j	 0.5850	 0.5060
k	 0.6080	 0.5320
l	 0.6680	 0.5630
m	 0.6910	 0.5220
n	 0.7300	 0.5450
o	 0.6830	 0.5170
p	 0.7640	 0.5410
q	 0.6490	 0.5290
r	 0.6640	 0.5270
s	 0.7000	 0.5420
t	 0.7280	 0.5290
u	 0.3480	 0.4730
v	 0.7620	 0.5430
x	 0.7020	 0.4860
y	 0.5250	 0.5390
z	 0.3830	 0.4520