



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:18 AM UTC

PDB ID : 6O8W / pdb_00006o8w
EMDB ID : EMD-0656
Title : Cryo-EM image reconstruction of the 70S Ribosome *Enterococcus faecalis* Class01
Authors : Jogl, G.; Khayat, R.
Deposited on : 2019-03-12
Resolution : 3.53 Å (reported)
Based on initial models : 5LI0, 4YBB

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

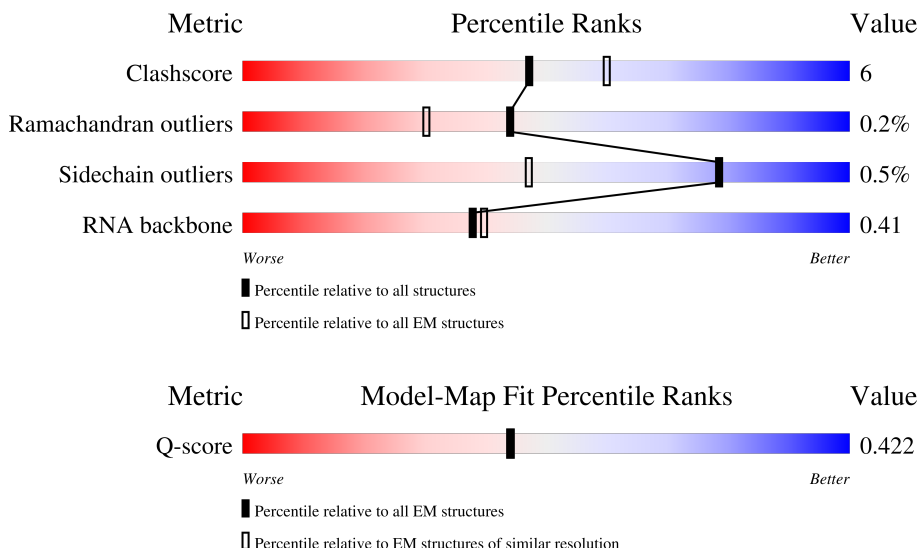
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.53 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	12947 (3.03 - 4.02)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	1523	
2	c	204	
3	d	201	

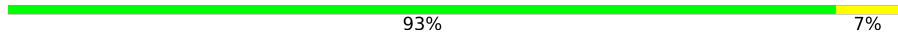
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Mol	Chain	Length	Quality of chain
4	e	163	
5	f	97	
6	g	154	
7	h	131	
8	i	128	
9	j	99	
10	k	117	
11	l	136	
12	m	112	
13	n	60	
14	o	88	
15	p	89	
16	q	83	
17	r	66	
18	s	78	
19	t	81	
20	u	76	
21	v	5	
22	A	2903	
23	B	116	
24	C	275	
25	D	207	
26	E	206	
27	F	177	
28	G	176	

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Mol	Chain	Length	Quality of chain
29	K	145	
30	L	122	
31	M	146	
32	N	141	
33	O	123	
34	P	117	
35	Q	114	
36	R	118	
37	S	102	
38	T	112	
39	U	89	
40	V	101	
41	W	94	
42	X	76	
43	Y	54	
44	Z	61	
45	0	58	
46	1	59	
47	2	56	
48	3	49	
49	4	44	
50	5	64	
51	6	38	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 139953 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1523	Total	C	N	O	P	0	0
			32646	14564	5967	10592	1523		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	204	Total	C	N	O	S	0	0
			1610	1012	303	292	3		

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1620	1016	303	297	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	163	Total	C	N	O	S	0	0
			1204	759	222	221	2		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	97	Total	C	N	O	S	0	0
			795	501	137	154	3		

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	154	Total	C	N	O	S	0	0
			1229	765	236	222	6		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			1041	662	184	193	2		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	128	Total	C	N	O	S	0	0
			990	615	197	177	1		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	99	Total	C	N	O	S	0	0
			800	504	147	147	2		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	117	Total	C	N	O	S	0	0
			863	533	165	161	4		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	136	Total	C	N	O	S	0	0
			1065	661	214	188	2		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	112	Total	C	N	O	S	0	0
			884	540	180	163	1		

- Molecule 13 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	60	Total	C	N	O	S	0	0
			492	310	100	77	5		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	o	88	Total	C	N	O	S	0	0
			741	455	152	133	1		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	89	Total	C	N	O	S	0	0
			708	448	131	127	2		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	q	83	Total	C	N	O	S	0	0
			681	427	127	124	3		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	66	Total	C	N	O	S	0	0
			537	343	99	94	1		

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	78	Total	C	N	O	S	0	0
			634	410	113	109	2		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	81	Total	C	N	O	S	0	0
			610	372	119	117	2		

- Molecule 20 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	u	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 21 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	5	Total	C	N	O	P	0	0
			100	45	11	39	5		

- Molecule 22 is a RNA chain called 50S subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	A	2903	Total	C	N	O	P	0	0
			62301	27808	11456	20134	2903		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	B	116	Total	C	N	O	P	0	0
			2478	1106	442	814	116		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	275	Total	C	N	O	S	0	0
			2113	1310	415	381	7		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	207	Total	C	N	O	S	0	0
			1578	993	292	289	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	206	Total	C	N	O	S	0	0
			1573	983	290	298	2		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	177	Total	C	N	O	S	0	0
			1391	886	239	260	6		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	176	Total	C	N	O	S	0	0
			1344	841	244	255	4		

- Molecule 29 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	K	145	Total	C	N	O	S	0	0
			1129	713	205	207	4		

- Molecule 30 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L	122	Total	C	N	O	S	0	0
			921	573	176	170	2		

- Molecule 31 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M	146	Total	C	N	O	S	0	0
			1094	676	212	205	1		

- Molecule 32 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	N	141	Total	C	N	O	S	0	0
			1118	710	216	185	7		

- Molecule 33 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	O	123	Total	C	N	O	S	0	0
			978	602	190	183	3		

- Molecule 34 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	P	112	Total	C	N	O	S	0	0
			862	533	169	159	1		

- Molecule 35 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	Q	114	Total	C	N	O		
			923	581	185	157	0	0

- Molecule 36 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	R	118	Total	C	N	O	S	
			950	602	184	160	4	0

- Molecule 37 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	S	102	Total	C	N	O	S	
			783	499	139	143	2	0

- Molecule 38 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	T	112	Total	C	N	O	S	
			848	531	156	159	2	0

- Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	U	89	Total	C	N	O	S	
			720	458	127	132	3	0

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	V	101	Total	C	N	O	S	
			762	485	135	140	2	0

- Molecule 41 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	W	94	Total	C	N	O	S	
			758	479	135	140	4	0

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	X	76	Total	C	N	O	0	0
			571	350	109	112		

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Y	54	Total	C	N	O	S	0	0
			425	265	86	72	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	51	ALA	THR	conflict	UNP A0A1B4XRZ8

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Z	61	Total	C	N	O	S	0	0
			504	314	94	95	1		

- Molecule 45 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	0	58	Total	C	N	O	S	0	0
			434	270	81	82	1		

- Molecule 46 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	59	Total	C	N	O	S	0	0
			472	300	74	96	2		

- Molecule 47 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	56	Total	C	N	O	S	0	0
			428	261	88	73	6		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	3	49	Total	C	N	O	S	0	0
			419	253	86	76	4		

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	4	44	Total	C	N	O	S	0	0
			374	227	91	54	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	5	64	Total	C	N	O	S	0	0
			521	320	122	77	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	6	38	Total	C	N	O	S	0	0
			304	188	66	44	6		

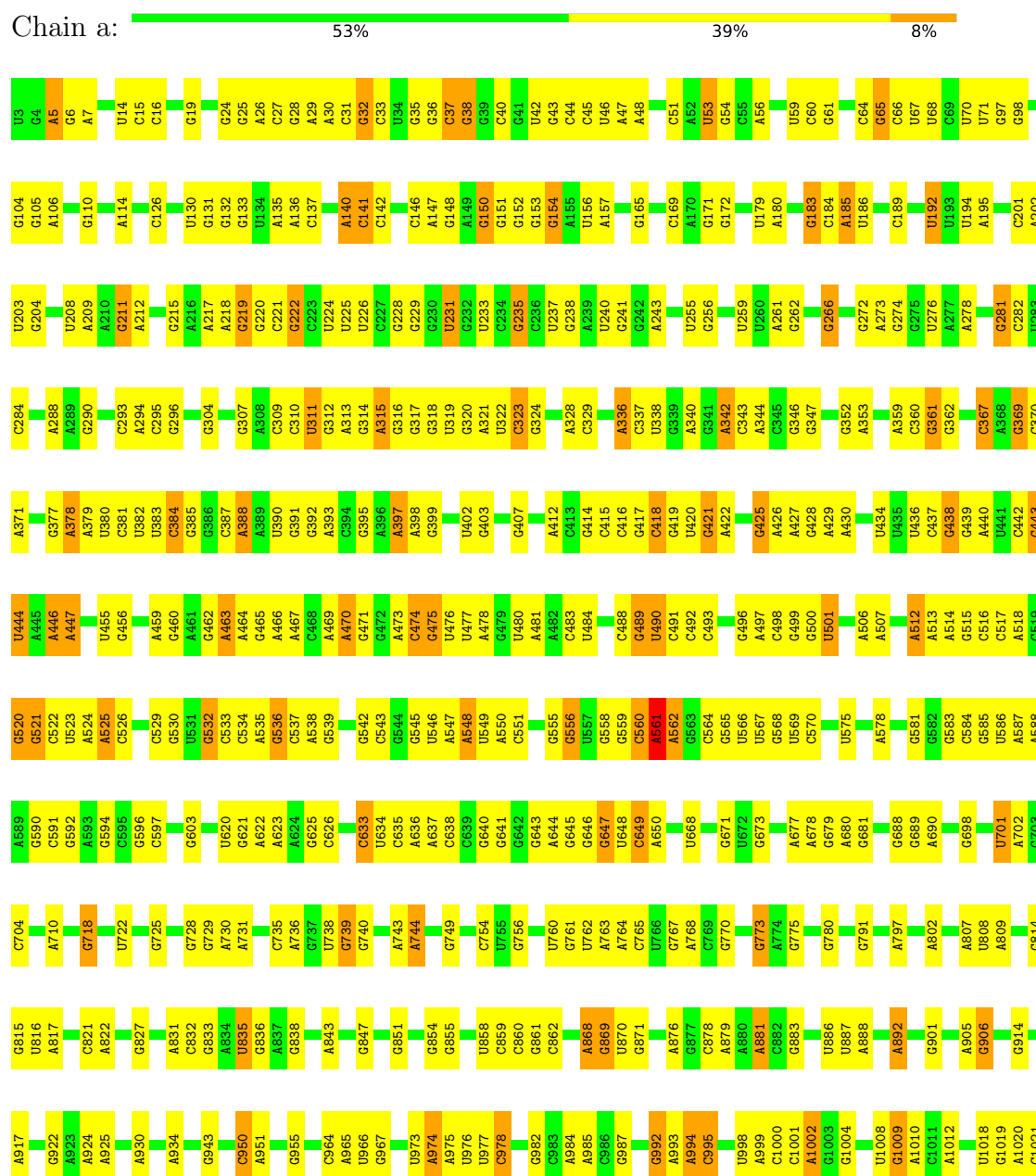
- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

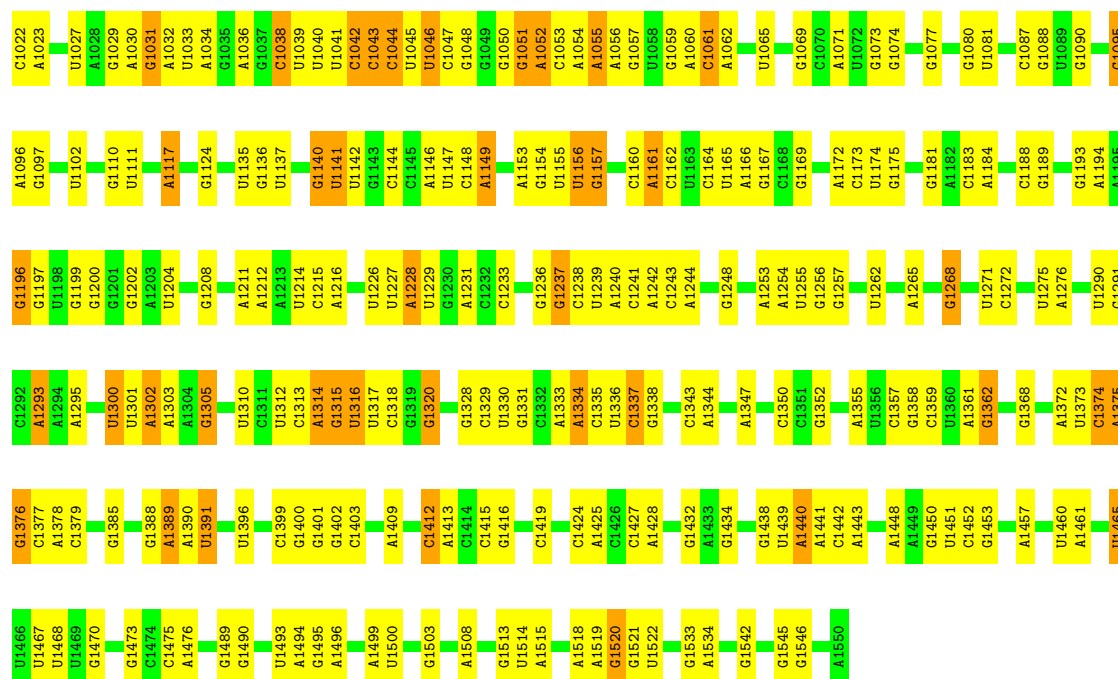
Mol	Chain	Residues	Atoms		AltConf
52	n	1	Total	Zn	0
			1	1	
52	2	1	Total	Zn	0
			1	1	
52	3	1	Total	Zn	0
			1	1	
52	6	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

• Molecule 1: 16S rRNA



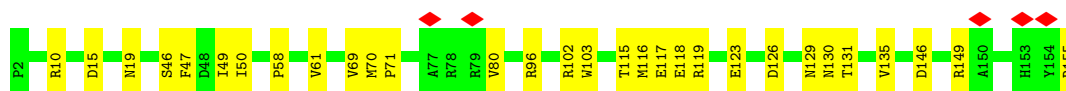


Chain f:  90% 10%



- Molecule 6: 30S ribosomal protein S7

Chain g:  81% 19%



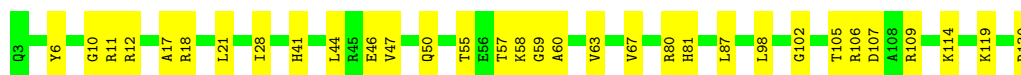
- Molecule 7: 30S ribosomal protein S8

Chain h:  85% 15%



- Molecule 8: 30S ribosomal protein S9

Chain i:  75% 25%



- Molecule 9: 30S ribosomal protein S10

Chain j:  81% 19%



- Molecule 10: 30S ribosomal protein S11

Chain k:  88% 12%



- Molecule 11: 30S ribosomal protein S12

Chain l:  71% 28%





- Molecule 12: 30S ribosomal protein S13

Chain m: 82% 18%



- Molecule 13: 30S ribosomal protein S14 type Z

Chain n: 83% 17%



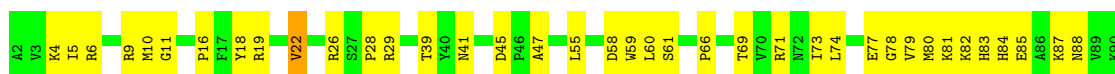
- Molecule 14: 30S ribosomal protein S15

Chain o: 85% 15%



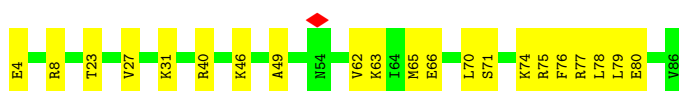
- Molecule 15: 30S ribosomal protein S16

Chain p: 57% 42%



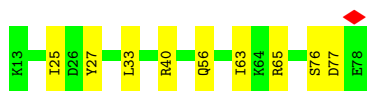
- Molecule 16: 30S ribosomal protein S17

Chain q: 75% 25%



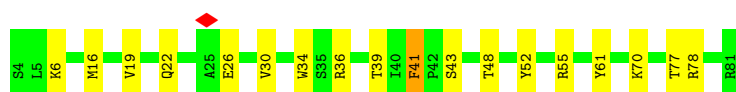
- Molecule 17: 30S ribosomal protein S18

Chain r: 86% 14%

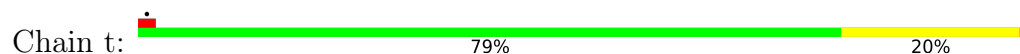


- Molecule 18: 30S ribosomal protein S19

Chain s: 77% 22%



- Molecule 19: 30S ribosomal protein S20



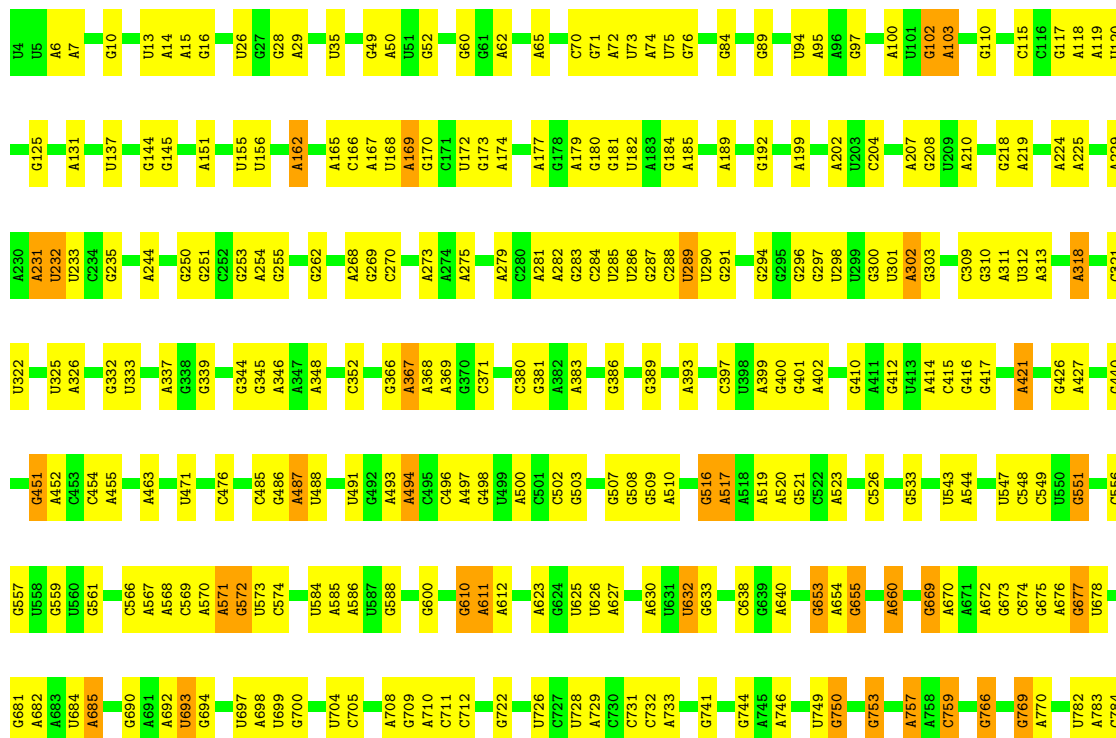
- Molecule 20: tRNA



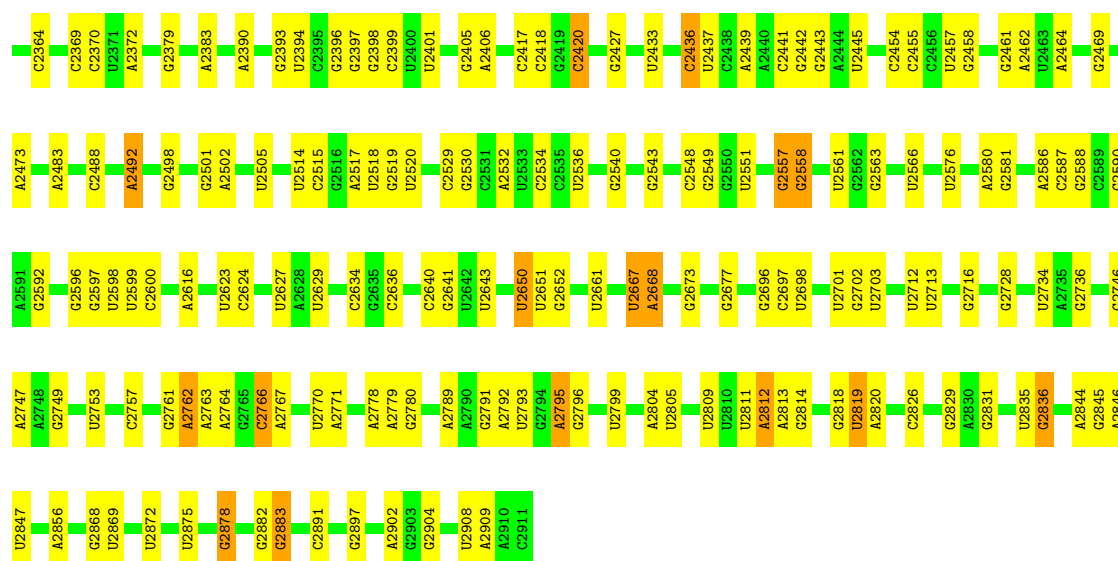
- Molecule 21: mRNA



- Molecule 22: 50S subunit

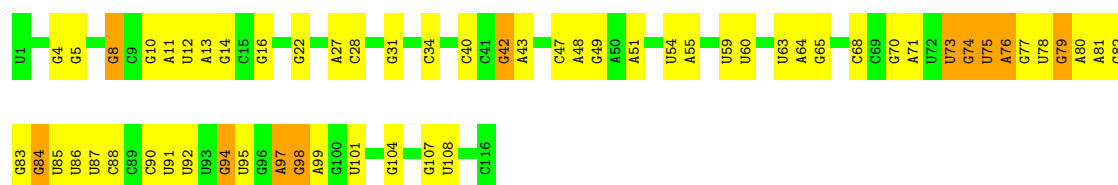


C2272	A2155	A1927	A1787	U1535	C1440	C1330	U1214	U1123	U1052	U965	G893	G785
U2276	A2156	C1928	G1790	A1536	C1441	U1336	A1215	A1124	A1053	U966	A894	U786
U2279	G2157	U1931	G1793	U1539	G1443	U1338	G1217	A1125	G1057	C967	A898	U787
A2280	G2158	G1943	U1794	U1542	U1448	G1345	G1224	G1127	A1060	U969	G899	U788
A2281	A2055	G1944	U1795	U1543	U1449	G1346	U1225	G1128	A1061	U970	G900	A789
A2282	C2057	G1945	U1796	U1551	U1450	C1350	C1234	G1129	A1062	U971	A901	A790
A2283	C2058	C1948	U1797	A1552	U1451	U1357	G1235	G1130	U1063	A902	A902	A791
A2284	C2059	G1949	U1798	A1553	U1452	A1357	G1236	G1131	G1064	A903	A903	A792
G2290	C2060	U1951	A1800	A1559	U1454	A1358	U1237	C1132	G1065	A904	A904	A804
C2297	C2061	A1952	A1801	G1565	U1455	G1359	U1238	U1134	A1066	A905	G905	G805
C2298	A2074	U1953	G1813	G1566	C1456	U1365	U1239	A1135	A1067	A906	A906	G808
C2299	C2075	C1955	C1814	C1567	A1457	U1366	A1241	A1136	A1068	G908	C908	G815
A2301	A2076	U1969	A1815	G1568	U1461	G1373	G1244	U1137	A1069	A907	A907	G816
A2302	U2082	U1970	G1821	A1572	U1462	G1374	G1249	G1070	A1071	C908	C908	G817
G2305	G2083	C1971	U1822	G1573	A1469	G1375	U1254	A1072	A1072	G909	G909	G820
C2306	C2084	U1972	A1823	A1576	C1470	U1376	C1255	U1073	U1073	A932	A932	A821
C2307	G2086	C1976	G1825	U1584	G1471	U1377	G1256	G1079	G1079	G934	G934	A822
G2317	U2090	C1977	U1826	G1585	U1475	U1388	A1257	U1080	U1080	G935	G935	A823
U2318	G2107	U1978	U1827	A1586	U1487	G1394	G1262	U1081	G1081	A936	A936	U824
U2319	U2182	A1980	A1829	G1589	C1488	G1395	U1268	U1082	U1082	U936	U936	U825
U2320	G2114	G1981	A1830	A1590	G1489	G1396	G1269	U1083	U1083	G937	G937	G832
U2321	C2115	A1984	A1831	A1591	U1490	G1397	U1270	U1084	U1084	A938	A938	A833
U2322	U2116	U1985	A1832	G1592	U1491	G1400	G1271	U1085	U1085	U939	U939	U836
U2323	A2117	G1986	A1833	U1593	G1492	A1401	G1272	U1086	U1086	U940	U940	A840
A2324	U2123	U1989	G1842	C1600	G1494	G1404	A1274	U1087	U1087	U941	U941	G845
G2325	U2124	U1990	A1843	U1601	U1495	G1405	G1275	U1088	U1088	A942	A942	C846
U2326	A2125	U1991	A1867	A1602	U1496	G1406	C1276	U1089	U1089	C939	C939	G849
U2327	C2126	U1992	A1868	A1603	U1497	G1407	G1277	U1090	U1090	A943	A943	U850
U2328	U2127	U1993	G1871	A1604	U1500	G1411	U1285	U1091	U1091	U944	U944	C852
A2333	A2128	U2005	G1872	C1605	A1501	U1415	U1286	U1092	U1092	U945	U945	C853
G2335	G2129	G2006	A1887	A1606	G1502	U1416	G1287	U1093	U1093	U946	U946	C854
A2336	A2130	U2007	G1881	A1612	U1503	G1417	A1288	U1094	U1094	A947	A947	A860
G2337	U2131	U2008	G1882	G1613	G1504	G1417	G1289	U1095	U1095	U948	U948	G867
U2338	A2132	A2011	C1882	G1614	U1507	A1420	A1290	U1096	U1096	U949	U949	U868
G2339	G2134	U2034	G1886	A1615	G1508	A1421	U1292	U1097	U1097	A950	A950	G872
U2340	C2139	U2025	A1896	A1616	U1509	C1422	G1293	U1098	U1098	A951	A951	U874
A2341	A2140	A2027	G1897	G1630	A1510	A1423	A1302	U1099	U1099	A952	A952	A875
A2342	G2141	G2035	A1898	A1631	C1510	G1424	G1303	U1100	U1100	C955	C955	U885
A2343	C2142	U2036	U1900	A1632	G1514	G1425	U1307	U1101	U1101	G956	G956	U886
G2348	C2143	G2035	G1768	A1633	G1519	G1428	G1308	U1102	U1102	G957	G957	U887
A2349	G2144	U2036	A1769	A1634	A1520	A1429	A1309	U1103	U1103	A958	A958	A888
A2350	U2145	G2043	G1770	A1635	G1521	U1430	A1310	U1104	U1104	U960	U960	G889
A2255	G2147	A2044	G1771	A1636	U1525	U1431	A1311	U1105	U1105	A1048	A1048	A890
G2256	A2148	A2045	G1772	A1637	G1531	U1432	G1319	U1106	U1106	A1049	A1049	A891
U2259	G2149	G2046	A1773	U1645	G1532	U1436	A1322	U1107	U1107	C963	C963	U892
G2369	A2150	U2047	G1784	U1646	A1532	U1437	A1323	U1108	U1108	A964	A964	
A2360	G2154	G2049	G1785			A1439		U1109	U1109			
C2361								U1110	U1110			
								U1111	U1111			
								U1112	U1112			
								U1113	U1113			
								U1114	U1114			
								U1115	U1115			
								U1116	U1116			
								U1117	U1117			
								U1118	U1118			
								U1119	U1119			
								U1120	U1120			
								U1121	U1121			
								U1122	U1122			



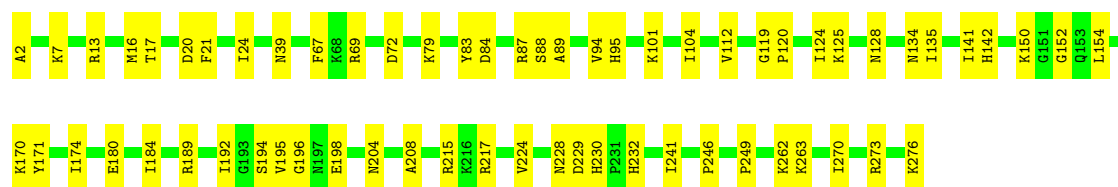
• Molecule 23: 5S rRNA

Chain B: 49% 41% 9%



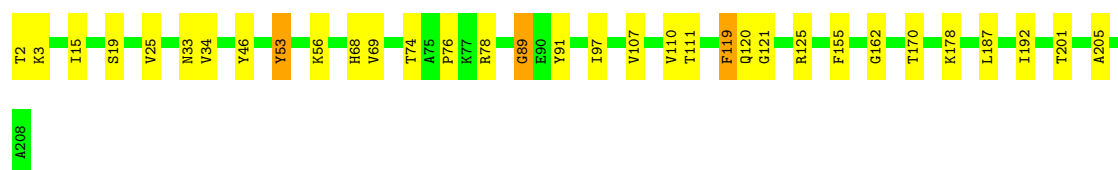
• Molecule 24: 50S ribosomal protein L2

Chain C: 77% 23%



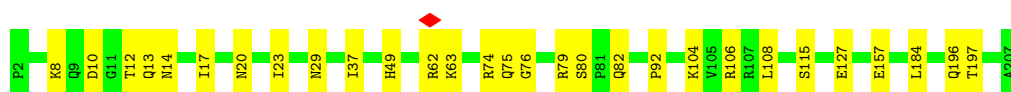
• Molecule 25: 50S ribosomal protein L3

Chain D: 84% 14%



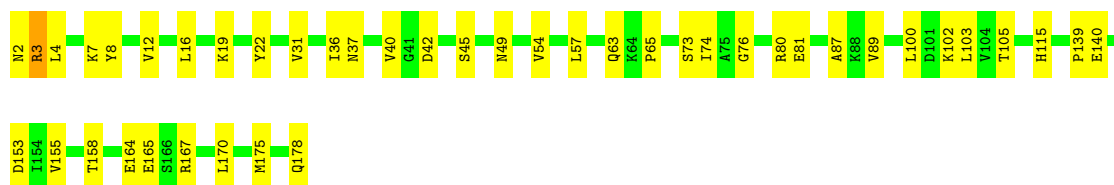
• Molecule 26: 50S ribosomal protein L4

Chain E: 86% 14%



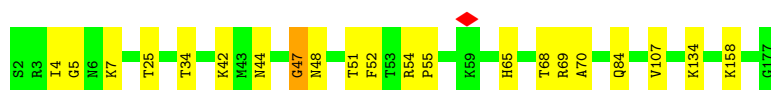
- Molecule 27: 50S ribosomal protein L5

Chain F:  76% 24%



- Molecule 28: 50S ribosomal protein L6

Chain G:  88% 11%

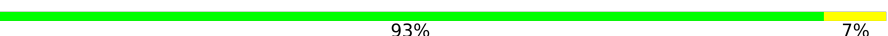


- Molecule 29: 50S ribosomal protein L13

Chain K:  84% 15%



- Molecule 30: 50S ribosomal protein L14

Chain L:  93% 7%



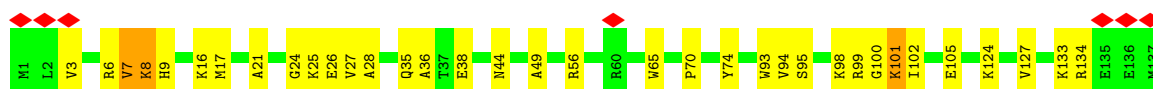
- Molecule 31: 50S ribosomal protein L15

Chain M:  85% 14%



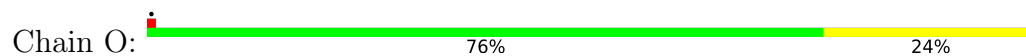
- Molecule 32: 50S ribosomal protein L16

Chain N:  7% 74% 23%

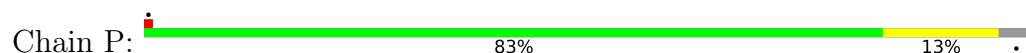




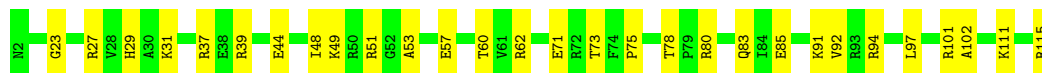
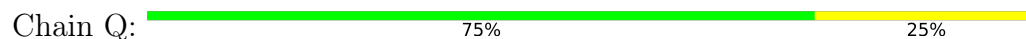
- Molecule 33: 50S ribosomal protein L17



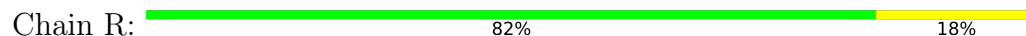
- Molecule 34: 50S ribosomal protein L18



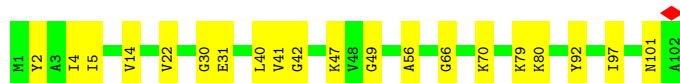
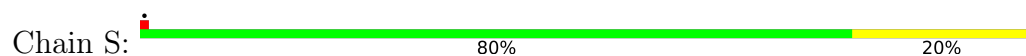
- Molecule 35: 50S ribosomal protein L19



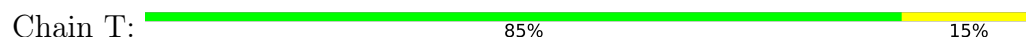
- Molecule 36: 50S ribosomal protein L20



- Molecule 37: 50S ribosomal protein L21



- Molecule 38: 50S ribosomal protein L22



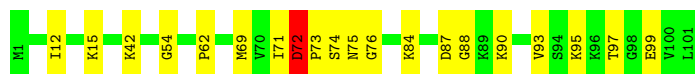
- Molecule 39: 50S ribosomal protein L23

Chain U:  83% 12% . .



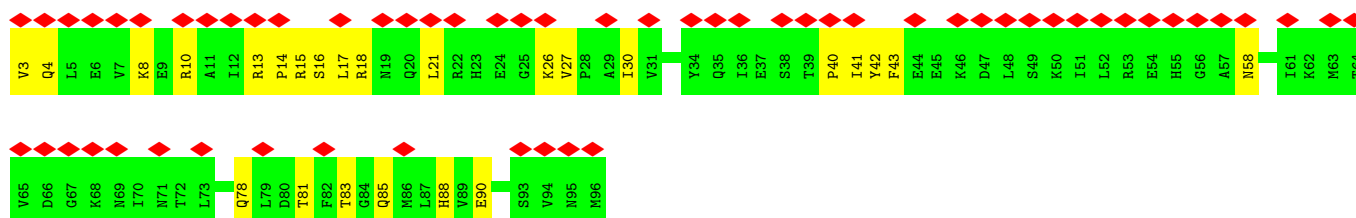
- Molecule 40: 50S ribosomal protein L24

Chain V:  80% 19% .



- Molecule 41: 50S ribosomal protein L25

Chain W:  63% 73% 27%



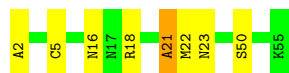
- Molecule 42: 50S ribosomal protein L27

Chain X:  89% 11%



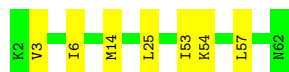
- Molecule 43: 50S ribosomal protein L28

Chain Y:  85% 13% .



- Molecule 44: 50S ribosomal protein L29

Chain Z:  89% 11%

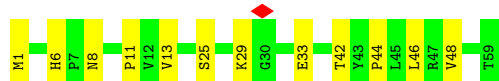
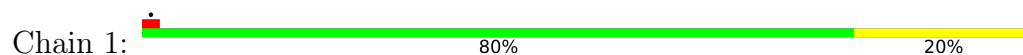


- Molecule 45: 50S ribosomal protein L30

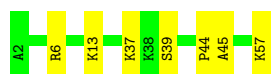
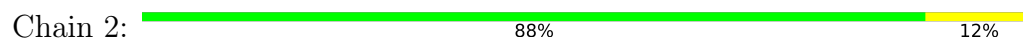
Chain 0:  79% 21%



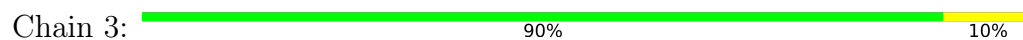
- Molecule 46: 50S ribosomal protein L31 type B



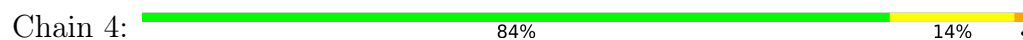
- Molecule 47: 50S ribosomal protein L32



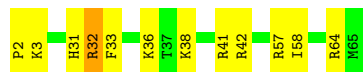
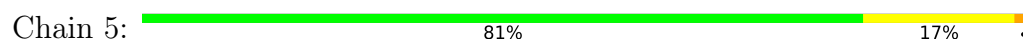
- Molecule 48: 50S ribosomal protein L33



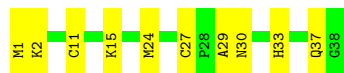
- Molecule 49: 50S ribosomal protein L34



- Molecule 50: 50S ribosomal protein L35



- Molecule 51: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35466	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.098	Depositor
Minimum map value	-0.790	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.238	Depositor
Map size ($\text{\AA}$)	482.68, 482.68, 482.68	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.097, 1.097, 1.097	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.60	6/36545 (0.0%)	0.45	2/56995 (0.0%)
2	c	0.29	0/1635	0.57	0/2197
3	d	2.50	1/1650 (0.1%)	0.70	2/2217 (0.1%)
4	e	0.33	0/1217	0.62	0/1641
5	f	0.30	0/807	0.54	0/1087
6	g	0.26	0/1249	0.59	1/1682 (0.1%)
7	h	0.32	0/1054	0.61	0/1417
8	i	0.27	0/1003	0.64	0/1343
9	j	0.29	0/812	0.69	0/1093
10	k	0.30	0/878	0.61	2/1185 (0.2%)
11	l	0.31	0/1082	0.74	0/1453
12	m	0.26	0/890	0.63	0/1195
13	n	0.28	0/504	0.65	0/669
14	o	0.32	0/751	0.62	0/1001
15	p	0.32	0/720	0.66	0/966
16	q	0.28	0/689	0.59	0/920
17	r	0.32	0/544	0.63	0/728
18	s	0.26	0/650	0.58	0/872
19	t	0.25	0/612	0.58	0/818
20	u	0.31	0/1813	0.46	0/2823
21	v	0.26	0/109	1.39	3/166 (1.8%)
22	A	0.46	0/69780	0.49	3/108830 (0.0%)
23	B	0.38	0/2769	0.53	1/4311 (0.0%)
24	C	0.54	0/2145	0.80	1/2881 (0.0%)
25	D	0.52	0/1599	0.79	0/2145
26	E	0.45	0/1594	0.66	0/2156
27	F	0.31	0/1409	0.64	0/1894
28	G	0.35	0/1362	0.65	0/1833
29	K	0.52	0/1148	0.72	0/1548
30	L	0.51	0/928	0.74	1/1245 (0.1%)
31	M	0.45	0/1102	0.85	2/1470 (0.1%)
32	N	0.46	0/1141	0.84	2/1519 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	O	0.52	0/985	0.87	3/1320 (0.2%)
34	P	0.40	0/870	0.66	0/1163
35	Q	0.49	0/935	0.69	0/1256
36	R	0.54	0/963	0.78	0/1280
37	S	0.46	0/793	0.72	0/1063
38	T	0.47	0/857	0.73	0/1156
39	U	0.46	0/727	0.87	4/972 (0.4%)
40	V	0.39	0/769	0.81	3/1027 (0.3%)
41	W	0.27	0/769	0.70	0/1034
42	X	0.51	0/576	0.68	0/770
43	Y	0.40	0/431	0.67	0/574
44	Z	0.37	0/505	0.61	0/672
45	0	0.46	0/434	0.66	0/583
46	1	0.29	0/486	0.72	0/661
47	2	0.51	0/434	0.66	0/575
48	3	0.36	0/423	0.57	0/563
49	4	0.52	0/377	0.71	0/491
50	5	0.47	0/527	0.77	0/687
51	6	0.48	0/309	0.65	0/409
All	All	0.54	7/152361 (0.0%)	0.54	30/228556 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	c	0	1
3	d	0	3
11	l	0	2
18	s	0	1
19	t	0	1
24	C	0	3
25	D	0	2
26	E	0	1
27	F	0	1
28	G	0	1
29	K	0	1
31	M	0	2
32	N	0	5
33	O	0	1
35	Q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
37	S	0	1
40	V	0	3
42	X	0	1
43	Y	0	1
46	1	0	1
49	4	0	1
All	All	0	34

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	d	2	SER	CA-CB	101.01	3.55	1.53
1	a	561	A	C6-N1	41.74	2.19	1.35
1	a	561	A	N3-C4	40.47	2.15	1.34
1	a	561	A	C2-N3	40.27	2.14	1.33
1	a	561	A	N1-C2	40.13	2.14	1.34
1	a	561	A	C5-C6	38.99	2.19	1.41
1	a	561	A	C5-C4	34.30	2.07	1.38

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	v	18	U	O3'-P-O5'	-15.42	80.87	104.00
3	d	2	SER	CB-CA-C	10.32	129.71	110.10
3	d	2	SER	CA-CB-OG	8.02	127.14	111.10
39	U	49	LYS	CA-C-N	7.45	135.37	121.97
39	U	49	LYS	C-N-CA	7.45	135.37	121.97
33	O	41	ARG	CA-CB-CG	6.86	127.81	114.10
40	V	71	ILE	CA-C-N	6.72	138.19	121.80
40	V	71	ILE	C-N-CA	6.72	138.19	121.80
32	N	9	HIS	CA-C-N	6.30	133.58	121.54
32	N	9	HIS	C-N-CA	6.30	133.58	121.54
33	O	41	ARG	CB-CG-CD	-6.22	96.99	111.30
6	g	69	VAL	N-CA-C	-5.91	106.51	113.42
1	a	561	A	N1-C2-N3	-5.85	111.74	129.30
23	B	98	G	P-O3'-C3'	5.78	128.87	120.20
31	M	15	VAL	CA-C-N	5.64	132.32	121.54
31	M	15	VAL	C-N-CA	5.64	132.32	121.54
21	v	18	U	P-O3'-C3'	-5.50	111.96	120.20
33	O	41	ARG	CB-CA-C	-5.47	102.22	110.92
21	v	18	U	OP2-P-O3'	5.47	124.41	108.00
10	k	38	HIS	CA-C-N	5.47	131.54	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	k	38	HIS	C-N-CA	5.47	131.54	121.70
22	A	1604	A	P-O3'-C3'	5.26	128.10	120.20
39	U	51	ALA	CA-C-N	5.22	131.51	121.54
39	U	51	ALA	C-N-CA	5.22	131.51	121.54
22	A	693	U	P-O3'-C3'	5.14	127.91	120.20
1	a	561	A	C2-N3-C4	5.13	125.98	110.60
30	L	64	ARG	CA-CB-CG	5.12	124.33	114.10
22	A	1584	G	P-O3'-C3'	5.09	127.84	120.20
40	V	72	ASP	N-CA-C	5.04	120.96	109.81
24	C	224	VAL	N-CA-C	-5.00	107.57	113.42

There are no chirality outliers.

All (34) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
46	1	48	VAL	Peptide
49	4	3	ARG	Peptide
24	C	154	LEU	Peptide
24	C	198	GLU	Peptide
24	C	83	TYR	Peptide
25	D	53	TYR	Peptide
25	D	89	GLY	Peptide
26	E	80	SER	Peptide
27	F	3	ARG	Peptide
28	G	47	GLY	Peptide
29	K	45	PHE	Peptide
31	M	30	THR	Peptide
31	M	85	PHE	Peptide
32	N	101	LYS	Peptide
32	N	133	LYS	Peptide
32	N	24	GLY	Peptide
32	N	7	VAL	Peptide
32	N	8	LYS	Peptide
33	O	60	ARG	Peptide
35	Q	49	LYS	Peptide
37	S	49	GLY	Peptide
40	V	72	ASP	Peptide
40	V	87	ASP	Peptide
40	V	97	THR	Peptide
42	X	49	GLN	Peptide
43	Y	21	ALA	Peptide
2	c	22	TRP	Peptide

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Mol	Chain	Res	Type	Group
3	d	187	TYR	Peptide
3	d	188	PRO	Peptide
3	d	189	GLU	Peptide
11	l	133	LYS	Peptide
11	l	37	ASN	Peptide
18	s	41	PHE	Peptide
19	t	66	ILE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32646	0	16441	355	0
2	c	1610	0	1653	19	0
3	d	1620	0	1641	43	0
4	e	1204	0	1280	17	0
5	f	795	0	789	6	0
6	g	1229	0	1259	20	0
7	h	1041	0	1092	14	0
8	i	990	0	1035	24	0
9	j	800	0	846	13	0
10	k	863	0	882	8	0
11	l	1065	0	1133	28	0
12	m	884	0	932	13	0
13	n	492	0	509	8	0
14	o	741	0	756	9	0
15	p	708	0	746	29	0
16	q	681	0	719	13	0
17	r	537	0	572	6	0
18	s	634	0	649	12	0
19	t	610	0	640	13	0
20	u	1623	0	821	25	0
21	v	100	0	52	0	0
22	A	62301	0	31306	415	0
23	B	2478	0	1246	24	0
24	C	2113	0	2195	39	0
25	D	1578	0	1658	21	0
26	E	1573	0	1617	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	F	1391	0	1449	28	0
28	G	1344	0	1373	15	0
29	K	1129	0	1167	16	0
30	L	921	0	981	4	0
31	M	1094	0	1145	15	0
32	N	1118	0	1180	20	0
33	O	978	0	1010	17	0
34	P	862	0	884	7	0
35	Q	923	0	977	22	0
36	R	950	0	1009	17	0
37	S	783	0	823	13	0
38	T	848	0	901	12	0
39	U	720	0	772	11	0
40	V	762	0	821	14	0
41	W	758	0	780	20	0
42	X	571	0	575	7	0
43	Y	425	0	460	5	0
44	Z	504	0	538	5	0
45	0	434	0	470	9	0
46	1	472	0	440	8	0
47	2	428	0	445	6	0
48	3	419	0	435	4	0
49	4	374	0	424	5	0
50	5	521	0	576	12	0
51	6	304	0	338	7	0
52	2	1	0	0	0	0
52	3	1	0	0	0	0
52	6	1	0	0	0	0
52	n	1	0	0	0	0
All	All	139953	0	92442	1283	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 6.

All (1283) 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)
1:a:561:A:C4	1:a:561:A:C5	2.07	1.32
1:a:561:A:C5	1:a:561:A:C6	2.19	1.31
22:A:2818:G:C2	22:A:2818:G:C4	2.20	1.25
1:a:561:A:C2	1:a:561:A:N1	2.14	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:561:A:C4	1:a:561:A:N3	2.15	1.15
1:a:561:A:C2	1:a:561:A:N3	2.14	1.15
22:A:2757:C:C6	22:A:2757:C:C4	2.34	1.13
23:B:88:C:C2	23:B:88:C:C4	2.32	1.11
1:a:561:A:C6	1:a:561:A:N1	2.19	1.11
22:A:2878:G:C4	22:A:2878:G:C6	2.39	1.06
8:i:46:GLU:O	8:i:50:GLN:HB2	1.55	1.04
22:A:275:A:H62	22:A:296:G:N2	1.56	1.03
22:A:2761:G:N2	22:A:2771:A:H62	1.62	0.97
42:X:50:ARG:CG	42:X:50:ARG:NE	2.28	0.96
1:a:222:G:H1	1:a:231:U:H3	1.01	0.95
1:a:1019:G:C2	1:a:1052:A:N6	2.34	0.95
22:A:2761:G:H21	22:A:2771:A:N6	1.65	0.93
1:a:220:G:H1	1:a:233:U:H3	1.09	0.93
1:a:59:U:H3	1:a:110:G:H1	0.95	0.92
24:C:88:SER:C	24:C:89:ALA:CA	2.42	0.92
1:a:1257:G:H1	1:a:1310:U:H3	0.96	0.92
1:a:1460:U:H3	1:a:1473:G:H1	1.15	0.92
22:A:275:A:N6	22:A:296:G:H21	1.66	0.92
25:D:155:PHE:CG	25:D:155:PHE:CA	2.53	0.92
22:A:1039:U:H3	22:A:1195:A:N6	1.67	0.91
33:O:14:LYS:CE	33:O:14:LYS:CG	2.50	0.89
1:a:1135:U:H3	1:a:1169:G:H1	1.20	0.88
22:A:2114:U:H3	22:A:2203:G:H1	0.91	0.88
22:A:2150:A:C2	22:A:2170:G:N1	2.40	0.88
22:A:2576:U:C5	22:A:2576:U:N1	2.37	0.87
22:A:275:A:H62	22:A:296:G:H21	0.89	0.84
1:a:425:G:H21	1:a:447:A:H62	1.20	0.84
22:A:1926:A:H62	22:A:1931:U:H3	1.23	0.84
31:M:133:GLN:CG	31:M:133:GLN:NE2	2.41	0.83
40:V:62:PRO:C	40:V:62:PRO:CB	2.52	0.83
20:u:19:G:H1	22:A:2128:A:N6	1.75	0.83
19:t:59:MET:O	19:t:63:LYS:HB3	1.79	0.82
45:0:6:ILE:CA	45:0:7:THR:N	2.42	0.82
29:K:61:ASP:CA	29:K:62:LYS:N	2.43	0.82
22:A:1039:U:H3	22:A:1195:A:H62	0.83	0.81
22:A:2761:G:H21	22:A:2771:A:H62	0.82	0.81
37:S:30:GLY:CA	37:S:31:GLU:N	2.43	0.81
35:Q:101:ARG:CA	35:Q:102:ALA:N	2.43	0.81
24:C:262:LYS:CA	24:C:263:LYS:N	2.44	0.81
1:a:464:A:H62	1:a:501:U:H3	1.28	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1019:G:N2	1:a:1052:A:C6	2.48	0.80
28:G:69:ARG:CA	28:G:70:ALA:N	2.44	0.80
1:a:425:G:N2	1:a:447:A:H62	1.81	0.79
27:F:80:ARG:CG	27:F:80:ARG:NE	2.47	0.78
22:A:2878:G:C6	22:A:2878:G:N7	2.52	0.77
1:a:65:G:H1	1:a:106:A:H2	1.29	0.77
1:a:780:G:H1	1:a:827:G:HO2'	1.32	0.75
22:A:902:A:N7	22:A:903:G:N2	2.35	0.73
22:A:2701:U:H3	22:A:2736:G:H1	1.35	0.73
22:A:2394:U:C2'	22:A:2394:U:N1	2.52	0.73
22:A:2279:U:O2	22:A:2290:G:C2	2.41	0.72
29:K:61:ASP:CA	29:K:61:ASP:O	2.37	0.72
6:g:70:MET:HG2	6:g:96:ARG:HG2	1.71	0.72
22:A:2697:C:O2	22:A:2697:C:N3	2.21	0.72
31:M:133:GLN:CG	31:M:133:GLN:OE1	2.38	0.72
1:a:561:A:N1	3:d:2:SER:HA	2.05	0.72
24:C:262:LYS:CA	24:C:262:LYS:O	2.38	0.72
15:p:9:ARG:HE	15:p:29:ARG:HH22	1.38	0.72
37:S:30:GLY:CA	37:S:30:GLY:O	2.38	0.72
35:Q:101:ARG:O	35:Q:102:ALA:N	2.24	0.71
40:V:72:ASP:HB2	40:V:76:GLY:H	1.55	0.71
28:G:69:ARG:CA	28:G:69:ARG:O	2.39	0.71
29:K:61:ASP:O	29:K:62:LYS:N	2.24	0.71
24:C:262:LYS:O	24:C:263:LYS:N	2.24	0.71
31:M:133:GLN:NE2	31:M:133:GLN:OE1	2.24	0.71
35:Q:101:ARG:CA	35:Q:101:ARG:O	2.39	0.71
45:O:6:ILE:CA	45:O:6:ILE:O	2.39	0.70
1:a:1053:C:H2'	1:a:1054:A:H8	1.55	0.70
20:u:19:G:H1	22:A:2128:A:H62	1.36	0.70
1:a:1019:G:N2	1:a:1052:A:C5	2.59	0.70
26:E:115:SER:CA	26:E:115:SER:OG	2.40	0.70
37:S:30:GLY:O	37:S:31:GLU:N	2.24	0.70
22:A:2464:A:H62	22:A:2515:C:H42	1.39	0.69
1:a:1019:G:N2	1:a:1052:A:N6	2.40	0.69
47:2:57:LYS:CA	47:2:57:LYS:O	2.39	0.69
28:G:69:ARG:O	28:G:70:ALA:N	2.26	0.69
40:V:62:PRO:C	40:V:62:PRO:N	2.51	0.69
20:u:19:G:N1	22:A:2128:A:N6	2.40	0.68
20:u:57:G:N1	22:A:2126:A:C2	2.61	0.68
45:O:6:ILE:O	45:O:7:THR:N	2.26	0.68
23:B:16:G:H1	23:B:63:U:H3	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:561:A:C6	3:d:2:SER:CB	2.77	0.68
1:a:391:G:H1	1:a:402:U:H3	1.41	0.67
29:K:77:ARG:HH22	29:K:100:ARG:HH11	1.42	0.67
22:A:366:G:H1	40:V:15:LYS:HE3	1.60	0.66
12:m:81:MET:HG3	12:m:82:GLU:HG3	1.77	0.66
20:u:19:G:N2	22:A:2128:A:N7	2.44	0.66
22:A:2139:G:H21	22:A:2187:A:H62	1.43	0.66
1:a:1023:A:N1	1:a:1038:C:N3	2.44	0.66
1:a:561:A:C4	3:d:2:SER:CB	2.79	0.65
1:a:464:A:N7	1:a:501:U:O4	2.29	0.65
22:A:162:A:N7	22:A:167:A:N6	2.43	0.65
22:A:1454:U:N3	22:A:1456:G:N1	2.43	0.65
24:C:94:VAL:HG21	24:C:104:ILE:HD12	1.78	0.65
22:A:84:G:H1	22:A:102:G:HO2'	1.44	0.65
15:p:41:ASN:HB3	15:p:47:ALA:HB1	1.80	0.65
1:a:307:G:H21	1:a:623:A:H61	1.45	0.64
22:A:287:G:H22	22:A:289:U:H5'	1.61	0.64
46:1:13:VAL:HB	46:1:44:PRO:HB3	1.79	0.64
22:A:510:A:OP1	26:E:79:ARG:NH2	2.31	0.64
1:a:561:A:C5	3:d:2:SER:CB	2.81	0.64
5:f:9:ILE:HG12	5:f:95:ILE:HG12	1.78	0.64
22:A:1815:A:OP2	24:C:150:LYS:NZ	2.30	0.64
35:Q:62:ARG:HG2	35:Q:71:GLU:HG2	1.80	0.64
19:t:74:ASP:O	19:t:78:LEU:HB2	1.97	0.64
22:A:2697:C:N3	22:A:2697:C:N1	2.37	0.64
18:s:39:THR:HA	18:s:70:LYS:HA	1.79	0.64
22:A:1254:U:OP1	36:R:15:LYS:NZ	2.31	0.64
22:A:2130:G:H1	22:A:2180:G:H21	1.45	0.63
22:A:346:A:N7	22:A:367:A:N6	2.46	0.63
22:A:1288:A:H5''	36:R:13:ARG:HH12	1.64	0.63
1:a:679:G:H22	1:a:756:G:H1	1.47	0.63
4:e:161:VAL:HG13	4:e:162:GLU:HG2	1.81	0.63
22:A:1039:U:N3	22:A:1195:A:N6	2.36	0.63
22:A:2090:U:OP2	22:A:2252:G:N2	2.31	0.63
15:p:9:ARG:HG2	15:p:29:ARG:HH12	1.63	0.63
1:a:561:A:C2	3:d:2:SER:CB	2.82	0.63
22:A:1454:U:N3	22:A:1456:G:C6	2.57	0.63
31:M:79:LEU:HD21	31:M:117:LEU:HB2	1.81	0.63
22:A:731:C:OP1	24:C:217:ARG:NH2	2.31	0.62
22:A:785:G:H21	22:A:790:A:H61	1.45	0.62
22:A:1039:U:C2	22:A:1195:A:N6	2.66	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1114:G:N3	22:A:1115:C:N4	2.46	0.62
32:N:17:MET:SD	32:N:17:MET:N	2.72	0.62
22:A:2027:A:N3	38:T:93:ARG:NH2	2.46	0.62
11:l:127:ARG:HG3	11:l:133:LYS:HG2	1.82	0.62
37:S:14:VAL:HG13	37:S:97:ILE:HD13	1.81	0.62
1:a:561:A:C4	3:d:2:SER:CA	2.83	0.62
22:A:1050:A:OP1	36:R:66:ASN:ND2	2.32	0.62
11:l:41:PRO:HG2	11:l:42:GLN:HG2	1.82	0.62
22:A:1396:G:H22	22:A:2228:C:H42	1.46	0.61
22:A:2697:C:O2	22:A:2697:C:N1	2.32	0.61
1:a:561:A:C6	3:d:2:SER:CA	2.83	0.61
1:a:475:G:N2	1:a:489:G:O2'	2.33	0.61
6:g:119:ARG:O	6:g:123:GLU:HB2	2.00	0.61
22:A:2218:C:H2'	22:A:2219:A:H8	1.65	0.61
23:B:12:U:OP2	42:X:83:ARG:NH2	2.33	0.61
27:F:4:LEU:HA	27:F:7:LYS:HB2	1.82	0.61
1:a:1475:C:OP1	19:t:26:ASN:ND2	2.33	0.61
22:A:262:G:H21	22:A:660:A:H8	1.49	0.61
27:F:139:PRO:HB2	46:l:46:LEU:HD22	1.83	0.61
1:a:1062:A:N6	1:a:1226:U:O2'	2.33	0.61
38:T:73:SER:HB2	38:T:115:LYS:HE3	1.83	0.61
22:A:2636:C:O2'	22:A:2836:G:N2	2.33	0.61
1:a:465:G:H5''	15:p:45:ASP:HB2	1.82	0.60
1:a:561:A:N3	3:d:2:SER:N	2.49	0.60
22:A:2883:G:H21	33:O:4:ARG:HH22	1.48	0.60
22:A:1499:G:H22	22:A:2716:G:H22	1.49	0.60
22:A:2182:G:N2	22:A:2185:A:O4'	2.33	0.60
25:D:125:ARG:NE	25:D:162:GLY:O	2.32	0.60
1:a:1419:C:H42	1:a:1513:G:H1	1.48	0.60
27:F:37:ASN:HB2	27:F:153:ASP:HB2	1.84	0.60
31:M:75:ALA:HB2	31:M:106:LYS:H	1.66	0.60
1:a:1204:U:OP1	9:j:53:ARG:NH2	2.35	0.60
22:A:1454:U:O2	22:A:1456:G:N2	2.34	0.60
1:a:391:G:H5''	15:p:6:ARG:HB2	1.84	0.60
22:A:2540:G:H1	22:A:2551:U:H3	1.49	0.60
22:A:380:C:H2'	22:A:381:G:H8	1.65	0.60
33:O:24:LEU:HG	33:O:30:ILE:HD12	1.84	0.60
22:A:632:U:H2'	22:A:633:G:H8	1.67	0.60
22:A:2401:U:O2'	42:X:50:ARG:NH1	2.35	0.60
1:a:1248:G:OP1	8:i:119:LYS:NZ	2.34	0.60
15:p:81:LYS:O	15:p:85:GLU:HB2	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:486:G:H21	22:A:494:A:N6	1.99	0.60
1:a:1043:C:N4	1:a:1052:A:N1	2.50	0.59
22:A:905:G:N2	22:A:949:U:O4	2.35	0.59
22:A:2139:G:N2	22:A:2187:A:H62	1.99	0.59
1:a:422:A:OP1	3:d:109:ARG:NH2	2.35	0.59
1:a:838:G:HO2'	7:h:2:VAL:N	1.98	0.59
22:A:568:A:H2	22:A:2055:U:H3	1.49	0.59
1:a:315:A:OP2	1:a:316:G:N2	2.35	0.59
22:A:1359:G:OP1	38:T:103:LYS:NZ	2.32	0.59
1:a:397:A:H2'	1:a:398:A:H8	1.68	0.59
1:a:1271:U:O2'	1:a:1293:A:N6	2.35	0.59
29:K:69:LYS:HA	29:K:72:ASP:HB2	1.84	0.59
1:a:420:U:H1'	1:a:513:A:H2'	1.83	0.59
1:a:1412:C:OP2	4:e:29:ARG:NH2	2.35	0.59
22:A:2150:A:N1	22:A:2170:G:O6	2.36	0.59
36:R:41:ASN:HA	36:R:44:TYR:HD2	1.67	0.59
22:A:854:C:H1'	22:A:1262:G:H21	1.66	0.59
22:A:2394:U:N1	22:A:2394:U:O4'	2.35	0.59
1:a:1343:C:H2'	1:a:1344:A:H8	1.67	0.59
1:a:1427:C:H2'	1:a:1428:A:H8	1.68	0.59
16:q:70:LEU:HD11	16:q:77:ARG:HE	1.67	0.59
22:A:874:U:H2'	22:A:875:A:H8	1.67	0.59
22:A:1140:C:N4	22:A:1145:U:O4	2.36	0.59
22:A:2875:U:OP1	35:Q:115:ARG:NH2	2.33	0.59
28:G:52:PHE:H	28:G:69:ARG:HH22	1.50	0.59
1:a:141:C:O2	15:p:26:ARG:NH2	2.36	0.58
22:A:1118:C:O2'	22:A:1128:A:N3	2.35	0.58
7:h:25:LEU:HB3	7:h:62:VAL:HB	1.85	0.58
12:m:94:GLY:HA2	12:m:109:ARG:HH12	1.68	0.58
7:h:12:THR:HG22	7:h:15:ARG:HH21	1.68	0.58
22:A:2321:G:OP1	22:A:2322:G:N2	2.37	0.58
26:E:63:LYS:HG2	26:E:76:GLY:HA2	1.86	0.58
1:a:518:A:H62	11:l:125:GLN:HE21	1.52	0.58
20:u:26:A:H61	20:u:44:G:H1	1.52	0.58
22:A:1831:G:OP1	24:C:87:ARG:NH2	2.36	0.58
50:5:33:PHE:O	50:5:41:ARG:NH2	2.36	0.58
1:a:434:U:H3	1:a:439:G:H1	1.50	0.58
1:a:1029:G:H21	1:a:1032:A:H62	1.51	0.58
22:A:638:C:O2'	26:E:104:LYS:NZ	2.36	0.58
22:A:2327:C:H1'	27:F:37:ASN:HD21	1.68	0.58
22:A:2520:U:O2	22:A:2597:G:N2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:561:A:N1	3:d:2:SER:CB	2.67	0.58
1:a:1137:U:H3	1:a:1167:G:H1	1.50	0.58
22:A:1457:A:H61	22:A:1630:G:H5'	1.67	0.58
22:A:2767:A:O2'	51:6:15:LYS:NZ	2.37	0.58
25:D:33:ASN:ND2	25:D:97:ILE:O	2.34	0.58
26:E:12:THR:HG22	26:E:13:GLN:HG3	1.85	0.58
32:N:28:ALA:O	32:N:134:ARG:NH2	2.36	0.58
1:a:561:A:C2	3:d:2:SER:CA	2.86	0.57
2:c:11:ARG:NH2	2:c:176:THR:O	2.38	0.57
1:a:59:U:O2	1:a:110:G:N2	2.31	0.57
1:a:673:G:OP1	14:o:8:LYS:NZ	2.37	0.57
22:A:1499:G:H1	22:A:2716:G:H1	1.50	0.57
23:B:95:U:OP2	41:W:13:ARG:NH1	2.37	0.57
32:N:70:PRO:HA	32:N:95:SER:HB3	1.86	0.57
8:i:28:ILE:HA	8:i:63:VAL:HB	1.87	0.57
23:B:75:U:OP2	41:W:18:ARG:NH1	2.38	0.57
33:O:7:GLY:H	33:O:13:ARG:HE	1.50	0.57
42:X:27:SER:O	42:X:29:ARG:NH1	2.37	0.57
22:A:1183:A:OP1	29:K:28:ARG:NH2	2.37	0.57
24:C:67:PHE:HB3	24:C:152:GLY:H	1.70	0.57
1:a:419:G:OP2	3:d:112:ARG:NH2	2.37	0.57
1:a:740:G:OP1	1:a:869:G:N2	2.38	0.57
3:d:12:SER:HB3	3:d:29:ARG:HH22	1.70	0.57
22:A:1449:U:OP1	22:A:1633:A:N6	2.37	0.57
24:C:124:ILE:HG23	24:C:192:ILE:HD13	1.86	0.57
1:a:201:C:N4	16:q:4:GLU:OE1	2.37	0.57
11:l:7:LEU:HD22	11:l:12:ARG:HD2	1.86	0.57
22:A:1400:G:OP2	43:Y:2:ALA:N	2.37	0.57
1:a:525:A:O2'	1:a:556:G:N2	2.38	0.57
1:a:1087:C:H2'	1:a:1088:G:H8	1.70	0.57
15:p:60:LEU:HD21	15:p:66:PRO:HD3	1.86	0.57
36:R:52:GLN:HG2	36:R:55:ARG:HD2	1.86	0.57
37:S:5:ILE:HD12	37:S:14:VAL:HG21	1.87	0.57
40:V:75:ASN:ND2	40:V:99:GLU:OE2	2.38	0.57
1:a:529:C:H2'	1:a:530:G:H8	1.69	0.57
3:d:80:GLU:O	3:d:86:ASN:ND2	2.37	0.57
22:A:2114:U:O2	22:A:2203:G:N2	2.31	0.57
2:c:24:ALA:HB2	2:c:58:ARG:HH12	1.69	0.56
14:o:26:GLU:HG2	14:o:81:LEU:HD11	1.85	0.56
15:p:74:LEU:O	15:p:79:VAL:N	2.34	0.56
1:a:1200:G:H4'	8:i:109:ARG:HH22	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:54:ILE:HG12	2:c:67:ILE:HG22	1.87	0.56
33:O:22:THR:HG21	33:O:67:ARG:H	1.70	0.56
34:P:45:ILE:HG12	34:P:52:THR:HG22	1.87	0.56
45:O:5:LYS:HG2	45:O:36:THR:HG22	1.87	0.56
1:a:217:A:O2'	1:a:235:G:N2	2.39	0.56
1:a:561:A:C2	3:d:2:SER:HB3	2.40	0.56
1:a:965:A:OP1	12:m:100:GLN:NE2	2.33	0.56
1:a:1374:C:O2'	1:a:1377:C:N4	2.38	0.56
22:A:1755:C:H2'	22:A:1756:U:H4'	1.86	0.56
26:E:49:HIS:HD2	26:E:92:PRO:HB2	1.70	0.56
29:K:63:VAL:O	29:K:94:ARG:NH2	2.38	0.56
1:a:338:U:H3	1:a:342:A:H62	1.52	0.56
22:A:1256:G:OP1	36:R:22:LYS:NZ	2.38	0.56
28:G:84:GLN:HG2	28:G:134:LYS:HG2	1.88	0.56
27:F:40:VAL:HG12	27:F:42:ASP:H	1.69	0.56
1:a:361:G:OP2	35:Q:39:ARG:NH1	2.39	0.56
1:a:437:C:O2	1:a:438:G:N1	2.39	0.56
1:a:561:A:C5	3:d:2:SER:CA	2.88	0.56
14:o:29:ILE:HD11	14:o:81:LEU:HD13	1.87	0.56
46:1:33:GLU:HB2	46:1:44:PRO:HG2	1.87	0.56
50:5:36:LYS:O	50:5:41:ARG:NH2	2.34	0.56
22:A:1710:G:N2	22:A:2006:G:OP2	2.37	0.56
22:A:2702:G:N1	22:A:2734:U:OP2	2.35	0.56
41:W:10:ARG:HD3	41:W:40:PRO:HB2	1.87	0.56
47:2:37:LYS:HZ1	47:2:45:ALA:HB3	1.71	0.56
1:a:561:A:C6	3:d:2:SER:HB2	2.39	0.56
25:D:69:VAL:HG21	25:D:76:PRO:HA	1.88	0.56
35:Q:53:ALA:H	35:Q:57:GLU:HG2	1.69	0.56
22:A:860:A:N3	22:A:983:U:O2'	2.38	0.55
22:A:1143:A:N6	22:A:1144:C:N3	2.53	0.55
22:A:1454:U:C2	22:A:1456:G:N1	2.75	0.55
32:N:65:TRP:HB2	32:N:105:GLU:HB2	1.88	0.55
1:a:390:U:OP1	15:p:69:THR:OG1	2.21	0.55
1:a:560:C:OP2	3:d:55:GLN:NE2	2.39	0.55
7:h:79:ARG:NH2	7:h:81:SER:O	2.38	0.55
3:d:156:VAL:O	3:d:162:ARG:NH2	2.39	0.55
15:p:83:HIS:O	15:p:87:LYS:HB2	2.06	0.55
22:A:2483:A:O2'	32:N:56:ARG:NH1	2.39	0.55
27:F:31:VAL:HG22	27:F:158:THR:HG22	1.88	0.55
1:a:1004:G:H21	1:a:1031:G:H22	1.54	0.55
23:B:47:C:H2'	23:B:48:A:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:67:U:H3	1:a:104:G:H1	1.55	0.55
1:a:1023:A:N6	1:a:1038:C:N4	2.55	0.55
22:A:1756:U:O2'	22:A:1760:G:N2	2.39	0.55
23:B:78:U:H2'	23:B:79:G:H21	1.71	0.55
25:D:178:LYS:HB2	25:D:187:LEU:HD12	1.88	0.55
27:F:54:VAL:HG13	27:F:65:PRO:HD2	1.87	0.55
43:Y:5:CYS:SG	43:Y:50:SER:OG	2.63	0.55
1:a:892:A:OP1	7:h:15:ARG:NH1	2.36	0.55
1:a:1442:C:H2'	1:a:1443:A:H8	1.72	0.55
22:A:2856:A:H62	22:A:2882:G:N2	2.05	0.55
32:N:27:VAL:HG23	32:N:102:ILE:HD13	1.89	0.55
32:N:36:ALA:H	32:N:100:GLY:HA2	1.72	0.55
1:a:561:A:N3	3:d:2:SER:CB	2.70	0.55
1:a:1262:U:O2	1:a:1305:G:O6	2.25	0.55
2:c:63:VAL:HB	2:c:98:VAL:HA	1.88	0.55
18:s:34:TRP:HD1	18:s:36:ARG:H	1.55	0.55
1:a:1056:A:H2'	1:a:1057:G:H8	1.71	0.55
22:A:669:G:H1	31:M:71:ARG:HH12	1.54	0.55
22:A:2255:A:H2'	22:A:2256:G:H8	1.72	0.55
1:a:760:U:H2'	1:a:761:G:H8	1.72	0.55
22:A:345:G:N2	22:A:517:A:N7	2.55	0.55
1:a:1164:C:OP2	8:i:11:ARG:NH2	2.40	0.55
1:a:1262:U:C2	1:a:1305:G:O6	2.59	0.55
22:A:1330:C:O2	33:O:67:ARG:NH2	2.40	0.55
22:A:1455:U:N3	22:A:1457:A:C8	2.69	0.55
22:A:2529:C:H2'	22:A:2530:G:H8	1.70	0.55
30:L:73:ASP:OD1	35:Q:80:ARG:NH1	2.39	0.55
1:a:1162:C:O2	8:i:18:ARG:NH1	2.39	0.54
1:a:1390:A:N7	6:g:10:ARG:NH1	2.55	0.54
22:A:516:G:N1	22:A:519:A:OP2	2.40	0.54
26:E:14:ASN:ND2	26:E:127:GLU:OE2	2.40	0.54
49:4:34:ARG:HH11	49:4:39:ARG:HD2	1.72	0.54
1:a:1416:G:O6	1:a:1520:G:N2	2.40	0.54
8:i:106:ARG:NH1	8:i:107:ASP:O	2.40	0.54
22:A:2085:A:H2'	22:A:2086:G:H8	1.72	0.54
15:p:74:LEU:HB3	15:p:79:VAL:HB	1.89	0.54
22:A:145:G:OP1	39:U:34:ASN:ND2	2.41	0.54
22:A:1106:U:O2'	22:A:1109:A:N6	2.40	0.54
22:A:2047:A:O2'	22:A:2049:G:OP2	2.24	0.54
1:a:261:A:N1	1:a:293:C:O2'	2.41	0.54
1:a:1453:G:OP2	19:t:29:ARG:NH1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1178:G:H21	29:K:109:MET:HE1	1.71	0.54
22:A:2856:A:H62	22:A:2882:G:H21	1.54	0.54
25:D:19:SER:O	35:Q:80:ARG:NH2	2.40	0.54
9:j:10:LEU:HB2	9:j:72:ARG:HB2	1.88	0.54
22:A:744:G:O2'	22:A:766:G:N2	2.41	0.54
22:A:1133:G:N1	22:A:1138:A:N7	2.47	0.54
22:A:2061:C:H2'	22:A:2062:G:H8	1.73	0.54
24:C:39:ASN:OD1	24:C:215:ARG:NH1	2.41	0.54
22:A:451:G:OP2	22:A:2420:C:O2'	2.26	0.54
22:A:1081:U:H2'	22:A:1082:G:H8	1.72	0.54
1:a:37:C:O2	1:a:38:G:N1	2.41	0.54
1:a:311:U:N3	1:a:317:G:O6	2.37	0.54
1:a:688:G:H2'	1:a:689:G:C8	2.42	0.54
1:a:1181:G:N1	1:a:1184:A:OP2	2.31	0.54
3:d:94:ARG:HG2	3:d:96:ASP:H	1.71	0.54
23:B:8:G:H1	23:B:108:U:H3	1.56	0.54
37:S:4:ILE:HD12	37:S:40:LEU:HD12	1.89	0.54
1:a:924:A:H2'	1:a:925:A:H8	1.73	0.54
1:a:994:A:O2'	1:a:1337:C:O2	2.23	0.54
22:A:485:C:OP1	36:R:2:ALA:N	2.41	0.54
22:A:2054:U:OP2	29:K:112:LYS:NZ	2.39	0.54
22:A:2520:U:N3	22:A:2597:G:N1	2.48	0.54
22:A:2125:U:O4	22:A:2162:G:N2	2.41	0.54
1:a:312:G:O2'	1:a:314:G:N7	2.39	0.53
5:f:29:PHE:HA	5:f:32:ILE:HG12	1.91	0.53
12:m:16:VAL:O	12:m:20:THR:OG1	2.26	0.53
41:W:8:LYS:HB2	41:W:42:TYR:HB2	1.90	0.53
1:a:65:G:O6	1:a:106:A:N1	2.41	0.53
5:f:29:PHE:HZ	5:f:87:ASN:HD21	1.56	0.53
22:A:872:G:H5'	31:M:38:GLN:HE21	1.72	0.53
22:A:1508:G:H21	22:A:1590:A:H2	1.55	0.53
1:a:360:C:OP2	35:Q:37:ARG:NH1	2.42	0.53
1:a:1045:U:H3	1:a:1050:G:H1	1.55	0.53
22:A:1926:A:N7	22:A:1931:U:O4	2.41	0.53
32:N:3:VAL:HG11	32:N:6:ARG:HE	1.72	0.53
1:a:797:A:H62	1:a:815:G:H21	1.57	0.53
22:A:1692:G:O2'	33:O:116:ASP:OD2	2.24	0.53
22:A:1793:U:H5''	22:A:1794:A:H5''	1.90	0.53
6:g:58:PRO:HA	6:g:61:VAL:HG12	1.91	0.53
15:p:73:ILE:HG13	15:p:74:LEU:HD12	1.90	0.53
32:N:38:GLU:HB2	32:N:127:VAL:HG13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:16:C:OP1	4:e:135:ASN:ND2	2.42	0.53
1:a:1200:G:O2'	8:i:109:ARG:NH1	2.38	0.53
1:a:1237:G:OP1	18:s:78:ARG:NH1	2.39	0.53
26:E:20:ASN:HD22	26:E:23:ILE:HD12	1.72	0.53
28:G:5:GLY:HA3	28:G:65:HIS:HB3	1.91	0.53
1:a:474:C:N3	1:a:490:U:O4	2.42	0.53
1:a:1362:G:O6	8:i:12:ARG:NH2	2.42	0.53
15:p:6:ARG:NH2	15:p:28:PRO:O	2.41	0.53
22:A:1038:C:OP1	36:R:84:LYS:NZ	2.37	0.53
1:a:754:C:H1'	14:o:46:HIS:HE1	1.73	0.53
1:a:1193:G:N2	1:a:1196:G:OP2	2.42	0.53
15:p:11:GLY:HA2	15:p:16:PRO:HA	1.89	0.53
22:A:674:C:O2'	22:A:678:U:OP1	2.27	0.53
24:C:180:GLU:HG2	24:C:273:ARG:HA	1.90	0.53
29:K:126:TYR:OH	29:K:133:HIS:NE2	2.41	0.53
1:a:1023:A:N6	1:a:1038:C:C4	2.76	0.53
22:A:325:U:H2'	22:A:326:A:H8	1.73	0.53
22:A:782:U:H2'	22:A:783:A:C8	2.43	0.53
23:B:83:G:H2'	23:B:84:G:C8	2.44	0.53
1:a:1362:G:N2	1:a:1389:A:OP2	2.42	0.52
22:A:2150:A:N1	22:A:2170:G:C6	2.76	0.52
24:C:230:HIS:HE1	24:C:232:HIS:HD2	1.56	0.52
1:a:565:G:O2'	11:l:129:LYS:NZ	2.39	0.52
22:A:1033:A:OP2	36:R:51:ARG:NH2	2.42	0.52
22:A:1319:G:N2	22:A:1322:A:OP2	2.42	0.52
22:A:2276:U:O2'	22:A:2342:A:N3	2.39	0.52
25:D:34:VAL:HG21	25:D:74:THR:HG21	1.91	0.52
27:F:8:TYR:HA	27:F:12:VAL:HB	1.91	0.52
32:N:138:GLY:HA2	41:W:58:ASN:HD21	1.74	0.52
38:T:74:LEU:HD23	38:T:114:GLU:HA	1.90	0.52
1:a:377:G:N2	1:a:380:U:OP2	2.42	0.52
1:a:964:C:OP1	12:m:108:THR:OG1	2.26	0.52
22:A:1454:U:O2	22:A:1456:G:C2	2.62	0.52
15:p:79:VAL:O	15:p:83:HIS:N	2.42	0.52
22:A:275:A:N6	22:A:296:G:N2	2.38	0.52
22:A:1950:A:OP2	22:A:1976:C:N4	2.40	0.52
22:A:2698:U:OP2	35:Q:51:ARG:NH1	2.42	0.52
1:a:1021:C:N4	1:a:1041:U:OP1	2.42	0.52
28:G:54:ARG:HH12	28:G:68:THR:HG1	1.58	0.52
20:u:19:G:N2	22:A:2127:C:N3	2.44	0.52
29:K:34:ALA:O	29:K:38:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:P:33:ILE:HD13	34:P:104:VAL:HG23	1.92	0.52
48:3:21:LYS:NZ	48:3:28:ASP:O	2.43	0.52
1:a:312:G:N2	1:a:316:G:H22	2.06	0.52
1:a:1140:G:N2	1:a:1141:U:O4	2.37	0.52
22:A:491:U:O2	22:A:493:A:N6	2.42	0.52
22:A:2025:U:OP2	38:T:21:LYS:NZ	2.38	0.52
22:A:2142:C:N3	22:A:2174:G:N2	2.58	0.52
24:C:135:ILE:HG21	24:C:141:ILE:HD11	1.90	0.52
33:O:19:ASP:OD1	33:O:67:ARG:NH2	2.43	0.52
1:a:1331:G:N2	1:a:1333:A:N7	2.58	0.52
6:g:146:ASP:HA	6:g:149:ARG:HB2	1.91	0.52
22:A:824:U:O4	24:C:228:ASN:ND2	2.25	0.52
22:A:900:G:H22	22:A:956:C:H5	1.57	0.52
45:0:7:THR:HG22	45:0:34:THR:HG22	1.91	0.52
51:6:11:CYS:SG	51:6:33:HIS:NE2	2.83	0.52
1:a:224:U:O2	1:a:229:G:N2	2.40	0.52
4:e:82:PRO:HD2	4:e:147:LEU:HD11	1.92	0.52
16:q:31:LYS:O	16:q:40:ARG:NH2	2.43	0.52
18:s:16:MET:HA	18:s:19:VAL:HG12	1.92	0.52
22:A:769:G:H22	24:C:208:ALA:HB3	1.73	0.52
1:a:346:G:HO2'	19:t:3:ASN:N	2.07	0.52
1:a:561:A:N3	3:d:2:SER:CA	2.73	0.52
15:p:71:ARG:HG3	15:p:80:MET:HG3	1.92	0.52
28:G:42:LYS:HG3	28:G:55:PRO:HD3	1.91	0.52
18:s:22:GLN:NE2	18:s:26:GLU:O	2.43	0.51
22:A:1087:G:N2	22:A:1150:G:O2'	2.39	0.51
24:C:120:PRO:O	24:C:134:ASN:ND2	2.43	0.51
42:X:80:ARG:HA	42:X:86:LYS:HA	1.92	0.51
1:a:562:A:OP1	3:d:3:ARG:NH2	2.43	0.51
24:C:125:LYS:H	24:C:128:ASN:HD22	1.58	0.51
9:j:36:VAL:HG23	9:j:76:ILE:HG12	1.91	0.51
20:u:34:G:H2'	20:u:35:A:H8	1.76	0.51
22:A:1122:U:O2'	22:A:1126:A:N6	2.34	0.51
22:A:1131:G:OP1	22:A:1142:C:O2'	2.27	0.51
27:F:42:ASP:O	27:F:49:ASN:ND2	2.44	0.51
1:a:151:G:H1	1:a:183:G:H1	1.57	0.51
1:a:561:A:N1	3:d:2:SER:CA	2.72	0.51
1:a:914:G:N2	1:a:917:A:OP2	2.42	0.51
1:a:1019:G:H22	1:a:1051:G:H3'	1.76	0.51
2:c:23:TYR:O	2:c:58:ARG:NH1	2.43	0.51
3:d:64:ASN:HB3	3:d:66:ARG:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:41:LYS:HD3	7:h:49:VAL:HG22	1.91	0.51
22:A:610:G:N1	22:A:2045:A:OP1	2.37	0.51
22:A:1500:A:H4'	22:A:1501:A:H5'	1.92	0.51
22:A:2272:C:O2'	22:A:2441:C:OP2	2.28	0.51
35:Q:60:THR:HG22	35:Q:73:THR:HG22	1.92	0.51
47:2:37:LYS:HD3	47:2:44:PRO:HD2	1.92	0.51
1:a:1012:A:N1	1:a:1061:C:O2'	2.39	0.51
8:i:130:ARG:HH22	20:u:33:U:H5	1.58	0.51
14:o:89:ARG:NH1	22:A:757:A:OP2	2.32	0.51
20:u:9:A:OP2	20:u:46:G:N2	2.40	0.51
22:A:1498:G:H2'	22:A:1499:G:H8	1.76	0.51
22:A:2141:G:H21	22:A:2187:A:H1'	1.76	0.51
22:A:2394:U:O4'	22:A:2394:U:C6	2.63	0.51
20:u:23:A:H2'	20:u:24:G:C8	2.46	0.51
22:A:273:A:OP2	22:A:297:G:N1	2.43	0.51
22:A:556:C:OP1	47:2:13:LYS:NZ	2.35	0.51
22:A:873:C:O2'	50:5:57:ARG:NH2	2.43	0.51
1:a:1009:G:N7	1:a:1228:A:N6	2.59	0.51
3:d:153:LYS:HA	3:d:156:VAL:HB	1.93	0.51
22:A:333:U:O2'	40:V:90:LYS:NZ	2.43	0.51
26:E:37:ILE:HG23	26:E:184:LEU:HD21	1.91	0.51
35:Q:91:LYS:HD2	35:Q:111:LYS:HD2	1.93	0.51
22:A:2279:U:O2	22:A:2290:G:N2	2.44	0.51
24:C:79:LYS:HA	24:C:112:VAL:HG13	1.92	0.51
39:U:53:VAL:HG13	39:U:80:VAL:HG22	1.92	0.51
1:a:633:C:N4	1:a:636:A:OP2	2.44	0.51
1:a:640:G:H2'	1:a:641:G:H8	1.75	0.51
16:q:65:MET:HE3	16:q:79:LEU:HD11	1.92	0.51
20:u:68:C:H2'	20:u:69:G:H8	1.75	0.51
22:A:231:A:N3	22:A:232:U:N3	2.59	0.51
22:A:1657:A:N6	38:T:97:SER:O	2.41	0.51
40:V:12:ILE:HD11	40:V:69:MET:HG2	1.93	0.51
40:V:84:LYS:HB2	40:V:93:VAL:HG21	1.92	0.51
6:g:115:THR:HG22	6:g:117:GLU:H	1.75	0.51
16:q:8:ARG:HB2	16:q:65:MET:HG3	1.92	0.51
25:D:2:THR:OG1	25:D:3:LYS:N	2.44	0.51
27:F:36:ILE:HB	27:F:89:VAL:HB	1.93	0.51
50:5:57:ARG:HG3	50:5:58:ILE:HG13	1.92	0.51
4:e:96:MET:HE1	4:e:140:THR:HG23	1.93	0.50
6:g:80:VAL:HG21	6:g:155:ARG:HD3	1.91	0.50
8:i:47:VAL:HG13	8:i:80:ARG:HH21	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:86:ASN:OD1	11:l:112:ARG:NH2	2.44	0.50
16:q:23:THR:OG1	16:q:74:LYS:NZ	2.44	0.50
22:A:1193:C:OP1	36:R:92:ARG:NH2	2.44	0.50
27:F:65:PRO:HB2	27:F:87:ALA:HB1	1.93	0.50
1:a:222:G:N2	1:a:231:U:O2	2.34	0.50
1:a:791:G:N2	1:a:817:A:OP2	2.39	0.50
1:a:1442:C:H2'	1:a:1443:A:C8	2.46	0.50
22:A:1525:U:O2	22:A:1552:A:N6	2.44	0.50
22:A:672:A:O2'	22:A:2418:C:OP1	2.28	0.50
22:A:1262:G:OP1	37:S:70:LYS:NZ	2.43	0.50
22:A:2145:A:O4'	22:A:2172:A:N6	2.44	0.50
22:A:2370:C:H5'	42:X:33:LYS:HZ3	1.76	0.50
29:K:58:ILE:HG23	29:K:129:ALA:HA	1.93	0.50
33:O:21:THR:HG22	33:O:40:VAL:HG13	1.92	0.50
8:i:44:LEU:HB3	8:i:47:VAL:HB	1.93	0.50
9:j:53:ARG:NH2	9:j:63:GLU:OE1	2.44	0.50
15:p:55:LEU:O	15:p:59:TRP:HB2	2.11	0.50
22:A:1421:A:O2'	22:A:1432:U:O2	2.28	0.50
22:A:2155:A:H2'	22:A:2156:A:C8	2.46	0.50
28:G:7:LYS:HD2	28:G:69:ARG:HB3	1.93	0.50
1:a:156:U:H2'	1:a:157:A:H8	1.76	0.50
1:a:442:C:OP2	3:d:28:ARG:NH2	2.44	0.50
1:a:543:C:N4	11:l:59:ASN:OD1	2.44	0.50
22:A:911:U:H5''	32:N:8:LYS:HB2	1.94	0.50
32:N:100:GLY:HA3	41:W:81:THR:HB	1.94	0.50
1:a:512:A:H2'	1:a:513:A:H8	1.76	0.50
1:a:1391:U:O4	6:g:10:ARG:NH1	2.44	0.50
22:A:2139:G:H22	22:A:2186:U:H5'	1.76	0.50
22:A:2154:G:H1	22:A:2165:U:H3	1.60	0.50
27:F:73:SER:HB3	27:F:81:GLU:HG3	1.93	0.50
23:B:68:C:H41	23:B:104:G:H1	1.60	0.50
27:F:57:LEU:HD12	27:F:65:PRO:HG3	1.94	0.50
1:a:133:G:O2'	16:q:8:ARG:NH2	2.45	0.50
1:a:1056:A:H2'	1:a:1057:G:C8	2.47	0.50
15:p:77:GLU:O	15:p:82:LYS:NZ	2.45	0.50
22:A:653:G:N1	22:A:655:G:OP2	2.44	0.50
22:A:2299:C:OP2	48:3:22:ASN:ND2	2.44	0.50
34:P:53:LEU:O	34:P:86:LYS:NZ	2.34	0.50
39:U:51:ALA:O	39:U:81:THR:OG1	2.28	0.50
48:3:21:LYS:NZ	48:3:47:GLU:OE1	2.44	0.50
22:A:192:G:O6	22:A:208:G:O2'	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:924:C:H41	22:A:934:G:H21	1.60	0.50
23:B:34:C:N4	23:B:47:C:O2	2.39	0.50
1:a:1029:G:N2	1:a:1033:U:O2	2.45	0.49
1:a:1374:C:OP1	13:n:22:THR:OG1	2.30	0.49
11:l:94:LEU:HB2	11:l:115:LEU:HD12	1.93	0.49
22:A:337:A:OP2	40:V:95:LYS:NZ	2.44	0.49
22:A:2369:C:O2'	42:X:33:LYS:NZ	2.33	0.49
25:D:120:GLN:H	25:D:125:ARG:HH22	1.59	0.49
45:0:50:ILE:HG22	45:0:53:LEU:HB2	1.94	0.49
1:a:59:U:O4	1:a:110:G:O6	2.29	0.49
1:a:506:A:H2'	1:a:507:A:H8	1.76	0.49
1:a:1135:U:H2'	1:a:1136:G:H8	1.77	0.49
8:i:98:LEU:O	8:i:102:GLY:N	2.44	0.49
12:m:68:ASP:O	12:m:72:GLU:N	2.45	0.49
15:p:84:HIS:HB2	15:p:88:ASN:HD22	1.77	0.49
22:A:2158:G:O2'	22:A:2161:A:N1	2.39	0.49
22:A:2799:U:O2	25:D:68:HIS:NE2	2.44	0.49
24:C:230:HIS:HE1	24:C:232:HIS:CD2	2.30	0.49
1:a:436:U:OP2	1:a:437:C:N4	2.45	0.49
1:a:1452:C:OP1	19:t:29:ARG:NH2	2.41	0.49
2:c:24:ALA:HB3	2:c:28:TYR:HD1	1.76	0.49
7:h:29:ALA:HA	7:h:33:LYS:HD2	1.95	0.49
22:A:290:U:H2'	22:A:291:G:H8	1.76	0.49
22:A:486:G:H21	22:A:494:A:H61	1.60	0.49
1:a:222:G:O6	1:a:231:U:O4	2.30	0.49
1:a:465:G:H3'	1:a:466:A:H5'	1.94	0.49
8:i:55:THR:HG21	8:i:87:LEU:HB3	1.93	0.49
22:A:508:G:OP2	49:4:37:LYS:NZ	2.44	0.49
22:A:2169:A:H3'	22:A:2170:G:H8	1.77	0.49
28:G:44:ASN:ND2	28:G:51:THR:O	2.30	0.49
1:a:698:G:O6	1:a:722:U:O2	2.30	0.49
1:a:1046:U:O4	1:a:1050:G:N2	2.46	0.49
1:a:1065:U:OP1	13:n:2:ALA:N	2.45	0.49
3:d:25:GLU:HG2	3:d:29:ARG:HH11	1.78	0.49
22:A:283:G:N2	22:A:287:G:O6	2.45	0.49
22:A:2123:U:H2'	22:A:2124:G:C8	2.47	0.49
32:N:49:ALA:HB1	32:N:124:LYS:HD3	1.94	0.49
1:a:171:G:H2'	1:a:172:G:H8	1.78	0.49
1:a:470:A:H3'	1:a:471:G:H8	1.78	0.49
1:a:1156:U:O2'	1:a:1157:G:O4'	2.31	0.49
1:a:1495:G:H2'	1:a:1496:A:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:115:LEU:HD13	4:e:123:ILE:HD13	1.95	0.49
22:A:1095:G:N2	22:A:1125:A:N1	2.57	0.49
22:A:2492:A:OP2	51:6:2:LYS:NZ	2.39	0.49
23:B:76:A:H5''	23:B:97:A:H61	1.77	0.49
25:D:121:GLY:O	25:D:125:ARG:NH1	2.45	0.49
27:F:63:GLN:HA	46:1:6:HIS:HD2	1.77	0.49
36:R:70:ARG:HB2	36:R:76:TYR:HE1	1.77	0.49
1:a:1042:C:O2'	1:a:1044:C:N4	2.46	0.49
22:A:1768:C:H5	35:Q:94:ARG:HH22	1.60	0.49
22:A:1793:U:O2	22:A:1797:A:N6	2.46	0.49
39:U:50:VAL:HG12	39:U:51:ALA:H	1.77	0.49
15:p:78:GLY:O	15:p:82:LYS:N	2.38	0.49
22:A:369:A:O2'	22:A:371:C:OP2	2.27	0.49
22:A:1068:A:H2'	22:A:1069:A:C8	2.47	0.49
46:1:11:PRO:HA	46:1:25:SER:HA	1.95	0.49
12:m:86:TYR:OH	12:m:90:ARG:NH2	2.45	0.48
22:A:1396:G:O6	22:A:2228:C:O2	2.31	0.48
23:B:73:U:O3'	41:W:18:ARG:NH2	2.47	0.48
41:W:21:LEU:HB3	41:W:26:LYS:HB2	1.94	0.48
1:a:53:U:H2'	1:a:54:G:C8	2.49	0.48
22:A:1767:G:N2	22:A:1770:G:OP2	2.46	0.48
22:A:2396:G:H21	50:5:42:ARG:HH22	1.59	0.48
1:a:5:A:H1'	4:e:108:GLY:HA2	1.96	0.48
1:a:520:G:H2'	1:a:521:G:H8	1.78	0.48
1:a:1254:A:H62	1:a:1314:A:H62	1.61	0.48
27:F:74:ILE:HG22	27:F:76:GLY:H	1.78	0.48
1:a:520:G:H5'	1:a:549:U:H2'	1.95	0.48
22:A:192:G:H21	22:A:210:A:H62	1.61	0.48
22:A:1096:G:N2	22:A:1142:C:OP2	2.47	0.48
22:A:1337:A:N6	22:A:1669:G:O2'	2.46	0.48
25:D:15:ILE:HD12	25:D:25:VAL:HG21	1.95	0.48
1:a:395:G:N2	1:a:398:A:OP2	2.35	0.48
13:n:24:CYS:SG	13:n:25:GLU:N	2.87	0.48
22:A:6:A:H2'	22:A:7:A:C8	2.48	0.48
22:A:1093:U:OP2	22:A:1140:C:O2'	2.29	0.48
22:A:1097:A:N6	22:A:1127:G:O5'	2.43	0.48
1:a:32:G:O6	11:l:128:SER:OG	2.25	0.48
1:a:439:G:H2'	1:a:440:A:H8	1.78	0.48
18:s:34:TRP:CD1	18:s:36:ARG:H	2.31	0.48
22:A:415:C:H2'	22:A:416:G:H8	1.79	0.48
22:A:1635:C:H2'	22:A:1636:A:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:459:A:H2'	1:a:460:G:C8	2.48	0.48
1:a:992:G:O5'	1:a:1373:U:O2'	2.32	0.48
1:a:1253:A:OP1	1:a:1350:C:O2'	2.32	0.48
2:c:154:GLY:HA3	2:c:195:LEU:HG	1.94	0.48
3:d:139:VAL:HG22	3:d:176:SER:HB3	1.96	0.48
22:A:421:A:OP1	43:Y:16:ASN:ND2	2.40	0.48
22:A:1124:A:N7	22:A:1145:U:O2'	2.39	0.48
22:A:1488:G:N2	22:A:1593:U:O2	2.46	0.48
27:F:16:LEU:HD23	27:F:19:LYS:HD2	1.95	0.48
31:M:92:THR:H	31:M:96:LEU:HD22	1.79	0.48
1:a:65:G:N1	1:a:106:A:H2	2.05	0.48
1:a:1160:C:H4'	1:a:1161:A:H5'	1.96	0.48
22:A:1071:G:N3	51:6:37:GLN:NE2	2.55	0.48
25:D:111:THR:HG22	25:D:170:THR:HG22	1.95	0.48
35:Q:23:GLY:HA3	35:Q:92:VAL:HG21	1.95	0.48
49:4:4:THR:O	49:4:6:GLN:N	2.46	0.48
1:a:65:G:C6	1:a:106:A:N1	2.82	0.48
1:a:545:G:N2	1:a:545:G:OP2	2.47	0.48
7:h:114:THR:HG23	7:h:117:GLU:H	1.79	0.48
22:A:1136:A:H2'	22:A:1137:U:C2	2.49	0.48
31:M:97:LYS:HG3	31:M:98:GLU:H	1.78	0.48
37:S:66:GLY:O	37:S:92:TYR:N	2.47	0.48
1:a:506:A:H2'	1:a:507:A:C8	2.48	0.48
1:a:739:G:OP2	1:a:870:U:O2'	2.31	0.48
1:a:1432:G:O2'	1:a:1499:A:N6	2.46	0.48
6:g:130:ASN:HA	6:g:135:VAL:HG21	1.96	0.48
18:s:48:THR:HA	18:s:61:TYR:HA	1.96	0.48
22:A:1752:U:H2'	22:A:1753:G:H8	1.79	0.48
1:a:5:A:N7	4:e:112:ARG:NH2	2.60	0.47
1:a:237:U:H2'	1:a:238:G:C8	2.49	0.47
1:a:467:A:OP1	1:a:496:G:N2	2.44	0.47
22:A:785:G:N2	22:A:790:A:H61	2.11	0.47
22:A:1111:G:N2	22:A:1130:U:OP2	2.47	0.47
22:A:2034:A:H62	47:2:6:ARG:CZ	2.27	0.47
27:F:102:LYS:NZ	27:F:140:GLU:OE2	2.39	0.47
29:K:86:LYS:HB3	29:K:88:VAL:HG23	1.96	0.47
49:4:1:MET:HE3	49:4:3:ARG:HH12	1.79	0.47
1:a:473:A:N6	1:a:491:C:N3	2.61	0.47
1:a:1333:A:N6	1:a:1334:A:N3	2.62	0.47
4:e:115:LEU:HD21	4:e:144:LEU:HD11	1.95	0.47
22:A:1531:G:O6	22:A:1543:U:O2	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:U:48:VAL:HG13	39:U:85:ASP:HB2	1.96	0.47
1:a:65:G:N1	1:a:106:A:C2	2.60	0.47
1:a:536:G:H21	1:a:551:C:H5'	1.79	0.47
4:e:12:GLU:N	4:e:40:GLY:O	2.44	0.47
6:g:46:SER:HB3	6:g:117:GLU:HB2	1.95	0.47
10:k:33:MET:HG3	10:k:44:TRP:HB3	1.96	0.47
22:A:502:C:N4	22:A:503:G:O6	2.47	0.47
22:A:1131:G:H1	22:A:1139:G:H8	1.62	0.47
22:A:2175:C:H2'	22:A:2176:G:C8	2.49	0.47
24:C:270:ILE:HG21	24:C:273:ARG:HE	1.78	0.47
25:D:89:GLY:O	25:D:91:TYR:N	2.47	0.47
41:W:27:VAL:HB	41:W:43:PHE:HB2	1.97	0.47
1:a:906:G:O2'	1:a:922:G:O6	2.29	0.47
22:A:1871:G:N2	22:A:1900:U:O4	2.47	0.47
22:A:2667:U:H3'	22:A:2668:A:H8	1.78	0.47
26:E:49:HIS:CD2	26:E:92:PRO:HB2	2.49	0.47
2:c:49:ALA:O	2:c:69:THR:OG1	2.28	0.47
5:f:50:ARG:HA	5:f:60:GLU:HA	1.96	0.47
20:u:51:U:H3	20:u:63:G:H22	1.61	0.47
22:A:2436:C:H2'	50:5:32:ARG:HH22	1.79	0.47
22:A:2650:U:O2'	25:D:46:TYR:OH	2.22	0.47
34:P:59:LEU:HD22	34:P:64:SER:HB3	1.95	0.47
1:a:140:A:N6	1:a:340:A:N1	2.61	0.47
1:a:1010:A:O2'	13:n:12:ARG:NH2	2.47	0.47
22:A:832:G:N7	22:A:2454:C:O2'	2.46	0.47
22:A:2457:U:H2'	22:A:2458:G:H8	1.80	0.47
27:F:115:HIS:O	27:F:178:GLN:NE2	2.48	0.47
32:N:98:LYS:HG2	32:N:99:ARG:HB2	1.96	0.47
1:a:272:G:H2'	1:a:273:A:C8	2.49	0.47
1:a:517:C:H4'	11:l:129:LYS:HZ3	1.80	0.47
1:a:567:U:H2'	1:a:568:G:C8	2.50	0.47
1:a:1401:G:H2'	1:a:1402:G:C8	2.49	0.47
3:d:151:THR:HA	3:d:154:GLU:HB3	1.97	0.47
7:h:45:PHE:HD1	7:h:74:ILE:HG22	1.79	0.47
9:j:11:LYS:HB2	9:j:97:ASN:HD22	1.78	0.47
11:l:67:ARG:HA	11:l:77:THR:HA	1.95	0.47
22:A:1268:G:H2'	22:A:1269:G:H8	1.79	0.47
23:B:12:U:OP2	23:B:68:C:O2'	2.33	0.47
27:F:164:GLU:HG2	27:F:167:ARG:HD2	1.95	0.47
1:a:346:G:O2'	19:t:3:ASN:N	2.48	0.47
1:a:1175:G:O6	1:a:1197:G:O6	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:6:PRO:HB2	4:e:8:HIS:HD2	1.79	0.47
22:A:520:A:O2'	40:V:42:LYS:O	2.32	0.47
51:6:30:ASN:HB2	51:6:33:HIS:CD2	2.50	0.47
1:a:384:C:H2'	1:a:385:G:C8	2.49	0.47
12:m:87:ARG:O	12:m:91:HIS:HB2	2.15	0.47
22:A:2260:G:H2'	22:A:2261:A:H8	1.80	0.47
23:B:74:G:OP1	41:W:10:ARG:NH1	2.48	0.47
1:a:529:C:H2'	1:a:530:G:C8	2.50	0.47
1:a:729:G:H2'	1:a:730:A:C8	2.49	0.47
1:a:1257:G:O6	1:a:1310:U:O4	2.33	0.47
35:Q:31:LYS:HD2	35:Q:80:ARG:HA	1.97	0.47
46:1:11:PRO:O	46:1:42:THR:OG1	2.33	0.47
50:5:38:LYS:HA	50:5:41:ARG:HG2	1.96	0.47
1:a:1390:A:H62	6:g:10:ARG:HH12	1.63	0.46
22:A:498:G:H22	22:A:509:G:H2'	1.80	0.46
22:A:1234:C:H2'	22:A:1235:G:H8	1.80	0.46
22:A:2085:A:H2'	22:A:2086:G:C8	2.49	0.46
26:E:10:ASP:OD1	26:E:10:ASP:N	2.48	0.46
30:L:63:VAL:HG22	30:L:106:LEU:HD11	1.97	0.46
1:a:336:A:H61	1:a:347:G:H1	1.62	0.46
1:a:378:A:OP2	11:l:44:ARG:NE	2.48	0.46
1:a:391:G:O6	1:a:402:U:O4	2.33	0.46
1:a:517:C:OP1	11:l:128:SER:N	2.33	0.46
1:a:1374:C:H1'	1:a:1377:C:H41	1.80	0.46
1:a:1401:G:H2'	1:a:1402:G:H8	1.80	0.46
3:d:107:THR:HG23	3:d:110:GLN:H	1.79	0.46
9:j:52:ILE:HA	9:j:62:ARG:HG2	1.96	0.46
22:A:697:U:H2'	22:A:698:A:C8	2.50	0.46
22:A:728:U:H2'	22:A:729:A:H8	1.81	0.46
22:A:1710:G:O2'	22:A:2005:U:O4	2.32	0.46
22:A:2420:C:C2	31:M:69:ILE:HD11	2.50	0.46
1:a:868:A:N6	1:a:869:G:O6	2.48	0.46
1:a:1031:G:H21	1:a:1233:C:H1'	1.80	0.46
6:g:49:ILE:HG21	6:g:118:GLU:HG2	1.96	0.46
8:i:6:TYR:HB2	8:i:21:LEU:HB3	1.97	0.46
9:j:8:ILE:HD12	9:j:25:ILE:HD12	1.97	0.46
16:q:71:SER:HB2	16:q:74:LYS:HG2	1.96	0.46
22:A:783:A:H2'	22:A:784:C:H6	1.79	0.46
22:A:785:G:H21	22:A:790:A:N6	2.11	0.46
22:A:996:G:OP2	32:N:16:LYS:NZ	2.48	0.46
23:B:42:G:OP1	46:1:1:MET:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1331:G:N2	1:a:1334:A:O4'	2.43	0.46
1:a:1475:C:H2'	1:a:1476:A:H8	1.80	0.46
22:A:1345:G:O6	22:A:1649:G:N2	2.48	0.46
1:a:532:G:N2	1:a:548:A:OP2	2.47	0.46
1:a:1427:C:H2'	1:a:1428:A:C8	2.50	0.46
14:o:63:ARG:HH12	14:o:87:LEU:HD13	1.79	0.46
22:A:401:G:H2'	22:A:402:A:H8	1.79	0.46
22:A:630:A:OP1	50:5:64:ARG:NH2	2.48	0.46
22:A:1132:C:H2'	22:A:1133:G:C8	2.50	0.46
22:A:2300:A:H2'	48:3:26:ASN:HD21	1.80	0.46
1:a:1071:A:N3	2:c:155:ARG:NH1	2.63	0.46
1:a:1315:G:H4'	1:a:1316:U:H5'	1.97	0.46
1:a:1329:C:OP2	18:s:6:LYS:NZ	2.48	0.46
7:h:28:PRO:HA	7:h:59:VAL:HG12	1.96	0.46
15:p:5:ILE:HG22	15:p:22:VAL:HG23	1.98	0.46
20:u:47:U:O2'	20:u:50:U:OP1	2.30	0.46
22:A:969:U:O2'	45:0:40:ASN:ND2	2.49	0.46
22:A:2259:U:H5''	22:A:2260:G:H5'	1.97	0.46
32:N:44:ASN:HD21	32:N:93:TRP:HB2	1.81	0.46
39:U:49:LYS:HB3	39:U:50:VAL:HG23	1.98	0.46
2:c:146:LYS:HB2	2:c:202:TYR:HD2	1.81	0.46
6:g:126:ASP:HA	6:g:129:ASN:HB2	1.97	0.46
22:A:1388:U:H1'	22:A:1616:A:H2	1.81	0.46
24:C:13:ARG:HD3	24:C:16:MET:HG3	1.97	0.46
1:a:314:G:H2'	1:a:315:A:C8	2.51	0.46
1:a:459:A:H2'	1:a:460:G:H8	1.81	0.46
1:a:578:A:HO2'	1:a:581:G:HO2'	1.62	0.46
1:a:626:C:H42	1:a:645:G:H22	1.63	0.46
10:k:25:SER:H	10:k:88:GLY:HA3	1.79	0.46
10:k:89:PRO:HD3	10:k:114:THR:HG21	1.98	0.46
16:q:62:VAL:HG21	16:q:78:LEU:HG	1.97	0.46
22:A:836:U:OP2	26:E:62:ARG:NH1	2.44	0.46
22:A:1096:G:H1'	22:A:1141:U:H1'	1.97	0.46
22:A:2520:U:O4	22:A:2597:G:O6	2.34	0.46
23:B:68:C:H5	23:B:104:G:H22	1.62	0.46
23:B:75:U:O2'	41:W:78:GLN:NE2	2.38	0.46
24:C:69:ARG:O	24:C:189:ARG:NH1	2.49	0.46
1:a:558:G:H2'	1:a:559:G:C8	2.51	0.46
22:A:1697:A:O2'	25:D:119:PHE:O	2.31	0.46
22:A:2764:A:O2'	22:A:2766:C:N4	2.41	0.46
1:a:146:C:H2'	1:a:147:A:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:955:G:OP1	6:g:102:ARG:NH1	2.42	0.46
1:a:1424:C:H2'	1:a:1425:A:H8	1.81	0.46
22:A:1132:C:H2'	22:A:1133:G:H8	1.80	0.46
22:A:1307:C:H5''	22:A:1308:G:H5'	1.98	0.46
22:A:2341:A:H2'	22:A:2342:A:C8	2.51	0.46
30:L:9:ARG:O	30:L:84:ALA:N	2.48	0.46
33:O:66:VAL:HG11	33:O:86:LEU:HB2	1.97	0.46
34:P:36:SER:OG	34:P:39:ASN:N	2.46	0.46
45:O:15:ARG:HH12	45:O:52:HIS:CD2	2.34	0.46
1:a:266:G:N1	1:a:281:G:O6	2.50	0.45
1:a:1375:A:O2'	1:a:1376:G:O4'	2.33	0.45
20:u:68:C:H2'	20:u:69:G:C8	2.50	0.45
22:A:2114:U:O4	22:A:2203:G:O6	2.34	0.45
24:C:230:HIS:CD2	24:C:249:PRO:HB3	2.51	0.45
32:N:21:ALA:HB1	32:N:99:ARG:HH12	1.81	0.45
40:V:84:LYS:HD2	40:V:93:VAL:HG11	1.98	0.45
1:a:276:U:OP2	19:t:73:ARG:NH2	2.50	0.45
1:a:831:A:OP1	1:a:1542:G:O2'	2.33	0.45
2:c:83:VAL:HG13	2:c:100:ILE:HD11	1.98	0.45
22:A:1119:C:H2'	22:A:1120:A:C8	2.51	0.45
1:a:237:U:H2'	1:a:238:G:H8	1.81	0.45
1:a:421:G:O2'	3:d:113:GLN:OE1	2.29	0.45
1:a:689:G:H2'	1:a:690:A:H8	1.79	0.45
1:a:1055:A:H2'	1:a:1056:A:C8	2.52	0.45
1:a:1142:U:O4	9:j:9:ARG:NH1	2.49	0.45
1:a:1357:C:H2'	1:a:1358:G:C8	2.51	0.45
3:d:6:GLY:O	3:d:109:ARG:NH1	2.49	0.45
20:u:9:A:H62	20:u:23:A:H62	1.63	0.45
22:A:454:C:H2'	22:A:455:A:H8	1.82	0.45
22:A:1712:A:O2'	22:A:2563:G:OP1	2.33	0.45
22:A:2501:G:H2'	22:A:2502:A:H8	1.81	0.45
1:a:1320:G:N2	1:a:1347:A:OP2	2.41	0.45
13:n:24:CYS:HB2	13:n:40:CYS:HB3	1.98	0.45
19:t:66:ILE:HG21	19:t:70:LYS:HD3	1.98	0.45
22:A:573:U:O2'	36:R:49:ASP:OD2	2.29	0.45
22:A:1867:A:H2'	22:A:1868:A:C8	2.51	0.45
24:C:95:HIS:CE1	24:C:101:LYS:HE2	2.51	0.45
25:D:56:LYS:HE3	25:D:78:ARG:HA	1.98	0.45
26:E:8:LYS:HD3	26:E:14:ASN:HD21	1.81	0.45
1:a:1135:U:O2	1:a:1169:G:N2	2.41	0.45
1:a:1465:U:O4	1:a:1470:G:N2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:14:ILE:HG22	2:c:15:ILE:HG23	1.97	0.45
12:m:94:GLY:O	12:m:109:ARG:NH2	2.47	0.45
22:A:885:U:H2'	22:A:886:U:H4'	1.97	0.45
22:A:948:A:OP2	32:N:25:LYS:HB2	2.17	0.45
1:a:272:G:H2'	1:a:273:A:H8	1.82	0.45
1:a:1399:C:H2'	1:a:1400:G:H8	1.80	0.45
1:a:367:C:O2'	1:a:369:G:OP1	2.28	0.45
1:a:391:G:H2'	1:a:392:G:H8	1.82	0.45
1:a:1237:G:OP2	1:a:1337:C:N4	2.49	0.45
3:d:61:TYR:OH	3:d:91:LEU:O	2.26	0.45
22:A:753:G:H22	22:A:759:C:H42	1.65	0.45
22:A:1590:A:C4	22:A:1591:A:H8	2.35	0.45
24:C:2:ALA:N	24:C:20:ASP:OD2	2.50	0.45
33:O:8:ARG:NH1	33:O:16:MET:SD	2.90	0.45
35:Q:27:ARG:HB2	35:Q:85:GLU:HB2	1.99	0.45
41:W:78:GLN:HG2	41:W:88:HIS:HB2	1.99	0.45
1:a:42:U:H2'	1:a:43:G:H8	1.81	0.45
1:a:64:C:H2'	1:a:65:G:C8	2.51	0.45
1:a:338:U:O4	1:a:342:A:N7	2.50	0.45
1:a:1010:A:C5	1:a:1231:A:H4'	2.51	0.45
1:a:1489:G:H2'	1:a:1490:G:C8	2.52	0.45
15:p:58:ASP:O	15:p:61:SER:OG	2.32	0.45
20:u:76:A:N6	22:A:2436:C:O4'	2.49	0.45
22:A:1757:U:H2'	22:A:1758:C:C4	2.52	0.45
33:O:66:VAL:HG21	33:O:86:LEU:HD12	1.99	0.45
1:a:323:C:H2'	1:a:324:G:H8	1.81	0.45
3:d:78:ILE:HG22	3:d:80:GLU:H	1.82	0.45
8:i:57:THR:HA	8:i:58:LYS:HA	1.65	0.45
15:p:81:LYS:O	15:p:85:GLU:CB	2.65	0.45
17:r:40:ARG:O	17:r:76:SER:OG	2.29	0.45
22:A:137:U:H3	22:A:144:G:H1	1.65	0.45
22:A:1192:C:H2'	22:A:1193:C:H6	1.82	0.45
1:a:46:U:H3	1:a:377:G:H1'	1.82	0.45
1:a:1090:G:O2'	1:a:1117:A:N1	2.45	0.45
8:i:10:GLY:O	8:i:17:ALA:N	2.49	0.45
11:l:97:GLY:HA2	11:l:108:TYR:HD1	1.82	0.45
16:q:27:VAL:HG22	16:q:46:LYS:HG2	1.97	0.45
22:A:1955:C:N4	22:A:1979:C:O4'	2.50	0.45
22:A:2342:A:H2'	22:A:2343:A:C8	2.51	0.45
36:R:60:LEU:HD23	36:R:60:LEU:HA	1.83	0.45
1:a:352:G:H2'	1:a:353:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:520:G:H2'	1:a:521:G:C8	2.52	0.44
1:a:881:A:H2	1:a:934:A:H4'	1.82	0.44
1:a:1019:G:H22	1:a:1051:G:H8	1.64	0.44
1:a:1148:C:N3	1:a:1149:A:N6	2.66	0.44
15:p:18:TYR:O	15:p:39:THR:OG1	2.35	0.44
22:A:523:A:O2'	40:V:54:GLY:O	2.35	0.44
22:A:1179:G:H5''	29:K:73:LYS:HE3	1.98	0.44
22:A:1532:A:N6	22:A:1542:U:H3	2.15	0.44
22:A:2342:A:H2'	22:A:2343:A:H8	1.80	0.44
22:A:2396:G:H21	50:5:42:ARG:NH2	2.14	0.44
23:B:27:A:H2'	23:B:28:C:H6	1.82	0.44
41:W:8:LYS:H	41:W:41:ILE:HG23	1.82	0.44
1:a:807:A:O2'	1:a:809:A:N7	2.45	0.44
3:d:101:ARG:HD2	3:d:163:PRO:HG2	1.99	0.44
15:p:82:LYS:HA	15:p:85:GLU:HB3	2.00	0.44
22:A:302:A:H2'	22:A:303:G:C8	2.53	0.44
22:A:872:G:H2'	22:A:873:C:C6	2.53	0.44
22:A:890:A:H2'	22:A:891:A:C8	2.52	0.44
22:A:1030:A:O2'	22:A:1032:C:OP2	2.27	0.44
22:A:1422:C:H2'	22:A:1423:A:H8	1.83	0.44
22:A:1813:G:O5'	24:C:276:LYS:NZ	2.50	0.44
22:A:1833:A:N1	24:C:276:LYS:HE2	2.33	0.44
50:5:2:PRO:HB2	50:5:3:LYS:H	1.60	0.44
1:a:569:U:H2'	1:a:570:C:H6	1.82	0.44
1:a:1033:U:N3	1:a:1034:A:N7	2.66	0.44
11:l:102:ASP:OD1	11:l:102:ASP:N	2.50	0.44
22:A:333:U:O3'	40:V:90:LYS:NZ	2.49	0.44
22:A:412:G:O2'	22:A:440:G:O6	2.25	0.44
22:A:2811:U:O2	22:A:2812:A:N6	2.50	0.44
41:W:15:ARG:O	41:W:17:LEU:N	2.49	0.44
41:W:83:THR:HB	41:W:85:GLN:HG2	1.98	0.44
1:a:567:U:O2'	11:l:41:PRO:O	2.35	0.44
1:a:701:U:O2'	1:a:718:G:N2	2.50	0.44
1:a:950:C:O2'	1:a:1359:C:OP2	2.34	0.44
1:a:1533:G:H2'	1:a:1534:A:C8	2.53	0.44
3:d:15:LEU:HD13	3:d:56:LYS:HA	1.99	0.44
22:A:290:U:H2'	22:A:291:G:C8	2.51	0.44
26:E:29:ASN:HD22	26:E:108:LEU:HD21	1.82	0.44
38:T:85:PRO:O	38:T:105:THR:OG1	2.33	0.44
44:Z:3:VAL:HA	44:Z:6:ILE:HD12	1.99	0.44
44:Z:14:MET:HG3	44:Z:57:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:974:A:C8	18:s:55:ARG:HD2	2.51	0.44
1:a:1375:A:O2'	1:a:1376:G:O5'	2.35	0.44
3:d:94:ARG:HG3	3:d:131:SER:HA	1.99	0.44
4:e:96:MET:HE2	4:e:115:LEU:HD11	2.00	0.44
16:q:63:LYS:NZ	16:q:80:GLU:OE1	2.50	0.44
22:A:269:G:H21	22:A:318:A:H61	1.65	0.44
22:A:1240:A:H2'	22:A:1241:A:C8	2.52	0.44
24:C:72:ASP:HB3	24:C:119:GLY:HA2	1.99	0.44
29:K:48:HIS:HB2	29:K:49:VAL:HG23	2.00	0.44
3:d:112:ARG:HA	3:d:115:VAL:HG12	1.98	0.44
12:m:14:ARG:HB3	12:m:44:ARG:HA	1.99	0.44
20:u:19:G:H2'	22:A:2126:A:H1'	1.99	0.44
22:A:302:A:H2'	22:A:303:G:H8	1.83	0.44
22:A:1441:C:H2'	22:A:1442:A:H8	1.83	0.44
22:A:2276:U:OP1	22:A:2401:U:O2'	2.28	0.44
24:C:17:THR:OG1	24:C:204:ASN:N	2.46	0.44
28:G:51:THR:HA	28:G:69:ARG:HH12	1.82	0.44
1:a:32:G:C8	11:l:133:LYS:HG3	2.53	0.44
17:r:33:LEU:HD21	17:r:63:ILE:HG22	2.00	0.44
22:A:502:C:H2'	22:A:503:G:H8	1.83	0.44
22:A:655:G:O2'	26:E:106:ARG:NH2	2.50	0.44
22:A:820:G:N1	24:C:229:ASP:OD2	2.39	0.44
41:W:14:PRO:HB2	41:W:18:ARG:HE	1.83	0.44
1:a:384:C:H2'	1:a:385:G:H8	1.81	0.44
1:a:1059:G:H2'	1:a:1060:A:C8	2.53	0.44
22:A:416:G:H2'	22:A:417:G:H8	1.83	0.44
24:C:241:ILE:HD13	24:C:246:PRO:HB3	1.99	0.44
17:r:27:TYR:HE1	17:r:65:ARG:HB3	1.82	0.44
22:A:2149:G:H1	22:A:2170:G:H22	1.65	0.44
1:a:418:C:H5'	3:d:130:PRO:HD2	2.00	0.43
1:a:464:A:H3'	1:a:465:G:H8	1.83	0.43
1:a:816:U:H2'	1:a:817:A:H8	1.82	0.43
9:j:4:GLN:HB2	9:j:77:VAL:HA	2.00	0.43
17:r:25:ILE:H	17:r:25:ILE:HG13	1.53	0.43
22:A:557:G:O5'	38:T:23:ARG:NH1	2.51	0.43
22:A:699:U:H2'	22:A:700:G:H8	1.83	0.43
22:A:1498:G:H2'	22:A:1499:G:C8	2.53	0.43
22:A:2673:G:OP2	28:G:158:LYS:NZ	2.51	0.43
24:C:142:HIS:CD2	24:C:194:SER:HA	2.53	0.43
32:N:35:GLN:HB3	32:N:100:GLY:HA2	1.99	0.43
35:Q:48:ILE:HG23	35:Q:97:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:42:U:H2'	1:a:43:G:C8	2.53	0.43
1:a:192:U:O4	1:a:211:G:O6	2.36	0.43
1:a:704:C:H5''	10:k:31:ILE:HD11	1.99	0.43
3:d:26:LEU:HD23	3:d:29:ARG:HD3	1.99	0.43
22:A:169:A:H3'	22:A:170:G:H8	1.83	0.43
22:A:699:U:H2'	22:A:700:G:C8	2.53	0.43
22:A:987:A:H2'	22:A:988:C:C6	2.53	0.43
22:A:1457:A:N6	22:A:1630:G:OP2	2.51	0.43
27:F:170:LEU:HB3	27:F:175:MET:HG3	2.00	0.43
35:Q:27:ARG:HG2	35:Q:44:GLU:HG2	2.00	0.43
41:W:14:PRO:HG2	41:W:18:ARG:HH21	1.84	0.43
12:m:24:GLY:HA3	12:m:65:VAL:HG22	2.01	0.43
19:t:50:TYR:CZ	19:t:83:LYS:HB2	2.53	0.43
22:A:28:G:O2'	22:A:551:G:N2	2.52	0.43
22:A:626:U:H2'	22:A:627:A:C8	2.53	0.43
22:A:890:A:H2'	22:A:891:A:H8	1.83	0.43
22:A:967:C:H2'	22:A:968:A:H8	1.82	0.43
22:A:1422:C:H2'	22:A:1423:A:C8	2.53	0.43
30:L:5:GLU:HA	30:L:20:LEU:HD22	2.00	0.43
33:O:112:PRO:HA	33:O:119:PRO:HA	2.00	0.43
1:a:730:A:H2'	1:a:731:A:C8	2.54	0.43
9:j:59:LYS:HB3	9:j:59:LYS:HE3	1.86	0.43
22:A:1823:A:H2'	22:A:1824:A:C8	2.54	0.43
22:A:2536:U:O2'	22:A:2661:U:OP1	2.34	0.43
22:A:2795:A:H5''	22:A:2796:G:H5'	2.00	0.43
31:M:94:VAL:O	31:M:96:LEU:N	2.51	0.43
1:a:439:G:H2'	1:a:440:A:C8	2.53	0.43
1:a:743:A:H2'	1:a:744:A:C8	2.54	0.43
4:e:156:LEU:HB3	7:h:73:VAL:HG12	2.01	0.43
9:j:8:ILE:HG22	9:j:100:ILE:HA	2.00	0.43
22:A:610:G:OP2	37:S:79:LYS:NZ	2.43	0.43
22:A:681:G:H21	22:A:685:A:H62	1.65	0.43
22:A:1208:C:H2'	22:A:1209:A:H8	1.83	0.43
27:F:3:ARG:HH12	27:F:105:THR:HG21	1.84	0.43
1:a:97:G:O2'	1:a:98:G:O4'	2.33	0.43
10:k:20:VAL:O	10:k:35:THR:OG1	2.34	0.43
22:A:84:G:H21	22:A:103:A:H2	1.65	0.43
22:A:1303:G:N7	38:T:20:ARG:HD2	2.34	0.43
22:A:2762:A:H2'	22:A:2763:A:H8	1.83	0.43
26:E:17:ILE:HD11	26:E:196:GLN:HG2	2.00	0.43
1:a:192:U:H3	1:a:211:G:H1	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:194:U:H2'	1:a:195:A:C8	2.53	0.43
1:a:762:U:H2'	1:a:763:A:C4	2.53	0.43
1:a:833:G:O2'	1:a:835:U:OP2	2.31	0.43
22:A:60:G:H1'	22:A:74:A:H2'	2.01	0.43
22:A:1822:U:O2'	22:A:1823:A:O4'	2.36	0.43
22:A:2143:C:H2'	22:A:2173:G:H1	1.84	0.43
22:A:2166:C:N4	22:A:2167:G:O6	2.52	0.43
22:A:2514:U:O2	22:A:2518:U:N3	2.52	0.43
22:A:2819:U:H2'	22:A:2820:A:H8	1.82	0.43
24:C:174:ILE:HD12	24:C:184:ILE:HD12	2.00	0.43
40:V:72:ASP:O	40:V:74:SER:N	2.52	0.43
1:a:388:A:O2'	1:a:467:A:N6	2.51	0.43
1:a:1350:C:OP1	1:a:1352:G:N2	2.44	0.43
18:s:41:PHE:O	18:s:43:SER:N	2.52	0.43
22:A:571:A:H4'	22:A:572:G:C8	2.54	0.43
22:A:893:G:H2'	22:A:894:A:H8	1.84	0.43
22:A:1039:U:O4	22:A:1195:A:N7	2.51	0.43
22:A:1119:C:H5	22:A:1128:A:H5''	1.84	0.43
23:B:49:G:OP2	34:P:67:THR:OG1	2.32	0.43
26:E:75:GLN:HE22	26:E:82:GLN:NE2	2.16	0.43
1:a:146:C:H2'	1:a:147:A:C8	2.54	0.43
1:a:322:U:H5''	1:a:323:C:H5	1.84	0.43
1:a:994:A:H5''	1:a:995:C:H5	1.84	0.43
1:a:1144:C:O2'	8:i:18:ARG:NH1	2.51	0.43
20:u:57:G:O6	22:A:2126:A:N1	2.52	0.43
22:A:454:C:H2'	22:A:455:A:C8	2.53	0.43
22:A:487:A:OP1	36:R:5:LYS:NZ	2.43	0.43
22:A:885:U:N3	22:A:886:U:H1'	2.34	0.43
22:A:1424:G:H2'	22:A:1425:G:H8	1.83	0.43
24:C:195:VAL:HG12	24:C:196:GLY:H	1.84	0.43
28:G:54:ARG:NH1	28:G:68:THR:OG1	2.43	0.43
35:Q:29:HIS:HD2	35:Q:83:GLN:HB2	1.84	0.43
37:S:41:VAL:HB	37:S:47:LYS:HB2	2.01	0.43
1:a:337:C:H2'	1:a:338:U:C6	2.53	0.42
1:a:397:A:H2'	1:a:398:A:C8	2.51	0.42
1:a:620:U:N3	1:a:647:G:N1	2.67	0.42
8:i:114:LYS:HE2	8:i:114:LYS:HB3	1.89	0.42
20:u:5:G:H2'	20:u:6:G:H8	1.84	0.42
20:u:57:G:N1	22:A:2126:A:H2	2.15	0.42
22:A:325:U:H2'	22:A:326:A:C8	2.53	0.42
22:A:573:U:H2'	22:A:574:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:898:A:N6	22:A:961:G:O6	2.52	0.42
22:A:940:G:H2'	22:A:941:A:C4	2.54	0.42
22:A:1507:U:HO2'	22:A:1572:A:HO2'	1.64	0.42
23:B:59:U:H2'	23:B:60:U:C6	2.53	0.42
23:B:94:G:H2'	23:B:95:U:C6	2.54	0.42
25:D:107:VAL:HG12	25:D:205:ALA:HB3	2.01	0.42
28:G:25:THR:HG22	28:G:34:THR:HG22	2.00	0.42
31:M:49:GLY:HA2	50:5:57:ARG:HD3	2.01	0.42
38:T:29:ILE:HD11	38:T:41:LEU:HD21	2.01	0.42
1:a:208:U:H2'	1:a:209:A:H8	1.83	0.42
1:a:221:C:H2'	1:a:222:G:C8	2.54	0.42
22:A:1783:A:O2'	22:A:1972:C:OP1	2.36	0.42
22:A:2328:A:H2'	22:A:2329:U:C6	2.55	0.42
26:E:157:GLU:OE2	26:E:197:THR:OG1	2.32	0.42
1:a:153:G:H2'	1:a:154:G:C8	2.54	0.42
1:a:466:A:N6	1:a:496:G:O2'	2.52	0.42
1:a:689:G:H2'	1:a:690:A:C8	2.53	0.42
1:a:768:A:OP1	14:o:69:TYR:OH	2.35	0.42
1:a:1002:A:N3	18:s:52:TYR:OH	2.50	0.42
6:g:15:ASP:HB2	6:g:19:ASN:H	1.83	0.42
11:l:120:VAL:HG22	11:l:122:ASP:H	1.84	0.42
14:o:49:ASP:OD1	14:o:50:HIS:N	2.53	0.42
22:A:410:G:OP2	22:A:463:A:N6	2.53	0.42
22:A:526:C:O2'	38:T:65:ASN:ND2	2.41	0.42
22:A:931:C:H2'	22:A:932:G:H8	1.85	0.42
35:Q:75:PRO:HG2	35:Q:78:THR:HG23	2.01	0.42
22:A:2305:U:OP1	22:A:2394:U:O2'	2.38	0.42
22:A:2557:G:H2'	22:A:2558:G:C8	2.54	0.42
22:A:2908:U:H2'	22:A:2909:A:C8	2.55	0.42
39:U:24:LYS:HG2	39:U:81:THR:HG22	2.02	0.42
1:a:150:G:H2'	1:a:151:G:C8	2.53	0.42
1:a:994:A:H1'	1:a:1334:A:C2	2.54	0.42
4:e:107:ALA:HB1	4:e:111:VAL:HG13	2.01	0.42
6:g:47:PHE:HA	6:g:50:ILE:HD12	2.01	0.42
15:p:71:ARG:HA	15:p:80:MET:HG3	2.01	0.42
20:u:19:G:O2'	22:A:2126:A:O3'	2.36	0.42
20:u:57:G:C6	22:A:2126:A:N1	2.87	0.42
22:A:625:U:H5''	31:M:16:ARG:HH22	1.84	0.42
22:A:1752:U:H2'	22:A:1753:G:C8	2.54	0.42
22:A:1826:A:H2'	22:A:1827:U:C6	2.55	0.42
22:A:2305:U:H2'	22:A:2306:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:W:3:VAL:HG12	41:W:4:GLN:HG3	2.01	0.42
43:Y:18:ARG:HH11	43:Y:22:MET:HB3	1.84	0.42
1:a:566:U:H5'	11:l:129:LYS:HE3	2.02	0.42
1:a:690:A:H1'	10:k:118:HIS:CD2	2.54	0.42
1:a:1194:A:H5''	8:i:105:THR:HG22	2.02	0.42
1:a:1402:G:H2'	1:a:1403:C:H6	1.83	0.42
19:t:69:ASN:HA	19:t:72:ASN:HB2	2.01	0.42
27:F:2:ASN:HB3	27:F:3:ARG:H	1.63	0.42
31:M:12:SER:O	31:M:12:SER:OG	2.38	0.42
36:R:17:VAL:HG11	36:R:36:LYS:HG2	2.01	0.42
44:Z:6:ILE:HG22	44:Z:14:MET:HE1	2.02	0.42
45:0:23:VAL:HG13	45:0:28:LEU:HB2	2.01	0.42
50:5:31:HIS:HB3	50:5:32:ARG:H	1.40	0.42
1:a:105:G:H2'	1:a:106:A:C8	2.55	0.42
1:a:336:A:N6	1:a:347:G:H1	2.17	0.42
1:a:370:C:H2'	1:a:371:A:C8	2.55	0.42
1:a:728:G:H2'	1:a:729:G:C8	2.54	0.42
1:a:1243:C:H2'	1:a:1244:A:C8	2.55	0.42
8:i:10:GLY:N	8:i:17:ALA:O	2.53	0.42
9:j:42:LEU:HB2	9:j:71:LYS:HB2	2.01	0.42
22:A:172:U:H2'	22:A:173:G:H8	1.84	0.42
22:A:1514:G:O6	22:A:1565:G:N2	2.52	0.42
24:C:170:LYS:HB3	24:C:171:TYR:CD1	2.55	0.42
41:W:78:GLN:H	41:W:88:HIS:HB3	1.84	0.42
1:a:978:C:H1'	1:a:1216:A:N1	2.35	0.42
22:A:1060:A:N1	22:A:1181:U:O2'	2.50	0.42
22:A:2640:C:H2'	22:A:2641:G:C8	2.55	0.42
23:B:16:G:O6	23:B:63:U:O4	2.38	0.42
25:D:111:THR:OG1	25:D:201:THR:OG1	2.28	0.42
39:U:56:LEU:HD12	39:U:77:LYS:HD2	2.01	0.42
46:1:8:ASN:HB3	46:1:29:LYS:NZ	2.34	0.42
1:a:1265:A:H2	1:a:1385:G:H1'	1.84	0.42
4:e:57:PRO:HA	4:e:60:ILE:HG12	2.02	0.42
11:l:26:LYS:HB3	11:l:38:VAL:HG11	2.01	0.42
22:A:1023:A:N6	22:A:1024:G:O6	2.52	0.42
22:A:1095:G:O5'	22:A:1141:U:N3	2.53	0.42
22:A:1406:C:H2'	22:A:1407:G:C8	2.55	0.42
22:A:2826:C:O2'	47:2:39:SER:OG	2.38	0.42
25:D:120:GLN:H	25:D:125:ARG:NH2	2.16	0.42
33:O:64:THR:OG1	33:O:65:PHE:N	2.52	0.42
1:a:597:C:OP2	1:a:773:G:N1	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:735:C:O3'	17:r:56:GLN:NE2	2.53	0.42
1:a:1439:U:H2'	1:a:1440:A:C8	2.55	0.42
1:a:1493:U:H2'	1:a:1494:A:H8	1.85	0.42
22:A:675:G:H4'	22:A:677:G:H4'	2.02	0.42
22:A:746:A:OP1	24:C:7:LYS:NZ	2.36	0.42
22:A:1237:U:H1'	36:R:4:VAL:HG22	2.02	0.42
22:A:1872:G:O2'	22:A:1898:A:N6	2.53	0.42
27:F:100:LEU:HD23	27:F:103:LEU:HD12	2.02	0.42
1:a:130:U:H2'	1:a:131:G:H8	1.84	0.41
1:a:462:G:O6	1:a:463:A:N6	2.53	0.41
1:a:1073:G:H1'	2:c:194:LYS:HD2	2.01	0.41
1:a:1236:G:H4'	18:s:77:THR:HG21	2.02	0.41
2:c:179:ALA:HB1	2:c:181:ILE:HG23	2.02	0.41
8:i:59:GLY:HA3	8:i:60:ALA:HA	1.68	0.41
11:l:53:MET:N	11:l:63:ARG:O	2.40	0.41
22:A:275:A:N6	22:A:296:G:C2	2.87	0.41
22:A:922:G:OP2	22:A:934:G:N1	2.53	0.41
22:A:1406:C:H2'	22:A:1407:G:H8	1.84	0.41
22:A:1635:C:H2'	22:A:1636:A:C8	2.55	0.41
22:A:1926:A:N6	22:A:1931:U:H3	2.03	0.41
22:A:2144:G:N2	22:A:2173:G:OP2	2.53	0.41
22:A:2260:G:H2'	22:A:2261:A:C8	2.54	0.41
25:D:110:VAL:HG11	25:D:192:ILE:HG12	2.01	0.41
39:U:48:VAL:HG11	39:U:82:LEU:HD13	2.01	0.41
1:a:924:A:H2'	1:a:925:A:C8	2.53	0.41
3:d:88:MET:HE1	3:d:190:ILE:HD11	2.02	0.41
7:h:58:GLY:HA3	7:h:59:VAL:HA	1.59	0.41
13:n:42:ILE:H	13:n:42:ILE:HG13	1.67	0.41
22:A:1009:G:H2'	22:A:1010:U:C6	2.55	0.41
22:A:1762:C:H2'	22:A:1763:A:H8	1.85	0.41
22:A:1996:U:H2'	22:A:1997:U:C6	2.55	0.41
27:F:42:ASP:O	27:F:45:SER:OG	2.30	0.41
33:O:73:VAL:HG22	33:O:82:VAL:HA	2.02	0.41
33:O:110:THR:OG1	33:O:111:GLU:N	2.53	0.41
37:S:2:TYR:HB2	37:S:42:GLY:HA3	2.02	0.41
37:S:56:ALA:HA	37:S:101:ASN:HD21	1.85	0.41
1:a:184:C:H2'	1:a:185:A:C8	2.55	0.41
1:a:219:G:H2'	1:a:220:G:H8	1.84	0.41
1:a:575:U:OP2	1:a:581:G:N2	2.50	0.41
1:a:698:G:N2	10:k:40:ASN:OD1	2.44	0.41
1:a:1074:G:H1	1:a:1214:U:H3	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1165:U:O4	1:a:1166:A:N6	2.54	0.41
22:A:1573:G:N1	22:A:1589:G:N7	2.68	0.41
22:A:2762:A:H5''	28:G:4:ILE:HD13	2.03	0.41
24:C:84:ASP:HB3	24:C:87:ARG:H	1.86	0.41
29:K:61:ASP:N	29:K:62:LYS:N	2.68	0.41
31:M:86:GLU:OE1	31:M:86:GLU:N	2.53	0.41
1:a:426:A:N6	1:a:443:G:N3	2.68	0.41
1:a:1450:G:H2'	1:a:1451:U:C6	2.55	0.41
7:h:11:LEU:HD22	7:h:79:ARG:HG3	2.02	0.41
16:q:66:GLU:OE1	16:q:75:ARG:NH1	2.54	0.41
19:t:74:ASP:HA	19:t:77:ARG:HG2	2.01	0.41
22:A:682:A:N1	22:A:2383:A:O2'	2.49	0.41
1:a:61:G:H1	1:a:106:A:H61	1.69	0.41
1:a:208:U:H2'	1:a:209:A:C8	2.56	0.41
1:a:328:A:H2'	1:a:329:C:C6	2.56	0.41
1:a:444:U:N3	1:a:446:A:C8	2.81	0.41
1:a:640:G:H2'	1:a:641:G:C8	2.54	0.41
1:a:1071:A:H62	1:a:1215:C:H42	1.68	0.41
1:a:1290:U:H2'	1:a:1291:G:C8	2.56	0.41
1:a:1424:C:H2'	1:a:1425:A:C8	2.55	0.41
2:c:71:LYS:HD2	2:c:74:MET:HG3	2.03	0.41
2:c:86:LEU:O	2:c:90:LEU:HB2	2.20	0.41
6:g:116:MET:HA	6:g:119:ARG:HE	1.84	0.41
11:l:32:LYS:H	11:l:32:LYS:HD2	1.86	0.41
11:l:69:ARG:HB2	11:l:75:GLU:HG2	2.01	0.41
15:p:10:MET:SD	15:p:19:ARG:NE	2.94	0.41
20:u:19:G:C6	22:A:2128:A:N6	2.88	0.41
22:A:1374:G:H2'	22:A:1375:G:C8	2.55	0.41
22:A:2124:G:O2'	22:A:2134:G:O4'	2.37	0.41
33:O:45:GLU:HG2	33:O:104:TYR:HD2	1.85	0.41
1:a:821:C:H2'	1:a:822:A:H8	1.86	0.41
2:c:68:HIS:HB3	2:c:105:ILE:HB	2.03	0.41
4:e:81:ILE:H	4:e:81:ILE:HG13	1.67	0.41
22:A:401:G:H2'	22:A:402:A:C8	2.55	0.41
22:A:889:G:H1	22:A:971:U:H3	1.69	0.41
22:A:1063:U:OP2	22:A:1065:G:O2'	2.38	0.41
22:A:2305:U:H3	22:A:2355:G:H1	1.67	0.41
22:A:2590:G:OP2	22:A:2590:G:N2	2.53	0.41
34:P:77:LYS:HG2	34:P:114:ASN:HD21	1.85	0.41
1:a:273:A:H2'	1:a:274:G:H8	1.86	0.41
1:a:491:C:H2'	1:a:492:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:892:A:H1'	7:h:12:THR:HG21	2.01	0.41
1:a:1087:C:H2'	1:a:1088:G:C8	2.53	0.41
1:a:1095:G:H2'	1:a:1096:A:C8	2.56	0.41
1:a:1188:C:H2'	1:a:1189:G:C8	2.56	0.41
1:a:1302:A:H2	1:a:1368:G:H1'	1.85	0.41
6:g:126:ASP:O	6:g:131:THR:N	2.41	0.41
8:i:10:GLY:HA2	8:i:81:HIS:HB2	2.01	0.41
8:i:109:ARG:HA	8:i:109:ARG:HD3	1.90	0.41
9:j:52:ILE:HG22	9:j:62:ARG:HG2	2.03	0.41
22:A:704:U:H2'	22:A:705:C:H6	1.85	0.41
22:A:907:A:H61	22:A:956:C:H42	1.69	0.41
22:A:2043:G:N1	22:A:2047:A:OP2	2.40	0.41
1:a:465:G:O3'	15:p:45:ASP:N	2.51	0.41
1:a:854:G:H2'	1:a:855:G:C8	2.55	0.41
11:l:87:LEU:HD12	11:l:110:ILE:HD12	2.03	0.41
13:n:23:ARG:HA	13:n:33:VAL:HG11	2.02	0.41
14:o:80:GLU:O	14:o:84:ARG:HB2	2.20	0.41
22:A:115:C:H4'	39:U:32:ARG:HH22	1.85	0.41
22:A:626:U:H2'	22:A:627:A:H8	1.86	0.41
22:A:1208:C:H2'	22:A:1209:A:C8	2.56	0.41
35:Q:92:VAL:HG12	35:Q:94:ARG:H	1.86	0.41
51:6:27:CYS:HB3	51:6:29:ALA:H	1.85	0.41
1:a:688:G:O3'	5:f:92:ARG:NH2	2.51	0.41
1:a:797:A:H62	1:a:815:G:N2	2.17	0.41
5:f:38:ALA:HB2	5:f:76:ALA:HB1	2.02	0.41
6:g:70:MET:HA	6:g:71:PRO:HD3	1.89	0.41
12:m:108:THR:HG22	12:m:109:ARG:HG3	2.02	0.41
16:q:49:ALA:HA	16:q:76:PHE:HB2	2.03	0.41
22:A:500:A:H62	22:A:509:G:H8	1.68	0.41
22:A:509:G:H22	49:4:37:LYS:NZ	2.18	0.41
22:A:732:C:H2'	22:A:733:A:H8	1.86	0.41
22:A:749:U:H2'	22:A:750:G:C8	2.56	0.41
22:A:992:G:O2'	22:A:993:A:H5''	2.21	0.41
22:A:1014:A:OP2	37:S:80:LYS:NZ	2.41	0.41
22:A:1753:G:H2'	22:A:1754:A:C8	2.56	0.41
22:A:2150:A:H2	22:A:2170:G:N1	2.05	0.41
24:C:21:PHE:HB3	24:C:24:ILE:HD12	2.03	0.41
27:F:3:ARG:HB3	27:F:7:LYS:HD2	2.02	0.41
27:F:22:TYR:OH	27:F:165:GLU:OE2	2.38	0.41
36:R:63:ALA:HA	36:R:66:ASN:ND2	2.36	0.41
39:U:19:ALA:HB1	39:U:24:LYS:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:W:30:ILE:HD12	41:W:90:GLU:HG2	2.03	0.41
1:a:621:G:H5''	1:a:622:A:H5'	2.03	0.41
1:a:738:U:O2	1:a:871:G:O2'	2.35	0.41
22:A:1650:U:H6	22:A:1650:U:H2'	1.70	0.41
22:A:2712:U:H2'	22:A:2713:U:C6	2.56	0.41
43:Y:21:ALA:O	43:Y:23:ASN:N	2.49	0.41
1:a:14:U:H2'	1:a:15:C:C6	2.56	0.40
1:a:352:G:H2'	1:a:353:A:C8	2.56	0.40
3:d:9:TRP:CZ3	3:d:25:GLU:HB2	2.56	0.40
10:k:28:ASN:OD1	10:k:28:ASN:N	2.53	0.40
12:m:2:ALA:HA	12:m:3:ARG:HA	1.78	0.40
32:N:26:GLU:HG3	32:N:101:LYS:NZ	2.36	0.40
11:l:2:PRO:HD2	11:l:7:LEU:HD21	2.02	0.40
11:l:113:GLY:HA3	11:l:131:GLY:HA3	2.03	0.40
22:A:73:U:OP2	44:Z:54:LYS:NZ	2.54	0.40
22:A:173:G:H2'	22:A:174:A:H8	1.86	0.40
22:A:281:A:H2'	22:A:282:A:C8	2.55	0.40
22:A:611:A:N6	22:A:2048:U:OP1	2.54	0.40
22:A:1103:G:H21	22:A:1117:A:H61	1.68	0.40
22:A:2162:G:H2'	22:A:2163:U:H6	1.86	0.40
23:B:4:G:H2'	23:B:5:G:C8	2.57	0.40
26:E:184:LEU:HD23	26:E:184:LEU:HA	1.91	0.40
1:a:1268:G:N1	1:a:1300:U:O4	2.55	0.40
2:c:147:GLY:HA2	2:c:170:GLY:HA3	2.02	0.40
11:l:81:PRO:HG2	11:l:112:ARG:HG2	2.03	0.40
11:l:123:ARG:HE	11:l:126:SER:HG	1.63	0.40
20:u:55:U:N3	20:u:58:A:OP2	2.45	0.40
22:A:2116:U:H2'	22:A:2117:A:C8	2.56	0.40
22:A:2144:G:H4'	22:A:2172:A:C6	2.56	0.40
1:a:130:U:H2'	1:a:131:G:C8	2.57	0.40
1:a:649:C:H2'	1:a:650:A:H8	1.85	0.40
4:e:97:LYS:HA	4:e:98:PRO:HD3	1.94	0.40
13:n:41:ARG:HG2	13:n:42:ILE:HG23	2.03	0.40
17:r:40:ARG:NH2	17:r:77:ASP:OD1	2.54	0.40
19:t:49:LEU:HA	19:t:52:GLU:HB2	2.04	0.40
22:A:669:G:N2	22:A:672:A:OP2	2.41	0.40
22:A:1630:G:H1'	22:A:1631:A:C4	2.55	0.40
22:A:2328:A:H1'	27:F:155:VAL:HG11	2.04	0.40
51:6:1:MET:HE1	51:6:24:MET:HE1	2.03	0.40
1:a:677:A:H2'	1:a:678:A:C8	2.57	0.40
2:c:40:LYS:HD2	2:c:40:LYS:HA	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:71:PRO:HG3	6:g:103:TRP:CZ3	2.56	0.40
22:A:70:C:H2'	22:A:71:G:C8	2.57	0.40
22:A:94:U:H2'	22:A:95:A:H8	1.87	0.40
22:A:173:G:H2'	22:A:174:A:C8	2.57	0.40
22:A:783:A:H2'	22:A:784:C:C6	2.55	0.40
22:A:2306:U:H2'	22:A:2307:C:H6	1.86	0.40
38:T:36:ASP:O	38:T:39:SER:OG	2.32	0.40
44:Z:14:MET:HE3	44:Z:53:ILE:HG23	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	c	202/204 (99%)	178 (88%)	24 (12%)	0	100	100
3	d	199/201 (99%)	169 (85%)	30 (15%)	0	100	100
4	e	161/163 (99%)	142 (88%)	19 (12%)	0	100	100
5	f	95/97 (98%)	86 (90%)	9 (10%)	0	100	100
6	g	152/154 (99%)	137 (90%)	15 (10%)	0	100	100
7	h	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
8	i	126/128 (98%)	109 (86%)	16 (13%)	1 (1%)	16	50
9	j	97/99 (98%)	83 (86%)	14 (14%)	0	100	100
10	k	115/117 (98%)	95 (83%)	20 (17%)	0	100	100
11	l	134/136 (98%)	103 (77%)	30 (22%)	1 (1%)	18	52
12	m	110/112 (98%)	85 (77%)	25 (23%)	0	100	100
13	n	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
14	o	86/88 (98%)	76 (88%)	10 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	p	87/89 (98%)	72 (83%)	15 (17%)	0	100	100
16	q	81/83 (98%)	67 (83%)	14 (17%)	0	100	100
17	r	64/66 (97%)	52 (81%)	12 (19%)	0	100	100
18	s	76/78 (97%)	59 (78%)	17 (22%)	0	100	100
19	t	79/81 (98%)	70 (89%)	9 (11%)	0	100	100
24	C	269/275 (98%)	241 (90%)	28 (10%)	0	100	100
25	D	205/207 (99%)	178 (87%)	27 (13%)	0	100	100
26	E	204/206 (99%)	174 (85%)	30 (15%)	0	100	100
27	F	175/177 (99%)	150 (86%)	25 (14%)	0	100	100
28	G	172/176 (98%)	141 (82%)	29 (17%)	2 (1%)	10	42
29	K	141/145 (97%)	124 (88%)	17 (12%)	0	100	100
30	L	120/122 (98%)	104 (87%)	16 (13%)	0	100	100
31	M	144/146 (99%)	102 (71%)	40 (28%)	2 (1%)	9	38
32	N	139/141 (99%)	115 (83%)	24 (17%)	0	100	100
33	O	121/123 (98%)	96 (79%)	25 (21%)	0	100	100
34	P	108/117 (92%)	92 (85%)	16 (15%)	0	100	100
35	Q	110/114 (96%)	101 (92%)	9 (8%)	0	100	100
36	R	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
37	S	98/102 (96%)	89 (91%)	9 (9%)	0	100	100
38	T	110/112 (98%)	98 (89%)	12 (11%)	0	100	100
39	U	87/89 (98%)	68 (78%)	18 (21%)	1 (1%)	11	44
40	V	98/101 (97%)	71 (72%)	24 (24%)	3 (3%)	3	24
41	W	92/94 (98%)	73 (79%)	18 (20%)	1 (1%)	11	44
42	X	74/76 (97%)	64 (86%)	10 (14%)	0	100	100
43	Y	52/54 (96%)	42 (81%)	10 (19%)	0	100	100
44	Z	59/61 (97%)	56 (95%)	3 (5%)	0	100	100
45	0	54/58 (93%)	50 (93%)	4 (7%)	0	100	100
46	1	57/59 (97%)	42 (74%)	15 (26%)	0	100	100
47	2	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
48	3	47/49 (96%)	41 (87%)	6 (13%)	0	100	100
49	4	42/44 (96%)	37 (88%)	5 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	5	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	36
51	6	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
All	All	5097/5211 (98%)	4343 (85%)	742 (15%)	12 (0%)	44	73

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	G	48	ASN
40	V	73	PRO
8	i	41	HIS
28	G	47	GLY
31	M	95	VAL
40	V	88	GLY
41	W	16	SER
31	M	98	GLU
39	U	50	VAL
50	5	32	ARG
11	l	39	ASN
40	V	72	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	c	162/162 (100%)	162 (100%)	0	100	100
3	d	175/175 (100%)	175 (100%)	0	100	100
4	e	126/126 (100%)	126 (100%)	0	100	100
5	f	86/86 (100%)	86 (100%)	0	100	100
6	g	131/131 (100%)	131 (100%)	0	100	100
7	h	112/112 (100%)	111 (99%)	1 (1%)	70	76
8	i	101/101 (100%)	100 (99%)	1 (1%)	68	75
9	j	90/90 (100%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	k	91/91 (100%)	90 (99%)	1 (1%)	65	74
11	l	118/118 (100%)	118 (100%)	0	100	100
12	m	95/95 (100%)	95 (100%)	0	100	100
13	n	51/51 (100%)	51 (100%)	0	100	100
14	o	78/78 (100%)	78 (100%)	0	100	100
15	p	79/79 (100%)	77 (98%)	2 (2%)	42	63
16	q	76/76 (100%)	76 (100%)	0	100	100
17	r	57/57 (100%)	57 (100%)	0	100	100
18	s	68/68 (100%)	67 (98%)	1 (2%)	57	71
19	t	62/62 (100%)	62 (100%)	0	100	100
24	C	225/225 (100%)	225 (100%)	0	100	100
25	D	169/170 (99%)	167 (99%)	2 (1%)	63	73
26	E	171/172 (99%)	170 (99%)	1 (1%)	78	80
27	F	153/154 (99%)	153 (100%)	0	100	100
28	G	146/146 (100%)	145 (99%)	1 (1%)	76	78
29	K	122/122 (100%)	121 (99%)	1 (1%)	73	77
30	L	98/98 (100%)	98 (100%)	0	100	100
31	M	111/112 (99%)	110 (99%)	1 (1%)	70	76
32	N	112/112 (100%)	109 (97%)	3 (3%)	39	62
33	O	104/105 (99%)	103 (99%)	1 (1%)	68	75
34	P	86/91 (94%)	84 (98%)	2 (2%)	44	64
35	Q	97/97 (100%)	97 (100%)	0	100	100
36	R	94/94 (100%)	94 (100%)	0	100	100
37	S	83/83 (100%)	82 (99%)	1 (1%)	63	73
38	T	94/95 (99%)	94 (100%)	0	100	100
39	U	80/80 (100%)	78 (98%)	2 (2%)	42	63
40	V	84/85 (99%)	84 (100%)	0	100	100
41	W	85/85 (100%)	85 (100%)	0	100	100
42	X	60/61 (98%)	60 (100%)	0	100	100
43	Y	47/47 (100%)	47 (100%)	0	100	100
44	Z	55/55 (100%)	54 (98%)	1 (2%)	51	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	0	49/49 (100%)	49 (100%)	0	100	100
46	1	55/55 (100%)	55 (100%)	0	100	100
47	2	46/46 (100%)	46 (100%)	0	100	100
48	3	49/49 (100%)	49 (100%)	0	100	100
49	4	39/39 (100%)	39 (100%)	0	100	100
50	5	51/51 (100%)	51 (100%)	0	100	100
51	6	35/35 (100%)	35 (100%)	0	100	100
All	All	4358/4371 (100%)	4336 (100%)	22 (0%)	78	81

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	h	74	ILE
8	i	67	VAL
10	k	113	VAL
15	p	4	LYS
15	p	22	VAL
18	s	30	VAL
25	D	53	TYR
25	D	119	PHE
26	E	74	ARG
28	G	107	VAL
29	K	45	PHE
31	M	77	VAL
32	N	7	VAL
32	N	74	TYR
32	N	94	VAL
33	O	121	VAL
34	P	91	VAL
34	P	103	ARG
37	S	22	VAL
39	U	48	VAL
39	U	50	VAL
44	Z	25	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (76) such sidechains are listed below:

Mol	Chain	Res	Type
2	c	64	ASN

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Mol	Chain	Res	Type
2	c	99	HIS
2	c	125	ASN
4	e	8	HIS
4	e	43	ASN
5	f	67	ASN
5	f	87	ASN
6	g	28	ASN
6	g	106	ASN
7	h	57	GLN
8	i	31	ASN
8	i	126	GLN
9	j	97	ASN
10	k	22	HIS
10	k	118	HIS
11	l	90	HIS
11	l	125	GLN
13	n	52	GLN
14	o	37	ASN
14	o	51	HIS
14	o	62	HIS
15	p	83	HIS
15	p	88	ASN
16	q	6	ASN
17	r	56	GLN
18	s	22	GLN
18	s	69	HIS
19	t	24	GLN
19	t	69	ASN
19	t	72	ASN
24	C	95	HIS
24	C	134	ASN
24	C	230	HIS
25	D	135	HIS
26	E	14	ASN
26	E	20	ASN
26	E	29	ASN
26	E	49	HIS
26	E	75	GLN
26	E	141	GLN
26	E	145	ASN
26	E	169	ASN
27	F	37	ASN

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Mol	Chain	Res	Type
28	G	71	ASN
28	G	74	ASN
29	K	48	HIS
31	M	27	ASN
31	M	38	GLN
32	N	44	ASN
33	O	61	GLN
34	P	39	ASN
35	Q	12	GLN
36	R	66	ASN
36	R	81	HIS
37	S	88	HIS
37	S	90	GLN
38	T	46	ASN
39	U	52	ASN
40	V	18	ASN
40	V	49	GLN
41	W	55	HIS
41	W	58	ASN
41	W	71	ASN
41	W	78	GLN
43	Y	17	ASN
43	Y	23	ASN
43	Y	32	ASN
43	Y	34	GLN
45	0	40	ASN
46	1	41	ASN
47	2	40	HIS
48	3	26	ASN
50	5	4	GLN
50	5	31	HIS
50	5	34	HIS
51	6	30	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1520/1523 (99%)	414 (27%)	0
20	u	75/76 (98%)	26 (34%)	0
21	v	4/5 (80%)	1 (25%)	0
22	A	2900/2903 (99%)	714 (24%)	21 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
23	B	115/116 (99%)	38 (33%)	3 (2%)
All	All	4614/4623 (99%)	1193 (25%)	24 (0%)

All (1193) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	5	A
1	a	6	G
1	a	7	A
1	a	19	G
1	a	24	G
1	a	25	G
1	a	26	A
1	a	27	C
1	a	28	G
1	a	29	A
1	a	30	A
1	a	31	C
1	a	32	G
1	a	33	C
1	a	35	G
1	a	36	G
1	a	37	C
1	a	38	G
1	a	40	C
1	a	44	C
1	a	45	C
1	a	47	A
1	a	48	A
1	a	51	C
1	a	53	U
1	a	56	A
1	a	60	C
1	a	65	G
1	a	66	C
1	a	68	U
1	a	70	U
1	a	71	U
1	a	114	A
1	a	126	C
1	a	132	G
1	a	135	A

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Mol	Chain	Res	Type
1	a	136	A
1	a	137	C
1	a	140	A
1	a	141	C
1	a	142	C
1	a	148	G
1	a	150	G
1	a	152	G
1	a	154	G
1	a	165	G
1	a	169	C
1	a	179	U
1	a	180	A
1	a	183	G
1	a	185	A
1	a	186	U
1	a	189	C
1	a	192	U
1	a	202	A
1	a	203	U
1	a	204	G
1	a	211	G
1	a	212	A
1	a	215	G
1	a	218	A
1	a	219	G
1	a	222	G
1	a	225	U
1	a	226	U
1	a	228	G
1	a	231	U
1	a	235	G
1	a	240	U
1	a	241	G
1	a	243	A
1	a	255	U
1	a	256	G
1	a	259	U
1	a	262	G
1	a	266	G
1	a	278	A
1	a	281	G

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Mol	Chain	Res	Type
1	a	282	C
1	a	284	C
1	a	288	A
1	a	290	G
1	a	294	A
1	a	295	C
1	a	296	G
1	a	304	G
1	a	309	C
1	a	310	C
1	a	311	U
1	a	313	A
1	a	315	A
1	a	318	G
1	a	319	U
1	a	320	G
1	a	321	A
1	a	323	C
1	a	336	A
1	a	342	A
1	a	343	C
1	a	344	A
1	a	359	A
1	a	361	G
1	a	362	G
1	a	367	C
1	a	369	G
1	a	378	A
1	a	379	A
1	a	381	C
1	a	382	U
1	a	383	U
1	a	384	C
1	a	387	C
1	a	388	A
1	a	393	A
1	a	397	A
1	a	399	G
1	a	403	G
1	a	407	G
1	a	412	A
1	a	414	G

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Mol	Chain	Res	Type
1	a	415	C
1	a	416	C
1	a	417	G
1	a	418	C
1	a	421	G
1	a	425	G
1	a	427	A
1	a	428	G
1	a	429	A
1	a	430	A
1	a	438	G
1	a	443	G
1	a	444	U
1	a	446	A
1	a	447	A
1	a	455	U
1	a	456	G
1	a	463	A
1	a	469	A
1	a	470	A
1	a	474	C
1	a	475	G
1	a	476	U
1	a	477	U
1	a	478	A
1	a	480	U
1	a	481	A
1	a	483	C
1	a	484	U
1	a	488	C
1	a	489	G
1	a	490	U
1	a	493	C
1	a	497	A
1	a	498	C
1	a	499	G
1	a	500	G
1	a	501	U
1	a	512	A
1	a	514	A
1	a	515	G
1	a	516	C

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Mol	Chain	Res	Type
1	a	520	G
1	a	521	G
1	a	522	C
1	a	523	U
1	a	524	A
1	a	525	A
1	a	526	C
1	a	532	G
1	a	533	C
1	a	534	C
1	a	535	A
1	a	536	G
1	a	537	C
1	a	538	A
1	a	539	G
1	a	542	G
1	a	546	U
1	a	547	A
1	a	548	A
1	a	550	A
1	a	555	G
1	a	556	G
1	a	560	C
1	a	561	A
1	a	562	A
1	a	564	C
1	a	583	G
1	a	584	C
1	a	585	G
1	a	586	U
1	a	587	A
1	a	588	A
1	a	590	G
1	a	591	C
1	a	592	G
1	a	594	G
1	a	596	G
1	a	603	G
1	a	625	G
1	a	633	C
1	a	634	U
1	a	635	C

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Mol	Chain	Res	Type
1	a	637	A
1	a	638	C
1	a	643	G
1	a	644	A
1	a	646	G
1	a	647	G
1	a	648	U
1	a	649	C
1	a	668	U
1	a	671	G
1	a	680	A
1	a	681	G
1	a	701	U
1	a	702	A
1	a	710	A
1	a	718	G
1	a	725	G
1	a	736	A
1	a	739	G
1	a	744	A
1	a	749	G
1	a	764	A
1	a	765	C
1	a	767	G
1	a	770	G
1	a	773	G
1	a	775	G
1	a	802	A
1	a	808	U
1	a	814	G
1	a	832	C
1	a	835	U
1	a	836	G
1	a	843	A
1	a	847	G
1	a	851	G
1	a	858	U
1	a	859	C
1	a	860	C
1	a	861	G
1	a	862	C
1	a	868	A

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Mol	Chain	Res	Type
1	a	869	G
1	a	876	A
1	a	878	C
1	a	879	A
1	a	881	A
1	a	883	G
1	a	886	U
1	a	887	U
1	a	888	A
1	a	892	A
1	a	901	G
1	a	905	A
1	a	906	G
1	a	930	A
1	a	943	G
1	a	950	C
1	a	951	A
1	a	966	U
1	a	967	G
1	a	973	U
1	a	974	A
1	a	975	A
1	a	976	U
1	a	977	U
1	a	978	C
1	a	982	G
1	a	984	A
1	a	985	A
1	a	987	G
1	a	992	G
1	a	993	A
1	a	994	A
1	a	995	C
1	a	998	U
1	a	999	A
1	a	1000	C
1	a	1001	C
1	a	1002	A
1	a	1008	U
1	a	1009	G
1	a	1018	U
1	a	1020	A

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Mol	Chain	Res	Type
1	a	1022	C
1	a	1027	U
1	a	1030	A
1	a	1031	G
1	a	1036	A
1	a	1038	C
1	a	1039	U
1	a	1040	U
1	a	1042	C
1	a	1043	C
1	a	1044	C
1	a	1046	U
1	a	1047	C
1	a	1048	G
1	a	1051	G
1	a	1052	A
1	a	1055	A
1	a	1061	C
1	a	1069	G
1	a	1077	G
1	a	1080	G
1	a	1081	U
1	a	1095	G
1	a	1097	G
1	a	1102	U
1	a	1110	G
1	a	1111	U
1	a	1117	A
1	a	1124	G
1	a	1140	G
1	a	1141	U
1	a	1146	A
1	a	1147	U
1	a	1149	A
1	a	1153	A
1	a	1154	G
1	a	1155	U
1	a	1156	U
1	a	1157	G
1	a	1161	A
1	a	1172	A
1	a	1173	C

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Mol	Chain	Res	Type
1	a	1174	U
1	a	1183	C
1	a	1196	G
1	a	1199	G
1	a	1202	G
1	a	1208	G
1	a	1211	A
1	a	1212	A
1	a	1227	U
1	a	1228	A
1	a	1229	U
1	a	1237	G
1	a	1238	C
1	a	1239	U
1	a	1240	A
1	a	1241	C
1	a	1242	A
1	a	1255	U
1	a	1256	G
1	a	1268	G
1	a	1272	C
1	a	1275	U
1	a	1276	A
1	a	1293	A
1	a	1295	A
1	a	1300	U
1	a	1301	U
1	a	1302	A
1	a	1303	A
1	a	1305	G
1	a	1312	U
1	a	1313	C
1	a	1314	A
1	a	1315	G
1	a	1316	U
1	a	1317	U
1	a	1318	C
1	a	1320	G
1	a	1328	G
1	a	1330	U
1	a	1334	A
1	a	1335	C

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Mol	Chain	Res	Type
1	a	1336	U
1	a	1337	C
1	a	1338	G
1	a	1355	A
1	a	1361	A
1	a	1362	G
1	a	1372	A
1	a	1374	C
1	a	1375	A
1	a	1376	G
1	a	1378	A
1	a	1379	C
1	a	1388	G
1	a	1389	A
1	a	1391	U
1	a	1396	U
1	a	1409	A
1	a	1412	C
1	a	1413	A
1	a	1415	C
1	a	1434	G
1	a	1438	G
1	a	1440	A
1	a	1441	A
1	a	1448	A
1	a	1457	A
1	a	1461	A
1	a	1465	U
1	a	1467	U
1	a	1468	U
1	a	1500	U
1	a	1503	G
1	a	1508	A
1	a	1514	U
1	a	1515	A
1	a	1518	A
1	a	1519	A
1	a	1520	G
1	a	1521	G
1	a	1522	U
1	a	1545	G
1	a	1546	G

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Mol	Chain	Res	Type
20	u	4	C
20	u	8	U
20	u	9	A
20	u	13	C
20	u	15	G
20	u	17	C
20	u	18	G
20	u	19	G
20	u	20	U
20	u	21	A
20	u	24	G
20	u	26	A
20	u	44	G
20	u	46	G
20	u	47	U
20	u	48	C
20	u	49	C
20	u	54	U
20	u	55	U
20	u	56	C
20	u	57	G
20	u	58	A
20	u	59	U
20	u	74	C
20	u	75	C
20	u	76	A
21	v	17	U
22	A	10	G
22	A	13	U
22	A	14	A
22	A	15	A
22	A	16	G
22	A	26	U
22	A	29	A
22	A	35	U
22	A	49	G
22	A	50	A
22	A	52	G
22	A	62	A
22	A	65	A
22	A	72	A
22	A	75	U

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Mol	Chain	Res	Type
22	A	76	G
22	A	89	G
22	A	97	G
22	A	100	A
22	A	102	G
22	A	103	A
22	A	110	G
22	A	117	G
22	A	118	A
22	A	119	A
22	A	120	U
22	A	125	G
22	A	131	A
22	A	151	A
22	A	155	U
22	A	156	U
22	A	162	A
22	A	165	A
22	A	166	C
22	A	168	U
22	A	169	A
22	A	177	A
22	A	180	G
22	A	181	G
22	A	182	U
22	A	184	G
22	A	185	A
22	A	189	A
22	A	199	A
22	A	202	A
22	A	204	C
22	A	207	A
22	A	218	G
22	A	219	A
22	A	224	A
22	A	225	A
22	A	229	A
22	A	231	A
22	A	232	U
22	A	233	U
22	A	235	G
22	A	244	A

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Mol	Chain	Res	Type
22	A	250	G
22	A	251	G
22	A	253	G
22	A	254	A
22	A	255	G
22	A	268	A
22	A	270	C
22	A	279	A
22	A	284	C
22	A	285	U
22	A	286	U
22	A	288	C
22	A	289	U
22	A	294	G
22	A	298	U
22	A	300	G
22	A	301	U
22	A	302	A
22	A	309	C
22	A	310	G
22	A	312	U
22	A	313	A
22	A	318	A
22	A	321	C
22	A	322	U
22	A	332	G
22	A	339	G
22	A	344	G
22	A	348	A
22	A	352	C
22	A	367	A
22	A	368	A
22	A	383	A
22	A	386	G
22	A	389	G
22	A	393	A
22	A	397	C
22	A	399	A
22	A	400	G
22	A	414	A
22	A	421	A
22	A	426	G

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Mol	Chain	Res	Type
22	A	451	G
22	A	452	A
22	A	471	U
22	A	476	C
22	A	487	A
22	A	488	U
22	A	494	A
22	A	496	C
22	A	497	A
22	A	507	G
22	A	516	G
22	A	517	A
22	A	521	G
22	A	533	G
22	A	543	U
22	A	544	A
22	A	547	U
22	A	548	C
22	A	549	C
22	A	551	G
22	A	561	G
22	A	566	C
22	A	567	A
22	A	569	C
22	A	570	A
22	A	571	A
22	A	572	G
22	A	584	U
22	A	585	A
22	A	586	A
22	A	588	G
22	A	600	G
22	A	610	G
22	A	611	A
22	A	612	A
22	A	623	A
22	A	632	U
22	A	640	A
22	A	653	G
22	A	654	A
22	A	655	G
22	A	660	A

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Mol	Chain	Res	Type
22	A	669	G
22	A	670	A
22	A	673	G
22	A	676	A
22	A	677	G
22	A	684	U
22	A	685	A
22	A	690	G
22	A	692	A
22	A	693	U
22	A	694	G
22	A	708	A
22	A	709	G
22	A	710	A
22	A	711	C
22	A	712	C
22	A	722	G
22	A	726	U
22	A	741	G
22	A	750	G
22	A	753	G
22	A	757	A
22	A	759	C
22	A	766	G
22	A	769	G
22	A	770	A
22	A	787	U
22	A	788	G
22	A	792	A
22	A	804	A
22	A	805	G
22	A	808	G
22	A	815	G
22	A	816	C
22	A	817	G
22	A	822	A
22	A	823	A
22	A	824	U
22	A	825	U
22	A	832	G
22	A	833	A
22	A	840	A

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Mol	Chain	Res	Type
22	A	845	G
22	A	846	C
22	A	849	G
22	A	851	U
22	A	852	C
22	A	867	U
22	A	868	U
22	A	886	U
22	A	887	G
22	A	888	A
22	A	891	A
22	A	892	U
22	A	900	G
22	A	901	U
22	A	902	A
22	A	903	G
22	A	905	G
22	A	907	A
22	A	908	C
22	A	909	U
22	A	910	G
22	A	919	A
22	A	920	G
22	A	921	G
22	A	923	G
22	A	924	C
22	A	925	C
22	A	927	A
22	A	928	U
22	A	932	G
22	A	933	G
22	A	934	G
22	A	935	U
22	A	936	U
22	A	939	C
22	A	943	U
22	A	944	U
22	A	945	C
22	A	946	A
22	A	947	G
22	A	948	A
22	A	950	A

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Mol	Chain	Res	Type
22	A	951	A
22	A	952	A
22	A	955	C
22	A	956	C
22	A	957	G
22	A	958	A
22	A	959	A
22	A	960	U
22	A	961	G
22	A	964	A
22	A	966	U
22	A	967	C
22	A	981	A
22	A	983	U
22	A	985	A
22	A	986	G
22	A	991	C
22	A	992	G
22	A	993	A
22	A	994	G
22	A	995	U
22	A	997	A
22	A	998	U
22	A	1001	G
22	A	1007	U
22	A	1014	A
22	A	1016	G
22	A	1023	A
22	A	1026	C
22	A	1028	A
22	A	1029	G
22	A	1036	A
22	A	1037	G
22	A	1045	C
22	A	1048	A
22	A	1051	A
22	A	1053	A
22	A	1057	G
22	A	1061	A
22	A	1062	G
22	A	1063	U
22	A	1064	G

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Mol	Chain	Res	Type
22	A	1065	G
22	A	1066	A
22	A	1073	U
22	A	1079	G
22	A	1085	C
22	A	1087	G
22	A	1092	C
22	A	1093	U
22	A	1094	A
22	A	1096	G
22	A	1097	A
22	A	1098	U
22	A	1100	U
22	A	1101	U
22	A	1102	G
22	A	1104	C
22	A	1106	U
22	A	1107	A
22	A	1111	G
22	A	1112	C
22	A	1113	A
22	A	1114	G
22	A	1116	C
22	A	1117	A
22	A	1118	C
22	A	1120	A
22	A	1121	U
22	A	1122	U
22	A	1125	A
22	A	1127	G
22	A	1128	A
22	A	1129	G
22	A	1130	U
22	A	1131	G
22	A	1134	U
22	A	1135	A
22	A	1137	U
22	A	1138	A
22	A	1139	G
22	A	1140	C
22	A	1141	U
22	A	1142	C

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Mol	Chain	Res	Type
22	A	1143	A
22	A	1144	C
22	A	1145	U
22	A	1146	A
22	A	1147	G
22	A	1148	U
22	A	1149	C
22	A	1150	G
22	A	1151	A
22	A	1152	G
22	A	1157	C
22	A	1166	A
22	A	1167	A
22	A	1168	A
22	A	1171	G
22	A	1172	U
22	A	1174	C
22	A	1175	C
22	A	1179	G
22	A	1181	U
22	A	1182	A
22	A	1212	A
22	A	1214	U
22	A	1215	A
22	A	1217	G
22	A	1224	G
22	A	1244	G
22	A	1249	G
22	A	1257	A
22	A	1272	G
22	A	1273	G
22	A	1275	G
22	A	1277	G
22	A	1285	G
22	A	1287	G
22	A	1290	A
22	A	1292	U
22	A	1293	G
22	A	1302	A
22	A	1308	G
22	A	1309	A
22	A	1310	A

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Mol	Chain	Res	Type
22	A	1311	A
22	A	1336	U
22	A	1337	A
22	A	1338	U
22	A	1350	C
22	A	1357	A
22	A	1365	U
22	A	1366	C
22	A	1373	G
22	A	1376	U
22	A	1377	U
22	A	1388	U
22	A	1394	G
22	A	1396	G
22	A	1397	G
22	A	1401	A
22	A	1404	G
22	A	1407	G
22	A	1411	G
22	A	1415	U
22	A	1416	G
22	A	1417	G
22	A	1420	A
22	A	1428	G
22	A	1429	A
22	A	1431	A
22	A	1432	U
22	A	1436	U
22	A	1439	A
22	A	1443	G
22	A	1448	U
22	A	1449	U
22	A	1450	U
22	A	1451	U
22	A	1452	G
22	A	1453	U
22	A	1455	U
22	A	1456	G
22	A	1457	A
22	A	1461	A
22	A	1462	U
22	A	1469	A

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Mol	Chain	Res	Type
22	A	1470	C
22	A	1471	G
22	A	1475	U
22	A	1487	U
22	A	1488	G
22	A	1489	C
22	A	1491	U
22	A	1492	G
22	A	1493	C
22	A	1494	G
22	A	1495	A
22	A	1496	U
22	A	1497	U
22	A	1500	A
22	A	1501	A
22	A	1502	G
22	A	1503	U
22	A	1504	G
22	A	1509	U
22	A	1510	C
22	A	1519	G
22	A	1521	G
22	A	1525	U
22	A	1531	G
22	A	1535	U
22	A	1536	A
22	A	1539	U
22	A	1551	U
22	A	1552	A
22	A	1559	A
22	A	1566	A
22	A	1567	C
22	A	1568	G
22	A	1573	G
22	A	1576	A
22	A	1584	G
22	A	1585	U
22	A	1586	A
22	A	1589	G
22	A	1590	A
22	A	1592	G
22	A	1600	C

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Mol	Chain	Res	Type
22	A	1601	G
22	A	1603	C
22	A	1604	A
22	A	1605	C
22	A	1606	A
22	A	1612	A
22	A	1613	A
22	A	1615	A
22	A	1623	C
22	A	1629	A
22	A	1630	G
22	A	1631	A
22	A	1632	A
22	A	1633	A
22	A	1634	A
22	A	1635	C
22	A	1645	U
22	A	1646	A
22	A	1650	U
22	A	1651	A
22	A	1653	A
22	A	1673	A
22	A	1677	U
22	A	1689	A
22	A	1690	G
22	A	1691	C
22	A	1717	G
22	A	1718	C
22	A	1737	C
22	A	1738	G
22	A	1741	A
22	A	1747	G
22	A	1756	U
22	A	1757	U
22	A	1758	C
22	A	1770	G
22	A	1777	G
22	A	1778	G
22	A	1784	G
22	A	1787	A
22	A	1790	G
22	A	1795	U

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Mol	Chain	Res	Type
22	A	1796	C
22	A	1798	A
22	A	1799	A
22	A	1801	A
22	A	1814	C
22	A	1815	A
22	A	1821	G
22	A	1822	U
22	A	1823	A
22	A	1828	G
22	A	1829	A
22	A	1830	A
22	A	1842	G
22	A	1843	A
22	A	1872	G
22	A	1881	G
22	A	1882	C
22	A	1886	G
22	A	1896	A
22	A	1913	A
22	A	1917	G
22	A	1919	C
22	A	1920	G
22	A	1927	A
22	A	1928	C
22	A	1943	G
22	A	1944	G
22	A	1948	C
22	A	1952	A
22	A	1953	U
22	A	1969	U
22	A	1970	U
22	A	1977	C
22	A	1978	G
22	A	1979	C
22	A	1981	C
22	A	1984	A
22	A	1985	A
22	A	1986	G
22	A	1989	G
22	A	1990	U
22	A	1996	U

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Mol	Chain	Res	Type
22	A	2005	U
22	A	2006	G
22	A	2007	U
22	A	2011	A
22	A	2035	G
22	A	2036	U
22	A	2044	A
22	A	2045	A
22	A	2046	G
22	A	2047	A
22	A	2048	U
22	A	2057	C
22	A	2066	G
22	A	2069	C
22	A	2070	G
22	A	2074	A
22	A	2075	G
22	A	2076	A
22	A	2082	U
22	A	2083	G
22	A	2084	G
22	A	2107	G
22	A	2115	G
22	A	2125	U
22	A	2126	A
22	A	2127	C
22	A	2129	G
22	A	2130	G
22	A	2131	A
22	A	2132	U
22	A	2134	G
22	A	2139	G
22	A	2140	A
22	A	2141	G
22	A	2144	G
22	A	2145	A
22	A	2146	U
22	A	2148	A
22	A	2149	G
22	A	2155	A
22	A	2158	G
22	A	2159	C

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Mol	Chain	Res	Type
22	A	2160	U
22	A	2161	A
22	A	2162	G
22	A	2165	U
22	A	2166	C
22	A	2168	G
22	A	2170	G
22	A	2174	G
22	A	2178	U
22	A	2182	G
22	A	2183	G
22	A	2184	G
22	A	2186	U
22	A	2187	A
22	A	2198	G
22	A	2200	U
22	A	2213	A
22	A	2217	G
22	A	2218	C
22	A	2227	U
22	A	2228	C
22	A	2239	A
22	A	2252	G
22	A	2253	G
22	A	2280	A
22	A	2282	A
22	A	2283	A
22	A	2284	G
22	A	2297	C
22	A	2298	C
22	A	2301	A
22	A	2302	A
22	A	2317	G
22	A	2318	G
22	A	2319	U
22	A	2323	A
22	A	2325	A
22	A	2333	A
22	A	2334	A
22	A	2336	A
22	A	2337	G
22	A	2339	G

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Mol	Chain	Res	Type
22	A	2341	A
22	A	2348	G
22	A	2349	A
22	A	2350	A
22	A	2359	G
22	A	2361	C
22	A	2364	C
22	A	2372	A
22	A	2379	G
22	A	2390	A
22	A	2393	G
22	A	2397	G
22	A	2398	G
22	A	2399	C
22	A	2405	G
22	A	2406	A
22	A	2417	C
22	A	2420	C
22	A	2427	G
22	A	2433	U
22	A	2436	C
22	A	2437	U
22	A	2439	A
22	A	2442	G
22	A	2443	G
22	A	2445	U
22	A	2455	C
22	A	2461	G
22	A	2462	A
22	A	2469	G
22	A	2473	A
22	A	2488	C
22	A	2492	A
22	A	2498	G
22	A	2505	U
22	A	2517	A
22	A	2519	G
22	A	2532	A
22	A	2534	C
22	A	2543	G
22	A	2548	C
22	A	2549	G

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Mol	Chain	Res	Type
22	A	2557	G
22	A	2558	G
22	A	2561	U
22	A	2566	U
22	A	2580	A
22	A	2581	G
22	A	2586	A
22	A	2587	C
22	A	2588	G
22	A	2592	G
22	A	2596	G
22	A	2598	U
22	A	2599	U
22	A	2600	C
22	A	2616	A
22	A	2623	U
22	A	2624	C
22	A	2627	U
22	A	2629	U
22	A	2634	C
22	A	2643	U
22	A	2650	U
22	A	2651	U
22	A	2652	G
22	A	2667	U
22	A	2668	A
22	A	2677	G
22	A	2696	G
22	A	2703	U
22	A	2728	G
22	A	2746	G
22	A	2747	A
22	A	2749	G
22	A	2753	U
22	A	2762	A
22	A	2766	C
22	A	2770	U
22	A	2778	A
22	A	2779	A
22	A	2780	G
22	A	2789	A
22	A	2791	G

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Mol	Chain	Res	Type
22	A	2792	A
22	A	2793	U
22	A	2795	A
22	A	2804	A
22	A	2805	U
22	A	2809	U
22	A	2812	A
22	A	2813	A
22	A	2814	G
22	A	2819	U
22	A	2829	G
22	A	2831	G
22	A	2835	U
22	A	2836	G
22	A	2844	A
22	A	2845	G
22	A	2846	A
22	A	2847	U
22	A	2868	G
22	A	2869	U
22	A	2872	U
22	A	2878	G
22	A	2883	G
22	A	2891	C
22	A	2897	G
22	A	2902	A
22	A	2904	G
23	B	8	G
23	B	10	G
23	B	11	A
23	B	13	A
23	B	14	G
23	B	22	G
23	B	31	G
23	B	40	C
23	B	42	G
23	B	43	A
23	B	51	A
23	B	54	U
23	B	55	A
23	B	64	A
23	B	65	G

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Mol	Chain	Res	Type
23	B	70	G
23	B	71	A
23	B	73	U
23	B	74	G
23	B	75	U
23	B	76	A
23	B	77	G
23	B	79	G
23	B	80	A
23	B	81	A
23	B	82	G
23	B	84	G
23	B	85	U
23	B	86	U
23	B	87	U
23	B	91	U
23	B	92	U
23	B	94	G
23	B	97	A
23	B	98	G
23	B	99	A
23	B	101	U
23	B	107	G

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	A	179	A
22	A	311	A
22	A	427	A
22	A	559	G
22	A	654	A
22	A	693	U
22	A	890	A
22	A	934	G
22	A	949	U
22	A	963	C
22	A	994	G
22	A	1101	U
22	A	1147	G
22	A	1239	U
22	A	1431	A

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Mol	Chain	Res	Type
22	A	1584	G
22	A	1585	U
22	A	1604	A
22	A	1605	C
22	A	2317	G
22	A	2813	A
23	B	73	U
23	B	90	C
23	B	98	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	a	3
22	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	928:U	O3'	931:C	P	13.85
1	a	71:U	O3'	97:G	P	13.64
1	A	1579:U	O3'	1583:A	P	5.91
1	a	465:G	O3'	466:A	P	5.38
1	a	519:C	O3'	520:G	P	3.31

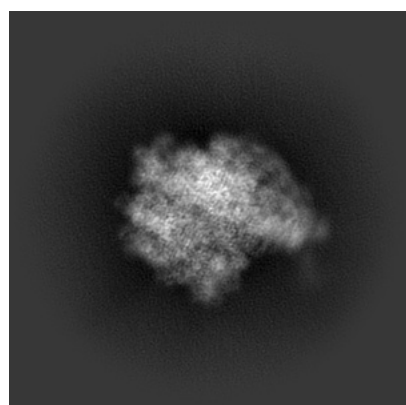
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0656. These allow visual inspection of the internal detail of the map and identification of artifacts.

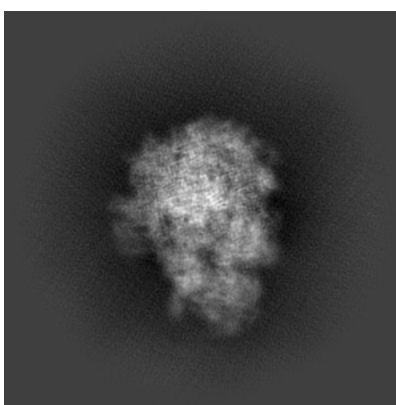
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

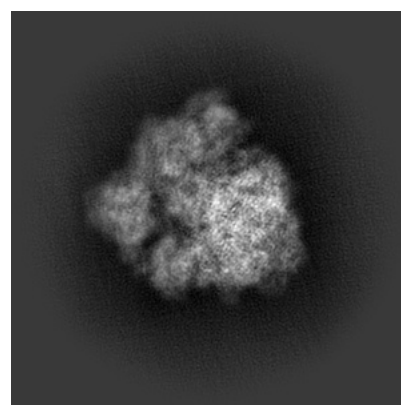
6.1.1 Primary map



X



Y

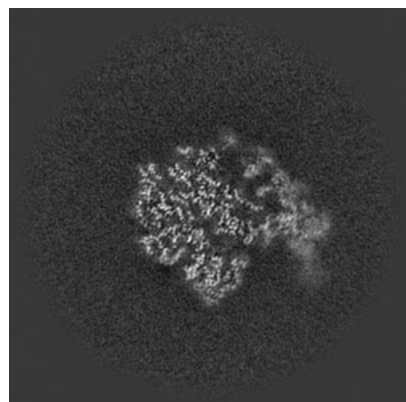


Z

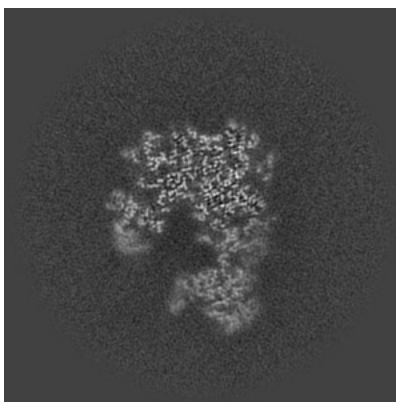
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

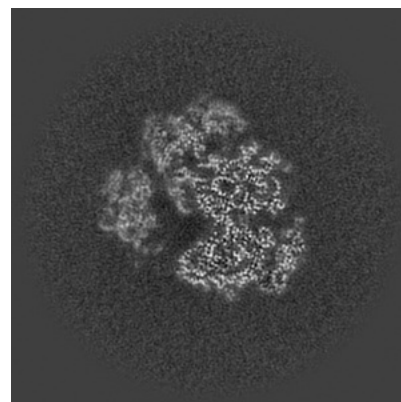
6.2.1 Primary map



X Index: 220



Y Index: 220

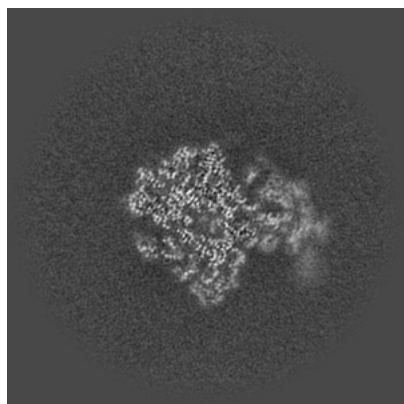


Z Index: 220

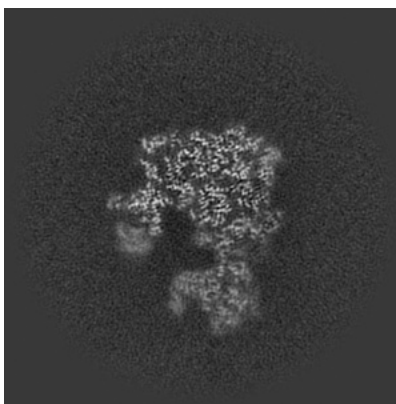
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

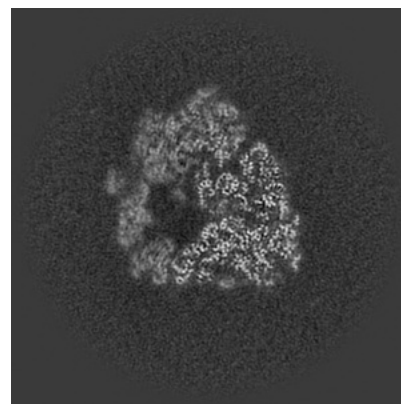
6.3.1 Primary map



X Index: 226



Y Index: 228

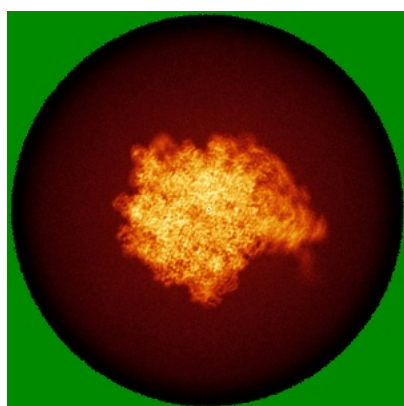


Z Index: 209

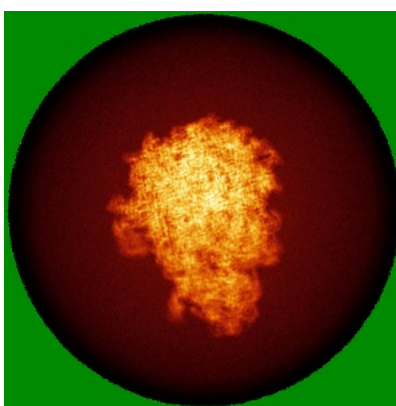
The images above show the largest variance slices of the map in three orthogonal directions.

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

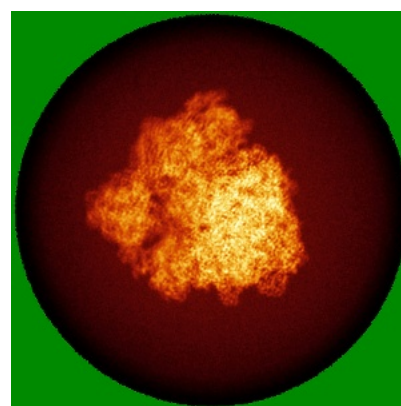
6.4.1 Primary map



X



Y

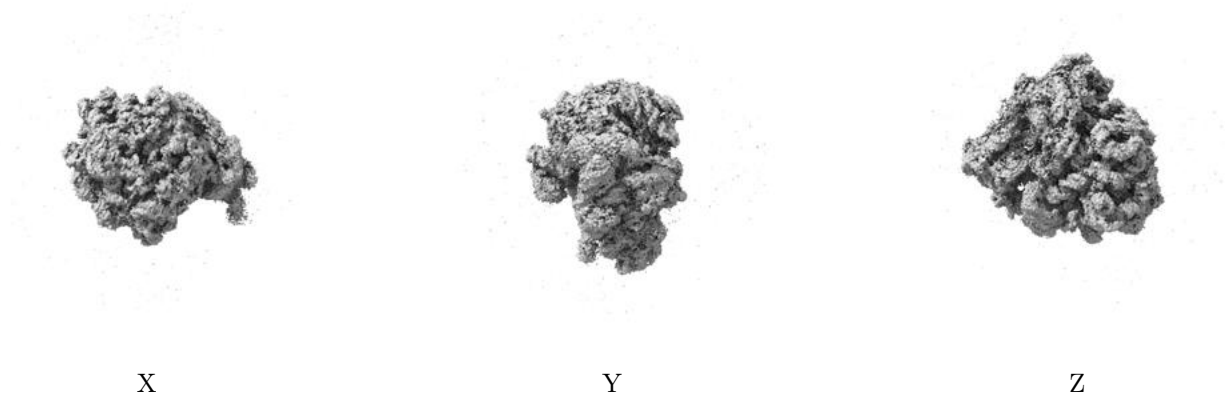


Z

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

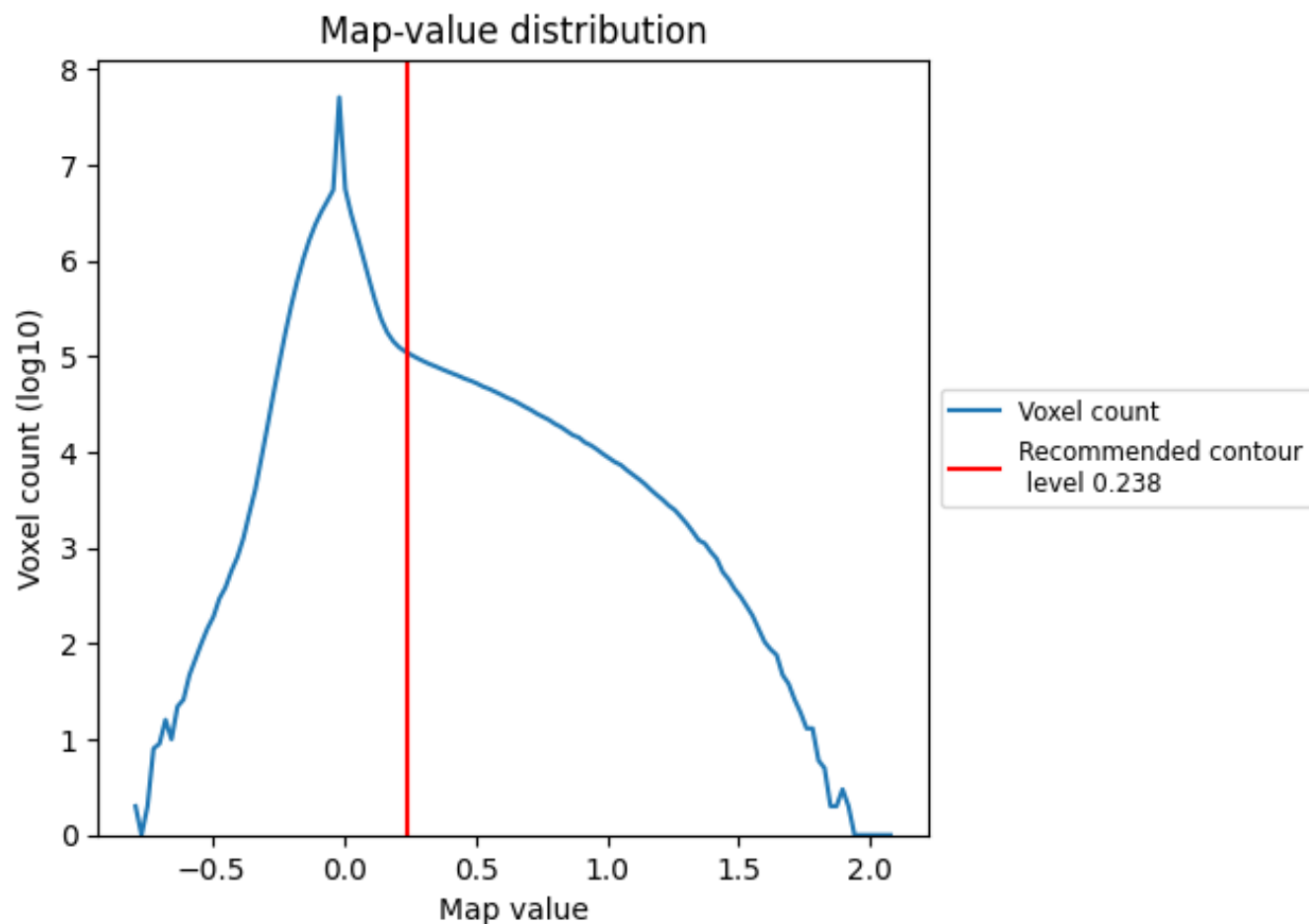
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

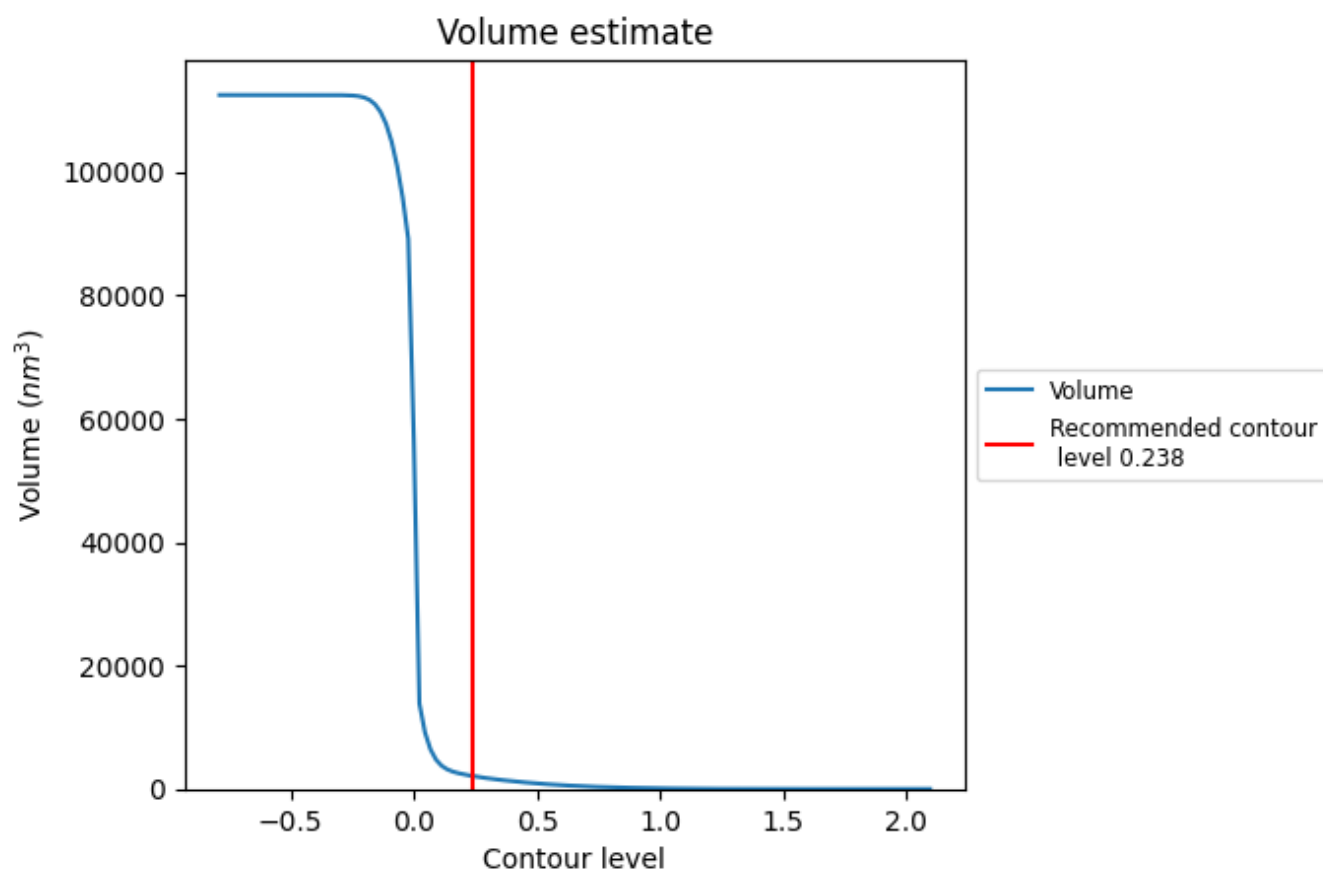
This section contains the results of statistical analysis of the map.

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.

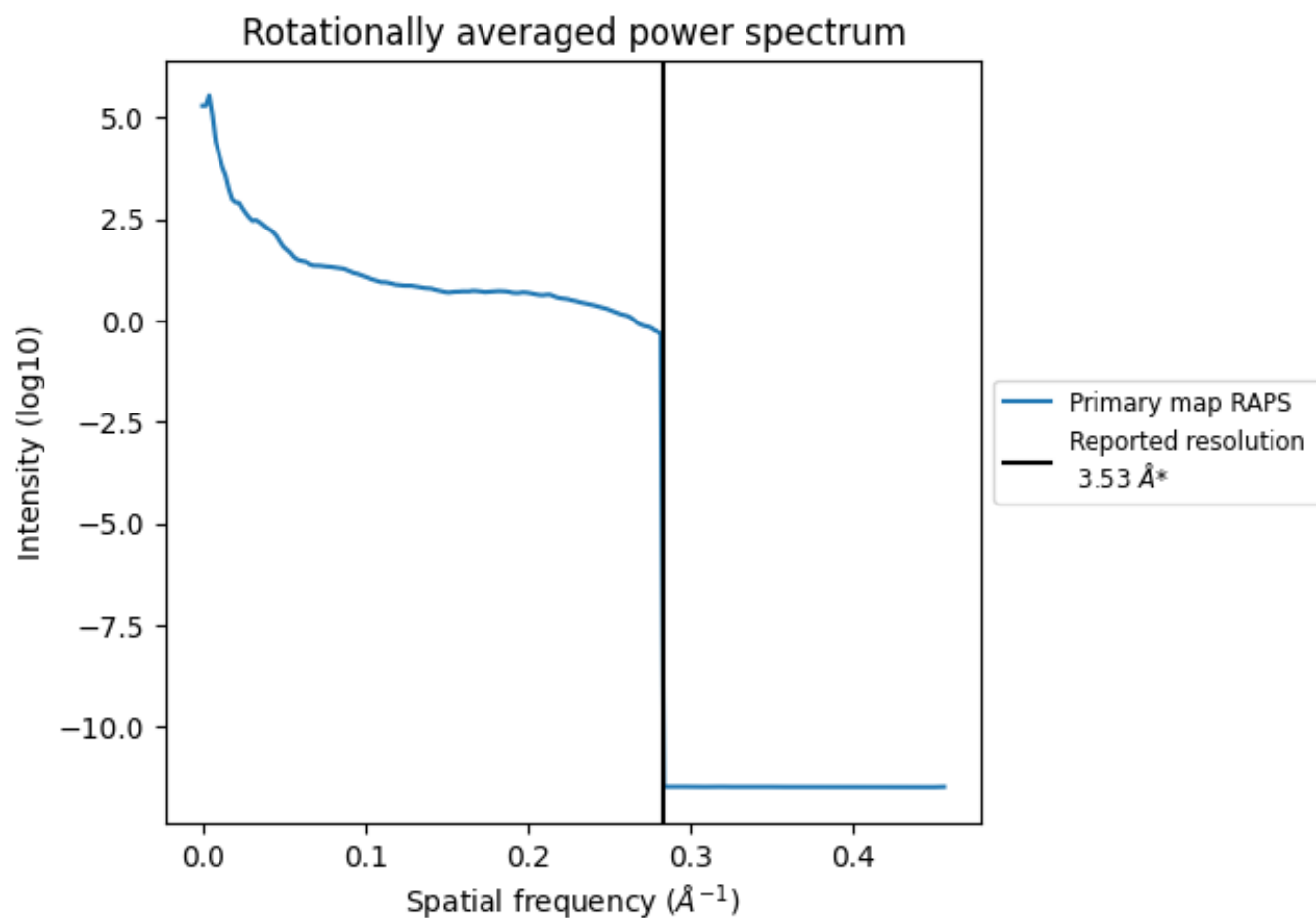
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2103 nm^3 ; this corresponds to an approximate mass of 1899 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 0.283 Å⁻¹

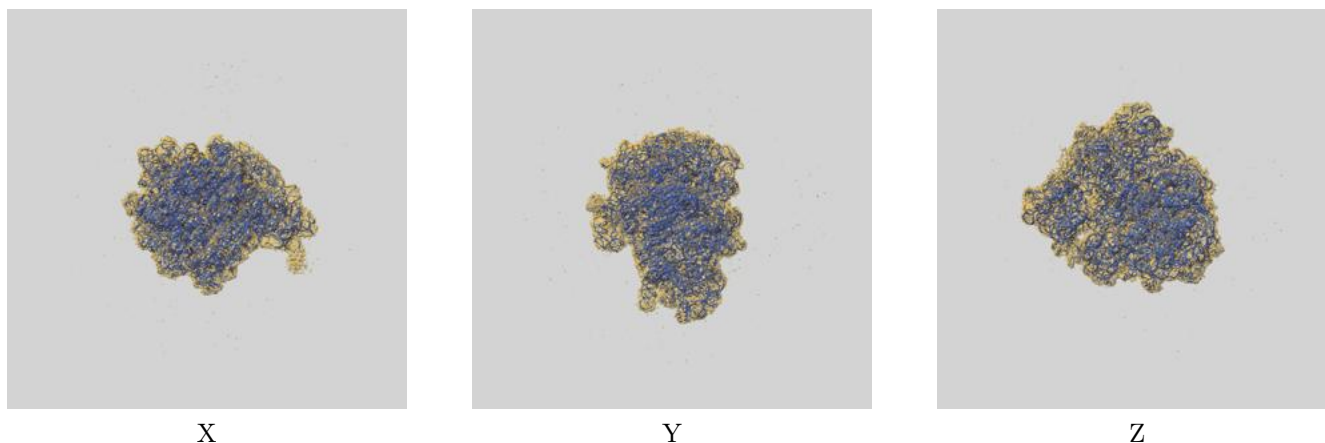
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

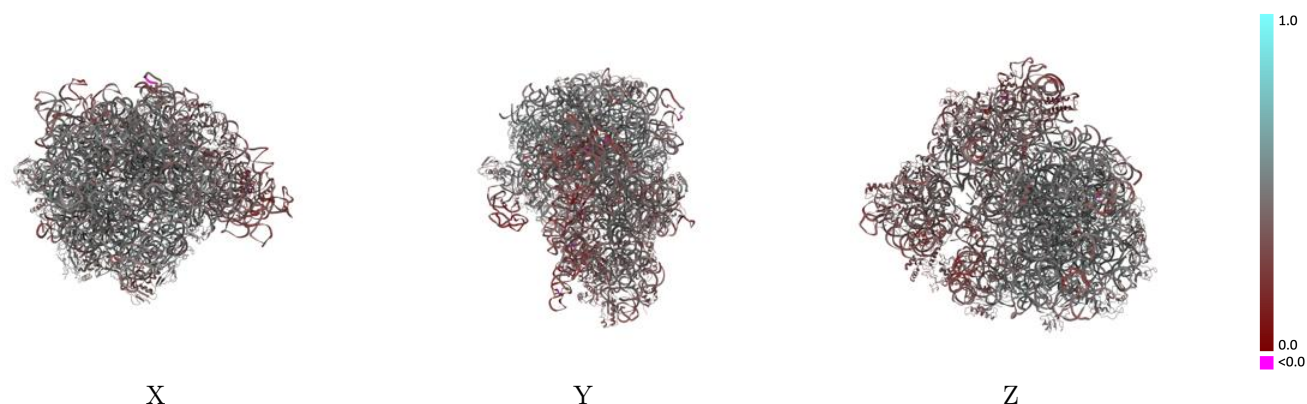
This section contains information regarding the fit between EMDB map EMD-0656 and PDB model 6O8W. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



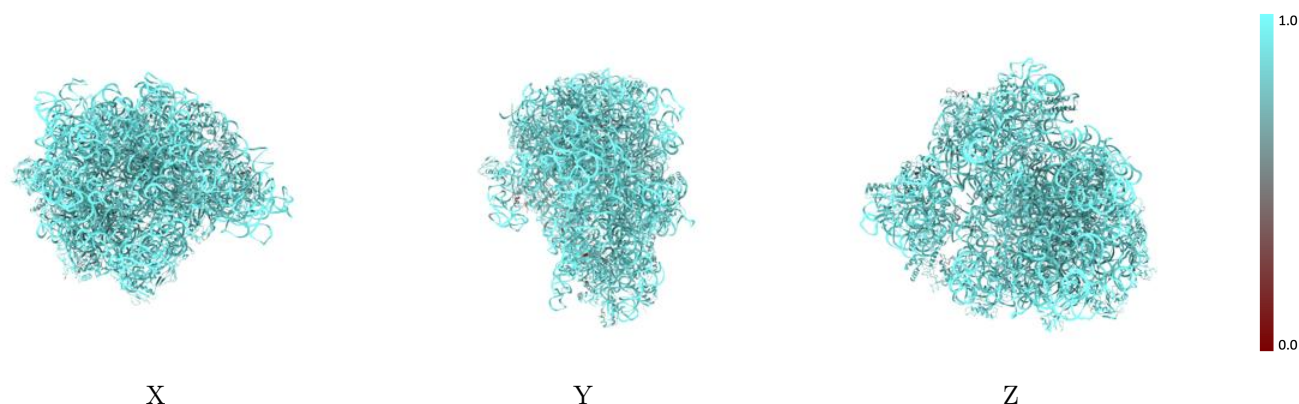
The images above show the 3D surface view of the map at the recommended contour level 0.238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



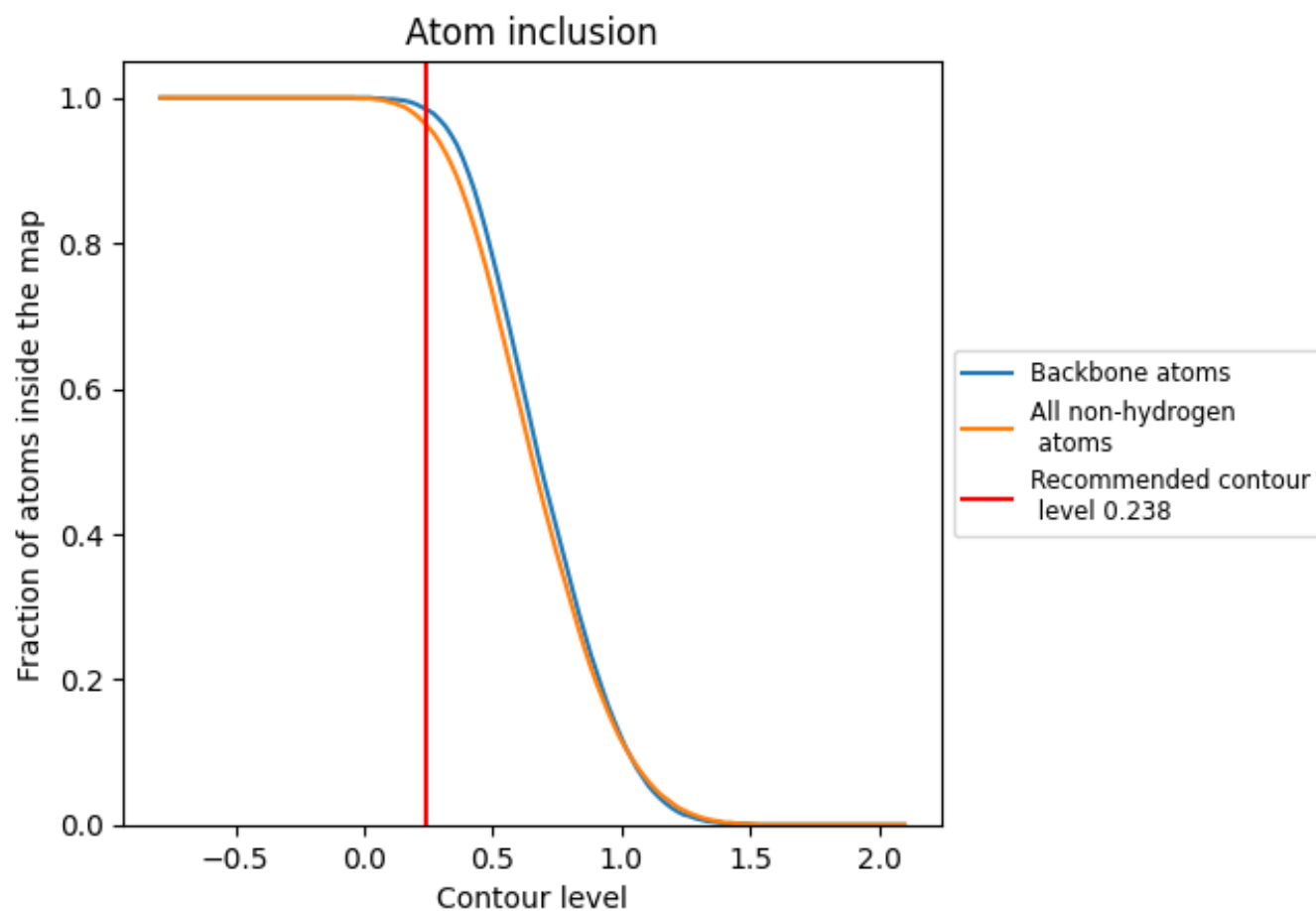
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.238).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.4220
0	 0.9250	 0.4750
1	 0.9010	 0.2830
2	 0.9570	 0.4810
3	 0.9360	 0.4750
4	 0.9290	 0.4550
5	 0.9330	 0.4840
6	 0.9700	 0.4810
A	 0.9920	 0.4520
B	 0.9940	 0.4030
C	 0.9310	 0.4740
D	 0.9390	 0.4820
E	 0.9420	 0.4600
F	 0.8580	 0.3350
G	 0.9060	 0.4000
K	 0.9350	 0.4660
L	 0.9130	 0.4900
M	 0.9500	 0.4780
N	 0.8220	 0.4190
O	 0.9340	 0.4600
P	 0.9080	 0.3870
Q	 0.9130	 0.4650
R	 0.9120	 0.4460
S	 0.9230	 0.4770
T	 0.9460	 0.4730
U	 0.9300	 0.4470
V	 0.9070	 0.4290
W	 0.3690	 0.3130
X	 0.9400	 0.4890
Y	 0.9710	 0.4960
Z	 0.9040	 0.4170
a	 0.9910	 0.3860
c	 0.9000	 0.3740
d	 0.8350	 0.3200
e	 0.9020	 0.4160



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Chain	Atom inclusion	Q-score
f	 0.8760	 0.4240
g	 0.8500	 0.3170
h	 0.9150	 0.3940
i	 0.9400	 0.3680
j	 0.8680	 0.3610
k	 0.8820	 0.4040
l	 0.8670	 0.3440
m	 0.8920	 0.3050
n	 0.9580	 0.3810
o	 0.8850	 0.3800
p	 0.9030	 0.3150
q	 0.8540	 0.3660
r	 0.8790	 0.3940
s	 0.9000	 0.2810
t	 0.8380	 0.2850
u	 0.9900	 0.3890
v	 0.9800	 0.4700