



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:34 AM UTC

PDB ID : 8VIO / pdb_00008vio
EMDB ID : EMD-43267
Title : Structure of Mycobacterium smegmatis HflX bound to a 70S ribosome
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.;
Agrawal, R.K.
Deposited on : 2024-01-05
Resolution : 3.26 Å (reported)
Based on initial models : 5O61, 6DZI

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

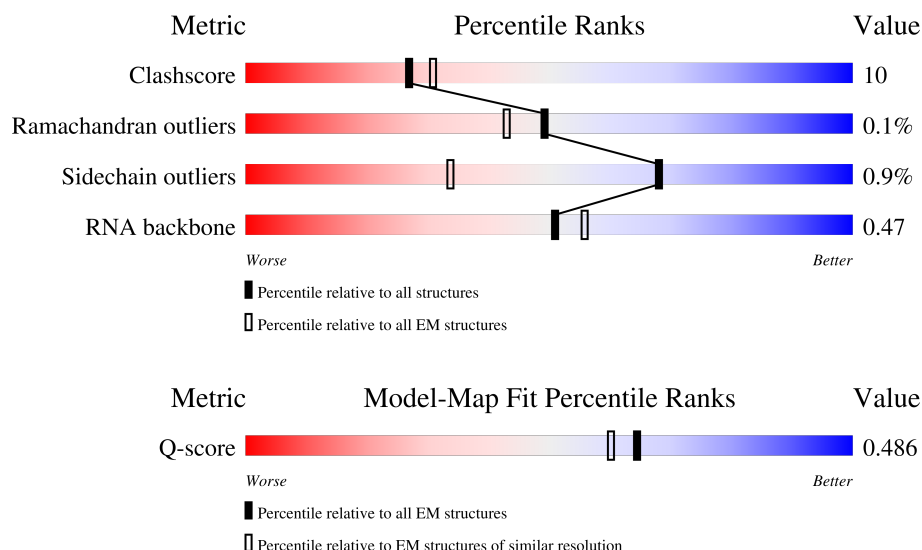
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 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.



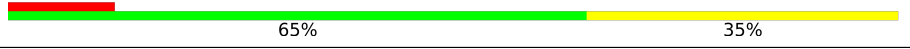
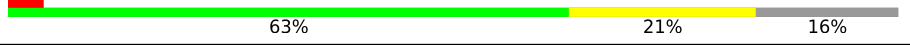
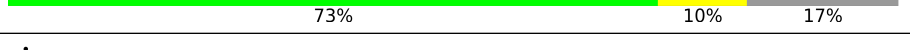
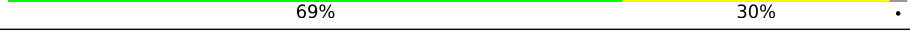
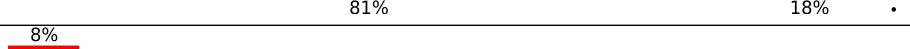
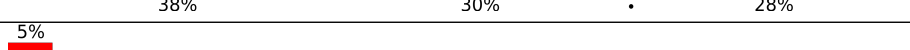
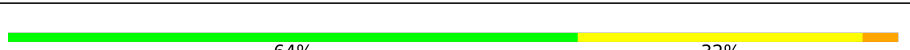
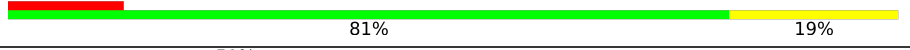
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14557 (2.76 - 3.76)

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	Y	64	
2	c	55	
3	g	75	

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Mol	Chain	Length	Quality of chain
4	r	84	
5	l	33	
6	j	201	
7	k	214	
8	l	96	
9	n	132	
10	q	138	
11	s	124	
12	v	89	
13	w	156	
14	x	98	
15	z	86	
16	h	277	
17	3	24	
18	A	3120	
19	B	118	
20	C	278	
21	D	217	
22	E	215	
23	F	187	
24	G	179	
25	H	151	
26	I	175	
27	J	142	
28	K	147	

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Mol	Chain	Length	Quality of chain
29	L	122	
30	M	147	
31	N	138	
32	O	199	
33	P	127	
34	Q	113	
35	R	129	
36	S	103	
37	T	153	
38	U	100	
39	V	105	
40	W	215	
41	X	88	
42	Z	77	
43	2	61	
44	b	57	
45	d	47	
46	e	64	
47	f	37	
48	5	77	
49	a	1528	
50	i	275	
51	m	156	
52	o	150	
53	p	101	

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Mol	Chain	Length	Quality of chain
54	t	124	23%49%38%13%
55	y	93	13%53%35%12%
56	4	470	55%40%17%43%
57	u	61	34%57%7%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 152629 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 2 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 3 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 4 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	r	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 5 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	j	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 7 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	k	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	l	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 9 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	n	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	q	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	s	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 12 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	v	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 13 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	w	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 14 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	x	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 15 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	z	85	Total	C	N	O		0	0
			660	402	139	119			

- Molecule 16 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 17 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	3	23	Total	C	N	O		0	0
			189	111	50	28			

- Molecule 18 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 19 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 20 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 21 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 22 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 23 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 24 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 25 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 26 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 27 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 28 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	K	145	Total	C	N	O	S	0	0
			1125	719	206	199	1		

- Molecule 29 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 30 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 31 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 32 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 33 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	P	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 34 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 35 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	R	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 36 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	S	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 37 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 38 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 39 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 40 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 41 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 44 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 45 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 46 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 47 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 48 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 49 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 50 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	i	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 51 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	m	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 52 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	o	126	Total	C	N	O		0	0
			994	630	194	170			

- Molecule 53 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	p	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 54 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	t	108	Total	C	N	O	S	0	0
			877	535	180	159	3		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 56 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	267	Total	C	N	O	S	0	0
			2058	1275	383	397	3		

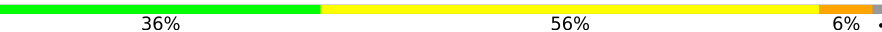
- Molecule 57 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	u	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

3 Residue-property plots [i](#)

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

- Molecule 1: 50S Ribosomal Protein L28

Chain Y: 



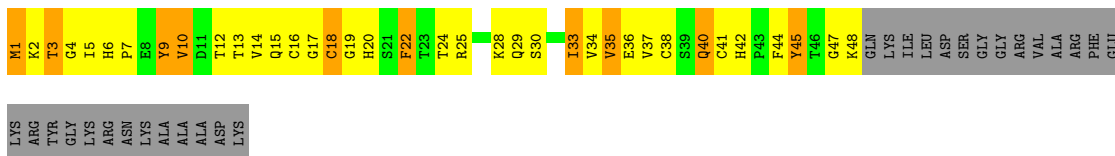
- Molecule 2: 50S Ribosomal Protein L33

Chain c: 



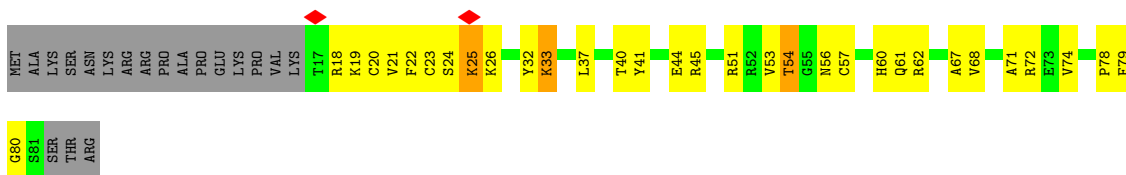
- Molecule 3: 50S Ribosomal Protein L31

Chain g: 



- Molecule 4: 30S Ribosomal Protein S18

Chain r: 

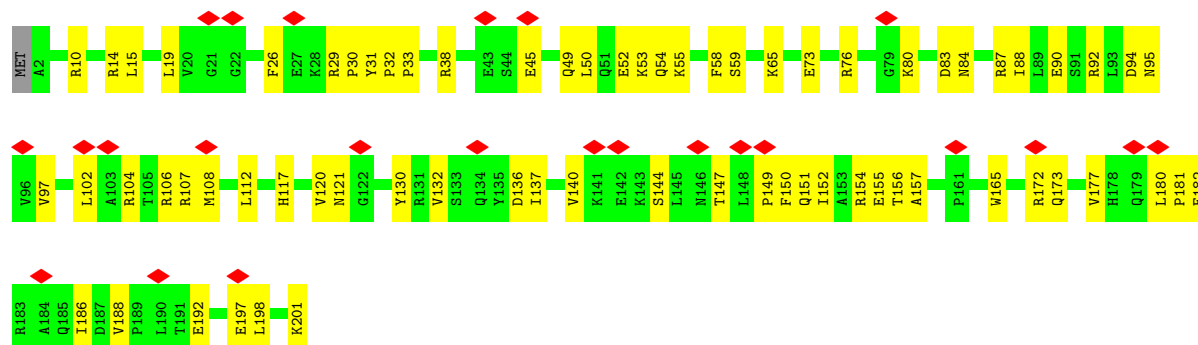


- Molecule 5: Conserved domain protein

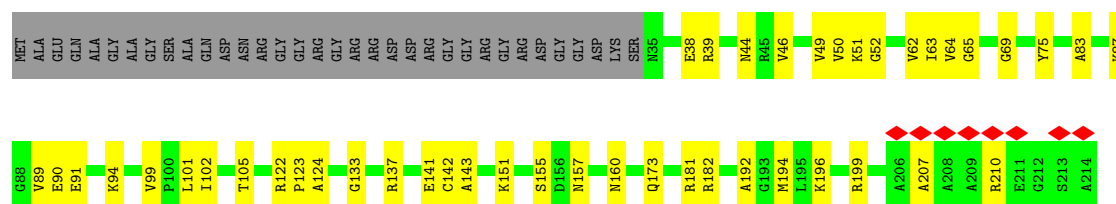
Chain 1: 



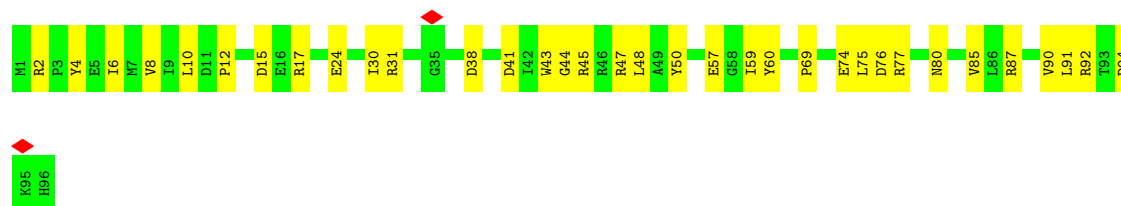
- Molecule 6: 30S ribosomal protein S4



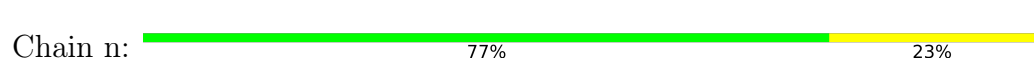
- Molecule 7: 30S Ribosomal Protein S5



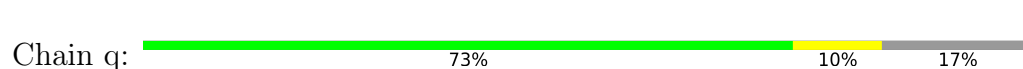
- Molecule 8: 30S ribosomal protein S6



- Molecule 9: 30S Ribosomal Protein S8

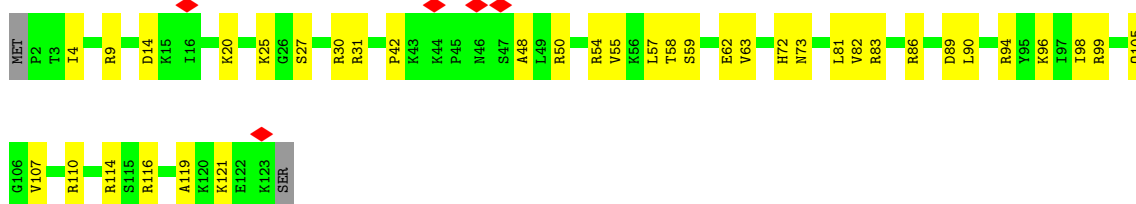


- Molecule 10: 30S ribosomal protein S11

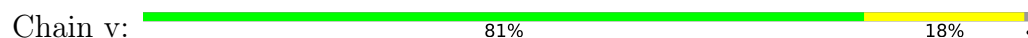




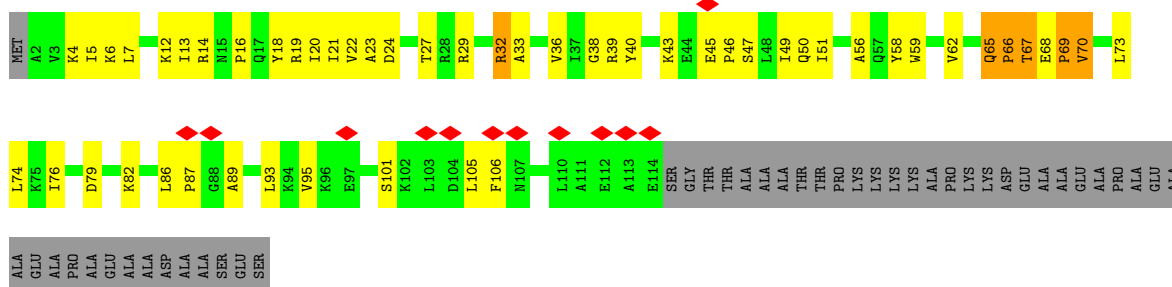
• Molecule 11: 30S ribosomal protein S12



• Molecule 12: 30S Ribosomal Protein S15



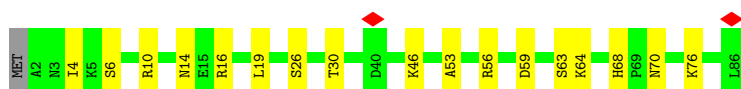
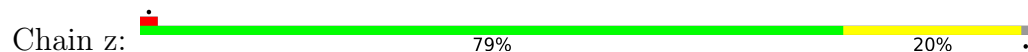
• Molecule 13: 30S ribosomal protein S16



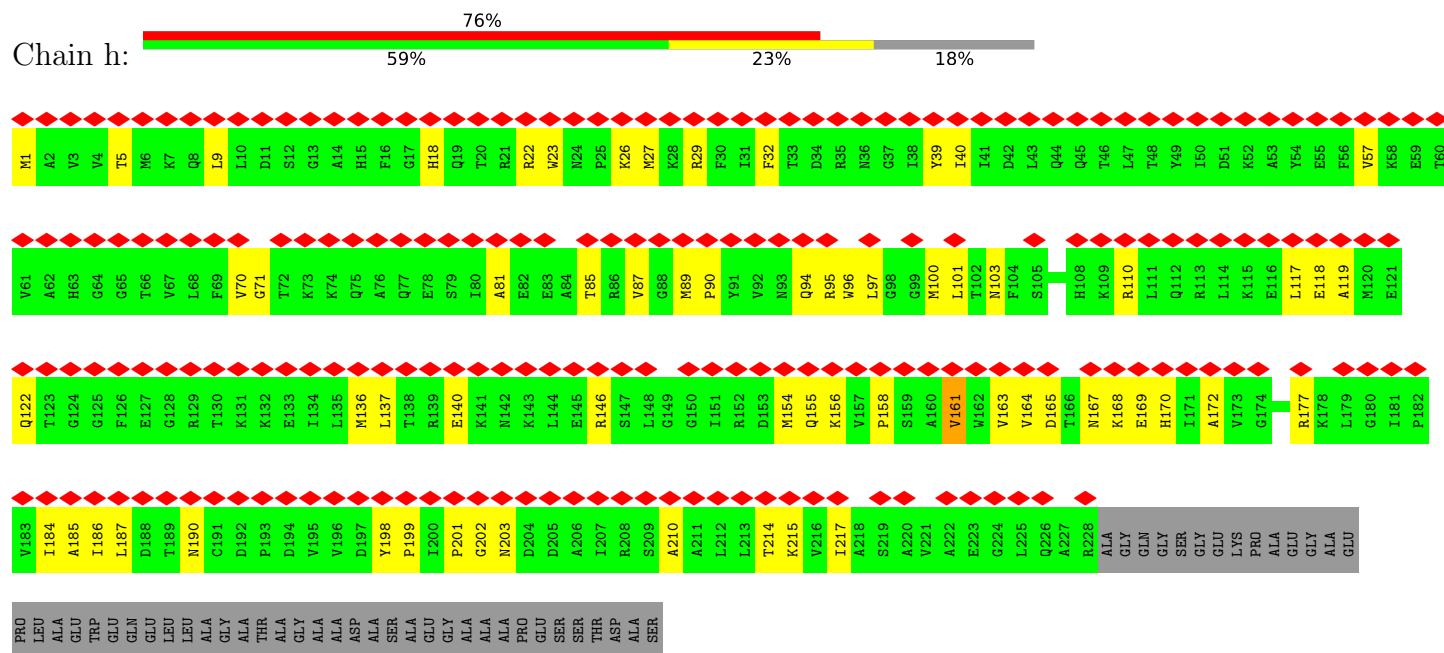
• Molecule 14: 30S ribosomal protein S17



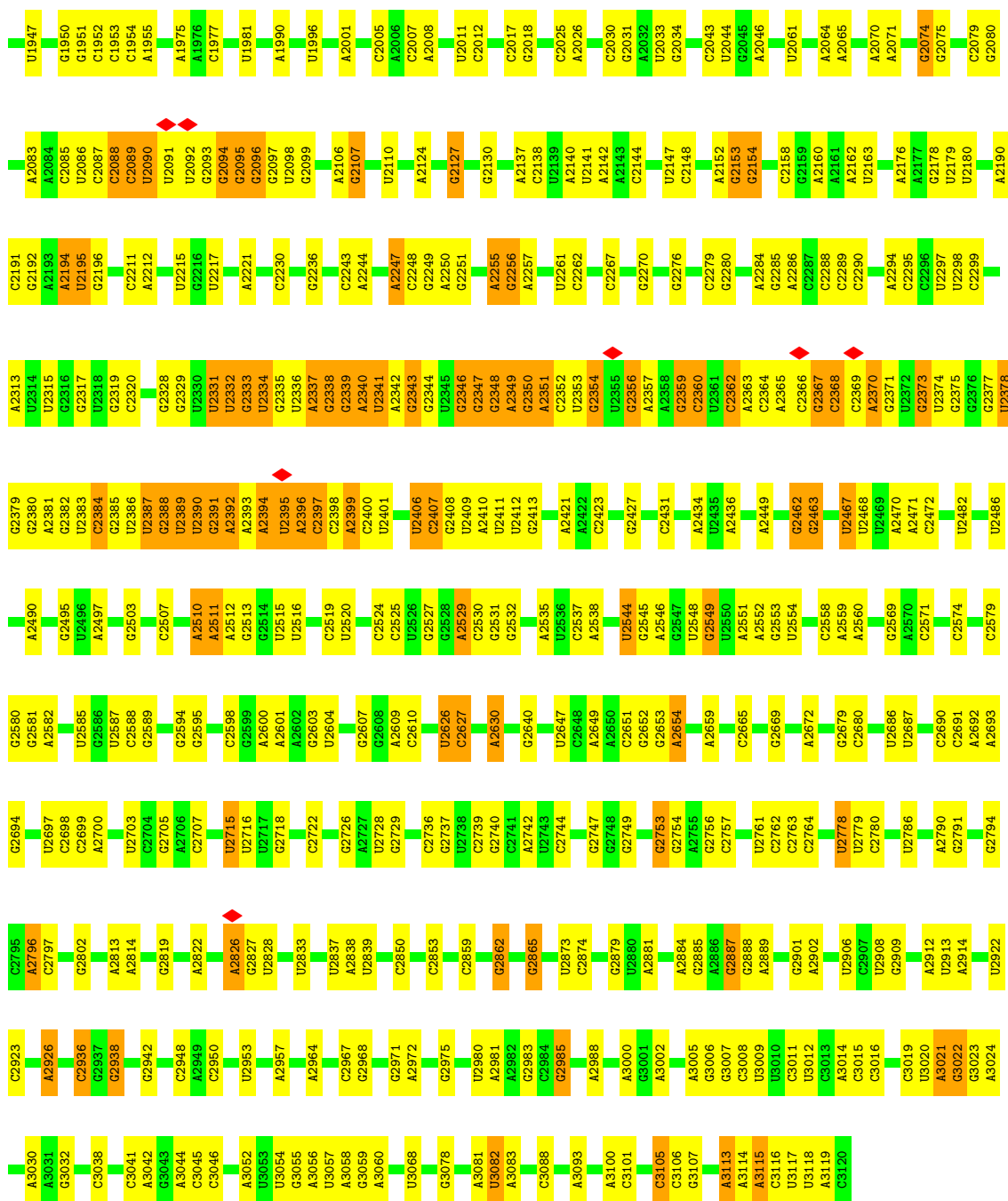
• Molecule 15: 30S ribosomal protein S20



- Molecule 16: 30S Ribosomal Protein S2

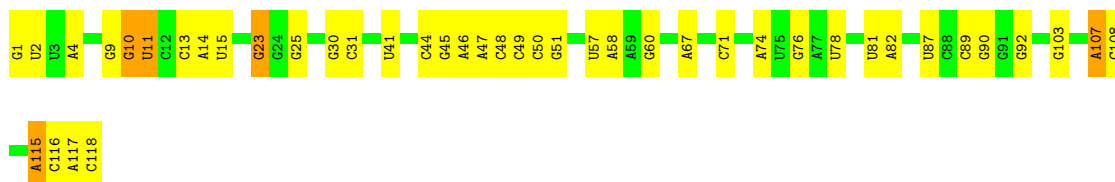


U1798	G1696	U1608	C1548	C1465	G1339	U1223	C1159	G1083	U947	A800	C692	G608	G476
G1803	G1696	G1609	G1549	C1466	G1343	G1224	G1160	G1083	G948	U801	C692	G609	C481
G1804	G1610	C1610	U1467	U1467	G1344	G1225	C1161	C1068	C949	A696	A696	C610	U482
G1805	A1611	U1612	A1468	A1468	G1345	C1227	A1163	G1072	A950	U699	U699	C618	G483
U1809	C1705	U1613	C1472	C1472	U1349	A1228	A1164	U1076	A958	G815	C705	C619	C484
A1810	A1706	G1616	G1473	G1473	G1350	A1229	G1165	A1076	U959	A830	G706	G620	A489
C1811	G1707	C1617	A1474	A1474	G1351	U1231	A1166	A1077	G960	A831	G707	G621	A490
G1815	A1714	C1617	G1475	G1475	G1352	G1232	A1168	G1078	G967	G832	U709	C622	U491
U1716	A1715	C1617	C1477	C1477	G1353	A1233	U1171	C1079	C968	U839	U709	A623	C492
U1717	A1716	C1621	C1478	C1478	U1362	U1234	C1171	U1080	G974	G716	G716	G624	U493
G1818	U1717	G1622	G1479	G1479	G1363	U1235	A1172	C1081	U975	C845	C717	A633	G494
G1819	C1718	U1624	A1480	A1480	U1364	G1236	G1173	C1082	U976	U857	C718	C634	G498
C1825	C1719	G1625	G1486	G1486	G1365	U1237	A1174	U1083	U977	U858	A721	G635	G499
A1826	G1720	A1563	U1487	U1487	G1366	C1239	G1176	C1085	G977	G708	G708	U636	C502
A1834	U1723	A1627	U1487	U1487	G1367	G1240	G1177	C1086	A978	U709	G728	G637	A503
U1727	A1728	A1628	A1493	A1493	A1368	U1245	U1178	G1087	G980	G863	G729	U641	G504
U1728	U1729	U1630	U1494	U1494	A1369	U1246	U1179	U1088	U981	G868	A731	G642	C505
G1849	G1632	A1631	A1499	A1499	U1370	U1250	G1180	A1091	U982	C872	C734	G643	A511
A1850	U1730	G1633	A1500	A1500	G1371	A1251	C1181	G1092	G986	G872	U735	G644	G512
G1851	C1634	C1634	C1501	C1501	A1377	G1252	U1183	A1093	G986	G872	U735	G645	A517
A1852	A1635	A1635	G1502	G1502	G1378	G1253	U1184	G1094	C992	A879	A738	U646	A520
A1853	A1636	U1506	U1506	U1506	G1379	G1254	A1185	A1101	G993	G880	A738	G647	A520
G1854	G1637	G1507	G1507	G1507	A1380	G1255	G1186	G1102	U995	U888	U739	A648	A520
A1855	C1638	A1508	A1508	A1508	G1381	G1256	G1187	G1105	G996	G890	A740	G653	U643
G1856	G1639	U1509	U1509	U1509	U1382	G1257	A1188	C1112	G997	G891	G742	U654	U544
A1737	A1640	A1510	A1510	A1510	G1386	C1258	G1189	G1113	G998	G891	G745	G655	G551
U1641	U1641	U1511	U1511	U1511	A1387	G1259	C1190	G1114	A896	A896	U746	A663	A554
G1642	G1642	C1514	C1514	C1514	U1388	G1260	G1191	G1115	C1001	A898	U748	G665	G555
A1648	A1648	C1515	C1515	C1515	A1389	A1261	G1192	A1118	C1002	G900	A751	A666	G556
C1649	G1649	A1518	A1518	A1518	A1415	G1270	G1193	A1119	C1003	A908	A752	A667	G561
G1650	C1651	G1522	G1522	G1522	A1416	A1274	C1194	G1140	A1005	U911	A753	A670	A567
C1652	A1656	G1528	G1528	G1528	G1425	G1281	C1122	G1137	A1007	C912	A754	G671	A568
G1657	G1657	U1529	U1529	U1529	U1428	C1282	G1129	G1130	G1007	U911	A755	G672	G569
G1664	G1664	G1530	G1530	G1530	A1429	C1283	G1131	G1131	G1008	A917	A756	C673	U570
A1673	A1673	U1531	U1531	U1531	C1430	U1292	A1203	U1137	U1009	G920	A758	U674	A571
G1674	G1674	G1532	G1532	G1532	U1431	G1293	A1204	G1140	U1010	G920	A759	G675	G587
U1675	U1675	C1535	C1535	C1535	C1435	U1294	G1205	G1143	A1011	C927	A760	A588	A588
G1676	G1676	U1536	U1536	U1536	C1436	G1295	G1206	A1144	C1012	U928	G765	A590	A590
G1677	G1677	U1537	U1537	U1537	C1436	U1296	G1207	A1145	U1013	C929	G766	C681	G591
U1678	U1678	G1538	G1538	G1538	C1440	C1298	U1208	G1154	G1014	C932	G768	A682	A592
A1679	A1679	U1539	U1539	U1539	U1444	G1302	G1211	U1151	A1025	G932	G771	G683	G593
A1680	U1681	U1540	U1540	U1540	G1456	U1303	U1212	G1152	C1037	A934	G772	G684	U594
G1684	C1684	A1542	A1542	A1542	C1318	C1318	A1213	U1153	U1044	A935	G773	G685	A595
G1685	A1543	U1543	U1543	U1543	U1459	G1326	A1214	G1154	U1044	U941	G774	A688	C596
U1690	U1544	C1544	C1544	C1544	U1459	G1326	A1215	G1157	A1047	U942	G784	G690	G604
A1691	A1546	A1546	A1546	A1546	G1462	G1335	U1219	U1158	A1048	U942	G784	G690	G605
A1792	G1547	G1547	G1547	G1547	G1462	G1335	A1221	C1222	A1058	U942	G784	G690	G605
U1787	G1786	A1787	A1787	A1787	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605
G1788	G1788	U1593	U1593	U1593	G1456	U1303	U1212	U1151	A1058	U942	G784	G690	G605
A1789	G1789	A1542	A1542	A1542	C1318	C1318	A1213	U1152	A1058	U942	G784	G690	G605
G1933	G1933	U1595	U1595	U1595	U1459	G1326	A1214	G1154	A1058	U942	G784	G690	G605
U1937	U1937	C1596	C1596	C1596	U1459	G1326	A1215	G1154	A1058	U942	G784	G690	G605
G1938	G1938	U1597	U1597	U1597	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605
U1938	G1938	U1598	U1598	U1598	G1462	G1335	A1221	C1222	A1058	U942	G784	G690	G605
U1937	U1937	U1599	U1599	U1599	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605
G1938	G1938	G1600	G1600	G1600	G1462	G1335	A1221	C1222	A1058	U942	G784	G690	G605
U1937	U1937	U1601	U1601	U1601	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605
G1938	G1938	G1603	G1603	G1603	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605
U1937	U1937	G1604	G1604	G1604	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605
G1938	G1938	G1605	G1605	G1605	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605
U1937	U1937	G1606	G1606	G1606	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605
G1938	G1938	C1607	C1607	C1607	G1462	G1335	U1219	U1158	A1058	U942	G784	G690	G605



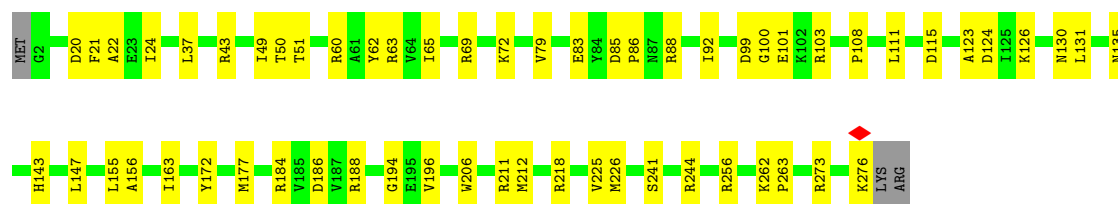
• Molecule 19: 5S ribosomal RNA

Chain B: 64% 32%



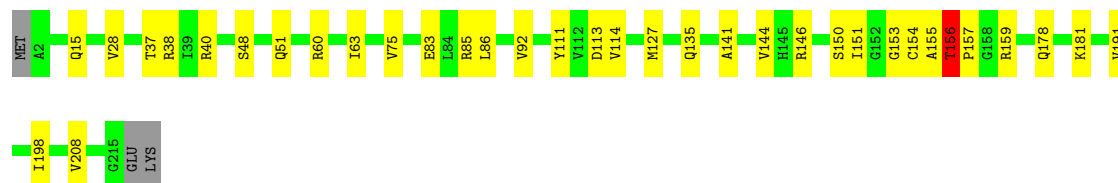
• Molecule 20: 50S ribosomal protein L2

Chain C:  78% 21% .



- Molecule 21: 50S ribosomal protein L3

Chain D:  82% 16% .



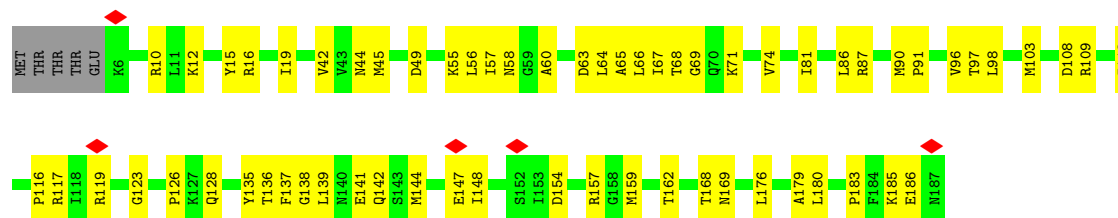
- Molecule 22: 50S Ribosomal Protein L4

Chain E:  85% 13% .



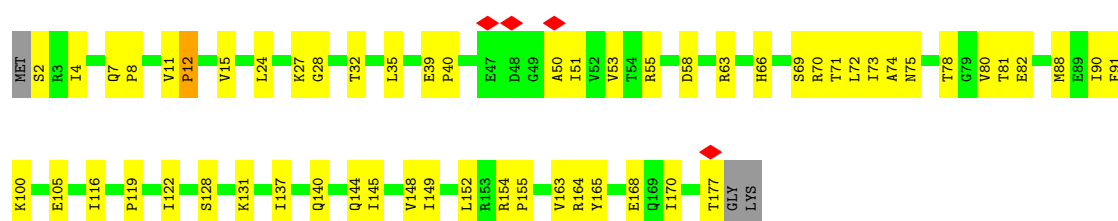
- Molecule 23: 50S Ribosomal Protein L5

Chain F:  64% 34% .

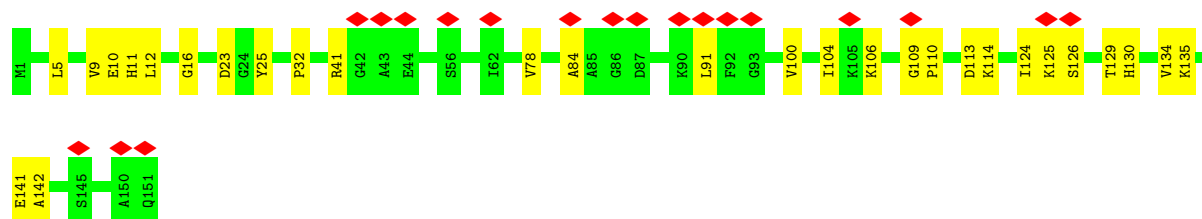
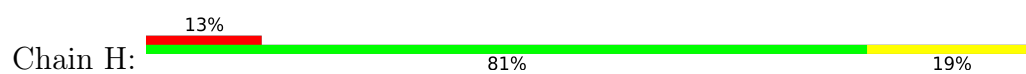


- Molecule 24: 50S ribosomal protein L6

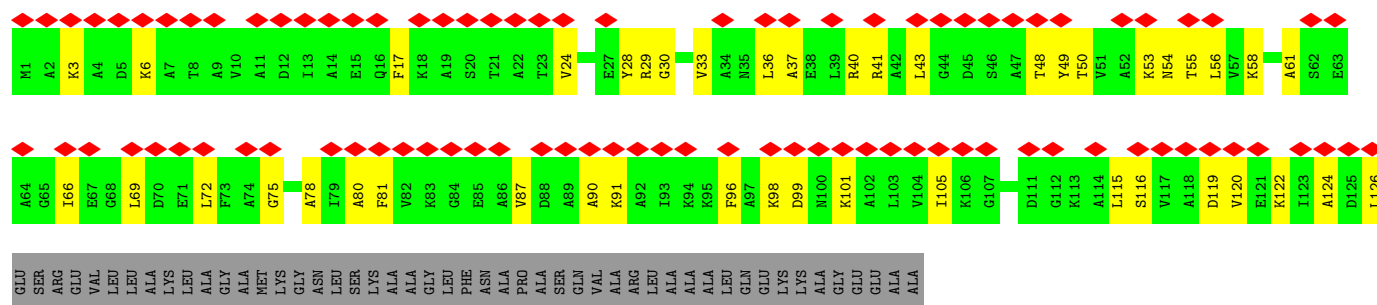
Chain G:  66% 31% .



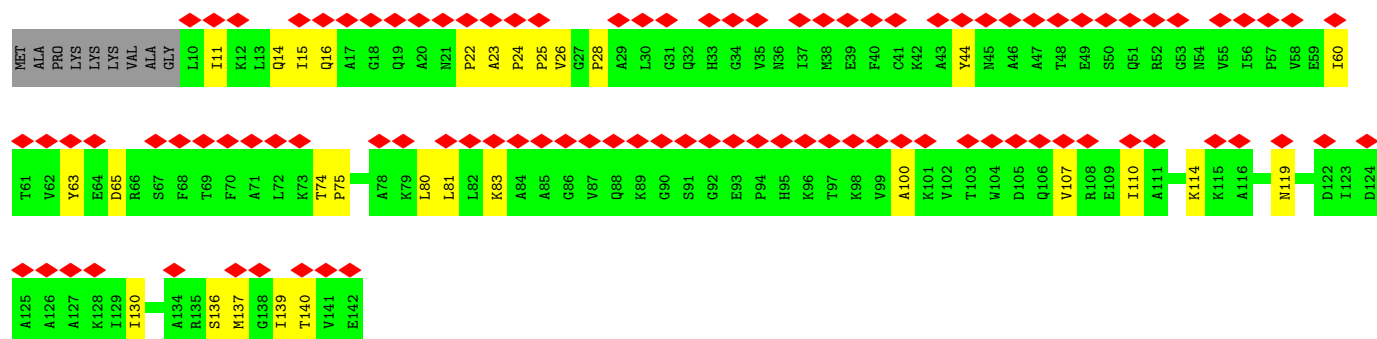
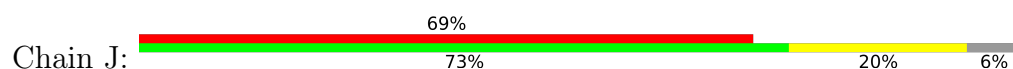
- Molecule 25: 50S ribosomal protein L9



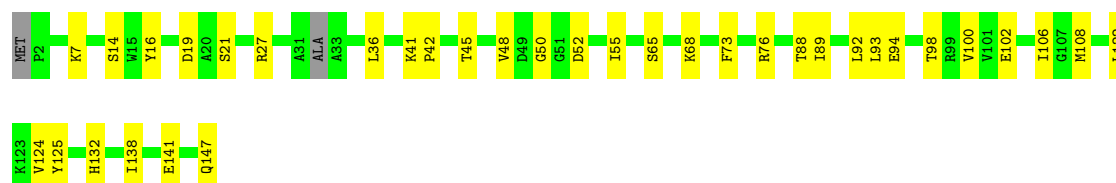
- Molecule 26: 50S ribosomal protein L10



- Molecule 27: 50S ribosomal protein L11

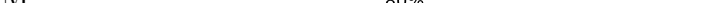


- Molecule 28: 50S Ribosomal Protein L13



- Molecule 29: 50S ribosomal protein L14

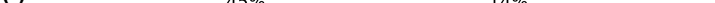
M1
I2
L8
D12
I22
R23
V24
R30
R31
Y32
A33
D37
K59
Y76
I77
K78
F79
N82
P93
R107
M112
X113
I114
V115
V121
L122

- Chain M:  80% 19% .

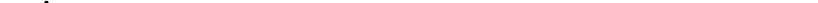
MET
SER
V3
H7
R21
V22
G23
R24
S28
K29
T32
E51
G52
G53
Q64
N65
M59
R60
L61
K65
Q76
V80
N84
G94
V95
D96
E97
L98
V99
V104
S108
L109
V110
L113
L118
N127
S130

- Chain N: 81% 17%

R1
I20
G30
I42
S49 A50
I58
K59 R60
K63
V64
P65
I66
N67
F70 D71
M83
K87
E91
A92
A95
N96
V97
E105
R120
A121
K124
R134
E135
E136
GLN PHE

- Chain O:  45% 14% 41%

ALA	ARG	MET
GLU	ARG	P2
GLU	ARG	K3
GLU	ALA	P4
GLU	ALA	
ALA	SER	G7
LYS	GLN	P8
ASP	ALA	R9
THR	LYS	L10
LYS	ALA	
	ASP	S14
	GLU	
	ARG	T37
	ALA	E38
	ASP	P39
	GLU	K40
	LYS	A41
	ALA	R42
	ASP	
	GLU	R45
	LYS	
	ALA	E49
	GLU	
	THR	K57
	VAL	
	GLU	N62
	GLU	
	GLU	I70
	THR	R71
	THR	D72
	GLU	K73
	ALA	
	PRO	V76
	ALA	
	GLU	Y87
	GLU	A88
	SER	D89
	THR	
	GLU	T95
	ALA	
	ALA	R103
	ALA	
	GLU	D106
	GLU	
	THR	M110
	VAL	
	GLU	L115
	GLU	V116
	THR	R117
	THR	E118
	GLU	K119
	ALA	THR
	PRO	VAL
	ALA	THR
	GLU	ASP
	GLU	GLU
	SER	ALA
	THR	ASN
	GLU	ARG

- Chain P:  75% 24%

Year	Publications
1987	1
1988	2
1989	3
1990	4
1991	5
1992	6
1993	7
1994	8
1995	9
1996	10
1997	11
1998	12
1999	13
2000	14
2001	15
2002	16
2003	17
2004	18
2005	19
2006	20
2007	21
2008	22
2009	23
2010	24
2011	25
2012	26
2013	27
2014	28
2015	29
2016	30
2017	31
2018	32
2019	33
2020	34
2021	35
2022	36
2023	37
2024	38
2025	39
2026	40

- Chain Q: 77% 22%

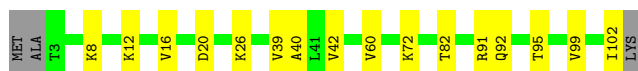
M1	N2	T3	L4	D5	L12	P17	T18	F19	E33	R48	R49	Q50	G51	S55	E56	T57	F58	T59	V60	R61	V69	E70	R71	T72	F73	H76	I83	K95	P113
----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------

- Chain R:  83% 13% .



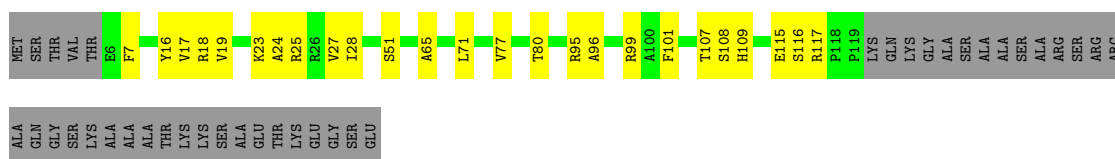
- Molecule 36: 50S Ribosomal Protein L21

Chain S: 82% 16% .



- Molecule 37: 50S Ribosomal Protein L22

Chain T: 58% 16% 25%



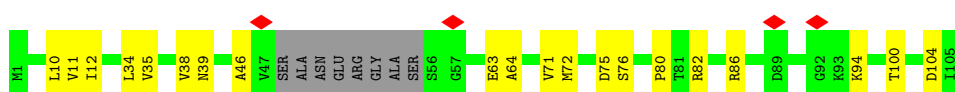
- Molecule 38: 50S Ribosomal Protein L23

Chain U: 83% 14% .



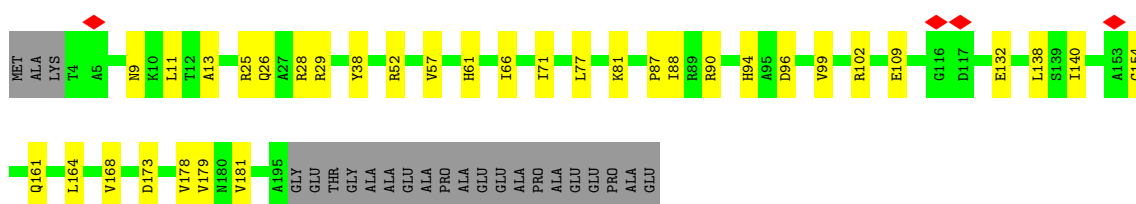
- Molecule 39: 50S ribosomal protein L24

Chain V: 73% 19% 8%



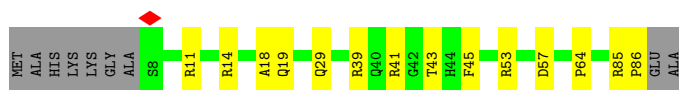
- Molecule 40: 50S ribosomal protein L25

Chain W: 73% 16% 11%



- Molecule 41: 50S ribosomal protein L27

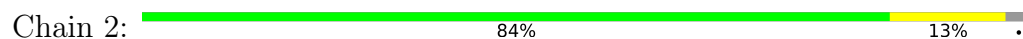
Chain X: 74% 16% 10%



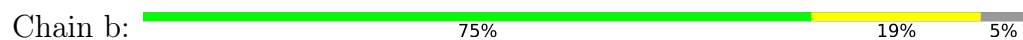
- Molecule 42: 50S ribosomal protein L29



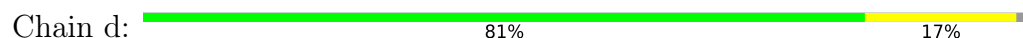
- Molecule 43: 50S ribosomal protein L30



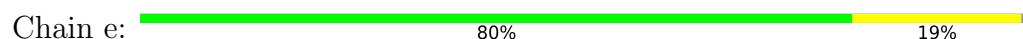
- Molecule 44: 50S ribosomal protein L32



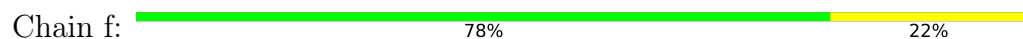
- Molecule 45: 50S ribosomal protein L34



- Molecule 46: 50S ribosomal protein L35



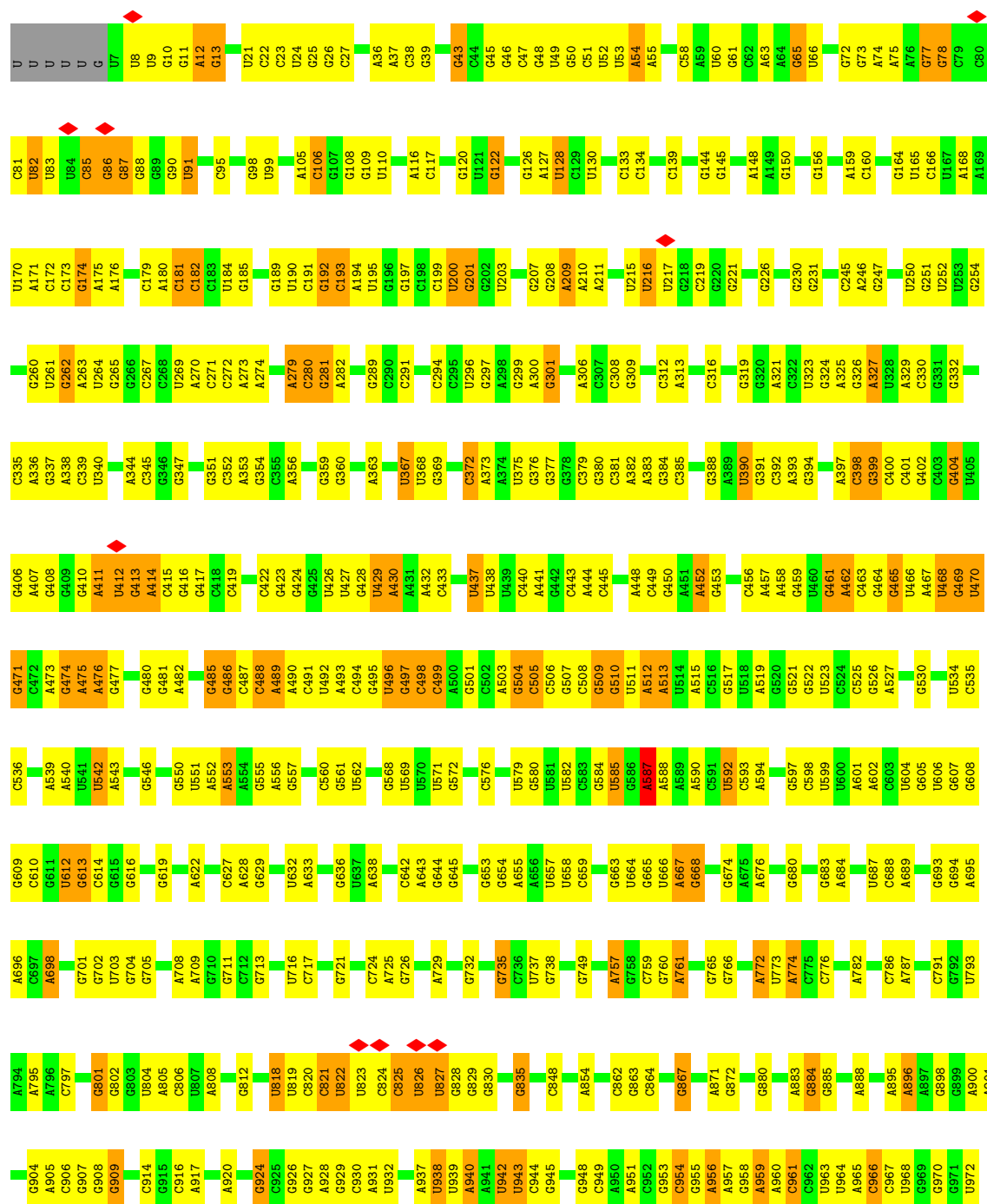
- Molecule 47: 50S ribosomal protein L36

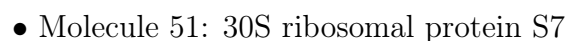


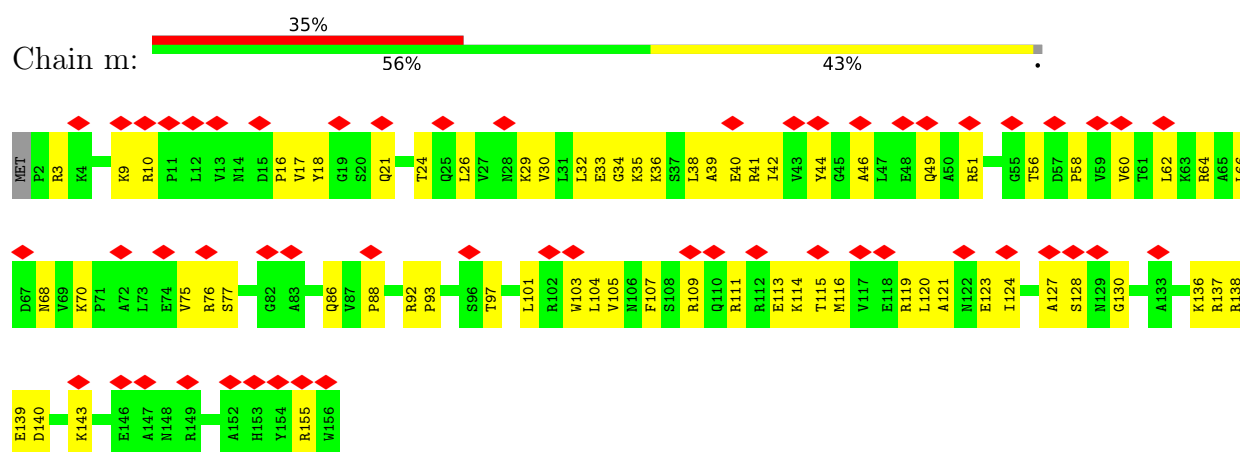
- Molecule 48: E-tRNA



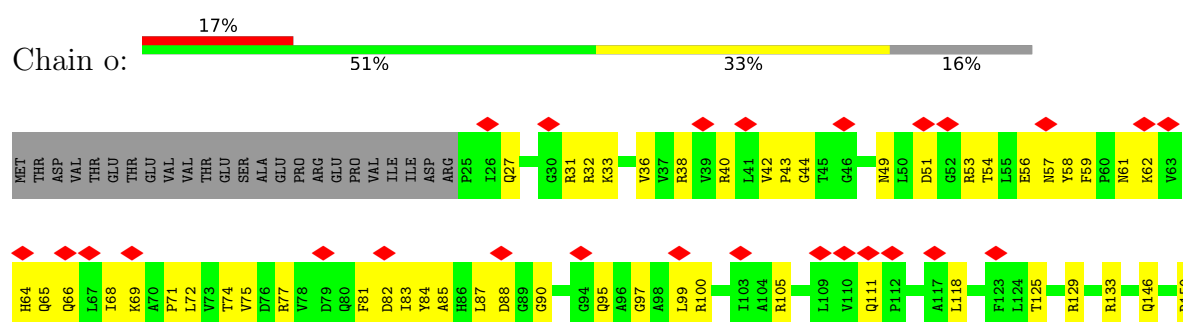
- Molecule 49: 16S ribosomal RNA



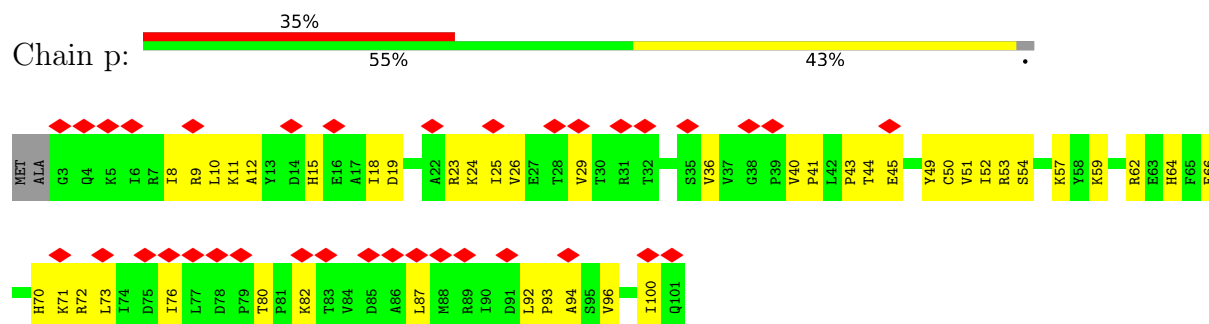




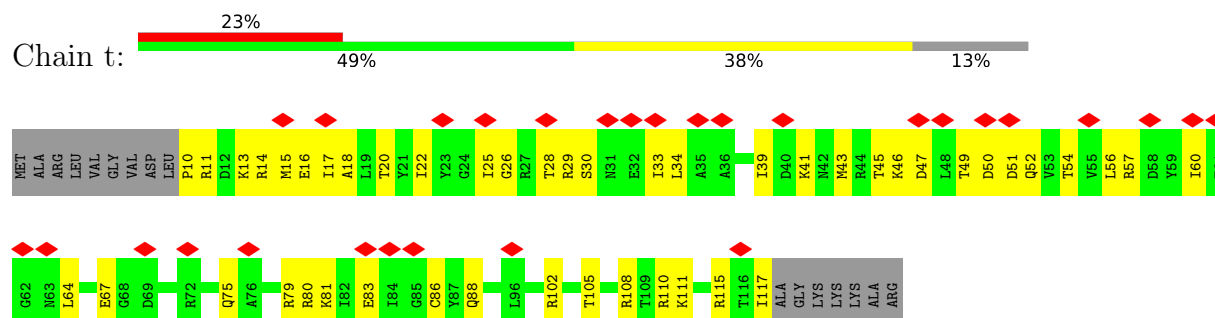
• Molecule 52: 30S ribosomal protein S9



• Molecule 53: 30S ribosomal protein S10



• Molecule 54: 30S ribosomal protein S13



• Molecule 55: 30S ribosomal protein S19





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48443	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 ($e^-/\text{\AA}^2$)	51.22	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.845	Depositor
Minimum map value	-1.224	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.083	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	433.19998, 433.19998, 433.19998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.083, 1.083, 1.083	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	Y	1.25	0/478	1.26	5/641 (0.8%)
2	c	0.99	0/413	1.08	2/553 (0.4%)
3	g	0.63	0/372	1.07	2/503 (0.4%)
4	r	0.96	0/518	1.11	5/693 (0.7%)
5	l	0.19	0/280	0.32	0/359
6	j	0.16	0/1672	0.39	0/2251
7	k	0.20	0/1312	0.39	0/1772
8	l	0.22	0/782	0.33	0/1059
9	n	0.21	0/1025	0.33	0/1385
10	q	0.18	0/873	0.31	0/1180
11	s	0.20	0/969	0.42	0/1294
12	v	0.21	0/729	0.28	0/977
13	w	0.92	3/908 (0.3%)	1.10	4/1226 (0.3%)
14	x	0.17	0/759	0.37	0/1016
15	z	0.15	0/663	0.31	0/882
16	h	0.14	0/1822	0.41	1/2457 (0.0%)
17	3	0.24	0/191	0.31	0/247
18	A	0.28	0/75001	0.32	0/117027
19	B	0.21	0/2821	0.28	0/4396
20	C	0.29	0/2153	0.35	0/2895
21	D	0.36	0/1609	0.48	2/2165 (0.1%)
22	E	0.26	0/1592	0.36	0/2153
23	F	0.43	2/1467 (0.1%)	0.86	5/1973 (0.3%)
24	G	0.27	0/1369	0.53	2/1848 (0.1%)
25	H	0.17	0/1027	0.39	0/1398
26	I	0.12	0/925	0.29	0/1246
27	J	0.15	0/1006	0.44	0/1364
28	K	0.29	0/1151	0.35	0/1557
29	L	0.29	0/946	0.35	0/1268
30	M	0.27	0/1091	0.43	0/1457
31	N	0.23	0/1118	0.33	0/1506
32	O	0.29	0/945	0.37	0/1267
33	P	0.20	0/966	0.30	0/1298
34	Q	0.63	2/921 (0.2%)	0.50	0/1236

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	R	0.31	0/1000	0.31	0/1341
36	S	0.27	0/764	0.32	0/1030
37	T	0.30	0/887	0.34	0/1204
38	U	0.26	0/766	0.33	0/1030
39	V	0.21	0/738	0.36	0/987
40	W	0.18	0/1443	0.30	0/1970
41	X	0.27	0/595	0.32	0/798
42	Z	0.23	0/534	0.30	0/713
43	2	0.28	0/477	0.27	0/640
44	b	0.29	0/427	0.33	0/572
45	d	0.31	0/380	0.40	0/500
46	e	0.28	0/507	0.33	0/672
47	f	0.24	0/303	0.29	0/401
48	5	0.16	0/1835	0.33	0/2859
49	a	0.33	6/36309 (0.0%)	0.32	2/56657 (0.0%)
50	i	0.16	0/1684	0.43	0/2261
51	m	0.16	0/1252	0.43	0/1690
52	o	0.16	0/1012	0.42	0/1362
53	p	0.17	0/802	0.43	0/1086
54	t	0.16	0/884	0.47	0/1180
55	y	0.16	0/680	0.43	0/915
56	4	0.14	0/2085	0.35	0/2829
57	u	0.67	0/488	1.07	5/650 (0.8%)
All	All	0.31	13/165726 (0.0%)	0.37	35/247896 (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
34	Q	0	1
50	i	0	3
All	All	0	4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	a	587	A	N3-C4	23.33	1.81	1.34
49	a	587	A	C6-N1	22.68	1.80	1.35
49	a	587	A	N1-C2	22.54	1.79	1.34
49	a	587	A	C2-N3	21.88	1.77	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	w	32	ARG	CD-NE	19.57	1.73	1.46
49	a	587	A	C5-C6	16.67	1.74	1.41
13	w	32	ARG	NE-CZ	16.13	1.50	1.33
49	a	587	A	C5-C4	15.41	1.69	1.38
23	F	116	PRO	CB-CG	-11.66	0.91	1.49
23	F	116	PRO	CG-CD	-8.05	1.23	1.50
34	Q	5	ASP	CA-C	-7.59	1.43	1.52
34	Q	5	ASP	C-O	-5.89	1.15	1.23
13	w	65	GLN	CA-C	-5.12	1.46	1.52

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	w	32	ARG	CD-NE-CZ	19.90	152.26	124.40
23	F	116	PRO	CA-CB-CG	-19.30	67.83	104.50
23	F	116	PRO	N-CD-CG	-18.93	74.80	103.20
23	F	116	PRO	CB-CG-CD	17.47	162.00	106.10
13	w	65	GLN	CA-C-N	16.80	136.82	119.85
13	w	65	GLN	C-N-CA	16.80	136.82	119.85
24	G	12	PRO	CA-N-CD	-12.67	94.26	112.00
23	F	116	PRO	CA-N-CD	-8.90	99.53	112.00
4	r	25	LYS	N-CA-C	-8.77	100.72	111.33
49	a	587	A	N1-C2-N3	-8.15	104.86	129.30
13	w	66	PRO	N-CA-C	8.10	124.26	111.38
21	D	156	THR	CA-C-N	-7.77	110.46	119.32
21	D	156	THR	C-N-CA	-7.77	110.46	119.32
3	g	2	LYS	N-CA-C	-7.20	104.59	113.15
4	r	61	GLN	N-CA-C	-7.01	103.72	111.36
24	G	12	PRO	N-CD-CG	-6.72	93.11	103.20
1	Y	21	SER	N-CA-C	-6.65	105.05	112.57
57	u	15	LYS	N-CA-C	-6.55	105.16	113.02
57	u	7	VAL	N-CA-C	-6.51	103.53	110.36
57	u	10	ALA	N-CA-C	-6.32	105.14	112.92
2	c	45	CYS	N-CA-C	-6.08	105.52	113.12
1	Y	11	GLY	CA-C-N	-6.05	113.52	119.76
1	Y	11	GLY	C-N-CA	-6.05	113.52	119.76
57	u	22	THR	N-CA-C	5.92	118.81	109.39
49	a	587	A	C2-N3-C4	5.88	128.25	110.60
57	u	17	ALA	N-CA-C	5.68	119.31	112.38
1	Y	40	THR	N-CA-C	-5.47	103.67	110.41
16	h	161	VAL	N-CA-C	-5.47	108.51	113.71
4	r	74	VAL	N-CA-C	-5.45	107.06	111.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	r	44	GLU	N-CA-C	-5.28	106.84	113.28
2	c	22	ASN	N-CA-C	5.22	119.78	113.41
1	Y	38	ALA	N-CA-C	5.20	117.20	107.99
3	g	40	GLN	N-CA-C	-5.18	106.91	113.18
4	r	51	ARG	N-CA-C	-5.12	107.42	113.97
23	F	116	PRO	N-CA-CB	-5.09	98.36	103.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	Q	4	LEU	Mainchain
50	i	158	GLY	Peptide
50	i	160	ALA	Peptide
50	i	75	VAL	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	Y	470	0	484	36	0
2	c	405	0	411	17	0
3	g	364	0	352	47	0
4	r	513	0	540	38	0
5	l	280	0	342	11	0
6	j	1641	0	1668	52	0
7	k	1296	0	1360	30	0
8	l	771	0	797	20	0
9	n	1010	0	1046	24	0
10	q	855	0	863	10	0
11	s	958	0	1045	30	0
12	v	720	0	760	10	0
13	w	891	0	935	76	0
14	x	748	0	795	24	0
15	z	660	0	712	12	0
16	h	1793	0	1839	48	0
17	3	189	0	205	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	A	66981	0	33700	733	0
19	B	2522	0	1285	27	0
20	C	2110	0	2165	46	0
21	D	1587	0	1630	29	0
22	E	1569	0	1607	21	0
23	F	1445	0	1476	48	0
24	G	1348	0	1399	39	0
25	H	1018	0	988	20	0
26	I	918	0	959	37	0
27	J	990	0	1021	22	0
28	K	1125	0	1161	23	0
29	L	938	0	1000	14	0
30	M	1078	0	1151	22	0
31	N	1092	0	1128	16	0
32	O	928	0	972	20	0
33	P	956	0	991	20	0
34	Q	907	0	938	19	0
35	R	988	0	1038	14	0
36	S	754	0	802	11	0
37	T	873	0	909	14	0
38	U	756	0	802	10	0
39	V	732	0	782	15	0
40	W	1428	0	1443	26	0
41	X	586	0	601	12	0
42	Z	531	0	541	9	0
43	2	474	0	500	7	0
44	b	423	0	463	8	0
45	d	377	0	411	5	0
46	e	502	0	541	9	0
47	f	299	0	324	6	0
48	5	1643	0	836	29	0
49	a	32439	0	16321	663	0
50	i	1660	0	1707	54	0
51	m	1232	0	1282	60	0
52	o	994	0	1050	47	0
53	p	788	0	819	41	0
54	t	877	0	922	44	0
55	y	662	0	677	28	0
56	4	2058	0	2093	59	0
57	u	477	0	503	50	0
All	All	152629	0	103092	2485	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 10.

All (2485) 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)
13:w:32:ARG:NE	49:a:587:A:C2	1.73	1.53
49:a:587:A:C2	49:a:587:A:N3	1.77	1.53
13:w:32:ARG:NE	49:a:587:A:C6	1.78	1.51
49:a:587:A:C2	49:a:587:A:N1	1.79	1.50
13:w:32:ARG:NE	13:w:32:ARG:CD	1.73	1.48
49:a:587:A:C6	49:a:587:A:N1	1.80	1.46
49:a:587:A:N3	49:a:587:A:C4	1.81	1.46
13:w:32:ARG:NE	49:a:587:A:N3	1.72	1.35
13:w:68:GLU:CD	13:w:69:PRO:HD3	1.51	1.33
13:w:32:ARG:NE	49:a:587:A:C4	2.00	1.29
13:w:32:ARG:NE	49:a:587:A:C5	2.05	1.24
13:w:32:ARG:CZ	49:a:587:A:C4	2.24	1.20
34:Q:1:MET:C	34:Q:2:ASN:OD1	1.83	1.20
13:w:32:ARG:CZ	49:a:587:A:N3	2.05	1.18
13:w:32:ARG:CZ	49:a:587:A:C2	2.30	1.14
13:w:32:ARG:CD	49:a:587:A:C4	2.32	1.12
13:w:32:ARG:HD2	49:a:587:A:C4	1.85	1.11
3:g:16:CYS:HA	3:g:35:VAL:HG13	1.09	1.09
13:w:32:ARG:NH1	49:a:587:A:N3	2.02	1.08
49:a:1137:G:H21	49:a:1160:A:N6	1.51	1.07
13:w:32:ARG:CD	49:a:587:A:N3	2.19	1.06
13:w:68:GLU:CD	13:w:69:PRO:CD	2.33	1.02
4:r:24:SER:HA	49:a:826:U:P	1.99	1.01
57:u:8:HIS:HA	57:u:11:ASN:HB2	1.39	1.01
13:w:32:ARG:CZ	49:a:587:A:C5	2.44	1.01
49:a:1137:G:N2	49:a:1160:A:H61	1.60	0.99
13:w:32:ARG:CZ	49:a:587:A:C6	2.45	0.98
23:F:87:ARG:HG2	23:F:90:MET:HE3	1.47	0.97
2:c:35:ARG:HE	2:c:52:LYS:HE2	1.30	0.96
24:G:39:GLU:HG2	24:G:40:PRO:HD3	1.46	0.96
49:a:1244:G:H1	49:a:1253:U:H3	1.09	0.96
49:a:72:G:N2	49:a:148:A:N1	2.13	0.96
13:w:32:ARG:CD	49:a:587:A:C2	2.50	0.95
49:a:185:G:H1	49:a:203:U:H3	1.12	0.95
3:g:1:MET:HG2	19:B:44:C:H5"	1.49	0.94
13:w:68:GLU:CG	13:w:69:PRO:HD3	1.96	0.94
49:a:592:U:H3	49:a:608:G:H1	1.15	0.94
49:a:1010:C:N4	49:a:1014:U:H3	1.66	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:1010:C:H42	49:a:1014:U:H3	0.95	0.93
13:w:32:ARG:NH1	49:a:587:A:C4	2.36	0.92
49:a:1137:G:H21	49:a:1160:A:H61	0.93	0.92
18:A:1171:C:N3	18:A:1224:G:N1	2.24	0.84
13:w:32:ARG:CD	49:a:587:A:C5	2.60	0.83
49:a:1338:G:H2'	49:a:1339:A:H8	1.44	0.83
13:w:68:GLU:OE1	13:w:69:PRO:CD	2.27	0.82
13:w:69:PRO:HG3	49:a:375:U:OP1	1.80	0.82
53:p:11:LYS:HZ3	53:p:71:LYS:HD3	1.44	0.82
49:a:82:U:H3	49:a:87:G:H1	1.26	0.82
4:r:24:SER:HA	49:a:826:U:OP1	1.79	0.81
16:h:89:MET:HE3	16:h:90:PRO:HD2	1.61	0.81
18:A:332:C:O2	18:A:349:G:N2	2.13	0.81
49:a:489:A:H8	49:a:523:U:HO2'	1.26	0.81
49:a:1333:U:H3	49:a:1354:G:H1	1.28	0.81
51:m:101:LEU:HA	51:m:104:LEU:HB2	1.62	0.81
52:o:42:VAL:HG13	52:o:82:ASP:HB3	1.62	0.81
49:a:1204:C:H5'	49:a:1205:U:H5''	1.64	0.80
18:A:1203:A:H61	26:l:36:LEU:HD23	1.46	0.80
34:Q:1:MET:O	34:Q:2:ASN:OD1	1.98	0.80
13:w:5:ILE:O	13:w:67:THR:HG22	1.81	0.80
49:a:1112:C:N3	49:a:1123:G:N1	2.29	0.79
49:a:1219:A:C8	49:a:1283:U:N3	2.50	0.79
57:u:6:LEU:HA	57:u:9:LYS:HG3	1.64	0.79
5:l:2:GLY:N	49:a:551:U:HO2'	1.80	0.79
18:A:2747:G:HO2'	18:A:2988:A:HO2'	1.30	0.79
13:w:19:ARG:HA	13:w:39:ARG:HA	1.64	0.79
18:A:2359:G:H1	18:A:2378:U:H3	1.29	0.79
3:g:16:CYS:HA	3:g:35:VAL:CG1	2.04	0.78
18:A:1171:C:O2	18:A:1224:G:N2	2.14	0.78
13:w:68:GLU:OE1	13:w:68:GLU:N	2.16	0.77
18:A:1825:C:N4	18:A:1840:G:OP2	2.18	0.77
49:a:959:A:HO2'	49:a:963:U:H3	1.32	0.77
18:A:2085:C:O2	18:A:2097:G:N2	2.17	0.77
49:a:1038:G:N2	49:a:1183:U:O4	2.17	0.77
49:a:1219:A:N7	49:a:1283:U:O2	2.18	0.77
9:n:9:ASP:HA	9:n:12:THR:HG22	1.66	0.76
13:w:32:ARG:CD	49:a:587:A:N1	2.48	0.76
13:w:32:ARG:CD	49:a:587:A:C6	2.69	0.76
18:A:2367:G:O2'	18:A:2370:A:N6	2.18	0.76
49:a:1329:G:H5''	52:o:129:ARG:HG2	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:J:80:LEU:HD23	27:J:110:ILE:HG23	1.68	0.76
24:G:119:PRO:HG2	24:G:122:ILE:HD12	1.66	0.75
56:4:441:ALA:HB3	56:4:452:LYS:HD3	1.67	0.75
53:p:53:ARG:HH11	57:u:45:ARG:HH11	1.34	0.75
18:A:1573:U:O2	18:A:1597:G:O6	2.04	0.75
4:r:54:THR:HG22	4:r:56:ASN:H	1.52	0.75
1:Y:25:THR:HG22	1:Y:26:SER:H	1.49	0.75
18:A:332:C:N3	18:A:349:G:N1	2.34	0.74
57:u:3:LYS:HG3	57:u:6:LEU:HD12	1.68	0.74
49:a:592:U:O4	49:a:608:G:O6	2.04	0.74
9:n:85:LEU:HD12	11:s:4:ILE:HG13	1.68	0.74
49:a:1112:C:O2	49:a:1123:G:N2	2.20	0.74
49:a:1027:G:H5'	57:u:4:LYS:HG3	1.70	0.74
40:W:87:PRO:HA	40:W:90:ARG:HH21	1.53	0.74
49:a:461:G:O2'	49:a:463:C:N4	2.21	0.74
3:g:1:MET:CG	19:B:44:C:H5''	2.17	0.74
13:w:20:ILE:HD11	13:w:73:LEU:HD23	1.70	0.74
1:Y:3:ALA:HA	1:Y:31:PRO:HD2	1.70	0.73
18:A:499:G:OP2	18:A:2630:A:O2'	2.05	0.73
18:A:3008:C:O2'	21:D:38:ARG:NH2	2.21	0.73
20:C:124:ASP:OD2	20:C:126:LYS:NZ	2.21	0.73
49:a:474:G:H2'	49:a:476:A:H8	1.53	0.73
49:a:1208:A:OP2	54:t:111:LYS:NZ	2.20	0.73
49:a:144:G:H1	49:a:172:C:H42	1.34	0.73
1:Y:18:VAL:HG22	1:Y:24:ARG:HG2	1.70	0.73
18:A:1566:A:O2'	18:A:1605:G:N2	2.22	0.73
49:a:1131:G:H21	53:p:41:PRO:HD2	1.54	0.73
18:A:2520:U:OP2	33:P:20:ARG:NH2	2.21	0.72
20:C:273:ARG:HE	20:C:276:LYS:HG2	1.53	0.72
13:w:32:ARG:HD3	49:a:587:A:C2	2.24	0.72
18:A:2703:U:O2	56:4:236:GLN:NE2	2.22	0.72
15:z:59:ASP:OD2	15:z:76:LYS:NZ	2.23	0.72
43:2:26:LEU:O	43:2:37:ARG:NH2	2.22	0.72
55:y:46:GLY:H	55:y:62:VAL:HG23	1.52	0.72
23:F:45:MET:HE3	23:F:64:LEU:HG	1.72	0.72
1:Y:39:VAL:HG22	1:Y:46:LYS:HG2	1.71	0.72
18:A:2463:G:OP1	20:C:244:ARG:NH2	2.22	0.72
18:A:1632:G:N2	18:A:1633:U:O4	2.23	0.72
18:A:2085:C:N3	18:A:2097:G:N1	2.36	0.72
56:4:371:ILE:HD12	56:4:391:PHE:HB2	1.71	0.72
57:u:53:LEU:HB2	57:u:56:VAL:HG11	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:324:C:O2	18:A:452:G:N2	2.17	0.71
18:A:1554:U:H2'	18:A:1555:A:C8	2.24	0.71
11:s:30:ARG:HB3	11:s:57:LEU:HD21	1.71	0.71
18:A:960:G:N2	18:A:960:G:OP2	2.22	0.71
56:4:253:TYR:O	56:4:258:LYS:NZ	2.23	0.71
4:r:22:PHE:HE1	4:r:37:LEU:HD21	1.54	0.71
9:n:5:ASP:OD2	9:n:79:ARG:NH1	2.23	0.71
18:A:2362:C:H2'	18:A:2363:A:H8	1.52	0.71
18:A:284:G:O6	18:A:302:U:C4	2.43	0.71
18:A:3020:U:H4'	18:A:3022:G:H1	1.56	0.71
42:Z:62:ARG:NH1	42:Z:65:GLU:OE2	2.24	0.71
49:a:1056:C:N4	49:a:1060:A:OP2	2.22	0.71
7:k:151:LYS:NZ	49:a:13:G:OP2	2.21	0.71
18:A:3014:A:H62	18:A:3113:A:H2	1.36	0.71
48:5:4:G:O2'	48:5:5:G:O5'	2.07	0.71
20:C:72:LYS:NZ	20:C:99:ASP:OD1	2.23	0.71
54:t:10:PRO:HG2	54:t:18:ALA:HA	1.73	0.71
57:u:8:HIS:CA	57:u:11:ASN:HB2	2.18	0.71
18:A:2338:G:O2'	18:A:2388:G:N2	2.24	0.71
18:A:1627:U:H2'	18:A:1628:A:H2'	1.73	0.70
18:A:2236:G:N7	37:T:23:LYS:NZ	2.37	0.70
18:A:3012:U:O2'	18:A:3030:A:N3	2.24	0.70
34:Q:2:ASN:OD1	34:Q:2:ASN:N	2.21	0.70
57:u:8:HIS:HA	57:u:11:ASN:CB	2.21	0.70
18:A:759:G:H1	41:X:64:PRO:HB3	1.57	0.70
18:A:2350:G:N2	18:A:2383:U:O4	2.25	0.70
3:g:16:CYS:CA	3:g:35:VAL:HG13	2.05	0.70
53:p:50:CYS:SG	53:p:62:ARG:HD3	2.32	0.70
16:h:71:GLY:HA2	16:h:164:VAL:HG11	1.73	0.70
3:g:1:MET:SD	3:g:1:MET:N	2.65	0.69
3:g:17:GLY:H	3:g:35:VAL:HG22	1.56	0.69
13:w:68:GLU:OE1	13:w:69:PRO:HD2	1.91	0.69
51:m:92:ARG:HD3	51:m:93:PRO:HD2	1.74	0.69
48:5:51:U:H3	48:5:65:G:H1	1.39	0.69
49:a:967:C:O2	55:y:55:ARG:NH2	2.25	0.69
18:A:2802:G:H21	21:D:135:GLN:HE21	1.39	0.69
4:r:25:LYS:CG	49:a:825:C:H5'	2.23	0.69
7:k:157:ASN:ND2	49:a:23:C:OP2	2.25	0.69
26:I:33:VAL:HA	26:I:36:LEU:HB2	1.75	0.69
41:X:53:ARG:NH1	41:X:57:ASP:OD1	2.25	0.69
49:a:975:G:O2'	49:a:976:A:N7	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:l:12:PRO:O	8:l:45:ARG:NH1	2.26	0.69
18:A:679:G:OP2	30:M:24:ARG:NH2	2.26	0.69
33:P:48:HIS:ND1	33:P:64:SER:OG	2.24	0.69
18:A:1365:G:OP2	30:M:24:ARG:NH1	2.26	0.68
18:A:451:U:H2'	18:A:452:G:C8	2.29	0.68
21:D:156:THR:O	21:D:157:PRO:C	2.34	0.68
49:a:145:G:H1	49:a:171:A:H61	1.38	0.68
25:H:78:VAL:HG11	25:H:104:ILE:HD13	1.75	0.68
49:a:1040:U:OP1	53:p:53:ARG:NH2	2.27	0.68
6:j:104:ARG:NH2	49:a:408:G:O3'	2.26	0.68
15:z:16:ARG:NH1	15:z:16:ARG:O	2.25	0.68
18:A:2527:G:H21	23:F:136:THR:HG21	1.59	0.68
49:a:694:G:H2'	49:a:695:A:C8	2.29	0.68
49:a:1329:G:N2	49:a:1357:A:OP2	2.26	0.68
3:g:42:HIS:CE1	3:g:44:PHE:HB3	2.29	0.68
6:j:87:ARG:HD2	6:j:180:LEU:HB3	1.76	0.68
18:A:490:A:N6	18:A:511:A:N1	2.39	0.68
47:f:1:MET:HE3	47:f:35:ARG:HB3	1.74	0.68
49:a:1159:G:N2	49:a:1162:G:OP2	2.25	0.68
18:A:699:U:OP2	22:E:105:LYS:NZ	2.27	0.68
49:a:1035:A:H2'	50:i:156:ARG:HH22	1.59	0.68
13:w:32:ARG:NH2	49:a:587:A:C6	2.61	0.68
18:A:1561:C:OP2	18:A:1562:C:N4	2.27	0.68
20:C:37:LEU:HD13	20:C:62:TYR:HB2	1.74	0.68
8:l:10:LEU:HB2	8:l:59:ILE:HB	1.76	0.68
18:A:1223:U:H2'	18:A:1224:G:C8	2.29	0.68
18:A:2255:A:N3	18:A:2679:G:O2'	2.22	0.68
31:N:42:ILE:HD12	31:N:97:VAL:HG21	1.76	0.67
9:n:10:PHE:HB2	9:n:33:LYS:HE3	1.76	0.67
52:o:43:PRO:HA	52:o:81:PHE:HA	1.75	0.67
18:A:587:G:N1	18:A:590:A:OP2	2.28	0.67
18:A:994:A:N6	18:A:1014:G:O2'	2.27	0.67
18:A:1256:G:N2	28:K:108:MET:SD	2.64	0.67
18:A:1568:C:H1'	18:A:1604:G:H1	1.59	0.67
18:A:2407:C:H2'	18:A:2408:G:C8	2.30	0.67
49:a:1066:U:H3	49:a:1079:G:H22	1.41	0.67
54:t:49:THR:OG1	54:t:51:ASP:OD1	2.12	0.67
49:a:82:U:O2	49:a:87:G:N2	2.25	0.67
18:A:571:A:H4'	39:V:46:ALA:HB2	1.76	0.67
6:j:107:ARG:NH1	49:a:407:A:OP1	2.27	0.67
18:A:1720:G:N2	20:C:99:ASP:O	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:n:16:ASN:ND2	49:a:806:C:O2	2.28	0.67
4:r:23:CYS:SG	4:r:60:HIS:ND1	2.67	0.67
18:A:2971:G:H5'	24:G:71:THR:HG21	1.76	0.67
49:a:1167:G:H1	52:o:133:ARG:H	1.43	0.67
49:a:1231:A:H4'	52:o:90:GLY:H	1.60	0.67
18:A:2865:G:OP2	28:K:76:ARG:NH1	2.28	0.67
20:C:101:GLU:OE2	20:C:103:ARG:NE	2.28	0.67
18:A:470:G:N2	18:A:481:C:N3	2.43	0.66
18:A:2885:G:C5	56:4:462:THR:HG23	2.31	0.66
50:i:72:PRO:HA	50:i:75:VAL:HB	1.77	0.66
18:A:2697:U:H1'	56:4:286:ARG:HD3	1.76	0.66
54:t:75:GLN:O	54:t:79:ARG:N	2.21	0.66
57:u:53:LEU:HB2	57:u:56:VAL:CG1	2.26	0.66
49:a:1272:G:C2	49:a:1273:C:H1'	2.31	0.66
2:c:37:GLU:HG2	2:c:52:LYS:HG3	1.78	0.66
49:a:1269:A:N3	49:a:1335:G:O2'	2.28	0.66
6:j:10:ARG:NH2	49:a:523:U:OP2	2.29	0.66
18:A:705:C:H2'	18:A:706:G:H5''	1.78	0.66
46:e:16:ARG:NH2	46:e:59:ASN:OD1	2.29	0.66
3:g:28:LYS:HD2	3:g:33:ILE:HG12	1.76	0.66
16:h:163:VAL:HB	16:h:185:ALA:HB2	1.78	0.66
39:V:75:ASP:OD2	39:V:100:THR:OG1	2.13	0.66
49:a:380:G:N2	49:a:383:A:OP2	2.26	0.66
49:a:1220:A:OP2	51:m:109:ARG:NH1	2.29	0.66
49:a:1282:G:H4'	49:a:1283:U:H5''	1.76	0.66
18:A:288:U:H4'	18:A:289:A:H5'	1.77	0.66
49:a:1127:A:O2'	52:o:27:GLN:OE1	2.14	0.66
50:i:125:ASN:O	50:i:126:ARG:NH1	2.29	0.66
13:w:68:GLU:HG2	13:w:69:PRO:HD3	1.76	0.65
3:g:14:VAL:HG11	3:g:35:VAL:HG12	1.78	0.65
23:F:186:GLU:N	23:F:186:GLU:OE2	2.28	0.65
17:3:8:LYS:HG2	17:3:11:ARG:HH12	1.61	0.65
18:A:1560:U:H2'	18:A:1561:C:H6	1.60	0.65
19:B:15:U:OP2	19:B:71:C:O2'	2.13	0.65
18:A:1211:G:H21	18:A:1216:A:H62	1.44	0.65
49:a:693:G:H2'	49:a:694:G:C8	2.32	0.65
18:A:284:G:N1	18:A:302:U:N3	2.44	0.65
18:A:2387:U:H3'	18:A:2388:G:C8	2.31	0.65
38:U:4:ILE:O	42:Z:26:LYS:NZ	2.29	0.65
18:A:2359:G:O6	18:A:2378:U:O4	2.14	0.65
18:A:2529:A:H5''	23:F:138:GLY:HA3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:987:A:H1'	49:a:1008:C:H1'	1.78	0.65
11:s:114:ARG:HB3	11:s:119:ALA:HB3	1.77	0.65
34:Q:61:ARG:NH1	34:Q:70:GLU:OE1	2.30	0.65
18:A:1201:G:N2	18:A:1204:A:OP2	2.24	0.65
25:H:126:SER:O	25:H:130:HIS:NE2	2.29	0.65
18:A:1186:G:O2'	18:A:1187:A:N7	2.30	0.65
18:A:1259:U:OP2	28:K:65:SER:OG	2.13	0.65
24:G:164:ARG:HD2	24:G:168:GLU:HG3	1.78	0.65
32:O:57:LYS:O	32:O:62:ASN:ND2	2.30	0.65
6:j:104:ARG:H	6:j:108:MET:HE2	1.61	0.65
18:A:2560:A:H61	41:X:43:THR:HG21	1.61	0.65
22:E:132:GLU:OE2	22:E:132:GLU:N	2.29	0.65
18:A:1628:A:H4'	18:A:1630:U:H5'	1.79	0.64
13:w:45:GLU:HG2	13:w:46:PRO:HD3	1.78	0.64
18:A:1545:C:H2'	18:A:1546:A:H8	1.63	0.64
18:A:1558:C:H2'	18:A:1559:A:H8	1.60	0.64
24:G:15:VAL:HG12	24:G:28:GLY:HA3	1.78	0.64
24:G:100:LYS:NZ	24:G:105:GLU:OE1	2.23	0.64
33:P:9:ASN:ND2	33:P:11:SER:OG	2.24	0.64
11:s:114:ARG:NH2	49:a:481:G:OP1	2.28	0.64
18:A:1367:G:N7	35:R:36:LYS:NZ	2.44	0.64
49:a:1054:G:O4'	49:a:1082:A:N6	2.31	0.64
18:A:1558:C:H2'	18:A:1559:A:C8	2.31	0.64
49:a:192:G:H2'	49:a:193:C:H2'	1.79	0.64
49:a:481:G:H2'	49:a:482:A:C8	2.33	0.64
49:a:1237:C:OP2	49:a:1260:A:N6	2.28	0.64
52:o:69:LYS:HA	52:o:72:LEU:HD23	1.77	0.64
11:s:14:ASP:OD1	49:a:542:U:O2'	2.15	0.64
49:a:85:C:H1'	49:a:86:G:N7	2.13	0.64
49:a:940:A:N3	55:y:55:ARG:NE	2.45	0.64
50:i:76:ILE:HA	50:i:82:GLU:HB3	1.80	0.64
14:x:34:LYS:O	14:x:62:HIS:ND1	2.27	0.64
16:h:184:ILE:HG22	16:h:198:TYR:HB2	1.79	0.64
21:D:156:THR:HB	21:D:157:PRO:HD3	1.78	0.64
18:A:774:G:N2	22:E:36:GLN:OE1	2.27	0.64
18:A:1854:U:O2'	18:A:1977:C:O2'	2.14	0.64
31:N:67:ASN:ND2	31:N:105:GLU:OE2	2.24	0.64
52:o:77:ARG:HH12	52:o:111:GLN:HE22	1.46	0.64
13:w:65:GLN:NE2	49:a:133:C:O2'	2.26	0.64
18:A:997:G:O6	18:A:1010:U:O2	2.15	0.64
49:a:481:G:H2'	49:a:482:A:H8	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:1277:U:O2'	54:t:14:ARG:NH2	2.27	0.64
7:k:39:ARG:NE	7:k:141:GLU:OE2	2.30	0.64
11:s:31:ARG:NH1	49:a:363:A:OP2	2.31	0.64
18:A:981:U:O2'	18:A:982:A:OP2	2.12	0.64
18:A:1194:C:OP1	31:N:60:ARG:NH1	2.31	0.64
18:A:1281:G:H21	36:S:92:GLN:HE22	1.46	0.64
51:m:113:GLU:HB3	51:m:119:ARG:HB2	1.80	0.63
6:j:136:ASP:H	6:j:177:VAL:HG22	1.63	0.63
49:a:1338:G:H2'	49:a:1339:A:C8	2.30	0.63
6:j:29:ARG:NH1	49:a:427:U:OP2	2.31	0.63
18:A:1365:G:N7	30:M:21:ARG:NH2	2.44	0.63
18:A:1596:C:H3'	18:A:1597:G:H8	1.63	0.63
52:o:83:ILE:HG13	52:o:85:ALA:H	1.63	0.63
53:p:53:ARG:HH11	57:u:45:ARG:NH1	1.97	0.63
4:r:25:LYS:HG3	49:a:825:C:H5'	1.80	0.63
18:A:297:G:N1	18:A:298:G:O6	2.32	0.63
37:T:115:GLU:OE1	37:T:117:ARG:NH1	2.32	0.63
49:a:653:G:H2'	49:a:654:G:C8	2.33	0.63
49:a:654:G:H2'	49:a:655:A:H8	1.63	0.63
51:m:140:ASP:HA	51:m:143:LYS:HE3	1.81	0.63
52:o:59:PHE:O	52:o:65:GLN:NE2	2.32	0.63
18:A:289:A:HO2'	18:A:303:G:HO2'	1.45	0.63
49:a:1219:A:N7	49:a:1283:U:C2	2.65	0.63
18:A:2106:A:H3'	18:A:2107:G:H5''	1.81	0.63
49:a:184:U:H2'	49:a:185:G:H8	1.62	0.63
49:a:1004:G:N1	49:a:1005:G:O6	2.32	0.63
49:a:1141:G:O6	49:a:1163:G:N2	2.26	0.63
52:o:62:LYS:O	52:o:66:GLN:NE2	2.31	0.63
52:o:68:ILE:HG23	52:o:99:LEU:HD11	1.80	0.63
54:t:15:MET:HA	54:t:18:ALA:HB3	1.81	0.63
55:y:32:LYS:HA	55:y:50:ALA:H	1.63	0.63
14:x:23:ALA:HB1	14:x:40:LEU:HD11	1.81	0.63
18:A:1996:U:OP2	18:A:2001:A:N6	2.31	0.63
18:A:2519:C:OP2	33:P:24:ARG:NH2	2.31	0.63
24:G:80:VAL:HA	24:G:137:ILE:HD11	1.80	0.63
13:w:51:ILE:HD11	13:w:56:ALA:HB2	1.80	0.63
15:z:6:SER:OG	49:a:65:G:N7	2.31	0.63
18:A:2083:A:N6	18:A:2099:G:O2'	2.31	0.63
18:A:308:U:H2'	18:A:309:G:H8	1.64	0.63
18:A:3078:G:N2	18:A:3081:A:OP2	2.30	0.62
28:K:45:THR:HB	28:K:48:VAL:HG12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:4:229:MET:HA	56:4:232:ILE:HD12	1.81	0.62
8:l:44:GLY:HA2	8:l:60:TYR:H	1.64	0.62
18:A:1201:G:H21	18:A:1203:A:H8	1.46	0.62
18:A:2693:A:N6	18:A:2705:G:O2'	2.32	0.62
51:m:137:ARG:HA	51:m:140:ASP:HB2	1.81	0.62
18:A:1554:U:H3	18:A:1617:C:N4	1.96	0.62
50:i:7:PRO:HD2	50:i:184:TYR:CD2	2.33	0.62
51:m:114:LYS:O	51:m:115:THR:OG1	2.14	0.62
56:4:234:ASP:O	56:4:238:GLY:N	2.30	0.62
4:r:24:SER:O	4:r:25:LYS:C	2.42	0.62
8:l:74:GLU:OE2	8:l:77:ARG:NH2	2.30	0.62
16:h:154:MET:SD	16:h:155:GLN:N	2.72	0.62
16:h:167:ASN:ND2	16:h:190:ASN:OD1	2.32	0.62
18:A:325:U:O2	18:A:450:G:O6	2.17	0.62
18:A:2975:G:H4'	24:G:4:ILE:HG12	1.81	0.62
54:t:54:THR:HA	54:t:57:ARG:HD2	1.81	0.62
18:A:1000:C:O2	18:A:1008:G:N2	2.32	0.62
18:A:306:U:H5''	25:H:41:ARG:HD3	1.81	0.62
18:A:2354:G:N3	18:A:2356:G:N2	2.46	0.62
23:F:12:LYS:HE2	23:F:16:ARG:HH21	1.65	0.62
24:G:168:GLU:OE1	24:G:168:GLU:N	2.32	0.62
49:a:980:G:H1	49:a:1023:U:H3	1.48	0.62
49:a:1091:A:N6	50:i:176:HIS:O	2.32	0.62
56:4:371:ILE:HG22	56:4:393:SER:HB2	1.82	0.62
49:a:598:C:N4	49:a:601:A:OP2	2.32	0.62
18:A:1886:A:N3	18:A:1888:C:N4	2.47	0.62
49:a:705:G:OP1	49:a:835:G:N2	2.28	0.62
6:j:120:VAL:HG12	6:j:121:ASN:H	1.65	0.62
18:A:247:G:O6	46:e:12:LYS:NZ	2.28	0.61
18:A:1195:A:H2	18:A:1206:A:H8	1.48	0.61
24:G:27:LYS:HG3	24:G:32:THR:HG22	1.80	0.61
26:I:69:LEU:HG	26:I:72:LEU:HB2	1.82	0.61
28:K:141:GLU:OE2	28:K:141:GLU:N	2.26	0.61
49:a:250:U:O2	49:a:252:U:N3	2.33	0.61
16:h:23:TRP:CG	16:h:39:TYR:HH	2.18	0.61
18:A:1159:C:H2'	18:A:1160:G:H8	1.65	0.61
18:A:2362:C:H2'	18:A:2363:A:C8	2.35	0.61
18:A:3005:A:H5''	18:A:3006:G:H5'	1.83	0.61
49:a:1065:U:H5''	49:a:1066:U:H5	1.65	0.61
11:s:55:VAL:HG11	11:s:82:VAL:HG11	1.82	0.61
18:A:1162:G:OP1	26:I:6:LYS:NZ	2.27	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:C:155:LEU:HD13	20:C:177:MET:HE1	1.82	0.61
1:Y:28:ARG:HD3	1:Y:30:ASN:OD1	1.99	0.61
18:A:1094:G:HO2'	18:A:1274:A:HO2'	1.46	0.61
51:m:49:GLN:HB2	51:m:121:ALA:HB1	1.82	0.61
13:w:69:PRO:CG	49:a:375:U:OP1	2.48	0.61
18:A:81:A:N1	18:A:96:G:O2'	2.33	0.61
18:A:935:A:H4'	18:A:951:G:H22	1.66	0.61
18:A:1223:U:H2'	18:A:1224:G:H8	1.64	0.61
18:A:2780:C:O2	56:4:216:ARG:NH1	2.32	0.61
49:a:1410:C:H2'	49:a:1411:A:H8	1.64	0.61
51:m:51:ARG:HG3	51:m:58:PRO:HD3	1.83	0.61
16:h:97:LEU:HB3	49:a:1083:C:H5''	1.81	0.61
18:A:1640:A:O2'	18:A:1641:U:OP1	2.17	0.61
19:B:10:G:O2'	19:B:11:U:OP1	2.19	0.61
49:a:1486:A:H2	49:a:1489:G:H1	1.49	0.61
55:y:53:ASP:HB3	55:y:76:PRO:HG2	1.82	0.61
3:g:42:HIS:HE1	3:g:44:PHE:HB3	1.63	0.61
13:w:32:ARG:HD3	49:a:587:A:N3	2.13	0.61
49:a:937:A:N6	49:a:1206:U:O4	2.23	0.61
49:a:819:U:H3	49:a:829:G:H22	1.49	0.61
50:i:76:ILE:HD13	50:i:83:ALA:HB2	1.82	0.61
16:h:95:ARG:NH1	49:a:1080:C:OP2	2.33	0.61
18:A:2378:U:H3'	18:A:2379:G:H8	1.65	0.61
49:a:1244:G:O6	49:a:1253:U:O4	2.19	0.61
51:m:68:ASN:ND2	51:m:128:SER:O	2.26	0.61
18:A:341:C:N3	18:A:342:C:N4	2.47	0.61
18:A:1536:A:H2'	18:A:1537:U:O4'	2.01	0.61
18:A:1077:A:H61	31:N:83:MET:HE2	1.65	0.60
49:a:1232:A:N3	49:a:1352:C:O2'	2.34	0.60
18:A:1186:G:N2	18:A:1213:A:O3'	2.34	0.60
49:a:1110:A:H61	49:a:1125:G:H1'	1.66	0.60
18:A:672:C:H4'	35:R:31:LEU:HD21	1.82	0.60
18:A:1162:G:O2'	18:A:1229:A:N6	2.34	0.60
22:E:150:GLU:OE1	22:E:150:GLU:N	2.32	0.60
49:a:612:U:H5'	49:a:613:G:C8	2.36	0.60
52:o:54:THR:HG23	52:o:57:ASN:H	1.65	0.60
57:u:3:LYS:O	57:u:4:LYS:C	2.45	0.60
5:1:25:ARG:HH11	5:1:25:ARG:HG3	1.66	0.60
32:O:89:ASP:OD1	32:O:89:ASP:N	2.34	0.60
34:Q:113:ARG:HD2	49:a:1425:G:H1	1.66	0.60
49:a:1070:U:O2'	49:a:1153:U:OP1	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:1219:A:H8	49:a:1283:U:N3	2.00	0.60
8:l:2:ARG:HD2	8:l:69:PRO:HG3	1.84	0.60
23:F:123:GLY:O	23:F:185:LYS:NZ	2.30	0.60
49:a:165:U:H2'	49:a:166:C:C6	2.37	0.60
49:a:1259:G:OP2	49:a:1259:G:N2	2.24	0.60
49:a:1299:C:OP1	57:u:17:ALA:HB3	2.02	0.60
10:q:93:VAL:HG21	10:q:106:ILE:HD11	1.82	0.60
49:a:416:G:H2'	49:a:417:G:H8	1.66	0.60
51:m:88:PRO:O	51:m:155:ARG:NH2	2.35	0.60
1:Y:5:CYS:SG	1:Y:6:ASP:N	2.74	0.60
3:g:3:THR:O	3:g:5:ILE:N	2.35	0.60
18:A:84:U:O2	42:Z:45:ARG:NH2	2.34	0.60
49:a:1027:G:H5'	57:u:4:LYS:HE3	1.84	0.60
54:t:50:ASP:O	54:t:54:THR:OG1	2.18	0.60
1:Y:63:ARG:O	1:Y:64:ALA:C	2.43	0.60
52:o:133:ARG:NH2	57:u:61:TRP:CD1	2.70	0.60
11:s:89:ASP:OD2	49:a:503:A:N6	2.33	0.60
18:A:1530:G:N2	18:A:1805:G:H22	2.00	0.60
23:F:119:ARG:NH1	54:t:83:GLU:OE2	2.34	0.60
18:A:335:G:O2'	18:A:336:C:OP1	2.12	0.59
18:A:1260:C:O2'	28:K:27:ARG:NH1	2.34	0.59
18:A:1758:G:H21	18:A:1759:A:H62	1.50	0.59
27:J:22:PRO:HD2	27:J:26:VAL:HG22	1.83	0.59
49:a:72:G:N2	49:a:148:A:C6	2.70	0.59
13:w:67:THR:HG23	13:w:70:VAL:HG13	1.84	0.59
18:A:2034:G:OP1	20:C:88:ARG:NH2	2.35	0.59
30:M:113:LEU:HD23	30:M:130:SER:HB2	1.84	0.59
39:V:10:LEU:HD23	39:V:80:PRO:HG3	1.83	0.59
18:A:1815:G:OP2	38:U:43:LYS:NZ	2.36	0.59
30:M:61:LEU:HD21	46:e:24:ARG:HD2	1.84	0.59
18:A:1457:A:O2'	18:A:1459:U:OP2	2.20	0.59
20:C:24:ILE:HG23	20:C:83:GLU:HA	1.84	0.59
24:G:116:ILE:HG21	24:G:149:ILE:HD11	1.84	0.59
44:b:10:ARG:O	44:b:14:ARG:HG2	2.02	0.59
49:a:1374:U:H2'	49:a:1375:G:C8	2.37	0.59
49:a:1320:G:O2'	49:a:1321:A:OP1	2.19	0.59
6:j:154:ARG:O	6:j:173:GLN:NE2	2.35	0.59
7:k:69:GLY:N	7:k:143:ALA:O	2.36	0.59
23:F:142:GLN:OE1	23:F:157:ARG:N	2.25	0.59
38:U:34:HIS:ND1	38:U:36:ASP:OD2	2.35	0.59
50:i:53:ASP:HB2	50:i:68:HIS:HD2	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:g:24:THR:HG22	3:g:25:ARG:H	1.68	0.59
18:A:217:G:H22	18:A:235:U:H4'	1.67	0.59
18:A:1532:G:O2'	18:A:1803:A:N1	2.32	0.59
18:A:1560:U:H2'	18:A:1561:C:C6	2.38	0.59
18:A:3052:A:OP1	21:D:60:ARG:NH2	2.32	0.59
40:W:77:LEU:HD21	40:W:138:LEU:HD21	1.83	0.59
49:a:1418:G:H2'	49:a:1419:C:C6	2.38	0.59
6:j:90:GLU:OE1	6:j:95:ASN:ND2	2.34	0.59
18:A:718:C:O2'	18:A:772:U:OP1	2.20	0.59
18:A:1545:C:N3	18:A:1626:G:N2	2.50	0.59
18:A:2249:G:H2'	18:A:2250:A:C8	2.37	0.59
55:y:37:ARG:O	55:y:70:LYS:NZ	2.29	0.59
57:u:6:LEU:O	57:u:7:VAL:C	2.44	0.59
11:s:73:ASN:ND2	11:s:105:GLN:OE1	2.35	0.59
18:A:1379:G:OP1	44:b:16:ARG:NH2	2.22	0.59
18:A:2383:U:C5	18:A:2384:C:H1'	2.37	0.59
25:H:124:ILE:HG22	25:H:125:LYS:H	1.68	0.59
49:a:469:G:H2'	49:a:470:U:O4'	2.03	0.59
49:a:1198:C:H5'	57:u:9:LYS:HD2	1.83	0.59
18:A:610:C:O2	18:A:646:U:O2'	2.21	0.58
18:A:1189:G:N3	18:A:1207:G:O2'	2.30	0.58
49:a:1241:G:N2	49:a:1256:A:OP2	2.32	0.58
18:A:2127:G:OP2	20:C:241:SER:OG	2.19	0.58
54:t:10:PRO:HG2	54:t:18:ALA:CA	2.33	0.58
56:4:412:GLU:OE2	56:4:454:ARG:NH1	2.36	0.58
4:r:20:CYS:HB3	4:r:23:CYS:HB2	1.84	0.58
13:w:6:LYS:HE3	13:w:24:ASP:O	2.04	0.58
18:A:1631:A:O2'	18:A:1632:G:O4'	2.20	0.58
18:A:2378:U:H3'	18:A:2379:G:C8	2.39	0.58
49:a:928:A:O2'	49:a:1315:A:N3	2.34	0.58
23:F:57:ILE:HD12	23:F:91:PRO:HB2	1.85	0.58
49:a:495:G:H2'	49:a:496:U:H6	1.69	0.58
49:a:1104:G:O2'	49:a:1126:G:N1	2.35	0.58
48:5:36:A:H4'	48:5:37:U:OP2	2.03	0.58
49:a:1203:G:OP1	55:y:78:ARG:NH2	2.17	0.58
6:j:54:GLN:HB3	6:j:58:PHE:HE2	1.69	0.58
18:A:1603:G:H2'	18:A:1604:G:C8	2.39	0.58
32:O:106:ASP:OD1	32:O:106:ASP:N	2.35	0.58
48:5:42:C:O2'	49:a:1320:G:N3	2.36	0.58
50:i:133:MET:HE1	50:i:153:CYS:HB2	1.85	0.58
13:w:68:GLU:OE1	13:w:69:PRO:HD3	1.90	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:1112:C:O2	36:S:12:LYS:NZ	2.30	0.58
18:A:1204:A:O2'	18:A:1205:G:N7	2.35	0.58
18:A:1258:C:OP2	28:K:68:LYS:NZ	2.30	0.58
49:a:644:G:H22	49:a:721:G:H1	1.52	0.58
49:a:1231:A:O2'	49:a:1232:A:OP1	2.19	0.58
51:m:109:ARG:HB2	51:m:119:ARG:NH2	2.19	0.58
3:g:16:CYS:HB2	3:g:20:HIS:O	2.03	0.58
31:N:91:GLU:HG2	31:N:92:TRP:CE3	2.39	0.58
49:a:390:U:H2'	49:a:391:G:H8	1.67	0.58
49:a:926:G:N1	49:a:1320:G:OP2	2.32	0.58
49:a:979:U:H2'	49:a:980:G:H8	1.68	0.58
18:A:747:A:H2	18:A:768:G:H21	1.52	0.58
18:A:994:A:OP2	18:A:1014:G:N2	2.37	0.58
18:A:2412:U:H2'	18:A:2413:G:C8	2.38	0.58
20:C:108:PRO:HD2	20:C:111:LEU:HD22	1.85	0.58
48:5:1:C:H42	48:5:73:A:H61	1.51	0.58
49:a:296:U:O2'	49:a:536:C:O2	2.22	0.58
53:p:29:VAL:HG22	53:p:87:LEU:HD11	1.86	0.58
32:O:10:LEU:HD13	32:O:40:LYS:HG2	1.86	0.57
49:a:485:G:H2'	49:a:486:G:C8	2.39	0.57
7:k:65:GLY:HA3	7:k:142:CYS:HB3	1.84	0.57
17:3:8:LYS:NZ	18:A:1078:G:O6	2.36	0.57
49:a:192:G:N1	49:a:195:U:OP2	2.32	0.57
49:a:297:G:N2	49:a:300:A:OP2	2.37	0.57
49:a:498:C:H5''	49:a:499:C:C6	2.39	0.57
57:u:43:CYS:O	57:u:44:LEU:C	2.47	0.57
18:A:2600:A:N3	33:P:121:ARG:NH2	2.51	0.57
40:W:178:VAL:HG12	40:W:179:VAL:HG23	1.86	0.57
49:a:928:A:H2'	49:a:929:G:H8	1.69	0.57
50:i:3:GLN:OE1	50:i:3:GLN:N	2.37	0.57
54:t:22:ILE:HB	54:t:25:ILE:HG22	1.87	0.57
54:t:81:LYS:HB3	54:t:86:CYS:HB3	1.86	0.57
4:r:19:LYS:HB3	49:a:827:U:OP1	2.03	0.57
18:A:2211:C:H2'	18:A:2212:A:H8	1.69	0.57
18:A:2826:A:H4'	56:4:204:GLY:HA2	1.86	0.57
49:a:993:G:O6	49:a:1002:U:O2	2.22	0.57
55:y:36:ARG:NH2	55:y:72:GLY:O	2.38	0.57
4:r:22:PHE:CE1	4:r:37:LEU:HD21	2.39	0.57
18:A:928:U:H2'	18:A:929:C:C6	2.39	0.57
4:r:24:SER:HA	49:a:826:U:OP2	2.03	0.57
18:A:2552:A:H2'	18:A:2553:G:C8	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:1130:C:H2'	49:a:1131:G:H8	1.70	0.57
52:o:82:ASP:OD1	52:o:83:ILE:N	2.37	0.57
18:A:2909:G:OP1	34:Q:48:ARG:NH1	2.27	0.57
18:A:2971:G:OP1	24:G:75:ASN:ND2	2.37	0.57
20:C:20:ASP:O	20:C:22:ALA:N	2.38	0.57
13:w:23:ALA:HB1	13:w:27:THR:HG21	1.87	0.57
43:2:10:ARG:HB2	43:2:53:LEU:HD23	1.87	0.57
49:a:109:G:H2'	49:a:110:U:C6	2.40	0.57
49:a:312:C:H2'	49:a:313:A:C8	2.40	0.57
52:o:53:ARG:HG2	52:o:58:TYR:HE2	1.70	0.57
3:g:10:VAL:O	3:g:25:ARG:HG3	2.03	0.57
18:A:752:C:H2'	18:A:753:A:H8	1.68	0.57
26:I:24:VAL:HG23	26:I:80:ALA:HB3	1.86	0.57
49:a:791:C:O2'	49:a:883:A:N1	2.37	0.57
51:m:21:GLN:HA	51:m:24:THR:HB	1.86	0.57
56:4:347:ARG:HA	56:4:350:ILE:HG12	1.87	0.57
28:K:42:PRO:HB3	35:R:68:ALA:HB2	1.87	0.57
48:5:75:C:H4'	48:5:76:C:OP2	2.05	0.57
52:o:75:VAL:HG13	52:o:77:ARG:HG2	1.86	0.57
54:t:10:PRO:O	54:t:45:THR:HG21	2.05	0.57
57:u:14:PRO:HB2	57:u:16:PHE:O	2.05	0.57
4:r:40:THR:HB	4:r:41:TYR:CD2	2.40	0.56
12:v:39:LEU:HD22	12:v:56:LEU:HB2	1.85	0.56
18:A:1565:A:O2'	18:A:1566:A:O5'	2.21	0.56
21:D:114:VAL:HG22	21:D:208:VAL:HG12	1.87	0.56
54:t:10:PRO:CG	54:t:13:LYS:HE2	2.35	0.56
8:l:50:TYR:OH	8:l:87:ARG:NH1	2.35	0.56
18:A:2387:U:H3'	18:A:2388:G:H8	1.69	0.56
49:a:21:U:H2'	49:a:22:C:H6	1.70	0.56
49:a:60:U:H2'	49:a:61:G:H8	1.71	0.56
49:a:128:U:H1'	49:a:262:G:H21	1.70	0.56
50:i:7:PRO:O	50:i:11:ARG:HG2	2.05	0.56
1:Y:8:CYS:SG	1:Y:52:CYS:SG	3.01	0.56
3:g:25:ARG:O	23:F:109:ARG:NH1	2.38	0.56
9:n:13:ARG:HD2	9:n:27:LEU:HD23	1.86	0.56
11:s:72:HIS:HA	11:s:99:ARG:HH22	1.69	0.56
13:w:67:THR:HG21	49:a:376:G:OP1	2.05	0.56
18:A:1189:G:H1'	18:A:1207:G:H2'	1.87	0.56
18:A:2317:G:H5'	25:H:25:TYR:HD1	1.71	0.56
18:A:2530:C:H5''	18:A:2531:G:H2'	1.87	0.56
49:a:372:C:N4	49:a:388:G:OP2	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:942:U:H4'	49:a:943:U:O5'	2.05	0.56
49:a:1040:U:H4'	53:p:53:ARG:O	2.04	0.56
49:a:1234:G:O6	49:a:1265:U:O2	2.24	0.56
51:m:29:LYS:HG3	51:m:101:LEU:HD23	1.87	0.56
18:A:1554:U:N3	18:A:1617:C:N4	2.53	0.56
49:a:109:G:H2'	49:a:110:U:H6	1.71	0.56
49:a:1436:G:O2'	49:a:1438:G:OP1	2.24	0.56
7:k:160:ASN:ND2	49:a:23:C:OP1	2.36	0.56
26:I:96:PHE:HA	26:I:99:ASP:HB3	1.87	0.56
36:S:16:VAL:HG21	36:S:99:VAL:HG21	1.87	0.56
18:A:1621:C:H2'	18:A:1622:G:C5	2.41	0.56
49:a:264:U:H2'	49:a:265:G:O4'	2.05	0.56
49:a:495:G:H2'	49:a:496:U:C6	2.41	0.56
53:p:12:ALA:HB3	53:p:18:ILE:HB	1.88	0.56
55:y:39:THR:HA	55:y:70:LYS:HG2	1.88	0.56
4:r:18:ARG:HD3	4:r:18:ARG:H	1.70	0.56
13:w:65:GLN:NE2	49:a:134:C:H5'	2.21	0.56
18:A:332:C:H2'	18:A:333:C:C6	2.41	0.56
18:A:2243:C:N4	18:A:2244:A:H62	2.04	0.56
20:C:143:HIS:ND1	20:C:194:GLY:O	2.37	0.56
52:o:77:ARG:NH1	52:o:111:GLN:HE22	2.03	0.56
57:u:23:ARG:HG3	57:u:28:GLY:O	2.06	0.56
19:B:78:U:OP1	40:W:28:ARG:NH2	2.38	0.56
20:C:21:PHE:HB3	20:C:24:ILE:HG13	1.87	0.56
34:Q:19:PHE:O	34:Q:49:ARG:NH1	2.39	0.56
49:a:1091:A:N1	50:i:177:THR:OG1	2.34	0.56
54:t:39:ILE:HD13	54:t:56:LEU:HB2	1.87	0.56
54:t:47:ASP:N	54:t:47:ASP:OD1	2.38	0.56
18:A:2270:G:H5'	44:b:16:ARG:HG3	1.88	0.56
18:A:3032:G:H5''	21:D:63:ILE:HG23	1.88	0.56
18:A:2374:U:H2'	18:A:2375:G:H8	1.70	0.56
20:C:65:ILE:H	20:C:65:ILE:HD12	1.71	0.56
20:C:131:LEU:HD12	20:C:135:ASN:HB2	1.87	0.56
22:E:64:LYS:NZ	22:E:76:GLN:O	2.38	0.56
45:d:37:ARG:NH1	45:d:44:ALA:O	2.38	0.56
49:a:440:C:H2'	49:a:441:A:H8	1.71	0.56
56:4:456:PRO:O	56:4:460:ALA:N	2.39	0.56
9:n:22:HIS:O	9:n:66:TYR:OH	2.23	0.55
18:A:2043:C:O2'	18:A:2195:U:OP2	2.24	0.55
19:B:117:A:O2'	19:B:118:C:O4'	2.15	0.55
9:n:114:THR:OG1	9:n:115:ASP:N	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:808:A:O2'	18:A:1468:A:N3	2.39	0.55
49:a:1267:U:H3'	49:a:1268:C:H5'	1.87	0.55
1:Y:56:ILE:HA	1:Y:61:VAL:HG22	1.88	0.55
13:w:21:ILE:HD11	13:w:33:ALA:HB3	1.88	0.55
33:P:43:SER:OG	33:P:44:ALA:N	2.39	0.55
49:a:1077:C:O2'	49:a:1150:A:N3	2.38	0.55
49:a:1410:C:H2'	49:a:1411:A:C8	2.41	0.55
18:A:1565:A:H2'	18:A:1566:A:C4	2.42	0.55
18:A:2537:C:O4'	23:F:44:ASN:ND2	2.37	0.55
23:F:19:ILE:HD12	23:F:179:ALA:HB1	1.88	0.55
49:a:737:U:H2'	49:a:738:G:O4'	2.06	0.55
6:j:45:GLU:OE2	7:k:137:ARG:NH2	2.39	0.55
6:j:87:ARG:HG3	6:j:181:PRO:HG2	1.89	0.55
6:j:95:ASN:OD1	6:j:106:ARG:NH2	2.39	0.55
11:s:50:ARG:HD2	11:s:90:LEU:HD11	1.89	0.55
18:A:473:C:O2'	18:A:476:G:N2	2.39	0.55
22:E:158:ILE:HD13	22:E:197:SER:HB3	1.89	0.55
49:a:1415:G:O2'	49:a:1452:A:N6	2.40	0.55
51:m:42:ILE:O	51:m:46:ALA:N	2.40	0.55
54:t:34:LEU:HB3	54:t:41:LYS:HB3	1.88	0.55
55:y:31:ILE:HD13	55:y:47:HIS:HB3	1.87	0.55
6:j:15:LEU:HD21	6:j:54:GLN:HB2	1.86	0.55
18:A:283:U:O2	18:A:303:G:O6	2.23	0.55
18:A:2579:C:H1'	41:X:39:ARG:HH11	1.71	0.55
18:A:2753:G:H5''	18:A:2754:G:H5''	1.88	0.55
49:a:928:A:H2'	49:a:929:G:C8	2.41	0.55
56:4:230:LYS:HA	56:4:233:ARG:HE	1.72	0.55
7:k:133:GLY:HA3	49:a:13:G:H5'	1.88	0.55
18:A:2587:U:OP2	46:e:43:ARG:NH2	2.34	0.55
49:a:880:G:N2	49:a:883:A:OP2	2.39	0.55
49:a:1041:G:N7	50:i:2:GLY:N	2.54	0.55
51:m:16:PRO:HB2	52:o:66:GLN:HG2	1.89	0.55
10:q:120:SER:OG	10:q:121:ASP:N	2.39	0.55
18:A:670:A:OP1	18:A:1370:U:O2'	2.24	0.55
18:A:2085:C:N4	18:A:2097:G:O6	2.37	0.55
21:D:154:CYS:O	21:D:155:ALA:HB3	2.06	0.55
40:W:173:ASP:OD1	40:W:173:ASP:N	2.39	0.55
49:a:145:G:H1	49:a:171:A:N6	2.05	0.55
49:a:1328:A:H62	49:a:1358:A:H62	1.55	0.55
52:o:40:ARG:HG3	52:o:84:TYR:HB2	1.87	0.55
1:Y:19:SER:OG	1:Y:20:HIS:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:980:C:O2'	18:A:981:U:O5'	2.24	0.55
18:A:1538:G:H2'	18:A:1539:A:C8	2.42	0.55
49:a:1130:C:H2'	49:a:1131:G:C8	2.41	0.55
49:a:1231:A:H2'	49:a:1232:A:C8	2.41	0.55
55:y:41:ILE:HG22	55:y:43:ASP:H	1.72	0.55
18:A:2967:C:OP1	47:f:33:LYS:NZ	2.40	0.55
49:a:49:U:H2'	49:a:50:G:C8	2.42	0.55
49:a:1014:U:H2'	49:a:1015:G:C8	2.42	0.55
49:a:1099:C:OP1	52:o:105:ARG:NH1	2.34	0.55
54:t:13:LYS:HB2	54:t:17:ILE:HG13	1.88	0.55
56:4:319:LEU:HD13	56:4:353:VAL:HG21	1.88	0.55
3:g:42:HIS:HB3	3:g:45:TYR:HB2	1.89	0.54
14:x:36:ILE:HG13	14:x:61:ALA:HB3	1.89	0.54
18:A:284:G:O6	18:A:302:U:O4	2.24	0.54
18:A:1122:C:H2'	18:A:1129:G:H2'	1.89	0.54
22:E:90:VAL:HG23	22:E:91:HIS:H	1.72	0.54
36:S:60:VAL:HG22	36:S:102:ILE:HG12	1.89	0.54
51:m:136:LYS:O	51:m:140:ASP:N	2.36	0.54
57:u:9:LYS:HA	57:u:12:LYS:HE2	1.89	0.54
1:Y:14:PHE:HZ	18:A:1480:A:C8	2.25	0.54
2:c:53:GLU:HG2	2:c:54:SER:N	2.22	0.54
5:1:12:MET:HE1	49:a:1503:A:H5'	1.87	0.54
6:j:49:GLN:HB3	6:j:198:LEU:HB2	1.88	0.54
18:A:2884:A:N1	56:4:432:ARG:NH1	2.55	0.54
27:J:75:PRO:HB2	27:J:80:LEU:HD13	1.89	0.54
30:M:51:GLU:OE2	46:e:57:ARG:NH2	2.36	0.54
49:a:1184:C:H5'	57:u:27:CYS:HB2	1.89	0.54
50:i:46:LEU:HD23	50:i:51:ILE:HD11	1.89	0.54
56:4:305:ARG:O	56:4:306:HIS:ND1	2.39	0.54
3:g:16:CYS:SG	3:g:38:CYS:HB3	2.48	0.54
7:k:173:GLN:OE1	7:k:181:ARG:NH1	2.39	0.54
18:A:947:U:H2'	18:A:948:G:H8	1.72	0.54
49:a:145:G:O2'	49:a:1429:A:N3	2.41	0.54
49:a:427:U:H1'	49:a:521:G:H5'	1.89	0.54
49:a:1198:C:OP1	57:u:9:LYS:HD2	2.07	0.54
52:o:88:ASP:O	52:o:95:GLN:NE2	2.41	0.54
55:y:34:TRP:CD1	55:y:35:SER:HG	2.25	0.54
1:Y:37:ARG:HG3	18:A:2423:C:OP1	2.08	0.54
18:A:445:U:H4'	18:A:446:G:O5'	2.06	0.54
18:A:2802:G:N2	21:D:135:GLN:HE21	2.05	0.54
49:a:75:A:H61	49:a:95:C:H1'	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:122:G:HO2'	49:a:614:C:HO2'	1.42	0.54
2:c:6:ASP:O	2:c:7:VAL:C	2.49	0.54
4:r:22:PHE:CE1	4:r:37:LEU:HD11	2.43	0.54
6:j:19:LEU:HD22	6:j:59:SER:HB3	1.89	0.54
14:x:83:SER:OG	49:a:254:G:OP1	2.25	0.54
18:A:328:C:H2'	18:A:329:U:O4'	2.07	0.54
49:a:979:U:H2'	49:a:980:G:C8	2.42	0.54
18:A:263:G:O2'	18:A:517:A:N3	2.36	0.54
18:A:1037:C:O2'	41:X:29:GLN:NE2	2.41	0.54
18:A:2097:G:H2'	18:A:2098:U:C6	2.43	0.54
18:A:2142:A:O2'	18:A:2144:C:N4	2.40	0.54
49:a:540:A:H5'	49:a:546:G:N2	2.23	0.54
49:a:642:C:H2'	49:a:643:A:C8	2.42	0.54
49:a:695:A:H2'	49:a:696:A:C8	2.42	0.54
49:a:1251:G:H2'	49:a:1252:G:H8	1.72	0.54
50:i:75:VAL:HG12	50:i:76:ILE:H	1.73	0.54
16:h:27:MET:SD	16:h:29:ARG:NH2	2.80	0.54
18:A:298:G:H2'	18:A:299:G:O4'	2.07	0.54
18:A:2366:C:H3'	18:A:2367:G:H8	1.73	0.54
29:L:1:MET:HG2	29:L:32:TYR:CG	2.42	0.54
49:a:269:U:H2'	49:a:270:A:C8	2.42	0.54
5:1:18:ARG:NH1	49:a:884:G:H5'	2.23	0.54
24:G:154:ARG:HD3	24:G:155:PRO:HD2	1.89	0.54
50:i:23:TYR:OH	53:p:11:LYS:HG2	2.07	0.54
51:m:105:VAL:HG12	51:m:123:GLU:HB3	1.89	0.54
3:g:33:ILE:HG22	3:g:34:VAL:H	1.72	0.54
8:l:17:ARG:NH1	18:A:1560:U:O2	2.41	0.54
18:A:1528:G:H2'	18:A:1529:U:C6	2.43	0.54
18:A:2357:A:N6	18:A:2380:G:H1'	2.23	0.54
50:i:56:ILE:HD13	50:i:66:ASP:HB2	1.88	0.54
50:i:175:LEU:HD13	50:i:182:ILE:HD12	1.88	0.54
3:g:22:PHE:HD2	3:g:22:PHE:N	2.05	0.54
18:A:284:G:C6	18:A:302:U:N3	2.76	0.54
18:A:290:C:O2'	18:A:301:U:O4	2.18	0.54
24:G:128:SER:HB3	24:G:131:LYS:HG2	1.90	0.54
26:I:115:LEU:HD23	26:I:119:ASP:HB3	1.90	0.54
44:b:37:ARG:HG3	44:b:54:LEU:HD22	1.90	0.54
49:a:1274:C:OP2	51:m:41:ARG:NH2	2.40	0.54
2:c:47:THR:HG22	2:c:48:HIS:N	2.23	0.53
3:g:14:VAL:CG1	3:g:35:VAL:HG12	2.38	0.53
6:j:31:TYR:CG	6:j:38:ARG:HD2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:q:136:ARG:NH1	49:a:776:C:O3'	2.42	0.53
18:A:1224:G:N3	26:I:28:TYR:OH	2.41	0.53
18:A:1231:U:H2'	18:A:1232:G:H8	1.72	0.53
18:A:3019:C:H5''	18:A:3020:U:H3	1.71	0.53
49:a:294:C:OP1	49:a:590:A:O2'	2.26	0.53
49:a:676:A:N3	49:a:766:G:O2'	2.37	0.53
9:n:50:ARG:HH12	9:n:63:GLN:HE22	1.56	0.53
18:A:1118:A:OP2	18:A:1273:G:N1	2.31	0.53
18:A:2756:G:O2'	18:A:2881:A:N1	2.39	0.53
19:B:92:G:OP2	40:W:25:ARG:NH1	2.40	0.53
21:D:150:SER:OG	21:D:151:ILE:N	2.41	0.53
23:F:74:VAL:HG21	23:F:91:PRO:HB3	1.90	0.53
31:N:58:ILE:HG13	31:N:59:LYS:H	1.73	0.53
49:a:72:G:C2	49:a:148:A:N1	2.75	0.53
50:i:12:LEU:HD11	57:u:51:GLY:CA	2.38	0.53
50:i:151:VAL:HG22	50:i:200:VAL:HG13	1.90	0.53
6:j:144:SER:O	6:j:172:ARG:NH2	2.41	0.53
13:w:5:ILE:O	13:w:67:THR:CG2	2.53	0.53
18:A:2407:C:H2'	18:A:2408:G:H8	1.73	0.53
26:I:105:ILE:HG21	26:I:120:VAL:HG11	1.90	0.53
49:a:77:G:C2	49:a:78:G:C8	2.97	0.53
56:4:254:THR:OG1	56:4:303:PHE:O	2.25	0.53
56:4:256:ALA:HB1	56:4:331:VAL:HG12	1.91	0.53
18:A:150:C:H2'	18:A:151:A:H8	1.73	0.53
18:A:1731:A:H2'	18:A:1732:U:C6	2.43	0.53
48:5:70:C:H2'	48:5:71:G:H8	1.72	0.53
49:a:1220:A:H1'	51:m:116:MET:SD	2.48	0.53
1:Y:14:PHE:HZ	18:A:1480:A:N7	2.06	0.53
11:s:25:LYS:HE2	11:s:59:SER:HB2	1.91	0.53
18:A:1179:U:C4	27:J:14:GLN:HB2	2.44	0.53
18:A:1212:U:N3	18:A:1215:U:OP2	2.34	0.53
18:A:2124:A:H1'	18:A:2194:A:H2'	1.91	0.53
26:I:116:SER:H	26:I:119:ASP:HB2	1.72	0.53
20:C:186:ASP:OD2	20:C:188:ARG:NH2	2.42	0.53
50:i:93:LEU:O	50:i:94:THR:HG22	2.09	0.53
52:o:74:THR:HB	52:o:118:LEU:HD21	1.90	0.53
53:p:11:LYS:NZ	53:p:71:LYS:HD3	2.20	0.53
18:A:2089:C:H2'	18:A:2090:U:C6	2.44	0.53
18:A:2373:G:H2'	18:A:2374:U:C6	2.43	0.53
49:a:1008:C:H2'	49:a:1009:C:C5	2.43	0.53
49:a:1324:C:H2'	49:a:1325:G:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:s:42:PRO:HG3	11:s:50:ARG:HH21	1.73	0.53
15:z:10:ARG:O	15:z:14:ASN:HB2	2.09	0.53
18:A:2367:G:H4'	18:A:2368:C:C5	2.44	0.53
49:a:66:U:O2'	49:a:379:C:O2	2.26	0.53
49:a:654:G:H2'	49:a:655:A:C8	2.44	0.53
49:a:1287:G:H22	49:a:1313:G:H1'	1.74	0.53
54:t:10:PRO:HB3	54:t:13:LYS:HE2	1.91	0.53
57:u:45:ARG:O	57:u:46:GLU:C	2.52	0.53
16:h:32:PHE:HB3	16:h:40:ILE:HB	1.91	0.53
18:A:928:U:H2'	18:A:929:C:H6	1.74	0.53
18:A:1000:C:H2'	18:A:1001:C:H5''	1.90	0.53
18:A:1606:G:H2'	18:A:1607:C:C6	2.44	0.53
18:A:3118:U:H2'	18:A:3119:A:C8	2.44	0.53
24:G:39:GLU:HG2	24:G:40:PRO:CD	2.31	0.53
26:I:28:TYR:HB3	26:I:78:ALA:HB2	1.91	0.53
40:W:109:GLU:HG2	40:W:132:GLU:HB3	1.91	0.53
49:a:1036:U:H2'	49:a:1037:G:H8	1.74	0.53
52:o:49:ASN:HB3	52:o:84:TYR:HA	1.91	0.53
9:n:96:ARG:NH1	9:n:115:ASP:OD2	2.41	0.53
9:n:109:SER:HA	49:a:622:A:N7	2.24	0.53
18:A:1541:G:H2'	18:A:1542:A:O4'	2.08	0.53
26:I:43:LEU:HD22	26:I:49:TYR:HB2	1.89	0.53
28:K:41:LYS:NZ	28:K:50:GLY:O	2.34	0.53
49:a:1131:G:H4'	53:p:43:PRO:HB3	1.91	0.53
7:k:50:VAL:HG13	7:k:52:GLY:H	1.74	0.52
18:A:1610:C:H2'	18:A:1611:A:C8	2.44	0.52
39:V:75:ASP:OD1	39:V:76:SER:N	2.40	0.52
51:m:62:LEU:O	51:m:66:LEU:HB2	2.09	0.52
53:p:54:SER:OG	53:p:57:LYS:O	2.27	0.52
3:g:22:PHE:N	3:g:22:PHE:CD2	2.77	0.52
19:B:4:A:N1	19:B:23:G:O2'	2.37	0.52
26:I:17:PHE:CZ	26:I:66:ILE:HB	2.44	0.52
26:I:53:LYS:HB3	26:I:56:LEU:HB2	1.92	0.52
49:a:21:U:H2'	49:a:22:C:C6	2.43	0.52
49:a:87:G:H2'	49:a:88:G:H8	1.74	0.52
49:a:927:G:N2	49:a:1316:G:O2'	2.42	0.52
49:a:1000:U:H2'	49:a:1001:G:H8	1.73	0.52
49:a:1127:A:H2'	49:a:1128:C:C6	2.45	0.52
53:p:15:HIS:HB2	53:p:70:HIS:HD2	1.74	0.52
1:Y:39:VAL:CG2	1:Y:46:LYS:HG2	2.37	0.52
18:A:1177:G:H2'	18:A:1178:U:C5	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:1787:A:H2'	20:C:86:PRO:HG3	1.91	0.52
18:A:2983:G:N2	24:G:140:GLN:OE1	2.43	0.52
49:a:522:G:H2'	49:a:523:U:C6	2.44	0.52
49:a:1361:C:O2	51:m:76:ARG:NH1	2.29	0.52
53:p:59:LYS:HG2	53:p:62:ARG:HH22	1.73	0.52
54:t:16:GLU:HA	54:t:30:SER:HB3	1.91	0.52
4:r:78:PRO:C	4:r:80:GLY:H	2.17	0.52
10:q:128:ASN:ND2	49:a:698:A:O5'	2.41	0.52
16:h:103:ASN:ND2	49:a:1053:U:O2	2.42	0.52
18:A:159:A:N3	18:A:2431:C:O2'	2.39	0.52
18:A:681:C:H2'	18:A:682:A:H8	1.74	0.52
18:A:1145:A:H61	18:A:1245:U:H5	1.57	0.52
18:A:1788:G:H5'	20:C:60:ARG:HA	1.91	0.52
18:A:2388:G:H21	18:A:2389:U:H1'	1.74	0.52
25:H:84:ALA:HB2	25:H:91:LEU:HD23	1.90	0.52
27:J:23:ALA:HB3	27:J:24:PRO:HD3	1.91	0.52
49:a:25:G:H2'	49:a:26:G:C8	2.44	0.52
49:a:78:G:O6	49:a:91:U:O4	2.26	0.52
49:a:1310:C:OP1	54:t:28:THR:HB	2.10	0.52
6:j:165:TRP:CE2	6:j:181:PRO:HB3	2.45	0.52
18:A:196:A:N6	18:A:2654:A:O2'	2.42	0.52
18:A:1640:A:H2'	18:A:1642:G:N7	2.24	0.52
30:M:55:MET:O	30:M:60:ARG:NH1	2.39	0.52
48:5:44:A:H2'	48:5:45:A:C8	2.43	0.52
49:a:105:A:H5'	49:a:106:C:H5	1.73	0.52
57:u:7:VAL:HG12	57:u:11:ASN:HD21	1.74	0.52
2:c:15:CYS:SG	2:c:18:CYS:SG	3.07	0.52
3:g:1:MET:C	3:g:3:THR:H	2.17	0.52
4:r:21:VAL:O	4:r:22:PHE:C	2.53	0.52
14:x:34:LYS:HE3	14:x:62:HIS:HE1	1.73	0.52
16:h:70:VAL:HG21	16:h:96:TRP:HE3	1.74	0.52
18:A:857:U:H2'	18:A:858:A:C8	2.45	0.52
18:A:1281:G:H21	36:S:92:GLN:NE2	2.07	0.52
49:a:312:C:H2'	49:a:313:A:H8	1.74	0.52
52:o:54:THR:OG1	52:o:56:GLU:OE1	2.23	0.52
54:t:17:ILE:O	54:t:20:THR:OG1	2.26	0.52
2:c:53:GLU:HG2	2:c:54:SER:H	1.74	0.52
8:l:24:GLU:OE1	8:l:31:ARG:NH2	2.43	0.52
16:h:110:ARG:NH1	49:a:1084:G:O3'	2.42	0.52
18:A:752:C:H2'	18:A:753:A:C8	2.44	0.52
18:A:977:G:H2'	18:A:978:A:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:1195:A:H2	18:A:1206:A:C8	2.27	0.52
18:A:1809:U:H2'	18:A:1810:A:H8	1.75	0.52
18:A:2394:A:N3	18:A:2395:U:O2'	2.38	0.52
18:A:2515:U:H2'	18:A:2516:U:C6	2.45	0.52
20:C:79:VAL:HG22	20:C:115:ASP:H	1.75	0.52
21:D:157:PRO:O	21:D:159:ARG:HG2	2.10	0.52
40:W:26:GLN:OE1	40:W:29:ARG:NH2	2.42	0.52
49:a:914:C:OP2	51:m:3:ARG:NH1	2.42	0.52
1:Y:8:CYS:HB3	1:Y:55:CYS:SG	2.50	0.52
5:1:25:ARG:HD3	5:1:29:ARG:HH21	1.75	0.52
6:j:112:LEU:O	6:j:117:HIS:ND1	2.36	0.52
11:s:54:ARG:NH1	11:s:62:GLU:OE2	2.42	0.52
18:A:1349:U:H2'	18:A:1350:G:O4'	2.09	0.52
24:G:2:SER:HA	24:G:66:HIS:HD2	1.75	0.52
26:I:61:ALA:HB1	26:I:66:ILE:HG23	1.91	0.52
49:a:498:C:H4'	49:a:499:C:O5'	2.09	0.52
49:a:761:A:O2'	49:a:1506:U:O2	2.27	0.52
49:a:1324:C:H2'	49:a:1325:G:C8	2.45	0.52
15:z:4:ILE:HG22	15:z:6:SER:H	1.75	0.52
16:h:18:HIS:CD2	16:h:190:ASN:HD22	2.28	0.52
18:A:181:A:H2'	18:A:182:C:H6	1.74	0.52
18:A:1690:A:H2'	18:A:1691:A:C8	2.45	0.52
18:A:2486:U:P	41:X:19:GLN:HE21	2.33	0.52
32:O:42:ARG:HH11	32:O:42:ARG:HG2	1.75	0.52
42:Z:13:LEU:HB3	42:Z:17:GLU:HG3	1.92	0.52
49:a:78:G:H1	49:a:91:U:H3	1.55	0.52
49:a:184:U:H2'	49:a:185:G:C8	2.44	0.52
51:m:9:LYS:HZ3	51:m:10:ARG:HG2	1.74	0.52
54:t:10:PRO:CB	54:t:13:LYS:HE2	2.39	0.52
1:Y:27:ARG:O	1:Y:27:ARG:HG3	2.09	0.52
18:A:242:G:O2'	18:A:254:G:O6	2.27	0.52
18:A:618:C:OP1	18:A:653:G:N2	2.37	0.52
18:A:1225:G:N3	26:I:29:ARG:NH2	2.58	0.52
19:B:41:U:N3	19:B:45:G:OP2	2.41	0.52
33:P:70:VAL:HG12	33:P:83:ARG:HG3	1.92	0.52
49:a:1040:U:H2'	49:a:1041:G:H8	1.75	0.52
49:a:1104:G:H1'	49:a:1105:U:H5	1.74	0.52
49:a:1210:A:H2'	49:a:1211:C:H6	1.75	0.52
49:a:1354:G:H2'	49:a:1355:U:C6	2.44	0.52
50:i:83:ALA:HB1	50:i:87:ARG:HH21	1.75	0.52
3:g:12:THR:HG22	3:g:13:THR:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:n:39:ILE:HD11	9:n:112:LEU:HB3	1.92	0.51
18:A:2363:A:H2'	18:A:2364:C:C6	2.45	0.51
27:J:16:GLN:O	27:J:44:TYR:OH	2.22	0.51
49:a:1067:G:H22	49:a:1079:G:H1'	1.75	0.51
52:o:133:ARG:HH21	57:u:61:TRP:CD1	2.28	0.51
18:A:633:A:H2'	18:A:634:C:C6	2.45	0.51
18:A:929:C:H1'	18:A:1339:G:N2	2.25	0.51
18:A:1612:U:H2'	18:A:1613:G:C8	2.44	0.51
18:A:2005:C:H5''	20:C:225:VAL:HG11	1.92	0.51
18:A:2334:U:HO2'	18:A:2341:U:HO2'	1.59	0.51
18:A:2364:C:O2'	18:A:2365:A:H5''	2.10	0.51
33:P:73:ILE:HG22	33:P:75:GLY:H	1.75	0.51
40:W:25:ARG:O	40:W:29:ARG:HG3	2.11	0.51
43:2:9:VAL:HG12	43:2:10:ARG:HG2	1.92	0.51
49:a:582:U:O2	49:a:616:G:O6	2.28	0.51
49:a:997:A:H3'	49:a:998:G:C8	2.45	0.51
4:r:23:CYS:SG	4:r:57:CYS:SG	3.04	0.51
20:C:156:ALA:HB2	20:C:163:ILE:HG13	1.91	0.51
21:D:114:VAL:HG11	21:D:198:ILE:HD12	1.92	0.51
23:F:128:GLN:NE2	23:F:135:TYR:OH	2.43	0.51
37:T:65:ALA:HB1	37:T:71:LEU:HD12	1.92	0.51
49:a:1100:U:H2'	49:a:1101:C:C6	2.46	0.51
49:a:1206:U:O2'	55:y:78:ARG:HD2	2.11	0.51
55:y:6:LYS:HA	55:y:6:LYS:HE3	1.91	0.51
1:Y:28:ARG:NH2	18:A:1480:A:H8	2.07	0.51
2:c:6:ASP:OD1	2:c:6:ASP:N	2.42	0.51
18:A:382:A:OP2	39:V:82:ARG:NH2	2.43	0.51
49:a:508:C:H3'	49:a:509:G:H5''	1.92	0.51
50:i:69:THR:HG21	50:i:75:VAL:HG21	1.91	0.51
2:c:12:THR:HG21	2:c:21:ARG:HH11	1.74	0.51
8:l:31:ARG:NH1	8:l:38:ASP:OD2	2.42	0.51
18:A:331:U:HO2'	18:A:332:C:H6	1.58	0.51
18:A:2757:C:OP1	18:A:2889:A:O2'	2.28	0.51
23:F:45:MET:HE2	23:F:159:MET:HE3	1.92	0.51
25:H:124:ILE:O	25:H:125:LYS:HG2	2.11	0.51
27:J:23:ALA:O	27:J:28:PRO:HD2	2.11	0.51
27:J:74:THR:HG21	27:J:114:LYS:HG2	1.91	0.51
49:a:1056:C:H3'	49:a:1058:U:OP2	2.09	0.51
49:a:1183:U:O2'	57:u:29:ARG:HB2	2.10	0.51
50:i:23:TYR:CZ	53:p:11:LYS:HG2	2.45	0.51
32:O:95:THR:HG22	32:O:115:LEU:HD23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R:58:ARG:O	35:R:62:ILE:HG12	2.10	0.51
49:a:120:G:H4'	49:a:291:C:O2'	2.10	0.51
49:a:190:U:H2'	49:a:191:C:C6	2.45	0.51
49:a:335:C:H2'	49:a:336:A:H8	1.74	0.51
49:a:555:G:O2'	49:a:801:G:OP2	2.27	0.51
49:a:956:A:P	57:u:29:ARG:HH22	2.33	0.51
8:l:76:ASP:O	8:l:80:ASN:ND2	2.40	0.51
9:n:79:ARG:NH2	9:n:81:SER:O	2.43	0.51
18:A:1410:C:H5''	32:O:71:ARG:HH11	1.76	0.51
18:A:3082:U:H2'	18:A:3083:A:H8	1.75	0.51
19:B:1:G:H2'	19:B:2:U:C6	2.46	0.51
35:R:3:ARG:HH12	35:R:5:LYS:HE3	1.76	0.51
49:a:1197:U:H2'	49:a:1198:C:C6	2.46	0.51
13:w:12:LYS:NZ	49:a:598:C:O2	2.43	0.51
18:A:2495:G:OP1	41:X:18:ALA:HB1	2.11	0.51
26:I:122:LYS:O	26:I:126:LEU:HD12	2.11	0.51
13:w:20:ILE:N	13:w:38:GLY:O	2.43	0.51
18:A:383:U:H5'	39:V:72:MET:HE1	1.92	0.51
18:A:1573:U:O2	18:A:1597:G:C6	2.64	0.51
18:A:2862:G:OP1	21:D:85:ARG:NH2	2.44	0.51
19:B:51:G:H5''	33:P:76:ASP:OD2	2.11	0.51
49:a:492:U:H2'	49:a:493:A:C8	2.45	0.51
49:a:1220:A:H62	49:a:1281:A:N6	2.09	0.51
56:4:284:THR:O	56:4:285:ARG:HG3	2.10	0.51
4:r:41:TYR:HE1	4:r:54:THR:HG23	1.75	0.51
7:k:182:ARG:NH2	9:n:43:GLU:HB3	2.26	0.51
18:A:623:A:OP1	35:R:53:ARG:NH1	2.44	0.51
18:A:745:G:OP1	46:e:19:THR:OG1	2.23	0.51
18:A:1900:C:H2'	18:A:1901:C:C6	2.46	0.51
18:A:2610:C:O2'	41:X:41:ARG:NH1	2.43	0.51
27:J:15:ILE:O	27:J:44:TYR:OH	2.29	0.51
49:a:1221:U:OP2	51:m:119:ARG:NH2	2.44	0.51
2:c:47:THR:HG22	2:c:48:HIS:H	1.76	0.50
5:1:18:ARG:HH12	49:a:884:G:H5'	1.76	0.50
18:A:256:A:H2'	18:A:257:A:H8	1.76	0.50
18:A:332:C:N4	18:A:349:G:O6	2.43	0.50
18:A:482:U:H2'	18:A:483:G:H8	1.75	0.50
18:A:1234:U:H2'	18:A:1235:U:C6	2.45	0.50
23:F:154:ASP:OD1	23:F:154:ASP:N	2.43	0.50
25:H:9:VAL:HG13	25:H:12:LEU:HB2	1.93	0.50
54:t:108:ARG:C	54:t:110:ARG:H	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:j:52:GLU:HA	6:j:55:LYS:HE3	1.92	0.50
16:h:210:ALA:O	16:h:214:THR:HG22	2.11	0.50
18:A:332:C:H2'	18:A:333:C:H6	1.76	0.50
18:A:2230:C:O2'	18:A:3044:A:N3	2.44	0.50
31:N:50:ALA:HB1	31:N:121:ALA:HB1	1.92	0.50
49:a:1277:U:HO2'	54:t:14:ARG:HH22	1.58	0.50
50:i:169:ARG:NH1	50:i:171:GLY:O	2.45	0.50
4:r:33:LYS:NZ	4:r:33:LYS:HB3	2.27	0.50
6:j:192:GLU:OE1	6:j:192:GLU:N	2.44	0.50
14:x:20:ARG:HB3	14:x:78:GLU:HB3	1.93	0.50
18:A:1690:A:H2'	18:A:1691:A:H8	1.76	0.50
26:I:87:VAL:HG12	26:I:91:LYS:HG3	1.94	0.50
32:O:72:ASP:OD1	32:O:73:LYS:N	2.44	0.50
50:i:23:TYR:CD2	50:i:23:TYR:O	2.64	0.50
53:p:92:LEU:HD12	53:p:93:PRO:HD2	1.93	0.50
15:z:53:ALA:O	15:z:56:ARG:NH2	2.45	0.50
18:A:544:U:OP2	38:U:70:ARG:NH2	2.39	0.50
18:A:1569:A:C5	18:A:1570:C:H1'	2.47	0.50
18:A:1696:G:O2'	18:A:1736:G:O6	2.28	0.50
18:A:2544:U:O2'	18:A:2545:G:OP2	2.26	0.50
18:A:2761:U:H2'	18:A:2762:C:H6	1.77	0.50
19:B:76:G:H21	40:W:94:HIS:CD2	2.29	0.50
30:M:104:VAL:HG11	30:M:110:VAL:HG23	1.93	0.50
49:a:384:G:H2'	49:a:385:C:C6	2.47	0.50
49:a:444:A:H2'	49:a:445:C:C6	2.46	0.50
49:a:584:G:H2'	49:a:585:U:O4'	2.11	0.50
49:a:821:C:H2'	49:a:822:U:O4'	2.12	0.50
49:a:1167:G:H5'	49:a:1168:G:C8	2.46	0.50
53:p:40:VAL:HG23	53:p:73:LEU:HB2	1.93	0.50
3:g:12:THR:HG22	3:g:13:THR:N	2.26	0.50
11:s:81:LEU:HD23	11:s:98:ILE:HD11	1.92	0.50
16:h:161:VAL:HG12	16:h:184:ILE:HG12	1.93	0.50
18:A:911:U:H2'	18:A:912:C:C6	2.46	0.50
18:A:1552:A:N6	18:A:1616:A:OP2	2.45	0.50
18:A:2398:C:H2'	18:A:2399:A:C8	2.46	0.50
31:N:63:LYS:HD2	31:N:65:TRP:CZ2	2.47	0.50
48:5:29:C:H2'	48:5:30:G:H8	1.76	0.50
49:a:390:U:H2'	49:a:391:G:C8	2.46	0.50
6:j:50:LEU:O	6:j:54:GLN:HG2	2.12	0.50
11:s:57:LEU:HD23	11:s:58:THR:N	2.26	0.50
18:A:365:U:H2'	18:A:366:G:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:551:G:N2	18:A:554:A:OP2	2.37	0.50
18:A:672:C:H2'	18:A:673:C:C6	2.47	0.50
18:A:858:A:O2'	18:A:1877:U:OP1	2.30	0.50
18:A:1083:G:C2'	18:A:1084:U:H5'	2.42	0.50
18:A:2470:A:H2'	18:A:2471:A:C8	2.46	0.50
35:R:73:ASP:O	35:R:114:ARG:NH2	2.45	0.50
38:U:62:ARG:HG3	38:U:81:ARG:HH12	1.76	0.50
49:a:60:U:H2'	49:a:61:G:C8	2.46	0.50
49:a:579:U:O2	49:a:619:G:O6	2.28	0.50
49:a:1036:U:H2'	49:a:1037:G:C8	2.46	0.50
49:a:1112:C:N4	49:a:1123:G:O6	2.44	0.50
4:r:24:SER:CA	49:a:826:U:OP1	2.56	0.50
18:A:93:A:O3'	42:Z:43:ASN:ND2	2.41	0.50
18:A:403:U:O2'	18:A:422:A:N3	2.43	0.50
18:A:1185:A:N7	56:4:292:GLY:HA2	2.27	0.50
18:A:1809:U:H2'	18:A:1810:A:C8	2.46	0.50
18:A:3117:U:H2'	18:A:3118:U:C6	2.47	0.50
48:5:28:U:H2'	48:5:29:C:C6	2.47	0.50
49:a:185:G:N2	49:a:203:U:O2	2.35	0.50
49:a:1311:G:H3'	49:a:1312:U:O4'	2.11	0.50
4:r:21:VAL:HG23	4:r:22:PHE:H	1.75	0.50
8:l:92:ARG:NH2	8:l:94:ASP:OD2	2.45	0.50
18:A:502:C:H2'	18:A:503:A:H8	1.75	0.50
18:A:1157:G:H4'	40:W:52:ARG:HH12	1.76	0.50
18:A:1564:A:H3'	18:A:1565:A:H8	1.77	0.50
18:A:2097:G:H2'	18:A:2098:U:H6	1.76	0.50
18:A:2873:U:H2'	18:A:2874:C:H6	1.76	0.50
30:M:84:ASN:HB2	30:M:118:LEU:HD12	1.92	0.50
49:a:273:A:N6	49:a:274:A:N1	2.60	0.50
9:n:98:LEU:HB2	9:n:102:GLY:H	1.77	0.50
18:A:2412:U:H2'	18:A:2413:G:H8	1.76	0.50
18:A:2515:U:O2'	18:A:2598:C:O2	2.29	0.50
18:A:2922:U:H2'	18:A:2923:C:C6	2.47	0.50
22:E:129:GLU:OE2	22:E:129:GLU:N	2.45	0.50
24:G:69:SER:O	24:G:73:ILE:HG12	2.12	0.50
40:W:154:GLY:HA2	40:W:181:VAL:O	2.12	0.50
49:a:996:G:N2	49:a:998:G:H3'	2.25	0.50
53:p:36:VAL:HG12	53:p:76:ILE:HD13	1.93	0.50
55:y:54:GLY:O	55:y:55:ARG:NH1	2.43	0.50
16:h:169:GLU:HB3	16:h:172:ALA:HB3	1.93	0.49
18:A:131:A:H2'	18:A:132:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:402:G:H2'	22:E:138:THR:HG21	1.94	0.49
18:A:1559:A:N6	18:A:1613:G:O6	2.45	0.49
18:A:2761:U:H2'	18:A:2762:C:C6	2.47	0.49
32:O:42:ARG:HG2	32:O:42:ARG:NH1	2.27	0.49
32:O:45:ARG:O	32:O:49:GLU:HG3	2.12	0.49
45:d:23:LEU:HD12	45:d:23:LEU:O	2.11	0.49
46:e:29:ARG:NH1	46:e:41:THR:O	2.45	0.49
49:a:489:A:H8	49:a:523:U:O2'	1.90	0.49
49:a:959:A:N6	49:a:1205:U:OP1	2.45	0.49
49:a:1022:G:H2'	49:a:1023:U:O4'	2.12	0.49
51:m:35:LYS:HD2	51:m:38:LEU:HD12	1.94	0.49
51:m:68:ASN:HB3	51:m:130:GLY:HA3	1.94	0.49
53:p:43:PRO:O	53:p:71:LYS:NZ	2.28	0.49
53:p:50:CYS:HB2	53:p:64:HIS:CD2	2.47	0.49
8:l:91:LEU:HD21	49:a:716:U:H5''	1.94	0.49
14:x:92:GLU:OE2	14:x:94:LEU:HD13	2.12	0.49
16:h:165:ASP:OD2	16:h:168:LYS:HB2	2.13	0.49
18:A:329:U:O2'	18:A:446:G:N2	2.46	0.49
34:Q:48:ARG:HG3	34:Q:95:LYS:HG3	1.93	0.49
37:T:17:VAL:O	37:T:107:THR:OG1	2.19	0.49
38:U:52:VAL:HG21	38:U:86:LEU:HD22	1.93	0.49
49:a:688:C:H2'	49:a:689:A:H8	1.77	0.49
49:a:1334:C:H2'	49:a:1335:G:C8	2.46	0.49
3:g:6:HIS:CE1	23:F:71:LYS:H	2.30	0.49
7:k:50:VAL:HG22	7:k:51:LYS:H	1.78	0.49
18:A:292:G:N2	18:A:343:U:H2'	2.28	0.49
49:a:175:A:C2	49:a:176:A:C8	3.00	0.49
49:a:1206:U:OP1	54:t:102:ARG:HA	2.12	0.49
49:a:1211:C:H2'	49:a:1212:A:H8	1.78	0.49
56:4:289:PHE:HE2	56:4:408:GLY:HA2	1.78	0.49
18:A:335:G:HO2'	18:A:336:C:P	2.34	0.49
18:A:2030:C:O2	20:C:50:THR:OG1	2.26	0.49
49:a:954:C:O3'	53:p:59:LYS:HE2	2.11	0.49
49:a:1251:G:H2'	49:a:1252:G:C8	2.47	0.49
35:R:120:ASP:OD2	35:R:123:ALA:N	2.46	0.49
49:a:156:G:N2	49:a:159:A:OP2	2.45	0.49
49:a:504:G:H2'	49:a:505:C:C6	2.48	0.49
53:p:59:LYS:O	53:p:62:ARG:NH1	2.40	0.49
6:j:197:GLU:O	49:a:12:A:N6	2.46	0.49
24:G:24:LEU:HD22	24:G:73:ILE:HD12	1.95	0.49
49:a:940:A:H1'	55:y:55:ARG:HE	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:j:26:PHE:O	6:j:30:PRO:HD3	2.12	0.49
6:j:80:LYS:HB2	6:j:83:ASP:OD1	2.12	0.49
18:A:114:G:OP2	18:A:116:A:O2'	2.24	0.49
18:A:979:G:H2'	18:A:980:C:C6	2.48	0.49
18:A:1159:C:H2'	18:A:1160:G:C8	2.48	0.49
18:A:2640:G:H5''	30:M:65:LYS:HD2	1.95	0.49
20:C:177:MET:HE3	20:C:177:MET:HB3	1.73	0.49
38:U:81:ARG:NH1	38:U:81:ARG:HB2	2.28	0.49
49:a:786:C:H2'	49:a:787:A:H8	1.77	0.49
49:a:895:A:H4'	49:a:896:A:O5'	2.12	0.49
11:s:107:VAL:HG23	11:s:110:ARG:HB2	1.94	0.49
12:v:8:LYS:NZ	49:a:638:A:OP1	2.30	0.49
18:A:429:A:H2'	18:A:430:A:H8	1.78	0.49
18:A:896:A:OP1	20:C:218:ARG:NH2	2.29	0.49
18:A:1621:C:H2'	18:A:1622:G:C8	2.48	0.49
18:A:1706:A:H2'	18:A:1707:G:H8	1.77	0.49
18:A:1720:G:O2'	20:C:100:GLY:O	2.24	0.49
18:A:2527:G:N2	23:F:136:THR:HG21	2.27	0.49
23:F:42:VAL:HG12	23:F:97:THR:HG22	1.95	0.49
24:G:12:PRO:O	24:G:12:PRO:HD2	2.09	0.49
49:a:86:G:H2'	49:a:87:G:C8	2.48	0.49
1:Y:21:SER:O	1:Y:22:HIS:C	2.54	0.49
18:A:2074:G:N2	18:A:2110:U:O4	2.46	0.49
18:A:2094:G:O2'	18:A:2095:G:H8	1.96	0.49
18:A:2390:U:O2'	18:A:2391:G:O5'	2.29	0.49
23:F:136:THR:HG23	23:F:162:THR:HB	1.95	0.49
49:a:407:A:H2'	49:a:408:G:C8	2.48	0.49
49:a:1497:A:H2'	49:a:1498:C:C6	2.48	0.49
56:4:437:GLY:HA3	56:4:455:VAL:HG12	1.94	0.49
18:A:436:C:H2'	18:A:437:G:O4'	2.13	0.49
18:A:1227:C:H2'	18:A:1228:A:C4	2.48	0.49
49:a:632:U:O4	49:a:732:G:O2'	2.22	0.49
49:a:804:U:H2'	49:a:805:A:H8	1.78	0.49
49:a:1432:C:H2'	49:a:1433:C:C6	2.48	0.49
3:g:41:CYS:O	3:g:42:HIS:C	2.56	0.48
18:A:621:U:H2'	18:A:622:C:C6	2.48	0.48
18:A:2288:C:H2'	18:A:2289:C:H6	1.78	0.48
20:C:273:ARG:NE	20:C:276:LYS:HG2	2.24	0.48
40:W:66:ILE:H	40:W:66:ILE:HD12	1.78	0.48
48:5:4:G:O2'	48:5:5:G:H8	1.96	0.48
49:a:414:A:H62	49:a:430:A:H61	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:1071:U:H5'	49:a:1153:U:OP1	2.12	0.48
53:p:24:LYS:HE2	53:p:92:LEU:HD13	1.94	0.48
5:1:25:ARG:HA	5:1:28:ARG:HH21	1.78	0.48
18:A:1003:A:O2'	18:A:1005:A:N7	2.38	0.48
18:A:1084:U:O2'	18:A:1085:G:OP1	2.31	0.48
18:A:1303:U:H4'	36:S:82:THR:HG23	1.95	0.48
18:A:2377:G:H2'	18:A:2378:U:O4'	2.13	0.48
18:A:2942:G:O2'	18:A:3068:U:OP1	2.24	0.48
20:C:206:TRP:O	20:C:211:ARG:HD3	2.13	0.48
25:H:5:LEU:O	25:H:16:GLY:N	2.35	0.48
49:a:443:C:N4	49:a:444:A:H62	2.10	0.48
49:a:929:G:H2'	49:a:930:C:C6	2.48	0.48
49:a:1425:G:H5'	49:a:1426:C:H5	1.78	0.48
56:4:457:ALA:HB3	56:4:458:PRO:HD3	1.95	0.48
8:l:15:ASP:OD1	8:l:15:ASP:N	2.36	0.48
13:w:7:LEU:HG	13:w:18:TYR:HB3	1.94	0.48
40:W:161:GLN:OE1	40:W:161:GLN:N	2.46	0.48
49:a:411:A:O3'	49:a:412:U:H4'	2.14	0.48
49:a:960:A:O2'	49:a:961:C:OP1	2.25	0.48
49:a:1051:C:H2'	49:a:1052:G:C8	2.48	0.48
52:o:66:GLN:HG3	52:o:69:LYS:HE3	1.95	0.48
52:o:87:LEU:HD22	52:o:95:GLN:HB3	1.95	0.48
56:4:353:VAL:HA	56:4:356:GLU:HG2	1.96	0.48
18:A:668:U:H2'	18:A:669:G:C8	2.48	0.48
18:A:1199:U:H2'	18:A:1200:U:C6	2.48	0.48
18:A:1222:C:H2'	18:A:1223:U:H6	1.77	0.48
56:4:289:PHE:CZ	56:4:407:MET:HB3	2.47	0.48
57:u:35:ARG:O	57:u:36:LYS:C	2.55	0.48
13:w:65:GLN:NE2	49:a:133:C:O3'	2.46	0.48
16:h:97:LEU:HD13	49:a:1083:C:H3'	1.94	0.48
18:A:935:A:H4'	18:A:951:G:N2	2.29	0.48
18:A:1565:A:H2'	18:A:1566:A:C5	2.48	0.48
23:F:147:GLU:OE1	23:F:147:GLU:N	2.36	0.48
29:L:107:ARG:HH12	34:Q:33:GLU:HB2	1.79	0.48
48:5:32:G:O2'	49:a:1322:G:O2'	2.31	0.48
49:a:604:U:H2'	49:a:605:G:H8	1.77	0.48
49:a:725:A:H2'	49:a:726:G:H8	1.79	0.48
56:4:370:LYS:HZ1	56:4:395:ARG:HH11	1.62	0.48
18:A:2294:A:H2'	18:A:2295:C:C6	2.49	0.48
23:F:55:LYS:HA	23:F:58:ASN:HD21	1.79	0.48
25:H:10:GLU:OE1	25:H:11:HIS:ND1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:444:A:N6	49:a:471:G:O6	2.47	0.48
50:i:56:ILE:HG12	50:i:64:ARG:C	2.39	0.48
3:g:9:TYR:CD2	3:g:25:ARG:HG2	2.48	0.48
4:r:24:SER:C	4:r:26:LYS:N	2.65	0.48
18:A:228:A:H2'	18:A:229:U:H5''	1.96	0.48
18:A:1201:G:O3'	26:I:40:ARG:NH2	2.46	0.48
18:A:2395:U:OP2	18:A:2397:C:N4	2.27	0.48
28:K:55:ILE:HD12	28:K:132:HIS:HD2	1.78	0.48
49:a:398:C:H2'	49:a:399:G:H8	1.79	0.48
49:a:1208:A:C5	55:y:83:HIS:CE1	3.02	0.48
57:u:40:CYS:O	57:u:41:ARG:C	2.55	0.48
7:k:90:GLU:O	7:k:94:LYS:HD3	2.13	0.48
10:q:58:HIS:CE1	49:a:667:A:H5''	2.49	0.48
16:h:70:VAL:HG21	16:h:96:TRP:CE3	2.48	0.48
18:A:225:A:H1'	18:A:230:G:N2	2.28	0.48
18:A:273:A:H62	18:A:313:G:H21	1.62	0.48
18:A:999:C:H2'	18:A:1000:C:C6	2.48	0.48
18:A:2654:A:N3	18:A:2654:A:H2'	2.29	0.48
18:A:2679:G:H2'	18:A:2680:C:C6	2.49	0.48
25:H:100:VAL:O	25:H:104:ILE:HG12	2.14	0.48
40:W:109:GLU:HA	40:W:132:GLU:HA	1.95	0.48
49:a:512:A:O2'	49:a:513:A:OP1	2.29	0.48
49:a:1285:C:H3'	49:a:1286:G:H8	1.79	0.48
52:o:32:ARG:HG3	52:o:33:LYS:H	1.79	0.48
56:4:248:VAL:HG12	56:4:327:LEU:HB3	1.96	0.48
11:s:30:ARG:NH2	11:s:59:SER:HB3	2.29	0.48
18:A:295:U:H3	18:A:340:A:H61	1.59	0.48
18:A:897:A:C2	20:C:226:MET:HG2	2.49	0.48
18:A:2391:G:H2'	18:A:2392:A:C8	2.49	0.48
18:A:2764:C:O2'	18:A:2964:A:N3	2.42	0.48
19:B:46:A:C4	19:B:47:A:C8	3.01	0.48
25:H:109:GLY:N	25:H:110:PRO:HD2	2.29	0.48
29:L:115:VAL:HG13	29:L:121:VAL:HG21	1.96	0.48
49:a:323:U:H2'	49:a:324:G:O4'	2.13	0.48
49:a:976:A:C2	57:u:5:ALA:HB2	2.48	0.48
49:a:1027:G:C5'	57:u:4:LYS:HG3	2.42	0.48
49:a:1125:G:N2	49:a:1127:A:H62	2.11	0.48
49:a:1218:C:O2'	49:a:1317:U:O4'	2.21	0.48
56:4:380:ALA:HA	56:4:383:ARG:HB2	1.96	0.48
34:Q:71:ARG:HG2	34:Q:73:PHE:CZ	2.49	0.48
40:W:9:ASN:HD21	40:W:61:HIS:CE1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:279:A:H4'	49:a:280:C:H5'	1.95	0.48
49:a:1018:C:H2'	49:a:1020:G:N7	2.29	0.48
49:a:1170:U:H4'	50:i:10:PHE:CE1	2.49	0.48
50:i:22:TRP:NE1	57:u:54:PRO:HG3	2.28	0.48
53:p:8:ILE:HG23	53:p:100:ILE:HG13	1.95	0.48
55:y:3:ARG:HH12	55:y:10:PHE:HB2	1.79	0.48
1:Y:25:THR:HG22	1:Y:26:SER:N	2.24	0.47
18:A:2249:G:H2'	18:A:2250:A:H8	1.79	0.47
18:A:2985:G:H1'	24:G:144:GLN:HE22	1.79	0.47
18:A:3105:C:O2'	18:A:3107:G:OP2	2.32	0.47
24:G:81:THR:HB	24:G:82:GLU:OE1	2.14	0.47
36:S:8:LYS:HD3	36:S:40:ALA:HB2	1.96	0.47
39:V:35:VAL:HB	39:V:38:VAL:HG22	1.96	0.47
49:a:269:U:H2'	49:a:270:A:H8	1.78	0.47
49:a:393:A:C2	49:a:394:G:C8	3.02	0.47
49:a:907:G:C2	49:a:909:G:C8	3.02	0.47
49:a:1002:U:H2'	49:a:1003:C:C6	2.48	0.47
50:i:62:ARG:HB2	50:i:99:GLN:HE22	1.79	0.47
3:g:35:VAL:HG23	3:g:36:GLU:N	2.28	0.47
7:k:75:TYR:N	7:k:91:GLU:OE1	2.41	0.47
13:w:32:ARG:CG	49:a:587:A:C6	2.97	0.47
14:x:38:VAL:O	14:x:59:VAL:N	2.47	0.47
15:z:68:HIS:ND1	15:z:70:ASN:OD1	2.46	0.47
24:G:2:SER:OG	24:G:55:ARG:NH2	2.45	0.47
27:J:83:LYS:HD3	27:J:83:LYS:HA	1.69	0.47
49:a:505:C:H2'	49:a:506:C:C6	2.49	0.47
49:a:606:U:H2'	49:a:607:G:C8	2.49	0.47
49:a:1217:A:H2'	49:a:1218:C:C6	2.48	0.47
49:a:1257:G:H2'	49:a:1258:C:O4'	2.14	0.47
49:a:1488:G:OP1	49:a:1491:A:H4'	2.14	0.47
52:o:97:GLY:O	52:o:100:ARG:HG2	2.13	0.47
54:t:22:ILE:HG23	54:t:67:GLU:CD	2.39	0.47
56:4:246:PRO:HD2	56:4:295:PHE:HA	1.96	0.47
57:u:59:SER:HG	57:u:61:TRP:HE3	1.62	0.47
6:j:54:GLN:HB3	6:j:58:PHE:CE2	2.49	0.47
7:k:83:ALA:O	7:k:87:LYS:HG2	2.14	0.47
16:h:186:ILE:HD11	16:h:203:ASN:H	1.78	0.47
18:A:68:A:H5''	18:A:70:A:C8	2.49	0.47
18:A:341:C:H2'	18:A:342:C:C5	2.49	0.47
18:A:1185:A:OP1	56:4:288:GLU:HB3	2.15	0.47
18:A:1705:C:H2'	18:A:1706:A:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:37:A:H2'	49:a:38:C:C6	2.49	0.47
49:a:1054:G:H2'	49:a:1055:U:H4'	1.97	0.47
49:a:1108:C:H2'	49:a:1109:C:C6	2.50	0.47
7:k:75:TYR:CE2	49:a:1059:G:H5'	2.49	0.47
7:k:196:LYS:HG2	7:k:199:ARG:HH22	1.78	0.47
16:h:57:VAL:HG21	16:h:217:ILE:HD11	1.96	0.47
18:A:218:A:N3	18:A:234:U:O2'	2.33	0.47
18:A:1905:G:N2	18:A:1920:G:O6	2.48	0.47
18:A:3045:C:H2'	18:A:3046:C:O4'	2.14	0.47
21:D:38:ARG:HB3	21:D:51:GLN:HB3	1.96	0.47
38:U:95:LEU:O	38:U:95:LEU:HD23	2.15	0.47
41:X:85:ARG:HG3	41:X:86:PRO:HD2	1.96	0.47
49:a:1151:A:H8	49:a:1151:A:OP2	1.98	0.47
49:a:1247:G:O2'	49:a:1249:G:O6	2.32	0.47
4:r:23:CYS:HG	4:r:60:HIS:CG	2.32	0.47
7:k:44:ASN:ND2	49:a:21:U:OP1	2.38	0.47
8:l:6:ILE:HG12	8:l:90:VAL:HG13	1.94	0.47
13:w:32:ARG:NH1	49:a:588:A:C8	2.82	0.47
16:h:167:ASN:O	16:h:170:HIS:ND1	2.38	0.47
18:A:365:U:H2'	18:A:366:G:C8	2.49	0.47
18:A:1367:G:N2	35:R:37:GLU:OE2	2.38	0.47
18:A:2317:G:H5'	25:H:25:TYR:CD1	2.49	0.47
24:G:8:PRO:HB2	24:G:50:ALA:HB1	1.96	0.47
49:a:664:U:H2'	49:a:665:G:O4'	2.14	0.47
54:t:60:ILE:HA	54:t:64:LEU:HB2	1.97	0.47
18:A:986:G:O2'	31:N:71:ASP:OD1	2.32	0.47
18:A:1186:G:H4'	18:A:1187:A:OP2	2.13	0.47
18:A:1590:G:H2'	18:A:1591:U:C6	2.50	0.47
18:A:1606:G:H8	18:A:1606:G:OP2	1.97	0.47
18:A:2147:U:H2'	18:A:2148:C:C6	2.49	0.47
48:5:28:U:H2'	48:5:29:C:H6	1.80	0.47
49:a:1277:U:HO2'	54:t:14:ARG:NH2	2.13	0.47
51:m:138:ARG:NH1	51:m:139:GLU:OE2	2.46	0.47
6:j:33:PRO:HB3	49:a:427:U:OP1	2.14	0.47
18:A:287:A:H1'	18:A:289:A:C8	2.50	0.47
18:A:389:G:H21	18:A:412:A:H61	1.62	0.47
18:A:635:G:O2'	18:A:636:U:O5'	2.31	0.47
18:A:1072:G:OP1	31:N:87:LYS:NZ	2.43	0.47
18:A:1770:G:OP1	18:A:1937:U:O2'	2.20	0.47
18:A:2365:A:H2'	18:A:2366:C:H6	1.80	0.47
18:A:2603:G:H2'	18:A:2604:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:3057:U:H2'	18:A:3058:A:H8	1.79	0.47
19:B:60:G:H4'	33:P:12:GLU:HB3	1.97	0.47
26:I:3:LYS:HD3	26:I:6:LYS:HE3	1.95	0.47
30:M:55:MET:HE3	30:M:59:MET:HE3	1.97	0.47
48:5:41:C:O2	49:a:1321:A:O2'	2.30	0.47
49:a:494:C:H2'	49:a:495:G:H8	1.79	0.47
49:a:606:U:H2'	49:a:607:G:H8	1.80	0.47
49:a:1039:C:H2'	49:a:1040:U:C6	2.50	0.47
49:a:1102:A:H2'	49:a:1103:U:O4'	2.14	0.47
52:o:51:ASP:OD1	52:o:53:ARG:NE	2.47	0.47
57:u:3:LYS:O	57:u:7:VAL:HG23	2.14	0.47
18:A:290:C:O2'	18:A:291:C:O4'	2.32	0.47
18:A:502:C:H2'	18:A:503:A:C8	2.50	0.47
18:A:1650:G:H2'	18:A:1651:C:C6	2.50	0.47
18:A:2552:A:H2'	18:A:2553:G:H8	1.80	0.47
18:A:2697:U:O2'	56:4:286:ARG:HB2	2.15	0.47
26:I:98:LYS:HD2	26:I:101:LYS:HE3	1.97	0.47
27:J:100:ALA:O	27:J:140:THR:OG1	2.27	0.47
49:a:45:G:C2	49:a:46:G:N7	2.83	0.47
49:a:1458:G:H2'	49:a:1459:G:O4'	2.15	0.47
53:p:19:ASP:HB2	53:p:72:ARG:HH12	1.79	0.47
3:g:28:LYS:HD2	3:g:33:ILE:HG23	1.96	0.47
9:n:98:LEU:HA	9:n:98:LEU:HD23	1.81	0.47
12:v:65:ARG:HD3	49:a:735:G:OP1	2.15	0.47
18:A:308:U:H2'	18:A:309:G:C8	2.48	0.47
18:A:435:A:H2'	18:A:436:C:C6	2.50	0.47
18:A:929:C:H1'	18:A:1339:G:H21	1.79	0.47
18:A:2715:U:H5''	18:A:2794:G:H5''	1.97	0.47
18:A:3038:C:OP1	32:O:42:ARG:NH2	2.47	0.47
19:B:81:U:H2'	19:B:82:A:C8	2.50	0.47
26:I:40:ARG:HA	26:I:43:LEU:HB2	1.97	0.47
27:J:11:ILE:HD11	27:J:60:ILE:HD12	1.96	0.47
42:Z:21:LYS:HB2	42:Z:21:LYS:HE2	1.61	0.47
49:a:598:C:H5'	49:a:599:U:H5''	1.96	0.47
49:a:1094:C:H2'	49:a:1095:U:C6	2.50	0.47
49:a:1096:U:N3	49:a:1166:G:N3	2.63	0.47
49:a:1110:A:C8	49:a:1127:A:C5	3.03	0.47
49:a:1219:A:H8	49:a:1283:U:H3	1.50	0.47
49:a:1414:C:H2'	49:a:1415:G:O4'	2.14	0.47
49:a:1506:U:H2'	49:a:1507:G:H8	1.80	0.47
50:i:12:LEU:HD11	57:u:51:GLY:HA3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:i:110:SER:O	50:i:110:SER:OG	2.30	0.47
3:g:29:GLN:O	3:g:30:SER:C	2.55	0.47
7:k:101:LEU:O	7:k:102:ILE:HD13	2.15	0.47
12:v:74:ASP:OD2	12:v:77:ARG:N	2.36	0.47
18:A:59:G:H5'	18:A:60:A:OP2	2.15	0.47
18:A:1545:C:H2'	18:A:1546:A:C8	2.46	0.47
18:A:2008:A:H5''	20:C:212:MET:HG3	1.97	0.47
18:A:2601:A:O2'	33:P:127:PHE:O	2.28	0.47
27:J:74:THR:HG21	27:J:114:LYS:HA	1.97	0.47
37:T:18:ARG:HH11	37:T:18:ARG:HG2	1.80	0.47
39:V:34:LEU:HD11	39:V:63:GLU:HB3	1.97	0.47
49:a:37:A:H2'	49:a:38:C:H6	1.80	0.47
49:a:496:U:H5''	49:a:497:G:N2	2.30	0.47
49:a:552:A:H5'	49:a:553:A:OP2	2.15	0.47
49:a:924:G:N2	52:o:146:GLN:OE1	2.46	0.47
49:a:968:U:H1'	55:y:55:ARG:HH11	1.78	0.47
49:a:1005:G:H2'	49:a:1006:U:C6	2.50	0.47
52:o:59:PHE:HZ	52:o:87:LEU:HD11	1.80	0.47
11:s:57:LEU:HD23	11:s:58:THR:H	1.79	0.46
15:z:26:SER:HB3	49:a:1442:G:H5''	1.97	0.46
18:A:1105:C:O2'	18:A:1118:A:N3	2.42	0.46
18:A:1673:A:H2'	18:A:1673:A:N3	2.28	0.46
18:A:1704:U:H2'	18:A:1705:C:C6	2.50	0.46
18:A:1716:A:H2'	18:A:1718:C:C5	2.50	0.46
18:A:1758:G:H21	18:A:1759:A:N6	2.12	0.46
18:A:1764:A:H2'	18:A:1765:A:C8	2.50	0.46
18:A:2070:A:H2'	18:A:2071:A:C8	2.50	0.46
18:A:2297:U:H2'	18:A:2298:U:C6	2.51	0.46
24:G:58:ASP:O	24:G:63:ARG:NH1	2.40	0.46
49:a:579:U:H2'	49:a:580:G:H8	1.80	0.46
49:a:980:G:H22	49:a:1023:U:H3	1.61	0.46
49:a:1089:C:C2	49:a:1090:A:C8	3.03	0.46
50:i:143:GLN:HG2	50:i:145:ASN:OD1	2.15	0.46
51:m:93:PRO:O	51:m:97:THR:HG23	2.16	0.46
53:p:53:ARG:HD2	57:u:45:ARG:NH1	2.30	0.46
13:w:32:ARG:HG3	49:a:587:A:C6	2.49	0.46
16:h:100:MET:HG3	16:h:101:LEU:N	2.30	0.46
18:A:292:G:H22	18:A:343:U:H2'	1.80	0.46
18:A:996:G:N2	18:A:997:G:O6	2.48	0.46
20:C:262:LYS:HG2	20:C:263:PRO:HD2	1.96	0.46
26:I:55:THR:HA	26:I:58:LYS:HD2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:W:102:ARG:HG2	40:W:138:LEU:HD11	1.98	0.46
41:X:43:THR:OG1	41:X:45:PHE:O	2.25	0.46
48:5:9:G:O2'	48:5:10:G:N7	2.48	0.46
49:a:23:C:H2'	49:a:24:U:C6	2.50	0.46
49:a:1329:G:O2'	49:a:1356:G:O6	2.23	0.46
53:p:15:HIS:HB2	53:p:70:HIS:CD2	2.49	0.46
53:p:52:ILE:HB	57:u:41:ARG:NE	2.31	0.46
55:y:50:ALA:HA	55:y:59:PRO:HA	1.95	0.46
1:Y:52:CYS:SG	1:Y:55:CYS:SG	3.05	0.46
1:Y:53:THR:HG21	18:A:2313:A:O2'	2.16	0.46
7:k:192:ALA:O	7:k:196:LYS:HG3	2.16	0.46
18:A:9:U:O2	18:A:2850:C:H4'	2.16	0.46
18:A:278:A:N1	18:A:309:G:C6	2.83	0.46
18:A:453:U:H2'	18:A:454:U:C6	2.51	0.46
18:A:1530:G:H22	18:A:1805:G:H1	1.64	0.46
18:A:2862:G:H8	18:A:2862:G:OP2	1.99	0.46
20:C:69:ARG:HG3	20:C:130:ASN:ND2	2.29	0.46
21:D:15:GLN:HE21	34:Q:55:SER:HA	1.80	0.46
21:D:127:MET:HE2	21:D:146:ARG:HG2	1.97	0.46
40:W:11:LEU:HD11	40:W:57:VAL:HG21	1.97	0.46
49:a:324:G:N2	49:a:327:A:OP2	2.41	0.46
49:a:1232:A:H62	49:a:1268:C:H42	1.62	0.46
49:a:1260:A:H1'	49:a:1263:C:N4	2.30	0.46
49:a:1281:A:N1	51:m:114:LYS:NZ	2.49	0.46
53:p:80:THR:HG22	53:p:82:LYS:H	1.79	0.46
55:y:31:ILE:HB	55:y:49:PHE:HD1	1.80	0.46
4:r:53:VAL:O	4:r:54:THR:C	2.58	0.46
14:x:43:ARG:HG3	14:x:43:ARG:HH11	1.80	0.46
18:A:6:G:N2	18:A:7:U:O4	2.45	0.46
18:A:608:C:H2'	18:A:609:G:H8	1.80	0.46
18:A:1164:A:C2	26:I:6:LYS:HB3	2.50	0.46
18:A:1561:C:H42	18:A:1610:C:H42	1.63	0.46
18:A:1628:A:H1'	18:A:1630:U:C4	2.51	0.46
18:A:2094:G:HO2'	18:A:2095:G:H8	1.57	0.46
18:A:2530:C:H3'	18:A:2531:G:H8	1.79	0.46
19:B:1:G:N1	19:B:117:A:H2	2.13	0.46
24:G:74:ALA:O	24:G:78:THR:HG22	2.15	0.46
29:L:76:TYR:HB2	34:Q:72:THR:HB	1.98	0.46
49:a:474:G:H2'	49:a:476:A:C8	2.42	0.46
49:a:1194:A:C5	49:a:1196:G:C5	3.04	0.46
49:a:1239:G:H2'	49:a:1240:C:C6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:1241:G:N2	49:a:1255:G:H2'	2.31	0.46
52:o:61:ASN:C	52:o:65:GLN:HE21	2.23	0.46
53:p:44:THR:OG1	53:p:45:GLU:N	2.48	0.46
3:g:7:PRO:HG2	23:F:69:GLY:C	2.41	0.46
6:j:186:ILE:HG22	6:j:188:VAL:HB	1.97	0.46
7:k:105:THR:HG21	7:k:124:ALA:H	1.80	0.46
8:l:48:LEU:HB3	8:l:50:TYR:O	2.16	0.46
10:q:109:LEU:HD22	10:q:114:LEU:HD12	1.96	0.46
18:A:417:C:H4'	39:V:72:MET:HE2	1.96	0.46
18:A:1154:G:C6	18:A:1238:G:C6	3.03	0.46
18:A:1231:U:H2'	18:A:1232:G:C8	2.49	0.46
18:A:1232:G:H2'	18:A:1233:A:H8	1.81	0.46
18:A:1675:U:O2'	18:A:1676:G:N7	2.49	0.46
19:B:49:C:H2'	19:B:50:C:H6	1.79	0.46
24:G:7:GLN:OE1	24:G:7:GLN:N	2.43	0.46
32:O:37:THR:HG22	32:O:39:PRO:HD2	1.98	0.46
37:T:77:VAL:HG21	37:T:117:ARG:HD2	1.96	0.46
49:a:904:G:H2'	49:a:905:A:C8	2.50	0.46
49:a:1133:G:H2'	49:a:1134:A:H8	1.80	0.46
49:a:1168:G:H21	57:u:60:SER:HB3	1.81	0.46
49:a:1212:A:H2'	49:a:1213:U:C6	2.49	0.46
49:a:1315:A:H2'	49:a:1316:G:O4'	2.15	0.46
4:r:22:PHE:C	4:r:24:SER:H	2.24	0.46
4:r:41:TYR:CE1	4:r:54:THR:HG23	2.51	0.46
16:h:119:ALA:HA	16:h:122:GLN:HE21	1.80	0.46
18:A:215:A:C8	18:A:520:A:N6	2.84	0.46
18:A:734:C:H2'	18:A:735:U:C6	2.51	0.46
18:A:1530:G:H2'	18:A:1531:C:H5''	1.98	0.46
18:A:1790:A:H2'	18:A:1791:A:C8	2.50	0.46
18:A:2482:U:O2'	18:A:2651:C:OP2	2.28	0.46
22:E:183:LEU:HA	22:E:183:LEU:HD12	1.74	0.46
40:W:81:LYS:N	40:W:96:ASP:O	2.44	0.46
49:a:38:C:H2'	49:a:39:G:H8	1.81	0.46
49:a:1187:G:H2'	49:a:1188:C:O4'	2.15	0.46
56:4:289:PHE:HZ	56:4:407:MET:HB3	1.81	0.46
18:A:1001:C:C5	18:A:1002:C:H1'	2.51	0.46
18:A:2261:U:H2'	18:A:2262:C:C6	2.51	0.46
21:D:154:CYS:O	21:D:155:ALA:CB	2.64	0.46
23:F:60:ALA:HB2	23:F:157:ARG:HD3	1.98	0.46
30:M:80:VAL:HG13	30:M:118:LEU:HD13	1.97	0.46
31:N:120:ARG:HA	31:N:120:ARG:HD3	1.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:O:7:GLY:O	32:O:9:ARG:NH1	2.49	0.46
49:a:1202:G:H5'	49:a:1303:U:H5	1.80	0.46
49:a:1375:G:N2	49:a:1486:A:H8	2.13	0.46
50:i:76:ILE:HG12	50:i:82:GLU:HG2	1.98	0.46
51:m:29:LYS:HG3	51:m:101:LEU:CD2	2.45	0.46
51:m:64:ARG:HD3	51:m:128:SER:O	2.15	0.46
53:p:12:ALA:HB2	53:p:96:VAL:HA	1.97	0.46
53:p:53:ARG:HD2	57:u:45:ARG:HH12	1.80	0.46
56:4:350:ILE:HG13	56:4:351:ASN:N	2.31	0.46
1:Y:63:ARG:HH12	18:A:2315:U:P	2.39	0.46
3:g:15:GLN:O	3:g:16:CYS:HB3	2.15	0.46
7:k:63:ILE:HD12	7:k:63:ILE:N	2.31	0.46
9:n:30:SER:OG	49:a:569:U:H5''	2.16	0.46
9:n:84:GLY:O	14:x:51:LYS:HG3	2.16	0.46
13:w:40:TYR:HD1	13:w:73:LEU:HD21	1.80	0.46
18:A:587:G:H22	18:A:590:A:H5'	1.80	0.46
18:A:899:G:H5'	18:A:900:G:OP1	2.15	0.46
18:A:1167:C:C2	18:A:1168:A:C8	3.04	0.46
18:A:1198:C:C2	18:A:1199:U:C5	3.04	0.46
18:A:1225:G:H4'	26:I:75:GLY:O	2.16	0.46
18:A:1283:C:H2'	18:A:1284:A:H8	1.81	0.46
18:A:2088:C:H2'	18:A:2089:C:C6	2.50	0.46
18:A:2365:A:H2'	18:A:2366:C:C6	2.51	0.46
18:A:2739:C:H2'	18:A:2740:G:H8	1.80	0.46
19:B:30:G:H2'	19:B:31:C:C6	2.51	0.46
23:F:135:TYR:CE2	23:F:137:PHE:HB3	2.51	0.46
29:L:59:LYS:HE3	29:L:59:LYS:HB2	1.66	0.46
32:O:87:TYR:OH	32:O:116:VAL:O	2.29	0.46
40:W:13:ALA:HB3	40:W:71:ILE:HG22	1.96	0.46
49:a:45:G:N2	49:a:402:G:C4	2.84	0.46
49:a:1054:G:O6	49:a:1063:U:O2	2.33	0.46
49:a:1070:U:H2'	49:a:1071:U:C6	2.49	0.46
56:4:219:MET:HB3	56:4:219:MET:HE2	1.78	0.46
7:k:38:GLU:HG2	7:k:64:VAL:HG22	1.98	0.46
13:w:40:TYR:CD1	13:w:73:LEU:HD21	2.51	0.46
18:A:678:A:O5'	22:E:90:VAL:HG21	2.16	0.46
18:A:1552:A:H61	18:A:1616:A:H8	1.64	0.46
29:L:93:PRO:HG3	29:L:114:ILE:HG12	1.97	0.46
43:2:23:LEU:HD23	43:2:23:LEU:HA	1.81	0.46
49:a:737:U:OP1	49:a:802:G:O2'	2.33	0.46
49:a:825:C:H2'	49:a:826:U:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:884:G:H2'	49:a:885:G:H8	1.81	0.46
49:a:970:G:O2'	49:a:998:G:N1	2.45	0.46
49:a:1017:C:O2'	49:a:1018:C:O4'	2.33	0.46
49:a:1110:A:O3'	52:o:40:ARG:NH2	2.49	0.46
49:a:1273:C:C2	49:a:1274:C:C5	3.04	0.46
50:i:87:ARG:HA	50:i:98:VAL:HG11	1.96	0.46
18:A:1194:C:H2'	18:A:1195:A:H8	1.81	0.46
18:A:1564:A:N3	18:A:1564:A:H2'	2.31	0.46
18:A:2007:C:H2'	18:A:2008:A:C8	2.51	0.46
18:A:2510:A:H4'	18:A:2511:A:O4'	2.16	0.46
18:A:2511:A:C5	18:A:2513:G:C8	3.04	0.46
41:X:11:ARG:O	41:X:14:ARG:NH1	2.31	0.46
49:a:1133:G:H4'	53:p:15:HIS:CE1	2.51	0.46
51:m:26:LEU:O	51:m:30:VAL:HG12	2.16	0.46
51:m:77:SER:HB2	51:m:86:GLN:HE22	1.79	0.46
57:u:41:ARG:HG3	57:u:42:ILE:N	2.31	0.46
13:w:45:GLU:HG2	13:w:46:PRO:CD	2.45	0.45
18:A:2095:G:O2'	18:A:2096:G:H8	1.99	0.45
18:A:2178:G:O2'	18:A:2180:U:O4	2.27	0.45
23:F:49:ASP:HB3	23:F:56:LEU:HD12	1.97	0.45
47:f:27:CYS:SG	47:f:28:SER:N	2.89	0.45
49:a:1312:U:OP2	54:t:26:GLY:N	2.39	0.45
2:c:14:ALA:HB2	2:c:21:ARG:HG2	1.99	0.45
15:z:46:LYS:HB3	15:z:46:LYS:HE2	1.80	0.45
18:A:1005:A:H2'	18:A:1006:G:O4'	2.17	0.45
18:A:1611:A:H2'	18:A:1612:U:C6	2.51	0.45
49:a:299:G:H2'	49:a:300:A:C8	2.51	0.45
49:a:416:G:H2'	49:a:417:G:C8	2.49	0.45
49:a:592:U:C4	49:a:608:G:O6	2.69	0.45
49:a:716:U:H2'	49:a:717:C:C6	2.52	0.45
56:4:240:ARG:HA	56:4:240:ARG:NH1	2.31	0.45
1:Y:64:ALA:HA	25:H:32:PRO:HB3	1.97	0.45
4:r:67:ALA:O	4:r:68:VAL:C	2.55	0.45
6:j:53:LYS:HD3	6:j:54:GLN:HE22	1.80	0.45
6:j:117:HIS:NE2	49:a:437:U:O2'	2.48	0.45
18:A:377:C:O3'	39:V:94:LYS:NZ	2.47	0.45
18:A:1559:A:H2'	18:A:1560:U:C6	2.51	0.45
18:A:1565:A:O2'	18:A:1566:A:O4'	2.34	0.45
18:A:2094:G:C4	18:A:2095:G:N7	2.85	0.45
20:C:85:ASP:HB2	20:C:92:ILE:HD13	1.97	0.45
51:m:123:GLU:O	51:m:127:ALA:N	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:t:15:MET:CE	54:t:43:MET:HB2	2.47	0.45
1:Y:56:ILE:HG12	1:Y:61:VAL:HG21	1.99	0.45
14:x:81:PRO:O	49:a:264:U:O2'	2.31	0.45
18:A:2:A:H2'	18:A:3:A:C8	2.51	0.45
18:A:239:U:HO2'	18:A:716:G:HO2'	1.60	0.45
18:A:774:G:H21	22:E:36:GLN:CD	2.21	0.45
23:F:141:GLU:OE2	23:F:141:GLU:HA	2.16	0.45
31:N:20:ILE:HD11	40:W:88:ILE:HG12	1.99	0.45
49:a:449:C:H2'	49:a:450:G:O4'	2.16	0.45
49:a:907:G:O2'	49:a:909:G:OP1	2.32	0.45
49:a:1328:A:C8	51:m:9:LYS:HE3	2.52	0.45
49:a:1491:A:H2'	49:a:1492:G:C8	2.52	0.45
54:t:25:ILE:O	54:t:30:SER:OG	2.25	0.45
16:h:94:GLN:NE2	16:h:146:ARG:HH21	2.15	0.45
18:A:181:A:H2'	18:A:182:C:C6	2.51	0.45
18:A:306:U:H2'	18:A:307:G:H8	1.82	0.45
18:A:747:A:H2'	18:A:748:U:O4'	2.16	0.45
18:A:1214:A:H2'	18:A:1215:U:O4'	2.16	0.45
18:A:2044:U:H5'	18:A:2195:U:H5'	1.98	0.45
23:F:68:THR:HG21	23:F:96:VAL:HG11	1.99	0.45
49:a:87:G:H2'	49:a:88:G:C8	2.50	0.45
49:a:1167:G:H2'	49:a:1167:G:N3	2.30	0.45
49:a:1287:G:N2	49:a:1313:G:H1'	2.31	0.45
51:m:75:VAL:HB	51:m:86:GLN:HB3	1.99	0.45
52:o:64:HIS:O	52:o:68:ILE:HD12	2.17	0.45
55:y:31:ILE:HB	55:y:49:PHE:CD1	2.51	0.45
12:v:35:ARG:HH21	12:v:59:LEU:HD11	1.82	0.45
14:x:12:ALA:HB2	49:a:226:G:H5''	1.98	0.45
16:h:23:TRP:CD1	16:h:39:TYR:HH	2.34	0.45
18:A:389:G:N1	18:A:392:A:OP2	2.47	0.45
18:A:1425:G:N2	18:A:1428:U:C4	2.85	0.45
18:A:2176:A:C5	29:L:22:ILE:HD12	2.52	0.45
18:A:2346:G:O6	18:A:2348:G:N2	2.49	0.45
32:O:110:MET:HE2	32:O:110:MET:HB2	1.70	0.45
45:d:19:HIS:HB2	45:d:47:ALA:HB3	1.97	0.45
49:a:246:A:C2	49:a:282:A:C5	3.04	0.45
49:a:437:U:O4	49:a:475:A:N7	2.49	0.45
49:a:486:G:H2'	49:a:487:C:C6	2.52	0.45
49:a:956:A:P	57:u:41:ARG:NH1	2.89	0.45
49:a:998:G:O2'	49:a:999:A:OP1	2.33	0.45
50:i:153:CYS:SG	50:i:157:LEU:HD11	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:p:49:TYR:O	53:p:51:VAL:HG13	2.17	0.45
2:c:48:HIS:HD2	18:A:2595:G:O2'	2.00	0.45
8:l:8:VAL:HG23	8:l:85:VAL:HG13	1.99	0.45
10:q:48:GLY:O	49:a:687:U:O2'	2.35	0.45
13:w:29:ARG:O	13:w:29:ARG:HD2	2.17	0.45
18:A:1854:U:HO2'	18:A:1977:C:HO2'	1.49	0.45
18:A:2288:C:H2'	18:A:2289:C:C6	2.51	0.45
20:C:123:ALA:HB3	20:C:131:LEU:HD22	1.98	0.45
29:L:2:ILE:HG13	29:L:8:LEU:HD21	1.99	0.45
48:5:26:C:H2'	48:5:27:G:C8	2.52	0.45
49:a:900:A:H2'	49:a:901:A:C8	2.51	0.45
49:a:1239:G:H2'	49:a:1240:C:H6	1.81	0.45
49:a:1422:G:H2'	49:a:1423:U:H6	1.82	0.45
55:y:19:VAL:HG21	55:y:44:PHE:HB3	1.98	0.45
3:g:18:CYS:HB2	3:g:41:CYS:SG	2.57	0.45
4:r:32:TYR:H	4:r:32:TYR:HD1	1.65	0.45
4:r:62:ARG:HA	4:r:62:ARG:HD2	1.70	0.45
13:w:22:VAL:O	13:w:33:ALA:HB1	2.16	0.45
16:h:97:LEU:HD22	49:a:1083:C:H5''	1.98	0.45
18:A:334:G:H2'	18:A:335:G:C8	2.52	0.45
18:A:336:C:H2'	18:A:337:U:O4'	2.17	0.45
18:A:681:C:H2'	18:A:682:A:C8	2.52	0.45
18:A:1553:C:H41	18:A:1617:C:H2'	1.81	0.45
18:A:1856:C:O2	18:A:2922:U:O2'	2.34	0.45
19:B:47:A:C5	19:B:48:C:C5	3.05	0.45
20:C:212:MET:HE3	20:C:212:MET:HB3	1.81	0.45
22:E:139:LYS:HA	22:E:139:LYS:HD3	1.75	0.45
23:F:135:TYR:O	23:F:162:THR:OG1	2.21	0.45
24:G:177:THR:C	56:4:242:ARG:HE	2.25	0.45
28:K:36:LEU:HD11	28:K:122:LEU:HB2	1.98	0.45
30:M:96:ASP:HA	30:M:99:VAL:HG22	1.98	0.45
49:a:199:C:H3'	49:a:201:G:H5''	1.98	0.45
49:a:335:C:H2'	49:a:336:A:C8	2.52	0.45
49:a:384:G:H2'	49:a:385:C:H6	1.80	0.45
49:a:627:C:H2'	49:a:628:A:C8	2.52	0.45
49:a:657:U:O2	49:a:757:A:O2'	2.34	0.45
49:a:1220:A:O2'	51:m:119:ARG:NH1	2.49	0.45
49:a:1261:A:O2'	49:a:1262:U:H5'	2.16	0.45
49:a:1382:C:C2	49:a:1486:A:N6	2.85	0.45
51:m:40:GLU:HG2	51:m:44:TYR:CE2	2.51	0.45
4:r:71:ALA:O	4:r:72:ARG:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:j:182:GLU:OE1	6:j:182:GLU:N	2.42	0.45
14:x:86:LYS:HE3	14:x:86:LYS:HB2	1.73	0.45
18:A:7:U:H2'	18:A:8:U:O4'	2.17	0.45
18:A:160:A:H3'	18:A:161:U:H5''	1.99	0.45
18:A:1818:C:N4	18:A:1819:G:O6	2.50	0.45
18:A:2756:G:N2	18:A:2887:G:O2'	2.50	0.45
49:a:280:C:H3'	49:a:281:G:H5'	1.99	0.45
49:a:398:C:H2'	49:a:399:G:C8	2.51	0.45
49:a:687:U:H2'	49:a:688:C:C6	2.51	0.45
49:a:930:C:OP1	54:t:108:ARG:N	2.49	0.45
49:a:1104:G:HO2'	49:a:1126:G:H1	1.54	0.45
49:a:1366:C:H3'	49:a:1367:C:H5''	1.98	0.45
51:m:17:VAL:HG13	51:m:18:TYR:CD2	2.52	0.45
51:m:105:VAL:HB	51:m:120:LEU:HD22	1.98	0.45
54:t:11:ARG:O	54:t:46:LYS:NZ	2.50	0.45
56:4:350:ILE:O	56:4:354:VAL:HG23	2.17	0.45
1:Y:5:CYS:SG	1:Y:8:CYS:SG	3.14	0.45
11:s:48:ALA:HB3	11:s:50:ARG:NH2	2.32	0.45
14:x:86:LYS:H	14:x:87:ARG:NH1	2.15	0.45
16:h:186:ILE:HG13	16:h:202:GLY:HA3	1.98	0.45
18:A:543:U:H3'	18:A:544:U:C5'	2.47	0.45
18:A:2364:C:O2'	18:A:2365:A:H8	2.00	0.45
18:A:2690:C:H5''	47:f:6:SER:HB3	1.98	0.45
22:E:29:PRO:HD3	22:E:120:ARG:HH21	1.81	0.45
26:I:33:VAL:O	26:I:37:ALA:N	2.32	0.45
49:a:150:G:H8	49:a:150:G:O5'	2.00	0.45
49:a:668:G:C5	49:a:680:G:C2	3.05	0.45
49:a:1310:C:O3'	54:t:29:ARG:HB2	2.17	0.45
51:m:32:LEU:HG	51:m:33:GLU:HG3	1.98	0.45
56:4:286:ARG:NE	56:4:294:PRO:HB2	2.32	0.45
7:k:122:ARG:HG3	7:k:123:PRO:HD2	1.99	0.44
11:s:86:ARG:HA	11:s:94:ARG:HA	1.98	0.44
12:v:47:LYS:O	12:v:53:ARG:NH2	2.50	0.44
18:A:1157:G:H4'	40:W:52:ARG:NH1	2.32	0.44
18:A:1174:G:H4'	18:A:1204:A:H8	1.82	0.44
18:A:2276:G:H4'	21:D:153:GLY:O	2.16	0.44
18:A:2331:U:H3'	18:A:2332:U:C6	2.53	0.44
18:A:2873:U:H2'	18:A:2874:C:C6	2.52	0.44
27:J:81:LEU:HB3	27:J:139:ILE:HD12	1.99	0.44
28:K:73:PHE:CE1	28:K:88:THR:HG22	2.51	0.44
29:L:78:LYS:HD3	34:Q:70:GLU:OE2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:O:116:VAL:HG13	32:O:118:GLU:OE1	2.17	0.44
40:W:81:LYS:HA	40:W:81:LYS:HD2	1.67	0.44
49:a:627:C:H2'	49:a:628:A:H8	1.82	0.44
49:a:1269:A:H1'	49:a:1336:C:H5'	1.97	0.44
50:i:48:ARG:HE	50:i:74:ILE:HG13	1.81	0.44
56:4:370:LYS:NZ	56:4:395:ARG:HH11	2.15	0.44
13:w:86:LEU:HB3	13:w:87:PRO:HD2	1.98	0.44
18:A:191:G:O2'	18:A:917:A:N3	2.46	0.44
18:A:556:G:OP2	45:d:40:LYS:NZ	2.50	0.44
18:A:1176:G:H2'	18:A:1177:G:C8	2.52	0.44
18:A:3009:U:H5'	21:D:38:ARG:HH22	1.82	0.44
20:C:65:ILE:HD12	20:C:65:ILE:N	2.33	0.44
33:P:78:LYS:O	33:P:81:SER:OG	2.31	0.44
40:W:38:TYR:O	40:W:99:VAL:HG12	2.16	0.44
43:2:21:GLU:OE2	43:2:24:ARG:NH1	2.49	0.44
49:a:46:G:H2'	49:a:47:C:O4'	2.17	0.44
49:a:437:U:H3	49:a:475:A:H62	1.65	0.44
49:a:571:U:H2'	49:a:572:G:H8	1.82	0.44
49:a:716:U:H2'	49:a:717:C:H6	1.82	0.44
54:t:81:LYS:HE2	54:t:88:GLN:HB3	1.98	0.44
56:4:262:LEU:HD13	56:4:299:ASP:HB2	1.99	0.44
9:n:35:ASN:HB3	9:n:112:LEU:HD12	1.99	0.44
11:s:116:ARG:NH1	49:a:530:G:O2'	2.49	0.44
13:w:65:GLN:HA	13:w:66:PRO:HD2	1.41	0.44
16:h:177:ARG:HD2	16:h:177:ARG:HA	1.72	0.44
18:A:1087:G:H2'	18:A:1088:U:C6	2.53	0.44
18:A:1538:G:O6	18:A:1635:A:H2	2.00	0.44
18:A:1651:C:H2'	18:A:1652:A:H8	1.83	0.44
18:A:1952:C:H2'	18:A:1953:C:C6	2.51	0.44
18:A:2679:G:H2'	18:A:2680:C:H6	1.83	0.44
18:A:2914:A:OP2	32:O:14:SER:OG	2.23	0.44
19:B:10:G:O2'	19:B:11:U:H5'	2.18	0.44
20:C:147:LEU:HD23	20:C:147:LEU:HA	1.73	0.44
23:F:117:ARG:HG2	23:F:144:MET:HA	1.98	0.44
27:J:22:PRO:HG2	27:J:25:PRO:HG2	1.99	0.44
49:a:667:A:C2	49:a:684:A:C5	3.06	0.44
49:a:1299:C:C2	57:u:16:PHE:HE1	2.35	0.44
49:a:1322:G:H2'	49:a:1323:U:O4'	2.17	0.44
49:a:1457:G:H2'	49:a:1458:G:C8	2.52	0.44
54:t:49:THR:OG1	54:t:52:GLN:OE1	2.29	0.44
18:A:217:G:N2	18:A:235:U:H4'	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:1129:G:H21	28:K:147:GLN:NE2	2.16	0.44
18:A:1541:G:O5'	18:A:1541:G:H8	2.00	0.44
18:A:3007:G:H2'	18:A:3008:C:C6	2.52	0.44
25:H:113:ASP:OD1	25:H:114:LYS:N	2.50	0.44
39:V:86:ARG:NH2	39:V:104:ASP:OD1	2.46	0.44
49:a:1002:U:H2'	49:a:1003:C:H6	1.83	0.44
49:a:1235:G:O4'	49:a:1338:G:H5''	2.17	0.44
49:a:1329:G:H8	52:o:129:ARG:O	2.01	0.44
49:a:1333:U:O2'	51:m:33:GLU:OE1	2.34	0.44
50:i:118:GLY:O	50:i:122:GLN:HG3	2.18	0.44
57:u:6:LEU:HD22	57:u:23:ARG:NH2	2.33	0.44
1:Y:23:ARG:HB3	1:Y:23:ARG:CZ	2.46	0.44
6:j:65:LYS:HG2	49:a:526:G:OP1	2.18	0.44
8:l:30:ILE:HD11	8:l:75:LEU:HD22	1.98	0.44
11:s:83:ARG:HH12	11:s:96:LYS:HD2	1.81	0.44
14:x:38:VAL:HG11	14:x:76:LEU:HD11	1.99	0.44
18:A:150:C:H2'	18:A:151:A:C8	2.51	0.44
18:A:1000:C:N4	18:A:1001:C:H41	2.14	0.44
18:A:1044:U:O2	43:2:24:ARG:NH2	2.50	0.44
18:A:1137:U:OP1	18:A:1153:U:O2'	2.20	0.44
18:A:2140:A:H8	18:A:2140:A:OP2	2.01	0.44
18:A:2707:C:N3	31:N:124:LYS:NZ	2.65	0.44
18:A:2859:C:O2'	21:D:83:GLU:OE1	2.31	0.44
18:A:2901:G:H2'	18:A:2902:A:C8	2.53	0.44
18:A:3055:G:H2'	18:A:3100:A:N6	2.32	0.44
28:K:16:TYR:HD1	28:K:138:ILE:HB	1.83	0.44
32:O:103:ARG:HE	32:O:110:MET:HE1	1.80	0.44
33:P:56:ASN:N	33:P:56:ASN:OD1	2.51	0.44
56:4:230:LYS:HA	56:4:233:ARG:NE	2.31	0.44
9:n:84:GLY:O	14:x:51:LYS:NZ	2.46	0.44
13:w:58:TYR:O	13:w:62:VAL:HG13	2.18	0.44
14:x:86:LYS:NZ	49:a:254:G:O3'	2.51	0.44
17:3:22:PRO:HB3	18:A:1102:G:H2'	2.00	0.44
18:A:250:G:H4'	30:M:59:MET:SD	2.58	0.44
18:A:482:U:H2'	18:A:483:G:C8	2.52	0.44
18:A:980:C:HO2'	18:A:981:U:P	2.41	0.44
18:A:1381:G:O2'	18:A:2236:G:O6	2.30	0.44
18:A:1539:A:H2'	18:A:1540:U:C6	2.52	0.44
18:A:1762:C:H2'	18:A:1763:G:O4'	2.18	0.44
18:A:2579:C:H1'	41:X:39:ARG:NH1	2.33	0.44
18:A:2736:C:H2'	18:A:2737:G:O4'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:3115:A:H2'	18:A:3116:C:H6	1.83	0.44
36:S:72:LYS:HD2	36:S:91:ARG:HG3	2.00	0.44
49:a:749:G:H4'	49:a:1497:A:H4'	2.00	0.44
49:a:930:C:P	54:t:108:ARG:H	2.41	0.44
49:a:1196:G:C5	49:a:1197:U:C5	3.06	0.44
50:i:96:LYS:HZ3	50:i:97:GLN:HG3	1.82	0.44
52:o:31:ARG:HD3	52:o:36:VAL:HG12	1.99	0.44
11:s:27:SER:HB2	11:s:30:ARG:HD3	2.00	0.44
18:A:1195:A:C2	18:A:1206:A:H8	2.31	0.44
18:A:3118:U:H2'	18:A:3119:A:H8	1.82	0.44
24:G:164:ARG:HD3	24:G:170:ILE:HD13	2.00	0.44
25:H:134:VAL:HG22	25:H:142:ALA:HB3	2.00	0.44
36:S:26:LYS:HA	36:S:95:THR:OG1	2.18	0.44
44:b:47:ALA:HA	44:b:52:VAL:HG12	2.00	0.44
48:5:17:C:OP1	48:5:62:C:H5'	2.18	0.44
49:a:359:G:H2'	49:a:360:G:O4'	2.18	0.44
49:a:1087:C:C4	49:a:1088:G:C8	3.06	0.44
49:a:1129:U:O2	52:o:38:ARG:NH2	2.51	0.44
49:a:1434:U:O2'	49:a:1435:U:H5''	2.17	0.44
51:m:103:TRP:HA	51:m:107:PHE:HB3	2.00	0.44
51:m:104:LEU:O	51:m:107:PHE:N	2.45	0.44
56:4:406:ARG:NH1	56:4:409:GLU:OE2	2.39	0.44
2:c:27:LYS:HG3	2:c:28:ASN:O	2.18	0.44
6:j:97:VAL:HB	6:j:102:LEU:HD22	2.00	0.44
7:k:46:VAL:HG21	49:a:1060:A:H5''	2.00	0.44
11:s:30:ARG:HA	11:s:30:ARG:HD2	1.81	0.44
13:w:39:ARG:NH1	13:w:50:GLN:OE1	2.51	0.44
18:A:21:G:H2'	18:A:22:U:H6	1.83	0.44
18:A:1194:C:C2	18:A:1195:A:C8	3.06	0.44
18:A:1479:G:H4'	18:A:2025:C:H5	1.82	0.44
18:A:1546:A:N6	18:A:1625:G:O6	2.50	0.44
27:J:107:VAL:HG13	27:J:130:ILE:HB	2.00	0.44
49:a:1231:A:HO2'	49:a:1232:A:P	2.40	0.44
50:i:68:HIS:CE1	50:i:103:LEU:HB3	2.52	0.44
51:m:16:PRO:CB	52:o:66:GLN:HG2	2.48	0.44
52:o:42:VAL:O	52:o:44:GLY:N	2.48	0.44
1:Y:57:LYS:O	1:Y:58:ALA:C	2.60	0.44
2:c:52:LYS:HG2	2:c:53:GLU:N	2.33	0.44
3:g:1:MET:C	3:g:3:THR:N	2.76	0.44
3:g:29:GLN:O	3:g:29:GLN:HG2	2.18	0.44
14:x:35:THR:HA	14:x:62:HIS:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:h:70:VAL:O	16:h:164:VAL:HG21	2.18	0.44
18:A:335:G:H2'	18:A:336:C:C6	2.53	0.44
18:A:1000:C:C4	18:A:1001:C:H5	2.36	0.44
18:A:1270:G:H21	35:R:77:ASN:HD22	1.65	0.44
18:A:1673:A:C5	18:A:2926:A:C8	3.05	0.44
18:A:2391:G:H1'	48:5:57:C:C5	2.53	0.44
34:Q:17:PRO:HG3	34:Q:83:ILE:O	2.18	0.44
49:a:373:A:N3	49:a:462:A:N6	2.66	0.44
49:a:593:C:H2'	49:a:594:A:C8	2.53	0.44
49:a:848:C:OP1	49:a:1057:G:N2	2.50	0.44
49:a:1133:G:H2'	49:a:1134:A:C8	2.53	0.44
51:m:30:VAL:HB	51:m:101:LEU:HD21	2.00	0.44
53:p:25:ILE:O	53:p:29:VAL:HG23	2.17	0.44
54:t:15:MET:HE3	54:t:43:MET:HB2	2.00	0.44
1:Y:18:VAL:HG13	1:Y:22:HIS:HA	1.99	0.43
6:j:73:GLU:OE1	6:j:88:ILE:HD13	2.18	0.43
18:A:188:G:O6	18:A:204:G:O2'	2.29	0.43
18:A:441:G:H2'	18:A:442:U:C6	2.52	0.43
18:A:2299:C:OP2	18:A:2462:G:N2	2.48	0.43
18:A:2553:G:H2'	18:A:2554:U:C6	2.53	0.43
18:A:2588:C:H2'	18:A:2589:G:O4'	2.17	0.43
23:F:176:LEU:HD23	23:F:180:LEU:HD23	2.00	0.43
24:G:11:VAL:HB	24:G:51:ILE:HD11	1.99	0.43
24:G:91:PHE:HD2	24:G:164:ARG:HE	1.66	0.43
34:Q:12:LEU:HD22	34:Q:76:HIS:CE1	2.53	0.43
43:2:37:ARG:HD3	43:2:37:ARG:HA	1.73	0.43
46:e:29:ARG:NH1	46:e:45:ASP:HB3	2.34	0.43
49:a:1291:G:N2	49:a:1311:G:H1'	2.32	0.43
50:i:59:THR:HB	53:p:94:ALA:HB2	2.00	0.43
18:A:131:A:H2'	18:A:132:C:H6	1.83	0.43
18:A:1208:U:C2	18:A:1220:C:H1'	2.52	0.43
18:A:1472:C:H2'	18:A:1473:G:O4'	2.18	0.43
18:A:1706:A:H2'	18:A:1707:G:C8	2.52	0.43
18:A:2406:U:HO2'	18:A:2407:C:H6	1.63	0.43
18:A:2626:U:H4'	18:A:2627:C:OP2	2.17	0.43
21:D:37:THR:HG22	21:D:75:VAL:HG21	2.00	0.43
23:F:15:TYR:HA	23:F:19:ILE:HB	2.00	0.43
23:F:63:ASP:O	23:F:67:ILE:HD12	2.17	0.43
28:K:93:LEU:HG	28:K:100:VAL:HG21	1.99	0.43
55:y:42:PRO:O	55:y:45:ILE:HG12	2.18	0.43
1:Y:63:ARG:NH1	18:A:2315:U:P	2.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:16:GLU:OE2	2:c:52:LYS:HB3	2.18	0.43
9:n:109:SER:HA	49:a:622:A:C8	2.53	0.43
18:A:323:C:H42	18:A:453:U:H3	1.66	0.43
18:A:947:U:H2'	18:A:948:G:C8	2.51	0.43
18:A:1172:A:O3'	26:I:30:GLY:HA2	2.18	0.43
18:A:1363:G:C5	35:R:3:ARG:HB2	2.52	0.43
26:I:48:THR:O	26:I:81:PHE:N	2.51	0.43
31:N:70:PRO:HA	31:N:95:ALA:HB2	2.00	0.43
49:a:1251:G:C2	49:a:1252:G:C5	3.06	0.43
51:m:51:ARG:HA	51:m:56:THR:O	2.18	0.43
55:y:40:ILE:HD12	55:y:66:MET:HE2	2.00	0.43
7:k:207:ALA:HA	7:k:210:ARG:HG2	2.00	0.43
18:A:1194:C:H2'	18:A:1195:A:C8	2.54	0.43
18:A:1202:A:OP1	26:I:50:THR:HA	2.18	0.43
18:A:1294:U:H2'	18:A:1295:U:H6	1.83	0.43
18:A:1476:G:H2'	18:A:1477:C:C6	2.54	0.43
26:I:41:ARG:NH2	27:J:119:ASN:OD1	2.52	0.43
28:K:98:THR:HG23	28:K:124:VAL:HG13	2.00	0.43
30:M:28:SER:OG	30:M:29:LYS:N	2.52	0.43
49:a:818:U:H3	49:a:830:G:H1	1.66	0.43
49:a:1210:A:H2'	49:a:1211:C:C6	2.53	0.43
49:a:1241:G:H22	49:a:1255:G:H2'	1.83	0.43
53:p:10:LEU:HB3	53:p:18:ILE:HD11	1.99	0.43
7:k:151:LYS:HA	7:k:151:LYS:HD2	1.75	0.43
9:n:88:TYR:CD1	9:n:126:GLU:HB2	2.53	0.43
18:A:1236:G:H2'	18:A:1237:U:O4'	2.17	0.43
18:A:1435:C:C5	18:A:1444:U:H5''	2.52	0.43
18:A:2154:G:O2'	18:A:2192:G:O6	2.33	0.43
18:A:2334:U:O2'	18:A:2341:U:O2'	2.27	0.43
18:A:2380:G:OP2	18:A:2380:G:H8	2.01	0.43
18:A:3057:U:H2'	18:A:3058:A:C8	2.52	0.43
26:I:101:LYS:HD3	26:I:101:LYS:HA	1.73	0.43
49:a:211:A:H8	49:a:211:A:OP1	2.02	0.43
49:a:1161:A:H5'	52:o:125:THR:HG23	1.99	0.43
49:a:1235:G:O2'	49:a:1236:G:H5'	2.19	0.43
56:4:286:ARG:CZ	56:4:294:PRO:HB2	2.49	0.43
57:u:8:HIS:C	57:u:11:ASN:HB2	2.43	0.43
16:h:187:LEU:HD12	16:h:199:PRO:HB2	1.99	0.43
18:A:362:A:H2'	18:A:363:A:O4'	2.19	0.43
18:A:685:G:N3	18:A:685:G:H2'	2.34	0.43
18:A:967:G:H2'	18:A:968:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:1171:C:N4	18:A:1224:G:O6	2.23	0.43
18:A:2551:A:H2'	18:A:2552:A:C8	2.54	0.43
18:A:3019:C:N4	18:A:3021:A:C8	2.87	0.43
21:D:111:TYR:HE1	21:D:181:LYS:HB2	1.83	0.43
28:K:89:ILE:HD11	28:K:100:VAL:HG13	2.00	0.43
37:T:27:VAL:HG11	37:T:51:SER:HB3	2.00	0.43
49:a:43:G:C6	49:a:404:G:C6	3.06	0.43
49:a:1096:U:O2	49:a:1166:G:H1'	2.17	0.43
49:a:1310:C:O2'	54:t:29:ARG:NE	2.47	0.43
50:i:161:GLU:OE2	50:i:161:GLU:N	2.44	0.43
3:g:7:PRO:HG3	23:F:65:ALA:O	2.18	0.43
18:A:429:A:H2'	18:A:430:A:C8	2.53	0.43
18:A:1664:G:C6	18:A:1769:G:C6	3.07	0.43
18:A:2289:C:H2'	18:A:2290:C:H6	1.84	0.43
24:G:7:GLN:HG3	24:G:70:ARG:HH21	1.83	0.43
24:G:35:LEU:HD11	24:G:72:LEU:HD23	2.00	0.43
27:J:25:PRO:HB2	27:J:26:VAL:HG13	2.01	0.43
33:P:100:VAL:HG22	33:P:125:LEU:HD12	2.01	0.43
49:a:308:C:H2'	49:a:309:G:C8	2.54	0.43
49:a:724:C:H2'	49:a:725:A:H8	1.84	0.43
49:a:1096:U:C2	49:a:1166:G:H1'	2.53	0.43
49:a:1515:A:H2'	49:a:1516:U:O4'	2.18	0.43
56:4:250:ILE:HG12	56:4:298:THR:O	2.19	0.43
56:4:354:VAL:O	56:4:358:ASP:N	2.52	0.43
12:v:68:LYS:HB2	12:v:68:LYS:HE3	1.88	0.43
14:x:35:THR:HG21	14:x:86:LYS:HZ1	1.84	0.43
16:h:214:THR:HA	16:h:217:ILE:HG22	2.01	0.43
18:A:1199:U:H2'	18:A:1200:U:H6	1.84	0.43
18:A:2088:C:H2'	18:A:2089:C:C5	2.53	0.43
28:K:7:LYS:HA	28:K:7:LYS:HD3	1.78	0.43
29:L:30:ARG:NH2	29:L:37:ASP:OD2	2.52	0.43
30:M:99:VAL:HG12	30:M:104:VAL:HG23	2.01	0.43
31:N:30:GLY:O	31:N:134:ARG:NH2	2.52	0.43
44:b:45:LYS:O	44:b:49:LEU:HG	2.19	0.43
48:5:31:G:H2'	48:5:32:G:C8	2.54	0.43
49:a:199:C:H5''	49:a:200:U:OP2	2.19	0.43
49:a:498:C:H5''	49:a:499:C:C5	2.54	0.43
49:a:905:A:H2'	49:a:906:C:C6	2.54	0.43
49:a:1087:C:N3	49:a:1088:G:C8	2.87	0.43
49:a:1220:A:H62	49:a:1281:A:H62	1.67	0.43
51:m:36:LYS:HA	51:m:39:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:w:93:LEU:HG	13:w:95:VAL:HG22	1.99	0.43
18:A:98:U:H3'	18:A:99:G:H5'	2.01	0.43
18:A:483:G:H2'	18:A:484:C:C6	2.54	0.43
18:A:663:A:N3	18:A:663:A:H2'	2.34	0.43
18:A:2339:G:H3'	18:A:2340:A:H8	1.83	0.43
18:A:2467:U:H2'	18:A:2468:U:C6	2.53	0.43
18:A:2669:G:OP1	22:E:75:ARG:NH1	2.39	0.43
18:A:2686:U:H2'	18:A:2687:U:C6	2.54	0.43
21:D:141:ALA:HB1	21:D:144:VAL:HG12	2.01	0.43
28:K:92:LEU:HD12	28:K:92:LEU:HA	1.81	0.43
33:P:69:ASP:OD1	33:P:69:ASP:N	2.51	0.43
34:Q:51:GLY:HA2	34:Q:56:GLU:CD	2.44	0.43
47:f:12:ASP:OD1	47:f:12:ASP:N	2.48	0.43
49:a:382:A:H2'	49:a:383:A:C8	2.54	0.43
49:a:411:A:N7	49:a:413:G:N2	2.66	0.43
49:a:998:G:HO2'	49:a:999:A:P	2.41	0.43
49:a:1141:G:H22	49:a:1158:G:N2	2.17	0.43
49:a:1339:A:H61	49:a:1348:G:H1	1.67	0.43
3:g:14:VAL:HG13	3:g:33:ILE:C	2.44	0.43
3:g:45:TYR:OH	23:F:183:PRO:HD3	2.18	0.43
13:w:74:LEU:HD22	13:w:79:ASP:HB2	2.00	0.43
16:h:154:MET:O	16:h:156:LYS:HB2	2.19	0.43
16:h:187:LEU:HB3	16:h:201:PRO:HA	2.01	0.43
18:A:21:G:H2'	18:A:22:U:C6	2.54	0.43
18:A:34:C:H2'	18:A:35:A:C8	2.54	0.43
18:A:974:G:O2'	18:A:975:U:P	2.76	0.43
18:A:1115:G:OP1	35:R:92:ARG:HD2	2.18	0.43
18:A:1786:G:OP1	20:C:211:ARG:NH2	2.52	0.43
18:A:2195:U:H1'	20:C:241:SER:HB3	2.01	0.43
18:A:2399:A:H2'	18:A:2400:C:C6	2.54	0.43
19:B:107:A:H2'	19:B:108:C:C6	2.54	0.43
22:E:58:VAL:HG21	22:E:80:ARG:HB3	2.01	0.43
49:a:708:A:H2'	49:a:709:A:C8	2.54	0.43
49:a:1165:G:H3'	49:a:1166:G:C8	2.54	0.43
50:i:117:GLN:HE21	50:i:121:GLU:HG2	1.84	0.43
56:4:287:GLY:HA3	56:4:295:PHE:CZ	2.53	0.43
57:u:7:VAL:HG12	57:u:11:ASN:ND2	2.34	0.43
1:Y:48:ARG:NH1	1:Y:48:ARG:HB2	2.34	0.42
15:z:64:LYS:HD3	15:z:64:LYS:HA	1.75	0.42
18:A:41:A:H2'	18:A:42:G:O4'	2.18	0.42
18:A:353:G:C2	18:A:443:C:O2	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:967:G:H2'	18:A:968:C:H6	1.84	0.42
18:A:992:C:H2'	18:A:993:G:O4'	2.19	0.42
18:A:996:G:N2	18:A:997:G:N7	2.67	0.42
18:A:2256:G:N2	18:A:2796:A:OP2	2.52	0.42
18:A:2515:U:H2'	18:A:2516:U:H6	1.82	0.42
18:A:3019:C:H3'	18:A:3020:U:O2	2.19	0.42
21:D:86:LEU:HD12	21:D:92:VAL:HG22	2.01	0.42
23:F:66:LEU:HD12	23:F:66:LEU:HA	1.92	0.42
36:S:16:VAL:HG23	36:S:20:ASP:HB2	2.01	0.42
48:5:34:U:H2'	48:5:35:C:H5''	2.00	0.42
49:a:487:C:OP2	49:a:488:C:O2'	2.29	0.42
49:a:965:A:H5'	49:a:966:C:OP2	2.19	0.42
49:a:1359:U:O4	51:m:9:LYS:HD3	2.19	0.42
49:a:1423:U:H3'	49:a:1424:G:H8	1.84	0.42
4:r:18:ARG:O	4:r:19:LYS:HB3	2.19	0.42
5:1:4:VAL:O	5:1:8:ARG:HG2	2.19	0.42
5:1:22:ARG:HD3	5:1:25:ARG:NH2	2.35	0.42
5:1:30:LYS:HE2	5:1:30:LYS:HB2	1.93	0.42
11:s:30:ARG:CB	11:s:57:LEU:HD21	2.46	0.42
16:h:154:MET:HE1	16:h:158:PRO:HD3	2.01	0.42
18:A:88:A:H1'	18:A:89:A:C8	2.55	0.42
18:A:2350:G:H1'	18:A:2351:A:N7	2.33	0.42
24:G:90:ILE:HG22	24:G:163:VAL:HG22	2.00	0.42
48:5:35:C:OP2	52:o:150:ARG:NH2	2.52	0.42
49:a:72:G:C8	49:a:73:G:C8	3.07	0.42
49:a:127:A:O2'	49:a:128:U:H5''	2.19	0.42
49:a:367:U:O5'	49:a:394:G:N2	2.52	0.42
50:i:64:ARG:HG2	50:i:99:GLN:CD	2.45	0.42
56:4:207:LYS:HD2	56:4:207:LYS:HA	1.87	0.42
56:4:280:LEU:HA	56:4:301:VAL:HG23	2.00	0.42
12:v:23:GLY:HA3	49:a:636:G:N2	2.35	0.42
18:A:277:U:H2'	18:A:278:A:C8	2.54	0.42
18:A:383:U:C6	39:V:80:PRO:HG2	2.55	0.42
18:A:669:G:O2'	18:A:1369:A:OP1	2.37	0.42
18:A:1182:C:C4	18:A:1183:U:C4	3.07	0.42
18:A:1225:G:H5''	26:I:54:ASN:OD1	2.19	0.42
18:A:1600:G:H2'	18:A:1601:G:C8	2.55	0.42
18:A:2328:G:C2	18:A:2408:G:C2	3.08	0.42
18:A:2410:A:H2'	18:A:2411:U:H6	1.84	0.42
18:A:2763:C:H4'	47:f:3:VAL:HG21	2.01	0.42
18:A:2936:C:OP1	18:A:2938:G:H4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:B:50:C:H2'	19:B:51:G:H8	1.83	0.42
20:C:63:ARG:O	20:C:65:ILE:HD12	2.19	0.42
36:S:39:VAL:HG11	36:S:42:VAL:HG22	2.01	0.42
49:a:930:C:H2'	49:a:931:A:H8	1.84	0.42
49:a:1230:C:H2'	49:a:1231:A:H5''	2.00	0.42
49:a:1231:A:C2	49:a:1353:G:H1'	2.55	0.42
49:a:1390:C:C2	49:a:1391:A:C8	3.07	0.42
49:a:1422:G:H2'	49:a:1423:U:C6	2.55	0.42
49:a:1472:G:H2'	49:a:1473:A:H8	1.83	0.42
51:m:56:THR:HB	51:m:60:VAL:HB	2.02	0.42
54:t:80:ARG:O	54:t:83:GLU:HG3	2.19	0.42
56:4:455:VAL:O	56:4:460:ALA:HB2	2.20	0.42
1:Y:2:ALA:HA	1:Y:33:ILE:HG12	2.01	0.42
1:Y:17:SER:O	1:Y:17:SER:OG	2.33	0.42
3:g:15:GLN:O	3:g:16:CYS:CB	2.66	0.42
6:j:84:ASN:OD1	6:j:87:ARG:NH2	2.53	0.42
13:w:49:ILE:HD12	13:w:76:ILE:HG21	2.01	0.42
18:A:368:U:O2'	18:A:369:G:H5'	2.19	0.42
18:A:604:C:O2'	37:T:25:ARG:NH2	2.52	0.42
21:D:154:CYS:O	21:D:154:CYS:SG	2.75	0.42
23:F:126:PRO:HD3	23:F:185:LYS:HB2	2.01	0.42
23:F:139:LEU:HD23	23:F:159:MET:SD	2.59	0.42
27:J:63:TYR:HB2	27:J:65:ASP:OD1	2.20	0.42
27:J:110:ILE:HB	27:J:130:ILE:HD13	2.00	0.42
29:L:24:VAL:HG13	29:L:33:ALA:HB2	2.02	0.42
29:L:107:ARG:HD2	29:L:112:MET:HE1	2.01	0.42
44:b:9:SER:O	44:b:13:THR:HG23	2.19	0.42
48:5:51:U:H2'	48:5:52:C:C6	2.54	0.42
48:5:54:G:H2'	48:5:55:U:C6	2.55	0.42
49:a:444:A:H2'	49:a:445:C:H6	1.84	0.42
49:a:1095:U:H2'	49:a:1096:U:H6	1.84	0.42
50:i:78:ARG:HG3	50:i:79:ARG:HG3	2.00	0.42
56:4:253:TYR:CE1	56:4:304:VAL:HA	2.54	0.42
8:l:2:ARG:HB2	8:l:4:TYR:HE1	1.84	0.42
12:v:12:LEU:HD13	12:v:22:THR:HG22	2.02	0.42
18:A:183:G:O2'	18:A:216:A:N3	2.47	0.42
18:A:419:G:C5	18:A:420:G:H1'	2.54	0.42
18:A:908:A:OP2	18:A:2294:A:O2'	2.37	0.42
18:A:949:C:C2	18:A:950:A:C8	3.08	0.42
18:A:1080:U:H2'	18:A:1081:C:H6	1.84	0.42
18:A:1430:C:H2'	18:A:1431:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:2011:U:H2'	18:A:2012:C:H6	1.85	0.42
18:A:2031:G:H4'	20:C:51:THR:HG21	2.00	0.42
18:A:2061:U:O3'	20:C:256:ARG:NH1	2.53	0.42
18:A:2079:C:H2'	18:A:2080:G:H8	1.83	0.42
18:A:2347:G:H5'	18:A:2348:G:N7	2.35	0.42
18:A:3022:G:H2'	18:A:3023:G:O4'	2.18	0.42
27:J:137:MET:HG2	27:J:139:ILE:HG13	2.01	0.42
49:a:207:G:H2'	49:a:208:G:H8	1.84	0.42
49:a:658:U:H2'	49:a:659:C:H6	1.84	0.42
49:a:944:C:H2'	49:a:945:G:O4'	2.19	0.42
49:a:1014:U:O2'	49:a:1015:G:OP1	2.31	0.42
49:a:1312:U:O4	49:a:1313:G:N1	2.52	0.42
49:a:1328:A:N3	51:m:10:ARG:NH2	2.68	0.42
49:a:1407:U:H2'	49:a:1408:A:C8	2.54	0.42
5:1:25:ARG:O	5:1:29:ARG:HG3	2.20	0.42
6:j:152:ILE:HG23	6:j:157:ALA:HB2	2.02	0.42
13:w:4:LYS:HD3	49:a:377:G:OP1	2.19	0.42
13:w:14:ARG:O	13:w:16:PRO:HD3	2.19	0.42
18:A:1174:G:N1	18:A:1220:C:OP2	2.52	0.42
18:A:1212:U:H3'	18:A:1213:A:H5''	2.01	0.42
18:A:1849:G:N2	18:A:1852:A:OP2	2.48	0.42
18:A:2388:G:N2	18:A:2389:U:H1'	2.33	0.42
18:A:3008:C:H2'	18:A:3009:U:O4'	2.19	0.42
24:G:122:ILE:HD13	24:G:145:ILE:HG21	2.02	0.42
49:a:415:C:C6	49:a:416:G:C8	3.08	0.42
49:a:1047:A:N1	49:a:1088:G:O2'	2.50	0.42
49:a:1206:U:O2	55:y:78:ARG:HD3	2.19	0.42
52:o:71:PRO:O	52:o:74:THR:OG1	2.37	0.42
54:t:57:ARG:HA	54:t:60:ILE:HG12	2.02	0.42
4:r:23:CYS:O	49:a:826:U:P	2.78	0.42
11:s:121:LYS:NZ	49:a:481:G:OP2	2.46	0.42
18:A:248:G:H5'	18:A:250:G:N7	2.34	0.42
18:A:688:A:H2'	18:A:689:U:C6	2.54	0.42
18:A:815:G:O2'	18:A:1850:A:N3	2.46	0.42
18:A:1637:G:H2'	18:A:1638:C:H6	1.83	0.42
18:A:2337:A:N3	18:A:2389:U:H2'	2.35	0.42
18:A:3019:C:H3'	18:A:3020:U:C2	2.54	0.42
23:F:44:ASN:C	23:F:44:ASN:OD1	2.62	0.42
23:F:98:LEU:HB3	23:F:103:MET:HB3	2.02	0.42
29:L:79:PHE:CD1	34:Q:69:VAL:HG12	2.55	0.42
35:R:117:LEU:HD23	35:R:117:LEU:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:427:U:OP2	49:a:428:G:O2'	2.30	0.42
49:a:432:A:C2	49:a:433:C:H1'	2.54	0.42
49:a:492:U:H2'	49:a:493:A:H8	1.84	0.42
49:a:1054:G:OP1	49:a:1082:A:N6	2.33	0.42
49:a:1294:G:N1	49:a:1308:C:C4	2.88	0.42
49:a:1369:G:H2'	49:a:1370:G:H8	1.84	0.42
50:i:156:ARG:HB2	50:i:160:ALA:HA	2.01	0.42
56:4:449:THR:O	56:4:451:ILE:HG13	2.20	0.42
3:g:1:MET:HG3	19:B:45:G:OP1	2.20	0.42
6:j:92:ARG:HB3	6:j:94:ASP:OD1	2.19	0.42
7:k:62:VAL:HG11	7:k:89:VAL:HG23	2.01	0.42
15:z:16:ARG:NH1	15:z:19:LEU:HB2	2.35	0.42
18:A:58:G:C6	18:A:92:G:C2	3.08	0.42
18:A:73:C:C2	18:A:108:A:C2	3.08	0.42
18:A:367:U:H2'	18:A:368:U:O4'	2.20	0.42
18:A:974:G:O2'	18:A:975:U:O5'	2.34	0.42
18:A:1734:C:H2'	18:A:1735:U:C6	2.55	0.42
18:A:1953:C:H2'	18:A:1954:C:O4'	2.20	0.42
18:A:2152:A:H2'	18:A:2153:G:O4'	2.19	0.42
22:E:30:ASN:O	22:E:34:MET:HG3	2.18	0.42
49:a:1110:A:C4	49:a:1111:G:C8	3.08	0.42
49:a:1131:G:O2'	49:a:1132:U:H5'	2.19	0.42
49:a:1342:A:H2'	49:a:1343:G:C8	2.54	0.42
3:g:16:CYS:SG	3:g:18:CYS:N	2.93	0.42
6:j:53:LYS:HD3	6:j:54:GLN:NE2	2.35	0.42
6:j:130:TYR:HD2	6:j:132:VAL:HG23	1.85	0.42
6:j:137:ILE:HG13	13:w:106:PHE:CE1	2.55	0.42
6:j:147:THR:HG22	6:j:149:PRO:HG2	2.02	0.42
13:w:13:ILE:HG21	49:a:47:C:OP1	2.20	0.42
18:A:423:C:H2'	18:A:424:G:O4'	2.20	0.42
18:A:751:A:H2'	18:A:752:C:C6	2.54	0.42
18:A:1157:G:H4'	40:W:52:ARG:HH22	1.84	0.42
18:A:1561:C:N4	18:A:1610:C:H42	2.18	0.42
18:A:1656:A:H2'	18:A:1657:G:H8	1.85	0.42
18:A:2333:G:O2'	18:A:2343:G:O4'	2.35	0.42
18:A:2349:A:O2'	18:A:2350:G:O5'	2.23	0.42
21:D:113:ASP:OD1	21:D:178:GLN:HA	2.19	0.42
23:F:142:GLN:HG3	23:F:148:ILE:HD13	2.02	0.42
30:M:22:VAL:HG12	30:M:29:LYS:HD2	2.02	0.42
33:P:47:ILE:HD11	33:P:112:ARG:HD2	2.02	0.42
37:T:95:ARG:HG3	37:T:101:PHE:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:210:A:HO2'	49:a:221:G:HO2'	1.62	0.42
49:a:805:A:H2'	49:a:806:C:H6	1.83	0.42
49:a:1124:G:H2'	49:a:1125:G:C8	2.55	0.42
49:a:1231:A:H2'	49:a:1232:A:H8	1.85	0.42
49:a:1491:A:C5	49:a:1514:G:C2	3.08	0.42
51:m:75:VAL:HA	51:m:88:PRO:HA	2.01	0.42
2:c:24:ILE:O	2:c:24:ILE:HG23	2.19	0.42
3:g:28:LYS:CD	3:g:33:ILE:HG12	2.47	0.42
11:s:20:LYS:HE2	11:s:20:LYS:HB2	1.83	0.42
13:w:45:GLU:CG	13:w:46:PRO:HD3	2.49	0.42
16:h:1:MET:HE2	16:h:1:MET:HB2	1.86	0.42
18:A:637:G:HO2'	18:A:638:U:H6	1.68	0.42
18:A:1486:G:N2	18:A:1487:U:O4	2.53	0.42
18:A:1518:A:O2'	18:A:1692:G:O2'	2.33	0.42
20:C:43:ARG:NH2	20:C:49:ILE:HD11	2.35	0.42
20:C:143:HIS:CD2	20:C:196:VAL:HG22	2.55	0.42
25:H:106:LYS:HE3	25:H:106:LYS:HB2	1.90	0.42
31:N:58:ILE:HG13	31:N:59:LYS:N	2.34	0.42
49:a:416:G:C2	49:a:417:G:N7	2.87	0.42
49:a:441:A:H2'	49:a:441:A:N3	2.35	0.42
49:a:1133:G:O5'	53:p:15:HIS:NE2	2.53	0.42
49:a:1138:A:C8	49:a:1162:G:C2	3.08	0.42
50:i:189:ALA:HB3	50:i:196:ILE:HB	2.02	0.42
56:4:289:PHE:HE2	56:4:408:GLY:CA	2.31	0.42
3:g:47:GLY:O	3:g:48:LYS:C	2.63	0.41
14:x:33:GLN:NE2	49:a:273:A:O2'	2.42	0.41
16:h:26:LYS:HA	16:h:26:LYS:HD2	1.70	0.41
16:h:136:MET:O	16:h:140:GLU:HG2	2.20	0.41
18:A:388:U:H2'	18:A:389:G:O4'	2.20	0.41
18:A:941:U:O2'	30:M:53:GLY:HA3	2.20	0.41
18:A:974:G:HO2'	18:A:975:U:P	2.43	0.41
18:A:1562:C:H6	18:A:1562:C:H2'	1.71	0.41
18:A:3000:A:C6	18:A:3006:G:H1'	2.55	0.41
24:G:88:MET:HE3	24:G:165:TYR:CD1	2.55	0.41
25:H:23:ASP:OD1	25:H:23:ASP:N	2.52	0.41
26:I:69:LEU:HD12	26:I:72:LEU:HD13	2.02	0.41
48:5:24:C:C2	48:5:25:U:C5	3.07	0.41
48:5:24:C:H2'	48:5:25:U:C6	2.55	0.41
49:a:26:G:H2'	49:a:27:C:H6	1.85	0.41
49:a:271:C:H2'	49:a:272:C:H6	1.85	0.41
49:a:485:G:O2'	49:a:486:G:OP1	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:562:U:OP2	49:a:738:G:N1	2.42	0.41
49:a:1110:A:N6	49:a:1125:G:H1'	2.33	0.41
49:a:1183:U:H1'	57:u:42:ILE:HD12	2.02	0.41
49:a:1260:A:H1'	49:a:1263:C:H42	1.84	0.41
49:a:1270:A:H2'	49:a:1271:A:H8	1.85	0.41
49:a:1418:G:H2'	49:a:1419:C:H6	1.84	0.41
50:i:11:ARG:O	50:i:16:THR:OG1	2.23	0.41
51:m:113:GLU:OE1	51:m:119:ARG:HB2	2.20	0.41
52:o:66:GLN:HA	52:o:69:LYS:HG3	2.01	0.41
8:l:47:ARG:HA	8:l:57:GLU:HG2	2.03	0.41
18:A:28:C:O2'	18:A:1353:G:OP1	2.38	0.41
18:A:422:A:O2'	22:E:170:ARG:NH2	2.53	0.41
18:A:608:C:H2'	18:A:609:G:C8	2.55	0.41
18:A:1174:G:H4'	18:A:1204:A:C8	2.55	0.41
18:A:1180:G:H1'	27:J:136:SER:HB2	2.02	0.41
18:A:1810:A:H2'	18:A:1811:C:C6	2.55	0.41
18:A:2163:U:OP1	18:A:2828:U:O2'	2.38	0.41
18:A:2524:C:H2'	18:A:2525:C:C6	2.55	0.41
18:A:2691:C:H2'	18:A:2692:A:O4'	2.20	0.41
18:A:3054:U:O2	21:D:60:ARG:HD3	2.20	0.41
21:D:40:ARG:O	21:D:48:SER:HA	2.20	0.41
25:H:135:LYS:HB3	25:H:141:GLU:HG2	2.02	0.41
29:L:8:LEU:HD23	29:L:82:ASN:HB3	2.02	0.41
33:P:26:ARG:HD2	33:P:26:ARG:HA	1.92	0.41
39:V:39:ASN:OD1	39:V:64:ALA:HB3	2.19	0.41
49:a:300:A:H2'	49:a:301:G:O4'	2.20	0.41
49:a:560:C:H2'	49:a:561:G:O4'	2.20	0.41
49:a:1117:U:H1'	49:a:1118:A:H2'	2.02	0.41
51:m:70:LYS:HE2	51:m:70:LYS:HB3	1.83	0.41
55:y:63:THR:O	55:y:66:MET:HG2	2.21	0.41
16:h:117:LEU:HD13	16:h:137:LEU:HG	2.02	0.41
18:A:691:U:H2'	18:A:692:C:C6	2.54	0.41
18:A:1294:U:H2'	18:A:1295:U:C6	2.54	0.41
18:A:1770:G:H2'	18:A:1771:U:C6	2.54	0.41
18:A:2580:G:H2'	18:A:2581:G:O4'	2.21	0.41
18:A:2778:U:H2'	18:A:2779:U:C6	2.55	0.41
18:A:2813:A:H2'	18:A:2814:A:H8	1.85	0.41
18:A:3023:G:H2'	18:A:3024:A:C8	2.55	0.41
24:G:70:ARG:HH11	24:G:74:ALA:HB2	1.85	0.41
26:I:98:LYS:HD2	26:I:98:LYS:HA	1.90	0.41
30:M:76:GLN:HG3	30:M:108:SER:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:P:19:LEU:HD23	33:P:19:LEU:HA	1.91	0.41
46:e:23:VAL:HG13	46:e:47:ARG:HB3	2.01	0.41
49:a:593:C:H2'	49:a:594:A:H8	1.85	0.41
49:a:658:U:H2'	49:a:659:C:C6	2.55	0.41
49:a:938:U:H2'	49:a:939:U:O4'	2.20	0.41
49:a:1056:C:H42	49:a:1060:A:P	2.40	0.41
49:a:1121:G:O2'	49:a:1122:U:H5'	2.20	0.41
1:Y:14:PHE:CZ	18:A:1480:A:N7	2.88	0.41
13:w:68:GLU:CG	13:w:69:PRO:CD	2.84	0.41
16:h:18:HIS:CE1	16:h:22:ARG:HB3	2.56	0.41
18:A:1176:G:C6	18:A:1177:G:C6	3.08	0.41
18:A:1554:U:O2	18:A:1617:C:N3	2.53	0.41
18:A:1557:C:C2	18:A:1558:C:C5	3.09	0.41
18:A:1684:C:H2'	18:A:1685:G:H8	1.86	0.41
18:A:1705:C:H2'	18:A:1706:A:C8	2.54	0.41
18:A:2366:C:H3'	18:A:2367:G:C8	2.52	0.41
18:A:2396:A:H2'	18:A:2397:C:C6	2.55	0.41
21:D:28:VAL:HG13	21:D:191:VAL:HG13	2.03	0.41
22:E:154:VAL:HG13	22:E:175:VAL:HG22	2.01	0.41
37:T:16:TYR:CD1	37:T:109:HIS:HE1	2.38	0.41
37:T:19:VAL:O	37:T:108:SER:OG	2.29	0.41
42:Z:13:LEU:H	42:Z:13:LEU:HD12	1.86	0.41
49:a:392:C:H2'	49:a:393:A:H8	1.85	0.41
49:a:863:G:H2'	49:a:864:C:O4'	2.20	0.41
49:a:986:G:HO2'	49:a:987:A:HO2'	1.57	0.41
49:a:1100:U:H2'	49:a:1101:C:H6	1.83	0.41
52:o:97:GLY:HA2	52:o:100:ARG:HD3	2.03	0.41
56:4:382:LEU:HD23	56:4:382:LEU:HA	1.89	0.41
6:j:92:ARG:NH2	6:j:94:ASP:OD2	2.35	0.41
16:h:5:THR:O	16:h:9:LEU:HG	2.20	0.41
16:h:81:ALA:O	16:h:85:THR:OG1	2.30	0.41
16:h:154:MET:O	16:h:155:GLN:HG3	2.21	0.41
18:A:1318:C:O2	30:M:7:HIS:HB3	2.20	0.41
18:A:1703:G:C6	18:A:1727:A:C2	3.09	0.41
18:A:1804:G:H2'	18:A:1805:G:O4'	2.21	0.41
18:A:2594:G:H2'	18:A:2595:G:O4'	2.20	0.41
23:F:139:LEU:HD21	23:F:144:MET:SD	2.61	0.41
28:K:19:ASP:OD2	28:K:21:SER:OG	2.32	0.41
30:M:94:GLY:H	30:M:97:GLU:HB2	1.84	0.41
34:Q:59:THR:HG22	34:Q:72:THR:HG23	2.02	0.41
49:a:173:C:O2'	49:a:174:G:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:181:C:C2	49:a:182:C:C5	3.08	0.41
49:a:1039:C:H2'	49:a:1040:U:H6	1.86	0.41
49:a:1369:G:H2'	49:a:1370:G:C8	2.56	0.41
56:4:246:PRO:O	56:4:296:VAL:N	2.29	0.41
1:Y:8:CYS:HG	1:Y:55:CYS:HG	1.67	0.41
4:r:22:PHE:CE2	4:r:41:TYR:CZ	3.09	0.41
6:j:201:LYS:HB2	49:a:12:A:C6	2.54	0.41
11:s:27:SER:HB3	49:a:363:A:N7	2.35	0.41
14:x:17:ARG:HG3	49:a:193:C:C4	2.54	0.41
18:A:302:U:H1'	18:A:303:G:H8	1.85	0.41
18:A:1178:U:O4'	18:A:1179:U:H3'	2.21	0.41
18:A:1594:G:H2'	18:A:1595:G:H8	1.86	0.41
18:A:1854:U:H2'	18:A:1855:A:H8	1.85	0.41
18:A:2094:G:C2	18:A:2095:G:C5	3.09	0.41
18:A:2289:C:H2'	18:A:2290:C:C6	2.56	0.41
18:A:2471:A:H2'	18:A:2472:C:H6	1.85	0.41
18:A:2548:U:H5''	18:A:2549:G:H5'	2.01	0.41
22:E:184:ASN:ND2	22:E:187:ASP:OD2	2.48	0.41
26:I:87:VAL:HG21	26:I:126:LEU:O	2.21	0.41
39:V:12:ILE:HD13	39:V:12:ILE:HA	1.85	0.41
48:5:53:G:C6	48:5:64:G:C6	3.08	0.41
48:5:72:C:H2'	48:5:73:A:C8	2.56	0.41
49:a:230:G:H2'	49:a:231:G:O4'	2.20	0.41
49:a:260:G:H2'	49:a:261:U:C6	2.55	0.41
49:a:263:A:H2'	49:a:264:U:C6	2.55	0.41
49:a:382:A:H2'	49:a:383:A:H8	1.86	0.41
49:a:467:A:N6	49:a:468:U:O2	2.53	0.41
49:a:1355:U:O2	51:m:34:GLY:HA3	2.20	0.41
50:i:19:LYS:HB3	50:i:19:LYS:HE2	1.89	0.41
51:m:33:GLU:HG3	51:m:33:GLU:H	1.63	0.41
53:p:23:ARG:HA	53:p:26:VAL:HG22	2.02	0.41
3:g:16:CYS:HB3	3:g:19:GLY:H	1.85	0.41
6:j:151:GLN:HB3	6:j:154:ARG:HH21	1.85	0.41
6:j:155:GLU:O	6:j:156:THR:OG1	2.29	0.41
7:k:69:GLY:O	7:k:99:VAL:N	2.47	0.41
17:3:8:LYS:HA	17:3:11:ARG:NH1	2.36	0.41
18:A:1201:G:N2	18:A:1203:A:H8	2.15	0.41
18:A:1627:U:H2'	18:A:1628:A:C8	2.56	0.41
18:A:2879:G:O2'	18:A:2888:G:O6	2.33	0.41
38:U:47:GLU:OE2	38:U:53:LYS:HA	2.21	0.41
49:a:216:U:O2	49:a:216:U:H2'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:a:400:C:H2'	49:a:401:C:O4'	2.20	0.41
49:a:410:G:H2'	49:a:429:U:O4	2.21	0.41
49:a:872:G:O2'	49:a:888:A:N6	2.53	0.41
49:a:929:G:H2'	49:a:930:C:H6	1.83	0.41
49:a:1081:A:O3'	49:a:1082:A:H4'	2.18	0.41
49:a:1272:G:N3	49:a:1272:G:H2'	2.36	0.41
49:a:1408:A:H2'	49:a:1409:A:O4'	2.21	0.41
50:i:122:GLN:O	50:i:127:VAL:HG12	2.21	0.41
56:4:422:ILE:HD13	56:4:429:LEU:HD13	2.02	0.41
57:u:59:SER:OG	57:u:61:TRP:HE3	2.02	0.41
4:r:21:VAL:HG23	4:r:22:PHE:N	2.36	0.41
4:r:78:PRO:C	4:r:80:GLY:N	2.79	0.41
9:n:108:THR:OG1	9:n:109:SER:N	2.54	0.41
10:q:49:ASN:HA	49:a:663:G:N2	2.35	0.41
12:v:60:VAL:HG21	18:A:830:A:C8	2.55	0.41
13:w:22:VAL:HG21	13:w:59:TRP:CD1	2.55	0.41
14:x:17:ARG:HH12	14:x:20:ARG:H	1.67	0.41
14:x:17:ARG:NH1	14:x:18:GLY:O	2.54	0.41
18:A:289:A:O2'	18:A:303:G:O2'	2.23	0.41
18:A:1514:C:C2	18:A:1515:C:C5	3.09	0.41
18:A:1621:C:H2'	18:A:1622:G:N7	2.36	0.41
18:A:1886:A:H4'	18:A:1887:A:O5'	2.21	0.41
18:A:2338:G:C8	18:A:2340:A:C5	3.09	0.41
19:B:115:A:H2'	19:B:116:C:C6	2.55	0.41
28:K:102:GLU:O	28:K:106:ILE:HG12	2.20	0.41
32:O:70:ILE:HD11	32:O:76:VAL:HB	2.02	0.41
37:T:96:ALA:O	37:T:99:ARG:HG2	2.21	0.41
49:a:26:G:H4'	49:a:867:G:C8	2.55	0.41
49:a:337:G:C2	49:a:338:A:C5	3.08	0.41
49:a:485:G:HO2'	49:a:486:G:P	2.43	0.41
49:a:488:C:O4'	49:a:489:A:H2	2.03	0.41
49:a:981:C:O2'	49:a:1022:G:N2	2.53	0.41
49:a:1146:G:C8	49:a:1147:G:C8	3.09	0.41
49:a:1264:C:H3'	49:a:1265:U:H5''	2.03	0.41
49:a:1269:A:H2'	49:a:1270:A:C8	2.55	0.41
50:i:135:LYS:HA	50:i:138:GLN:HB2	2.03	0.41
3:g:38:CYS:SG	3:g:40:GLN:HB2	2.61	0.41
6:j:53:LYS:HD2	6:j:198:LEU:HD21	2.03	0.41
6:j:140:VAL:HG21	6:j:150:PHE:CZ	2.56	0.41
9:n:10:PHE:CD1	9:n:27:LEU:HD22	2.56	0.41
10:q:134:LYS:HD2	49:a:1507:G:OP1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:s:9:ARG:NH1	49:a:862:C:OP1	2.51	0.41
16:h:118:GLU:O	16:h:122:GLN:HG3	2.21	0.41
18:A:263:G:H2'	18:A:264:G:O4'	2.21	0.41
18:A:469:G:N2	18:A:482:U:H1'	2.35	0.41
18:A:490:A:N6	18:A:491:U:O4	2.54	0.41
18:A:664:A:H5''	18:A:665:G:OP2	2.21	0.41
18:A:857:U:H2'	18:A:858:A:H8	1.86	0.41
18:A:958:A:H2'	18:A:959:U:C6	2.56	0.41
18:A:1566:A:H2'	18:A:1567:C:H5''	2.03	0.41
18:A:1594:G:H2'	18:A:1595:G:C8	2.55	0.41
18:A:1791:A:H2'	18:A:1792:A:C8	2.56	0.41
18:A:3059:G:C4	18:A:3060:A:C8	3.08	0.41
19:B:117:A:H2'	19:B:118:C:C6	2.56	0.41
22:E:166:ALA:O	22:E:170:ARG:HG3	2.20	0.41
23:F:10:ARG:HD3	23:F:108:ASP:OD1	2.21	0.41
23:F:168:THR:OG1	23:F:169:ASN:N	2.53	0.41
24:G:116:ILE:HD11	24:G:152:LEU:HD11	2.03	0.41
25:H:12:LEU:HD23	25:H:12:LEU:HA	1.87	0.41
26:I:122:LYS:HG2	26:I:126:LEU:HD12	2.03	0.41
33:P:40:VAL:HG11	33:P:113:ILE:HD12	2.03	0.41
33:P:46:HIS:HB3	33:P:65:SER:HB2	2.03	0.41
35:R:95:LEU:HD23	35:R:95:LEU:HA	1.84	0.41
37:T:7:PHE:HB3	37:T:116:SER:O	2.21	0.41
39:V:11:VAL:HG12	39:V:71:VAL:HG12	2.02	0.41
49:a:53:U:O2'	49:a:54:A:H2'	2.21	0.41
49:a:98:G:H2'	49:a:99:U:H6	1.85	0.41
49:a:339:C:H2'	49:a:340:U:C6	2.56	0.41
49:a:534:U:H2'	49:a:535:C:C6	2.55	0.41
49:a:959:A:O2'	49:a:963:U:N3	2.27	0.41
49:a:1146:G:H5''	49:a:1147:G:N7	2.36	0.41
49:a:1480:C:C2	49:a:1481:G:C8	3.09	0.41
49:a:1486:A:H2	49:a:1489:G:H22	1.68	0.41
56:4:445:THR:OG1	56:4:448:GLY:O	2.30	0.41
13:w:47:SER:HB3	49:a:452:A:C2	2.56	0.41
14:x:32:MET:HB2	14:x:35:THR:OG1	2.21	0.41
18:A:543:U:C5	18:A:561:G:H5'	2.56	0.41
18:A:1302:G:H8	18:A:1302:G:O5'	2.03	0.41
18:A:1547:G:N2	18:A:1624:U:H1'	2.36	0.41
18:A:1651:C:H2'	18:A:1652:A:C8	2.56	0.41
18:A:2370:A:H2'	18:A:2371:G:O4'	2.21	0.41
18:A:2410:A:H2'	18:A:2411:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:2971:G:H21	18:A:2981:A:H62	1.68	0.41
26:I:90:ALA:HB1	26:I:124:ALA:HB2	2.02	0.41
28:K:14:SER:O	28:K:52:ASP:HB3	2.20	0.41
28:K:125:TYR:OH	28:K:132:HIS:NE2	2.37	0.41
32:O:3:LYS:HA	32:O:4:PRO:HD3	1.93	0.41
38:U:24:ILE:HD13	38:U:28:VAL:O	2.21	0.41
40:W:164:LEU:HB3	40:W:168:VAL:HG23	2.02	0.41
42:Z:7:PRO:HA	42:Z:10:LEU:HB2	2.03	0.41
42:Z:20:ASP:O	42:Z:24:GLU:HG2	2.21	0.41
48:5:24:C:H2'	48:5:25:U:H6	1.85	0.41
49:a:335:C:C2	49:a:336:A:C8	3.09	0.41
49:a:937:A:O2'	55:y:83:HIS:NE2	2.40	0.41
49:a:966:C:N3	49:a:1203:G:C2	2.89	0.41
49:a:1037:G:C4	49:a:1038:G:C8	3.09	0.41
49:a:1232:A:H62	49:a:1268:C:N4	2.18	0.41
50:i:106:LYS:HB3	50:i:106:LYS:HE2	1.94	0.41
4:r:19:LYS:CB	49:a:827:U:OP1	2.67	0.40
6:j:76:ARG:HH21	49:a:593:C:P	2.43	0.40
13:w:43:LYS:HA	49:a:450:G:H4'	2.03	0.40
15:z:63:SER:OG	49:a:209:A:H5''	2.21	0.40
18:A:932:C:H2'	18:A:933:G:O4'	2.22	0.40
18:A:1198:C:H2'	18:A:1199:U:C6	2.56	0.40
18:A:2247:A:H2'	18:A:2248:C:C6	2.56	0.40
18:A:2367:G:H4'	18:A:2368:C:H5	1.86	0.40
20:C:172:TYR:HB3	20:C:184:ARG:HD2	2.02	0.40
23:F:113:ILE:HD13	23:F:113:ILE:HA	1.95	0.40
49:a:72:G:H21	49:a:148:A:N6	2.19	0.40
49:a:496:U:O2	49:a:496:U:H2'	2.21	0.40
49:a:609:G:H2'	49:a:610:C:O4'	2.20	0.40
49:a:996:G:H22	49:a:998:G:H3'	1.86	0.40
49:a:1329:G:H22	49:a:1357:A:P	2.44	0.40
49:a:1333:U:O4	49:a:1354:G:O6	2.40	0.40
54:t:115:ARG:HB3	54:t:117:ILE:HD11	2.02	0.40
56:4:382:LEU:HD22	56:4:386:LEU:HD13	2.04	0.40
57:u:14:PRO:HB3	57:u:19:ARG:HB2	2.03	0.40
1:Y:3:ALA:O	1:Y:12:PRO:HD3	2.21	0.40
2:c:40:LYS:O	2:c:51:HIS:CE1	2.74	0.40
3:g:35:VAL:HG23	3:g:37:VAL:N	2.36	0.40
7:k:194:MET:HE2	7:k:194:MET:HB3	1.93	0.40
13:w:82:LYS:HD3	13:w:89:ALA:H	1.86	0.40
18:A:13:G:H5''	44:b:14:ARG:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A:1506:U:C2	18:A:1509:U:O4	2.75	0.40
18:A:1900:C:H2'	18:A:1901:C:H6	1.86	0.40
18:A:2908:U:OP1	34:Q:57:THR:HG21	2.21	0.40
19:B:74:A:N3	19:B:74:A:H2'	2.36	0.40
24:G:53:VAL:HG23	24:G:66:HIS:CE1	2.56	0.40
48:5:22:A:H2'	48:5:23:G:O4'	2.22	0.40
49:a:498:C:H2'	49:a:510:G:C8	2.57	0.40
49:a:759:C:H2'	49:a:760:G:O4'	2.21	0.40
49:a:772:A:O2'	49:a:774:A:N7	2.49	0.40
49:a:1139:C:N4	49:a:1141:G:C2	2.89	0.40
49:a:1243:U:H3'	49:a:1244:G:H8	1.87	0.40
51:m:46:ALA:CB	51:m:124:ILE:HD12	2.51	0.40
51:m:111:ARG:O	51:m:113:GLU:N	2.54	0.40
54:t:33:ILE:HD12	54:t:64:LEU:HD11	2.03	0.40
10:q:96:LYS:HB2	10:q:122:VAL:O	2.21	0.40
13:w:101:SER:O	13:w:105:LEU:HG	2.21	0.40
16:h:215:LYS:HA	16:h:215:LYS:HD2	1.90	0.40
18:A:1000:C:N4	18:A:1002:C:O2	2.54	0.40
18:A:1118:A:H2'	18:A:1119:A:C8	2.57	0.40
18:A:1500:A:O2'	18:A:1511:U:O2	2.38	0.40
18:A:1550:G:C6	18:A:1621:C:C4	3.09	0.40
18:A:1950:G:C2	18:A:1951:G:C8	3.10	0.40
18:A:2819:G:N2	18:A:2822:A:OP2	2.50	0.40
19:B:1:G:N1	19:B:117:A:C2	2.90	0.40
30:M:110:VAL:O	30:M:127:ASN:HB2	2.22	0.40
49:a:325:A:H2'	49:a:326:G:O4'	2.22	0.40
49:a:1099:C:H2'	49:a:1100:U:H6	1.86	0.40
49:a:1106:U:O4	53:p:9:ARG:NH1	2.55	0.40
49:a:1137:G:N2	49:a:1160:A:N6	2.33	0.40
49:a:1178:A:H8	49:a:1178:A:OP2	2.05	0.40
49:a:1291:G:C6	49:a:1311:G:C5	3.09	0.40
50:i:122:GLN:HB3	50:i:127:VAL:HG11	2.03	0.40
57:u:38:GLY:O	57:u:39:LEU:HD23	2.22	0.40
6:j:165:TRP:CD2	6:j:181:PRO:HB3	2.56	0.40
18:A:728:G:H2'	18:A:729:C:C6	2.56	0.40
18:A:800:A:C8	18:A:888:U:C4	3.10	0.40
18:A:1538:G:H8	18:A:1538:G:P	2.45	0.40
18:A:1600:G:H2'	18:A:1601:G:H8	1.86	0.40
18:A:1717:U:H5''	18:A:1718:C:H5	1.87	0.40
18:A:2328:G:C6	18:A:2329:G:N7	2.89	0.40
23:F:81:ILE:HG13	23:F:86:LEU:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:T:24:ALA:O	37:T:28:ILE:HG12	2.22	0.40
45:d:29:ALA:O	45:d:33:ILE:HG12	2.21	0.40
49:a:448:A:OP2	49:a:465:G:N2	2.27	0.40
49:a:804:U:H2'	49:a:805:A:C8	2.56	0.40
49:a:981:C:H1'	49:a:1022:G:H22	1.87	0.40
49:a:1014:U:HO2'	49:a:1015:G:P	2.42	0.40
49:a:1336:C:C2	49:a:1337:A:C8	3.09	0.40
1:Y:36:VAL:HG22	1:Y:49:ILE:CG1	2.52	0.40
4:r:72:ARG:HD3	4:r:78:PRO:O	2.22	0.40
6:j:14:ARG:HD3	6:j:32:PRO:HB3	2.02	0.40
8:l:41:ASP:OD2	8:l:43:TRP:HD1	2.05	0.40
16:h:87:VAL:HG23	16:h:89:MET:H	1.87	0.40
18:A:624:G:O2'	18:A:648:A:N6	2.54	0.40
18:A:771:G:H2'	18:A:772:U:O4'	2.22	0.40
18:A:1250:U:H3'	18:A:1251:A:H5''	2.04	0.40
18:A:2070:A:H2'	18:A:2071:A:H8	1.86	0.40
18:A:2211:C:H2'	18:A:2212:A:C8	2.54	0.40
18:A:2339:G:H3'	18:A:2340:A:C8	2.55	0.40
18:A:2359:G:H2'	18:A:2360:C:C6	2.57	0.40
18:A:2538:A:H5'	23:F:42:VAL:HG21	2.03	0.40
49:a:601:A:H2'	49:a:602:A:H8	1.86	0.40
49:a:1008:C:H2'	49:a:1009:C:C6	2.57	0.40
49:a:1039:C:O2'	49:a:1040:U:H5'	2.22	0.40
49:a:1117:U:O2'	49:a:1118:A:H5''	2.21	0.40
49:a:1130:C:P	52:o:31:ARG:HH12	2.44	0.40
49:a:1320:G:HO2'	49:a:1321:A:P	2.43	0.40
50:i:34:GLU:O	50:i:38:ILE:HG12	2.21	0.40
51:m:70:LYS:C	51:m:138:ARG:HH21	2.29	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	
1	Y	61/64 (95%)	49 (80%)	12 (20%)	0	100	100
2	c	47/55 (86%)	46 (98%)	1 (2%)	0	100	100
3	g	46/75 (61%)	33 (72%)	10 (22%)	3 (6%)	1	7
4	r	63/84 (75%)	53 (84%)	10 (16%)	0	100	100
5	l	30/33 (91%)	30 (100%)	0	0	100	100
6	j	198/201 (98%)	167 (84%)	31 (16%)	0	100	100
7	k	178/214 (83%)	168 (94%)	10 (6%)	0	100	100
8	l	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
9	n	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
10	q	113/138 (82%)	103 (91%)	10 (9%)	0	100	100
11	s	120/124 (97%)	106 (88%)	14 (12%)	0	100	100
12	v	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
13	w	111/156 (71%)	91 (82%)	20 (18%)	0	100	100
14	x	92/98 (94%)	85 (92%)	7 (8%)	0	100	100
15	z	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
16	h	226/277 (82%)	204 (90%)	22 (10%)	0	100	100
17	3	21/24 (88%)	21 (100%)	0	0	100	100
20	C	273/278 (98%)	258 (94%)	15 (6%)	0	100	100
21	D	212/217 (98%)	195 (92%)	16 (8%)	1 (0%)	24	55
22	E	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
23	F	180/187 (96%)	165 (92%)	15 (8%)	0	100	100
24	G	174/179 (97%)	165 (95%)	9 (5%)	0	100	100
25	H	149/151 (99%)	141 (95%)	8 (5%)	0	100	100
26	I	124/175 (71%)	115 (93%)	9 (7%)	0	100	100
27	J	131/142 (92%)	112 (86%)	19 (14%)	0	100	100
28	K	141/147 (96%)	133 (94%)	8 (6%)	0	100	100
29	L	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
30	M	143/147 (97%)	127 (89%)	16 (11%)	0	100	100
31	N	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
32	O	116/199 (58%)	110 (95%)	6 (5%)	0	100	100
33	P	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
34	Q	111/113 (98%)	101 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	R	122/129 (95%)	117 (96%)	5 (4%)	0	100	100
36	S	98/103 (95%)	94 (96%)	4 (4%)	0	100	100
37	T	112/153 (73%)	107 (96%)	5 (4%)	0	100	100
38	U	95/100 (95%)	89 (94%)	6 (6%)	0	100	100
39	V	93/105 (89%)	84 (90%)	9 (10%)	0	100	100
40	W	190/215 (88%)	182 (96%)	8 (4%)	0	100	100
41	X	77/88 (88%)	74 (96%)	3 (4%)	0	100	100
42	Z	62/77 (80%)	62 (100%)	0	0	100	100
43	2	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
44	b	52/57 (91%)	52 (100%)	0	0	100	100
45	d	44/47 (94%)	44 (100%)	0	0	100	100
46	e	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
47	f	35/37 (95%)	35 (100%)	0	0	100	100
50	i	206/275 (75%)	173 (84%)	33 (16%)	0	100	100
51	m	153/156 (98%)	131 (86%)	22 (14%)	0	100	100
52	o	124/150 (83%)	103 (83%)	21 (17%)	0	100	100
53	p	97/101 (96%)	89 (92%)	8 (8%)	0	100	100
54	t	106/124 (86%)	88 (83%)	18 (17%)	0	100	100
55	y	80/93 (86%)	67 (84%)	13 (16%)	0	100	100
56	4	265/470 (56%)	250 (94%)	15 (6%)	0	100	100
57	u	58/61 (95%)	48 (83%)	10 (17%)	0	100	100
All	All	6224/7149 (87%)	5721 (92%)	499 (8%)	4 (0%)	49	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	g	4	GLY
3	g	3	THR
21	D	156	THR
3	g	10	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	50/51 (98%)	47 (94%)	3 (6%)	17	44
2	c	47/52 (90%)	44 (94%)	3 (6%)	16	42
3	g	43/63 (68%)	36 (84%)	7 (16%)	2	10
4	r	55/72 (76%)	51 (93%)	4 (7%)	13	38
5	l	30/31 (97%)	30 (100%)	0	100	100
6	j	175/176 (99%)	175 (100%)	0	100	100
7	k	127/147 (86%)	125 (98%)	2 (2%)	55	70
8	l	85/85 (100%)	85 (100%)	0	100	100
9	n	107/108 (99%)	107 (100%)	0	100	100
10	q	89/105 (85%)	89 (100%)	0	100	100
11	s	103/105 (98%)	102 (99%)	1 (1%)	68	75
12	v	76/77 (99%)	75 (99%)	1 (1%)	61	73
13	w	92/118 (78%)	88 (96%)	4 (4%)	26	52
14	x	80/83 (96%)	79 (99%)	1 (1%)	61	73
15	z	69/70 (99%)	68 (99%)	1 (1%)	59	72
16	h	191/218 (88%)	191 (100%)	0	100	100
17	3	18/19 (95%)	18 (100%)	0	100	100
20	C	215/218 (99%)	215 (100%)	0	100	100
21	D	160/163 (98%)	160 (100%)	0	100	100
22	E	169/173 (98%)	169 (100%)	0	100	100
23	F	151/156 (97%)	151 (100%)	0	100	100
24	G	148/150 (99%)	147 (99%)	1 (1%)	76	79
25	H	90/116 (78%)	89 (99%)	1 (1%)	65	75
26	I	89/120 (74%)	89 (100%)	0	100	100
27	J	102/108 (94%)	102 (100%)	0	100	100
28	K	119/120 (99%)	118 (99%)	1 (1%)	73	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	L	100/100 (100%)	99 (99%)	1 (1%)	68	75
30	M	112/114 (98%)	111 (99%)	1 (1%)	70	76
31	N	114/116 (98%)	113 (99%)	1 (1%)	70	76
32	O	97/158 (61%)	97 (100%)	0	100	100
33	P	93/94 (99%)	92 (99%)	1 (1%)	65	75
34	Q	100/100 (100%)	98 (98%)	2 (2%)	48	66
35	R	97/99 (98%)	97 (100%)	0	100	100
36	S	81/83 (98%)	81 (100%)	0	100	100
37	T	90/117 (77%)	89 (99%)	1 (1%)	65	75
38	U	83/85 (98%)	83 (100%)	0	100	100
39	V	81/86 (94%)	81 (100%)	0	100	100
40	W	155/168 (92%)	154 (99%)	1 (1%)	78	81
41	X	58/63 (92%)	58 (100%)	0	100	100
42	Z	58/66 (88%)	57 (98%)	1 (2%)	53	69
43	2	52/54 (96%)	52 (100%)	0	100	100
44	b	43/46 (94%)	43 (100%)	0	100	100
45	d	35/36 (97%)	35 (100%)	0	100	100
46	e	53/54 (98%)	53 (100%)	0	100	100
47	f	35/35 (100%)	35 (100%)	0	100	100
50	i	170/212 (80%)	168 (99%)	2 (1%)	63	74
51	m	131/132 (99%)	131 (100%)	0	100	100
52	o	102/125 (82%)	102 (100%)	0	100	100
53	p	89/90 (99%)	88 (99%)	1 (1%)	65	75
54	t	93/104 (89%)	92 (99%)	1 (1%)	65	75
55	y	73/84 (87%)	73 (100%)	0	100	100
56	4	220/372 (59%)	220 (100%)	0	100	100
57	u	49/50 (98%)	46 (94%)	3 (6%)	17	44
All	All	5144/5747 (90%)	5098 (99%)	46 (1%)	68	76

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

Mol	Chain	Res	Type
1	Y	36	VAL

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Mol	Chain	Res	Type
1	Y	48	ARG
1	Y	52	CYS
2	c	6	ASP
2	c	7	VAL
2	c	18	CYS
3	g	1	MET
3	g	9	TYR
3	g	18	CYS
3	g	22	PHE
3	g	33	ILE
3	g	35	VAL
3	g	45	TYR
4	r	33	LYS
4	r	45	ARG
4	r	54	THR
4	r	79	PHE
7	k	49	VAL
7	k	155	SER
11	s	63	VAL
12	v	20	THR
13	w	36	VAL
13	w	67	THR
13	w	69	PRO
13	w	70	VAL
14	x	79	THR
15	z	30	THR
24	G	148	VAL
25	H	129	THR
28	K	94	GLU
29	L	12	ASP
30	M	32	THR
31	N	49	SER
33	P	101	VAL
34	Q	2	ASN
34	Q	3	THR
37	T	80	THR
40	W	140	ILE
42	Z	44	ASN
50	i	170	GLU
50	i	182	ILE
53	p	66	GLU
54	t	105	THR

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Mol	Chain	Res	Type
57	u	6	LEU
57	u	31	HIS
57	u	44	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (79) such sidechains are listed below:

Mol	Chain	Res	Type
1	Y	22	HIS
2	c	20	HIS
2	c	22	ASN
2	c	48	HIS
2	c	49	GLN
2	c	51	HIS
5	l	17	HIS
7	k	95	ASN
8	l	28	ASN
9	n	93	ASN
10	q	127	HIS
12	v	28	GLN
12	v	37	GLN
13	w	65	GLN
15	z	22	GLN
15	z	52	HIS
15	z	71	GLN
15	z	74	ASN
16	h	18	HIS
16	h	44	GLN
16	h	94	GLN
16	h	112	GLN
16	h	122	GLN
17	3	17	ASN
20	C	87	ASN
20	C	91	ASN
20	C	109	GLN
20	C	203	ASN
21	D	15	GLN
21	D	80	HIS
21	D	130	HIS
22	E	100	GLN
22	E	208	ASN
23	F	34	GLN
23	F	58	ASN

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Mol	Chain	Res	Type
23	F	128	GLN
23	F	169	ASN
24	G	66	HIS
24	G	98	GLN
24	G	144	GLN
25	H	111	ASN
25	H	151	GLN
26	I	35	ASN
28	K	147	GLN
30	M	107	ASN
31	N	57	HIS
32	O	61	HIS
33	P	9	ASN
35	R	72	ASN
35	R	122	ASN
36	S	47	ASN
36	S	92	GLN
36	S	93	GLN
38	U	58	ASN
40	W	156	GLN
40	W	169	ASN
41	X	12	ASN
41	X	19	GLN
42	Z	52	GLN
43	2	19	GLN
44	b	12	ASN
44	b	19	GLN
50	i	68	HIS
50	i	117	GLN
50	i	125	ASN
51	m	14	ASN
51	m	28	ASN
51	m	86	GLN
51	m	148	ASN
52	o	64	HIS
52	o	111	GLN
53	p	47	ASN
54	t	106	ASN
55	y	14	HIS
56	4	330	HIS
56	4	344	ASN
56	4	444	HIS

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Mol	Chain	Res	Type
57	u	11	ASN
57	u	25	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
18	A	3118/3120 (99%)	610 (19%)	25 (0%)
19	B	117/118 (99%)	15 (12%)	1 (0%)
48	5	76/77 (98%)	21 (27%)	2 (2%)
49	a	1510/1528 (98%)	448 (29%)	0
All	All	4821/4843 (99%)	1094 (22%)	28 (0%)

All (1094) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
18	A	7	U
18	A	9	U
18	A	12	G
18	A	20	G
18	A	31	U
18	A	47	U
18	A	55	G
18	A	59	G
18	A	60	A
18	A	61	G
18	A	68	A
18	A	71	A
18	A	72	G
18	A	91	C
18	A	94	G
18	A	98	U
18	A	99	G
18	A	102	C
18	A	115	A
18	A	116	A
18	A	117	U
18	A	125	C
18	A	133	G
18	A	137	G
18	A	140	G
18	A	161	U

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Mol	Chain	Res	Type
18	A	164	A
18	A	175	G
18	A	176	G
18	A	180	A
18	A	195	A
18	A	198	A
18	A	200	C
18	A	203	A
18	A	212	A
18	A	214	G
18	A	215	A
18	A	221	A
18	A	227	A
18	A	228	A
18	A	229	U
18	A	230	G
18	A	231	U
18	A	248	G
18	A	250	G
18	A	265	A
18	A	266	U
18	A	268	G
18	A	270	U
18	A	275	C
18	A	276	G
18	A	283	U
18	A	285	U
18	A	286	G
18	A	287	A
18	A	288	U
18	A	289	A
18	A	290	C
18	A	291	C
18	A	292	G
18	A	296	A
18	A	297	G
18	A	300	G
18	A	302	U
18	A	303	G
18	A	305	G
18	A	312	G
18	A	314	G

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Mol	Chain	Res	Type
18	A	315	U
18	A	317	G
18	A	318	U
18	A	319	G
18	A	322	A
18	A	323	C
18	A	324	C
18	A	326	A
18	A	328	C
18	A	330	U
18	A	331	U
18	A	332	C
18	A	336	C
18	A	338	C
18	A	339	U
18	A	342	C
18	A	344	G
18	A	345	G
18	A	350	A
18	A	351	G
18	A	357	U
18	A	358	G
18	A	361	A
18	A	364	A
18	A	366	G
18	A	369	G
18	A	370	U
18	A	384	G
18	A	387	U
18	A	393	U
18	A	406	A
18	A	412	A
18	A	413	G
18	A	417	C
18	A	424	G
18	A	434	G
18	A	437	G
18	A	445	U
18	A	446	G
18	A	450	G
18	A	452	G
18	A	454	U

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Mol	Chain	Res	Type
18	A	460	G
18	A	474	G
18	A	489	A
18	A	493	U
18	A	494	G
18	A	498	G
18	A	505	C
18	A	512	G
18	A	543	U
18	A	544	U
18	A	555	G
18	A	568	A
18	A	569	G
18	A	589	A
18	A	590	A
18	A	591	G
18	A	592	A
18	A	594	U
18	A	595	A
18	A	596	C
18	A	605	G
18	A	617	U
18	A	618	C
18	A	619	C
18	A	620	G
18	A	623	A
18	A	634	C
18	A	635	G
18	A	636	U
18	A	637	G
18	A	638	U
18	A	641	U
18	A	642	G
18	A	644	G
18	A	647	G
18	A	655	G
18	A	665	G
18	A	666	A
18	A	667	A
18	A	675	G
18	A	678	A
18	A	679	G

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Mol	Chain	Res	Type
18	A	684	G
18	A	685	G
18	A	696	A
18	A	706	G
18	A	707	G
18	A	708	G
18	A	709	U
18	A	721	A
18	A	728	G
18	A	730	G
18	A	731	A
18	A	738	A
18	A	740	A
18	A	742	G
18	A	747	A
18	A	755	A
18	A	757	G
18	A	759	G
18	A	760	U
18	A	765	G
18	A	766	G
18	A	768	G
18	A	784	G
18	A	801	U
18	A	832	G
18	A	839	U
18	A	845	C
18	A	862	U
18	A	863	G
18	A	868	C
18	A	872	G
18	A	879	A
18	A	880	G
18	A	890	G
18	A	891	G
18	A	897	A
18	A	899	G
18	A	900	G
18	A	920	G
18	A	927	C
18	A	942	U
18	A	974	G

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Mol	Chain	Res	Type
18	A	975	U
18	A	981	U
18	A	982	A
18	A	993	G
18	A	994	A
18	A	997	G
18	A	1001	C
18	A	1002	C
18	A	1003	A
18	A	1005	A
18	A	1006	G
18	A	1007	G
18	A	1010	U
18	A	1011	A
18	A	1012	C
18	A	1013	U
18	A	1014	G
18	A	1025	A
18	A	1044	U
18	A	1047	A
18	A	1048	A
18	A	1049	G
18	A	1058	A
18	A	1063	G
18	A	1068	C
18	A	1076	A
18	A	1078	G
18	A	1084	U
18	A	1085	G
18	A	1091	A
18	A	1092	G
18	A	1101	A
18	A	1114	G
18	A	1130	C
18	A	1131	G
18	A	1140	G
18	A	1143	G
18	A	1144	A
18	A	1151	U
18	A	1164	A
18	A	1165	G
18	A	1175	A

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Mol	Chain	Res	Type
18	A	1178	U
18	A	1181	G
18	A	1184	U
18	A	1185	A
18	A	1186	G
18	A	1187	A
18	A	1188	A
18	A	1189	G
18	A	1190	C
18	A	1191	A
18	A	1192	G
18	A	1201	G
18	A	1202	A
18	A	1205	G
18	A	1206	A
18	A	1207	G
18	A	1208	U
18	A	1213	A
18	A	1219	U
18	A	1225	G
18	A	1227	C
18	A	1229	A
18	A	1230	G
18	A	1234	U
18	A	1238	G
18	A	1240	G
18	A	1250	U
18	A	1251	A
18	A	1253	C
18	A	1254	G
18	A	1260	C
18	A	1261	A
18	A	1292	U
18	A	1293	G
18	A	1298	C
18	A	1326	G
18	A	1335	G
18	A	1339	G
18	A	1343	G
18	A	1344	A
18	A	1345	G
18	A	1351	G

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Mol	Chain	Res	Type
18	A	1353	G
18	A	1362	A
18	A	1365	G
18	A	1371	G
18	A	1377	A
18	A	1380	A
18	A	1386	G
18	A	1387	A
18	A	1389	U
18	A	1415	A
18	A	1416	A
18	A	1436	C
18	A	1440	C
18	A	1456	G
18	A	1462	G
18	A	1465	C
18	A	1467	U
18	A	1474	A
18	A	1480	A
18	A	1493	A
18	A	1494	U
18	A	1499	A
18	A	1501	C
18	A	1502	G
18	A	1507	G
18	A	1508	A
18	A	1510	A
18	A	1522	G
18	A	1529	U
18	A	1531	C
18	A	1532	G
18	A	1533	U
18	A	1534	C
18	A	1538	G
18	A	1541	G
18	A	1543	A
18	A	1545	C
18	A	1549	G
18	A	1550	G
18	A	1551	U
18	A	1553	C
18	A	1554	U

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Mol	Chain	Res	Type
18	A	1563	A
18	A	1565	A
18	A	1566	A
18	A	1567	C
18	A	1570	C
18	A	1573	U
18	A	1574	G
18	A	1579	C
18	A	1587	G
18	A	1588	G
18	A	1589	G
18	A	1596	C
18	A	1597	G
18	A	1599	U
18	A	1600	G
18	A	1603	G
18	A	1605	G
18	A	1606	G
18	A	1608	U
18	A	1609	G
18	A	1610	C
18	A	1623	U
18	A	1624	U
18	A	1627	U
18	A	1628	A
18	A	1629	G
18	A	1630	U
18	A	1631	A
18	A	1632	G
18	A	1633	U
18	A	1634	C
18	A	1636	A
18	A	1639	G
18	A	1640	A
18	A	1641	U
18	A	1648	A
18	A	1649	C
18	A	1673	A
18	A	1674	G
18	A	1676	G
18	A	1678	U
18	A	1679	A

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Mol	Chain	Res	Type
18	A	1680	A
18	A	1681	U
18	A	1703	G
18	A	1714	A
18	A	1717	U
18	A	1723	U
18	A	1728	U
18	A	1729	A
18	A	1730	U
18	A	1731	A
18	A	1737	A
18	A	1738	G
18	A	1754	G
18	A	1755	A
18	A	1756	G
18	A	1757	U
18	A	1767	U
18	A	1769	G
18	A	1778	A
18	A	1786	G
18	A	1789	A
18	A	1798	U
18	A	1826	A
18	A	1834	A
18	A	1864	U
18	A	1866	C
18	A	1867	G
18	A	1869	G
18	A	1870	U
18	A	1871	G
18	A	1872	A
18	A	1892	G
18	A	1933	G
18	A	1938	G
18	A	1947	U
18	A	1955	A
18	A	1975	A
18	A	1981	U
18	A	1990	A
18	A	2017	C
18	A	2018	G
18	A	2026	A

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Mol	Chain	Res	Type
18	A	2033	U
18	A	2046	A
18	A	2064	A
18	A	2065	A
18	A	2074	G
18	A	2075	G
18	A	2086	U
18	A	2087	C
18	A	2088	C
18	A	2089	C
18	A	2090	U
18	A	2091	U
18	A	2092	U
18	A	2093	G
18	A	2094	G
18	A	2095	G
18	A	2096	G
18	A	2107	G
18	A	2127	G
18	A	2130	G
18	A	2137	A
18	A	2138	C
18	A	2141	U
18	A	2153	G
18	A	2154	G
18	A	2158	C
18	A	2160	A
18	A	2162	A
18	A	2179	U
18	A	2190	A
18	A	2191	C
18	A	2194	A
18	A	2195	U
18	A	2196	G
18	A	2215	U
18	A	2217	U
18	A	2221	A
18	A	2247	A
18	A	2251	G
18	A	2255	A
18	A	2256	G
18	A	2257	A

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Mol	Chain	Res	Type
18	A	2267	C
18	A	2279	C
18	A	2280	G
18	A	2284	A
18	A	2285	G
18	A	2286	A
18	A	2319	G
18	A	2320	C
18	A	2331	U
18	A	2332	U
18	A	2333	G
18	A	2334	U
18	A	2335	G
18	A	2336	U
18	A	2337	A
18	A	2338	G
18	A	2339	G
18	A	2340	A
18	A	2341	U
18	A	2342	A
18	A	2343	G
18	A	2344	G
18	A	2346	G
18	A	2347	G
18	A	2348	G
18	A	2349	A
18	A	2350	G
18	A	2351	A
18	A	2352	C
18	A	2354	G
18	A	2356	G
18	A	2359	G
18	A	2360	C
18	A	2362	C
18	A	2367	G
18	A	2368	C
18	A	2369	C
18	A	2370	A
18	A	2373	G
18	A	2378	U
18	A	2381	A
18	A	2382	G

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Mol	Chain	Res	Type
18	A	2384	C
18	A	2385	G
18	A	2386	U
18	A	2387	U
18	A	2388	G
18	A	2389	U
18	A	2390	U
18	A	2391	G
18	A	2392	A
18	A	2393	A
18	A	2394	A
18	A	2395	U
18	A	2396	A
18	A	2397	C
18	A	2399	A
18	A	2401	U
18	A	2406	U
18	A	2407	C
18	A	2409	U
18	A	2421	A
18	A	2427	G
18	A	2434	A
18	A	2436	A
18	A	2449	A
18	A	2462	G
18	A	2463	G
18	A	2467	U
18	A	2490	A
18	A	2497	A
18	A	2503	G
18	A	2507	C
18	A	2510	A
18	A	2511	A
18	A	2512	A
18	A	2529	A
18	A	2532	G
18	A	2535	A
18	A	2544	U
18	A	2546	A
18	A	2549	G
18	A	2558	C
18	A	2559	A

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Mol	Chain	Res	Type
18	A	2569	G
18	A	2571	C
18	A	2574	C
18	A	2582	A
18	A	2585	U
18	A	2607	G
18	A	2609	A
18	A	2627	C
18	A	2630	A
18	A	2647	U
18	A	2649	A
18	A	2652	G
18	A	2653	G
18	A	2654	A
18	A	2659	A
18	A	2665	C
18	A	2672	A
18	A	2694	G
18	A	2698	C
18	A	2699	C
18	A	2700	A
18	A	2715	U
18	A	2716	U
18	A	2718	G
18	A	2722	C
18	A	2726	G
18	A	2728	U
18	A	2729	G
18	A	2742	A
18	A	2744	C
18	A	2749	G
18	A	2753	G
18	A	2778	U
18	A	2786	U
18	A	2790	A
18	A	2791	G
18	A	2796	A
18	A	2797	C
18	A	2826	A
18	A	2827	G
18	A	2833	U
18	A	2837	U

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Mol	Chain	Res	Type
18	A	2838	A
18	A	2839	U
18	A	2853	C
18	A	2862	G
18	A	2865	G
18	A	2887	G
18	A	2906	U
18	A	2912	A
18	A	2913	U
18	A	2926	A
18	A	2936	C
18	A	2938	G
18	A	2948	C
18	A	2950	C
18	A	2953	U
18	A	2957	A
18	A	2968	G
18	A	2972	A
18	A	2980	U
18	A	2985	G
18	A	3002	A
18	A	3011	C
18	A	3015	C
18	A	3016	C
18	A	3021	A
18	A	3022	G
18	A	3041	C
18	A	3042	A
18	A	3056	A
18	A	3082	U
18	A	3088	C
18	A	3093	A
18	A	3101	C
18	A	3105	C
18	A	3106	C
18	A	3113	A
18	A	3114	A
18	A	3115	A
19	B	9	G
19	B	11	U
19	B	13	C
19	B	14	A

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Mol	Chain	Res	Type
19	B	23	G
19	B	25	G
19	B	57	U
19	B	58	A
19	B	67	A
19	B	87	U
19	B	89	C
19	B	90	G
19	B	103	G
19	B	107	A
19	B	115	A
48	5	5	G
48	5	6	G
48	5	12	G
48	5	15	G
48	5	19	G
48	5	20	G
48	5	21	U
48	5	22	A
48	5	27	G
48	5	33	C
48	5	34	U
48	5	35	C
48	5	36	A
48	5	37	U
48	5	47	G
48	5	48	U
48	5	53	G
48	5	69	C
48	5	75	C
48	5	76	C
48	5	77	A
49	a	8	U
49	a	9	U
49	a	10	G
49	a	11	G
49	a	12	A
49	a	13	G
49	a	36	A
49	a	43	G
49	a	48	G
49	a	51	C

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Mol	Chain	Res	Type
49	a	52	U
49	a	54	A
49	a	55	A
49	a	58	C
49	a	63	A
49	a	65	G
49	a	74	A
49	a	77	G
49	a	78	G
49	a	81	C
49	a	82	U
49	a	83	U
49	a	85	C
49	a	86	G
49	a	87	G
49	a	90	G
49	a	91	U
49	a	106	C
49	a	108	G
49	a	116	A
49	a	117	C
49	a	122	G
49	a	126	G
49	a	128	U
49	a	130	U
49	a	139	C
49	a	160	C
49	a	164	G
49	a	168	A
49	a	170	U
49	a	174	G
49	a	179	C
49	a	180	A
49	a	181	C
49	a	182	C
49	a	189	G
49	a	192	G
49	a	193	C
49	a	194	A
49	a	197	G
49	a	200	U
49	a	201	G

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Mol	Chain	Res	Type
49	a	209	A
49	a	215	U
49	a	216	U
49	a	217	U
49	a	219	C
49	a	245	C
49	a	247	G
49	a	251	G
49	a	262	G
49	a	267	C
49	a	279	A
49	a	280	C
49	a	281	G
49	a	289	G
49	a	301	G
49	a	306	A
49	a	316	C
49	a	319	G
49	a	321	A
49	a	327	A
49	a	329	A
49	a	330	C
49	a	332	G
49	a	344	A
49	a	345	C
49	a	347	G
49	a	351	G
49	a	352	C
49	a	353	A
49	a	354	G
49	a	356	A
49	a	367	U
49	a	368	U
49	a	369	G
49	a	372	C
49	a	381	C
49	a	390	U
49	a	397	A
49	a	398	C
49	a	399	G
49	a	404	G
49	a	406	G

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Mol	Chain	Res	Type
49	a	411	A
49	a	412	U
49	a	413	G
49	a	414	A
49	a	419	C
49	a	422	C
49	a	423	G
49	a	424	G
49	a	426	U
49	a	429	U
49	a	430	A
49	a	437	U
49	a	438	U
49	a	452	A
49	a	453	G
49	a	456	C
49	a	457	A
49	a	458	A
49	a	459	G
49	a	461	G
49	a	462	A
49	a	464	G
49	a	465	G
49	a	466	U
49	a	468	U
49	a	469	G
49	a	470	U
49	a	471	G
49	a	473	A
49	a	474	G
49	a	475	A
49	a	476	A
49	a	477	G
49	a	480	G
49	a	485	G
49	a	486	G
49	a	488	C
49	a	489	A
49	a	490	A
49	a	491	C
49	a	496	U
49	a	497	G

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Mol	Chain	Res	Type
49	a	498	C
49	a	499	C
49	a	501	G
49	a	504	G
49	a	505	C
49	a	507	G
49	a	509	G
49	a	510	G
49	a	511	U
49	a	512	A
49	a	513	A
49	a	515	A
49	a	517	G
49	a	519	A
49	a	525	C
49	a	527	A
49	a	539	A
49	a	542	U
49	a	543	A
49	a	550	G
49	a	553	A
49	a	556	A
49	a	557	G
49	a	568	G
49	a	576	C
49	a	585	U
49	a	587	A
49	a	592	U
49	a	597	G
49	a	612	U
49	a	613	G
49	a	629	G
49	a	633	A
49	a	645	G
49	a	666	U
49	a	667	A
49	a	668	G
49	a	674	G
49	a	683	G
49	a	698	A
49	a	701	G
49	a	702	G

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Mol	Chain	Res	Type
49	a	703	U
49	a	704	G
49	a	711	G
49	a	713	G
49	a	729	A
49	a	735	G
49	a	757	A
49	a	761	A
49	a	765	G
49	a	772	A
49	a	773	U
49	a	774	A
49	a	782	A
49	a	793	U
49	a	795	A
49	a	797	C
49	a	801	G
49	a	808	A
49	a	812	G
49	a	818	U
49	a	820	C
49	a	821	C
49	a	822	U
49	a	823	U
49	a	824	C
49	a	825	C
49	a	826	U
49	a	827	U
49	a	828	G
49	a	835	G
49	a	854	A
49	a	867	G
49	a	871	A
49	a	884	G
49	a	896	A
49	a	898	G
49	a	908	G
49	a	909	G
49	a	916	C
49	a	917	A
49	a	920	A
49	a	924	G

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Mol	Chain	Res	Type
49	a	932	U
49	a	938	U
49	a	940	A
49	a	942	U
49	a	943	U
49	a	948	G
49	a	949	C
49	a	951	A
49	a	953	G
49	a	954	C
49	a	955	G
49	a	956	A
49	a	957	A
49	a	958	G
49	a	959	A
49	a	961	C
49	a	964	U
49	a	966	C
49	a	972	U
49	a	973	U
49	a	974	U
49	a	975	G
49	a	976	A
49	a	984	A
49	a	987	A
49	a	988	C
49	a	989	G
49	a	990	C
49	a	993	G
49	a	996	G
49	a	997	A
49	a	998	G
49	a	999	A
49	a	1000	U
49	a	1005	G
49	a	1006	U
49	a	1007	U
49	a	1008	C
49	a	1013	G
49	a	1014	U
49	a	1015	G
49	a	1017	C

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Mol	Chain	Res	Type
49	a	1019	U
49	a	1020	G
49	a	1023	U
49	a	1025	C
49	a	1026	A
49	a	1030	G
49	a	1031	G
49	a	1033	G
49	a	1034	C
49	a	1035	A
49	a	1040	U
49	a	1044	G
49	a	1045	U
49	a	1048	G
49	a	1054	G
49	a	1055	U
49	a	1056	C
49	a	1059	G
49	a	1061	G
49	a	1065	U
49	a	1066	U
49	a	1068	G
49	a	1069	G
49	a	1070	U
49	a	1074	G
49	a	1075	U
49	a	1078	C
49	a	1079	G
49	a	1080	C
49	a	1081	A
49	a	1082	A
49	a	1083	C
49	a	1084	G
49	a	1086	G
49	a	1104	G
49	a	1105	U
49	a	1110	A
49	a	1114	C
49	a	1115	G
49	a	1116	U
49	a	1117	U
49	a	1118	A

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Mol	Chain	Res	Type
49	a	1120	G
49	a	1121	G
49	a	1122	U
49	a	1123	G
49	a	1127	A
49	a	1131	G
49	a	1137	G
49	a	1138	A
49	a	1140	U
49	a	1141	G
49	a	1143	C
49	a	1144	G
49	a	1145	G
49	a	1147	G
49	a	1149	C
49	a	1150	A
49	a	1151	A
49	a	1152	C
49	a	1153	U
49	a	1154	C
49	a	1158	G
49	a	1159	G
49	a	1160	A
49	a	1163	G
49	a	1164	U
49	a	1165	G
49	a	1166	G
49	a	1168	G
49	a	1177	A
49	a	1178	A
49	a	1179	G
49	a	1182	A
49	a	1192	U
49	a	1193	U
49	a	1194	A
49	a	1198	C
49	a	1199	C
49	a	1200	A
49	a	1204	C
49	a	1205	U
49	a	1206	U
49	a	1207	C

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Mol	Chain	Res	Type
49	a	1208	A
49	a	1219	A
49	a	1220	A
49	a	1221	U
49	a	1222	G
49	a	1226	G
49	a	1228	U
49	a	1229	A
49	a	1231	A
49	a	1232	A
49	a	1234	G
49	a	1236	G
49	a	1237	C
49	a	1238	U
49	a	1239	G
49	a	1240	C
49	a	1241	G
49	a	1242	A
49	a	1244	G
49	a	1245	C
49	a	1248	U
49	a	1249	G
49	a	1250	A
49	a	1251	G
49	a	1253	U
49	a	1254	G
49	a	1256	A
49	a	1257	G
49	a	1258	C
49	a	1259	G
49	a	1260	A
49	a	1261	A
49	a	1262	U
49	a	1265	U
49	a	1266	U
49	a	1267	U
49	a	1272	G
49	a	1273	C
49	a	1275	G
49	a	1276	G
49	a	1278	C
49	a	1279	U

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Mol	Chain	Res	Type
49	a	1281	A
49	a	1283	U
49	a	1284	U
49	a	1287	G
49	a	1296	C
49	a	1299	C
49	a	1302	C
49	a	1305	G
49	a	1311	G
49	a	1312	U
49	a	1317	U
49	a	1320	G
49	a	1321	A
49	a	1322	G
49	a	1328	A
49	a	1329	G
49	a	1331	A
49	a	1333	U
49	a	1335	G
49	a	1338	G
49	a	1343	G
49	a	1344	C
49	a	1346	A
49	a	1347	C
49	a	1351	G
49	a	1353	G
49	a	1357	A
49	a	1359	U
49	a	1367	C
49	a	1380	C
49	a	1381	A
49	a	1382	C
49	a	1383	C
49	a	1384	G
49	a	1402	G
49	a	1425	G
49	a	1426	C
49	a	1429	A
49	a	1432	C
49	a	1433	C
49	a	1435	U
49	a	1436	G

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Mol	Chain	Res	Type
49	a	1437	U
49	a	1438	G
49	a	1459	G
49	a	1476	A
49	a	1477	A
49	a	1478	G
49	a	1481	G
49	a	1483	A
49	a	1486	A
49	a	1488	G
49	a	1489	G
49	a	1490	U
49	a	1501	G
49	a	1502	A
49	a	1503	A
49	a	1504	G
49	a	1513	G
49	a	1514	G

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	A	97	U
18	A	316	U
18	A	335	G
18	A	357	U
18	A	445	U
18	A	567	A
18	A	899	G
18	A	942	U
18	A	974	G
18	A	980	C
18	A	981	U
18	A	998	G
18	A	1004	C
18	A	1084	U
18	A	1186	G
18	A	1549	G
18	A	1573	U
18	A	1629	G
18	A	1630	U
18	A	2094	G

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Mol	Chain	Res	Type
18	A	2349	A
18	A	2353	U
18	A	2381	A
18	A	2384	C
18	A	2626	U
19	B	10	G
48	5	36	A
48	5	75	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

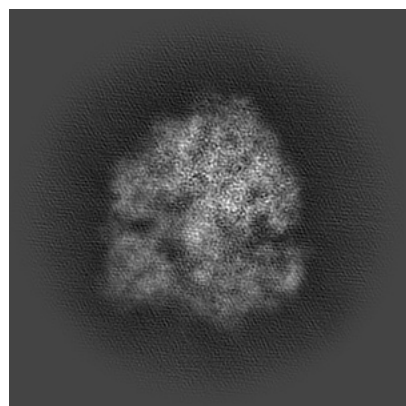
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43267. These allow visual inspection of the internal detail of the map and identification of artifacts.

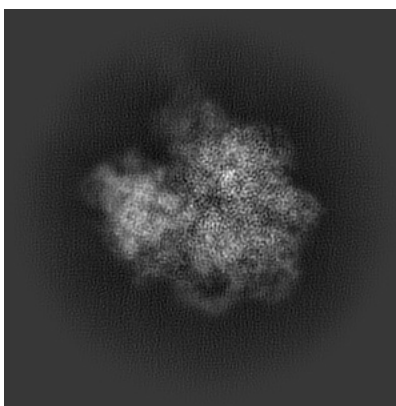
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

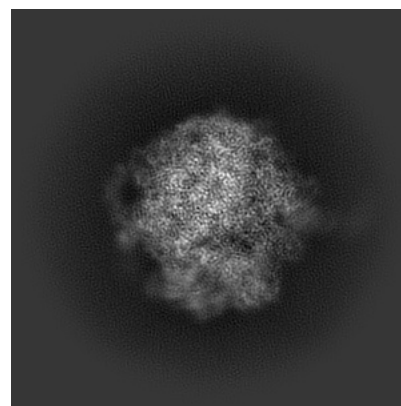
6.1.1 Primary map



X

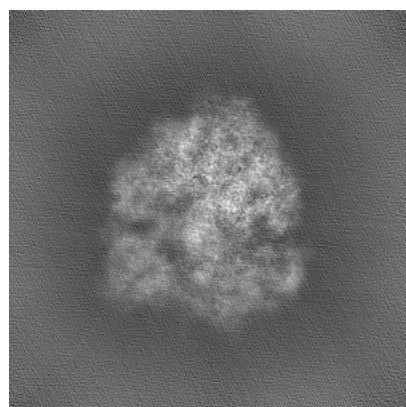


Y

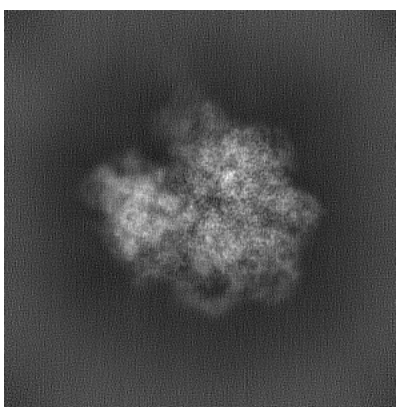


Z

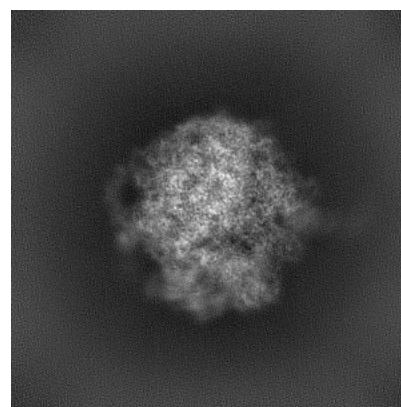
6.1.2 Raw map



X



Y

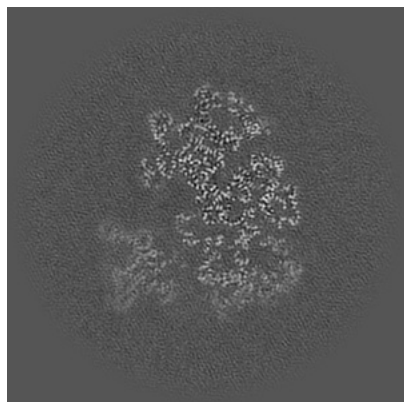


Z

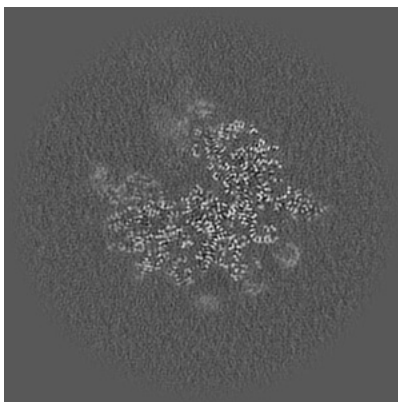
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

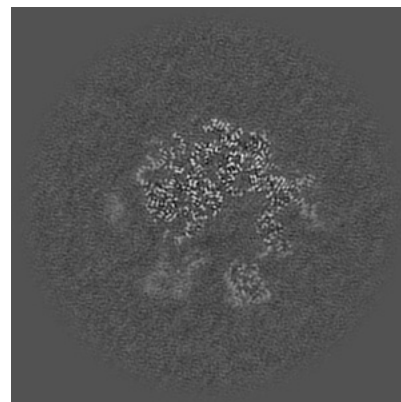
6.2.1 Primary map



X Index: 200

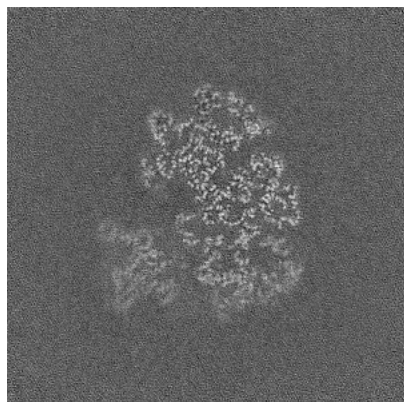


Y Index: 200

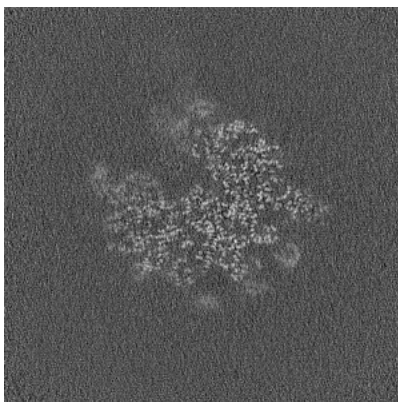


Z Index: 200

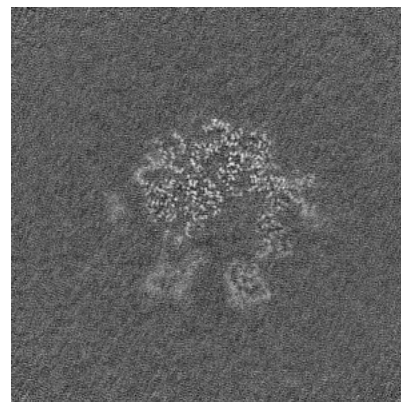
6.2.2 Raw map



X Index: 200



Y Index: 200

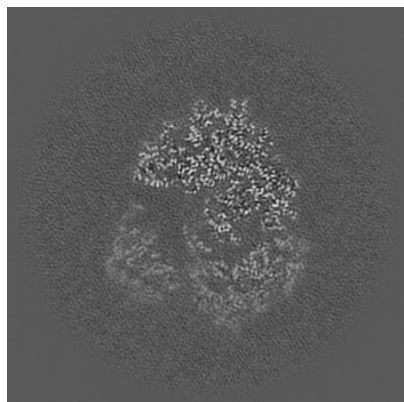


Z Index: 200

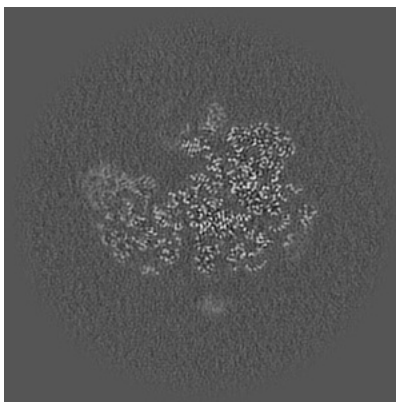
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

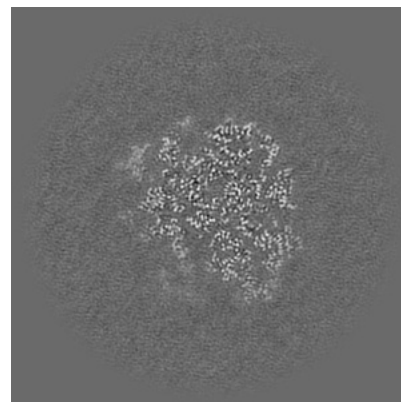
6.3.1 Primary map



X Index: 214

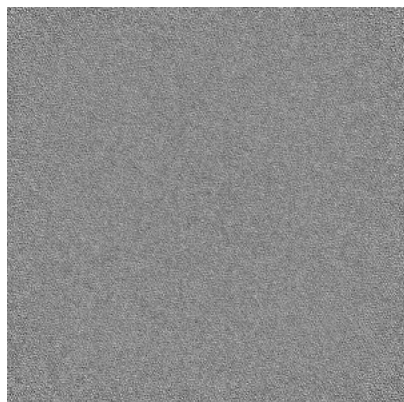


Y Index: 213

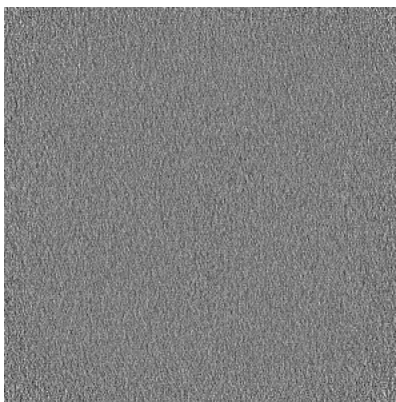


Z Index: 230

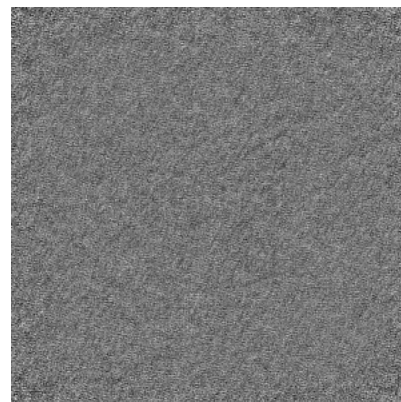
6.3.2 Raw map



X Index: 0



Y Index: 0

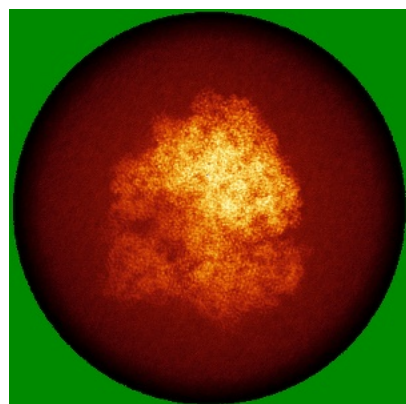


Z Index: 0

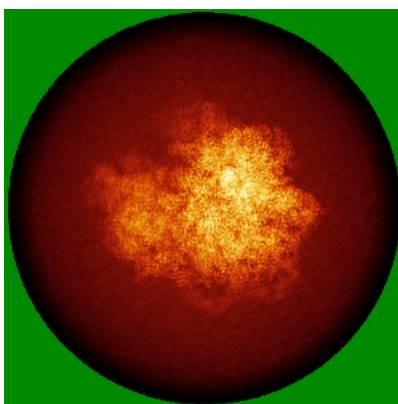
The images above show the largest variance slices of the map in three orthogonal directions.

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

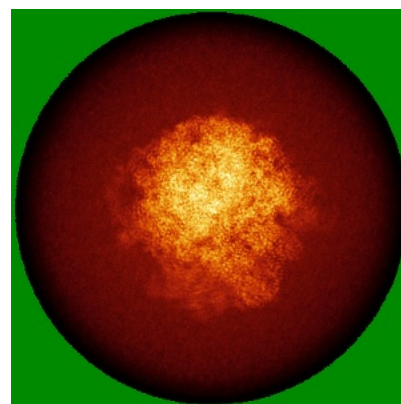
6.4.1 Primary map



X

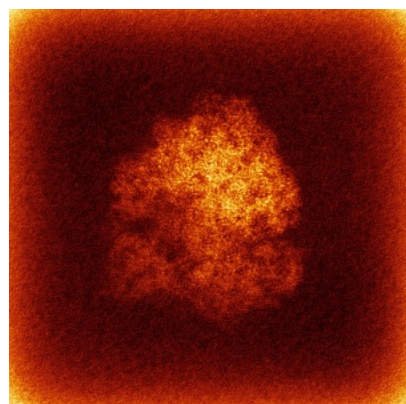


Y

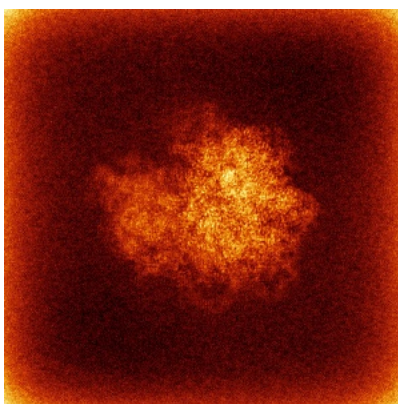


Z

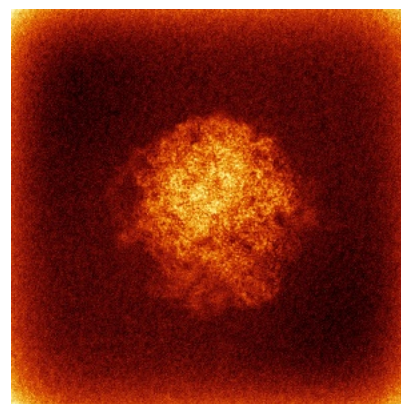
6.4.2 Raw map



X



Y

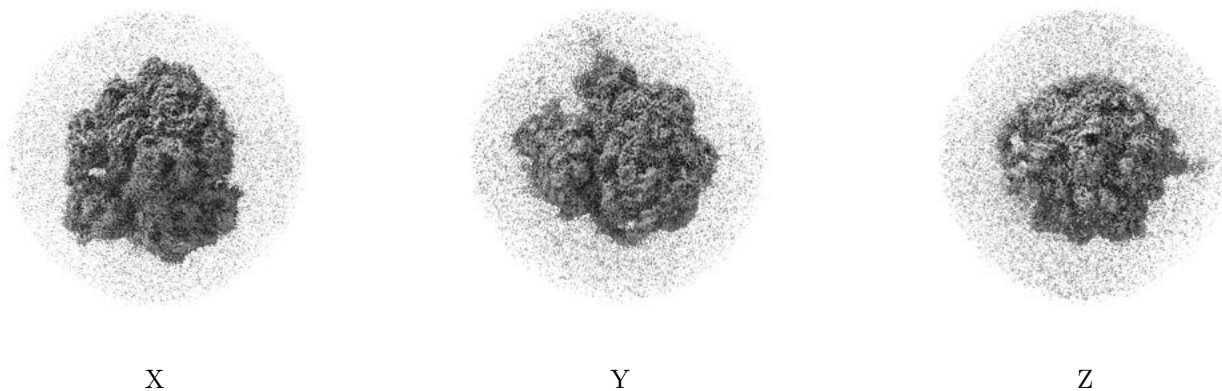


Z

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.

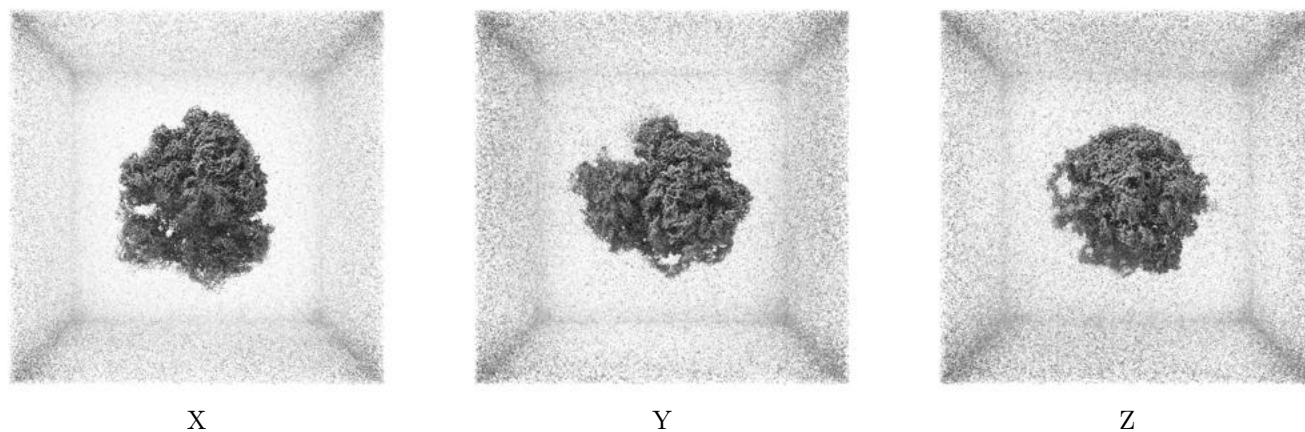
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

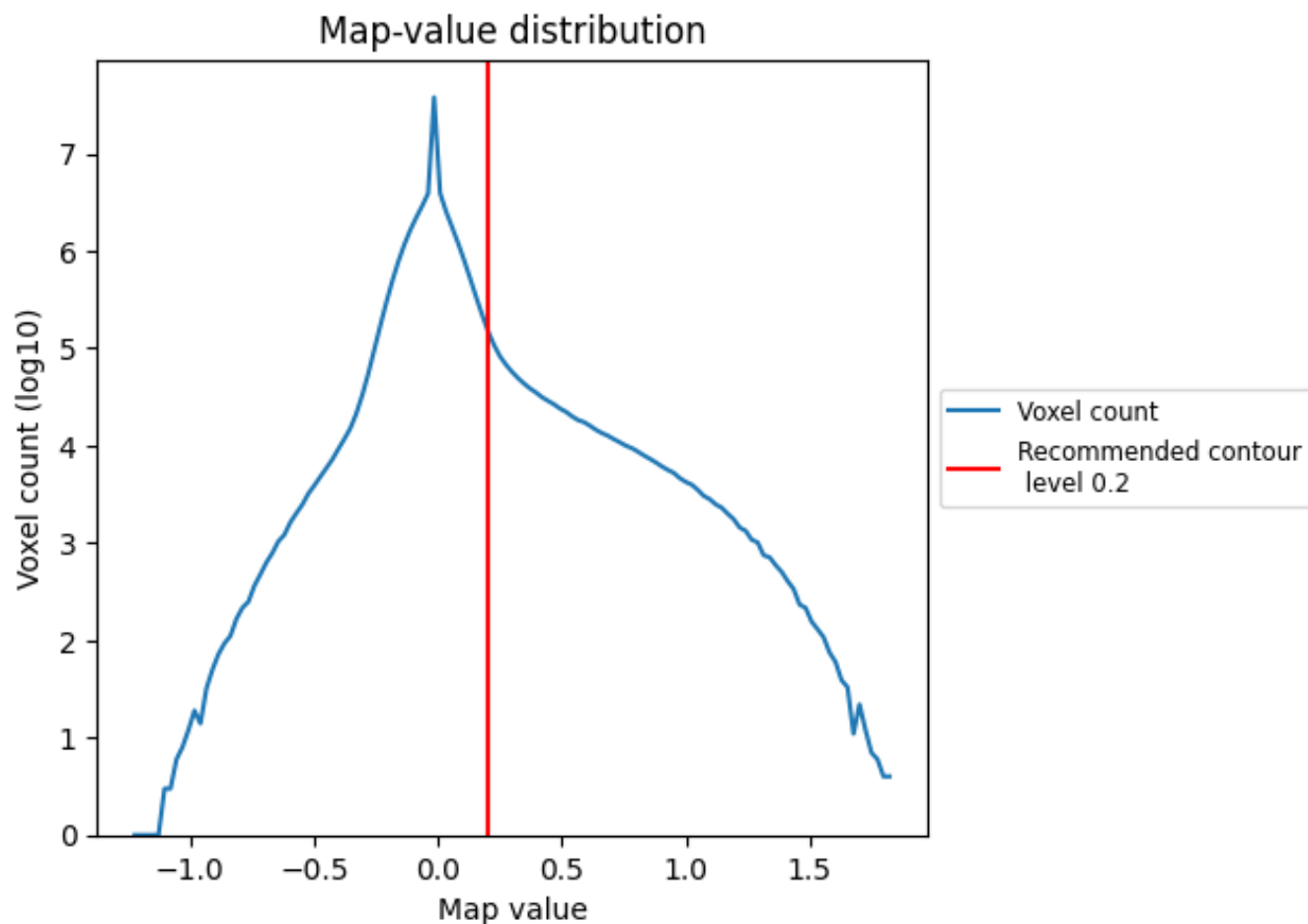
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

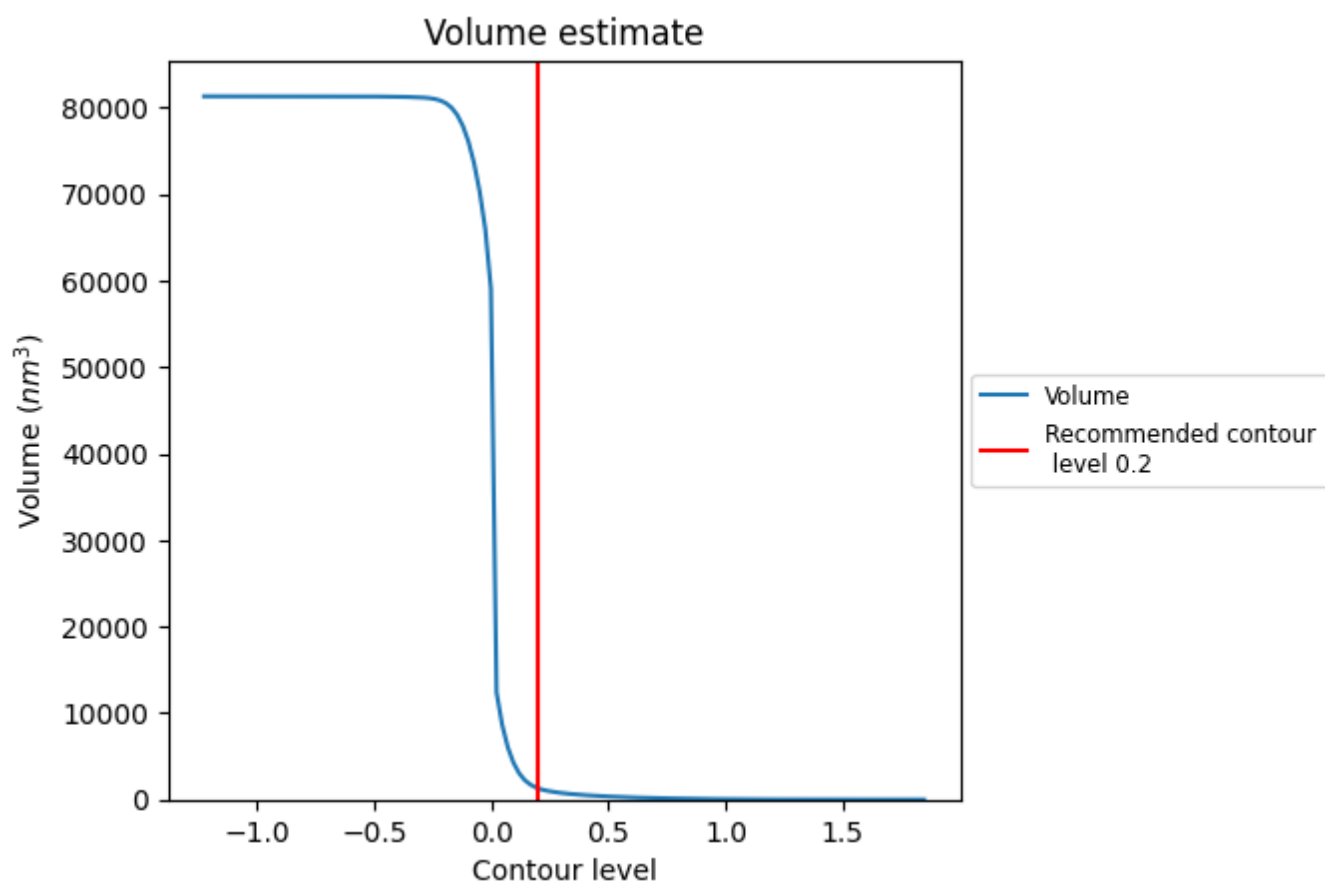
This section contains the results of statistical analysis of the map.

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.

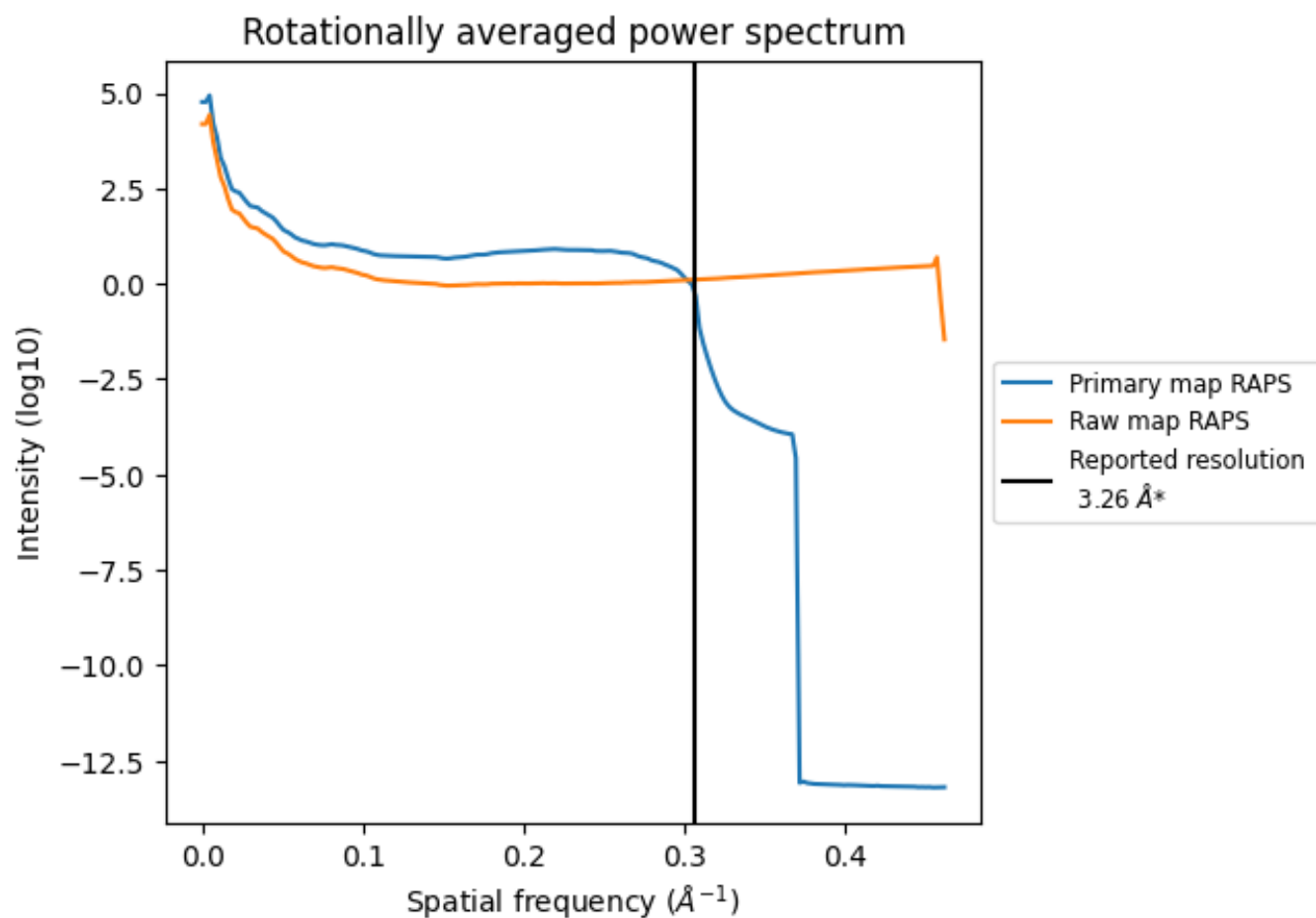
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1311 nm³; this corresponds to an approximate mass of 1184 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 ⓘ

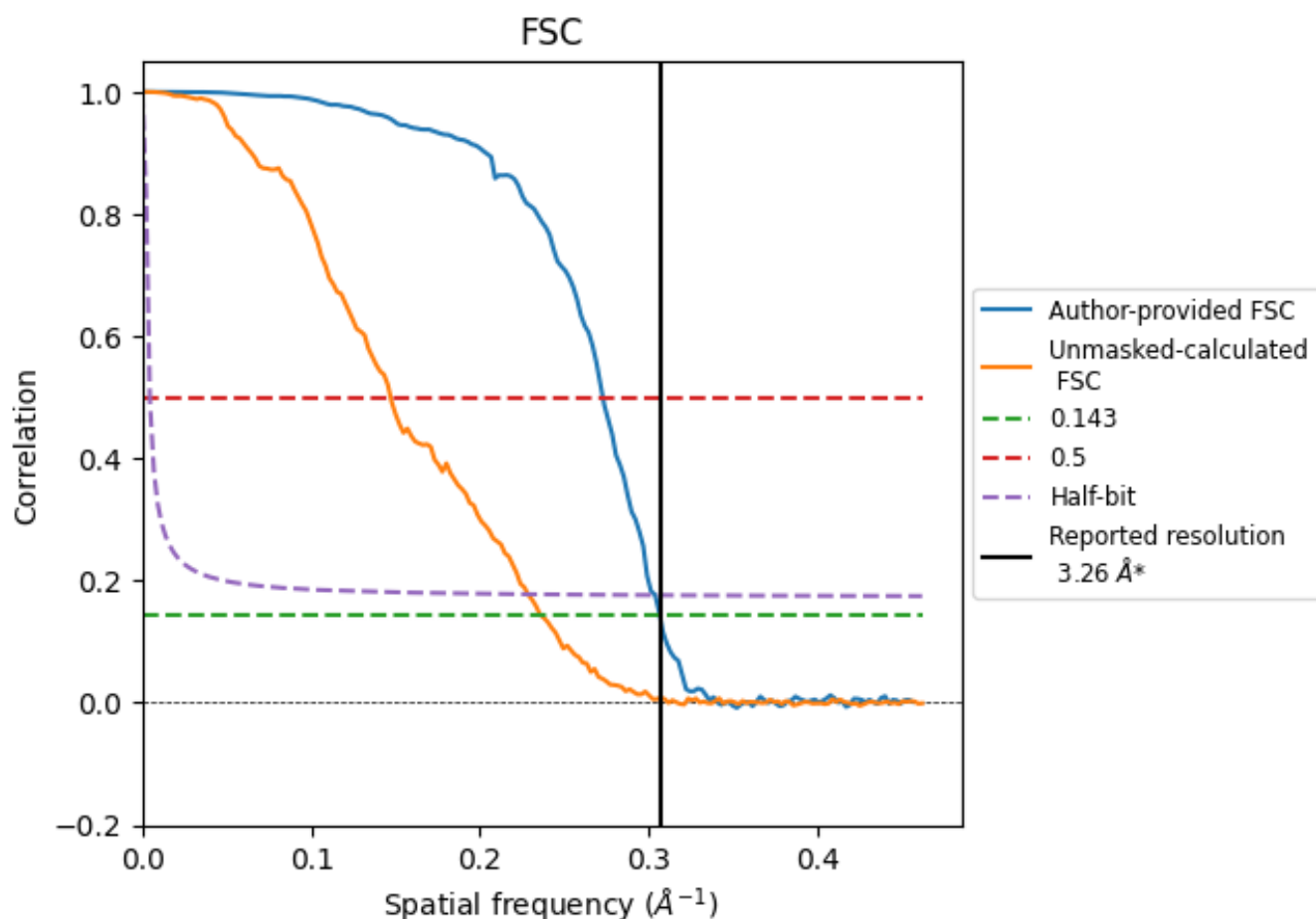


*Reported resolution corresponds to spatial frequency of 0.307 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.307 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.26	-	-
Author-provided FSC curve	3.26	3.67	3.29
Unmasked-calculated*	4.24	6.80	4.38

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.24 differs from the reported value 3.26 by more than 10 %

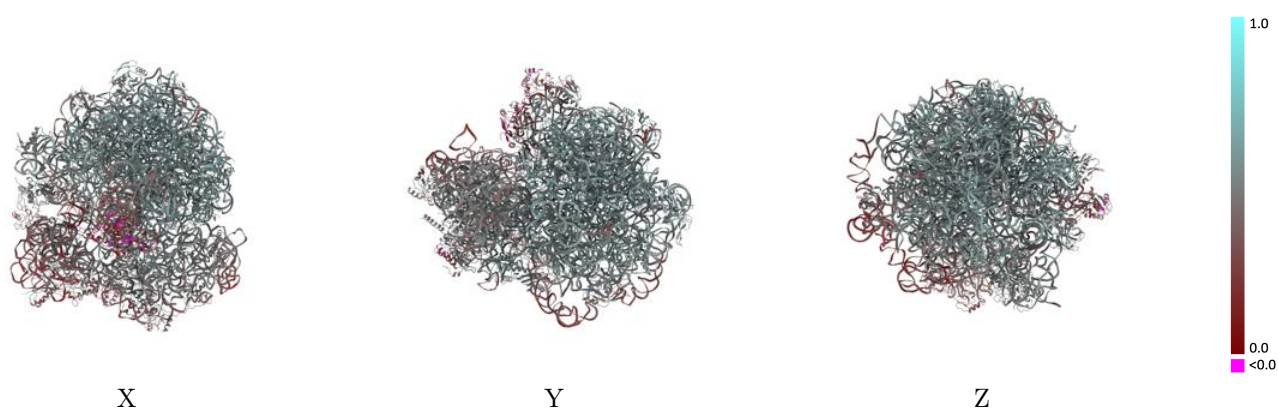
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43267 and PDB model 8VIO. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

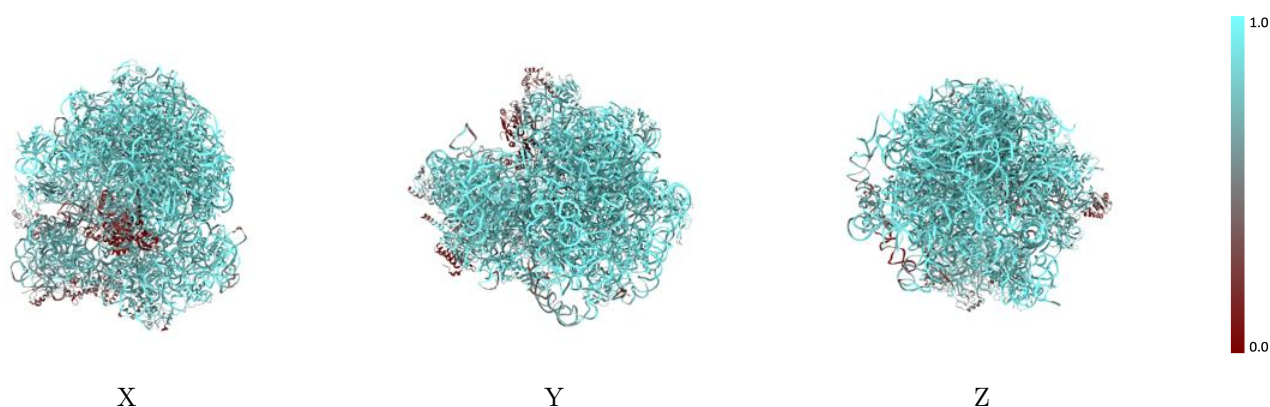
This section was not generated.

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



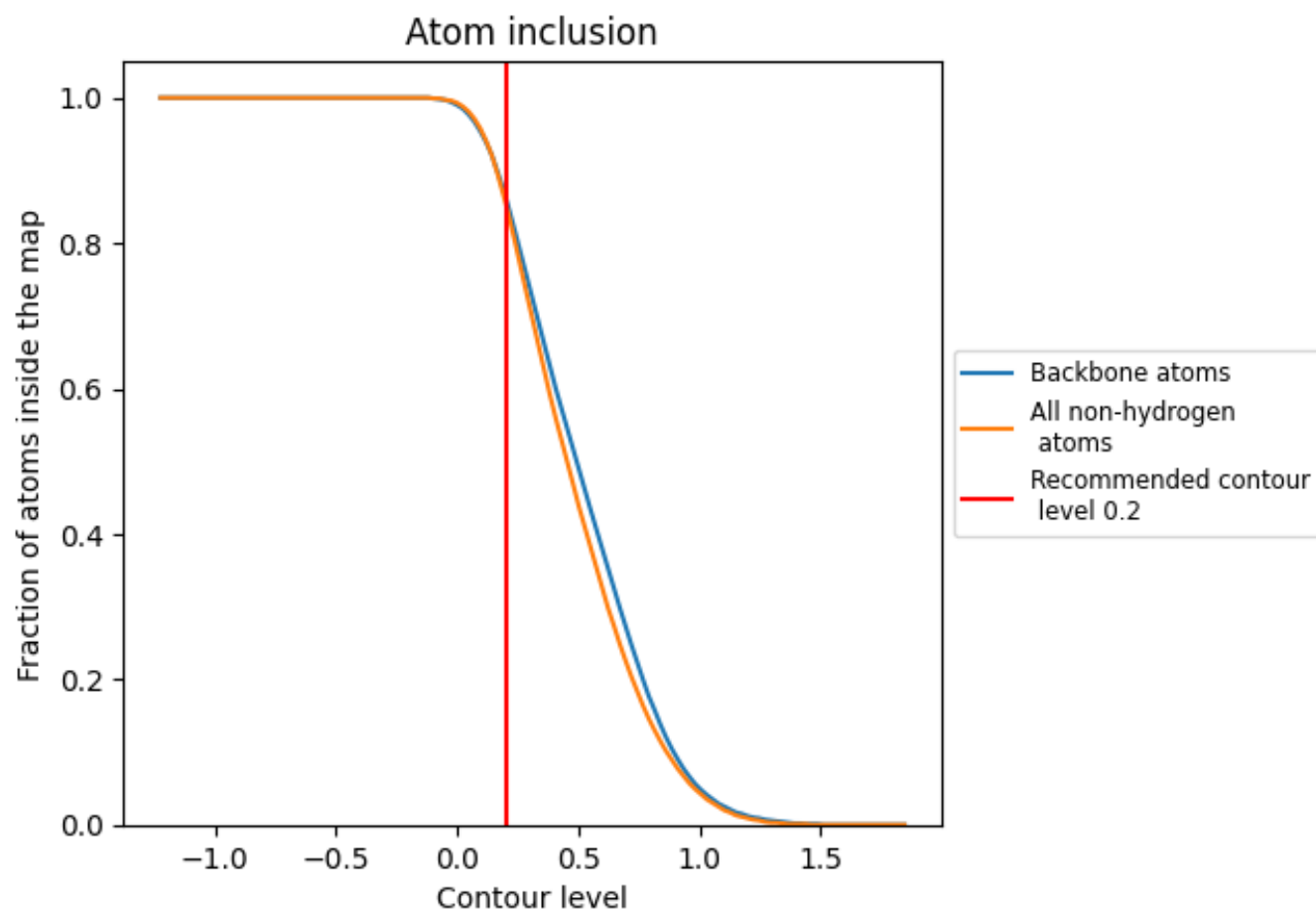
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8550	 0.4860
1	 0.8320	 0.5550
2	 0.9480	 0.5780
3	 0.9610	 0.5920
4	 0.0800	 0.3100
5	 0.8090	 0.4030
A	 0.9170	 0.5050
B	 0.9460	 0.4970
C	 0.9320	 0.5780
D	 0.9440	 0.5770
E	 0.9130	 0.5590
F	 0.8260	 0.4890
G	 0.8320	 0.4940
H	 0.7040	 0.4630
I	 0.3060	 0.2700
J	 0.2460	 0.2590
K	 0.9440	 0.5730
L	 0.9100	 0.5690
M	 0.9240	 0.5640
N	 0.8990	 0.5690
O	 0.9440	 0.5720
P	 0.8940	 0.5230
Q	 0.9140	 0.5720
R	 0.9390	 0.5750
S	 0.9310	 0.5770
T	 0.9230	 0.5690
U	 0.9050	 0.5560
V	 0.8400	 0.5230
W	 0.8030	 0.5200
X	 0.9220	 0.5760
Y	 0.9120	 0.5660
Z	 0.9180	 0.5600
a	 0.8800	 0.4460
b	 0.9450	 0.5710
c	 0.8930	 0.5680



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Chain	Atom inclusion	Q-score
d	 0.9510	 0.5870
e	 0.9480	 0.5860
f	 0.9200	 0.5790
g	 0.8000	 0.4580
h	 0.1200	 0.2780
i	 0.6000	 0.4120
j	 0.6850	 0.4460
k	 0.8260	 0.5240
l	 0.8640	 0.5170
m	 0.5080	 0.3380
n	 0.8950	 0.5450
o	 0.6040	 0.3900
p	 0.5290	 0.4030
q	 0.8900	 0.5400
r	 0.8320	 0.5140
s	 0.7800	 0.5060
t	 0.5420	 0.3710
u	 0.7830	 0.4640
v	 0.9060	 0.5430
w	 0.7340	 0.4770
x	 0.7990	 0.4900
y	 0.6340	 0.4000
z	 0.8080	 0.4710