



Full wwPDB EM Validation Report ⓘ

Mar 26, 2026 – 04:07 AM UTC

PDB ID : 5LMU / pdb_00005lmu
EMDB ID : EMD-4080
Title : Structure of bacterial 30S-IF3-mRNA-tRNA translation pre-initiation complex, closed form (state-4)
Authors : Hussain, T.; Llacer, J.L.; Wimberly, B.T.; Ramakrishnan, V.
Deposited on : 2016-08-01
Resolution : 4.00 Å(reported)

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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

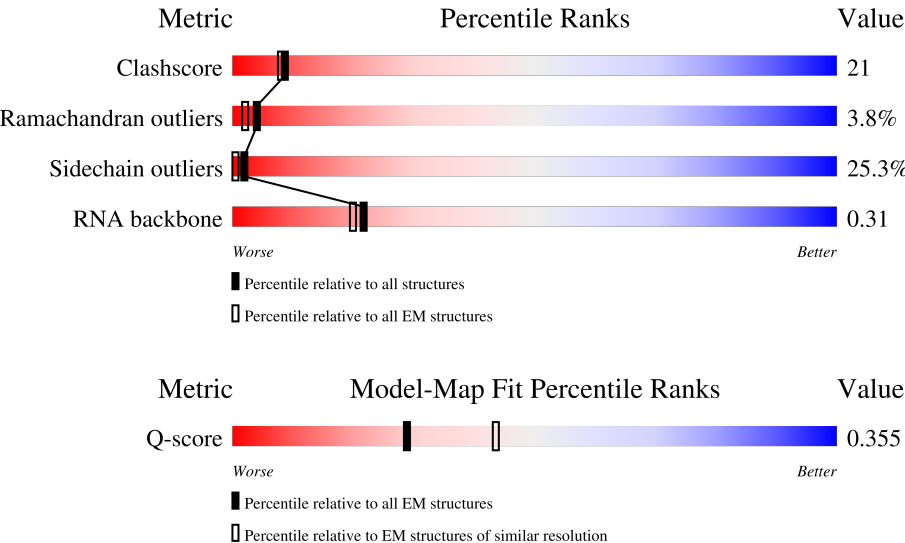
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	7587 (3.50 - 4.50)

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

Mol	Chain	Length	Quality of chain
1	A	1522	
2	B	256	
3	C	239	

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	132	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	V	27	
22	X	171	
23	Y	42	
24	Z	77	

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 55195 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1515	Total	C	N	O	P	0	0
			32548	14490	6022	10523	1513		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	234	Total	C	N	O	S	0	0
			1900	1213	341	341	5		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1612	1016	314	281	1		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	150	Total	C	N	O	S	0	0
			1146	724	217	201	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	127	Total	C	N	O	0	0
			1010	639	197	174		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			792	498	156	137	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	118	Total	C	N	O	S	0	0
			937	579	193	163	2		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	83	Total	C	N	O	S	0	0
			700	443	139	117	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	99	Total	C	N	O	S	0	0
			823	528	151	142	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	73	Total	C	N	O	0	0
			598	381	118	99		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	82	Total	C	N	O	S	0	0
			655	419	120	114	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	24	Total	C	N	O	0	0
			208	128	50	30		

- Molecule 22 is a protein called Translation initiation factor IF-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	164	Total	C	N	O	S	0	0
			1336	841	245	241	9		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	20	Total	C	N	O	P	0	0
			439	196	89	134	20		

- Molecule 24 is a RNA chain called tRNAi.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	77	Total	C	N	O	P	0	0
			1646	735	297	536	77	1	

- Molecule 25 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
25	A	78	Total	Mg	0
			78	78	
25	L	1	Total	Mg	0
			1	1	
25	Z	1	Total	Mg	0
			1	1	

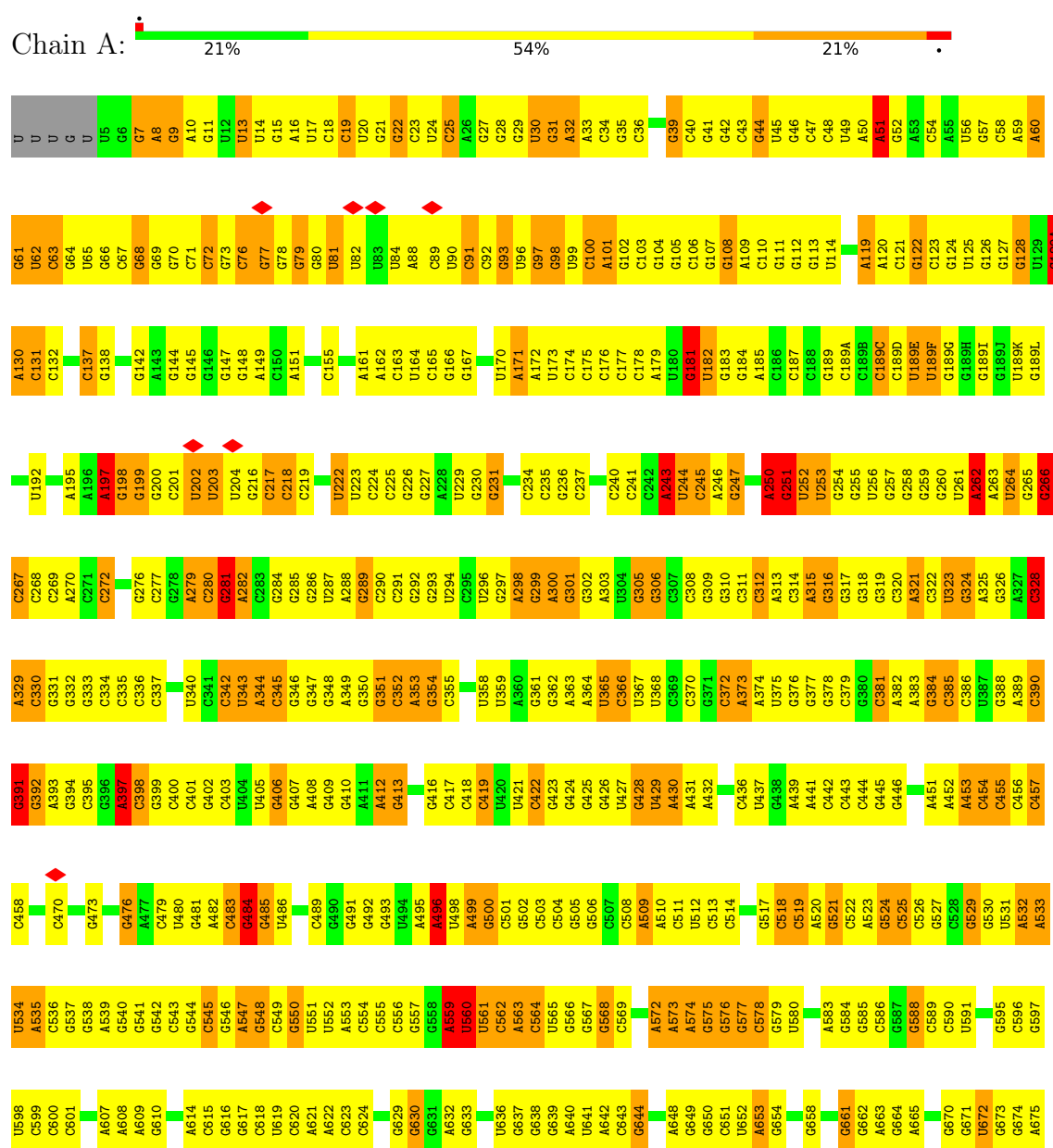
- Molecule 26 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
26	D	1	Total	Zn	0
			1	1	
26	N	1	Total	Zn	0
			1	1	

3 Residue-property plots

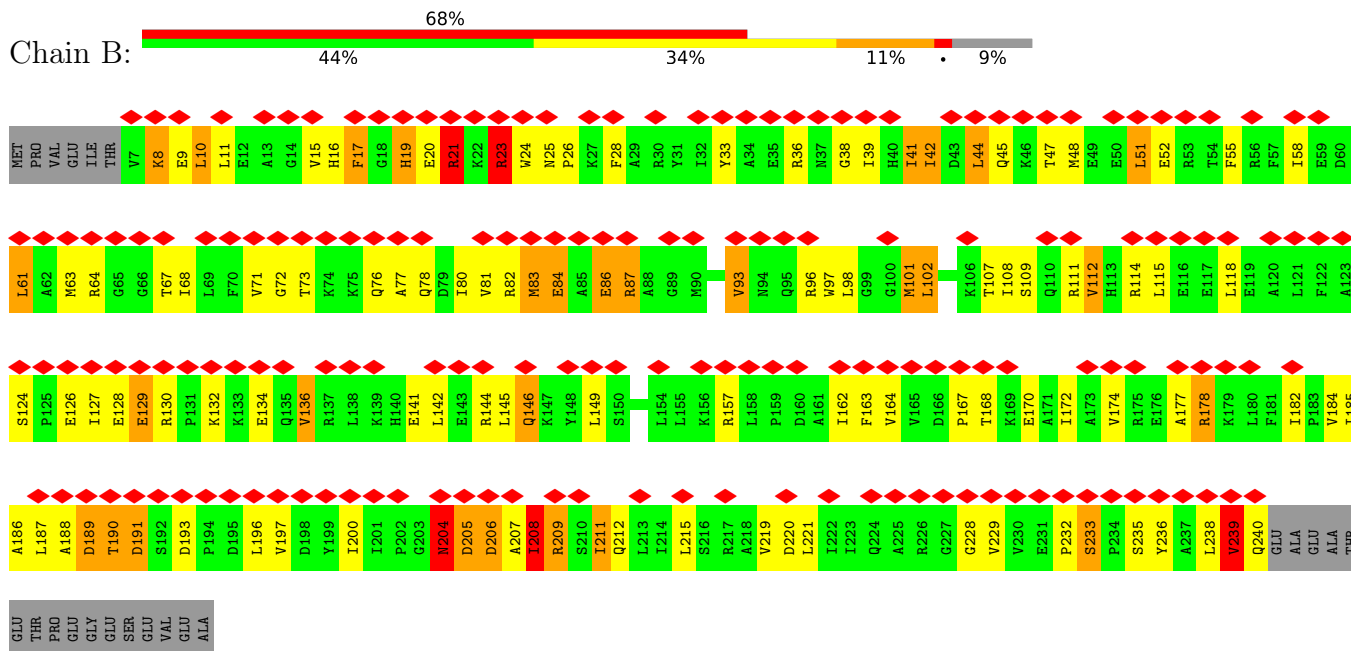
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

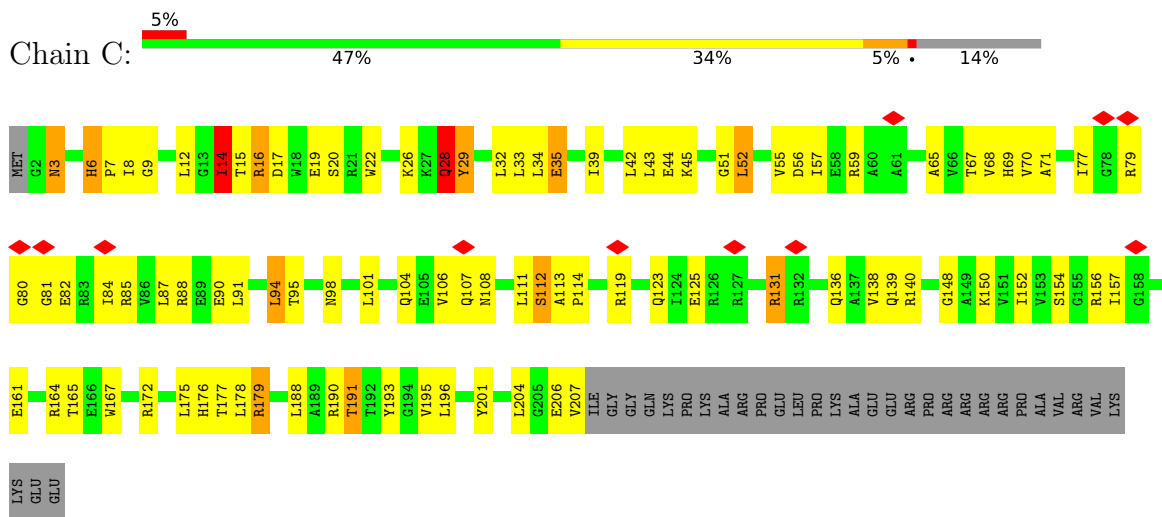


U1537	G1475	C1335	G1266	G1138	U1073	A1004	U943	C890	G809	U743	A676
C1538	U1407	C1336	G1207	G1139	G1074	A1005	G944	G881	C810	C744	U677
C1539	C1407	A1339	C1208	C1140	C1075	C1008	G945	C882	C811	C745	U678
U1540	C1477	A1339	C1209	C1141	C1076	G1009	A946	C883	C812	C746	C679
U1541	C1478	A1339	C1210	G1144	U1077	G1012	G947	U884	U813	C747	C680
U1542	C1409	G1342	U1211	C1145	U1078	U1013	A949	G885	A814	C748	C681
C	G1410	G1343	U1212	C1146	A1080	G1014	U950	G887	A815	C749	G682
U	C1411	G1344	A1213	A1147	A1081	A1015	U951	G888	A816	C750	G683
	C1412	U1345	G1214	C1148	G1082	A1016	U952	G889	U820	C751	A687
	A1413	G1346	G1215	U1149	U1083	A1017	G953	A890	G752	C752	G688
	U1414	G1347	G1216	C1150	U1084	G1018	G954	U891	A753	C753	G689
	G1415	C1217	C1217	A1151	U1085	C1017	U955	U892	G754	C754	G690
	U1416	U1281	C1218	A1152	U1086	C1018	U956	C893	G755	C755	G691
	A1349	C1282	U1219	C1153	G1087	G1022	U957	C894	G756	C756	U692
	A1350	C1283	G1220	G1154	G1088	G1023	U958	G895	C760	C760	U693
	U1351	C1284	G1221	G1155	U1089	G1024	A959	C896	C761	C762	A694
	C1352	A1285	G1222	U1159	U1090	U1025	U960	U827	C763	C763	A695
	G1353	A1286	C1223	G1160	U1091	G1026	U961	A828	C764	C764	A696
	G1354	A1287	U1224	U1161	U1092	C1027	G962	C832	C765	C765	C701
	G1355	A1288	A1225	G1171	U1093	C1028	G963	U833	A766	A766	A702
	G1356	A1289	C1226	C1172	U1094	C1029	A964	G902	A767	A767	G703
	A1367	G1293	A1227	C1173	A1101	C1030	A965	G903	U834	A768	A704
	U1368	C1294	C1228	G1174	U1102	G1030A	G966	G904	U835	C770	C707
	C1359	G1295	C1229	U1175	U1103	C1030B	C967	G906	U836	C771	G708
	A1360	G1296	C1230	C1176	U1104	C1030C	A968	A900	G837	G772	G709
	G1361	C1297	G1231	G1177	U1105	A1030D	A969	A901	U838	G773	G710
	C1362	C1298	G1232	C1178	U1106	G1031	C970	A902	C840	G774	G711
	C1363	A1299	U1233	G1179	U1107	G1032	G971	A903	U841	C775	A712
	A1363A	G1300	C1234	A1180	U1108	C1033	A972	A904	C848	A777	G713
	C1364	U1301	G1235	U1181	U1109	C1034	A973	A905	C849	A778	G714
	G1365	U1302	U1236	G1182	U1110	A1041	A974	A906	U850	C779	G715
	C1366	G1303	A1237	U1183	U1111	A1042	A975	A907	G851	A780	A716
	C1367	G1304	C1238	A1184	U1112	G1043	A976	A908	G852	A781	C717
	G1368	G1305	A1239	G1185	U1113	A1044	A977	A909	G853	A782	C718
	C1369	G1306	U1240	U1186	U1114	C1045	A978	U920	G854	C719	C719
	G1370	U1307	U1241	G1187	U1115	U1046	C980	U921	C855	C720	C720
	G1371	G1310	C1242	U1188	U1116	A1046	U981	G922	C856	G721	G721
	U1372	G1311	C1243	G1189	U1117	G1060	C985	G923	G857	A722	A722
	G1373	G1312	C1244	C1190	U1118	C1061	A986	G924	G858	G723	G723
	C1378	U1313	A1245	G1191	U1119	C1062	A987	C924	G861	G724	G724
	G1379	C1314	C1246	C1192	U1120	C1063	A988	C925	G862	G725	G725
	U1380	U1315	U1247	G1193	U1121	C1064	G987	G926	G863	C726	C726
	U1381	U1316	U1248	U1194	U1122	A1065	C989	G927	A864	G727	G727
	U1381	G1317	C1249	C1195	U1123	U1066	C990	G928	A865	A728	A728
	C1384	A1318	A1250	C1196	U1124	C1067	U991	G929	C866	A729	A729
	G1385	A1319	A1251	U1197	U1125	C1068	U992	C930	C867	A730	G730
	G1386	C1320	A1252	G1198	U1126	G1069	G993	C931	C868	C731	G731
	G1387	C1321	G1253	U1199	U1127	C1070	A994	C932	G869	C732	C732
	G1388	C1322	C1254	G1200	U1128	U1071	C995	C933	G796	C733	C733
	C1389	G1323	G1255	A1201	C1129	U1072	G996	C934	C797	C734	G734
	C1390	A1324	A1256	G1202	U1130	U1065	G997	A935	C798	C735	C735
	U1391	C1325	U1257	G1203	U1131	C1066	C998	C936	A872	C736	C736
	U1392	C1326	G1258	C1204	G1132	C1067	C999	C937	A873	A737	A737
	U1393	C1327	G1259	A1205	U1133	U1068	U1000	A938	C874	C738	C738
	A1394	C1328	C1260	U1205	G1134	G1069	A1001	G939	G875	C739	C739
	C1395	G1331	A1261	U1206	U1135	C1070	G1001	C940	C805	U740	U740
	A1396	A1332	C1262	C1203	U1136	U1071	G1002	G941	C806	G741	G741
	C1397	A1333	C1263	U1204	U1137	C1072	G1003	G942	C807	G742	G742
	A1398	G1334	G1265	U1205	C1137				C808		

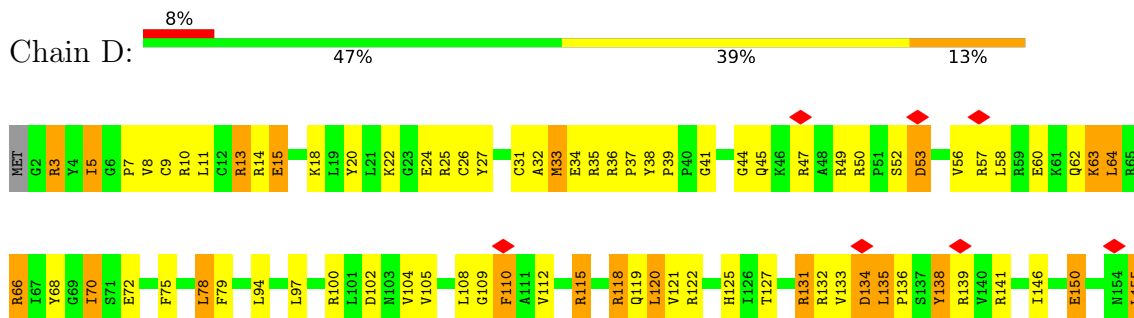
• Molecule 2: 30S ribosomal protein S2

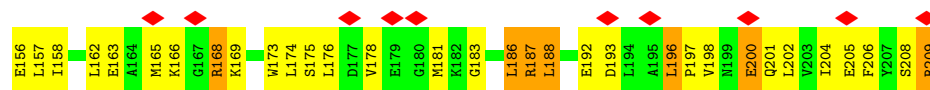


• Molecule 3: 30S ribosomal protein S3

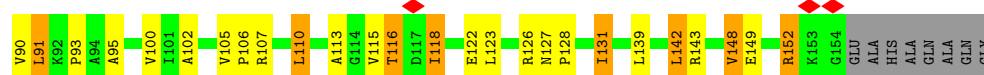
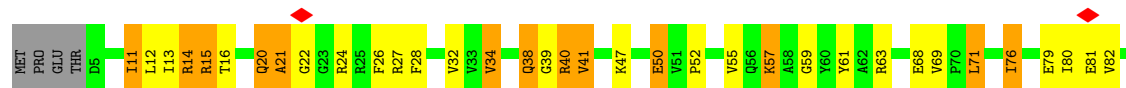


• Molecule 4: 30S ribosomal protein S4

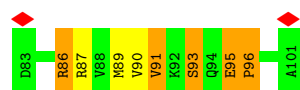
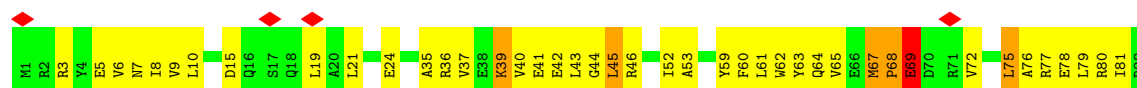




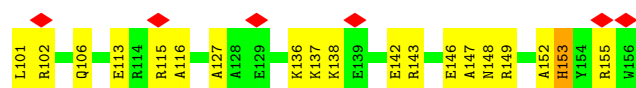
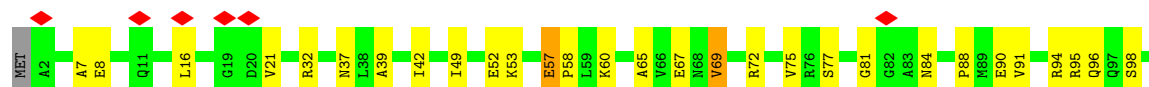
• Molecule 5: 30S ribosomal protein S5



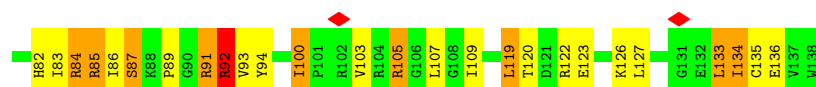
• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7



• Molecule 8: 30S ribosomal protein S8



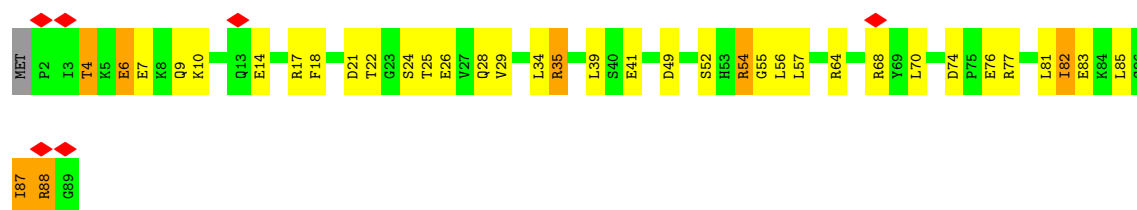
• Molecule 9: 30S ribosomal protein S9



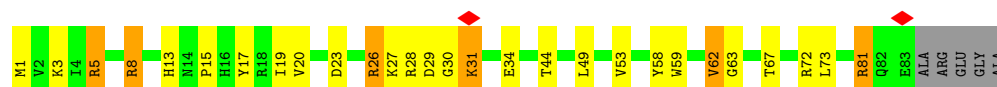
- Molecule 14: 30S ribosomal protein S14 type Z



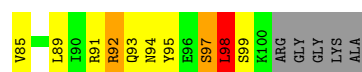
- Molecule 15: 30S ribosomal protein S15



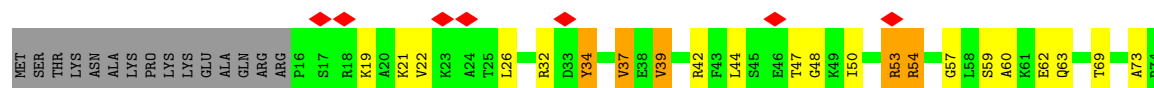
- Molecule 16: 30S ribosomal protein S16



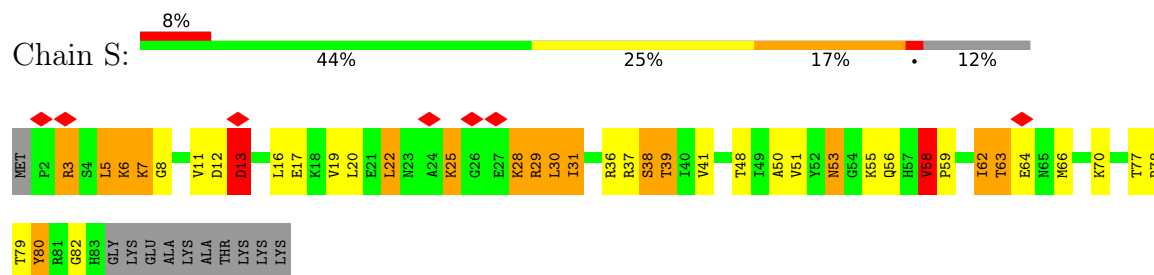
- Molecule 17: 30S ribosomal protein S17



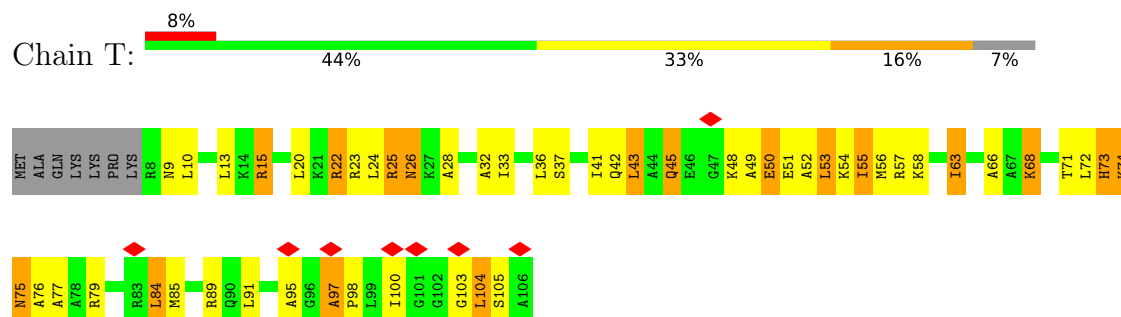
- Molecule 18: 30S ribosomal protein S18



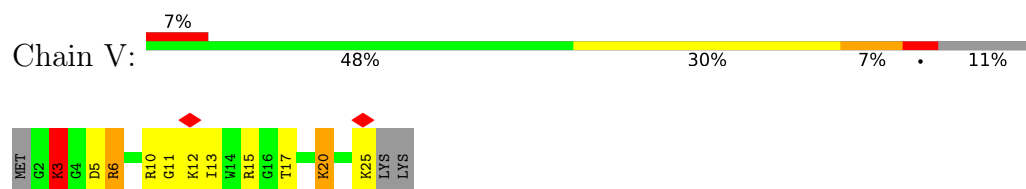
- Molecule 19: 30S ribosomal protein S19



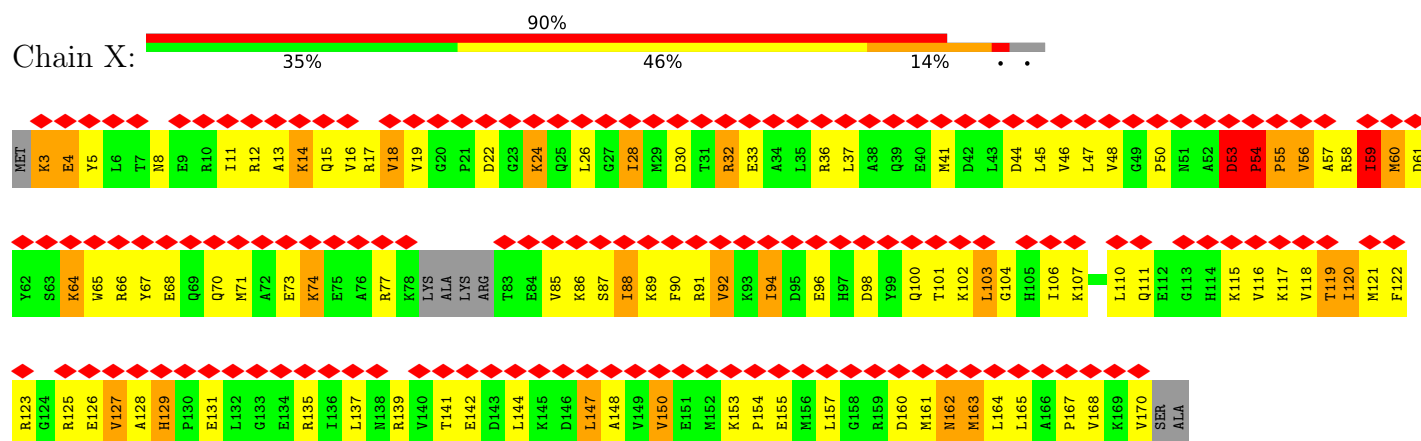
- Molecule 20: 30S ribosomal protein S20



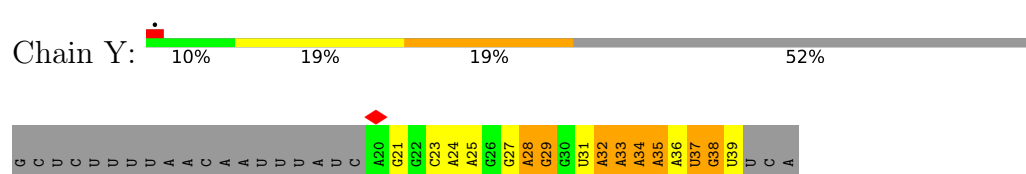
- Molecule 21: 30S ribosomal protein Thx



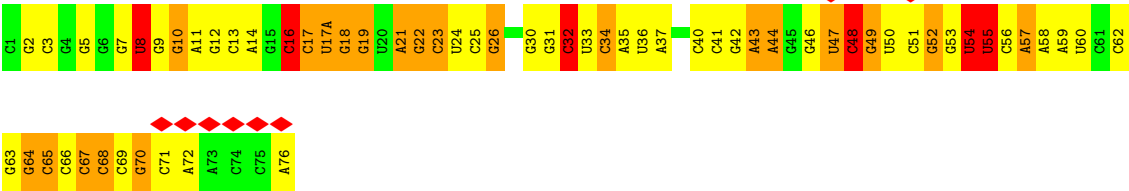
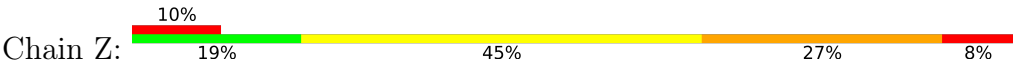
- Molecule 22: Translation initiation factor IF-3



- Molecule 23: mRNA



● Molecule 24: tRNAi



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26949	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	OTHER	Depositor
Maximum map value	0.704	Depositor
Minimum map value	-0.271	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	348.4, 348.4, 348.4	wwPDB
Map dimensions	260, 260, 260	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, PSU, G7M, ZN, MG, OMC, 4SU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.42	0/36426	0.85	86/56837 (0.2%)
2	B	0.69	0/1935	1.26	3/2609 (0.1%)
3	C	0.57	0/1636	1.10	6/2205 (0.3%)
4	D	0.52	0/1733	1.20	8/2318 (0.3%)
5	E	0.55	0/1162	1.18	7/1564 (0.4%)
6	F	0.54	0/856	1.19	4/1154 (0.3%)
7	G	0.52	0/1276	1.17	0/1709
8	H	0.54	0/1136	1.07	3/1527 (0.2%)
9	I	0.54	0/1029	1.04	1/1379 (0.1%)
10	J	0.58	0/805	1.13	4/1082 (0.4%)
11	K	0.61	0/900	1.17	2/1213 (0.2%)
12	L	0.49	0/986	1.08	5/1320 (0.4%)
13	M	0.57	0/947	1.21	6/1270 (0.5%)
14	N	0.51	0/501	1.03	0/664
15	O	0.59	0/745	1.25	0/992
16	P	0.51	0/716	0.96	0/963
17	Q	0.48	0/836	1.03	1/1117 (0.1%)
18	R	0.55	0/604	1.12	0/801
19	S	0.57	0/670	1.14	1/903 (0.1%)
20	T	0.56	0/765	1.31	2/1007 (0.2%)
21	V	0.46	0/212	1.06	0/277
22	X	0.79	1/1354 (0.1%)	1.39	7/1813 (0.4%)
23	Y	0.46	0/493	0.90	0/766
24	Z	0.53	1/1721 (0.1%)	0.89	5/2682 (0.2%)
All	All	0.48	2/59444 (0.0%)	0.96	151/88172 (0.2%)

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
1	A	0	2
19	S	0	1
22	X	0	2
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	X	4	GLU	C-O	5.82	1.30	1.23
24	Z	8	4SU	O3'-P	5.79	1.62	1.56

All (151) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	X	4	GLU	N-CA-CB	-15.66	83.86	110.95
1	A	266	G	C2'-C3'-O3'	11.58	126.87	109.50
1	A	1145	C	C2'-C3'-O3'	10.72	125.58	109.50
1	A	1498	U	C2'-C3'-O3'	10.30	124.96	109.50
22	X	4	GLU	CB-CA-C	-10.18	96.78	111.23
1	A	1346	A	C2'-C3'-O3'	10.11	124.67	109.50
1	A	792	A	C2'-C3'-O3'	10.06	124.58	109.50
1	A	1301	U	C2'-C3'-O3'	9.86	124.29	109.50
6	F	67	MET	N-CA-C	9.56	116.58	108.07
6	F	95	GLU	CA-C-N	9.23	131.38	119.84
6	F	95	GLU	C-N-CA	9.23	131.38	119.84
1	A	509	A	C4'-C3'-O3'	9.13	126.69	113.00
22	X	4	GLU	N-CA-C	8.95	124.71	107.44
1	A	687	A	C2'-C3'-O3'	8.88	122.82	109.50
1	A	372	C	C2'-C3'-O3'	8.66	122.49	109.50
1	A	1380	U	C2'-C3'-O3'	8.66	122.49	109.50
1	A	965	A	C2'-C3'-O3'	8.58	122.36	109.50
24	Z	47	U	C2'-C3'-O3'	8.38	122.06	109.50
1	A	181	G	C4'-C3'-O3'	8.32	121.88	109.40
2	B	239	VAL	N-CA-C	-8.18	105.94	113.71
1	A	181	G	C2'-C3'-O3'	7.86	121.28	109.50
4	D	169	LYS	N-CA-C	7.86	121.00	109.69
5	E	22	GLY	N-CA-C	7.85	122.15	112.73
1	A	281	G	C2'-C3'-O3'	7.67	121.01	109.50
1	A	1492	A	C4'-C3'-O3'	7.65	124.47	113.00
1	A	428	G	C2'-C3'-O3'	7.57	120.85	109.50
1	A	51	A	C2'-C3'-O3'	7.56	120.83	109.50
1	A	197	A	C2'-C3'-O3'	7.39	120.59	109.50
22	X	53	ASP	CA-C-N	7.35	127.95	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	X	53	ASP	C-N-CA	7.35	127.95	120.38
1	A	960	U	C2'-C3'-O3'	7.33	120.50	109.50
1	A	7	G	C2'-C3'-O3'	7.31	120.47	109.50
4	D	135	LEU	CA-C-N	7.31	127.02	119.56
4	D	135	LEU	C-N-CA	7.31	127.02	119.56
10	J	37	PRO	N-CA-C	-7.25	97.53	112.47
13	M	15	VAL	CB-CA-C	-7.11	102.78	111.88
1	A	60	A	C2'-C3'-O3'	7.08	120.12	109.50
1	A	560	U	C2'-C3'-O3'	7.04	120.06	109.50
5	E	76	ILE	CB-CA-C	7.02	117.25	110.16
1	A	559	A	C2'-C3'-O3'	6.96	119.94	109.50
3	C	28	GLN	N-CA-C	6.95	124.03	113.61
13	M	108	ARG	N-CA-C	6.92	119.71	111.33
1	A	508	C	C4'-C3'-O3'	6.84	119.66	109.40
1	A	960	U	C4'-C3'-O3'	6.77	119.56	109.40
4	D	38	TYR	CA-C-N	6.75	127.33	120.38
4	D	38	TYR	C-N-CA	6.75	127.33	120.38
1	A	559	A	C4'-C3'-O3'	6.74	119.50	109.40
3	C	14	ILE	N-CA-C	6.72	123.31	109.34
4	D	63	LYS	N-CA-C	-6.61	102.95	111.02
1	A	1190	G	C2'-C3'-O3'	6.50	123.46	113.70
1	A	1225	A	C2'-C3'-O3'	-6.50	103.95	113.70
20	T	97	ALA	CA-C-N	6.47	127.93	119.84
20	T	97	ALA	C-N-CA	6.47	127.93	119.84
1	A	1101	A	C2'-C3'-O3'	6.47	119.20	109.50
1	A	748	C	C2'-C3'-O3'	6.46	119.19	109.50
1	A	496	A	C4'-C3'-O3'	6.45	119.08	109.40
2	B	19	HIS	N-CA-C	6.44	118.91	108.34
1	A	1285	A	C2'-C3'-O3'	6.44	119.16	109.50
1	A	913	A	C2'-C3'-O3'	6.42	119.13	109.50
1	A	1182	G	C2'-C3'-O3'	6.40	119.09	109.50
1	A	991	U	C4'-C3'-O3'	-6.35	103.47	113.00
1	A	1065	U	C2'-C3'-O3'	6.35	119.03	109.50
1	A	1225	A	C4'-C3'-O3'	-6.30	103.54	113.00
24	Z	48	C	C4'-C3'-O3'	6.25	118.78	109.40
1	A	1028	C	C4'-C3'-O3'	6.24	122.36	113.00
12	L	60	LEU	N-CA-C	6.24	118.89	109.41
1	A	1205	U	C4'-C3'-O3'	-6.23	103.66	113.00
1	A	328	C	C2'-C3'-O3'	6.21	118.82	109.50
1	A	1125	U	C1'-C2'-O2'	-6.16	102.56	111.80
24	Z	17(A)	U	C2'-C3'-O3'	6.08	118.62	109.50
1	A	916	G	C4'-C3'-O3'	-6.07	103.90	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1201	A	C2'-C3'-O3'	6.05	118.57	109.50
13	M	40	ASN	CA-C-N	6.02	125.90	119.28
13	M	40	ASN	C-N-CA	6.02	125.90	119.28
1	A	243	A	C4'-C3'-O3'	6.02	118.43	109.40
1	A	1300	G	C2'-C3'-O3'	6.01	118.52	109.50
1	A	747	C	C4'-C3'-O3'	-6.00	104.00	113.00
1	A	262	A	C4'-C3'-O3'	-5.99	104.01	113.00
12	L	47	LYS	CA-C-N	-5.95	114.10	120.47
12	L	47	LYS	C-N-CA	-5.95	114.10	120.47
10	J	88	LEU	N-CA-C	-5.93	106.21	113.50
1	A	1201	A	C4'-C3'-O3'	5.92	118.29	109.40
1	A	484	G	C2'-C3'-O3'	5.90	118.35	109.50
1	A	1285	A	C4'-C3'-O3'	5.86	118.19	109.40
1	A	243	A	C2'-C3'-O3'	5.86	118.28	109.50
1	A	51	A	C4'-C3'-O3'	5.83	118.14	109.40
1	A	1305	G	C4'-C3'-O3'	-5.82	104.27	113.00
1	A	499	A	C4'-C3'-O3'	5.82	118.12	109.40
1	A	1288	A	C4'-C3'-O3'	-5.72	104.43	113.00
1	A	1257	U	C4'-C3'-O3'	5.70	117.94	109.40
5	E	76	ILE	CA-C-N	5.69	126.95	119.84
5	E	76	ILE	C-N-CA	5.69	126.95	119.84
1	A	306	G	C4'-C3'-O3'	-5.69	104.47	113.00
1	A	60	A	C4'-C3'-O3'	5.68	117.92	109.40
19	S	58	VAL	N-CA-C	5.67	114.74	108.05
12	L	30	ALA	CA-C-N	5.66	126.92	119.84
12	L	30	ALA	C-N-CA	5.66	126.92	119.84
1	A	1101	A	C4'-C3'-O3'	5.66	117.88	109.40
1	A	251	G	C4'-C3'-O3'	5.64	117.87	109.40
5	E	50	GLU	N-CA-C	5.63	117.83	108.99
22	X	54	PRO	N-CA-C	5.63	117.57	110.70
1	A	391	G	C4'-C3'-O3'	-5.62	104.56	113.00
8	H	135	CYS	N-CA-C	5.62	118.36	108.75
1	A	323	U	C4'-C3'-O3'	-5.60	104.60	113.00
8	H	119	LEU	N-CA-C	5.57	115.90	108.38
1	A	364	A	C4'-C3'-O3'	-5.52	104.72	113.00
22	X	129	HIS	O-C-N	5.50	124.73	120.38
1	A	1180	A	C4'-C3'-O3'	-5.50	104.76	113.00
8	H	91	ARG	N-CA-C	-5.50	107.83	114.75
1	A	1200	C	C2'-C3'-O3'	-5.48	105.48	113.70
1	A	1257	U	C2'-C3'-O3'	5.44	117.66	109.50
4	D	110	PHE	N-CA-C	-5.43	106.15	112.89
1	A	509	A	C2'-C3'-O3'	-5.42	105.58	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	250	A	C4'-C3'-O3'	5.40	117.50	109.40
1	A	484	G	C4'-C3'-O3'	5.38	117.46	109.40
1	A	315	A	C2'-C3'-O3'	5.37	117.56	109.50
1	A	422	C	C4'-C3'-O3'	-5.37	101.34	109.40
17	Q	98	LEU	N-CA-C	5.37	118.93	112.38
13	M	110	ARG	N-CA-C	-5.35	107.40	114.04
24	Z	16	C	C2'-C3'-O3'	5.35	117.52	109.50
1	A	62	U	C4'-C3'-O3'	-5.30	105.05	113.00
13	M	25	ILE	N-CA-C	5.28	116.32	108.46
2	B	86	GLU	N-CA-C	-5.27	107.50	114.04
1	A	1196	U	C3'-C2'-O2'	5.24	118.56	110.70
1	A	1356	G	C4'-C3'-O3'	-5.24	105.15	113.00
1	A	746	A	C4'-C3'-O3'	-5.22	105.16	113.00
4	D	33	MET	N-CA-C	-5.21	105.75	112.68
1	A	653	A	C2'-C3'-O3'	5.20	117.30	109.50
24	Z	7	G	C2'-C3'-O3'	5.20	117.30	109.50
5	E	95	ALA	CA-C-N	5.20	126.34	119.84
5	E	95	ALA	C-N-CA	5.20	126.34	119.84
10	J	6	ILE	N-CA-C	5.17	115.50	107.28
6	F	95	GLU	N-CA-C	5.15	117.92	110.14
1	A	312	C	C4'-C3'-O3'	-5.15	105.28	113.00
1	A	25	C	C4'-C3'-O3'	-5.14	105.28	113.00
1	A	129(A)	G	C2'-C3'-O3'	5.13	117.20	109.50
1	A	499	A	C2'-C3'-O3'	-5.12	101.81	109.50
1	A	1357	A	C4'-C3'-O3'	-5.08	105.37	113.00
3	C	29	TYR	CA-C-N	5.08	127.40	120.54
3	C	29	TYR	C-N-CA	5.08	127.40	120.54
1	A	1504	G	C2'-C3'-O3'	5.07	117.11	109.50
3	C	6	HIS	CA-C-N	5.07	124.38	118.85
3	C	6	HIS	C-N-CA	5.07	124.38	118.85
9	I	70	LYS	N-CA-C	5.05	117.19	111.02
1	A	1233	G	C4'-C3'-O3'	-5.04	105.44	113.00
10	J	81	THR	N-CA-C	-5.04	105.47	110.97
1	A	792	A	C4'-C3'-O3'	5.04	116.95	109.40
1	A	1237	C	C4'-C3'-O3'	-5.03	105.45	113.00
1	A	397	A	C2'-C3'-O3'	5.01	121.22	113.70
11	K	57	THR	CA-C-N	5.01	126.11	119.84
11	K	57	THR	C-N-CA	5.01	126.11	119.84

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1445	C	Sidechain
1	A	218	C	Sidechain
19	S	3	ARG	Peptide
22	X	3	LYS	Peptide
22	X	53	ASP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32548	0	16440	1269	0
2	B	1900	0	1951	72	0
3	C	1612	0	1675	61	0
4	D	1703	0	1767	93	0
5	E	1146	0	1207	46	0
6	F	843	0	857	27	0
7	G	1257	0	1296	15	0
8	H	1116	0	1177	20	0
9	I	1010	0	1037	32	0
10	J	792	0	834	99	0
11	K	885	0	904	17	0
12	L	970	0	1057	31	0
13	M	937	0	995	18	0
14	N	492	0	531	16	0
15	O	734	0	771	15	0
16	P	700	0	720	19	0
17	Q	823	0	891	24	0
18	R	598	0	670	17	0
19	S	655	0	672	26	0
20	T	763	0	861	46	0
21	V	208	0	221	9	0
22	X	1336	0	1388	87	0
23	Y	439	0	219	18	0
24	Z	1646	0	843	56	0
25	A	78	0	0	3	0
25	L	1	0	0	0	0
25	Z	1	0	0	0	0
26	D	1	0	0	1	0
26	N	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	55195	0	38984	1980	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 21.

All (1980) 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)
10:J:38:ILE:HG23	10:J:71:LEU:CB	1.24	1.66
10:J:38:ILE:CG2	10:J:71:LEU:HB3	1.04	1.50
1:A:412:A:N3	4:D:35:ARG:NH1	1.66	1.44
1:A:1358:U:H3	1:A:1363(A):A:N6	1.13	1.43
1:A:1061:G:C5'	10:J:59:SER:OG	1.68	1.39
1:A:262:A:H5'	20:T:73:HIS:CE1	1.59	1.37
4:D:13:ARG:NH2	4:D:36:ARG:NH2	1.69	1.36
1:A:439:A:OP2	1:A:493:G:N2	1.57	1.34
10:J:48:THR:CG2	10:J:60:ARG:HD3	1.58	1.34
3:C:8:ILE:CD1	3:C:16:ARG:HH21	1.41	1.32
4:D:13:ARG:NH2	4:D:36:ARG:HH21	1.19	1.30
10:J:38:ILE:HG22	10:J:71:LEU:O	1.27	1.29
4:D:13:ARG:HH21	4:D:36:ARG:NH2	1.31	1.23
1:A:1358:U:O4	1:A:1363(A):A:N1	1.71	1.22
1:A:1061:G:H5'	10:J:59:SER:OG	1.18	1.19
10:J:38:ILE:CG2	10:J:71:LEU:CB	1.95	1.16
10:J:38:ILE:HG21	10:J:71:LEU:HB3	1.24	1.15
3:C:8:ILE:HD13	3:C:16:ARG:NH2	1.62	1.14
1:A:439:A:OP2	1:A:493:G:C2	2.02	1.12
1:A:1348:U:H2'	1:A:1349:A:H8	1.10	1.12
10:J:6:ILE:HG13	10:J:72:VAL:HB	1.31	1.12
10:J:38:ILE:HG23	10:J:71:LEU:CA	1.81	1.10
1:A:412:A:C4	4:D:35:ARG:NH1	2.19	1.09
4:D:13:ARG:CZ	4:D:36:ARG:HH21	1.65	1.08
1:A:1458:G:H5''	20:T:32:ALA:HB2	1.37	1.07
10:J:38:ILE:CG2	10:J:71:LEU:O	2.03	1.06
10:J:8:LEU:CB	10:J:70:ARG:HB2	1.86	1.05
10:J:8:LEU:HB3	10:J:70:ARG:HB2	1.12	1.04
3:C:8:ILE:HG12	3:C:16:ARG:HE	1.20	1.04
10:J:48:THR:HG22	10:J:60:ARG:CD	1.88	1.04
10:J:48:THR:HG22	10:J:60:ARG:HD3	1.08	1.04
1:A:413:G:N7	4:D:35:ARG:NH2	2.08	1.02
1:A:262:A:C5'	20:T:73:HIS:HE1	1.76	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:8:ILE:CD1	3:C:16:ARG:NH2	2.19	0.98
16:P:59:TRP:O	16:P:62:VAL:HG23	1.61	0.98
24:Z:71:C:H2'	24:Z:72:A:H8	1.25	0.98
1:A:96:U:H2'	1:A:97:G:C8	2.00	0.97
1:A:1398:A:N6	5:E:21:ALA:O	1.97	0.97
3:C:8:ILE:HD13	3:C:16:ARG:HH21	0.83	0.97
1:A:1391:U:H2'	1:A:1392:G:H8	1.31	0.96
10:J:16:LEU:HD23	10:J:70:ARG:HG2	1.48	0.96
10:J:38:ILE:CG2	10:J:71:LEU:C	2.39	0.96
10:J:49:VAL:O	10:J:60:ARG:HG3	1.65	0.95
1:A:436:C:H2'	1:A:437:U:H6	1.32	0.94
10:J:6:ILE:N	10:J:72:VAL:O	2.00	0.94
10:J:48:THR:HG21	10:J:60:ARG:HD3	1.50	0.93
1:A:262:A:C5'	20:T:73:HIS:CE1	2.50	0.93
1:A:1061:G:H5''	10:J:59:SER:OG	1.66	0.93
1:A:1038:C:H2'	1:A:1039:C:H6	1.31	0.93
1:A:1080:A:O3'	5:E:16:THR:CG2	2.16	0.93
4:D:13:ARG:HH21	4:D:36:ARG:HH22	1.01	0.93
10:J:38:ILE:HG21	10:J:71:LEU:HD12	1.50	0.93
1:A:664:G:H22	1:A:741:G:H1	0.98	0.93
1:A:1348:U:H2'	1:A:1349:A:C8	2.02	0.93
1:A:1391:U:H2'	1:A:1392:G:C8	2.04	0.92
1:A:1533:C:OP1	1:A:1533:C:H4'	1.69	0.92
1:A:576:G:H3'	1:A:577:G:H5''	1.51	0.91
9:I:26:VAL:HB	9:I:33:PHE:HB2	1.51	0.91
10:J:8:LEU:HB3	10:J:70:ARG:CB	2.00	0.90
15:O:35:ARG:HG2	15:O:35:ARG:HH11	1.34	0.90
1:A:920:U:H2'	1:A:921:U:C6	2.06	0.89
1:A:148:G:H2'	1:A:149:A:C8	2.07	0.89
1:A:439:A:OP2	1:A:493:G:N1	2.05	0.89
1:A:1458:G:OP1	20:T:32:ALA:HA	1.74	0.87
16:P:59:TRP:O	16:P:62:VAL:CG2	2.23	0.87
6:F:35:ALA:HA	6:F:67:MET:HB3	1.57	0.87
10:J:38:ILE:HG22	10:J:71:LEU:C	1.98	0.86
1:A:1507:A:H2'	1:A:1508:G:C8	2.10	0.86
22:X:111:GLN:HG3	22:X:147:LEU:HD21	1.55	0.86
1:A:398:C:H2'	1:A:399:G:H8	1.39	0.86
9:I:5:TYR:OH	9:I:7:THR:OG1	1.88	0.86
10:J:61:GLU:OE1	10:J:63:PHE:CZ	2.29	0.86
10:J:38:ILE:HG21	10:J:71:LEU:CD1	2.05	0.85
1:A:946:A:H2'	1:A:947:G:C8	2.11	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:51:ARG:HG2	9:I:56:LEU:HD11	1.59	0.85
9:I:8:GLY:HA2	9:I:79:LEU:HD12	1.59	0.85
10:J:6:ILE:CG1	10:J:72:VAL:HB	2.06	0.85
1:A:1219:U:H2'	1:A:1220:G:H8	1.41	0.85
22:X:3:LYS:HB3	22:X:66:ARG:HH22	1.41	0.85
1:A:1061:G:H5'	10:J:59:SER:CB	2.07	0.84
22:X:3:LYS:HB3	22:X:66:ARG:NH2	1.92	0.84
1:A:436:C:H2'	1:A:437:U:C6	2.12	0.83
1:A:674:G:H2'	1:A:675:A:H8	1.42	0.83
1:A:1457:G:H5''	1:A:1457:G:C8	2.12	0.83
22:X:58:ARG:HH22	24:Z:19:G:H2'	1.40	0.83
1:A:564:C:O2	1:A:564:C:H2'	1.77	0.83
2:B:19:HIS:O	2:B:190:THR:HG22	1.79	0.82
1:A:262:A:H5'	20:T:73:HIS:HE1	1.07	0.82
1:A:658:G:C2	1:A:749:C:N3	2.48	0.82
1:A:71:C:H2'	1:A:72:C:O4'	1.79	0.82
1:A:97:G:H2'	1:A:98:G:C8	2.14	0.82
1:A:1219:U:H2'	1:A:1220:G:C8	2.16	0.81
24:Z:71:C:H2'	24:Z:72:A:C8	2.14	0.81
22:X:19:VAL:O	22:X:58:ARG:HA	1.81	0.81
1:A:30:U:H3'	1:A:31:G:H5''	1.63	0.81
20:T:15:ARG:HG2	20:T:15:ARG:HH11	1.46	0.80
24:Z:36:U:H2'	24:Z:37:A:H8	1.45	0.80
18:R:37:VAL:HG21	18:R:78:LEU:HB3	1.62	0.80
2:B:215:LEU:O	2:B:219:VAL:HG23	1.82	0.80
1:A:1507:A:H2'	1:A:1508:G:H8	1.44	0.80
1:A:553:A:H2'	1:A:554:C:C6	2.16	0.80
1:A:1356:G:H2'	1:A:1357:A:C8	2.16	0.80
1:A:10:A:H2'	1:A:11:G:H8	1.47	0.80
11:K:15:ALA:HA	11:K:77:MET:HA	1.64	0.80
1:A:750:G:H1'	15:O:22:THR:OG1	1.82	0.79
2:B:212:GLN:HG3	2:B:239:VAL:CG2	2.12	0.79
1:A:1513:A:H2'	1:A:1514:C:C6	2.17	0.79
1:A:745:C:H2'	1:A:746:A:C8	2.17	0.79
3:C:8:ILE:HG12	3:C:16:ARG:NE	1.96	0.79
9:I:5:TYR:HH	9:I:7:THR:HG1	1.14	0.79
10:J:38:ILE:CB	10:J:71:LEU:HB3	2.09	0.79
1:A:1080:A:O3'	5:E:16:THR:HG21	1.83	0.79
10:J:48:THR:CG2	10:J:60:ARG:CD	2.50	0.79
1:A:17:U:H2'	1:A:18:C:C6	2.17	0.78
1:A:946:A:H2'	1:A:947:G:H8	1.47	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:6:ILE:HG13	10:J:72:VAL:CB	2.12	0.78
1:A:977:A:H2'	1:A:978:A:H5''	1.66	0.78
1:A:373:A:H2'	1:A:374:A:H8	1.49	0.78
22:X:106:ILE:HG12	22:X:116:VAL:HG11	1.66	0.78
1:A:262:A:H5'	20:T:73:HIS:NE2	1.99	0.77
13:M:22:ILE:HG22	13:M:24:GLY:H	1.48	0.77
1:A:1327:C:H5''	21:V:20:LYS:HB2	1.66	0.77
1:A:1347:G:C8	9:I:107:ARG:HB3	2.19	0.77
9:I:46:ALA:HA	9:I:78:LYS:HB2	1.67	0.77
10:J:8:LEU:CB	10:J:70:ARG:CB	2.61	0.77
1:A:1264:C:H2'	1:A:1265:G:H8	1.50	0.77
4:D:165:MET:HA	4:D:168:ARG:HG2	1.66	0.77
1:A:20:U:H2'	1:A:21:G:O4'	1.84	0.77
1:A:24:U:H2'	1:A:25:C:C6	2.20	0.76
10:J:35:SER:HB2	10:J:73:ASP:HB3	1.67	0.76
1:A:880:C:H2'	1:A:881:G:H8	1.49	0.76
1:A:1255:G:H2'	1:A:1279:A:N6	2.01	0.76
1:A:737:A:H2'	1:A:738:C:C6	2.21	0.76
18:R:32:ARG:HA	18:R:69:THR:HG21	1.68	0.76
1:A:1399:C:C2	1:A:1502:A:N6	2.54	0.76
1:A:81:U:O2'	1:A:88:A:N6	2.19	0.75
1:A:1095:U:OP1	1:A:1108:G:N1	2.18	0.75
1:A:1228:C:H5'	13:M:108:ARG:HH22	1.51	0.75
1:A:1293:G:H2'	1:A:1294:G:H8	1.51	0.75
1:A:148:G:H2'	1:A:149:A:H8	1.50	0.75
1:A:263:A:OP1	20:T:79:ARG:HD3	1.86	0.75
24:Z:23:C:H2'	24:Z:24:U:C6	2.21	0.75
1:A:351:G:H4'	1:A:352:C:OP1	1.87	0.75
1:A:1121:U:H2'	1:A:1122:U:C6	2.21	0.75
10:J:51:ARG:N	10:J:59:SER:O	2.19	0.75
10:J:49:VAL:O	10:J:60:ARG:CG	2.35	0.75
1:A:1038:C:H2'	1:A:1039:C:C6	2.19	0.75
1:A:124:G:H2'	1:A:125:U:O4'	1.87	0.74
1:A:714:G:H2'	1:A:715:A:C8	2.21	0.74
1:A:559:A:H4'	1:A:560:U:H5''	1.69	0.74
1:A:1458:G:C5'	20:T:32:ALA:HB2	2.15	0.74
24:Z:33:U:N3	24:Z:36:U:OP2	2.21	0.74
1:A:266:G:C8	1:A:266:G:H5''	2.22	0.74
24:Z:55:PSU:O2'	24:Z:57:A:N7	2.18	0.74
1:A:81:U:H4'	1:A:81:U:OP1	1.88	0.73
3:C:22:TRP:CZ3	3:C:29:TYR:CD1	2.77	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:67:TYR:O	22:X:71:MET:HG3	1.88	0.73
24:Z:63:G:H2'	24:Z:64:G:H8	1.52	0.73
1:A:524:G:C6	1:A:525:C:N4	2.56	0.73
1:A:922:G:H2'	1:A:923:A:C8	2.24	0.73
1:A:184:G:H2'	1:A:185:A:H8	1.53	0.73
1:A:343:U:O2'	1:A:346:G:O6	2.04	0.73
1:A:728:A:H2'	1:A:729:A:C8	2.23	0.73
1:A:302:G:H2'	1:A:303:A:C8	2.24	0.73
1:A:736:C:H2'	1:A:737:A:C8	2.24	0.73
1:A:78:G:H2'	1:A:79:G:O4'	1.89	0.72
1:A:101:A:H2'	1:A:102:G:H8	1.53	0.72
1:A:600:C:H2'	1:A:601:C:C6	2.24	0.72
17:Q:94:ASN:O	17:Q:97:SER:HB3	1.89	0.72
19:S:28:LYS:HD3	19:S:29:ARG:H	1.53	0.72
1:A:1281:U:H3	10:J:5:ARG:HH12	1.35	0.72
1:A:1014:A:H2'	1:A:1015:A:C8	2.24	0.72
1:A:1135:U:H4'	1:A:1136:U:C5	2.23	0.72
1:A:917:G:H2'	1:A:918:A:C8	2.23	0.72
5:E:14:ARG:HG3	5:E:14:ARG:NH1	2.05	0.72
4:D:15:GLU:HG2	4:D:63:LYS:HG3	1.72	0.72
1:A:576:G:H3'	1:A:577:G:C5'	2.20	0.72
1:A:1445:C:C2	1:A:1458:G:C2	2.78	0.72
19:S:13:ASP:HA	19:S:16:LEU:HB3	1.71	0.72
1:A:664:G:N2	1:A:741:G:H1	1.81	0.71
3:C:14:ILE:HD13	3:C:14:ILE:N	2.04	0.71
23:Y:38:G:H1	24:Z:34:C:H42	1.38	0.71
5:E:14:ARG:HG3	5:E:14:ARG:HH11	1.56	0.71
6:F:7:ASN:HB2	6:F:89:MET:HB3	1.70	0.71
1:A:92:C:H2'	1:A:93:G:C8	2.24	0.71
20:T:63:ILE:HG23	20:T:72:LEU:HD13	1.73	0.71
1:A:109:A:H2'	1:A:326:G:N2	2.05	0.71
1:A:1475:G:H2'	1:A:1476:G:C8	2.26	0.71
2:B:93:VAL:HG11	2:B:97:TRP:HD1	1.56	0.71
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.73	0.70
10:J:60:ARG:HB3	10:J:60:ARG:HH21	1.55	0.70
12:L:53:ARG:HG2	12:L:53:ARG:HH11	1.54	0.70
1:A:920:U:H2'	1:A:921:U:H6	1.52	0.70
1:A:1016:A:H2'	1:A:1017:G:O4'	1.91	0.70
1:A:72:C:H42	1:A:97:G:H1	1.39	0.70
1:A:1293:G:H2'	1:A:1294:G:C8	2.26	0.70
2:B:212:GLN:HG3	2:B:239:VAL:HG21	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:9:CYS:SG	26:D:300:ZN:ZN	1.79	0.70
4:D:201:GLN:HG2	4:D:205:GLU:OE1	1.91	0.70
1:A:769:G:N2	1:A:770:C:C2	2.60	0.70
1:A:10:A:H2'	1:A:11:G:C8	2.27	0.70
1:A:1121:U:H2'	1:A:1122:U:H6	1.57	0.70
1:A:544:G:OP1	4:D:62:GLN:HG3	1.91	0.70
1:A:658:G:N2	1:A:749:C:C2	2.60	0.70
1:A:914:A:H2'	1:A:915:A:H8	1.55	0.70
1:A:1518:A:H2'	1:A:1519:A:C8	2.26	0.70
22:X:64:LYS:O	22:X:68:GLU:HG2	1.92	0.70
1:A:224:C:H2'	1:A:225:C:C6	2.27	0.69
1:A:575:G:H4'	1:A:576:G:H5''	1.74	0.69
1:A:662:G:H2'	1:A:663:A:C8	2.26	0.69
1:A:728:A:H2'	1:A:729:A:H8	1.57	0.69
1:A:864:A:H2'	1:A:865:A:C8	2.26	0.69
1:A:1097:C:H2'	1:A:1098:C:C6	2.27	0.69
8:H:91:ARG:HD3	12:L:7:ILE:HG21	1.73	0.69
1:A:335:C:H2'	1:A:336:C:C6	2.27	0.69
23:Y:27:G:H2'	23:Y:28:A:O4'	1.91	0.69
1:A:1354:C:H2'	1:A:1355:G:H8	1.57	0.69
22:X:137:LEU:HD12	22:X:154:PRO:HB3	1.74	0.69
1:A:1287:A:H2'	1:A:1288:A:C8	2.27	0.69
2:B:112:VAL:HG23	2:B:149:LEU:HB3	1.75	0.69
10:J:38:ILE:HG23	10:J:71:LEU:C	2.12	0.69
1:A:585:G:H4'	12:L:8:ASN:HD21	1.58	0.69
1:A:973:G:H3'	1:A:974:A:H5''	1.73	0.69
1:A:1256:A:N6	1:A:1278:U:C2	2.61	0.69
8:H:12:ARG:HD3	8:H:26:VAL:HG12	1.74	0.69
10:J:61:GLU:OE1	10:J:63:PHE:CE2	2.45	0.69
19:S:11:VAL:HA	19:S:38:SER:HB3	1.75	0.69
22:X:61:ASP:HB3	22:X:64:LYS:HB3	1.75	0.69
1:A:578:C:OP1	25:A:1668:MG:MG	1.36	0.68
1:A:841:U:H6	1:A:841:U:H5''	1.56	0.68
1:A:1106:G:H5''	3:C:172:ARG:HG2	1.74	0.68
10:J:23:ILE:HG21	10:J:72:VAL:HG11	1.74	0.68
1:A:1358:U:C4	1:A:1363(A):A:N1	2.59	0.68
1:A:579:G:H2'	1:A:580:U:C6	2.29	0.68
1:A:736:C:H2'	1:A:737:A:H8	1.58	0.68
1:A:772:U:H2'	1:A:773:G:C8	2.29	0.68
2:B:8:LYS:HD2	2:B:9:GLU:H	1.58	0.68
24:Z:36:U:H2'	24:Z:37:A:C8	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:975:A:H4'	1:A:976:G:H5'	1.75	0.68
1:A:24:U:H2'	1:A:25:C:H6	1.57	0.68
1:A:99:U:H2'	1:A:100:C:C6	2.28	0.68
1:A:412:A:C2	4:D:35:ARG:NH1	2.60	0.68
1:A:1281:U:H5'	1:A:1282:C:H5	1.59	0.68
1:A:322:C:H2'	1:A:323:U:H6	1.58	0.68
1:A:674:G:H2'	1:A:675:A:C8	2.28	0.68
1:A:1513:A:H2'	1:A:1514:C:H6	1.57	0.68
1:A:1518:A:H2'	1:A:1519:A:H8	1.58	0.68
1:A:568:G:N2	1:A:883:C:C2	2.61	0.68
1:A:914:A:H2'	1:A:915:A:C8	2.28	0.68
1:A:222:U:H2'	1:A:223:U:C6	2.29	0.68
6:F:52:ILE:HD11	18:R:77:GLY:HA3	1.75	0.68
1:A:216:G:H2'	1:A:217:C:C6	2.29	0.68
10:J:6:ILE:HD11	10:J:72:VAL:HG11	1.75	0.68
1:A:352:C:H4'	1:A:354:G:OP1	1.94	0.67
10:J:40:LEU:HB2	10:J:69:ASN:HB3	1.77	0.67
1:A:797:C:OP1	11:K:124:LYS:HG3	1.94	0.67
1:A:84:U:H2'	1:A:88:A:O4'	1.94	0.67
1:A:299:G:H2'	1:A:300:A:C8	2.30	0.67
1:A:1488:G:H2'	1:A:1489:G:H8	1.58	0.67
1:A:729:A:H2'	1:A:730:G:H8	1.59	0.67
1:A:1263:C:H2'	1:A:1264:C:C6	2.30	0.67
10:J:49:VAL:HG22	10:J:61:GLU:O	1.94	0.67
1:A:302:G:H2'	1:A:303:A:H8	1.60	0.67
1:A:524:G:C2	1:A:525:C:N3	2.62	0.67
20:T:42:GLN:O	20:T:45:GLN:HB2	1.95	0.67
1:A:413:G:N7	4:D:35:ARG:CZ	2.57	0.67
1:A:1099:G:C6	1:A:1100:C:N3	2.63	0.67
1:A:1349:A:H3'	1:A:1350:A:H8	1.60	0.67
3:C:22:TRP:CH2	3:C:29:TYR:CE1	2.82	0.67
13:M:97:PRO:HG2	13:M:103:THR:HG22	1.77	0.67
3:C:28:GLN:O	3:C:32:LEU:HG	1.95	0.67
2:B:212:GLN:HG3	2:B:239:VAL:HG22	1.77	0.67
1:A:632:A:H2'	1:A:633:G:O4'	1.94	0.66
15:O:35:ARG:HG2	15:O:35:ARG:NH1	2.09	0.66
22:X:127:VAL:HG23	22:X:128:ALA:H	1.60	0.66
1:A:1126:U:H1'	1:A:1280:A:C6	2.29	0.66
3:C:22:TRP:CH2	3:C:29:TYR:HE1	2.12	0.66
12:L:73:GLU:H	12:L:110:VAL:HG11	1.60	0.66
22:X:88:ILE:HG22	22:X:118:VAL:HG13	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:62:HIS:HB2	14:N:59:ALA:HB3	1.77	0.66
1:A:197:A:H4'	1:A:198:G:O5'	1.94	0.66
1:A:568:G:C2	1:A:883:C:N3	2.63	0.66
1:A:1218:C:H2'	1:A:1219:U:C6	2.30	0.66
19:S:56:GLN:HB3	19:S:58:VAL:HG13	1.78	0.66
1:A:96:U:H2'	1:A:97:G:H8	1.55	0.66
5:E:15:ARG:HG3	5:E:15:ARG:O	1.94	0.66
1:A:1161:C:H2'	1:A:1162:C:C6	2.31	0.66
18:R:48:GLY:H	18:R:83:GLU:HB2	1.61	0.66
22:X:11:ILE:HG12	22:X:47:LEU:HD22	1.78	0.66
24:Z:63:G:H2'	24:Z:64:G:C8	2.30	0.66
1:A:33:A:H2'	1:A:34:C:C6	2.31	0.66
1:A:1040:U:H2'	1:A:1041:A:C8	2.31	0.66
1:A:1363(A):A:H1'	1:A:1365:G:C5	2.31	0.66
1:A:491:G:H2'	1:A:492:G:O4'	1.96	0.65
1:A:499:A:C6	1:A:547:A:C8	2.84	0.65
1:A:69:G:H1	1:A:100:C:H42	1.43	0.65
1:A:874:G:N2	1:A:875:C:C2	2.65	0.65
1:A:1151:A:O2'	1:A:1152:A:H8	1.79	0.65
1:A:1312:G:N2	1:A:1326:C:C2	2.65	0.65
4:D:173:TRP:HB2	4:D:187:ARG:O	1.96	0.65
1:A:1264:C:H2'	1:A:1265:G:C8	2.29	0.65
15:O:82:ILE:HG21	15:O:88:ARG:HE	1.61	0.65
22:X:48:VAL:HG21	22:X:58:ARG:HE	1.62	0.65
22:X:110:LEU:HD22	22:X:148:ALA:HB2	1.79	0.65
23:Y:28:A:H3'	23:Y:29:G:C8	2.32	0.65
1:A:1361:G:C6	1:A:1362:C:N3	2.65	0.65
3:C:44:GLU:HG2	3:C:52:LEU:HD11	1.78	0.65
3:C:77:ILE:HA	3:C:84:ILE:HB	1.79	0.65
1:A:1504:G:H4'	1:A:1505:G:O5'	1.97	0.65
1:A:354:G:N2	1:A:355:C:C2	2.65	0.65
1:A:1353:G:N2	1:A:1354:C:C2	2.64	0.65
10:J:61:GLU:OE2	14:N:45:ARG:NH1	2.29	0.65
1:A:1151:A:O2'	1:A:1152:A:C8	2.50	0.65
5:E:100:VAL:HG13	5:E:118:ILE:HD11	1.79	0.65
22:X:15:GLN:HB3	22:X:28:ILE:HG22	1.79	0.65
22:X:88:ILE:HG23	22:X:102:LYS:HD3	1.79	0.65
1:A:397:A:H3'	1:A:397:A:N3	2.12	0.64
1:A:1095:U:H2'	1:A:1096:C:C6	2.31	0.64
1:A:97:G:H2'	1:A:98:G:H8	1.58	0.64
1:A:409:G:OP2	4:D:22:LYS:HB3	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:C:H2'	1:A:443:C:C6	2.33	0.64
1:A:416:G:C6	1:A:417:C:N3	2.65	0.64
1:A:1151:A:HO2'	1:A:1152:A:H8	1.44	0.64
1:A:539:A:H2'	1:A:540:G:C8	2.32	0.64
1:A:1128:C:H1'	1:A:1146:A:H61	1.63	0.64
3:C:22:TRP:HZ3	3:C:29:TYR:HD1	1.45	0.64
22:X:157:LEU:HB2	22:X:160:ASP:HB2	1.78	0.64
1:A:1456:G:H3'	1:A:1457:G:O4'	1.97	0.64
2:B:71:VAL:HA	2:B:93:VAL:HG12	1.79	0.64
3:C:22:TRP:CZ3	3:C:29:TYR:CE1	2.85	0.64
4:D:13:ARG:CZ	4:D:36:ARG:NH2	2.39	0.64
9:I:112:LYS:HG2	9:I:118:LYS:HA	1.79	0.64
24:Z:48:C:H4'	24:Z:49:G:H5''	1.80	0.64
1:A:1354:C:H2'	1:A:1355:G:C8	2.32	0.64
1:A:772:U:H2'	1:A:773:G:H8	1.63	0.63
3:C:22:TRP:CZ3	3:C:29:TYR:HD1	2.15	0.63
3:C:8:ILE:HD11	3:C:16:ARG:NH2	2.12	0.63
13:M:108:ARG:HE	13:M:114:ARG:HG2	1.62	0.63
1:A:744:C:H2'	1:A:745:C:C6	2.34	0.63
1:A:34:C:H2'	1:A:35:G:H8	1.64	0.63
24:Z:43:A:H2'	24:Z:44:A:C8	2.33	0.63
1:A:505:G:H5'	1:A:534:U:H2'	1.80	0.63
1:A:725:G:N2	1:A:726:C:C2	2.67	0.63
4:D:3:ARG:HA	4:D:3:ARG:CZ	2.28	0.63
9:I:10:ARG:HA	9:I:104:ARG:HH12	1.63	0.63
22:X:90:PHE:HB2	22:X:120:ILE:HD13	1.79	0.63
1:A:588:G:N2	1:A:589:C:C2	2.67	0.63
1:A:585:G:H4'	12:L:8:ASN:ND2	2.13	0.63
1:A:965:A:O5'	1:A:965:A:H8	1.82	0.63
1:A:107:G:C2	1:A:108:G:H1'	2.34	0.63
1:A:1492:A:H2'	1:A:1493:A:H5''	1.80	0.63
6:F:41:GLU:HB2	6:F:62:TRP:HE3	1.64	0.63
20:T:63:ILE:HG12	20:T:72:LEU:HD11	1.80	0.63
1:A:352:C:OP2	25:A:1639:MG:MG	1.42	0.62
2:B:84:GLU:HA	2:B:87:ARG:HB2	1.80	0.62
1:A:1443:G:C6	1:A:1444:C:N4	2.66	0.62
4:D:33:MET:HA	4:D:36:ARG:O	1.99	0.62
1:A:170:U:H2'	1:A:171:A:H8	1.64	0.62
18:R:59:SER:HB3	18:R:62:GLU:HB2	1.80	0.62
1:A:110:C:H2'	1:A:111:G:O4'	1.99	0.62
1:A:1355:G:H2'	1:A:1356:G:H8	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:38:ILE:HG21	10:J:71:LEU:CB	1.99	0.62
10:J:48:THR:HG22	10:J:60:ARG:CG	2.29	0.62
1:A:1456:G:C4	1:A:1457:G:H1'	2.34	0.62
1:A:1492:A:H3'	1:A:1492:A:H8	1.65	0.62
14:N:27:CYS:SG	26:N:101:ZN:ZN	1.88	0.62
1:A:79:G:H2'	1:A:80:G:C8	2.34	0.62
1:A:598:U:H2'	1:A:599:C:H6	1.65	0.62
10:J:38:ILE:HG23	10:J:71:LEU:HB3	0.64	0.62
22:X:96:GLU:O	22:X:100:GLN:HG3	2.00	0.62
1:A:663:A:H2'	1:A:664:G:O4'	1.99	0.62
1:A:34:C:H2'	1:A:35:G:C8	2.34	0.62
2:B:162:ILE:HD12	2:B:177:ALA:HB2	1.81	0.62
15:O:17:ARG:HE	15:O:77:ARG:HD2	1.65	0.62
1:A:322:C:H2'	1:A:323:U:C6	2.34	0.62
1:A:1004:A:H5''	1:A:1025:U:C5	2.35	0.62
1:A:1342:C:H2'	1:A:1343:G:H8	1.65	0.62
1:A:1425:U:H2'	1:A:1426:C:C6	2.34	0.62
4:D:78:LEU:HD22	4:D:97:LEU:HG	1.81	0.62
1:A:21:G:H2'	1:A:22:G:C8	2.34	0.62
1:A:198:G:H1	1:A:219:C:N4	1.98	0.62
1:A:999:C:O2	1:A:1043:C:O2	2.17	0.62
4:D:11:LEU:HD13	4:D:66:ARG:HG2	1.82	0.62
5:E:40:ARG:HG2	5:E:40:ARG:HH11	1.64	0.62
1:A:376:G:H2'	1:A:377:G:H8	1.65	0.61
1:A:543:C:H2'	1:A:544:G:C8	2.35	0.61
1:A:681:C:C2	1:A:710:G:N2	2.68	0.61
1:A:216:G:C6	1:A:217:C:N4	2.68	0.61
1:A:413:G:C5	4:D:35:ARG:NH2	2.68	0.61
1:A:1305:G:O2'	1:A:1306:A:H8	1.82	0.61
3:C:131:ARG:NH1	5:E:50:GLU:HB3	2.14	0.61
1:A:373:A:H2'	1:A:374:A:C8	2.34	0.61
1:A:583:A:O2'	17:Q:91:ARG:HG3	2.00	0.61
1:A:952:U:H2'	1:A:953:G:H8	1.65	0.61
1:A:1536:C:H42	23:Y:29:G:H1	1.47	0.61
1:A:269:C:H2'	1:A:270:A:C8	2.36	0.61
1:A:1333:A:H2'	1:A:1334:G:O4'	2.00	0.61
2:B:177:ALA:HB1	2:B:182:ILE:O	2.01	0.61
1:A:262:A:H2'	1:A:263:A:C8	2.35	0.61
1:A:824:C:H42	1:A:876:G:H1	1.48	0.61
1:A:1368:G:N2	1:A:1369:C:C2	2.68	0.61
1:A:259:G:H2'	1:A:260:G:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:712:A:H2'	1:A:713:G:O4'	2.00	0.61
1:A:1106:G:N2	1:A:1107:C:C2	2.68	0.61
1:A:1323:G:H2'	1:A:1324:A:C8	2.36	0.61
1:A:1361:G:C2	1:A:1362:C:O2	2.53	0.61
4:D:133:VAL:HG11	4:D:138:TYR:HD2	1.66	0.61
5:E:14:ARG:HH11	5:E:14:ARG:CG	2.14	0.61
1:A:187:C:C2	20:T:105:SER:HB2	2.36	0.61
1:A:1287:A:H5'	1:A:1287:A:H8	1.65	0.61
3:C:131:ARG:HH12	5:E:52:PRO:HD2	1.64	0.61
4:D:196:LEU:HB3	4:D:198:VAL:HG12	1.81	0.61
10:J:78:ASN:HB2	10:J:81:THR:H	1.65	0.61
22:X:16:VAL:HB	22:X:57:ALA:HB2	1.82	0.61
4:D:201:GLN:HA	4:D:204:ILE:HD12	1.81	0.61
1:A:68:G:H5''	1:A:68:G:C8	2.35	0.60
1:A:222:U:H2'	1:A:223:U:H6	1.65	0.60
1:A:1003:G:N2	1:A:1038:C:C2	2.69	0.60
1:A:662:G:H2'	1:A:663:A:H8	1.64	0.60
1:A:975:A:C8	1:A:975:A:H5'	2.37	0.60
10:J:16:LEU:CD2	10:J:70:ARG:HG2	2.28	0.60
22:X:157:LEU:HD12	22:X:160:ASP:HB2	1.82	0.60
1:A:122:G:N1	1:A:123:C:C2	2.70	0.60
1:A:184:G:H2'	1:A:185:A:C8	2.35	0.60
1:A:1127:G:N2	1:A:1145:C:C2	2.69	0.60
1:A:1342:C:H2'	1:A:1343:G:C8	2.36	0.60
2:B:118:LEU:HB3	2:B:142:LEU:HD11	1.82	0.60
10:J:5:ARG:HA	10:J:73:ASP:HA	1.83	0.60
1:A:1182:G:H4'	1:A:1183:A:O5'	2.01	0.60
1:A:746:A:H2'	1:A:747:C:C6	2.36	0.60
1:A:1025:U:H2'	1:A:1026:G:C8	2.37	0.60
1:A:1126:U:O2	1:A:1126:U:H2'	2.00	0.60
1:A:78:G:H2'	1:A:79:G:C1'	2.31	0.60
1:A:598:U:H2'	1:A:599:C:C6	2.36	0.60
20:T:15:ARG:HH11	20:T:15:ARG:CG	2.14	0.60
1:A:181:G:H4'	1:A:182:U:H5'	1.84	0.60
1:A:1056:U:O2	1:A:1056:U:H2'	2.00	0.60
1:A:524:G:C2	1:A:525:C:C4	2.90	0.60
1:A:584:G:H2'	1:A:585:G:H8	1.67	0.60
1:A:865:A:O5'	1:A:865:A:H8	1.84	0.60
1:A:992:U:H4'	1:A:993:G:O5'	2.02	0.60
2:B:19:HIS:HB2	2:B:204:ASN:HA	1.84	0.60
19:S:12:ASP:H	19:S:38:SER:HB3	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:C:H2'	1:A:321:A:C8	2.36	0.60
3:C:29:TYR:OH	14:N:54:PRO:HD2	2.02	0.60
1:A:600:C:H2'	1:A:601:C:H6	1.67	0.59
1:A:658:G:C2	1:A:749:C:C2	2.90	0.59
1:A:1001(A):G:N2	1:A:1040:U:C2	2.69	0.59
1:A:1248:A:H2'	1:A:1249:C:C6	2.37	0.59
1:A:127:G:C2	1:A:235:C:N3	2.70	0.59
1:A:344:A:H4'	1:A:345:C:OP2	2.02	0.59
1:A:365:U:O2	1:A:365:U:H2'	2.01	0.59
2:B:15:VAL:HG21	2:B:209:ARG:HG3	1.82	0.59
3:C:6:HIS:HD2	3:C:9:GLY:H	1.49	0.59
1:A:755:G:N2	1:A:756:C:C2	2.70	0.59
1:A:1128:C:H2'	1:A:1139:G:N7	2.16	0.59
1:A:289:G:N2	1:A:290:C:C2	2.70	0.59
1:A:1163:C:C2	1:A:1174:G:N2	2.71	0.59
20:T:53:LEU:HB3	20:T:100:ILE:HG22	1.83	0.59
22:X:111:GLN:HG3	22:X:147:LEU:CD2	2.28	0.59
1:A:683:G:N2	1:A:708:C:C2	2.70	0.59
2:B:21:ARG:HA	2:B:39:ILE:HA	1.84	0.59
2:B:82:ARG:O	2:B:86:GLU:HB2	2.01	0.59
10:J:27:ALA:HB1	10:J:34:VAL:HG21	1.85	0.59
10:J:51:ARG:HB2	10:J:59:SER:O	2.01	0.59
5:E:81:GLU:HG3	5:E:90:VAL:HG22	1.85	0.59
1:A:127:G:N2	1:A:235:C:C2	2.71	0.59
1:A:517:G:N1	1:A:533:A:OP2	2.29	0.59
1:A:552:U:H2'	1:A:553:A:C8	2.38	0.59
1:A:1125:U:H5'	1:A:1126:U:H5	1.67	0.59
7:G:39:ALA:HA	7:G:42:ILE:HD12	1.83	0.59
1:A:412:A:H1'	4:D:35:ARG:NH1	2.18	0.59
1:A:766:A:OP2	25:A:1629:MG:MG	1.44	0.59
1:A:975:A:H4'	1:A:976:G:C5'	2.32	0.59
1:A:1530:G:H2'	1:A:1531:A:C8	2.38	0.59
1:A:555:C:H2'	1:A:556:C:C6	2.37	0.59
1:A:564:C:O2	1:A:564:C:C2'	2.50	0.59
10:J:38:ILE:CG2	10:J:71:LEU:CA	2.58	0.59
1:A:1232:U:H5''	9:I:124:GLN:O	2.03	0.58
20:T:54:LYS:HA	20:T:57:ARG:HD3	1.85	0.58
20:T:72:LEU:HD22	20:T:77:ALA:HA	1.84	0.58
22:X:87:SER:HA	22:X:117:LYS:O	2.03	0.58
1:A:19:C:H2'	1:A:20:U:C6	2.39	0.58
1:A:198:G:H2'	1:A:199:G:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1312:G:C2	1:A:1326:C:C2	2.92	0.58
1:A:1492:A:H3'	1:A:1492:A:C8	2.37	0.58
11:K:48:ILE:HD11	11:K:64:ALA:HB2	1.84	0.58
1:A:98:G:H2'	1:A:99:U:O4'	2.03	0.58
1:A:584:G:H2'	1:A:585:G:C8	2.39	0.58
1:A:1216:G:N2	1:A:1217:C:C2	2.72	0.58
1:A:518:C:H5''	1:A:519:C:C6	2.39	0.58
1:A:914:A:C4	1:A:915:A:N7	2.71	0.58
22:X:86:LYS:O	22:X:116:VAL:HA	2.04	0.58
1:A:145:G:C2	1:A:178:C:N3	2.72	0.58
1:A:1355:G:H2'	1:A:1356:G:C8	2.39	0.58
2:B:174:VAL:HG13	2:B:184:VAL:HG21	1.86	0.58
10:J:23:ILE:CG2	10:J:72:VAL:HG11	2.33	0.58
10:J:38:ILE:HG21	10:J:71:LEU:CG	2.34	0.58
1:A:975:A:C8	1:A:975:A:C5'	2.86	0.58
1:A:202:U:H4'	1:A:203:U:OP1	2.03	0.58
1:A:312:C:H2'	1:A:313:A:C8	2.39	0.58
1:A:1203:C:H2'	1:A:1204:A:H8	1.68	0.58
2:B:209:ARG:HA	2:B:239:VAL:CG1	2.34	0.58
1:A:761:G:C6	1:A:762:C:N3	2.72	0.58
1:A:767:A:H2'	1:A:768:A:O4'	2.03	0.58
6:F:5:GLU:HB2	6:F:91:VAL:HG12	1.86	0.58
1:A:1439:C:O2	1:A:1463:C:O2	2.22	0.58
2:B:178:ARG:HA	2:B:178:ARG:HH11	1.68	0.58
2:B:200:ILE:H	2:B:200:ILE:HD12	1.68	0.58
10:J:6:ILE:CD1	10:J:72:VAL:HB	2.34	0.58
24:Z:8:4SU:O2	24:Z:21:A:H2	1.86	0.58
1:A:198:G:H1	1:A:219:C:H42	1.51	0.57
1:A:1134:G:H1	1:A:1140:C:H42	1.52	0.57
3:C:29:TYR:OH	14:N:54:PRO:CD	2.52	0.57
4:D:133:VAL:HG11	4:D:138:TYR:CD2	2.39	0.57
1:A:174:C:H2'	1:A:175:C:H6	1.69	0.57
1:A:269:C:H2'	1:A:270:A:H8	1.68	0.57
1:A:1488:G:H2'	1:A:1489:G:C8	2.38	0.57
1:A:1512:U:H2'	1:A:1513:A:H8	1.69	0.57
5:E:20:GLN:OE1	5:E:20:GLN:HA	2.02	0.57
1:A:128:G:C2	1:A:234:C:C2	2.92	0.57
1:A:589:C:O2	1:A:651:C:O2	2.22	0.57
1:A:769:G:N1	1:A:770:C:C4	2.71	0.57
1:A:1114:C:C2	1:A:1187:G:C2	2.93	0.57
1:A:1392:G:N2	1:A:1502:A:H8	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1456:G:H2'	1:A:1457:G:O4'	2.05	0.57
20:T:51:GLU:HA	20:T:54:LYS:HE3	1.87	0.57
1:A:308:C:H2'	1:A:309:G:H8	1.70	0.57
1:A:392:G:H2'	1:A:393:A:C8	2.39	0.57
1:A:1039:C:H2'	1:A:1040:U:C6	2.39	0.57
3:C:85:ARG:NH1	3:C:88:ARG:HB3	2.20	0.57
4:D:35:ARG:HG2	4:D:36:ARG:HG3	1.87	0.57
18:R:21:LYS:HE3	18:R:57:GLY:HA3	1.86	0.57
1:A:174:C:H2'	1:A:175:C:C6	2.39	0.57
1:A:777:A:H2'	1:A:778:G:C8	2.39	0.57
1:A:838:G:C2	1:A:849:C:C2	2.92	0.57
1:A:1002:G:H2'	1:A:1003:G:O4'	2.05	0.57
2:B:73:THR:HB	2:B:170:GLU:HG2	1.86	0.57
1:A:67:C:H2'	1:A:68:G:C8	2.40	0.57
1:A:1281:U:H5'	1:A:1282:C:C5	2.39	0.57
1:A:216:G:C2	1:A:217:C:N3	2.73	0.57
1:A:1435:G:H2'	1:A:1436:U:C6	2.40	0.57
1:A:1457:G:C8	1:A:1457:G:C5'	2.85	0.57
2:B:114:ARG:HH11	2:B:118:LEU:HD11	1.69	0.57
5:E:69:VAL:HG11	5:E:113:ALA:HB1	1.86	0.57
1:A:652:U:O4	1:A:752:G:O2'	2.17	0.57
1:A:1097:C:H2'	1:A:1098:C:H6	1.70	0.57
1:A:128:G:N2	1:A:234:C:C2	2.72	0.57
1:A:131:C:H2'	1:A:132:C:C6	2.39	0.57
1:A:419:C:H42	1:A:424:G:H1	1.52	0.57
1:A:629:G:H2'	1:A:630:G:O4'	2.05	0.57
1:A:1512:U:H2'	1:A:1513:A:C8	2.40	0.57
18:R:48:GLY:N	18:R:83:GLU:HB2	2.19	0.57
1:A:1105:A:H2'	1:A:1106:G:H8	1.69	0.56
1:A:1222:G:N2	1:A:1223:C:C2	2.73	0.56
1:A:255:G:H2'	1:A:256:U:C6	2.40	0.56
1:A:662:G:C2	1:A:744:C:O2	2.58	0.56
1:A:1315:U:O2'	1:A:1360:A:N3	2.37	0.56
2:B:115:LEU:HD11	2:B:146:GLN:HG3	1.87	0.56
17:Q:82:MET:O	17:Q:85:VAL:HB	2.05	0.56
19:S:28:LYS:CD	19:S:29:ARG:H	2.18	0.56
20:T:43:LEU:HB3	20:T:52:ALA:HB2	1.86	0.56
1:A:30:U:H3'	1:A:31:G:C5'	2.33	0.56
1:A:35:G:H2'	1:A:36:C:C6	2.40	0.56
1:A:794:A:H2'	1:A:795:C:C6	2.40	0.56
1:A:806:C:H2'	1:A:807:A:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1218:C:H2'	1:A:1219:U:H6	1.70	0.56
1:A:1414:U:H2'	1:A:1415:G:C8	2.39	0.56
4:D:200:GLU:O	4:D:204:ILE:HG13	2.05	0.56
5:E:28:PHE:HD2	5:E:50:GLU:HA	1.71	0.56
1:A:279:A:OP2	17:Q:95:TYR:OH	2.21	0.56
1:A:864:A:C2	1:A:865:A:C2	2.94	0.56
1:A:1416:G:H2'	1:A:1417:G:O4'	2.05	0.56
4:D:201:GLN:HE21	5:E:100:VAL:HG23	1.69	0.56
5:E:91:LEU:HD11	5:E:110:LEU:HD11	1.88	0.56
5:E:148:VAL:HG22	5:E:152:ARG:HE	1.71	0.56
13:M:4:ILE:HA	13:M:57:ARG:HG3	1.87	0.56
1:A:880:C:H2'	1:A:881:G:C8	2.36	0.56
1:A:1256:A:H1'	1:A:1258:G:C4	2.40	0.56
23:Y:38:G:H1	24:Z:34:C:N4	2.02	0.56
1:A:29:G:N2	1:A:555:C:C2	2.74	0.56
1:A:814:A:H2'	1:A:816:A:H5''	1.87	0.56
1:A:1233:G:C6	1:A:1234:C:N4	2.73	0.56
1:A:259:G:C2	1:A:268:C:C2	2.93	0.56
1:A:401:C:H2'	1:A:402:G:H8	1.71	0.56
24:Z:49:G:C2	24:Z:66:C:C2	2.94	0.56
1:A:21:G:C2	1:A:22:G:C5	2.93	0.56
1:A:834:C:C2	1:A:853:G:C2	2.94	0.56
1:A:954:G:H21	1:A:1227:A:H62	1.53	0.56
1:A:1023:G:H2'	1:A:1023:G:N3	2.21	0.56
4:D:33:MET:CA	4:D:36:ARG:O	2.52	0.56
5:E:11:ILE:HG21	5:E:105:VAL:HG13	1.88	0.56
11:K:84:VAL:HG11	11:K:95:ILE:HD11	1.88	0.56
1:A:280:C:O2	17:Q:38:ARG:HG3	2.06	0.56
1:A:543:C:H2'	1:A:544:G:H8	1.70	0.56
2:B:61:LEU:HD11	2:B:68:ILE:HG13	1.87	0.56
7:G:146:GLU:HA	7:G:149:ARG:HG2	1.88	0.56
20:T:89:ARG:HH12	20:T:105:SER:H	1.54	0.56
1:A:68:G:C8	1:A:68:G:C5'	2.88	0.55
1:A:79:G:H2'	1:A:80:G:H8	1.68	0.55
1:A:913:A:H4'	1:A:914:A:O5'	2.06	0.55
1:A:1314:C:H2'	1:A:1315:U:C6	2.41	0.55
1:A:398:C:H2'	1:A:399:G:C8	2.31	0.55
1:A:397:A:H5''	1:A:398:C:OP1	2.06	0.55
1:A:671:G:C2	1:A:736:C:N3	2.74	0.55
1:A:891:U:H2'	1:A:892:A:H8	1.72	0.55
1:A:1438:G:N2	1:A:1439:C:C2	2.74	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:35:ARG:HH11	15:O:35:ARG:CG	2.11	0.55
22:X:33:GLU:O	22:X:37:LEU:HG	2.06	0.55
24:Z:35:A:H2'	24:Z:36:U:C6	2.41	0.55
1:A:301:G:H2'	1:A:302:G:H8	1.71	0.55
1:A:690:G:OP2	11:K:27:ASN:HB3	2.06	0.55
1:A:1050:G:C2	1:A:1209:C:O2	2.60	0.55
1:A:1310:G:N2	1:A:1328:C:C2	2.74	0.55
18:R:34:TYR:CD1	18:R:34:TYR:N	2.74	0.55
1:A:512:U:H2'	1:A:513:C:C6	2.42	0.55
1:A:725:G:N1	1:A:726:C:C4	2.75	0.55
1:A:917:G:H2'	1:A:918:A:H8	1.71	0.55
1:A:316:G:H2'	1:A:317:G:H8	1.71	0.55
1:A:774:G:C2	1:A:806:C:C2	2.94	0.55
1:A:991:U:C4	1:A:1212:U:H1'	2.42	0.55
1:A:1327:C:H5''	21:V:20:LYS:CB	2.36	0.55
2:B:102:LEU:HD21	2:B:162:ILE:HD11	1.88	0.55
22:X:45:LEU:HD12	22:X:59:ILE:HG12	1.88	0.55
1:A:279:A:H5''	1:A:280:C:H3'	1.89	0.55
1:A:878:G:H2'	1:A:879:C:C6	2.41	0.55
1:A:1317:C:H2'	1:A:1318:A:O4'	2.07	0.55
1:A:1484:C:H2'	1:A:1485:U:O4'	2.06	0.55
1:A:1533:C:OP1	1:A:1533:C:C4'	2.50	0.55
23:Y:34:A:H3'	23:Y:35:A:H8	1.72	0.55
1:A:385:C:H2'	1:A:386:C:O4'	2.07	0.55
1:A:482:A:C2	1:A:483:C:H1'	2.42	0.55
2:B:126:GLU:HA	2:B:129:GLU:HB3	1.88	0.55
13:M:39:ILE:HD13	13:M:56:LEU:HG	1.89	0.55
21:V:6:ARG:HB3	21:V:15:ARG:HH11	1.72	0.55
1:A:35:G:C6	1:A:36:C:N4	2.75	0.55
1:A:100:C:H2'	1:A:101:A:C8	2.42	0.55
1:A:786:G:C2	1:A:797:C:C2	2.94	0.55
1:A:1060:C:O2	1:A:1198:G:C2	2.60	0.55
11:K:34:ASP:HB2	11:K:35:PRO:CD	2.37	0.55
19:S:30:LEU:HD22	19:S:50:ALA:HB2	1.88	0.55
20:T:63:ILE:HG23	20:T:72:LEU:CD1	2.37	0.55
1:A:36:C:O2'	1:A:501:C:OP1	2.25	0.55
1:A:90:U:H2'	1:A:91:C:C6	2.42	0.55
1:A:542:G:C6	1:A:543:C:N4	2.74	0.55
20:T:56:MET:SD	20:T:103:GLY:HA3	2.47	0.55
1:A:46:G:O2'	1:A:365:U:H1'	2.07	0.54
1:A:403:C:H5''	4:D:136:PRO:HD2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:743:U:H2'	1:A:744:C:C6	2.42	0.54
1:A:1124:G:H1	1:A:1149:C:H42	1.54	0.54
1:A:1284:C:H2'	1:A:1285:A:C8	2.42	0.54
1:A:1459:C:OP1	20:T:28:ALA:HA	2.07	0.54
1:A:1534:A:H61	23:Y:31:U:H3	1.54	0.54
22:X:18:VAL:HG12	22:X:59:ILE:HD11	1.89	0.54
1:A:255:G:C2	1:A:272:C:C2	2.94	0.54
1:A:1237:C:H5''	1:A:1238:A:O4'	2.08	0.54
1:A:1369:C:H2'	1:A:1370:G:C8	2.43	0.54
4:D:157:LEU:HG	4:D:158:ILE:HD12	1.90	0.54
10:J:6:ILE:HD11	10:J:23:ILE:HG21	1.87	0.54
22:X:45:LEU:HG	22:X:57:ALA:HB1	1.89	0.54
1:A:381:C:H2'	1:A:382:A:O4'	2.07	0.54
1:A:1000:U:H2'	1:A:1001:A:O4'	2.07	0.54
18:R:73:ALA:HA	18:R:76:LEU:HD12	1.89	0.54
3:C:57:ILE:HA	3:C:65:ALA:O	2.08	0.54
4:D:163:GLU:HA	4:D:166:LYS:HD2	1.89	0.54
9:I:111:ARG:HD3	9:I:113:LYS:HG2	1.89	0.54
1:A:617:G:N1	1:A:618:C:C4	2.76	0.54
1:A:952:U:H2'	1:A:953:G:C8	2.43	0.54
1:A:977:A:H8	1:A:1223:C:N3	2.06	0.54
1:A:1106:G:N1	1:A:1107:C:C4	2.75	0.54
1:A:1287:A:H2'	1:A:1288:A:H8	1.73	0.54
1:A:1358:U:N3	1:A:1363(A):A:N6	1.95	0.54
3:C:150:LYS:HE2	3:C:152:ILE:HD11	1.90	0.54
5:E:14:ARG:O	5:E:14:ARG:HG2	2.07	0.54
19:S:17:GLU:HA	19:S:20:LEU:HG	1.89	0.54
1:A:61:G:H2'	1:A:62:U:O4'	2.07	0.54
1:A:942:G:H2'	1:A:942:G:N3	2.22	0.54
1:A:1484:C:H6	1:A:1484:C:O5'	1.90	0.54
1:A:1536:C:N4	23:Y:29:G:H1	2.05	0.54
15:O:87:ILE:HG22	15:O:88:ARG:H	1.72	0.54
1:A:70:G:C2	1:A:100:C:C2	2.95	0.54
1:A:88:A:H3'	1:A:89:C:C6	2.43	0.54
1:A:806:C:H2'	1:A:807:A:H8	1.73	0.54
1:A:1283:G:N2	1:A:1284:C:C2	2.76	0.54
7:G:88:PRO:HG3	7:G:148:ASN:O	2.08	0.54
8:H:89:PRO:HA	8:H:92:ARG:HD2	1.89	0.54
24:Z:16:C:H2'	24:Z:17:C:C6	2.42	0.54
1:A:333:G:N2	1:A:334:C:C2	2.75	0.54
1:A:680:C:H2'	1:A:681:C:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1410:G:H2'	1:A:1411:C:C6	2.43	0.54
2:B:20:GLU:HB3	2:B:23:ARG:HD2	1.88	0.54
8:H:10:LEU:HD13	8:H:83:ILE:HG12	1.90	0.54
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.48	0.54
22:X:137:LEU:HB3	22:X:163:MET:SD	2.48	0.54
1:A:444:C:H2'	1:A:445:G:H8	1.72	0.54
1:A:563:A:H2'	1:A:567:G:C8	2.43	0.54
1:A:945:G:H2'	1:A:945:G:N3	2.23	0.54
1:A:1323:G:H2'	1:A:1324:A:H8	1.72	0.54
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.89	0.54
1:A:132:C:N3	1:A:231:G:C2	2.76	0.54
1:A:874:G:N1	1:A:875:C:C4	2.75	0.54
2:B:77:ALA:HA	2:B:80:ILE:HD12	1.90	0.54
4:D:209:ARG:HB3	4:D:209:ARG:HH11	1.73	0.54
1:A:28:G:O2'	1:A:296:U:OP1	2.26	0.53
1:A:45:U:H2'	1:A:46:G:C8	2.43	0.53
1:A:67:C:H2'	1:A:68:G:H8	1.72	0.53
1:A:343:U:O3'	1:A:344:A:H8	1.92	0.53
1:A:521:G:N2	1:A:522:C:C2	2.77	0.53
1:A:1250:A:H4'	9:I:67:GLY:HA2	1.90	0.53
16:P:59:TRP:CE3	16:P:62:VAL:HG21	2.43	0.53
1:A:22:G:C6	1:A:23:C:C4	2.96	0.53
1:A:81:U:H2'	1:A:84:U:O4	2.07	0.53
1:A:525:C:H2'	1:A:526:C:C6	2.44	0.53
1:A:696:A:N3	1:A:786:G:O2'	2.39	0.53
1:A:931:C:O2	1:A:1387:G:C2	2.61	0.53
1:A:972:C:O2	1:A:972:C:H2'	2.07	0.53
1:A:877:C:H2'	1:A:878:G:C8	2.43	0.53
1:A:877:C:H2'	1:A:878:G:H8	1.74	0.53
1:A:1456:G:N2	1:A:1457:G:C5	2.77	0.53
4:D:10:ARG:HH11	4:D:10:ARG:HG3	1.73	0.53
10:J:8:LEU:HB2	10:J:70:ARG:CB	2.37	0.53
1:A:122:G:C2	1:A:123:C:C2	2.96	0.53
1:A:164:U:H2'	1:A:165:C:C6	2.43	0.53
1:A:1029:C:H2'	1:A:1030:C:C6	2.44	0.53
1:A:1475:G:H2'	1:A:1476:G:H8	1.73	0.53
15:O:85:LEU:HB2	15:O:87:ILE:HD11	1.90	0.53
1:A:129(A):G:H4'	1:A:130:A:O5'	2.08	0.53
1:A:200:G:C2	1:A:218:C:C2	2.96	0.53
1:A:358:U:H2'	1:A:359:U:O4'	2.09	0.53
1:A:455:C:H2'	1:A:456:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1217:C:H2'	1:A:1218:C:O4'	2.09	0.53
1:A:1511:G:H2'	1:A:1512:U:O4'	2.09	0.53
4:D:3:ARG:HA	4:D:3:ARG:NE	2.23	0.53
24:Z:51:C:H42	24:Z:63:G:H1	1.56	0.53
24:Z:64:G:C2	24:Z:65:C:C2	2.97	0.53
1:A:92:C:H2'	1:A:93:G:H8	1.73	0.53
1:A:1361:G:C5	1:A:1362:C:N3	2.77	0.53
1:A:1422:G:H1	1:A:1478:C:N4	2.07	0.53
1:A:1030(B):C:H2'	1:A:1030(C):G:O4'	2.09	0.53
1:A:1234:C:H2'	1:A:1235:U:C6	2.44	0.53
1:A:1235:U:H2'	1:A:1236:A:O4'	2.09	0.53
5:E:115:VAL:HG11	5:E:118:ILE:HG23	1.90	0.53
10:J:4:ILE:HB	10:J:74:ILE:HD12	1.90	0.53
11:K:13:GLN:HE21	11:K:75:TYR:HA	1.73	0.53
22:X:16:VAL:HG12	22:X:55:PRO:HB2	1.91	0.53
1:A:122:G:C6	1:A:123:C:C4	2.97	0.53
1:A:500:G:C6	1:A:501:C:N4	2.77	0.53
1:A:671:G:N2	1:A:736:C:C2	2.77	0.53
3:C:16:ARG:HB3	3:C:16:ARG:HH11	1.74	0.53
6:F:95:GLU:HB3	6:F:96:PRO:HD2	1.90	0.53
12:L:86:ARG:HG2	12:L:99:HIS:HB2	1.91	0.53
1:A:102:G:N2	1:A:103:C:C2	2.77	0.53
1:A:313:A:H2'	1:A:314:C:C6	2.44	0.53
1:A:392:G:H2'	1:A:393:A:H8	1.73	0.53
1:A:823:G:N2	1:A:824:C:C2	2.77	0.53
1:A:1015:A:H2'	1:A:1016:A:C8	2.44	0.53
10:J:27:ALA:HB2	10:J:85:LEU:HD11	1.89	0.53
16:P:13:HIS:C	16:P:15:PRO:HD3	2.34	0.53
1:A:72:C:N4	1:A:97:G:H1	2.06	0.53
1:A:502:G:H2'	1:A:503:C:O4'	2.09	0.53
1:A:810:C:H2'	1:A:811:C:O4'	2.09	0.53
1:A:872:A:C8	1:A:874:G:C8	2.97	0.53
1:A:974:A:H8	1:A:974:A:OP1	1.92	0.53
1:A:1030:C:H42	1:A:1031:G:H1	1.56	0.53
1:A:1105:A:H2'	1:A:1106:G:C8	2.44	0.53
1:A:1190:G:H5'	3:C:176:HIS:CE1	2.44	0.53
1:A:1363(A):A:H1'	1:A:1365:G:N7	2.23	0.53
17:Q:69:LYS:H	17:Q:70:ARG:HD2	1.73	0.53
1:A:1130:A:H2'	1:A:1131:G:C8	2.43	0.52
16:P:5:ARG:HH21	16:P:28:ARG:HA	1.73	0.52
1:A:173:U:H5'	1:A:197:A:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:A:H5''	20:T:76:ALA:HB2	1.90	0.52
1:A:1386:G:H2'	1:A:1387:G:H8	1.74	0.52
8:H:49:GLU:HG3	8:H:60:ARG:HB2	1.90	0.52
17:Q:92:ARG:O	17:Q:95:TYR:HB2	2.09	0.52
1:A:788:U:H2'	1:A:789:U:O4'	2.08	0.52
1:A:985:C:C2	1:A:1221:G:N2	2.78	0.52
1:A:1095:U:P	1:A:1108:G:H1	2.29	0.52
4:D:109:GLY:HA3	4:D:165:MET:HG3	1.89	0.52
17:Q:81:ARG:HH21	17:Q:84:LEU:HB2	1.75	0.52
1:A:998:G:N2	1:A:999:C:C2	2.77	0.52
1:A:1351:U:H2'	1:A:1352:C:H6	1.74	0.52
12:L:39:VAL:HG23	12:L:57:LYS:HB2	1.91	0.52
1:A:165:C:H2'	1:A:166:G:H8	1.74	0.52
1:A:258:G:N2	1:A:269:C:C2	2.77	0.52
1:A:872:A:C4	1:A:874:G:N7	2.78	0.52
3:C:157:ILE:HD12	3:C:164:ARG:HB3	1.91	0.52
1:A:145:G:N2	1:A:178:C:C2	2.78	0.52
1:A:1225:A:H4'	19:S:78:ARG:HD3	1.92	0.52
1:A:1405:G:H1	1:A:1496:C:H42	1.57	0.52
1:A:1434:A:H2'	1:A:1435:G:O4'	2.10	0.52
2:B:10:LEU:HG	2:B:48:MET:HG3	1.92	0.52
22:X:144:LEU:HD11	22:X:165:LEU:HD13	1.91	0.52
1:A:77:G:H3'	1:A:77:G:C8	2.44	0.52
1:A:291:C:H2'	1:A:292:G:H8	1.74	0.52
1:A:550:G:H2'	1:A:551:U:C6	2.45	0.52
1:A:777:A:H2'	1:A:778:G:H8	1.75	0.52
1:A:838:G:N2	1:A:849:C:C2	2.78	0.52
1:A:884:U:H4'	1:A:885:G:H5''	1.90	0.52
1:A:988:G:N1	1:A:989:C:C2	2.77	0.52
4:D:32:ALA:O	4:D:36:ARG:O	2.28	0.52
10:J:60:ARG:NH2	10:J:60:ARG:CB	2.73	0.52
14:N:59:ALA:HB1	14:N:61:TRP:HZ3	1.75	0.52
20:T:66:ALA:HB3	20:T:72:LEU:HD12	1.90	0.52
1:A:99:U:H2'	1:A:100:C:H6	1.75	0.52
1:A:560:U:H5''	1:A:561:U:H5'	1.92	0.52
1:A:1017:G:C2	1:A:1018:C:C2	2.97	0.52
2:B:33:TYR:HB2	2:B:42:ILE:C	2.35	0.52
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.92	0.52
4:D:121:VAL:O	4:D:134:ASP:HA	2.10	0.52
10:J:60:ARG:HB3	10:J:60:ARG:NH2	2.23	0.52
20:T:72:LEU:HB3	20:T:77:ALA:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:G:O2'	1:A:282:A:OP2	2.25	0.52
1:A:354:G:C6	1:A:355:C:N4	2.78	0.52
1:A:416:G:H2'	1:A:417:C:O4'	2.10	0.52
1:A:1478:C:H2'	1:A:1479:C:C6	2.44	0.52
24:Z:50:U:H2'	24:Z:51:C:C6	2.45	0.52
1:A:76:C:H2'	1:A:77:G:H5'	1.91	0.52
1:A:738:C:H5''	6:F:69:GLU:HB2	1.92	0.52
1:A:761:G:C2	1:A:762:C:C2	2.98	0.52
1:A:966:G:N3	24:Z:34:C:H5'	2.23	0.52
1:A:1129:C:O5'	1:A:1130:A:H5'	2.09	0.52
1:A:1233:G:N2	1:A:1234:C:C2	2.78	0.52
10:J:6:ILE:HD11	10:J:72:VAL:CG1	2.40	0.52
1:A:407:G:C2	1:A:436:C:C2	2.98	0.51
3:C:15:THR:HG21	3:C:178:LEU:O	2.10	0.51
6:F:45:LEU:HA	6:F:59:TYR:HA	1.92	0.51
24:Z:18:G:H21	24:Z:57:A:H2'	1.74	0.51
1:A:234:C:H2'	1:A:235:C:C6	2.45	0.51
1:A:376:G:H2'	1:A:377:G:C8	2.45	0.51
1:A:1144:G:C2	1:A:1145:C:N3	2.78	0.51
1:A:1222:G:N1	1:A:1223:C:C4	2.78	0.51
3:C:22:TRP:HB3	3:C:59:ARG:H	1.75	0.51
5:E:102:ALA:HB1	5:E:106:PRO:HB2	1.91	0.51
24:Z:49:G:N2	24:Z:66:C:C2	2.78	0.51
24:Z:52:G:H2'	24:Z:53:G:C8	2.46	0.51
1:A:399:G:C6	1:A:400:C:N4	2.79	0.51
1:A:883:C:H2'	1:A:884:U:C6	2.45	0.51
1:A:1114:C:C2	1:A:1187:G:N2	2.79	0.51
17:Q:21:VAL:HG21	17:Q:59:ILE:HD11	1.92	0.51
1:A:481:G:O2'	1:A:483:C:N4	2.42	0.51
1:A:536:C:H2'	1:A:537:G:C8	2.45	0.51
1:A:913:A:O2'	1:A:914:A:OP2	2.24	0.51
1:A:1074:G:C2	1:A:1075:C:C2	2.98	0.51
1:A:1082:G:H2'	1:A:1083:U:O4'	2.10	0.51
9:I:127:LYS:HE2	24:Z:34:C:OP2	2.10	0.51
14:N:24:CYS:HB2	14:N:40:CYS:HB3	1.91	0.51
20:T:84:LEU:HD23	20:T:85:MET:HG3	1.92	0.51
24:Z:70:G:H2'	24:Z:71:C:C6	2.45	0.51
1:A:198:G:H2'	1:A:199:G:H8	1.76	0.51
1:A:672:U:H3	1:A:734:G:H1	1.59	0.51
1:A:1070:U:H2'	1:A:1071:C:H6	1.75	0.51
2:B:72:GLY:HA3	2:B:81:VAL:HG21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:U:O2'	1:A:541:G:OP1	2.28	0.51
1:A:609:A:C4	1:A:610:G:C8	2.98	0.51
1:A:681:C:N3	1:A:710:G:C2	2.79	0.51
1:A:1520:G:H2'	1:A:1521:G:C8	2.46	0.51
3:C:94:LEU:HB3	3:C:95:THR:HG23	1.92	0.51
4:D:102:ASP:HB3	4:D:136:PRO:HB3	1.92	0.51
1:A:132:C:C2	1:A:231:G:N2	2.79	0.51
1:A:172:A:H2'	1:A:174:C:H5	1.76	0.51
1:A:1256:A:H4'	1:A:1258:G:O4'	2.11	0.51
1:A:1373:G:N7	9:I:11:LYS:NZ	2.59	0.51
5:E:40:ARG:HG2	5:E:40:ARG:NH1	2.23	0.51
6:F:45:LEU:HD12	6:F:59:TYR:HD2	1.75	0.51
11:K:21:ILE:HG12	11:K:30:VAL:HG22	1.92	0.51
17:Q:48:GLU:HB2	17:Q:50:LYS:HB2	1.92	0.51
1:A:725:G:C2	1:A:726:C:C4	2.98	0.51
1:A:1486:G:N3	1:A:1486:G:H2'	2.25	0.51
2:B:189:ASP:N	2:B:189:ASP:OD1	2.44	0.51
13:M:23:TYR:HB3	13:M:67:GLU:HA	1.93	0.51
1:A:1252:A:H2'	1:A:1253:G:O4'	2.10	0.51
1:A:1300:G:HO2'	1:A:1301:U:P	2.34	0.51
1:A:1441:G:O2'	1:A:1460:A:N6	2.43	0.51
17:Q:45:HIS:HA	17:Q:69:LYS:HE2	1.92	0.51
22:X:122:PHE:CE2	22:X:161:MET:HB2	2.46	0.51
1:A:69:G:H1	1:A:100:C:N4	2.09	0.51
1:A:236:G:C2	1:A:237:C:C2	2.99	0.51
1:A:1353:G:N1	1:A:1354:C:C4	2.79	0.51
4:D:25:ARG:C	4:D:27:TYR:H	2.17	0.51
1:A:568:G:C2	1:A:883:C:C2	2.99	0.50
1:A:616:G:H2'	1:A:617:G:H8	1.75	0.50
1:A:887:G:H3'	1:A:888:G:H8	1.74	0.50
1:A:1225:A:H2'	1:A:1225:A:N3	2.26	0.50
1:A:1431:C:C2	1:A:1470:G:N2	2.79	0.50
1:A:718:G:H5'	11:K:117:ASN:HB2	1.93	0.50
3:C:77:ILE:HD13	3:C:84:ILE:HD12	1.93	0.50
9:I:16:ARG:HH21	9:I:64:THR:HG21	1.76	0.50
10:J:83:GLU:HA	10:J:86:MET:HB2	1.93	0.50
22:X:126:GLU:HA	22:X:129:HIS:HB2	1.94	0.50
1:A:250:A:H4'	1:A:251:G:O5'	2.11	0.50
1:A:354:G:C2	1:A:355:C:C4	2.99	0.50
1:A:1038:C:C6	1:A:1039:C:H5	2.30	0.50
1:A:1064:G:H21	1:A:1190:G:H2'	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:C:H1'	1:A:1179:A:C5	2.47	0.50
1:A:1255:G:O2'	1:A:1258:G:N3	2.43	0.50
1:A:1412:C:H2'	1:A:1413:A:O4'	2.10	0.50
2:B:167:PRO:HG3	2:B:186:ALA:HB1	1.94	0.50
22:X:90:PHE:HD1	22:X:94:ILE:HD11	1.75	0.50
22:X:154:PRO:HD3	22:X:163:MET:HE3	1.92	0.50
1:A:316:G:H2'	1:A:317:G:C8	2.45	0.50
1:A:539:A:H2'	1:A:540:G:H8	1.73	0.50
1:A:597:G:H2'	1:A:598:U:H5'	1.94	0.50
1:A:910:C:H2'	1:A:911:U:O4'	2.12	0.50
1:A:1060:C:C2	1:A:1198:G:N1	2.80	0.50
1:A:1068:G:N2	1:A:1069:C:C2	2.80	0.50
1:A:1103:C:H2'	1:A:1104:G:O4'	2.11	0.50
1:A:1189:C:OP1	10:J:51:ARG:NH2	2.44	0.50
2:B:15:VAL:HG11	2:B:209:ARG:HG3	1.93	0.50
4:D:187:ARG:CZ	4:D:188:LEU:O	2.59	0.50
5:E:127:ASN:O	5:E:131:ILE:HB	2.10	0.50
7:G:16:LEU:HD11	9:I:42:ARG:HD2	1.94	0.50
13:M:3:ARG:HB3	13:M:7:VAL:HA	1.94	0.50
1:A:101:A:H2'	1:A:102:G:C8	2.41	0.50
1:A:137:C:H1'	16:P:63:GLY:HA3	1.94	0.50
1:A:407:G:C2	1:A:436:C:O2	2.65	0.50
1:A:965:A:O5'	1:A:965:A:C8	2.63	0.50
1:A:1134:G:N2	1:A:1141:C:C2	2.79	0.50
1:A:1198:G:H2'	1:A:1199:U:C6	2.47	0.50
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.93	0.50
5:E:139:LEU:HA	5:E:142:LEU:HD12	1.94	0.50
12:L:67:THR:HB	12:L:96:VAL:HG22	1.93	0.50
1:A:590:C:N3	1:A:650:G:C2	2.79	0.50
1:A:1074:G:C6	1:A:1075:C:N3	2.80	0.50
1:A:1417:G:H22	1:A:1482:G:H2'	1.76	0.50
1:A:1462:G:N2	1:A:1463:C:C2	2.80	0.50
24:Z:64:G:C5	24:Z:65:C:C4	3.00	0.50
1:A:57:G:C6	1:A:58:C:N3	2.80	0.50
1:A:500:G:H2'	1:A:501:C:C6	2.47	0.50
1:A:975:A:H5'	1:A:975:A:H8	1.76	0.50
1:A:1410:G:C6	1:A:1411:C:N4	2.80	0.50
3:C:131:ARG:NH1	5:E:52:PRO:HD2	2.27	0.50
4:D:60:GLU:HG2	4:D:202:LEU:HB2	1.93	0.50
1:A:56:U:H2'	1:A:57:G:C8	2.47	0.50
1:A:64:G:H4'	1:A:65:U:H5''	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:G:H2'	1:A:184:G:O4'	2.11	0.50
1:A:572:A:N1	1:A:864:A:C5	2.79	0.50
1:A:678:U:H2'	1:A:679:C:C6	2.47	0.50
1:A:947:G:H2'	1:A:948:C:O4'	2.11	0.50
1:A:1390:U:H2'	1:A:1391:U:C6	2.47	0.50
1:A:1408:A:OP1	22:X:123:ARG:HB3	2.12	0.50
8:H:85:ARG:C	8:H:85:ARG:HD3	2.37	0.50
1:A:680:C:H2'	1:A:681:C:H6	1.77	0.50
1:A:1251:A:H2'	1:A:1252:A:O4'	2.12	0.50
1:A:1365:G:C2	1:A:1366:C:C2	3.00	0.50
4:D:20:TYR:HA	4:D:26:CYS:HB3	1.94	0.50
4:D:58:LEU:HD23	4:D:206:PHE:CE2	2.47	0.50
16:P:27:LYS:C	16:P:29:ASP:H	2.20	0.50
19:S:30:LEU:HA	19:S:48:THR:O	2.12	0.50
22:X:150:VAL:HG23	22:X:165:LEU:HG	1.92	0.50
1:A:259:G:H2'	1:A:260:G:H8	1.76	0.49
1:A:260:G:H2'	1:A:261:U:C6	2.47	0.49
1:A:333:G:C6	1:A:334:C:N4	2.80	0.49
1:A:648:A:H2'	1:A:649:G:H8	1.77	0.49
1:A:1008:C:H2'	1:A:1009:G:O4'	2.12	0.49
1:A:1121:U:O5'	1:A:1121:U:H6	1.94	0.49
1:A:1485:U:H2'	1:A:1486:G:H8	1.77	0.49
3:C:106:VAL:HG11	3:C:112:SER:HB2	1.94	0.49
11:K:126:ARG:C	11:K:128:ALA:N	2.68	0.49
22:X:28:ILE:HG12	22:X:54:PRO:HG3	1.94	0.49
1:A:375:U:H4'	16:P:17:TYR:CE2	2.47	0.49
1:A:953:G:H2'	1:A:954:G:O4'	2.11	0.49
1:A:1241:G:N2	1:A:1242:C:C2	2.81	0.49
1:A:1368:G:OP1	10:J:62:HIS:NE2	2.43	0.49
1:A:1420:C:H2'	1:A:1421:G:H8	1.76	0.49
4:D:13:ARG:HA	4:D:33:MET:HE1	1.95	0.49
4:D:68:TYR:HD2	4:D:97:LEU:HD13	1.78	0.49
4:D:70:ILE:HD13	4:D:75:PHE:HD2	1.77	0.49
20:T:37:SER:O	20:T:41:ILE:HG13	2.12	0.49
22:X:118:VAL:HG12	22:X:137:LEU:HD22	1.94	0.49
1:A:370:C:C2	1:A:392:G:N2	2.80	0.49
1:A:412:A:H1'	4:D:35:ARG:HH12	1.74	0.49
1:A:499:A:N6	1:A:547:A:C8	2.80	0.49
1:A:734:G:H21	18:R:75:ILE:HD11	1.78	0.49
1:A:761:G:C6	1:A:762:C:C4	3.00	0.49
1:A:1001(A):G:N1	1:A:1002:G:C6	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:138:TYR:CD1	4:D:138:TYR:C	2.90	0.49
8:H:87:SER:HB2	8:H:133:LEU:O	2.11	0.49
24:Z:55:PSU:C6	24:Z:57:A:OP2	2.65	0.49
1:A:768:A:C4	1:A:769:G:C8	3.00	0.49
1:A:828:A:H4'	1:A:828:A:OP1	2.11	0.49
1:A:1073:U:OP2	5:E:57:LYS:HE2	2.11	0.49
2:B:83:MET:HG3	2:B:238:LEU:HD22	1.94	0.49
1:A:588:G:N1	1:A:589:C:C4	2.80	0.49
1:A:902:G:H2'	1:A:903:G:H8	1.78	0.49
1:A:947:G:C2	1:A:948:C:C2	3.00	0.49
1:A:1074:G:C6	1:A:1075:C:C4	3.00	0.49
1:A:1104:G:H4'	2:B:111:ARG:CZ	2.42	0.49
3:C:85:ARG:HH11	3:C:88:ARG:HB3	1.78	0.49
4:D:201:GLN:NE2	5:E:116:THR:OG1	2.46	0.49
1:A:354:G:N1	1:A:355:C:C4	2.81	0.49
1:A:439:A:C8	1:A:496:A:N1	2.79	0.49
1:A:876:G:C6	1:A:877:C:N4	2.81	0.49
1:A:1443:G:C2	1:A:1444:C:N3	2.81	0.49
2:B:15:VAL:HG21	2:B:209:ARG:CG	2.42	0.49
5:E:57:LYS:O	5:E:61:TYR:HD1	1.96	0.49
12:L:55:VAL:HG12	12:L:56:ALA:H	1.78	0.49
23:Y:28:A:H3'	23:Y:29:G:H8	1.76	0.49
1:A:945:G:C2	1:A:946:A:C8	3.01	0.49
1:A:1074:G:C5	1:A:1075:C:C4	3.01	0.49
1:A:1266:G:N2	1:A:1270:C:C2	2.81	0.49
4:D:138:TYR:C	4:D:138:TYR:HD1	2.21	0.49
1:A:18:C:H2'	1:A:19:C:O4'	2.13	0.49
1:A:22:G:C2	1:A:23:C:C2	3.00	0.49
1:A:77:G:C8	1:A:77:G:C3'	2.96	0.49
1:A:658:G:C6	1:A:749:C:N4	2.81	0.49
1:A:994:A:N7	1:A:1216:G:H4'	2.28	0.49
1:A:1508:G:C2	1:A:1509:C:C2	3.01	0.49
3:C:39:ILE:O	3:C:43:LEU:HG	2.13	0.49
4:D:58:LEU:HD23	4:D:206:PHE:HE2	1.77	0.49
7:G:65:ALA:O	7:G:69:VAL:HG23	2.13	0.49
10:J:19:SER:HA	10:J:22:LYS:HB2	1.95	0.49
1:A:19:C:H2'	1:A:20:U:H6	1.77	0.49
1:A:84:U:O5'	1:A:84:U:H6	1.95	0.49
1:A:688:G:C6	1:A:689:C:N4	2.81	0.49
1:A:1244:C:H2'	1:A:1245:A:C8	2.48	0.49
1:A:1365:G:C6	1:A:1366:C:C4	3.00	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1407:C:H5''	22:X:123:ARG:HG3	1.94	0.49
1:A:439:A:C8	1:A:496:A:C2	3.01	0.49
1:A:1191:A:H2'	1:A:1192:C:C6	2.48	0.49
2:B:111:ARG:HD3	2:B:145:LEU:HD21	1.94	0.49
7:G:98:SER:HA	7:G:101:LEU:HD12	1.95	0.49
22:X:45:LEU:CG	22:X:57:ALA:HB1	2.43	0.49
1:A:32:A:H2'	1:A:33:A:C8	2.47	0.48
1:A:189(D):C:H3'	1:A:189(E):U:C6	2.48	0.48
1:A:584:G:C4	1:A:585:G:C8	3.01	0.48
1:A:792:A:H4'	1:A:793:U:H5'	1.95	0.48
1:A:939:G:H2'	1:A:940:C:C6	2.48	0.48
1:A:1392:G:H21	1:A:1502:A:H8	1.59	0.48
1:A:189:G:C2	1:A:189(A):C:C2	3.01	0.48
1:A:192:U:H1'	20:T:103:GLY:HA2	1.95	0.48
1:A:942:G:C6	1:A:1342:C:N3	2.81	0.48
1:A:976:G:C8	1:A:1358:U:C2	3.01	0.48
1:A:1281:U:H4'	1:A:1282:C:OP2	2.13	0.48
13:M:39:ILE:HG13	13:M:55:ARG:HH21	1.78	0.48
1:A:243:A:H4'	1:A:244:U:O5'	2.13	0.48
1:A:444:C:H2'	1:A:445:G:C8	2.49	0.48
1:A:729:A:H2'	1:A:730:G:C8	2.45	0.48
1:A:1217:C:N4	1:A:1218:C:N4	2.61	0.48
1:A:1320:C:H2'	1:A:1321:C:O4'	2.13	0.48
1:A:1399:C:N3	1:A:1502:A:N6	2.61	0.48
18:R:37:VAL:HG22	18:R:79:LEU:HG	1.94	0.48
22:X:5:TYR:HB2	22:X:46:VAL:HG12	1.96	0.48
1:A:402:G:N2	1:A:403:C:C2	2.81	0.48
1:A:505:G:H1	1:A:526:C:H42	1.60	0.48
1:A:548:G:C6	1:A:549:C:N4	2.80	0.48
1:A:867:G:N2	1:A:868:C:C2	2.81	0.48
1:A:1123:A:H4'	10:J:37:PRO:HD2	1.95	0.48
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.95	0.48
10:J:4:ILE:HA	10:J:100:THR:HA	1.94	0.48
17:Q:57:VAL:HG12	17:Q:76:LEU:HA	1.94	0.48
19:S:62:ILE:HG13	19:S:66:MET:SD	2.53	0.48
1:A:15:G:H2'	1:A:16:A:C8	2.49	0.48
1:A:112:G:C2	1:A:113:G:C8	3.00	0.48
1:A:266:G:O2'	1:A:267:C:OP2	2.22	0.48
1:A:309:G:H2'	1:A:310:G:H8	1.78	0.48
1:A:542:G:N2	1:A:543:C:C2	2.82	0.48
1:A:546:G:OP2	4:D:72:GLU:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:881:G:C2	1:A:882:C:C2	3.02	0.48
1:A:1001(A):G:C6	1:A:1002:G:O6	2.66	0.48
1:A:1511:G:C6	1:A:1512:U:N3	2.81	0.48
2:B:44:LEU:HA	2:B:47:THR:HB	1.95	0.48
4:D:97:LEU:HD23	4:D:100:ARG:HD3	1.94	0.48
5:E:139:LEU:O	5:E:142:LEU:HB2	2.14	0.48
8:H:85:ARG:HH21	8:H:134:ILE:HG22	1.77	0.48
1:A:287:U:H2'	1:A:288:A:H8	1.77	0.48
1:A:453:A:H2'	1:A:454:C:C6	2.48	0.48
1:A:532:A:O2'	1:A:533:A:H5'	2.14	0.48
1:A:836:G:H1	1:A:850:U:H3	1.62	0.48
1:A:1086:U:O5'	1:A:1086:U:H6	1.96	0.48
1:A:1163:C:N3	1:A:1174:G:C2	2.82	0.48
1:A:1233:G:H2'	1:A:1234:C:C6	2.49	0.48
1:A:1306:A:H2'	1:A:1307:U:O4'	2.14	0.48
4:D:162:LEU:O	4:D:166:LYS:N	2.46	0.48
6:F:43:LEU:HB2	6:F:60:PHE:HB2	1.96	0.48
19:S:63:THR:HG22	19:S:64:GLU:H	1.79	0.48
1:A:170:U:H2'	1:A:171:A:C8	2.46	0.48
1:A:405:U:H5''	1:A:406:G:O4'	2.14	0.48
1:A:1081:G:P	5:E:16:THR:CG2	3.01	0.48
3:C:69:HIS:HA	3:C:104:GLN:O	2.14	0.48
22:X:115:LYS:HD3	22:X:164:LEU:HD11	1.96	0.48
1:A:549:C:H2'	1:A:550:G:H8	1.79	0.48
10:J:60:ARG:HH21	10:J:60:ARG:CB	2.25	0.48
11:K:83:ILE:HG12	11:K:109:VAL:HG12	1.96	0.48
18:R:34:TYR:H	18:R:34:TYR:HD1	1.58	0.48
1:A:105:G:C2	1:A:106:C:C2	3.01	0.48
1:A:256:U:H2'	1:A:257:G:C8	2.49	0.48
1:A:590:C:H2'	1:A:591:U:C6	2.48	0.48
1:A:648:A:H2'	1:A:649:G:C8	2.49	0.48
1:A:966:G:H8	1:A:966:G:OP1	1.96	0.48
1:A:1286:A:C8	1:A:1286:A:H3'	2.49	0.48
2:B:101:MET:HG3	2:B:108:ILE:HD13	1.95	0.48
1:A:362:G:H5''	12:L:61:THR:HB	1.96	0.48
1:A:1358:U:O4	1:A:1363(A):A:C2	2.59	0.48
3:C:148:GLY:HA3	3:C:172:ARG:O	2.14	0.48
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.95	0.48
6:F:78:GLU:HA	6:F:81:ILE:HD12	1.95	0.48
11:K:20:TYR:HE2	11:K:33:THR:HG21	1.78	0.48
18:R:53:ARG:HE	18:R:60:ALA:HA	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.95	0.48
1:A:15:G:H2'	1:A:16:A:H8	1.78	0.47
1:A:276:G:C2	1:A:277:C:C2	3.02	0.47
1:A:293:G:C4	1:A:305:G:N2	2.82	0.47
1:A:418:C:C2	1:A:426:G:C2	3.02	0.47
1:A:521:G:N1	1:A:522:C:C4	2.82	0.47
1:A:1147:C:H4'	9:I:5:TYR:CE2	2.49	0.47
1:A:1244:C:H2'	1:A:1245:A:H8	1.79	0.47
1:A:1492:A:C8	1:A:1492:A:C3'	2.97	0.47
4:D:206:PHE:CD1	4:D:206:PHE:C	2.92	0.47
5:E:152:ARG:HB2	8:H:43:GLY:HA3	1.96	0.47
12:L:89:ARG:HA	12:L:97:ARG:HA	1.96	0.47
1:A:177:C:H2'	1:A:178:C:C6	2.49	0.47
1:A:229:U:H2'	1:A:230:G:H8	1.79	0.47
1:A:328:C:H4'	1:A:329:A:O5'	2.15	0.47
1:A:365:U:O2	1:A:365:U:C2'	2.62	0.47
1:A:585:G:C2	1:A:586:C:C2	3.02	0.47
1:A:720:C:H2'	1:A:721:G:N7	2.29	0.47
1:A:1216:G:N1	1:A:1217:C:C4	2.82	0.47
1:A:1305:G:O2'	1:A:1306:A:C8	2.64	0.47
4:D:66:ARG:HH11	4:D:66:ARG:HB2	1.79	0.47
21:V:3:LYS:O	21:V:11:GLY:HA2	2.14	0.47
22:X:45:LEU:HD11	22:X:57:ALA:HB1	1.95	0.47
1:A:390:C:H2'	1:A:391:G:H8	1.79	0.47
1:A:399:G:N2	1:A:400:C:C2	2.83	0.47
1:A:680:C:C2	1:A:711:G:N2	2.82	0.47
1:A:778:G:C2	1:A:779:C:C2	3.03	0.47
1:A:1079:G:N2	1:A:1080:A:C2	2.82	0.47
1:A:1144:G:C6	1:A:1145:C:N4	2.82	0.47
1:A:1427:U:H2'	1:A:1428:A:C8	2.49	0.47
1:A:80:G:H3'	1:A:81:U:H5''	1.97	0.47
1:A:109:A:H2'	1:A:326:G:H21	1.78	0.47
1:A:128:G:C2	1:A:234:C:N3	2.81	0.47
1:A:178:C:H2'	1:A:179:A:H8	1.79	0.47
1:A:416:G:C6	1:A:417:C:C4	3.02	0.47
1:A:579:G:H5'	1:A:728:A:H1'	1.95	0.47
1:A:1112:C:O2	3:C:179:ARG:HB2	2.15	0.47
1:A:1266:G:C2	1:A:1270:C:N3	2.83	0.47
1:A:1287:A:H5'	1:A:1287:A:C8	2.47	0.47
1:A:1301:U:H1'	1:A:1302:U:OP1	2.15	0.47
1:A:1397:C:O2	1:A:1397:C:H2'	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:76:ALA:HB2	6:F:90:VAL:HG21	1.96	0.47
24:Z:43:A:H2'	24:Z:44:A:O4'	2.13	0.47
24:Z:64:G:C6	24:Z:65:C:C4	3.03	0.47
1:A:79:G:C2'	1:A:80:G:H8	2.28	0.47
1:A:312:C:H2'	1:A:313:A:H8	1.79	0.47
1:A:928:G:H1	1:A:1389:C:H42	1.62	0.47
1:A:1406:U:H2'	1:A:1407:C:H6	1.80	0.47
4:D:39:PRO:O	4:D:44:GLY:HA3	2.14	0.47
5:E:15:ARG:HD3	5:E:26:PHE:CD1	2.49	0.47
22:X:45:LEU:CD1	22:X:57:ALA:HB1	2.44	0.47
1:A:373:A:H3'	1:A:373:A:OP2	2.15	0.47
1:A:601:C:C2	1:A:638:G:N2	2.83	0.47
1:A:1039:C:H2'	1:A:1040:U:H6	1.76	0.47
1:A:1479:C:H2'	1:A:1480:G:H8	1.79	0.47
1:A:1505:G:H4'	1:A:1506:U:H5''	1.97	0.47
4:D:155:LEU:HB3	4:D:158:ILE:HD13	1.96	0.47
13:M:25:ILE:HG12	13:M:29:ARG:HB3	1.96	0.47
22:X:5:TYR:HD2	22:X:65:TRP:HH2	1.63	0.47
24:Z:36:U:C2	24:Z:37:A:C8	3.02	0.47
1:A:33:A:H2'	1:A:34:C:H6	1.76	0.47
1:A:43:C:H2'	1:A:44:G:C8	2.49	0.47
1:A:67:C:H42	1:A:102:G:H1	1.61	0.47
1:A:155:C:H42	1:A:166:G:H1	1.62	0.47
1:A:585:G:C6	1:A:586:C:C4	3.03	0.47
1:A:689:C:H2'	1:A:690:G:C8	2.50	0.47
1:A:768:A:C5	1:A:769:G:C8	3.03	0.47
1:A:784:C:C2	1:A:799:G:N2	2.83	0.47
1:A:815:A:O2'	1:A:1527:C:H1'	2.15	0.47
1:A:942:G:C2	1:A:1342:C:O2	2.68	0.47
1:A:998:G:N1	1:A:999:C:C4	2.83	0.47
1:A:1017:G:C6	1:A:1018:C:C4	3.02	0.47
1:A:1050:G:N2	1:A:1051:C:C2	2.83	0.47
1:A:1133:G:H1	1:A:1141:C:H42	1.63	0.47
1:A:1312:G:C2	1:A:1326:C:N3	2.82	0.47
1:A:1456:G:C3'	1:A:1457:G:O4'	2.63	0.47
2:B:87:ARG:HB3	2:B:219:VAL:HG11	1.96	0.47
2:B:188:ALA:HB3	2:B:200:ILE:HG23	1.96	0.47
7:G:143:ARG:O	7:G:147:ALA:N	2.43	0.47
17:Q:51:TYR:HE1	17:Q:76:LEU:HB2	1.80	0.47
22:X:17:ARG:HB2	22:X:54:PRO:O	2.14	0.47
23:Y:37:U:O2	23:Y:37:U:H2'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:10:G:N2	24:Z:26:G:H1'	2.30	0.47
1:A:113:G:H2'	1:A:114:U:C6	2.49	0.47
1:A:122:G:C6	1:A:123:C:N3	2.82	0.47
1:A:189:G:C6	1:A:189(A):C:C4	3.03	0.47
1:A:394:G:N2	1:A:395:C:C2	2.83	0.47
1:A:505:G:H2'	1:A:506:G:C8	2.49	0.47
1:A:636:U:H5'	17:Q:2:PRO:HG3	1.97	0.47
1:A:962:C:H2'	1:A:963:G:O4'	2.14	0.47
1:A:1532:U:O5'	1:A:1532:U:H6	1.98	0.47
3:C:45:LYS:HD3	3:C:45:LYS:HA	1.65	0.47
20:T:74:LYS:HA	20:T:74:LYS:HD2	1.52	0.47
22:X:11:ILE:HD11	22:X:45:LEU:O	2.14	0.47
1:A:68:G:C5'	1:A:68:G:H8	2.28	0.47
1:A:412:A:C1'	4:D:35:ARG:NH1	2.78	0.47
1:A:484:G:H4'	1:A:485:G:O5'	2.15	0.47
1:A:1223:C:P	19:S:78:ARG:HH22	2.37	0.47
1:A:1255:G:O2'	1:A:1258:G:H1'	2.15	0.47
22:X:103:LEU:HA	22:X:106:ILE:HD12	1.96	0.47
24:Z:16:C:H5'	24:Z:17:C:H2'	1.97	0.47
1:A:19:C:O2	1:A:917:G:C2	2.68	0.47
1:A:27:G:H2'	1:A:28:G:O4'	2.14	0.47
1:A:70:G:C2	1:A:100:C:O2	2.68	0.47
1:A:225:C:H2'	1:A:226:G:H8	1.80	0.47
1:A:391:G:H5''	16:P:8:ARG:NH1	2.30	0.47
1:A:778:G:C6	1:A:779:C:C4	3.03	0.47
1:A:807:A:H2'	1:A:808:C:C6	2.50	0.47
1:A:868:C:H2'	1:A:869:G:O4'	2.14	0.47
1:A:1116:C:C2	1:A:1185:G:C2	3.03	0.47
1:A:1128:C:H1'	1:A:1146:A:N6	2.28	0.47
1:A:1452:C:H4'	1:A:1456:G:O4'	2.15	0.47
1:A:1539:C:C2	23:Y:27:G:N2	2.83	0.47
22:X:106:ILE:O	22:X:110:LEU:HG	2.14	0.47
1:A:200:G:N2	1:A:218:C:C2	2.83	0.46
1:A:577:G:C2	1:A:578:C:C2	3.03	0.46
1:A:601:C:H42	1:A:637:G:H1	1.63	0.46
2:B:51:LEU:HD23	2:B:55:PHE:CZ	2.51	0.46
2:B:83:MET:SD	2:B:235:SER:HB2	2.54	0.46
9:I:5:TYR:CZ	9:I:7:THR:OG1	2.68	0.46
22:X:85:VAL:HG22	22:X:115:LYS:HD2	1.96	0.46
22:X:155:GLU:HB2	22:X:162:ASN:ND2	2.30	0.46
1:A:453:A:H4'	16:P:72:ARG:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1276:G:H2'	1:A:1277:C:O4'	2.15	0.46
6:F:9:VAL:HG12	6:F:86:ARG:HG3	1.97	0.46
9:I:13:ALA:HB2	9:I:68:GLY:HA3	1.98	0.46
20:T:55:ILE:HA	20:T:58:LYS:HD2	1.97	0.46
22:X:13:ALA:HB3	22:X:47:LEU:HD21	1.97	0.46
1:A:794:A:H2'	1:A:795:C:H6	1.78	0.46
1:A:857:C:H2'	1:A:858:G:C8	2.50	0.46
1:A:886:G:C2	1:A:912:C:O2	2.69	0.46
1:A:1070:U:OP1	5:E:20:GLN:HG3	2.15	0.46
1:A:1125:U:H5'	1:A:1126:U:C5	2.48	0.46
1:A:1456:G:C2	1:A:1457:G:C4	3.03	0.46
1:A:439:A:C6	1:A:441:A:H1'	2.50	0.46
1:A:931:C:C2	1:A:1387:G:C2	3.03	0.46
1:A:1325:C:H4'	21:V:17:THR:HG21	1.98	0.46
1:A:1384:C:H2'	1:A:1385:G:C8	2.50	0.46
1:A:1509:C:H2'	1:A:1510:U:O4'	2.16	0.46
1:A:390:C:H6	1:A:390:C:O5'	1.98	0.46
1:A:1356:G:N2	1:A:1357:A:C2	2.83	0.46
1:A:1447:A:OP2	1:A:1452:C:H5	1.99	0.46
3:C:154:SER:HA	3:C:165:THR:HA	1.96	0.46
4:D:25:ARG:C	4:D:27:TYR:N	2.71	0.46
9:I:10:ARG:HD3	9:I:105:ASP:HB3	1.96	0.46
22:X:18:VAL:HB	22:X:26:LEU:HB2	1.97	0.46
22:X:102:LYS:O	22:X:106:ILE:HG13	2.16	0.46
1:A:253:U:H2'	1:A:254:G:H8	1.79	0.46
1:A:473:G:H5''	16:P:81:ARG:NH2	2.30	0.46
1:A:568:G:N1	1:A:883:C:C4	2.84	0.46
1:A:617:G:N2	1:A:618:C:C2	2.83	0.46
1:A:734:G:C2	1:A:735:C:C2	3.03	0.46
1:A:790:A:H8	1:A:790:A:O5'	1.98	0.46
1:A:985:C:C2	1:A:1221:G:C2	3.04	0.46
1:A:1119:C:H2'	1:A:1120:G:H8	1.81	0.46
2:B:207:ALA:O	2:B:209:ARG:N	2.48	0.46
3:C:8:ILE:CG1	3:C:16:ARG:HH21	2.19	0.46
3:C:125:GLU:HA	3:C:191:THR:HG23	1.97	0.46
8:H:24:THR:HG22	8:H:61:VAL:HB	1.98	0.46
20:T:74:LYS:HE2	20:T:75:ASN:H	1.80	0.46
24:Z:54:5MU:N3	24:Z:58:A:C8	2.83	0.46
1:A:236:G:C6	1:A:237:C:C4	3.04	0.46
1:A:377:G:H2'	1:A:378:G:C8	2.50	0.46
1:A:524:G:N2	1:A:525:C:C2	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:553:A:H2'	1:A:554:C:H6	1.74	0.46
1:A:745:C:H2'	1:A:746:A:H8	1.78	0.46
1:A:1283:G:C6	1:A:1284:C:N4	2.84	0.46
3:C:56:ASP:HB2	3:C:67:THR:HB	1.97	0.46
9:I:89:ASN:HD21	9:I:91:ASP:HB2	1.79	0.46
12:L:60:LEU:HB3	12:L:62:SER:H	1.80	0.46
22:X:47:LEU:HD23	22:X:50:PRO:HB3	1.98	0.46
23:Y:32:A:H4'	23:Y:33:A:OP2	2.14	0.46
1:A:51:A:C6	1:A:353:A:C2	3.04	0.46
1:A:416:G:C2	1:A:417:C:C2	3.03	0.46
1:A:513:C:H2'	1:A:514:C:C6	2.51	0.46
1:A:658:G:C2	1:A:749:C:C4	3.03	0.46
1:A:1060:C:N3	1:A:1198:G:C6	2.84	0.46
1:A:1094:G:O2'	1:A:1095:U:P	2.74	0.46
1:A:1129:C:H4'	1:A:1130:A:H3'	1.97	0.46
6:F:72:VAL:O	6:F:75:LEU:HG	2.16	0.46
22:X:5:TYR:HD2	22:X:65:TRP:CH2	2.34	0.46
22:X:32:ARG:O	22:X:36:ARG:HG3	2.15	0.46
1:A:662:G:C6	1:A:744:C:N3	2.84	0.46
1:A:688:G:H2'	1:A:689:C:C6	2.50	0.46
1:A:825:G:C6	1:A:826:C:C4	3.04	0.46
1:A:1003:G:N2	1:A:1038:C:O2	2.48	0.46
11:K:16:SER:HB2	11:K:79:SER:HB3	1.97	0.46
13:M:86:CYS:SG	13:M:87:TYR:N	2.89	0.46
1:A:57:G:C5	1:A:58:C:C4	3.04	0.46
1:A:98:G:H2'	1:A:99:U:C6	2.51	0.46
1:A:308:C:H2'	1:A:309:G:C8	2.51	0.46
1:A:399:G:C2	1:A:400:C:C2	3.04	0.46
1:A:573:A:C5	1:A:574:A:C2	3.04	0.46
1:A:1245:A:H2'	1:A:1246:C:C6	2.50	0.46
1:A:1339:A:H1'	24:Z:41:C:H1'	1.97	0.46
1:A:1487:G:H2'	1:A:1488:G:C8	2.51	0.46
10:J:40:LEU:HB2	10:J:69:ASN:CB	2.45	0.46
1:A:8:A:C4	4:D:209:ARG:HD3	2.50	0.45
1:A:13:U:N3	1:A:915:A:N6	2.64	0.45
1:A:88:A:H8	1:A:88:A:O5'	1.99	0.45
1:A:109:A:C2'	1:A:326:G:N2	2.79	0.45
1:A:148:G:C2	1:A:175:C:C2	3.05	0.45
1:A:299:G:C6	1:A:300:A:C6	3.04	0.45
1:A:377:G:H2'	1:A:378:G:H8	1.80	0.45
1:A:473:G:OP1	16:P:81:ARG:NH1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:562:C:H41	1:A:884:U:H2'	1.81	0.45
1:A:957:U:H2'	1:A:959:A:OP2	2.16	0.45
1:A:1056:U:O2	1:A:1056:U:C2'	2.64	0.45
1:A:1257:U:H4'	1:A:1258:G:O5'	2.16	0.45
1:A:1305:G:H1'	1:A:1332:A:N6	2.31	0.45
1:A:1368:G:N1	1:A:1369:C:C4	2.84	0.45
3:C:156:ARG:HH21	3:C:161:GLU:HA	1.81	0.45
15:O:74:ASP:OD2	15:O:77:ARG:HB2	2.16	0.45
17:Q:74:LEU:HG	17:Q:75:ARG:HG2	1.96	0.45
24:Z:70:G:H2'	24:Z:71:C:O4'	2.16	0.45
1:A:182:U:OP2	1:A:183:G:C8	2.69	0.45
1:A:348:G:H2'	1:A:349:A:H8	1.80	0.45
1:A:500:G:N2	1:A:501:C:C2	2.85	0.45
1:A:502:G:C2	1:A:503:C:C2	3.04	0.45
1:A:568:G:C6	1:A:883:C:N4	2.85	0.45
1:A:1191:A:H2'	1:A:1192:C:H6	1.81	0.45
3:C:35:GLU:HB3	3:C:59:ARG:HH22	1.82	0.45
9:I:16:ARG:HB2	9:I:64:THR:HB	1.96	0.45
22:X:141:THR:HG22	22:X:165:LEU:HD21	1.99	0.45
1:A:14:U:N3	1:A:17:U:OP2	2.47	0.45
1:A:76:C:C2'	1:A:77:G:H5'	2.46	0.45
1:A:128:G:H4'	17:Q:3:LYS:HG3	1.98	0.45
1:A:416:G:C5	1:A:417:C:C4	3.04	0.45
1:A:429:U:H4'	1:A:430:A:O5'	2.16	0.45
1:A:500:G:C2	1:A:501:C:N3	2.84	0.45
1:A:682:G:H1	1:A:708:C:H42	1.64	0.45
1:A:841:U:H5'	1:A:848:C:O4'	2.17	0.45
1:A:1119:C:C2	1:A:1155:G:N2	2.84	0.45
1:A:1508:G:C6	1:A:1509:C:C4	3.04	0.45
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.98	0.45
6:F:39:LYS:H	6:F:39:LYS:HD2	1.80	0.45
10:J:38:ILE:CG1	10:J:71:LEU:HB3	2.46	0.45
17:Q:9:VAL:O	17:Q:21:VAL:HA	2.17	0.45
22:X:17:ARG:HE	22:X:56:VAL:HG22	1.82	0.45
24:Z:48:C:C4'	24:Z:49:G:H5''	2.44	0.45
24:Z:70:G:C6	24:Z:71:C:N4	2.84	0.45
1:A:9:G:H5'	5:E:122:GLU:CD	2.41	0.45
1:A:165:C:H2'	1:A:166:G:C8	2.50	0.45
1:A:318:G:N2	1:A:336:C:C2	2.85	0.45
1:A:419:C:N4	1:A:424:G:H1	2.13	0.45
1:A:505:G:C6	1:A:535:A:C2	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:760:G:O2'	17:Q:98:LEU:HB3	2.15	0.45
1:A:769:G:H2'	1:A:769:G:N3	2.29	0.45
1:A:916:G:H2'	1:A:917:G:H8	1.81	0.45
1:A:947:G:C6	1:A:948:C:C4	3.04	0.45
1:A:1220:G:H2'	1:A:1221:G:O4'	2.17	0.45
1:A:1327:C:H2'	1:A:1328:C:C6	2.51	0.45
1:A:1515:C:H2'	1:A:1516:G:C8	2.52	0.45
19:S:6:LYS:HD2	19:S:7:LYS:H	1.80	0.45
1:A:42:G:C6	1:A:43:C:C4	3.05	0.45
1:A:223:U:H5'	20:T:68:LYS:HZ1	1.82	0.45
1:A:893:C:H2'	1:A:894:G:O4'	2.17	0.45
1:A:986:A:C6	1:A:1220:G:N1	2.85	0.45
1:A:1070:U:H2'	1:A:1071:C:C6	2.51	0.45
1:A:1086:U:H3	1:A:1099:G:H22	1.62	0.45
1:A:1256:A:H62	1:A:1278:U:H1'	1.82	0.45
12:L:53:ARG:HG2	12:L:53:ARG:NH1	2.28	0.45
1:A:129(A):G:O2'	1:A:130:A:OP2	2.34	0.45
1:A:407:G:H5''	4:D:115:ARG:HD3	1.99	0.45
1:A:790:A:H2'	1:A:791:G:C8	2.52	0.45
1:A:1080:A:H5''	5:E:16:THR:HG21	1.98	0.45
1:A:1171:G:C2	1:A:1172:C:C2	3.05	0.45
1:A:1207:G:C2	1:A:1208:C:C2	3.05	0.45
1:A:1353:G:C2	1:A:1354:C:C4	3.05	0.45
2:B:28:PHE:CD2	2:B:190:THR:HA	2.52	0.45
2:B:189:ASP:HB3	2:B:205:ASP:H	1.81	0.45
4:D:64:LEU:HG	4:D:198:VAL:HG21	1.99	0.45
1:A:431:A:H2'	1:A:432:A:O4'	2.17	0.45
1:A:692:U:H2'	1:A:694:A:OP2	2.17	0.45
1:A:1466:C:H2'	1:A:1467:G:O4'	2.17	0.45
1:A:1489:G:C2	1:A:1490:C:C2	3.05	0.45
3:C:6:HIS:CD2	3:C:9:GLY:H	2.30	0.45
24:Z:11:A:H2'	24:Z:12:G:H8	1.82	0.45
1:A:161:A:H2'	1:A:162:A:O4'	2.17	0.45
1:A:623:C:H2'	1:A:624:C:O4'	2.17	0.45
1:A:643:C:H2'	1:A:644:G:C8	2.51	0.45
1:A:661:G:C2	1:A:745:C:N3	2.85	0.45
1:A:683:G:C2	1:A:708:C:N3	2.85	0.45
1:A:885:G:H1	1:A:912:C:H42	1.64	0.45
1:A:903:G:C2	1:A:904:C:C2	3.05	0.45
1:A:1216:G:H5''	14:N:5:ALA:CB	2.47	0.45
1:A:1282:C:O2	1:A:1282:C:H2'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:187:LEU:CD1	2:B:205:ASP:HA	2.47	0.45
9:I:4:TYR:HA	9:I:87:GLN:NE2	2.32	0.45
1:A:1081:G:P	5:E:16:THR:HG22	2.57	0.45
1:A:1207:G:C6	1:A:1208:C:C4	3.05	0.45
4:D:33:MET:C	4:D:36:ARG:O	2.60	0.45
5:E:71:LEU:HD11	5:E:115:VAL:HG22	1.99	0.45
10:J:38:ILE:HG12	10:J:71:LEU:CB	2.47	0.45
19:S:6:LYS:HB2	19:S:7:LYS:HE3	1.99	0.45
23:Y:23:C:H2'	23:Y:24:A:O4'	2.17	0.45
1:A:725:G:C6	1:A:726:C:N4	2.85	0.45
1:A:885:G:C2	1:A:913:A:C2	3.05	0.45
1:A:1012:U:H2'	1:A:1013:G:O4'	2.17	0.45
1:A:1050:G:C6	1:A:1051:C:N4	2.85	0.45
1:A:1486:G:C2	1:A:1487:G:O4'	2.70	0.45
17:Q:68:ARG:HG3	17:Q:68:ARG:O	2.17	0.45
17:Q:91:ARG:O	17:Q:94:ASN:HB2	2.17	0.45
23:Y:23:C:H2'	23:Y:24:A:C8	2.52	0.45
1:A:41:G:H2'	1:A:42:G:H8	1.82	0.44
1:A:284:G:H2'	1:A:285:G:C8	2.53	0.44
1:A:316:G:H1	1:A:337:C:H42	1.64	0.44
1:A:568:G:C6	1:A:569:C:N4	2.85	0.44
1:A:740:U:H2'	1:A:741:G:H8	1.82	0.44
1:A:928:G:H1	1:A:1389:C:N4	2.15	0.44
1:A:936:C:H2'	1:A:937:A:O4'	2.16	0.44
1:A:976:G:C5	1:A:1362:C:H5	2.35	0.44
1:A:1099:G:C2	1:A:1100:C:O2	2.71	0.44
1:A:1196:U:O2'	1:A:1197:G:OP2	2.24	0.44
1:A:1230:C:H5'	24:Z:30:G:H5''	1.99	0.44
1:A:1241:G:C2	1:A:1242:C:C2	3.04	0.44
1:A:1406:U:H2'	1:A:1407:C:C6	2.52	0.44
10:J:57:LYS:HG2	10:J:58:ASP:N	2.32	0.44
19:S:11:VAL:HA	19:S:38:SER:CB	2.45	0.44
24:Z:24:U:H2'	24:Z:25:C:H6	1.81	0.44
1:A:19:C:N3	1:A:917:G:C6	2.85	0.44
1:A:237:C:H5''	17:Q:25:ARG:CZ	2.47	0.44
1:A:373:A:C2	1:A:482:A:C6	3.04	0.44
1:A:769:G:H4'	1:A:1513:A:H4'	1.99	0.44
1:A:1038:C:C5	1:A:1039:C:H5	2.35	0.44
1:A:1348:U:C2	1:A:1349:A:C8	3.05	0.44
6:F:8:ILE:CD1	6:F:63:TYR:HD2	2.30	0.44
10:J:70:ARG:HD3	10:J:70:ARG:HA	1.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:33:THR:HA	11:K:39:PRO:HA	1.98	0.44
19:S:22:LEU:HA	19:S:25:LYS:HB2	1.99	0.44
22:X:88:ILE:HG21	22:X:106:ILE:HD11	1.99	0.44
1:A:113:G:H1'	1:A:354:G:H5'	1.99	0.44
12:L:6:THR:O	12:L:9:GLN:HB2	2.17	0.44
12:L:90:VAL:HG11	12:L:93:LEU:HD12	2.00	0.44
15:O:4:THR:HB	15:O:6:GLU:OE2	2.17	0.44
20:T:22:ARG:HA	20:T:25:ARG:HG2	2.00	0.44
23:Y:36:A:H2'	23:Y:37:U:O4'	2.17	0.44
1:A:42:G:N1	1:A:43:C:C2	2.86	0.44
1:A:91:C:C6	1:A:91:C:OP2	2.70	0.44
1:A:105:G:H2'	1:A:106:C:C6	2.51	0.44
1:A:413:G:N1	4:D:36:ARG:NH1	2.65	0.44
1:A:590:C:C2	1:A:650:G:C2	3.05	0.44
1:A:881:G:C6	1:A:882:C:C4	3.05	0.44
1:A:989:C:H2'	1:A:990:C:H6	1.82	0.44
1:A:1030:C:N4	1:A:1031:G:H1	2.15	0.44
1:A:1076:C:N3	1:A:1082:G:C2	2.85	0.44
1:A:1222:G:C2	1:A:1223:C:C2	3.06	0.44
4:D:201:GLN:HE22	5:E:116:THR:HA	1.83	0.44
7:G:115:ARG:HG2	7:G:116:ALA:H	1.82	0.44
11:K:65:ALA:HB1	11:K:98:LEU:HD12	1.99	0.44
20:T:43:LEU:HB3	20:T:52:ALA:CB	2.47	0.44
20:T:72:LEU:HD22	20:T:77:ALA:CA	2.48	0.44
22:X:89:LYS:HG2	22:X:119:THR:HB	1.98	0.44
24:Z:11:A:H2'	24:Z:12:G:C8	2.53	0.44
1:A:42:G:C2	1:A:43:C:C2	3.06	0.44
1:A:291:C:O2	1:A:310:G:C2	2.71	0.44
1:A:409:G:H3'	1:A:410:G:H8	1.83	0.44
1:A:430:A:P	4:D:8:VAL:H	2.40	0.44
1:A:734:G:C6	1:A:735:C:C4	3.06	0.44
1:A:774:G:N2	1:A:806:C:C2	2.86	0.44
1:A:841:U:H5''	1:A:841:U:C6	2.45	0.44
1:A:861:G:C2	1:A:862:C:C2	3.06	0.44
1:A:922:G:C2	1:A:923:A:C4	3.06	0.44
1:A:1028:C:H2'	1:A:1029:C:O4'	2.18	0.44
1:A:1187:G:C6	1:A:1188:A:C6	3.06	0.44
1:A:1462:G:N1	1:A:1463:C:C4	2.86	0.44
7:G:37:ASN:HD21	9:I:42:ARG:H	1.64	0.44
13:M:108:ARG:O	13:M:112:GLY:N	2.50	0.44
19:S:5:LEU:HD23	19:S:6:LYS:HE3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:31:G:H2'	24:Z:32:OMC:O4'	2.18	0.44
24:Z:49:G:C2	24:Z:66:C:N3	2.86	0.44
1:A:284:G:H2'	1:A:285:G:H8	1.83	0.44
1:A:344:A:H5''	1:A:345:C:H5	1.83	0.44
1:A:408:A:H2'	1:A:409:G:O4'	2.18	0.44
1:A:500:G:C2	1:A:501:C:C2	3.06	0.44
1:A:501:C:H2'	1:A:502:G:C8	2.52	0.44
1:A:548:G:C2	1:A:549:C:C2	3.06	0.44
1:A:577:G:N2	1:A:578:C:C2	2.85	0.44
1:A:608:A:C4	1:A:609:A:C8	3.06	0.44
1:A:763:G:C2	1:A:764:C:C2	3.05	0.44
1:A:1060:C:C2	1:A:1198:G:C2	3.06	0.44
1:A:1115:C:C2	1:A:1186:G:N2	2.86	0.44
1:A:1371:G:OP1	9:I:11:LYS:O	2.35	0.44
1:A:1418:A:H3'	1:A:1419:G:H8	1.83	0.44
1:A:1456:G:C2'	1:A:1457:G:O4'	2.64	0.44
4:D:173:TRP:CZ3	4:D:193:ASP:HB3	2.53	0.44
5:E:91:LEU:HD21	5:E:110:LEU:HD21	2.00	0.44
6:F:37:VAL:HG13	6:F:65:VAL:HG12	1.99	0.44
8:H:86:ILE:HD11	8:H:136:GLU:HB2	1.99	0.44
11:K:126:ARG:C	11:K:128:ALA:H	2.24	0.44
15:O:54:ARG:HG3	15:O:55:GLY:N	2.31	0.44
1:A:276:G:C6	1:A:277:C:C4	3.06	0.44
1:A:329:A:H4'	1:A:330:C:OP1	2.17	0.44
1:A:373:A:H3'	1:A:373:A:P	2.58	0.44
1:A:446:G:N2	1:A:489:C:C2	2.86	0.44
1:A:456:C:C2	1:A:476:G:C2	3.05	0.44
1:A:890:G:O2'	1:A:906:G:O6	2.28	0.44
1:A:1225:A:H5''	1:A:1226:C:OP2	2.17	0.44
4:D:186:LEU:HB2	4:D:187:ARG:H	1.57	0.44
22:X:135:ARG:O	22:X:139:ARG:HB2	2.18	0.44
1:A:301:G:C4	1:A:302:G:C8	3.06	0.44
1:A:715:A:H2'	1:A:716:A:C8	2.53	0.44
1:A:751:U:H4'	15:O:24:SER:HA	2.00	0.44
1:A:862:C:H2'	1:A:863:U:O4'	2.17	0.44
1:A:926:G:H3'	1:A:1505:G:H21	1.83	0.44
1:A:1064:G:N2	1:A:1190:G:H2'	2.33	0.44
1:A:1515:C:H2'	1:A:1516:G:H8	1.82	0.44
2:B:19:HIS:HB3	2:B:189:ASP:HB2	2.00	0.44
2:B:97:TRP:CH2	2:B:101:MET:HB2	2.53	0.44
3:C:35:GLU:HG2	3:C:95:THR:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:120:LEU:HD11	4:D:157:LEU:HD11	1.99	0.44
22:X:3:LYS:CB	22:X:66:ARG:HH22	2.21	0.44
24:Z:67:C:H2'	24:Z:68:C:C6	2.53	0.44
1:A:79:G:H3'	1:A:80:G:H8	1.83	0.44
1:A:324:G:H8	1:A:324:G:OP2	2.01	0.44
1:A:792:A:H4'	1:A:793:U:C5'	2.48	0.44
1:A:820:U:H4'	1:A:821:G:OP2	2.17	0.44
1:A:836:G:H2'	1:A:837:G:C8	2.53	0.44
1:A:865:A:C2	1:A:866:C:C2	3.06	0.44
1:A:923:A:O2'	1:A:1399:C:OP2	2.31	0.44
1:A:975:A:H4'	1:A:976:G:O5'	2.18	0.44
1:A:1200:C:H2'	1:A:1200:C:O2	2.17	0.44
3:C:113:ALA:N	3:C:114:PRO:CD	2.81	0.44
8:H:14:ARG:NH2	8:H:83:ILE:O	2.51	0.44
12:L:7:ILE:HG12	12:L:8:ASN:H	1.83	0.44
23:Y:31:U:H2'	23:Y:32:A:O4'	2.18	0.44
24:Z:56:C:H2'	24:Z:57:A:C8	2.53	0.44
1:A:262:A:H4'	20:T:75:ASN:OD1	2.18	0.43
1:A:504:C:C2	1:A:542:G:C2	3.06	0.43
1:A:544:G:H2'	1:A:545:C:O4'	2.17	0.43
1:A:616:G:H2'	1:A:617:G:C8	2.52	0.43
1:A:825:G:C2	1:A:826:C:C2	3.06	0.43
1:A:886:G:C4	1:A:887:G:C8	3.06	0.43
1:A:1022:G:H2'	1:A:1023:G:C8	2.53	0.43
1:A:1233:G:C2	1:A:1234:C:C2	3.06	0.43
6:F:3:ARG:HG3	6:F:93:SER:HB3	1.99	0.43
10:J:9:ARG:HG3	10:J:95:GLU:HB3	2.00	0.43
10:J:45:ARG:O	10:J:64:GLU:HA	2.18	0.43
12:L:117:ARG:HD2	12:L:122:THR:HB	2.00	0.43
19:S:30:LEU:HD21	19:S:59:PRO:HB3	1.99	0.43
22:X:5:TYR:CD2	22:X:48:VAL:HG12	2.53	0.43
22:X:90:PHE:HD1	22:X:94:ILE:CD1	2.30	0.43
24:Z:22:G:N2	24:Z:23:C:C2	2.86	0.43
1:A:80:G:H3'	1:A:81:U:C5'	2.48	0.43
1:A:374:A:C6	1:A:375:U:C4	3.05	0.43
1:A:383:A:C5	1:A:384:G:H1'	2.53	0.43
1:A:413:G:H1	4:D:36:ARG:NH1	2.16	0.43
1:A:643:C:H2'	1:A:644:G:H8	1.82	0.43
1:A:673:G:H2'	1:A:674:G:C8	2.52	0.43
1:A:1228:C:H6	1:A:1228:C:H5''	1.83	0.43
1:A:1498:U:H1'	1:A:1499:A:N7	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:73:THR:HG23	2:B:96:ARG:HA	2.00	0.43
2:B:132:LYS:O	2:B:136:VAL:HB	2.18	0.43
3:C:154:SER:HB3	3:C:165:THR:HG23	1.99	0.43
22:X:141:THR:HG21	22:X:163:MET:HE1	1.99	0.43
24:Z:70:G:C5	24:Z:71:C:C4	3.06	0.43
1:A:148:G:C2	1:A:149:A:C5	3.06	0.43
1:A:391:G:H2'	1:A:392:G:O4'	2.18	0.43
1:A:538:G:H5''	12:L:114:LYS:HB2	2.00	0.43
1:A:542:G:H2'	1:A:543:C:C6	2.53	0.43
1:A:670:G:H1	1:A:736:C:H42	1.65	0.43
1:A:923:A:H2'	1:A:924:C:O4'	2.19	0.43
1:A:941:G:H2'	1:A:942:G:O4'	2.17	0.43
1:A:974:A:H4'	1:A:975:A:H3'	2.00	0.43
1:A:987:G:H2'	1:A:988:G:C8	2.53	0.43
1:A:1418:A:H8	1:A:1482:G:H21	1.66	0.43
1:A:1501:C:N4	1:A:1504:G:C2	2.85	0.43
6:F:67:MET:HE3	6:F:68:PRO:HG2	2.00	0.43
16:P:26:ARG:HH21	16:P:31:LYS:HB3	1.83	0.43
20:T:63:ILE:HG23	20:T:77:ALA:HB1	2.00	0.43
22:X:147:LEU:O	22:X:167:PRO:HA	2.18	0.43
1:A:333:G:C2	1:A:334:C:C4	3.06	0.43
1:A:549:C:H2'	1:A:550:G:C8	2.54	0.43
1:A:577:G:C6	1:A:578:C:C4	3.06	0.43
1:A:766:A:C2	1:A:814:A:C2	3.07	0.43
1:A:941:G:N1	1:A:1343:G:C6	2.86	0.43
1:A:1231:G:C6	1:A:1232:U:C4	3.06	0.43
3:C:26:LYS:NZ	10:J:45:ARG:HE	2.16	0.43
6:F:43:LEU:HB3	6:F:46:ARG:HD2	2.00	0.43
16:P:59:TRP:HA	16:P:62:VAL:CG2	2.49	0.43
22:X:104:GLY:HA2	22:X:107:LYS:HD2	1.99	0.43
1:A:35:G:C6	1:A:550:G:N1	2.87	0.43
1:A:109:A:C2'	1:A:326:G:H21	2.32	0.43
1:A:171:A:H2'	1:A:172:A:C8	2.54	0.43
1:A:529:G:H5'	1:A:530:G:OP2	2.19	0.43
1:A:639:G:H2'	1:A:640:A:H8	1.83	0.43
1:A:761:G:C5	1:A:762:C:C4	3.07	0.43
1:A:900:A:H2'	1:A:901:A:C8	2.54	0.43
1:A:1061:G:P	10:J:59:SER:OG	2.76	0.43
1:A:1445:C:O2	1:A:1458:G:C2	2.71	0.43
1:A:1447:A:OP2	1:A:1452:C:C5	2.71	0.43
2:B:87:ARG:HH12	2:B:233:SER:H	1.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:76:ALA:O	6:F:80:ARG:HG3	2.19	0.43
1:A:147:G:C2	1:A:176:C:C2	3.07	0.43
1:A:189(K):U:H2'	1:A:189(L):G:C8	2.53	0.43
1:A:264:U:H2'	1:A:265:G:O4'	2.18	0.43
1:A:1233:G:C2	1:A:1234:C:C4	3.06	0.43
1:A:1262:C:H2'	1:A:1263:C:C6	2.53	0.43
1:A:1487:G:C2'	1:A:1488:G:C8	3.02	0.43
12:L:27:LEU:HG	12:L:28:LYS:N	2.34	0.43
17:Q:56:VAL:HG13	17:Q:77:VAL:HB	2.01	0.43
1:A:259:G:N2	1:A:268:C:C2	2.86	0.43
1:A:972:C:OP1	10:J:57:LYS:HD2	2.19	0.43
1:A:1076:C:H2'	1:A:1077:G:C8	2.53	0.43
1:A:1327:C:C5'	21:V:20:LYS:HB2	2.44	0.43
1:A:1438:G:N1	1:A:1439:C:C4	2.86	0.43
13:M:96:LEU:HD23	13:M:97:PRO:HD2	2.01	0.43
1:A:13:U:H3	1:A:915:A:N6	2.16	0.43
1:A:286:G:H2'	1:A:287:U:O4'	2.18	0.43
1:A:298:A:C6	1:A:299:G:C2	3.07	0.43
1:A:310:G:C6	1:A:311:C:C4	3.06	0.43
1:A:317:G:P	1:A:353:A:H61	2.41	0.43
1:A:551:U:H2'	1:A:552:U:C6	2.54	0.43
1:A:755:G:N1	1:A:756:C:C4	2.86	0.43
1:A:855:G:C6	1:A:856:C:C4	3.07	0.43
1:A:902:G:H2'	1:A:903:G:C8	2.54	0.43
1:A:972:C:P	10:J:57:LYS:HD2	2.59	0.43
1:A:977:A:C2'	1:A:978:A:H5''	2.42	0.43
1:A:977:A:H1'	1:A:982:U:O4	2.18	0.43
1:A:1126:U:O2	1:A:1126:U:C2'	2.66	0.43
1:A:1440:C:C2	1:A:1462:G:N2	2.87	0.43
2:B:193:ASP:HB3	2:B:196:LEU:HD12	2.00	0.43
3:C:152:ILE:HG12	3:C:167:TRP:HD1	1.84	0.43
8:H:91:ARG:CD	12:L:7:ILE:HG21	2.46	0.43
9:I:93:ARG:C	9:I:95:LYS:H	2.27	0.43
22:X:14:LYS:H	22:X:14:LYS:HG3	1.43	0.43
22:X:120:ILE:HG22	22:X:121:MET:N	2.33	0.43
1:A:59:A:H3'	1:A:331:G:H22	1.84	0.43
1:A:71:C:C4	1:A:72:C:C5	3.07	0.43
1:A:293:G:C6	1:A:294:U:C4	3.07	0.43
1:A:412:A:C1'	4:D:35:ARG:HH12	2.31	0.43
1:A:1134:G:H1	1:A:1140:C:N4	2.15	0.43
1:A:1135:U:O2'	1:A:1138:G:O6	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1315:U:H2'	1:A:1316:G:O4'	2.19	0.43
1:A:1526:G:C6	1:A:1527:C:N4	2.87	0.43
10:J:27:ALA:CB	10:J:34:VAL:HG21	2.48	0.43
12:L:46:LYS:HB3	12:L:48:PRO:HD2	1.99	0.43
19:S:53:ASN:HD22	19:S:53:ASN:HA	1.60	0.43
1:A:119:A:H2'	1:A:240:C:H41	1.84	0.43
1:A:246:A:N3	1:A:247:G:H1'	2.33	0.43
1:A:289:G:N1	1:A:290:C:C4	2.87	0.43
1:A:707:C:H4'	11:K:20:TYR:CG	2.54	0.43
1:A:1176:A:H2'	1:A:1177:G:C8	2.53	0.43
1:A:1492:A:N7	12:L:47:LYS:HA	2.34	0.43
3:C:6:HIS:NE2	3:C:8:ILE:HB	2.34	0.43
4:D:120:LEU:O	4:D:125:HIS:HB2	2.19	0.43
8:H:64:LYS:HB3	8:H:79:VAL:HG11	2.01	0.43
9:I:2:GLU:HG2	9:I:20:ARG:HG2	2.00	0.43
10:J:6:ILE:CG1	10:J:72:VAL:CB	2.86	0.43
10:J:50:ILE:HD13	14:N:41:ARG:HH11	1.84	0.43
12:L:5:PRO:HB2	12:L:6:THR:H	1.65	0.43
15:O:6:GLU:H	15:O:6:GLU:CD	2.26	0.43
22:X:11:ILE:HD13	22:X:45:LEU:HD23	2.00	0.43
22:X:54:PRO:HA	22:X:55:PRO:HD2	1.89	0.43
22:X:118:VAL:HG12	22:X:137:LEU:CD2	2.49	0.43
1:A:63:C:H42	1:A:104:G:H1	1.66	0.42
1:A:235:C:H2'	1:A:236:G:H8	1.84	0.42
1:A:390:C:H2'	1:A:391:G:C8	2.54	0.42
1:A:1347:G:H8	9:I:107:ARG:HB3	1.79	0.42
1:A:1358:U:H2'	1:A:1359:C:O4'	2.19	0.42
2:B:25:ASN:HA	2:B:26:PRO:HD3	1.75	0.42
2:B:93:VAL:HG11	2:B:97:TRP:CD1	2.45	0.42
10:J:62:HIS:HB2	14:N:59:ALA:CB	2.46	0.42
24:Z:51:C:N4	24:Z:63:G:H1	2.17	0.42
1:A:58:C:O5'	1:A:58:C:H6	2.02	0.42
1:A:105:G:C6	1:A:106:C:C4	3.06	0.42
1:A:109:A:H5'	1:A:110:C:H5	1.83	0.42
1:A:189(C):C:C2	1:A:189(I):G:N2	2.87	0.42
1:A:299:G:H2'	1:A:300:A:H8	1.82	0.42
1:A:319:G:C2	1:A:320:C:C2	3.07	0.42
1:A:542:G:C2	1:A:543:C:C2	3.07	0.42
1:A:824:C:N4	1:A:876:G:H1	2.16	0.42
1:A:916:G:H2'	1:A:917:G:C8	2.54	0.42
1:A:951:G:C6	1:A:1231:G:C6	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1499:A:C4	1:A:1500:A:C8	3.07	0.42
15:O:26:GLU:HB3	15:O:81:LEU:HD21	2.01	0.42
1:A:244:U:H4'	1:A:245:C:H5''	2.01	0.42
1:A:809:G:N1	1:A:810:C:C2	2.87	0.42
1:A:931:C:C2	1:A:1387:G:N1	2.87	0.42
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.34	0.42
1:A:1220:G:H2'	1:A:1221:G:C8	2.55	0.42
1:A:1353:G:P	21:V:3:LYS:HZ1	2.42	0.42
1:A:1363:C:H5'	1:A:1363(A):A:O5'	2.19	0.42
4:D:100:ARG:HH22	4:D:118:ARG:HH22	1.65	0.42
5:E:41:VAL:HG13	5:E:113:ALA:HA	2.02	0.42
5:E:105:VAL:HB	5:E:106:PRO:CD	2.46	0.42
7:G:81:GLY:N	23:Y:32:A:OP1	2.52	0.42
12:L:24:VAL:HG13	12:L:98:TYR:HE1	1.84	0.42
1:A:39:G:C6	1:A:40:C:C4	3.08	0.42
1:A:108:G:H5'	1:A:109:A:H5''	2.02	0.42
1:A:234:C:H2'	1:A:235:C:H6	1.85	0.42
1:A:504:C:N3	1:A:542:G:C2	2.87	0.42
1:A:514:C:H42	1:A:537:G:H1	1.66	0.42
1:A:573:A:C6	1:A:574:A:N1	2.87	0.42
1:A:598:U:H4'	8:H:94:TYR:CG	2.55	0.42
1:A:1050:G:N1	1:A:1051:C:C4	2.88	0.42
1:A:1106:G:C2	1:A:1107:C:C4	3.08	0.42
1:A:1206:G:H2'	1:A:1207:G:C8	2.55	0.42
24:Z:18:G:N2	24:Z:57:A:H2'	2.35	0.42
24:Z:40:C:H2'	24:Z:41:C:C6	2.54	0.42
1:A:67:C:OP1	1:A:199:G:H4'	2.20	0.42
1:A:903:G:C6	1:A:904:C:C4	3.08	0.42
1:A:967:C:C4	1:A:968:A:C6	3.07	0.42
1:A:1218:C:H2'	1:A:1219:U:C5	2.53	0.42
1:A:1356:G:C2	1:A:1367:C:C2	3.07	0.42
1:A:1540:U:H3	23:Y:25:A:H61	1.66	0.42
10:J:49:VAL:CG2	10:J:61:GLU:O	2.64	0.42
24:Z:18:G:H1'	24:Z:57:A:C2	2.55	0.42
24:Z:34:C:H2'	24:Z:35:A:C8	2.54	0.42
1:A:21:G:C2	1:A:22:G:C6	3.07	0.42
1:A:366:C:H1'	1:A:394:G:H22	1.85	0.42
1:A:932:C:C2	1:A:1386:G:C2	3.08	0.42
1:A:1171:G:H2'	1:A:1172:C:C6	2.55	0.42
2:B:186:ALA:CB	2:B:197:VAL:HG11	2.49	0.42
12:L:110:VAL:HG23	12:L:120:TYR:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:1:MET:HE3	16:P:3:LYS:HE2	2.02	0.42
20:T:63:ILE:HA	20:T:72:LEU:HD12	2.01	0.42
24:Z:53:G:N2	24:Z:62:C:C2	2.87	0.42
1:A:301:G:H2'	1:A:302:G:C8	2.52	0.42
1:A:1081:G:H2'	1:A:1082:G:O4'	2.19	0.42
1:A:1228:C:H5'	13:M:108:ARG:NH2	2.27	0.42
1:A:1281:U:H3'	1:A:1282:C:C5	2.54	0.42
4:D:53:ASP:O	4:D:57:ARG:HD2	2.19	0.42
12:L:87:GLY:HA2	12:L:98:TYR:HA	2.02	0.42
13:M:22:ILE:HB	13:M:25:ILE:HB	2.02	0.42
16:P:59:TRP:O	16:P:62:VAL:HG22	2.13	0.42
19:S:50:ALA:HA	19:S:58:VAL:O	2.19	0.42
1:A:284:G:C2	1:A:285:G:C5	3.07	0.42
1:A:333:G:C2	1:A:334:C:C2	3.08	0.42
1:A:333:G:N1	1:A:334:C:C4	2.88	0.42
1:A:763:G:C6	1:A:764:C:C4	3.08	0.42
1:A:786:G:N2	1:A:797:C:C2	2.87	0.42
1:A:814:A:C8	1:A:816:A:C8	3.07	0.42
1:A:939:G:H5''	7:G:102:ARG:CZ	2.49	0.42
1:A:956:U:H2'	1:A:957:U:O4'	2.19	0.42
1:A:1082:G:C2	1:A:1083:U:C2	3.08	0.42
1:A:1284:C:H2'	1:A:1285:A:N7	2.35	0.42
5:E:59:GLY:O	5:E:63:ARG:HD3	2.19	0.42
6:F:8:ILE:HD13	6:F:63:TYR:HD2	1.84	0.42
9:I:26:VAL:HB	9:I:33:PHE:CB	2.36	0.42
10:J:83:GLU:CA	10:J:86:MET:HB2	2.50	0.42
1:A:57:G:C6	1:A:58:C:C4	3.08	0.42
1:A:70:G:N1	1:A:100:C:N3	2.68	0.42
1:A:310:G:C2	1:A:311:C:C2	3.08	0.42
1:A:457:C:H2'	1:A:458:C:H6	1.85	0.42
1:A:501:C:H2'	1:A:502:G:H8	1.84	0.42
1:A:583:A:H2'	1:A:584:G:O4'	2.19	0.42
1:A:614:A:H2'	1:A:615:C:C6	2.55	0.42
1:A:620:C:N3	4:D:135:LEU:HD22	2.35	0.42
1:A:1081:G:C4	1:A:1082:G:C8	3.07	0.42
1:A:1419:G:C6	1:A:1420:C:C4	3.08	0.42
1:A:1423:G:C6	1:A:1424:C:C4	3.08	0.42
8:H:100:ILE:H	8:H:100:ILE:HG13	1.60	0.42
1:A:34:C:H1'	12:L:32:PHE:CZ	2.55	0.42
1:A:424:G:H2'	1:A:425:G:C8	2.55	0.42
1:A:502:G:C6	1:A:503:C:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:G:H2'	1:A:506:G:H8	1.84	0.42
1:A:559:A:H4'	1:A:560:U:C5'	2.44	0.42
1:A:823:G:C2	1:A:824:C:C2	3.07	0.42
1:A:1243:C:H2'	1:A:1244:C:O4'	2.20	0.42
1:A:1306:A:C2	1:A:1307:U:H1'	2.55	0.42
1:A:1494:G:C6	1:A:1495:U:C4	3.08	0.42
6:F:6:VAL:HB	6:F:63:TYR:HB2	2.02	0.42
20:T:50:GLU:HG2	20:T:100:ILE:HB	2.02	0.42
21:V:10:ARG:HA	21:V:13:ILE:HD12	2.02	0.42
22:X:44:ASP:O	22:X:60:MET:O	2.37	0.42
22:X:45:LEU:HA	22:X:59:ILE:HA	2.01	0.42
22:X:70:GLN:O	22:X:74:LYS:HD2	2.19	0.42
1:A:129(A):G:N3	1:A:189(F):U:H5''	2.35	0.41
1:A:216:G:C2	1:A:217:C:C2	3.08	0.41
1:A:399:G:C6	1:A:400:C:C4	3.08	0.41
1:A:402:G:C6	1:A:403:C:N4	2.88	0.41
1:A:412:A:N9	4:D:35:ARG:NH1	2.65	0.41
1:A:774:G:C2	1:A:806:C:N3	2.88	0.41
1:A:823:G:N1	1:A:824:C:C4	2.88	0.41
1:A:1050:G:N1	1:A:1209:C:C2	2.88	0.41
1:A:1162:C:C2	1:A:1175:G:C2	3.08	0.41
1:A:1353:G:C6	1:A:1354:C:N4	2.88	0.41
1:A:1514:C:H2'	1:A:1515:C:C6	2.55	0.41
2:B:80:ILE:HD11	2:B:208:ILE:HG22	2.02	0.41
7:G:152:ALA:HB1	7:G:155:ARG:HH21	1.85	0.41
10:J:38:ILE:HG12	10:J:71:LEU:HB3	2.01	0.41
18:R:54:ARG:NH1	18:R:54:ARG:HB2	2.34	0.41
20:T:15:ARG:CG	20:T:15:ARG:NH1	2.80	0.41
1:A:57:G:C2	1:A:58:C:C2	3.08	0.41
1:A:456:C:H2'	1:A:457:C:C6	2.55	0.41
1:A:524:G:N2	1:A:525:C:N3	2.67	0.41
1:A:563:A:O2'	1:A:566:G:O2'	2.27	0.41
1:A:922:G:H2'	1:A:923:A:H8	1.83	0.41
1:A:929:G:C6	1:A:930:C:C4	3.08	0.41
1:A:1276:G:C2	1:A:1277:C:C2	3.09	0.41
1:A:1489:G:C6	1:A:1490:C:C4	3.08	0.41
6:F:8:ILE:HD13	6:F:63:TYR:CD2	2.55	0.41
15:O:17:ARG:HE	15:O:77:ARG:CD	2.31	0.41
16:P:27:LYS:C	16:P:29:ASP:N	2.78	0.41
22:X:106:ILE:HA	22:X:116:VAL:HG21	2.01	0.41
1:A:102:G:N1	1:A:103:C:C4	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:G:O3'	4:D:14:ARG:NH2	2.52	0.41
1:A:548:G:N2	1:A:549:C:C2	2.87	0.41
1:A:673:G:H1	1:A:717:C:H42	1.68	0.41
1:A:911:U:OP2	12:L:97:ARG:NH2	2.52	0.41
1:A:985:C:H2'	1:A:986:A:C8	2.55	0.41
1:A:1346:A:C8	1:A:1348:U:C2	3.08	0.41
19:S:39:THR:HA	19:S:70:LYS:HA	2.01	0.41
20:T:72:LEU:HD13	20:T:77:ALA:CB	2.50	0.41
1:A:229:U:H2'	1:A:230:G:C8	2.55	0.41
1:A:256:U:H2'	1:A:257:G:H8	1.85	0.41
1:A:297:G:O2'	1:A:299:G:N7	2.50	0.41
1:A:319:G:C6	1:A:320:C:C4	3.08	0.41
1:A:500:G:C2	1:A:501:C:C4	3.09	0.41
1:A:601:C:C2	1:A:638:G:C2	3.09	0.41
1:A:621:A:H2'	1:A:622:A:C8	2.56	0.41
1:A:867:G:C2	1:A:868:C:C2	3.08	0.41
1:A:929:G:C2	1:A:930:C:C2	3.09	0.41
2:B:163:PHE:HA	2:B:185:ILE:HB	2.01	0.41
4:D:62:GLN:HB3	4:D:66:ARG:NH1	2.35	0.41
4:D:105:VAL:HG13	4:D:110:PHE:HB2	2.02	0.41
10:J:34:VAL:H	10:J:75:ILE:HB	1.85	0.41
22:X:150:VAL:HG21	22:X:163:MET:HE2	2.01	0.41
1:A:39:G:C2	1:A:40:C:C2	3.08	0.41
1:A:109:A:C6	1:A:326:G:C6	3.08	0.41
1:A:391:G:H4'	16:P:8:ARG:HH22	1.86	0.41
1:A:584:G:C5	1:A:585:G:N7	2.88	0.41
1:A:689:C:H2'	1:A:690:G:O4'	2.21	0.41
1:A:1076:C:H2'	1:A:1077:G:H8	1.86	0.41
1:A:1202:G:H2'	1:A:1203:C:O4'	2.21	0.41
1:A:1485:U:H2'	1:A:1486:G:C8	2.55	0.41
1:A:1526:G:C2	1:A:1527:C:C2	3.08	0.41
2:B:48:MET:HA	2:B:51:LEU:HD12	2.02	0.41
2:B:142:LEU:O	2:B:146:GLN:HB2	2.21	0.41
3:C:150:LYS:HB3	3:C:201:TYR:HB2	2.02	0.41
13:M:78:ILE:O	13:M:82:MET:N	2.49	0.41
1:A:342:C:H42	1:A:347:G:H1	1.69	0.41
1:A:725:G:C2	1:A:726:C:C2	3.09	0.41
1:A:1132:C:H2'	1:A:1133:G:C8	2.55	0.41
1:A:1162:C:C2	1:A:1175:G:N2	2.89	0.41
1:A:1186:G:H4'	9:I:110:GLU:HG3	2.02	0.41
2:B:55:PHE:HD1	2:B:58:ILE:HD12	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:6:HIS:HA	3:C:7:PRO:HD3	1.74	0.41
3:C:123:GLN:HE22	3:C:140:ARG:HH22	1.67	0.41
22:X:22:ASP:HB2	22:X:24:LYS:HG3	2.02	0.41
1:A:99:U:C2	1:A:100:C:C5	3.08	0.41
1:A:109:A:C4	1:A:326:G:C2	3.08	0.41
1:A:125:U:H2'	1:A:126:G:C8	2.55	0.41
1:A:363:A:C6	12:L:31:PRO:HD2	2.55	0.41
1:A:556:C:H2'	1:A:557:G:O4'	2.20	0.41
1:A:918:A:H2'	1:A:919:A:C8	2.56	0.41
1:A:922:G:C2'	1:A:923:A:C8	2.99	0.41
1:A:939:G:C2	1:A:940:C:C2	3.08	0.41
1:A:1030(A):G:N2	1:A:1030(D):A:C8	2.88	0.41
1:A:1233:G:C2	1:A:1234:C:N3	2.89	0.41
1:A:1286:A:H3'	1:A:1286:A:H8	1.85	0.41
4:D:9:CYS:SG	4:D:26:CYS:SG	3.18	0.41
5:E:93:PRO:HG3	8:H:105:ARG:HD3	2.03	0.41
7:G:57:GLU:HA	7:G:58:PRO:HD2	1.90	0.41
9:I:4:TYR:CZ	9:I:88:TYR:HD1	2.39	0.41
14:N:3:ARG:C	14:N:5:ALA:H	2.29	0.41
18:R:44:LEU:HD23	18:R:48:GLY:HA2	2.03	0.41
22:X:92:VAL:HG11	22:X:129:HIS:CD2	2.55	0.41
1:A:542:G:N1	1:A:543:C:C4	2.88	0.41
1:A:567:G:H2'	1:A:568:G:O4'	2.21	0.41
1:A:687:A:H4'	1:A:688:G:O5'	2.20	0.41
1:A:832:C:O2	1:A:855:G:C2	2.74	0.41
1:A:1101:A:H4'	1:A:1102:A:O5'	2.20	0.41
4:D:138:TYR:HD1	4:D:139:ARG:N	2.19	0.41
10:J:79:ARG:O	10:J:83:GLU:HB2	2.21	0.41
10:J:84:GLN:HE21	10:J:84:GLN:HB2	1.64	0.41
10:J:92:THR:H	10:J:94:VAL:HG23	1.86	0.41
13:M:22:ILE:HG22	13:M:24:GLY:N	2.26	0.41
17:Q:29:HIS:HD2	17:Q:36:ILE:HD11	1.86	0.41
24:Z:71:C:C2'	24:Z:72:A:H8	2.13	0.41
1:A:70:G:N1	1:A:100:C:C2	2.89	0.41
1:A:103:C:H2'	1:A:104:G:H8	1.86	0.41
1:A:402:G:C2	1:A:403:C:C2	3.09	0.41
1:A:524:G:N1	1:A:525:C:N4	2.69	0.41
1:A:532:A:H62	3:C:193:TYR:HB3	1.86	0.41
1:A:746:A:H2'	1:A:747:C:H6	1.84	0.41
1:A:748:C:H1'	1:A:749:C:C5	2.55	0.41
1:A:861:G:C6	1:A:862:C:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:886:G:C6	1:A:912:C:N3	2.89	0.41
1:A:895:G:C2	1:A:896:C:C2	3.08	0.41
1:A:957:U:O2	1:A:960:U:C2	2.73	0.41
1:A:1050:G:C2	1:A:1051:C:C2	3.09	0.41
1:A:1088:G:C6	1:A:1089:G:C5	3.09	0.41
1:A:1106:G:C2	1:A:1107:C:C2	3.09	0.41
1:A:1144:G:H21	1:A:1146:A:H62	1.69	0.41
1:A:1253:G:C2	1:A:1254:C:C2	3.09	0.41
1:A:1387:G:C2	1:A:1388:C:C2	3.09	0.41
1:A:1410:G:C5	1:A:1411:C:C4	3.09	0.41
2:B:19:HIS:CE1	2:B:206:ASP:HB2	2.56	0.41
2:B:109:SER:O	2:B:112:VAL:HG12	2.21	0.41
2:B:178:ARG:NE	2:B:196:LEU:O	2.47	0.41
3:C:9:GLY:HA3	14:N:49:HIS:HA	2.03	0.41
7:G:153:HIS:C	7:G:155:ARG:H	2.29	0.41
9:I:125:TYR:CD1	9:I:125:TYR:C	2.99	0.41
10:J:27:ALA:CB	10:J:85:LEU:HD11	2.50	0.41
10:J:30:SER:HB3	10:J:84:GLN:HE22	1.85	0.41
13:M:15:VAL:O	13:M:19:LEU:HG	2.21	0.41
18:R:26:LEU:HD11	18:R:39:VAL:HG22	2.03	0.41
18:R:32:ARG:HA	18:R:69:THR:CG2	2.45	0.41
19:S:6:LYS:CD	19:S:7:LYS:H	2.33	0.41
1:A:70:G:C6	1:A:100:C:N3	2.89	0.41
1:A:137:C:H2'	1:A:138:G:H8	1.86	0.41
1:A:378:G:C2	1:A:379:C:C2	3.08	0.41
1:A:677:U:H3	1:A:713:G:H22	1.69	0.41
1:A:1327:C:H2'	1:A:1328:C:H6	1.86	0.41
1:A:1368:G:H5''	14:N:61:TRP:HZ2	1.86	0.41
1:A:1419:G:C2	1:A:1420:C:C2	3.09	0.41
2:B:87:ARG:NH1	2:B:233:SER:H	2.19	0.41
4:D:26:CYS:HA	4:D:31:CYS:HB2	2.03	0.41
8:H:82:HIS:NE2	8:H:84:ARG:HB2	2.35	0.41
10:J:76:ASN:HA	10:J:77:PRO:HD2	1.96	0.41
22:X:119:THR:HG22	22:X:160:ASP:HB3	2.01	0.41
1:A:35:G:C2	1:A:36:C:N3	2.89	0.40
1:A:245:C:C2	1:A:284:G:C2	3.08	0.40
1:A:252:U:H2'	1:A:253:U:C6	2.56	0.40
1:A:522:C:H2'	1:A:523:A:C8	2.56	0.40
1:A:575:G:H4'	1:A:576:G:C5'	2.48	0.40
1:A:779:C:N4	1:A:780:A:N1	2.69	0.40
1:A:943:U:H2'	1:A:944:G:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1102:A:H2'	1:A:1103:C:C6	2.56	0.40
1:A:1116:C:H3'	1:A:1117:G:H5''	2.02	0.40
1:A:1193:G:N2	1:A:1194:U:C2	2.89	0.40
1:A:1298:C:H4'	1:A:1299:A:O5'	2.22	0.40
1:A:1456:G:C2	1:A:1457:G:N9	2.88	0.40
2:B:25:ASN:H	2:B:191:ASP:HA	1.86	0.40
4:D:175:SER:O	4:D:183:GLY:HA2	2.20	0.40
4:D:196:LEU:HD13	4:D:197:PRO:HD2	2.03	0.40
6:F:42:GLU:C	6:F:44:GLY:H	2.28	0.40
10:J:38:ILE:O	10:J:71:LEU:N	2.49	0.40
16:P:58:TYR:O	16:P:62:VAL:HG22	2.21	0.40
1:A:91:C:OP2	1:A:91:C:H6	2.03	0.40
1:A:976:G:C4	1:A:1363(A):A:N6	2.89	0.40
1:A:980:C:C5	1:A:981:U:C2	3.10	0.40
1:A:1031:G:O5'	1:A:1031:G:H8	2.04	0.40
1:A:1065:U:O2'	1:A:1066:C:OP2	2.30	0.40
1:A:1071:C:H2'	1:A:1072:G:C8	2.57	0.40
2:B:208:ILE:HA	2:B:211:ILE:HD12	2.03	0.40
2:B:236:TYR:HA	2:B:239:VAL:HG23	2.04	0.40
4:D:79:PHE:CZ	4:D:204:ILE:HA	2.57	0.40
5:E:34:VAL:HG21	5:E:63:ARG:NE	2.36	0.40
12:L:71:PRO:HB2	12:L:120:TYR:HE1	1.85	0.40
14:N:7:ILE:O	14:N:7:ILE:HG22	2.21	0.40
19:S:58:VAL:HA	19:S:59:PRO:HD3	1.87	0.40
22:X:110:LEU:HD13	22:X:148:ALA:CB	2.51	0.40
1:A:240:C:H2'	1:A:241:C:C6	2.57	0.40
1:A:363:A:OP2	12:L:34:ARG:HB3	2.21	0.40
1:A:457:C:H2'	1:A:458:C:C6	2.56	0.40
1:A:520:A:N1	1:A:536:C:H1'	2.36	0.40
1:A:932:C:C2	1:A:1386:G:N2	2.90	0.40
1:A:1027:C:C2'	1:A:1028:C:H5'	2.51	0.40
1:A:1251:A:O5'	1:A:1251:A:H8	2.05	0.40
1:A:1261:A:N6	1:A:1274:G:O2'	2.55	0.40
2:B:36:ARG:HB2	2:B:41:ILE:HD13	2.02	0.40
8:H:91:ARG:HA	17:Q:34:LYS:HB3	2.03	0.40
19:S:80:TYR:CE2	19:S:82:GLY:HA3	2.56	0.40
20:T:26:ASN:ND2	20:T:71:THR:HA	2.36	0.40
22:X:17:ARG:HB2	22:X:54:PRO:HB2	2.03	0.40
1:A:199:G:C2	1:A:219:C:N3	2.90	0.40
1:A:361:G:H2'	1:A:362:G:O4'	2.21	0.40
1:A:1064:G:C4	1:A:1066:C:C4	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1253:G:C6	1:A:1254:C:C4	3.09	0.40
3:C:26:LYS:H	3:C:26:LYS:HG2	1.64	0.40
3:C:70:VAL:HB	3:C:71:ALA:H	1.81	0.40
10:J:51:ARG:HG3	14:N:45:ARG:NH1	2.37	0.40
19:S:31:ILE:HD13	19:S:31:ILE:HA	1.87	0.40
22:X:120:ILE:HG13	22:X:161:MET:HB3	2.03	0.40
1:A:79:G:C3'	1:A:80:G:H8	2.34	0.40
1:A:104:G:C2	1:A:105:G:C5	3.09	0.40
1:A:675:A:C4	1:A:676:A:C8	3.09	0.40
1:A:876:G:C2	1:A:877:C:N3	2.89	0.40
1:A:985:C:N3	1:A:1221:G:C2	2.90	0.40
1:A:1197:G:OP1	1:A:1198:G:OP2	2.40	0.40
1:A:1305:G:OP2	21:V:5:ASP:HB2	2.22	0.40
1:A:1384:C:H2'	1:A:1385:G:H8	1.86	0.40
1:A:1430:C:C2	1:A:1471:G:N2	2.89	0.40
4:D:131:ARG:HH11	4:D:131:ARG:HB2	1.87	0.40
8:H:4:ASP:HA	8:H:5:PRO:HD3	1.80	0.40
10:J:6:ILE:HG22	10:J:98:ILE:HA	2.03	0.40
20:T:89:ARG:HG3	20:T:104:LEU:HD22	2.03	0.40
22:X:5:TYR:CD2	22:X:65:TRP:HH2	2.40	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	232/256 (91%)	184 (79%)	33 (14%)	15 (6%)	1	15
3	C	204/239 (85%)	174 (85%)	26 (13%)	4 (2%)	6	33
4	D	206/209 (99%)	176 (85%)	26 (13%)	4 (2%)	6	34
5	E	148/162 (91%)	125 (84%)	19 (13%)	4 (3%)	4	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	99/101 (98%)	87 (88%)	7 (7%)	5 (5%)	1	18
7	G	153/156 (98%)	132 (86%)	18 (12%)	3 (2%)	6	33
8	H	136/138 (99%)	125 (92%)	9 (7%)	2 (2%)	8	38
9	I	125/128 (98%)	104 (83%)	14 (11%)	7 (6%)	1	17
10	J	96/105 (91%)	79 (82%)	12 (12%)	5 (5%)	1	18
11	K	117/129 (91%)	94 (80%)	17 (14%)	6 (5%)	1	18
12	L	122/132 (92%)	95 (78%)	24 (20%)	3 (2%)	4	29
13	M	116/126 (92%)	100 (86%)	13 (11%)	3 (3%)	4	29
14	N	58/61 (95%)	44 (76%)	9 (16%)	5 (9%)	0	10
15	O	86/89 (97%)	77 (90%)	7 (8%)	2 (2%)	5	31
16	P	81/88 (92%)	71 (88%)	8 (10%)	2 (2%)	4	29
17	Q	97/105 (92%)	82 (84%)	10 (10%)	5 (5%)	1	18
18	R	71/88 (81%)	62 (87%)	8 (11%)	1 (1%)	9	39
19	S	80/93 (86%)	63 (79%)	12 (15%)	5 (6%)	1	15
20	T	97/106 (92%)	81 (84%)	11 (11%)	5 (5%)	1	18
21	V	22/27 (82%)	19 (86%)	1 (4%)	2 (9%)	0	10
22	X	160/171 (94%)	137 (86%)	17 (11%)	6 (4%)	2	22
All	All	2506/2709 (92%)	2111 (84%)	301 (12%)	94 (4%)	4	22

All (94) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	21	ARG
2	B	24	TRP
2	B	229	VAL
4	D	37	PRO
5	E	21	ALA
6	F	69	GLU
6	F	96	PRO
12	L	27	LEU
14	N	15	LYS
19	S	6	LYS
20	T	98	PRO
21	V	3	LYS
22	X	54	PRO
22	X	127	VAL

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Mol	Chain	Res	Type
2	B	134	GLU
3	C	81	GLY
4	D	5	ILE
7	G	7	ALA
7	G	153	HIS
9	I	41	VAL
9	I	58	HIS
9	I	119	ALA
10	J	34	VAL
10	J	55	LYS
11	K	14	VAL
11	K	50	TYR
11	K	55	LYS
11	K	126	ARG
12	L	16	GLU
12	L	45	PRO
14	N	14	PRO
17	Q	67	LYS
19	S	30	LEU
22	X	8	ASN
2	B	17	PHE
2	B	38	GLY
2	B	204	ASN
2	B	228	GLY
2	B	233	SER
3	C	3	ASN
3	C	51	GLY
6	F	93	SER
7	G	53	LYS
8	H	92	ARG
9	I	54	ASP
10	J	54	PHE
11	K	123	LYS
13	M	100	GLY
14	N	22	THR
15	O	88	ARG
17	Q	68	ARG
19	S	13	ASP
20	T	9	ASN
20	T	97	ALA
2	B	130	ARG
6	F	53	ALA

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Mol	Chain	Res	Type
8	H	5	PRO
9	I	56	LEU
11	K	127	LYS
13	M	10	PRO
14	N	23	ARG
16	P	30	GLY
17	Q	97	SER
17	Q	99	SER
20	T	95	ALA
21	V	6	ARG
2	B	23	ARG
4	D	150	GLU
16	P	31	LYS
18	R	87	ARG
20	T	49	ALA
22	X	55	PRO
22	X	56	VAL
2	B	78	GLN
5	E	38	GLN
6	F	68	PRO
14	N	17	LYS
15	O	18	PHE
19	S	80	TYR
4	D	41	GLY
22	X	59	ILE
2	B	208	ILE
2	B	232	PRO
5	E	128	PRO
9	I	22	GLY
9	I	44	VAL
10	J	37	PRO
10	J	91	PRO
13	M	113	PRO
19	S	8	GLY
3	C	80	GLY
17	Q	47	PRO
2	B	127	ILE
5	E	39	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	202/220 (92%)	150 (74%)	52 (26%)	0	4
3	C	160/188 (85%)	117 (73%)	43 (27%)	0	4
4	D	180/181 (99%)	130 (72%)	50 (28%)	0	3
5	E	115/123 (94%)	80 (70%)	35 (30%)	0	2
6	F	90/90 (100%)	73 (81%)	17 (19%)	1	11
7	G	126/127 (99%)	102 (81%)	24 (19%)	1	10
8	H	119/119 (100%)	79 (66%)	40 (34%)	0	2
9	I	98/99 (99%)	78 (80%)	20 (20%)	1	8
10	J	87/92 (95%)	69 (79%)	18 (21%)	1	7
11	K	90/99 (91%)	68 (76%)	22 (24%)	1	5
12	L	104/109 (95%)	76 (73%)	28 (27%)	0	4
13	M	94/101 (93%)	78 (83%)	16 (17%)	2	13
14	N	49/50 (98%)	37 (76%)	12 (24%)	1	5
15	O	79/80 (99%)	53 (67%)	26 (33%)	0	2
16	P	72/74 (97%)	58 (81%)	14 (19%)	1	10
17	Q	94/97 (97%)	75 (80%)	19 (20%)	1	9
18	R	64/77 (83%)	46 (72%)	18 (28%)	0	3
19	S	71/80 (89%)	48 (68%)	23 (32%)	0	2
20	T	76/82 (93%)	52 (68%)	24 (32%)	0	2
21	V	19/22 (86%)	15 (79%)	4 (21%)	1	7
22	X	145/150 (97%)	110 (76%)	35 (24%)	1	5
All	All	2134/2260 (94%)	1594 (75%)	540 (25%)	2	4

All (540) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	8	LYS

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Mol	Chain	Res	Type
2	B	10	LEU
2	B	11	LEU
2	B	16	HIS
2	B	17	PHE
2	B	21	ARG
2	B	23	ARG
2	B	41	ILE
2	B	42	ILE
2	B	44	LEU
2	B	45	GLN
2	B	51	LEU
2	B	52	GLU
2	B	61	LEU
2	B	63	MET
2	B	64	ARG
2	B	67	THR
2	B	76	GLN
2	B	83	MET
2	B	84	GLU
2	B	87	ARG
2	B	93	VAL
2	B	98	LEU
2	B	101	MET
2	B	102	LEU
2	B	107	THR
2	B	112	VAL
2	B	124	SER
2	B	128	GLU
2	B	129	GLU
2	B	136	VAL
2	B	141	GLU
2	B	144	ARG
2	B	146	GLN
2	B	157	ARG
2	B	164	VAL
2	B	168	THR
2	B	172	ILE
2	B	178	ARG
2	B	189	ASP
2	B	190	THR
2	B	191	ASP
2	B	204	ASN

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Mol	Chain	Res	Type
2	B	205	ASP
2	B	206	ASP
2	B	208	ILE
2	B	209	ARG
2	B	211	ILE
2	B	220	ASP
2	B	221	LEU
2	B	239	VAL
2	B	240	GLN
3	C	3	ASN
3	C	12	LEU
3	C	14	ILE
3	C	16	ARG
3	C	17	ASP
3	C	19	GLU
3	C	20	SER
3	C	28	GLN
3	C	33	LEU
3	C	34	LEU
3	C	35	GLU
3	C	42	LEU
3	C	52	LEU
3	C	55	VAL
3	C	68	VAL
3	C	79	ARG
3	C	82	GLU
3	C	87	LEU
3	C	90	GLU
3	C	91	LEU
3	C	94	LEU
3	C	98	ASN
3	C	101	LEU
3	C	107	GLN
3	C	108	ASN
3	C	111	LEU
3	C	112	SER
3	C	119	ARG
3	C	131	ARG
3	C	136	GLN
3	C	138	VAL
3	C	139	GLN
3	C	175	LEU

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Mol	Chain	Res	Type
3	C	177	THR
3	C	179	ARG
3	C	188	LEU
3	C	190	ARG
3	C	191	THR
3	C	195	VAL
3	C	196	LEU
3	C	204	LEU
3	C	206	GLU
3	C	207	VAL
4	D	3	ARG
4	D	5	ILE
4	D	13	ARG
4	D	15	GLU
4	D	18	LYS
4	D	24	GLU
4	D	34	GLU
4	D	45	GLN
4	D	47	ARG
4	D	49	ARG
4	D	50	ARG
4	D	52	SER
4	D	53	ASP
4	D	56	VAL
4	D	64	LEU
4	D	66	ARG
4	D	70	ILE
4	D	78	LEU
4	D	94	LEU
4	D	104	VAL
4	D	108	LEU
4	D	112	VAL
4	D	115	ARG
4	D	118	ARG
4	D	119	GLN
4	D	120	LEU
4	D	122	ARG
4	D	127	THR
4	D	131	ARG
4	D	132	ARG
4	D	134	ASP
4	D	138	TYR

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Mol	Chain	Res	Type
4	D	141	ARG
4	D	146	ILE
4	D	150	GLU
4	D	155	LEU
4	D	156	GLU
4	D	168	ARG
4	D	174	LEU
4	D	176	LEU
4	D	178	VAL
4	D	181	MET
4	D	186	LEU
4	D	187	ARG
4	D	188	LEU
4	D	192	GLU
4	D	196	LEU
4	D	200	GLU
4	D	208	SER
4	D	209	ARG
5	E	11	ILE
5	E	12	LEU
5	E	13	ILE
5	E	14	ARG
5	E	15	ARG
5	E	20	GLN
5	E	24	ARG
5	E	27	ARG
5	E	32	VAL
5	E	34	VAL
5	E	38	GLN
5	E	40	ARG
5	E	41	VAL
5	E	47	LYS
5	E	55	VAL
5	E	57	LYS
5	E	68	GLU
5	E	71	LEU
5	E	76	ILE
5	E	79	GLU
5	E	80	ILE
5	E	82	VAL
5	E	91	LEU
5	E	107	ARG

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Mol	Chain	Res	Type
5	E	110	LEU
5	E	116	THR
5	E	118	ILE
5	E	123	LEU
5	E	126	ARG
5	E	131	ILE
5	E	142	LEU
5	E	143	ARG
5	E	148	VAL
5	E	149	GLU
5	E	152	ARG
6	F	10	LEU
6	F	15	ASP
6	F	19	LEU
6	F	21	LEU
6	F	24	GLU
6	F	36	ARG
6	F	39	LYS
6	F	40	VAL
6	F	45	LEU
6	F	61	LEU
6	F	64	GLN
6	F	69	GLU
6	F	75	LEU
6	F	77	ARG
6	F	79	LEU
6	F	86	ARG
6	F	91	VAL
7	G	8	GLU
7	G	21	VAL
7	G	32	ARG
7	G	49	ILE
7	G	52	GLU
7	G	57	GLU
7	G	60	LYS
7	G	67	GLU
7	G	69	VAL
7	G	72	ARG
7	G	75	VAL
7	G	77	SER
7	G	84	ASN
7	G	90	GLU

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Mol	Chain	Res	Type
7	G	91	VAL
7	G	94	ARG
7	G	95	ARG
7	G	96	GLN
7	G	106	GLN
7	G	113	GLU
7	G	136	LYS
7	G	137	LYS
7	G	138	LYS
7	G	142	GLU
8	H	6	ILE
8	H	8	ASP
8	H	10	LEU
8	H	11	THR
8	H	14	ARG
8	H	17	THR
8	H	18	ARG
8	H	19	VAL
8	H	21	LYS
8	H	23	SER
8	H	29	SER
8	H	34	GLU
8	H	38	ILE
8	H	41	ARG
8	H	46	LYS
8	H	49	GLU
8	H	50	ARG
8	H	53	VAL
8	H	56	LYS
8	H	60	ARG
8	H	75	ARG
8	H	77	GLU
8	H	84	ARG
8	H	85	ARG
8	H	87	SER
8	H	92	ARG
8	H	93	VAL
8	H	100	ILE
8	H	103	VAL
8	H	105	ARG
8	H	107	LEU
8	H	109	ILE

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Mol	Chain	Res	Type
8	H	119	LEU
8	H	120	THR
8	H	122	ARG
8	H	123	GLU
8	H	126	LYS
8	H	127	LEU
8	H	133	LEU
8	H	134	ILE
9	I	7	THR
9	I	19	LEU
9	I	26	VAL
9	I	34	ASN
9	I	38	GLN
9	I	40	LEU
9	I	54	ASP
9	I	60	ASP
9	I	78	LYS
9	I	85	LEU
9	I	87	GLN
9	I	93	ARG
9	I	95	LYS
9	I	96	LEU
9	I	99	LEU
9	I	111	ARG
9	I	113	LYS
9	I	118	LYS
9	I	125	TYR
9	I	128	ARG
10	J	5	ARG
10	J	8	LEU
10	J	16	LEU
10	J	17	ASP
10	J	38	ILE
10	J	42	THR
10	J	51	ARG
10	J	57	LYS
10	J	61	GLU
10	J	62	HIS
10	J	69	ASN
10	J	70	ARG
10	J	71	LEU
10	J	82	ILE

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Mol	Chain	Res	Type
10	J	84	GLN
10	J	85	LEU
10	J	94	VAL
10	J	99	LYS
11	K	12	ARG
11	K	16	SER
11	K	29	ILE
11	K	40	ILE
11	K	41	THR
11	K	44	SER
11	K	48	ILE
11	K	54	ARG
11	K	57	THR
11	K	62	GLN
11	K	63	LEU
11	K	66	LEU
11	K	77	MET
11	K	78	GLN
11	K	87	THR
11	K	92	GLU
11	K	93	GLN
11	K	98	LEU
11	K	107	SER
11	K	109	VAL
11	K	116	HIS
11	K	117	ASN
12	L	7	ILE
12	L	15	ARG
12	L	17	LYS
12	L	19	ARG
12	L	24	VAL
12	L	27	LEU
12	L	39	VAL
12	L	41	ARG
12	L	43	VAL
12	L	44	THR
12	L	47	LYS
12	L	55	VAL
12	L	59	ARG
12	L	60	LEU
12	L	67	THR
12	L	70	ILE

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Mol	Chain	Res	Type
12	L	79	GLU
12	L	81	SER
12	L	84	LEU
12	L	86	ARG
12	L	90	VAL
12	L	93	LEU
12	L	97	ARG
12	L	104	VAL
12	L	114	LYS
12	L	122	THR
12	L	126	LYS
12	L	127	GLU
13	M	4	ILE
13	M	9	ILE
13	M	15	VAL
13	M	17	VAL
13	M	32	GLU
13	M	45	VAL
13	M	48	LEU
13	M	54	VAL
13	M	69	GLU
13	M	70	LEU
13	M	79	LYS
13	M	80	ARG
13	M	102	ARG
13	M	110	ARG
13	M	115	LYS
13	M	116	THR
14	N	7	ILE
14	N	8	GLU
14	N	9	LYS
14	N	12	ARG
14	N	18	VAL
14	N	26	ARG
14	N	31	ARG
14	N	33	VAL
14	N	41	ARG
14	N	44	LEU
14	N	50	LYS
14	N	53	LEU
15	O	4	THR
15	O	6	GLU

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Mol	Chain	Res	Type
15	O	7	GLU
15	O	9	GLN
15	O	10	LYS
15	O	14	GLU
15	O	21	ASP
15	O	25	THR
15	O	28	GLN
15	O	29	VAL
15	O	34	LEU
15	O	35	ARG
15	O	39	LEU
15	O	41	GLU
15	O	49	ASP
15	O	52	SER
15	O	54	ARG
15	O	56	LEU
15	O	57	LEU
15	O	64	ARG
15	O	68	ARG
15	O	70	LEU
15	O	76	GLU
15	O	82	ILE
15	O	83	GLU
15	O	87	ILE
16	P	5	ARG
16	P	8	ARG
16	P	19	ILE
16	P	20	VAL
16	P	23	ASP
16	P	26	ARG
16	P	34	GLU
16	P	44	THR
16	P	49	LEU
16	P	53	VAL
16	P	62	VAL
16	P	67	THR
16	P	73	LEU
16	P	81	ARG
17	Q	7	THR
17	Q	16	GLN
17	Q	23	VAL
17	Q	34	LYS

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Mol	Chain	Res	Type
17	Q	41	LYS
17	Q	52	LYS
17	Q	56	VAL
17	Q	59	ILE
17	Q	60	ILE
17	Q	62	SER
17	Q	63	ARG
17	Q	65	ILE
17	Q	68	ARG
17	Q	76	LEU
17	Q	82	MET
17	Q	89	LEU
17	Q	92	ARG
17	Q	93	GLN
17	Q	98	LEU
18	R	19	LYS
18	R	22	VAL
18	R	34	TYR
18	R	37	VAL
18	R	39	VAL
18	R	42	ARG
18	R	47	THR
18	R	50	ILE
18	R	53	ARG
18	R	54	ARG
18	R	63	GLN
18	R	75	ILE
18	R	81	PHE
18	R	83	GLU
18	R	84	LYS
18	R	86	VAL
18	R	87	ARG
18	R	88	LYS
19	S	3	ARG
19	S	5	LEU
19	S	7	LYS
19	S	13	ASP
19	S	19	VAL
19	S	22	LEU
19	S	25	LYS
19	S	28	LYS
19	S	29	ARG

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Mol	Chain	Res	Type
19	S	31	ILE
19	S	36	ARG
19	S	37	ARG
19	S	38	SER
19	S	39	THR
19	S	41	VAL
19	S	51	VAL
19	S	53	ASN
19	S	55	LYS
19	S	58	VAL
19	S	62	ILE
19	S	63	THR
19	S	77	THR
19	S	79	THR
20	T	10	LEU
20	T	13	LEU
20	T	15	ARG
20	T	20	LEU
20	T	22	ARG
20	T	23	ARG
20	T	24	LEU
20	T	25	ARG
20	T	26	ASN
20	T	33	ILE
20	T	36	LEU
20	T	43	LEU
20	T	45	GLN
20	T	48	LYS
20	T	50	GLU
20	T	53	LEU
20	T	55	ILE
20	T	63	ILE
20	T	68	LYS
20	T	73	HIS
20	T	74	LYS
20	T	75	ASN
20	T	84	LEU
20	T	104	LEU
21	V	3	LYS
21	V	12	LYS
21	V	20	LYS
21	V	25	LYS

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Mol	Chain	Res	Type
22	X	4	GLU
22	X	12	ARG
22	X	14	LYS
22	X	18	VAL
22	X	24	LYS
22	X	28	ILE
22	X	30	ASP
22	X	32	ARG
22	X	41	MET
22	X	53	ASP
22	X	59	ILE
22	X	60	MET
22	X	64	LYS
22	X	73	GLU
22	X	74	LYS
22	X	77	ARG
22	X	88	ILE
22	X	91	ARG
22	X	92	VAL
22	X	94	ILE
22	X	98	ASP
22	X	101	THR
22	X	103	LEU
22	X	119	THR
22	X	120	ILE
22	X	125	ARG
22	X	131	GLU
22	X	142	GLU
22	X	147	LEU
22	X	150	VAL
22	X	153	LYS
22	X	162	ASN
22	X	163	MET
22	X	168	VAL
22	X	170	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	16	HIS
2	B	25	ASN
2	B	45	GLN

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Mol	Chain	Res	Type
2	B	146	GLN
2	B	212	GLN
2	B	224	GLN
3	C	6	HIS
3	C	31	HIS
3	C	107	GLN
3	C	108	ASN
3	C	118	GLN
3	C	123	GLN
3	C	136	GLN
3	C	170	GLN
3	C	176	HIS
4	D	45	GLN
4	D	74	GLN
4	D	201	GLN
6	F	18	GLN
6	F	64	GLN
6	F	100	ASN
7	G	28	ASN
7	G	68	ASN
8	H	70	GLN
9	I	87	GLN
9	I	124	GLN
10	J	33	GLN
10	J	68	HIS
10	J	78	ASN
10	J	84	GLN
11	K	13	GLN
11	K	38	ASN
12	L	8	ASN
12	L	49	ASN
12	L	76	ASN
12	L	99	HIS
13	M	12	ASN
13	M	62	ASN
14	N	52	GLN
15	O	37	ASN
15	O	46	HIS
15	O	50	HIS
15	O	62	GLN
16	P	13	HIS
18	R	36	ASN

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Mol	Chain	Res	Type
18	R	63	GLN
19	S	53	ASN
20	T	26	ASN
22	X	25	GLN
22	X	129	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1509/1522 (99%)	460 (30%)	109 (7%)
23	Y	19/42 (45%)	10 (52%)	1 (5%)
24	Z	76/77 (98%)	37 (48%)	5 (6%)
All	All	1604/1641 (97%)	507 (31%)	115 (7%)

All (507) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	G
1	A	13	U
1	A	19	C
1	A	22	G
1	A	30	U
1	A	31	G
1	A	32	A
1	A	39	G
1	A	44	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	52	G
1	A	54	C
1	A	60	A
1	A	61	G
1	A	63	C
1	A	66	G
1	A	68	G
1	A	72	C
1	A	73	G

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Mol	Chain	Res	Type
1	A	76	C
1	A	77	G
1	A	79	G
1	A	81	U
1	A	82	U
1	A	91	C
1	A	93	G
1	A	97	G
1	A	98	G
1	A	100	C
1	A	101	A
1	A	108	G
1	A	120	A
1	A	121	C
1	A	122	G
1	A	128	G
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	137	C
1	A	142	G
1	A	144	G
1	A	151	A
1	A	163	C
1	A	167	G
1	A	171	A
1	A	181	G
1	A	182	U
1	A	189(C)	C
1	A	189(E)	U
1	A	189(F)	U
1	A	189(G)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	199	G
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	217	C
1	A	222	U

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Mol	Chain	Res	Type
1	A	227	G
1	A	231	G
1	A	243	A
1	A	244	U
1	A	245	C
1	A	247	G
1	A	250	A
1	A	251	G
1	A	252	U
1	A	253	U
1	A	262	A
1	A	264	U
1	A	266	G
1	A	267	C
1	A	272	C
1	A	279	A
1	A	280	C
1	A	281	G
1	A	282	A
1	A	289	G
1	A	298	A
1	A	299	G
1	A	300	A
1	A	301	G
1	A	305	G
1	A	306	G
1	A	315	A
1	A	316	G
1	A	321	A
1	A	324	G
1	A	325	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	340	U
1	A	342	C
1	A	343	U
1	A	344	A
1	A	345	C
1	A	350	G
1	A	351	G

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Mol	Chain	Res	Type
1	A	352	C
1	A	353	A
1	A	354	G
1	A	365	U
1	A	367	U
1	A	368	U
1	A	373	A
1	A	381	C
1	A	384	G
1	A	385	C
1	A	388	G
1	A	389	A
1	A	390	C
1	A	391	G
1	A	392	G
1	A	397	A
1	A	398	C
1	A	406	G
1	A	412	A
1	A	413	G
1	A	419	C
1	A	421	U
1	A	422	C
1	A	423	G
1	A	428	G
1	A	429	U
1	A	430	A
1	A	451	A
1	A	452	A
1	A	453	A
1	A	454	C
1	A	455	C
1	A	457	C
1	A	470	C
1	A	476	G
1	A	479	C
1	A	480	U
1	A	483	C
1	A	484	G
1	A	485	G
1	A	486	U
1	A	495	A

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Mol	Chain	Res	Type
1	A	496	A
1	A	498	U
1	A	500	G
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	521	G
1	A	524	G
1	A	525	C
1	A	527	G
1	A	529	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	535	A
1	A	545	C
1	A	547	A
1	A	548	G
1	A	550	G
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	563	A
1	A	564	C
1	A	565	U
1	A	568	G
1	A	572	A
1	A	573	A
1	A	574	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	578	C
1	A	588	G
1	A	596	C
1	A	607	A
1	A	619	U
1	A	630	G
1	A	641	U

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Mol	Chain	Res	Type
1	A	642	A
1	A	644	G
1	A	653	A
1	A	654	G
1	A	665	A
1	A	672	U
1	A	683	G
1	A	688	G
1	A	689	C
1	A	693	G
1	A	695	A
1	A	701	C
1	A	702	A
1	A	703	G
1	A	704	A
1	A	713	G
1	A	716	A
1	A	717	C
1	A	720	C
1	A	721	G
1	A	723	U
1	A	731	G
1	A	748	C
1	A	749	C
1	A	752	G
1	A	753	A
1	A	755	G
1	A	760	G
1	A	764	C
1	A	777	A
1	A	782	A
1	A	785	G
1	A	787	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	804	U
1	A	805	C
1	A	810	C
1	A	812	C
1	A	815	A
1	A	817	C

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Mol	Chain	Res	Type
1	A	820	U
1	A	828	A
1	A	835	U
1	A	839	U
1	A	840	C
1	A	841	U
1	A	851	G
1	A	855	G
1	A	864	A
1	A	865	A
1	A	873	A
1	A	876	G
1	A	877	C
1	A	885	G
1	A	887	G
1	A	889	A
1	A	891	U
1	A	900	A
1	A	902	G
1	A	914	A
1	A	919	A
1	A	922	G
1	A	926	G
1	A	927	G
1	A	931	C
1	A	932	C
1	A	933	G
1	A	934	C
1	A	935	A
1	A	942	G
1	A	946	A
1	A	950	U
1	A	956	U
1	A	958	A
1	A	960	U
1	A	961	U
1	A	966	G
1	A	968	A
1	A	969	A
1	A	971	G
1	A	972	C
1	A	974	A

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Mol	Chain	Res	Type
1	A	975	A
1	A	976	G
1	A	977	A
1	A	989	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	995	C
1	A	998	G
1	A	1000	U
1	A	1005	A
1	A	1009	G
1	A	1023	G
1	A	1024	G
1	A	1025	U
1	A	1026	G
1	A	1028	C
1	A	1029	C
1	A	1030	C
1	A	1030(A)	G
1	A	1037	C
1	A	1045	C
1	A	1046	A
1	A	1050	G
1	A	1051	C
1	A	1053	G
1	A	1054	C
1	A	1060	C
1	A	1065	U
1	A	1066	C
1	A	1074	G
1	A	1085	U
1	A	1086	U
1	A	1089	G
1	A	1094	G
1	A	1095	U
1	A	1096	C
1	A	1101	A
1	A	1102	A
1	A	1104	G
1	A	1108	G

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Mol	Chain	Res	Type
1	A	1115	C
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1128	C
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1133	G
1	A	1134	G
1	A	1135	U
1	A	1136	U
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1145	C
1	A	1146	A
1	A	1150	U
1	A	1151	A
1	A	1152	A
1	A	1154	G
1	A	1155	G
1	A	1159	U
1	A	1160	G
1	A	1170	A
1	A	1183	A
1	A	1184	G
1	A	1187	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1211	U
1	A	1212	U
1	A	1214	C
1	A	1215	G
1	A	1225	A

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Mol	Chain	Res	Type
1	A	1227	A
1	A	1236	A
1	A	1238	A
1	A	1239	A
1	A	1240	U
1	A	1241	G
1	A	1249	C
1	A	1250	A
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1260	C
1	A	1270	C
1	A	1273	G
1	A	1278	U
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1288	A
1	A	1295	G
1	A	1298	C
1	A	1299	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1312	G
1	A	1317	C
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1321	C
1	A	1322	C
1	A	1323	G
1	A	1332	A
1	A	1335	C
1	A	1336	C

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Mol	Chain	Res	Type
1	A	1345	U
1	A	1346	A
1	A	1347	G
1	A	1349	A
1	A	1353	G
1	A	1357	A
1	A	1361	G
1	A	1362	C
1	A	1363	C
1	A	1363(A)	A
1	A	1364	U
1	A	1370	G
1	A	1378	C
1	A	1379	G
1	A	1381	U
1	A	1394	A
1	A	1395	C
1	A	1396	A
1	A	1397	C
1	A	1398	A
1	A	1399	C
1	A	1412	C
1	A	1413	A
1	A	1418	A
1	A	1419	G
1	A	1424	C
1	A	1428	A
1	A	1440	C
1	A	1442	G
1	A	1443	G
1	A	1447	A
1	A	1452	C
1	A	1456	G
1	A	1457	G
1	A	1458	G
1	A	1481	U
1	A	1483	A
1	A	1484	C
1	A	1488	G
1	A	1492	A
1	A	1493	A
1	A	1494	G

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Mol	Chain	Res	Type
1	A	1497	G
1	A	1499	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1534	A
1	A	1536	C
1	A	1538	C
1	A	1539	C
1	A	1541	U
23	Y	21	G
23	Y	28	A
23	Y	29	G
23	Y	32	A
23	Y	33	A
23	Y	34	A
23	Y	35	A
23	Y	37	U
23	Y	38	G
23	Y	39	U
24	Z	2	G
24	Z	3	C
24	Z	5	G
24	Z	8	4SU
24	Z	9	G
24	Z	10	G
24	Z	13	C
24	Z	14	A
24	Z	16	C
24	Z	17	C
24	Z	17(A)	U
24	Z	18	G
24	Z	19	G
24	Z	21	A
24	Z	22	G
24	Z	23	C

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Mol	Chain	Res	Type
24	Z	26	G
24	Z	32	OMC
24	Z	34	C
24	Z	42	G
24	Z	43	A
24	Z	44	A
24	Z	47	U
24	Z	48	C
24	Z	49	G
24	Z	52	G
24	Z	54	5MU
24	Z	55	PSU
24	Z	57	A
24	Z	59	A
24	Z	64	G
24	Z	65	C
24	Z	67	C
24	Z	68	C
24	Z	69	C
24	Z	70	G
24	Z	76	A

All (115) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	A
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	202	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	281	G

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Mol	Chain	Res	Type
1	A	305	G
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	366	C
1	A	367	U
1	A	372	C
1	A	389	A
1	A	391	G
1	A	397	A
1	A	412	A
1	A	428	G
1	A	429	U
1	A	484	G
1	A	485	G
1	A	495	A
1	A	496	A
1	A	509	A
1	A	518	C
1	A	524	G
1	A	531	U
1	A	559	A
1	A	560	U
1	A	562	C
1	A	595	G
1	A	641	U
1	A	653	A
1	A	661	G
1	A	687	A
1	A	701	C
1	A	703	G
1	A	748	C
1	A	792	A
1	A	839	U
1	A	850	U
1	A	864	A
1	A	884	U
1	A	897	C
1	A	913	A
1	A	932	C
1	A	960	U

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Mol	Chain	Res	Type
1	A	965	A
1	A	968	A
1	A	975	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	1028	C
1	A	1030	C
1	A	1064	G
1	A	1065	U
1	A	1101	A
1	A	1128	C
1	A	1145	C
1	A	1151	A
1	A	1182	G
1	A	1190	G
1	A	1196	U
1	A	1200	C
1	A	1201	A
1	A	1212	U
1	A	1226	C
1	A	1239	A
1	A	1240	U
1	A	1257	U
1	A	1278	U
1	A	1279	A
1	A	1285	A
1	A	1287	A
1	A	1298	C
1	A	1299	A
1	A	1300	G
1	A	1301	U
1	A	1322	C
1	A	1331	G
1	A	1335	C
1	A	1345	U
1	A	1346	A
1	A	1364	U
1	A	1380	U
1	A	1419	G
1	A	1442(B)	A
1	A	1447	A

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Mol	Chain	Res	Type
1	A	1452	C
1	A	1457	G
1	A	1483	A
1	A	1492	A
1	A	1498	U
1	A	1503	A
1	A	1504	G
1	A	1533	C
23	Y	32	A
24	Z	3	C
24	Z	9	G
24	Z	47	U
24	Z	48	C
24	Z	60	U

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	4SU	Z	8	24	18,21,22	1.77	5 (27%)	25,30,33	2.43	8 (32%)
24	G7M	Z	46	24	23,26,27	2.43	5 (21%)	34,39,42	3.01	13 (38%)
24	5MU	Z	54	24	19,22,23	1.57	4 (21%)	27,32,35	1.85	6 (22%)
24	PSU	Z	55	24	18,21,22	1.47	3 (16%)	21,30,33	2.46	6 (28%)
24	OMC	Z	32	24	19,22,23	0.93	1 (5%)	25,31,34	1.27	3 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	4SU	Z	8	24	-	0/7/25/26	0/2/2/2
24	G7M	Z	46	24	-	0/7/25/26	0/3/3/3
24	5MU	Z	54	24	-	3/7/25/26	0/2/2/2
24	PSU	Z	55	24	-	5/7/25/26	0/2/2/2
24	OMC	Z	32	24	-	3/9/27/28	0/2/2/2

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	Z	46	G7M	C8-N7	7.98	1.46	1.33
24	Z	55	PSU	C6-C5	4.61	1.40	1.35
24	Z	46	G7M	C8-N9	4.58	1.48	1.35
24	Z	8	4SU	C4-S4	-4.54	1.60	1.68
24	Z	46	G7M	C5-C4	4.19	1.48	1.38
24	Z	54	5MU	C6-C5	3.82	1.40	1.34
24	Z	46	G7M	C5-N7	-3.68	1.34	1.39
24	Z	8	4SU	C2-N1	3.61	1.44	1.38
24	Z	54	5MU	C4-C5	2.87	1.49	1.44
24	Z	54	5MU	C2-N1	2.78	1.42	1.38
24	Z	8	4SU	C4-N3	-2.34	1.35	1.37
24	Z	54	5MU	C4-N3	-2.32	1.34	1.38
24	Z	8	4SU	C6-C5	2.21	1.40	1.35
24	Z	32	OMC	C6-C5	2.19	1.40	1.35
24	Z	46	G7M	C5-C6	2.16	1.49	1.43
24	Z	55	PSU	C4-N3	-2.14	1.34	1.38
24	Z	8	4SU	C5-C4	-2.11	1.40	1.42
24	Z	55	PSU	C4-C5	2.06	1.50	1.44

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	Z	46	G7M	CN7-N7-C8	-8.30	112.22	124.79
24	Z	46	G7M	N9-C8-N7	-6.58	96.51	112.48
24	Z	46	G7M	C8-N7-C5	6.10	115.41	107.78
24	Z	55	PSU	C6-C5-C4	-5.83	114.24	118.17
24	Z	55	PSU	N1-C2-N3	5.76	121.24	115.17
24	Z	46	G7M	N9-C4-N3	5.68	137.32	125.95
24	Z	8	4SU	C4-N3-C2	-5.51	122.03	127.31
24	Z	46	G7M	C5-C4-N3	-4.99	118.72	128.15
24	Z	54	5MU	N3-C2-N1	4.82	121.17	114.89
24	Z	8	4SU	N3-C2-N1	4.68	120.98	114.89
24	Z	46	G7M	CN7-N7-C5	4.46	132.36	126.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	Z	55	PSU	O2-C2-N1	-4.43	118.22	122.79
24	Z	8	4SU	C5-C4-N3	4.41	118.85	114.75
24	Z	46	G7M	C2-N3-C4	4.41	119.89	112.30
24	Z	8	4SU	C5-C4-S4	-4.27	119.43	124.31
24	Z	46	G7M	C8-N9-C4	4.15	117.36	107.09
24	Z	8	4SU	C6-N1-C2	-3.73	116.46	121.00
24	Z	8	4SU	C1'-N1-C2	3.67	124.18	117.59
24	Z	55	PSU	C4-N3-C2	-3.54	121.49	126.37
24	Z	54	5MU	C4-N3-C2	-3.51	122.73	127.34
24	Z	54	5MU	C5-C4-N3	3.40	118.28	115.32
24	Z	32	OMC	O2-C2-N3	-3.36	117.03	122.33
24	Z	8	4SU	C3'-C2'-C1'	2.79	106.75	101.46
24	Z	46	G7M	C1'-N9-C8	-2.78	117.36	126.74
24	Z	55	PSU	O3'-C3'-C4'	2.77	119.05	111.08
24	Z	46	G7M	O6-C6-C5	-2.67	122.06	128.01
24	Z	54	5MU	C3'-C2'-C1'	2.61	106.41	101.46
24	Z	54	5MU	C6-N1-C2	-2.56	118.75	121.30
24	Z	8	4SU	O2-C2-N3	-2.52	116.85	121.49
24	Z	46	G7M	O4'-C4'-C3'	-2.43	100.32	105.15
24	Z	54	5MU	O4-C4-C5	-2.42	122.15	124.92
24	Z	32	OMC	C1'-N1-C2	2.40	123.75	118.44
24	Z	46	G7M	C5-C6-N1	2.24	116.47	111.84
24	Z	55	PSU	C3'-C2'-C1'	2.17	104.25	101.69
24	Z	32	OMC	O2-C2-N1	2.04	122.90	118.90
24	Z	46	G7M	C6-C5-N7	2.00	134.68	132.17

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	Z	32	OMC	O4'-C4'-C5'-O5'
24	Z	54	5MU	O4'-C4'-C5'-O5'
24	Z	55	PSU	C2'-C1'-C5-C4
24	Z	55	PSU	C2'-C1'-C5-C6
24	Z	55	PSU	C3'-C4'-C5'-O5'
24	Z	55	PSU	O4'-C4'-C5'-O5'
24	Z	32	OMC	C3'-C4'-C5'-O5'
24	Z	54	5MU	C3'-C4'-C5'-O5'
24	Z	55	PSU	C4'-C5'-O5'-P
24	Z	32	OMC	C2'-C1'-N1-C6
24	Z	54	5MU	C4'-C5'-O5'-P

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	Z	8	4SU	1	0
24	Z	54	5MU	1	0
24	Z	55	PSU	2	0
24	Z	32	OMC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 82 ligands modelled in this entry, 82 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	5
23	Y	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1442(A):G	O3'	1442(B):A	P	5.11

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	84:U	O3'	88:A	P	5.07
1	A	93:G	O3'	96:U	P	4.99
1	A	204:U	O3'	216:G	P	4.97
1	A	841:U	O3'	848:C	P	4.05
1	Y	28:A	O3'	29:G	P	3.21

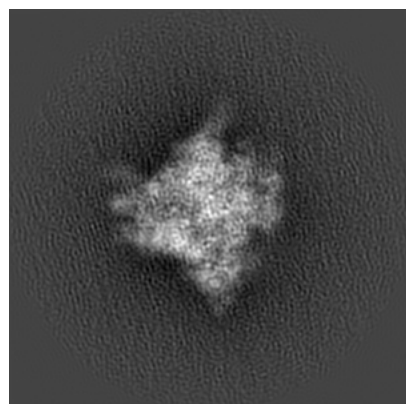
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4080. These allow visual inspection of the internal detail of the map and identification of artifacts.

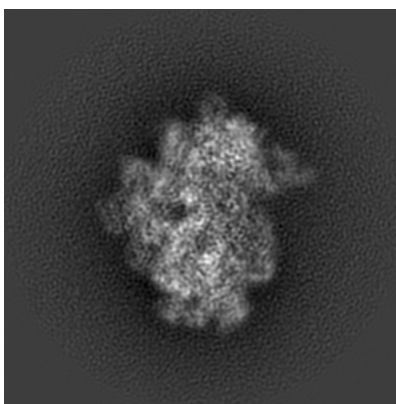
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

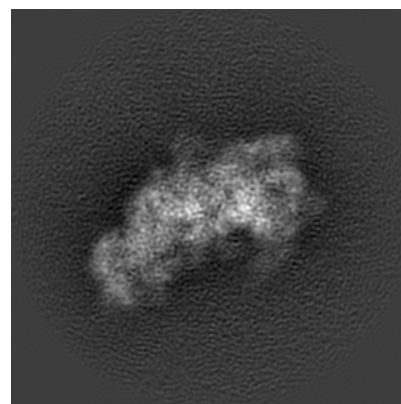
6.1.1 Primary map



X

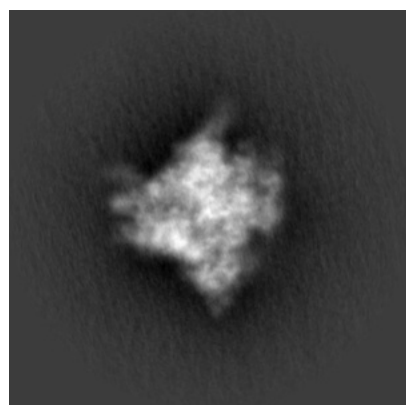


Y

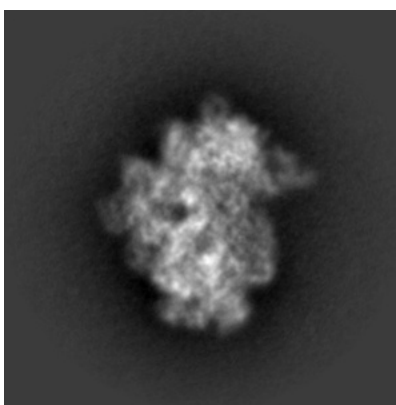


Z

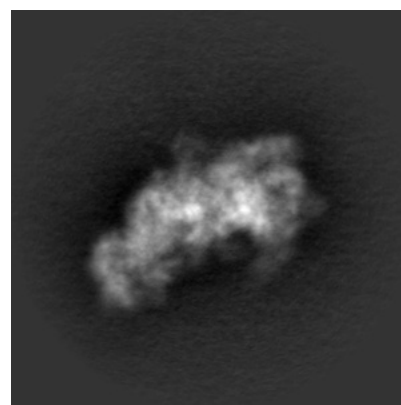
6.1.2 Raw map



X



Y

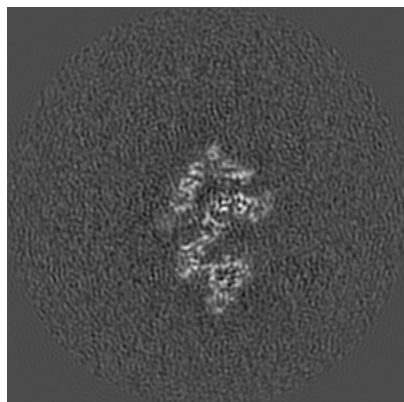


Z

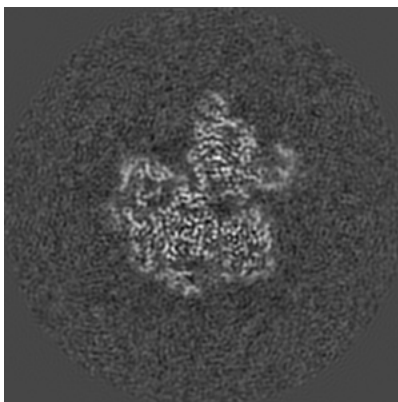
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

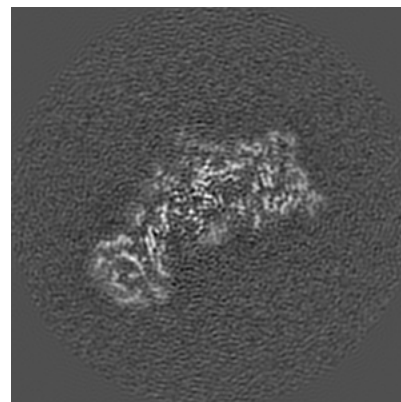
6.2.1 Primary map



X Index: 130

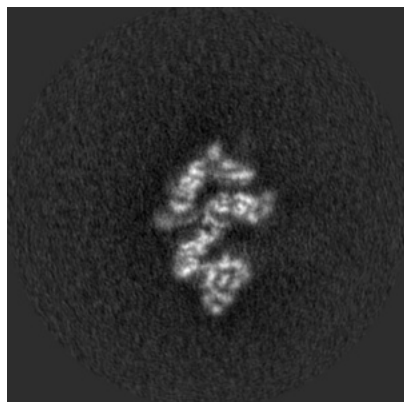


Y Index: 130

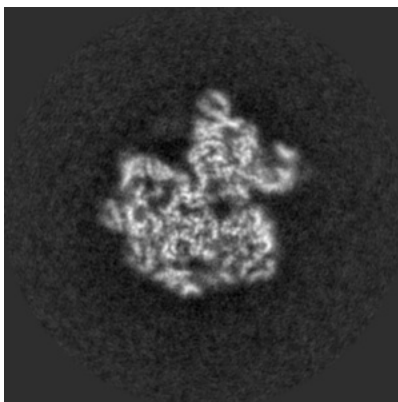


Z Index: 130

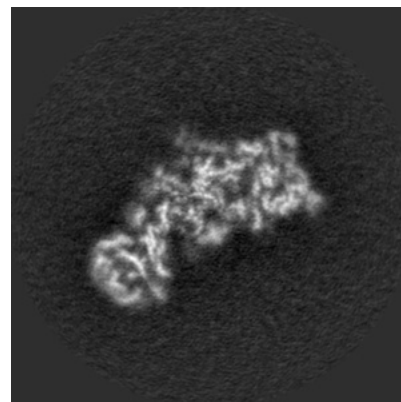
6.2.2 Raw map



X Index: 130



Y Index: 130

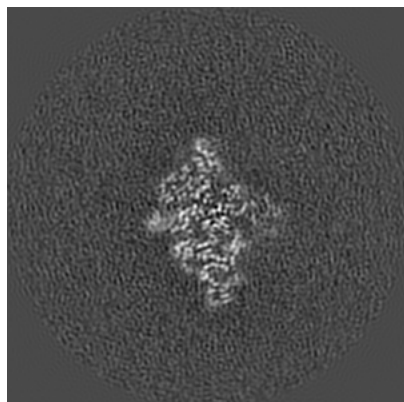


Z Index: 130

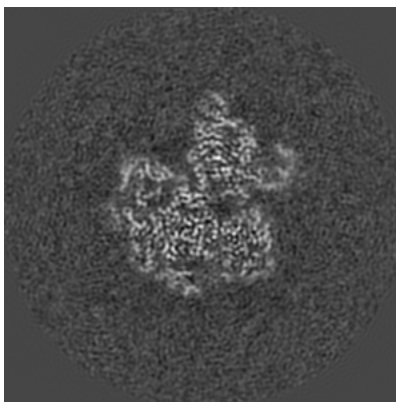
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

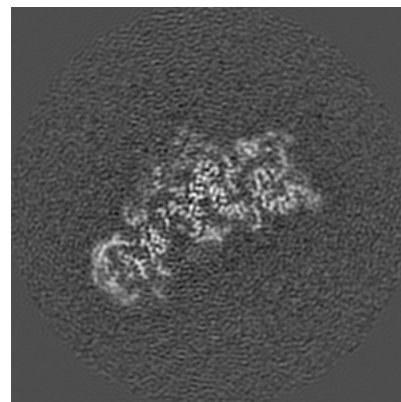
6.3.1 Primary map



X Index: 119

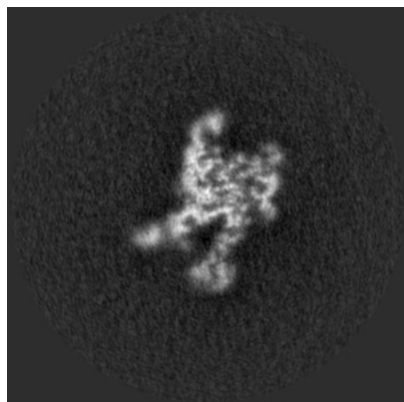


Y Index: 130

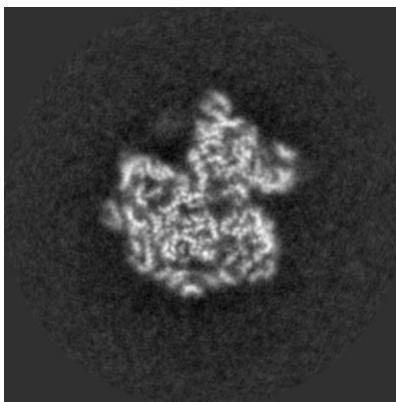


Z Index: 128

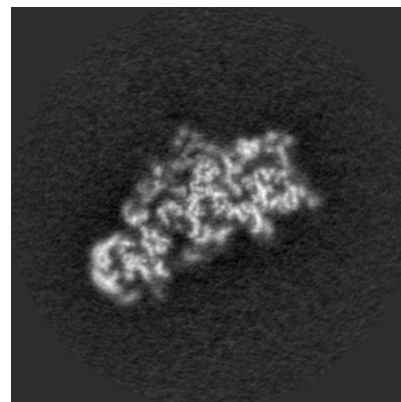
6.3.2 Raw map



X Index: 161



Y Index: 129

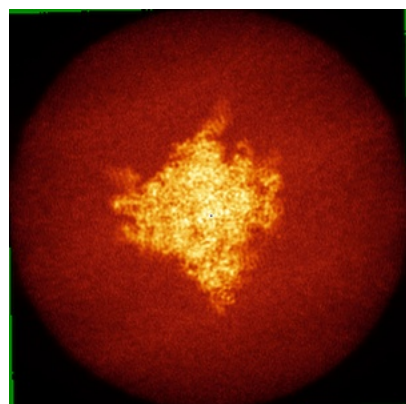


Z Index: 127

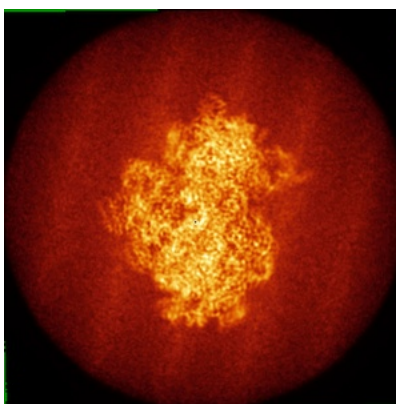
The images above show the largest variance slices of the map in three orthogonal directions.

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

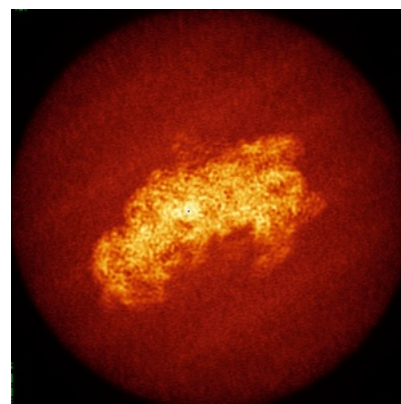
6.4.1 Primary map



X

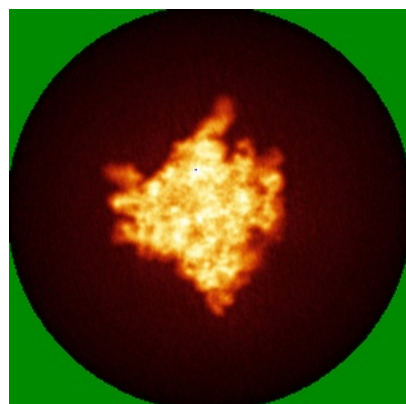


Y

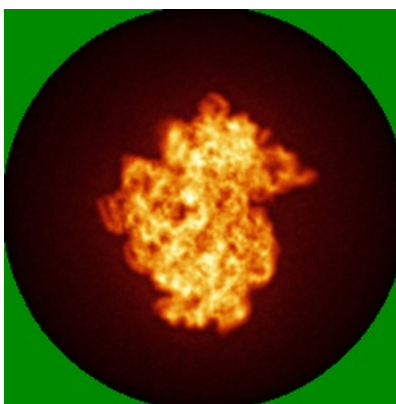


Z

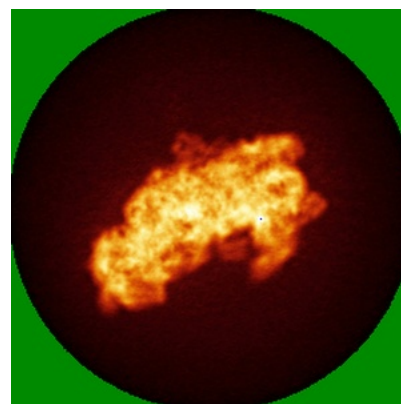
6.4.2 Raw map



X



Y

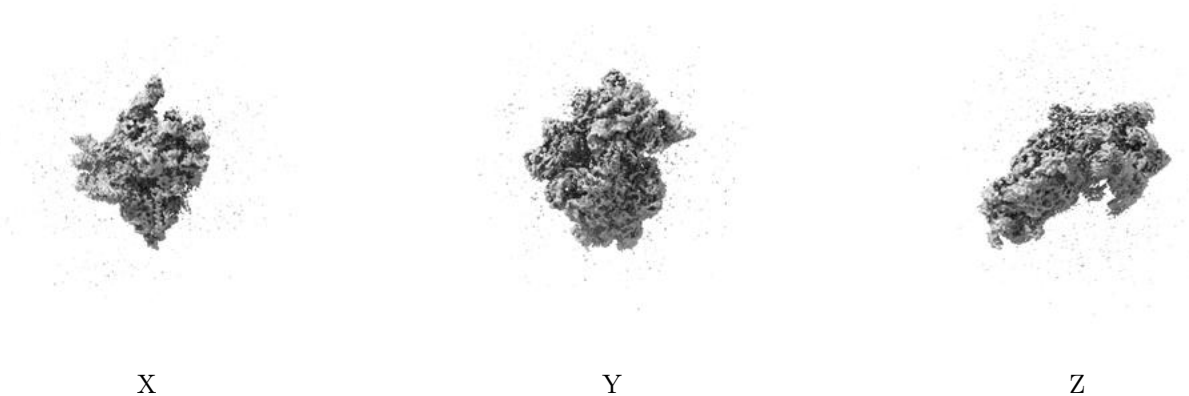


Z

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.

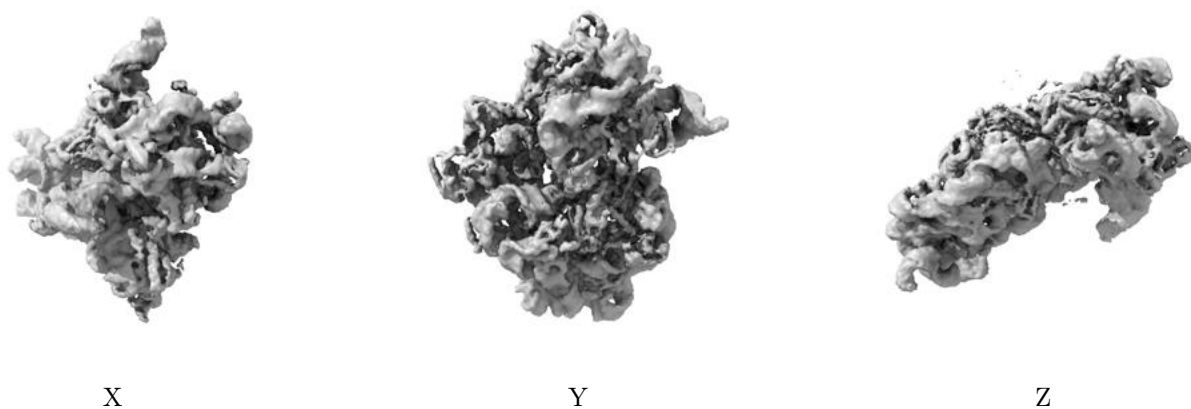
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

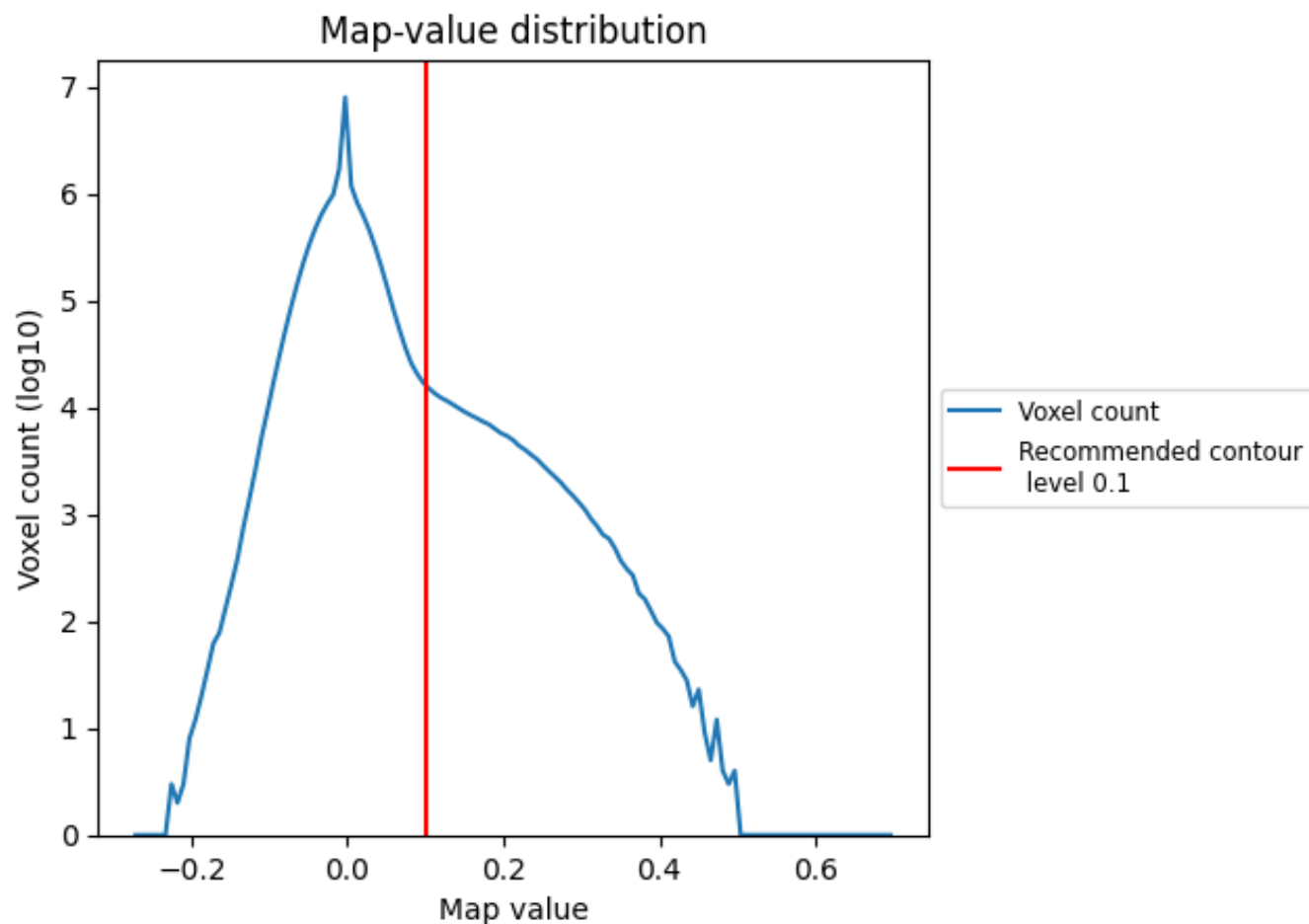
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

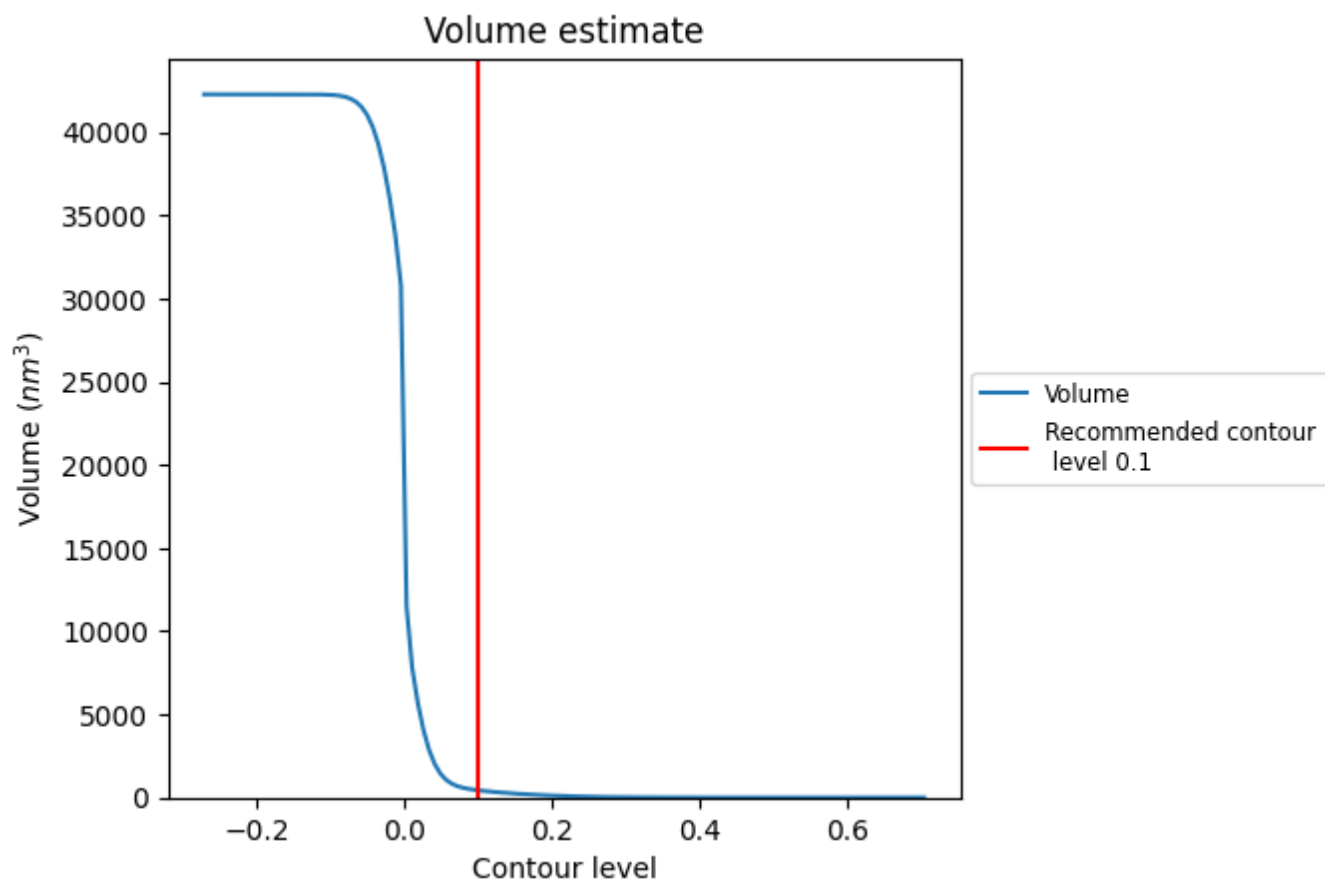
This section contains the results of statistical analysis of the map.

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.

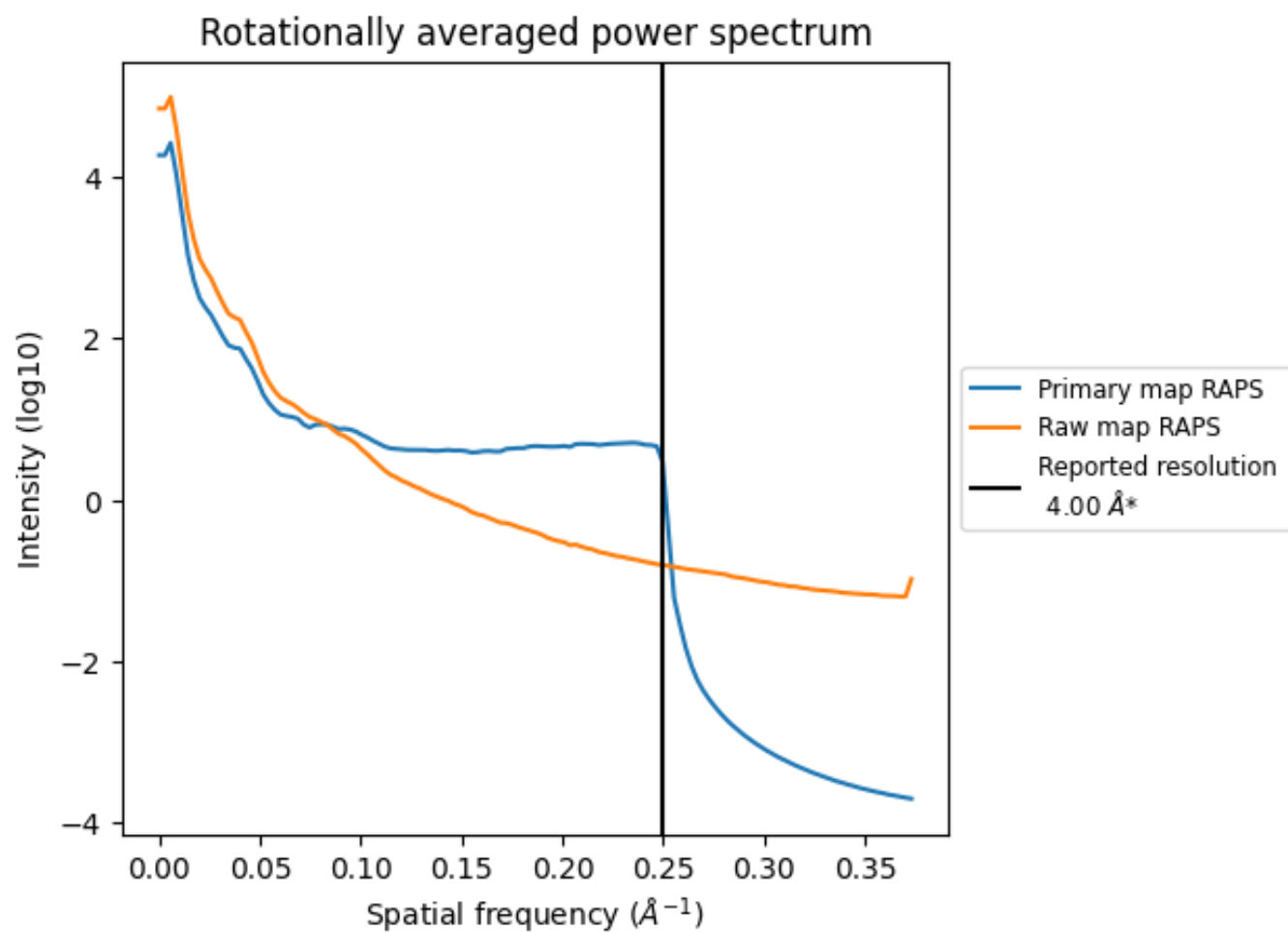
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 435 nm³; this corresponds to an approximate mass of 393 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 ⓘ

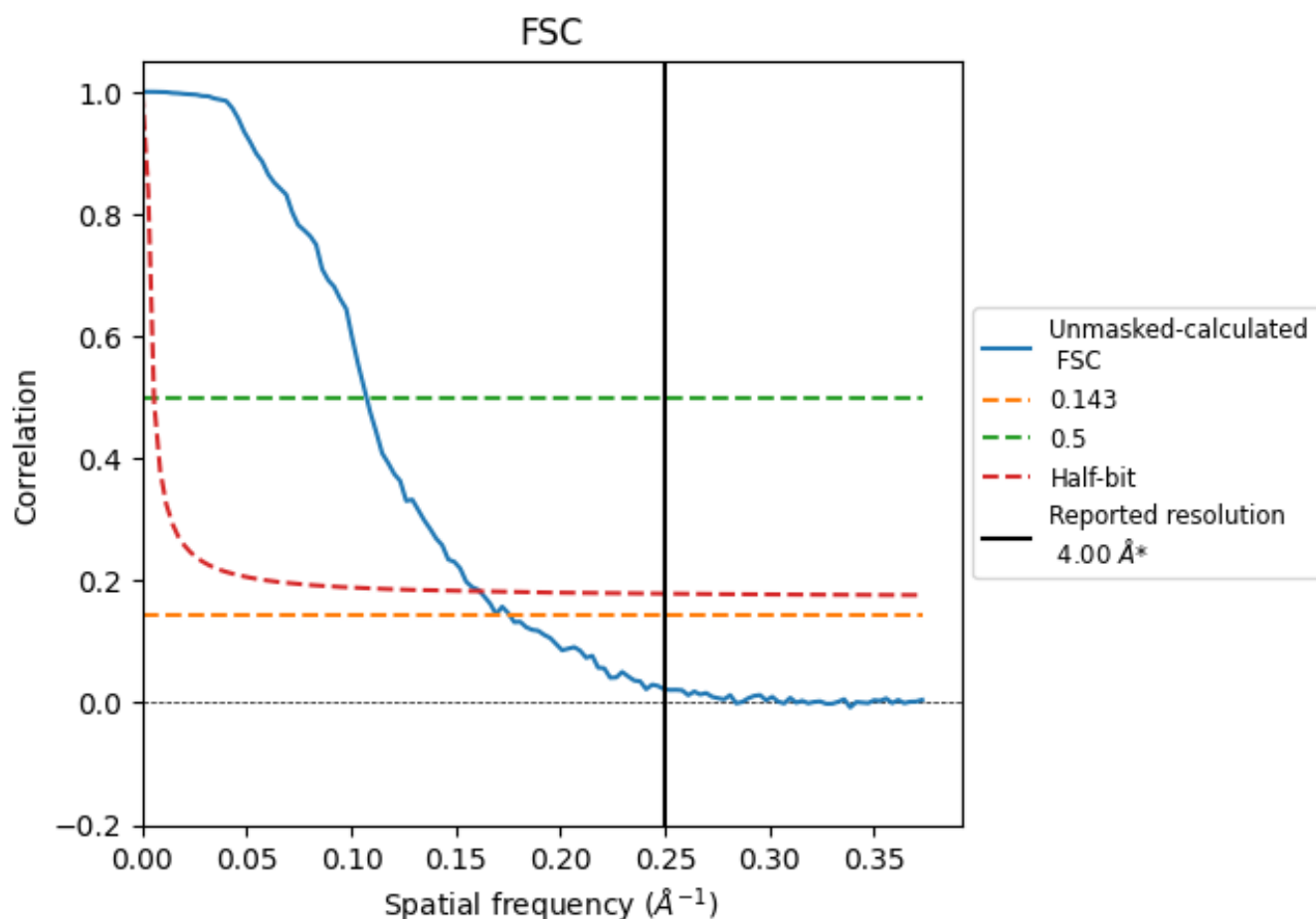


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

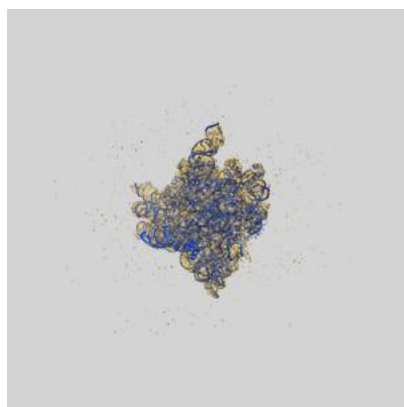
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.69	9.32	6.19

*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 5.69 differs from the reported value 4.0 by more than 10 %

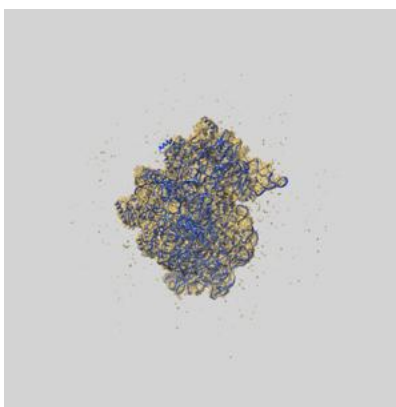
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4080 and PDB model 5LMU. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

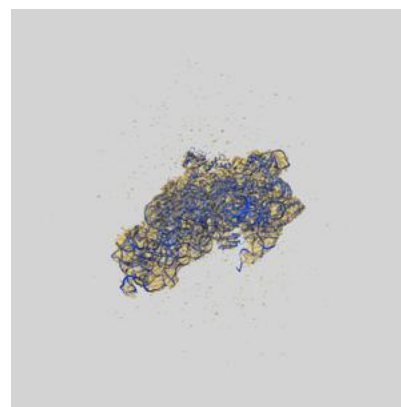
9.1 Map-model overlay [i](#)



X



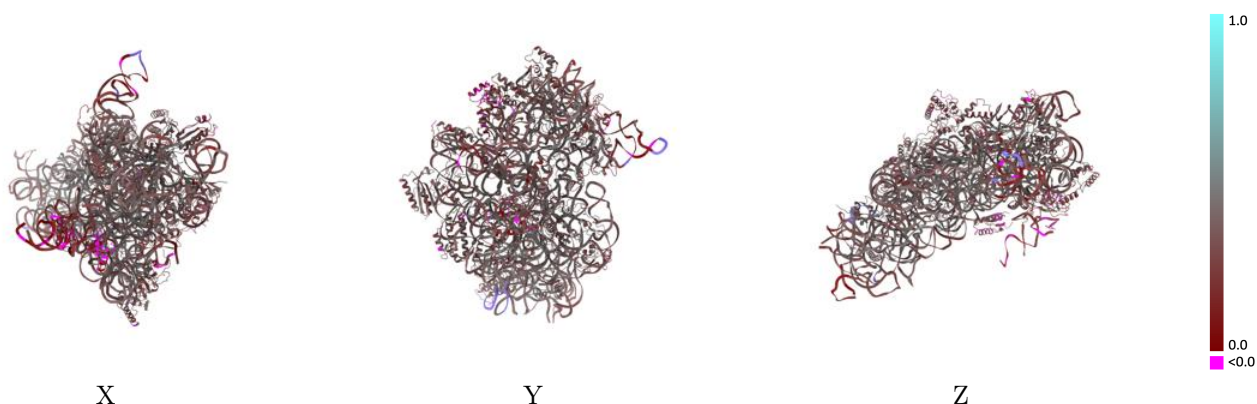
Y



Z

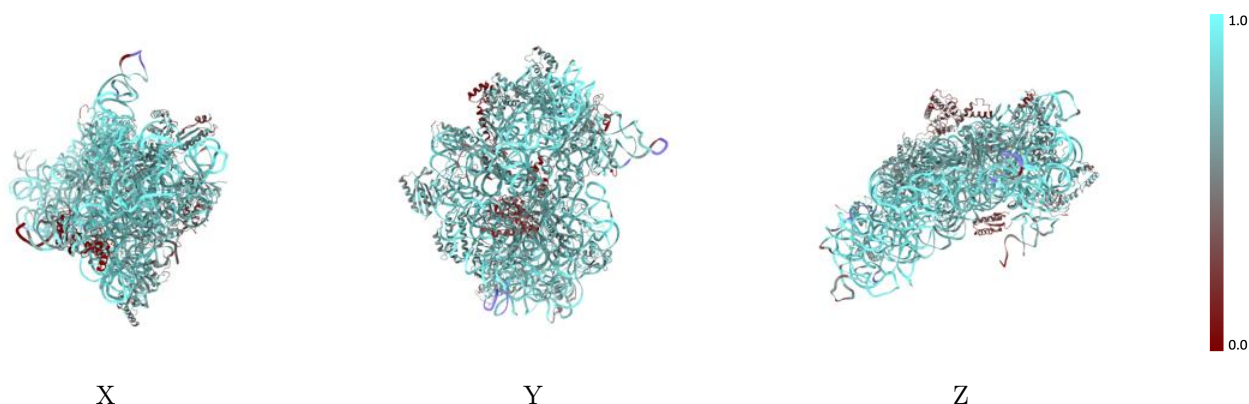
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



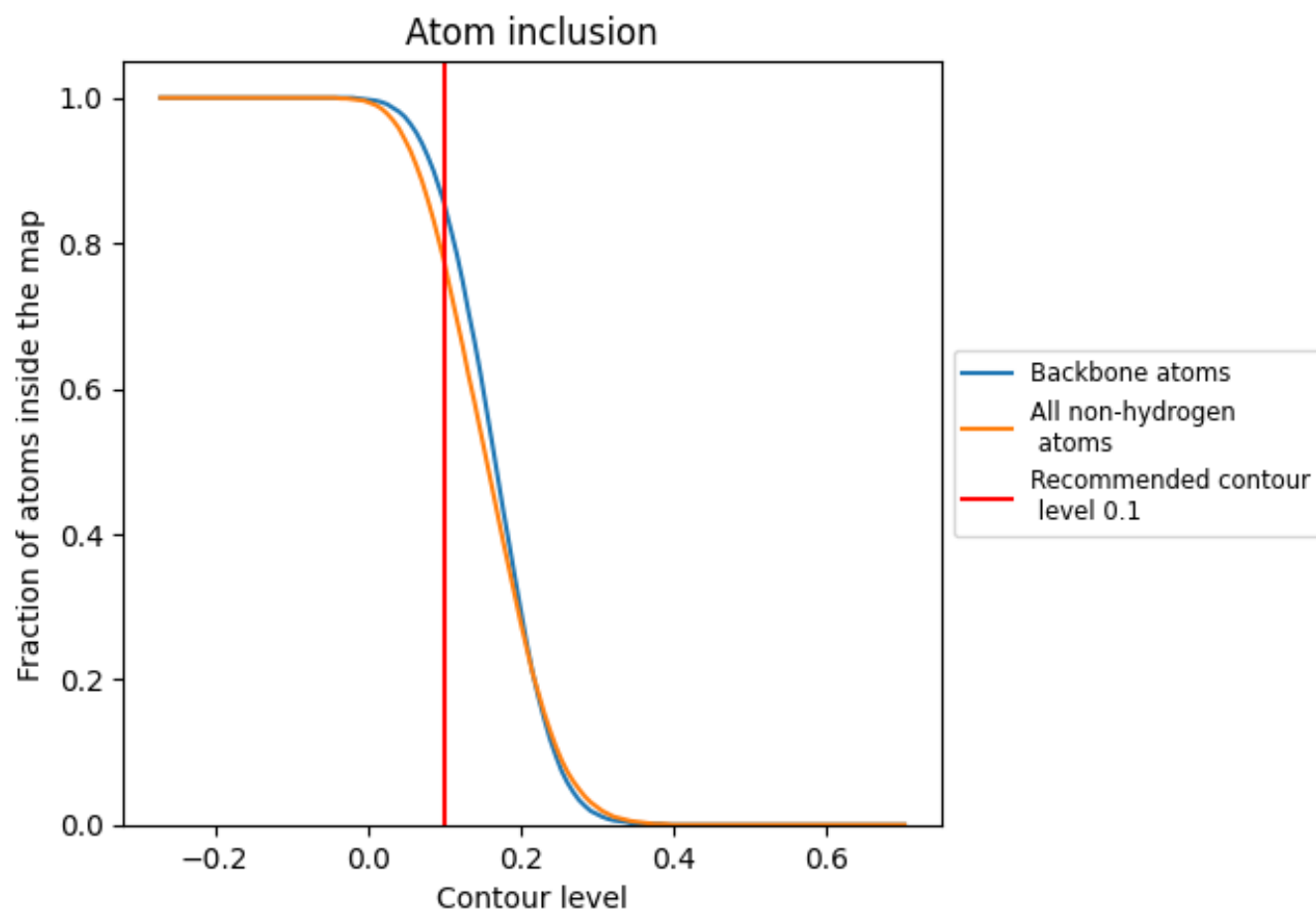
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 78% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7760	 0.3550
A	 0.8820	 0.3710
B	 0.2920	 0.2820
C	 0.6890	 0.3870
D	 0.6780	 0.3620
E	 0.6920	 0.3980
F	 0.6460	 0.3530
G	 0.6610	 0.3550
H	 0.6850	 0.3790
I	 0.6910	 0.3680
J	 0.5780	 0.3320
K	 0.6640	 0.3540
L	 0.6920	 0.4180
M	 0.6860	 0.3420
N	 0.7350	 0.4010
O	 0.6650	 0.3500
P	 0.7420	 0.3990
Q	 0.6980	 0.4060
R	 0.6420	 0.3500
S	 0.6750	 0.3360
T	 0.6620	 0.3310
V	 0.7490	 0.3640
X	 0.1150	 0.1040
Y	 0.7450	 0.2960
Z	 0.7240	 0.1910

