



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 07:16 AM UTC

PDB ID : 8S8G / pdb_00008s8g
EMDB ID : EMD-19804
Title : Structure of a yeast 48S-AUC preinitiation complex in closed conformation
(model py48S-AUC-2.1)
Authors : Villamayor-Belinchon, L.; Sharma, P.; Llacer, J.L.; Hussain, T.
Deposited on : 2024-03-06
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:

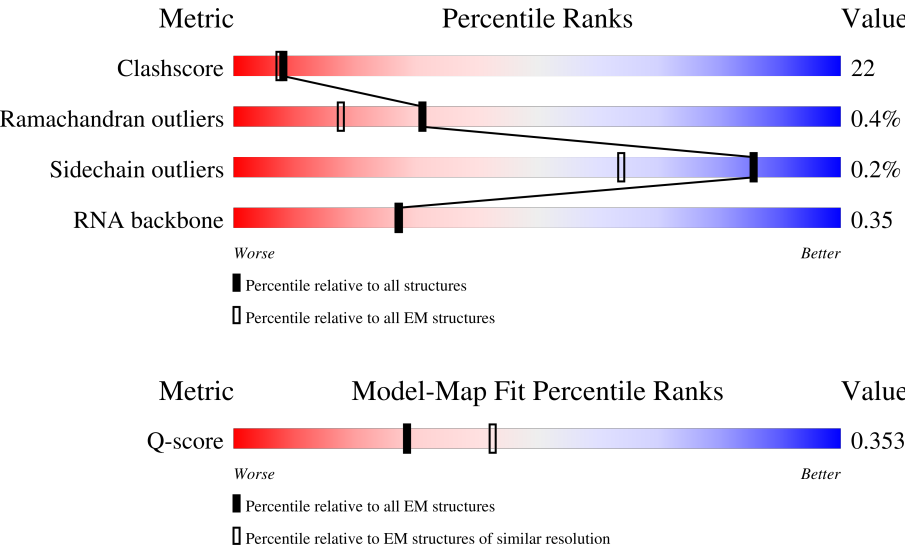
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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.



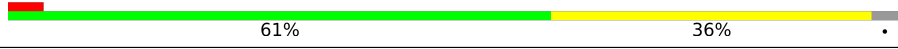
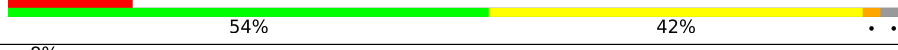
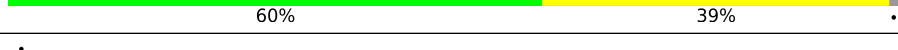
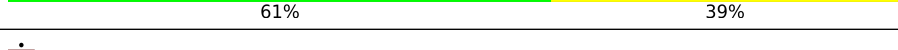
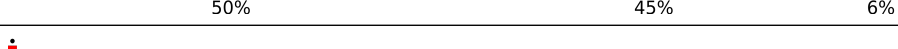
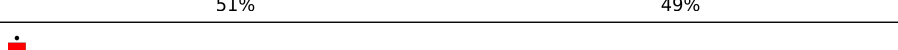
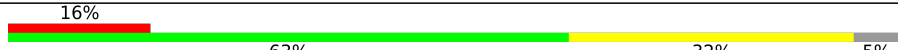
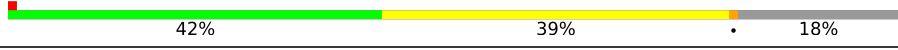
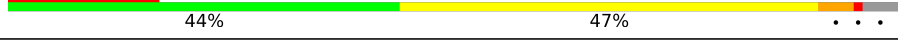
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	2	1798	7% 23% 56% 21%
2	A	254	5% 44% 42% 14%
3	B	255	5% 53% 35% 12%

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Mol	Chain	Length	Quality of chain
4	C	259	
5	E	261	
6	G	236	
7	H	190	
8	I	201	
9	J	188	
10	L	156	
11	N	151	
12	O	137	
13	V	87	
14	W	130	
15	X	145	
16	Y	135	
17	a	119	
18	b	82	
19	e	63	
20	h	25	
21	D	237	
22	F	227	
23	K	106	
24	M	134	
25	P	142	
26	Q	143	
27	R	136	
28	S	146	

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Mol	Chain	Length	Quality of chain
29	T	144	
30	U	117	
31	Z	108	
32	c	67	
33	d	56	
34	f	150	
35	g	326	
36	i	153	
37	3	49	
38	1	75	
39	j	304	
40	k	527	
41	l	285	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
38	M2G	1	26	-	-	X	-
38	5MC	1	48	-	-	X	-

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 86935 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1798	Total	C	N	O	P	0	0
			38190	17073	6722	12597	1798		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	219	Total	C	N	O	S	0	0
			1702	1085	299	316	2		

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	225	Total	C	N	O	S	0	0
			1796	1135	330	328	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	220	Total	C	N	O	S	0	0
			1648	1053	291	300	4		

- Molecule 5 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	260	Total	C	N	O	S	0	0
			2078	1322	393	359	4		

- Molecule 6 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	230	Total	C	N	O	S	0	0
			1832	1146	352	330	4		

- Molecule 7 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	184	Total	C	N	O	0	0
			1483	950	270	263		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	188	Total	C	N	O	S	0	0
			1489	923	300	265	1		

- Molecule 9 is a protein called KLLA0E23673p.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	182	Total	C	N	O	S	0	0
			1471	929	287	254	1		

- Molecule 10 is a protein called KLLA0A10483p.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	155	Total	C	N	O	S	0	0
			1248	798	237	210	3		

- Molecule 11 is a protein called KLLA0F18040p.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	151	Total	C	N	O	S	0	0
			1195	761	224	207	3		

- Molecule 12 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	129	Total	C	N	O	S	0	0
			955	585	191	176	3		

- Molecule 13 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 15 is a protein called KLLA0B11231p.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	X	144	Total	C	N	O	S	0	0
			1119	708	218	191	2		

- Molecule 16 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Y	134	Total	C	N	O	S	0	0
			1061	665	207	189			

- Molecule 17 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	102	Total	C	N	O	S	0	0
			797	492	168	132	5		

- Molecule 18 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	81	Total	C	N	O	S	0	0
			609	379	112	113	5		

- Molecule 19 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	e	60	Total	C	N	O	S	0	0
			472	295	96	80	1		

- Molecule 20 is a protein called 40S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	h	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 21 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D	227	Total	C	N	O	S	0	0
			1774	1126	320	323	5		

- Molecule 22 is a protein called KLLA0D10659p.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	F	206	Total	C	N	O	S	0	0
			1609	1008	298	300	3		

- Molecule 23 is a protein called KLLA0B08173p.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K	96	Total	C	N	O	S	0	0
			809	533	129	146	1		

- Molecule 24 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	M	117	Total	C	N	O		0	0
			885	553	161	171			

- Molecule 25 is a protein called KLLA0F07843p.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	117	Total	C	N	O	S	0	0
			923	592	165	161	5		

- Molecule 26 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Q	141	Total	C	N	O		0	0
			1105	709	204	192			

- Molecule 27 is a protein called KLLA0B01474p.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	R	130	Total	C	N	O	S	0	0
			1033	643	194	193	3		

- Molecule 28 is a protein called KLLA0B01562p.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	145	Total	C	N	O	S	0	0
			1189	739	239	209	2		

- Molecule 29 is a protein called KLLA0A07194p.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	143	Total	C	N	O		0	0
			1110	693	210	207			

- Molecule 30 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	78	Total	C	N	O	S	0	0
			594	376	111	106	1		

- Molecule 32 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	64	Total	C	N	O	S	0	0
			499	308	99	91	1		

- Molecule 33 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	55	Total	C	N	O	S	0	0
			461	289	93	78	1		

- Molecule 34 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	74	Total	C	N	O	S	0	0
			584	374	111	95	4		

- Molecule 35 is a protein called KLLA0E12277p.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	320	Total	C	N	O	S	0	0
			2469	1561	432	471	5		

- Molecule 36 is a protein called Eukaryotic translation initiation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	99	Total	C	N	O	S	0	0
			799	494	153	147	5		

- Molecule 37 is a RNA chain called mRNA (5'-R(P*AP*AP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
37	3	26	Total	C	N	O	P	0	0
			536	242	84	184	26		

- Molecule 38 is a RNA chain called Met-tRNAi.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	1	75	Total	C	N	O	P	0	0
			1639	734	298	531	76		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	267	Total	C	N	O	S	0	0
			2145	1369	358	407	11		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	470	Total	C	N	O	S	0	0
			3596	2279	633	666	18		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 2 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	134	Total	C	N	O	S	0	0
			1083	689	194	193	7		

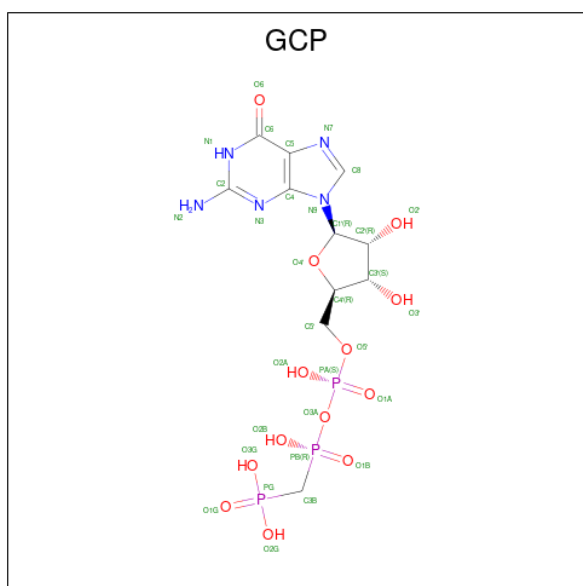
- Molecule 42 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
42	2	113	Total	Mg	0
			113	113	
42	T	1	Total	Mg	0
			1	1	
42	i	1	Total	Mg	0
			1	1	
42	k	1	Total	Mg	0
			1	1	

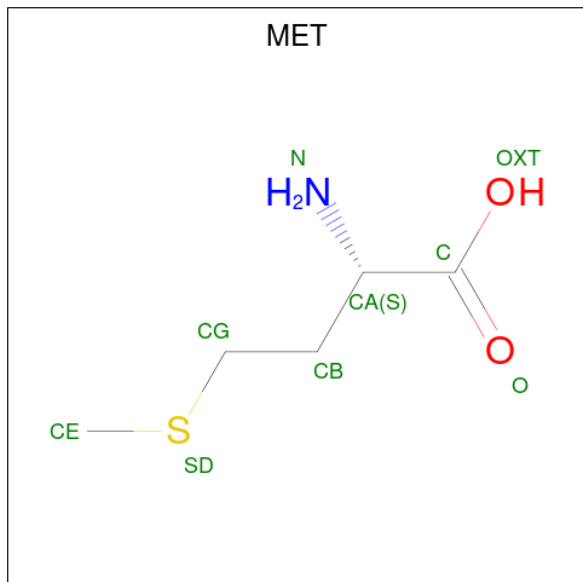
- Molecule 43 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
43	a	1	Total	Zn	0
			1	1	
43	b	1	Total	Zn	0
			1	1	
43	f	1	Total	Zn	0
			1	1	

- Molecule 44 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



- Molecule 45 is METHIONINE (CCD ID: MET) (formula: $C_5H_{11}NO_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
45	k	1	8	5	1	1	1	0

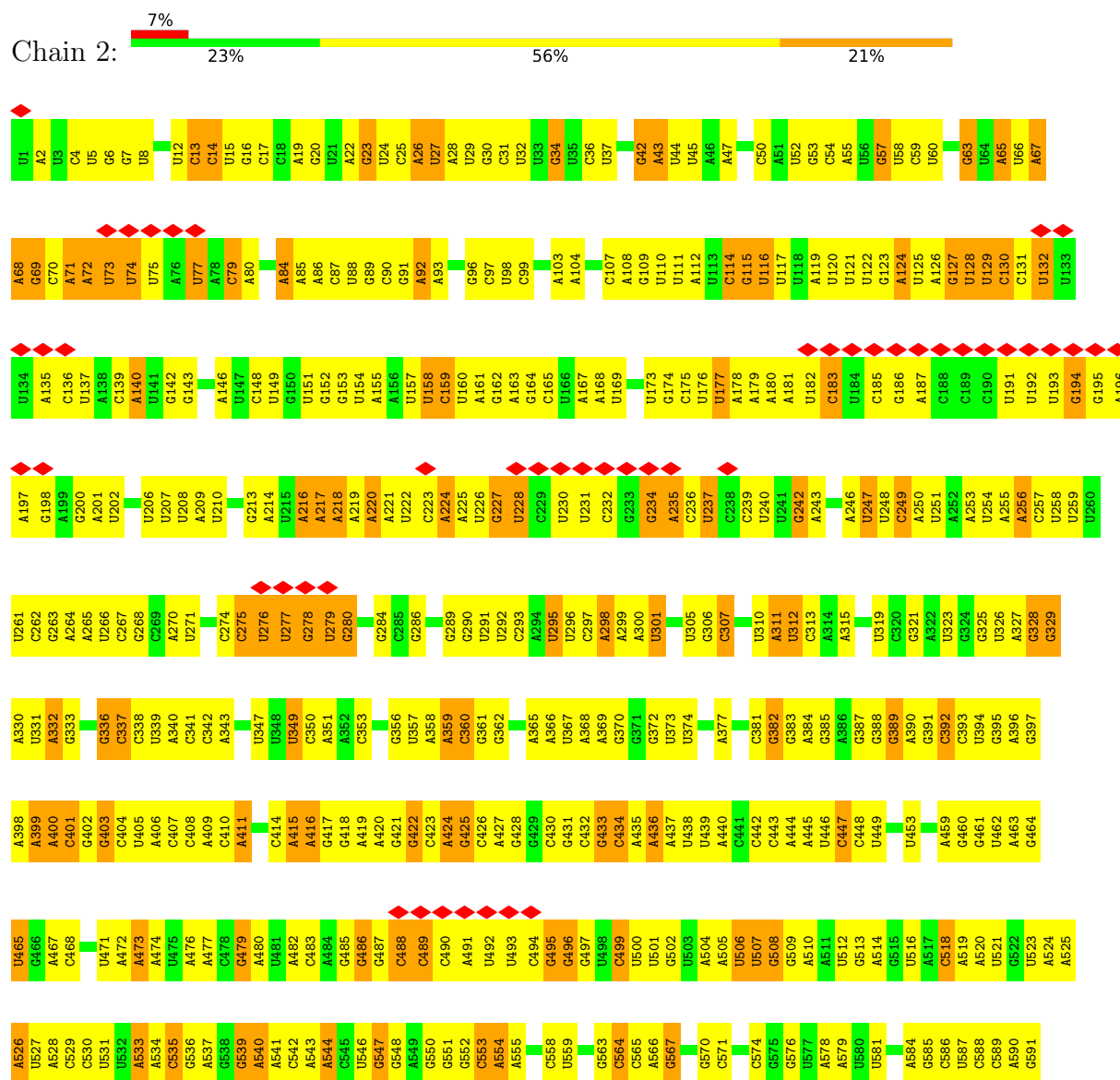
- Molecule 46 is water.

Mol	Chain	Residues	Atoms		AltConf
46	2	3	Total	O	0
			3	3	

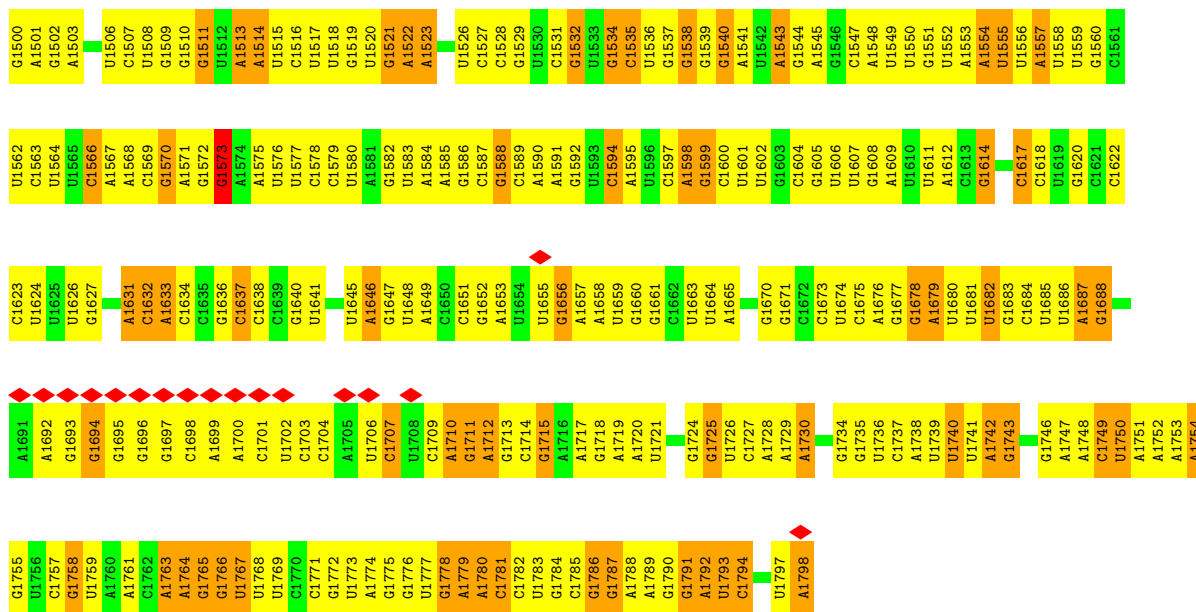
3 Residue-property plots

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: 18S ribosomal RNA



C1439	C1440	U1441	A1442	G1443	A1444		U1447	U1448	C1449	U1450	G1451	G1452	G1453	C1454	C1455	G1456	C1457	A1458	C1459	G1460	C1461	G1462	G1463	G1464	C1465	U1466	C1467	C1468	A1469	C1470	U1471	G1472	A1473	C1474	G1475	G1476	A1477	G1478	C1479	C1480	A1481	G1482	C1483	G1484		A1485	G1486	U1487	U1488	C1489	A1490	A1491	C1492	C1493	C1494	U1495	G1496	G1497	C1498	C1499			
G1370	A1371		U1376			U1379	A1380	G1381	A1382	G1383	G1384	G1385	G1386	C1387	U1388	A1389	U1390	C1391	G1392		U1396	C1397	A1398	A1399	G1400	C1401	C1402	G1403	A1404	U1405	G1406	A1407	U1408	A1409	G1410	U1411	U1412	U1413	G1414	A1415	G1416	G1417	C1418		A1423	C1424	A1425	G1426	U1427	U1428	G1429	U1430	G1431	U1432	G1433	A1434	U1435	G1436	U1437	C1438			
G1307	C1308	U1309	U1310	A1311	A1312	U1313	U1314	C1315	C1316	G1317	A1318	U1319	A1320	C1321	C1322	G1323	A1324	A1325	C1326	G1327	A1328	G1329	A1330	C1331	C1332	U1333	U1334	A1335	A1336	C1337	C1338	U1339	A1340	A1343	A1344	A1345	U1346	A1347	G1348	G1349		G1353	C1354	U1355	G1356	C1357	C1358	A1359	C1360	U1361	U1362	G1363	C1364	U1365	G1366	U1367	U1368	U1369					
A1243	G1244	C1245	U1246	C1247	U1248	U1249	U1250	C1251	U1252	U1253	G1254	A1255	U1256	U1257	C1258	U1259	U1260	U1261	G1262	G1263	G1264	U1265	G1266	C1267	U1268	G1269		C1272	C1273	A1274	U1275	G1276	G1277	C1278	C1279	G1280	U1281	U1282	C1283	U1284	U1285	A1286	G1287	U1288	U1289	G1290	G1291	U1292	G1293		G1296	U1297	G1298	A1299	U1300	U1301	U1302	U1306					
U1180	U1181	A1182	A1183	U1184	U1185		A1188	C1189	B1190	B1191	A1192	A1193	C1194	A1195	C1196	G1197	A1198	G1199	G1200	A1201	A1202	A1203		C1206	A1207	C1208	C1209	C1210	A1211	G1212	U1213	C1214	C1215	A1216	G1217	A1218	C1219	A1220	C1221	A1222	A1223	U1224	A1225	A1226	G1227	A1228	U1229	U1230		A1233	C1234	A1235	G1236	A1237	U1238	U1239	G1240	A1241	G1242				
A1115	U1116	G1117		G1121	C1122	A1123	A1124	G1125	C1126	C1127		A1131	A1132	C1133	U1134	U1135	A1136	A1137		G1140	A1141	A1142	U1143	U1144	G1145	A1146	C1147	U1148	G1149	A1150	A1151	G1152	G1153	C1154	C1155	A1156	G1157	C1158	A1159	C1160	C1161	A1162	G1163	G1164	A1165	G1166	U1167	G1168	G1169	A1170	C1171	C1172	C1173	U1174	G1175	C1176	G1177	C1178	C1179				
U1048	G1049	U1050	U1051	G1052	U1053	U1054	U1055	U1056	U1057	C1058	U1059		U1062	G1063	A1064	G1065	C1066	C1067	A1068		C1071	G1072	G1073	C1074	A1075	C1076	C1077	U1078	U1079	A1080	C1081	G1082	A1083	G1084	A1085	A1086	A1087		A1090	A1091	A1092		C1095	U1096	U1097	U1098	G1099	G1100	G1101	U1102	U1103	U1104	G1106	G1107	G1108		A1112	G1113	U1114				
G979		A982	G983	G984	G985	G986	A987	U988	C989	G990	A991	A992	G993	A994	U995	A996	A997	U998		A1002	U1003		C1006	G1007	G941	C942	A943	U944	U945	U946	G947	C948	C949	A950	A951	G952	G953	A954	C955	U956	U957	U958	U959	U960	C961	A962	U963	G1033	G1034	A965	A966	U967	U968	U969	A970	A971	A972	A973	C974	G975	U976	A977	A978
U915	U916	A917	U918	U919	U920	G921	A922	G923	A924	A925	U926	U927	A928		U931	A932	C933	U934		A938	A939		G940	G941	C942	A943	U944	U945	U946	G947	C948	C949	A950	A951	G952	G953	A954	C955	U956	U957	U958	U959	U960	C961	A962	U963	G1033	G1034	A965	A966	U967	U968	U969	A970	A971	A972	A973	C974	G975	U976	A977	A978	
U853	A854	A855	U856	U857	A858	U859	U860	A861	A862	U863	U864	G865	G866	G867	A868	C869	G870	G871	U872		G875	G876	G877	G878	C879	G880	U881	U882	U883	G884	U885	A886	U887	G888	G889	U890	U891	U892	U893	G894	U895	U896	A897	G898	U899	G900	G901	U902	G903	A904	A905	A906		C909	U910	U911	G912	G913					
C785	G786	A787	A788	U789	U790	U791	U792	U793	U794		U798	U799	G800	G801	A802	A803		U806	U807	G808	G809	A810	U811	U812	A813	G814	G815	A816	C817	G818	U819	U820	U821	G822	G823	U824	U825	C826	U827	A828	U829	U830	U831	U832	G833	U834	U835	G836	G837		U840	C841	U842	A843	G844	U845	A846		A849				
U658	G659	A660	C661	U662	U663	U664	A665	U666		U667	U668	C669	G670	C671	G672	C673	A674	C675		U679	U680	U681	U682	U683	U684	U685	C686	U687	G688		U691	C692	U693	U694	U695	U696	U697	U698	U699	C700	U701	G702	U703	C704	U705	U706	U707	U708	C709	U710	G711	U712	U713	C714	U715	C716	C717	U718	U719	G720			
U592	A593	G594	C595	G596	U597	A598	U599	A600	U601	U602		A605	G606	U607	G608	G609	U610	U611	G612	C613		A618	A619	A620	A621	A622	G623	C624	U625	C626	G627	U628	A629		U632		A635	C636	U637	U638	U639	G640	G641	G642	U643	C644	U645	G646	G647	U648	U649	G650	U651	C652	C653	G654	G655	U656	C657				



• Molecule 2: Small ribosomal subunit protein uS2

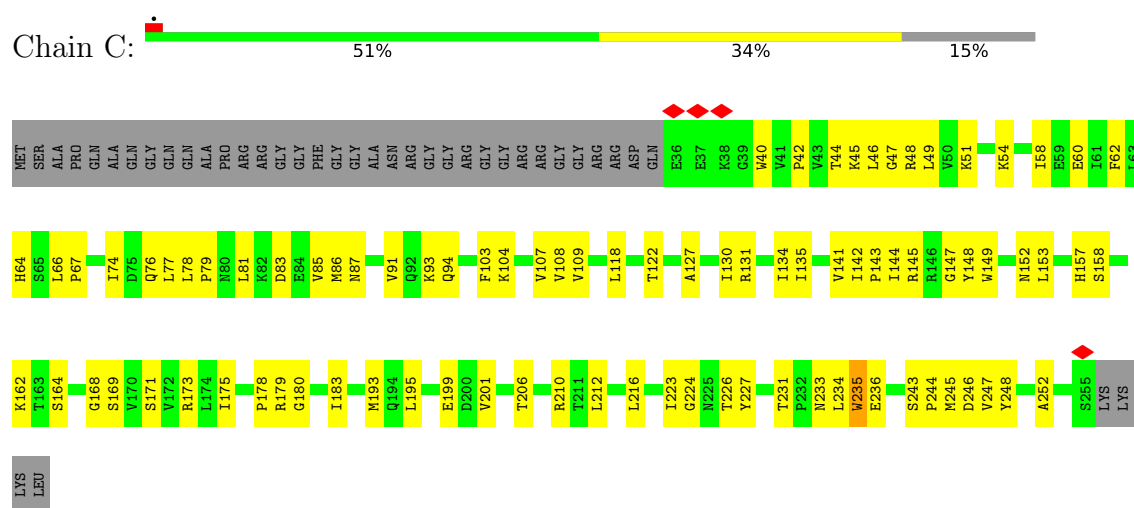


• Molecule 3: Small ribosomal subunit protein eS1

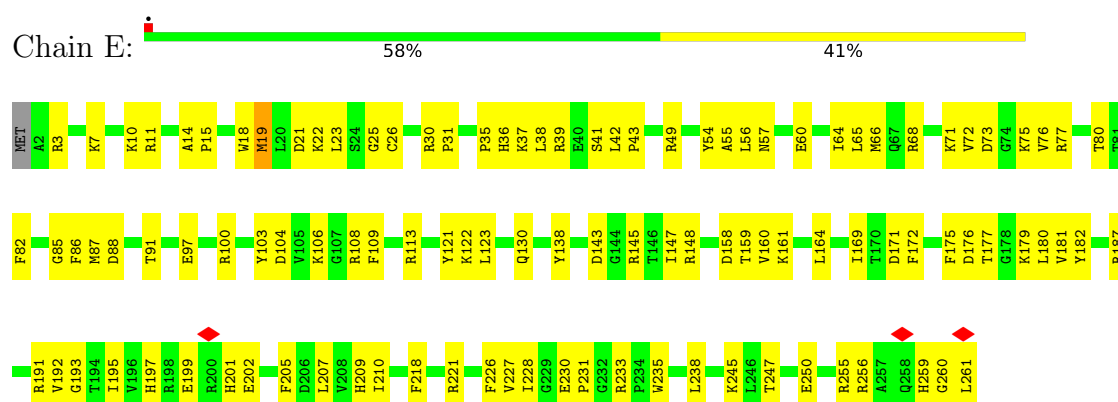


ILE
LEU
GLU
THR
VAL

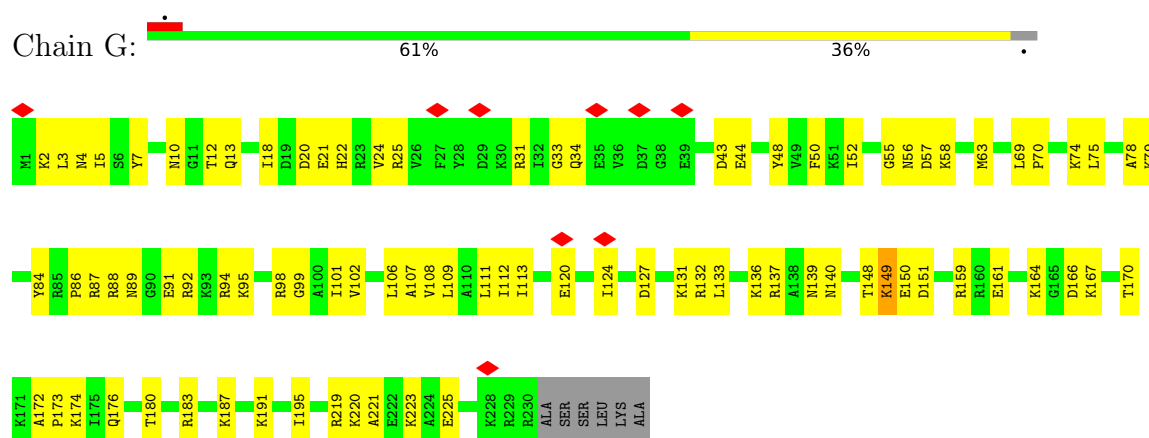
• Molecule 4: Small ribosomal subunit protein uS5



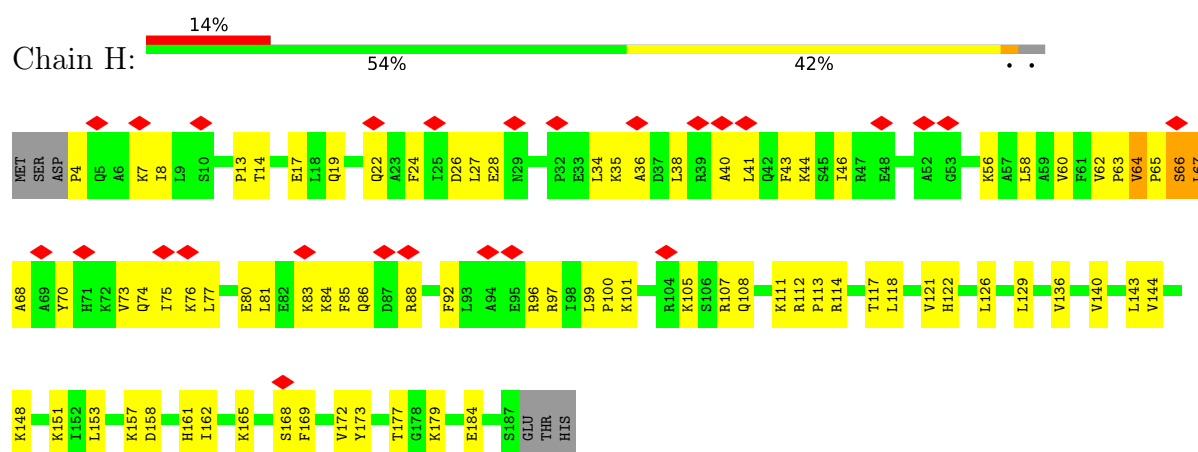
• Molecule 5: 40S ribosomal protein S4



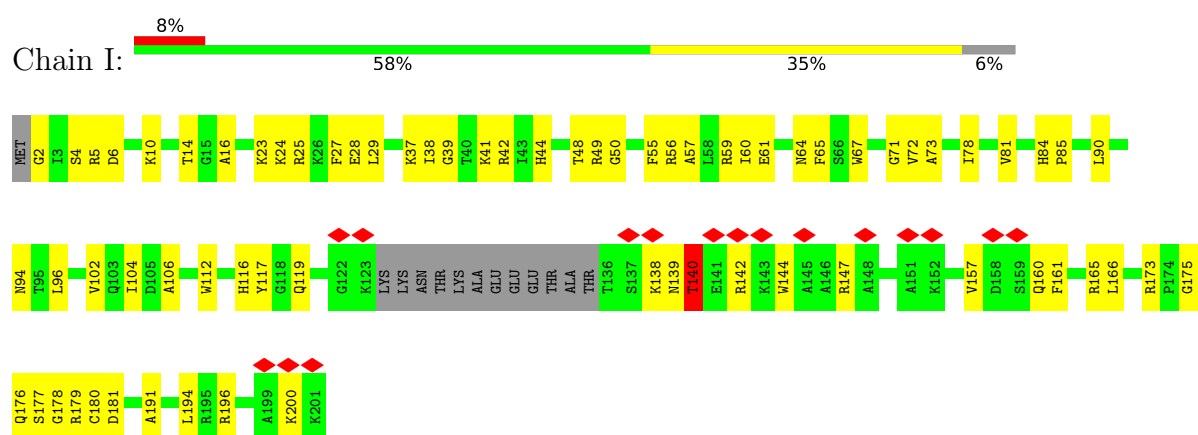
• Molecule 6: Small ribosomal subunit protein eS6



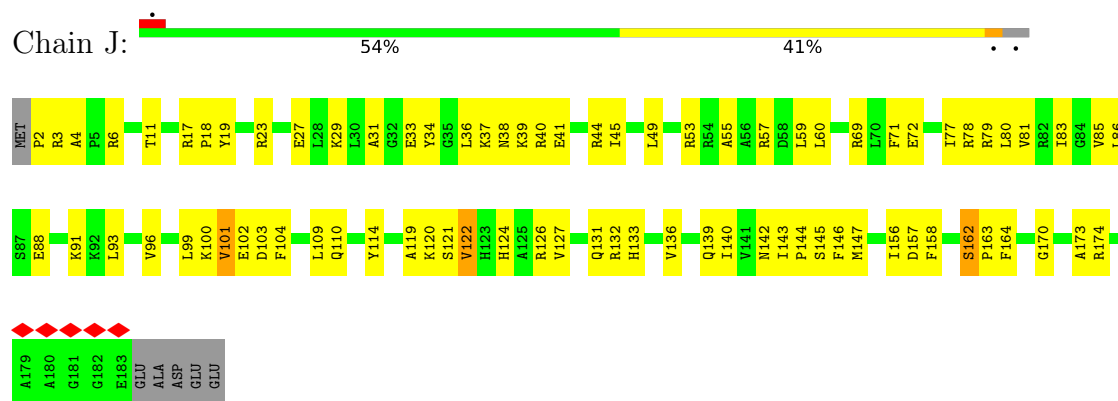
• Molecule 7: 40S ribosomal protein S7



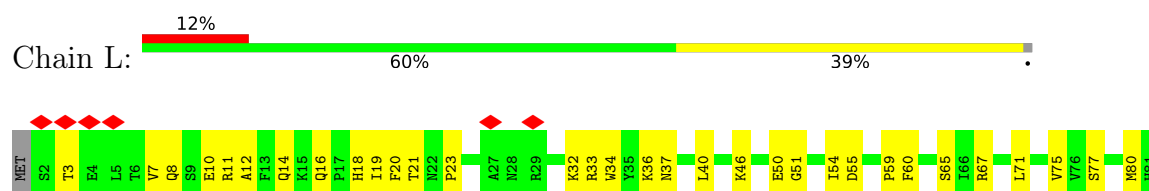
• Molecule 8: 40S ribosomal protein S8

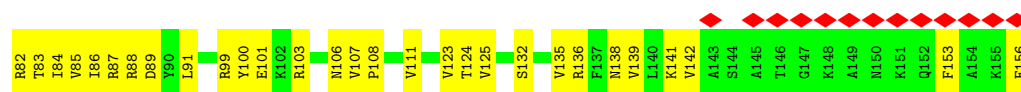


• Molecule 9: KLLA0E23673p

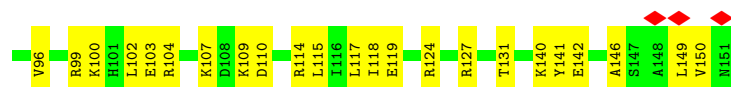


• Molecule 10: KLLA0A10483p

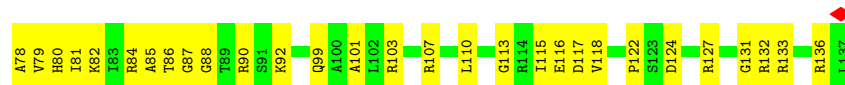
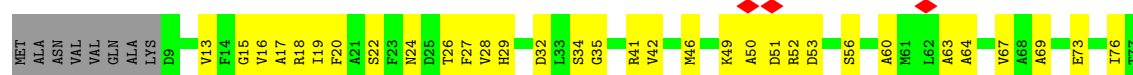




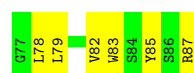
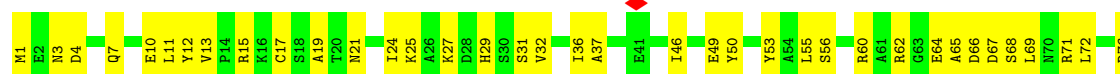
• Molecule 11: KLLA0F18040p



• Molecule 12: Small ribosomal subunit protein uS11



• Molecule 13: 40S ribosomal protein S21



• Molecule 14: Small ribosomal subunit protein uS8



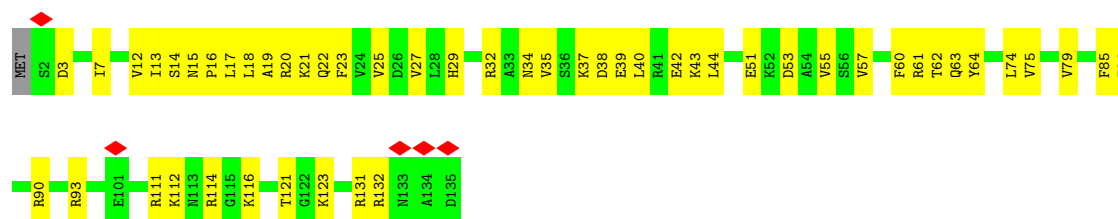
• Molecule 15: KLLA0B11231p

Chain X: 



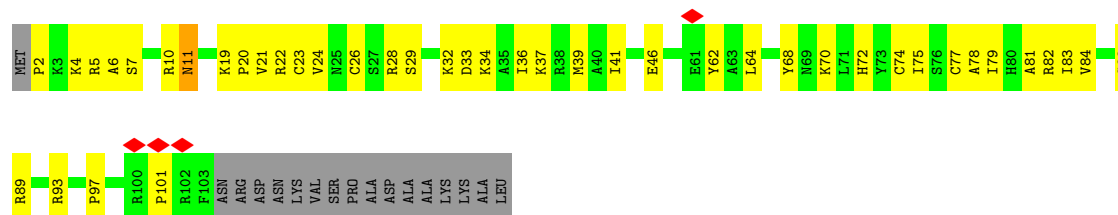
- Molecule 16: 40S ribosomal protein S24

Chain Y: 



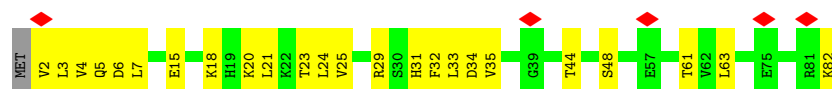
- Molecule 17: 40S ribosomal protein S26

Chain a: 



- Molecule 18: 40S ribosomal protein S27

Chain b: 



- Molecule 19: 40S ribosomal protein S30

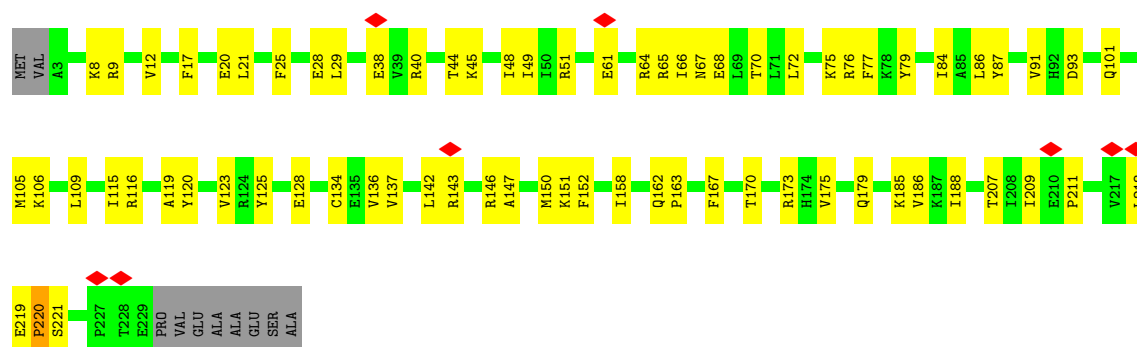
Chain e: 



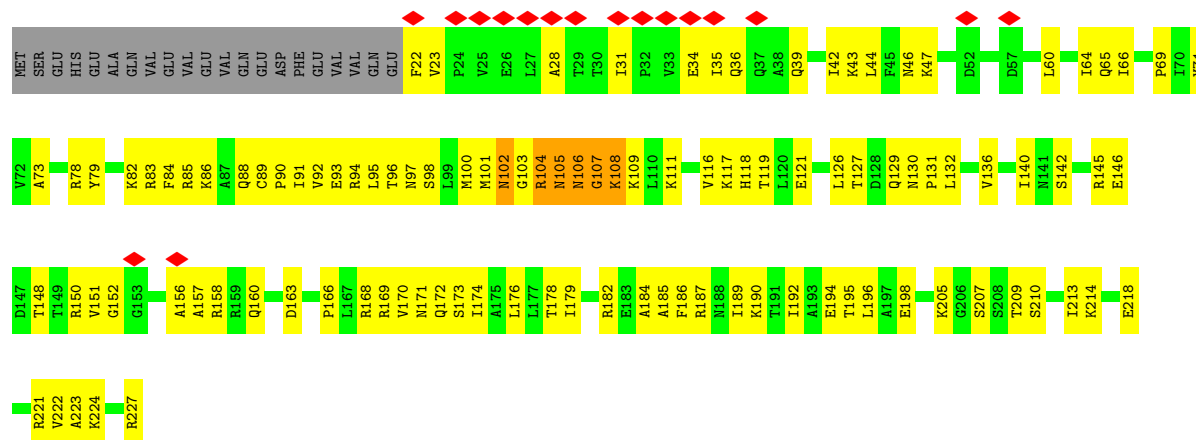
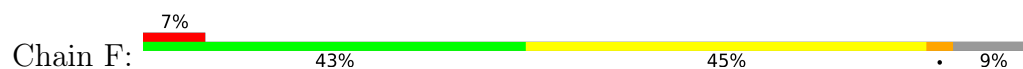
- Molecule 20: 40S ribosomal protein L41-A

Chain h: 

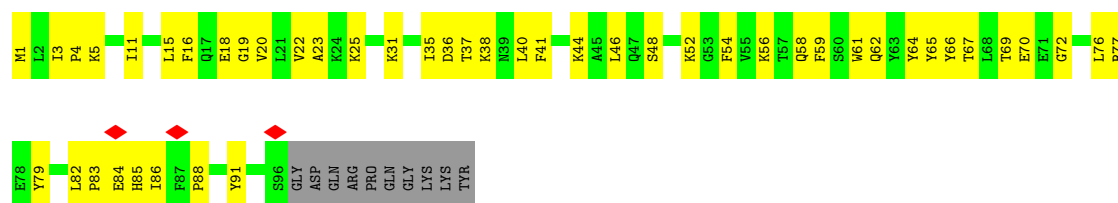
- Molecule 21: 40S ribosomal protein S3



- Molecule 22: KLLA0D10659p

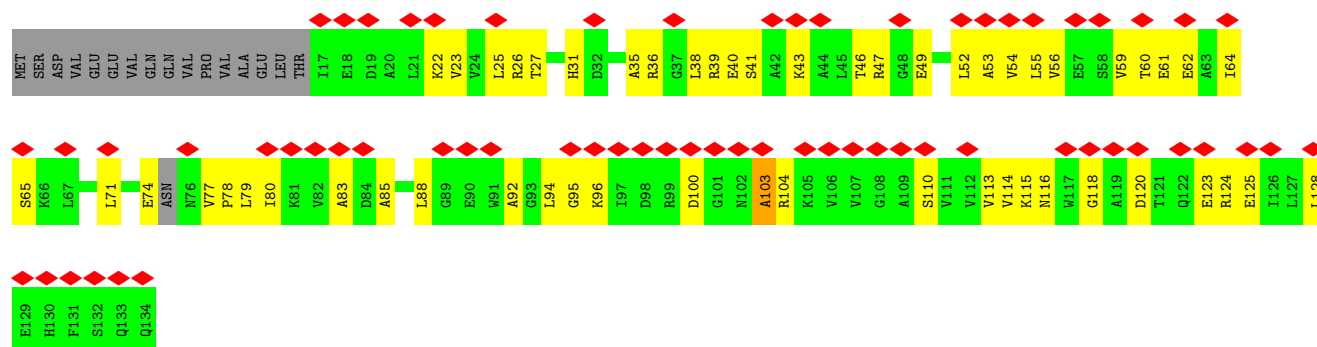


- Molecule 23: KLLA0B08173p

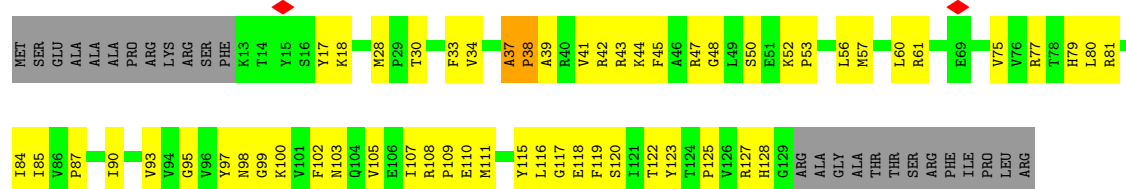


- Molecule 24: 40S ribosomal protein S12

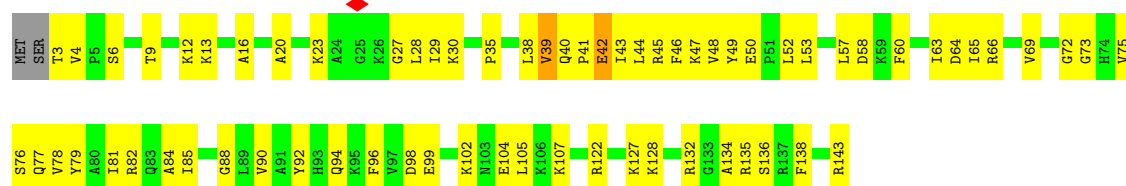




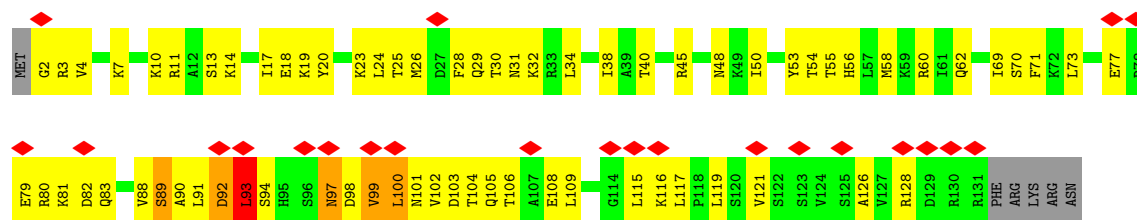
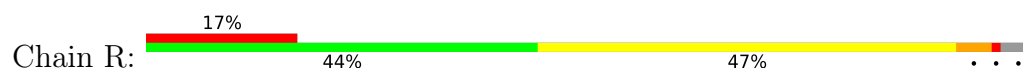
• Molecule 25: KLLA0F07843p



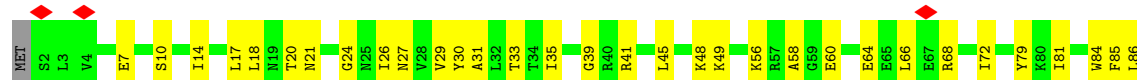
• Molecule 26: Small ribosomal subunit protein uS9

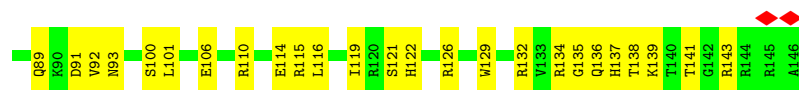


• Molecule 27: KLLA0B01474p

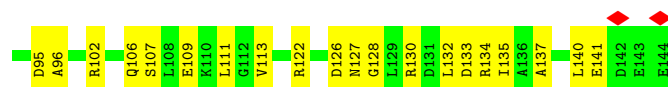


• Molecule 28: KLLA0B01562p

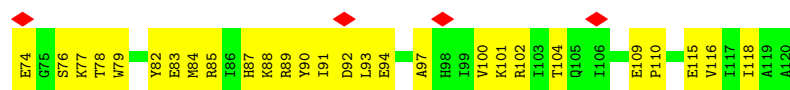
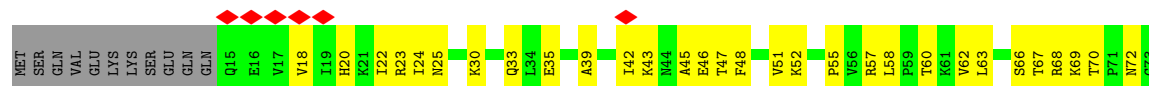




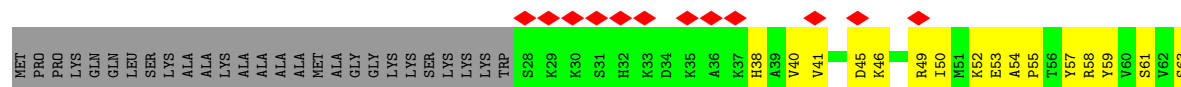
• Molecule 29: KLLA0A07194p



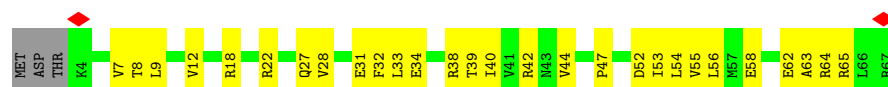
• Molecule 30: Small ribosomal subunit protein uS10



• Molecule 31: 40S ribosomal protein S25



• Molecule 32: Small ribosomal subunit protein eS28

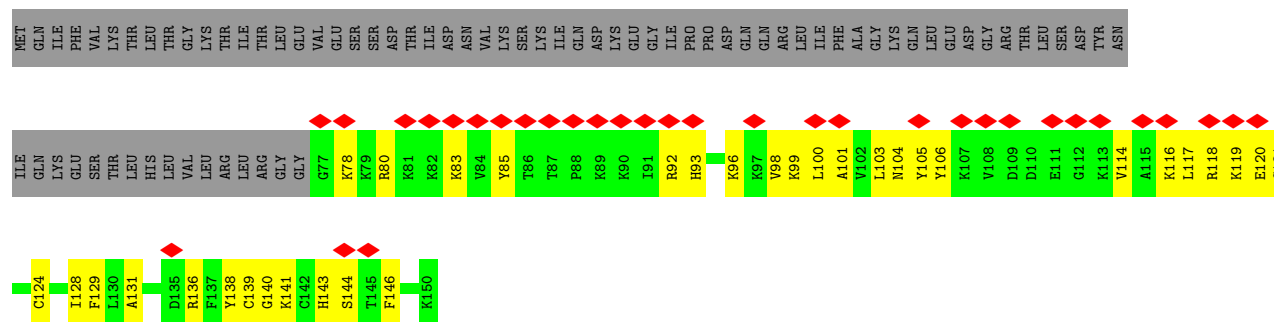
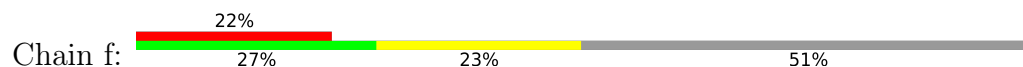


• Molecule 33: Small ribosomal subunit protein uS14

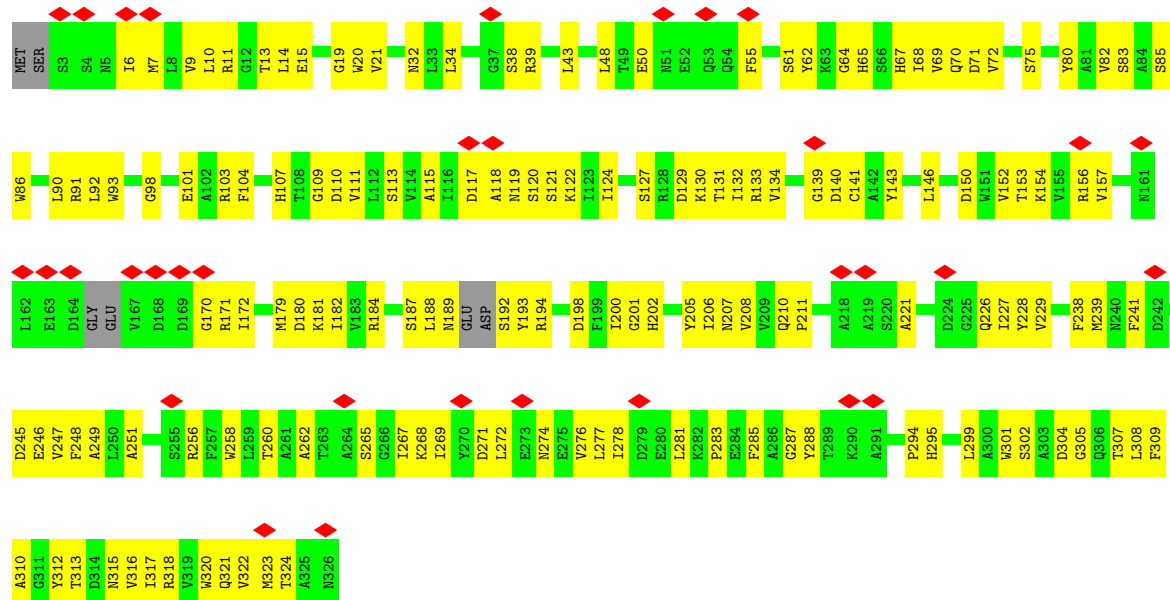




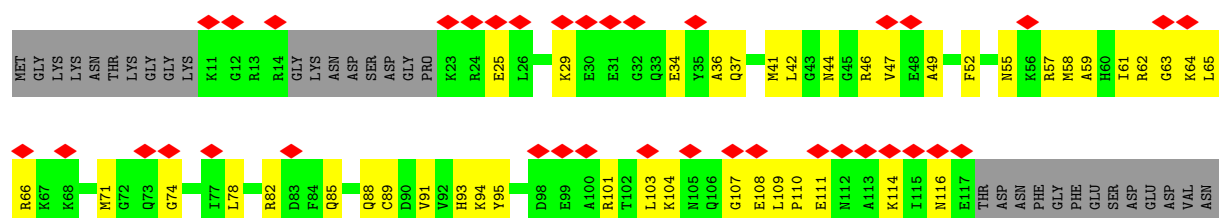
• Molecule 34: Small ribosomal subunit protein eS31

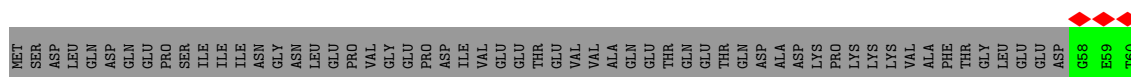


• Molecule 35: KLLA0E12277p



• Molecule 36: Eukaryotic translation initiation factor 1A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30016	Depositor
Resolution determination method	FSC 3 SIGMA CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.506	Depositor
Minimum map value	-0.346	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	402.0, 402.0, 402.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: 5MC, B8N, H2U, ZN, 7MG, 2MG, MA6, T6A, 1MG, PSU, M2G, 1MA, GCP, MG, RIA

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	2	0.14	0/42410	0.35	0/66079
2	A	0.19	0/1742	0.46	0/2383
3	B	0.20	0/1820	0.48	0/2448
4	C	0.23	0/1678	0.53	1/2277 (0.0%)
5	E	0.19	0/2122	0.48	2/2861 (0.1%)
6	G	0.18	0/1855	0.43	0/2479
7	H	0.26	0/1507	0.56	0/2028
8	I	0.31	1/1515 (0.1%)	0.50	0/2029
9	J	0.24	0/1495	0.55	1/2001 (0.0%)
10	L	0.17	0/1276	0.46	0/1718
11	N	0.21	0/1218	0.49	0/1638
12	O	0.22	0/966	0.51	0/1297
13	V	0.23	0/696	0.46	0/938
14	W	0.27	0/1039	0.52	0/1399
15	X	0.18	0/1137	0.45	0/1516
16	Y	0.17	0/1075	0.41	0/1433
17	a	0.26	0/810	0.59	1/1087 (0.1%)
18	b	0.20	0/619	0.48	0/837
19	e	0.20	0/480	0.50	0/640
20	h	0.23	0/234	0.49	0/300
21	D	0.24	0/1800	0.49	0/2421
22	F	0.19	0/1628	0.62	5/2198 (0.2%)
23	K	0.16	0/831	0.45	0/1123
24	M	0.17	0/891	0.58	0/1201
25	P	0.29	0/942	0.71	5/1269 (0.4%)
26	Q	0.28	0/1125	0.55	0/1510
27	R	0.31	0/1044	0.60	0/1402
28	S	0.19	0/1208	0.49	0/1624
29	T	0.19	0/1129	0.40	0/1520
30	U	0.26	0/857	0.56	0/1158
31	Z	0.16	0/603	0.41	0/814
32	c	0.17	0/501	0.45	0/673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.23	0/473	0.53	0/629
34	f	0.17	0/597	0.49	0/795
35	g	0.19	0/2523	0.50	0/3434
36	i	0.17	0/807	0.43	0/1072
37	3	0.10	0/595	0.28	0/920
38	1	0.25	0/1529	0.58	3/2376 (0.1%)
39	j	0.22	0/2177	0.55	0/2931
40	k	0.19	0/3657	0.48	0/4946
41	l	0.16	0/1099	0.47	1/1469 (0.1%)
All	All	0.19	1/91710 (0.0%)	0.43	19/132873 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	I	140	THR	N-CA	5.45	1.53	1.46

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	F	104	ARG	N-CA-C	-15.04	94.19	112.54
4	C	235	TRP	N-CA-C	10.00	122.17	111.28
22	F	107	GLY	N-CA-C	-8.56	100.92	111.45
25	P	37	ALA	CA-C-N	7.83	127.85	119.78
25	P	37	ALA	C-N-CA	7.83	127.85	119.78
22	F	102	ASN	N-CA-C	-7.50	101.04	111.39
38	1	27	C	N1-C1'-C2'	-7.19	101.21	112.00
5	E	19	MET	CB-CG-SD	-6.99	91.72	112.70
9	J	164	PHE	N-CA-C	-6.51	103.62	113.51
25	P	38	PRO	N-CA-C	6.05	120.83	111.21
22	F	106	ASN	CA-C-N	-6.04	116.72	121.86
22	F	106	ASN	C-N-CA	-6.04	116.72	121.86
38	1	27	C	C3'-C2'-O2'	5.86	119.49	110.70
41	l	238	THR	N-CA-C	5.76	117.56	111.28
17	a	97	PRO	CA-N-CD	-5.54	104.25	112.00
38	1	27	C	C2'-C3'-O3'	-5.50	105.45	113.70
25	P	48	GLY	CA-C-N	-5.39	115.11	121.90
25	P	48	GLY	C-N-CA	-5.39	115.11	121.90
5	E	19	MET	CA-CB-CG	5.18	124.46	114.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	38190	0	19211	1349	0
2	A	1702	0	1695	98	0
3	B	1796	0	1874	83	0
4	C	1648	0	1727	98	0
5	E	2078	0	2157	102	0
6	G	1832	0	1919	90	0
7	H	1483	0	1579	86	0
8	I	1489	0	1504	77	0
9	J	1471	0	1554	81	0
10	L	1248	0	1311	60	0
11	N	1195	0	1263	56	0
12	O	955	0	987	64	0
13	V	687	0	682	45	0
14	W	1021	0	1056	71	0
15	X	1119	0	1198	51	0
16	Y	1061	0	1111	52	0
17	a	797	0	835	52	0
18	b	609	0	629	17	0
19	e	472	0	508	21	0
20	h	233	0	284	14	0
21	D	1774	0	1855	60	0
22	F	1609	0	1679	120	0
23	K	809	0	810	43	0
24	M	885	0	917	43	0
25	P	923	0	960	70	0
26	Q	1105	0	1170	69	0
27	R	1033	0	1082	69	0
28	S	1189	0	1211	58	0
29	T	1110	0	1124	55	0
30	U	845	0	913	53	0
31	Z	594	0	590	37	0
32	c	499	0	536	27	0
33	d	461	0	448	31	0
34	f	584	0	601	47	0
35	g	2469	0	2403	134	0
36	i	799	0	804	41	0
37	3	536	0	277	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	1	1639	0	852	88	0
39	j	2145	0	2216	151	0
40	k	3596	0	3713	154	0
41	l	1083	0	1123	36	0
42	2	113	0	0	0	0
42	T	1	0	0	0	0
42	i	1	0	0	0	0
42	k	1	0	0	0	0
43	a	1	0	0	0	0
43	b	1	0	0	0	0
43	f	1	0	0	0	0
44	k	32	0	14	8	0
45	k	8	0	8	2	0
46	2	3	0	0	0	0
All	All	86935	0	68390	3374	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 22.

All (3374) 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)
8:I:140:THR:HG23	8:I:144:TRP:CZ3	1.47	1.48
38:1:26:M2G:HM22	38:1:44:A:N1	1.44	1.31
3:B:8:ARG:O	3:B:9:LEU:CD1	1.80	1.29
39:j:74:LEU:HB2	39:j:89:ARG:NH1	1.46	1.28
22:F:103:GLY:HA3	22:F:106:ASN:OD1	1.28	1.25
22:F:98:SER:O	22:F:101:MET:HE2	1.07	1.22
3:B:8:ARG:O	3:B:9:LEU:HD12	1.04	1.17
8:I:140:THR:CG2	8:I:144:TRP:CZ3	2.32	1.12
22:F:98:SER:O	22:F:101:MET:CE	2.03	1.05
22:F:104:ARG:HG3	22:F:105:ASN:ND2	1.71	1.05
1:2:1547:C:OP1	25:P:38:PRO:CG	2.06	1.03
1:2:1547:C:OP1	25:P:38:PRO:HG2	1.57	1.03
34:f:105:TYR:C	34:f:117:LEU:HD23	1.84	1.02
38:1:20:A:N6	38:1:57:G:N2	2.08	1.01
1:2:485:G:H1	1:2:500:U:H3	1.07	1.00
1:2:1266:G:H1	1:2:1440:U:H3	1.04	1.00
40:k:113:LYS:HE2	44:k:601:GCP:O3G	1.62	1.00
34:f:105:TYR:O	34:f:117:LEU:HD23	1.63	0.98
1:2:1586:G:H1	1:2:1606:U:H3	1.11	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:f:106:TYR:HE2	34:f:116:LYS:HE2	1.25	0.97
5:E:26:CYS:SG	9:J:2:PRO:O	2.22	0.97
38:1:26:M2G:CM2	38:1:44:A:N1	2.27	0.96
3:B:141:ALA:HB1	3:B:207:LEU:HD11	1.46	0.95
39:j:74:LEU:HB2	39:j:89:ARG:CZ	1.95	0.95
22:F:101:MET:HE1	22:F:178:THR:CG2	1.98	0.94
1:2:1293:G:H1	1:2:1302:U:H3	1.14	0.94
1:2:570:G:H5''	15:X:114:LYS:HE2	1.50	0.94
39:j:74:LEU:CB	39:j:89:ARG:NH1	2.29	0.94
39:j:72:VAL:HG11	39:j:89:ARG:HB3	1.49	0.94
22:F:103:GLY:CA	22:F:106:ASN:OD1	2.17	0.92
14:W:24:GLN:NE2	18:b:5:GLN:OE1	2.02	0.92
38:1:27:C:HO2'	38:1:28:A:H8	1.14	0.92
23:K:77:ARG:HD3	23:K:84:GLU:HA	1.51	0.92
4:C:64:HIS:HA	13:V:15:ARG:HH12	1.35	0.91
1:2:1213:U:HO2'	33:d:2:ALA:N	1.69	0.90
1:2:855:A:N7	7:H:96:ARG:NH1	2.18	0.90
1:2:965:A:OP2	11:N:124:ARG:NH1	2.04	0.90
22:F:163:ASP:OD2	32:c:42:ARG:NH1	2.06	0.89
23:K:56:LYS:HZ3	23:K:58:GLN:HB2	1.38	0.88
39:j:198:ILE:HG21	40:k:335:GLY:HA2	1.54	0.88
22:F:100:MET:HE3	22:F:107:GLY:O	1.74	0.88
1:2:520:A:N3	16:Y:34:ASN:ND2	2.21	0.88
38:1:20:A:N6	38:1:57:G:H21	1.71	0.88
35:g:316:VAL:O	35:g:318:ARG:NH1	2.07	0.88
12:O:50:ALA:O	12:O:52:ARG:NH1	2.06	0.87
1:2:1782:C:H41	20:h:5:TRP:HE1	1.23	0.87
4:C:143:PRO:HG2	4:C:227:TYR:HE2	1.36	0.87
19:e:38:LEU:HD21	19:e:42:ARG:HH21	1.38	0.87
39:j:74:LEU:HB2	39:j:89:ARG:HH12	1.39	0.87
1:2:1480:C:H4'	26:Q:77:GLN:HE22	1.37	0.87
11:N:110:ASP:OD2	11:N:114:ARG:NH1	2.07	0.87
39:j:205:LEU:HD13	40:k:330:ILE:HB	1.54	0.86
8:I:140:THR:HG23	8:I:144:TRP:HZ3	1.09	0.86
10:L:3:THR:HG21	10:L:7:VAL:HG23	1.58	0.86
1:2:28:A:N1	1:2:597:U:C4	2.44	0.86
22:F:101:MET:HE3	22:F:182:ARG:HH22	1.39	0.86
4:C:40:TRP:HE1	4:C:51:LYS:HB2	1.40	0.86
1:2:1564:U:H5''	28:S:39:GLY:H	1.39	0.86
10:L:101:GLU:OE2	15:X:13:ARG:NH1	2.09	0.86
36:i:62:ARG:NH1	36:i:63:GLY:O	2.09	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1:9:1MG:H4'	38:1:45:U:O2'	1.76	0.85
34:f:106:TYR:CE2	34:f:116:LYS:HE2	2.11	0.85
36:i:71:MET:HE1	36:i:91:VAL:HG21	1.56	0.85
26:Q:94:GLN:HB2	26:Q:102:LYS:HD3	1.56	0.85
17:a:11:ASN:O	17:a:11:ASN:ND2	2.09	0.85
1:2:1653:A:N6	1:2:1743:G:O2'	2.10	0.85
1:2:296:U:OP1	5:E:37:LYS:NZ	2.10	0.84
1:2:1290:G:H1	1:2:1323:G:H22	1.22	0.84
1:2:7:G:N7	4:C:210:ARG:NH2	2.25	0.84
1:2:1247:C:OP2	34:f:93:HIS:ND1	2.11	0.84
1:2:1661:G:H1	1:2:1736:U:H3	1.24	0.84
1:2:66:U:H3	6:G:173:PRO:HD3	1.40	0.84
21:D:105:MET:HE1	21:D:119:ALA:HA	1.59	0.84
1:2:995:U:H3	1:2:1007:G:H1	1.19	0.83
25:P:38:PRO:HA	25:P:42:ARG:HB2	1.57	0.83
4:C:235:TRP:CD1	14:W:68:ARG:HD2	2.12	0.83
1:2:1238:U:O2	1:2:1245:C:N4	2.12	0.83
7:H:62:VAL:HG12	7:H:64:VAL:H	1.44	0.82
38:1:74:C:H4'	38:1:75:C:H5'	1.61	0.82
40:k:105:THR:HG22	40:k:215:LEU:HD22	1.62	0.82
38:1:50:U:O4	38:1:64:RIA:N6	2.10	0.82
1:2:1277:G:N2	1:2:1431:G:O6	2.11	0.82
39:j:71:ALA:HB1	39:j:85:LEU:HD21	1.61	0.82
3:B:144:ARG:HB3	3:B:206:PRO:HB2	1.62	0.82
22:F:101:MET:HE1	22:F:178:THR:HG21	1.61	0.81
23:K:82:LEU:HD12	23:K:83:PRO:HD2	1.62	0.81
39:j:72:VAL:CG1	39:j:89:ARG:HE	1.93	0.81
1:2:92:A:H5''	1:2:93:A:H5''	1.60	0.81
25:P:105:VAL:HG11	25:P:119:PHE:HB3	1.63	0.81
10:L:108:PRO:HB2	10:L:135:VAL:HG12	1.61	0.81
22:F:36:GLN:HG3	26:Q:57:LEU:HD12	1.61	0.81
10:L:3:THR:OG1	10:L:82:ARG:NH1	2.13	0.81
25:P:39:ALA:H	25:P:42:ARG:HB3	1.45	0.81
1:2:983:G:H1	1:2:1016:U:H5	1.27	0.81
35:g:258:TRP:HB3	35:g:269:ILE:HD11	1.63	0.81
1:2:1386:A:OP2	27:R:32:LYS:NZ	2.15	0.80
40:k:148:TYR:HB3	40:k:183:TYR:HB3	1.64	0.80
1:2:544:A:H2'	19:e:31:LYS:HD2	1.62	0.80
39:j:74:LEU:CB	39:j:89:ARG:HH12	1.93	0.80
1:2:893:U:H2'	1:2:894:G:H8	1.46	0.80
31:Z:61:SER:H	31:Z:64:VAL:HB	1.44	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:3:LEU:HB3	2:A:7:PHE:HD2	1.47	0.80
24:M:54:VAL:HG22	24:M:80:ILE:HB	1.64	0.80
34:f:136:ARG:HH22	34:f:138:TYR:HB2	1.45	0.80
1:2:299:A:H2'	1:2:300:A:C8	2.16	0.79
1:2:1365:C:O2'	29:T:7:ARG:NH1	2.15	0.79
35:g:43:LEU:HD11	35:g:83:SER:HB3	1.63	0.79
6:G:219:ARG:HH12	6:G:223:LYS:HB2	1.48	0.79
1:2:1330:A:OP1	27:R:45:ARG:NH1	2.15	0.79
12:O:53:ASP:HB2	12:O:56:SER:HB2	1.62	0.79
1:2:1787:G:OP2	12:O:132:ARG:NH2	2.16	0.79
4:C:180:GLY:O	9:J:53:ARG:NH1	2.16	0.79
25:P:50:SER:HB3	25:P:53:PRO:HD2	1.65	0.79
1:2:1531:C:OP2	31:Z:77:ARG:NH2	2.16	0.79
21:D:49:ILE:HG22	21:D:87:TYR:HB2	1.63	0.79
9:J:23:ARG:NH1	9:J:27:GLU:OE1	2.14	0.78
40:k:113:LYS:CE	44:k:601:GCP:O3G	2.30	0.78
30:U:63:LEU:O	30:U:83:GLU:HA	1.84	0.78
1:2:763:G:OP2	9:J:79:ARG:NH2	2.16	0.78
1:2:1594:C:OP1	33:d:16:LYS:NZ	2.15	0.78
19:e:43:ARG:HG3	19:e:54:ARG:HH22	1.49	0.78
40:k:359:ILE:HB	40:k:371:LYS:HB3	1.65	0.78
34:f:116:LYS:HB3	34:f:129:PHE:CZ	2.19	0.78
8:I:104:ILE:O	8:I:165:ARG:HA	1.83	0.78
19:e:43:ARG:HG3	19:e:54:ARG:NH2	1.97	0.78
12:O:84:ARG:NH1	12:O:85:ALA:O	2.15	0.78
1:2:905:A:O2'	39:j:53:ARG:NH1	2.16	0.78
22:F:101:MET:HE1	22:F:178:THR:HG23	1.64	0.78
1:2:1541:A:N6	1:2:1566:C:O2'	2.17	0.78
1:2:497:G:H1'	1:2:499:C:H41	1.48	0.77
29:T:137:ALA:O	29:T:141:GLU:HG3	1.82	0.77
1:2:460:G:OP1	9:J:2:PRO:HG2	1.85	0.77
1:2:1227:G:HO2'	34:f:100:LEU:H	1.32	0.77
1:2:959:U:H5'	11:N:55:ARG:HD3	1.65	0.77
24:M:46:THR:OG1	34:f:116:LYS:NZ	2.17	0.77
1:2:566:A:OP1	15:X:70:LYS:NZ	2.17	0.77
1:2:976:A:H62	1:2:1023:U:H3	1.31	0.77
36:i:71:MET:HE2	36:i:94:LYS:HB2	1.66	0.76
38:1:10:2MG:N2	38:1:25:C:O2	2.17	0.76
1:2:761:G:N2	1:2:762:A:N7	2.32	0.76
1:2:1486:G:H3'	1:2:1513:A:H61	1.51	0.76
1:2:990:G:N2	1:2:1013:G:O6	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1547:C:OP1	25:P:38:PRO:CB	2.34	0.76
1:2:890:A:H2'	1:2:891:A:H8	1.51	0.76
1:2:1152:G:OP1	17:a:82:ARG:NH2	2.18	0.76
1:2:1592:G:OP2	1:2:1594:C:N4	2.19	0.76
22:F:96:THR:HG22	22:F:116:VAL:HG11	1.67	0.76
7:H:144:VAL:HG13	14:W:49:GLU:OE2	1.84	0.76
26:Q:41:PRO:HG2	26:Q:44:LEU:HD12	1.67	0.76
40:k:351:ASP:HB2	40:k:377:ILE:HD12	1.68	0.76
1:2:952:G:H2'	1:2:953:G:H8	1.49	0.76
39:j:160:PRO:HG2	39:j:166:LEU:HD11	1.66	0.76
1:2:1396:U:H3'	1:2:1397:C:H5'	1.66	0.75
5:E:23:LEU:HD21	9:J:6:ARG:HD3	1.68	0.75
38:l:62:C:H2'	38:l:63:G:H8	1.51	0.75
11:N:45:LEU:HD12	11:N:49:GLN:HG3	1.66	0.75
11:N:146:ALA:HA	11:N:149:LEU:HB2	1.68	0.75
22:F:100:MET:CE	22:F:107:GLY:O	2.34	0.75
1:2:13:C:H1'	1:2:1298:G:H21	1.52	0.75
1:2:1591:A:H2'	1:2:1592:G:H8	1.49	0.75
35:g:71:ASP:OD2	35:g:154:LYS:NZ	2.19	0.75
39:j:195:TYR:OH	40:k:371:LYS:NZ	2.16	0.75
1:2:1785:C:H2'	1:2:1786:G:H8	1.51	0.75
26:Q:60:PHE:HB2	26:Q:63:ILE:HG13	1.69	0.75
39:j:204:ALA:HB2	39:j:254:VAL:HG21	1.66	0.75
40:k:330:ILE:HG23	40:k:333:LEU:HD12	1.68	0.75
1:2:627:G:N1	1:2:969:A:OP2	2.15	0.75
5:E:199:GLU:OE2	5:E:209:HIS:ND1	2.20	0.75
14:W:50:PHE:HB3	14:W:63:VAL:HG23	1.68	0.75
18:b:20:LYS:HG3	18:b:21:LEU:HD12	1.67	0.75
30:U:68:ARG:HD2	30:U:70:THR:HG22	1.69	0.75
4:C:149:TRP:O	14:W:97:ARG:NH2	2.19	0.75
1:2:246:A:H4'	10:L:36:LYS:HZ2	1.51	0.75
1:2:863:U:OP2	14:W:57:ARG:NH2	2.19	0.74
2:A:20:ALA:HB2	2:A:172:LEU:HD13	1.69	0.74
7:H:177:THR:HG23	7:H:179:LYS:H	1.52	0.74
34:f:105:TYR:O	34:f:117:LEU:CD2	2.34	0.74
35:g:90:LEU:HB2	35:g:104:PHE:HB2	1.70	0.74
1:2:922:A:H2'	1:2:923:A:C8	2.21	0.74
22:F:101:MET:HB2	22:F:182:ARG:NH2	2.02	0.74
23:K:56:LYS:NZ	23:K:58:GLN:HB2	2.03	0.74
39:j:33:TYR:HB3	39:j:45:MET:HE1	1.67	0.74
39:j:127:TYR:HB3	39:j:132:TRP:CZ3	2.22	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1358:C:H5''	29:T:134:ARG:HH12	1.53	0.74
9:J:80:LEU:HB3	9:J:86:LEU:HD23	1.69	0.74
1:2:479:G:H1	1:2:507:U:H3	1.35	0.74
9:J:99:LEU:HD13	9:J:104:PHE:HZ	1.52	0.74
35:g:71:ASP:OD2	35:g:156:ARG:NH2	2.21	0.74
38:1:3:C:H4'	39:j:185:ARG:HH22	1.51	0.74
3:B:5:LYS:NZ	3:B:7:LYS:HA	2.03	0.74
1:2:1682:U:O2	1:2:1715:G:O6	2.06	0.74
5:E:15:PRO:HB3	5:E:39:ARG:HD3	1.70	0.74
14:W:30:SER:OG	14:W:58:SER:O	2.05	0.74
28:S:138:THR:HA	28:S:141:THR:HG22	1.68	0.74
1:2:1021:C:H4'	1:2:1124:A:H61	1.52	0.73
26:Q:39:VAL:HG22	26:Q:45:ARG:HE	1.51	0.73
1:2:1357:G:O2'	29:T:133:ASP:OD2	2.06	0.73
10:L:123:VAL:HG22	10:L:142:VAL:HG12	1.69	0.73
11:N:83:GLU:HG2	11:N:84:ILE:HD12	1.69	0.73
22:F:86:LYS:HG2	22:F:94:ARG:HH22	1.53	0.73
3:B:5:LYS:C	3:B:7:LYS:H	1.95	0.73
1:2:870:G:H2'	1:2:871:G:C8	2.22	0.73
1:2:1661:G:N2	1:2:1736:U:O2	2.19	0.73
21:D:76:ARG:O	21:D:76:ARG:NH1	2.21	0.73
21:D:40:ARG:HE	30:U:110:PRO:HD3	1.53	0.73
1:2:1547:C:OP1	25:P:38:PRO:HB2	1.88	0.73
3:B:114:VAL:HA	3:B:142:PHE:HE2	1.51	0.73
30:U:52:LYS:HB3	30:U:93:LEU:HD23	1.71	0.73
35:g:202:HIS:HD2	35:g:206:ILE:HG12	1.53	0.73
3:B:106:THR:OG1	12:O:116:GLU:OE1	2.05	0.73
35:g:13:THR:HG22	35:g:318:ARG:HG3	1.70	0.73
39:j:7:ARG:N	39:j:40:ASP:OD1	2.21	0.73
1:2:1780:MA6:H4'	20:h:1:MET:HE1	1.71	0.73
1:2:1560:G:OP1	29:T:89:ARG:NH2	2.21	0.72
35:g:171:ARG:HA	35:g:188:LEU:O	1.89	0.72
1:2:760:A:N1	1:2:789:U:C4	2.57	0.72
4:C:118:LEU:HD11	4:C:216:LEU:HB3	1.70	0.72
11:N:49:GLN:HA	11:N:52:VAL:HG12	1.69	0.72
39:j:213:THR:O	39:j:217:GLN:NE2	2.21	0.72
8:I:140:THR:HG23	8:I:144:TRP:CH2	2.18	0.72
1:2:383:G:H2'	1:2:384:A:C8	2.24	0.72
1:2:1085:A:O2'	1:2:1297:U:O4	2.06	0.72
1:2:1477:A:H2'	1:2:1478:G:H8	1.54	0.72
9:J:34:TYR:O	9:J:110:GLN:NE2	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:S:115:ARG:HD2	28:S:119:ILE:HD11	1.70	0.72
1:2:949:C:H4'	11:N:104:ARG:HH12	1.54	0.72
7:H:27:LEU:HB3	7:H:34:LEU:HD21	1.71	0.72
8:I:57:ALA:HB2	8:I:178:GLY:HA2	1.70	0.72
2:A:55:GLU:HB3	13:V:79:LEU:HD12	1.70	0.72
40:k:146:LYS:NZ	40:k:168:LYS:O	2.22	0.72
1:2:142:G:H2'	1:2:143:G:C8	2.24	0.72
1:2:437:A:H1'	1:2:464:G:H22	1.55	0.71
1:2:886:A:H61	1:2:924:G:H1	1.35	0.71
28:S:115:ARG:HD2	28:S:119:ILE:CD1	2.20	0.71
10:L:8:GLN:HA	10:L:14:GLN:HE22	1.54	0.71
22:F:104:ARG:HG3	22:F:105:ASN:HD21	1.51	0.71
28:S:134:ARG:HB2	28:S:136:GLN:HE22	1.55	0.71
2:A:38:TYR:HE2	27:R:109:LEU:HB2	1.53	0.71
10:L:14:GLN:OE1	10:L:14:GLN:N	2.23	0.71
2:A:11:SER:HA	27:R:115:LEU:HD21	1.72	0.71
4:C:145:ARG:HE	13:V:10:GLU:HG2	1.54	0.71
8:I:116:HIS:O	8:I:147:ARG:NH1	2.22	0.71
4:C:234:LEU:CD1	13:V:13:VAL:HG23	2.21	0.71
1:2:521:U:H5''	16:Y:37:LYS:HG3	1.71	0.71
1:2:589:C:H2'	1:2:590:A:H8	1.56	0.71
1:2:1553:A:H5''	25:P:44:LYS:HZ2	1.54	0.71
16:Y:7:ILE:HD13	16:Y:43:LYS:HB3	1.71	0.71
34:f:116:LYS:HB3	34:f:129:PHE:HZ	1.53	0.71
1:2:1637:5MC:H2'	1:2:1638:C:O4'	1.91	0.71
1:2:337:C:H1'	8:I:5:ARG:HB2	1.72	0.71
9:J:99:LEU:HD13	9:J:104:PHE:CZ	2.25	0.70
12:O:17:ALA:HB3	12:O:81:ILE:HA	1.73	0.70
13:V:66:ASP:OD1	13:V:67:ASP:N	2.24	0.70
30:U:68:ARG:HH12	30:U:77:LYS:HA	1.55	0.70
1:2:1252:U:H5''	34:f:128:ILE:HD11	1.73	0.70
34:f:139:CYS:HB2	34:f:146:PHE:HB3	1.73	0.70
40:k:78:GLN:HE22	40:k:98:GLN:HE22	1.39	0.70
1:2:444:A:H2'	1:2:445:A:H8	1.56	0.70
1:2:1670:G:H2'	1:2:1671:G:H8	1.56	0.70
5:E:55:ALA:HB1	5:E:60:GLU:HG3	1.73	0.70
8:I:173:ARG:HG3	8:I:176:GLN:HB2	1.73	0.70
1:2:370:G:N2	1:2:611:U:O2	2.24	0.70
27:R:13:SER:O	27:R:17:ILE:HG12	1.91	0.70
1:2:57:G:OP1	16:Y:112:LYS:NZ	2.25	0.70
1:2:638:U:OP2	7:H:101:LYS:NZ	2.20	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1532:G:N7	31:Z:77:ARG:NH1	2.39	0.70
40:k:466:ILE:HA	40:k:499:ILE:HG12	1.72	0.70
40:k:221:ASN:HD21	40:k:250:LYS:HD3	1.57	0.69
10:L:33:ARG:NH1	10:L:51:GLY:O	2.25	0.69
1:2:1469:A:OP1	22:F:187:ARG:NH1	2.24	0.69
14:W:44:HIS:NE2	14:W:112:ASP:OD2	2.26	0.69
1:2:28:A:N1	1:2:597:U:O4	2.25	0.69
1:2:531:U:OP1	9:J:132:ARG:NH1	2.21	0.69
1:2:1464:G:O2'	1:2:1600:C:OP1	2.10	0.69
1:2:1481:A:H2'	1:2:1482:G:C8	2.26	0.69
1:2:1482:G:H21	1:2:1604:C:H1'	1.56	0.69
6:G:58:LYS:HA	6:G:107:ALA:HB2	1.73	0.69
7:H:83:LYS:O	7:H:86:GLN:NE2	2.26	0.69
39:j:7:ARG:NH2	39:j:10:GLU:O	2.26	0.69
1:2:1626:U:H2'	1:2:1627:G:C8	2.28	0.69
22:F:105:ASN:HB3	22:F:108:LYS:HD2	1.73	0.69
35:g:6:ILE:HG21	35:g:256:ARG:HH12	1.57	0.69
3:B:144:ARG:HD3	3:B:208:GLN:HB3	1.75	0.69
1:2:636:C:O2	7:H:114:ARG:NH1	2.25	0.69
1:2:1564:U:H5''	28:S:39:GLY:N	2.06	0.69
1:2:1656:G:O6	1:2:1741:U:O2	2.11	0.69
29:T:44:GLU:OE1	29:T:44:GLU:N	2.26	0.69
3:B:114:VAL:HA	3:B:142:PHE:CE2	2.27	0.69
27:R:115:LEU:HG	27:R:117:LEU:HD23	1.75	0.69
30:U:45:ALA:HB3	30:U:52:LYS:HZ2	1.56	0.69
1:2:479:G:O6	1:2:507:U:O4	2.11	0.69
6:G:78:ALA:HB2	6:G:92:ARG:HG3	1.75	0.69
7:H:140:VAL:HB	14:W:52:TYR:HB3	1.75	0.69
1:2:887:U:H2'	1:2:888:U:C6	2.29	0.68
10:L:36:LYS:NZ	10:L:37:ASN:O	2.26	0.68
28:S:91:ASP:O	28:S:93:ASN:N	2.26	0.68
35:g:21:VAL:HG11	35:g:317:ILE:HD11	1.74	0.68
1:2:164:G:O2'	6:G:131:LYS:NZ	2.26	0.68
8:I:140:THR:CG2	8:I:144:TRP:HZ3	1.85	0.68
24:M:25:LEU:HD13	24:M:92:ALA:HA	1.75	0.68
24:M:52:LEU:HB2	24:M:114:VAL:HB	1.76	0.68
40:k:147:ILE:HG23	40:k:295:ASN:HD21	1.56	0.68
11:N:20:ARG:HH21	14:W:56:HIS:HB3	1.58	0.68
39:j:72:VAL:C	39:j:89:ARG:HH21	2.00	0.68
1:2:159:C:N4	1:2:160:U:C4	2.62	0.68
1:2:162:G:OP2	1:2:162:G:N2	2.21	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:433:G:H21	1:2:435:A:H8	1.42	0.68
1:2:1044:C:H2'	1:2:1045:G:H8	1.58	0.68
4:C:78:LEU:HD13	4:C:81:LEU:HD21	1.74	0.68
7:H:101:LYS:HZ3	7:H:112:ARG:HH12	1.42	0.68
31:Z:68:ARG:HB2	31:Z:70:LYS:HE2	1.75	0.68
38:1:46:7MG:O2'	38:1:48:5MC:OP2	2.08	0.68
39:j:21:MET:SD	39:j:68:ASN:HB3	2.34	0.68
25:P:110:GLU:OE1	25:P:110:GLU:N	2.22	0.68
1:2:63:G:O2'	1:2:169:U:OP1	2.12	0.68
2:A:84:ARG:NH1	2:A:203:PHE:O	2.26	0.68
1:2:916:U:O2	12:O:41:ARG:NH1	2.27	0.68
7:H:143:LEU:HA	14:W:49:GLU:OE1	1.93	0.68
21:D:44:THR:HG23	21:D:45:LYS:HG3	1.75	0.68
1:2:1038:A:O2'	1:2:1039:G:O5'	2.11	0.68
31:Z:49:ARG:HH12	31:Z:53:GLU:HB3	1.60	0.68
1:2:1474:C:H5''	29:T:44:GLU:OE2	1.94	0.67
3:B:112:SER:HA	17:a:68:TYR:HE2	1.58	0.67
4:C:236:GLU:OE1	4:C:236:GLU:N	2.17	0.67
40:k:377:ILE:HA	40:k:400:THR:HG22	1.76	0.67
1:2:778:G:H5'	1:2:780:A:N1	2.09	0.67
1:2:862:A:O5'	14:W:57:ARG:NH2	2.27	0.67
29:T:140:LEU:O	29:T:140:LEU:HD23	1.93	0.67
39:j:25:GLN:NE2	39:j:35:LYS:H	1.91	0.67
1:2:687:C:H5'	14:W:119:LYS:HE3	1.76	0.67
2:A:50:VAL:O	2:A:53:THR:OG1	2.10	0.67
5:E:230:GLU:HB3	5:E:233:ARG:HB3	1.76	0.67
6:G:180:THR:HG23	6:G:183:ARG:H	1.59	0.67
35:g:210:GLN:NE2	35:g:211:PRO:O	2.28	0.67
3:B:5:LYS:HZ2	3:B:7:LYS:HA	1.57	0.67
40:k:320:SER:HB2	40:k:407:CYS:HA	1.76	0.67
2:A:26:ALA:HB1	2:A:149:LEU:HB2	1.74	0.67
6:G:161:GLU:OE1	6:G:170:THR:OG1	2.11	0.67
9:J:23:ARG:O	9:J:27:GLU:HG3	1.95	0.67
1:2:1585:A:O2'	22:F:106:ASN:ND2	2.28	0.67
1:2:1660:G:H2'	1:2:1661:G:H8	1.60	0.67
35:g:20:TRP:CD1	35:g:39:ARG:HD2	2.30	0.67
9:J:81:VAL:HG21	9:J:91:LYS:HZ3	1.57	0.67
1:2:566:A:H5''	15:X:70:LYS:HZ1	1.60	0.67
8:I:25:ARG:N	8:I:28:GLU:OE2	2.27	0.67
10:L:7:VAL:HG22	10:L:14:GLN:HE21	1.59	0.67
29:T:140:LEU:HD23	29:T:140:LEU:C	2.19	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:396:A:H4'	8:I:50:GLY:HA2	1.76	0.67
1:2:787:A:OP2	5:E:108:ARG:NH2	2.27	0.67
21:D:61:GLU:HB3	21:D:64:ARG:HD3	1.77	0.67
35:g:172:ILE:HB	35:g:188:LEU:HB2	1.75	0.67
1:2:129:U:O4'	1:2:263:G:N1	2.28	0.67
1:2:339:U:H2'	1:2:340:A:H8	1.60	0.67
1:2:938:A:H2'	1:2:939:A:C8	2.30	0.67
9:J:109:LEU:HB2	9:J:146:PHE:HB3	1.77	0.67
12:O:15:GLY:N	12:O:78:ALA:O	2.24	0.67
35:g:107:HIS:ND1	35:g:129:ASP:OD2	2.24	0.67
38:1:42:U:H2'	38:1:43:G:O4'	1.94	0.67
39:j:72:VAL:O	39:j:89:ARG:NH2	2.28	0.67
30:U:22:ILE:HD13	30:U:100:VAL:HG11	1.76	0.66
1:2:798:A:H4'	5:E:201:HIS:NE2	2.09	0.66
20:h:22:ALA:HA	20:h:25:LYS:HE3	1.77	0.66
31:Z:57:TYR:HE1	31:Z:68:ARG:HH21	1.43	0.66
33:d:30:LEU:HA	33:d:39:ASP:HA	1.77	0.66
36:i:37:GLN:HE22	36:i:74:GLY:HA2	1.61	0.66
39:j:193:PHE:HA	40:k:406:LEU:HD21	1.77	0.66
1:2:339:U:H2'	1:2:340:A:C8	2.30	0.66
1:2:403:G:O2'	6:G:91:GLU:OE1	2.13	0.66
7:H:101:LYS:NZ	7:H:112:ARG:HH12	1.92	0.66
1:2:1746:G:H2'	1:2:1747:A:C8	2.30	0.66
26:Q:41:PRO:C	26:Q:43:ILE:H	2.03	0.66
39:j:47:LEU:HG	39:j:49:SER:H	1.60	0.66
29:T:109:GLU:OE1	29:T:122:ARG:NH1	2.29	0.66
9:J:18:PRO:HA	9:J:23:ARG:HH22	1.61	0.66
1:2:65:A:OP1	6:G:174:LYS:NZ	2.28	0.66
1:2:1100:G:H5''	14:W:76:SER:HB3	1.78	0.66
1:2:1102:U:OP1	15:X:8:GLY:N	2.28	0.66
3:B:41:ARG:NH2	3:B:231:LEU:O	2.28	0.66
35:g:285:PHE:CE2	35:g:294:PRO:HG2	2.31	0.66
41:l:177:ILE:HD12	41:l:180:ILE:HD11	1.77	0.66
1:2:1683:G:H2'	1:2:1684:C:C6	2.31	0.66
7:H:157:LYS:HD2	7:H:158:ASP:HB2	1.77	0.66
8:I:81:VAL:HG12	8:I:94:ASN:HA	1.77	0.66
30:U:66:SER:C	30:U:79:TRP:HZ3	2.04	0.66
1:2:15:U:O2'	1:2:619:A:N6	2.29	0.66
1:2:208:U:H1'	8:I:181:ASP:OD2	1.96	0.66
1:2:1496:G:H5''	29:T:72:GLY:HA3	1.78	0.66
4:C:85:VAL:HG12	4:C:107:VAL:HG22	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:88:GLU:OE1	9:J:88:GLU:N	2.24	0.66
5:E:64:ILE:HD11	16:Y:18:LEU:HG	1.78	0.65
25:P:81:ARG:NH2	25:P:117:GLY:O	2.29	0.65
1:2:1173:C:O2'	1:2:1195:A:N6	2.29	0.65
1:2:1203:A:N3	33:d:10:HIS:NE2	2.43	0.65
35:g:15:GLU:N	35:g:15:GLU:OE2	2.28	0.65
1:2:383:G:H2'	1:2:384:A:H8	1.59	0.65
1:2:530:C:O2	16:Y:62:THR:OG1	2.09	0.65
25:P:57:MET:O	25:P:61:ARG:HG3	1.97	0.65
26:Q:30:LYS:NZ	29:T:8:ASP:OD1	2.29	0.65
32:c:31:GLU:HB3	32:c:39:THR:HG22	1.77	0.65
1:2:710:U:H2'	1:2:711:G:C5	2.31	0.65
1:2:883:A:H2'	1:2:884:G:C8	2.31	0.65
2:A:30:GLN:HE21	2:A:46:ASN:HD22	1.44	0.65
5:E:71:LYS:HB3	5:E:91:THR:HB	1.78	0.65
6:G:5:ILE:HD11	6:G:113:ILE:HB	1.77	0.65
25:P:18:LYS:HE2	28:S:92:VAL:HG12	1.79	0.65
35:g:11:ARG:HH22	35:g:50:GLU:HA	1.62	0.65
1:2:882:C:H2'	1:2:883:A:C8	2.31	0.65
22:F:60:LEU:HD12	22:F:170:VAL:HG23	1.77	0.65
26:Q:12:LYS:HA	26:Q:16:ALA:O	1.97	0.65
38:1:16:H2U:O3'	38:1:61:C:OP1	2.14	0.65
1:2:1645:U:H2'	1:2:1646:A:C8	2.32	0.65
3:B:160:HIS:HB3	3:B:205:PHE:HE2	1.61	0.65
7:H:96:ARG:NH1	7:H:97:ARG:H	1.93	0.65
1:2:249:C:H2'	1:2:250:A:H8	1.60	0.65
2:A:148:ASP:OD1	2:A:149:LEU:N	2.29	0.65
4:C:234:LEU:HD11	13:V:13:VAL:HG23	1.79	0.65
30:U:68:ARG:HH22	30:U:77:LYS:HE3	1.61	0.65
1:2:367:U:O4	1:2:368:A:N6	2.29	0.65
1:2:525:A:OP2	16:Y:93:ARG:NH2	2.29	0.65
1:2:1122:C:H2'	1:2:1123:A:C4	2.32	0.65
6:G:10:ASN:ND2	6:G:127:ASP:O	2.30	0.65
24:M:31:HIS:HB2	24:M:116:ASN:ND2	2.12	0.65
24:M:120:ASP:HA	24:M:124:ARG:HG2	1.77	0.65
27:R:24:LEU:HD23	27:R:34:LEU:HD22	1.79	0.65
34:f:121:CYS:HB3	34:f:128:ILE:HG23	1.79	0.65
40:k:144:ASN:HB3	40:k:188:HIS:NE2	2.11	0.65
1:2:685:A:H2'	1:2:686:C:C6	2.31	0.65
1:2:1498:C:OP1	29:T:122:ARG:NH2	2.30	0.65
5:E:88:ASP:HA	5:E:122:LYS:HE3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1:9:1MG:OP2	38:1:46:7MG:O3'	2.14	0.65
1:2:149:U:OP1	16:Y:123:LYS:NZ	2.25	0.65
1:2:107:C:H2'	1:2:108:A:H8	1.61	0.64
1:2:357:U:H2'	1:2:359:A:C8	2.32	0.64
1:2:1062:U:H3'	1:2:1063:G:H8	1.61	0.64
1:2:1162:A:OP1	22:F:150:ARG:NH2	2.30	0.64
1:2:1720:A:H5''	6:G:75:LEU:HD11	1.77	0.64
4:C:87:ASN:HB2	4:C:212:LEU:HD13	1.79	0.64
19:e:56:MET:N	19:e:56:MET:SD	2.70	0.64
1:2:1320:A:N6	2:A:135:GLU:OE2	2.30	0.64
4:C:54:LYS:HD2	4:C:248:TYR:HE2	1.61	0.64
32:c:64:ARG:NH2	37:3:23:A:N3	2.45	0.64
1:2:519:A:H2'	1:2:520:A:C8	2.32	0.64
1:2:1559:U:H2'	1:2:1560:G:H8	1.61	0.64
2:A:119:ARG:HH22	4:C:246:ASP:HB2	1.63	0.64
5:E:64:ILE:HD12	16:Y:17:LEU:HB3	1.78	0.64
12:O:18:ARG:HA	12:O:82:LYS:HB2	1.79	0.64
28:S:116:LEU:HA	28:S:119:ILE:HD13	1.79	0.64
30:U:63:LEU:HB2	30:U:84:MET:HB2	1.80	0.64
6:G:50:PHE:HB3	6:G:111:LEU:HD12	1.80	0.64
35:g:302:SER:OG	35:g:304:ASP:OD1	2.13	0.64
40:k:315:LEU:HB2	40:k:417:VAL:HB	1.79	0.64
1:2:867:G:H5''	11:N:91:LEU:HD21	1.79	0.64
1:2:1759:U:O2'	37:3:30:U:OP1	2.13	0.64
8:I:106:ALA:HB2	8:I:166:LEU:HD23	1.79	0.64
25:P:111:MET:HE2	25:P:111:MET:HA	1.79	0.64
35:g:20:TRP:HB2	35:g:39:ARG:HG3	1.78	0.64
1:2:1086:A:H2'	1:2:1087:A:C8	2.32	0.64
1:2:1786:G:OP1	12:O:127:ARG:NH2	2.30	0.64
2:A:39:LYS:HZ1	27:R:105:GLN:HG3	1.62	0.64
20:h:2:ARG:HG2	20:h:5:TRP:HE3	1.62	0.64
1:2:65:A:H2	1:2:84:A:H62	1.45	0.64
35:g:132:ILE:HD11	35:g:152:VAL:HG11	1.80	0.64
40:k:209:ALA:HA	40:k:239:MET:SD	2.38	0.64
1:2:158:U:O2'	6:G:87:ARG:NE	2.31	0.64
3:B:107:THR:OG1	12:O:117:ASP:O	2.16	0.64
35:g:67:HIS:ND1	35:g:86:TRP:HB2	2.13	0.64
40:k:121:SER:HB3	40:k:145:ALA:HB2	1.80	0.64
1:2:753:A:H5''	5:E:187:ARG:HH12	1.62	0.64
33:d:20:GLN:N	33:d:20:GLN:OE1	2.31	0.64
1:2:153:G:H3'	16:Y:132:ARG:HH22	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:899:A:H3'	1:2:900:G:H21	1.61	0.64
35:g:113:SER:OG	35:g:153:THR:O	2.16	0.64
1:2:14:C:OP1	4:C:169:SER:OG	2.13	0.63
1:2:1170:A:H2'	1:2:1171:G:C8	2.33	0.63
5:E:179:LYS:HA	5:E:231:PRO:HD3	1.80	0.63
12:O:22:SER:OG	12:O:24:ASN:O	2.16	0.63
12:O:26:THR:HG21	12:O:60:ALA:HB2	1.79	0.63
22:F:107:GLY:O	22:F:108:LYS:C	2.41	0.63
1:2:683:C:N4	1:2:684:A:N6	2.47	0.63
1:2:867:G:H2'	1:2:868:A:H8	1.64	0.63
1:2:886:A:N6	1:2:924:G:H1	1.95	0.63
3:B:32:ILE:HB	3:B:43:VAL:HB	1.80	0.63
40:k:314:ARG:HD2	40:k:344:ASN:HD21	1.63	0.63
25:P:81:ARG:NH2	25:P:120:SER:O	2.32	0.63
30:U:55:PRO:HA	30:U:91:ILE:HG12	1.79	0.63
35:g:64:GLY:O	35:g:91:ARG:NH1	2.32	0.63
35:g:117:ASP:OD2	35:g:121:SER:OG	2.16	0.63
38:1:36:U:H2'	38:1:37:T6A:H8	1.63	0.63
1:2:399:A:H4'	1:2:400:A:H5''	1.81	0.63
1:2:1345:A:OP2	1:2:1347:A:N6	2.25	0.63
1:2:112:A:O2'	10:L:67:ARG:NH1	2.31	0.63
1:2:638:U:H5'	7:H:101:LYS:HE3	1.81	0.63
1:2:845:G:H2'	1:2:846:A:C8	2.34	0.63
1:2:1157:C:H42	1:2:1162:A:H61	1.47	0.63
5:E:22:LYS:HG3	5:E:23:LEU:HD12	1.80	0.63
8:I:67:TRP:O	8:I:71:GLY:N	2.32	0.63
1:2:645:U:H2'	1:2:646:G:H8	1.63	0.63
1:2:842:U:O4	1:2:843:A:N6	2.31	0.63
1:2:866:G:O6	1:2:961:C:N4	2.31	0.63
12:O:131:GLY:O	17:a:22:ARG:NH2	2.30	0.63
27:R:17:ILE:HD12	27:R:58:MET:HE2	1.81	0.63
38:1:16:H2U:H4'	38:1:16:H2U:OP1	1.98	0.63
39:j:48:LEU:HD23	39:j:51:LEU:HD13	1.81	0.63
1:2:1198:G:H2'	1:2:1198:G:N3	2.12	0.63
3:B:174:ARG:O	3:B:178:ASN:ND2	2.31	0.63
25:P:81:ARG:NH2	25:P:120:SER:OG	2.30	0.63
30:U:39:ALA:O	30:U:42:ILE:HG22	1.99	0.63
35:g:207:ASN:ND2	35:g:248:PHE:HA	2.14	0.63
1:2:992:A:OP1	1:2:1775:G:N2	2.31	0.63
1:2:1227:G:O2'	34:f:100:LEU:N	2.28	0.63
12:O:115:ILE:HG22	17:a:62:TYR:HE2	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:159:C:N4	1:2:160:U:O4	2.32	0.63
1:2:1679:A:H2	1:2:1718:G:H21	1.47	0.63
1:2:1793:U:OP2	17:a:4:LYS:NZ	2.32	0.63
4:C:142:ILE:HD11	13:V:27:LYS:HG2	1.79	0.63
27:R:14:LYS:HG3	27:R:69:ILE:HG22	1.81	0.63
39:j:174:SER:O	39:j:178:THR:OG1	2.16	0.63
40:k:76:PRO:HD3	40:k:170:ILE:HD11	1.81	0.63
40:k:426:ILE:HG23	40:k:523:LEU:HB3	1.80	0.63
1:2:151:U:O2	6:G:4:ASN:ND2	2.32	0.62
1:2:1168:G:N1	1:2:1573:7MG:OP2	2.31	0.62
1:2:1680:U:P	6:G:31:ARG:HH12	2.21	0.62
10:L:86:ILE:HG22	10:L:107:VAL:O	1.98	0.62
11:N:54:LEU:HD12	11:N:60:VAL:HG21	1.80	0.62
27:R:31:ASN:HD22	27:R:55:THR:HG22	1.63	0.62
39:j:72:VAL:CG1	39:j:89:ARG:NE	2.61	0.62
1:2:1431:G:H2'	1:2:1432:U:C6	2.35	0.62
1:2:1584:A:H5''	26:Q:136:SER:HB2	1.80	0.62
7:H:158:ASP:OD1	7:H:161:HIS:ND1	2.32	0.62
8:I:104:ILE:HB	8:I:166:LEU:HB2	1.80	0.62
1:2:196:A:N6	8:I:139:ASN:OD1	2.32	0.62
1:2:1141:A:H5''	17:a:2:PRO:HB3	1.81	0.62
1:2:1609:A:O3'	22:F:97:ASN:ND2	2.31	0.62
35:g:227:ILE:HB	35:g:241:PHE:HB2	1.79	0.62
40:k:227:PRO:HD3	40:k:444:LYS:HE2	1.80	0.62
1:2:129:U:OP1	1:2:131:C:N4	2.30	0.62
1:2:291:U:H2'	1:2:292:U:C6	2.34	0.62
22:F:86:LYS:HE3	22:F:94:ARG:HH12	1.65	0.62
40:k:503:ARG:HG3	40:k:512:ILE:HD13	1.81	0.62
1:2:1254:G:O2'	1:2:1255:A:N7	2.33	0.62
17:a:24:VAL:N	17:a:72:HIS:O	2.31	0.62
1:2:297:C:O3'	5:E:30:ARG:NH2	2.32	0.62
1:2:336:G:O3'	8:I:10:LYS:NZ	2.32	0.62
1:2:1121:G:O2'	1:2:1123:A:N6	2.30	0.62
1:2:1513:A:O2'	1:2:1515:U:OP2	2.18	0.62
24:M:95:GLY:HA3	24:M:104:ARG:HD3	1.81	0.62
39:j:147:LEU:HD22	39:j:154:VAL:HG22	1.82	0.62
1:2:1115:A:OP1	20:h:14:LYS:NZ	2.23	0.62
1:2:1157:C:H42	1:2:1162:A:N6	1.98	0.62
1:2:1201:A:N6	1:2:1455:C:OP1	2.32	0.62
1:2:1472:G:H2'	1:2:1473:A:H8	1.64	0.62
39:j:7:ARG:HD2	39:j:40:ASP:OD2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1170:A:H2'	1:2:1171:G:H8	1.63	0.62
1:2:1190:B8N:N34	38:1:34:C:OP1	2.32	0.62
1:2:1212:G:O2'	1:2:1243:A:N6	2.33	0.62
9:J:136:VAL:HG21	9:J:146:PHE:HE2	1.64	0.62
21:D:136:VAL:HG22	21:D:186:VAL:HG12	1.82	0.62
32:c:42:ARG:HA	32:c:63:ALA:HB2	1.82	0.62
35:g:294:PRO:HB3	35:g:313:THR:OG1	2.00	0.62
39:j:51:LEU:HD11	39:j:63:ILE:HD11	1.82	0.62
39:j:72:VAL:HG13	39:j:89:ARG:NH2	2.15	0.62
8:I:27:PHE:HB3	8:I:49:ARG:HH22	1.63	0.62
21:D:209:ILE:O	27:R:20:TYR:OH	2.14	0.62
1:2:29:U:H2'	1:2:30:G:H8	1.65	0.62
1:2:353:C:H5''	8:I:16:ALA:HB2	1.82	0.62
1:2:997:A:N6	1:2:1003:U:OP2	2.32	0.62
2:A:60:ALA:O	2:A:64:ILE:HG12	2.00	0.62
3:B:5:LYS:O	3:B:7:LYS:N	2.32	0.62
5:E:72:VAL:HG11	5:E:82:PHE:HE2	1.62	0.62
33:d:38:ILE:HD11	33:d:42:SER:HB3	1.79	0.62
40:k:110:ALA:H	44:k:601:GCP:H3B2	1.65	0.62
1:2:44:U:OP2	1:2:436:A:N6	2.32	0.61
1:2:115:G:OP2	10:L:65:SER:OG	2.18	0.61
25:P:39:ALA:N	25:P:42:ARG:HB3	2.15	0.61
1:2:403:G:O5'	6:G:88:ARG:NH2	2.33	0.61
21:D:28:GLU:OE1	23:K:58:GLN:NE2	2.33	0.61
38:1:9:1MG:O5'	38:1:46:7MG:H1'	1.99	0.61
1:2:391:G:OP1	1:2:1727:C:O2'	2.19	0.61
1:2:1552:U:OP2	25:P:47:ARG:NH2	2.32	0.61
1:2:1793:U:H5'	17:a:79:ILE:HD11	1.83	0.61
5:E:23:LEU:HA	9:J:3:ARG:NH2	2.15	0.61
16:Y:18:LEU:HA	16:Y:85:PHE:HE2	1.65	0.61
1:2:816:A:H61	1:2:853:U:H3	1.46	0.61
1:2:1201:A:N6	1:2:1455:C:O2	2.34	0.61
38:1:27:C:O2'	38:1:28:A:H8	1.80	0.61
1:2:923:A:H2'	1:2:924:G:C8	2.35	0.61
1:2:1040:G:H2'	1:2:1041:G:C8	2.34	0.61
1:2:1548:A:P	25:P:42:ARG:HH21	2.24	0.61
11:N:46:THR:OG1	11:N:49:GLN:OE1	2.18	0.61
14:W:31:SER:O	14:W:35:ILE:HG12	2.00	0.61
1:2:394:U:O2'	6:G:89:ASN:ND2	2.34	0.61
35:g:104:PHE:HE1	35:g:139:GLY:HA2	1.66	0.61
35:g:271:ASP:OD2	35:g:274:ASN:ND2	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:131:C:H4'	1:2:132:U:H4'	1.83	0.61
1:2:554:A:H2'	1:2:555:A:C8	2.35	0.61
1:2:896:C:H42	1:2:913:G:H2'	1.66	0.61
1:2:1338:C:O2'	1:2:1340:A:N7	2.32	0.61
6:G:43:ASP:OD1	6:G:44:GLU:N	2.34	0.61
22:F:95:LEU:HA	22:F:174:ILE:HD11	1.83	0.61
1:2:326:U:H2'	1:2:327:A:C8	2.35	0.61
1:2:835:U:H2'	1:2:836:G:C8	2.35	0.61
1:2:1793:U:H3'	17:a:5:ARG:HH22	1.65	0.61
39:j:8:PHE:HE1	39:j:109:HIS:HB2	1.65	0.61
39:j:222:LEU:HD11	40:k:324:ASN:HB3	1.81	0.61
1:2:299:A:H2'	1:2:300:A:H8	1.65	0.61
1:2:404:C:O2'	6:G:92:ARG:O	2.18	0.61
1:2:588:C:H4'	19:e:57:ASN:HB2	1.81	0.61
1:2:855:A:H62	7:H:96:ARG:NE	1.99	0.61
1:2:1280:G:O3'	30:U:76:SER:OG	2.19	0.61
35:g:115:ALA:HB3	35:g:124:ILE:HB	1.82	0.61
35:g:267:ILE:HB	35:g:281:LEU:HB2	1.80	0.61
39:j:72:VAL:HG11	39:j:89:ARG:HE	1.64	0.61
40:k:151:GLN:HG2	40:k:184:LYS:HE3	1.83	0.61
1:2:28:A:C6	1:2:597:U:O4	2.54	0.61
1:2:1617:C:H2'	1:2:1618:C:H6	1.66	0.61
2:A:59:LEU:O	2:A:63:ILE:HG12	2.01	0.61
17:a:33:ASP:OD1	17:a:34:LYS:N	2.32	0.61
25:P:111:MET:HE1	28:S:119:ILE:HG23	1.82	0.61
1:2:405:U:H2'	1:2:406:A:C8	2.36	0.60
22:F:103:GLY:C	22:F:105:ASN:N	2.50	0.60
26:Q:90:VAL:HG13	26:Q:102:LYS:HD2	1.82	0.60
39:j:60:GLN:OE1	39:j:60:GLN:N	2.34	0.60
23:K:15:LEU:O	23:K:19:GLY:N	2.26	0.60
1:2:1319:U:H2'	1:2:1321:A:H5'	1.84	0.60
1:2:1591:A:H2'	1:2:1592:G:C8	2.34	0.60
8:I:85:PRO:O	10:L:11:ARG:NH1	2.35	0.60
40:k:432:ILE:HG12	40:k:515:ALA:HB1	1.84	0.60
1:2:1190:B8N:O2'	1:2:1191:C:O4'	2.19	0.60
1:2:1240:G:OP1	25:P:77:ARG:NH1	2.33	0.60
1:2:1498:C:OP1	29:T:106:GLN:NE2	2.35	0.60
1:2:1710:A:C6	1:2:1711:G:H1'	2.36	0.60
4:C:64:HIS:HA	13:V:15:ARG:NH1	2.11	0.60
5:E:182:TYR:N	5:E:226:PHE:O	2.34	0.60
26:Q:104:GLU:HA	26:Q:107:LYS:HD2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1356:G:H2'	1:2:1357:G:H8	1.66	0.60
2:A:42:PRO:HB2	27:R:126:ALA:HB2	1.83	0.60
22:F:104:ARG:CG	22:F:105:ASN:ND2	2.57	0.60
1:2:1045:G:OP1	3:B:157:GLN:NE2	2.33	0.60
1:2:1660:G:H2'	1:2:1661:G:C8	2.37	0.60
35:g:115:ALA:O	35:g:124:ILE:N	2.32	0.60
39:j:7:ARG:NH1	39:j:9:TYR:O	2.35	0.60
1:2:506:U:H3'	1:2:507:U:H5''	1.84	0.60
1:2:1551:G:O6	25:P:43:ARG:NH1	2.34	0.60
3:B:8:ARG:C	3:B:9:LEU:HD12	2.12	0.60
22:F:148:THR:HG21	22:F:222:VAL:HG12	1.83	0.60
40:k:129:LYS:O	40:k:131:GLU:N	2.35	0.60
1:2:234:G:H2'	1:2:235:A:C8	2.37	0.60
1:2:609:G:O2'	1:2:612:G:O2'	2.16	0.60
1:2:712:U:H3	1:2:726:G:H21	1.49	0.60
1:2:1076:C:H2'	1:2:1077:C:H6	1.66	0.60
1:2:1402:C:H2'	1:2:1403:G:H8	1.67	0.60
1:2:1488:A:OP1	21:D:9:ARG:NH2	2.35	0.60
5:E:121:TYR:OH	5:E:235:TRP:O	2.19	0.60
6:G:221:ALA:O	6:G:225:GLU:HG2	2.01	0.60
30:U:35:GLU:OE2	30:U:89:ARG:NE	2.25	0.60
39:j:149:ILE:HG13	39:j:150:ILE:HG23	1.83	0.60
1:2:1782:C:H41	20:h:5:TRP:NE1	1.95	0.60
2:A:70:PRO:O	2:A:73:VAL:HG12	2.02	0.60
18:b:34:ASP:OD2	18:b:82:LYS:HD3	2.01	0.60
35:g:134:VAL:HB	35:g:143:TYR:HB2	1.83	0.60
1:2:121:U:H2'	1:2:122:U:C6	2.37	0.60
1:2:735:C:O2'	1:2:736:C:O5'	2.20	0.60
1:2:1580:U:H1'	1:2:1612:A:H62	1.67	0.60
1:2:1601:U:H2'	1:2:1602:U:H6	1.67	0.60
2:A:38:TYR:HH	27:R:108:GLU:CD	2.10	0.60
2:A:125:ASP:OD1	2:A:164:ASN:ND2	2.35	0.60
28:S:72:ILE:HA	28:S:79:TYR:CE2	2.36	0.60
34:f:119:LYS:O	34:f:120:GLU:HB3	2.02	0.60
35:g:14:LEU:HB2	35:g:317:ILE:HB	1.83	0.60
38:1:20:A:N6	38:1:57:G:C2	2.70	0.60
1:2:180:A:H2'	1:2:181:A:C8	2.37	0.59
1:2:925:A:H2'	1:2:926:C:C6	2.37	0.59
1:2:952:G:H2'	1:2:953:G:C8	2.35	0.59
1:2:1475:G:H1'	29:T:48:GLN:HE22	1.67	0.59
3:B:48:VAL:HG21	3:B:61:LEU:HD21	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:172:LEU:HD23	3:B:193:ILE:HD11	1.83	0.59
5:E:199:GLU:HB2	5:E:207:LEU:HB2	1.83	0.59
8:I:60:ILE:HD12	8:I:180:CYS:HB2	1.84	0.59
12:O:107:ARG:HH12	32:c:38:ARG:HH12	1.48	0.59
26:Q:52:LEU:HG	26:Q:60:PHE:HZ	1.67	0.59
30:U:84:MET:HE2	33:d:52:PHE:CD1	2.37	0.59
34:f:104:ASN:O	34:f:117:LEU:HG	2.00	0.59
1:2:403:G:H2'	1:2:404:C:C6	2.37	0.59
1:2:883:A:H2'	1:2:884:G:H8	1.67	0.59
1:2:1670:G:H2'	1:2:1671:G:C8	2.38	0.59
7:H:13:PRO:HD2	7:H:17:GLU:OE2	2.02	0.59
38:1:33:U:N3	38:1:36:U:OP2	2.35	0.59
39:j:72:VAL:HG13	39:j:89:ARG:NE	2.18	0.59
39:j:251:ILE:HA	39:j:254:VAL:HG22	1.84	0.59
40:k:148:TYR:OH	40:k:169:GLU:O	2.12	0.59
1:2:367:U:O2	1:2:372:G:O6	2.20	0.59
1:2:601:U:H2'	1:2:602:U:C6	2.36	0.59
1:2:1589:C:H2'	1:2:1590:A:H8	1.67	0.59
1:2:1683:G:H2'	1:2:1684:C:H6	1.67	0.59
2:A:26:ALA:HB2	2:A:48:ILE:HD11	1.83	0.59
4:C:131:ARG:O	4:C:135:ILE:HD12	2.02	0.59
5:E:36:HIS:CG	5:E:85:GLY:HA3	2.37	0.59
21:D:106:LYS:HG3	21:D:175:VAL:HG22	1.84	0.59
40:k:129:LYS:HB2	40:k:132:LEU:HB2	1.84	0.59
5:E:143:ASP:HB2	5:E:145:ARG:HG3	1.84	0.59
11:N:102:LEU:HD12	11:N:115:LEU:HD13	1.84	0.59
39:j:147:LEU:HD23	39:j:151:ASP:HB3	1.83	0.59
1:2:590:A:H2'	1:2:591:G:C8	2.38	0.59
1:2:1648:U:H2'	1:2:1649:A:C8	2.38	0.59
8:I:160:GLN:HG2	8:I:166:LEU:HD13	1.84	0.59
1:2:843:A:H2'	1:2:844:G:C8	2.37	0.59
1:2:1044:C:H2'	1:2:1045:G:C8	2.37	0.59
1:2:1198:G:H4'	1:2:1199:G:O5'	2.02	0.59
12:O:60:ALA:HB1	12:O:101:ALA:HB2	1.84	0.59
31:Z:45:ASP:OD1	31:Z:46:LYS:N	2.36	0.59
38:1:19:G:O5'	38:1:60:A:N6	2.35	0.59
1:2:351:A:OP2	15:X:13:ARG:NH2	2.36	0.59
1:2:788:A:C2	1:2:789:U:H1'	2.38	0.59
1:2:809:G:C2	7:H:111:LYS:HB2	2.38	0.59
1:2:984:G:H22	1:2:1015:C:H5	1.51	0.59
3:B:29:TRP:CE2	3:B:47:LEU:HD21	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:38:LEU:HD21	7:H:73:VAL:HG21	1.84	0.59
1:2:165:C:O2'	6:G:133:LEU:O	2.19	0.59
6:G:57:ASP:OD1	6:G:58:LYS:N	2.36	0.59
16:Y:16:PRO:HA	16:Y:19:ALA:HA	1.85	0.59
32:c:34:GLU:OE1	32:c:34:GLU:N	2.35	0.59
35:g:150:ASP:HB3	35:g:179:MET:HB3	1.83	0.59
38:1:75:C:O2'	40:k:324:ASN:O	2.21	0.59
39:j:151:ASP:OD2	39:j:153:THR:OG1	2.20	0.59
39:j:226:PRO:HD3	40:k:408:ARG:HD3	1.84	0.59
1:2:553:C:N4	1:2:570:G:O6	2.36	0.59
7:H:27:LEU:HB3	7:H:34:LEU:CD2	2.33	0.59
8:I:81:VAL:HA	8:I:102:VAL:HG12	1.85	0.59
12:O:15:GLY:O	12:O:80:HIS:N	2.33	0.59
13:V:55:LEU:HD21	13:V:65:ALA:HB1	1.83	0.59
28:S:84:TRP:HA	28:S:89:GLN:HE21	1.68	0.59
1:2:1412:U:H5''	27:R:3:ARG:HD3	1.85	0.59
1:2:1470:C:O2	1:2:1532:G:N2	2.35	0.59
4:C:74:ILE:HG21	4:C:141:VAL:HG21	1.85	0.59
13:V:64:GLU:OE2	18:b:2:VAL:N	2.36	0.59
38:1:47:H2U:H3'	38:1:49:5MC:OP1	2.02	0.59
38:1:47:H2U:H4'	38:1:48:5MC:OP2	2.02	0.59
1:2:415:A:H5'	1:2:416:A:C8	2.38	0.58
1:2:858:A:O2'	11:N:73:ARG:NH1	2.36	0.58
1:2:1124:A:C8	1:2:1125:G:H1'	2.37	0.58
2:A:155:TYR:O	13:V:60:ARG:NH2	2.35	0.58
10:L:7:VAL:O	10:L:14:GLN:NE2	2.36	0.58
22:F:34:GLU:O	22:F:39:GLN:NE2	2.36	0.58
24:M:23:VAL:O	24:M:27:THR:HG23	2.03	0.58
39:j:75:ARG:NE	39:j:84:ASP:OD2	2.35	0.58
1:2:563:G:N2	1:2:576:G:OP1	2.36	0.58
19:e:41:THR:HA	19:e:45:VAL:HG12	1.85	0.58
1:2:1293:G:N2	1:2:1302:U:O2	2.33	0.58
1:2:1322:C:H2'	1:2:1323:G:C8	2.38	0.58
1:2:1477:A:OP1	29:T:57:ARG:NE	2.28	0.58
11:N:31:ASP:O	11:N:35:GLU:HG2	2.03	0.58
26:Q:127:LYS:HA	26:Q:134:ALA:HA	1.85	0.58
27:R:93:LEU:HD23	27:R:100:LEU:HG	1.84	0.58
31:Z:90:LYS:NZ	31:Z:104:ALA:HA	2.19	0.58
35:g:184:ARG:NE	35:g:198:ASP:OD1	2.25	0.58
41:l:173:ILE:HG12	41:l:212:VAL:HG22	1.85	0.58
1:2:142:G:P	6:G:139:ASN:HD22	2.25	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1611:U:H5''	22:F:171:ASN:HD21	1.67	0.58
1:2:1617:C:O2	32:c:22:ARG:NH2	2.36	0.58
3:B:45:LYS:HB2	12:O:13:VAL:HG23	1.83	0.58
5:E:103:TYR:CE1	5:E:109:PHE:HE1	2.22	0.58
22:F:105:ASN:HB3	22:F:108:LYS:HZ2	1.67	0.58
28:S:24:GLY:HA2	28:S:58:ALA:HB3	1.85	0.58
35:g:170:GLY:O	35:g:189:ASN:ND2	2.37	0.58
1:2:67:A:O2'	1:2:69:G:OP1	2.21	0.58
1:2:99:C:OP2	1:2:377:A:O2'	2.19	0.58
1:2:477:A:O2'	9:J:124:HIS:ND1	2.34	0.58
1:2:1427:G:H2'	1:2:1428:U:C6	2.38	0.58
1:2:1522:A:H2'	1:2:1523:A:C8	2.38	0.58
1:2:1737:C:H2'	1:2:1738:A:H8	1.67	0.58
18:b:23:THR:OG1	18:b:25:VAL:O	2.22	0.58
35:g:221:ALA:HB1	35:g:247:VAL:HG11	1.86	0.58
36:i:29:LYS:HB2	36:i:34:GLU:HA	1.85	0.58
38:1:62:C:H2'	38:1:63:G:C8	2.37	0.58
1:2:312:U:O4	1:2:1115:A:N6	2.37	0.58
1:2:697:C:H3'	1:2:698:U:H5''	1.85	0.58
1:2:1506:U:H2'	1:2:1507:C:C6	2.39	0.58
1:2:1589:C:H2'	1:2:1590:A:C8	2.39	0.58
38:1:10:2MG:C5	38:1:26:M2G:HM12	2.39	0.58
1:2:158:U:O2'	6:G:87:ARG:NH2	2.37	0.58
1:2:407:C:O2'	1:2:1730:A:O2'	2.19	0.58
1:2:845:G:N2	1:2:845:G:OP2	2.37	0.58
1:2:931:U:O3'	17:a:32:LYS:NZ	2.37	0.58
1:2:1356:G:H2'	1:2:1357:G:C8	2.39	0.58
5:E:191:ARG:HD3	5:E:218:PHE:CE2	2.38	0.58
8:I:117:TYR:O	8:I:119:GLN:NE2	2.31	0.58
12:O:103:ARG:HH12	12:O:107:ARG:HH21	1.51	0.58
35:g:62:TYR:HE1	35:g:98:GLY:HA2	1.69	0.58
36:i:58:MET:O	36:i:88:GLN:NE2	2.36	0.58
1:2:751:G:H2'	1:2:752:A:C8	2.39	0.58
3:B:8:ARG:O	3:B:9:LEU:HD13	1.93	0.58
9:J:17:ARG:O	9:J:23:ARG:NH2	2.36	0.58
31:Z:89:ILE:HG21	31:Z:101:TYR:HB3	1.86	0.58
21:D:120:TYR:HA	21:D:123:VAL:HG12	1.86	0.58
23:K:25:LYS:HD2	23:K:59:PHE:CE1	2.38	0.58
1:2:332:A:OP2	8:I:48:THR:OG1	2.19	0.58
1:2:1548:A:P	25:P:42:ARG:NH2	2.77	0.58
5:E:54:TYR:O	16:Y:20:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:F:101:MET:CE	22:F:178:THR:HG21	2.32	0.58
23:K:83:PRO:HB2	23:K:85:HIS:CD2	2.39	0.58
29:T:78:LYS:HA	29:T:95:ASP:OD1	2.03	0.58
1:2:256:A:N3	8:I:64:ASN:ND2	2.52	0.57
1:2:312:U:O4'	1:2:1117:G:N2	2.37	0.57
1:2:519:A:H2'	1:2:520:A:H8	1.67	0.57
2:A:36:TYR:OH	2:A:56:LYS:NZ	2.32	0.57
7:H:34:LEU:HD23	7:H:34:LEU:O	2.04	0.57
39:j:72:VAL:HG13	39:j:89:ARG:HH21	1.68	0.57
40:k:356:ARG:CZ	40:k:424:PRO:HD2	2.34	0.57
1:2:510:A:H5'	9:J:173:ALA:HB2	1.86	0.57
1:2:520:A:H2'	1:2:521:U:C6	2.39	0.57
1:2:622:A:N6	1:2:969:A:OP1	2.37	0.57
1:2:897:A:N6	1:2:913:G:H1'	2.19	0.57
1:2:1466:U:H1'	29:T:88:VAL:HG23	1.86	0.57
1:2:1554:A:OP2	25:P:44:LYS:NZ	2.37	0.57
1:2:1785:C:H2'	1:2:1786:G:C8	2.38	0.57
2:A:6:THR:O	2:A:191:ARG:NH1	2.28	0.57
3:B:7:LYS:O	3:B:7:LYS:HG3	2.03	0.57
28:S:68:ARG:O	28:S:72:ILE:HG12	2.04	0.57
38:1:3:C:H4'	39:j:185:ARG:NH2	2.17	0.57
1:2:247:U:H5'	10:L:36:LYS:HE3	1.86	0.57
1:2:613:C:OP1	15:X:3:LYS:NZ	2.24	0.57
1:2:1768:U:H2'	1:2:1769:U:C6	2.39	0.57
4:C:234:LEU:HG	4:C:234:LEU:O	2.04	0.57
11:N:38:ILE:HB	11:N:42:ARG:HH12	1.70	0.57
14:W:35:ILE:O	14:W:39:GLN:HG3	2.04	0.57
17:a:93:ARG:NE	17:a:93:ARG:HA	2.19	0.57
24:M:85:ALA:HB1	24:M:110:SER:H	1.68	0.57
26:Q:44:LEU:HD11	26:Q:75:VAL:HG12	1.86	0.57
28:S:56:LYS:HE3	28:S:60:GLU:HB3	1.87	0.57
28:S:139:LYS:O	28:S:143:ARG:NH2	2.37	0.57
1:2:140:A:H61	6:G:187:LYS:HB2	1.70	0.57
1:2:976:A:N6	1:2:1023:U:H3	2.00	0.57
3:B:67:GLU:N	3:B:67:GLU:OE2	2.36	0.57
35:g:67:HIS:CG	35:g:68:ILE:H	2.21	0.57
35:g:130:LYS:HE2	35:g:150:ASP:HA	1.87	0.57
38:1:12:G:H2'	38:1:13:C:C6	2.39	0.57
1:2:182:U:H2'	1:2:183:C:C6	2.39	0.57
1:2:1159:A:H2'	1:2:1160:C:C6	2.39	0.57
2:A:16:LEU:HG	2:A:172:LEU:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:F:86:LYS:O	22:F:94:ARG:NH2	2.37	0.57
29:T:37:VAL:HG12	29:T:39:THR:H	1.70	0.57
38:1:42:U:C2	38:1:43:G:C8	2.93	0.57
1:2:403:G:O4'	6:G:88:ARG:NH1	2.37	0.57
1:2:863:U:O5'	14:W:28:ARG:NH2	2.38	0.57
1:2:1143:U:H2'	1:2:1144:U:C6	2.39	0.57
1:2:1227:G:H2'	34:f:99:LYS:HD2	1.87	0.57
1:2:1481:A:OP2	1:2:1519:G:N2	2.35	0.57
3:B:66:VAL:HG12	12:O:34:SER:HA	1.86	0.57
22:F:190:LYS:NZ	22:F:198:GLU:OE1	2.29	0.57
28:S:41:ARG:NH2	29:T:36:ILE:O	2.36	0.57
39:j:32:ALA:HB3	39:j:46:ILE:HG12	1.87	0.57
1:2:1317:G:H2'	1:2:1318:A:C8	2.39	0.57
1:2:1645:U:H2'	1:2:1646:A:H8	1.70	0.57
10:L:16:GLN:HE22	10:L:33:ARG:HD2	1.69	0.57
16:Y:12:VAL:HA	16:Y:23:PHE:HB3	1.86	0.57
39:j:14:PRO:HD3	39:j:39:TYR:CZ	2.40	0.57
1:2:1200:G:N2	1:2:1598:A:O4'	2.37	0.57
1:2:1522:A:N3	1:2:1588:G:O2'	2.32	0.57
2:A:39:LYS:NZ	27:R:105:GLN:HG3	2.20	0.57
36:i:104:LYS:NZ	36:i:110:PRO:O	2.37	0.57
40:k:95:ILE:HG23	40:k:185:LEU:HD23	1.86	0.57
1:2:1171:G:H21	29:T:88:VAL:HG21	1.70	0.57
1:2:1798:A:N6	37:3:20:A:O2'	2.34	0.57
10:L:132:SER:OG	10:L:135:VAL:HG22	2.04	0.57
19:e:14:VAL:O	19:e:18:THR:OG1	2.21	0.57
21:D:116:ARG:NH2	37:3:39:U:O4	2.38	0.57
38:1:36:U:H2'	38:1:37:T6A:C8	2.39	0.57
39:j:212:SER:HB2	39:j:217:GLN:HA	1.87	0.57
1:2:332:A:H2'	1:2:333:G:C8	2.40	0.57
1:2:683:C:N4	1:2:684:A:H62	2.02	0.57
1:2:882:C:H2'	1:2:883:A:H8	1.70	0.57
1:2:959:U:O4'	11:N:55:ARG:NH1	2.38	0.57
1:2:1301:U:H2'	1:2:1302:U:H6	1.70	0.57
1:2:1319:U:O2'	1:2:1321:A:OP1	2.18	0.57
2:A:118:PRO:O	2:A:141:ILE:HD12	2.04	0.57
21:D:146:ARG:NH1	37:3:36:U:H3	2.03	0.57
23:K:3:ILE:HD12	23:K:4:PRO:HD2	1.87	0.57
1:2:696:C:P	7:H:100:PRO:HG3	2.46	0.56
1:2:1043:U:H5	1:2:1073:G:H1	1.52	0.56
1:2:1066:C:O4'	3:B:148:ASN:ND2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:102:PHE:HD2	2:A:131:GLN:HG2	1.70	0.56
4:C:58:ILE:H	4:C:58:ILE:HD12	1.69	0.56
9:J:157:ASP:OD1	9:J:158:PHE:N	2.36	0.56
26:Q:30:LYS:HZ2	26:Q:35:PRO:HD3	1.70	0.56
3:B:36:SER:HA	3:B:41:ARG:HE	1.69	0.56
7:H:99:LEU:HD22	7:H:112:ARG:HD3	1.87	0.56
13:V:83:TRP:CH2	13:V:85:TYR:HD2	2.22	0.56
22:F:105:ASN:HA	22:F:108:LYS:HE3	1.87	0.56
38:l:47:H2U:H2'	38:l:50:U:P	2.45	0.56
39:j:74:LEU:N	39:j:89:ARG:NH2	2.53	0.56
39:j:204:ALA:HB1	39:j:251:ILE:HG13	1.87	0.56
40:k:290:ASN:ND2	41:l:134:LEU:HD11	2.20	0.56
1:2:357:U:O2'	1:2:359:A:OP1	2.23	0.56
1:2:959:U:OP2	11:N:55:ARG:NH1	2.38	0.56
1:2:1131:A:H2'	1:2:1132:A:H8	1.70	0.56
1:2:1381:G:P	30:U:89:ARG:HH22	2.27	0.56
1:2:1480:C:P	1:2:1519:G:H22	2.28	0.56
1:2:1481:A:N3	1:2:1605:G:O2'	2.33	0.56
4:C:244:PRO:HA	4:C:247:VAL:HG12	1.86	0.56
5:E:171:ASP:OD1	5:E:172:PHE:N	2.36	0.56
10:L:77:SER:HB3	10:L:85:VAL:HB	1.86	0.56
11:N:38:ILE:HG21	11:N:78:ASN:HD22	1.70	0.56
23:K:37:THR:HB	23:K:41:PHE:HE1	1.69	0.56
24:M:71:LEU:HD12	34:f:114:VAL:HG21	1.86	0.56
30:U:69:LYS:HB2	30:U:78:THR:HG23	1.87	0.56
39:j:205:LEU:HD12	39:j:220:VAL:HB	1.87	0.56
41:l:165:CYS:SG	41:l:166:LEU:N	2.78	0.56
1:2:808:G:H2'	1:2:809:G:C8	2.40	0.56
1:2:1058:C:H5'	1:2:1059:U:O5'	2.04	0.56
3:B:121:ILE:HG12	3:B:161:ILE:HG23	1.87	0.56
4:C:86:MET:HE1	4:C:108:VAL:HB	1.87	0.56
4:C:143:PRO:HG2	4:C:227:TYR:CE2	2.29	0.56
35:g:109:GLY:N	35:g:129:ASP:HB3	2.21	0.56
1:2:274:C:O2'	1:2:276:U:O4	2.19	0.56
1:2:863:U:H3'	14:W:28:ARG:NH2	2.20	0.56
3:B:179:SER:OG	3:B:183:GLN:HB2	2.06	0.56
12:O:16:VAL:HG12	12:O:18:ARG:HG3	1.87	0.56
16:Y:20:ARG:HH11	16:Y:74:LEU:HD21	1.69	0.56
35:g:6:ILE:HG12	35:g:256:ARG:HH22	1.71	0.56
1:2:888:U:H2'	1:2:889:C:H6	1.71	0.56
1:2:1213:U:O2'	33:d:2:ALA:N	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1626:U:H2'	1:2:1627:G:H8	1.69	0.56
1:2:1749:C:H2'	1:2:1750:U:H6	1.71	0.56
28:S:119:ILE:CG2	28:S:121:SER:HB3	2.36	0.56
35:g:117:ASP:N	35:g:122:LYS:O	2.33	0.56
39:j:21:MET:HB2	39:j:98:CYS:SG	2.46	0.56
40:k:113:LYS:HG2	40:k:217:LEU:HD12	1.87	0.56
1:2:157:U:O2'	1:2:159:C:OP2	2.22	0.56
10:L:80:MET:HE3	10:L:83:THR:OG1	2.06	0.56
17:a:4:LYS:HD3	17:a:5:ARG:HE	1.69	0.56
24:M:36:ARG:HH22	24:M:94:LEU:HD13	1.71	0.56
33:d:41:GLN:HG3	33:d:42:SER:N	2.21	0.56
41:l:247:LYS:HD2	41:l:258:VAL:HG21	1.88	0.56
1:2:1380:A:H5''	30:U:60:THR:HG23	1.88	0.56
1:2:1680:U:OP1	6:G:31:ARG:NH2	2.33	0.56
5:E:88:ASP:OD2	5:E:122:LYS:NZ	2.32	0.56
6:G:74:LYS:HD2	6:G:94:ARG:HG2	1.88	0.56
40:k:94:ILE:HG23	40:k:391:VAL:HG21	1.87	0.56
40:k:380:LEU:HB3	40:k:396:ILE:HD11	1.88	0.56
41:l:186:ARG:HH21	41:l:234:VAL:HA	1.71	0.56
1:2:97:C:H2'	1:2:98:U:H6	1.69	0.56
2:A:30:GLN:HE21	2:A:46:ASN:ND2	2.03	0.56
2:A:90:ALA:HA	2:A:95:ALA:HB3	1.86	0.56
9:J:33:GLU:N	9:J:33:GLU:OE2	2.39	0.56
24:M:60:THR:O	24:M:61:GLU:HG3	2.04	0.56
29:T:13:ASP:OD1	29:T:14:PHE:N	2.38	0.56
30:U:101:LYS:HA	30:U:104:THR:HG22	1.88	0.56
40:k:239:MET:O	40:k:239:MET:HG2	2.05	0.56
1:2:14:C:H5'	4:C:169:SER:OG	2.06	0.56
1:2:824:U:H2'	1:2:825:U:C6	2.41	0.56
7:H:8:ILE:O	7:H:43:PHE:HD2	1.89	0.56
14:W:42:GLN:NE2	14:W:50:PHE:HD1	2.04	0.56
21:D:40:ARG:NE	30:U:110:PRO:HD3	2.20	0.56
27:R:88:VAL:O	27:R:90:ALA:N	2.39	0.56
30:U:42:ILE:HD12	30:U:52:LYS:NZ	2.21	0.56
1:2:127:G:C2	6:G:195:ILE:HD11	2.42	0.55
1:2:654:G:OP2	1:2:673:C:N4	2.39	0.55
4:C:127:ALA:O	4:C:131:ARG:HG3	2.05	0.55
15:X:53:VAL:HA	15:X:74:VAL:HG12	1.88	0.55
23:K:54:PHE:HB3	23:K:72:GLY:HA2	1.88	0.55
1:2:926:C:H1'	12:O:124:ASP:O	2.06	0.55
1:2:1754:A:OP2	36:i:66:ARG:NH1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:56:LEU:N	5:E:60:GLU:OE2	2.39	0.55
11:N:83:GLU:OE1	11:N:83:GLU:N	2.37	0.55
16:Y:13:ILE:HB	16:Y:22:GLN:HE21	1.69	0.55
34:f:100:LEU:HB3	34:f:103:LEU:HD13	1.87	0.55
40:k:127:ARG:NH2	44:k:601:GCP:O2B	2.39	0.55
1:2:107:C:H2'	1:2:108:A:C8	2.40	0.55
1:2:1299:A:OP1	4:C:104:LYS:NZ	2.39	0.55
1:2:1682:U:C2	1:2:1715:G:O6	2.59	0.55
1:2:1757:C:H2'	1:2:1758:G:C8	2.41	0.55
9:J:139:GLN:OE1	16:Y:63:GLN:NE2	2.39	0.55
11:N:46:THR:H	11:N:49:GLN:NE2	2.03	0.55
14:W:38:LEU:O	14:W:41:MET:HB2	2.06	0.55
1:2:242:G:H2'	1:2:243:A:H8	1.71	0.55
1:2:349:U:O2'	1:2:969:A:N1	2.37	0.55
1:2:1416:G:O5'	26:Q:128:LYS:HE2	2.05	0.55
1:2:1798:A:O2'	17:a:101:PRO:HD2	2.07	0.55
5:E:100:ARG:NH2	5:E:121:TYR:O	2.39	0.55
11:N:36:GLN:HG3	11:N:40:TYR:HE2	1.72	0.55
27:R:26:MET:HE1	27:R:58:MET:HB3	1.88	0.55
30:U:45:ALA:HB3	30:U:52:LYS:NZ	2.20	0.55
35:g:229:VAL:HG13	35:g:238:PHE:HB3	1.88	0.55
1:2:29:U:H2'	1:2:30:G:C8	2.41	0.55
1:2:1737:C:H2'	1:2:1738:A:C8	2.42	0.55
2:A:148:ASP:HB2	2:A:164:ASN:OD1	2.07	0.55
7:H:28:GLU:HB2	7:H:35:LYS:HG3	1.88	0.55
16:Y:14:SER:HA	16:Y:21:LYS:HD2	1.88	0.55
35:g:6:ILE:HA	35:g:324:THR:HG23	1.88	0.55
39:j:163:LYS:HD3	39:j:166:LEU:HD12	1.88	0.55
1:2:1152:G:H2'	1:2:1153:G:C8	2.40	0.55
4:C:145:ARG:H	4:C:226:THR:HG21	1.72	0.55
4:C:236:GLU:H	4:C:236:GLU:CD	2.11	0.55
14:W:42:GLN:NE2	14:W:50:PHE:CD1	2.75	0.55
23:K:31:LYS:NZ	23:K:36:ASP:O	2.39	0.55
24:M:27:THR:HB	24:M:118:GLY:HA3	1.88	0.55
25:P:127:ARG:NH2	25:P:128:HIS:O	2.40	0.55
26:Q:94:GLN:HB2	26:Q:102:LYS:CD	2.32	0.55
28:S:45:LEU:HD11	29:T:36:ILE:HD13	1.88	0.55
35:g:301:TRP:CE2	35:g:308:LEU:HD13	2.42	0.55
1:2:193:U:H3'	1:2:194:G:H4'	1.89	0.55
1:2:1145:G:H2'	1:2:1146:A:C8	2.42	0.55
1:2:1545:A:O2'	28:S:89:GLN:O	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:171:SER:HB2	4:C:206:THR:CG2	2.37	0.55
11:N:5:HIS:HB3	11:N:117:LEU:HD23	1.89	0.55
26:Q:143:ARG:NH1	38:1:35:A:OP2	2.38	0.55
33:d:23:ILE:HG13	33:d:38:ILE:HD13	1.88	0.55
40:k:497:GLU:O	40:k:499:ILE:HG13	2.06	0.55
1:2:77:U:H1'	6:G:159:ARG:NH2	2.21	0.55
2:A:160:ILE:HG21	2:A:173:ILE:HD11	1.89	0.55
3:B:213:ARG:HD2	3:B:214:LYS:HB2	1.89	0.55
23:K:16:PHE:CD1	23:K:76:LEU:HD11	2.42	0.55
34:f:131:ALA:N	34:f:138:TYR:O	2.35	0.55
1:2:153:G:H3'	16:Y:132:ARG:NH2	2.21	0.55
1:2:403:G:H2'	1:2:404:C:H6	1.71	0.55
1:2:408:C:H2'	1:2:409:A:H8	1.71	0.55
1:2:525:A:OP1	16:Y:93:ARG:NE	2.37	0.55
1:2:1246:U:OP1	34:f:93:HIS:N	2.29	0.55
1:2:1597:C:H5'	1:2:1598:A:OP2	2.07	0.55
5:E:191:ARG:NE	5:E:245:LYS:HG2	2.22	0.55
9:J:27:GLU:OE2	9:J:39:LYS:HD3	2.06	0.55
9:J:109:LEU:HD13	9:J:146:PHE:HD2	1.71	0.55
22:F:103:GLY:HA3	22:F:106:ASN:CG	2.20	0.55
22:F:117:LYS:O	22:F:121:GLU:HG2	2.07	0.55
22:F:194:GLU:OE1	31:Z:63:SER:OG	2.24	0.55
35:g:245:ASP:OD2	35:g:265:SER:N	2.37	0.55
39:j:72:VAL:CG2	39:j:89:ARG:HE	2.19	0.55
1:2:1405:U:H2'	1:2:1406:G:C8	2.41	0.55
15:X:75:GLN:NE2	15:X:76:LEU:O	2.39	0.55
31:Z:50:ILE:HG22	31:Z:70:LYS:HD2	1.89	0.55
35:g:269:ILE:HG23	35:g:278:ILE:HG13	1.87	0.55
39:j:153:THR:HA	39:j:156:GLU:HG2	1.89	0.55
1:2:163:A:H5'	6:G:112:ILE:HD11	1.89	0.54
1:2:579:A:O2'	1:2:581:U:OP2	2.19	0.54
1:2:1157:C:N4	1:2:1162:A:H61	2.04	0.54
1:2:1168:G:N3	1:2:1573:7MG:HM72	2.22	0.54
1:2:1219:C:H5''	23:K:52:LYS:HD3	1.90	0.54
6:G:18:ILE:HD11	6:G:20:ASP:HB3	1.89	0.54
8:I:72:VAL:HG21	8:I:112:TRP:CZ2	2.42	0.54
22:F:176:LEU:HA	22:F:179:ILE:HG22	1.89	0.54
22:F:207:SER:OG	22:F:209:THR:OG1	2.23	0.54
26:Q:41:PRO:O	26:Q:43:ILE:N	2.40	0.54
35:g:229:VAL:HG11	35:g:272:LEU:HD11	1.89	0.54
39:j:8:PHE:O	39:j:132:TRP:NE1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:286:GLN:OE1	44:k:601:GCP:H2'	2.07	0.54
1:2:222:U:H2'	1:2:223:C:C6	2.42	0.54
1:2:733:A:H5'	1:2:734:A:N7	2.22	0.54
1:2:865:G:H2'	1:2:866:G:H8	1.72	0.54
1:2:1172:C:OP1	28:S:141:THR:OG1	2.25	0.54
1:2:1783:U:H2'	1:2:1784:G:H8	1.72	0.54
9:J:71:PHE:HD2	9:J:72:GLU:HG3	1.72	0.54
15:X:69:ARG:HG3	15:X:117:ILE:HG12	1.89	0.54
24:M:71:LEU:O	24:M:74:GLU:HG3	2.07	0.54
29:T:111:LEU:HD22	29:T:113:VAL:HG13	1.89	0.54
35:g:111:VAL:HA	35:g:127:SER:HB2	1.90	0.54
1:2:163:A:H2'	1:2:164:G:C8	2.42	0.54
1:2:398:A:H4'	5:E:3:ARG:HG3	1.89	0.54
1:2:961:C:H3'	11:N:70:LYS:HZ2	1.71	0.54
5:E:123:LEU:HD12	5:E:160:VAL:O	2.07	0.54
7:H:64:VAL:N	7:H:65:PRO:HD3	2.22	0.54
30:U:51:VAL:HG13	30:U:94:GLU:HB2	1.89	0.54
30:U:70:THR:O	33:d:40:ARG:NH1	2.33	0.54
38:1:26:M2G:HM22	38:1:44:A:C2	2.34	0.54
40:k:174:CYS:HA	40:k:183:TYR:CE2	2.43	0.54
40:k:217:LEU:HG	40:k:247:LEU:HD12	1.88	0.54
1:2:256:A:H1'	8:I:73:ALA:HB3	1.90	0.54
1:2:997:A:H2'	1:2:998:PSU:C6	2.43	0.54
1:2:1162:A:N3	1:2:1611:U:O2'	2.32	0.54
1:2:1782:C:N4	20:h:5:TRP:HE1	2.01	0.54
4:C:147:GLY:N	4:C:158:SER:O	2.38	0.54
5:E:19:MET:SD	5:E:108:ARG:HD2	2.47	0.54
10:L:132:SER:O	10:L:136:ARG:NH1	2.35	0.54
13:V:7:GLN:OE1	13:V:7:GLN:N	2.40	0.54
24:M:56:VAL:HG13	24:M:83:ALA:HA	1.89	0.54
28:S:17:LEU:HD21	28:S:66:LEU:HD22	1.89	0.54
30:U:109:GLU:HB2	30:U:110:PRO:HD2	1.89	0.54
39:j:216:MET:HE1	39:j:239:LYS:HB2	1.88	0.54
1:2:115:G:N7	10:L:67:ARG:NH2	2.55	0.54
2:A:53:THR:O	2:A:57:ILE:HD12	2.08	0.54
6:G:22:HIS:HA	6:G:25:ARG:NE	2.23	0.54
25:P:90:ILE:HD13	25:P:107:ILE:HG22	1.89	0.54
35:g:202:HIS:CD2	35:g:206:ILE:HG12	2.39	0.54
38:1:57:G:H2'	38:1:58:1MA:C8	2.43	0.54
39:j:181:ALA:HB2	39:j:235:LEU:HD13	1.88	0.54
1:2:405:U:H2'	1:2:406:A:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:598:A:N3	15:X:47:SER:OG	2.25	0.54
1:2:790:A:C5	1:2:791:U:N3	2.75	0.54
1:2:1107:G:H4'	1:2:1108:G:H5''	1.89	0.54
1:2:1480:C:H2'	1:2:1481:A:H5''	1.88	0.54
2:A:166:GLY:O	2:A:167:LYS:HG2	2.08	0.54
21:D:28:GLU:HB3	21:D:29:LEU:HD12	1.89	0.54
22:F:92:VAL:O	22:F:96:THR:HG23	2.07	0.54
24:M:36:ARG:NH2	24:M:94:LEU:HD13	2.23	0.54
26:Q:79:TYR:O	26:Q:82:ARG:HG2	2.08	0.54
39:j:74:LEU:N	39:j:89:ARG:HH22	2.05	0.54
1:2:216:A:O2'	1:2:217:A:OP1	2.25	0.54
1:2:789:U:H5	1:2:790:A:C4	2.26	0.54
1:2:976:A:N7	1:2:1023:U:O4	2.41	0.54
1:2:1439:C:H2'	1:2:1440:U:C6	2.43	0.54
1:2:1623:C:H2'	1:2:1624:U:H6	1.73	0.54
1:2:1792:A:OP2	17:a:4:LYS:NZ	2.36	0.54
6:G:159:ARG:HD3	6:G:172:ALA:HB2	1.90	0.54
27:R:116:LYS:HD2	27:R:117:LEU:N	2.23	0.54
40:k:253:LEU:HD11	41:l:239:CYS:HB3	1.89	0.54
1:2:97:C:H2'	1:2:98:U:C6	2.42	0.54
1:2:898:G:H8	3:B:3:VAL:O	1.91	0.54
1:2:1550:U:OP2	25:P:43:ARG:NH2	2.37	0.54
1:2:1559:U:H2'	1:2:1560:G:C8	2.43	0.54
1:2:1612:A:OP2	22:F:86:LYS:NZ	2.41	0.54
13:V:17:CYS:SG	13:V:56:SER:N	2.77	0.54
14:W:3:ARG:NH2	14:W:28:ARG:HH12	2.06	0.54
15:X:83:VAL:HG21	15:X:122:PHE:CE2	2.43	0.54
23:K:77:ARG:NH2	23:K:86:ILE:O	2.32	0.54
26:Q:6:SER:HB2	26:Q:23:LYS:HG2	1.88	0.54
35:g:62:TYR:HB3	35:g:93:TRP:CZ3	2.42	0.54
41:l:189:GLU:O	41:l:193:GLN:HG2	2.07	0.54
1:2:709:C:H2'	1:2:710:U:H4'	1.89	0.54
13:V:37:ALA:HA	13:V:50:TYR:HB3	1.89	0.54
17:a:83:ILE:H	17:a:83:ILE:HD12	1.72	0.54
22:F:103:GLY:O	22:F:106:ASN:CG	2.51	0.54
29:T:71:VAL:O	29:T:122:ARG:N	2.37	0.54
32:c:52:ASP:OD1	32:c:53:ILE:N	2.41	0.54
38:1:2:G:H2'	38:1:3:C:C6	2.43	0.54
38:1:9:1MG:H4'	38:1:45:U:C2'	2.38	0.54
41:l:241:SER:C	41:l:242:ILE:HD12	2.33	0.54
1:2:753:A:H5''	5:E:187:ARG:NH1	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:171:SER:O	4:C:206:THR:HG22	2.08	0.54
12:O:28:VAL:HG13	12:O:67:VAL:HG11	1.90	0.54
22:F:136:VAL:O	22:F:140:ILE:HG12	2.08	0.54
27:R:93:LEU:HD22	27:R:99:VAL:HA	1.89	0.54
40:k:124:GLN:HG2	40:k:126:VAL:H	1.73	0.54
1:2:179:A:H2'	1:2:180:A:O4'	2.07	0.53
1:2:471:U:H2'	1:2:472:A:C8	2.44	0.53
2:A:84:ARG:NH2	27:R:82:ASP:OD1	2.40	0.53
12:O:118:VAL:HG12	12:O:118:VAL:O	2.09	0.53
30:U:22:ILE:HG13	30:U:118:ILE:HA	1.90	0.53
1:2:79:C:OP1	6:G:172:ALA:HB3	2.07	0.53
1:2:1085:A:H5'	4:C:169:SER:HB3	1.89	0.53
1:2:1577:U:H2'	1:2:1578:C:H6	1.73	0.53
1:2:1598:A:H2'	1:2:1599:G:H5''	1.88	0.53
7:H:24:PHE:HA	7:H:27:LEU:HD13	1.90	0.53
7:H:66:SER:C	7:H:68:ALA:N	2.65	0.53
9:J:59:LEU:HD12	9:J:69:ARG:HA	1.90	0.53
10:L:21:THR:O	10:L:23:PRO:HD3	2.08	0.53
12:O:20:PHE:O	12:O:27:PHE:N	2.32	0.53
21:D:219:GLU:HB2	21:D:220:PRO:HD3	1.90	0.53
25:P:45:PHE:CZ	25:P:84:ILE:HD11	2.42	0.53
39:j:147:LEU:CD2	39:j:151:ASP:HB3	2.37	0.53
1:2:218:A:C6	1:2:842:U:H1'	2.43	0.53
1:2:419:A:H2'	1:2:420:A:C8	2.43	0.53
1:2:762:A:P	9:J:79:ARG:HH22	2.30	0.53
1:2:1056:U:H4'	3:B:202:LYS:HE3	1.90	0.53
1:2:1163:G:H2'	1:2:1164:G:C8	2.43	0.53
1:2:1467:A:H2'	1:2:1468:C:C6	2.43	0.53
1:2:1659:U:H2'	1:2:1660:G:H8	1.73	0.53
1:2:1778:G:H2'	1:2:1779:A:C8	2.43	0.53
39:j:127:TYR:HB3	39:j:132:TRP:CH2	2.43	0.53
40:k:108:HIS:HB3	40:k:111:HIS:CD2	2.44	0.53
1:2:55:A:H3'	1:2:402:G:H22	1.72	0.53
1:2:400:A:O2'	1:2:401:C:H4'	2.08	0.53
1:2:946:U:H2'	1:2:947:G:H8	1.71	0.53
1:2:1175:G:O2'	1:2:1194:C:O2'	2.24	0.53
1:2:1659:U:H2'	1:2:1660:G:C8	2.43	0.53
2:A:39:LYS:HD3	27:R:108:GLU:OE2	2.08	0.53
11:N:140:LYS:HE3	11:N:142:GLU:OE2	2.09	0.53
12:O:19:ILE:N	12:O:82:LYS:O	2.40	0.53
15:X:69:ARG:NH1	15:X:116:ASP:OD1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:U:82:TYR:HB3	33:d:52:PHE:HB3	1.89	0.53
35:g:104:PHE:CE1	35:g:139:GLY:HA2	2.43	0.53
1:2:593:A:OP2	9:J:38:ASN:ND2	2.42	0.53
1:2:1314:U:O2	27:R:4:VAL:HG11	2.09	0.53
1:2:1548:A:H2'	1:2:1549:U:C6	2.44	0.53
2:A:75:ALA:HB3	2:A:86:VAL:HG13	1.91	0.53
4:C:153:LEU:HA	13:V:4:ASP:OD2	2.09	0.53
6:G:48:TYR:CD1	6:G:113:ILE:HD11	2.43	0.53
6:G:219:ARG:NH2	6:G:220:LYS:HA	2.24	0.53
14:W:35:ILE:HD11	14:W:61:ILE:HD11	1.91	0.53
16:Y:15:ASN:HD22	16:Y:20:ARG:HE	1.54	0.53
24:M:59:VAL:HG11	24:M:64:ILE:HD11	1.90	0.53
34:f:131:ALA:HB3	34:f:138:TYR:HB3	1.88	0.53
35:g:208:VAL:HG11	35:g:249:ALA:HA	1.91	0.53
1:2:207:U:H2'	1:2:208:U:C6	2.44	0.53
1:2:255:A:H2'	1:2:256:A:C8	2.43	0.53
3:B:135:LEU:HD23	3:B:217:LEU:HA	1.90	0.53
22:F:94:ARG:HG2	22:F:174:ILE:HD13	1.90	0.53
28:S:30:TYR:O	28:S:33:THR:OG1	2.25	0.53
38:1:14:A:H2'	38:1:15:G:C6	2.43	0.53
1:2:447:C:OP1	5:E:49:ARG:NH2	2.38	0.53
1:2:1794:C:N4	17:a:6:ALA:H	2.05	0.53
7:H:28:GLU:HG3	7:H:35:LYS:HE3	1.90	0.53
15:X:83:VAL:HG22	15:X:84:THR:H	1.72	0.53
39:j:186:ALA:HB2	39:j:244:LEU:HD11	1.90	0.53
40:k:250:LYS:O	40:k:254:MET:HE2	2.09	0.53
1:2:342:C:H2'	1:2:343:A:H8	1.74	0.53
1:2:1584:A:H1'	1:2:1609:A:N6	2.24	0.53
1:2:1749:C:H2'	1:2:1750:U:C6	2.44	0.53
2:A:52:LYS:O	2:A:56:LYS:HG2	2.08	0.53
34:f:117:LEU:HD22	34:f:117:LEU:N	2.23	0.53
40:k:98:GLN:HE21	40:k:391:VAL:HG23	1.74	0.53
1:2:512:U:H2'	1:2:513:G:C8	2.43	0.53
1:2:649:U:O2'	1:2:650:G:OP1	2.23	0.53
1:2:1193:A:H2'	1:2:1194:C:O4'	2.09	0.53
2:A:38:TYR:CE1	2:A:39:LYS:HG2	2.44	0.53
12:O:79:VAL:HG21	12:O:110:LEU:HD13	1.90	0.53
13:V:3:ASN:OD1	13:V:4:ASP:N	2.37	0.53
22:F:89:CYS:SG	22:F:94:ARG:HB2	2.49	0.53
27:R:77:GLU:OE2	27:R:80:ARG:NH2	2.42	0.53
38:1:3:C:H2'	38:1:4:G:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:j:75:ARG:HH22	39:j:77:ASP:HB2	1.74	0.53
1:2:219:A:N7	1:2:831:U:H1'	2.22	0.53
1:2:773:C:OP1	5:E:22:LYS:HG2	2.08	0.53
1:2:861:A:O2'	1:2:962:A:N1	2.36	0.53
1:2:1182:A:C6	25:P:100:LYS:NZ	2.77	0.53
1:2:1337:C:H2'	1:2:1338:C:C6	2.44	0.53
1:2:1622:C:H2'	1:2:1623:C:C6	2.44	0.53
3:B:210:VAL:O	3:B:211:HIS:ND1	2.41	0.53
4:C:49:LEU:HD21	4:C:252:ALA:HB2	1.89	0.53
15:X:103:LEU:HD13	15:X:126:LYS:HD3	1.91	0.53
21:D:218:LEU:HG	21:D:221:SER:OG	2.08	0.53
22:F:101:MET:HB2	22:F:182:ARG:HH22	1.72	0.53
36:i:36:ALA:HB1	36:i:49:ALA:HB1	1.90	0.53
40:k:297:PHE:O	40:k:301:THR:OG1	2.17	0.53
1:2:694:U:O2'	7:H:97:ARG:HA	2.09	0.52
1:2:1233:A:H4'	34:f:143:HIS:CD2	2.44	0.52
1:2:1455:C:H4'	28:S:137:HIS:CD2	2.44	0.52
1:2:1614:G:O2'	32:c:18:ARG:HD2	2.09	0.52
6:G:148:THR:HB	6:G:151:ASP:OD2	2.09	0.52
22:F:105:ASN:HB3	22:F:108:LYS:NZ	2.25	0.52
31:Z:90:LYS:HZ1	31:Z:104:ALA:HA	1.74	0.52
38:1:26:M2G:HM23	38:1:45:U:H3	1.73	0.52
40:k:187:ARG:HH22	40:k:298:ILE:HG22	1.72	0.52
1:2:71:A:H2'	1:2:72:A:C4	2.44	0.52
1:2:463:A:C2	1:2:464:G:C8	2.97	0.52
1:2:811:A:H62	1:2:857:G:H2'	1.75	0.52
1:2:888:U:H2'	1:2:889:C:C6	2.44	0.52
1:2:1112:A:OP1	1:2:1114:U:H1'	2.08	0.52
3:B:171:ILE:HG21	3:B:197:ILE:HG12	1.92	0.52
17:a:26:CYS:SG	17:a:28:ARG:HB2	2.49	0.52
21:D:116:ARG:NH1	21:D:150:MET:HE1	2.24	0.52
22:F:107:GLY:O	22:F:109:LYS:N	2.42	0.52
22:F:169:ARG:HH12	32:c:55:VAL:HG21	1.73	0.52
22:F:210:SER:HB3	22:F:213:ILE:HG22	1.92	0.52
24:M:23:VAL:HG11	24:M:124:ARG:NH2	2.24	0.52
31:Z:71:LEU:HD13	31:Z:76:ALA:HA	1.91	0.52
39:j:77:ASP:HB3	39:j:82:TYR:N	2.24	0.52
1:2:1081:C:O2	13:V:62:ARG:NH2	2.42	0.52
1:2:1172:C:H5'	1:2:1541:A:O2'	2.10	0.52
1:2:1337:C:H2'	1:2:1338:C:H6	1.74	0.52
1:2:1391:C:H2'	1:2:1392:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:38:ILE:HB	11:N:42:ARG:NH1	2.24	0.52
17:a:21:VAL:HG11	17:a:72:HIS:HD1	1.73	0.52
27:R:23:LYS:HE3	35:g:179:MET:HE2	1.91	0.52
36:i:62:ARG:NH1	36:i:64:LYS:HB3	2.25	0.52
38:1:11:C:H2'	38:1:12:G:C8	2.45	0.52
39:j:254:VAL:O	39:j:258:TYR:CD2	2.62	0.52
40:k:382:ALA:HB3	40:k:387:LEU:HD12	1.90	0.52
1:2:200:G:H2'	1:2:201:A:C8	2.44	0.52
1:2:871:G:H2'	1:2:872:U:O4'	2.08	0.52
2:A:102:PHE:CE2	2:A:132:ALA:HA	2.45	0.52
3:B:8:ARG:C	3:B:9:LEU:CD1	2.76	0.52
14:W:25:VAL:HB	14:W:63:VAL:HG12	1.91	0.52
18:b:15:GLU:O	18:b:29:ARG:NH2	2.28	0.52
36:i:104:LYS:HD3	36:i:109:LEU:HD21	1.90	0.52
40:k:103:ILE:HG12	40:k:213:ALA:HB3	1.92	0.52
41:l:171:LYS:HG3	41:l:214:LYS:HG2	1.91	0.52
1:2:88:U:H2'	1:2:89:G:H8	1.73	0.52
1:2:862:A:N7	1:2:963:U:O4	2.43	0.52
1:2:1290:G:H1	1:2:1323:G:N2	2.00	0.52
3:B:204:ILE:HG22	3:B:205:PHE:CD2	2.45	0.52
38:1:16:H2U:N3	38:1:59:A:H2	2.08	0.52
40:k:320:SER:HB3	40:k:412:LEU:HB2	1.92	0.52
40:k:431:GLU:HG3	40:k:482:MET:SD	2.49	0.52
1:2:349:U:H4'	1:2:350:C:H5''	1.92	0.52
1:2:608:U:O3'	15:X:19:ARG:NH2	2.43	0.52
1:2:1275:U:OP1	21:D:147:ALA:N	2.42	0.52
1:2:1427:G:H2'	1:2:1428:U:H6	1.73	0.52
1:2:1526:U:O2'	26:Q:42:GLU:OE2	2.16	0.52
2:A:52:LYS:NZ	13:V:82:VAL:O	2.24	0.52
3:B:160:HIS:O	3:B:164:ILE:HG12	2.10	0.52
5:E:23:LEU:HA	9:J:3:ARG:HH22	1.74	0.52
5:E:65:LEU:HD12	5:E:80:THR:HG22	1.91	0.52
8:I:85:PRO:HB3	10:L:12:ALA:HB2	1.90	0.52
11:N:34:VAL:O	11:N:38:ILE:HG12	2.09	0.52
25:P:39:ALA:H	25:P:42:ARG:CB	2.18	0.52
31:Z:54:ALA:O	31:Z:89:ILE:HD11	2.10	0.52
36:i:37:GLN:NE2	36:i:74:GLY:HA2	2.24	0.52
36:i:61:ILE:HA	36:i:91:VAL:HG12	1.91	0.52
36:i:103:LEU:HD22	36:i:108:GLU:HG3	1.92	0.52
1:2:57:G:C2	1:2:91:G:C2	2.98	0.52
1:2:219:A:C8	1:2:831:U:H1'	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:958:U:C6	11:N:61:THR:HG23	2.44	0.52
1:2:1472:G:H2'	1:2:1473:A:C8	2.44	0.52
1:2:1502:G:H2'	1:2:1503:A:C4	2.45	0.52
30:U:68:ARG:NH2	30:U:77:LYS:HE3	2.24	0.52
33:d:36:LEU:HB3	33:d:38:ILE:HG22	1.91	0.52
40:k:97:ARG:HB3	40:k:387:LEU:HD21	1.91	0.52
40:k:463:MET:HB3	40:k:502:SER:OG	2.09	0.52
1:2:86:A:H2'	1:2:87:C:H6	1.74	0.52
1:2:88:U:C2	1:2:89:G:C8	2.98	0.52
1:2:598:A:H2'	1:2:599:U:C6	2.45	0.52
1:2:992:A:N6	1:2:1010:G:O2'	2.43	0.52
10:L:111:VAL:HA	10:L:139:VAL:HG22	1.90	0.52
29:T:40:SER:OG	29:T:43:ASN:OD1	2.19	0.52
29:T:57:ARG:HD2	29:T:80:TYR:CE2	2.45	0.52
35:g:6:ILE:C	35:g:7:MET:HE2	2.35	0.52
38:l:68:G:OP2	41:l:253:ARG:NH1	2.42	0.52
39:j:211:MET:O	39:j:211:MET:HE3	2.10	0.52
39:j:217:GLN:HB3	39:j:219:LYS:HZ3	1.74	0.52
40:k:216:LEU:HD23	40:k:246:ILE:HG12	1.91	0.52
1:2:1021:C:H4'	1:2:1124:A:N6	2.23	0.52
1:2:1521:G:N7	29:T:68:ARG:NH1	2.57	0.52
1:2:1794:C:C4	17:a:93:ARG:NH2	2.77	0.52
1:2:1794:C:H6	17:a:7:SER:HB3	1.75	0.52
3:B:5:LYS:C	3:B:7:LYS:N	2.61	0.52
9:J:126:ARG:HG2	19:e:33:ARG:HD3	1.91	0.52
10:L:19:ILE:HG12	10:L:34:TRP:HB2	1.90	0.52
25:P:37:ALA:O	25:P:41:VAL:HB	2.10	0.52
26:Q:16:ALA:HB2	26:Q:72:GLY:HA3	1.91	0.52
27:R:104:THR:OG1	27:R:105:GLN:OE1	2.27	0.52
28:S:17:LEU:HD11	28:S:66:LEU:HB3	1.92	0.52
34:f:139:CYS:SG	34:f:140:GLY:N	2.80	0.52
38:l:7:G:O2'	38:l:49:5MC:O4'	2.28	0.52
41:l:241:SER:O	41:l:242:ILE:HG13	2.10	0.52
1:2:108:A:H2'	1:2:109:G:C8	2.44	0.52
1:2:295:U:H2'	1:2:296:U:C6	2.45	0.52
1:2:567:G:OP2	15:X:70:LYS:NZ	2.33	0.52
1:2:1159:A:H2'	1:2:1160:C:H6	1.74	0.52
2:A:140:ASN:HD22	4:C:67:PRO:HD3	1.75	0.52
11:N:96:VAL:HG11	11:N:150:VAL:HG11	1.90	0.52
24:M:96:LYS:O	24:M:103:ALA:HB3	2.09	0.52
29:T:14:PHE:HZ	29:T:132:LEU:HD13	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:127:ARG:HH12	40:k:136:ILE:C	2.18	0.52
1:2:165:C:O2'	6:G:131:LYS:HD2	2.10	0.51
1:2:552:G:OP2	1:2:553:C:O2'	2.20	0.51
1:2:802:A:N7	7:H:105:LYS:NZ	2.58	0.51
1:2:898:G:H5''	3:B:3:VAL:HG23	1.92	0.51
1:2:1513:A:O2'	1:2:1514:A:OP1	2.29	0.51
16:Y:3:ASP:OD2	16:Y:32:ARG:NH1	2.43	0.51
21:D:72:LEU:HD22	23:K:65:TYR:HD1	1.74	0.51
38:1:14:A:H2'	38:1:15:G:C5	2.44	0.51
39:j:21:MET:HG2	39:j:69:ASP:O	2.10	0.51
40:k:118:ARG:HD3	40:k:124:GLN:HG3	1.91	0.51
40:k:243:HIS:HB3	40:k:302:ILE:HG12	1.91	0.51
1:2:1063:G:O2'	3:B:204:ILE:O	2.28	0.51
1:2:1163:G:H2'	1:2:1164:G:H8	1.74	0.51
1:2:1590:A:H2'	1:2:1591:A:H8	1.74	0.51
4:C:180:GLY:C	9:J:53:ARG:HH12	2.15	0.51
7:H:63:PRO:HB2	7:H:65:PRO:HD3	1.91	0.51
14:W:27:ILE:HB	14:W:61:ILE:HB	1.93	0.51
25:P:77:ARG:HB2	25:P:102:PHE:CG	2.45	0.51
26:Q:44:LEU:HB3	26:Q:78:VAL:HG11	1.92	0.51
30:U:67:THR:HG23	33:d:40:ARG:HB2	1.92	0.51
35:g:70:GLN:HG2	35:g:86:TRP:HE1	1.75	0.51
38:1:37:T6A:H153	38:1:38:A:H2	1.76	0.51
1:2:221:A:H2'	1:2:222:U:C6	2.45	0.51
1:2:331:U:O2'	8:I:5:ARG:NH2	2.44	0.51
1:2:476:A:O3'	19:e:33:ARG:NH2	2.28	0.51
1:2:957:U:P	18:b:20:LYS:HE2	2.51	0.51
4:C:162:LYS:HD2	14:W:95:PRO:HA	1.91	0.51
11:N:33:VAL:HG21	11:N:66:ILE:HD12	1.92	0.51
21:D:66:ILE:HG13	21:D:67:ASN:N	2.25	0.51
30:U:58:LEU:HD22	30:U:88:LYS:HG2	1.91	0.51
34:f:136:ARG:NH2	34:f:138:TYR:HB2	2.20	0.51
38:1:26:M2G:HN1	38:1:44:A:H61	1.59	0.51
39:j:255:ILE:HG13	39:j:262:CYS:SG	2.50	0.51
1:2:57:G:N3	1:2:91:G:N2	2.58	0.51
1:2:1590:A:H2'	1:2:1591:A:C8	2.45	0.51
14:W:115:GLU:HA	14:W:118:ARG:HE	1.75	0.51
35:g:75:SER:HB3	35:g:80:TYR:HB2	1.92	0.51
38:1:14:A:OP2	38:1:14:A:H8	1.93	0.51
39:j:170:LYS:HA	39:j:173:ILE:HG12	1.92	0.51
39:j:247:ALA:O	39:j:251:ILE:HD12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:349:LEU:HG	40:k:388:LYS:HA	1.93	0.51
1:2:862:A:OP1	14:W:57:ARG:NH1	2.42	0.51
1:2:890:A:H2'	1:2:891:A:C8	2.38	0.51
1:2:1439:C:H2'	1:2:1440:U:H6	1.75	0.51
1:2:1768:U:H2'	1:2:1769:U:H6	1.74	0.51
1:2:1771:C:OP2	20:h:2:ARG:NE	2.41	0.51
11:N:119:GLU:OE1	11:N:141:TYR:HE2	1.93	0.51
16:Y:86:GLU:OE1	16:Y:90:ARG:HD2	2.11	0.51
21:D:211:PRO:HD3	27:R:19:LYS:HG2	1.92	0.51
29:T:38:LYS:HD3	29:T:43:ASN:C	2.36	0.51
35:g:283:PRO:HG2	35:g:312:TYR:OH	2.11	0.51
39:j:12:LYS:O	39:j:39:TYR:OH	2.29	0.51
39:j:72:VAL:HG13	39:j:89:ARG:CZ	2.40	0.51
1:2:77:U:H1'	6:G:159:ARG:HH21	1.73	0.51
1:2:373:U:H2'	1:2:374:U:C6	2.45	0.51
1:2:1206:C:O2'	1:2:1207:A:OP2	2.21	0.51
1:2:1263:G:N2	1:2:1264:G:N3	2.58	0.51
1:2:1358:C:H5''	29:T:134:ARG:NH1	2.23	0.51
1:2:1568:A:H2'	1:2:1569:C:O4'	2.11	0.51
4:C:145:ARG:HB2	4:C:227:TYR:CE1	2.46	0.51
5:E:14:ALA:HB1	5:E:18:TRP:CE3	2.46	0.51
5:E:103:TYR:HB2	5:E:182:TYR:OH	2.11	0.51
24:M:31:HIS:HB2	24:M:116:ASN:HD21	1.75	0.51
28:S:27:ASN:O	28:S:31:ALA:N	2.40	0.51
39:j:72:VAL:CG1	39:j:89:ARG:HB3	2.31	0.51
39:j:74:LEU:CD1	39:j:89:ARG:NH1	2.74	0.51
40:k:172:PRO:HD2	40:k:183:TYR:HB2	1.91	0.51
1:2:968:C:H4'	1:2:1103:U:O2'	2.11	0.51
1:2:996:G:H1	1:2:1006:5MC:N4	2.09	0.51
1:2:1607:U:H5''	26:Q:75:VAL:HG22	1.93	0.51
1:2:1757:C:H2'	1:2:1758:G:H8	1.74	0.51
4:C:42:PRO:HB2	4:C:48:ARG:HG2	1.91	0.51
8:I:27:PHE:CB	8:I:49:ARG:HH22	2.24	0.51
9:J:127:VAL:O	9:J:131:GLN:HG2	2.11	0.51
22:F:101:MET:CE	22:F:178:THR:CG2	2.82	0.51
23:K:11:ILE:HG22	23:K:35:ILE:HG12	1.91	0.51
27:R:71:PHE:HE2	27:R:73:LEU:HB2	1.76	0.51
38:1:47:H2U:H2'	38:1:50:U:OP1	2.10	0.51
1:2:1056:U:O2'	1:2:1058:C:OP2	2.27	0.51
1:2:1520:U:O3'	29:T:78:LYS:NZ	2.41	0.51
3:B:146:GLN:NE2	3:B:206:PRO:HG3	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:48:TYR:CG	6:G:113:ILE:HD11	2.46	0.51
23:K:48:SER:O	23:K:52:LYS:HG2	2.10	0.51
25:P:98:ASN:OD1	25:P:122:THR:HA	2.10	0.51
33:d:21:CYS:O	33:d:22:ARG:HG2	2.11	0.51
35:g:140:ASP:OD1	35:g:141:CYS:N	2.43	0.51
38:1:23:C:N4	38:1:24:G:O6	2.43	0.51
38:1:53:G:H2'	38:1:54:A:H8	1.75	0.51
1:2:194:G:OP1	1:2:227:G:H5'	2.11	0.51
1:2:1791:G:C4	17:a:75:ILE:HD11	2.46	0.51
2:A:175:TYR:CD2	2:A:199:PRO:HB3	2.46	0.51
4:C:173:ARG:HB3	4:C:175:ILE:HD11	1.93	0.51
8:I:173:ARG:O	8:I:177:SER:N	2.41	0.51
13:V:1:MET:SD	13:V:1:MET:N	2.83	0.51
25:P:75:VAL:HA	25:P:93:VAL:HG13	1.93	0.51
26:Q:52:LEU:HB3	26:Q:57:LEU:HD21	1.92	0.51
30:U:23:ARG:HE	30:U:92:ASP:HB3	1.75	0.51
34:f:143:HIS:CG	34:f:144:SER:N	2.79	0.51
36:i:78:LEU:HB3	36:i:93:HIS:HB3	1.93	0.51
36:i:104:LYS:HZ1	36:i:111:GLU:HA	1.76	0.51
37:3:26:A:H2	39:j:57:ARG:HH22	1.58	0.51
41:l:232:GLU:HG3	41:l:233:TYR:CD2	2.46	0.51
1:2:148:C:OP1	16:Y:121:THR:OG1	2.26	0.51
1:2:222:U:H2'	1:2:223:C:H6	1.74	0.51
1:2:638:U:OP1	7:H:101:LYS:HD2	2.11	0.51
2:A:109:ASN:OD1	2:A:111:ILE:HG22	2.11	0.51
5:E:36:HIS:CD2	5:E:85:GLY:HA3	2.46	0.51
5:E:158:ASP:OD1	5:E:175:PHE:N	2.40	0.51
8:I:56:ARG:NH2	8:I:175:GLY:O	2.37	0.51
10:L:21:THR:HG22	10:L:32:LYS:H	1.74	0.51
23:K:69:THR:HG22	23:K:70:GLU:H	1.75	0.51
25:P:99:GLY:C	25:P:100:LYS:HD3	2.35	0.51
40:k:426:ILE:HD11	40:k:490:PRO:HB3	1.93	0.51
1:2:151:U:H5'	6:G:13:GLN:HE22	1.76	0.50
1:2:431:G:H2'	1:2:432:C:C6	2.46	0.50
1:2:1097:U:H1'	14:W:71:LYS:HD3	1.93	0.50
1:2:1101:G:H2'	1:2:1102:U:O4'	2.11	0.50
1:2:1626:U:H5'	17:a:88:SER:HA	1.92	0.50
2:A:8:ASP:OD1	2:A:9:LEU:N	2.44	0.50
4:C:67:PRO:HA	13:V:29:HIS:CE1	2.46	0.50
5:E:86:PHE:CZ	5:E:87:MET:HE3	2.46	0.50
28:S:119:ILE:HG22	28:S:121:SER:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1:57:G:H2'	38:1:58:1MA:H8	1.74	0.50
40:k:281:VAL:HG23	41:l:134:LEU:HD23	1.93	0.50
40:k:355:ILE:HB	40:k:373:ILE:HB	1.93	0.50
44:k:601:GCP:N2	41:l:239:CYS:HB3	2.26	0.50
41:l:235:THR:OG1	41:l:242:ILE:HG13	2.11	0.50
1:2:270:A:C2	1:2:284:G:C6	2.99	0.50
1:2:449:U:H5''	5:E:7:LYS:HD3	1.92	0.50
1:2:487:G:N1	1:2:488:C:O2	2.44	0.50
1:2:989:C:H2'	1:2:990:G:O4'	2.11	0.50
1:2:1508:U:H2'	1:2:1509:G:C8	2.47	0.50
1:2:1508:U:H2'	1:2:1509:G:H8	1.75	0.50
1:2:1532:G:O2'	31:Z:72:GLY:O	2.29	0.50
1:2:1563:C:H2'	1:2:1564:U:C6	2.46	0.50
1:2:1611:U:C5'	22:F:171:ASN:HD21	2.25	0.50
1:2:1711:G:H3'	1:2:1712:A:C8	2.46	0.50
3:B:29:TRP:CD2	3:B:47:LEU:HD21	2.47	0.50
5:E:41:SER:OG	5:E:42:LEU:N	2.44	0.50
5:E:182:TYR:HD1	5:E:192:VAL:HG22	1.76	0.50
7:H:14:THR:O	7:H:17:GLU:HG2	2.11	0.50
7:H:77:LEU:HD22	7:H:92:PHE:HZ	1.76	0.50
15:X:58:GLY:C	15:X:68:ILE:HD11	2.36	0.50
15:X:69:ARG:HB3	15:X:86:PHE:HE1	1.75	0.50
24:M:35:ALA:HB1	24:M:40:GLU:HB3	1.94	0.50
26:Q:27:GLY:N	26:Q:63:ILE:O	2.42	0.50
32:c:65:ARG:HB2	37:3:23:A:N6	2.26	0.50
1:2:700:C:H2'	1:2:701:U:C6	2.46	0.50
1:2:994:A:H2'	1:2:995:U:O4'	2.11	0.50
1:2:1036:C:O2	14:W:16:ASN:ND2	2.43	0.50
1:2:1210:A:N6	1:2:1451:G:O6	2.44	0.50
2:A:20:ALA:O	2:A:21:ARG:HG2	2.11	0.50
7:H:101:LYS:HD3	7:H:112:ARG:HH22	1.76	0.50
8:I:67:TRP:O	8:I:71:GLY:CA	2.60	0.50
22:F:43:LYS:H	22:F:71:TYR:HE1	1.60	0.50
26:Q:38:LEU:HD11	29:T:10:PRO:HG3	1.93	0.50
1:2:26:A:H2'	1:2:27:U:C6	2.47	0.50
1:2:79:C:H3'	1:2:80:A:H8	1.76	0.50
1:2:168:A:OP2	6:G:137:ARG:NH2	2.44	0.50
1:2:550:G:H2'	1:2:551:G:H8	1.77	0.50
1:2:1359:A:O2'	29:T:2:PRO:HB2	2.11	0.50
1:2:1399:A:OP1	27:R:56:HIS:NE2	2.36	0.50
1:2:1601:U:H2'	1:2:1602:U:C6	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:53:GLY:HA2	3:B:56:ASN:OD1	2.11	0.50
10:L:59:PRO:HD3	10:L:138:ASN:HD21	1.76	0.50
11:N:127:ARG:O	11:N:131:THR:HG23	2.12	0.50
13:V:71:ARG:NH1	18:b:4:VAL:HG21	2.25	0.50
25:P:34:VAL:HG22	25:P:45:PHE:CD2	2.45	0.50
39:j:216:MET:HE3	39:j:235:LEU:H	1.77	0.50
40:k:157:GLU:N	40:k:158:PRO:HD2	2.26	0.50
40:k:324:ASN:HD21	40:k:404:PRO:HG3	1.75	0.50
41:l:201:THR:HG21	41:l:217:PHE:HE2	1.75	0.50
1:2:12:U:H2'	1:2:13:C:C6	2.47	0.50
1:2:208:U:N3	1:2:209:A:N7	2.59	0.50
1:2:428:G:OP1	1:2:437:A:O2'	2.25	0.50
1:2:444:A:H1'	1:2:524:A:OP1	2.12	0.50
1:2:836:G:H2'	1:2:837:G:C8	2.46	0.50
1:2:1049:G:H5'	1:2:1050:G:OP2	2.11	0.50
1:2:1079:U:H2'	1:2:1080:A:C8	2.47	0.50
1:2:1233:A:O2'	34:f:143:HIS:HD2	1.93	0.50
1:2:1746:G:H2'	1:2:1747:A:H8	1.73	0.50
6:G:70:PRO:HD3	6:G:101:ILE:HD12	1.92	0.50
7:H:13:PRO:HB2	7:H:14:THR:HG23	1.94	0.50
10:L:101:GLU:HB2	15:X:12:ALA:HB3	1.93	0.50
11:N:38:ILE:HG13	11:N:42:ARG:HH22	1.77	0.50
17:a:39:MET:SD	17:a:70:LYS:HE2	2.52	0.50
22:F:64:ILE:HG23	22:F:91:ILE:HB	1.93	0.50
36:i:116:ASN:O	41:l:169:GLY:N	2.45	0.50
1:2:841:C:H2'	1:2:842:U:C6	2.46	0.50
1:2:1681:U:H2'	1:2:1682:U:O4'	2.10	0.50
5:E:38:LEU:HD11	5:E:39:ARG:HH21	1.76	0.50
6:G:69:LEU:HD12	6:G:70:PRO:HD2	1.93	0.50
12:O:107:ARG:NH1	32:c:38:ARG:HH12	2.09	0.50
14:W:6:VAL:HG22	14:W:34:ILE:HD11	1.94	0.50
14:W:11:LEU:HA	14:W:14:ILE:HG22	1.93	0.50
25:P:79:HIS:HA	25:P:97:TYR:HB2	1.93	0.50
27:R:104:THR:HG22	27:R:121:VAL:HG13	1.93	0.50
35:g:91:ARG:HD3	35:g:103:ARG:HG3	1.94	0.50
38:1:26:M2G:CM2	38:1:44:A:C2	2.93	0.50
38:1:52:G:N2	38:1:64:RIA:O2X	2.44	0.50
1:2:760:A:N1	1:2:789:U:O4	2.43	0.50
1:2:1034:G:OP2	11:N:9:LYS:NZ	2.23	0.50
1:2:1541:A:N6	1:2:1566:C:HO2'	2.08	0.50
1:2:1711:G:H2'	1:2:1711:G:N3	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1788:A:H2'	1:2:1789:A:C8	2.47	0.50
3:B:127:VAL:HG21	3:B:176:VAL:HG21	1.93	0.50
15:X:103:LEU:HB3	15:X:126:LYS:HB2	1.93	0.50
25:P:50:SER:HB3	25:P:53:PRO:CD	2.40	0.50
27:R:97:ASN:ND2	27:R:97:ASN:O	2.44	0.50
28:S:45:LEU:HA	28:S:48:LYS:HG2	1.94	0.50
31:Z:49:ARG:NH1	31:Z:53:GLU:HB3	2.26	0.50
34:f:104:ASN:O	34:f:117:LEU:CD2	2.59	0.50
40:k:464:VAL:HG11	40:k:485:LEU:HD13	1.92	0.50
1:2:216:A:H2'	1:2:217:A:C8	2.47	0.50
1:2:751:G:H2'	1:2:752:A:H8	1.77	0.50
1:2:1286:A:N1	1:2:1327:G:O2'	2.45	0.50
1:2:1401:C:OP1	27:R:2:GLY:N	2.45	0.50
1:2:1553:A:H5''	25:P:44:LYS:NZ	2.25	0.50
2:A:38:TYR:CD1	2:A:39:LYS:HG2	2.47	0.50
3:B:143:THR:HG21	3:B:156:ALA:HB2	1.94	0.50
6:G:74:LYS:HD2	6:G:94:ARG:CG	2.42	0.50
7:H:19:GLN:HA	7:H:22:GLN:OE1	2.11	0.50
7:H:27:LEU:C	7:H:34:LEU:HD22	2.36	0.50
15:X:105:ALA:O	15:X:123:LYS:N	2.45	0.50
23:K:62:GLN:NE2	33:d:23:ILE:O	2.42	0.50
27:R:25:THR:O	27:R:31:ASN:ND2	2.36	0.50
27:R:117:LEU:O	27:R:119:LEU:HG	2.11	0.50
36:i:109:LEU:HD23	36:i:109:LEU:H	1.77	0.50
40:k:129:LYS:HD3	40:k:132:LEU:HD22	1.94	0.50
41:l:230:ILE:HA	41:l:234:VAL:HG22	1.94	0.50
1:2:119:A:C4	1:2:396:A:N1	2.80	0.50
1:2:563:G:N1	1:2:579:A:OP2	2.41	0.50
1:2:1402:C:H2'	1:2:1403:G:C8	2.47	0.50
1:2:1773:U:H2'	1:2:1774:A:C8	2.47	0.50
2:A:92:HIS:ND1	2:A:202:TYR:OH	2.31	0.50
5:E:161:LYS:HB3	5:E:171:ASP:H	1.77	0.50
10:L:71:LEU:HD12	10:L:88:ARG:HD2	1.93	0.50
14:W:87:GLU:O	14:W:90:THR:OG1	2.25	0.50
14:W:94:LEU:HD22	14:W:100:GLY:HA3	1.93	0.50
22:F:151:VAL:HG11	22:F:160:GLN:HB2	1.94	0.50
27:R:34:LEU:O	27:R:38:ILE:HG12	2.11	0.50
40:k:360:VAL:HG22	40:k:490:PRO:HG2	1.94	0.50
1:2:213:G:N2	1:2:251:U:O4	2.45	0.49
1:2:445:A:N6	1:2:460:G:H21	2.10	0.49
1:2:686:C:H5''	14:W:118:ARG:NH1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1096:U:H6	4:C:173:ARG:HD2	1.76	0.49
1:2:1465:C:H2'	1:2:1466:U:C6	2.47	0.49
2:A:3:LEU:HB3	2:A:7:PHE:CD2	2.38	0.49
15:X:89:ASN:HB3	15:X:136:TRP:CG	2.47	0.49
26:Q:69:VAL:HG11	26:Q:81:ILE:HD11	1.93	0.49
35:g:268:LYS:HD2	35:g:277:LEU:HD11	1.94	0.49
36:i:104:LYS:NZ	36:i:111:GLU:HA	2.27	0.49
39:j:32:ALA:HB3	39:j:46:ILE:CG1	2.42	0.49
39:j:98:CYS:HA	39:j:101:LYS:HE2	1.94	0.49
1:2:122:U:O3'	5:E:77:ARG:NH2	2.45	0.49
1:2:445:A:H5''	5:E:57:ASN:HD21	1.77	0.49
1:2:909:C:H2'	1:2:910:U:C6	2.47	0.49
1:2:977:A:C4	1:2:978:A:C8	3.00	0.49
1:2:1532:G:OP2	31:Z:74:SER:HB3	2.12	0.49
4:C:40:TRP:CD1	4:C:51:LYS:HD3	2.47	0.49
5:E:104:ASP:N	5:E:108:ARG:O	2.26	0.49
13:V:12:TYR:CD2	13:V:12:TYR:O	2.65	0.49
21:D:8:LYS:HB2	30:U:63:LEU:HD21	1.94	0.49
36:i:41:MET:HA	36:i:47:VAL:HG23	1.94	0.49
39:j:72:VAL:HG11	39:j:89:ARG:CB	2.32	0.49
1:2:209:A:OP2	10:L:18:HIS:NE2	2.38	0.49
1:2:1297:U:O2'	1:2:1298:G:O5'	2.29	0.49
8:I:157:VAL:HG12	8:I:161:PHE:CE2	2.47	0.49
10:L:99:ARG:HB2	15:X:12:ALA:HB2	1.94	0.49
22:F:105:ASN:HB3	22:F:108:LYS:CD	2.43	0.49
22:F:130:ASN:OD1	22:F:131:PRO:HD2	2.12	0.49
24:M:55:LEU:HD21	24:M:65:SER:HA	1.94	0.49
30:U:57:ARG:HG3	30:U:89:ARG:NH1	2.27	0.49
40:k:436:LEU:HD23	40:k:513:GLY:HA3	1.94	0.49
1:2:357:U:H2'	1:2:359:A:H8	1.74	0.49
1:2:594:G:H2'	1:2:595:C:C6	2.47	0.49
1:2:897:A:H4'	12:O:46:MET:HE2	1.94	0.49
1:2:951:A:H2'	1:2:952:G:H8	1.77	0.49
1:2:1012:A:C6	1:2:1013:G:C2	3.00	0.49
1:2:1430:U:H4'	1:2:1431:G:O5'	2.11	0.49
1:2:1537:G:H22	28:S:26:ILE:HD11	1.78	0.49
5:E:97:GLU:OE1	5:E:113:ARG:HD3	2.11	0.49
8:I:6:ASP:N	8:I:6:ASP:OD1	2.45	0.49
10:L:75:VAL:HG13	10:L:84:ILE:HD11	1.93	0.49
24:M:36:ARG:O	24:M:40:GLU:HB2	2.12	0.49
24:M:46:THR:CB	34:f:116:LYS:NZ	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:154:LYS:HG3	35:g:208:VAL:HA	1.94	0.49
39:j:192:CYS:HA	39:j:261:VAL:H	1.76	0.49
39:j:217:GLN:HB3	39:j:219:LYS:NZ	2.28	0.49
1:2:855:A:H62	7:H:96:ARG:CZ	2.25	0.49
1:2:976:A:N6	1:2:1023:U:C2	2.81	0.49
1:2:1675:C:OP1	8:I:42:ARG:NH2	2.35	0.49
2:A:24:LEU:HD22	2:A:41:ARG:NH1	2.27	0.49
2:A:205:ARG:HH12	2:A:209:GLU:HG3	1.78	0.49
4:C:231:THR:HG22	4:C:233:ASN:H	1.77	0.49
6:G:69:LEU:O	6:G:99:GLY:HA3	2.12	0.49
8:I:191:ALA:O	8:I:194:LEU:HB3	2.12	0.49
21:D:134:CYS:SG	21:D:188:ILE:HG13	2.52	0.49
30:U:62:VAL:HG22	30:U:85:ARG:HG2	1.93	0.49
38:1:27:C:O2'	38:1:28:A:C8	2.60	0.49
1:2:148:C:O2	6:G:132:ARG:NH2	2.45	0.49
1:2:330:A:H3'	8:I:176:GLN:HE22	1.78	0.49
1:2:760:A:C6	1:2:789:U:O4	2.66	0.49
2:A:102:PHE:HE2	2:A:132:ALA:HA	1.78	0.49
4:C:67:PRO:HA	13:V:29:HIS:HE1	1.76	0.49
5:E:106:LYS:HB2	5:E:108:ARG:NH1	2.27	0.49
24:M:52:LEU:HD12	24:M:114:VAL:HG11	1.94	0.49
28:S:64:GLU:N	28:S:64:GLU:OE2	2.45	0.49
31:Z:53:GLU:HB2	31:Z:57:TYR:CE2	2.47	0.49
1:2:60:U:H3	1:2:63:G:P	2.35	0.49
1:2:208:U:C2	1:2:209:A:C8	3.01	0.49
1:2:223:C:H2'	1:2:224:A:C8	2.48	0.49
1:2:917:U:H2'	1:2:918:A:H8	1.77	0.49
1:2:954:A:H2'	1:2:955:C:C6	2.48	0.49
1:2:1131:A:H2'	1:2:1132:A:C8	2.48	0.49
5:E:159:THR:HG21	5:E:227:VAL:O	2.13	0.49
6:G:7:TYR:HD1	6:G:113:ILE:HG23	1.77	0.49
9:J:41:GLU:O	9:J:45:ILE:HD12	2.11	0.49
21:D:75:LYS:HE2	23:K:18:GLU:CD	2.38	0.49
31:Z:38:HIS:HE1	31:Z:66:VAL:O	1.95	0.49
1:2:5:U:O2'	1:2:552:G:H4'	2.13	0.49
1:2:551:G:N1	1:2:552:G:C6	2.81	0.49
1:2:1511:G:O2'	1:2:1513:A:N3	2.45	0.49
1:2:1582:G:O2'	1:2:1608:G:O6	2.29	0.49
4:C:145:ARG:HB2	4:C:227:TYR:CD1	2.48	0.49
12:O:20:PHE:HB3	12:O:27:PHE:HB2	1.94	0.49
16:Y:35:VAL:O	16:Y:35:VAL:HG12	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:U:67:THR:HG21	33:d:44:ARG:HG3	1.95	0.49
35:g:43:LEU:O	35:g:61:SER:HA	2.13	0.49
39:j:39:TYR:HE2	39:j:42:ILE:HD12	1.78	0.49
39:j:124:GLU:OE2	39:j:125:GLU:HG3	2.13	0.49
39:j:181:ALA:HA	39:j:234:ALA:O	2.13	0.49
40:k:221:ASN:ND2	40:k:250:LYS:HD3	2.24	0.49
1:2:658:C:H2'	1:2:659:G:H8	1.78	0.49
1:2:774:A:C2	1:2:786:G:C6	3.01	0.49
1:2:995:U:O2	1:2:1007:G:N2	2.39	0.49
1:2:1096:U:O3'	4:C:173:ARG:NH1	2.46	0.49
1:2:1472:G:OP1	22:F:111:LYS:NZ	2.36	0.49
1:2:1738:A:H2'	1:2:1739:U:C6	2.48	0.49
5:E:247:THR:HB	5:E:250:GLU:OE1	2.13	0.49
10:L:16:GLN:HB2	10:L:19:ILE:HD13	1.94	0.49
15:X:46:SER:OG	15:X:48:HIS:O	2.31	0.49
21:D:93:ASP:N	21:D:93:ASP:OD1	2.46	0.49
39:j:73:VAL:HG22	39:j:85:LEU:HD12	1.93	0.49
40:k:146:LYS:HB3	40:k:148:TYR:CE2	2.48	0.49
1:2:903:G:C6	1:2:904:A:C6	3.01	0.49
1:2:997:A:H2'	1:2:998:PSU:H6	1.77	0.49
1:2:1134:U:H2'	1:2:1135:U:C6	2.48	0.49
1:2:1793:U:H3'	17:a:5:ARG:NH2	2.28	0.49
2:A:70:PRO:HB3	2:A:94:GLY:HA3	1.95	0.49
6:G:219:ARG:NH1	6:G:223:LYS:HB2	2.24	0.49
12:O:50:ALA:C	12:O:52:ARG:H	2.21	0.49
12:O:88:GLY:HA2	12:O:122:PRO:HD3	1.94	0.49
13:V:10:GLU:OE1	13:V:10:GLU:N	2.46	0.49
16:Y:20:ARG:NH1	16:Y:74:LEU:HD21	2.28	0.49
17:a:21:VAL:HG11	17:a:72:HIS:ND1	2.27	0.49
23:K:64:TYR:HB3	23:K:66:TYR:CE2	2.47	0.49
24:M:52:LEU:HD23	24:M:128:LEU:HD11	1.95	0.49
35:g:188:LEU:HA	35:g:193:TYR:HA	1.95	0.49
36:i:114:LYS:HD3	41:l:167:ARG:H	1.78	0.49
39:j:167:ASP:OD1	39:j:168:GLU:N	2.46	0.49
40:k:65:ARG:NH2	40:k:165:LYS:HD3	2.28	0.49
1:2:43:A:O2'	1:2:99:C:OP1	2.20	0.48
1:2:296:U:H2'	1:2:297:C:C6	2.48	0.48
1:2:638:U:H2'	7:H:101:LYS:HG3	1.95	0.48
1:2:1097:U:OP2	4:C:164:SER:OG	2.27	0.48
1:2:1160:C:H1'	1:2:1617:C:H42	1.78	0.48
1:2:1480:C:O2'	26:Q:77:GLN:NE2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1544:G:O6	1:2:1545:A:N6	2.46	0.48
10:L:111:VAL:HG12	10:L:139:VAL:HG21	1.94	0.48
21:D:109:LEU:HD11	21:D:115:ILE:HG22	1.95	0.48
24:M:43:LYS:O	24:M:46:THR:HG22	2.13	0.48
24:M:123:GLU:C	24:M:124:ARG:HD2	2.38	0.48
28:S:84:TRP:CE3	28:S:85:PHE:HB2	2.48	0.48
35:g:117:ASP:OD1	35:g:118:ALA:N	2.44	0.48
1:2:30:G:C6	1:2:596:G:C6	3.00	0.48
1:2:72:A:H1'	1:2:73:U:C5	2.47	0.48
1:2:91:G:H2'	1:2:92:A:O4'	2.12	0.48
1:2:194:G:O6	8:I:142:ARG:NH1	2.41	0.48
1:2:388:G:H2'	1:2:389:G:O4'	2.13	0.48
1:2:885:U:H2'	1:2:886:A:C8	2.48	0.48
1:2:1015:C:H2'	1:2:1016:U:O4'	2.13	0.48
1:2:1299:A:H5''	4:C:91:VAL:HG11	1.94	0.48
1:2:1396:U:H5	1:2:1398:A:C5	2.30	0.48
8:I:173:ARG:HA	8:I:173:ARG:NE	2.28	0.48
13:V:56:SER:O	13:V:60:ARG:HG3	2.13	0.48
15:X:19:ARG:O	15:X:23:ARG:HG2	2.12	0.48
31:Z:74:SER:HA	31:Z:77:ARG:HH22	1.78	0.48
35:g:107:HIS:CD2	35:g:133:ARG:HD2	2.48	0.48
39:j:25:GLN:HE22	39:j:35:LYS:H	1.59	0.48
39:j:134:LEU:HD22	39:j:144:ALA:HB1	1.95	0.48
40:k:114:SER:O	40:k:118:ARG:HG3	2.13	0.48
40:k:416:VAL:HG21	40:k:492:CYS:HB2	1.95	0.48
1:2:52:U:N3	1:2:53:G:N7	2.62	0.48
1:2:434:C:N3	15:X:46:SER:OG	2.42	0.48
1:2:495:G:H2'	1:2:496:G:C8	2.49	0.48
1:2:977:A:H1'	1:2:1786:G:H1'	1.95	0.48
1:2:1426:2MG:HM22	1:2:1427:G:C2	2.48	0.48
4:C:93:LYS:HG2	4:C:94:GLN:N	2.28	0.48
6:G:33:GLY:H	6:G:52:ILE:HG13	1.78	0.48
9:J:29:LYS:HD2	19:e:44:PHE:HD2	1.78	0.48
23:K:88:PRO:HD2	23:K:91:TYR:CD2	2.47	0.48
25:P:17:TYR:HD2	25:P:18:LYS:HG2	1.78	0.48
39:j:26:GLN:O	39:j:27:ILE:HD13	2.13	0.48
1:2:7:G:H2'	1:2:8:U:H5''	1.94	0.48
1:2:914:A:N3	1:2:914:A:H2'	2.28	0.48
1:2:1387:C:OP1	27:R:48:ASN:ND2	2.46	0.48
1:2:1528:C:OP2	31:Z:95:HIS:HD2	1.96	0.48
1:2:1651:C:H2'	1:2:1652:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:49:ASN:O	2:A:53:THR:HG23	2.12	0.48
5:E:31:PRO:HG2	5:E:38:LEU:HB2	1.95	0.48
9:J:29:LYS:HD2	19:e:44:PHE:CD2	2.49	0.48
14:W:25:VAL:HB	14:W:63:VAL:CG1	2.44	0.48
21:D:51:ARG:HB3	21:D:91:VAL:HG12	1.95	0.48
35:g:321:GLN:OE1	35:g:322:VAL:N	2.46	0.48
40:k:493:THR:HA	40:k:497:GLU:OE1	2.13	0.48
1:2:181:A:H2'	1:2:182:U:C6	2.48	0.48
1:2:225:A:C2	1:2:835:U:C4	3.02	0.48
1:2:406:A:H2'	1:2:407:C:C6	2.48	0.48
1:2:585:G:H2'	1:2:586:C:C6	2.49	0.48
1:2:812:U:N3	10:L:153:PHE:HB2	2.28	0.48
1:2:1302:U:O2'	1:2:1321:A:OP2	2.28	0.48
16:Y:15:ASN:O	16:Y:19:ALA:N	2.46	0.48
21:D:72:LEU:HG	23:K:20:VAL:HG21	1.95	0.48
25:P:77:ARG:HB2	25:P:102:PHE:CD2	2.47	0.48
39:j:169:LEU:HD12	39:j:170:LYS:HD2	1.96	0.48
1:2:159:C:C4	1:2:160:U:C4	3.01	0.48
1:2:1085:A:H2'	1:2:1086:A:O4'	2.13	0.48
1:2:1318:A:H2'	1:2:1319:U:O4'	2.13	0.48
1:2:1466:U:H2'	1:2:1467:A:O4'	2.14	0.48
1:2:1617:C:H2'	1:2:1618:C:C6	2.48	0.48
1:2:1676:A:H2'	1:2:1677:G:O4'	2.14	0.48
3:B:112:SER:HA	17:a:68:TYR:CE2	2.43	0.48
4:C:46:LEU:HD13	4:C:66:LEU:CD2	2.44	0.48
4:C:224:GLY:O	13:V:25:LYS:NZ	2.47	0.48
7:H:101:LYS:NZ	7:H:117:THR:OG1	2.46	0.48
9:J:49:LEU:HD12	9:J:104:PHE:CE2	2.49	0.48
11:N:38:ILE:HG21	11:N:78:ASN:ND2	2.28	0.48
14:W:42:GLN:HG3	14:W:47:ILE:HG23	1.95	0.48
14:W:70:ASN:OD1	14:W:71:LYS:N	2.47	0.48
35:g:307:THR:HG22	35:g:321:GLN:NE2	2.29	0.48
38:1:53:G:H2'	38:1:54:A:C8	2.48	0.48
39:j:89:ARG:O	39:j:89:ARG:HG2	2.14	0.48
40:k:118:ARG:HD3	40:k:124:GLN:HA	1.95	0.48
40:k:347:PHE:CZ	40:k:419:ALA:HB2	2.49	0.48
1:2:253:A:H2'	1:2:254:U:C6	2.48	0.48
1:2:300:A:H4'	8:I:27:PHE:CE1	2.48	0.48
1:2:757:A:O3'	5:E:22:LYS:NZ	2.45	0.48
1:2:1254:G:O6	24:M:39:ARG:NH1	2.46	0.48
1:2:1309:U:H2'	1:2:1310:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:55:GLU:HA	2:A:58:VAL:HG22	1.96	0.48
2:A:140:ASN:ND2	4:C:67:PRO:HD3	2.29	0.48
6:G:7:TYR:HD2	6:G:10:ASN:OD1	1.97	0.48
6:G:98:ARG:HG2	6:G:106:LEU:HD21	1.94	0.48
11:N:119:GLU:OE1	11:N:119:GLU:HA	2.13	0.48
39:j:185:ARG:HA	39:j:230:LEU:O	2.14	0.48
41:l:157:LYS:HD3	41:l:159:ARG:HB2	1.95	0.48
1:2:331:U:OP2	8:I:176:GLN:NE2	2.47	0.48
1:2:529:C:O2	16:Y:61:ARG:NH2	2.46	0.48
1:2:1086:A:OP2	1:2:1086:A:H8	1.97	0.48
1:2:1198:G:H5''	33:d:29:GLY:HA2	1.95	0.48
1:2:1474:C:H2'	1:2:1475:G:C8	2.49	0.48
1:2:1500:G:O6	29:T:102:ARG:NH2	2.43	0.48
1:2:1563:C:H2'	1:2:1564:U:H6	1.79	0.48
2:A:78:SER:O	2:A:83:GLN:NE2	2.46	0.48
2:A:89:TYR:HD1	2:A:178:ALA:HB2	1.79	0.48
7:H:58:LEU:HD11	7:H:88:ARG:HD2	1.96	0.48
8:I:41:LYS:HA	8:I:59:ARG:O	2.14	0.48
9:J:140:ILE:O	16:Y:64:TYR:HE2	1.97	0.48
14:W:6:VAL:HG23	14:W:29:PRO:HG2	1.96	0.48
16:Y:39:GLU:O	16:Y:42:GLU:HG3	2.14	0.48
26:Q:98:ASP:OD1	26:Q:99:GLU:N	2.41	0.48
27:R:25:THR:OG1	27:R:30:THR:OG1	2.31	0.48
38:1:14:A:H2	38:1:48:5MC:HN41	1.60	0.48
38:1:27:C:O2'	38:1:28:A:O5'	2.30	0.48
39:j:74:LEU:HB3	39:j:89:ARG:HH12	1.75	0.48
1:2:66:U:OP1	6:G:136:LYS:NZ	2.41	0.48
1:2:257:C:O2	8:I:179:ARG:NH1	2.47	0.48
1:2:414:C:O2'	1:2:417:G:O6	2.19	0.48
1:2:485:G:O6	1:2:500:U:O4	2.31	0.48
1:2:1382:A:H2'	1:2:1383:G:O4'	2.13	0.48
1:2:1757:C:O2'	1:2:1778:G:O6	2.30	0.48
3:B:185:THR:O	3:B:189:ILE:HG12	2.14	0.48
9:J:60:LEU:HD21	9:J:93:LEU:HG	1.96	0.48
16:Y:15:ASN:OD1	16:Y:17:LEU:HB2	2.14	0.48
22:F:78:ARG:HH22	26:Q:122:ARG:CZ	2.25	0.48
22:F:82:LYS:HB2	22:F:85:ARG:HD3	1.96	0.48
29:T:140:LEU:C	29:T:140:LEU:CD2	2.86	0.48
1:2:296:U:H2'	1:2:297:C:H6	1.78	0.48
1:2:392:C:H2'	1:2:393:C:C6	2.48	0.48
1:2:749:U:H2'	1:2:750:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:763:G:H5''	9:J:78:ARG:NH2	2.29	0.48
23:K:5:LYS:HE3	23:K:79:TYR:OH	2.14	0.48
29:T:31:PRO:HG2	29:T:34:VAL:HG13	1.96	0.48
35:g:245:ASP:OD1	35:g:246:GLU:N	2.47	0.48
35:g:307:THR:HG22	35:g:321:GLN:HE22	1.79	0.48
36:i:78:LEU:HD23	36:i:93:HIS:HB3	1.96	0.48
1:2:28:A:C2	1:2:597:U:C5	3.01	0.47
1:2:786:G:C6	1:2:787:A:C5	3.01	0.47
1:2:1076:C:H2'	1:2:1077:C:C6	2.48	0.47
1:2:1079:U:H2'	1:2:1080:A:H8	1.79	0.47
1:2:1217:G:H22	1:2:1442:A:P	2.36	0.47
1:2:1234:C:C2	1:2:1235:A:C8	3.02	0.47
2:A:129:ASP:O	2:A:133:ILE:HG12	2.13	0.47
8:I:160:GLN:CG	8:I:166:LEU:HD13	2.44	0.47
12:O:13:VAL:HG13	12:O:76:ILE:HA	1.96	0.47
12:O:69:ALA:O	12:O:73:GLU:HG2	2.13	0.47
27:R:103:ASP:OD2	27:R:105:GLN:HB2	2.14	0.47
35:g:202:HIS:HE1	35:g:228:TYR:HB2	1.79	0.47
38:l:66:C:H2'	38:l:67:G:C8	2.49	0.47
39:j:198:ILE:HG13	39:j:199:ASP:N	2.29	0.47
40:k:286:GLN:HB3	41:l:262:CYS:HB3	1.96	0.47
1:2:387:G:C6	1:2:409:A:C6	3.01	0.47
1:2:749:U:H5''	14:W:83:ILE:HG12	1.97	0.47
1:2:869:C:H2'	1:2:870:G:H8	1.79	0.47
1:2:958:U:H4'	11:N:16:ILE:HG22	1.96	0.47
1:2:1106:G:O2'	1:2:1107:G:H5'	2.14	0.47
1:2:1367:G:H5''	29:T:69:LYS:HD3	1.96	0.47
4:C:62:PHE:CE2	4:C:143:PRO:HD3	2.49	0.47
5:E:36:HIS:NE2	5:E:88:ASP:OD1	2.46	0.47
5:E:205:PHE:HD1	5:E:221:ARG:HD2	1.78	0.47
9:J:85:VAL:HG13	9:J:103:ASP:HB3	1.95	0.47
22:F:142:SER:OG	22:F:173:SER:HB2	2.15	0.47
23:K:37:THR:HB	23:K:41:PHE:CE1	2.49	0.47
31:Z:54:ALA:HB3	31:Z:55:PRO:HD3	1.94	0.47
35:g:181:LYS:HD2	35:g:205:TYR:HA	1.96	0.47
1:2:396:A:H2'	1:2:397:G:O4'	2.15	0.47
1:2:1085:A:H5''	4:C:168:GLY:O	2.14	0.47
1:2:1791:G:H4'	1:2:1792:A:OP1	2.14	0.47
2:A:38:TYR:CE2	27:R:109:LEU:HB2	2.40	0.47
4:C:64:HIS:C	13:V:15:ARG:HH22	2.22	0.47
6:G:56:ASN:OD1	6:G:108:VAL:HB	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:137:ARG:HG2	6:G:140:ASN:H	1.79	0.47
14:W:6:VAL:HG21	14:W:29:PRO:HB2	1.95	0.47
22:F:65:GLN:HG3	22:F:88:GLN:C	2.39	0.47
25:P:33:PHE:CD2	25:P:45:PHE:HE2	2.32	0.47
38:1:10:2MG:H2'	38:1:11:C:C6	2.49	0.47
40:k:206:SER:OG	40:k:318:ILE:HD13	2.13	0.47
1:2:311:A:N1	1:2:353:C:N4	2.63	0.47
1:2:365:A:H2'	1:2:366:A:H8	1.80	0.47
1:2:564:C:OP2	36:i:64:LYS:HD2	2.14	0.47
1:2:599:U:OP2	15:X:108:GLY:HA2	2.13	0.47
1:2:692:C:H2'	1:2:693:U:C6	2.50	0.47
1:2:1150:A:H2'	1:2:1151:A:C8	2.50	0.47
1:2:1490:A:O2'	1:2:1491:A:O4'	2.32	0.47
1:2:1521:G:H21	1:2:1521:G:P	2.38	0.47
4:C:40:TRP:NE1	4:C:51:LYS:HB2	2.18	0.47
7:H:85:PHE:HB3	7:H:88:ARG:HE	1.80	0.47
14:W:111:MET:HE3	14:W:116:ALA:HB2	1.96	0.47
16:Y:21:LYS:HB2	16:Y:75:VAL:HG12	1.97	0.47
35:g:180:ASP:HB2	35:g:182:ILE:HG22	1.96	0.47
39:j:195:TYR:HE1	40:k:373:ILE:HA	1.79	0.47
40:k:227:PRO:HG3	40:k:444:LYS:HG2	1.95	0.47
1:2:893:U:H2'	1:2:894:G:C8	2.36	0.47
1:2:1146:A:O2'	1:2:1634:C:OP2	2.29	0.47
1:2:1201:A:H8	1:2:1206:C:H42	1.61	0.47
1:2:1679:A:O3'	6:G:31:ARG:NH1	2.47	0.47
1:2:1783:U:P	12:O:133:ARG:HH12	2.36	0.47
2:A:183:ARG:HD3	2:A:191:ARG:HB2	1.95	0.47
25:P:110:GLU:H	25:P:110:GLU:CD	2.17	0.47
1:2:36:C:H2'	1:2:37:U:H6	1.80	0.47
1:2:297:C:H5''	5:E:38:LEU:HD23	1.94	0.47
1:2:471:U:OP1	9:J:11:THR:HG22	2.14	0.47
1:2:836:G:C2	1:2:837:G:C5	3.02	0.47
1:2:1036:C:H2'	1:2:1037:U:C6	2.49	0.47
1:2:1230:U:OP1	1:2:1258:U:O2'	2.27	0.47
1:2:1475:G:H2'	1:2:1476:G:C8	2.50	0.47
1:2:1480:C:H4'	26:Q:77:GLN:NE2	2.17	0.47
1:2:1726:U:H2'	1:2:1727:C:C6	2.50	0.47
6:G:55:GLY:C	6:G:63:MET:HE3	2.40	0.47
13:V:46:ILE:HG22	13:V:49:GLU:OE1	2.15	0.47
25:P:100:LYS:HD3	25:P:100:LYS:N	2.29	0.47
27:R:7:LYS:HD2	27:R:11:ARG:HE	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:S:119:ILE:HG22	28:S:121:SER:N	2.29	0.47
31:Z:46:LYS:O	31:Z:50:ILE:HG23	2.14	0.47
39:j:36:LEU:HD12	39:j:39:TYR:CD2	2.50	0.47
40:k:66:LYS:O	40:k:69:PHE:N	2.46	0.47
40:k:78:GLN:HE22	40:k:98:GLN:NE2	2.09	0.47
40:k:384:GLN:HG2	40:k:385:ASN:CG	2.40	0.47
1:2:12:U:H1'	1:2:1299:A:H1'	1.97	0.47
1:2:278:G:N1	1:2:280:G:C6	2.82	0.47
1:2:396:A:C6	1:2:397:G:C2	3.02	0.47
1:2:445:A:C5'	5:E:57:ASN:HD21	2.27	0.47
1:2:551:G:C6	1:2:552:G:O6	2.67	0.47
1:2:803:A:N3	14:W:105:THR:OG1	2.45	0.47
1:2:904:A:H4'	12:O:52:ARG:HD2	1.97	0.47
1:2:1326:C:H2'	1:2:1327:G:H8	1.79	0.47
3:B:129:THR:OG1	3:B:133:TYR:HB2	2.15	0.47
5:E:202:GLU:OE1	10:L:40:LEU:HD13	2.13	0.47
8:I:160:GLN:NE2	8:I:165:ARG:O	2.48	0.47
10:L:91:LEU:HD23	10:L:100:TYR:HB3	1.97	0.47
14:W:40:VAL:HG11	14:W:103:ILE:HD12	1.97	0.47
21:D:9:ARG:HA	21:D:12:VAL:HG22	1.97	0.47
22:F:43:LYS:HB3	22:F:46:ASN:HA	1.97	0.47
22:F:84:PHE:CZ	32:c:47:PRO:HB2	2.50	0.47
25:P:95:GLY:HA2	25:P:103:ASN:O	2.15	0.47
34:f:78:LYS:NZ	34:f:80:ARG:HD3	2.30	0.47
34:f:105:TYR:CA	34:f:117:LEU:HD23	2.42	0.47
36:i:42:LEU:HB2	36:i:46:ARG:C	2.40	0.47
36:i:63:GLY:C	36:i:65:LEU:H	2.23	0.47
38:1:6:C:H2'	38:1:7:G:C8	2.49	0.47
39:j:9:TYR:C	39:j:132:TRP:HE1	2.22	0.47
1:2:152:G:H5''	16:Y:131:ARG:NH2	2.29	0.47
1:2:329:G:OP1	8:I:173:ARG:NH2	2.48	0.47
1:2:539:G:O2'	1:2:540:A:O5'	2.31	0.47
1:2:789:U:C5	1:2:790:A:C5	3.03	0.47
1:2:1217:G:H1'	1:2:1264:G:H22	1.79	0.47
1:2:1226:A:H5''	1:2:1228:G:O4'	2.15	0.47
1:2:1575:A:H2'	1:2:1576:U:O4'	2.15	0.47
1:2:1584:A:OP1	26:Q:134:ALA:N	2.47	0.47
1:2:1742:A:H3'	1:2:1743:G:H8	1.80	0.47
1:2:1772:G:H2'	1:2:1773:U:C6	2.50	0.47
4:C:223:ILE:O	4:C:226:THR:HG22	2.15	0.47
6:G:3:LEU:HD23	6:G:18:ILE:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:40:ALA:C	7:H:41:LEU:HD12	2.40	0.47
14:W:76:SER:OG	14:W:77:PRO:HD3	2.15	0.47
22:F:95:LEU:CA	22:F:174:ILE:HD11	2.44	0.47
23:K:15:LEU:HD22	23:K:46:LEU:HD21	1.97	0.47
23:K:22:VAL:HG23	23:K:23:ALA:H	1.80	0.47
31:Z:84:GLU:OE2	31:Z:89:ILE:HB	2.15	0.47
34:f:92:ARG:HH21	34:f:93:HIS:HB3	1.79	0.47
35:g:113:SER:OG	35:g:154:LYS:HA	2.14	0.47
38:l:15:G:H1	38:l:48:5MC:HN41	1.63	0.47
40:k:440:LEU:HD21	40:k:510:ARG:HD2	1.97	0.47
1:2:27:U:H2'	1:2:28:A:H8	1.80	0.47
1:2:278:G:N2	1:2:280:G:C2	2.83	0.47
1:2:392:C:OP1	8:I:2:GLY:N	2.47	0.47
1:2:552:G:H3'	1:2:553:C:H2'	1.97	0.47
1:2:710:U:H2'	1:2:711:G:N7	2.29	0.47
1:2:862:A:H62	1:2:963:U:H3	1.62	0.47
1:2:1080:A:O2'	1:2:1081:C:H2'	2.15	0.47
1:2:1334:U:H2'	1:2:1335:A:C8	2.50	0.47
2:A:158:VAL:HB	13:V:69:LEU:HD23	1.96	0.47
6:G:33:GLY:N	6:G:52:ILE:O	2.42	0.47
8:I:84:HIS:CD2	8:I:90:LEU:HD13	2.50	0.47
11:N:75:LEU:O	11:N:79:GLY:N	2.48	0.47
12:O:133:ARG:HA	17:a:28:ARG:NH1	2.30	0.47
21:D:207:THR:HB	27:R:40:THR:HG22	1.97	0.47
25:P:100:LYS:HE2	25:P:100:LYS:HB2	1.68	0.47
38:l:20:A:C8	38:l:60:A:N6	2.83	0.47
39:j:72:VAL:HG11	39:j:89:ARG:NE	2.28	0.47
1:2:342:C:C2	1:2:343:A:C8	3.02	0.47
1:2:726:G:H2'	1:2:727:C:C6	2.49	0.47
1:2:835:U:H2'	1:2:836:G:H8	1.79	0.47
3:B:153:THR:HB	3:B:155:TYR:CE1	2.50	0.47
7:H:35:LYS:HG2	7:H:36:ALA:H	1.80	0.47
7:H:60:VAL:HG22	7:H:92:PHE:HA	1.96	0.47
8:I:5:ARG:NH1	8:I:29:LEU:O	2.48	0.47
8:I:38:ILE:HA	8:I:60:ILE:O	2.15	0.47
8:I:39:GLY:HA2	8:I:61:GLU:OE2	2.14	0.47
8:I:138:LYS:HG3	8:I:139:ASN:N	2.28	0.47
13:V:11:LEU:HG	13:V:12:TYR:CD1	2.50	0.47
15:X:54:LEU:HG	15:X:55:GLU:OE1	2.14	0.47
17:a:77:CYS:O	17:a:81:ALA:N	2.39	0.47
21:D:163:PRO:O	21:D:167:PHE:N	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:132:ARG:HG2	26:Q:138:PHE:CE1	2.50	0.47
33:d:21:CYS:HB3	33:d:25:GLY:N	2.30	0.47
1:2:464:G:H2'	1:2:465:PSU:H6	1.80	0.46
1:2:477:A:H2	1:2:509:G:H22	1.63	0.46
1:2:642:G:O6	1:2:692:C:N4	2.48	0.46
1:2:720:G:N1	1:2:722:G:O6	2.47	0.46
1:2:901:G:H2'	1:2:902:U:C6	2.50	0.46
1:2:1126:G:C6	1:2:1127:C:C4	3.03	0.46
1:2:1242:G:H2'	1:2:1242:G:N3	2.30	0.46
1:2:1260:G:H2'	1:2:1261:U:C6	2.50	0.46
1:2:1752:A:H2'	36:i:44:ASN:HD22	1.79	0.46
9:J:145:SER:C	9:J:147:MET:H	2.23	0.46
26:Q:41:PRO:C	26:Q:43:ILE:N	2.67	0.46
26:Q:143:ARG:HH12	38:1:35:A:P	2.38	0.46
28:S:41:ARG:HG3	28:S:85:PHE:HE1	1.79	0.46
28:S:45:LEU:HD23	28:S:85:PHE:CE2	2.50	0.46
30:U:25:ASN:OD1	30:U:115:GLU:HB3	2.15	0.46
32:c:7:VAL:HG13	32:c:55:VAL:HG13	1.96	0.46
34:f:98:VAL:HB	34:f:101:ALA:HB2	1.97	0.46
39:j:39:TYR:CG	39:j:40:ASP:N	2.83	0.46
39:j:145:PHE:O	39:j:149:ILE:HG23	2.15	0.46
1:2:1327:G:C2	1:2:1328:A:C8	3.04	0.46
1:2:1475:G:H1'	29:T:48:GLN:NE2	2.30	0.46
2:A:37:VAL:HG21	2:A:46:ASN:ND2	2.30	0.46
3:B:104:ASP:OD1	3:B:105:PHE:N	2.49	0.46
3:B:172:LEU:O	3:B:176:VAL:HG22	2.15	0.46
5:E:11:ARG:HD3	5:E:21:ASP:O	2.14	0.46
5:E:25:GLY:O	9:J:3:ARG:NH1	2.47	0.46
15:X:60:GLU:OE1	15:X:60:GLU:N	2.48	0.46
17:a:79:ILE:HD13	17:a:84:VAL:HG13	1.97	0.46
22:F:224:LYS:HA	22:F:227:ARG:CZ	2.46	0.46
25:P:80:LEU:O	25:P:116:LEU:HD11	2.15	0.46
26:Q:73:GLY:N	26:Q:76:SER:OG	2.49	0.46
1:2:36:C:H2'	1:2:37:U:C6	2.50	0.46
1:2:93:A:H4'	5:E:3:ARG:HH12	1.80	0.46
1:2:373:U:H2'	1:2:374:U:H6	1.79	0.46
1:2:406:A:H2'	1:2:407:C:H6	1.80	0.46
1:2:640:G:H2'	1:2:641:G:O4'	2.15	0.46
1:2:756:A:C4	1:2:757:A:C8	3.03	0.46
1:2:842:U:C4	1:2:843:A:N6	2.83	0.46
1:2:880:A:N1	1:2:947:G:C6	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1380:A:O2'	1:2:1381:G:H5''	2.16	0.46
1:2:1641:U:O2	1:2:1778:G:N2	2.48	0.46
5:E:72:VAL:N	5:E:75:LYS:O	2.48	0.46
7:H:118:LEU:O	7:H:122:HIS:ND1	2.47	0.46
22:F:64:ILE:HG22	22:F:66:ILE:HG23	1.96	0.46
22:F:168:ARG:CZ	22:F:172:GLN:HE21	2.29	0.46
25:P:28:MET:SD	25:P:87:PRO:HG2	2.55	0.46
38:1:8:U:O2'	38:1:11:C:OP2	2.26	0.46
40:k:123:VAL:HB	40:k:143:ALA:HB1	1.97	0.46
40:k:357:PRO:HG2	40:k:415:GLN:HE21	1.79	0.46
1:2:93:A:H61	1:2:395:G:H1'	1.79	0.46
1:2:1035:A:H2'	1:2:1036:C:H6	1.81	0.46
1:2:1501:A:C6	1:2:1502:G:C6	3.03	0.46
1:2:1780:MA6:H8	1:2:1780:MA6:O5'	2.15	0.46
11:N:36:GLN:HG3	11:N:40:TYR:CE2	2.49	0.46
24:M:77:VAL:N	24:M:78:PRO:HD2	2.30	0.46
26:Q:39:VAL:HG11	26:Q:48:VAL:HG11	1.96	0.46
35:g:119:ASN:OD1	35:g:120:SER:N	2.39	0.46
40:k:95:ILE:HD11	40:k:187:ARG:HA	1.98	0.46
1:2:89:G:C6	1:2:90:C:C4	3.03	0.46
1:2:946:U:H2'	1:2:947:G:C8	2.49	0.46
1:2:1183:A:C2	1:2:1453:G:H1'	2.50	0.46
4:C:62:PHE:CD2	4:C:143:PRO:HG3	2.50	0.46
4:C:107:VAL:HG11	4:C:134:ILE:HG13	1.98	0.46
9:J:121:SER:O	9:J:124:HIS:N	2.36	0.46
10:L:87:ARG:NH1	10:L:89:ASP:OD1	2.49	0.46
11:N:3:ARG:N	11:N:3:ARG:HD2	2.31	0.46
12:O:133:ARG:HB2	12:O:136:ARG:NH1	2.31	0.46
16:Y:111:ARG:HG2	16:Y:114:ARG:HH21	1.81	0.46
25:P:118:GLU:OE1	25:P:118:GLU:N	2.34	0.46
31:Z:89:ILE:CG2	31:Z:101:TYR:HB3	2.46	0.46
35:g:92:LEU:HG	35:g:101:GLU:OE2	2.14	0.46
40:k:140:LEU:HD11	40:k:318:ILE:HG12	1.96	0.46
1:2:365:A:H2'	1:2:366:A:C8	2.51	0.46
1:2:399:A:H5''	8:I:25:ARG:HA	1.97	0.46
1:2:1147:C:H2'	1:2:1148:G:H8	1.80	0.46
1:2:1249:U:H5'	1:2:1250:U:OP2	2.15	0.46
1:2:1332:C:H2'	1:2:1333:U:C6	2.51	0.46
1:2:1517:U:H2'	1:2:1518:U:C5	2.50	0.46
1:2:1631:A:H4'	1:2:1632:C:H5''	1.97	0.46
4:C:157:HIS:CE1	4:C:179:ARG:HG2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:256:ARG:O	5:E:259:HIS:ND1	2.49	0.46
6:G:79:LYS:NZ	6:G:86:PRO:HD2	2.31	0.46
9:J:18:PRO:HG2	9:J:19:TYR:CD1	2.50	0.46
10:L:14:GLN:HG2	10:L:54:ILE:HD13	1.97	0.46
11:N:71:ILE:H	11:N:71:ILE:HD12	1.81	0.46
14:W:19:LYS:HB2	14:W:19:LYS:HE3	1.73	0.46
14:W:41:MET:O	14:W:45:GLY:N	2.49	0.46
14:W:81:VAL:HG13	14:W:85:ASP:HB2	1.97	0.46
24:M:43:LYS:HA	24:M:46:THR:HG22	1.98	0.46
29:T:77:ASN:OD1	29:T:96:ALA:N	2.48	0.46
35:g:312:TYR:H	35:g:318:ARG:HH12	1.63	0.46
39:j:254:VAL:O	39:j:258:TYR:HD2	1.99	0.46
40:k:462:LEU:HD22	40:k:503:ARG:HA	1.98	0.46
1:2:645:U:H2'	1:2:646:G:C8	2.49	0.46
1:2:700:C:O2'	1:2:701:U:OP1	2.28	0.46
1:2:1077:C:H2'	1:2:1078:U:H6	1.81	0.46
1:2:1096:U:C6	4:C:173:ARG:HD2	2.50	0.46
1:2:1739:U:H2'	1:2:1740:U:C6	2.51	0.46
2:A:83:GLN:HG2	2:A:99:ALA:HB1	1.96	0.46
2:A:157:ASP:OD2	13:V:32:VAL:HG21	2.16	0.46
5:E:193:GLY:HA3	5:E:210:ILE:CG2	2.46	0.46
8:I:112:TRP:CH2	8:I:117:TYR:HE2	2.33	0.46
40:k:201:MET:O	40:k:204:MET:HG3	2.15	0.46
40:k:378:VAL:N	40:k:399:GLY:O	2.48	0.46
1:2:96:G:H2'	1:2:97:C:H6	1.81	0.46
1:2:112:A:HO2'	10:L:67:ARG:HH11	1.62	0.46
1:2:236:C:H4'	1:2:237:U:C2	2.49	0.46
1:2:261:U:H2'	1:2:262:C:C6	2.51	0.46
1:2:488:C:N3	1:2:489:C:N4	2.64	0.46
1:2:599:U:C4	1:2:600:A:N7	2.84	0.46
1:2:883:A:H5''	3:B:136:ARG:CZ	2.46	0.46
1:2:947:G:H2'	1:2:948:C:C6	2.51	0.46
1:2:978:A:H4'	1:2:1784:G:H21	1.81	0.46
1:2:990:G:N2	1:2:1013:G:C6	2.82	0.46
1:2:1145:G:H2'	1:2:1146:A:H8	1.79	0.46
1:2:1195:A:OP2	1:2:1462:G:N2	2.48	0.46
1:2:1201:A:H62	1:2:1454:C:H3'	1.79	0.46
1:2:1426:2MG:HM22	1:2:1427:G:N3	2.31	0.46
1:2:1540:G:O3'	1:2:1541:A:H8	1.99	0.46
1:2:1556:U:H4'	28:S:135:GLY:HA3	1.97	0.46
22:F:104:ARG:CG	22:F:105:ASN:HD21	2.25	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:F:192:ILE:HD12	22:F:192:ILE:H	1.81	0.46
26:Q:104:GLU:OE1	26:Q:105:LEU:HD12	2.14	0.46
30:U:57:ARG:HG3	30:U:89:ARG:CZ	2.45	0.46
31:Z:57:TYR:OH	31:Z:68:ARG:NE	2.44	0.46
40:k:256:GLU:HG2	41:l:139:PHE:CE2	2.51	0.46
40:k:434:TYR:HE2	40:k:483:ALA:HB2	1.81	0.46
1:2:15:U:H2'	1:2:16:G:O4'	2.16	0.46
1:2:210:U:OP1	10:L:20:PHE:HB2	2.16	0.46
1:2:275:C:O2'	1:2:276:U:H5''	2.16	0.46
1:2:589:C:H2'	1:2:590:A:C8	2.45	0.46
1:2:743:U:H2'	1:2:744:U:O4'	2.16	0.46
1:2:774:A:N6	1:2:785:C:O2	2.45	0.46
1:2:884:G:OP1	3:B:136:ARG:NH1	2.49	0.46
2:A:197:ILE:H	2:A:197:ILE:HD12	1.80	0.46
9:J:53:ARG:HE	9:J:53:ARG:HB3	1.48	0.46
22:F:186:PHE:CD1	22:F:187:ARG:HG3	2.51	0.46
27:R:29:GLN:O	27:R:32:LYS:HG2	2.16	0.46
28:S:27:ASN:HB3	28:S:30:TYR:HD2	1.81	0.46
32:c:44:VAL:HG21	32:c:54:LEU:HD11	1.98	0.46
35:g:110:ASP:N	35:g:110:ASP:OD1	2.48	0.46
35:g:304:ASP:OD1	35:g:305:GLY:N	2.48	0.46
40:k:506:GLU:O	40:k:508:HIS:N	2.49	0.46
41:l:244:THR:OG1	41:l:258:VAL:O	2.24	0.46
1:2:292:U:H2'	1:2:293:C:C6	2.51	0.46
1:2:419:A:H2'	1:2:420:A:H8	1.81	0.46
1:2:472:A:OP1	9:J:44:ARG:NH1	2.43	0.46
1:2:749:U:H5''	14:W:83:ILE:CG1	2.46	0.46
1:2:1227:G:OP2	24:M:38:LEU:HG	2.15	0.46
1:2:1262:G:H2'	1:2:1263:G:O4'	2.16	0.46
1:2:1379:U:H1'	1:2:1514:A:N6	2.31	0.46
1:2:1784:G:H2'	1:2:1785:C:C6	2.51	0.46
1:2:1791:G:C2	17:a:75:ILE:HD11	2.51	0.46
3:B:133:TYR:CE1	3:B:221:PRO:HD2	2.50	0.46
6:G:3:LEU:CD1	6:G:109:LEU:HB2	2.46	0.46
9:J:100:LYS:O	9:J:102:GLU:N	2.49	0.46
15:X:3:LYS:O	15:X:5:LYS:N	2.40	0.46
22:F:118:HIS:HE1	31:Z:95:HIS:ND1	2.14	0.46
23:K:54:PHE:CD1	23:K:72:GLY:HA2	2.51	0.46
24:M:125:GLU:OE2	24:M:125:GLU:N	2.43	0.46
26:Q:99:GLU:OE2	35:g:61:SER:N	2.49	0.46
28:S:49:LYS:HG3	28:S:81:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:U:18:VAL:HG23	30:U:20:HIS:HE1	1.80	0.46
39:j:7:ARG:NH1	39:j:132:TRP:CZ2	2.84	0.46
39:j:64:ARG:O	39:j:67:LYS:HG2	2.16	0.46
39:j:216:MET:HE3	39:j:234:ALA:HA	1.98	0.46
1:2:97:C:O2	1:2:424:A:O2'	2.30	0.45
1:2:97:C:H1'	1:2:425:G:H5'	1.97	0.45
1:2:279:U:H1'	1:2:280:G:OP2	2.15	0.45
1:2:434:C:N4	15:X:46:SER:HB2	2.31	0.45
1:2:867:G:C2	1:2:960:U:C2	3.04	0.45
1:2:869:C:H2'	1:2:870:G:C8	2.50	0.45
1:2:967:U:H2'	1:2:968:C:O4'	2.15	0.45
1:2:1712:A:H2'	1:2:1713:G:C8	2.51	0.45
2:A:119:ARG:NH2	4:C:243:SER:HB3	2.30	0.45
4:C:60:GLU:O	4:C:64:HIS:ND1	2.45	0.45
4:C:76:GLN:OE1	4:C:76:GLN:HA	2.16	0.45
4:C:94:GLN:OE1	4:C:94:GLN:HA	2.15	0.45
19:e:54:ARG:HG3	19:e:54:ARG:HH11	1.81	0.45
22:F:145:ARG:HD3	32:c:55:VAL:HG11	1.98	0.45
30:U:42:ILE:HD12	30:U:52:LYS:HZ1	1.80	0.45
40:k:286:GLN:HG2	44:k:601:GCP:C5	2.46	0.45
1:2:93:A:C4'	5:E:3:ARG:HH12	2.29	0.45
1:2:473:A:H5'	9:J:144:PRO:HG2	1.98	0.45
1:2:701:U:H3	1:2:737:A:H2	1.62	0.45
1:2:739:G:H2'	1:2:740:A:C8	2.51	0.45
1:2:1306:U:H3	1:2:1317:G:H21	1.64	0.45
1:2:1460:G:H2'	1:2:1461:C:C6	2.52	0.45
1:2:1557:A:C5	28:S:134:ARG:HD2	2.52	0.45
3:B:194:ASN:OD1	3:B:210:VAL:HB	2.16	0.45
4:C:66:LEU:HD21	4:C:245:MET:SD	2.56	0.45
5:E:228:ILE:HD13	5:E:238:LEU:HD21	1.98	0.45
7:H:80:GLU:OE1	7:H:81:LEU:HD22	2.16	0.45
7:H:117:THR:O	7:H:121:VAL:HG23	2.16	0.45
8:I:37:LYS:H	8:I:59:ARG:H	1.64	0.45
26:Q:13:LYS:HG2	26:Q:76:SER:HA	1.99	0.45
27:R:100:LEU:O	27:R:102:VAL:HG13	2.16	0.45
28:S:7:GLU:HG2	28:S:10:SER:HB3	1.99	0.45
39:j:70:VAL:HG11	39:j:95:ILE:HG22	1.97	0.45
40:k:462:LEU:HD22	40:k:503:ARG:HG2	1.98	0.45
1:2:327:A:H2'	1:2:328:G:O4'	2.16	0.45
1:2:523:U:H1'	1:2:526:A:N7	2.31	0.45
1:2:906:A:H1'	1:2:996:G:O2'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1210:A:C6	1:2:1451:G:C6	3.04	0.45
1:2:1506:U:H2'	1:2:1507:C:H6	1.81	0.45
6:G:102:VAL:HG13	6:G:106:LEU:HD12	1.97	0.45
9:J:3:ARG:HD2	9:J:3:ARG:HA	1.68	0.45
9:J:45:ILE:HG22	9:J:101:VAL:HG23	1.98	0.45
17:a:37:LYS:NZ	17:a:72:HIS:NE2	2.65	0.45
21:D:101:GLN:OE1	21:D:101:GLN:HA	2.16	0.45
38:1:48:5MC:HM51	38:1:59:A:C6	2.51	0.45
40:k:313:PRO:HA	40:k:345:GLY:HA3	1.98	0.45
1:2:14:C:H2'	1:2:15:U:C6	2.51	0.45
1:2:109:G:C6	1:2:110:U:C2	3.04	0.45
1:2:381:C:H2'	1:2:382:G:H8	1.82	0.45
1:2:1201:A:H8	1:2:1206:C:N4	2.14	0.45
1:2:1364:C:H5'	26:Q:66:ARG:NH2	2.32	0.45
1:2:1527:C:H2'	1:2:1528:C:C6	2.52	0.45
6:G:166:ASP:OD1	6:G:167:LYS:N	2.50	0.45
7:H:74:GLN:O	7:H:75:ILE:C	2.60	0.45
17:a:93:ARG:HA	17:a:93:ARG:CZ	2.46	0.45
19:e:24:GLN:OE1	19:e:24:GLN:HA	2.17	0.45
22:F:166:PRO:HD3	32:c:54:LEU:HD13	1.97	0.45
25:P:33:PHE:HD2	25:P:45:PHE:HE2	1.64	0.45
28:S:14:ILE:HG23	28:S:21:ASN:OD1	2.17	0.45
35:g:19:GLY:N	35:g:315:ASN:OD1	2.49	0.45
35:g:241:PHE:HZ	35:g:272:LEU:HA	1.81	0.45
38:1:16:H2U:H1'	38:1:60:A:C2	2.50	0.45
38:1:26:M2G:C2'	38:1:27:C:H5'	2.47	0.45
1:2:42:G:N2	1:2:45:U:H3	2.15	0.45
1:2:236:C:H2'	1:2:833:G:O4'	2.16	0.45
1:2:295:U:H2'	1:2:296:U:H6	1.80	0.45
1:2:652:C:H2'	1:2:653:C:O4'	2.17	0.45
1:2:683:C:H42	1:2:684:A:N6	2.14	0.45
1:2:1357:G:O3'	29:T:130:ARG:HG2	2.17	0.45
1:2:1464:G:H2'	1:2:1465:C:C6	2.51	0.45
1:2:1580:U:H5''	26:Q:135:ARG:HD2	1.98	0.45
4:C:44:THR:O	4:C:47:GLY:N	2.41	0.45
4:C:83:ASP:HB3	4:C:109:VAL:HG12	1.98	0.45
4:C:171:SER:HB2	4:C:206:THR:HG22	1.97	0.45
4:C:178:PRO:HG3	9:J:57:ARG:HD3	1.98	0.45
7:H:26:ASP:HB3	7:H:84:LYS:HZ3	1.82	0.45
7:H:67:LEU:HD12	7:H:70:TYR:HB2	1.98	0.45
9:J:132:ARG:HG3	9:J:142:ASN:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:O:86:THR:HG21	12:O:90:ARG:HB3	1.98	0.45
17:a:10:ARG:O	17:a:11:ASN:HB3	2.17	0.45
23:K:25:LYS:HD2	23:K:59:PHE:CZ	2.51	0.45
25:P:123:TYR:OH	28:S:126:ARG:NH2	2.35	0.45
30:U:18:VAL:HG23	30:U:20:HIS:CE1	2.51	0.45
36:i:59:ALA:HA	36:i:89:CYS:O	2.16	0.45
36:i:64:LYS:HG2	36:i:64:LYS:O	2.16	0.45
38:1:6:C:N3	38:1:68:G:N1	2.64	0.45
1:2:24:U:H2'	1:2:26:A:H8	1.81	0.45
1:2:88:U:H2'	1:2:89:G:C8	2.50	0.45
1:2:116:U:H2'	1:2:117:U:C6	2.51	0.45
1:2:249:C:H2'	1:2:250:A:C8	2.45	0.45
1:2:391:G:H2'	1:2:392:C:O4'	2.17	0.45
1:2:521:U:H5''	16:Y:37:LYS:CG	2.42	0.45
1:2:527:U:C2	1:2:528:A:C8	3.04	0.45
1:2:1167:U:H2'	1:2:1168:G:H8	1.82	0.45
1:2:1483:C:H1'	1:2:1604:C:H4'	1.98	0.45
4:C:157:HIS:NE2	4:C:179:ARG:HG2	2.32	0.45
9:J:136:VAL:HG21	9:J:146:PHE:CE2	2.48	0.45
9:J:162:SER:O	9:J:162:SER:OG	2.31	0.45
14:W:8:ALA:HA	14:W:74:VAL:HG11	1.97	0.45
25:P:28:MET:HE1	25:P:33:PHE:N	2.31	0.45
35:g:226:GLN:HB3	35:g:228:TYR:CE1	2.52	0.45
40:k:110:ALA:H	44:k:601:GCP:C3B	2.28	0.45
1:2:6:G:C5	4:C:210:ARG:NH2	2.85	0.45
1:2:442:C:O2'	1:2:444:A:N1	2.49	0.45
1:2:566:A:H5''	15:X:70:LYS:NZ	2.29	0.45
1:2:574:C:H41	15:X:65:ASN:ND2	2.14	0.45
1:2:686:C:H5''	14:W:118:ARG:HH12	1.82	0.45
1:2:693:U:H5'	1:2:695:U:H5''	1.98	0.45
1:2:1209:C:H2'	1:2:1210:A:H8	1.82	0.45
1:2:1234:C:O2	34:f:136:ARG:NH2	2.50	0.45
1:2:1475:G:C6	1:2:1529:G:N1	2.85	0.45
1:2:1765:G:H4'	1:2:1766:G:O5'	2.17	0.45
2:A:105:GLY:O	2:A:109:ASN:HB3	2.16	0.45
3:B:213:ARG:HD2	3:B:214:LYS:CB	2.46	0.45
7:H:24:PHE:HE1	7:H:77:LEU:HD11	1.82	0.45
7:H:66:SER:C	7:H:68:ALA:H	2.25	0.45
7:H:101:LYS:HZ2	7:H:112:ARG:HH22	1.65	0.45
14:W:15:ASN:HD21	14:W:71:LYS:HG3	1.81	0.45
22:F:146:GLU:CD	22:F:227:ARG:HH21	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Z:75:LEU:HD23	31:Z:75:LEU:H	1.81	0.45
35:g:131:THR:HG22	35:g:146:LEU:HG	1.98	0.45
39:j:22:VAL:HG12	39:j:36:LEU:HD22	1.99	0.45
39:j:205:LEU:HD12	40:k:330:ILE:HD12	1.99	0.45
40:k:84:PHE:HA	40:k:87:LEU:HG	1.99	0.45
40:k:97:ARG:O	40:k:387:LEU:HD11	2.16	0.45
40:k:239:MET:O	40:k:240:LYS:HB2	2.16	0.45
40:k:292:ASP:OD1	40:k:293:ALA:N	2.50	0.45
40:k:359:ILE:HD12	40:k:373:ILE:HG12	1.99	0.45
40:k:410:ASP:OD1	40:k:410:ASP:N	2.47	0.45
1:2:93:A:N6	1:2:395:G:H1'	2.32	0.45
1:2:291:U:H2'	1:2:292:U:H6	1.76	0.45
1:2:900:G:C6	1:2:901:G:C6	3.05	0.45
1:2:966:A:H2'	1:2:967:U:C6	2.52	0.45
1:2:979:G:H4'	1:2:1774:A:H4'	1.98	0.45
1:2:1049:G:O6	1:2:1068:A:N6	2.49	0.45
1:2:1116:U:H2'	1:2:1117:G:C8	2.52	0.45
1:2:1413:U:H2'	1:2:1414:G:H8	1.80	0.45
1:2:1555:U:O2'	1:2:1556:U:H2'	2.17	0.45
1:2:1648:U:H2'	1:2:1649:A:H8	1.81	0.45
1:2:1664:U:H2'	1:2:1665:A:O4'	2.17	0.45
1:2:1750:U:H2'	1:2:1751:A:C8	2.51	0.45
2:A:63:ILE:CD1	13:V:36:ILE:HG12	2.47	0.45
9:J:170:GLY:HA2	9:J:174:ARG:NH1	2.32	0.45
28:S:18:LEU:O	28:S:20:THR:HG23	2.16	0.45
35:g:72:VAL:HA	35:g:82:VAL:O	2.17	0.45
35:g:271:ASP:OD1	35:g:274:ASN:HB2	2.16	0.45
39:j:166:LEU:O	39:j:170:LYS:HD3	2.16	0.45
40:k:65:ARG:HH22	40:k:165:LYS:HD3	1.82	0.45
1:2:53:G:H2'	1:2:54:C:C6	2.52	0.45
1:2:326:U:H4'	10:L:10:GLU:OE2	2.17	0.45
1:2:433:G:N2	1:2:435:A:H8	2.10	0.45
1:2:485:G:H2'	1:2:486:G:C8	2.52	0.45
1:2:585:G:H2'	1:2:586:C:H6	1.82	0.45
1:2:625:U:H2'	1:2:626:C:H6	1.80	0.45
1:2:961:C:H3'	11:N:70:LYS:NZ	2.31	0.45
1:2:987:A:H2'	1:2:988:U:C6	2.52	0.45
1:2:1436:G:H2'	1:2:1437:C:H6	1.82	0.45
1:2:1787:G:N7	12:O:132:ARG:NH1	2.65	0.45
5:E:18:TRP:HE1	5:E:42:LEU:HA	1.82	0.45
8:I:14:THR:HG23	8:I:16:ALA:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:W:15:ASN:ND2	14:W:71:LYS:HG3	2.31	0.45
14:W:24:GLN:N	14:W:24:GLN:OE1	2.49	0.45
17:a:89:ARG:HH11	17:a:89:ARG:HG3	1.81	0.45
22:F:79:TYR:OH	22:F:89:CYS:HA	2.15	0.45
24:M:100:ASP:N	24:M:100:ASP:OD1	2.50	0.45
26:Q:52:LEU:HG	26:Q:60:PHE:CZ	2.49	0.45
27:R:103:ASP:OD1	27:R:106:THR:HG22	2.17	0.45
28:S:115:ARG:HE	28:S:116:LEU:HD22	1.82	0.45
30:U:24:ILE:CD1	30:U:116:VAL:HG22	2.46	0.45
35:g:274:ASN:O	35:g:276:VAL:HG13	2.16	0.45
41:l:186:ARG:HH22	41:l:244:THR:HG23	1.81	0.45
1:2:513:G:H2'	1:2:514:A:H8	1.81	0.45
1:2:858:A:N1	11:N:76:LYS:NZ	2.65	0.45
1:2:991:A:O2'	1:2:1783:U:O2	2.32	0.45
1:2:1150:A:H2'	1:2:1151:A:H8	1.80	0.45
1:2:1308:C:C4	1:2:1309:U:C4	3.05	0.45
1:2:1343:A:H2'	1:2:1344:A:C8	2.52	0.45
2:A:4:PRO:HG2	2:A:6:THR:HG22	1.97	0.45
2:A:59:LEU:HD23	2:A:158:VAL:HG21	1.98	0.45
4:C:144:ILE:HG13	4:C:223:ILE:HG23	1.98	0.45
5:E:35:PRO:HB2	5:E:36:HIS:HD2	1.83	0.45
16:Y:15:ASN:ND2	16:Y:18:LEU:HD12	2.32	0.45
21:D:38:GLU:OE2	21:D:49:ILE:HG12	2.16	0.45
24:M:49:GLU:O	24:M:115:LYS:HA	2.17	0.45
27:R:100:LEU:O	27:R:101:ASN:C	2.60	0.45
29:T:38:LYS:O	29:T:39:THR:OG1	2.23	0.45
31:Z:53:GLU:HB2	31:Z:57:TYR:HE2	1.80	0.45
32:c:56:LEU:HB3	32:c:58:GLU:O	2.17	0.45
35:g:310:ALA:C	35:g:318:ARG:NH2	2.75	0.45
39:j:18:ASP:OD1	39:j:73:VAL:HB	2.17	0.45
40:k:106:ILE:HG13	40:k:216:LEU:HA	1.98	0.45
40:k:433:ASN:O	40:k:515:ALA:HA	2.17	0.45
1:2:73:U:O2'	1:2:74:U:O4'	2.35	0.44
1:2:842:U:H2'	1:2:843:A:C8	2.52	0.44
1:2:1411:U:O2'	1:2:1414:G:OP1	2.31	0.44
1:2:1657:A:H2'	1:2:1658:A:C8	2.52	0.44
1:2:1713:G:H2'	1:2:1714:C:C6	2.52	0.44
1:2:1779:A:N6	1:2:1780:MA6:H93	2.32	0.44
3:B:54:LEU:O	3:B:55:LYS:HB2	2.17	0.44
6:G:219:ARG:HH12	6:G:223:LYS:CB	2.24	0.44
13:V:24:ILE:HD12	13:V:31:SER:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:a:36:ILE:HG21	17:a:78:ALA:HB2	1.99	0.44
22:F:42:ILE:HA	22:F:71:TYR:CE1	2.52	0.44
25:P:52:LYS:HB3	25:P:80:LEU:HD11	1.99	0.44
27:R:19:LYS:C	27:R:20:TYR:HD1	2.25	0.44
29:T:128:GLY:O	29:T:132:LEU:HD23	2.17	0.44
39:j:24:VAL:HA	39:j:34:VAL:HG12	1.99	0.44
39:j:172:TYR:CE2	39:j:176:ARG:HG3	2.52	0.44
1:2:125:U:O4	1:2:290:G:N1	2.47	0.44
1:2:257:C:H2'	1:2:258:U:C6	2.51	0.44
1:2:411:A:C8	1:2:421:G:C2	3.05	0.44
1:2:453:U:C5	5:E:66:MET:HE1	2.51	0.44
1:2:637:U:OP1	1:2:637:U:H4'	2.15	0.44
1:2:927:U:H3'	1:2:943:A:O2'	2.16	0.44
1:2:949:C:C4'	11:N:104:ARG:HH12	2.28	0.44
1:2:1447:U:H2'	1:2:1448:U:C6	2.52	0.44
1:2:1781:C:OP2	20:h:1:MET:HE2	2.17	0.44
2:A:190:ASP:OD1	2:A:190:ASP:N	2.47	0.44
4:C:234:LEU:HD11	13:V:13:VAL:CG2	2.46	0.44
9:J:114:TYR:HA	9:J:119:ALA:CB	2.47	0.44
15:X:6:PRO:HG2	15:X:15:LEU:HD22	1.99	0.44
24:M:85:ALA:HA	24:M:88:LEU:HB3	2.00	0.44
25:P:37:ALA:N	25:P:38:PRO:CD	2.80	0.44
25:P:85:ILE:HD13	25:P:111:MET:HB3	1.99	0.44
29:T:20:SER:O	29:T:24:ARG:HG2	2.18	0.44
32:c:27:GLN:NE2	32:c:65:ARG:HA	2.33	0.44
39:j:46:ILE:HG22	39:j:85:LEU:C	2.42	0.44
40:k:84:PHE:HB3	40:k:309:PHE:CD2	2.52	0.44
40:k:356:ARG:HH21	40:k:418:GLY:HA3	1.82	0.44
1:2:103:A:H1'	1:2:307:C:N4	2.32	0.44
1:2:362:G:C2	1:2:381:C:C2	3.06	0.44
1:2:1182:A:C6	1:2:1183:A:C6	3.06	0.44
1:2:1259:U:O2'	1:2:1260:G:H8	2.00	0.44
1:2:1332:C:H2'	1:2:1333:U:H6	1.80	0.44
1:2:1710:A:H2'	1:2:1711:G:H4'	1.99	0.44
7:H:75:ILE:HG13	7:H:76:LYS:H	1.81	0.44
9:J:114:TYR:CD2	9:J:122:VAL:HB	2.53	0.44
12:O:80:HIS:HA	12:O:113:GLY:O	2.17	0.44
14:W:110:ILE:HD12	14:W:126:LEU:HD11	1.99	0.44
15:X:6:PRO:O	15:X:15:LEU:HD21	2.17	0.44
25:P:108:ARG:O	25:P:111:MET:HB2	2.17	0.44
38:1:47:H2U:H5''	38:1:47:H2U:H61	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:106:ILE:C	40:k:113:LYS:HD3	2.43	0.44
41:l:257:MET:HG3	41:l:266:ARG:O	2.18	0.44
1:2:340:A:H2'	1:2:341:C:C6	2.53	0.44
1:2:551:G:C6	1:2:552:G:C6	3.06	0.44
1:2:588:C:C4'	19:e:57:ASN:HB2	2.47	0.44
1:2:654:G:P	1:2:673:C:H42	2.39	0.44
1:2:760:A:C2	1:2:761:G:H1'	2.52	0.44
1:2:768:C:C2	9:J:143:ILE:HD13	2.53	0.44
1:2:828:A:N6	1:2:843:A:H61	2.16	0.44
1:2:926:C:H2'	1:2:927:U:C6	2.52	0.44
1:2:1343:A:H4'	1:2:1344:A:OP1	2.17	0.44
1:2:1450:U:H2'	1:2:1451:G:C8	2.52	0.44
1:2:1738:A:H2'	1:2:1739:U:H6	1.82	0.44
2:A:139:VAL:HG13	2:A:141:ILE:HG12	1.98	0.44
3:B:105:PHE:HZ	3:B:211:HIS:HB3	1.81	0.44
9:J:23:ARG:HD2	9:J:27:GLU:OE1	2.18	0.44
10:L:156:PHE:CD2	11:N:77:SER:HA	2.52	0.44
22:F:152:GLY:HA3	22:F:158:ARG:H	1.83	0.44
27:R:92:ASP:O	27:R:93:LEU:C	2.61	0.44
30:U:47:THR:HG23	30:U:48:PHE:CD1	2.51	0.44
35:g:9:VAL:HB	35:g:323:MET:SD	2.58	0.44
35:g:34:LEU:HD22	35:g:309:PHE:CD2	2.53	0.44
35:g:65:HIS:ND1	35:g:85:SER:HB3	2.33	0.44
35:g:157:VAL:O	35:g:211:PRO:HG2	2.17	0.44
36:i:25:GLU:H	36:i:25:GLU:CD	2.25	0.44
39:j:72:VAL:HG13	39:j:89:ARG:HE	1.69	0.44
40:k:314:ARG:C	40:k:315:LEU:HD12	2.42	0.44
40:k:395:LEU:H	40:k:395:LEU:HD12	1.83	0.44
1:2:643:U:H2'	1:2:644:C:C6	2.53	0.44
1:2:681:U:O2'	1:2:682:U:O4'	2.27	0.44
1:2:743:U:P	7:H:107:ARG:HD3	2.58	0.44
1:2:766:PSU:H5'	1:2:767:U:H5''	2.00	0.44
1:2:840:U:C4	1:2:841:C:C4	3.05	0.44
1:2:905:A:O5'	12:O:52:ARG:NH1	2.51	0.44
1:2:1049:G:C6	1:2:1068:A:C6	3.05	0.44
1:2:1227:G:H22	24:M:59:VAL:HB	1.82	0.44
1:2:1673:C:N3	1:2:1725:G:N1	2.66	0.44
2:A:80:THR:HA	2:A:83:GLN:HE22	1.83	0.44
2:A:166:GLY:C	2:A:168:HIS:H	2.25	0.44
3:B:141:ALA:C	3:B:142:PHE:HD1	2.26	0.44
5:E:3:ARG:HD3	5:E:3:ARG:H	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:14:ALA:HB1	5:E:18:TRP:HE3	1.81	0.44
5:E:35:PRO:HB2	5:E:36:HIS:CD2	2.52	0.44
7:H:4:PRO:HA	7:H:7:LYS:HE3	1.98	0.44
9:J:3:ARG:CZ	9:J:4:ALA:HB3	2.47	0.44
9:J:18:PRO:HG2	9:J:19:TYR:HD1	1.81	0.44
12:O:64:ALA:HA	12:O:67:VAL:HG22	2.00	0.44
12:O:99:GLN:HB3	17:a:46:GLU:OE2	2.18	0.44
14:W:11:LEU:HB3	14:W:72:CYS:SG	2.57	0.44
26:Q:81:ILE:O	26:Q:85:ILE:HG12	2.18	0.44
30:U:20:HIS:NE2	30:U:97:ALA:HB2	2.33	0.44
35:g:20:TRP:HB2	35:g:39:ARG:CG	2.45	0.44
35:g:285:PHE:HZ	35:g:312:TYR:CE2	2.36	0.44
39:j:39:TYR:CE2	39:j:42:ILE:HD12	2.53	0.44
1:2:24:U:H2'	1:2:26:A:C8	2.53	0.44
1:2:163:A:H2'	1:2:164:G:H8	1.81	0.44
1:2:646:G:C6	1:2:688:G:C6	3.04	0.44
1:2:649:U:C4	1:2:685:A:N1	2.86	0.44
1:2:1475:G:H1'	29:T:48:GLN:OE1	2.18	0.44
1:2:1523:A:H8	1:2:1523:A:OP2	2.01	0.44
5:E:100:ARG:HH21	5:E:122:LYS:HA	1.83	0.44
8:I:65:PHE:HE1	8:I:78:ILE:HD11	1.83	0.44
12:O:53:ASP:HB2	12:O:56:SER:CB	2.41	0.44
21:D:17:PHE:O	21:D:20:GLU:HB2	2.18	0.44
22:F:126:LEU:HA	31:Z:58:ARG:HD2	1.99	0.44
22:F:152:GLY:HA3	22:F:157:ALA:HA	2.00	0.44
36:i:61:ILE:CG2	36:i:66:ARG:HA	2.47	0.44
38:1:18:G:P	38:1:18:G:H8	2.41	0.44
39:j:24:VAL:HG11	39:j:63:ILE:HG23	2.00	0.44
40:k:214:ALA:HB3	40:k:244:VAL:HG22	2.00	0.44
41:l:186:ARG:NH1	41:l:245:GLU:HA	2.32	0.44
1:2:220:A:C2	1:2:840:U:C2	3.05	0.44
1:2:785:C:O3'	5:E:255:ARG:NH1	2.51	0.44
1:2:978:A:N3	1:2:1773:U:O2'	2.49	0.44
1:2:1071:C:H2'	1:2:1072:G:C8	2.53	0.44
1:2:1084:G:H5'	1:2:1085:A:OP2	2.18	0.44
1:2:1178:G:H2'	1:2:1179:C:O4'	2.18	0.44
1:2:1214:C:H5'	33:d:2:ALA:N	2.33	0.44
1:2:1423:A:O2'	1:2:1424:C:H5'	2.18	0.44
1:2:1481:A:H2'	1:2:1482:G:H8	1.77	0.44
1:2:1636:G:C6	1:2:1637:5MC:N3	2.85	0.44
3:B:47:LEU:HD23	3:B:47:LEU:HA	1.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:127:ALA:O	4:C:130:ILE:HG22	2.18	0.44
21:D:116:ARG:HH12	21:D:150:MET:HE1	1.83	0.44
21:D:179:GLN:OE1	21:D:179:GLN:N	2.47	0.44
35:g:287:GLY:C	35:g:288:TYR:HD1	2.26	0.44
38:1:20:A:H62	38:1:57:G:N2	2.08	0.44
40:k:142:TYR:CE2	45:k:603:MET:HB3	2.53	0.44
1:2:22:A:H2'	1:2:23:G:O4'	2.18	0.44
1:2:128:U:H4'	1:2:130:C:C5	2.52	0.44
1:2:278:G:C6	1:2:280:G:C6	3.05	0.44
1:2:356:G:H2'	1:2:357:U:C6	2.53	0.44
1:2:533:A:C5	1:2:534:A:C8	3.06	0.44
1:2:860:U:H4'	11:N:20:ARG:NH2	2.33	0.44
1:2:1144:U:H2'	1:2:1145:G:H8	1.83	0.44
1:2:1144:U:H4'	4:C:93:LYS:HE3	2.00	0.44
1:2:1274:A:N1	1:2:1436:G:C4	2.86	0.44
1:2:1513:A:H1'	1:2:1516:C:N4	2.33	0.44
1:2:1632:C:H1'	37:3:35:C:H5	1.83	0.44
1:2:1694:G:H2'	1:2:1706:U:O2'	2.17	0.44
2:A:73:VAL:HG13	2:A:95:ALA:HA	1.99	0.44
6:G:21:GLU:O	6:G:24:VAL:HG12	2.18	0.44
16:Y:38:ASP:OD1	16:Y:39:GLU:N	2.51	0.44
16:Y:44:LEU:HB2	16:Y:55:VAL:HG21	2.00	0.44
16:Y:57:VAL:HB	16:Y:60:PHE:CE2	2.53	0.44
20:h:3:ALA:O	20:h:7:LYS:HB2	2.18	0.44
22:F:224:LYS:HG3	22:F:227:ARG:NH1	2.32	0.44
23:K:54:PHE:HD1	23:K:72:GLY:HA2	1.83	0.44
24:M:53:ALA:O	24:M:79:LEU:HA	2.18	0.44
27:R:28:PHE:HD1	27:R:55:THR:HG21	1.83	0.44
30:U:30:LYS:HD2	30:U:33:GLN:HG3	1.98	0.44
36:i:61:ILE:HG22	36:i:66:ARG:HA	1.99	0.44
1:2:157:U:C4	1:2:419:A:H4'	2.52	0.44
1:2:300:A:C6	1:2:301:U:C4	3.06	0.44
1:2:666:U:H2'	1:2:667:G:H8	1.82	0.44
1:2:878:G:H2'	1:2:879:C:C6	2.52	0.44
1:2:932:A:C6	1:2:934:U:N3	2.86	0.44
1:2:1033:C:N3	1:2:1101:G:N1	2.66	0.44
1:2:1035:A:H2'	1:2:1036:C:C6	2.53	0.44
1:2:1043:U:H2'	1:2:1044:C:C6	2.53	0.44
1:2:1095:C:OP2	14:W:71:LYS:NZ	2.40	0.44
1:2:1233:A:H4'	34:f:143:HIS:NE2	2.33	0.44
1:2:1475:G:C6	1:2:1529:G:C6	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:105:PHE:CZ	3:B:211:HIS:HB3	2.53	0.44
3:B:111:ARG:HB3	17:a:68:TYR:HD2	1.83	0.44
3:B:140:ILE:HD11	3:B:213:ARG:CZ	2.48	0.44
4:C:145:ARG:HH21	13:V:1:MET:HG3	1.83	0.44
6:G:167:LYS:HB3	6:G:167:LYS:HE2	1.81	0.44
9:J:40:ARG:NE	9:J:40:ARG:HA	2.33	0.44
11:N:99:ARG:HH21	11:N:115:LEU:HD21	1.83	0.44
16:Y:29:HIS:ND1	16:Y:32:ARG:O	2.41	0.44
17:a:19:LYS:HE2	17:a:20:PRO:HD2	1.99	0.44
18:b:2:VAL:O	18:b:3:LEU:HB3	2.18	0.44
22:F:83:ARG:HG2	22:F:84:PHE:CD1	2.53	0.44
22:F:118:HIS:CE1	31:Z:98:GLN:HE21	2.36	0.44
26:Q:3:THR:OG1	26:Q:4:VAL:N	2.51	0.44
34:f:124:CYS:SG	34:f:141:LYS:HG2	2.58	0.44
37:3:22:U:O2'	37:3:23:A:N3	2.42	0.44
39:j:74:LEU:H	39:j:89:ARG:HH22	1.64	0.44
40:k:281:VAL:CG2	41:l:134:LEU:HD23	2.48	0.44
1:2:19:A:H2'	1:2:20:G:H8	1.82	0.43
1:2:175:C:H2'	1:2:176:U:C6	2.53	0.43
1:2:277:U:O5'	1:2:278:G:N2	2.50	0.43
1:2:442:C:N3	1:2:461:G:N1	2.67	0.43
1:2:1227:G:HO2'	34:f:100:LEU:N	2.08	0.43
4:C:233:ASN:O	4:C:233:ASN:ND2	2.51	0.43
12:O:32:ASP:OD1	12:O:35:GLY:N	2.50	0.43
18:b:7:LEU:O	18:b:24:LEU:HD13	2.18	0.43
19:e:37:ARG:O	19:e:41:THR:HG23	2.18	0.43
23:K:1:MET:SD	23:K:3:ILE:HB	2.58	0.43
34:f:124:CYS:HB3	34:f:128:ILE:HG21	2.00	0.43
35:g:258:TRP:CD1	35:g:271:ASP:HB3	2.53	0.43
39:j:22:VAL:HG21	39:j:34:VAL:HG21	2.00	0.43
1:2:174:G:N1	1:2:265:A:OP1	2.48	0.43
1:2:310:U:OP2	15:X:20:ARG:NH1	2.51	0.43
1:2:550:G:N7	1:2:581:U:C2	2.87	0.43
1:2:571:C:OP1	15:X:109:ARG:HD2	2.18	0.43
1:2:959:U:H6	1:2:959:U:P	2.41	0.43
1:2:960:U:H5''	11:N:71:ILE:HD13	1.99	0.43
1:2:1078:U:H2'	1:2:1079:U:C6	2.53	0.43
1:2:1199:G:H3'	1:2:1199:G:P	2.58	0.43
1:2:1386:A:C6	1:2:1409:A:N7	2.86	0.43
1:2:1475:G:C2	1:2:1476:G:C5	3.05	0.43
1:2:1646:A:H2'	1:2:1647:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:30:GLN:HE22	2:A:149:LEU:HB3	1.83	0.43
3:B:2:ALA:HB2	12:O:51:ASP:OD2	2.18	0.43
3:B:189:ILE:HB	3:B:190:PRO:HD3	2.00	0.43
4:C:58:ILE:CD1	4:C:78:LEU:HG	2.48	0.43
6:G:2:LYS:O	6:G:108:VAL:HA	2.18	0.43
10:L:59:PRO:HG2	10:L:60:PHE:CD2	2.53	0.43
11:N:100:LYS:O	11:N:103:GLU:HG3	2.18	0.43
17:a:21:VAL:CG1	17:a:72:HIS:HD1	2.31	0.43
23:K:1:MET:HE1	23:K:3:ILE:HB	2.00	0.43
25:P:125:PRO:HB3	28:S:129:TRP:CZ2	2.54	0.43
26:Q:58:ASP:OD1	26:Q:58:ASP:N	2.49	0.43
39:j:100:GLU:OE1	39:j:104:LYS:HE3	2.18	0.43
39:j:129:THR:HG21	39:j:161:PRO:HD3	1.99	0.43
40:k:353:ILE:HA	40:k:419:ALA:HA	1.99	0.43
40:k:435:PHE:HD2	40:k:514:TRP:CZ2	2.36	0.43
1:2:57:G:C4	1:2:91:G:N2	2.86	0.43
1:2:518:C:C4	1:2:533:A:C8	3.06	0.43
1:2:635:A:N1	1:2:860:U:C4	2.86	0.43
1:2:774:A:N1	1:2:785:C:N3	2.66	0.43
1:2:1147:C:H2'	1:2:1148:G:C8	2.54	0.43
10:L:21:THR:CG2	10:L:32:LYS:H	2.31	0.43
15:X:75:GLN:NE2	15:X:80:GLY:HA2	2.33	0.43
18:b:18:LYS:O	18:b:29:ARG:NH2	2.43	0.43
22:F:60:LEU:HD13	22:F:166:PRO:HB3	2.00	0.43
25:P:30:THR:O	25:P:34:VAL:HG23	2.19	0.43
27:R:71:PHE:CE2	27:R:73:LEU:HB2	2.53	0.43
28:S:86:LEU:H	28:S:89:GLN:NE2	2.16	0.43
28:S:89:GLN:OE1	28:S:89:GLN:N	2.51	0.43
28:S:119:ILE:HG21	28:S:121:SER:HB3	2.00	0.43
30:U:70:THR:OG1	30:U:72:ASN:OD1	2.32	0.43
33:d:13:LYS:HA	33:d:13:LYS:HE3	2.00	0.43
33:d:41:GLN:HG3	33:d:42:SER:H	1.84	0.43
35:g:117:ASP:HB2	35:g:122:LYS:HB2	2.01	0.43
35:g:156:ARG:HB3	35:g:211:PRO:HD3	2.00	0.43
39:j:85:LEU:HD23	39:j:86:SER:N	2.33	0.43
40:k:107:GLY:N	40:k:113:LYS:HD3	2.33	0.43
41:l:134:LEU:HD12	41:l:137:ARG:HD3	2.00	0.43
41:l:249:GLU:HB2	41:l:256:PHE:CD2	2.53	0.43
1:2:520:A:H2'	1:2:521:U:H6	1.81	0.43
1:2:962:A:N7	11:N:70:LYS:HE3	2.33	0.43
1:2:1114:U:H2'	1:2:1115:A:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1519:G:O2'	1:2:1521:G:OP2	2.32	0.43
1:2:1577:U:H2'	1:2:1578:C:C6	2.52	0.43
2:A:74:VAL:HG12	2:A:96:THR:HB	2.01	0.43
11:N:87:ASP:O	11:N:91:LEU:HD23	2.19	0.43
12:O:132:ARG:HG3	17:a:29:SER:HB3	2.00	0.43
16:Y:57:VAL:HB	16:Y:60:PHE:CZ	2.53	0.43
35:g:154:LYS:HA	35:g:154:LYS:HD3	1.76	0.43
35:g:238:PHE:HD2	35:g:239:MET:HG3	1.83	0.43
39:j:72:VAL:O	39:j:85:LEU:HG	2.19	0.43
1:2:220:A:C6	1:2:840:U:C4	3.06	0.43
1:2:782:G:C8	16:Y:12:VAL:HG22	2.53	0.43
1:2:1182:A:C5	25:P:100:LYS:NZ	2.86	0.43
1:2:1213:U:H5'	1:2:1245:C:O2'	2.17	0.43
1:2:1595:A:P	33:d:19:ARG:HH22	2.41	0.43
2:A:182:LEU:HD22	2:A:187:ALA:HB3	2.01	0.43
3:B:183:GLN:O	3:B:187:LYS:HG2	2.18	0.43
4:C:148:TYR:OH	4:C:153:LEU:O	2.32	0.43
8:I:138:LYS:CG	8:I:139:ASN:N	2.82	0.43
13:V:53:TYR:CE1	13:V:72:LEU:HB3	2.53	0.43
16:Y:13:ILE:HB	16:Y:22:GLN:NE2	2.34	0.43
21:D:170:THR:HA	21:D:186:VAL:O	2.19	0.43
22:F:185:ALA:CB	22:F:192:ILE:HG13	2.48	0.43
27:R:10:LYS:HG2	27:R:53:TYR:CE2	2.53	0.43
28:S:29:VAL:O	28:S:33:THR:HG23	2.18	0.43
32:c:12:VAL:HG23	32:c:28:VAL:HB	2.01	0.43
35:g:38:SER:O	35:g:69:VAL:HB	2.18	0.43
38:1:10:2MG:O6	38:1:26:M2G:C2	2.72	0.43
38:1:37:T6A:H153	38:1:38:A:C2	2.52	0.43
1:2:34:G:O2'	1:2:514:A:O2'	2.37	0.43
1:2:658:C:H2'	1:2:659:G:C8	2.54	0.43
1:2:695:U:H4'	1:2:696:C:OP2	2.17	0.43
1:2:786:G:C4	1:2:787:A:C8	3.06	0.43
1:2:946:U:OP1	3:B:162:ARG:HG3	2.18	0.43
1:2:1157:C:N4	1:2:1580:U:C4	2.87	0.43
1:2:1387:C:N4	1:2:1389:A:H1'	2.33	0.43
1:2:1474:C:H2'	1:2:1475:G:H8	1.83	0.43
1:2:1578:C:H2'	1:2:1579:C:C6	2.54	0.43
1:2:1647:G:H2'	1:2:1648:U:C6	2.54	0.43
3:B:103:MET:SD	3:B:104:ASP:N	2.91	0.43
5:E:181:VAL:HG21	5:E:195:ILE:HD11	2.01	0.43
10:L:55:ASP:HA	10:L:82:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:125:VAL:HG23	10:L:139:VAL:HA	2.00	0.43
21:D:21:LEU:HD12	21:D:25:PHE:CE2	2.54	0.43
27:R:88:VAL:C	27:R:90:ALA:H	2.26	0.43
29:T:28:LEU:HD12	29:T:107:SER:HB2	1.99	0.43
32:c:9:LEU:HB3	32:c:33:LEU:HD12	1.99	0.43
35:g:39:ARG:HG2	35:g:68:ILE:HG12	2.00	0.43
39:j:146:LYS:O	39:j:149:ILE:HG12	2.19	0.43
1:2:327:A:C4	1:2:328:G:C8	3.07	0.43
1:2:393:C:H2'	1:2:394:U:C6	2.53	0.43
1:2:548:G:H1	1:2:588:C:H5	1.67	0.43
1:2:1220:A:H2'	1:2:1221:C:C6	2.53	0.43
1:2:1314:U:OP1	1:2:1327:G:N2	2.52	0.43
1:2:1380:A:O2'	1:2:1381:G:H8	2.01	0.43
5:E:11:ARG:NH1	5:E:21:ASP:O	2.33	0.43
7:H:56:LYS:HE3	7:H:56:LYS:HB2	1.79	0.43
11:N:25:TRP:HB2	18:b:82:LYS:HE3	2.00	0.43
12:O:42:VAL:HG23	12:O:46:MET:SD	2.59	0.43
17:a:23:CYS:SG	17:a:74:CYS:N	2.72	0.43
29:T:73:VAL:HG11	29:T:102:ARG:HG3	2.01	0.43
40:k:98:GLN:HE21	40:k:391:VAL:CG2	2.31	0.43
40:k:286:GLN:HE21	41:l:262:CYS:HB3	1.82	0.43
40:k:428:THR:O	40:k:487:LEU:HG	2.19	0.43
1:2:31:C:OP1	15:X:140:LYS:NZ	2.29	0.43
1:2:66:U:N3	6:G:173:PRO:HD3	2.20	0.43
1:2:445:A:C6	1:2:446:U:C4	3.07	0.43
1:2:554:A:C5	9:J:19:TYR:CE2	3.07	0.43
1:2:619:A:O2'	1:2:620:A:H5'	2.19	0.43
1:2:768:C:H5'	9:J:146:PHE:HE1	1.84	0.43
1:2:768:C:H2'	1:2:769:A:C8	2.54	0.43
1:2:809:G:N3	7:H:111:LYS:HB2	2.34	0.43
1:2:1234:C:H2'	1:2:1235:A:O4'	2.18	0.43
1:2:1296:G:O2'	1:2:1298:G:O6	2.34	0.43
1:2:1523:A:N3	1:2:1587:C:O2'	2.51	0.43
1:2:1656:G:O6	1:2:1741:U:C2	2.72	0.43
2:A:43:ASP:O	27:R:128:ARG:NE	2.51	0.43
2:A:77:SER:HB2	2:A:86:VAL:HG21	2.01	0.43
19:e:13:LYS:HE2	19:e:13:LYS:HB2	1.84	0.43
28:S:106:GLU:OE1	28:S:110:ARG:NH1	2.51	0.43
28:S:114:GLU:HA	28:S:114:GLU:OE2	2.17	0.43
34:f:83:LYS:HD3	34:f:85:TYR:OH	2.18	0.43
35:g:10:LEU:HD13	35:g:318:ARG:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:117:ASP:HB2	35:g:122:LYS:H	1.83	0.43
35:g:187:SER:OG	35:g:194:ARG:O	2.30	0.43
35:g:208:VAL:HG21	35:g:249:ALA:HA	2.01	0.43
37:3:32:U:O2'	37:3:33:C:O4'	2.33	0.43
39:j:77:ASP:OD1	39:j:81:GLY:N	2.51	0.43
40:k:347:PHE:O	40:k:390:ALA:N	2.51	0.43
1:2:736:C:H2'	1:2:737:A:C8	2.53	0.43
1:2:974:C:C2	1:2:975:G:C8	3.06	0.43
1:2:986:G:OP2	1:2:986:G:H8	2.02	0.43
1:2:1165:A:H2'	1:2:1166:G:O4'	2.18	0.43
1:2:1167:U:C2	1:2:1168:G:C8	3.07	0.43
1:2:1182:A:N6	25:P:122:THR:O	2.52	0.43
1:2:1195:A:H4'	1:2:1196:C:H5''	2.01	0.43
1:2:1207:A:H5''	1:2:1208:C:OP2	2.18	0.43
1:2:1262:G:C2	1:2:1263:G:H1'	2.53	0.43
3:B:125:VAL:HG22	3:B:127:VAL:HG13	2.00	0.43
5:E:147:ILE:HG21	5:E:169:ILE:HG23	2.00	0.43
8:I:44:HIS:HB2	8:I:56:ARG:HB2	2.00	0.43
12:O:87:GLY:HA2	12:O:92:LYS:HA	2.00	0.43
12:O:127:ARG:HG3	17:a:22:ARG:NH1	2.34	0.43
15:X:43:PHE:O	15:X:45:GLY:N	2.48	0.43
16:Y:112:LYS:HD2	16:Y:116:LYS:HE3	2.01	0.43
23:K:61:TRP:CD2	33:d:23:ILE:HD12	2.54	0.43
26:Q:49:TYR:HB3	26:Q:53:LEU:HD23	2.00	0.43
26:Q:60:PHE:O	26:Q:60:PHE:CG	2.71	0.43
27:R:50:ILE:O	27:R:54:THR:HG23	2.19	0.43
28:S:100:SER:C	28:S:101:LEU:HD12	2.44	0.43
28:S:115:ARG:O	28:S:119:ILE:HD12	2.19	0.43
35:g:62:TYR:HB3	35:g:93:TRP:CH2	2.54	0.43
36:i:78:LEU:HB2	36:i:95:TYR:OH	2.19	0.43
38:1:42:U:C4	38:1:43:G:N7	2.86	0.43
38:1:66:C:H2'	38:1:67:G:H8	1.84	0.43
39:j:198:ILE:HD13	40:k:335:GLY:HA2	2.01	0.43
1:2:71:A:H62	6:G:164:LYS:HD2	1.84	0.43
1:2:644:C:H2'	1:2:645:U:C6	2.53	0.43
1:2:649:U:H2'	1:2:650:G:C8	2.54	0.43
1:2:991:A:N7	1:2:1012:A:C6	2.87	0.43
1:2:1399:A:OP1	27:R:60:ARG:NH1	2.52	0.43
1:2:1617:C:C2	32:c:22:ARG:NH2	2.87	0.43
1:2:1657:A:H2'	1:2:1658:A:H8	1.84	0.43
3:B:35:PRO:HD2	3:B:38:PHE:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:171:ILE:HD11	3:B:196:GLU:HB3	2.00	0.43
4:C:193:MET:HG3	4:C:201:VAL:HG11	2.00	0.43
13:V:67:ASP:OD1	13:V:87:ARG:NH2	2.52	0.43
14:W:77:PRO:HG2	14:W:79:PHE:CE1	2.53	0.43
20:h:1:MET:HB2	20:h:1:MET:HE3	1.68	0.43
22:F:166:PRO:HG2	32:c:52:ASP:OD1	2.19	0.43
23:K:61:TRP:CE2	33:d:23:ILE:HD12	2.53	0.43
26:Q:9:THR:HG21	26:Q:88:GLY:HA2	2.01	0.43
38:1:10:2MG:HM23	38:1:11:C:H1'	2.00	0.43
1:2:185:C:N4	1:2:186:G:O6	2.52	0.42
1:2:227:G:C2	1:2:228:U:C4	3.07	0.42
1:2:347:U:OP1	10:L:106:ASN:ND2	2.42	0.42
1:2:448:C:H2'	1:2:449:U:C6	2.53	0.42
1:2:508:G:H2'	1:2:509:G:C8	2.54	0.42
1:2:812:U:H3	10:L:153:PHE:HB2	1.84	0.42
1:2:1080:A:O2'	1:2:1081:C:O5'	2.31	0.42
1:2:1235:A:C4	1:2:1236:G:C8	3.07	0.42
1:2:1362:U:O2	1:2:1363:G:H5'	2.19	0.42
1:2:1450:U:H2'	1:2:1451:G:H8	1.82	0.42
1:2:1611:U:H5''	22:F:171:ASN:ND2	2.31	0.42
1:2:1623:C:H2'	1:2:1624:U:C6	2.54	0.42
1:2:1758:G:H1'	1:2:1779:A:H2	1.84	0.42
1:2:1791:G:C5	17:a:75:ILE:HD11	2.54	0.42
3:B:127:VAL:HG11	3:B:176:VAL:HG21	2.00	0.42
21:D:119:ALA:HB1	21:D:152:PHE:CD2	2.54	0.42
21:D:221:SER:HB2	35:g:200:ILE:O	2.19	0.42
24:M:22:LYS:HE2	24:M:26:ARG:HD2	2.00	0.42
35:g:172:ILE:HB	35:g:188:LEU:HD12	1.99	0.42
36:i:25:GLU:OE2	36:i:25:GLU:N	2.41	0.42
36:i:103:LEU:O	36:i:107:GLY:N	2.52	0.42
38:1:16:H2U:H2'	38:1:60:A:H1'	2.01	0.42
39:j:186:ALA:HB3	39:j:230:LEU:HD12	2.01	0.42
40:k:78:GLN:CD	40:k:387:LEU:HD22	2.43	0.42
1:2:87:C:C4	1:2:88:U:C5	3.08	0.42
1:2:197:A:H2'	1:2:198:G:O4'	2.20	0.42
1:2:408:C:H2'	1:2:409:A:C8	2.53	0.42
1:2:799:U:H2'	1:2:800:G:H8	1.84	0.42
1:2:858:A:OP1	7:H:113:PRO:HB3	2.18	0.42
1:2:917:U:H2'	1:2:918:A:C8	2.52	0.42
1:2:967:U:C4	1:2:968:C:C4	3.07	0.42
1:2:1383:G:H2'	1:2:1384:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1604:C:H2'	1:2:1605:G:C8	2.54	0.42
2:A:16:LEU:HD23	2:A:176:LEU:HD21	2.01	0.42
3:B:120:LEU:HD23	3:B:120:LEU:H	1.83	0.42
7:H:66:SER:O	7:H:68:ALA:N	2.53	0.42
7:H:136:VAL:HG12	7:H:153:LEU:O	2.19	0.42
7:H:151:LYS:HD3	7:H:184:GLU:CD	2.44	0.42
22:F:42:ILE:HG22	22:F:69:PRO:HB2	2.01	0.42
22:F:71:TYR:HB2	26:Q:50:GLU:OE1	2.18	0.42
22:F:105:ASN:HB3	22:F:108:LYS:CE	2.48	0.42
31:Z:40:VAL:HG13	31:Z:41:VAL:HG23	2.00	0.42
35:g:6:ILE:HG12	35:g:256:ARG:NH2	2.32	0.42
38:1:23:C:H2'	38:1:24:G:C8	2.54	0.42
39:j:74:LEU:CD1	39:j:89:ARG:HH11	2.32	0.42
1:2:246:A:O3'	10:L:36:LYS:HE3	2.18	0.42
1:2:608:U:O2'	15:X:19:ARG:NH2	2.53	0.42
1:2:609:G:OP2	15:X:19:ARG:NH1	2.37	0.42
1:2:815:G:H2'	1:2:816:A:H8	1.84	0.42
1:2:945:U:H2'	1:2:946:U:C6	2.55	0.42
1:2:1077:C:H2'	1:2:1078:U:C6	2.54	0.42
1:2:1180:U:H2'	1:2:1181:U:O4'	2.20	0.42
1:2:1316:C:H2'	1:2:1317:G:O4'	2.19	0.42
1:2:1386:A:N6	1:2:1409:A:N7	2.67	0.42
1:2:1426:2MG:N2	30:U:74:GLU:OE1	2.46	0.42
1:2:1448:U:H2'	1:2:1449:C:C6	2.53	0.42
1:2:1471:U:O4	22:F:182:ARG:NE	2.51	0.42
1:2:1540:G:N2	1:2:1567:A:OP2	2.51	0.42
1:2:1586:G:C6	1:2:1587:C:C4	3.06	0.42
1:2:1611:U:N3	1:2:1612:A:N1	2.67	0.42
1:2:1792:A:H3'	17:a:4:LYS:NZ	2.35	0.42
7:H:44:LYS:HB2	7:H:44:LYS:HE3	1.85	0.42
13:V:17:CYS:HB2	13:V:56:SER:HB2	2.01	0.42
13:V:85:TYR:CE1	18:b:6:ASP:OD1	2.71	0.42
22:F:43:LYS:HD3	22:F:47:LYS:C	2.44	0.42
22:F:73:ALA:HB1	22:F:96:THR:HG21	2.01	0.42
23:K:82:LEU:HD21	23:K:86:ILE:HG21	2.00	0.42
26:Q:46:PHE:O	26:Q:49:TYR:HB2	2.19	0.42
26:Q:92:TYR:CD1	26:Q:96:PHE:HD2	2.36	0.42
29:T:6:VAL:O	29:T:9:VAL:HG12	2.20	0.42
36:i:65:LEU:O	36:i:65:LEU:HD23	2.19	0.42
40:k:132:LEU:HD23	40:k:137:THR:HA	2.01	0.42
1:2:142:G:OP1	6:G:139:ASN:ND2	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:700:C:HO2'	1:2:701:U:P	2.42	0.42
1:2:806:A:H2'	1:2:807:U:H6	1.85	0.42
1:2:1125:G:H5'	20:h:11:ARG:HD3	2.01	0.42
1:2:1391:C:H2'	1:2:1392:G:C8	2.53	0.42
1:2:1465:C:H2'	1:2:1466:U:H6	1.85	0.42
1:2:1477:A:H4'	29:T:15:ILE:HD13	2.00	0.42
1:2:1562:U:H2'	1:2:1563:C:C6	2.55	0.42
3:B:70:LEU:HD12	3:B:82:ARG:HB3	2.01	0.42
5:E:260:GLY:C	5:E:261:LEU:HD12	2.44	0.42
6:G:63:MET:HE1	6:G:106:LEU:HD13	2.01	0.42
7:H:99:LEU:HA	7:H:100:PRO:HD2	1.89	0.42
7:H:101:LYS:HD3	7:H:112:ARG:NH2	2.34	0.42
13:V:76:ASP:HB3	13:V:78:LEU:HD23	2.00	0.42
16:Y:21:LYS:HB2	16:Y:75:VAL:CG1	2.50	0.42
22:F:205:LYS:H	22:F:205:LYS:HG2	1.68	0.42
25:P:84:ILE:HA	25:P:115:TYR:HA	2.00	0.42
26:Q:132:ARG:HG2	26:Q:138:PHE:HE1	1.85	0.42
30:U:102:ARG:NE	30:U:102:ARG:HA	2.35	0.42
31:Z:76:ALA:O	31:Z:80:LEU:HG	2.18	0.42
35:g:32:ASN:HA	35:g:48:LEU:HB2	2.02	0.42
35:g:43:LEU:HB2	35:g:62:TYR:HD2	1.83	0.42
39:j:19:ILE:HD13	39:j:72:VAL:HG23	2.00	0.42
40:k:254:MET:HE3	40:k:254:MET:HB2	1.90	0.42
1:2:206:U:O2	8:I:179:ARG:NH2	2.53	0.42
1:2:664:U:H2'	1:2:665:A:C8	2.54	0.42
1:2:938:A:H2'	1:2:939:A:H8	1.78	0.42
1:2:1011:U:C4	1:2:1012:A:N6	2.88	0.42
1:2:1038:A:O2'	1:2:1039:G:H8	2.03	0.42
1:2:1415:A:H2'	1:2:1416:G:O4'	2.19	0.42
1:2:1735:G:H2'	1:2:1736:U:C6	2.54	0.42
1:2:1786:G:C2	1:2:1787:G:C4	3.08	0.42
12:O:133:ARG:HB2	12:O:136:ARG:HH11	1.84	0.42
16:Y:25:VAL:HG12	16:Y:27:VAL:HG13	2.00	0.42
24:M:46:THR:HG23	24:M:47:ARG:N	2.35	0.42
29:T:18:TYR:CD1	29:T:135:ILE:HG13	2.54	0.42
29:T:126:ASP:OD1	29:T:127:ASN:N	2.52	0.42
39:j:32:ALA:HB1	39:j:34:VAL:HG13	2.00	0.42
39:j:254:VAL:HA	39:j:257:LYS:NZ	2.34	0.42
40:k:487:LEU:HD13	40:k:490:PRO:HA	2.01	0.42
1:2:201:A:H2'	1:2:202:U:C6	2.55	0.42
1:2:246:A:H4'	10:L:36:LYS:NZ	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:399:A:OP2	8:I:25:ARG:NH2	2.53	0.42
1:2:609:G:C6	1:2:613:C:C2	3.07	0.42
1:2:793:U:H5''	1:2:794:U:O5'	2.19	0.42
2:A:101:ARG:NH1	2:A:103:THR:HA	2.35	0.42
8:I:112:TRP:CZ3	8:I:117:TYR:HE2	2.37	0.42
8:I:196:ARG:O	8:I:200:LYS:HG2	2.20	0.42
8:I:196:ARG:NH2	10:L:11:ARG:HA	2.35	0.42
13:V:17:CYS:O	13:V:21:ASN:N	2.50	0.42
14:W:79:PHE:HD2	14:W:89:TRP:HZ2	1.68	0.42
26:Q:29:ILE:HA	26:Q:65:ILE:HB	2.02	0.42
35:g:90:LEU:HD22	35:g:111:VAL:HG21	2.02	0.42
1:2:30:G:H2'	1:2:31:C:C6	2.55	0.42
1:2:124:A:O2'	5:E:148:ARG:NH2	2.43	0.42
1:2:307:C:OP2	10:L:103:ARG:NH2	2.52	0.42
1:2:325:G:C2	1:2:342:C:C2	3.08	0.42
1:2:744:U:H2'	1:2:745:U:O4'	2.19	0.42
1:2:870:G:C6	1:2:956:G:N1	2.88	0.42
1:2:1023:U:OP1	1:2:1126:G:O2'	2.38	0.42
1:2:1085:A:H2'	1:2:1086:A:C8	2.54	0.42
1:2:1217:G:O2'	1:2:1264:G:N2	2.53	0.42
1:2:1219:C:H2'	1:2:1220:A:H8	1.85	0.42
1:2:1331:C:O2'	21:D:162:GLN:HG2	2.20	0.42
1:2:1706:U:H2'	1:2:1707:C:C5	2.54	0.42
2:A:73:VAL:HG23	2:A:120:LEU:HD22	2.00	0.42
4:C:85:VAL:HG11	4:C:130:ILE:HD11	2.01	0.42
4:C:152:ASN:O	4:C:153:LEU:HD22	2.20	0.42
11:N:107:LYS:O	11:N:109:LYS:N	2.53	0.42
23:K:38:LYS:HE2	23:K:38:LYS:HB2	1.87	0.42
24:M:60:THR:C	24:M:62:GLU:H	2.28	0.42
25:P:57:MET:HE2	25:P:61:ARG:NH1	2.34	0.42
30:U:43:LYS:O	30:U:46:GLU:HG3	2.19	0.42
33:d:41:GLN:H	33:d:41:GLN:HG2	1.69	0.42
35:g:201:GLY:C	35:g:228:TYR:HE2	2.28	0.42
38:l:10:2MG:H2'	38:l:11:C:H6	1.83	0.42
39:j:96:ILE:HA	39:j:99:GLU:OE1	2.20	0.42
39:j:149:ILE:HG22	39:j:173:ILE:HD12	2.00	0.42
39:j:186:ALA:CB	39:j:244:LEU:HD11	2.50	0.42
40:k:463:MET:HB3	40:k:502:SER:HG	1.83	0.42
41:l:157:LYS:HG2	41:l:158:PHE:H	1.84	0.42
1:2:268:G:C5	1:2:286:G:C2	3.08	0.42
1:2:326:U:H2'	1:2:327:A:H8	1.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:599:U:P	15:X:108:GLY:HA2	2.59	0.42
1:2:636:C:H5''	1:2:637:U:OP2	2.20	0.42
1:2:779:A:H1'	1:2:781:A:N6	2.35	0.42
1:2:825:U:H2'	1:2:826:C:H4'	2.01	0.42
1:2:1212:G:O3'	1:2:1243:A:N6	2.53	0.42
1:2:1236:G:H3'	1:2:1237:A:H8	1.84	0.42
1:2:1592:G:H5'	33:d:33:LYS:NZ	2.35	0.42
4:C:93:LYS:HG2	4:C:94:GLN:H	1.85	0.42
5:E:15:PRO:HD2	5:E:18:TRP:CE3	2.55	0.42
6:G:31:ARG:HG3	6:G:34:GLN:OE1	2.20	0.42
9:J:31:ALA:HA	9:J:36:LEU:HD12	2.01	0.42
9:J:80:LEU:HA	9:J:83:ILE:HG12	2.01	0.42
12:O:86:THR:CG2	12:O:90:ARG:HB3	2.49	0.42
14:W:111:MET:HB3	14:W:111:MET:HE2	1.49	0.42
14:W:111:MET:CG	14:W:115:GLU:HB3	2.50	0.42
21:D:79:TYR:CD2	21:D:84:ILE:HD11	2.55	0.42
22:F:90:PRO:HB2	22:F:93:GLU:HG2	2.02	0.42
22:F:101:MET:O	22:F:102:ASN:HB2	2.20	0.42
22:F:224:LYS:NZ	22:F:227:ARG:HH12	2.17	0.42
29:T:27:LYS:HD3	29:T:27:LYS:HA	1.82	0.42
33:d:20:GLN:HG2	33:d:22:ARG:H	1.84	0.42
36:i:52:PHE:HB3	36:i:110:PRO:HD2	2.02	0.42
41:l:228:ARG:O	41:l:232:GLU:HG2	2.20	0.42
1:2:72:A:H1'	1:2:73:U:C4	2.55	0.42
1:2:177:U:H5	6:G:191:LYS:NZ	2.18	0.42
1:2:242:G:H2'	1:2:243:A:C8	2.52	0.42
1:2:535:C:H3'	1:2:536:G:H8	1.85	0.42
1:2:639:U:O2'	7:H:148:LYS:NZ	2.49	0.42
1:2:786:G:C6	1:2:787:A:C6	3.08	0.42
1:2:898:G:C5'	3:B:3:VAL:HG23	2.49	0.42
2:A:14:ALA:O	2:A:18:LEU:HG	2.19	0.42
2:A:102:PHE:CD1	2:A:102:PHE:O	2.73	0.42
2:A:193:GLN:HA	2:A:194:PRO:HD3	1.90	0.42
2:A:205:ARG:NH1	2:A:209:GLU:HG3	2.35	0.42
5:E:60:GLU:O	5:E:64:ILE:HG12	2.20	0.42
9:J:131:GLN:HB2	9:J:133:HIS:CD2	2.55	0.42
12:O:81:ILE:O	12:O:115:ILE:HD12	2.19	0.42
14:W:80:ASN:ND2	14:W:124:LYS:HG2	2.34	0.42
17:a:83:ILE:HD12	17:a:83:ILE:N	2.35	0.42
21:D:76:ARG:HA	21:D:76:ARG:HD2	1.90	0.42
22:F:35:ILE:HD13	26:Q:49:TYR:HE2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:P:17:TYR:O	25:P:18:LYS:HD3	2.19	0.42
29:T:25:GLN:HG2	29:T:27:LYS:H	1.85	0.42
31:Z:95:HIS:CD2	31:Z:96:SER:N	2.87	0.42
32:c:8:THR:HG21	32:c:32:PHE:CD2	2.55	0.42
35:g:271:ASP:CG	35:g:274:ASN:HB2	2.45	0.42
39:j:95:ILE:HG13	39:j:96:ILE:N	2.35	0.42
39:j:203:ASP:HA	39:j:206:LYS:HD2	2.02	0.42
1:2:298:A:P	5:E:30:ARG:HH22	2.43	0.42
1:2:372:G:N2	1:2:602:U:O3'	2.53	0.42
1:2:426:C:C4	1:2:427:A:N7	2.87	0.42
1:2:691:U:N3	1:2:692:C:N4	2.67	0.42
1:2:802:A:H62	7:H:105:LYS:NZ	2.18	0.42
1:2:862:A:H2'	1:2:864:A:C8	2.55	0.42
1:2:947:G:H2'	1:2:948:C:H6	1.85	0.42
1:2:1216:A:C5	23:K:40:LEU:HD11	2.55	0.42
1:2:1404:A:OP1	22:F:85:ARG:NH2	2.39	0.42
1:2:1417:G:O3'	33:d:54:LYS:HE3	2.20	0.42
1:2:1578:C:H2'	1:2:1579:C:H6	1.84	0.42
1:2:1673:C:H2'	1:2:1674:U:C6	2.54	0.42
3:B:36:SER:N	3:B:41:ARG:HH21	2.17	0.42
5:E:180:LEU:HB2	5:E:231:PRO:HA	2.02	0.42
6:G:21:GLU:O	6:G:25:ARG:HD3	2.20	0.42
7:H:179:LYS:HD3	7:H:179:LYS:HA	1.74	0.42
15:X:83:VAL:HG22	15:X:84:THR:N	2.33	0.42
16:Y:40:LEU:HD23	16:Y:40:LEU:HA	1.87	0.42
23:K:44:LYS:HD3	23:K:44:LYS:HA	1.63	0.42
27:R:26:MET:CE	27:R:58:MET:HB3	2.49	0.42
35:g:308:LEU:HB3	35:g:320:TRP:HB2	2.00	0.42
38:1:8:U:H3	38:1:13:C:H41	1.65	0.42
38:1:21:A:N3	38:1:48:5MC:HM52	2.35	0.42
38:1:56:C:OP1	39:j:114:TYR:OH	2.30	0.42
1:2:305:U:H2'	1:2:306:G:C8	2.56	0.41
1:2:410:C:H2'	1:2:411:A:O4'	2.20	0.41
1:2:1191:C:OP1	1:2:1193:A:H5'	2.19	0.41
1:2:1379:U:H1'	1:2:1514:A:H61	1.85	0.41
1:2:1383:G:H2'	1:2:1384:G:C8	2.55	0.41
1:2:1398:A:H4'	27:R:60:ARG:NH2	2.35	0.41
1:2:1585:A:H1'	22:F:106:ASN:HD22	1.84	0.41
1:2:1598:A:OP1	1:2:1598:A:H4'	2.20	0.41
1:2:1656:G:H2'	1:2:1656:G:N3	2.35	0.41
6:G:148:THR:HG22	6:G:150:GLU:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:168:SER:O	7:H:172:VAL:HG12	2.20	0.41
10:L:36:LYS:HA	10:L:36:LYS:HD2	1.85	0.41
21:D:17:PHE:HE1	21:D:77:PHE:CD2	2.38	0.41
21:D:49:ILE:HG21	21:D:49:ILE:HD13	1.73	0.41
21:D:162:GLN:N	21:D:163:PRO:HD2	2.35	0.41
23:K:25:LYS:HD3	23:K:62:GLN:HG3	2.01	0.41
28:S:35:ILE:HD12	28:S:35:ILE:H	1.85	0.41
28:S:84:TRP:O	28:S:85:PHE:HB3	2.20	0.41
39:j:193:PHE:HE1	40:k:411:ARG:HH12	1.66	0.41
40:k:317:VAL:HA	40:k:340:GLY:HA2	2.02	0.41
1:2:19:A:H2'	1:2:20:G:C8	2.55	0.41
1:2:32:U:O2'	1:2:593:A:N1	2.44	0.41
1:2:154:U:OP2	16:Y:132:ARG:NH1	2.54	0.41
1:2:168:A:H5'	6:G:176:GLN:HG3	2.02	0.41
1:2:326:U:O4	1:2:327:A:N6	2.54	0.41
1:2:385:G:OP1	8:I:23:LYS:HG2	2.19	0.41
1:2:461:G:C6	1:2:462:U:C4	3.08	0.41
1:2:479:G:O6	1:2:507:U:C4	2.72	0.41
1:2:629:A:H1'	1:2:969:A:N6	2.36	0.41
1:2:1034:G:C6	1:2:1100:G:C6	3.07	0.41
1:2:1058:C:H6	1:2:1058:C:H2'	1.69	0.41
1:2:1167:U:H2'	1:2:1168:G:C8	2.56	0.41
1:2:1277:G:H2'	1:2:1278:C:O4'	2.21	0.41
1:2:1476:G:C6	1:2:1477:A:C5	3.08	0.41
4:C:145:ARG:H	4:C:226:THR:CG2	2.33	0.41
7:H:46:ILE:HG12	7:H:60:VAL:HA	2.02	0.41
7:H:77:LEU:HD22	7:H:92:PHE:CZ	2.54	0.41
10:L:124:THR:CG2	10:L:141:LYS:HB3	2.50	0.41
12:O:49:LYS:HZ1	39:j:88:ARG:NE	2.18	0.41
12:O:103:ARG:NH1	12:O:107:ARG:HH21	2.17	0.41
21:D:68:GLU:OE2	23:K:67:THR:HG23	2.19	0.41
22:F:22:PHE:CD2	22:F:23:VAL:HG23	2.55	0.41
22:F:119:THR:HG21	22:F:196:LEU:HG	2.02	0.41
22:F:221:ARG:HH22	39:j:45:MET:HB3	1.85	0.41
23:K:35:ILE:HG23	23:K:37:THR:H	1.85	0.41
39:j:118:LYS:HD3	39:j:118:LYS:HA	1.68	0.41
1:2:63:G:O5'	1:2:63:G:H8	2.04	0.41
1:2:114:C:C2	1:2:247:U:C2	3.08	0.41
1:2:402:G:H8	1:2:402:G:O5'	2.03	0.41
1:2:624:C:H2'	1:2:625:U:C6	2.56	0.41
1:2:644:C:H2'	1:2:645:U:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:959:U:O5'	11:N:62:GLN:NE2	2.53	0.41
1:2:1080:A:H2'	1:2:1082:G:N7	2.36	0.41
1:2:1085:A:C6	1:2:1086:A:C6	3.08	0.41
1:2:1107:G:H2'	15:X:25:ALA:HB1	2.00	0.41
1:2:1492:C:H2'	1:2:1493:C:C6	2.55	0.41
1:2:1687:A:H2'	1:2:1688:G:N7	2.35	0.41
1:2:1767:U:O2'	1:2:1768:U:H5'	2.21	0.41
5:E:18:TRP:CZ2	5:E:43:PRO:HD3	2.55	0.41
6:G:12:THR:OG1	6:G:124:ILE:O	2.36	0.41
6:G:112:ILE:HD13	6:G:112:ILE:HA	1.90	0.41
11:N:114:ARG:O	11:N:118:ILE:HG12	2.20	0.41
15:X:11:SER:O	15:X:15:LEU:HD23	2.18	0.41
20:h:8:LYS:HE3	20:h:12:ARG:NH2	2.36	0.41
21:D:70:THR:OG1	21:D:86:LEU:HG	2.21	0.41
22:F:31:ILE:H	22:F:31:ILE:HD12	1.85	0.41
26:Q:41:PRO:HG2	26:Q:78:VAL:HG21	2.02	0.41
27:R:18:GLU:OE1	27:R:70:SER:N	2.47	0.41
27:R:79:GLU:O	27:R:83:GLN:HG2	2.20	0.41
35:g:285:PHE:HE2	35:g:294:PRO:HG2	1.81	0.41
35:g:299:LEU:HD12	35:g:308:LEU:HD11	2.02	0.41
39:j:77:ASP:HB3	39:j:82:TYR:H	1.85	0.41
39:j:198:ILE:HD13	40:k:335:GLY:CA	2.50	0.41
40:k:108:HIS:CD2	40:k:228:GLN:NE2	2.88	0.41
1:2:69:G:C6	1:2:70:C:C4	3.09	0.41
1:2:427:A:H3'	1:2:428:G:H8	1.85	0.41
1:2:554:A:C4	9:J:19:TYR:HE2	2.39	0.41
1:2:632:U:H5'	15:X:8:GLY:HA3	2.01	0.41
1:2:1147:C:O2'	1:2:1763:A:N1	2.52	0.41
1:2:1600:C:H2'	1:2:1601:U:C6	2.56	0.41
2:A:53:THR:O	2:A:56:LYS:N	2.54	0.41
4:C:40:TRP:HD1	4:C:51:LYS:HD3	1.84	0.41
5:E:87:MET:SD	5:E:123:LEU:HB3	2.61	0.41
7:H:38:LEU:HA	7:H:41:LEU:HD13	2.03	0.41
8:I:55:PHE:HB2	8:I:177:SER:O	2.20	0.41
12:O:127:ARG:HG3	17:a:22:ARG:HH12	1.86	0.41
17:a:41:ILE:HG12	17:a:68:TYR:CD1	2.55	0.41
18:b:61:THR:O	18:b:63:LEU:HD12	2.20	0.41
19:e:20:LYS:NZ	19:e:21:VAL:O	2.51	0.41
21:D:48:ILE:HB	21:D:86:LEU:HD22	2.03	0.41
21:D:137:VAL:HG22	21:D:151:LYS:HG2	2.02	0.41
22:F:44:LEU:HD22	22:F:132:LEU:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:F:105:ASN:HD22	22:F:108:LYS:HZ1	1.68	0.41
26:Q:127:LYS:HD2	26:Q:128:LYS:N	2.35	0.41
29:T:51:GLU:HA	29:T:51:GLU:OE2	2.20	0.41
31:Z:59:TYR:CZ	31:Z:61:SER:HB3	2.56	0.41
38:1:39:C:H2'	38:1:40:C:H6	1.85	0.41
39:j:71:ALA:CB	39:j:85:LEU:HD21	2.42	0.41
1:2:12:U:H2'	1:2:13:C:H6	1.86	0.41
1:2:162:G:H2'	1:2:163:A:C8	2.55	0.41
1:2:258:U:O2	8:I:179:ARG:NH2	2.52	0.41
1:2:554:A:C5	9:J:19:TYR:HE2	2.38	0.41
1:2:590:A:H2'	1:2:591:G:H8	1.84	0.41
1:2:636:C:OP1	14:W:32:LYS:N	2.53	0.41
1:2:927:U:H4'	12:O:124:ASP:OD2	2.21	0.41
1:2:954:A:H2'	1:2:955:C:H6	1.85	0.41
1:2:967:U:H1'	1:2:1102:U:O2'	2.21	0.41
1:2:1169:G:C2	1:2:1170:A:C8	3.08	0.41
1:2:1311:A:H8	1:2:1311:A:OP1	2.04	0.41
1:2:1387:C:H6	27:R:28:PHE:CZ	2.38	0.41
1:2:1405:U:H2'	1:2:1406:G:H8	1.84	0.41
1:2:1436:G:H2'	1:2:1437:C:C6	2.55	0.41
1:2:1451:G:H2'	1:2:1452:G:H8	1.85	0.41
1:2:1611:U:C4	1:2:1612:A:N1	2.88	0.41
1:2:1712:A:H2'	1:2:1713:G:H8	1.85	0.41
2:A:24:LEU:HD22	2:A:41:ARG:HH11	1.85	0.41
2:A:188:LEU:HD22	2:A:195:TRP:CD1	2.56	0.41
4:C:183:ILE:HD11	4:C:199:GLU:HA	2.02	0.41
5:E:176:ASP:OD1	5:E:177:THR:N	2.54	0.41
9:J:136:VAL:HG22	9:J:156:ILE:HD13	2.02	0.41
9:J:170:GLY:HA2	9:J:174:ARG:HH11	1.86	0.41
14:W:82:LYS:HB3	14:W:82:LYS:HE2	1.95	0.41
22:F:127:THR:O	22:F:129:GLN:HB3	2.20	0.41
25:P:17:TYR:CD2	25:P:18:LYS:HG2	2.55	0.41
27:R:17:ILE:CD1	27:R:58:MET:HE2	2.49	0.41
29:T:22:LEU:HB3	29:T:55:TYR:HD1	1.85	0.41
35:g:200:ILE:O	35:g:200:ILE:HG13	2.21	0.41
35:g:295:HIS:H	35:g:313:THR:CG2	2.33	0.41
38:1:15:G:H1	38:1:48:5MC:N4	2.17	0.41
38:1:38:A:H2'	38:1:39:C:O4'	2.20	0.41
40:k:512:ILE:HG13	40:k:513:GLY:N	2.35	0.41
1:2:65:A:N1	1:2:85:A:N6	2.69	0.41
1:2:387:G:O6	1:2:409:A:N6	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:525:A:C5	1:2:526:A:C8	3.08	0.41
1:2:548:G:O2'	1:2:555:A:N1	2.50	0.41
1:2:566:A:O2'	19:e:14:VAL:HG22	2.20	0.41
1:2:743:U:OP1	7:H:108:GLN:N	2.49	0.41
1:2:786:G:H4'	5:E:255:ARG:NH2	2.35	0.41
1:2:977:A:H2'	1:2:978:A:O4'	2.20	0.41
1:2:983:G:H2'	1:2:984:G:H8	1.86	0.41
1:2:1210:A:C6	1:2:1211:G:C5	3.09	0.41
1:2:1276:G:C6	1:2:1434:A:C6	3.08	0.41
1:2:1280:G:H2'	1:2:1281:U:C6	2.55	0.41
1:2:1477:A:N3	1:2:1478:G:C8	2.89	0.41
4:C:108:VAL:HG12	4:C:195:LEU:HD22	2.03	0.41
7:H:75:ILE:HG13	7:H:76:LYS:N	2.36	0.41
8:I:37:LYS:HA	8:I:37:LYS:HD3	1.93	0.41
8:I:67:TRP:O	8:I:71:GLY:HA2	2.21	0.41
12:O:29:HIS:ND1	12:O:41:ARG:HG3	2.36	0.41
13:V:19:ALA:HB1	13:V:68:SER:HB2	2.01	0.41
18:b:31:HIS:O	18:b:48:SER:OG	2.32	0.41
20:h:2:ARG:CZ	20:h:5:TRP:HZ3	2.32	0.41
22:F:97:ASN:O	22:F:100:MET:HG2	2.20	0.41
22:F:189:ILE:HG21	31:Z:66:VAL:HG21	2.02	0.41
25:P:90:ILE:HD12	25:P:109:PRO:HA	2.02	0.41
26:Q:6:SER:CB	26:Q:23:LYS:HG2	2.50	0.41
26:Q:28:LEU:HD21	26:Q:66:ARG:HE	1.85	0.41
26:Q:90:VAL:CG1	26:Q:102:LYS:HD2	2.51	0.41
26:Q:94:GLN:HG3	26:Q:102:LYS:HE2	2.02	0.41
39:j:21:MET:HE3	39:j:102:TYR:CD1	2.56	0.41
40:k:147:ILE:HG23	40:k:295:ASN:ND2	2.29	0.41
45:k:603:MET:HE3	45:k:603:MET:O	2.20	0.41
1:2:597:U:C5	1:2:598:A:C5	3.08	0.41
1:2:691:U:C4	1:2:692:C:N4	2.85	0.41
1:2:926:C:O2'	12:O:124:ASP:HB3	2.21	0.41
1:2:951:A:H2'	1:2:952:G:C8	2.55	0.41
1:2:990:G:O2'	1:2:1013:G:N2	2.53	0.41
1:2:1163:G:C2	1:2:1164:G:C5	3.09	0.41
1:2:1537:G:N2	28:S:26:ILE:HD11	2.36	0.41
1:2:1543:A:OP1	28:S:132:ARG:HD3	2.20	0.41
1:2:1632:C:H5'	1:2:1633:A:C8	2.56	0.41
5:E:130:GLN:HB3	5:E:138:TYR:CZ	2.56	0.41
7:H:44:LYS:NZ	7:H:63:PRO:HA	2.36	0.41
8:I:78:ILE:HG21	8:I:96:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:46:LYS:O	10:L:50:GLU:HG2	2.20	0.41
14:W:30:SER:CB	14:W:61:ILE:HG12	2.49	0.41
14:W:51:GLU:N	14:W:62:VAL:O	2.53	0.41
21:D:142:LEU:O	21:D:143:ARG:HG2	2.20	0.41
21:D:211:PRO:HD3	27:R:20:TYR:HE1	1.86	0.41
22:F:146:GLU:HG2	22:F:223:ALA:HB1	2.03	0.41
24:M:53:ALA:HB3	24:M:79:LEU:HD23	2.01	0.41
26:Q:47:LYS:HG3	26:Q:82:ARG:HE	1.85	0.41
27:R:7:LYS:CD	27:R:11:ARG:HG3	2.50	0.41
27:R:58:MET:O	27:R:62:GLN:HG2	2.20	0.41
30:U:68:ARG:NH1	30:U:77:LYS:HA	2.30	0.41
30:U:101:LYS:HB3	30:U:102:ARG:HH22	1.85	0.41
34:f:99:LYS:HG3	34:f:100:LEU:HD13	2.02	0.41
36:i:62:ARG:NH1	36:i:65:LEU:HB2	2.36	0.41
40:k:322:ASP:N	40:k:407:CYS:O	2.54	0.41
1:2:124:A:H2'	1:2:125:U:O4'	2.20	0.41
1:2:153:G:H1'	6:G:56:ASN:ND2	2.36	0.41
1:2:158:U:O2'	6:G:87:ARG:CZ	2.68	0.41
1:2:789:U:H5	1:2:790:A:C5	2.39	0.41
1:2:1025:A:H4'	1:2:1027:C:C5	2.56	0.41
1:2:1140:G:C6	1:2:1141:A:C6	3.08	0.41
1:2:1209:C:H2'	1:2:1210:A:C8	2.55	0.41
1:2:1424:C:H3'	1:2:1425:A:H4'	2.02	0.41
1:2:1776:G:H2'	1:2:1777:U:C6	2.56	0.41
3:B:103:MET:HB3	3:B:215:VAL:HB	2.01	0.41
4:C:77:LEU:O	4:C:79:PRO:HD3	2.21	0.41
4:C:103:PHE:O	4:C:122:THR:HA	2.21	0.41
5:E:181:VAL:HG11	5:E:195:ILE:HG13	2.02	0.41
6:G:63:MET:HE2	6:G:63:MET:HB3	2.00	0.41
9:J:3:ARG:HD2	9:J:4:ALA:N	2.36	0.41
9:J:55:ALA:O	9:J:59:LEU:HD23	2.21	0.41
12:O:63:ALA:O	12:O:67:VAL:HG13	2.21	0.41
16:Y:51:GLU:OE1	16:Y:51:GLU:N	2.27	0.41
34:f:117:LEU:HB2	34:f:129:PHE:HE2	1.86	0.41
39:j:216:MET:HG2	39:j:235:LEU:HD23	2.02	0.41
1:2:57:G:H2'	1:2:58:U:O4'	2.21	0.41
1:2:96:G:OP2	5:E:10:LYS:NZ	2.52	0.41
1:2:277:U:P	1:2:278:G:H21	2.44	0.41
1:2:462:U:H2'	1:2:463:A:H8	1.85	0.41
1:2:606:G:N1	1:2:612:G:H5'	2.35	0.41
1:2:661:C:H4'	1:2:662:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:743:U:P	7:H:108:GLN:H	2.44	0.41
1:2:745:U:C2	1:2:746:A:C8	3.09	0.41
1:2:801:G:O2'	14:W:107:SER:HB2	2.21	0.41
1:2:853:U:O4	1:2:854:A:N6	2.54	0.41
1:2:1073:G:H2'	1:2:1074:C:C6	2.55	0.41
1:2:1140:G:C2	1:2:1141:A:C4	3.09	0.41
1:2:1141:A:H2'	1:2:1142:A:O4'	2.21	0.41
1:2:1182:A:C2	25:P:100:LYS:NZ	2.89	0.41
1:2:1243:A:N3	1:2:1243:A:H2'	2.35	0.41
1:2:1314:U:P	1:2:1327:G:H22	2.44	0.41
1:2:1353:G:C5	1:2:1370:G:C6	3.09	0.41
1:2:1548:A:N1	1:2:1560:G:C6	2.89	0.41
1:2:1566:C:HO2'	1:2:1567:A:H8	1.64	0.41
1:2:1595:A:P	33:d:19:ARG:HH12	2.43	0.41
1:2:1677:G:O2'	1:2:1678:G:H5'	2.21	0.41
2:A:38:TYR:OH	27:R:108:GLU:OE2	2.31	0.41
2:A:56:LYS:HG3	2:A:161:PRO:HD3	2.03	0.41
2:A:67:ILE:HD11	2:A:120:LEU:HB2	2.03	0.41
2:A:206:ASN:HB2	2:A:209:GLU:OE2	2.21	0.41
6:G:52:ILE:HG22	6:G:111:LEU:HD11	2.02	0.41
6:G:149:LYS:HD2	6:G:149:LYS:HA	1.78	0.41
8:I:140:THR:HA	8:I:144:TRP:HZ3	1.85	0.41
10:L:16:GLN:CB	10:L:19:ILE:HD13	2.51	0.41
10:L:55:ASP:OD1	10:L:82:ARG:NE	2.54	0.41
14:W:74:VAL:HG23	14:W:126:LEU:O	2.21	0.41
21:D:173:ARG:HD3	21:D:173:ARG:HA	1.77	0.41
22:F:28:ALA:HB3	26:Q:28:LEU:HB2	2.01	0.41
25:P:97:TYR:OH	25:P:99:GLY:O	2.35	0.41
25:P:119:PHE:HD1	25:P:119:PHE:HA	1.63	0.41
26:Q:23:LYS:HB2	26:Q:64:ASP:OD2	2.21	0.41
27:R:117:LEU:HD13	27:R:117:LEU:HA	1.90	0.41
30:U:60:THR:HG22	30:U:87:HIS:ND1	2.35	0.41
35:g:14:LEU:HD21	35:g:55:PHE:HB3	2.03	0.41
35:g:48:LEU:HD21	35:g:309:PHE:HZ	1.86	0.41
35:g:247:VAL:HA	35:g:262:ALA:O	2.21	0.41
36:i:55:ASN:OD1	36:i:57:ARG:NH2	2.53	0.41
38:1:12:G:C6	38:1:24:G:N1	2.89	0.41
41:l:223:GLU:O	41:l:227:ARG:HG3	2.20	0.41
1:2:235:A:O2'	1:2:237:U:O2	2.33	0.41
1:2:387:G:OP2	1:2:422:G:O2'	2.35	0.41
1:2:430:C:H2'	1:2:431:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:624:C:H2'	1:2:625:U:H6	1.86	0.41
1:2:760:A:N1	1:2:788:A:N6	2.68	0.41
1:2:918:A:H2'	1:2:919:U:C6	2.56	0.41
1:2:977:A:H2'	1:2:978:A:H8	1.86	0.41
1:2:1052:G:H2'	1:2:1053:U:C6	2.56	0.41
1:2:1227:G:C2'	34:f:99:LYS:HD2	2.51	0.41
1:2:1403:G:H2'	1:2:1404:A:H8	1.86	0.41
1:2:1535:C:C2	1:2:1570:2MG:C2	3.08	0.41
1:2:1582:G:O2'	1:2:1583:U:OP2	2.39	0.41
1:2:1634:C:C2	1:2:1763:A:N6	2.88	0.41
2:A:195:TRP:O	2:A:197:ILE:N	2.54	0.41
5:E:15:PRO:HD2	5:E:18:TRP:CZ3	2.56	0.41
6:G:79:LYS:HE2	6:G:86:PRO:HG2	2.03	0.41
9:J:77:ILE:O	9:J:81:VAL:HG23	2.21	0.41
16:Y:53:ASP:HB2	16:Y:79:VAL:HG22	2.03	0.41
17:a:19:LYS:HE2	17:a:19:LYS:HB3	1.78	0.41
18:b:32:PHE:O	18:b:33:LEU:HD23	2.21	0.41
22:F:93:GLU:O	22:F:96:THR:OG1	2.37	0.41
22:F:214:LYS:O	22:F:218:GLU:HG2	2.20	0.41
24:M:41:SER:HA	24:M:113:VAL:HG21	2.03	0.41
27:R:77:GLU:HG3	27:R:81:LYS:HD3	2.03	0.41
30:U:68:ARG:HH12	30:U:77:LYS:CA	2.30	0.41
35:g:318:ARG:HD3	35:g:318:ARG:N	2.36	0.41
40:k:94:ILE:HG12	40:k:389:PHE:HE2	1.85	0.41
40:k:463:MET:HE2	40:k:502:SER:OG	2.20	0.41
1:2:155:A:N6	1:2:417:G:C5	2.89	0.40
1:2:546:U:N3	1:2:547:G:N7	2.69	0.40
1:2:621:A:H4'	1:2:622:A:OP1	2.21	0.40
1:2:686:C:H2'	1:2:687:C:C6	2.56	0.40
1:2:760:A:C6	1:2:761:G:C4	3.10	0.40
1:2:918:A:OP1	12:O:18:ARG:NH1	2.53	0.40
1:2:1413:U:O2'	1:2:1414:G:H5'	2.21	0.40
1:2:1431:G:C1'	33:d:41:GLN:HE22	2.34	0.40
1:2:1600:C:H2'	1:2:1601:U:O4'	2.22	0.40
1:2:1638:C:O2	1:2:1761:A:N6	2.54	0.40
1:2:1717:A:H2'	1:2:1718:G:O4'	2.21	0.40
3:B:33:LYS:O	3:B:98:THR:OG1	2.37	0.40
5:E:73:ASP:HA	5:E:164:LEU:HD11	2.03	0.40
5:E:181:VAL:HG22	5:E:182:TYR:H	1.86	0.40
5:E:230:GLU:HG2	5:E:231:PRO:HD2	2.03	0.40
7:H:38:LEU:C	7:H:41:LEU:HD13	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:e:55:LYS:HG2	19:e:58:PRO:HB3	2.01	0.40
22:F:107:GLY:C	22:F:109:LYS:N	2.79	0.40
25:P:118:GLU:HB2	28:S:122:HIS:HB3	2.03	0.40
28:S:84:TRP:CD1	28:S:84:TRP:H	2.39	0.40
35:g:20:TRP:HB2	35:g:39:ARG:HD2	2.02	0.40
35:g:62:TYR:CE1	35:g:98:GLY:HA2	2.53	0.40
35:g:117:ASP:CB	35:g:122:LYS:H	2.34	0.40
35:g:251:ALA:O	35:g:260:THR:OG1	2.33	0.40
39:j:56:ILE:CG2	39:j:59:ILE:HG13	2.51	0.40
40:k:126:VAL:O	40:k:127:ARG:HB2	2.20	0.40
40:k:217:LEU:HD23	40:k:247:LEU:HB2	2.02	0.40
40:k:236:ILE:HG23	40:k:241:LEU:HB2	2.03	0.40
1:2:158:U:C5	16:Y:116:LYS:HB3	2.56	0.40
1:2:361:G:C6	1:2:382:G:C6	3.09	0.40
1:2:704:C:H4'	1:2:705:U:O5'	2.20	0.40
1:2:810:A:N6	7:H:113:PRO:HD3	2.36	0.40
1:2:828:A:O2'	1:2:829:U:OP2	2.22	0.40
1:2:875:G:H1'	1:2:943:A:O4'	2.21	0.40
1:2:1030:U:H4'	1:2:1031:G:OP2	2.22	0.40
1:2:1161:C:H4'	32:c:22:ARG:HD3	2.03	0.40
1:2:1202:A:C5	1:2:1553:A:C6	3.08	0.40
1:2:1469:A:P	22:F:187:ARG:HH11	2.44	0.40
1:2:1647:G:H2'	1:2:1648:U:H6	1.86	0.40
1:2:1758:G:H1'	1:2:1779:A:C2	2.56	0.40
1:2:1766:G:H4'	1:2:1767:U:H5''	2.03	0.40
2:A:54:TRP:HA	2:A:57:ILE:HD13	2.03	0.40
2:A:163:ASN:O	2:A:169:SER:OG	2.37	0.40
5:E:68:ARG:HH11	5:E:76:VAL:HG21	1.87	0.40
9:J:120:LYS:O	9:J:121:SER:HB3	2.20	0.40
16:Y:29:HIS:HB2	16:Y:32:ARG:HB3	2.03	0.40
17:a:11:ASN:ND2	17:a:11:ASN:C	2.78	0.40
21:D:125:TYR:O	21:D:128:GLU:HG3	2.22	0.40
22:F:156:ALA:O	22:F:158:ARG:HG2	2.21	0.40
22:F:184:ALA:HB3	22:F:195:THR:HB	2.03	0.40
26:Q:20:ALA:HB2	26:Q:84:ALA:HB1	2.03	0.40
39:j:109:HIS:ND1	39:j:127:TYR:OH	2.52	0.40
40:k:227:PRO:O	40:k:230:SER:OG	2.29	0.40
1:2:66:U:P	6:G:173:PRO:HA	2.61	0.40
1:2:1131:A:OP1	15:X:30:LYS:NZ	2.24	0.40
1:2:1222:A:C4	1:2:1223:A:C8	3.09	0.40
1:2:1225:A:O3'	1:2:1228:G:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1585:A:H2'	1:2:1586:G:H8	1.86	0.40
1:2:1779:A:H2'	1:2:1780:MA6:C8	2.51	0.40
4:C:46:LEU:HD13	4:C:66:LEU:HD22	2.03	0.40
4:C:227:TYR:CE2	13:V:12:TYR:OH	2.66	0.40
5:E:197:HIS:HB3	5:E:209:HIS:HB2	2.03	0.40
6:G:84:TYR:HD1	6:G:95:LYS:HE3	1.86	0.40
7:H:129:LEU:HD21	7:H:169:PHE:CG	2.56	0.40
9:J:114:TYR:HA	9:J:119:ALA:HB2	2.03	0.40
14:W:73:GLY:HA3	14:W:128:PHE:CZ	2.56	0.40
21:D:77:PHE:N	21:D:77:PHE:CD1	2.87	0.40
21:D:137:VAL:HB	21:D:185:LYS:HB2	2.03	0.40
23:K:11:ILE:HA	23:K:35:ILE:HD11	2.03	0.40
27:R:89:SER:C	27:R:91:LEU:H	2.29	0.40
31:Z:52:LYS:HB3	31:Z:52:LYS:HE2	1.84	0.40
34:f:118:ARG:N	34:f:118:ARG:HD2	2.37	0.40
35:g:271:ASP:CG	35:g:274:ASN:HD22	2.26	0.40
39:j:6:CYS:SG	39:j:123:LEU:HB3	2.62	0.40
39:j:97:LYS:O	39:j:100:GLU:HG3	2.21	0.40
40:k:358:GLY:HA3	40:k:373:ILE:HG13	2.03	0.40
41:l:171:LYS:HE3	41:l:173:ILE:HD11	2.03	0.40
1:2:28:A:C6	1:2:29:U:C4	3.10	0.40
1:2:638:U:O4'	7:H:118:LEU:HD21	2.20	0.40
1:2:698:U:H2'	1:2:699:U:C6	2.57	0.40
1:2:915:U:H3	12:O:41:ARG:NH2	2.19	0.40
1:2:958:U:H5''	11:N:16:ILE:HA	2.02	0.40
1:2:1176:C:H4'	1:2:1188:A:N6	2.36	0.40
1:2:1353:G:C5	1:2:1354:C:C5	3.10	0.40
1:2:1447:U:H2'	1:2:1448:U:H6	1.86	0.40
1:2:1538:G:H2'	1:2:1539:G:O4'	2.21	0.40
2:A:39:LYS:HZ2	2:A:39:LYS:HG3	1.42	0.40
4:C:64:HIS:HB2	4:C:66:LEU:CD1	2.51	0.40
6:G:48:TYR:OH	6:G:120:GLU:HA	2.21	0.40
7:H:162:ILE:HG23	7:H:165:LYS:HB2	2.02	0.40
8:I:78:ILE:HD13	8:I:180:CYS:SG	2.61	0.40
9:J:37:LYS:HA	19:e:33:ARG:HA	2.04	0.40
9:J:96:VAL:O	9:J:99:LEU:HG	2.21	0.40
13:V:83:TRP:HH2	13:V:85:TYR:HD2	1.65	0.40
15:X:48:HIS:HA	15:X:104:LEU:O	2.21	0.40
17:a:64:LEU:HA	17:a:64:LEU:HD23	1.85	0.40
22:F:28:ALA:N	26:Q:27:GLY:O	2.55	0.40
27:R:92:ASP:O	27:R:94:SER:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:c:40:ILE:HD11	32:c:62:GLU:HB3	2.04	0.40
34:f:96:LYS:HB3	34:f:96:LYS:HE2	1.86	0.40
35:g:101:GLU:N	35:g:101:GLU:OE1	2.54	0.40
35:g:192:SER:O	35:g:194:ARG:NE	2.50	0.40
40:k:71:GLU:O	40:k:182:ARG:NH1	2.31	0.40
40:k:236:ILE:HG23	40:k:241:LEU:HD12	2.03	0.40
1:2:68:A:N6	6:G:132:ARG:HG2	2.37	0.40
1:2:360:C:H2'	1:2:361:G:C8	2.56	0.40
1:2:479:G:C2	1:2:480:A:C8	3.10	0.40
1:2:609:G:C2	1:2:613:C:C4	3.09	0.40
1:2:610:U:O5'	15:X:5:LYS:NZ	2.53	0.40
1:2:1150:A:OP2	1:2:1764:A:O2'	2.37	0.40
1:2:1235:A:C6	1:2:1236:G:C5	3.10	0.40
1:2:1291:G:N1	1:2:1323:G:C2	2.90	0.40
1:2:1534:G:C5	1:2:1536:U:C2	3.09	0.40
1:2:1549:U:H2'	1:2:1550:U:H6	1.86	0.40
1:2:1711:G:C6	1:2:1712:A:C6	3.10	0.40
1:2:1720:A:H2'	1:2:1721:U:O4'	2.21	0.40
3:B:23:PRO:HB3	3:B:26:ARG:NH2	2.37	0.40
7:H:126:LEU:HD12	7:H:173:TYR:CZ	2.56	0.40
8:I:4:SER:OG	8:I:24:LYS:HD2	2.21	0.40
14:W:83:ILE:O	14:W:86:VAL:HG22	2.22	0.40
14:W:111:MET:HG2	14:W:115:GLU:HB3	2.02	0.40
18:b:35:VAL:HG12	18:b:44:THR:O	2.22	0.40
21:D:65:ARG:O	21:D:68:GLU:HB3	2.22	0.40
21:D:158:ILE:O	21:D:158:ILE:HG23	2.21	0.40
25:P:56:LEU:O	25:P:60:LEU:HD23	2.22	0.40
30:U:58:LEU:HD11	30:U:90:TYR:CD1	2.56	0.40
32:c:33:LEU:HD23	32:c:33:LEU:HA	1.86	0.40
34:f:104:ASN:O	34:f:117:LEU:CG	2.68	0.40
36:i:65:LEU:HD21	36:i:71:MET:HE3	2.03	0.40
36:i:82:ARG:HB2	36:i:85:GLN:O	2.21	0.40
36:i:101:ARG:CZ	36:i:104:LYS:HB3	2.52	0.40
40:k:280:ILE:O	41:l:131:TYR:HB2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	217/254 (85%)	191 (88%)	26 (12%)	0	100	100
3	B	221/255 (87%)	192 (87%)	27 (12%)	2 (1%)	14	48
4	C	218/259 (84%)	198 (91%)	19 (9%)	1 (0%)	24	60
5	E	258/261 (99%)	234 (91%)	24 (9%)	0	100	100
6	G	228/236 (97%)	214 (94%)	14 (6%)	0	100	100
7	H	182/190 (96%)	152 (84%)	28 (15%)	2 (1%)	11	44
8	I	184/201 (92%)	163 (89%)	20 (11%)	1 (0%)	24	60
9	J	180/188 (96%)	154 (86%)	22 (12%)	4 (2%)	5	31
10	L	153/156 (98%)	135 (88%)	18 (12%)	0	100	100
11	N	149/151 (99%)	138 (93%)	11 (7%)	0	100	100
12	O	127/137 (93%)	107 (84%)	20 (16%)	0	100	100
13	V	85/87 (98%)	74 (87%)	11 (13%)	0	100	100
14	W	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
15	X	142/145 (98%)	122 (86%)	20 (14%)	0	100	100
16	Y	132/135 (98%)	124 (94%)	8 (6%)	0	100	100
17	a	100/119 (84%)	82 (82%)	18 (18%)	0	100	100
18	b	79/82 (96%)	68 (86%)	11 (14%)	0	100	100
19	e	58/63 (92%)	53 (91%)	5 (9%)	0	100	100
20	h	23/25 (92%)	23 (100%)	0	0	100	100
21	D	225/237 (95%)	210 (93%)	14 (6%)	1 (0%)	30	65
22	F	204/227 (90%)	182 (89%)	21 (10%)	1 (0%)	24	60
23	K	94/106 (89%)	84 (89%)	10 (11%)	0	100	100
24	M	113/134 (84%)	91 (80%)	21 (19%)	1 (1%)	14	48
25	P	115/142 (81%)	97 (84%)	18 (16%)	0	100	100
26	Q	139/143 (97%)	119 (86%)	18 (13%)	2 (1%)	9	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	R	128/136 (94%)	104 (81%)	19 (15%)	5 (4%)	2	22
28	S	143/146 (98%)	124 (87%)	19 (13%)	0	100	100
29	T	141/144 (98%)	128 (91%)	13 (9%)	0	100	100
30	U	104/117 (89%)	96 (92%)	8 (8%)	0	100	100
31	Z	76/108 (70%)	68 (90%)	8 (10%)	0	100	100
32	c	62/67 (92%)	55 (89%)	7 (11%)	0	100	100
33	d	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
34	f	72/150 (48%)	55 (76%)	17 (24%)	0	100	100
35	g	314/326 (96%)	277 (88%)	37 (12%)	0	100	100
36	i	95/153 (62%)	83 (87%)	12 (13%)	0	100	100
39	j	263/304 (86%)	238 (90%)	24 (9%)	1 (0%)	30	65
40	k	468/527 (89%)	433 (92%)	32 (7%)	3 (1%)	21	57
41	l	126/285 (44%)	120 (95%)	5 (4%)	1 (1%)	16	52
All	All	5798/6582 (88%)	5152 (89%)	621 (11%)	25 (0%)	31	65

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	6	ASN
8	I	140	THR
26	Q	42	GLU
27	R	93	LEU
27	R	98	ASP
40	k	130	ASP
22	F	108	LYS
40	k	507	LYS
7	H	66	SER
7	H	67	LEU
9	J	163	PRO
24	M	103	ALA
27	R	89	SER
39	j	40	ASP
3	B	221	PRO
27	R	97	ASN
27	R	99	VAL
4	C	45	LYS
9	J	162	SER

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Mol	Chain	Res	Type
21	D	220	PRO
26	Q	39	VAL
40	k	127	ARG
9	J	101	VAL
9	J	122	VAL
41	l	242	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	180/211 (85%)	180 (100%)	0	100	100
3	B	202/228 (89%)	201 (100%)	1 (0%)	81	82
4	C	177/203 (87%)	177 (100%)	0	100	100
5	E	223/224 (100%)	223 (100%)	0	100	100
6	G	192/200 (96%)	191 (100%)	1 (0%)	81	82
7	H	164/170 (96%)	163 (99%)	1 (1%)	78	81
8	I	147/159 (92%)	147 (100%)	0	100	100
9	J	153/158 (97%)	153 (100%)	0	100	100
10	L	136/137 (99%)	136 (100%)	0	100	100
11	N	128/128 (100%)	128 (100%)	0	100	100
12	O	97/104 (93%)	97 (100%)	0	100	100
13	V	73/73 (100%)	73 (100%)	0	100	100
14	W	110/111 (99%)	110 (100%)	0	100	100
15	X	119/120 (99%)	119 (100%)	0	100	100
16	Y	108/109 (99%)	108 (100%)	0	100	100
17	a	83/100 (83%)	82 (99%)	1 (1%)	63	73
18	b	71/72 (99%)	71 (100%)	0	100	100
19	e	51/55 (93%)	51 (100%)	0	100	100
20	h	23/23 (100%)	23 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	D	188/196 (96%)	188 (100%)	0	100	100
22	F	174/194 (90%)	173 (99%)	1 (1%)	78	81
23	K	88/96 (92%)	88 (100%)	0	100	100
24	M	93/109 (85%)	93 (100%)	0	100	100
25	P	99/119 (83%)	99 (100%)	0	100	100
26	Q	117/119 (98%)	116 (99%)	1 (1%)	70	76
27	R	116/124 (94%)	113 (97%)	3 (3%)	40	61
28	S	127/129 (98%)	127 (100%)	0	100	100
29	T	117/118 (99%)	117 (100%)	0	100	100
30	U	96/107 (90%)	96 (100%)	0	100	100
31	Z	59/88 (67%)	59 (100%)	0	100	100
32	c	55/59 (93%)	55 (100%)	0	100	100
33	d	47/48 (98%)	47 (100%)	0	100	100
34	f	60/133 (45%)	60 (100%)	0	100	100
35	g	264/272 (97%)	264 (100%)	0	100	100
36	i	83/130 (64%)	83 (100%)	0	100	100
39	j	240/274 (88%)	240 (100%)	0	100	100
40	k	393/449 (88%)	393 (100%)	0	100	100
41	l	125/246 (51%)	125 (100%)	0	100	100
All	All	4978/5595 (89%)	4969 (100%)	9 (0%)	85	87

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	3	VAL
6	G	149	LYS
7	H	64	VAL
17	a	11	ASN
22	F	105	ASN
26	Q	40	GLN
27	R	92	ASP
27	R	93	LEU
27	R	100	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	30	GLN
2	A	46	ASN
2	A	49	ASN
3	B	74	GLN
3	B	146	GLN
3	B	178	ASN
4	C	225	ASN
5	E	17	HIS
5	E	216	ASN
5	E	224	ASN
7	H	110	GLN
7	H	164	ASN
8	I	116	HIS
9	J	48	GLN
10	L	8	GLN
13	V	70	ASN
14	W	12	ASN
15	X	75	GLN
16	Y	15	ASN
17	a	80	HIS
18	b	49	HIS
21	D	162	GLN
22	F	105	ASN
22	F	106	ASN
23	K	85	HIS
24	M	102	ASN
24	M	116	ASN
26	Q	8	GLN
26	Q	21	HIS
27	R	97	ASN
29	T	93	HIS
29	T	127	ASN
31	Z	38	HIS
34	f	95	HIS
34	f	143	HIS
36	i	88	GLN
40	k	78	GLN
40	k	144	ASN
40	k	243	HIS
40	k	344	ASN
40	k	369	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1797/1798 (99%)	593 (32%)	23 (1%)
37	3	25/49 (51%)	16 (64%)	0
38	1	71/75 (94%)	31 (43%)	8 (11%)
All	All	1893/1922 (98%)	640 (33%)	31 (1%)

All (640) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	13	C
1	2	14	C
1	2	17	C
1	2	23	G
1	2	25	C
1	2	26	A
1	2	27	U
1	2	34	G
1	2	42	G
1	2	43	A
1	2	47	A
1	2	50	C
1	2	57	G
1	2	59	C
1	2	63	G
1	2	65	A
1	2	67	A
1	2	68	A
1	2	69	G
1	2	71	A
1	2	72	A
1	2	73	U
1	2	74	U
1	2	75	U
1	2	77	U
1	2	79	C
1	2	84	A
1	2	92	A
1	2	104	A
1	2	111	U
1	2	114	C
1	2	115	G
1	2	116	U

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Mol	Chain	Res	Type
1	2	123	G
1	2	124	A
1	2	126	A
1	2	127	G
1	2	128	U
1	2	129	U
1	2	130	C
1	2	132	U
1	2	135	A
1	2	136	C
1	2	137	U
1	2	139	C
1	2	140	A
1	2	146	A
1	2	158	U
1	2	159	C
1	2	161	A
1	2	167	A
1	2	173	U
1	2	177	U
1	2	178	A
1	2	183	C
1	2	187	A
1	2	191	U
1	2	192	U
1	2	194	G
1	2	195	G
1	2	214	A
1	2	217	A
1	2	218	A
1	2	220	A
1	2	224	A
1	2	226	U
1	2	227	G
1	2	228	U
1	2	230	U
1	2	231	U
1	2	232	C
1	2	234	G
1	2	235	A
1	2	237	U
1	2	239	C

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Mol	Chain	Res	Type
1	2	240	U
1	2	242	G
1	2	247	U
1	2	248	U
1	2	249	C
1	2	256	A
1	2	259	U
1	2	264	A
1	2	266	U
1	2	267	C
1	2	271	U
1	2	275	C
1	2	276	U
1	2	278	G
1	2	280	G
1	2	289	G
1	2	295	U
1	2	298	A
1	2	301	U
1	2	307	C
1	2	311	A
1	2	312	U
1	2	313	C
1	2	315	A
1	2	319	U
1	2	321	G
1	2	323	U
1	2	328	G
1	2	329	G
1	2	332	A
1	2	336	G
1	2	337	C
1	2	338	C
1	2	349	U
1	2	358	A
1	2	359	A
1	2	360	C
1	2	369	A
1	2	382	G
1	2	389	G
1	2	390	A
1	2	392	C

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Mol	Chain	Res	Type
1	2	399	A
1	2	400	A
1	2	401	C
1	2	403	G
1	2	411	A
1	2	415	A
1	2	416	A
1	2	418	G
1	2	422	G
1	2	423	C
1	2	424	A
1	2	425	G
1	2	433	G
1	2	434	C
1	2	436	A
1	2	438	U
1	2	439	U
1	2	440	A
1	2	443	C
1	2	447	C
1	2	459	A
1	2	467	A
1	2	468	C
1	2	473	A
1	2	474	A
1	2	479	G
1	2	482	A
1	2	483	C
1	2	486	G
1	2	488	C
1	2	489	C
1	2	490	C
1	2	491	A
1	2	492	U
1	2	493	U
1	2	494	C
1	2	495	G
1	2	496	G
1	2	499	C
1	2	501	U
1	2	502	G
1	2	504	A

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Mol	Chain	Res	Type
1	2	505	A
1	2	506	U
1	2	507	U
1	2	508	G
1	2	516	U
1	2	518	C
1	2	526	A
1	2	533	A
1	2	535	C
1	2	537	A
1	2	539	G
1	2	540	A
1	2	541	A
1	2	542	C
1	2	543	A
1	2	544	A
1	2	547	G
1	2	553	C
1	2	554	A
1	2	558	C
1	2	559	U
1	2	564	C
1	2	565	C
1	2	567	G
1	2	578	A
1	2	584	A
1	2	587	U
1	2	593	A
1	2	594	G
1	2	605	A
1	2	610	U
1	2	618	A
1	2	619	A
1	2	620	A
1	2	621	A
1	2	622	A
1	2	623	G
1	2	632	U
1	2	637	U
1	2	638	U
1	2	641	G
1	2	647	G

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Mol	Chain	Res	Type
1	2	650	G
1	2	651	U
1	2	652	C
1	2	653	C
1	2	659	G
1	2	663	U
1	2	664	U
1	2	666	U
1	2	671	C
1	2	672	G
1	2	673	C
1	2	675	C
1	2	679	U
1	2	680	U
1	2	681	U
1	2	684	A
1	2	685	A
1	2	686	C
1	2	691	U
1	2	693	U
1	2	694	U
1	2	695	U
1	2	696	C
1	2	697	C
1	2	700	C
1	2	701	U
1	2	702	G
1	2	704	C
1	2	707	A
1	2	709	C
1	2	710	U
1	2	711	G
1	2	712	U
1	2	713	A
1	2	714	C
1	2	715	U
1	2	716	C
1	2	717	C
1	2	718	U
1	2	719	U
1	2	720	G
1	2	721	U

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Mol	Chain	Res	Type
1	2	722	G
1	2	727	C
1	2	730	G
1	2	732	G
1	2	733	A
1	2	734	A
1	2	736	C
1	2	738	G
1	2	741	C
1	2	742	U
1	2	753	A
1	2	755	A
1	2	762	A
1	2	765	G
1	2	766	PSU
1	2	771	A
1	2	774	A
1	2	778	G
1	2	779	A
1	2	780	A
1	2	781	A
1	2	782	G
1	2	783	C
1	2	788	A
1	2	792	A
1	2	793	U
1	2	794	U
1	2	811	A
1	2	813	A
1	2	814	G
1	2	818	G
1	2	819	U
1	2	820	U
1	2	821	U
1	2	822	G
1	2	823	G
1	2	826	C
1	2	827	U
1	2	828	A
1	2	829	U
1	2	832	U
1	2	836	G

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Mol	Chain	Res	Type
1	2	837	G
1	2	840	U
1	2	845	G
1	2	849	A
1	2	855	A
1	2	856	U
1	2	859	U
1	2	860	U
1	2	861	A
1	2	862	A
1	2	863	U
1	2	876	G
1	2	885	U
1	2	896	C
1	2	897	A
1	2	904	A
1	2	905	A
1	2	910	U
1	2	911	U
1	2	912	G
1	2	913	G
1	2	915	U
1	2	916	U
1	2	917	U
1	2	919	U
1	2	920	U
1	2	927	U
1	2	928	A
1	2	932	A
1	2	934	U
1	2	941	G
1	2	944	U
1	2	950	A
1	2	958	U
1	2	959	U
1	2	965	A
1	2	969	A
1	2	973	A
1	2	982	A
1	2	985	G
1	2	986	G
1	2	987	A

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Mol	Chain	Res	Type
1	2	991	A
1	2	995	U
1	2	1002	A
1	2	1008	U
1	2	1011	U
1	2	1015	C
1	2	1025	A
1	2	1026	A
1	2	1027	C
1	2	1030	U
1	2	1031	G
1	2	1038	A
1	2	1039	G
1	2	1041	G
1	2	1042	A
1	2	1048	U
1	2	1049	G
1	2	1050	G
1	2	1051	U
1	2	1052	G
1	2	1054	U
1	2	1055	U
1	2	1057	U
1	2	1058	C
1	2	1059	U
1	2	1065	C
1	2	1075	A
1	2	1081	C
1	2	1082	G
1	2	1084	G
1	2	1086	A
1	2	1090	A
1	2	1091	A
1	2	1092	A
1	2	1095	C
1	2	1096	U
1	2	1097	U
1	2	1099	G
1	2	1103	U
1	2	1112	A
1	2	1113	G
1	2	1123	A

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Mol	Chain	Res	Type
1	2	1125	G
1	2	1131	A
1	2	1137	A
1	2	1149	G
1	2	1150	A
1	2	1155	C
1	2	1157	C
1	2	1158	C
1	2	1163	G
1	2	1166	G
1	2	1169	G
1	2	1184	U
1	2	1185	U
1	2	1188	A
1	2	1189	C
1	2	1190	B8N
1	2	1192	A
1	2	1193	A
1	2	1198	G
1	2	1199	G
1	2	1206	C
1	2	1207	A
1	2	1211	G
1	2	1216	A
1	2	1217	G
1	2	1224	U
1	2	1226	A
1	2	1227	G
1	2	1228	G
1	2	1230	U
1	2	1236	G
1	2	1237	A
1	2	1241	A
1	2	1243	A
1	2	1244	G
1	2	1245	C
1	2	1246	U
1	2	1247	C
1	2	1249	U
1	2	1250	U
1	2	1251	C
1	2	1254	G

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Mol	Chain	Res	Type
1	2	1255	A
1	2	1256	U
1	2	1258	U
1	2	1259	U
1	2	1260	G
1	2	1268	U
1	2	1269	G
1	2	1272	G
1	2	1275	U
1	2	1283	C
1	2	1284	U
1	2	1287	G
1	2	1289	PSU
1	2	1298	G
1	2	1300	U
1	2	1306	U
1	2	1313	U
1	2	1314	U
1	2	1315	G
1	2	1320	A
1	2	1321	A
1	2	1323	G
1	2	1324	A
1	2	1336	A
1	2	1337	C
1	2	1339	U
1	2	1340	A
1	2	1343	A
1	2	1344	A
1	2	1345	A
1	2	1347	A
1	2	1349	G
1	2	1359	A
1	2	1360	C
1	2	1361	U
1	2	1362	U
1	2	1363	G
1	2	1366	G
1	2	1369	U
1	2	1370	G
1	2	1371	A
1	2	1376	U

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Mol	Chain	Res	Type
1	2	1381	G
1	2	1388	U
1	2	1390	U
1	2	1396	U
1	2	1397	C
1	2	1398	A
1	2	1400	G
1	2	1401	C
1	2	1408	A
1	2	1409	A
1	2	1410	G
1	2	1411	U
1	2	1413	U
1	2	1414	G
1	2	1416	G
1	2	1418	C
1	2	1423	A
1	2	1424	C
1	2	1425	A
1	2	1426	2MG
1	2	1431	G
1	2	1434	A
1	2	1442	A
1	2	1443	G
1	2	1444	A
1	2	1453	G
1	2	1455	C
1	2	1457	C
1	2	1458	A
1	2	1459	C
1	2	1464	G
1	2	1467	A
1	2	1469	A
1	2	1471	U
1	2	1475	G
1	2	1476	G
1	2	1481	A
1	2	1482	G
1	2	1484	G
1	2	1488	A
1	2	1489	C
1	2	1490	A

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Mol	Chain	Res	Type
1	2	1491	A
1	2	1494	U
1	2	1510	G
1	2	1511	G
1	2	1514	A
1	2	1521	G
1	2	1522	A
1	2	1523	A
1	2	1532	G
1	2	1534	G
1	2	1535	C
1	2	1538	G
1	2	1540	G
1	2	1543	A
1	2	1554	A
1	2	1555	U
1	2	1557	A
1	2	1558	U
1	2	1566	C
1	2	1571	A
1	2	1572	G
1	2	1573	7MG
1	2	1588	G
1	2	1594	C
1	2	1598	A
1	2	1599	G
1	2	1614	G
1	2	1617	C
1	2	1620	G
1	2	1631	A
1	2	1632	C
1	2	1633	A
1	2	1640	G
1	2	1646	A
1	2	1655	U
1	2	1656	G
1	2	1663	U
1	2	1678	G
1	2	1679	A
1	2	1682	U
1	2	1685	U
1	2	1686	U

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Mol	Chain	Res	Type
1	2	1687	A
1	2	1688	G
1	2	1692	A
1	2	1693	G
1	2	1694	G
1	2	1695	G
1	2	1696	G
1	2	1697	G
1	2	1698	C
1	2	1699	A
1	2	1700	A
1	2	1701	C
1	2	1702	U
1	2	1703	C
1	2	1704	C
1	2	1707	C
1	2	1709	C
1	2	1710	A
1	2	1711	G
1	2	1712	A
1	2	1715	G
1	2	1719	A
1	2	1724	G
1	2	1725	G
1	2	1728	A
1	2	1729	A
1	2	1730	A
1	2	1734	G
1	2	1740	U
1	2	1742	A
1	2	1743	G
1	2	1748	A
1	2	1749	C
1	2	1750	U
1	2	1753	A
1	2	1754	A
1	2	1755	G
1	2	1758	G
1	2	1763	A
1	2	1764	A
1	2	1766	G
1	2	1767	U

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Mol	Chain	Res	Type
1	2	1778	G
1	2	1779	A
1	2	1781	C
1	2	1786	G
1	2	1787	G
1	2	1790	G
1	2	1791	G
1	2	1792	A
1	2	1793	U
1	2	1794	C
1	2	1797	U
1	2	1798	A
37	3	16	U
37	3	19	A
37	3	20	A
37	3	22	U
37	3	23	A
37	3	24	U
37	3	25	A
37	3	26	A
37	3	29	A
37	3	32	U
37	3	33	C
37	3	35	C
37	3	36	U
37	3	37	U
37	3	38	C
37	3	40	C
38	1	4	G
38	1	8	U
38	1	9	1MG
38	1	13	C
38	1	14	A
38	1	15	G
38	1	16	H2U
38	1	19	G
38	1	20	A
38	1	21	A
38	1	22	G
38	1	23	C
38	1	24	G
38	1	25	C

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Mol	Chain	Res	Type
38	1	26	M2G
38	1	27	C
38	1	28	A
38	1	41	C
38	1	43	G
38	1	44	A
38	1	45	U
38	1	46	7MG
38	1	47	H2U
38	1	48	5MC
38	1	50	U
38	1	56	C
38	1	58	1MA
38	1	60	A
38	1	61	C
38	1	73	A
38	1	75	C

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	74	U
1	2	216	A
1	2	217	A
1	2	239	C
1	2	277	U
1	2	279	U
1	2	423	C
1	2	649	U
1	2	670	G
1	2	695	U
1	2	700	C
1	2	721	U
1	2	828	A
1	2	1080	A
1	2	1198	G
1	2	1206	C
1	2	1255	A
1	2	1343	A
1	2	1430	U
1	2	1470	C
1	2	1513	A

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Mol	Chain	Res	Type
1	2	1571	A
1	2	1765	G
38	1	8	U
38	1	14	A
38	1	24	G
38	1	25	C
38	1	27	C
38	1	43	G
38	1	44	A
38	1	74	C

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

23 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	$\# Z > 2$
38	1MA	1	58	38	21,25,26	3.16	6 (28%)	30,37,40	2.51	8 (26%)
38	2MG	1	10	38	23,26,27	2.91	8 (34%)	33,38,41	2.18	11 (33%)
38	M2G	1	26	38	24,27,28	1.33	4 (16%)	33,40,43	2.08	8 (24%)
1	PSU	2	465	1	18,21,22	4.44	7 (38%)	21,30,33	1.90	5 (23%)
1	PSU	2	766	1	18,21,22	4.45	7 (38%)	21,30,33	2.11	6 (28%)
1	B8N	2	1190	1	25,29,30	3.35	7 (28%)	28,42,45	2.00	9 (32%)
38	5MC	1	49	38	19,22,23	3.94	8 (42%)	26,32,35	1.07	3 (11%)
1	5MC	2	1637	1	19,22,23	3.83	8 (42%)	26,32,35	0.93	1 (3%)
38	7MG	1	46	38	23,26,27	3.64	11 (47%)	27,39,42	2.21	9 (33%)
38	1MG	1	9	38	23,26,27	3.33	7 (30%)	33,39,42	2.30	8 (24%)
1	2MG	2	1426	1,42	23,26,27	2.90	8 (34%)	33,38,41	2.18	9 (27%)
1	7MG	2	1573	1,38	23,26,27	3.59	11 (47%)	27,39,42	2.22	9 (33%)
1	MA6	2	1780	1	23,26,27	1.40	4 (17%)	33,38,41	3.22	11 (33%)
38	5MC	1	48	38	19,22,23	3.84	8 (42%)	26,32,35	1.18	2 (7%)
38	T6A	1	37	38	31,34,35	1.81	7 (22%)	43,49,52	2.16	13 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	H2U	1	16	38	18,21,22	3.13	4 (22%)	19,30,33	1.36	4 (21%)
1	5MC	2	1006	1	19,22,23	3.84	8 (42%)	26,32,35	1.11	3 (11%)
1	PSU	2	120	1	18,21,22	4.45	7 (38%)	21,30,33	1.98	6 (28%)
1	2MG	2	1570	1	23,26,27	2.92	8 (34%)	33,38,41	2.15	10 (30%)
1	PSU	2	998	1	18,21,22	4.42	7 (38%)	21,30,33	1.94	6 (28%)
1	PSU	2	1289	1	18,21,22	4.46	7 (38%)	21,30,33	1.86	5 (23%)
38	H2U	1	47	38	18,21,22	3.16	4 (22%)	19,30,33	1.43	4 (21%)
38	RIA	1	64	38	35,38,39	4.66	14 (40%)	50,57,60	1.97	12 (24%)

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
38	1MA	1	58	38	-	2/7/25/26	0/3/3/3
38	2MG	1	10	38	-	0/9/27/28	0/3/3/3
38	M2G	1	26	38	-	1/11/29/30	0/3/3/3
1	PSU	2	465	1	-	0/7/25/26	0/2/2/2
1	PSU	2	766	1	-	2/7/25/26	0/2/2/2
1	B8N	2	1190	1	-	5/16/34/35	0/2/2/2
38	5MC	1	49	38	-	0/7/25/26	0/2/2/2
1	5MC	2	1637	1	-	0/7/25/26	0/2/2/2
38	7MG	1	46	38	-	1/7/37/38	0/3/3/3
38	1MG	1	9	38	-	2/7/25/26	0/3/3/3
1	2MG	2	1426	1,42	-	0/9/27/28	0/3/3/3
1	7MG	2	1573	1,38	-	2/7/37/38	0/3/3/3
1	MA6	2	1780	1	-	3/11/29/30	0/3/3/3
38	5MC	1	48	38	-	3/7/25/26	0/2/2/2
38	T6A	1	37	38	-	5/23/41/42	0/3/3/3
38	H2U	1	16	38	-	1/7/38/39	0/2/2/2
1	5MC	2	1006	1	-	0/7/25/26	0/2/2/2
1	PSU	2	120	1	-	1/7/25/26	0/2/2/2
1	2MG	2	1570	1	-	2/9/27/28	0/3/3/3
1	PSU	2	998	1	-	0/7/25/26	0/2/2/2
1	PSU	2	1289	1	-	3/7/25/26	0/2/2/2
38	H2U	1	47	38	-	4/7/38/39	0/2/2/2
38	RIA	1	64	38	-	3/17/51/52	0/4/4/4

All (170) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	64	RIA	C1'-C2'	-16.24	1.32	1.52
1	2	1289	PSU	C6-C5	11.90	1.48	1.35
1	2	766	PSU	C6-C5	11.76	1.48	1.35
1	2	120	PSU	C6-C5	11.72	1.48	1.35
1	2	465	PSU	C6-C5	11.70	1.48	1.35
1	2	998	PSU	C6-C5	11.53	1.48	1.35
38	1	64	RIA	O1'-C1'	11.36	1.61	1.41
1	2	120	PSU	C2-N1	10.03	1.49	1.36
1	2	465	PSU	C2-N1	9.92	1.49	1.36
38	1	47	H2U	C2-N1	9.90	1.49	1.35
1	2	766	PSU	C2-N1	9.89	1.49	1.36
1	2	998	PSU	C2-N1	9.86	1.49	1.36
1	2	1289	PSU	C2-N1	9.85	1.49	1.36
38	1	58	1MA	C2-N3	9.82	1.48	1.30
38	1	16	H2U	C2-N1	9.75	1.49	1.35
38	1	48	5MC	C6-C5	9.40	1.49	1.34
38	1	64	RIA	C2A-C1A	-9.37	1.30	1.53
38	1	49	5MC	C6-C5	9.33	1.49	1.34
1	2	1637	5MC	C6-C5	9.29	1.49	1.34
38	1	64	RIA	O4'-C1A	9.21	1.63	1.42
38	1	9	1MG	C2-N2	9.20	1.50	1.34
1	2	1006	5MC	C6-C5	8.81	1.49	1.34
1	2	1573	7MG	C8-N9	8.68	1.51	1.45
38	1	46	7MG	C8-N9	8.53	1.51	1.45
1	2	1190	B8N	C6-N1	8.29	1.56	1.36
1	2	766	PSU	C2-N3	7.82	1.50	1.37
1	2	998	PSU	C2-N3	7.80	1.50	1.37
1	2	1570	2MG	C2-N3	7.76	1.46	1.32
1	2	120	PSU	C2-N3	7.76	1.50	1.37
1	2	465	PSU	C2-N3	7.74	1.50	1.37
1	2	1289	PSU	C2-N3	7.71	1.50	1.37
1	2	1426	2MG	C2-N3	7.60	1.46	1.32
38	1	10	2MG	C2-N3	7.59	1.46	1.32
1	2	1190	B8N	C4-N3	-7.48	1.27	1.40
1	2	1190	B8N	C4-C5	7.36	1.64	1.47
38	1	58	1MA	C4-N3	7.19	1.50	1.35
38	1	9	1MG	C2-N3	7.13	1.44	1.33
38	1	46	7MG	C5-N7	7.13	1.44	1.35
1	2	1006	5MC	C4-N3	6.97	1.45	1.34
1	2	1637	5MC	C4-N3	6.94	1.45	1.34
38	1	48	5MC	C4-N3	6.86	1.45	1.34
38	1	49	5MC	C5-C4	6.85	1.49	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	49	5MC	C4-N3	6.85	1.45	1.34
1	2	1573	7MG	C5-N7	6.84	1.44	1.35
1	2	1006	5MC	C5-C4	6.71	1.49	1.44
1	2	1570	2MG	C4-N3	6.70	1.49	1.34
1	2	1426	2MG	C4-N3	6.70	1.49	1.34
38	1	10	2MG	C4-N3	6.61	1.49	1.34
38	1	9	1MG	C4-N3	6.60	1.49	1.34
38	1	47	H2U	C2-N3	6.60	1.49	1.38
38	1	16	H2U	C2-N3	6.58	1.49	1.38
38	1	64	RIA	O1'-C4'	-6.53	1.30	1.45
1	2	1006	5MC	C2-N3	6.41	1.49	1.36
38	1	48	5MC	C2-N3	6.32	1.48	1.36
38	1	49	5MC	C2-N3	6.31	1.48	1.36
1	2	1637	5MC	C2-N3	6.12	1.48	1.36
38	1	64	RIA	O4'-C4A	-6.10	1.31	1.45
38	1	46	7MG	C2-N3	6.03	1.47	1.33
1	2	1637	5MC	C5-C4	6.00	1.48	1.44
38	1	46	7MG	C4-N3	5.94	1.47	1.34
1	2	1573	7MG	C2-N3	5.90	1.47	1.33
38	1	10	2MG	C2-N2	5.88	1.45	1.33
38	1	64	RIA	C6-N6	5.86	1.49	1.34
1	2	1570	2MG	C2-N2	5.82	1.45	1.33
38	1	48	5MC	C5-C4	5.81	1.48	1.44
1	2	1190	B8N	C2-N1	5.81	1.56	1.39
1	2	1426	2MG	C2-N2	5.79	1.45	1.33
1	2	1573	7MG	C4-N3	5.70	1.47	1.34
38	1	46	7MG	C4-N9	5.41	1.44	1.37
38	1	9	1MG	C2-N1	5.38	1.46	1.37
1	2	120	PSU	C6-N1	5.31	1.45	1.36
1	2	1573	7MG	C4-N9	5.29	1.44	1.37
1	2	465	PSU	C6-N1	5.28	1.44	1.36
1	2	1289	PSU	C6-N1	5.25	1.44	1.36
1	2	998	PSU	C6-N1	5.25	1.44	1.36
38	1	37	T6A	C10-N11	5.21	1.49	1.35
38	1	37	T6A	C10-N6	5.17	1.48	1.37
1	2	766	PSU	C6-N1	5.13	1.44	1.36
38	1	10	2MG	C2-N1	5.08	1.44	1.36
38	1	47	H2U	C4-N3	5.06	1.46	1.37
1	2	1190	B8N	C6-C5	5.04	1.42	1.35
38	1	46	7MG	C2-N2	5.03	1.45	1.34
38	1	58	1MA	C2-N1	4.97	1.46	1.35
1	2	1570	2MG	C2-N1	4.96	1.44	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1573	7MG	C2-N2	4.93	1.45	1.34
1	2	1426	2MG	C2-N1	4.92	1.44	1.36
38	1	16	H2U	C4-N3	4.91	1.45	1.37
1	2	1637	5MC	C6-N1	4.87	1.46	1.38
38	1	48	5MC	C6-N1	4.79	1.46	1.38
38	1	49	5MC	C6-N1	4.72	1.46	1.38
38	1	49	5MC	C2-N1	4.69	1.49	1.40
1	2	1190	B8N	C1'-C5	-4.60	1.39	1.50
38	1	48	5MC	C2-N1	4.54	1.49	1.40
38	1	49	5MC	C4-N4	4.51	1.45	1.34
1	2	1637	5MC	C4-N4	4.49	1.45	1.34
1	2	1006	5MC	C4-N4	4.45	1.45	1.34
1	2	1006	5MC	C6-N1	4.43	1.45	1.38
1	2	1006	5MC	C2-N1	4.35	1.49	1.40
38	1	48	5MC	C4-N4	4.31	1.45	1.34
1	2	1637	5MC	C2-N1	4.23	1.48	1.40
38	1	58	1MA	C5-C6	4.02	1.54	1.43
38	1	46	7MG	C2-N1	3.94	1.47	1.37
1	2	1289	PSU	C4-N3	3.90	1.46	1.38
1	2	998	PSU	C4-N3	3.90	1.46	1.38
1	2	766	PSU	C4-N3	3.88	1.46	1.38
1	2	465	PSU	C4-N3	3.85	1.46	1.38
1	2	1780	MA6	C6-N6	3.83	1.47	1.36
1	2	1573	7MG	C2-N1	3.83	1.46	1.37
1	2	120	PSU	C4-N3	3.76	1.45	1.38
38	1	9	1MG	O6-C6	-3.73	1.15	1.23
1	2	1573	7MG	C5-C6	3.63	1.52	1.43
38	1	46	7MG	C5-C6	3.61	1.52	1.43
38	1	9	1MG	C5-C6	3.46	1.54	1.45
38	1	46	7MG	C6-N1	3.37	1.45	1.38
38	1	9	1MG	C5-N7	-3.26	1.32	1.39
1	2	1573	7MG	C6-N1	3.24	1.44	1.38
38	1	26	M2G	C5-C4	3.22	1.47	1.38
38	1	58	1MA	C5-N7	-3.16	1.32	1.39
38	1	64	RIA	O3A-C3A	-3.13	1.35	1.43
38	1	64	RIA	C5-N7	-3.11	1.33	1.39
38	1	64	RIA	O2'-C2'	3.06	1.50	1.43
1	2	1780	MA6	C5-C4	-2.98	1.33	1.39
1	2	1426	2MG	C5-N7	-2.96	1.33	1.39
38	1	26	M2G	C2-N2	2.95	1.40	1.35
1	2	1570	2MG	C5-N7	-2.93	1.33	1.39
38	1	10	2MG	C5-N7	-2.88	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	64	RIA	O2A-C2A	2.86	1.51	1.43
1	2	1006	5MC	O2-C2	-2.75	1.18	1.23
38	1	48	5MC	O2-C2	-2.73	1.18	1.23
1	2	1637	5MC	O2-C2	-2.70	1.18	1.23
38	1	49	5MC	O2-C2	-2.69	1.18	1.23
38	1	37	T6A	C5-N7	-2.64	1.34	1.39
38	1	47	H2U	O2-C2	-2.53	1.18	1.23
38	1	16	H2U	O2-C2	-2.53	1.18	1.23
1	2	1573	7MG	O6-C6	-2.52	1.18	1.23
38	1	10	2MG	C5-C6	2.52	1.53	1.44
38	1	10	2MG	C6-N1	2.51	1.43	1.38
1	2	1426	2MG	C5-C6	2.51	1.53	1.44
38	1	46	7MG	O6-C6	-2.50	1.18	1.23
1	2	766	PSU	O4-C4	-2.50	1.18	1.23
1	2	1289	PSU	O4-C4	-2.49	1.18	1.23
1	2	1570	2MG	C5-C6	2.49	1.53	1.44
1	2	998	PSU	O4-C4	-2.49	1.18	1.23
1	2	120	PSU	O4-C4	-2.47	1.18	1.23
1	2	465	PSU	O4-C4	-2.47	1.18	1.23
1	2	1426	2MG	C6-N1	2.46	1.43	1.38
1	2	1426	2MG	O6-C6	-2.44	1.18	1.23
38	1	26	M2G	C6-N1	-2.44	1.34	1.38
38	1	10	2MG	O6-C6	-2.43	1.19	1.23
1	2	1570	2MG	C6-N1	2.41	1.43	1.38
1	2	1570	2MG	O6-C6	-2.39	1.19	1.23
38	1	37	T6A	ODA-C13	2.39	1.29	1.22
1	2	1190	B8N	O4'-C1'	-2.35	1.40	1.43
38	1	64	RIA	O3'-C3'	-2.35	1.37	1.43
38	1	37	T6A	C6-N6	2.33	1.44	1.39
1	2	1780	MA6	C5-N7	-2.30	1.34	1.39
38	1	64	RIA	P'-O5'	2.29	1.67	1.60
38	1	37	T6A	C2-N1	2.25	1.37	1.33
38	1	64	RIA	C2-N1	2.19	1.37	1.33
1	2	766	PSU	O2-C2	-2.14	1.18	1.23
1	2	120	PSU	O2-C2	-2.13	1.18	1.23
38	1	37	T6A	C5-C4	-2.13	1.35	1.39
38	1	58	1MA	CM1-N1	-2.12	1.42	1.46
1	2	465	PSU	O2-C2	-2.10	1.18	1.23
38	1	46	7MG	C5-C4	2.10	1.44	1.37
1	2	998	PSU	O2-C2	-2.09	1.18	1.23
1	2	1289	PSU	O2-C2	-2.09	1.18	1.23
1	2	1780	MA6	C8-N9	-2.06	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	26	M2G	C5-N7	-2.04	1.35	1.39
1	2	1573	7MG	C8-N7	2.01	1.52	1.42

All (162) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1780	MA6	N1-C6-N6	-11.95	102.30	116.86
1	2	1780	MA6	C5-C6-N6	7.81	137.70	125.33
38	1	58	1MA	C1'-N9-C8	-7.34	105.89	126.73
38	1	26	M2G	C5-C4-N3	-6.79	117.58	128.39
1	2	1426	2MG	C2-N3-C4	6.63	120.30	112.00
38	1	9	1MG	C1'-N9-C4	-6.50	107.29	126.49
38	1	10	2MG	C2-N3-C4	6.45	120.07	112.00
38	1	58	1MA	C1'-N9-C4	6.43	145.48	126.49
1	2	1570	2MG	C2-N3-C4	6.41	120.02	112.00
38	1	9	1MG	C1'-N9-C8	6.07	143.97	126.73
1	2	1780	MA6	N1-C2-N3	-5.93	119.60	128.58
38	1	37	T6A	N3-C2-N1	-5.89	119.66	128.58
38	1	64	RIA	N3-C2-N1	-5.76	119.87	128.58
38	1	64	RIA	C5-C4-N3	-5.58	119.03	126.72
1	2	1426	2MG	C5-C4-N3	-5.40	119.79	128.39
1	2	1570	2MG	C5-C4-N3	-5.27	120.00	128.39
38	1	9	1MG	C5-C4-N3	-5.26	120.02	128.39
38	1	10	2MG	C5-C4-N3	-5.19	120.13	128.39
38	1	58	1MA	C5-C4-N3	-5.18	119.64	127.27
38	1	46	7MG	C5-C6-N1	5.11	119.92	110.94
38	1	37	T6A	C12-N11-C10	5.06	130.41	121.99
1	2	1573	7MG	C5-C6-N1	5.04	119.81	110.94
38	1	26	M2G	N9-C4-N3	5.04	136.03	125.95
38	1	37	T6A	C5-C4-N3	-4.91	119.96	126.72
1	2	1190	B8N	C5-C4-N3	4.82	124.90	116.15
38	1	26	M2G	C2-N3-C4	4.81	121.41	112.51
1	2	1573	7MG	C2-N3-C4	4.80	120.58	112.30
38	1	58	1MA	N1-C2-N3	-4.74	120.36	126.00
1	2	120	PSU	C4-N3-C2	-4.72	119.88	126.37
1	2	766	PSU	C4-N3-C2	-4.71	119.89	126.37
1	2	766	PSU	N1-C2-N3	4.68	120.11	115.17
38	1	46	7MG	C2-N3-C4	4.65	120.31	112.30
1	2	465	PSU	C4-N3-C2	-4.59	120.05	126.37
1	2	998	PSU	C4-N3-C2	-4.59	120.05	126.37
1	2	1289	PSU	C4-N3-C2	-4.52	120.15	126.37
1	2	1190	B8N	C4-N3-C2	-4.44	120.16	125.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1573	7MG	C5-C4-N3	-4.36	119.94	128.13
1	2	120	PSU	N1-C2-N3	4.35	119.76	115.17
1	2	998	PSU	N1-C2-N3	4.28	119.68	115.17
1	2	1780	MA6	N9-C8-N7	-4.27	107.89	113.94
38	1	64	RIA	N6-C6-N1	-4.26	108.90	118.38
1	2	465	PSU	N1-C2-N3	4.25	119.65	115.17
1	2	1780	MA6	C5-C4-N3	-4.21	120.91	126.72
38	1	46	7MG	C5-C4-N3	-4.19	120.27	128.13
1	2	1289	PSU	N1-C2-N3	4.14	119.53	115.17
38	1	37	T6A	C4-C5-C6	4.13	120.21	116.78
1	2	1570	2MG	C2-N1-C6	-4.08	119.62	124.55
38	1	10	2MG	C2-N1-C6	-4.03	119.68	124.55
1	2	1426	2MG	C2-N1-C6	-4.01	119.70	124.55
38	1	64	RIA	N3-C4-N9	3.98	133.93	127.17
38	1	46	7MG	C4-C5-N7	3.95	110.04	105.38
38	1	58	1MA	C2-N3-C4	3.77	119.92	112.53
38	1	37	T6A	N9-C8-N7	-3.77	108.59	113.94
1	2	1190	B8N	N3-C2-N1	3.73	121.28	116.72
38	1	64	RIA	N9-C8-N7	-3.70	108.69	113.94
1	2	766	PSU	C6-C5-C4	3.69	120.67	118.17
38	1	37	T6A	N6-C10-N11	3.69	118.84	113.77
1	2	1573	7MG	C4-C5-N7	3.64	109.68	105.38
38	1	9	1MG	C2-N3-C4	3.59	120.05	111.98
1	2	766	PSU	C6-N1-C2	-3.59	119.36	122.69
38	1	48	5MC	C5-C6-N1	-3.59	119.42	123.31
38	1	64	RIA	C2-N3-C4	3.58	120.58	111.83
1	2	998	PSU	C6-N1-C2	-3.58	119.37	122.69
1	2	1573	7MG	C5-C4-N9	3.56	110.89	106.33
38	1	10	2MG	N1-C2-N2	3.53	120.16	116.56
1	2	1780	MA6	C2-N1-C6	3.51	120.41	111.83
1	2	1426	2MG	N1-C2-N2	3.48	120.12	116.56
38	1	9	1MG	N9-C4-N3	3.42	132.80	125.95
38	1	37	T6A	C2-N3-C4	3.40	120.14	111.83
1	2	1190	B8N	C1'-C5-C4	3.31	122.64	117.61
1	2	1570	2MG	N9-C4-N3	3.30	132.56	125.95
1	2	1289	PSU	C6-N1-C2	-3.30	119.63	122.69
1	2	465	PSU	C6-N1-C2	-3.29	119.63	122.69
1	2	1780	MA6	C4-C5-C6	3.29	119.32	115.91
1	2	120	PSU	C6-N1-C2	-3.27	119.66	122.69
1	2	1780	MA6	C2-N3-C4	3.25	119.76	111.83
1	2	1426	2MG	N9-C4-N3	3.23	132.41	125.95
1	2	1006	5MC	CM5-C5-C6	-3.22	118.49	122.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	1	9	1MG	N9-C8-N7	-3.21	107.44	113.40
1	2	1570	2MG	N1-C2-N2	3.15	119.78	116.56
1	2	120	PSU	C6-C5-C4	3.10	120.27	118.17
38	1	16	H2U	C5-C6-N1	3.09	120.86	111.52
38	1	37	T6A	O10-C10-N6	-3.07	118.18	123.64
38	1	47	H2U	N3-C2-N1	3.05	119.72	116.65
38	1	26	M2G	C6-C5-N7	3.05	135.84	130.29
38	1	47	H2U	C5-C4-N3	3.05	119.93	116.69
38	1	10	2MG	N9-C4-N3	2.99	131.94	125.95
1	2	766	PSU	O2-C2-N1	-2.98	119.71	122.79
38	1	58	1MA	N9-C8-N7	-2.95	107.92	113.40
38	1	64	RIA	C5-C6-N6	2.94	130.57	123.29
38	1	47	H2U	C5-C6-N1	2.94	120.40	111.52
38	1	46	7MG	O6-C6-C5	-2.91	120.48	127.62
38	1	46	7MG	N9-C4-N3	2.89	129.70	125.46
38	1	16	H2U	N3-C2-N1	2.89	119.55	116.65
38	1	46	7MG	C5-C4-N9	2.88	110.03	106.33
1	2	1573	7MG	C2-N1-C6	-2.87	119.90	125.11
38	1	64	RIA	C1'-C2'-C3'	2.87	105.86	102.29
38	1	10	2MG	N9-C8-N7	-2.86	108.10	113.40
38	1	58	1MA	N9-C4-N3	2.86	133.41	126.90
38	1	9	1MG	C5-C6-N1	2.84	120.27	115.02
38	1	37	T6A	N3-C4-N9	2.84	132.00	127.17
1	2	1190	B8N	C31-N3-C4	2.84	121.19	117.18
1	2	1570	2MG	N9-C8-N7	-2.79	108.23	113.40
38	1	26	M2G	C4-C5-N7	-2.79	106.26	110.67
38	1	16	H2U	C5-C4-N3	2.77	119.63	116.69
38	1	46	7MG	C2-N1-C6	-2.77	120.09	125.11
1	2	998	PSU	O2-C2-N1	-2.75	119.95	122.79
1	2	1573	7MG	O6-C6-C5	-2.75	120.87	127.62
1	2	1289	PSU	O2-C2-N1	-2.66	120.04	122.79
1	2	1780	MA6	C4-N9-C8	2.64	108.51	105.74
38	1	64	RIA	C5-N7-C8	2.63	107.59	103.45
1	2	465	PSU	O2-C2-N1	-2.63	120.08	122.79
1	2	465	PSU	C6-C5-C4	2.62	119.94	118.17
1	2	1570	2MG	C5-C6-N1	2.62	119.93	113.25
1	2	1780	MA6	C5-N7-C8	2.62	107.56	103.45
38	1	37	T6A	C5-N7-C8	2.61	107.56	103.45
1	2	120	PSU	O2-C2-N1	-2.61	120.10	122.79
1	2	1426	2MG	N9-C8-N7	-2.60	108.57	113.40
1	2	998	PSU	C6-C5-C4	2.58	119.92	118.17
1	2	1426	2MG	C5-C6-N1	2.58	119.82	113.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	1	48	5MC	C5-C4-N4	-2.55	117.80	121.39
38	1	10	2MG	C5-C6-N1	2.54	119.72	113.25
1	2	1573	7MG	N9-C4-N3	2.53	129.16	125.46
1	2	1780	MA6	N3-C4-N9	2.53	131.47	127.17
1	2	1570	2MG	O6-C6-C5	-2.49	119.96	126.53
1	2	1573	7MG	N9-C8-N7	2.49	106.89	103.37
1	2	1426	2MG	O6-C6-C5	-2.48	119.99	126.53
38	1	10	2MG	O6-C6-C5	-2.44	120.09	126.53
1	2	1006	5MC	C5-C4-N3	-2.41	119.29	121.75
38	1	49	5MC	C5-C6-N1	-2.40	120.70	123.31
38	1	64	RIA	C1'-O2A-C2A	-2.40	112.28	117.98
1	2	1637	5MC	C5-C4-N3	-2.39	119.31	121.75
38	1	26	M2G	O6-C6-C5	-2.33	120.39	126.53
38	1	64	RIA	C6-C5-C4	2.33	120.36	117.18
1	2	1006	5MC	C5-C6-N1	-2.31	120.81	123.31
38	1	46	7MG	N9-C8-N7	2.31	106.64	103.37
38	1	47	H2U	O2-C2-N1	-2.30	120.34	123.10
38	1	10	2MG	C1'-N9-C4	-2.30	119.69	126.49
38	1	9	1MG	C8-N7-C5	2.30	108.36	104.26
1	2	1190	B8N	O4'-C1'-C2'	2.29	108.32	105.15
1	2	1190	B8N	O4-C4-C5	-2.29	118.62	122.58
38	1	16	H2U	O2-C2-N1	-2.29	120.35	123.10
1	2	1190	B8N	O4-C4-N3	-2.16	116.48	119.99
1	2	1426	2MG	N1-C2-N3	-2.15	120.06	123.68
1	2	766	PSU	O4'-C1'-C2'	2.13	108.10	105.15
1	2	1289	PSU	C6-C5-C4	2.13	119.61	118.17
38	1	10	2MG	C8-N7-C5	2.11	108.02	104.26
38	1	10	2MG	N1-C2-N3	-2.11	120.13	123.68
38	1	58	1MA	C8-N7-C5	2.11	108.01	104.26
38	1	49	5MC	O2-C2-N3	-2.10	119.03	122.33
1	2	998	PSU	O4'-C1'-C2'	2.09	108.04	105.15
38	1	64	RIA	O1'-C1'-C2'	2.09	107.63	104.98
1	2	1570	2MG	N1-C2-N3	-2.08	120.17	123.68
38	1	26	M2G	C5-C6-N1	2.08	118.54	113.25
38	1	49	5MC	C5-C4-N3	-2.07	119.63	121.75
38	1	37	T6A	C4-C5-N7	-2.05	108.24	110.58
38	1	37	T6A	C5-C4-N9	2.04	108.04	105.81
38	1	26	M2G	C8-N7-C5	2.04	107.89	104.26
38	1	37	T6A	N6-C6-N1	2.04	122.81	117.54
1	2	1190	B8N	C32-C31-N3	2.03	115.71	112.16
1	2	120	PSU	O4'-C1'-C2'	2.03	107.96	105.15
1	2	1570	2MG	C8-N7-C5	2.00	107.83	104.26

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	2	766	PSU	O4'-C4'-C5'-O5'
1	2	1190	B8N	O4'-C4'-C5'-O5'
1	2	1289	PSU	O4'-C4'-C5'-O5'
1	2	1780	MA6	C5-C6-N6-C10
1	2	1780	MA6	N1-C6-N6-C10
38	1	9	1MG	O4'-C4'-C5'-O5'
38	1	16	H2U	C4'-C5'-O5'-P
38	1	37	T6A	C14-C12-N11-C10
38	1	37	T6A	N11-C12-C14-O14
38	1	37	T6A	C13-C12-C14-O14
38	1	37	T6A	C13-C12-C14-C15
38	1	58	1MA	O4'-C4'-C5'-O5'
38	1	64	RIA	C5'-O5'-P'-O2X
38	1	64	RIA	C5'-O5'-P'-O3X
1	2	766	PSU	C3'-C4'-C5'-O5'
1	2	1289	PSU	C3'-C4'-C5'-O5'
38	1	9	1MG	C3'-C4'-C5'-O5'
1	2	1573	7MG	O4'-C4'-C5'-O5'
1	2	1573	7MG	C3'-C4'-C5'-O5'
38	1	47	H2U	O4'-C4'-C5'-O5'
1	2	1190	B8N	C3'-C4'-C5'-O5'
38	1	47	H2U	C3'-C4'-C5'-O5'
38	1	58	1MA	C3'-C4'-C5'-O5'
38	1	37	T6A	N11-C12-C14-C15
1	2	1190	B8N	N34-C33-C34-O36
38	1	48	5MC	O4'-C4'-C5'-O5'
38	1	64	RIA	C5'-O5'-P'-O1X
1	2	1289	PSU	C4'-C5'-O5'-P
38	1	47	H2U	C4'-C5'-O5'-P
1	2	1190	B8N	N34-C33-C34-O35
38	1	48	5MC	C3'-C4'-C5'-O5'
38	1	46	7MG	C4'-C5'-O5'-P
1	2	1780	MA6	C5-C6-N6-C9
1	2	1570	2MG	C2'-C1'-N9-C8
38	1	48	5MC	C4'-C5'-O5'-P
1	2	1190	B8N	O4'-C1'-C5-C4
1	2	1570	2MG	C2'-C1'-N9-C4
1	2	120	PSU	O4'-C4'-C5'-O5'
38	1	26	M2G	C3'-C4'-C5'-O5'
38	1	47	H2U	O4'-C1'-N1-C6

There are no ring outliers.

21 monomers are involved in 61 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	1	58	1MA	2	0
38	1	10	2MG	6	0
38	1	26	M2G	9	0
1	2	465	PSU	1	0
1	2	766	PSU	1	0
1	2	1190	B8N	2	0
38	1	49	5MC	2	0
1	2	1637	5MC	2	0
38	1	46	7MG	3	0
38	1	9	1MG	4	0
1	2	1426	2MG	3	0
1	2	1573	7MG	2	0
1	2	1780	MA6	4	0
38	1	48	5MC	7	0
38	1	37	T6A	4	0
38	1	16	H2U	5	0
1	2	1006	5MC	1	0
1	2	1570	2MG	1	0
1	2	998	PSU	2	0
38	1	47	H2U	5	0
38	1	64	RIA	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 121 ligands modelled in this entry, 119 are monoatomic - leaving 2 for Mogul analysis.

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
44	GCP	k	601	-	32,34,34	1.47	7 (21%)	49,54,54	1.79	8 (16%)
45	MET	k	603	-	6,7,8	0.50	0	2,7,9	0.35	0

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
44	GCP	k	601	-	-	0/19/38/38	0/3/3/3
45	MET	k	603	-	-	1/5/6/8	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	k	601	GCP	C5-C4	3.19	1.47	1.38
44	k	601	GCP	PG-O3G	2.92	1.61	1.55
44	k	601	GCP	PG-O2G	2.90	1.61	1.55
44	k	601	GCP	PB-O3A	2.76	1.61	1.58
44	k	601	GCP	C6-N1	-2.41	1.34	1.38
44	k	601	GCP	PB-O2B	2.06	1.61	1.56
44	k	601	GCP	C5-N7	-2.00	1.35	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	k	601	GCP	C5-C4-N3	-6.19	118.54	128.39
44	k	601	GCP	C2-N3-C4	5.04	120.98	112.30
44	k	601	GCP	N9-C4-N3	4.57	135.09	125.95
44	k	601	GCP	PB-O3A-PA	-3.65	120.45	132.37
44	k	601	GCP	C6-C5-N7	3.21	136.13	130.29
44	k	601	GCP	C4-C5-N7	-2.58	106.58	110.67
44	k	601	GCP	C3'-C2'-C1'	2.28	105.77	101.46
44	k	601	GCP	O6-C6-C5	-2.09	121.02	126.53

There are no chirality outliers.

All (1) torsion outliers are listed below:

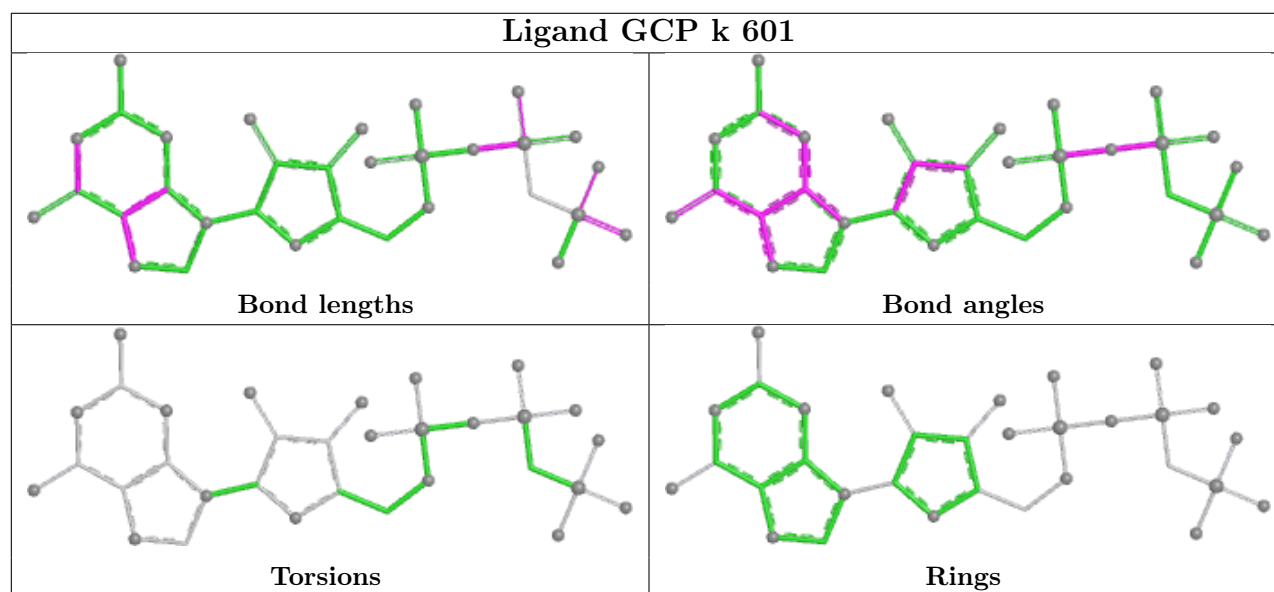
Mol	Chain	Res	Type	Atoms
45	k	603	MET	CB-CG-SD-CE

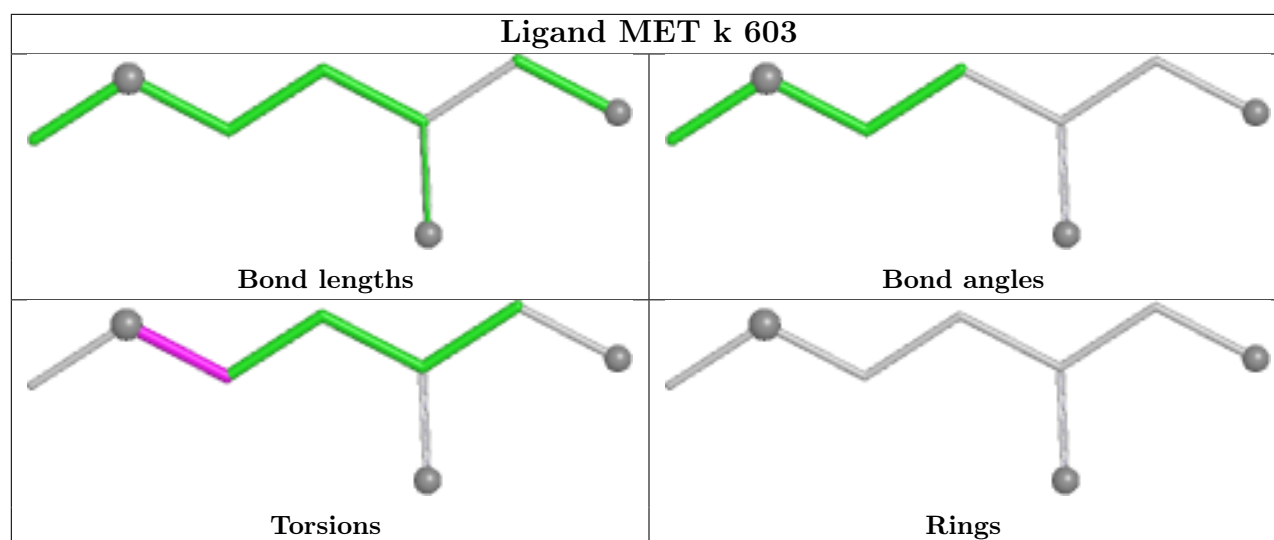
There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	k	601	GCP	8	0
45	k	603	MET	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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
38	1	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	64:RIA	O3'	65:G	P	8.39
1	1	16:H2U	O3'	18:G	P	4.94
1	1	63:G	O3'	64:RIA	P	3.65

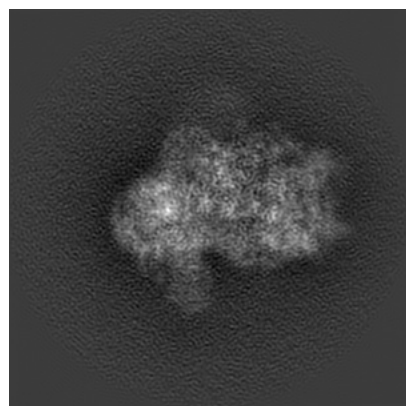
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19804. These allow visual inspection of the internal detail of the map and identification of artifacts.

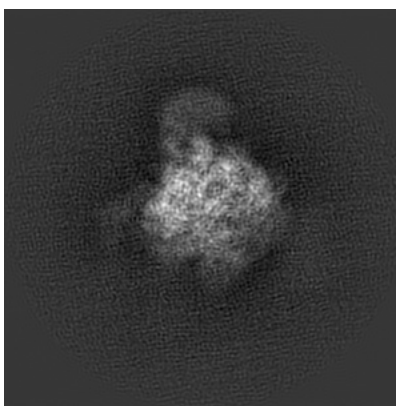
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

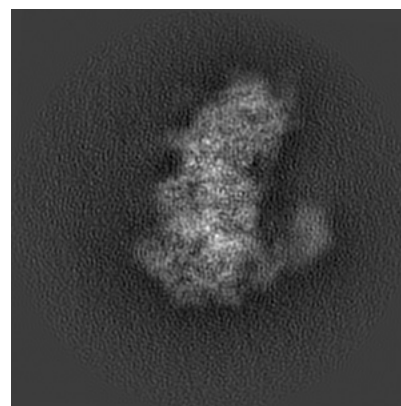
6.1.1 Primary map



X

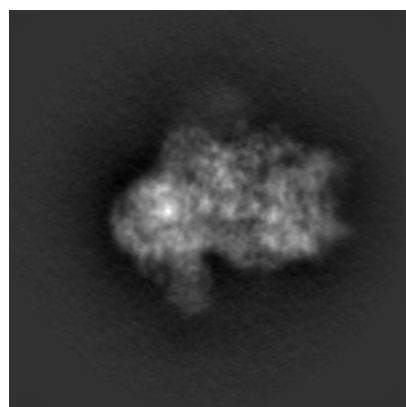


Y

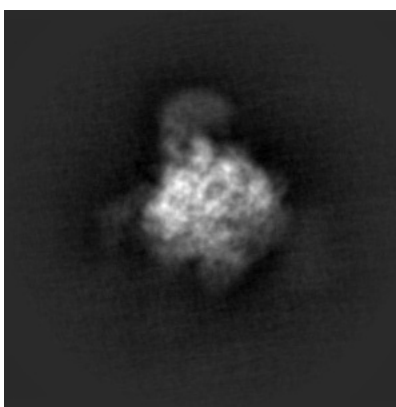


Z

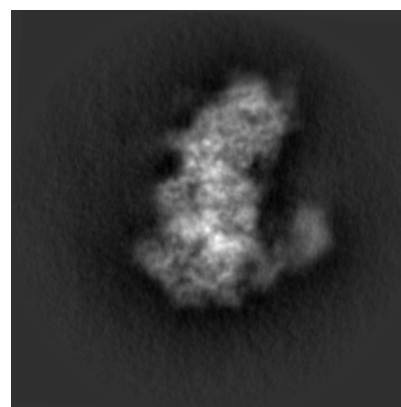
6.1.2 Raw map



X



Y

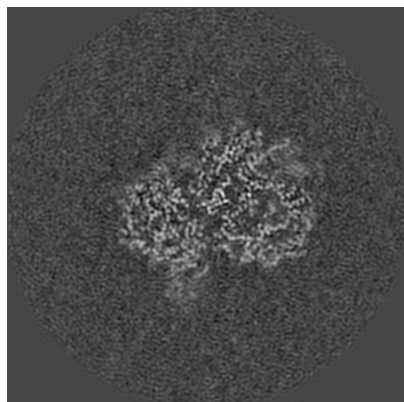


Z

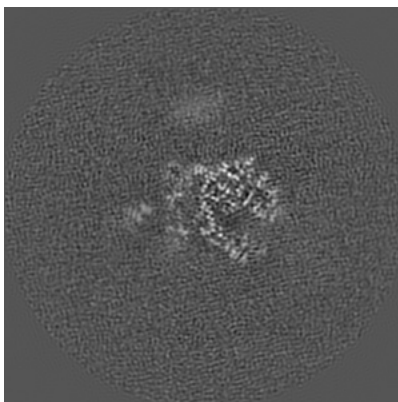
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

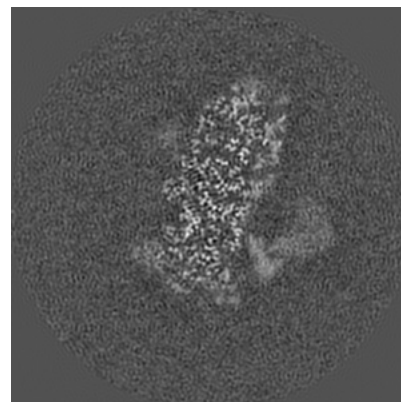
6.2.1 Primary map



X Index: 150

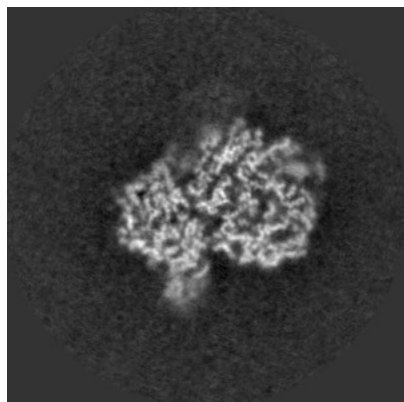


Y Index: 150

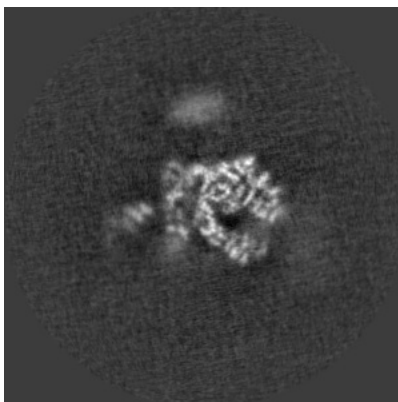


Z Index: 150

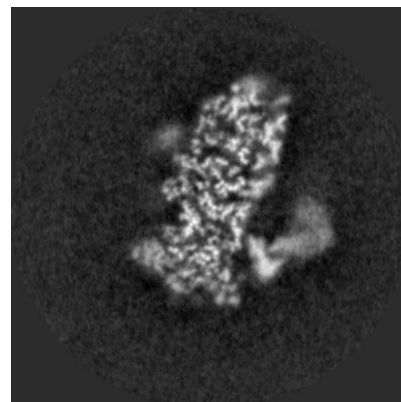
6.2.2 Raw map



X Index: 150



Y Index: 150

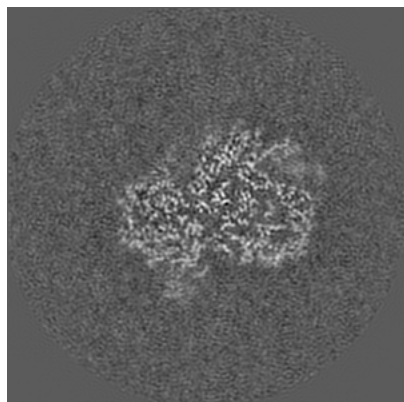


Z Index: 150

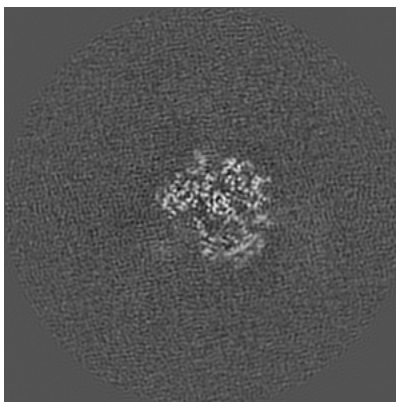
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

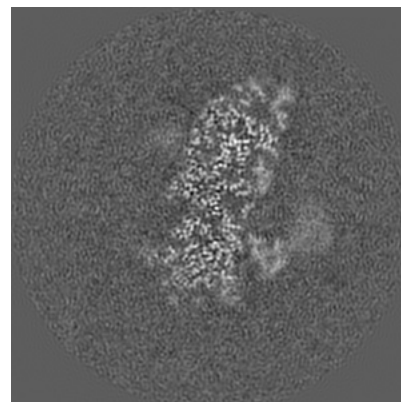
6.3.1 Primary map



X Index: 151

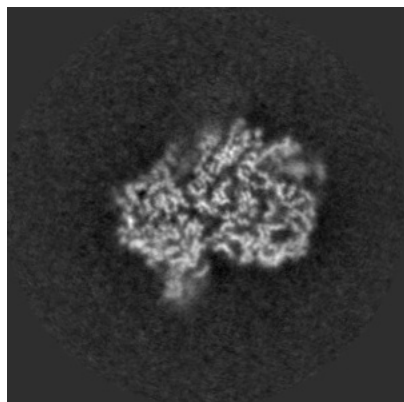


Y Index: 162

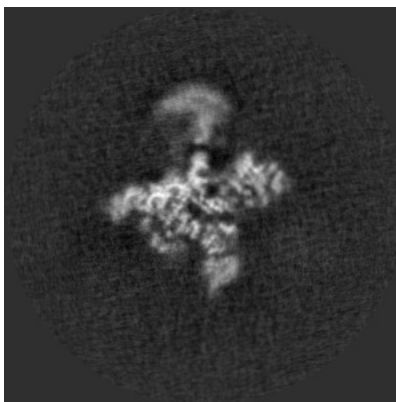


Z Index: 146

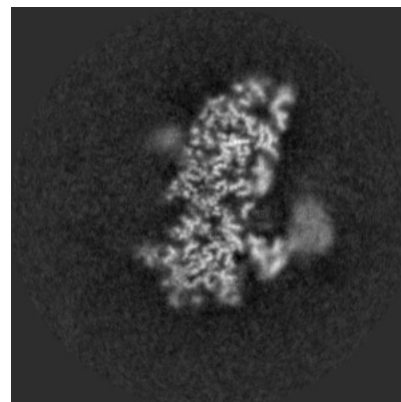
6.3.2 Raw map



X Index: 151



Y Index: 124

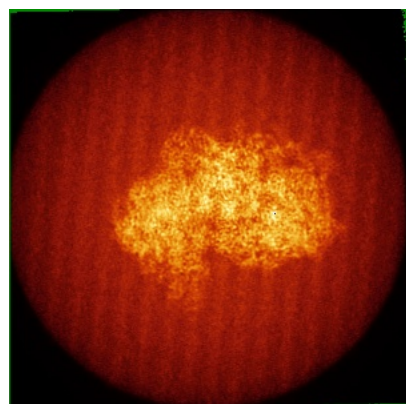


Z Index: 146

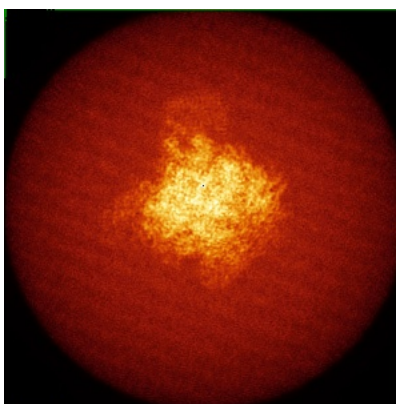
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

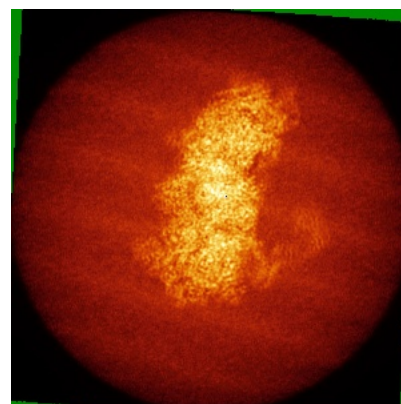
6.4.1 Primary map



X

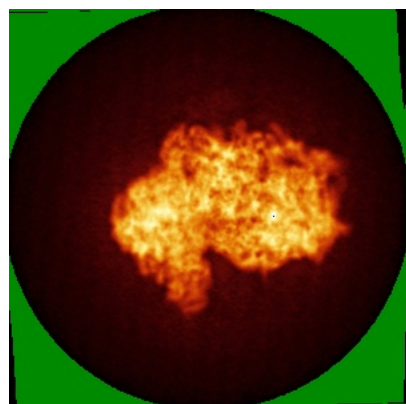


Y

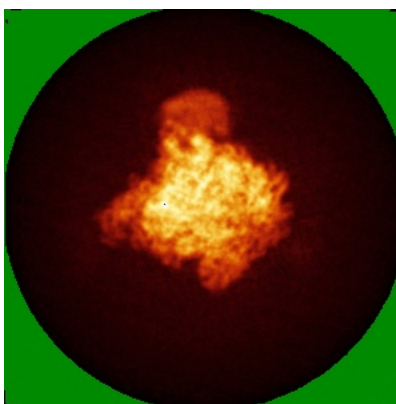


Z

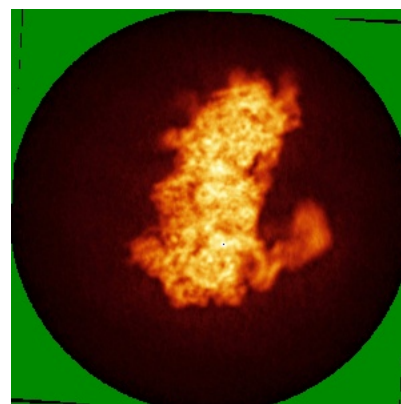
6.4.2 Raw map



X



Y

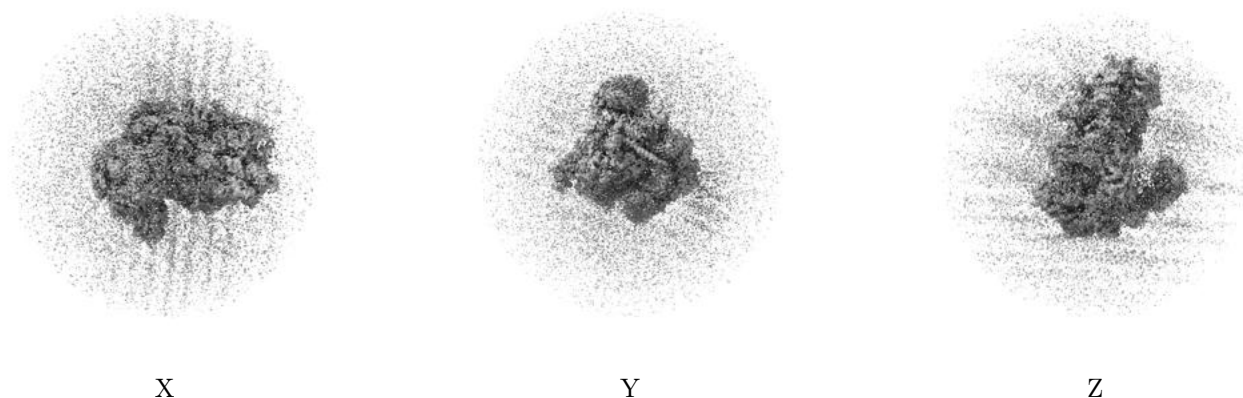


Z

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.

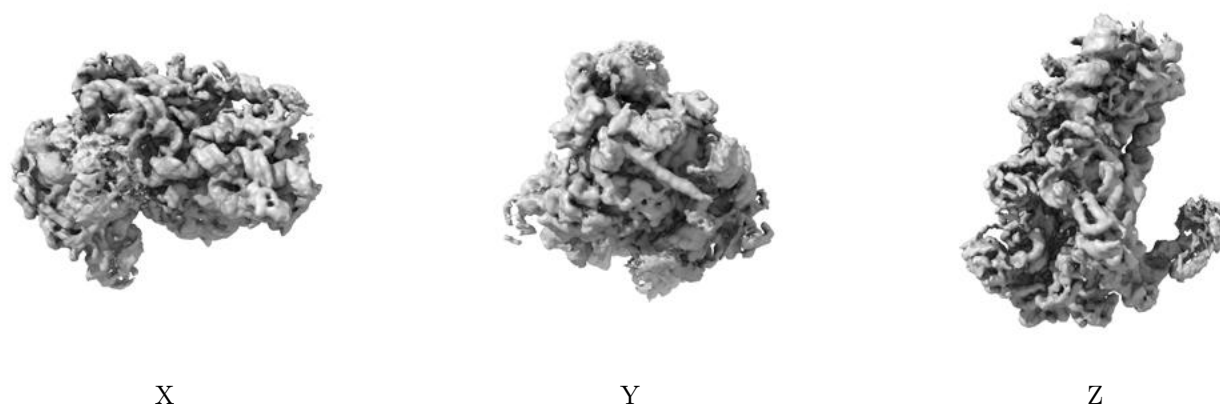
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

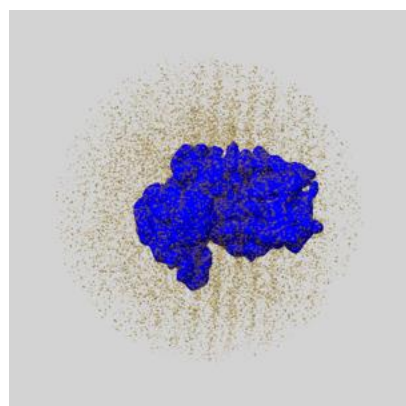
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

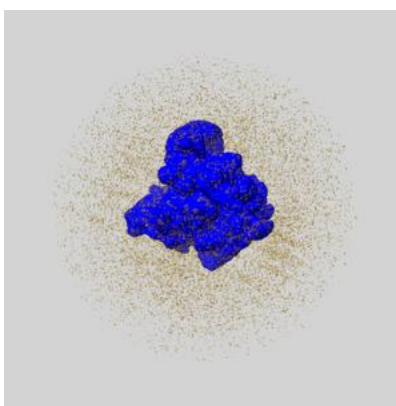
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

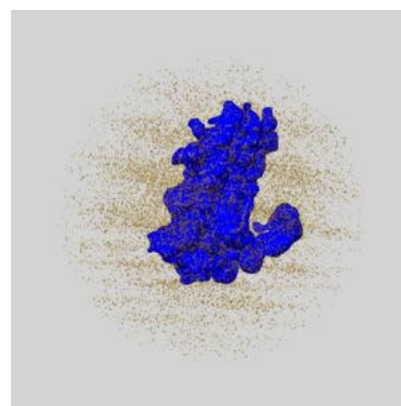
6.6.1 emd_19804_msk_1.map [i](#)



X



Y

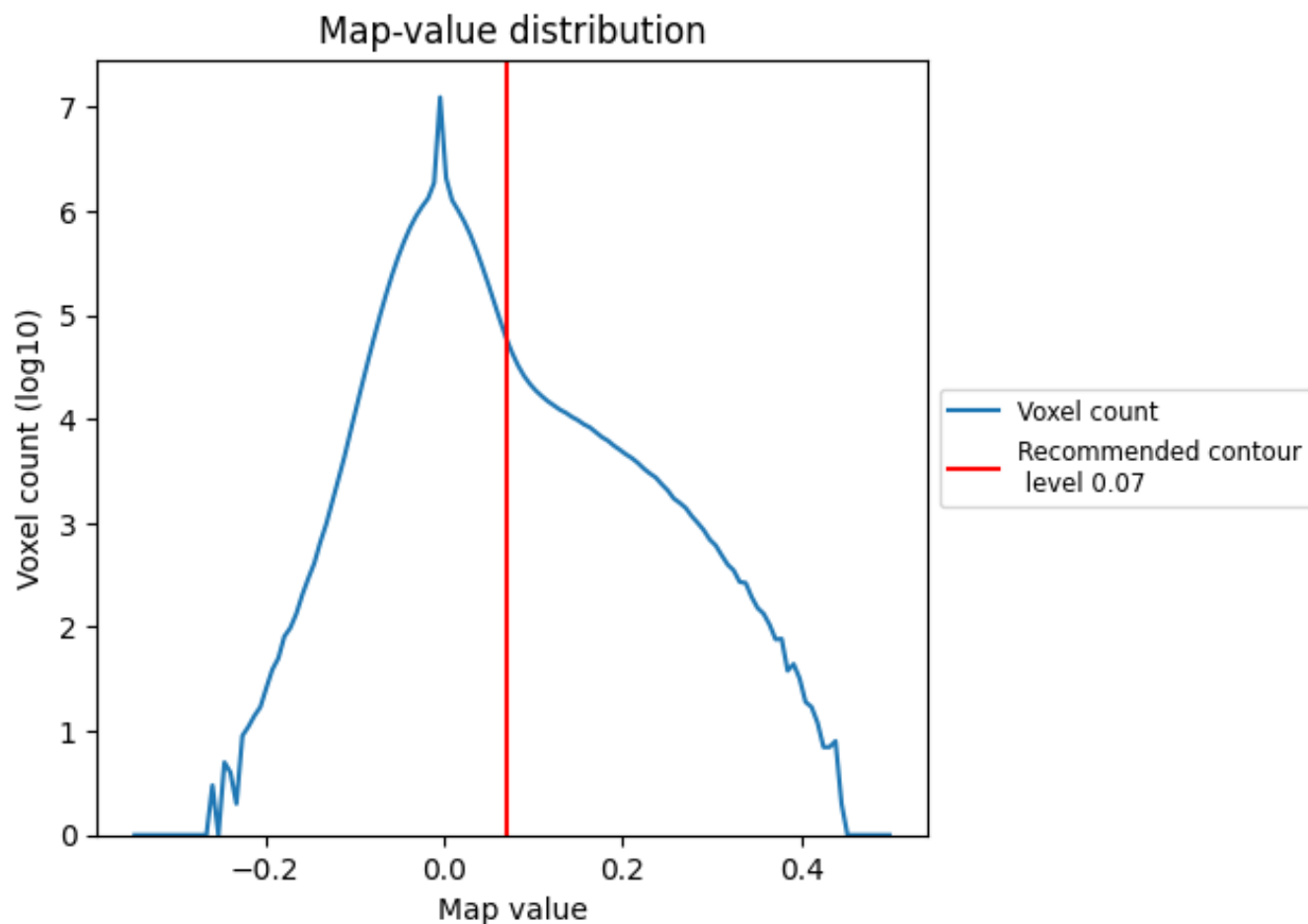


Z

7 Map analysis [i](#)

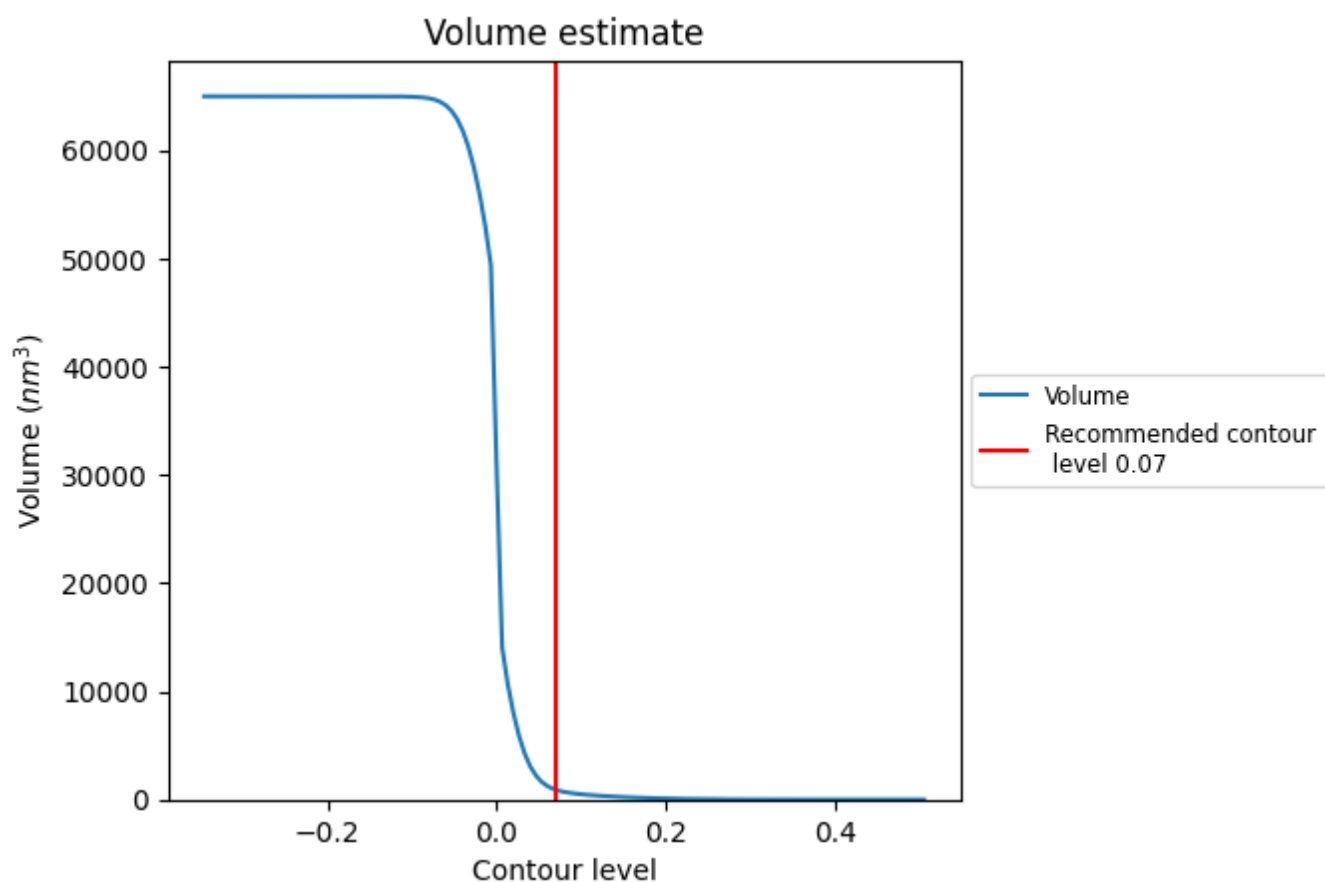
This section contains the results of statistical analysis of the map.

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.

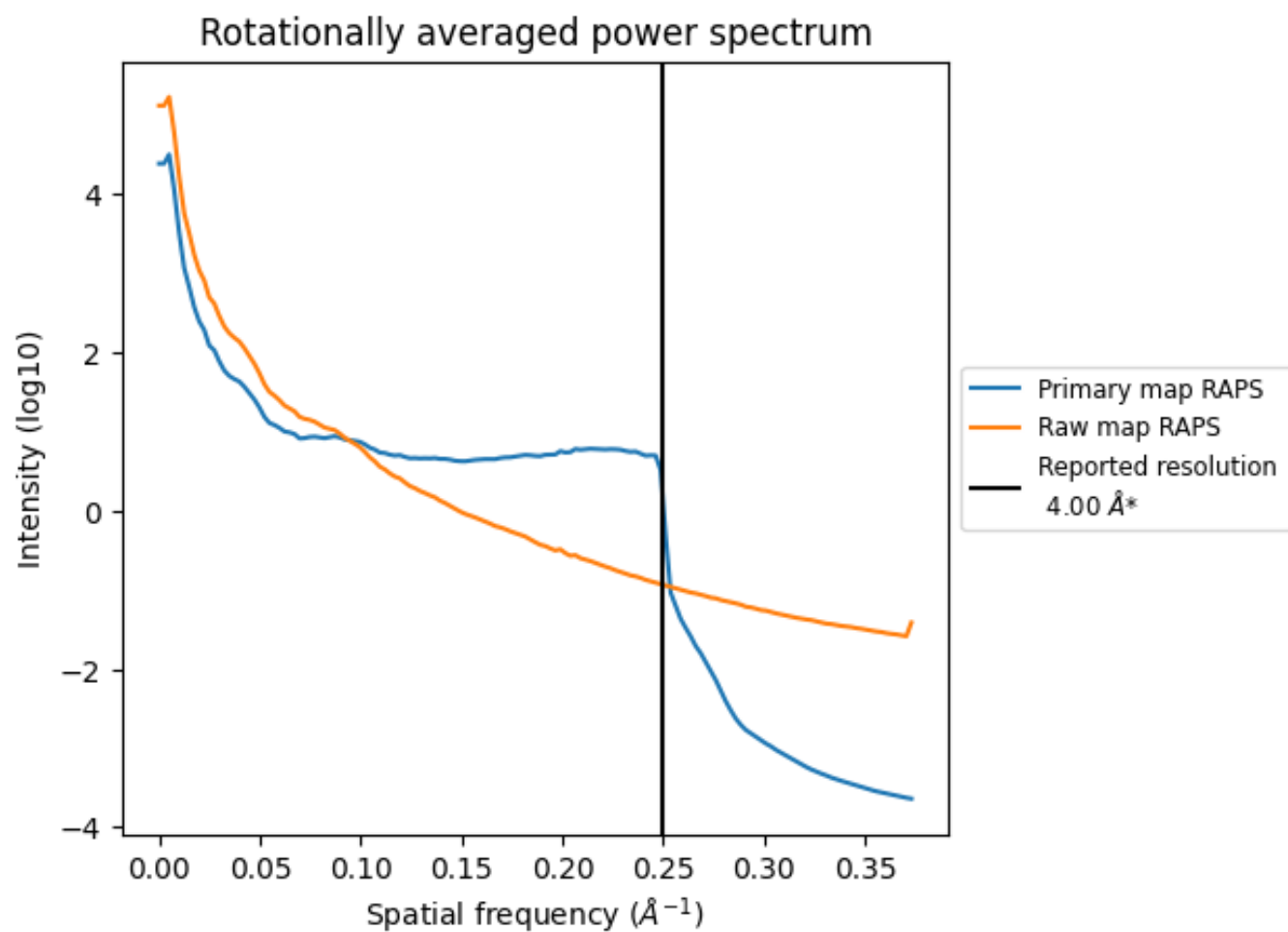
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 907 nm³; this corresponds to an approximate mass of 819 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 ⓘ

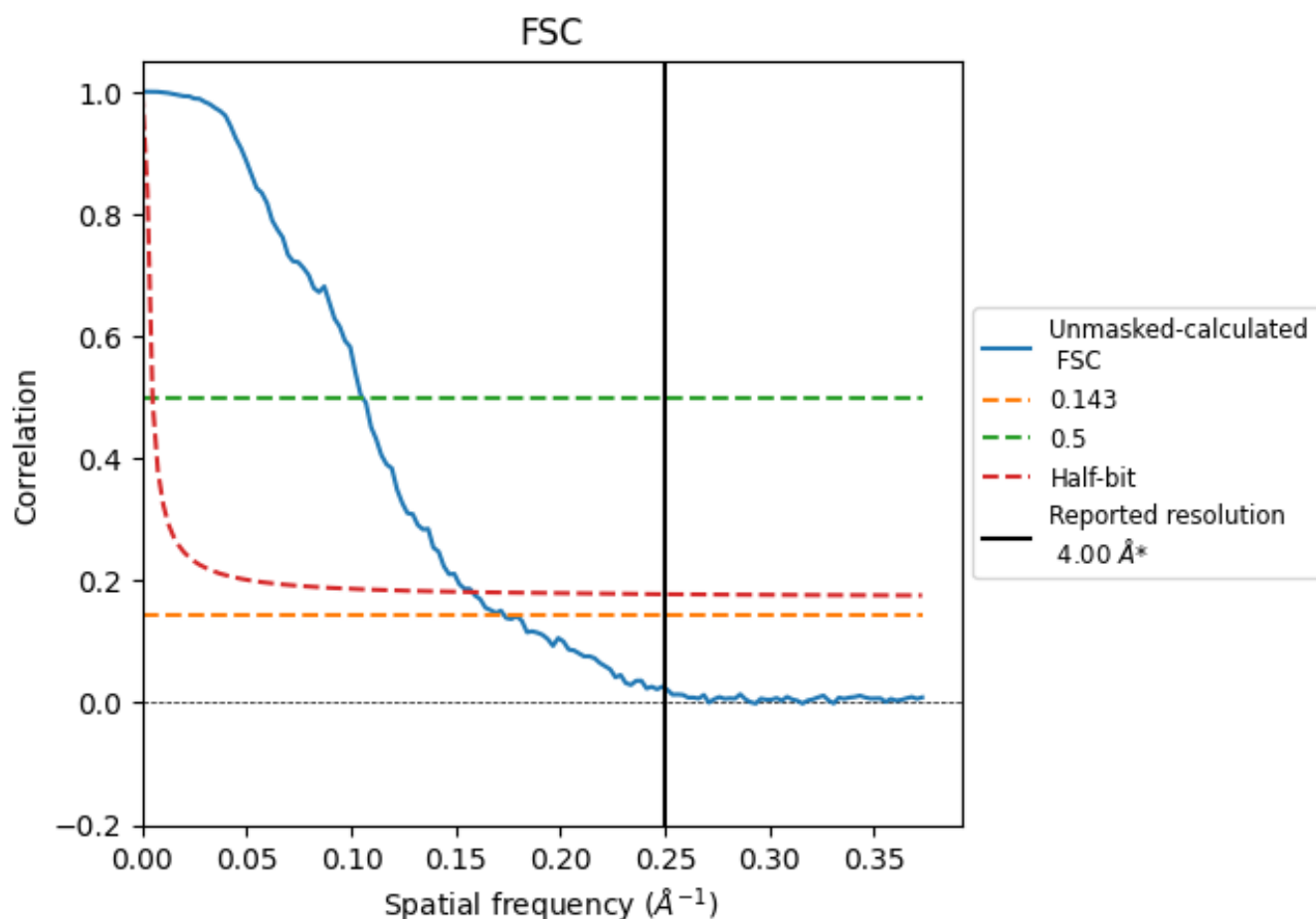


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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](#)

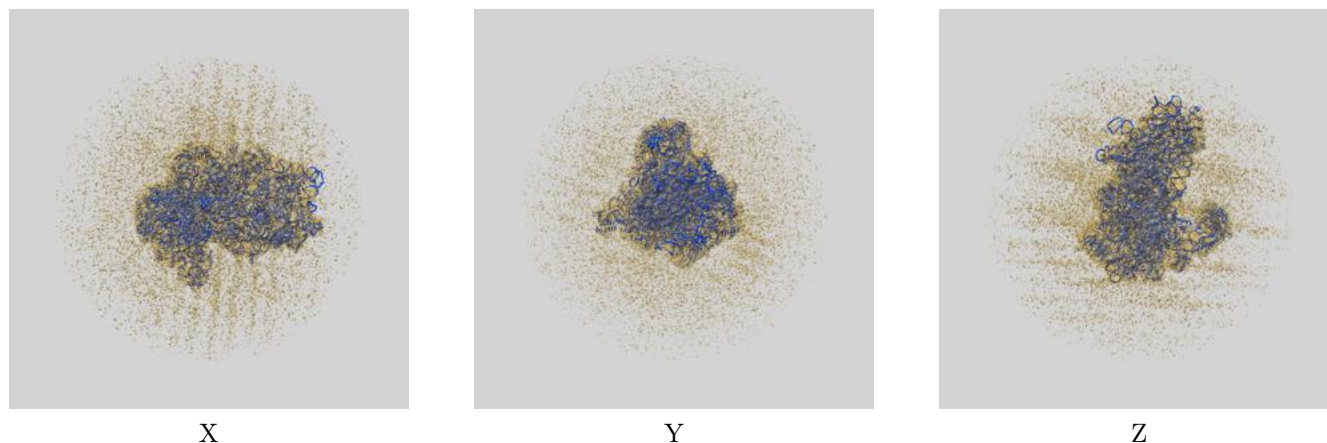
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Threesig
Reported by author	-	-	-	4.00
Author-provided FSC curve	-	-	-	-
Unmasked-calculated*	5.77	9.51	6.33	3.86

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

9 Map-model fit [i](#)

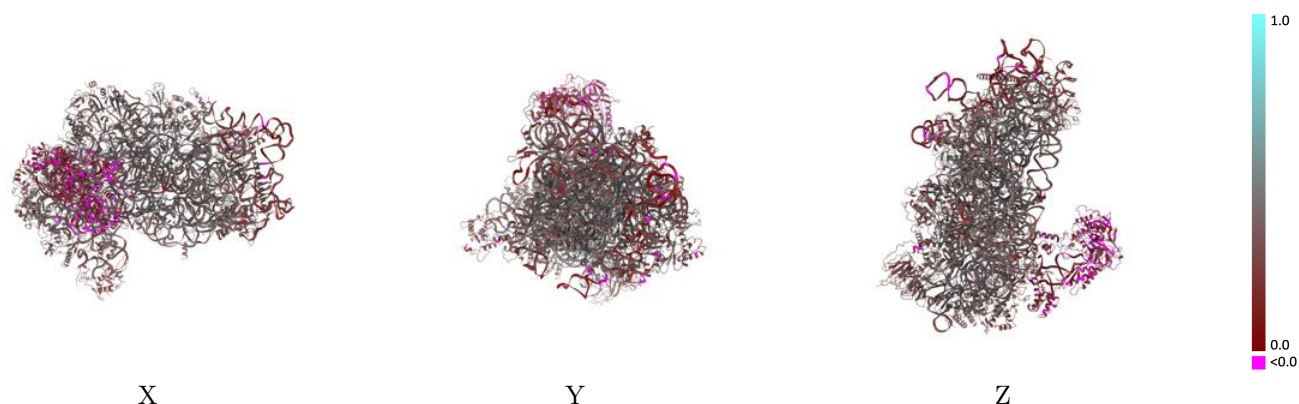
This section contains information regarding the fit between EMDB map EMD-19804 and PDB model 8S8G. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



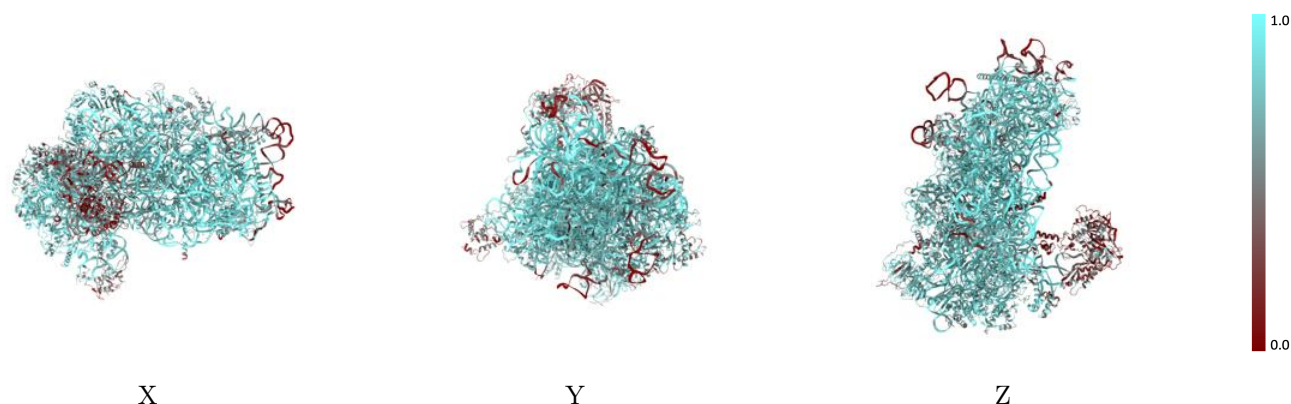
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



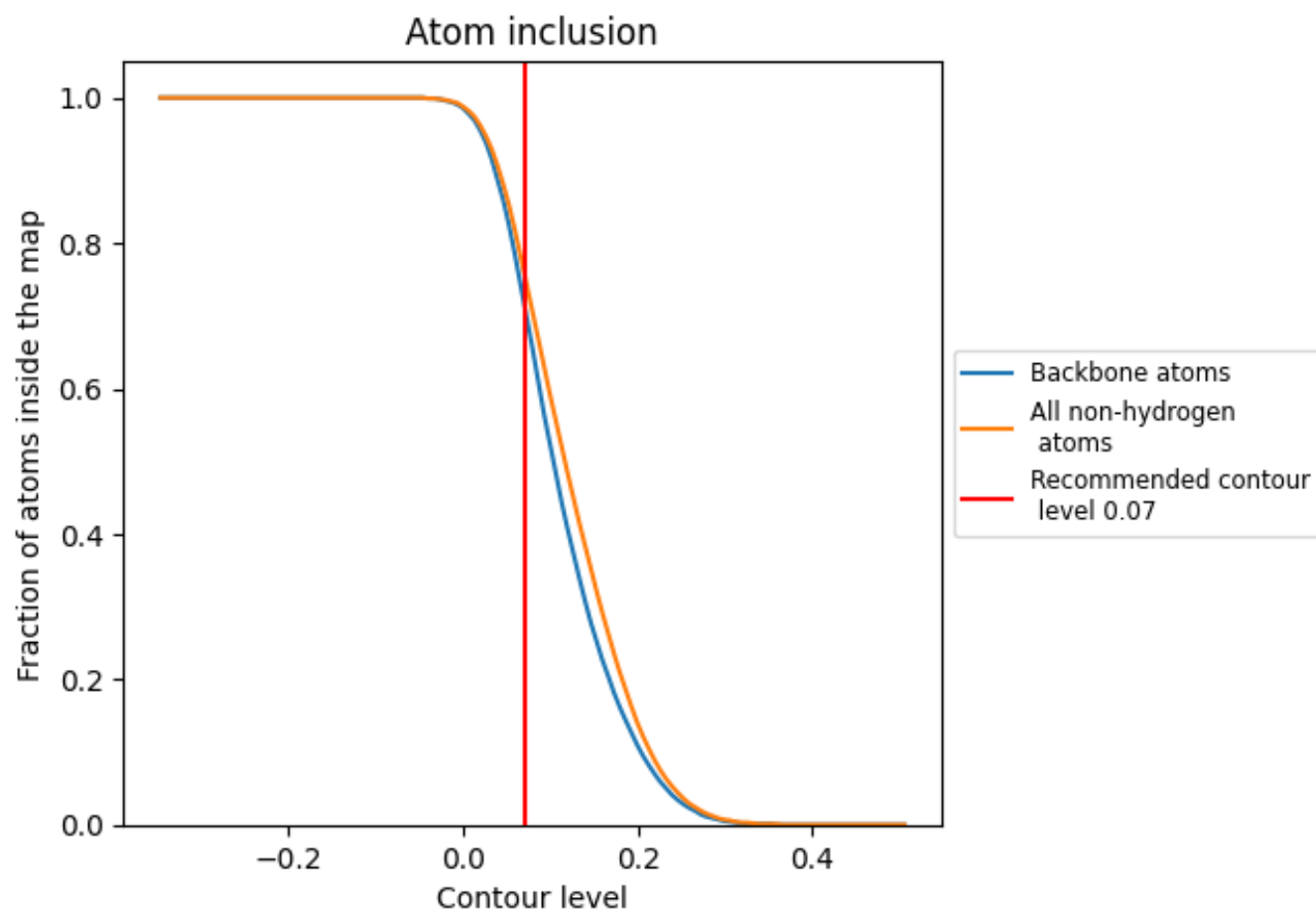
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7610	 0.3530
1	 0.8150	 0.2240
2	 0.8710	 0.3690
3	 0.4010	 0.3040
A	 0.7570	 0.3840
B	 0.7550	 0.3810
C	 0.8110	 0.4300
D	 0.7430	 0.4010
E	 0.8260	 0.4230
F	 0.7410	 0.3910
G	 0.7640	 0.3430
H	 0.6620	 0.3580
I	 0.7480	 0.3760
J	 0.7940	 0.4120
K	 0.7560	 0.3470
L	 0.7420	 0.4110
M	 0.3470	 0.2380
N	 0.8100	 0.4050
O	 0.8030	 0.4130
P	 0.8140	 0.3610
Q	 0.7950	 0.3960
R	 0.6660	 0.3650
S	 0.8100	 0.3810
T	 0.8350	 0.3890
U	 0.7000	 0.3810
V	 0.8010	 0.4150
W	 0.7940	 0.4350
X	 0.7940	 0.4380
Y	 0.8110	 0.3940
Z	 0.6420	 0.3000
a	 0.7940	 0.4370
b	 0.7490	 0.4020
c	 0.7520	 0.4140
d	 0.8390	 0.4190
e	 0.7180	 0.3990



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Chain	Atom inclusion	Q-score
f	 0.4520	 0.2290
g	 0.7220	 0.3420
h	 0.1980	 0.2910
i	 0.5180	 0.3520
j	 0.5240	 0.1910
k	 0.2720	 0.0820
l	 0.0850	 0.1410