



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 04:17 PM UTC

PDB ID : 8S8I / pdb_00008s8i
EMDB ID : EMD-19806
Title : Structure of a yeast 48S-AUC preinitiation complex in closed conformation
(model py48S-AUC-eIF1)
Authors : Villamayor-Belinchon, L.; Sharma, P.; Llacer, J.L.; Hussain, T.
Deposited on : 2024-03-06
Resolution : 4.30 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:

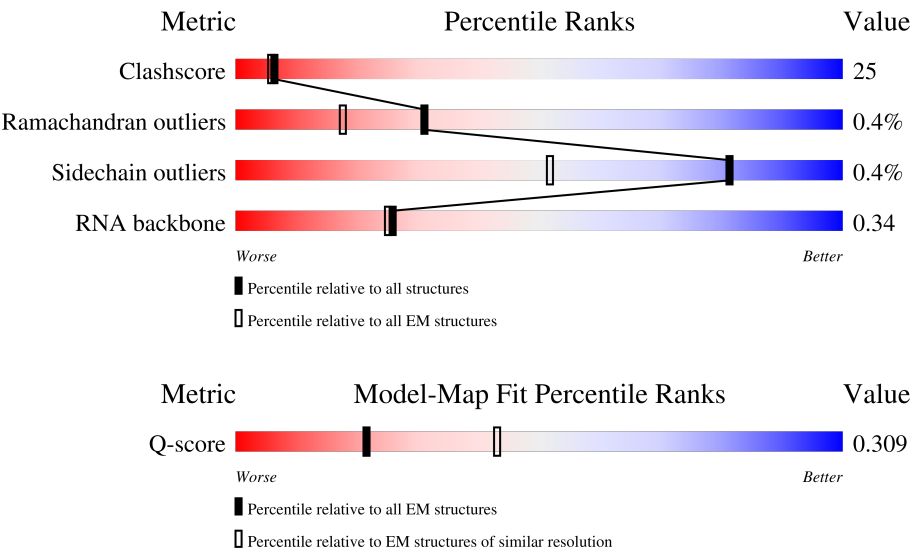
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.30 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.



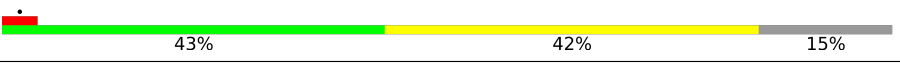
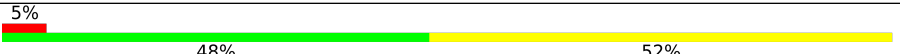
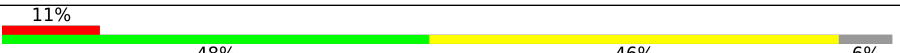
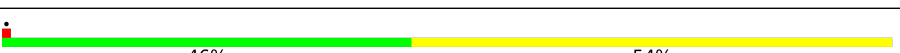
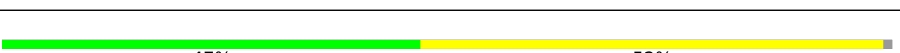
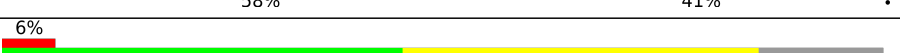
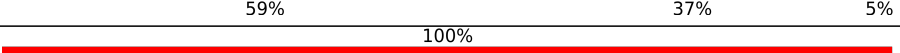
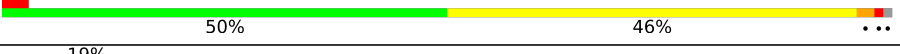
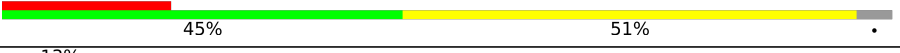
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	
2	A	254	
3	B	255	

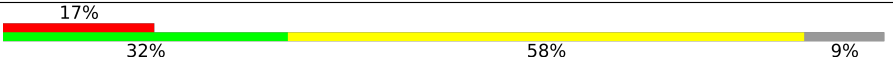
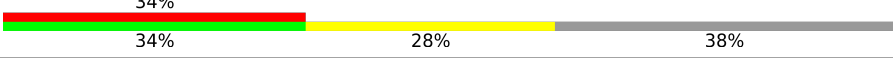
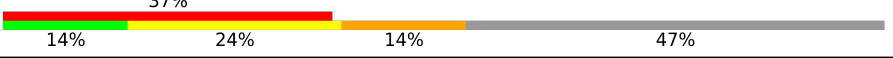
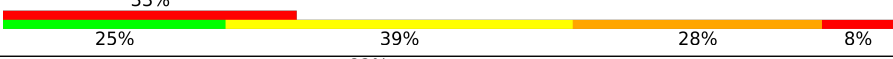
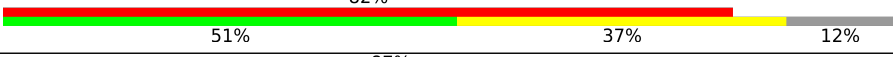
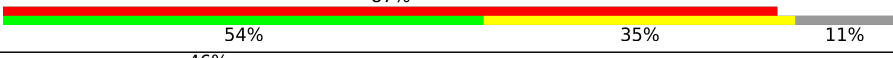
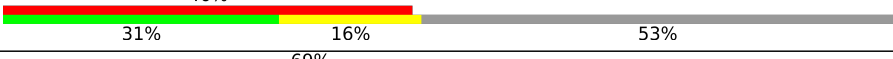
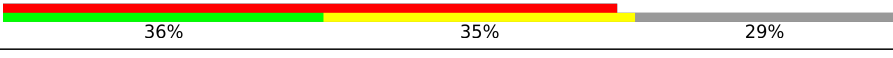
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Mol	Chain	Length	Quality of chain
4	C	259	
5	E	261	
6	G	236	
7	H	190	
8	I	201	
9	J	188	
10	L	156	
11	N	151	
12	O	137	
13	V	87	
14	W	130	
15	X	145	
16	Y	135	
17	a	119	
18	b	82	
19	e	63	
20	h	25	
21	D	237	
22	F	227	
23	K	106	
24	M	134	
25	P	142	
26	Q	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	
42	m	108	

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
45	GCP	k	601	-	-	X	-

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 87328 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	1789	Total	C	N	O	P	0	0
			38003	16989	6694	12531	1789		

- 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	95	Total	C	N	O	S	0	0
			764	474	142	143	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
			2139	1366	355	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 a protein called Eukaryotic translation initiation factor eIF-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	77	Total	C	N	O	S	0	0
			619	395	109	111	4		

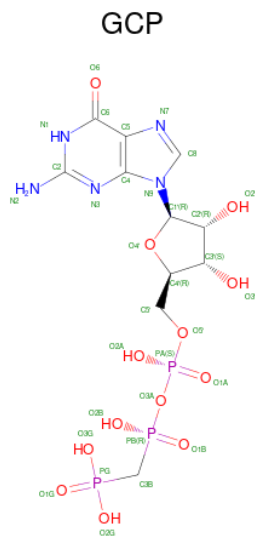
- Molecule 43 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
43	2	114	Total	Mg	0
			114	114	
43	S	1	Total	Mg	0
			1	1	
43	i	1	Total	Mg	0
			1	1	
43	k	1	Total	Mg	0
			1	1	

- Molecule 44 is ZINC ION (CCD ID: ZN) (formula: Zn).

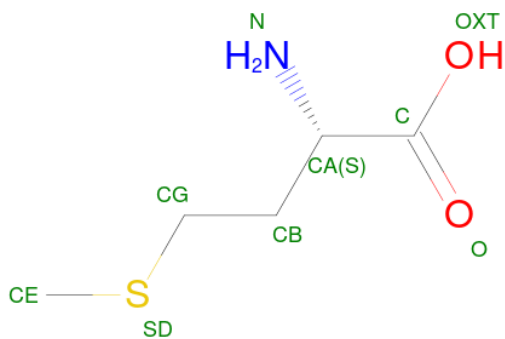
Mol	Chain	Residues	Atoms		AltConf
44	a	1	Total	Zn	0
			1	1	
44	b	1	Total	Zn	0
			1	1	
44	f	1	Total	Zn	0
			1	1	
44	l	1	Total	Zn	0
			1	1	

- Molecule 45 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
45	k	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 46 is METHIONINE (CCD ID: MET) (formula: $\text{C}_5\text{H}_{11}\text{NO}_2\text{S}$).



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

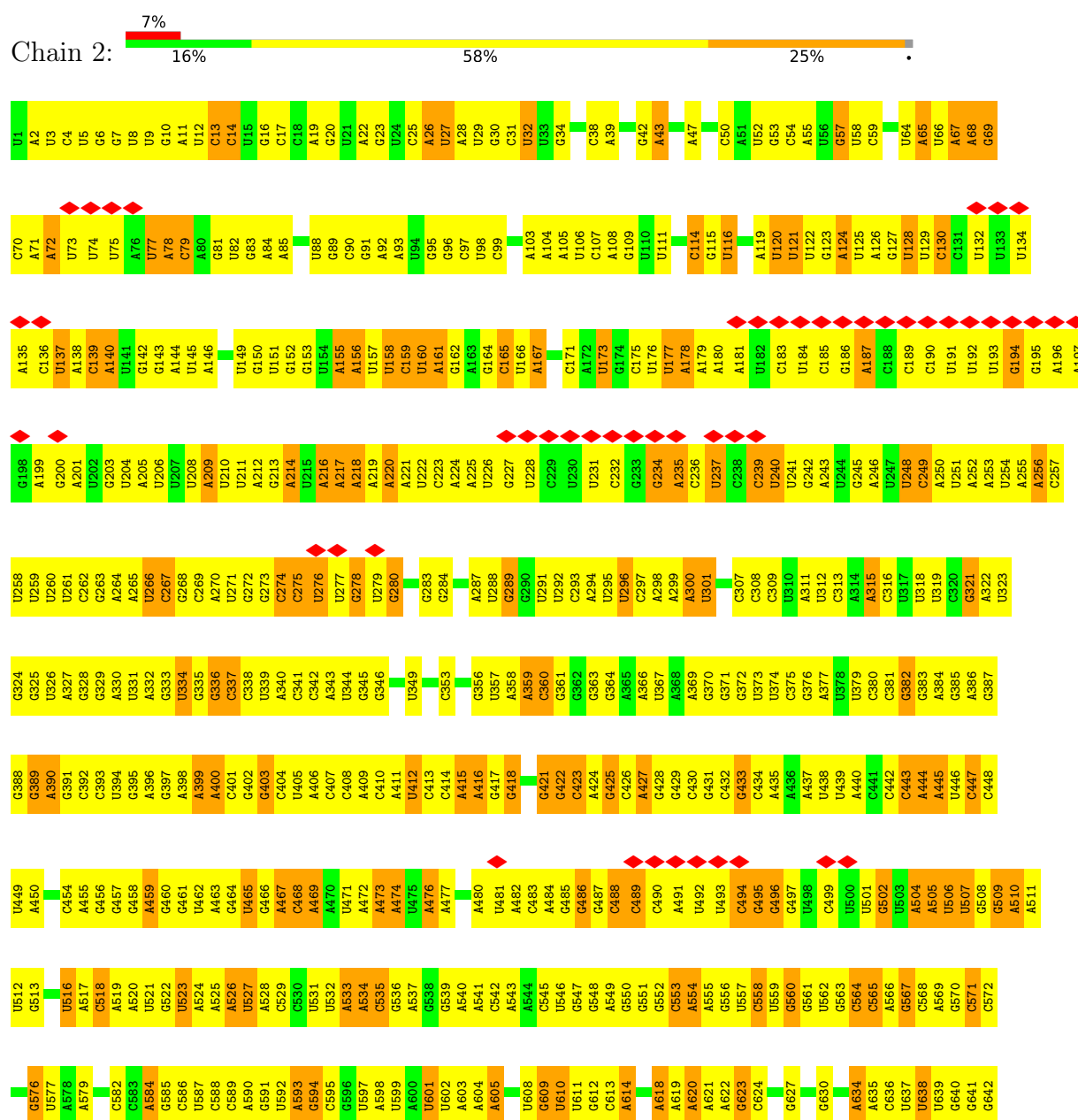
- Molecule 47 is water.

Mol	Chain	Residues	Atoms		AltConf
47	2	3	Total 3	O 3	0

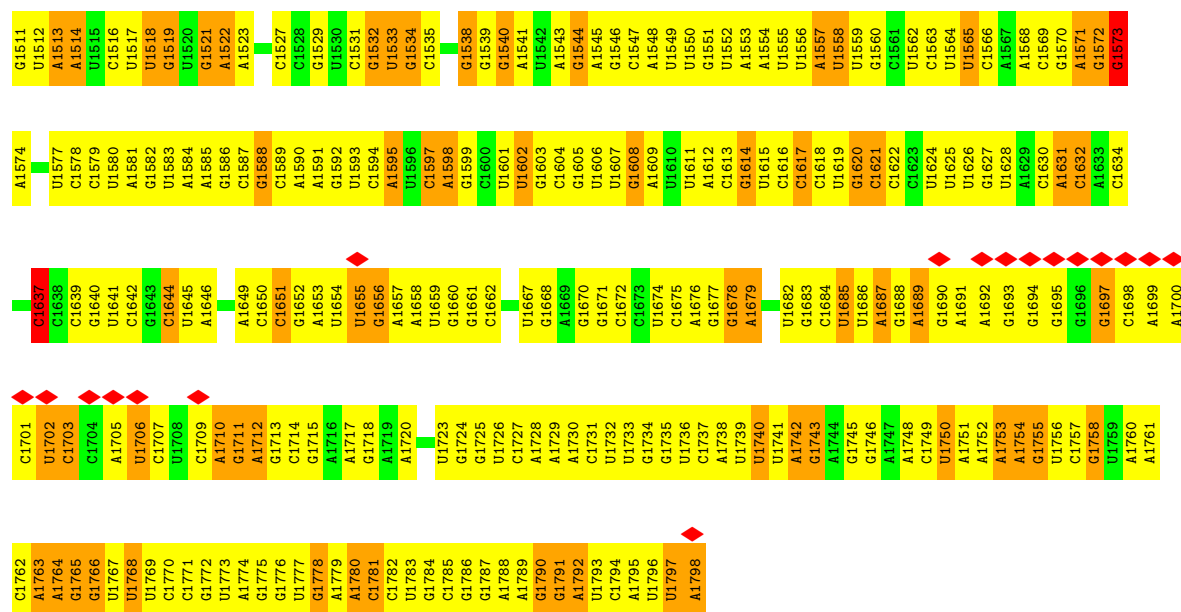
3 Residue-property plots

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

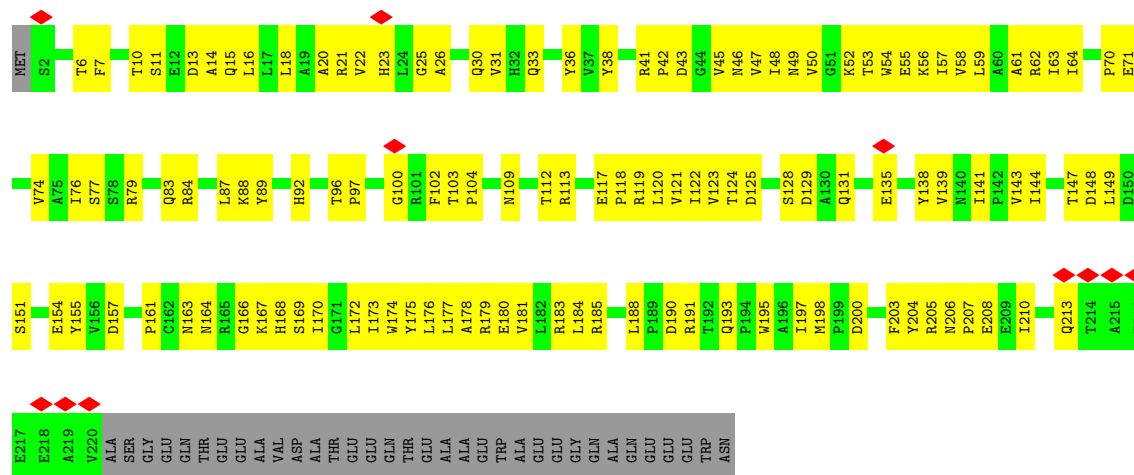


C1449	U1388	A1325	U1261	G1199	U1135	U1011	A950	A886	G823	G763	G703
U1450	A1389	C1326	G1262	G1200	A1136	A1012	A951	U887	U824	U764	C704
U1451	U1390	C1327	G1263	G1201	A1137	A1013	U951	U888	U825	U765	U705
G1452	C1391	G1328	G1264	A1202	G1138	U1014	G952	C889	C826	U766	G646
G1453	G1392	C1329	U1265	A1203	U1139	C1015	G953	A890	U827	U767	A706
C1454	A1330	G1266	C1204	C1204	G1140	U1016	A954	A891	A828	C768	C707
C1455	C1331	G1267	G1268	U1205	A1141	U1079	C955	U892	U829	U769	C708
C1456	C1332	U1268	C1206	C1206	A1142	A1080	G956	U893	U830	A770	C709
C1457	U1333	G1269	A1207	A1207	U1143	G1081	U957	G894	U831	A771	U710
G1460	U1334	G1270	C1208	C1208	U1144	G1082	U958	U895	U832	U772	G711
C1461	A1335	U1271	C1209	C1209	U1145	A1083	U959	C896	G833	C773	G712
G1462	A1336	G1272	A1210	A1210	A1146	G1084	U960	A897	U834	A774	U713
C1463	C1337	C1273	G1211	G1211	A1085	A1025	C961	G898	G836	G775	A713
G1464	C1338	A1274	G1212	G1212	A1086	A1026	A962	A899	G837	G776	C714
C1465	U1339	U1275	U1213	U1213	A1087	C1027	U963	G900	U838	C777	U715
C1466	A1340	G1276	C1214	C1214	A1151	U1028	U964	U901	U839	G778	C716
U1466	U1405	G1277	G1215	G1215	A1090	A1029	A965	U902	U840	A779	U717
A1467	G1406	C1278	A1216	A1216	A1091	U1030	A966	G903	C941	U780	C718
C1468	G1407	C1279	G1217	G1217	A1092	G1031	U967	A904	U842	A781	C717
A1469	A1343	C1278	A1218	A1218	G1093	C1032	C968	A905	A843	U782	U718
C1470	A1344	U1281	C1219	C1219	U1094	C1033	A969	A906	G844	C783	U719
U1470	U1346	U1282	U1282	A1220	C1159	G1034	A970	C945	U794	U784	G720
U1471	C1283	U1283	C1283	U1224	U1096	A1035	G971	C909	A846	C785	U721
U1472	A1347	U1284	U1284	A1225	U1097	C1036	A972	U910	A947	G786	U722
A1473	G1350	G1287	G1287	A1226	U1098	U1037	A973	U911	C948	A787	G723
C1474	U1351	U1288	U1288	G1227	G1099	A1038	C974	G912	A849	A788	G724
G1475	U1352	U1289	U1289	G1228	G1100	G1039	G975	G913	U850	U789	G723
G1476	A1415	U1289	U1289	A1228	G1101	G1040	A976	A914	C951	U790	G724
A1477	G1416	U1289	U1289	A1229	G1102	G1041	A977	U915	G852	U791	U725
U1478	C1354	G1290	G1290	A1230	U1103	A1042	A978	U916	U853	A792	U726
C1479	U1355	U1291	U1291	U1231	G1104	U1043	G979	U917	A854	U793	C727
C1480	G1356	G1292	G1292	G1232	U1105	C1044	U979	A918	A855	U794	G671
A1481	C1357	G1293	G1293	G1233	G1106	G1045	U982	U919	U856	A795	A728
U1482	G1358	G1294	A1233	A1233	G1107	G1046	G983	U920	A858	G796	G729
C1483	A1359	A1295	A1295	C1234	G1171	G1047	G984	U859	U860	A674	C730
A1484	C1360	G1296	G1296	A1235	C1172	U1048	G985	U861	U861	C797	G731
C1485	U1361	U1297	U1297	G1236	C1173	G1049	G986	A922	U862	U798	C732
A1486	G1362	G1298	G1298	A1237	U1174	G1050	A987	G924	U863	G800	A733
U1487	C1363	A1299	U1238	U1238	G1110	U1051	U988	A925	U864	G801	A734
A1488	G1364	U1300	U1239	U1239	A1112	U1052	C989	C926	A802	A733	G678
C1489	C1365	U1300	G1240	G1240	G1177	G1052	G990	U927	G865	A803	C735
A1490	G1366	U1304	A1241	A1241	U1114	U1053	A991	A928	G866	U804	C736
A1491	C1367	C1305	G1242	G1242	U1115	U1054	A992	A929	G867	A805	C737
C1492	U1368	U1306	A1243	A1243	U1116	U1055	A992	C930	A868	A806	U837
C1493	U1369	U1306	G1244	G1244	G1117	U1056	U995	U931	C969	U807	C683
U1494	G1370	U1309	C1245	C1245	A1182	U1057	U996	C930	C969	G738	A684
A1495	C1371	U1310	U1246	U1246	A1183	C1058	G997	C932	G870	G808	A685
C1496	A1371	A1311	C1247	C1247	U1184	U1059	A997	C933	G871	G809	U691
G1496	C1372	U1312	U1248	U1248	U1185	U1060	U998	U934	U872	A810	A745
C1497	U1373	A1312	U1248	U1248	U1186	U1061	C999	G935	C873	A811	C741
C1498	G1374	U1313	U1249	U1249	U1187	A1062	C999	G935	C873	C887	C742
U1499	U1375	U1314	U1250	U1250	A1188	U1063	A1000	C936	G874	U812	U742
C1499	C1376	G1315	C1251	C1251	C1189	U1062	G997	G937	G875	A813	G688
G1500	U1377	C1316	U1252	U1252	B81190	G1063	A1001	A938	G876	G814	U743
A1501	C1378	G1317	C1253	C1253	U1185	A1064	A1002	A939	G877	G815	U744
G1502	U1441	U1378	G1254	G1254	C1191	C1065	U1003	A939	G878	A816	A745
A1503	A1442	A1318	G1254	G1254	A1192	C1066	A1004	A940	C879	A816	A746
C1504	G1380	U1319	U1255	U1255	C1193	C1066	C1005	G941	C879	C817	C747
C1505	A1381	A1320	U1256	U1256	C1194	C1067	C1006	A880	A830	G818	U748
U1506	U1444	A1321	U1257	U1257	A1195	A1068	G1007	U944	U883	U819	U749
C1507	C1445	A1321	U1257	U1257	A1196	C1069	U1008	U945	A883	U820	U750
U1508	G1385	G1322	U1258	U1258	C1196	C1070	C1009	U946	U883	U821	G684
G1509	U1437	C1323	G1323	G1323	G1197	C1071	C1009	U946	U883	G822	C697
C1510	U1448	C1387	A1324	G1260	G1198	G1072	G1010	G947	U885	A753	U698



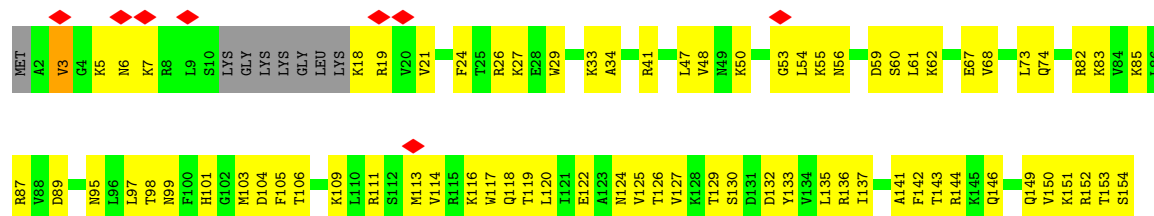
• Molecule 2: Small ribosomal subunit protein uS2

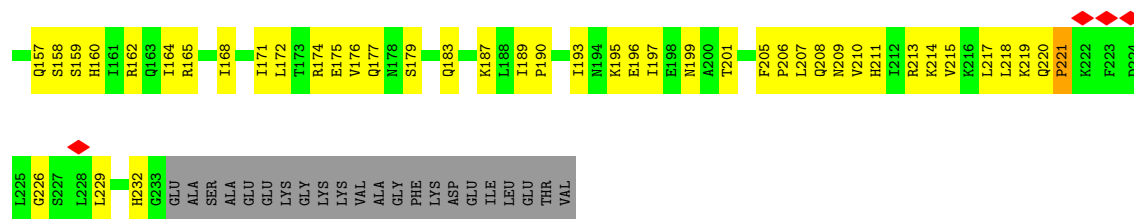
Chain A: 37% 49% 14%



• Molecule 3: Small ribosomal subunit protein eS1

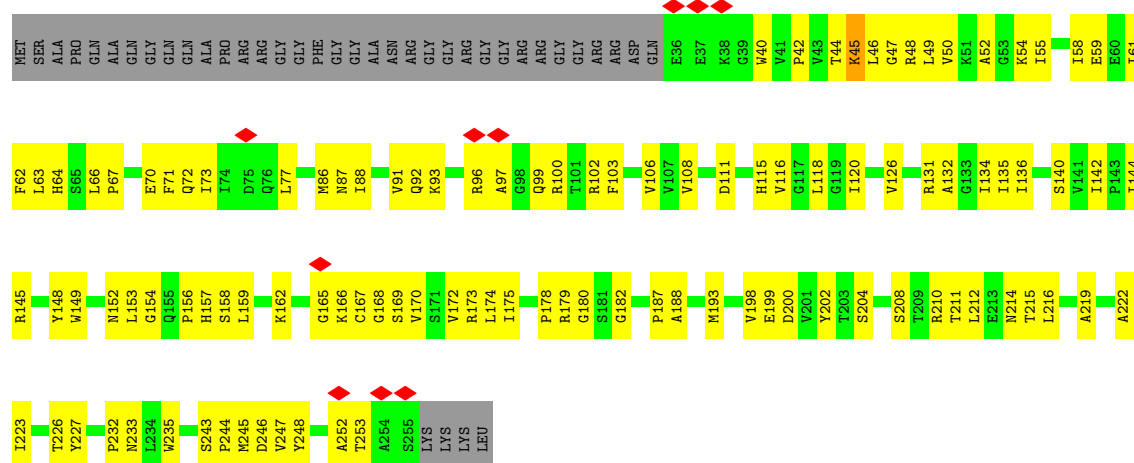
Chain B: 5% 42% 45% 12%





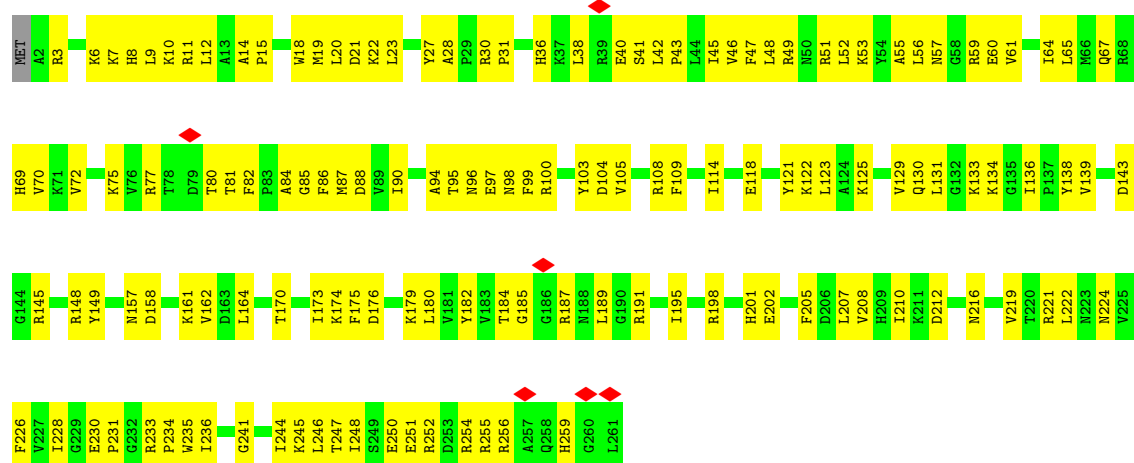
• Molecule 4: Small ribosomal subunit protein uS5

Chain C: 43% 42% 15%



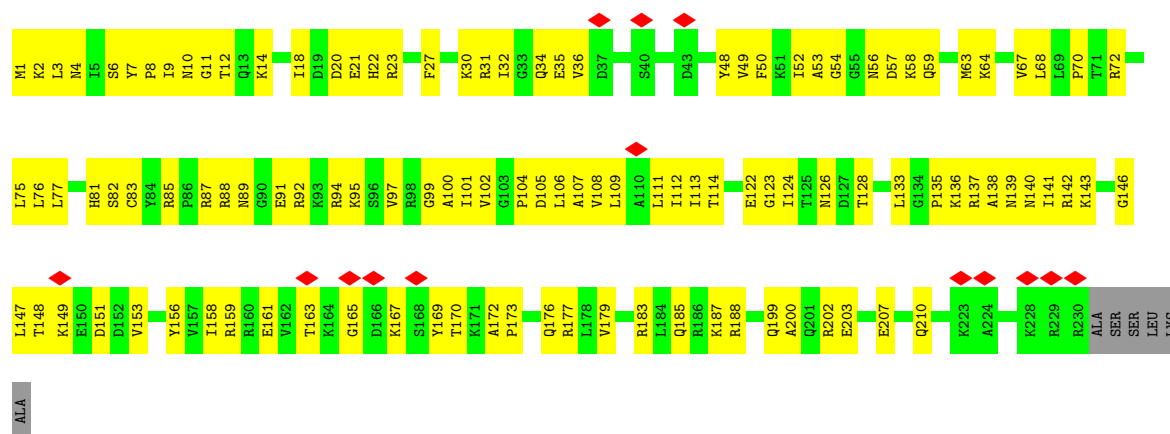
• Molecule 5: 40S ribosomal protein S4

Chain E: 46% 54%

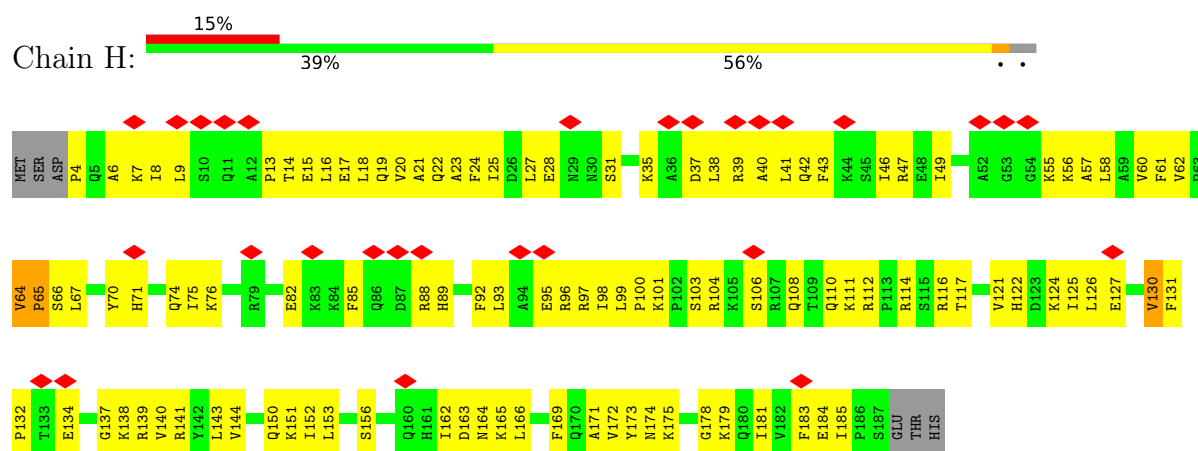


• Molecule 6: Small ribosomal subunit protein eS6

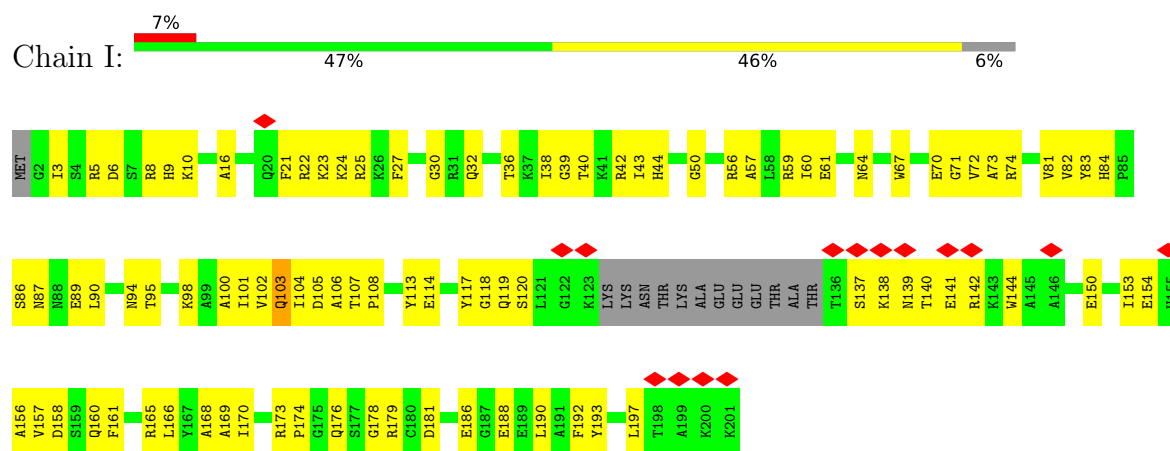
Chain G: 6% 49% 48%



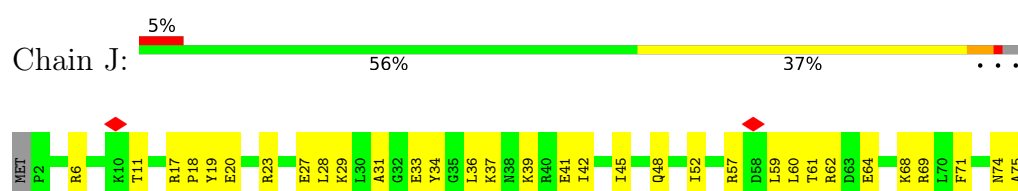
• Molecule 7: 40S ribosomal protein S7

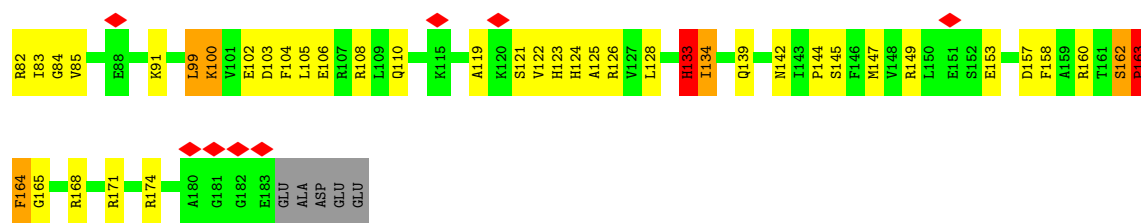


• Molecule 8: 40S ribosomal protein S8

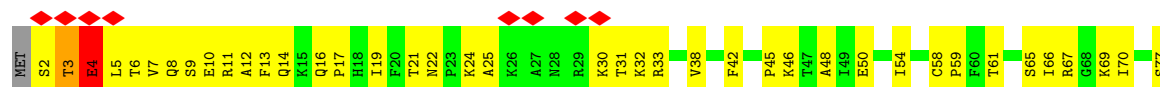


• Molecule 9: KLLA0E23673p





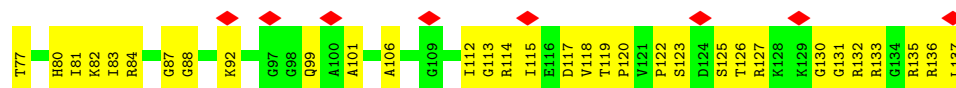
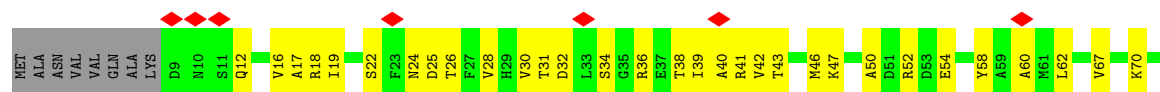
• Molecule 10: KLLA0A10483p



• Molecule 11: KLLA0F18040p

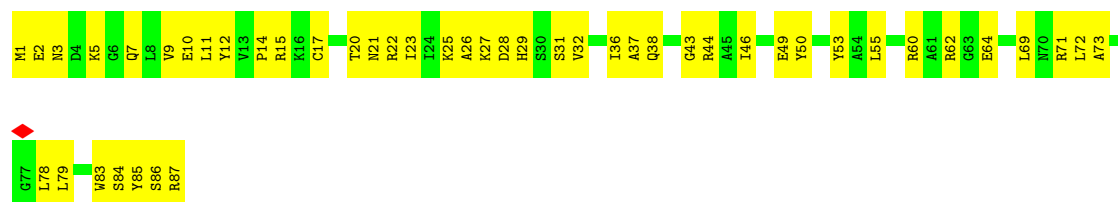


• Molecule 12: Small ribosomal subunit protein uS11



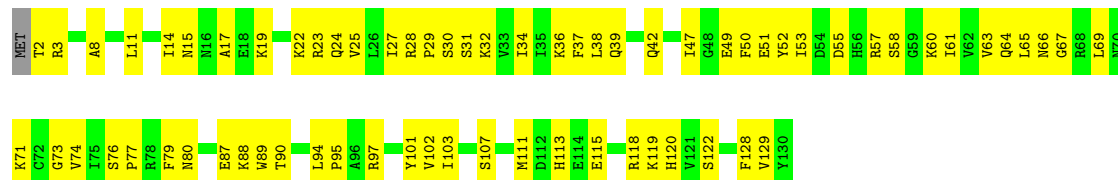
• Molecule 13: 40S ribosomal protein S21





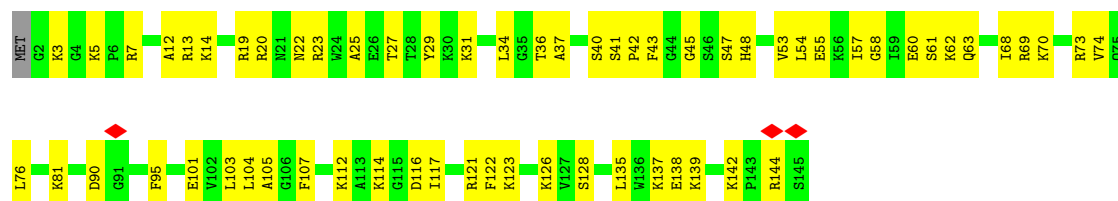
- Molecule 14: Small ribosomal subunit protein uS8

Chain W: 47% 52%



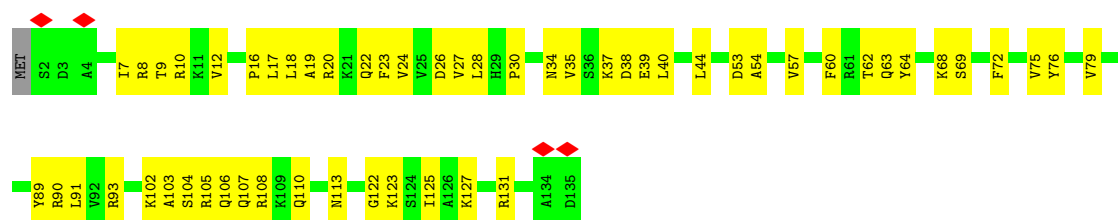
- Molecule 15: KLLA0B11231p

Chain X: 57% 43%



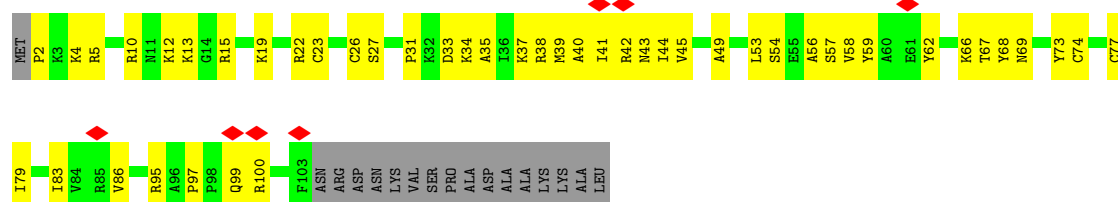
- Molecule 16: 40S ribosomal protein S24

Chain Y: 58% 41%



- Molecule 17: 40S ribosomal protein S26

Chain a: 6% 45% 40% 14%



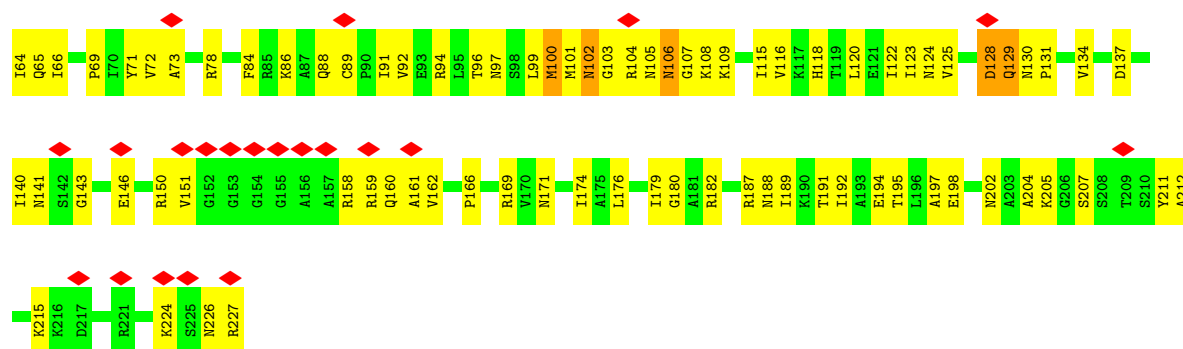
-
- The chart displays the distribution of 1000 samples across 100 categories. The categories are labeled on the y-axis, and the x-axis represents the count of samples. The bars are colored in a repeating pattern of yellow, green, and grey. Red diamonds are placed above certain bars, indicating specific categories of interest.
- | Category | Count (approx.) | Color | Marked |
|----------|-----------------|--------|--------|
| K82 | 10 | Green | Yes |
| MET | 10 | Grey | No |
| V2 | 10 | Yellow | No |
| L3 | 10 | Yellow | No |
| V4 | 10 | Yellow | No |
| O5 | 10 | Yellow | No |
| D6 | 10 | Yellow | No |
| T11 | 10 | Yellow | No |
| S14 | 10 | Yellow | No |
| R17 | 10 | Yellow | No |
| K18 | 10 | Yellow | No |
| R19 | 10 | Green | No |
| K20 | 10 | Yellow | No |
| L21 | 10 | Yellow | No |
| K22 | 10 | Yellow | No |
| T23 | 10 | Yellow | No |
| L24 | 10 | Green | No |
| V25 | 10 | Yellow | No |
| Q26 | 10 | Yellow | No |
| R29 | 10 | Yellow | No |
| F32 | 10 | Yellow | No |
| L33 | 10 | Green | No |
| D34 | 10 | Yellow | No |
| V35 | 10 | Green | No |
| K36 | 10 | Yellow | No |
| C37 | 10 | Yellow | No |
| P38 | 10 | Yellow | No |
| I43 | 10 | Yellow | No |
| F47 | 10 | Yellow | No |
| S48 | 10 | Green | No |
| H49 | 10 | Yellow | No |
| A50 | 10 | Yellow | No |
| Q51 | 10 | Yellow | No |
| C56 | 10 | Yellow | No |
| E57 | 10 | Green | Yes |
| S58 | 10 | Yellow | No |
| T61 | 10 | Green | Yes |
| T65 | 10 | Yellow | No |
| K70 | 10 | Yellow | No |
| A71 | 10 | Green | No |
| K72 | 10 | Green | No |
| L73 | 10 | Green | No |
| S74 | 10 | Green | No |
| E75 | 10 | Green | No |
| G76 | 10 | Green | No |
| T77 | 10 | Yellow | No |
| S78 | 10 | Yellow | No |
| F79 | 10 | Yellow | No |
| R80 | 10 | Yellow | No |
| H81 | 10 | Yellow | No |

- [illegible]

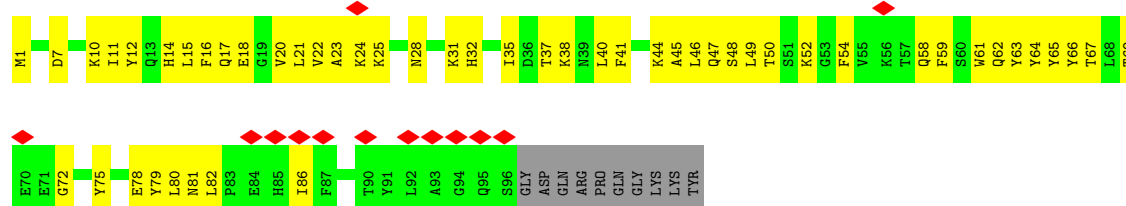
- | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| M1 | R2 | A3 | K4 | W5 | R6 | K7 | K8 | R9 | T10 | R11 | R12 | L13 | K14 | R15 | K16 | R17 | R18 | K19 | V20 | R21 | A22 | R23 | S24 | K25 |
|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- | |
|------|
| V175 | L176 | L177 | L178 | L179 | G183 | L184 | K185 | L202 | P203 | P209 | D204 | A205 | V206 | T207 | E210 | P211 | K212 | V217 | S221 | V222 | Y225 | R226 | P227 | T228 | E229 | PRO | VAL | GLU | ALA | ALA | GLU | SER | ALA | | | | | | | | | | | | | | | |
| K75 | R76 | F77 | K78 | K79 | R80 | R81 | G82 | T83 | I84 | R88 | E89 | R90 | Y91 | R94 | Y99 | A100 | Q101 | M105 | K106 | F107 | K108 | L109 | L110 | A114 | I115 | R116 | R117 | V122 | K141 | L142 | R143 | A144 | A145 | R146 | A147 | K148 | S149 | M150 | I158 | H159 | S160 | G161 | Q162 | P163 | F167 | A171 | T172 | R173 |
| MET | VAL | A3 | S6 | K7 | R8 | R9 | K10 | D14 | F17 | E20 | E23 | F24 | T25 | T26 | R27 | E28 | L29 | A30 | G33 | Y34 | V37 | E38 | V39 | R40 | V41 | T42 | K45 | T46 | E47 | I50 | R51 | A52 | T53 | K54 | V55 | V58 | V59 | G60 | E61 | R64 | R65 | I66 | E68 | L69 | I73 | E74 | | |

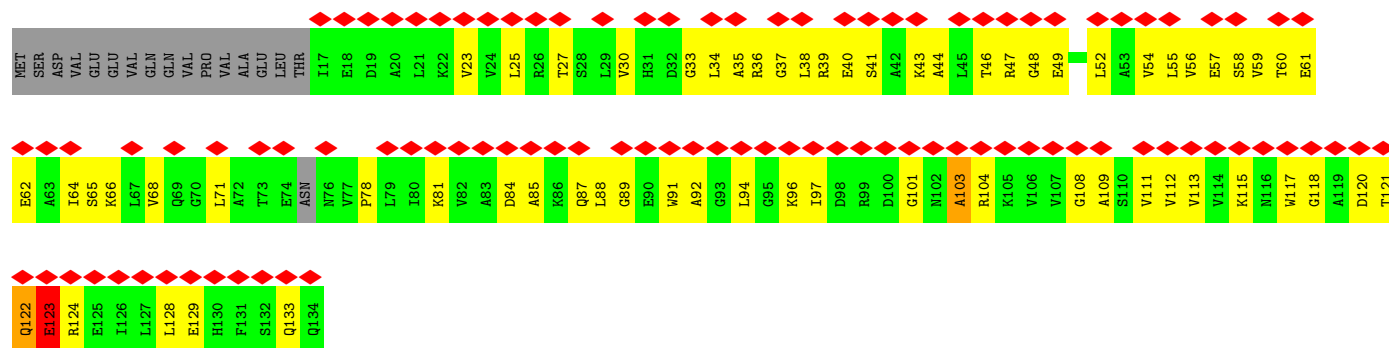
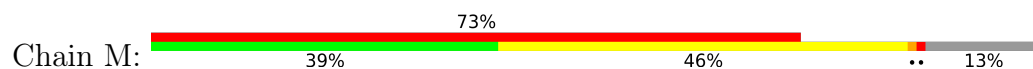
- | MET | SER | HIS | GLU | ALA | GLN | VAL | GLU | VAL | GLU | VAL | GLN | ASP | PHE | GLU | VAL | VAL | GLN | GLU |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| F22 | V23 | F24 | V25 | E26 | L27 | A28 | T29 | T30 | I31 | P32 | V33 | E34 | I35 | Q36 | Q37 | A38 | Q39 | I42 |
| K43 | F44 | F45 | N46 | K47 | W48 | S49 | F50 | K55 | D57 | A58 | S59 | L60 | V61 | D62 | V63 | V64 | V65 | V66 |



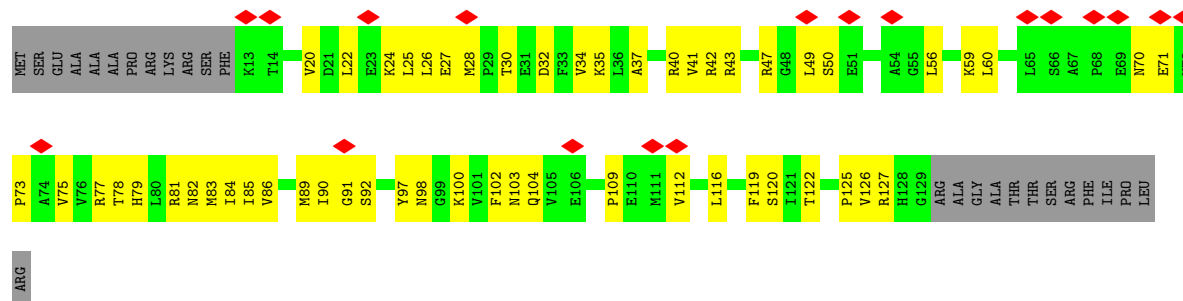
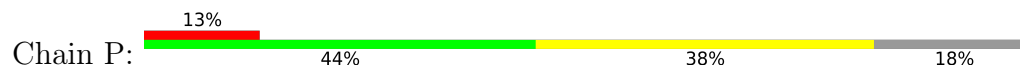
• Molecule 23: KLLA0B08173p



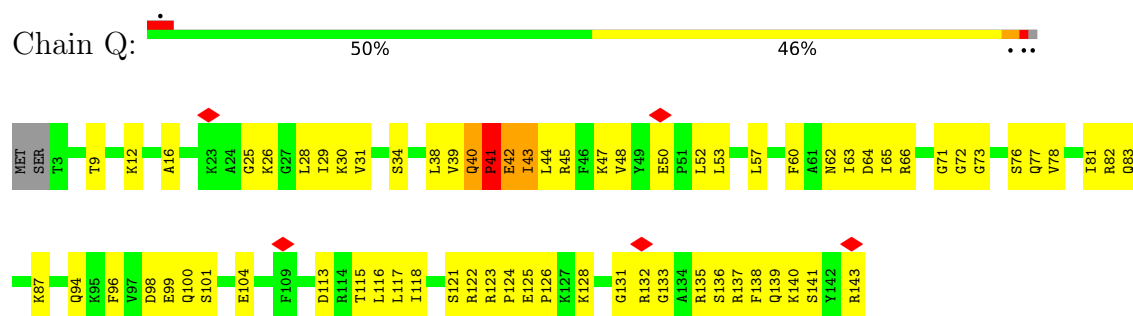
• Molecule 24: 40S ribosomal protein S12



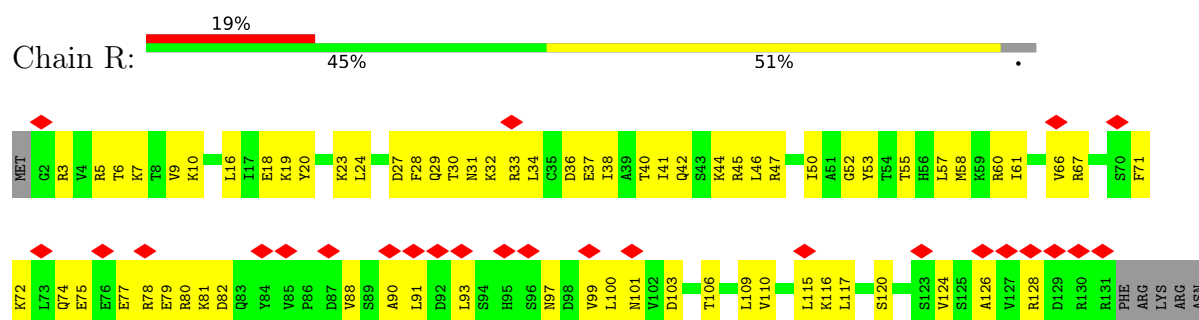
• Molecule 25: KLLA0F07843p



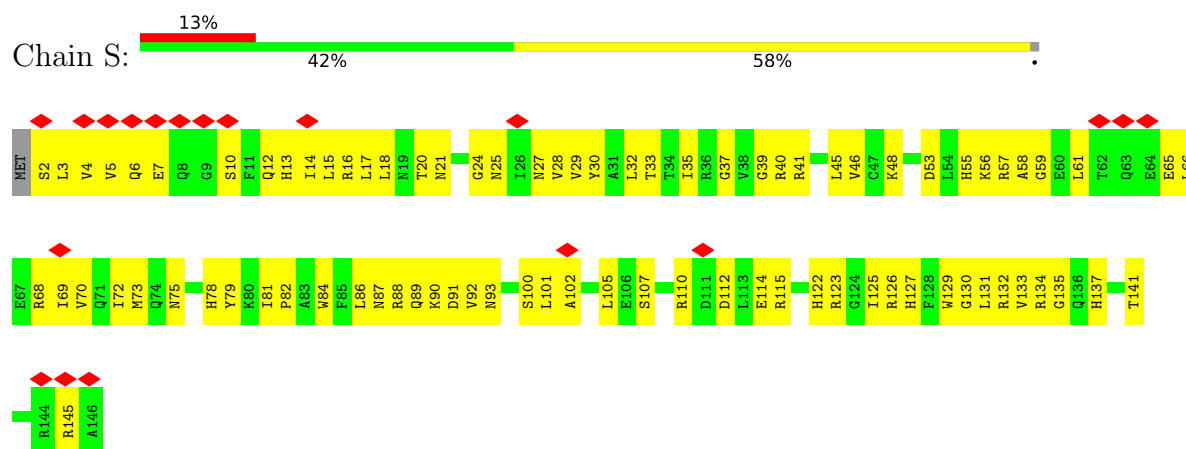
- Molecule 26: Small ribosomal subunit protein uS9



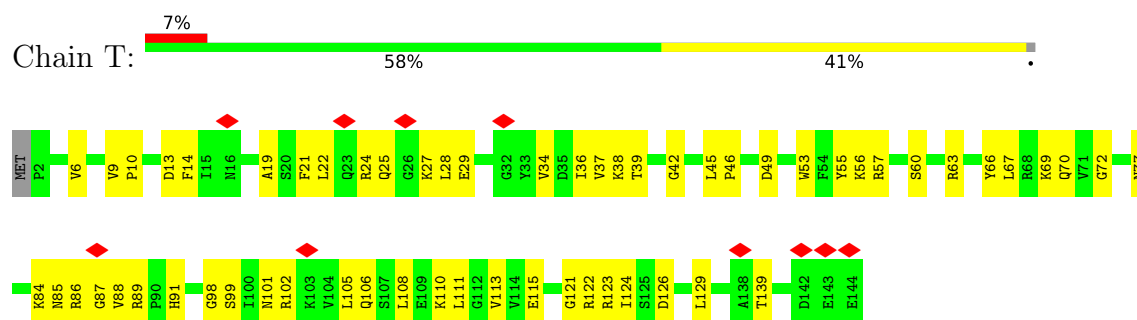
- Molecule 27: KLLA0B01474p



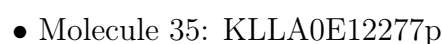
- Molecule 28: KLLA0B01562p

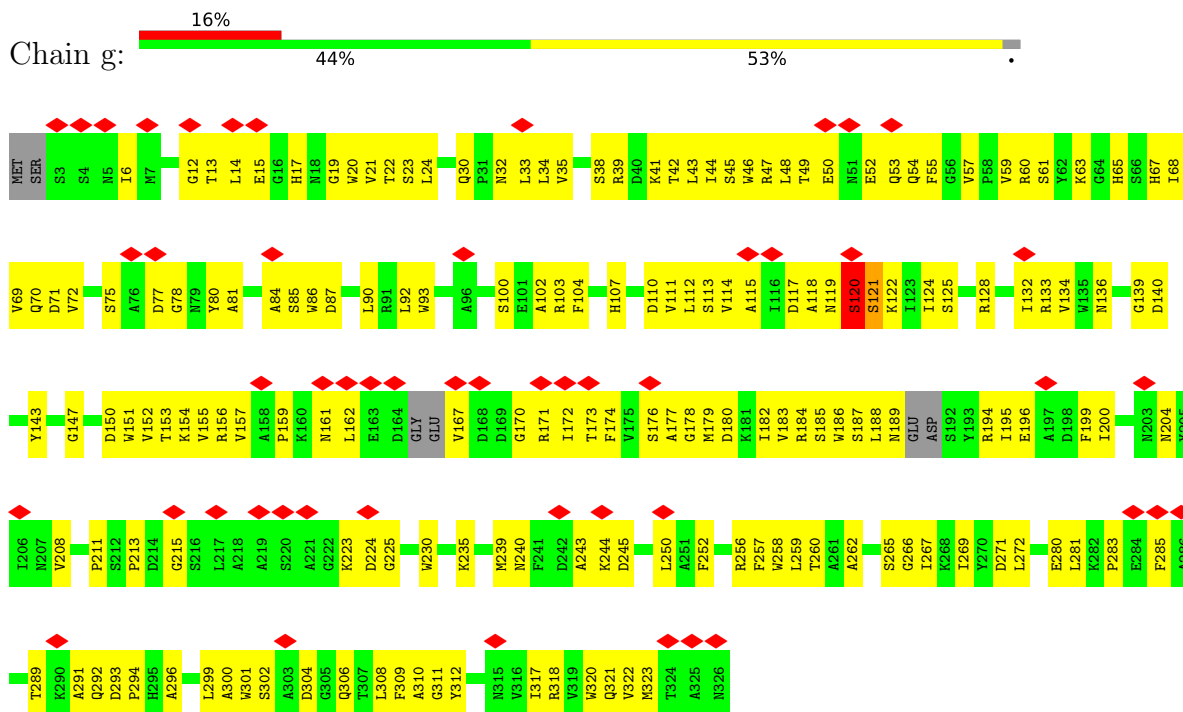


- Molecule 29: KLLA0A07194p

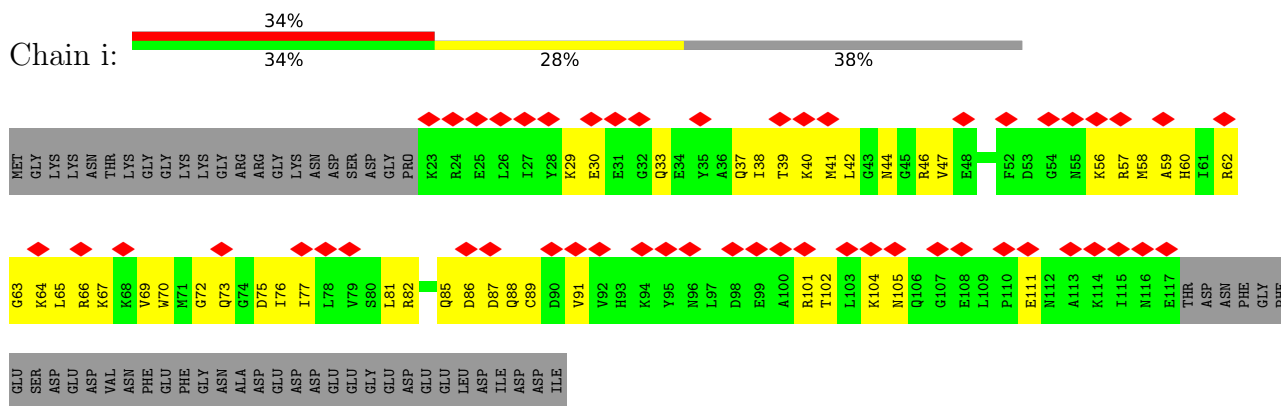


- Molecule 30: Small ribosomal subunit protein uS10

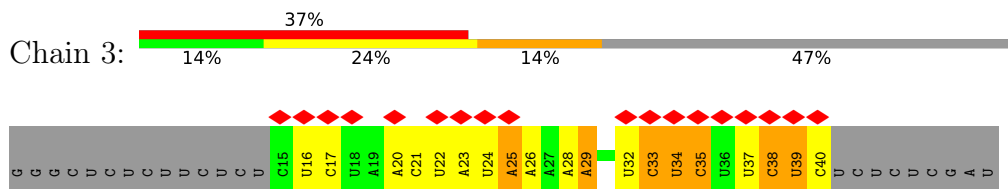




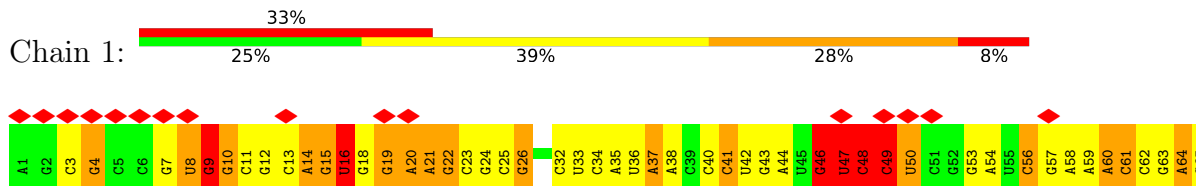
- Molecule 36: Eukaryotic translation initiation factor 1A

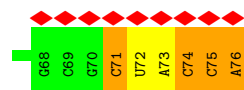


- Molecule 37: mRNA (5'-R(P*AP*AP*U)-3')

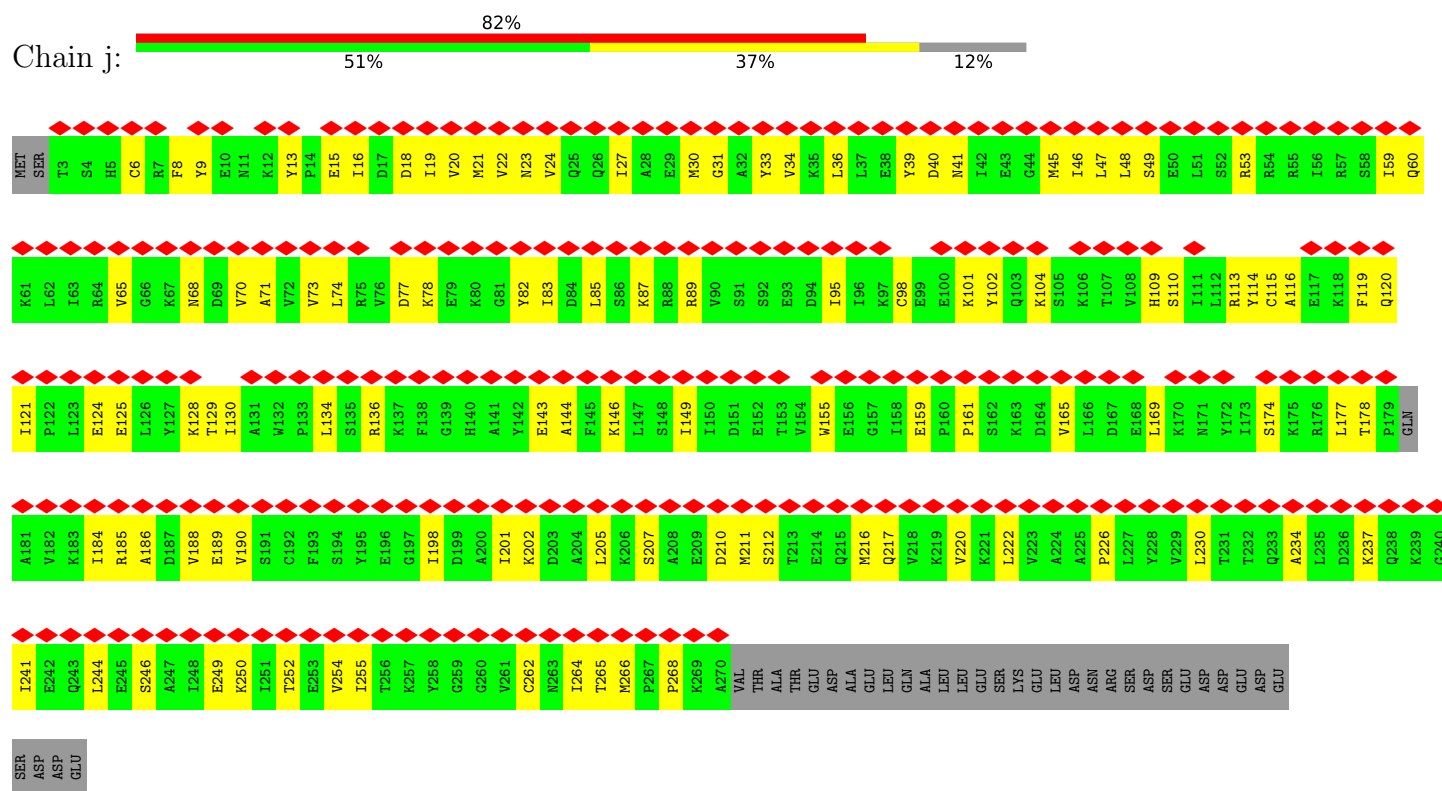


- Molecule 38: Met-tRNAⁱ

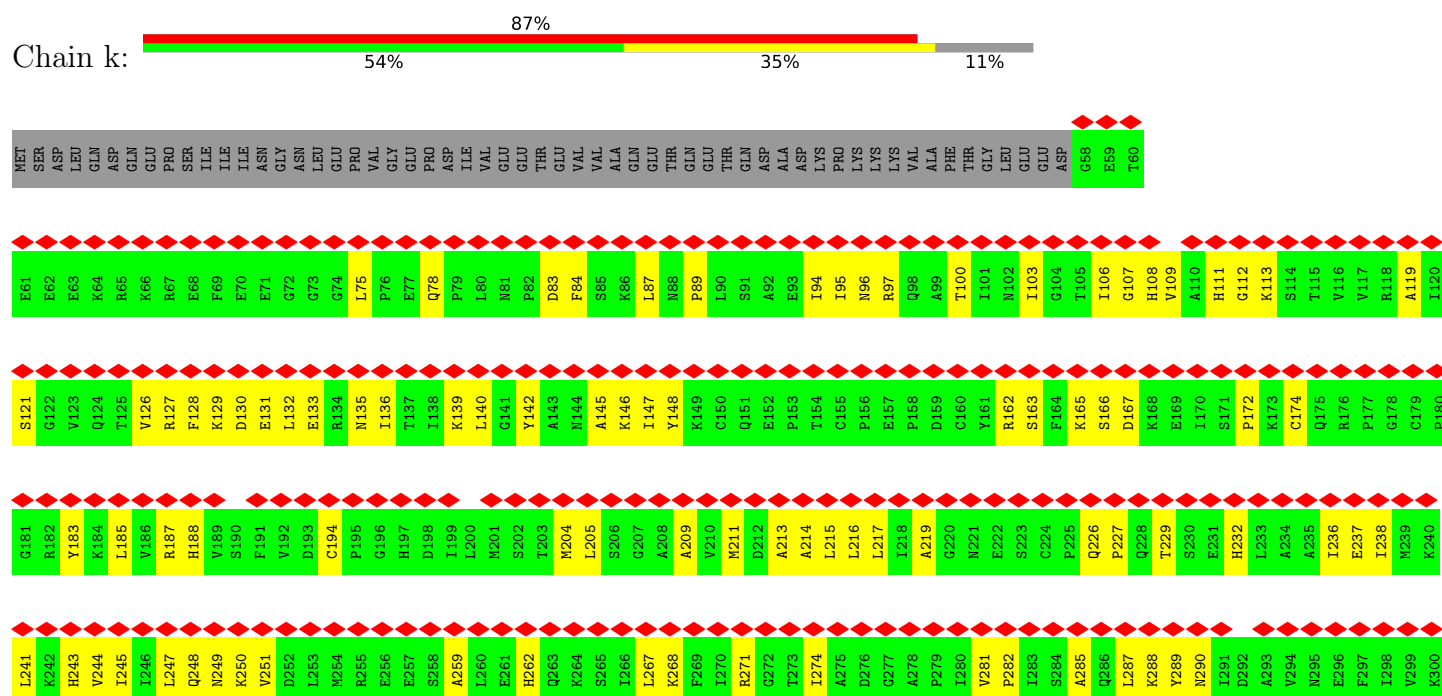


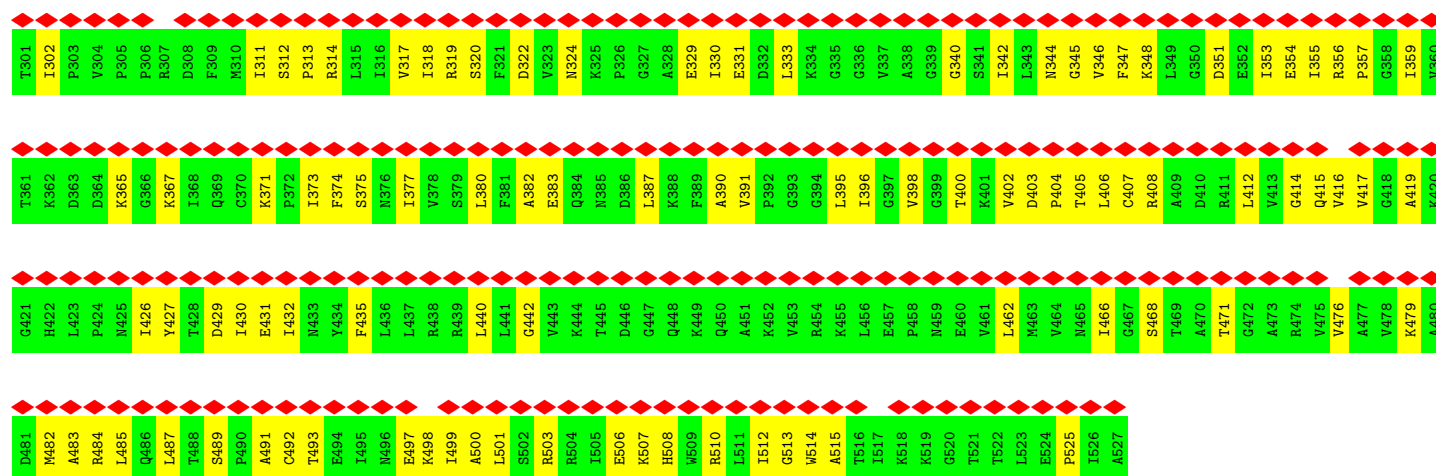


• Molecule 39: Eukaryotic translation initiation factor 2 subunit alpha

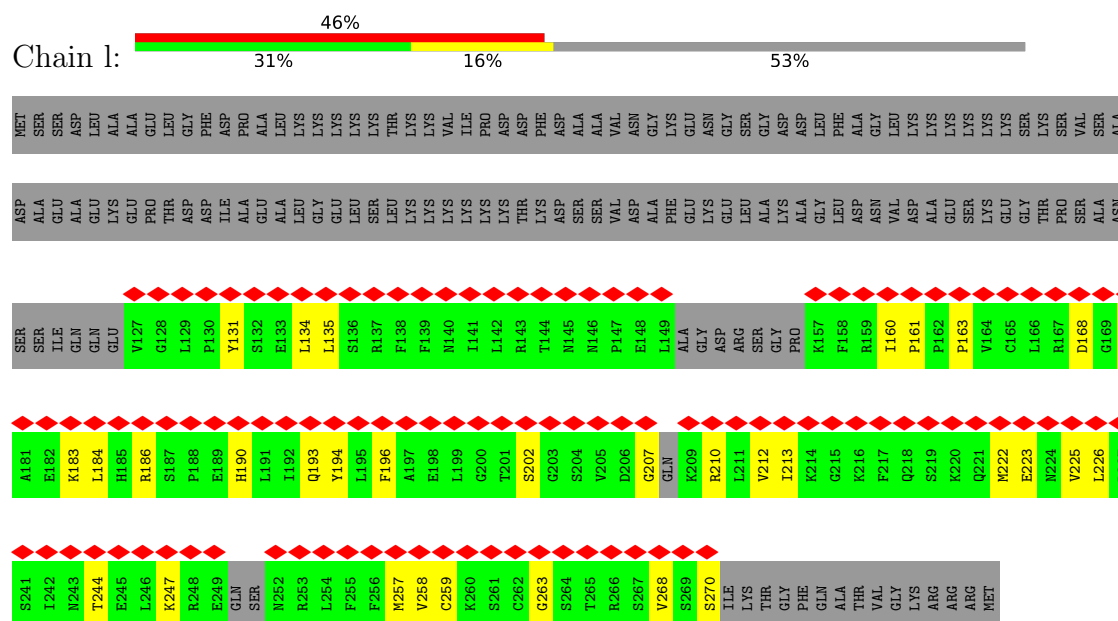


• Molecule 40: Eukaryotic translation initiation factor 2 subunit gamma

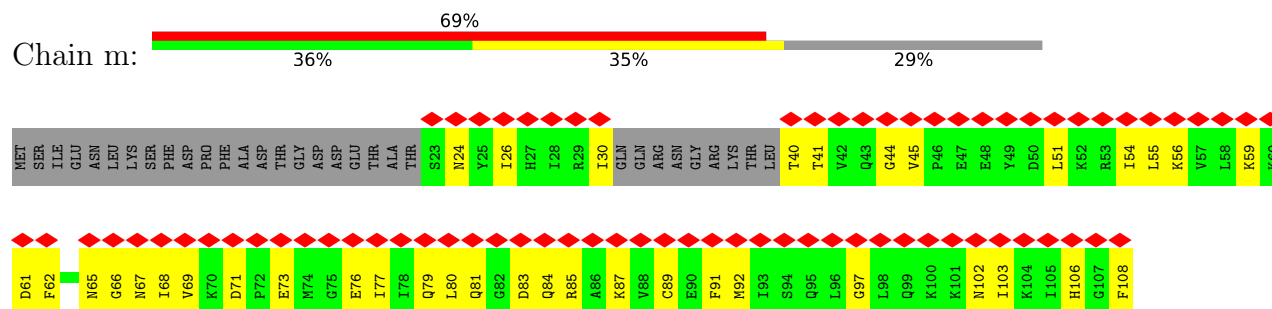




• Molecule 41: Eukaryotic translation initiation factor 2 subunit beta



• Molecule 42: Eukaryotic translation initiation factor eIF-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26818	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	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	0.330	Depositor
Minimum map value	-0.169	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.06	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: 7MG, RIA, 2MG, MG, PSU, ZN, B8N, H2U, MA6, 1MA, 5MC, T6A, M2G, 1MG, GCP

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	0.22	0/42201	0.34	0/65752
2	A	0.23	0/1742	0.47	0/2383
3	B	0.23	0/1820	0.53	0/2448
4	C	0.24	0/1678	0.47	0/2277
5	E	0.24	0/2122	0.50	0/2861
6	G	0.17	0/1855	0.40	0/2479
7	H	0.26	0/1507	0.62	3/2028 (0.1%)
8	I	0.21	0/1515	0.48	0/2029
9	J	0.33	0/1495	0.65	5/2001 (0.2%)
10	L	0.28	0/1276	0.48	0/1718
11	N	0.20	0/1218	0.41	0/1638
12	O	0.23	0/966	0.56	1/1297 (0.1%)
13	V	0.22	0/696	0.46	0/938
14	W	0.29	0/1039	0.54	0/1399
15	X	0.25	0/1137	0.51	0/1516
16	Y	0.21	0/1075	0.47	0/1433
17	a	0.23	0/810	0.53	0/1087
18	b	0.19	0/619	0.42	0/837
19	e	0.20	0/480	0.47	0/640
20	h	0.18	0/234	0.44	0/300
21	D	0.19	0/1800	0.44	0/2421
22	F	0.28	0/1628	0.50	0/2198
23	K	0.21	0/831	0.49	0/1123
24	M	0.28	0/891	0.60	0/1201
25	P	0.20	0/942	0.50	0/1269
26	Q	0.28	0/1125	0.64	2/1510 (0.1%)
27	R	0.31	0/1044	0.62	0/1402
28	S	0.18	0/1208	0.47	0/1624
29	T	0.19	0/1129	0.41	0/1520
30	U	0.21	0/857	0.57	0/1158
31	Z	0.21	0/603	0.54	0/814
32	c	0.20	0/501	0.41	0/673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.23	0/473	0.57	0/629
34	f	0.15	0/597	0.51	0/795
35	g	0.21	0/2523	0.46	0/3434
36	i	0.19	0/773	0.52	0/1031
37	3	0.13	0/595	0.27	0/920
38	1	0.20	0/1529	0.34	0/2376
39	j	0.17	0/2171	0.45	0/2924
40	k	0.17	0/3657	0.44	0/4946
41	l	0.15	0/1099	0.41	0/1469
42	m	0.16	0/626	0.46	0/835
All	All	0.22	0/92087	0.42	11/133333 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	H	65	PRO	N-CA-C	-8.64	102.36	114.98
26	Q	43	ILE	N-CA-C	-7.97	106.14	113.71
26	Q	40	GLN	CA-C-O	-6.71	112.70	119.08
9	J	163	PRO	CA-N-CD	-6.46	102.95	112.00
9	J	163	PRO	N-CA-CB	-5.69	97.27	103.25
7	H	130	VAL	CA-C-N	-5.36	113.88	119.83
7	H	130	VAL	C-N-CA	-5.36	113.88	119.83
9	J	163	PRO	N-CA-C	5.15	123.09	112.47
9	J	162	SER	CA-C-N	5.07	126.17	119.84
9	J	162	SER	C-N-CA	5.07	126.17	119.84
12	O	130	GLY	N-CA-C	5.02	121.63	114.85

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	38003	0	19119	1658	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1702	0	1695	117	0
3	B	1796	0	1874	142	0
4	C	1648	0	1727	105	0
5	E	2078	0	2157	142	0
6	G	1832	0	1919	101	0
7	H	1483	0	1579	112	0
8	I	1489	0	1504	93	0
9	J	1471	0	1554	82	0
10	L	1248	0	1311	74	0
11	N	1195	0	1263	69	0
12	O	955	0	987	70	0
13	V	687	0	682	48	0
14	W	1021	0	1056	85	0
15	X	1119	0	1198	61	0
16	Y	1061	0	1111	64	0
17	a	797	0	835	63	0
18	b	609	0	628	32	0
19	e	472	0	508	23	0
20	h	233	0	284	15	0
21	D	1774	0	1855	83	0
22	F	1609	0	1679	132	0
23	K	809	0	810	55	0
24	M	885	0	917	59	0
25	P	923	0	960	51	0
26	Q	1105	0	1170	77	0
27	R	1033	0	1082	73	0
28	S	1189	0	1211	81	0
29	T	1110	0	1124	56	0
30	U	845	0	913	80	0
31	Z	594	0	590	43	0
32	c	499	0	536	26	0
33	d	461	0	448	44	0
34	f	584	0	602	39	0
35	g	2469	0	2403	156	0
36	i	764	0	762	37	0
37	3	536	0	277	11	0
38	1	1639	0	852	56	0
39	j	2139	0	2205	98	0
40	k	3596	0	3712	136	0
41	l	1083	0	1121	39	0
42	m	619	0	646	33	0
43	2	114	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	S	1	0	0	0	0
43	i	1	0	0	0	0
43	k	1	0	0	0	0
44	a	1	0	0	0	0
44	b	1	0	0	0	0
44	f	1	0	0	0	0
44	l	1	0	0	0	0
45	k	32	0	14	10	0
46	k	8	0	8	1	0
47	2	3	0	0	0	0
All	All	87328	0	68888	3915	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 25.

All (3915) 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)
45:k:601:GCP:O3'	41:l:238:THR:HG21	1.28	1.29
45:k:601:GCP:O2'	41:l:238:THR:HB	1.33	1.24
1:2:1471:U:C5	22:F:105:ASN:ND2	2.14	1.12
1:2:1677:G:N2	1:2:1720:A:H62	1.46	1.11
1:2:1471:U:C6	22:F:105:ASN:ND2	2.19	1.10
22:F:162:VAL:HB	32:c:45:LYS:HE3	1.32	1.10
12:O:127:ARG:NH1	17:a:22:ARG:NH1	2.00	1.10
3:B:3:VAL:HG12	39:j:89:ARG:HB3	1.35	1.08
3:B:3:VAL:CG1	39:j:89:ARG:HB3	1.84	1.08
1:2:1677:G:H21	1:2:1720:A:N6	1.52	1.07
12:O:127:ARG:NH1	17:a:22:ARG:HH12	1.52	1.07
45:k:601:GCP:HO2'	41:l:238:THR:HB	0.93	1.07
1:2:1355:U:H3	1:2:1366:G:H1	1.06	1.04
1:2:1464:G:H5'	26:Q:132:ARG:HH12	1.27	0.98
12:O:127:ARG:HH12	17:a:22:ARG:NH1	1.58	0.96
45:k:601:GCP:O3'	41:l:238:THR:CG2	2.12	0.96
28:S:16:ARG:HH21	28:S:21:ASN:HA	1.29	0.95
12:O:127:ARG:HH12	17:a:22:ARG:HH12	0.97	0.94
1:2:1352:U:H3	1:2:1370:G:H1	1.07	0.93
1:2:1682:U:H3	1:2:1715:G:H1	1.01	0.92
1:2:477:A:H2	1:2:509:G:H1	1.16	0.91
1:2:1290:G:H1	1:2:1323:G:H22	1.17	0.91
22:F:96:THR:HG22	22:F:116:VAL:HG11	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:k:601:GCP:O2'	41:l:238:THR:CB	2.19	0.91
1:2:654:G:H1	1:2:676:U:H3	0.94	0.89
3:B:3:VAL:CG1	39:j:89:ARG:HE	1.85	0.89
1:2:161:A:H3'	1:2:162:G:H21	1.38	0.89
38:1:74:C:H4'	38:1:75:C:H5'	1.56	0.88
1:2:886:A:H61	1:2:924:G:H1	1.18	0.88
45:k:601:GCP:HO3'	41:l:238:THR:HG21	1.35	0.88
1:2:521:U:H5''	16:Y:37:LYS:HG3	1.54	0.87
1:2:899:A:H3'	1:2:900:G:H21	1.37	0.87
31:Z:58:ARG:HA	31:Z:103:ARG:HH12	1.39	0.87
21:D:105:MET:HE1	21:D:122:VAL:HG11	1.56	0.86
34:f:139:CYS:HB2	34:f:146:PHE:HB3	1.57	0.86
1:2:935:G:N7	17:a:15:ARG:NH1	2.23	0.86
35:g:92:LEU:HB3	35:g:102:ALA:HB3	1.57	0.86
30:U:68:ARG:HD2	30:U:70:THR:HG22	1.56	0.86
41:l:230:ILE:HA	41:l:234:VAL:HB	1.56	0.86
1:2:954:A:OP2	11:N:3:ARG:NH1	2.07	0.86
42:m:67:ASN:H	42:m:79:GLN:HB2	1.41	0.85
1:2:7:G:N7	4:C:210:ARG:NH2	2.23	0.85
1:2:786:G:H5'	5:E:255:ARG:HH22	1.42	0.85
1:2:867:G:H1	1:2:959:U:H3	1.22	0.85
2:A:36:TYR:HB2	2:A:149:LEU:HD11	1.59	0.85
1:2:1551:G:N7	25:P:43:ARG:NH2	2.25	0.84
5:E:42:LEU:HD21	5:E:47:PHE:HB2	1.57	0.84
35:g:172:ILE:HB	35:g:188:LEU:HB3	1.60	0.84
11:N:5:HIS:HB3	11:N:117:LEU:HD11	1.59	0.83
30:U:63:LEU:HB2	30:U:84:MET:HB3	1.58	0.83
1:2:1213:U:HO2'	33:d:2:ALA:N	1.77	0.83
3:B:103:MET:HB3	3:B:215:VAL:HG12	1.61	0.83
1:2:142:G:H2'	1:2:143:G:C8	2.13	0.83
1:2:520:A:N3	16:Y:34:ASN:ND2	2.26	0.83
1:2:952:G:H2'	1:2:953:G:H8	1.41	0.83
1:2:1172:C:O2	1:2:1599:G:N2	2.12	0.82
40:k:359:ILE:HB	40:k:371:LYS:HB2	1.58	0.82
1:2:433:G:H21	1:2:435:A:H8	1.22	0.82
21:D:76:ARG:HB2	23:K:22:VAL:HG11	1.61	0.82
3:B:3:VAL:HG12	39:j:89:ARG:CB	2.10	0.82
22:F:105:ASN:O	22:F:108:LYS:HG2	1.80	0.81
1:2:1497:G:H1	1:2:1506:U:H3	1.26	0.81
10:L:77:SER:HB3	10:L:85:VAL:HB	1.61	0.81
1:2:635:A:H5''	14:W:31:SER:HB2	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:T:42:GLY:HA2	29:T:84:LYS:HD3	1.61	0.81
35:g:115:ALA:HB3	35:g:124:ILE:HB	1.63	0.80
39:j:8:PHE:HE1	39:j:109:HIS:HB2	1.44	0.80
1:2:917:U:H2'	1:2:918:A:H8	1.46	0.80
1:2:256:A:H1'	8:I:73:ALA:HB3	1.63	0.80
14:W:27:ILE:HB	14:W:61:ILE:HB	1.62	0.80
1:2:139:C:N4	1:2:280:G:OP1	2.15	0.79
1:2:984:G:H1	1:2:1015:C:H5	1.29	0.79
14:W:49:GLU:H	14:W:64:GLN:HE21	1.30	0.79
22:F:104:ARG:O	22:F:108:LYS:NZ	2.14	0.79
40:k:147:ILE:HD12	40:k:187:ARG:HB3	1.63	0.79
1:2:771:A:O2'	9:J:6:ARG:NH2	2.14	0.79
1:2:865:G:OP1	11:N:1:MET:N	2.16	0.79
1:2:1500:G:N2	1:2:1503:A:OP2	2.15	0.79
38:l:19:G:N7	39:j:113:ARG:NH2	2.32	0.78
8:I:157:VAL:HG13	8:I:160:GLN:HE21	1.47	0.78
12:O:30:VAL:O	12:O:41:ARG:NH1	2.14	0.78
1:2:66:U:H3	6:G:173:PRO:HD3	1.45	0.78
18:b:18:LYS:O	18:b:29:ARG:NH2	2.16	0.78
1:2:1544:G:OP1	28:S:127:HIS:NE2	2.15	0.77
1:2:927:U:OP1	17:a:19:LYS:NZ	2.17	0.77
1:2:1166:G:OP1	22:F:103:GLY:HA3	1.83	0.77
1:2:1341:C:H4'	35:g:103:ARG:HH12	1.50	0.77
14:W:22:LYS:HE2	18:b:3:LEU:HD13	1.66	0.77
1:2:824:U:H2'	1:2:825:U:H6	1.47	0.77
12:O:47:LYS:HD2	12:O:62:LEU:HB3	1.66	0.77
1:2:869:C:O2	18:b:51:GLN:NE2	2.17	0.77
14:W:65:LEU:HG	14:W:67:GLY:H	1.50	0.77
1:2:1392:G:OP1	35:g:292:GLN:NE2	2.18	0.77
4:C:162:LYS:HE2	14:W:95:PRO:HA	1.64	0.77
1:2:886:A:N6	1:2:924:G:H1	1.83	0.76
41:l:160:ILE:HD13	41:l:230:ILE:HD13	1.67	0.76
1:2:1586:G:H1	1:2:1606:U:H3	1.31	0.76
1:2:1677:G:H21	1:2:1720:A:H62	0.78	0.76
7:H:89:HIS:HB3	7:H:165:LYS:HE3	1.67	0.76
40:k:377:ILE:HA	40:k:400:THR:HG22	1.66	0.76
1:2:1345:A:OP2	1:2:1347:A:N6	2.18	0.76
1:2:983:G:H2'	1:2:984:G:H8	1.50	0.76
7:H:139:ARG:HB2	7:H:151:LYS:HB2	1.68	0.76
3:B:3:VAL:HB	39:j:89:ARG:NH2	2.00	0.76
26:Q:94:GLN:HG2	26:Q:99:GLU:HG3	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:536:G:H2'	9:J:171:ARG:HH21	1.51	0.76
39:j:198:ILE:HG22	39:j:202:LYS:HE3	1.67	0.76
23:K:38:LYS:HB2	23:K:41:PHE:CE2	2.20	0.76
1:2:923:A:H2'	1:2:924:G:C8	2.20	0.75
8:I:39:GLY:HA2	8:I:61:GLU:HB3	1.68	0.75
25:P:125:PRO:HB2	25:P:127:ARG:HH22	1.50	0.75
7:H:56:LYS:NZ	7:H:57:ALA:O	2.19	0.75
38:1:53:G:H2'	38:1:54:A:H8	1.52	0.75
1:2:1085:A:H2'	1:2:1086:A:C8	2.21	0.75
12:O:131:GLY:O	17:a:22:ARG:NH2	2.20	0.75
21:D:28:GLU:HG2	23:K:58:GLN:HG2	1.69	0.75
40:k:148:TYR:HB3	40:k:183:TYR:HB3	1.67	0.75
1:2:1531:C:OP2	31:Z:77:ARG:NH2	2.20	0.75
13:V:14:PRO:HG2	13:V:23:ILE:HD11	1.68	0.75
1:2:533:A:H3'	1:2:534:A:H8	1.51	0.75
10:L:91:LEU:HD12	10:L:100:TYR:HB3	1.68	0.75
24:M:25:LEU:HD13	24:M:92:ALA:HA	1.66	0.75
3:B:5:LYS:NZ	3:B:7:LYS:HA	2.02	0.74
23:K:32:HIS:N	23:K:37:THR:O	2.19	0.74
39:j:8:PHE:CE1	39:j:109:HIS:HB2	2.22	0.74
21:D:202:LEU:O	27:R:42:GLN:NE2	2.21	0.74
1:2:1053:U:H2'	1:2:1054:U:C6	2.22	0.74
1:2:1611:U:H5''	22:F:171:ASN:HD21	1.50	0.74
26:Q:39:VAL:O	26:Q:45:ARG:NH1	2.21	0.74
25:P:60:LEU:HD12	25:P:92:SER:HB3	1.67	0.74
1:2:1469:A:OP1	22:F:187:ARG:NH2	2.19	0.74
1:2:1486:G:H3'	1:2:1513:A:H61	1.52	0.74
15:X:103:LEU:HB2	15:X:126:LYS:HB2	1.69	0.74
35:g:134:VAL:HB	35:g:143:TYR:HB2	1.70	0.74
1:2:1164:G:H4'	22:F:101:MET:HE1	1.67	0.74
1:2:1198:G:H22	33:d:31:ILE:HD13	1.53	0.74
3:B:3:VAL:HB	39:j:89:ARG:HH21	1.51	0.74
1:2:345:G:H4'	10:L:80:MET:HE1	1.68	0.73
14:W:53:ILE:HB	14:W:60:LYS:HB2	1.70	0.73
24:M:66:LYS:HZ1	34:f:111:GLU:HA	1.53	0.73
1:2:13:C:O2'	1:2:1298:G:N2	2.20	0.73
40:k:320:SER:HB3	40:k:412:LEU:HB2	1.69	0.73
3:B:3:VAL:HG11	39:j:89:ARG:HB3	1.70	0.73
1:2:1034:G:OP2	11:N:9:LYS:NZ	2.20	0.73
2:A:41:ARG:HH21	27:R:124:VAL:HG11	1.54	0.73
1:2:396:A:H4'	8:I:50:GLY:HA2	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:620:A:O2'	1:2:1105:U:O2'	2.05	0.73
1:2:339:U:H2'	1:2:340:A:H8	1.52	0.73
1:2:1679:A:N6	1:2:1718:G:O2'	2.21	0.73
21:D:51:ARG:HB3	21:D:91:VAL:HG22	1.71	0.73
28:S:4:VAL:HG22	28:S:6:GLN:H	1.54	0.73
22:F:150:ARG:HH22	22:F:158:ARG:N	1.85	0.73
30:U:68:ARG:HH12	30:U:77:LYS:HA	1.53	0.72
1:2:151:U:O2	6:G:4:ASN:ND2	2.23	0.72
1:2:780:A:N7	16:Y:8:ARG:NH1	2.37	0.72
12:O:133:ARG:HB2	12:O:136:ARG:HH21	1.53	0.72
1:2:774:A:N6	1:2:785:C:O2	2.22	0.72
26:Q:143:ARG:NH1	38:1:35:A:OP1	2.23	0.72
1:2:1233:A:O2'	34:f:138:TYR:OH	2.06	0.72
1:2:1471:U:C4	22:F:105:ASN:ND2	2.56	0.72
3:B:34:ALA:HB3	3:B:41:ARG:HA	1.72	0.72
14:W:25:VAL:HG22	14:W:63:VAL:HG22	1.70	0.72
31:Z:71:LEU:HD13	31:Z:76:ALA:HA	1.71	0.72
1:2:761:G:N2	1:2:762:A:N7	2.38	0.72
2:A:154:GLU:N	2:A:154:GLU:OE2	2.21	0.72
1:2:566:A:OP1	15:X:70:LYS:NZ	2.23	0.72
1:2:1675:C:OP1	8:I:42:ARG:NH1	2.23	0.72
1:2:297:C:H5''	5:E:38:LEU:HD22	1.71	0.72
1:2:925:A:OP1	1:2:1015:C:O2'	2.08	0.72
1:2:862:A:OP1	14:W:57:ARG:NH1	2.23	0.72
1:2:1434:A:OP2	21:D:27:ARG:NH2	2.21	0.72
30:U:98:HIS:HB2	30:U:102:ARG:HH12	1.52	0.72
41:l:186:ARG:NH1	41:l:244:THR:O	2.19	0.72
1:2:824:U:H2'	1:2:825:U:C6	2.25	0.72
1:2:925:A:H2'	1:2:926:C:C6	2.24	0.72
1:2:1592:G:OP2	1:2:1594:C:N4	2.23	0.72
1:2:592:U:H4'	1:2:594:G:H4'	1.72	0.71
1:2:906:A:N3	1:2:996:G:O2'	2.22	0.71
1:2:1674:U:OP1	8:I:44:HIS:ND1	2.21	0.71
14:W:90:THR:HG23	14:W:94:LEU:HD12	1.69	0.71
16:Y:12:VAL:HG12	16:Y:23:PHE:HB3	1.71	0.71
22:F:27:LEU:HD23	22:F:30:THR:HA	1.70	0.71
30:U:17:VAL:HA	30:U:96:PRO:HB3	1.71	0.71
42:m:41:THR:OG1	42:m:79:GLN:OE1	2.06	0.71
1:2:1114:U:H2'	1:2:1115:A:H8	1.55	0.71
1:2:1357:G:H1'	29:T:129:LEU:HD22	1.72	0.71
1:2:1472:G:H2'	1:2:1473:A:H8	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:16:LEU:HD21	2:A:172:LEU:HD11	1.72	0.71
30:U:68:ARG:HH22	30:U:77:LYS:HD2	1.55	0.71
38:l:56:C:H41	39:j:114:TYR:HA	1.54	0.71
9:J:41:GLU:N	9:J:41:GLU:OE2	2.21	0.71
1:2:398:A:H4'	5:E:3:ARG:HB2	1.73	0.71
1:2:1164:G:H5''	22:F:101:MET:HE2	1.71	0.71
40:k:237:GLU:HB3	40:k:274:ILE:HD12	1.71	0.71
1:2:342:C:H2'	1:2:343:A:H8	1.56	0.71
1:2:1212:G:O2'	1:2:1243:A:N6	2.23	0.71
1:2:1254:G:N7	24:M:39:ARG:NH1	2.38	0.71
1:2:1386:A:OP2	27:R:32:LYS:NZ	2.23	0.71
22:F:31:ILE:HD11	22:F:36:GLN:HB3	1.71	0.71
1:2:205:A:OP1	5:E:133:LYS:NZ	2.20	0.71
14:W:22:LYS:HZ1	18:b:3:LEU:HD22	1.56	0.71
1:2:1170:A:H2'	1:2:1171:G:C8	2.26	0.71
1:2:1170:A:H2'	1:2:1171:G:H8	1.55	0.71
5:E:7:LYS:HA	5:E:30:ARG:HH21	1.56	0.71
35:g:13:THR:HG22	35:g:318:ARG:HG3	1.72	0.71
40:k:373:ILE:HD13	40:k:406:LEU:HD11	1.72	0.71
1:2:1241:A:OP1	25:P:59:LYS:NZ	2.24	0.71
13:V:17:CYS:HG	13:V:20:THR:HG1	1.38	0.71
26:Q:40:GLN:O	26:Q:42:GLU:N	2.22	0.71
1:2:811:A:O2'	11:N:76:LYS:NZ	2.23	0.71
1:2:1114:U:H5''	20:h:10:THR:HG21	1.73	0.70
1:2:1498:C:OP1	29:T:122:ARG:NH2	2.24	0.70
3:B:82:ARG:NH2	3:B:103:MET:HG2	2.06	0.70
7:H:156:SER:HA	7:H:185:ILE:HD11	1.71	0.70
35:g:32:ASN:HA	35:g:48:LEU:HB2	1.73	0.70
2:A:121:VAL:HG23	2:A:141:ILE:HG21	1.73	0.70
9:J:27:GLU:HG3	9:J:39:LYS:HD3	1.74	0.70
39:j:174:SER:O	39:j:178:THR:OG1	2.07	0.70
1:2:339:U:H2'	1:2:340:A:C8	2.26	0.70
1:2:917:U:H2'	1:2:918:A:C8	2.25	0.70
29:T:21:PHE:O	29:T:24:ARG:N	2.19	0.70
30:U:28:SER:HB3	30:U:34:LEU:HD12	1.73	0.70
38:l:33:U:N3	38:l:36:U:OP2	2.25	0.70
1:2:328:G:H2'	1:2:329:G:H8	1.55	0.70
1:2:1480:C:H5	1:2:1523:A:H62	1.39	0.70
8:I:137:SER:O	8:I:140:THR:OG1	2.08	0.70
1:2:1044:C:H2'	1:2:1045:G:H8	1.56	0.70
2:A:30:GLN:HE21	2:A:46:ASN:HD22	1.40	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:O:127:ARG:HH11	17:a:22:ARG:NH1	1.90	0.70
1:2:1198:G:N3	33:d:40:ARG:NH2	2.39	0.70
23:K:15:LEU:HD23	23:K:21:LEU:HD13	1.74	0.70
28:S:41:ARG:HD3	29:T:38:LYS:HZ1	1.56	0.70
39:j:46:ILE:HD13	39:j:87:LYS:HZ2	1.57	0.70
18:b:73:LEU:HG	18:b:75:GLU:H	1.57	0.69
40:k:213:ALA:HB1	40:k:302:ILE:HD13	1.73	0.69
1:2:932:A:OP2	17:a:37:LYS:NZ	2.23	0.69
1:2:1045:G:OP1	3:B:157:GLN:NE2	2.25	0.69
6:G:76:LEU:HD11	6:G:92:ARG:HB3	1.73	0.69
1:2:511:A:H5''	9:J:163:PRO:HG2	1.74	0.69
1:2:642:G:O6	1:2:692:C:N4	2.25	0.69
7:H:139:ARG:HH12	14:W:53:ILE:HA	1.58	0.69
1:2:521:U:O2'	16:Y:60:PHE:O	2.10	0.69
1:2:550:G:H2'	1:2:551:G:C8	2.26	0.69
10:L:10:GLU:OE2	10:L:14:GLN:NE2	2.25	0.69
1:2:90:C:H2'	1:2:91:G:C8	2.26	0.69
1:2:1033:C:HO2'	14:W:2:THR:N	1.91	0.69
28:S:112:ASP:OD1	28:S:115:ARG:NH2	2.26	0.69
1:2:1381:G:O5'	30:U:89:ARG:NH2	2.26	0.69
7:H:139:ARG:NH2	14:W:53:ILE:HD13	2.06	0.69
10:L:92:HIS:HB3	10:L:101:GLU:HB3	1.73	0.69
35:g:267:ILE:HB	35:g:281:LEU:HB2	1.75	0.69
42:m:89:CYS:HA	42:m:92:MET:SD	2.33	0.69
1:2:153:G:OP1	6:G:2:LYS:NZ	2.25	0.69
1:2:790:A:H2'	1:2:791:U:C6	2.27	0.69
1:2:863:U:O2	18:b:22:LYS:NZ	2.23	0.69
1:2:1671:G:OP1	6:G:94:ARG:NH2	2.25	0.69
3:B:82:ARG:HH22	3:B:103:MET:HG2	1.55	0.69
5:E:11:ARG:NH1	5:E:21:ASP:OD1	2.26	0.69
8:I:104:ILE:HB	8:I:166:LEU:HB2	1.72	0.69
27:R:101:ASN:HA	27:R:120:SER:HB3	1.74	0.69
35:g:153:THR:HG23	35:g:178:GLY:HA2	1.75	0.69
39:j:101:LYS:HA	39:j:104:LYS:HE2	1.73	0.69
1:2:1628:U:HO2'	1:2:1762:C:HO2'	1.41	0.69
36:i:33:GLN:OE1	36:i:33:GLN:N	2.26	0.69
1:2:1644:C:O2	36:i:46:ARG:NH2	2.26	0.69
2:A:119:ARG:NH2	4:C:245:MET:O	2.26	0.69
12:O:135:ARG:HD3	12:O:137:LEU:HD23	1.75	0.69
22:F:105:ASN:O	22:F:108:LYS:CG	2.40	0.69
24:M:33:GLY:HA2	24:M:115:LYS:HE2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:S:126:ARG:HE	28:S:131:LEU:HB2	1.56	0.69
39:j:189:GLU:HB3	39:j:265:THR:HG23	1.75	0.69
1:2:1487:U:OP2	1:2:1513:A:N6	2.25	0.68
1:2:447:C:OP1	5:E:49:ARG:NH2	2.26	0.68
13:V:55:LEU:HD11	13:V:69:LEU:HD21	1.75	0.68
24:M:129:GLU:HA	24:M:133:GLN:HB3	1.74	0.68
30:U:97:ALA:O	30:U:101:LYS:N	2.25	0.68
35:g:308:LEU:HB2	35:g:320:TRP:HB2	1.75	0.68
1:2:1145:G:O2'	4:C:96:ARG:NH2	2.26	0.68
7:H:139:ARG:HH22	14:W:53:ILE:HA	1.56	0.68
35:g:289:THR:H	35:g:292:GLN:HE22	1.39	0.68
1:2:142:G:OP1	6:G:139:ASN:ND2	2.26	0.68
1:2:747:C:O3'	14:W:80:ASN:ND2	2.27	0.68
8:I:84:HIS:HD2	8:I:87:ASN:H	1.41	0.68
29:T:88:VAL:HB	29:T:89:ARG:HH12	1.59	0.68
32:c:29:ARG:HG2	32:c:41:VAL:HG22	1.76	0.68
36:i:41:MET:HG2	36:i:47:VAL:HG23	1.76	0.68
39:j:129:THR:HG23	39:j:130:ILE:HG13	1.73	0.68
1:2:204:U:H2'	1:2:205:A:H8	1.59	0.68
1:2:477:A:N1	1:2:509:G:O6	2.26	0.68
8:I:32:GLN:O	8:I:56:ARG:NH2	2.23	0.68
12:O:60:ALA:HB1	12:O:101:ALA:HB2	1.75	0.68
14:W:28:ARG:HB3	14:W:29:PRO:HD3	1.75	0.68
1:2:1551:G:N2	1:2:1554:A:OP2	2.27	0.68
1:2:1782:C:H2'	1:2:1783:U:C6	2.29	0.68
26:Q:28:LEU:O	26:Q:65:ILE:N	2.26	0.68
26:Q:34:SER:HB2	26:Q:38:LEU:HD23	1.75	0.68
26:Q:50:GLU:OE1	26:Q:82:ARG:NH1	2.27	0.68
3:B:3:VAL:CG2	39:j:89:ARG:HH21	2.07	0.68
35:g:115:ALA:HB1	35:g:157:VAL:HG13	1.76	0.68
1:2:1145:G:H2'	1:2:1146:A:C8	2.29	0.68
14:W:115:GLU:HG2	14:W:118:ARG:HH12	1.59	0.68
23:K:10:LYS:HZ1	23:K:14:HIS:HB2	1.58	0.68
1:2:952:G:H2'	1:2:953:G:C8	2.28	0.68
1:2:1481:A:H2'	1:2:1482:G:C8	2.28	0.68
3:B:74:GLN:HE21	3:B:189:ILE:HG21	1.58	0.68
5:E:6:LYS:O	5:E:30:ARG:NH2	2.26	0.68
22:F:115:ILE:HD13	22:F:192:ILE:HD13	1.74	0.68
14:W:50:PHE:HB2	14:W:63:VAL:HG12	1.74	0.68
1:2:894:G:N1	1:2:917:U:C4	2.62	0.67
6:G:32:ILE:HA	6:G:52:ILE:HG23	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:95:ILE:HD11	40:k:187:ARG:HA	1.75	0.67
1:2:387:G:OP2	1:2:422:G:O2'	2.13	0.67
1:2:1346:U:OP2	30:U:23:ARG:NH2	2.27	0.67
5:E:212:ASP:OD1	5:E:216:ASN:N	2.20	0.67
8:I:103:GLN:HA	8:I:166:LEU:O	1.93	0.67
12:O:112:ILE:HD13	17:a:53:LEU:HD12	1.77	0.67
25:P:70:ASN:OD1	25:P:71:GLU:N	2.27	0.67
1:2:760:A:N1	1:2:789:U:C4	2.63	0.67
1:2:1773:U:H3	1:2:1784:G:H1	1.43	0.67
6:G:21:GLU:OE2	6:G:22:HIS:ND1	2.27	0.67
29:T:49:ASP:OD1	29:T:53:TRP:N	2.27	0.67
1:2:186:G:O2'	1:2:187:A:N7	2.26	0.67
1:2:512:U:H2'	1:2:513:G:C8	2.30	0.67
1:2:1788:A:H2'	1:2:1789:A:C8	2.29	0.67
3:B:3:VAL:CB	39:j:89:ARG:HE	2.07	0.67
3:B:3:VAL:HB	39:j:89:ARG:NE	2.08	0.67
22:F:176:LEU:HD21	22:F:215:LYS:HB2	1.76	0.67
28:S:122:HIS:HA	28:S:125:ILE:HD12	1.76	0.67
36:i:67:LYS:HD2	37:3:33:C:H4'	1.76	0.67
1:2:1297:U:O2	4:C:214:ASN:ND2	2.27	0.67
38:1:10:2MG:HM23	38:1:11:C:H1'	1.77	0.67
40:k:282:PRO:O	40:k:290:ASN:ND2	2.27	0.67
1:2:140:A:H8	6:G:179:VAL:HG22	1.60	0.67
1:2:249:C:H2'	1:2:250:A:H8	1.58	0.67
1:2:928:A:H3'	1:2:930:C:H41	1.59	0.67
1:2:589:C:H5'	19:e:56:MET:HE1	1.77	0.67
1:2:1007:G:OP1	12:O:135:ARG:NH2	2.28	0.67
4:C:162:LYS:HA	4:C:174:LEU:O	1.95	0.67
38:1:16:H2U:H2'	38:1:60:A:H1'	1.77	0.67
1:2:883:A:H2'	1:2:884:G:C8	2.30	0.67
1:2:1472:G:H2'	1:2:1473:A:C8	2.30	0.67
1:2:1607:U:O2	22:F:109:LYS:NZ	2.28	0.67
10:L:101:GLU:OE2	15:X:13:ARG:NH1	2.28	0.67
14:W:23:ARG:HH21	14:W:66:ASN:HA	1.60	0.67
39:j:136:ARG:O	39:j:136:ARG:NE	2.25	0.67
1:2:870:G:H2'	1:2:871:G:C8	2.30	0.67
5:E:45:ILE:HD11	5:E:80:THR:HB	1.77	0.67
9:J:59:LEU:HD21	9:J:69:ARG:HG3	1.77	0.67
24:M:49:GLU:HB2	24:M:115:LYS:HG3	1.77	0.67
3:B:3:VAL:CB	39:j:89:ARG:HH21	2.08	0.66
22:F:102:ASN:HD22	22:F:102:ASN:N	1.92	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:917:U:OP1	12:O:84:ARG:NH1	2.28	0.66
2:A:210:ILE:HG12	27:R:81:LYS:HE2	1.78	0.66
3:B:144:ARG:HB2	3:B:208:GLN:HB3	1.76	0.66
21:D:221:SER:OG	35:g:200:ILE:O	2.12	0.66
1:2:1201:A:N6	1:2:1455:C:OP1	2.29	0.66
5:E:55:ALA:HB1	5:E:60:GLU:HG3	1.76	0.66
11:N:83:GLU:HG2	11:N:84:ILE:HG12	1.77	0.66
25:P:85:ILE:HG22	25:P:112:VAL:HG12	1.76	0.66
1:2:1428:U:H1'	30:U:72:ASN:HD22	1.60	0.66
7:H:41:LEU:HD23	7:H:70:TYR:HE1	1.60	0.66
16:Y:123:LYS:O	16:Y:127:LYS:NZ	2.29	0.66
26:Q:99:GLU:OE1	35:g:60:ARG:HA	1.95	0.66
29:T:14:PHE:HA	29:T:139:THR:HG21	1.77	0.66
1:2:786:G:OP1	5:E:255:ARG:NH2	2.27	0.66
1:2:1581:A:OP1	26:Q:135:ARG:NH2	2.28	0.66
21:D:76:ARG:HG3	21:D:77:PHE:CD1	2.31	0.66
1:2:445:A:H5''	5:E:57:ASN:HD22	1.59	0.66
3:B:3:VAL:HB	39:j:89:ARG:HE	1.58	0.66
17:a:44:ILE:HG23	17:a:45:VAL:HG23	1.77	0.66
22:F:137:ASP:OD1	22:F:141:ASN:ND2	2.27	0.66
1:2:165:C:O2'	6:G:133:LEU:O	2.11	0.66
1:2:798:A:O3'	5:E:201:HIS:NE2	2.28	0.66
1:2:1194:C:N4	26:Q:143:ARG:O	2.29	0.66
1:2:1216:A:OP1	23:K:1:MET:N	2.27	0.66
1:2:1319:U:O2'	1:2:1321:A:OP1	2.12	0.66
40:k:217:LEU:HB3	40:k:249:ASN:HD21	1.58	0.66
1:2:1282:U:H3'	1:2:1283:C:H2'	1.78	0.66
1:2:1466:U:H1'	29:T:88:VAL:HG13	1.77	0.66
24:M:56:VAL:HG11	24:M:85:ALA:HB2	1.78	0.66
38:1:14:A:H2'	38:1:15:G:C4	2.30	0.66
1:2:291:U:H2'	1:2:292:U:C6	2.30	0.66
1:2:1069:C:H5''	18:b:17:ARG:HH21	1.61	0.66
30:U:68:ARG:HA	30:U:79:TRP:CD1	2.31	0.66
35:g:34:LEU:HD22	35:g:46:TRP:CE3	2.31	0.66
35:g:45:SER:O	35:g:59:VAL:N	2.25	0.66
40:k:129:LYS:O	40:k:131:GLU:N	2.29	0.66
1:2:1209:C:H2'	1:2:1210:A:H8	1.61	0.66
9:J:153:GLU:OE1	9:J:153:GLU:N	2.28	0.66
32:c:19:THR:HG22	32:c:20:GLY:H	1.60	0.66
1:2:103:A:H4'	1:2:105:A:C8	2.32	0.65
1:2:703:G:H3'	1:2:704:C:H3'	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1322:C:H2'	1:2:1323:G:C8	2.32	0.65
1:2:1336:A:O5'	26:Q:123:ARG:NH1	2.29	0.65
6:G:58:LYS:NZ	6:G:104:PRO:O	2.28	0.65
25:P:90:ILE:HD13	25:P:109:PRO:HA	1.78	0.65
1:2:99:C:OP2	1:2:377:A:O2'	2.13	0.65
1:2:107:C:H2'	1:2:108:A:H8	1.61	0.65
1:2:1584:A:H62	1:2:1608:G:H21	1.43	0.65
29:T:37:VAL:HG12	29:T:39:THR:H	1.61	0.65
1:2:1135:U:O4	15:X:112:LYS:NZ	2.30	0.65
1:2:1333:U:H4'	33:d:55:TYR:HD2	1.62	0.65
4:C:59:GLU:OE1	4:C:59:GLU:N	2.26	0.65
5:E:185:GLY:N	5:E:224:ASN:OD1	2.30	0.65
35:g:17:HIS:HE2	35:g:46:TRP:HH2	1.45	0.65
1:2:152:G:H2'	1:2:153:G:H8	1.61	0.65
28:S:17:LEU:HD11	28:S:66:LEU:HD22	1.79	0.65
33:d:3:HIS:HB3	33:d:6:VAL:HB	1.78	0.65
3:B:126:THR:HG22	3:B:136:ARG:HG3	1.78	0.65
6:G:58:LYS:HA	6:G:107:ALA:HB2	1.77	0.65
33:d:29:GLY:HA2	33:d:40:ARG:HH21	1.61	0.65
1:2:1543:A:H3'	28:S:134:ARG:HH21	1.62	0.65
16:Y:105:ARG:HG2	16:Y:108:ARG:HH21	1.61	0.65
26:Q:9:THR:HB	26:Q:87:LYS:HD3	1.77	0.65
35:g:176:SER:HB3	35:g:186:TRP:HE1	1.60	0.65
38:1:19:G:OP1	38:1:57:G:N2	2.30	0.65
1:2:10:G:O2'	4:C:92:GLN:OE1	2.15	0.65
1:2:1125:G:OP2	20:h:18:ARG:NH2	2.29	0.65
5:E:56:LEU:N	5:E:60:GLU:OE2	2.28	0.65
1:2:1201:A:HO2'	1:2:1205:U:H3	1.45	0.65
1:2:1391:C:H2'	1:2:1392:G:H8	1.61	0.65
1:2:1580:U:OP1	26:Q:135:ARG:NH1	2.30	0.65
10:L:30:LYS:HG3	10:L:31:THR:H	1.62	0.65
15:X:23:ARG:HG2	15:X:29:TYR:CD2	2.32	0.65
1:2:627:G:N1	1:2:969:A:OP2	2.23	0.65
1:2:1774:A:H2'	1:2:1775:G:H8	1.62	0.65
4:C:148:TYR:OH	4:C:153:LEU:O	2.04	0.65
12:O:43:THR:HG22	12:O:46:MET:HG2	1.77	0.65
22:F:78:ARG:HG2	26:Q:122:ARG:HD2	1.78	0.65
27:R:110:VAL:HG13	27:R:117:LEU:HD12	1.78	0.65
33:d:20:GLN:N	33:d:20:GLN:OE1	2.29	0.65
35:g:151:TRP:HB2	35:g:179:MET:HG2	1.79	0.65
1:2:1143:U:H2'	1:2:1144:U:C6	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:70:TYR:O	7:H:74:GLN:HB2	1.97	0.64
1:2:758:U:OP1	5:E:22:LYS:NZ	2.30	0.64
17:a:43:ASN:OD1	17:a:66:LYS:NZ	2.26	0.64
24:M:56:VAL:HG22	24:M:88:LEU:HD13	1.79	0.64
27:R:28:PHE:HA	27:R:55:THR:HG21	1.80	0.64
1:2:1500:G:O6	29:T:102:ARG:NH2	2.29	0.64
1:2:1774:A:H2'	1:2:1775:G:C8	2.32	0.64
2:A:33:GLN:NE2	13:V:64:GLU:OE2	2.29	0.64
2:A:104:PRO:HB3	2:A:131:GLN:HG2	1.78	0.64
4:C:99:GLN:N	4:C:99:GLN:OE1	2.30	0.64
35:g:93:TRP:HD1	35:g:100:SER:HA	1.61	0.64
35:g:147:GLY:HA3	35:g:184:ARG:HH12	1.62	0.64
36:i:82:ARG:NH2	36:i:85:GLN:OE1	2.30	0.64
1:2:705:U:H2'	1:2:706:A:H8	1.63	0.64
1:2:1590:A:H2'	1:2:1591:A:H8	1.62	0.64
1:2:1652:G:H22	1:2:1743:G:H2'	1.62	0.64
2:A:179:ARG:HH11	2:A:183:ARG:HD2	1.62	0.64
4:C:145:ARG:HB3	4:C:226:THR:HB	1.79	0.64
26:Q:136:SER:O	26:Q:137:ARG:NE	2.29	0.64
40:k:259:ALA:HB1	41:l:135:LEU:HD11	1.79	0.64
1:2:1190:B8N:N34	38:1:34:C:OP1	2.30	0.64
1:2:1413:U:OP1	27:R:45:ARG:NH2	2.28	0.64
1:2:1609:A:O3'	22:F:97:ASN:ND2	2.29	0.64
8:I:106:ALA:HB2	8:I:166:LEU:HG	1.80	0.64
1:2:216:A:H2'	1:2:217:A:H8	1.62	0.64
1:2:878:G:H2'	1:2:879:C:C6	2.32	0.64
6:G:68:LEU:H	6:G:100:ALA:HB3	1.61	0.64
9:J:142:ASN:ND2	16:Y:64:TYR:OH	2.29	0.64
28:S:130:GLY:O	28:S:145:ARG:NH1	2.31	0.64
39:j:198:ILE:HG13	40:k:404:PRO:HD3	1.80	0.64
1:2:19:A:H2'	1:2:20:G:H8	1.62	0.64
1:2:1317:G:H2'	1:2:1318:A:C8	2.32	0.64
1:2:1582:G:O2'	1:2:1608:G:O6	2.15	0.64
28:S:123:ARG:HD3	28:S:133:VAL:HG21	1.80	0.64
13:V:5:LYS:HB2	13:V:7:GLN:HE22	1.63	0.64
21:D:76:ARG:HG3	21:D:77:PHE:HD1	1.63	0.64
40:k:140:LEU:HD12	40:k:318:ILE:HD12	1.80	0.64
1:2:293:C:H2'	1:2:294:A:H8	1.62	0.64
1:2:751:G:H2'	1:2:752:A:H8	1.63	0.64
1:2:778:G:H1	16:Y:10:ARG:HD3	1.60	0.64
3:B:87:ARG:HB2	3:B:101:HIS:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:64:HIS:CE1	4:C:243:SER:HA	2.33	0.64
15:X:23:ARG:HG2	15:X:29:TYR:HD2	1.63	0.64
35:g:170:GLY:O	35:g:189:ASN:ND2	2.31	0.64
41:l:163:PRO:HB3	41:l:174:PHE:HZ	1.61	0.64
1:2:443:C:H6	16:Y:105:ARG:HH12	1.45	0.64
1:2:1653:A:N6	1:2:1743:G:O2'	2.26	0.64
3:B:201:THR:HG21	3:B:207:LEU:HD23	1.79	0.64
4:C:157:HIS:CG	4:C:179:ARG:HD2	2.33	0.64
23:K:64:TYR:HB3	23:K:66:TYR:CZ	2.33	0.64
1:2:27:U:H2'	1:2:28:A:H8	1.63	0.63
1:2:29:U:H2'	1:2:30:G:H8	1.62	0.63
1:2:383:G:H2'	1:2:384:A:C8	2.33	0.63
1:2:406:A:H2'	1:2:407:C:C6	2.33	0.63
1:2:811:A:H4'	1:2:812:U:H5''	1.80	0.63
1:2:1595:A:OP2	33:d:32:ARG:NH1	2.31	0.63
1:2:1773:U:P	20:h:11:ARG:HH12	2.22	0.63
3:B:3:VAL:HB	39:j:89:ARG:CZ	2.28	0.63
16:Y:8:ARG:HH12	16:Y:10:ARG:HH21	1.45	0.63
35:g:136:ASN:HD21	35:g:140:ASP:HB2	1.62	0.63
39:j:70:VAL:HG11	39:j:95:ILE:HG23	1.80	0.63
40:k:382:ALA:HB3	40:k:387:LEU:HD12	1.79	0.63
1:2:476:A:OP2	19:e:28:LYS:NZ	2.31	0.63
3:B:82:ARG:NH2	3:B:83:LYS:O	2.26	0.63
3:B:87:ARG:NH1	3:B:99:ASN:OD1	2.31	0.63
4:C:149:TRP:O	14:W:97:ARG:NH2	2.27	0.63
10:L:16:GLN:HE22	10:L:33:ARG:HA	1.63	0.63
40:k:251:VAL:HG21	40:k:282:PRO:HB3	1.80	0.63
1:2:748:U:O2'	14:W:122:SER:O	2.14	0.63
10:L:8:GLN:HE22	10:L:13:PHE:HA	1.63	0.63
38:1:42:U:H2'	38:1:43:G:C8	2.34	0.63
1:2:1641:U:H1'	1:2:1778:G:H21	1.64	0.63
7:H:96:ARG:HE	7:H:97:ARG:N	1.97	0.63
1:2:1165:A:OP1	22:F:102:ASN:N	2.29	0.63
1:2:1271:U:O2'	1:2:1274:A:OP2	2.15	0.63
1:2:1589:C:H2'	1:2:1590:A:C8	2.33	0.63
3:B:5:LYS:HZ1	3:B:7:LYS:HD2	1.63	0.63
10:L:127:GLN:HG2	10:L:137:PHE:HE1	1.63	0.63
11:N:19:SER:OG	11:N:21:ASN:OD1	2.16	0.63
1:2:194:G:O6	8:I:142:ARG:NH2	2.31	0.63
1:2:751:G:H2'	1:2:752:A:C8	2.33	0.63
1:2:773:C:OP1	5:E:22:LYS:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1309:U:O2'	1:2:1400:G:O2'	2.17	0.63
1:2:1352:U:O2	1:2:1370:G:N2	2.26	0.63
4:C:162:LYS:HG2	4:C:175:ILE:HA	1.80	0.63
7:H:138:LYS:O	7:H:139:ARG:NH1	2.31	0.63
23:K:37:THR:HB	23:K:41:PHE:HZ	1.63	0.63
1:2:563:G:N1	1:2:579:A:OP2	2.31	0.63
1:2:1144:U:H4'	4:C:93:LYS:HE3	1.81	0.63
1:2:1784:G:P	12:O:136:ARG:HH22	2.21	0.63
7:H:139:ARG:HH21	14:W:51:GLU:CD	2.07	0.63
23:K:38:LYS:HB2	23:K:41:PHE:HE2	1.63	0.63
28:S:3:LEU:HB3	31:Z:82:HIS:ND1	2.13	0.63
25:P:27:GLU:N	25:P:27:GLU:OE2	2.32	0.63
42:m:59:LYS:HZ2	42:m:65:ASN:HA	1.64	0.63
1:2:433:G:N2	1:2:435:A:H3'	2.14	0.63
28:S:87:ASN:HB3	28:S:100:SER:H	1.62	0.63
39:j:244:LEU:HD13	39:j:268:PRO:HB3	1.81	0.63
42:m:51:LEU:HA	42:m:54:ILE:HD12	1.81	0.63
1:2:788:A:C2	1:2:789:U:H1'	2.34	0.62
2:A:183:ARG:NH2	2:A:193:GLN:O	2.32	0.62
23:K:10:LYS:NZ	23:K:14:HIS:HB2	2.14	0.62
1:2:1464:G:OP1	26:Q:132:ARG:NH1	2.32	0.62
1:2:1736:U:H2'	1:2:1737:C:C6	2.34	0.62
12:O:114:ARG:HD3	17:a:62:TYR:HE1	1.65	0.62
23:K:61:TRP:NE1	33:d:23:ILE:HG23	2.14	0.62
26:Q:16:ALA:HB2	26:Q:72:GLY:HA3	1.81	0.62
40:k:476:VAL:HB	40:k:484:ARG:HG3	1.80	0.62
1:2:77:U:H1'	6:G:159:ARG:HH22	1.65	0.62
1:2:208:U:O2'	8:I:181:ASP:OD1	2.12	0.62
1:2:810:A:C5	7:H:110:GLN:HG2	2.33	0.62
6:G:138:ALA:HA	6:G:141:ILE:HD12	1.81	0.62
8:I:87:ASN:HB3	8:I:89:GLU:HG3	1.80	0.62
9:J:163:PRO:O	9:J:165:GLY:N	2.32	0.62
15:X:54:LEU:HD22	15:X:73:ARG:HH12	1.63	0.62
21:D:46:THR:HB	21:D:84:ILE:HG12	1.80	0.62
26:Q:73:GLY:N	26:Q:76:SER:OG	2.33	0.62
40:k:313:PRO:HA	40:k:345:GLY:HA3	1.80	0.62
1:2:487:G:N1	1:2:488:C:O2	2.32	0.62
1:2:649:U:O2'	1:2:650:G:OP1	2.15	0.62
1:2:1431:G:H2'	1:2:1432:U:C6	2.34	0.62
1:2:1523:A:N3	1:2:1587:C:O2'	2.31	0.62
2:A:26:ALA:HB2	2:A:48:ILE:HD11	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:38:VAL:HG23	10:L:66:ILE:HD13	1.81	0.62
26:Q:83:GLN:NE2	26:Q:117:LEU:O	2.32	0.62
30:U:63:LEU:O	30:U:83:GLU:HA	2.00	0.62
1:2:694:U:O3'	7:H:97:ARG:NH1	2.32	0.62
6:G:58:LYS:NZ	6:G:106:LEU:O	2.32	0.62
7:H:144:VAL:HA	14:W:42:GLN:HE22	1.64	0.62
7:H:166:LEU:HB2	7:H:183:PHE:HD2	1.63	0.62
27:R:24:LEU:O	35:g:223:LYS:NZ	2.28	0.62
36:i:59:ALA:HA	36:i:89:CYS:O	2.00	0.62
1:2:1295:A:OP1	2:A:138:TYR:OH	2.15	0.62
6:G:32:ILE:HD11	6:G:63:MET:HG2	1.81	0.62
12:O:127:ARG:NH1	12:O:127:ARG:HB3	2.15	0.62
16:Y:68:LYS:NZ	16:Y:69:SER:O	2.27	0.62
18:b:23:THR:OG1	18:b:25:VAL:O	2.18	0.62
22:F:162:VAL:HB	32:c:45:LYS:CE	2.19	0.62
32:c:25:VAL:HG12	32:c:45:LYS:HG3	1.81	0.62
42:m:85:ARG:NH1	42:m:106:HIS:O	2.32	0.62
1:2:292:U:H2'	1:2:293:C:C6	2.35	0.62
6:G:50:PHE:HB3	6:G:111:LEU:HD11	1.80	0.62
9:J:108:ARG:HH21	9:J:110:GLN:HE22	1.48	0.62
24:M:59:VAL:HG21	24:M:65:SER:HB3	1.80	0.62
5:E:180:LEU:HD13	5:E:231:PRO:HA	1.82	0.62
5:E:182:TYR:N	5:E:226:PHE:O	2.33	0.62
13:V:17:CYS:N	13:V:22:ARG:O	2.32	0.62
21:D:40:ARG:HB3	21:D:47:GLU:HB2	1.81	0.62
35:g:30:GLN:HE21	35:g:33:LEU:HD13	1.65	0.62
1:2:442:C:H3'	16:Y:105:ARG:HD2	1.81	0.62
1:2:1275:U:O5'	21:D:141:LYS:NZ	2.29	0.62
6:G:87:ARG:N	6:G:91:GLU:OE2	2.29	0.62
8:I:81:VAL:HA	8:I:102:VAL:HG12	1.81	0.62
19:e:41:THR:HA	19:e:45:VAL:HB	1.82	0.62
1:2:855:A:N6	7:H:96:ARG:HD2	2.14	0.62
3:B:133:TYR:HA	3:B:219:LYS:O	2.00	0.62
4:C:154:GLY:HA2	13:V:3:ASN:HD21	1.64	0.62
6:G:1:MET:N	6:G:18:ILE:O	2.30	0.62
34:f:131:ALA:HB3	34:f:138:TYR:HB3	1.80	0.62
39:j:15:GLU:HG3	39:j:18:ASP:HB3	1.81	0.62
40:k:243:HIS:HB3	40:k:302:ILE:HG12	1.82	0.62
42:m:84:GLN:HB3	42:m:87:LYS:HB2	1.82	0.62
1:2:520:A:H2'	1:2:521:U:C6	2.35	0.61
1:2:1293:G:H2'	1:2:1294:G:H8	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1335:A:O2'	26:Q:123:ARG:NH1	2.32	0.61
3:B:3:VAL:HG12	39:j:89:ARG:HE	1.64	0.61
1:2:249:C:H2'	1:2:250:A:C8	2.35	0.61
1:2:863:U:OP2	14:W:57:ARG:NH2	2.32	0.61
1:2:1477:A:OP1	29:T:57:ARG:NE	2.25	0.61
2:A:54:TRP:HA	2:A:57:ILE:HD12	1.82	0.61
28:S:88:ARG:HG2	28:S:91:ASP:HA	1.82	0.61
35:g:6:ILE:HG21	35:g:258:TRP:HH2	1.65	0.61
1:2:108:A:H2'	1:2:109:G:C8	2.35	0.61
1:2:1590:A:H2'	1:2:1591:A:C8	2.35	0.61
12:O:12:GLN:OE1	12:O:77:THR:OG1	2.14	0.61
17:a:40:ALA:N	17:a:69:ASN:O	2.33	0.61
27:R:18:GLU:HA	27:R:71:PHE:HB3	1.82	0.61
30:U:115:GLU:N	30:U:115:GLU:OE2	2.33	0.61
39:j:20:VAL:HB	39:j:36:LEU:HD11	1.81	0.61
1:2:58:U:O2'	1:2:450:A:N3	2.33	0.61
1:2:1086:A:H2'	1:2:1087:A:C8	2.36	0.61
1:2:1741:U:H2'	1:2:1742:A:C8	2.34	0.61
21:D:23:GLU:OE2	33:d:46:LYS:NZ	2.32	0.61
1:2:384:A:OP1	8:I:25:ARG:NH2	2.32	0.61
1:2:484:A:H2'	1:2:485:G:H8	1.65	0.61
1:2:1611:U:H5''	22:F:171:ASN:ND2	2.14	0.61
1:2:1682:U:O2	1:2:1715:G:N2	2.24	0.61
22:F:109:LYS:H	22:F:109:LYS:HD2	1.65	0.61
35:g:6:ILE:HG12	35:g:256:ARG:HH12	1.66	0.61
1:2:357:U:H2'	1:2:359:A:C8	2.34	0.61
1:2:846:A:H2'	1:2:847:C:C6	2.36	0.61
1:2:1067:C:H2'	1:2:1068:A:H8	1.66	0.61
1:2:1488:A:OP1	21:D:9:ARG:NH2	2.34	0.61
21:D:173:ARG:CZ	21:D:174:HIS:H	2.13	0.61
35:g:80:TYR:HB3	35:g:92:LEU:HD11	1.83	0.61
2:A:64:ILE:HD11	2:A:122:ILE:HD11	1.81	0.61
5:E:64:ILE:HD11	16:Y:18:LEU:HD12	1.82	0.61
9:J:125:ALA:HA	9:J:128:LEU:HD12	1.82	0.61
24:M:34:LEU:HB3	24:M:36:ARG:HG3	1.83	0.61
40:k:113:LYS:HG2	40:k:217:LEU:HD12	1.80	0.61
1:2:189:C:N4	1:2:195:G:O6	2.34	0.61
1:2:299:A:H2'	1:2:300:A:C8	2.35	0.61
1:2:1793:U:H3'	17:a:5:ARG:HH21	1.64	0.61
7:H:150:GLN:HB2	7:H:181:ILE:HG12	1.82	0.61
35:g:262:ALA:HB2	35:g:299:LEU:HD11	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1:76:A:O2'	46:k:602:MET:O	2.18	0.61
1:2:5:U:H2'	1:2:6:G:H8	1.66	0.61
1:2:52:U:H2'	1:2:53:G:H8	1.66	0.61
1:2:890:A:H2'	1:2:891:A:H8	1.66	0.61
1:2:1181:U:H3	1:2:1184:U:H5''	1.64	0.61
1:2:1685:U:N3	1:2:1712:A:N1	2.48	0.61
2:A:7:PHE:HE2	13:V:43:GLY:HA2	1.66	0.61
4:C:40:TRP:CD1	4:C:72:GLN:HE21	2.19	0.61
7:H:62:VAL:HG12	7:H:64:VAL:H	1.66	0.61
12:O:92:LYS:NZ	17:a:69:ASN:OD1	2.32	0.61
41:l:184:LEU:HD22	41:l:234:VAL:HG11	1.83	0.61
1:2:1164:G:C4'	22:F:101:MET:HE1	2.30	0.61
1:2:1439:C:O2'	1:2:1445:C:N4	2.33	0.61
3:B:26:ARG:O	3:B:50:LYS:N	2.32	0.61
24:M:84:ASP:O	24:M:88:LEU:N	2.27	0.61
24:M:96:LYS:O	24:M:104:ARG:NH1	2.34	0.61
35:g:15:GLU:N	35:g:15:GLU:OE2	2.33	0.61
1:2:477:A:OP1	19:e:33:ARG:NH1	2.27	0.60
1:2:590:A:H2'	1:2:591:G:C8	2.35	0.60
1:2:1626:U:H2'	1:2:1627:G:C8	2.36	0.60
35:g:296:ALA:HA	35:g:312:TYR:HA	1.82	0.60
40:k:357:PRO:HG2	40:k:415:GLN:HE21	1.65	0.60
1:2:803:A:C8	14:W:107:SER:HA	2.36	0.60
1:2:945:U:H4'	3:B:165:ARG:NH2	2.16	0.60
1:2:1649:A:H2'	1:2:1650:C:H6	1.67	0.60
6:G:8:PRO:HG2	6:G:9:ILE:HD12	1.82	0.60
27:R:44:LYS:HE2	27:R:47:ARG:HH22	1.64	0.60
41:l:184:LEU:HD13	41:l:234:VAL:HG21	1.83	0.60
1:2:1145:G:O3'	4:C:96:ARG:NH2	2.35	0.60
4:C:199:GLU:OE2	4:C:199:GLU:N	2.34	0.60
17:a:33:ASP:OD1	17:a:34:LYS:N	2.32	0.60
24:M:25:LEU:HD21	24:M:112:VAL:HG11	1.83	0.60
7:H:130:VAL:HG22	7:H:169:PHE:CD2	2.35	0.60
10:L:111:VAL:HG12	10:L:139:VAL:HG21	1.81	0.60
12:O:83:ILE:HD13	17:a:44:ILE:HD11	1.84	0.60
12:O:106:ALA:HB2	17:a:53:LEU:HD13	1.83	0.60
25:P:125:PRO:HG2	25:P:127:ARG:HH12	1.66	0.60
35:g:117:ASP:HB2	35:g:122:LYS:H	1.65	0.60
1:2:548:G:H1	1:2:588:C:H5	1.49	0.60
1:2:887:U:H2'	1:2:888:U:C6	2.36	0.60
1:2:1617:C:H2'	1:2:1618:C:H6	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:247:THR:HB	5:E:250:GLU:HG2	1.84	0.60
14:W:103:ILE:HD11	14:W:129:VAL:HG22	1.82	0.60
16:Y:35:VAL:HG23	16:Y:40:LEU:HD11	1.83	0.60
21:D:7:LYS:HA	21:D:10:LYS:HZ3	1.65	0.60
21:D:207:THR:OG1	27:R:40:THR:OG1	2.16	0.60
22:F:60:LEU:HD21	22:F:169:ARG:HH11	1.65	0.60
40:k:268:LYS:HA	40:k:271:ARG:HE	1.66	0.60
1:2:914:A:H5''	1:2:915:U:H5	1.66	0.60
1:2:1418:C:H3'	1:2:1419:A:H8	1.66	0.60
2:A:26:ALA:HB1	2:A:149:LEU:HB2	1.82	0.60
24:M:55:LEU:HB3	24:M:68:VAL:HG11	1.84	0.60
1:2:448:C:H4'	5:E:8:HIS:CD2	2.36	0.60
1:2:912:G:H5'	1:2:913:G:C8	2.37	0.60
1:2:1319:U:H2'	1:2:1321:A:H5'	1.84	0.60
1:2:1661:G:H1	1:2:1736:U:H3	1.50	0.60
7:H:85:PHE:HB3	7:H:88:ARG:HD3	1.84	0.60
8:I:90:LEU:HG	8:I:95:THR:HB	1.82	0.60
10:L:59:PRO:HG3	10:L:138:ASN:ND2	2.16	0.60
10:L:133:LYS:C	10:L:136:ARG:HH12	2.10	0.60
38:1:63:G:N2	38:1:64:RIA:O5'	2.28	0.60
1:2:930:C:H5'	3:B:114:VAL:HG22	1.84	0.60
1:2:1086:A:OP2	1:2:1086:A:H8	1.84	0.60
1:2:883:A:OP1	3:B:136:ARG:NH2	2.35	0.60
1:2:1448:U:HO2'	33:d:7:TRP:CD1	2.19	0.60
7:H:98:ILE:HG13	7:H:121:VAL:HG21	1.83	0.60
35:g:47:ARG:HG3	35:g:59:VAL:HG22	1.83	0.60
40:k:172:PRO:HD2	40:k:183:TYR:HB2	1.83	0.60
40:k:482:MET:SD	40:k:483:ALA:N	2.75	0.60
1:2:645:U:H2'	1:2:646:G:H8	1.66	0.60
1:2:1217:G:N2	1:2:1442:A:OP2	2.33	0.60
1:2:1353:G:O6	1:2:1368:U:O2	2.20	0.60
1:2:1752:A:N7	1:2:1753:A:N6	2.50	0.60
16:Y:89:TYR:CE2	16:Y:90:ARG:HG3	2.37	0.60
22:F:105:ASN:O	22:F:106:ASN:O	2.20	0.60
39:j:47:LEU:HD23	39:j:49:SER:H	1.66	0.60
41:l:207:GLY:O	41:l:210:ARG:NH1	2.33	0.60
1:2:1149:G:H3'	1:2:1766:G:H21	1.65	0.59
2:A:166:GLY:O	2:A:168:HIS:ND1	2.30	0.59
7:H:67:LEU:HG	7:H:71:HIS:CE1	2.37	0.59
37:3:28:A:O2'	38:1:37:T6A:ODA	2.13	0.59
39:j:6:CYS:SG	39:j:124:GLU:HA	2.42	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:m:26:ILE:HB	42:m:103:ILE:HG13	1.82	0.59
1:2:257:C:O4'	8:I:64:ASN:ND2	2.35	0.59
1:2:321:G:O3'	8:I:10:LYS:NZ	2.29	0.59
1:2:484:A:H2'	1:2:485:G:C8	2.37	0.59
1:2:523:U:O2'	1:2:526:A:N7	2.34	0.59
1:2:872:U:O2'	1:2:1046:G:OP1	2.20	0.59
1:2:1519:G:O2'	1:2:1521:G:OP2	2.19	0.59
1:2:1571:A:H4'	1:2:1572:G:O5'	2.02	0.59
1:2:1783:U:OP1	12:O:136:ARG:NH1	2.35	0.59
22:F:25:VAL:HG11	26:Q:57:LEU:HG	1.84	0.59
1:2:252:A:OP1	5:E:134:LYS:N	2.35	0.59
1:2:328:G:H2'	1:2:329:G:C8	2.37	0.59
1:2:1162:A:N3	1:2:1611:U:O2'	2.30	0.59
1:2:1545:A:O2'	28:S:89:GLN:N	2.36	0.59
1:2:127:G:O3'	1:2:177:U:N3	2.36	0.59
1:2:548:G:H2'	1:2:549:A:H8	1.66	0.59
1:2:1391:C:H5''	35:g:292:GLN:HG3	1.84	0.59
1:2:1557:A:O5'	28:S:135:GLY:HA3	2.03	0.59
3:B:193:ILE:O	3:B:197:ILE:HG12	2.02	0.59
1:2:29:U:O3'	15:X:126:LYS:NZ	2.32	0.59
1:2:324:G:H2'	1:2:325:G:H8	1.68	0.59
16:Y:38:ASP:OD1	16:Y:39:GLU:N	2.36	0.59
1:2:121:U:H2'	1:2:122:U:C6	2.37	0.59
1:2:445:A:H2'	1:2:446:U:H6	1.68	0.59
1:2:1416:G:H4'	26:Q:128:LYS:HE2	1.84	0.59
1:2:1476:G:H5'	29:T:57:ARG:HH21	1.67	0.59
1:2:1749:C:H2'	1:2:1750:U:C6	2.36	0.59
9:J:78:ARG:HA	9:J:81:VAL:HG22	1.84	0.59
1:2:353:C:H5''	8:I:16:ALA:HB2	1.84	0.59
1:2:380:C:H2'	1:2:381:C:H6	1.67	0.59
1:2:860:U:H4'	11:N:20:ARG:HH22	1.66	0.59
1:2:1009:C:H3'	1:2:1010:G:H8	1.68	0.59
9:J:108:ARG:HE	9:J:110:GLN:NE2	2.01	0.59
24:M:94:LEU:O	24:M:104:ARG:NE	2.33	0.59
35:g:171:ARG:HH11	35:g:187:SER:HB2	1.68	0.59
1:2:1362:U:H5''	1:2:1363:G:H8	1.68	0.59
1:2:1750:U:H2'	1:2:1751:A:C8	2.37	0.59
2:A:164:ASN:HA	2:A:170:ILE:HD11	1.84	0.59
6:G:6:SER:HB3	6:G:112:ILE:HG22	1.84	0.59
8:I:118:GLY:HA3	8:I:144:TRP:CZ3	2.38	0.59
22:F:180:GLY:HA2	22:F:211:TYR:HD2	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:W:11:LEU:HA	14:W:14:ILE:HD12	1.84	0.59
19:e:49:LEU:O	19:e:54:ARG:NH2	2.36	0.59
24:M:47:ARG:HG3	24:M:48:GLY:H	1.68	0.59
26:Q:52:LEU:HG	26:Q:60:PHE:HZ	1.68	0.59
1:2:1513:A:O2'	1:2:1514:A:OP1	2.16	0.59
7:H:99:LEU:HD23	7:H:112:ARG:HB2	1.85	0.59
25:P:86:VAL:HG12	25:P:89:MET:HE3	1.85	0.59
29:T:86:ARG:HB2	29:T:89:ARG:HB2	1.85	0.59
36:i:85:GLN:HB3	36:i:88:GLN:HB3	1.84	0.59
39:j:129:THR:OG1	39:j:159:GLU:O	2.19	0.59
1:2:19:A:H2'	1:2:20:G:C8	2.37	0.58
1:2:324:G:OP1	10:L:134:THR:OG1	2.11	0.58
1:2:331:U:O2'	8:I:5:ARG:NH1	2.36	0.58
1:2:445:A:H2'	1:2:446:U:C6	2.38	0.58
1:2:1367:G:H5''	29:T:69:LYS:HD3	1.84	0.58
1:2:1712:A:H2'	1:2:1713:G:C8	2.38	0.58
1:2:1757:C:O3'	42:m:81:GLN:NE2	2.36	0.58
2:A:167:LYS:HE2	2:A:204:TYR:HB3	1.85	0.58
3:B:197:ILE:HG21	3:B:210:VAL:HG21	1.85	0.58
13:V:31:SER:HA	13:V:55:LEU:O	2.03	0.58
15:X:76:LEU:HD12	15:X:81:LYS:HB2	1.85	0.58
35:g:50:GLU:OE1	35:g:50:GLU:N	2.36	0.58
35:g:84:ALA:HB2	35:g:114:VAL:HG23	1.84	0.58
39:j:22:VAL:O	39:j:68:ASN:HA	2.03	0.58
1:2:123:G:C6	1:2:294:A:C6	2.90	0.58
1:2:520:A:H2'	1:2:521:U:H6	1.68	0.58
1:2:553:C:N4	1:2:570:G:O6	2.37	0.58
1:2:687:C:OP1	14:W:119:LYS:NZ	2.31	0.58
1:2:1067:C:H2'	1:2:1068:A:C8	2.38	0.58
3:B:82:ARG:NE	3:B:104:ASP:O	2.36	0.58
16:Y:104:SER:HB2	16:Y:107:GLN:NE2	2.17	0.58
16:Y:105:ARG:HA	16:Y:108:ARG:HE	1.68	0.58
41:l:232:GLU:HG3	41:l:233:TYR:HD1	1.66	0.58
1:2:97:C:H2'	1:2:98:U:H6	1.69	0.58
1:2:1099:G:O2'	14:W:74:VAL:O	2.17	0.58
1:2:1168:G:N3	1:2:1573:7MG:HM72	2.18	0.58
1:2:1672:C:OP1	6:G:92:ARG:NH1	2.36	0.58
7:H:62:VAL:HG11	7:H:67:LEU:HD13	1.84	0.58
22:F:84:PHE:CZ	32:c:47:PRO:HB2	2.37	0.58
1:2:142:G:P	6:G:139:ASN:HD22	2.26	0.58
1:2:437:A:HI1'	1:2:464:G:H22	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:974:C:H5'	11:N:109:LYS:HE3	1.84	0.58
1:2:1145:G:H2'	1:2:1146:A:H8	1.68	0.58
1:2:1239:U:O3'	1:2:1240:G:N2	2.32	0.58
1:2:1404:A:H2'	1:2:1405:U:H6	1.69	0.58
1:2:1778:G:H2'	1:2:1779:A:C8	2.39	0.58
27:R:32:LYS:HG3	27:R:47:ARG:HD3	1.85	0.58
35:g:20:TRP:CE3	35:g:39:ARG:HD2	2.39	0.58
1:2:327:A:H2'	1:2:328:G:H8	1.69	0.58
1:2:716:C:N4	1:2:722:G:O6	2.37	0.58
1:2:1413:U:H2'	1:2:1414:G:H8	1.68	0.58
3:B:127:VAL:HG21	3:B:176:VAL:HG11	1.85	0.58
21:D:101:GLN:O	21:D:105:MET:HG2	2.04	0.58
40:k:365:LYS:O	40:k:367:LYS:NZ	2.36	0.58
1:2:843:A:H2'	1:2:844:G:C8	2.38	0.58
1:2:1195:A:H4'	1:2:1196:C:H5''	1.85	0.58
1:2:1219:C:H2'	1:2:1220:A:H8	1.68	0.58
1:2:1240:G:OP1	25:P:77:ARG:NE	2.36	0.58
3:B:118:GLN:NE2	3:B:119:THR:O	2.36	0.58
32:c:44:VAL:C	32:c:45:LYS:HD3	2.28	0.58
35:g:20:TRP:HB2	35:g:39:ARG:HG3	1.85	0.58
36:i:62:ARG:HD3	36:i:63:GLY:O	2.04	0.58
1:2:569:A:N6	15:X:116:ASP:OD1	2.34	0.58
1:2:576:G:H21	36:i:64:LYS:H	1.51	0.58
1:2:1240:G:H2'	1:2:1241:A:C4	2.39	0.58
1:2:1280:G:O3'	30:U:76:SER:OG	2.19	0.58
2:A:22:VAL:HG22	2:A:169:SER:HB2	1.83	0.58
22:F:60:LEU:HD12	22:F:140:ILE:HG12	1.85	0.58
1:2:126:A:N1	1:2:262:C:O2'	2.32	0.58
1:2:392:C:H2'	1:2:393:C:C6	2.39	0.58
1:2:926:C:O2	12:O:125:SER:OG	2.19	0.58
1:2:1226:A:N1	24:M:36:ARG:NH2	2.47	0.58
3:B:172:LEU:O	3:B:176:VAL:HG12	2.03	0.58
4:C:142:ILE:HD11	13:V:27:LYS:HG2	1.85	0.58
7:H:140:VAL:CG2	14:W:52:TYR:HB3	2.34	0.58
9:J:36:LEU:HB3	9:J:41:GLU:OE1	2.03	0.58
26:Q:41:PRO:C	26:Q:43:ILE:H	2.10	0.58
1:2:69:G:H2'	1:2:70:C:H6	1.69	0.58
1:2:77:U:O2	6:G:159:ARG:NH1	2.37	0.58
1:2:296:U:H2'	1:2:297:C:C6	2.39	0.58
1:2:1043:U:H2'	1:2:1044:C:C6	2.39	0.58
3:B:209:ASN:HD22	3:B:211:HIS:CE1	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:40:GLU:OE2	5:E:103:TYR:OH	2.10	0.58
8:I:104:ILE:O	8:I:165:ARG:HA	2.04	0.58
8:I:173:ARG:HB2	8:I:176:GLN:HB2	1.85	0.58
13:V:10:GLU:OE1	13:V:11:LEU:N	2.36	0.58
16:Y:53:ASP:HB2	16:Y:79:VAL:HG22	1.84	0.58
22:F:105:ASN:C	22:F:108:LYS:HZ2	2.11	0.58
28:S:137:HIS:O	28:S:141:THR:OG1	2.17	0.58
41:l:173:ILE:HD12	41:l:212:VAL:HG22	1.85	0.58
1:2:257:C:H2'	1:2:258:U:C6	2.39	0.58
1:2:1737:C:H2'	1:2:1738:A:H8	1.69	0.58
2:A:175:TYR:OH	2:A:197:ILE:O	2.21	0.58
3:B:59:ASP:OD1	3:B:60:SER:N	2.37	0.58
9:J:75:ALA:HA	9:J:78:ARG:HE	1.68	0.58
27:R:66:VAL:HG22	27:R:67:ARG:H	1.68	0.58
35:g:75:SER:OG	35:g:77:ASP:OD1	2.19	0.58
1:2:780:A:O5'	1:2:781:A:N6	2.37	0.57
1:2:1736:U:H2'	1:2:1737:C:H6	1.68	0.57
9:J:31:ALA:HA	9:J:36:LEU:HD12	1.86	0.57
16:Y:54:ALA:O	16:Y:76:TYR:N	2.34	0.57
21:D:61:GLU:OE2	21:D:64:ARG:NH1	2.35	0.57
22:F:105:ASN:O	22:F:106:ASN:C	2.47	0.57
33:d:21:CYS:O	33:d:22:ARG:HG2	2.04	0.57
35:g:65:HIS:ND1	35:g:87:ASP:OD2	2.30	0.57
42:m:106:HIS:HB3	42:m:108:PHE:HD2	1.68	0.57
1:2:1077:C:H2'	1:2:1078:U:C6	2.39	0.57
1:2:1689:A:H2'	1:2:1690:G:C8	2.38	0.57
5:E:72:VAL:HB	5:E:77:ARG:HG3	1.86	0.57
16:Y:122:GLY:HA2	16:Y:125:ILE:HD13	1.86	0.57
21:D:6:SER:HB2	21:D:9:ARG:HG2	1.86	0.57
39:j:149:ILE:HD11	39:j:177:LEU:HB3	1.85	0.57
1:2:219:A:C8	1:2:831:U:H1'	2.40	0.57
1:2:517:A:O2'	1:2:533:A:N6	2.36	0.57
1:2:650:G:O6	1:2:684:A:N6	2.37	0.57
1:2:716:C:OP2	1:2:717:C:N4	2.28	0.57
1:2:1151:A:H2'	1:2:1152:G:H8	1.68	0.57
1:2:1240:G:O5'	25:P:77:ARG:NH2	2.22	0.57
1:2:1679:A:H2	1:2:1718:G:H21	1.52	0.57
13:V:53:TYR:CZ	13:V:72:LEU:HB3	2.39	0.57
15:X:58:GLY:H	36:i:85:GLN:NE2	2.02	0.57
30:U:68:ARG:HG3	30:U:70:THR:O	2.04	0.57
35:g:289:THR:H	35:g:292:GLN:NE2	2.00	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1085:A:H5''	4:C:168:GLY:C	2.29	0.57
1:2:1754:A:H62	36:i:67:LYS:HA	1.69	0.57
5:E:100:ARG:NH2	5:E:118:GLU:O	2.31	0.57
9:J:108:ARG:HE	9:J:110:GLN:HE22	1.50	0.57
23:K:17:GLN:NE2	23:K:18:GLU:HG2	2.20	0.57
30:U:34:LEU:HD22	30:U:89:ARG:HD2	1.85	0.57
34:f:138:TYR:OH	34:f:143:HIS:HB2	2.03	0.57
35:g:85:SER:OG	35:g:87:ASP:OD1	2.19	0.57
1:2:877:G:H2'	1:2:878:G:H8	1.68	0.57
1:2:1210:A:N3	25:P:97:TYR:OH	2.31	0.57
1:2:1388:U:H5'	27:R:3:ARG:HD3	1.87	0.57
1:2:1658:A:H2'	1:2:1659:U:C6	2.40	0.57
1:2:1742:A:H3'	1:2:1743:G:H8	1.70	0.57
8:I:67:TRP:O	8:I:71:GLY:HA2	2.04	0.57
11:N:1:MET:HB2	11:N:9:LYS:HE3	1.85	0.57
11:N:101:HIS:NE2	11:N:108:ASP:OD2	2.38	0.57
40:k:248:GLN:HB2	40:k:282:PRO:HA	1.86	0.57
1:2:27:U:H2'	1:2:28:A:C8	2.39	0.57
1:2:69:G:H2'	1:2:70:C:C6	2.38	0.57
1:2:95:G:H4'	5:E:8:HIS:ND1	2.20	0.57
1:2:406:A:H2'	1:2:407:C:H6	1.70	0.57
1:2:1219:C:H2'	1:2:1220:A:C8	2.40	0.57
1:2:1655:U:OP1	1:2:1656:G:O2'	2.20	0.57
2:A:84:ARG:NH1	2:A:203:PHE:O	2.25	0.57
9:J:119:ALA:O	9:J:124:HIS:ND1	2.23	0.57
10:L:14:GLN:HB3	10:L:54:ILE:HG21	1.84	0.57
12:O:22:SER:OG	12:O:24:ASN:O	2.23	0.57
27:R:24:LEU:HD23	27:R:34:LEU:HD13	1.85	0.57
35:g:150:ASP:HB3	35:g:179:MET:HB2	1.86	0.57
40:k:103:ILE:HG12	40:k:213:ALA:HB3	1.86	0.57
40:k:217:LEU:HD23	40:k:247:LEU:HB2	1.86	0.57
1:2:487:G:C2	1:2:488:C:H1'	2.39	0.57
1:2:922:A:H2'	1:2:923:A:C8	2.39	0.57
1:2:1070:U:H2'	1:2:1071:C:C6	2.40	0.57
1:2:1375:U:O2	1:2:1377:C:N4	2.31	0.57
1:2:1554:A:H5''	25:P:40:ARG:HH21	1.70	0.57
3:B:153:THR:OG1	3:B:154:SER:N	2.38	0.57
14:W:11:LEU:HD12	14:W:37:PHE:HE2	1.69	0.57
17:a:22:ARG:NE	17:a:27:SER:O	2.36	0.57
22:F:198:GLU:O	22:F:202:ASN:ND2	2.38	0.57
24:M:66:LYS:HZ1	34:f:111:GLU:HG2	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:171:ARG:NH2	35:g:189:ASN:OD1	2.37	0.57
40:k:431:GLU:HG3	40:k:484:ARG:HH21	1.69	0.57
1:2:763:G:H2'	1:2:764:U:C6	2.40	0.57
1:2:1214:C:O4'	33:d:2:ALA:N	2.38	0.57
1:2:1556:U:OP1	28:S:122:HIS:ND1	2.36	0.57
3:B:160:HIS:O	3:B:164:ILE:HG12	2.04	0.57
5:E:47:PHE:HZ	5:E:99:PHE:HD2	1.52	0.57
6:G:147:LEU:HD23	6:G:153:VAL:HG23	1.86	0.57
11:N:118:ILE:HD13	11:N:121:ARG:HD2	1.86	0.57
13:V:1:MET:HA	13:V:10:GLU:HB2	1.86	0.57
31:Z:46:LYS:O	31:Z:50:ILE:HG12	2.05	0.57
1:2:1671:G:H2'	1:2:1672:C:C6	2.40	0.57
7:H:96:ARG:HE	7:H:97:ARG:H	1.53	0.57
10:L:8:GLN:NE2	10:L:13:PHE:HA	2.20	0.57
14:W:30:SER:OG	14:W:58:SER:O	2.22	0.57
22:F:134:VAL:HG13	22:F:204:ALA:HB2	1.86	0.57
22:F:150:ARG:HB3	32:c:22:ARG:HH12	1.70	0.57
24:M:35:ALA:HB3	24:M:113:VAL:HB	1.86	0.57
36:i:58:MET:HE1	36:i:60:HIS:CE1	2.40	0.57
1:2:878:G:H2'	1:2:879:C:H6	1.67	0.57
1:2:1396:U:H5	1:2:1398:A:C6	2.23	0.57
4:C:116:VAL:HG22	4:C:144:ILE:HD11	1.87	0.57
13:V:73:ALA:O	13:V:78:LEU:N	2.36	0.57
15:X:22:ASN:O	15:X:22:ASN:ND2	2.38	0.57
17:a:38:ARG:HG3	17:a:83:ILE:HD11	1.86	0.57
28:S:30:TYR:O	28:S:33:THR:OG1	2.21	0.57
1:2:467:A:N1	1:2:593:A:O2'	2.31	0.56
1:2:1146:A:H5'	4:C:96:ARG:NH2	2.20	0.56
1:2:1209:C:H2'	1:2:1210:A:C8	2.39	0.56
1:2:1435:U:H4'	21:D:176:LEU:HD13	1.86	0.56
5:E:185:GLY:C	5:E:224:ASN:HD21	2.13	0.56
23:K:1:MET:HA	23:K:1:MET:HE2	1.87	0.56
23:K:12:TYR:HA	23:K:15:LEU:HD12	1.87	0.56
25:P:86:VAL:H	25:P:89:MET:HE3	1.70	0.56
31:Z:89:ILE:CG2	31:Z:101:TYR:HB3	2.35	0.56
40:k:355:ILE:HB	40:k:373:ILE:HB	1.87	0.56
41:l:168:ASP:O	41:l:170:LYS:N	2.37	0.56
1:2:97:C:H2'	1:2:98:U:C6	2.40	0.56
1:2:107:C:H2'	1:2:108:A:C8	2.40	0.56
1:2:200:G:H2'	1:2:201:A:C8	2.41	0.56
1:2:1341:C:H4'	35:g:103:ARG:NH1	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1521:G:OP1	1:2:1521:G:N2	2.31	0.56
4:C:182:GLY:N	4:C:200:ASP:OD1	2.38	0.56
5:E:18:TRP:HE1	5:E:42:LEU:HA	1.71	0.56
8:I:114:GLU:HA	8:I:118:GLY:HA2	1.87	0.56
12:O:30:VAL:C	12:O:41:ARG:HH12	2.10	0.56
30:U:58:LEU:HD21	30:U:90:TYR:HD1	1.69	0.56
38:1:11:C:H2'	38:1:12:G:C8	2.40	0.56
41:l:171:LYS:HG2	41:l:173:ILE:HD11	1.85	0.56
1:2:462:U:H2'	1:2:463:A:H8	1.71	0.56
1:2:517:A:O2'	1:2:518:C:H5''	2.06	0.56
1:2:550:G:H2'	1:2:551:G:H8	1.67	0.56
1:2:592:U:OP2	9:J:39:LYS:HB2	2.05	0.56
1:2:694:U:O2'	7:H:97:ARG:NH1	2.38	0.56
1:2:761:G:H22	1:2:762:A:H62	1.54	0.56
1:2:842:U:H2'	1:2:843:A:C8	2.40	0.56
1:2:945:U:H4'	3:B:165:ARG:HH22	1.70	0.56
1:2:1163:G:H2'	1:2:1164:G:H8	1.70	0.56
1:2:1168:G:N1	1:2:1573:7MG:OP2	2.39	0.56
1:2:1198:G:N3	1:2:1198:G:H2'	2.21	0.56
1:2:1293:G:H2'	1:2:1294:G:C8	2.40	0.56
1:2:1601:U:H2'	1:2:1602:U:C6	2.40	0.56
1:2:1749:C:H2'	1:2:1750:U:H6	1.70	0.56
2:A:25:GLY:HA3	2:A:163:ASN:ND2	2.20	0.56
10:L:10:GLU:OE1	10:L:12:ALA:N	2.34	0.56
22:F:39:GLN:HG2	26:Q:53:LEU:HD22	1.87	0.56
22:F:160:GLN:N	22:F:160:GLN:OE1	2.38	0.56
33:d:30:LEU:HD21	33:d:37:ASN:HA	1.86	0.56
40:k:403:ASP:OD2	40:k:405:THR:OG1	2.15	0.56
1:2:720:G:N2	1:2:720:G:OP2	2.37	0.56
1:2:1270:G:OP1	34:f:77:GLY:N	2.39	0.56
2:A:195:TRP:CZ2	2:A:197:ILE:HD11	2.41	0.56
5:E:103:TYR:CE1	5:E:109:PHE:HE1	2.24	0.56
7:H:58:LEU:N	7:H:89:HIS:O	2.33	0.56
7:H:162:ILE:HG23	7:H:165:LYS:HB3	1.87	0.56
8:I:57:ALA:HB2	8:I:178:GLY:HA2	1.86	0.56
15:X:62:LYS:HD2	15:X:116:ASP:HA	1.85	0.56
22:F:37:GLN:HG3	22:F:38:ALA:H	1.68	0.56
22:F:150:ARG:HH22	22:F:158:ARG:H	1.53	0.56
39:j:220:VAL:HG11	39:j:230:LEU:HD23	1.87	0.56
40:k:351:ASP:HB2	40:k:377:ILE:HD12	1.88	0.56
1:2:66:U:OP1	6:G:136:LYS:NZ	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:383:G:H2'	1:2:384:A:H8	1.67	0.56
1:2:693:U:O2'	1:2:694:U:N3	2.37	0.56
1:2:1532:G:O2'	31:Z:73:GLY:HA3	2.05	0.56
1:2:1554:A:H8	25:P:40:ARG:NH2	2.03	0.56
3:B:122:GLU:OE2	3:B:213:ARG:NH2	2.36	0.56
3:B:213:ARG:HH11	3:B:214:LYS:HD2	1.70	0.56
17:a:41:ILE:HA	17:a:68:TYR:CE1	2.40	0.56
22:F:124:ASN:O	22:F:128:ASP:HA	2.04	0.56
1:2:1289:PSU:H2'	1:2:1290:G:C8	2.41	0.56
1:2:1667:U:H3'	1:2:1668:G:H8	1.71	0.56
3:B:114:VAL:HA	3:B:142:PHE:HE2	1.69	0.56
7:H:46:ILE:HG12	7:H:60:VAL:HG23	1.86	0.56
30:U:16:GLU:HB2	30:U:98:HIS:CD2	2.40	0.56
39:j:188:VAL:HG23	39:j:264:ILE:HD13	1.87	0.56
40:k:214:ALA:HB3	40:k:244:VAL:HA	1.87	0.56
1:2:92:A:OP1	5:E:7:LYS:NZ	2.39	0.56
1:2:403:G:H2'	1:2:404:C:H6	1.70	0.56
1:2:564:C:O2'	1:2:576:G:N2	2.39	0.56
1:2:1650:C:H2'	1:2:1651:C:H6	1.71	0.56
3:B:67:GLU:OE2	3:B:83:LYS:HB3	2.06	0.56
3:B:133:TYR:HE2	3:B:220:GLN:HG3	1.71	0.56
7:H:49:ILE:HB	7:H:57:ALA:HB3	1.86	0.56
1:2:162:G:N2	1:2:162:G:OP2	2.38	0.56
1:2:446:U:H2'	1:2:447:C:O4'	2.05	0.56
1:2:601:U:H2'	1:2:602:U:C6	2.40	0.56
1:2:643:U:H2'	1:2:644:C:C6	2.41	0.56
1:2:1379:U:H3'	1:2:1380:A:H8	1.70	0.56
1:2:1552:U:O3'	25:P:47:ARG:NH2	2.39	0.56
7:H:55:LYS:HD3	7:H:89:HIS:NE2	2.21	0.56
7:H:74:GLN:NE2	7:H:92:PHE:HB2	2.21	0.56
13:V:25:LYS:HB2	13:V:28:ASP:HB2	1.86	0.56
16:Y:8:ARG:NH1	16:Y:10:ARG:HH21	2.03	0.56
16:Y:22:GLN:N	16:Y:22:GLN:OE1	2.38	0.56
21:D:76:ARG:HG2	23:K:65:TYR:HE1	1.71	0.56
35:g:154:LYS:HD2	35:g:208:VAL:HG23	1.87	0.56
38:1:15:G:H1	38:1:48:5MC:N4	2.04	0.56
42:m:59:LYS:HZ2	42:m:66:GLY:H	1.53	0.56
1:2:367:U:O2	1:2:372:G:O6	2.23	0.56
1:2:750:U:H2'	1:2:751:G:H8	1.70	0.56
1:2:1404:A:H2'	1:2:1405:U:C6	2.40	0.56
1:2:1562:U:H2'	1:2:1563:C:H6	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:193:ILE:O	3:B:196:GLU:HG2	2.06	0.56
7:H:82:GLU:OE2	7:H:165:LYS:NZ	2.26	0.56
28:S:123:ARG:HA	28:S:133:VAL:HG21	1.88	0.56
35:g:14:LEU:HB2	35:g:317:ILE:HB	1.87	0.56
35:g:265:SER:OG	35:g:280:GLU:OE2	2.22	0.56
1:2:627:G:OP1	11:N:120:SER:OG	2.23	0.56
1:2:636:C:OP1	14:W:32:LYS:HD3	2.06	0.56
1:2:1527:C:H5'	26:Q:42:GLU:OE2	2.05	0.56
1:2:1568:A:H2'	1:2:1569:C:O4'	2.06	0.56
2:A:74:VAL:HG22	2:A:96:THR:HB	1.88	0.56
3:B:105:PHE:CZ	3:B:211:HIS:HB3	2.41	0.56
7:H:130:VAL:HG22	7:H:169:PHE:CE2	2.41	0.56
15:X:121:ARG:HG3	15:X:122:PHE:CE1	2.41	0.56
22:F:92:VAL:O	22:F:96:THR:HG23	2.05	0.56
30:U:65:ILE:HD11	33:d:34:TYR:HE2	1.71	0.56
1:2:295:U:H2'	1:2:296:U:C6	2.41	0.55
1:2:340:A:H2'	1:2:341:C:C6	2.41	0.55
1:2:525:A:P	16:Y:93:ARG:HH21	2.29	0.55
1:2:913:G:H4'	1:2:914:A:O4'	2.06	0.55
1:2:1621:C:H2'	1:2:1622:C:H6	1.71	0.55
35:g:183:VAL:HB	35:g:199:PHE:HB2	1.88	0.55
35:g:213:PRO:HD3	35:g:252:PHE:HB3	1.87	0.55
36:i:104:LYS:O	36:i:104:LYS:NZ	2.39	0.55
40:k:219:ALA:HB1	40:k:250:LYS:HD2	1.88	0.55
1:2:1028:U:OP2	17:a:12:LYS:NZ	2.33	0.55
1:2:1096:U:O3'	4:C:173:ARG:NH1	2.39	0.55
1:2:1265:U:H2'	1:2:1266:G:H8	1.71	0.55
3:B:104:ASP:OD1	3:B:105:PHE:N	2.39	0.55
5:E:36:HIS:CG	5:E:85:GLY:HA3	2.41	0.55
12:O:17:ALA:HA	12:O:30:VAL:HA	1.88	0.55
25:P:24:LYS:HB3	25:P:28:MET:HE3	1.87	0.55
27:R:77:GLU:OE1	27:R:80:ARG:NE	2.37	0.55
28:S:100:SER:HB3	28:S:105:LEU:HA	1.89	0.55
29:T:77:ASN:HD21	29:T:98:GLY:HA2	1.70	0.55
1:2:324:G:H2'	1:2:325:G:C8	2.40	0.55
1:2:637:U:OP2	14:W:32:LYS:HD2	2.06	0.55
1:2:888:U:H2'	1:2:889:C:H6	1.71	0.55
1:2:1198:G:H4'	1:2:1199:G:O5'	2.04	0.55
1:2:1405:U:H2'	1:2:1406:G:C8	2.42	0.55
1:2:1710:A:H2'	1:2:1711:G:H4'	1.88	0.55
6:G:163:THR:HG22	6:G:165:GLY:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:157:ASP:OD1	9:J:158:PHE:N	2.39	0.55
14:W:55:ASP:OD2	14:W:57:ARG:HB2	2.05	0.55
20:h:2:ARG:HB2	20:h:5:TRP:HB2	1.88	0.55
29:T:124:ILE:HG21	29:T:129:LEU:HD12	1.88	0.55
30:U:62:VAL:HA	30:U:84:MET:O	2.06	0.55
30:U:63:LEU:HD12	33:d:34:TYR:CZ	2.41	0.55
40:k:414:GLY:HA2	40:k:468:SER:HB3	1.88	0.55
1:2:896:C:O2'	1:2:913:G:N2	2.38	0.55
1:2:1243:A:C5	1:2:1245:C:H1'	2.42	0.55
1:2:1275:U:H4'	21:D:141:LYS:HZ3	1.71	0.55
3:B:67:GLU:HB2	3:B:85:LYS:NZ	2.20	0.55
12:O:39:ILE:O	12:O:41:ARG:NH1	2.39	0.55
27:R:10:LYS:HG2	27:R:53:TYR:CZ	2.42	0.55
29:T:38:LYS:O	29:T:39:THR:OG1	2.24	0.55
35:g:93:TRP:CD1	35:g:100:SER:HA	2.41	0.55
39:j:185:ARG:HA	39:j:230:LEU:O	2.06	0.55
40:k:287:LEU:HB3	40:k:289:TYR:CD2	2.41	0.55
1:2:926:C:H2'	1:2:927:U:C6	2.41	0.55
1:2:1408:A:H5''	26:Q:118:ILE:HD11	1.89	0.55
1:2:1785:C:H2'	1:2:1786:G:H8	1.72	0.55
23:K:32:HIS:CE1	23:K:35:ILE:HD12	2.41	0.55
24:M:44:ALA:HA	24:M:49:GLU:OE2	2.07	0.55
27:R:31:ASN:HA	27:R:34:LEU:HD12	1.89	0.55
34:f:139:CYS:HB3	34:f:143:HIS:HA	1.88	0.55
1:2:72:A:OP1	1:2:72:A:H4'	2.06	0.55
1:2:1044:C:H2'	1:2:1045:G:C8	2.39	0.55
1:2:1488:A:H1'	1:2:1489:C:C2	2.41	0.55
1:2:1601:U:H2'	1:2:1602:U:H6	1.72	0.55
2:A:123:VAL:HG13	2:A:129:ASP:HB2	1.89	0.55
3:B:103:MET:O	3:B:214:LYS:HA	2.07	0.55
9:J:168:ARG:HG2	9:J:174:ARG:HD2	1.89	0.55
12:O:26:THR:O	12:O:43:THR:OG1	2.24	0.55
14:W:17:ALA:HB1	14:W:22:LYS:HG3	1.89	0.55
24:M:47:ARG:NH2	34:f:126:PRO:O	2.40	0.55
1:2:371:G:H1'	1:2:611:U:H3	1.72	0.55
1:2:853:U:O4	1:2:854:A:N6	2.40	0.55
1:2:958:U:H5''	11:N:15:ALA:O	2.07	0.55
1:2:990:G:N2	1:2:1013:G:O6	2.40	0.55
2:A:119:ARG:HE	4:C:245:MET:HE1	1.72	0.55
35:g:21:VAL:HA	35:g:38:SER:HA	1.86	0.55
40:k:113:LYS:NZ	45:k:601:GCP:O3G	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:216:LEU:HD11	40:k:229:THR:HB	1.89	0.55
1:2:522:G:N1	1:2:527:U:OP2	2.39	0.55
1:2:645:U:H2'	1:2:646:G:C8	2.42	0.55
1:2:891:A:H2'	1:2:892:U:C6	2.42	0.55
1:2:910:U:O4	3:B:6:ASN:ND2	2.35	0.55
1:2:1626:U:H2'	1:2:1627:G:H8	1.71	0.55
4:C:157:HIS:ND1	4:C:179:ARG:HD2	2.22	0.55
9:J:121:SER:O	9:J:124:HIS:N	2.34	0.55
10:L:6:THR:O	10:L:9:SER:OG	2.24	0.55
12:O:16:VAL:HG12	12:O:18:ARG:HG3	1.88	0.55
36:i:82:ARG:HH21	36:i:88:GLN:HG2	1.72	0.55
39:j:190:VAL:HB	40:k:405:THR:HG21	1.88	0.55
1:2:31:C:O2'	1:2:546:U:OP1	2.25	0.55
1:2:797:C:OP1	10:L:69:LYS:NZ	2.39	0.55
1:2:1107:G:H4'	1:2:1108:G:H5''	1.89	0.55
1:2:1140:G:H2'	1:2:1141:A:C8	2.42	0.55
4:C:193:MET:HE1	4:C:223:ILE:HD12	1.87	0.55
19:e:14:VAL:O	19:e:18:THR:HG23	2.06	0.55
23:K:16:PHE:HE2	23:K:82:LEU:HG	1.72	0.55
34:f:100:LEU:HB3	34:f:103:LEU:HD13	1.89	0.55
1:2:14:C:OP1	4:C:169:SER:OG	2.18	0.55
1:2:155:A:O2'	1:2:156:A:O4'	2.23	0.55
1:2:254:U:H2'	1:2:255:A:H8	1.72	0.55
1:2:833:G:H8	1:2:833:G:OP2	1.90	0.55
1:2:1487:U:OP1	21:D:9:ARG:NH1	2.40	0.55
7:H:55:LYS:HG2	7:H:56:LYS:H	1.72	0.55
14:W:57:ARG:NH1	18:b:26:GLN:OE1	2.40	0.55
15:X:43:PHE:O	15:X:45:GLY:N	2.39	0.55
35:g:306:GLN:HG2	35:g:322:VAL:HB	1.89	0.55
40:k:353:ILE:O	40:k:375:SER:N	2.40	0.55
1:2:423:C:O2'	1:2:425:G:OP1	2.24	0.54
4:C:180:GLY:N	4:C:200:ASP:OD2	2.40	0.54
8:I:84:HIS:HD2	8:I:87:ASN:N	2.04	0.54
12:O:87:GLY:HA2	12:O:92:LYS:HA	1.90	0.54
18:b:32:PHE:CE1	18:b:47:PHE:HD1	2.25	0.54
22:F:44:LEU:HD11	22:F:73:ALA:HB2	1.89	0.54
29:T:115:GLU:OE2	29:T:123:ARG:NE	2.39	0.54
35:g:283:PRO:HG3	35:g:320:TRP:HZ2	1.71	0.54
39:j:136:ARG:HE	39:j:136:ARG:C	2.15	0.54
40:k:330:ILE:HG23	40:k:333:LEU:HD12	1.89	0.54
1:2:142:G:H2'	1:2:143:G:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:789:U:H5	1:2:790:A:C5	2.25	0.54
1:2:1293:G:O4'	2:A:109:ASN:ND2	2.40	0.54
1:2:1703:C:O2'	1:2:1706:U:O2	2.24	0.54
4:C:111:ASP:OD2	4:C:115:HIS:ND1	2.30	0.54
14:W:73:GLY:O	14:W:128:PHE:N	2.35	0.54
26:Q:44:LEU:HB3	26:Q:78:VAL:HG11	1.88	0.54
40:k:466:ILE:HA	40:k:499:ILE:HG12	1.90	0.54
1:2:331:U:OP2	8:I:176:GLN:NE2	2.34	0.54
1:2:1164:G:H5''	22:F:101:MET:CE	2.35	0.54
7:H:139:ARG:HH22	14:W:53:ILE:CA	2.19	0.54
9:J:124:HIS:CE1	9:J:128:LEU:HD11	2.43	0.54
12:O:42:VAL:HG11	12:O:47:LYS:HZ1	1.72	0.54
14:W:111:MET:SD	14:W:115:GLU:HB2	2.47	0.54
27:R:5:ARG:HD2	27:R:53:TYR:HD1	1.73	0.54
35:g:90:LEU:HB2	35:g:104:PHE:HB2	1.89	0.54
38:1:10:2MG:C2	38:1:26:M2G:H1'	2.42	0.54
40:k:112:GLY:HA2	45:k:601:GCP:O1A	2.07	0.54
1:2:325:G:H2'	1:2:326:U:C6	2.42	0.54
1:2:448:C:H4'	5:E:8:HIS:HD2	1.73	0.54
1:2:670:G:O2'	1:2:671:C:OP1	2.19	0.54
1:2:959:U:H5'	11:N:55:ARG:HH11	1.71	0.54
1:2:1317:G:H2'	1:2:1318:A:H8	1.72	0.54
1:2:1628:U:O2'	1:2:1762:C:O2'	2.16	0.54
1:2:1637:5MC:HN41	1:2:1761:A:H61	1.54	0.54
20:h:4:LYS:HD3	20:h:5:TRP:HE1	1.73	0.54
39:j:222:LEU:HD21	40:k:324:ASN:HB3	1.88	0.54
1:2:1114:U:H2'	1:2:1115:A:C8	2.40	0.54
1:2:1201:A:O2'	1:2:1205:U:N3	2.34	0.54
2:A:207:PRO:O	2:A:210:ILE:HG22	2.07	0.54
7:H:35:LYS:HZ1	7:H:39:ARG:HH22	1.56	0.54
7:H:144:VAL:HA	14:W:42:GLN:NE2	2.23	0.54
21:D:7:LYS:HD2	21:D:10:LYS:NZ	2.23	0.54
21:D:59:VAL:HA	21:D:66:ILE:HG12	1.88	0.54
24:M:47:ARG:HE	34:f:126:PRO:HG2	1.73	0.54
35:g:180:ASP:HB3	35:g:182:ILE:HG12	1.89	0.54
39:j:255:ILE:HD13	39:j:262:CYS:HB2	1.90	0.54
41:l:194:TYR:OH	41:l:228:ARG:NH2	2.41	0.54
1:2:152:G:H5''	16:Y:131:ARG:CZ	2.38	0.54
1:2:153:G:H1'	6:G:56:ASN:ND2	2.22	0.54
1:2:774:A:N6	1:2:785:C:C2	2.70	0.54
7:H:152:ILE:HD13	7:H:181:ILE:HG23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:O:99:GLN:NE2	17:a:45:VAL:HA	2.22	0.54
14:W:36:LYS:NZ	14:W:39:GLN:OE1	2.26	0.54
15:X:37:ALA:O	15:X:41:SER:OG	2.26	0.54
17:a:54:SER:O	17:a:57:SER:OG	2.20	0.54
30:U:22:ILE:HG13	30:U:118:ILE:HA	1.89	0.54
35:g:34:LEU:O	35:g:45:SER:HA	2.07	0.54
40:k:94:ILE:HG23	40:k:391:VAL:HG21	1.89	0.54
42:m:55:LEU:HB2	42:m:68:ILE:HD11	1.89	0.54
1:2:38:C:H2'	1:2:39:A:C8	2.43	0.54
1:2:173:U:H3	1:2:265:A:H62	1.55	0.54
1:2:1000:A:H2'	1:2:1001:G:C8	2.43	0.54
1:2:1554:A:H5''	25:P:40:ARG:NH2	2.23	0.54
4:C:193:MET:HA	4:C:193:MET:HE3	1.89	0.54
6:G:122:GLU:HG2	6:G:123:GLY:H	1.72	0.54
7:H:143:LEU:HA	14:W:49:GLU:OE1	2.07	0.54
8:I:150:GLU:OE1	8:I:150:GLU:N	2.41	0.54
10:L:118:GLN:NE2	10:L:145:ALA:O	2.40	0.54
12:O:81:ILE:HG23	12:O:115:ILE:HD12	1.89	0.54
15:X:61:SER:OG	15:X:62:LYS:N	2.40	0.54
15:X:61:SER:OG	15:X:116:ASP:HB2	2.08	0.54
16:Y:102:LYS:HD3	16:Y:108:ARG:HH12	1.73	0.54
35:g:42:THR:HG22	35:g:63:LYS:HA	1.89	0.54
38:1:53:G:H2'	38:1:54:A:C8	2.38	0.54
1:2:82:U:H2'	1:2:83:G:O4'	2.07	0.54
1:2:234:G:H2'	1:2:235:A:C8	2.43	0.54
1:2:443:C:OP1	16:Y:102:LYS:NZ	2.34	0.54
1:2:801:G:H2'	1:2:802:A:C8	2.42	0.54
1:2:1040:G:H2'	1:2:1041:G:C8	2.42	0.54
1:2:1131:A:H2'	1:2:1132:A:H8	1.72	0.54
1:2:1428:U:O2'	30:U:72:ASN:ND2	2.41	0.54
7:H:139:ARG:NH2	14:W:51:GLU:OE2	2.41	0.54
8:I:157:VAL:O	8:I:160:GLN:HG2	2.08	0.54
10:L:16:GLN:HE22	10:L:33:ARG:HG3	1.72	0.54
17:a:74:CYS:SG	17:a:77:CYS:HB2	2.48	0.54
21:D:7:LYS:HA	21:D:10:LYS:NZ	2.23	0.54
30:U:16:GLU:HB2	30:U:98:HIS:HD2	1.71	0.54
35:g:104:PHE:CD2	35:g:139:GLY:HA2	2.43	0.54
1:2:115:G:OP2	10:L:65:SER:OG	2.26	0.54
1:2:366:A:H2'	1:2:367:U:O4'	2.08	0.54
1:2:623:G:H2'	1:2:624:C:C6	2.43	0.54
1:2:700:C:O2'	1:2:701:U:OP1	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1236:G:H2'	1:2:1237:A:H8	1.72	0.54
1:2:1470:C:H4'	1:2:1471:U:O5'	2.07	0.54
1:2:1480:C:H2'	1:2:1481:A:H5''	1.90	0.54
3:B:21:VAL:HB	3:B:26:ARG:HH12	1.72	0.54
5:E:103:TYR:HE2	5:E:184:THR:HA	1.72	0.54
5:E:248:ILE:O	5:E:251:GLU:HG3	2.08	0.54
8:I:140:THR:O	8:I:144:TRP:HD1	1.91	0.54
30:U:34:LEU:CD2	30:U:89:ARG:HD2	2.37	0.54
35:g:24:LEU:HD11	35:g:311:GLY:N	2.23	0.54
1:2:1038:A:O2'	1:2:1039:G:O5'	2.24	0.54
1:2:1265:U:H2'	1:2:1266:G:C8	2.43	0.54
1:2:1290:G:H22	1:2:1323:G:N2	2.05	0.54
5:E:252:ARG:HH11	5:E:256:ARG:HH12	1.53	0.54
7:H:42:GLN:OE1	7:H:43:PHE:N	2.39	0.54
11:N:92:ILE:O	11:N:96:VAL:HG23	2.08	0.54
22:F:86:LYS:HG2	22:F:94:ARG:NH2	2.23	0.54
23:K:44:LYS:O	23:K:47:GLN:HG2	2.08	0.54
25:P:81:ARG:NH2	25:P:120:SER:O	2.41	0.54
26:Q:96:PHE:O	35:g:60:ARG:NH2	2.41	0.54
31:Z:57:TYR:O	31:Z:103:ARG:NH1	2.41	0.54
31:Z:58:ARG:HA	31:Z:103:ARG:NH1	2.18	0.54
40:k:487:LEU:HD13	40:k:491:ALA:HB3	1.89	0.54
1:2:638:U:C5	7:H:100:PRO:HA	2.43	0.53
1:2:895:U:H2'	1:2:896:C:C2	2.44	0.53
1:2:1046:G:H2'	1:2:1047:G:C8	2.42	0.53
1:2:1460:G:H2'	1:2:1461:C:C6	2.43	0.53
1:2:1559:U:H2'	1:2:1560:G:H8	1.74	0.53
2:A:155:TYR:O	13:V:60:ARG:NH2	2.41	0.53
3:B:5:LYS:NZ	3:B:7:LYS:HD2	2.22	0.53
38:1:42:U:H2'	38:1:43:G:H8	1.73	0.53
40:k:416:VAL:HG21	40:k:492:CYS:HB2	1.90	0.53
1:2:152:G:H2'	1:2:153:G:C8	2.42	0.53
1:2:164:G:H2'	1:2:165:C:C6	2.44	0.53
1:2:253:A:H2'	1:2:254:U:C6	2.43	0.53
1:2:589:C:H5'	19:e:56:MET:CE	2.38	0.53
1:2:654:G:O6	1:2:676:U:O4	2.27	0.53
1:2:877:G:H2'	1:2:878:G:C8	2.43	0.53
1:2:913:G:HO2'	1:2:914:A:H8	1.56	0.53
1:2:1430:U:H4'	1:2:1431:G:O5'	2.08	0.53
1:2:1651:C:H2'	1:2:1652:G:O4'	2.08	0.53
11:N:142:GLU:CD	11:N:143:SER:H	2.16	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:F:106:ASN:O	22:F:108:LYS:NZ	2.41	0.53
22:F:109:LYS:HD2	22:F:109:LYS:N	2.23	0.53
23:K:15:LEU:HD11	23:K:46:LEU:HD21	1.89	0.53
26:Q:115:THR:HA	26:Q:118:ILE:HG22	1.90	0.53
35:g:30:GLN:NE2	35:g:78:GLY:O	2.41	0.53
39:j:71:ALA:HB1	39:j:85:LEU:HD21	1.90	0.53
40:k:217:LEU:HB3	40:k:249:ASN:ND2	2.24	0.53
1:2:186:G:H21	1:2:197:A:H8	1.55	0.53
1:2:689:G:H2'	1:2:690:A:C8	2.44	0.53
1:2:751:G:C6	1:2:798:A:N1	2.77	0.53
1:2:1355:U:O2	1:2:1366:G:N2	2.28	0.53
12:O:99:GLN:HE22	17:a:45:VAL:HA	1.72	0.53
21:D:116:ARG:HE	37:3:39:U:H3	1.54	0.53
23:K:22:VAL:HG23	23:K:23:ALA:H	1.74	0.53
27:R:41:ILE:HG23	27:R:46:LEU:HD22	1.90	0.53
35:g:225:GLY:O	35:g:243:ALA:N	2.28	0.53
1:2:312:U:O4'	1:2:1117:G:N2	2.41	0.53
1:2:519:A:H2'	1:2:520:A:C8	2.43	0.53
1:2:1001:G:O2'	42:m:65:ASN:ND2	2.41	0.53
2:A:79:ARG:C	2:A:83:GLN:HE22	2.16	0.53
5:E:136:ILE:HG21	5:E:148:ARG:HH11	1.74	0.53
7:H:166:LEU:HB2	7:H:183:PHE:CD2	2.42	0.53
22:F:45:PHE:HB2	22:F:48:TRP:HZ3	1.73	0.53
23:K:25:LYS:HG3	23:K:64:TYR:CE2	2.43	0.53
27:R:72:LYS:HA	27:R:75:GLU:CD	2.34	0.53
28:S:25:ASN:O	28:S:57:ARG:NH1	2.41	0.53
30:U:55:PRO:HA	30:U:91:ILE:HG12	1.88	0.53
33:d:2:ALA:HA	33:d:7:TRP:HB2	1.90	0.53
35:g:43:LEU:HD12	35:g:93:TRP:CZ3	2.43	0.53
40:k:97:ARG:NH2	40:k:166:SER:O	2.34	0.53
1:2:866:G:O6	1:2:961:C:N4	2.41	0.53
1:2:1080:A:O2'	1:2:1081:C:O5'	2.23	0.53
1:2:1461:C:H2'	1:2:1462:G:H8	1.73	0.53
1:2:1650:C:H2'	1:2:1651:C:C6	2.43	0.53
1:2:1786:G:H5''	12:O:132:ARG:NH1	2.24	0.53
5:E:251:GLU:O	5:E:255:ARG:HG2	2.08	0.53
6:G:12:THR:HG21	6:G:124:ILE:HA	1.90	0.53
8:I:138:LYS:NZ	8:I:142:ARG:HH21	2.05	0.53
33:d:13:LYS:HG3	33:d:14:PHE:HD1	1.73	0.53
1:2:989:C:H2'	1:2:990:G:O4'	2.09	0.53
1:2:1378:U:H2'	1:2:1379:U:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1621:C:H2'	1:2:1622:C:C6	2.42	0.53
5:E:31:PRO:HG2	5:E:38:LEU:HB2	1.90	0.53
11:N:46:THR:HG22	11:N:49:GLN:CD	2.33	0.53
16:Y:86:GLU:OE2	16:Y:90:ARG:NE	2.37	0.53
21:D:160:SER:OG	21:D:161:GLY:N	2.42	0.53
39:j:246:SER:O	39:j:249:GLU:HG3	2.08	0.53
42:m:59:LYS:NZ	42:m:66:GLY:H	2.07	0.53
1:2:893:U:H2'	1:2:894:G:H8	1.73	0.53
1:2:1171:G:H2'	1:2:1172:C:C6	2.43	0.53
1:2:1191:C:O3'	26:Q:140:LYS:NZ	2.41	0.53
1:2:1227:G:O2'	34:f:100:LEU:HD22	2.08	0.53
1:2:1240:G:P	25:P:77:ARG:HE	2.32	0.53
3:B:24:PHE:HA	3:B:27:LYS:HB2	1.90	0.53
4:C:131:ARG:O	4:C:134:ILE:HG22	2.09	0.53
7:H:16:LEU:HA	7:H:19:GLN:NE2	2.24	0.53
11:N:98:VAL:HG23	11:N:115:LEU:HD12	1.90	0.53
24:M:78:PRO:HB2	24:M:128:LEU:HD22	1.89	0.53
24:M:96:LYS:C	24:M:103:ALA:HB3	2.34	0.53
30:U:38:SER:O	30:U:42:ILE:HG12	2.09	0.53
1:2:463:A:C2	1:2:464:G:C8	2.97	0.53
1:2:611:U:H3'	1:2:612:G:H2'	1.90	0.53
1:2:756:A:C4	1:2:757:A:C8	2.97	0.53
1:2:871:G:N2	1:2:1046:G:H4'	2.24	0.53
1:2:1711:G:H3'	1:2:1712:A:H8	1.73	0.53
1:2:1784:G:OP2	12:O:136:ARG:NH2	2.32	0.53
2:A:53:THR:HG22	2:A:161:PRO:HG2	1.91	0.53
7:H:153:LEU:HD12	7:H:184:GLU:OE2	2.09	0.53
7:H:171:ALA:O	7:H:175:LYS:HG2	2.09	0.53
11:N:88:LEU:O	11:N:92:ILE:HG12	2.09	0.53
22:F:106:ASN:OD1	22:F:107:GLY:N	2.41	0.53
34:f:119:LYS:HD3	34:f:137:PHE:HD2	1.73	0.53
1:2:1256:U:O2'	23:K:1:MET:O	2.19	0.53
1:2:1563:C:H2'	1:2:1564:U:C6	2.43	0.53
5:E:176:ASP:H	5:E:179:LYS:HE3	1.74	0.53
7:H:96:ARG:NH1	7:H:116:ARG:HG3	2.24	0.53
19:e:20:LYS:NZ	19:e:22:GLU:OE1	2.41	0.53
23:K:75:TYR:O	23:K:78:GLU:HG3	2.09	0.53
28:S:29:VAL:O	28:S:33:THR:HG23	2.09	0.53
30:U:84:MET:HB2	33:d:52:PHE:CE2	2.43	0.53
35:g:260:THR:HG22	35:g:269:ILE:HG12	1.91	0.53
35:g:266:GLY:HA3	35:g:281:LEU:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:322:ASP:OD2	40:k:408:ARG:NH1	2.41	0.53
1:2:123:G:O6	1:2:294:A:N6	2.42	0.53
1:2:327:A:H2'	1:2:328:G:C8	2.44	0.53
1:2:373:U:H2'	1:2:374:U:C6	2.43	0.53
1:2:1052:G:H2'	1:2:1053:U:C6	2.44	0.53
5:E:48:LEU:HD12	5:E:61:VAL:HG13	1.91	0.53
7:H:126:LEU:HB2	7:H:173:TYR:CE1	2.44	0.53
8:I:70:GLU:OE1	8:I:70:GLU:N	2.38	0.53
12:O:16:VAL:O	12:O:31:THR:N	2.32	0.53
12:O:17:ALA:HB3	12:O:81:ILE:HD13	1.90	0.53
16:Y:28:LEU:HD23	16:Y:30:PRO:HD3	1.90	0.53
34:f:107:LYS:HB3	34:f:115:ALA:HB3	1.90	0.53
1:2:156:A:H2	1:2:418:G:H21	1.56	0.52
1:2:337:C:H1'	8:I:5:ARG:HB2	1.91	0.52
1:2:345:G:OP1	10:L:79:ARG:NH1	2.43	0.52
1:2:883:A:H2'	1:2:884:G:H8	1.69	0.52
1:2:1639:C:H2'	1:2:1640:G:C8	2.44	0.52
1:2:1739:U:H2'	1:2:1740:U:C6	2.44	0.52
2:A:42:PRO:HB2	27:R:126:ALA:HB2	1.90	0.52
3:B:164:ILE:O	3:B:168:ILE:HD12	2.09	0.52
4:C:42:PRO:O	4:C:48:ARG:NH2	2.41	0.52
6:G:49:VAL:O	6:G:113:ILE:HD12	2.10	0.52
11:N:86:GLU:HG2	11:N:87:ASP:N	2.24	0.52
16:Y:7:ILE:HD12	16:Y:27:VAL:HG12	1.91	0.52
22:F:65:GLN:NE2	22:F:88:GLN:OE1	2.41	0.52
22:F:146:GLU:OE2	22:F:227:ARG:NE	2.39	0.52
35:g:281:LEU:HD23	35:g:320:TRP:CE2	2.45	0.52
1:2:11:A:N3	1:2:1299:A:O2'	2.40	0.52
1:2:968:C:H4'	1:2:1103:U:O2'	2.10	0.52
1:2:998:PSU:H2'	1:2:999:C:C2	2.44	0.52
1:2:1214:C:H2'	1:2:1215:C:C6	2.44	0.52
1:2:1315:G:H2'	1:2:1316:C:H6	1.74	0.52
9:J:108:ARG:NH1	9:J:145:SER:OG	2.40	0.52
21:D:25:PHE:CD2	21:D:50:ILE:HD13	2.43	0.52
24:M:120:ASP:O	24:M:124:ARG:NH1	2.41	0.52
28:S:82:PRO:HB2	28:S:84:TRP:CD1	2.45	0.52
38:1:21:A:O2'	38:1:22:G:H5''	2.08	0.52
1:2:58:U:OP1	1:2:455:A:O2'	2.23	0.52
1:2:160:U:O2'	1:2:161:A:OP2	2.25	0.52
1:2:345:G:OP2	10:L:79:ARG:NH2	2.31	0.52
1:2:396:A:H2'	1:2:397:G:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:405:U:H2'	1:2:406:A:C8	2.43	0.52
1:2:552:G:H3'	1:2:553:C:H2'	1.91	0.52
1:2:753:A:OP2	5:E:187:ARG:N	2.42	0.52
1:2:765:G:C6	9:J:149:ARG:HG2	2.44	0.52
1:2:906:A:H4'	39:j:53:ARG:NH2	2.24	0.52
1:2:1657:A:H2'	1:2:1658:A:C8	2.44	0.52
35:g:293:ASP:OD1	35:g:293:ASP:N	2.42	0.52
1:2:54:C:H5'	16:Y:110:GLN:OE1	2.09	0.52
1:2:90:C:H2'	1:2:91:G:H8	1.71	0.52
1:2:445:A:P	5:E:59:ARG:HH12	2.32	0.52
1:2:567:G:H4'	15:X:90:ASP:OD1	2.09	0.52
1:2:568:C:N4	15:X:116:ASP:OD2	2.43	0.52
1:2:804:U:O4	1:2:805:A:N6	2.42	0.52
1:2:818:G:C2	1:2:852:G:C2	2.98	0.52
1:2:1080:A:O2'	1:2:1081:C:H2'	2.10	0.52
1:2:1160:C:H2'	1:2:1161:C:C6	2.44	0.52
1:2:1204:C:H2'	1:2:1205:U:O4'	2.09	0.52
1:2:1778:G:H2'	1:2:1779:A:H8	1.73	0.52
1:2:1779:A:O3'	20:h:9:ARG:NH2	2.43	0.52
3:B:41:ARG:HH21	3:B:232:HIS:HB3	1.73	0.52
21:D:24:PHE:HE2	23:K:65:TYR:CD1	2.27	0.52
35:g:117:ASP:O	35:g:118:ALA:C	2.52	0.52
36:i:86:ASP:OD1	36:i:87:ASP:N	2.43	0.52
39:j:31:GLY:HA3	39:j:46:ILE:O	2.10	0.52
1:2:29:U:H2'	1:2:30:G:C8	2.44	0.52
1:2:96:G:H2'	1:2:97:C:H6	1.75	0.52
1:2:602:U:H2'	1:2:603:A:C8	2.43	0.52
1:2:1199:G:H3'	1:2:1199:G:P	2.49	0.52
4:C:187:PRO:HD3	9:J:17:ARG:HH12	1.75	0.52
8:I:36:THR:HG21	8:I:174:PRO:HB2	1.91	0.52
12:O:19:ILE:HG13	12:O:28:VAL:HG12	1.92	0.52
14:W:101:TYR:HA	14:W:113:HIS:CD2	2.45	0.52
30:U:67:THR:OG1	30:U:80:ASP:OD1	2.27	0.52
33:d:19:ARG:NH2	33:d:32:ARG:HH11	2.07	0.52
40:k:226:GLN:HE21	40:k:229:THR:HG21	1.74	0.52
1:2:130:C:N4	1:2:178:A:OP2	2.33	0.52
1:2:395:G:N2	1:2:397:G:H3'	2.25	0.52
1:2:883:A:H5''	3:B:136:ARG:CZ	2.38	0.52
5:E:9:LEU:HD21	5:E:14:ALA:HB2	1.91	0.52
9:J:20:GLU:OE1	9:J:20:GLU:N	2.41	0.52
15:X:36:THR:O	15:X:40:SER:OG	2.20	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:57:ILE:HD12	36:i:85:GLN:HE21	1.75	0.52
25:P:27:GLU:O	25:P:28:MET:HE2	2.10	0.52
38:1:19:G:OP2	38:1:60:A:N6	2.43	0.52
41:l:163:PRO:HB3	41:l:174:PHE:CZ	2.44	0.52
1:2:1398:A:H2'	1:2:1399:A:C8	2.45	0.52
1:2:1564:U:H2'	1:2:1565:U:C6	2.44	0.52
4:C:52:ALA:HB1	4:C:54:LYS:HE2	1.91	0.52
6:G:49:VAL:HG13	6:G:114:THR:HB	1.91	0.52
22:F:124:ASN:HB2	22:F:131:PRO:HG3	1.91	0.52
28:S:7:GLU:HB3	28:S:10:SER:HB3	1.92	0.52
28:S:28:VAL:O	28:S:32:LEU:HG	2.08	0.52
29:T:66:TYR:O	29:T:124:ILE:HD11	2.10	0.52
1:2:454:C:H3'	1:2:455:A:H8	1.75	0.52
1:2:1599:G:N3	29:T:89:ARG:NH2	2.57	0.52
1:2:1788:A:P	17:a:10:ARG:HH12	2.32	0.52
4:C:44:THR:O	4:C:47:GLY:N	2.37	0.52
6:G:7:TYR:O	6:G:11:GLY:HA2	2.10	0.52
10:L:69:LYS:O	10:L:127:GLN:HG3	2.09	0.52
11:N:113:PHE:O	11:N:116:ILE:HG22	2.09	0.52
12:O:39:ILE:H	12:O:41:ARG:NH1	2.08	0.52
15:X:107:PHE:CD1	15:X:123:LYS:HG3	2.44	0.52
22:F:39:GLN:HE22	22:F:42:ILE:HA	1.74	0.52
22:F:72:VAL:HG21	26:Q:47:LYS:HG2	1.91	0.52
27:R:16:LEU:HD11	27:R:38:ILE:HD12	1.92	0.52
1:2:599:U:H1'	15:X:47:SER:OG	2.10	0.52
1:2:686:C:H4'	14:W:118:ARG:HD2	1.90	0.52
1:2:930:C:O2'	1:2:931:U:OP1	2.27	0.52
1:2:1299:A:H5''	4:C:91:VAL:HG21	1.91	0.52
10:L:45:PRO:HG2	10:L:48:ALA:HB2	1.90	0.52
14:W:15:ASN:O	14:W:19:LYS:HG2	2.10	0.52
34:f:121:CYS:HB3	34:f:128:ILE:HG23	1.91	0.52
35:g:47:ARG:HH11	35:g:57:VAL:HG13	1.74	0.52
1:2:161:A:H3'	1:2:162:G:N2	2.17	0.52
1:2:1107:G:N1	15:X:22:ASN:ND2	2.56	0.52
2:A:62:ARG:NH2	13:V:37:ALA:O	2.39	0.52
2:A:206:ASN:ND2	2:A:208:GLU:OE2	2.43	0.52
3:B:213:ARG:NH1	3:B:214:LYS:HD2	2.25	0.52
6:G:147:LEU:HD21	6:G:156:TYR:HD2	1.74	0.52
12:O:18:ARG:HE	12:O:82:LYS:HD3	1.75	0.52
23:K:64:TYR:HB3	23:K:66:TYR:CE1	2.45	0.52
23:K:69:THR:HG23	23:K:72:GLY:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:U:102:ARG:HA	30:U:105:GLN:HG3	1.91	0.52
40:k:108:HIS:HB3	40:k:111:HIS:CE1	2.45	0.52
1:2:180:A:H2'	1:2:181:A:C8	2.44	0.51
1:2:561:G:H2'	1:2:562:U:H6	1.75	0.51
1:2:565:C:H2'	1:2:566:A:O4'	2.09	0.51
1:2:958:U:OP2	18:b:20:LYS:NZ	2.42	0.51
1:2:1659:U:H2'	1:2:1660:G:C8	2.45	0.51
24:M:66:LYS:NZ	34:f:111:GLU:HG2	2.24	0.51
26:Q:30:LYS:HB2	26:Q:66:ARG:HG2	1.91	0.51
27:R:16:LEU:HD21	27:R:38:ILE:HD11	1.91	0.51
28:S:13:HIS:O	28:S:24:GLY:N	2.43	0.51
30:U:68:ARG:NH1	30:U:77:LYS:HA	2.23	0.51
31:Z:103:ARG:HD3	31:Z:103:ARG:H	1.76	0.51
36:i:40:LYS:HZ3	36:i:42:LEU:HA	1.74	0.51
1:2:91:G:H2'	1:2:92:A:O4'	2.10	0.51
1:2:160:U:OP2	6:G:87:ARG:NH2	2.37	0.51
1:2:216:A:H2'	1:2:217:A:C8	2.42	0.51
1:2:989:C:H5	1:2:1013:G:H1	1.58	0.51
1:2:1385:G:O2'	1:2:1409:A:N6	2.38	0.51
1:2:1550:U:H2'	1:2:1551:G:O4'	2.10	0.51
2:A:205:ARG:HH12	2:A:213:GLN:HG3	1.74	0.51
5:E:103:TYR:CE2	5:E:184:THR:HA	2.45	0.51
11:N:4:MET:HE2	11:N:124:ARG:CZ	2.40	0.51
27:R:91:LEU:O	27:R:93:LEU:N	2.43	0.51
31:Z:40:VAL:HG23	31:Z:41:VAL:HG23	1.91	0.51
35:g:49:THR:HG21	35:g:57:VAL:HG12	1.92	0.51
40:k:95:ILE:HG23	40:k:185:LEU:HD23	1.90	0.51
40:k:356:ARG:HH12	40:k:525:PRO:HG3	1.75	0.51
1:2:248:U:N3	10:L:17:PRO:O	2.43	0.51
1:2:700:C:H2'	1:2:701:U:C6	2.46	0.51
1:2:884:G:N2	12:O:123:SER:OG	2.44	0.51
1:2:1043:U:H2'	1:2:1044:C:H6	1.75	0.51
1:2:1323:G:H4'	2:A:113:ARG:HH21	1.75	0.51
1:2:1471:U:C4	22:F:192:ILE:HD12	2.46	0.51
2:A:30:GLN:OE1	2:A:149:LEU:HB3	2.10	0.51
4:C:208:SER:O	4:C:211:THR:HG22	2.10	0.51
5:E:30:ARG:O	5:E:81:THR:OG1	2.26	0.51
5:E:143:ASP:HB2	5:E:145:ARG:HG3	1.92	0.51
6:G:105:ASP:OD1	6:G:105:ASP:N	2.41	0.51
7:H:38:LEU:C	7:H:41:LEU:HD13	2.36	0.51
8:I:138:LYS:HZ2	8:I:142:ARG:HH21	1.56	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:W:31:SER:H	14:W:34:ILE:HD12	1.75	0.51
17:a:23:CYS:SG	17:a:74:CYS:N	2.71	0.51
33:d:37:ASN:O	33:d:37:ASN:ND2	2.33	0.51
40:k:215:LEU:HD22	40:k:247:LEU:HD11	1.91	0.51
40:k:430:ILE:HG13	40:k:485:LEU:HB2	1.92	0.51
40:k:431:GLU:HG3	40:k:484:ARG:NH2	2.26	0.51
1:2:324:G:O6	1:2:343:A:N6	2.44	0.51
1:2:970:A:C2	1:2:971:G:H1'	2.45	0.51
1:2:1044:C:N3	1:2:1073:G:N1	2.57	0.51
1:2:1069:C:H2'	1:2:1070:U:C6	2.45	0.51
1:2:1159:A:H2'	1:2:1160:C:C6	2.45	0.51
1:2:1233:A:O5'	1:2:1244:G:O2'	2.25	0.51
3:B:187:LYS:HG2	3:B:193:ILE:HD11	1.93	0.51
6:G:14:LYS:HE2	6:G:124:ILE:HB	1.92	0.51
16:Y:62:THR:HG23	16:Y:69:SER:HB2	1.91	0.51
22:F:84:PHE:HE2	32:c:49:ARG:HG3	1.75	0.51
27:R:19:LYS:C	27:R:20:TYR:HD1	2.19	0.51
1:2:611:U:OP2	15:X:5:LYS:NZ	2.42	0.51
1:2:1164:G:O3'	22:F:101:MET:HE1	2.10	0.51
1:2:1326:C:H2'	1:2:1327:G:O4'	2.10	0.51
1:2:1583:U:OP1	26:Q:125:GLU:N	2.26	0.51
3:B:109:LYS:HG3	3:B:113:MET:SD	2.51	0.51
4:C:64:HIS:CE1	4:C:244:PRO:HD3	2.45	0.51
13:V:49:GLU:OE2	13:V:49:GLU:N	2.44	0.51
21:D:50:ILE:HG22	21:D:88:ALA:HA	1.90	0.51
26:Q:40:GLN:C	26:Q:42:GLU:H	2.19	0.51
26:Q:48:VAL:HG13	26:Q:78:VAL:HG13	1.92	0.51
27:R:29:GLN:O	27:R:33:ARG:HG2	2.11	0.51
35:g:300:ALA:HB3	35:g:309:PHE:HB2	1.92	0.51
1:2:589:C:H2'	1:2:590:A:H8	1.74	0.51
1:2:1204:C:O2'	33:d:12:ARG:NH1	2.44	0.51
1:2:1503:A:O2'	1:2:1560:G:N3	2.43	0.51
1:2:1589:C:H2'	1:2:1590:A:H8	1.73	0.51
1:2:1793:U:H3'	17:a:5:ARG:NH2	2.25	0.51
5:E:250:GLU:O	5:E:254:ARG:NE	2.43	0.51
6:G:135:PRO:HD2	6:G:158:ILE:HD12	1.91	0.51
6:G:137:ARG:HB3	6:G:140:ASN:OD1	2.11	0.51
7:H:21:ALA:HA	7:H:24:PHE:HD2	1.75	0.51
8:I:188:GLU:OE1	8:I:188:GLU:N	2.44	0.51
17:a:41:ILE:O	37:3:21:C:O2'	2.23	0.51
25:P:83:MET:HE2	25:P:83:MET:HA	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:R:57:LEU:O	27:R:61:ILE:HG12	2.10	0.51
27:R:74:GLN:O	27:R:78:ARG:HG2	2.10	0.51
32:c:16:LEU:HB2	32:c:27:GLN:HB3	1.92	0.51
1:2:268:G:H2'	1:2:269:C:H6	1.75	0.51
1:2:1035:A:H2'	1:2:1036:C:H6	1.76	0.51
1:2:1381:G:P	30:U:89:ARG:HH21	2.34	0.51
2:A:11:SER:HA	27:R:115:LEU:HD21	1.92	0.51
4:C:232:PRO:HA	4:C:235:TRP:CE2	2.46	0.51
5:E:36:HIS:HB2	5:E:41:SER:HB2	1.92	0.51
10:L:5:LEU:O	10:L:6:THR:OG1	2.21	0.51
24:M:33:GLY:HA2	24:M:115:LYS:HB3	1.93	0.51
24:M:35:ALA:O	24:M:41:SER:OG	2.29	0.51
32:c:12:VAL:HG13	32:c:50:GLU:HA	1.91	0.51
35:g:52:GLU:HG3	35:g:53:GLN:H	1.75	0.51
39:j:220:VAL:CG1	39:j:230:LEU:HD23	2.40	0.51
42:m:40:THR:HG21	42:m:83:ASP:HA	1.93	0.51
1:2:915:U:H2'	1:2:916:U:C6	2.45	0.51
1:2:1144:U:N3	1:2:1145:G:N7	2.58	0.51
1:2:1659:U:H2'	1:2:1660:G:H8	1.75	0.51
3:B:89:ASP:OD1	3:B:89:ASP:N	2.44	0.51
3:B:98:THR:H	3:B:232:HIS:CE1	2.29	0.51
5:E:72:VAL:N	5:E:75:LYS:O	2.44	0.51
6:G:48:TYR:HB3	6:G:50:PHE:CE1	2.45	0.51
13:V:5:LYS:HB2	13:V:7:GLN:NE2	2.26	0.51
19:e:10:ARG:O	19:e:10:ARG:HG3	2.11	0.51
21:D:24:PHE:HE2	23:K:65:TYR:CG	2.29	0.51
26:Q:131:GLY:O	26:Q:133:GLY:N	2.44	0.51
28:S:65:GLU:O	28:S:68:ARG:HG2	2.10	0.51
35:g:159:PRO:HD2	35:g:215:GLY:HA2	1.93	0.51
35:g:208:VAL:HG21	35:g:250:LEU:H	1.76	0.51
1:2:566:A:H5'	19:e:9:ALA:HA	1.92	0.51
1:2:1021:C:H4'	1:2:1124:A:H61	1.75	0.51
1:2:1066:C:OP2	3:B:151:LYS:NZ	2.40	0.51
1:2:1236:G:H2'	1:2:1237:A:C8	2.45	0.51
3:B:48:VAL:HG21	3:B:61:LEU:HD21	1.92	0.51
4:C:156:PRO:HD2	13:V:9:VAL:HG21	1.93	0.51
4:C:173:ARG:HB3	4:C:204:SER:OG	2.10	0.51
6:G:7:TYR:HB2	6:G:124:ILE:HD11	1.93	0.51
6:G:67:VAL:HG11	6:G:99:GLY:HA2	1.92	0.51
6:G:207:GLU:O	6:G:210:GLN:HG3	2.11	0.51
13:V:83:TRP:CH2	13:V:85:TYR:HA	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:F:159:ARG:O	22:F:226:ASN:ND2	2.44	0.51
26:Q:41:PRO:O	26:Q:43:ILE:N	2.44	0.51
31:Z:65:LEU:HB3	31:Z:71:LEU:HD12	1.92	0.51
40:k:204:MET:HG3	40:k:232:HIS:CE1	2.44	0.51
1:2:533:A:C2	1:2:534:A:H1'	2.46	0.51
1:2:750:U:H2'	1:2:751:G:C8	2.46	0.51
1:2:966:A:OP2	11:N:4:MET:HE1	2.12	0.51
1:2:1240:G:O4'	25:P:77:ARG:NH2	2.44	0.51
1:2:1456:G:H21	25:P:126:VAL:HG21	1.75	0.51
1:2:1782:C:H2'	1:2:1783:U:H6	1.72	0.51
5:E:98:ASN:O	5:E:114:ILE:N	2.40	0.51
5:E:122:LYS:HD3	5:E:145:ARG:NH1	2.26	0.51
9:J:80:LEU:O	9:J:84:GLY:N	2.44	0.51
10:L:127:GLN:HG2	10:L:137:PHE:CE1	2.44	0.51
25:P:32:ASP:HA	25:P:35:LYS:HE2	1.93	0.51
41:l:190:HIS:O	41:l:193:GLN:HG3	2.10	0.51
1:2:586:C:H2'	1:2:587:U:C6	2.46	0.50
1:2:652:C:H2'	1:2:653:C:O4'	2.10	0.50
1:2:802:A:O2'	7:H:104:ARG:NH2	2.44	0.50
1:2:977:A:C4	1:2:978:A:C8	3.00	0.50
1:2:1577:U:H2'	1:2:1578:C:C6	2.47	0.50
1:2:1720:A:H5''	6:G:75:LEU:HD11	1.92	0.50
5:E:252:ARG:HH11	5:E:256:ARG:NH1	2.09	0.50
22:F:27:LEU:HB3	22:F:30:THR:HG22	1.92	0.50
23:K:20:VAL:HG12	23:K:67:THR:HA	1.92	0.50
24:M:60:THR:O	24:M:61:GLU:HG3	2.11	0.50
28:S:57:ARG:HH12	31:Z:40:VAL:HB	1.76	0.50
40:k:317:VAL:HA	40:k:340:GLY:HA2	1.93	0.50
1:2:43:A:H1'	1:2:377:A:H1'	1.93	0.50
1:2:477:A:OP1	19:e:37:ARG:NH2	2.45	0.50
1:2:749:U:H2'	1:2:750:U:C6	2.45	0.50
1:2:863:U:H3'	14:W:28:ARG:HH21	1.76	0.50
1:2:1242:G:H2'	1:2:1242:G:N3	2.25	0.50
1:2:1649:A:H2'	1:2:1650:C:C6	2.46	0.50
3:B:103:MET:CB	3:B:215:VAL:HG12	2.37	0.50
4:C:58:ILE:HD12	4:C:62:PHE:CE2	2.46	0.50
8:I:158:ASP:HA	8:I:161:PHE:CD2	2.47	0.50
11:N:64:LYS:HE2	11:N:70:LYS:HG3	1.93	0.50
16:Y:89:TYR:OH	16:Y:90:ARG:NH1	2.44	0.50
26:Q:138:PHE:O	26:Q:139:GLN:HG3	2.12	0.50
31:Z:89:ILE:HG21	31:Z:101:TYR:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:19:GLY:O	35:g:38:SER:HB2	2.11	0.50
35:g:132:ILE:HD11	35:g:152:VAL:HG21	1.93	0.50
35:g:136:ASN:ND2	35:g:140:ASP:HB2	2.25	0.50
39:j:134:LEU:HB3	39:j:144:ALA:CB	2.41	0.50
39:j:222:LEU:HD12	40:k:330:ILE:HG12	1.92	0.50
41:l:174:PHE:CE2	41:l:176:ASN:HB3	2.46	0.50
1:2:554:A:N3	9:J:19:TYR:HE2	2.10	0.50
1:2:808:G:H2'	1:2:809:G:C8	2.45	0.50
1:2:966:A:H2'	1:2:967:U:C6	2.46	0.50
1:2:976:A:N7	1:2:1023:U:O4	2.44	0.50
1:2:1533:U:C4	22:F:189:ILE:HD13	2.47	0.50
1:2:1711:G:H3'	1:2:1712:A:C8	2.46	0.50
2:A:117:GLU:HG3	2:A:117:GLU:O	2.11	0.50
2:A:198:MET:HG2	2:A:200:ASP:OD1	2.11	0.50
3:B:171:ILE:O	3:B:175:GLU:HG2	2.11	0.50
5:E:228:ILE:HD11	5:E:236:ILE:HG22	1.92	0.50
15:X:60:GLU:OE2	15:X:68:ILE:HG13	2.11	0.50
23:K:24:LYS:HA	23:K:63:TYR:HA	1.94	0.50
23:K:28:ASN:H	23:K:40:LEU:HD11	1.76	0.50
28:S:12:GLN:O	28:S:59:GLY:HA3	2.11	0.50
28:S:65:GLU:HA	28:S:68:ARG:HG2	1.93	0.50
32:c:42:ARG:HA	32:c:63:ALA:HB3	1.93	0.50
1:2:143:G:OP1	6:G:143:LYS:NZ	2.43	0.50
1:2:471:U:H2'	1:2:472:A:C8	2.46	0.50
1:2:751:G:C6	1:2:798:A:C6	2.99	0.50
1:2:865:G:H2'	1:2:866:G:H8	1.76	0.50
1:2:1415:A:H2'	1:2:1416:G:O4'	2.10	0.50
2:A:59:LEU:O	2:A:63:ILE:HG12	2.11	0.50
4:C:132:ALA:O	4:C:136:ILE:HG12	2.10	0.50
6:G:122:GLU:O	6:G:126:ASN:ND2	2.45	0.50
26:Q:28:LEU:HB2	26:Q:64:ASP:HA	1.93	0.50
28:S:75:ASN:HD21	28:S:78:HIS:CE1	2.29	0.50
40:k:119:ALA:HA	40:k:288:LYS:HE2	1.94	0.50
1:2:381:C:C2	1:2:382:G:C8	3.00	0.50
1:2:883:A:H4'	3:B:124:ASN:HD21	1.76	0.50
1:2:893:U:H2'	1:2:894:G:C8	2.46	0.50
1:2:1341:C:H4'	35:g:103:ARG:HH22	1.75	0.50
1:2:1752:A:H2'	36:i:44:ASN:HB2	1.93	0.50
3:B:135:LEU:HD12	3:B:217:LEU:HA	1.93	0.50
14:W:23:ARG:HH11	14:W:23:ARG:HG3	1.76	0.50
22:F:63:TYR:CE2	22:F:166:PRO:HB2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:12:LYS:HD2	26:Q:16:ALA:O	2.12	0.50
29:T:29:GLU:CD	29:T:29:GLU:H	2.19	0.50
30:U:44:ASN:HA	30:U:47:THR:HG22	1.93	0.50
34:f:120:GLU:OE2	34:f:127:GLY:N	2.44	0.50
35:g:321:GLN:HB3	35:g:323:MET:HE3	1.93	0.50
1:2:52:U:H2'	1:2:53:G:C8	2.44	0.50
1:2:196:A:N1	8:I:139:ASN:ND2	2.44	0.50
1:2:566:A:H1'	19:e:14:VAL:HG23	1.93	0.50
1:2:946:U:H2'	1:2:947:G:C8	2.47	0.50
1:2:1450:U:H2'	1:2:1451:G:C8	2.46	0.50
1:2:1488:A:H2'	1:2:1488:A:OP2	2.12	0.50
1:2:1496:G:H5''	29:T:72:GLY:HA3	1.93	0.50
1:2:1497:G:H2'	1:2:1498:C:C6	2.47	0.50
4:C:244:PRO:HA	4:C:247:VAL:HG12	1.93	0.50
9:J:23:ARG:O	9:J:27:GLU:OE1	2.29	0.50
10:L:97:TYR:O	10:L:99:ARG:HG2	2.12	0.50
12:O:25:ASP:HA	12:O:54:GLU:HB3	1.94	0.50
22:F:191:THR:OG1	22:F:194:GLU:HG2	2.12	0.50
24:M:52:LEU:HD12	24:M:128:LEU:HD11	1.94	0.50
24:M:56:VAL:HG12	24:M:58:SER:N	2.27	0.50
27:R:27:ASP:HB3	27:R:30:THR:HG22	1.94	0.50
29:T:66:TYR:HD2	29:T:67:LEU:HD22	1.76	0.50
35:g:23:SER:OG	35:g:70:GLN:O	2.15	0.50
35:g:157:VAL:HA	35:g:174:PHE:HB3	1.92	0.50
40:k:319:ARG:HH21	40:k:395:LEU:HD21	1.75	0.50
40:k:342:ILE:HD12	40:k:396:ILE:HD12	1.94	0.50
1:2:10:G:C6	1:2:11:A:C5	2.99	0.50
1:2:338:C:H2'	1:2:339:U:H6	1.76	0.50
1:2:571:C:H2'	1:2:572:C:C6	2.47	0.50
1:2:891:A:H2'	1:2:892:U:H6	1.76	0.50
1:2:969:A:H2'	1:2:970:A:H5'	1.94	0.50
1:2:1203:A:H61	33:d:15:GLY:HA3	1.76	0.50
5:E:104:ASP:N	5:E:108:ARG:O	2.32	0.50
11:N:141:TYR:CE1	11:N:146:ALA:HB2	2.47	0.50
22:F:151:VAL:HB	22:F:160:GLN:CD	2.37	0.50
28:S:14:ILE:C	28:S:15:LEU:HD12	2.37	0.50
1:2:309:C:P	15:X:20:ARG:HH12	2.34	0.50
1:2:318:U:H4'	1:2:322:A:C8	2.47	0.50
1:2:488:C:N3	1:2:489:C:N4	2.60	0.50
1:2:1004:A:H2'	1:2:1005:C:C6	2.46	0.50
1:2:1563:C:H2'	1:2:1564:U:H6	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1583:U:H2'	1:2:1584:A:H8	1.76	0.50
2:A:119:ARG:NH1	4:C:246:ASP:HA	2.26	0.50
5:E:175:PHE:HZ	5:E:198:ARG:HG3	1.76	0.50
7:H:40:ALA:C	7:H:41:LEU:HD12	2.37	0.50
7:H:139:ARG:NH2	14:W:53:ILE:HA	2.25	0.50
11:N:16:ILE:O	18:b:26:GLN:NE2	2.45	0.50
11:N:38:ILE:HB	11:N:42:ARG:HH12	1.76	0.50
13:V:11:LEU:HG	13:V:12:TYR:HD1	1.77	0.50
15:X:137:LYS:HB3	15:X:139:LYS:NZ	2.26	0.50
21:D:29:LEU:HB2	21:D:34:TYR:HB2	1.93	0.50
35:g:185:SER:O	35:g:196:GLU:HB2	2.11	0.50
35:g:204:ASN:HB2	35:g:224:ASP:CG	2.37	0.50
1:2:221:A:H2'	1:2:222:U:H6	1.77	0.50
1:2:300:A:H4'	8:I:27:PHE:CE1	2.46	0.50
1:2:737:A:HO2'	1:2:738:G:H8	1.60	0.50
1:2:864:A:OP2	14:W:3:ARG:NH2	2.45	0.50
2:A:79:ARG:O	2:A:83:GLN:NE2	2.45	0.50
18:b:73:LEU:HD23	18:b:73:LEU:H	1.76	0.50
27:R:115:LEU:HD22	27:R:117:LEU:HG	1.93	0.50
30:U:29:THR:OG1	30:U:84:MET:HE1	2.11	0.50
35:g:24:LEU:HD11	35:g:311:GLY:H	1.77	0.50
38:1:9:1MG:OP2	38:1:46:7MG:O3'	2.30	0.50
40:k:427:TYR:HE2	40:k:493:THR:HB	1.75	0.50
1:2:334:U:H2'	1:2:335:G:C8	2.46	0.49
1:2:886:A:N1	1:2:924:G:N2	2.54	0.49
1:2:1194:C:H42	26:Q:143:ARG:C	2.17	0.49
1:2:1213:U:O5'	1:2:1243:A:N6	2.44	0.49
13:V:38:GLN:HB2	13:V:46:ILE:HB	1.94	0.49
16:Y:12:VAL:HA	16:Y:22:GLN:O	2.12	0.49
17:a:97:PRO:O	17:a:99:GLN:N	2.42	0.49
22:F:102:ASN:N	22:F:102:ASN:ND2	2.60	0.49
23:K:49:LEU:HD13	23:K:54:PHE:HD2	1.77	0.49
30:U:44:ASN:ND2	30:U:103:ILE:HG12	2.27	0.49
40:k:128:PHE:HZ	40:k:139:LYS:HB2	1.77	0.49
1:2:32:U:O2'	1:2:593:A:N1	2.44	0.49
1:2:433:G:H2'	1:2:435:A:OP2	2.12	0.49
1:2:473:A:H5'	9:J:144:PRO:HG2	1.94	0.49
1:2:844:G:H2'	1:2:845:G:H5''	1.94	0.49
1:2:925:A:H2'	1:2:926:C:H6	1.75	0.49
1:2:1035:A:H2'	1:2:1036:C:C6	2.48	0.49
1:2:1064:A:H2'	1:2:1065:C:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1112:A:OP1	1:2:1114:U:H1'	2.12	0.49
1:2:1279:C:H5''	30:U:69:LYS:NZ	2.27	0.49
1:2:1280:G:H2'	1:2:1281:U:C6	2.47	0.49
1:2:1437:C:H2'	1:2:1438:C:C6	2.47	0.49
1:2:1545:A:H4'	28:S:88:ARG:HG3	1.93	0.49
7:H:31:SER:O	7:H:35:LYS:HG2	2.12	0.49
7:H:61:PHE:HB3	7:H:95:GLU:HB2	1.94	0.49
7:H:174:ASN:O	7:H:178:GLY:N	2.42	0.49
22:F:54:GLU:OE1	22:F:54:GLU:N	2.45	0.49
35:g:162:LEU:O	35:g:167:VAL:N	2.45	0.49
38:l:18:G:O6	39:j:110:SER:OG	2.26	0.49
1:2:245:G:H2'	1:2:246:A:C8	2.48	0.49
1:2:392:C:H4'	1:2:1672:C:H5'	1.93	0.49
1:2:411:A:C8	1:2:421:G:C2	3.01	0.49
1:2:1006:5MC:O3'	12:O:135:ARG:NH1	2.46	0.49
1:2:1304:U:H5''	1:2:1305:C:H5	1.77	0.49
1:2:1745:G:H2'	1:2:1746:G:H8	1.77	0.49
8:I:104:ILE:HG22	8:I:106:ALA:H	1.77	0.49
8:I:138:LYS:HZ3	8:I:142:ARG:HE	1.60	0.49
9:J:77:ILE:HD11	9:J:91:LYS:HA	1.94	0.49
10:L:93:TYR:HD1	10:L:100:TYR:CE1	2.30	0.49
12:O:40:ALA:HB1	12:O:67:VAL:HG22	1.93	0.49
22:F:42:ILE:HG23	22:F:71:TYR:CE1	2.47	0.49
28:S:84:TRP:CD1	28:S:84:TRP:H	2.30	0.49
38:l:8:U:H4'	38:l:9:1MG:OP2	2.12	0.49
39:j:201:ILE:O	39:j:205:LEU:HD23	2.12	0.49
41:l:172:THR:OG1	41:l:213:ILE:HG13	2.12	0.49
1:2:373:U:H2'	1:2:374:U:H6	1.76	0.49
1:2:559:U:C2	1:2:560:G:C8	3.01	0.49
1:2:963:U:H5'	11:N:128:TYR:HE1	1.77	0.49
1:2:1025:A:O4'	1:2:1027:C:N4	2.45	0.49
1:2:1034:G:H2'	1:2:1035:A:C8	2.48	0.49
1:2:1726:U:H2'	1:2:1727:C:C6	2.47	0.49
1:2:1738:A:H2'	1:2:1739:U:C6	2.47	0.49
4:C:47:GLY:O	4:C:50:VAL:HB	2.12	0.49
4:C:50:VAL:HG21	4:C:73:ILE:HG12	1.94	0.49
23:K:7:ASP:O	23:K:11:ILE:HG12	2.12	0.49
24:M:39:ARG:HE	24:M:43:LYS:HE3	1.78	0.49
35:g:6:ILE:HG21	35:g:258:TRP:CH2	2.47	0.49
35:g:260:THR:HG21	35:g:308:LEU:HD11	1.94	0.49
39:j:48:LEU:HD11	39:j:59:ILE:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:865:G:OP1	11:N:2:GLY:N	2.34	0.49
1:2:924:G:H2'	1:2:925:A:H8	1.76	0.49
1:2:1427:G:H2'	1:2:1428:U:H6	1.77	0.49
1:2:1562:U:H2'	1:2:1563:C:C6	2.47	0.49
1:2:1594:C:H3'	33:d:32:ARG:HH12	1.75	0.49
1:2:1606:U:H2'	1:2:1607:U:C6	2.47	0.49
1:2:1778:G:OP2	42:m:56:LYS:NZ	2.45	0.49
5:E:51:ARG:O	5:E:53:LYS:NZ	2.45	0.49
6:G:7:TYR:CZ	6:G:9:ILE:HB	2.48	0.49
6:G:32:ILE:HG12	6:G:54:GLY:H	1.76	0.49
6:G:82:SER:OG	6:G:83:CYS:N	2.44	0.49
6:G:85:ARG:O	6:G:87:ARG:NH1	2.45	0.49
18:b:56:CYS:SG	18:b:58:SER:OG	2.68	0.49
21:D:29:LEU:CB	21:D:34:TYR:HB2	2.42	0.49
22:F:57:ASP:OD2	22:F:59:SER:HB3	2.12	0.49
23:K:32:HIS:ND1	23:K:35:ILE:HD12	2.27	0.49
30:U:68:ARG:NH2	30:U:77:LYS:HD2	2.26	0.49
35:g:84:ALA:HB1	35:g:111:VAL:HG12	1.94	0.49
35:g:107:HIS:HE1	35:g:133:ARG:HB2	1.76	0.49
35:g:243:ALA:O	35:g:244:LYS:HG2	2.12	0.49
39:j:130:ILE:HG12	39:j:155:TRP:HH2	1.76	0.49
1:2:70:C:H2'	1:2:71:A:O4'	2.12	0.49
1:2:785:C:O3'	5:E:255:ARG:NH1	2.46	0.49
1:2:885:U:H3'	1:2:886:A:H8	1.78	0.49
1:2:1210:A:H2'	1:2:1211:G:O4'	2.13	0.49
1:2:1645:U:H2'	1:2:1646:A:H8	1.78	0.49
1:2:1656:G:O6	1:2:1741:U:O2	2.30	0.49
1:2:1741:U:H2'	1:2:1742:A:H8	1.74	0.49
1:2:1778:G:C8	42:m:59:LYS:HG3	2.48	0.49
3:B:124:ASN:OD1	3:B:125:VAL:N	2.45	0.49
4:C:157:HIS:CE1	4:C:179:ARG:HD2	2.46	0.49
5:E:255:ARG:O	5:E:259:HIS:NE2	2.46	0.49
6:G:159:ARG:HG3	6:G:170:THR:OG1	2.12	0.49
10:L:89:ASP:OD1	10:L:90:TYR:N	2.46	0.49
11:N:54:LEU:HD12	11:N:60:VAL:HG21	1.95	0.49
25:P:83:MET:SD	25:P:84:ILE:N	2.86	0.49
28:S:107:SER:O	28:S:110:ARG:NH2	2.45	0.49
40:k:96:ASN:OD1	40:k:97:ARG:N	2.45	0.49
40:k:128:PHE:CZ	40:k:139:LYS:HD2	2.47	0.49
1:2:983:G:H1	1:2:1016:U:H5	1.60	0.49
1:2:1046:G:H2'	1:2:1047:G:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1206:C:O2'	1:2:1207:A:OP2	2.26	0.49
1:2:1433:G:O6	23:K:64:TYR:OH	2.27	0.49
2:A:10:THR:OG1	2:A:11:SER:N	2.45	0.49
5:E:118:GLU:OE1	5:E:121:TYR:OH	2.16	0.49
7:H:124:LYS:O	7:H:127:GLU:HG3	2.13	0.49
12:O:88:GLY:HA2	12:O:122:PRO:HD3	1.95	0.49
29:T:22:LEU:HB3	29:T:55:TYR:HD2	1.77	0.49
35:g:86:TRP:HA	35:g:110:ASP:HB2	1.94	0.49
35:g:90:LEU:HD11	35:g:125:SER:HB2	1.93	0.49
1:2:88:U:C2	1:2:89:G:C8	3.01	0.49
1:2:630:G:N2	1:2:1103:U:OP1	2.45	0.49
1:2:768:C:H2'	1:2:769:A:O4'	2.13	0.49
1:2:866:G:OP1	11:N:3:ARG:HA	2.12	0.49
1:2:1146:A:H5'	4:C:96:ARG:HH21	1.77	0.49
1:2:1641:U:H2'	1:2:1642:C:C6	2.48	0.49
9:J:41:GLU:O	9:J:45:ILE:HG12	2.13	0.49
21:D:61:GLU:CD	21:D:61:GLU:H	2.17	0.49
30:U:57:ARG:HA	30:U:89:ARG:HG2	1.94	0.49
40:k:227:PRO:HB2	40:k:442:GLY:HA2	1.95	0.49
1:2:404:C:O2'	6:G:92:ARG:O	2.27	0.49
1:2:535:C:H3'	1:2:536:G:H8	1.78	0.49
1:2:654:G:H2'	1:2:655:G:C8	2.48	0.49
1:2:738:G:H2'	1:2:739:G:C8	2.48	0.49
1:2:751:G:C2	1:2:752:A:C5	3.01	0.49
1:2:871:G:H2'	1:2:872:U:O4'	2.13	0.49
1:2:977:A:H2'	1:2:978:A:O4'	2.13	0.49
1:2:1066:C:OP1	3:B:150:VAL:HG12	2.13	0.49
1:2:1737:C:H2'	1:2:1738:A:C8	2.46	0.49
3:B:141:ALA:HB1	3:B:207:LEU:HD11	1.95	0.49
4:C:157:HIS:O	4:C:198:VAL:HG23	2.13	0.49
8:I:6:ASP:OD2	8:I:8:ARG:HB2	2.13	0.49
15:X:55:GLU:OE1	15:X:73:ARG:NH2	2.46	0.49
18:b:11:THR:O	18:b:14:SER:OG	2.20	0.49
21:D:114:ALA:HB3	21:D:117:ARG:HB3	1.93	0.49
23:K:81:ASN:ND2	24:M:30:VAL:HG13	2.28	0.49
28:S:91:ASP:O	28:S:93:ASN:N	2.40	0.49
30:U:83:GLU:OE2	33:d:55:TYR:N	2.42	0.49
35:g:41:LYS:HB3	35:g:65:HIS:O	2.13	0.49
40:k:215:LEU:HD23	40:k:245:ILE:HB	1.94	0.49
41:l:163:PRO:HG2	41:l:223:GLU:HG2	1.95	0.49
1:2:12:U:H1'	1:2:1299:A:H1'	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:324:G:C6	1:2:343:A:C6	3.01	0.49
1:2:653:C:H2'	1:2:654:G:H8	1.78	0.49
1:2:1785:C:OP1	12:O:127:ARG:NH2	2.45	0.49
5:E:15:PRO:HG2	5:E:18:TRP:CZ3	2.47	0.49
7:H:22:GLN:HA	7:H:25:ILE:HD12	1.95	0.49
9:J:160:ARG:HH22	16:Y:30:PRO:HA	1.78	0.49
9:J:163:PRO:O	9:J:164:PHE:C	2.56	0.49
15:X:69:ARG:HG3	15:X:117:ILE:HG22	1.94	0.49
28:S:61:LEU:HD12	28:S:65:GLU:HG3	1.94	0.49
32:c:44:VAL:HG11	32:c:48:VAL:HG11	1.95	0.49
35:g:23:SER:HB2	35:g:72:VAL:HG23	1.94	0.49
36:i:101:ARG:O	36:i:104:LYS:HB3	2.13	0.49
38:1:22:G:H2'	38:1:22:G:N3	2.27	0.49
40:k:312:SER:OG	40:k:314:ARG:NH1	2.46	0.49
40:k:471:THR:OG1	40:k:489:SER:OG	2.29	0.49
1:2:266:U:OP1	6:G:183:ARG:NE	2.46	0.48
1:2:1229:A:H62	1:2:1254:G:H21	1.61	0.48
1:2:1356:G:H2'	1:2:1357:G:C8	2.48	0.48
1:2:1476:G:H5'	29:T:57:ARG:NH2	2.27	0.48
1:2:1500:G:N2	1:2:1502:G:H3'	2.28	0.48
1:2:1532:G:O2'	31:Z:72:GLY:O	2.24	0.48
4:C:106:VAL:HG23	4:C:120:ILE:HG22	1.94	0.48
6:G:59:GLN:OE1	6:G:72:ARG:NH1	2.31	0.48
7:H:67:LEU:HD12	7:H:70:TYR:HB2	1.95	0.48
10:L:2:SER:O	10:L:4:GLU:N	2.46	0.48
10:L:67:ARG:O	10:L:127:GLN:HB2	2.13	0.48
28:S:41:ARG:NH2	29:T:36:ILE:O	2.42	0.48
39:j:210:ASP:OD1	39:j:211:MET:N	2.46	0.48
1:2:609:G:O5'	15:X:19:ARG:NH1	2.45	0.48
1:2:653:C:H5''	1:2:673:C:N4	2.28	0.48
1:2:1581:A:N1	1:2:1609:A:H5''	2.28	0.48
1:2:1653:A:H62	1:2:1743:G:HO2'	1.58	0.48
2:A:157:ASP:OD1	13:V:60:ARG:NE	2.41	0.48
5:E:207:LEU:HD12	5:E:219:VAL:HG22	1.95	0.48
9:J:121:SER:O	9:J:121:SER:OG	2.31	0.48
15:X:142:LYS:HG2	15:X:144:ARG:H	1.77	0.48
26:Q:31:VAL:O	26:Q:34:SER:OG	2.30	0.48
26:Q:41:PRO:HB2	26:Q:44:LEU:HB2	1.95	0.48
27:R:34:LEU:O	27:R:38:ILE:HG12	2.13	0.48
36:i:102:THR:O	36:i:105:ASN:N	2.46	0.48
39:j:252:THR:HA	39:j:255:ILE:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:380:LEU:HD23	40:k:398:VAL:HG12	1.94	0.48
41:l:233:TYR:OH	41:l:270:SER:O	2.26	0.48
1:2:256:A:N3	8:I:64:ASN:ND2	2.60	0.48
1:2:708:C:C2	1:2:710:U:H5	2.31	0.48
1:2:885:U:H2'	1:2:886:A:C8	2.49	0.48
1:2:890:A:H2'	1:2:891:A:C8	2.48	0.48
1:2:1335:A:H2'	1:2:1336:A:O4'	2.13	0.48
4:C:73:ILE:O	4:C:77:LEU:HD23	2.13	0.48
4:C:131:ARG:O	4:C:135:ILE:HG12	2.14	0.48
6:G:142:ARG:O	6:G:146:GLY:N	2.46	0.48
7:H:137:GLY:HA3	7:H:153:LEU:HB2	1.94	0.48
8:I:113:TYR:CE1	8:I:117:TYR:HB2	2.49	0.48
22:F:107:GLY:HA2	22:F:109:LYS:NZ	2.28	0.48
22:F:162:VAL:CB	32:c:45:LYS:HE3	2.22	0.48
26:Q:41:PRO:C	26:Q:43:ILE:N	2.71	0.48
31:Z:50:ILE:HD12	31:Z:70:LYS:NZ	2.28	0.48
1:2:26:A:H2'	1:2:27:U:C6	2.48	0.48
1:2:268:G:H2'	1:2:269:C:C6	2.49	0.48
1:2:403:G:H2'	1:2:404:C:C6	2.47	0.48
1:2:564:C:OP2	36:i:62:ARG:NH2	2.46	0.48
1:2:860:U:H4'	11:N:20:ARG:NH2	2.28	0.48
1:2:902:U:O2'	1:2:904:A:N7	2.38	0.48
1:2:932:A:C6	1:2:934:U:N3	2.82	0.48
1:2:951:A:H2'	1:2:952:G:H8	1.78	0.48
1:2:1106:G:O2'	1:2:1107:G:H5'	2.14	0.48
1:2:1182:A:C2	25:P:100:LYS:HG3	2.49	0.48
1:2:1182:A:N6	25:P:122:THR:O	2.46	0.48
1:2:1370:G:H2'	1:2:1371:A:H8	1.78	0.48
1:2:1765:G:H4'	1:2:1766:G:O5'	2.11	0.48
4:C:145:ARG:HD2	4:C:227:TYR:CE1	2.48	0.48
5:E:67:GLN:HG3	5:E:69:HIS:ND1	2.28	0.48
5:E:121:TYR:CG	5:E:161:LYS:HE3	2.48	0.48
5:E:173:ILE:HD11	5:E:235:TRP:NE1	2.29	0.48
21:D:222:VAL:HG22	35:g:230:TRP:HZ3	1.78	0.48
22:F:42:ILE:HG12	22:F:71:TYR:CZ	2.48	0.48
22:F:89:CYS:SG	22:F:94:ARG:NH1	2.86	0.48
25:P:83:MET:HB3	25:P:116:LEU:HD12	1.95	0.48
31:Z:83:LEU:HD21	31:Z:89:ILE:HG13	1.95	0.48
36:i:57:ARG:HH12	36:i:81:LEU:HD11	1.78	0.48
1:2:261:U:H2'	1:2:262:C:C6	2.48	0.48
1:2:789:U:C5	1:2:790:A:C5	3.00	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:861:A:H4'	14:W:57:ARG:HD2	1.95	0.48
1:2:862:A:N7	1:2:963:U:O4	2.46	0.48
1:2:888:U:H2'	1:2:889:C:C6	2.47	0.48
1:2:959:U:O2'	11:N:48:SER:O	2.31	0.48
1:2:985:G:H3'	1:2:986:G:H8	1.79	0.48
1:2:988:U:H2'	1:2:989:C:O4'	2.13	0.48
1:2:1604:C:H2'	1:2:1605:G:C8	2.48	0.48
1:2:1756:U:O2'	42:m:84:GLN:OE1	2.30	0.48
3:B:179:SER:HB3	3:B:183:GLN:OE1	2.14	0.48
5:E:9:LEU:HD13	5:E:30:ARG:HA	1.95	0.48
6:G:64:LYS:NZ	6:G:82:SER:O	2.39	0.48
6:G:122:GLU:HG2	6:G:123:GLY:N	2.29	0.48
9:J:37:LYS:HG2	19:e:33:ARG:N	2.29	0.48
10:L:59:PRO:HB3	10:L:66:ILE:HD11	1.96	0.48
12:O:137:LEU:HD11	37:3:25:A:C5	2.49	0.48
34:f:140:GLY:HA2	34:f:143:HIS:HB3	1.96	0.48
35:g:43:LEU:HD12	35:g:93:TRP:HZ3	1.78	0.48
40:k:237:GLU:HG2	40:k:274:ILE:HB	1.95	0.48
1:2:123:G:P	5:E:77:ARG:HH22	2.37	0.48
1:2:507:U:N3	1:2:508:G:N7	2.61	0.48
1:2:836:G:H2'	1:2:837:G:O4'	2.14	0.48
1:2:1338:C:O2'	1:2:1340:A:N7	2.46	0.48
1:2:1455:C:H4'	28:S:137:HIS:CD2	2.49	0.48
1:2:1784:G:H2'	1:2:1785:C:C6	2.48	0.48
6:G:7:TYR:O	6:G:11:GLY:CA	2.62	0.48
11:N:132:VAL:HG13	11:N:134:VAL:HG23	1.95	0.48
16:Y:106:GLN:O	16:Y:110:GLN:HG2	2.13	0.48
22:F:50:PHE:CE2	22:F:69:PRO:HA	2.48	0.48
22:F:161:ALA:CB	22:F:227:ARG:HA	2.44	0.48
22:F:176:LEU:HG	22:F:212:ALA:HA	1.94	0.48
26:Q:60:PHE:HB2	26:Q:63:ILE:HG13	1.96	0.48
27:R:33:ARG:O	27:R:36:ASP:HB2	2.14	0.48
1:2:274:C:H5''	1:2:275:C:OP2	2.14	0.48
1:2:338:C:H2'	1:2:339:U:C6	2.49	0.48
1:2:627:G:P	11:N:124:ARG:HH21	2.37	0.48
1:2:763:G:C5'	9:J:78:ARG:HH22	2.26	0.48
1:2:900:G:H2'	1:2:901:G:O4'	2.14	0.48
1:2:901:G:H2'	1:2:902:U:C6	2.48	0.48
1:2:1288:U:H2'	1:2:1289:PSU:H6	1.78	0.48
1:2:1365:C:OP1	26:Q:66:ARG:NE	2.38	0.48
1:2:1392:G:C6	1:2:1403:G:C6	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1501:A:H2'	1:2:1502:G:C8	2.49	0.48
1:2:1657:A:H2'	1:2:1658:A:H8	1.78	0.48
1:2:1754:A:N6	36:i:69:VAL:O	2.36	0.48
3:B:83:LYS:NZ	3:B:106:THR:HA	2.29	0.48
5:E:161:LYS:O	5:E:170:THR:N	2.38	0.48
6:G:10:ASN:HD22	6:G:128:THR:HG23	1.78	0.48
7:H:99:LEU:HD12	7:H:100:PRO:HD2	1.95	0.48
11:N:130:ARG:HD3	11:N:137:PRO:HA	1.96	0.48
18:b:36:LYS:HB2	18:b:78:SER:OG	2.14	0.48
21:D:148:LYS:NZ	21:D:150:MET:HB2	2.28	0.48
28:S:4:VAL:HG22	28:S:6:GLN:N	2.26	0.48
30:U:68:ARG:NH1	30:U:78:THR:H	2.12	0.48
31:Z:49:ARG:O	31:Z:53:GLU:HG2	2.13	0.48
39:j:77:ASP:HB3	39:j:82:TYR:H	1.79	0.48
1:2:938:A:H2'	1:2:939:A:C8	2.49	0.48
1:2:1134:U:H2'	1:2:1135:U:C6	2.48	0.48
1:2:1315:G:H2'	1:2:1316:C:C6	2.49	0.48
1:2:1331:C:O2'	21:D:162:GLN:HB3	2.14	0.48
1:2:1486:G:H3'	1:2:1513:A:N6	2.25	0.48
1:2:1564:U:H5''	28:S:39:GLY:H	1.79	0.48
1:2:1565:U:H5'	28:S:37:GLY:H	1.79	0.48
1:2:1754:A:N6	36:i:66:ARG:O	2.46	0.48
3:B:171:ILE:HG13	3:B:174:ARG:NH2	2.29	0.48
10:L:78:THR:HA	10:L:84:ILE:HD12	1.96	0.48
23:K:25:LYS:HG3	23:K:64:TYR:HE2	1.79	0.48
30:U:16:GLU:OE1	30:U:101:LYS:NZ	2.43	0.48
30:U:113:ASP:OD1	30:U:114:VAL:N	2.46	0.48
38:1:24:G:H2'	38:1:25:C:C6	2.49	0.48
38:1:47:H2U:H4'	38:1:48:5MC:OP2	2.13	0.48
40:k:205:LEU:HD13	40:k:500:ALA:HB3	1.95	0.48
1:2:54:C:P	16:Y:110:GLN:HE22	2.37	0.48
1:2:775:G:C6	1:2:785:C:C4	3.01	0.48
1:2:1266:G:O2'	1:2:1446:G:O2'	2.28	0.48
1:2:1372:C:H2'	1:2:1373:U:C6	2.49	0.48
1:2:1577:U:O2'	26:Q:139:GLN:HA	2.14	0.48
5:E:75:LYS:HD2	5:E:77:ARG:CZ	2.44	0.48
5:E:87:MET:HE3	5:E:123:LEU:HB3	1.95	0.48
7:H:139:ARG:NH1	14:W:53:ILE:HA	2.26	0.48
8:I:38:ILE:HD12	8:I:60:ILE:O	2.13	0.48
11:N:146:ALA:O	11:N:150:VAL:HG22	2.14	0.48
13:V:17:CYS:SG	13:V:20:THR:N	2.87	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:b:32:PHE:HE1	18:b:47:PHE:HD1	1.61	0.48
22:F:37:GLN:HG3	22:F:38:ALA:N	2.29	0.48
22:F:101:MET:HB2	22:F:182:ARG:CZ	2.44	0.48
22:F:129:GLN:O	22:F:130:ASN:C	2.55	0.48
29:T:25:GLN:HG2	29:T:27:LYS:H	1.79	0.48
35:g:285:PHE:CE2	35:g:294:PRO:HD2	2.49	0.48
41:l:229:TYR:HA	41:l:232:GLU:HG2	1.96	0.48
1:2:267:C:OP1	6:G:176:GLN:NE2	2.42	0.48
1:2:586:C:H2'	1:2:587:U:H6	1.79	0.48
1:2:780:A:H4'	1:2:781:A:C5	2.49	0.48
1:2:815:G:H2'	1:2:816:A:H8	1.78	0.48
1:2:880:A:N1	1:2:947:G:C6	2.82	0.48
1:2:974:C:H3'	1:2:975:G:H8	1.77	0.48
1:2:1198:G:C4	33:d:40:ARG:NH2	2.82	0.48
1:2:1427:G:H2'	1:2:1428:U:C6	2.48	0.48
1:2:1551:G:H4'	33:d:14:PHE:CZ	2.49	0.48
1:2:1776:G:H2'	1:2:1777:U:O4'	2.14	0.48
2:A:117:GLU:HG3	4:C:45:LYS:HE3	1.96	0.48
3:B:187:LYS:O	3:B:190:PRO:HD2	2.14	0.48
7:H:131:PHE:CD1	7:H:131:PHE:C	2.92	0.48
8:I:3:ILE:O	8:I:30:GLY:N	2.37	0.48
8:I:104:ILE:HD11	8:I:168:ALA:HB3	1.95	0.48
10:L:69:LYS:HD2	10:L:70:ILE:H	1.79	0.48
11:N:69:ASN:HB2	11:N:74:ILE:HD11	1.95	0.48
16:Y:86:GLU:HB3	16:Y:91:LEU:HD21	1.95	0.48
22:F:125:VAL:O	31:Z:58:ARG:NH2	2.30	0.48
27:R:71:PHE:H	27:R:74:GLN:HE21	1.59	0.48
28:S:28:VAL:HG12	28:S:58:ALA:HA	1.95	0.48
35:g:283:PRO:HG3	35:g:320:TRP:CZ2	2.48	0.48
1:2:293:C:H2'	1:2:294:A:C8	2.46	0.47
1:2:1518:U:H4'	1:2:1521:G:N2	2.29	0.47
2:A:183:ARG:O	13:V:44:ARG:NH1	2.47	0.47
5:E:47:PHE:HD1	5:E:48:LEU:HD23	1.79	0.47
5:E:97:GLU:HB3	5:E:99:PHE:CE1	2.49	0.47
5:E:129:VAL:HG22	5:E:139:VAL:HG23	1.96	0.47
5:E:162:VAL:HG12	5:E:164:LEU:H	1.79	0.47
9:J:45:ILE:HG13	9:J:105:LEU:HD21	1.96	0.47
18:b:34:ASP:HB2	18:b:43:ILE:HD11	1.96	0.47
21:D:143:ARG:NH1	37:3:38:C:O2	2.36	0.47
21:D:205:ALA:O	27:R:42:GLN:NE2	2.47	0.47
23:K:61:TRP:CE2	33:d:23:ILE:HD12	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:R:5:ARG:HD2	27:R:53:TYR:CD1	2.48	0.47
30:U:35:GLU:HB3	30:U:89:ARG:HH12	1.79	0.47
33:d:21:CYS:N	33:d:26:SER:O	2.47	0.47
34:f:81:LYS:HG2	34:f:82:LYS:H	1.78	0.47
38:1:7:G:O2'	38:1:49:5MC:H6	1.96	0.47
39:j:116:ALA:O	39:j:120:GLN:N	2.47	0.47
40:k:501:LEU:HD11	40:k:515:ALA:HB2	1.96	0.47
1:2:116:U:O2'	1:2:332:A:N3	2.47	0.47
1:2:1107:G:H2'	15:X:25:ALA:HB1	1.96	0.47
1:2:1164:G:O3'	22:F:101:MET:CE	2.62	0.47
1:2:1329:G:H2'	1:2:1330:A:O4'	2.14	0.47
1:2:1343:A:H2'	1:2:1344:A:C8	2.49	0.47
1:2:1564:U:H5''	28:S:39:GLY:N	2.29	0.47
1:2:1757:C:C2	1:2:1758:G:C8	3.02	0.47
4:C:118:LEU:O	4:C:140:SER:OG	2.32	0.47
6:G:159:ARG:NE	6:G:172:ALA:HB2	2.29	0.47
10:L:58:CYS:HG	10:L:61:THR:H	1.62	0.47
11:N:33:VAL:HG21	11:N:66:ILE:HG21	1.95	0.47
13:V:71:ARG:HD2	18:b:4:VAL:HG11	1.96	0.47
17:a:74:CYS:SG	17:a:77:CYS:N	2.68	0.47
17:a:97:PRO:C	17:a:99:GLN:H	2.21	0.47
28:S:72:ILE:HG23	28:S:79:TYR:HD2	1.79	0.47
1:2:690:A:H2'	1:2:691:U:O4'	2.15	0.47
1:2:875:G:C6	1:2:935:G:C6	3.03	0.47
1:2:1138:A:C5	1:2:1139:G:C8	3.02	0.47
4:C:103:PHE:CD2	4:C:126:VAL:HG22	2.49	0.47
7:H:9:LEU:HD21	7:H:21:ALA:HB2	1.96	0.47
9:J:145:SER:HB3	9:J:147:MET:HE3	1.97	0.47
16:Y:23:PHE:CE1	16:Y:75:VAL:HG23	2.49	0.47
16:Y:40:LEU:O	16:Y:44:LEU:HD23	2.15	0.47
17:a:12:LYS:HB2	17:a:33:ASP:OD2	2.14	0.47
18:b:38:PRO:HD3	18:b:77:THR:HG22	1.96	0.47
23:K:59:PHE:CZ	23:K:62:GLN:HA	2.50	0.47
29:T:25:GLN:NE2	29:T:27:LYS:HD2	2.29	0.47
1:2:429:G:H2'	1:2:430:C:C6	2.50	0.47
1:2:1066:C:H2'	1:2:1067:C:C6	2.50	0.47
1:2:1172:C:H2'	1:2:1173:C:H6	1.78	0.47
1:2:1198:G:H22	33:d:31:ILE:CD1	2.26	0.47
1:2:1228:G:N2	1:2:1254:G:O2'	2.48	0.47
1:2:1233:A:H3'	1:2:1244:G:H2'	1.97	0.47
1:2:1506:U:H2'	1:2:1507:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1671:G:H2'	1:2:1672:C:H6	1.79	0.47
1:2:1779:A:H2'	1:2:1780:MA6:C8	2.44	0.47
2:A:31:VAL:HG22	2:A:33:GLN:H	1.80	0.47
2:A:188:LEU:HD21	2:A:195:TRP:CG	2.48	0.47
5:E:86:PHE:C	5:E:88:ASP:H	2.21	0.47
14:W:14:ILE:HG13	14:W:27:ILE:HD11	1.96	0.47
15:X:107:PHE:CE2	15:X:114:LYS:HG2	2.49	0.47
17:a:13:LYS:O	17:a:13:LYS:HG2	2.14	0.47
22:F:50:PHE:CD2	22:F:69:PRO:HA	2.50	0.47
24:M:23:VAL:O	24:M:27:THR:HG23	2.14	0.47
35:g:257:PHE:CD2	35:g:272:LEU:HB2	2.50	0.47
40:k:84:PHE:CE2	40:k:348:LYS:HE2	2.50	0.47
45:k:601:GCP:O3'	41:l:238:THR:CB	2.61	0.47
41:l:247:LYS:HD3	41:l:258:VAL:HG21	1.96	0.47
1:2:81:G:H2'	1:2:82:U:O4'	2.15	0.47
1:2:140:A:OP1	6:G:149:LYS:NZ	2.47	0.47
1:2:842:U:H2'	1:2:843:A:H8	1.80	0.47
1:2:935:G:H2'	1:2:936:C:H6	1.78	0.47
1:2:1055:U:N3	1:2:1062:U:O4	2.48	0.47
1:2:1291:G:H2'	1:2:1292:U:O2	2.15	0.47
1:2:1497:G:H2'	1:2:1498:C:H6	1.80	0.47
1:2:1613:C:P	32:c:47:PRO:HB3	2.54	0.47
1:2:1632:C:H1'	37:3:35:C:C5	2.50	0.47
1:2:1658:A:H2'	1:2:1659:U:H6	1.77	0.47
1:2:1679:A:O3'	6:G:31:ARG:NH1	2.42	0.47
1:2:1777:U:H2'	1:2:1779:A:OP2	2.14	0.47
3:B:175:GLU:OE1	3:B:187:LYS:NZ	2.47	0.47
7:H:8:ILE:HD11	7:H:21:ALA:HB1	1.97	0.47
9:J:74:ASN:O	9:J:78:ARG:HG3	2.14	0.47
10:L:17:PRO:O	10:L:19:ILE:HD12	2.14	0.47
20:h:5:TRP:N	20:h:5:TRP:CD1	2.83	0.47
29:T:85:ASN:O	29:T:87:GLY:N	2.43	0.47
30:U:78:THR:O	30:U:79:TRP:HD1	1.98	0.47
35:g:301:TRP:CE2	35:g:308:LEU:HD21	2.49	0.47
36:i:63:GLY:C	36:i:65:LEU:H	2.22	0.47
1:2:67:A:H2'	1:2:69:G:H8	1.79	0.47
1:2:210:U:H2'	1:2:211:U:C6	2.48	0.47
1:2:245:G:H8	5:E:202:GLU:OE2	1.97	0.47
1:2:321:G:H8	1:2:321:G:OP2	1.98	0.47
1:2:409:A:H2'	1:2:410:C:C6	2.50	0.47
1:2:556:G:O4'	19:e:57:ASN:ND2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:987:A:H2'	1:2:988:U:C6	2.50	0.47
1:2:1227:G:OP2	24:M:38:LEU:HG	2.14	0.47
1:2:1652:G:N2	1:2:1743:G:H2'	2.29	0.47
1:2:1683:G:C6	1:2:1715:G:C6	3.03	0.47
2:A:87:LEU:HD23	2:A:97:PRO:HB2	1.96	0.47
3:B:118:GLN:HE21	3:B:143:THR:N	2.13	0.47
3:B:174:ARG:HA	3:B:177:GLN:HE21	1.79	0.47
8:I:67:TRP:O	8:I:71:GLY:CA	2.62	0.47
8:I:84:HIS:CD2	8:I:86:SER:H	2.32	0.47
9:J:48:GLN:O	9:J:52:ILE:HG12	2.14	0.47
11:N:88:LEU:HD12	11:N:125:LEU:HB3	1.96	0.47
12:O:81:ILE:HG23	12:O:115:ILE:HA	1.97	0.47
13:V:17:CYS:O	13:V:21:ASN:N	2.36	0.47
14:W:24:GLN:NE2	18:b:5:GLN:H	2.13	0.47
26:Q:39:VAL:HG21	26:Q:48:VAL:HG21	1.95	0.47
30:U:68:ARG:NE	30:U:79:TRP:HE1	2.11	0.47
31:Z:58:ARG:HD2	31:Z:103:ARG:HH22	1.80	0.47
38:l:4:G:P	39:j:185:ARG:HH12	2.38	0.47
40:k:503:ARG:HG3	40:k:512:ILE:HD13	1.95	0.47
1:2:22:A:H2'	1:2:23:G:H8	1.79	0.47
1:2:116:U:H4'	1:2:333:G:H1'	1.96	0.47
1:2:415:A:H5'	1:2:416:A:C8	2.50	0.47
1:2:511:A:H5''	9:J:163:PRO:CG	2.42	0.47
1:2:780:A:H62	16:Y:10:ARG:NH2	2.13	0.47
1:2:785:C:O2'	5:E:255:ARG:NH1	2.48	0.47
1:2:786:G:H5'	5:E:255:ARG:NH2	2.20	0.47
1:2:818:G:N3	1:2:852:G:N2	2.63	0.47
1:2:932:A:OP1	3:B:116:LYS:NZ	2.41	0.47
1:2:958:U:C6	11:N:61:THR:HB	2.49	0.47
1:2:1133:C:H2'	1:2:1134:U:C6	2.50	0.47
1:2:1234:C:OP2	1:2:1244:G:H8	1.97	0.47
1:2:1311:A:H2'	1:2:1312:A:C8	2.50	0.47
1:2:1449:C:H2'	1:2:1450:U:C6	2.50	0.47
1:2:1450:U:H2'	1:2:1451:G:H8	1.78	0.47
1:2:1501:A:H8	1:2:1501:A:OP1	1.97	0.47
1:2:1738:A:H2'	1:2:1739:U:H6	1.80	0.47
2:A:18:LEU:HG	2:A:23:HIS:NE2	2.30	0.47
2:A:47:VAL:HG11	27:R:109:LEU:HD21	1.97	0.47
3:B:67:GLU:HB2	3:B:85:LYS:HZ1	1.78	0.47
3:B:133:TYR:CE2	3:B:220:GLN:HG3	2.49	0.47
5:E:205:PHE:HD2	5:E:221:ARG:HD2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:32:ILE:HG23	6:G:53:ALA:HA	1.97	0.47
8:I:36:THR:HB	8:I:57:ALA:O	2.15	0.47
10:L:42:PHE:HE2	10:L:140:LEU:HD13	1.78	0.47
12:O:80:HIS:CD2	12:O:114:ARG:HB2	2.50	0.47
14:W:49:GLU:N	14:W:64:GLN:HE21	2.03	0.47
17:a:73:TYR:HB3	17:a:78:ALA:HB2	1.96	0.47
21:D:207:THR:O	27:R:40:THR:OG1	2.26	0.47
22:F:45:PHE:HB2	22:F:48:TRP:CZ3	2.50	0.47
26:Q:99:GLU:OE1	26:Q:99:GLU:N	2.47	0.47
27:R:27:ASP:O	27:R:31:ASN:ND2	2.48	0.47
28:S:41:ARG:HD3	29:T:38:LYS:NZ	2.29	0.47
30:U:22:ILE:HG21	30:U:100:VAL:HG11	1.95	0.47
32:c:43:ASN:HB2	32:c:45:LYS:HZ2	1.78	0.47
35:g:302:SER:OG	35:g:304:ASP:OD1	2.18	0.47
1:2:255:A:H2'	1:2:256:A:C8	2.50	0.47
1:2:543:A:O3'	19:e:31:LYS:NZ	2.42	0.47
1:2:638:U:OP1	7:H:112:ARG:NH2	2.42	0.47
1:2:752:A:C6	1:2:753:A:N1	2.83	0.47
1:2:909:C:H2'	1:2:910:U:C6	2.50	0.47
1:2:1362:U:H5''	1:2:1363:G:C8	2.49	0.47
1:2:1481:A:H4'	26:Q:71:GLY:HA2	1.96	0.47
4:C:167:CYS:O	4:C:170:VAL:HG12	2.15	0.47
6:G:36:VAL:HG12	6:G:50:PHE:HB2	1.97	0.47
6:G:88:ARG:HG3	6:G:89:ASN:N	2.30	0.47
7:H:38:LEU:HA	7:H:41:LEU:HD22	1.96	0.47
7:H:162:ILE:HG23	7:H:165:LYS:CB	2.44	0.47
8:I:70:GLU:OE2	8:I:72:VAL:HG22	2.15	0.47
10:L:10:GLU:OE1	10:L:11:ARG:N	2.48	0.47
10:L:24:LYS:HB3	10:L:24:LYS:HE2	1.80	0.47
12:O:84:ARG:HG3	12:O:120:PRO:HD3	1.97	0.47
13:V:26:ALA:HB1	13:V:27:LYS:NZ	2.30	0.47
22:F:118:HIS:HD2	31:Z:98:GLN:HE21	1.62	0.47
24:M:57:GLU:HG3	24:M:81:LYS:HG2	1.97	0.47
26:Q:40:GLN:C	26:Q:42:GLU:N	2.72	0.47
26:Q:99:GLU:CD	35:g:61:SER:H	2.22	0.47
28:S:35:ILE:HG23	28:S:102:ALA:HB2	1.95	0.47
30:U:24:ILE:HG22	30:U:116:VAL:HG22	1.97	0.47
30:U:57:ARG:HG3	30:U:89:ARG:HG2	1.97	0.47
32:c:27:GLN:NE2	32:c:43:ASN:OD1	2.48	0.47
35:g:110:ASP:OD2	35:g:128:ARG:NE	2.48	0.47
39:j:241:ILE:HD12	39:j:268:PRO:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:m:85:ARG:HH22	42:m:108:PHE:HB2	1.80	0.47
1:2:54:C:OP1	16:Y:110:GLN:NE2	2.48	0.47
1:2:210:U:H2'	1:2:211:U:H6	1.80	0.47
1:2:387:G:C6	1:2:409:A:C6	3.03	0.47
1:2:471:U:OP1	9:J:11:THR:HG22	2.15	0.47
1:2:739:G:H2'	1:2:740:A:C8	2.50	0.47
1:2:933:C:N3	1:2:1076:C:H4'	2.30	0.47
1:2:1608:G:O2'	22:F:109:LYS:HE2	2.14	0.47
2:A:89:TYR:HE2	2:A:177:LEU:HB3	1.79	0.47
5:E:42:LEU:HB2	5:E:109:PHE:HE2	1.80	0.47
5:E:157:ASN:ND2	5:E:222:LEU:HD21	2.30	0.47
9:J:64:GLU:HA	9:J:69:ARG:NH1	2.30	0.47
11:N:40:TYR:HB3	11:N:50:ILE:HD12	1.96	0.47
21:D:42:THR:HB	21:D:45:LYS:O	2.14	0.47
22:F:55:VAL:HG13	22:F:140:ILE:HD11	1.96	0.47
35:g:120:SER:O	35:g:121:SER:C	2.57	0.47
42:m:26:ILE:HG23	42:m:44:GLY:O	2.14	0.47
1:2:242:G:H2'	1:2:243:A:H8	1.79	0.47
1:2:761:G:N2	1:2:762:A:H62	2.12	0.47
1:2:778:G:H5'	1:2:780:A:N1	2.30	0.47
1:2:869:C:H2'	1:2:870:G:H8	1.80	0.47
1:2:1069:C:H5''	18:b:17:ARG:NH2	2.26	0.47
1:2:1242:G:OP1	1:2:1242:G:N2	2.48	0.47
1:2:1403:G:H2'	1:2:1404:A:H8	1.79	0.47
1:2:1582:G:H22	1:2:1609:A:P	2.38	0.47
1:2:1763:A:C5	1:2:1765:G:C6	3.03	0.47
6:G:57:ASP:OD1	6:G:58:LYS:N	2.48	0.47
7:H:35:LYS:C	7:H:37:ASP:H	2.21	0.47
8:I:118:GLY:HA3	8:I:144:TRP:CH2	2.50	0.47
13:V:38:GLN:HG2	13:V:50:TYR:HA	1.97	0.47
18:b:2:VAL:O	18:b:3:LEU:HB2	2.14	0.47
21:D:74:GLU:OE1	21:D:81:ARG:HA	2.15	0.47
28:S:45:LEU:HA	28:S:48:LYS:HD2	1.97	0.47
29:T:108:LEU:HG	29:T:113:VAL:HG23	1.96	0.47
35:g:182:ILE:HG23	35:g:200:ILE:HG13	1.97	0.47
38:1:37:T6A:H153	38:1:38:A:C2	2.50	0.47
40:k:353:ILE:HG13	40:k:419:ALA:HA	1.95	0.47
1:2:92:A:N6	6:G:89:ASN:OD1	2.48	0.46
1:2:236:C:H4'	1:2:237:U:C6	2.50	0.46
1:2:374:U:H2'	1:2:375:C:H6	1.80	0.46
1:2:1614:G:H2'	1:2:1615:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1754:A:N1	36:i:70:TRP:HA	2.30	0.46
2:A:206:ASN:O	2:A:210:ILE:N	2.45	0.46
6:G:64:LYS:NZ	6:G:81:HIS:HB3	2.30	0.46
7:H:47:ARG:O	7:H:58:LEU:HD12	2.15	0.46
9:J:100:LYS:HB2	9:J:102:GLU:OE2	2.15	0.46
11:N:135:LEU:HD13	11:N:139:TRP:CG	2.49	0.46
16:Y:16:PRO:C	16:Y:19:ALA:H	2.24	0.46
26:Q:77:GLN:O	26:Q:81:ILE:HG13	2.15	0.46
33:d:29:GLY:HA2	33:d:40:ARG:NH2	2.29	0.46
40:k:353:ILE:HG12	40:k:417:VAL:HG12	1.97	0.46
1:2:14:C:H5'	4:C:169:SER:OG	2.15	0.46
1:2:409:A:H2'	1:2:410:C:H6	1.80	0.46
1:2:843:A:H2'	1:2:844:G:H8	1.77	0.46
1:2:1085:A:O2'	1:2:1086:A:O5'	2.32	0.46
1:2:1091:A:C6	1:2:1093:G:C4	3.03	0.46
1:2:1443:G:C2	34:f:89:LYS:HA	2.50	0.46
1:2:1608:G:OP1	22:F:109:LYS:HD3	2.15	0.46
1:2:1697:G:H5''	1:2:1702:U:H5'	1.96	0.46
2:A:11:SER:O	2:A:14:ALA:N	2.48	0.46
4:C:40:TRP:NE1	4:C:72:GLN:HE21	2.13	0.46
6:G:70:PRO:HD3	6:G:101:ILE:HD12	1.97	0.46
7:H:20:VAL:HG12	7:H:85:PHE:CZ	2.50	0.46
7:H:134:GLU:CD	11:N:21:ASN:HD21	2.23	0.46
15:X:74:VAL:HG21	15:X:104:LEU:HD11	1.97	0.46
27:R:29:GLN:O	27:R:32:LYS:HB3	2.15	0.46
35:g:44:ILE:HB	35:g:46:TRP:CH2	2.50	0.46
35:g:153:THR:N	35:g:177:ALA:O	2.46	0.46
36:i:38:ILE:HD12	36:i:75:ASP:HB3	1.96	0.46
40:k:248:GLN:HE22	40:k:262:HIS:HD2	1.63	0.46
40:k:320:SER:HB2	40:k:407:CYS:HA	1.97	0.46
1:2:598:A:H2'	1:2:599:U:C6	2.50	0.46
1:2:710:U:O4	1:2:730:G:N1	2.49	0.46
1:2:827:U:O4	1:2:828:A:N6	2.49	0.46
1:2:1106:G:H2'	1:2:1107:G:N3	2.30	0.46
1:2:1470:C:O2'	22:F:188:ASN:O	2.32	0.46
1:2:1548:A:H2'	1:2:1549:U:C6	2.50	0.46
1:2:1588:G:OP1	29:T:91:HIS:HB2	2.15	0.46
3:B:133:TYR:CZ	3:B:221:PRO:HD2	2.51	0.46
3:B:159:SER:N	3:B:162:ARG:HH21	2.14	0.46
5:E:187:ARG:HB3	5:E:187:ARG:CZ	2.44	0.46
9:J:27:GLU:HB2	9:J:42:ILE:HD13	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:33:GLU:C	9:J:34:TYR:HD1	2.22	0.46
17:a:26:CYS:SG	17:a:74:CYS:HB3	2.54	0.46
21:D:65:ARG:NE	21:D:68:GLU:OE1	2.47	0.46
24:M:88:LEU:O	24:M:92:ALA:HB2	2.16	0.46
27:R:37:GLU:HG2	27:R:38:ILE:N	2.30	0.46
27:R:88:VAL:O	27:R:90:ALA:N	2.48	0.46
28:S:18:LEU:HD22	28:S:101:LEU:HD23	1.97	0.46
29:T:110:LYS:HD3	29:T:110:LYS:HA	1.67	0.46
31:Z:50:ILE:HD12	31:Z:70:LYS:HZ3	1.80	0.46
1:2:254:U:H2'	1:2:255:A:C8	2.49	0.46
1:2:334:U:O2'	10:L:130:PRO:O	2.34	0.46
1:2:699:U:N3	1:2:740:A:H2	2.12	0.46
1:2:836:G:H2'	1:2:837:G:C1'	2.45	0.46
1:2:850:U:H2'	1:2:851:C:H6	1.80	0.46
1:2:1198:G:H5''	33:d:40:ARG:NH2	2.31	0.46
1:2:1398:A:OP2	27:R:60:ARG:NH2	2.48	0.46
1:2:1421:U:H2'	1:2:1422:A:O4'	2.15	0.46
1:2:1585:A:H1'	22:F:106:ASN:ND2	2.31	0.46
3:B:120:LEU:HD23	3:B:120:LEU:H	1.80	0.46
3:B:142:PHE:C	3:B:207:LEU:HD12	2.40	0.46
4:C:87:ASN:OD1	4:C:88:ILE:N	2.49	0.46
5:E:94:ALA:O	5:E:95:THR:OG1	2.28	0.46
9:J:29:LYS:O	9:J:33:GLU:HG2	2.15	0.46
17:a:58:VAL:HG23	17:a:59:TYR:HD2	1.79	0.46
28:S:125:ILE:HG23	28:S:129:TRP:CZ3	2.49	0.46
1:2:54:C:O2'	1:2:458:G:N7	2.40	0.46
1:2:66:U:P	6:G:173:PRO:HA	2.56	0.46
1:2:186:G:N2	1:2:197:A:OP2	2.37	0.46
1:2:222:U:H2'	1:2:223:C:C6	2.50	0.46
1:2:337:C:H2'	1:2:338:C:C6	2.51	0.46
1:2:545:C:H2'	1:2:546:U:C6	2.50	0.46
1:2:550:G:N1	1:2:551:G:C6	2.84	0.46
1:2:935:G:H2'	1:2:936:C:C6	2.51	0.46
1:2:974:C:OP1	11:N:109:LYS:NZ	2.48	0.46
1:2:1287:G:N2	1:2:1327:G:H1'	2.31	0.46
1:2:1683:G:H2'	1:2:1684:C:C6	2.51	0.46
1:2:1775:G:H2'	1:2:1776:G:C8	2.50	0.46
4:C:49:LEU:HD12	4:C:54:LYS:HB2	1.97	0.46
6:G:14:LYS:NZ	6:G:123:GLY:H	2.14	0.46
10:L:93:TYR:HD1	10:L:100:TYR:HE1	1.61	0.46
14:W:31:SER:OG	14:W:32:LYS:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:a:39:MET:HA	17:a:39:MET:HE3	1.95	0.46
22:F:91:ILE:HD11	22:F:174:ILE:HD11	1.97	0.46
25:P:98:ASN:OD1	25:P:122:THR:HA	2.15	0.46
27:R:57:LEU:O	27:R:60:ARG:HB3	2.15	0.46
30:U:28:SER:OG	30:U:30:LYS:O	2.24	0.46
41:l:232:GLU:HG3	41:l:233:TYR:CD1	2.48	0.46
1:2:219:A:H3'	1:2:220:A:H5''	1.97	0.46
1:2:613:C:H2'	1:2:614:A:H8	1.80	0.46
1:2:623:G:H2'	1:2:624:C:H6	1.81	0.46
1:2:1185:U:H2'	1:2:1186:U:O4'	2.16	0.46
1:2:1225:A:H4'	1:2:1228:G:H4'	1.98	0.46
1:2:1238:U:H2'	1:2:1239:U:C6	2.50	0.46
1:2:1339:U:OP1	1:2:1340:A:H8	1.97	0.46
1:2:1341:C:OP1	35:g:103:ARG:NH2	2.49	0.46
2:A:167:LYS:NZ	2:A:204:TYR:O	2.29	0.46
4:C:61:ILE:HD13	4:C:66:LEU:HD12	1.95	0.46
8:I:83:TYR:HD2	8:I:101:ILE:HD13	1.79	0.46
8:I:84:HIS:CG	8:I:90:LEU:HD22	2.51	0.46
8:I:154:GLU:CD	8:I:156:ALA:H	2.23	0.46
8:I:158:ASP:HA	8:I:161:PHE:HD2	1.81	0.46
15:X:3:LYS:O	15:X:5:LYS:N	2.35	0.46
24:M:47:ARG:HG3	24:M:48:GLY:N	2.28	0.46
35:g:171:ARG:HG2	35:g:173:THR:HG23	1.97	0.46
38:1:64:RIA:N3	38:1:64:RIA:H2A	2.30	0.46
39:j:220:VAL:HG12	39:j:230:LEU:HA	1.97	0.46
40:k:435:PHE:HB2	40:k:514:TRP:CE2	2.51	0.46
1:2:554:A:H2'	1:2:555:A:C8	2.51	0.46
1:2:634:A:H2'	1:2:635:A:O4'	2.15	0.46
1:2:636:C:OP2	14:W:31:SER:OG	2.33	0.46
1:2:869:C:H2'	1:2:870:G:C8	2.51	0.46
1:2:906:A:H4'	39:j:53:ARG:HH21	1.80	0.46
1:2:1234:C:C2	1:2:1235:A:C8	3.04	0.46
1:2:1547:C:P	25:P:42:ARG:HH22	2.37	0.46
1:2:1670:G:H2'	1:2:1671:G:H8	1.80	0.46
1:2:1768:U:H2'	1:2:1769:U:C6	2.51	0.46
2:A:71:GLU:OE2	2:A:96:THR:OG1	2.34	0.46
3:B:5:LYS:HZ3	3:B:7:LYS:HA	1.78	0.46
4:C:170:VAL:HG11	4:C:214:ASN:C	2.40	0.46
5:E:130:GLN:HB2	5:E:138:TYR:CZ	2.50	0.46
8:I:157:VAL:HA	8:I:160:GLN:HG2	1.97	0.46
10:L:69:LYS:H	10:L:127:GLN:CD	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:W:8:ALA:HA	14:W:74:VAL:HG11	1.97	0.46
34:f:98:VAL:HB	34:f:101:ALA:HB2	1.97	0.46
35:g:67:HIS:HB2	35:g:87:ASP:HB3	1.98	0.46
39:j:9:TYR:HD2	39:j:39:TYR:CE2	2.34	0.46
40:k:128:PHE:O	40:k:132:LEU:HB2	2.16	0.46
1:2:89:G:C6	1:2:90:C:C4	3.04	0.46
1:2:214:A:N6	1:2:241:U:H3'	2.30	0.46
1:2:442:C:P	16:Y:105:ARG:HG3	2.56	0.46
1:2:1533:U:OP2	31:Z:38:HIS:NE2	2.47	0.46
1:2:1577:U:H2'	1:2:1578:C:H6	1.80	0.46
1:2:1685:U:H1'	1:2:1713:G:N2	2.31	0.46
4:C:145:ARG:HH22	4:C:233:ASN:HD21	1.64	0.46
9:J:139:GLN:HE21	16:Y:63:GLN:HE22	1.63	0.46
14:W:73:GLY:N	14:W:128:PHE:O	2.49	0.46
16:Y:8:ARG:HB2	16:Y:26:ASP:OD1	2.15	0.46
22:F:205:LYS:HE3	22:F:207:SER:HB2	1.97	0.46
30:U:20:HIS:CE1	30:U:97:ALA:H	2.34	0.46
34:f:135:ASP:O	34:f:150:LYS:N	2.43	0.46
35:g:39:ARG:HG2	35:g:68:ILE:HG23	1.98	0.46
39:j:143:GLU:HA	39:j:146:LYS:HG2	1.98	0.46
1:2:325:G:H2'	1:2:326:U:H6	1.79	0.46
1:2:434:C:H2'	1:2:435:A:O4'	2.16	0.46
1:2:446:U:O2'	5:E:27:TYR:O	2.28	0.46
1:2:967:U:C4	1:2:968:C:N3	2.84	0.46
1:2:1042:A:H2'	1:2:1042:A:N3	2.30	0.46
1:2:1184:U:C4	1:2:1456:G:C4	3.04	0.46
1:2:1554:A:H2'	25:P:40:ARG:HH21	1.81	0.46
1:2:1613:C:OP1	32:c:47:PRO:HB3	2.15	0.46
5:E:52:LEU:HD11	5:E:99:PHE:HE2	1.80	0.46
8:I:170:ILE:HG23	8:I:181:ASP:O	2.16	0.46
11:N:102:LEU:HD12	11:N:115:LEU:HD13	1.97	0.46
17:a:42:ARG:HH12	17:a:67:THR:HG23	1.81	0.46
18:b:37:CYS:SG	18:b:38:PRO:HD2	2.56	0.46
39:j:30:MET:HE1	39:j:45:MET:HB2	1.98	0.46
39:j:129:THR:HG21	39:j:161:PRO:HD3	1.98	0.46
40:k:78:GLN:OE1	40:k:387:LEU:HB3	2.16	0.46
1:2:323:U:N3	1:2:324:G:N7	2.64	0.46
1:2:677:G:H2'	1:2:678:G:C8	2.51	0.46
1:2:820:U:C4	1:2:851:C:N3	2.84	0.46
1:2:1288:U:H2'	1:2:1289:PSU:C6	2.50	0.46
1:2:1437:C:H2'	1:2:1438:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1467:A:H2'	1:2:1468:C:H6	1.81	0.46
1:2:1509:G:H2'	1:2:1510:G:C8	2.51	0.46
1:2:1532:G:OP2	1:2:1532:G:H8	1.99	0.46
1:2:1760:A:O2'	1:2:1781:C:OP1	2.25	0.46
3:B:54:LEU:O	3:B:55:LYS:HB2	2.16	0.46
8:I:119:GLN:O	8:I:120:SER:OG	2.31	0.46
9:J:62:ARG:HH12	9:J:68:LYS:HD3	1.80	0.46
12:O:70:LYS:HA	12:O:70:LYS:HD3	1.78	0.46
12:O:84:ARG:HB2	12:O:118:VAL:HG13	1.98	0.46
13:V:86:SER:C	13:V:87:ARG:HH11	2.24	0.46
21:D:53:THR:OG1	21:D:54:LYS:N	2.50	0.46
22:F:84:PHE:CE2	32:c:49:ARG:HG3	2.51	0.46
30:U:61:LYS:HB2	30:U:86:ILE:CG2	2.46	0.46
40:k:107:GLY:HA2	40:k:229:THR:HG22	1.98	0.46
40:k:432:ILE:CG1	40:k:515:ALA:HB1	2.45	0.46
1:2:300:A:H3'	1:2:301:U:H6	1.81	0.45
1:2:430:C:H2'	1:2:431:G:H8	1.81	0.45
1:2:462:U:H2'	1:2:463:A:C8	2.50	0.45
1:2:550:G:C6	1:2:551:G:C6	3.04	0.45
1:2:809:G:N3	7:H:111:LYS:HB2	2.30	0.45
1:2:826:C:H2'	1:2:827:U:C6	2.50	0.45
1:2:867:G:OP1	11:N:121:ARG:NH1	2.48	0.45
1:2:1127:C:H2'	1:2:1128:U:C6	2.51	0.45
1:2:1312:A:C4	1:2:1314:U:H5'	2.52	0.45
1:2:1336:A:P	26:Q:123:ARG:HH12	2.39	0.45
3:B:19:ARG:HG2	3:B:19:ARG:O	2.16	0.45
8:I:100:ALA:O	8:I:169:ALA:HA	2.16	0.45
15:X:42:PRO:HA	15:X:81:LYS:HD3	1.98	0.45
15:X:48:HIS:CD2	15:X:105:ALA:HB2	2.51	0.45
21:D:69:LEU:O	21:D:73:ILE:HG12	2.16	0.45
39:j:155:TRP:HZ2	39:j:169:LEU:HD22	1.81	0.45
40:k:97:ARG:O	40:k:387:LEU:HD11	2.16	0.45
1:2:122:U:H5''	5:E:77:ARG:NH1	2.31	0.45
1:2:389:G:H2'	1:2:1729:A:H4'	1.98	0.45
1:2:448:C:H2'	1:2:449:U:C6	2.52	0.45
1:2:985:G:H3'	1:2:986:G:C8	2.51	0.45
1:2:995:U:H2'	1:2:996:G:C8	2.51	0.45
1:2:1144:U:C2	1:2:1145:G:C8	3.04	0.45
1:2:1439:C:H2'	1:2:1440:U:C6	2.51	0.45
1:2:1574:A:H1'	38:l:41:C:H1'	1.98	0.45
1:2:1594:C:O2	33:d:32:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1723:U:H2'	1:2:1724:G:C8	2.52	0.45
4:C:86:MET:HE1	4:C:108:VAL:N	2.31	0.45
5:E:246:LEU:HD12	5:E:254:ARG:HH22	1.81	0.45
6:G:12:THR:HB	6:G:124:ILE:HG13	1.98	0.45
8:I:103:GLN:HB3	8:I:165:ARG:HB3	1.98	0.45
10:L:108:PRO:HG2	10:L:134:THR:HB	1.97	0.45
15:X:53:VAL:HG22	15:X:74:VAL:HG12	1.97	0.45
22:F:64:ILE:HG22	22:F:66:ILE:HG23	1.98	0.45
22:F:143:GLY:HA3	22:F:169:ARG:HG2	1.99	0.45
22:F:150:ARG:HB2	22:F:159:ARG:NH1	2.31	0.45
25:P:77:ARG:HD2	25:P:102:PHE:CE1	2.52	0.45
35:g:20:TRP:HE3	35:g:39:ARG:HD2	1.81	0.45
39:j:13:TYR:CZ	39:j:78:LYS:HA	2.51	0.45
39:j:216:MET:HE3	39:j:234:ALA:HA	1.98	0.45
40:k:440:LEU:HD11	40:k:510:ARG:HB3	1.98	0.45
1:2:119:A:H3'	1:2:120:PSU:H6	1.81	0.45
1:2:146:A:H2'	1:2:146:A:N3	2.31	0.45
1:2:200:G:H2'	1:2:201:A:H8	1.80	0.45
1:2:408:C:H2'	1:2:409:A:H8	1.81	0.45
1:2:743:U:C4	1:2:808:G:N1	2.85	0.45
1:2:850:U:H2'	1:2:851:C:C6	2.51	0.45
1:2:894:G:N1	1:2:917:U:N3	2.64	0.45
1:2:1122:C:H2'	1:2:1123:A:O4'	2.16	0.45
1:2:1151:A:H2'	1:2:1152:G:C8	2.49	0.45
1:2:1320:A:O5'	2:A:104:PRO:HG3	2.16	0.45
1:2:1343:A:O2'	1:2:1344:A:OP1	2.28	0.45
1:2:1390:U:H2'	1:2:1391:C:C6	2.51	0.45
1:2:1467:A:H2'	1:2:1468:C:C6	2.51	0.45
1:2:1551:G:O6	25:P:43:ARG:NE	2.50	0.45
1:2:1645:U:H2'	1:2:1646:A:C8	2.51	0.45
2:A:184:LEU:C	13:V:44:ARG:HH12	2.22	0.45
5:E:11:ARG:HA	5:E:28:ALA:HB2	1.97	0.45
5:E:191:ARG:HG2	5:E:245:LYS:HB2	1.99	0.45
6:G:27:PHE:HE1	6:G:36:VAL:HG11	1.80	0.45
11:N:31:ASP:OD1	11:N:32:GLY:N	2.50	0.45
25:P:37:ALA:HB1	25:P:41:VAL:HG11	1.98	0.45
39:j:234:ALA:HB1	39:j:237:LYS:HA	1.98	0.45
41:l:180:ILE:HD12	41:l:226:LEU:HD21	1.98	0.45
1:2:429:G:H2'	1:2:430:C:H6	1.82	0.45
1:2:567:G:H4'	15:X:90:ASP:CG	2.41	0.45
1:2:646:G:C6	1:2:688:G:C6	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:762:A:C2'	1:2:763:G:H5'	2.46	0.45
1:2:1009:C:H3'	1:2:1010:G:C8	2.50	0.45
1:2:1046:G:O6	1:2:1071:C:N4	2.49	0.45
1:2:1077:C:H2'	1:2:1078:U:H6	1.78	0.45
1:2:1273:C:O2	1:2:1425:A:O2'	2.29	0.45
1:2:1482:G:H1	1:2:1589:C:H1'	1.81	0.45
1:2:1559:U:H4'	1:2:1597:C:O2'	2.16	0.45
3:B:168:ILE:HA	3:B:171:ILE:HG22	1.98	0.45
3:B:217:LEU:HD23	3:B:218:LEU:N	2.31	0.45
5:E:56:LEU:HD11	16:Y:72:PHE:CE2	2.51	0.45
5:E:233:ARG:NH1	5:E:234:PRO:O	2.50	0.45
6:G:2:LYS:O	6:G:108:VAL:HA	2.16	0.45
8:I:141:GLU:HA	8:I:144:TRP:HB2	1.98	0.45
9:J:103:ASP:O	9:J:106:GLU:HG2	2.16	0.45
10:L:46:LYS:O	10:L:50:GLU:HG2	2.17	0.45
15:X:34:LEU:HB2	15:X:36:THR:HG23	1.98	0.45
21:D:148:LYS:HZ1	21:D:150:MET:HE3	1.82	0.45
24:M:109:ALA:C	24:M:111:VAL:H	2.25	0.45
29:T:84:LYS:HB2	29:T:86:ARG:HG2	1.97	0.45
31:Z:90:LYS:NZ	31:Z:105:THR:HG22	2.32	0.45
39:j:33:TYR:HA	39:j:45:MET:HA	1.98	0.45
1:2:1067:C:H5'	27:R:128:ARG:HD2	1.99	0.45
1:2:1280:G:H2'	1:2:1281:U:H6	1.80	0.45
1:2:1423:A:O2'	1:2:1424:C:H5'	2.17	0.45
1:2:1448:U:H2'	1:2:1449:C:C6	2.50	0.45
1:2:1503:A:H4'	1:2:1560:G:O2'	2.16	0.45
11:N:138:ASN:OD1	11:N:139:TRP:N	2.49	0.45
12:O:38:THR:HG22	12:O:41:ARG:HH21	1.81	0.45
17:a:10:ARG:HG2	17:a:33:ASP:OD2	2.16	0.45
21:D:225:TYR:CE2	35:g:195:ILE:HD11	2.51	0.45
22:F:189:ILE:HG21	31:Z:66:VAL:HG11	1.99	0.45
23:K:58:GLN:O	23:K:65:TYR:HB2	2.17	0.45
25:P:81:ARG:NH2	25:P:120:SER:OG	2.47	0.45
27:R:100:LEU:O	27:R:100:LEU:HD12	2.17	0.45
39:j:77:ASP:HB3	39:j:82:TYR:N	2.32	0.45
1:2:137:U:H2'	1:2:138:A:C8	2.52	0.45
1:2:149:U:C2	1:2:164:G:N2	2.85	0.45
1:2:199:A:H2'	1:2:200:G:C8	2.52	0.45
1:2:360:C:H2'	1:2:361:G:H8	1.82	0.45
1:2:806:A:H2'	1:2:807:U:C6	2.52	0.45
1:2:928:A:O5'	1:2:930:C:N4	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1115:A:OP1	20:h:17:ARG:NH2	2.46	0.45
1:2:1120:C:N4	1:2:1126:G:O6	2.50	0.45
1:2:1261:U:H2'	1:2:1262:G:C8	2.51	0.45
1:2:1460:G:H2'	1:2:1461:C:H6	1.81	0.45
1:2:1462:G:H4'	26:Q:141:SER:HB2	1.99	0.45
1:2:1624:U:H2'	1:2:1625:U:H6	1.81	0.45
1:2:1797:U:C4	3:B:152:ARG:HD2	2.52	0.45
6:G:76:LEU:HD12	6:G:77:LEU:N	2.31	0.45
7:H:4:PRO:HA	7:H:7:LYS:HE3	1.99	0.45
10:L:59:PRO:HG3	10:L:138:ASN:HD21	1.79	0.45
30:U:50:LEU:HB3	30:U:95:ALA:HB2	1.99	0.45
38:1:35:A:H2'	38:1:36:U:C6	2.52	0.45
38:1:60:A:H2'	38:1:61:C:H5	1.81	0.45
42:m:30:ILE:HG13	42:m:85:ARG:CZ	2.46	0.45
1:2:90:C:O2'	1:2:450:A:H5''	2.17	0.45
1:2:1101:G:OP1	14:W:76:SER:OG	2.31	0.45
1:2:1494:U:O2	1:2:1509:G:O6	2.35	0.45
1:2:1789:A:OP2	17:a:10:ARG:HD2	2.17	0.45
2:A:190:ASP:OD1	2:A:190:ASP:N	2.50	0.45
3:B:144:ARG:HB2	3:B:208:GLN:CB	2.45	0.45
6:G:161:GLU:HA	6:G:170:THR:HA	1.99	0.45
7:H:117:THR:O	7:H:121:VAL:HG23	2.16	0.45
7:H:122:HIS:HA	7:H:125:ILE:HG12	1.99	0.45
9:J:77:ILE:O	9:J:81:VAL:HG13	2.16	0.45
9:J:85:VAL:HG11	9:J:104:PHE:CD1	2.52	0.45
23:K:80:LEU:HB3	23:K:82:LEU:HD23	1.98	0.45
24:M:54:VAL:HG11	24:M:88:LEU:HD11	1.99	0.45
24:M:123:GLU:O	24:M:124:ARG:C	2.59	0.45
27:R:106:THR:O	27:R:110:VAL:HG23	2.16	0.45
33:d:13:LYS:HG3	33:d:14:PHE:CD1	2.50	0.45
35:g:52:GLU:CG	35:g:53:GLN:H	2.29	0.45
35:g:117:ASP:OD1	35:g:118:ALA:N	2.50	0.45
40:k:165:LYS:HD2	40:k:167:ASP:H	1.81	0.45
1:2:93:A:H8	1:2:398:A:O4'	2.00	0.45
1:2:106:U:OP1	8:I:8:ARG:NH2	2.49	0.45
1:2:329:G:C6	1:2:330:A:C6	3.05	0.45
1:2:408:C:H2'	1:2:409:A:C8	2.52	0.45
1:2:477:A:C2	1:2:509:G:N1	2.65	0.45
1:2:870:G:C6	1:2:956:G:C6	3.05	0.45
1:2:965:A:OP2	11:N:124:ARG:NH1	2.44	0.45
1:2:1174:U:OP2	28:S:137:HIS:ND1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1237:A:C5	1:2:1238:U:C4	3.05	0.45
1:2:1332:C:H2'	1:2:1333:U:H6	1.81	0.45
1:2:1584:A:H62	1:2:1608:G:N2	2.10	0.45
2:A:49:ASN:O	2:A:53:THR:HG23	2.16	0.45
4:C:149:TRP:HZ3	9:J:60:LEU:HD22	1.81	0.45
5:E:64:ILE:HD11	16:Y:18:LEU:CD1	2.44	0.45
5:E:65:LEU:HD13	5:E:70:VAL:HG21	1.99	0.45
5:E:208:VAL:HG13	5:E:210:ILE:HD11	1.98	0.45
6:G:185:GLN:HA	6:G:188:ARG:CZ	2.47	0.45
12:O:133:ARG:HB2	12:O:136:ARG:NH2	2.27	0.45
22:F:159:ARG:HB2	22:F:226:ASN:HD22	1.81	0.45
29:T:88:VAL:HB	29:T:89:ARG:NH1	2.28	0.45
30:U:58:LEU:HD21	30:U:90:TYR:CD1	2.51	0.45
31:Z:55:PRO:HA	31:Z:103:ARG:HG2	1.98	0.45
35:g:71:ASP:HB2	35:g:112:LEU:O	2.16	0.45
35:g:172:ILE:O	35:g:187:SER:HA	2.17	0.45
38:1:24:G:H2'	38:1:25:C:H6	1.82	0.45
40:k:174:CYS:HA	40:k:183:TYR:CE2	2.52	0.45
40:k:267:LEU:O	40:k:271:ARG:HG3	2.17	0.45
40:k:462:LEU:HD22	40:k:503:ARG:HA	1.99	0.45
1:2:384:A:P	8:I:25:ARG:HH22	2.39	0.45
1:2:740:A:H2'	1:2:741:C:O4'	2.17	0.45
1:2:951:A:H2'	1:2:952:G:C8	2.52	0.45
1:2:1150:A:H2'	1:2:1151:A:H8	1.82	0.45
1:2:1428:U:H1'	30:U:72:ASN:ND2	2.28	0.45
1:2:1511:G:O2'	1:2:1513:A:N3	2.45	0.45
1:2:1595:A:C8	33:d:14:PHE:CD2	3.04	0.45
1:2:1731:C:H2'	1:2:1732:U:C6	2.52	0.45
3:B:5:LYS:HZ2	3:B:7:LYS:HA	1.78	0.45
3:B:33:LYS:HG3	3:B:95:ASN:HD21	1.82	0.45
3:B:59:ASP:HA	3:B:62:LYS:HE2	1.99	0.45
4:C:45:LYS:HB3	4:C:252:ALA:HB1	1.99	0.45
6:G:167:LYS:NZ	6:G:169:TYR:HB2	2.31	0.45
10:L:3:THR:HB	10:L:7:VAL:HA	1.99	0.45
11:N:35:GLU:HA	11:N:38:ILE:HG12	1.99	0.45
14:W:23:ARG:O	14:W:65:LEU:N	2.25	0.45
24:M:56:VAL:HG12	24:M:58:SER:H	1.82	0.45
25:P:20:VAL:HG13	25:P:24:LYS:HB2	1.99	0.45
28:S:61:LEU:HD23	28:S:61:LEU:H	1.81	0.45
29:T:28:LEU:H	29:T:111:LEU:HD21	1.81	0.45
30:U:24:ILE:HG13	30:U:24:ILE:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:U:98:HIS:CE1	30:U:99:ILE:HG23	2.52	0.45
34:f:96:LYS:HB2	34:f:96:LYS:HE3	1.63	0.45
1:2:142:G:N7	6:G:177:ARG:NH2	2.52	0.45
1:2:261:U:H2'	1:2:262:C:H6	1.82	0.45
1:2:340:A:H2'	1:2:341:C:H6	1.81	0.45
1:2:570:G:H5''	15:X:114:LYS:HE3	1.98	0.45
1:2:610:U:H2'	1:2:611:U:C6	2.52	0.45
1:2:939:A:H2'	1:2:940:A:H8	1.82	0.45
1:2:1198:G:N2	33:d:31:ILE:HD13	2.28	0.45
1:2:1475:G:C6	1:2:1529:G:C6	3.05	0.45
1:2:1683:G:H2'	1:2:1684:C:H6	1.81	0.45
2:A:176:LEU:O	2:A:180:GLU:OE1	2.34	0.45
4:C:50:VAL:HG22	4:C:55:ILE:HD11	1.99	0.45
5:E:103:TYR:HE1	5:E:109:PHE:HE1	1.65	0.45
9:J:145:SER:C	9:J:147:MET:H	2.25	0.45
27:R:77:GLU:HA	27:R:80:ARG:HG2	1.98	0.45
33:d:30:LEU:HA	33:d:39:ASP:HA	1.99	0.45
36:i:29:LYS:HB2	36:i:33:GLN:O	2.16	0.45
36:i:37:GLN:OE1	36:i:76:ILE:HG13	2.17	0.45
39:j:119:PHE:HB3	39:j:121:ILE:HG13	1.99	0.45
40:k:442:GLY:HA3	40:k:510:ARG:NH2	2.32	0.45
1:2:5:U:H2'	1:2:6:G:C8	2.48	0.44
1:2:122:U:O3'	5:E:77:ARG:NH2	2.47	0.44
1:2:330:A:H2'	1:2:331:U:C6	2.52	0.44
1:2:477:A:N1	1:2:509:G:C6	2.84	0.44
1:2:609:G:O2'	1:2:612:G:O3'	2.34	0.44
1:2:704:C:H1'	1:2:705:U:H4'	2.00	0.44
1:2:809:G:H21	7:H:108:GLN:HB2	1.82	0.44
1:2:933:C:C4	1:2:1076:C:H4'	2.53	0.44
1:2:1168:G:C2	1:2:1573:7MG:HM72	2.52	0.44
1:2:1243:A:H2'	1:2:1243:A:N3	2.32	0.44
1:2:1275:U:OP1	21:D:146:ARG:NH2	2.50	0.44
1:2:1554:A:H1'	1:2:1558:U:OP2	2.16	0.44
1:2:1581:A:H5'	26:Q:135:ARG:HH21	1.81	0.44
1:2:1712:A:H2'	1:2:1713:G:H8	1.80	0.44
2:A:52:LYS:O	2:A:56:LYS:HG2	2.17	0.44
3:B:97:LEU:HD13	3:B:232:HIS:HB2	1.98	0.44
3:B:171:ILE:HD13	3:B:197:ILE:HD13	1.98	0.44
4:C:148:TYR:CE2	4:C:156:PRO:HB3	2.52	0.44
8:I:61:GLU:OE1	8:I:61:GLU:N	2.50	0.44
9:J:59:LEU:CD2	9:J:69:ARG:HG3	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:V:36:ILE:O	13:V:50:TYR:HB2	2.17	0.44
27:R:75:GLU:O	27:R:79:GLU:OE1	2.34	0.44
35:g:30:GLN:OE1	35:g:30:GLN:N	2.51	0.44
38:1:41:C:H2'	38:1:42:U:C6	2.52	0.44
1:2:212:A:H2'	1:2:213:G:O4'	2.17	0.44
1:2:220:A:C6	1:2:840:U:C4	3.05	0.44
1:2:570:G:H5''	15:X:114:LYS:CE	2.47	0.44
1:2:760:A:C6	1:2:761:G:C4	3.05	0.44
1:2:809:G:C2	7:H:111:LYS:HB2	2.51	0.44
1:2:1084:G:H5'	1:2:1085:A:OP2	2.16	0.44
1:2:1137:A:H2'	1:2:1138:A:C8	2.53	0.44
1:2:1158:C:H4'	1:2:1578:C:OP1	2.16	0.44
1:2:1163:G:H2'	1:2:1164:G:C8	2.50	0.44
1:2:1304:U:H5''	1:2:1305:C:C5	2.52	0.44
1:2:1439:C:H2'	1:2:1440:U:H6	1.83	0.44
1:2:1450:U:OP1	33:d:10:HIS:ND1	2.45	0.44
1:2:1583:U:H2'	1:2:1584:A:C8	2.52	0.44
1:2:1599:G:C4	29:T:89:ARG:CZ	3.00	0.44
1:2:1730:A:H2'	1:2:1731:C:C6	2.52	0.44
2:A:41:ARG:NH1	2:A:43:ASP:OD2	2.51	0.44
11:N:61:THR:OG1	11:N:62:GLN:N	2.48	0.44
11:N:87:ASP:OD1	11:N:88:LEU:N	2.49	0.44
14:W:47:ILE:HD11	14:W:63:VAL:HB	2.00	0.44
22:F:25:VAL:HG21	26:Q:57:LEU:HD21	1.99	0.44
23:K:69:THR:CG2	23:K:72:GLY:H	2.30	0.44
27:R:66:VAL:HG22	27:R:67:ARG:N	2.31	0.44
27:R:88:VAL:C	27:R:90:ALA:H	2.25	0.44
31:Z:103:ARG:HD3	31:Z:103:ARG:N	2.32	0.44
36:i:30:GLU:HB3	36:i:33:GLN:HE22	1.81	0.44
40:k:135:ASN:C	40:k:136:ILE:HD12	2.41	0.44
1:2:53:G:O2'	16:Y:106:GLN:NE2	2.51	0.44
1:2:65:A:N7	1:2:83:G:N1	2.65	0.44
1:2:287:A:H2'	1:2:288:U:O4'	2.17	0.44
1:2:381:C:P	5:E:10:LYS:HD2	2.58	0.44
1:2:494:C:H3'	1:2:495:G:C8	2.52	0.44
1:2:760:A:H3'	1:2:761:G:H8	1.82	0.44
1:2:1553:A:O2'	25:P:82:ASN:ND2	2.23	0.44
1:2:1582:G:H3'	26:Q:124:PRO:HA	1.99	0.44
1:2:1676:A:H2'	1:2:1677:G:O4'	2.16	0.44
2:A:118:PRO:HG2	2:A:141:ILE:HD13	2.00	0.44
3:B:118:GLN:HE21	3:B:143:THR:H	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:27:PHE:CE1	6:G:36:VAL:HG11	2.52	0.44
7:H:103:SER:O	7:H:106:SER:OG	2.35	0.44
11:N:38:ILE:HG13	11:N:42:ARG:HH22	1.82	0.44
21:D:107:PHE:O	21:D:110:LEU:HG	2.17	0.44
22:F:122:ILE:HG12	31:Z:59:TYR:CE1	2.53	0.44
22:F:176:LEU:HD11	22:F:215:LYS:HG3	1.99	0.44
26:Q:52:LEU:HG	26:Q:60:PHE:CZ	2.49	0.44
28:S:2:SER:C	31:Z:82:HIS:HE1	2.25	0.44
40:k:432:ILE:HG22	40:k:483:ALA:O	2.17	0.44
1:2:157:U:O2'	1:2:158:U:H5'	2.16	0.44
1:2:385:G:H2'	1:2:386:A:C8	2.52	0.44
1:2:444:A:H1'	1:2:524:A:H5'	2.00	0.44
1:2:772:G:H5'	9:J:6:ARG:NH1	2.33	0.44
1:2:914:A:N3	1:2:914:A:H2'	2.33	0.44
1:2:1065:C:H4'	3:B:149:GLN:CD	2.43	0.44
1:2:1492:C:H2'	1:2:1493:C:C6	2.52	0.44
1:2:1745:G:H2'	1:2:1746:G:C8	2.51	0.44
1:2:1756:U:H2'	1:2:1757:C:C6	2.52	0.44
1:2:1768:U:C4	1:2:1791:G:N1	2.85	0.44
2:A:122:ILE:HD13	2:A:144:ILE:HB	1.99	0.44
3:B:53:GLY:HA2	3:B:56:ASN:OD1	2.17	0.44
4:C:172:VAL:HG21	4:C:219:ALA:HA	1.99	0.44
4:C:178:PRO:HG3	9:J:57:ARG:HE	1.82	0.44
5:E:131:LEU:HD23	5:E:131:LEU:HA	1.82	0.44
14:W:73:GLY:HA3	14:W:128:PHE:CZ	2.52	0.44
15:X:107:PHE:HB2	15:X:121:ARG:O	2.18	0.44
24:M:27:THR:HB	24:M:118:GLY:HA3	1.99	0.44
26:Q:101:SER:HA	26:Q:104:GLU:CD	2.42	0.44
28:S:125:ILE:O	28:S:129:TRP:HE3	2.00	0.44
34:f:94:LYS:NZ	34:f:95:HIS:HB3	2.33	0.44
35:g:259:LEU:HB2	35:g:272:LEU:HD21	1.98	0.44
39:j:124:GLU:OE2	39:j:125:GLU:HG3	2.17	0.44
40:k:347:PHE:CE1	40:k:353:ILE:HD12	2.52	0.44
41:l:259:CYS:HB3	41:l:263:GLY:H	1.81	0.44
1:2:178:A:H2'	1:2:179:A:O4'	2.17	0.44
1:2:250:A:C2	5:E:131:LEU:HD12	2.53	0.44
1:2:312:U:O4	1:2:1129:G:H1'	2.18	0.44
1:2:363:G:N2	1:2:380:C:C2	2.85	0.44
1:2:504:A:OP2	1:2:505:A:H1'	2.18	0.44
1:2:554:A:O2'	1:2:555:A:O4'	2.16	0.44
1:2:754:A:H5''	1:2:755:A:H5''	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:798:A:H4'	5:E:201:HIS:CD2	2.53	0.44
1:2:899:A:C8	1:2:900:G:N2	2.86	0.44
2:A:124:THR:HG22	2:A:174:TRP:HZ2	1.83	0.44
2:A:177:LEU:O	2:A:181:VAL:HG13	2.18	0.44
3:B:29:TRP:CZ3	3:B:47:LEU:HD21	2.52	0.44
3:B:68:VAL:HG21	3:B:73:LEU:HD11	1.99	0.44
4:C:63:LEU:HB3	4:C:64:HIS:HD2	1.82	0.44
11:N:45:LEU:HB2	11:N:50:ILE:HD11	1.99	0.44
13:V:12:TYR:O	13:V:12:TYR:CG	2.70	0.44
14:W:101:TYR:HA	14:W:113:HIS:NE2	2.32	0.44
24:M:117:TRP:HE1	24:M:124:ARG:HB3	1.82	0.44
30:U:100:VAL:HA	30:U:103:ILE:HD12	1.98	0.44
35:g:156:ARG:HB2	35:g:211:PRO:HD3	1.98	0.44
39:j:184:ILE:HD12	39:j:234:ALA:HB2	1.99	0.44
40:k:106:ILE:HD13	40:k:236:ILE:HD12	1.98	0.44
42:m:67:ASN:N	42:m:79:GLN:HB2	2.22	0.44
1:2:25:C:H5''	1:2:26:A:H5''	1.99	0.44
1:2:274:C:O2'	1:2:276:U:O4	2.35	0.44
1:2:335:G:O6	8:I:5:ARG:NE	2.30	0.44
1:2:390:A:O2'	1:2:1728:A:H4'	2.17	0.44
1:2:883:A:H5''	3:B:136:ARG:NH1	2.32	0.44
1:2:910:U:O2	3:B:5:LYS:HD2	2.17	0.44
1:2:1443:G:N1	34:f:88:PRO:O	2.46	0.44
1:2:1517:U:H2'	1:2:1518:U:C5	2.52	0.44
1:2:1605:G:H2'	1:2:1606:U:H6	1.83	0.44
1:2:1640:G:N2	1:2:1778:G:H22	2.16	0.44
2:A:41:ARG:NE	27:R:103:ASP:OD2	2.51	0.44
2:A:76:ILE:HD13	2:A:121:VAL:HG13	2.00	0.44
3:B:82:ARG:NH2	3:B:104:ASP:H	2.15	0.44
3:B:116:LYS:HB3	3:B:117:TRP:CD1	2.53	0.44
5:E:241:GLY:O	5:E:244:ILE:HG12	2.17	0.44
7:H:134:GLU:OE2	11:N:19:SER:OG	2.36	0.44
8:I:73:ALA:O	8:I:74:ARG:NH1	2.49	0.44
9:J:18:PRO:HG2	9:J:19:TYR:HD1	1.83	0.44
20:h:13:LEU:HD23	20:h:17:ARG:HD3	2.00	0.44
22:F:105:ASN:C	22:F:108:LYS:NZ	2.74	0.44
26:Q:41:PRO:HG2	26:Q:78:VAL:HG21	1.99	0.44
30:U:41:ILE:HD12	30:U:103:ILE:HG22	2.00	0.44
35:g:59:VAL:HG12	35:g:60:ARG:HG3	1.99	0.44
37:3:34:U:O2'	37:3:35:C:H5''	2.17	0.44
40:k:188:HIS:CE1	40:k:383:GLU:HG3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:238:ILE:HG23	40:k:514:TRP:HB3	2.00	0.44
1:2:216:A:O2'	1:2:217:A:OP1	2.27	0.44
1:2:219:A:H3'	1:2:831:U:O2'	2.18	0.44
1:2:431:G:H2'	1:2:432:C:C6	2.53	0.44
1:2:488:C:C2	1:2:489:C:N4	2.86	0.44
1:2:553:C:H4'	9:J:19:TYR:HB3	1.99	0.44
1:2:588:C:H2'	1:2:589:C:C6	2.53	0.44
1:2:869:C:H1'	18:b:51:GLN:NE2	2.33	0.44
1:2:894:G:C2	1:2:917:U:C2	3.05	0.44
1:2:997:A:H2'	1:2:998:PSU:C6	2.53	0.44
1:2:1249:U:O2'	34:f:133:HIS:HA	2.17	0.44
1:2:1316:C:H2'	1:2:1317:G:O4'	2.18	0.44
1:2:1630:C:N4	1:2:1631:A:H62	2.16	0.44
2:A:43:ASP:OD1	2:A:45:VAL:N	2.51	0.44
3:B:3:VAL:HG21	39:j:89:ARG:HH21	1.79	0.44
3:B:111:ARG:CZ	17:a:68:TYR:H	2.31	0.44
3:B:127:VAL:HG21	3:B:176:VAL:HG21	2.00	0.44
4:C:64:HIS:HA	13:V:15:ARG:NH1	2.32	0.44
4:C:96:ARG:HA	4:C:96:ARG:NE	2.33	0.44
5:E:48:LEU:O	5:E:53:LYS:N	2.51	0.44
7:H:6:ALA:HA	7:H:9:LEU:HD12	1.99	0.44
10:L:116:ARG:HE	10:L:117:VAL:H	1.66	0.44
12:O:50:ALA:C	12:O:52:ARG:H	2.26	0.44
21:D:14:ASP:O	21:D:17:PHE:HB3	2.18	0.44
23:K:44:LYS:HD2	23:K:47:GLN:NE2	2.33	0.44
27:R:36:ASP:OD1	27:R:47:ARG:NE	2.41	0.44
28:S:73:MET:HE1	28:S:101:LEU:HG	1.99	0.44
30:U:99:ILE:O	30:U:103:ILE:HG13	2.18	0.44
35:g:54:GLN:HG2	35:g:54:GLN:O	2.16	0.44
36:i:39:THR:OG1	36:i:56:LYS:NZ	2.47	0.44
38:1:60:A:H2'	38:1:61:C:C5	2.53	0.44
40:k:209:ALA:HB1	40:k:498:LYS:HE3	2.00	0.44
1:2:393:C:H2'	1:2:394:U:H6	1.83	0.44
1:2:1032:C:H2'	1:2:1033:C:H6	1.83	0.44
1:2:1080:A:N6	1:2:1090:A:N7	2.66	0.44
1:2:1192:A:C8	1:2:1281:U:H4'	2.53	0.44
1:2:1192:A:H8	1:2:1192:A:OP1	2.01	0.44
1:2:1356:G:H2'	1:2:1357:G:H8	1.82	0.44
1:2:1388:U:O2	1:2:1388:U:H2'	2.18	0.44
1:2:1531:C:N4	1:2:1532:G:O6	2.50	0.44
1:2:1584:A:H2	22:F:106:ASN:HD21	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1732:U:H2'	1:2:1733:U:C6	2.52	0.44
1:2:1775:G:H2'	1:2:1776:G:H8	1.82	0.44
7:H:13:PRO:HB2	7:H:14:THR:HG23	1.99	0.44
10:L:3:THR:O	10:L:4:GLU:HB2	2.18	0.44
12:O:83:ILE:HG21	17:a:44:ILE:HD11	1.98	0.44
12:O:117:ASP:OD2	12:O:119:THR:HG22	2.18	0.44
14:W:25:VAL:HG22	14:W:63:VAL:CG2	2.43	0.44
14:W:115:GLU:HG2	14:W:118:ARG:NH1	2.30	0.44
15:X:138:GLU:N	15:X:138:GLU:OE2	2.51	0.44
24:M:71:LEU:HD13	34:f:114:VAL:HG21	2.00	0.44
24:M:87:GLN:O	24:M:91:TRP:CD1	2.71	0.44
24:M:89:GLY:HA3	24:M:108:GLY:HA2	1.98	0.44
28:S:5:VAL:HG11	31:Z:44:GLN:HG2	1.99	0.44
31:Z:60:VAL:HB	31:Z:101:TYR:HB2	1.99	0.44
39:j:226:PRO:HD3	40:k:408:ARG:HD3	1.99	0.44
41:l:176:ASN:OD1	41:l:179:ASP:HB2	2.18	0.44
1:2:278:G:N2	1:2:280:G:C2	2.86	0.44
1:2:468:C:C4	1:2:469:A:C5	3.06	0.44
1:2:484:A:C2	1:2:502:G:N1	2.86	0.44
1:2:649:U:HO2'	1:2:650:G:P	2.39	0.44
1:2:961:C:H2'	1:2:962:A:O4'	2.18	0.44
1:2:992:A:N3	1:2:992:A:H2'	2.33	0.44
1:2:1259:U:O2'	1:2:1260:G:H8	2.01	0.44
1:2:1323:G:H8	1:2:1323:G:OP2	2.01	0.44
1:2:1476:G:H3'	1:2:1477:A:H8	1.83	0.44
1:2:1496:G:O3'	29:T:121:GLY:HA2	2.18	0.44
4:C:48:ARG:HH11	4:C:253:THR:H	1.66	0.44
5:E:23:LEU:HD23	5:E:23:LEU:H	1.83	0.44
8:I:6:ASP:O	8:I:9:HIS:ND1	2.51	0.44
8:I:153:ILE:HD12	8:I:161:PHE:HE2	1.83	0.44
9:J:102:GLU:OE2	9:J:102:GLU:N	2.42	0.44
10:L:22:ASN:OD1	10:L:25:ALA:N	2.50	0.44
13:V:11:LEU:HD23	13:V:11:LEU:H	1.81	0.44
18:b:49:HIS:NE2	18:b:70:LYS:HG3	2.33	0.44
22:F:105:ASN:O	22:F:108:LYS:NZ	2.42	0.44
25:P:56:LEU:HD22	25:P:78:THR:HG21	1.99	0.44
30:U:71:PRO:HB3	33:d:41:GLN:HB3	2.00	0.44
36:i:41:MET:HE3	36:i:72:GLY:C	2.43	0.44
36:i:77:ILE:HG21	36:i:91:VAL:HG22	1.99	0.44
39:j:24:VAL:HG12	39:j:65:VAL:HG23	1.99	0.44
1:2:779:A:H1'	1:2:781:A:N6	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1046:G:H1	1:2:1070:U:H3	1.65	0.43
1:2:1052:G:C2	1:2:1066:C:C2	3.05	0.43
1:2:1234:C:H5'	34:f:143:HIS:CD2	2.53	0.43
1:2:1417:G:H2'	1:2:1418:C:H6	1.82	0.43
1:2:1444:A:H2'	1:2:1444:A:OP2	2.18	0.43
1:2:1480:C:P	1:2:1519:G:H22	2.41	0.43
3:B:168:ILE:HG23	3:B:172:LEU:HD23	2.00	0.43
9:J:108:ARG:NH2	9:J:110:GLN:HE22	2.14	0.43
10:L:135:VAL:O	10:L:136:ARG:HD2	2.17	0.43
16:Y:10:ARG:HB3	16:Y:24:VAL:HG13	2.00	0.43
27:R:115:LEU:HD23	27:R:116:LYS:N	2.33	0.43
28:S:53:ASP:HB3	28:S:56:LYS:HB2	2.00	0.43
29:T:45:LEU:HG	29:T:46:PRO:HD2	2.00	0.43
29:T:66:TYR:HA	29:T:124:ILE:HG12	2.00	0.43
34:f:92:ARG:HH21	34:f:94:LYS:HA	1.83	0.43
39:j:230:LEU:HD13	39:j:244:LEU:HD21	1.99	0.43
42:m:26:ILE:O	42:m:103:ILE:HA	2.18	0.43
1:2:54:C:OP1	16:Y:113:ASN:ND2	2.51	0.43
1:2:468:C:H2'	1:2:469:A:O4'	2.17	0.43
1:2:554:A:C4	9:J:19:TYR:HE2	2.36	0.43
1:2:960:U:OP2	11:N:62:GLN:NE2	2.41	0.43
1:2:1141:A:H5''	17:a:2:PRO:HB3	2.00	0.43
1:2:1275:U:O5'	21:D:147:ALA:HB2	2.18	0.43
1:2:1499:C:OP2	29:T:106:GLN:NE2	2.51	0.43
1:2:1533:U:H5'	1:2:1534:G:C8	2.53	0.43
1:2:1579:C:O2'	1:2:1580:U:H5'	2.17	0.43
1:2:1735:G:H2'	1:2:1736:U:O4'	2.17	0.43
4:C:165:GLY:HA3	4:C:222:ALA:HB2	2.00	0.43
5:E:7:LYS:HA	5:E:30:ARG:NH2	2.29	0.43
6:G:148:THR:HB	6:G:151:ASP:OD2	2.18	0.43
7:H:41:LEU:HD23	7:H:70:TYR:CE1	2.47	0.43
7:H:75:ILE:HG13	7:H:76:LYS:H	1.83	0.43
12:O:52:ARG:CZ	22:F:158:ARG:HH12	2.31	0.43
13:V:7:GLN:OE1	13:V:7:GLN:N	2.51	0.43
21:D:27:ARG:O	23:K:58:GLN:NE2	2.51	0.43
22:F:84:PHE:CE1	32:c:47:PRO:HB2	2.54	0.43
27:R:24:LEU:HB3	27:R:58:MET:HE1	2.00	0.43
27:R:47:ARG:HA	27:R:50:ILE:HG22	2.00	0.43
28:S:33:THR:HG21	28:S:40:ARG:HG2	2.00	0.43
28:S:90:LYS:HD3	28:S:90:LYS:HA	1.77	0.43
30:U:42:ILE:O	30:U:46:GLU:OE1	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:c:31:GLU:HB3	32:c:39:THR:HG22	2.01	0.43
35:g:22:THR:OG1	35:g:69:VAL:O	2.23	0.43
40:k:354:GLU:HA	40:k:373:ILE:O	2.17	0.43
41:l:186:ARG:NH2	41:l:257:MET:HE1	2.33	0.43
42:m:45:VAL:HB	42:m:76:GLU:HB2	2.00	0.43
1:2:484:A:C2	1:2:485:G:C5	3.07	0.43
1:2:914:A:H3'	1:2:915:U:C6	2.53	0.43
1:2:1207:A:N1	1:2:1453:G:N2	2.65	0.43
1:2:1240:G:C8	25:P:79:HIS:HB2	2.52	0.43
1:2:1342:U:O4	1:2:1343:A:N6	2.51	0.43
1:2:1717:A:H2'	1:2:1718:G:O4'	2.17	0.43
2:A:38:TYR:HB2	2:A:49:ASN:OD1	2.19	0.43
2:A:179:ARG:HD2	2:A:183:ARG:HD2	2.00	0.43
5:E:31:PRO:HG3	5:E:43:PRO:HG3	2.00	0.43
5:E:179:LYS:O	5:E:195:ILE:HG22	2.19	0.43
7:H:70:TYR:HB3	7:H:92:PHE:HD2	1.83	0.43
9:J:28:LEU:HD21	19:e:40:TYR:HA	2.00	0.43
18:b:47:PHE:HE2	18:b:49:HIS:HB2	1.82	0.43
22:F:161:ALA:HB3	22:F:227:ARG:HA	2.00	0.43
31:Z:50:ILE:HD11	31:Z:70:LYS:HD2	2.01	0.43
34:f:92:ARG:NH2	34:f:94:LYS:HA	2.33	0.43
35:g:20:TRP:HB2	35:g:39:ARG:HH11	1.83	0.43
35:g:301:TRP:NE1	35:g:308:LEU:HD21	2.34	0.43
38:1:71:C:H2'	38:1:72:U:H6	1.83	0.43
1:2:143:G:H2'	1:2:144:A:O4'	2.17	0.43
1:2:897:A:C8	1:2:911:U:C4	3.06	0.43
1:2:919:U:H5'	1:2:920:U:OP2	2.18	0.43
1:2:1029:A:C6	1:2:1790:G:C6	3.06	0.43
1:2:1060:U:H3'	1:2:1061:A:C2	2.54	0.43
1:2:1078:U:H2'	1:2:1079:U:O4'	2.19	0.43
1:2:1201:A:H61	1:2:1455:C:H5'	1.82	0.43
1:2:1215:C:O2'	1:2:1442:A:N1	2.49	0.43
1:2:1642:C:O2'	42:m:61:ASP:O	2.20	0.43
1:2:1795:A:H4'	17:a:95:ARG:HG3	2.00	0.43
2:A:125:ASP:HB2	2:A:128:SER:OG	2.18	0.43
4:C:71:PHE:CG	4:C:135:ILE:HD12	2.53	0.43
4:C:118:LEU:HD11	4:C:216:LEU:HB3	2.00	0.43
4:C:188:ALA:HB1	4:C:216:LEU:HD11	2.01	0.43
5:E:136:ILE:HG23	5:E:149:TYR:CE1	2.53	0.43
9:J:82:ARG:HE	9:J:149:ARG:NE	2.16	0.43
10:L:10:GLU:HG3	10:L:14:GLN:HE22	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:14:GLN:HB3	10:L:54:ILE:HG13	2.00	0.43
10:L:16:GLN:NE2	10:L:33:ARG:HG3	2.34	0.43
14:W:69:LEU:HD11	14:W:71:LYS:C	2.43	0.43
23:K:46:LEU:O	23:K:50:THR:HG23	2.18	0.43
28:S:65:GLU:O	28:S:69:ILE:HG12	2.17	0.43
29:T:101:ASN:O	29:T:105:LEU:HD23	2.18	0.43
38:1:20:A:N3	38:1:20:A:H2'	2.34	0.43
41:l:196:PHE:CD1	41:l:202:SER:HA	2.54	0.43
1:2:239:C:H4'	1:2:240:U:OP2	2.18	0.43
1:2:272:G:C6	1:2:283:G:N3	2.87	0.43
1:2:372:G:C6	1:2:373:U:C4	3.06	0.43
1:2:405:U:H2'	1:2:406:A:H8	1.82	0.43
1:2:613:C:H2'	1:2:614:A:C8	2.54	0.43
1:2:710:U:H2'	1:2:711:G:C4	2.54	0.43
1:2:799:U:H2'	1:2:800:G:H8	1.82	0.43
1:2:909:C:H2'	1:2:910:U:H6	1.83	0.43
1:2:1084:G:C5'	4:C:166:LYS:HZ1	2.32	0.43
1:2:1197:G:C6	1:2:1199:G:C6	3.06	0.43
1:2:1210:A:C6	1:2:1211:G:C5	3.07	0.43
1:2:1231:U:H2'	1:2:1232:G:C8	2.53	0.43
1:2:1262:G:H2'	1:2:1263:G:O4'	2.18	0.43
1:2:1578:C:H4'	26:Q:137:ARG:HB2	2.00	0.43
2:A:54:TRP:O	2:A:58:VAL:HG13	2.18	0.43
2:A:109:ASN:HB3	2:A:112:THR:HG23	2.00	0.43
2:A:179:ARG:HD3	2:A:183:ARG:CZ	2.48	0.43
2:A:190:ASP:OD1	2:A:193:GLN:NE2	2.52	0.43
3:B:137:ILE:HG13	3:B:215:VAL:HG23	2.00	0.43
5:E:18:TRP:CD1	5:E:46:VAL:HG11	2.53	0.43
5:E:98:ASN:HB2	5:E:114:ILE:O	2.18	0.43
6:G:35:GLU:HA	6:G:50:PHE:O	2.18	0.43
7:H:101:LYS:HB2	7:H:101:LYS:HE3	1.82	0.43
8:I:22:ARG:HG3	8:I:22:ARG:O	2.18	0.43
22:F:192:ILE:O	22:F:195:THR:OG1	2.25	0.43
31:Z:90:LYS:HE2	31:Z:104:ALA:HA	2.00	0.43
35:g:152:VAL:HA	35:g:178:GLY:HA3	2.01	0.43
38:1:64:RIA:H3A	38:1:65:G:H5'	2.00	0.43
40:k:247:LEU:HD23	40:k:281:VAL:HB	2.00	0.43
1:2:43:A:C8	1:2:377:A:C2	3.07	0.43
1:2:504:A:H2'	1:2:506:U:O2	2.18	0.43
1:2:644:C:H2'	1:2:645:U:C6	2.53	0.43
1:2:960:U:O2'	11:N:86:GLU:OE2	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1034:G:H2'	1:2:1035:A:H8	1.83	0.43
1:2:1047:G:H2'	1:2:1048:U:H6	1.84	0.43
1:2:1125:G:H2'	1:2:1126:G:H8	1.84	0.43
1:2:1140:G:H2'	1:2:1141:A:H8	1.84	0.43
1:2:1230:U:OP1	1:2:1258:U:O2'	2.16	0.43
1:2:1434:A:H1'	21:D:174:HIS:CE1	2.54	0.43
3:B:98:THR:O	3:B:232:HIS:NE2	2.44	0.43
5:E:64:ILE:HD12	16:Y:17:LEU:HB3	2.00	0.43
10:L:99:ARG:HE	14:W:79:PHE:HE1	1.67	0.43
10:L:99:ARG:HB2	15:X:12:ALA:HB2	1.99	0.43
16:Y:18:LEU:HB2	16:Y:20:ARG:NE	2.33	0.43
16:Y:23:PHE:CZ	16:Y:75:VAL:HG23	2.54	0.43
21:D:148:LYS:HE3	37:3:38:C:H42	1.83	0.43
27:R:72:LYS:HA	27:R:75:GLU:OE2	2.19	0.43
33:d:30:LEU:HD23	33:d:31:ILE:N	2.34	0.43
36:i:39:THR:O	36:i:73:GLN:NE2	2.51	0.43
40:k:83:ASP:O	40:k:87:LEU:HG	2.19	0.43
40:k:211:MET:SD	40:k:241:LEU:HD13	2.59	0.43
1:2:10:G:C4	1:2:11:A:C8	3.06	0.43
1:2:93:A:C8	1:2:398:A:C4	3.07	0.43
1:2:262:C:H2'	1:2:263:G:C8	2.54	0.43
1:2:345:G:N3	1:2:346:G:C8	2.86	0.43
1:2:360:C:H2'	1:2:361:G:C8	2.53	0.43
1:2:528:A:H2'	1:2:529:C:C6	2.54	0.43
1:2:568:C:H2'	1:2:569:A:O4'	2.19	0.43
1:2:777:C:N4	16:Y:10:ARG:HD2	2.33	0.43
1:2:859:U:OP1	7:H:114:ARG:NH1	2.52	0.43
1:2:1207:A:H2'	1:2:1207:A:N3	2.34	0.43
1:2:1234:C:H5'	34:f:143:HIS:HD2	1.82	0.43
1:2:1422:A:O2'	4:C:97:ALA:HB3	2.17	0.43
1:2:1675:C:C4	1:2:1723:U:C4	3.07	0.43
3:B:5:LYS:HG2	3:B:7:LYS:H	1.83	0.43
3:B:82:ARG:NE	3:B:82:ARG:HA	2.34	0.43
7:H:21:ALA:HA	7:H:24:PHE:CD2	2.54	0.43
8:I:192:PHE:CD2	10:L:13:PHE:HD2	2.36	0.43
10:L:67:ARG:HH12	10:L:129:ARG:HB2	1.83	0.43
21:D:33:GLY:HA3	21:D:53:THR:OG1	2.19	0.43
21:D:34:TYR:OH	21:D:37:VAL:HG12	2.19	0.43
21:D:109:LEU:HD23	21:D:175:VAL:HG11	2.00	0.43
23:K:16:PHE:HZ	23:K:86:ILE:HG23	1.83	0.43
24:M:60:THR:C	24:M:62:GLU:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Z:54:ALA:HB3	31:Z:55:PRO:HD3	2.01	0.43
32:c:14:LYS:HA	32:c:14:LYS:HD2	1.80	0.43
33:d:21:CYS:C	33:d:23:ILE:H	2.27	0.43
35:g:155:VAL:HG22	35:g:176:SER:HB2	2.01	0.43
35:g:161:ASN:OD1	35:g:162:LEU:N	2.51	0.43
1:2:68:A:O5'	1:2:69:G:H5''	2.19	0.43
1:2:93:A:H1'	5:E:3:ARG:HG3	1.99	0.43
1:2:294:A:C6	1:2:295:U:C4	3.07	0.43
1:2:324:G:OP1	10:L:132:SER:OG	2.32	0.43
1:2:388:G:H3'	1:2:389:G:H21	1.84	0.43
1:2:586:C:H5''	19:e:26:LYS:HZ1	1.83	0.43
1:2:598:A:N3	15:X:48:HIS:HE1	2.17	0.43
1:2:868:A:H61	1:2:957:U:H5	1.67	0.43
1:2:1249:U:H1'	34:f:133:HIS:CE1	2.54	0.43
1:2:1386:A:C2	1:2:1410:G:C5	3.07	0.43
1:2:1475:G:H2'	1:2:1476:G:C8	2.54	0.43
1:2:1782:C:H5	20:h:5:TRP:CH2	2.37	0.43
2:A:21:ARG:HH11	2:A:21:ARG:HG3	1.83	0.43
2:A:143:VAL:HG23	2:A:157:ASP:H	1.83	0.43
7:H:38:LEU:HD12	7:H:38:LEU:O	2.18	0.43
11:N:16:ILE:HG13	11:N:17:PRO:HD2	1.99	0.43
12:O:127:ARG:HH11	17:a:22:ARG:HH11	1.63	0.43
20:h:16:LYS:NZ	20:h:23:ARG:HH12	2.17	0.43
22:F:47:LYS:HB2	22:F:48:TRP:CE3	2.53	0.43
22:F:84:PHE:HZ	32:c:47:PRO:HB2	1.80	0.43
24:M:97:ILE:HG23	24:M:101:GLY:HA2	2.00	0.43
25:P:75:VAL:HG13	25:P:104:GLN:HE22	1.83	0.43
27:R:103:ASP:HB2	27:R:106:THR:HG22	2.00	0.43
28:S:5:VAL:HG21	31:Z:44:GLN:OE1	2.18	0.43
28:S:125:ILE:HG23	28:S:129:TRP:CE3	2.54	0.43
30:U:69:LYS:HB3	30:U:78:THR:HG23	2.00	0.43
35:g:34:LEU:HD12	35:g:309:PHE:CE2	2.54	0.43
39:j:40:ASP:OD1	39:j:41:ASN:N	2.44	0.43
40:k:282:PRO:HD3	41:l:131:TYR:CD1	2.53	0.43
40:k:285:ALA:HB3	45:k:601:GCP:N7	2.34	0.43
40:k:354:GLU:HB3	40:k:374:PHE:CD2	2.54	0.43
42:m:71:ASP:O	42:m:73:GLU:N	2.51	0.43
1:2:208:U:H2'	1:2:209:A:C8	2.54	0.43
1:2:273:G:H2'	1:2:274:C:C6	2.53	0.43
1:2:679:U:H3'	1:2:680:U:H5''	2.01	0.43
1:2:870:G:H2'	1:2:871:G:H8	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:954:A:H2'	1:2:955:C:C6	2.54	0.43
1:2:1146:A:O2'	1:2:1634:C:OP2	2.31	0.43
1:2:1407:G:N1	1:2:1410:G:OP2	2.51	0.43
1:2:1533:U:H5	22:F:188:ASN:C	2.27	0.43
1:2:1619:U:C4	1:2:1620:G:N7	2.87	0.43
2:A:15:GLN:HE21	27:R:117:LEU:HA	1.83	0.43
2:A:61:ALA:HA	2:A:181:VAL:HG12	2.01	0.43
5:E:7:LYS:C	5:E:30:ARG:HE	2.26	0.43
5:E:179:LYS:HA	5:E:231:PRO:HD3	2.01	0.43
5:E:180:LEU:HB2	5:E:230:GLU:C	2.44	0.43
6:G:102:VAL:HG13	6:G:106:LEU:HD12	2.01	0.43
9:J:62:ARG:NH2	9:J:68:LYS:HB3	2.33	0.43
15:X:62:LYS:HZ1	15:X:117:ILE:C	2.26	0.43
21:D:55:VAL:HA	21:D:58:VAL:HB	2.01	0.43
28:S:46:VAL:HG23	28:S:72:ILE:HG22	1.99	0.43
29:T:88:VAL:HG12	29:T:89:ARG:HH22	1.84	0.43
35:g:107:HIS:ND1	35:g:133:ARG:HD2	2.34	0.43
38:1:32:C:C4	38:1:33:U:C4	3.07	0.43
38:1:71:C:H2'	38:1:72:U:C6	2.54	0.43
40:k:148:TYR:O	40:k:162:ARG:N	2.45	0.43
40:k:330:ILE:HG23	40:k:333:LEU:CD1	2.49	0.43
1:2:78:A:H2'	1:2:79:C:O4'	2.19	0.43
1:2:204:U:H2'	1:2:205:A:C8	2.46	0.43
1:2:558:C:H2'	1:2:559:U:C6	2.53	0.43
1:2:608:U:O4	15:X:25:ALA:HB3	2.19	0.43
1:2:700:C:O2'	1:2:701:U:P	2.77	0.43
1:2:735:C:O2'	1:2:736:C:O5'	2.29	0.43
1:2:1099:G:O4'	15:X:7:ARG:NH2	2.52	0.43
1:2:1133:C:H2'	1:2:1134:U:H6	1.84	0.43
1:2:1434:A:HO2'	21:D:174:HIS:CE1	2.30	0.43
1:2:1477:A:H5''	29:T:60:SER:HB2	2.01	0.43
2:A:70:PRO:HG3	2:A:185:ARG:HH22	1.84	0.43
2:A:89:TYR:CD2	2:A:174:TRP:HE3	2.37	0.43
2:A:169:SER:O	2:A:173:ILE:HG12	2.19	0.43
4:C:70:GLU:HB3	4:C:72:GLN:NE2	2.34	0.43
4:C:153:LEU:HD12	4:C:153:LEU:HA	1.82	0.43
4:C:170:VAL:HG21	4:C:215:THR:HA	1.99	0.43
6:G:9:ILE:HD12	6:G:9:ILE:H	1.84	0.43
10:L:123:VAL:HG22	10:L:142:VAL:HG22	2.01	0.43
18:b:20:LYS:O	18:b:21:LEU:HB2	2.19	0.43
21:D:163:PRO:HB3	21:D:167:PHE:HD2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:P:22:LEU:O	25:P:26:LEU:HG	2.18	0.43
31:Z:58:ARG:HA	31:Z:58:ARG:HD2	1.75	0.43
32:c:17:GLY:O	32:c:26:THR:HG23	2.18	0.43
33:d:22:ARG:HG2	33:d:37:ASN:O	2.19	0.43
1:2:71:A:H5''	1:2:72:A:OP2	2.19	0.42
1:2:336:G:H1'	1:2:338:C:OP2	2.19	0.42
1:2:460:G:H2'	1:2:461:G:H8	1.84	0.42
1:2:551:G:H2'	1:2:552:G:C8	2.54	0.42
1:2:560:G:C2	1:2:561:G:C8	3.06	0.42
1:2:587:U:P	19:e:26:LYS:HE3	2.59	0.42
1:2:874:G:O6	1:2:951:A:N1	2.52	0.42
1:2:1249:U:OP2	1:2:1249:U:H6	2.02	0.42
1:2:1276:G:H2'	1:2:1277:G:C8	2.53	0.42
1:2:1277:G:H2'	1:2:1278:C:O4'	2.19	0.42
1:2:1776:G:N1	1:2:1782:C:N3	2.67	0.42
3:B:226:GLY:HA2	3:B:229:LEU:HG	2.01	0.42
4:C:100:ARG:HH12	4:C:102:ARG:NE	2.16	0.42
5:E:208:VAL:O	5:E:219:VAL:HA	2.18	0.42
7:H:20:VAL:HG12	7:H:85:PHE:CE2	2.53	0.42
11:N:127:ARG:O	11:N:131:THR:HG23	2.19	0.42
13:V:84:SER:O	13:V:87:ARG:NH1	2.52	0.42
21:D:27:ARG:HB3	23:K:58:GLN:OE1	2.19	0.42
21:D:99:VAL:HG22	21:D:171:ALA:HB2	2.01	0.42
21:D:141:LYS:HZ2	21:D:147:ALA:HA	1.84	0.42
21:D:148:LYS:HZ2	21:D:150:MET:HB2	1.84	0.42
28:S:92:VAL:HG13	28:S:92:VAL:O	2.19	0.42
30:U:99:ILE:HG13	30:U:100:VAL:N	2.34	0.42
34:f:136:ARG:CB	34:f:149:GLN:HA	2.49	0.42
35:g:81:ALA:O	35:g:92:LEU:HD12	2.19	0.42
35:g:310:ALA:O	35:g:317:ILE:HA	2.19	0.42
38:1:12:G:C6	38:1:24:G:N1	2.87	0.42
40:k:429:ASP:HB3	40:k:484:ARG:NH1	2.33	0.42
1:2:124:A:H2'	1:2:125:U:O4'	2.20	0.42
1:2:242:G:H2'	1:2:243:A:C8	2.54	0.42
1:2:496:G:H5'	1:2:497:G:OP2	2.19	0.42
1:2:516:U:H5'	1:2:517:A:OP2	2.19	0.42
1:2:548:G:H2'	1:2:549:A:C8	2.51	0.42
1:2:604:A:C5	1:2:605:A:C2	3.07	0.42
1:2:946:U:H2'	1:2:947:G:H8	1.81	0.42
1:2:1502:G:H2'	1:2:1503:A:C8	2.54	0.42
1:2:1540:G:O3'	1:2:1541:A:H8	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1557:A:C4	28:S:134:ARG:HD2	2.54	0.42
1:2:1780:MA6:OP1	20:h:9:ARG:NH2	2.51	0.42
2:A:20:ALA:HB3	2:A:22:VAL:HG23	2.02	0.42
4:C:49:LEU:HD11	4:C:248:TYR:HB3	2.01	0.42
4:C:232:PRO:HA	4:C:235:TRP:CD1	2.54	0.42
5:E:175:PHE:CZ	5:E:198:ARG:HG3	2.55	0.42
5:E:185:GLY:HA2	5:E:189:LEU:HD13	2.01	0.42
9:J:61:THR:HG22	14:W:87:GLU:OE1	2.19	0.42
11:N:33:VAL:O	11:N:37:ILE:HG13	2.19	0.42
21:D:173:ARG:NH1	21:D:174:HIS:H	2.18	0.42
22:F:42:ILE:HG12	22:F:71:TYR:OH	2.19	0.42
29:T:6:VAL:O	29:T:9:VAL:HG12	2.18	0.42
29:T:34:VAL:O	29:T:36:ILE:HD12	2.19	0.42
36:i:40:LYS:NZ	36:i:42:LEU:HD23	2.34	0.42
39:j:19:ILE:HB	39:j:98:CYS:SG	2.59	0.42
39:j:130:ILE:HG12	39:j:155:TRP:CH2	2.54	0.42
40:k:426:ILE:HG12	40:k:492:CYS:SG	2.59	0.42
40:k:479:LYS:HD2	40:k:482:MET:HB3	2.01	0.42
1:2:364:G:C5	1:2:376:G:C2	3.07	0.42
1:2:511:A:H2'	1:2:512:U:C6	2.54	0.42
1:2:680:U:O2'	1:2:682:U:OP1	2.27	0.42
1:2:953:G:C6	1:2:954:A:C6	3.08	0.42
1:2:1389:A:C4	1:2:1390:U:C5	3.07	0.42
1:2:1617:C:H2'	1:2:1618:C:C6	2.48	0.42
2:A:77:SER:HB2	2:A:124:THR:HG21	2.00	0.42
2:A:88:LYS:HG3	2:A:92:HIS:CE1	2.54	0.42
3:B:171:ILE:HG23	3:B:172:LEU:HD22	2.01	0.42
12:O:112:ILE:HG12	17:a:56:ALA:O	2.18	0.42
13:V:32:VAL:HG22	13:V:55:LEU:HB2	2.01	0.42
14:W:34:ILE:O	14:W:38:LEU:HD23	2.20	0.42
14:W:88:LYS:HD2	14:W:89:TRP:N	2.34	0.42
15:X:90:ASP:HB3	19:e:12:GLY:HA2	2.01	0.42
15:X:101:GLU:OE2	15:X:128:SER:HA	2.18	0.42
21:D:25:PHE:HD2	21:D:50:ILE:HD13	1.82	0.42
23:K:31:LYS:HA	23:K:31:LYS:HE3	2.01	0.42
27:R:6:THR:OG1	27:R:7:LYS:N	2.52	0.42
34:f:100:LEU:HD12	34:f:103:LEU:HD11	2.00	0.42
40:k:108:HIS:CE1	40:k:109:VAL:HG22	2.54	0.42
40:k:512:ILE:HG13	40:k:513:GLY:N	2.34	0.42
1:2:209:A:C6	1:2:210:U:C4	3.07	0.42
1:2:221:A:N7	1:2:832:U:C2	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:278:G:N1	1:2:280:G:C6	2.87	0.42
1:2:338:C:C2	1:2:339:U:C5	3.07	0.42
1:2:345:G:H2'	1:2:346:G:H8	1.85	0.42
1:2:345:G:C4'	10:L:80:MET:HE1	2.43	0.42
1:2:413:C:C4	1:2:414:C:C4	3.07	0.42
1:2:511:A:H2'	1:2:512:U:O4'	2.20	0.42
1:2:531:U:H2'	1:2:532:U:O4'	2.20	0.42
1:2:639:U:H2'	1:2:640:G:O4'	2.18	0.42
1:2:789:U:H6	1:2:789:U:H2'	1.62	0.42
1:2:886:A:C5	1:2:887:U:C5	3.07	0.42
1:2:941:G:OP1	1:2:976:A:O2'	2.35	0.42
1:2:1038:A:H4'	13:V:62:ARG:NH2	2.34	0.42
1:2:1359:A:N3	1:2:1359:A:H2'	2.35	0.42
1:2:1685:U:C4	1:2:1687:A:C5	3.08	0.42
1:2:1795:A:O2'	17:a:95:ARG:O	2.25	0.42
2:A:50:VAL:O	2:A:53:THR:OG1	2.23	0.42
3:B:129:THR:OG1	3:B:130:SER:N	2.51	0.42
3:B:215:VAL:HG13	3:B:215:VAL:O	2.19	0.42
5:E:12:LEU:HA	5:E:12:LEU:HD23	1.83	0.42
12:O:32:ASP:OD2	12:O:34:SER:HB3	2.19	0.42
17:a:79:ILE:HD11	17:a:86:VAL:HG23	2.01	0.42
29:T:66:TYR:HE1	29:T:129:LEU:HG	1.85	0.42
29:T:70:GLN:OE1	29:T:121:GLY:HA3	2.20	0.42
29:T:89:ARG:HA	29:T:89:ARG:NE	2.34	0.42
35:g:157:VAL:O	35:g:211:PRO:HG2	2.20	0.42
35:g:271:ASP:OD1	35:g:271:ASP:N	2.51	0.42
42:m:80:LEU:HD21	42:m:84:GLN:HB2	2.00	0.42
1:2:127:G:O2'	1:2:128:U:H5'	2.20	0.42
1:2:155:A:H2	1:2:414:C:H1'	1.84	0.42
1:2:321:G:O2'	8:I:10:LYS:NZ	2.52	0.42
1:2:393:C:H2'	1:2:394:U:C6	2.54	0.42
1:2:568:C:C4	1:2:569:A:C5	3.08	0.42
1:2:709:C:H42	1:2:730:G:H2'	1.84	0.42
1:2:751:G:N1	1:2:752:A:C6	2.88	0.42
1:2:997:A:C6	1:2:998:PSU:C2	3.07	0.42
1:2:1062:U:H2'	1:2:1063:G:O4'	2.20	0.42
1:2:1112:A:C8	1:2:1114:U:C2	3.08	0.42
1:2:1416:G:H2'	1:2:1417:G:H8	1.84	0.42
1:2:1471:U:N1	22:F:105:ASN:ND2	2.66	0.42
1:2:1502:G:OP1	29:T:99:SER:N	2.36	0.42
1:2:1544:G:P	28:S:127:HIS:HE2	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1615:U:H2'	1:2:1616:C:C6	2.55	0.42
1:2:1731:C:H2'	1:2:1732:U:H6	1.85	0.42
2:A:6:THR:O	2:A:191:ARG:NH1	2.52	0.42
2:A:16:LEU:HD23	2:A:172:LEU:HD21	2.01	0.42
4:C:45:LYS:HD3	4:C:252:ALA:HB1	2.02	0.42
4:C:64:HIS:HA	13:V:15:ARG:CZ	2.49	0.42
5:E:118:GLU:HA	5:E:121:TYR:CE2	2.54	0.42
6:G:3:LEU:HD13	6:G:109:LEU:HB2	2.01	0.42
7:H:139:ARG:CB	7:H:151:LYS:HB2	2.46	0.42
10:L:78:THR:HG21	10:L:118:GLN:C	2.45	0.42
11:N:120:SER:O	11:N:124:ARG:HG3	2.20	0.42
13:V:86:SER:HB2	18:b:6:ASP:HB2	2.01	0.42
21:D:146:ARG:HE	21:D:147:ALA:N	2.17	0.42
25:P:77:ARG:HD2	25:P:102:PHE:CZ	2.54	0.42
31:Z:38:HIS:HB3	31:Z:72:GLY:HA2	2.01	0.42
35:g:34:LEU:HB3	35:g:46:TRP:HB2	2.01	0.42
39:j:250:LYS:O	39:j:254:VAL:HG23	2.19	0.42
40:k:484:ARG:HD3	40:k:485:LEU:N	2.34	0.42
1:2:67:A:C6	1:2:84:A:C8	3.08	0.42
1:2:217:A:C6	1:2:829:U:C4	3.08	0.42
1:2:274:C:H2'	1:2:275:C:O4'	2.20	0.42
1:2:278:G:C6	1:2:280:G:C6	3.07	0.42
1:2:332:A:H2'	1:2:333:G:N9	2.35	0.42
1:2:343:A:C6	1:2:344:U:C4	3.07	0.42
1:2:407:C:H2'	1:2:408:C:C6	2.55	0.42
1:2:412:U:O2	1:2:412:U:H2'	2.20	0.42
1:2:460:G:H2'	1:2:461:G:C8	2.55	0.42
1:2:618:A:N3	1:2:1140:G:H1'	2.34	0.42
1:2:1045:G:C6	1:2:1072:G:N1	2.88	0.42
1:2:1257:U:H6	1:2:1257:U:H2'	1.68	0.42
1:2:1275:U:H4'	21:D:141:LYS:NZ	2.34	0.42
1:2:1279:C:OP1	33:d:44:ARG:NH2	2.43	0.42
1:2:1297:U:OP1	1:2:1297:U:H6	2.02	0.42
1:2:1331:C:H4'	21:D:203:PRO:HB3	2.01	0.42
1:2:1387:C:O2'	27:R:52:GLY:HA3	2.19	0.42
1:2:1409:A:H5''	26:Q:121:SER:HB3	2.02	0.42
1:2:1778:G:C4	1:2:1779:A:C8	3.08	0.42
2:A:143:VAL:O	2:A:157:ASP:HB2	2.19	0.42
3:B:18:LYS:C	3:B:19:ARG:HD3	2.44	0.42
5:E:21:ASP:HB2	5:E:23:LEU:HD23	2.01	0.42
7:H:15:GLU:O	7:H:18:LEU:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:99:LEU:O	9:J:100:LYS:C	2.62	0.42
10:L:69:LYS:HB3	10:L:127:GLN:OE1	2.20	0.42
10:L:135:VAL:C	10:L:136:ARG:HD2	2.45	0.42
15:X:95:PHE:CE2	15:X:135:LEU:HB3	2.55	0.42
17:a:73:TYR:CD2	17:a:83:ILE:HG21	2.55	0.42
24:M:71:LEU:HD21	34:f:106:TYR:HB3	2.00	0.42
28:S:66:LEU:O	28:S:70:VAL:HG23	2.19	0.42
40:k:127:ARG:O	40:k:133:GLU:HA	2.20	0.42
42:m:24:ASN:O	42:m:102:ASN:ND2	2.53	0.42
1:2:329:G:C6	1:2:330:A:C5	3.08	0.42
1:2:370:G:H2'	1:2:371:G:O4'	2.20	0.42
1:2:459:A:H3'	1:2:460:G:H8	1.85	0.42
1:2:568:C:H41	15:X:69:ARG:HH22	1.67	0.42
1:2:756:A:C2	1:2:757:A:H1'	2.55	0.42
1:2:760:A:C6	1:2:789:U:O4	2.72	0.42
1:2:1025:A:N7	1:2:1770:C:O2'	2.49	0.42
1:2:1063:G:C6	1:2:1064:A:C5	3.08	0.42
1:2:1097:U:O2	14:W:71:LYS:NZ	2.23	0.42
1:2:1177:G:C6	1:2:1460:G:C6	3.08	0.42
1:2:1656:G:C6	1:2:1742:A:C5	3.08	0.42
1:2:1760:A:C4	1:2:1761:A:C8	3.07	0.42
1:2:1790:G:OP2	17:a:4:LYS:HB2	2.19	0.42
2:A:13:ASP:OD1	2:A:14:ALA:N	2.53	0.42
2:A:195:TRP:CH2	2:A:197:ILE:HD11	2.55	0.42
3:B:82:ARG:HA	3:B:82:ARG:HE	1.85	0.42
3:B:193:ILE:HA	3:B:196:GLU:OE2	2.20	0.42
5:E:11:ARG:NH1	5:E:20:LEU:HB3	2.35	0.42
5:E:82:PHE:CD1	5:E:82:PHE:C	2.98	0.42
5:E:158:ASP:CG	5:E:174:LYS:HA	2.44	0.42
6:G:64:LYS:HB2	6:G:97:VAL:HG21	2.01	0.42
7:H:64:VAL:N	7:H:65:PRO:HD3	2.33	0.42
11:N:110:ASP:OD1	11:N:111:ALA:N	2.52	0.42
20:h:8:LYS:O	20:h:12:ARG:HG2	2.20	0.42
22:F:32:PRO:HB2	22:F:35:ILE:HG13	2.01	0.42
24:M:64:ILE:HG13	24:M:65:SER:N	2.34	0.42
26:Q:25:GLY:N	26:Q:62:ASN:O	2.53	0.42
35:g:14:LEU:HD22	35:g:46:TRP:CD1	2.55	0.42
35:g:54:GLN:OE1	35:g:54:GLN:N	2.45	0.42
38:l:15:G:H1	38:l:48:5MC:HN42	1.68	0.42
39:j:16:ILE:HG23	39:j:74:LEU:O	2.20	0.42
40:k:427:TYR:CE2	40:k:493:THR:HB	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:206:U:O2	8:I:179:ARG:NH2	2.53	0.42
1:2:579:A:C6	1:2:582:C:C2	3.08	0.42
1:2:782:G:C4	1:2:783:C:C5	3.08	0.42
1:2:991:A:OP2	1:2:1010:G:N1	2.42	0.42
1:2:1139:G:C2	1:2:1140:G:C8	3.08	0.42
1:2:1389:A:C6	1:2:1390:U:C4	3.08	0.42
1:2:1514:A:OP2	30:U:88:LYS:HE2	2.19	0.42
1:2:1678:G:OP2	1:2:1678:G:H8	2.02	0.42
1:2:1757:C:H2'	1:2:1758:G:C8	2.55	0.42
2:A:157:ASP:CG	13:V:60:ARG:HH21	2.27	0.42
15:X:14:LYS:HE2	15:X:14:LYS:HB3	1.79	0.42
16:Y:57:VAL:HB	16:Y:60:PHE:CE2	2.55	0.42
18:b:34:ASP:OD1	18:b:80:ARG:HB3	2.19	0.42
22:F:28:ALA:HB2	26:Q:26:LYS:HG3	2.02	0.42
30:U:98:HIS:HA	30:U:101:LYS:HE2	2.01	0.42
35:g:194:ARG:HD3	35:g:194:ARG:HA	1.86	0.42
39:j:27:ILE:HG23	39:j:31:GLY:O	2.20	0.42
1:2:71:A:H1'	1:2:81:G:N2	2.35	0.42
1:2:84:A:H3'	1:2:85:A:H8	1.84	0.42
1:2:203:G:OP1	1:2:203:G:H3'	2.20	0.42
1:2:220:A:OP2	1:2:831:U:O2'	2.34	0.42
1:2:391:G:OP1	8:I:24:LYS:NZ	2.48	0.42
1:2:445:A:H5''	5:E:57:ASN:ND2	2.30	0.42
1:2:474:A:P	9:J:126:ARG:HH21	2.43	0.42
1:2:688:G:C6	1:2:689:G:C5	3.08	0.42
1:2:807:U:H2'	1:2:808:G:C8	2.54	0.42
1:2:1034:G:C6	1:2:1100:G:C6	3.07	0.42
1:2:1359:A:H3'	1:2:1360:C:C6	2.54	0.42
1:2:1531:C:OP1	31:Z:74:SER:HB2	2.20	0.42
2:A:77:SER:O	2:A:100:GLY:N	2.52	0.42
4:C:212:LEU:HA	4:C:212:LEU:HD12	1.87	0.42
5:E:42:LEU:O	5:E:84:ALA:N	2.46	0.42
5:E:125:LYS:HB2	5:E:226:PHE:CE1	2.55	0.42
6:G:48:TYR:HB3	6:G:50:PHE:HE1	1.82	0.42
7:H:169:PHE:HA	7:H:172:VAL:HG12	2.02	0.42
8:I:21:PHE:CD2	8:I:22:ARG:HG2	2.54	0.42
14:W:15:ASN:OD1	14:W:71:LYS:HB2	2.20	0.42
16:Y:8:ARG:HH12	16:Y:10:ARG:NH2	2.13	0.42
16:Y:103:ALA:HB3	16:Y:108:ARG:HD2	2.00	0.42
17:a:31:PRO:O	17:a:35:ALA:HB2	2.20	0.42
19:e:30:PRO:HB2	19:e:34:ALA:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:285:PHE:CD2	35:g:294:PRO:HD2	2.54	0.42
35:g:306:GLN:NE2	35:g:322:VAL:O	2.50	0.42
1:2:11:A:O2'	4:C:91:VAL:HG23	2.20	0.42
1:2:106:U:H2'	1:2:107:C:O4'	2.19	0.42
1:2:121:U:H2'	1:2:122:U:H6	1.83	0.42
1:2:245:G:C2	1:2:246:A:C4	3.08	0.42
1:2:426:C:H2'	1:2:427:A:O4'	2.19	0.42
1:2:585:G:C6	1:2:586:C:C4	3.08	0.42
1:2:685:A:H2'	1:2:686:C:C5	2.55	0.42
1:2:825:U:N3	1:2:846:A:N1	2.68	0.42
1:2:859:U:O4'	7:H:114:ARG:HD2	2.20	0.42
1:2:1274:A:C6	1:2:1436:G:C5	3.07	0.42
1:2:1277:G:OP1	21:D:185:LYS:NZ	2.52	0.42
1:2:1478:G:H3'	1:2:1479:C:C6	2.55	0.42
1:2:1501:A:C5	28:S:84:TRP:CE2	3.08	0.42
4:C:152:ASN:ND2	13:V:2:GLU:O	2.34	0.42
5:E:72:VAL:HG22	5:E:90:ILE:HD12	2.01	0.42
6:G:76:LEU:HD12	6:G:77:LEU:H	1.84	0.42
7:H:17:GLU:HA	7:H:20:VAL:HG22	2.02	0.42
8:I:186:GLU:O	8:I:190:LEU:N	2.41	0.42
11:N:99:ARG:O	11:N:103:GLU:HG3	2.20	0.42
14:W:102:VAL:H	14:W:113:HIS:CD2	2.38	0.42
15:X:27:THR:O	15:X:31:LYS:HG2	2.20	0.42
23:K:12:TYR:HD2	23:K:79:TYR:CE2	2.38	0.42
23:K:48:SER:O	23:K:52:LYS:HG2	2.20	0.42
29:T:19:ALA:HB2	29:T:56:LYS:HA	2.01	0.42
30:U:40:ASN:C	30:U:40:ASN:HD22	2.27	0.42
30:U:46:GLU:C	30:U:49:LYS:H	2.28	0.42
30:U:83:GLU:OE1	30:U:83:GLU:N	2.53	0.42
32:c:10:ALA:HA	32:c:32:PHE:HA	2.02	0.42
32:c:60:GLU:OE1	32:c:60:GLU:N	2.47	0.42
33:d:21:CYS:HB3	33:d:25:GLY:H	1.85	0.42
39:j:23:ASN:O	39:j:34:VAL:HB	2.19	0.42
39:j:125:GLU:HA	39:j:128:LYS:HE3	2.01	0.42
1:2:149:U:H2'	1:2:150:G:O4'	2.20	0.41
1:2:323:U:H1'	1:2:345:G:O2'	2.20	0.41
1:2:374:U:H2'	1:2:375:C:C6	2.54	0.41
1:2:646:G:H2'	1:2:647:G:H1'	2.01	0.41
1:2:715:U:O2	1:2:724:G:N2	2.53	0.41
1:2:894:G:C6	1:2:917:U:C4	3.07	0.41
1:2:1006:5MC:H2'	1:2:1007:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1077:C:C2	1:2:1078:U:C5	3.07	0.41
1:2:1184:U:C2	1:2:1456:G:C6	3.08	0.41
1:2:1200:G:C6	1:2:1593:U:N3	2.88	0.41
1:2:1246:U:H2'	1:2:1247:C:O4'	2.20	0.41
1:2:1279:C:O2'	30:U:70:THR:HB	2.20	0.41
1:2:1386:A:N7	1:2:1409:A:N6	2.68	0.41
1:2:1678:G:O2'	1:2:1718:G:N2	2.53	0.41
2:A:210:ILE:HG12	27:R:81:LYS:CE	2.49	0.41
3:B:117:TRP:CD2	3:B:152:ARG:NH1	2.88	0.41
4:C:93:LYS:O	4:C:99:GLN:HA	2.20	0.41
4:C:158:SER:OG	4:C:159:LEU:N	2.52	0.41
5:E:36:HIS:CE1	5:E:85:GLY:HA3	2.55	0.41
6:G:50:PHE:HB3	6:G:111:LEU:CD1	2.49	0.41
7:H:23:ALA:O	7:H:27:LEU:HD23	2.20	0.41
7:H:141:ARG:HD3	14:W:49:GLU:OE1	2.20	0.41
17:a:58:VAL:HG23	17:a:59:TYR:CD2	2.55	0.41
21:D:33:GLY:O	21:D:53:THR:HG23	2.20	0.41
21:D:105:MET:SD	21:D:122:VAL:HG21	2.60	0.41
26:Q:28:LEU:HB2	26:Q:64:ASP:CB	2.49	0.41
31:Z:89:ILE:HD13	31:Z:103:ARG:HA	2.01	0.41
34:f:118:ARG:O	34:f:119:LYS:HG3	2.19	0.41
35:g:199:PHE:HZ	35:g:235:LYS:HG2	1.85	0.41
35:g:239:MET:SD	35:g:240:ASN:N	2.93	0.41
35:g:258:TRP:CD1	35:g:271:ASP:HA	2.55	0.41
35:g:289:THR:O	35:g:291:ALA:N	2.53	0.41
38:1:11:C:H2'	38:1:12:G:H8	1.84	0.41
38:1:49:5MC:H2'	38:1:50:U:C5	2.55	0.41
39:j:143:GLU:O	39:j:146:LYS:HG2	2.20	0.41
39:j:198:ILE:O	39:j:201:ILE:HG12	2.20	0.41
40:k:108:HIS:CG	40:k:109:VAL:N	2.88	0.41
40:k:329:GLU:HB3	40:k:331:GLU:OE1	2.20	0.41
41:l:233:TYR:CE2	41:l:268:VAL:HG12	2.54	0.41
1:2:95:G:C4	1:2:96:G:C8	3.08	0.41
1:2:363:G:C2	1:2:380:C:C2	3.08	0.41
1:2:379:U:H5'	1:2:380:C:H5	1.84	0.41
1:2:867:G:C2	1:2:868:A:C8	3.08	0.41
1:2:924:G:H2'	1:2:925:A:C8	2.54	0.41
1:2:979:G:H4'	1:2:1774:A:H4'	2.01	0.41
1:2:1796:U:C4	17:a:38:ARG:CZ	3.03	0.41
2:A:55:GLU:HB3	13:V:79:LEU:HD22	2.02	0.41
3:B:67:GLU:CD	3:B:83:LYS:HB3	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:135:LEU:HD23	3:B:137:ILE:HD11	2.02	0.41
8:I:107:THR:N	8:I:108:PRO:HD2	2.35	0.41
9:J:128:LEU:O	9:J:133:HIS:HB2	2.20	0.41
9:J:134:ILE:HA	9:J:158:PHE:HA	2.01	0.41
11:N:40:TYR:O	11:N:43:LYS:HB2	2.20	0.41
13:V:20:THR:C	13:V:22:ARG:H	2.28	0.41
14:W:36:LYS:HB3	14:W:36:LYS:HE3	1.81	0.41
20:h:4:LYS:HD3	20:h:5:TRP:NE1	2.35	0.41
21:D:158:ILE:O	21:D:158:ILE:HG23	2.20	0.41
25:P:103:ASN:ND2	25:P:120:SER:HA	2.35	0.41
26:Q:98:ASP:OD1	26:Q:99:GLU:N	2.53	0.41
26:Q:126:PRO:HG2	26:Q:128:LYS:NZ	2.35	0.41
27:R:23:LYS:HA	27:R:23:LYS:HD3	1.89	0.41
27:R:41:ILE:HG21	27:R:47:ARG:HB2	2.02	0.41
28:S:122:HIS:HA	28:S:125:ILE:HB	2.02	0.41
28:S:132:ARG:HH22	28:S:145:ARG:NH1	2.17	0.41
35:g:12:GLY:HA3	35:g:55:PHE:HB2	2.02	0.41
38:1:36:U:H2'	38:1:37:T6A:H8	1.85	0.41
38:1:41:C:H5'	39:j:60:GLN:NE2	2.36	0.41
40:k:89:PRO:HB3	40:k:100:THR:OG1	2.21	0.41
42:m:40:THR:OG1	42:m:80:LEU:HB3	2.19	0.41
1:2:5:U:O2'	1:2:552:G:H4'	2.19	0.41
1:2:140:A:H61	6:G:187:LYS:HB2	1.86	0.41
1:2:159:C:O3'	6:G:95:LYS:NZ	2.53	0.41
1:2:220:A:C2	1:2:840:U:C2	3.08	0.41
1:2:245:G:C6	1:2:246:A:C6	3.09	0.41
1:2:250:A:H2	5:E:131:LEU:HD12	1.85	0.41
1:2:874:G:OP1	3:B:158:SER:HB3	2.20	0.41
1:2:928:A:C5	1:2:929:A:C5	3.09	0.41
1:2:1015:C:C5	1:2:1016:U:C2	3.08	0.41
1:2:1030:U:H4'	1:2:1031:G:OP2	2.21	0.41
1:2:1123:A:H2'	1:2:1124:A:C8	2.55	0.41
1:2:1169:G:C6	1:2:1572:G:C6	3.08	0.41
1:2:1677:G:O2'	1:2:1678:G:H5'	2.20	0.41
1:2:1788:A:P	17:a:10:ARG:HH22	2.42	0.41
2:A:139:VAL:HG13	2:A:141:ILE:HG13	2.01	0.41
7:H:101:LYS:HA	7:H:112:ARG:NH2	2.35	0.41
7:H:162:ILE:C	7:H:164:ASN:H	2.28	0.41
8:I:81:VAL:N	8:I:94:ASN:OD1	2.47	0.41
8:I:153:ILE:HD12	8:I:161:PHE:CE2	2.55	0.41
17:a:49:ALA:O	17:a:53:LEU:HD23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:M:49:GLU:OE1	24:M:49:GLU:N	2.54	0.41
39:j:207:SER:O	39:j:250:LYS:NZ	2.42	0.41
1:2:58:U:O2'	1:2:450:A:H1'	2.19	0.41
1:2:98:U:O2'	1:2:99:C:H5'	2.20	0.41
1:2:289:G:N3	1:2:289:G:H2'	2.36	0.41
1:2:294:A:C5	1:2:295:U:C4	3.09	0.41
1:2:334:U:C4	1:2:335:G:C6	3.08	0.41
1:2:465:PSU:C2	1:2:466:G:C5	3.08	0.41
1:2:760:A:C2	1:2:761:G:H1'	2.55	0.41
1:2:803:A:N7	14:W:107:SER:HA	2.35	0.41
1:2:937:G:N1	1:2:941:G:C6	2.88	0.41
1:2:958:U:O5'	11:N:14:SER:HB2	2.21	0.41
1:2:1139:G:H2'	1:2:1140:G:H8	1.84	0.41
1:2:1149:G:C6	1:2:1766:G:C6	3.07	0.41
1:2:1677:G:C2	1:2:1720:A:N6	2.85	0.41
1:2:1754:A:OP1	1:2:1754:A:H2'	2.21	0.41
2:A:148:ASP:OD2	2:A:164:ASN:N	2.54	0.41
16:Y:54:ALA:HB1	16:Y:76:TYR:O	2.21	0.41
19:e:30:PRO:HG2	19:e:38:LEU:HD23	2.02	0.41
22:F:48:TRP:CD1	22:F:131:PRO:HD2	2.55	0.41
22:F:128:ASP:O	22:F:129:GLN:C	2.63	0.41
23:K:37:THR:HB	23:K:41:PHE:CZ	2.49	0.41
26:Q:100:GLN:O	26:Q:104:GLU:OE1	2.38	0.41
28:S:16:ARG:C	28:S:17:LEU:HD12	2.45	0.41
28:S:61:LEU:HB2	28:S:65:GLU:OE2	2.21	0.41
30:U:34:LEU:HD23	30:U:34:LEU:C	2.45	0.41
30:U:47:THR:HG23	30:U:48:PHE:HD1	1.85	0.41
38:1:16:H2U:HN3	38:1:48:5MC:HM51	1.84	0.41
1:2:428:G:C2	1:2:429:G:C8	3.09	0.41
1:2:551:G:C6	1:2:552:G:C6	3.08	0.41
1:2:568:C:H41	15:X:69:ARG:HH12	1.67	0.41
1:2:705:U:N3	1:2:732:G:N3	2.69	0.41
1:2:752:A:H2	1:2:796:G:H22	1.68	0.41
1:2:787:A:C2	5:E:19:MET:HE1	2.55	0.41
1:2:973:A:H2'	1:2:974:C:H6	1.86	0.41
1:2:1270:G:H2'	1:2:1271:U:C6	2.55	0.41
1:2:1481:A:C5	1:2:1522:A:C5	3.08	0.41
1:2:1538:G:H2'	1:2:1539:G:O4'	2.19	0.41
1:2:1591:A:H2'	1:2:1592:G:H8	1.86	0.41
1:2:1713:G:H2'	1:2:1714:C:O4'	2.21	0.41
1:2:1755:G:C2	1:2:1756:U:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1778:G:C6	1:2:1779:A:C5	3.08	0.41
4:C:149:TRP:CZ3	4:C:178:PRO:HB3	2.56	0.41
6:G:20:ASP:OD1	6:G:23:ARG:HG2	2.20	0.41
6:G:200:ALA:O	6:G:203:GLU:HG3	2.20	0.41
22:F:60:LEU:HD11	22:F:169:ARG:NH1	2.35	0.41
22:F:105:ASN:O	22:F:108:LYS:CD	2.68	0.41
22:F:176:LEU:O	22:F:179:ILE:HG22	2.20	0.41
22:F:224:LYS:HG2	22:F:227:ARG:NH1	2.35	0.41
23:K:45:ALA:O	23:K:49:LEU:HD23	2.21	0.41
30:U:42:ILE:HD11	30:U:91:ILE:HD13	2.01	0.41
34:f:136:ARG:HH11	34:f:138:TYR:HB2	1.85	0.41
40:k:121:SER:HB3	40:k:145:ALA:HB2	2.03	0.41
40:k:194:CYS:HB3	40:k:204:MET:HG2	2.02	0.41
40:k:287:LEU:HB3	40:k:289:TYR:HD2	1.81	0.41
1:2:315:A:H2'	1:2:316:C:H6	1.83	0.41
1:2:393:C:O4'	6:G:92:ARG:NH2	2.53	0.41
1:2:594:G:H2'	1:2:595:C:H6	1.85	0.41
1:2:612:G:H5'	1:2:1098:U:O2	2.19	0.41
1:2:752:A:C5	1:2:753:A:C6	3.08	0.41
1:2:758:U:C2	1:2:759:U:C6	3.09	0.41
1:2:760:A:N1	1:2:789:U:O4	2.54	0.41
1:2:811:A:H62	1:2:858:A:H5'	1.86	0.41
1:2:897:A:N1	1:2:910:U:O2'	2.46	0.41
1:2:966:A:OP2	1:2:966:A:H8	2.04	0.41
1:2:987:A:H2'	1:2:988:U:H6	1.84	0.41
1:2:1032:C:H2'	1:2:1033:C:C6	2.56	0.41
1:2:1102:U:H5'	1:2:1103:U:P	2.61	0.41
1:2:1149:G:C6	1:2:1766:G:C5	3.08	0.41
1:2:1218:A:C2	1:2:1219:C:H1'	2.56	0.41
1:2:1253:U:H2'	1:2:1254:G:C8	2.55	0.41
1:2:1312:A:N3	1:2:1314:U:H5'	2.36	0.41
1:2:1357:G:H5'	29:T:126:ASP:OD1	2.20	0.41
1:2:1656:G:C6	1:2:1742:A:C6	3.08	0.41
1:2:1739:U:H2'	1:2:1740:U:H6	1.84	0.41
2:A:42:PRO:HB2	27:R:126:ALA:CB	2.51	0.41
2:A:168:HIS:CD2	2:A:203:PHE:HE2	2.38	0.41
3:B:195:LYS:O	3:B:199:ASN:ND2	2.54	0.41
5:E:104:ASP:OD1	5:E:105:VAL:N	2.52	0.41
6:G:14:LYS:HZ3	6:G:123:GLY:H	1.68	0.41
7:H:61:PHE:HE1	7:H:93:LEU:HD12	1.85	0.41
8:I:157:VAL:HG12	8:I:161:PHE:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:193:TYR:O	8:I:197:LEU:HD23	2.19	0.41
12:O:80:HIS:HA	12:O:113:GLY:O	2.20	0.41
15:X:54:LEU:HD22	15:X:73:ARG:HH22	1.84	0.41
21:D:20:GLU:OE2	23:K:61:TRP:HE3	2.03	0.41
26:Q:29:ILE:HD12	26:Q:65:ILE:HD12	2.02	0.41
27:R:20:TYR:CD2	27:R:38:ILE:HD12	2.56	0.41
35:g:308:LEU:C	35:g:309:PHE:HD1	2.29	0.41
38:l:62:C:H2'	38:l:63:G:H8	1.85	0.41
40:k:75:LEU:HD13	40:k:97:ARG:CZ	2.49	0.41
40:k:346:VAL:HG13	40:k:390:ALA:O	2.20	0.41
40:k:356:ARG:HB3	40:k:416:VAL:HG23	2.02	0.41
1:2:12:U:O2'	1:2:1299:A:N3	2.48	0.41
1:2:399:A:H4'	1:2:400:A:H5''	2.03	0.41
1:2:525:A:H2'	1:2:526:A:O4'	2.19	0.41
1:2:608:U:H1'	15:X:19:ARG:HH11	1.86	0.41
1:2:760:A:N1	1:2:788:A:N6	2.68	0.41
1:2:778:G:H1	16:Y:10:ARG:CD	2.28	0.41
1:2:1044:C:C2	1:2:1073:G:N1	2.89	0.41
1:2:1120:C:H2'	1:2:1121:G:H8	1.84	0.41
1:2:1276:G:O3'	21:D:183:GLY:HA3	2.20	0.41
1:2:1328:A:H2'	1:2:1329:G:O4'	2.21	0.41
1:2:1339:U:O4	26:Q:9:THR:HA	2.21	0.41
1:2:1372:C:H2'	1:2:1373:U:H6	1.84	0.41
1:2:1473:A:H2'	1:2:1474:C:O4'	2.19	0.41
1:2:1481:A:O2'	1:2:1482:G:O4'	2.36	0.41
1:2:1516:C:H2'	1:2:1517:U:C6	2.55	0.41
1:2:1517:U:H5''	1:2:1518:U:OP2	2.21	0.41
1:2:1624:U:H2'	1:2:1625:U:C6	2.56	0.41
1:2:1710:A:C2'	1:2:1711:G:H4'	2.50	0.41
1:2:1753:A:H5''	15:X:63:GLN:OE1	2.21	0.41
1:2:1771:C:H2'	1:2:1772:G:H8	1.85	0.41
2:A:55:GLU:O	2:A:58:VAL:HG22	2.20	0.41
2:A:147:THR:OG1	2:A:151:SER:HB3	2.20	0.41
5:E:94:ALA:C	5:E:96:ASN:H	2.28	0.41
5:E:244:ILE:HD11	5:E:246:LEU:HD11	2.02	0.41
7:H:96:ARG:HG2	7:H:121:VAL:CG2	2.51	0.41
8:I:83:TYR:OH	10:L:11:ARG:HB3	2.21	0.41
14:W:23:ARG:NH2	14:W:66:ASN:HA	2.30	0.41
16:Y:27:VAL:HG23	16:Y:69:SER:HB3	2.03	0.41
25:P:30:THR:O	25:P:34:VAL:HG23	2.21	0.41
25:P:73:PRO:HD2	25:P:91:GLY:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:12:LYS:HD2	26:Q:12:LYS:HA	1.90	0.41
35:g:113:SER:HB2	35:g:153:THR:O	2.21	0.41
35:g:155:VAL:O	35:g:156:ARG:HD2	2.20	0.41
40:k:281:VAL:HG13	41:l:134:LEU:HD13	2.01	0.41
40:k:435:PHE:HB2	40:k:514:TRP:NE1	2.35	0.41
1:2:57:G:C2	1:2:91:G:C2	3.09	0.41
1:2:214:A:H62	1:2:241:U:H3'	1.85	0.41
1:2:560:G:C6	1:2:584:A:C6	3.09	0.41
1:2:718:U:O2'	1:2:719:U:O5'	2.39	0.41
1:2:830:U:H2'	1:2:831:U:O4'	2.20	0.41
1:2:1168:G:N2	1:2:1573:7MG:H81	2.36	0.41
1:2:1179:C:H2'	1:2:1180:U:C6	2.55	0.41
1:2:1202:A:C5	1:2:1553:A:C6	3.09	0.41
1:2:1547:C:OP1	25:P:42:ARG:NH1	2.36	0.41
1:2:1798:A:H8	17:a:100:ARG:HA	1.85	0.41
2:A:84:ARG:NE	27:R:82:ASP:OD1	2.23	0.41
3:B:132:ASP:HB3	3:B:221:PRO:HB3	2.01	0.41
8:I:22:ARG:O	8:I:23:LYS:C	2.64	0.41
9:J:80:LEU:HA	9:J:83:ILE:HG22	2.02	0.41
9:J:123:HIS:ND1	19:e:33:ARG:HD2	2.36	0.41
10:L:14:GLN:CB	10:L:54:ILE:HG13	2.50	0.41
10:L:79:ARG:C	10:L:80:MET:HE2	2.46	0.41
11:N:54:LEU:HD13	11:N:58:HIS:ND1	2.35	0.41
12:O:127:ARG:HB3	12:O:127:ARG:CZ	2.51	0.41
21:D:61:GLU:HG2	21:D:64:ARG:HD3	2.03	0.41
21:D:79:TYR:HB3	21:D:83:THR:HB	2.03	0.41
22:F:63:TYR:HE2	22:F:166:PRO:HB2	1.84	0.41
22:F:71:TYR:CE1	26:Q:53:LEU:HD13	2.55	0.41
22:F:123:ILE:HD11	22:F:197:ALA:HA	2.03	0.41
23:K:16:PHE:CE2	23:K:82:LEU:HG	2.54	0.41
24:M:36:ARG:HD2	24:M:94:LEU:HD21	2.02	0.41
24:M:60:THR:C	24:M:61:GLU:HG3	2.45	0.41
26:Q:131:GLY:HA3	26:Q:136:SER:O	2.21	0.41
28:S:89:GLN:C	28:S:91:ASP:H	2.29	0.41
30:U:109:GLU:HB2	30:U:110:PRO:HD2	2.02	0.41
31:Z:83:LEU:O	31:Z:88:ILE:HD12	2.21	0.41
34:f:107:LYS:HB2	34:f:117:LEU:HD11	2.03	0.41
35:g:6:ILE:HD12	35:g:6:ILE:HA	1.91	0.41
35:g:112:LEU:HD11	35:g:128:ARG:HG3	2.02	0.41
39:j:21:MET:HG3	39:j:68:ASN:HB3	2.01	0.41
42:m:62:PHE:CZ	42:m:91:PHE:HB2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:39:A:H5'	9:J:6:ARG:HG3	2.03	0.41
1:2:146:A:C5	1:2:167:A:N6	2.89	0.41
1:2:151:U:H4'	6:G:14:LYS:HA	2.02	0.41
1:2:217:A:H4'	1:2:218:A:OP1	2.21	0.41
1:2:220:A:N6	1:2:832:U:O4	2.53	0.41
1:2:253:A:H2'	1:2:254:U:H6	1.83	0.41
1:2:328:G:H5''	8:I:98:LYS:HG3	2.02	0.41
1:2:535:C:C4	1:2:536:G:C5	3.09	0.41
1:2:709:C:H41	1:2:730:G:H21	1.69	0.41
1:2:884:G:OP1	3:B:136:ARG:NH1	2.53	0.41
1:2:1064:A:H4'	3:B:205:PHE:CD1	2.56	0.41
1:2:1150:A:H2'	1:2:1151:A:C8	2.56	0.41
1:2:1398:A:C6	1:2:1399:A:C6	3.09	0.41
1:2:1408:A:H1'	1:2:1409:A:H5'	2.02	0.41
1:2:1413:U:O2'	1:2:1414:G:H5'	2.20	0.41
1:2:1677:G:N2	1:2:1720:A:N6	2.29	0.41
1:2:1770:C:H3'	20:h:2:ARG:HH22	1.86	0.41
2:A:30:GLN:HG2	2:A:46:ASN:ND2	2.35	0.41
2:A:102:PHE:O	2:A:103:THR:OG1	2.37	0.41
2:A:128:SER:OG	2:A:129:ASP:N	2.54	0.41
3:B:67:GLU:OE1	3:B:68:VAL:N	2.54	0.41
3:B:142:PHE:O	3:B:208:GLN:N	2.54	0.41
5:E:64:ILE:HD13	5:E:64:ILE:HA	1.81	0.41
6:G:143:LYS:HB2	6:G:143:LYS:HE3	1.90	0.41
7:H:141:ARG:HD2	7:H:143:LEU:HD22	2.03	0.41
8:I:43:ILE:HD13	8:I:57:ALA:HA	2.02	0.41
8:I:82:VAL:HG22	8:I:197:LEU:HD11	2.02	0.41
8:I:139:ASN:OD1	8:I:142:ARG:NH1	2.54	0.41
8:I:157:VAL:HG12	8:I:161:PHE:CZ	2.56	0.41
9:J:28:LEU:HD11	19:e:39:LEU:HG	2.02	0.41
9:J:62:ARG:HH22	9:J:68:LYS:HB3	1.85	0.41
9:J:100:LYS:H	9:J:100:LYS:HG2	1.56	0.41
10:L:21:THR:HA	10:L:32:LYS:NZ	2.36	0.41
11:N:138:ASN:OD1	11:N:138:ASN:C	2.64	0.41
12:O:52:ARG:NH1	22:F:158:ARG:HH12	2.19	0.41
12:O:58:TYR:O	12:O:62:LEU:HG	2.21	0.41
14:W:77:PRO:HG2	14:W:79:PHE:CE2	2.56	0.41
14:W:101:TYR:HA	14:W:113:HIS:HE2	1.85	0.41
22:F:120:LEU:HD12	22:F:131:PRO:HB2	2.03	0.41
22:F:151:VAL:HB	22:F:160:GLN:NE2	2.36	0.41
24:M:37:GLY:O	24:M:41:SER:OG	2.26	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:U:98:HIS:ND1	30:U:99:ILE:HG23	2.35	0.41
35:g:84:ALA:HA	35:g:90:LEU:HD23	2.03	0.41
38:l:3:C:H4'	39:j:185:ARG:HH22	1.85	0.41
38:l:40:C:H2'	38:l:41:C:H6	1.86	0.41
40:k:506:GLU:O	40:k:508:HIS:N	2.54	0.41
41:l:161:PRO:HG3	41:l:183:LYS:HD3	2.02	0.41
42:m:51:LEU:HD23	42:m:54:ILE:HD12	2.03	0.41
42:m:92:MET:O	42:m:97:GLY:N	2.45	0.41
1:2:175:C:N4	1:2:265:A:OP2	2.54	0.41
1:2:300:A:C6	1:2:301:U:C4	3.09	0.41
1:2:309:C:N3	1:2:356:G:N1	2.69	0.41
1:2:345:G:P	10:L:79:ARG:HH12	2.43	0.41
1:2:558:C:H2'	1:2:559:U:H6	1.86	0.41
1:2:635:A:N1	1:2:860:U:C4	2.89	0.41
1:2:780:A:O2'	16:Y:9:THR:O	2.32	0.41
1:2:841:C:H2'	1:2:842:U:C6	2.56	0.41
1:2:934:U:C4	17:a:15:ARG:CZ	3.04	0.41
1:2:1171:G:H2'	1:2:1172:C:H6	1.84	0.41
1:2:1187:G:C6	1:2:1197:G:C6	3.09	0.41
1:2:1260:G:H2'	1:2:1261:U:C6	2.56	0.41
1:2:1764:A:OP2	1:2:1792:A:H5'	2.21	0.41
3:B:114:VAL:HA	3:B:142:PHE:CE2	2.53	0.41
5:E:36:HIS:ND1	5:E:85:GLY:HA3	2.35	0.41
6:G:30:LYS:NZ	6:G:34:GLN:HB3	2.36	0.41
6:G:199:GLN:OE1	6:G:202:ARG:NH2	2.54	0.41
7:H:24:PHE:O	7:H:28:GLU:HG3	2.21	0.41
9:J:45:ILE:HG23	9:J:104:PHE:HD2	1.86	0.41
9:J:85:VAL:HG11	9:J:104:PHE:HD1	1.86	0.41
13:V:71:ARG:HD3	18:b:4:VAL:HG21	2.02	0.41
16:Y:7:ILE:HG23	16:Y:27:VAL:HG12	2.03	0.41
17:a:42:ARG:NH1	17:a:67:THR:HG23	2.36	0.41
21:D:78:LYS:N	21:D:78:LYS:HD2	2.35	0.41
22:F:58:ALA:O	22:F:61:VAL:HG12	2.21	0.41
24:M:46:THR:OG1	34:f:127:GLY:HA2	2.21	0.41
24:M:57:GLU:HG3	24:M:81:LYS:O	2.21	0.41
24:M:115:LYS:HE2	24:M:115:LYS:HB3	1.89	0.41
26:Q:113:ASP:O	26:Q:116:LEU:HG	2.20	0.41
27:R:6:THR:O	27:R:9:VAL:HG12	2.21	0.41
28:S:27:ASN:HD21	28:S:55:HIS:HA	1.85	0.41
28:S:110:ARG:O	28:S:114:GLU:OE1	2.38	0.41
30:U:30:LYS:HD3	30:U:33:GLN:CD	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:3:29:A:H62	38:1:37:T6A:N11	2.19	0.41
39:j:73:VAL:HG13	39:j:83:ILE:HG23	2.03	0.41
40:k:142:TYR:HB2	40:k:319:ARG:HH22	1.85	0.41
40:k:402:VAL:HG11	40:k:406:LEU:HD22	2.03	0.41
1:2:155:A:H2'	1:2:156:A:C8	2.55	0.40
1:2:221:A:O2'	1:2:222:U:H5'	2.21	0.40
1:2:455:A:H2'	1:2:456:G:C8	2.56	0.40
1:2:749:U:H2'	1:2:750:U:H6	1.86	0.40
1:2:762:A:C6	1:2:763:G:C5	3.09	0.40
1:2:774:A:C5	1:2:786:G:C2	3.09	0.40
1:2:863:U:P	14:W:57:ARG:HH21	2.43	0.40
1:2:1200:G:N2	1:2:1598:A:N3	2.69	0.40
1:2:1315:G:OP1	27:R:6:THR:OG1	2.23	0.40
1:2:1331:C:O2'	21:D:163:PRO:HD3	2.21	0.40
1:2:1370:G:H2'	1:2:1371:A:C8	2.56	0.40
1:2:1562:U:C2	1:2:1563:C:C5	3.08	0.40
2:A:38:TYR:O	2:A:47:VAL:HB	2.20	0.40
2:A:135:GLU:HA	2:A:138:TYR:HB2	2.02	0.40
3:B:18:LYS:O	3:B:19:ARG:HD3	2.21	0.40
4:C:148:TYR:CD1	4:C:152:ASN:HA	2.56	0.40
7:H:96:ARG:O	7:H:98:ILE:HD12	2.22	0.40
7:H:131:PHE:N	7:H:132:PRO:HD2	2.36	0.40
8:I:40:THR:OG1	8:I:59:ARG:HD3	2.21	0.40
10:L:30:LYS:HG3	10:L:31:THR:N	2.33	0.40
22:F:100:MET:HE2	22:F:100:MET:HB2	1.69	0.40
28:S:81:ILE:HA	28:S:82:PRO:HD3	1.94	0.40
30:U:42:ILE:O	30:U:45:ALA:HB3	2.21	0.40
30:U:104:THR:O	30:U:108:ILE:HD11	2.21	0.40
37:3:32:U:H2'	37:3:33:C:C2	2.57	0.40
1:2:485:G:H2'	1:2:486:G:C8	2.56	0.40
1:2:693:U:H2'	1:2:695:U:C5	2.56	0.40
1:2:1403:G:H2'	1:2:1404:A:C8	2.56	0.40
1:2:1776:G:N2	1:2:1782:C:C2	2.90	0.40
2:A:163:ASN:OD1	2:A:164:ASN:N	2.53	0.40
3:B:158:SER:C	3:B:162:ARG:HH21	2.29	0.40
4:C:46:LEU:O	4:C:50:VAL:HG23	2.21	0.40
4:C:67:PRO:HA	13:V:29:HIS:CE1	2.57	0.40
7:H:97:ARG:HD2	7:H:97:ARG:HA	1.90	0.40
10:L:133:LYS:O	10:L:136:ARG:NH1	2.46	0.40
22:F:105:ASN:HA	22:F:108:LYS:HD2	2.04	0.40
23:K:20:VAL:C	23:K:21:LEU:HD12	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:P:103:ASN:ND2	25:P:119:PHE:O	2.54	0.40
30:U:25:ASN:OD1	30:U:90:TYR:HB2	2.21	0.40
38:1:36:U:H2'	38:1:37:T6A:C8	2.55	0.40
39:j:21:MET:HG2	39:j:102:TYR:CG	2.56	0.40
39:j:115:CYS:SG	39:j:165:VAL:HG13	2.62	0.40
1:2:328:G:C4	1:2:329:G:C8	3.09	0.40
1:2:991:A:O2'	1:2:1783:U:O2	2.25	0.40
1:2:1388:U:O4'	1:2:1410:G:N2	2.54	0.40
1:2:1548:A:C6	1:2:1560:G:C6	3.10	0.40
1:2:1670:G:H2'	1:2:1671:G:C8	2.56	0.40
12:O:41:ARG:HA	12:O:41:ARG:HD2	1.83	0.40
14:W:120:HIS:O	14:W:120:HIS:ND1	2.54	0.40
18:b:65:THR:OG1	18:b:72:LYS:HE3	2.22	0.40
25:P:20:VAL:HG12	25:P:25:LEU:HG	2.03	0.40
27:R:30:THR:O	27:R:34:LEU:HG	2.21	0.40
28:S:57:ARG:HD3	28:S:57:ARG:HA	1.96	0.40
29:T:39:THR:HG21	29:T:53:TRP:CH2	2.56	0.40
30:U:68:ARG:HH22	30:U:77:LYS:HA	1.87	0.40
31:Z:95:HIS:CD2	31:Z:96:SER:N	2.90	0.40
36:i:57:ARG:NH1	36:i:81:LEU:HD11	2.37	0.40
36:i:104:LYS:HE2	36:i:111:GLU:HB3	2.03	0.40
39:j:186:ALA:HB1	39:j:266:MET:O	2.22	0.40
1:2:7:G:H2'	1:2:8:U:H5''	2.02	0.40
1:2:123:G:C6	1:2:124:A:C5	3.09	0.40
1:2:127:G:H1'	1:2:177:U:H3	1.86	0.40
1:2:212:A:C6	1:2:252:A:C6	3.09	0.40
1:2:213:G:N2	1:2:251:U:O4	2.55	0.40
1:2:476:A:H61	1:2:510:A:H61	1.69	0.40
1:2:519:A:C6	1:2:520:A:C6	3.09	0.40
1:2:771:A:C4	1:2:772:G:C8	3.09	0.40
1:2:894:G:H1'	12:O:36:ARG:O	2.22	0.40
1:2:1041:G:N2	1:2:1076:C:O2	2.54	0.40
1:2:1228:G:N1	24:M:40:GLU:OE2	2.33	0.40
1:2:1760:A:N3	1:2:1761:A:C8	2.89	0.40
1:2:1795:A:C4'	17:a:95:ARG:HG3	2.51	0.40
3:B:111:ARG:NH2	17:a:68:TYR:H	2.20	0.40
3:B:125:VAL:HG22	3:B:127:VAL:HG13	2.03	0.40
4:C:175:ILE:HB	4:C:202:TYR:HB2	2.02	0.40
5:E:100:ARG:HH12	5:E:114:ILE:HG21	1.87	0.40
5:E:252:ARG:HD3	9:J:71:PHE:CE2	2.56	0.40
7:H:75:ILE:HG13	7:H:76:LYS:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:D:45:LYS:HG3	21:D:82:GLY:O	2.22	0.40
22:F:99:LEU:HD12	22:F:99:LEU:HA	1.91	0.40
25:P:49:LEU:O	25:P:50:SER:OG	2.36	0.40
28:S:17:LEU:O	28:S:20:THR:OG1	2.31	0.40
29:T:10:PRO:HB2	29:T:13:ASP:OD1	2.21	0.40
35:g:243:ALA:C	35:g:245:ASP:H	2.29	0.40
38:l:74:C:N4	40:k:133:GLU:OE2	2.55	0.40
39:j:186:ALA:HB3	39:j:244:LEU:HD11	2.03	0.40
40:k:146:LYS:O	40:k:163:SER:HA	2.22	0.40
40:k:311:ILE:HD13	40:k:344:ASN:CG	2.46	0.40
1:2:55:A:H2'	1:2:402:G:H1	1.87	0.40
1:2:114:C:C4	1:2:246:A:C6	3.10	0.40
1:2:270:A:C2	1:2:284:G:C6	3.09	0.40
1:2:391:G:H2'	1:2:392:C:H6	1.87	0.40
1:2:639:U:O2	7:H:179:LYS:NZ	2.55	0.40
1:2:1065:C:O2'	3:B:146:GLN:OE1	2.40	0.40
1:2:1247:C:C2	1:2:1248:U:C5	3.10	0.40
1:2:1341:C:C2	1:2:1342:U:C5	3.09	0.40
1:2:1350:G:H2'	1:2:1351:U:H6	1.86	0.40
1:2:1479:C:P	29:T:63:ARG:HH12	2.44	0.40
1:2:1519:G:H2'	1:2:1521:G:N2	2.37	0.40
1:2:1557:A:C8	28:S:134:ARG:HB3	2.57	0.40
2:A:15:GLN:NE2	27:R:117:LEU:HD23	2.36	0.40
2:A:120:LEU:HD23	2:A:121:VAL:N	2.37	0.40
2:A:178:ALA:HA	2:A:181:VAL:HG22	2.04	0.40
3:B:205:PHE:CG	3:B:206:PRO:HD2	2.57	0.40
4:C:50:VAL:HG21	4:C:73:ILE:HG23	2.03	0.40
4:C:149:TRP:CZ3	9:J:60:LEU:HD22	2.55	0.40
5:E:179:LYS:HE2	5:E:179:LYS:HB2	1.80	0.40
8:I:105:ASP:HA	8:I:165:ARG:HH21	1.86	0.40
12:O:46:MET:HA	12:O:46:MET:HE3	2.03	0.40
22:F:118:HIS:HD2	31:Z:98:GLN:NE2	2.19	0.40
28:S:86:LEU:HB2	28:S:89:GLN:HG2	2.02	0.40
31:Z:89:ILE:CD1	31:Z:103:ARG:HG3	2.52	0.40
35:g:34:LEU:HD23	35:g:35:VAL:N	2.37	0.40
39:j:212:SER:HB2	39:j:217:GLN:HA	2.04	0.40
41:l:222:MET:HA	41:l:225:VAL:HB	2.02	0.40
42:m:69:VAL:O	42:m:77:ILE:HB	2.21	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%)	193 (89%)	24 (11%)	0	100	100
3	B	221/255 (87%)	189 (86%)	31 (14%)	1 (0%)	24	62
4	C	218/259 (84%)	197 (90%)	20 (9%)	1 (0%)	24	62
5	E	258/261 (99%)	224 (87%)	34 (13%)	0	100	100
6	G	228/236 (97%)	211 (92%)	17 (8%)	0	100	100
7	H	182/190 (96%)	157 (86%)	23 (13%)	2 (1%)	11	45
8	I	184/201 (92%)	162 (88%)	22 (12%)	0	100	100
9	J	180/188 (96%)	151 (84%)	24 (13%)	5 (3%)	4	24
10	L	153/156 (98%)	135 (88%)	16 (10%)	2 (1%)	9	41
11	N	149/151 (99%)	137 (92%)	12 (8%)	0	100	100
12	O	127/137 (93%)	108 (85%)	19 (15%)	0	100	100
13	V	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
14	W	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
15	X	142/145 (98%)	114 (80%)	28 (20%)	0	100	100
16	Y	132/135 (98%)	123 (93%)	9 (7%)	0	100	100
17	a	100/119 (84%)	81 (81%)	19 (19%)	0	100	100
18	b	79/82 (96%)	66 (84%)	13 (16%)	0	100	100
19	e	58/63 (92%)	50 (86%)	8 (14%)	0	100	100
20	h	23/25 (92%)	23 (100%)	0	0	100	100
21	D	225/237 (95%)	208 (92%)	17 (8%)	0	100	100
22	F	204/227 (90%)	182 (89%)	21 (10%)	1 (0%)	24	62
23	K	94/106 (89%)	82 (87%)	12 (13%)	0	100	100
24	M	113/134 (84%)	92 (81%)	17 (15%)	4 (4%)	3	20
25	P	115/142 (81%)	97 (84%)	18 (16%)	0	100	100
26	Q	139/143 (97%)	120 (86%)	17 (12%)	2 (1%)	9	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	R	128/136 (94%)	106 (83%)	21 (16%)	1 (1%)	16	52
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%)	97 (93%)	7 (7%)	0	100	100
31	Z	76/108 (70%)	68 (90%)	8 (10%)	0	100	100
32	c	62/67 (92%)	57 (92%)	5 (8%)	0	100	100
33	d	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
34	f	72/150 (48%)	52 (72%)	20 (28%)	0	100	100
35	g	314/326 (96%)	280 (89%)	33 (10%)	1 (0%)	36	71
36	i	93/153 (61%)	81 (87%)	12 (13%)	0	100	100
39	j	263/304 (86%)	238 (90%)	25 (10%)	0	100	100
40	k	468/527 (89%)	431 (92%)	33 (7%)	4 (1%)	14	49
41	l	126/285 (44%)	122 (97%)	4 (3%)	0	100	100
42	m	73/108 (68%)	64 (88%)	9 (12%)	0	100	100
All	All	5869/6690 (88%)	5190 (88%)	655 (11%)	24 (0%)	31	66

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	H	66	SER
9	J	163	PRO
9	J	164	PHE
22	F	106	ASN
24	M	123	GLU
26	Q	41	PRO
26	Q	42	GLU
10	L	3	THR
40	k	130	ASP
40	k	497	GLU
40	k	507	LYS
24	M	103	ALA
24	M	122	GLN
35	g	120	SER
3	B	221	PRO
24	M	121	THR
4	C	45	LYS
10	L	4	GLU

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Mol	Chain	Res	Type
7	H	163	ASP
9	J	133	HIS
27	R	99	VAL
9	J	122	VAL
9	J	162	SER
40	k	126	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	180/211 (85%)	180 (100%)	0	100	100
3	B	202/228 (89%)	201 (100%)	1 (0%)	81	81
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%)	192 (100%)	0	100	100
7	H	164/170 (96%)	163 (99%)	1 (1%)	78	80
8	I	147/159 (92%)	146 (99%)	1 (1%)	76	79
9	J	153/158 (97%)	148 (97%)	5 (3%)	33	55
10	L	136/137 (99%)	135 (99%)	1 (1%)	76	79
11	N	128/128 (100%)	128 (100%)	0	100	100
12	O	97/104 (93%)	96 (99%)	1 (1%)	68	76
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%)	83 (100%)	0	100	100
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%)	170 (98%)	4 (2%)	44	64
23	K	88/96 (92%)	88 (100%)	0	100	100
24	M	93/109 (85%)	91 (98%)	2 (2%)	45	64
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%)	115 (99%)	1 (1%)	70	76
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%)	46 (98%)	1 (2%)	47	65
34	f	60/133 (45%)	60 (100%)	0	100	100
35	g	264/272 (97%)	261 (99%)	3 (1%)	65	74
36	i	80/130 (62%)	80 (100%)	0	100	100
39	j	239/274 (87%)	239 (100%)	0	100	100
40	k	393/449 (88%)	393 (100%)	0	100	100
41	l	125/246 (51%)	125 (100%)	0	100	100
42	m	69/96 (72%)	69 (100%)	0	100	100
All	All	5043/5691 (89%)	5021 (100%)	22 (0%)	81	82

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

Mol	Chain	Res	Type
3	B	3	VAL
7	H	64	VAL
8	I	103	GLN
9	J	99	LEU
9	J	100	LYS
9	J	133	HIS
9	J	134	ILE
9	J	163	PRO
10	L	4	GLU
12	O	126	THR

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Mol	Chain	Res	Type
22	F	100	MET
22	F	102	ASN
22	F	128	ASP
22	F	129	GLN
24	M	122	GLN
24	M	123	GLU
26	Q	41	PRO
27	R	97	ASN
33	d	37	ASN
35	g	119	ASN
35	g	120	SER
35	g	121	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	23	HIS
2	A	30	GLN
2	A	109	ASN
3	B	118	GLN
3	B	177	GLN
3	B	211	HIS
4	C	64	HIS
4	C	76	GLN
5	E	57	ASN
5	E	216	ASN
6	G	119	GLN
6	G	140	ASN
7	H	29	ASN
7	H	74	GLN
7	H	150	GLN
8	I	52	ASN
8	I	160	GLN
9	J	139	GLN
10	L	92	HIS
11	N	49	GLN
14	W	64	GLN
14	W	80	ASN
16	Y	106	GLN
16	Y	107	GLN
16	Y	110	GLN
18	b	9	HIS

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Mol	Chain	Res	Type
18	b	19	HIS
21	D	67	ASN
21	D	162	GLN
21	D	165	ASN
22	F	39	GLN
22	F	40	GLN
22	F	102	ASN
22	F	118	HIS
22	F	226	ASN
23	K	17	GLN
23	K	32	HIS
23	K	58	GLN
24	M	116	ASN
25	P	103	ASN
26	Q	40	GLN
28	S	13	HIS
28	S	19	ASN
28	S	55	HIS
28	S	74	GLN
28	S	75	ASN
30	U	44	ASN
30	U	72	ASN
32	c	27	GLN
32	c	43	ASN
34	f	143	HIS
35	g	53	GLN
35	g	240	ASN
36	i	85	GLN
39	j	23	ASN
39	j	41	ASN
40	k	249	ASN
40	k	262	HIS
40	k	263	GLN
40	k	369	GLN
42	m	65	ASN
42	m	81	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1787/1798 (99%)	645 (36%)	26 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
37	3	25/49 (51%)	16 (64%)	0
38	1	71/75 (94%)	28 (39%)	3 (4%)
All	All	1883/1922 (97%)	689 (36%)	29 (1%)

All (689) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	U
1	2	4	C
1	2	9	U
1	2	13	C
1	2	14	C
1	2	16	G
1	2	17	C
1	2	26	A
1	2	27	U
1	2	32	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	64	U
1	2	65	A
1	2	67	A
1	2	68	A
1	2	69	G
1	2	72	A
1	2	73	U
1	2	74	U
1	2	75	U
1	2	77	U
1	2	78	A
1	2	79	C
1	2	104	A
1	2	111	U
1	2	114	C
1	2	116	U
1	2	121	U

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Mol	Chain	Res	Type
1	2	124	A
1	2	128	U
1	2	129	U
1	2	130	C
1	2	132	U
1	2	134	U
1	2	135	A
1	2	136	C
1	2	137	U
1	2	139	C
1	2	140	A
1	2	145	U
1	2	155	A
1	2	156	A
1	2	158	U
1	2	159	C
1	2	160	U
1	2	161	A
1	2	165	C
1	2	166	U
1	2	167	A
1	2	171	C
1	2	173	U
1	2	176	U
1	2	177	U
1	2	178	A
1	2	183	C
1	2	184	U
1	2	185	C
1	2	187	A
1	2	190	C
1	2	191	U
1	2	192	U
1	2	193	U
1	2	194	G
1	2	209	A
1	2	214	A
1	2	217	A
1	2	218	A
1	2	220	A
1	2	224	A
1	2	225	A

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Mol	Chain	Res	Type
1	2	226	U
1	2	227	G
1	2	228	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
1	2	240	U
1	2	248	U
1	2	249	C
1	2	256	A
1	2	259	U
1	2	260	U
1	2	264	A
1	2	266	U
1	2	267	C
1	2	271	U
1	2	274	C
1	2	275	C
1	2	276	U
1	2	278	G
1	2	280	G
1	2	289	G
1	2	296	U
1	2	298	A
1	2	300	A
1	2	301	U
1	2	307	C
1	2	308	C
1	2	311	A
1	2	313	C
1	2	315	A
1	2	319	U
1	2	321	G
1	2	334	U
1	2	336	G
1	2	337	C
1	2	349	U
1	2	358	A
1	2	359	A

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Mol	Chain	Res	Type
1	2	360	C
1	2	369	A
1	2	382	G
1	2	389	G
1	2	390	A
1	2	399	A
1	2	400	A
1	2	401	C
1	2	403	G
1	2	412	U
1	2	415	A
1	2	416	A
1	2	417	G
1	2	418	G
1	2	421	G
1	2	422	G
1	2	423	C
1	2	424	A
1	2	425	G
1	2	427	A
1	2	433	G
1	2	438	U
1	2	439	U
1	2	440	A
1	2	443	C
1	2	444	A
1	2	445	A
1	2	447	C
1	2	457	G
1	2	459	A
1	2	467	A
1	2	468	C
1	2	469	A
1	2	473	A
1	2	474	A
1	2	476	A
1	2	480	A
1	2	481	U
1	2	482	A
1	2	483	C
1	2	486	G
1	2	488	C

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Mol	Chain	Res	Type
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
1	2	505	A
1	2	506	U
1	2	507	U
1	2	509	G
1	2	510	A
1	2	516	U
1	2	518	C
1	2	523	U
1	2	526	A
1	2	527	U
1	2	533	A
1	2	534	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	547	G
1	2	553	C
1	2	554	A
1	2	557	U
1	2	558	C
1	2	560	G
1	2	564	C
1	2	565	C
1	2	567	G
1	2	571	C
1	2	576	G
1	2	577	U

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Mol	Chain	Res	Type
1	2	584	A
1	2	593	A
1	2	594	G
1	2	597	U
1	2	601	U
1	2	605	A
1	2	609	G
1	2	610	U
1	2	614	A
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	634	A
1	2	638	U
1	2	641	G
1	2	647	G
1	2	648	U
1	2	650	G
1	2	652	C
1	2	653	C
1	2	657	C
1	2	658	C
1	2	671	C
1	2	675	C
1	2	679	U
1	2	680	U
1	2	681	U
1	2	682	U
1	2	684	A
1	2	685	A
1	2	686	C
1	2	688	G
1	2	692	C
1	2	693	U
1	2	694	U
1	2	695	U
1	2	696	C
1	2	697	C
1	2	701	U

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Mol	Chain	Res	Type
1	2	702	G
1	2	704	C
1	2	705	U
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	717	C
1	2	718	U
1	2	719	U
1	2	720	G
1	2	721	U
1	2	723	G
1	2	724	G
1	2	727	C
1	2	730	G
1	2	731	C
1	2	732	G
1	2	733	A
1	2	734	A
1	2	736	C
1	2	737	A
1	2	738	G
1	2	739	G
1	2	741	C
1	2	742	U
1	2	743	U
1	2	745	U
1	2	753	A
1	2	755	A
1	2	763	G
1	2	765	G
1	2	766	PSU
1	2	767	U
1	2	771	A
1	2	774	A
1	2	778	G
1	2	779	A
1	2	780	A

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Mol	Chain	Res	Type
1	2	781	A
1	2	782	G
1	2	783	C
1	2	786	G
1	2	787	A
1	2	788	A
1	2	789	U
1	2	792	A
1	2	793	U
1	2	794	U
1	2	809	G
1	2	811	A
1	2	812	U
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	830	U
1	2	832	U
1	2	836	G
1	2	837	G
1	2	839	U
1	2	840	U
1	2	843	A
1	2	845	G
1	2	849	A
1	2	852	G
1	2	862	A
1	2	863	U
1	2	864	A
1	2	869	C
1	2	874	G
1	2	876	G
1	2	884	G

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Mol	Chain	Res	Type
1	2	885	U
1	2	895	U
1	2	896	C
1	2	897	A
1	2	905	A
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	930	C
1	2	931	U
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	963	U
1	2	965	A
1	2	966	A
1	2	969	A
1	2	970	A
1	2	972	A
1	2	973	A
1	2	982	A
1	2	985	G
1	2	986	G
1	2	987	A
1	2	991	A
1	2	992	A
1	2	995	U
1	2	997	A
1	2	998	PSU
1	2	999	C
1	2	1002	A
1	2	1008	U
1	2	1009	C

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Mol	Chain	Res	Type
1	2	1011	U
1	2	1015	C
1	2	1016	U
1	2	1020	C
1	2	1024	A
1	2	1025	A
1	2	1026	A
1	2	1027	C
1	2	1029	A
1	2	1030	U
1	2	1031	G
1	2	1035	A
1	2	1038	A
1	2	1039	G
1	2	1041	G
1	2	1042	A
1	2	1043	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	1060	U
1	2	1062	U
1	2	1066	C
1	2	1075	A
1	2	1081	C
1	2	1082	G
1	2	1084	G
1	2	1085	A
1	2	1086	A
1	2	1091	A
1	2	1095	C
1	2	1096	U
1	2	1097	U
1	2	1099	G
1	2	1100	G
1	2	1103	U

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Mol	Chain	Res	Type
1	2	1108	G
1	2	1110	G
1	2	1113	G
1	2	1114	U
1	2	1125	G
1	2	1137	A
1	2	1149	G
1	2	1150	A
1	2	1156	A
1	2	1157	C
1	2	1158	C
1	2	1163	G
1	2	1166	G
1	2	1170	A
1	2	1182	A
1	2	1184	U
1	2	1185	U
1	2	1187	G
1	2	1189	C
1	2	1190	B8N
1	2	1193	A
1	2	1195	A
1	2	1198	G
1	2	1199	G
1	2	1201	A
1	2	1207	A
1	2	1211	G
1	2	1216	A
1	2	1217	G
1	2	1224	U
1	2	1227	G
1	2	1228	G
1	2	1230	U
1	2	1236	G
1	2	1237	A
1	2	1240	G
1	2	1241	A
1	2	1242	G
1	2	1243	A
1	2	1244	G
1	2	1245	C
1	2	1247	C

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Mol	Chain	Res	Type
1	2	1249	U
1	2	1250	U
1	2	1251	C
1	2	1254	G
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	1274	A
1	2	1275	U
1	2	1283	C
1	2	1284	U
1	2	1296	G
1	2	1298	G
1	2	1300	U
1	2	1305	C
1	2	1306	U
1	2	1313	U
1	2	1314	U
1	2	1315	G
1	2	1319	U
1	2	1320	A
1	2	1321	A
1	2	1323	G
1	2	1324	A
1	2	1337	C
1	2	1339	U
1	2	1341	C
1	2	1343	A
1	2	1344	A
1	2	1345	A
1	2	1347	A
1	2	1355	U
1	2	1356	G
1	2	1359	A
1	2	1360	C
1	2	1361	U
1	2	1362	U
1	2	1363	G

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Mol	Chain	Res	Type
1	2	1364	C
1	2	1365	C
1	2	1369	U
1	2	1370	G
1	2	1376	U
1	2	1379	U
1	2	1380	A
1	2	1388	U
1	2	1389	A
1	2	1390	U
1	2	1393	G
1	2	1396	U
1	2	1397	C
1	2	1400	G
1	2	1401	C
1	2	1407	G
1	2	1408	A
1	2	1409	A
1	2	1411	U
1	2	1412	U
1	2	1413	U
1	2	1414	G
1	2	1418	C
1	2	1423	A
1	2	1424	C
1	2	1425	A
1	2	1426	2MG
1	2	1429	C
1	2	1431	G
1	2	1442	A
1	2	1443	G
1	2	1444	A
1	2	1455	C
1	2	1456	G
1	2	1457	C
1	2	1464	G
1	2	1467	A
1	2	1469	A
1	2	1471	U
1	2	1472	G
1	2	1476	G
1	2	1481	A

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Mol	Chain	Res	Type
1	2	1482	G
1	2	1483	C
1	2	1484	G
1	2	1488	A
1	2	1489	C
1	2	1490	A
1	2	1491	A
1	2	1494	U
1	2	1498	C
1	2	1499	C
1	2	1510	G
1	2	1512	U
1	2	1513	A
1	2	1514	A
1	2	1518	U
1	2	1519	G
1	2	1521	G
1	2	1522	A
1	2	1532	G
1	2	1533	U
1	2	1534	G
1	2	1535	C
1	2	1538	G
1	2	1540	G
1	2	1544	G
1	2	1546	G
1	2	1555	U
1	2	1557	A
1	2	1558	U
1	2	1565	U
1	2	1566	C
1	2	1571	A
1	2	1572	G
1	2	1573	7MG
1	2	1588	G
1	2	1595	A
1	2	1597	C
1	2	1598	A
1	2	1602	U
1	2	1603	G
1	2	1608	G
1	2	1612	A

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Mol	Chain	Res	Type
1	2	1614	G
1	2	1617	C
1	2	1620	G
1	2	1621	C
1	2	1631	A
1	2	1632	C
1	2	1637	5MC
1	2	1644	C
1	2	1651	C
1	2	1654	U
1	2	1655	U
1	2	1656	G
1	2	1662	C
1	2	1678	G
1	2	1679	A
1	2	1685	U
1	2	1686	U
1	2	1687	A
1	2	1688	G
1	2	1689	A
1	2	1691	A
1	2	1692	A
1	2	1693	G
1	2	1694	G
1	2	1695	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	1705	A
1	2	1706	U
1	2	1707	C
1	2	1709	C
1	2	1710	A
1	2	1711	G
1	2	1712	A
1	2	1725	G
1	2	1734	G
1	2	1740	U

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Mol	Chain	Res	Type
1	2	1742	A
1	2	1743	G
1	2	1748	A
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
1	2	1768	U
1	2	1778	G
1	2	1781	C
1	2	1787	G
1	2	1790	G
1	2	1791	G
1	2	1792	A
1	2	1794	C
1	2	1797	U
1	2	1798	A
37	3	16	U
37	3	17	C
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	33	C
37	3	34	U
37	3	35	C
37	3	37	U
37	3	38	C
37	3	39	U
37	3	40	C
38	1	4	G
38	1	8	U
38	1	9	1MG
38	1	13	C

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Mol	Chain	Res	Type
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	41	C
38	1	44	A
38	1	46	7MG
38	1	47	H2U
38	1	48	5MC
38	1	49	5MC
38	1	50	U
38	1	56	C
38	1	59	A
38	1	60	A
38	1	61	C
38	1	71	C
38	1	73	A
38	1	74	C
38	1	75	C
38	1	76	A

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	72	A
1	2	74	U
1	2	216	A
1	2	217	A
1	2	226	U
1	2	239	C
1	2	277	U
1	2	279	U
1	2	649	U
1	2	670	G
1	2	695	U
1	2	700	C
1	2	781	A
1	2	828	A

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Mol	Chain	Res	Type
1	2	930	C
1	2	998	PSU
1	2	1080	A
1	2	1198	G
1	2	1206	C
1	2	1343	A
1	2	1430	U
1	2	1470	C
1	2	1513	A
1	2	1571	A
1	2	1765	G
1	2	1797	U
38	1	8	U
38	1	48	5MC
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	T6A	1	37	38	31,34,35	1.76	9 (29%)	43,49,52	2.08	13 (30%)
38	7MG	1	46	38	23,26,27	3.61	11 (47%)	27,39,42	2.18	9 (33%)
1	B8N	2	1190	1	25,29,30	3.36	8 (32%)	28,42,45	2.02	7 (25%)
1	PSU	2	465	1	18,21,22	4.35	7 (38%)	21,30,33	1.91	5 (23%)
38	1MG	1	9	38	23,26,27	3.29	8 (34%)	33,39,42	2.41	8 (24%)
38	RIA	1	64	38	35,38,39	4.63	14 (40%)	50,57,60	2.15	12 (24%)
1	PSU	2	120	1	18,21,22	4.44	7 (38%)	21,30,33	2.03	5 (23%)
1	7MG	2	1573	1	23,26,27	3.48	10 (43%)	27,39,42	2.17	9 (33%)
38	1MA	1	58	38	21,25,26	3.14	6 (28%)	30,37,40	2.34	8 (26%)
38	H2U	1	16	38	18,21,22	3.09	4 (22%)	19,30,33	1.43	4 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	2	1780	1	23,26,27	1.39	4 (17%)	33,38,41	3.25	11 (33%)
1	PSU	2	1289	1	18,21,22	4.42	7 (38%)	21,30,33	1.83	5 (23%)
1	2MG	2	1426	43,1	23,26,27	2.85	9 (39%)	33,38,41	2.28	10 (30%)
1	PSU	2	998	1	18,21,22	4.34	8 (44%)	21,30,33	2.00	5 (23%)
38	5MC	1	49	38	19,22,23	3.91	8 (42%)	26,32,35	1.05	1 (3%)
1	5MC	2	1006	1	19,22,23	3.80	8 (42%)	26,32,35	1.04	2 (7%)
1	5MC	2	1637	1	19,22,23	3.74	8 (42%)	26,32,35	1.14	2 (7%)
1	PSU	2	766	1	18,21,22	4.35	8 (44%)	21,30,33	2.15	6 (28%)
38	M2G	1	26	38	24,27,28	2.67	8 (33%)	33,40,43	1.68	7 (21%)
38	2MG	1	10	38	23,26,27	2.92	8 (34%)	33,38,41	2.11	10 (30%)
38	H2U	1	47	38	18,21,22	3.19	4 (22%)	19,30,33	1.38	4 (21%)
38	5MC	1	48	38	19,22,23	3.86	8 (42%)	26,32,35	1.10	1 (3%)
1	2MG	2	1570	1	23,26,27	2.87	9 (39%)	33,38,41	2.24	10 (30%)

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	T6A	1	37	38	-	2/23/41/42	0/3/3/3
38	7MG	1	46	38	-	1/7/37/38	0/3/3/3
1	B8N	2	1190	1	-	2/16/34/35	0/2/2/2
1	PSU	2	465	1	-	0/7/25/26	0/2/2/2
38	1MG	1	9	38	-	2/7/25/26	0/3/3/3
38	RIA	1	64	38	-	10/17/51/52	0/4/4/4
1	PSU	2	120	1	-	0/7/25/26	0/2/2/2
1	7MG	2	1573	1	-	2/7/37/38	0/3/3/3
38	1MA	1	58	38	-	2/7/25/26	0/3/3/3
38	H2U	1	16	38	-	7/7/38/39	0/2/2/2
1	MA6	2	1780	1	-	2/11/29/30	0/3/3/3
1	PSU	2	1289	1	-	0/7/25/26	0/2/2/2
1	2MG	2	1426	43,1	-	0/9/27/28	0/3/3/3
1	PSU	2	998	1	-	4/7/25/26	0/2/2/2
38	5MC	1	49	38	-	2/7/25/26	0/2/2/2
1	5MC	2	1006	1	-	0/7/25/26	0/2/2/2
1	5MC	2	1637	1	-	3/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	2	766	1	-	2/7/25/26	0/2/2/2
38	M2G	1	26	38	-	2/11/29/30	0/3/3/3
38	2MG	1	10	38	-	0/9/27/28	0/3/3/3
38	H2U	1	47	38	-	4/7/38/39	0/2/2/2
38	5MC	1	48	38	-	3/7/25/26	0/2/2/2
1	2MG	2	1570	1	-	1/9/27/28	0/3/3/3

All (181) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	64	RIA	C1'-C2'	-16.34	1.32	1.52
1	2	1289	PSU	C6-C5	11.64	1.48	1.35
1	2	120	PSU	C6-C5	11.61	1.48	1.35
1	2	465	PSU	C6-C5	11.51	1.48	1.35
1	2	766	PSU	C6-C5	11.31	1.47	1.35
1	2	998	PSU	C6-C5	11.22	1.47	1.35
38	1	64	RIA	O1'-C1'	11.01	1.61	1.41
1	2	120	PSU	C2-N1	10.08	1.49	1.36
38	1	47	H2U	C2-N1	9.98	1.49	1.35
1	2	1289	PSU	C2-N1	9.95	1.49	1.36
1	2	766	PSU	C2-N1	9.88	1.49	1.36
1	2	465	PSU	C2-N1	9.75	1.49	1.36
38	1	58	1MA	C2-N3	9.74	1.48	1.30
1	2	998	PSU	C2-N1	9.67	1.49	1.36
38	1	16	H2U	C2-N1	9.66	1.49	1.35
38	1	48	5MC	C6-C5	9.28	1.49	1.34
38	1	49	5MC	C6-C5	9.23	1.49	1.34
38	1	64	RIA	C2A-C1A	-9.23	1.30	1.53
38	1	9	1MG	C2-N2	9.09	1.50	1.34
1	2	1637	5MC	C6-C5	9.01	1.49	1.34
38	1	64	RIA	O4'-C1A	8.99	1.62	1.42
1	2	1006	5MC	C6-C5	8.98	1.49	1.34
38	1	46	7MG	C8-N9	8.65	1.51	1.45
1	2	1573	7MG	C8-N9	8.35	1.51	1.45
1	2	1190	B8N	C6-N1	8.31	1.56	1.36
38	1	10	2MG	C2-N3	7.78	1.46	1.32
1	2	1190	B8N	C4-N3	-7.75	1.26	1.40
1	2	998	PSU	C2-N3	7.62	1.50	1.37
1	2	1570	2MG	C2-N3	7.61	1.46	1.32
1	2	120	PSU	C2-N3	7.55	1.49	1.37
1	2	766	PSU	C2-N3	7.50	1.49	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1289	PSU	C2-N3	7.44	1.49	1.37
1	2	1426	2MG	C2-N3	7.39	1.46	1.32
1	2	465	PSU	C2-N3	7.36	1.49	1.37
1	2	1190	B8N	C4-C5	7.33	1.64	1.47
38	1	58	1MA	C4-N3	7.22	1.50	1.35
38	1	46	7MG	C5-N7	7.21	1.44	1.35
38	1	49	5MC	C4-N3	7.01	1.45	1.34
38	1	9	1MG	C2-N3	6.88	1.44	1.33
38	1	48	5MC	C4-N3	6.82	1.45	1.34
1	2	1006	5MC	C4-N3	6.81	1.45	1.34
38	1	26	M2G	C4-N3	6.79	1.49	1.34
38	1	10	2MG	C4-N3	6.68	1.49	1.34
38	1	47	H2U	C2-N3	6.65	1.49	1.38
38	1	49	5MC	C5-C4	6.63	1.49	1.44
38	1	48	5MC	C5-C4	6.62	1.49	1.44
38	1	64	RIA	O1'-C4'	-6.58	1.30	1.45
1	2	1570	2MG	C4-N3	6.51	1.49	1.34
1	2	1006	5MC	C5-C4	6.48	1.49	1.44
38	1	26	M2G	C2-N2	6.47	1.47	1.35
1	2	1637	5MC	C4-N3	6.47	1.44	1.34
1	2	1573	7MG	C5-N7	6.41	1.43	1.35
38	1	49	5MC	C2-N3	6.41	1.49	1.36
38	1	9	1MG	C4-N3	6.39	1.48	1.34
38	1	16	H2U	C2-N3	6.39	1.49	1.38
1	2	1426	2MG	C4-N3	6.36	1.48	1.34
38	1	64	RIA	O4'-C4A	-6.34	1.30	1.45
1	2	1006	5MC	C2-N3	6.25	1.48	1.36
38	1	48	5MC	C2-N3	6.19	1.48	1.36
1	2	1637	5MC	C5-C4	6.08	1.48	1.44
38	1	26	M2G	C2-N3	6.06	1.46	1.32
1	2	1637	5MC	C2-N3	6.05	1.48	1.36
1	2	1573	7MG	C2-N3	5.97	1.47	1.33
38	1	10	2MG	C2-N2	5.94	1.45	1.33
38	1	64	RIA	C6-N6	5.93	1.49	1.34
38	1	46	7MG	C2-N3	5.91	1.47	1.33
38	1	46	7MG	C4-N3	5.78	1.47	1.34
1	2	1190	B8N	C2-N1	5.71	1.55	1.39
1	2	1573	7MG	C4-N3	5.70	1.47	1.34
1	2	1426	2MG	C2-N2	5.65	1.45	1.33
1	2	1570	2MG	C2-N2	5.56	1.45	1.33
1	2	120	PSU	C6-N1	5.44	1.45	1.36
1	2	1289	PSU	C6-N1	5.37	1.45	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	9	1MG	C2-N1	5.25	1.46	1.37
1	2	465	PSU	C6-N1	5.20	1.44	1.36
1	2	1573	7MG	C4-N9	5.17	1.44	1.37
38	1	47	H2U	C4-N3	5.13	1.46	1.37
1	2	766	PSU	C6-N1	5.10	1.44	1.36
1	2	998	PSU	C6-N1	5.07	1.44	1.36
38	1	46	7MG	C4-N9	5.06	1.44	1.37
38	1	37	T6A	C10-N6	5.03	1.48	1.37
38	1	46	7MG	C2-N2	5.00	1.45	1.34
38	1	16	H2U	C4-N3	4.94	1.45	1.37
1	2	1190	B8N	C6-C5	4.94	1.42	1.35
38	1	58	1MA	C2-N1	4.89	1.45	1.35
1	2	1570	2MG	C2-N1	4.83	1.44	1.36
1	2	1426	2MG	C2-N1	4.78	1.44	1.36
38	1	37	T6A	C10-N11	4.77	1.48	1.35
38	1	10	2MG	C2-N1	4.74	1.44	1.36
1	2	1573	7MG	C2-N2	4.71	1.45	1.34
38	1	48	5MC	C6-N1	4.67	1.46	1.38
1	2	1190	B8N	C1'-C5	-4.64	1.39	1.50
38	1	49	5MC	C2-N1	4.61	1.49	1.40
38	1	49	5MC	C6-N1	4.58	1.45	1.38
1	2	1637	5MC	C2-N1	4.55	1.49	1.40
38	1	49	5MC	C4-N4	4.47	1.45	1.34
1	2	1006	5MC	C4-N4	4.45	1.45	1.34
1	2	1637	5MC	C6-N1	4.41	1.45	1.38
1	2	1006	5MC	C6-N1	4.39	1.45	1.38
1	2	1637	5MC	C4-N4	4.33	1.45	1.34
38	1	48	5MC	C4-N4	4.31	1.45	1.34
38	1	48	5MC	C2-N1	4.30	1.49	1.40
1	2	1006	5MC	C2-N1	4.09	1.48	1.40
38	1	58	1MA	C5-C6	3.99	1.54	1.43
38	1	46	7MG	C2-N1	3.89	1.47	1.37
38	1	9	1MG	O6-C6	-3.84	1.15	1.23
1	2	998	PSU	C4-N3	3.83	1.46	1.38
1	2	1780	MA6	C6-N6	3.74	1.47	1.36
1	2	1573	7MG	C2-N1	3.70	1.46	1.37
1	2	1289	PSU	C4-N3	3.70	1.45	1.38
1	2	120	PSU	C4-N3	3.69	1.45	1.38
1	2	465	PSU	C4-N3	3.69	1.45	1.38
38	1	46	7MG	C5-C6	3.64	1.52	1.43
38	1	26	M2G	C2-N1	3.61	1.45	1.36
1	2	766	PSU	C4-N3	3.58	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1573	7MG	C5-C6	3.50	1.52	1.43
38	1	9	1MG	C5-C6	3.43	1.54	1.45
38	1	46	7MG	C6-N1	3.29	1.45	1.38
38	1	9	1MG	C5-N7	-3.28	1.32	1.39
38	1	58	1MA	C5-N7	-3.11	1.32	1.39
38	1	64	RIA	O3A-C3A	-3.08	1.35	1.43
38	1	64	RIA	O2'-C2'	3.06	1.50	1.43
1	2	1570	2MG	C5-N7	-3.06	1.32	1.39
38	1	10	2MG	C5-N7	-3.03	1.33	1.39
1	2	1426	2MG	C5-N7	-3.01	1.33	1.39
1	2	1780	MA6	C5-C4	-2.99	1.33	1.39
38	1	64	RIA	O2A-C2A	2.97	1.51	1.43
1	2	1006	5MC	O2-C2	-2.95	1.18	1.23
38	1	64	RIA	C5-N7	-2.94	1.33	1.39
1	2	1573	7MG	C6-N1	2.92	1.44	1.38
1	2	1637	5MC	O2-C2	-2.87	1.18	1.23
38	1	26	M2G	C5-N7	-2.82	1.33	1.39
38	1	48	5MC	O2-C2	-2.81	1.18	1.23
38	1	37	T6A	C5-N7	-2.76	1.34	1.39
1	2	1426	2MG	O6-C6	-2.70	1.18	1.23
38	1	49	5MC	O2-C2	-2.67	1.18	1.23
1	2	766	PSU	O4-C4	-2.66	1.18	1.23
1	2	998	PSU	O4-C4	-2.65	1.18	1.23
38	1	26	M2G	C6-N1	2.62	1.43	1.38
1	2	1289	PSU	O4-C4	-2.60	1.18	1.23
1	2	465	PSU	O4-C4	-2.59	1.18	1.23
38	1	26	M2G	C5-C6	2.58	1.54	1.44
1	2	1573	7MG	O6-C6	-2.58	1.18	1.23
1	2	120	PSU	O4-C4	-2.57	1.18	1.23
1	2	1570	2MG	O6-C6	-2.54	1.18	1.23
38	1	16	H2U	O2-C2	-2.52	1.18	1.23
38	1	10	2MG	O6-C6	-2.50	1.18	1.23
38	1	46	7MG	O6-C6	-2.49	1.18	1.23
38	1	47	H2U	O2-C2	-2.49	1.18	1.23
1	2	1426	2MG	C5-C6	2.48	1.53	1.44
1	2	1780	MA6	C5-N7	-2.44	1.34	1.39
38	1	10	2MG	C5-C6	2.40	1.53	1.44
1	2	1570	2MG	C5-C6	2.39	1.53	1.44
38	1	64	RIA	O3'-C3'	-2.38	1.37	1.43
1	2	1426	2MG	C6-N1	2.36	1.43	1.38
1	2	1190	B8N	O4'-C1'	-2.32	1.40	1.43
38	1	26	M2G	O6-C6	-2.30	1.19	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	998	PSU	O4'-C1'	-2.29	1.40	1.43
1	2	1570	2MG	C6-N1	2.28	1.43	1.38
1	2	766	PSU	O4'-C1'	-2.26	1.40	1.43
38	1	37	T6A	C5-C4	-2.22	1.35	1.39
1	2	465	PSU	O2-C2	-2.22	1.18	1.23
1	2	1289	PSU	O2-C2	-2.18	1.18	1.23
38	1	37	T6A	ODA-C13	2.18	1.28	1.22
38	1	64	RIA	P'-O5'	2.17	1.67	1.60
1	2	120	PSU	O2-C2	-2.17	1.18	1.23
38	1	10	2MG	C6-N1	2.17	1.42	1.38
1	2	766	PSU	O2-C2	-2.17	1.18	1.23
38	1	9	1MG	C4-N9	-2.16	1.32	1.38
1	2	1780	MA6	C8-N9	-2.15	1.33	1.37
1	2	998	PSU	O2-C2	-2.13	1.18	1.23
38	1	37	T6A	C6-N6	2.12	1.43	1.39
38	1	58	1MA	CM1-N1	-2.10	1.42	1.46
38	1	37	T6A	C2-N1	2.07	1.37	1.33
38	1	64	RIA	C2-N1	2.07	1.37	1.33
1	2	1426	2MG	C4-N9	-2.07	1.32	1.38
38	1	46	7MG	C5-C4	2.07	1.44	1.37
1	2	1570	2MG	C4-N9	-2.04	1.32	1.38
38	1	37	T6A	C4-N9	-2.04	1.33	1.37
1	2	1190	B8N	O2-C2	-2.01	1.18	1.22
38	1	37	T6A	O10-C10	-2.01	1.19	1.23

All (154) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1780	MA6	N1-C6-N6	-12.00	102.23	116.86
1	2	1780	MA6	C5-C6-N6	7.76	137.61	125.33
38	1	9	1MG	C1'-N9-C4	-7.14	105.38	126.49
38	1	58	1MA	C1'-N9-C8	-6.62	107.91	126.73
1	2	1426	2MG	C2-N3-C4	6.57	120.22	112.00
38	1	9	1MG	C1'-N9-C8	6.48	145.14	126.73
38	1	64	RIA	C5-C4-N3	-6.33	118.00	126.72
38	1	10	2MG	C2-N3-C4	6.28	119.86	112.00
1	2	1570	2MG	C2-N3-C4	6.08	119.61	112.00
38	1	37	T6A	N3-C2-N1	-6.07	119.39	128.58
1	2	1780	MA6	N1-C2-N3	-5.76	119.87	128.58
38	1	58	1MA	C1'-N9-C4	5.74	143.44	126.49
38	1	64	RIA	N3-C2-N1	-5.66	120.02	128.58
38	1	10	2MG	C5-C4-N3	-5.35	119.87	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1570	2MG	C5-C4-N3	-5.34	119.89	128.39
1	2	1426	2MG	C5-C4-N3	-5.31	119.93	128.39
38	1	26	M2G	C5-C4-N3	-5.21	120.09	128.39
1	2	766	PSU	C4-N3-C2	-5.21	119.20	126.37
1	2	1190	B8N	C5-C4-N3	5.16	125.53	116.15
38	1	46	7MG	C5-C6-N1	5.05	119.83	110.94
1	2	120	PSU	C4-N3-C2	-5.01	119.47	126.37
1	2	1573	7MG	C5-C6-N1	4.94	119.63	110.94
38	1	9	1MG	C5-C4-N3	-4.92	120.56	128.39
1	2	1780	MA6	C5-C4-N3	-4.90	119.97	126.72
38	1	64	RIA	N6-C6-N1	-4.90	107.46	118.38
1	2	465	PSU	C4-N3-C2	-4.87	119.66	126.37
38	1	58	1MA	N1-C2-N3	-4.79	120.31	126.00
1	2	1289	PSU	C4-N3-C2	-4.75	119.83	126.37
38	1	58	1MA	C5-C4-N3	-4.72	120.32	127.27
1	2	1190	B8N	C4-N3-C2	-4.69	119.85	125.62
1	2	998	PSU	C4-N3-C2	-4.68	119.92	126.37
1	2	766	PSU	N1-C2-N3	4.67	120.09	115.17
1	2	1426	2MG	C2-N1-C6	-4.67	118.91	124.55
38	1	46	7MG	C2-N3-C4	4.53	120.10	112.30
1	2	1573	7MG	C5-C4-N3	-4.51	119.66	128.13
1	2	1570	2MG	C2-N1-C6	-4.51	119.10	124.55
1	2	120	PSU	N1-C2-N3	4.50	119.92	115.17
38	1	37	T6A	C12-N11-C10	4.47	129.43	121.99
38	1	64	RIA	N3-C4-N9	4.45	134.74	127.17
38	1	37	T6A	C5-C4-N3	-4.39	120.68	126.72
1	2	465	PSU	N1-C2-N3	4.34	119.74	115.17
1	2	1573	7MG	C2-N3-C4	4.27	119.66	112.30
1	2	998	PSU	N1-C2-N3	4.12	119.52	115.17
38	1	46	7MG	C5-C4-N3	-4.10	120.43	128.13
1	2	1289	PSU	N1-C2-N3	4.09	119.48	115.17
1	2	1780	MA6	N9-C8-N7	-4.09	108.14	113.94
1	2	1426	2MG	N1-C2-N2	4.08	120.73	116.56
38	1	48	5MC	C5-C6-N1	-4.08	118.88	123.31
38	1	37	T6A	N9-C8-N7	-4.07	108.16	113.94
38	1	10	2MG	C2-N1-C6	-4.01	119.70	124.55
1	2	1190	B8N	C1'-C5-C4	3.96	123.61	117.61
38	1	64	RIA	C2-N3-C4	3.92	121.40	111.83
38	1	26	M2G	C2-N3-C4	3.91	119.74	112.51
1	2	766	PSU	C6-C5-C4	3.89	120.80	118.17
38	1	46	7MG	C4-C5-N7	3.82	109.89	105.38
1	2	1780	MA6	C4-C5-C6	3.78	119.82	115.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1573	7MG	C4-C5-N7	3.76	109.82	105.38
38	1	64	RIA	N9-C8-N7	-3.74	108.63	113.94
38	1	9	1MG	N9-C8-N7	-3.72	106.50	113.40
38	1	37	T6A	C4-C5-C6	3.62	119.79	116.78
1	2	1570	2MG	N1-C2-N2	3.62	120.26	116.56
1	2	998	PSU	C6-N1-C2	-3.61	119.34	122.69
38	1	58	1MA	C2-N3-C4	3.58	119.56	112.53
38	1	9	1MG	C2-N3-C4	3.52	119.90	111.98
1	2	1190	B8N	N3-C2-N1	3.51	121.01	116.72
38	1	64	RIA	C5-C6-N6	3.49	131.92	123.29
38	1	10	2MG	N9-C4-N3	3.46	132.88	125.95
1	2	120	PSU	C6-C5-C4	3.40	120.47	118.17
1	2	1780	MA6	C2-N3-C4	3.40	120.12	111.83
38	1	16	H2U	N3-C2-N1	3.39	120.06	116.65
1	2	1780	MA6	C2-N1-C6	3.37	120.06	111.83
1	2	1570	2MG	N9-C4-N3	3.30	132.55	125.95
38	1	37	T6A	C2-N3-C4	3.24	119.74	111.83
38	1	64	RIA	C1'-O2A-C2A	-3.23	110.32	117.98
1	2	1573	7MG	C2-N1-C6	-3.17	119.36	125.11
1	2	1573	7MG	C5-C4-N9	3.15	110.37	106.33
38	1	9	1MG	N9-C4-N3	3.14	132.24	125.95
38	1	46	7MG	C5-C4-N9	3.13	110.34	106.33
38	1	58	1MA	N9-C8-N7	-3.09	107.67	113.40
1	2	1573	7MG	N9-C4-N3	3.08	129.97	125.46
1	2	1780	MA6	N3-C4-N9	3.06	132.36	127.17
38	1	26	M2G	N9-C4-N3	3.05	132.06	125.95
38	1	47	H2U	N3-C2-N1	3.05	119.71	116.65
38	1	47	H2U	C5-C6-N1	3.05	120.74	111.52
38	1	37	T6A	N6-C10-N11	3.05	117.96	113.77
1	2	120	PSU	C6-N1-C2	-3.04	119.87	122.69
1	2	1570	2MG	N9-C8-N7	-3.02	107.81	113.40
1	2	1426	2MG	N9-C4-N3	2.98	131.92	125.95
1	2	1190	B8N	O4-C4-N3	-2.98	115.15	119.99
1	2	1637	5MC	C5-C6-N1	-2.97	120.09	123.31
1	2	766	PSU	C6-N1-C2	-2.93	119.97	122.69
38	1	10	2MG	N9-C8-N7	-2.93	107.97	113.40
38	1	64	RIA	C5-N7-C8	2.90	108.01	103.45
1	2	465	PSU	C6-N1-C2	-2.89	120.01	122.69
1	2	1570	2MG	CM2-N2-C2	-2.89	117.45	123.65
38	1	46	7MG	O6-C6-C5	-2.86	120.60	127.62
38	1	46	7MG	C2-N1-C6	-2.84	119.96	125.11
1	2	1426	2MG	N9-C8-N7	-2.84	108.14	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	1	26	M2G	N9-C8-N7	-2.82	108.18	113.40
38	1	16	H2U	C5-C6-N1	2.82	120.04	111.52
1	2	1289	PSU	C6-N1-C2	-2.80	120.09	122.69
38	1	47	H2U	C5-C4-N3	2.79	119.65	116.69
38	1	9	1MG	C5-C6-N1	2.77	120.15	115.02
1	2	1426	2MG	C5-C6-N1	2.74	120.23	113.25
1	2	1780	MA6	C5-N7-C8	2.71	107.72	103.45
1	2	998	PSU	O2-C2-N1	-2.69	120.01	122.79
38	1	37	T6A	C5-N7-C8	2.68	107.66	103.45
38	1	9	1MG	C8-N7-C5	2.67	109.01	104.26
1	2	1573	7MG	O6-C6-C5	-2.64	121.14	127.62
38	1	10	2MG	C5-C6-N1	2.60	119.88	113.25
1	2	1570	2MG	C5-C6-N1	2.59	119.85	113.25
38	1	46	7MG	N9-C4-N3	2.57	129.23	125.46
38	1	16	H2U	O2-C2-N1	-2.56	120.03	123.10
38	1	16	H2U	C5-C4-N3	2.56	119.41	116.69
1	2	766	PSU	O2-C2-N1	-2.55	120.16	122.79
38	1	26	M2G	C5-C6-N1	2.55	119.74	113.25
1	2	1570	2MG	O6-C6-C5	-2.55	119.81	126.53
38	1	64	RIA	C6-C5-C4	2.53	120.63	117.18
1	2	1006	5MC	CM5-C5-C6	-2.51	119.45	122.85
1	2	1426	2MG	O6-C6-C5	-2.50	119.93	126.53
38	1	26	M2G	O6-C6-C5	-2.50	119.95	126.53
38	1	37	T6A	C13-C12-N11	-2.49	104.70	110.17
1	2	1637	5MC	O2-C2-N3	-2.48	118.42	122.33
38	1	10	2MG	O6-C6-C5	-2.47	120.02	126.53
38	1	58	1MA	N9-C4-N3	2.46	132.50	126.90
38	1	37	T6A	N3-C4-N9	2.44	131.32	127.17
1	2	465	PSU	O2-C2-N1	-2.43	120.28	122.79
1	2	465	PSU	C6-C5-C4	2.42	119.81	118.17
38	1	49	5MC	C5-C4-N3	-2.41	119.28	121.75
1	2	1190	B8N	O4'-C1'-C2'	2.34	108.39	105.15
38	1	46	7MG	N9-C8-N7	2.34	106.68	103.37
38	1	64	RIA	C4A-O4'-C1A	-2.32	104.35	109.47
38	1	64	RIA	C1'-C2'-C3'	2.29	105.14	102.29
1	2	1573	7MG	N9-C8-N7	2.29	106.61	103.37
1	2	998	PSU	O4'-C1'-C2'	2.28	108.31	105.15
1	2	1006	5MC	C5-C4-N3	-2.26	119.44	121.75
1	2	1780	MA6	C4-N9-C8	2.26	108.11	105.74
1	2	1426	2MG	C1'-N9-C4	-2.23	119.91	126.49
1	2	1570	2MG	C8-N7-C5	2.18	108.14	104.26
38	1	58	1MA	C8-N7-C5	2.17	108.12	104.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	766	PSU	O4'-C1'-C2'	2.16	108.14	105.15
1	2	120	PSU	O2-C2-N1	-2.15	120.57	122.79
38	1	10	2MG	C8-N7-C5	2.11	108.01	104.26
38	1	37	T6A	C4-N9-C8	2.10	107.94	105.74
1	2	1289	PSU	C6-C5-C4	2.08	119.58	118.17
38	1	47	H2U	O2-C2-N1	-2.08	120.60	123.10
1	2	1190	B8N	C31-N3-C2	2.07	120.70	117.64
38	1	10	2MG	N1-C2-N2	2.06	118.66	116.56
38	1	37	T6A	C4-C5-N7	-2.06	108.23	110.58
38	1	26	M2G	C8-N7-C5	2.05	107.91	104.26
38	1	10	2MG	N1-C2-N3	-2.04	120.24	123.68
1	2	1426	2MG	C8-N7-C5	2.03	107.88	104.26
1	2	1289	PSU	O2-C2-N1	-2.02	120.70	122.79
38	1	37	T6A	C5-C4-N9	2.01	108.00	105.81

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	2	1190	B8N	O4'-C4'-C5'-O5'
1	2	1190	B8N	C3'-C4'-C5'-O5'
1	2	1637	5MC	O4'-C4'-C5'-O5'
38	1	9	1MG	O4'-C4'-C5'-O5'
38	1	9	1MG	C3'-C4'-C5'-O5'
38	1	16	H2U	C4'-C5'-O5'-P
38	1	16	H2U	O4'-C1'-N1-C6
38	1	37	T6A	C14-C12-N11-C10
38	1	49	5MC	O4'-C4'-C5'-O5'
38	1	64	RIA	C2'-C1'-O2A-C2A
38	1	64	RIA	C2A-C1A-N9-C4
38	1	64	RIA	C5'-O5'-P'-O1X
1	2	766	PSU	C3'-C4'-C5'-O5'
1	2	766	PSU	O4'-C4'-C5'-O5'
38	1	16	H2U	C3'-C4'-C5'-O5'
38	1	47	H2U	O4'-C4'-C5'-O5'
38	1	64	RIA	C2A-C1A-N9-C8
38	1	37	T6A	C13-C12-N11-C10
1	2	1573	7MG	C3'-C4'-C5'-O5'
38	1	16	H2U	O4'-C4'-C5'-O5'
38	1	47	H2U	C3'-C4'-C5'-O5'
38	1	48	5MC	O4'-C4'-C5'-O5'
38	1	58	1MA	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
38	1	16	H2U	C2'-C1'-N1-C6
1	2	1573	7MG	O4'-C4'-C5'-O5'
1	2	1637	5MC	C3'-C4'-C5'-O5'
38	1	48	5MC	C3'-C4'-C5'-O5'
38	1	49	5MC	C3'-C4'-C5'-O5'
38	1	26	M2G	C3'-C4'-C5'-O5'
38	1	58	1MA	C3'-C4'-C5'-O5'
38	1	64	RIA	O1'-C1'-O2A-C2A
1	2	998	PSU	O4'-C4'-C5'-O5'
38	1	48	5MC	C4'-C5'-O5'-P
38	1	16	H2U	C2'-C1'-N1-C2
1	2	1780	MA6	O4'-C4'-C5'-O5'
1	2	998	PSU	C3'-C4'-C5'-O5'
38	1	64	RIA	C3'-C4'-C5'-O5'
38	1	16	H2U	O4'-C1'-N1-C2
1	2	998	PSU	O4'-C1'-C5-C4
38	1	46	7MG	C4'-C5'-O5'-P
38	1	64	RIA	C3A-C2A-O2A-C1'
38	1	47	H2U	C2'-C1'-N1-C6
38	1	26	M2G	O4'-C4'-C5'-O5'
38	1	47	H2U	C4'-C5'-O5'-P
1	2	998	PSU	O4'-C1'-C5-C6
38	1	64	RIA	C5'-O5'-P'-O2X
38	1	64	RIA	O1'-C4'-C5'-O5'
38	1	64	RIA	C1A-C2A-O2A-C1'
1	2	1637	5MC	C2'-C1'-N1-C2
1	2	1570	2MG	C4'-C5'-O5'-P
1	2	1780	MA6	C3'-C4'-C5'-O5'

There are no ring outliers.

19 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	1	37	T6A	5	0
38	1	46	7MG	1	0
1	2	1190	B8N	1	0
1	2	465	PSU	1	0
38	1	9	1MG	2	0
38	1	64	RIA	3	0
1	2	120	PSU	1	0
1	2	1573	7MG	4	0
38	1	16	H2U	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2	1780	MA6	2	0
1	2	1289	PSU	3	0
1	2	998	PSU	3	0
38	1	49	5MC	2	0
1	2	1006	5MC	2	0
1	2	1637	5MC	1	0
38	1	26	M2G	1	0
38	1	10	2MG	2	0
38	1	47	H2U	1	0
38	1	48	5MC	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 123 ligands modelled in this entry, 121 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
46	MET	k	602	-	6,7,8	0.51	0	2,7,9	0.09	0
45	GCP	k	601	-	32,34,34	1.47	7 (21%)	49,54,54	1.80	8 (16%)

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
46	MET	k	602	-	-	1/5/6/8	-
45	GCP	k	601	-	-	1/19/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	k	601	GCP	C5-C4	3.19	1.47	1.38
45	k	601	GCP	PG-O3G	2.92	1.61	1.55
45	k	601	GCP	PG-O2G	2.88	1.61	1.55
45	k	601	GCP	PB-O3A	2.79	1.61	1.58
45	k	601	GCP	C6-N1	-2.43	1.34	1.38
45	k	601	GCP	PB-O2B	2.05	1.61	1.56
45	k	601	GCP	C5-N7	-2.03	1.35	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	k	601	GCP	C5-C4-N3	-6.20	118.52	128.39
45	k	601	GCP	C2-N3-C4	5.07	121.04	112.30
45	k	601	GCP	N9-C4-N3	4.59	135.14	125.95
45	k	601	GCP	PB-O3A-PA	-3.64	120.50	132.37
45	k	601	GCP	C6-C5-N7	3.24	136.19	130.29
45	k	601	GCP	C4-C5-N7	-2.60	106.55	110.67
45	k	601	GCP	C3'-C2'-C1'	2.27	105.76	101.46
45	k	601	GCP	O6-C6-C5	-2.11	120.97	126.53

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	k	602	MET	CB-CG-SD-CE
45	k	601	GCP	C5'-O5'-PA-O1A

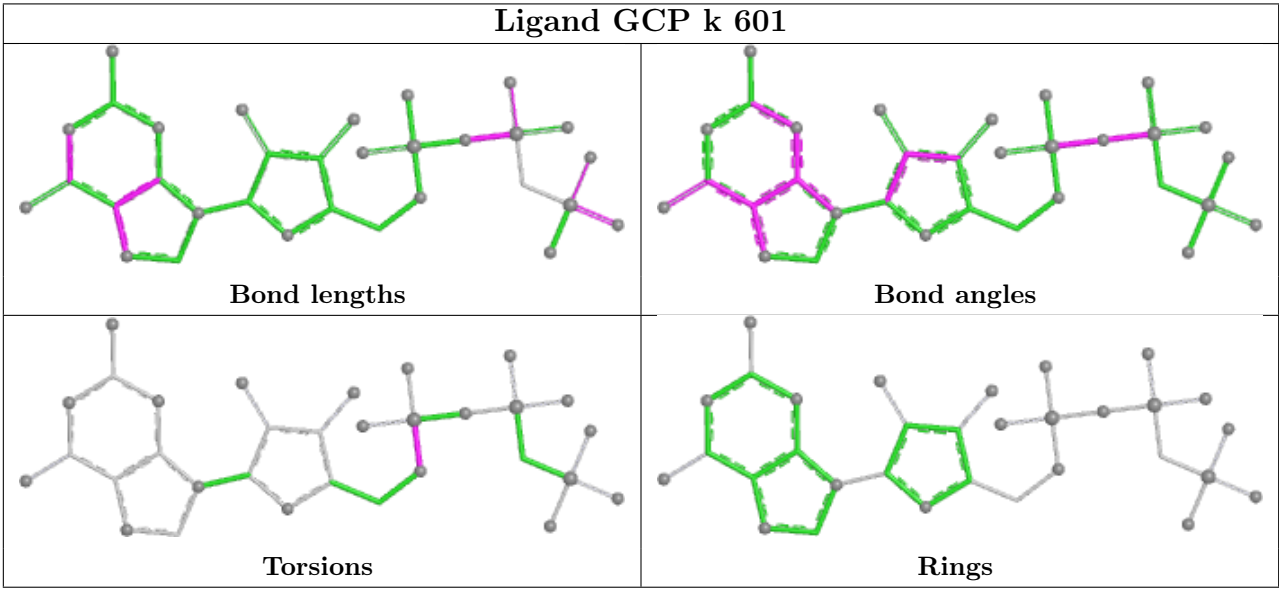
There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
46	k	602	MET	1	0
45	k	601	GCP	10	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	7.03
1	1	63:G	O3'	64:RIA	P	5.87
1	1	16:H2U	O3'	18:G	P	4.04

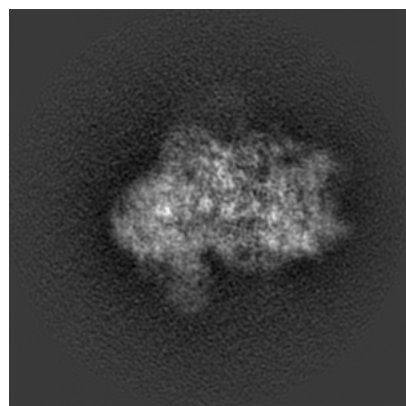
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19806. These allow visual inspection of the internal detail of the map and identification of artifacts.

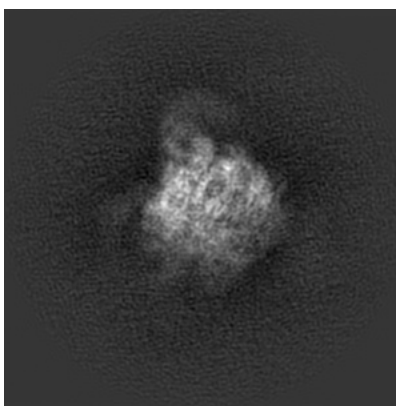
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

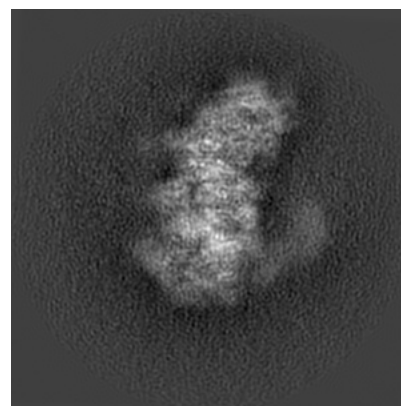
6.1.1 Primary map



X

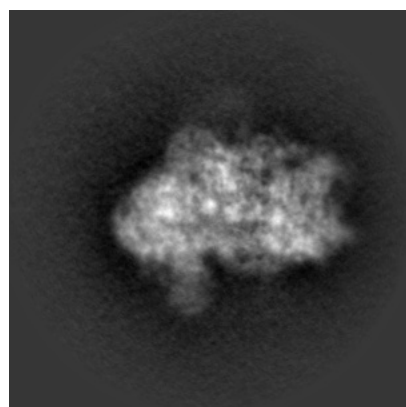


Y

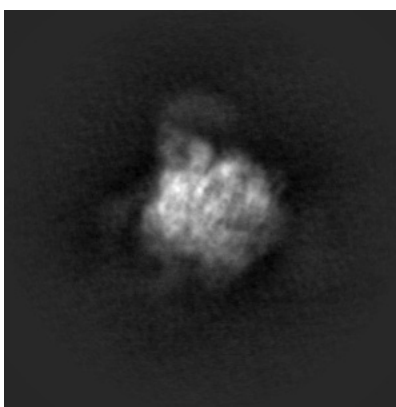


Z

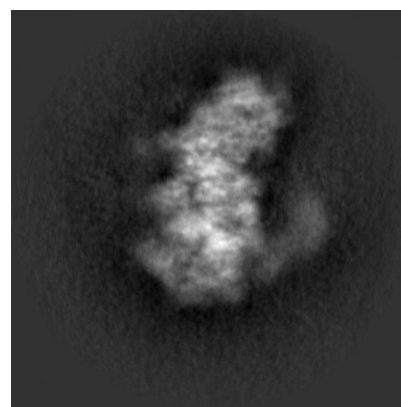
6.1.2 Raw map



X



Y

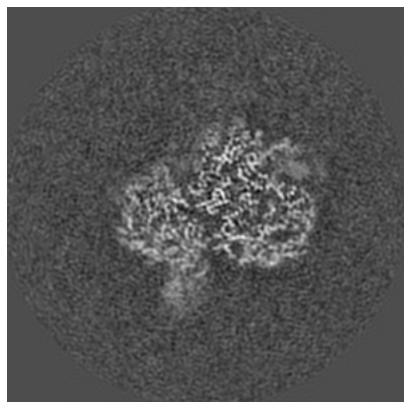


Z

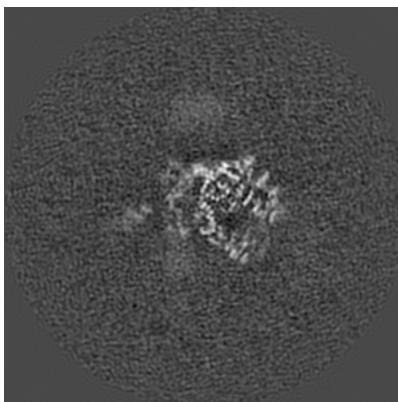
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

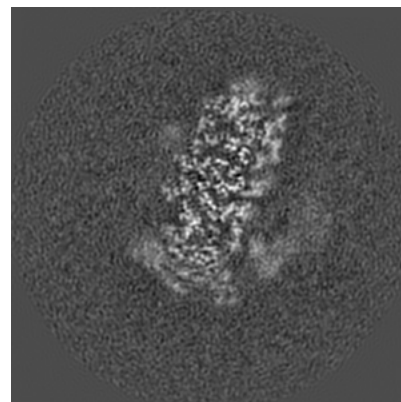
6.2.1 Primary map



X Index: 150

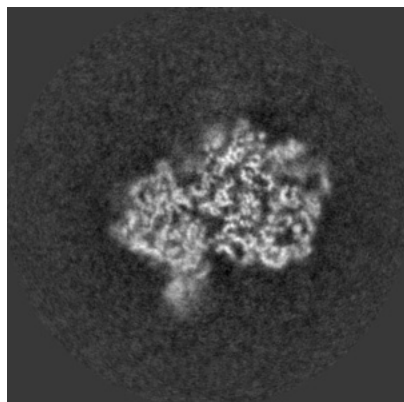


Y Index: 150

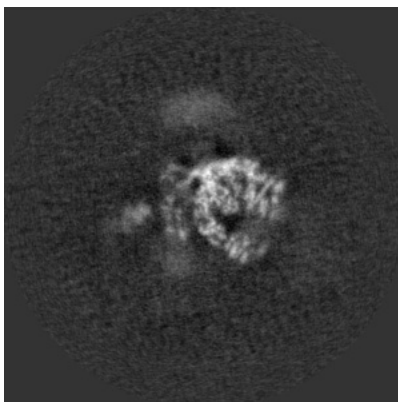


Z Index: 150

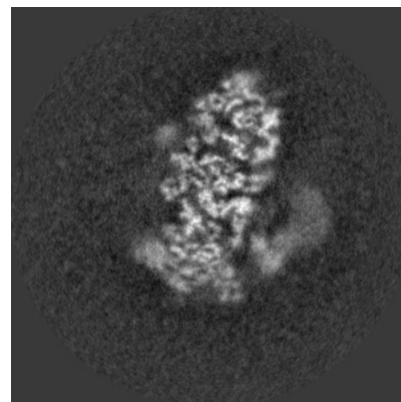
6.2.2 Raw map



X Index: 150



Y Index: 150

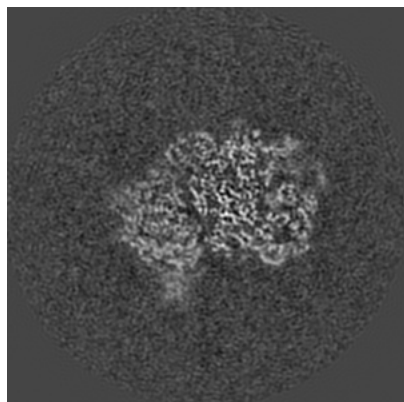


Z Index: 150

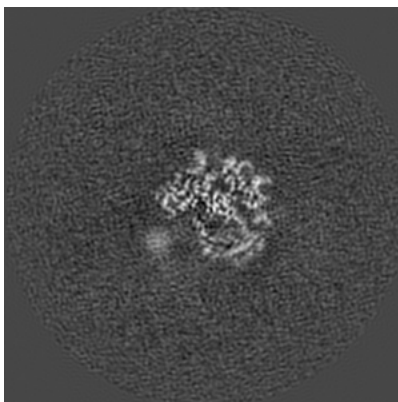
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

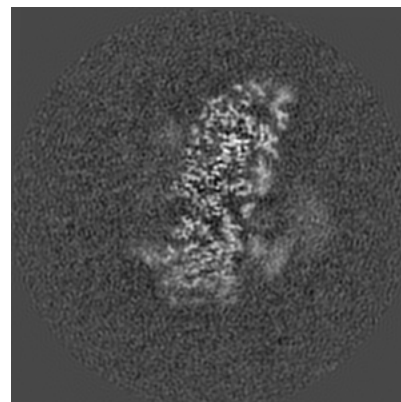
6.3.1 Primary map



X Index: 154

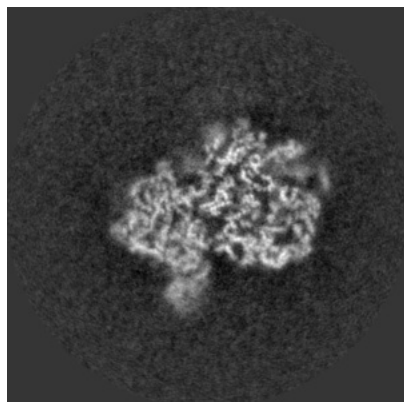


Y Index: 162

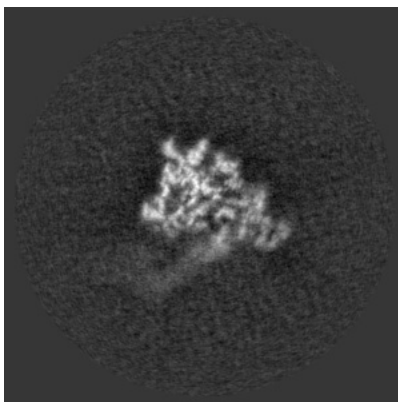


Z Index: 146

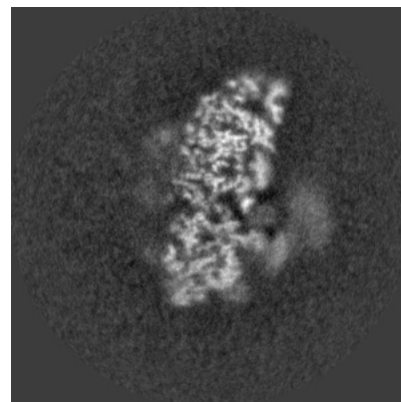
6.3.2 Raw map



X Index: 149



Y Index: 201

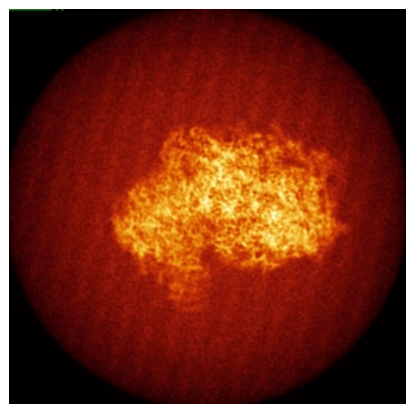


Z Index: 143

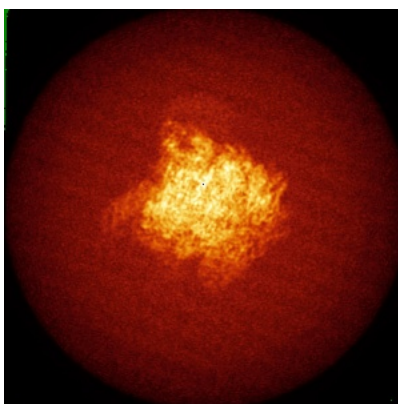
The images above show the largest variance slices of the map in three orthogonal directions.

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

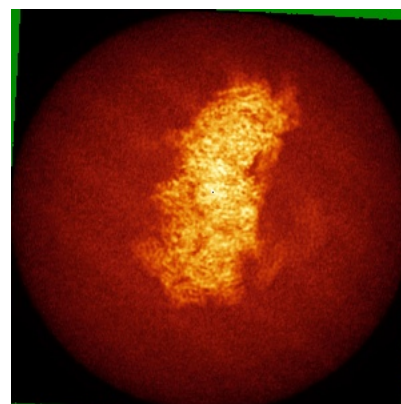
6.4.1 Primary map



X

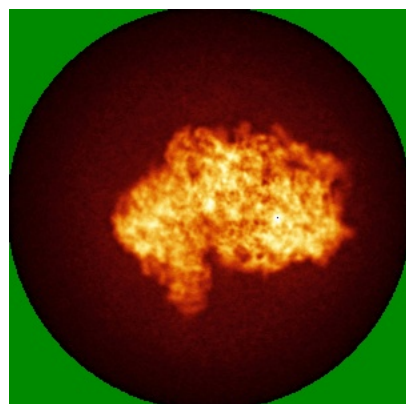


Y

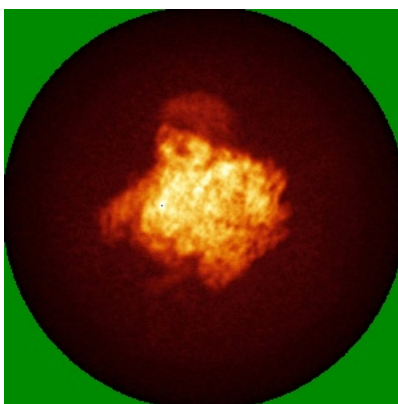


Z

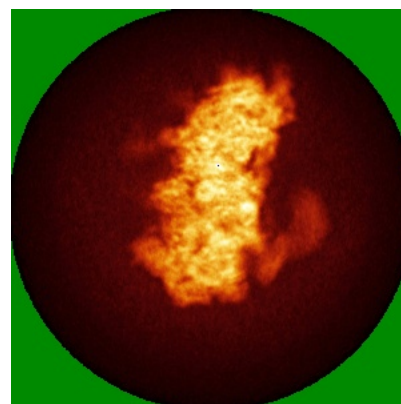
6.4.2 Raw map



X



Y

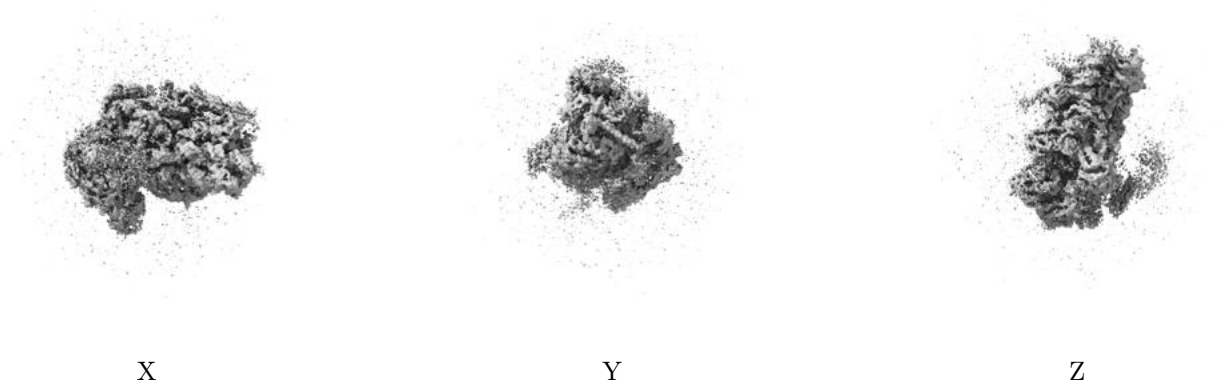


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. 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.

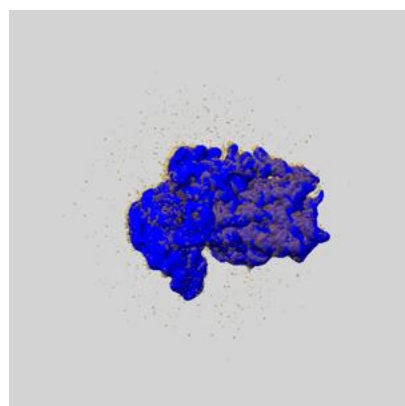
6.6 Mask visualisation [i](#)

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

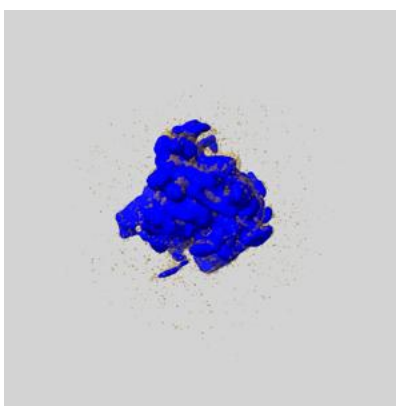
A mask typically either:

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

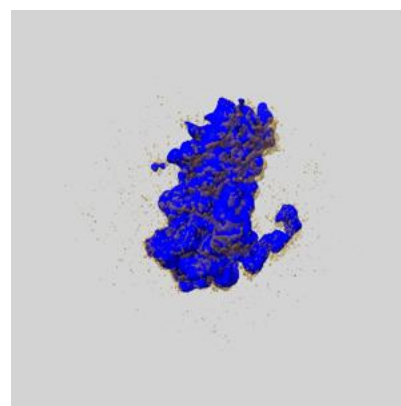
6.6.1 emd_19806_msk_1.map [i](#)



X



Y

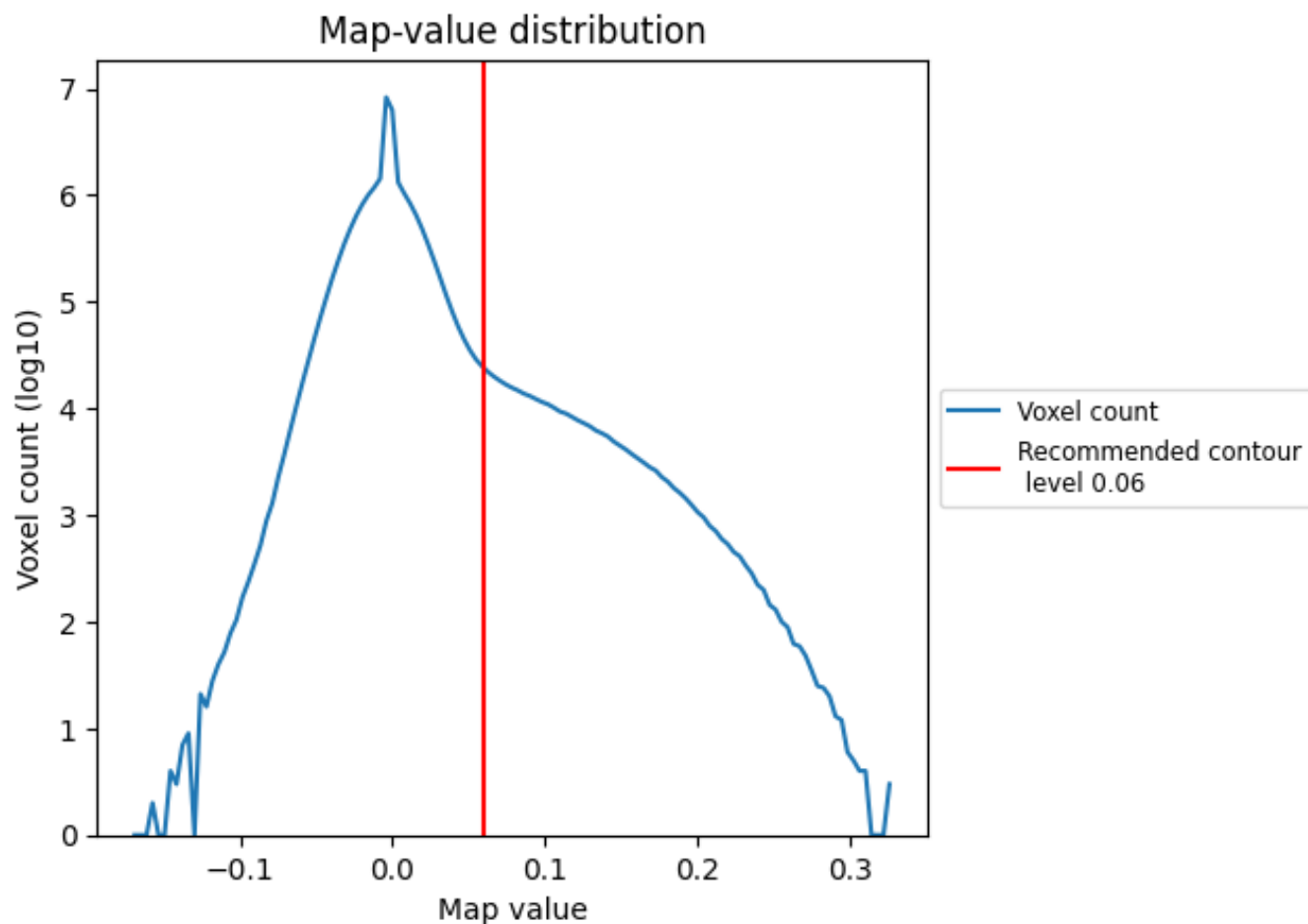


Z

7 Map analysis [i](#)

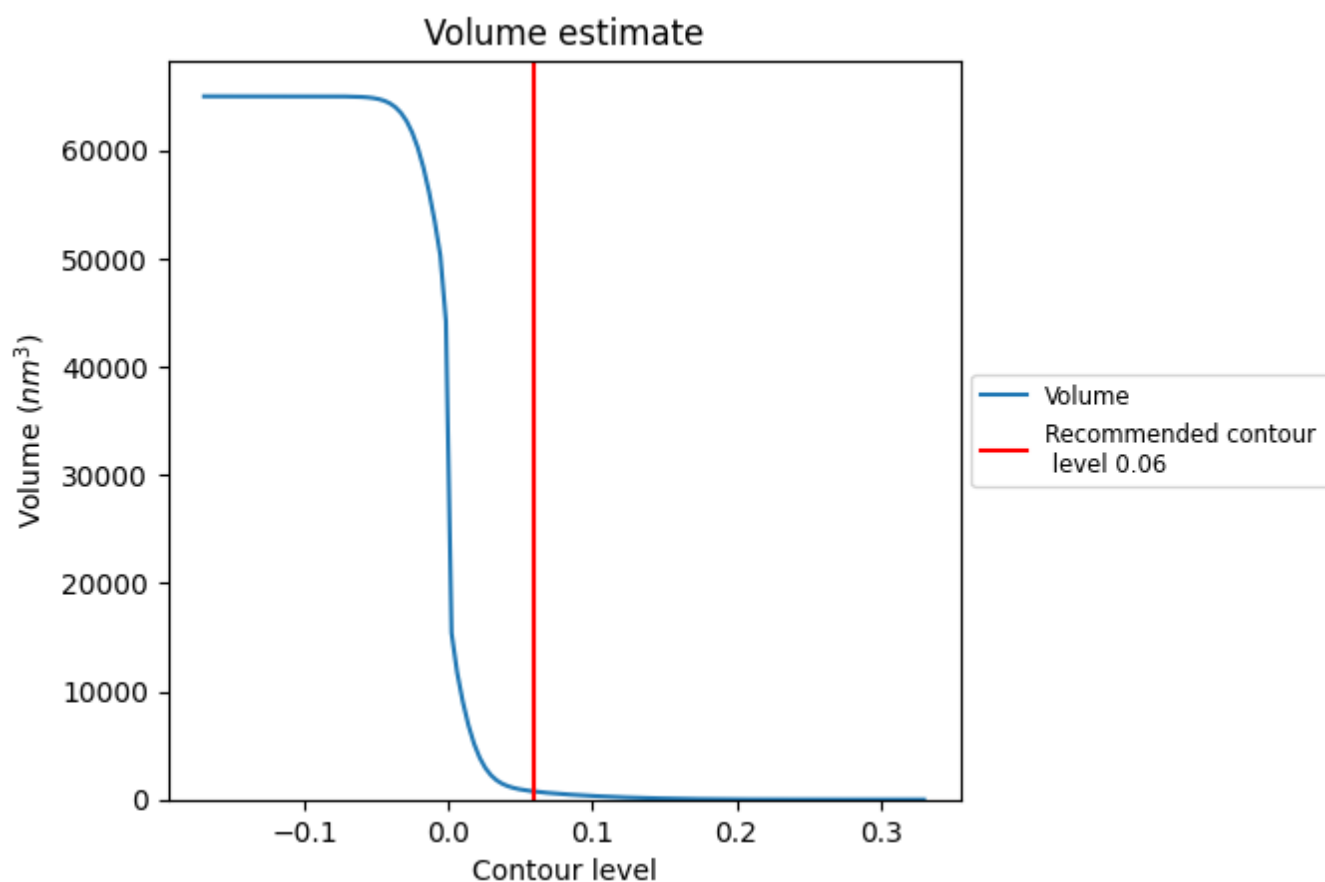
This section contains the results of statistical analysis of the map.

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.

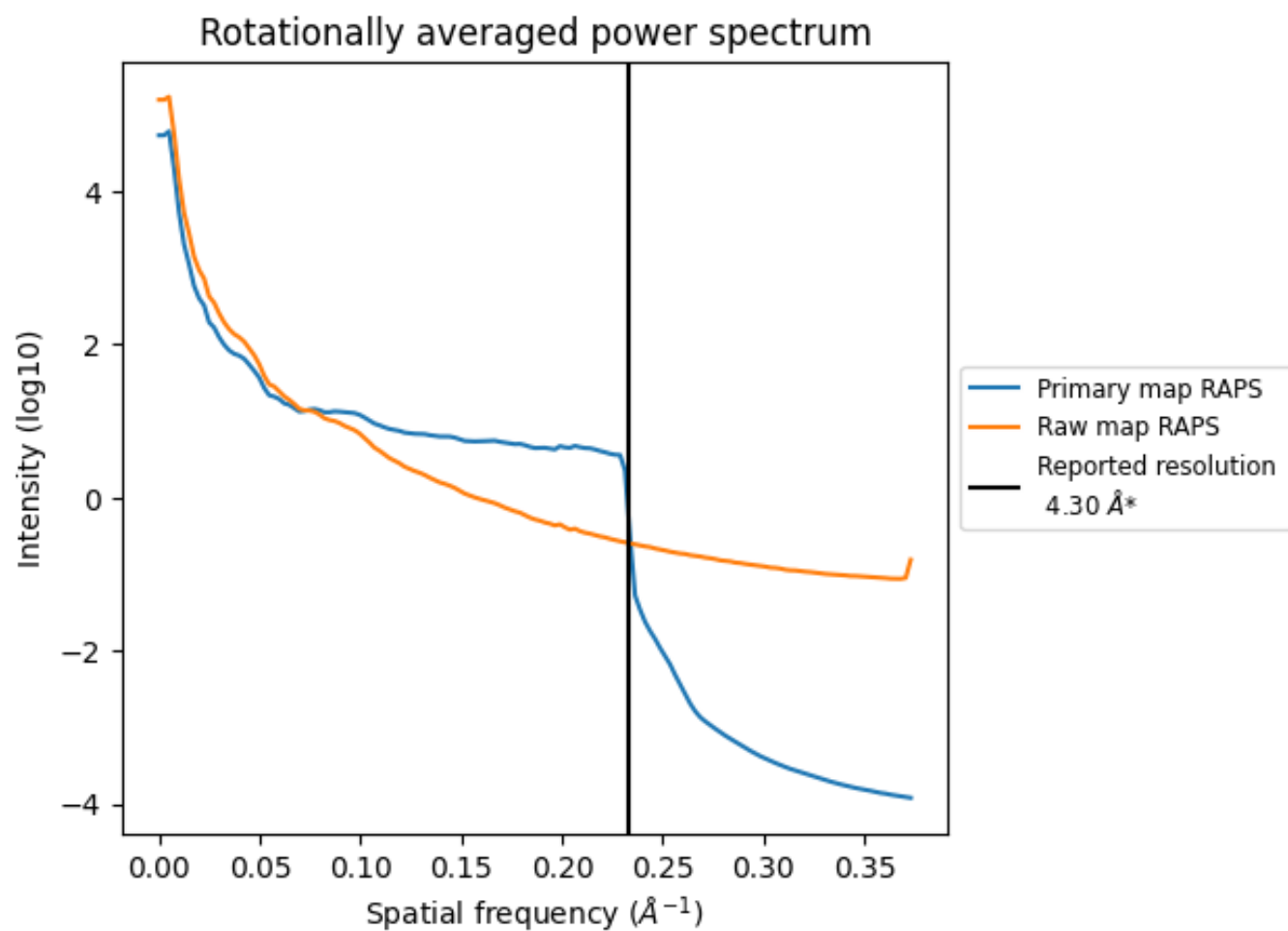
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 744 nm³; this corresponds to an approximate mass of 672 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 ⓘ

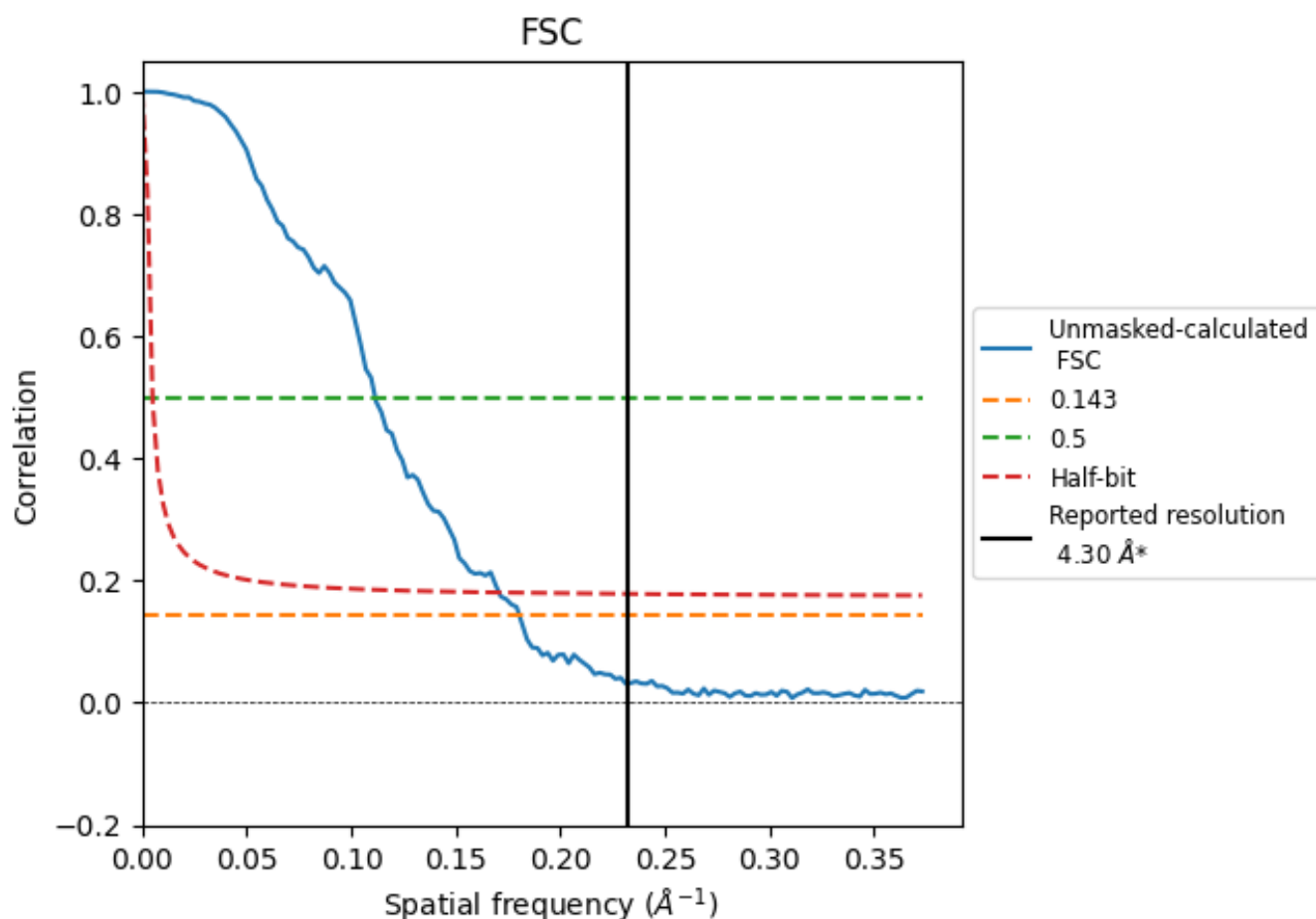


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 0.233 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

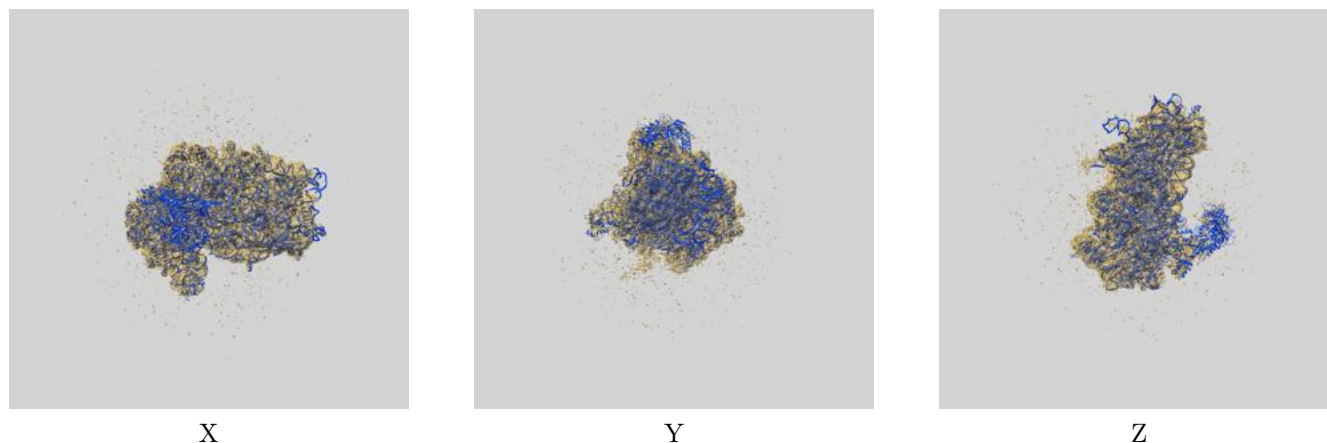
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.54	8.97	5.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.54 differs from the reported value 4.3 by more than 10 %

9 Map-model fit [i](#)

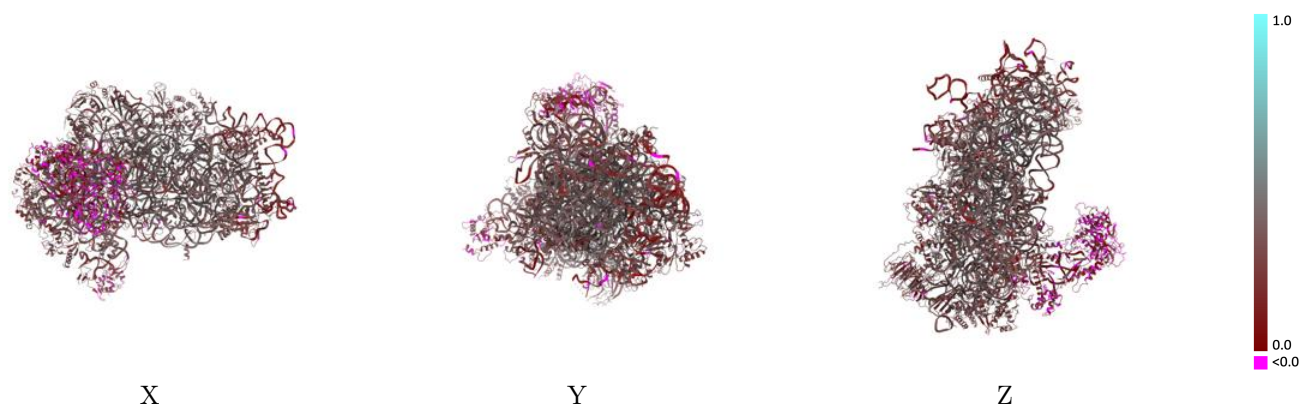
This section contains information regarding the fit between EMDB map EMD-19806 and PDB model 8S8I. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



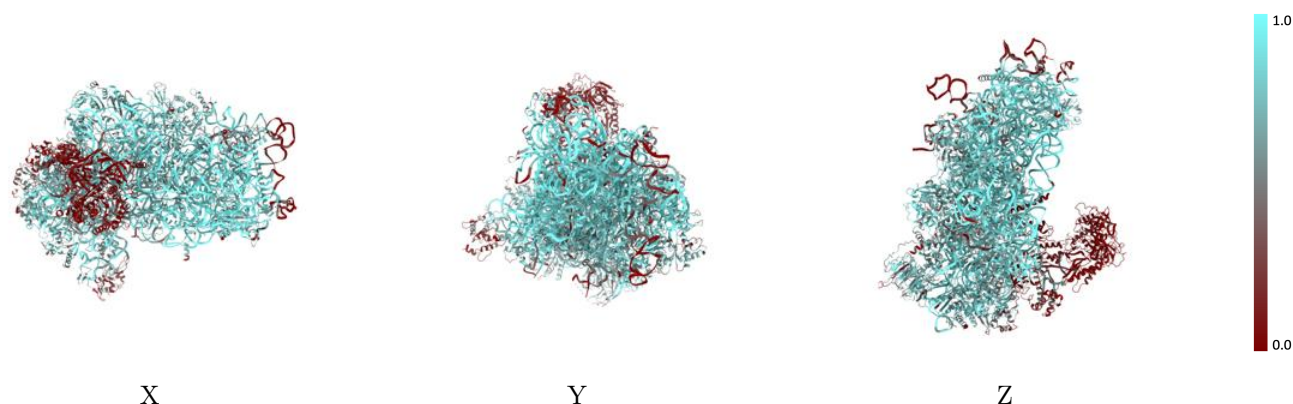
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



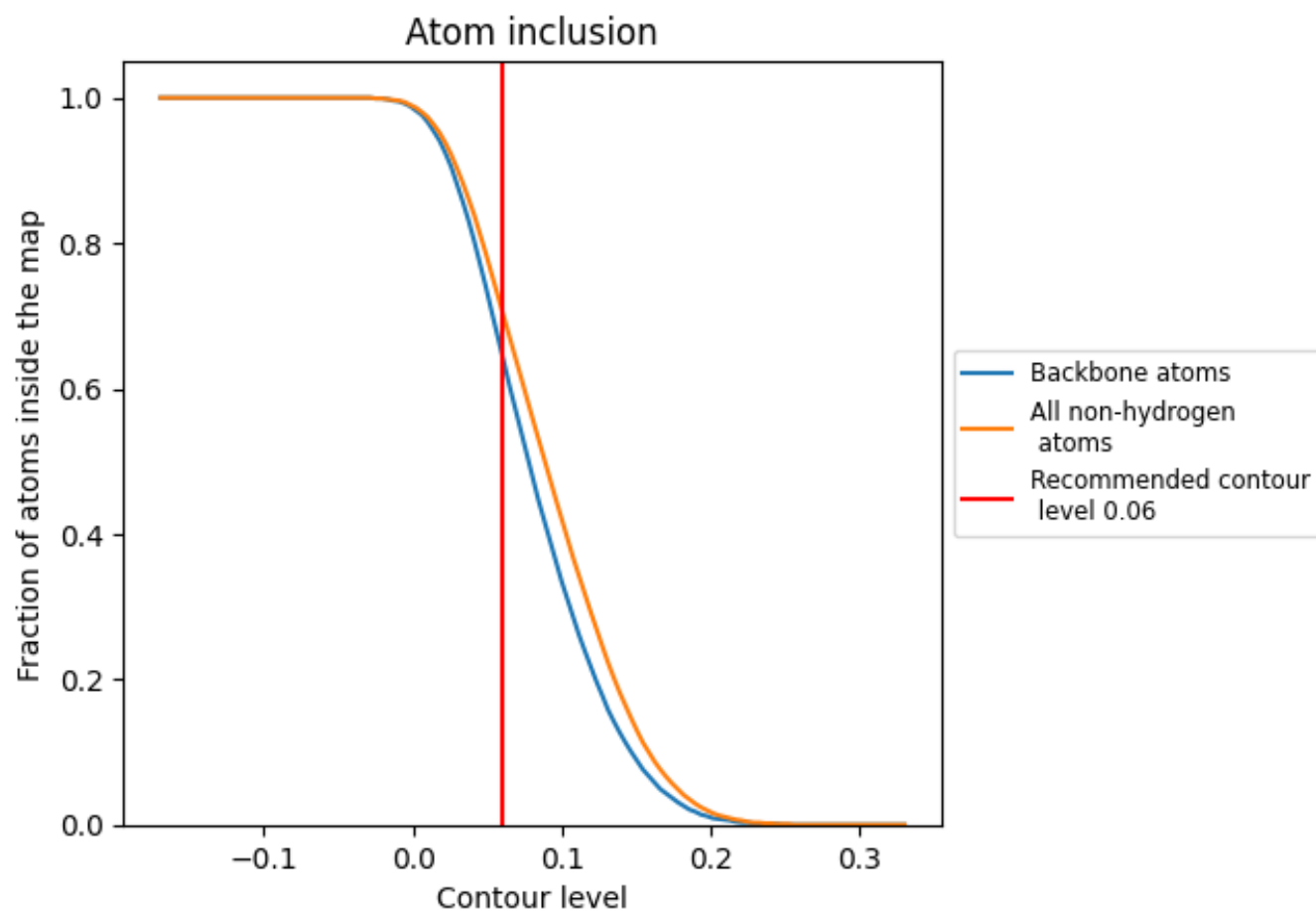
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 71% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7080	 0.3090
1	 0.5620	 0.1870
2	 0.8790	 0.3360
3	 0.2980	 0.3010
A	 0.7530	 0.3390
B	 0.7380	 0.3180
C	 0.7530	 0.3700
D	 0.6640	 0.3330
E	 0.7750	 0.3730
F	 0.6600	 0.3260
G	 0.7680	 0.3060
H	 0.6180	 0.3050
I	 0.7490	 0.3440
J	 0.7440	 0.3490
K	 0.6830	 0.2770
L	 0.7150	 0.3660
M	 0.1900	 0.1540
N	 0.7710	 0.3480
O	 0.7290	 0.3390
P	 0.6820	 0.2860
Q	 0.7520	 0.3260
R	 0.6280	 0.2980
S	 0.6880	 0.2880
T	 0.7740	 0.3000
U	 0.5950	 0.3060
V	 0.8040	 0.3590
W	 0.7760	 0.3790
X	 0.7580	 0.3830
Y	 0.7980	 0.3370
Z	 0.4060	 0.2540
a	 0.7200	 0.3750
b	 0.7390	 0.3590
c	 0.6160	 0.3460
d	 0.7850	 0.3390
e	 0.6550	 0.3690



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Chain	Atom inclusion	Q-score
f	 0.4120	 0.1930
g	 0.6530	 0.2820
h	 0.0660	 0.2370
i	 0.3830	 0.2990
j	 0.1040	 0.1350
k	 0.0370	 0.0900
l	 0.0290	 0.1370
m	 0.0640	 0.2100