



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 21, 2026 – 10:18 am BST

PDB ID : 2UUB / pdb_00002uub
Title : Structure of the *Thermus thermophilus* 30S ribosomal subunit complexed with a Valine-ASL with cmo5U in position 34 bound to an mRNA with a GUU-codon in the A-site and paromomycin.
Authors : Weixlbaumer, A.; Murphy, F.V.; Dziergowska, A.; Malkiewicz, A.; Vendeix, F.A.P.; Agris, P.F.; Ramakrishnan, V.
Deposited on : 2007-03-01
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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](#) ①) were used in the production of this report:

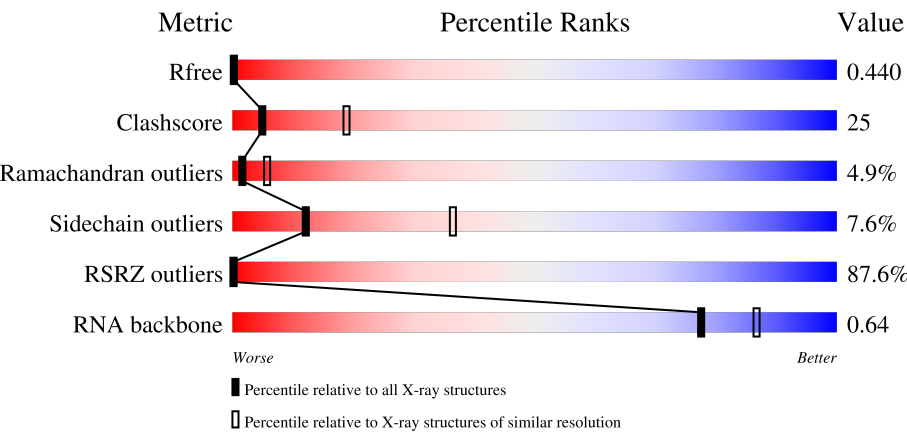
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1522	94% 45% 43% 9% ..
2	B	256	75% 28% 54% 9% 8%
3	C	239	77% 32% 44% 10% 13%
4	D	209	83% 54% 40% ..

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Mol	Chain	Length	Quality of chain
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	135	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	
22	X	6	
23	Y	17	

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
25	MG	A	1603	-	-	-	X
25	MG	A	1604	-	-	-	X
25	MG	A	1605	-	-	-	X
25	MG	A	1606	-	-	-	X
25	MG	A	1607	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1610	-	-	-	X
25	MG	A	1612	-	-	-	X
25	MG	A	1618	-	-	-	X
25	MG	A	1622	-	-	-	X
25	MG	A	1625	-	-	-	X
25	MG	A	1628	-	-	-	X
25	MG	A	1630	-	-	-	X
25	MG	A	1631	-	-	-	X
25	MG	A	1632	-	-	-	X
25	MG	A	1634	-	-	-	X
25	MG	A	1636	-	-	-	X
25	MG	A	1637	-	-	-	X
25	MG	A	1638	-	-	-	X
25	MG	A	1641	-	-	-	X
25	MG	A	1643	-	-	-	X
25	MG	A	1644	-	-	-	X
25	MG	A	1652	-	-	-	X
25	MG	A	1654	-	-	-	X
25	MG	A	1655	-	-	-	X
25	MG	A	1657	-	-	-	X
25	MG	A	1659	-	-	-	X
25	MG	A	1662	-	-	-	X
25	MG	A	1663	-	-	-	X
25	MG	A	1665	-	-	-	X
25	MG	A	1667	-	-	-	X
25	MG	A	1669	-	-	-	X
25	MG	A	1671	-	-	-	X
25	MG	A	1673	-	-	-	X
25	MG	A	1676	-	-	-	X
25	MG	A	1678	-	-	-	X
25	MG	A	1680	-	-	-	X
25	MG	A	1681	-	-	-	X
25	MG	A	1683	-	-	-	X
25	MG	A	1684	-	-	-	X
25	MG	A	1685	-	-	-	X
25	MG	A	1686	-	-	-	X
25	MG	A	1687	-	-	-	X
25	MG	A	1688	-	-	-	X
25	MG	A	1692	-	-	-	X
25	MG	A	1694	-	-	-	X
25	MG	A	1696	-	-	-	X
25	MG	A	1701	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1702	-	-	-	X
25	MG	A	1705	-	-	-	X
25	MG	A	1706	-	-	-	X
25	MG	A	1708	-	-	-	X
25	MG	A	1710	-	-	-	X
25	MG	A	1711	-	-	-	X
25	MG	A	1713	-	-	-	X
25	MG	A	1714	-	-	-	X
25	MG	A	1715	-	-	-	X
25	MG	A	1716	-	-	-	X
25	MG	A	1717	-	-	-	X
25	MG	A	1721	-	-	-	X
25	MG	A	1724	-	-	-	X
25	MG	A	1730	-	-	-	X
25	MG	A	1731	-	-	-	X
25	MG	A	1734	-	-	-	X
25	MG	A	1735	-	-	-	X
25	MG	A	1736	-	-	-	X
25	MG	A	1737	-	-	-	X
25	MG	A	1740	-	-	-	X
25	MG	A	1741	-	-	-	X
25	MG	A	1742	-	-	-	X
25	MG	A	1747	-	-	-	X
25	MG	A	1748	-	-	-	X
25	MG	A	1754	-	-	-	X
25	MG	A	1766	-	-	-	X
25	MG	A	1767	-	-	-	X
25	MG	A	1771	-	-	-	X
25	MG	A	1777	-	-	-	X
25	MG	A	1781	-	-	-	X
25	MG	A	1782	-	-	-	X
25	MG	A	1784	-	-	-	X
25	MG	A	1785	-	-	-	X
25	MG	A	1790	-	-	-	X
25	MG	A	1793	-	-	-	X
25	MG	A	1796	-	-	-	X
25	MG	A	1798	-	-	-	X
25	MG	A	1800	-	-	-	X
25	MG	A	1801	-	-	-	X
25	MG	A	1802	-	-	-	X
25	MG	E	201	-	-	-	X
25	MG	N	101	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
26	K	A	1808	-	-	-	X
26	K	A	1809	-	-	-	X
26	K	A	1811	-	-	-	X
26	K	A	1813	-	-	-	X
26	K	A	1814	-	-	-	X
26	K	A	1816	-	-	-	X
26	K	A	1817	-	-	-	X
26	K	A	1818	-	-	-	X
26	K	A	1822	-	-	-	X
26	K	A	1825	-	-	-	X
26	K	A	1828	-	-	-	X
26	K	A	1829	-	-	-	X
26	K	A	1831	-	-	-	X

2 Entry composition [i](#)

There are 27 unique types of molecules in this entry. The entry contains 52363 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1512	Total	C	N	O	P	0	0	0
			32489	14462	6011	10505	1511			

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	235	Total	C	N	O	S	0	0	1
			1901	1213	342	341	5			

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	207	Total	C	N	O	S	0	0	1
			1613	1016	315	281	1			

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	151	Total	C	N	O	S	0	0	1
			1147	724	218	201	4			

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

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

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	99	Total	C	N	O	S	0	0	1
			793	498	157	137	1			

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	125	Total	C	N	O	S	0	0	1
			971	611	196	163	1			

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14.

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

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	84	Total	C	N	O	S	0	0	1
			701	443	140	117	1			

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	104	Total	C	N	O	S	0	0	0
			857	547	160	148	2			

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	1
			648	414	120	112	2			

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	25	Total	C	N	O	0	0	1
			209	128	51	30			

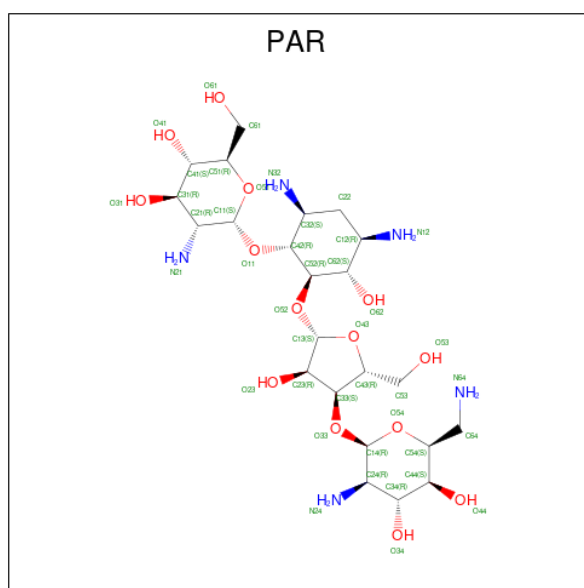
- Molecule 22 is a RNA chain called 5'-R(*GP*UP*UP*AP*AP*AP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	X	5	Total	C	N	O	P	0	0	0
			104	48	19	33	4			

- Molecule 23 is a RNA chain called 5'-R(*CP*CP*UP*CP*CP*CP*UP*CM0P*AP*CP*6MZP*AP*GP*GP*AP*GP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	Y	11	Total	C	N	O	P	0	0	0
			235	107	41	77	10			

- Molecule 24 is PAROMOMYCIN (CCD ID: PAR) (formula: C₂₃H₄₅N₅O₁₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	A	1	Total	C	N	O	0	0
			42	23	5	14		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	203	Total	Mg	0	0
			203	203		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	B	1	Total 1	Mg 1	0	0
25	D	1	Total 1	Mg 1	0	0
25	E	2	Total 2	Mg 2	0	0
25	F	1	Total 1	Mg 1	0	0
25	G	1	Total 1	Mg 1	0	0
25	H	1	Total 1	Mg 1	0	0
25	I	1	Total 1	Mg 1	0	0
25	M	1	Total 1	Mg 1	0	0
25	N	1	Total 1	Mg 1	0	0
25	Q	3	Total 3	Mg 3	0	0
25	S	1	Total 1	Mg 1	0	0
25	X	1	Total 1	Mg 1	0	0

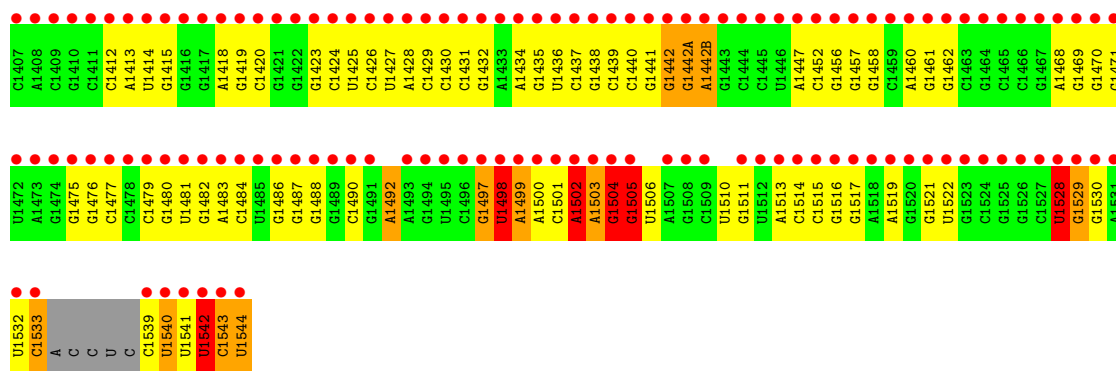
- Molecule 26 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	A	34	Total 34	K 34	0	0
26	E	1	Total 1	K 1	0	0

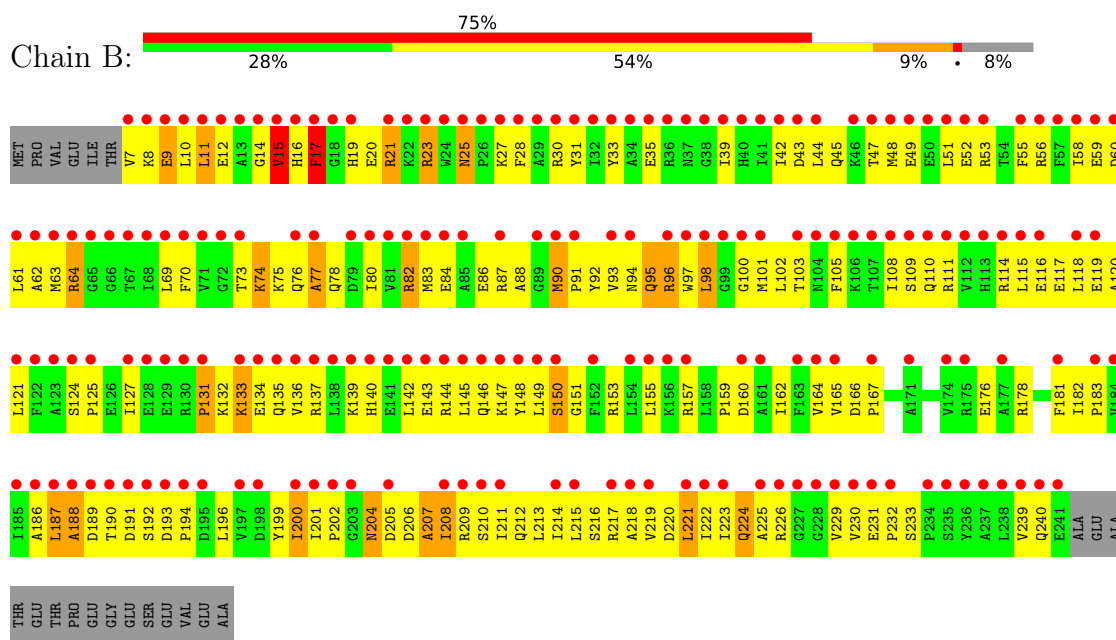
- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
27	D	1	Total 1	Zn 1	0	0
27	N	1	Total 1	Zn 1	0	0

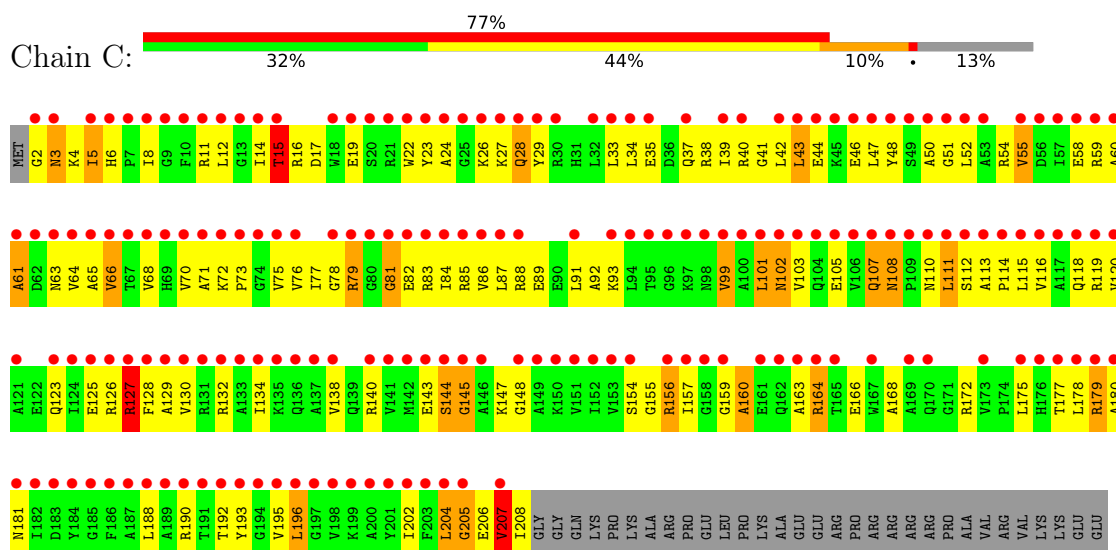
G1347	A1287	A1227	G1166	G1106	A1046	C991	U871	U804	C744	A684	C624
U1348	A1288	C1228	A1168	C1107	G1047	C992	A872	C805	C745	G685	G625
A1349	A1289	A1229	A1169	G1108	U1048	G993	A873	C806	A746	U686	U626
A1350	G1290	C1230	A1170	C1109	U1049	G994	G874	A807	C747	A687	G627
U1351	G1291	G1231	G1171	A1110	C1050	C995	A875	G808	C748	G688	G628
C1352	U1292	U1232	G1172	C1111	G1051	A996	G876	G809	C749	C689	G629
G1353	G1293	G1233	G1173	C1112	U1052	U997	C877	C810	G750	G690	G630
C1354	G1294	U1234	G1174	C1113	U1053	G998	C878	C811	U751	G691	G631
G1355	G1295	U1235	G1175	C1114	C1054	C999	C879	C812	G752	U692	A632
A1356	C1296	A1236	C1115	C1115	U1055	C900	G880	U813	A753	G693	G633
G1357	C1297	C1237	A1176	C1116	U1056	G941	G881	U814	C754	A694	C634
U1358	A1298	A1238	G1178	G1117	G1057	G942	C882	A815	G755	A695	G635
C1359	C1299	U1239	A1179	C1118	U1058	U943	C883	A816	C756	U696	U636
A1360	A1300	U1240	A1180	C1119	C1059	G944	U884	C817	U757	G697	G637
G1361	U1301	G1241	G1181	G1120	U1060	G945	G885	G818	G758	G698	G638
C1362	G1302	C1242	G1182	U1121	G1061	A946	A879	A819	A759	C699	G639
C1363	C1303	C1243	A1183	G1122	U1062	G947	G887	U820	G760	U700	A640
A1363A	G1304	C1244	G1184	A1123	C1063	C948	G888	G821	G761	C701	U641
U1364	G1305	A1245	G1185	G1124	U1064	A949	A889	C822	C762	A702	A642
G1365	A1306	G1246	G1186	U1125	C1065	U950	G890	G823	G763	G703	C643
C1366	U1307	U1247	G1187	U1126	U1066	G951	G891	G824	C764	A704	G644
G1367	U1308	A1248	A1188	G1127	A1067	U952	A892	G825	G765	U705	G645
C1368	G1309	C1249	C1189	G1128	U1068	G953	C893	C826	A766	A706	U646
U1369	C1310	A1250	G1190	C1129	C1069	G954	G894	U827	A767	C707	C647
G1370	G1311	A1251	A1191	A1130	U1070	U955	G895	A828	A768	C708	A648
C1371	G1312	C1252	C1192	G1131	C1071	U956	C896	C829	G769	G709	G649
U1372	U1313	G1253	G1193	C1132	U1072	U957	G897	G830	C770	G710	G650
G1373	C1314	C1254	U1194	G1133	U1073	A958	G898	U831	G771	G711	C651
A1374	U1315	G1255	G1195	G1134	G1074	C1018	C899	C832	U772	A712	U652
C1375	G1316	A1256	U1196	U1135	C1075	U960	A900	U833	G773	C713	A653
U1376	C1317	U1257	U1197	U1136	G1076	U961	A901	C834	G774	G714	G654
A1377	G1318	G1258	G1198	C1137	U1077	C962	G902	U835	G775	A715	A655
C1378	A1319	C1259	U1199	G1138	U1078	G963	G903	G836	A776	G716	C656
G1379	C1320	C1260	C1200	G1139	G1079	A964	C904	G837	A777	C717	G657
U1380	C1321	A1261	A1201	C1140	A1080	A965	U905	U838	C778	G718	G658
C1381	C1322	C1262	G1202	G1141	U1081	G966	A907	C840	A780	C719	G659
C1382	G1323	C1263	C1203	G1142	G1082	C967	G908	U841	U781	G721	G661
A1383	A1324	G1264	A1204	G1143	U1083	A968	A909	C849	A782	A722	A663
C1384	C1325	U1265	U1205	C1144	U1084	A969	C910	U850	C783	U723	G664
G1385	G1326	G1266	G1206	G1145	U1085	G971	U911	G851	G784	G724	A665
C1386	C1327	C1267	G1207	C1146	G1086	C972	C912	G852	G785	C725	G666
G1387	G1328	A1268	C1208	A1147	G1087	G973	A913	G853	G786	G726	G667
C1388	A1329	C1269	C1209	U1148	G1088	A974	A914	G854	A787	G727	G668
U1389	U1330	G1270	C1210	C1149	U1089	A975	A915	G855	U788	A728	G669
A1390	C1331	U1271	U1211	U1150	U1090	G976	G916	U858	A789	A729	U670
U1391	A1332	G1272	U1212	A1151	A1091	A977	G917	G859	G791	G731	G671
C1392	A1333	G1273	A1213	C1152	A1092	A978	A918	A860	A792	C732	U672
U1393	G1334	G1274	C1153	G1154	G1093	C979	U920	G861	U793	A733	G673
A1394	C1335	A1275	G1215	G1155	U1095	C980	U921	C862	A794	G734	G674
C1395	G1336	G1276	G1216	G1156	C1096	U981	U922	U863	C795	G735	A675
A1396	G1337	C1277	C1217	G1157	C1097	U982	G923	U864	C796	C736	U676
C1397	U1338	U1278	C1218	A1157	G1098	A983	A924	A865	G797	A737	U677
A1398	A1339	A1279	U1219	C1158	G1099	C984	G925	A866	G798	G738	U678
G1401	C1340	U1281	G1221	G1159	U1100	U985	G926	A867	G799	C739	C679
C1402	C1341	G1282	C1161	C1160	A1101	A986	C927	G868	G800	U740	G680
C1403	G1343	G1283	C1162	A1102	A1102	G987	G928	C869	U801	G741	G681
G1404	C1344	G1284	C1163	G1103	C1043	C988	G929	G870	A802	G742	G682
U1405	U1345	A1285	A1164	G1104	C1044	C989	G930	U870	G803	U743	G683
A1406	A1346	C1226	C1165	A1105	C1045	C990					



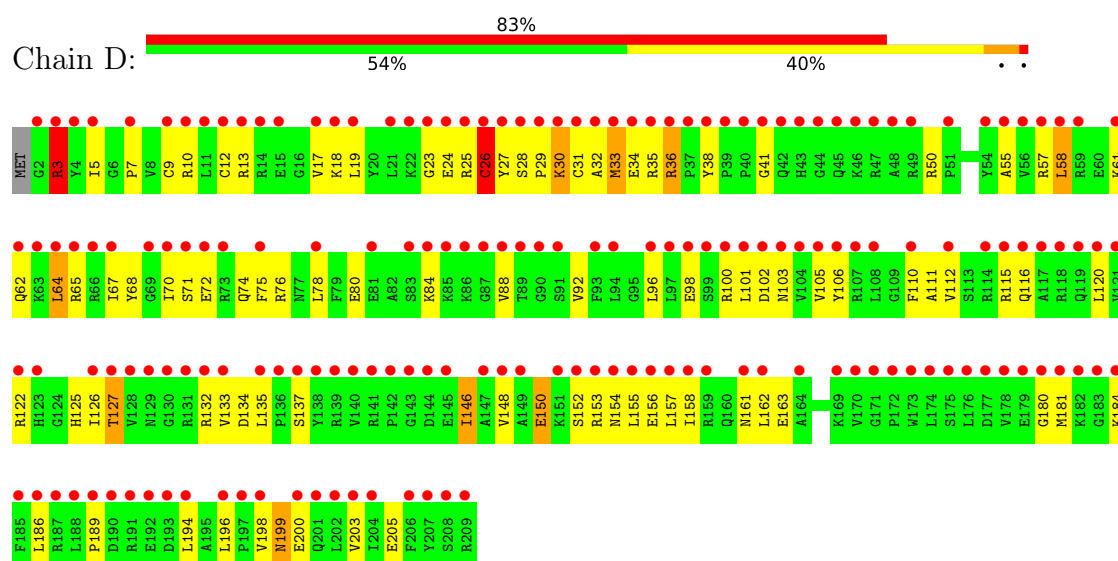
• Molecule 2: 30S RIBOSOMAL PROTEIN S2



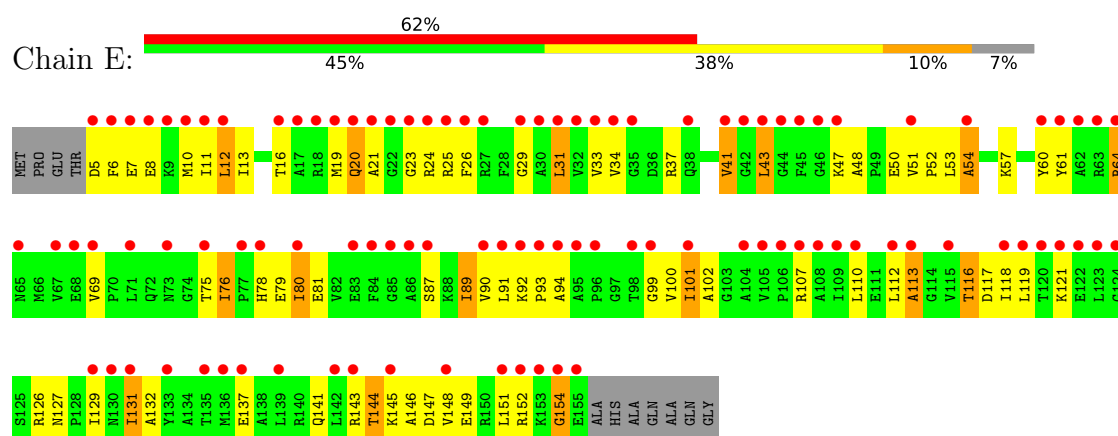
• Molecule 3: 30S RIBOSOMAL PROTEIN S3



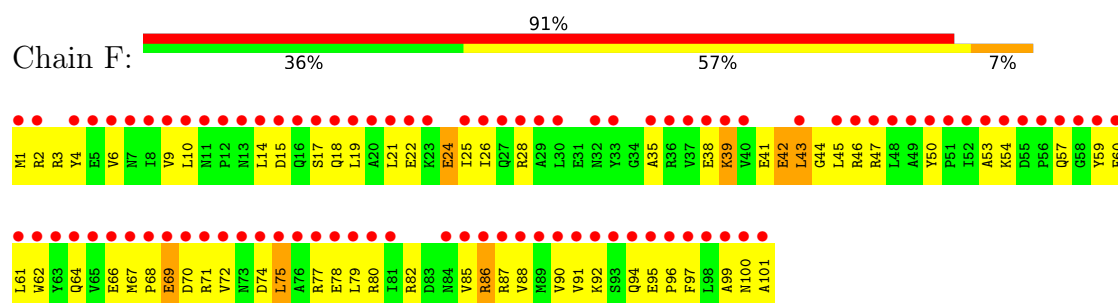
• Molecule 4: 30S RIBOSOMAL PROTEIN S4



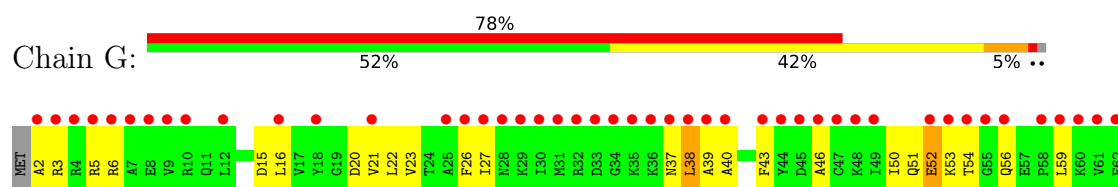
• Molecule 5: 30S RIBOSOMAL PROTEIN S5

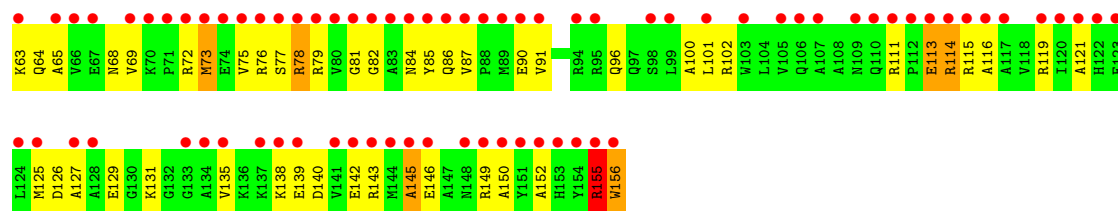


• Molecule 6: 30S RIBOSOMAL PROTEIN S6

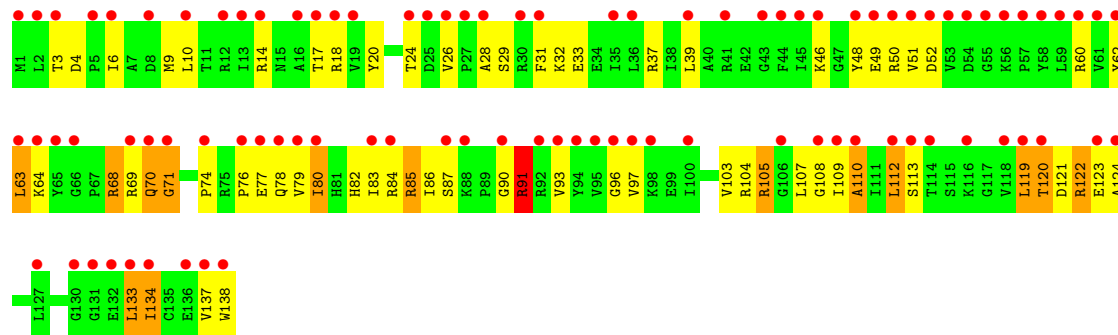


• Molecule 7: 30S RIBOSOMAL PROTEIN S7

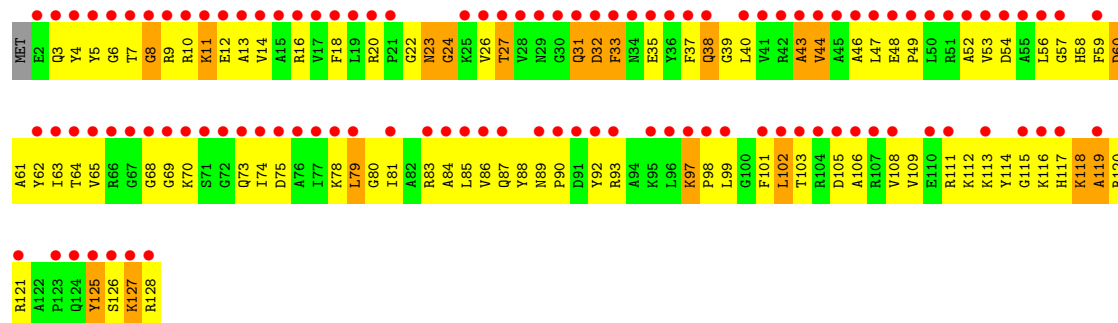
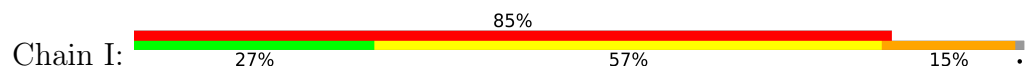




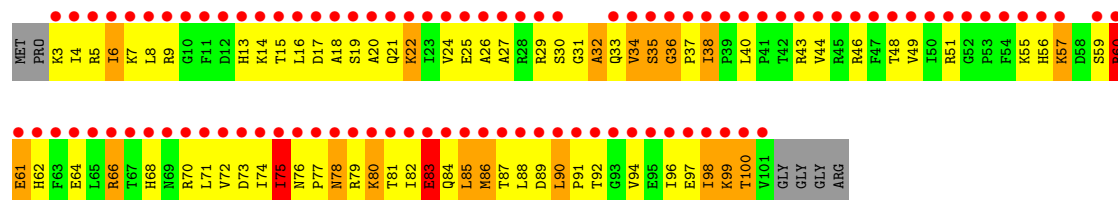
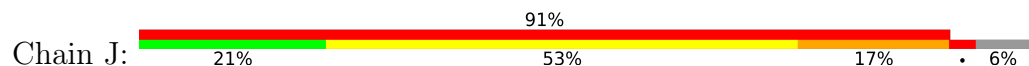
• Molecule 8: 30S RIBOSOMAL PROTEIN S8



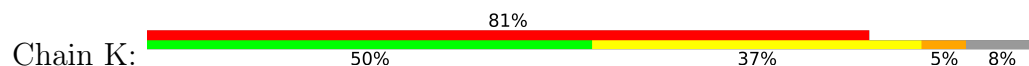
• Molecule 9: 30S RIBOSOMAL PROTEIN S9

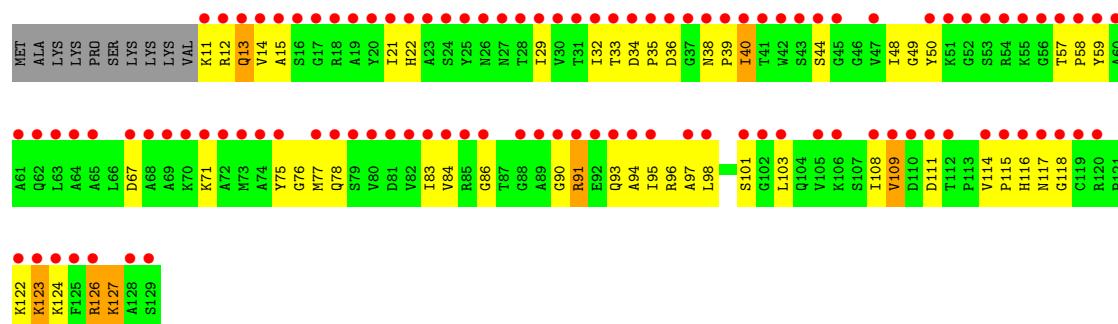


• Molecule 10: 30S RIBOSOMAL PROTEIN S10

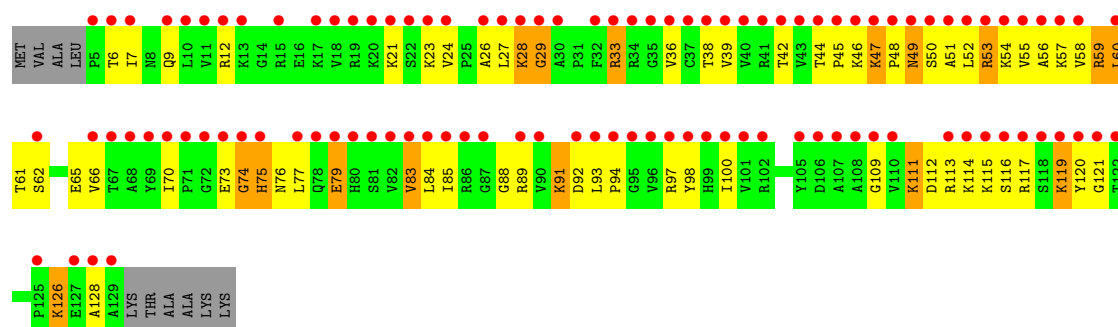
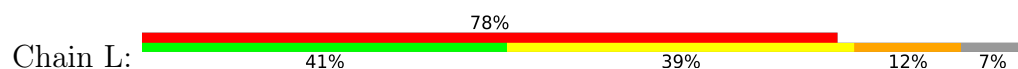


• Molecule 11: 30S RIBOSOMAL PROTEIN S11

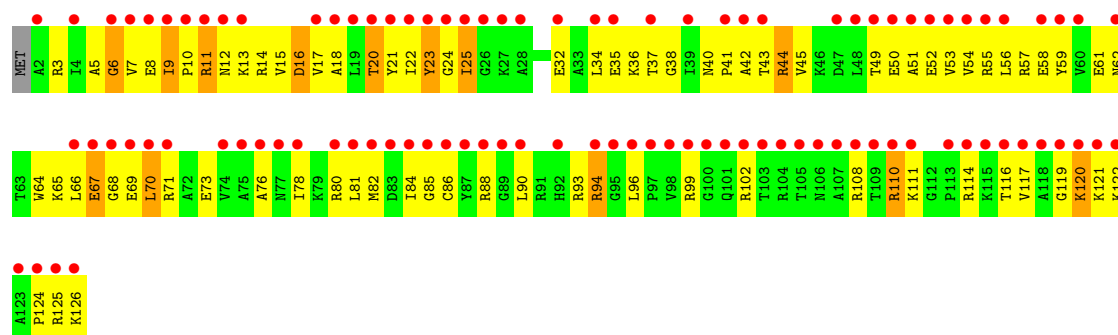
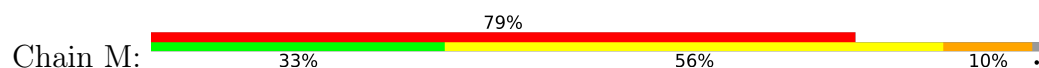




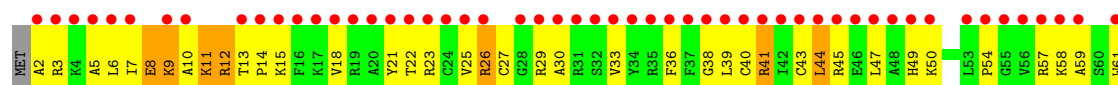
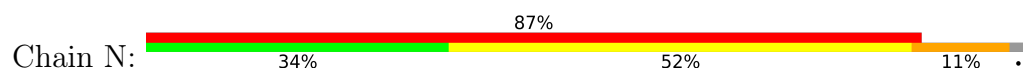
● Molecule 12: 30S RIBOSOMAL PROTEIN S12



● Molecule 13: 30S RIBOSOMAL PROTEIN S13

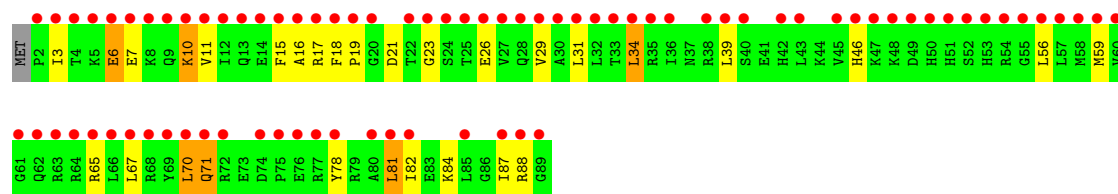


● Molecule 14: 30S RIBOSOMAL PROTEIN S14

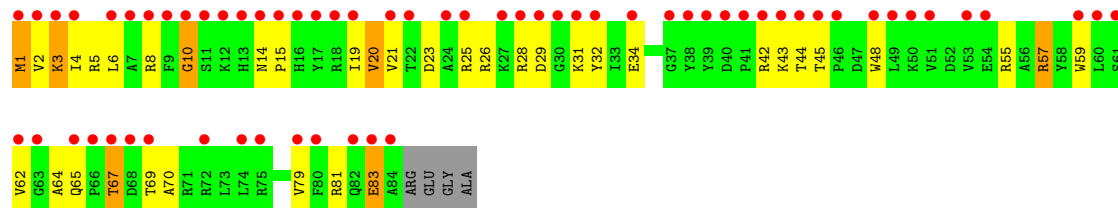


● Molecule 15: 30S RIBOSOMAL PROTEIN S15

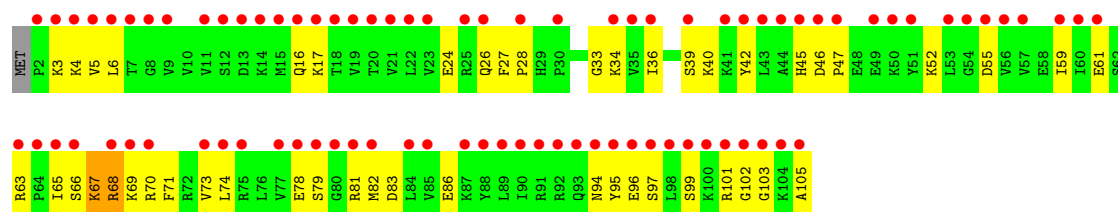
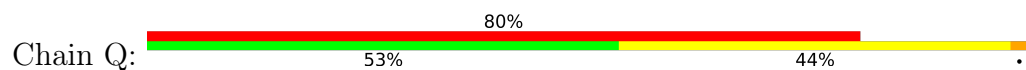




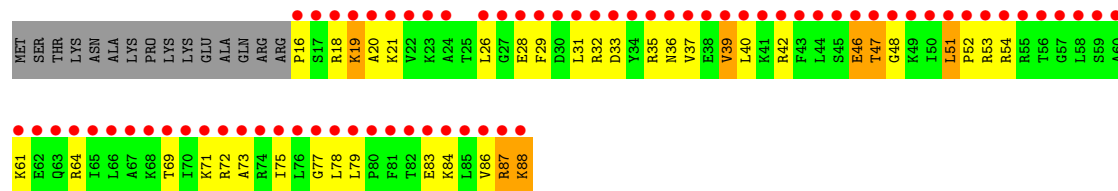
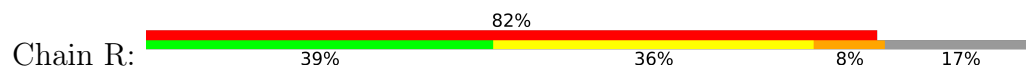
• Molecule 16: 30S RIBOSOMAL PROTEIN S16



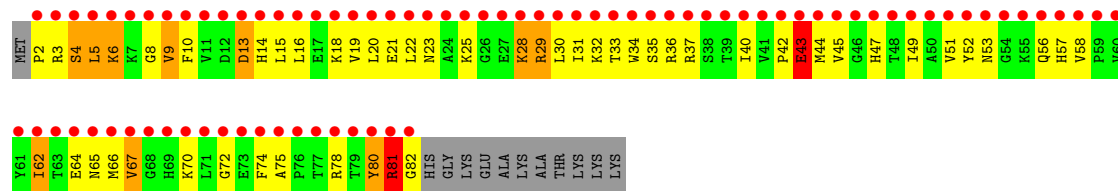
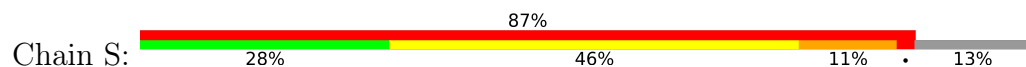
• Molecule 17: 30S RIBOSOMAL PROTEIN S17



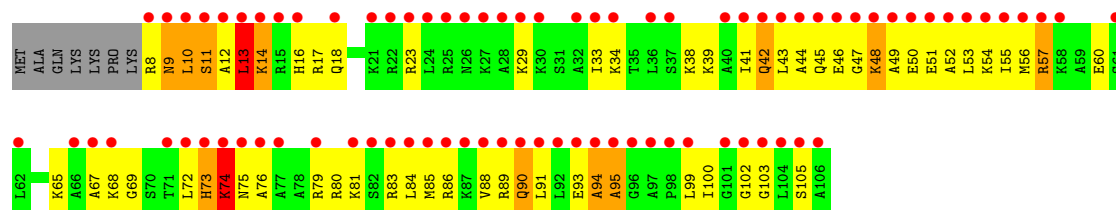
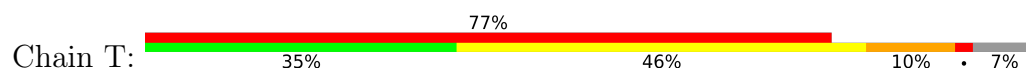
• Molecule 18: 30S RIBOSOMAL PROTEIN S18



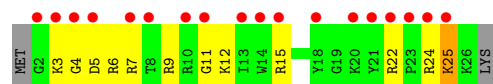
• Molecule 19: 30S RIBOSOMAL PROTEIN S19



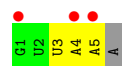
• Molecule 20: 30S RIBOSOMAL PROTEIN S20



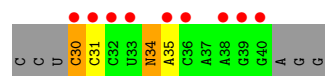
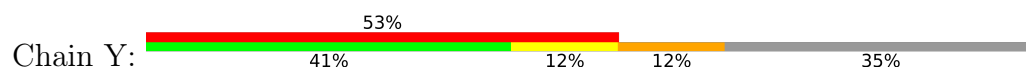
• Molecule 21: 30S RIBOSOMAL PROTEIN THX



• Molecule 22: 5'-R(*GP*UP*UP*AP*AP*AP)-3'



• Molecule 23: 5'-R(*CP*CP*UP*CP*CP*CP*UP*CM0P*AP*CP*6MZP*AP *GP*GP*AP*GP*G)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	400.44Å 400.44Å 173.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.99 – 2.80 29.99 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.99-2.80) 97.5 (29.99-2.80)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.45Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.219 , 0.243 0.439 , 0.440	Depositor DCC
R_{free} test set	24813 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	51.4	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.71	EDS
Total number of atoms	52363	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.77% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PAR, K, 6MZ, ZN, MG, CM0

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.47	1/36365 (0.0%)	0.67	65/56754 (0.1%)
2	B	0.45	1/1936 (0.1%)	1.04	9/2611 (0.3%)
3	C	0.47	1/1637 (0.1%)	0.98	8/2207 (0.4%)
4	D	0.46	0/1733	0.97	5/2318 (0.2%)
5	E	0.58	1/1163 (0.1%)	1.09	7/1566 (0.4%)
6	F	0.38	0/856	0.90	1/1154 (0.1%)
7	G	0.45	0/1276	0.93	2/1709 (0.1%)
8	H	0.57	0/1136	1.16	11/1527 (0.7%)
9	I	0.42	0/1029	1.01	3/1379 (0.2%)
10	J	0.48	1/806 (0.1%)	0.99	3/1084 (0.3%)
11	K	0.51	0/900	1.08	5/1213 (0.4%)
12	L	0.56	1/987 (0.1%)	1.24	10/1322 (0.8%)
13	M	0.44	0/1008	0.93	2/1347 (0.1%)
14	N	0.45	0/501	0.90	1/664 (0.2%)
15	O	0.44	0/745	0.85	0/992
16	P	0.56	1/717 (0.1%)	1.02	3/965 (0.3%)
17	Q	0.53	0/870	1.12	3/1159 (0.3%)
18	R	0.43	0/604	1.01	4/801 (0.5%)
19	S	0.44	1/662 (0.2%)	1.06	3/892 (0.3%)
20	T	0.55	0/765	1.12	4/1007 (0.4%)
21	U	0.64	1/213 (0.5%)	0.85	0/279
22	X	0.51	0/116	0.76	0/179
23	Y	0.46	0/206	0.81	1/314 (0.3%)
All	All	0.48	9/56231 (0.0%)	0.80	150/83443 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	2	34

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1540	U	O3'-P	-9.56	1.46	1.61
3	C	207	VAL	C-N	-5.89	1.25	1.33
10	J	100	THR	C-N	-5.66	1.25	1.33
2	B	240	GLN	C-N	-5.50	1.25	1.33
12	L	128	ALA	C-N	-5.46	1.25	1.33
19	S	81	ARG	C-N	-5.42	1.25	1.33
21	U	25	LYS	C-N	-5.14	1.26	1.33
16	P	83	GLU	C-N	-5.14	1.26	1.33
5	E	154	GLY	C-N	-5.02	1.26	1.33

All (150) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	U	C2'-C3'-O3'	14.97	131.96	109.50
1	A	1503	A	C2'-C3'-O3'	13.84	130.27	109.50
1	A	484	G	C2'-C3'-O3'	13.32	129.47	109.50
1	A	366	C	C2'-C3'-O3'	13.26	129.38	109.50
1	A	115	G	C2'-C3'-O3'	13.13	129.19	109.50
1	A	181	G	C2'-C3'-O3'	13.08	129.12	109.50
1	A	243	A	C2'-C3'-O3'	13.02	129.02	109.50
1	A	575	G	C2'-C3'-O3'	12.72	128.59	109.50
1	A	559	A	C2'-C3'-O3'	12.37	128.05	109.50
20	T	13	LEU	N-CA-C	-12.28	97.82	112.92
1	A	812	C	C2'-C3'-O3'	12.05	127.58	109.50
1	A	372	C	C2'-C3'-O3'	11.53	126.80	109.50
1	A	60	A	C2'-C3'-O3'	11.33	126.50	109.50
1	A	687	A	C2'-C3'-O3'	11.33	126.50	109.50
12	L	26	ALA	N-CA-C	-10.90	96.62	111.55
1	A	965	A	C2'-C3'-O3'	10.69	125.53	109.50
20	T	75	ASN	N-CA-C	-10.41	100.59	113.18
1	A	266	G	C2'-C3'-O3'	10.40	125.10	109.50
1	A	533	A	C2'-C3'-O3'	10.06	124.59	109.50
12	L	119	LYS	N-CA-C	-10.00	95.72	110.52
1	A	1067	A	C2'-C3'-O3'	9.80	124.20	109.50
8	H	79	VAL	N-CA-C	-9.70	101.41	110.82
1	A	428	G	C2'-C3'-O3'	9.49	123.73	109.50
9	I	60	ASP	N-CA-C	-9.25	94.92	109.72
1	A	812	C	C4'-C3'-O3'	9.08	123.02	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	366	C	C4'-C3'-O3'	8.75	122.52	109.40
1	A	1503	A	C4'-C3'-O3'	8.73	122.50	109.40
1	A	748	C	C2'-C3'-O3'	8.71	122.57	109.50
4	D	33	MET	N-CA-C	-8.70	102.84	113.19
3	C	205	GLY	N-CA-C	8.44	122.78	111.72
8	H	134	ILE	N-CA-C	8.38	118.46	110.42
1	A	559	A	C4'-C3'-O3'	8.32	121.89	109.40
20	T	14	LYS	N-CA-C	-8.30	102.19	111.82
12	L	29	GLY	N-CA-C	-8.24	101.66	114.10
1	A	1299	A	N9-C1'-C2'	7.90	123.85	112.00
1	A	1301	U	C2'-C3'-O3'	7.86	121.28	109.50
11	K	116	HIS	N-CA-C	-7.80	102.11	112.72
1	A	243	A	C4'-C3'-O3'	7.75	121.02	109.40
9	I	39	GLY	N-CA-C	-7.69	103.88	114.64
1	A	687	A	C4'-C3'-O3'	7.52	120.68	109.40
1	A	1505	G	C2'-C3'-O3'	7.50	124.95	113.70
19	S	80	TYR	N-CA-C	7.50	121.62	109.40
11	K	91	ARG	N-CA-C	-7.49	102.48	111.69
1	A	181	G	C4'-C3'-O3'	7.48	120.62	109.40
1	A	484	G	C4'-C3'-O3'	7.37	120.45	109.40
1	A	281	G	C2'-C3'-O3'	7.35	120.53	109.50
4	D	26	CYS	N-CA-C	-7.32	104.80	113.21
18	R	47	THR	N-CA-C	-7.28	100.31	110.35
1	A	1281	U	C2'-C3'-O3'	7.25	120.38	109.50
1	A	60	A	C4'-C3'-O3'	7.18	120.17	109.40
3	C	130	VAL	N-CA-C	7.16	117.24	110.30
1	A	509	A	C2'-C3'-O3'	7.13	124.40	113.70
12	L	88	GLY	N-CA-C	-7.03	96.53	113.18
1	A	1528	U	C2'-C3'-O3'	7.01	120.01	109.50
12	L	23	LYS	N-CA-C	-6.96	104.67	113.02
1	A	1285	A	C2'-C3'-O3'	6.94	119.92	109.50
8	H	120	THR	N-CA-C	-6.85	101.48	110.53
17	Q	79	SER	N-CA-C	6.76	116.96	108.45
13	M	25	ILE	N-CA-C	6.75	117.58	107.80
5	E	26	PHE	N-CA-C	6.66	120.38	110.52
2	B	133	LYS	N-CA-C	-6.64	105.24	113.15
2	B	90	MET	N-CA-C	6.45	118.02	109.83
1	A	115	G	C4'-C3'-O3'	6.44	119.06	109.40
18	R	51	LEU	CA-C-N	6.42	126.38	120.21
18	R	51	LEU	C-N-CA	6.42	126.38	120.21
5	E	23	GLY	N-CA-C	6.42	119.49	110.38
17	Q	67	LYS	N-CA-C	-6.40	102.05	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	69	VAL	N-CA-C	6.33	114.15	107.76
7	G	87	VAL	N-CA-C	6.31	114.13	107.76
1	A	1129	C	C2'-C3'-O3'	6.31	118.96	109.50
11	K	40	ILE	N-CA-C	-6.28	106.41	111.81
10	J	75	ILE	N-CA-C	6.25	122.33	109.34
13	M	11	ARG	N-CA-C	6.19	117.91	108.07
16	P	20	VAL	N-CA-C	6.16	119.11	108.95
23	Y	30	C	N1-C1'-C2'	6.15	121.23	112.00
1	A	250	A	C2'-C3'-O3'	6.15	118.72	109.50
8	H	96	GLY	N-CA-C	-6.11	104.40	112.82
3	C	66	VAL	N-CA-C	6.09	112.72	106.21
1	A	993	G	N9-C1'-C2'	6.08	123.13	114.00
20	T	74	LYS	N-CA-C	6.08	123.74	110.80
5	E	48	ALA	N-CA-C	6.05	113.57	108.13
7	G	85	TYR	N-CA-C	6.05	118.81	109.07
2	B	17	PHE	N-CA-C	6.02	123.62	110.80
1	A	344	A	C2'-C3'-O3'	6.00	118.50	109.50
1	A	1544	U	C2'-C3'-O3'	-5.98	100.53	109.50
3	C	111	LEU	N-CA-C	-5.96	104.54	112.94
8	H	28	ALA	N-CA-C	5.95	118.89	110.50
5	E	54	ALA	N-CA-C	-5.92	104.75	111.14
10	J	66	ARG	N-CA-C	5.90	117.90	108.41
1	A	1498	U	C4'-C3'-O3'	5.89	118.24	109.40
8	H	80	ILE	CB-CA-C	-5.88	106.64	113.22
1	A	1502	A	N9-C1'-C2'	5.87	122.81	114.00
14	N	38	GLY	N-CA-C	-5.87	107.56	115.36
8	H	84	ARG	N-CA-C	5.86	118.67	108.76
1	A	119	A	C2'-C3'-O3'	5.86	118.29	109.50
12	L	60	LEU	N-CA-C	5.85	119.14	110.48
2	B	186	ALA	N-CA-C	5.85	117.41	108.52
11	K	126	ARG	N-CA-C	5.84	118.76	109.24
1	A	701	C	C2'-C3'-O3'	5.83	118.24	109.50
2	B	77	ALA	N-CA-C	-5.78	106.09	114.12
1	A	328	C	N1-C1'-C2'	5.74	122.61	114.00
3	C	99	VAL	N-CA-C	5.73	118.09	108.81
8	H	68	ARG	N-CA-C	-5.70	102.97	110.43
1	A	129(A)	G	C2'-C3'-O3'	5.69	118.04	109.50
11	K	50	TYR	N-CA-C	5.69	118.26	110.24
5	E	113	ALA	N-CA-C	-5.68	106.31	113.18
16	P	3	LYS	N-CA-C	5.67	118.31	109.52
16	P	19	ILE	N-CA-C	-5.66	101.37	108.84
1	A	1200	C	C2'-C3'-O3'	-5.64	105.25	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1201	A	C2'-C3'-O3'	5.63	117.95	109.50
10	J	60	ARG	N-CA-C	5.59	122.70	110.80
2	B	64	ARG	N-CA-C	-5.55	105.86	113.30
1	A	1331	G	C2'-C3'-O3'	5.53	117.80	109.50
1	A	533	A	C4'-C3'-O3'	5.52	117.67	109.40
8	H	69	ARG	N-CA-C	5.50	117.61	109.69
18	R	46	GLU	N-CA-C	-5.45	105.34	111.28
2	B	200	ILE	N-CA-C	5.44	116.82	108.71
12	L	49	ASN	N-CA-C	5.44	118.85	110.42
2	B	110	GLN	N-CA-C	-5.43	105.76	112.38
4	D	72	GLU	N-CA-C	-5.41	105.55	111.82
19	S	4	SER	N-CA-C	5.40	117.18	109.14
3	C	145	GLY	N-CA-C	5.38	123.05	115.30
19	S	14	HIS	N-CA-C	-5.37	105.12	110.97
3	C	5	ILE	CB-CA-C	-5.35	103.89	111.28
9	I	63	ILE	N-CA-C	5.34	116.42	108.46
6	F	60	PHE	N-CA-C	5.32	118.49	109.76
2	B	188	ALA	N-CA-C	5.32	118.15	109.59
1	A	1279	A	N9-C1'-C2'	5.30	119.95	112.00
1	A	1504	G	O4'-C1'-C2'	5.30	111.10	105.80
8	H	110	ALA	N-CA-C	-5.29	101.03	109.23
1	A	1542	U	C5'-C4'-C3'	-5.28	108.08	116.00
1	A	63	C	C5'-C4'-C3'	-5.24	108.13	116.00
1	A	1299	A	C4'-C3'-O3'	-5.24	105.14	113.00
1	A	410	G	C2'-C3'-O3'	5.22	121.54	113.70
1	A	1182	G	C2'-C3'-O3'	5.22	117.32	109.50
4	D	163	GLU	N-CA-C	-5.21	105.50	111.07
4	D	29	PRO	N-CA-C	-5.19	105.47	112.48
12	L	83	VAL	N-CA-C	5.19	115.66	108.23
3	C	33	LEU	N-CA-C	-5.18	104.65	111.96
1	A	960	U	C4'-C3'-O3'	5.17	117.16	109.40
8	H	71	GLY	N-CA-C	5.11	122.76	112.34
1	A	1049	U	C2'-C3'-O3'	5.11	117.16	109.50
1	A	992	U	C2'-C3'-O3'	5.07	117.11	109.50
12	L	61	THR	N-CA-C	-5.07	106.36	112.54
1	A	1190	G	C4'-C3'-O3'	-5.06	105.41	113.00
1	A	993	G	C2'-C3'-O3'	5.05	117.08	109.50
1	A	353	A	C5'-C4'-O4'	-5.05	102.23	109.80
12	L	42	THR	N-CA-C	-5.02	101.45	109.23
5	E	102	ALA	N-CA-C	5.01	116.46	108.79
17	Q	83	ASP	N-CA-C	-5.01	105.89	111.36

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	366	C	C3'
1	A	1503	A	C3'

All (34) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1049	U	Sidechain
1	A	1067	A	Sidechain
1	A	107	G	Sidechain
1	A	1077	G	Sidechain
1	A	1078	U	Sidechain
1	A	1085	U	Sidechain
1	A	1196	U	Sidechain
1	A	1299	A	Sidechain
1	A	1380	U	Sidechain
1	A	145	G	Sidechain
1	A	1490	C	Sidechain
1	A	195	A	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	297	G	Sidechain
1	A	362	G	Sidechain
1	A	380	G	Sidechain
1	A	387	U	Sidechain
1	A	528	C	Sidechain
1	A	536	C	Sidechain
1	A	575	G	Sidechain
1	A	587	G	Sidechain
1	A	639	G	Sidechain
1	A	652	U	Sidechain
1	A	664	G	Sidechain
1	A	691	G	Sidechain
1	A	727	G	Sidechain
1	A	760	G	Sidechain
1	A	879	C	Sidechain
1	A	884	U	Sidechain
1	A	898	G	Sidechain
1	A	940	C	Sidechain
1	A	993	G	Sidechain

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	A	32489	0	16399	795	0
2	B	1901	0	1951	219	0
3	C	1613	0	1677	163	0
4	D	1703	0	1765	116	0
5	E	1147	0	1207	75	0
6	F	843	0	857	67	0
7	G	1257	0	1296	99	0
8	H	1116	0	1177	61	0
9	I	1010	0	1036	109	0
10	J	793	0	835	142	0
11	K	885	0	904	51	0
12	L	971	0	1057	80	0
13	M	997	0	1072	90	0
14	N	492	0	530	60	0
15	O	734	0	771	38	0
16	P	701	0	720	45	0
17	Q	857	0	928	53	0
18	R	598	0	670	49	0
19	S	648	0	673	65	0
20	T	763	0	861	71	0
21	U	209	0	221	17	0
22	X	104	0	55	4	0
23	Y	235	0	124	7	0
24	A	42	0	45	1	0
25	A	203	0	0	0	0
25	B	1	0	0	0	0
25	D	1	0	0	0	0
25	E	2	0	0	0	0
25	F	1	0	0	0	0
25	G	1	0	0	0	0
25	H	1	0	0	0	0
25	I	1	0	0	0	0
25	M	1	0	0	0	0
25	N	1	0	0	0	0
25	Q	3	0	0	0	0
25	S	1	0	0	0	0
25	X	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	A	34	0	0	0	0
26	E	1	0	0	0	0
27	D	1	0	0	0	0
27	N	1	0	0	1	0
All	All	52363	0	36831	2241	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 (2241) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1539:C:O5'	7:G:82:GLY:CA	1.86	1.22
1:A:1532:U:C2'	1:A:1533:C:H5''	1.68	1.22
1:A:402:G:H2'	1:A:403:C:H5''	1.20	1.18
10:J:99:LYS:HD3	10:J:100:THR:H	1.06	1.18
1:A:1539:C:O5'	7:G:82:GLY:HA2	1.42	1.15
1:A:243:A:H4'	1:A:244:U:H5'	1.19	1.14
1:A:1532:U:H2'	1:A:1533:C:C5'	1.78	1.12
1:A:1539:C:C4'	7:G:82:GLY:HA2	1.80	1.12
3:C:50:ALA:HB1	3:C:70:VAL:HG11	1.27	1.11
12:L:60:LEU:HD11	12:L:85:ILE:HD12	1.32	1.09
2:B:142:LEU:HG	2:B:146:GLN:HE21	1.18	1.07
7:G:73:MET:HE2	7:G:90:GLU:HA	1.32	1.06
3:C:14:ILE:HG22	3:C:15:THR:H	1.17	1.06
10:J:32:ALA:HB1	10:J:75:ILE:HG13	1.38	1.06
18:R:19:LYS:HG3	18:R:20:ALA:H	1.18	1.05
1:A:1532:U:H2'	1:A:1533:C:H5''	1.09	1.05
1:A:1539:C:C5'	7:G:82:GLY:HA2	1.88	1.03
19:S:33:THR:HG22	19:S:35:SER:H	1.24	1.03
20:T:73:HIS:O	20:T:74:LYS:HB2	1.59	1.03
1:A:1539:C:O4'	7:G:82:GLY:HA2	1.56	1.03
1:A:402:G:C2'	1:A:403:C:H5''	1.89	1.01
15:O:87:ILE:HG22	15:O:88:ARG:H	1.19	1.01
3:C:70:VAL:HG12	3:C:72:LYS:H	1.22	1.00
7:G:75:VAL:HG21	7:G:86:GLN:HB3	1.44	1.00
10:J:4:ILE:HD11	10:J:74:ILE:HD12	1.41	1.00
1:A:1539:C:C4'	7:G:82:GLY:CA	2.41	0.99
12:L:27:LEU:O	12:L:29:GLY:N	1.96	0.98
10:J:4:ILE:HA	10:J:100:THR:HA	1.43	0.97
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.46	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:97:LYS:HA	9:I:102:LEU:HD21	1.48	0.95
19:S:36:ARG:HH21	19:S:53:ASN:HA	1.32	0.95
20:T:50:GLU:HA	20:T:100:ILE:HG22	1.49	0.94
2:B:118:LEU:HD22	2:B:142:LEU:HD13	1.51	0.93
5:E:144:THR:HG22	5:E:147:ASP:H	1.31	0.93
5:E:50:GLU:HG3	5:E:52:PRO:HD2	1.49	0.93
1:A:1060:C:C5	3:C:2:GLY:HA3	2.05	0.92
2:B:17:PHE:HB3	2:B:44:LEU:HD21	1.48	0.91
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.52	0.91
1:A:1125:U:H3	10:J:5:ARG:HH21	1.11	0.91
13:M:49:THR:HG22	13:M:51:ALA:H	1.32	0.91
8:H:120:THR:OG1	8:H:123:GLU:HG3	1.71	0.91
1:A:1152:A:H5''	10:J:13:HIS:CD2	2.06	0.91
1:A:1086:U:H3	1:A:1099:G:H22	1.15	0.90
5:E:8:GLU:HB3	5:E:34:VAL:HG23	1.52	0.90
10:J:37:PRO:HA	10:J:72:VAL:HG22	1.53	0.90
13:M:3:ARG:HD3	13:M:9:ILE:HG23	1.50	0.90
1:A:371:G:O2'	1:A:372:C:H5'	1.70	0.90
2:B:111:ARG:HB3	2:B:149:LEU:HD11	1.51	0.90
3:C:64:VAL:HB	3:C:99:VAL:HG21	1.51	0.90
3:C:126:ARG:HA	3:C:127:ARG:HH21	1.33	0.90
8:H:122:ARG:HB3	8:H:122:ARG:HH11	1.36	0.90
1:A:129(A):G:O2'	1:A:189(F):U:H2'	1.71	0.89
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.54	0.89
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.50	0.89
10:J:38:ILE:HD11	10:J:71:LEU:HD12	1.55	0.89
1:A:1054:C:H2'	1:A:1055:A:H5''	1.55	0.89
1:A:1250:A:H4'	9:I:68:GLY:H	1.34	0.89
12:L:38:THR:HG22	12:L:39:VAL:HG23	1.54	0.88
1:A:243:A:C4'	1:A:244:U:H5'	2.04	0.88
13:M:22:ILE:HD12	13:M:25:ILE:HD12	1.55	0.88
9:I:65:VAL:HG11	9:I:73:GLN:HB3	1.56	0.88
10:J:99:LYS:HD3	10:J:100:THR:N	1.88	0.87
1:A:975:A:H4'	1:A:976:G:H5''	1.56	0.87
2:B:178:ARG:HH22	8:H:68:ARG:HH22	1.18	0.87
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.38	0.87
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.54	0.87
1:A:1060:C:H5	3:C:2:GLY:HA3	1.39	0.87
1:A:1528:U:O2'	1:A:1529:G:H3'	1.75	0.86
1:A:1123:A:H4'	10:J:37:PRO:HD2	1.53	0.86
6:F:1:MET:HE3	6:F:66:GLU:HG2	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:38:ILE:HG13	10:J:71:LEU:HB3	1.58	0.86
3:C:47:LEU:HD23	3:C:68:VAL:HG11	1.59	0.85
9:I:70:LYS:O	9:I:74:ILE:HG13	1.77	0.85
1:A:192:U:H4'	20:T:102:GLY:O	1.76	0.85
4:D:98:GLU:HG2	4:D:189:PRO:HG3	1.58	0.85
3:C:91:LEU:HD21	3:C:99:VAL:HG22	1.58	0.84
12:L:126:LYS:HD2	12:L:126:LYS:O	1.76	0.84
2:B:16:HIS:NE2	2:B:214:ILE:HD11	1.92	0.84
2:B:165:VAL:HG23	2:B:166:ASP:H	1.40	0.84
10:J:8:LEU:HB2	10:J:70:ARG:HB2	1.58	0.84
19:S:22:LEU:HD13	19:S:28:LYS:HB3	1.60	0.84
3:C:156:ARG:HD2	3:C:160:ALA:O	1.78	0.84
5:E:80:ILE:CD1	5:E:91:LEU:HB2	2.07	0.84
10:J:9:ARG:HB3	10:J:9:ARG:NH1	1.92	0.84
5:E:81:GLU:HG3	5:E:90:VAL:HG22	1.60	0.84
1:A:250:A:H4'	1:A:251:G:O5'	1.77	0.83
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.18	0.83
10:J:32:ALA:H	10:J:78:ASN:ND2	1.76	0.83
15:O:10:LYS:HD3	15:O:10:LYS:C	2.03	0.83
19:S:15:LEU:HA	19:S:18:LYS:HB3	1.60	0.83
1:A:1539:C:O4'	7:G:82:GLY:CA	2.26	0.83
5:E:12:LEU:HD13	5:E:31:LEU:HB2	1.59	0.83
1:A:1305:G:H5'	21:U:4:GLY:HA3	1.61	0.83
18:R:87:ARG:O	18:R:88:LYS:HB2	1.77	0.82
15:O:17:ARG:HG3	15:O:17:ARG:HH11	1.43	0.82
20:T:53:LEU:O	20:T:57:ARG:HD2	1.79	0.82
18:R:87:ARG:HG2	18:R:88:LYS:H	1.45	0.82
3:C:8:ILE:HG23	3:C:16:ARG:HG2	1.60	0.82
1:A:1250:A:H4'	9:I:68:GLY:N	1.95	0.82
1:A:1054:C:O2	1:A:1054:C:H3'	1.79	0.81
9:I:93:ARG:NH1	9:I:93:ARG:HB3	1.94	0.81
2:B:219:VAL:HA	2:B:222:ILE:HD12	1.61	0.81
6:F:15:ASP:H	6:F:18:GLN:NE2	1.77	0.81
10:J:49:VAL:HG23	14:N:41:ARG:HB2	1.60	0.81
13:M:88:ARG:HD2	19:S:3:ARG:HH21	1.44	0.81
1:A:1026:G:H2'	1:A:1027:C:H5''	1.61	0.81
7:G:140:ASP:HA	7:G:143:ARG:HH11	1.44	0.81
9:I:8:GLY:HA2	9:I:79:LEU:HD13	1.61	0.81
12:L:27:LEU:C	12:L:29:GLY:H	1.89	0.81
6:F:2:ARG:NE	6:F:69:GLU:HG2	1.95	0.81
15:O:39:LEU:HD12	15:O:56:LEU:HB2	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1257:U:H4'	1:A:1258:G:OP2	1.81	0.81
6:F:22:GLU:OE2	6:F:82:ARG:HD3	1.81	0.81
20:T:53:LEU:HB2	20:T:100:ILE:CG2	2.11	0.81
1:A:351:G:H4'	1:A:352:C:OP1	1.81	0.80
2:B:223:ILE:HD12	2:B:224:GLN:N	1.95	0.80
10:J:34:VAL:HG22	10:J:74:ILE:HG23	1.62	0.80
3:C:91:LEU:HD11	3:C:99:VAL:HG23	1.62	0.80
1:A:1161:C:H2'	1:A:1162:C:H6	1.47	0.80
2:B:178:ARG:HH22	8:H:68:ARG:NH2	1.79	0.80
15:O:78:TYR:CZ	15:O:82:ILE:HD11	2.16	0.80
2:B:75:LYS:HA	2:B:78:GLN:HB2	1.65	0.79
2:B:204:ASN:C	2:B:204:ASN:HD22	1.90	0.79
12:L:75:HIS:CD2	12:L:77:LEU:H	2.01	0.79
7:G:140:ASP:HA	7:G:143:ARG:NH1	1.97	0.79
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.63	0.79
1:A:371:G:C2'	1:A:372:C:H5'	2.13	0.79
18:R:46:GLU:H	18:R:46:GLU:CD	1.90	0.79
20:T:45:GLN:HB2	20:T:91:LEU:HD13	1.65	0.79
11:K:21:ILE:HD12	11:K:95:ILE:HD13	1.65	0.78
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.64	0.78
12:L:24:VAL:O	12:L:24:VAL:HG12	1.82	0.78
1:A:1391:U:H2'	1:A:1392:G:C8	2.18	0.78
1:A:402:G:H2'	1:A:403:C:C5'	2.10	0.78
1:A:1539:C:H4'	7:G:82:GLY:N	1.99	0.78
8:H:9:MET:SD	8:H:32:LYS:HG2	2.24	0.78
10:J:32:ALA:CB	10:J:75:ILE:HG13	2.14	0.78
17:Q:96:GLU:O	17:Q:102:GLY:HA2	1.84	0.78
1:A:818:G:O2'	1:A:819:A:H5''	1.83	0.78
1:A:946:A:H2'	1:A:947:G:C8	2.20	0.77
1:A:247:G:OP2	17:Q:99:SER:HB2	1.83	0.77
1:A:975:A:H5'	1:A:975:A:H8	1.50	0.77
1:A:1305:G:N2	1:A:1331:G:O2'	2.18	0.77
10:J:46:ARG:HG2	10:J:46:ARG:HH11	1.47	0.77
13:M:3:ARG:HA	13:M:8:GLU:O	1.85	0.77
1:A:939:G:H5''	7:G:102:ARG:NH2	1.99	0.77
10:J:76:ASN:C	10:J:78:ASN:H	1.91	0.77
3:C:14:ILE:HG22	3:C:15:THR:N	1.98	0.76
7:G:54:THR:HG22	7:G:56:GLN:H	1.49	0.76
2:B:134:GLU:HG2	2:B:137:ARG:HH21	1.48	0.76
10:J:61:GLU:OE1	14:N:45:ARG:NH1	2.18	0.76
1:A:1539:C:O5'	7:G:82:GLY:N	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:31:GLN:O	9:I:32:ASP:HB3	1.86	0.76
1:A:437:U:H5''	4:D:155:LEU:HD22	1.65	0.76
1:A:1075:C:H5'	2:B:103:THR:HG21	1.68	0.76
1:A:1255:G:OP2	10:J:43:ARG:NH2	2.19	0.76
2:B:142:LEU:HG	2:B:146:GLN:NE2	1.99	0.76
12:L:74:GLY:O	12:L:75:HIS:HB3	1.82	0.76
18:R:19:LYS:HG3	18:R:20:ALA:N	1.99	0.76
1:A:1502:A:H2	1:A:1505:G:H1	1.31	0.76
3:C:35:GLU:HG2	3:C:59:ARG:HH22	1.50	0.76
1:A:580:U:H2'	1:A:581:G:O4'	1.85	0.75
1:A:718:G:H5'	11:K:117:ASN:ND2	2.00	0.75
1:A:1054:C:H42	23:Y:34:CM0:C1'	1.98	0.75
3:C:14:ILE:O	3:C:16:ARG:N	2.18	0.75
6:F:3:ARG:HH11	6:F:3:ARG:HG3	1.50	0.75
3:C:119:ARG:HE	3:C:140:ARG:NE	1.85	0.75
15:O:87:ILE:HG22	15:O:88:ARG:N	1.97	0.75
17:Q:82:MET:O	17:Q:86:GLU:HG2	1.87	0.75
9:I:128:ARG:O	13:M:126:LYS:HD2	1.87	0.75
10:J:49:VAL:CG2	14:N:41:ARG:HB2	2.16	0.75
1:A:1539:C:C5'	7:G:82:GLY:CA	2.56	0.75
2:B:7:VAL:HG12	2:B:221:LEU:HD23	1.68	0.74
11:K:126:ARG:O	11:K:127:LYS:HB2	1.86	0.74
1:A:1027:C:H6	1:A:1027:C:H5'	1.52	0.74
1:A:1492:A:OP1	12:L:47:LYS:N	2.17	0.74
3:C:116:VAL:HG21	3:C:202:ILE:HD11	1.70	0.74
10:J:9:ARG:HB3	10:J:9:ARG:HH11	1.50	0.74
1:A:1539:C:O5'	7:G:82:GLY:C	2.30	0.74
2:B:231:GLU:HB3	2:B:232:PRO:HD2	1.70	0.74
12:L:47:LYS:HB3	12:L:48:PRO:CD	2.18	0.74
18:R:19:LYS:CG	18:R:20:ALA:H	1.98	0.74
1:A:1144:G:N2	1:A:1146:A:H62	1.86	0.74
2:B:15:VAL:HG11	2:B:209:ARG:HB2	1.70	0.73
8:H:122:ARG:HB3	8:H:122:ARG:NH1	2.02	0.73
1:A:1080:A:H5''	5:E:16:THR:HG21	1.69	0.73
3:C:64:VAL:HG23	3:C:99:VAL:HG11	1.70	0.73
2:B:204:ASN:ND2	2:B:206:ASP:H	1.86	0.73
9:I:16:ARG:HB2	9:I:64:THR:HB	1.71	0.73
10:J:82:ILE:O	10:J:86:MET:HB2	1.87	0.73
13:M:40:ASN:HB3	13:M:43:THR:HG23	1.68	0.73
14:N:41:ARG:HG2	14:N:41:ARG:HH11	1.54	0.73
1:A:243:A:H4'	1:A:244:U:C5'	2.10	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1356:G:H2'	1:A:1357:A:C8	2.23	0.73
1:A:1216:G:H5''	14:N:5:ALA:CB	2.18	0.73
10:J:5:ARG:HA	10:J:73:ASP:OD1	1.89	0.73
11:K:84:VAL:HG11	11:K:91:ARG:HD3	1.69	0.73
12:L:83:VAL:HG21	12:L:100:ILE:HG23	1.70	0.73
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.24	0.73
9:I:69:GLY:O	9:I:73:GLN:HG3	1.88	0.72
10:J:30:SER:HB3	10:J:84:GLN:HE21	1.52	0.72
3:C:64:VAL:O	3:C:99:VAL:HB	1.89	0.72
12:L:59:ARG:HB2	12:L:59:ARG:HH11	1.52	0.72
15:O:6:GLU:H	15:O:6:GLU:CD	1.97	0.72
2:B:23:ARG:HD2	2:B:23:ARG:O	1.89	0.72
2:B:87:ARG:NH1	2:B:233:SER:HB2	2.04	0.72
9:I:93:ARG:HB3	9:I:93:ARG:HH11	1.52	0.72
1:A:1137:C:H4'	1:A:1138:G:C2	2.23	0.72
3:C:47:LEU:CD2	3:C:68:VAL:HG11	2.20	0.72
2:B:75:LYS:HB2	2:B:76:GLN:NE2	2.04	0.72
1:A:1532:U:C2'	1:A:1533:C:C5'	2.50	0.72
2:B:178:ARG:HH21	2:B:196:LEU:C	1.98	0.72
20:T:50:GLU:HG3	20:T:100:ILE:HB	1.71	0.72
18:R:18:ARG:O	18:R:19:LYS:HB3	1.89	0.72
4:D:36:ARG:HG2	4:D:38:TYR:OH	1.89	0.72
1:A:246:A:O2'	17:Q:99:SER:HB3	1.89	0.72
1:A:677:U:H3	1:A:713:G:H22	1.38	0.72
1:A:706:A:O4'	11:K:29:ILE:HD11	1.90	0.72
13:M:81:LEU:HD13	13:M:88:ARG:HD3	1.70	0.71
1:A:1381:U:H1'	7:G:78:ARG:NH2	2.05	0.71
17:Q:67:LYS:CA	17:Q:70:ARG:HH12	2.03	0.71
15:O:39:LEU:CD1	15:O:56:LEU:HB2	2.21	0.71
13:M:17:VAL:O	13:M:20:THR:HB	1.91	0.71
8:H:112:LEU:N	8:H:112:LEU:HD23	2.06	0.71
2:B:96:ARG:N	2:B:96:ARG:HD2	2.05	0.71
2:B:86:GLU:C	2:B:88:ALA:H	1.98	0.71
5:E:147:ASP:O	5:E:151:LEU:HD13	1.91	0.71
15:O:56:LEU:HA	15:O:59:MET:HE2	1.72	0.71
1:A:664:G:H22	1:A:741:G:H1	1.36	0.70
1:A:759:A:H61	17:Q:94:ASN:HD21	1.39	0.70
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.72	0.70
10:J:32:ALA:HB2	10:J:76:ASN:HB2	1.72	0.70
10:J:80:LYS:HA	10:J:83:GLU:OE2	1.91	0.70
23:Y:30:C:O2	23:Y:30:C:H2'	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:58:GLU:HB2	3:C:65:ALA:HB3	1.73	0.70
10:J:90:LEU:H	10:J:91:PRO:CD	2.04	0.70
1:A:673:G:H2'	1:A:674:G:C8	2.26	0.70
12:L:53:ARG:HG2	12:L:93:LEU:HD11	1.73	0.70
1:A:1014:A:C2	1:A:1219:U:H1'	2.25	0.70
5:E:89:ILE:HD13	5:E:90:VAL:N	2.05	0.70
11:K:48:ILE:HG22	11:K:49:GLY:H	1.55	0.70
1:A:1065:U:H5''	1:A:1190:G:N2	2.07	0.70
1:A:532:A:N1	3:C:156:ARG:NH2	2.40	0.70
1:A:1054:C:C2'	1:A:1055:A:H5''	2.22	0.70
1:A:1542:U:C3'	1:A:1543:C:H5''	2.21	0.70
1:A:180:U:H2'	1:A:181:G:H5'	1.71	0.70
1:A:1038:C:H2'	1:A:1039:C:C6	2.26	0.70
1:A:789:U:OP1	1:A:1539:C:N4	2.25	0.69
2:B:42:ILE:H	2:B:42:ILE:HD12	1.57	0.69
4:D:3:ARG:HH11	4:D:115:ARG:HD2	1.57	0.69
5:E:11:ILE:HB	5:E:31:LEU:HB3	1.74	0.69
5:E:79:GLU:HG3	5:E:93:PRO:HD2	1.74	0.69
3:C:14:ILE:CG2	3:C:15:THR:H	1.99	0.69
5:E:5:ASP:CG	5:E:6:PHE:H	1.99	0.69
1:A:1542:U:H3'	1:A:1543:C:H5''	1.75	0.69
11:K:13:GLN:HA	11:K:75:TYR:O	1.91	0.69
8:H:103:VAL:HG21	8:H:109:ILE:O	1.92	0.69
5:E:145:LYS:O	5:E:149:GLU:HG2	1.93	0.69
2:B:78:GLN:HG3	2:B:94:ASN:OD1	1.92	0.69
18:R:33:ASP:OD2	18:R:36:ASN:HB2	1.93	0.69
3:C:123:GLN:O	3:C:128:PHE:HB2	1.93	0.69
7:G:15:ASP:HB3	7:G:20:ASP:H	1.58	0.69
9:I:3:GLN:HB3	9:I:20:ARG:HG2	1.74	0.69
13:M:67:GLU:O	13:M:69:GLU:N	2.26	0.69
10:J:57:LYS:HE2	10:J:60:ARG:NH2	2.08	0.68
5:E:89:ILE:HD13	5:E:90:VAL:H	1.58	0.68
1:A:1024:G:H3'	1:A:1025:U:H5''	1.75	0.68
8:H:29:SER:OG	8:H:32:LYS:HB2	1.93	0.68
10:J:29:ARG:HG3	10:J:84:GLN:HE22	1.58	0.68
17:Q:63:ARG:O	17:Q:65:ILE:HD12	1.92	0.68
3:C:70:VAL:HG12	3:C:71:ALA:N	2.06	0.68
3:C:77:ILE:O	3:C:83:ARG:HB3	1.93	0.68
10:J:4:ILE:HD11	10:J:74:ILE:CD1	2.18	0.68
14:N:26:ARG:HH21	14:N:47:LEU:CD2	2.07	0.68
2:B:21:ARG:HH12	2:B:23:ARG:HG2	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:6:ILE:HG22	10:J:97:GLU:O	1.93	0.68
19:S:5:LEU:O	19:S:6:LYS:HB2	1.92	0.68
1:A:1539:C:C5'	7:G:82:GLY:N	2.56	0.68
1:A:1216:G:H5''	14:N:5:ALA:HB2	1.76	0.68
2:B:178:ARG:NH2	8:H:68:ARG:HH22	1.89	0.68
12:L:57:LYS:HE3	12:L:65:GLU:HG2	1.76	0.68
1:A:542:G:OP1	4:D:10:ARG:NH2	2.27	0.68
1:A:1305:G:H22	1:A:1331:G:C2'	2.06	0.68
1:A:1425:U:H2'	1:A:1426:C:C6	2.28	0.68
2:B:230:VAL:HG12	2:B:231:GLU:N	2.09	0.68
4:D:30:LYS:HB3	4:D:35:ARG:HH21	1.58	0.68
10:J:27:ALA:HA	10:J:81:THR:HG23	1.76	0.68
1:A:412:A:N6	4:D:35:ARG:HB3	2.09	0.67
1:A:1497:G:C2'	1:A:1498:U:H5'	2.24	0.67
2:B:218:ALA:O	2:B:222:ILE:HG13	1.94	0.67
10:J:21:GLN:HE21	10:J:21:GLN:HA	1.58	0.67
16:P:10:GLY:HA3	16:P:14:ASN:O	1.94	0.67
1:A:1241:G:H2'	1:A:1242:C:C6	2.28	0.67
9:I:118:LYS:O	9:I:120:ARG:N	2.27	0.67
1:A:953:G:H1'	13:M:125:ARG:HB2	1.77	0.67
1:A:991:U:O2'	1:A:992:U:H5'	1.95	0.67
1:A:1442(A):G:H4'	1:A:1442(B):A:H5'	1.76	0.67
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.75	0.67
1:A:954:G:H4'	13:M:120:LYS:HB3	1.74	0.67
1:A:1539:C:H4'	7:G:82:GLY:CA	2.25	0.67
2:B:74:LYS:HE2	2:B:166:ASP:HB2	1.77	0.67
10:J:30:SER:CB	10:J:84:GLN:HE21	2.07	0.67
11:K:33:THR:HG22	11:K:39:PRO:HA	1.75	0.67
2:B:52:GLU:HG2	2:B:56:ARG:NH2	2.09	0.67
2:B:87:ARG:HH11	2:B:233:SER:HB2	1.58	0.67
9:I:8:GLY:HA2	9:I:79:LEU:HB3	1.76	0.67
20:T:50:GLU:HA	20:T:100:ILE:CG2	2.24	0.67
20:T:53:LEU:HB2	20:T:100:ILE:HG23	1.75	0.67
1:A:406:G:H5''	4:D:5:ILE:HG23	1.77	0.67
4:D:162:LEU:HD12	4:D:181:MET:HE2	1.76	0.67
10:J:35:SER:HB3	10:J:73:ASP:HB2	1.76	0.67
1:A:1435:G:H2'	1:A:1436:U:C6	2.29	0.67
2:B:28:PHE:CD2	2:B:190:THR:HA	2.30	0.67
12:L:83:VAL:HG21	12:L:100:ILE:CG2	2.24	0.67
18:R:39:VAL:O	18:R:42:ARG:HB2	1.95	0.67
1:A:1539:C:C4'	7:G:82:GLY:N	2.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:25:ASN:HD22	2:B:25:ASN:C	2.02	0.67
2:B:124:SER:O	2:B:127:ILE:HG13	1.95	0.67
3:C:35:GLU:CG	3:C:59:ARG:HH22	2.07	0.67
2:B:111:ARG:HB3	2:B:149:LEU:CD1	2.22	0.66
2:B:189:ASP:HB3	2:B:191:ASP:OD1	1.96	0.66
3:C:119:ARG:HG3	3:C:119:ARG:HH11	1.60	0.66
19:S:20:LEU:HD12	19:S:21:GLU:N	2.10	0.66
1:A:149:A:H2'	1:A:150:C:C6	2.31	0.66
1:A:1130:A:H3'	1:A:1130:A:OP2	1.95	0.66
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.03	0.66
11:K:126:ARG:O	11:K:127:LYS:HE2	1.96	0.66
3:C:50:ALA:HB1	3:C:70:VAL:CG1	2.17	0.66
4:D:30:LYS:C	4:D:32:ALA:H	2.03	0.66
20:T:39:LYS:HD3	20:T:55:ILE:HD13	1.76	0.66
1:A:1182:G:O2'	1:A:1183:A:OP2	2.13	0.66
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.61	0.66
4:D:35:ARG:O	4:D:36:ARG:HB2	1.93	0.66
21:U:5:ASP:O	21:U:11:GLY:HA3	1.96	0.66
1:A:1117:G:H5'	1:A:1117:G:H8	1.61	0.66
3:C:91:LEU:HD11	3:C:99:VAL:CG2	2.26	0.66
10:J:33:GLN:CB	10:J:75:ILE:HD11	2.26	0.66
11:K:14:VAL:HG21	11:K:40:ILE:HD11	1.77	0.66
12:L:47:LYS:HB3	12:L:48:PRO:HD3	1.78	0.66
1:A:190:U:O2	20:T:105:SER:HB2	1.96	0.66
1:A:579:G:H5'	1:A:728:A:H1'	1.77	0.66
1:A:1016:A:H2'	1:A:1017:G:O4'	1.96	0.66
13:M:50:GLU:O	13:M:54:VAL:HG23	1.96	0.66
15:O:3:ILE:HD13	15:O:34:LEU:HD13	1.77	0.66
12:L:60:LEU:HD11	12:L:85:ILE:CD1	2.18	0.66
2:B:132:LYS:HB3	2:B:136:VAL:HG23	1.77	0.66
8:H:86:ILE:HG21	8:H:133:LEU:HD13	1.77	0.66
8:H:110:ALA:HB3	8:H:121:ASP:HB3	1.78	0.66
4:D:3:ARG:NH1	4:D:115:ARG:HD2	2.11	0.65
4:D:70:ILE:HG22	4:D:71:SER:O	1.95	0.65
7:G:113:GLU:HG2	7:G:119:ARG:HG2	1.78	0.65
19:S:52:TYR:HA	19:S:56:GLN:O	1.95	0.65
23:Y:34:CM0:C8	23:Y:34:CM0:O4	2.44	0.65
1:A:299:G:H2'	1:A:300:A:C8	2.30	0.65
4:D:31:CYS:C	4:D:33:MET:H	2.04	0.65
18:R:88:LYS:HB3	18:R:88:LYS:NZ	2.11	0.65
10:J:31:GLY:HA3	10:J:81:THR:OG1	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:57:ARG:NH1	16:P:79:VAL:O	2.30	0.65
1:A:201:C:H4'	1:A:202:U:OP1	1.96	0.65
1:A:1132:C:H2'	1:A:1133:G:H8	1.62	0.65
8:H:51:VAL:HG11	8:H:60:ARG:HH11	1.62	0.65
15:O:87:ILE:CG2	15:O:88:ARG:H	2.02	0.65
13:M:37:THR:HG23	13:M:55:ARG:HD2	1.79	0.65
19:S:18:LYS:O	19:S:22:LEU:HG	1.95	0.65
1:A:384:G:H2'	1:A:385:C:C6	2.32	0.65
1:A:1189:C:P	10:J:51:ARG:HH22	2.20	0.65
7:G:37:ASN:HD21	9:I:40:LEU:HA	1.60	0.65
12:L:83:VAL:HG22	12:L:84:LEU:N	2.11	0.65
1:A:1142:G:H2'	1:A:1143:G:O4'	1.97	0.65
2:B:21:ARG:HH11	2:B:21:ARG:HG3	1.62	0.65
10:J:3:LYS:HA	10:J:74:ILE:O	1.95	0.65
18:R:32:ARG:HA	18:R:69:THR:HG21	1.78	0.65
1:A:1427:U:H2'	1:A:1428:A:C8	2.32	0.65
19:S:30:LEU:O	19:S:31:ILE:HD13	1.96	0.65
2:B:8:LYS:O	2:B:9:GLU:HB2	1.96	0.65
2:B:45:GLN:O	2:B:48:MET:HB2	1.97	0.65
2:B:114:ARG:HH11	2:B:118:LEU:HD12	1.61	0.65
3:C:188:LEU:HD21	3:C:195:VAL:HG11	1.79	0.65
1:A:35:G:H2'	1:A:36:C:C6	2.31	0.64
2:B:142:LEU:O	2:B:146:GLN:HG3	1.97	0.64
1:A:818:G:C2'	1:A:819:A:H5''	2.26	0.64
4:D:189:PRO:HB2	4:D:194:LEU:HD21	1.79	0.64
4:D:146:ILE:N	4:D:146:ILE:HD12	2.12	0.64
9:I:106:ALA:O	9:I:108:VAL:HG23	1.97	0.64
13:M:15:VAL:HG23	13:M:43:THR:O	1.97	0.64
1:A:473:G:O2'	1:A:474:G:H5'	1.98	0.64
1:A:1125:U:H3	10:J:5:ARG:NH2	1.89	0.64
2:B:140:HIS:HA	2:B:143:GLU:OE1	1.97	0.64
2:B:230:VAL:HG12	2:B:231:GLU:H	1.61	0.64
8:H:91:ARG:HG3	12:L:7:ILE:HG13	1.78	0.64
17:Q:3:LYS:HB3	17:Q:61:GLU:HB2	1.79	0.64
1:A:1352:C:H2'	1:A:1353:G:C8	2.33	0.64
1:A:1510:U:H2'	1:A:1511:G:C8	2.32	0.64
2:B:14:GLY:C	2:B:15:VAL:HG22	2.22	0.64
9:I:93:ARG:HH11	9:I:93:ARG:CB	2.10	0.64
9:I:115:GLY:O	9:I:116:LYS:HD3	1.98	0.64
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.79	0.64
1:A:108:G:H5'	1:A:109:A:H5''	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:909:A:OP1	12:L:21:LYS:HE2	1.97	0.64
2:B:61:LEU:HD21	2:B:160:ASP:CB	2.27	0.64
19:S:5:LEU:O	19:S:6:LYS:CB	2.46	0.64
19:S:13:ASP:HA	19:S:16:LEU:HB3	1.80	0.64
1:A:266:G:H5''	1:A:268:C:H41	1.63	0.64
1:A:1152:A:H2'	1:A:1153:C:C6	2.33	0.64
8:H:119:LEU:HD12	8:H:124:ALA:HA	1.79	0.64
11:K:58:PRO:HA	11:K:90:GLY:HA3	1.80	0.64
1:A:420:U:H2'	1:A:422:C:C5	2.32	0.64
1:A:1053:G:C3'	1:A:1054:C:H5'	2.27	0.64
3:C:188:LEU:HD21	3:C:195:VAL:CG1	2.28	0.64
1:A:1250:A:H2'	1:A:1251:A:C8	2.33	0.63
7:G:73:MET:HE1	7:G:90:GLU:HG2	1.80	0.63
2:B:80:ILE:HD13	2:B:212:GLN:HB2	1.80	0.63
4:D:78:LEU:HD22	4:D:96:LEU:HB3	1.79	0.63
12:L:47:LYS:HE3	22:X:3:U:OP1	1.99	0.63
13:M:65:LYS:HG3	13:M:69:GLU:OE2	1.97	0.63
9:I:53:VAL:HG21	9:I:85:LEU:HD21	1.78	0.63
6:F:47:ARG:HA	6:F:57:GLN:HG2	1.78	0.63
13:M:58:GLU:HA	13:M:58:GLU:OE2	1.97	0.63
1:A:662:G:H2'	1:A:663:A:C8	2.33	0.63
3:C:125:GLU:HG2	3:C:190:ARG:O	1.99	0.63
5:E:13:ILE:HA	5:E:29:GLY:O	1.98	0.63
10:J:21:GLN:HA	10:J:21:GLN:NE2	2.14	0.63
1:A:928:G:O2'	1:A:1533:C:OP1	2.14	0.63
1:A:1181:G:H2'	1:A:1182:G:C5	2.33	0.63
1:A:1540:U:O2'	1:A:1541:U:H5'	1.99	0.63
5:E:80:ILE:HD12	5:E:80:ILE:H	1.63	0.63
7:G:79:ARG:HH22	7:G:82:GLY:H	1.45	0.63
14:N:57:ARG:HG2	14:N:58:LYS:H	1.64	0.63
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.79	0.63
7:G:146:GLU:HG2	7:G:149:ARG:HH21	1.63	0.63
14:N:26:ARG:HE	14:N:47:LEU:HD11	1.62	0.63
1:A:975:A:H5'	1:A:975:A:C8	2.33	0.63
1:A:1066:C:O2'	1:A:1067:A:H5'	1.99	0.63
1:A:1497:G:H2'	1:A:1498:U:H5'	1.80	0.63
1:A:629:G:H2'	1:A:630:G:C4'	2.29	0.63
12:L:27:LEU:HB2	12:L:62:SER:HB2	1.80	0.63
4:D:150:GLU:HA	4:D:153:ARG:HG3	1.80	0.62
14:N:43:CYS:SG	27:N:102:ZN:ZN	1.87	0.62
4:D:70:ILE:HG23	4:D:74:GLN:HB2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:953:G:H5'	1:A:965:A:H61	1.62	0.62
1:A:1281:U:H5'	1:A:1282:C:H5	1.64	0.62
3:C:132:ARG:HB3	3:C:132:ARG:HH11	1.65	0.62
13:M:49:THR:HG22	13:M:51:ALA:N	2.11	0.62
1:A:112:G:H4'	1:A:389:A:H5''	1.81	0.62
1:A:1027:C:H42	1:A:1034:G:H1	1.47	0.62
2:B:80:ILE:HD11	2:B:208:ILE:HG22	1.81	0.62
2:B:134:GLU:HG2	2:B:137:ARG:NH2	2.14	0.62
10:J:46:ARG:NH1	10:J:64:GLU:HB3	2.13	0.62
11:K:90:GLY:HA2	11:K:93:GLN:HB2	1.80	0.62
12:L:83:VAL:HG22	12:L:84:LEU:H	1.64	0.62
1:A:759:A:H61	17:Q:94:ASN:ND2	1.96	0.62
3:C:91:LEU:HD23	3:C:92:ALA:N	2.14	0.62
16:P:20:VAL:HG11	16:P:32:TYR:CB	2.30	0.62
1:A:281:G:O2'	1:A:282:A:OP2	2.17	0.62
3:C:129:ALA:HB3	3:C:132:ARG:NH1	2.15	0.62
1:A:105:G:H2'	1:A:106:C:C6	2.34	0.62
1:A:524:G:H2'	1:A:525:C:C6	2.35	0.62
5:E:6:PHE:HB3	5:E:34:VAL:HG22	1.81	0.62
14:N:23:ARG:NH1	14:N:30:ALA:HB2	2.15	0.62
1:A:344:A:H4'	1:A:345:C:OP2	1.99	0.62
2:B:98:LEU:HD23	2:B:98:LEU:N	2.14	0.62
2:B:139:LYS:C	2:B:139:LYS:HD3	2.25	0.62
3:C:6:HIS:HD2	3:C:8:ILE:H	1.47	0.62
4:D:126:ILE:HG22	4:D:127:THR:N	2.13	0.62
1:A:969:A:H61	13:M:126:LYS:CB	2.13	0.62
1:A:1060:C:H2'	1:A:1061:G:H8	1.63	0.62
1:A:1532:U:O2'	1:A:1533:C:H5''	2.00	0.62
2:B:84:GLU:OE1	2:B:216:SER:HA	1.99	0.62
2:B:132:LYS:HA	2:B:135:GLN:HB2	1.82	0.62
3:C:102:ASN:N	3:C:102:ASN:HD22	1.97	0.62
3:C:111:LEU:HD21	3:C:144:SER:HB2	1.80	0.62
6:F:21:LEU:O	6:F:25:ILE:HG13	2.00	0.62
8:H:60:ARG:HH11	8:H:60:ARG:HG3	1.65	0.62
9:I:97:LYS:CA	9:I:102:LEU:HD21	2.27	0.62
9:I:125:TYR:H	9:I:125:TYR:HD2	1.48	0.62
1:A:266:G:H5'	1:A:266:G:C8	2.35	0.62
6:F:14:LEU:HA	6:F:18:GLN:NE2	2.15	0.62
6:F:80:ARG:NH1	6:F:88:VAL:HB	2.15	0.62
9:I:117:HIS:C	9:I:118:LYS:HG3	2.24	0.62
11:K:11:LYS:HD2	11:K:11:LYS:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:28:PHE:HD1	2:B:194:PRO:HG3	1.65	0.61
1:A:1052:U:H2'	1:A:1055:A:OP1	2.00	0.61
1:A:1054:C:O2	1:A:1054:C:C3'	2.48	0.61
3:C:148:GLY:HA3	3:C:172:ARG:O	2.00	0.61
8:H:119:LEU:HB3	8:H:123:GLU:HB2	1.82	0.61
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.82	0.61
3:C:110:ASN:ND2	3:C:140:ARG:HB3	2.16	0.61
3:C:112:SER:HB3	3:C:115:LEU:HD12	1.83	0.61
2:B:204:ASN:HD22	2:B:206:ASP:H	1.47	0.61
3:C:77:ILE:C	3:C:83:ARG:HB3	2.24	0.61
3:C:132:ARG:HB3	3:C:132:ARG:NH1	2.15	0.61
7:G:111:ARG:HB3	7:G:113:GLU:OE2	2.00	0.61
1:A:410:G:H2'	1:A:429:U:C5	2.36	0.61
1:A:539:A:H2'	1:A:540:G:C8	2.35	0.61
1:A:1502:A:H2	1:A:1505:G:N1	1.97	0.61
5:E:80:ILE:HD12	5:E:91:LEU:HB2	1.81	0.61
10:J:9:ARG:HH11	10:J:9:ARG:CB	2.13	0.61
13:M:14:ARG:NH1	13:M:16:ASP:OD2	2.34	0.61
19:S:43:GLU:H	19:S:43:GLU:CD	2.07	0.61
19:S:80:TYR:CZ	19:S:81:ARG:HB3	2.36	0.61
1:A:706:A:C4'	11:K:29:ILE:HD11	2.31	0.61
9:I:4:TYR:HB3	9:I:87:GLN:HB2	1.82	0.61
12:L:83:VAL:CG2	12:L:100:ILE:HG23	2.31	0.61
19:S:64:GLU:O	19:S:67:VAL:HG23	2.01	0.61
1:A:1391:U:H2'	1:A:1392:G:H8	1.66	0.61
1:A:1392:G:O2'	1:A:1502:A:H5''	2.01	0.61
5:E:80:ILE:HD13	5:E:91:LEU:HD12	1.82	0.61
13:M:54:VAL:O	13:M:58:GLU:HG2	2.01	0.61
13:M:66:LEU:O	13:M:67:GLU:O	2.19	0.61
8:H:4:ASP:CG	8:H:85:ARG:HH11	2.09	0.61
10:J:6:ILE:CD1	10:J:72:VAL:HB	2.30	0.61
10:J:84:GLN:O	10:J:88:LEU:HD12	2.01	0.61
20:T:72:LEU:O	20:T:72:LEU:HG	2.01	0.61
1:A:701:C:H5''	1:A:703:G:O4'	2.01	0.61
7:G:75:VAL:CG2	7:G:86:GLN:HB3	2.25	0.61
13:M:119:GLY:O	13:M:121:LYS:HG3	2.00	0.61
16:P:34:GLU:OE2	16:P:55:ARG:HD3	2.00	0.61
1:A:363:A:H62	12:L:28:LYS:HE3	1.66	0.61
1:A:938:A:H5'	7:G:76:ARG:HH21	1.66	0.61
1:A:946:A:H2'	1:A:947:G:H8	1.66	0.61
1:A:1148:U:H2'	1:A:1149:C:O4'	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:80:ILE:O	8:H:80:ILE:HG22	2.00	0.61
20:T:56:MET:HE2	20:T:88:VAL:HG11	1.81	0.61
1:A:1120:G:H2'	1:A:1121:U:C6	2.37	0.60
2:B:144:ARG:HA	2:B:147:LYS:HE2	1.84	0.60
14:N:9:LYS:HE3	14:N:21:TYR:O	2.01	0.60
1:A:1042:G:O2'	1:A:1043:C:H5'	2.01	0.60
1:A:1481:U:H2'	1:A:1482:G:O4'	2.00	0.60
2:B:92:TYR:CD2	2:B:151:GLY:HA3	2.37	0.60
5:E:11:ILE:HD11	5:E:33:VAL:HG21	1.82	0.60
9:I:48:GLU:N	9:I:49:PRO:HD2	2.16	0.60
10:J:79:ARG:HG2	10:J:79:ARG:HH11	1.65	0.60
1:A:1053:G:H3'	1:A:1054:C:H5'	1.84	0.60
1:A:1379:G:O6	7:G:2:ALA:HB3	2.00	0.60
6:F:22:GLU:O	6:F:26:ILE:HG13	2.01	0.60
13:M:65:LYS:O	13:M:66:LEU:HD23	2.00	0.60
21:U:6:ARG:HH21	21:U:15:ARG:NE	1.98	0.60
2:B:95:GLN:C	2:B:96:ARG:HD2	2.27	0.60
3:C:47:LEU:N	3:C:47:LEU:HD12	2.16	0.60
13:M:125:ARG:HD2	13:M:126:LYS:N	2.16	0.60
1:A:1135:U:H4'	1:A:1136:U:H5	1.66	0.60
1:A:1154:G:H2'	1:A:1155:G:H8	1.66	0.60
14:N:8:GLU:O	14:N:10:ALA:N	2.35	0.60
1:A:1038:C:H2'	1:A:1039:C:H6	1.66	0.60
1:A:1423:G:O2'	1:A:1424:C:H5'	2.01	0.60
10:J:32:ALA:H	10:J:78:ASN:HD21	1.45	0.60
10:J:38:ILE:CD1	10:J:71:LEU:HD12	2.28	0.60
12:L:56:ALA:HB2	12:L:70:ILE:HD11	1.83	0.60
14:N:26:ARG:HH21	14:N:47:LEU:HG	1.65	0.60
16:P:57:ARG:HG2	16:P:57:ARG:HH11	1.65	0.60
1:A:269:C:H2'	1:A:270:A:C8	2.37	0.60
5:E:24:ARG:HG2	5:E:24:ARG:HH11	1.66	0.60
11:K:34:ASP:OD2	11:K:38:ASN:HB2	2.01	0.60
19:S:44:MET:HA	19:S:47:HIS:HD2	1.67	0.60
1:A:17:U:H2'	1:A:18:C:C6	2.36	0.60
3:C:29:TYR:OH	14:N:54:PRO:HD2	2.02	0.60
3:C:157:ILE:CD1	3:C:166:GLU:HG3	2.31	0.60
4:D:25:ARG:C	4:D:27:TYR:H	2.08	0.60
1:A:1116:C:C2'	1:A:1117:G:H5''	2.31	0.60
2:B:165:VAL:HG23	2:B:166:ASP:N	2.13	0.60
14:N:57:ARG:HG2	14:N:58:LYS:N	2.16	0.60
1:A:254:G:OP1	17:Q:67:LYS:O	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1425:U:H2'	1:A:1426:C:H6	1.65	0.60
3:C:89:GLU:O	3:C:93:LYS:HG2	2.01	0.60
5:E:20:GLN:NE2	5:E:21:ALA:O	2.35	0.60
1:A:1181:G:H4'	1:A:1182:G:OP1	2.01	0.59
2:B:165:VAL:O	2:B:187:LEU:O	2.20	0.59
4:D:24:GLU:OE1	4:D:25:ARG:N	2.34	0.59
5:E:12:LEU:CD1	5:E:31:LEU:HB2	2.32	0.59
8:H:90:GLY:O	8:H:91:ARG:HB2	2.02	0.59
21:U:6:ARG:HE	21:U:15:ARG:CD	2.14	0.59
1:A:620:C:N1	4:D:135:LEU:HD13	2.17	0.59
1:A:1014:A:H2'	1:A:1015:A:C8	2.37	0.59
1:A:1201:A:H4'	1:A:1202:G:O5'	2.01	0.59
2:B:181:PHE:CD2	8:H:70:GLN:HB3	2.37	0.59
4:D:9:CYS:O	4:D:13:ARG:HG3	2.02	0.59
6:F:101:ALA:HB2	18:R:28:GLU:HG3	1.84	0.59
16:P:57:ARG:HH11	16:P:57:ARG:CG	2.15	0.59
4:D:64:LEU:HD12	4:D:75:PHE:HZ	1.67	0.59
7:G:64:GLN:HE21	7:G:68:ASN:ND2	2.00	0.59
10:J:76:ASN:O	10:J:78:ASN:N	2.32	0.59
17:Q:101:ARG:HA	17:Q:101:ARG:HE	1.65	0.59
1:A:1152:A:H5'	10:J:70:ARG:HH22	1.67	0.59
1:A:1401:G:C2	1:A:1402:C:H1'	2.37	0.59
2:B:19:HIS:NE2	2:B:206:ASP:HB3	2.17	0.59
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.84	0.59
1:A:1024:G:C3'	1:A:1025:U:H5''	2.32	0.59
2:B:92:TYR:CE2	2:B:151:GLY:HA3	2.37	0.59
20:T:93:GLU:C	20:T:95:ALA:H	2.10	0.59
17:Q:68:ARG:N	17:Q:70:ARG:NH1	2.51	0.59
21:U:6:ARG:HH21	21:U:15:ARG:HE	1.50	0.59
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.37	0.59
5:E:152:ARG:NH2	8:H:107:LEU:O	2.34	0.59
19:S:44:MET:C	19:S:62:ILE:HD13	2.27	0.59
4:D:18:LYS:NZ	4:D:31:CYS:HB3	2.17	0.59
5:E:43:LEU:HD11	5:E:132:ALA:HB1	1.85	0.59
7:G:46:ALA:O	7:G:50:ILE:HG12	2.01	0.59
11:K:48:ILE:HG22	11:K:49:GLY:N	2.17	0.59
12:L:46:LYS:O	12:L:48:PRO:HD2	2.03	0.59
1:A:1251:A:H5''	9:I:12:GLU:OE2	2.03	0.59
2:B:137:ARG:NH1	2:B:137:ARG:HB2	2.17	0.59
20:T:10:LEU:O	20:T:13:LEU:HG	2.03	0.59
8:H:87:SER:HA	8:H:93:VAL:HG23	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:90:LEU:N	10:J:91:PRO:CD	2.66	0.59
13:M:37:THR:CG2	13:M:55:ARG:HD2	2.33	0.59
1:A:353:A:H5'	1:A:353:A:H8	1.67	0.58
1:A:1062:U:H2'	1:A:1063:C:C6	2.38	0.58
1:A:1066:C:C2'	1:A:1067:A:H5'	2.33	0.58
1:A:1412:C:H2'	1:A:1413:A:C8	2.38	0.58
1:A:1438:G:H2'	1:A:1439:C:C6	2.38	0.58
3:C:64:VAL:CG2	3:C:99:VAL:HG11	2.33	0.58
17:Q:67:LYS:HA	17:Q:70:ARG:NH1	2.16	0.58
20:T:73:HIS:O	20:T:74:LYS:CB	2.42	0.58
21:U:12:LYS:HB3	21:U:22:ARG:HD2	1.85	0.58
1:A:1116:C:O2'	1:A:1117:G:H5''	2.02	0.58
4:D:36:ARG:HG2	4:D:38:TYR:CZ	2.39	0.58
9:I:125:TYR:CD2	9:I:125:TYR:N	2.70	0.58
1:A:421:U:H5'	1:A:422:C:C5	2.38	0.58
1:A:1068:G:OP2	1:A:1068:G:H8	1.86	0.58
2:B:61:LEU:HD21	2:B:160:ASP:HB3	1.85	0.58
9:I:99:LEU:HB3	9:I:101:PHE:CE1	2.38	0.58
20:T:60:GLU:HG3	20:T:81:LYS:HG2	1.83	0.58
1:A:1118:C:H1'	1:A:1179:A:C4	2.38	0.58
2:B:215:LEU:O	2:B:219:VAL:HG23	2.03	0.58
6:F:101:ALA:HB1	18:R:28:GLU:OE1	2.04	0.58
12:L:60:LEU:HD21	12:L:66:VAL:HG22	1.85	0.58
16:P:20:VAL:CG1	16:P:21:VAL:N	2.67	0.58
2:B:124:SER:HB2	2:B:125:PRO:HD2	1.85	0.58
12:L:109:GLY:HA3	12:L:121:GLY:O	2.03	0.58
16:P:20:VAL:CG1	16:P:32:TYR:HB2	2.33	0.58
3:C:164:ARG:HB2	3:C:164:ARG:HH11	1.69	0.58
1:A:528:C:H5'	1:A:535:A:C6	2.39	0.58
1:A:1325:C:P	21:U:6:ARG:HH22	2.26	0.58
6:F:19:LEU:HD11	6:F:59:TYR:CE2	2.39	0.58
12:L:115:LYS:C	12:L:117:ARG:H	2.12	0.58
19:S:33:THR:HG22	19:S:34:TRP:N	2.19	0.58
3:C:73:PRO:HD3	3:C:105:GLU:HG3	1.86	0.58
1:A:1161:C:H2'	1:A:1162:C:C6	2.35	0.58
1:A:1532:U:H2'	1:A:1533:C:H5'	1.81	0.58
14:N:14:PRO:O	14:N:15:LYS:HB2	2.01	0.58
1:A:1020:U:H2'	1:A:1021:G:H8	1.68	0.58
1:A:1123:A:O2'	10:J:38:ILE:HG23	2.04	0.58
1:A:1149:C:H2'	1:A:1150:U:C6	2.39	0.58
1:A:1228:C:H4'	13:M:116:THR:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1393:U:O4'	1:A:1502:A:H5'	2.04	0.58
24:A:1601:PAR:H642	24:A:1601:PAR:H43	1.85	0.58
6:F:19:LEU:HD11	6:F:59:TYR:CZ	2.39	0.58
6:F:42:GLU:HG3	6:F:61:LEU:HD23	1.84	0.58
1:A:977:A:H2'	1:A:978:A:H5'	1.86	0.57
4:D:58:LEU:O	4:D:58:LEU:HD22	2.04	0.57
4:D:184:LYS:HG2	4:D:186:LEU:HD23	1.85	0.57
5:E:144:THR:HG23	5:E:146:ALA:H	1.69	0.57
9:I:8:GLY:CA	9:I:79:LEU:HB3	2.33	0.57
16:P:57:ARG:HH12	16:P:79:VAL:HA	1.69	0.57
20:T:53:LEU:HD23	20:T:56:MET:HE3	1.86	0.57
10:J:46:ARG:HH11	10:J:64:GLU:HB3	1.70	0.57
1:A:1397:C:H4'	1:A:1398:A:OP2	2.03	0.57
1:A:1310:G:O6	19:S:2:PRO:HB3	2.05	0.57
6:F:22:GLU:OE2	6:F:22:GLU:HA	2.04	0.57
12:L:75:HIS:CD2	12:L:75:HIS:C	2.82	0.57
13:M:57:ARG:O	13:M:61:GLU:HG3	2.05	0.57
1:A:992:U:H4'	1:A:993:G:O5'	2.05	0.57
1:A:1106:G:H5''	3:C:172:ARG:HG2	1.86	0.57
7:G:77:SER:HB2	7:G:86:GLN:OE1	2.04	0.57
15:O:65:ARG:HH11	15:O:65:ARG:HG2	1.69	0.57
1:A:818:G:C3'	1:A:819:A:H5''	2.34	0.57
1:A:1056:U:H5'	3:C:163:ALA:HB2	1.86	0.57
1:A:1300:G:O2'	1:A:1301:U:H6	1.87	0.57
1:A:1343:G:H2'	1:A:1344:C:C6	2.39	0.57
2:B:137:ARG:HB2	2:B:137:ARG:CZ	2.34	0.57
3:C:58:GLU:O	3:C:64:VAL:HA	2.05	0.57
3:C:58:GLU:HG2	10:J:92:THR:HG21	1.87	0.57
4:D:10:ARG:HH11	4:D:10:ARG:HG3	1.70	0.57
4:D:32:ALA:C	4:D:34:GLU:H	2.11	0.57
16:P:26:ARG:HD2	16:P:31:LYS:O	2.05	0.57
18:R:47:THR:HG22	18:R:48:GLY:H	1.69	0.57
1:A:1054:C:H5	1:A:1196:U:C5	2.23	0.57
1:A:1256:A:H5'	1:A:1258:G:N3	2.20	0.57
1:A:1305:G:H22	1:A:1331:G:HO2'	1.51	0.57
1:A:1381:U:H1'	7:G:78:ARG:HH21	1.70	0.57
6:F:19:LEU:C	6:F:19:LEU:HD23	2.29	0.57
7:G:121:ALA:O	7:G:125:MET:HG3	2.05	0.57
9:I:10:ARG:HG2	9:I:75:ASP:CB	2.35	0.57
9:I:111:ARG:HD3	9:I:112:LYS:N	2.19	0.57
14:N:22:THR:HG23	14:N:33:VAL:CG2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:C:H2'	1:A:270:A:H8	1.69	0.57
1:A:1366:C:H2'	1:A:1367:C:C6	2.39	0.57
4:D:122:ARG:HA	4:D:122:ARG:HE	1.69	0.57
7:G:16:LEU:HD22	7:G:16:LEU:N	2.20	0.57
20:T:89:ARG:O	20:T:93:GLU:HG3	2.05	0.57
1:A:1027:C:N4	1:A:1034:G:H1	2.03	0.57
1:A:1392:G:N2	1:A:1502:A:H8	2.02	0.57
1:A:1404:C:H2'	1:A:1405:G:C8	2.39	0.57
21:U:9:ARG:NH1	21:U:22:ARG:HA	2.20	0.57
1:A:539:A:OP1	12:L:114:LYS:HE2	2.05	0.57
1:A:629:G:H2'	1:A:630:G:O4'	2.04	0.57
1:A:960:U:O2	1:A:960:U:H2'	2.03	0.57
1:A:1053:G:O5'	1:A:1054:C:H5'	2.05	0.57
2:B:42:ILE:HD12	2:B:42:ILE:N	2.20	0.57
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.87	0.57
11:K:29:ILE:HG22	11:K:44:SER:HB2	1.87	0.57
1:A:1262:C:H2'	1:A:1263:C:C6	2.40	0.56
3:C:6:HIS:CD2	3:C:8:ILE:HB	2.40	0.56
6:F:10:LEU:HD23	6:F:85:VAL:HA	1.87	0.56
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.86	0.56
1:A:743:U:H2'	1:A:744:C:C6	2.40	0.56
12:L:28:LYS:HB3	12:L:33:ARG:HH12	1.70	0.56
13:M:11:ARG:HG3	13:M:12:ASN:N	2.20	0.56
14:N:33:VAL:HG23	14:N:33:VAL:O	2.04	0.56
1:A:337:C:H2'	1:A:338:A:C8	2.40	0.56
1:A:860:A:H2'	1:A:861:G:O4'	2.05	0.56
1:A:1125:U:H5'	1:A:1126:U:H5	1.70	0.56
2:B:142:LEU:CG	2:B:146:GLN:HE21	2.06	0.56
12:L:38:THR:HG22	12:L:39:VAL:CG2	2.30	0.56
13:M:35:GLU:C	13:M:37:THR:H	2.14	0.56
15:O:70:LEU:HD12	15:O:78:TYR:HA	1.88	0.56
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.40	0.56
20:T:65:LYS:O	20:T:68:LYS:HG3	2.05	0.56
1:A:738:C:OP1	6:F:92:LYS:HD3	2.05	0.56
1:A:1225:A:H2'	1:A:1226:C:C5	2.41	0.56
7:G:73:MET:HE2	7:G:90:GLU:CA	2.22	0.56
13:M:40:ASN:HD22	13:M:41:PRO:N	2.04	0.56
13:M:40:ASN:ND2	13:M:42:ALA:H	2.04	0.56
19:S:36:ARG:NH2	19:S:75:ALA:O	2.22	0.56
3:C:195:VAL:HG12	3:C:196:LEU:N	2.20	0.56
4:D:65:ARG:HG3	4:D:75:PHE:CD1	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:19:LEU:HD23	6:F:19:LEU:O	2.05	0.56
14:N:8:GLU:OE1	14:N:8:GLU:C	2.48	0.56
2:B:225:ALA:O	2:B:226:ARG:HG3	2.05	0.56
10:J:32:ALA:HB2	10:J:76:ASN:HD22	1.70	0.56
2:B:74:LYS:O	2:B:75:LYS:HB2	2.04	0.56
2:B:75:LYS:CA	2:B:78:GLN:HB2	2.34	0.56
1:A:166:G:O2'	1:A:167:G:H5'	2.04	0.56
2:B:223:ILE:HD13	2:B:229:VAL:HA	1.88	0.56
3:C:64:VAL:N	3:C:99:VAL:HG11	2.21	0.56
13:M:78:ILE:O	13:M:82:MET:HG3	2.06	0.56
15:O:10:LYS:HD3	15:O:10:LYS:O	2.05	0.56
20:T:57:ARG:HG2	20:T:102:GLY:O	2.06	0.56
1:A:716:A:N3	11:K:117:ASN:O	2.39	0.56
1:A:1367:C:H5'	10:J:60:ARG:NH1	2.19	0.56
1:A:1413:A:H2	1:A:1487:G:H22	1.54	0.56
1:A:1428:A:H2'	1:A:1429:C:C6	2.41	0.56
7:G:5:ARG:HD2	7:G:6:ARG:O	2.06	0.56
9:I:10:ARG:HD3	9:I:105:ASP:HB3	1.87	0.56
12:L:55:VAL:HG12	12:L:56:ALA:N	2.20	0.56
13:M:84:ILE:O	13:M:84:ILE:HG13	2.06	0.56
14:N:26:ARG:HH21	14:N:47:LEU:CG	2.19	0.56
20:T:13:LEU:H	20:T:13:LEU:HD12	1.71	0.56
21:U:6:ARG:HE	21:U:15:ARG:HD2	1.69	0.56
1:A:91:C:H2'	1:A:92:C:H6	1.71	0.56
1:A:1504:G:O2'	1:A:1505:G:OP2	2.23	0.56
2:B:114:ARG:O	2:B:118:LEU:HB2	2.05	0.56
3:C:60:ALA:O	3:C:61:ALA:HB2	2.05	0.56
7:G:72:ARG:O	7:G:73:MET:HE3	2.06	0.56
10:J:7:LYS:HZ1	10:J:40:LEU:HD11	1.69	0.56
11:K:14:VAL:O	11:K:15:ALA:HB3	2.06	0.56
19:S:66:MET:HE3	19:S:74:PHE:CE2	2.41	0.56
1:A:377:G:OP1	16:P:3:LYS:HD3	2.06	0.55
1:A:840:C:H4'	1:A:848:C:O2	2.06	0.55
1:A:1299:A:C8	1:A:1301:U:H1'	2.41	0.55
2:B:19:HIS:HD2	2:B:189:ASP:OD1	1.88	0.55
10:J:32:ALA:O	10:J:34:VAL:HG23	2.05	0.55
17:Q:97:SER:HA	17:Q:102:GLY:CA	2.36	0.55
1:A:968:A:H4'	1:A:969:A:OP2	2.05	0.55
1:A:1281:U:H4'	1:A:1282:C:OP2	2.06	0.55
2:B:223:ILE:C	2:B:225:ALA:H	2.13	0.55
3:C:52:LEU:HD23	3:C:52:LEU:H	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:35:ARG:O	4:D:36:ARG:CB	2.54	0.55
5:E:80:ILE:HD12	5:E:80:ILE:N	2.20	0.55
10:J:3:LYS:HB3	10:J:75:ILE:HA	1.88	0.55
11:K:67:ASP:OD1	11:K:71:LYS:HE3	2.05	0.55
1:A:718:G:C5'	11:K:117:ASN:ND2	2.68	0.55
1:A:1514:C:O2'	1:A:1515:C:H5'	2.07	0.55
8:H:120:THR:HG1	8:H:123:GLU:HG3	1.71	0.55
10:J:46:ARG:HH11	10:J:46:ARG:CG	2.19	0.55
10:J:49:VAL:O	10:J:60:ARG:HA	2.06	0.55
15:O:17:ARG:HG3	15:O:17:ARG:NH1	2.17	0.55
1:A:575:G:OP1	1:A:575:G:H4'	2.07	0.55
1:A:1277:C:O2'	1:A:1279:A:H1'	2.06	0.55
2:B:17:PHE:HB3	2:B:44:LEU:CD2	2.28	0.55
2:B:114:ARG:NH1	2:B:118:LEU:HD12	2.21	0.55
2:B:181:PHE:CE2	8:H:70:GLN:HB3	2.42	0.55
4:D:148:VAL:CG1	4:D:158:ILE:HD13	2.36	0.55
15:O:78:TYR:CE1	15:O:82:ILE:HD11	2.40	0.55
1:A:613:C:O2'	1:A:614:A:H5'	2.07	0.55
1:A:737:A:H2'	1:A:738:C:C6	2.40	0.55
1:A:1060:C:C5	3:C:2:GLY:CA	2.85	0.55
1:A:1427:U:H2'	1:A:1428:A:H8	1.70	0.55
13:M:5:ALA:O	13:M:6:GLY:C	2.49	0.55
20:T:53:LEU:HB2	20:T:100:ILE:HG21	1.87	0.55
1:A:973:G:H3'	1:A:974:A:H5''	1.89	0.55
1:A:1247:U:O2'	1:A:1248:A:H5'	2.06	0.55
1:A:1499:A:O2'	1:A:1500:A:H5'	2.07	0.55
2:B:20:GLU:HB2	2:B:190:THR:OG1	2.07	0.55
2:B:60:ASP:CG	2:B:64:ARG:HH22	2.14	0.55
7:G:64:GLN:HE21	7:G:68:ASN:HD21	1.54	0.55
13:M:40:ASN:HD22	13:M:41:PRO:CD	2.20	0.55
18:R:46:GLU:CD	18:R:46:GLU:N	2.64	0.55
1:A:627:G:O2'	1:A:628:G:H5'	2.07	0.55
1:A:780:A:O2'	1:A:781:A:H5''	2.07	0.55
2:B:189:ASP:HB2	2:B:205:ASP:OD2	2.07	0.55
5:E:11:ILE:HD11	5:E:33:VAL:CG2	2.37	0.55
6:F:21:LEU:O	6:F:24:GLU:HG3	2.06	0.55
9:I:5:TYR:O	9:I:84:ALA:HA	2.07	0.55
10:J:30:SER:HB2	10:J:80:LYS:HG3	1.88	0.55
10:J:60:ARG:O	10:J:61:GLU:HB3	2.07	0.55
18:R:47:THR:HG22	18:R:48:GLY:N	2.22	0.55
1:A:56:U:H2'	1:A:57:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:832:C:O2'	1:A:833:U:H5'	2.06	0.55
1:A:1144:G:H21	1:A:1146:A:H62	1.54	0.55
3:C:17:ASP:O	3:C:54:ARG:NH2	2.40	0.55
3:C:55:VAL:O	3:C:55:VAL:HG12	2.05	0.55
9:I:78:LYS:HD3	9:I:101:PHE:HD2	1.72	0.55
10:J:7:LYS:HZ1	10:J:71:LEU:HD23	1.72	0.55
16:P:26:ARG:CD	16:P:31:LYS:O	2.55	0.55
1:A:180:U:C2'	1:A:181:G:H5'	2.37	0.55
1:A:397:A:H5'	1:A:398:C:OP1	2.07	0.55
1:A:1116:C:H2'	1:A:1117:G:C5'	2.37	0.55
1:A:1330:U:OP1	13:M:23:TYR:O	2.24	0.55
2:B:82:ARG:HA	2:B:92:TYR:CE1	2.42	0.55
3:C:110:ASN:HD22	3:C:140:ARG:HB3	1.72	0.55
9:I:22:GLY:N	9:I:58:HIS:O	2.40	0.55
9:I:37:PHE:O	9:I:40:LEU:HG	2.07	0.55
1:A:631:G:H2'	1:A:632:A:C8	2.41	0.55
2:B:12:GLU:HA	2:B:12:GLU:OE2	2.06	0.55
2:B:60:ASP:HB3	2:B:64:ARG:HH12	1.71	0.55
4:D:70:ILE:CG2	4:D:74:GLN:HB2	2.37	0.55
7:G:79:ARG:NH2	7:G:82:GLY:H	2.05	0.55
10:J:6:ILE:HD12	10:J:6:ILE:O	2.06	0.55
13:M:81:LEU:CD1	13:M:88:ARG:HD3	2.35	0.55
1:A:814:A:H2'	1:A:816:A:H5''	1.89	0.54
1:A:913:A:OP1	12:L:91:LYS:HE2	2.07	0.54
7:G:129:GLU:CD	7:G:131:LYS:HE2	2.32	0.54
9:I:8:GLY:HA3	9:I:80:GLY:H	1.72	0.54
9:I:31:GLN:HG2	9:I:35:GLU:HG3	1.89	0.54
15:O:29:VAL:HG11	15:O:67:LEU:HD21	1.88	0.54
19:S:15:LEU:O	19:S:19:VAL:HG12	2.07	0.54
1:A:1152:A:H5''	10:J:13:HIS:CG	2.40	0.54
1:A:1152:A:H2'	1:A:1153:C:H6	1.72	0.54
1:A:1286:A:C8	1:A:1287:A:H4'	2.42	0.54
1:A:1394:A:C5	1:A:1501:C:H4'	2.42	0.54
12:L:74:GLY:O	12:L:75:HIS:CB	2.52	0.54
12:L:111:LYS:O	12:L:112:ASP:HB2	2.06	0.54
13:M:13:LYS:HE2	13:M:21:TYR:OH	2.07	0.54
19:S:20:LEU:HA	19:S:23:ASN:ND2	2.22	0.54
1:A:1001(A):G:H3'	1:A:1002:G:H8	1.72	0.54
1:A:1074:G:O3'	2:B:103:THR:CG2	2.56	0.54
1:A:1425:U:H3	1:A:1475:G:H1	1.55	0.54
2:B:137:ARG:NH1	2:B:137:ARG:CB	2.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:64:VAL:N	3:C:99:VAL:CG1	2.70	0.54
5:E:51:VAL:HB	5:E:52:PRO:CD	2.32	0.54
19:S:15:LEU:HD12	19:S:16:LEU:N	2.21	0.54
1:A:382:A:C2	1:A:383:A:C4	2.96	0.54
1:A:403:C:H6	1:A:403:C:H5'	1.72	0.54
1:A:620:C:C2	4:D:135:LEU:HD13	2.42	0.54
1:A:1355:G:O2'	1:A:1356:G:H5'	2.07	0.54
3:C:164:ARG:HH22	3:C:166:GLU:CD	2.15	0.54
5:E:144:THR:HB	5:E:147:ASP:OD2	2.07	0.54
12:L:111:LYS:CA	12:L:111:LYS:HE3	2.37	0.54
1:A:287:U:O2'	1:A:288:A:H5'	2.08	0.54
2:B:69:LEU:HD23	2:B:70:PHE:N	2.23	0.54
3:C:23:TYR:C	3:C:23:TYR:CD2	2.86	0.54
4:D:196:LEU:C	4:D:198:VAL:H	2.16	0.54
9:I:53:VAL:CG2	9:I:85:LEU:HD21	2.37	0.54
14:N:41:ARG:HG2	14:N:41:ARG:NH1	2.21	0.54
16:P:59:TRP:HA	16:P:62:VAL:HG22	1.89	0.54
1:A:537:G:OP1	12:L:113:ARG:NH2	2.40	0.54
1:A:1056:U:H5'	3:C:163:ALA:CB	2.38	0.54
1:A:1273:G:H2'	1:A:1274:G:O4'	2.07	0.54
5:E:51:VAL:O	5:E:54:ALA:HB3	2.08	0.54
9:I:31:GLN:O	9:I:32:ASP:CB	2.54	0.54
10:J:49:VAL:HG21	14:N:41:ARG:O	2.08	0.54
15:O:18:PHE:HB2	15:O:19:PRO:HD2	1.89	0.54
18:R:18:ARG:O	18:R:19:LYS:CB	2.56	0.54
1:A:226:G:O2'	1:A:227:G:H5'	2.08	0.54
1:A:1347:G:O2'	1:A:1348:U:P	2.64	0.54
4:D:62:GLN:HE22	4:D:65:ARG:NH1	2.06	0.54
6:F:3:ARG:HH11	6:F:3:ARG:CG	2.20	0.54
10:J:30:SER:HB2	10:J:80:LYS:O	2.08	0.54
13:M:96:LEU:O	13:M:110:ARG:NH1	2.41	0.54
1:A:974:A:OP2	14:N:41:ARG:NH1	2.41	0.54
2:B:206:ASP:O	2:B:207:ALA:HB2	2.07	0.54
7:G:135:VAL:O	7:G:139:GLU:HG3	2.07	0.54
19:S:40:ILE:HG23	19:S:62:ILE:HD12	1.90	0.54
1:A:1241:G:H2'	1:A:1242:C:H6	1.72	0.54
3:C:34:LEU:HD23	14:N:25:VAL:HG21	1.90	0.54
12:L:83:VAL:HG11	12:L:100:ILE:HD13	1.89	0.54
1:A:536:C:H2'	1:A:537:G:C8	2.42	0.54
1:A:620:C:H2'	1:A:621:A:O4'	2.08	0.54
1:A:1000:U:H2'	1:A:1001:A:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:137:GLU:OE1	5:E:141:GLN:NE2	2.39	0.54
12:L:111:LYS:HE3	12:L:111:LYS:HA	1.90	0.54
12:L:119:LYS:O	12:L:120:TYR:HB2	2.08	0.54
1:A:168:G:O2'	1:A:169:C:H5'	2.08	0.53
1:A:723:U:O2	1:A:723:U:H2'	2.07	0.53
1:A:759:A:N6	17:Q:94:ASN:HD21	2.06	0.53
9:I:8:GLY:HA3	9:I:80:GLY:N	2.24	0.53
9:I:11:LYS:O	9:I:11:LYS:HG2	2.07	0.53
1:A:923:A:OP1	5:E:21:ALA:HB2	2.08	0.53
1:A:1125:U:N3	10:J:5:ARG:NH2	2.54	0.53
1:A:1152:A:OP1	10:J:68:HIS:ND1	2.41	0.53
1:A:1441:G:H4'	1:A:1442:G:C5	2.44	0.53
2:B:105:PHE:HE1	2:B:155:LEU:HD23	1.73	0.53
3:C:27:LYS:HB2	3:C:28:GLN:HE21	1.73	0.53
3:C:58:GLU:CG	10:J:92:THR:HG21	2.38	0.53
3:C:64:VAL:CB	3:C:99:VAL:HG11	2.37	0.53
4:D:199:ASN:HD22	4:D:199:ASN:C	2.15	0.53
6:F:4:TYR:CE1	6:F:92:LYS:HG2	2.43	0.53
10:J:79:ARG:HG2	10:J:79:ARG:NH1	2.22	0.53
12:L:27:LEU:C	12:L:29:GLY:N	2.57	0.53
20:T:94:ALA:O	20:T:95:ALA:HB2	2.07	0.53
1:A:1104:G:OP1	2:B:111:ARG:HD2	2.09	0.53
1:A:1479:C:H2'	1:A:1480:G:H8	1.73	0.53
2:B:14:GLY:O	2:B:15:VAL:HG13	2.08	0.53
2:B:213:LEU:HD23	2:B:213:LEU:C	2.33	0.53
3:C:40:ARG:O	3:C:44:GLU:HG3	2.08	0.53
10:J:18:ALA:C	10:J:20:ALA:H	2.15	0.53
13:M:90:LEU:O	13:M:94:ARG:HG2	2.07	0.53
15:O:6:GLU:CD	15:O:6:GLU:N	2.65	0.53
1:A:21:G:H2'	1:A:22:G:C8	2.44	0.53
2:B:187:LEU:HD23	2:B:201:ILE:O	2.09	0.53
3:C:107:GLN:O	3:C:108:ASN:HB3	2.07	0.53
7:G:38:LEU:C	7:G:38:LEU:HD12	2.32	0.53
8:H:86:ILE:HD12	8:H:133:LEU:HD22	1.89	0.53
12:L:50:SER:O	12:L:51:ALA:HB2	2.08	0.53
1:A:192:U:H4'	20:T:102:GLY:C	2.33	0.53
1:A:1057:G:O2'	1:A:1058:G:H5'	2.08	0.53
1:A:1191:A:OP1	3:C:4:LYS:HE2	2.09	0.53
1:A:1320:C:OP1	19:S:70:LYS:HE2	2.08	0.53
2:B:7:VAL:C	2:B:8:LYS:HG3	2.32	0.53
2:B:213:LEU:HD22	2:B:214:ILE:HD13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:70:VAL:CG1	3:C:71:ALA:N	2.72	0.53
9:I:37:PHE:O	9:I:38:GLN:C	2.52	0.53
9:I:56:LEU:O	9:I:56:LEU:HD23	2.08	0.53
1:A:255:G:H1'	17:Q:16:GLN:NE2	2.24	0.53
1:A:1311:G:N7	19:S:2:PRO:HA	2.24	0.53
2:B:21:ARG:HG3	2:B:21:ARG:NH1	2.23	0.53
19:S:4:SER:OG	19:S:5:LEU:N	2.42	0.53
1:A:918:A:H2'	1:A:919:A:C8	2.44	0.53
1:A:1178:G:N2	1:A:1180:A:H3'	2.23	0.53
3:C:157:ILE:HD13	3:C:166:GLU:HG3	1.90	0.53
13:M:93:ARG:NH1	13:M:93:ARG:HB2	2.24	0.53
1:A:254:G:O2'	1:A:255:G:H5'	2.08	0.53
1:A:384:G:H2'	1:A:385:C:H6	1.72	0.53
1:A:969:A:H61	13:M:126:LYS:HB2	1.72	0.53
2:B:188:ALA:HB3	2:B:200:ILE:HD11	1.90	0.53
9:I:97:LYS:HB3	9:I:98:PRO:HD3	1.91	0.53
1:A:353:A:H5'	1:A:353:A:C8	2.44	0.53
1:A:390:C:H2'	1:A:391:G:C8	2.44	0.53
1:A:839:U:O2	1:A:839:U:H2'	2.08	0.53
10:J:4:ILE:HG12	10:J:74:ILE:HB	1.90	0.53
10:J:20:ALA:O	10:J:24:VAL:HG23	2.09	0.53
18:R:88:LYS:HB3	18:R:88:LYS:HZ3	1.74	0.53
20:T:14:LYS:O	20:T:18:GLN:HG3	2.09	0.53
1:A:458:C:H2'	1:A:460:G:O4'	2.08	0.53
1:A:1020:U:H2'	1:A:1021:G:C8	2.44	0.53
1:A:1279:A:H5''	1:A:1280:A:OP1	2.09	0.53
1:A:1318:A:H1'	19:S:37:ARG:HH11	1.74	0.53
3:C:34:LEU:HD11	3:C:38:ARG:CZ	2.39	0.53
10:J:35:SER:N	10:J:73:ASP:O	2.38	0.53
1:A:328:C:O2	1:A:328:C:H2'	2.09	0.52
4:D:68:TYR:CB	4:D:70:ILE:HD13	2.39	0.52
11:K:76:GLY:O	11:K:78:GLN:HG3	2.09	0.52
18:R:73:ALA:CB	18:R:79:LEU:HD12	2.39	0.52
1:A:337:C:H2'	1:A:338:A:H8	1.73	0.52
1:A:750:G:N3	15:O:23:GLY:HA3	2.24	0.52
3:C:34:LEU:HD13	3:C:34:LEU:C	2.34	0.52
6:F:35:ALA:HA	6:F:67:MET:HB3	1.90	0.52
6:F:42:GLU:HG3	6:F:61:LEU:CD2	2.38	0.52
10:J:76:ASN:C	10:J:78:ASN:N	2.61	0.52
20:T:79:ARG:O	20:T:83:ARG:HG3	2.10	0.52
1:A:370:C:O2'	1:A:371:G:H5'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:119:ARG:HG3	3:C:119:ARG:NH1	2.23	0.52
4:D:30:LYS:C	4:D:32:ALA:N	2.68	0.52
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.44	0.52
13:M:124:PRO:CB	13:M:126:LYS:HE2	2.40	0.52
15:O:26:GLU:HG3	15:O:81:LEU:HG	1.90	0.52
20:T:56:MET:CE	20:T:88:VAL:HG11	2.38	0.52
1:A:410:G:H4'	1:A:411:A:OP1	2.10	0.52
1:A:818:G:H3'	1:A:819:A:C5'	2.40	0.52
1:A:1054:C:H2'	1:A:1055:A:C5'	2.36	0.52
1:A:1072:G:H2'	1:A:1073:U:C6	2.45	0.52
4:D:23:GLY:HA3	4:D:112:VAL:HG22	1.90	0.52
4:D:24:GLU:C	4:D:26:CYS:H	2.17	0.52
4:D:32:ALA:C	4:D:34:GLU:N	2.63	0.52
4:D:64:LEU:CD1	4:D:75:PHE:HZ	2.22	0.52
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.45	0.52
9:I:127:LYS:HG2	9:I:128:ARG:N	2.23	0.52
10:J:33:GLN:HB2	10:J:75:ILE:HD11	1.90	0.52
10:J:74:ILE:HD13	10:J:81:THR:HG21	1.90	0.52
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.73	0.52
13:M:90:LEU:HD22	13:M:94:ARG:NH1	2.24	0.52
14:N:22:THR:HG23	14:N:33:VAL:HG21	1.92	0.52
3:C:35:GLU:HG2	3:C:59:ARG:NH2	2.23	0.52
3:C:129:ALA:HB3	3:C:132:ARG:CZ	2.40	0.52
10:J:32:ALA:CB	10:J:78:ASN:HD21	2.23	0.52
10:J:59:SER:O	10:J:60:ARG:HB2	2.09	0.52
1:A:1262:C:H2'	1:A:1263:C:H6	1.73	0.52
1:A:1342:C:O2'	1:A:1343:G:H5'	2.09	0.52
2:B:111:ARG:NE	2:B:111:ARG:HA	2.23	0.52
17:Q:68:ARG:HG2	17:Q:68:ARG:HH11	1.75	0.52
1:A:427:U:OP1	4:D:13:ARG:NH2	2.42	0.52
1:A:818:G:C3'	1:A:819:A:C5'	2.87	0.52
2:B:86:GLU:C	2:B:88:ALA:N	2.68	0.52
3:C:116:VAL:O	3:C:120:VAL:HG23	2.08	0.52
7:G:150:ALA:O	11:K:57:THR:HG21	2.09	0.52
11:K:108:ILE:N	11:K:108:ILE:HD12	2.24	0.52
11:K:115:PRO:C	11:K:117:ASN:H	2.16	0.52
18:R:16:PRO:HB2	18:R:18:ARG:CZ	2.39	0.52
1:A:189(A):C:H2'	1:A:189(B):C:C6	2.45	0.52
1:A:814:A:H2'	1:A:816:A:C5'	2.40	0.52
2:B:10:LEU:HG	2:B:48:MET:HE2	1.92	0.52
5:E:93:PRO:HG2	8:H:105:ARG:NH2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:15:ASP:H	6:F:18:GLN:HE21	1.55	0.52
10:J:90:LEU:H	10:J:91:PRO:HD2	1.75	0.52
1:A:1542:U:H2'	1:A:1543:C:H5''	1.92	0.52
3:C:126:ARG:O	3:C:128:PHE:N	2.43	0.52
13:M:13:LYS:O	13:M:45:VAL:HG23	2.10	0.52
19:S:16:LEU:O	19:S:20:LEU:HG	2.10	0.52
1:A:828:A:H4'	1:A:828:A:OP1	2.10	0.52
2:B:118:LEU:HD23	2:B:118:LEU:C	2.35	0.52
9:I:84:ALA:O	9:I:87:GLN:HB2	2.10	0.52
10:J:85:LEU:O	10:J:87:THR:N	2.43	0.52
1:A:1314:C:OP2	19:S:6:LYS:HG3	2.10	0.51
1:A:1331:G:O2'	1:A:1332:A:P	2.67	0.51
2:B:55:PHE:HD2	2:B:58:ILE:HD12	1.75	0.51
3:C:34:LEU:O	3:C:34:LEU:HD22	2.10	0.51
7:G:126:ASP:CG	7:G:131:LYS:HE3	2.35	0.51
11:K:34:ASP:C	11:K:34:ASP:OD1	2.52	0.51
11:K:108:ILE:O	11:K:109:VAL:HG23	2.10	0.51
17:Q:5:VAL:HA	17:Q:59:ILE:O	2.10	0.51
19:S:42:PRO:C	19:S:44:MET:H	2.17	0.51
1:A:1026:G:C2'	1:A:1027:C:H5''	2.37	0.51
1:A:1128:C:H5'	9:I:16:ARG:NH2	2.24	0.51
2:B:193:ASP:HB3	2:B:196:LEU:HD13	1.92	0.51
7:G:146:GLU:HG2	7:G:149:ARG:NH2	2.25	0.51
19:S:44:MET:HE2	19:S:49:ILE:HD11	1.91	0.51
1:A:1125:U:H5'	1:A:1126:U:C5	2.45	0.51
8:H:120:THR:OG1	8:H:122:ARG:HG2	2.10	0.51
10:J:8:LEU:HB3	10:J:16:LEU:HD22	1.92	0.51
14:N:44:LEU:HD12	14:N:44:LEU:O	2.10	0.51
1:A:1014:A:H2	1:A:1219:U:H1'	1.71	0.51
2:B:61:LEU:HD21	2:B:160:ASP:HB2	1.91	0.51
2:B:135:GLN:O	2:B:139:LYS:HB2	2.11	0.51
13:M:3:ARG:HD3	13:M:9:ILE:CG2	2.32	0.51
1:A:1207:G:H2'	1:A:1208:C:H6	1.75	0.51
2:B:139:LYS:HD3	2:B:139:LYS:O	2.10	0.51
2:B:230:VAL:CG1	2:B:231:GLU:H	2.23	0.51
4:D:162:LEU:HD13	4:D:181:MET:HG2	1.92	0.51
9:I:78:LYS:HD3	9:I:101:PHE:CD2	2.44	0.51
10:J:51:ARG:HG2	10:J:60:ARG:O	2.11	0.51
1:A:189(B):C:H2'	1:A:189(C):C:C6	2.46	0.51
1:A:617:G:H4'	16:P:44:THR:O	2.10	0.51
1:A:939:G:H5''	7:G:102:ARG:HH22	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:992:U:H4'	1:A:993:G:O4'	2.11	0.51
1:A:1331:G:O2'	1:A:1332:A:OP2	2.26	0.51
3:C:50:ALA:CB	3:C:70:VAL:HG11	2.19	0.51
3:C:127:ARG:HE	3:C:127:ARG:N	2.08	0.51
5:E:144:THR:CG2	5:E:146:ALA:HB3	2.41	0.51
8:H:49:GLU:HG2	8:H:62:TYR:HE2	1.75	0.51
11:K:21:ILE:CD1	11:K:95:ILE:HD13	2.37	0.51
1:A:841:U:H3'	1:A:848:C:O4'	2.10	0.51
1:A:1143:G:H2'	1:A:1144:G:C8	2.46	0.51
1:A:1347:G:C2'	1:A:1348:U:OP2	2.59	0.51
6:F:38:GLU:O	6:F:39:LYS:HB3	2.11	0.51
11:K:33:THR:HG22	11:K:39:PRO:CA	2.39	0.51
13:M:125:ARG:O	13:M:126:LYS:C	2.54	0.51
1:A:186:C:O2	20:T:85:MET:HE1	2.11	0.51
1:A:639:G:O2'	1:A:640:A:H5'	2.10	0.51
1:A:1053:G:C3'	1:A:1054:C:C5'	2.88	0.51
6:F:47:ARG:N	6:F:47:ARG:HD3	2.26	0.51
13:M:40:ASN:HB3	13:M:43:THR:CG2	2.37	0.51
15:O:82:ILE:HD13	15:O:88:ARG:HG3	1.92	0.51
1:A:262:A:H5'	20:T:74:LYS:HG3	1.92	0.51
2:B:108:ILE:O	2:B:111:ARG:HB2	2.10	0.51
4:D:126:ILE:HG22	4:D:127:THR:H	1.76	0.51
6:F:64:GLN:O	6:F:64:GLN:HG2	2.10	0.51
9:I:7:THR:O	9:I:8:GLY:O	2.29	0.51
9:I:114:TYR:CE1	10:J:59:SER:O	2.63	0.51
10:J:15:THR:O	10:J:18:ALA:N	2.38	0.51
1:A:123:C:OP1	1:A:312:C:H5'	2.11	0.51
1:A:1300:G:HO2'	1:A:1301:U:H6	1.56	0.51
3:C:34:LEU:HD23	14:N:25:VAL:CG2	2.41	0.51
8:H:112:LEU:N	8:H:112:LEU:CD2	2.74	0.51
9:I:8:GLY:HA2	9:I:79:LEU:CD1	2.38	0.51
10:J:80:LYS:HB2	10:J:80:LYS:NZ	2.26	0.51
17:Q:68:ARG:HH11	17:Q:68:ARG:CG	2.24	0.51
18:R:21:LYS:HE3	18:R:54:ARG:O	2.11	0.51
1:A:1487:G:O2'	1:A:1488:G:H5'	2.11	0.50
1:A:1521:G:H2'	1:A:1522:U:C6	2.46	0.50
2:B:15:VAL:CG1	2:B:209:ARG:HB2	2.40	0.50
4:D:152:SER:C	4:D:154:ASN:H	2.17	0.50
10:J:48:THR:OG1	10:J:62:HIS:CD2	2.64	0.50
14:N:6:LEU:C	14:N:8:GLU:H	2.19	0.50
16:P:43:LYS:HG2	16:P:48:TRP:CE2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:52:LYS:N	17:Q:55:ASP:OD2	2.41	0.50
17:Q:66:SER:OG	17:Q:69:LYS:HB3	2.12	0.50
4:D:92:VAL:O	4:D:96:LEU:HD13	2.11	0.50
13:M:49:THR:HB	13:M:52:GLU:HG3	1.92	0.50
14:N:36:PHE:O	14:N:36:PHE:CD1	2.65	0.50
15:O:39:LEU:HD12	15:O:56:LEU:HD13	1.93	0.50
1:A:164:U:H2'	1:A:165:C:C6	2.46	0.50
1:A:718:G:C4'	11:K:117:ASN:ND2	2.74	0.50
1:A:969:A:H61	13:M:126:LYS:HB3	1.75	0.50
1:A:1230:C:O2'	1:A:1231:G:H5'	2.11	0.50
1:A:1303:C:H2'	1:A:1304:G:H5'	1.93	0.50
1:A:1366:C:H2'	1:A:1367:C:H6	1.75	0.50
1:A:1542:U:C2'	1:A:1543:C:H5''	2.41	0.50
2:B:188:ALA:CB	2:B:200:ILE:HD11	2.42	0.50
7:G:79:ARG:HH12	7:G:81:GLY:HA2	1.76	0.50
8:H:50:ARG:HG2	8:H:50:ARG:HH11	1.76	0.50
9:I:9:ARG:NE	9:I:14:VAL:HG12	2.27	0.50
10:J:18:ALA:C	10:J:20:ALA:N	2.65	0.50
19:S:80:TYR:CE1	19:S:81:ARG:HB3	2.46	0.50
1:A:921:U:O2	5:E:19:MET:HB2	2.11	0.50
1:A:1143:G:H2'	1:A:1144:G:H8	1.74	0.50
1:A:1369:C:H2'	1:A:1370:G:C8	2.46	0.50
1:A:1475:G:H2'	1:A:1476:G:H8	1.75	0.50
2:B:28:PHE:CD1	2:B:194:PRO:HG3	2.45	0.50
5:E:116:THR:HG23	5:E:117:ASP:OD2	2.12	0.50
17:Q:33:GLY:O	17:Q:34:LYS:C	2.54	0.50
17:Q:59:ILE:HD13	17:Q:73:VAL:HA	1.93	0.50
19:S:15:LEU:O	19:S:19:VAL:N	2.44	0.50
20:T:86:ARG:HG2	20:T:90:GLN:HE22	1.76	0.50
1:A:1187:G:OP1	9:I:113:LYS:HE2	2.11	0.50
2:B:118:LEU:CD2	2:B:142:LEU:HB2	2.42	0.50
6:F:53:ALA:O	6:F:54:LYS:HB2	2.11	0.50
7:G:79:ARG:HH22	7:G:81:GLY:HA2	1.76	0.50
8:H:20:TYR:CE1	8:H:76:PRO:HG2	2.46	0.50
8:H:51:VAL:HG11	8:H:60:ARG:HG3	1.94	0.50
9:I:10:ARG:HG2	9:I:75:ASP:HB2	1.92	0.50
11:K:57:THR:CG2	11:K:58:PRO:HD2	2.41	0.50
17:Q:27:PHE:CZ	17:Q:36:ILE:HD11	2.47	0.50
1:A:551:U:H2'	1:A:552:U:C6	2.46	0.50
1:A:920:U:H2'	1:A:921:U:C6	2.47	0.50
1:A:939:G:H2'	1:A:940:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:20:GLU:OE2	2:B:189:ASP:OD1	2.29	0.50
2:B:51:LEU:O	2:B:55:PHE:HB2	2.12	0.50
2:B:75:LYS:HB2	2:B:76:GLN:HE21	1.77	0.50
3:C:42:LEU:C	3:C:44:GLU:H	2.20	0.50
9:I:79:LEU:HD22	9:I:83:ARG:HG3	1.93	0.50
10:J:6:ILE:HG22	10:J:98:ILE:HA	1.93	0.50
1:A:56:U:H2'	1:A:57:G:H8	1.77	0.50
1:A:487:A:H2'	1:A:488:C:O4'	2.11	0.50
1:A:1101:A:H4'	1:A:1102:A:O5'	2.12	0.50
1:A:1486:G:H2'	1:A:1487:G:O4'	2.12	0.50
5:E:92:LYS:HB3	5:E:119:LEU:HB2	1.93	0.50
5:E:144:THR:O	5:E:148:VAL:HG23	2.11	0.50
9:I:125:TYR:HD2	9:I:125:TYR:N	2.09	0.50
1:A:216:G:H1'	1:A:217:C:C6	2.46	0.50
1:A:945:G:C2	1:A:946:A:C8	3.00	0.50
1:A:1007:C:O2'	1:A:1008:C:H5'	2.12	0.50
1:A:1201:A:O2'	1:A:1202:G:OP2	2.23	0.50
2:B:144:ARG:HA	2:B:147:LYS:HG2	1.94	0.50
3:C:181:ASN:ND2	3:C:204:LEU:CD1	2.74	0.50
7:G:6:ARG:HB3	7:G:6:ARG:HH11	1.77	0.50
10:J:35:SER:CB	10:J:73:ASP:HB2	2.41	0.50
13:M:84:ILE:O	13:M:86:CYS:N	2.42	0.50
16:P:4:ILE:HA	16:P:20:VAL:O	2.11	0.50
1:A:154:C:O2'	1:A:155:C:H5'	2.12	0.50
4:D:13:ARG:HD2	4:D:36:ARG:O	2.12	0.50
4:D:31:CYS:C	4:D:33:MET:N	2.70	0.50
5:E:80:ILE:HD13	5:E:91:LEU:HB2	1.91	0.50
9:I:47:LEU:C	9:I:49:PRO:HD2	2.36	0.50
19:S:20:LEU:HA	19:S:23:ASN:HD22	1.76	0.50
1:A:405:U:H3'	1:A:406:G:H5'	1.94	0.49
1:A:1096:C:H2'	1:A:1097:C:H6	1.76	0.49
10:J:20:ALA:C	10:J:22:LYS:H	2.20	0.49
14:N:3:ARG:NH1	14:N:6:LEU:HD11	2.27	0.49
14:N:7:ILE:O	14:N:7:ILE:HG22	2.12	0.49
14:N:8:GLU:OE1	14:N:9:LYS:N	2.45	0.49
17:Q:69:LYS:C	17:Q:70:ARG:HD2	2.37	0.49
18:R:16:PRO:HB2	18:R:18:ARG:NE	2.27	0.49
1:A:477:A:O2'	1:A:479:C:H5'	2.12	0.49
1:A:528:C:H41	12:L:49:ASN:ND2	2.10	0.49
1:A:954:G:H21	1:A:1227:A:H62	1.60	0.49
1:A:1170:A:H2'	1:A:1171:G:O4'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:82:ARG:O	2:B:86:GLU:HG3	2.12	0.49
2:B:157:ARG:HH11	2:B:157:ARG:HG3	1.76	0.49
3:C:11:ARG:NH1	3:C:177:THR:O	2.45	0.49
10:J:4:ILE:O	10:J:73:ASP:HA	2.12	0.49
1:A:189(I):G:O2'	1:A:189(J):G:H5'	2.11	0.49
1:A:980:C:H2'	1:A:981:U:O4'	2.13	0.49
1:A:1060:C:H2'	1:A:1061:G:C8	2.46	0.49
1:A:1497:G:O2'	1:A:1498:U:H5'	2.12	0.49
1:A:1539:C:P	7:G:82:GLY:C	2.95	0.49
2:B:25:ASN:HD22	2:B:27:LYS:H	1.60	0.49
2:B:35:GLU:HA	2:B:39:ILE:O	2.12	0.49
5:E:57:LYS:HG2	5:E:61:TYR:CE2	2.48	0.49
16:P:81:ARG:HG2	16:P:83:GLU:HG2	1.94	0.49
1:A:399:G:H2'	1:A:400:C:C6	2.46	0.49
1:A:627:G:H2'	1:A:628:G:H8	1.78	0.49
1:A:974:A:OP2	14:N:29:ARG:NH2	2.43	0.49
1:A:1181:G:O2'	1:A:1182:G:O5'	2.30	0.49
1:A:1216:G:O2'	1:A:1217:C:H5'	2.12	0.49
1:A:1539:C:C5'	7:G:82:GLY:H	2.24	0.49
2:B:42:ILE:H	2:B:42:ILE:CD1	2.24	0.49
3:C:64:VAL:H	3:C:99:VAL:CG1	2.26	0.49
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.13	0.49
13:M:11:ARG:CG	13:M:12:ASN:N	2.75	0.49
14:N:8:GLU:C	14:N:10:ALA:N	2.70	0.49
1:A:145:G:O2'	1:A:146:G:H5'	2.12	0.49
1:A:741:G:O2'	1:A:742:G:H5'	2.12	0.49
1:A:757:U:H2'	1:A:758:G:O4'	2.13	0.49
1:A:1116:C:H2'	1:A:1117:G:H5''	1.94	0.49
1:A:1120:G:H2'	1:A:1121:U:H6	1.77	0.49
1:A:1201:A:HO2'	1:A:1202:G:P	2.35	0.49
1:A:1456:G:H2'	1:A:1457:G:O4'	2.12	0.49
2:B:217:ARG:HA	2:B:220:ASP:OD2	2.13	0.49
4:D:105:VAL:HG13	4:D:110:PHE:HB2	1.94	0.49
7:G:51:GLN:C	7:G:53:LYS:H	2.20	0.49
7:G:65:ALA:HB1	7:G:127:ALA:CB	2.42	0.49
13:M:14:ARG:HG3	13:M:44:ARG:HH21	1.77	0.49
18:R:37:VAL:HG22	18:R:78:LEU:HB3	1.94	0.49
18:R:39:VAL:CG1	18:R:40:LEU:N	2.75	0.49
13:M:40:ASN:HD22	13:M:40:ASN:C	2.19	0.49
1:A:197:A:N1	1:A:220:G:O2'	2.45	0.49
1:A:390:C:O3'	16:P:28:ARG:NH2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1022:G:H2'	1:A:1023:G:H8	1.76	0.49
1:A:1182:G:H4'	1:A:1183:A:O5'	2.12	0.49
4:D:100:ARG:HH12	4:D:137:SER:HB3	1.77	0.49
1:A:109:A:H2'	1:A:326:G:N2	2.27	0.49
1:A:685:G:O2'	1:A:686:U:H5'	2.13	0.49
1:A:1532:U:C3'	1:A:1533:C:C5'	2.90	0.49
2:B:119:GLU:HG2	2:B:142:LEU:HD11	1.95	0.49
8:H:119:LEU:CD1	8:H:124:ALA:HA	2.41	0.49
9:I:87:GLN:O	9:I:88:TYR:C	2.56	0.49
16:P:1:MET:HE3	16:P:65:GLN:HB2	1.95	0.49
18:R:36:ASN:OD1	18:R:39:VAL:HB	2.13	0.49
20:T:43:LEU:HD13	20:T:51:GLU:HG3	1.95	0.49
1:A:495:A:H4'	1:A:496:A:O5'	2.11	0.49
1:A:1128:C:O2'	1:A:1130:A:N7	2.45	0.49
1:A:1136:U:H5''	1:A:1137:C:OP2	2.13	0.49
1:A:1385:G:O2'	1:A:1386:G:H5'	2.13	0.49
1:A:1431:C:H2'	1:A:1432:G:O4'	2.13	0.49
11:K:34:ASP:OD1	11:K:36:ASP:N	2.42	0.49
1:A:60:A:H4'	1:A:61:G:O5'	2.13	0.49
1:A:1218:C:H2'	1:A:1219:U:C6	2.47	0.49
1:A:105:G:H2'	1:A:106:C:H6	1.77	0.48
1:A:624:C:O2'	1:A:625:G:H5'	2.13	0.48
1:A:913:A:P	12:L:91:LYS:HE2	2.53	0.48
8:H:50:ARG:HG2	8:H:50:ARG:NH1	2.28	0.48
10:J:34:VAL:H	10:J:75:ILE:HG12	1.78	0.48
18:R:26:LEU:HD23	18:R:29:PHE:CE2	2.48	0.48
20:T:76:ALA:O	20:T:80:ARG:HG3	2.13	0.48
1:A:797:C:O2'	1:A:798:G:H5'	2.11	0.48
1:A:900:A:H2'	1:A:901:A:C8	2.48	0.48
1:A:1300:G:O2'	1:A:1301:U:P	2.71	0.48
2:B:115:LEU:O	2:B:119:GLU:HG3	2.13	0.48
2:B:221:LEU:O	2:B:221:LEU:HD13	2.13	0.48
4:D:157:LEU:HD11	4:D:161:ASN:HD21	1.77	0.48
6:F:3:ARG:NH1	6:F:38:GLU:OE1	2.46	0.48
6:F:14:LEU:HA	6:F:18:GLN:HE21	1.78	0.48
10:J:26:ALA:HB3	10:J:85:LEU:CD2	2.44	0.48
17:Q:67:LYS:CA	17:Q:70:ARG:NH1	2.74	0.48
19:S:66:MET:HE3	19:S:74:PHE:CZ	2.47	0.48
20:T:8:ARG:O	20:T:9:ASN:CB	2.61	0.48
1:A:191:G:N2	20:T:85:MET:HE1	2.27	0.48
1:A:436:C:O2'	1:A:437:U:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:445:G:O2'	1:A:446:G:H5'	2.12	0.48
1:A:556:C:O2'	1:A:557:G:H5'	2.13	0.48
6:F:41:GLU:HB2	6:F:62:TRP:HB3	1.95	0.48
7:G:15:ASP:OD2	7:G:16:LEU:N	2.46	0.48
7:G:78:ARG:HD3	7:G:79:ARG:O	2.13	0.48
12:L:117:ARG:O	12:L:119:LYS:O	2.31	0.48
13:M:23:TYR:O	13:M:25:ILE:N	2.45	0.48
14:N:9:LYS:HD3	14:N:9:LYS:C	2.39	0.48
1:A:382:A:O2'	1:A:383:A:H5'	2.13	0.48
1:A:839:U:O2	1:A:839:U:C2'	2.61	0.48
1:A:853:G:O2'	1:A:854:G:H5'	2.13	0.48
8:H:24:THR:HG22	8:H:63:LEU:HD21	1.96	0.48
8:H:51:VAL:HG11	8:H:60:ARG:NH1	2.27	0.48
9:I:27:THR:HG23	9:I:62:TYR:HA	1.96	0.48
6:F:46:ARG:HG2	6:F:47:ARG:N	2.28	0.48
8:H:60:ARG:HG3	8:H:60:ARG:NH1	2.28	0.48
9:I:57:GLY:C	9:I:58:HIS:ND1	2.71	0.48
12:L:58:VAL:O	12:L:65:GLU:HA	2.13	0.48
12:L:79:GLU:O	12:L:79:GLU:HG2	2.14	0.48
15:O:17:ARG:HD3	15:O:26:GLU:CD	2.39	0.48
1:A:184:G:H2'	1:A:185:A:H8	1.78	0.48
1:A:242:C:H2'	1:A:243:A:H5'	1.96	0.48
1:A:254:G:OP1	17:Q:68:ARG:HB3	2.13	0.48
1:A:650:G:O2'	1:A:651:C:H5'	2.14	0.48
1:A:1132:C:H2'	1:A:1133:G:C8	2.45	0.48
3:C:19:GLU:HG2	3:C:54:ARG:HE	1.79	0.48
3:C:64:VAL:HB	3:C:99:VAL:CG2	2.33	0.48
3:C:70:VAL:HG12	3:C:71:ALA:H	1.77	0.48
16:P:28:ARG:NH1	16:P:29:ASP:CG	2.71	0.48
1:A:979:C:H2'	1:A:980:C:H5'	1.95	0.48
2:B:204:ASN:ND2	2:B:206:ASP:N	2.60	0.48
3:C:188:LEU:C	3:C:188:LEU:HD13	2.39	0.48
4:D:112:VAL:HG12	4:D:116:GLN:CD	2.39	0.48
15:O:17:ARG:HD3	15:O:26:GLU:OE2	2.14	0.48
20:T:47:GLY:O	20:T:49:ALA:N	2.45	0.48
1:A:328:C:O2	1:A:328:C:C2'	2.61	0.48
1:A:1157:A:H4'	1:A:1158:C:O5'	2.13	0.48
1:A:1353:G:H2'	1:A:1354:C:C6	2.48	0.48
1:A:1402:C:O2	1:A:1500:A:N1	2.46	0.48
1:A:1470:G:O2'	1:A:1471:G:H5'	2.14	0.48
1:A:1513:A:H2'	1:A:1514:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:230:VAL:CG1	2:B:231:GLU:N	2.75	0.48
4:D:80:GLU:O	4:D:84:LYS:HG3	2.13	0.48
7:G:20:ASP:OD1	7:G:22:LEU:HB3	2.14	0.48
9:I:4:TYR:CD2	9:I:88:TYR:HB2	2.49	0.48
20:T:38:LYS:O	20:T:41:ILE:HG12	2.13	0.48
1:A:173:U:H6	1:A:198:G:HO2'	1.58	0.48
1:A:438:G:OP1	4:D:125:HIS:HE1	1.97	0.48
1:A:1296:C:H4'	1:A:1302:U:C5	2.48	0.48
1:A:1320:C:H2'	1:A:1321:C:O4'	2.14	0.48
3:C:108:ASN:HD21	3:C:144:SER:HB3	1.77	0.48
12:L:45:PRO:HD3	12:L:51:ALA:O	2.14	0.48
13:M:66:LEU:O	13:M:67:GLU:C	2.56	0.48
19:S:51:VAL:O	19:S:58:VAL:HG22	2.14	0.48
1:A:625:G:H2'	1:A:626:U:C6	2.49	0.48
2:B:80:ILE:HD11	2:B:208:ILE:CG2	2.43	0.48
2:B:212:GLN:NE2	2:B:216:SER:HB3	2.29	0.48
3:C:19:GLU:CG	3:C:54:ARG:HE	2.27	0.48
3:C:61:ALA:C	3:C:63:ASN:H	2.22	0.48
16:P:5:ARG:HH21	16:P:28:ARG:HA	1.79	0.48
17:Q:97:SER:HA	17:Q:102:GLY:HA3	1.95	0.48
1:A:882:C:O2'	1:A:883:C:H5'	2.14	0.47
1:A:945:G:H2'	1:A:945:G:N3	2.29	0.47
1:A:1144:G:N2	1:A:1146:A:N6	2.59	0.47
1:A:1298:C:H4'	1:A:1299:A:O4'	2.14	0.47
2:B:132:LYS:N	2:B:132:LYS:HD2	2.29	0.47
6:F:62:TRP:CB	18:R:35:ARG:HH12	2.27	0.47
6:F:67:MET:HB2	6:F:68:PRO:CD	2.39	0.47
9:I:24:GLY:HA2	9:I:59:PHE:O	2.14	0.47
10:J:7:LYS:NZ	10:J:71:LEU:HD23	2.28	0.47
14:N:26:ARG:O	14:N:26:ARG:HG3	2.14	0.47
15:O:18:PHE:HD1	15:O:19:PRO:O	1.97	0.47
17:Q:3:LYS:HB3	17:Q:61:GLU:CB	2.44	0.47
1:A:707:C:H2'	1:A:708:C:H6	1.78	0.47
1:A:981:U:H5'	14:N:21:TYR:CE1	2.48	0.47
1:A:1117:G:H5'	1:A:1117:G:C8	2.46	0.47
1:A:1123:A:O3'	10:J:36:GLY:HA3	2.15	0.47
1:A:1333:A:H2'	1:A:1334:G:O4'	2.14	0.47
1:A:1386:G:H2'	1:A:1387:G:H8	1.78	0.47
2:B:21:ARG:NH1	2:B:23:ARG:HG2	2.27	0.47
4:D:58:LEU:O	4:D:62:GLN:HG2	2.14	0.47
4:D:148:VAL:HG13	4:D:158:ILE:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:38:LEU:HD12	7:G:38:LEU:O	2.14	0.47
19:S:16:LEU:O	19:S:19:VAL:HG12	2.14	0.47
20:T:57:ARG:CZ	20:T:102:GLY:HA3	2.44	0.47
1:A:114:U:O2'	1:A:115:G:H5'	2.14	0.47
1:A:682:G:O2'	1:A:683:G:H5'	2.14	0.47
1:A:953:G:H1'	13:M:125:ARG:CB	2.43	0.47
1:A:1000:U:O2'	1:A:1001:A:H5'	2.14	0.47
1:A:1231:G:H4'	9:I:126:SER:OG	2.13	0.47
1:A:1238:A:N7	1:A:1303:C:H1'	2.28	0.47
1:A:1392:G:H21	1:A:1502:A:H8	1.63	0.47
3:C:87:LEU:C	3:C:89:GLU:N	2.72	0.47
4:D:76:ARG:O	4:D:80:GLU:HG2	2.15	0.47
7:G:52:GLU:HG2	7:G:52:GLU:O	2.13	0.47
9:I:26:VAL:HG13	9:I:61:ALA:HB3	1.96	0.47
9:I:111:ARG:HD3	9:I:112:LYS:C	2.39	0.47
9:I:126:SER:O	9:I:128:ARG:N	2.47	0.47
12:L:53:ARG:NH1	12:L:92:ASP:OD2	2.47	0.47
16:P:4:ILE:HG13	16:P:64:ALA:HB1	1.95	0.47
1:A:189(K):U:H2'	1:A:189(L):G:C8	2.49	0.47
1:A:547:A:H4'	1:A:548:G:O5'	2.13	0.47
1:A:559:A:OP1	5:E:126:ARG:NH2	2.44	0.47
1:A:1305:G:H5'	21:U:4:GLY:CA	2.40	0.47
1:A:1326:C:OP1	21:U:12:LYS:NZ	2.43	0.47
2:B:47:THR:HA	2:B:202:PRO:HG2	1.97	0.47
2:B:74:LYS:C	2:B:76:GLN:H	2.22	0.47
2:B:224:GLN:O	2:B:224:GLN:HG2	2.14	0.47
3:C:102:ASN:N	3:C:102:ASN:ND2	2.61	0.47
4:D:146:ILE:N	4:D:146:ILE:CD1	2.77	0.47
6:F:99:ALA:O	6:F:100:ASN:C	2.57	0.47
7:G:79:ARG:HA	7:G:84:ASN:HA	1.96	0.47
9:I:56:LEU:HD23	9:I:56:LEU:C	2.39	0.47
1:A:539:A:H2'	1:A:540:G:H8	1.76	0.47
1:A:848:C:O2'	1:A:849:C:H5'	2.14	0.47
1:A:976:G:H5'	1:A:1358:U:O2'	2.14	0.47
1:A:1053:G:C4'	1:A:1054:C:H5'	2.44	0.47
1:A:1133:G:H2'	1:A:1134:G:H8	1.78	0.47
2:B:83:MET:O	2:B:86:GLU:N	2.47	0.47
4:D:19:LEU:HD22	4:D:67:ILE:HG13	1.96	0.47
9:I:32:ASP:O	9:I:33:PHE:C	2.57	0.47
9:I:33:PHE:CE1	9:I:47:LEU:HD21	2.50	0.47
10:J:19:SER:OG	10:J:91:PRO:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:44:VAL:HG22	10:J:66:ARG:HE	1.79	0.47
12:L:73:GLU:O	12:L:74:GLY:O	2.32	0.47
14:N:39:LEU:HD13	14:N:47:LEU:HD12	1.97	0.47
16:P:20:VAL:CG1	16:P:32:TYR:CB	2.92	0.47
16:P:43:LYS:HG3	16:P:48:TRP:CD2	2.49	0.47
19:S:80:TYR:CG	19:S:81:ARG:N	2.82	0.47
20:T:57:ARG:NE	20:T:102:GLY:HA3	2.29	0.47
1:A:266:G:O2'	1:A:267:C:OP2	2.33	0.47
1:A:420:U:C2'	1:A:421:U:H5''	2.45	0.47
3:C:46:GLU:HB2	3:C:47:LEU:HD12	1.96	0.47
3:C:195:VAL:O	3:C:196:LEU:HD22	2.14	0.47
5:E:129:ILE:H	5:E:129:ILE:HD12	1.79	0.47
9:I:86:VAL:HG13	9:I:90:PRO:HA	1.96	0.47
11:K:33:THR:HB	11:K:38:ASN:C	2.40	0.47
16:P:67:THR:HG22	16:P:70:ALA:H	1.80	0.47
17:Q:67:LYS:C	17:Q:70:ARG:NH1	2.72	0.47
20:T:10:LEU:HD12	20:T:12:ALA:H	1.79	0.47
1:A:245:C:O2'	1:A:246:A:H5'	2.15	0.47
1:A:344:A:O5'	1:A:345:C:H5	1.97	0.47
1:A:977:A:C2'	1:A:978:A:H5'	2.43	0.47
1:A:1152:A:OP1	10:J:13:HIS:HB2	2.14	0.47
1:A:1457:G:O2'	1:A:1458:G:H5'	2.14	0.47
1:A:1476:G:O2'	1:A:1477:C:H5'	2.14	0.47
2:B:10:LEU:HD22	2:B:11:LEU:HD23	1.96	0.47
2:B:75:LYS:HE2	2:B:96:ARG:HH22	1.79	0.47
2:B:116:GLU:HG2	2:B:153:ARG:HH12	1.79	0.47
6:F:44:GLY:HA2	6:F:59:TYR:CE1	2.50	0.47
7:G:16:LEU:HD22	7:G:16:LEU:H	1.80	0.47
9:I:102:LEU:HD12	9:I:103:THR:N	2.30	0.47
10:J:26:ALA:HB1	10:J:84:GLN:HB2	1.96	0.47
11:K:122:LYS:O	11:K:123:LYS:C	2.58	0.47
12:L:28:LYS:HB3	12:L:28:LYS:HE2	1.77	0.47
13:M:6:GLY:O	13:M:8:GLU:N	2.48	0.47
13:M:8:GLU:HA	13:M:8:GLU:OE2	2.14	0.47
13:M:80:ARG:O	13:M:84:ILE:HG12	2.15	0.47
13:M:124:PRO:HB2	13:M:126:LYS:HE2	1.97	0.47
14:N:11:LYS:C	14:N:13:THR:N	2.71	0.47
19:S:62:ILE:HA	19:S:66:MET:SD	2.55	0.47
1:A:243:A:N6	1:A:281:G:O2'	2.48	0.47
1:A:408:A:O2'	1:A:409:G:H5'	2.13	0.47
1:A:743:U:H2'	1:A:744:C:H6	1.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1268:A:H2'	1:A:1269:A:C8	2.49	0.47
1:A:1310:G:N7	19:S:2:PRO:HD3	2.30	0.47
1:A:1460:A:H2'	1:A:1461:G:O4'	2.15	0.47
1:A:1480:G:O2'	1:A:1481:U:H5'	2.15	0.47
2:B:10:LEU:HD23	2:B:10:LEU:C	2.39	0.47
2:B:15:VAL:HG21	2:B:210:SER:HA	1.97	0.47
4:D:64:LEU:CD1	4:D:75:PHE:CZ	2.97	0.47
5:E:5:ASP:CG	5:E:6:PHE:N	2.68	0.47
7:G:78:ARG:HD3	7:G:79:ARG:N	2.30	0.47
10:J:90:LEU:N	10:J:91:PRO:HD2	2.28	0.47
1:A:272:C:O2'	1:A:273:A:H5'	2.15	0.47
9:I:5:TYR:CG	9:I:6:GLY:N	2.83	0.47
1:A:472:A:H2'	1:A:473:G:O4'	2.14	0.47
1:A:1096:C:H2'	1:A:1097:C:C6	2.49	0.47
1:A:1352:C:H2'	1:A:1353:G:H8	1.77	0.47
3:C:155:GLY:O	3:C:157:ILE:N	2.45	0.47
7:G:146:GLU:CD	7:G:146:GLU:C	2.83	0.47
10:J:3:LYS:N	10:J:3:LYS:HD3	2.30	0.47
10:J:60:ARG:O	10:J:61:GLU:CB	2.61	0.47
10:J:64:GLU:OE2	10:J:66:ARG:HD2	2.15	0.47
10:J:80:LYS:O	10:J:83:GLU:HB2	2.15	0.47
12:L:89:ARG:CB	12:L:97:ARG:HA	2.45	0.47
14:N:44:LEU:HD12	14:N:44:LEU:C	2.39	0.47
16:P:3:LYS:O	16:P:21:VAL:HA	2.15	0.47
16:P:20:VAL:HG12	16:P:21:VAL:N	2.30	0.47
1:A:138:G:O2'	1:A:139:G:H5'	2.15	0.46
1:A:542:G:H5'	4:D:41:GLY:HA3	1.96	0.46
1:A:1405:G:O2'	1:A:1406:U:H5'	2.15	0.46
3:C:88:ARG:NH1	3:C:101:LEU:H	2.13	0.46
9:I:117:HIS:C	9:I:118:LYS:CG	2.88	0.46
16:P:67:THR:HG22	16:P:69:THR:N	2.30	0.46
17:Q:101:ARG:HE	17:Q:101:ARG:CA	2.29	0.46
19:S:4:SER:O	19:S:5:LEU:HG	2.14	0.46
1:A:1126:U:O2	1:A:1126:U:H2'	2.16	0.46
1:A:1179:A:H2'	1:A:1180:A:O4'	2.16	0.46
1:A:1327:C:O2'	1:A:1328:C:H5'	2.15	0.46
11:K:83:ILE:N	11:K:83:ILE:HD12	2.30	0.46
16:P:42:ARG:O	16:P:43:LYS:C	2.58	0.46
19:S:81:ARG:CG	19:S:81:ARG:O	2.61	0.46
20:T:34:LYS:O	20:T:38:LYS:HG3	2.15	0.46
1:A:109:A:H5'	1:A:110:C:C5	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:A:C6	4:D:35:ARG:HB3	2.49	0.46
2:B:95:GLN:OE1	2:B:95:GLN:HA	2.15	0.46
3:C:60:ALA:HB3	3:C:63:ASN:HD22	1.81	0.46
13:M:22:ILE:CD1	13:M:25:ILE:HD12	2.36	0.46
1:A:1321:C:O2'	19:S:78:ARG:NH2	2.41	0.46
1:A:1429:C:H2'	1:A:1430:C:C6	2.51	0.46
3:C:35:GLU:OE2	3:C:59:ARG:NH1	2.46	0.46
4:D:68:TYR:HB3	4:D:70:ILE:HD13	1.98	0.46
4:D:101:LEU:O	4:D:102:ASP:C	2.59	0.46
4:D:199:ASN:C	4:D:199:ASN:ND2	2.73	0.46
9:I:31:GLN:HG2	9:I:35:GLU:CG	2.46	0.46
9:I:33:PHE:HZ	9:I:46:ALA:HB3	1.80	0.46
10:J:20:ALA:C	10:J:22:LYS:N	2.74	0.46
15:O:71:GLN:HB3	15:O:78:TYR:CD1	2.50	0.46
18:R:87:ARG:HG2	18:R:88:LYS:N	2.22	0.46
1:A:1102:A:H2'	1:A:1103:C:C6	2.51	0.46
1:A:1191:A:OP2	3:C:3:ASN:ND2	2.49	0.46
1:A:1250:A:H5'	9:I:68:GLY:O	2.16	0.46
1:A:1414:U:H2'	1:A:1415:G:H8	1.80	0.46
1:A:1424:C:O2'	1:A:1425:U:H5'	2.15	0.46
2:B:33:TYR:HB2	2:B:43:ASP:HA	1.97	0.46
4:D:76:ARG:HG2	4:D:76:ARG:HH11	1.81	0.46
4:D:148:VAL:HG11	4:D:158:ILE:HD13	1.98	0.46
5:E:12:LEU:HD22	5:E:12:LEU:C	2.40	0.46
7:G:6:ARG:HH11	7:G:6:ARG:CB	2.28	0.46
17:Q:65:ILE:HD12	17:Q:65:ILE:N	2.30	0.46
1:A:629:G:H3'	1:A:630:G:H5''	1.98	0.46
1:A:668:G:O2'	15:O:46:HIS:HD2	1.99	0.46
1:A:1129:C:O2'	1:A:1130:A:P	2.73	0.46
1:A:1196:U:C5	22:X:5:A:H1'	2.51	0.46
2:B:19:HIS:HB2	2:B:204:ASN:OD1	2.16	0.46
4:D:61:LYS:HD2	4:D:61:LYS:C	2.40	0.46
4:D:126:ILE:CG2	4:D:127:THR:N	2.77	0.46
10:J:15:THR:O	10:J:16:LEU:C	2.59	0.46
10:J:90:LEU:H	10:J:91:PRO:HD3	1.80	0.46
12:L:75:HIS:CD2	12:L:76:ASN:N	2.84	0.46
13:M:125:ARG:HD2	13:M:125:ARG:C	2.40	0.46
17:Q:59:ILE:CG2	17:Q:71:PHE:CD1	2.96	0.46
1:A:45:U:H2'	1:A:46:G:C8	2.51	0.46
1:A:401:C:O2'	1:A:402:G:H5'	2.16	0.46
1:A:1128:C:O2'	1:A:1130:A:C8	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:ARG:NH1	2:B:199:TYR:CD2	2.84	0.46
3:C:23:TYR:CD2	3:C:24:ALA:N	2.84	0.46
3:C:126:ARG:O	3:C:127:ARG:C	2.59	0.46
4:D:17:VAL:HG12	4:D:18:LYS:N	2.30	0.46
4:D:25:ARG:C	4:D:27:TYR:N	2.73	0.46
5:E:99:GLY:O	5:E:117:ASP:HA	2.15	0.46
14:N:10:ALA:O	14:N:12:ARG:N	2.49	0.46
17:Q:68:ARG:CG	17:Q:68:ARG:NH1	2.77	0.46
18:R:31:LEU:O	18:R:69:THR:HG21	2.15	0.46
1:A:196:A:OP1	20:T:68:LYS:NZ	2.49	0.46
4:D:76:ARG:HG2	4:D:76:ARG:NH1	2.31	0.46
4:D:132:ARG:HB2	4:D:132:ARG:HH11	1.80	0.46
6:F:28:ARG:HH11	6:F:28:ARG:HG3	1.81	0.46
8:H:82:HIS:O	8:H:137:VAL:HA	2.16	0.46
19:S:28:LYS:O	19:S:29:ARG:C	2.58	0.46
20:T:57:ARG:CG	20:T:102:GLY:O	2.63	0.46
1:A:619:U:N3	4:D:134:ASP:OD2	2.45	0.46
1:A:1047:G:O2'	1:A:1048:G:H5'	2.15	0.46
2:B:14:GLY:O	2:B:15:VAL:HG22	2.15	0.46
3:C:73:PRO:O	3:C:76:VAL:N	2.47	0.46
3:C:75:VAL:O	3:C:83:ARG:HG2	2.16	0.46
4:D:36:ARG:C	4:D:38:TYR:H	2.24	0.46
5:E:7:GLU:CD	5:E:37:ARG:HH21	2.24	0.46
9:I:97:LYS:HG2	9:I:102:LEU:HD21	1.98	0.46
16:P:28:ARG:HH11	16:P:29:ASP:CG	2.24	0.46
1:A:865:A:H5'	1:A:1078:U:O4	2.16	0.46
1:A:1229:A:H2'	1:A:1230:C:C6	2.51	0.46
1:A:1250:A:C4'	9:I:68:GLY:H	2.17	0.46
2:B:52:GLU:HG2	2:B:56:ARG:HH21	1.79	0.46
2:B:100:GLY:N	2:B:176:GLU:OE2	2.46	0.46
4:D:24:GLU:O	4:D:25:ARG:HB3	2.16	0.46
4:D:184:LYS:HE3	4:D:184:LYS:HB2	1.78	0.46
14:N:33:VAL:HA	14:N:40:CYS:HA	1.98	0.46
18:R:26:LEU:HD21	18:R:39:VAL:HG22	1.98	0.46
18:R:71:LYS:O	18:R:75:ILE:HG13	2.16	0.46
1:A:189:G:H2'	1:A:189(A):C:C6	2.51	0.45
1:A:1116:C:H2'	1:A:1117:G:H5'	1.97	0.45
1:A:1347:G:O2'	1:A:1348:U:OP2	2.33	0.45
1:A:1532:U:C3'	1:A:1533:C:H5''	2.42	0.45
2:B:10:LEU:O	2:B:12:GLU:N	2.49	0.45
2:B:77:ALA:CB	2:B:211:ILE:HD13	2.33	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:57:ARG:HD3	4:D:205:GLU:HB2	1.98	0.45
9:I:10:ARG:HG2	9:I:75:ASP:HB3	1.99	0.45
10:J:46:ARG:NH1	10:J:46:ARG:CG	2.77	0.45
13:M:120:LYS:NZ	13:M:122:LYS:HB3	2.31	0.45
19:S:33:THR:HG22	19:S:34:TRP:H	1.79	0.45
20:T:53:LEU:CB	20:T:100:ILE:HG23	2.45	0.45
20:T:67:ALA:O	20:T:73:HIS:CE1	2.70	0.45
1:A:586:C:O2'	1:A:587:G:H5'	2.17	0.45
1:A:1001:A:H2	1:A:1001(A):G:N7	2.15	0.45
1:A:1054:C:N3	23:Y:34:CM0:O4'	2.49	0.45
1:A:1353:G:O2'	1:A:1354:C:H5'	2.16	0.45
2:B:98:LEU:O	2:B:101:MET:HG3	2.16	0.45
3:C:101:LEU:O	3:C:101:LEU:HD22	2.17	0.45
5:E:20:GLN:HE21	5:E:20:GLN:HB3	1.56	0.45
8:H:63:LEU:HD22	8:H:63:LEU:H	1.81	0.45
17:Q:95:TYR:C	17:Q:97:SER:H	2.24	0.45
19:S:45:VAL:N	19:S:62:ILE:HD13	2.31	0.45
1:A:502:G:H2'	1:A:503:C:O4'	2.16	0.45
1:A:978:A:O2'	1:A:1322:C:N3	2.47	0.45
1:A:1281:U:H5'	1:A:1282:C:C5	2.48	0.45
1:A:1312:G:O2'	1:A:1313:U:H5'	2.15	0.45
2:B:74:LYS:O	2:B:75:LYS:CB	2.63	0.45
2:B:87:ARG:HD3	2:B:233:SER:OG	2.16	0.45
3:C:195:VAL:CG1	3:C:196:LEU:N	2.80	0.45
4:D:100:ARG:HB3	4:D:102:ASP:OD1	2.17	0.45
5:E:100:VAL:O	5:E:107:ARG:NH2	2.49	0.45
6:F:62:TRP:CG	18:R:35:ARG:NH1	2.84	0.45
7:G:69:VAL:HG12	7:G:100:ALA:HA	1.99	0.45
8:H:87:SER:CB	8:H:93:VAL:H	2.29	0.45
12:L:59:ARG:HB2	12:L:59:ARG:NH1	2.26	0.45
17:Q:17:LYS:HA	17:Q:46:ASP:O	2.16	0.45
1:A:340:U:H2'	1:A:341:C:C6	2.51	0.45
1:A:663:A:H5''	18:R:61:LYS:HE3	1.99	0.45
1:A:1353:G:H2'	1:A:1354:C:H6	1.82	0.45
2:B:52:GLU:CG	2:B:56:ARG:NH2	2.79	0.45
2:B:78:GLN:HE22	2:B:96:ARG:HH12	1.64	0.45
2:B:109:SER:C	2:B:111:ARG:N	2.74	0.45
4:D:64:LEU:O	4:D:64:LEU:HD22	2.15	0.45
6:F:62:TRP:HB2	18:R:35:ARG:NH1	2.32	0.45
6:F:97:PHE:HB2	18:R:32:ARG:NH2	2.32	0.45
12:L:57:LYS:HE3	12:L:65:GLU:CG	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:11:LYS:O	14:N:13:THR:N	2.50	0.45
1:A:413:G:N2	1:A:428:G:H1'	2.31	0.45
1:A:443:C:H2'	1:A:444:C:H6	1.81	0.45
1:A:782:A:H2'	1:A:783:C:O4'	2.16	0.45
1:A:974:A:P	14:N:41:ARG:HH12	2.38	0.45
1:A:1019:C:O2'	1:A:1020:U:H5'	2.17	0.45
1:A:1192:C:C5	1:A:1193:G:C8	3.05	0.45
1:A:1325:C:P	21:U:6:ARG:NH2	2.89	0.45
1:A:1331:G:HO2'	1:A:1332:A:P	2.40	0.45
2:B:137:ARG:CB	2:B:137:ARG:HH11	2.29	0.45
7:G:21:VAL:HG23	7:G:22:LEU:N	2.31	0.45
9:I:97:LYS:CB	9:I:98:PRO:HD3	2.46	0.45
10:J:22:LYS:NZ	10:J:22:LYS:HB2	2.31	0.45
18:R:86:VAL:O	18:R:87:ARG:HB3	2.16	0.45
1:A:530:G:O6	22:X:3:U:H1'	2.17	0.45
1:A:1074:G:O3'	2:B:103:THR:HG22	2.16	0.45
1:A:1260:C:O5'	1:A:1284:C:H4'	2.16	0.45
1:A:1468:A:H2'	1:A:1469:G:O4'	2.17	0.45
13:M:5:ALA:HB2	13:M:22:ILE:HD13	1.99	0.45
13:M:37:THR:HG22	13:M:37:THR:O	2.17	0.45
16:P:81:ARG:HH11	16:P:81:ARG:HB2	1.82	0.45
17:Q:97:SER:HA	17:Q:102:GLY:HA2	1.99	0.45
19:S:8:GLY:O	19:S:9:VAL:C	2.59	0.45
20:T:53:LEU:HD23	20:T:56:MET:CE	2.45	0.45
1:A:189(A):C:H2'	1:A:189(B):C:H6	1.81	0.45
1:A:495:A:O4'	1:A:496:A:C8	2.70	0.45
1:A:626:U:O2'	1:A:627:G:H5'	2.17	0.45
1:A:983:A:H5'	1:A:984:C:OP2	2.16	0.45
1:A:1207:G:H2'	1:A:1208:C:C6	2.51	0.45
1:A:1405:G:H1'	1:A:1519:A:C4'	2.46	0.45
1:A:1483:A:H2'	1:A:1484:C:O4'	2.16	0.45
2:B:132:LYS:C	2:B:134:GLU:H	2.23	0.45
3:C:156:ARG:CD	3:C:160:ALA:O	2.58	0.45
4:D:64:LEU:HB2	4:D:198:VAL:HG11	1.97	0.45
11:K:111:ASP:CG	18:R:84:LYS:HE3	2.41	0.45
12:L:60:LEU:CD2	12:L:66:VAL:HG22	2.47	0.45
15:O:18:PHE:C	15:O:18:PHE:CD1	2.94	0.45
20:T:43:LEU:HD12	20:T:52:ALA:HA	1.98	0.45
20:T:57:ARG:NH2	20:T:102:GLY:HA3	2.32	0.45
1:A:833:U:H2'	1:A:834:C:C6	2.51	0.45
1:A:1258:G:O2'	1:A:1259:C:H5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1434:A:H2'	1:A:1435:G:O4'	2.17	0.45
3:C:52:LEU:H	3:C:52:LEU:CD2	2.29	0.45
7:G:26:PHE:HD1	7:G:101:LEU:HD22	1.82	0.45
11:K:32:ILE:CG2	11:K:77:MET:HE3	2.46	0.45
12:L:83:VAL:CG2	12:L:84:LEU:H	2.30	0.45
20:T:39:LYS:CD	20:T:55:ILE:HD13	2.46	0.45
1:A:103:C:P	20:T:17:ARG:NH1	2.90	0.45
1:A:501:C:H2'	1:A:502:G:H8	1.82	0.45
1:A:642:A:C2	8:H:113:SER:O	2.70	0.45
1:A:983:A:HO2'	1:A:1049:U:HO2'	1.64	0.45
1:A:1091:U:H2'	1:A:1093:A:OP2	2.16	0.45
1:A:1169:A:H2'	1:A:1170:A:C8	2.51	0.45
1:A:1370:G:O2'	1:A:1371:G:H5'	2.17	0.45
1:A:1371:G:O3'	9:I:69:GLY:HA3	2.17	0.45
4:D:5:ILE:HG22	4:D:5:ILE:O	2.16	0.45
7:G:78:ARG:HD3	7:G:78:ARG:C	2.42	0.45
9:I:48:GLU:N	9:I:49:PRO:CD	2.80	0.45
1:A:149:A:H2'	1:A:150:C:H6	1.77	0.45
1:A:658:G:H2'	1:A:659:U:C6	2.52	0.45
1:A:714:G:H2'	1:A:715:A:C8	2.52	0.45
1:A:1095:U:H2'	1:A:1096:C:C6	2.51	0.45
1:A:1137:C:H4'	1:A:1138:G:N1	2.32	0.45
2:B:115:LEU:HD11	2:B:146:GLN:HG2	1.99	0.45
2:B:204:ASN:HD22	2:B:206:ASP:N	2.14	0.45
2:B:213:LEU:O	2:B:217:ARG:HG2	2.17	0.45
3:C:42:LEU:C	3:C:44:GLU:N	2.75	0.45
10:J:26:ALA:HB3	10:J:85:LEU:HD23	1.99	0.45
12:L:28:LYS:HB3	12:L:33:ARG:NH1	2.32	0.45
13:M:23:TYR:HB2	13:M:67:GLU:CD	2.42	0.45
14:N:45:ARG:O	14:N:49:HIS:CD2	2.70	0.45
1:A:413:G:N2	1:A:429:U:OP2	2.37	0.44
1:A:833:U:H2'	1:A:834:C:H6	1.83	0.44
1:A:1060:C:OP1	14:N:45:ARG:NH2	2.50	0.44
1:A:1121:U:H2'	1:A:1122:U:C6	2.52	0.44
1:A:1405:G:O4'	1:A:1519:A:H4'	2.17	0.44
5:E:60:TYR:CE1	5:E:64:ARG:CZ	2.99	0.44
6:F:62:TRP:HB2	18:R:35:ARG:HH12	1.82	0.44
7:G:156:TRP:CD1	7:G:156:TRP:C	2.95	0.44
10:J:57:LYS:CE	10:J:60:ARG:NH2	2.78	0.44
10:J:89:ASP:C	10:J:90:LEU:HG	2.42	0.44
12:L:89:ARG:HB3	12:L:97:ARG:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:11:LYS:C	14:N:13:THR:H	2.25	0.44
1:A:1288:A:H2'	1:A:1289:A:C8	2.53	0.44
1:A:1305:G:H5''	21:U:4:GLY:C	2.42	0.44
6:F:95:GLU:O	6:F:96:PRO:C	2.58	0.44
7:G:6:ARG:CB	7:G:6:ARG:NH1	2.81	0.44
20:T:23:ARG:HG2	20:T:23:ARG:NH1	2.31	0.44
1:A:665:A:N3	1:A:732:C:H2'	2.33	0.44
1:A:1054:C:C2'	1:A:1055:A:C5'	2.94	0.44
1:A:1116:C:C2'	1:A:1117:G:C5'	2.94	0.44
2:B:97:TRP:CZ2	2:B:102:LEU:HD13	2.46	0.44
3:C:43:LEU:HD22	3:C:43:LEU:N	2.33	0.44
6:F:77:ARG:HD2	6:F:77:ARG:C	2.43	0.44
12:L:44:THR:HA	12:L:45:PRO:HD3	1.81	0.44
12:L:52:LEU:O	12:L:54:LYS:HD2	2.18	0.44
13:M:66:LEU:O	13:M:70:LEU:HB2	2.18	0.44
16:P:20:VAL:HG11	16:P:32:TYR:HB3	1.97	0.44
19:S:44:MET:HB2	19:S:62:ILE:CD1	2.47	0.44
20:T:69:GLY:O	20:T:73:HIS:CD2	2.71	0.44
1:A:16:A:N1	1:A:919:A:H2	2.15	0.44
1:A:32:A:H2'	1:A:33:A:C8	2.52	0.44
1:A:1153:C:P	10:J:13:HIS:HE2	2.39	0.44
1:A:1539:C:H4'	7:G:81:GLY:C	2.42	0.44
4:D:100:ARG:HH12	4:D:137:SER:CB	2.31	0.44
5:E:75:THR:HG23	5:E:76:ILE:O	2.18	0.44
12:L:83:VAL:CG2	12:L:84:LEU:N	2.79	0.44
19:S:80:TYR:O	19:S:82:GLY:N	2.51	0.44
1:A:129(A):G:O2'	1:A:130:A:OP2	2.35	0.44
1:A:782:A:O3'	1:A:1515:C:H4'	2.18	0.44
1:A:835:U:OP1	18:R:64:ARG:NH2	2.36	0.44
1:A:911:U:H2'	1:A:912:C:C6	2.52	0.44
1:A:1347:G:N2	1:A:1373:G:H2'	2.33	0.44
2:B:102:LEU:N	2:B:102:LEU:HD12	2.32	0.44
2:B:116:GLU:HG2	2:B:153:ARG:NH1	2.33	0.44
7:G:23:VAL:O	7:G:27:ILE:HG12	2.18	0.44
7:G:116:ALA:HA	7:G:119:ARG:CZ	2.47	0.44
8:H:6:ILE:HD11	8:H:31:PHE:CD2	2.53	0.44
8:H:33:GLU:HG3	8:H:48:TYR:CE1	2.53	0.44
10:J:8:LEU:CD2	10:J:96:ILE:HG12	2.47	0.44
10:J:37:PRO:CA	10:J:72:VAL:HG22	2.37	0.44
12:L:55:VAL:CG1	12:L:56:ALA:N	2.80	0.44
12:L:75:HIS:HD2	12:L:76:ASN:N	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:10:GLY:HA3	16:P:15:PRO:HA	2.00	0.44
17:Q:59:ILE:CG2	17:Q:71:PHE:HB3	2.46	0.44
20:T:29:LYS:O	20:T:33:ILE:HG13	2.18	0.44
1:A:520:A:O2'	12:L:73:GLU:HG2	2.17	0.44
1:A:954:G:H2'	1:A:955:U:C6	2.53	0.44
1:A:1131:G:H2'	1:A:1132:C:C6	2.52	0.44
3:C:147:LYS:HE2	3:C:205:GLY:HA2	2.00	0.44
4:D:61:LYS:HA	4:D:203:VAL:HG22	1.99	0.44
4:D:189:PRO:HB2	4:D:194:LEU:CD2	2.45	0.44
5:E:10:MET:O	5:E:10:MET:HG3	2.17	0.44
7:G:26:PHE:CD1	7:G:101:LEU:HD22	2.52	0.44
17:Q:24:GLU:HG2	17:Q:39:SER:HB3	1.99	0.44
1:A:854:G:C6	1:A:855:G:N7	2.86	0.44
1:A:1003:G:N2	1:A:1039:C:C6	2.86	0.44
1:A:1030:C:H2'	1:A:1030(A):G:H8	1.83	0.44
1:A:1475:G:H2'	1:A:1476:G:C8	2.52	0.44
2:B:20:GLU:HB2	2:B:190:THR:HG1	1.83	0.44
2:B:30:ARG:HG3	2:B:31:TYR:CD2	2.53	0.44
2:B:73:THR:O	2:B:73:THR:HG22	2.18	0.44
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.71	0.44
2:B:155:LEU:HD21	2:B:159:PRO:HD3	1.99	0.44
3:C:134:ILE:O	3:C:138:VAL:HG23	2.18	0.44
7:G:152:ALA:O	7:G:155:ARG:HD3	2.17	0.44
8:H:17:THR:HB	8:H:78:GLN:OE1	2.17	0.44
9:I:10:ARG:O	9:I:13:ALA:HB3	2.18	0.44
15:O:15:PHE:CE2	15:O:84:LYS:HD3	2.52	0.44
20:T:38:LYS:O	20:T:42:GLN:HB2	2.18	0.44
20:T:56:MET:HE2	20:T:88:VAL:CG1	2.46	0.44
1:A:447:G:H2'	1:A:485:G:N2	2.32	0.44
1:A:643:C:H2'	1:A:644:G:H8	1.82	0.44
1:A:838:G:H2'	1:A:839:U:H5''	2.00	0.44
1:A:1053:G:H4'	1:A:1054:C:H4'	2.00	0.44
1:A:1481:U:O2'	1:A:1482:G:H5'	2.17	0.44
4:D:24:GLU:CD	4:D:25:ARG:H	2.25	0.44
6:F:2:ARG:CD	6:F:69:GLU:HG2	2.47	0.44
7:G:59:LEU:HD11	7:G:63:LYS:HE2	1.99	0.44
11:K:101:SER:C	11:K:103:LEU:H	2.26	0.44
12:L:115:LYS:O	12:L:117:ARG:N	2.50	0.44
13:M:99:ARG:HG2	13:M:99:ARG:HH11	1.82	0.44
19:S:13:ASP:OD2	19:S:13:ASP:N	2.46	0.44
20:T:39:LYS:O	20:T:43:LEU:HG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:C:H5''	1:A:365:U:O4	2.18	0.44
1:A:191:G:H22	20:T:85:MET:HE1	1.82	0.44
1:A:407:G:O2'	4:D:116:GLN:HG3	2.18	0.44
1:A:820:U:H4'	1:A:821:G:OP2	2.18	0.44
1:A:1069:C:O3'	5:E:25:ARG:NH1	2.51	0.44
1:A:1305:G:C5'	21:U:4:GLY:HA3	2.39	0.44
2:B:132:LYS:HB3	2:B:136:VAL:CG2	2.46	0.44
3:C:16:ARG:HG3	3:C:17:ASP:H	1.83	0.44
3:C:73:PRO:HA	3:C:76:VAL:HG23	2.00	0.44
3:C:78:GLY:HA3	3:C:83:ARG:CB	2.48	0.44
6:F:45:LEU:HD12	6:F:45:LEU:O	2.18	0.44
6:F:75:LEU:HD22	6:F:79:LEU:HD11	1.99	0.44
9:I:115:GLY:C	9:I:116:LYS:HD3	2.43	0.44
1:A:189(L):G:H2'	1:A:190:U:C6	2.53	0.43
1:A:251:G:H4'	1:A:252:U:O5'	2.17	0.43
1:A:369:C:O2'	1:A:370:C:H5'	2.18	0.43
1:A:1115:C:H1'	14:N:61:TRP:O	2.18	0.43
2:B:62:ALA:C	2:B:64:ARG:H	2.26	0.43
2:B:88:ALA:C	2:B:90:MET:H	2.24	0.43
2:B:223:ILE:HA	2:B:226:ARG:HH21	1.82	0.43
3:C:39:ILE:HG22	3:C:40:ARG:N	2.33	0.43
3:C:42:LEU:O	3:C:44:GLU:N	2.51	0.43
6:F:68:PRO:HG2	6:F:71:ARG:HG3	2.00	0.43
17:Q:45:HIS:CD2	17:Q:47:PRO:HD3	2.53	0.43
1:A:106:C:O2'	1:A:107:G:H5'	2.18	0.43
1:A:243:A:C2	1:A:246:A:C8	3.07	0.43
1:A:881:G:H2'	1:A:882:C:O4'	2.18	0.43
1:A:1379:G:O2'	1:A:1380:U:H5'	2.18	0.43
3:C:22:TRP:CE3	3:C:22:TRP:O	2.71	0.43
4:D:152:SER:C	4:D:154:ASN:N	2.76	0.43
19:S:16:LEU:C	19:S:19:VAL:HG12	2.44	0.43
20:T:43:LEU:HB2	20:T:52:ALA:HB2	2.00	0.43
1:A:895:G:H2'	1:A:896:C:C6	2.54	0.43
1:A:989:C:O2'	1:A:990:C:H5'	2.17	0.43
1:A:1053:G:H3'	1:A:1054:C:C5'	2.46	0.43
1:A:1181:G:H2'	1:A:1182:G:C4	2.53	0.43
3:C:11:ARG:O	3:C:12:LEU:C	2.61	0.43
3:C:66:VAL:O	3:C:66:VAL:HG12	2.19	0.43
3:C:159:GLY:HA2	3:C:193:TYR:CZ	2.53	0.43
4:D:31:CYS:O	4:D:32:ALA:HB3	2.18	0.43
6:F:78:GLU:HA	6:F:78:GLU:OE2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:53:ARG:CG	12:L:93:LEU:HD11	2.44	0.43
13:M:13:LYS:O	13:M:14:ARG:C	2.61	0.43
14:N:8:GLU:C	14:N:10:ALA:H	2.26	0.43
1:A:179:A:H2'	1:A:180:U:C6	2.53	0.43
1:A:263:A:OP2	20:T:79:ARG:NH1	2.52	0.43
1:A:429:U:H4'	1:A:430:A:O5'	2.19	0.43
1:A:567:G:H2'	1:A:568:G:O4'	2.18	0.43
1:A:841:U:H3'	1:A:848:C:C5'	2.49	0.43
1:A:1203:C:OP1	14:N:2:ALA:N	2.52	0.43
2:B:21:ARG:HG3	2:B:21:ARG:H	1.63	0.43
2:B:137:ARG:HH11	2:B:137:ARG:HB3	1.83	0.43
2:B:223:ILE:HA	2:B:226:ARG:NH2	2.34	0.43
6:F:91:VAL:HG11	18:R:72:ARG:NH1	2.33	0.43
10:J:25:GLU:C	10:J:27:ALA:H	2.26	0.43
10:J:46:ARG:HG2	10:J:46:ARG:NH1	2.22	0.43
10:J:62:HIS:HB3	14:N:59:ALA:HB3	1.99	0.43
21:U:24:ARG:HG2	21:U:24:ARG:HH11	1.84	0.43
1:A:300:A:H1'	1:A:565:U:O2	2.18	0.43
1:A:376:G:P	16:P:67:THR:HG21	2.58	0.43
1:A:601:C:O2'	1:A:602:A:H5'	2.18	0.43
1:A:1125:U:H6	1:A:1125:U:H5''	1.82	0.43
1:A:1138:G:C6	1:A:1140:C:H1'	2.53	0.43
8:H:122:ARG:H	8:H:122:ARG:CD	2.32	0.43
9:I:16:ARG:NH1	9:I:64:THR:HG21	2.34	0.43
12:L:119:LYS:O	12:L:120:TYR:CB	2.65	0.43
20:T:23:ARG:HG2	20:T:23:ARG:HH11	1.84	0.43
1:A:407:G:H2'	1:A:408:A:H8	1.84	0.43
1:A:434:U:H2'	1:A:435:C:C6	2.53	0.43
1:A:501:C:H2'	1:A:502:G:C8	2.54	0.43
1:A:954:G:H2'	1:A:955:U:H6	1.84	0.43
1:A:1181:G:HO2'	1:A:1182:G:C5'	2.32	0.43
1:A:1256:A:H62	1:A:1278:U:H5'	1.84	0.43
1:A:1320:C:O2'	1:A:1321:C:H5'	2.18	0.43
1:A:1479:C:H2'	1:A:1480:G:C8	2.53	0.43
2:B:148:TYR:C	2:B:150:SER:H	2.26	0.43
2:B:189:ASP:OD1	2:B:205:ASP:OD1	2.37	0.43
3:C:107:GLN:NE2	3:C:107:GLN:H	2.16	0.43
3:C:126:ARG:HA	3:C:127:ARG:NH2	2.16	0.43
3:C:178:LEU:C	3:C:180:ALA:H	2.27	0.43
5:E:76:ILE:CG2	5:E:78:HIS:O	2.67	0.43
9:I:43:ALA:O	9:I:44:VAL:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:4:ILE:HD11	10:J:74:ILE:CG1	2.48	0.43
10:J:29:ARG:H	10:J:29:ARG:HG2	1.64	0.43
10:J:81:THR:C	10:J:83:GLU:N	2.76	0.43
20:T:53:LEU:HD12	20:T:100:ILE:HG23	2.01	0.43
1:A:438:G:O2'	1:A:494:U:O4	2.37	0.43
1:A:1108:G:H5'	1:A:1191:A:H4'	2.01	0.43
1:A:1229:A:H2'	1:A:1230:C:H6	1.84	0.43
1:A:1302:U:OP2	13:M:17:VAL:HG13	2.19	0.43
1:A:1314:C:OP2	19:S:6:LYS:CD	2.67	0.43
1:A:1332:A:C2	1:A:1333:A:C4	3.07	0.43
3:C:68:VAL:HG12	3:C:70:VAL:HG23	1.99	0.43
3:C:134:ILE:HG22	3:C:168:ALA:HB3	2.00	0.43
5:E:144:THR:HG23	5:E:146:ALA:N	2.33	0.43
7:G:51:GLN:C	7:G:53:LYS:N	2.76	0.43
13:M:57:ARG:HE	13:M:57:ARG:HB2	1.62	0.43
23:Y:30:C:O2	23:Y:31:C:H5	2.01	0.43
1:A:89:C:O5'	1:A:89:C:H6	2.02	0.43
1:A:344:A:O2'	1:A:345:C:OP1	2.36	0.43
1:A:456:C:H2'	1:A:457:C:C6	2.54	0.43
1:A:1036:G:H2'	1:A:1037:C:O4'	2.19	0.43
1:A:1287:A:H2'	1:A:1288:A:C8	2.54	0.43
1:A:1440:C:H2'	1:A:1441:G:O4'	2.18	0.43
2:B:14:GLY:C	2:B:15:VAL:CG2	2.92	0.43
3:C:11:ARG:O	3:C:14:ILE:O	2.36	0.43
3:C:47:LEU:N	3:C:47:LEU:CD1	2.79	0.43
4:D:155:LEU:O	4:D:156:GLU:C	2.62	0.43
5:E:76:ILE:HG23	5:E:78:HIS:H	1.83	0.43
5:E:112:LEU:HA	5:E:112:LEU:HD23	1.84	0.43
6:F:53:ALA:O	6:F:54:LYS:CB	2.67	0.43
7:G:50:ILE:O	7:G:54:THR:HB	2.19	0.43
10:J:4:ILE:O	10:J:4:ILE:HG13	2.19	0.43
10:J:48:THR:HG23	10:J:62:HIS:CD2	2.53	0.43
12:L:75:HIS:CD2	12:L:77:LEU:N	2.78	0.43
16:P:28:ARG:NH1	16:P:29:ASP:OD1	2.52	0.43
1:A:184:G:H2'	1:A:185:A:C8	2.53	0.43
1:A:333:G:H4'	20:T:16:HIS:CD2	2.53	0.43
2:B:74:LYS:HE2	2:B:166:ASP:CB	2.46	0.43
6:F:1:MET:CE	6:F:66:GLU:HG2	2.39	0.43
6:F:3:ARG:CG	6:F:3:ARG:NH1	2.80	0.43
6:F:68:PRO:HB2	6:F:70:ASP:OD1	2.18	0.43
8:H:86:ILE:HD13	8:H:133:LEU:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:128:ARG:HH11	9:I:128:ARG:HG3	1.84	0.43
13:M:11:ARG:HG3	13:M:12:ASN:H	1.84	0.43
13:M:124:PRO:HB3	13:M:126:LYS:HE2	2.00	0.43
19:S:20:LEU:HD12	19:S:21:GLU:HG3	1.99	0.43
1:A:262:A:C6	1:A:263:A:C6	3.07	0.43
1:A:1250:A:H4'	9:I:68:GLY:CA	2.49	0.43
1:A:1516:G:N1	1:A:1519:A:OP2	2.52	0.43
2:B:59:GLU:O	2:B:60:ASP:C	2.62	0.43
3:C:164:ARG:HH11	3:C:164:ARG:CB	2.30	0.43
5:E:31:LEU:HD23	5:E:31:LEU:HA	1.83	0.43
18:R:51:LEU:HA	18:R:52:PRO:HD3	1.78	0.43
1:A:374:A:C6	1:A:375:U:C4	3.06	0.42
1:A:443:C:H2'	1:A:444:C:C6	2.54	0.42
1:A:551:U:H2'	1:A:552:U:H6	1.84	0.42
1:A:649:G:O2'	1:A:650:G:H5'	2.19	0.42
1:A:1061:G:H1'	10:J:56:HIS:CE1	2.54	0.42
1:A:1288:A:H1'	1:A:1352:C:O2'	2.19	0.42
1:A:1289:A:H2'	1:A:1290:G:H5'	2.01	0.42
1:A:1543:C:C2'	1:A:1544:U:H5'	2.49	0.42
2:B:93:VAL:HG11	2:B:97:TRP:CD1	2.54	0.42
3:C:43:LEU:HA	3:C:47:LEU:HD13	2.00	0.42
4:D:100:ARG:O	4:D:103:ASN:HB3	2.19	0.42
4:D:103:ASN:O	4:D:106:TYR:HB3	2.19	0.42
6:F:41:GLU:O	6:F:43:LEU:N	2.52	0.42
8:H:91:ARG:CG	12:L:7:ILE:HG13	2.47	0.42
9:I:20:ARG:O	9:I:59:PHE:HA	2.18	0.42
9:I:37:PHE:O	9:I:38:GLN:O	2.37	0.42
9:I:118:LYS:O	9:I:119:ALA:HB3	2.18	0.42
12:L:115:LYS:C	12:L:117:ARG:N	2.77	0.42
19:S:40:ILE:CG2	19:S:62:ILE:HD12	2.48	0.42
1:A:176:C:H2'	1:A:177:C:H6	1.85	0.42
1:A:339:C:H2'	1:A:340:U:C6	2.54	0.42
1:A:718:G:H4'	11:K:117:ASN:HD21	1.83	0.42
1:A:761:G:H21	17:Q:105:ALA:HB1	1.83	0.42
1:A:921:U:O2'	5:E:19:MET:O	2.28	0.42
1:A:1152:A:H5'	10:J:70:ARG:NH2	2.34	0.42
7:G:78:ARG:HH11	7:G:78:ARG:HG3	1.84	0.42
7:G:142:GLU:O	7:G:145:ALA:HB3	2.19	0.42
9:I:10:ARG:HD2	9:I:11:LYS:N	2.35	0.42
10:J:3:LYS:CB	10:J:75:ILE:HA	2.48	0.42
14:N:50:LYS:HE2	14:N:50:LYS:HB3	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:57:ARG:NH1	16:P:57:ARG:CG	2.78	0.42
1:A:54:C:H2'	1:A:352:C:H41	1.84	0.42
1:A:436:C:H2'	1:A:437:U:C6	2.55	0.42
1:A:731:G:H5'	1:A:766:A:H4'	2.00	0.42
1:A:939:G:H5''	7:G:102:ARG:CZ	2.48	0.42
1:A:1024:G:H2'	1:A:1025:U:O4'	2.19	0.42
2:B:78:GLN:CG	2:B:94:ASN:OD1	2.64	0.42
17:Q:67:LYS:C	17:Q:70:ARG:HH12	2.27	0.42
1:A:746:A:O2'	1:A:747:C:H5'	2.19	0.42
1:A:818:G:H3'	1:A:819:A:H5'	2.01	0.42
1:A:1149:C:OP1	9:I:14:VAL:HG11	2.19	0.42
1:A:1277:C:O2'	1:A:1279:A:H8	2.02	0.42
1:A:1301:U:O2'	1:A:1302:U:OP1	2.35	0.42
2:B:131:PRO:C	2:B:133:LYS:H	2.26	0.42
3:C:64:VAL:HB	3:C:99:VAL:HG11	2.01	0.42
4:D:194:LEU:HD22	4:D:194:LEU:N	2.34	0.42
6:F:10:LEU:HD21	6:F:85:VAL:HG22	2.01	0.42
10:J:55:LYS:HG3	10:J:56:HIS:N	2.34	0.42
14:N:22:THR:CG2	14:N:33:VAL:CG2	2.97	0.42
15:O:17:ARG:NH1	15:O:17:ARG:CG	2.80	0.42
15:O:82:ILE:HD13	15:O:88:ARG:CG	2.50	0.42
1:A:222:U:H2'	1:A:223:U:C6	2.54	0.42
1:A:1331:G:O6	21:U:7:ARG:NH2	2.53	0.42
1:A:1461:G:O2'	1:A:1462:G:H5'	2.19	0.42
1:A:1543:C:O2'	1:A:1544:U:H5'	2.19	0.42
2:B:49:GLU:O	2:B:52:GLU:HB3	2.19	0.42
7:G:111:ARG:NH1	7:G:113:GLU:OE2	2.50	0.42
10:J:34:VAL:C	10:J:36:GLY:H	2.26	0.42
11:K:124:LYS:O	11:K:124:LYS:HG2	2.19	0.42
13:M:23:TYR:N	13:M:67:GLU:OE2	2.52	0.42
13:M:108:ARG:NH2	13:M:114:ARG:HA	2.33	0.42
1:A:91:C:H2'	1:A:92:C:C6	2.51	0.42
1:A:179:A:O2'	1:A:180:U:H5'	2.20	0.42
1:A:335:C:H2'	1:A:336:C:C6	2.54	0.42
1:A:393:A:O2'	1:A:394:G:H5'	2.19	0.42
1:A:960:U:H1'	1:A:1223:C:H5'	2.02	0.42
1:A:1055:A:N6	1:A:1206:G:C5	2.87	0.42
1:A:1305:G:C8	1:A:1305:G:OP2	2.72	0.42
1:A:1479:C:O2'	1:A:1480:G:H5'	2.19	0.42
3:C:179:ARG:O	3:C:179:ARG:HG3	2.19	0.42
3:C:207:VAL:HG12	3:C:208:ILE:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:108:ILE:HG22	11:K:109:VAL:N	2.35	0.42
12:L:75:HIS:NE2	12:L:77:LEU:HB2	2.35	0.42
13:M:34:LEU:HD13	13:M:41:PRO:HA	2.02	0.42
13:M:52:GLU:O	13:M:53:VAL:C	2.61	0.42
17:Q:4:LYS:HE3	17:Q:6:LEU:HD21	2.02	0.42
1:A:961:U:O2'	1:A:962:C:H5'	2.20	0.42
1:A:969:A:N6	13:M:126:LYS:HE3	2.35	0.42
1:A:1174:G:O2'	1:A:1175:G:H5'	2.20	0.42
2:B:75:LYS:HD3	2:B:78:GLN:OE1	2.19	0.42
2:B:90:MET:HA	2:B:91:PRO:HD3	1.77	0.42
2:B:132:LYS:HD2	2:B:135:GLN:NE2	2.34	0.42
2:B:164:VAL:HG11	2:B:167:PRO:HA	2.02	0.42
3:C:48:TYR:O	3:C:51:GLY:N	2.51	0.42
4:D:61:LYS:NZ	4:D:62:GLN:NE2	2.67	0.42
4:D:110:PHE:N	4:D:110:PHE:CD1	2.88	0.42
4:D:148:VAL:HG11	4:D:158:ILE:HG21	2.02	0.42
5:E:10:MET:SD	5:E:13:ILE:HG23	2.60	0.42
5:E:131:ILE:HD13	5:E:131:ILE:HA	1.85	0.42
6:F:1:MET:HE1	6:F:66:GLU:O	2.19	0.42
7:G:23:VAL:HG13	7:G:43:PHE:CE2	2.55	0.42
7:G:129:GLU:OE1	7:G:131:LYS:HE2	2.19	0.42
9:I:65:VAL:CG1	9:I:73:GLN:HB3	2.40	0.42
10:J:57:LYS:HG3	10:J:57:LYS:O	2.19	0.42
15:O:87:ILE:O	15:O:88:ARG:HB2	2.19	0.42
21:U:9:ARG:HH11	21:U:22:ARG:HA	1.84	0.42
1:A:577:G:H1'	1:A:816:A:N3	2.35	0.42
1:A:662:G:O2'	1:A:836:G:H5'	2.19	0.42
1:A:1126:U:O2'	1:A:1127:G:H5'	2.19	0.42
1:A:1127:G:O2'	9:I:16:ARG:NH2	2.53	0.42
1:A:1227:A:OP2	13:M:111:LYS:HE3	2.20	0.42
1:A:1419:G:O2'	1:A:1420:C:H5'	2.20	0.42
2:B:223:ILE:HD12	2:B:223:ILE:C	2.45	0.42
3:C:79:ARG:C	3:C:81:GLY:H	2.28	0.42
3:C:123:GLN:HE22	3:C:140:ARG:HH22	1.68	0.42
7:G:72:ARG:HH12	7:G:138:LYS:NZ	2.17	0.42
9:I:81:ILE:O	9:I:85:LEU:HB2	2.20	0.42
10:J:35:SER:O	10:J:36:GLY:O	2.38	0.42
16:P:43:LYS:CG	16:P:48:TRP:CD2	3.02	0.42
1:A:376:G:OP2	16:P:67:THR:HG21	2.20	0.42
1:A:435:C:O2'	1:A:436:C:H5'	2.20	0.42
1:A:1190:G:C2'	1:A:1191:A:OP2	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1367:C:H5'	10:J:60:ARG:HH12	1.85	0.42
3:C:70:VAL:CG1	3:C:71:ALA:H	2.32	0.42
7:G:73:MET:CE	7:G:90:GLU:HG2	2.49	0.42
10:J:16:LEU:HD23	10:J:94:VAL:HG22	2.02	0.42
10:J:34:VAL:HA	10:J:74:ILE:HA	2.02	0.42
13:M:23:TYR:CE2	13:M:71:ARG:HG3	2.54	0.42
14:N:6:LEU:C	14:N:8:GLU:N	2.77	0.42
17:Q:78:GLU:OE2	17:Q:81:ARG:HD2	2.19	0.42
1:A:560:U:H4'	1:A:561:U:O5'	2.20	0.42
1:A:1312:G:N7	19:S:3:ARG:O	2.52	0.42
3:C:206:GLU:HB3	3:C:207:VAL:H	1.52	0.42
4:D:18:LYS:HZ3	4:D:31:CYS:HB3	1.85	0.42
7:G:149:ARG:HD2	11:K:59:TYR:CE1	2.55	0.42
9:I:53:VAL:O	9:I:54:ASP:HB2	2.20	0.42
12:L:126:LYS:HD2	12:L:126:LYS:C	2.43	0.42
1:A:448:A:C4	1:A:487:A:C2	3.08	0.41
1:A:961:U:C2'	1:A:962:C:H5'	2.50	0.41
1:A:1019:C:C2'	1:A:1020:U:H5'	2.50	0.41
1:A:1394:A:C6	1:A:1501:C:H4'	2.55	0.41
1:A:1437:C:H2'	1:A:1438:G:H8	1.84	0.41
1:A:1539:C:H2'	1:A:1540:U:H5'	2.02	0.41
4:D:58:LEU:HD22	4:D:62:GLN:HG2	2.02	0.41
4:D:68:TYR:HB2	4:D:70:ILE:HD13	2.02	0.41
9:I:89:ASN:O	9:I:92:TYR:HB2	2.20	0.41
10:J:74:ILE:O	10:J:76:ASN:N	2.49	0.41
11:K:21:ILE:HD13	11:K:94:ALA:HB3	2.02	0.41
11:K:34:ASP:HB2	11:K:35:PRO:CD	2.50	0.41
11:K:97:ALA:O	11:K:101:SER:HB3	2.20	0.41
11:K:109:VAL:HG22	18:R:86:VAL:HA	2.02	0.41
13:M:40:ASN:HD22	13:M:41:PRO:HD2	1.84	0.41
13:M:114:ARG:HG2	13:M:114:ARG:HH11	1.85	0.41
1:A:9:G:OP2	5:E:121:LYS:NZ	2.33	0.41
1:A:707:C:H2'	1:A:708:C:C6	2.54	0.41
1:A:971:G:C8	1:A:1365:G:H4'	2.55	0.41
1:A:974:A:H8	1:A:974:A:OP1	2.03	0.41
1:A:1250:A:H2'	1:A:1251:A:H8	1.84	0.41
3:C:113:ALA:N	3:C:202:ILE:HD12	2.35	0.41
3:C:181:ASN:ND2	3:C:204:LEU:HD13	2.34	0.41
5:E:78:HIS:CD2	8:H:107:LEU:HD12	2.55	0.41
5:E:87:SER:HB3	5:E:131:ILE:HD13	2.03	0.41
8:H:105:ARG:HG3	8:H:105:ARG:HH11	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:4:A:N6	23:Y:34:CM0:O9	2.52	0.41
1:A:108:G:H5'	1:A:109:A:C5'	2.48	0.41
1:A:189(E):U:O2'	1:A:189(F):U:H5'	2.20	0.41
1:A:255:G:O6	1:A:266:G:O6	2.38	0.41
1:A:528:C:H5'	1:A:535:A:N6	2.35	0.41
1:A:1108:G:H4'	1:A:1191:A:O4'	2.20	0.41
1:A:1154:G:H2'	1:A:1155:G:C8	2.51	0.41
1:A:1277:C:O2'	1:A:1279:A:C8	2.74	0.41
2:B:116:GLU:C	2:B:118:LEU:N	2.78	0.41
2:B:182:ILE:O	2:B:183:PRO:C	2.63	0.41
3:C:113:ALA:N	3:C:114:PRO:CD	2.83	0.41
4:D:162:LEU:CD1	4:D:181:MET:HE2	2.47	0.41
4:D:180:GLY:O	4:D:181:MET:C	2.63	0.41
8:H:104:ARG:CZ	8:H:138:TRP:CZ3	3.02	0.41
9:I:7:THR:O	9:I:8:GLY:C	2.62	0.41
9:I:23:ASN:HB3	9:I:60:ASP:OD1	2.20	0.41
14:N:9:LYS:C	14:N:11:LYS:H	2.27	0.41
20:T:56:MET:HE2	20:T:88:VAL:CB	2.50	0.41
23:Y:34:CM0:O8	23:Y:35:A:N6	2.53	0.41
1:A:671:G:O2'	1:A:672:U:H5'	2.21	0.41
1:A:1130:A:P	1:A:1131:G:OP2	2.79	0.41
1:A:1323:G:H2'	1:A:1324:A:C8	2.56	0.41
1:A:1346:A:O4'	1:A:1348:U:C6	2.74	0.41
1:A:1381:U:O2'	1:A:1382:C:H5'	2.19	0.41
2:B:210:SER:O	2:B:214:ILE:HG12	2.20	0.41
3:C:60:ALA:O	3:C:61:ALA:CB	2.67	0.41
3:C:82:GLU:O	3:C:86:VAL:HG23	2.20	0.41
4:D:162:LEU:HD23	4:D:162:LEU:HA	1.91	0.41
6:F:28:ARG:HG3	6:F:28:ARG:NH1	2.36	0.41
7:G:27:ILE:HD12	7:G:40:ALA:HA	2.03	0.41
7:G:91:VAL:HG12	7:G:96:GLN:HG3	2.01	0.41
11:K:86:GLY:O	11:K:91:ARG:NH1	2.54	0.41
19:S:19:VAL:HG13	19:S:20:LEU:N	2.34	0.41
20:T:44:ALA:C	20:T:46:GLU:H	2.27	0.41
1:A:143:A:H2	1:A:220:G:H22	1.68	0.41
1:A:953:G:C5'	1:A:965:A:H61	2.31	0.41
1:A:1054:C:H5	1:A:1196:U:C4	2.37	0.41
1:A:1338:G:H2'	1:A:1339:A:C8	2.55	0.41
4:D:12:CYS:SG	4:D:19:LEU:O	2.78	0.41
5:E:101:ILE:N	5:E:101:ILE:CD1	2.84	0.41
5:E:126:ARG:O	5:E:127:ASN:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:46:LYS:N	8:H:64:LYS:HG3	2.36	0.41
13:M:59:TYR:CD1	13:M:59:TYR:C	2.98	0.41
15:O:7:GLU:O	15:O:11:VAL:HG12	2.20	0.41
1:A:35:G:H2'	1:A:36:C:H6	1.79	0.41
1:A:130:A:C8	17:Q:63:ARG:HG3	2.55	0.41
1:A:263:A:P	20:T:79:ARG:NH1	2.93	0.41
1:A:646:U:H2'	1:A:647:C:C6	2.54	0.41
1:A:1067:A:N3	1:A:1068:G:H1'	2.36	0.41
1:A:1251:A:H5'	9:I:12:GLU:CG	2.50	0.41
1:A:1418:A:H2'	1:A:1419:G:O4'	2.20	0.41
2:B:145:LEU:O	2:B:149:LEU:HB2	2.20	0.41
3:C:143:GLU:C	3:C:145:GLY:H	2.29	0.41
3:C:206:GLU:O	3:C:207:VAL:C	2.64	0.41
5:E:20:GLN:O	5:E:21:ALA:C	2.64	0.41
5:E:41:VAL:HG13	5:E:113:ALA:HA	2.03	0.41
7:G:79:ARG:CB	7:G:84:ASN:HA	2.50	0.41
7:G:114:ARG:H	7:G:114:ARG:HG2	1.58	0.41
14:N:23:ARG:HH12	14:N:30:ALA:HB2	1.85	0.41
15:O:16:ALA:C	15:O:18:PHE:N	2.78	0.41
1:A:119:A:H4'	1:A:120:A:O5'	2.20	0.41
1:A:952:U:H2'	1:A:953:G:H8	1.85	0.41
1:A:1151:A:O2'	1:A:1152:A:H8	2.03	0.41
1:A:1315:U:OP2	19:S:6:LYS:NZ	2.54	0.41
2:B:108:ILE:HD13	2:B:108:ILE:HA	1.92	0.41
2:B:189:ASP:HB2	2:B:205:ASP:CG	2.46	0.41
4:D:126:ILE:CG2	4:D:127:THR:H	2.34	0.41
13:M:35:GLU:O	13:M:37:THR:N	2.51	0.41
14:N:39:LEU:CD1	14:N:47:LEU:HD12	2.51	0.41
16:P:6:LEU:N	16:P:6:LEU:HD12	2.35	0.41
18:R:26:LEU:HD13	18:R:42:ARG:NH1	2.35	0.41
1:A:421:U:H5'	1:A:422:C:H5	1.83	0.41
1:A:881:G:OP2	12:L:12:ARG:NH2	2.54	0.41
1:A:1222:G:O2'	1:A:1223:C:H5'	2.21	0.41
1:A:1306:A:N6	1:A:1331:G:H1'	2.35	0.41
2:B:200:ILE:HG23	2:B:202:PRO:HD3	2.02	0.41
2:B:216:SER:OG	2:B:217:ARG:N	2.53	0.41
3:C:115:LEU:HD23	3:C:118:GLN:OE1	2.20	0.41
8:H:14:ARG:O	8:H:18:ARG:HD3	2.21	0.41
17:Q:65:ILE:HG21	17:Q:69:LYS:HE2	2.02	0.41
17:Q:78:GLU:OE2	17:Q:81:ARG:CD	2.69	0.41
20:T:93:GLU:C	20:T:95:ALA:N	2.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:C:H2'	1:A:68:G:C8	2.56	0.41
1:A:310:G:H5''	16:P:31:LYS:HB2	2.03	0.41
1:A:436:C:H2'	1:A:437:U:H6	1.85	0.41
1:A:536:C:H2'	1:A:537:G:H8	1.81	0.41
1:A:598:U:H2'	1:A:599:C:H6	1.86	0.41
1:A:861:G:O2'	1:A:862:C:H5'	2.20	0.41
1:A:1318:A:H5''	19:S:10:PHE:CD1	2.56	0.41
1:A:1390:U:H2'	1:A:1391:U:C6	2.56	0.41
1:A:1402:C:H2'	1:A:1403:C:O4'	2.20	0.41
2:B:93:VAL:HG11	2:B:97:TRP:HD1	1.84	0.41
2:B:118:LEU:C	2:B:120:ALA:N	2.76	0.41
2:B:204:ASN:C	2:B:204:ASN:ND2	2.62	0.41
3:C:3:ASN:OD1	3:C:3:ASN:N	2.54	0.41
3:C:83:ARG:C	3:C:85:ARG:H	2.29	0.41
3:C:89:GLU:OE2	3:C:93:LYS:HE2	2.19	0.41
7:G:39:ALA:O	7:G:40:ALA:C	2.64	0.41
7:G:115:ARG:O	7:G:116:ALA:C	2.63	0.41
9:I:49:PRO:O	9:I:52:ALA:HB3	2.21	0.41
11:K:98:LEU:HA	11:K:101:SER:HB3	2.03	0.41
15:O:16:ALA:C	15:O:18:PHE:H	2.28	0.41
16:P:23:ASP:OD1	16:P:25:ARG:N	2.52	0.41
16:P:26:ARG:HD3	16:P:31:LYS:N	2.36	0.41
16:P:28:ARG:HG3	16:P:29:ASP:OD2	2.21	0.41
18:R:53:ARG:HG3	18:R:53:ARG:HH11	1.86	0.41
19:S:32:LYS:HD2	19:S:57:HIS:CD2	2.55	0.41
20:T:8:ARG:O	20:T:9:ASN:HB3	2.21	0.41
1:A:189(D):C:H2'	1:A:189(E):U:O4'	2.21	0.41
1:A:264:U:H2'	1:A:265:G:O4'	2.21	0.41
1:A:421:U:H5'	1:A:422:C:C6	2.55	0.41
1:A:1160:G:O2'	1:A:1161:C:H5'	2.21	0.41
1:A:1235:U:H2'	1:A:1236:A:O4'	2.21	0.41
1:A:1244:C:O2'	1:A:1245:A:H5'	2.21	0.41
1:A:1258:G:H2'	1:A:1259:C:C6	2.56	0.41
1:A:1288:A:N1	1:A:1371:G:H1'	2.35	0.41
2:B:51:LEU:HD22	2:B:55:PHE:CE1	2.56	0.41
2:B:97:TRP:CH2	2:B:176:GLU:CD	2.90	0.41
2:B:192:SER:O	2:B:194:PRO:HD3	2.21	0.41
3:C:76:VAL:O	3:C:83:ARG:CG	2.69	0.41
5:E:47:LYS:HB2	5:E:47:LYS:HE2	1.84	0.41
5:E:126:ARG:NH1	5:E:126:ARG:HG3	2.35	0.41
7:G:113:GLU:CD	7:G:113:GLU:H	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:112:LEU:HD23	8:H:112:LEU:H	1.80	0.41
12:L:93:LEU:O	12:L:94:PRO:C	2.64	0.41
13:M:16:ASP:O	13:M:17:VAL:C	2.63	0.41
18:R:47:THR:HG23	18:R:83:GLU:O	2.20	0.41
20:T:11:SER:C	20:T:13:LEU:H	2.29	0.41
1:A:686:U:O4	1:A:703:G:H1'	2.21	0.40
1:A:1314:C:OP2	19:S:6:LYS:CG	2.69	0.40
1:A:1320:C:C2	19:S:72:GLY:HA3	2.56	0.40
1:A:1347:G:H2'	1:A:1373:G:H1	1.86	0.40
1:A:1539:C:H2'	1:A:1539:C:O2	2.21	0.40
2:B:15:VAL:HB	2:B:210:SER:HB2	2.03	0.40
3:C:39:ILE:C	3:C:41:GLY:N	2.77	0.40
5:E:110:LEU:HD13	5:E:118:ILE:HG21	2.03	0.40
6:F:94:GLN:CD	18:R:32:ARG:HD3	2.46	0.40
11:K:32:ILE:HG22	11:K:77:MET:HE3	2.02	0.40
16:P:43:LYS:HA	16:P:48:TRP:HB3	2.03	0.40
19:S:40:ILE:HB	19:S:67:VAL:O	2.20	0.40
1:A:411:A:C5	1:A:429:U:C5	3.09	0.40
1:A:509:A:H5''	4:D:55:ALA:HB2	2.03	0.40
1:A:517:G:N3	1:A:531:U:H5'	2.37	0.40
1:A:1030:C:O2'	1:A:1030(A):G:H5'	2.22	0.40
1:A:1058:G:C6	1:A:1059:C:N3	2.89	0.40
1:A:1405:G:C1'	1:A:1519:A:H4'	2.51	0.40
2:B:25:ASN:ND2	2:B:27:LYS:H	2.18	0.40
2:B:157:ARG:HG3	2:B:157:ARG:NH1	2.36	0.40
2:B:181:PHE:HD2	8:H:70:GLN:HB3	1.84	0.40
4:D:12:CYS:SG	4:D:19:LEU:HB2	2.61	0.40
5:E:143:ARG:NH1	8:H:77:GLU:OE2	2.44	0.40
6:F:99:ALA:HB2	18:R:31:LEU:CD1	2.51	0.40
11:K:22:HIS:HB3	11:K:29:ILE:HG12	2.02	0.40
17:Q:40:LYS:HD2	17:Q:42:TYR:CE1	2.56	0.40
19:S:15:LEU:O	19:S:16:LEU:C	2.64	0.40
20:T:51:GLU:O	20:T:54:LYS:HB3	2.21	0.40
1:A:371:G:C2'	1:A:372:C:C5'	2.93	0.40
1:A:985:C:H2'	1:A:986:A:C8	2.56	0.40
1:A:1392:G:N2	1:A:1502:A:C8	2.85	0.40
1:A:1498:U:H4'	1:A:1519:A:C2	2.55	0.40
5:E:126:ARG:HG3	5:E:126:ARG:HH11	1.85	0.40
6:F:86:ARG:O	6:F:87:ARG:HG2	2.22	0.40
7:G:79:ARG:HH22	7:G:82:GLY:N	2.15	0.40
9:I:18:PHE:HB2	9:I:62:TYR:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:97:LYS:HA	9:I:102:LEU:CD2	2.36	0.40
9:I:102:LEU:HD12	9:I:103:THR:H	1.85	0.40
10:J:18:ALA:O	10:J:20:ALA:N	2.54	0.40
15:O:65:ARG:HG2	15:O:65:ARG:NH1	2.34	0.40
1:A:73:G:O2'	1:A:76:C:H5'	2.21	0.40
1:A:88:A:H2'	1:A:89:C:O4'	2.21	0.40
1:A:267:C:OP2	17:Q:67:LYS:HD2	2.21	0.40
1:A:390:C:H2'	1:A:391:G:H8	1.85	0.40
1:A:706:A:H4'	11:K:29:ILE:HD11	2.04	0.40
1:A:828:A:H2'	1:A:829:G:O4'	2.21	0.40
1:A:1004:A:N7	1:A:1026:G:C5	2.89	0.40
1:A:1110:A:O5'	1:A:1110:A:H8	2.04	0.40
1:A:1152:A:H4'	10:J:17:ASP:OD2	2.21	0.40
3:C:76:VAL:O	3:C:83:ARG:HG3	2.22	0.40
3:C:126:ARG:C	3:C:128:PHE:N	2.80	0.40
8:H:68:ARG:HH11	8:H:68:ARG:HG2	1.86	0.40
8:H:108:GLY:HA3	8:H:138:TRP:HB3	2.03	0.40
9:I:57:GLY:O	9:I:58:HIS:ND1	2.54	0.40
10:J:64:GLU:HG2	14:N:59:ALA:HB2	2.04	0.40
13:M:73:GLU:O	13:M:76:ALA:HB3	2.21	0.40
1:A:192:U:H2'	1:A:193:C:C6	2.57	0.40
1:A:333:G:C4'	20:T:16:HIS:CD2	3.04	0.40
1:A:619:U:O2	4:D:133:VAL:HA	2.22	0.40
1:A:933:G:OP2	7:G:3:ARG:HB3	2.21	0.40
1:A:1163:C:H2'	1:A:1164:G:H8	1.85	0.40
1:A:1190:G:OP1	3:C:4:LYS:HA	2.20	0.40
1:A:1314:C:O2'	1:A:1315:U:H5'	2.20	0.40
1:A:1351:U:O2'	1:A:1352:C:H5'	2.21	0.40
2:B:92:TYR:CE2	2:B:151:GLY:CA	3.03	0.40
2:B:178:ARG:HH12	8:H:74:PRO:HB3	1.86	0.40
3:C:84:ILE:O	3:C:88:ARG:HG3	2.21	0.40
4:D:19:LEU:HD22	4:D:67:ILE:CG1	2.51	0.40
4:D:28:SER:C	4:D:30:LYS:H	2.30	0.40
5:E:94:ALA:HB2	5:E:119:LEU:HG	2.03	0.40
6:F:6:VAL:HG22	6:F:90:VAL:HG22	2.04	0.40
9:I:112:LYS:C	9:I:112:LYS:HD3	2.47	0.40
13:M:32:GLU:OE1	13:M:64:TRP:HZ2	2.05	0.40
17:Q:68:ARG:N	17:Q:70:ARG:HH12	2.20	0.40
20:T:57:ARG:CG	20:T:57:ARG:HH11	2.34	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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	233/256 (91%)	173 (74%)	48 (21%)	12 (5%)	1	5
3	C	205/239 (86%)	153 (75%)	36 (18%)	16 (8%)	1	2
4	D	206/209 (99%)	179 (87%)	22 (11%)	5 (2%)	4	17
5	E	149/162 (92%)	143 (96%)	5 (3%)	1 (1%)	18	47
6	F	99/101 (98%)	84 (85%)	13 (13%)	2 (2%)	6	21
7	G	153/156 (98%)	130 (85%)	20 (13%)	3 (2%)	6	21
8	H	136/138 (99%)	127 (93%)	6 (4%)	3 (2%)	5	19
9	I	125/128 (98%)	103 (82%)	10 (8%)	12 (10%)	0	1
10	J	97/105 (92%)	68 (70%)	15 (16%)	14 (14%)	0	0
11	K	117/129 (91%)	102 (87%)	11 (9%)	4 (3%)	3	11
12	L	123/135 (91%)	103 (84%)	14 (11%)	6 (5%)	1	6
13	M	123/126 (98%)	89 (72%)	23 (19%)	11 (9%)	0	1
14	N	58/61 (95%)	47 (81%)	8 (14%)	3 (5%)	1	5
15	O	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
16	P	82/88 (93%)	73 (89%)	8 (10%)	1 (1%)	10	34
17	Q	102/105 (97%)	91 (89%)	10 (10%)	1 (1%)	12	38
18	R	71/88 (81%)	61 (86%)	8 (11%)	2 (3%)	4	14
19	S	79/93 (85%)	62 (78%)	8 (10%)	9 (11%)	0	1
20	T	97/106 (92%)	80 (82%)	9 (9%)	8 (8%)	0	1
21	U	23/27 (85%)	19 (83%)	2 (9%)	2 (9%)	0	1
All	All	2364/2541 (93%)	1962 (83%)	287 (12%)	115 (5%)	1	6

All (115) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	15	VAL

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Mol	Chain	Res	Type
2	B	17	PHE
2	B	207	ALA
3	C	15	THR
3	C	61	ALA
3	C	127	ARG
3	C	207	VAL
4	D	36	ARG
8	H	71	GLY
8	H	91	ARG
9	I	8	GLY
9	I	23	ASN
9	I	38	GLN
10	J	75	ILE
10	J	85	LEU
10	J	86	MET
11	K	127	LYS
12	L	28	LYS
12	L	47	LYS
12	L	74	GLY
12	L	79	GLU
13	M	23	TYR
13	M	67	GLU
13	M	68	GLY
14	N	9	LYS
14	N	11	LYS
18	R	19	LYS
19	S	6	LYS
19	S	9	VAL
19	S	29	ARG
19	S	67	VAL
19	S	81	ARG
20	T	74	LYS
20	T	95	ALA
2	B	11	LEU
2	B	74	LYS
3	C	79	ARG
3	C	160	ALA
4	D	88	VAL
7	G	155	ARG
8	H	70	GLN
9	I	33	PHE
9	I	127	LYS

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Mol	Chain	Res	Type
10	J	34	VAL
10	J	36	GLY
10	J	57	LYS
10	J	60	ARG
10	J	61	GLU
10	J	83	GLU
10	J	90	LEU
11	K	118	GLY
12	L	75	HIS
13	M	6	GLY
13	M	24	GLY
18	R	87	ARG
19	S	5	LEU
19	S	43	GLU
20	T	9	ASN
20	T	99	LEU
2	B	208	ILE
3	C	3	ASN
3	C	43	LEU
3	C	81	GLY
3	C	156	ARG
4	D	30	LYS
6	F	39	LYS
6	F	42	GLU
7	G	145	ALA
9	I	11	LYS
9	I	32	ASP
10	J	78	ASN
11	K	12	ARG
11	K	13	GLN
13	M	36	LYS
13	M	120	LYS
14	N	12	ARG
16	P	10	GLY
19	S	28	LYS
20	T	48	LYS
2	B	9	GLU
2	B	95	GLN
3	C	144	SER
7	G	52	GLU
9	I	43	ALA
13	M	38	GLY

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Mol	Chain	Res	Type
19	S	25	LYS
20	T	94	ALA
20	T	103	GLY
21	U	3	LYS
21	U	25	LYS
2	B	150	SER
3	C	102	ASN
4	D	3	ARG
4	D	200	GLU
10	J	32	ALA
12	L	116	SER
13	M	85	GLY
20	T	11	SER
2	B	131	PRO
2	B	224	GLN
3	C	103	VAL
3	C	179	ARG
9	I	119	ALA
10	J	35	SER
13	M	7	VAL
13	M	117	VAL
2	B	239	VAL
10	J	77	PRO
9	I	24	GLY
3	C	108	ASN
9	I	44	VAL
9	I	109	VAL
17	Q	103	GLY
3	C	55	VAL
5	E	154	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	202/220 (92%)	188 (93%)	14 (7%)	14 41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	160/188 (85%)	146 (91%)	14 (9%)	9	29
4	D	180/181 (99%)	171 (95%)	9 (5%)	22	54
5	E	115/123 (94%)	101 (88%)	14 (12%)	5	16
6	F	90/90 (100%)	83 (92%)	7 (8%)	11	35
7	G	126/127 (99%)	119 (94%)	7 (6%)	19	50
8	H	119/119 (100%)	105 (88%)	14 (12%)	5	17
9	I	98/99 (99%)	90 (92%)	8 (8%)	10	33
10	J	87/92 (95%)	79 (91%)	8 (9%)	8	27
11	K	90/99 (91%)	86 (96%)	4 (4%)	25	59
12	L	104/111 (94%)	97 (93%)	7 (7%)	15	42
13	M	100/101 (99%)	90 (90%)	10 (10%)	7	24
14	N	49/50 (98%)	44 (90%)	5 (10%)	7	23
15	O	79/80 (99%)	72 (91%)	7 (9%)	9	29
16	P	72/74 (97%)	66 (92%)	6 (8%)	10	32
17	Q	96/97 (99%)	92 (96%)	4 (4%)	26	61
18	R	64/77 (83%)	62 (97%)	2 (3%)	35	70
19	S	71/80 (89%)	67 (94%)	4 (6%)	19	50
20	T	76/82 (93%)	68 (90%)	8 (10%)	6	22
21	U	19/22 (86%)	19 (100%)	0	100	100
All	All	1997/2112 (95%)	1845 (92%)	152 (8%)	12	36

All (152) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	15	VAL
2	B	21	ARG
2	B	23	ARG
2	B	25	ASN
2	B	63	MET
2	B	82	ARG
2	B	96	ARG
2	B	98	LEU
2	B	117	GLU
2	B	121	LEU
2	B	162	ILE

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Mol	Chain	Res	Type
2	B	187	LEU
2	B	204	ASN
2	B	221	LEU
3	C	5	ILE
3	C	15	THR
3	C	26	LYS
3	C	28	GLN
3	C	37	GLN
3	C	101	LEU
3	C	107	GLN
3	C	127	ARG
3	C	154	SER
3	C	164	ARG
3	C	175	LEU
3	C	192	THR
3	C	196	LEU
3	C	204	LEU
4	D	3	ARG
4	D	26	CYS
4	D	50	ARG
4	D	58	LEU
4	D	64	LEU
4	D	127	THR
4	D	146	ILE
4	D	150	GLU
4	D	199	ASN
5	E	12	LEU
5	E	20	GLN
5	E	31	LEU
5	E	41	VAL
5	E	43	LEU
5	E	53	LEU
5	E	64	ARG
5	E	76	ILE
5	E	80	ILE
5	E	89	ILE
5	E	101	ILE
5	E	116	THR
5	E	131	ILE
5	E	144	THR
6	F	17	SER
6	F	24	GLU

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Mol	Chain	Res	Type
6	F	43	LEU
6	F	69	GLU
6	F	74	ASP
6	F	75	LEU
6	F	86	ARG
7	G	38	LEU
7	G	73	MET
7	G	78	ARG
7	G	113	GLU
7	G	114	ARG
7	G	155	ARG
7	G	156	TRP
8	H	3	THR
8	H	26	VAL
8	H	37	ARG
8	H	39	LEU
8	H	52	ASP
8	H	63	LEU
8	H	85	ARG
8	H	91	ARG
8	H	97	VAL
8	H	105	ARG
8	H	112	LEU
8	H	119	LEU
8	H	122	ARG
8	H	133	LEU
9	I	27	THR
9	I	31	GLN
9	I	79	LEU
9	I	97	LYS
9	I	102	LEU
9	I	118	LYS
9	I	121	ARG
9	I	125	TYR
10	J	6	ILE
10	J	14	LYS
10	J	22	LYS
10	J	38	ILE
10	J	80	LYS
10	J	83	GLU
10	J	98	ILE
10	J	99	LYS

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Mol	Chain	Res	Type
11	K	96	ARG
11	K	109	VAL
11	K	114	VAL
11	K	123	LYS
12	L	33	ARG
12	L	36	VAL
12	L	53	ARG
12	L	59	ARG
12	L	91	LYS
12	L	111	LYS
12	L	126	LYS
13	M	9	ILE
13	M	16	ASP
13	M	20	THR
13	M	44	ARG
13	M	56	LEU
13	M	62	ASN
13	M	70	LEU
13	M	94	ARG
13	M	102	ARG
13	M	110	ARG
14	N	8	GLU
14	N	18	VAL
14	N	26	ARG
14	N	41	ARG
14	N	44	LEU
15	O	6	GLU
15	O	10	LYS
15	O	31	LEU
15	O	34	LEU
15	O	70	LEU
15	O	71	GLN
15	O	81	LEU
16	P	1	MET
16	P	2	VAL
16	P	8	ARG
16	P	45	THR
16	P	57	ARG
16	P	67	THR
17	Q	26	GLN
17	Q	28	PRO
17	Q	68	ARG

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Mol	Chain	Res	Type
17	Q	74	LEU
18	R	39	VAL
18	R	88	LYS
19	S	13	ASP
19	S	43	GLU
19	S	62	ILE
19	S	65	ASN
20	T	10	LEU
20	T	13	LEU
20	T	42	GLN
20	T	48	LYS
20	T	57	ARG
20	T	73	HIS
20	T	84	LEU
20	T	90	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	25	ASN
2	B	40	HIS
2	B	78	GLN
2	B	110	GLN
2	B	135	GLN
2	B	146	GLN
2	B	204	ASN
3	C	6	HIS
3	C	28	GLN
3	C	31	HIS
3	C	37	GLN
3	C	63	ASN
3	C	98	ASN
3	C	102	ASN
3	C	107	GLN
3	C	108	ASN
3	C	110	ASN
3	C	118	GLN
3	C	123	GLN
3	C	136	GLN
3	C	176	HIS
3	C	181	ASN
4	D	42	GLN

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Mol	Chain	Res	Type
4	D	62	GLN
4	D	123	HIS
4	D	160	GLN
4	D	161	ASN
4	D	199	ASN
4	D	201	GLN
5	E	20	GLN
5	E	73	ASN
6	F	18	GLN
6	F	27	GLN
6	F	32	ASN
6	F	64	GLN
6	F	73	ASN
7	G	37	ASN
7	G	64	GLN
7	G	68	ASN
7	G	96	GLN
7	G	106	GLN
9	I	23	ASN
9	I	73	GLN
10	J	21	GLN
10	J	33	GLN
10	J	76	ASN
10	J	78	ASN
10	J	84	GLN
11	K	22	HIS
11	K	38	ASN
11	K	62	GLN
11	K	104	GLN
11	K	117	ASN
12	L	49	ASN
12	L	75	HIS
12	L	78	GLN
13	M	40	ASN
13	M	62	ASN
14	N	49	HIS
15	O	13	GLN
15	O	37	ASN
15	O	46	HIS
15	O	71	GLN
16	P	14	ASN
16	P	16	HIS

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Mol	Chain	Res	Type
16	P	65	GLN
16	P	76	GLN
17	Q	94	ASN
19	S	14	HIS
19	S	47	HIS
19	S	56	GLN
19	S	57	HIS
20	T	18	GLN
20	T	73	HIS
20	T	90	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1510/1522 (99%)	191 (12%)	58 (3%)
22	X	4/6 (66%)	0	0
23	Y	10/17 (58%)	0	0
All	All	1524/1545 (98%)	191 (12%)	58 (3%)

All (191) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	61	G
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	195	A
1	A	197	A

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Mol	Chain	Res	Type
1	A	202	U
1	A	203	U
1	A	216	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	282	A
1	A	289	G
1	A	316	G
1	A	321	A
1	A	328	C
1	A	332	G
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C
1	A	403	C
1	A	406	G
1	A	411	A
1	A	412	A
1	A	413	G
1	A	414	A
1	A	421	U
1	A	428	G
1	A	429	U
1	A	439	A
1	A	442	C
1	A	452	A
1	A	484	G
1	A	485	G
1	A	496	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C

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Mol	Chain	Res	Type
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	588	G
1	A	630	G
1	A	631	G
1	A	653	A
1	A	665	A
1	A	688	G
1	A	701	C
1	A	702	A
1	A	723	U
1	A	731	G
1	A	749	C
1	A	755	G
1	A	777	A
1	A	781	A
1	A	794	A
1	A	813	U
1	A	816	A
1	A	817	C
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	902	G
1	A	914	A
1	A	926	G

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Mol	Chain	Res	Type
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	965	A
1	A	966	G
1	A	969	A
1	A	971	G
1	A	972	C
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	978	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1026	G
1	A	1027	C
1	A	1050	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1068	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1117	G
1	A	1125	U
1	A	1126	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1136	U
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1146	A
1	A	1152	A

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Mol	Chain	Res	Type
1	A	1159	U
1	A	1182	G
1	A	1183	A
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1227	A
1	A	1238	A
1	A	1258	G
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1305	G
1	A	1320	C
1	A	1332	A
1	A	1346	A
1	A	1348	U
1	A	1364	U
1	A	1398	A
1	A	1442	G
1	A	1442(A)	G
1	A	1442(B)	A
1	A	1452	C
1	A	1492	A
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1529	G

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Mol	Chain	Res	Type
1	A	1530	G
1	A	1533	C
1	A	1542	U
1	A	1543	C

All (58) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	201	C
1	A	243	A
1	A	250	A
1	A	266	G
1	A	281	G
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	410	G
1	A	428	G
1	A	484	G
1	A	495	A
1	A	509	A
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	701	C
1	A	748	C
1	A	793	U
1	A	812	C
1	A	819	A
1	A	960	U
1	A	965	A
1	A	992	U

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Mol	Chain	Res	Type
1	A	993	G
1	A	1049	U
1	A	1067	A
1	A	1129	C
1	A	1181	G
1	A	1182	G
1	A	1190	G
1	A	1201	A
1	A	1257	U
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1331	G
1	A	1347	G
1	A	1397	C
1	A	1447	A
1	A	1498	U
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1528	U
1	A	1543	C

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

2 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	$\# Z > 2$
23	6MZ	Y	37	23	22,25,26	0.56	0	30,36,39	0.59	0
23	CM0	Y	34	23	22,26,27	1.47	3 (13%)	28,37,40	2.99	3 (10%)

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
23	6MZ	Y	37	23	-	0/9/27/28	0/3/3/3
23	CM0	Y	34	23	-	5/12/30/31	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	Y	34	CM0	O9-C8	4.31	1.36	1.22
23	Y	34	CM0	O5-C7	3.91	1.53	1.44
23	Y	34	CM0	O8-C8	-2.30	1.23	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	Y	34	CM0	C7-O5-C5	14.37	136.39	117.58
23	Y	34	CM0	O5-C7-C8	5.34	122.47	110.88
23	Y	34	CM0	O4-C4-N3	-2.26	115.79	120.12

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	Y	34	CM0	C4-C5-O5-C7
23	Y	34	CM0	C6-C5-O5-C7
23	Y	34	CM0	C8-C7-O5-C5
23	Y	34	CM0	O5-C7-C8-O8
23	Y	34	CM0	O5-C7-C8-O9

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	Y	34	CM0	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 256 ligands modelled in this entry, 255 are monoatomic - leaving 1 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	$\# Z > 2$
24	PAR	A	1601	-	45,45,45	1.56	10 (22%)	64,67,67	1.25	8 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	PAR	A	1601	-	-	5/18/94/94	0/4/4/4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1601	PAR	C64-C54	4.49	1.58	1.52
24	A	1601	PAR	O54-C14	3.43	1.50	1.41
24	A	1601	PAR	C52-C42	3.05	1.58	1.52
24	A	1601	PAR	C31-C21	2.76	1.57	1.53
24	A	1601	PAR	C11-C21	2.43	1.57	1.52
24	A	1601	PAR	C34-C24	2.34	1.56	1.53
24	A	1601	PAR	C14-C24	2.18	1.56	1.52
24	A	1601	PAR	O51-C11	2.04	1.47	1.41
24	A	1601	PAR	O54-C54	2.03	1.49	1.44
24	A	1601	PAR	C62-C52	2.01	1.57	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1601	PAR	O33-C14-C24	4.26	115.56	108.22
24	A	1601	PAR	O54-C54-C64	3.73	112.95	106.01
24	A	1601	PAR	C14-O54-C54	3.44	120.44	113.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1601	PAR	O52-C13-C23	2.63	113.41	107.96
24	A	1601	PAR	O11-C11-C21	2.39	112.34	108.22
24	A	1601	PAR	C11-O51-C51	2.29	118.19	113.69
24	A	1601	PAR	O52-C13-O43	-2.23	109.01	111.43
24	A	1601	PAR	C22-C32-C42	2.12	114.88	109.53

There are no chirality outliers.

All (5) torsion outliers are listed below:

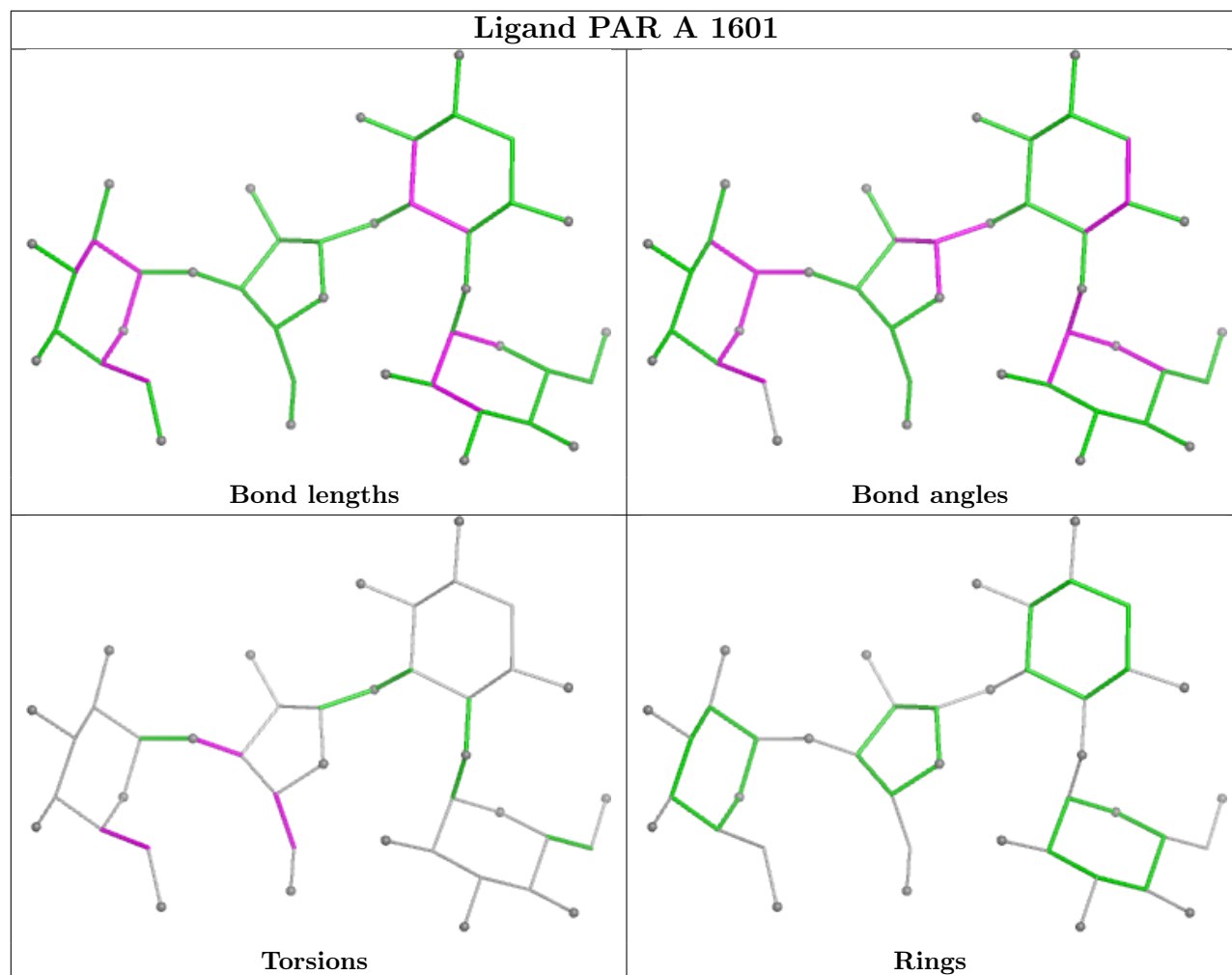
Mol	Chain	Res	Type	Atoms
24	A	1601	PAR	C44-C54-C64-N64
24	A	1601	PAR	C33-C43-C53-O53
24	A	1601	PAR	O43-C43-C53-O53
24	A	1601	PAR	O54-C54-C64-N64
24	A	1601	PAR	C43-C33-O33-C14

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1601	PAR	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1512/1522 (99%)	3.77	1427 (94%)  	29, 55, 119, 166	0
2	B	235/256 (91%)	3.43	193 (82%)  	47, 82, 126, 148	0
3	C	207/239 (86%)	3.68	183 (88%)  	47, 75, 110, 117	0
4	D	208/209 (99%)	3.43	174 (83%)  	45, 60, 82, 89	0
5	E	151/162 (93%)	2.77	101 (66%)  	30, 46, 63, 85	0
6	F	101/101 (100%)	4.06	92 (91%)  	56, 79, 92, 101	0
7	G	155/156 (99%)	2.94	121 (78%)  	52, 72, 110, 127	0
8	H	138/138 (100%)	2.82	92 (66%)  	29, 44, 63, 68	0
9	I	127/128 (99%)	3.40	109 (85%)  	43, 82, 101, 104	0
10	J	99/105 (94%)	4.17	96 (96%)  	44, 103, 140, 145	0
11	K	119/129 (92%)	3.81	105 (88%)  	33, 59, 80, 103	0
12	L	125/135 (92%)	3.37	105 (84%)  	22, 51, 72, 108	0
13	M	125/126 (99%)	3.52	99 (79%)  	47, 69, 125, 159	0
14	N	60/61 (98%)	4.07	53 (88%)  	49, 66, 90, 98	0
15	O	88/89 (98%)	3.97	79 (89%)  	40, 60, 79, 104	0
16	P	84/88 (95%)	2.92	63 (75%)  	36, 48, 59, 91	0
17	Q	104/105 (99%)	3.65	84 (80%)  	32, 53, 98, 127	0
18	R	73/88 (82%)	4.18	72 (98%)  	49, 66, 103, 132	0
19	S	81/93 (87%)	4.38	81 (100%)  	63, 85, 107, 116	0
20	T	99/106 (93%)	3.38	82 (82%)  	35, 53, 80, 85	0
21	U	25/27 (92%)	2.93	18 (72%)  	44, 56, 81, 87	0
22	X	5/6 (83%)	2.36	3 (60%)  	51, 52, 85, 109	0
23	Y	9/17 (52%)	3.32	9 (100%)  	57, 78, 113, 120	0
All	All	3930/4086 (96%)	3.60	3441 (87%)  	22, 60, 113, 166	0

All (3441) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
17	Q	105	ALA	13.9
3	C	103	VAL	12.3
3	C	101	LEU	12.0
19	S	4	SER	11.8
4	D	32	ALA	11.7
18	R	20	ALA	11.7
14	N	2	ALA	10.9
19	S	15	LEU	10.8
13	M	125	ARG	10.8
13	M	85	GLY	10.7
6	F	79	LEU	10.3
17	Q	16	GLN	10.2
3	C	66	VAL	10.2
8	H	106	GLY	10.2
6	F	84	ASN	10.0
13	M	124	PRO	10.0
3	C	120	VAL	10.0
20	T	47	GLY	9.9
13	M	104	ARG	9.8
14	N	3	ARG	9.7
2	B	203	GLY	9.7
16	P	30	GLY	9.7
4	D	151	LYS	9.6
15	O	56	LEU	9.6
1	A	1482	G	9.5
2	B	228	GLY	9.4
8	H	1	MET	9.4
19	S	34	TRP	9.4
3	C	68	VAL	9.4
17	Q	21	VAL	9.3
1	A	1129	C	9.2
12	L	39	VAL	9.1
7	G	153	HIS	9.1
3	C	195	VAL	9.1
15	O	25	THR	8.9
9	I	106	ALA	8.7
10	J	18	ALA	8.6
17	Q	95	TYR	8.6
17	Q	65	ILE	8.5
19	S	18	LYS	8.5
3	C	196	LEU	8.5
3	C	2	GLY	8.4

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Mol	Chain	Res	Type	RSRZ
4	D	42	GLN	8.4
15	O	66	LEU	8.4
1	A	1541	U	8.3
11	K	69	ALA	8.3
1	A	159	G	8.3
6	F	75	LEU	8.2
20	T	40	ALA	8.2
1	A	989	C	8.2
8	H	79	VAL	8.2
4	D	30	LYS	8.1
1	A	160	A	8.1
20	T	103	GLY	8.1
1	A	1474	G	8.0
6	F	73	ASN	8.0
20	T	12	ALA	8.0
18	R	50	ILE	8.0
6	F	10	LEU	8.0
15	O	67	LEU	8.0
1	A	704	A	8.0
2	B	138	LEU	7.9
2	B	35	GLU	7.9
4	D	31	CYS	7.9
1	A	1013	G	7.8
7	G	2	ALA	7.7
2	B	80	ILE	7.7
2	B	99	GLY	7.7
1	A	1433	A	7.7
6	F	85	VAL	7.7
6	F	8	ILE	7.7
9	I	33	PHE	7.6
19	S	3	ARG	7.6
10	J	54	PHE	7.6
1	A	1419	G	7.6
5	E	101	ILE	7.6
18	R	78	LEU	7.6
13	M	103	THR	7.6
11	K	51	LYS	7.6
14	N	21	TYR	7.5
2	B	229	VAL	7.5
18	R	76	LEU	7.5
18	R	51	LEU	7.5
1	A	1354	C	7.5

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Mol	Chain	Res	Type	RSRZ
4	D	133	VAL	7.4
5	E	20	GLN	7.4
1	A	1014	A	7.4
1	A	1055	A	7.4
10	J	39	PRO	7.4
5	E	92	LYS	7.4
1	A	1147	C	7.4
2	B	7	VAL	7.3
1	A	161	A	7.3
7	G	76	ARG	7.3
17	Q	57	VAL	7.3
1	A	1030(D)	A	7.2
8	H	124	ALA	7.2
3	C	7	PRO	7.2
4	D	35	ARG	7.2
20	T	48	LYS	7.1
10	J	90	LEU	7.1
10	J	93	GLY	7.1
1	A	152	A	7.1
1	A	493	G	7.1
1	A	1049	U	7.1
1	A	985	C	7.1
19	S	49	ILE	7.0
10	J	67	THR	7.0
1	A	435	C	7.0
1	A	436	C	7.0
13	M	114	ARG	7.0
1	A	700	G	7.0
1	A	703	G	7.0
15	O	33	THR	7.0
17	Q	99	SER	7.0
14	N	37	PHE	7.0
11	K	31	THR	7.0
15	O	30	ALA	7.0
11	K	50	TYR	6.9
1	A	490	G	6.9
11	K	118	GLY	6.9
1	A	349	A	6.9
1	A	1016	A	6.9
1	A	366	C	6.9
1	A	1124	G	6.9
1	A	196	A	6.9

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Mol	Chain	Res	Type	RSRZ
1	A	1426	C	6.9
15	O	55	GLY	6.9
1	A	1001(A)	G	6.9
16	P	63	GLY	6.8
10	J	56	HIS	6.8
10	J	37	PRO	6.8
3	C	75	VAL	6.8
14	N	34	TYR	6.8
7	G	88	PRO	6.8
6	F	6	VAL	6.8
5	E	95	ALA	6.8
2	B	221	LEU	6.8
8	H	13	ILE	6.8
10	J	4	ILE	6.8
1	A	275	G	6.8
1	A	999	C	6.8
1	A	1145	C	6.8
4	D	119	GLN	6.8
11	K	39	PRO	6.8
17	Q	91	ARG	6.7
9	I	36	TYR	6.7
19	S	79	THR	6.7
1	A	156	G	6.7
1	A	630	G	6.7
1	A	1060	C	6.7
17	Q	20	THR	6.7
1	A	1219	U	6.7
13	M	117	VAL	6.7
4	D	169	LYS	6.7
4	D	115	ARG	6.7
15	O	31	LEU	6.7
15	O	49	ASP	6.7
4	D	39	PRO	6.7
12	L	107	ALA	6.7
6	F	7	ASN	6.7
7	G	141	VAL	6.7
4	D	36	ARG	6.6
14	N	16	PHE	6.6
13	M	116	THR	6.6
1	A	1017	G	6.6
4	D	25	ARG	6.6
1	A	1319	A	6.6

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Mol	Chain	Res	Type	RSRZ
15	O	52	SER	6.6
15	O	45	VAL	6.6
9	I	29	ASN	6.6
19	S	14	HIS	6.6
3	C	192	THR	6.5
2	B	188	ALA	6.5
12	L	115	LYS	6.5
18	R	67	ALA	6.5
8	H	44	PHE	6.5
4	D	2	GLY	6.5
1	A	410	G	6.5
1	A	413	G	6.5
1	A	1030(C)	G	6.5
11	K	95	ILE	6.5
17	Q	64	PRO	6.5
4	D	106	TYR	6.5
1	A	1043	C	6.5
1	A	1163	C	6.5
1	A	1046	A	6.5
17	Q	12	SER	6.4
1	A	1012	U	6.4
18	R	58	LEU	6.4
10	J	21	GLN	6.4
15	O	53	HIS	6.4
20	T	71	THR	6.4
20	T	85	MET	6.4
18	R	60	ALA	6.4
15	O	51	HIS	6.4
1	A	1094	G	6.4
6	F	57	GLN	6.3
2	B	108	ILE	6.3
11	K	28	THR	6.3
1	A	533	A	6.3
2	B	77	ALA	6.3
6	F	99	ALA	6.3
2	B	42	ILE	6.3
11	K	20	TYR	6.3
1	A	988	G	6.3
18	R	40	LEU	6.3
1	A	696	A	6.3
1	A	1256	A	6.3
18	R	54	ARG	6.3

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Mol	Chain	Res	Type	RSRZ
5	E	119	LEU	6.3
19	S	69	HIS	6.3
1	A	481	G	6.3
1	A	1143	G	6.3
2	B	192	SER	6.3
10	J	60	ARG	6.3
1	A	1473	A	6.2
9	I	102	LEU	6.2
1	A	1221	G	6.2
1	A	1130	A	6.2
1	A	1056	U	6.2
11	K	32	ILE	6.2
15	O	69	TYR	6.2
1	A	1226	C	6.2
11	K	58	PRO	6.2
3	C	132	ARG	6.2
13	M	119	GLY	6.2
4	D	138	TYR	6.2
6	F	93	SER	6.2
3	C	127	ARG	6.2
19	S	60	VAL	6.2
1	A	1441	G	6.2
17	Q	100	LYS	6.2
3	C	102	ASN	6.1
1	A	716	A	6.1
1	A	777	A	6.1
1	A	992	U	6.1
1	A	77	G	6.1
18	R	47	THR	6.1
18	R	52	PRO	6.1
11	K	83	ILE	6.1
1	A	341	C	6.1
1	A	1128	C	6.1
3	C	149	ALA	6.1
7	G	150	ALA	6.1
1	A	57	G	6.1
1	A	289	G	6.1
1	A	775	G	6.1
1	A	1001	A	6.1
13	M	123	ALA	6.1
1	A	742	G	6.1
19	S	33	THR	6.1

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Mol	Chain	Res	Type	RSRZ
5	E	22	GLY	6.1
1	A	1445	C	6.0
10	J	34	VAL	6.0
12	L	79	GLU	6.0
12	L	95	GLY	6.0
1	A	1422	G	6.0
1	A	498	U	6.0
7	G	85	TYR	6.0
13	M	87	TYR	6.0
1	A	54	C	6.0
4	D	21	LEU	6.0
2	B	22	LYS	6.0
14	N	58	LYS	6.0
1	A	351	G	6.0
1	A	631	G	6.0
1	A	1154	G	6.0
15	O	26	GLU	6.0
13	M	49	THR	6.0
13	M	81	LEU	6.0
19	S	6	LYS	6.0
4	D	3	ARG	6.0
6	F	29	ALA	6.0
1	A	476	G	6.0
1	A	1511	G	6.0
13	M	121	LYS	6.0
1	A	977	A	6.0
4	D	110	PHE	6.0
10	J	94	VAL	6.0
20	T	88	VAL	6.0
1	A	813	U	5.9
21	U	4	GLY	5.9
1	A	64	G	5.9
11	K	61	ALA	5.9
13	M	28	ALA	5.9
1	A	1041	A	5.9
5	E	41	VAL	5.9
6	F	90	VAL	5.9
19	S	5	LEU	5.9
10	J	35	SER	5.9
1	A	439	A	5.9
1	A	1468	A	5.9
1	A	1223	C	5.9

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Mol	Chain	Res	Type	RSRZ
2	B	105	PHE	5.9
1	A	346	G	5.9
1	A	438	G	5.9
1	A	1305	G	5.9
1	A	1137	C	5.9
16	P	24	ALA	5.9
14	N	32	SER	5.9
5	E	23	GLY	5.8
1	A	715	A	5.8
1	A	278	G	5.8
1	A	319	G	5.8
1	A	1421	G	5.8
8	H	2	LEU	5.8
2	B	90	MET	5.8
12	L	28	LYS	5.8
10	J	23	ILE	5.8
1	A	1210	C	5.8
9	I	56	LEU	5.8
11	K	129	SER	5.8
17	Q	98	LEU	5.8
2	B	226	ARG	5.8
18	R	72	ARG	5.8
12	L	129	ALA	5.8
19	S	77	THR	5.8
1	A	1146	A	5.8
1	A	418	C	5.8
1	A	1463	C	5.8
1	A	361	G	5.8
1	A	688	G	5.8
2	B	152	PHE	5.8
10	J	69	ASN	5.8
1	A	672	U	5.8
2	B	29	ALA	5.7
9	I	15	ALA	5.7
4	D	209	ARG	5.7
15	O	54	ARG	5.7
1	A	455	C	5.7
1	A	470	C	5.7
4	D	135	LEU	5.7
9	I	47	LEU	5.7
1	A	266	G	5.7
1	A	800	G	5.7

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Mol	Chain	Res	Type	RSRZ
1	A	1042	G	5.7
1	A	1475	G	5.7
4	D	171	GLY	5.7
12	L	35	GLY	5.7
12	L	116	SER	5.7
11	K	36	ASP	5.7
1	A	705	U	5.7
1	A	1414	U	5.7
20	T	72	LEU	5.7
1	A	369	C	5.7
2	B	214	ILE	5.7
13	M	102	ARG	5.7
4	D	26	CYS	5.7
19	S	80	TYR	5.7
1	A	445	G	5.6
1	A	1220	G	5.6
1	A	1312	G	5.6
1	A	1469	G	5.6
17	Q	90	ILE	5.6
1	A	1260	C	5.6
4	D	185	PHE	5.6
5	E	110	LEU	5.6
12	L	102	ARG	5.6
19	S	20	LEU	5.6
4	D	28	SER	5.6
2	B	189	ASP	5.6
1	A	423	G	5.6
1	A	1139	G	5.6
2	B	208	ILE	5.6
9	I	6	GLY	5.6
10	J	6	ILE	5.6
6	F	72	VAL	5.6
17	Q	19	VAL	5.6
1	A	576	G	5.6
1	A	1053	G	5.6
1	A	1443	G	5.6
2	B	122	PHE	5.6
4	D	22	LYS	5.6
3	C	116	VAL	5.6
7	G	87	VAL	5.6
13	M	60	VAL	5.6
1	A	449	C	5.6

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Mol	Chain	Res	Type	RSRZ
1	A	805	C	5.6
1	A	899	C	5.6
3	C	15	THR	5.6
8	H	100	ILE	5.6
2	B	209	ARG	5.6
11	K	91	ARG	5.6
12	L	43	VAL	5.6
1	A	1003	G	5.6
1	A	1207	G	5.6
1	A	1271	G	5.6
1	A	58	C	5.5
1	A	1362	C	5.5
10	J	65	LEU	5.5
3	C	130	VAL	5.5
1	A	622	A	5.5
15	O	50	HIS	5.5
4	D	102	ASP	5.5
1	A	102	G	5.5
1	A	265	G	5.5
1	A	316	G	5.5
1	A	388	G	5.5
1	A	409	G	5.5
1	A	1523	G	5.5
10	J	70	ARG	5.5
12	L	113	ARG	5.5
13	M	126	LYS	5.5
17	Q	68	ARG	5.5
21	U	7	ARG	5.5
2	B	51	LEU	5.5
12	L	52	LEU	5.5
1	A	990	C	5.5
7	G	134	ALA	5.5
11	K	38	ASN	5.5
1	A	130	A	5.5
1	A	448	A	5.5
1	A	1531	A	5.5
11	K	40	ILE	5.5
18	R	65	ILE	5.5
20	T	99	LEU	5.5
1	A	714	G	5.5
1	A	993	G	5.5
1	A	189(C)	C	5.5

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Mol	Chain	Res	Type	RSRZ
1	A	720	C	5.5
1	A	726	C	5.5
1	A	408	A	5.5
14	N	22	THR	5.5
1	A	428	G	5.5
1	A	670	G	5.5
1	A	1489	G	5.5
1	A	165	C	5.5
6	F	92	LYS	5.5
8	H	131	GLY	5.4
17	Q	18	THR	5.4
1	A	274	A	5.4
19	S	40	ILE	5.4
1	A	1007	C	5.4
6	F	58	GLY	5.4
11	K	56	GLY	5.4
18	R	33	ASP	5.4
18	R	81	PHE	5.4
12	L	120	TYR	5.4
1	A	172	A	5.4
5	E	18	ARG	5.4
3	C	162	GLN	5.4
2	B	16	HIS	5.4
7	G	120	ILE	5.4
6	F	88	VAL	5.4
11	K	14	VAL	5.4
13	M	17	VAL	5.4
1	A	492	G	5.4
1	A	1255	G	5.4
18	R	73	ALA	5.4
17	Q	63	ARG	5.4
6	F	16	GLN	5.4
13	M	53	VAL	5.4
14	N	20	ALA	5.4
1	A	372	C	5.4
1	A	1018	C	5.4
10	J	45	ARG	5.4
1	A	39	G	5.4
1	A	167	G	5.4
1	A	774	G	5.4
1	A	1122	U	5.4
2	B	14	GLY	5.3

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Mol	Chain	Res	Type	RSRZ
12	L	26	ALA	5.3
2	B	125	PRO	5.3
3	C	202	ILE	5.3
2	B	31	TYR	5.3
1	A	276	G	5.3
1	A	350	G	5.3
1	A	649	G	5.3
1	A	1497	G	5.3
17	Q	14	LYS	5.3
1	A	279	A	5.3
1	A	1279	A	5.3
11	K	35	PRO	5.3
6	F	14	LEU	5.3
19	S	22	LEU	5.3
1	A	1200	C	5.3
13	M	122	LYS	5.3
4	D	105	VAL	5.3
1	A	434	U	5.3
1	A	588	G	5.3
1	A	1084	G	5.3
1	A	1278	U	5.3
12	L	41	ARG	5.3
14	N	48	ALA	5.3
1	A	733	A	5.3
14	N	47	LEU	5.3
2	B	109	SER	5.3
19	S	7	LYS	5.3
10	J	47	PHE	5.3
1	A	1039	C	5.3
1	A	1267	C	5.3
2	B	37	ASN	5.3
6	F	11	ASN	5.3
1	A	1485	U	5.3
1	A	683	G	5.3
1	A	1442(A)	G	5.3
1	A	1488	G	5.3
1	A	51	A	5.3
1	A	60	A	5.3
1	A	1502	A	5.3
9	I	70	LYS	5.3
19	S	52	TYR	5.3
12	L	55	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
19	S	51	VAL	5.3
20	T	97	ALA	5.2
1	A	335	C	5.2
2	B	200	ILE	5.2
8	H	83	ILE	5.2
1	A	21	G	5.2
1	A	529	G	5.2
1	A	579	G	5.2
1	A	741	G	5.2
1	A	1198	G	5.2
9	I	65	VAL	5.2
14	N	6	LEU	5.2
2	B	47	THR	5.2
1	A	245	C	5.2
1	A	1000	U	5.2
1	A	1254	C	5.2
3	C	141	VAL	5.2
11	K	79	SER	5.2
15	O	27	VAL	5.2
1	A	1225	A	5.2
1	A	776	G	5.2
1	A	878	G	5.2
11	K	122	LYS	5.2
11	K	41	THR	5.2
11	K	105	VAL	5.2
18	R	34	TYR	5.2
20	T	11	SER	5.2
13	M	50	GLU	5.2
2	B	238	LEU	5.2
12	L	77	LEU	5.2
11	K	106	LYS	5.2
1	A	69	G	5.2
1	A	447	G	5.2
1	A	537	G	5.2
1	A	654	G	5.2
1	A	769	G	5.2
1	A	1178	G	5.2
1	A	1266	G	5.2
2	B	67	THR	5.2
4	D	13	ARG	5.2
14	N	33	VAL	5.2
2	B	28	PHE	5.2

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Mol	Chain	Res	Type	RSRZ
1	A	443	C	5.2
17	Q	79	SER	5.2
12	L	100	ILE	5.2
1	A	499	A	5.1
1	A	1434	A	5.1
1	A	1480	G	5.1
7	G	26	PHE	5.1
9	I	37	PHE	5.1
3	C	22	TRP	5.1
9	I	96	LEU	5.1
4	D	33	MET	5.1
10	J	86	MET	5.1
1	A	195	A	5.1
1	A	1213	A	5.1
10	J	42	THR	5.1
11	K	33	THR	5.1
16	P	39	TYR	5.1
20	T	94	ALA	5.1
1	A	370	C	5.1
3	C	88	ARG	5.1
8	H	50	ARG	5.1
1	A	766	A	5.1
1	A	918	A	5.1
1	A	1513	A	5.1
12	L	47	LYS	5.1
16	P	31	LYS	5.1
13	M	9	ILE	5.1
6	F	20	ALA	5.1
1	A	1446	U	5.1
21	U	10	ARG	5.1
1	A	424	G	5.1
11	K	82	VAL	5.1
1	A	248	C	5.1
1	A	739	C	5.1
3	C	97	LYS	5.1
18	R	63	GLN	5.1
3	C	5	ILE	5.1
8	H	55	GLY	5.1
3	C	177	THR	5.0
6	F	30	LEU	5.0
1	A	52	G	5.0
1	A	189	G	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	657	G	5.0
1	A	1224	G	5.0
1	A	1274	G	5.0
8	H	80	ILE	5.0
1	A	569	C	5.0
1	A	1051	C	5.0
1	A	574	A	5.0
1	A	737	A	5.0
2	B	144	ARG	5.0
3	C	59	ARG	5.0
1	A	264	U	5.0
1	A	1052	U	5.0
9	I	28	VAL	5.0
19	S	71	LEU	5.0
19	S	31	ILE	5.0
9	I	119	ALA	5.0
1	A	444	C	5.0
1	A	880	C	5.0
1	A	972	C	5.0
1	A	987	G	5.0
1	A	1061	G	5.0
2	B	68	ILE	5.0
4	D	132	ARG	5.0
13	M	97	PRO	5.0
14	N	14	PRO	5.0
16	P	15	PRO	5.0
1	A	174	C	5.0
1	A	419	C	5.0
1	A	612	C	5.0
1	A	1228	C	5.0
1	A	1156	G	5.0
4	D	123	HIS	5.0
1	A	547	A	5.0
1	A	1377	A	5.0
21	U	24	ARG	5.0
13	M	120	LYS	5.0
3	C	198	VAL	5.0
6	F	4	TYR	5.0
12	L	83	VAL	5.0
1	A	352	C	4.9
1	A	1141	C	4.9
1	A	1322	C	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	1404	C	4.9
1	A	1459	C	4.9
1	A	1539	C	4.9
15	O	87	ILE	4.9
15	O	24	SER	4.9
1	A	65	U	4.9
1	A	182	U	4.9
1	A	363	A	4.9
1	A	373	A	4.9
8	H	30	ARG	4.9
10	J	9	ARG	4.9
13	M	52	GLU	4.9
7	G	80	VAL	4.9
11	K	29	ILE	4.9
3	C	67	THR	4.9
1	A	706	A	4.9
1	A	1004	A	4.9
5	E	93	PRO	4.9
5	E	106	PRO	4.9
1	A	189(G)	G	4.9
1	A	1026	G	4.9
1	A	1190	G	4.9
1	A	1458	G	4.9
4	D	170	VAL	4.9
11	K	21	ILE	4.9
12	L	80	HIS	4.9
9	I	125	TYR	4.9
5	E	5	ASP	4.9
17	Q	104	LYS	4.9
10	J	91	PRO	4.9
1	A	268	C	4.9
1	A	271	C	4.9
1	A	745	C	4.9
1	A	897	C	4.9
1	A	653	A	4.9
7	G	75	VAL	4.9
1	A	362	G	4.9
1	A	629	G	4.9
1	A	1142	G	4.9
1	A	1144	G	4.9
4	D	181	MET	4.9
3	C	29	TYR	4.9

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Mol	Chain	Res	Type	RSRZ
20	T	74	LYS	4.9
2	B	235	SER	4.9
19	S	35	SER	4.9
5	E	96	PRO	4.9
4	D	97	LEU	4.9
1	A	479	C	4.9
1	A	879	C	4.9
2	B	93	VAL	4.9
1	A	477	A	4.9
1	A	1275	A	4.9
3	C	83	ARG	4.9
3	C	128	PHE	4.9
4	D	14	ARG	4.9
17	Q	70	ARG	4.9
1	A	371	G	4.8
1	A	396	G	4.8
1	A	1202	G	4.8
1	A	1222	G	4.8
1	A	1311	G	4.8
19	S	68	GLY	4.8
9	I	13	ALA	4.8
20	T	98	PRO	4.8
5	E	12	LEU	4.8
2	B	230	VAL	4.8
11	K	80	VAL	4.8
4	D	161	ASN	4.8
11	K	108	ILE	4.8
15	O	59	MET	4.8
7	G	43	PHE	4.8
1	A	32	A	4.8
1	A	162	A	4.8
1	A	994	A	4.8
15	O	61	GLY	4.8
15	O	76	GLU	4.8
15	O	22	THR	4.8
1	A	129(A)	G	4.8
1	A	406	G	4.8
1	A	639	G	4.8
1	A	674	G	4.8
1	A	685	G	4.8
1	A	752	G	4.8
1	A	1034	G	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	1310	G	4.8
1	A	1331	G	4.8
1	A	1464	G	4.8
3	C	94	LEU	4.8
6	F	98	LEU	4.8
14	N	25	VAL	4.8
1	A	531	U	4.8
1	A	717	C	4.8
1	A	984	C	4.8
1	A	1045	C	4.8
1	A	1066	C	4.8
1	A	1162	C	4.8
1	A	1035	A	4.8
1	A	1357	A	4.8
2	B	123	ALA	4.8
4	D	29	PRO	4.8
4	D	136	PRO	4.8
4	D	178	VAL	4.8
10	J	3	LYS	4.8
10	J	19	SER	4.8
1	A	1023	G	4.8
1	A	582	U	4.8
7	G	154	TYR	4.8
9	I	62	TYR	4.8
17	Q	103	GLY	4.8
1	A	269	C	4.8
1	A	599	C	4.8
1	A	681	C	4.8
1	A	814	A	4.8
1	A	1418	A	4.8
1	A	1452	C	4.8
1	A	1465	C	4.8
1	A	1519	A	4.8
9	I	64	THR	4.8
3	C	57	ILE	4.8
6	F	9	VAL	4.8
6	F	26	ILE	4.8
11	K	30	VAL	4.8
14	N	57	ARG	4.8
3	C	10	PHE	4.8
1	A	421	U	4.8
1	A	437	U	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	1512	U	4.8
1	A	625	G	4.8
1	A	668	G	4.8
1	A	1050	G	4.8
1	A	1197	G	4.8
1	A	1316	G	4.8
11	K	68	ALA	4.8
13	M	13	LYS	4.7
6	F	40	VAL	4.7
8	H	53	VAL	4.7
12	L	24	VAL	4.7
1	A	336	C	4.7
1	A	728	A	4.7
1	A	781	A	4.7
1	A	794	A	4.7
1	A	892	A	4.7
1	A	1208	C	4.7
3	C	123	GLN	4.7
19	S	73	GLU	4.7
2	B	69	LEU	4.7
1	A	384	G	4.7
1	A	869	G	4.7
10	J	74	ILE	4.7
9	I	14	VAL	4.7
18	R	30	ASP	4.7
19	S	11	VAL	4.7
19	S	12	ASP	4.7
1	A	189(B)	C	4.7
1	A	441	A	4.7
1	A	983	A	4.7
1	A	1005	A	4.7
1	A	1289	A	4.7
1	A	1442(B)	A	4.7
2	B	17	PHE	4.7
8	H	87	SER	4.7
14	N	28	GLY	4.7
1	A	244	U	4.7
20	T	14	LYS	4.7
2	B	97	TRP	4.7
3	C	182	ILE	4.7
3	C	201	TYR	4.7
4	D	158	ILE	4.7

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Mol	Chain	Res	Type	RSRZ
17	Q	51	TYR	4.7
6	F	37	VAL	4.7
10	J	24	VAL	4.7
18	R	82	THR	4.7
1	A	548	G	4.7
1	A	713	G	4.7
1	A	758	G	4.7
1	A	1048	G	4.7
1	A	1182	G	4.7
1	A	1504	G	4.7
1	A	187	C	4.7
1	A	322	C	4.7
1	A	1027	C	4.7
1	A	1277	C	4.7
1	A	1282	C	4.7
6	F	22	GLU	4.7
1	A	957	U	4.7
1	A	1427	U	4.7
11	K	12	ARG	4.7
15	O	77	ARG	4.7
17	Q	60	ILE	4.7
8	H	17	THR	4.7
20	T	105	SER	4.7
1	A	181	G	4.7
1	A	851	G	4.7
1	A	1160	G	4.7
1	A	1323	G	4.7
1	A	1467	G	4.7
4	D	19	LEU	4.7
7	G	25	ALA	4.7
13	M	118	ALA	4.7
1	A	360	A	4.7
1	A	1176	A	4.7
1	A	1287	A	4.7
1	A	783	C	4.7
1	A	1363	C	4.7
23	Y	31	C	4.7
8	H	8	ASP	4.6
2	B	133	LYS	4.6
11	K	55	LYS	4.6
5	E	91	LEU	4.6
12	L	118	SER	4.6

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Mol	Chain	Res	Type	RSRZ
8	H	74	PRO	4.6
10	J	10	GLY	4.6
13	M	10	PRO	4.6
15	O	62	GLN	4.6
20	T	106	ALA	4.6
9	I	83	ARG	4.6
16	P	42	ARG	4.6
11	K	114	VAL	4.6
1	A	33	A	4.6
1	A	495	A	4.6
1	A	532	A	4.6
1	A	773	G	4.6
1	A	1015	A	4.6
1	A	291	C	4.6
1	A	342	C	4.6
1	A	656	C	4.6
1	A	995	C	4.6
1	A	1159	U	4.6
1	A	1259	C	4.6
1	A	1314	C	4.6
1	A	1481	U	4.6
4	D	27	TYR	4.6
7	G	63	LYS	4.6
3	C	62	ASP	4.6
10	J	85	LEU	4.6
3	C	163	ALA	4.6
9	I	42	ARG	4.6
14	N	30	ALA	4.6
2	B	39	ILE	4.6
17	Q	5	VAL	4.6
10	J	15	THR	4.6
1	A	686	U	4.6
1	A	7	G	4.6
1	A	318	G	4.6
1	A	398	C	4.6
1	A	1304	G	4.6
3	C	175	LEU	4.6
10	J	40	LEU	4.6
19	S	70	LYS	4.6
9	I	7	THR	4.6
18	R	56	THR	4.6
1	A	676	A	4.6

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Mol	Chain	Res	Type	RSRZ
10	J	8	LEU	4.6
12	L	12	ARG	4.6
1	A	744	C	4.6
1	A	1030(B)	C	4.6
1	A	1411	C	4.6
1	A	1431	C	4.6
1	A	473	G	4.6
1	A	491	G	4.6
1	A	521	G	4.6
1	A	690	G	4.6
1	A	711	G	4.6
1	A	1131	G	4.6
1	A	1272	G	4.6
1	A	1353	G	4.6
3	C	20	SER	4.6
11	K	44	SER	4.6
19	S	53	ASN	4.6
3	C	18	TRP	4.5
1	A	173	U	4.5
1	A	697	U	4.5
1	A	1447	A	4.5
13	M	51	ALA	4.5
14	N	7	ILE	4.5
11	K	52	GLY	4.5
17	Q	54	GLY	4.5
8	H	123	GLU	4.5
1	A	689	C	4.5
1	A	893	C	4.5
1	A	1214	C	4.5
10	J	44	VAL	4.5
15	O	10	LYS	4.5
1	A	247	G	4.5
1	A	953	G	4.5
1	A	1355	G	4.5
20	T	61	SER	4.5
2	B	101	MET	4.5
6	F	86	ARG	4.5
1	A	841	U	4.5
10	J	77	PRO	4.5
16	P	51	VAL	4.5
1	A	753	A	4.5
1	A	504	C	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	1113	C	4.5
20	T	56	MET	4.5
18	R	31	LEU	4.5
1	A	450	G	4.5
1	A	734	G	4.5
1	A	1253	G	4.5
1	A	1416	G	4.5
1	A	1461	G	4.5
10	J	43	ARG	4.5
2	B	236	TYR	4.5
7	G	151	TYR	4.5
3	C	84	ILE	4.5
2	B	81	VAL	4.5
15	O	11	VAL	4.5
1	A	374	A	4.5
1	A	675	A	4.5
20	T	16	HIS	4.5
1	A	483	C	4.5
1	A	806	C	4.5
1	A	1008	C	4.5
1	A	1030	C	4.5
12	L	44	THR	4.5
7	G	36	LYS	4.5
8	H	98	LYS	4.5
19	S	2	PRO	4.5
1	A	61	G	4.5
1	A	391	G	4.5
1	A	823	G	4.5
3	C	64	VAL	4.5
6	F	38	GLU	4.5
2	B	10	LEU	4.5
10	J	11	PHE	4.5
20	T	91	LEU	4.5
6	F	52	ILE	4.4
18	R	70	ILE	4.4
1	A	699	C	4.4
1	A	1038	C	4.4
1	A	1478	C	4.4
6	F	33	TYR	4.4
6	F	53	ALA	4.4
11	K	65	ALA	4.4
11	K	74	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
12	L	45	PRO	4.4
17	Q	78	GLU	4.4
1	A	164	U	4.4
1	A	839	U	4.4
1	A	1199	U	4.4
1	A	1283	G	4.4
3	C	178	LEU	4.4
9	I	19	LEU	4.4
5	E	64	ARG	4.4
18	R	64	ARG	4.4
11	K	116	HIS	4.4
5	E	130	ASN	4.4
12	L	114	LYS	4.4
1	A	197	A	4.4
2	B	227	GLY	4.4
5	E	35	GLY	4.4
6	F	50	TYR	4.4
2	B	241	GLU	4.4
1	A	385	C	4.4
11	K	85	ARG	4.4
15	O	39	LEU	4.4
15	O	63	ARG	4.4
1	A	429	U	4.4
1	A	486	U	4.4
1	A	1313	U	4.4
1	A	1393	U	4.4
1	A	484	G	4.4
1	A	517	G	4.4
1	A	1273	G	4.4
1	A	1417	G	4.4
2	B	124	SER	4.4
1	A	722	A	4.4
1	A	807	A	4.4
3	C	48	TYR	4.4
3	C	148	GLY	4.4
4	D	112	VAL	4.4
3	C	142	MET	4.4
9	I	5	TYR	4.4
3	C	12	LEU	4.4
5	E	63	ARG	4.4
14	N	31	ARG	4.4
18	R	42	ARG	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	1029	C	4.4
1	A	1126	U	4.4
1	A	1472	U	4.4
3	C	110	ASN	4.4
9	I	49	PRO	4.4
11	K	89	ALA	4.4
2	B	112	VAL	4.4
3	C	153	VAL	4.4
12	L	18	VAL	4.4
1	A	107	G	4.4
1	A	347	G	4.4
1	A	426	G	4.4
1	A	585	G	4.4
1	A	725	G	4.4
1	A	894	G	4.4
1	A	1002	G	4.4
1	A	1432	G	4.4
18	R	38	GLU	4.4
4	D	194	LEU	4.4
15	O	68	ARG	4.4
18	R	74	ARG	4.4
5	E	109	ILE	4.4
1	A	169	C	4.4
1	A	241	C	4.4
1	A	242	C	4.4
1	A	488	C	4.4
1	A	634	C	4.4
1	A	1140	C	4.4
1	A	190	U	4.4
13	M	107	ALA	4.3
3	C	138	VAL	4.3
14	N	56	VAL	4.3
11	K	102	GLY	4.3
5	E	155	GLU	4.3
20	T	93	GLU	4.3
3	C	43	LEU	4.3
9	I	31	GLN	4.3
16	P	25	ARG	4.3
1	A	297	G	4.3
1	A	425	G	4.3
1	A	666	G	4.3
1	A	902	G	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	916	G	4.3
1	A	1171	G	4.3
5	E	6	PHE	4.3
16	P	80	PHE	4.3
1	A	246	A	4.3
1	A	767	A	4.3
1	A	1123	A	4.3
1	A	1268	A	4.3
15	O	12	ILE	4.3
4	D	193	ASP	4.3
1	A	253	U	4.3
1	A	442	C	4.3
1	A	643	C	4.3
1	A	719	C	4.3
1	A	797	C	4.3
1	A	804	U	4.3
1	A	1019	C	4.3
1	A	1420	C	4.3
1	A	1436	U	4.3
1	A	1533	C	4.3
7	G	83	ALA	4.3
8	H	19	VAL	4.3
3	C	81	GLY	4.3
3	C	204	LEU	4.3
9	I	9	ARG	4.3
9	I	35	GLU	4.3
11	K	63	LEU	4.3
14	N	36	PHE	4.3
18	R	43	PHE	4.3
2	B	127	ILE	4.3
8	H	6	ILE	4.3
1	A	50	A	4.3
1	A	411	A	4.3
1	A	727	G	4.3
1	A	872	A	4.3
1	A	958	A	4.3
1	A	1036	G	4.3
1	A	1231	G	4.3
1	A	1398	A	4.3
1	A	1415	G	4.3
1	A	1476	G	4.3
5	E	19	MET	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	223	U	4.3
1	A	387	U	4.3
1	A	1211	U	4.3
19	S	82	GLY	4.3
2	B	154	LEU	4.3
1	A	76	C	4.3
1	A	153	C	4.3
1	A	240	C	4.3
1	A	283	C	4.3
1	A	290	C	4.3
1	A	330	C	4.3
1	A	1071	C	4.3
1	A	1262	C	4.3
2	B	135	GLN	4.3
6	F	25	ILE	4.3
15	O	82	ILE	4.3
11	K	22	HIS	4.3
2	B	198	ASP	4.3
2	B	136	VAL	4.3
2	B	234	PRO	4.3
9	I	55	ALA	4.3
2	B	46	LYS	4.3
9	I	115	GLY	4.3
1	A	35	G	4.3
1	A	73	G	4.3
1	A	399	G	4.3
1	A	691	G	4.3
1	A	731	G	4.3
1	A	1064	G	4.3
1	A	1356	G	4.3
1	A	480	U	4.3
1	A	422	C	4.3
1	A	1006	C	4.3
1	A	1209	C	4.3
6	F	63	TYR	4.3
6	F	56	PRO	4.3
12	L	23	LYS	4.3
12	L	58	VAL	4.3
16	P	41	PRO	4.3
4	D	187	ARG	4.3
17	Q	11	VAL	4.3
1	A	1269	A	4.2

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Mol	Chain	Res	Type	RSRZ
17	Q	7	THR	4.2
11	K	42	TRP	4.2
1	A	302	G	4.2
1	A	635	G	4.2
1	A	1024	G	4.2
1	A	1133	G	4.2
1	A	1300	G	4.2
1	A	454	C	4.2
1	A	1484	C	4.2
12	L	57	LYS	4.2
14	N	9	LYS	4.2
17	Q	50	LYS	4.2
18	R	61	LYS	4.2
20	T	57	ARG	4.2
3	C	200	ALA	4.2
10	J	88	LEU	4.2
15	O	81	LEU	4.2
14	N	55	GLY	4.2
1	A	430	A	4.2
1	A	684	A	4.2
1	A	695	A	4.2
1	A	1250	A	4.2
1	A	1375	A	4.2
1	A	1483	A	4.2
10	J	55	LYS	4.2
17	Q	17	LYS	4.2
1	A	31	G	4.2
1	A	108	G	4.2
1	A	682	G	4.2
1	A	976	G	4.2
1	A	1181	G	4.2
2	B	15	VAL	4.2
2	B	131	PRO	4.2
1	A	123	C	4.2
1	A	201	C	4.2
1	A	219	C	4.2
1	A	234	C	4.2
1	A	624	C	4.2
2	B	145	LEU	4.2
3	C	60	ALA	4.2
4	D	64	LEU	4.2
2	B	128	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
3	C	35	GLU	4.2
19	S	10	PHE	4.2
1	A	494	U	4.2
1	A	788	U	4.2
1	A	816	A	4.2
1	A	1135	U	4.2
1	A	1425	U	4.2
3	C	86	VAL	4.2
2	B	13	ALA	4.2
3	C	91	LEU	4.2
8	H	93	VAL	4.2
13	M	7	VAL	4.2
9	I	43	ALA	4.2
13	M	2	ALA	4.2
19	S	30	LEU	4.2
1	A	221	C	4.2
1	A	225	C	4.2
1	A	317	G	4.2
1	A	541	G	4.2
1	A	581	G	4.2
1	A	754	C	4.2
1	A	765	G	4.2
1	A	1371	G	4.2
1	A	1405	G	4.2
1	A	1440	C	4.2
15	O	36	ILE	4.2
2	B	190	THR	4.2
10	J	99	LYS	4.2
14	N	4	LYS	4.2
14	N	15	LYS	4.2
18	R	41	LYS	4.2
3	C	23	TYR	4.2
6	F	65	VAL	4.2
4	D	55	ALA	4.2
3	C	13	GLY	4.2
1	A	417	C	4.1
1	A	157	G	4.1
1	A	191	G	4.1
1	A	251	G	4.1
1	A	485	G	4.1
1	A	595	G	4.1
1	A	724	G	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	1031	G	4.1
1	A	1456	G	4.1
12	L	119	LYS	4.1
7	G	37	ASN	4.1
13	M	80	ARG	4.1
19	S	65	ASN	4.1
4	D	96	LEU	4.1
18	R	24	ALA	4.1
19	S	50	ALA	4.1
1	A	101	A	4.1
19	S	27	GLU	4.1
9	I	81	ILE	4.1
10	J	38	ILE	4.1
3	C	150	LYS	4.1
6	F	70	ASP	4.1
7	G	78	ARG	4.1
1	A	103	C	4.1
1	A	556	C	4.1
1	A	600	C	4.1
1	A	1270	C	4.1
5	E	31	LEU	4.1
15	O	43	LEU	4.1
1	A	66	G	4.1
1	A	286	G	4.1
1	A	1022	G	4.1
3	C	193	TYR	4.1
4	D	38	TYR	4.1
11	K	115	PRO	4.1
3	C	129	ALA	4.1
20	T	49	ALA	4.1
16	P	10	GLY	4.1
1	A	353	A	4.1
1	A	611	A	4.1
1	A	702	A	4.1
1	A	759	A	4.1
4	D	18	LYS	4.1
9	I	127	LYS	4.1
17	Q	41	LYS	4.1
13	M	11	ARG	4.1
15	O	65	ARG	4.1
4	D	140	VAL	4.1
6	F	91	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
4	D	40	PRO	4.1
8	H	5	PRO	4.1
1	A	770	C	4.1
1	A	1153	C	4.1
1	A	1444	C	4.1
1	A	1514	C	4.1
1	A	1515	C	4.1
6	F	17	SER	4.1
1	A	56	U	4.1
1	A	138	G	4.1
1	A	166	G	4.1
1	A	348	G	4.1
1	A	460	G	4.1
1	A	671	G	4.1
1	A	798	G	4.1
1	A	863	U	4.1
1	A	945	G	4.1
1	A	1088	G	4.1
1	A	1368	G	4.1
2	B	9	GLU	4.1
4	D	200	GLU	4.1
12	L	7	ILE	4.1
18	R	62	GLU	4.1
4	D	118	ARG	4.1
10	J	12	ASP	4.1
11	K	57	THR	4.1
7	G	59	LEU	4.1
19	S	16	LEU	4.1
9	I	26	VAL	4.1
5	E	17	ALA	4.1
13	M	75	ALA	4.1
5	E	154	GLY	4.1
6	F	54	LYS	4.1
7	G	70	LYS	4.1
1	A	513	C	4.1
17	Q	97	SER	4.1
1	A	343	U	4.1
13	M	88	ARG	4.1
18	R	29	PHE	4.1
6	F	64	GLN	4.1
1	A	446	G	4.1
1	A	475	G	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	644	G	4.1
1	A	836	G	4.1
17	Q	22	LEU	4.0
1	A	535	A	4.0
1	A	1044	A	4.0
14	N	18	VAL	4.0
15	O	75	PRO	4.0
11	K	64	ALA	4.0
11	K	128	ALA	4.0
14	N	61	TRP	4.0
16	P	50	LYS	4.0
10	J	52	GLY	4.0
1	A	277	C	4.0
1	A	359	U	4.0
1	A	723	U	4.0
1	A	960	U	4.0
1	A	1218	C	4.0
9	I	3	GLN	4.0
13	M	101	GLN	4.0
18	R	79	LEU	4.0
2	B	202	PRO	4.0
1	A	254	G	4.0
1	A	301	G	4.0
1	A	407	G	4.0
1	A	540	G	4.0
1	A	1134	G	4.0
1	A	1423	G	4.0
7	G	145	ALA	4.0
12	L	128	ALA	4.0
19	S	24	ALA	4.0
20	T	81	LYS	4.0
1	A	356	A	4.0
1	A	1067	A	4.0
4	D	90	GLY	4.0
6	F	97	PHE	4.0
3	C	154	SER	4.0
10	J	59	SER	4.0
3	C	87	LEU	4.0
4	D	101	LEU	4.0
1	A	618	C	4.0
1	A	1407	C	4.0
15	O	42	HIS	4.0

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Mol	Chain	Res	Type	RSRZ
5	E	42	GLY	4.0
1	A	1280	A	4.0
16	P	8	ARG	4.0
19	S	81	ARG	4.0
1	A	139	G	4.0
1	A	803	G	4.0
1	A	1030(A)	G	4.0
1	A	1057	G	4.0
1	A	1258	G	4.0
1	A	1290	G	4.0
4	D	174	LEU	4.0
6	F	19	LEU	4.0
15	O	57	LEU	4.0
20	T	53	LEU	4.0
10	J	33	GLN	4.0
1	A	114	U	4.0
1	A	950	U	4.0
3	C	180	ALA	4.0
10	J	89	ASP	4.0
1	A	339	C	4.0
1	A	1321	C	4.0
3	C	124	ILE	4.0
9	I	69	GLY	4.0
4	D	145	GLU	4.0
16	P	48	TRP	4.0
1	A	344	A	4.0
1	A	412	A	4.0
2	B	240	GLN	4.0
1	A	260	G	4.0
1	A	474	G	4.0
1	A	771	G	4.0
1	A	778	G	4.0
1	A	821	G	4.0
1	A	1276	G	4.0
1	A	1517	G	4.0
19	S	38	SER	4.0
13	M	82	MET	4.0
19	S	63	THR	4.0
1	A	1136	U	3.9
10	J	75	ILE	3.9
8	H	25	ASP	3.9
7	G	149	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
21	U	2	GLY	3.9
1	A	295	C	3.9
1	A	848	C	3.9
1	A	979	C	3.9
1	A	1028	C	3.9
1	A	1059	C	3.9
1	A	1242	C	3.9
1	A	119	A	3.9
1	A	978	A	3.9
1	A	986	A	3.9
1	A	1460	A	3.9
17	Q	23	VAL	3.9
10	J	53	PRO	3.9
3	C	133	ALA	3.9
4	D	149	ALA	3.9
14	N	59	ALA	3.9
1	A	200	G	3.9
1	A	281	G	3.9
1	A	500	G	3.9
1	A	570	G	3.9
1	A	1387	G	3.9
1	A	1392	G	3.9
1	A	1487	G	3.9
1	A	427	U	3.9
1	A	850	U	3.9
1	A	1532	U	3.9
4	D	10	ARG	3.9
14	N	29	ARG	3.9
13	M	68	GLY	3.9
3	C	161	GLU	3.9
2	B	11	LEU	3.9
4	D	176	LEU	3.9
1	A	150	C	3.9
1	A	489	C	3.9
1	A	849	C	3.9
1	A	862	C	3.9
1	A	1367	C	3.9
13	M	21	TYR	3.9
23	Y	36	C	3.9
3	C	118	GLN	3.9
9	I	108	VAL	3.9
7	G	98	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	149	A	3.9
1	A	414	A	3.9
1	A	496	A	3.9
1	A	621	A	3.9
1	A	663	A	3.9
1	A	1332	A	3.9
4	D	66	ARG	3.9
6	F	49	ALA	3.9
1	A	323	U	3.9
1	A	340	U	3.9
1	A	619	U	3.9
1	A	1085	U	3.9
1	A	1307	U	3.9
12	L	72	GLY	3.9
16	P	68	ASP	3.9
7	G	146	GLU	3.9
1	A	148	G	3.9
1	A	515	G	3.9
1	A	584	G	3.9
1	A	730	G	3.9
1	A	1337	G	3.9
1	A	1442	G	3.9
3	C	181	ASN	3.9
13	M	12	ASN	3.9
4	D	148	VAL	3.9
18	R	22	VAL	3.9
1	A	71	C	3.9
1	A	514	C	3.9
1	A	526	C	3.9
1	A	623	C	3.9
1	A	1103	C	3.9
10	J	50	ILE	3.9
6	F	77	ARG	3.9
9	I	10	ARG	3.9
9	I	20	ARG	3.9
12	L	81	SER	3.9
14	N	41	ARG	3.9
1	A	143	A	3.9
1	A	659	U	3.9
2	B	12	GLU	3.9
9	I	113	LYS	3.9
11	K	71	LYS	3.9

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Mol	Chain	Res	Type	RSRZ
15	O	85	LEU	3.9
17	Q	77	VAL	3.9
19	S	19	VAL	3.9
1	A	255	G	3.9
1	A	597	G	3.9
1	A	664	G	3.9
1	A	971	G	3.9
1	A	1047	G	3.9
1	A	1177	G	3.9
2	B	21	ARG	3.9
4	D	49	ARG	3.9
4	D	67	ILE	3.9
1	A	137	C	3.9
1	A	525	C	3.9
1	A	564	C	3.9
1	A	645	C	3.9
1	A	748	C	3.9
1	A	808	C	3.9
1	A	1037	C	3.9
3	C	74	GLY	3.8
19	S	54	GLY	3.8
11	K	103	LEU	3.8
10	J	63	PHE	3.8
1	A	53	A	3.8
1	A	729	A	3.8
1	A	768	A	3.8
1	A	1340	A	3.8
8	H	26	VAL	3.8
8	H	51	VAL	3.8
4	D	116	GLN	3.8
9	I	34	ASN	3.8
3	C	73	PRO	3.8
5	E	131	ILE	3.8
6	F	51	PRO	3.8
13	M	99	ARG	3.8
15	O	46	HIS	3.8
3	C	189	ALA	3.8
1	A	158	G	3.8
1	A	299	G	3.8
1	A	331	G	3.8
1	A	1068	G	3.8
5	E	75	THR	3.8

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Mol	Chain	Res	Type	RSRZ
5	E	98	THR	3.8
18	R	21	LYS	3.8
19	S	48	THR	3.8
4	D	23	GLY	3.8
17	Q	6	LEU	3.8
1	A	536	C	3.8
1	A	589	C	3.8
1	A	756	C	3.8
1	A	896	C	3.8
1	A	1335	C	3.8
6	F	5	GLU	3.8
6	F	66	GLU	3.8
1	A	90	U	3.8
1	A	655	A	3.8
10	J	101	VAL	3.8
12	L	40	VAL	3.8
3	C	85	ARG	3.8
19	S	36	ARG	3.8
12	L	69	TYR	3.8
3	C	146	ALA	3.8
7	G	116	ALA	3.8
7	G	138	LYS	3.8
2	B	149	LEU	3.8
17	Q	43	LEU	3.8
12	L	32	PHE	3.8
18	R	17	SER	3.8
4	D	24	GLU	3.8
7	G	74	GLU	3.8
1	A	41	G	3.8
1	A	111	G	3.8
1	A	189(J)	G	3.8
1	A	1215	G	3.8
1	A	1265	G	3.8
19	S	44	MET	3.8
1	A	381	C	3.8
1	A	501	C	3.8
1	A	1132	C	3.8
3	C	106	VAL	3.8
6	F	74	ASP	3.8
14	N	40	CYS	3.8
17	Q	73	VAL	3.8
1	A	1248	A	3.8

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Mol	Chain	Res	Type	RSRZ
9	I	92	TYR	3.8
3	C	53	ALA	3.8
14	N	5	ALA	3.8
3	C	33	LEU	3.8
13	M	48	LEU	3.8
9	I	2	GLU	3.8
10	J	30	SER	3.8
12	L	22	SER	3.8
4	D	139	ARG	3.8
9	I	107	ARG	3.8
12	L	97	ARG	3.8
20	T	33	ILE	3.8
1	A	306	G	3.8
1	A	380	G	3.8
1	A	834	C	3.8
1	A	944	G	3.8
1	A	1373	G	3.8
2	B	110	GLN	3.8
15	O	19	PRO	3.8
16	P	66	PRO	3.8
1	A	204	U	3.8
1	A	1522	U	3.8
3	C	108	ASN	3.8
9	I	4	TYR	3.8
16	P	17	TYR	3.8
1	A	55	A	3.8
1	A	171	A	3.8
1	A	510	A	3.8
14	N	39	LEU	3.8
2	B	38	GLY	3.8
2	B	129	GLU	3.7
6	F	69	GLU	3.7
20	T	50	GLU	3.7
12	L	62	SER	3.7
10	J	28	ARG	3.7
2	B	41	ILE	3.7
2	B	222	ILE	3.7
18	R	71	LYS	3.7
16	P	46	PRO	3.7
19	S	13	ASP	3.7
12	L	56	ALA	3.7
1	A	34	C	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	47	C	3.7
1	A	121	C	3.7
1	A	596	C	3.7
1	A	810	C	3.7
16	P	49	LEU	3.7
18	R	66	LEU	3.7
21	U	18	TYR	3.7
1	A	1164	G	3.7
1	A	1526	G	3.7
5	E	44	GLY	3.7
1	A	116	A	3.7
1	A	393	A	3.7
1	A	520	A	3.7
1	A	632	A	3.7
1	A	746	A	3.7
1	A	907	A	3.7
1	A	1252	A	3.7
9	I	59	PHE	3.7
6	F	87	ARG	3.7
9	I	66	ARG	3.7
21	U	22	ARG	3.7
6	F	81	ILE	3.7
18	R	59	SER	3.7
7	G	53	LYS	3.7
9	I	11	LYS	3.7
3	C	136	GLN	3.7
18	R	80	PRO	3.7
2	B	187	LEU	3.7
2	B	237	ALA	3.7
16	P	7	ALA	3.7
11	K	119	CYS	3.7
11	K	25	TYR	3.7
1	A	1040	U	3.7
1	A	1498	U	3.7
9	I	68	GLY	3.7
1	A	188	C	3.7
1	A	337	C	3.7
1	A	395	C	3.7
1	A	1424	C	3.7
3	C	82	GLU	3.7
17	Q	61	GLU	3.7
1	A	305	G	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	617	G	3.7
1	A	1033	G	3.7
1	A	1117	G	3.7
1	A	1334	G	3.7
7	G	3	ARG	3.7
23	Y	40	G	3.7
1	A	864	A	3.7
1	A	1201	A	3.7
1	A	1251	A	3.7
1	A	1518	A	3.7
4	D	182	LYS	3.7
2	B	201	ILE	3.7
4	D	5	ILE	3.7
9	I	17	VAL	3.7
12	L	101	VAL	3.7
19	S	62	ILE	3.7
3	C	49	SER	3.7
12	L	50	SER	3.7
3	C	100	ALA	3.7
6	F	45	LEU	3.7
7	G	73	MET	3.7
3	C	145	GLY	3.7
11	K	88	GLY	3.7
1	A	252	U	3.7
1	A	1196	U	3.7
7	G	72	ARG	3.7
9	I	111	ARG	3.7
10	J	25	GLU	3.7
21	U	15	ARG	3.7
10	J	87	THR	3.7
18	R	19	LYS	3.7
19	S	32	LYS	3.7
1	A	314	C	3.7
1	A	701	C	3.7
1	A	784	C	3.7
1	A	866	C	3.7
1	A	1297	C	3.7
4	D	203	VAL	3.7
17	Q	59	ILE	3.7
1	A	432	A	3.7
1	A	482	A	3.7
1	A	572	A	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	780	A	3.7
1	A	792	A	3.7
1	A	1236	A	3.7
1	A	22	G	3.7
1	A	115	G	3.7
1	A	122	G	3.7
1	A	616	G	3.7
1	A	830	G	3.7
1	A	973	G	3.7
1	A	1216	G	3.7
1	A	1471	G	3.7
6	F	12	PRO	3.7
8	H	70	GLN	3.7
5	E	108	ALA	3.7
4	D	190	ASP	3.7
2	B	96	ARG	3.7
9	I	57	GLY	3.7
13	M	24	GLY	3.7
17	Q	94	ASN	3.7
10	J	14	LYS	3.7
19	S	28	LYS	3.7
1	A	835	U	3.7
3	C	55	VAL	3.7
13	M	78	ILE	3.7
13	M	109	THR	3.7
1	A	308	C	3.6
1	A	379	C	3.6
1	A	1165	C	3.6
1	A	1203	C	3.6
1	A	1501	C	3.6
13	M	41	PRO	3.6
2	B	19	HIS	3.6
3	C	47	LEU	3.6
6	F	21	LEU	3.6
12	L	84	LEU	3.6
17	Q	84	LEU	3.6
4	D	175	SER	3.6
1	A	315	A	3.6
1	A	397	A	3.6
1	A	782	A	3.6
1	A	259	G	3.6
1	A	1521	G	3.6

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Mol	Chain	Res	Type	RSRZ
13	M	26	GLY	3.6
18	R	77	GLY	3.6
2	B	94	ASN	3.6
7	G	18	TYR	3.6
4	D	70	ILE	3.6
4	D	162	LEU	3.6
9	I	21	PRO	3.6
20	T	104	LEU	3.6
3	C	61	ALA	3.6
1	A	386	C	3.6
1	A	904	C	3.6
1	A	1054	C	3.6
1	A	1430	C	3.6
1	A	1477	C	3.6
1	A	1329	A	3.6
2	B	147	LYS	3.6
2	B	156	LYS	3.6
18	R	88	LYS	3.6
19	S	25	LYS	3.6
19	S	55	LYS	3.6
2	B	55	PHE	3.6
7	G	62	PHE	3.6
11	K	90	GLY	3.6
1	A	113	G	3.6
1	A	189(H)	G	3.6
1	A	232	G	3.6
1	A	606	G	3.6
1	A	721	G	3.6
1	A	829	G	3.6
1	A	1155	G	3.6
1	A	1206	G	3.6
2	B	165	VAL	3.6
20	T	9	ASN	3.6
7	G	47	CYS	3.6
1	A	911	U	3.6
2	B	215	LEU	3.6
12	L	78	GLN	3.6
20	T	76	ALA	3.6
2	B	27	LYS	3.6
9	I	126	SER	3.6
10	J	22	LYS	3.6
2	B	163	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
2	B	89	GLY	3.6
15	O	20	GLY	3.6
1	A	511	C	3.6
8	H	52	ASP	3.6
1	A	329	A	3.6
1	A	1111	A	3.6
7	G	113	GLU	3.6
11	K	84	VAL	3.6
12	L	36	VAL	3.6
15	O	29	VAL	3.6
11	K	117	ASN	3.6
19	S	61	TYR	3.6
6	F	43	LEU	3.6
10	J	71	LEU	3.6
1	A	37	U	3.6
1	A	512	U	3.6
1	A	593	G	3.6
1	A	626	U	3.6
1	A	887	G	3.6
1	A	888	G	3.6
1	A	906	G	3.6
1	A	1361	G	3.6
19	S	57	HIS	3.6
3	C	121	ALA	3.6
20	T	30	LYS	3.6
3	C	144	SER	3.6
6	F	60	PHE	3.6
14	N	38	GLY	3.6
20	T	41	ILE	3.6
4	D	173	TRP	3.6
7	G	21	VAL	3.6
7	G	33	ASP	3.6
17	Q	55	ASP	3.6
5	E	61	TYR	3.6
1	A	946	A	3.6
1	A	1318	A	3.6
4	D	120	LEU	3.6
10	J	7	LYS	3.5
13	M	27	LYS	3.5
1	A	1205	U	3.5
12	L	19	ARG	3.5
15	O	35	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
18	R	32	ARG	3.5
19	S	37	ARG	3.5
1	A	46	G	3.5
1	A	326	G	3.5
1	A	558	G	3.5
1	A	658	G	3.5
1	A	881	G	3.5
1	A	1079	G	3.5
1	A	1138	G	3.5
1	A	1530	G	3.5
13	M	95	GLY	3.5
17	Q	36	ILE	3.5
4	D	17	VAL	3.5
9	I	53	VAL	3.5
18	R	37	VAL	3.5
7	G	156	TRP	3.5
16	P	6	LEU	3.5
6	F	39	LYS	3.5
1	A	355	C	3.5
1	A	586	C	3.5
1	A	1263	C	3.5
1	A	1284	C	3.5
2	B	137	ARG	3.5
3	C	169	ALA	3.5
7	G	6	ARG	3.5
16	P	18	ARG	3.5
20	T	77	ALA	3.5
20	T	89	ARG	3.5
11	K	62	GLN	3.5
1	A	13	U	3.5
1	A	249	U	3.5
1	A	652	U	3.5
1	A	1348	U	3.5
4	D	126	ILE	3.5
9	I	63	ILE	3.5
10	J	36	GLY	3.5
10	J	96	ILE	3.5
1	A	38	G	3.5
1	A	44	G	3.5
1	A	566	G	3.5
1	A	604	G	3.5
1	A	785	G	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	1370	G	3.5
1	A	1508	G	3.5
20	T	13	LEU	3.5
13	M	111	LYS	3.5
15	O	48	LYS	3.5
2	B	183	PRO	3.5
4	D	4	TYR	3.5
19	S	39	THR	3.5
12	L	117	ARG	3.5
3	C	69	HIS	3.5
10	J	62	HIS	3.5
10	J	68	HIS	3.5
11	K	19	ALA	3.5
11	K	97	ALA	3.5
20	T	44	ALA	3.5
1	A	185	A	3.5
1	A	224	C	3.5
1	A	487	A	3.5
1	A	518	C	3.5
1	A	519	C	3.5
1	A	747	C	3.5
1	A	959	A	3.5
1	A	1188	A	3.5
1	A	1317	C	3.5
1	A	1366	C	3.5
11	K	125	PHE	3.5
16	P	19	ILE	3.5
1	A	170	U	3.5
3	C	25	GLY	3.5
3	C	197	GLY	3.5
4	D	198	VAL	3.5
15	O	60	VAL	3.5
7	G	99	LEU	3.5
15	O	32	LEU	3.5
4	D	46	LYS	3.5
10	J	80	LYS	3.5
12	L	21	LYS	3.5
14	N	54	PRO	3.5
4	D	65	ARG	3.5
14	N	19	ARG	3.5
1	A	144	G	3.5
1	A	292	G	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	333	G	3.5
1	A	354	G	3.5
1	A	550	G	3.5
1	A	755	G	3.5
1	A	1309	G	3.5
1	A	1435	G	3.5
1	A	1520	G	3.5
13	M	77	ASN	3.5
2	B	70	PHE	3.5
3	C	134	ILE	3.5
9	I	101	PHE	3.5
1	A	194	C	3.5
1	A	267	C	3.5
1	A	964	A	3.5
1	A	1172	C	3.5
1	A	1363(A)	A	3.5
1	A	367	U	3.5
1	A	740	U	3.5
1	A	1315	U	3.5
3	C	52	LEU	3.5
5	E	71	LEU	3.5
13	M	34	LEU	3.5
15	O	8	LYS	3.5
17	Q	96	GLU	3.5
3	C	30	ARG	3.5
13	M	55	ARG	3.5
3	C	117	ALA	3.5
3	C	137	ALA	3.5
5	E	65	ASN	3.5
9	I	87	GLN	3.4
3	C	39	ILE	3.4
16	P	9	PHE	3.4
1	A	592	G	3.4
1	A	886	G	3.4
2	B	18	GLY	3.4
8	H	71	GLY	3.4
4	D	188	LEU	3.4
5	E	151	LEU	3.4
13	M	56	LEU	3.4
16	P	12	LYS	3.4
20	T	68	LYS	3.4
20	T	92	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	509	A	3.4
1	A	1229	A	3.4
1	A	1333	A	3.4
1	A	1408	A	3.4
1	A	19	C	3.4
1	A	189(F)	U	3.4
1	A	390	C	3.4
1	A	749	C	3.4
1	A	905	U	3.4
1	A	1397	C	3.4
23	Y	30	C	3.4
6	F	62	TRP	3.4
8	H	16	ALA	3.4
10	J	26	ALA	3.4
8	H	45	ILE	3.4
10	J	82	ILE	3.4
3	C	199	LYS	3.4
7	G	137	LYS	3.4
8	H	97	VAL	3.4
11	K	17	GLY	3.4
13	M	96	LEU	3.4
1	A	189(I)	G	3.4
1	A	954	G	3.4
1	A	998	G	3.4
1	A	534	U	3.4
1	A	1257	U	3.4
1	A	1406	U	3.4
1	A	583	A	3.4
4	D	197	PRO	3.4
1	A	23	C	3.4
1	A	89	C	3.4
1	A	154	C	3.4
1	A	272	C	3.4
1	A	1389	C	3.4
4	D	152	SER	3.4
20	T	95	ALA	3.4
4	D	62	GLN	3.4
14	N	42	ILE	3.4
20	T	55	ILE	3.4
2	B	239	VAL	3.4
4	D	58	LEU	3.4
7	G	69	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
7	G	124	LEU	3.4
9	I	41	VAL	3.4
9	I	67	GLY	3.4
12	L	96	VAL	3.4
10	J	61	GLU	3.4
3	C	79	ARG	3.4
15	O	17	ARG	3.4
14	N	43	CYS	3.4
12	L	94	PRO	3.4
12	L	125	PRO	3.4
1	A	202	U	3.4
1	A	431	A	3.4
1	A	539	A	3.4
1	A	557	G	3.4
1	A	874	G	3.4
1	A	895	G	3.4
1	A	903	G	3.4
1	A	949	A	3.4
1	A	1179	A	3.4
1	A	1401	G	3.4
1	A	1428	A	3.4
3	C	187	ALA	3.4
2	B	58	ILE	3.4
7	G	27	ILE	3.4
1	A	72	C	3.4
1	A	456	C	3.4
1	A	1320	C	3.4
1	A	1342	C	3.4
2	B	33	TYR	3.4
3	C	93	LYS	3.4
12	L	9	GLN	3.4
11	K	27	ASN	3.4
5	E	43	LEU	3.4
20	T	62	LEU	3.4
7	G	133	GLY	3.4
2	B	111	ARG	3.4
3	C	105	GLU	3.4
7	G	52	GLU	3.4
13	M	113	PRO	3.4
3	C	65	ALA	3.4
3	C	71	ALA	3.4
5	E	94	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
10	J	20	ALA	3.4
1	A	591	U	3.4
1	A	891	U	3.4
11	K	43	SER	3.4
4	D	206	PHE	3.4
1	A	250	A	3.4
16	P	40	ASP	3.4
12	L	10	LEU	3.3
1	A	68	G	3.3
1	A	79	G	3.3
1	A	117	G	3.3
1	A	1058	G	3.3
1	A	1074	G	3.3
1	A	1104	G	3.3
1	A	1127	G	3.3
1	A	1173	G	3.3
1	A	1347	G	3.3
10	J	49	VAL	3.3
13	M	54	VAL	3.3
1	A	163	C	3.3
1	A	811	C	3.3
1	A	970	C	3.3
7	G	32	ARG	3.3
14	N	23	ARG	3.3
15	O	64	ARG	3.3
10	J	97	GLU	3.3
4	D	189	PRO	3.3
2	B	140	HIS	3.3
17	Q	3	LYS	3.3
1	A	404	U	3.3
1	A	801	U	3.3
1	A	956	U	3.3
1	A	1330	U	3.3
3	C	28	GLN	3.3
7	G	110	GLN	3.3
3	C	32	LEU	3.3
9	I	85	LEU	3.3
2	B	160	ASP	3.3
21	U	21	TYR	3.3
2	B	130	ARG	3.3
5	E	46	GLY	3.3
7	G	4	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
11	K	26	ASN	3.3
19	S	29	ARG	3.3
20	T	96	GLY	3.3
1	A	273	A	3.3
1	A	640	A	3.3
1	A	1092	A	3.3
1	A	1192	C	3.3
1	A	184	G	3.3
1	A	199	G	3.3
1	A	257	G	3.3
1	A	394	G	3.3
1	A	524	G	3.3
1	A	825	G	3.3
1	A	926	G	3.3
1	A	1072	G	3.3
1	A	1120	G	3.3
2	B	194	PRO	3.3
17	Q	82	MET	3.3
8	H	10	LEU	3.3
11	K	98	LEU	3.3
10	J	92	THR	3.3
1	A	192	U	3.3
3	C	40	ARG	3.3
4	D	104	VAL	3.3
20	T	15	ARG	3.3
8	H	58	TYR	3.3
1	A	1169	A	3.3
1	A	1306	A	3.3
1	A	67	C	3.3
1	A	312	C	3.3
1	A	543	C	3.3
23	Y	32	C	3.3
17	Q	44	ALA	3.3
20	T	73	HIS	3.3
1	A	146	G	3.3
1	A	183	G	3.3
1	A	799	G	3.3
1	A	951	G	3.3
9	I	40	LEU	3.3
6	F	80	ARG	3.3
17	Q	35	VAL	3.3
19	S	58	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
19	S	78	ARG	3.3
4	D	71	SER	3.3
1	A	81	U	3.3
1	A	203	U	3.3
1	A	1070	U	3.3
1	A	1358	U	3.3
15	O	78	TYR	3.3
7	G	90	GLU	3.3
9	I	12	GLU	3.3
10	J	83	GLU	3.3
10	J	95	GLU	3.3
11	K	92	GLU	3.3
4	D	85	LYS	3.3
12	L	17	LYS	3.3
2	B	232	PRO	3.3
1	A	364	A	3.3
1	A	815	A	3.3
1	A	937	A	3.3
17	Q	45	HIS	3.3
4	D	11	LEU	3.3
20	T	10	LEU	3.3
1	A	679	C	3.3
1	A	738	C	3.3
1	A	1325	C	3.3
1	A	1352	C	3.3
1	A	1437	C	3.3
9	I	16	ARG	3.3
10	J	79	ARG	3.3
11	K	78	GLN	3.3
3	C	95	THR	3.3
1	A	238	G	3.3
1	A	502	G	3.3
1	A	718	G	3.3
3	C	205	GLY	3.3
7	G	34	GLY	3.3
13	M	100	GLY	3.3
20	T	102	GLY	3.3
8	H	48	TYR	3.2
13	M	59	TYR	3.2
1	A	565	U	3.2
2	B	134	GLU	3.2
2	B	141	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
9	I	105	ASP	3.2
5	E	11	ILE	3.2
12	L	70	ILE	3.2
3	C	176	HIS	3.2
6	F	61	LEU	3.2
9	I	79	LEU	3.2
1	A	327	A	3.2
1	A	968	A	3.2
1	A	975	A	3.2
1	A	1152	A	3.2
11	K	47	VAL	3.2
17	Q	26	GLN	3.2
17	Q	56	VAL	3.2
20	T	45	GLN	3.2
1	A	1063	C	3.2
1	A	1195	C	3.2
1	A	1249	C	3.2
3	C	185	GLY	3.2
4	D	41	GLY	3.2
5	E	47	LYS	3.2
5	E	8	GLU	3.2
16	P	34	GLU	3.2
7	G	45	ASP	3.2
1	A	669	U	3.2
1	A	763	G	3.2
1	A	952	U	3.2
1	A	1089	G	3.2
3	C	24	ALA	3.2
5	E	90	VAL	3.2
7	G	135	VAL	3.2
8	H	95	VAL	3.2
6	F	18	GLN	3.2
1	A	389	A	3.2
1	A	865	A	3.2
1	A	1191	A	3.2
1	A	1261	A	3.2
12	L	29	GLY	3.2
12	L	67	THR	3.2
1	A	1114	C	3.2
8	H	76	PRO	3.2
1	A	256	U	3.2
1	A	365	U	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	516	U	3.2
2	B	61	LEU	3.2
7	G	16	LEU	3.2
6	F	2	ARG	3.2
7	G	107	ALA	3.2
12	L	51	ALA	3.2
14	N	53	LEU	3.2
17	Q	92	ARG	3.2
1	A	6	G	3.2
1	A	42	G	3.2
1	A	124	G	3.2
1	A	1175	G	3.2
3	C	99	VAL	3.2
4	D	121	VAL	3.2
5	E	34	VAL	3.2
11	K	109	VAL	3.2
18	R	39	VAL	3.2
10	J	57	LYS	3.2
13	M	115	LYS	3.2
20	T	34	LYS	3.2
5	E	124	GLY	3.2
11	K	37	GLY	3.2
4	D	127	THR	3.2
16	P	22	THR	3.2
1	A	151	A	3.2
1	A	1503	A	3.2
17	Q	15	MET	3.2
4	D	9	CYS	3.2
16	P	11	SER	3.2
2	B	191	ASP	3.2
1	A	620	C	3.2
1	A	708	C	3.2
1	A	1116	C	3.2
1	A	1388	C	3.2
4	D	73	ARG	3.2
8	H	18	ARG	3.2
9	I	128	ARG	3.2
17	Q	101	ARG	3.2
1	A	827	U	3.2
19	S	47	HIS	3.2
3	C	207	VAL	3.2
5	E	67	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
17	Q	9	VAL	3.2
1	A	97	G	3.2
1	A	284	G	3.2
1	A	471	G	3.2
1	A	627	G	3.2
1	A	917	G	3.2
1	A	1010	G	3.2
1	A	1193	G	3.2
4	D	87	GLY	3.2
15	O	89	GLY	3.2
6	F	1	MET	3.2
10	J	64	GLU	3.2
16	P	83	GLU	3.2
15	O	3	ILE	3.2
1	A	687	A	3.1
1	A	1102	A	3.1
1	A	1180	A	3.1
1	A	1183	A	3.1
1	A	1396	A	3.1
3	C	11	ARG	3.1
3	C	190	ARG	3.1
7	G	101	LEU	3.1
8	H	59	LEU	3.1
9	I	121	ARG	3.1
10	J	29	ARG	3.1
11	K	101	SER	3.1
2	B	225	ALA	3.1
8	H	46	LYS	3.1
1	A	189(D)	C	3.1
1	A	522	C	3.1
1	A	826	C	3.1
1	A	1395	C	3.1
3	C	158	GLY	3.1
12	L	74	GLY	3.1
12	L	121	GLY	3.1
10	J	81	THR	3.1
2	B	91	PRO	3.1
2	B	223	ILE	3.1
1	A	78	G	3.1
1	A	377	G	3.1
1	A	527	G	3.1
1	A	542	G	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	575	G	3.1
1	A	650	G	3.1
1	A	709	G	3.1
1	A	760	G	3.1
1	A	761	G	3.1
1	A	1021	G	3.1
1	A	1365	G	3.1
1	A	1494	G	3.1
1	A	1525	G	3.1
2	B	30	ARG	3.1
18	R	87	ARG	3.1
12	L	105	TYR	3.1
5	E	86	ALA	3.1
11	K	53	SER	3.1
1	A	288	A	3.1
1	A	1500	A	3.1
12	L	49	ASN	3.1
12	L	90	VAL	3.1
1	A	991	U	3.1
1	A	1232	U	3.1
1	A	1372	U	3.1
1	A	193	C	3.1
1	A	233	C	3.1
1	A	779	C	3.1
2	B	83	MET	3.1
7	G	56	GLN	3.1
16	P	82	GLN	3.1
17	Q	93	GLN	3.1
2	B	50	GLU	3.1
7	G	142	GLU	3.1
21	U	23	PRO	3.1
2	B	217	ARG	3.1
13	M	70	LEU	3.1
13	M	94	ARG	3.1
15	O	70	LEU	3.1
2	B	139	LYS	3.1
2	B	40	HIS	3.1
1	A	376	G	3.1
1	A	392	G	3.1
2	B	197	VAL	3.1
3	C	56	ASP	3.1
8	H	31	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
9	I	18	PHE	3.1
4	D	129	ASN	3.1
5	E	51	VAL	3.1
5	E	69	VAL	3.1
7	G	84	ASN	3.1
1	A	889	A	3.1
1	A	938	A	3.1
1	A	1151	A	3.1
1	A	1212	U	3.1
9	I	124	GLN	3.1
2	B	66	GLY	3.1
3	C	159	GLY	3.1
23	Y	33	U	3.1
8	H	136	GLU	3.1
1	A	178	C	3.1
1	A	433	C	3.1
1	A	812	C	3.1
1	A	1326	C	3.1
2	B	118	LEU	3.1
3	C	156	ARG	3.1
9	I	51	ARG	3.1
13	M	66	LEU	3.1
19	S	42	PRO	3.1
11	K	11	LYS	3.1
4	D	99	SER	3.1
6	F	89	MET	3.1
14	N	24	CYS	3.1
19	S	23	ASN	3.1
2	B	72	GLY	3.1
4	D	44	GLY	3.1
7	G	82	GLY	3.1
20	T	101	GLY	3.1
1	A	26	A	3.1
1	A	59	A	3.1
1	A	559	A	3.1
1	A	567	G	3.1
1	A	750	G	3.1
1	A	909	A	3.1
1	A	915	A	3.1
1	A	1288	A	3.1
1	A	641	U	3.1
1	A	1301	U	3.1

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Mol	Chain	Res	Type	RSRZ
3	C	152	ILE	3.1
4	D	204	ILE	3.1
2	B	119	GLU	3.1
4	D	142	PRO	3.1
5	E	121	LYS	3.1
1	A	186	C	3.1
1	A	189(A)	C	3.1
1	A	307	C	3.1
1	A	311	C	3.1
1	A	736	C	3.1
1	A	824	C	3.1
1	A	1246	C	3.1
1	A	1303	C	3.1
1	A	1429	C	3.1
1	A	1466	C	3.1
13	M	18	ALA	3.0
13	M	23	TYR	3.0
13	M	98	VAL	3.0
19	S	46	GLY	3.0
18	R	75	ILE	3.0
20	T	86	ARG	3.0
2	B	121	LEU	3.0
3	C	143	GLU	3.0
7	G	58	PRO	3.0
18	R	28	GLU	3.0
19	S	17	GLU	3.0
1	A	270	A	3.0
1	A	313	A	3.0
1	A	368	U	3.0
1	A	1065	U	3.0
1	A	1235	U	3.0
1	A	1308	U	3.0
22	X	5	A	3.0
2	B	103	THR	3.0
12	L	42	THR	3.0
1	A	357	G	3.0
1	A	890	G	3.0
2	B	161	ALA	3.0
3	C	50	ALA	3.0
6	F	35	ALA	3.0
1	A	63	C	3.0
1	A	458	C	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	931	C	3.0
1	A	1264	C	3.0
1	A	1412	C	3.0
3	C	183	ASP	3.0
6	F	94	GLN	3.0
16	P	14	ASN	3.0
4	D	59	ARG	3.0
7	G	49	ILE	3.0
16	P	65	GLN	3.0
19	S	56	GLN	3.0
8	H	12	ARG	3.0
4	D	108	LEU	3.0
4	D	37	PRO	3.0
12	L	48	PRO	3.0
1	A	757	U	3.0
9	I	103	THR	3.0
1	A	819	A	3.0
1	A	859	A	3.0
1	A	1204	A	3.0
3	C	70	VAL	3.0
7	G	105	VAL	3.0
16	P	79	VAL	3.0
1	A	126	G	3.0
1	A	189(L)	G	3.0
1	A	506	G	3.0
1	A	544	G	3.0
1	A	867	G	3.0
1	A	132	C	3.0
1	A	735	C	3.0
1	A	764	C	3.0
3	C	27	LYS	3.0
8	H	56	LYS	3.0
10	J	98	ILE	3.0
13	M	39	ILE	3.0
10	J	17	ASP	3.0
10	J	73	ASP	3.0
11	K	110	ASP	3.0
15	O	74	ASP	3.0
16	P	60	LEU	3.0
16	P	61	SER	3.0
14	N	46	GLU	3.0
2	B	107	THR	3.0

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Mol	Chain	Res	Type	RSRZ
7	G	54	THR	3.0
8	H	114	THR	3.0
1	A	62	U	3.0
1	A	1020	U	3.0
12	L	110	VAL	3.0
13	M	74	VAL	3.0
13	M	92	HIS	3.0
1	A	109	A	3.0
1	A	472	A	3.0
1	A	969	A	3.0
1	A	1157	A	3.0
20	T	83	ARG	3.0
17	Q	80	GLY	3.0
1	A	310	G	3.0
1	A	660	G	3.0
1	A	1108	G	3.0
1	A	1174	G	3.0
1	A	1505	G	3.0
7	G	109	ASN	3.0
21	U	5	ASP	3.0
1	A	1369	C	3.0
12	L	127	GLU	3.0
17	Q	2	PRO	3.0
4	D	89	THR	3.0
9	I	44	VAL	3.0
1	A	751	U	3.0
1	A	1125	U	3.0
12	L	99	HIS	3.0
5	E	152	ARG	2.9
7	G	5	ARG	2.9
8	H	60	ARG	2.9
1	A	451	A	2.9
1	A	802	A	2.9
4	D	54	TYR	2.9
4	D	144	ASP	2.9
1	A	70	G	2.9
1	A	324	G	2.9
1	A	530	G	2.9
1	A	1032	G	2.9
1	A	1294	G	2.9
1	A	1244	C	2.9
1	A	1527	C	2.9

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Mol	Chain	Res	Type	RSRZ
3	C	203	PHE	2.9
7	G	66	VAL	2.9
12	L	66	VAL	2.9
18	R	69	THR	2.9
21	U	8	THR	2.9
11	K	123	LYS	2.9
1	A	921	U	2.9
1	A	1194	U	2.9
2	B	56	ARG	2.9
13	M	90	LEU	2.9
7	G	44	TYR	2.9
16	P	37	GLY	2.9
20	T	90	GLN	2.9
1	A	298	A	2.9
1	A	325	A	2.9
1	A	452	A	2.9
1	A	790	A	2.9
3	C	109	PRO	2.9
7	G	71	PRO	2.9
13	M	67	GLU	2.9
5	E	73	ASN	2.9
7	G	144	MET	2.9
11	K	34	ASP	2.9
5	E	21	ALA	2.9
3	C	26	LYS	2.9
3	C	186	PHE	2.9
2	B	113	HIS	2.9
8	H	24	THR	2.9
1	A	136	C	2.9
1	A	651	C	2.9
1	A	1327	C	2.9
5	E	27	ARG	2.9
1	A	128	G	2.9
1	A	538	G	2.9
1	A	1011	G	2.9
1	A	1081	G	2.9
1	A	1457	G	2.9
1	A	45	U	2.9
1	A	129	U	2.9
1	A	180	U	2.9
1	A	261	U	2.9
1	A	793	U	2.9

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Mol	Chain	Res	Type	RSRZ
17	Q	74	LEU	2.9
3	C	78	GLY	2.9
15	O	28	GLN	2.9
2	B	167	PRO	2.9
4	D	98	GLU	2.9
13	M	8	GLU	2.9
1	A	243	A	2.9
1	A	712	A	2.9
1	A	1374	A	2.9
2	B	60	ASP	2.9
2	B	193	ASP	2.9
7	G	121	ALA	2.9
9	I	71	SER	2.9
18	R	49	LYS	2.9
20	T	28	ALA	2.9
21	U	20	LYS	2.9
5	E	26	PHE	2.9
2	B	23	ARG	2.9
5	E	143	ARG	2.9
16	P	44	THR	2.9
2	B	211	ILE	2.9
8	H	109	ILE	2.9
13	M	4	ILE	2.9
1	A	91	C	2.9
1	A	1121	U	2.9
1	A	15	G	2.9
1	A	147	G	2.9
1	A	1379	G	2.9
3	C	104	GLN	2.9
4	D	7	PRO	2.9
4	D	63	LYS	2.9
20	T	29	LYS	2.9
1	A	140	A	2.9
7	G	115	ARG	2.9
10	J	46	ARG	2.9
11	K	112	THR	2.9
16	P	67	THR	2.9
2	B	44	LEU	2.9
13	M	84	ILE	2.9
17	Q	53	LEU	2.9
18	R	85	LEU	2.9
3	C	80	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
4	D	183	GLY	2.8
1	A	334	C	2.8
1	A	561	U	2.8
1	A	680	C	2.8
1	A	912	C	2.8
1	A	980	C	2.8
1	A	1025	U	2.8
1	A	1109	C	2.8
1	A	1237	C	2.8
2	B	106	LYS	2.8
20	T	54	LYS	2.8
1	A	236	G	2.8
1	A	546	G	2.8
1	A	809	G	2.8
1	A	1185	G	2.8
2	B	177	ALA	2.8
5	E	24	ARG	2.8
7	G	148	ASN	2.8
14	N	35	ARG	2.8
4	D	91	SER	2.8
16	P	16	HIS	2.8
5	E	16	THR	2.8
1	A	263	A	2.8
1	A	461	A	2.8
5	E	10	MET	2.8
7	G	86	GLN	2.8
20	T	18	GLN	2.8
9	I	25	LYS	2.8
20	T	87	LYS	2.8
5	E	7	GLU	2.8
13	M	35	GLU	2.8
20	T	46	GLU	2.8
1	A	1542	U	2.8
2	B	148	TYR	2.8
1	A	328	C	2.8
1	A	554	C	2.8
1	A	877	C	2.8
3	C	21	ARG	2.8
3	C	42	LEU	2.8
9	I	91	ASP	2.8
18	R	26	LEU	2.8
1	A	127	G	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	142	G	2.8
1	A	168	G	2.8
1	A	698	G	2.8
1	A	947	G	2.8
1	A	1166	G	2.8
1	A	1470	G	2.8
1	A	282	A	2.8
1	A	1499	A	2.8
5	E	99	GLY	2.8
9	I	8	GLY	2.8
9	I	78	LYS	2.8
4	D	179	GLU	2.8
15	O	14	GLU	2.8
6	F	59	TYR	2.8
15	O	88	ARG	2.8
1	A	30	U	2.8
2	B	186	ALA	2.8
9	I	52	ALA	2.8
2	B	142	LEU	2.8
5	E	78	HIS	2.8
5	E	112	LEU	2.8
8	H	36	LEU	2.8
1	A	40	C	2.8
1	A	106	C	2.8
1	A	110	C	2.8
1	A	403	C	2.8
1	A	962	C	2.8
1	A	1189	C	2.8
1	A	1328	C	2.8
1	A	1409	C	2.8
9	I	32	ASP	2.8
11	K	111	ASP	2.8
16	P	27	LYS	2.8
8	H	43	GLY	2.8
7	G	106	GLN	2.8
11	K	13	GLN	2.8
15	O	9	GLN	2.8
1	A	300	A	2.8
1	A	338	A	2.8
1	A	553	A	2.8
1	A	908	A	2.8
7	G	143	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
8	H	138	TRP	2.8
2	B	181	PHE	2.8
11	K	60	ALA	2.8
15	O	15	PHE	2.8
4	D	196	LEU	2.8
6	F	48	LEU	2.8
9	I	99	LEU	2.8
3	C	6	HIS	2.8
3	C	45	LYS	2.8
3	C	165	THR	2.8
8	H	64	LYS	2.8
9	I	97	LYS	2.8
13	M	105	THR	2.8
17	Q	69	LYS	2.8
20	T	27	LYS	2.8
1	A	840	C	2.8
1	A	1490	C	2.8
3	C	46	GLU	2.7
10	J	5	ARG	2.7
13	M	108	ARG	2.7
19	S	9	VAL	2.7
1	A	9	G	2.7
1	A	262	A	2.7
1	A	416	G	2.7
1	A	860	A	2.7
1	A	914	A	2.7
5	E	62	ALA	2.7
11	K	15	ALA	2.7
13	M	76	ALA	2.7
1	A	963	G	2.7
8	H	112	LEU	2.7
11	K	59	TYR	2.7
23	Y	39	G	2.7
5	E	145	LYS	2.7
16	P	43	LYS	2.7
18	R	23	LYS	2.7
11	K	67	ASP	2.7
12	L	106	ASP	2.7
2	B	100	GLY	2.7
2	B	26	PRO	2.7
2	B	36	ARG	2.7
2	B	87	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	114	ARG	2.7
3	C	164	ARG	2.7
4	D	191	ARG	2.7
7	G	79	ARG	2.7
9	I	104	ARG	2.7
12	L	15	ARG	2.7
16	P	72	ARG	2.7
20	T	79	ARG	2.7
1	A	43	C	2.7
1	A	528	C	2.7
1	A	1161	C	2.7
1	A	1230	C	2.7
1	A	1496	C	2.7
2	B	59	GLU	2.7
2	B	164	VAL	2.7
8	H	39	LEU	2.7
17	Q	42	TYR	2.7
1	A	415	A	2.7
1	A	1093	A	2.7
1	A	1110	A	2.7
7	G	29	LYS	2.7
15	O	5	LYS	2.7
1	A	49	U	2.7
1	A	405	U	2.7
1	A	560	U	2.7
1	A	587	G	2.7
1	A	594	G	2.7
1	A	693	G	2.7
1	A	789	U	2.7
1	A	838	G	2.7
1	A	1241	G	2.7
2	B	104	ASN	2.7
3	C	98	ASN	2.7
8	H	120	THR	2.7
14	N	13	THR	2.7
4	D	130	GLY	2.7
4	D	47	ARG	2.7
4	D	100	ARG	2.7
4	D	208	SER	2.7
6	F	36	ARG	2.7
15	O	72	ARG	2.7
2	B	116	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
3	C	151	VAL	2.7
1	A	732	C	2.7
1	A	1439	C	2.7
4	D	94	LEU	2.7
8	H	133	LEU	2.7
14	N	10	ALA	2.7
15	O	16	ALA	2.7
2	B	24	TRP	2.7
7	G	31	MET	2.7
1	A	303	A	2.7
1	A	996	A	2.7
1	A	5	U	2.7
1	A	552	U	2.7
1	A	772	U	2.7
1	A	1247	U	2.7
10	J	78	ASN	2.7
4	D	180	GLY	2.7
7	G	155	ARG	2.7
9	I	30	GLY	2.7
18	R	18	ARG	2.7
1	A	29	G	2.7
1	A	786	G	2.7
1	A	941	G	2.7
3	C	112	SER	2.7
9	I	110	GLU	2.7
16	P	21	VAL	2.7
16	P	53	VAL	2.7
3	C	34	LEU	2.7
5	E	80	ILE	2.7
20	T	43	LEU	2.7
7	G	40	ALA	2.7
10	J	27	ALA	2.7
2	B	8	LYS	2.7
17	Q	87	LYS	2.7
10	J	13	HIS	2.7
21	U	14	TRP	2.7
1	A	320	C	2.7
1	A	457	C	2.7
1	A	948	C	2.7
1	A	1243	C	2.7
5	E	60	TYR	2.7
2	B	53	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
20	T	8	ARG	2.7
3	C	194	GLY	2.7
7	G	81	GLY	2.7
9	I	72	GLY	2.7
12	L	5	PRO	2.7
3	C	44	GLU	2.7
3	C	125	GLU	2.7
5	E	122	GLU	2.7
6	F	95	GLU	2.7
19	S	64	GLU	2.7
3	C	188	LEU	2.7
6	F	23	LYS	2.6
11	K	124	LYS	2.6
1	A	104	G	2.6
1	A	1082	G	2.6
1	A	1462	G	2.6
1	A	1529	G	2.6
22	X	1	G	2.6
6	F	46	ARG	2.6
8	H	92	ARG	2.6
9	I	93	ARG	2.6
18	R	35	ARG	2.6
1	A	36	C	2.6
1	A	503	C	2.6
1	A	795	C	2.6
1	A	967	C	2.6
1	A	1359	C	2.6
5	E	85	GLY	2.6
18	R	16	PRO	2.6
1	A	870	U	2.6
1	A	981	U	2.6
1	A	1376	U	2.6
2	B	76	GLN	2.6
3	C	19	GLU	2.6
3	C	115	LEU	2.6
5	E	68	GLU	2.6
12	L	60	LEU	2.6
18	R	86	VAL	2.6
19	S	67	VAL	2.6
1	A	648	A	2.6
5	E	45	PHE	2.6
5	E	84	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
7	G	46	ALA	2.6
1	A	309	G	2.6
1	A	577	G	2.6
1	A	861	G	2.6
1	A	898	G	2.6
1	A	1184	G	2.6
1	A	1293	G	2.6
11	K	18	ARG	2.6
3	C	9	GLY	2.6
1	A	235	C	2.6
1	A	590	C	2.6
1	A	910	C	2.6
8	H	88	LYS	2.6
3	C	173	VAL	2.6
4	D	81	GLU	2.6
5	E	32	VAL	2.6
18	R	44	LEU	2.6
18	R	46	GLU	2.6
1	A	24	U	2.6
1	A	420	U	2.6
1	A	134	A	2.6
1	A	1413	A	2.6
23	Y	38	A	2.6
5	E	25	ARG	2.6
12	L	86	ARG	2.6
3	C	167	TRP	2.6
4	D	207	TYR	2.6
12	L	46	LYS	2.6
1	A	231	G	2.6
1	A	378	G	2.6
1	A	637	G	2.6
1	A	662	G	2.6
1	A	673	G	2.6
1	A	791	G	2.6
1	A	1106	G	2.6
3	C	76	VAL	2.6
8	H	63	LEU	2.6
10	J	48	THR	2.6
12	L	38	THR	2.6
3	C	58	GLU	2.6
11	K	77	MET	2.6
15	O	58	MET	2.6

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Mol	Chain	Res	Type	RSRZ
4	D	117	ALA	2.6
11	K	23	ALA	2.6
1	A	135	C	2.6
1	A	883	C	2.6
1	A	1344	C	2.6
1	A	83	U	2.6
1	A	833	U	2.6
12	L	75	HIS	2.6
18	R	45	SER	2.6
3	C	140	ARG	2.6
6	F	71	ARG	2.6
14	N	45	ARG	2.6
1	A	900	A	2.6
6	F	96	PRO	2.6
12	L	13	LYS	2.6
12	L	71	PRO	2.6
19	S	8	GLY	2.6
19	S	26	GLY	2.6
8	H	127	LEU	2.6
15	O	34	LEU	2.6
6	F	67	MET	2.6
7	G	30	ILE	2.6
2	B	84	GLU	2.6
13	M	69	GLU	2.6
3	C	63	ASN	2.6
1	A	966	G	2.5
1	A	1186	G	2.5
1	A	1291	G	2.5
17	Q	46	ASP	2.6
1	A	304	U	2.5
1	A	375	U	2.5
1	A	677	U	2.5
2	B	175	ARG	2.5
4	D	107	ARG	2.5
6	F	47	ARG	2.5
12	L	89	ARG	2.5
15	O	38	ARG	2.5
11	K	24	SER	2.5
7	G	35	LYS	2.5
12	L	20	LYS	2.5
21	U	25	LYS	2.5
3	C	96	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
9	I	98	PRO	2.5
9	I	123	PRO	2.5
11	K	75	TYR	2.5
16	P	38	TYR	2.5
8	H	134	ILE	2.5
8	H	137	VAL	2.5
4	D	201	GLN	2.5
5	E	120	THR	2.5
9	I	48	GLU	2.5
11	K	93	GLN	2.5
15	O	13	GLN	2.5
16	P	54	GLU	2.5
9	I	45	ALA	2.5
20	T	52	ALA	2.5
3	C	179	ARG	2.5
4	D	141	ARG	2.5
8	H	84	ARG	2.5
1	A	358	U	2.5
1	A	1091	U	2.5
9	I	95	LYS	2.5
9	I	116	LYS	2.5
1	A	80	G	2.5
1	A	610	G	2.5
1	A	633	G	2.5
1	A	638	G	2.5
1	A	667	G	2.5
1	A	852	G	2.5
5	E	123	LEU	2.5
9	I	90	PRO	2.5
16	P	74	LEU	2.5
19	S	59	PRO	2.5
20	T	36	LEU	2.5
5	E	105	VAL	2.5
1	A	642	A	2.5
1	A	965	A	2.5
1	A	1394	A	2.5
8	H	3	THR	2.5
8	H	77	GLU	2.5
10	J	100	THR	2.5
12	L	73	GLU	2.5
20	T	51	GLU	2.5
15	O	18	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	62	ALA	2.5
15	O	80	ALA	2.5
3	C	119	ARG	2.5
7	G	94	ARG	2.5
11	K	126	ARG	2.5
17	Q	75	ARG	2.5
8	H	54	ASP	2.5
1	A	118	U	2.5
1	A	692	U	2.5
1	A	1292	U	2.5
3	C	51	GLY	2.5
7	G	89	MET	2.5
18	R	27	GLY	2.5
1	A	92	C	2.5
1	A	218	C	2.5
1	A	934	C	2.5
1	A	1069	C	2.5
1	A	1158	C	2.5
1	A	1296	C	2.5
1	A	28	G	2.5
1	A	1087	G	2.5
1	A	1491	G	2.5
17	Q	88	TYR	2.5
7	G	8	GLU	2.5
3	C	37	GLN	2.5
3	C	191	THR	2.5
4	D	93	PHE	2.5
10	J	84	GLN	2.5
1	A	179	A	2.5
1	A	321	A	2.5
1	A	901	A	2.5
8	H	14	ARG	2.5
13	M	71	ARG	2.5
3	C	135	LYS	2.5
4	D	43	HIS	2.5
2	B	155	LEU	2.5
5	E	139	LEU	2.5
20	T	84	LEU	2.5
2	B	150	SER	2.5
1	A	678	U	2.5
1	A	1062	U	2.5
1	A	1095	U	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	8	ILE	2.5
4	D	83	SER	2.5
5	E	87	SER	2.5
7	G	9	VAL	2.5
4	D	15	GLU	2.5
6	F	78	GLU	2.5
8	H	132	GLU	2.5
3	C	107	GLN	2.5
4	D	131	ARG	2.5
8	H	28	ALA	2.5
12	L	53	ARG	2.5
20	T	22	ARG	2.5
1	A	1118	C	2.5
13	M	20	THR	2.5
15	O	4	THR	2.5
20	T	21	LYS	2.5
1	A	93	G	2.5
1	A	112	G	2.5
1	A	925	G	2.5
1	A	927	G	2.5
1	A	1187	G	2.5
1	A	1295	G	2.5
1	A	573	A	2.5
1	A	607	A	2.5
1	A	1285	A	2.5
4	D	12	CYS	2.5
20	T	26	ASN	2.5
2	B	79	ASP	2.4
2	B	115	LEU	2.4
3	C	111	LEU	2.4
4	D	177	ASP	2.4
4	D	202	LEU	2.4
7	G	125	MET	2.4
4	D	51	PRO	2.4
2	B	184	VAL	2.4
15	O	23	GLY	2.4
18	R	48	GLY	2.4
1	A	125	U	2.4
1	A	189(K)	U	2.4
1	A	1540	U	2.4
7	G	119	ARG	2.4
7	G	123	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
11	K	120	ARG	2.4
14	N	26	ARG	2.4
7	G	127	ALA	2.4
8	H	65	TYR	2.4
14	N	50	LYS	2.4
15	O	71	GLN	2.4
18	R	84	LYS	2.4
16	P	69	THR	2.4
16	P	13	HIS	2.4
1	A	817	C	2.4
1	A	868	C	2.4
1	A	1509	C	2.4
1	A	1524	C	2.4
4	D	103	ASN	2.4
6	F	13	ASN	2.4
10	J	76	ASN	2.4
4	D	155	LEU	2.4
4	D	157	LEU	2.4
1	A	383	A	2.4
1	A	828	A	2.4
1	A	1299	A	2.4
23	Y	35	A	2.4
1	A	942	G	2.4
1	A	1410	G	2.4
4	D	172	PRO	2.4
10	J	41	PRO	2.4
12	L	92	ASP	2.4
2	B	71	VAL	2.4
4	D	56	VAL	2.4
4	D	57	ARG	2.4
7	G	114	ARG	2.4
11	K	16	SER	2.4
1	A	96	U	2.4
1	A	296	U	2.4
1	A	571	U	2.4
1	A	1073	U	2.4
1	A	1090	U	2.4
1	A	1345	U	2.4
4	D	34	GLU	2.4
12	L	54	LYS	2.4
15	O	47	LYS	2.4
19	S	74	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	34	ALA	2.4
2	B	85	ALA	2.4
12	L	30	ALA	2.4
13	M	19	LEU	2.4
17	Q	89	LEU	2.4
13	M	106	ASN	2.4
1	A	237	C	2.4
1	A	549	C	2.4
1	A	1096	C	2.4
1	A	1119	C	2.4
5	E	77	PRO	2.4
7	G	91	VAL	2.4
17	Q	13	ASP	2.4
21	U	11	GLY	2.4
1	A	1360	A	2.4
7	G	95	ARG	2.4
11	K	70	LYS	2.4
1	A	145	G	2.4
1	A	402	G	2.4
1	A	1343	G	2.4
4	D	156	GLU	2.4
4	D	192	GLU	2.4
17	Q	49	GLU	2.4
19	S	21	GLU	2.4
13	M	42	ALA	2.4
9	I	38	GLN	2.4
1	A	20	U	2.4
1	A	961	U	2.4
1	A	982	U	2.4
1	A	1083	U	2.4
1	A	1380	U	2.4
2	B	73	THR	2.4
12	L	122	THR	2.4
16	P	1	MET	2.4
9	I	50	LEU	2.4
13	M	22	ILE	2.4
4	D	154	ASN	2.4
9	I	89	ASN	2.4
18	R	36	ASN	2.4
4	D	128	VAL	2.4
8	H	118	VAL	2.4
11	K	86	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
16	P	62	VAL	2.4
17	Q	102	GLY	2.4
19	S	45	VAL	2.4
4	D	84	LYS	2.4
6	F	28	ARG	2.4
6	F	55	ASP	2.4
13	M	86	CYS	2.4
20	T	23	ARG	2.4
20	T	58	LYS	2.4
1	A	555	C	2.4
1	A	822	C	2.4
1	A	832	C	2.4
1	A	1383	C	2.4
1	A	913	A	2.4
2	B	57	PHE	2.4
2	B	143	GLU	2.4
18	R	83	GLU	2.4
6	F	76	ALA	2.4
7	G	7	ALA	2.4
9	I	76	ALA	2.4
2	B	146	GLN	2.4
7	G	77	SER	2.4
15	O	40	SER	2.4
17	Q	66	SER	2.4
20	T	82	SER	2.4
1	A	105	G	2.4
1	A	227	G	2.4
1	A	285	G	2.4
1	A	884	U	2.4
1	A	997	U	2.4
1	A	1516	G	2.4
12	L	93	LEU	2.4
2	B	32	ILE	2.4
5	E	118	ILE	2.4
15	O	2	PRO	2.4
17	Q	28	PRO	2.4
2	B	64	ARG	2.3
8	H	116	LYS	2.3
10	J	72	VAL	2.3
2	B	65	GLY	2.3
5	E	29	GLY	2.3
13	M	89	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
13	M	110	ARG	2.3
17	Q	81	ARG	2.3
19	S	75	ALA	2.3
1	A	48	C	2.3
1	A	175	C	2.3
1	A	762	C	2.3
1	A	1217	C	2.3
6	F	27	GLN	2.3
8	H	78	GLN	2.3
20	T	42	GLN	2.3
1	A	16	A	2.3
1	A	1080	A	2.3
1	A	1286	A	2.3
2	B	98	LEU	2.3
1	A	222	U	2.3
1	A	551	U	2.3
1	A	1148	U	2.3
1	A	1240	U	2.3
1	A	1281	U	2.3
1	A	1302	U	2.3
17	Q	4	LYS	2.3
1	A	876	G	2.3
1	A	939	G	2.3
4	D	114	ARG	2.3
12	L	33	ARG	2.3
4	D	75	PHE	2.3
2	B	171	ALA	2.3
20	T	67	ALA	2.3
9	I	73	GLN	2.3
11	K	73	MET	2.3
7	G	12	LEU	2.3
17	Q	39	SER	2.3
20	T	37	SER	2.3
1	A	1075	C	2.3
1	A	1115	C	2.3
1	A	1543	C	2.3
5	E	135	THR	2.3
1	A	614	A	2.3
1	A	1238	A	2.3
8	H	62	TYR	2.3
9	I	77	ILE	2.3
12	L	85	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
22	X	4	A	2.3
4	D	61	LYS	2.3
4	D	159	ARG	2.3
8	H	69	ARG	2.3
17	Q	25	ARG	2.3
1	A	332	G	2.3
1	A	568	G	2.3
1	A	1338	G	2.3
3	C	113	ALA	2.3
4	D	147	ALA	2.3
2	B	43	ASP	2.3
5	E	142	LEU	2.3
12	L	27	LEU	2.3
9	I	117	HIS	2.3
4	D	137	SER	2.3
2	B	82	ARG	2.3
7	G	111	ARG	2.3
12	L	34	ARG	2.3
3	C	114	PRO	2.3
1	A	796	C	2.3
1	A	287	U	2.3
1	A	453	A	2.3
1	A	1495	U	2.3
1	A	1507	A	2.3
16	P	2	VAL	2.3
8	H	96	GLY	2.3
8	H	130	GLY	2.3
3	C	3	ASN	2.3
6	F	100	ASN	2.3
2	B	52	GLU	2.3
2	B	63	MET	2.3
5	E	104	ALA	2.3
13	M	32	GLU	2.3
19	S	43	GLU	2.3
20	T	32	ALA	2.3
5	E	38	GLN	2.3
8	H	119	LEU	2.3
9	I	54	ASP	2.3
9	I	75	ASP	2.3
7	G	48	LYS	2.3
16	P	3	LYS	2.3
1	A	198	G	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	922	G	2.3
1	A	1233	G	2.3
1	A	1438	G	2.3
13	M	25	ILE	2.3
13	M	37	THR	2.3
16	P	59	TRP	2.3
3	C	184	TYR	2.3
5	E	33	VAL	2.3
5	E	148	VAL	2.3
8	H	57	PRO	2.3
8	H	94	TYR	2.3
9	I	86	VAL	2.3
4	D	143	GLY	2.3
7	G	55	GLY	2.3
13	M	6	GLY	2.3
1	A	523	A	2.2
1	A	875	C	2.2
1	A	1098	C	2.2
1	A	1149	C	2.2
1	A	1346	A	2.2
1	A	1378	C	2.2
1	A	1479	C	2.2
15	O	6	GLU	2.2
4	D	186	LEU	2.2
4	D	45	GLN	2.2
16	P	4	ILE	2.2
20	T	25	ARG	2.2
4	D	88	VAL	2.2
19	S	41	VAL	2.2
1	A	661	G	2.2
1	A	933	G	2.2
2	B	48	MET	2.2
1	A	580	U	2.2
2	B	218	ALA	2.2
5	E	113	ALA	2.2
7	G	128	ALA	2.2
20	T	66	ALA	2.2
1	A	345	C	2.2
1	A	707	C	2.2
1	A	932	C	2.2
1	A	940	C	2.2
1	A	1349	A	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1384	C	2.2
7	G	28	ASN	2.2
8	H	35	ILE	2.2
5	E	107	ARG	2.2
8	H	41	ARG	2.2
6	F	68	PRO	2.2
7	G	61	VAL	2.2
12	L	82	VAL	2.2
17	Q	30	PRO	2.2
8	H	66	GLY	2.2
12	L	87	GLY	2.2
18	R	57	GLY	2.2
3	C	72	LYS	2.2
1	A	220	G	2.2
1	A	628	G	2.2
1	A	710	G	2.2
1	A	1009	G	2.2
4	D	78	LEU	2.2
7	G	139	GLU	2.2
10	J	16	LEU	2.2
14	N	44	LEU	2.2
15	O	7	GLU	2.2
1	A	12	U	2.2
1	A	14	U	2.2
1	A	955	U	2.2
20	T	75	ASN	2.2
1	A	935	A	2.2
1	A	601	C	2.2
1	A	1403	C	2.2
2	B	205	ASP	2.2
13	M	83	ASP	2.2
8	H	27	PRO	2.2
12	L	11	VAL	2.2
19	S	76	PRO	2.2
8	H	108	GLY	2.2
8	H	113	SER	2.2
11	K	45	GLY	2.2
17	Q	8	GLY	2.2
14	N	17	LYS	2.2
20	T	24	LEU	2.2
9	I	84	ALA	2.2
3	C	14	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
10	J	66	ARG	2.2
18	R	55	ARG	2.2
21	U	13	ILE	2.2
1	A	82	U	2.2
13	M	62	ASN	2.2
1	A	885	G	2.2
7	G	122	HIS	2.2
1	A	694	A	2.2
1	A	787	A	2.2
1	A	176	C	2.2
19	S	66	MET	2.2
4	D	69	GLY	2.2
4	D	184	LYS	2.2
18	R	68	LYS	2.2
16	P	32	TYR	2.2
7	G	38	LEU	2.2
5	E	54	ALA	2.2
5	E	137	GLU	2.2
12	L	68	ALA	2.2
16	P	28	ARG	2.1
1	A	294	U	2.1
1	A	943	U	2.1
5	E	153	LYS	2.1
16	P	45	THR	2.1
21	U	3	LYS	2.1
7	G	103	TRP	2.1
1	A	280	C	2.1
1	A	1100	C	2.1
8	H	110	ALA	2.1
12	L	108	ALA	2.1
4	D	72	GLU	2.1
5	E	83	GLU	2.1
8	H	49	GLU	2.1
5	E	129	ILE	2.1
6	F	32	ASN	2.1
1	A	1078	U	2.1
17	Q	47	PRO	2.1
7	G	60	LYS	2.1
13	M	47	ASP	2.1
1	A	563	A	2.1
1	A	1170	A	2.1
3	C	131	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
4	D	122	ARG	2.1
5	E	30	ALA	2.1
5	E	133	TYR	2.1
7	G	65	ALA	2.1
7	G	117	ALA	2.1
7	G	152	ALA	2.1
1	A	1486	G	2.1
2	B	49	GLU	2.1
1	A	930	C	2.1
4	D	86	LYS	2.1
7	G	112	PRO	2.1
17	Q	34	LYS	2.1
1	A	605	U	2.1
1	A	871	U	2.1
8	H	90	GLY	2.1
3	C	126	ARG	2.1
4	D	153	ARG	2.1
7	G	10	ARG	2.1
10	J	51	ARG	2.1
11	K	54	ARG	2.1
18	R	53	ARG	2.1
2	B	185	ILE	2.1
6	F	101	ALA	2.1
9	I	74	ILE	2.1
11	K	72	ALA	2.1
11	K	94	ALA	2.1
16	P	84	ALA	2.1
1	A	1350	A	2.1
1	A	1493	A	2.1
2	B	210	SER	2.1
12	L	37	CYS	2.1
1	A	25	C	2.1
1	A	155	C	2.1
14	N	49	HIS	2.1
1	A	929	G	2.1
1	A	1150	U	2.1
1	A	1351	U	2.1
1	A	1544	U	2.1
2	B	157	ARG	2.1
11	K	81	ASP	2.1
13	M	43	THR	2.1
16	P	29	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
16	P	75	ARG	2.1
4	D	48	ALA	2.1
7	G	39	ALA	2.1
9	I	46	ALA	2.1
2	B	231	GLU	2.1
12	L	98	TYR	2.1
3	C	170	GLN	2.0
5	E	9	LYS	2.0
1	A	88	A	2.0
1	A	919	A	2.0
2	B	174	VAL	2.0
2	B	219	VAL	2.0
1	A	615	C	2.0
2	B	25	ASN	2.0
1	A	837	G	2.0
1	A	858	G	2.0
12	L	109	GLY	2.0
1	A	133	U	2.0
1	A	1390	U	2.0
1	A	1528	U	2.0
3	C	157	ILE	2.0
12	L	6	THR	2.0
6	F	15	ASP	2.0
13	M	58	GLU	2.0
1	A	8	A	2.0
1	A	382	A	2.0
1	A	923	A	2.0
19	S	72	GLY	2.0
1	A	647	C	2.0
1	A	1402	C	2.0
4	D	164	ALA	2.0
9	I	27	THR	2.0
2	B	195	ASP	2.0
1	A	258	G	2.0
7	G	67	GLU	2.0
5	E	136	MET	2.0
5	E	115	VAL	2.0
8	H	61	VAL	2.0
17	Q	85	VAL	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
23	CM0	Y	34	25/26	0.59	0.20	64,69,71,72	0
23	6MZ	Y	37	23/24	0.82	0.17	60,64,65,66	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
25	MG	A	1643	1/1	-0.20	0.68	66,66,66,66	0
25	MG	A	1631	1/1	-0.14	0.42	59,59,59,59	0
25	MG	A	1721	1/1	-0.14	0.89	68,68,68,68	0
25	MG	A	1608	1/1	-0.12	0.36	74,74,74,74	0
25	MG	A	1731	1/1	-0.09	1.18	82,82,82,82	0
25	MG	A	1736	1/1	-0.03	1.39	72,72,72,72	0
25	MG	A	1630	1/1	0.00	0.66	90,90,90,90	0
25	MG	A	1747	1/1	0.01	0.70	55,55,55,55	0
25	MG	A	1742	1/1	0.04	0.41	78,78,78,78	0
25	MG	A	1710	1/1	0.04	0.97	95,95,95,95	0
25	MG	N	101	1/1	0.08	0.77	104,104,104,104	0
26	K	E	203	1/1	0.09	0.28	93,93,93,93	0
25	MG	F	201	1/1	0.12	0.25	49,49,49,49	0
26	K	A	1808	1/1	0.13	0.70	81,81,81,81	0
25	MG	A	1714	1/1	0.13	0.73	60,60,60,60	0
26	K	A	1810	1/1	0.14	0.30	102,102,102,102	0
25	MG	A	1753	1/1	0.14	0.26	35,35,35,35	0
25	MG	A	1673	1/1	0.16	0.47	67,67,67,67	0
25	MG	A	1637	1/1	0.16	0.83	68,68,68,68	0
26	K	A	1820	1/1	0.17	0.33	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1684	1/1	0.20	1.03	92,92,92,92	0
25	MG	A	1622	1/1	0.20	0.76	78,78,78,78	0
26	K	A	1809	1/1	0.20	0.77	92,92,92,92	0
26	K	A	1828	1/1	0.21	0.70	99,99,99,99	0
25	MG	A	1789	1/1	0.21	0.28	51,51,51,51	0
25	MG	A	1661	1/1	0.23	0.33	44,44,44,44	0
25	MG	A	1785	1/1	0.24	1.02	81,81,81,81	0
25	MG	A	1611	1/1	0.24	0.18	13,13,13,13	0
25	MG	A	1612	1/1	0.25	0.49	48,48,48,48	0
25	MG	A	1625	1/1	0.25	0.58	49,49,49,49	0
25	MG	A	1655	1/1	0.25	0.50	64,64,64,64	0
25	MG	A	1605	1/1	0.26	0.93	70,70,70,70	0
25	MG	A	1614	1/1	0.26	0.40	91,91,91,91	0
25	MG	A	1652	1/1	0.27	0.51	60,60,60,60	0
25	MG	A	1717	1/1	0.28	0.57	79,79,79,79	0
25	MG	A	1775	1/1	0.28	0.19	33,33,33,33	0
25	MG	A	1748	1/1	0.28	0.77	70,70,70,70	0
25	MG	A	1696	1/1	0.30	0.70	96,96,96,96	0
25	MG	A	1606	1/1	0.30	0.68	54,54,54,54	0
25	MG	A	1711	1/1	0.31	0.56	57,57,57,57	0
25	MG	A	1800	1/1	0.32	0.46	42,42,42,42	0
26	K	A	1821	1/1	0.32	0.40	90,90,90,90	0
25	MG	A	1685	1/1	0.33	0.79	81,81,81,81	0
26	K	A	1816	1/1	0.33	0.46	120,120,120,120	0
25	MG	A	1656	1/1	0.34	0.34	69,69,69,69	0
26	K	A	1817	1/1	0.34	0.77	108,108,108,108	0
25	MG	A	1724	1/1	0.34	0.61	55,55,55,55	0
25	MG	A	1793	1/1	0.34	0.42	45,45,45,45	0
25	MG	A	1634	1/1	0.34	0.53	30,30,30,30	0
25	MG	A	1802	1/1	0.34	0.93	82,82,82,82	0
25	MG	A	1638	1/1	0.35	0.44	60,60,60,60	0
25	MG	A	1692	1/1	0.36	0.42	51,51,51,51	0
25	MG	A	1657	1/1	0.37	0.50	74,74,74,74	0
25	MG	A	1787	1/1	0.37	0.34	48,48,48,48	0
26	K	A	1832	1/1	0.37	0.30	103,103,103,103	0
25	MG	Q	202	1/1	0.37	0.15	39,39,39,39	0
26	K	A	1818	1/1	0.38	0.45	110,110,110,110	0
25	MG	A	1766	1/1	0.38	0.49	65,65,65,65	0
25	MG	A	1782	1/1	0.39	0.58	49,49,49,49	0
25	MG	A	1737	1/1	0.40	0.61	56,56,56,56	0
25	MG	A	1705	1/1	0.40	0.48	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1607	1/1	0.41	0.72	91,91,91,91	0
25	MG	A	1798	1/1	0.41	0.41	52,52,52,52	0
25	MG	A	1688	1/1	0.41	0.61	76,76,76,76	0
25	MG	A	1759	1/1	0.42	0.30	44,44,44,44	0
25	MG	A	1629	1/1	0.43	0.31	56,56,56,56	0
25	MG	A	1761	1/1	0.43	0.24	48,48,48,48	0
25	MG	A	1735	1/1	0.43	0.67	96,96,96,96	0
25	MG	S	101	1/1	0.43	0.30	45,45,45,45	0
25	MG	A	1754	1/1	0.43	0.42	51,51,51,51	0
25	MG	A	1633	1/1	0.44	0.38	69,69,69,69	0
26	K	A	1814	1/1	0.44	0.46	95,95,95,95	0
25	MG	A	1642	1/1	0.45	0.33	48,48,48,48	0
25	MG	A	1723	1/1	0.45	0.30	47,47,47,47	0
25	MG	A	1677	1/1	0.45	0.17	89,89,89,89	0
25	MG	A	1666	1/1	0.45	0.37	57,57,57,57	0
25	MG	A	1790	1/1	0.46	0.43	45,45,45,45	0
25	MG	A	1715	1/1	0.46	0.61	68,68,68,68	0
25	MG	A	1681	1/1	0.46	0.73	82,82,82,82	0
26	K	A	1811	1/1	0.46	0.54	86,86,86,86	0
26	K	A	1819	1/1	0.46	0.39	96,96,96,96	0
25	MG	A	1718	1/1	0.47	0.30	51,51,51,51	0
25	MG	A	1610	1/1	0.47	0.79	50,50,50,50	0
25	MG	A	1621	1/1	0.47	0.31	59,59,59,59	0
25	MG	A	1686	1/1	0.47	0.75	34,34,34,34	0
25	MG	A	1730	1/1	0.47	0.73	84,84,84,84	0
26	K	A	1807	1/1	0.48	0.33	76,76,76,76	0
25	MG	A	1751	1/1	0.48	0.35	61,61,61,61	0
26	K	A	1833	1/1	0.48	0.32	99,99,99,99	0
26	K	A	1805	1/1	0.48	0.14	68,68,68,68	0
25	MG	A	1767	1/1	0.49	0.40	61,61,61,61	0
26	K	A	1815	1/1	0.49	0.28	119,119,119,119	0
25	MG	A	1665	1/1	0.50	0.49	49,49,49,49	0
25	MG	A	1741	1/1	0.50	0.50	74,74,74,74	0
25	MG	A	1623	1/1	0.51	0.36	54,54,54,54	0
26	K	A	1830	1/1	0.51	0.36	97,97,97,97	0
25	MG	A	1784	1/1	0.51	0.80	79,79,79,79	0
25	MG	A	1771	1/1	0.51	0.60	58,58,58,58	0
26	K	A	1835	1/1	0.51	0.36	114,114,114,114	0
25	MG	A	1618	1/1	0.51	0.69	60,60,60,60	0
25	MG	A	1794	1/1	0.52	0.36	47,47,47,47	0
26	K	A	1822	1/1	0.52	0.42	100,100,100,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1702	1/1	0.52	0.63	50,50,50,50	0
25	MG	A	1667	1/1	0.52	0.54	47,47,47,47	0
25	MG	A	1716	1/1	0.53	0.77	66,66,66,66	0
25	MG	A	1709	1/1	0.53	0.39	46,46,46,46	0
26	K	A	1829	1/1	0.54	0.42	94,94,94,94	0
25	MG	A	1680	1/1	0.54	0.42	39,39,39,39	0
25	MG	A	1635	1/1	0.54	0.23	43,43,43,43	0
25	MG	A	1763	1/1	0.55	0.19	47,47,47,47	0
26	K	A	1834	1/1	0.55	0.23	91,91,91,91	0
26	K	A	1806	1/1	0.56	0.21	72,72,72,72	0
25	MG	A	1620	1/1	0.56	0.36	51,51,51,51	0
25	MG	A	1792	1/1	0.56	0.12	54,54,54,54	0
26	K	A	1825	1/1	0.56	0.55	107,107,107,107	0
26	K	A	1831	1/1	0.57	0.48	95,95,95,95	0
25	MG	A	1801	1/1	0.57	0.47	56,56,56,56	0
26	K	A	1838	1/1	0.57	0.35	120,120,120,120	0
25	MG	A	1617	1/1	0.57	0.26	25,25,25,25	0
25	MG	A	1693	1/1	0.58	0.37	43,43,43,43	0
25	MG	A	1669	1/1	0.58	0.81	74,74,74,74	0
25	MG	A	1627	1/1	0.58	0.16	39,39,39,39	0
25	MG	A	1760	1/1	0.59	0.22	41,41,41,41	0
25	MG	A	1728	1/1	0.59	0.40	47,47,47,47	0
25	MG	A	1745	1/1	0.59	0.13	29,29,29,29	0
25	MG	A	1641	1/1	0.60	0.47	38,38,38,38	0
25	MG	A	1632	1/1	0.60	0.48	72,72,72,72	0
25	MG	A	1624	1/1	0.60	0.37	74,74,74,74	0
25	MG	A	1602	1/1	0.60	0.12	45,45,45,45	0
26	K	A	1836	1/1	0.60	0.36	92,92,92,92	0
25	MG	A	1701	1/1	0.60	0.51	65,65,65,65	0
25	MG	A	1654	1/1	0.60	0.52	48,48,48,48	0
25	MG	A	1678	1/1	0.61	0.59	91,91,91,91	0
25	MG	A	1676	1/1	0.62	0.50	45,45,45,45	0
25	MG	A	1671	1/1	0.62	0.50	74,74,74,74	0
25	MG	A	1628	1/1	0.62	0.81	51,51,51,51	0
25	MG	A	1796	1/1	0.63	0.44	46,46,46,46	0
25	MG	A	1640	1/1	0.63	0.27	46,46,46,46	0
26	K	A	1812	1/1	0.63	0.21	91,91,91,91	0
25	MG	A	1780	1/1	0.63	0.23	38,38,38,38	0
25	MG	A	1749	1/1	0.63	0.19	34,34,34,34	0
25	MG	A	1694	1/1	0.63	0.56	50,50,50,50	0
25	MG	A	1662	1/1	0.63	0.64	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1786	1/1	0.63	0.24	63,63,63,63	0
25	MG	I	201	1/1	0.64	0.35	67,67,67,67	0
25	MG	A	1695	1/1	0.64	0.38	43,43,43,43	0
25	MG	A	1648	1/1	0.64	0.35	46,46,46,46	0
25	MG	A	1604	1/1	0.65	0.62	49,49,49,49	0
25	MG	A	1603	1/1	0.65	0.64	75,75,75,75	0
26	K	A	1824	1/1	0.65	0.16	83,83,83,83	0
25	MG	A	1663	1/1	0.65	0.59	55,55,55,55	0
25	MG	A	1644	1/1	0.65	0.46	73,73,73,73	0
25	MG	A	1791	1/1	0.66	0.23	56,56,56,56	0
25	MG	A	1697	1/1	0.66	0.35	51,51,51,51	0
25	MG	A	1664	1/1	0.66	0.37	35,35,35,35	0
25	MG	A	1706	1/1	0.66	0.52	56,56,56,56	0
25	MG	D	302	1/1	0.67	0.16	41,41,41,41	0
25	MG	A	1740	1/1	0.67	0.56	51,51,51,51	0
25	MG	A	1729	1/1	0.67	0.25	68,68,68,68	0
25	MG	A	1777	1/1	0.67	0.60	69,69,69,69	0
25	MG	A	1659	1/1	0.67	0.56	50,50,50,50	0
25	MG	A	1636	1/1	0.67	0.40	32,32,32,32	0
25	MG	A	1739	1/1	0.68	0.40	53,53,53,53	0
26	K	A	1813	1/1	0.68	0.47	88,88,88,88	0
25	MG	A	1613	1/1	0.68	0.21	44,44,44,44	0
25	MG	A	1762	1/1	0.68	0.29	38,38,38,38	0
25	MG	A	1682	1/1	0.69	0.26	51,51,51,51	0
25	MG	A	1757	1/1	0.69	0.13	32,32,32,32	0
25	MG	A	1750	1/1	0.70	0.23	65,65,65,65	0
25	MG	A	1722	1/1	0.70	0.26	57,57,57,57	0
25	MG	A	1660	1/1	0.70	0.38	43,43,43,43	0
25	MG	A	1626	1/1	0.70	0.18	44,44,44,44	0
25	MG	A	1755	1/1	0.70	0.23	56,56,56,56	0
26	K	A	1826	1/1	0.71	0.21	83,83,83,83	0
25	MG	A	1781	1/1	0.71	0.41	53,53,53,53	0
25	MG	A	1647	1/1	0.71	0.35	41,41,41,41	0
25	MG	Q	203	1/1	0.71	0.27	63,63,63,63	0
25	MG	A	1774	1/1	0.72	0.21	14,14,14,14	0
25	MG	A	1704	1/1	0.72	0.38	57,57,57,57	0
25	MG	A	1734	1/1	0.72	0.42	40,40,40,40	0
25	MG	A	1779	1/1	0.72	0.26	37,37,37,37	0
25	MG	A	1768	1/1	0.72	0.37	45,45,45,45	0
25	MG	A	1788	1/1	0.72	0.11	19,19,19,19	0
25	MG	A	1698	1/1	0.72	0.25	16,16,16,16	0
25	MG	A	1776	1/1	0.73	0.33	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1799	1/1	0.73	0.25	69,69,69,69	0
25	MG	A	1674	1/1	0.73	0.19	39,39,39,39	0
25	MG	A	1645	1/1	0.73	0.24	35,35,35,35	0
25	MG	A	1619	1/1	0.73	0.13	44,44,44,44	0
25	MG	A	1765	1/1	0.73	0.17	34,34,34,34	0
25	MG	E	201	1/1	0.73	0.48	50,50,50,50	0
25	MG	A	1732	1/1	0.73	0.35	34,34,34,34	0
25	MG	A	1797	1/1	0.73	0.09	74,74,74,74	0
24	PAR	A	1601	42/42	0.74	0.27	43,47,64,68	0
25	MG	A	1720	1/1	0.74	0.14	38,38,38,38	0
25	MG	A	1713	1/1	0.74	0.76	56,56,56,56	0
26	K	A	1827	1/1	0.75	0.15	85,85,85,85	0
25	MG	A	1700	1/1	0.75	0.25	37,37,37,37	0
25	MG	A	1803	1/1	0.76	0.19	44,44,44,44	0
26	K	A	1837	1/1	0.76	0.30	93,93,93,93	0
25	MG	A	1699	1/1	0.76	0.15	32,32,32,32	0
25	MG	A	1687	1/1	0.76	0.73	62,62,62,62	0
25	MG	A	1725	1/1	0.77	0.15	29,29,29,29	0
25	MG	A	1707	1/1	0.77	0.11	20,20,20,20	0
25	MG	A	1764	1/1	0.77	0.21	27,27,27,27	0
25	MG	A	1708	1/1	0.77	0.47	46,46,46,46	0
25	MG	A	1683	1/1	0.77	0.47	48,48,48,48	0
25	MG	A	1743	1/1	0.77	0.25	38,38,38,38	0
25	MG	A	1670	1/1	0.77	0.26	45,45,45,45	0
25	MG	A	1783	1/1	0.78	0.36	57,57,57,57	0
25	MG	A	1773	1/1	0.78	0.25	30,30,30,30	0
25	MG	A	1769	1/1	0.78	0.18	32,32,32,32	0
25	MG	A	1726	1/1	0.78	0.19	35,35,35,35	0
25	MG	A	1795	1/1	0.78	0.11	41,41,41,41	0
27	ZN	D	301	1/1	0.78	0.22	81,81,81,81	0
25	MG	M	201	1/1	0.79	0.15	35,35,35,35	0
25	MG	A	1738	1/1	0.79	0.24	34,34,34,34	0
25	MG	G	201	1/1	0.79	0.29	58,58,58,58	0
25	MG	A	1733	1/1	0.79	0.23	40,40,40,40	0
25	MG	A	1770	1/1	0.80	0.19	11,11,11,11	0
25	MG	A	1675	1/1	0.80	0.17	36,36,36,36	0
25	MG	A	1772	1/1	0.80	0.12	24,24,24,24	0
25	MG	X	101	1/1	0.81	0.16	27,27,27,27	0
25	MG	A	1615	1/1	0.81	0.13	42,42,42,42	0
25	MG	A	1639	1/1	0.81	0.43	48,48,48,48	0
25	MG	H	201	1/1	0.82	0.12	37,37,37,37	0
25	MG	A	1746	1/1	0.83	0.14	31,31,31,31	0

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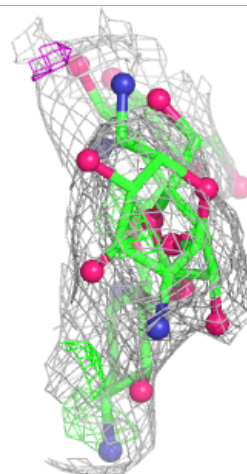
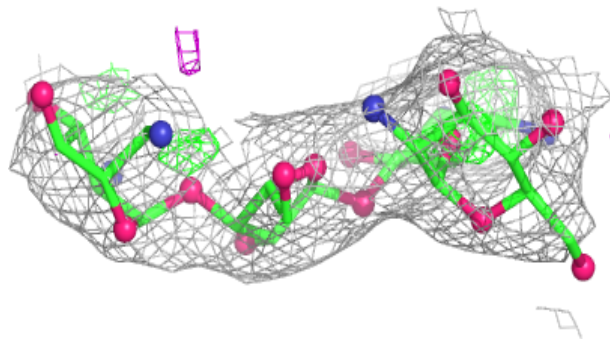
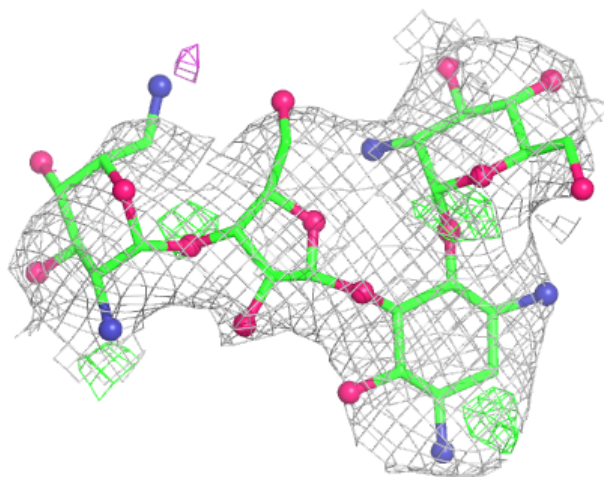
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	MG	A	1703	1/1	0.83	0.22	31,31,31,31	0
25	MG	Q	201	1/1	0.83	0.32	52,52,52,52	0
26	K	A	1823	1/1	0.84	0.34	85,85,85,85	0
25	MG	A	1668	1/1	0.84	0.63	106,106,106,106	0
25	MG	A	1756	1/1	0.84	0.16	43,43,43,43	0
25	MG	A	1804	1/1	0.84	0.21	88,88,88,88	0
25	MG	B	301	1/1	0.84	0.11	36,36,36,36	0
25	MG	A	1712	1/1	0.84	0.13	16,16,16,16	0
25	MG	A	1758	1/1	0.85	0.07	20,20,20,20	0
25	MG	A	1719	1/1	0.85	0.36	42,42,42,42	0
25	MG	A	1650	1/1	0.86	0.16	47,47,47,47	0
25	MG	A	1672	1/1	0.86	0.26	27,27,27,27	0
25	MG	A	1679	1/1	0.86	0.24	27,27,27,27	0
25	MG	A	1690	1/1	0.87	0.25	43,43,43,43	0
25	MG	A	1658	1/1	0.87	0.11	18,18,18,18	0
25	MG	A	1744	1/1	0.87	0.10	26,26,26,26	0
25	MG	A	1727	1/1	0.88	0.18	27,27,27,27	0
25	MG	A	1609	1/1	0.88	0.49	37,37,37,37	0
25	MG	E	202	1/1	0.89	0.16	52,52,52,52	0
25	MG	A	1616	1/1	0.89	0.26	30,30,30,30	0
25	MG	A	1689	1/1	0.89	0.14	34,34,34,34	0
25	MG	A	1646	1/1	0.89	0.42	48,48,48,48	0
25	MG	A	1653	1/1	0.90	0.12	1,1,1,1	0
25	MG	A	1649	1/1	0.90	0.33	50,50,50,50	0
27	ZN	N	102	1/1	0.90	0.07	69,69,69,69	0
25	MG	A	1778	1/1	0.91	0.09	44,44,44,44	0
25	MG	A	1651	1/1	0.92	0.34	34,34,34,34	0
25	MG	A	1691	1/1	0.93	0.22	28,28,28,28	0
25	MG	A	1752	1/1	0.93	0.18	42,42,42,42	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PAR A 1601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.