



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:29 PM GMT

PDB ID : 1FFK  
Title : CRYSTAL STRUCTURE OF THE LARGE RIBOSOMAL SUBUNIT FROM HALOARCUA MARISMORTUI AT 2.4 ANGSTROM RESOLUTION  
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Deposited on : 2000-07-25  
Resolution : 2.40 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

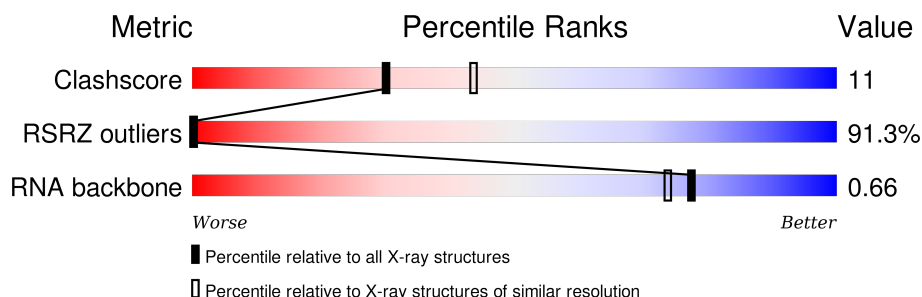
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
Clashscore	102246	3407 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)
RNA backbone	2183	1073 (2.90-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	0	2922	<div> <div>74%</div> <div> <div>49%</div> <div>34%</div> <div>8%</div> <div>7%</div> </div> </div>
2	9	122	<div> <div>93%</div> <div> <div>43%</div> <div>43%</div> <div>11%</div> </div> </div>
3	A	239	<div> <div>99%</div> <div>98%</div> </div>
4	B	337	<div> <div>99%</div> <div>99%</div> </div>
5	C	246	<div> <div>100%</div> <div>100%</div> </div>
6	D	176	<div> <div>79%</div> <div>80%</div> <div>20%</div> </div>
7	E	119	<div> <div>97%</div> <div>97%</div> </div>
8	F	157	<div> <div>100%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
9	G	145	98% 
10	H	132	100% 
11	I	194	100% 
12	J	164	87% 
13	K	186	100% 
14	L	115	100% 
15	M	148	97% 
16	N	95	100% 
17	O	154	97% 
18	P	84	93% 
19	Q	119	100% 
20	R	66	80% 
21	S	70	93% 
22	T	154	100% 
23	U	91	93% 
24	V	143	99% 
25	W	73	100% 
26	X	56	100% 
27	Y	49	63% 
28	Z	92	100% 
29	1	177	97% 

## 2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 64281 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 23S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2706	Total	C	N	O	P	0	0	0
			58012	25885	10685	18737	2705			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	560	C	U	CONFLICT	GB 3377779

- Molecule 2 is a RNA chain called 5S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	9	122	Total	C	N	O	P	0	0	0
			2600	1160	472	847	121			

- Molecule 3 is a protein called RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
3	A	237	Total	C	0	0	237
			237	237			

- Molecule 4 is a protein called RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
4	B	337	Total	C	0	0	337
			337	337			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLU	DELETION	UNP P20279
B	311	PHE	-	INSERTION	UNP P20279

- Molecule 5 is a protein called RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	C	246	Total C 246 246	0	0	246

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	73	LEU	GLN	CONFLICT	UNP P12735

- Molecule 6 is a protein called RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	D	140	Total C 140 140	0	0	140

- Molecule 7 is a protein called RIBOSOMAL PROTEIN L7AE.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
7	E	118	Total C 118 118	0	0	118

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	108	LEU	-	INSERTION	UNP P12743
E	109	GLU	-	INSERTION	UNP P12743
E	110	GLU	-	INSERTION	UNP P12743

- Molecule 8 is a protein called RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
8	F	157	Total C 157 157	0	0	157

- Molecule 9 is a protein called RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
9	G	142	Total C 142 142	0	0	142

- Molecule 10 is a protein called RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
10	H	132	Total C 132 132	0	0	132

- Molecule 11 is a protein called RIBOSOMAL PROTEIN L15E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
11	I	194	Total C 194 194	0	0	194

- Molecule 12 is a protein called RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
12	J	143	Total C 143 143	0	0	143

- Molecule 13 is a protein called RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
13	K	186	Total C 186 186	0	0	186

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	186	LEU	-	INSERTION	UNP P14123

- Molecule 14 is a protein called RIBOSOMAL PROTEIN L18E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
14	L	115	Total C 115 115	0	0	115

- Molecule 15 is a protein called RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
15	M	143	Total C 143 143	0	0	143

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	71	LYS	TYR	CONFLICT	UNP P14119

- Molecule 16 is a protein called RIBOSOMAL PROTEIN L21E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
16	N	95	Total C 95 95	0	0	95

- Molecule 17 is a protein called RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
17	O	150	Total C 150 150	0	0	150

- Molecule 18 is a protein called RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
18	P	78	Total C 78 78	0	0	78

- Molecule 19 is a protein called RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
19	Q	119	Total C 119 119	0	0	119

- Molecule 20 is a protein called RIBOSOMAL PROTEIN L24E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
20	R	53	Total C 53 53	0	0	53

- Molecule 21 is a protein called RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
21	S	65	Total C 65 65	0	0	65

- Molecule 22 is a protein called RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
22	T	154	Total C 154 154	0	0	154

- Molecule 23 is a protein called RIBOSOMAL PROTEIN L31E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
23	U	85	Total C 85 85	0	0	85

- Molecule 24 is a protein called RIBOSOMAL PROTEIN L32E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
24	V	143	Total C 143 143	0	0	143

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	109	ASN	ALA	CONFLICT	UNP P12736

- Molecule 25 is a protein called RIBOSOMAL PROTEIN L37AE.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
25	W	73	Total C 73 73	0	0	73

- Molecule 26 is a protein called RIBOSOMAL PROTEIN L37E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
26	X	56	Total C 56 56	0	0	56

- Molecule 27 is a protein called RIBOSOMAL PROTEIN L39E.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
27	Y	31	Total C 31 31	0	0	31

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	11	LYS	LEU	CONFLICT	UNP P22452
Y	24	TYR	TRP	CONFLICT	UNP P22452
Y	42	TRP	TYR	CONFLICT	UNP P22452

- Molecule 28 is a protein called RIBOSOMAL PROTEIN L44E.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
28	Z	92	Total C 92 92	0	0	92

- Molecule 29 is a protein called RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
29	1	172	Total C 172 172	0	0	172

- Molecule 30 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
30	X	1	Total Cd 1 1	0	0
30	W	1	Total Cd 1 1	0	0
30	R	1	Total Cd 1 1	0	0
30	Z	1	Total Cd 1 1	0	0

- Molecule 31 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
31	0	1	Total K 1 1	0	0

- Molecule 32 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	0	2	Total Mg 2 2	0	0

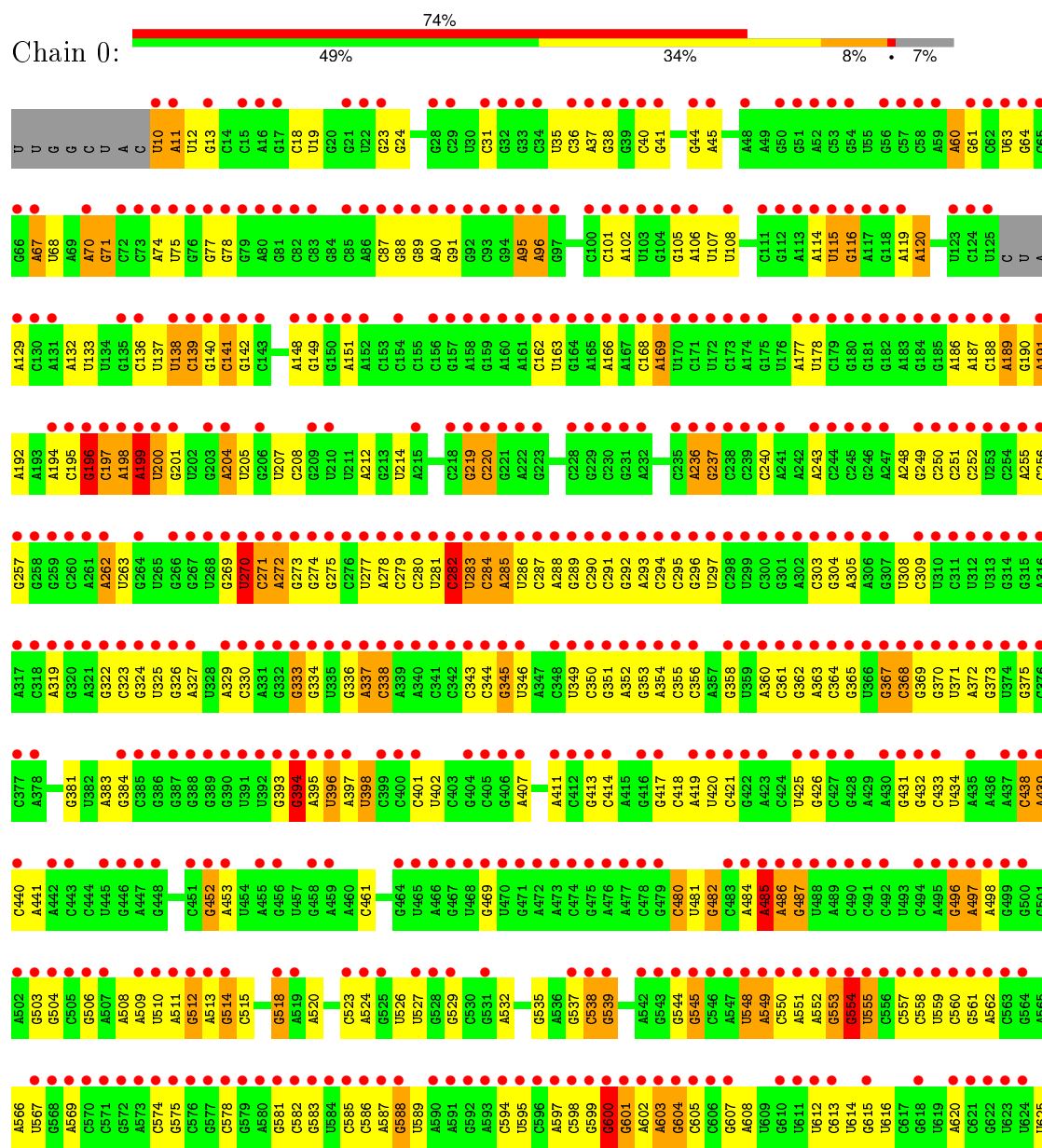
- Molecule 33 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	0	6	Total O 6 6	0	0

### 3 Residue-property plots

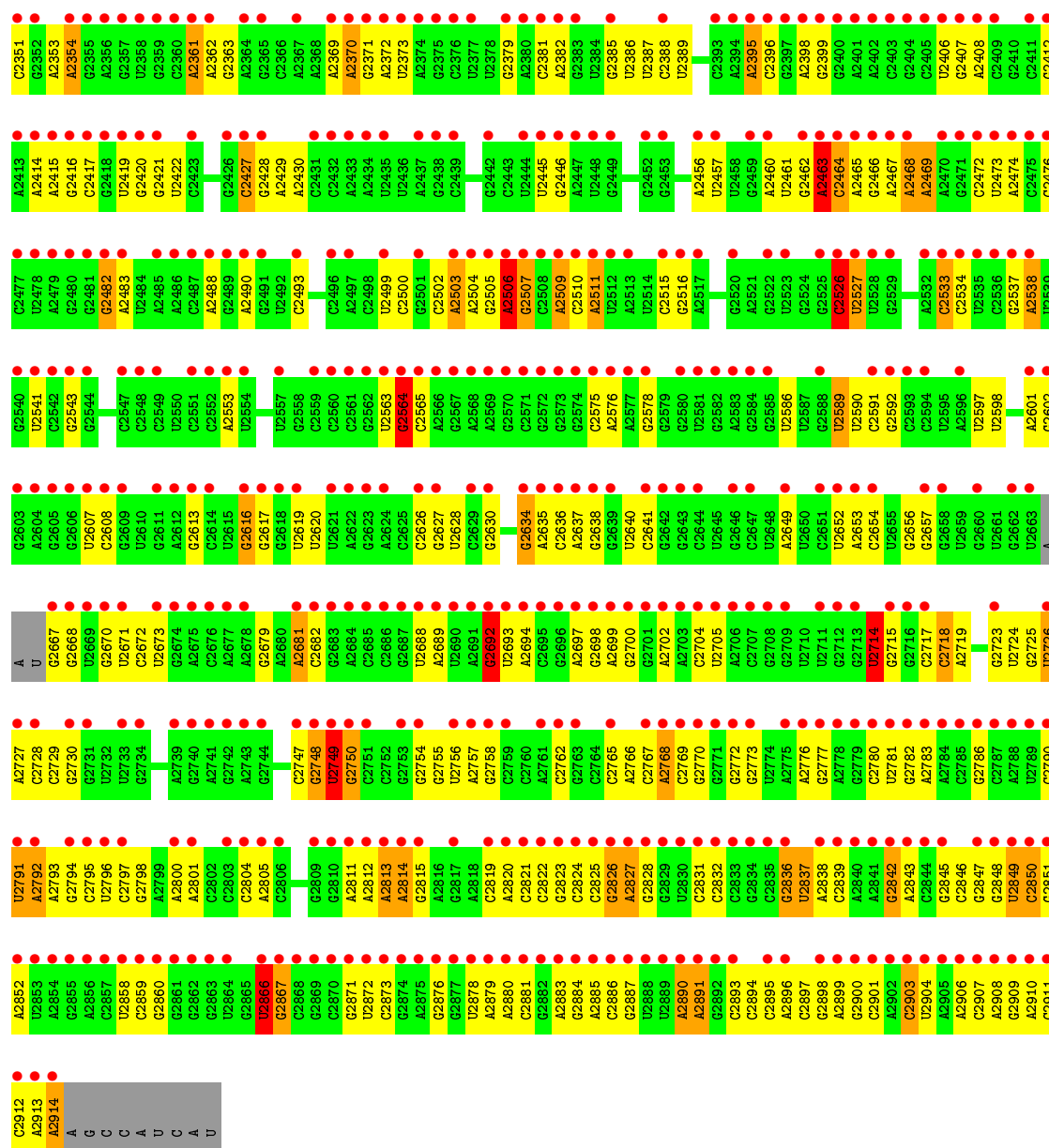
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

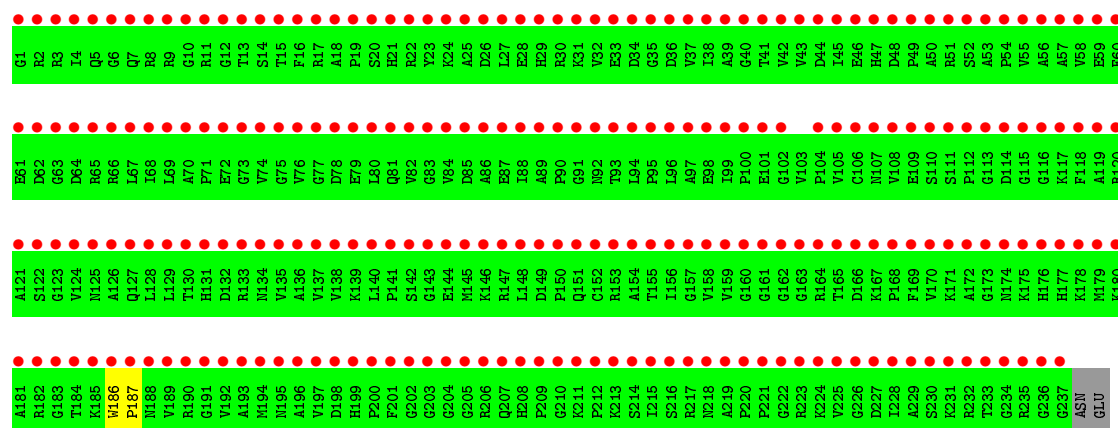
#### • Molecule 1: 23S rRNA



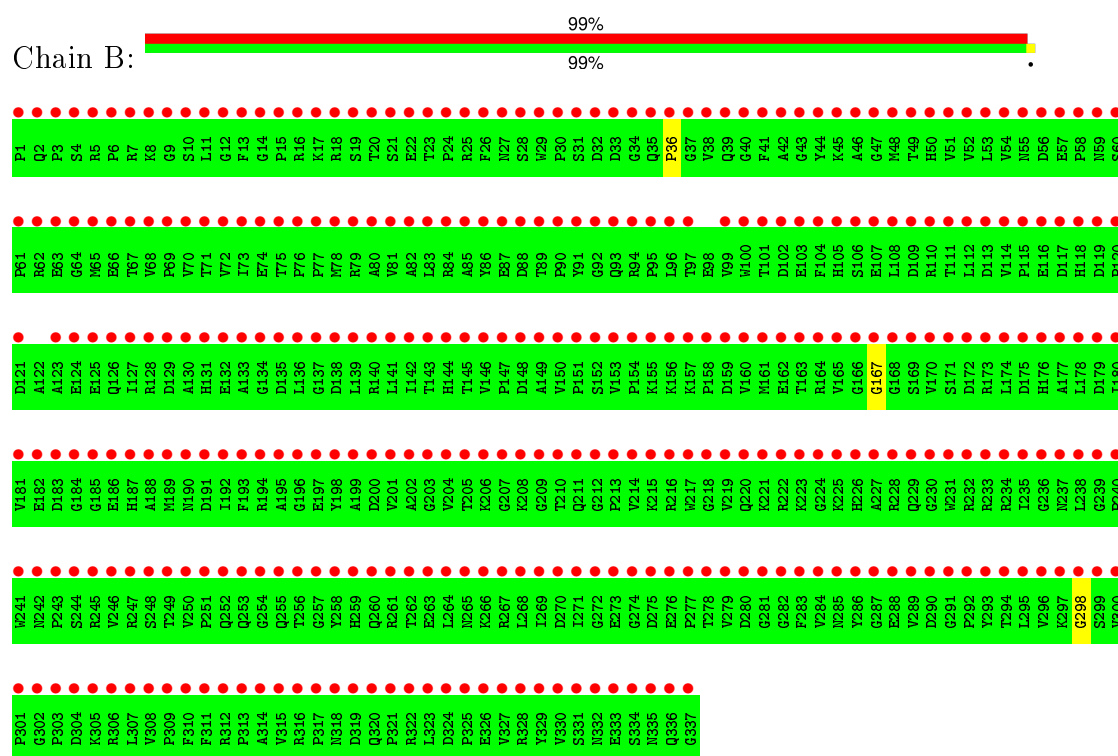
G1421	A1355	A1294	A1232	G1112	G1049	G	A926	A746	A686	U626
U1422	A1356	G1295	A1236	G1113	G1050	A	A929	G747	G687	G627
C1423	A1357	A1296	U1237	U1114	G1051	G	A930	C748	A688	A628
A1424	U1297	U1297	U1237	U1115	G1052	U	G931	C749	G689	G629
G1425	U1298	U1298	C1238	U1116	G1053	C	C932	A750	G690	A630
C1426	G1299	U1299	G1239	U1117	G1054	C	C933	A751	G691	A631
A1427	U1300	G1300	G1240	U1118	G1055	G	C934	C752	A692	A632
G1430	U1301	U1301	G1241	U1119	U1056	C	G935	U753	G693	C633
G1433	U1304	U1304	A1242	U1120	U1057	A	C936	G754	A694	C634
A1434	U1305	U1305	C1243	G1121	A1058	C	G937	G755	G695	A635
G1437	U1306	U1306	U1244	U1122	G1059	A	G938	G756	G696	C637
U1438	U1307	U1307	C1245	A1123	C1060	C	A939	C757	G697	C638
G1439	A1308	U1308	A1246	C1124	C1061	U1001	G940	A758	A698	A639
U1440	U1309	U1309	A1247	U1125	U1062	G	G941	C759	G699	G640
G1441	U1310	U1310	U1248	C1126	U1063	U1003	U942	G760	A700	G641
A1442	G1311	G1311	C1250	U1128	U1064	A	U943	C762	G702	G642
G1443	G1312	G1312	C1251	U1129	U1065	A	U944	G763	G703	A643
U1444	A1313	A1313	A1252	U1130	A1066	U1006	U945	C764	G704	G644
G1445	U1314	U1314	C1253	G1131	C1067	A	U946	G765	G705	U645
U1446	G1315	G1315	A1254	A1132	C1068	U1008	U947	A766	G706	G646
A1447	G1316	G1316	C1255	A1133	A1069	U1009	U948	C767	G707	U647
U1448	G1317	G1317	A1256	G1134	A1070	A	U949	A768	A708	G648
G1449	A1318	A1318	C1257	G1072	G1072	C	U950	C769	G709	U649
U1450	G1319	G1319	G1258	A1073	A1073	A	A951	C770	G710	C650
C1451	U1320	U1320	A1259	U1135	A1074	U1013	G952	G771	G711	U651
G1452	A1321	A1321	G1260	G1137	G1075	A	G953	C772	G712	C652
U1453	G1322	G1322	U1261	U1138	A1076	U1016	U954	A773	U713	C653
G1454	G1323	G1323	C1262	U1139	G1076	A	U955	C774	U714	A654
U1455	A1324	A1324	A1263	C1140	A1077	U1017	U956	G775	U	U655
G1456	G1325	G1325	U1264	U1141	C1080	C	U957	A776	G716	G656
U1457	U1326	U1326	C1265	C1142	A1081	U1019	G958	C777	G717	G657
A1458	G1327	G1327	U1266	G1143	A1082	A	C959	U777	C718	C658
G1459	A1328	A1328	C1267	A1144	C1083	U1021	G960	C778	C719	U659
U1460	G1329	G1329	U1268	G1145	C1084	U1022	A961	U779	G720	A660
C1461	U1330	U1330	U1270	C1147	G1087	U1023	G962	C781	A721	G661
U1462	A1331	A1331	A1271	U1148	A1088	C	C963	G782	G722	U662
G1463	G1332	G1332	C1272	U1149	G1089	U1025	G964	C783	G723	C663
U1464	U1333	U1333	U1273	U1150	A1090	C	U965	A784	G724	U664
G1465	C1334	C1334	G1274	G1151	U1091	U1026	U966	U785	C725	A665
U1466	U1335	U1335	A1275	C1152	A1092	U1027	U967	G786	G726	A666
C1467	C1336	C1336	C1276	U1153	G1093	U1029	G968	C787	G727	C667
U1468	A1337	A1337	U1277	A1154	G1094	U1030	U969	A788	G728	G668
G1469	U1338	U1338	A1278	G1155	U1095	A	U970	C789	G729	U669
U1470	G1339	G1339	C1279	C1156	U1096	U1032	U	A790	G730	G670
A1471	U1340	U1340	U1280	G1157	A1097	C	U	A791	U731	A671
U1472	C1341	C1341	C1281	U1158	G1098	U1033	U	C792	C732	U672
G1473	A1342	A1342	U1282	G1159	G1099	C	C	A793	U733	U673
U1474	G1343	G1343	G1283	G1160	G1000	U1036	U	U794	U734	A674
C1475	U1344	U1344	A1284	A	U1001	G1037	C	G795	C735	U675
U1476	A1345	A1345	G1285	G	C1102	G1038	C	A796	A736	C676
G1477	U1346	U1346	U1286	G	C1103	U1039	C	A797	A737	C677
U1478	A1347	A1347	A1287	U	C1104	A1040	U	G798	U738	G678
A1479	G1348	G1348	C1288	G	C1105	U1041	U	C799	G739	G679
U1480	U1349	U1349	U1289	A	G1006	U1042	C	G800	G740	G680
G1481	C1350	C1350	C1290	C	A1107	C1043	C	U801	C741	A681
U1482	U1351	U1351	U1291	U	G1108	G1044	G	G802	G742	A682
C1483	A1352	A1352	G1292	U	U1109	U1045	A	C803	G743	G683
U1484	G1353	G1353	U1293	A	G1110	G1046	G	U804	G744	G684
G1485	U1354	U1354	A1293	A	U1111	G1048	G	G805	G745	C685

G2287	C	U	G	C2104	U2042	G1979	H1918	A1857	G1795	A1733	U1671	G1610	G1546	G1484
G2288	C	C	A	C2105	U2043	U1960	A1919	A1858	A1796	C1734	G1672	G1611	A1947	A1485
G2289	G	G	G	C2106	G2044	A1981	A1920	A1859	A1797	C1735	U1673	A1612	A1947	
U2290	G	A	A	U2107	G2045	U1982	A1921	U1860	G1798	A1736		A1613	U1488	
A2291	U	C	C	A2108	G2046	C1983	G1923	C1862	G1799	A1737	G1676	G1614	C1551	G1489
C2292	G	A	A	U2109	C2047		G1924	G1863	A1801	G1738	U1677	A1615	C1552	G1490
G2293	C	C	C	G2110			A1925	C1864	A1802	G1739	U1678	A1616	C1553	G1491
G2294	C	U	U	G2111	G2050		G1926	A1865	G1803	C1679	C1679	C1617	U1564	A1492
U2297	C	U	A	A2112	G2051		A1927	A1866	A1804	U1740	C1680	C1618	C1555	A1493
A2300	C	C	A	C2113	U2052		G1928	G1867	A1805	G1743	A1681	C1620	C1556	A1494
A2301	C	C	C	C2114	G2053		G1929	A1868	G1806	G1744	A1682	C1621	C1557	C1495
A2302	C	A	C	U2115	A2054		A1930	A1869	A1807	G1745	A1684	G1622	C1558	G1496
A2303	C	C	C	U2116	A2055		A1931	A1870	C1806	A1746	A1685	C1623	C1559	G1497
A2304	C	C	C	U2117	C2056		G1932						U	G1498
A2305	C	C	C	C2118	U2057		G1933	G1873	C1809	C1750	C1686	U1624	U1561	
A2306	C	C	C	C2119	G2058		G1934	U1874	C1810	C1687	C1687	U1625	C1562	A1501
A2307	C	C	C	U2120	U2059		A1935	A1875	A1811	G1751	G1688	A1626	C1563	A1502
A2308	C	C	C	G2121	A2060		G1936	C1876	G1812	G1752	A1689	G1627	C1564	U1503
A2309	C	C	C	G2122	C2061		C1937	G1877	A1815	C1753	C1690	G1628	C1565	U1504
A2310	C	C	C	G2123	A2062		U1937	G1878	A1816	A1754	C1691	G1629	C1566	U1505
A2311	C	C	C	C2124	U2063		G1938	A1879	C1817	A1755	C1692	A1631	C1567	U1506
A2312	C	C	C	U2125	G2064		U1939	U1880	A1818	G1756	A1693	A1632	C1568	C1507
A2313	C	C	C	C2126	C2065			A1881	C1819	U1757	A1694	C1633	U1569	C1508
A2314	C	C	C	G2127	U2066			G1882	G1820	U1758	G1695	C1634	C1570	C1509
A2315	C	C	C	U2128	C2067		A1942	A1883	A1821	U1759	G1696	G1635	C1571	G1510
A2316	C	C	C	U2129	A2068		G1943	U1884	A1822	G1760	G1697	U1636	A1572	U1511
A2317	C	C	C	C2130	G2069		G1944	A1885	G1823	C1761	U1698	G1637	A1573	G1512
A2318	C	C	C	U2131	U2070		G1945	A1886	A1824	C1763	C1699	C1574	C1575	C1513
A2319	C	C	C	C2132	C2071		A1946	U1887	U1825	C1764	C1700	C1576	C1576	C1514
A2320	C	C	C	U2133	G2072		G1947	A1888	A1826	G1765	U1702	G1640	C1577	G1515
A2321	C	C	C	G2134	C2073		A1948	G1889	G1827	U1766	G1703	A1641	C1578	C1516
A2322	C	C	C	U2135	A2074		G1950	U1890	A1828	A1767	G1704	A1642	C1579	U1517
A2323	C	C	C	C2136	G2075		G1951	A1891	A1829	C1768	G1705	C1644	A1581	A1518
A2324	C	C	C	A	U2076		U	A1892	C1830	C1769	G1706	U1645	C1580	U1519
A2325	C	C	C	U2137	G2077		A	A1893	U1831	G1770	G1707	G1646	C1582	G1521
A2326	C	C	C	G2138	U2078		A	A1894	U1832	U1771	G1708	G1647	U1583	A1522
A2327	C	C	C	U2139	A2079		C	A1895	U1833	C1772	G1709	G1648	C1584	G1523
A2328	C	C	C	C2140	G2080		U	A1896	U1834	G1773	A1710	G1649	C1585	U1524
A2329	C	C	C	U2141	A2081		A	U1897	A1836	A1775	G1713	C1651	C1586	G1525
A2330	C	C	C	C2142	G2082		U	A1898	G1837	A1776	G1714	C1652	U1587	A1526
A2331	C	C	C	U2143	C2083		G	A1899	U1838	G1777	A1711	U1653	C1588	A1527
A2332	C	C	C	C2144	A2084		A	A1900	A1839	A1778	C1715	U1654	C1589	A1528
A2333	C	C	C	U2145	C2085		C	A1901	A1840	A1779	U1716	G1655	A1590	G1529
A2334	C	C	C	G2146	G2086		C	G1902				G1656	A1591	U1530
A2335	C	C	C	U2147	A2087		U	G1903	A1843	G1780	A1717	A1657	C1592	U1531
A2336	C	C	C	C2148	U2088		C	A1904	A1844	G1781	G1718	C1658	C1593	G1532
A2337	C	C	C	U2149	G2089		A	U1905	A1845	G1782	G1719	A1659	C1594	A1533
A2338	C	C	C	C2150	C2090		U	U1906	A1846	A1783		G1660	C1595	C1534
A2339	C	C	C	U2151	A2091		A	U1907	U1847	U1784	U1722	G1661	G1596	G1535
A2340	C	C	C	G2152	G2092		C	A1908	A1847	G1785	G1723	A1662	C1597	C1536
A2341	C	C	C	U2153	U2093		U	G1909	A1848	C1786	U1724	G1663	C1602	C1537
A2342	C	C	C	C2154	A2094		G	A1910	G1849	C1787	C1725	A1664	U1538	U1539
A2343	C	C	C	U2155	G2095		A	U1911	U1850	U1788	G1726	A1665	G1540	G1540
A2344	C	C	C	C2156	C2096		U	U1912	U1851	G1789	G1727	C1666	G1604	G1541
A2345	C	C	C	U2157	A2097		A	A1852	A1852	C1790	G1728	A1667	G1605	G1542
A2346	C	C	C	G2158	C2098		C	C1853	C1853	U1791	A1729	U1668	A1606	G1543
A2347	C	C	C	U2159	U2099		U	U1913	A1854	C1792	C1730	U1669	G1607	U1544
A2348	C	C	C	C2160	A2100		C	G1914	G1855	C1793	A1732	G1670	C1609	G1545
A2349	C	C	C	U2101	G2101		U	U1915	G1856					
A2350	C	C	C	G2102	C2102		U	U1916	G1857					
A2351	C	C	C	A2103	G2103		U	G1917	C1856					

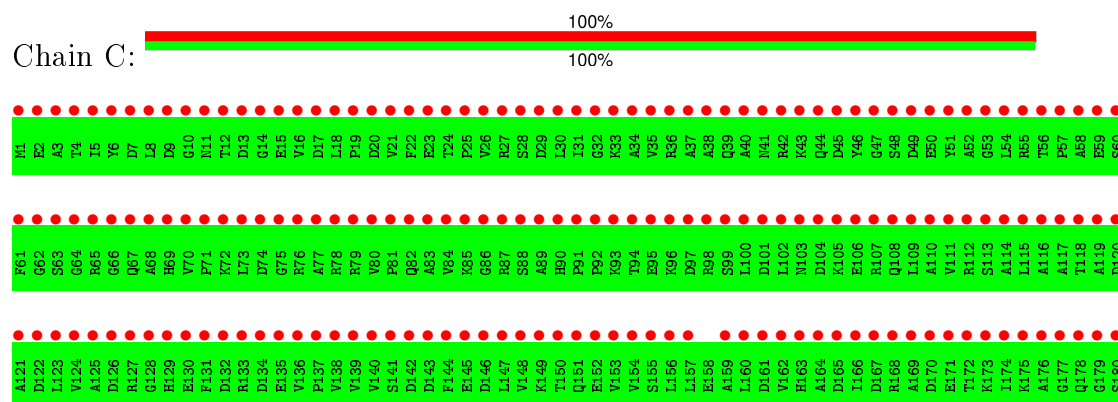


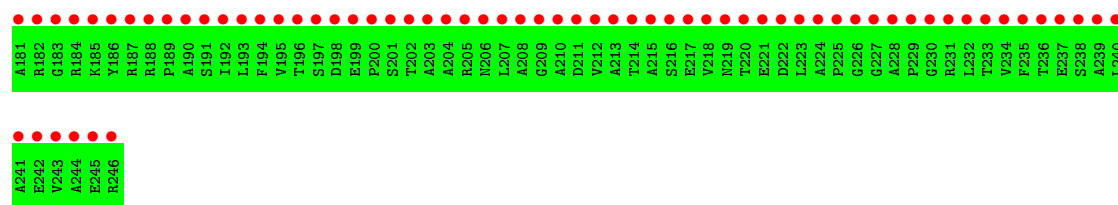


● Molecule 4: RIBOSOMAL PROTEIN L3

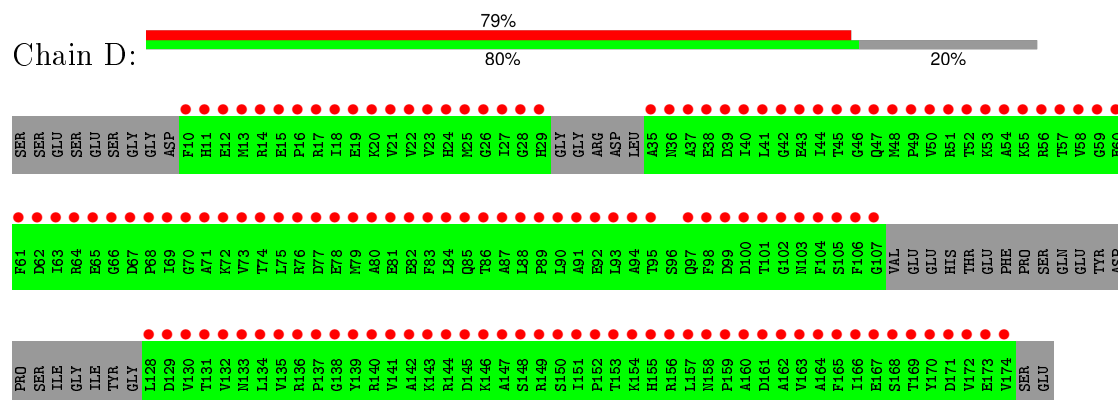


● Molecule 5: RIBOSOMAL PROTEIN L4

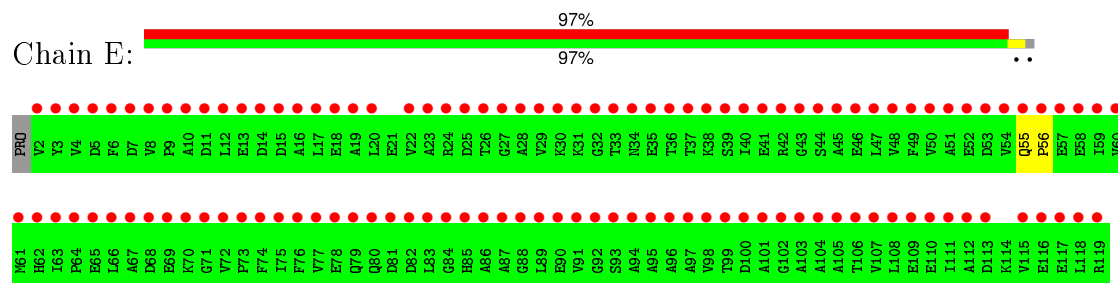




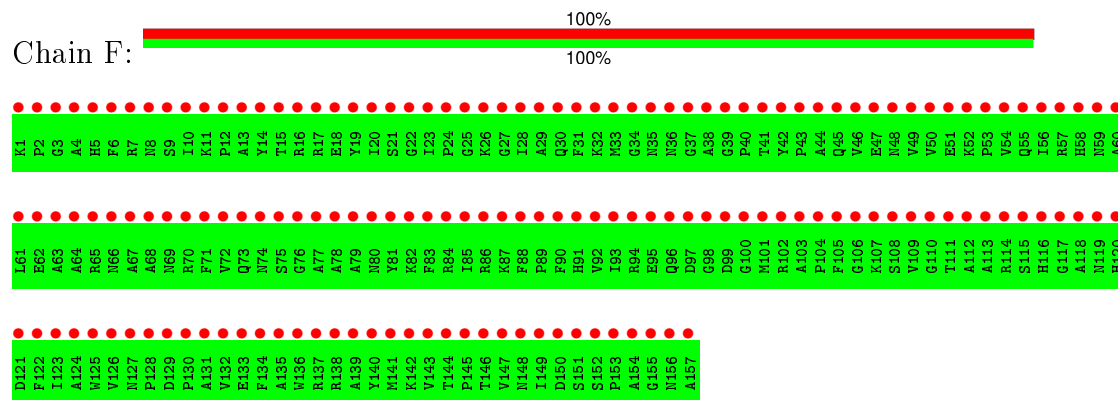
• Molecule 6: RIBOSOMAL PROTEIN L5



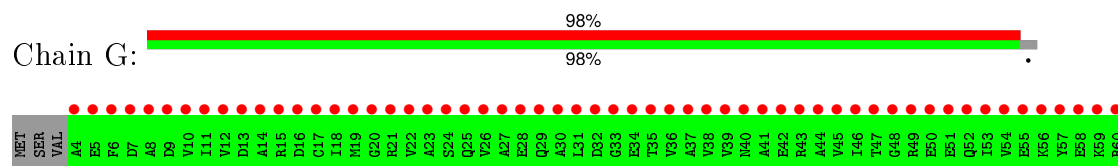
• Molecule 7: RIBOSOMAL PROTEIN L7AE

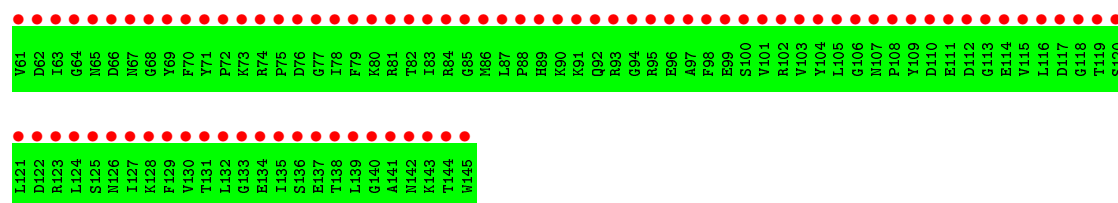


• Molecule 8: RIBOSOMAL PROTEIN L10E

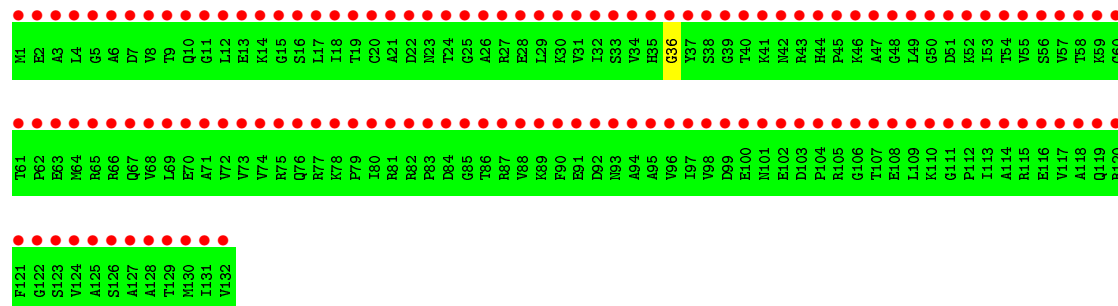


• Molecule 9: RIBOSOMAL PROTEIN L13

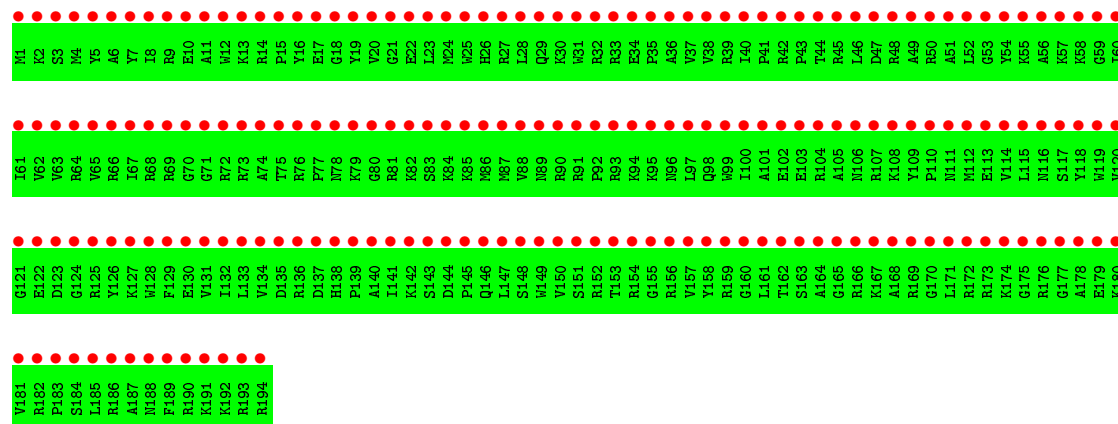




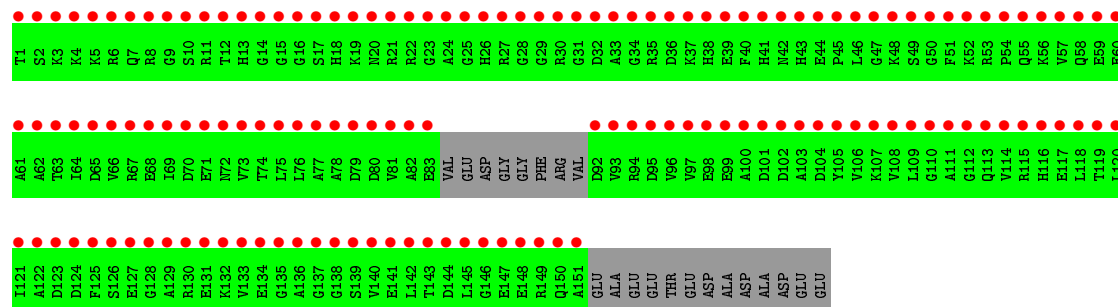
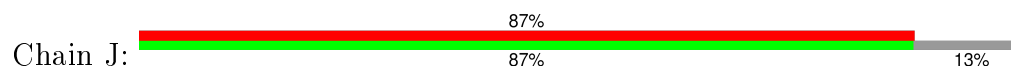
• Molecule 10: RIBOSOMAL PROTEIN L14



• Molecule 11: RIBOSOMAL PROTEIN L15E

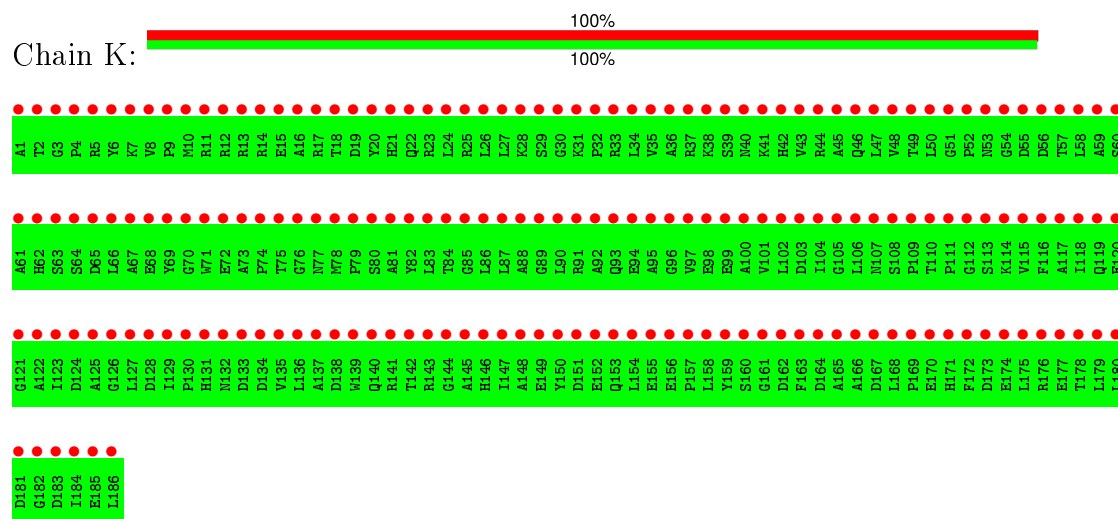


• Molecule 12: RIBOSOMAL PROTEIN L15

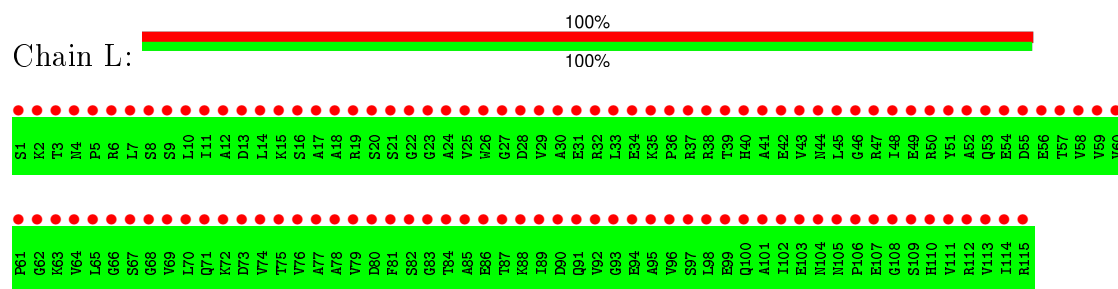




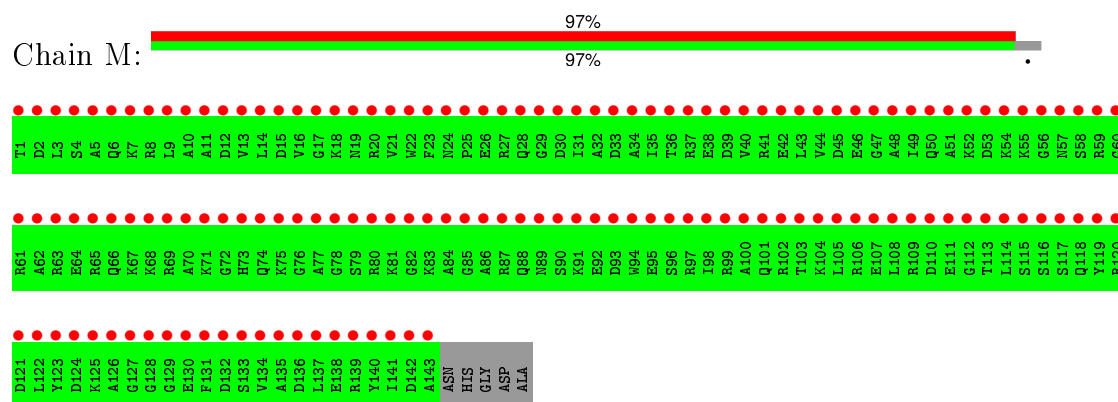
- Molecule 13: RIBOSOMAL PROTEIN L18



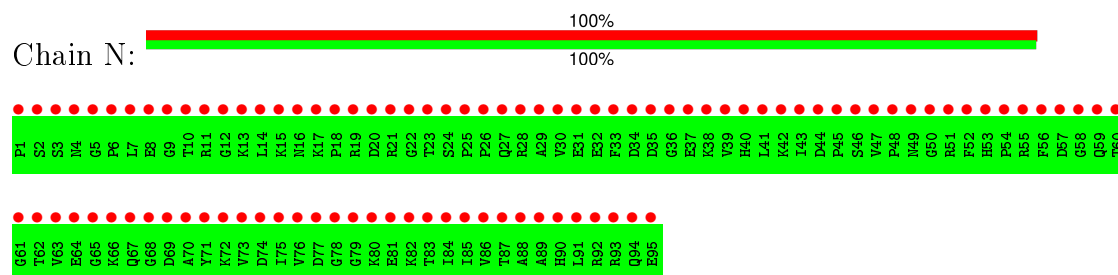
- Molecule 14: RIBOSOMAL PROTEIN L18E



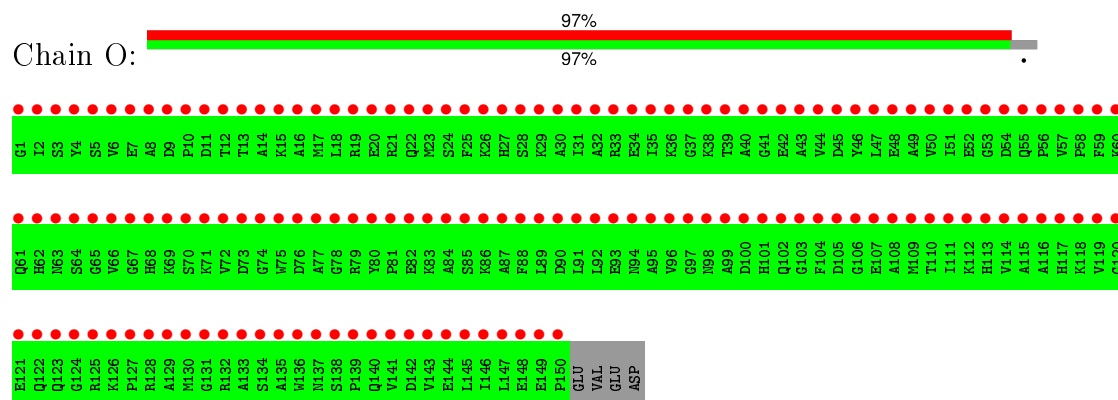
- Molecule 15: RIBOSOMAL PROTEIN L19



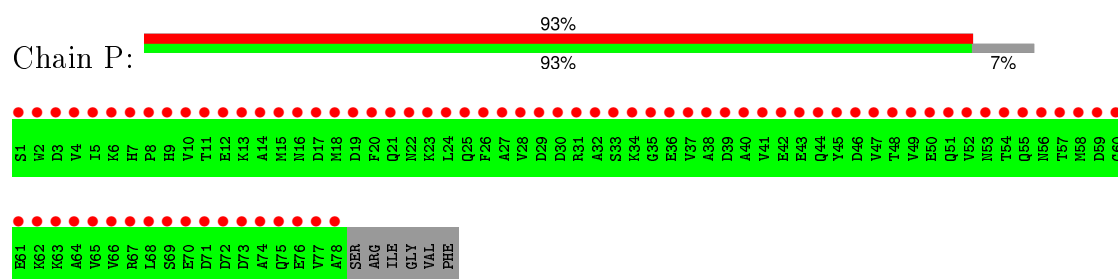
- Molecule 16: RIBOSOMAL PROTEIN L21E



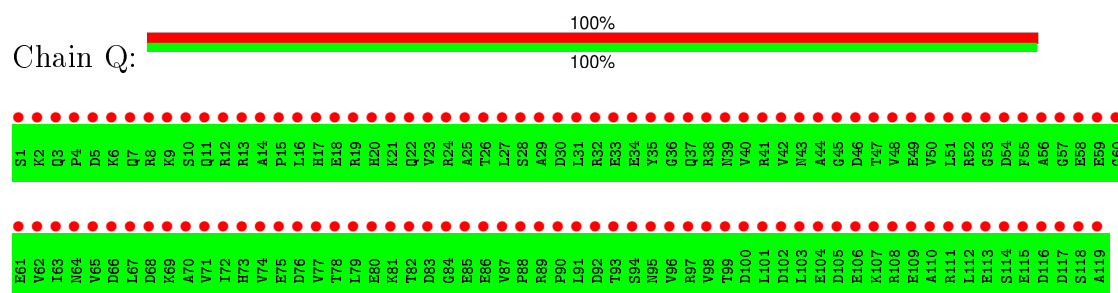
- Molecule 17: RIBOSOMAL PROTEIN L22



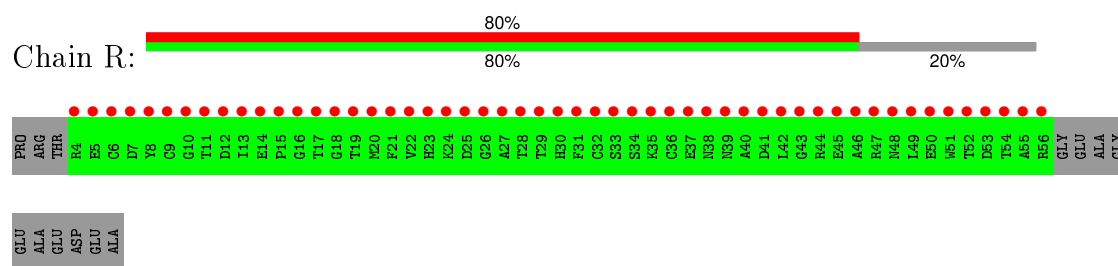
- Molecule 18: RIBOSOMAL PROTEIN L23



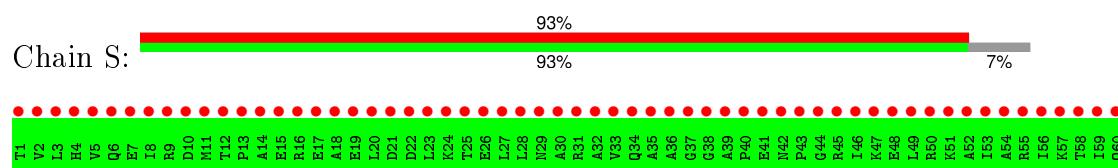
- Molecule 19: RIBOSOMAL PROTEIN L24

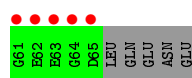


- Molecule 20: RIBOSOMAL PROTEIN L24E

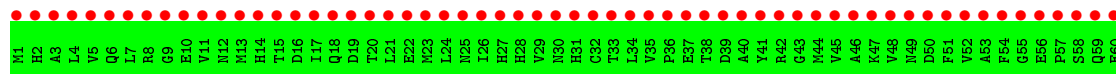


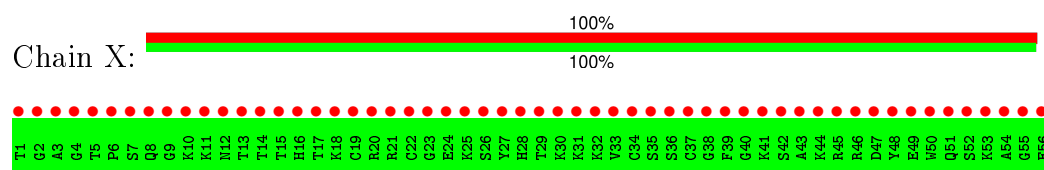
- Molecule 21: RIBOSOMAL PROTEIN L29



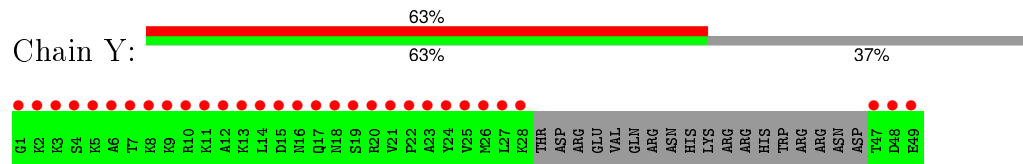


• Molecule 22: RIBOSOMAL PROTEIN L30

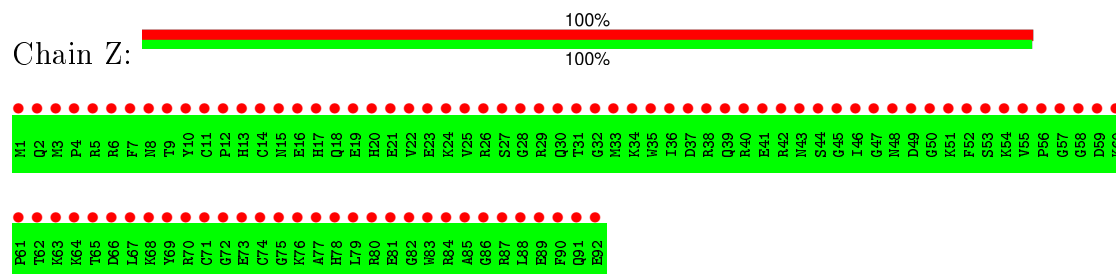




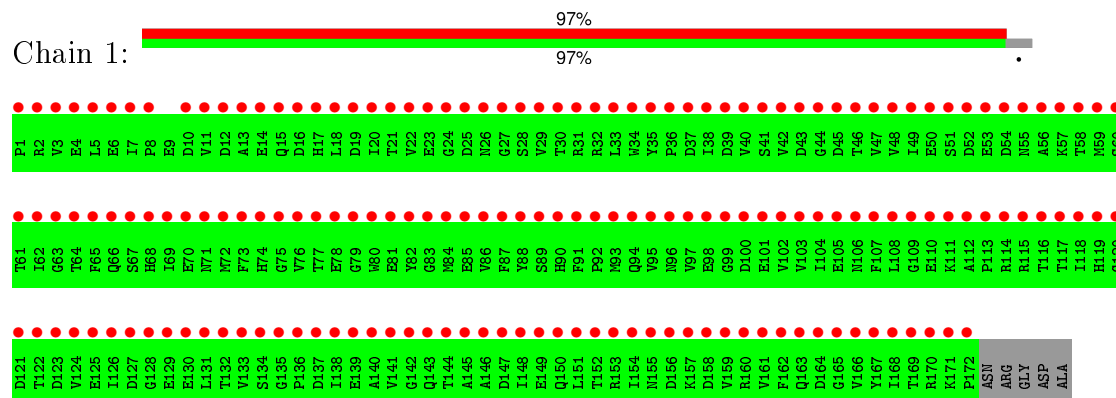
• Molecule 27: RIBOSOMAL PROTEIN L39E



• Molecule 28: RIBOSOMAL PROTEIN L44E



• Molecule 29: RIBOSOMAL PROTEIN L6



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	211.66Å 299.67Å 573.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.00 – 2.40 89.24 – 2.40	Depositor EDS
% Data completeness (in resolution range)	82.3 (90.00-2.40) 95.5 (89.24-2.40)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.28 (at 2.40Å)	Xtriage
Refinement program	TNT, CNS	Depositor
R, $R_{free}$	0.252 , 0.261 0.337 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	42.3	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.04 , -7.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 701272 reflections	Xtriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	64281	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.51% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: K, MG, CD

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	0	0.47	0/64945	0.72	73/101281 (0.1%)
2	9	0.35	0/2905	0.75	4/4528 (0.1%)
All	All	0.46	0/67850	0.72	77/105809 (0.1%)

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	0	18	45
2	9	2	0
All	All	20	45

There are no bond length outliers.

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2749	U	C2'-C3'-O3'	11.07	133.85	109.50
1	0	904	U	C2'-C3'-O3'	10.39	132.35	109.50
1	0	1981	A	C2'-C3'-O3'	10.23	132.00	109.50
1	0	2692	G	N9-C1'-C2'	10.09	127.12	114.00
2	9	3	A	C2'-C3'-O3'	9.58	130.57	109.50
1	0	894	A	C2'-C3'-O3'	9.38	130.13	109.50
1	0	1059	G	C2'-C3'-O3'	8.85	128.97	109.50
1	0	713	U	C2'-C3'-O3'	8.71	128.66	109.50
1	0	1309	U	C2'-C3'-O3'	8.66	128.56	109.50
1	0	191	A	C2'-C3'-O3'	8.64	128.51	109.50
1	0	2616	G	C2'-C3'-O3'	8.34	127.84	109.50
1	0	480	C	C2'-C3'-O3'	8.34	127.84	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	394	G	C2'-C3'-O3'	8.29	127.75	109.50
1	0	2482	G	C2'-C3'-O3'	8.25	127.66	109.50
1	0	282	C	C2'-C3'-O3'	8.13	127.39	109.50
1	0	1406	A	C2'-C3'-O3'	8.13	127.38	109.50
1	0	1835	U	C2'-C3'-O3'	8.11	127.34	109.50
1	0	1907	U	C2'-C3'-O3'	8.04	127.20	109.50
1	0	600	G	C2'-C3'-O3'	7.99	127.08	109.50
1	0	1853	C	C2'-C3'-O3'	7.97	127.05	109.50
1	0	2714	U	C2'-C3'-O3'	7.97	127.04	109.50
1	0	2321	A	C2'-C3'-O3'	7.91	126.89	109.50
1	0	2427	C	C2'-C3'-O3'	7.69	126.42	109.50
1	0	1699	C	C2'-C3'-O3'	7.68	126.39	109.50
1	0	2370	A	C2'-C3'-O3'	7.60	126.22	109.50
1	0	1506	U	C2'-C3'-O3'	7.48	125.96	109.50
1	0	554	G	C2'-C3'-O3'	7.44	125.87	109.50
2	9	28	U	C2'-C3'-O3'	7.31	125.58	109.50
1	0	2813	A	C2'-C3'-O3'	7.24	125.43	109.50
1	0	199	A	C2'-C3'-O3'	7.22	125.38	109.50
1	0	2283	G	C2'-C3'-O3'	7.17	125.26	109.50
1	0	452	G	N9-C1'-C2'	6.97	123.06	114.00
1	0	1214	G	C2'-C3'-O3'	6.96	124.84	113.70
1	0	1379	A	C2'-C3'-O3'	6.90	124.74	113.70
1	0	1690	C	C2'-C3'-O3'	6.86	124.67	113.70
1	0	196	G	C2'-C3'-O3'	6.83	124.63	113.70
1	0	1979	G	C2'-C3'-O3'	6.76	124.51	113.70
1	0	856	G	N9-C1'-C2'	6.74	122.76	114.00
1	0	548	U	C2'-C3'-O3'	6.55	124.19	113.70
1	0	1072	G	N9-C1'-C2'	6.46	122.39	114.00
1	0	1995	G	N9-C1'-C2'	6.44	122.37	114.00
1	0	2090	G	C2'-C3'-O3'	6.28	123.75	113.70
1	0	2692	G	O4'-C1'-N9	6.22	113.17	108.20
1	0	1682	A	N9-C1'-C2'	6.15	122.00	114.00
1	0	2083	A	C2'-C3'-O3'	6.14	123.52	113.70
1	0	1214	G	C4'-C3'-O3'	6.13	125.26	113.00
1	0	1126	C	C2'-C3'-O3'	6.12	123.50	113.70
1	0	2395	A	C2'-C3'-O3'	6.11	123.48	113.70
1	0	2258	A	C2'-C3'-O3'	5.97	123.26	113.70
1	0	191	A	C4'-C3'-O3'	5.95	124.89	113.00
1	0	1120	U	C5'-C4'-C3'	-5.85	106.64	116.00
1	0	1524	U	N1-C1'-C2'	-5.74	105.69	112.00
1	0	1448	A	C2'-C3'-O3'	5.68	122.79	113.70
2	9	39	U	N1-C1'-C2'	5.67	121.38	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1819	G	C5'-C4'-C3'	5.53	124.84	116.00
1	0	2506	A	N9-C1'-C2'	-5.51	105.94	112.00
1	0	1108	G	C2'-C3'-O3'	5.49	122.48	113.70
1	0	2914	A	C2'-C3'-O3'	5.36	122.27	113.70
1	0	1214	G	C4'-C3'-C2'	5.30	107.90	102.60
1	0	600	G	C4'-C3'-O3'	5.30	123.60	113.00
1	0	452	G	C2'-C3'-O3'	5.30	122.18	113.70
1	0	777	U	O4'-C1'-N1	5.29	112.43	108.20
1	0	1683	G	C2'-C3'-O3'	5.27	122.13	113.70
2	9	1	U	N1-C1'-C2'	5.26	120.84	114.00
1	0	1907	U	C4'-C3'-O3'	5.20	123.41	113.00
1	0	2316	G	N9-C1'-C2'	5.18	120.73	114.00
1	0	535	G	N9-C1'-C2'	5.15	120.70	114.00
1	0	2074	A	N9-C1'-C2'	5.14	120.68	114.00
1	0	1615	A	C5'-C4'-C3'	5.12	124.18	116.00
1	0	1369	A	N9-C1'-C2'	5.11	120.65	114.00
1	0	2427	C	C4'-C3'-O3'	5.10	123.19	113.00
1	0	2526	C	C2'-C3'-O3'	5.09	121.84	113.70
1	0	2506	A	O4'-C1'-N9	5.08	112.26	108.20
1	0	1835	U	C4'-C3'-O3'	5.07	123.13	113.00
1	0	1504	A	C1'-O4'-C4'	-5.05	105.86	109.90
1	0	857	A	C2'-C3'-O3'	5.05	121.78	113.70
1	0	894	A	C4'-C3'-O3'	5.01	123.01	113.00

All (20) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	0	191	A	C3'
1	0	282	C	C3'
1	0	600	G	C3'
1	0	894	A	C3'
1	0	904	U	C3'
1	0	1214	G	C3'
1	0	1309	U	C3'
1	0	1699	C	C3'
1	0	1835	U	C3'
1	0	1853	C	C3'
1	0	1907	U	C3'
1	0	1981	A	C3'
1	0	2083	A	C3'
1	0	2427	C	C3'
1	0	2482	G	C3'

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Mol	Chain	Res	Type	Atom
1	0	2692	G	C1'
1	0	2714	U	C3'
1	0	2749	U	C3'
2	9	1	U	C1'
2	9	3	A	C3'

All (45) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1122	U	Sidechain
1	0	1342	C	Sidechain
1	0	138	U	Sidechain
1	0	1417	G	Sidechain
1	0	1430	G	Sidechain
1	0	1524	U	Sidechain
1	0	1525	G	Sidechain
1	0	1555	G	Sidechain
1	0	1614	G	Sidechain
1	0	1682	A	Sidechain
1	0	1809	G	Sidechain
1	0	1819	G	Sidechain
1	0	1829	A	Sidechain
1	0	1848	G	Sidechain
1	0	1863	G	Sidechain
1	0	1867	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	189	A	Sidechain
1	0	1950	G	Sidechain
1	0	1972	U	Sidechain
1	0	1979	G	Sidechain
1	0	1995	G	Sidechain
1	0	2312	G	Sidechain
1	0	2313	C	Sidechain
1	0	2463	A	Sidechain
1	0	2493	C	Sidechain
1	0	2503	A	Sidechain
1	0	2506	A	Sidechain
1	0	2543	G	Sidechain
1	0	2564	G	Sidechain
1	0	2607	U	Sidechain
1	0	262	A	Sidechain

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Mol	Chain	Res	Type	Group
1	0	2630	G	Sidechain
1	0	270	U	Sidechain
1	0	2842	G	Sidechain
1	0	2866	U	Sidechain
1	0	333	G	Sidechain
1	0	396	U	Sidechain
1	0	469	G	Sidechain
1	0	482	G	Sidechain
1	0	485	A	Sidechain
1	0	518	G	Sidechain
1	0	529	G	Sidechain
1	0	791	A	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	0	58012	0	29282	976	0
2	9	2600	0	1326	62	0
3	A	237	0	0	1	0
4	B	337	0	0	2	0
5	C	246	0	0	0	0
6	D	140	0	0	0	0
7	E	118	0	0	1	0
8	F	157	0	0	0	0
9	G	142	0	0	0	0
10	H	132	0	0	1	0
11	I	194	0	0	0	0
12	J	143	0	0	0	0
13	K	186	0	0	0	0
14	L	115	0	0	0	0
15	M	143	0	0	0	0
16	N	95	0	0	0	0
17	O	150	0	0	0	0
18	P	78	0	0	0	0
19	Q	119	0	0	0	0
20	R	53	0	0	0	0
21	S	65	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	T	154	0	0	0	0
23	U	85	0	0	1	0
24	V	143	0	0	2	0
25	W	73	0	0	0	0
26	X	56	0	0	0	0
27	Y	31	0	0	0	0
28	Z	92	0	0	0	0
29	1	172	0	0	0	0
30	R	1	0	0	0	0
30	W	1	0	0	0	0
30	X	1	0	0	0	0
30	Z	1	0	0	0	0
31	0	1	0	0	0	0
32	0	2	0	0	0	0
33	0	6	0	0	0	0
All	All	64281	0	30608	1040	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 11.

All (1040) 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)
2:9:76:G:H3'	2:9:77:A:H5''	1.29	1.10
1:0:1682:A:H2	1:0:1696:U:H3	1.05	1.01
1:0:795:G:H2'	1:0:817:G:H22	1.25	1.00
1:0:326:G:H1	1:0:330:C:H5	1.03	1.00
1:0:1355:A:O2'	1:0:1356:A:H3'	1.60	1.00
2:9:56:A:H2'	2:9:57:A:H5''	1.44	0.99
1:0:1147:C:H2'	1:0:1148:C:H5''	1.47	0.95
1:0:337:A:H2	1:0:1314:U:HO2'	1.00	0.95
1:0:2768:A:H2'	1:0:2769:C:O4'	1.66	0.94
1:0:289:G:H22	1:0:363:A:H2	1.08	0.93
1:0:282:C:H1'	1:0:368:C:N4	1.82	0.93
1:0:2717:C:C2'	1:0:2718:C:H5''	2.00	0.92
1:0:560:C:H42	1:0:597:A:H61	1.01	0.91
1:0:1751:G:H2'	1:0:1752:G:H5''	1.51	0.91
1:0:1116:U:HO2'	1:0:1118:A:H2	0.91	0.90
1:0:10:U:HO2'	1:0:11:A:H8	0.99	0.90
1:0:2890:A:H8	1:0:2890:A:H5''	1.37	0.90
1:0:1701:A:H4'	1:0:1702:U:H5''	1.54	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1088:A:O2'	1:0:1089:G:H5''	1.71	0.90
1:0:45:A:H2	1:0:115:U:H3	0.94	0.89
1:0:199:A:O2'	1:0:200:U:H5''	1.72	0.88
1:0:2506:A:O2'	1:0:2507:G:H8	1.56	0.87
1:0:289:G:N2	1:0:363:A:H2	1.74	0.86
1:0:288:A:H61	1:0:364:C:H42	1.19	0.86
1:0:506:G:H22	1:0:509:A:H5'	1.43	0.84
1:0:2717:C:H2'	1:0:2718:C:H5''	1.57	0.84
1:0:1835:U:H5	1:0:1840:A:N7	1.77	0.82
1:0:283:U:H3'	1:0:284:C:C6	2.14	0.82
1:0:817:G:H4'	1:0:818:A:OP1	1.80	0.82
1:0:795:G:N2	1:0:817:G:H2'	1.94	0.81
1:0:795:G:H2'	1:0:817:G:N2	1.94	0.81
1:0:1147:C:C2'	1:0:1148:C:H5''	2.10	0.81
1:0:1106:A:H8	1:0:1106:A:H5'	1.46	0.81
1:0:371:U:H2'	1:0:372:A:C8	2.17	0.81
1:0:2812:A:H2	1:0:2814:A:H62	1.25	0.80
1:0:2090:G:H2'	1:0:2091:G:C8	2.17	0.79
1:0:2316:G:H4'	1:0:2316:G:OP1	1.81	0.79
2:9:29:C:H2'	2:9:30:C:H5'	1.65	0.79
2:9:56:A:C2'	2:9:57:A:H5''	2.13	0.78
1:0:2251:G:H2'	1:0:2252:A:C8	2.18	0.78
1:0:281:U:H2'	1:0:282:C:O4'	1.84	0.78
1:0:485:A:N3	1:0:487:G:H5''	1.98	0.78
1:0:1590:A:N6	1:0:1605:G:H1'	1.99	0.78
1:0:1148:C:H5'	1:0:1148:C:H6	1.49	0.77
1:0:2506:A:HO2'	1:0:2507:G:H8	0.79	0.77
1:0:45:A:H2	1:0:115:U:N3	1.77	0.77
1:0:506:G:H22	1:0:509:A:C5'	1.97	0.77
1:0:1088:A:H4'	1:0:1089:G:OP1	1.85	0.77
2:9:39:U:H1'	2:9:44:A:H61	1.50	0.76
1:0:1149:U:H5''	1:0:1151:G:O4'	1.84	0.76
1:0:2878:U:H2'	1:0:2879:A:O4'	1.86	0.76
1:0:796:A:N6	1:0:817:G:H1'	2.01	0.76
1:0:877:G:H5'	1:0:878:G:OP1	1.86	0.73
1:0:2103:A:H62	1:0:2538:A:H2	1.37	0.73
1:0:1438:G:N2	1:0:1685:A:H8	1.86	0.73
1:0:139:C:H4'	1:0:140:G:H5'	1.71	0.72
1:0:2866:U:H4'	1:0:2867:G:H5'	1.71	0.72
2:9:28:U:H2'	2:9:29:C:C6	2.24	0.72
1:0:1669:A:H2'	1:0:1670:G:C8	2.25	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:39:U:H1'	2:9:44:A:N6	2.05	0.72
1:0:2586:U:H3	1:0:2592:G:H22	1.37	0.71
1:0:2765:C:H4'	4:B:298:GLY:CA	2.20	0.71
1:0:544:G:H2'	1:0:545:G:H5''	1.72	0.71
2:9:76:G:C3'	2:9:77:A:H5''	2.16	0.71
1:0:1589:G:N2	1:0:1605:G:H2'	2.04	0.71
1:0:2851:G:O2'	1:0:2852:A:H5'	1.90	0.71
1:0:1972:U:H2'	1:0:1973:A:H5'	1.71	0.71
1:0:2903:C:H5'	1:0:2903:C:H6	1.54	0.71
1:0:2717:C:O2'	1:0:2718:C:H5''	1.89	0.71
1:0:2909:G:O2'	1:0:2910:A:H5'	1.91	0.71
1:0:138:U:H6	1:0:140:G:H1	1.39	0.71
1:0:371:U:H2'	1:0:372:A:H8	1.54	0.70
1:0:2866:U:H1'	1:0:2891:A:C4	2.25	0.70
1:0:952:G:H4'	1:0:953:G:OP1	1.91	0.70
1:0:1441:G:O2'	1:0:1442:A:H5'	1.90	0.70
1:0:67:A:OP2	1:0:108:U:H5'	1.91	0.70
1:0:2505:G:O2'	1:0:2506:A:H5'	1.91	0.70
1:0:1523:G:H2'	1:0:1524:U:C6	2.26	0.70
1:0:1119:G:N2	1:0:1246:A:C2	2.57	0.69
1:0:1751:G:C2'	1:0:1752:G:H5''	2.22	0.69
1:0:326:G:N1	1:0:330:C:H5	1.83	0.69
1:0:1681:G:H4'	1:0:1682:A:C8	2.27	0.69
1:0:2827:A:H2'	1:0:2828:G:O4'	1.92	0.69
1:0:362:G:H2'	1:0:363:A:H8	1.57	0.69
1:0:1819:G:H2'	1:0:1820:G:H4'	1.74	0.69
1:0:1209:C:H2'	1:0:1210:G:H8	1.57	0.69
1:0:219:G:H3'	1:0:220:C:H5''	1.75	0.69
1:0:603:A:H4'	1:0:604:G:O5'	1.91	0.69
1:0:2321:A:O2'	1:0:2322:U:H3'	1.93	0.69
1:0:1641:A:H2'	1:0:1642:A:H5'	1.75	0.69
1:0:2238:A:O2'	1:0:2239:C:H5'	1.93	0.68
2:9:14:G:H5'	2:9:14:G:H8	1.58	0.68
1:0:855:U:H4'	1:0:856:G:O5'	1.91	0.68
1:0:2756:U:H3	1:0:2896:A:H2	1.41	0.68
1:0:95:A:H5''	1:0:96:A:H3'	1.74	0.68
1:0:1380:U:O2	1:0:1380:U:H2'	1.92	0.68
1:0:12:U:H2'	1:0:13:G:H5'	1.75	0.68
1:0:1590:A:H61	1:0:1605:G:H1'	1.58	0.68
1:0:2890:A:C8	1:0:2890:A:H5''	2.26	0.68
1:0:553:G:O2'	1:0:554:G:H5'	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1666:C:H2'	1:0:1667:A:H8	1.59	0.68
1:0:74:A:H2'	1:0:75:U:C6	2.28	0.68
1:0:1313:A:H5''	24:V:113:GLY:CA	2.23	0.67
1:0:1730:G:H5'	1:0:1731:C:C5	2.30	0.67
1:0:2250:G:H2'	1:0:2251:G:C8	2.29	0.67
1:0:162:C:H2'	1:0:163:U:H5'	1.76	0.67
1:0:284:C:H1'	1:0:285:A:OP2	1.94	0.67
1:0:1116:U:O2'	1:0:1118:A:H2	1.70	0.67
1:0:1561:U:H2'	1:0:1562:C:H6	1.60	0.67
2:9:49:G:O2'	2:9:50:G:H5'	1.95	0.67
1:0:545:G:H8	1:0:545:G:H5'	1.60	0.67
1:0:1118:A:H3'	1:0:1118:A:H8	1.60	0.67
1:0:1158:G:O2'	1:0:1159:G:H5'	1.95	0.67
1:0:2251:G:H2'	1:0:2252:A:H8	1.58	0.66
1:0:1684:A:O2'	1:0:1685:A:H5''	1.94	0.66
1:0:681:G:H4'	1:0:682:A:O5'	1.95	0.66
1:0:337:A:H2	1:0:1314:U:O2'	1.76	0.66
1:0:544:G:C2'	1:0:545:G:H5''	2.26	0.66
1:0:285:A:N6	1:0:367:G:H1'	2.11	0.66
1:0:1667:A:H2'	1:0:1668:U:C6	2.31	0.66
1:0:1701:A:H5''	1:0:1702:U:H3'	1.77	0.66
1:0:960:G:H2'	1:0:960:G:N3	2.11	0.66
1:0:1130:U:H2'	1:0:1131:G:O4'	1.96	0.65
1:0:1106:A:C8	1:0:1106:A:H5'	2.29	0.65
1:0:1448:A:H5'	1:0:1507:C:OP1	1.96	0.65
1:0:289:G:O2'	1:0:290:C:H5'	1.96	0.65
1:0:2894:C:O2'	1:0:2895:C:H5'	1.97	0.65
1:0:95:A:C5'	1:0:96:A:H3'	2.27	0.65
1:0:1613:C:H2'	1:0:1614:G:O4'	1.96	0.65
1:0:285:A:H62	1:0:367:G:H1'	1.61	0.64
2:9:29:C:C2'	2:9:30:C:H5'	2.26	0.64
1:0:601:G:O2'	1:0:602:A:H5'	1.96	0.64
1:0:2670:G:O2'	1:0:2671:U:H5'	1.97	0.64
1:0:10:U:H1'	1:0:532:A:H62	1.63	0.64
1:0:2598:U:H5''	10:H:36:GLY:CA	2.28	0.64
1:0:1579:C:H2'	1:0:1580:A:C8	2.33	0.64
1:0:1355:A:OP1	1:0:1355:A:H4'	1.98	0.64
1:0:2253:G:H2'	1:0:2254:G:H8	1.63	0.64
1:0:1438:G:N2	1:0:1684:A:HO2'	1.95	0.64
1:0:1217:G:H2'	1:0:1218:U:C6	2.33	0.64
1:0:1766:U:O2	1:0:1778:A:H5'	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:420:U:H2'	1:0:421:C:C6	2.33	0.64
1:0:1947:G:H2'	1:0:1948:G:H8	1.62	0.64
1:0:1778:A:H2'	1:0:1779:A:H5'	1.79	0.64
2:9:13:A:O2'	2:9:14:G:H5''	1.98	0.63
2:9:25:G:O2'	2:9:26:C:H5'	1.98	0.63
1:0:1118:A:H3'	1:0:1118:A:C8	2.32	0.63
1:0:350:C:O2'	1:0:351:G:H5'	1.99	0.63
1:0:362:G:H2'	1:0:363:A:C8	2.33	0.63
1:0:372:A:H2'	1:0:373:G:H8	1.64	0.63
1:0:2908:A:H2'	1:0:2909:G:O4'	1.98	0.63
1:0:1947:G:H2'	1:0:1948:G:C8	2.34	0.63
1:0:349:U:O2'	1:0:350:C:H5'	1.98	0.63
1:0:582:C:H2'	1:0:583:G:H8	1.64	0.63
1:0:795:G:H1'	1:0:818:A:N6	2.14	0.63
2:9:107:C:H2'	2:9:108:C:C6	2.34	0.63
1:0:646:G:H2'	1:0:647:U:C6	2.34	0.62
1:0:432:G:O2'	1:0:433:C:H5'	1.99	0.62
1:0:1438:G:N2	1:0:1684:A:O2'	2.31	0.62
1:0:538:C:H5''	1:0:539:G:C8	2.34	0.62
1:0:1525:G:H5'	1:0:1526:A:OP2	1.99	0.62
2:9:92:G:H2'	2:9:93:A:C8	2.33	0.62
2:9:55:U:H4'	2:9:56:A:O5'	1.99	0.62
1:0:2849:U:O2'	1:0:2850:C:OP2	2.17	0.62
1:0:1211:G:O2'	1:0:1212:C:H5'	1.98	0.62
1:0:2266:A:H2'	1:0:2267:G:C8	2.35	0.62
1:0:613:C:H2'	1:0:614:U:H6	1.64	0.62
1:0:2289:G:H21	1:0:2291:A:H2	1.47	0.62
1:0:2387:U:H2'	1:0:2388:C:C6	2.35	0.62
1:0:1450:C:O2'	1:0:1493:A:H2'	1.99	0.62
1:0:1474:C:H6	1:0:1474:C:H5'	1.65	0.62
1:0:2591:C:H2'	1:0:2592:G:O4'	1.99	0.62
2:9:20:G:O2'	2:9:21:G:H5'	1.99	0.62
1:0:702:G:O2'	1:0:703:G:H5'	2.00	0.62
1:0:999:C:H2'	1:0:1000:C:C6	2.35	0.61
1:0:2316:G:C4'	1:0:2316:G:OP1	2.47	0.61
1:0:671:A:O2'	1:0:672:G:H2'	2.00	0.61
1:0:625:U:H5''	1:0:1044:C:N4	2.15	0.61
1:0:2502:C:C2'	1:0:2503:A:H5'	2.30	0.61
2:9:22:G:O3'	2:9:23:U:H4'	2.01	0.61
1:0:1741:U:H5'	1:0:1742:A:OP1	2.01	0.61
1:0:968:G:O2'	1:0:969:G:H5'	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2504:A:H2'	1:0:2505:G:O4'	2.01	0.61
1:0:283:U:C5	1:0:284:C:N4	2.68	0.61
1:0:2533:C:H5'	1:0:2533:C:H6	1.66	0.61
1:0:1120:U:H5'	1:0:1121:G:OP2	2.00	0.61
1:0:283:U:H3'	1:0:284:C:C5	2.35	0.60
1:0:1477:C:H5'	1:0:1868:G:C5'	2.31	0.60
1:0:1714:C:O2'	1:0:1715:C:H5'	2.00	0.60
1:0:1149:U:O2'	1:0:1150:A:OP2	2.15	0.60
1:0:255:A:H2'	1:0:256:C:C6	2.36	0.60
1:0:796:A:H62	1:0:817:G:H1'	1.64	0.60
1:0:2506:A:O2'	1:0:2507:G:C8	2.40	0.60
1:0:1528:A:H2'	1:0:1529:G:O4'	2.01	0.60
1:0:1377:C:H6	1:0:1377:C:H5'	1.66	0.60
1:0:1856:C:O2'	1:0:1857:A:OP2	2.19	0.60
1:0:2112:A:H2'	1:0:2113:G:C8	2.37	0.59
1:0:2240:U:O2'	1:0:2241:C:H5'	2.02	0.59
1:0:256:C:H2'	1:0:257:G:O4'	2.03	0.59
1:0:283:U:H5''	1:0:284:C:OP2	2.02	0.59
2:9:91:C:H2'	2:9:92:G:O4'	2.03	0.59
1:0:1636:G:O2'	1:0:1637:A:H5'	2.02	0.59
1:0:1557:G:O2'	1:0:1558:C:H5'	2.02	0.59
1:0:367:G:O2'	1:0:368:C:O5'	2.16	0.59
1:0:2488:A:H61	1:0:2534:C:H42	1.50	0.59
1:0:795:G:C2'	1:0:817:G:N2	2.64	0.59
1:0:372:A:H2'	1:0:373:G:C8	2.38	0.59
1:0:599:G:O2'	1:0:600:G:H5'	2.03	0.59
1:0:2900:G:H2'	1:0:2901:C:O4'	2.02	0.59
1:0:1506:U:H6	1:0:1506:U:H5'	1.67	0.59
1:0:2507:G:H2'	1:0:2510:C:H42	1.67	0.59
1:0:1964:U:H2'	1:0:1965:C:C6	2.38	0.59
1:0:1342:C:O2'	1:0:1343:C:H5'	2.03	0.59
1:0:1515:A:H2'	1:0:1516:C:C6	2.38	0.59
1:0:290:C:O2'	1:0:291:C:H5'	2.03	0.59
1:0:820:G:H4'	1:0:856:G:H5'	1.84	0.59
1:0:74:A:H2'	1:0:75:U:H6	1.67	0.59
1:0:2361:A:H2'	1:0:2362:A:C8	2.37	0.59
1:0:219:G:OP2	1:0:220:C:H5''	2.03	0.58
1:0:1280:A:H3'	1:0:1280:A:OP1	2.03	0.58
1:0:63:U:O2'	1:0:64:G:H5'	2.02	0.58
1:0:279:C:O2'	1:0:280:C:H5'	2.03	0.58
1:0:514:G:OP1	1:0:514:G:H3'	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2697:A:H2'	1:0:2698:G:O4'	2.03	0.58
1:0:945:U:H2'	1:0:946:C:H6	1.69	0.58
2:9:28:U:H5''	2:9:28:U:H6	1.68	0.58
1:0:1730:G:H5'	1:0:1731:C:C6	2.38	0.58
1:0:2635:A:O2'	1:0:2636:C:H5'	2.03	0.58
1:0:1701:A:H4'	1:0:1702:U:C5'	2.30	0.58
1:0:1579:C:H2'	1:0:1580:A:H8	1.68	0.58
1:0:1804:A:H2'	1:0:1805:G:C8	2.39	0.58
1:0:2907:C:H2'	1:0:2908:A:O4'	2.04	0.58
1:0:1064:U:H2'	1:0:1065:G:C8	2.39	0.58
1:0:2866:U:H4'	1:0:2867:G:C5'	2.32	0.58
1:0:1497:G:H4'	1:0:1627:G:O2'	2.03	0.58
1:0:282:C:O2'	1:0:283:U:H4'	2.03	0.58
1:0:2679:G:H2'	1:0:2681:A:OP2	2.03	0.58
1:0:2819:C:H2'	1:0:2820:A:C8	2.38	0.58
1:0:803:C:O2'	1:0:804:C:H5'	2.03	0.58
1:0:574:C:O2'	1:0:575:G:H5'	2.03	0.58
1:0:945:U:H2'	1:0:946:C:C6	2.38	0.58
2:9:22:G:O3'	2:9:23:U:C4'	2.52	0.58
1:0:2780:C:H2'	1:0:2781:U:C6	2.38	0.58
1:0:795:G:C2'	1:0:817:G:H22	2.08	0.57
4:B:36:PRO:CA	4:B:167:GLY:CA	2.82	0.57
1:0:1522:A:O2'	1:0:1523:G:H5'	2.05	0.57
1:0:1477:C:O2'	1:0:1478:U:H5'	2.03	0.57
1:0:1805:G:H2'	1:0:1806:G:H8	1.68	0.57
1:0:703:G:O2'	1:0:704:C:H5'	2.04	0.57
1:0:2699:A:H2'	1:0:2700:G:O4'	2.05	0.57
1:0:195:C:H2'	1:0:196:G:H5'	1.84	0.57
1:0:1667:A:H2'	1:0:1668:U:H6	1.68	0.57
1:0:561:G:H2'	1:0:562:A:H8	1.67	0.57
2:9:14:G:H5'	2:9:14:G:C8	2.39	0.57
1:0:1313:A:OP1	24:V:113:GLY:CA	2.53	0.57
1:0:2526:C:O2'	1:0:2527:U:H5'	2.05	0.57
1:0:2748:G:O2'	1:0:2749:U:OP2	2.20	0.57
1:0:807:A:H2'	1:0:808:A:O4'	2.03	0.57
1:0:1147:C:H2'	1:0:1148:C:C5'	2.26	0.57
1:0:1562:C:H3'	1:0:1563:G:C8	2.40	0.57
2:9:26:C:O2'	2:9:27:C:H5'	2.05	0.57
2:9:29:C:H2'	2:9:30:C:C5'	2.34	0.57
1:0:1304:U:H2'	1:0:1305:C:C6	2.40	0.57
1:0:1214:G:HO2'	1:0:1215:A:H8	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1333:U:H2'	1:0:1334:C:C6	2.40	0.56
1:0:660:A:H4'	1:0:661:G:O5'	2.04	0.56
1:0:396:U:O2'	1:0:418:C:H4'	2.05	0.56
1:0:598:C:H2'	1:0:599:G:H8	1.70	0.56
1:0:2812:A:C2	1:0:2814:A:N6	2.69	0.56
1:0:1438:G:H21	1:0:1685:A:H8	1.52	0.56
1:0:1556:G:O2'	1:0:1557:G:H5'	2.05	0.56
1:0:1577:U:O2'	1:0:1578:C:H5'	2.05	0.56
1:0:1950:G:HO2'	1:0:1951:G:C5'	2.18	0.56
1:0:566:A:H2'	1:0:567:U:O4'	2.06	0.56
1:0:2825:C:H4'	1:0:2826:G:O5'	2.05	0.56
1:0:2414:A:H2'	1:0:2415:A:C8	2.40	0.56
1:0:1056:U:H2'	1:0:1057:A:O4'	2.05	0.56
1:0:1682:A:H2	1:0:1696:U:N3	1.89	0.56
1:0:326:G:O2'	1:0:327:A:H5'	2.05	0.56
1:0:281:U:O2'	1:0:282:C:H5'	2.05	0.56
1:0:1586:G:O2'	1:0:1587:U:H5'	2.06	0.56
1:0:2814:A:H3'	1:0:2814:A:OP2	2.05	0.56
1:0:1641:A:C2'	1:0:1642:A:H5'	2.35	0.56
1:0:1666:C:H2'	1:0:1667:A:C8	2.41	0.56
1:0:1555:G:O2'	1:0:1556:G:P	2.64	0.56
1:0:1214:G:H4'	1:0:1215:A:OP1	2.06	0.56
1:0:1735:C:O2'	1:0:1736:A:H5'	2.06	0.56
1:0:560:C:O2'	1:0:561:G:H5'	2.06	0.55
1:0:2468:A:H4'	1:0:2469:A:OP1	2.06	0.55
1:0:1250:C:O2'	1:0:1251:C:H5'	2.05	0.55
1:0:1072:G:O2'	1:0:1073:A:H8	1.89	0.55
1:0:1523:G:C6	1:0:1524:U:O4	2.60	0.55
1:0:1210:G:O2'	1:0:1211:G:H5'	2.06	0.55
2:9:59:C:H2'	2:9:60:C:C6	2.40	0.55
1:0:37:A:H2'	1:0:38:G:H8	1.70	0.55
1:0:1289:C:O2'	1:0:1290:G:H5'	2.07	0.55
1:0:1438:G:N2	1:0:1685:A:C8	2.73	0.55
1:0:1515:A:H2'	1:0:1516:C:H6	1.69	0.55
1:0:303:C:O2'	1:0:304:G:H5'	2.06	0.55
1:0:684:G:H2'	1:0:685:C:C6	2.41	0.55
1:0:1450:C:H4'	1:0:1451:C:OP2	2.06	0.55
1:0:1697:G:O2'	1:0:1698:U:H5'	2.05	0.55
1:0:137:U:H2'	1:0:139:C:C5	2.41	0.55
1:0:138:U:H6	1:0:140:G:N1	2.03	0.55
1:0:1909:A:H2'	1:0:1910:A:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2072:G:C6	1:0:2533:C:H1'	2.42	0.55
1:0:1495:C:H2'	1:0:1496:G:C8	2.42	0.55
1:0:1014:A:H2'	1:0:1015:C:H5'	1.88	0.55
1:0:817:G:O2'	1:0:818:A:H8	1.90	0.54
1:0:370:G:O2'	1:0:371:U:H5'	2.07	0.54
1:0:2692:G:H8	1:0:2693:U:C5	2.25	0.54
1:0:2250:G:H2'	1:0:2251:G:H8	1.72	0.54
1:0:2237:G:H1'	1:0:2238:A:C8	2.42	0.54
1:0:1450:C:O2'	1:0:1494:A:H5'	2.07	0.54
2:9:103:A:H2'	2:9:104:A:H8	1.71	0.54
1:0:2016:U:H2'	1:0:2017:U:C6	2.42	0.54
1:0:1761:U:H2'	1:0:1762:C:C6	2.42	0.54
1:0:2237:G:O2'	1:0:2238:A:C8	2.60	0.54
1:0:1804:A:H2'	1:0:1805:G:H8	1.71	0.54
1:0:1123:A:C2	1:0:1129:C:H4'	2.43	0.54
1:0:1367:A:H2'	1:0:1368:U:O4'	2.08	0.54
1:0:2769:C:H2'	1:0:2770:G:O4'	2.07	0.54
1:0:2795:C:O2'	1:0:2796:U:H5'	2.08	0.54
1:0:1088:A:H1'	1:0:1260:G:H21	1.72	0.54
1:0:2718:C:H6	1:0:2718:C:H5'	1.73	0.54
2:9:2:U:O5'	2:9:3:A:H5'	2.07	0.54
1:0:1730:G:C6	23:U:18:ARG:CA	2.90	0.54
1:0:2291:A:C8	1:0:2309:C:H5'	2.42	0.54
1:0:2717:C:H2'	1:0:2718:C:C5'	2.32	0.54
1:0:1741:U:O2'	1:0:2723:G:H4'	2.08	0.54
1:0:889:C:H2'	1:0:890:C:C6	2.43	0.54
1:0:344:C:H2'	1:0:345:G:O4'	2.08	0.54
1:0:1965:C:H6	1:0:1965:C:O5'	1.90	0.53
1:0:2681:A:N6	1:0:2714:U:H4'	2.22	0.53
1:0:37:A:H2'	1:0:38:G:C8	2.43	0.53
1:0:88:G:H2'	1:0:89:G:C8	2.43	0.53
1:0:1423:C:O2'	1:0:1424:A:H5'	2.08	0.53
1:0:597:A:O2'	1:0:598:C:H5'	2.09	0.53
1:0:1603:A:H5'	1:0:1605:G:O4'	2.07	0.53
1:0:1220:U:H2'	1:0:1221:G:H8	1.73	0.53
1:0:1327:G:N2	1:0:1329:A:H3'	2.23	0.53
1:0:1790:C:H2'	1:0:1791:U:H6	1.72	0.53
1:0:2463:A:O2'	1:0:2464:C:OP1	2.23	0.53
1:0:1972:U:C2'	1:0:1973:A:H5'	2.37	0.53
1:0:695:C:H2'	1:0:696:C:C6	2.43	0.53
1:0:2912:C:H2'	1:0:2913:A:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1933:G:O2'	1:0:1934:A:H5'	2.08	0.53
1:0:2051:G:O2'	1:0:2052:U:H5'	2.08	0.53
1:0:367:G:H4'	1:0:368:C:OP1	2.07	0.53
1:0:1925:G:O2'	1:0:1926:G:H5'	2.09	0.53
1:0:881:C:OP1	1:0:883:U:H5	1.90	0.53
1:0:1245:C:O5'	1:0:1245:C:H6	1.90	0.53
1:0:1118:A:C8	1:0:1118:A:C3'	2.92	0.53
1:0:2250:G:N2	1:0:2251:G:H1'	2.22	0.53
1:0:1218:U:H2'	1:0:1219:U:C6	2.44	0.53
1:0:1477:C:H5'	1:0:1868:G:H5''	1.90	0.53
1:0:790:A:H2'	1:0:791:A:O4'	2.09	0.53
1:0:1116:U:O2'	1:0:1118:A:C2	2.46	0.53
1:0:646:G:H2'	1:0:647:U:H6	1.73	0.53
1:0:187:A:H3'	1:0:188:C:C6	2.43	0.53
1:0:413:G:H2'	1:0:414:C:C6	2.44	0.53
1:0:820:G:H5'	1:0:821:U:H5'	1.90	0.53
1:0:2866:U:O2'	1:0:2867:G:P	2.67	0.52
1:0:2692:G:C8	1:0:2693:U:H5	2.26	0.52
1:0:873:G:H21	1:0:876:A:H62	1.56	0.52
1:0:204:A:C2'	1:0:205:U:H5'	2.39	0.52
1:0:282:C:H1'	1:0:368:C:H42	1.68	0.52
1:0:1471:A:H2'	1:0:1472:C:C6	2.43	0.52
1:0:1098:A:H2'	1:0:1099:G:O4'	2.10	0.52
1:0:2858:U:H2'	1:0:2859:C:C6	2.44	0.52
1:0:282:C:O2'	1:0:283:U:C4'	2.57	0.52
1:0:1588:G:C6	1:0:1589:G:N1	2.77	0.52
2:9:23:U:H3	2:9:54:A:H5''	1.74	0.52
1:0:1333:U:H2'	1:0:1334:C:H6	1.74	0.52
1:0:236:A:H4'	1:0:237:G:OP1	2.10	0.52
1:0:1117:A:N1	1:0:1244:U:H2'	2.23	0.52
1:0:503:G:H2'	1:0:504:G:H8	1.74	0.52
1:0:737:A:H2'	1:0:738:G:O4'	2.10	0.52
1:0:666:A:H2'	1:0:667:C:O4'	2.09	0.52
1:0:280:C:O2'	1:0:281:U:H5'	2.10	0.52
1:0:484:A:N1	1:0:506:G:H4'	2.24	0.52
1:0:1589:G:H22	1:0:1605:G:H2'	1.73	0.52
1:0:1950:G:O2'	1:0:1951:G:O5'	2.23	0.52
1:0:1398:G:H2'	1:0:1399:A:C8	2.44	0.52
1:0:282:C:H2'	1:0:283:U:O4'	2.09	0.52
1:0:1835:U:C5	1:0:1840:A:N7	2.69	0.52
1:0:2909:G:O2'	1:0:2910:A:C5'	2.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1309:U:H2'	1:0:1310:U:C5'	2.40	0.52
1:0:2472:C:O2'	1:0:2634:G:H4'	2.10	0.52
1:0:2768:A:C2'	1:0:2769:C:O4'	2.51	0.52
1:0:1132:A:N6	1:0:1229:C:H2'	2.24	0.52
1:0:817:G:O2'	1:0:818:A:C8	2.62	0.52
1:0:1591:A:H4'	1:0:1592:G:O5'	2.09	0.52
1:0:2345:A:OP1	1:0:2346:C:H5	1.92	0.52
1:0:1066:U:H2'	1:0:1067:A:C8	2.45	0.52
1:0:2597:U:H2'	1:0:2598:U:H5'	1.91	0.52
2:9:107:C:H2'	2:9:108:C:H6	1.75	0.52
1:0:2727:A:H2'	1:0:2728:C:H5'	1.92	0.51
1:0:2906:A:H5'	1:0:2907:C:O4'	2.10	0.51
1:0:1561:U:H2'	1:0:1562:C:C6	2.44	0.51
1:0:1060:C:H2'	1:0:1061:C:H6	1.75	0.51
1:0:249:G:O2'	1:0:250:C:H5'	2.11	0.51
1:0:2791:U:H1'	1:0:2792:A:H5''	1.92	0.51
1:0:289:G:N2	1:0:363:A:C2	2.61	0.51
1:0:612:U:H2'	1:0:613:C:C6	2.45	0.51
1:0:1616:A:H2'	1:0:1618:G:C8	2.46	0.51
1:0:2667:G:O2'	1:0:2668:G:H5'	2.10	0.51
1:0:842:C:O2	1:0:1693:A:H2'	2.11	0.51
1:0:2509:A:OP2	1:0:2510:C:H5	1.92	0.51
1:0:2445:U:H2'	1:0:2446:G:C8	2.46	0.51
1:0:272:A:C2	1:0:369:G:H5''	2.46	0.51
2:9:106:C:O2'	2:9:107:C:H5'	2.11	0.51
1:0:1042:U:O2'	1:0:1043:C:H5'	2.10	0.51
1:0:289:G:N1	1:0:363:A:C2	2.77	0.51
1:0:581:G:O2'	1:0:582:C:H5'	2.11	0.51
1:0:1804:A:O2'	1:0:1805:G:H5'	2.10	0.51
1:0:1790:C:H2'	1:0:1791:U:C6	2.45	0.51
1:0:1099:G:OP1	2:9:87:U:H2'	2.11	0.51
1:0:1008:C:H2'	1:0:1009:U:C6	2.45	0.51
2:9:114:G:H2'	2:9:115:C:C6	2.46	0.51
1:0:559:U:O2'	1:0:560:C:H5'	2.10	0.51
1:0:1217:G:H2'	1:0:1218:U:H6	1.75	0.51
1:0:255:A:H2'	1:0:256:C:H6	1.73	0.51
2:9:64:C:C2'	2:9:65:A:H5'	2.41	0.51
1:0:1909:A:N1	1:0:2128:G:H1'	2.26	0.51
1:0:2242:U:O2'	1:0:2243:C:O5'	2.29	0.51
1:0:1386:G:O2'	1:0:1387:G:H5'	2.11	0.51
1:0:834:G:H3'	1:0:835:U:H4'	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2564:G:OP2	1:0:2565:C:H5'	2.11	0.50
1:0:939:A:H4'	1:0:940:G:O5'	2.11	0.50
1:0:1132:A:H2'	1:0:1133:A:C8	2.46	0.50
1:0:1072:G:O2'	1:0:1073:A:P	2.69	0.50
1:0:941:G:O2'	1:0:942:U:H5'	2.12	0.50
1:0:1006:A:H2'	1:0:1007:A:C8	2.47	0.50
1:0:553:G:C2'	1:0:554:G:H5'	2.42	0.50
2:9:103:A:O2'	2:9:104:A:H5'	2.10	0.50
1:0:2348:C:O2'	1:0:2349:G:H5'	2.11	0.50
1:0:2766:A:O2'	1:0:2767:C:H5'	2.11	0.50
1:0:2064:U:H5'	1:0:2652:U:O3'	2.12	0.50
1:0:2578:G:H5'	1:0:2578:G:H8	1.76	0.50
1:0:291:C:H2'	1:0:292:G:O4'	2.12	0.50
1:0:2300:A:H4'	1:0:2301:A:O5'	2.12	0.50
1:0:1730:G:H4'	1:0:1731:C:O5'	2.12	0.50
1:0:555:U:H6	1:0:555:U:OP2	1.95	0.50
1:0:1072:G:H1'	1:0:1088:A:N6	2.27	0.50
1:0:485:A:O2'	1:0:487:G:H5'	2.11	0.50
1:0:1342:C:C2'	1:0:1343:C:H5'	2.41	0.50
1:0:2133:U:H4'	1:0:2134:G:H5'	1.93	0.50
2:9:52:A:O2'	2:9:53:G:H5'	2.12	0.50
1:0:848:C:H2'	1:0:849:C:C6	2.46	0.50
1:0:2756:U:N3	1:0:2896:A:H2	2.09	0.49
2:9:25:G:H3'	2:9:25:G:OP1	2.12	0.49
1:0:2515:C:C2'	1:0:2516:G:H5'	2.43	0.49
1:0:1380:U:O2	1:0:1380:U:C2'	2.60	0.49
1:0:195:C:C2'	1:0:196:G:H5'	2.42	0.49
1:0:2726:U:O2	1:0:2749:U:O5'	2.30	0.49
1:0:2242:U:O2'	1:0:2243:C:P	2.69	0.49
1:0:2502:C:H2'	1:0:2503:A:H5'	1.93	0.49
1:0:969:G:H2'	1:0:970:U:C6	2.48	0.49
1:0:2681:A:C6	1:0:2714:U:H4'	2.48	0.49
1:0:10:U:O2'	1:0:11:A:P	2.69	0.49
1:0:2290:U:H4'	1:0:2291:A:OP1	2.12	0.49
1:0:496:G:H4'	1:0:497:A:OP1	2.12	0.49
2:9:42:C:H5'	2:9:43:G:OP2	2.12	0.49
1:0:1887:U:H2'	1:0:1888:C:C6	2.48	0.49
1:0:2656:G:O2'	1:0:2657:G:H5'	2.12	0.49
1:0:284:C:H1'	1:0:285:A:P	2.52	0.49
1:0:2765:C:H2'	1:0:2766:A:C8	2.48	0.49
1:0:604:G:H4'	1:0:605:C:O5'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2381:C:H2'	1:0:2382:A:C8	2.48	0.49
1:0:2903:C:O2'	1:0:2904:U:H5'	2.12	0.49
1:0:629:A:H2'	1:0:630:A:O4'	2.13	0.49
1:0:1461:U:H2'	1:0:1462:C:C6	2.48	0.49
1:0:44:G:H21	1:0:45:A:H62	1.60	0.49
2:9:102:G:O2'	2:9:103:A:H5'	2.13	0.49
1:0:1309:U:C2'	1:0:1310:U:H5'	2.42	0.49
1:0:939:A:O2'	1:0:940:G:OP2	2.30	0.49
1:0:639:A:H2'	1:0:640:G:C8	2.47	0.49
1:0:1477:C:C5'	1:0:1868:G:H5''	2.43	0.49
1:0:199:A:C2'	1:0:200:U:H5''	2.43	0.49
1:0:2782:G:O6	1:0:2790:C:H5''	2.13	0.49
2:9:103:A:H2'	2:9:104:A:C8	2.48	0.49
1:0:2242:U:O2'	1:0:2243:C:C6	2.63	0.49
1:0:1511:U:O2'	1:0:1512:G:H5'	2.13	0.49
1:0:2842:G:H2'	1:0:2843:A:H5'	1.95	0.49
1:0:2011:A:H4'	1:0:2012:U:O5'	2.13	0.49
1:0:2912:C:O2'	1:0:2913:A:H5'	2.12	0.48
1:0:2883:A:H2'	1:0:2884:G:O4'	2.13	0.48
1:0:1946:C:H2'	1:0:1971:G:C8	2.47	0.48
1:0:1072:G:O2'	1:0:1073:A:C8	2.66	0.48
1:0:1669:A:H2'	1:0:1670:G:H8	1.72	0.48
1:0:2279:G:N2	1:0:2463:A:H1'	2.28	0.48
1:0:2329:C:O2'	1:0:2330:U:H5'	2.12	0.48
1:0:2804:C:H2'	1:0:2805:A:O4'	2.12	0.48
1:0:907:A:H2'	1:0:908:A:H8	1.77	0.48
1:0:322:G:O2'	1:0:323:C:H5'	2.14	0.48
1:0:887:G:H2'	1:0:888:U:C6	2.48	0.48
1:0:2266:A:H2'	1:0:2267:G:H8	1.79	0.48
1:0:1568:G:O2'	1:0:1569:U:H5'	2.12	0.48
1:0:2473:U:O3'	1:0:2474:A:H3'	2.14	0.48
1:0:1000:C:H2'	1:0:1001:U:O4'	2.13	0.48
1:0:1140:C:O2'	1:0:1141:U:H5'	2.14	0.48
1:0:352:A:H2'	1:0:353:G:C8	2.49	0.48
1:0:2103:A:N7	1:0:2538:A:N1	2.62	0.48
1:0:1209:C:O2'	1:0:1210:G:H5'	2.12	0.48
2:9:108:C:O2'	2:9:109:G:H5'	2.14	0.48
1:0:1214:G:O2'	1:0:1215:A:H8	1.96	0.48
1:0:1657:A:H2'	1:0:1658:A:C8	2.49	0.48
1:0:1425:G:O2'	1:0:1426:C:H5'	2.13	0.48
1:0:1257:C:H2'	1:0:1258:G:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1624:A:O2'	1:0:1625:U:P	2.71	0.48
1:0:2387:U:H2'	1:0:2388:C:H6	1.77	0.48
1:0:197:C:OP2	1:0:198:A:H8	1.97	0.48
1:0:1950:G:O2'	1:0:1951:G:P	2.71	0.48
1:0:1329:A:H2'	1:0:1330:A:C8	2.48	0.48
1:0:938:G:HO2'	1:0:939:A:H8	1.54	0.48
1:0:1773:G:N2	1:0:1774:G:C8	2.82	0.48
1:0:1120:U:H5''	1:0:1120:U:C6	2.48	0.48
1:0:1503:U:H2'	1:0:1504:A:O4'	2.13	0.48
1:0:1662:C:H2'	1:0:1663:G:O4'	2.14	0.48
1:0:2886:C:O2'	1:0:2887:G:H5'	2.13	0.48
1:0:598:C:O2'	1:0:599:G:H5'	2.13	0.48
1:0:162:C:C2'	1:0:163:U:H5'	2.43	0.48
1:0:1805:G:H2'	1:0:1806:G:C8	2.47	0.48
1:0:555:U:OP2	1:0:555:U:C6	2.67	0.48
1:0:353:G:O2'	1:0:354:A:H5'	2.14	0.48
1:0:440:C:H2'	1:0:441:A:C8	2.48	0.48
1:0:2074:A:H4'	1:0:2075:G:OP1	2.13	0.48
1:0:557:C:O2'	1:0:558:C:H5'	2.14	0.48
1:0:1307:A:H2'	1:0:1308:A:C8	2.49	0.48
1:0:1153:C:O2'	1:0:1154:A:H5'	2.14	0.48
1:0:116:G:H5'	1:0:129:A:H2'	1.94	0.48
1:0:284:C:H6	1:0:284:C:OP2	1.95	0.47
1:0:2252:A:H2'	1:0:2253:G:O4'	2.14	0.47
1:0:12:U:C2'	1:0:13:G:H5'	2.43	0.47
1:0:1463:A:H2'	1:0:1464:U:C6	2.48	0.47
1:0:2353:A:H4'	1:0:2354:A:O5'	2.14	0.47
1:0:544:G:H2'	1:0:545:G:C5'	2.44	0.47
1:0:2264:A:H2'	1:0:2265:U:C6	2.48	0.47
1:0:2257:G:H4'	1:0:2259:C:C2	2.49	0.47
1:0:2381:C:H2'	1:0:2382:A:H8	1.79	0.47
1:0:958:G:H2'	1:0:959:C:C6	2.49	0.47
1:0:2836:G:H4'	1:0:2837:U:OP1	2.14	0.47
1:0:1119:G:N2	1:0:1246:A:N1	2.62	0.47
2:9:3:A:N7	2:9:25:G:N2	2.62	0.47
1:0:2692:G:H8	1:0:2693:U:H5	1.61	0.47
1:0:393:G:O2'	1:0:394:G:H5'	2.15	0.47
1:0:613:C:H2'	1:0:614:U:C6	2.48	0.47
1:0:2748:G:H4'	1:0:2749:U:H5'	1.96	0.47
1:0:2372:A:H2'	1:0:2373:U:C6	2.50	0.47
1:0:2320:U:H4'	1:0:2321:A:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1791:U:O2'	1:0:1792:C:H5'	2.13	0.47
1:0:2842:G:C2'	1:0:2843:A:H5'	2.45	0.47
1:0:2885:A:H2'	1:0:2886:C:H6	1.78	0.47
1:0:2385:G:H2'	1:0:2386:U:C6	2.50	0.47
1:0:795:G:H21	1:0:817:G:H2'	1.78	0.47
1:0:952:G:N3	1:0:2302:A:H2'	2.30	0.47
1:0:2238:A:C2'	1:0:2239:C:H5'	2.45	0.47
1:0:2697:A:H2'	1:0:2698:G:C8	2.50	0.47
1:0:2415:A:H2'	1:0:2416:G:H5'	1.95	0.47
1:0:1865:A:H2'	1:0:1866:A:C8	2.50	0.47
1:0:425:U:O2'	1:0:426:G:H5'	2.15	0.47
1:0:817:G:HO2'	1:0:818:A:H8	1.49	0.47
1:0:506:G:H22	1:0:509:A:H5''	1.80	0.47
1:0:136:C:H2'	1:0:137:U:O4'	2.14	0.47
1:0:1948:G:O2'	1:0:1949:G:H5'	2.14	0.47
1:0:940:G:O2'	1:0:941:G:H5'	2.15	0.47
2:9:96:C:H2'	2:9:97:U:C6	2.50	0.47
1:0:2326:U:H2'	1:0:2327:A:C8	2.49	0.47
1:0:35:U:H2'	1:0:36:C:C6	2.49	0.47
1:0:101:C:O2'	1:0:102:A:H5'	2.13	0.47
1:0:2672:C:H2'	1:0:2673:U:H6	1.79	0.47
1:0:1160:G:H21	1:0:1207:A:H62	1.63	0.47
1:0:1355:A:OP1	1:0:1355:A:C4'	2.63	0.47
1:0:1605:G:H5''	1:0:1605:G:C8	2.50	0.47
1:0:1730:G:C5'	1:0:1731:C:C6	2.97	0.47
1:0:637:C:H2'	1:0:638:C:C6	2.50	0.47
1:0:2897:C:O2'	1:0:2898:G:H5'	2.15	0.47
1:0:1127:C:OP1	1:0:1128:U:H5	1.96	0.47
1:0:2511:A:H5'	1:0:2511:A:H8	1.80	0.47
1:0:1447:U:H3'	1:0:1506:U:O2	2.14	0.47
1:0:197:C:OP2	1:0:198:A:C8	2.68	0.47
1:0:2255:A:O2'	1:0:2256:G:H5'	2.14	0.47
1:0:2350:G:O2'	1:0:2351:C:H5'	2.14	0.47
1:0:1544:U:O2'	1:0:1545:C:H5'	2.15	0.47
1:0:2398:A:H2'	1:0:2399:G:O4'	2.14	0.47
1:0:1218:U:H2'	1:0:1219:U:H6	1.80	0.47
1:0:1015:C:H2'	1:0:1016:U:C6	2.50	0.47
1:0:1878:G:O2'	1:0:1879:U:OP2	2.32	0.47
1:0:550:C:O2'	1:0:551:A:H5'	2.14	0.47
1:0:438:C:O2'	1:0:439:A:OP1	2.30	0.46
1:0:284:C:C1'	1:0:285:A:OP2	2.61	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:508:A:H2'	1:0:509:A:H5''	1.96	0.46
1:0:506:G:N2	1:0:509:A:H5'	2.21	0.46
1:0:1603:A:H4'	1:0:1604:G:OP2	2.14	0.46
1:0:946:C:H2'	1:0:947:U:C6	2.51	0.46
1:0:1309:U:H2'	1:0:1310:U:H5'	1.96	0.46
1:0:90:A:H2'	1:0:91:G:O4'	2.14	0.46
1:0:1321:A:H2'	1:0:1322:G:C8	2.50	0.46
1:0:2005:G:H3'	1:0:2005:G:OP2	2.14	0.46
1:0:2129:U:H2'	1:0:2130:C:C6	2.50	0.46
1:0:1552:G:H2'	1:0:1553:C:C6	2.49	0.46
1:0:2589:U:H2'	1:0:2590:U:C6	2.50	0.46
1:0:1109:U:OP1	1:0:1110:G:H5''	2.15	0.46
1:0:681:G:O2'	1:0:682:A:OP2	2.29	0.46
1:0:293:A:O2'	1:0:294:C:H5'	2.16	0.46
1:0:2754:G:O2'	1:0:2755:G:H5'	2.15	0.46
1:0:1527:A:C2	1:0:1528:A:C5	3.03	0.46
1:0:2064:U:H5'	1:0:2652:U:H4'	1.98	0.46
1:0:702:G:HO2'	1:0:703:G:H5'	1.81	0.46
1:0:1496:G:H5'	1:0:1572:A:H1'	1.98	0.46
1:0:2004:U:O5'	1:0:2004:U:H6	1.99	0.46
1:0:999:C:O2'	1:0:1000:C:H5'	2.15	0.46
1:0:354:A:H2'	1:0:355:C:C6	2.51	0.46
1:0:657:G:H2'	1:0:658:C:C6	2.51	0.46
1:0:2105:C:H2'	1:0:2106:C:C6	2.51	0.46
1:0:1825:U:O2'	1:0:1826:C:H5'	2.16	0.46
2:9:76:G:H3'	2:9:77:A:C5'	2.21	0.46
1:0:2251:G:C6	1:0:2252:A:C6	3.04	0.46
1:0:1730:G:H5'	1:0:1731:C:H5	1.80	0.46
1:0:1947:G:N2	1:0:1966:U:C2	2.84	0.46
1:0:939:A:O2'	1:0:940:G:P	2.74	0.46
1:0:2073:G:OP2	1:0:2490:A:H5'	2.16	0.46
1:0:2430:A:N6	1:0:2460:A:H2	2.14	0.46
1:0:1345:A:H2'	1:0:1346:U:C6	2.51	0.46
1:0:18:C:H2'	1:0:19:U:C6	2.51	0.46
1:0:2000:G:O2'	1:0:2001:G:H5'	2.16	0.46
1:0:2866:U:O2'	1:0:2867:G:OP2	2.29	0.46
1:0:2911:C:O2'	1:0:2912:C:H5'	2.15	0.46
1:0:295:C:O2'	1:0:296:G:H5'	2.15	0.46
1:0:337:A:H2	1:0:1314:U:C2'	2.29	0.46
1:0:1450:C:C4'	1:0:1451:C:OP2	2.64	0.46
1:0:945:U:O2'	1:0:946:C:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2871:G:H2'	1:0:2872:U:C6	2.51	0.46
1:0:2575:C:H2'	1:0:2576:A:O4'	2.16	0.46
1:0:2772:G:O2'	1:0:2773:G:H5'	2.15	0.46
1:0:1114:A:H2'	1:0:1115:U:C6	2.51	0.46
1:0:1422:U:H2'	1:0:1423:C:C6	2.50	0.46
1:0:1114:A:H2'	1:0:1115:U:H6	1.80	0.46
1:0:1607:A:H2'	1:0:1608:G:O4'	2.15	0.46
1:0:168:C:O2'	1:0:169:A:H5'	2.16	0.46
1:0:2831:C:H2'	1:0:2832:C:H5'	1.96	0.46
1:0:279:C:H2'	1:0:280:C:H6	1.80	0.45
1:0:1586:G:H2'	1:0:1587:U:O4'	2.16	0.45
1:0:2819:C:H2'	1:0:2820:A:H8	1.81	0.45
1:0:2255:A:H2'	1:0:2256:G:O4'	2.16	0.45
1:0:2456:A:H2'	1:0:2457:U:C6	2.51	0.45
1:0:1080:C:O2'	1:0:1081:A:OP1	2.26	0.45
1:0:141:C:C2'	1:0:141:C:O2	2.63	0.45
1:0:1965:C:H2'	1:0:1966:U:C6	2.52	0.45
1:0:2781:U:O2'	1:0:2782:G:H5'	2.16	0.45
1:0:693:A:H2'	1:0:694:A:C8	2.51	0.45
1:0:204:A:O2'	1:0:205:U:H5'	2.16	0.45
1:0:296:G:O2'	1:0:297:U:H5'	2.16	0.45
1:0:2831:C:C2'	1:0:2832:C:H5'	2.46	0.45
1:0:2653:A:H2'	1:0:2654:C:C6	2.51	0.45
1:0:947:U:O2'	1:0:948:G:H5'	2.16	0.45
1:0:2416:G:H2'	1:0:2417:C:C6	2.52	0.45
1:0:2074:A:O2'	1:0:2075:G:P	2.75	0.45
1:0:1315:G:H4'	1:0:1316:G:OP2	2.17	0.45
1:0:747:G:H2'	1:0:748:C:C6	2.51	0.45
1:0:40:C:O2'	1:0:41:G:H5'	2.16	0.45
1:0:1573:A:H2'	1:0:1574:C:O4'	2.16	0.45
1:0:2776:A:H2'	1:0:2777:G:O4'	2.16	0.45
1:0:2871:G:H2'	1:0:2872:U:H6	1.81	0.45
1:0:2251:G:C2	1:0:2252:A:C4	3.05	0.45
1:0:582:C:H2'	1:0:583:G:C8	2.48	0.45
1:0:683:G:O2'	1:0:684:G:H5'	2.16	0.45
1:0:696:C:O2'	1:0:731:U:OP1	2.34	0.45
1:0:549:A:O2'	1:0:550:C:H5'	2.16	0.45
1:0:2429:A:H2'	1:0:2430:A:C8	2.51	0.45
1:0:728:C:H2'	1:0:729:C:H6	1.81	0.45
1:0:1965:C:O2'	1:0:1966:U:H5'	2.16	0.45
1:0:2242:U:H4'	1:0:2243:C:OP1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2729:C:O2'	1:0:2730:G:H5'	2.17	0.45
1:0:274:G:O2'	1:0:275:G:H5'	2.17	0.45
1:0:2115:U:H2'	1:0:2116:U:C6	2.52	0.45
2:9:55:U:O2'	2:9:56:A:OP2	2.26	0.45
1:0:2890:A:C2'	1:0:2891:A:OP2	2.65	0.45
1:0:2765:C:H2'	1:0:2766:A:H8	1.82	0.45
1:0:219:G:O2'	1:0:220:C:P	2.75	0.45
1:0:2133:U:N3	1:0:2259:C:OP2	2.45	0.45
1:0:631:A:N3	1:0:2073:G:O2'	2.49	0.45
1:0:1535:G:H2'	1:0:1536:C:C6	2.52	0.45
1:0:1815:A:H2'	1:0:1816:C:O4'	2.17	0.45
1:0:2499:U:O2'	1:0:2500:C:H5'	2.16	0.45
1:0:1526:A:H1'	1:0:1527:A:N7	2.32	0.45
1:0:1730:G:C5'	1:0:1731:C:H6	2.29	0.45
1:0:695:C:H2'	1:0:696:C:H6	1.82	0.45
1:0:1978:A:O2'	1:0:1979:G:OP1	2.24	0.45
2:9:18:U:O2'	2:9:19:G:H5'	2.16	0.45
1:0:1928:C:H2'	1:0:1929:G:O4'	2.17	0.45
1:0:816:G:C6	1:0:817:G:N1	2.85	0.45
1:0:2506:A:O2'	1:0:2507:G:O5'	2.34	0.45
1:0:2112:A:H2'	1:0:2113:G:H8	1.79	0.45
1:0:248:A:H5'	1:0:249:G:OP2	2.17	0.45
2:9:95:C:O2'	2:9:96:C:H5'	2.17	0.45
1:0:1120:U:H6	1:0:1120:U:H5''	1.82	0.45
2:9:94:G:O2'	2:9:95:C:H5'	2.17	0.45
1:0:2672:C:O2'	1:0:2673:U:H5'	2.17	0.45
1:0:956:G:H2'	1:0:957:A:O4'	2.17	0.45
1:0:1406:A:H4'	1:0:1407:A:O5'	2.17	0.45
1:0:305:A:C5	1:0:329:A:C2	3.05	0.45
1:0:1283:G:O2'	1:0:1284:G:H5'	2.16	0.45
1:0:282:C:H3'	1:0:283:U:H5'	1.99	0.44
1:0:1116:U:H3	1:0:1246:A:H62	1.66	0.44
1:0:820:G:O2'	1:0:856:G:H4'	2.17	0.44
1:0:1327:G:C2	1:0:1329:A:H3'	2.53	0.44
1:0:2419:U:H5''	1:0:2420:G:H5'	1.99	0.44
1:0:1148:C:C5'	1:0:1148:C:H6	2.25	0.44
1:0:1118:A:H8	1:0:1119:G:H5''	1.83	0.44
1:0:219:G:HO2'	1:0:220:C:P	2.40	0.44
1:0:1496:G:H2'	1:0:1497:G:C8	2.52	0.44
1:0:638:C:H2'	1:0:639:A:C8	2.52	0.44
1:0:1882:C:O2'	1:0:2012:U:OP2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:438:C:O2'	1:0:439:A:P	2.75	0.44
1:0:2106:C:H2'	1:0:2107:U:C6	2.52	0.44
1:0:141:C:H2'	1:0:141:C:O2	2.17	0.44
1:0:1433:G:O2'	1:0:1434:A:H5'	2.18	0.44
2:9:71:C:O2'	2:9:72:C:H5'	2.17	0.44
1:0:790:A:H1'	1:0:1710:A:H2'	1.99	0.44
1:0:1006:A:N1	1:0:2311:A:H1'	2.31	0.44
1:0:2688:U:O2'	1:0:2689:A:H5'	2.17	0.44
1:0:419:A:H1'	1:0:1921:A:C2	2.53	0.44
1:0:1902:G:H2'	1:0:1903:U:C6	2.51	0.44
1:0:1930:A:H2'	1:0:1931:A:C8	2.52	0.44
1:0:920:C:H5''	1:0:921:G:O5'	2.17	0.44
1:0:1149:U:H4'	1:0:1150:A:H5''	1.98	0.44
1:0:1380:U:H5	1:0:2043:U:O2'	2.00	0.44
1:0:2388:C:O2'	1:0:2389:U:H5'	2.17	0.44
1:0:2515:C:H2'	1:0:2516:G:H5'	1.98	0.44
1:0:907:A:H2'	1:0:908:A:C8	2.51	0.44
1:0:383:A:H2'	1:0:384:G:O4'	2.18	0.44
1:0:140:G:H3'	1:0:140:G:H8	1.83	0.44
1:0:2563:U:H2'	1:0:2565:C:O5'	2.16	0.44
1:0:324:G:O2'	1:0:325:U:H5'	2.18	0.44
1:0:270:U:O2'	1:0:271:C:P	2.75	0.44
1:0:2279:G:C2	1:0:2463:A:H1'	2.53	0.44
2:9:52:A:C2'	2:9:53:G:H5'	2.48	0.44
2:9:35:C:H5'	2:9:36:C:OP2	2.18	0.44
1:0:319:A:H4'	1:0:338:C:C4	2.53	0.44
1:0:1587:U:C4	1:0:1588:G:C6	3.06	0.44
1:0:2256:G:O2'	1:0:2257:G:H5'	2.17	0.44
1:0:2885:A:H2'	1:0:2886:C:C6	2.52	0.44
1:0:766:A:O2'	1:0:767:A:H5''	2.18	0.44
1:0:2247:C:O2'	1:0:2248:C:H5'	2.18	0.44
1:0:45:A:H5'	1:0:45:A:C8	2.53	0.44
1:0:1517:U:O2'	1:0:1518:A:H5'	2.18	0.44
1:0:294:C:H2'	1:0:295:C:O4'	2.18	0.44
1:0:858:U:H2'	1:0:859:C:H6	1.82	0.44
1:0:212:A:O4'	1:0:214:U:C6	2.70	0.44
1:0:615:G:H2'	1:0:616:U:C6	2.52	0.44
1:0:2846:C:H2'	1:0:2847:G:H8	1.82	0.44
1:0:1589:G:N2	1:0:1605:G:C2'	2.80	0.44
1:0:95:A:H5''	1:0:96:A:C3'	2.45	0.44
1:0:243:A:H61	1:0:269:G:H1'	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:61:C:H2'	2:9:62:A:H8	1.83	0.44
1:0:1739:G:O2'	1:0:1740:U:H5'	2.18	0.44
1:0:105:G:O2'	1:0:106:A:H5'	2.18	0.44
1:0:219:G:H3'	1:0:220:C:C5'	2.45	0.43
1:0:1141:U:O2'	1:0:1142:C:H5'	2.18	0.43
1:0:2372:A:H2'	1:0:2373:U:H6	1.83	0.43
1:0:401:C:H2'	1:0:402:U:C6	2.52	0.43
1:0:283:U:H5	1:0:284:C:H41	1.66	0.43
1:0:1524:U:O2'	1:0:1525:G:P	2.76	0.43
1:0:1761:U:H2'	1:0:1762:C:H6	1.82	0.43
1:0:343:C:O2'	1:0:344:C:H5'	2.18	0.43
1:0:2074:A:O2'	1:0:2076:U:OP2	2.24	0.43
1:0:1878:G:O2'	1:0:1879:U:C6	2.66	0.43
1:0:2419:U:H5''	1:0:2420:G:C5'	2.48	0.43
1:0:1609:C:H2'	1:0:1610:G:H8	1.83	0.43
1:0:2312:G:C2'	1:0:2313:C:H5'	2.48	0.43
1:0:2793:A:H2'	1:0:2794:G:H5'	1.99	0.43
1:0:2781:U:C2'	1:0:2782:G:H5'	2.48	0.43
1:0:1950:G:H4'	1:0:1951:G:OP1	2.17	0.43
1:0:2859:C:O2'	1:0:2860:G:H5'	2.18	0.43
1:0:737:A:O2'	1:0:738:G:H5'	2.18	0.43
1:0:1399:A:H2'	1:0:1400:C:C6	2.54	0.43
1:0:1060:C:H2'	1:0:1061:C:C6	2.52	0.43
1:0:1643:C:O2'	1:0:1644:C:H5'	2.18	0.43
1:0:1246:A:O2'	1:0:1247:A:H3'	2.18	0.43
1:0:45:A:H5'	1:0:45:A:H8	1.83	0.43
1:0:140:G:C8	1:0:140:G:H3'	2.53	0.43
1:0:2780:C:H2'	1:0:2781:U:H6	1.82	0.43
1:0:875:A:H5'	1:0:876:A:C2	2.53	0.43
1:0:2330:U:H4'	1:0:2331:C:OP1	2.19	0.43
1:0:1968:A:H2'	1:0:1969:A:C8	2.53	0.43
1:0:735:C:C5	1:0:736:A:C5	3.06	0.43
1:0:2756:U:N3	1:0:2896:A:C2	2.71	0.43
1:0:204:A:H2'	1:0:205:U:H5'	2.01	0.43
1:0:2460:A:O2'	1:0:2461:U:O4'	2.36	0.43
1:0:706:G:HO2'	1:0:707:C:H6	1.67	0.43
1:0:1901:G:O2'	1:0:1902:G:H5'	2.18	0.43
1:0:2619:U:H2'	1:0:2620:U:C6	2.53	0.43
1:0:1850:U:H2'	1:0:1851:G:H8	1.82	0.43
1:0:95:A:H5'	1:0:96:A:H3'	1.99	0.43
2:9:59:C:H2'	2:9:60:C:H6	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:631:A:C6	1:0:2074:A:H5'	2.53	0.43
1:0:2312:G:H2'	1:0:2313:C:H5'	2.01	0.43
1:0:1768:C:H2'	1:0:1769:C:O4'	2.18	0.43
1:0:588:G:O2'	1:0:589:U:P	2.77	0.43
1:0:2694:A:C2	1:0:2702:A:C4	3.07	0.43
1:0:963:C:H2'	1:0:964:G:C8	2.54	0.43
1:0:1823:G:O2'	1:0:1824:C:H5'	2.18	0.43
1:0:1641:A:H2'	1:0:1642:A:C5'	2.46	0.43
1:0:1379:A:O2'	1:0:1380:U:H5''	2.19	0.43
1:0:2133:U:H4'	1:0:2134:G:C5'	2.48	0.43
1:0:728:C:H2'	1:0:729:C:C6	2.54	0.43
1:0:858:U:H2'	1:0:859:C:C6	2.53	0.43
1:0:1869:A:H2'	1:0:1870:C:O4'	2.19	0.43
1:0:2407:G:O2'	1:0:2408:A:H5'	2.18	0.43
1:0:485:A:H1'	1:0:486:A:H5'	2.00	0.43
1:0:1730:G:N3	1:0:1730:G:H2'	2.34	0.43
1:0:1496:G:H2'	1:0:1497:G:H8	1.83	0.43
1:0:2692:G:C8	1:0:2693:U:C5	3.02	0.43
2:9:52:A:H2'	2:9:53:G:O4'	2.19	0.43
1:0:2078:U:O2'	1:0:2079:G:H5'	2.19	0.43
2:9:117:G:H2'	2:9:118:C:C6	2.54	0.43
1:0:2838:A:H2'	1:0:2839:C:C6	2.54	0.43
1:0:288:A:N1	1:0:364:C:N3	2.67	0.43
1:0:1521:C:O2'	1:0:1522:A:H5'	2.19	0.43
1:0:1666:C:O2'	1:0:1667:A:H5'	2.19	0.43
1:0:2291:A:H5''	1:0:2292:C:C5'	2.49	0.43
1:0:1902:G:H2'	1:0:1903:U:O4'	2.18	0.43
1:0:2406:U:O2'	1:0:2407:G:H5'	2.19	0.43
1:0:1053:G:O2'	1:0:1054:G:H5'	2.19	0.43
1:0:364:C:H2'	1:0:365:G:O4'	2.18	0.42
1:0:2909:G:H2'	1:0:2910:A:H8	1.83	0.42
1:0:603:A:O2'	1:0:604:G:OP2	2.36	0.42
1:0:1518:A:H2'	1:0:1519:U:C6	2.54	0.42
1:0:807:A:N1	1:0:808:A:C2	2.87	0.42
1:0:1791:U:H2'	1:0:1792:C:C6	2.54	0.42
1:0:1887:U:H2'	1:0:1888:C:H6	1.83	0.42
1:0:2511:A:H5'	1:0:2511:A:C8	2.53	0.42
1:0:1363:G:H2'	1:0:1364:G:C8	2.54	0.42
1:0:2899:A:O2'	1:0:2900:G:H5'	2.19	0.42
1:0:2134:G:O6	1:0:2258:A:H5''	2.18	0.42
1:0:2430:A:N6	1:0:2460:A:C2	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:72:C:O2'	2:9:73:G:H5'	2.18	0.42
1:0:764:C:H2'	1:0:765:G:O4'	2.19	0.42
1:0:653:C:H2'	1:0:654:A:C8	2.54	0.42
1:0:2626:C:H2'	1:0:2627:G:C8	2.54	0.42
1:0:1894:C:N4	1:0:1939:U:H2'	2.34	0.42
1:0:23:G:H1'	1:0:520:A:N6	2.35	0.42
1:0:1369:A:H8	1:0:1369:A:OP1	2.01	0.42
1:0:846:A:O2'	1:0:847:C:H5'	2.19	0.42
1:0:1021:G:O2'	1:0:1022:A:H5'	2.18	0.42
1:0:369:G:C2	1:0:370:G:C8	3.08	0.42
1:0:1072:G:O2'	1:0:1073:A:OP2	2.34	0.42
1:0:2301:A:H5''	1:0:2302:A:H5'	2.01	0.42
1:0:947:U:H2'	1:0:948:G:C8	2.54	0.42
1:0:2748:G:H4'	1:0:2749:U:C5'	2.50	0.42
1:0:286:U:H2'	1:0:287:C:C6	2.54	0.42
1:0:598:C:C4	1:0:599:G:N7	2.87	0.42
1:0:1308:A:O2'	1:0:1309:U:H5'	2.20	0.42
1:0:2872:U:H2'	1:0:2873:C:H6	1.84	0.42
1:0:1594:C:O2'	1:0:1595:G:H5'	2.18	0.42
7:E:55:GLN:CA	7:E:56:PRO:CA	2.97	0.42
1:0:607:G:H2'	1:0:608:A:O4'	2.20	0.42
1:0:360:A:H2'	1:0:361:C:O4'	2.19	0.42
1:0:1092:A:H2'	1:0:1093:G:C8	2.54	0.42
1:0:1088:A:O2'	1:0:1089:G:C5'	2.57	0.42
1:0:67:A:H5''	1:0:68:U:H3'	2.02	0.42
1:0:1526:A:O4'	1:0:1527:A:C5	2.72	0.42
1:0:1495:C:H2'	1:0:1496:G:H8	1.83	0.42
1:0:1462:C:H2'	1:0:1463:A:C8	2.55	0.42
1:0:1569:U:H3'	1:0:1570:C:H5'	2.00	0.42
1:0:1142:C:O2'	1:0:1143:G:H5'	2.19	0.42
1:0:2885:A:O2'	1:0:2886:C:H5'	2.19	0.42
1:0:1545:C:H2'	1:0:1546:G:O4'	2.20	0.42
1:0:2847:G:O2'	1:0:2848:G:H5'	2.19	0.42
1:0:2335:C:H2'	1:0:2336:G:C8	2.55	0.42
1:0:119:A:H2'	1:0:120:A:H5''	2.02	0.42
1:0:2724:U:H2'	1:0:2725:G:O4'	2.19	0.42
1:0:2276:U:H2'	1:0:2277:U:C6	2.55	0.42
1:0:2415:A:C2'	1:0:2416:G:H5'	2.49	0.42
1:0:2563:U:O2'	1:0:2564:G:H3'	2.20	0.42
1:0:70:A:H4'	1:0:71:G:O5'	2.18	0.42
3:A:186:TRP:CA	3:A:187:PRO:CA	2.98	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:60:A:O2'	1:0:61:G:H5'	2.19	0.42
1:0:200:U:OP1	1:0:200:U:C6	2.73	0.42
1:0:2253:G:O2'	1:0:2254:G:H5'	2.20	0.42
1:0:1846:U:H2'	1:0:1847:A:C5	2.55	0.42
1:0:240:C:H5''	1:0:270:U:O4	2.20	0.42
2:9:3:A:H62	2:9:25:G:H1	1.66	0.42
1:0:1516:C:H2'	1:0:1517:U:C6	2.54	0.42
1:0:2004:U:H2'	1:0:2005:G:OP1	2.20	0.42
1:0:1850:U:H2'	1:0:1851:G:C8	2.54	0.42
1:0:333:G:O2'	1:0:334:G:H5'	2.20	0.42
1:0:1298:U:H2'	1:0:1299:G:C8	2.54	0.42
1:0:1798:C:O2	1:0:1798:C:H2'	2.19	0.42
1:0:850:U:H2'	1:0:851:C:O4'	2.19	0.42
2:9:56:A:C3'	2:9:57:A:H5''	2.50	0.42
1:0:1280:A:H8	1:0:1280:A:O5'	2.03	0.42
1:0:1805:G:O2'	1:0:1806:G:H5'	2.20	0.42
1:0:1626:A:H2'	1:0:1627:G:C5'	2.50	0.42
1:0:345:G:H2'	1:0:346:U:H6	1.85	0.42
1:0:1039:G:H2'	1:0:1040:A:O4'	2.20	0.42
1:0:594:C:O2'	1:0:595:U:H5'	2.20	0.42
1:0:811:C:H2'	1:0:812:A:C8	2.54	0.42
1:0:1457:U:O2'	1:0:1458:A:H5'	2.20	0.42
1:0:345:G:H2'	1:0:346:U:C6	2.55	0.42
1:0:2325:C:H2'	1:0:2326:U:C6	2.55	0.42
1:0:2326:U:H4'	1:0:2412:G:C4'	2.50	0.42
1:0:2627:G:H2'	1:0:2628:U:C6	2.54	0.42
1:0:778:C:H2'	1:0:779:U:O4'	2.20	0.42
1:0:375:G:C4	1:0:411:A:C6	3.08	0.42
1:0:1050:G:C6	1:0:1051:C:C4	3.08	0.42
1:0:1155:G:H2'	1:0:1156:C:C6	2.55	0.42
1:0:2025:G:O2'	1:0:2026:C:H5'	2.19	0.42
1:0:558:C:N3	1:0:600:G:C2	2.88	0.41
1:0:552:A:H3'	1:0:553:G:C5'	2.49	0.41
1:0:1735:C:H2'	1:0:1736:A:C8	2.54	0.41
1:0:2242:U:O2'	1:0:2243:C:H2'	2.19	0.41
1:0:1787:C:H4'	1:0:2883:A:O4'	2.20	0.41
1:0:1878:G:O2'	1:0:1879:U:P	2.76	0.41
1:0:2335:C:H2'	1:0:2336:G:H8	1.84	0.41
1:0:364:C:H2'	1:0:365:G:C8	2.54	0.41
1:0:2253:G:N3	1:0:2254:G:C8	2.88	0.41
1:0:433:C:O2'	1:0:434:U:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1555:G:H4'	1:0:1630:A:H2	1.85	0.41
1:0:2488:A:N6	1:0:2534:C:H42	2.16	0.41
1:0:2821:C:H2'	1:0:2822:C:C6	2.55	0.41
1:0:281:U:O2	1:0:369:G:C2	2.73	0.41
1:0:1150:A:H4'	1:0:1151:G:OP2	2.19	0.41
1:0:694:A:H2'	1:0:695:C:H5'	2.03	0.41
1:0:2258:A:H1'	1:0:2259:C:OP2	2.19	0.41
2:9:97:U:H2'	2:9:98:C:C6	2.55	0.41
1:0:243:A:H61	1:0:269:G:C1'	2.33	0.41
1:0:106:A:O2'	1:0:107:U:H5'	2.20	0.41
1:0:810:G:O2'	1:0:811:C:H5'	2.21	0.41
1:0:77:G:O2'	1:0:78:G:H5'	2.20	0.41
1:0:659:A:N3	1:0:746:A:C2	2.89	0.41
1:0:1427:A:H61	1:0:1440:U:H1'	1.84	0.41
1:0:1706:G:H1'	1:0:1712:A:H61	1.85	0.41
1:0:281:U:C2'	1:0:282:C:O4'	2.60	0.41
1:0:553:G:O4'	1:0:1325:G:H5'	2.20	0.41
1:0:2820:A:H2'	1:0:2821:C:C6	2.54	0.41
1:0:1020:A:H2'	1:0:1021:G:C8	2.55	0.41
1:0:1706:G:C6	1:0:1707:G:C6	3.08	0.41
1:0:2124:G:H2'	1:0:2125:G:H8	1.84	0.41
1:0:251:C:H2'	1:0:252:C:C6	2.56	0.41
1:0:1993:C:C4	1:0:1994:A:C6	3.08	0.41
1:0:2120:U:H2'	1:0:2121:G:O4'	2.21	0.41
1:0:578:C:O2	1:0:1112:G:H4'	2.20	0.41
1:0:2249:G:C2	1:0:2253:G:C6	3.09	0.41
2:9:39:U:H3'	2:9:40:C:H5''	2.02	0.41
1:0:877:G:C5'	1:0:878:G:OP1	2.65	0.41
1:0:95:A:H4'	1:0:96:A:O5'	2.20	0.41
1:0:2893:C:O2'	1:0:2894:C:H5'	2.20	0.41
1:0:1627:G:O2'	1:0:1628:G:H5'	2.20	0.41
1:0:1914:C:C2	1:0:1926:G:C2	3.08	0.41
1:0:2515:C:H2'	1:0:2516:G:C5'	2.50	0.41
1:0:2836:G:O2'	1:0:2837:U:P	2.78	0.41
1:0:23:G:C6	1:0:24:G:N1	2.89	0.41
2:9:76:G:C8	2:9:77:A:H2'	2.55	0.41
1:0:602:A:O2'	1:0:605:C:H4'	2.21	0.41
1:0:1064:U:H2'	1:0:1065:G:H8	1.85	0.41
1:0:1626:A:C2'	1:0:1627:G:H5'	2.50	0.41
1:0:2064:U:H2'	1:0:2065:C:C6	2.55	0.41
1:0:2845:G:O2'	1:0:2846:C:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:132:A:H2'	1:0:133:U:C6	2.55	0.41
1:0:569:A:H5''	1:0:587:A:N1	2.36	0.41
1:0:2640:U:H2'	1:0:2641:C:C6	2.56	0.41
1:0:1269:G:H2'	1:0:1270:U:C6	2.56	0.41
1:0:1029:U:H5'	1:0:1031:G:N7	2.36	0.41
1:0:289:G:C2	1:0:363:A:H2	2.34	0.41
1:0:355:C:O2'	1:0:356:C:H5'	2.21	0.41
1:0:2773:G:H22	1:0:2801:A:H2	1.69	0.41
1:0:1029:U:O2'	1:0:1273:C:OP1	2.30	0.41
1:0:1676:G:O2'	1:0:1677:U:H5'	2.20	0.41
1:0:526:U:H2'	1:0:527:U:C6	2.56	0.41
1:0:1538:C:O2'	1:0:1539:U:H5'	2.21	0.41
1:0:277:U:O2'	1:0:278:A:H5'	2.21	0.41
1:0:2238:A:C2	1:0:2239:C:C6	3.09	0.41
1:0:1665:G:O2'	1:0:1666:C:H5'	2.20	0.41
1:0:255:A:O2'	1:0:256:C:H5'	2.20	0.41
1:0:2004:U:C2'	1:0:2005:G:OP1	2.69	0.41
1:0:512:G:O3'	1:0:513:A:H8	2.04	0.41
1:0:523:C:H2'	1:0:524:A:C8	2.56	0.41
1:0:2757:A:H2'	1:0:2758:G:O4'	2.21	0.41
1:0:934:C:H2'	1:0:935:G:C8	2.56	0.41
1:0:1391:G:H2'	1:0:1392:A:H5'	2.01	0.41
1:0:1088:A:HO2'	1:0:1089:G:H5''	1.79	0.41
1:0:2823:G:O2'	1:0:2824:C:H5'	2.21	0.41
1:0:2824:C:O3'	1:0:2825:C:H6	2.04	0.41
1:0:1209:C:H2'	1:0:1210:G:C8	2.45	0.41
1:0:1964:U:O2'	1:0:1965:C:H5'	2.21	0.41
2:9:1:U:O2'	2:9:3:A:OP1	2.38	0.41
1:0:431:G:O2'	1:0:432:G:H5'	2.20	0.41
1:0:1555:G:O2'	1:0:1556:G:H8	2.03	0.41
1:0:24:G:N2	1:0:518:G:H1'	2.35	0.41
1:0:2336:G:O2'	1:0:2337:G:H5'	2.20	0.41
1:0:2135:A:O2'	1:0:2136:G:H5'	2.20	0.41
1:0:2880:A:H2'	1:0:2881:C:O4'	2.21	0.41
1:0:585:C:H2'	1:0:586:C:C6	2.56	0.41
1:0:627:G:H2'	1:0:2071:C:C4	2.56	0.41
1:0:1659:A:H2'	1:0:1660:G:O4'	2.21	0.41
1:0:2239:C:O2'	1:0:2240:U:H5'	2.21	0.41
1:0:1474:C:C6	1:0:1474:C:H5'	2.49	0.41
1:0:394:G:H2'	1:0:398:U:C6	2.56	0.41
1:0:2334:C:O2'	1:0:2335:C:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:282:C:C2'	1:0:283:U:C5'	2.99	0.40
1:0:2823:G:C5'	1:0:2827:A:H5'	2.51	0.40
1:0:2362:A:H2'	1:0:2363:G:C8	2.55	0.40
1:0:2445:U:H2'	1:0:2446:G:H8	1.84	0.40
1:0:1782:G:O2'	1:0:1783:A:H5'	2.21	0.40
1:0:1236:A:H2'	1:0:1237:U:O4'	2.20	0.40
1:0:272:A:N1	1:0:369:G:C5'	2.84	0.40
1:0:598:C:H2'	1:0:599:G:C8	2.52	0.40
1:0:482:G:H4'	1:0:508:A:N1	2.36	0.40
1:0:2825:C:C2	1:0:2826:G:C5	3.09	0.40
1:0:2597:U:C2'	1:0:2598:U:H5'	2.51	0.40
1:0:1555:G:HO2'	1:0:1556:G:P	2.44	0.40
1:0:934:C:H2'	1:0:935:G:H8	1.87	0.40
1:0:1453:G:H2'	1:0:1454:U:O4'	2.20	0.40
1:0:207:U:H2'	1:0:208:C:C6	2.56	0.40
1:0:10:U:C2'	1:0:11:A:OP2	2.69	0.40
1:0:194:A:C2'	1:0:195:C:H5'	2.52	0.40
1:0:735:C:C2'	1:0:736:A:H5'	2.50	0.40
1:0:2704:C:H2'	1:0:2705:U:O4'	2.21	0.40
1:0:270:U:O2'	1:0:271:C:OP2	2.33	0.40
1:0:284:C:H4'	1:0:285:A:C8	2.57	0.40
1:0:2265:U:H2'	1:0:2266:A:C8	2.56	0.40
1:0:946:C:H2'	1:0:947:U:H6	1.85	0.40
1:0:907:A:H4'	1:0:1328:A:C2	2.56	0.40
1:0:735:C:H2'	1:0:736:A:H5'	2.03	0.40
1:0:148:A:O2'	1:0:149:G:H5'	2.22	0.40
1:0:1796:A:H2'	1:0:1797:A:C8	2.57	0.40
1:0:189:A:H2'	1:0:190:G:O4'	2.22	0.40
1:0:271:C:H4'	1:0:272:A:O5'	2.22	0.40
1:0:2252:A:H2'	1:0:2253:G:H5'	2.04	0.40
1:0:2252:A:H2'	1:0:2253:G:C5'	2.51	0.40
1:0:140:G:C8	1:0:140:G:C3'	3.04	0.40
1:0:196:G:H1'	1:0:197:C:OP2	2.21	0.40
1:0:807:A:N1	1:0:808:A:N3	2.69	0.40
2:9:64:C:O2'	2:9:65:A:H5'	2.22	0.40
1:0:2797:C:O2'	1:0:2798:G:H5'	2.22	0.40
1:0:177:A:H2'	1:0:178:U:O4'	2.22	0.40
1:0:2750:G:H8	1:0:2750:G:O5'	2.05	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2697/2922 (92%)	334 (12%)	107 (3%)
2	9	122/122 (100%)	17 (13%)	5 (4%)
All	All	2819/3044 (92%)	351 (12%)	112 (3%)

All (351) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	11	A
1	0	31	C
1	0	60	A
1	0	67	A
1	0	70	A
1	0	71	G
1	0	87	C
1	0	95	A
1	0	96	A
1	0	114	A
1	0	115	U
1	0	116	G
1	0	120	A
1	0	139	C
1	0	141	C
1	0	142	G
1	0	151	A
1	0	166	A
1	0	169	A
1	0	186	A
1	0	192	A
1	0	196	G
1	0	197	C

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Mol	Chain	Res	Type
1	0	198	A
1	0	200	U
1	0	201	G
1	0	204	A
1	0	219	G
1	0	220	C
1	0	236	A
1	0	237	G
1	0	262	A
1	0	263	U
1	0	271	C
1	0	272	A
1	0	273	G
1	0	282	C
1	0	283	U
1	0	284	C
1	0	285	A
1	0	308	U
1	0	309	C
1	0	336	G
1	0	337	A
1	0	345	G
1	0	358	G
1	0	368	C
1	0	381	G
1	0	395	A
1	0	397	A
1	0	398	U
1	0	407	A
1	0	417	G
1	0	439	A
1	0	453	A
1	0	461	C
1	0	481	U
1	0	485	A
1	0	486	A
1	0	487	G
1	0	497	A
1	0	498	A
1	0	510	U
1	0	511	A
1	0	512	G

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Mol	Chain	Res	Type
1	0	514	G
1	0	515	C
1	0	537	G
1	0	538	C
1	0	539	G
1	0	545	G
1	0	548	U
1	0	549	A
1	0	553	G
1	0	554	G
1	0	555	U
1	0	588	G
1	0	600	G
1	0	601	G
1	0	604	G
1	0	620	A
1	0	632	A
1	0	660	A
1	0	682	A
1	0	688	A
1	0	699	C
1	0	700	A
1	0	701	U
1	0	714	U
1	0	759	C
1	0	777	U
1	0	809	G
1	0	817	G
1	0	818	A
1	0	821	U
1	0	835	U
1	0	840	U
1	0	856	G
1	0	857	A
1	0	858	U
1	0	868	G
1	0	869	G
1	0	875	A
1	0	877	G
1	0	878	G
1	0	885	G
1	0	895	A

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Mol	Chain	Res	Type
1	0	898	G
1	0	905	C
1	0	920	C
1	0	921	G
1	0	923	A
1	0	940	G
1	0	953	G
1	0	960	G
1	0	961	A
1	0	965	A
1	0	1006	A
1	0	1008	C
1	0	1029	U
1	0	1045	G
1	0	1059	G
1	0	1060	C
1	0	1072	G
1	0	1073	A
1	0	1081	A
1	0	1089	G
1	0	1106	A
1	0	1107	A
1	0	1108	G
1	0	1109	U
1	0	1110	G
1	0	1119	G
1	0	1124	A
1	0	1126	C
1	0	1127	C
1	0	1130	U
1	0	1137	G
1	0	1148	C
1	0	1149	U
1	0	1150	A
1	0	1160	G
1	0	1215	A
1	0	1216	G
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1245	C
1	0	1279	U

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Mol	Chain	Res	Type
1	0	1287	A
1	0	1289	C
1	0	1309	U
1	0	1310	U
1	0	1330	A
1	0	1331	A
1	0	1341	A
1	0	1342	C
1	0	1353	C
1	0	1355	A
1	0	1360	C
1	0	1369	A
1	0	1370	G
1	0	1377	C
1	0	1380	U
1	0	1407	A
1	0	1409	G
1	0	1449	G
1	0	1451	C
1	0	1474	C
1	0	1485	A
1	0	1488	U
1	0	1492	A
1	0	1506	U
1	0	1507	C
1	0	1524	U
1	0	1525	G
1	0	1526	A
1	0	1527	A
1	0	1528	A
1	0	1535	G
1	0	1556	G
1	0	1563	G
1	0	1564	C
1	0	1592	G
1	0	1593	C
1	0	1604	G
1	0	1605	G
1	0	1606	A
1	0	1624	A
1	0	1625	U
1	0	1626	A

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Mol	Chain	Res	Type
1	0	1633	C
1	0	1634	G
1	0	1656	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1691	A
1	0	1692	C
1	0	1693	A
1	0	1699	C
1	0	1700	C
1	0	1701	A
1	0	1710	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1731	C
1	0	1732	A
1	0	1752	G
1	0	1774	G
1	0	1778	A
1	0	1798	C
1	0	1819	G
1	0	1820	G
1	0	1829	A
1	0	1835	U
1	0	1836	A
1	0	1853	C
1	0	1854	C
1	0	1857	A
1	0	1879	U
1	0	1907	U
1	0	1908	G
1	0	1919	A
1	0	1942	A
1	0	1951	G
1	0	1971	G
1	0	1973	A
1	0	1979	G
1	0	1980	U
1	0	1981	A
1	0	1982	C

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Mol	Chain	Res	Type
1	0	1996	U
1	0	2005	G
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G
1	0	2033	G
1	0	2034	U
1	0	2063	U
1	0	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2075	G
1	0	2077	C
1	0	2083	A
1	0	2084	C
1	0	2091	G
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2110	G
1	0	2238	A
1	0	2243	C
1	0	2258	A
1	0	2259	C
1	0	2271	G
1	0	2272	G
1	0	2283	G
1	0	2284	G
1	0	2291	A
1	0	2316	G
1	0	2317	C
1	0	2322	U
1	0	2354	A
1	0	2361	A
1	0	2369	A
1	0	2370	A
1	0	2371	G
1	0	2379	G
1	0	2396	C
1	0	2422	U

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Mol	Chain	Res	Type
1	0	2427	C
1	0	2428	G
1	0	2462	G
1	0	2464	C
1	0	2466	G
1	0	2467	A
1	0	2469	A
1	0	2476	C
1	0	2482	G
1	0	2483	A
1	0	2507	G
1	0	2509	A
1	0	2511	A
1	0	2527	U
1	0	2533	C
1	0	2537	G
1	0	2538	A
1	0	2541	U
1	0	2553	A
1	0	2564	G
1	0	2589	U
1	0	2601	A
1	0	2602	G
1	0	2608	C
1	0	2613	G
1	0	2617	G
1	0	2634	G
1	0	2637	A
1	0	2638	G
1	0	2649	A
1	0	2681	A
1	0	2682	C
1	0	2714	U
1	0	2715	G
1	0	2719	A
1	0	2726	U
1	0	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2762	C
1	0	2768	A

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Mol	Chain	Res	Type
1	0	2783	A
1	0	2786	G
1	0	2792	A
1	0	2800	A
1	0	2811	A
1	0	2814	A
1	0	2815	G
1	0	2826	G
1	0	2827	A
1	0	2837	U
1	0	2850	C
1	0	2867	G
1	0	2876	G
1	0	2890	A
1	0	2891	A
1	0	2903	C
1	0	2914	A
2	9	2	U
2	9	4	G
2	9	14	G
2	9	23	U
2	9	24	U
2	9	25	G
2	9	29	C
2	9	34	A
2	9	41	C
2	9	43	G
2	9	56	A
2	9	57	A
2	9	66	G
2	9	77	A
2	9	87	U
2	9	114	G
2	9	122	C

All (112) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	10	U
1	0	95	A
1	0	115	U
1	0	191	A

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Mol	Chain	Res	Type
1	0	196	G
1	0	199	A
1	0	270	U
1	0	282	C
1	0	283	U
1	0	284	C
1	0	338	C
1	0	367	G
1	0	394	G
1	0	438	C
1	0	452	G
1	0	480	C
1	0	485	A
1	0	496	G
1	0	514	G
1	0	548	U
1	0	554	G
1	0	600	G
1	0	603	A
1	0	681	G
1	0	699	C
1	0	713	U
1	0	817	G
1	0	855	U
1	0	857	A
1	0	877	G
1	0	894	A
1	0	904	U
1	0	939	A
1	0	952	G
1	0	1044	C
1	0	1059	G
1	0	1072	G
1	0	1080	C
1	0	1088	A
1	0	1106	A
1	0	1108	G
1	0	1126	C
1	0	1137	G
1	0	1149	U
1	0	1214	G
1	0	1237	U

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Mol	Chain	Res	Type
1	0	1309	U
1	0	1329	A
1	0	1352	A
1	0	1369	A
1	0	1379	A
1	0	1406	A
1	0	1408	U
1	0	1448	A
1	0	1450	C
1	0	1506	U
1	0	1534	C
1	0	1591	A
1	0	1603	A
1	0	1605	G
1	0	1624	A
1	0	1683	G
1	0	1690	C
1	0	1699	C
1	0	1835	U
1	0	1853	C
1	0	1856	C
1	0	1907	U
1	0	1950	G
1	0	1978	A
1	0	1979	G
1	0	1981	A
1	0	2011	A
1	0	2074	A
1	0	2076	U
1	0	2083	A
1	0	2090	G
1	0	2242	U
1	0	2258	A
1	0	2282	U
1	0	2283	G
1	0	2290	U
1	0	2316	G
1	0	2321	A
1	0	2370	A
1	0	2395	A
1	0	2421	G
1	0	2427	C

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Mol	Chain	Res	Type
1	0	2463	A
1	0	2465	A
1	0	2467	A
1	0	2468	A
1	0	2482	G
1	0	2526	C
1	0	2616	G
1	0	2692	G
1	0	2714	U
1	0	2718	C
1	0	2748	G
1	0	2749	U
1	0	2791	U
1	0	2813	A
1	0	2814	A
1	0	2836	G
1	0	2849	U
1	0	2866	U
1	0	2890	A
2	9	1	U
2	9	3	A
2	9	28	U
2	9	55	U
2	9	65	A

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.



There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	0	2706/2922 (92%)	2.87	2156 (79%) 0 0	12, 29, 60, 87	0
2	9	122/122 (100%)	3.77	114 (93%) 0 0	22, 42, 67, 106	0
3	A	237/239 (99%)	8.12	236 (99%) 0 0	16, 35, 64, 78	0
4	B	337/337 (100%)	8.74	335 (99%) 0 0	18, 42, 65, 72	0
5	C	246/246 (100%)	8.36	245 (99%) 0 0	14, 31, 54, 76	0
6	D	140/176 (79%)	7.87	139 (99%) 0 0	49, 80, 90, 94	0
7	E	118/119 (99%)	5.77	116 (98%) 0 0	32, 51, 69, 72	0
8	F	157/157 (100%)	9.68	157 (100%) 0 0	33, 56, 81, 93	0
9	G	142/145 (97%)	8.81	142 (100%) 0 0	22, 38, 58, 68	0
10	H	132/132 (100%)	7.59	132 (100%) 0 0	20, 37, 55, 63	0
11	I	194/194 (100%)	10.95	194 (100%) 0 0	22, 36, 54, 66	0
12	J	143/164 (87%)	9.10	143 (100%) 0 0	21, 46, 73, 85	0
13	K	186/186 (100%)	8.86	186 (100%) 0 0	40, 65, 83, 87	0
14	L	115/115 (100%)	6.64	115 (100%) 0 0	28, 38, 55, 65	0
15	M	143/148 (96%)	9.10	143 (100%) 0 0	24, 38, 49, 58	0
16	N	95/95 (100%)	9.85	95 (100%) 0 0	20, 32, 53, 65	0
17	O	150/154 (97%)	9.44	150 (100%) 0 0	19, 31, 49, 58	0
18	P	78/84 (92%)	6.86	78 (100%) 0 0	27, 38, 63, 65	0
19	Q	119/119 (100%)	6.31	119 (100%) 0 0	28, 39, 56, 67	0
20	R	53/66 (80%)	6.98	53 (100%) 0 0	29, 43, 55, 58	0
21	S	65/70 (92%)	6.91	65 (100%) 0 0	35, 51, 77, 83	0
22	T	154/154 (100%)	8.60	154 (100%) 0 0	24, 35, 51, 56	0
23	U	85/91 (93%)	10.03	85 (100%) 0 0	29, 47, 73, 80	0
24	V	143/143 (100%)	7.67	142 (99%) 0 0	18, 33, 62, 76	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	W	73/73 (100%)	8.47	73 (100%) 0 0	36, 43, 57, 62	0
26	X	56/56 (100%)	13.37	56 (100%) 0 0	17, 27, 35, 41	0
27	Y	31/49 (63%)	9.74	31 (100%) 0 0	25, 33, 55, 61	0
28	Z	92/92 (100%)	8.48	92 (100%) 0 0	23, 40, 51, 63	0
29	1	172/177 (97%)	6.37	171 (99%) 0 0	31, 48, 64, 71	0
All	All	6484/6825 (95%)	6.04	5917 (91%) 0 0	12, 36, 70, 106	0

All (5917) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	D	86	THR	34.8
6	D	63	ILE	30.5
12	J	81	VAL	29.8
13	K	166	ALA	26.3
6	D	106	PHE	25.9
6	D	49	PRO	25.1
13	K	162	ASP	25.0
4	B	156	LYS	24.8
6	D	170	TYR	23.5
8	F	99	ASP	23.5
12	J	143	THR	22.2
26	X	1	THR	21.1
3	A	37	VAL	20.9
5	C	61	PHE	20.9
6	D	22	VAL	20.7
26	X	5	THR	20.2
8	F	98	GLY	20.0
17	O	133	ALA	19.5
6	D	93	LEU	19.4
4	B	1	PRO	18.9
8	F	101	MET	18.8
4	B	116	GLU	18.7
5	C	63	SER	18.6
23	U	80	GLU	18.5
26	X	2	GLY	18.5
26	X	19	CYS	18.4
23	U	23	HIS	18.3
17	O	11	ASP	18.2
26	X	37	CYS	18.0
11	I	77	PRO	17.8

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Mol	Chain	Res	Type	RSRZ
26	X	34	CYS	17.8
5	C	62	GLY	17.6
6	D	158	ASN	17.6
12	J	83	GLU	17.6
4	B	241	TRP	17.5
24	V	116	LYS	17.4
11	I	80	GLY	17.3
26	X	22	CYS	17.3
5	C	60	SER	17.3
26	X	50	TRP	17.2
5	C	80	VAL	17.2
12	J	14	GLY	17.2
4	B	167	GLY	17.2
5	C	56	THR	17.2
12	J	24	ALA	17.0
4	B	231	TRP	17.0
17	O	130	MET	17.0
8	F	100	GLY	16.9
5	C	68	ALA	16.8
26	X	6	PRO	16.8
5	C	64	GLY	16.8
26	X	52	SER	16.8
12	J	43	HIS	16.7
26	X	48	TYR	16.6
10	H	61	THR	16.6
23	U	81	GLY	16.6
17	O	136	TRP	16.6
26	X	54	ALA	16.6
17	O	129	ALA	16.5
5	C	77	ALA	16.5
11	I	87	MET	16.5
23	U	19	ALA	16.5
11	I	187	ALA	16.3
17	O	135	ALA	16.3
5	C	70	VAL	16.3
26	X	33	VAL	16.2
23	U	21	PRO	16.2
26	X	3	ALA	16.2
12	J	26	HIS	16.1
17	O	134	SER	16.0
12	J	42	ASN	16.0
5	C	67	GLN	16.0

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Mol	Chain	Res	Type	RSRZ
11	I	189	PHE	15.9
11	I	99	TRP	15.8
9	G	63	ILE	15.7
17	O	131	GLY	15.7
8	F	10	ILE	15.6
12	J	18	HIS	15.6
8	F	103	ALA	15.6
11	I	88	VAL	15.6
4	B	244	SER	15.6
11	I	118	TYR	15.5
11	I	75	THR	15.4
11	I	78	ASN	15.4
11	I	183	PRO	15.4
11	I	119	TRP	15.3
11	I	193	ARG	15.3
4	B	243	PRO	15.3
12	J	33	ALA	15.2
17	O	132	ARG	15.2
23	U	22	ASN	15.1
12	J	15	GLY	15.1
11	I	157	VAL	15.1
4	B	256	THR	15.0
17	O	66	VAL	15.0
23	U	17	ALA	15.0
5	C	54	LEU	14.9
5	C	84	VAL	14.9
11	I	158	TYR	14.9
23	U	16	ASP	14.8
11	I	37	VAL	14.8
12	J	23	GLY	14.8
23	U	14	LEU	14.8
5	C	58	ALA	14.8
5	C	69	HIS	14.8
8	F	104	PRO	14.7
12	J	151	ALA	14.7
11	I	36	ALA	14.6
17	O	124	GLY	14.6
3	A	90	PRO	14.6
12	J	40	PHE	14.6
5	C	71	PRO	14.5
5	C	65	ARG	14.5
11	I	89	ASN	14.5

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Mol	Chain	Res	Type	RSRZ
26	X	4	GLY	14.5
11	I	185	LEU	14.5
5	C	245	GLU	14.5
5	C	89	ALA	14.5
12	J	12	THR	14.5
4	B	300	VAL	14.5
4	B	235	ILE	14.4
4	B	301	PRO	14.4
5	C	51	TYR	14.4
5	C	75	GLY	14.4
26	X	35	SER	14.4
8	F	102	ARG	14.3
5	C	52	ALA	14.3
4	B	250	VAL	14.3
4	B	219	VAL	14.3
11	I	184	SER	14.3
5	C	81	PRO	14.3
5	C	73	LEU	14.2
11	I	149	TRP	14.2
11	I	97	LEU	14.2
9	G	65	ASN	14.2
12	J	38	HIS	14.2
8	F	105	PHE	14.2
11	I	35	PRO	14.2
26	X	8	GLN	14.2
8	F	96	GLN	14.1
4	B	242	ASN	14.1
11	I	38	VAL	14.1
16	N	1	PRO	14.1
11	I	117	SER	14.1
26	X	7	SER	14.1
26	X	29	THR	14.0
9	G	64	GLY	14.0
11	I	194	ARG	14.0
12	J	20	ASN	14.0
24	V	53	LEU	13.9
5	C	46	TYR	13.9
28	Z	46	ILE	13.9
4	B	248	SER	13.9
26	X	27	TYR	13.9
4	B	227	ALA	13.9
28	Z	35	TRP	13.9

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Mol	Chain	Res	Type	RSRZ
5	C	83	ALA	13.8
4	B	246	VAL	13.8
12	J	36	ASP	13.8
3	A	13	THR	13.8
4	B	249	THR	13.8
23	U	15	ARG	13.7
4	B	210	THR	13.7
6	D	94	ALA	13.7
11	I	126	TYR	13.7
11	I	74	ALA	13.7
4	B	240	PRO	13.7
17	O	127	PRO	13.7
29	1	16	ASP	13.7
3	A	14	SER	13.7
12	J	17	SER	13.7
26	X	39	PHE	13.6
24	V	51	GLY	13.6
5	C	74	ASP	13.6
26	X	14	THR	13.6
28	Z	56	PRO	13.6
26	X	13	THR	13.6
8	F	12	PRO	13.6
12	J	46	LEU	13.6
24	V	4	GLY	13.6
23	U	64	ALA	13.5
4	B	251	PRO	13.5
26	X	26	SER	13.5
4	B	238	LEU	13.5
9	G	69	TYR	13.5
9	G	70	PHE	13.5
11	I	168	ALA	13.4
10	H	109	LEU	13.4
11	I	188	ASN	13.4
16	N	2	SER	13.4
11	I	115	LEU	13.4
4	B	15	PRO	13.4
11	I	155	GLY	13.4
4	B	214	VAL	13.3
11	I	72	ARG	13.3
24	V	60	ILE	13.3
11	I	153	THR	13.3
26	X	51	GLN	13.3

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Mol	Chain	Res	Type	RSRZ
5	C	79	ARG	13.3
12	J	31	GLY	13.3
11	I	164	ALA	13.3
13	K	165	ALA	13.2
8	F	9	SER	13.2
5	C	94	THR	13.2
13	K	65	ASP	13.2
11	I	81	ARG	13.2
11	I	92	PRO	13.2
11	I	114	VAL	13.2
29	1	86	VAL	13.1
5	C	92	PRO	13.1
4	B	217	TRP	13.1
5	C	48	SER	13.1
11	I	100	ILE	13.1
8	F	8	ASN	13.1
3	A	196	ALA	13.1
26	X	43	ALA	13.1
12	J	41	HIS	13.0
16	N	3	SER	13.0
17	O	125	ARG	13.0
23	U	26	ALA	13.0
4	B	170	VAL	13.0
12	J	29	GLY	13.0
17	O	128	ARG	13.0
26	X	36	SER	13.0
11	I	161	LEU	13.0
4	B	138	ASP	13.0
11	I	86	MET	13.0
3	A	15	THR	13.0
12	J	25	GLY	13.0
23	U	12	ILE	13.0
12	J	13	HIS	13.0
3	A	179	MET	13.0
23	U	29	ALA	13.0
8	F	54	VAL	12.9
4	B	4	SER	12.9
8	F	6	PHE	12.9
9	G	67	ASN	12.9
23	U	13	PRO	12.9
1	0	1951	G	12.9
28	Z	57	GLY	12.9

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Mol	Chain	Res	Type	RSRZ
24	V	46	TRP	12.9
26	X	9	GLY	12.9
5	C	90	HIS	12.8
24	V	42	VAL	12.8
11	I	171	LEU	12.8
26	X	56	GLU	12.8
12	J	28	GLY	12.8
12	J	35	ARG	12.8
15	M	62	ALA	12.8
17	O	137	ASN	12.8
11	I	109	TYR	12.8
27	Y	7	THR	12.8
3	A	194	MET	12.8
8	F	117	GLY	12.8
3	A	172	ALA	12.8
9	G	145	TRP	12.7
17	O	80	TYR	12.7
15	M	113	THR	12.7
11	I	163	SER	12.7
4	B	13	PHE	12.7
11	I	70	GLY	12.7
24	V	27	GLY	12.7
4	B	67	THR	12.7
1	0	2237	G	12.7
4	B	237	ASN	12.7
18	P	2	TRP	12.7
11	I	16	TYR	12.7
25	W	57	CYS	12.7
26	X	38	GLY	12.7
11	I	192	LYS	12.7
12	J	1	THR	12.6
15	M	116	SER	12.6
4	B	298	GLY	12.6
11	I	76	ARG	12.6
13	K	50	LEU	12.6
26	X	47	ASP	12.6
25	W	14	PHE	12.6
11	I	186	ARG	12.6
15	M	94	TRP	12.6
13	K	71	TRP	12.5
8	F	4	ALA	12.5
15	M	114	LEU	12.5

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Mol	Chain	Res	Type	RSRZ
3	A	197	VAL	12.5
4	B	303	PRO	12.5
12	J	27	ARG	12.5
26	X	15	THR	12.5
28	Z	55	VAL	12.5
4	B	252	GLN	12.5
5	C	66	GLY	12.5
4	B	245	ARG	12.4
5	C	53	GLY	12.4
4	B	213	PRO	12.4
5	C	76	ARG	12.4
11	I	67	ILE	12.4
4	B	148	ASP	12.4
28	Z	48	ASN	12.4
5	C	222	ASP	12.4
23	U	30	MET	12.4
17	O	59	PHE	12.4
28	Z	43	ASN	12.4
23	U	59	TRP	12.4
16	N	76	VAL	12.4
12	J	45	PRO	12.3
13	K	52	PRO	12.3
13	K	59	ALA	12.3
5	C	86	GLY	12.3
11	I	181	VAL	12.3
24	V	54	SER	12.3
3	A	4	ILE	12.3
3	A	181	ALA	12.3
4	B	224	GLY	12.3
22	T	11	VAL	12.3
22	T	15	THR	12.3
4	B	209	GLY	12.3
12	J	47	GLY	12.3
11	I	79	LYS	12.3
27	Y	19	SER	12.3
26	X	17	THR	12.3
27	Y	21	VAL	12.3
6	D	60	GLU	12.3
12	J	9	GLY	12.3
4	B	3	PRO	12.3
17	O	23	MET	12.3
8	F	146	THR	12.3

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Mol	Chain	Res	Type	RSRZ
23	U	66	THR	12.3
26	X	12	ASN	12.3
11	I	91	ARG	12.3
3	A	18	ALA	12.2
4	B	299	SER	12.2
4	B	236	GLY	12.2
12	J	16	GLY	12.2
3	A	189	VAL	12.2
5	C	91	PRO	12.2
17	O	126	LYS	12.2
5	C	78	ARG	12.2
13	K	70	GLY	12.2
26	X	42	SER	12.2
16	N	84	ILE	12.2
8	F	118	ALA	12.1
11	I	54	TYR	12.1
15	M	115	SER	12.1
23	U	27	ASP	12.1
4	B	2	GLN	12.1
8	F	125	TRP	12.1
11	I	25	TRP	12.1
27	Y	1	GLY	12.1
11	I	154	ARG	12.1
15	M	22	TRP	12.1
5	C	135	GLU	12.1
15	M	119	TYR	12.1
11	I	182	ARG	12.1
17	O	67	GLY	12.1
3	A	192	VAL	12.1
11	I	105	ALA	12.1
3	A	23	TYR	12.1
4	B	253	GLN	12.1
4	B	226	HIS	12.1
15	M	108	LEU	12.1
17	O	56	PRO	12.1
12	J	10	SER	12.1
11	I	116	ASN	12.0
23	U	83	ALA	12.0
8	F	143	VAL	12.0
10	H	40	THR	12.0
5	C	72	LYS	12.0
11	I	101	ALA	12.0

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Mol	Chain	Res	Type	RSRZ
17	O	123	GLN	12.0
24	V	66	THR	12.0
2	9	23	U	12.0
28	Z	44	SER	12.0
8	F	140	TYR	12.0
16	N	4	ASN	12.0
8	F	5	HIS	12.0
16	N	79	GLY	12.0
25	W	18	TYR	12.0
23	U	18	ARG	12.0
4	B	233	ARG	12.0
18	P	58	MET	11.9
4	B	254	GLY	11.9
12	J	30	ARG	11.9
16	N	75	ILE	11.9
6	D	107	GLY	11.9
22	T	41	TYR	11.9
9	G	141	ALA	11.9
5	C	57	PRO	11.9
12	J	32	ASP	11.9
11	I	165	GLY	11.9
23	U	62	GLY	11.9
8	F	63	ALA	11.9
5	C	49	ASP	11.9
11	I	120	VAL	11.9
11	I	134	VAL	11.9
13	K	139	TRP	11.9
11	I	156	ARG	11.9
4	B	258	TYR	11.9
8	F	2	PRO	11.9
13	K	97	VAL	11.9
5	C	55	ARG	11.9
16	N	83	THR	11.9
21	S	8	ILE	11.9
13	K	1	ALA	11.9
16	N	6	PRO	11.9
18	P	77	VAL	11.8
15	M	141	ILE	11.8
3	A	186	TRP	11.8
26	X	46	ARG	11.8
8	F	106	GLY	11.8
16	N	62	THR	11.8

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Mol	Chain	Res	Type	RSRZ
17	O	119	VAL	11.8
4	B	257	GLY	11.8
16	N	91	LEU	11.8
11	I	98	GLN	11.8
8	F	145	PRO	11.8
10	H	62	PRO	11.8
13	K	49	THR	11.8
6	D	132	VAL	11.8
4	B	232	ARG	11.8
8	F	19	TYR	11.8
23	U	60	ALA	11.7
4	B	302	GLY	11.7
11	I	162	THR	11.7
16	N	73	VAL	11.7
11	I	106	ASN	11.7
12	J	78	ALA	11.7
3	A	210	GLY	11.7
4	B	14	GLY	11.7
28	Z	28	GLY	11.7
24	V	44	THR	11.7
15	M	134	VAL	11.7
3	A	205	GLY	11.7
24	V	43	SER	11.7
28	Z	47	GLY	11.7
9	G	57	TYR	11.7
9	G	71	TYR	11.7
25	W	10	PRO	11.7
11	I	166	ARG	11.7
17	O	25	PHE	11.7
3	A	1	GLY	11.7
11	I	73	ARG	11.7
12	J	57	VAL	11.7
12	J	34	GLY	11.7
17	O	77	ALA	11.7
24	V	67	VAL	11.6
11	I	190	ARG	11.6
12	J	2	SER	11.6
8	F	153	PRO	11.6
4	B	9	GLY	11.6
16	N	33	PHE	11.6
3	A	10	GLY	11.6
11	I	90	ARG	11.6

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Mol	Chain	Res	Type	RSRZ
24	V	62	GLY	11.6
25	W	19	GLY	11.6
23	U	65	ASN	11.6
27	Y	12	ALA	11.6
15	M	123	TYR	11.6
22	T	44	MET	11.6
11	I	15	PRO	11.6
11	I	150	VAL	11.6
13	K	48	VAL	11.6
27	Y	14	LEU	11.6
13	K	95	ALA	11.6
23	U	25	ARG	11.6
8	F	14	TYR	11.6
3	A	191	GLY	11.6
8	F	13	ALA	11.5
15	M	98	ILE	11.5
27	Y	6	ALA	11.5
5	C	47	GLY	11.5
16	N	95	GLU	11.5
17	O	24	SER	11.5
19	Q	1	SER	11.5
11	I	137	ASP	11.5
24	V	59	GLY	11.5
16	N	54	PRO	11.5
13	K	57	THR	11.5
5	C	88	SER	11.5
16	N	85	ILE	11.5
22	T	26	ILE	11.5
22	T	48	VAL	11.5
4	B	234	ARG	11.5
11	I	112	MET	11.5
16	N	77	ASP	11.5
3	A	203	GLY	11.5
13	K	35	VAL	11.5
17	O	138	SER	11.5
28	Z	53	SER	11.5
8	F	60	ALA	11.5
4	B	230	GLY	11.4
11	I	82	LYS	11.4
4	B	204	VAL	11.4
22	T	38	THR	11.4
11	I	71	GLY	11.4

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Mol	Chain	Res	Type	RSRZ
8	F	56	ILE	11.4
8	F	115	SER	11.4
8	F	144	THR	11.4
17	O	64	SER	11.4
22	T	14	HIS	11.4
24	V	52	GLN	11.4
16	N	14	LEU	11.4
15	M	140	TYR	11.4
8	F	64	ALA	11.4
11	I	129	PHE	11.4
24	V	49	PRO	11.4
6	D	29	HIS	11.4
17	O	68	HIS	11.4
3	A	201	PHE	11.4
13	K	172	PHE	11.4
15	M	21	VAL	11.4
27	Y	4	SER	11.4
26	X	11	LYS	11.4
15	M	57	ASN	11.4
23	U	24	LYS	11.3
15	M	112	GLY	11.3
26	X	21	ARG	11.3
9	G	66	ASP	11.3
11	I	151	SER	11.3
25	W	31	ILE	11.3
11	I	159	ARG	11.3
24	V	35	ASP	11.3
11	I	83	SER	11.3
3	A	195	ASN	11.3
8	F	92	VAL	11.3
8	F	136	TRP	11.3
27	Y	18	ASN	11.3
3	A	187	PRO	11.3
3	A	221	PRO	11.3
4	B	91	TYR	11.3
23	U	11	THR	11.3
15	M	16	VAL	11.3
25	W	55	TRP	11.3
4	B	228	ARG	11.3
5	C	59	GLU	11.3
11	I	96	ASN	11.3
17	O	141	VAL	11.3

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Mol	Chain	Res	Type	RSRZ
13	K	4	PRO	11.3
17	O	81	PRO	11.3
4	B	239	GLY	11.2
15	M	13	VAL	11.2
13	K	100	ALA	11.2
3	A	200	PRO	11.2
4	B	229	GLN	11.2
15	M	58	SER	11.2
8	F	113	ALA	11.2
3	A	16	PHE	11.2
15	M	60	GLY	11.2
11	I	61	ILE	11.2
12	J	37	LYS	11.2
11	I	131	VAL	11.2
22	T	13	MET	11.2
11	I	152	ARG	11.2
26	X	23	GLY	11.2
11	I	40	ILE	11.2
25	W	39	CYS	11.2
9	G	62	ASP	11.2
13	K	135	VAL	11.2
3	A	225	VAL	11.2
13	K	36	ALA	11.2
13	K	186	LEU	11.1
15	M	110	ASP	11.1
26	X	28	HIS	11.1
8	F	53	PRO	11.1
13	K	9	PRO	11.1
16	N	63	VAL	11.1
5	C	40	ALA	11.1
9	G	61	VAL	11.1
11	I	49	ALA	11.1
16	N	71	TYR	11.1
23	U	68	SER	11.1
1	0	284	C	11.1
17	O	139	PRO	11.1
11	I	12	TRP	11.1
17	O	122	GLN	11.1
4	B	207	GLY	11.1
16	N	36	GLY	11.1
28	Z	58	GLY	11.1
12	J	44	GLU	11.1

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Mol	Chain	Res	Type	RSRZ
4	B	212	GLY	11.1
4	B	304	ASP	11.1
11	I	65	VAL	11.1
8	F	116	HIS	11.0
12	J	19	LYS	11.0
8	F	112	ALA	11.0
22	T	40	ALA	11.0
25	W	26	VAL	11.0
9	G	113	GLY	11.0
13	K	51	GLY	11.0
15	M	105	LEU	11.0
10	H	42	ASN	11.0
15	M	76	GLY	11.0
11	I	191	LYS	11.0
3	A	3	ARG	11.0
25	W	44	PHE	11.0
6	D	59	GLY	11.0
17	O	57	VAL	11.0
15	M	143	ALA	11.0
22	T	45	VAL	11.0
23	U	52	PRO	11.0
9	G	98	PHE	11.0
26	X	10	LYS	11.0
15	M	56	GLY	11.0
17	O	75	TRP	11.0
3	A	204	GLY	11.0
9	G	53	ILE	11.0
11	I	178	ALA	11.0
15	M	5	ALA	11.0
4	B	10	SER	10.9
3	A	2	ARG	10.9
11	I	93	ARG	10.9
27	Y	17	GLN	10.9
4	B	19	SER	10.9
17	O	121	GLU	10.9
15	M	86	ALA	10.9
22	T	5	VAL	10.9
25	W	15	GLY	10.9
8	F	93	ILE	10.9
11	I	69	ARG	10.9
8	F	11	LYS	10.9
4	B	20	THR	10.9

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Mol	Chain	Res	Type	RSRZ
17	O	63	ASN	10.9
22	T	23	MET	10.9
4	B	205	THR	10.9
10	H	39	GLY	10.9
23	U	87	ALA	10.9
5	C	100	LEU	10.9
8	F	120	HIS	10.9
24	V	37	HIS	10.9
15	M	126	ALA	10.9
25	W	37	TYR	10.9
23	U	67	PRO	10.9
27	Y	22	PRO	10.9
8	F	109	VAL	10.8
11	I	63	VAL	10.8
19	Q	55	PHE	10.8
3	A	215	ILE	10.8
11	I	5	TYR	10.8
17	O	84	ALA	10.8
3	A	173	GLY	10.8
26	X	55	GLY	10.8
3	A	5	GLN	10.8
4	B	211	GLN	10.8
23	U	63	ARG	10.8
7	E	109	GLU	10.8
3	A	19	PRO	10.8
11	I	4	MET	10.8
25	W	16	PRO	10.8
28	Z	49	ASP	10.8
15	M	11	ALA	10.8
3	A	184	THR	10.8
17	O	28	SER	10.8
22	T	124	GLY	10.8
3	A	212	PRO	10.8
28	Z	1	MET	10.8
5	C	87	ARG	10.8
8	F	97	ASP	10.8
27	Y	16	ASN	10.8
8	F	50	VAL	10.8
4	B	337	GLY	10.8
26	X	41	LYS	10.8
15	M	51	ALA	10.8
24	V	57	ARG	10.8

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Mol	Chain	Res	Type	RSRZ
11	I	121	GLY	10.8
28	Z	45	GLY	10.8
24	V	58	ARG	10.8
8	F	152	SER	10.7
26	X	16	HIS	10.7
17	O	120	GLY	10.7
26	X	32	LYS	10.7
12	J	51	PHE	10.7
17	O	62	HIS	10.7
22	T	17	ILE	10.7
9	G	94	GLY	10.7
16	N	39	VAL	10.7
25	W	79	VAL	10.7
16	N	56	PHE	10.7
13	K	61	ALA	10.7
16	N	29	ALA	10.7
4	B	247	ARG	10.7
1	0	2251	G	10.7
8	F	20	ILE	10.7
11	I	167	LYS	10.7
9	G	17	CYS	10.7
22	T	32	CYS	10.7
21	S	18	ALA	10.7
24	V	45	SER	10.7
4	B	65	MET	10.7
13	K	6	TYR	10.7
11	I	62	VAL	10.7
11	I	84	LYS	10.7
16	N	45	PRO	10.7
12	J	61	ALA	10.7
17	O	87	ALA	10.7
11	I	175	GLY	10.7
24	V	56	GLN	10.7
17	O	50	VAL	10.7
12	J	49	SER	10.7
15	M	135	ALA	10.6
16	N	89	ALA	10.6
11	I	145	PRO	10.6
4	B	51	VAL	10.6
5	C	82	GLN	10.6
16	N	86	VAL	10.6
5	C	97	ASP	10.6

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Mol	Chain	Res	Type	RSRZ
4	B	202	ALA	10.6
8	F	135	ALA	10.6
12	J	39	GLU	10.6
12	J	7	GLN	10.6
16	N	94	GLN	10.6
13	K	76	GLY	10.6
15	M	133	SER	10.6
26	X	45	ARG	10.6
3	A	229	ALA	10.6
15	M	4	SER	10.6
28	Z	40	ARG	10.6
9	G	14	ALA	10.6
6	D	13	MET	10.6
6	D	41	LEU	10.6
13	K	53	ASN	10.6
11	I	141	ILE	10.6
15	M	53	ASP	10.6
15	M	111	GLU	10.6
8	F	3	GLY	10.6
26	X	30	LYS	10.6
3	A	8	ARG	10.6
11	I	125	ARG	10.6
4	B	153	VAL	10.5
12	J	22	ARG	10.5
16	N	88	ALA	10.5
11	I	170	GLY	10.5
12	J	145	LEU	10.5
17	O	58	PRO	10.5
28	Z	36	ILE	10.5
29	1	154	ILE	10.5
3	A	198	ASP	10.5
4	B	284	VAL	10.5
13	K	126	GLY	10.5
16	N	9	GLY	10.5
4	B	6	PRO	10.5
16	N	18	PRO	10.5
23	U	20	GLU	10.5
12	J	8	ARG	10.5
15	M	117	SER	10.5
17	O	51	ILE	10.5
4	B	56	ASP	10.5
13	K	21	HIS	10.5

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Mol	Chain	Res	Type	RSRZ
13	K	125	ALA	10.5
23	U	58	ALA	10.5
4	B	218	GLY	10.5
8	F	111	THR	10.5
16	N	90	HIS	10.5
13	K	54	GLY	10.5
24	V	64	GLY	10.5
24	V	69	ALA	10.5
28	Z	42	ARG	10.5
16	N	52	PHE	10.5
13	K	58	LEU	10.5
11	I	128	TRP	10.5
11	I	132	ILE	10.5
3	A	193	ALA	10.5
5	C	45	ASP	10.5
9	G	31	LEU	10.5
26	X	20	ARG	10.5
15	M	77	ALA	10.4
23	U	57	ALA	10.4
6	D	77	ASP	10.4
13	K	101	VAL	10.4
17	O	72	VAL	10.4
9	G	138	THR	10.4
11	I	147	LEU	10.4
16	N	41	LEU	10.4
25	W	11	THR	10.4
4	B	7	ARG	10.4
17	O	30	ALA	10.4
26	X	31	LYS	10.4
22	T	29	VAL	10.4
25	W	24	VAL	10.4
28	Z	52	PHE	10.4
15	M	1	THR	10.4
22	T	90	TYR	10.4
13	K	122	ALA	10.4
28	Z	39	GLN	10.4
9	G	139	LEU	10.4
17	O	31	ILE	10.4
23	U	55	ASN	10.4
18	P	59	ASP	10.4
28	Z	37	ASP	10.4
11	I	136	ARG	10.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
15	M	70	ALA	10.4
16	N	60	THR	10.4
23	U	50	LEU	10.4
15	M	103	THR	10.4
15	M	122	LEU	10.4
23	U	85	VAL	10.4
11	I	124	GLY	10.4
4	B	255	GLN	10.4
24	V	114	ALA	10.4
22	T	36	PRO	10.4
4	B	18	ARG	10.4
15	M	17	GLY	10.4
16	N	93	ARG	10.4
27	Y	47	THR	10.4
22	T	153	MET	10.4
23	U	32	LEU	10.4
17	O	2	ILE	10.4
9	G	119	THR	10.3
16	N	10	THR	10.3
13	K	10	MET	10.3
13	K	175	LEU	10.3
25	W	20	LEU	10.3
8	F	28	ILE	10.3
15	M	90	SER	10.3
4	B	274	GLY	10.3
8	F	108	SER	10.3
22	T	16	ASP	10.3
3	A	209	PRO	10.3
8	F	59	ASN	10.3
24	V	55	LYS	10.3
27	Y	15	ASP	10.3
11	I	138	HIS	10.3
16	N	65	GLY	10.3
8	F	78	ALA	10.3
12	J	11	ARG	10.3
17	O	8	ALA	10.3
4	B	5	ARG	10.3
9	G	129	PHE	10.3
17	O	22	GLN	10.3
9	G	26	VAL	10.3
8	F	154	ALA	10.3
4	B	21	SER	10.3

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Mol	Chain	Res	Type	RSRZ
4	B	54	VAL	10.3
16	N	40	HIS	10.3
1	0	1523	G	10.2
8	F	85	ILE	10.2
19	Q	4	PRO	10.2
4	B	16	ARG	10.2
9	G	10	VAL	10.2
11	I	172	ARG	10.2
15	M	109	ARG	10.2
26	X	49	GLU	10.2
17	O	116	ALA	10.2
22	T	106	THR	10.2
11	I	59	GLY	10.2
13	K	168	LEU	10.2
6	D	10	PHE	10.2
17	O	53	GLY	10.2
3	A	177	HIS	10.2
5	C	85	LYS	10.2
15	M	142	ASP	10.2
4	B	222	ARG	10.2
11	I	111	ASN	10.2
29	1	165	GLY	10.2
8	F	141	MET	10.2
6	D	89	PRO	10.2
17	O	78	GLY	10.2
13	K	78	MET	10.2
11	I	179	GLU	10.2
28	Z	41	GLU	10.2
12	J	54	PRO	10.2
13	K	130	PRO	10.2
23	U	31	ILE	10.2
25	W	54	ILE	10.2
9	G	92	GLN	10.2
8	F	58	HIS	10.2
9	G	89	HIS	10.2
3	A	49	PRO	10.1
11	I	60	ILE	10.1
9	G	100	SER	10.1
12	J	21	ARG	10.1
13	K	106	LEU	10.1
4	B	26	PHE	10.1
13	K	20	TYR	10.1

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Mol	Chain	Res	Type	RSRZ
8	F	119	ASN	10.1
3	A	11	ARG	10.1
23	U	33	ILE	10.1
13	K	60	SER	10.1
4	B	308	VAL	10.1
20	R	9	CYS	10.1
8	F	67	ALA	10.1
8	F	88	PHE	10.1
1	0	2345	A	10.1
13	K	55	ASP	10.1
28	Z	59	ASP	10.1
11	I	176	ARG	10.1
6	D	138	GLY	10.1
22	T	27	HIS	10.1
3	A	121	ALA	10.1
25	W	52	THR	10.1
13	K	127	LEU	10.1
22	T	83	TRP	10.1
3	A	21	HIS	10.1
17	O	27	HIS	10.1
23	U	28	LYS	10.1
22	T	3	ALA	10.1
24	V	50	ARG	10.1
10	H	24	THR	10.1
11	I	160	GLY	10.1
14	L	36	PRO	10.1
16	N	48	PRO	10.1
24	V	36	HIS	10.1
13	K	113	SER	10.0
9	G	97	ALA	10.0
29	1	118	ILE	10.0
13	K	34	LEU	10.0
3	A	170	VAL	10.0
17	O	32	ALA	10.0
24	V	26	VAL	10.0
1	0	1949	G	10.0
3	A	228	ILE	10.0
9	G	68	GLY	10.0
17	O	65	GLY	10.0
13	K	56	ASP	10.0
1	0	2238	A	10.0
15	M	96	SER	10.0

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Mol	Chain	Res	Type	RSRZ
26	X	24	GLU	10.0
8	F	55	GLN	10.0
19	Q	53	GLY	10.0
26	X	53	LYS	10.0
3	A	208	HIS	10.0
16	N	7	LEU	10.0
17	O	47	LEU	10.0
22	T	24	LEU	10.0
3	A	214	SER	10.0
4	B	195	ALA	10.0
9	G	41	ALA	10.0
10	H	36	GLY	10.0
16	N	5	GLY	10.0
16	N	78	GLY	10.0
13	K	2	THR	10.0
4	B	136	LEU	10.0
12	J	97	VAL	10.0
22	T	52	VAL	10.0
9	G	82	THR	10.0
16	N	87	THR	10.0
22	T	107	LEU	10.0
4	B	44	TYR	10.0
10	H	33	SER	10.0
4	B	17	LYS	9.9
17	O	17	MET	9.9
1	0	1950	G	9.9
15	M	100	ALA	9.9
22	T	53	ALA	9.9
17	O	143	VAL	9.9
9	G	72	PRO	9.9
10	H	37	TYR	9.9
17	O	70	SER	9.9
19	Q	10	SER	9.9
26	X	40	GLY	9.9
16	N	81	GLU	9.9
28	Z	31	THR	9.9
28	Z	71	CYS	9.9
4	B	165	VAL	9.9
24	V	29	PRO	9.9
5	C	99	SER	9.9
4	B	286	TYR	9.9
26	X	18	LYS	9.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
9	G	131	THR	9.9
13	K	115	VAL	9.9
22	T	79	VAL	9.9
24	V	112	VAL	9.9
15	M	79	SER	9.9
3	A	234	GLY	9.9
3	A	50	ALA	9.9
13	K	45	ALA	9.9
22	T	35	VAL	9.9
28	Z	50	GLY	9.9
13	K	118	ILE	9.9
1	0	2252	A	9.9
3	A	176	HIS	9.9
8	F	139	ALA	9.9
15	M	10	ALA	9.9
8	F	15	THR	9.9
22	T	114	PRO	9.9
9	G	130	VAL	9.9
13	K	3	GLY	9.9
13	K	29	SER	9.9
16	N	43	ILE	9.9
11	I	19	TYR	9.8
25	W	42	CYS	9.8
9	G	4	ALA	9.8
5	C	172	THR	9.8
18	P	60	GLY	9.8
22	T	20	THR	9.8
11	I	180	LYS	9.8
19	Q	116	ASP	9.8
15	M	106	ARG	9.8
20	R	6	CYS	9.8
6	D	35	ALA	9.8
23	U	38	ALA	9.8
26	X	44	LYS	9.8
18	P	1	SER	9.8
22	T	105	THR	9.8
4	B	11	LEU	9.8
4	B	307	LEU	9.8
13	K	24	LEU	9.8
13	K	102	LEU	9.8
17	O	18	LEU	9.8
22	T	21	LEU	9.8

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Mol	Chain	Res	Type	RSRZ
8	F	68	ALA	9.8
16	N	35	ASP	9.8
28	Z	54	LYS	9.8
9	G	136	SER	9.8
18	P	33	SER	9.8
21	S	49	LEU	9.8
4	B	72	VAL	9.8
11	I	20	VAL	9.8
3	A	6	GLY	9.8
11	I	24	MET	9.8
28	Z	61	PRO	9.8
3	A	165	THR	9.8
17	O	55	GLN	9.8
11	I	46	LEU	9.8
8	F	22	GLY	9.7
25	W	22	ILE	9.7
16	N	92	ARG	9.7
4	B	154	PRO	9.7
10	H	121	PHE	9.7
10	H	94	ALA	9.7
15	M	84	ALA	9.7
24	V	41	ARG	9.7
14	L	1	SER	9.7
8	F	94	ARG	9.7
3	A	12	GLY	9.7
8	F	123	ILE	9.7
10	H	31	VAL	9.7
11	I	8	ILE	9.7
17	O	6	VAL	9.7
17	O	114	VAL	9.7
21	S	42	ASN	9.7
5	C	183	GLY	9.7
11	I	133	LEU	9.7
11	I	123	ASP	9.7
22	T	19	ASP	9.7
25	W	29	VAL	9.7
16	N	23	THR	9.7
15	M	88	GLN	9.7
25	W	56	VAL	9.7
27	Y	20	ARG	9.7
9	G	88	PRO	9.7
9	G	19	MET	9.7

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Mol	Chain	Res	Type	RSRZ
5	C	34	ALA	9.7
18	P	27	ALA	9.7
9	G	52	GLN	9.7
16	N	58	GLY	9.7
22	T	43	GLY	9.7
11	I	107	ARG	9.7
6	D	141	VAL	9.7
8	F	49	VAL	9.7
9	G	12	VAL	9.7
11	I	6	ALA	9.7
12	J	100	ALA	9.7
13	K	18	THR	9.7
24	V	137	VAL	9.6
27	Y	25	VAL	9.6
4	B	225	LYS	9.6
17	O	115	ALA	9.6
24	V	31	PHE	9.6
3	A	17	ARG	9.6
4	B	73	ILE	9.6
14	L	111	VAL	9.6
11	I	1	MET	9.6
11	I	173	ARG	9.6
11	I	177	GLY	9.6
12	J	50	GLY	9.6
22	T	145	GLY	9.6
4	B	262	THR	9.6
4	B	27	ASN	9.6
22	T	12	ASN	9.6
12	J	102	ASP	9.6
4	B	203	GLY	9.6
9	G	36	VAL	9.6
5	C	181	ALA	9.6
13	K	84	THR	9.6
11	I	104	ARG	9.6
15	M	59	ARG	9.6
25	W	12	GLY	9.6
9	G	78	ILE	9.6
6	D	71	ALA	9.6
8	F	134	PHE	9.6
18	P	57	THR	9.6
12	J	75	LEU	9.6
3	A	223	ARG	9.6

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Mol	Chain	Res	Type	RSRZ
11	I	31	TRP	9.6
13	K	184	ILE	9.6
10	H	1	MET	9.6
25	W	70	THR	9.6
5	C	180	SER	9.6
22	T	89	ASP	9.6
9	G	48	GLY	9.6
22	T	139	GLY	9.6
24	V	70	GLY	9.6
4	B	314	ALA	9.6
11	I	68	ARG	9.6
16	N	74	ASP	9.6
24	V	75	THR	9.6
12	J	146	GLY	9.5
4	B	220	GLN	9.5
3	A	9	ARG	9.5
5	C	186	TYR	9.5
17	O	54	ASP	9.5
3	A	219	ALA	9.5
13	K	16	ALA	9.5
9	G	47	THR	9.5
21	S	1	THR	9.5
28	Z	65	THR	9.5
11	I	28	LEU	9.5
15	M	14	LEU	9.5
25	W	45	PRO	9.5
17	O	117	HIS	9.5
22	T	1	MET	9.5
11	I	56	ALA	9.5
16	N	19	ARG	9.5
5	C	35	VAL	9.5
10	H	57	VAL	9.5
10	H	38	SER	9.5
17	O	40	ALA	9.5
4	B	12	GLY	9.5
15	M	78	GLY	9.5
17	O	79	ARG	9.5
10	H	17	LEU	9.5
15	M	19	ASN	9.5
22	T	91	ASP	9.5
8	F	132	VAL	9.5
17	O	85	SER	9.5

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Mol	Chain	Res	Type	RSRZ
17	O	140	GLN	9.5
4	B	216	ARG	9.5
12	J	103	ALA	9.5
17	O	1	GLY	9.5
13	K	110	THR	9.5
4	B	24	PRO	9.5
4	B	317	PRO	9.5
5	C	225	PRO	9.5
9	G	20	GLY	9.5
25	W	51	SER	9.5
4	B	201	VAL	9.5
18	P	32	ALA	9.5
13	K	161	GLY	9.5
28	Z	32	GLY	9.5
4	B	318	ASN	9.5
9	G	142	ASN	9.5
22	T	68	THR	9.5
27	Y	3	LYS	9.5
29	1	122	THR	9.5
10	H	79	PRO	9.4
16	N	25	PRO	9.4
11	I	148	SER	9.4
16	N	61	GLY	9.4
15	M	124	ASP	9.4
16	N	20	ASP	9.4
16	N	49	ASN	9.4
22	T	54	PHE	9.4
3	A	67	LEU	9.4
13	K	74	PRO	9.4
23	U	61	ARG	9.4
3	A	183	GLY	9.4
13	K	96	GLY	9.4
15	M	128	GLY	9.4
5	C	101	ASP	9.4
8	F	124	ALA	9.4
9	G	23	ALA	9.4
16	N	70	ALA	9.4
22	T	97	ALA	9.4
16	N	30	VAL	9.4
16	N	47	VAL	9.4
1	0	2253	G	9.4
3	A	27	LEU	9.4

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Mol	Chain	Res	Type	RSRZ
4	B	95	PRO	9.4
4	B	151	PRO	9.4
13	K	111	PRO	9.4
11	I	85	LYS	9.4
25	W	43	GLY	9.4
29	1	10	ASP	9.4
27	Y	10	ARG	9.4
9	G	30	ALA	9.4
4	B	327	VAL	9.4
11	I	53	GLY	9.4
16	N	12	GLY	9.4
3	A	230	SER	9.4
8	F	107	LYS	9.4
6	D	48	MET	9.4
20	R	11	THR	9.4
4	B	160	VAL	9.4
15	M	3	LEU	9.4
15	M	23	PHE	9.4
22	T	128	VAL	9.4
23	U	5	PHE	9.4
9	G	76	ASP	9.4
3	A	199	HIS	9.4
1	0	999	C	9.4
3	A	190	ARG	9.4
29	1	3	VAL	9.4
9	G	77	GLY	9.4
15	M	132	ASP	9.4
23	U	46	ASP	9.4
4	B	42	ALA	9.4
22	T	46	ALA	9.4
8	F	40	PRO	9.4
11	I	110	PRO	9.4
28	Z	51	LYS	9.4
3	A	226	GLY	9.4
8	F	110	GLY	9.4
8	F	91	HIS	9.3
3	A	168	PRO	9.3
13	K	138	ASP	9.3
15	M	136	ASP	9.3
17	O	76	ASP	9.3
28	Z	33	MET	9.3
17	O	89	LEU	9.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
24	V	5	LEU	9.3
3	A	207	GLN	9.3
8	F	24	PRO	9.3
11	I	44	THR	9.3
9	G	105	LEU	9.3
13	K	136	LEU	9.3
4	B	28	SER	9.3
11	I	94	LYS	9.3
13	K	146	HIS	9.3
5	C	44	GLN	9.3
15	M	82	GLY	9.3
20	R	15	PRO	9.3
13	K	87	LEU	9.3
22	T	4	LEU	9.3
14	L	113	VAL	9.3
28	Z	25	VAL	9.3
10	H	41	LYS	9.3
3	A	220	PRO	9.3
5	C	37	ALA	9.3
8	F	79	ALA	9.3
13	K	73	ALA	9.3
11	I	33	ARG	9.3
11	I	3	SER	9.3
11	I	143	SER	9.3
11	I	169	ARG	9.3
15	M	63	ARG	9.3
28	Z	38	ARG	9.3
23	U	70	ILE	9.3
16	N	53	HIS	9.3
4	B	150	VAL	9.3
11	I	135	ASP	9.3
22	T	39	ASP	9.3
23	U	72	VAL	9.3
12	J	99	GLU	9.3
25	W	58	GLY	9.3
1	0	2136	G	9.3
16	N	26	PRO	9.3
9	G	8	ALA	9.3
18	P	30	ASP	9.2
11	I	18	GLY	9.2
16	N	11	ARG	9.2
3	A	56	ALA	9.2

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Mol	Chain	Res	Type	RSRZ
9	G	37	ALA	9.2
3	A	52	SER	9.2
10	H	54	THR	9.2
13	K	116	PHE	9.2
4	B	287	GLY	9.2
5	C	139	VAL	9.2
22	T	84	VAL	9.2
11	I	139	PRO	9.2
5	C	213	ALA	9.2
13	K	81	ALA	9.2
13	K	117	ALA	9.2
17	O	49	ALA	9.2
3	A	169	PHE	9.2
4	B	52	VAL	9.2
12	J	101	ASP	9.2
24	V	65	ASP	9.2
11	I	95	LYS	9.2
4	B	285	ASN	9.2
8	F	149	ILE	9.2
4	B	289	VAL	9.2
11	I	66	ARG	9.2
15	M	25	PRO	9.2
10	H	71	ALA	9.2
22	T	88	THR	9.2
3	A	188	ASN	9.2
9	G	132	LEU	9.2
25	W	13	ARG	9.2
13	K	64	SER	9.2
3	A	7	GLN	9.2
22	T	115	THR	9.2
4	B	208	LYS	9.2
26	X	25	LYS	9.2
13	K	62	HIS	9.2
13	K	39	SER	9.2
22	T	102	SER	9.2
3	A	222	GLY	9.2
8	F	29	ALA	9.2
29	1	13	ALA	9.2
22	T	62	LEU	9.1
23	U	34	ARG	9.1
4	B	49	THR	9.1
11	I	140	ALA	9.1

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Mol	Chain	Res	Type	RSRZ
13	K	37	ARG	9.1
5	C	95	GLU	9.1
4	B	48	MET	9.1
22	T	96	LEU	9.1
7	E	60	VAL	9.1
4	B	59	ASN	9.1
9	G	33	GLY	9.1
4	B	46	ALA	9.1
14	L	24	ALA	9.1
15	M	121	ASP	9.1
23	U	37	LEU	9.1
28	Z	3	MET	9.1
16	N	17	LYS	9.1
25	W	60	CYS	9.1
4	B	321	PRO	9.1
15	M	89	ASN	9.1
5	C	214	THR	9.1
6	D	147	ALA	9.1
25	W	50	ALA	9.1
28	Z	67	LEU	9.1
3	A	174	ASN	9.1
7	E	93	SER	9.1
8	F	148	ASN	9.1
10	H	3	ALA	9.1
12	J	63	THR	9.1
28	Z	62	THR	9.1
15	M	80	ARG	9.1
4	B	277	PRO	9.1
6	D	150	SER	9.1
16	N	50	GLY	9.1
22	T	111	GLY	9.1
9	G	22	VAL	9.1
10	H	116	GLU	9.1
11	I	39	ARG	9.1
18	P	54	THR	9.1
23	U	74	ALA	9.1
4	B	166	GLY	9.1
9	G	135	ILE	9.1
13	K	129	ILE	9.1
5	C	176	ALA	9.1
3	A	35	GLY	9.0
4	B	64	GLY	9.0

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Mol	Chain	Res	Type	RSRZ
24	V	109	ASN	9.0
9	G	117	ASP	9.0
21	S	65	ASP	9.0
9	G	75	PRO	9.0
29	1	28	SER	9.0
3	A	45	ILE	9.0
9	G	93	ARG	9.0
13	K	43	VAL	9.0
17	O	110	THR	9.0
5	C	102	LEU	9.0
13	K	82	TYR	9.0
4	B	133	ALA	9.0
15	M	73	HIS	9.0
17	O	16	ALA	9.0
11	I	23	LEU	9.0
22	T	18	GLN	9.0
22	T	73	LEU	9.0
8	F	114	ARG	9.0
5	C	96	LYS	9.0
9	G	46	ILE	9.0
11	I	102	GLU	9.0
23	U	10	VAL	9.0
6	D	171	ASP	9.0
11	I	144	ASP	9.0
17	O	142	ASP	9.0
22	T	138	LEU	9.0
21	S	11	MET	9.0
10	H	44	HIS	9.0
4	B	8	LYS	9.0
24	V	77	VAL	9.0
4	B	143	THR	9.0
9	G	85	GLY	9.0
9	G	106	GLY	9.0
22	T	100	LEU	9.0
22	T	112	LEU	9.0
4	B	158	PRO	9.0
11	I	146	GLN	9.0
24	V	71	PHE	9.0
16	N	82	LYS	9.0
9	G	44	ALA	9.0
14	L	26	TRP	9.0
29	1	88	TYR	9.0

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Mol	Chain	Res	Type	RSRZ
13	K	169	PRO	9.0
12	J	52	LYS	9.0
5	C	41	ASN	9.0
15	M	138	GLU	9.0
16	N	64	GLU	9.0
4	B	281	GLY	9.0
22	T	95	GLY	9.0
8	F	147	VAL	8.9
8	F	21	SER	8.9
24	V	13	SER	8.9
17	O	91	LEU	8.9
6	D	85	GLN	8.9
16	N	57	ASP	8.9
3	A	135	VAL	8.9
10	H	118	ALA	8.9
13	K	8	VAL	8.9
9	G	109	TYR	8.9
9	G	18	ILE	8.9
17	O	14	ALA	8.9
1	0	1520	G	8.9
12	J	105	TYR	8.9
4	B	23	THR	8.9
4	B	278	THR	8.9
5	C	169	ALA	8.9
13	K	142	THR	8.9
20	R	28	THR	8.9
22	T	143	THR	8.9
3	A	43	VAL	8.9
16	N	34	ASP	8.9
23	U	9	VAL	8.9
3	A	141	PRO	8.9
5	C	189	PRO	8.9
8	F	89	PRO	8.9
22	T	118	LEU	8.9
24	V	61	LYS	8.9
15	M	131	PHE	8.9
24	V	120	ILE	8.9
16	N	46	SER	8.9
25	W	53	SER	8.9
24	V	40	LYS	8.9
18	P	4	VAL	8.9
21	S	45	ARG	8.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	W	69	TYR	8.9
1	0	283	U	8.9
4	B	33	ASP	8.9
8	F	121	ASP	8.9
29	1	104	ILE	8.9
14	L	41	ALA	8.9
15	M	48	ALA	8.9
4	B	58	PRO	8.9
6	D	152	PRO	8.9
11	I	43	PRO	8.9
15	M	129	GLY	8.9
17	O	74	GLY	8.9
4	B	221	LYS	8.9
1	0	282	C	8.9
10	H	16	SER	8.9
22	T	93	ILE	8.9
27	Y	49	GLU	8.9
10	H	47	ALA	8.8
13	K	25	ARG	8.8
29	1	56	ALA	8.8
3	A	54	PRO	8.8
24	V	34	GLN	8.8
25	W	67	GLY	8.8
28	Z	74	CYS	8.8
17	O	46	TYR	8.8
24	V	136	TYR	8.8
3	A	20	SER	8.8
3	A	216	SER	8.8
12	J	6	ARG	8.8
17	O	146	ILE	8.8
4	B	259	HIS	8.8
10	H	9	THR	8.8
3	A	157	GLY	8.8
9	G	124	LEU	8.8
23	U	43	VAL	8.8
28	Z	14	CYS	8.8
4	B	198	TYR	8.8
8	F	75	SER	8.8
28	Z	69	TYR	8.8
4	B	294	THR	8.8
9	G	144	THR	8.8
29	1	21	THR	8.8

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Mol	Chain	Res	Type	RSRZ
11	I	41	PRO	8.8
11	I	52	LEU	8.8
22	T	150	LEU	8.8
10	H	132	VAL	8.8
9	G	86	MET	8.8
8	F	156	ASN	8.8
7	E	3	TYR	8.8
20	R	21	PHE	8.8
13	K	104	ILE	8.8
22	T	136	GLY	8.8
4	B	309	PRO	8.8
13	K	32	PRO	8.8
8	F	61	LEU	8.8
17	O	145	LEU	8.8
9	G	54	VAL	8.8
23	U	48	VAL	8.8
10	H	101	ASN	8.8
13	K	77	ASN	8.8
4	B	43	GLY	8.8
14	L	108	GLY	8.8
8	F	7	ARG	8.8
24	V	105	ALA	8.8
4	B	53	LEU	8.8
9	G	121	LEU	8.8
15	M	64	GLU	8.8
22	T	94	SER	8.8
3	A	47	HIS	8.8
13	K	105	GLY	8.8
7	E	94	ALA	8.8
11	I	34	GLU	8.8
27	Y	26	MET	8.8
12	J	137	GLY	8.8
14	L	37	ARG	8.8
5	C	9	ASP	8.8
13	K	123	ILE	8.7
18	P	74	ALA	8.7
15	M	137	LEU	8.7
3	A	55	VAL	8.7
9	G	115	VAL	8.7
10	H	55	VAL	8.7
28	Z	27	SER	8.7
15	M	101	GLN	8.7

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Mol	Chain	Res	Type	RSRZ
17	O	88	PHE	8.7
9	G	11	ILE	8.7
13	K	92	ALA	8.7
22	T	77	ALA	8.7
8	F	51	GLU	8.7
14	L	8	SER	8.7
7	E	100	ASP	8.7
10	H	8	VAL	8.7
7	E	56	PRO	8.7
4	B	271	ILE	8.7
11	I	14	ARG	8.7
13	K	5	ARG	8.7
19	Q	8	ARG	8.7
15	M	139	ARG	8.7
4	B	268	LEU	8.7
29	1	108	LEU	8.7
5	C	179	GLY	8.7
4	B	279	VAL	8.7
15	M	40	VAL	8.7
22	T	131	PRO	8.7
4	B	283	PHE	8.7
3	A	152	CYS	8.7
14	L	22	GLY	8.7
20	R	34	SER	8.7
1	0	1528	A	8.7
3	A	182	ARG	8.7
4	B	68	VAL	8.7
15	M	65	ARG	8.7
4	B	115	PRO	8.7
5	C	103	ASN	8.7
8	F	31	PHE	8.7
3	A	119	ALA	8.7
8	F	23	ILE	8.7
25	W	59	HIS	8.7
8	F	81	TYR	8.7
15	M	87	ARG	8.7
9	G	143	LYS	8.7
20	R	20	MET	8.7
3	A	134	ASN	8.7
16	N	16	ASN	8.7
22	T	110	GLN	8.7
6	D	153	THR	8.6

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Mol	Chain	Res	Type	RSRZ
21	S	12	THR	8.6
3	A	53	ALA	8.6
15	M	34	ALA	8.6
9	G	87	LEU	8.6
9	G	91	LYS	8.6
29	1	167	TYR	8.6
19	Q	5	ASP	8.6
19	Q	90	PRO	8.6
20	R	17	THR	8.6
4	B	31	SER	8.6
6	D	148	SER	8.6
27	Y	11	LYS	8.6
1	0	370	G	8.6
28	Z	15	ASN	8.6
13	K	134	ASP	8.6
6	D	174	VAL	8.6
16	N	55	ARG	8.6
15	M	127	GLY	8.6
23	U	40	HIS	8.6
3	A	25	ALA	8.6
8	F	122	PHE	8.6
28	Z	85	ALA	8.6
19	Q	112	LEU	8.6
28	Z	88	LEU	8.6
1	0	369	G	8.6
22	T	50	ASP	8.6
16	N	80	LYS	8.6
8	F	25	GLY	8.6
16	N	22	GLY	8.6
4	B	111	THR	8.6
1	0	970	U	8.6
17	O	73	ASP	8.6
5	C	200	PRO	8.6
6	D	16	PRO	8.6
3	A	57	ALA	8.6
8	F	71	PHE	8.6
15	M	32	ALA	8.6
13	K	91	ARG	8.6
13	K	179	LEU	8.6
24	V	47	ARG	8.6
28	Z	11	CYS	8.6
29	1	97	VAL	8.6

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Mol	Chain	Res	Type	RSRZ
10	H	56	SER	8.6
15	M	67	LYS	8.6
15	M	104	LYS	8.6
5	C	244	ALA	8.6
15	M	102	ARG	8.6
21	S	58	THR	8.6
3	A	118	PHE	8.6
18	P	64	ALA	8.6
22	T	51	PHE	8.6
8	F	95	GLU	8.6
13	K	121	GLY	8.6
17	O	113	HIS	8.6
27	Y	2	LYS	8.6
13	K	150	TYR	8.6
18	P	28	VAL	8.5
20	R	29	THR	8.5
22	T	116	LEU	8.5
4	B	269	ILE	8.5
21	S	64	GLY	8.5
1	0	280	C	8.5
1	0	1000	C	8.5
5	C	19	PRO	8.5
22	T	72	PRO	8.5
24	V	74	PRO	8.5
9	G	38	VAL	8.5
25	W	28	ASP	8.5
28	Z	9	THR	8.5
22	T	152	ALA	8.5
2	9	25	G	8.5
4	B	142	ILE	8.5
10	H	53	ILE	8.5
22	T	109	GLU	8.5
5	C	161	ASP	8.5
13	K	133	ASP	8.5
9	G	45	VAL	8.5
28	Z	10	TYR	8.5
10	H	90	PHE	8.5
29	1	91	PHE	8.5
9	G	60	ARG	8.5
16	N	21	ARG	8.5
8	F	150	ASP	8.5
3	A	180	LYS	8.5

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Mol	Chain	Res	Type	RSRZ
22	T	25	ASN	8.5
5	C	208	ALA	8.5
15	M	69	ARG	8.5
5	C	31	ILE	8.5
4	B	30	PRO	8.5
21	S	43	PRO	8.5
29	1	26	ASN	8.5
25	W	17	ARG	8.5
3	A	158	VAL	8.5
10	H	34	VAL	8.5
8	F	155	GLY	8.5
11	I	11	ALA	8.5
22	T	135	GLY	8.5
22	T	76	ASP	8.5
1	0	2254	G	8.5
3	A	160	GLY	8.5
22	T	127	GLY	8.5
24	V	39	LYS	8.5
21	S	54	ALA	8.5
22	T	125	HIS	8.5
13	K	109	PRO	8.5
4	B	272	GLY	8.4
10	H	58	THR	8.4
14	L	39	THR	8.4
15	M	12	ASP	8.4
13	K	98	GLU	8.4
22	T	49	ASN	8.4
5	C	182	ARG	8.4
12	J	55	GLN	8.4
22	T	121	PRO	8.4
27	Y	8	LYS	8.4
22	T	74	GLU	8.4
10	H	23	ASN	8.4
25	W	25	ARG	8.4
25	W	68	ALA	8.4
4	B	215	LYS	8.4
10	H	29	LEU	8.4
12	J	3	LYS	8.4
13	K	26	LEU	8.4
13	K	108	SER	8.4
21	S	44	GLY	8.4
15	M	15	ASP	8.4

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Mol	Chain	Res	Type	RSRZ
3	A	106	CYS	8.4
4	B	223	LYS	8.4
14	L	33	LEU	8.4
4	B	147	PRO	8.4
13	K	79	PRO	8.4
9	G	24	SER	8.4
29	1	35	TYR	8.4
9	G	55	GLU	8.4
1	0	599	G	8.4
4	B	92	GLY	8.4
11	I	50	ARG	8.4
22	T	31	HIS	8.4
17	O	61	GLN	8.4
3	A	58	VAL	8.4
7	E	91	VAL	8.4
13	K	27	LEU	8.4
3	A	202	GLY	8.4
3	A	206	ARG	8.4
4	B	261	ARG	8.4
17	O	60	LYS	8.4
29	1	116	THR	8.4
10	H	69	LEU	8.4
25	W	71	PRO	8.4
3	A	22	ARG	8.4
7	E	25	ASP	8.4
1	0	497	A	8.4
5	C	178	GLN	8.4
20	R	51	TRP	8.4
4	B	163	THR	8.4
13	K	67	ALA	8.4
22	T	101	LEU	8.4
8	F	30	GLN	8.4
13	K	159	TYR	8.4
17	O	111	ILE	8.4
15	M	18	LYS	8.3
8	F	57	ARG	8.3
5	C	215	ALA	8.3
13	K	19	ASP	8.3
24	V	2	ALA	8.3
11	I	122	GLU	8.3
13	K	47	LEU	8.3
13	K	86	LEU	8.3

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Mol	Chain	Res	Type	RSRZ
9	G	107	ASN	8.3
5	C	6	TYR	8.3
15	M	49	ILE	8.3
4	B	106	SER	8.3
14	L	61	PRO	8.3
17	O	43	ALA	8.3
4	B	295	LEU	8.3
15	M	54	LYS	8.3
20	R	42	LEU	8.3
23	U	49	ARG	8.3
16	N	24	SER	8.3
21	S	14	ALA	8.3
28	Z	86	GLY	8.3
10	H	72	VAL	8.3
28	Z	22	VAL	8.3
9	G	84	ARG	8.3
22	T	108	ARG	8.3
24	V	33	ARG	8.3
1	0	960	G	8.3
11	I	142	LYS	8.3
14	L	51	TYR	8.3
3	A	162	GLY	8.3
22	T	9	GLY	8.3
22	T	33	THR	8.3
4	B	80	ALA	8.3
5	C	98	ARG	8.3
8	F	80	ASN	8.3
4	B	310	PHE	8.3
3	A	114	ASP	8.3
22	T	146	ILE	8.3
3	A	123	GLY	8.3
11	I	7	TYR	8.3
8	F	43	PRO	8.3
11	I	32	ARG	8.3
8	F	157	ALA	8.3
16	N	59	GLN	8.3
4	B	315	VAL	8.3
4	B	330	VAL	8.3
6	D	50	VAL	8.3
9	G	103	VAL	8.3
17	O	19	ARG	8.3
17	O	5	SER	8.3

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Mol	Chain	Res	Type	RSRZ
8	F	69	ASN	8.3
13	K	131	HIS	8.3
15	M	24	ASN	8.3
5	C	117	ALA	8.3
15	M	9	LEU	8.3
22	T	7	LEU	8.3
24	V	25	ARG	8.3
3	A	163	GLY	8.2
9	G	118	GLY	8.2
24	V	113	GLY	8.2
17	O	3	SER	8.2
27	Y	28	LYS	8.2
3	A	233	THR	8.2
9	G	104	TYR	8.2
13	K	93	GLN	8.2
16	N	67	GLN	8.2
4	B	29	TRP	8.2
6	D	21	VAL	8.2
8	F	90	PHE	8.2
15	M	61	ARG	8.2
13	K	182	GLY	8.2
24	V	110	SER	8.2
21	S	13	PRO	8.2
10	H	21	ALA	8.2
14	L	30	ALA	8.2
19	Q	70	ALA	8.2
17	O	33	ARG	8.2
10	H	123	SER	8.2
3	A	145	MET	8.2
8	F	128	PRO	8.2
2	9	2	U	8.2
11	I	174	LYS	8.2
19	Q	119	ALA	8.2
1	0	2506	A	8.2
12	J	59	GLU	8.2
28	Z	83	TRP	8.2
4	B	305	LYS	8.2
8	F	17	ARG	8.2
9	G	49	ARG	8.2
12	J	4	LYS	8.2
12	J	149	ARG	8.2
10	H	26	ALA	8.2

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Mol	Chain	Res	Type	RSRZ
20	R	46	ALA	8.2
22	T	67	ALA	8.2
22	T	34	LEU	8.2
24	V	79	GLY	8.2
10	H	68	VAL	8.2
6	D	168	SER	8.2
15	M	97	ARG	8.2
29	1	41	SER	8.2
23	U	84	ILE	8.2
8	F	33	MET	8.2
4	B	149	ALA	8.2
8	F	44	ALA	8.2
11	I	113	GLU	8.2
12	J	62	ALA	8.2
4	B	196	GLY	8.2
4	B	293	TYR	8.2
1	0	279	C	8.2
12	J	5	LYS	8.2
6	D	51	ARG	8.2
22	T	130	HIS	8.2
5	C	174	ILE	8.2
13	K	157	PRO	8.2
18	P	8	PRO	8.2
12	J	48	LYS	8.2
14	L	72	LYS	8.2
11	I	9	ARG	8.2
24	V	32	ASN	8.2
4	B	270	ASP	8.2
22	T	28	HIS	8.2
4	B	60	SER	8.2
5	C	140	VAL	8.1
15	M	95	GLU	8.1
9	G	56	LYS	8.1
16	N	38	LYS	8.1
29	1	168	ILE	8.1
4	B	264	LEU	8.1
4	B	265	ASN	8.1
13	K	107	ASN	8.1
4	B	76	PRO	8.1
20	R	52	THR	8.1
6	D	36	ASN	8.1
8	F	38	ALA	8.1

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Mol	Chain	Res	Type	RSRZ
12	J	82	ALA	8.1
14	L	101	ALA	8.1
11	I	26	HIS	8.1
13	K	42	HIS	8.1
8	F	1	LYS	8.1
22	T	113	SER	8.1
11	I	48	ARG	8.1
4	B	192	ILE	8.1
5	C	50	GLU	8.1
10	H	11	GLY	8.1
11	I	21	GLY	8.1
17	O	82	GLU	8.1
29	1	49	ILE	8.1
4	B	206	LYS	8.1
22	T	70	ALA	8.1
22	T	119	HIS	8.1
3	A	122	SER	8.1
7	E	39	SER	8.1
5	C	212	VAL	8.1
9	G	7	ASP	8.1
15	M	52	LYS	8.1
16	N	15	LYS	8.1
10	H	18	ILE	8.1
5	C	203	ALA	8.1
14	L	10	LEU	8.1
14	L	21	SER	8.1
23	U	45	GLU	8.1
17	O	118	LYS	8.1
24	V	48	LYS	8.1
25	W	61	GLY	8.1
2	9	1	U	8.1
4	B	187	HIS	8.1
10	H	97	ILE	8.1
11	I	45	ARG	8.1
5	C	240	LEU	8.1
3	A	44	ASP	8.1
4	B	47	GLY	8.1
5	C	32	GLY	8.1
10	H	15	GLY	8.1
13	K	12	ARG	8.1
15	M	20	ARG	8.1
16	N	51	ARG	8.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
5	C	93	LYS	8.1
22	T	6	GLN	8.0
24	V	1	GLN	8.0
28	Z	30	GLN	8.0
15	M	92	GLU	8.0
15	M	99	ARG	8.0
17	O	83	LYS	8.0
19	Q	65	VAL	8.0
22	T	65	VAL	8.0
5	C	38	ALA	8.0
5	C	190	ALA	8.0
13	K	83	LEU	8.0
15	M	43	LEU	8.0
13	K	128	ASP	8.0
8	F	127	ASN	8.0
13	K	144	GLY	8.0
14	L	66	GLY	8.0
19	Q	11	GLN	8.0
5	C	39	GLN	8.0
9	G	28	GLU	8.0
1	0	575	G	8.0
25	W	23	ARG	8.0
4	B	325	PRO	8.0
6	D	165	PHE	8.0
25	W	33	HIS	8.0
4	B	75	THR	8.0
4	B	145	THR	8.0
10	H	19	THR	8.0
12	J	60	GLU	8.0
11	I	29	GLN	8.0
24	V	38	LYS	8.0
27	Y	48	ASP	8.0
1	0	1965	C	8.0
3	A	161	GLY	8.0
22	T	8	ARG	8.0
1	0	601	G	8.0
4	B	81	VAL	8.0
13	K	173	ASP	8.0
15	M	2	ASP	8.0
15	M	8	ARG	8.0
28	Z	84	ARG	8.0
3	A	70	ALA	8.0

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Mol	Chain	Res	Type	RSRZ
5	C	227	GLY	8.0
5	C	241	ALA	8.0
29	1	18	LEU	8.0
27	Y	13	LYS	8.0
12	J	125	PHE	8.0
9	G	32	ASP	8.0
5	C	28	SER	8.0
10	H	107	THR	8.0
6	D	70	GLY	8.0
10	H	128	ALA	8.0
11	I	51	ALA	8.0
19	Q	15	PRO	8.0
10	H	43	ARG	8.0
12	J	144	ASP	8.0
15	M	45	ASP	8.0
4	B	34	GLY	8.0
6	D	23	VAL	8.0
15	M	72	GLY	8.0
22	T	30	ASN	8.0
1	0	2250	G	8.0
13	K	145	ALA	8.0
25	W	62	TYR	8.0
13	K	44	ARG	8.0
13	K	163	PHE	7.9
16	N	32	GLU	7.9
9	G	133	GLY	7.9
15	M	83	LYS	7.9
24	V	135	THR	7.9
6	D	135	VAL	7.9
9	G	39	VAL	7.9
24	V	139	VAL	7.9
10	H	95	ALA	7.9
9	G	29	GLN	7.9
14	L	114	ILE	7.9
21	S	6	GLN	7.9
27	Y	27	LEU	7.9
3	A	71	PRO	7.9
27	Y	9	LYS	7.9
4	B	130	ALA	7.9
4	B	260	GLN	7.9
22	T	132	VAL	7.9
9	G	116	LEU	7.9

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Mol	Chain	Res	Type	RSRZ
16	N	69	ASP	7.9
17	O	90	ASP	7.9
21	S	7	GLU	7.9
22	T	86	GLU	7.9
22	T	75	GLY	7.9
3	A	164	ARG	7.9
3	A	136	ALA	7.9
16	N	72	LYS	7.9
21	S	53	ILE	7.9
3	A	218	ASN	7.9
29	1	67	SER	7.9
22	T	10	GLU	7.9
4	B	144	HIS	7.9
22	T	141	HIS	7.9
29	1	158	ASP	7.9
5	C	114	ALA	7.9
18	P	14	ALA	7.9
4	B	189	MET	7.9
3	A	95	PRO	7.9
4	B	152	SER	7.9
9	G	51	GLU	7.9
12	J	58	GLN	7.9
3	A	154	ALA	7.9
5	C	124	VAL	7.9
19	Q	56	ALA	7.9
1	0	200	U	7.9
4	B	306	ARG	7.9
9	G	108	PRO	7.9
17	O	35	ILE	7.9
25	W	40	PRO	7.9
9	G	140	GLY	7.9
5	C	194	PHE	7.9
1	0	1929	G	7.9
13	K	94	GLU	7.9
23	U	88	GLU	7.9
4	B	296	VAL	7.9
6	D	73	VAL	7.9
24	V	30	GLN	7.9
4	B	71	THR	7.8
11	I	17	GLU	7.8
14	L	18	ALA	7.8
10	H	45	PRO	7.8

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Mol	Chain	Res	Type	RSRZ
20	R	36	CYS	7.8
4	B	323	LEU	7.8
13	K	90	LEU	7.8
25	W	47	LEU	7.8
1	0	2344	G	7.8
3	A	227	ASP	7.8
21	S	17	GLU	7.8
11	I	127	LYS	7.8
6	D	52	THR	7.8
6	D	68	PRO	7.8
20	R	22	VAL	7.8
5	C	104	ASP	7.8
10	H	32	ILE	7.8
23	U	42	SER	7.8
15	M	28	GLN	7.8
8	F	83	PHE	7.8
8	F	131	ALA	7.8
15	M	107	GLU	7.8
16	N	8	GLU	7.8
29	1	140	ALA	7.8
22	T	66	LEU	7.8
7	E	2	VAL	7.8
11	I	64	ARG	7.8
18	P	47	VAL	7.8
17	O	4	TYR	7.8
6	D	19	GLU	7.8
22	T	103	GLU	7.8
15	M	68	LYS	7.8
16	N	13	LYS	7.8
14	L	106	PRO	7.8
28	Z	79	LEU	7.8
17	O	20	GLU	7.8
3	A	185	LYS	7.8
14	L	23	GLY	7.8
22	T	64	THR	7.8
29	1	152	THR	7.8
4	B	324	ASP	7.8
13	K	103	ASP	7.8
4	B	169	SER	7.8
14	L	82	SER	7.8
21	S	60	GLN	7.8
6	D	44	ILE	7.8

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Mol	Chain	Res	Type	RSRZ
16	N	31	GLU	7.8
19	Q	2	LYS	7.8
13	K	33	ARG	7.8
4	B	100	TRP	7.8
4	B	280	ASP	7.8
5	C	229	PRO	7.8
15	M	118	GLN	7.8
5	C	3	ALA	7.8
7	E	95	ALA	7.8
11	I	103	GLU	7.8
13	K	185	GLU	7.8
23	U	47	ALA	7.8
29	1	33	LEU	7.8
17	O	101	HIS	7.8
9	G	101	VAL	7.7
29	1	40	VAL	7.7
1	0	598	C	7.7
14	L	102	ILE	7.7
18	P	31	ARG	7.7
7	E	27	GLY	7.7
21	S	61	GLY	7.7
4	B	36	PRO	7.7
7	E	96	ALA	7.7
18	P	9	HIS	7.7
3	A	51	ARG	7.7
13	K	23	ARG	7.7
9	G	83	ILE	7.7
10	H	111	GLY	7.7
13	K	89	GLY	7.7
23	U	51	ASP	7.7
10	H	125	ALA	7.7
14	L	17	ALA	7.7
19	Q	12	ARG	7.7
29	1	155	ASN	7.7
5	C	138	VAL	7.7
15	M	93	ASP	7.7
16	N	37	GLU	7.7
8	F	27	GLY	7.7
13	K	69	TYR	7.7
14	L	97	SER	7.7
19	Q	13	ARG	7.7
28	Z	90	PHE	7.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
21	S	52	ALA	7.7
6	D	169	THR	7.7
3	A	171	LYS	7.7
5	C	239	ALA	7.7
10	H	114	ALA	7.7
20	R	40	ALA	7.7
28	Z	77	ALA	7.7
13	K	66	LEU	7.7
28	Z	82	GLY	7.7
7	E	54	VAL	7.7
14	L	25	VAL	7.7
9	G	58	GLU	7.7
15	M	125	LYS	7.7
3	A	78	ASP	7.7
22	T	126	ASP	7.7
28	Z	7	PHE	7.7
13	K	88	ALA	7.7
14	L	98	LEU	7.7
25	W	66	GLY	7.7
11	I	42	ARG	7.7
28	Z	34	LYS	7.7
1	0	281	U	7.7
3	A	26	ASP	7.7
29	1	51	SER	7.7
23	U	77	PHE	7.7
4	B	282	GLY	7.7
9	G	73	LYS	7.7
11	I	130	GLU	7.7
18	P	61	GLU	7.7
22	T	22	GLU	7.7
22	T	104	GLU	7.7
21	S	56	ILE	7.6
9	G	13	ASP	7.6
13	K	124	ASP	7.6
3	A	211	LYS	7.6
6	D	87	ALA	7.6
1	0	1525	G	7.6
1	0	1948	G	7.6
29	1	93	MET	7.6
4	B	93	GLN	7.6
22	T	137	GLN	7.6
3	A	137	VAL	7.6

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Mol	Chain	Res	Type	RSRZ
14	L	76	VAL	7.6
29	1	156	ASP	7.6
17	O	69	LYS	7.6
5	C	36	ARG	7.6
8	F	86	ARG	7.6
23	U	41	PHE	7.6
25	W	75	ALA	7.6
8	F	42	TYR	7.6
19	Q	3	GLN	7.6
11	I	47	ASP	7.6
12	J	104	ASP	7.6
19	Q	6	LYS	7.6
22	T	87	HIS	7.6
24	V	63	LYS	7.6
28	Z	63	LYS	7.6
3	A	108	VAL	7.6
18	P	5	ILE	7.6
19	Q	42	VAL	7.6
29	1	102	VAL	7.6
29	1	124	VAL	7.6
3	A	91	GLY	7.6
6	D	101	THR	7.6
5	C	125	ALA	7.6
9	G	27	ALA	7.6
14	L	52	ALA	7.6
8	F	52	LYS	7.6
23	U	7	GLU	7.6
9	G	16	ASP	7.6
10	H	66	ARG	7.6
14	L	105	ASN	7.6
18	P	56	ASN	7.6
25	W	27	ARG	7.6
23	U	54	ILE	7.6
13	K	148	ALA	7.6
14	L	12	ALA	7.6
1	0	1521	C	7.6
3	A	142	SER	7.6
24	V	73	SER	7.6
5	C	195	VAL	7.6
6	D	137	PRO	7.6
7	E	22	VAL	7.6
10	H	104	PRO	7.6

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Mol	Chain	Res	Type	RSRZ
17	O	29	LYS	7.6
19	Q	62	VAL	7.6
20	R	10	GLY	7.6
13	K	46	GLN	7.6
6	D	145	ASP	7.6
5	C	193	LEU	7.6
14	L	7	LEU	7.6
29	1	17	HIS	7.6
4	B	134	GLY	7.6
10	H	5	GLY	7.6
20	R	18	GLY	7.6
20	R	33	SER	7.6
4	B	319	ASP	7.6
4	B	85	ALA	7.6
5	C	30	LEU	7.6
6	D	142	ALA	7.6
18	P	40	ALA	7.6
27	Y	23	ALA	7.6
16	N	42	LYS	7.5
16	N	66	LYS	7.5
22	T	37	GLU	7.5
2	9	24	U	7.5
10	H	86	THR	7.5
22	T	2	HIS	7.5
15	M	50	GLN	7.5
7	E	44	SER	7.5
13	K	17	ARG	7.5
15	M	33	ASP	7.5
10	H	129	THR	7.5
22	T	47	LYS	7.5
5	C	210	ALA	7.5
7	E	51	ALA	7.5
17	O	95	ALA	7.5
28	Z	80	ARG	7.5
19	Q	71	VAL	7.5
4	B	320	GLN	7.5
1	0	1527	A	7.5
10	H	12	LEU	7.5
13	K	30	GLY	7.5
10	H	99	ASP	7.5
22	T	81	ASP	7.5
1	0	1157	C	7.5

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Mol	Chain	Res	Type	RSRZ
9	G	126	ASN	7.5
13	K	40	ASN	7.5
3	A	124	VAL	7.5
4	B	35	GLN	7.5
15	M	66	GLN	7.5
17	O	21	ARG	7.5
4	B	171	SER	7.5
17	O	10	PRO	7.5
22	T	120	PRO	7.5
5	C	184	ARG	7.5
22	T	42	ARG	7.5
3	A	156	ILE	7.5
15	M	91	LYS	7.5
29	1	20	ILE	7.5
29	1	38	ILE	7.5
18	P	41	VAL	7.5
7	E	84	GLY	7.5
10	H	60	GLY	7.5
4	B	313	PRO	7.5
29	1	36	PRO	7.5
4	B	322	ARG	7.5
23	U	56	GLU	7.5
7	E	62	HIS	7.5
29	1	144	THR	7.5
3	A	68	ILE	7.5
5	C	166	ILE	7.5
6	D	139	TYR	7.5
12	J	96	VAL	7.5
12	J	138	GLY	7.5
18	P	66	VAL	7.5
19	Q	40	VAL	7.5
29	1	166	VAL	7.5
2	9	32	G	7.5
22	T	58	SER	7.5
3	A	213	LYS	7.4
9	G	74	ARG	7.4
27	Y	5	LYS	7.4
6	D	151	ILE	7.4
8	F	76	GLY	7.4
1	0	2508	C	7.4
18	P	65	VAL	7.4
19	Q	98	VAL	7.4

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Mol	Chain	Res	Type	RSRZ
5	C	224	ALA	7.4
29	1	15	GLN	7.4
17	O	104	PHE	7.4
4	B	200	ASP	7.4
20	R	7	ASP	7.4
24	V	28	LYS	7.4
3	A	82	VAL	7.4
5	C	111	VAL	7.4
8	F	72	VAL	7.4
29	1	103	VAL	7.4
6	D	37	ALA	7.4
29	1	80	TRP	7.4
18	P	29	ASP	7.4
3	A	93	THR	7.4
9	G	95	ARG	7.4
17	O	13	THR	7.4
21	S	59	ILE	7.4
4	B	104	PHE	7.4
9	G	90	LYS	7.4
4	B	159	ASP	7.4
4	B	275	ASP	7.4
28	Z	66	ASP	7.4
1	0	1210	G	7.4
7	E	37	THR	7.4
8	F	151	SER	7.4
10	H	113	ILE	7.4
19	Q	9	LYS	7.4
17	O	92	LEU	7.4
19	Q	16	LEU	7.4
28	Z	4	PRO	7.4
3	A	166	ASP	7.4
16	N	68	GLY	7.4
12	J	56	LYS	7.4
13	K	178	THR	7.4
4	B	263	GLU	7.4
6	D	12	GLU	7.4
8	F	48	ASN	7.4
10	H	93	ASN	7.4
13	K	147	ILE	7.4
10	H	49	LEU	7.4
14	L	29	VAL	7.4
29	1	76	VAL	7.4

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Mol	Chain	Res	Type	RSRZ
24	V	81	HIS	7.4
29	1	136	PRO	7.4
10	H	50	GLY	7.4
11	I	108	LYS	7.4
24	V	68	GLU	7.4
7	E	40	ILE	7.4
5	C	198	ASP	7.4
5	C	228	ALA	7.4
1	0	969	G	7.3
4	B	69	PRO	7.3
19	Q	88	PRO	7.3
5	C	226	GLY	7.3
13	K	38	LYS	7.3
4	B	161	MET	7.3
17	O	9	ASP	7.3
5	C	110	ALA	7.3
4	B	146	VAL	7.3
8	F	130	PRO	7.3
1	0	1522	A	7.3
4	B	329	TYR	7.3
29	1	96	ASN	7.3
17	O	86	LYS	7.3
18	P	55	GLN	7.3
25	W	34	LYS	7.3
4	B	22	GLU	7.3
13	K	99	GLU	7.3
6	D	134	LEU	7.3
14	L	27	GLY	7.3
19	Q	14	ALA	7.3
12	J	108	VAL	7.3
8	F	36	ASN	7.3
11	I	13	LYS	7.3
22	T	59	GLN	7.3
4	B	32	ASP	7.3
9	G	122	ASP	7.3
16	N	44	ASP	7.3
14	L	84	THR	7.3
24	V	108	ILE	7.3
25	W	32	LYS	7.3
10	H	67	GLN	7.3
18	P	73	ASP	7.3
14	L	40	HIS	7.3

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Mol	Chain	Res	Type	RSRZ
21	S	25	THR	7.3
5	C	177	GLY	7.3
4	B	61	PRO	7.3
14	L	95	ALA	7.3
29	1	145	ALA	7.3
6	D	103	ASN	7.3
9	G	99	GLU	7.3
5	C	202	THR	7.3
24	V	6	THR	7.3
20	R	44	ARG	7.3
29	1	115	ARG	7.3
21	S	40	PRO	7.3
28	Z	12	PRO	7.3
5	C	223	LEU	7.3
7	E	59	ILE	7.3
14	L	4	ASN	7.3
18	P	16	ASN	7.3
4	B	70	VAL	7.3
4	B	135	ASP	7.3
8	F	46	VAL	7.3
22	T	92	ASP	7.3
29	1	42	VAL	7.3
3	A	175	LYS	7.3
6	D	79	MET	7.3
9	G	81	ARG	7.3
5	C	230	GLY	7.3
5	C	236	THR	7.3
10	H	127	ALA	7.2
24	V	76	ALA	7.2
13	K	7	LYS	7.2
13	K	31	LYS	7.2
29	1	47	VAL	7.2
29	1	141	VAL	7.2
28	Z	17	HIS	7.2
29	1	99	GLY	7.2
8	F	129	ASP	7.2
22	T	57	PRO	7.2
29	1	92	PRO	7.2
3	A	140	LEU	7.2
4	B	178	LEU	7.2
22	T	129	LYS	7.2
23	U	69	LYS	7.2

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Mol	Chain	Res	Type	RSRZ
23	U	75	ALA	7.2
3	A	120	ARG	7.2
7	E	55	GLN	7.2
5	C	220	THR	7.2
3	A	153	ARG	7.2
5	C	109	LEU	7.2
5	C	123	LEU	7.2
19	Q	51	LEU	7.2
22	T	99	ALA	7.2
5	C	216	SER	7.2
8	F	126	VAL	7.2
10	H	35	HIS	7.2
3	A	116	GLY	7.2
4	B	336	GLN	7.2
4	B	45	LYS	7.2
5	C	233	THR	7.2
13	K	181	ASP	7.2
5	C	159	ALA	7.2
10	H	6	ALA	7.2
14	L	78	ALA	7.2
7	E	92	GLY	7.2
9	G	59	LYS	7.2
11	I	2	LYS	7.2
5	C	234	VAL	7.2
3	A	48	ASP	7.2
5	C	1	MET	7.2
28	Z	8	ASN	7.2
29	1	45	ASP	7.2
17	O	12	THR	7.2
4	B	292	PRO	7.2
19	Q	25	ALA	7.2
28	Z	60	LYS	7.2
13	K	80	SER	7.2
14	L	67	SER	7.2
10	H	122	GLY	7.2
14	L	68	GLY	7.2
9	G	9	ASP	7.2
16	N	28	ARG	7.2
18	P	39	ASP	7.2
18	P	11	THR	7.2
29	1	132	THR	7.2
15	M	7	LYS	7.2

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Mol	Chain	Res	Type	RSRZ
1	0	2336	G	7.2
1	0	2698	G	7.2
15	M	130	GLU	7.2
15	M	37	ARG	7.2
10	H	74	VAL	7.2
12	J	106	VAL	7.2
14	L	58	VAL	7.2
29	1	8	PRO	7.2
14	L	32	ARG	7.1
15	M	120	ARG	7.1
20	R	55	ALA	7.1
17	O	26	LYS	7.1
1	0	1279	U	7.1
8	F	133	GLU	7.1
3	A	102	GLY	7.1
14	L	46	GLY	7.1
7	E	87	ALA	7.1
19	Q	110	ALA	7.1
21	S	36	ALA	7.1
17	O	94	ASN	7.1
4	B	63	GLU	7.1
14	L	34	GLU	7.1
19	Q	72	ILE	7.1
23	U	86	GLU	7.1
1	0	1158	G	7.1
1	0	1159	G	7.1
4	B	193	PHE	7.1
5	C	21	VAL	7.1
9	G	79	PHE	7.1
3	A	217	ARG	7.1
3	A	235	ARG	7.1
3	A	237	GLY	7.1
4	B	37	GLY	7.1
4	B	155	LYS	7.1
6	D	155	HIS	7.1
5	C	29	ASP	7.1
18	P	69	SER	7.1
4	B	66	GLU	7.1
4	B	335	ASN	7.1
6	D	164	ALA	7.1
18	P	45	TYR	7.1
5	C	218	VAL	7.1

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Mol	Chain	Res	Type	RSRZ
18	P	62	LYS	7.1
29	1	22	VAL	7.1
7	E	33	THR	7.1
22	T	61	THR	7.1
1	0	808	A	7.1
5	C	170	ASP	7.1
17	O	41	GLY	7.1
4	B	188	ALA	7.1
8	F	73	GLN	7.1
14	L	77	ALA	7.1
24	V	124	ALA	7.1
8	F	142	LYS	7.1
14	L	60	VAL	7.1
3	A	36	ASP	7.1
3	A	149	ASP	7.1
1	0	2241	C	7.1
1	0	2909	G	7.1
7	E	86	ALA	7.1
7	E	103	ALA	7.1
29	1	151	LEU	7.1
20	R	8	TYR	7.1
9	G	112	ASP	7.1
4	B	89	THR	7.1
5	C	26	VAL	7.1
25	W	74	VAL	7.1
13	K	119	GLN	7.1
29	1	77	THR	7.1
4	B	55	ASN	7.1
28	Z	5	ARG	7.1
28	Z	29	ARG	7.1
6	D	160	ALA	7.1
8	F	47	GLU	7.1
13	K	137	ALA	7.1
19	Q	31	LEU	7.1
14	L	89	ILE	7.1
22	T	78	ASP	7.1
4	B	185	GLY	7.1
7	E	6	PHE	7.1
14	L	31	GLU	7.1
4	B	83	LEU	7.0
12	J	122	ALA	7.0
1	0	2637	A	7.0

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Mol	Chain	Res	Type	RSRZ
10	H	80	ILE	7.0
13	K	22	GLN	7.0
29	1	24	GLY	7.0
8	F	16	ARG	7.0
9	G	42	GLU	7.0
17	O	52	GLU	7.0
19	Q	23	VAL	7.0
13	K	154	LEU	7.0
1	0	1625	U	7.0
4	B	88	ASP	7.0
4	B	39	GLN	7.0
29	1	94	GLN	7.0
9	G	50	GLU	7.0
10	H	48	GLY	7.0
1	0	367	G	7.0
20	R	13	ILE	7.0
19	Q	78	THR	7.0
14	L	74	VAL	7.0
3	A	224	LYS	7.0
23	U	44	ASP	7.0
1	0	804	C	7.0
3	A	115	GLY	7.0
4	B	41	PHE	7.0
5	C	12	THR	7.0
10	H	92	ASP	7.0
25	W	30	GLU	7.0
5	C	119	ALA	7.0
4	B	50	HIS	7.0
29	1	90	HIS	7.0
17	O	150	PRO	7.0
4	B	334	SER	7.0
14	L	3	THR	7.0
3	A	66	ARG	7.0
4	B	25	ARG	7.0
22	T	69	ARG	7.0
22	T	148	ASP	7.0
6	D	163	VAL	7.0
24	V	93	VAL	7.0
6	D	102	GLY	7.0
18	P	78	ALA	7.0
4	B	267	ARG	7.0
15	M	30	ASP	7.0

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Mol	Chain	Res	Type	RSRZ
21	S	21	ASP	7.0
10	H	117	VAL	7.0
7	E	88	GLY	7.0
13	K	41	LYS	7.0
17	O	71	LYS	7.0
8	F	62	GLU	7.0
17	O	34	GLU	7.0
1	0	2769	C	7.0
9	G	125	SER	7.0
12	J	53	ARG	7.0
6	D	74	THR	7.0
25	W	36	LYS	7.0
15	M	27	ARG	6.9
23	U	53	SER	6.9
1	0	2239	C	6.9
13	K	68	GLU	6.9
13	K	120	GLU	6.9
13	K	149	GLU	6.9
23	U	35	GLU	6.9
5	C	206	ASN	6.9
19	Q	95	ASN	6.9
17	O	44	VAL	6.9
9	G	43	ARG	6.9
7	E	66	LEU	6.9
19	Q	22	GLN	6.9
29	1	112	ALA	6.9
29	1	60	SER	6.9
1	0	1211	G	6.9
1	0	1666	C	6.9
15	M	85	GLY	6.9
17	O	39	THR	6.9
4	B	311	PHE	6.9
21	S	9	ARG	6.9
9	G	80	LYS	6.9
5	C	8	LEU	6.9
10	H	84	ASP	6.9
15	M	39	ASP	6.9
20	R	37	GLU	6.9
5	C	113	SER	6.9
5	C	141	SER	6.9
1	0	810	G	6.9
4	B	194	ARG	6.9

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Mol	Chain	Res	Type	RSRZ
10	H	77	ARG	6.9
29	1	69	ILE	6.9
3	A	231	LYS	6.9
7	E	48	VAL	6.9
1	0	372	A	6.9
14	L	109	SER	6.9
5	C	43	LYS	6.9
21	S	34	GLN	6.9
6	D	100	ASP	6.9
21	S	30	ALA	6.9
21	S	35	ALA	6.9
4	B	328	ARG	6.9
15	M	81	LYS	6.9
1	0	2255	A	6.9
8	F	66	ASN	6.9
4	B	97	THR	6.9
10	H	51	ASP	6.9
10	H	131	ILE	6.9
1	0	368	C	6.9
6	D	157	LEU	6.9
10	H	87	ARG	6.9
14	L	79	VAL	6.9
4	B	87	GLU	6.9
23	U	82	GLU	6.9
8	F	34	GLY	6.9
3	A	29	HIS	6.9
6	D	27	ILE	6.9
25	W	38	LYS	6.9
29	1	148	ILE	6.9
22	T	71	GLU	6.8
3	A	42	VAL	6.8
14	L	5	PRO	6.8
3	A	40	GLY	6.8
5	C	128	GLY	6.8
22	T	123	GLY	6.8
6	D	82	GLU	6.8
3	A	60	PHE	6.8
14	L	20	SER	6.8
3	A	39	ALA	6.8
7	E	4	VAL	6.8
24	V	133	ASN	6.8
11	I	58	LYS	6.8

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Mol	Chain	Res	Type	RSRZ
5	C	167	ASP	6.8
29	1	52	ASP	6.8
4	B	173	ARG	6.8
10	H	65	ARG	6.8
1	0	285	A	6.8
14	L	81	PHE	6.8
19	Q	118	SER	6.8
24	V	8	LYS	6.8
6	D	80	ALA	6.8
14	L	65	LEU	6.8
17	O	147	LEU	6.8
7	E	72	VAL	6.8
21	S	22	ASP	6.8
8	F	138	ARG	6.8
11	I	27	ARG	6.8
1	0	2910	A	6.8
17	O	37	GLY	6.8
22	T	144	GLU	6.8
28	Z	81	GLU	6.8
17	O	96	VAL	6.8
19	Q	7	GLN	6.8
11	I	55	LYS	6.8
3	A	38	ILE	6.8
3	A	110	SER	6.8
9	G	120	SER	6.8
13	K	85	GLY	6.8
14	L	19	ARG	6.8
20	R	26	GLY	6.8
4	B	82	ALA	6.8
12	J	111	ALA	6.8
11	I	57	LYS	6.8
14	L	43	VAL	6.8
20	R	32	CYS	6.8
1	0	2004	U	6.8
14	L	57	THR	6.8
4	B	331	SER	6.8
22	T	80	ASP	6.8
24	V	101	GLY	6.8
29	1	34	TRP	6.8
3	A	104	PRO	6.8
5	C	121	ALA	6.8
5	C	147	LEU	6.8

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Mol	Chain	Res	Type	RSRZ
6	D	54	ALA	6.8
18	P	52	VAL	6.8
13	K	75	THR	6.8
15	M	36	THR	6.8
24	V	9	THR	6.8
3	A	178	LYS	6.8
5	C	197	SER	6.8
6	D	61	PHE	6.7
18	P	18	MET	6.7
4	B	174	LEU	6.7
6	D	91	ALA	6.7
9	G	114	GLU	6.7
19	Q	44	ALA	6.7
28	Z	16	GLU	6.7
4	B	94	ARG	6.7
24	V	119	ARG	6.7
10	H	76	GLN	6.7
14	L	11	ILE	6.7
4	B	90	PRO	6.7
5	C	235	PHE	6.7
20	R	39	ASN	6.7
5	C	150	THR	6.7
9	G	123	ARG	6.7
13	K	14	ARG	6.7
15	M	55	LYS	6.7
19	Q	19	ARG	6.7
7	E	19	ALA	6.7
22	T	149	LEU	6.7
25	W	78	ALA	6.7
19	Q	117	ASP	6.7
6	D	172	VAL	6.7
12	J	133	VAL	6.7
14	L	92	VAL	6.7
24	V	106	VAL	6.7
28	Z	18	GLN	6.7
29	1	150	GLN	6.7
29	1	113	PRO	6.7
6	D	140	ARG	6.7
28	Z	26	ARG	6.7
3	A	130	THR	6.7
1	0	514	G	6.7
10	H	119	GLN	6.7

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Mol	Chain	Res	Type	RSRZ
29	1	62	ILE	6.7
24	V	85	PHE	6.7
15	M	71	LYS	6.7
29	1	83	GLY	6.7
3	A	159	VAL	6.7
4	B	316	ARG	6.7
13	K	171	HIS	6.7
8	F	74	ASN	6.7
6	D	83	PHE	6.7
29	1	1	PRO	6.6
6	D	14	ARG	6.6
10	H	105	ARG	6.6
23	U	71	ARG	6.6
23	U	76	ARG	6.6
8	F	77	ALA	6.6
21	S	39	ALA	6.6
20	R	23	HIS	6.6
1	0	365	G	6.6
1	0	600	G	6.6
19	Q	94	SER	6.6
5	C	33	LYS	6.6
13	K	140	GLN	6.6
8	F	41	THR	6.6
3	A	46	GLU	6.6
9	G	127	ILE	6.6
14	L	62	GLY	6.6
14	L	93	GLY	6.6
29	1	59	MET	6.6
24	V	24	HIS	6.6
29	1	37	ASP	6.6
4	B	181	VAL	6.6
19	Q	87	VAL	6.6
5	C	133	ARG	6.6
13	K	15	GLU	6.6
19	Q	39	ASN	6.6
17	O	97	GLY	6.6
14	L	35	LYS	6.6
14	L	45	LEU	6.6
17	O	36	LYS	6.6
7	E	79	GLN	6.6
8	F	18	GLU	6.6
1	0	1665	G	6.6

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Mol	Chain	Res	Type	RSRZ
12	J	64	ILE	6.6
4	B	191	ASP	6.6
5	C	127	ARG	6.6
9	G	137	GLU	6.6
19	Q	34	GLU	6.6
21	S	63	GLU	6.6
29	1	19	ASP	6.6
20	R	38	ASN	6.6
14	L	75	THR	6.6
1	0	2770	G	6.6
17	O	7	GLU	6.6
19	Q	17	HIS	6.6
15	M	35	ILE	6.6
19	Q	63	ILE	6.6
22	T	147	ASP	6.6
1	0	272	A	6.6
10	H	46	LYS	6.6
29	1	172	PRO	6.6
21	S	41	GLU	6.6
8	F	137	ARG	6.6
29	1	12	ASP	6.6
6	D	40	ILE	6.6
7	E	63	ILE	6.6
1	0	1526	A	6.6
17	O	144	GLU	6.6
7	E	36	THR	6.6
10	H	83	PRO	6.6
14	L	115	ARG	6.5
19	Q	50	VAL	6.5
29	1	95	VAL	6.5
5	C	142	ASP	6.5
6	D	143	LYS	6.5
5	C	22	PHE	6.5
25	W	65	ALA	6.5
5	C	14	GLY	6.5
13	K	112	GLY	6.5
3	A	112	PRO	6.5
13	K	114	LYS	6.5
20	R	19	THR	6.5
25	W	73	THR	6.5
10	H	88	VAL	6.5
29	1	74	HIS	6.5

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Mol	Chain	Res	Type	RSRZ
4	B	333	GLU	6.5
5	C	191	SER	6.5
4	B	157	LYS	6.5
5	C	42	ARG	6.5
4	B	291	GLY	6.5
22	T	140	LYS	6.5
1	0	322	G	6.5
4	B	176	HIS	6.5
5	C	137	PRO	6.5
5	C	108	GLN	6.5
10	H	103	ASP	6.5
24	V	95	ASP	6.5
6	D	57	THR	6.5
2	9	122	C	6.5
1	0	289	G	6.5
4	B	297	LYS	6.5
15	M	74	GLN	6.5
25	W	48	LYS	6.5
17	O	103	GLY	6.5
5	C	192	ILE	6.5
14	L	48	ILE	6.5
18	P	15	MET	6.5
5	C	196	THR	6.5
25	W	21	LYS	6.5
29	1	58	THR	6.5
8	F	70	ARG	6.5
1	0	2346	C	6.5
5	C	238	SER	6.5
5	C	243	VAL	6.5
12	J	73	VAL	6.5
3	A	89	ALA	6.5
17	O	99	ALA	6.5
29	1	126	ILE	6.5
5	C	246	ARG	6.5
6	D	136	ARG	6.5
23	U	8	ARG	6.5
5	C	16	VAL	6.5
9	G	34	GLU	6.5
3	A	113	GLY	6.5
12	J	110	GLY	6.5
28	Z	24	LYS	6.5
1	0	809	G	6.5

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Mol	Chain	Res	Type	RSRZ
1	0	1610	G	6.5
9	G	25	GLN	6.5
10	H	81	ARG	6.5
28	Z	2	GLN	6.5
3	A	74	VAL	6.4
4	B	38	VAL	6.4
6	D	39	ASP	6.4
7	E	81	ASP	6.4
10	H	20	CYS	6.4
14	L	28	ASP	6.4
19	Q	68	ASP	6.4
7	E	17	LEU	6.4
6	D	149	ARG	6.4
28	Z	13	HIS	6.4
3	A	24	LYS	6.4
5	C	185	LYS	6.4
24	V	100	ASP	6.4
13	K	153	GLN	6.4
29	1	14	GLU	6.4
29	1	107	PHE	6.4
15	M	75	LYS	6.4
13	K	164	ASP	6.4
4	B	57	GLU	6.4
6	D	90	LEU	6.4
7	E	85	HIS	6.4
1	0	573	A	6.4
12	J	67	ARG	6.4
13	K	141	ARG	6.4
18	P	35	GLY	6.4
24	V	117	ARG	6.4
17	O	15	LYS	6.4
19	Q	77	VAL	6.4
11	I	10	GLU	6.4
22	T	122	ARG	6.4
24	V	3	ARG	6.4
29	1	54	ASP	6.4
4	B	168	GLY	6.4
1	0	2509	A	6.4
29	1	169	THR	6.4
5	C	148	VAL	6.4
6	D	130	VAL	6.4
3	A	28	GLU	6.4

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Mol	Chain	Res	Type	RSRZ
19	Q	35	TYR	6.4
29	1	89	SER	6.4
4	B	62	ARG	6.4
12	J	65	ASP	6.4
5	C	209	GLY	6.4
18	P	26	PHE	6.4
10	H	14	LYS	6.3
5	C	162	VAL	6.3
5	C	204	ALA	6.3
15	M	44	VAL	6.3
24	V	17	ALA	6.3
10	H	70	GLU	6.3
1	0	1964	U	6.3
6	D	95	THR	6.3
19	Q	38	ARG	6.3
19	Q	47	THR	6.3
25	W	49	ARG	6.3
3	A	107	ASN	6.3
3	A	69	LEU	6.3
14	L	64	VAL	6.3
19	Q	67	LEU	6.3
24	V	88	VAL	6.3
6	D	25	MET	6.3
19	Q	24	ARG	6.3
23	U	73	ARG	6.3
4	B	117	ASP	6.3
4	B	172	ASP	6.3
14	L	80	ASP	6.3
19	Q	66	ASP	6.3
15	M	46	GLU	6.3
1	0	806	A	6.3
1	0	1518	A	6.3
5	C	201	SER	6.3
9	G	15	ARG	6.3
4	B	190	ASN	6.3
6	D	11	HIS	6.3
21	S	46	ILE	6.3
24	V	14	ASP	6.3
5	C	106	GLU	6.3
1	0	1529	G	6.3
1	0	2826	G	6.3
8	F	26	LYS	6.3

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Mol	Chain	Res	Type	RSRZ
3	A	65	ARG	6.3
3	A	128	LEU	6.3
21	S	31	ARG	6.3
1	0	559	U	6.3
10	H	10	GLN	6.3
5	C	211	ASP	6.3
13	K	177	GLU	6.3
17	O	45	ASP	6.3
12	J	128	GLY	6.3
15	M	29	GLY	6.3
19	Q	36	GLY	6.3
19	Q	45	GLY	6.3
1	0	716	G	6.3
4	B	199	ALA	6.3
5	C	25	PRO	6.3
24	V	132	LEU	6.3
1	0	1524	U	6.3
5	C	132	ASP	6.3
22	T	98	PHE	6.3
5	C	5	ILE	6.3
7	E	26	THR	6.3
4	B	312	ARG	6.3
10	H	115	ARG	6.3
22	T	55	GLY	6.3
4	B	77	PRO	6.3
24	V	82	PRO	6.3
6	D	53	LYS	6.3
28	Z	64	LYS	6.3
1	0	362	G	6.3
8	F	65	ARG	6.3
28	Z	87	ARG	6.3
12	J	112	GLY	6.2
29	1	79	GLY	6.2
3	A	64	ASP	6.2
5	C	20	ASP	6.2
5	C	116	ALA	6.2
7	E	45	ALA	6.2
20	R	48	ASN	6.2
25	W	82	ALA	6.2
13	K	176	ARG	6.2
21	S	2	VAL	6.2
10	H	64	MET	6.2

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Mol	Chain	Res	Type	RSRZ
5	C	24	THR	6.2
19	Q	82	THR	6.2
10	H	110	LYS	6.2
21	S	20	LEU	6.2
24	V	20	LEU	6.2
3	A	59	GLU	6.2
3	A	109	GLU	6.2
13	K	72	GLU	6.2
3	A	146	LYS	6.2
4	B	40	GLY	6.2
4	B	74	GLU	6.2
10	H	2	GLU	6.2
17	O	148	GLU	6.2
13	K	180	LEU	6.2
2	9	40	C	6.2
8	F	45	GLN	6.2
4	B	137	GLY	6.2
6	D	45	THR	6.2
7	E	74	PHE	6.2
12	J	74	THR	6.2
4	B	326	GLU	6.2
1	0	2349	G	6.2
2	9	110	G	6.2
8	F	87	LYS	6.2
10	H	4	LEU	6.2
12	J	140	VAL	6.2
13	K	63	SER	6.2
24	V	91	HIS	6.2
22	T	85	ALA	6.2
5	C	154	VAL	6.2
7	E	68	ASP	6.2
29	1	147	ASP	6.2
10	H	52	LYS	6.2
13	K	132	ASN	6.2
29	1	106	ASN	6.2
29	1	68	HIS	6.2
7	E	9	PRO	6.2
15	M	42	GLU	6.2
9	G	102	ARG	6.2
1	0	1947	G	6.2
4	B	332	ASN	6.1
7	E	50	VAL	6.1

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Mol	Chain	Res	Type	RSRZ
4	B	101	THR	6.1
9	G	6	PHE	6.1
19	Q	99	THR	6.1
13	K	143	ARG	6.1
18	P	17	ASP	6.1
1	0	1552	G	6.1
2	9	50	G	6.1
3	A	105	VAL	6.1
17	O	109	MET	6.1
29	1	48	VAL	6.1
29	1	66	GLN	6.1
9	G	21	ARG	6.1
19	Q	83	ASP	6.1
24	V	11	ASP	6.1
3	A	94	LEU	6.1
12	J	136	ALA	6.1
29	1	146	ALA	6.1
7	E	65	GLU	6.1
13	K	28	LYS	6.1
14	L	2	LYS	6.1
29	1	134	SER	6.1
1	0	2871	G	6.1
22	T	133	LYS	6.1
28	Z	76	LYS	6.1
5	C	129	HIS	6.1
1	0	2879	A	6.1
19	Q	92	ASP	6.1
1	0	574	C	6.1
10	H	85	GLY	6.1
12	J	98	GLU	6.1
1	0	373	G	6.1
15	M	6	GLN	6.1
3	A	96	LEU	6.1
13	K	160	SER	6.1
20	R	5	GLU	6.1
24	V	143	GLU	6.1
3	A	75	GLY	6.1
6	D	146	LYS	6.1
17	O	106	GLY	6.1
24	V	115	ARG	6.1
19	Q	79	LEU	6.1
1	0	572	G	6.1

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Mol	Chain	Res	Type	RSRZ
12	J	129	ALA	6.1
10	H	100	GLU	6.1
20	R	50	GLU	6.1
19	Q	102	ASP	6.1
20	R	24	LYS	6.1
15	M	41	ARG	6.1
1	0	1209	C	6.1
19	Q	18	GLU	6.1
19	Q	113	GLU	6.1
1	0	2700	G	6.1
24	V	102	ASP	6.1
4	B	184	GLY	6.0
10	H	25	GLY	6.0
4	B	114	VAL	6.0
20	R	49	LEU	6.0
10	H	7	ASP	6.0
13	K	13	ARG	6.0
10	H	63	GLU	6.0
12	J	66	VAL	6.0
24	V	129	ILE	6.0
1	0	363	A	6.0
1	0	807	A	6.0
5	C	122	ASP	6.0
5	C	134	ASP	6.0
12	J	142	LEU	6.0
19	Q	91	LEU	6.0
4	B	124	GLU	6.0
8	F	37	GLY	6.0
29	1	27	GLY	6.0
3	A	155	THR	6.0
10	H	98	VAL	6.0
28	Z	20	HIS	6.0
21	S	27	LEU	6.0
24	V	72	ARG	6.0
7	E	35	GLU	6.0
4	B	183	ASP	6.0
21	S	33	VAL	6.0
5	C	217	GLU	6.0
6	D	18	ILE	6.0
7	E	118	LEU	6.0
1	0	2699	A	6.0
9	G	40	ASN	6.0

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Mol	Chain	Res	Type	RSRZ
7	E	57	GLU	6.0
8	F	84	ARG	6.0
19	Q	89	ARG	6.0
19	Q	74	VAL	6.0
6	D	69	ILE	6.0
1	0	1216	G	6.0
1	0	2337	G	6.0
1	0	2823	G	6.0
3	A	86	ALA	6.0
1	0	1667	A	6.0
1	0	2335	C	6.0
2	9	51	A	6.0
6	D	144	ARG	6.0
14	L	42	GLU	6.0
29	1	161	VAL	6.0
7	E	97	ALA	6.0
7	E	101	ALA	6.0
18	P	53	ASN	6.0
10	H	27	ARG	6.0
1	0	1555	G	5.9
2	9	53	G	5.9
1	0	558	C	5.9
1	0	2135	A	5.9
24	V	134	PRO	5.9
18	P	48	THR	5.9
16	N	27	GLN	5.9
17	O	108	ALA	5.9
7	E	64	PRO	5.9
1	0	2512	U	5.9
1	0	1151	G	5.9
1	0	1217	G	5.9
7	E	90	GLU	5.9
15	M	26	GLU	5.9
18	P	37	VAL	5.9
3	A	62	ASP	5.9
4	B	180	ILE	5.9
1	0	560	C	5.9
13	K	11	ARG	5.9
20	R	43	GLY	5.9
21	S	55	ARG	5.9
29	1	55	ASN	5.9
3	A	76	VAL	5.9

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Mol	Chain	Res	Type	RSRZ
18	P	12	GLU	5.9
25	W	35	LYS	5.9
12	J	95	ASP	5.9
20	R	53	ASP	5.9
1	0	577	G	5.9
2	9	21	G	5.9
10	H	13	GLU	5.9
22	T	82	GLU	5.9
10	H	120	ARG	5.9
12	J	79	ASP	5.9
21	S	10	ASP	5.9
29	1	85	GLU	5.9
12	J	132	LYS	5.9
24	V	96	LEU	5.9
3	A	127	GLN	5.9
14	L	53	GLN	5.9
19	Q	60	GLY	5.9
21	S	37	GLY	5.9
4	B	140	ARG	5.9
5	C	188	ARG	5.9
7	E	77	VAL	5.9
10	H	124	VAL	5.9
21	S	23	LEU	5.9
15	M	31	ILE	5.9
4	B	197	GLU	5.9
10	H	112	PRO	5.9
22	T	134	GLU	5.9
6	D	42	GLY	5.8
10	H	78	LYS	5.8
7	E	34	ASN	5.8
29	1	63	GLY	5.8
12	J	70	ASP	5.8
12	J	123	ASP	5.8
9	G	111	GLU	5.8
23	U	36	HIS	5.8
1	0	2912	C	5.8
10	H	96	VAL	5.8
3	A	236	GLY	5.8
22	T	63	GLU	5.8
4	B	99	VAL	5.8
1	0	255	A	5.8
22	T	154	ARG	5.8

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Mol	Chain	Res	Type	RSRZ
5	C	118	THR	5.8
13	K	156	GLU	5.8
22	T	60	GLU	5.8
29	1	98	GLU	5.8
14	L	83	GLY	5.8
21	S	28	LEU	5.8
20	R	27	ALA	5.8
1	0	2870	C	5.8
5	C	2	GLU	5.8
5	C	199	GLU	5.8
29	1	119	HIS	5.8
6	D	66	GLY	5.8
14	L	55	ASP	5.8
1	0	1902	G	5.8
1	0	2829	G	5.8
2	9	109	G	5.8
17	O	48	GLU	5.8
19	Q	64	ASN	5.8
20	R	47	ARG	5.8
6	D	81	GLU	5.8
19	Q	115	GLU	5.8
28	Z	72	GLY	5.8
1	0	1519	U	5.8
3	A	150	PRO	5.8
24	V	99	VAL	5.8
19	Q	37	GLN	5.8
14	L	110	HIS	5.8
4	B	162	GLU	5.8
14	L	38	ARG	5.8
17	O	149	GLU	5.8
20	R	41	ASP	5.8
5	C	219	ASN	5.8
1	0	371	U	5.8
6	D	97	GLN	5.8
4	B	131	HIS	5.8
5	C	149	LYS	5.8
3	A	77	GLY	5.8
18	P	20	PHE	5.8
19	Q	103	LEU	5.8
18	P	76	GLU	5.7
19	Q	69	LYS	5.7
29	1	53	GLU	5.7

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Mol	Chain	Res	Type	RSRZ
3	A	111	SER	5.7
24	V	18	ARG	5.7
24	V	16	ASP	5.7
21	S	38	GLY	5.7
4	B	139	LEU	5.7
20	R	31	PHE	5.7
11	I	30	LYS	5.7
28	Z	89	GLU	5.7
5	C	187	ARG	5.7
29	1	43	ASP	5.7
5	C	4	THR	5.7
29	1	84	MET	5.7
17	O	112	LYS	5.7
21	S	48	GLU	5.7
29	1	111	LYS	5.7
2	9	65	A	5.7
3	A	32	VAL	5.7
13	K	151	ASP	5.7
19	Q	46	ASP	5.7
29	1	61	THR	5.7
18	P	6	LYS	5.7
1	0	2510	C	5.7
1	0	1634	G	5.7
1	0	278	A	5.7
1	0	1280	A	5.7
14	L	13	ASP	5.7
4	B	107	GLU	5.7
3	A	73	GLY	5.7
10	H	30	LYS	5.7
4	B	113	ASP	5.7
12	J	126	SER	5.7
18	P	63	LYS	5.7
24	V	84	GLY	5.7
29	1	75	GLY	5.7
3	A	99	ILE	5.7
5	C	145	GLU	5.7
5	C	242	GLU	5.7
13	K	167	ASP	5.7
18	P	75	GLN	5.7
29	1	25	ASP	5.7
6	D	104	PHE	5.7
7	E	76	PHE	5.7

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Mol	Chain	Res	Type	RSRZ
18	P	67	ARG	5.7
29	1	109	GLY	5.7
1	0	1215	A	5.7
3	A	84	VAL	5.7
3	A	41	THR	5.7
1	0	2850	C	5.7
3	A	147	ARG	5.7
24	V	92	ASN	5.7
2	9	73	G	5.6
12	J	93	VAL	5.6
18	P	21	GLN	5.6
18	P	25	GLN	5.6
18	P	72	ASP	5.6
1	0	288	A	5.6
1	0	1207	A	5.6
1	0	1627	G	5.6
1	0	2914	A	5.6
19	Q	85	GLU	5.6
20	R	35	LYS	5.6
21	S	51	LYS	5.6
29	1	157	LYS	5.6
24	V	142	SER	5.6
14	L	85	ALA	5.6
4	B	110	ARG	5.6
14	L	6	ARG	5.6
3	A	87	GLU	5.6
19	Q	21	LYS	5.6
5	C	10	GLY	5.6
6	D	99	ASP	5.6
6	D	129	ASP	5.6
19	Q	54	ASP	5.6
3	A	117	LYS	5.6
4	B	266	LYS	5.6
10	H	91	GLU	5.6
17	O	93	GLU	5.6
12	J	119	THR	5.6
17	O	98	ASN	5.6
7	E	61	MET	5.6
15	M	47	GLY	5.6
28	Z	75	GLY	5.6
1	0	1669	A	5.6
14	L	14	LEU	5.6

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Mol	Chain	Res	Type	RSRZ
23	U	39	LYS	5.6
3	A	92	ASN	5.6
1	0	2697	A	5.6
12	J	76	LEU	5.6
1	0	324	G	5.6
1	0	583	G	5.6
1	0	1160	G	5.6
1	0	1611	G	5.6
1	0	1805	G	5.6
1	0	2248	C	5.6
19	Q	26	THR	5.6
24	V	21	THR	5.6
3	A	63	GLY	5.6
24	V	131	VAL	5.6
3	A	232	ARG	5.6
1	0	549	A	5.5
4	B	123	ALA	5.5
3	A	167	LYS	5.5
4	B	84	ARG	5.5
10	H	75	ARG	5.5
21	S	50	ARG	5.5
7	E	89	LEU	5.5
21	S	3	LEU	5.5
20	R	56	ARG	5.5
29	1	2	ARG	5.5
5	C	120	ASP	5.5
1	0	2375	G	5.5
1	0	2505	G	5.5
12	J	114	VAL	5.5
14	L	69	VAL	5.5
19	Q	81	LYS	5.5
19	Q	108	ARG	5.5
6	D	26	GLY	5.5
19	Q	100	ASP	5.5
19	Q	48	VAL	5.5
1	0	1670	G	5.5
7	E	12	LEU	5.5
19	Q	43	ASN	5.5
18	P	38	ALA	5.5
20	R	12	ASP	5.5
29	1	162	PHE	5.5
7	E	41	GLU	5.5

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Mol	Chain	Res	Type	RSRZ
9	G	128	LYS	5.5
1	0	603	A	5.5
5	C	112	ARG	5.5
14	L	59	VAL	5.5
1	0	323	C	5.5
5	C	157	LEU	5.5
1	0	561	G	5.5
3	A	100	PRO	5.5
4	B	108	LEU	5.5
5	C	163	HIS	5.5
14	L	86	GLU	5.5
15	M	38	GLU	5.5
7	E	71	GLY	5.5
1	0	2507	G	5.5
6	D	133	ASN	5.5
7	E	111	ILE	5.5
11	I	22	GLU	5.5
12	J	72	ASN	5.5
21	S	5	VAL	5.5
5	C	156	LEU	5.5
12	J	150	GLN	5.4
2	9	43	G	5.4
7	E	117	GLU	5.4
24	V	90	VAL	5.4
29	1	101	GLU	5.4
3	A	125	ASN	5.4
1	0	2869	G	5.4
27	Y	24	TYR	5.4
10	H	102	GLU	5.4
23	U	79	GLU	5.4
1	0	735	C	5.4
6	D	67	ASP	5.4
7	E	5	ASP	5.4
22	T	117	ARG	5.4
29	1	135	GLY	5.4
12	J	69	ILE	5.4
10	H	73	VAL	5.4
3	A	80	LEU	5.4
1	0	1208	C	5.4
29	1	65	PHE	5.4
4	B	273	GLU	5.4
3	A	97	ALA	5.4

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Mol	Chain	Res	Type	RSRZ
7	E	67	ALA	5.4
1	0	2511	A	5.4
7	E	31	LYS	5.4
18	P	3	ASP	5.4
29	1	105	GLU	5.4
7	E	32	GLY	5.4
21	S	4	HIS	5.4
29	1	142	GLY	5.4
5	C	18	LEU	5.4
29	1	5	LEU	5.4
6	D	105	SER	5.4
1	0	375	G	5.4
1	0	2350	G	5.4
2	9	31	C	5.4
29	1	64	THR	5.4
12	J	127	GLU	5.4
20	R	45	GLU	5.4
22	T	151	GLU	5.4
25	W	64	ILE	5.4
24	V	141	VAL	5.3
29	1	164	ASP	5.4
1	0	1926	G	5.3
1	0	2334	C	5.3
1	0	2786	G	5.3
4	B	78	MET	5.3
12	J	77	ALA	5.3
5	C	173	LYS	5.3
1	0	968	G	5.3
6	D	62	ASP	5.3
5	C	175	LYS	5.3
12	J	109	LEU	5.3
6	D	58	VAL	5.3
14	L	96	VAL	5.3
4	B	105	HIS	5.3
1	0	1144	A	5.3
1	0	1154	A	5.3
17	O	38	LYS	5.3
1	0	138	U	5.3
1	0	1496	G	5.3
1	0	2316	G	5.3
19	Q	84	GLY	5.3
24	V	111	LYS	5.3

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Mol	Chain	Res	Type	RSRZ
21	S	16	ARG	5.3
29	1	128	GLY	5.3
1	0	1628	G	5.3
10	H	22	ASP	5.3
14	L	15	LYS	5.3
24	V	94	ASP	5.3
5	C	152	GLU	5.3
1	0	578	C	5.3
5	C	207	LEU	5.3
6	D	84	LEU	5.3
9	G	134	GLU	5.3
1	0	817	G	5.3
1	0	2333	G	5.3
20	R	54	THR	5.3
24	V	80	LYS	5.3
1	0	361	C	5.2
1	0	2911	C	5.2
4	B	179	ASP	5.2
1	0	360	A	5.2
3	A	126	ALA	5.2
18	P	49	VAL	5.2
29	1	133	VAL	5.2
1	0	1143	G	5.2
1	0	2249	G	5.2
2	9	16	G	5.2
7	E	30	LYS	5.2
3	A	144	GLU	5.2
29	1	44	GLY	5.2
17	O	100	ASP	5.2
29	1	39	ASP	5.2
13	K	158	LEU	5.2
18	P	68	LEU	5.2
8	F	35	ASN	5.2
1	0	1904	A	5.2
12	J	107	LYS	5.2
28	Z	23	GLU	5.2
6	D	47	GLN	5.2
19	Q	32	ARG	5.2
10	H	59	LYS	5.2
1	0	254	C	5.2
9	G	5	GLU	5.2
23	U	78	GLU	5.2

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Mol	Chain	Res	Type	RSRZ
1	0	2908	A	5.2
28	Z	78	HIS	5.2
24	V	78	ARG	5.2
1	0	91	G	5.2
1	0	2748	G	5.2
4	B	96	LEU	5.2
4	B	141	LEU	5.2
6	D	75	LEU	5.2
17	O	42	GLU	5.2
18	P	44	GLN	5.2
1	0	1919	A	5.2
9	G	110	ASP	5.2
5	C	131	PHE	5.2
6	D	46	GLY	5.2
4	B	288	GLU	5.2
14	L	47	ARG	5.2
7	E	43	GLY	5.2
1	0	1221	G	5.2
1	0	2338	G	5.2
1	0	2772	G	5.2
29	1	46	THR	5.2
28	Z	68	LYS	5.2
21	S	32	ALA	5.1
14	L	9	SER	5.1
1	0	576	C	5.1
1	0	1156	C	5.1
21	S	24	LYS	5.1
24	V	86	GLU	5.1
5	C	136	VAL	5.1
7	E	69	GLU	5.1
1	0	2825	C	5.1
1	0	1113	G	5.1
3	A	143	GLY	5.1
1	0	2890	A	5.1
6	D	24	HIS	5.1
18	P	7	HIS	5.1
6	D	166	ILE	5.1
1	0	2240	U	5.1
1	0	2242	U	5.1
19	Q	93	THR	5.1
29	1	29	VAL	5.1
21	S	47	LYS	5.1

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Mol	Chain	Res	Type	RSRZ
17	O	107	GLU	5.1
22	T	56	GLU	5.1
5	C	27	ARG	5.1
12	J	130	ARG	5.1
14	L	73	ASP	5.1
17	O	105	ASP	5.1
4	B	120	PRO	5.1
9	G	96	GLU	5.1
4	B	128	ARG	5.1
19	Q	101	LEU	5.1
1	0	90	A	5.1
6	D	154	LYS	5.1
24	V	138	GLU	5.1
19	Q	111	ARG	5.1
7	E	47	LEU	5.1
7	E	83	LEU	5.1
4	B	177	ALA	5.1
1	0	1903	U	5.1
7	E	78	GLU	5.1
1	0	1589	G	5.1
25	W	46	LYS	5.0
25	W	63	LYS	5.0
1	0	1914	C	5.0
4	B	186	GLU	5.0
7	E	112	ALA	5.0
1	0	2768	A	5.0
29	1	50	GLU	5.0
24	V	23	ARG	5.0
6	D	72	LYS	5.0
19	Q	28	SER	5.0
19	Q	114	SER	5.0
4	B	86	TYR	5.0
14	L	99	GLU	5.0
20	R	16	GLY	5.0
19	Q	73	HIS	5.0
29	1	143	GLN	5.0
4	B	164	ARG	5.0
6	D	56	ARG	5.0
14	L	44	ASN	5.0
20	R	25	ASP	5.0
29	1	159	VAL	5.0
12	J	141	GLU	5.0

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Mol	Chain	Res	Type	RSRZ
18	P	43	GLU	5.0
19	Q	104	GLU	5.0
28	Z	21	GLU	5.0
1	0	1603	A	5.0
7	E	20	LEU	5.0
1	0	2771	G	5.0
9	G	35	THR	5.0
5	C	130	GLU	5.0
1	0	1355	A	5.0
1	0	2880	A	5.0
3	A	133	ARG	5.0
14	L	104	ASN	5.0
21	S	29	ASN	5.0
29	1	170	ARG	5.0
4	B	276	GLU	5.0
23	U	6	GLU	5.0
29	1	4	GLU	5.0
1	0	2352	G	5.0
1	0	311	C	5.0
2	9	46	C	5.0
14	L	63	LYS	4.9
1	0	1630	A	4.9
4	B	175	ASP	4.9
7	E	53	ASP	4.9
5	C	144	PHE	4.9
6	D	17	ARG	4.9
6	D	38	GLU	4.9
10	H	82	ARG	4.9
18	P	24	LEU	4.9
18	P	22	ASN	4.9
1	0	295	C	4.9
2	9	63	C	4.9
7	E	13	GLU	4.9
29	1	31	ARG	4.9
1	0	353	G	4.9
1	0	496	G	4.9
1	0	2516	G	4.9
1	0	2874	G	4.9
3	A	138	VAL	4.9
1	0	1915	U	4.9
6	D	88	LEU	4.9
19	Q	30	ASP	4.9

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Mol	Chain	Res	Type	RSRZ
25	W	76	GLY	4.9
5	C	13	ASP	4.9
6	D	161	ASP	4.9
28	Z	19	GLU	4.9
29	1	78	GLU	4.9
10	H	130	MET	4.9
29	1	72	MET	4.9
17	O	102	GLN	4.9
22	T	142	ASP	4.9
1	0	2878	U	4.9
7	E	115	VAL	4.9
20	R	14	GLU	4.9
4	B	79	ARG	4.9
1	0	296	G	4.9
1	0	2892	G	4.9
2	9	22	G	4.9
5	C	151	GLN	4.9
28	Z	91	GLN	4.9
6	D	55	LYS	4.9
19	Q	107	LYS	4.9
13	K	183	ASP	4.9
2	9	3	A	4.9
5	C	171	GLU	4.9
7	E	58	GLU	4.9
29	1	6	GLU	4.9
29	1	71	ASN	4.9
1	0	803	C	4.9
1	0	1153	C	4.9
5	C	232	LEU	4.9
18	P	10	VAL	4.9
7	E	23	ALA	4.9
1	0	307	G	4.9
29	1	11	VAL	4.8
29	1	139	GLU	4.8
24	V	10	PRO	4.8
20	R	4	ARG	4.8
1	0	1967	U	4.8
1	0	736	A	4.8
2	9	52	A	4.8
6	D	98	PHE	4.8
6	D	167	GLU	4.8
7	E	107	VAL	4.8

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Mol	Chain	Res	Type	RSRZ
1	0	1281	C	4.8
29	1	120	GLY	4.8
1	0	1214	G	4.8
7	E	14	ASP	4.8
7	E	16	ALA	4.8
21	S	57	LYS	4.8
1	0	287	C	4.8
12	J	113	GLN	4.8
18	P	51	GLN	4.8
24	V	104	GLU	4.8
12	J	80	ASP	4.8
12	J	118	LEU	4.8
18	P	46	ASP	4.8
19	Q	52	ARG	4.8
1	0	358	G	4.8
19	Q	58	GLU	4.8
29	1	82	TYR	4.8
7	E	80	GLN	4.8
7	E	38	LYS	4.8
5	C	7	ASP	4.8
28	Z	70	ARG	4.8
10	H	106	GLY	4.8
1	0	602	A	4.8
1	0	1145	G	4.8
1	0	2355	G	4.8
1	0	2913	A	4.8
1	0	717	C	4.8
5	C	15	GLU	4.8
6	D	65	GLU	4.8
5	C	105	LYS	4.8
1	0	812	A	4.8
1	0	1150	A	4.8
1	0	1137	G	4.8
1	0	1155	G	4.8
1	0	1619	G	4.8
2	9	49	G	4.8
14	L	56	GLU	4.8
19	Q	86	GLU	4.8
4	B	132	GLU	4.7
13	K	170	GLU	4.7
14	L	112	ARG	4.7
4	B	119	ASP	4.7

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Mol	Chain	Res	Type	RSRZ
5	C	17	ASP	4.7
1	0	2332	A	4.7
1	0	326	G	4.7
1	0	2667	G	4.7
7	E	18	GLU	4.7
12	J	94	ARG	4.7
24	V	121	GLU	4.7
24	V	128	GLY	4.7
1	0	2247	C	4.7
1	0	104	G	4.7
29	1	160	ARG	4.7
7	E	29	VAL	4.7
1	0	1517	U	4.7
3	A	98	GLU	4.7
18	P	70	GLU	4.7
19	Q	41	ARG	4.7
29	1	114	ARG	4.7
5	C	165	ASP	4.7
19	Q	27	LEU	4.7
1	0	1806	G	4.7
14	L	71	GLN	4.7
25	W	41	VAL	4.7
1	0	366	U	4.7
12	J	116	HIS	4.7
18	P	23	LYS	4.7
1	0	1562	C	4.7
6	D	15	GLU	4.7
13	K	174	GLU	4.7
1	0	604	G	4.7
1	0	738	G	4.7
3	A	83	GLY	4.7
29	1	30	THR	4.7
3	A	88	ILE	4.7
10	H	28	GLU	4.7
1	0	1664	A	4.7
1	0	2348	C	4.7
24	V	19	LEU	4.7
2	9	54	A	4.7
24	V	98	GLY	4.7
7	E	15	ASP	4.6
10	H	126	SER	4.6
24	V	97	GLU	4.6

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Mol	Chain	Res	Type	RSRZ
20	R	30	HIS	4.6
29	1	137	ASP	4.6
12	J	139	SER	4.6
5	C	115	LEU	4.6
4	B	125	GLU	4.6
1	0	294	C	4.6
14	L	87	THR	4.6
18	P	13	LYS	4.6
5	C	221	GLU	4.6
1	0	1629	G	4.6
7	E	102	GLY	4.6
24	V	89	ARG	4.6
1	0	1626	A	4.6
6	D	128	LEU	4.6
1	0	76	G	4.6
29	1	70	GLU	4.6
1	0	581	G	4.6
1	0	1563	G	4.6
1	0	2851	G	4.6
1	0	309	C	4.6
1	0	1147	C	4.6
1	0	2873	C	4.6
1	0	2886	C	4.6
1	0	262	A	4.6
1	0	2374	A	4.6
5	C	107	ARG	4.6
24	V	107	ARG	4.6
3	A	34	ASP	4.6
24	V	122	GLU	4.6
3	A	129	LEU	4.6
29	1	131	LEU	4.6
14	L	100	GLN	4.6
1	0	89	G	4.5
1	0	219	G	4.5
2	9	35	C	4.5
2	9	61	C	4.5
3	A	30	ARG	4.5
25	W	80	MET	4.5
2	9	44	A	4.5
1	0	1966	U	4.5
1	0	2872	U	4.5
24	V	125	GLU	4.5

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Mol	Chain	Res	Type	RSRZ
12	J	92	ASP	4.5
1	0	78	G	4.5
1	0	1497	G	4.5
1	0	1925	G	4.5
1	0	2701	G	4.5
1	0	2887	G	4.5
1	0	2691	A	4.5
1	0	1029	U	4.5
1	0	711	G	4.5
1	0	1218	U	4.5
3	A	72	GLU	4.5
5	C	160	LEU	4.5
19	Q	109	GLU	4.5
5	C	164	ALA	4.5
7	E	73	PRO	4.5
13	K	152	GLU	4.5
19	Q	80	GLU	4.5
1	0	571	C	4.5
1	0	310	U	4.5
1	0	258	G	4.5
1	0	1636	G	4.5
1	0	1927	A	4.5
2	9	76	G	4.5
19	Q	105	ASP	4.5
6	D	43	GLU	4.5
19	Q	97	ARG	4.5
25	W	77	LYS	4.5
4	B	290	ASP	4.5
29	1	100	ASP	4.5
2	9	55	U	4.4
7	E	7	ASP	4.4
1	0	585	C	4.4
1	0	2351	C	4.4
2	9	29	C	4.4
28	Z	92	GLU	4.4
1	0	1586	G	4.4
19	Q	76	ASP	4.4
1	0	1615	A	4.4
1	0	2891	A	4.4
1	0	273	G	4.4
1	0	2256	G	4.4
1	0	2257	G	4.4

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Mol	Chain	Res	Type	RSRZ
6	D	78	GLU	4.4
24	V	123	GLU	4.4
1	0	491	C	4.4
1	0	1253	C	4.4
1	0	1913	C	4.4
1	0	2347	C	4.4
1	0	95	A	4.4
1	0	1783	A	4.4
3	A	139	LYS	4.4
1	0	1605	G	4.4
5	C	231	ARG	4.4
29	1	32	ARG	4.4
1	0	2820	A	4.4
7	E	82	ASP	4.4
24	V	127	ALA	4.4
1	0	290	C	4.4
14	L	90	ASP	4.4
25	W	81	LYS	4.4
29	1	117	THR	4.4
2	9	66	G	4.3
18	P	36	GLU	4.3
24	V	7	GLU	4.3
24	V	15	GLU	4.3
7	E	24	ARG	4.3
7	E	46	GLU	4.3
1	0	292	G	4.3
2	9	74	G	4.3
1	0	2513	A	4.3
1	0	1219	U	4.3
8	F	82	LYS	4.3
1	0	364	C	4.3
1	0	1213	C	4.3
1	0	1785	G	4.3
24	V	103	THR	4.3
1	0	291	C	4.3
1	0	300	C	4.3
7	E	116	GLU	4.3
14	L	94	GLU	4.3
3	A	148	LEU	4.3
7	E	108	LEU	4.3
1	0	257	G	4.3
1	0	805	G	4.3

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Mol	Chain	Res	Type	RSRZ
1	0	2438	G	4.3
1	0	2855	G	4.3
2	9	19	G	4.3
1	0	584	U	4.3
1	0	1585	C	4.3
1	0	504	G	4.3
1	0	938	G	4.3
1	0	1592	G	4.3
1	0	2567	G	4.3
1	0	1804	A	4.3
1	0	2824	C	4.3
4	B	121	ASP	4.3
12	J	124	ASP	4.3
14	L	50	ARG	4.3
1	0	266	G	4.2
1	0	2421	G	4.2
1	0	562	A	4.2
3	A	33	GLU	4.2
1	0	728	C	4.2
2	9	26	C	4.2
2	9	33	U	4.2
3	A	101	GLU	4.2
1	0	802	G	4.2
2	9	17	G	4.2
7	E	70	LYS	4.2
1	0	302	A	4.2
2	9	57	A	4.2
7	E	42	ARG	4.2
29	1	153	ARG	4.2
1	0	1114	A	4.2
1	0	1424	A	4.2
1	0	2848	G	4.2
12	J	148	GLU	4.2
19	Q	29	ALA	4.2
29	1	7	ILE	4.2
18	P	42	GLU	4.2
1	0	1612	A	4.2
2	9	18	U	4.2
5	C	155	SER	4.2
18	P	34	LYS	4.2
1	0	314	G	4.2
1	0	320	G	4.2

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Mol	Chain	Res	Type	RSRZ
1	0	702	G	4.2
2	9	108	C	4.2
1	0	201	G	4.2
1	0	1579	C	4.2
1	0	1917	G	4.2
2	9	15	C	4.2
29	1	87	PHE	4.2
12	J	120	LEU	4.2
1	0	374	U	4.2
1	0	2291	A	4.1
2	9	67	C	4.1
1	0	503	G	4.1
1	0	1878	G	4.1
1	0	2564	G	4.1
28	Z	6	ARG	4.1
1	0	321	A	4.1
1	0	1624	A	4.1
1	0	2258	A	4.1
10	H	108	GLU	4.1
12	J	147	GLU	4.1
25	W	72	GLU	4.1
1	0	2696	G	4.1
7	E	99	THR	4.1
1	0	1515	A	4.1
1	0	2504	A	4.1
1	0	2831	C	4.1
1	0	1663	G	4.1
3	A	79	GLU	4.1
1	0	354	A	4.1
1	0	811	C	4.1
1	0	2885	A	4.1
2	9	62	A	4.1
1	0	1001	U	4.1
5	C	23	GLU	4.1
1	0	1512	G	4.1
7	E	8	VAL	4.1
29	1	163	GLN	4.1
1	0	286	U	4.1
4	B	112	LEU	4.1
1	0	2882	G	4.1
14	L	49	GLU	4.1
24	V	22	GLN	4.1

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Mol	Chain	Res	Type	RSRZ
6	D	156	ARG	4.1
1	0	1222	A	4.1
1	0	1559	A	4.1
1	0	1570	C	4.1
1	0	2875	A	4.1
1	0	2902	A	4.1
24	V	126	ASP	4.1
1	0	1441	G	4.0
1	0	1781	G	4.0
14	L	16	SER	4.0
7	E	75	ILE	4.0
29	1	149	GLU	4.0
1	0	2852	A	4.0
2	9	59	C	4.0
1	0	61	G	4.0
1	0	77	G	4.0
1	0	1021	G	4.0
1	0	1284	G	4.0
1	0	2692	G	4.0
1	0	2877	G	4.0
18	P	19	ASP	4.0
1	0	1764	C	4.0
1	0	1278	A	4.0
1	0	1631	A	4.0
7	E	105	ALA	4.0
1	0	605	C	4.0
21	S	19	GLU	4.0
24	V	118	GLU	4.0
1	0	1621	G	4.0
1	0	2867	G	4.0
1	0	298	C	4.0
1	0	423	A	4.0
2	9	38	A	4.0
6	D	162	ALA	4.0
5	C	168	ARG	4.0
1	0	256	C	4.0
1	0	2731	G	4.0
2	9	72	C	4.0
12	J	71	GLU	4.0
1	0	498	A	4.0
1	0	737	A	4.0
6	D	64	ARG	4.0

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Mol	Chain	Res	Type	RSRZ
7	E	28	ALA	3.9
1	0	351	G	3.9
1	0	543	G	3.9
1	0	964	G	3.9
1	0	1970	G	3.9
1	0	2446	G	3.9
1	0	1442	A	3.9
1	0	1637	A	3.9
1	0	1668	U	3.9
2	9	39	U	3.9
1	0	421	C	3.9
4	B	126	GLN	3.9
1	0	422	G	3.9
1	0	597	A	3.9
1	0	710	G	3.9
1	0	1588	G	3.9
1	0	1608	G	3.9
1	0	2074	A	3.9
1	0	2503	A	3.9
2	9	34	A	3.9
5	C	143	ASP	3.9
6	D	20	LYS	3.9
18	P	71	ASP	3.9
1	0	1142	C	3.9
1	0	2881	C	3.9
5	C	153	VAL	3.9
7	E	113	ASP	3.9
1	0	1110	G	3.9
1	0	1809	G	3.9
1	0	1587	U	3.9
3	A	31	LYS	3.9
1	0	1507	C	3.9
1	0	2526	C	3.9
14	L	70	LEU	3.9
24	V	83	SER	3.9
1	0	1591	A	3.9
1	0	1801	A	3.9
1	0	544	G	3.9
1	0	1112	G	3.9
1	0	1812	G	3.9
1	0	2005	G	3.9
5	C	11	ASN	3.9

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Mol	Chain	Res	Type	RSRZ
1	0	1803	C	3.9
1	0	129	A	3.9
4	B	102	ASP	3.9
1	0	87	C	3.9
1	0	719	C	3.9
1	0	1788	U	3.8
1	0	2884	G	3.8
1	0	1146	C	3.8
21	S	62	GLU	3.8
1	0	510	U	3.8
8	F	32	LYS	3.8
1	0	45	A	3.8
1	0	88	G	3.8
19	Q	59	GLU	3.8
1	0	2854	A	3.8
18	P	50	GLU	3.8
1	0	500	G	3.8
1	0	1072	G	3.8
1	0	2638	G	3.8
1	0	2828	G	3.8
3	A	151	GLN	3.8
1	0	96	A	3.8
1	0	411	A	3.8
1	0	939	A	3.8
19	Q	20	HIS	3.8
1	0	1979	G	3.8
1	0	2323	G	3.8
12	J	115	ARG	3.8
1	0	593	A	3.8
28	Z	73	GLU	3.8
29	1	81	GLU	3.8
29	1	57	LYS	3.8
1	0	591	A	3.7
1	0	1682	A	3.7
1	0	2479	A	3.7
5	C	146	ASP	3.7
19	Q	33	GLU	3.7
29	1	129	GLU	3.7
1	0	85	C	3.7
1	0	2747	C	3.7
2	9	41	C	3.7
1	0	301	G	3.7

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Mol	Chain	Res	Type	RSRZ
1	0	304	G	3.7
1	0	1604	G	3.7
3	A	131	HIS	3.7
1	0	246	G	3.7
1	0	394	G	3.7
1	0	795	G	3.7
1	0	2134	G	3.7
2	9	68	G	3.7
29	1	110	GLU	3.7
1	0	2907	C	3.7
1	0	1807	U	3.7
1	0	644	G	3.7
1	0	720	G	3.7
1	0	724	G	3.7
1	0	730	G	3.7
1	0	1556	G	3.7
1	0	1908	G	3.7
1	0	2128	G	3.7
1	0	2449	G	3.7
1	0	2900	G	3.7
1	0	965	A	3.7
1	0	58	C	3.7
1	0	93	C	3.7
1	0	1212	C	3.7
1	0	2795	C	3.7
13	K	155	GLU	3.7
1	0	1224	G	3.7
1	0	1498	G	3.7
1	0	2416	G	3.7
6	D	28	GLY	3.7
2	9	111	U	3.7
1	0	2565	C	3.7
1	0	1614	G	3.7
1	0	2570	G	3.7
1	0	2327	A	3.7
1	0	2694	A	3.7
1	0	2739	A	3.7
1	0	2329	C	3.6
2	9	30	C	3.6
12	J	68	GLU	3.6
1	0	588	G	3.6
1	0	1567	A	3.6

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Mol	Chain	Res	Type	RSRZ
1	0	1789	G	3.6
1	0	2324	G	3.6
1	0	2568	A	3.6
1	0	2740	G	3.6
1	0	582	C	3.6
1	0	1790	C	3.6
1	0	1906	C	3.6
29	1	73	PHE	3.6
29	1	125	GLU	3.6
1	0	587	A	3.6
1	0	1622	G	3.6
1	0	2408	A	3.6
1	0	1613	C	3.6
1	0	1792	C	3.6
1	0	2804	C	3.6
19	Q	96	VAL	3.6
12	J	131	GLU	3.6
1	0	1912	A	3.6
1	0	940	G	3.6
1	0	1901	G	3.6
1	0	1289	C	3.6
1	0	10	U	3.6
1	0	1220	U	3.6
1	0	1530	U	3.6
1	0	1577	U	3.6
1	0	1857	A	3.6
1	0	2030	A	3.6
1	0	2706	A	3.6
1	0	2814	A	3.6
1	0	2896	A	3.6
1	0	259	G	3.6
1	0	579	G	3.6
1	0	856	G	3.6
1	0	1576	G	3.6
2	9	75	G	3.6
1	0	590	A	3.6
2	9	77	A	3.6
1	0	492	C	3.6
1	0	512	G	3.6
1	0	1223	G	3.6
5	C	126	ASP	3.6
1	0	67	A	3.5

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Mol	Chain	Res	Type	RSRZ
1	0	397	A	3.5
2	9	71	C	3.5
1	0	1481	G	3.5
1	0	1780	G	3.5
2	9	94	G	3.5
3	A	85	ASP	3.5
1	0	1246	A	3.5
1	0	1642	A	3.5
1	0	1973	A	3.5
1	0	2373	U	3.5
1	0	2788	A	3.5
1	0	1513	C	3.5
1	0	1808	C	3.5
1	0	2515	C	3.5
6	D	159	PRO	3.5
1	0	727	G	3.5
1	0	1568	G	3.5
1	0	2404	G	3.5
4	B	127	ILE	3.5
1	0	1968	A	3.5
19	Q	49	GLU	3.5
1	0	553	G	3.5
1	0	1802	G	3.5
1	0	2742	G	3.5
1	0	2863	G	3.5
1	0	713	U	3.5
29	1	138	ILE	3.5
1	0	2566	A	3.5
1	0	893	C	3.5
7	E	10	ALA	3.5
1	0	267	G	3.5
1	0	564	G	3.5
1	0	592	G	3.5
1	0	1557	G	3.5
1	0	2072	G	3.5
1	0	344	C	3.5
1	0	1408	U	3.5
1	0	2705	U	3.5
1	0	196	G	3.5
1	0	681	G	3.5
1	0	697	G	3.5
1	0	1312	G	3.5

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Mol	Chain	Res	Type	RSRZ
1	0	1550	A	3.4
24	V	130	ARG	3.4
10	H	89	LYS	3.4
7	E	52	GLU	3.4
1	0	775	G	3.4
1	0	863	G	3.4
1	0	1089	G	3.4
1	0	1923	G	3.4
1	0	1933	G	3.4
1	0	1609	C	3.4
1	0	2463	A	3.4
4	B	129	ASP	3.4
1	0	703	G	3.4
1	0	2709	G	3.4
1	0	2713	G	3.4
2	9	20	G	3.4
21	S	26	GLU	3.4
24	V	87	GLU	3.4
1	0	490	C	3.4
1	0	586	C	3.4
1	0	876	A	3.4
1	0	1920	C	3.4
3	A	132	ASP	3.4
1	0	33	G	3.4
1	0	499	G	3.4
1	0	891	G	3.4
1	0	2482	G	3.4
1	0	2617	G	3.4
1	0	124	C	3.4
1	0	252	C	3.4
1	0	570	C	3.4
1	0	2785	C	3.4
1	0	2822	C	3.4
1	0	2857	C	3.4
2	9	121	C	3.4
1	0	1895	A	3.4
1	0	714	U	3.4
1	0	1130	U	3.4
1	0	1511	U	3.4
1	0	31	C	3.4
1	0	237	G	3.4
1	0	705	C	3.4

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Mol	Chain	Res	Type	RSRZ
14	L	107	GLU	3.4
1	0	293	A	3.4
1	0	1797	A	3.4
1	0	2447	A	3.4
12	J	121	ILE	3.4
4	B	103	GLU	3.4
1	0	1620	C	3.4
1	0	116	G	3.4
1	0	199	A	3.4
1	0	329	A	3.4
1	0	502	A	3.4
1	0	670	G	3.4
1	0	709	G	3.4
1	0	870	G	3.4
1	0	1135	G	3.4
1	0	1510	G	3.4
1	0	1590	A	3.4
1	0	1974	G	3.4
1	0	2420	G	3.4
1	0	2460	A	3.4
1	0	2708	G	3.4
1	0	2845	G	3.4
1	0	1244	U	3.3
1	0	271	C	3.3
1	0	2821	C	3.3
1	0	901	G	3.3
1	0	1386	G	3.3
1	0	2407	G	3.3
1	0	2483	A	3.3
1	0	2616	G	3.3
1	0	2741	A	3.3
1	0	2836	G	3.3
1	0	75	U	3.3
4	B	109	ASP	3.3
19	Q	61	GLU	3.3
23	U	4	ASP	3.3
2	9	107	C	3.3
1	0	476	A	3.3
2	9	56	A	3.3
1	0	743	G	3.3
1	0	1438	G	3.3
1	0	1976	G	3.3

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Mol	Chain	Res	Type	RSRZ
1	0	2817	G	3.3
1	0	1936	C	3.3
1	0	2360	C	3.3
1	0	2456	A	3.3
1	0	2703	A	3.3
6	D	173	GLU	3.3
1	0	871	G	3.3
1	0	376	C	3.3
1	0	734	U	3.3
1	0	1148	C	3.3
1	0	2534	C	3.3
2	9	48	C	3.3
2	9	118	C	3.3
7	E	106	THR	3.3
1	0	165	A	3.3
1	0	569	A	3.3
1	0	1580	A	3.3
1	0	1701	A	3.3
1	0	2538	A	3.3
2	9	45	A	3.3
1	0	336	G	3.3
1	0	1283	G	3.3
1	0	2009	G	3.3
1	0	2489	G	3.3
19	Q	106	GLU	3.3
29	1	130	GLU	3.3
1	0	1905	U	3.3
12	J	135	GLY	3.3
1	0	813	C	3.3
2	9	64	C	3.3
2	9	95	C	3.3
1	0	542	A	3.3
7	E	49	PHE	3.3
1	0	948	G	3.3
1	0	2289	G	3.3
2	9	88	G	3.3
2	9	114	G	3.3
1	0	235	C	3.2
5	C	237	GLU	3.2
1	0	161	A	3.2
1	0	485	A	3.2
1	0	547	A	3.2

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Mol	Chain	Res	Type	RSRZ
1	0	1329	A	3.2
1	0	1427	A	3.2
1	0	2702	A	3.2
1	0	2789	U	3.2
6	D	92	GLU	3.2
1	0	182	G	3.2
1	0	274	G	3.2
1	0	745	G	3.2
1	0	1444	G	3.2
1	0	1543	G	3.2
1	0	1932	G	3.2
1	0	2562	G	3.2
2	9	58	G	3.2
1	0	341	C	3.2
1	0	2695	C	3.2
1	0	74	A	3.2
1	0	317	A	3.2
2	9	120	A	3.2
1	0	79	G	3.2
1	0	892	G	3.2
1	0	1489	G	3.2
1	0	2861	G	3.2
1	0	959	C	3.2
1	0	1271	A	3.2
1	0	2468	A	3.2
1	0	2883	A	3.2
1	0	902	G	3.2
1	0	1087	G	3.2
1	0	2013	G	3.2
1	0	2046	G	3.2
1	0	2283	G	3.2
1	0	2782	G	3.2
2	9	101	G	3.2
1	0	880	C	3.2
1	0	2259	C	3.2
2	9	42	C	3.2
2	9	116	C	3.2
1	0	432	G	3.2
1	0	607	G	3.2
1	0	828	G	3.2
1	0	868	G	3.2
1	0	879	C	3.2

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Mol	Chain	Res	Type	RSRZ
1	0	898	G	3.2
1	0	1516	C	3.2
1	0	1655	G	3.2
1	0	1938	G	3.2
1	0	2773	G	3.2
1	0	2833	C	3.2
1	0	2847	G	3.2
1	0	1561	U	3.2
1	0	1671	U	3.2
1	0	895	A	3.2
1	0	1152	A	3.2
1	0	1476	A	3.2
1	0	2622	A	3.2
1	0	276	C	3.2
1	0	56	G	3.2
1	0	878	G	3.2
1	0	1036	G	3.2
1	0	2102	G	3.2
1	0	2876	G	3.2
5	C	205	ARG	3.1
1	0	319	A	3.1
1	0	270	U	3.1
1	0	594	C	3.1
1	0	712	C	3.1
1	0	899	C	3.1
1	0	963	C	3.1
1	0	1769	C	3.1
14	L	88	LYS	3.1
1	0	81	G	3.1
1	0	333	G	3.1
1	0	924	G	3.1
1	0	1292	G	3.1
1	0	1571	G	3.1
1	0	1774	G	3.1
1	0	2267	G	3.1
1	0	2412	G	3.1
8	F	39	GLY	3.1
1	0	513	A	3.1
1	0	841	A	3.1
1	0	1369	A	3.1
1	0	2414	A	3.1
1	0	2517	A	3.1

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Mol	Chain	Res	Type	RSRZ
1	0	2612	A	3.1
1	0	1149	U	3.1
2	9	28	U	3.1
1	0	1578	C	3.1
1	0	1633	C	3.1
1	0	2686	C	3.1
1	0	2819	C	3.1
1	0	2893	C	3.1
2	9	60	C	3.1
2	9	113	C	3.1
2	9	115	C	3.1
3	A	81	GLN	3.1
1	0	249	G	3.1
1	0	487	G	3.1
1	0	627	G	3.1
1	0	1706	G	3.1
1	0	1828	G	3.1
1	0	2284	G	3.1
1	0	2466	G	3.1
1	0	2537	G	3.1
1	0	2860	G	3.1
1	0	160	A	3.1
1	0	1607	A	3.1
2	9	103	A	3.1
12	J	134	GLU	3.1
29	1	23	GLU	3.1
1	0	299	U	3.1
1	0	396	U	3.1
1	0	2830	U	3.1
1	0	2888	U	3.1
1	0	36	C	3.1
1	0	338	C	3.1
1	0	21	G	3.1
1	0	97	G	3.1
1	0	744	G	3.1
1	0	765	G	3.1
1	0	814	G	3.1
1	0	1093	G	3.1
1	0	1311	G	3.1
1	0	2383	G	3.1
1	0	52	A	3.1
1	0	1569	U	3.1

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Mol	Chain	Res	Type	RSRZ
1	0	1746	A	3.1
1	0	1767	A	3.1
1	0	1930	A	3.1
1	0	2904	U	3.1
1	0	1509	C	3.1
1	0	1946	C	3.1
1	0	1987	C	3.1
2	9	27	C	3.1
14	L	103	GLU	3.1
1	0	102	A	3.1
1	0	140	G	3.1
1	0	327	A	3.1
1	0	545	G	3.1
1	0	771	G	3.1
1	0	782	G	3.1
1	0	877	G	3.1
1	0	1924	A	3.1
1	0	2481	G	3.1
1	0	2712	G	3.1
1	0	2792	A	3.1
1	0	2827	A	3.1
1	0	550	C	3.1
1	0	2409	C	3.1
4	B	118	HIS	3.1
29	1	121	ASP	3.1
7	E	104	ALA	3.1
1	0	92	G	3.0
1	0	352	A	3.0
1	0	404	G	3.0
1	0	887	G	3.0
1	0	1108	G	3.0
1	0	1226	G	3.0
1	0	1449	G	3.0
1	0	1546	G	3.0
1	0	1799	G	3.0
1	0	2096	A	3.0
2	9	5	G	3.0
29	1	127	ASP	3.0
1	0	57	C	3.0
1	0	658	C	3.0
1	0	1564	C	3.0
1	0	1593	C	3.0

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Mol	Chain	Res	Type	RSRZ
1	0	1768	C	3.0
1	0	1380	U	3.0
1	0	2328	U	3.0
7	E	119	ARG	3.0
1	0	2372	A	3.0
1	0	2813	A	3.0
1	0	428	G	3.0
1	0	1039	G	3.0
1	0	1315	G	3.0
1	0	1475	G	3.0
1	0	1694	G	3.0
1	0	1819	G	3.0
1	0	2418	G	3.0
1	0	732	C	3.0
1	0	1008	C	3.0
1	0	1566	C	3.0
1	0	1699	C	3.0
1	0	2243	C	3.0
1	0	2269	C	3.0
1	0	313	U	3.0
1	0	306	A	3.0
1	0	700	A	3.0
1	0	1242	A	3.0
1	0	1778	A	3.0
2	9	47	A	3.0
1	0	885	G	3.0
1	0	2522	G	3.0
1	0	2862	G	3.0
1	0	1787	C	3.0
1	0	2554	U	3.0
2	9	119	C	3.0
29	1	171	LYS	3.0
1	0	788	A	3.0
1	0	2465	A	3.0
1	0	2435	U	3.0
1	0	2858	U	3.0
21	S	15	GLU	3.0
1	0	443	C	3.0
1	0	505	C	3.0
1	0	1126	C	3.0
1	0	1387	G	3.0
1	0	1762	C	3.0

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Mol	Chain	Res	Type	RSRZ
1	0	2068	G	3.0
1	0	2357	G	3.0
1	0	2475	C	3.0
1	0	2580	G	3.0
3	A	61	GLU	3.0
1	0	472	A	3.0
1	0	519	A	3.0
1	0	671	A	3.0
1	0	846	A	3.0
1	0	1040	A	3.0
1	0	1352	A	3.0
1	0	2054	A	3.0
1	0	2089	A	3.0
1	0	2437	A	3.0
1	0	65	C	3.0
1	0	1450	C	3.0
1	0	2396	C	3.0
1	0	2868	C	3.0
1	0	669	G	3.0
1	0	836	G	3.0
1	0	1425	G	3.0
1	0	1697	G	3.0
1	0	1765	G	3.0
1	0	1896	G	3.0
1	0	1971	G	3.0
1	0	2730	G	3.0
1	0	2763	G	3.0
1	0	312	U	3.0
1	0	325	U	3.0
1	0	1028	U	3.0
1	0	818	A	3.0
1	0	2433	A	3.0
1	0	40	C	3.0
1	0	1928	C	3.0
1	0	2901	C	3.0
1	0	452	G	2.9
1	0	554	G	2.9
1	0	1131	G	2.9
1	0	1795	G	2.9
1	0	2898	G	2.9
1	0	359	U	2.9
1	0	495	A	2.9

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Mol	Chain	Res	Type	RSRZ
1	0	1448	A	2.9
1	0	1494	A	2.9
1	0	2689	A	2.9
1	0	260	C	2.9
1	0	318	C	2.9
1	0	668	C	2.9
1	0	2065	C	2.9
1	0	209	G	2.9
1	0	387	G	2.9
1	0	388	G	2.9
1	0	390	G	2.9
1	0	471	G	2.9
1	0	792	G	2.9
1	0	918	G	2.9
1	0	1378	G	2.9
1	0	1800	G	2.9
1	0	2491	G	2.9
1	0	2529	G	2.9
1	0	2753	G	2.9
1	0	277	U	2.9
1	0	425	U	2.9
1	0	1111	U	2.9
1	0	1282	U	2.9
1	0	158	A	2.9
1	0	177	A	2.9
1	0	2395	A	2.9
1	0	2905	A	2.9
1	0	82	C	2.9
1	0	239	C	2.9
1	0	763	C	2.9
1	0	1892	C	2.9
1	0	1916	C	2.9
1	0	2647	C	2.9
1	0	1791	U	2.9
1	0	2320	U	2.9
2	9	112	U	2.9
1	0	641	G	2.9
1	0	1532	G	2.9
1	0	2379	G	2.9
1	0	1090	A	2.9
1	0	1252	A	2.9
1	0	1287	A	2.9

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Mol	Chain	Res	Type	RSRZ
1	0	1437	A	2.9
1	0	1661	A	2.9
1	0	2783	A	2.9
1	0	704	C	2.9
1	0	769	C	2.9
1	0	884	C	2.9
1	0	925	C	2.9
1	0	2405	C	2.9
1	0	2685	C	2.9
1	0	779	U	2.9
1	0	2016	U	2.9
1	0	334	G	2.9
1	0	634	G	2.9
1	0	772	G	2.9
1	0	2288	G	2.9
1	0	2520	G	2.9
1	0	2611	G	2.9
1	0	2683	G	2.9
1	0	2734	G	2.9
1	0	316	A	2.9
1	0	1934	A	2.9
1	0	2784	A	2.9
1	0	2805	A	2.9
1	0	197	C	2.9
1	0	1988	C	2.9
1	0	2008	U	2.9
1	0	2476	C	2.9
1	0	1316	G	2.9
1	0	2397	G	2.9
1	0	2663	U	2.9
1	0	2693	U	2.9
1	0	117	A	2.9
1	0	767	A	2.9
1	0	1081	A	2.9
1	0	1088	A	2.9
1	0	1754	A	2.9
1	0	2101	A	2.9
1	0	2321	A	2.9
1	0	2569	A	2.9
1	0	130	C	2.9
1	0	401	C	2.9
1	0	920	C	2.9

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Mol	Chain	Res	Type	RSRZ
1	0	1245	C	2.9
1	0	1793	C	2.9
1	0	833	G	2.8
1	0	1141	U	2.8
1	0	1324	G	2.8
1	0	1648	G	2.8
1	0	2080	G	2.8
1	0	2544	G	2.8
1	0	2646	G	2.8
1	0	2866	U	2.8
1	0	188	C	2.8
1	0	350	C	2.8
1	0	776	A	2.8
1	0	793	A	2.8
1	0	1686	C	2.8
1	0	2678	A	2.8
1	0	2707	C	2.8
2	9	37	C	2.8
1	0	1766	U	2.8
1	0	2290	U	2.8
1	0	38	G	2.8
1	0	315	G	2.8
1	0	345	G	2.8
1	0	456	G	2.8
1	0	506	G	2.8
1	0	691	G	2.8
1	0	1045	G	2.8
1	0	1794	G	2.8
1	0	2480	G	2.8
1	0	2810	G	2.8
2	9	100	G	2.8
1	0	148	A	2.8
1	0	168	C	2.8
1	0	305	A	2.8
1	0	538	C	2.8
1	0	546	C	2.8
1	0	1020	A	2.8
1	0	1581	A	2.8
1	0	1606	A	2.8
1	0	1662	C	2.8
1	0	642	G	2.8
1	0	661	G	2.8

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Mol	Chain	Res	Type	RSRZ
1	0	86	A	2.8
1	0	232	A	2.8
1	0	596	C	2.8
1	0	632	A	2.8
1	0	696	C	2.8
1	0	778	C	2.8
1	0	857	A	2.8
1	0	1353	C	2.8
1	0	1367	A	2.8
1	0	1399	A	2.8
1	0	1582	C	2.8
1	0	2011	A	2.8
1	0	2653	A	2.8
1	0	2899	A	2.8
1	0	2906	A	2.8
12	J	117	GLU	2.8
1	0	115	U	2.8
1	0	187	A	2.8
1	0	332	G	2.8
1	0	679	G	2.8
1	0	699	C	2.8
1	0	781	C	2.8
1	0	834	G	2.8
1	0	1037	G	2.8
1	0	1046	G	2.8
1	0	1406	A	2.8
1	0	1471	A	2.8
1	0	1491	G	2.8
1	0	1935	C	2.8
1	0	1975	C	2.8
1	0	2090	G	2.8
1	0	2370	A	2.8
1	0	2543	G	2.8
1	0	2649	A	2.8
1	0	2794	G	2.8
2	9	36	C	2.8
1	0	253	U	2.8
1	0	826	U	2.8
6	D	131	THR	2.8
1	0	762	C	2.8
1	0	889	C	2.8
1	0	1044	C	2.8

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Mol	Chain	Res	Type	RSRZ
1	0	1462	C	2.8
1	0	1558	C	2.8
1	0	2245	C	2.8
1	0	2376	C	2.8
1	0	2388	C	2.8
1	0	2464	C	2.8
1	0	2571	C	2.8
1	0	2636	C	2.8
1	0	80	A	2.8
1	0	447	A	2.8
1	0	746	A	2.8
1	0	882	A	2.8
1	0	1261	A	2.8
1	0	967	U	2.8
1	0	1683	G	2.8
1	0	1782	G	2.8
1	0	2563	U	2.8
1	0	2668	G	2.8
2	9	7	G	2.8
1	0	1102	C	2.7
1	0	1508	C	2.7
1	0	2406	U	2.7
1	0	189	A	2.7
1	0	897	A	2.7
1	0	2356	A	2.7
1	0	164	G	2.7
1	0	269	G	2.7
1	0	417	G	2.7
1	0	656	G	2.7
1	0	723	G	2.7
1	0	1325	G	2.7
1	0	1681	G	2.7
1	0	1703	G	2.7
1	0	1989	G	2.7
1	0	2001	G	2.7
1	0	2050	G	2.7
1	0	2110	G	2.7
1	0	2471	G	2.7
1	0	2670	G	2.7
1	0	555	U	2.7
1	0	556	C	2.7
1	0	1023	C	2.7

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Mol	Chain	Res	Type	RSRZ
1	0	2704	C	2.7
1	0	829	A	2.7
1	0	1922	A	2.7
1	0	2354	A	2.7
1	0	678	G	2.7
1	0	690	G	2.7
1	0	740	G	2.7
1	0	1002	G	2.7
1	0	1054	G	2.7
1	0	1269	G	2.7
1	0	1322	G	2.7
1	0	1323	G	2.7
1	0	1354	G	2.7
1	0	1660	G	2.7
1	0	1986	G	2.7
1	0	2058	G	2.7
7	E	98	VAL	2.7
1	0	864	U	2.7
1	0	2322	U	2.7
19	Q	57	GLY	2.7
1	0	139	C	2.7
1	0	741	C	2.7
1	0	838	C	2.7
1	0	890	C	2.7
1	0	1043	C	2.7
1	0	1365	C	2.7
1	0	2903	C	2.7
1	0	926	A	2.7
1	0	1307	A	2.7
1	0	2100	A	2.7
1	0	2112	A	2.7
1	0	1138	G	2.7
1	0	1391	G	2.7
1	0	1490	G	2.7
1	0	1945	G	2.7
1	0	1995	G	2.7
1	0	2000	G	2.7
1	0	2574	G	2.7
1	0	2642	G	2.7
1	0	2815	G	2.7
1	0	179	C	2.7
1	0	245	C	2.7

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Mol	Chain	Res	Type	RSRZ
1	0	342	C	2.7
1	0	881	C	2.7
1	0	946	C	2.7
1	0	1035	C	2.7
1	0	1361	C	2.7
1	0	1426	C	2.7
1	0	1824	C	2.7
1	0	1888	C	2.7
1	0	2844	C	2.7
1	0	241	A	2.7
1	0	843	A	2.7
1	0	1379	A	2.7
1	0	1656	A	2.7
1	0	2380	A	2.7
1	0	2778	A	2.7
6	D	76	ARG	2.7
1	0	469	G	2.7
1	0	752	G	2.7
1	0	830	G	2.7
1	0	850	U	2.7
1	0	1034	G	2.7
1	0	1100	G	2.7
1	0	1344	G	2.7
1	0	1460	G	2.7
1	0	1541	G	2.7
1	0	2044	G	2.7
1	0	2073	G	2.7
1	0	2285	G	2.7
1	0	2572	G	2.7
1	0	2585	G	2.7
1	0	2726	U	2.7
2	9	14	G	2.7
1	0	111	C	2.7
1	0	718	C	2.7
1	0	931	C	2.7
1	0	395	A	2.7
1	0	867	A	2.7
1	0	1463	A	2.7
1	0	2856	A	2.7
1	0	2849	U	2.7
1	0	105	G	2.7
1	0	816	G	2.7

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Mol	Chain	Res	Type	RSRZ
1	0	869	G	2.7
1	0	1295	G	2.7
1	0	1540	G	2.7
1	0	1595	G	2.7
1	0	1713	G	2.7
1	0	1730	G	2.7
1	0	2091	G	2.7
1	0	2270	G	2.7
1	0	2525	G	2.7
1	0	2658	G	2.7
1	0	385	C	2.7
1	0	474	C	2.7
1	0	557	C	2.7
1	0	764	C	2.7
1	0	936	C	2.7
1	0	1103	C	2.7
1	0	1403	C	2.7
1	0	1575	C	2.7
1	0	2106	C	2.7
1	0	2536	C	2.7
1	0	2767	C	2.7
1	0	922	A	2.7
1	0	1978	A	2.7
1	0	953	G	2.6
1	0	1265	G	2.6
1	0	1647	G	2.6
1	0	1851	G	2.6
1	0	2075	G	2.6
1	0	2359	G	2.6
1	0	2540	G	2.6
1	0	2716	G	2.6
1	0	839	C	2.6
1	0	1243	C	2.6
1	0	1553	C	2.6
1	0	1644	C	2.6
1	0	1650	C	2.6
1	0	1692	C	2.6
1	0	2029	C	2.6
1	0	2126	C	2.6
1	0	2548	C	2.6
1	0	2559	C	2.6
1	0	2594	C	2.6

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Mol	Chain	Res	Type	RSRZ
2	9	82	U	2.6
1	0	761	A	2.6
1	0	780	A	2.6
1	0	827	A	2.6
1	0	908	A	2.6
1	0	1459	A	2.6
1	0	2382	A	2.6
1	0	2470	A	2.6
14	L	54	GLU	2.6
1	0	17	G	2.6
1	0	28	G	2.6
1	0	39	G	2.6
1	0	135	G	2.6
1	0	672	G	2.6
1	0	742	G	2.6
1	0	1075	G	2.6
1	0	1385	G	2.6
1	0	1760	G	2.6
1	0	2113	G	2.6
1	0	2124	G	2.6
1	0	2592	G	2.6
1	0	2834	G	2.6
2	9	78	G	2.6
1	0	141	C	2.6
1	0	244	C	2.6
1	0	966	U	2.6
1	0	1025	C	2.6
1	0	1334	C	2.6
1	0	1343	C	2.6
1	0	1388	U	2.6
1	0	1856	C	2.6
1	0	2109	U	2.6
1	0	2432	C	2.6
1	0	2448	U	2.6
1	0	2688	U	2.6
1	0	2895	C	2.6
1	0	459	A	2.6
1	0	1248	A	2.6
1	0	1345	A	2.6
1	0	1729	A	2.6
1	0	1969	A	2.6
1	0	125	U	2.6

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Mol	Chain	Res	Type	RSRZ
1	0	393	G	2.6
1	0	747	G	2.6
1	0	1542	G	2.6
1	0	1688	G	2.6
1	0	1867	G	2.6
1	0	1891	G	2.6
1	0	2014	G	2.6
1	0	2330	U	2.6
1	0	2428	G	2.6
1	0	2602	G	2.6
1	0	2606	G	2.6
1	0	2715	G	2.6
1	0	355	C	2.6
1	0	405	C	2.6
1	0	1594	C	2.6
1	0	2002	C	2.6
1	0	2626	C	2.6
1	0	2676	C	2.6
1	0	2790	C	2.6
1	0	166	A	2.6
1	0	886	A	2.6
1	0	1274	A	2.6
1	0	1465	A	2.6
1	0	1684	A	2.6
1	0	1775	A	2.6
1	0	1836	A	2.6
1	0	2081	A	2.6
1	0	2118	A	2.6
1	0	2675	A	2.6
1	0	2727	A	2.6
2	9	13	A	2.6
1	0	855	U	2.6
1	0	883	U	2.6
1	0	1838	U	2.6
1	0	275	G	2.6
1	0	416	G	2.6
1	0	475	G	2.6
1	0	774	C	2.6
1	0	873	G	2.6
1	0	1228	C	2.6
1	0	1398	G	2.6
1	0	1415	G	2.6

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Mol	Chain	Res	Type	RSRZ
1	0	1430	G	2.6
1	0	1453	G	2.6
1	0	1584	C	2.6
1	0	1649	G	2.6
1	0	1676	G	2.6
1	0	1695	G	2.6
1	0	1725	C	2.6
1	0	1823	G	2.6
1	0	2079	G	2.6
1	0	2371	G	2.6
1	0	2426	G	2.6
1	0	2487	C	2.6
1	0	2627	G	2.6
1	0	113	A	2.6
1	0	261	A	2.6
1	0	486	A	2.6
1	0	654	A	2.6
1	0	688	A	2.6
1	0	1641	A	2.6
1	0	2601	A	2.6
1	0	2635	A	2.6
1	0	768	U	2.6
1	0	837	U	2.6
1	0	1412	U	2.6
1	0	1831	U	2.6
19	Q	75	GLU	2.6
1	0	162	C	2.6
1	0	729	C	2.6
1	0	770	C	2.6
1	0	783	C	2.6
1	0	1268	C	2.6
1	0	1735	C	2.6
1	0	1889	C	2.6
1	0	50	G	2.6
1	0	94	G	2.6
1	0	221	G	2.6
1	0	1409	G	2.6
1	0	1433	G	2.6
1	0	1726	G	2.6
1	0	1868	G	2.6
1	0	2304	G	2.6
1	0	2442	G	2.6

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Mol	Chain	Res	Type	RSRZ
1	0	435	A	2.6
1	0	1067	A	2.6
1	0	2677	A	2.6
7	E	110	GLU	2.6
1	0	1939	U	2.6
1	0	2419	U	2.6
1	0	2445	U	2.6
1	0	2527	U	2.6
1	0	1127	C	2.5
1	0	1257	C	2.5
1	0	1273	C	2.5
1	0	1617	C	2.5
1	0	2061	C	2.5
1	0	2066	C	2.5
1	0	2560	C	2.5
1	0	2759	C	2.5
1	0	32	G	2.5
1	0	64	G	2.5
1	0	180	G	2.5
1	0	184	G	2.5
1	0	185	G	2.5
1	0	264	G	2.5
1	0	413	G	2.5
1	0	800	G	2.5
1	0	1363	G	2.5
1	0	1445	G	2.5
1	0	1751	G	2.5
1	0	1820	G	2.5
1	0	2462	G	2.5
1	0	2573	G	2.5
1	0	2578	G	2.5
1	0	2582	G	2.5
1	0	595	U	2.5
1	0	875	A	2.5
1	0	1013	A	2.5
1	0	1506	U	2.5
1	0	1632	A	2.5
1	0	1657	A	2.5
1	0	1875	A	2.5
1	0	2038	A	2.5
1	0	2604	A	2.5
1	0	2864	U	2.5

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Mol	Chain	Res	Type	RSRZ
2	9	99	U	2.5
1	0	73	C	2.5
1	0	171	C	2.5
1	0	606	C	2.5
1	0	687	C	2.5
1	0	2056	C	2.5
1	0	2130	C	2.5
1	0	2268	C	2.5
1	0	2533	C	2.5
1	0	2549	C	2.5
1	0	2614	C	2.5
2	9	106	C	2.5
1	0	54	G	2.5
1	0	406	G	2.5
1	0	426	G	2.5
1	0	464	G	2.5
1	0	518	G	2.5
1	0	754	G	2.5
1	0	865	G	2.5
1	0	921	G	2.5
1	0	952	G	2.5
1	0	1327	G	2.5
1	0	1443	G	2.5
1	0	1535	G	2.5
1	0	1704	G	2.5
1	0	1719	G	2.5
1	0	2053	G	2.5
1	0	2275	G	2.5
1	0	37	A	2.5
1	0	477	A	2.5
1	0	1082	A	2.5
1	0	1291	A	2.5
1	0	1294	A	2.5
1	0	1390	A	2.5
1	0	1693	A	2.5
1	0	1822	A	2.5
1	0	1859	A	2.5
1	0	2311	A	2.5
1	0	2394	A	2.5
1	0	2497	A	2.5
1	0	238	C	2.5
1	0	433	C	2.5

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Mol	Chain	Res	Type	RSRZ
1	0	1551	C	2.5
1	0	1687	C	2.5
1	0	1862	C	2.5
1	0	2381	C	2.5
1	0	2417	C	2.5
1	0	2651	C	2.5
1	0	2859	C	2.5
1	0	103	U	2.5
1	0	831	U	2.5
1	0	1554	U	2.5
1	0	2297	U	2.5
1	0	51	G	2.5
1	0	118	G	2.5
1	0	203	G	2.5
1	0	684	G	2.5
1	0	2082	G	2.5
1	0	2385	G	2.5
1	0	236	A	2.5
1	0	756	A	2.5
1	0	766	A	2.5
1	0	861	A	2.5
1	0	1779	A	2.5
1	0	2434	A	2.5
1	0	2775	A	2.5
1	0	2811	A	2.5
1	0	250	C	2.5
1	0	563	C	2.5
1	0	613	C	2.5
1	0	1798	C	2.5
1	0	2088	C	2.5
1	0	2313	C	2.5
1	0	392	U	2.5
1	0	1635	U	2.5
1	0	2478	U	2.5
2	9	69	U	2.5
1	0	755	G	2.5
1	0	1059	G	2.5
1	0	1065	G	2.5
1	0	1533	A	2.5
1	0	1728	G	2.5
1	0	1736	A	2.5
1	0	2097	G	2.5

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Mol	Chain	Res	Type	RSRZ
1	0	2613	G	2.5
1	0	2662	G	2.5
1	0	707	C	2.5
1	0	847	C	2.5
1	0	900	U	2.5
1	0	1267	C	2.5
1	0	1574	C	2.5
1	0	2542	C	2.5
1	0	2669	U	2.5
1	0	247	A	2.5
1	0	331	A	2.5
1	0	437	A	2.5
1	0	631	A	2.5
1	0	758	A	2.5
1	0	1073	A	2.5
1	0	1413	A	2.5
1	0	2015	A	2.5
1	0	2305	A	2.5
1	0	2367	A	2.5
1	0	2402	A	2.5
1	0	2761	A	2.5
1	0	150	G	2.5
1	0	384	G	2.5
1	0	1027	G	2.5
1	0	1076	G	2.5
1	0	1468	G	2.5
1	0	1827	G	2.5
1	0	1837	G	2.5
1	0	2365	G	2.5
1	0	2660	G	2.5
1	0	1091	U	2.5
1	0	2619	U	2.5
1	0	195	C	2.5
1	0	412	C	2.5
1	0	1105	C	2.5
1	0	1140	C	2.5
1	0	1305	C	2.5
1	0	1404	C	2.5
1	0	2629	C	2.5
1	0	473	A	2.4
1	0	1255	A	2.4
1	0	1296	A	2.4

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Mol	Chain	Res	Type	RSRZ
1	0	1348	A	2.4
1	0	1414	A	2.4
1	0	1717	A	2.4
1	0	1843	A	2.4
1	0	2244	A	2.4
1	0	680	G	2.4
1	0	854	G	2.4
1	0	1333	U	2.4
1	0	1351	G	2.4
1	0	2052	U	2.4
1	0	2310	G	2.4
1	0	2453	G	2.4
1	0	2605	G	2.4
1	0	2623	G	2.4
1	0	2639	G	2.4
1	0	2723	G	2.4
1	0	2779	G	2.4
2	9	117	G	2.4
1	0	83	C	2.4
1	0	251	C	2.4
1	0	348	C	2.4
1	0	637	C	2.4
1	0	1250	C	2.4
1	0	1301	C	2.4
1	0	1894	C	2.4
1	0	2104	C	2.4
2	9	9	C	2.4
1	0	420	U	2.4
1	0	624	U	2.4
1	0	797	A	2.4
1	0	1691	A	2.4
1	0	1869	A	2.4
1	0	2039	A	2.4
1	0	386	G	2.4
1	0	568	G	2.4
1	0	610	G	2.4
1	0	1300	G	2.4
1	0	1410	G	2.4
1	0	2092	G	2.4
1	0	2111	G	2.4
1	0	2618	G	2.4
2	9	102	G	2.4

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Mol	Chain	Res	Type	RSRZ
1	0	136	C	2.4
1	0	663	C	2.4
1	0	1262	C	2.4
1	0	2575	C	2.4
1	0	1461	U	2.4
1	0	16	A	2.4
1	0	70	A	2.4
1	0	222	A	2.4
1	0	750	A	2.4
1	0	894	A	2.4
1	0	913	A	2.4
1	0	1337	A	2.4
1	0	1504	A	2.4
1	0	1755	A	2.4
1	0	2019	A	2.4
1	0	2415	A	2.4
1	0	2485	A	2.4
1	0	2490	A	2.4
1	0	66	G	2.4
1	0	156	C	2.4
1	0	159	G	2.4
1	0	303	C	2.4
1	0	667	C	2.4
1	0	798	G	2.4
1	0	1364	G	2.4
1	0	1538	C	2.4
1	0	1718	G	2.4
1	0	1752	G	2.4
1	0	1944	G	2.4
1	0	1982	C	2.4
1	0	2105	C	2.4
1	0	2423	C	2.4
1	0	2459	G	2.4
1	0	2552	C	2.4
1	0	2609	G	2.4
1	0	349	U	2.4
1	0	470	U	2.4
1	0	733	U	2.4
1	0	840	U	2.4
1	0	1101	U	2.4
1	0	1249	U	2.4
1	0	1306	U	2.4

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Mol	Chain	Res	Type	RSRZ
1	0	2473	U	2.4
1	0	131	A	2.4
1	0	511	A	2.4
1	0	629	A	2.4
1	0	790	A	2.4
1	0	1286	A	2.4
1	0	1358	A	2.4
1	0	2467	A	2.4
1	0	2757	A	2.4
1	0	400	C	2.4
1	0	650	C	2.4
1	0	726	C	2.4
1	0	853	C	2.4
1	0	910	C	2.4
1	0	1060	C	2.4
1	0	1277	C	2.4
1	0	1456	C	2.4
1	0	1679	C	2.4
1	0	1899	C	2.4
1	0	1911	C	2.4
1	0	2803	C	2.4
1	0	1050	G	2.4
1	0	1723	G	2.4
1	0	2272	G	2.4
1	0	2643	G	2.4
1	0	297	U	2.4
1	0	1696	U	2.4
1	0	2358	U	2.4
1	0	152	A	2.4
1	0	339	A	2.4
1	0	916	A	2.4
1	0	1012	A	2.4
1	0	1018	A	2.4
1	0	1330	A	2.4
1	0	1479	A	2.4
1	0	1811	A	2.4
1	0	1909	A	2.4
1	0	2060	A	2.4
1	0	100	C	2.4
1	0	101	C	2.4
1	0	759	C	2.4
1	0	896	C	2.4

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Mol	Chain	Res	Type	RSRZ
1	0	1439	C	2.4
1	0	1472	C	2.4
1	0	1474	C	2.4
1	0	1708	C	2.4
1	0	2682	C	2.4
1	0	2780	C	2.4
2	9	96	C	2.4
1	0	465	U	2.4
1	0	2523	U	2.4
1	0	206	G	2.4
1	0	231	G	2.4
1	0	528	G	2.4
1	0	537	G	2.4
1	0	636	G	2.4
1	0	1074	G	2.4
1	0	1290	G	2.4
1	0	1672	G	2.4
1	0	2093	G	2.4
2	9	90	G	2.4
1	0	552	A	2.3
1	0	693	A	2.3
1	0	844	A	2.3
1	0	1097	A	2.3
1	0	1492	A	2.3
1	0	1776	A	2.3
1	0	2361	A	2.3
2	9	80	A	2.3
2	9	93	A	2.3
1	0	230	C	2.3
1	0	623	U	2.3
1	0	1139	U	2.3
1	0	1256	C	2.3
1	0	1480	U	2.3
1	0	1654	U	2.3
1	0	1830	C	2.3
1	0	1850	U	2.3
1	0	1870	C	2.3
1	0	2561	C	2.3
1	0	2690	U	2.3
1	0	2781	U	2.3
14	L	91	GLN	2.3
1	0	458	G	2.3

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Mol	Chain	Res	Type	RSRZ
1	0	689	G	2.3
1	0	760	G	2.3
1	0	1241	G	2.3
1	0	1452	G	2.3
1	0	2045	G	2.3
1	0	2584	G	2.3
1	0	2657	G	2.3
2	9	92	G	2.3
1	0	198	A	2.3
1	0	643	A	2.3
1	0	659	A	2.3
1	0	1247	A	2.3
1	0	1821	A	2.3
1	0	2055	A	2.3
1	0	2486	A	2.3
1	0	63	U	2.3
1	0	468	U	2.3
1	0	1120	U	2.3
1	0	859	C	2.3
1	0	1010	C	2.3
1	0	1360	C	2.3
1	0	1514	C	2.3
1	0	2071	C	2.3
1	0	2292	C	2.3
1	0	2403	C	2.3
1	0	2654	C	2.3
1	0	446	G	2.3
1	0	467	G	2.3
1	0	525	G	2.3
1	0	640	G	2.3
1	0	824	G	2.3
1	0	958	G	2.3
1	0	1340	G	2.3
1	0	1744	G	2.3
1	0	1848	G	2.3
1	0	2125	G	2.3
2	9	4	G	2.3
1	0	2377	U	2.3
1	0	167	A	2.3
1	0	378	A	2.3
1	0	628	A	2.3
1	0	694	A	2.3

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Mol	Chain	Res	Type	RSRZ
1	0	819	A	2.3
1	0	1022	A	2.3
1	0	1839	A	2.3
1	0	1885	A	2.3
1	0	2812	A	2.3
1	0	218	C	2.3
1	0	915	C	2.3
1	0	1026	C	2.3
1	0	1534	C	2.3
1	0	2047	C	2.3
1	0	2411	C	2.3
1	0	2765	C	2.3
1	0	2806	C	2.3
1	0	2832	C	2.3
24	V	12	LEU	2.3
1	0	149	G	2.3
1	0	652	G	2.3
1	0	787	G	2.3
1	0	911	G	2.3
1	0	1339	G	2.3
1	0	1484	G	2.3
1	0	1745	G	2.3
1	0	2279	G	2.3
1	0	2687	G	2.3
1	0	2758	G	2.3
2	9	8	G	2.3
1	0	801	U	2.3
1	0	821	U	2.3
1	0	2282	U	2.3
1	0	2499	U	2.3
1	0	2673	U	2.3
1	0	2733	U	2.3
1	0	419	A	2.3
1	0	961	A	2.3
1	0	1458	A	2.3
1	0	1547	A	2.3
1	0	1733	A	2.3
1	0	1900	A	2.3
1	0	1994	A	2.3
1	0	2095	A	2.3
1	0	2577	A	2.3
1	0	173	C	2.3

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Mol	Chain	Res	Type	RSRZ
1	0	1893	C	2.3
1	0	2098	C	2.3
2	9	81	C	2.3
29	1	123	ASP	2.3
1	0	108	U	2.3
1	0	860	U	2.3
1	0	223	G	2.3
1	0	529	G	2.3
1	0	539	G	2.3
1	0	622	G	2.3
1	0	706	G	2.3
1	0	722	G	2.3
1	0	1094	G	2.3
1	0	1601	G	2.3
1	0	1756	G	2.3
1	0	2501	G	2.3
1	0	340	A	2.3
1	0	455	A	2.3
1	0	784	A	2.3
1	0	1341	A	2.3
1	0	2398	A	2.3
1	0	2413	A	2.3
1	0	2801	A	2.3
1	0	29	C	2.3
1	0	440	C	2.3
1	0	483	C	2.3
1	0	494	C	2.3
1	0	653	C	2.3
1	0	822	C	2.3
1	0	1227	C	2.3
1	0	1251	C	2.3
1	0	1451	C	2.3
1	0	1680	C	2.3
1	0	1690	C	2.3
1	0	1734	C	2.3
1	0	1993	C	2.3
1	0	2035	C	2.3
1	0	2114	C	2.3
1	0	2717	C	2.3
1	0	178	U	2.3
1	0	1835	U	2.3
1	0	1937	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	0	2444	U	2.3
1	0	44	G	2.3
1	0	531	G	2.3
1	0	648	G	2.3
1	0	657	G	2.3
1	0	739	G	2.3
1	0	1832	G	2.3
1	0	1898	G	2.3
1	0	2099	G	2.3
1	0	2777	G	2.3
1	0	204	A	2.3
1	0	442	A	2.3
1	0	620	A	2.3
1	0	791	A	2.3
1	0	1815	A	2.3
1	0	2260	A	2.3
1	0	2583	A	2.3
1	0	438	C	2.3
1	0	478	C	2.3
1	0	848	C	2.3
1	0	934	C	2.3
1	0	1033	C	2.3
1	0	1396	C	2.3
1	0	1469	C	2.3
1	0	1834	C	2.3
1	0	2287	C	2.3
4	B	182	GLU	2.2
1	0	163	U	2.2
1	0	548	U	2.2
1	0	1293	U	2.2
1	0	1770	U	2.2
1	0	2581	U	2.2
1	0	479	G	2.2
1	0	683	G	2.2
1	0	1031	G	2.2
1	0	1055	G	2.2
1	0	1299	G	2.2
1	0	1389	G	2.2
1	0	2041	G	2.2
1	0	2286	G	2.2
2	9	84	G	2.2
1	0	174	A	2.2

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Mol	Chain	Res	Type	RSRZ
1	0	337	A	2.2
1	0	430	A	2.2
1	0	639	A	2.2
1	0	773	A	2.2
1	0	1124	A	2.2
1	0	1356	A	2.2
1	0	1411	A	2.2
1	0	1482	A	2.2
1	0	1689	A	2.2
1	0	2083	A	2.2
1	0	2474	A	2.2
1	0	2838	A	2.2
1	0	34	C	2.2
1	0	1129	C	2.2
1	0	1536	C	2.2
1	0	1602	C	2.2
1	0	2261	C	2.2
1	0	2477	C	2.2
1	0	2496	C	2.2
1	0	2547	C	2.2
1	0	2787	C	2.2
1	0	210	U	2.2
1	0	1531	U	2.2
1	0	1833	U	2.2
1	0	2756	U	2.2
1	0	181	G	2.2
1	0	229	G	2.2
1	0	1053	G	2.2
1	0	1349	G	2.2
1	0	1416	G	2.2
1	0	1855	G	2.2
1	0	1863	G	2.2
1	0	2452	G	2.2
1	0	2588	G	2.2
1	0	2674	G	2.2
1	0	2744	G	2.2
1	0	453	A	2.2
1	0	489	A	2.2
1	0	666	A	2.2
1	0	912	A	2.2
1	0	937	C	2.2
1	0	1057	A	2.2

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Mol	Chain	Res	Type	RSRZ
1	0	888	U	2.2
1	0	1377	C	2.2
1	0	1421	C	2.2
1	0	1983	C	2.2
1	0	2364	A	2.2
1	0	2401	A	2.2
1	0	2028	U	2.2
1	0	2037	C	2.2
1	0	2266	A	2.2
1	0	2127	U	2.2
1	0	2276	U	2.2
1	0	2318	C	2.2
1	0	2644	C	2.2
1	0	2671	U	2.2
1	0	2839	C	2.2
2	9	85	A	2.2
2	9	97	U	2.2
1	0	815	U	2.2
1	0	1698	U	2.2
1	0	2652	U	2.2
1	0	2711	U	2.2
2	9	79	U	2.2
1	0	618	G	2.2
1	0	621	C	2.2
1	0	950	G	2.2
1	0	1229	C	2.2
1	0	1230	A	2.2
1	0	1254	C	2.2
1	0	1272	C	2.2
1	0	1375	A	2.2
1	0	1402	G	2.2
1	0	1600	G	2.2
1	0	1646	G	2.2
1	0	1709	G	2.2
1	0	1777	G	2.2
1	0	1786	C	2.2
1	0	1796	A	2.2
1	0	1990	C	2.2
1	0	2026	C	2.2
1	0	2280	A	2.2
1	0	2300	A	2.2
1	0	2302	A	2.2

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Mol	Chain	Res	Type	RSRZ
1	0	2317	C	2.2
1	0	2362	A	2.2
1	0	2532	A	2.2
1	0	2591	C	2.2
1	0	2593	C	2.2
1	0	391	U	2.2
1	0	1270	U	2.2
1	0	1285	U	2.2
1	0	2246	U	2.2
1	0	2535	U	2.2
7	E	11	ASP	2.2
1	0	551	A	2.2
1	0	905	C	2.2
1	0	923	A	2.2
1	0	1069	C	2.2
1	0	1080	C	2.2
1	0	1931	A	2.2
1	0	2776	A	2.2
1	0	13	G	2.2
1	0	112	G	2.2
1	0	1239	G	2.2
1	0	1319	G	2.2
1	0	2094	G	2.2
1	0	2293	G	2.2
1	0	2809	G	2.2
1	0	2842	G	2.2
1	0	22	U	2.2
1	0	268	U	2.2
1	0	346	U	2.2
1	0	1539	U	2.2
1	0	2277	U	2.2
1	0	2749	U	2.2
1	0	2796	U	2.2
1	0	62	C	2.2
1	0	106	A	2.2
1	0	114	A	2.2
1	0	183	A	2.2
1	0	186	A	2.2
1	0	356	C	2.2
1	0	407	A	2.2
1	0	484	A	2.2
1	0	580	A	2.2

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Mol	Chain	Res	Type	RSRZ
1	0	665	A	2.2
1	0	930	C	2.2
1	0	1049	C	2.2
1	0	1083	C	2.2
1	0	1318	A	2.2
1	0	1335	C	2.2
1	0	1392	A	2.2
1	0	1545	C	2.2
1	0	1999	C	2.2
1	0	2006	C	2.2
1	0	2393	C	2.2
1	0	2551	C	2.2
1	0	820	G	2.2
1	0	941	G	2.2
1	0	944	G	2.2
1	0	1240	G	2.2
1	0	1727	G	2.2
1	0	2051	G	2.2
1	0	527	U	2.2
1	0	611	U	2.2
1	0	612	U	2.2
1	0	1310	U	2.2
1	0	695	C	2.1
1	0	1019	C	2.1
1	0	1084	C	2.1
1	0	1332	C	2.1
1	0	1738	C	2.1
1	0	1772	C	2.1
1	0	151	A	2.1
1	0	929	A	2.1
1	0	1313	A	2.1
1	0	1678	A	2.1
1	0	2010	A	2.1
1	0	2488	A	2.1
1	0	2743	A	2.1
2	9	105	A	2.1
1	0	389	G	2.1
1	0	615	G	2.1
1	0	1877	G	2.1
1	0	1998	G	2.1
2	9	86	G	2.1
1	0	858	U	2.1

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Mol	Chain	Res	Type	RSRZ
1	0	945	U	2.1
1	0	1645	U	2.1
1	0	2607	U	2.1
1	0	220	C	2.1
1	0	228	C	2.1
1	0	638	C	2.1
1	0	849	C	2.1
1	0	1061	C	2.1
1	0	1420	C	2.1
1	0	1423	C	2.1
1	0	1537	C	2.1
1	0	1763	C	2.1
1	0	2751	C	2.1
1	0	194	A	2.1
1	0	630	A	2.1
1	0	708	A	2.1
1	0	1259	A	2.1
1	0	1321	A	2.1
1	0	1573	A	2.1
1	0	2576	A	2.1
1	0	2840	A	2.1
1	0	662	U	2.1
1	0	823	U	2.1
1	0	903	U	2.1
1	0	1347	U	2.1
1	0	2457	U	2.1
1	0	448	G	2.1
1	0	1258	G	2.1
1	0	1743	G	2.1
1	0	1849	G	2.1
1	0	2314	G	2.1
1	0	2399	G	2.1
1	0	240	C	2.1
1	0	377	C	2.1
1	0	633	C	2.1
1	0	1640	C	2.1
1	0	2439	C	2.1
1	0	2608	C	2.1
1	0	2641	C	2.1
1	0	2728	C	2.1
1	0	2762	C	2.1
1	0	48	A	2.1

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Mol	Chain	Res	Type	RSRZ
1	0	169	A	2.1
1	0	170	U	2.1
1	0	215	A	2.1
1	0	466	A	2.1
1	0	647	U	2.1
1	0	1017	U	2.1
1	0	1106	A	2.1
1	0	1440	U	2.1
1	0	1493	A	2.1
1	0	1918	U	2.1
1	0	1370	G	2.1
1	0	2023	G	2.1
1	0	143	C	2.1
1	0	343	C	2.1
1	0	399	C	2.1
1	0	451	C	2.1
1	0	677	C	2.1
1	0	845	U	2.1
1	0	1041	U	2.1
1	0	1395	C	2.1
1	0	1705	C	2.1
1	0	1750	C	2.1
1	0	1818	C	2.1
1	0	1864	C	2.1
1	0	2017	U	2.1
1	0	2059	U	2.1
1	0	2077	C	2.1
1	0	2129	U	2.1
1	0	2431	C	2.1
1	0	2493	C	2.1
1	0	2621	U	2.1
1	0	2835	C	2.1
2	9	89	C	2.1
1	0	191	A	2.1
1	0	1107	A	2.1
1	0	1232	A	2.1
1	0	1845	A	2.1
1	0	2684	A	2.1
1	0	23	G	2.1
1	0	142	G	2.1
1	0	175	G	2.1
1	0	431	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	0	1038	G	2.1
1	0	1048	G	2.1
1	0	1063	G	2.1
1	0	1260	G	2.1
1	0	1773	G	2.1
1	0	2070	G	2.1
1	0	2400	G	2.1
1	0	2750	G	2.1
1	0	172	U	2.1
1	0	777	U	2.1
1	0	832	U	2.1
1	0	872	U	2.1
1	0	1264	U	2.1
1	0	1304	U	2.1
1	0	1673	U	2.1
1	0	1887	U	2.1
1	0	2889	U	2.1
1	0	427	C	2.1
1	0	2472	C	2.1
1	0	11	A	2.1
1	0	509	A	2.1
1	0	955	A	2.1
1	0	1032	A	2.1
1	0	1616	A	2.1
1	0	1710	A	2.1
1	0	2553	A	2.1
1	0	2596	A	2.1
1	0	2681	A	2.1
1	0	646	G	2.1
1	0	786	G	2.1
1	0	2033	G	2.1
1	0	335	U	2.1
1	0	942	U	2.1
1	0	1051	C	2.0
1	0	1238	C	2.0
1	0	1342	C	2.0
1	0	1394	C	2.0
1	0	1652	C	2.0
1	0	1816	C	2.0
1	0	2319	C	2.0
1	0	2427	C	2.0
1	0	2797	C	2.0

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Mol	Chain	Res	Type	RSRZ
1	0	119	A	2.0
1	0	243	A	2.0
1	0	507	A	2.0
1	0	674	A	2.0
1	0	682	A	2.0
1	0	907	A	2.0
1	0	1098	A	2.0
1	0	1501	A	2.0
1	0	1942	A	2.0
1	0	2108	A	2.0
1	0	2264	A	2.0
1	0	2624	A	2.0
1	0	1064	U	2.0
1	0	1095	U	2.0
1	0	1276	U	2.0
1	0	1336	U	2.0
1	0	1454	U	2.0
1	0	1702	U	2.0
1	0	1758	U	2.0
1	0	1992	U	2.0
1	0	2057	U	2.0
1	0	2115	U	2.0
1	0	41	G	2.0
1	0	1024	G	2.0
1	0	1071	G	2.0
1	0	1099	G	2.0
1	0	1119	G	2.0
1	0	1376	G	2.0
1	0	2630	G	2.0
1	0	2754	G	2.0
1	0	15	C	2.0
1	0	72	C	2.0
1	0	330	C	2.0
1	0	414	C	2.0
1	0	1495	C	2.0
1	0	1844	C	2.0
1	0	1861	C	2.0
1	0	2294	C	2.0
2	9	91	C	2.0
1	0	59	A	2.0
1	0	439	A	2.0
1	0	914	A	2.0

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Mol	Chain	Res	Type	RSRZ
1	0	1317	A	2.0
1	0	1659	A	2.0
1	0	1712	A	2.0
1	0	1881	A	2.0
1	0	2022	A	2.0
1	0	2085	A	2.0
1	0	2274	A	2.0
1	0	2369	A	2.0
1	0	445	U	2.0
1	0	488	U	2.0
1	0	701	U	2.0
1	0	794	U	2.0
1	0	862	U	2.0
1	0	1003	U	2.0
1	0	1320	U	2.0
1	0	2528	U	2.0
1	0	2557	U	2.0
1	0	2853	U	2.0
1	0	157	G	2.0
1	0	1873	G	2.0
1	0	1884	G	2.0
1	0	2603	G	2.0
1	0	2634	G	2.0
1	0	53	C	2.0
1	0	154	C	2.0
1	0	523	C	2.0
1	0	676	C	2.0
1	0	1263	C	2.0
1	0	1374	C	2.0
1	0	1467	C	2.0
1	0	524	A	2.0
1	0	721	A	2.0
1	0	1653	A	2.0
1	0	1742	A	2.0
1	0	1858	A	2.0
1	0	1886	A	2.0
1	0	2800	A	2.0
1	0	2841	A	2.0
1	0	2843	A	2.0
2	9	104	A	2.0
1	0	123	U	2.0
1	0	567	U	2.0

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Mol	Chain	Res	Type	RSRZ
1	0	866	U	2.0
1	0	1047	U	2.0
1	0	1237	U	2.0
1	0	1503	U	2.0
1	0	2117	U	2.0
1	0	2541	U	2.0
1	0	2791	U	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
32	MG	0	2926	1/1	0.60	0.27	-2.02	30,30,30,30	0
32	MG	0	2925	1/1	0.75	0.14	-5.90	30,30,30,30	0
31	K	0	2924	1/1	0.87	0.09	-12.79	30,30,30,30	0
30	CD	Z	104	1/1	0.96	0.23	-	54,54,54,54	0
30	CD	R	101	1/1	0.96	0.12	-	39,39,39,39	0
30	CD	X	102	1/1	0.81	0.21	-	48,48,48,48	0
30	CD	W	103	1/1	0.95	0.13	-	30,30,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.