



Full wwPDB X-ray Structure Validation Report i

Feb 28, 2014 – 12:27 AM GMT

PDB ID : 3PYO
Title : Crystal structure of a complex containing domain 3 from the PSIV IGR IRES RNA bound to the 70S ribosome. This file contains the 50S subunit of the first 70S ribosome.
Authors : Zhu, J.; Korostelev, A.; Costantino, D.; Noller, H.F.; Kieft, J.S.
Deposited on : 2010-12-13
Resolution : 3.50 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

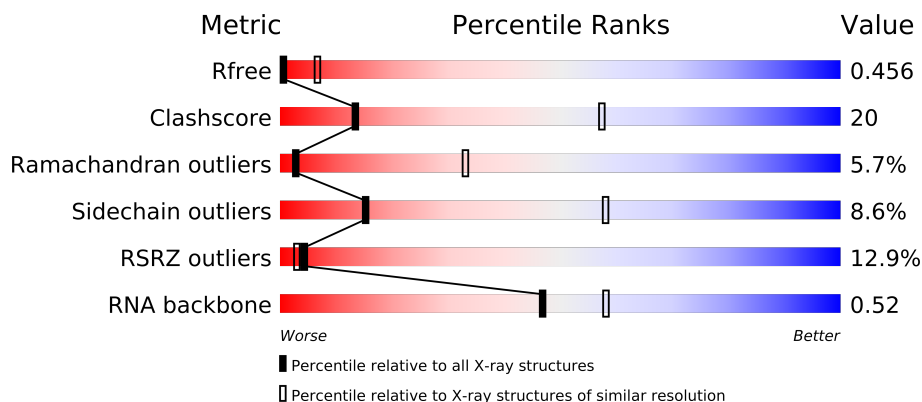
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1243 (3.70-3.30)
Clashscore	79885	1039 (3.66-3.34)
Ramachandran outliers	78287	1000 (3.66-3.34)
Sidechain outliers	78261	1000 (3.66-3.34)
RSRZ outliers	66119	1243 (3.70-3.30)
RNA backbone	1838	1007 (4.22-2.76)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	2879	
2	B	119	
3	C	271	
4	D	204	
5	E	202	
6	F	181	
7	G	159	
8	H	145	
9	I	65	
10	J	137	
11	K	122	
12	L	146	

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Mol	Chain	Length	Quality of chain
13	M	136	
14	N	117	
15	O	98	
16	P	137	
17	Q	116	
18	R	101	
19	S	112	
20	T	92	
21	U	100	
22	V	188	
23	W	76	
24	X	88	
25	Y	62	
26	Z	59	
27	1	30	
28	2	52	
29	3	44	
30	4	48	
31	5	63	

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 89438 atoms, of which 0 are hydrogen and 0 are deuterium.

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 ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	2760	Total	C	N	O	P	0	0	0
			59442	26456	11114	19113	2759			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1142	U	C	SEE REMARK 999	GB AE017221.1
A	2825	U	G	SEE REMARK 999	GB AE017221.1

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	271	Total	C	N	O	S	0	0	0
			2105	1329	416	357	3			

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	204	Total	C	N	O	S	0	0	0
			1564	988	299	271	6			

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	202	Total	C	N	O	S	0	0	0
			1587	1011	297	276	3			

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	181	Total	C	N	O	S	0	0	0
			1475	943	268	260	4			

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	159	Total	C	N	O	S	0	0	0
			1223	773	228	221	1			

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	145	Total	C	N	O	S	0	0	0
			1133	724	200	208	1			

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	32	Total	C	N	O	0	0	0
			254	157	49	48			

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	137	Total	C	N	O	S	0	0	0
			1097	707	205	182	3			

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	122	Total	C	N	O	S	0	0	0
			932	587	171	170	4			

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	136	Total	C	N	O	S	0	0	0
			1079	688	204	182	5			

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	117	Total	C	N	O		0	0	0
			960	599	202	159				

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	98	Total	C	N	O		0	0	0
			771	486	154	131				

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	137	Total	C	N	O	S	0	0	0
			1144	713	234	196	1			

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	116	Total	C	N	O	S	0	0	0
			953	601	201	150	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	?	-	PHE	DELETION	UNP Q72L76

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	112	Total	C	N	O	S	0	0	0
			891	560	175	154	2			

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	92	Total	C	N	O		0	0	0
			726	471	131	124				

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	100	Total	C	N	O	S	0	0	0
			776	500	148	124	4			

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	188	Total	C	N	O	S	0	0	0
			1492	950	265	275	2			

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	76	Total	C	N	O	S	0	0	0
			605	376	126	102	1			

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	X	88	Total	C	N	O		0	0	0
			695	435	141	119				

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	Y	62	Total	C	N	O	S	0	0	0
			521	325	102	92	2			

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Z	59	Total	C	N	O	S	0	0	0
			468	298	90	79	1			

- Molecule 27 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	1	30	Total	C	N	O	S	0	0	0
			226	142	36	44	4			

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	2	52	Total	C	N	O	S	0	0	0
			405	255	79	66	5			

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	3	44	Total	C	N	O	S	0	0	0
			381	235	77	65	4			

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	4	48	Total	C	N	O	S	0	0	0
			419	257	104	56	2			

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	5	63	Total	C	N	O	S	0	0	0
			508	326	101	79	2			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	P	12	Total	Mg	0	0
			12	12		
32	K	5	Total	Mg	0	0
			5	5		
32	B	27	Total	Mg	0	0
			27	27		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	6	244	Total 244	Mg 244	0	0
32	W	1	Total 1	Mg 1	0	0
32	N	2	Total 2	Mg 2	0	0
32	X	2	Total 2	Mg 2	0	0
32	2	2	Total 2	Mg 2	0	0
32	S	1	Total 1	Mg 1	0	0
32	J	3	Total 3	Mg 3	0	0
32	E	2	Total 2	Mg 2	0	0
32	V	3	Total 3	Mg 3	0	0
32	A	829	Total 829	Mg 829	0	0
32	R	1	Total 1	Mg 1	0	0
32	M	3	Total 3	Mg 3	0	0
32	1	1	Total 1	Mg 1	0	0
32	I	1	Total 1	Mg 1	0	0
32	U	2	Total 2	Mg 2	0	0
32	H	1	Total 1	Mg 1	0	0
32	C	9	Total 9	Mg 9	0	0
32	T	2	Total 2	Mg 2	0	0
32	O	1	Total 1	Mg 1	0	0
32	Y	3	Total 3	Mg 3	0	0
32	3	1	Total 1	Mg 1	0	0

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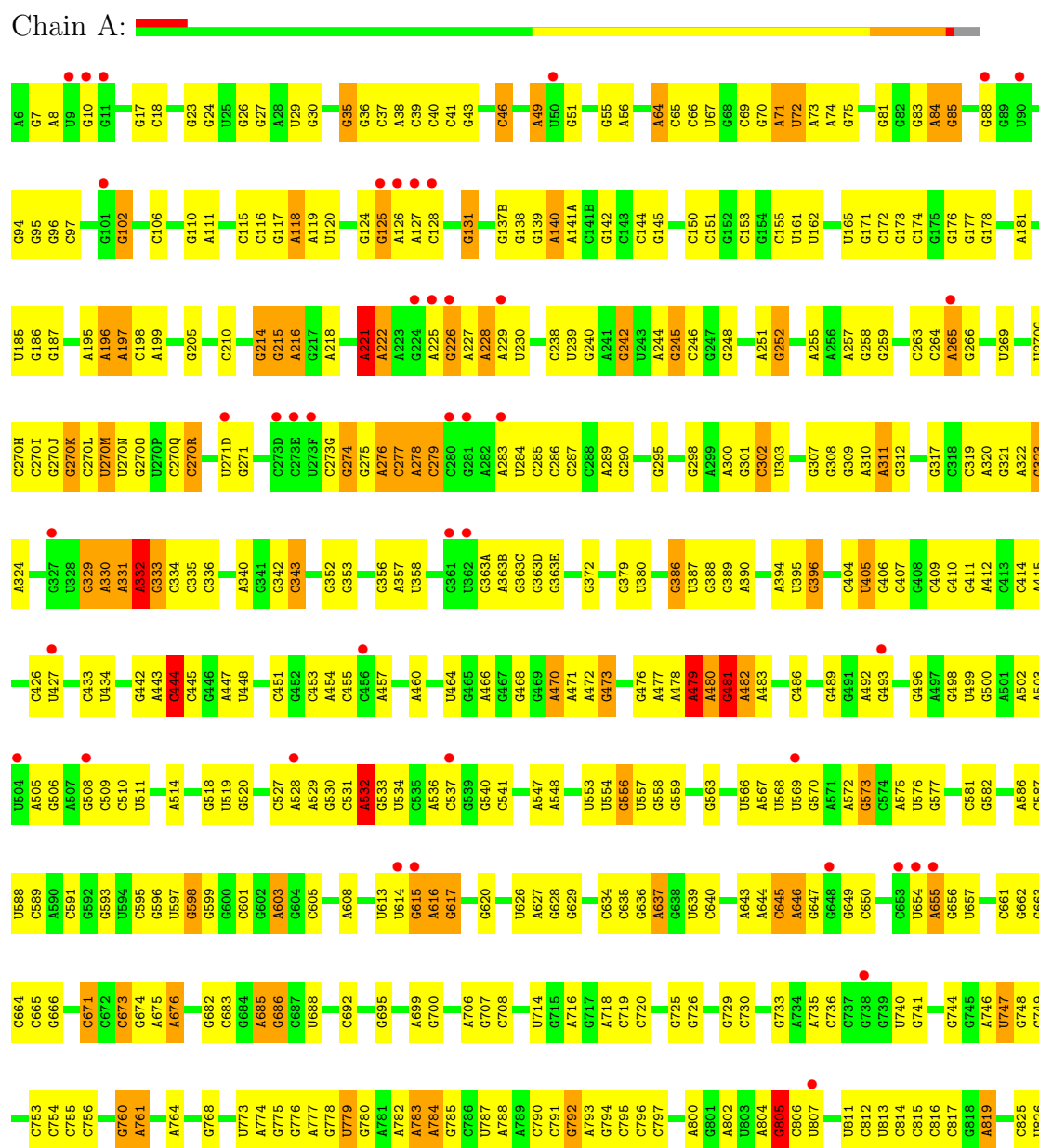
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	F	4	Total	Mg	0	0
			4	4		

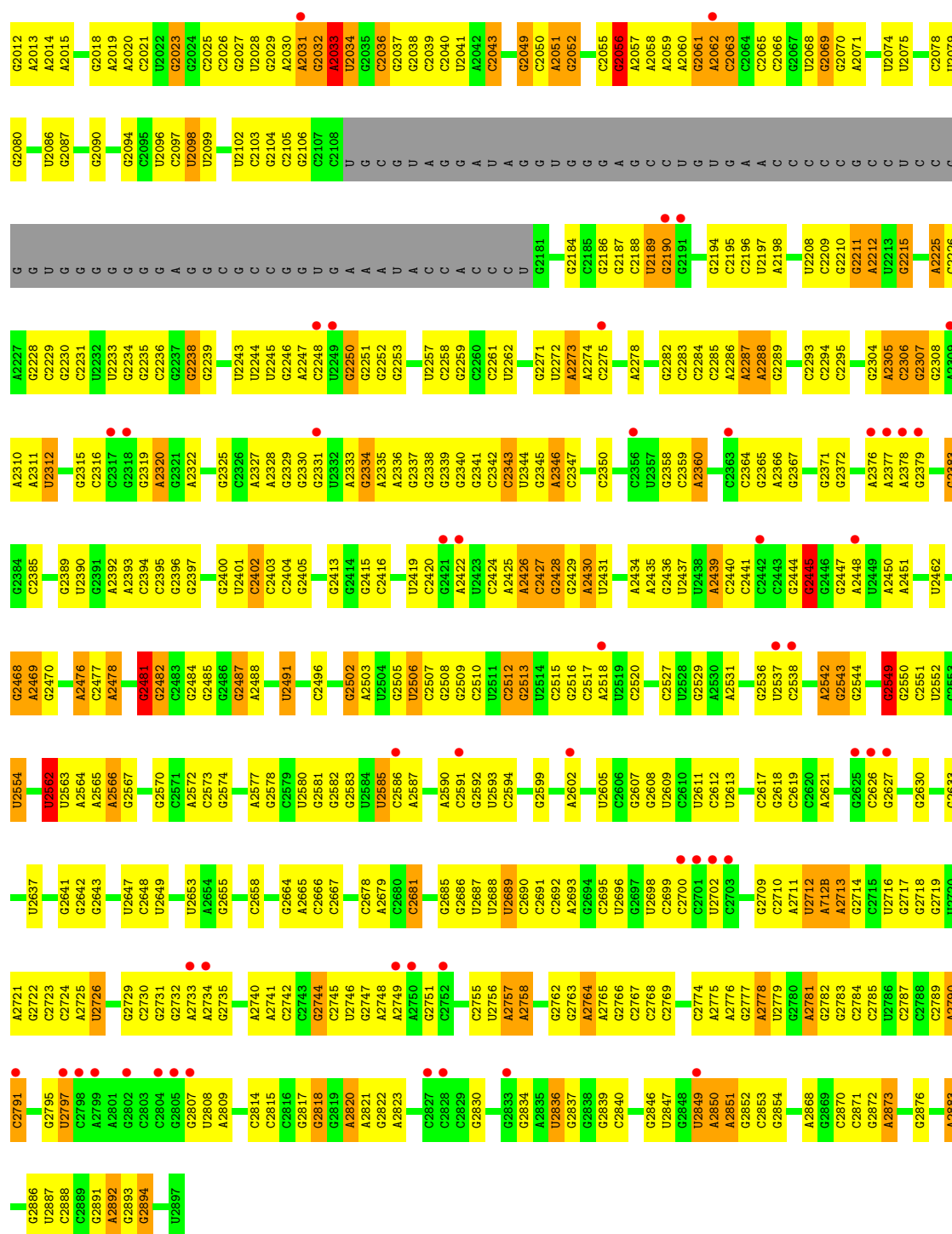
3 Residue-property plots

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 ($RSRZ > 2$). 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 ribosomal RNA

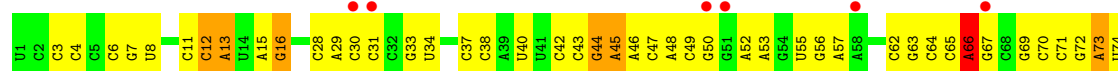


A1916	U1818	U1735	U1639	G1559	G1466	G1388	C1315	A1220	U1130	A980	A911	U827
U1917	A1819	C1741	C1640	G1563	C1467	G1389	U1316	A1221	C1135	A983	C912	U828
A1918	U1820	C1742	G1642	C1564	G1478	U1390	A1317	C1221	U1390	A983	U913	A829
C1920	G1824	G1743	G1643	C1565	G1479	U1391	C1318	C1222	U	G889	C914	G830
G1921	A1825	G1748	C1644	C1566	A1483	A1395	U1323	G1227	G1137	G890	C915	G831
U1926	G1826	A1749	G1645	A1567	G1484	U1396	G1324	G1228	G1138	A917	G916	G832
G1929	C1827	G1750	C1648	A1568	G1485	C1399	U1325	G1229	C1139	A918	U933	C834
A1930	G1828	C1751	G1649	A1569	A1486	G1400	G1326	G1230	C1140	A919	G919	A835
G1931	U1829	G1752	G1650	A1570	G1487	U1405	C1327	G1231	U1141	C994	G920	G836
U1932	C1830	C1753	A1652	G1573	G1488	C1404	G1328	G1232	U1142	C995	G921	C837
A1933	G1831	C1754	C1653	C1574	U1489	U1406	U1330	C1233	A1143	A996	C924	C838
U1934	U1832	A1759	A1654	C1575	A1490	U1407	A1331	G1239	G1144	C997	C925	U839
A1936	C1833	C1760	A1655	U1576	A1491	C1408	G1332	U1240	C1153	A1000	G929	C940
A1937	G1834	C1761	C1656	C1577	C1493	C1409	C1333	A1241	A1001	G1002	A941	A842
C1938	U1835	A1762	C1657	A1578	A1494	U1410	G1334	A1242	U1011	G1003	G932	G843
U1939	G1836	G1763	C1658	A1580	A1495	C1411	U1335	U1249	C1005	C1006	A933	C846
C1843	C1843	C1764	A1668	C1581	A1496	A1412	A1336	G1250	C1007	C1007	G934	U847
C1844	A1669	C1765	A1669	A1582	U1497	G1413	G1337	G1251	U	U	G938	A849
A1847	U1673	U1768	U1673	C1585	C1502	U1414	U1341	C1252	C1161	A1010	G939	G855
A1953	G1769	G1769	C1674	A1586	U1503	U1415	A1342	A1253	G1162	A1011	G940	C856
G1954	C1674	C1770	C1674	A1587	C1504	G1416	G1343	A1254	G1163	U1012	A941	C857
U1955	G1771	G1771	C1675	C1588	C1505	G1417	G1344	U1255	U1165	C1013	G942	U858
U1956	C1772	G1772	A1676	C1589	C1506	A1418	C1345	G1256	C1166	U1019	G943	G859
C1852	A1677	A1773	A1677	U1590	A1508	U1420	G1348	C1257	G1171	A1020	U944	A861
A1853	C1678	G1774	U1678	G1591	A1509	U1421	A1349	G1258	G1172	G1021	G945	G862
G1954	U1679	U1775	U1680	C1592	A1510	C1428	C1350	A1264	A1174	A1022	A946	A863
U1963	G1593	G1776	G1681	G1593	A1511	G1429	C1351	A1265	U1175	G1023	G947	C867
A1856	C1594	U1778	C1682	G1594	U1514	C1430	U1352	G1266	G1176	U1024	G948	G951
G1857	C1595	U1779	C1683	C1595	C1515	U1431	A1353	C1270	A1177	G1025	C951	U868
G1858	U1688	A1783	C1684	C1598	U1516	C1432	G1354	G1271	C1179	A1026	G952	G869
A1859	C1684	A1784	C1684	C1599	G1517	U1433	A1355	A1272	C1178	A1027	G953	A870
G1862	U1689	A1785	U1688	C1600	C1518	A1434	G1356	U1273	G1187	A1028	G954	U871
A1871	A1689	C1790	A1689	U1601	G1525	G1435	U1357	A1274	U188	G1029	C955	G875
A1872	U1692	A1791	U1692	U1602	G1526	C1437	A1358	U1275	A1189	G1030	G956	C885
A1884	U1693	U1794	C1694	A1603	A1528	U1438	A1360	A1276	G1190	A1032	U958	C886
C1885	G1695	C1795	G1695	C1604	A1529	G1444	U1361	G1284	U198	U1033	A960	A887
C1886	C1696	A1885	C1696	A1609	C1533	A1448	A1365	G1285	U199	C1040	C961	C888
C1887	G1697	C1797	G1697	A1610	G1534	C1445	G1368	C1289	G1107	C1041	G962	C889
G1888	C1699	U1798	G1699	C1611	U1535	G1447	G1369	C1290	U1108	A1046	G966	A890
A1889	A1700	C1800	G1700	C1612	A1536	G1448	U1373	C1291	U1109	G1047	C967	A896
G1899	G1801	G1801	U1709	G1613	C1537	A1498	A1374	U1292	C1110	A1050	G968	C897
U1901	A1802	C1802	C1710	A1614	G1538	C1450	C1375	C1293	A1111	G1051	U969	C898
A1900	C1803	A1803	C1710	C1615	G1539	C1451	A1378	U1300	G1112	C1052	C970	A899
C1901	U1804	C1804	G1717	A1616	U1540	U1453	A1379	A1301	C1121	G1056	C971	C903
G1902	A1809	A1809	C1717	C1617	G1541	A1454	U1454	A1308	G1122	A	G973	C904
G1903	C1726	G1726	U1726	A1618	A1543	G1461	A1381	A1309	C1123	G	C974A	U907
C1904	G1727	G1727	C1728	G1619	C1544	A1460	G1381	G1310	G1124	U	C974B	C908
U1905	A1729	A1729	C1729	G1620	A1545	C1462	A1384	G1311	G1125	C	G975	A909
G1907	G1813	G1813	A1729	A1632	A1546	C1463	C1385	U1312	A1126	U	G979	A910
A1913	G1816	G1816	G1733	G1633	C154B	C1464	C1386	U1313	A1127	G		
U1915	C1734	C1734	C1734	A1634	A1558	G1465	C1387	C1314	A1128	U		



• Molecule 2: 5S ribosomal RNA

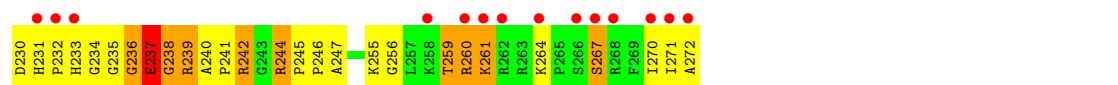
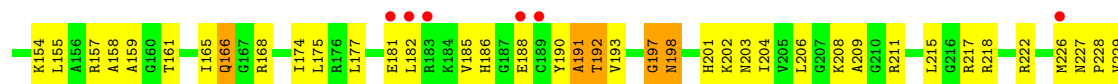
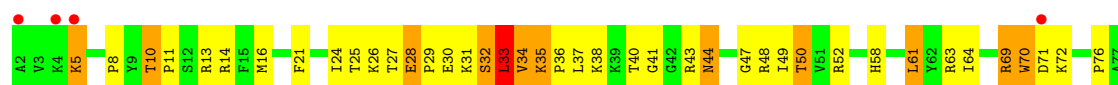
Chain B:





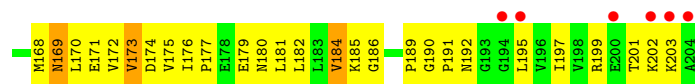
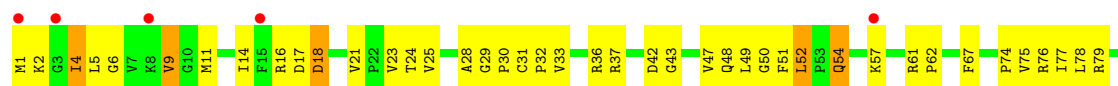
- Molecule 3: 50S ribosomal protein L2

Chain C:



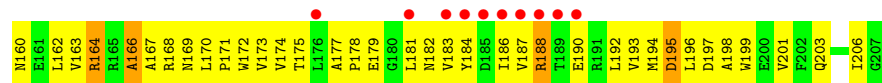
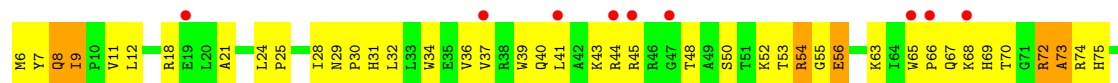
- Molecule 4: 50S ribosomal protein L3

Chain D: 



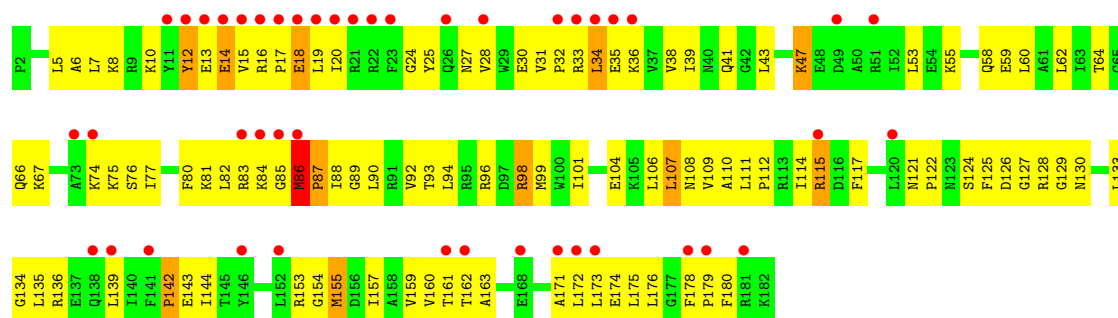
- Molecule 5: 50S ribosomal protein L4

Chain E:



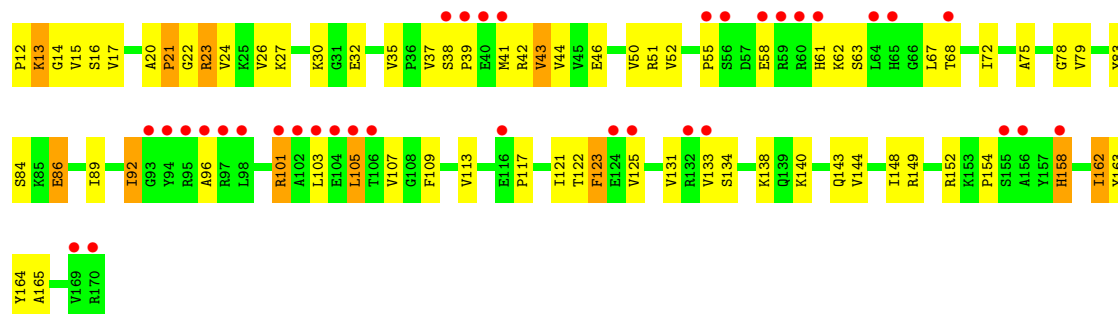
- Molecule 6: 50S ribosomal protein L5

Chain F:



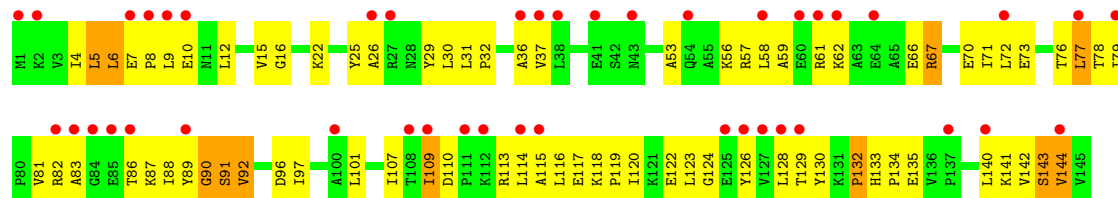
• Molecule 7: 50S ribosomal protein L6

Chain G:



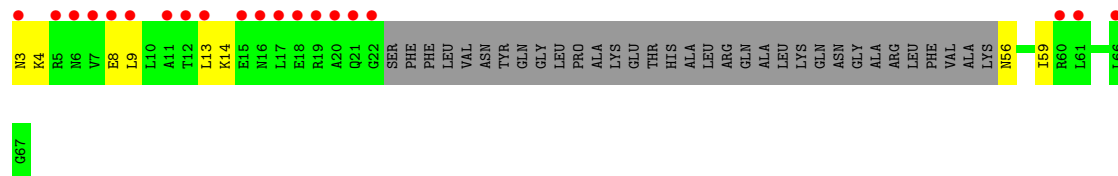
• Molecule 8: 50S ribosomal protein L9

Chain H:



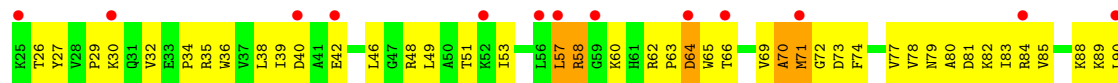
• Molecule 9: 50S ribosomal protein L10

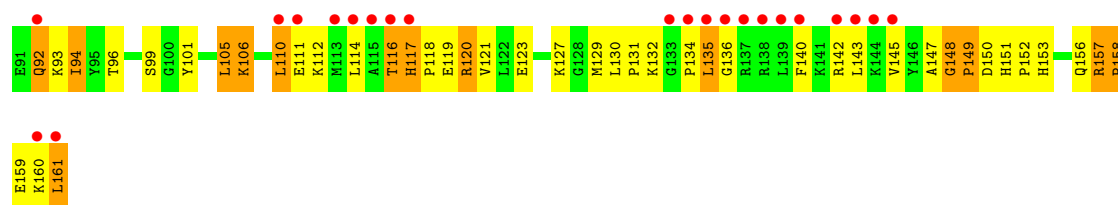
Chain I:



• Molecule 10: 50S ribosomal protein L13

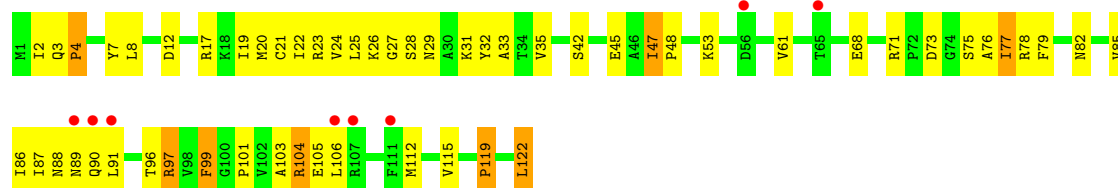
Chain J:





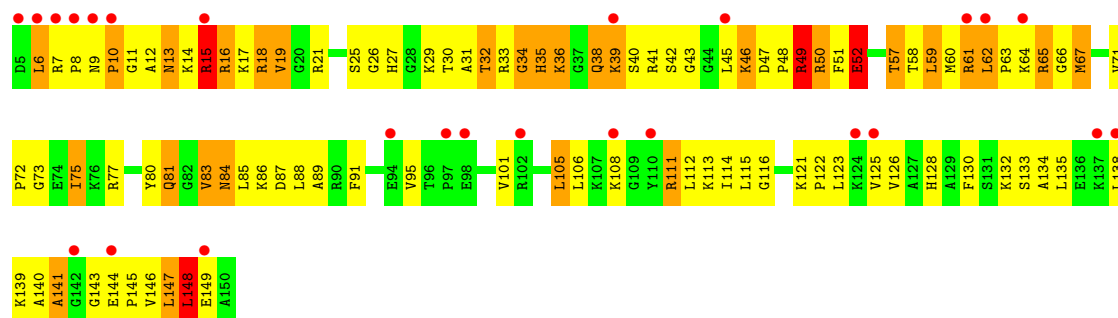
- Molecule 11: 50S ribosomal protein L14

Chain K:



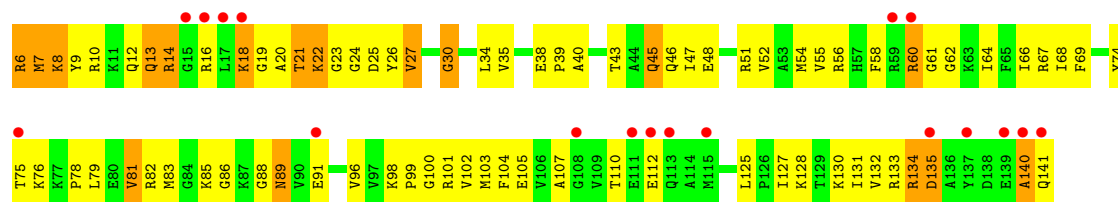
- Molecule 12: 50S ribosomal protein L15

Chain L:



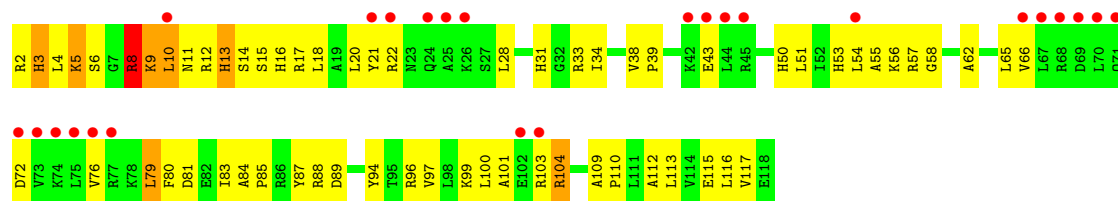
- Molecule 13: 50S ribosomal protein L16

Chain M:



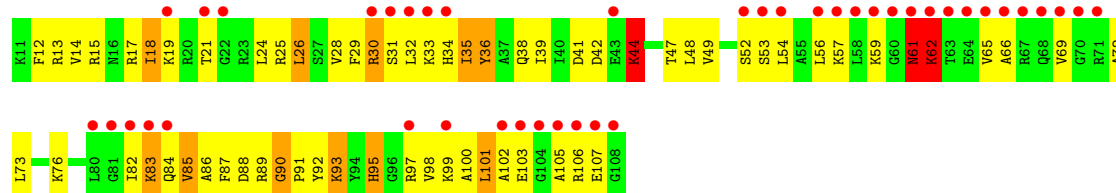
- Molecule 14: 50S ribosomal protein L17

Chain N:



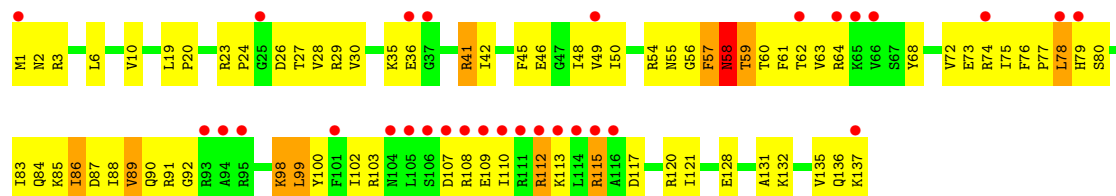
- Molecule 15: 50S ribosomal protein L18

Chain O:



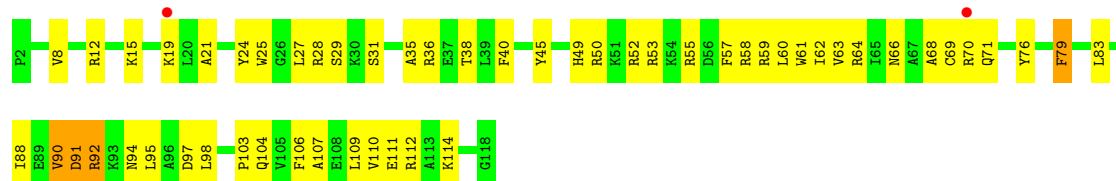
- Molecule 16: 50S ribosomal protein L19

Chain P:



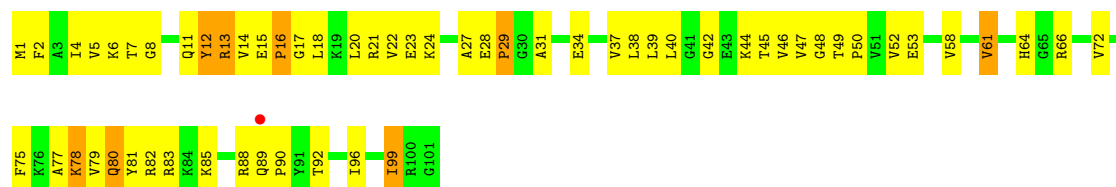
- Molecule 17: 50S ribosomal protein L20

Chain Q:



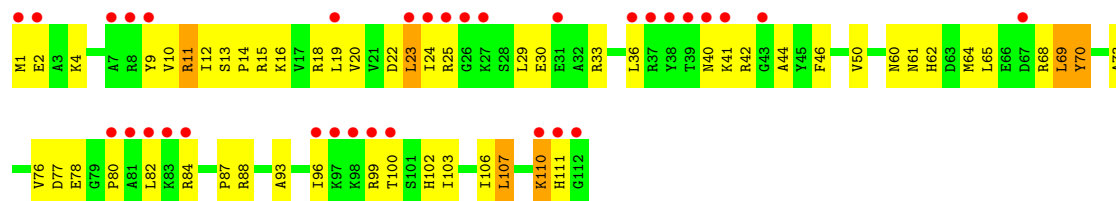
- Molecule 18: 50S ribosomal protein L21

Chain R:



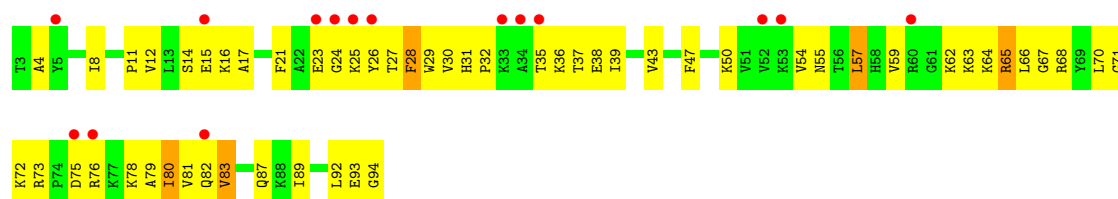
- Molecule 19: 50S ribosomal protein L22

Chain S:



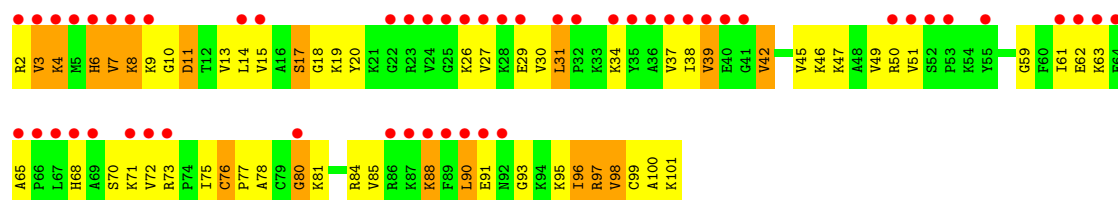
- Molecule 20: 50S ribosomal protein L23

Chain T:



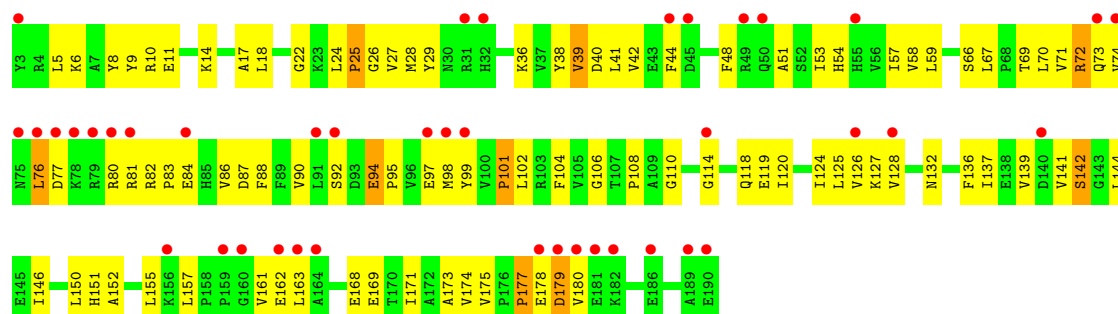
• Molecule 21: 50S ribosomal protein L24

Chain U:



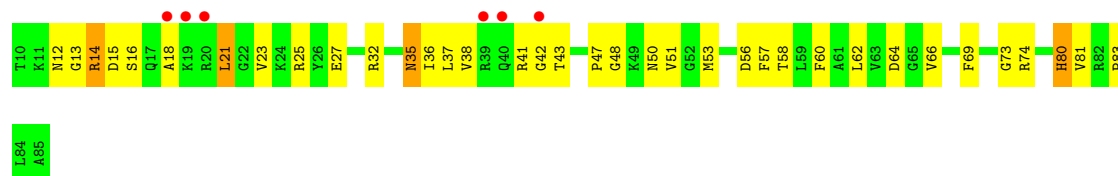
• Molecule 22: 50S ribosomal protein L25

Chain V:



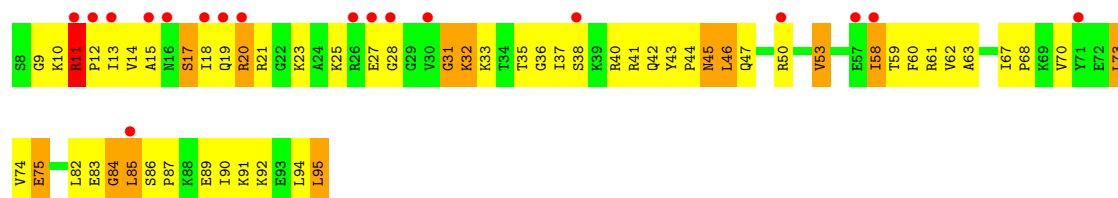
• Molecule 23: 50S ribosomal protein L27

Chain W:



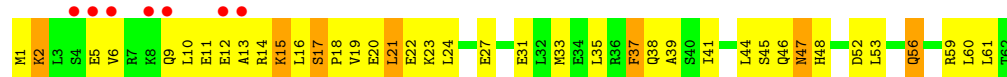
• Molecule 24: 50S ribosomal protein L28

Chain X:



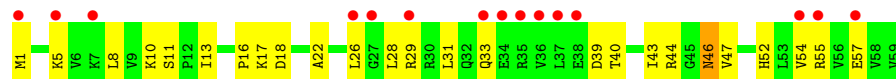
• Molecule 25: 50S ribosomal protein L29

Chain Y: 



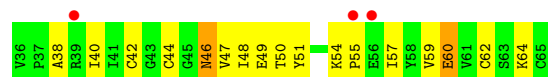
- Molecule 26: 50S ribosomal protein L30

Chain Z: 



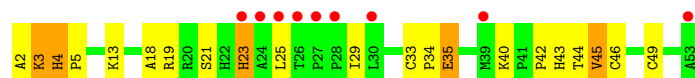
- Molecule 27: 50S ribosomal protein L31

Chain 1: 



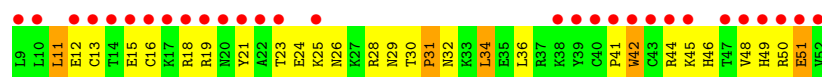
- Molecule 28: 50S ribosomal protein L32

Chain 2: 



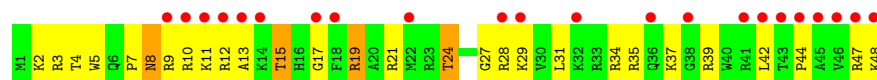
- Molecule 29: 50S ribosomal protein L33

Chain 3: 



- Molecule 30: 50S ribosomal protein L34

Chain 4: 



- Molecule 31: 50S ribosomal protein L35

Chain 5: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.94Å 455.59Å 618.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.50 60.01 – 3.49	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-3.50) 99.6 (60.01-3.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 3.49Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.233 , 0.264 0.445 , 0.456	Depositor DCC
R_{free} test set	7390 reflections (0.99%)	DCC
Wilson B-factor (Å ²)	106.2	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 46.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	1 of 746568 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.64	EDS
Total number of atoms	89438	wwPDB-VP
Average B, all atoms (Å ²)	110.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.51	0/66575	1.03	115/103930 (0.1%)
2	B	0.44	0/2853	0.92	1/4451 (0.0%)
3	C	0.33	0/2155	0.51	0/2905
4	D	0.27	0/1597	0.48	0/2153
5	E	0.29	0/1622	0.46	0/2194
6	F	0.23	0/1500	0.42	0/2017
7	G	0.22	0/1246	0.42	0/1682
8	H	0.29	0/1148	0.46	0/1552
9	I	0.21	0/252	0.38	0/333
10	J	0.26	0/1124	0.47	0/1515
11	K	0.27	0/942	0.48	0/1268
12	L	0.30	0/1131	0.56	0/1504
13	M	0.30	0/1099	0.49	0/1468
14	N	0.26	0/974	0.45	0/1302
15	O	0.23	0/779	0.42	0/1036
16	P	0.27	0/1158	0.44	0/1544
17	Q	0.29	0/970	0.46	0/1290
18	R	0.27	0/790	0.45	0/1057
19	S	0.31	0/902	0.51	0/1209
20	T	0.30	0/740	0.49	0/993
21	U	0.25	0/789	0.44	0/1051
22	V	0.23	0/1524	0.44	0/2068
23	W	0.26	0/613	0.43	0/816
24	X	0.30	0/702	0.56	0/932
25	Y	0.29	0/523	0.52	0/690
26	Z	0.23	0/473	0.41	0/634
27	1	0.20	0/229	0.38	0/309
28	2	0.28	0/419	0.51	0/567
29	3	0.21	0/388	0.40	0/518
30	4	0.34	0/427	0.52	0/561
31	5	0.31	0/516	0.50	0/679
All	All	0.46	0/96160	0.92	116/144228 (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
6	F	0	1
12	L	0	1
All	All	0	2

There are no bond length outliers.

All (116) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	945	A	C1'-O4'-C4'	-10.48	101.52	109.90
1	A	1786	A	C1'-O4'-C4'	-10.25	101.70	109.90
1	A	676	A	C1'-O4'-C4'	-9.48	102.32	109.90
1	A	2818	G	C1'-O4'-C4'	-9.24	102.51	109.90
1	A	945	A	O4'-C1'-N9	8.85	115.28	108.20
1	A	265	A	C3'-C2'-C1'	-8.68	94.55	101.50
1	A	1786	A	C3'-C2'-C1'	-8.01	95.09	101.50
1	A	761	A	N1-C6-N6	7.98	123.39	118.60
1	A	221	A	P-O3'-C3'	7.85	129.12	119.70
1	A	1614	A	C1'-O4'-C4'	-7.84	103.63	109.90
1	A	481	G	P-O3'-C3'	7.74	128.98	119.70
1	A	748	G	C1'-O4'-C4'	-7.71	103.73	109.90
1	A	1937	A	P-O3'-C3'	7.59	128.81	119.70
1	A	933	A	O4'-C1'-N9	7.32	114.06	108.20
1	A	945	A	C3'-C2'-C1'	-7.22	95.72	101.50
1	A	242	G	C3'-C2'-C1'	-7.05	95.86	101.50
1	A	1496	A	O4'-C1'-N9	6.94	113.75	108.20
1	A	332	A	P-O3'-C3'	6.92	128.00	119.70
1	A	1395	A	C1'-O4'-C4'	-6.82	104.44	109.90
1	A	1558	A	P-O3'-C3'	6.80	127.86	119.70
1	A	2506	U	O4'-C1'-N1	6.75	113.60	108.20
1	A	1542	G	P-O3'-C3'	6.70	127.75	119.70
1	A	989	G	C1'-O4'-C4'	-6.69	104.55	109.90
1	A	1984	G	C4'-C3'-C2'	-6.67	95.93	102.60
1	A	1698	A	C3'-C2'-C1'	-6.59	96.22	101.50
1	A	2445	G	C4'-C3'-C2'	-6.58	96.02	102.60
1	A	1022	G	P-O3'-C3'	6.58	127.59	119.70
1	A	1021	A	C3'-C2'-C1'	-6.56	96.25	101.50
1	A	1046	A	C5-C6-N1	-6.48	114.46	117.70
1	A	1379	A	P-O3'-C3'	6.47	127.46	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2049	G	C1'-O4'-C4'	-6.33	104.84	109.90
1	A	933	A	C4'-C3'-C2'	-6.32	96.28	102.60
1	A	1545	A	C1'-O4'-C4'	-6.29	104.87	109.90
1	A	210	C	C6-N1-C2	6.27	122.81	120.30
1	A	1786	A	N9-C1'-C2'	6.24	122.11	114.00
1	A	131	G	C1'-O4'-C4'	-6.24	104.91	109.90
1	A	2225	A	P-O3'-C3'	6.22	127.17	119.70
1	A	791	C	C3'-C2'-C1'	-6.21	96.53	101.50
1	A	1385	G	C3'-C2'-C1'	-6.20	96.54	101.50
1	A	859	G	C3'-C2'-C1'	-6.19	96.55	101.50
1	A	2613	U	C3'-C2'-C1'	-6.19	96.55	101.50
1	A	1761	C	C1'-O4'-C4'	-6.14	104.99	109.90
1	A	2447	G	P-O3'-C3'	6.12	127.05	119.70
1	A	1266	G	C3'-C2'-C1'	-6.09	96.62	101.50
1	A	372	G	O4'-C1'-N9	6.03	113.03	108.20
1	A	783	A	N1-C6-N6	5.98	122.19	118.60
1	A	989	G	O4'-C1'-N9	5.98	112.98	108.20
1	A	2052	G	C4'-C3'-C2'	-5.97	96.63	102.60
1	A	2056	G	N9-C4-C5	5.96	107.78	105.40
1	A	933	A	C1'-O4'-C4'	-5.93	105.15	109.90
1	A	938	G	C4'-C3'-C2'	-5.90	96.70	102.60
1	A	2033	A	P-O3'-C3'	5.89	126.76	119.70
1	A	825	C	C4'-C3'-C2'	-5.87	96.73	102.60
1	A	407	G	C4'-C3'-C2'	-5.86	96.74	102.60
1	A	783	A	C3'-C2'-C1'	-5.82	96.84	101.50
1	A	1427	A	P-O3'-C3'	5.82	126.68	119.70
1	A	1786	A	O4'-C1'-C2'	-5.82	99.98	105.80
1	A	1698	A	C1'-O4'-C4'	-5.78	105.28	109.90
1	A	444	C	C1'-O4'-C4'	-5.77	105.28	109.90
1	A	2428	G	P-O3'-C3'	5.76	126.61	119.70
1	A	807	U	C4'-C3'-C2'	-5.76	96.84	102.60
1	A	2278	A	C1'-O4'-C4'	-5.70	105.34	109.90
1	A	2883	A	O4'-C1'-N9	5.69	112.75	108.20
1	A	974(B)	C	C3'-C2'-C1'	-5.64	96.99	101.50
1	A	2098	U	P-O3'-C3'	5.63	126.46	119.70
1	A	761	A	N7-C8-N9	5.61	116.61	113.80
1	A	933	A	O4'-C4'-C3'	-5.60	98.40	104.00
1	A	1608	A	C1'-O4'-C4'	-5.60	105.42	109.90
1	A	2481	G	P-O3'-C3'	5.59	126.41	119.70
1	A	131	G	O4'-C4'-C3'	-5.57	98.43	104.00
1	A	2689	U	P-O3'-C3'	5.56	126.37	119.70
1	A	940	G	C4'-C3'-C2'	-5.51	97.09	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	226	G	C3'-C2'-C1'	-5.50	97.10	101.50
2	B	66	A	P-O3'-C3'	5.49	126.29	119.70
1	A	2562	U	C4'-C3'-C2'	-5.48	97.12	102.60
1	A	760	G	C4'-C3'-C2'	-5.42	97.18	102.60
1	A	95	G	C4'-C3'-C2'	-5.40	97.20	102.60
1	A	761	A	C6-C5-N7	-5.39	128.53	132.30
1	A	673	C	C4'-C3'-C2'	-5.39	97.21	102.60
1	A	1255	U	C1'-O4'-C4'	-5.38	105.60	109.90
1	A	1162	G	C4'-C3'-C2'	-5.37	97.23	102.60
1	A	527	C	O4'-C1'-N1	5.36	112.49	108.20
1	A	2681	C	C3'-C2'-C1'	-5.36	97.21	101.50
1	A	1022	G	C3'-C2'-C1'	5.36	105.79	101.50
1	A	2549	G	C4'-C3'-C2'	-5.35	97.25	102.60
1	A	2512	C	C4'-C3'-C2'	-5.34	97.26	102.60
1	A	956	G	C1'-O4'-C4'	-5.32	105.64	109.90
1	A	84	A	C3'-C2'-C1'	-5.30	97.26	101.50
1	A	372	G	C3'-C2'-C1'	-5.29	97.27	101.50
1	A	2049	G	C4'-C3'-C2'	-5.28	97.32	102.60
1	A	2056	G	C4'-C3'-C2'	-5.28	97.32	102.60
1	A	2818	G	O4'-C4'-C3'	-5.28	98.72	104.00
1	A	1936	A	P-O3'-C3'	5.27	126.02	119.70
1	A	807	U	O4'-C4'-C3'	-5.27	98.73	104.00
1	A	444	C	C4'-C3'-C2'	-5.26	97.34	102.60
1	A	479	A	C1'-O4'-C4'	-5.25	105.70	109.90
1	A	214	G	O4'-C1'-N9	5.22	112.38	108.20
1	A	1613	G	C4'-C3'-C2'	-5.21	97.39	102.60
1	A	601	C	C4'-C3'-C2'	-5.18	97.42	102.60
1	A	532	A	C1'-O4'-C4'	-5.15	105.78	109.90
1	A	2447	G	C3'-C2'-C1'	-5.14	97.38	101.50
1	A	2789	C	C1'-O4'-C4'	-5.13	105.80	109.90
1	A	1929	G	C3'-C2'-C1'	-5.12	97.40	101.50
1	A	974(B)	C	C1'-O4'-C4'	-5.09	105.82	109.90
1	A	692	C	C4'-C3'-C2'	-5.08	97.52	102.60
1	A	2744	G	C4'-C3'-C2'	-5.07	97.53	102.60
1	A	265	A	C1'-O4'-C4'	-5.04	105.87	109.90
1	A	1494	A	P-O3'-C3'	5.04	125.74	119.70
1	A	1189	A	O3'-P-O5'	-5.03	94.44	104.00
1	A	741	G	C4'-C3'-C2'	-5.03	97.57	102.60
1	A	671	C	C4'-C3'-C2'	-5.02	97.58	102.60
1	A	85	G	C3'-C2'-C1'	-5.02	97.49	101.50
1	A	35	G	C4'-C3'-C2'	-5.01	97.59	102.60
1	A	805	G	O4'-C1'-N9	5.01	112.21	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1504	C	N1-C1'-C2'	-5.00	106.50	112.00
1	A	1654	A	C4'-C3'-C2'	-5.00	97.60	102.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	F	75	LYS	Peptide
12	L	52	GLU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	59442	0	29966	1288	0
2	B	2551	0	1295	53	0
3	C	2105	0	2182	202	0
4	D	1564	0	1629	117	0
5	E	1587	0	1632	107	0
6	F	1475	0	1537	106	0
7	G	1223	0	1282	64	0
8	H	1133	0	1220	83	0
9	I	254	0	275	8	0
10	J	1097	0	1168	82	0
11	K	932	0	994	53	0
12	L	1114	0	1187	167	0
13	M	1079	0	1127	96	0
14	N	960	0	1021	73	0
15	O	771	0	832	67	0
16	P	1144	0	1211	68	0
17	Q	953	0	1013	71	0
18	R	779	0	852	76	0
19	S	891	0	951	50	0
20	T	726	0	778	58	0
21	U	776	0	870	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	V	1492	0	1513	94	0
23	W	605	0	628	36	0
24	X	695	0	764	69	0
25	Y	521	0	575	45	0
26	Z	468	0	523	20	0
27	1	226	0	225	17	0
28	2	405	0	420	27	0
29	3	381	0	391	28	0
30	4	419	0	467	30	0
31	5	508	0	576	54	0
32	1	1	0	0	0	0
32	2	2	0	0	0	0
32	3	1	0	0	0	0
32	6	244	0	0	0	0
32	A	829	0	0	0	0
32	B	27	0	0	0	0
32	C	9	0	0	0	0
32	E	2	0	0	0	0
32	F	4	0	0	0	0
32	H	1	0	0	0	0
32	I	1	0	0	0	0
32	J	3	0	0	0	0
32	K	5	0	0	0	0
32	M	3	0	0	0	0
32	N	2	0	0	0	0
32	O	1	0	0	0	0
32	P	12	0	0	0	0
32	R	1	0	0	0	0
32	S	1	0	0	0	0
32	T	2	0	0	0	0
32	U	2	0	0	0	0
32	V	3	0	0	0	0
32	W	1	0	0	0	0
32	X	2	0	0	0	0
32	Y	3	0	0	0	0
All	All	89438	0	59104	3008	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 20.

All (3008) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:33:ARG:HG3	12:L:36:LYS:HD3	1.31	1.12
12:L:128:HIS:HA	12:L:147:LEU:HB3	1.30	1.11
1:A:2015:A:H1'	28:2:2:ALA:HA	1.34	1.07
12:L:49:ARG:HG2	12:L:50:ARG:H	1.16	1.04
23:W:23:VAL:HA	23:W:38:VAL:HG22	1.37	1.03
15:O:24:LEU:HD12	15:O:84:GLN:HB3	1.38	1.03
8:H:92:VAL:HG13	8:H:120:ILE:HB	1.41	1.03
17:Q:92:ARG:HB2	17:Q:92:ARG:HH11	1.25	1.01
3:C:242:ARG:HD3	3:C:242:ARG:H	1.21	1.00
10:J:70:ALA:HB2	10:J:135:LEU:HD12	1.41	0.98
20:T:11:PRO:HA	20:T:28:PHE:HB3	1.47	0.97
1:A:2781:A:H5'	1:A:2782:G:H5'	1.44	0.97
1:A:1163:G:H2'	1:A:1164:G:H5''	1.46	0.96
12:L:50:ARG:HB2	31:5:60:LEU:HD11	1.47	0.96
1:A:1021:A:H3'	1:A:1021:A:H8	1.31	0.95
10:J:157:ARG:H	10:J:158:PRO:HD3	1.30	0.95
1:A:2420:C:OP1	31:5:34:TRP:HA	1.68	0.93
1:A:1021:A:H3'	1:A:1021:A:C8	2.04	0.93
1:A:1899:G:H21	1:A:1902:C:H41	1.08	0.93
7:G:16:SER:HB2	7:G:27:LYS:HB2	1.51	0.92
10:J:42:GLU:HA	10:J:82:LYS:HB3	1.50	0.92
13:M:22:LYS:HE2	13:M:22:LYS:HA	1.51	0.92
6:F:60:LEU:HD11	6:F:92:VAL:HG11	1.52	0.92
1:A:1019:U:HO2'	1:A:1021:A:H2	0.99	0.91
1:A:886:C:H2'	1:A:887:A:H4'	1.52	0.91
1:A:2068:U:H3	1:A:2430:A:H2	1.11	0.91
1:A:1046:A:N3	9:I:4:LYS:HD3	1.84	0.90
1:A:587:C:H42	12:L:33:ARG:HG2	1.34	0.90
1:A:2681:C:H5	1:A:2725:A:H62	0.98	0.90
22:V:18:LEU:HD23	22:V:25:PRO:HG3	1.52	0.90
1:A:761:A:H8	1:A:761:A:O5'	1.53	0.90
1:A:996:A:H4'	17:Q:92:ARG:NH1	1.87	0.89
19:S:24:ILE:HG21	19:S:36:LEU:HD21	1.55	0.89
1:A:547:A:H2'	1:A:548:A:C8	2.08	0.89
25:Y:2:LYS:HA	25:Y:5:GLU:CD	1.94	0.89
1:A:142:G:H4'	20:T:35:THR:HG21	1.55	0.88
12:L:49:ARG:HG2	12:L:50:ARG:N	1.83	0.88
1:A:780:G:H21	1:A:783:A:H62	1.14	0.88
12:L:114:ILE:HD11	12:L:130:PHE:CD1	2.07	0.88
7:G:89:ILE:HG12	7:G:162:ILE:HG22	1.56	0.88
1:A:197:A:H8	1:A:197:A:H5'	1.36	0.88
21:U:8:LYS:H	21:U:8:LYS:HZ2	1.19	0.87
7:G:101:ARG:HE	7:G:101:ARG:H	1.18	0.87

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:857:C:H4'	23:W:23:VAL:HG21	1.55	0.87
28:2:35:GLU:HB2	28:2:49:CYS:SG	2.14	0.87
11:K:3:GLN:HB2	11:K:4:PRO:HD2	1.54	0.87
5:E:67:GLN:O	5:E:67:GLN:HG3	1.73	0.87
1:A:270(J):G:HO2'	1:A:270(K):G:H8	1.19	0.86
21:U:81:LYS:HD2	21:U:96:ILE:HD12	1.57	0.86
1:A:2426:A:H3'	1:A:2427:C:H5''	1.56	0.86
27:1:50:THR:HG22	27:1:51:TYR:H	1.38	0.86
1:A:954:G:H5''	13:M:13:GLN:HG3	1.57	0.86
1:A:676:A:H8	1:A:2069:G:H21	1.24	0.86
1:A:2331:G:H4'	23:W:43:THR:H	1.38	0.86
15:O:35:ILE:HG12	15:O:101:LEU:HD21	1.57	0.85
1:A:2681:C:H5	1:A:2725:A:N6	1.74	0.85
25:Y:17:SER:HB3	25:Y:18:PRO:HD3	1.56	0.85
1:A:2712:U:H1'	1:A:712(B):A:C8	2.11	0.85
27:1:59:VAL:HG12	27:1:60:GLU:H	1.40	0.85
21:U:88:LYS:HE2	21:U:93:GLY:HA3	1.58	0.85
20:T:35:THR:O	20:T:39:ILE:HG12	1.77	0.85
17:Q:88:ILE:HB	17:Q:90:VAL:HG12	1.59	0.85
1:A:2439:A:H5'	1:A:2439:A:C8	2.13	0.84
8:H:5:LEU:HD23	8:H:5:LEU:H	1.39	0.84
21:U:45:VAL:HG22	21:U:62:GLU:HB3	1.59	0.84
1:A:1813:G:H1'	3:C:50:THR:HG21	1.59	0.84
21:U:2:ARG:HG2	21:U:3:VAL:HG23	1.59	0.84
6:F:41:GLN:HG2	6:F:155:MET:HB3	1.60	0.84
11:K:119:PRO:HB2	16:P:68:TYR:HE1	1.39	0.84
24:X:11:ARG:HB3	24:X:12:PRO:HD2	1.59	0.84
1:A:2426:A:H3'	1:A:2427:C:C5'	2.08	0.83
3:C:133:LEU:HD23	3:C:136:ILE:HD12	1.60	0.83
14:N:54:LEU:HD11	14:N:65:LEU:HD23	1.61	0.83
3:C:159:ALA:HB1	3:C:198:ASN:O	1.78	0.83
1:A:848:G:H2'	1:A:849:A:C8	2.14	0.83
22:V:97:GLU:HB3	22:V:125:LEU:HD21	1.60	0.82
1:A:1899:G:H21	1:A:1902:C:N4	1.74	0.82
16:P:26:ASP:HB2	16:P:91:ARG:HA	1.60	0.82
6:F:55:LYS:HD2	6:F:58:GLN:HE21	1.42	0.82
1:A:2744:G:H21	7:G:143:GLN:HE22	1.25	0.82
11:K:119:PRO:HB2	16:P:68:TYR:CE1	2.14	0.82
23:W:35:ASN:HD22	23:W:35:ASN:H	1.24	0.81
30:4:8:ASN:ND2	30:4:11:LYS:H	1.78	0.81
12:L:41:ARG:HH22	12:L:45:LEU:HB2	1.44	0.81
5:E:41:LEU:HA	5:E:44:ARG:HD3	1.62	0.81

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:245:G:H5'	12:L:73:GLY:HA2	1.61	0.81
1:A:947:G:C2'	1:A:948:G:H5''	2.10	0.81
21:U:78:ALA:HB3	21:U:81:LYS:HE3	1.63	0.81
4:D:91:VAL:HB	4:D:95:ILE:HD11	1.61	0.81
1:A:2327:A:H2'	1:A:2328:A:C8	2.15	0.81
12:L:89:ALA:HB1	12:L:121:LYS:HD3	1.62	0.81
19:S:13:SER:HB3	19:S:16:LYS:HD2	1.62	0.81
1:A:2400:G:H4'	29:3:19:ARG:HD3	1.61	0.81
7:G:162:ILE:HD13	7:G:162:ILE:H	1.46	0.81
17:Q:83:LEU:HG	17:Q:88:ILE:HD11	1.63	0.80
4:D:117:MET:HE1	4:D:136:ARG:HA	1.62	0.80
21:U:81:LYS:HD3	21:U:97:ARG:HB3	1.63	0.80
1:A:2873:A:C2	14:N:6:SER:HB2	2.17	0.80
6:F:109:VAL:HG11	6:F:142:PRO:HG3	1.61	0.79
1:A:996:A:H4'	17:Q:92:ARG:HH12	1.45	0.79
13:M:81:VAL:HG12	13:M:82:ARG:HG2	1.63	0.79
12:L:45:LEU:HD23	12:L:46:LYS:H	1.44	0.79
7:G:92:ILE:HD12	7:G:92:ILE:H	1.47	0.79
5:E:65:TRP:CZ3	5:E:75:HIS:HD2	2.01	0.79
26:Z:8:LEU:HD12	26:Z:31:LEU:HA	1.63	0.79
1:A:1579:A:H5'	1:A:1579:A:H8	1.45	0.79
12:L:6:LEU:HD23	12:L:6:LEU:H	1.48	0.79
1:A:773:U:C4'	3:C:47:GLY:HA3	2.13	0.79
1:A:2637:U:H5''	4:D:82:ARG:NH2	1.97	0.79
3:C:25:THR:O	3:C:27:THR:HG22	1.83	0.79
1:A:2394:C:OP1	12:L:63:PRO:HD2	1.83	0.78
11:K:35:VAL:HG11	11:K:103:ALA:HB3	1.65	0.78
22:V:77:ASP:HB2	22:V:84:GLU:HG3	1.63	0.78
31:5:54:GLU:HA	31:5:57:ARG:HH12	1.47	0.78
1:A:947:G:H2'	1:A:948:G:H5''	1.64	0.78
3:C:71:ASP:HB3	3:C:103:ARG:HH22	1.49	0.78
25:Y:16:LEU:HB2	25:Y:20:GLU:HG3	1.64	0.78
1:A:2025:C:H2'	1:A:2026:C:C6	2.17	0.78
3:C:244:ARG:HG3	3:C:245:PRO:HD2	1.65	0.78
15:O:24:LEU:O	15:O:86:ALA:HB3	1.82	0.78
1:A:1311:G:H5'	1:A:1311:G:H8	1.48	0.78
8:H:71:ILE:HG23	8:H:72:LEU:HD22	1.64	0.78
8:H:62:LYS:HB2	8:H:133:HIS:CE1	2.19	0.78
23:W:35:ASN:ND2	23:W:35:ASN:H	1.81	0.77
20:T:29:TRP:CZ3	20:T:78:LYS:HG3	2.19	0.77
1:A:1021:A:H62	1:A:1141:U:H3	1.32	0.77
1:A:1899:G:N2	1:A:1902:C:H41	1.79	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:8:LYS:HG3	13:M:9:TYR:H	1.50	0.77
1:A:587:C:N3	12:L:33:ARG:HD2	2.00	0.77
13:M:75:THR:HA	13:M:88:GLY:HA2	1.65	0.77
1:A:1006:C:O2	10:J:129:MET:HG2	1.84	0.77
3:C:264:LYS:O	3:C:267:SER:HB2	1.84	0.77
1:A:1658:C:OP1	4:D:132:HIS:ND1	2.16	0.77
12:L:36:LYS:HG3	12:L:41:ARG:HB2	1.67	0.77
3:C:242:ARG:N	3:C:242:ARG:HD3	1.98	0.77
6:F:66:GLN:HG2	6:F:67:LYS:H	1.48	0.77
16:P:27:THR:HG23	16:P:89:VAL:HG13	1.67	0.77
1:A:1210:A:C8	1:A:1210:A:H5''	2.20	0.77
1:A:1210:A:H5''	1:A:1210:A:H8	1.48	0.77
17:Q:24:TYR:HB2	17:Q:29:SER:HB3	1.65	0.77
17:Q:92:ARG:HB2	17:Q:92:ARG:NH1	1.98	0.77
1:A:773:U:H4'	3:C:47:GLY:HA3	1.66	0.77
1:A:125:G:H4'	1:A:126:A:OP2	1.84	0.76
15:O:49:VAL:HG12	15:O:73:LEU:HD23	1.67	0.76
5:E:53:THR:HG23	5:E:55:GLY:H	1.50	0.76
1:A:2210:G:N3	1:A:2210:G:H3'	2.00	0.76
1:A:1510:A:H2'	1:A:1511:A:C8	2.21	0.76
25:Y:39:ALA:HA	25:Y:45:SER:HB3	1.66	0.76
3:C:33:LEU:H	3:C:33:LEU:HD23	1.50	0.76
8:H:82:ARG:HB3	8:H:89:TYR:HB2	1.67	0.76
1:A:2377:A:H2'	1:A:2378:A:C8	2.21	0.76
1:A:948:G:H8	1:A:948:G:H5'	1.48	0.76
4:D:201:THR:HG22	4:D:202:LYS:H	1.50	0.76
1:A:140:A:H8	1:A:1408:C:HO2'	1.31	0.76
12:L:115:LEU:HA	12:L:134:ALA:HB2	1.67	0.75
4:D:2:LYS:HD3	4:D:95:ILE:HG22	1.67	0.75
1:A:1175:U:H2'	1:A:1176:G:H8	1.50	0.75
15:O:103:GLU:O	15:O:107:GLU:HG2	1.86	0.75
1:A:603:A:N1	1:A:655:A:H1'	2.00	0.75
7:G:35:VAL:HG21	7:G:75:ALA:HB2	1.66	0.75
12:L:122:PRO:HA	12:L:141:ALA:O	1.86	0.75
20:T:63:LYS:NZ	20:T:72:LYS:HB3	2.01	0.75
12:L:45:LEU:HD23	12:L:46:LYS:N	2.01	0.75
8:H:83:ALA:HB2	8:H:88:ILE:HD13	1.69	0.75
13:M:75:THR:HA	13:M:88:GLY:CA	2.16	0.75
1:A:343:C:H5'	1:A:343:C:H6	1.50	0.75
12:L:33:ARG:CG	12:L:36:LYS:HD3	2.13	0.75
1:A:2427:C:H5'	1:A:2427:C:H6	1.51	0.75
1:A:2039:C:H2'	1:A:2040:C:H6	1.52	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:201:THR:HG22	4:D:202:LYS:N	2.03	0.74
18:R:66:ARG:HD2	18:R:88:ARG:CZ	2.17	0.74
18:R:4:ILE:HB	18:R:39:LEU:HB2	1.67	0.74
19:S:1:MET:HE2	19:S:2:GLU:H	1.51	0.74
6:F:86:MET:SD	6:F:87:PRO:HD3	2.27	0.74
30:4:11:LYS:O	30:4:15:THR:HG23	1.87	0.74
3:C:30:GLU:CD	3:C:63:ARG:HE	1.90	0.74
3:C:227:ASN:HB3	3:C:228:PRO:HD2	1.69	0.74
21:U:27:VAL:HG12	21:U:39:VAL:HG22	1.69	0.74
21:U:71:LYS:NZ	21:U:71:LYS:HB2	2.03	0.74
20:T:50:LYS:H	20:T:87:GLN:HE22	1.35	0.74
20:T:30:VAL:HG11	20:T:39:ILE:HD12	1.69	0.74
11:K:71:ARG:HH12	16:P:74:ARG:HH22	1.36	0.74
1:A:1019:U:H3	1:A:114(B):A:H62	1.36	0.74
2:B:13:A:N7	2:B:70:C:H4'	2.02	0.74
3:C:118:VAL:HG22	3:C:119:ALA:H	1.53	0.74
1:A:2056:G:N2	28:2:4:HIS:O	2.21	0.73
10:J:157:ARG:N	10:J:158:PRO:HD3	2.03	0.73
22:V:48:PHE:HA	22:V:51:ALA:HB3	1.70	0.73
1:A:2025:C:H2'	1:A:2026:C:H6	1.51	0.73
1:A:2542:A:N3	1:A:2542:A:H5''	2.02	0.73
1:A:528:A:H8	1:A:528:A:H3'	1.53	0.73
2:B:43:C:H4'	6:F:98:ARG:HH12	1.52	0.73
10:J:157:ARG:H	10:J:158:PRO:CD	2.01	0.73
16:P:84:GLN:HG3	16:P:85:LYS:HG3	1.70	0.73
10:J:57:LEU:O	10:J:72:GLY:HA3	1.88	0.73
3:C:186:HIS:HD2	3:C:188:GLU:H	1.37	0.73
18:R:5:VAL:HG23	18:R:37:VAL:HG23	1.70	0.73
8:H:9:LEU:HB3	8:H:12:LEU:HD23	1.71	0.73
15:O:30:ARG:HB3	15:O:35:ILE:HD13	1.71	0.73
22:V:126:VAL:HG12	22:V:163:LEU:HA	1.71	0.73
1:A:2287:A:O2'	1:A:2288:A:H5''	1.88	0.73
14:N:10:LEU:HB2	14:N:17:ARG:HE	1.53	0.73
1:A:806:C:OP2	12:L:39:LYS:HD2	1.89	0.73
1:A:2469:A:H2	1:A:2481:G:H21	1.35	0.73
1:A:973:A:OP2	18:R:78:LYS:NZ	2.21	0.73
20:T:15:GLU:H	20:T:15:GLU:CD	1.91	0.73
21:U:96:ILE:HD11	21:U:99:CYS:HB2	1.69	0.72
31:5:57:ARG:HB2	31:5:57:ARG:NH1	2.04	0.72
14:N:10:LEU:HB2	14:N:17:ARG:NE	2.04	0.72
5:E:139:PHE:HB2	5:E:166:ALA:HB1	1.71	0.72
6:F:77:ILE:HG22	6:F:80:PHE:H	1.53	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:75:THR:HG21	13:M:85:LYS:NZ	2.04	0.72
1:A:547:A:H2'	1:A:548:A:H8	1.51	0.72
27:1:38:ALA:HA	27:1:55:PRO:HA	1.72	0.72
6:F:28:VAL:O	6:F:31:VAL:HG12	1.89	0.72
3:C:30:GLU:HG3	3:C:63:ARG:NH2	2.04	0.72
1:A:1314:C:H6	1:A:1314:C:H5'	1.55	0.72
1:A:848:G:C4	1:A:933:A:H8	2.07	0.72
4:D:51:PHE:HD1	4:D:52:LEU:HG	1.53	0.72
4:D:52:LEU:H	4:D:52:LEU:HD12	1.53	0.72
12:L:64:LYS:HB2	31:5:25:MET:HG3	1.72	0.72
1:A:106:C:H1'	21:U:2:ARG:HE	1.54	0.72
4:D:179:GLU:HB3	4:D:181:LEU:HD23	1.72	0.72
26:Z:43:ILE:O	26:Z:47:VAL:HG23	1.89	0.72
1:A:1021:A:C3'	1:A:1021:A:C8	2.72	0.72
1:A:528:A:H2	1:A:2043:C:H4'	1.54	0.72
1:A:2287:A:H62	1:A:2344:U:H3	1.37	0.72
8:H:110:ASP:HB2	8:H:113:ARG:HG2	1.70	0.72
10:J:65:TRP:HA	10:J:71:MET:HE1	1.72	0.72
1:A:556:G:H2'	1:A:557:U:C6	2.24	0.72
20:T:63:LYS:HD2	20:T:72:LYS:HA	1.72	0.71
5:E:155:LEU:HD23	5:E:186:ILE:HD13	1.71	0.71
30:4:35:ARG:HG3	30:4:42:LEU:HD11	1.71	0.71
22:V:163:LEU:HD23	22:V:163:LEU:H	1.55	0.71
3:C:27:THR:O	3:C:27:THR:HG23	1.91	0.71
1:A:2543:G:H8	1:A:2543:G:H5'	1.53	0.71
1:A:2075:U:H2'	1:A:2238:G:N2	2.05	0.71
29:3:42:TRP:HA	29:3:42:TRP:CE3	2.25	0.71
12:L:29:LYS:N	12:L:29:LYS:HD2	2.05	0.71
1:A:1343:G:H5'	1:A:1343:G:C8	2.24	0.71
12:L:49:ARG:CG	12:L:50:ARG:N	2.52	0.71
30:4:8:ASN:C	30:4:8:ASN:HD22	1.92	0.71
1:A:1311:G:H5'	1:A:1311:G:C8	2.26	0.71
3:C:147:LEU:HD13	3:C:155:LEU:HD11	1.71	0.71
12:L:59:LEU:HA	12:L:61:ARG:NE	2.05	0.71
1:A:1429:G:H2'	1:A:1430:C:C6	2.26	0.71
1:A:1516:U:H2'	1:A:1517:G:H8	1.56	0.71
24:X:17:SER:HB3	24:X:44:PRO:HD3	1.69	0.71
6:F:83:ARG:HG3	6:F:84:LYS:H	1.56	0.71
12:L:16:ARG:HE	12:L:17:LYS:N	1.89	0.71
31:5:26:LYS:HA	31:5:48:PHE:HE2	1.55	0.71
15:O:34:HIS:HA	15:O:54:LEU:HD23	1.72	0.71
1:A:2415:G:H4'	12:L:66:GLY:CA	2.20	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1336:A:H2'	1:A:1337:G:H8	1.55	0.71
6:F:19:LEU:HD11	6:F:172:LEU:HD13	1.72	0.71
13:M:43:THR:HB	13:M:45:GLN:HE21	1.54	0.71
21:U:31:LEU:HD23	21:U:31:LEU:H	1.54	0.71
16:P:26:ASP:CB	16:P:91:ARG:HA	2.21	0.70
6:F:7:LEU:HD23	6:F:10:LYS:HD2	1.74	0.70
1:A:796:C:H2'	1:A:797:C:C6	2.25	0.70
1:A:2740:A:H2'	1:A:2741:A:C8	2.26	0.70
1:A:141(A):A:H8	1:A:1595:G:H21	1.38	0.70
1:A:674:G:H1'	5:E:74:ARG:HD3	1.73	0.70
1:A:2261:C:C6	23:W:16:SER:HB3	2.27	0.70
30:4:12:ARG:NH2	30:4:44:PRO:HB3	2.05	0.70
8:H:56:LYS:HA	8:H:59:ALA:HB3	1.73	0.70
8:H:76:THR:HG22	8:H:141:LYS:HD3	1.74	0.70
30:4:5:TRP:NE1	30:4:7:PRO:HG3	2.06	0.70
12:L:26:GLY:HA2	12:L:30:THR:HG23	1.71	0.70
1:A:2036:C:H6	1:A:2036:C:H5'	1.57	0.70
1:A:2068:U:N3	1:A:2430:A:H2	1.89	0.70
21:U:8:LYS:N	21:U:8:LYS:HZ2	1.90	0.70
22:V:76:LEU:H	22:V:76:LEU:HD12	1.56	0.70
3:C:201:HIS:O	3:C:204:ILE:HG13	1.90	0.70
15:O:90:GLY:O	15:O:92:TYR:N	2.25	0.70
10:J:90:LEU:HD12	10:J:90:LEU:H	1.56	0.70
6:F:121:ASN:HD22	6:F:122:PRO:HD2	1.56	0.70
9:I:14:LYS:HE2	9:I:14:LYS:HA	1.72	0.70
20:T:27:THR:HB	20:T:80:ILE:HB	1.74	0.69
25:Y:2:LYS:H	25:Y:2:LYS:CD	2.05	0.69
20:T:50:LYS:H	20:T:87:GLN:NE2	1.90	0.69
1:A:760:G:H2'	1:A:761:A:H5'	1.74	0.69
1:A:1541:U:H3'	1:A:1542:G:O3'	1.92	0.69
17:Q:15:LYS:O	17:Q:19:LYS:HG3	1.92	0.69
1:A:1678:G:O5'	1:A:1678:G:H8	1.75	0.69
3:C:35:LYS:HG3	3:C:104:TYR:CE2	2.26	0.69
1:A:2023:G:H5'	1:A:2617:C:H4'	1.74	0.69
17:Q:50:ARG:HH22	18:R:72:VAL:HG12	1.58	0.69
24:X:83:GLU:HG2	24:X:84:GLY:H	1.57	0.69
10:J:36:TRP:HB2	10:J:156:GLN:HB2	1.75	0.69
24:X:50:ARG:HG2	24:X:59:THR:HG22	1.73	0.69
4:D:154:LYS:HA	4:D:154:LYS:HE3	1.74	0.69
1:A:1163:G:C2'	1:A:1164:G:H5''	2.23	0.69
1:A:1174:A:H3'	1:A:1175:U:H5''	1.73	0.69
1:A:2415:G:H4'	12:L:66:GLY:HA3	1.75	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1542:G:H1'	1:A:1543:A:C4	2.28	0.69
13:M:60:ARG:H	22:V:179:ASP:HB2	1.56	0.69
1:A:1544:C:H3'	1:A:1545:A:H5'	1.75	0.69
5:E:160:ASN:OD1	5:E:163:VAL:HG23	1.93	0.69
1:A:1899:G:N2	1:A:1902:C:N4	2.39	0.69
1:A:1046:A:H1'	9:I:4:LYS:CD	2.23	0.69
1:A:2062:A:O2'	1:A:2063:C:H5'	1.93	0.69
29:3:42:TRP:HA	29:3:42:TRP:HE3	1.58	0.68
29:3:15:GLU:OE2	29:3:18:ARG:HD2	1.92	0.68
28:2:45:VAL:HG12	28:2:46:CYS:H	1.56	0.68
24:X:11:ARG:HB3	24:X:12:PRO:CD	2.21	0.68
22:V:104:PHE:HA	22:V:139:VAL:HB	1.74	0.68
17:Q:55:ARG:HA	17:Q:58:ARG:HD2	1.73	0.68
24:X:27:GLU:HB2	24:X:33:LYS:HA	1.75	0.68
8:H:79:ILE:HB	8:H:144:VAL:HA	1.75	0.68
1:A:591:C:O2	31:5:2:PRO:HA	1.94	0.68
1:A:1516:U:H2'	1:A:1517:G:C8	2.29	0.68
13:M:24:GLY:HA2	13:M:101:ARG:HA	1.75	0.68
1:A:2056:G:N3	1:A:2056:G:H2'	2.08	0.68
1:A:733:G:N7	1:A:761:A:C6	2.62	0.68
1:A:528:A:C8	1:A:528:A:H3'	2.28	0.68
1:A:587:C:N4	12:L:33:ARG:HG2	2.08	0.68
1:A:860:U:H5	1:A:917:A:N7	1.91	0.68
2:B:55:U:H4'	6:F:27:ASN:HD21	1.58	0.68
3:C:155:LEU:HD23	3:C:177:LEU:HD21	1.74	0.68
7:G:43:VAL:HA	7:G:52:VAL:HG22	1.74	0.68
3:C:244:ARG:HG3	3:C:245:PRO:CD	2.24	0.68
1:A:1316:U:H2'	1:A:1317:A:C8	2.29	0.68
12:L:146:VAL:HG22	12:L:147:LEU:H	1.59	0.68
3:C:96:HIS:HD2	3:C:102:LYS:HG2	1.59	0.68
29:3:36:LEU:H	29:3:36:LEU:HD23	1.59	0.68
17:Q:90:VAL:HG13	17:Q:91:ASP:H	1.58	0.68
10:J:66:THR:HB	10:J:69:VAL:HG12	1.76	0.68
21:U:42:VAL:HG12	21:U:65:ALA:HB3	1.76	0.68
1:A:1826:G:H4'	3:C:242:ARG:HE	1.58	0.67
1:A:1175:U:H2'	1:A:1176:G:C8	2.29	0.67
8:H:87:LYS:HA	8:H:122:GLU:HA	1.76	0.67
3:C:217:ARG:HH11	3:C:217:ARG:HG2	1.59	0.67
22:V:108:PRO:HG3	22:V:141:VAL:HG22	1.75	0.67
1:A:1405:U:H2'	1:A:1406:U:C6	2.28	0.67
8:H:92:VAL:HA	8:H:96:ASP:OD2	1.95	0.67
1:A:2637:U:H5''	4:D:82:ARG:HH21	1.59	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:78:LYS:HD3	3:C:114:GLY:HA2	1.77	0.67
10:J:118:PRO:O	10:J:121:VAL:HG22	1.94	0.67
26:Z:8:LEU:CD1	26:Z:31:LEU:HD12	2.24	0.67
6:F:98:ARG:H	6:F:98:ARG:HD2	1.60	0.67
1:A:1046:A:H3'	1:A:1047:G:H5''	1.75	0.67
4:D:92:THR:HB	4:D:94:GLU:HG2	1.77	0.67
7:G:17:VAL:HG22	7:G:26:VAL:HG22	1.76	0.67
1:A:1657:C:H2'	1:A:1658:C:H6	1.59	0.67
3:C:144:ALA:HB3	3:C:192:THR:HG23	1.75	0.67
20:T:26:TYR:HB3	20:T:92:LEU:HD13	1.77	0.67
1:A:1336:A:H2'	1:A:1337:G:C8	2.30	0.67
4:D:30:PRO:HD3	4:D:180:ASN:ND2	2.10	0.67
1:A:1858:G:H1'	1:A:1884:A:N6	2.10	0.67
1:A:443:A:H2'	5:E:45:ARG:HH12	1.60	0.67
2:B:13:A:H5'	23:W:74:ARG:HH21	1.60	0.66
1:A:586:A:H5'	5:E:89:VAL:HG21	1.77	0.66
12:L:148:LEU:HD13	12:L:148:LEU:H	1.60	0.66
1:A:2822:G:H2'	1:A:2823:A:H5''	1.77	0.66
5:E:139:PHE:CB	5:E:166:ALA:HB1	2.25	0.66
12:L:62:LEU:HD11	31:5:27:THR:HA	1.77	0.66
31:5:22:VAL:HB	31:5:54:GLU:HG2	1.77	0.66
1:A:330:A:C2	1:A:1210:A:H2'	2.31	0.66
8:H:82:ARG:HB3	8:H:89:TYR:CB	2.24	0.66
3:C:186:HIS:CD2	3:C:188:GLU:H	2.14	0.66
1:A:1504:C:HO2'	1:A:1505:C:H6	1.41	0.66
1:A:65:C:H2'	1:A:66:C:H6	1.60	0.66
24:X:10:LYS:O	24:X:11:ARG:HG2	1.96	0.66
22:V:136:PHE:C	22:V:137:ILE:HD12	2.15	0.66
17:Q:92:ARG:HD2	17:Q:95:LEU:HG	1.77	0.66
3:C:94:LEU:HB2	3:C:104:TYR:HE1	1.60	0.66
25:Y:16:LEU:O	25:Y:20:GLU:HB2	1.95	0.66
12:L:111:ARG:HG3	12:L:128:HIS:CG	2.30	0.66
1:A:126:A:OP2	30:4:19:ARG:HB2	1.95	0.66
19:S:18:ARG:HG2	19:S:76:VAL:CG1	2.25	0.66
2:B:66:A:H61	2:B:107:U:H2'	1.60	0.66
1:A:1348:G:H2'	1:A:1349:A:H5''	1.77	0.66
18:R:40:LEU:HD23	18:R:47:VAL:HG23	1.78	0.66
20:T:8:ILE:H	20:T:8:ILE:HD12	1.60	0.66
1:A:1614:A:N6	19:S:87:PRO:HA	2.11	0.66
5:E:8:GLN:HA	5:E:21:ALA:HA	1.77	0.66
3:C:148:GLU:HB2	3:C:151:LYS:HD2	1.76	0.66
7:G:101:ARG:NE	7:G:101:ARG:H	1.93	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:59:LEU:HA	12:L:61:ARG:CZ	2.26	0.66
28:2:40:LYS:HE2	28:2:46:CYS:HB3	1.78	0.66
1:A:774:A:H2	1:A:787:U:HO2'	1.39	0.66
1:A:1778:U:H2'	1:A:1784:A:N6	2.11	0.66
3:C:238:GLY:O	3:C:239:ARG:C	2.33	0.65
1:A:1418:G:H8	1:A:1418:G:O5'	1.78	0.65
17:Q:110:VAL:O	17:Q:114:LYS:HG2	1.96	0.65
3:C:155:LEU:HD23	3:C:177:LEU:CD2	2.26	0.65
11:K:20:MET:HG2	11:K:21:CYS:O	1.96	0.65
1:A:251:A:C5	1:A:252:G:H1'	2.31	0.65
1:A:2392:A:H2	1:A:2424:C:H42	1.43	0.65
2:B:74:U:H2'	2:B:75:G:C8	2.31	0.65
1:A:673:C:H5''	5:E:81:PRO:HD2	1.78	0.65
1:A:1694:C:H5''	1:A:1694:C:H6	1.62	0.65
6:F:32:PRO:HB2	6:F:172:LEU:HD22	1.77	0.65
3:C:79:VAL:HG21	3:C:111:LEU:HD11	1.77	0.65
25:Y:46:GLN:O	25:Y:47:ASN:HB2	1.94	0.65
12:L:41:ARG:NH2	12:L:45:LEU:HD12	2.11	0.65
1:A:675:A:H4'	5:E:67:GLN:NE2	2.11	0.65
1:A:910:A:H62	13:M:12:GLN:HA	1.61	0.65
8:H:83:ALA:HB3	8:H:123:LEU:HD12	1.79	0.65
15:O:99:LYS:O	15:O:103:GLU:HB2	1.97	0.65
1:A:2359:C:H2'	1:A:2360:A:C8	2.32	0.65
1:A:1332:G:C8	1:A:1332:G:H5'	2.32	0.65
22:V:24:LEU:HB2	22:V:41:LEU:HD23	1.77	0.65
1:A:197:A:H5'	1:A:197:A:C8	2.24	0.65
1:A:342:G:C2'	1:A:343:C:H5''	2.27	0.65
17:Q:92:ARG:HD3	17:Q:94:ASN:HB3	1.79	0.65
29:3:11:LEU:HG	29:3:26:ASN:HB2	1.78	0.65
18:R:22:VAL:HG12	18:R:23:GLU:N	2.11	0.65
18:R:49:THR:HB	18:R:50:PRO:HD2	1.77	0.65
25:Y:6:VAL:O	25:Y:10:LEU:HG	1.96	0.65
1:A:860:U:O2'	1:A:861:A:H5'	1.96	0.65
3:C:142:VAL:HG23	3:C:192:THR:O	1.97	0.65
1:A:2724:C:OP1	4:D:118:LYS:HE3	1.97	0.65
1:A:140:A:H8	1:A:1408:C:O2'	1.79	0.64
1:A:528:A:C2	1:A:2043:C:H4'	2.32	0.64
1:A:1343:G:H5'	1:A:1343:G:H8	1.62	0.64
1:A:322:A:H3'	5:E:169:ASN:ND2	2.12	0.64
3:C:158:ALA:HB3	3:C:161:THR:HG21	1.79	0.64
1:A:2506:U:H5	1:A:2583:G:H1	1.45	0.64
1:A:588:U:H2'	1:A:589:C:C6	2.32	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:51:PHE:H	4:D:75:VAL:HB	1.62	0.64
28:2:40:LYS:CE	28:2:46:CYS:HB3	2.27	0.64
1:A:2078:C:H2'	1:A:2079:U:H6	1.62	0.64
1:A:270(G):U:H2'	1:A:270(H):C:C6	2.32	0.64
1:A:1794:U:H2'	1:A:1795:C:H6	1.62	0.64
1:A:1022:G:H8	10:J:92:GLN:NE2	1.96	0.64
1:A:1607:C:H4'	1:A:1608:A:O5'	1.97	0.64
26:Z:5:LYS:HB3	26:Z:57:GLU:HB2	1.80	0.64
1:A:2873:A:N3	14:N:6:SER:HB2	2.13	0.64
14:N:9:LYS:O	14:N:10:LEU:HG	1.96	0.64
13:M:83:MET:O	13:M:83:MET:HG3	1.98	0.64
20:T:70:LEU:HD23	20:T:71:GLY:N	2.13	0.64
23:W:37:LEU:O	23:W:38:VAL:HG23	1.98	0.64
10:J:36:TRP:HB2	10:J:156:GLN:CB	2.27	0.64
15:O:33:LYS:HD3	15:O:33:LYS:O	1.98	0.64
5:E:31:HIS:HB2	12:L:13:ASN:HB3	1.79	0.64
31:5:39:LYS:O	31:5:43:GLN:HG2	1.97	0.64
13:M:110:THR:HB	13:M:112:GLU:OE1	1.98	0.64
7:G:149:ARG:HA	7:G:162:ILE:CG1	2.28	0.64
1:A:1210:A:H4'	1:A:1211:U:O5'	1.98	0.64
2:B:79:C:H2'	2:B:80:U:O4'	1.97	0.64
1:A:2599:G:C8	3:C:237:GLU:HG3	2.32	0.64
15:O:31:SER:HB3	15:O:34:HIS:HB2	1.78	0.64
1:A:1529:A:H62	1:A:1542:G:N2	1.96	0.64
1:A:1007:C:O2'	10:J:131:PRO:HA	1.98	0.64
14:N:38:VAL:HB	14:N:39:PRO:HD3	1.80	0.64
1:A:2777:G:H5''	1:A:2778:A:H5'	1.78	0.64
1:A:664:C:H4'	1:A:941:A:OP1	1.98	0.64
3:C:270:ILE:O	3:C:271:ILE:HG13	1.97	0.64
3:C:206:LEU:O	3:C:211:ARG:HD3	1.98	0.64
1:A:811:U:O2	1:A:1250:G:H2'	1.98	0.64
1:A:185:U:H2'	1:A:186:G:C8	2.32	0.64
21:U:50:ARG:HD3	21:U:51:VAL:H	1.63	0.64
1:A:480:A:OP2	21:U:46:LYS:HE2	1.97	0.64
1:A:954:G:H5''	13:M:13:GLN:CG	2.27	0.63
14:N:79:LEU:HD23	14:N:83:ILE:HB	1.79	0.63
1:A:2271:G:OP1	23:W:18:ALA:HB1	1.97	0.63
1:A:1434:A:H2'	1:A:1435:G:C8	2.33	0.63
17:Q:90:VAL:HG23	18:R:39:LEU:HB3	1.81	0.63
1:A:948:G:H5'	1:A:948:G:C8	2.32	0.63
1:A:2210:G:H21	1:A:2211:G:H5'	1.64	0.63
22:V:24:LEU:HD21	22:V:86:VAL:CG2	2.29	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:11:C:H3'	2:B:12:C:H6	1.63	0.63
7:G:101:ARG:N	7:G:101:ARG:HE	1.94	0.63
24:X:13:ILE:HD11	24:X:15:ALA:HB2	1.79	0.63
24:X:46:LEU:O	24:X:46:LEU:HD23	1.99	0.63
1:A:1652:A:OP1	14:N:9:LYS:HE3	1.98	0.63
1:A:389:G:O6	12:L:71:VAL:HG23	1.97	0.63
1:A:2294:C:H2'	1:A:2295:C:H6	1.62	0.63
11:K:103:ALA:HB1	11:K:105:GLU:OE1	1.98	0.63
4:D:119:ARG:HD3	4:D:120:TRP:CE2	2.34	0.63
1:A:637:A:O5'	12:L:116:GLY:HA2	1.99	0.63
1:A:2401:U:H2'	1:A:2402:C:H5''	1.79	0.63
18:R:39:LEU:HD12	18:R:47:VAL:HG11	1.81	0.63
1:A:1314:C:H5'	1:A:1314:C:C6	2.34	0.63
1:A:1316:U:H2'	1:A:1317:A:H8	1.63	0.63
5:E:103:LYS:HA	5:E:106:ARG:HG3	1.78	0.63
24:X:86:SER:O	24:X:90:ILE:HG12	1.97	0.63
3:C:131:LEU:CD1	3:C:136:ILE:HG12	2.29	0.63
14:N:18:LEU:HD11	14:N:22:ARG:CZ	2.29	0.63
4:D:36:ARG:NH1	4:D:86:PRO:HD2	2.14	0.63
12:L:14:LYS:O	12:L:15:ARG:HB2	1.98	0.63
10:J:112:LYS:O	10:J:116:THR:HG22	1.99	0.63
1:A:1694:C:C5'	1:A:1694:C:H6	2.12	0.63
1:A:663:G:H5''	12:L:21:ARG:HD3	1.79	0.63
1:A:214:G:H1'	1:A:216:A:O2'	1.99	0.63
1:A:780:G:H21	1:A:783:A:N6	1.93	0.62
14:N:17:ARG:HG3	14:N:18:LEU:N	2.14	0.62
1:A:2402:C:H5'	1:A:2403:C:OP2	1.98	0.62
16:P:50:ILE:HA	16:P:99:LEU:HD11	1.81	0.62
1:A:1389:G:H2'	1:A:1390:U:C6	2.34	0.62
12:L:62:LEU:N	12:L:62:LEU:HD13	2.14	0.62
15:O:66:ALA:HB1	15:O:101:LEU:HD22	1.80	0.62
5:E:29:ASN:H	5:E:112:MET:HE1	1.64	0.62
1:A:1953:A:H2	1:A:2549:G:N3	1.97	0.62
1:A:510:C:H2'	1:A:511:U:O4'	1.99	0.62
1:A:242:G:C8	31:5:5:LYS:HG2	2.33	0.62
7:G:84:SER:HA	7:G:133:VAL:O	1.99	0.62
3:C:10:THR:HG23	3:C:13:ARG:CB	2.29	0.62
10:J:135:LEU:HD23	10:J:136:GLY:N	2.13	0.62
11:K:71:ARG:NH1	16:P:74:ARG:HH22	1.98	0.62
12:L:9:ASN:N	12:L:10:PRO:HD3	2.15	0.62
8:H:6:LEU:H	8:H:6:LEU:HD23	1.63	0.62
1:A:2687:U:C4	1:A:2688:U:C5	2.88	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:132:HIS:CD2	4:D:135:HIS:NE2	2.68	0.62
1:A:2075:U:H2'	1:A:2238:G:H22	1.63	0.62
17:Q:21:ALA:CB	17:Q:35:ALA:HB1	2.29	0.62
1:A:2350:C:H5''	31:5:42:ARG:HD3	1.81	0.62
1:A:2502:G:H5'	1:A:2503:A:H5''	1.81	0.62
11:K:104:ARG:HH11	11:K:104:ARG:HB3	1.63	0.62
12:L:16:ARG:NH1	12:L:18:ARG:HG3	2.15	0.62
22:V:102:LEU:HD23	22:V:137:ILE:HB	1.81	0.62
1:A:185:U:H4'	1:A:218:A:H4'	1.82	0.62
2:B:50:G:OP2	15:O:62:LYS:HD3	2.00	0.62
13:M:38:GLU:HB2	13:M:127:ILE:HG23	1.81	0.62
1:A:492:A:H2'	1:A:493:G:O4'	2.00	0.62
23:W:23:VAL:HA	23:W:38:VAL:CG2	2.24	0.62
21:U:7:VAL:HB	21:U:8:LYS:HZ2	1.65	0.62
1:A:81:G:H21	21:U:2:ARG:NH2	1.98	0.62
1:A:343:C:C6	1:A:343:C:H5'	2.32	0.62
8:H:78:THR:HA	8:H:143:SER:HB3	1.80	0.62
1:A:674:G:H2'	1:A:804:A:H61	1.62	0.62
24:X:73:LEU:HD21	24:X:94:LEU:HG	1.82	0.62
1:A:2186:G:H2'	1:A:2187:G:H8	1.65	0.62
24:X:25:LYS:HG2	24:X:35:THR:HG22	1.81	0.62
1:A:2577:A:H5''	1:A:2578:G:H5'	1.81	0.62
1:A:1937:A:O2'	1:A:1938:A:H5'	1.99	0.62
3:C:30:GLU:HG3	3:C:63:ARG:HH21	1.63	0.62
12:L:30:THR:HG22	12:L:31:ALA:N	2.15	0.62
10:J:127:LYS:HB2	10:J:140:PHE:CE1	2.35	0.62
1:A:273(G):C:H2'	1:A:274:G:H5''	1.82	0.62
1:A:1046:A:H1'	9:I:4:LYS:HD3	1.82	0.61
13:M:20:ALA:HB1	13:M:99:PRO:O	2.00	0.61
4:D:4:ILE:CG1	4:D:28:ALA:HB1	2.30	0.61
1:A:1021:A:O2'	1:A:1123:C:H5''	2.00	0.61
21:U:8:LYS:HE2	21:U:37:VAL:HG11	1.82	0.61
8:H:123:LEU:HD23	8:H:124:GLY:N	2.15	0.61
1:A:729:G:C5	3:C:208:LYS:HB2	2.35	0.61
5:E:199:TRP:O	5:E:203:GLN:HG2	2.00	0.61
1:A:2653:U:H3	1:A:2667:C:H42	1.48	0.61
3:C:21:PHE:O	3:C:24:ILE:HG22	2.00	0.61
3:C:108:PRO:HG3	3:C:143:HIS:CE1	2.36	0.61
11:K:2:ILE:HD11	11:K:82:ASN:HD22	1.65	0.61
1:A:1291:C:H2'	1:A:1292:U:C6	2.35	0.61
10:J:57:LEU:HD21	10:J:143:LEU:HB2	1.80	0.61
20:T:64:LYS:HG2	20:T:65:ARG:H	1.65	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2562:U:H1'	11:K:23:ARG:NH1	2.15	0.61
16:P:98:LYS:HB3	16:P:100:TYR:CE1	2.36	0.61
5:E:102:PRO:HB2	5:E:105:VAL:HG23	1.81	0.61
1:A:639:U:H2'	1:A:640:C:C6	2.35	0.61
1:A:7:G:H2'	1:A:8:A:H8	1.64	0.61
3:C:5:LYS:HD2	3:C:5:LYS:N	2.14	0.61
1:A:996:A:C4'	17:Q:92:ARG:HH12	2.12	0.61
3:C:25:THR:HG22	3:C:82:ILE:O	2.01	0.61
1:A:1678:G:N2	1:A:1989:G:H22	1.98	0.61
1:A:860:U:C5	1:A:917:A:N7	2.68	0.61
16:P:41:ARG:HD2	16:P:42:ILE:H	1.65	0.61
5:E:83:PHE:O	5:E:84:VAL:C	2.38	0.61
13:M:6:ARG:O	13:M:7:MET:HB2	2.00	0.61
7:G:55:PRO:HG2	7:G:61:HIS:HD2	1.63	0.61
1:A:245:G:H2'	1:A:246:C:H6	1.65	0.61
1:A:1408:C:C2	1:A:1595:G:N2	2.68	0.61
1:A:1388:G:H2'	1:A:1389:G:H8	1.64	0.61
19:S:78:GLU:OE2	19:S:99:ARG:HD3	2.00	0.61
1:A:2787:C:H1'	4:D:62:PRO:HG3	1.82	0.61
24:X:67:ILE:N	24:X:68:PRO:HD2	2.15	0.61
1:A:2850:A:C8	1:A:2850:A:H5'	2.36	0.61
23:W:21:LEU:HD12	23:W:21:LEU:H	1.66	0.61
3:C:31:LYS:O	3:C:36:PRO:HD3	2.01	0.61
12:L:140:ALA:O	12:L:141:ALA:HB2	2.00	0.61
4:D:51:PHE:CD1	4:D:52:LEU:HG	2.36	0.61
20:T:59:VAL:HB	20:T:76:ARG:HG3	1.81	0.61
4:D:32:PRO:HA	4:D:90:THR:HG22	1.83	0.61
4:D:173:VAL:HG12	4:D:174:ASP:H	1.65	0.61
10:J:62:ARG:NH2	10:J:64:ASP:HB2	2.15	0.61
21:U:90:LEU:HG	21:U:91:GLU:N	2.16	0.61
1:A:1358:G:O2'	1:A:1359:A:H5''	2.01	0.61
1:A:1542:G:H4'	1:A:1543:A:O5'	2.01	0.61
1:A:38:A:H2'	1:A:39:C:C6	2.35	0.61
19:S:65:LEU:HB2	19:S:68:ARG:HG2	1.82	0.61
1:A:245:G:O6	31:5:8:LYS:HE3	2.01	0.61
1:A:1311:G:H8	1:A:1311:G:C5'	2.12	0.61
8:H:126:TYR:H	8:H:142:VAL:HB	1.65	0.61
1:A:65:C:H2'	1:A:66:C:C6	2.35	0.61
31:5:57:ARG:HH11	31:5:57:ARG:HB2	1.66	0.60
5:E:53:THR:HG22	5:E:56:GLU:CD	2.22	0.60
1:A:2039:C:H2'	1:A:2040:C:C6	2.35	0.60
1:A:1543:A:H5'	1:A:1544:C:OP2	2.00	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:X:27:GLU:CB	24:X:33:LYS:HA	2.31	0.60
3:C:69:ARG:HH21	3:C:130:ALA:HB2	1.62	0.60
1:A:2078:C:H2'	1:A:2079:U:C6	2.36	0.60
1:A:1437:C:H2'	1:A:1438:U:C6	2.36	0.60
6:F:36:LYS:HB3	6:F:160:VAL:HB	1.83	0.60
30:4:8:ASN:ND2	30:4:8:ASN:C	2.54	0.60
24:X:31:GLY:O	24:X:32:LYS:HB2	2.01	0.60
1:A:1478:G:O2'	1:A:1558:A:H2	1.84	0.60
14:N:84:ALA:HB3	14:N:85:PRO:HD3	1.83	0.60
1:A:1309:G:H3'	30:4:9:ARG:HH12	1.65	0.60
7:G:68:THR:O	7:G:72:ILE:HG12	2.01	0.60
1:A:747:U:OP2	28:2:3:LYS:HD3	2.00	0.60
21:U:76:CYS:HB3	21:U:77:PRO:HD2	1.83	0.60
14:N:4:LEU:HG	14:N:4:LEU:O	2.01	0.60
31:5:22:VAL:HB	31:5:54:GLU:CG	2.31	0.60
3:C:61:LEU:O	3:C:63:ARG:NH1	2.34	0.60
14:N:10:LEU:CB	14:N:17:ARG:HE	2.13	0.60
1:A:2074:U:H2'	1:A:2075:U:C6	2.36	0.60
24:X:19:GLN:HG2	24:X:41:ARG:HB2	1.83	0.60
1:A:2893:G:H5''	1:A:2894:G:O4'	2.02	0.60
1:A:85:G:H5''	1:A:85:G:H8	1.66	0.60
3:C:34:VAL:O	3:C:35:LYS:HD3	2.01	0.60
24:X:83:GLU:HG2	24:X:84:GLY:N	2.17	0.60
20:T:8:ILE:HD12	20:T:8:ILE:N	2.16	0.60
12:L:38:GLN:HG3	12:L:39:LYS:H	1.66	0.60
1:A:2439:A:C5'	1:A:2439:A:C8	2.84	0.60
1:A:558:G:OP1	10:J:134:PRO:HD2	2.00	0.60
6:F:10:LYS:O	6:F:14:GLU:HB3	2.00	0.60
1:A:795:C:H2'	1:A:796:C:H6	1.66	0.60
10:J:117:HIS:CE1	10:J:120:ARG:HE	2.19	0.60
22:V:24:LEU:HD21	22:V:86:VAL:HG21	1.82	0.60
1:A:1771:C:HO2'	1:A:1786:A:H8	1.50	0.60
14:N:11:ASN:OD1	14:N:12:ARG:N	2.30	0.60
6:F:114:ILE:HG23	6:F:115:ARG:HD2	1.84	0.60
4:D:132:HIS:HA	4:D:135:HIS:NE2	2.15	0.60
1:A:153:C:OP1	24:X:92:LYS:HE2	2.02	0.60
5:E:164:ARG:HG3	5:E:175:THR:OG1	2.02	0.60
1:A:414:C:H2'	1:A:415:A:C8	2.37	0.60
3:C:28:GLU:HB3	3:C:29:PRO:HD3	1.84	0.60
11:K:53:LYS:N	11:K:53:LYS:HD2	2.17	0.60
21:U:8:LYS:NZ	21:U:8:LYS:H	1.95	0.60
26:Z:1:MET:SD	26:Z:40:THR:HA	2.42	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1429:G:H2'	1:A:1430:C:H6	1.66	0.60
24:X:19:GLN:NE2	24:X:41:ARG:HE	1.98	0.60
12:L:71:VAL:HB	12:L:72:PRO:HD3	1.84	0.60
1:A:2776:A:H4'	1:A:2777:G:H5''	1.83	0.60
19:S:40:ASN:O	19:S:41:LYS:HG2	2.02	0.60
15:O:24:LEU:HD13	15:O:82:ILE:HG23	1.82	0.60
9:I:4:LYS:HG2	9:I:8:GLU:HG3	1.84	0.60
13:M:30:GLY:HA2	13:M:107:ALA:HB2	1.83	0.60
1:A:760:G:C2'	1:A:761:A:H5'	2.31	0.59
11:K:3:GLN:CB	11:K:4:PRO:HD2	2.29	0.59
13:M:76:LYS:N	13:M:88:GLY:HA2	2.17	0.59
1:A:295:G:H4'	21:U:2:ARG:NH1	2.16	0.59
1:A:2038:G:H2'	1:A:2039:C:C6	2.36	0.59
8:H:113:ARG:HB2	8:H:130:TYR:CE1	2.37	0.59
13:M:38:GLU:O	13:M:127:ILE:HD13	2.02	0.59
1:A:2243:U:H2'	1:A:2244:U:C6	2.37	0.59
1:A:1803:A:H5''	1:A:1804:C:OP2	2.01	0.59
19:S:29:LEU:HD22	19:S:69:LEU:HD11	1.83	0.59
2:B:70:C:H2'	2:B:71:C:H6	1.68	0.59
5:E:170:LEU:HD12	5:E:171:PRO:HD2	1.84	0.59
20:T:47:PHE:HB3	20:T:89:ILE:HD12	1.84	0.59
1:A:1799:G:H8	3:C:181:GLU:CD	2.06	0.59
22:V:69:THR:HG22	22:V:90:VAL:HG22	1.84	0.59
1:A:2307:G:H2'	1:A:2308:G:H5'	1.82	0.59
1:A:2593:U:H2'	1:A:2594:C:C6	2.37	0.59
1:A:826:U:O2	1:A:832:G:C2	2.56	0.59
21:U:76:CYS:CB	21:U:77:PRO:HD2	2.32	0.59
1:A:835:A:OP1	31:5:52:LYS:HG2	2.02	0.59
2:B:13:A:H5'	23:W:74:ARG:NH2	2.16	0.59
4:D:9:VAL:HG22	4:D:25:VAL:HB	1.84	0.59
17:Q:104:GLN:HB3	18:R:44:LYS:HZ1	1.67	0.59
30:4:21:ARG:HB3	30:4:31:LEU:HD21	1.84	0.59
13:M:75:THR:HG21	13:M:85:LYS:HZ2	1.66	0.59
14:N:4:LEU:C	14:N:6:SER:H	2.05	0.59
3:C:267:SER:O	3:C:270:ILE:HG13	2.02	0.59
1:A:342:G:H2'	1:A:343:C:H5''	1.84	0.59
11:K:104:ARG:NH1	11:K:104:ARG:HB3	2.18	0.59
3:C:44:ASN:HB3	3:C:50:THR:HG21	1.84	0.59
4:D:50:GLY:HA3	4:D:75:VAL:HG11	1.84	0.59
24:X:19:GLN:HE21	24:X:41:ARG:HE	1.47	0.59
1:A:661:C:O3'	12:L:18:ARG:HG2	2.02	0.59
1:A:185:U:H2'	1:A:186:G:H8	1.67	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:91:PHE:CE2	12:L:95:VAL:HG12	2.37	0.59
1:A:839:U:H2'	1:A:840:C:C6	2.37	0.59
1:A:330:A:H2	1:A:1210:A:H2'	1.68	0.59
1:A:1264:G:OP1	28:2:19:ARG:NH2	2.33	0.59
1:A:442:G:H1'	5:E:48:THR:HG21	1.85	0.59
1:A:2476:A:H2'	1:A:2476:A:N3	2.17	0.59
10:J:80:ALA:O	10:J:83:ILE:HG13	2.01	0.59
18:R:38:LEU:HD23	18:R:39:LEU:N	2.17	0.59
1:A:1794:U:H2'	1:A:1795:C:C6	2.37	0.59
1:A:2392:A:OP1	31:5:32:LEU:HB3	2.02	0.59
1:A:2496:C:OP1	13:M:81:VAL:HG13	2.03	0.59
25:Y:13:ALA:O	25:Y:17:SER:HA	2.03	0.59
1:A:83:G:H22	1:A:102:G:H2'	1.65	0.59
1:A:779:U:H5'	3:C:49:ILE:HD11	1.85	0.59
18:R:12:TYR:OH	18:R:22:VAL:HG13	2.02	0.59
30:4:8:ASN:HD21	30:4:11:LYS:H	1.51	0.59
17:Q:50:ARG:NH2	18:R:72:VAL:HG12	2.17	0.59
1:A:2346:A:H5''	1:A:2383:G:H1'	1.84	0.59
5:E:178:PRO:HB3	5:E:201:VAL:HG11	1.83	0.59
1:A:426:C:H2'	1:A:427:U:H6	1.68	0.59
1:A:814:C:C5	12:L:27:HIS:NE2	2.71	0.59
18:R:38:LEU:O	18:R:39:LEU:HD13	2.03	0.59
20:T:12:VAL:HG12	20:T:28:PHE:HA	1.85	0.59
21:U:13:VAL:HG11	21:U:72:VAL:HB	1.84	0.59
27:1:50:THR:HG22	27:1:51:TYR:N	2.15	0.59
12:L:57:THR:HG23	12:L:59:LEU:CB	2.33	0.59
1:A:1188:U:O2'	1:A:1189:A:H5'	2.03	0.59
8:H:113:ARG:HB2	8:H:130:TYR:CZ	2.38	0.59
17:Q:36:ARG:HG2	17:Q:40:PHE:CE1	2.38	0.59
1:A:2563:U:O2	1:A:2565:A:H8	1.85	0.59
24:X:58:ILE:HD11	24:X:91:LYS:HG2	1.84	0.59
16:P:132:LYS:O	16:P:136:GLN:HG3	2.03	0.59
5:E:192:LEU:HD21	5:E:194:MET:HE3	1.84	0.59
5:E:80:ALA:O	5:E:83:PHE:HB2	2.02	0.59
22:V:58:VAL:HA	22:V:67:LEU:O	2.01	0.59
3:C:95:LEU:HD12	3:C:95:LEU:O	2.03	0.59
29:3:11:LEU:HD13	29:3:12:GLU:N	2.18	0.58
4:D:33:VAL:HG12	4:D:89:ASP:O	2.03	0.58
5:E:150:GLY:HA2	5:E:172:TRP:CE3	2.38	0.58
18:R:28:GLU:HB2	18:R:31:ALA:HB2	1.85	0.58
15:O:52:SER:HB2	15:O:56:LEU:HB2	1.85	0.58
1:A:1331:A:O2'	1:A:1332:G:H8	1.86	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:V:14:LYS:HB2	22:V:17:ALA:HB3	1.85	0.58
1:A:71:A:C2	20:T:31:HIS:HE1	2.21	0.58
4:D:132:HIS:CG	4:D:135:HIS:NE2	2.72	0.58
1:A:603:A:H61	1:A:655:A:H1'	1.68	0.58
8:H:53:ALA:O	8:H:57:ARG:HB2	2.04	0.58
31:5:37:SER:OG	31:5:40:GLU:HG2	2.03	0.58
12:L:32:THR:OG1	12:L:36:LYS:HB3	2.04	0.58
13:M:141:GLN:HG2	22:V:72:ARG:HA	1.84	0.58
3:C:271:ILE:O	3:C:272:ALA:HB3	2.03	0.58
20:T:63:LYS:HZ1	20:T:72:LYS:HB3	1.67	0.58
3:C:30:GLU:CG	3:C:63:ARG:HH21	2.16	0.58
4:D:36:ARG:HH12	4:D:86:PRO:HD2	1.68	0.58
1:A:7:G:H2'	1:A:8:A:C8	2.37	0.58
16:P:20:PRO:HD2	16:P:86:ILE:HG23	1.85	0.58
1:A:784:A:C5	3:C:229:VAL:HG21	2.38	0.58
3:C:70:TRP:CZ2	3:C:150:LYS:HA	2.38	0.58
1:A:942:G:H5'	12:L:35:HIS:HB2	1.86	0.58
20:T:26:TYR:O	20:T:81:VAL:HG22	2.03	0.58
4:D:92:THR:O	4:D:95:ILE:HG13	2.03	0.58
1:A:1657:C:H2'	1:A:1658:C:C6	2.38	0.58
5:E:164:ARG:O	5:E:168:ARG:HB2	2.03	0.58
1:A:1966:A:H4'	1:A:1967:C:OP1	2.02	0.58
10:J:119:GLU:O	10:J:123:GLU:HG3	2.04	0.58
1:A:278:A:H4'	1:A:279:C:OP1	2.04	0.58
1:A:476:G:H4'	1:A:502:A:N1	2.19	0.58
17:Q:92:ARG:HG2	18:R:11:GLN:NE2	2.19	0.58
10:J:39:ILE:HG22	10:J:40:ASP:O	2.03	0.58
8:H:114:LEU:HD21	8:H:128:LEU:HD13	1.85	0.58
12:L:18:ARG:CZ	12:L:18:ARG:HB3	2.34	0.58
25:Y:24:LEU:HD22	25:Y:60:LEU:HD13	1.85	0.58
1:A:2393:A:H5''	12:L:62:LEU:HB3	1.85	0.58
21:U:45:VAL:HA	21:U:62:GLU:HA	1.86	0.58
24:X:27:GLU:HB3	24:X:33:LYS:HG3	1.85	0.58
2:B:11:C:H3'	2:B:12:C:C6	2.39	0.58
1:A:1603:A:C8	1:A:1603:A:H5'	2.39	0.58
11:K:47:ILE:HG13	11:K:48:PRO:HD2	1.85	0.58
1:A:656:G:H2'	1:A:657:U:O4'	2.02	0.58
1:A:955:C:OP1	13:M:85:LYS:HE2	2.04	0.58
25:Y:17:SER:HB3	25:Y:18:PRO:CD	2.30	0.58
1:A:1331:A:HO2'	1:A:1332:G:H8	1.52	0.58
7:G:13:LYS:HE2	7:G:14:GLY:H	1.67	0.58
25:Y:38:GLN:O	25:Y:41:ILE:HG12	2.03	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:Y:2:LYS:H	25:Y:2:LYS:HD2	1.68	0.58
1:A:1311:G:C8	1:A:1311:G:C5'	2.86	0.58
6:F:83:ARG:HG3	6:F:84:LYS:N	2.17	0.58
1:A:2294:C:H2'	1:A:2295:C:C6	2.38	0.58
1:A:2393:A:C5'	12:L:62:LEU:HD12	2.34	0.58
25:Y:2:LYS:N	25:Y:2:LYS:HD2	2.19	0.58
3:C:35:LYS:HE3	3:C:104:TYR:CD2	2.38	0.58
8:H:130:TYR:CD2	8:H:132:PRO:HG3	2.39	0.58
1:A:2468:G:H22	1:A:2481:G:H2'	1.68	0.57
15:O:26:LEU:O	15:O:88:ASP:HB3	2.04	0.57
1:A:1540:G:H2'	1:A:1541:U:O4'	2.03	0.57
3:C:11:PRO:C	3:C:13:ARG:H	2.07	0.57
1:A:83:G:N2	1:A:102:G:H2'	2.19	0.57
1:A:1980:G:H3'	1:A:1981:A:H5''	1.85	0.57
6:F:47:LYS:HG3	6:F:82:LEU:HD22	1.86	0.57
1:A:832:G:OP1	12:L:40:SER:HB3	2.03	0.57
1:A:114(B):A:H4'	10:J:48:ARG:HH22	1.69	0.57
1:A:1568:G:P	3:C:63:ARG:HH22	2.27	0.57
5:E:195:ASP:OD2	5:E:197:ASP:HB3	2.04	0.57
1:A:2647:U:H2'	1:A:2648:C:C6	2.39	0.57
1:A:1993:U:H4'	4:D:128:SER:HB3	1.84	0.57
1:A:1566:A:O2'	1:A:1567:A:H5'	2.04	0.57
1:A:2233:U:H2'	1:A:2234:G:C8	2.40	0.57
1:A:2056:G:N2	1:A:2057:A:H1'	2.20	0.57
1:A:795:C:H2'	1:A:796:C:C6	2.39	0.57
1:A:221:A:H4'	1:A:222:A:O5'	2.03	0.57
4:D:1:MET:HB3	4:D:83:ASP:O	2.03	0.57
8:H:90:GLY:O	8:H:91:SER:HB2	2.02	0.57
1:A:2104:G:H2'	1:A:2105:C:C6	2.40	0.57
1:A:1587:A:H2'	1:A:1588:C:C6	2.39	0.57
1:A:1241:A:N3	1:A:1241:A:H5'	2.19	0.57
4:D:5:LEU:HB2	4:D:51:PHE:CD2	2.39	0.57
1:A:2376:A:N6	15:O:89:ARG:HD2	2.20	0.57
20:T:57:LEU:HD12	20:T:57:LEU:N	2.18	0.57
1:A:46:C:OP2	1:A:215:G:H2'	2.04	0.57
18:R:81:TYR:C	18:R:82:ARG:HG3	2.24	0.57
11:K:86:ILE:H	11:K:86:ILE:HD12	1.68	0.57
12:L:57:THR:HG23	12:L:59:LEU:HB2	1.87	0.57
28:2:33:CYS:SG	28:2:40:LYS:HE3	2.45	0.57
13:M:40:ALA:HB3	13:M:127:ILE:HD11	1.87	0.57
14:N:13:HIS:CE1	14:N:16:HIS:HB2	2.39	0.57
1:A:2607:G:H2'	1:A:2608:G:O4'	2.05	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:121:ILE:HD11	7:G:140:LYS:HD3	1.87	0.57
1:A:534:U:O2'	17:Q:49:HIS:HD2	1.87	0.57
11:K:122:LEU:HD13	16:P:72:VAL:HG11	1.86	0.57
10:J:148:GLY:HA3	10:J:149:PRO:O	2.05	0.57
2:B:30:C:OP2	15:O:32:LEU:HD11	2.03	0.57
8:H:142:VAL:HG12	8:H:143:SER:H	1.69	0.57
5:E:29:ASN:N	5:E:112:MET:HE1	2.19	0.57
2:B:111:U:H2'	2:B:112:G:H8	1.70	0.57
16:P:117:ASP:O	16:P:121:ILE:HG13	2.05	0.57
12:L:135:LEU:O	12:L:139:LYS:HB2	2.04	0.57
12:L:114:ILE:O	12:L:114:ILE:HD12	2.05	0.57
1:A:966:G:H2'	1:A:967:C:H6	1.69	0.57
27:1:48:ILE:H	27:1:48:ILE:HD12	1.70	0.57
1:A:1544:C:H3'	1:A:1545:A:C5'	2.33	0.57
3:C:217:ARG:HG2	3:C:217:ARG:NH1	2.19	0.57
3:C:130:ALA:HB2	3:C:192:THR:HB	1.86	0.57
1:A:1434:A:H2'	1:A:1435:G:H8	1.67	0.57
25:Y:38:GLN:HB3	25:Y:44:LEU:HB3	1.84	0.57
25:Y:23:LYS:O	25:Y:27:GLU:HG3	2.04	0.57
7:G:20:ALA:HB1	7:G:21:PRO:HD2	1.87	0.57
3:C:231:HIS:CG	3:C:232:PRO:HD2	2.40	0.57
1:A:1819:A:H4'	1:A:1820:U:H5''	1.86	0.57
18:R:64:HIS:CD2	18:R:92:THR:HG22	2.40	0.57
1:A:1046:A:C3'	1:A:1047:G:H5''	2.35	0.57
2:B:43:C:H2'	2:B:44:G:H5''	1.87	0.57
8:H:6:LEU:HA	8:H:15:VAL:HG13	1.87	0.57
7:G:55:PRO:HG2	7:G:61:HIS:CD2	2.40	0.57
3:C:8:PRO:HB3	3:C:14:ARG:CB	2.34	0.57
1:A:529:A:H62	1:A:2041:U:H3	1.53	0.57
1:A:2746:U:H2'	1:A:2747:G:H5'	1.87	0.57
26:Z:8:LEU:HB2	26:Z:28:LEU:HD23	1.86	0.57
5:E:52:LYS:HB3	5:E:56:GLU:O	2.05	0.57
1:A:528:A:C8	1:A:528:A:C3'	2.88	0.57
4:D:67:PHE:CE2	4:D:75:VAL:HG22	2.40	0.57
4:D:67:PHE:HE2	4:D:75:VAL:HG22	1.70	0.57
1:A:2633:G:O2'	4:D:61:ARG:HD3	2.05	0.57
24:X:37:ILE:CG2	24:X:38:SER:N	2.68	0.57
22:V:95:PRO:HB2	22:V:127:LYS:HE3	1.87	0.57
6:F:136:ARG:O	6:F:154:GLY:HA2	2.04	0.57
1:A:761:A:O5'	1:A:761:A:C8	2.45	0.56
1:A:556:G:H2'	1:A:557:U:H6	1.67	0.56
1:A:1275:A:C8	14:N:16:HIS:CD2	2.93	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:192:LEU:HD21	5:E:194:MET:CE	2.35	0.56
1:A:1360:A:H5'	1:A:1361:G:OP2	2.05	0.56
1:A:2790:A:H2'	1:A:2791:C:H5''	1.87	0.56
6:F:5:LEU:HD21	27:1:50:THR:HG23	1.87	0.56
1:A:2892:A:H2'	1:A:2893:G:H5'	1.87	0.56
16:P:19:LEU:HD13	16:P:78:LEU:HD22	1.87	0.56
6:F:81:LYS:O	6:F:82:LEU:HD23	2.04	0.56
2:B:87:G:H21	2:B:89(B):A:H62	1.52	0.56
1:A:301:G:C4	1:A:302:C:C5	2.93	0.56
5:E:32:LEU:C	5:E:32:LEU:HD23	2.26	0.56
3:C:125:ILE:HD12	3:C:125:ILE:H	1.70	0.56
1:A:195:A:OP1	12:L:46:LYS:HE2	2.06	0.56
12:L:115:LEU:HA	12:L:134:ALA:CB	2.35	0.56
15:O:49:VAL:HG13	15:O:76:LYS:HD2	1.87	0.56
1:A:2439:A:H8	1:A:2439:A:H5'	1.68	0.56
1:A:568:U:O4	18:R:78:LYS:NZ	2.37	0.56
10:J:62:ARG:HH21	10:J:64:ASP:HB2	1.69	0.56
1:A:278:A:H2'	1:A:279:C:O4'	2.06	0.56
1:A:626:U:O2	12:L:105:LEU:HB3	2.05	0.56
21:U:76:CYS:SG	21:U:77:PRO:HD2	2.46	0.56
29:3:11:LEU:HD11	29:3:51:GLU:HG3	1.86	0.56
1:A:779:U:OP1	3:C:49:ILE:HG13	2.04	0.56
1:A:1952:A:C5	11:K:22:ILE:HD12	2.41	0.56
1:A:1378:A:O2'	1:A:1379:A:H3'	2.06	0.56
26:Z:17:LYS:HD3	26:Z:17:LYS:C	2.26	0.56
1:A:828:U:H4'	1:A:831:G:N1	2.20	0.56
12:L:64:LYS:HD2	31:5:25:MET:SD	2.46	0.56
16:P:28:VAL:HA	16:P:89:VAL:HG12	1.86	0.56
4:D:84:PHE:CZ	4:D:86:PRO:HG3	2.41	0.56
1:A:1588:C:H2'	1:A:1589:C:H6	1.70	0.56
1:A:706:A:H2'	1:A:707:G:O4'	2.06	0.56
13:M:66:ILE:HG22	13:M:104:PHE:CD2	2.40	0.56
12:L:128:HIS:HA	12:L:147:LEU:CB	2.20	0.56
1:A:886:C:C2'	1:A:887:A:H4'	2.31	0.56
14:N:51:LEU:HD22	14:N:66:VAL:HG13	1.87	0.56
14:N:9:LYS:C	14:N:10:LEU:HG	2.26	0.56
3:C:126:GLN:O	3:C:193:VAL:HG11	2.05	0.56
16:P:80:SER:HB3	16:P:83:ILE:HG13	1.86	0.56
1:A:1826:G:H4'	3:C:242:ARG:NE	2.21	0.56
1:A:2744:G:N2	7:G:143:GLN:HE22	2.01	0.56
5:E:181:LEU:HD22	5:E:186:ILE:HD11	1.88	0.56
10:J:90:LEU:O	10:J:111:GLU:HG3	2.06	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:58:ARG:O	17:Q:62:ILE:HG12	2.05	0.56
1:A:966:G:H2'	1:A:967:C:C6	2.41	0.56
12:L:33:ARG:O	12:L:34:GLY:C	2.44	0.56
30:4:37:LYS:HD3	30:4:39:ARG:HE	1.70	0.56
1:A:581:C:H2'	1:A:582:G:H8	1.69	0.56
1:A:1373:A:H2'	1:A:1374:G:O4'	2.05	0.56
3:C:233:HIS:CE1	3:C:247:ALA:H	2.23	0.56
1:A:572:A:C2	1:A:2033:A:C2	2.93	0.56
1:A:343:C:C5'	1:A:343:C:H6	2.18	0.56
8:H:12:LEU:H	8:H:12:LEU:HD22	1.71	0.56
1:A:1156:A:H4'	1:A:1157:G:OP2	2.05	0.56
1:A:1655:A:H1'	4:D:113:PHE:CD2	2.41	0.56
1:A:276:A:H3'	1:A:277:C:H5''	1.88	0.56
2:B:8:U:H5''	15:O:15:ARG:HH22	1.71	0.56
1:A:1813:G:H1'	3:C:50:THR:CG2	2.35	0.56
6:F:110:ALA:O	6:F:114:ILE:HG13	2.06	0.56
29:3:13:CYS:SG	29:3:24:GLU:HG3	2.45	0.56
17:Q:95:LEU:O	17:Q:98:LEU:HG	2.05	0.55
20:T:30:VAL:HG12	20:T:31:HIS:N	2.21	0.55
3:C:44:ASN:HB3	3:C:50:THR:CG2	2.36	0.55
1:A:2517:C:C6	1:A:2542:A:C2	2.94	0.55
17:Q:68:ALA:O	17:Q:71:GLN:HB3	2.05	0.55
13:M:58:PHE:O	13:M:58:PHE:CD1	2.59	0.55
8:H:92:VAL:HG21	8:H:97:ILE:HD11	1.86	0.55
1:A:1173:G:H1'	1:A:1177:A:H61	1.71	0.55
16:P:59:THR:O	16:P:78:LEU:HB2	2.06	0.55
3:C:8:PRO:HB3	3:C:14:ARG:HB3	1.88	0.55
8:H:92:VAL:HG23	8:H:96:ASP:HB2	1.88	0.55
11:K:103:ALA:O	11:K:106:LEU:HD13	2.06	0.55
1:A:1430:C:H2'	1:A:1431:U:C6	2.41	0.55
14:N:101:ALA:HB2	28:2:44:THR:HG21	1.88	0.55
1:A:1187:G:H5''	18:R:81:TYR:CE2	2.41	0.55
17:Q:92:ARG:HD2	17:Q:95:LEU:CG	2.37	0.55
21:U:71:LYS:HB2	21:U:71:LYS:HZ2	1.70	0.55
18:R:77:ALA:O	18:R:79:VAL:N	2.39	0.55
1:A:1541:U:H3'	1:A:1542:G:C3'	2.37	0.55
29:3:11:LEU:HB2	29:3:26:ASN:H	1.70	0.55
5:E:203:GLN:HA	5:E:206:ILE:O	2.06	0.55
11:K:73:ASP:OD1	11:K:75:SER:HB3	2.07	0.55
1:A:2058:A:N6	1:A:2059:A:N6	2.54	0.55
1:A:747:U:C4	28:2:2:ALA:N	2.74	0.55
22:V:76:LEU:N	22:V:76:LEU:HD12	2.21	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1579:A:H5'	1:A:1579:A:C8	2.33	0.55
8:H:77:LEU:HD11	8:H:101:LEU:HB2	1.88	0.55
24:X:27:GLU:CD	24:X:33:LYS:HE3	2.27	0.55
22:V:8:TYR:HB2	22:V:38:TYR:CZ	2.41	0.55
25:Y:21:LEU:HD23	25:Y:22:GLU:N	2.22	0.55
1:A:2749:A:H4'	7:G:62:LYS:HB3	1.89	0.55
1:A:195:A:H61	1:A:198:C:H3'	1.72	0.55
1:A:2393:A:H5'	12:L:62:LEU:HD12	1.88	0.55
1:A:2439:A:H8	1:A:2439:A:C5'	2.20	0.55
1:A:2210:G:N2	1:A:2211:G:H5'	2.21	0.55
5:E:192:LEU:HD23	5:E:193:VAL:N	2.22	0.55
1:A:2305:A:H5''	6:F:134:GLY:HA3	1.88	0.55
1:A:1996:C:OP1	11:K:31:LYS:HE3	2.06	0.55
12:L:112:LEU:HD23	12:L:113:LYS:N	2.22	0.55
12:L:111:ARG:HG3	12:L:128:HIS:CB	2.36	0.55
30:4:34:ARG:HD2	30:4:39:ARG:HG3	1.87	0.55
1:A:1292:U:H2'	1:A:1293:C:C6	2.42	0.55
1:A:2815:C:O2'	28:2:43:HIS:HD2	1.88	0.55
7:G:44:VAL:O	7:G:50:VAL:HG13	2.07	0.55
1:A:1971:A:C4	3:C:241:PRO:HG3	2.41	0.55
20:T:12:VAL:HG12	20:T:27:THR:O	2.07	0.55
1:A:2036:C:C6	1:A:2036:C:H5'	2.39	0.55
1:A:775:G:C4	1:A:794:G:C8	2.94	0.55
1:A:2648:C:H2'	1:A:2649:U:C6	2.42	0.55
24:X:23:LYS:HB3	24:X:37:ILE:HG12	1.89	0.55
21:U:59:GLY:C	21:U:61:ILE:H	2.10	0.55
1:A:483:A:H4'	21:U:49:VAL:HG23	1.89	0.55
1:A:2014:A:H2'	1:A:2015:A:C8	2.42	0.55
31:5:14:VAL:HG13	31:5:22:VAL:HG13	1.89	0.55
3:C:182:LEU:O	3:C:271:ILE:HD12	2.06	0.55
26:Z:1:MET:HA	26:Z:39:ASP:HB3	1.88	0.55
1:A:323:G:H5'	5:E:169:ASN:HD21	1.71	0.55
11:K:24:VAL:HG23	11:K:33:ALA:HB2	1.89	0.55
4:D:111:ARG:HD2	4:D:160:TYR:CE1	2.42	0.55
31:5:52:LYS:N	31:5:53:PRO:HD2	2.22	0.55
1:A:2543:G:C8	1:A:2543:G:H5'	2.40	0.55
8:H:116:LEU:HD22	8:H:128:LEU:HD21	1.89	0.55
19:S:4:LYS:HG2	19:S:106:ILE:HG22	1.88	0.55
19:S:103:ILE:H	19:S:103:ILE:HD12	1.73	0.54
1:A:380:U:O2'	24:X:20:ARG:HB3	2.08	0.54
12:L:84:ASN:HB3	12:L:86:LYS:HG2	1.90	0.54
27:1:46:ASN:HB2	27:1:64:LYS:HB2	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:Z:26:LEU:HB2	26:Z:28:LEU:HD13	1.89	0.54
1:A:1005:C:O2'	10:J:51:THR:HG21	2.06	0.54
1:A:1510:A:H2'	1:A:1511:A:H8	1.72	0.54
15:O:34:HIS:ND1	15:O:54:LEU:HB2	2.22	0.54
1:A:270(Q):C:HO2'	1:A:270(R):C:H6	1.50	0.54
1:A:1932:A:H3'	1:A:1933:G:H8	1.72	0.54
1:A:1266:G:H5''	28:2:23:HIS:NE2	2.21	0.54
1:A:806:C:O2'	1:A:2445:G:H4'	2.07	0.54
13:M:81:VAL:CG1	13:M:82:ARG:HG2	2.37	0.54
6:F:173:LEU:HD23	6:F:176:LEU:HD12	1.89	0.54
1:A:2036:C:H6	1:A:2036:C:C5'	2.20	0.54
1:A:1448:G:H2'	1:A:149(B):A:C8	2.42	0.54
1:A:999:U:H5''	1:A:1154:G:O6	2.06	0.54
13:M:26:TYR:HA	22:V:81:ARG:HH21	1.72	0.54
1:A:1647:G:OP2	1:A:1647:G:H3'	2.08	0.54
1:A:1046:A:H1'	9:I:4:LYS:HD2	1.89	0.54
13:M:8:LYS:O	13:M:9:TYR:HB3	2.08	0.54
4:D:101:ARG:HD3	4:D:169:ASN:ND2	2.22	0.54
1:A:1434:A:H61	1:A:1558:A:N6	2.05	0.54
12:L:143:GLY:O	12:L:145:PRO:HD3	2.08	0.54
1:A:137(B):G:H2'	1:A:139:G:N7	2.23	0.54
1:A:1639:U:H2'	1:A:1640:C:H5''	1.88	0.54
1:A:270(J):G:O2'	1:A:270(K):G:H8	1.87	0.54
1:A:910:A:C4	13:M:13:GLN:NE2	2.76	0.54
23:W:35:ASN:N	23:W:35:ASN:ND2	2.55	0.54
30:4:34:ARG:HB3	30:4:42:LEU:HD22	1.88	0.54
1:A:1614:A:H61	19:S:88:ARG:H	1.56	0.54
12:L:125:VAL:O	12:L:145:PRO:HD2	2.07	0.54
1:A:1495:A:H2'	1:A:1496:A:N3	2.22	0.54
1:A:948:G:H8	1:A:948:G:C5'	2.20	0.54
1:A:64:A:O2'	20:T:71:GLY:HA3	2.07	0.54
1:A:319:C:H2'	1:A:320:A:C8	2.42	0.54
14:N:88:ARG:HG3	14:N:89:ASP:OD1	2.06	0.54
1:A:1833:U:H2'	1:A:1834:U:H6	1.72	0.54
1:A:576:U:H2'	1:A:577:G:C8	2.43	0.54
1:A:1161:C:O2'	18:R:23:GLU:HG2	2.08	0.54
18:R:38:LEU:HD22	18:R:52:VAL:HG11	1.90	0.54
20:T:23:GLU:HG3	20:T:24:GLY:H	1.72	0.54
3:C:25:THR:HG21	3:C:81:ALA:HB1	1.90	0.54
31:5:54:GLU:HA	31:5:57:ARG:NH1	2.20	0.54
1:A:2186:G:H2'	1:A:2187:G:C8	2.42	0.54
1:A:2305:A:C2	6:F:154:GLY:HA3	2.43	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2102:U:H2'	1:A:2103:C:C6	2.42	0.54
1:A:919:G:H5'	2:B:81:G:H1'	1.90	0.54
10:J:151:HIS:HD2	10:J:152:PRO:O	1.90	0.54
1:A:1161:C:O2'	18:R:8:GLY:HA2	2.08	0.54
20:T:28:PHE:HE2	20:T:92:LEU:HD11	1.71	0.54
12:L:62:LEU:H	12:L:62:LEU:HD22	1.73	0.54
25:Y:2:LYS:N	25:Y:2:LYS:CD	2.69	0.54
3:C:123:ALA:HB3	3:C:131:LEU:HD23	1.89	0.54
3:C:25:THR:HG21	3:C:81:ALA:CB	2.38	0.54
1:A:319:C:H2'	1:A:320:A:H8	1.73	0.54
3:C:246:PRO:HD2	3:C:255:LYS:HD3	1.89	0.54
23:W:51:VAL:N	23:W:62:LEU:HD12	2.22	0.54
13:M:54:MET:HG2	13:M:64:ILE:HD13	1.90	0.54
1:A:2729:G:H2'	1:A:2730:C:C6	2.43	0.54
1:A:2726:U:H5'	1:A:2726:U:O2	2.08	0.54
1:A:929:G:H8	1:A:929:G:O5'	1.90	0.54
6:F:60:LEU:HD11	6:F:92:VAL:CG1	2.30	0.54
15:O:35:ILE:CG1	15:O:101:LEU:HD21	2.34	0.54
8:H:101:LEU:HG	8:H:107:ILE:HG23	1.90	0.54
19:S:73:ALA:O	19:S:106:ILE:HG12	2.07	0.54
1:A:2731:G:C6	1:A:2732:G:O6	2.61	0.54
2:B:49:C:OP1	15:O:97:ARG:HG3	2.08	0.54
20:T:39:ILE:O	20:T:43:VAL:HG12	2.08	0.54
3:C:131:LEU:HA	3:C:190:TYR:CE2	2.43	0.54
5:E:53:THR:HG23	5:E:55:GLY:N	2.18	0.54
4:D:25:VAL:HG12	4:D:181:LEU:HD12	1.90	0.54
14:N:96:ARG:HH22	14:N:117:VAL:HG23	1.73	0.54
2:B:40:U:H6	2:B:40:U:O5'	1.91	0.54
17:Q:92:ARG:CD	17:Q:94:ASN:HB3	2.38	0.53
1:A:955:C:OP2	13:M:14:ARG:HD2	2.08	0.53
3:C:132:PRO:HD3	3:C:190:TYR:CZ	2.44	0.53
12:L:18:ARG:NH1	12:L:18:ARG:HB3	2.22	0.53
13:M:45:GLN:H	13:M:45:GLN:CD	2.10	0.53
13:M:112:GLU:H	13:M:112:GLU:CD	2.11	0.53
6:F:47:LYS:HG3	6:F:82:LEU:CD2	2.39	0.53
6:F:134:GLY:C	6:F:135:LEU:HD12	2.29	0.53
5:E:183:VAL:O	5:E:187:VAL:HG23	2.08	0.53
22:V:110:GLY:HA3	22:V:174:VAL:HG11	1.90	0.53
12:L:132:LYS:N	12:L:132:LYS:HD2	2.22	0.53
11:K:96:THR:O	11:K:97:ARG:C	2.47	0.53
7:G:27:LYS:HG2	7:G:32:GLU:HB2	1.90	0.53
1:A:911:A:C6	13:M:9:TYR:HE1	2.25	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:674:G:C1'	5:E:74:ARG:HD3	2.37	0.53
11:K:24:VAL:CG2	11:K:33:ALA:HB2	2.38	0.53
1:A:1154:G:H8	1:A:1154:G:O5'	1.90	0.53
1:A:320:A:H2'	5:E:136:THR:HG21	1.91	0.53
2:B:37:C:H2'	15:O:95:HIS:HE1	1.71	0.53
1:A:2032:G:O2'	4:D:145:LYS:HE2	2.09	0.53
18:R:22:VAL:HG12	18:R:23:GLU:H	1.73	0.53
12:L:88:LEU:HD22	12:L:114:ILE:HG21	1.90	0.53
1:A:2293:C:H4'	15:O:93:LYS:NZ	2.23	0.53
1:A:2050:C:H1'	4:D:156:MET:HE1	1.90	0.53
20:T:31:HIS:ND1	20:T:32:PRO:HD2	2.22	0.53
21:U:11:ASP:O	21:U:26:LYS:HA	2.09	0.53
1:A:2543:G:H2'	1:A:2544:G:C8	2.44	0.53
8:H:142:VAL:HG12	8:H:143:SER:N	2.23	0.53
1:A:1614:A:H62	19:S:93:ALA:HB2	1.73	0.53
1:A:1692:U:O2'	1:A:1693:U:H2'	2.08	0.53
1:A:2814:C:O2'	28:2:29:ILE:HG13	2.08	0.53
1:A:17:G:H4'	17:Q:25:TRP:CH2	2.43	0.53
1:A:1809:A:H2'	1:A:1810:A:C8	2.43	0.53
13:M:78:PRO:O	13:M:79:LEU:HB2	2.09	0.53
12:L:62:LEU:CD2	31:5:25:MET:HB2	2.38	0.53
10:J:42:GLU:HA	10:J:82:LYS:CB	2.32	0.53
6:F:41:GLN:HG2	6:F:155:MET:CB	2.37	0.53
31:5:50:LEU:HB2	31:5:54:GLU:HG3	1.91	0.53
25:Y:16:LEU:HB2	25:Y:20:GLU:CG	2.35	0.53
3:C:244:ARG:HG3	3:C:245:PRO:N	2.24	0.53
15:O:87:PHE:CE2	15:O:89:ARG:HA	2.43	0.53
16:P:57:PHE:O	16:P:59:THR:N	2.41	0.53
1:A:176:G:O2'	1:A:177:G:H5'	2.09	0.53
17:Q:92:ARG:NH2	18:R:11:GLN:H	2.06	0.53
16:P:26:ASP:HB2	16:P:90:GLN:O	2.09	0.53
1:A:1309:G:H3'	30:4:9:ARG:NH1	2.23	0.53
1:A:605:C:H1'	1:A:657:U:O2'	2.09	0.53
12:L:52:GLU:OE1	12:L:52:GLU:HA	2.08	0.53
3:C:242:ARG:CD	3:C:242:ARG:H	2.07	0.53
6:F:107:LEU:HA	6:F:111:LEU:HD12	1.91	0.53
11:K:68:GLU:HB3	11:K:78:ARG:HB2	1.89	0.53
4:D:9:VAL:HG13	4:D:25:VAL:O	2.09	0.53
22:V:108:PRO:HA	22:V:142:SER:O	2.08	0.53
7:G:109:PHE:CE1	7:G:152:ARG:HD3	2.44	0.53
2:B:30:C:H2'	2:B:31:C:H5'	1.90	0.53
10:J:49:LEU:O	10:J:53:ILE:HG13	2.09	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:P:1:MET:O	16:P:3:ARG:N	2.41	0.53
19:S:80:PRO:O	19:S:100:THR:HG22	2.09	0.53
13:M:48:GLU:O	13:M:52:VAL:HG12	2.08	0.53
1:A:637:A:OP1	12:L:133:SER:HB3	2.09	0.53
31:5:53:PRO:HB2	31:5:57:ARG:HH21	1.72	0.53
4:D:47:VAL:HG21	4:D:86:PRO:HD3	1.90	0.53
1:A:1257:C:H4'	5:E:83:PHE:CE2	2.44	0.53
17:Q:8:VAL:HG11	17:Q:12:ARG:CZ	2.39	0.53
1:A:1862:G:H2'	1:A:1863:G:H8	1.74	0.53
1:A:2056:G:N2	1:A:2057:A:C1'	2.72	0.53
1:A:1971:A:C5	3:C:241:PRO:HG3	2.44	0.53
31:5:34:TRP:CG	31:5:35:GLN:N	2.76	0.53
13:M:141:GLN:HA	22:V:71:VAL:O	2.08	0.53
13:M:140:ALA:HB3	22:V:53:ILE:HD13	1.90	0.53
24:X:27:GLU:CB	24:X:33:LYS:HG3	2.39	0.53
2:B:104:A:O4'	22:V:29:TYR:HE1	1.92	0.53
1:A:2401:U:C2'	1:A:2402:C:H5''	2.38	0.53
12:L:75:ILE:HD13	12:L:77:ARG:NE	2.24	0.53
13:M:68:ILE:HG23	13:M:103:MET:HA	1.91	0.53
1:A:1028:A:N6	1:A:1125:G:H2'	2.24	0.53
1:A:2422:A:N7	31:5:31:HIS:CE1	2.77	0.53
27:1:42:CYS:SG	27:1:46:ASN:HB3	2.48	0.53
1:A:2481:G:O2'	1:A:2482:G:P	2.67	0.53
14:N:12:ARG:HD3	14:N:16:HIS:ND1	2.24	0.53
1:A:1386:C:H2'	1:A:1387:C:H6	1.74	0.53
1:A:55:G:H2'	1:A:56:A:H8	1.73	0.53
5:E:18:ARG:O	5:E:18:ARG:HG3	2.08	0.53
18:R:6:LYS:O	18:R:37:VAL:HG21	2.10	0.52
5:E:63:LYS:HE3	5:E:75:HIS:O	2.09	0.52
1:A:270(L):C:H2'	1:A:270(M):U:H5''	1.91	0.52
21:U:95:LYS:HG2	21:U:100:ALA:HA	1.91	0.52
15:O:35:ILE:O	15:O:53:SER:HB2	2.09	0.52
12:L:143:GLY:C	12:L:145:PRO:HD3	2.30	0.52
15:O:41:ASP:OD2	15:O:44:LYS:HD3	2.09	0.52
1:A:676:A:H2	1:A:802:A:H61	1.57	0.52
1:A:2210:G:H21	1:A:2211:G:C5'	2.23	0.52
11:K:2:ILE:HG12	11:K:8:LEU:HD11	1.91	0.52
23:W:48:GLY:HA3	23:W:80:HIS:ND1	2.24	0.52
1:A:263:C:H2'	1:A:264:C:O4'	2.09	0.52
1:A:498:G:N3	21:U:47:LYS:HE3	2.24	0.52
25:Y:2:LYS:HA	25:Y:5:GLU:OE2	2.08	0.52
3:C:71:ASP:HB3	3:C:103:ARG:NH2	2.20	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:10:LEU:HD22	14:N:17:ARG:CD	2.40	0.52
14:N:21:TYR:HE2	14:N:43:GLU:HB3	1.73	0.52
8:H:76:THR:HA	8:H:141:LYS:HB2	1.90	0.52
13:M:60:ARG:H	22:V:179:ASP:CB	2.22	0.52
1:A:2358:G:C6	1:A:2359:C:C4	2.97	0.52
1:A:1276:A:O2'	14:N:16:HIS:HE1	1.92	0.52
8:H:66:GLU:HB3	8:H:67:ARG:NH1	2.24	0.52
18:R:15:GLU:HB3	18:R:16:PRO:HD2	1.92	0.52
1:A:1790:C:O2'	3:C:209:ALA:HB2	2.09	0.52
16:P:6:LEU:O	16:P:10:VAL:HG23	2.09	0.52
19:S:110:LYS:HG3	19:S:111:HIS:ND1	2.25	0.52
1:A:118:A:N3	1:A:178:G:H1'	2.25	0.52
16:P:48:ILE:H	16:P:48:ILE:HD12	1.73	0.52
31:5:50:LEU:HD13	31:5:57:ARG:CZ	2.40	0.52
8:H:72:LEU:HD12	8:H:140:LEU:HD13	1.91	0.52
1:A:1173:G:H3'	1:A:1174:A:C5'	2.40	0.52
4:D:33:VAL:HG23	4:D:47:VAL:HG13	1.90	0.52
1:A:1567:A:H2'	3:C:84:TYR:HE2	1.75	0.52
6:F:96:ARG:O	6:F:99:MET:HB3	2.09	0.52
1:A:1817:G:OP1	3:C:88:ARG:NH2	2.42	0.52
1:A:2774:C:H2'	1:A:2775:A:O4'	2.09	0.52
1:A:1164:G:H8	1:A:1164:G:C5'	2.22	0.52
25:Y:12:GLU:C	25:Y:14:ARG:H	2.13	0.52
12:L:58:THR:C	12:L:60:MET:H	2.12	0.52
5:E:29:ASN:H	5:E:112:MET:CE	2.22	0.52
1:A:1386:C:H2'	1:A:1387:C:C6	2.44	0.52
1:A:127:A:H5''	1:A:128:C:O4'	2.09	0.52
5:E:179:GLU:CD	5:E:179:GLU:H	2.12	0.52
3:C:242:ARG:CD	3:C:242:ARG:N	2.70	0.52
7:G:149:ARG:HA	7:G:162:ILE:HG12	1.91	0.52
1:A:2712:U:H1'	1:A:712(B):A:H8	1.66	0.52
4:D:201:THR:CG2	4:D:202:LYS:N	2.73	0.52
1:A:1027:A:C2	1:A:2488:A:H5'	2.45	0.52
3:C:233:HIS:HE1	3:C:247:ALA:H	1.58	0.52
3:C:31:LYS:HE3	3:C:33:LEU:HD21	1.92	0.52
25:Y:39:ALA:HA	25:Y:45:SER:CB	2.39	0.52
6:F:85:GLY:C	6:F:86:MET:HG3	2.30	0.52
1:A:819:A:C4	1:A:1189:A:C2	2.97	0.52
1:A:1953:A:C2	1:A:2549:G:N3	2.78	0.52
1:A:814:C:O2'	1:A:815:C:H5'	2.09	0.52
7:G:121:ILE:HD11	7:G:140:LYS:HB3	1.90	0.52
1:A:49:A:H5''	1:A:51:G:O4'	2.10	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:135:LEU:HD23	10:J:136:GLY:H	1.75	0.52
21:U:96:ILE:HG23	21:U:101:LYS:O	2.09	0.52
1:A:2822:G:O6	14:N:4:LEU:HD23	2.10	0.52
2:B:71:C:C2	2:B:72:G:C8	2.97	0.52
12:L:27:HIS:HE1	18:R:83:ARG:HH12	1.56	0.52
17:Q:8:VAL:HG11	17:Q:12:ARG:NE	2.24	0.52
1:A:298:G:P	21:U:85:VAL:HG22	2.49	0.52
1:A:871:U:H4'	13:M:69:PHE:CE2	2.45	0.52
1:A:1022:G:O2'	1:A:1023:U:OP2	2.25	0.52
13:M:58:PHE:HD1	13:M:58:PHE:O	1.91	0.52
5:E:36:VAL:O	5:E:40:GLN:HG3	2.08	0.52
17:Q:79:PHE:HE1	17:Q:83:LEU:HD21	1.75	0.52
21:U:81:LYS:CD	21:U:97:ARG:HB3	2.39	0.52
1:A:959:A:O2'	1:A:960:A:H5'	2.09	0.52
30:4:8:ASN:ND2	30:4:11:LYS:N	2.53	0.52
31:5:52:LYS:H	31:5:53:PRO:HD2	1.75	0.52
3:C:204:ILE:HD12	3:C:204:ILE:O	2.10	0.52
1:A:917:A:H2'	1:A:918:A:O4'	2.09	0.52
14:N:81:ASP:O	14:N:85:PRO:HG2	2.10	0.52
3:C:72:LYS:HE3	3:C:101:GLU:HG2	1.92	0.52
1:A:614:U:H4'	1:A:615:G:H5''	1.92	0.52
1:A:2094:G:N2	1:A:2196:C:H1'	2.24	0.52
1:A:2371:G:O2'	29:3:45:LYS:HB3	2.09	0.52
1:A:1206:G:C6	1:A:1207:C:C4	2.98	0.52
17:Q:88:ILE:HG13	17:Q:88:ILE:O	2.10	0.51
12:L:58:THR:C	12:L:61:ARG:HE	2.13	0.51
5:E:182:ASN:O	5:E:186:ILE:HG12	2.10	0.51
1:A:518:G:H4'	19:S:18:ARG:NH1	2.24	0.51
21:U:90:LEU:HG	21:U:91:GLU:HG2	1.92	0.51
18:R:28:GLU:HB2	18:R:31:ALA:CB	2.40	0.51
1:A:2747:G:O6	1:A:2755:C:H5''	2.10	0.51
1:A:380:U:O2	24:X:20:ARG:NH2	2.43	0.51
1:A:2188:C:H2'	1:A:2189:U:O4'	2.10	0.51
1:A:2090:G:H21	24:X:45:ASN:ND2	2.08	0.51
1:A:1537:C:H2'	1:A:1538:G:O4'	2.10	0.51
1:A:486:C:H4'	19:S:60:ASN:HD22	1.74	0.51
6:F:139:LEU:HA	6:F:144:ILE:HG21	1.91	0.51
20:T:11:PRO:HG3	25:Y:37:PHE:CE2	2.46	0.51
10:J:157:ARG:N	10:J:158:PRO:CD	2.65	0.51
13:M:75:THR:HA	13:M:88:GLY:HA3	1.89	0.51
6:F:74:LYS:HA	6:F:74:LYS:HE3	1.93	0.51
11:K:68:GLU:H	11:K:68:GLU:CD	2.13	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:107:ILE:HG13	8:H:109:ILE:HG23	1.92	0.51
1:A:2688:U:O2	1:A:2688:U:H3'	2.10	0.51
16:P:57:PHE:HE2	16:P:79:HIS:HB2	1.76	0.51
1:A:2094:G:P	8:H:22:LYS:HD2	2.50	0.51
22:V:94:GLU:H	22:V:94:GLU:CD	2.14	0.51
3:C:166:GLN:HE21	3:C:166:GLN:CA	2.22	0.51
1:A:566:U:H2'	1:A:567:A:O4'	2.10	0.51
1:A:2758:A:C4	7:G:67:LEU:HD21	2.45	0.51
1:A:830:G:H4'	1:A:831:G:OP2	2.11	0.51
1:A:780:G:N2	1:A:783:A:H62	1.95	0.51
21:U:37:VAL:HG21	21:U:72:VAL:HG21	1.93	0.51
1:A:848:G:C4	1:A:933:A:C8	2.95	0.51
1:A:2744:G:H21	7:G:143:GLN:NE2	2.02	0.51
7:G:92:ILE:CD1	7:G:92:ILE:H	2.22	0.51
5:E:155:LEU:CD2	5:E:186:ILE:HD13	2.39	0.51
15:O:26:LEU:HD13	15:O:87:PHE:HD1	1.76	0.51
1:A:389:G:C6	12:L:71:VAL:HG23	2.45	0.51
25:Y:46:GLN:OE1	25:Y:46:GLN:HA	2.09	0.51
1:A:588:U:H1'	5:E:90:PHE:CD1	2.45	0.51
1:A:943:U:OP2	12:L:38:GLN:CD	2.48	0.51
1:A:588:U:C2	5:E:90:PHE:CE1	2.99	0.51
20:T:30:VAL:HG11	20:T:39:ILE:CD1	2.38	0.51
1:A:661:C:H2'	1:A:662:G:C8	2.46	0.51
5:E:34:TRP:HB2	12:L:10:PRO:O	2.10	0.51
1:A:2105:C:H2'	1:A:2106:G:C8	2.45	0.51
15:O:15:ARG:O	15:O:19:LYS:HG3	2.10	0.51
19:S:19:LEU:HB3	28:2:25:LEU:CD1	2.40	0.51
1:A:144:C:H2'	1:A:145:G:C8	2.45	0.51
1:A:1444:G:H2'	1:A:1445:C:C5	2.46	0.51
17:Q:107:ALA:O	17:Q:111:GLU:HG2	2.11	0.51
1:A:69:C:O2'	1:A:70:G:H5'	2.11	0.51
17:Q:106:PHE:O	17:Q:110:VAL:HG23	2.10	0.51
12:L:83:VAL:O	12:L:114:ILE:HA	2.10	0.51
1:A:954:G:C5	1:A:955:C:C5	2.99	0.51
1:A:960:A:H61	13:M:82:ARG:HH21	1.58	0.51
1:A:603:A:H61	1:A:655:A:C1'	2.24	0.51
3:C:118:VAL:HG22	3:C:119:ALA:N	2.24	0.51
14:N:10:LEU:HB2	14:N:17:ARG:CZ	2.41	0.51
1:A:1188:U:C2'	1:A:1189:A:H5'	2.40	0.51
6:F:32:PRO:HA	6:F:162:THR:OG1	2.10	0.51
1:A:814:C:H5	12:L:27:HIS:NE2	2.08	0.51
13:M:58:PHE:CD1	13:M:61:GLY:HA3	2.45	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:72:ASP:O	14:N:76:VAL:HG12	2.11	0.51
1:A:1824:G:OP1	3:C:52:ARG:HD3	2.11	0.51
1:A:1344:G:H4'	1:A:1384:A:C5	2.46	0.51
1:A:719:C:H2'	1:A:720:C:H6	1.75	0.51
8:H:31:LEU:HB3	8:H:32:PRO:HD3	1.92	0.51
1:A:1022:G:H8	10:J:92:GLN:HE22	1.57	0.51
7:G:92:ILE:N	7:G:92:ILE:HD12	2.22	0.51
3:C:71:ASP:CB	3:C:103:ARG:HH22	2.20	0.51
1:A:363(D):G:H2'	1:A:363(E):G:H8	1.76	0.51
15:O:49:VAL:HG11	15:O:73:LEU:HA	1.92	0.51
1:A:2378:A:H2'	15:O:21:THR:HG21	1.92	0.51
2:B:71:C:C4	2:B:72:G:N7	2.79	0.51
6:F:77:ILE:HG22	6:F:80:PHE:N	2.24	0.51
1:A:2893:G:H3'	1:A:2894:G:H5'	1.93	0.51
17:Q:49:HIS:HA	17:Q:52:ARG:HB2	1.91	0.51
1:A:581:C:OP1	17:Q:31:SER:HB2	2.11	0.51
1:A:920:G:H2'	1:A:921:G:H8	1.76	0.51
26:Z:11:SER:OG	26:Z:13:ILE:HG12	2.10	0.51
18:R:13:ARG:HD2	18:R:13:ARG:C	2.31	0.51
17:Q:90:VAL:HG13	17:Q:91:ASP:N	2.26	0.51
17:Q:95:LEU:HD11	18:R:12:TYR:HA	1.92	0.51
21:U:71:LYS:HZ3	21:U:71:LYS:HB2	1.76	0.51
22:V:104:PHE:HB3	22:V:141:VAL:HG11	1.93	0.51
1:A:388:G:OP1	24:X:33:LYS:HB3	2.11	0.51
1:A:2777:G:C5'	1:A:2778:A:H5'	2.41	0.51
12:L:135:LEU:HD13	12:L:135:LEU:O	2.11	0.51
1:A:379:G:N2	24:X:20:ARG:HH12	2.08	0.51
1:A:2698:U:H2'	1:A:2699:C:C6	2.46	0.51
22:V:118:GLN:HB2	22:V:173:ALA:O	2.11	0.51
14:N:104:ARG:NH1	14:N:109:ALA:HB3	2.25	0.51
12:L:16:ARG:C	12:L:16:ARG:HE	2.14	0.51
1:A:597:U:O2'	12:L:15:ARG:HG2	2.10	0.51
16:P:100:TYR:HD2	16:P:103:ARG:NH2	2.09	0.51
1:A:2305:A:H3'	1:A:2306:C:H5''	1.92	0.51
29:3:30:THR:HG22	29:3:31:PRO:HD2	1.92	0.51
1:A:2795:G:H3'	1:A:2797:U:C5'	2.41	0.51
13:M:74:TYR:CD2	13:M:91:GLU:HB2	2.46	0.51
8:H:82:ARG:HG2	8:H:89:TYR:CD1	2.46	0.51
1:A:1335:U:H2'	1:A:1336:A:H8	1.76	0.51
1:A:2484:G:H5''	13:M:45:GLN:HB2	1.92	0.51
3:C:43:ARG:HB2	3:C:48:ARG:O	2.11	0.51
19:S:46:PHE:O	19:S:50:VAL:HG12	2.11	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:144(B):A:H5''	1:A:1445:C:H5	1.75	0.51
5:E:184:TYR:CE2	5:E:188:ARG:HD2	2.46	0.51
1:A:2840:C:H4'	14:N:53:HIS:CD2	2.46	0.51
1:A:2853:C:H2'	1:A:2854:G:H8	1.76	0.51
12:L:85:LEU:H	12:L:85:LEU:HD23	1.76	0.50
1:A:744:G:OP1	4:D:132:HIS:HB2	2.12	0.50
1:A:2038:G:H2'	1:A:2039:C:H6	1.76	0.50
1:A:94:G:H21	25:Y:47:ASN:ND2	2.09	0.50
22:V:5:LEU:HB3	22:V:59:LEU:HD23	1.92	0.50
1:A:2366:A:H2'	1:A:2367:G:O4'	2.11	0.50
12:L:33:ARG:HG3	12:L:36:LYS:CD	2.22	0.50
1:A:2822:G:H8	1:A:2822:G:O5'	1.95	0.50
24:X:90:ILE:O	24:X:94:LEU:HB2	2.10	0.50
24:X:45:ASN:ND2	24:X:47:GLN:HE21	2.10	0.50
15:O:36:TYR:N	15:O:36:TYR:CD1	2.79	0.50
1:A:2340:G:H2'	1:A:2341:G:H8	1.76	0.50
31:5:11:LYS:C	31:5:11:LYS:HD3	2.31	0.50
1:A:1111:A:N3	1:A:1112:G:H1'	2.26	0.50
1:A:593:G:O2'	31:5:62:LEU:HD13	2.11	0.50
17:Q:112:ARG:HH21	18:R:46:VAL:HG21	1.76	0.50
15:O:30:ARG:C	15:O:30:ARG:HD2	2.31	0.50
24:X:62:VAL:HG22	24:X:63:ALA:N	2.26	0.50
3:C:33:LEU:HD23	3:C:33:LEU:N	2.24	0.50
20:T:63:LYS:HZ2	20:T:72:LYS:HB3	1.76	0.50
15:O:26:LEU:HG	15:O:39:ILE:CD1	2.41	0.50
1:A:1541:U:H3'	1:A:1542:G:H3'	1.93	0.50
1:A:1404:C:O2'	1:A:1405:U:H5'	2.11	0.50
1:A:1504:C:O2'	1:A:1505:C:H6	1.95	0.50
1:A:2271:G:H2'	1:A:2272:U:C6	2.46	0.50
20:T:89:ILE:O	20:T:93:GLU:HG2	2.11	0.50
4:D:14:ILE:HD12	4:D:14:ILE:C	2.31	0.50
4:D:172:VAL:HG13	4:D:182:LEU:HD11	1.92	0.50
30:4:24:THR:O	30:4:28:ARG:HG3	2.11	0.50
1:A:1178:C:H2'	1:A:1179:C:H6	1.76	0.50
1:A:2208:U:O2'	1:A:2209:C:H5'	2.11	0.50
1:A:1929:G:N3	1:A:1929:G:H5''	2.26	0.50
12:L:147:LEU:HD13	12:L:148:LEU:O	2.12	0.50
22:V:125:LEU:HD23	22:V:126:VAL:N	2.26	0.50
3:C:244:ARG:HB2	3:C:244:ARG:HH11	1.77	0.50
10:J:57:LEU:HD11	10:J:142:ARG:HB2	1.92	0.50
10:J:127:LYS:HA	10:J:130:LEU:HD12	1.92	0.50
5:E:12:LEU:HB2	5:E:124:LEU:HD11	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2462:U:H1'	1:A:2491:U:O4	2.12	0.50
1:A:1010:A:H1'	1:A:1153:C:H1'	1.92	0.50
18:R:49:THR:HB	18:R:50:PRO:CD	2.42	0.50
15:O:14:VAL:O	15:O:18:ILE:HG12	2.12	0.50
6:F:74:LYS:HE2	6:F:84:LYS:HE3	1.94	0.50
1:A:2517:C:C5	1:A:2542:A:C2	2.99	0.50
6:F:25:TYR:CD1	6:F:30:GLU:HB3	2.47	0.50
1:A:270(H):C:H2'	1:A:270(I):C:H6	1.76	0.50
7:G:30:LYS:HB2	7:G:79:VAL:HA	1.94	0.50
1:A:1056:G:H8	1:A:1056:G:O5'	1.94	0.50
3:C:131:LEU:HD11	3:C:136:ILE:HG12	1.94	0.50
4:D:120:TRP:CD1	4:D:155:LYS:HB3	2.47	0.50
1:A:775:G:C5	1:A:794:G:C8	2.99	0.50
1:A:1980:G:H3'	1:A:1981:A:C5'	2.42	0.50
1:A:2320:A:N3	1:A:2320:A:H2'	2.25	0.50
1:A:116:C:H2'	1:A:117:G:C8	2.47	0.50
21:U:8:LYS:NZ	21:U:8:LYS:N	2.57	0.50
8:H:77:LEU:HG	8:H:101:LEU:HD13	1.94	0.50
12:L:17:LYS:O	12:L:19:VAL:HG22	2.12	0.50
1:A:481:G:H1'	1:A:506:G:N2	2.27	0.50
8:H:6:LEU:N	8:H:6:LEU:HD23	2.26	0.50
16:P:57:PHE:CG	16:P:58:ASN:N	2.80	0.50
19:S:4:LYS:HG2	19:S:106:ILE:CG2	2.42	0.50
1:A:1495:A:H2'	1:A:1495:A:N3	2.26	0.50
15:O:38:GLN:HB3	15:O:47:THR:CG2	2.41	0.50
23:W:37:LEU:HG	23:W:60:PHE:HA	1.92	0.50
1:A:310:A:OP1	21:U:18:GLY:HA2	2.11	0.50
1:A:2641:G:H5''	10:J:99:SER:HB3	1.93	0.50
1:A:41:C:H2'	1:A:43:G:O4'	2.11	0.50
2:B:46:A:H2'	2:B:47:C:C6	2.47	0.50
11:K:61:VAL:HG13	11:K:61:VAL:O	2.12	0.50
1:A:773:U:H4'	3:C:47:GLY:CA	2.39	0.50
1:A:646:A:H5'	1:A:646:A:N3	2.27	0.50
6:F:173:LEU:HA	6:F:176:LEU:HD12	1.94	0.50
8:H:4:ILE:HD11	8:H:16:GLY:HA2	1.94	0.50
1:A:37:C:H2'	1:A:38:A:C8	2.46	0.50
3:C:150:LYS:HA	3:C:150:LYS:HE3	1.94	0.50
22:V:39:VAL:HG21	22:V:44:PHE:CD2	2.47	0.50
1:A:2846:G:H2'	1:A:2847:U:O4'	2.11	0.50
1:A:1827:C:H2'	1:A:1828:G:O4'	2.12	0.49
3:C:132:PRO:HG3	3:C:190:TYR:CE1	2.46	0.49
22:V:76:LEU:H	22:V:76:LEU:CD1	2.24	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:774:A:H2	1:A:787:U:O2'	1.93	0.49
11:K:2:ILE:CD1	11:K:82:ASN:HD22	2.25	0.49
1:A:2894:G:N3	1:A:2894:G:H2'	2.27	0.49
1:A:581:C:H2'	1:A:582:G:C8	2.47	0.49
1:A:1165:U:H2'	1:A:1166:C:C6	2.47	0.49
1:A:903:C:H2'	1:A:904:C:C6	2.47	0.49
1:A:496:G:H1'	19:S:61:ASN:ND2	2.27	0.49
21:U:29:GLU:HB3	21:U:38:ILE:HB	1.94	0.49
25:Y:11:GLU:OE1	25:Y:11:GLU:N	2.43	0.49
17:Q:79:PHE:C	17:Q:79:PHE:CD1	2.85	0.49
17:Q:88:ILE:HB	17:Q:90:VAL:CG1	2.36	0.49
1:A:2246:G:H2'	1:A:2247:A:C8	2.48	0.49
1:A:1578:U:H2'	1:A:1579:A:H5''	1.94	0.49
1:A:390:A:C6	12:L:71:VAL:HG21	2.47	0.49
22:V:82:ARG:HG2	22:V:83:PRO:HD2	1.94	0.49
1:A:144:C:H2'	1:A:145:G:H8	1.77	0.49
6:F:16:ARG:O	6:F:20:ILE:HG12	2.12	0.49
1:A:2419:U:O4	31:5:30:ARG:CZ	2.60	0.49
1:A:1689:A:H62	1:A:1698:A:H2	1.59	0.49
1:A:114(B):A:N3	1:A:1144:G:C8	2.81	0.49
1:A:2394:C:H2'	1:A:2395:C:C6	2.48	0.49
1:A:956:G:N2	1:A:959:A:H3'	2.26	0.49
24:X:11:ARG:HB2	24:X:13:ILE:HG22	1.94	0.49
1:A:603:A:N6	1:A:655:A:H1'	2.27	0.49
1:A:1568:G:OP2	3:C:63:ARG:NH2	2.45	0.49
1:A:860:U:O2	1:A:860:U:O4'	2.29	0.49
21:U:20:TYR:CE1	21:U:42:VAL:HA	2.47	0.49
3:C:10:THR:HG23	3:C:13:ARG:HB3	1.94	0.49
8:H:57:ARG:O	8:H:61:ARG:HG3	2.12	0.49
14:N:103:ARG:HH12	14:N:110:PRO:HG3	1.78	0.49
1:A:150:C:H2'	1:A:151:C:C6	2.47	0.49
1:A:2010:G:H5''	19:S:42:ARG:HB2	1.94	0.49
11:K:112:MET:HA	11:K:115:VAL:HG22	1.93	0.49
5:E:143:ALA:HB1	5:E:148:LEU:HB2	1.94	0.49
2:B:63:G:H2'	2:B:64:C:C6	2.47	0.49
1:A:114(B):A:C4	1:A:1144:G:N7	2.80	0.49
31:5:33:ASN:ND2	31:5:34:TRP:H	2.11	0.49
3:C:81:ALA:HB3	3:C:94:LEU:HB3	1.95	0.49
13:M:60:ARG:N	22:V:179:ASP:HB2	2.26	0.49
1:A:1937:A:N7	1:A:1939:U:H2'	2.28	0.49
11:K:2:ILE:CG1	11:K:8:LEU:HD11	2.42	0.49
29:3:13:CYS:O	29:3:21:TYR:HA	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:52:VAL:O	13:M:56:ARG:HB2	2.12	0.49
29:3:16:CYS:SG	29:3:48:VAL:HG23	2.52	0.49
13:M:23:GLY:HA3	13:M:98:LYS:HB2	1.94	0.49
1:A:754:C:H2'	1:A:755:C:C6	2.47	0.49
1:A:1826:G:OP1	3:C:233:HIS:HD2	1.96	0.49
13:M:76:LYS:H	13:M:88:GLY:HA2	1.76	0.49
6:F:86:MET:H	6:F:87:PRO:CD	2.25	0.49
29:3:36:LEU:HB3	29:3:50:ARG:NH1	2.27	0.49
3:C:79:VAL:O	3:C:113:VAL:HG13	2.11	0.49
1:A:1437:C:H2'	1:A:1438:U:H6	1.78	0.49
5:E:125:LEU:HB3	5:E:196:LEU:HD23	1.94	0.49
1:A:2564:A:OP1	1:A:2648:C:H4'	2.13	0.49
14:N:87:TYR:OH	14:N:116:LEU:HB3	2.13	0.49
1:A:405:U:H3'	1:A:406:G:H5'	1.94	0.49
6:F:133:LEU:HD21	6:F:157:ILE:HG13	1.94	0.49
1:A:23:G:H2'	1:A:24:G:H8	1.77	0.49
1:A:1592:C:H2'	1:A:1593:G:H8	1.78	0.49
8:H:92:VAL:HG22	8:H:120:ILE:HD12	1.94	0.49
1:A:1970:A:H4'	1:A:1971:A:OP1	2.12	0.49
1:A:1022:G:C6	1:A:1140:C:C4	3.01	0.49
1:A:733:G:H8	1:A:733:G:O5'	1.96	0.49
4:D:5:LEU:HB2	4:D:51:PHE:HD2	1.77	0.49
1:A:557:U:H2'	1:A:558:G:H8	1.76	0.49
1:A:596:G:C6	1:A:597:U:C4	3.01	0.49
3:C:108:PRO:CG	3:C:143:HIS:CE1	2.96	0.49
6:F:130:ASN:OD1	6:F:160:VAL:HA	2.13	0.49
10:J:80:ALA:HB3	10:J:147:ALA:HB2	1.95	0.49
1:A:1833:U:C2	1:A:1834:U:C6	3.00	0.49
1:A:2258:C:H4'	1:A:2259:G:OP2	2.12	0.49
7:G:23:ARG:N	7:G:23:ARG:HD3	2.27	0.49
25:Y:14:ARG:HA	25:Y:17:SER:HB2	1.94	0.49
13:M:43:THR:OG1	13:M:46:GLN:HG3	2.12	0.49
1:A:795:C:O2'	1:A:796:C:H5'	2.13	0.49
1:A:2892:A:N6	1:A:2893:G:C2	2.81	0.49
1:A:1973:G:H2'	1:A:1974:C:H6	1.77	0.49
23:W:53:MET:HA	23:W:58:THR:O	2.13	0.49
23:W:50:ASN:HD22	23:W:83:PRO:HD3	1.78	0.49
11:K:12:ASP:OD1	11:K:85:VAL:HG13	2.13	0.49
1:A:783:A:H3'	1:A:783:A:C8	2.48	0.49
8:H:5:LEU:H	8:H:5:LEU:CD2	2.18	0.49
4:D:117:MET:CE	4:D:136:ARG:HA	2.38	0.49
1:A:1486:A:C6	1:A:1504:C:N4	2.80	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:4:21:ARG:HB3	30:4:31:LEU:CD2	2.43	0.49
3:C:105:ILE:CG1	3:C:106:ILE:HD12	2.42	0.49
1:A:2537:U:H2'	1:A:2538:C:H6	1.77	0.49
1:A:2012:G:O2'	19:S:96:ILE:HD11	2.12	0.49
6:F:153:ARG:NH1	6:F:153:ARG:HB3	2.27	0.49
1:A:747:U:O2	1:A:2014:A:H1'	2.12	0.49
24:X:13:ILE:HG23	24:X:14:VAL:H	1.77	0.49
4:D:101:ARG:HG2	4:D:171:GLU:HA	1.95	0.49
1:A:1614:A:C6	19:S:87:PRO:HA	2.48	0.49
24:X:58:ILE:HD11	24:X:91:LYS:CG	2.43	0.49
1:A:433:C:H2'	1:A:434:U:C6	2.48	0.49
1:A:110:G:C2	1:A:111:A:C8	3.01	0.49
1:A:1963:U:H2'	1:A:1963:U:O2	2.12	0.49
18:R:47:VAL:HG12	18:R:49:THR:O	2.13	0.49
3:C:25:THR:HG21	3:C:81:ALA:CA	2.43	0.49
1:A:1486:A:N6	1:A:1504:C:H42	2.09	0.49
12:L:95:VAL:HG23	12:L:125:VAL:HA	1.94	0.49
3:C:72:LYS:HE3	3:C:101:GLU:CB	2.43	0.49
16:P:107:ASP:O	16:P:110:ILE:HG22	2.12	0.49
1:A:1680:U:O2	1:A:1763:G:H3'	2.12	0.49
1:A:2784:C:H2'	1:A:2785:C:C6	2.48	0.49
10:J:160:LYS:CD	10:J:161:LEU:H	2.26	0.49
28:2:3:LYS:O	28:2:4:HIS:C	2.51	0.48
17:Q:79:PHE:HD1	17:Q:79:PHE:C	2.16	0.48
21:U:14:LEU:HD23	21:U:15:VAL:N	2.28	0.48
6:F:55:LYS:HD2	6:F:58:GLN:NE2	2.20	0.48
1:A:947:G:N2	1:A:971:C:C2	2.81	0.48
1:A:1431:U:H2'	1:A:1432:C:C6	2.48	0.48
1:A:2741:A:H2'	1:A:2742:C:O4'	2.13	0.48
29:3:11:LEU:HD21	29:3:51:GLU:CD	2.33	0.48
1:A:322:A:H3'	5:E:169:ASN:HD21	1.78	0.48
1:A:481:G:O2'	1:A:482:A:P	2.71	0.48
16:P:54:ARG:HA	16:P:59:THR:OG1	2.12	0.48
3:C:72:LYS:CE	3:C:101:GLU:HG2	2.42	0.48
1:A:2252:G:H2'	1:A:2253:G:H8	1.78	0.48
1:A:165:U:H2'	1:A:171:G:O4'	2.13	0.48
1:A:1270:C:H5''	1:A:1271:G:O5'	2.13	0.48
1:A:1001:A:H2'	1:A:1002:G:O4'	2.12	0.48
25:Y:1:MET:SD	25:Y:1:MET:O	2.71	0.48
18:R:47:VAL:HG13	18:R:52:VAL:N	2.28	0.48
1:A:2039:C:C2	1:A:2040:C:C5	3.01	0.48
8:H:77:LEU:O	8:H:143:SER:HB3	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2415:G:H4'	12:L:66:GLY:HA2	1.92	0.48
13:M:39:PRO:O	13:M:40:ALA:HB2	2.13	0.48
3:C:43:ARG:HB2	3:C:49:ILE:HA	1.96	0.48
16:P:58:ASN:HD22	16:P:58:ASN:C	2.17	0.48
12:L:138:LEU:HD11	12:L:144:GLU:HB3	1.94	0.48
1:A:1252:G:C2	1:A:1253:A:C2	3.01	0.48
1:A:996:A:H4'	17:Q:92:ARG:CZ	2.44	0.48
1:A:1171:G:H2'	1:A:1173:G:O4'	2.13	0.48
15:O:25:ARG:HD2	15:O:88:ASP:OD1	2.12	0.48
21:U:90:LEU:HG	21:U:91:GLU:H	1.77	0.48
1:A:2699:C:H2'	1:A:2700:C:O4'	2.13	0.48
1:A:1632:A:O5'	1:A:1632:A:H8	1.96	0.48
6:F:60:LEU:O	6:F:64:THR:HG22	2.14	0.48
20:T:30:VAL:HG21	20:T:79:ALA:HB3	1.94	0.48
1:A:675:A:H4'	5:E:67:GLN:HE21	1.76	0.48
6:F:55:LYS:O	6:F:59:GLU:HG3	2.14	0.48
15:O:89:ARG:O	15:O:90:GLY:O	2.31	0.48
1:A:478:A:C6	1:A:480:A:C6	3.01	0.48
1:A:1478:G:H2'	1:A:1479:G:H8	1.78	0.48
3:C:259:THR:O	3:C:260:ARG:HB2	2.14	0.48
1:A:2887:U:H2'	1:A:2888:C:H6	1.78	0.48
17:Q:60:LEU:HD23	17:Q:60:LEU:C	2.33	0.48
6:F:109:VAL:C	6:F:112:PRO:HD2	2.34	0.48
1:A:1509:A:H4'	1:A:1510:A:C1'	2.44	0.48
8:H:88:ILE:CG2	8:H:89:TYR:N	2.76	0.48
6:F:98:ARG:O	6:F:101:ILE:HG12	2.13	0.48
26:Z:40:THR:O	26:Z:44:ARG:HG3	2.13	0.48
25:Y:52:ASP:O	25:Y:56:GLN:HB2	2.14	0.48
19:S:12:ILE:HD12	19:S:46:PHE:CE2	2.49	0.48
1:A:1797:C:O2'	3:C:259:THR:HG23	2.14	0.48
10:J:26:THR:HG22	10:J:27:TYR:N	2.29	0.48
1:A:2335:A:H2'	15:O:13:ARG:HH22	1.78	0.48
1:A:1615:C:O2'	1:A:1616:A:H5'	2.13	0.48
11:K:88:ASN:OD1	11:K:89:ASN:N	2.47	0.48
22:V:10:ARG:HB3	22:V:36:LYS:HB3	1.95	0.48
21:U:2:ARG:C	21:U:4:LYS:H	2.17	0.48
31:5:53:PRO:HB2	31:5:57:ARG:NH2	2.28	0.48
17:Q:62:ILE:HD12	17:Q:76:TYR:CE1	2.48	0.48
8:H:86:THR:O	8:H:122:GLU:HG3	2.14	0.48
1:A:1478:G:O2'	1:A:1558:A:C2	2.66	0.48
5:E:28:ILE:O	5:E:30:PRO:HD3	2.13	0.48
6:F:128:ARG:HH21	6:F:130:ASN:HD21	1.61	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:V:10:ARG:HH21	22:V:26:GLY:H	1.62	0.48
1:A:1399:C:O2'	1:A:1400:G:H5'	2.14	0.48
1:A:1887:C:H3'	1:A:1888:G:H5''	1.96	0.48
1:A:792:G:H5''	1:A:793:A:H5'	1.94	0.48
3:C:25:THR:HG21	3:C:81:ALA:HA	1.95	0.48
1:A:2027:G:H2'	1:A:2028:U:O4'	2.14	0.48
14:N:17:ARG:O	14:N:20:LEU:HB3	2.14	0.48
1:A:661:C:H4'	12:L:16:ARG:HD2	1.95	0.48
1:A:2061:G:H5''	1:A:2503:A:C2	2.48	0.48
1:A:2815:C:O2'	28:2:43:HIS:CD2	2.66	0.48
1:A:2572:A:H62	4:D:145:LYS:HG3	1.79	0.48
1:A:903:C:H2'	1:A:904:C:H6	1.79	0.48
1:A:2537:U:H2'	1:A:2538:C:C6	2.49	0.48
1:A:1615:C:C6	1:A:1617:C:C5	3.01	0.48
2:B:78:A:C2	2:B:99:A:C4	3.02	0.48
1:A:649:G:H2'	1:A:650:C:C6	2.49	0.48
19:S:62:HIS:O	19:S:64:MET:HG3	2.14	0.48
1:A:855:G:H2'	1:A:856:C:C6	2.48	0.48
13:M:81:VAL:HG12	13:M:82:ARG:CG	2.41	0.48
25:Y:10:LEU:O	25:Y:13:ALA:HB3	2.13	0.48
23:W:32:ARG:CB	23:W:35:ASN:HD21	2.27	0.48
26:Z:8:LEU:HA	26:Z:54:VAL:HG12	1.95	0.48
3:C:94:LEU:HB2	3:C:104:TYR:CE1	2.47	0.48
1:A:1210:A:C5'	1:A:1210:A:H8	2.22	0.48
1:A:310:A:OP1	21:U:17:SER:O	2.31	0.48
7:G:46:GLU:HG3	7:G:51:ARG:NE	2.28	0.48
7:G:58:GLU:HB2	7:G:61:HIS:ND1	2.29	0.48
1:A:2244:U:O2'	1:A:2245:U:H5'	2.13	0.48
1:A:1639:U:H4'	1:A:2699:C:H4'	1.94	0.48
1:A:2334:G:H4'	1:A:2335:A:OP2	2.14	0.48
21:U:9:LYS:O	21:U:27:VAL:HG21	2.14	0.48
1:A:1517:G:H2'	1:A:1518:C:C6	2.49	0.48
1:A:242:G:N7	31:5:5:LYS:HG2	2.28	0.48
1:A:2850:A:H2'	1:A:2851:A:C8	2.49	0.48
2:B:8:U:H5''	15:O:15:ARG:NH2	2.29	0.48
5:E:37:VAL:HG13	5:E:184:TYR:HD1	1.78	0.48
10:J:77:VAL:HB	10:J:145:VAL:HG22	1.94	0.48
9:I:9:LEU:O	9:I:13:LEU:HG	2.13	0.48
16:P:24:PRO:HA	16:P:49:VAL:HG13	1.95	0.48
14:N:50:HIS:O	14:N:54:LEU:HB2	2.14	0.48
16:P:27:THR:CG2	16:P:90:GLN:HB3	2.44	0.48
3:C:154:LYS:C	3:C:155:LEU:HD12	2.34	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2599:G:N7	3:C:237:GLU:HG3	2.29	0.48
1:A:39:C:H2'	1:A:40:C:C6	2.49	0.48
18:R:81:TYR:O	18:R:82:ARG:HG3	2.13	0.48
16:P:60:THR:HG22	16:P:77:PRO:HA	1.96	0.48
8:H:117:GLU:HG3	8:H:118:LYS:N	2.28	0.48
1:A:409:C:O2'	1:A:410:G:H5'	2.13	0.48
3:C:40:THR:HG22	3:C:41:GLY:N	2.28	0.48
2:B:6:C:C2	2:B:115:G:N2	2.82	0.48
1:A:114(B):A:C4	1:A:1144:G:C8	3.01	0.47
21:U:76:CYS:CB	21:U:77:PRO:CD	2.92	0.47
31:5:14:VAL:CG1	31:5:22:VAL:HG13	2.43	0.47
1:A:124:G:N7	30:4:19:ARG:NH2	2.62	0.47
8:H:79:ILE:HG22	8:H:81:VAL:CG2	2.44	0.47
1:A:603:A:C6	1:A:655:A:H1'	2.48	0.47
1:A:2286:A:H4'	1:A:2287:A:O4'	2.14	0.47
1:A:661:C:H4'	12:L:16:ARG:CD	2.44	0.47
12:L:16:ARG:CZ	12:L:18:ARG:HG3	2.44	0.47
1:A:1478:G:N3	1:A:1479:G:C8	2.82	0.47
1:A:784:A:N7	3:C:229:VAL:HG21	2.29	0.47
22:V:5:LEU:HD23	22:V:6:LYS:N	2.29	0.47
8:H:25:TYR:O	8:H:29:TYR:HB3	2.14	0.47
19:S:84:ARG:HB2	19:S:96:ILE:HG22	1.96	0.47
1:A:1796:U:H2'	1:A:1797:C:C6	2.49	0.47
4:D:31:CYS:HB3	4:D:49:LEU:HB3	1.95	0.47
18:R:22:VAL:CG1	18:R:23:GLU:N	2.76	0.47
6:F:92:VAL:O	6:F:92:VAL:HG13	2.14	0.47
1:A:827:U:O2	1:A:2246:G:H4'	2.14	0.47
1:A:783:A:C3'	1:A:783:A:C8	2.97	0.47
13:M:81:VAL:HG12	13:M:82:ARG:N	2.29	0.47
1:A:1448:G:H21	1:A:1529:A:H2	1.62	0.47
1:A:861:A:H2'	1:A:862:G:O4'	2.15	0.47
1:A:1331:A:O2'	1:A:1332:G:C8	2.66	0.47
1:A:2512:C:H5''	1:A:2513:G:OP2	2.14	0.47
1:A:1040:C:H2'	1:A:1041:C:C6	2.49	0.47
1:A:239:U:O2'	1:A:240:G:H5'	2.14	0.47
1:A:634:C:H2'	1:A:635:C:C6	2.50	0.47
19:S:9:TYR:H	19:S:102:HIS:HD2	1.63	0.47
1:A:471:A:H2'	1:A:472:A:O4'	2.14	0.47
1:A:1289:C:H2'	1:A:1290:C:H6	1.79	0.47
1:A:2751:G:H2'	1:A:2751:G:N3	2.29	0.47
3:C:136:ILE:O	3:C:168:ARG:NH2	2.47	0.47
1:A:124:G:C5	30:4:19:ARG:NH2	2.82	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1504:C:O2'	1:A:1505:C:O5'	2.31	0.47
1:A:966:G:C6	1:A:967:C:N4	2.82	0.47
1:A:768:G:O2'	1:A:1379:A:N6	2.47	0.47
14:N:96:ARG:NH2	14:N:117:VAL:HG23	2.29	0.47
13:M:47:ILE:HG22	13:M:48:GLU:N	2.28	0.47
1:A:1871:A:H2'	1:A:1872:A:C8	2.50	0.47
1:A:714:U:O2	1:A:716:A:C8	2.67	0.47
15:O:69:VAL:O	15:O:72:ALA:HB3	2.14	0.47
14:N:54:LEU:HD23	14:N:62:ALA:HB1	1.97	0.47
4:D:171:GLU:HG2	4:D:185:LYS:HG2	1.96	0.47
1:A:2516:G:C6	1:A:2517:C:N4	2.83	0.47
4:D:51:PHE:HB3	4:D:52:LEU:HD12	1.96	0.47
1:A:363(A):G:H2'	1:A:363(B):A:H8	1.79	0.47
13:M:6:ARG:N	13:M:6:ARG:HE	2.12	0.47
5:E:126:VAL:O	5:E:196:LEU:HG	2.14	0.47
1:A:380:U:H1'	24:X:20:ARG:NH1	2.29	0.47
14:N:87:TYR:HE1	14:N:117:VAL:HG13	1.79	0.47
22:V:27:VAL:HG22	22:V:36:LYS:HA	1.95	0.47
15:O:85:VAL:HG11	15:O:106:ARG:HD2	1.95	0.47
1:A:356:G:H2'	1:A:357:A:C8	2.49	0.47
12:L:84:ASN:HA	12:L:115:LEU:O	2.15	0.47
1:A:2481:G:HO2'	1:A:2482:G:P	2.37	0.47
2:B:75:G:N1	2:B:102:G:N2	2.61	0.47
7:G:103:LEU:HD22	7:G:123:PHE:CE1	2.50	0.47
4:D:4:ILE:HG12	4:D:28:ALA:HB1	1.95	0.47
6:F:16:ARG:HB3	6:F:17:PRO:HD3	1.97	0.47
18:R:99:ILE:HD13	18:R:99:ILE:N	2.29	0.47
28:2:18:ALA:O	28:2:21:SER:HB2	2.14	0.47
3:C:76:PRO:HB3	3:C:116:GLN:HE21	1.80	0.47
1:A:1341:U:O4	20:T:16:LYS:HE2	2.14	0.47
6:F:104:GLU:O	6:F:108:ASN:HB2	2.14	0.47
1:A:1709:U:H2'	1:A:1710:C:C6	2.49	0.47
6:F:143:GLU:CD	6:F:143:GLU:H	2.17	0.47
1:A:1022:G:N2	1:A:114(B):A:C2	2.83	0.47
15:O:49:VAL:CG1	15:O:76:LYS:HB2	2.45	0.47
4:D:5:LEU:C	4:D:51:PHE:HE2	2.18	0.47
24:X:27:GLU:HB2	24:X:32:LYS:O	2.14	0.47
25:Y:41:ILE:HD11	25:Y:44:LEU:HD12	1.95	0.47
22:V:81:ARG:O	22:V:82:ARG:HB2	2.14	0.47
1:A:1326:U:O2'	1:A:1327:C:H5'	2.15	0.47
7:G:154:PRO:HB3	7:G:163:TYR:CE2	2.49	0.47
1:A:2836:U:C4	1:A:2883:A:N6	2.82	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:718:A:O5'	1:A:718:A:H8	1.96	0.47
31:5:60:LEU:C	31:5:62:LEU:H	2.17	0.47
17:Q:92:ARG:HG2	18:R:11:GLN:CD	2.35	0.47
3:C:238:GLY:O	3:C:240:ALA:N	2.48	0.47
19:S:24:ILE:HG21	19:S:36:LEU:CD2	2.36	0.47
1:A:270(L):C:H6	1:A:270(L):C:O5'	1.97	0.47
22:V:99:TYR:CE2	22:V:125:LEU:HD12	2.49	0.47
1:A:744:G:OP1	4:D:132:HIS:CB	2.62	0.47
8:H:83:ALA:CB	8:H:123:LEU:HD12	2.43	0.47
8:H:82:ARG:HB3	8:H:89:TYR:CG	2.49	0.47
8:H:130:TYR:HD2	8:H:132:PRO:HG3	1.80	0.47
7:G:51:ARG:O	7:G:52:VAL:HG23	2.15	0.47
19:S:14:PRO:O	19:S:15:ARG:C	2.52	0.47
1:A:2365:G:O6	31:5:39:LYS:HE3	2.15	0.47
1:A:1357:U:H2'	1:A:1358:G:O4'	2.15	0.47
12:L:126:VAL:HA	12:L:145:PRO:HB2	1.95	0.47
1:A:1495:A:H2'	1:A:1496:A:C2	2.50	0.47
1:A:2730:C:O2'	1:A:2731:G:H5'	2.14	0.47
1:A:628:G:H2'	1:A:629:G:H8	1.79	0.47
1:A:2784:C:H2'	1:A:2785:C:H6	1.80	0.47
4:D:49:LEU:O	4:D:78:LEU:HA	2.15	0.47
1:A:2836:U:H2'	1:A:2837:G:C8	2.50	0.47
1:A:1051:G:H2'	1:A:1052:C:C6	2.49	0.47
1:A:1121:C:H6	1:A:1121:C:O5'	1.98	0.47
22:V:119:GLU:HG3	22:V:119:GLU:O	2.14	0.47
23:W:66:VAL:O	23:W:81:VAL:HA	2.15	0.47
10:J:30:LYS:O	10:J:32:VAL:HG23	2.15	0.47
1:A:828:U:O2	1:A:828:U:H3'	2.15	0.47
18:R:6:LYS:HA	18:R:11:GLN:HB3	1.97	0.47
1:A:2247:A:H2'	1:A:2248:C:C6	2.50	0.47
21:U:13:VAL:HG13	21:U:73:ARG:O	2.14	0.47
21:U:88:LYS:HE2	21:U:93:GLY:CA	2.39	0.47
16:P:88:ILE:HG13	16:P:89:VAL:N	2.30	0.47
1:A:245:G:H2'	1:A:246:C:C6	2.49	0.47
3:C:33:LEU:O	3:C:35:LYS:N	2.48	0.47
1:A:2026:C:C2	1:A:2027:G:C8	3.03	0.47
4:D:103:ASP:OD1	4:D:201:THR:HG23	2.14	0.47
4:D:169:ASN:ND2	4:D:201:THR:HG21	2.30	0.47
12:L:140:ALA:O	12:L:141:ALA:CB	2.63	0.47
1:A:2261:C:H3'	23:W:16:SER:CB	2.45	0.47
5:E:157:VAL:HB	5:E:194:MET:HB3	1.96	0.47
11:K:79:PHE:HD2	16:P:72:VAL:HG22	1.78	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:636:G:OP1	12:L:132:LYS:HD3	2.15	0.47
30:4:24:THR:HG23	30:4:27:GLY:HA3	1.96	0.47
1:A:2887:U:H2'	1:A:2888:C:C6	2.50	0.47
1:A:2335:A:C8	1:A:2337:G:C5	3.02	0.47
23:W:12:ASN:O	23:W:14:ARG:HB2	2.15	0.47
18:R:14:VAL:HG13	18:R:96:ILE:HG13	1.97	0.47
1:A:329:G:H1	21:U:19:LYS:HE3	1.79	0.47
6:F:38:VAL:HG22	6:F:93:THR:HG23	1.97	0.47
14:N:31:HIS:HB2	14:N:34:ILE:HD11	1.97	0.47
1:A:915:C:H2'	1:A:916:G:C8	2.50	0.47
28:2:3:LYS:HD2	28:2:3:LYS:N	2.29	0.47
24:X:11:ARG:HD2	24:X:60:PHE:HD2	1.79	0.47
3:C:271:ILE:O	3:C:272:ALA:CB	2.63	0.47
18:R:78:LYS:HG3	18:R:79:VAL:HG23	1.97	0.47
6:F:81:LYS:C	6:F:82:LEU:HD23	2.35	0.47
1:A:1655:A:H1'	4:D:113:PHE:CE2	2.50	0.47
1:A:96:G:H4'	25:Y:48:HIS:CD2	2.50	0.47
1:A:1411:C:H2'	1:A:1412:A:C8	2.50	0.47
1:A:396:G:H1'	24:X:42:GLN:OE1	2.15	0.47
1:A:196:A:H2'	1:A:196:A:N3	2.29	0.47
21:U:76:CYS:O	21:U:77:PRO:C	2.52	0.47
21:U:10:GLY:HA2	21:U:27:VAL:HG23	1.96	0.47
24:X:19:GLN:HA	24:X:41:ARG:HA	1.96	0.47
2:B:106:G:C6	2:B:107:U:C4	3.03	0.47
4:D:86:PRO:HB2	4:D:87:GLU:H	1.41	0.47
11:K:79:PHE:CD2	16:P:72:VAL:HG22	2.50	0.47
1:A:753:C:H2'	1:A:754:C:H6	1.80	0.47
1:A:1506:C:H2'	1:A:1508:A:C8	2.50	0.47
1:A:909:A:H2'	1:A:912:C:H5	1.79	0.47
14:N:97:VAL:HA	14:N:113:LEU:O	2.15	0.47
3:C:25:THR:O	3:C:25:THR:HG23	2.14	0.46
3:C:25:THR:O	3:C:27:THR:N	2.49	0.46
31:5:54:GLU:O	31:5:58:ILE:HG12	2.14	0.46
11:K:77:ILE:HD13	11:K:78:ARG:N	2.30	0.46
13:M:35:VAL:HA	13:M:101:ARG:O	2.14	0.46
16:P:50:ILE:HA	16:P:99:LEU:CD1	2.45	0.46
1:A:966:G:C4	1:A:967:C:C5	3.03	0.46
14:N:53:HIS:O	14:N:56:LYS:HB3	2.15	0.46
1:A:1762:A:H8	1:A:1762:A:O5'	1.98	0.46
1:A:532:A:C8	1:A:2021:C:C5	3.03	0.46
3:C:37:LEU:HD12	3:C:38:LYS:H	1.79	0.46
2:B:56:G:H4'	2:B:57:A:C8	2.50	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1019:U:H3	1:A:114(B):A:N6	2.09	0.46
1:A:2393:A:H5''	12:L:62:LEU:HD12	1.97	0.46
13:M:75:THR:CA	13:M:88:GLY:HA2	2.40	0.46
8:H:12:LEU:N	8:H:12:LEU:HD22	2.30	0.46
14:N:10:LEU:HD23	14:N:21:TYR:OH	2.15	0.46
1:A:322:A:OP2	5:E:169:ASN:HB2	2.14	0.46
1:A:1602:U:H3'	1:A:1603:A:H5''	1.97	0.46
1:A:226:G:N2	1:A:228:A:H62	2.13	0.46
1:A:1567:A:H5''	3:C:58:HIS:CD2	2.50	0.46
10:J:58:ARG:C	10:J:60:LYS:H	2.18	0.46
1:A:2531:A:H2	1:A:2658:C:O2	1.98	0.46
18:R:34:GLU:HG3	18:R:58:VAL:HG22	1.97	0.46
10:J:34:PRO:HB3	10:J:74:PHE:CE1	2.50	0.46
25:Y:31:GLU:O	25:Y:35:LEU:HB2	2.15	0.46
2:B:28:C:H2'	2:B:29:A:O4'	2.15	0.46
1:A:1668:A:H4'	1:A:1669:A:O5'	2.16	0.46
1:A:943:U:OP1	12:L:38:GLN:HB3	2.16	0.46
12:L:128:HIS:CA	12:L:147:LEU:HB3	2.22	0.46
4:D:201:THR:O	4:D:202:LYS:HD3	2.15	0.46
1:A:2287:A:C6	1:A:2289:G:C4	3.03	0.46
15:O:39:ILE:O	15:O:48:LEU:HD13	2.15	0.46
1:A:510:C:OP1	1:A:511:U:OP2	2.34	0.46
1:A:2687:U:C4	1:A:2688:U:H5	2.33	0.46
1:A:2666:C:H3'	1:A:2667:C:C6	2.50	0.46
8:H:58:LEU:HD23	8:H:61:ARG:HD2	1.97	0.46
1:A:1187:G:O5'	1:A:1187:G:H8	1.98	0.46
1:A:380:U:O2'	24:X:20:ARG:HG2	2.16	0.46
1:A:2730:C:H4'	4:D:168:MET:O	2.15	0.46
1:A:2795:G:H3'	1:A:2797:U:H5''	1.95	0.46
1:A:1010:A:H1'	1:A:1153:C:C1'	2.45	0.46
3:C:76:PRO:CB	3:C:116:GLN:HE21	2.28	0.46
4:D:175:VAL:O	4:D:177:PRO:HD3	2.16	0.46
11:K:76:ALA:HB3	16:P:75:ILE:HB	1.97	0.46
5:E:132:VAL:HG23	5:E:133:ASN:N	2.30	0.46
12:L:128:HIS:HB3	12:L:147:LEU:HD23	1.98	0.46
1:A:2469:A:H5'	1:A:2470:G:OP2	2.15	0.46
1:A:1431:U:H2'	1:A:1432:C:H6	1.81	0.46
6:F:15:VAL:O	6:F:19:LEU:HG	2.15	0.46
6:F:6:ALA:HB1	6:F:10:LYS:HE3	1.97	0.46
1:A:2734:A:C8	1:A:2735:G:C8	3.04	0.46
1:A:1620:G:O2'	30:4:2:LYS:HG2	2.16	0.46
1:A:289:A:H2'	1:A:290:G:O4'	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:167:ALA:HB1	5:E:173:VAL:HG11	1.97	0.46
1:A:2190:G:H8	1:A:2190:G:H5'	1.79	0.46
1:A:1936:A:OP1	1:A:1936:A:H3'	2.15	0.46
1:A:2056:G:C2'	1:A:2056:G:N3	2.78	0.46
17:Q:69:CYS:SG	17:Q:79:PHE:HD2	2.38	0.46
12:L:85:LEU:HA	12:L:88:LEU:CB	2.45	0.46
16:P:27:THR:HA	16:P:48:ILE:HA	1.96	0.46
26:Z:28:LEU:HA	26:Z:33:GLN:OE1	2.16	0.46
1:A:2037:G:H2'	1:A:2038:G:C8	2.51	0.46
11:K:71:ARG:HH21	11:K:77:ILE:HG21	1.79	0.46
1:A:448:U:H1'	5:E:84:VAL:CG2	2.45	0.46
5:E:124:LEU:HD12	5:E:125:LEU:N	2.31	0.46
11:K:31:LYS:HB3	11:K:32:TYR:CE1	2.51	0.46
1:A:2830:G:N3	1:A:2883:A:H2	2.13	0.46
10:J:105:LEU:O	10:J:106:LYS:C	2.54	0.46
23:W:56:ASP:O	23:W:57:PHE:HB2	2.16	0.46
1:A:587:C:H42	12:L:33:ARG:CG	2.18	0.46
1:A:958:U:H5'	13:M:14:ARG:NH1	2.30	0.46
22:V:74:VAL:O	22:V:76:LEU:HD12	2.16	0.46
1:A:1173:G:H3'	1:A:1174:A:H5''	1.96	0.46
6:F:86:MET:O	6:F:87:PRO:O	2.34	0.46
6:F:53:LEU:CD1	6:F:88:ILE:HG12	2.46	0.46
14:N:21:TYR:CE2	14:N:43:GLU:HB3	2.50	0.46
24:X:27:GLU:HG2	24:X:28:GLY:N	2.30	0.46
8:H:15:VAL:HG12	8:H:16:GLY:N	2.30	0.46
16:P:30:VAL:HG12	16:P:86:ILE:CG1	2.45	0.46
1:A:2745:C:C4	1:A:2746:U:C4	3.03	0.46
1:A:2815:C:O2'	28:2:42:PRO:HB2	2.16	0.46
1:A:69:C:H2'	1:A:70:G:C8	2.50	0.46
22:V:28:MET:HE2	22:V:28:MET:HB3	1.80	0.46
29:3:34:LEU:N	29:3:34:LEU:HD13	2.31	0.46
3:C:69:ARG:HH12	3:C:117:VAL:CG2	2.29	0.46
1:A:2476:A:C2	1:A:2477:C:C6	3.03	0.46
18:R:24:LYS:HA	18:R:92:THR:HG23	1.97	0.46
1:A:2320:A:C8	1:A:2333:A:N6	2.83	0.46
4:D:78:LEU:N	4:D:78:LEU:HD23	2.30	0.46
16:P:63:VAL:O	16:P:73:GLU:HA	2.16	0.46
1:A:613:U:H4'	1:A:616:A:N6	2.31	0.46
1:A:258:G:H2'	1:A:259:G:H8	1.80	0.46
1:A:1449:G:H2'	1:A:1450:C:C6	2.50	0.46
1:A:2590:A:O2'	1:A:2591:C:H5'	2.15	0.46
1:A:394:A:O2'	1:A:395:U:H5'	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:38:GLN:CG	12:L:39:LYS:H	2.28	0.46
20:T:55:ASN:HB2	20:T:80:ILE:HG23	1.97	0.46
8:H:78:THR:HA	8:H:143:SER:CB	2.44	0.46
1:A:1678:G:H22	1:A:1989:G:H22	1.62	0.46
24:X:27:GLU:HG3	24:X:33:LYS:CD	2.46	0.46
2:B:79:C:H6	2:B:79:C:O5'	1.99	0.46
1:A:2273:A:H2'	1:A:2274:A:C8	2.50	0.46
1:A:221:A:N7	1:A:266:G:C5	2.84	0.46
1:A:534:U:O2'	17:Q:49:HIS:CD2	2.69	0.46
6:F:39:ILE:HG12	6:F:157:ILE:HG22	1.98	0.46
16:P:62:THR:HG22	16:P:75:ILE:HG13	1.98	0.46
1:A:451:C:H41	1:A:453:C:H3'	1.80	0.46
1:A:2764:A:N7	1:A:2766:G:C6	2.83	0.46
5:E:50:SER:HB2	5:E:94:PRO:HD3	1.97	0.46
16:P:29:ARG:HA	16:P:45:PHE:O	2.16	0.46
17:Q:69:CYS:CB	17:Q:79:PHE:HD2	2.29	0.46
10:J:92:GLN:O	10:J:94:ILE:HG13	2.16	0.46
1:A:71:A:OP1	1:A:72:U:H2'	2.16	0.46
5:E:63:LYS:HG2	5:E:65:TRP:O	2.15	0.46
24:X:11:ARG:HB2	24:X:13:ILE:CG2	2.45	0.46
1:A:558:G:H2'	1:A:559:G:H8	1.81	0.46
1:A:661:C:H4'	12:L:18:ARG:HG2	1.98	0.46
1:A:1317:A:N6	1:A:1336:A:N6	2.64	0.46
29:3:34:LEU:HD23	29:3:36:LEU:HD22	1.98	0.46
4:D:118:LYS:NZ	14:N:2:ARG:HH22	2.13	0.46
1:A:2666:C:H3'	1:A:2667:C:H6	1.81	0.46
1:A:2630:G:H1'	1:A:2894:G:H1'	1.98	0.46
3:C:70:TRP:CH2	3:C:150:LYS:HA	2.51	0.46
3:C:146:GLU:OE2	3:C:150:LYS:N	2.49	0.46
1:A:2647:U:H2'	1:A:2648:C:H6	1.80	0.46
1:A:2306:C:H4'	6:F:136:ARG:HH22	1.80	0.46
1:A:1833:U:C2	1:A:1834:U:C5	3.04	0.46
1:A:499:U:C4'	21:U:47:LYS:HZ1	2.29	0.46
16:P:109:GLU:HA	16:P:112:ARG:HG3	1.98	0.46
1:A:2252:G:H2'	1:A:2253:G:C8	2.51	0.46
1:A:155:C:H2'	1:A:161:U:H5'	1.98	0.46
23:W:14:ARG:O	23:W:15:ASP:HB2	2.16	0.46
1:A:2722:G:H4'	14:N:5:LYS:HB3	1.98	0.46
1:A:1354:A:C8	1:A:1355:G:C8	3.03	0.46
1:A:2678:C:H2'	1:A:2679:A:H8	1.81	0.46
10:J:81:ASP:N	10:J:81:ASP:OD1	2.48	0.46
13:M:134:ARG:O	13:M:135:ASP:HB2	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:587:C:C5	1:A:671:C:H1'	2.51	0.46
1:A:826:U:C5	1:A:828:U:H1'	2.50	0.46
1:A:833:U:H5''	12:L:48:PRO:HB2	1.97	0.46
20:T:24:GLY:O	20:T:83:VAL:HG22	2.15	0.46
6:F:64:THR:HG23	6:F:66:GLN:N	2.30	0.46
27:1:59:VAL:HG12	27:1:60:GLU:N	2.19	0.46
3:C:102:LYS:C	3:C:103:ARG:HG2	2.37	0.46
1:A:1006:C:H5'	10:J:51:THR:HG23	1.97	0.46
18:R:79:VAL:O	18:R:79:VAL:HG12	2.16	0.46
15:O:34:HIS:CG	15:O:54:LEU:HB2	2.51	0.46
3:C:130:ALA:HA	3:C:192:THR:HA	1.97	0.46
22:V:24:LEU:HD21	22:V:86:VAL:HG23	1.98	0.46
1:A:2667:C:H1'	7:G:109:PHE:HD2	1.81	0.46
1:A:919:G:H2'	1:A:920:G:C8	2.50	0.46
23:W:42:GLY:HA2	23:W:57:PHE:CD2	2.51	0.46
1:A:2627:G:H8	1:A:2627:G:O5'	1.99	0.46
21:U:68:HIS:ND1	21:U:70:SER:HB3	2.31	0.46
4:D:24:THR:HB	4:D:186:GLY:O	2.16	0.46
5:E:89:VAL:HG12	5:E:90:PHE:CD2	2.51	0.45
18:R:7:THR:HG23	18:R:22:VAL:HG11	1.98	0.45
1:A:1164:G:C8	1:A:1164:G:C5'	2.99	0.45
1:A:2392:A:H2	1:A:2424:C:N4	2.11	0.45
15:O:72:ALA:O	15:O:76:LYS:HG3	2.16	0.45
16:P:46:GLU:OE2	16:P:89:VAL:HG11	2.16	0.45
1:A:2027:G:C2	1:A:2028:U:H1'	2.51	0.45
1:A:2033:A:O2'	1:A:2034:U:P	2.74	0.45
6:F:25:TYR:CZ	6:F:32:PRO:HD3	2.51	0.45
18:R:72:VAL:CG2	18:R:85:LYS:HB3	2.46	0.45
5:E:198:ALA:O	5:E:201:VAL:HG12	2.15	0.45
1:A:1378:A:H4'	1:A:1379:A:OP1	2.15	0.45
9:I:56:ASN:HA	9:I:59:ILE:HD12	1.98	0.45
7:G:38:SER:HB2	7:G:41:MET:HG3	1.98	0.45
1:A:1599:C:OP2	20:T:36:LYS:HD3	2.15	0.45
1:A:1748:G:H2'	1:A:1749:A:C8	2.51	0.45
12:L:65:ARG:H	12:L:65:ARG:HD2	1.80	0.45
20:T:30:VAL:HG12	20:T:31:HIS:H	1.80	0.45
1:A:956:G:H22	1:A:959:A:H3'	1.81	0.45
27:1:57:ILE:HG22	27:1:59:VAL:CG2	2.46	0.45
1:A:947:G:H2'	1:A:948:G:C5'	2.43	0.45
1:A:125:G:H5'	30:4:19:ARG:HG3	1.97	0.45
1:A:2582:G:C2	1:A:2583:G:C8	3.03	0.45
10:J:62:ARG:CZ	10:J:64:ASP:HB2	2.46	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:414:C:H2'	1:A:415:A:H8	1.79	0.45
22:V:58:VAL:HG11	22:V:66:SER:HB2	1.98	0.45
1:A:270(Q):C:O2'	1:A:270(R):C:H6	1.98	0.45
1:A:628:G:H2'	1:A:629:G:C8	2.51	0.45
22:V:10:ARG:HG2	22:V:11:GLU:N	2.32	0.45
19:S:9:TYR:H	19:S:102:HIS:CD2	2.34	0.45
1:A:1750:G:H2'	1:A:1751:C:C6	2.52	0.45
6:F:174:GLU:HG2	6:F:180:PHE:CD1	2.51	0.45
4:D:54:GLN:HB2	4:D:74:PRO:O	2.16	0.45
10:J:63:PRO:O	17:Q:64:ARG:HD2	2.17	0.45
1:A:2585:U:H4'	1:A:2586:C:OP1	2.16	0.45
1:A:1850:G:C6	1:A:1851:U:C4	3.04	0.45
31:5:29:LYS:HB3	31:5:29:LYS:NZ	2.31	0.45
11:K:99:PHE:CD1	11:K:99:PHE:N	2.85	0.45
12:L:50:ARG:HD3	12:L:51:PHE:HB2	1.98	0.45
20:T:26:TYR:HE1	20:T:83:VAL:HG21	1.81	0.45
20:T:54:VAL:C	20:T:55:ASN:HD22	2.20	0.45
6:F:60:LEU:C	6:F:60:LEU:HD13	2.37	0.45
3:C:132:PRO:HD3	3:C:190:TYR:CE2	2.52	0.45
3:C:31:LYS:HA	3:C:31:LYS:HD2	1.65	0.45
4:D:101:ARG:HB3	4:D:169:ASN:HD22	1.82	0.45
18:R:72:VAL:HG22	18:R:85:LYS:O	2.16	0.45
1:A:779:U:P	3:C:49:ILE:HG13	2.56	0.45
5:E:192:LEU:C	5:E:192:LEU:HD23	2.37	0.45
1:A:1588:C:H2'	1:A:1589:C:C6	2.49	0.45
1:A:1995:U:H3'	1:A:1996:C:H2'	1.99	0.45
1:A:1709:U:C2	1:A:1750:G:C2	3.05	0.45
23:W:12:ASN:O	23:W:14:ARG:N	2.49	0.45
1:A:1354:A:H2'	1:A:1355:G:O4'	2.17	0.45
1:A:238:C:O2'	1:A:608:A:H1'	2.16	0.45
1:A:1427:A:H4'	1:A:1428:C:O5'	2.17	0.45
3:C:124:PRO:HG2	3:C:129:ASN:ND2	2.31	0.45
19:S:20:VAL:O	19:S:23:LEU:HB2	2.16	0.45
1:A:447:A:C5	1:A:473:G:C5	3.05	0.45
13:M:51:ARG:O	13:M:55:VAL:HG13	2.16	0.45
20:T:66:LEU:HD23	20:T:67:GLY:N	2.30	0.45
28:2:4:HIS:HB2	28:2:5:PRO:HD3	1.99	0.45
1:A:1971:A:N3	3:C:239:ARG:O	2.50	0.45
20:T:25:LYS:HE3	20:T:82:GLN:OE1	2.16	0.45
1:A:1021:A:H2'	1:A:1023:U:H5'	1.98	0.45
29:3:25:LYS:HD3	31:5:34:TRP:CZ3	2.51	0.45
22:V:71:VAL:HG11	22:V:74:VAL:CG2	2.46	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2516:G:O6	1:A:2517:C:N4	2.49	0.45
1:A:2542:A:C8	1:A:2544:G:O6	2.70	0.45
6:F:125:PHE:C	6:F:127:GLY:H	2.20	0.45
16:P:30:VAL:HG12	16:P:86:ILE:HG12	1.99	0.45
1:A:226:G:N2	1:A:227:A:C2	2.85	0.45
3:C:174:ILE:N	3:C:174:ILE:HD12	2.31	0.45
8:H:31:LEU:HD13	8:H:37:VAL:HA	1.98	0.45
1:A:1178:C:H2'	1:A:1179:C:C6	2.51	0.45
1:A:1973:G:H2'	1:A:1974:C:C6	2.51	0.45
19:S:20:VAL:HG11	19:S:44:ALA:HA	1.98	0.45
4:D:192:ASN:HD22	4:D:192:ASN:N	2.15	0.45
12:L:38:GLN:HG3	12:L:41:ARG:HG2	1.99	0.45
7:G:149:ARG:HD2	7:G:164:TYR:HE1	1.82	0.45
1:A:390:A:C5	12:L:71:VAL:HG21	2.52	0.45
1:A:1858:G:H1'	1:A:1884:A:H61	1.82	0.45
1:A:186:G:H2'	1:A:187:G:H8	1.82	0.45
5:E:83:PHE:O	5:E:86:GLY:N	2.45	0.45
1:A:36:G:N1	1:A:445:C:C4	2.84	0.45
1:A:919:G:C5'	2:B:81:G:H1'	2.46	0.45
1:A:868:U:C4	1:A:869:G:N7	2.85	0.45
19:S:70:TYR:O	19:S:107:LEU:HA	2.17	0.45
21:U:75:ILE:HG13	21:U:80:GLY:H	1.82	0.45
18:R:77:ALA:C	18:R:79:VAL:H	2.19	0.45
1:A:558:G:P	10:J:134:PRO:HD2	2.57	0.45
1:A:777:A:O2'	1:A:778:G:H5'	2.16	0.45
16:P:20:PRO:CD	16:P:86:ILE:HG23	2.46	0.45
3:C:70:TRP:C	3:C:70:TRP:CD1	2.90	0.45
1:A:1567:A:C8	3:C:84:TYR:CE2	3.05	0.45
1:A:2817:G:H21	1:A:2836:U:H1'	1.82	0.45
1:A:2722:G:H2'	1:A:2723:C:C6	2.51	0.45
7:G:38:SER:HB2	7:G:41:MET:CG	2.46	0.45
1:A:2436:G:C5	1:A:2437:U:C5	3.04	0.45
27:1:40:ILE:O	27:1:47:VAL:HA	2.16	0.45
4:D:21:VAL:HG12	4:D:23:VAL:HG13	1.99	0.45
1:A:2655:G:N2	1:A:2664:G:C5	2.85	0.45
1:A:553:U:O2'	1:A:554:U:H5'	2.16	0.45
28:2:4:HIS:HB2	28:2:5:PRO:CD	2.46	0.45
3:C:35:LYS:HA	3:C:35:LYS:HD2	1.62	0.45
1:A:2025:C:C2	1:A:2026:C:C5	3.05	0.45
1:A:1006:C:H1'	10:J:129:MET:HG2	1.99	0.45
4:D:201:THR:CG2	4:D:202:LYS:H	2.22	0.45
19:S:1:MET:HG3	19:S:2:GLU:N	2.32	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:9:LEU:HB2	8:H:12:LEU:HB2	1.98	0.45
14:N:10:LEU:HB2	14:N:17:ARG:NH2	2.31	0.45
1:A:1188:U:H4'	18:R:79:VAL:HG13	1.98	0.45
1:A:557:U:H2'	1:A:558:G:C8	2.51	0.45
1:A:1348:G:C2'	1:A:1349:A:H5''	2.45	0.45
3:C:11:PRO:C	3:C:13:ARG:N	2.70	0.45
1:A:2807:G:C6	1:A:2893:G:O6	2.69	0.45
1:A:2346:A:H5''	1:A:2383:G:C1'	2.46	0.45
7:G:13:LYS:HE2	7:G:14:GLY:N	2.32	0.45
1:A:1952:A:C4	11:K:22:ILE:HD12	2.50	0.45
1:A:356:G:H2'	1:A:357:A:H8	1.81	0.45
1:A:2552:U:H2'	1:A:2554:U:OP2	2.16	0.45
1:A:1489:U:HO2'	1:A:1490:A:H8	1.65	0.45
1:A:1208:C:C4	1:A:1209:G:N7	2.85	0.45
23:W:32:ARG:C	23:W:35:ASN:HD21	2.19	0.45
6:F:106:LEU:HB3	6:F:107:LEU:HD23	1.99	0.45
5:E:53:THR:C	5:E:55:GLY:N	2.70	0.45
21:U:27:VAL:O	21:U:27:VAL:HG23	2.16	0.45
4:D:6:GLY:HA2	4:D:51:PHE:CZ	2.51	0.45
10:J:116:THR:HG23	10:J:117:HIS:N	2.32	0.45
1:A:2850:A:H8	1:A:2850:A:H5'	1.79	0.45
1:A:301:G:C6	1:A:317:G:C6	3.05	0.45
1:A:979:G:H3'	1:A:980:A:H5''	1.99	0.45
1:A:244:A:C2	1:A:255:A:C4	3.05	0.45
1:A:994:C:OP1	17:Q:53:ARG:NH2	2.49	0.45
1:A:2580:U:H4'	4:D:130:GLY:HA2	1.98	0.45
1:A:1682:G:H2'	1:A:1683:C:C6	2.51	0.45
4:D:170:LEU:HB3	4:D:184:VAL:HG12	1.99	0.45
20:T:62:LYS:O	20:T:73:ARG:HB2	2.16	0.45
25:Y:33:MET:O	25:Y:37:PHE:HB2	2.17	0.45
1:A:1022:G:C5	1:A:1140:C:N4	2.85	0.45
1:A:142:G:H1'	20:T:37:THR:HG21	1.98	0.45
5:E:63:LYS:NZ	5:E:67:GLN:HE21	2.15	0.45
1:A:2712:U:O2'	1:A:712(B):A:P	2.75	0.45
1:A:1578:U:C2'	1:A:1579:A:H5''	2.46	0.45
6:F:88:ILE:HG13	6:F:89:GLY:N	2.30	0.45
1:A:66:C:H2'	1:A:67:U:H6	1.81	0.45
1:A:598:G:H2'	1:A:599:G:O4'	2.16	0.45
10:J:127:LYS:HB2	10:J:140:PHE:HE1	1.78	0.45
1:A:1291:C:H2'	1:A:1292:U:H6	1.79	0.45
3:C:5:LYS:H	3:C:5:LYS:HD2	1.80	0.45
21:U:90:LEU:N	21:U:90:LEU:HD23	2.31	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:105:LEU:H	12:L:105:LEU:HD12	1.82	0.45
23:W:50:ASN:ND2	23:W:83:PRO:HD3	2.31	0.45
1:A:454:A:H4'	1:A:455:C:OP2	2.17	0.45
7:G:105:LEU:N	7:G:105:LEU:HD13	2.31	0.45
12:L:50:ARG:HB3	31:5:60:LEU:HD21	1.98	0.45
13:M:85:LYS:HG3	13:M:86:GLY:N	2.32	0.45
4:D:91:VAL:HB	4:D:95:ILE:CD1	2.40	0.45
1:A:1006:C:C2	1:A:1138:G:N2	2.85	0.45
1:A:1658:C:OP1	4:D:132:HIS:O	2.34	0.45
1:A:2543:G:H2'	1:A:2544:G:O4'	2.17	0.45
1:A:2287:A:C4	1:A:2289:G:C8	3.04	0.45
13:M:101:ARG:HG3	13:M:102:VAL:N	2.32	0.45
22:V:22:GLY:O	22:V:41:LEU:HG	2.17	0.45
1:A:1478:G:C2	1:A:1479:G:C8	3.04	0.45
1:A:1390:U:O2'	1:A:1391:U:H5'	2.16	0.45
1:A:2850:A:H5''	1:A:2868:A:C2	2.51	0.45
10:J:62:ARG:NE	10:J:64:ASP:HB2	2.32	0.45
5:E:124:LEU:HB3	5:E:193:VAL:HG22	1.99	0.45
1:A:380:U:H4'	24:X:21:ARG:O	2.17	0.45
1:A:2196:C:O2'	1:A:2197:U:H5'	2.17	0.45
1:A:2259:G:C2	1:A:2282:G:N1	2.85	0.45
1:A:2886:G:H2'	1:A:2887:U:H6	1.82	0.45
5:E:54:ARG:HA	5:E:87:GLY:HA3	1.98	0.45
1:A:2315:G:H2'	1:A:2316:C:C6	2.52	0.45
10:J:156:GLN:O	10:J:157:ARG:HB2	2.17	0.44
6:F:58:GLN:O	6:F:62:LEU:HD13	2.17	0.44
8:H:82:ARG:HD2	8:H:89:TYR:CD2	2.52	0.44
1:A:2037:G:C6	1:A:2038:G:C6	3.05	0.44
10:J:57:LEU:CD1	10:J:142:ARG:HB2	2.48	0.44
15:O:90:GLY:O	15:O:92:TYR:CD1	2.69	0.44
3:C:211:ARG:O	3:C:215:LEU:HG	2.17	0.44
20:T:64:LYS:HG2	20:T:65:ARG:N	2.31	0.44
17:Q:104:GLN:HB3	18:R:44:LYS:NZ	2.32	0.44
1:A:102:G:H5''	1:A:102:G:H8	1.82	0.44
11:K:86:ILE:HD12	11:K:86:ILE:N	2.31	0.44
31:5:11:LYS:HB2	31:5:61:LEU:HD22	1.99	0.44
1:A:225:A:O2'	1:A:257:A:H4'	2.17	0.44
23:W:27:GLU:HB2	23:W:69:PHE:HD1	1.81	0.44
7:G:24:VAL:HG23	7:G:37:VAL:HG21	1.98	0.44
4:D:37:ARG:HD3	4:D:42:ASP:OD1	2.18	0.44
1:A:1900:A:N1	1:A:1970:A:C6	2.85	0.44
1:A:2250:G:C4	13:M:82:ARG:HG3	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:1:64:LYS:HA	27:1:64:LYS:HE3	2.00	0.44
1:A:2028:U:O4	1:A:2033:A:OP1	2.35	0.44
15:O:18:ILE:HA	15:O:21:THR:OG1	2.17	0.44
5:E:139:PHE:HB2	5:E:166:ALA:CB	2.45	0.44
1:A:1317:A:C6	1:A:1318:C:C4	3.05	0.44
12:L:30:THR:HG22	12:L:31:ALA:H	1.80	0.44
4:D:4:ILE:CG2	4:D:96:PHE:HE1	2.30	0.44
1:A:2809:A:C6	1:A:2892:A:C8	3.05	0.44
1:A:1603:A:H8	1:A:1603:A:H5'	1.81	0.44
2:B:111:U:HO2'	2:B:112:G:H8	1.62	0.44
22:V:92:SER:HB2	22:V:94:GLU:OE2	2.16	0.44
18:R:99:ILE:H	18:R:99:ILE:HD13	1.81	0.44
1:A:1600:C:O2'	1:A:1601:G:H5'	2.17	0.44
1:A:816:C:O2'	1:A:817:C:H5'	2.16	0.44
1:A:1916:A:H2'	1:A:1917:U:O4'	2.18	0.44
22:V:150:LEU:HD23	22:V:151:HIS:N	2.32	0.44
1:A:570:G:H2'	1:A:2030:A:C5	2.52	0.44
8:H:7:GLU:OE1	8:H:8:PRO:HD2	2.16	0.44
12:L:57:THR:C	12:L:59:LEU:H	2.21	0.44
10:J:116:THR:O	10:J:118:PRO:HD3	2.18	0.44
6:F:115:ARG:CD	6:F:115:ARG:H	2.31	0.44
1:A:17:G:H2'	1:A:18:C:C6	2.52	0.44
1:A:404:C:H4'	1:A:405:U:H5'	1.99	0.44
6:F:174:GLU:HG2	6:F:180:PHE:HD1	1.80	0.44
1:A:1487:G:H2'	1:A:1488:G:H8	1.81	0.44
1:A:142:G:H1'	20:T:37:THR:CG2	2.47	0.44
21:U:15:VAL:HG22	21:U:72:VAL:HG12	1.99	0.44
13:M:141:GLN:HE21	22:V:72:ARG:HG2	1.82	0.44
6:F:172:LEU:O	6:F:176:LEU:HG	2.17	0.44
10:J:116:THR:OG1	10:J:117:HIS:N	2.51	0.44
8:H:6:LEU:HD23	8:H:36:ALA:HA	1.99	0.44
1:A:2849:U:H4'	1:A:2868:A:C2	2.52	0.44
22:V:6:LYS:HG3	22:V:8:TYR:CZ	2.53	0.44
1:A:363(C):G:H2'	1:A:363(D):G:H8	1.83	0.44
1:A:357:A:H2'	1:A:358:U:C6	2.52	0.44
1:A:2820:A:O4'	14:N:5:LYS:HG3	2.17	0.44
22:V:54:HIS:CG	22:V:101:PRO:HG3	2.53	0.44
19:S:22:ASP:HA	19:S:25:ARG:HH12	1.83	0.44
1:A:71:A:C2	20:T:31:HIS:CE1	3.04	0.44
14:N:54:LEU:HD22	14:N:66:VAL:HG23	2.00	0.44
1:A:572:A:H5''	1:A:573:G:OP2	2.17	0.44
8:H:83:ALA:CA	8:H:89:TYR:HD1	2.29	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1654:A:OP2	14:N:3:HIS:NE2	2.51	0.44
7:G:123:PHE:HA	7:G:133:VAL:HA	1.99	0.44
1:A:1030:G:OP2	13:M:128:LYS:HE3	2.17	0.44
3:C:108:PRO:HB3	3:C:143:HIS:CE1	2.52	0.44
7:G:22:GLY:C	7:G:23:ARG:HD3	2.38	0.44
16:P:107:ASP:OD2	16:P:109:GLU:HB2	2.17	0.44
10:J:161:LEU:N	10:J:161:LEU:HD23	2.32	0.44
4:D:93:VAL:HG21	4:D:177:PRO:HA	1.99	0.44
12:L:65:ARG:N	12:L:65:ARG:HD2	2.33	0.44
29:3:41:PRO:HG3	29:3:49:HIS:HE1	1.82	0.44
3:C:226:MET:HB3	3:C:230:ASP:HB2	2.00	0.44
1:A:466:A:N3	1:A:683:C:H1'	2.32	0.44
4:D:176:ILE:HD12	4:D:176:ILE:N	2.33	0.44
4:D:176:ILE:O	4:D:176:ILE:HG22	2.17	0.44
1:A:1733:G:H8	1:A:1733:G:O5'	2.01	0.44
21:U:75:ILE:HG12	21:U:76:CYS:N	2.32	0.44
21:U:81:LYS:NZ	21:U:99:CYS:SG	2.91	0.44
13:M:141:GLN:N	22:V:53:ILE:HB	2.33	0.44
3:C:35:LYS:HB3	3:C:36:PRO:HD3	2.00	0.44
3:C:235:GLY:O	3:C:237:GLU:N	2.45	0.44
4:D:47:VAL:HG23	4:D:84:PHE:O	2.18	0.44
3:C:10:THR:HG23	3:C:13:ARG:HB2	1.97	0.44
1:A:2346:A:C2	1:A:2383:G:C2	3.06	0.44
1:A:813:U:H2'	1:A:814:C:C6	2.52	0.44
10:J:149:PRO:O	10:J:150:ASP:HB2	2.17	0.44
22:V:5:LEU:HD21	22:V:39:VAL:HB	1.99	0.44
22:V:110:GLY:HA2	22:V:146:ILE:HG23	1.99	0.44
1:A:1028:A:H61	1:A:1125:G:H2'	1.83	0.44
14:N:109:ALA:HA	14:N:110:PRO:HD3	1.84	0.44
22:V:54:HIS:HB3	22:V:101:PRO:HD3	1.99	0.44
4:D:190:GLY:HA2	4:D:191:PRO:HD3	1.74	0.44
1:A:2450:A:O2'	1:A:2451:A:H5'	2.18	0.44
1:A:1483:G:H2'	1:A:1484:G:C8	2.53	0.44
5:E:82:ILE:O	5:E:82:ILE:HG13	2.17	0.44
17:Q:92:ARG:CD	17:Q:95:LEU:H	2.31	0.44
17:Q:112:ARG:NH2	18:R:46:VAL:HG21	2.33	0.44
20:T:21:PHE:CD2	20:T:26:TYR:HD2	2.35	0.44
1:A:637:A:OP2	12:L:115:LEU:HB2	2.17	0.44
21:U:4:LYS:HD3	21:U:4:LYS:H	1.83	0.44
24:X:11:ARG:NH1	24:X:61:ARG:H	2.16	0.44
3:C:120:GLY:O	3:C:131:LEU:HB3	2.17	0.44
12:L:12:ALA:HB1	12:L:16:ARG:HB2	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:X:90:ILE:O	24:X:94:LEU:N	2.50	0.44
3:C:16:MET:HE1	3:C:208:LYS:HG2	1.99	0.44
1:A:1308:A:N6	1:A:1309:G:C2	2.86	0.44
14:N:11:ASN:O	14:N:12:ARG:HB2	2.18	0.44
6:F:16:ARG:HB3	6:F:17:PRO:CD	2.48	0.44
1:A:649:G:C5	1:A:650:C:C4	3.05	0.44
10:J:78:VAL:O	10:J:79:ASN:HB2	2.18	0.44
12:L:35:HIS:O	12:L:36:LYS:HB2	2.17	0.44
3:C:222:ARG:HH12	3:C:239:ARG:CZ	2.31	0.44
16:P:27:THR:HG22	16:P:90:GLN:HB3	1.98	0.44
1:A:1652:A:H2'	1:A:1653:G:O4'	2.18	0.44
1:A:598:G:H5'	12:L:15:ARG:CB	2.48	0.44
19:S:10:VAL:O	19:S:12:ILE:N	2.50	0.44
1:A:1615:C:C5	1:A:1617:C:C4	3.06	0.44
1:A:2591:C:H2'	1:A:2592:G:C8	2.53	0.44
1:A:1526:G:H2'	1:A:1527:G:C8	2.53	0.44
18:R:38:LEU:C	18:R:39:LEU:HD22	2.38	0.44
1:A:2285:C:H41	29:3:25:LYS:NZ	2.15	0.44
3:C:33:LEU:O	3:C:36:PRO:HD2	2.18	0.44
25:Y:16:LEU:N	25:Y:16:LEU:HD22	2.33	0.44
3:C:228:PRO:HD3	3:C:234:GLY:O	2.18	0.44
14:N:9:LYS:HD3	14:N:43:GLU:OE1	2.18	0.44
1:A:2376:A:H61	15:O:89:ARG:HG3	1.82	0.44
22:V:141:VAL:HA	22:V:144:LEU:HD23	2.00	0.44
19:S:14:PRO:O	19:S:18:ARG:HG3	2.18	0.44
2:B:102:G:H1'	22:V:73:GLN:HE22	1.82	0.44
1:A:322:A:P	5:E:169:ASN:HB2	2.58	0.44
5:E:11:VAL:HG13	5:E:196:LEU:HD21	2.00	0.44
3:C:72:LYS:HE3	3:C:101:GLU:HB3	1.99	0.44
1:A:1536:A:H5''	1:A:1537:C:OP2	2.17	0.44
1:A:405:U:H3'	1:A:406:G:C5'	2.48	0.44
4:D:77:ILE:HG22	4:D:78:LEU:N	2.33	0.44
1:A:1328:G:H2'	1:A:1330:C:C5	2.52	0.44
30:4:13:ALA:O	30:4:17:GLY:HA3	2.17	0.44
30:4:3:ARG:HA	30:4:3:ARG:HD3	1.75	0.44
27:1:46:ASN:HB2	27:1:64:LYS:CB	2.47	0.43
14:N:10:LEU:CB	14:N:17:ARG:NE	2.74	0.43
12:L:16:ARG:NH2	12:L:18:ARG:H	2.15	0.43
22:V:106:GLY:HA3	22:V:142:SER:HG	1.83	0.43
1:A:1694:C:C6	1:A:1694:C:C5'	2.96	0.43
1:A:863:A:OP1	13:M:21:THR:HB	2.18	0.43
12:L:27:HIS:CE1	18:R:83:ARG:HH12	2.35	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2094:G:OP1	8:H:22:LYS:HD2	2.17	0.43
8:H:29:TYR:C	8:H:32:PRO:HD2	2.38	0.43
1:A:616:A:C4'	1:A:617:G:OP1	2.66	0.43
1:A:2709:G:O2'	1:A:2710:C:H5'	2.18	0.43
1:A:2096:U:H2'	1:A:2097:C:C6	2.53	0.43
12:L:101:VAL:HG23	12:L:108:LYS:H	1.83	0.43
1:A:1285:G:C5	1:A:1329:U:C4	3.06	0.43
21:U:63:LYS:HE3	21:U:63:LYS:HB2	1.80	0.43
1:A:941:A:H4'	12:L:35:HIS:CD2	2.54	0.43
18:R:40:LEU:H	18:R:47:VAL:CG2	2.31	0.43
18:R:6:LYS:O	18:R:6:LYS:HG3	2.19	0.43
1:A:114(B):A:O2'	1:A:1143:A:H3'	2.17	0.43
21:U:6:HIS:O	21:U:7:VAL:O	2.35	0.43
1:A:1211:U:H4'	1:A:1212:G:OP2	2.18	0.43
15:O:26:LEU:HG	15:O:39:ILE:HD11	2.00	0.43
20:T:70:LEU:C	20:T:70:LEU:HD23	2.39	0.43
1:A:479:A:HO2'	1:A:481:G:H8	1.64	0.43
7:G:107:VAL:HG23	7:G:109:PHE:CE1	2.52	0.43
1:A:500:G:N2	1:A:502:A:H2'	2.33	0.43
25:Y:19:VAL:HG12	25:Y:23:LYS:HE3	2.00	0.43
15:O:36:TYR:HD1	15:O:36:TYR:H	1.64	0.43
1:A:2257:U:O2'	1:A:2258:C:H5'	2.18	0.43
1:A:699:A:H4'	1:A:1634:A:N7	2.33	0.43
18:R:89:GLN:HA	18:R:90:PRO:HD3	1.81	0.43
14:N:33:ARG:HG3	14:N:115:GLU:HG3	1.98	0.43
22:V:152:ALA:N	22:V:169:GLU:O	2.49	0.43
3:C:175:LEU:HD12	3:C:185:VAL:HG21	2.00	0.43
4:D:203:LYS:O	4:D:203:LYS:HD2	2.18	0.43
8:H:115:ALA:HB3	8:H:129:THR:O	2.18	0.43
1:A:1826:G:H2'	1:A:1827:C:H6	1.82	0.43
10:J:42:GLU:O	10:J:42:GLU:HG3	2.18	0.43
6:F:66:GLN:NE2	6:F:94:LEU:HB3	2.33	0.43
24:X:10:LYS:O	24:X:11:ARG:CG	2.66	0.43
26:Z:22:ALA:O	26:Z:26:LEU:HG	2.18	0.43
3:C:30:GLU:HG3	3:C:63:ARG:CZ	2.48	0.43
1:A:662:G:OP1	12:L:18:ARG:HD2	2.18	0.43
22:V:137:ILE:N	22:V:137:ILE:HD12	2.33	0.43
29:3:11:LEU:HA	29:3:11:LEU:HD22	1.89	0.43
1:A:2271:G:H2'	1:A:2272:U:H6	1.82	0.43
1:A:36:G:C5	1:A:37:C:C5	3.06	0.43
6:F:126:ASP:OD2	6:F:130:ASN:HB2	2.18	0.43
1:A:1655:A:H4'	4:D:115:GLY:N	2.33	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2050:C:H2'	1:A:2051:A:C8	2.53	0.43
17:Q:25:TRP:O	17:Q:28:ARG:HB3	2.18	0.43
3:C:166:GLN:HB2	3:C:174:ILE:HG22	2.00	0.43
1:A:1272:A:O2'	1:A:1273:U:H5'	2.18	0.43
1:A:2658:C:H4'	7:G:158:HIS:CE1	2.53	0.43
1:A:1525:G:H2'	1:A:1526:G:C8	2.54	0.43
1:A:2550:G:C6	1:A:2551:C:C4	3.07	0.43
1:A:997:G:O2'	1:A:998:C:H5'	2.18	0.43
1:A:836:G:H2'	1:A:837:C:C6	2.53	0.43
1:A:685:A:H1'	1:A:688:U:O4	2.18	0.43
15:O:98:VAL:O	15:O:101:LEU:HB2	2.18	0.43
25:Y:9:GLN:O	25:Y:12:GLU:HB3	2.19	0.43
16:P:61:PHE:CZ	16:P:76:PHE:HB2	2.54	0.43
1:A:479:A:H4'	1:A:480:A:O5'	2.18	0.43
25:Y:21:LEU:CD2	25:Y:22:GLU:HG3	2.49	0.43
1:A:1050:A:H2'	1:A:1051:G:C8	2.54	0.43
1:A:2590:A:H2'	1:A:2591:C:C6	2.54	0.43
1:A:869:G:C2	1:A:870:A:C8	3.06	0.43
1:A:816:C:H2'	1:A:817:C:H6	1.83	0.43
4:D:107:THR:O	4:D:190:GLY:HA2	2.18	0.43
1:A:2515:C:H1'	1:A:2570:G:N2	2.33	0.43
1:A:969:U:H2'	1:A:970:C:C6	2.53	0.43
1:A:1818:U:H2'	3:C:157:ARG:HG3	2.00	0.43
1:A:1461:G:O2'	1:A:1462:C:H5'	2.18	0.43
1:A:1717:G:C6	1:A:1743:G:C6	3.07	0.43
1:A:251:A:H5''	12:L:51:PHE:CE1	2.53	0.43
1:A:1826:G:H2'	1:A:1827:C:C6	2.53	0.43
1:A:2247:A:H2'	1:A:2248:C:H6	1.83	0.43
1:A:956:G:OP1	13:M:86:GLY:N	2.48	0.43
15:O:17:ARG:HG2	15:O:18:ILE:HD13	2.00	0.43
28:2:33:CYS:HB2	28:2:34:PRO:HD2	2.01	0.43
7:G:42:ARG:O	7:G:52:VAL:HA	2.18	0.43
3:C:142:VAL:HG23	3:C:192:THR:C	2.38	0.43
29:3:11:LEU:HD13	29:3:12:GLU:H	1.83	0.43
1:A:778:G:C5	1:A:779:U:C4	3.07	0.43
7:G:20:ALA:HB1	7:G:21:PRO:CD	2.47	0.43
1:A:1693:U:H1'	3:C:14:ARG:NH2	2.34	0.43
22:V:8:TYR:HB2	22:V:38:TYR:CE2	2.52	0.43
1:A:719:C:H2'	1:A:720:C:C6	2.53	0.43
1:A:532:A:N1	1:A:2020:A:H1'	2.34	0.43
5:E:50:SER:HA	5:E:92:PRO:O	2.17	0.43
1:A:1748:G:H2'	1:A:1749:A:H8	1.84	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:20:LEU:HD12	18:R:21:ARG:H	1.82	0.43
18:R:27:ALA:HB3	18:R:61:VAL:HG11	1.99	0.43
16:P:35:LYS:HB2	16:P:35:LYS:HE3	1.89	0.43
1:A:2015:A:N3	28:2:2:ALA:N	2.66	0.43
16:P:26:ASP:OD1	16:P:26:ASP:O	2.36	0.43
21:U:11:ASP:H	21:U:27:VAL:CG2	2.32	0.43
1:A:2286:A:C8	1:A:2287:A:N6	2.87	0.43
14:N:10:LEU:HD22	14:N:17:ARG:HD3	2.00	0.43
24:X:19:GLN:HG2	24:X:41:ARG:CB	2.46	0.43
1:A:1478:G:HO2'	1:A:1558:A:H2	1.63	0.43
12:L:8:PRO:C	12:L:10:PRO:HD3	2.39	0.43
27:1:48:ILE:N	27:1:48:ILE:HD12	2.34	0.43
18:R:61:VAL:HG23	18:R:61:VAL:O	2.18	0.43
1:A:2086:U:H2'	1:A:2087:G:C8	2.54	0.43
24:X:75:GLU:OE1	24:X:75:GLU:HA	2.19	0.43
12:L:86:LYS:HG3	12:L:87:ASP:N	2.34	0.43
3:C:25:THR:HG23	3:C:27:THR:HG22	2.01	0.43
31:5:21:LYS:HA	31:5:54:GLU:OE2	2.18	0.43
1:A:644:A:C2	1:A:646:A:C4	3.07	0.43
1:A:2850:A:H5''	1:A:2868:A:H2	1.83	0.43
13:M:104:PHE:HE1	13:M:125:LEU:HD11	1.83	0.43
1:A:379:G:N2	24:X:20:ARG:NH1	2.66	0.43
1:A:2839:G:C5	1:A:2840:C:C4	3.07	0.43
15:O:38:GLN:HB3	15:O:47:THR:HG23	1.99	0.43
22:V:40:ASP:OD1	22:V:42:VAL:HG12	2.19	0.43
1:A:519:U:H2'	1:A:520:G:H8	1.82	0.43
1:A:1464:C:H2'	1:A:1465:G:C8	2.54	0.43
26:Z:16:PRO:HB2	26:Z:18:ASP:OD1	2.18	0.43
1:A:2748:A:C2	1:A:2757:A:C4	3.06	0.43
5:E:70:THR:HG23	5:E:72:ARG:H	1.83	0.43
7:G:86:GLU:CD	7:G:86:GLU:H	2.22	0.43
8:H:72:LEU:HD12	8:H:140:LEU:CD1	2.48	0.43
14:N:8:ARG:CZ	14:N:43:GLU:HG3	2.49	0.43
1:A:644:A:O2'	1:A:645:C:H5''	2.18	0.43
15:O:31:SER:HB3	15:O:34:HIS:H	1.84	0.43
1:A:322:A:O4'	1:A:340:A:H1'	2.19	0.43
3:C:235:GLY:C	3:C:237:GLU:H	2.22	0.43
29:3:44:ARG:HB3	29:3:45:LYS:H	1.67	0.43
22:V:118:GLN:HG3	22:V:175:VAL:HG13	2.00	0.43
10:J:160:LYS:HD2	10:J:161:LEU:H	1.83	0.43
4:D:78:LEU:C	4:D:79:ARG:HD2	2.38	0.43
1:A:1239:G:O2'	1:A:1240:U:H5'	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:78:GLY:HA2	7:G:83:TYR:CE1	2.54	0.43
1:A:708:C:H6	1:A:708:C:O5'	2.01	0.43
1:A:843:G:C8	1:A:843:G:H5''	2.54	0.43
17:Q:79:PHE:HE2	17:Q:106:PHE:CZ	2.36	0.43
12:L:114:ILE:CD1	12:L:130:PHE:CD1	2.92	0.43
21:U:13:VAL:CG1	21:U:72:VAL:HB	2.48	0.43
22:V:71:VAL:HA	22:V:87:ASP:O	2.18	0.43
3:C:35:LYS:HZ1	3:C:104:TYR:H	1.66	0.43
12:L:57:THR:CG2	12:L:59:LEU:HB2	2.48	0.43
6:F:84:LYS:HG3	6:F:85:GLY:H	1.84	0.43
1:A:2562:U:H1'	11:K:23:ARG:HH12	1.81	0.43
22:V:38:TYR:CD1	22:V:38:TYR:O	2.72	0.43
14:N:104:ARG:HH11	14:N:104:ARG:HB2	1.84	0.43
1:A:433:C:O2'	1:A:434:U:H5'	2.19	0.43
1:A:2330:G:O2'	23:W:41:ARG:HB2	2.17	0.43
3:C:140:THR:O	3:C:165:ILE:HD12	2.18	0.43
1:A:2768:C:C4	1:A:2769:C:C5	3.07	0.43
1:A:2891:G:O5'	1:A:2891:G:H8	2.01	0.43
1:A:1191:G:OP1	12:L:35:HIS:CD2	2.72	0.43
6:F:5:LEU:O	6:F:8:LYS:HB3	2.19	0.43
23:W:43:THR:HG22	23:W:43:THR:O	2.19	0.43
26:Z:26:LEU:HB2	26:Z:28:LEU:CD1	2.48	0.43
1:A:643:A:C2	1:A:644:A:C4	3.07	0.43
1:A:1335:U:H2'	1:A:1336:A:C8	2.54	0.43
1:A:907:U:O2'	13:M:101:ARG:NH2	2.46	0.43
2:B:65:C:O2'	2:B:66:A:H5'	2.18	0.43
1:A:2777:G:H4'	1:A:2778:A:H5'	2.01	0.43
20:T:93:GLU:O	20:T:94:GLY:C	2.56	0.43
1:A:102:G:C8	1:A:102:G:H5''	2.54	0.43
1:A:302:C:O2'	1:A:303:U:H5'	2.19	0.43
1:A:855:G:H2'	1:A:856:C:H6	1.84	0.43
1:A:1961:C:O2'	1:A:1962:C:H5'	2.18	0.43
1:A:1232:G:H2'	1:A:1233:C:H6	1.84	0.43
25:Y:15:LYS:HA	25:Y:15:LYS:HE2	2.01	0.43
12:L:80:TYR:CE1	12:L:111:ARG:HG2	2.53	0.42
31:5:32:LEU:HD23	31:5:33:ASN:H	1.83	0.42
5:E:63:LYS:HZ1	5:E:67:GLN:NE2	2.17	0.42
3:C:132:PRO:HA	3:C:190:TYR:HA	2.01	0.42
22:V:48:PHE:CE2	22:V:71:VAL:HG21	2.54	0.42
3:C:27:THR:O	3:C:27:THR:CG2	2.62	0.42
3:C:32:SER:O	3:C:33:LEU:O	2.36	0.42
21:U:17:SER:HB2	21:U:71:LYS:HD2	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:197:ILE:HD11	4:D:199:ARG:HE	1.84	0.42
1:A:661:C:H2'	1:A:662:G:H8	1.83	0.42
6:F:161:THR:HG21	6:F:172:LEU:HD23	2.01	0.42
28:2:44:THR:HG22	28:2:45:VAL:N	2.34	0.42
13:M:24:GLY:HA2	13:M:100:GLY:C	2.39	0.42
1:A:1405:U:H2'	1:A:1406:U:H6	1.79	0.42
1:A:477:A:H2'	1:A:478:A:C8	2.54	0.42
4:D:36:ARG:HD3	4:D:85:ASN:HD21	1.84	0.42
4:D:111:ARG:HD2	4:D:160:TYR:HE1	1.84	0.42
1:A:1576:U:C2	1:A:1577:C:C5	3.07	0.42
1:A:116:C:O2'	1:A:117:G:H5'	2.19	0.42
1:A:2846:G:H2'	1:A:2847:U:C6	2.53	0.42
31:5:29:LYS:HG2	31:5:29:LYS:O	2.19	0.42
1:A:993:G:H1'	18:R:89:GLN:OE1	2.19	0.42
17:Q:59:ARG:O	17:Q:63:VAL:HG23	2.19	0.42
1:A:2389:G:H5''	1:A:2390:U:H5'	2.00	0.42
1:A:26:G:C6	1:A:27:G:N1	2.88	0.42
1:A:460:A:C6	1:A:470:A:C8	3.07	0.42
17:Q:90:VAL:O	17:Q:92:ARG:N	2.52	0.42
1:A:2394:C:H2'	1:A:2395:C:H6	1.84	0.42
20:T:35:THR:HB	20:T:38:GLU:H	1.84	0.42
6:F:8:LYS:O	6:F:12:TYR:HD1	2.02	0.42
15:O:49:VAL:HG13	15:O:76:LYS:HB2	2.01	0.42
1:A:2712:U:O2'	1:A:2713:A:H5'	2.19	0.42
1:A:848:G:N9	1:A:933:A:H8	2.16	0.42
31:5:14:VAL:HG22	31:5:24:ALA:HB2	2.01	0.42
1:A:1310:G:C3'	1:A:1311:G:H5''	2.49	0.42
1:A:2343:C:O2'	1:A:2344:U:H5'	2.19	0.42
1:A:1612:C:O3'	30:4:5:TRP:HD1	2.02	0.42
2:B:73:A:C4	2:B:104:A:C2	3.07	0.42
16:P:98:LYS:HB3	16:P:100:TYR:HE1	1.82	0.42
6:F:129:GLY:HA3	6:F:163:ALA:HB3	2.01	0.42
16:P:64:ARG:HA	16:P:72:VAL:O	2.19	0.42
8:H:66:GLU:O	8:H:70:GLU:HG2	2.20	0.42
24:X:45:ASN:HD21	24:X:47:GLN:NE2	2.17	0.42
1:A:2852:G:H2'	1:A:2853:C:C6	2.54	0.42
1:A:2846:G:H2'	1:A:2847:U:H6	1.84	0.42
17:Q:60:LEU:O	17:Q:60:LEU:HD23	2.19	0.42
1:A:616:A:H4'	1:A:617:G:OP1	2.19	0.42
1:A:2626:C:H2'	1:A:2627:G:O4'	2.19	0.42
7:G:122:THR:O	7:G:134:SER:HB2	2.19	0.42
1:A:1546:A:H2'	1:A:154(B):C:O4'	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:93:LYS:HB3	10:J:110:LEU:HB2	2.01	0.42
1:A:284:U:H2'	1:A:285:C:C6	2.54	0.42
1:A:1688:U:O2	1:A:1700:A:H8	2.02	0.42
1:A:2527:C:O5'	1:A:2527:C:H6	2.01	0.42
17:Q:92:ARG:HH21	18:R:11:GLN:H	1.67	0.42
5:E:63:LYS:NZ	5:E:67:GLN:NE2	2.67	0.42
1:A:910:A:C6	1:A:911:A:C6	3.08	0.42
13:M:141:GLN:NE2	22:V:72:ARG:HG2	2.35	0.42
4:D:171:GLU:HG3	4:D:171:GLU:O	2.19	0.42
11:K:71:ARG:HH12	16:P:74:ARG:NH2	2.11	0.42
6:F:13:GLU:O	6:F:14:GLU:HB2	2.19	0.42
22:V:102:LEU:HD21	22:V:124:ILE:HD11	2.02	0.42
1:A:94:G:N3	25:Y:47:ASN:ND2	2.66	0.42
1:A:2272:U:H5''	1:A:2273:A:OP1	2.19	0.42
1:A:840:C:H2'	1:A:841:A:C8	2.54	0.42
1:A:2563:U:H4'	11:K:28:SER:HA	2.00	0.42
16:P:56:GLY:O	16:P:59:THR:HG22	2.20	0.42
1:A:628:G:C6	1:A:636:G:C2	3.07	0.42
1:A:1790:C:H5''	1:A:1791:A:P	2.59	0.42
1:A:1536:A:O5'	1:A:1536:A:H8	2.02	0.42
1:A:471:A:O5'	1:A:471:A:H8	2.02	0.42
1:A:1683:C:H2'	1:A:1684:C:C6	2.55	0.42
1:A:2364:C:H1'	23:W:36:ILE:HD11	2.01	0.42
1:A:1414:G:C4	1:A:1415:U:C5	3.07	0.42
22:V:128:VAL:CG2	22:V:132:ASN:HB2	2.49	0.42
10:J:85:VAL:HG22	10:J:89:LYS:HG3	2.00	0.42
1:A:286:C:H2'	1:A:287:C:H6	1.83	0.42
14:N:55:ALA:HA	14:N:80:PHE:CE1	2.54	0.42
10:J:157:ARG:HG2	10:J:157:ARG:O	2.20	0.42
10:J:38:LEU:HD13	10:J:39:ILE:N	2.34	0.42
20:T:30:VAL:HG21	20:T:79:ALA:CB	2.50	0.42
1:A:637:A:C5'	12:L:116:GLY:HA2	2.49	0.42
1:A:572:A:H2'	1:A:573:G:O4'	2.20	0.42
8:H:88:ILE:HG13	8:H:144:VAL:HG11	2.02	0.42
21:U:31:LEU:HD23	21:U:31:LEU:N	2.26	0.42
2:B:73:A:H3'	2:B:74:U:C6	2.54	0.42
1:A:2777:G:H3'	1:A:2777:G:H8	1.84	0.42
24:X:35:THR:HB	24:X:36:GLY:H	1.54	0.42
1:A:301:G:H5'	1:A:334:C:O2'	2.19	0.42
13:M:66:ILE:HG22	13:M:104:PHE:HD2	1.82	0.42
1:A:1833:U:N3	1:A:1834:U:C5	2.88	0.42
1:A:2572:A:C8	4:D:144:ARG:HB3	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:150:C:H2'	1:A:151:C:H6	1.83	0.42
1:A:1324:G:H4'	1:A:1616:A:C2	2.54	0.42
1:A:909:A:C4	1:A:912:C:C5	3.07	0.42
14:N:100:LEU:HD21	14:N:113:LEU:HB2	2.02	0.42
1:A:1229:G:H2'	1:A:1230:C:C6	2.54	0.42
6:F:34:LEU:HD21	6:F:159:VAL:HG21	2.00	0.42
1:A:2716:U:O2'	1:A:2717:G:H5'	2.19	0.42
1:A:1954:G:N2	1:A:1956:U:H3	2.18	0.42
1:A:1648:C:H2'	1:A:1649:G:O5'	2.19	0.42
1:A:1109:C:H2'	1:A:1110:G:O4'	2.19	0.42
1:A:846:C:C2	1:A:847:U:C5	3.07	0.42
1:A:643:A:O2'	1:A:644:A:H5'	2.19	0.42
1:A:1541:U:C3'	1:A:1542:G:O3'	2.66	0.42
5:E:160:ASN:ND2	5:E:162:LEU:H	2.18	0.42
1:A:332:A:O2'	1:A:334:C:OP2	2.30	0.42
22:V:9:TYR:O	22:V:38:TYR:HE2	2.02	0.42
19:S:4:LYS:HA	19:S:106:ILE:HG22	2.02	0.42
13:M:26:TYR:CD1	13:M:26:TYR:O	2.72	0.42
4:D:11:MET:CB	4:D:24:THR:HA	2.50	0.42
1:A:335:C:C2	1:A:336:C:C5	3.07	0.42
4:D:110:GLY:HA2	4:D:162:ALA:HB2	2.01	0.42
1:A:1759:A:C8	1:A:2696:U:H1'	2.53	0.42
2:B:16:G:C6	2:B:69:G:C2	3.08	0.42
5:E:9:ILE:H	5:E:9:ILE:HD13	1.83	0.42
17:Q:79:PHE:HE1	17:Q:83:LEU:CD2	2.32	0.42
18:R:40:LEU:C	18:R:45:THR:HB	2.40	0.42
18:R:45:THR:O	18:R:46:VAL:C	2.56	0.42
27:1:42:CYS:HA	27:1:59:VAL:C	2.40	0.42
13:M:141:GLN:OXT	22:V:98:MET:HE3	2.19	0.42
7:G:46:GLU:HG3	7:G:51:ARG:CD	2.49	0.42
1:A:2809:A:N6	1:A:2892:A:C8	2.88	0.42
1:A:1996:C:H5	11:K:32:TYR:OH	2.03	0.42
13:M:74:TYR:O	13:M:89:ASN:N	2.53	0.42
8:H:118:LYS:HA	8:H:119:PRO:HD3	1.86	0.42
1:A:2767:C:H2'	1:A:2768:C:H6	1.84	0.42
13:M:18:LYS:HB3	13:M:19:GLY:H	1.63	0.42
1:A:536:A:H2'	1:A:537:C:C6	2.55	0.42
1:A:540:G:C4	1:A:541:C:C5	3.08	0.42
1:A:2212:A:HO2'	1:A:2215:G:C1'	2.32	0.42
3:C:218:ARG:HG3	3:C:218:ARG:HH11	1.84	0.42
22:V:70:LEU:HD23	22:V:70:LEU:N	2.34	0.42
1:A:588:U:H2'	1:A:589:C:H6	1.82	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:47:ASP:HB3	12:L:48:PRO:CA	2.49	0.42
1:A:1828:G:OP2	3:C:239:ARG:NH2	2.53	0.42
1:A:72:U:O2'	1:A:73:A:H5'	2.19	0.42
1:A:2711:A:OP1	1:A:712(B):A:P	2.78	0.42
4:D:91:VAL:CB	4:D:95:ILE:HD11	2.43	0.42
1:A:2262:U:H4'	1:A:2328:A:C2	2.55	0.42
3:C:31:LYS:HG3	3:C:33:LEU:HG	2.02	0.42
3:C:27:THR:CG2	3:C:83:GLU:HG2	2.50	0.42
3:C:147:LEU:HD13	3:C:155:LEU:CD1	2.45	0.42
24:X:43:TYR:HA	24:X:44:PRO:HD3	1.77	0.42
1:A:2484:G:C2	1:A:2485:G:C8	3.07	0.42
1:A:804:A:H5''	1:A:805:G:OP1	2.20	0.42
1:A:1678:G:O5'	1:A:1678:G:C8	2.64	0.42
17:Q:62:ILE:HD12	17:Q:76:TYR:CZ	2.54	0.42
29:3:34:LEU:HD13	29:3:34:LEU:H	1.85	0.42
3:C:79:VAL:HG11	3:C:111:LEU:CD1	2.50	0.42
12:L:7:ARG:O	12:L:10:PRO:HD3	2.19	0.42
1:A:426:C:C2	1:A:427:U:C5	3.08	0.42
25:Y:56:GLN:O	25:Y:60:LEU:HG	2.20	0.42
1:A:919:G:H2'	1:A:920:G:H8	1.85	0.42
1:A:56:A:C2	1:A:115:C:O2	2.73	0.42
1:A:2090:G:H21	24:X:45:ASN:HD21	1.67	0.42
1:A:363(D):G:H2'	1:A:363(E):G:C8	2.55	0.42
19:S:107:LEU:N	19:S:107:LEU:CD1	2.82	0.42
7:G:96:ALA:CB	7:G:105:LEU:HB3	2.49	0.42
1:A:286:C:C2	1:A:287:C:C5	3.07	0.42
10:J:35:ARG:O	10:J:73:ASP:HB3	2.20	0.42
1:A:665:C:O2'	1:A:666:G:H5'	2.20	0.42
13:M:130:LYS:HG2	13:M:131:ILE:N	2.33	0.42
4:D:97:LYS:HE2	4:D:97:LYS:HB3	1.91	0.42
1:A:2444:G:C6	1:A:2445:G:C5	3.08	0.42
10:J:40:ASP:OD1	10:J:42:GLU:HG2	2.20	0.42
1:A:948:G:OP1	1:A:962:G:OP1	2.38	0.42
6:F:111:LEU:N	6:F:112:PRO:CD	2.83	0.42
8:H:101:LEU:HG	8:H:107:ILE:CG2	2.49	0.42
19:S:18:ARG:HG2	19:S:76:VAL:HG11	2.02	0.42
14:N:2:ARG:HB3	14:N:3:HIS:CE1	2.54	0.42
5:E:106:ARG:H	5:E:106:ARG:HG2	1.54	0.42
18:R:28:GLU:OE1	18:R:31:ALA:HB2	2.19	0.42
1:A:514:A:H1'	1:A:581:C:O2'	2.19	0.42
3:C:105:ILE:HG13	3:C:106:ILE:HD12	2.02	0.42
1:A:2536:G:C6	1:A:2537:U:C4	3.08	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:260:ARG:O	3:C:261:LYS:C	2.58	0.42
1:A:1751:C:H2'	1:A:1752:C:C6	2.54	0.42
1:A:1465:G:C2	1:A:1466:G:C8	3.07	0.42
16:P:131:ALA:O	16:P:135:VAL:HG23	2.20	0.42
1:A:1107:G:O2'	1:A:1108:U:H5'	2.19	0.42
4:D:17:ASP:OD1	4:D:18:ASP:N	2.52	0.42
21:U:34:LYS:HE2	21:U:34:LYS:HB3	1.80	0.42
17:Q:83:LEU:HG	17:Q:88:ILE:CD1	2.43	0.42
20:T:26:TYR:CE1	20:T:83:VAL:HG21	2.55	0.42
31:5:25:MET:SD	31:5:47:LYS:HG2	2.59	0.42
31:5:33:ASN:ND2	31:5:34:TRP:N	2.67	0.42
21:U:30:VAL:HG13	21:U:37:VAL:HG12	2.01	0.42
22:V:97:GLU:HB3	22:V:125:LEU:CD2	2.43	0.42
1:A:1579:A:H2'	1:A:1580:A:C8	2.55	0.42
1:A:307:G:N1	1:A:310:A:OP2	2.53	0.42
1:A:464:U:H4'	30:4:5:TRP:CZ3	2.54	0.42
22:V:179:ASP:CG	22:V:180:VAL:N	2.73	0.42
1:A:1349:A:N6	1:A:1598:C:H42	2.18	0.42
1:A:1951:U:O2	1:A:1953:A:H8	2.03	0.42
1:A:2686:G:C5	1:A:2687:U:C4	3.08	0.42
6:F:128:ARG:HH21	6:F:130:ASN:ND2	2.17	0.42
3:C:145:VAL:HG12	3:C:146:GLU:O	2.20	0.42
1:A:1655:A:O2'	4:D:115:GLY:HA2	2.19	0.42
29:3:30:THR:CG2	29:3:31:PRO:HD2	2.48	0.42
3:C:261:LYS:HB2	3:C:261:LYS:NZ	2.35	0.42
19:S:70:TYR:HD2	19:S:70:TYR:H	1.68	0.42
1:A:1464:C:O2	1:A:1528:A:H2	2.03	0.42
11:K:17:ARG:HB2	11:K:45:GLU:HG3	2.02	0.42
7:G:12:PRO:O	7:G:15:VAL:HG22	2.20	0.42
1:A:2194:G:H2'	1:A:2195:C:H6	1.84	0.42
1:A:173:G:H2'	1:A:174:C:C6	2.55	0.42
1:A:2396:G:O2'	1:A:2397:G:H5'	2.20	0.42
16:P:23:ARG:NH2	16:P:120:ARG:HD3	2.35	0.42
18:R:4:ILE:HG22	18:R:5:VAL:N	2.35	0.42
12:L:85:LEU:HD21	12:L:116:GLY:O	2.20	0.42
3:C:190:TYR:O	3:C:191:ALA:HB2	2.20	0.42
12:L:61:ARG:HH11	31:5:13:ARG:HD2	1.84	0.42
1:A:1334:G:C6	1:A:1335:U:C4	3.07	0.42
6:F:18:GLU:HB3	6:F:175:LEU:HD13	2.02	0.42
1:A:1447:G:N3	1:A:1545:A:H2	2.18	0.42
1:A:388:G:OP1	24:X:33:LYS:CB	2.68	0.42
2:B:106:G:C5	2:B:107:U:C5	3.08	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:128:ARG:HG2	6:F:129:GLY:H	1.85	0.42
1:A:311:A:C8	1:A:332:A:C5	3.07	0.42
11:K:22:ILE:HG12	11:K:42:SER:H	1.85	0.42
4:D:144:ARG:HB3	4:D:145:LYS:H	1.57	0.42
1:A:2050:C:H1'	4:D:156:MET:CE	2.49	0.42
1:A:161:U:HO2'	1:A:162:U:H5	1.66	0.42
1:A:2590:A:C2	1:A:2605:U:C2	3.08	0.42
18:R:1:MET:SD	18:R:42:GLY:HA3	2.60	0.42
19:S:30:GLU:HA	19:S:33:ARG:HD2	2.02	0.42
1:A:2762:G:O2'	1:A:2763:G:H5'	2.20	0.42
1:A:924:C:H2'	1:A:925:C:C6	2.55	0.42
2:B:33:G:O2'	2:B:34:U:H5'	2.20	0.42
1:A:2870:C:H2'	1:A:2871:C:O4'	2.19	0.42
12:L:62:LEU:HD22	12:L:62:LEU:N	2.35	0.41
2:B:72:G:N2	2:B:103:U:C5	2.88	0.41
6:F:15:VAL:HG22	6:F:175:LEU:HB3	2.02	0.41
25:Y:46:GLN:O	25:Y:47:ASN:CB	2.61	0.41
1:A:811:U:H3'	12:L:25:SER:O	2.20	0.41
1:A:2809:A:N1	1:A:2892:A:C4	2.88	0.41
1:A:1374:G:C5	1:A:1375:C:C5	3.08	0.41
1:A:320:A:H5''	1:A:321:G:OP1	2.19	0.41
14:N:94:TYR:O	14:N:117:VAL:HG12	2.20	0.41
14:N:100:LEU:HD23	14:N:112:ALA:HA	2.02	0.41
1:A:1851:U:H2'	1:A:1852:C:H6	1.85	0.41
1:A:1284:A:H2'	1:A:1285:G:O4'	2.20	0.41
1:A:2718:G:H2'	1:A:2719:G:C8	2.55	0.41
5:E:117:ARG:HD2	5:E:190:GLU:O	2.20	0.41
1:A:2338:G:C2	1:A:2339:G:C8	3.08	0.41
1:A:71:A:H4'	1:A:72:U:H5''	2.02	0.41
15:O:66:ALA:HA	15:O:69:VAL:HG12	2.02	0.41
24:X:11:ARG:HG3	24:X:62:VAL:HA	2.02	0.41
12:L:57:THR:HG23	12:L:59:LEU:HB3	1.99	0.41
1:A:2210:G:C3'	1:A:2210:G:N3	2.77	0.41
21:U:17:SER:CB	21:U:71:LYS:HD2	2.50	0.41
1:A:2287:A:C5	1:A:2289:G:C5	3.08	0.41
1:A:388:G:C4	1:A:390:A:C6	3.09	0.41
1:A:1486:A:N6	1:A:1504:C:N4	2.68	0.41
13:M:127:ILE:HG22	13:M:128:LYS:N	2.36	0.41
1:A:2306:C:H4'	6:F:136:ARG:NH2	2.34	0.41
3:C:126:GLN:HG2	3:C:127:VAL:H	1.85	0.41
1:A:1027:A:N6	1:A:1126:A:N9	2.67	0.41
3:C:105:ILE:HG12	3:C:106:ILE:HD12	2.01	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:P:110:ILE:HD12	16:P:110:ILE:HA	1.86	0.41
10:J:27:TYR:O	10:J:29:PRO:HD3	2.20	0.41
1:A:2723:C:O5'	1:A:2723:C:H6	2.03	0.41
7:G:144:VAL:O	7:G:148:ILE:HG12	2.20	0.41
3:C:202:LYS:HG3	3:C:203:ASN:OD1	2.19	0.41
1:A:2065:C:H2'	1:A:2066:C:C6	2.55	0.41
1:A:735:A:H3'	1:A:736:C:C6	2.54	0.41
1:A:2509:G:C5	1:A:2510:C:C5	3.08	0.41
22:V:157:LEU:N	22:V:157:LEU:HD12	2.35	0.41
1:A:826:U:H2'	1:A:828:U:O4'	2.20	0.41
21:U:14:LEU:C	21:U:14:LEU:HD23	2.40	0.41
6:F:5:LEU:HD21	27:1:50:THR:CG2	2.50	0.41
21:U:2:ARG:HG2	21:U:3:VAL:N	2.35	0.41
3:C:32:SER:HA	3:C:36:PRO:HG2	2.01	0.41
20:T:15:GLU:N	20:T:15:GLU:CD	2.62	0.41
13:M:24:GLY:HA2	13:M:101:ARG:CA	2.46	0.41
13:M:20:ALA:O	13:M:21:THR:O	2.38	0.41
5:E:111:ALA:HB2	5:E:206:ILE:HD12	2.00	0.41
1:A:448:U:H1'	5:E:84:VAL:HG21	2.02	0.41
1:A:2593:U:H2'	1:A:2594:C:H6	1.81	0.41
1:A:2476:A:N1	1:A:2477:C:C4	2.88	0.41
18:R:28:GLU:HB3	18:R:29:PRO:HD2	2.02	0.41
1:A:1496:A:C8	1:A:1577:C:O2'	2.71	0.41
1:A:2013:A:H4'	19:S:96:ILE:HD12	2.02	0.41
1:A:1354:A:H8	1:A:1354:A:O5'	2.03	0.41
1:A:2070:G:H2'	1:A:2071:A:O4'	2.20	0.41
30:4:47:ARG:O	30:4:48:LYS:HB2	2.20	0.41
1:A:1676:A:N6	1:A:1677:A:C6	2.88	0.41
16:P:115:ARG:HG2	16:P:115:ARG:H	1.51	0.41
12:L:67:MET:HA	12:L:67:MET:HE3	2.02	0.41
17:Q:106:PHE:HA	17:Q:109:LEU:HD12	2.02	0.41
10:J:88:LYS:O	10:J:92:GLN:HB3	2.20	0.41
12:L:62:LEU:HA	12:L:63:PRO:HD3	1.77	0.41
1:A:960:A:H61	13:M:82:ARG:NH2	2.18	0.41
5:E:181:LEU:CD2	5:E:186:ILE:HD11	2.50	0.41
1:A:796:C:H2'	1:A:797:C:H6	1.81	0.41
10:J:114:LEU:HA	10:J:118:PRO:HB3	2.01	0.41
3:C:69:ARG:HH12	3:C:117:VAL:HG21	1.85	0.41
5:E:39:TRP:CD1	5:E:101:LEU:HB2	2.56	0.41
1:A:595:C:H2'	1:A:596:G:O4'	2.21	0.41
16:P:100:TYR:C	16:P:102:ILE:N	2.74	0.41
16:P:77:PRO:HB2	16:P:80:SER:HB2	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:28:ARG:HG3	17:Q:38:THR:OG1	2.19	0.41
1:A:486:C:H4'	19:S:60:ASN:ND2	2.35	0.41
1:A:1289:C:H2'	1:A:1290:C:C6	2.55	0.41
23:W:14:ARG:HE	23:W:14:ARG:HB2	1.50	0.41
1:A:2783:G:N2	4:D:37:ARG:HH12	2.19	0.41
15:O:102:ALA:HA	15:O:105:ALA:HB3	2.03	0.41
1:A:1695:G:N2	1:A:1696:G:C8	2.88	0.41
1:A:312:G:H5'	1:A:331:A:H2'	2.01	0.41
1:A:2228:G:C6	1:A:2229:C:C4	3.09	0.41
1:A:1203:G:C6	1:A:1204:A:C6	3.09	0.41
26:Z:55:ARG:HD3	26:Z:55:ARG:HA	1.65	0.41
12:L:81:GLN:HE21	12:L:81:GLN:HB2	1.59	0.41
1:A:1140:C:OP1	10:J:46:LEU:HB3	2.21	0.41
1:A:2420:C:P	31:5:34:TRP:HA	2.60	0.41
7:G:86:GLU:HG2	7:G:164:TYR:O	2.19	0.41
3:C:35:LYS:CB	3:C:36:PRO:HD3	2.50	0.41
1:A:1493:C:C4	1:A:2210:G:O2'	2.73	0.41
1:A:342:G:O2'	1:A:343:C:H5''	2.21	0.41
10:J:57:LEU:HA	10:J:57:LEU:HD13	1.72	0.41
4:D:181:LEU:HA	4:D:181:LEU:HD13	1.73	0.41
1:A:1543:A:H8	1:A:1543:A:H3'	1.85	0.41
1:A:482:A:H8	1:A:482:A:O5'	2.04	0.41
15:O:61:ASN:O	15:O:62:LYS:C	2.59	0.41
12:L:126:VAL:HG22	12:L:145:PRO:HB2	2.02	0.41
1:A:1265:A:H3'	28:2:19:ARG:NH1	2.36	0.41
13:M:61:GLY:O	22:V:177:PRO:HA	2.20	0.41
1:A:2487:G:H2'	1:A:2488:A:C8	2.56	0.41
1:A:755:C:H2'	1:A:756:C:C6	2.55	0.41
1:A:1270:C:H5''	1:A:1271:G:C5'	2.50	0.41
1:A:699:A:H2'	1:A:700:G:O4'	2.20	0.41
1:A:1696:G:C6	1:A:1697:G:C4	3.08	0.41
22:V:161:VAL:HG12	22:V:162:GLU:N	2.36	0.41
1:A:1581:G:H2'	1:A:1582:C:O4'	2.20	0.41
10:J:101:TYR:CD1	10:J:101:TYR:N	2.88	0.41
1:A:2284:C:O5'	1:A:2284:C:H6	2.03	0.41
26:Z:52:HIS:H	26:Z:52:HIS:CD2	2.37	0.41
12:L:36:LYS:O	12:L:38:GLN:HG2	2.19	0.41
1:A:2057:A:H2'	1:A:2058:A:O4'	2.21	0.41
18:R:38:LEU:O	18:R:52:VAL:HG12	2.21	0.41
1:A:114(B):A:C2	1:A:1144:G:C8	3.08	0.41
12:L:85:LEU:HA	12:L:88:LEU:HB2	2.01	0.41
1:A:675:A:C4'	5:E:67:GLN:NE2	2.81	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:95:LYS:HB3	21:U:99:CYS:O	2.20	0.41
25:Y:6:VAL:O	25:Y:9:GLN:HB2	2.21	0.41
1:A:846:C:H4'	1:A:847:U:O5'	2.21	0.41
1:A:933:A:H2'	1:A:934:G:H5'	2.03	0.41
8:H:133:HIS:HD2	8:H:135:GLU:HG2	1.85	0.41
6:F:87:PRO:O	6:F:88:ILE:HB	2.21	0.41
11:K:71:ARG:NH2	11:K:77:ILE:HG21	2.35	0.41
1:A:643:A:OP1	29:3:42:TRP:NE1	2.54	0.41
6:F:122:PRO:O	6:F:125:PHE:HD1	2.02	0.41
12:L:9:ASN:N	12:L:10:PRO:CD	2.83	0.41
5:E:150:GLY:HA2	5:E:172:TRP:CD2	2.56	0.41
1:A:302:C:H2'	1:A:303:U:C6	2.55	0.41
2:B:48:A:H2'	2:B:49:C:C6	2.55	0.41
1:A:2341:G:H2'	1:A:2342:C:C6	2.55	0.41
1:A:1750:G:H2'	1:A:1751:C:H6	1.84	0.41
5:E:72:ARG:O	5:E:73:ALA:O	2.38	0.41
6:F:178:PHE:HA	6:F:179:PRO:HD3	1.79	0.41
1:A:2642:G:O2'	1:A:2643:G:H5'	2.21	0.41
1:A:1351:C:C2	1:A:1381:G:C2	3.08	0.41
1:A:2235:G:H2'	1:A:2236:C:C6	2.55	0.41
2:B:52:A:H2'	2:B:53:A:O4'	2.21	0.41
2:B:3:C:H2'	2:B:4:C:C6	2.55	0.41
1:A:2721:A:H1'	1:A:2873:A:O2'	2.21	0.41
26:Z:26:LEU:HD21	26:Z:46:ASN:HB3	2.01	0.41
12:L:6:LEU:HD23	12:L:6:LEU:N	2.25	0.41
4:D:171:GLU:HG2	4:D:185:LYS:CG	2.50	0.41
1:A:1407:C:H2'	1:A:1408:C:C6	2.55	0.41
16:P:74:ARG:HD3	16:P:76:PHE:CE2	2.55	0.41
14:N:9:LYS:C	14:N:10:LEU:CG	2.89	0.41
8:H:109:ILE:HD13	8:H:109:ILE:N	2.35	0.41
6:F:161:THR:HG21	6:F:172:LEU:CD2	2.50	0.41
1:A:1308:A:H2'	1:A:1309:G:O4'	2.20	0.41
1:A:1804:C:H6	1:A:1804:C:O5'	2.04	0.41
1:A:1495:A:N3	1:A:1496:A:C2	2.89	0.41
19:S:84:ARG:HB2	19:S:96:ILE:CG2	2.51	0.41
1:A:1854:A:H62	1:A:1888:G:H8	1.69	0.41
1:A:2329:G:H2'	1:A:2330:G:C8	2.56	0.41
1:A:1414:G:C5	1:A:1415:U:C5	3.09	0.41
1:A:2618:G:C6	1:A:2619:C:C4	3.09	0.41
1:A:1214:A:H2'	1:A:1215:G:O4'	2.21	0.41
17:Q:66:ASN:HD21	17:Q:70:ARG:HH21	1.69	0.41
24:X:70:VAL:O	24:X:74:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:26:ALA:HA	8:H:30:LEU:HB2	2.02	0.41
1:A:2692:C:H2'	1:A:2693:A:H8	1.86	0.41
5:E:78:ILE:HD12	5:E:78:ILE:H	1.85	0.41
1:A:1794:U:H1'	1:A:1900:A:N3	2.35	0.41
20:T:24:GLY:HA3	20:T:82:GLN:HE22	1.86	0.41
7:G:101:ARG:HB2	7:G:117:PRO:HG2	2.03	0.41
21:U:76:CYS:CB	21:U:96:ILE:HD13	2.50	0.41
6:F:41:GLN:HB3	6:F:43:LEU:HD13	2.03	0.41
22:V:71:VAL:HG11	22:V:74:VAL:HG23	2.02	0.41
15:O:100:ALA:HA	15:O:103:GLU:HB3	2.01	0.41
1:A:1543:A:C8	1:A:1543:A:H3'	2.56	0.41
1:A:861:A:C2	1:A:917:A:C4	3.09	0.41
10:J:116:THR:HG23	10:J:117:HIS:H	1.86	0.41
5:E:101:LEU:O	5:E:106:ARG:NH1	2.53	0.41
1:A:2850:A:H2'	1:A:2851:A:O4'	2.20	0.41
1:A:85:G:H5''	1:A:85:G:C8	2.51	0.41
24:X:37:ILE:HG23	24:X:38:SER:N	2.36	0.41
1:A:1952:A:C2	11:K:22:ILE:HG23	2.55	0.41
1:A:1206:G:C5	1:A:1207:C:C5	3.09	0.41
30:4:24:THR:HG23	30:4:27:GLY:H	1.85	0.41
1:A:161:U:O2	1:A:165:U:O4	2.39	0.41
1:A:2817:G:H21	1:A:2836:U:C1'	2.33	0.41
1:A:912:C:C2	1:A:913:U:C5	3.09	0.41
7:G:105:LEU:HD22	7:G:113:VAL:HB	2.01	0.41
1:A:1239:G:C6	1:A:1240:U:C4	3.09	0.41
1:A:2695:C:H2'	1:A:2696:U:C6	2.56	0.41
20:T:14:SER:O	20:T:17:ALA:N	2.54	0.41
1:A:29:U:O2'	1:A:30:G:H5'	2.21	0.41
1:A:308:G:H2'	1:A:309:G:O4'	2.21	0.41
2:B:7:G:H5''	15:O:29:PHE:CD2	2.56	0.41
12:L:39:LYS:HD3	12:L:39:LYS:HA	1.71	0.41
12:L:48:PRO:O	12:L:49:ARG:C	2.59	0.41
1:A:1825:A:H2'	1:A:1826:G:C8	2.56	0.41
1:A:1826:G:C6	1:A:1827:C:C4	3.09	0.41
1:A:1164:G:H8	1:A:1164:G:H5''	1.86	0.41
1:A:733:G:N7	1:A:761:A:N6	2.68	0.41
6:F:5:LEU:HA	6:F:5:LEU:HD23	1.85	0.41
15:O:28:VAL:HG13	15:O:35:ILE:HD11	2.01	0.41
15:O:65:VAL:O	15:O:69:VAL:HG12	2.21	0.41
16:P:68:TYR:N	16:P:68:TYR:CD2	2.89	0.41
24:X:11:ARG:HH11	24:X:60:PHE:HA	1.85	0.41
22:V:51:ALA:HB1	22:V:57:ILE:HD11	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:V:53:ILE:CG2	22:V:71:VAL:HB	2.51	0.41
4:D:116:VAL:HG13	4:D:117:MET:N	2.35	0.41
1:A:773:U:C5'	3:C:47:GLY:HA3	2.51	0.41
1:A:2516:G:C6	1:A:2517:C:C4	3.08	0.41
2:B:106:G:O2'	2:B:107:U:H5'	2.20	0.41
5:E:28:ILE:HA	5:E:112:MET:HE3	2.03	0.41
3:C:108:PRO:HG3	3:C:143:HIS:NE2	2.36	0.41
1:A:1258:C:O4'	5:E:84:VAL:HG11	2.21	0.41
1:A:444:C:H2'	1:A:445:C:H6	1.85	0.41
5:E:177:ALA:HB1	5:E:178:PRO:HD2	2.03	0.41
11:K:47:ILE:HD12	11:K:47:ILE:HA	1.87	0.41
1:A:332:A:O2'	1:A:333:G:P	2.79	0.41
1:A:1374:G:H2'	1:A:1375:C:H6	1.86	0.41
1:A:2749:A:H4'	7:G:62:LYS:CB	2.51	0.41
19:S:10:VAL:HG21	19:S:103:ILE:HD13	2.01	0.41
13:M:132:VAL:HG11	22:V:81:ARG:NH1	2.36	0.41
23:W:51:VAL:HG21	23:W:80:HIS:HA	2.01	0.41
13:M:68:ILE:HD13	13:M:103:MET:HG3	2.02	0.41
1:A:1798:U:H5''	3:C:259:THR:O	2.21	0.41
1:A:1676:A:O5'	1:A:1676:A:H8	2.04	0.41
2:B:45:A:H2'	2:B:45:A:N3	2.35	0.41
24:X:95:LEU:HA	24:X:95:LEU:HD22	1.82	0.41
1:A:1765:C:H6	1:A:1765:C:O5'	2.04	0.41
5:E:24:LEU:HA	5:E:25:PRO:HD3	1.85	0.41
7:G:125:VAL:HG22	7:G:131:VAL:HG22	2.03	0.41
1:A:1368:G:C2	1:A:1369:G:C8	3.09	0.41
1:A:2304:G:H1	1:A:2312:U:H3	1.67	0.41
22:V:155:LEU:HD21	22:V:171:ILE:HG13	2.02	0.41
28:2:13:LYS:HB3	28:2:13:LYS:HE2	1.88	0.41
1:A:885:C:O5'	1:A:885:C:H6	2.04	0.41
1:A:533:G:N3	17:Q:45:TYR:CE1	2.89	0.41
5:E:6:MET:HB3	5:E:7:TYR:H	1.55	0.41
17:Q:57:PHE:HB3	17:Q:61:TRP:CZ2	2.55	0.41
1:A:725:G:C6	1:A:726:G:N1	2.89	0.41
1:A:1563:G:H2'	1:A:1564:C:H6	1.85	0.41
1:A:2507:C:C2	1:A:2508:G:C8	3.09	0.41
18:R:75:PHE:C	18:R:75:PHE:CD1	2.94	0.41
31:5:62:LEU:HB2	31:5:63:PRO:HD3	2.02	0.41
31:5:59:LYS:HA	31:5:62:LEU:HD11	2.03	0.41
1:A:195:A:H4'	1:A:251:A:O2'	2.21	0.41
18:R:22:VAL:CG1	18:R:23:GLU:H	2.32	0.41
1:A:270(K):G:H2'	1:A:270(L):C:O4'	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:117:MET:HB2	4:D:117:MET:HE3	1.92	0.41
12:L:57:THR:C	12:L:59:LEU:N	2.74	0.41
18:R:77:ALA:C	18:R:79:VAL:N	2.73	0.41
26:Z:40:THR:OG1	26:Z:43:ILE:HG12	2.20	0.41
6:F:115:ARG:HD2	6:F:115:ARG:N	2.36	0.41
10:J:83:ILE:HG22	10:J:84:ARG:O	2.21	0.41
1:A:1862:G:H2'	1:A:1863:G:C8	2.54	0.41
14:N:104:ARG:CB	14:N:104:ARG:HH11	2.33	0.41
2:B:62:C:C2	2:B:63:G:C8	3.09	0.41
1:A:2836:U:H2'	1:A:2837:G:H8	1.86	0.41
1:A:2586:C:O5'	1:A:2586:C:H6	2.04	0.41
23:W:27:GLU:HB2	23:W:69:PHE:CD1	2.55	0.41
1:A:172:C:H2'	1:A:173:G:H8	1.86	0.41
1:A:952:G:P	13:M:16:ARG:HH22	2.44	0.41
1:A:1831:G:C5	1:A:1832:C:C5	3.09	0.41
1:A:686:G:N2	1:A:788:A:H61	2.18	0.41
1:A:2230:G:C6	1:A:2231:C:C4	3.09	0.41
8:H:92:VAL:HG22	8:H:92:VAL:O	2.20	0.40
1:A:2685:G:N3	1:A:2725:A:C2	2.89	0.40
3:C:197:GLY:O	3:C:198:ASN:C	2.59	0.40
22:V:48:PHE:HE2	22:V:71:VAL:HG21	1.86	0.40
22:V:97:GLU:O	22:V:98:MET:HB3	2.20	0.40
1:A:2028:U:H2'	1:A:2029:G:C8	2.55	0.40
1:A:1509:A:H4'	1:A:1510:A:N9	2.36	0.40
1:A:1174:A:H3'	1:A:1175:U:C5'	2.46	0.40
12:L:122:PRO:O	12:L:123:LEU:HB3	2.21	0.40
14:N:14:SER:O	14:N:15:SER:C	2.60	0.40
1:A:972:G:H3'	1:A:973:A:H2'	2.04	0.40
1:A:646:A:H2'	1:A:647:G:O4'	2.20	0.40
24:X:84:GLY:O	24:X:85:LEU:C	2.59	0.40
1:A:1858:G:HO2'	1:A:1859:A:H8	1.66	0.40
11:K:7:TYR:CE1	11:K:20:MET:HB2	2.56	0.40
1:A:2777:G:C4'	1:A:2778:A:H5'	2.51	0.40
14:N:11:ASN:CG	14:N:12:ARG:H	2.21	0.40
16:P:19:LEU:HA	16:P:20:PRO:HD3	1.73	0.40
1:A:276:A:C3'	1:A:277:C:H5''	2.51	0.40
1:A:2749:A:H1'	7:G:63:SER:OG	2.21	0.40
19:S:82:LEU:HD23	19:S:84:ARG:NH2	2.36	0.40
14:N:28:LEU:HD23	14:N:34:ILE:HG12	2.02	0.40
1:A:1936:A:N3	1:A:1936:A:H5''	2.36	0.40
13:M:34:LEU:HD12	13:M:130:LYS:O	2.21	0.40
1:A:300:A:OP1	21:U:84:ARG:NH2	2.54	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2018:G:C6	1:A:2019:A:C6	3.09	0.40
1:A:1726:G:C2	1:A:1735:U:O2	2.74	0.40
1:A:1198:U:H2'	1:A:1199:U:C6	2.55	0.40
1:A:1502:C:O5'	1:A:1502:C:H6	2.04	0.40
1:A:2422:A:C5	1:A:2424:C:C4	3.09	0.40
13:M:22:LYS:CE	13:M:22:LYS:HA	2.35	0.40
1:A:827:U:H2'	1:A:2068:U:C2	2.56	0.40
13:M:141:GLN:O	22:V:53:ILE:HG22	2.20	0.40
23:W:32:ARG:CA	23:W:35:ASN:HD21	2.34	0.40
14:N:4:LEU:C	14:N:6:SER:N	2.72	0.40
31:5:13:ARG:HG3	31:5:14:VAL:HG23	2.02	0.40
1:A:2029:G:H2'	1:A:2031:A:OP1	2.22	0.40
1:A:603:A:C2	1:A:655:A:N3	2.89	0.40
6:F:53:LEU:HD13	6:F:88:ILE:HG12	2.03	0.40
14:N:14:SER:HA	14:N:17:ARG:HG2	2.03	0.40
4:D:5:LEU:HD22	4:D:197:ILE:HG22	2.02	0.40
8:H:128:LEU:HG	8:H:142:VAL:CG2	2.50	0.40
8:H:114:LEU:HA	8:H:130:TYR:HD1	1.86	0.40
1:A:1276:A:H5''	1:A:1276:A:H8	1.86	0.40
25:Y:24:LEU:HD23	25:Y:24:LEU:O	2.21	0.40
1:A:265:A:C8	1:A:266:G:H1'	2.55	0.40
1:A:534:U:H1'	17:Q:49:HIS:CD2	2.56	0.40
24:X:23:LYS:O	24:X:23:LYS:HG3	2.20	0.40
29:3:23:THR:O	29:3:24:GLU:HG2	2.22	0.40
5:E:40:GLN:O	5:E:43:LYS:HG2	2.21	0.40
3:C:174:ILE:N	3:C:174:ILE:CD1	2.84	0.40
1:A:69:C:H2'	1:A:70:G:H8	1.84	0.40
6:F:16:ARG:N	6:F:17:PRO:HD2	2.36	0.40
10:J:159:GLU:HG2	10:J:160:LYS:N	2.36	0.40
1:A:1271:G:O3'	1:A:1272:A:H4'	2.21	0.40
1:A:1203:G:C6	1:A:1204:A:N6	2.89	0.40
1:A:1918:A:O2'	1:A:1920:C:N4	2.54	0.40
13:M:67:ARG:HD2	13:M:105:GLU:OE2	2.21	0.40
10:J:132:LYS:HG2	10:J:132:LYS:H	1.61	0.40
1:A:252:G:OP2	12:L:50:ARG:NH2	2.49	0.40
12:L:39:LYS:CD	12:L:40:SER:H	2.35	0.40
3:C:236:GLY:O	3:C:238:GLY:N	2.54	0.40
12:L:62:LEU:HD22	12:L:62:LEU:O	2.22	0.40
1:A:2416:C:OP1	12:L:64:LYS:O	2.40	0.40
24:X:46:LEU:HB2	24:X:63:ALA:HA	2.04	0.40
1:A:1493:C:H2'	1:A:1493:C:O2	2.21	0.40
14:N:10:LEU:HD12	14:N:10:LEU:N	2.37	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:X:41:ARG:HD3	24:X:43:TYR:CE2	2.57	0.40
12:L:17:LYS:C	12:L:19:VAL:H	2.25	0.40
22:V:144:LEU:HD22	22:V:144:LEU:N	2.37	0.40
1:A:1858:G:H1'	1:A:1884:A:H62	1.86	0.40
1:A:480:A:H2'	1:A:480:A:N3	2.36	0.40
24:X:73:LEU:HD21	24:X:94:LEU:CG	2.49	0.40
3:C:107:ALA:HA	3:C:108:PRO:HD3	1.78	0.40
6:F:114:ILE:HB	6:F:117:PHE:HB2	2.02	0.40
1:A:839:U:H2'	1:A:840:C:H6	1.81	0.40
1:A:775:G:C2	1:A:777:A:N6	2.89	0.40
1:A:1344:G:H5'	1:A:1384:A:C6	2.56	0.40
4:D:76:ARG:HG2	4:D:77:ILE:HG13	2.03	0.40
1:A:1599:C:H2'	1:A:1600:C:C6	2.56	0.40
1:A:1488:G:C5	1:A:1489:U:C5	3.10	0.40
24:X:53:VAL:HG22	24:X:74:VAL:HG13	2.03	0.40
1:A:1221:C:H2'	1:A:122(A):C:C6	2.56	0.40
1:A:386:G:H4'	1:A:387:U:OP2	2.22	0.40
1:A:2404:C:H2'	1:A:2405:G:O4'	2.22	0.40
1:A:2574:G:H8	1:A:2574:G:O5'	2.04	0.40
1:A:1728:G:H8	1:A:1728:G:O5'	2.05	0.40
16:P:137:LYS:HD2	16:P:137:LYS:N	2.36	0.40
1:A:587:C:H4'	1:A:588:U:C6	2.57	0.40
12:L:47:ASP:HB3	12:L:48:PRO:HA	2.02	0.40
15:O:82:ILE:HG22	15:O:83:LYS:N	2.35	0.40
1:A:97:C:H5''	25:Y:2:LYS:HZ1	1.86	0.40
1:A:1310:G:H2'	1:A:1311:G:H5''	2.03	0.40
8:H:133:HIS:HA	8:H:134:PRO:HD3	1.92	0.40
1:A:141(A):A:C8	1:A:1408:C:H1'	2.57	0.40
6:F:171:ALA:O	6:F:175:LEU:HG	2.21	0.40
18:R:72:VAL:HG23	18:R:72:VAL:O	2.22	0.40
1:A:270(H):C:H2'	1:A:270(I):C:C6	2.56	0.40
4:D:85:ASN:HA	4:D:86:PRO:HD3	1.78	0.40
1:A:2477:C:HO2'	1:A:2478:A:P	2.44	0.40
1:A:2565:A:H5''	1:A:2566:A:OP2	2.22	0.40
19:S:50:VAL:HG11	19:S:103:ILE:HG21	2.04	0.40
2:B:37:C:C5	2:B:38:C:C5	3.09	0.40
13:M:78:PRO:C	13:M:79:LEU:HD12	2.42	0.40
1:A:118:A:H1'	1:A:178:G:O4'	2.22	0.40
1:A:875:G:N2	1:A:903:C:C2	2.90	0.40
6:F:133:LEU:HD23	6:F:133:LEU:N	2.36	0.40
6:F:39:ILE:HG23	6:F:157:ILE:HG22	2.04	0.40
27:1:40:ILE:HD12	27:1:40:ILE:N	2.36	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:83:TYR:CZ	7:G:138:LYS:HG3	2.56	0.40
1:A:2019:A:H5''	17:Q:27:LEU:HD12	2.04	0.40
1:A:1783:A:C2	1:A:2587:A:C4	3.10	0.40
1:A:1843:C:O2'	1:A:1844:C:H5'	2.22	0.40
21:U:98:VAL:HG22	21:U:98:VAL:O	2.21	0.40
1:A:2057:A:N6	1:A:2058:A:C6	2.89	0.40
3:C:35:LYS:O	3:C:64:ILE:HD12	2.21	0.40
8:H:88:ILE:HG22	8:H:89:TYR:N	2.35	0.40
8:H:114:LEU:HA	8:H:130:TYR:CD1	2.57	0.40
5:E:155:LEU:HA	5:E:174:VAL:HG23	2.03	0.40
1:A:468:G:N7	30:4:39:ARG:NH2	2.68	0.40
15:O:26:LEU:HB3	15:O:87:PHE:HA	2.03	0.40
15:O:87:PHE:HE2	15:O:89:ARG:HA	1.87	0.40
16:P:128:GLU:O	16:P:132:LYS:HG3	2.20	0.40
16:P:92:GLY:HA2	16:P:117:ASP:H	1.87	0.40
13:M:27:VAL:H	22:V:81:ARG:NH2	2.19	0.40
1:A:1647:G:P	1:A:1647:G:H3'	2.62	0.40
1:A:319:C:C2	1:A:320:A:C8	3.10	0.40
4:D:14:ILE:HD12	4:D:14:ILE:O	2.22	0.40
1:A:2846:G:C5	1:A:2847:U:C5	3.09	0.40
22:V:28:MET:HA	22:V:88:PHE:HB2	2.03	0.40
1:A:2764:A:N6	1:A:2766:G:C2	2.90	0.40
1:A:489:G:C5	1:A:1284:A:C2	3.09	0.40
11:K:90:GLN:O	11:K:91:LEU:HB2	2.21	0.40
14:N:99:LYS:HE3	14:N:99:LYS:HB3	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	269/271 (99%)	220 (82%)	31 (12%)	18 (7%)	2	28
4	D	202/204 (99%)	168 (83%)	26 (13%)	8 (4%)	5	44
5	E	200/202 (99%)	165 (82%)	28 (14%)	7 (4%)	6	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	179/181 (99%)	134 (75%)	37 (21%)	8 (4%)	4	40
7	G	157/159 (99%)	126 (80%)	27 (17%)	4 (2%)	9	57
8	H	143/145 (99%)	109 (76%)	28 (20%)	6 (4%)	4	43
9	I	28/65 (43%)	27 (96%)	1 (4%)	0	100	100
10	J	135/137 (98%)	108 (80%)	19 (14%)	8 (6%)	2	32
11	K	120/122 (98%)	105 (88%)	8 (7%)	7 (6%)	3	32
12	L	144/146 (99%)	94 (65%)	35 (24%)	15 (10%)	1	14
13	M	134/136 (98%)	98 (73%)	22 (16%)	14 (10%)	1	14
14	N	115/117 (98%)	97 (84%)	13 (11%)	5 (4%)	4	42
15	O	96/98 (98%)	65 (68%)	18 (19%)	13 (14%)	0	8
16	P	135/137 (98%)	99 (73%)	30 (22%)	6 (4%)	4	41
17	Q	114/116 (98%)	99 (87%)	13 (11%)	2 (2%)	13	65
18	R	99/101 (98%)	71 (72%)	19 (19%)	9 (9%)	1	18
19	S	110/112 (98%)	94 (86%)	14 (13%)	2 (2%)	13	65
20	T	90/92 (98%)	82 (91%)	7 (8%)	1 (1%)	21	77
21	U	98/100 (98%)	65 (66%)	22 (22%)	11 (11%)	1	13
22	V	186/188 (99%)	140 (75%)	36 (19%)	10 (5%)	3	35
23	W	74/76 (97%)	59 (80%)	12 (16%)	3 (4%)	4	44
24	X	86/88 (98%)	57 (66%)	20 (23%)	9 (10%)	1	14
25	Y	60/62 (97%)	48 (80%)	9 (15%)	3 (5%)	3	37
26	Z	57/59 (97%)	51 (90%)	5 (9%)	1 (2%)	13	65
27	1	28/30 (93%)	15 (54%)	10 (36%)	3 (11%)	1	13
28	2	50/52 (96%)	39 (78%)	8 (16%)	3 (6%)	2	31
29	3	42/44 (96%)	35 (83%)	2 (5%)	5 (12%)	1	11
30	4	46/48 (96%)	42 (91%)	4 (9%)	0	100	100
31	5	61/63 (97%)	43 (70%)	13 (21%)	5 (8%)	1	21
All	All	3258/3351 (97%)	2555 (78%)	517 (16%)	186 (6%)	3	33

All (186) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	26	LYS
3	C	33	LEU

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Mol	Chain	Res	Type
3	C	35	LYS
3	C	237	GLU
3	C	239	ARG
3	C	260	ARG
4	D	16	ARG
5	E	73	ALA
6	F	87	PRO
7	G	92	ILE
7	G	165	ALA
8	H	91	SER
10	J	116	THR
10	J	149	PRO
10	J	157	ARG
12	L	15	ARG
12	L	36	LYS
12	L	46	LYS
12	L	59	LEU
12	L	141	ALA
13	M	8	LYS
13	M	21	THR
15	O	12	PHE
15	O	59	LYS
15	O	62	LYS
15	O	90	GLY
15	O	91	PRO
16	P	58	ASN
16	P	115	ARG
18	R	53	GLU
18	R	78	LYS
19	S	110	LYS
21	U	3	VAL
21	U	7	VAL
22	V	178	GLU
23	W	47	PRO
24	X	11	ARG
25	Y	47	ASN
28	2	4	HIS
28	2	35	GLU
29	3	28	ARG
3	C	34	VAL
3	C	69	ARG
3	C	70	TRP

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Mol	Chain	Res	Type
3	C	106	ILE
3	C	197	GLY
4	D	86	PRO
5	E	84	VAL
6	F	14	GLU
6	F	24	GLY
6	F	86	MET
8	H	10	GLU
8	H	90	GLY
8	H	143	SER
10	J	106	LYS
10	J	153	HIS
12	L	11	GLY
12	L	34	GLY
12	L	149	GLU
13	M	7	MET
13	M	10	ARG
13	M	18	LYS
13	M	62	GLY
14	N	3	HIS
14	N	57	ARG
15	O	35	ILE
15	O	44	LYS
15	O	57	LYS
16	P	2	ASN
21	U	17	SER
21	U	42	VAL
21	U	80	GLY
21	U	98	VAL
22	V	114	GLY
22	V	120	ILE
22	V	177	PRO
22	V	179	ASP
23	W	13	GLY
23	W	73	GLY
24	X	85	LEU
31	5	3	LYS
3	C	125	ILE
3	C	238	GLY
4	D	18	ASP
5	E	68	LYS
5	E	127	GLU

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Mol	Chain	Res	Type
5	E	166	ALA
7	G	21	PRO
10	J	148	GLY
11	K	4	PRO
11	K	26	LYS
11	K	97	ARG
12	L	18	ARG
12	L	42	SER
12	L	49	ARG
12	L	148	LEU
13	M	133	ARG
14	N	58	GLY
15	O	95	HIS
16	P	36	GLU
18	R	17	GLY
18	R	29	PRO
18	R	80	GLN
21	U	88	LYS
21	U	96	ILE
22	V	168	GLU
24	X	9	GLY
24	X	31	GLY
24	X	32	LYS
25	Y	17	SER
27	1	44	CYS
27	1	62	CYS
29	3	31	PRO
29	3	46	HIS
31	5	34	TRP
31	5	35	GLN
3	C	32	SER
3	C	191	ALA
3	C	256	GLY
4	D	43	GLY
6	F	35	GLU
6	F	124	SER
8	H	132	PRO
10	J	70	ALA
11	K	29	ASN
12	L	65	ARG
13	M	81	VAL
13	M	134	ARG

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Mol	Chain	Res	Type
13	M	140	ALA
14	N	8	ARG
15	O	83	LYS
15	O	85	VAL
15	O	101	LEU
16	P	57	PHE
17	Q	91	ASP
18	R	2	PHE
19	S	11	ARG
20	T	4	ALA
21	U	39	VAL
21	U	90	LEU
22	V	80	ARG
22	V	142	SER
25	Y	15	LYS
26	Z	29	ARG
27	1	54	LYS
28	2	45	VAL
29	3	32	ASN
29	3	51	GLU
31	5	20	GLY
3	C	198	ASN
6	F	12	TYR
13	M	25	ASP
15	O	61	ASN
16	P	55	ASN
18	R	48	GLY
24	X	53	VAL
24	X	84	GLY
24	X	87	PRO
31	5	61	LEU
4	D	29	GLY
6	F	142	PRO
7	G	39	PRO
12	L	43	GLY
13	M	27	VAL
14	N	13	HIS
21	U	11	ASP
24	X	58	ILE
3	C	236	GLY
12	L	10	PRO
13	M	96	VAL

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Mol	Chain	Res	Type
5	E	131	GLY
11	K	27	GLY
18	R	61	VAL
4	D	4	ILE
13	M	30	GLY
18	R	16	PRO
22	V	39	VAL
4	D	189	PRO
5	E	82	ILE
8	H	144	VAL
11	K	101	PRO
11	K	119	PRO
17	Q	90	VAL
22	V	101	PRO
4	D	173	VAL
10	J	158	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	213/213 (100%)	192 (90%)	21 (10%)	11	49
4	D	165/165 (100%)	149 (90%)	16 (10%)	12	50
5	E	161/161 (100%)	148 (92%)	13 (8%)	17	61
6	F	155/155 (100%)	144 (93%)	11 (7%)	21	67
7	G	132/132 (100%)	123 (93%)	9 (7%)	22	70
8	H	122/122 (100%)	115 (94%)	7 (6%)	29	76
9	I	27/53 (51%)	26 (96%)	1 (4%)	45	86
10	J	116/116 (100%)	103 (89%)	13 (11%)	9	41
11	K	100/100 (100%)	92 (92%)	8 (8%)	17	61
12	L	112/112 (100%)	87 (78%)	25 (22%)	1	8
13	M	106/106 (100%)	98 (92%)	8 (8%)	19	65
14	N	100/100 (100%)	94 (94%)	6 (6%)	27	74
15	O	77/77 (100%)	68 (88%)	9 (12%)	8	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	P	121/121 (100%)	109 (90%)	12 (10%)	11	49
17	Q	92/92 (100%)	88 (96%)	4 (4%)	40	84
18	R	82/82 (100%)	77 (94%)	5 (6%)	26	73
19	S	91/91 (100%)	85 (93%)	6 (7%)	24	71
20	T	74/74 (100%)	67 (90%)	7 (10%)	12	51
21	U	84/84 (100%)	78 (93%)	6 (7%)	21	67
22	V	163/163 (100%)	159 (98%)	4 (2%)	60	91
23	W	61/61 (100%)	55 (90%)	6 (10%)	12	50
24	X	73/73 (100%)	61 (84%)	12 (16%)	3	20
25	Y	58/58 (100%)	51 (88%)	7 (12%)	7	36
26	Z	51/51 (100%)	49 (96%)	2 (4%)	43	85
27	1	27/27 (100%)	24 (89%)	3 (11%)	9	42
28	2	45/45 (100%)	43 (96%)	2 (4%)	39	83
29	3	43/43 (100%)	39 (91%)	4 (9%)	13	53
30	4	41/41 (100%)	34 (83%)	7 (17%)	3	18
31	5	53/53 (100%)	51 (96%)	2 (4%)	44	85
All	All	2745/2771 (99%)	2509 (91%)	236 (9%)	15	58

All (236) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	5	LYS
3	C	10	THR
3	C	28	GLU
3	C	33	LEU
3	C	44	ASN
3	C	50	THR
3	C	61	LEU
3	C	78	LYS
3	C	94	LEU
3	C	95	LEU
3	C	106	ILE
3	C	111	LEU
3	C	150	LYS
3	C	166	GLN
3	C	192	THR

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Mol	Chain	Res	Type
3	C	237	GLU
3	C	242	ARG
3	C	244	ARG
3	C	259	THR
3	C	261	LYS
3	C	267	SER
4	D	9	VAL
4	D	48	GLN
4	D	52	LEU
4	D	54	GLN
4	D	57	LYS
4	D	92	THR
4	D	118	LYS
4	D	119	ARG
4	D	132	HIS
4	D	141	ILE
4	D	144	ARG
4	D	154	LYS
4	D	160	TYR
4	D	169	ASN
4	D	184	VAL
4	D	195	LEU
5	E	8	GLN
5	E	9	ILE
5	E	54	ARG
5	E	56	GLU
5	E	66	PRO
5	E	69	HIS
5	E	72	ARG
5	E	83	PHE
5	E	95	ARG
5	E	106	ARG
5	E	164	ARG
5	E	188	ARG
5	E	195	ASP
6	F	18	GLU
6	F	33	ARG
6	F	34	LEU
6	F	47	LYS
6	F	76	SER
6	F	86	MET
6	F	90	LEU

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Mol	Chain	Res	Type
6	F	98	ARG
6	F	107	LEU
6	F	115	ARG
6	F	155	MET
7	G	13	LYS
7	G	23	ARG
7	G	43	VAL
7	G	86	GLU
7	G	101	ARG
7	G	105	LEU
7	G	123	PHE
7	G	158	HIS
7	G	162	ILE
8	H	5	LEU
8	H	6	LEU
8	H	67	ARG
8	H	73	GLU
8	H	77	LEU
8	H	92	VAL
8	H	109	ILE
9	I	3	ASN
10	J	57	LEU
10	J	58	ARG
10	J	64	ASP
10	J	71	MET
10	J	92	GLN
10	J	94	ILE
10	J	96	THR
10	J	105	LEU
10	J	110	LEU
10	J	117	HIS
10	J	120	ARG
10	J	135	LEU
10	J	161	LEU
11	K	19	ILE
11	K	25	LEU
11	K	47	ILE
11	K	77	ILE
11	K	87	ILE
11	K	99	PHE
11	K	104	ARG
11	K	122	LEU

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Mol	Chain	Res	Type
12	L	6	LEU
12	L	13	ASN
12	L	15	ARG
12	L	16	ARG
12	L	19	VAL
12	L	32	THR
12	L	35	HIS
12	L	38	GLN
12	L	39	LYS
12	L	49	ARG
12	L	50	ARG
12	L	52	GLU
12	L	57	THR
12	L	61	ARG
12	L	62	LEU
12	L	67	MET
12	L	75	ILE
12	L	81	GLN
12	L	83	VAL
12	L	84	ASN
12	L	105	LEU
12	L	106	LEU
12	L	111	ARG
12	L	147	LEU
12	L	148	LEU
13	M	6	ARG
13	M	13	GLN
13	M	14	ARG
13	M	22	LYS
13	M	45	GLN
13	M	60	ARG
13	M	89	ASN
13	M	135	ASP
14	N	5	LYS
14	N	8	ARG
14	N	9	LYS
14	N	10	LEU
14	N	79	LEU
14	N	104	ARG
15	O	18	ILE
15	O	26	LEU
15	O	30	ARG

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Mol	Chain	Res	Type
15	O	36	TYR
15	O	42	ASP
15	O	44	LYS
15	O	61	ASN
15	O	62	LYS
15	O	93	LYS
16	P	41	ARG
16	P	58	ASN
16	P	59	THR
16	P	78	LEU
16	P	86	ILE
16	P	87	ASP
16	P	89	VAL
16	P	98	LYS
16	P	99	LEU
16	P	108	ARG
16	P	112	ARG
16	P	113	LYS
17	Q	79	PHE
17	Q	92	ARG
17	Q	97	ASP
17	Q	103	PRO
18	R	12	TYR
18	R	13	ARG
18	R	18	LEU
18	R	80	GLN
18	R	99	ILE
19	S	11	ARG
19	S	23	LEU
19	S	69	LEU
19	S	70	TYR
19	S	77	ASP
19	S	107	LEU
20	T	28	PHE
20	T	57	LEU
20	T	65	ARG
20	T	68	ARG
20	T	75	ASP
20	T	80	ILE
20	T	83	VAL
21	U	4	LYS
21	U	6	HIS

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Mol	Chain	Res	Type
21	U	8	LYS
21	U	31	LEU
21	U	76	CYS
21	U	97	ARG
22	V	25	PRO
22	V	72	ARG
22	V	76	LEU
22	V	94	GLU
23	W	14	ARG
23	W	21	LEU
23	W	25	ARG
23	W	35	ASN
23	W	64	ASP
23	W	80	HIS
24	X	11	ARG
24	X	17	SER
24	X	18	ILE
24	X	20	ARG
24	X	40	ARG
24	X	45	ASN
24	X	46	LEU
24	X	73	LEU
24	X	75	GLU
24	X	82	LEU
24	X	89	GLU
24	X	95	LEU
25	Y	2	LYS
25	Y	21	LEU
25	Y	37	PHE
25	Y	53	LEU
25	Y	56	GLN
25	Y	59	ARG
25	Y	61	LEU
26	Z	10	LYS
26	Z	46	ASN
27	1	46	ASN
27	1	49	GLU
27	1	60	GLU
28	2	3	LYS
28	2	23	HIS
29	3	11	LEU
29	3	29	ASN

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Mol	Chain	Res	Type
29	3	34	LEU
29	3	42	TRP
30	4	4	THR
30	4	8	ASN
30	4	10	ARG
30	4	15	THR
30	4	19	ARG
30	4	24	THR
30	4	29	LYS
31	5	4	MET
31	5	30	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	58	HIS
3	C	87	ASN
3	C	96	HIS
3	C	116	GLN
3	C	126	GLN
3	C	166	GLN
3	C	186	HIS
3	C	198	ASN
3	C	227	ASN
3	C	233	HIS
4	D	60	ASN
4	D	66	HIS
4	D	129	HIS
4	D	143	ASN
4	D	169	ASN
4	D	192	ASN
5	E	67	GLN
5	E	69	HIS
5	E	75	HIS
5	E	169	ASN
6	F	27	ASN
6	F	58	GLN
6	F	66	GLN
6	F	108	ASN
6	F	121	ASN
7	G	143	GLN
7	G	147	ASN

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Mol	Chain	Res	Type
8	H	133	HIS
9	I	3	ASN
9	I	6	ASN
10	J	79	ASN
10	J	151	HIS
10	J	154	GLN
11	K	89	ASN
12	L	13	ASN
12	L	27	HIS
12	L	35	HIS
12	L	38	GLN
12	L	81	GLN
13	M	13	GLN
13	M	45	GLN
13	M	141	GLN
14	N	13	HIS
14	N	16	HIS
14	N	61	HIS
14	N	71	GLN
14	N	91	GLN
15	O	61	ASN
15	O	95	HIS
16	P	43	GLN
16	P	58	ASN
16	P	79	HIS
16	P	84	GLN
16	P	90	GLN
17	Q	49	HIS
17	Q	72	HIS
19	S	34	ASN
19	S	57	ASN
19	S	61	ASN
19	S	102	HIS
20	T	31	HIS
20	T	41	ASN
20	T	55	ASN
20	T	87	GLN
21	U	6	HIS
22	V	118	GLN
23	W	35	ASN
23	W	50	ASN
23	W	70	GLN

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Mol	Chain	Res	Type
24	X	19	GLN
24	X	45	ASN
24	X	56	GLN
24	X	66	HIS
25	Y	47	ASN
26	Z	19	GLN
26	Z	46	ASN
26	Z	52	HIS
27	1	46	ASN
28	2	43	HIS
29	3	29	ASN
30	4	8	ASN
30	4	36	GLN
31	5	31	HIS
31	5	33	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2757/2879 (95%)	410 (14%)	69 (2%)
2	B	118/119 (99%)	16 (13%)	1 (0%)
All	All	2875/2998 (95%)	426 (14%)	70 (2%)

All (426) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	G
1	A	35	G
1	A	46	C
1	A	49	A
1	A	64	A
1	A	71	A
1	A	72	U
1	A	74	A
1	A	75	G
1	A	84	A
1	A	88	G
1	A	102	G
1	A	118	A
1	A	119	A
1	A	120	U

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Mol	Chain	Res	Type
1	A	125	G
1	A	131	G
1	A	138	G
1	A	140	A
1	A	181	A
1	A	196	A
1	A	197	A
1	A	199	A
1	A	205	G
1	A	215	G
1	A	216	A
1	A	221	A
1	A	222	A
1	A	228	A
1	A	229	A
1	A	230	U
1	A	245	G
1	A	248	G
1	A	252	G
1	A	269	U
1	A	270(K)	G
1	A	270(M)	U
1	A	270(N)	U
1	A	270(O)	G
1	A	270(R)	C
1	A	271(D)	U
1	A	271	G
1	A	274	G
1	A	275	G
1	A	276	A
1	A	277	C
1	A	278	A
1	A	279	C
1	A	283	A
1	A	302	C
1	A	311	A
1	A	323	G
1	A	324	A
1	A	329	G
1	A	330	A
1	A	332	A
1	A	333	G

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Mol	Chain	Res	Type
1	A	343	C
1	A	352	G
1	A	353	G
1	A	386	G
1	A	396	G
1	A	405	U
1	A	411	G
1	A	412	A
1	A	444	C
1	A	457	A
1	A	470	A
1	A	473	G
1	A	480	A
1	A	481	G
1	A	482	A
1	A	505	A
1	A	508	G
1	A	509	C
1	A	530	G
1	A	531	C
1	A	532	A
1	A	556	G
1	A	563	G
1	A	569	U
1	A	573	G
1	A	575	A
1	A	598	G
1	A	603	A
1	A	615	G
1	A	617	G
1	A	620	G
1	A	627	A
1	A	637	A
1	A	645	C
1	A	646	A
1	A	654	U
1	A	655	A
1	A	686	G
1	A	695	G
1	A	730	C
1	A	740	U
1	A	746	A

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Mol	Chain	Res	Type
1	A	747	U
1	A	749	C
1	A	764	A
1	A	776	G
1	A	779	U
1	A	782	A
1	A	784	A
1	A	785	G
1	A	790	C
1	A	792	G
1	A	800	A
1	A	805	G
1	A	812	C
1	A	819	A
1	A	827	U
1	A	828	U
1	A	846	C
1	A	847	U
1	A	859	G
1	A	887	A
1	A	889	C
1	A	890	A
1	A	896	A
1	A	897	C
1	A	910	A
1	A	917	A
1	A	931	G
1	A	932	G
1	A	941	A
1	A	945	A
1	A	946	G
1	A	948	G
1	A	959	A
1	A	961	C
1	A	973	A
1	A	974(A)	G
1	A	974(B)	C
1	A	975	G
1	A	983	A
1	A	989	G
1	A	990	A
1	A	996	A

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Mol	Chain	Res	Type
1	A	1011	G
1	A	1012	U
1	A	1013	C
1	A	1022	G
1	A	1023	U
1	A	1025	G
1	A	1026	U
1	A	1033	U
1	A	1047	G
1	A	1112	G
1	A	1126	A
1	A	1129	A
1	A	1130	U
1	A	1135	C
1	A	1136	G
1	A	1139	G
1	A	114(B)	A
1	A	1144	G
1	A	1155	A
1	A	1164	G
1	A	1174	A
1	A	1175	U
1	A	1205	U
1	A	1210	A
1	A	1211	U
1	A	1220	A
1	A	1221	C
1	A	1227	G
1	A	1241	A
1	A	1242	A
1	A	1249	U
1	A	1250	G
1	A	1253	A
1	A	1256	G
1	A	1271	G
1	A	1272	A
1	A	1300	U
1	A	1301	A
1	A	1309	G
1	A	1311	G
1	A	1312	U
1	A	1314	C

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Mol	Chain	Res	Type
1	A	1329	U
1	A	1343	G
1	A	1345	C
1	A	1349	A
1	A	1352	U
1	A	1359	A
1	A	1360	A
1	A	1365	A
1	A	1368	G
1	A	1378	A
1	A	1379	A
1	A	1380	G
1	A	1384	A
1	A	1385	G
1	A	1386	C
1	A	1396	U
1	A	1416	G
1	A	1417	C
1	A	1420	U
1	A	1427	A
1	A	1428	C
1	A	144(B)	A
1	A	1453	A
1	A	1467	C
1	A	1483	G
1	A	1490	A
1	A	1493	C
1	A	1494	A
1	A	1495	A
1	A	1497	U
1	A	1505	C
1	A	1509	A
1	A	1510	A
1	A	1542	G
1	A	1543	A
1	A	1544	C
1	A	1545	A
1	A	1558	A
1	A	1559	G
1	A	1569	A
1	A	1579	A
1	A	1585	C

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Mol	Chain	Res	Type
1	A	1586	A
1	A	1598	C
1	A	1603	A
1	A	1604	C
1	A	1609	A
1	A	1610	A
1	A	1617	C
1	A	1618	A
1	A	1640	C
1	A	1647	G
1	A	1648	C
1	A	1673	U
1	A	1674	G
1	A	1694	C
1	A	1695	G
1	A	1696	G
1	A	1729	A
1	A	1763	G
1	A	1764	G
1	A	1773	A
1	A	1776	G
1	A	1786	A
1	A	1791	A
1	A	1800	C
1	A	1801	G
1	A	1803	A
1	A	1811	G
1	A	1816	G
1	A	1829	A
1	A	1838	C
1	A	1839	G
1	A	1847	A
1	A	1888	G
1	A	1889	A
1	A	1902	C
1	A	1903	G
1	A	1906	G
1	A	1913	A
1	A	1914	C
1	A	1929	G
1	A	1930	G
1	A	1936	A

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Mol	Chain	Res	Type
1	A	1938	A
1	A	1939	U
1	A	1955	U
1	A	1963	U
1	A	1966	A
1	A	1967	C
1	A	1970	A
1	A	1971	A
1	A	1972	A
1	A	1982	C
1	A	1991	U
1	A	1992	G
1	A	1993	U
1	A	1997	G
1	A	2004	G
1	A	2023	G
1	A	2031	A
1	A	2032	G
1	A	2033	A
1	A	2034	U
1	A	2036	C
1	A	2043	C
1	A	2049	G
1	A	2052	G
1	A	2055	C
1	A	2056	G
1	A	2060	A
1	A	2061	G
1	A	2062	A
1	A	2063	C
1	A	2069	G
1	A	2080	G
1	A	2099	U
1	A	2184	G
1	A	2189	U
1	A	2190	G
1	A	2198	A
1	A	2211	G
1	A	2212	A
1	A	2215	G
1	A	2225	A
1	A	2226	C

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Mol	Chain	Res	Type
1	A	2238	G
1	A	2239	G
1	A	2251	G
1	A	2273	A
1	A	2275	C
1	A	2283	C
1	A	2287	A
1	A	2288	A
1	A	2305	A
1	A	2306	C
1	A	2307	G
1	A	2310	A
1	A	2311	A
1	A	2312	U
1	A	2319	G
1	A	2320	A
1	A	2322	A
1	A	2325	G
1	A	2334	G
1	A	2336	A
1	A	2343	C
1	A	2345	G
1	A	2346	A
1	A	2347	C
1	A	2360	A
1	A	2372	G
1	A	2379	G
1	A	2383	G
1	A	2385	C
1	A	2402	C
1	A	2413	G
1	A	2425	A
1	A	2427	C
1	A	2428	G
1	A	2429	G
1	A	2430	A
1	A	2431	U
1	A	2434	A
1	A	2435	A
1	A	2439	A
1	A	2440	C
1	A	2441	C

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Mol	Chain	Res	Type
1	A	2445	G
1	A	2448	A
1	A	2469	A
1	A	2476	A
1	A	2478	A
1	A	2482	G
1	A	2487	G
1	A	2491	U
1	A	2502	G
1	A	2505	G
1	A	2513	G
1	A	2518	A
1	A	2520	C
1	A	2529	G
1	A	2542	A
1	A	2543	G
1	A	2549	G
1	A	2554	U
1	A	2562	U
1	A	2566	A
1	A	2567	G
1	A	2573	C
1	A	2602	A
1	A	2609	U
1	A	2611	U
1	A	2612	C
1	A	2621	A
1	A	2665	A
1	A	2690	C
1	A	2691	C
1	A	2702	U
1	A	2712	U
1	A	712(B)	A
1	A	2713	A
1	A	2714	G
1	A	2726	U
1	A	2733	A
1	A	2757	A
1	A	2758	A
1	A	2764	A
1	A	2765	A
1	A	2778	A

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Mol	Chain	Res	Type
1	A	2779	U
1	A	2781	A
1	A	2790	A
1	A	2791	C
1	A	2797	U
1	A	2808	U
1	A	2818	G
1	A	2820	A
1	A	2821	A
1	A	2834	G
1	A	2836	U
1	A	2850	A
1	A	2851	A
1	A	2872	G
1	A	2876	G
1	A	2892	A
1	A	2894	G
2	B	12	C
2	B	13	A
2	B	15	A
2	B	16	G
2	B	42	C
2	B	44	G
2	B	45	A
2	B	67	G
2	B	73	A
2	B	77	U
2	B	88	C
2	B	89(A)	G
2	B	90	C
2	B	108	C
2	B	109	G
2	B	112	G

All (70) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	102	G
1	A	119	A
1	A	120	U
1	A	131	G
1	A	199	A

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Mol	Chain	Res	Type
1	A	221	A
1	A	278	A
1	A	331	A
1	A	332	A
1	A	479	A
1	A	481	G
1	A	503	A
1	A	616	A
1	A	682	G
1	A	685	A
1	A	746	A
1	A	764	A
1	A	776	G
1	A	846	C
1	A	858	U
1	A	859	G
1	A	933	A
1	A	945	A
1	A	948	G
1	A	961	C
1	A	974(A)	G
1	A	989	G
1	A	1022	G
1	A	1157	G
1	A	1210	A
1	A	1221	C
1	A	1253	A
1	A	1311	G
1	A	1314	C
1	A	1343	G
1	A	1378	A
1	A	1379	A
1	A	1427	A
1	A	1494	A
1	A	1542	G
1	A	1558	A
1	A	1579	A
1	A	1603	A
1	A	1608	A
1	A	1694	C
1	A	1786	A
1	A	1800	C

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Mol	Chain	Res	Type
1	A	1929	G
1	A	1930	G
1	A	1937	A
1	A	2033	A
1	A	2051	A
1	A	2062	A
1	A	2098	U
1	A	2225	A
1	A	2250	G
1	A	2311	A
1	A	2426	A
1	A	2427	C
1	A	2439	A
1	A	2468	G
1	A	2481	G
1	A	2581	G
1	A	2585	U
1	A	2689	U
1	A	2756	U
1	A	2849	U
1	A	2850	A
1	A	2873	A
2	B	66	A

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 1162 ligands modelled in this entry, 1162 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.

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	2760/2879 (95%)	0.22	169 (6%) 21 9	38, 86, 205, 371	0
2	B	119/119 (100%)	0.53	11 (9%) 9 5	83, 149, 196, 251	0
3	C	271/271 (100%)	0.46	27 (9%) 8 5	24, 81, 150, 209	0
4	D	204/204 (100%)	0.57	20 (9%) 8 5	45, 96, 173, 331	0
5	E	202/202 (100%)	0.52	24 (11%) 5 4	32, 94, 172, 311	0
6	F	181/181 (100%)	1.22	44 (24%) 1 2	107, 202, 262, 297	0
7	G	159/159 (100%)	1.33	35 (22%) 1 2	102, 192, 269, 331	0
8	H	145/145 (100%)	1.46	43 (29%) 1 1	60, 224, 376, 453	0
9	I	32/65 (49%)	2.34	20 (62%) 0 1	163, 256, 325, 352	0
10	J	137/137 (100%)	1.15	35 (25%) 1 2	58, 105, 182, 221	0
11	K	122/122 (100%)	0.52	8 (6%) 18 8	48, 90, 142, 194	0
12	L	146/146 (100%)	1.05	25 (17%) 2 2	40, 114, 204, 306	0
13	M	136/136 (100%)	0.59	18 (13%) 4 3	57, 110, 205, 344	0
14	N	117/117 (100%)	0.95	25 (21%) 1 2	44, 92, 166, 282	0
15	O	98/98 (100%)	2.40	42 (42%) 1 1	89, 155, 230, 299	0
16	P	137/137 (100%)	1.06	30 (21%) 1 2	52, 115, 216, 248	0
17	Q	116/116 (100%)	0.33	2 (1%) 67 34	43, 88, 163, 244	0
18	R	101/101 (100%)	0.05	1 (0%) 79 47	55, 134, 187, 294	0
19	S	112/112 (100%)	1.21	33 (29%) 1 1	45, 78, 151, 250	0
20	T	92/92 (100%)	0.95	15 (16%) 2 2	57, 107, 174, 204	0
21	U	100/100 (100%)	2.39	53 (53%) 0 1	59, 139, 289, 344	0
22	V	188/188 (100%)	1.03	41 (21%) 1 2	80, 160, 224, 277	0
23	W	76/76 (100%)	0.52	6 (7%) 13 7	61, 101, 160, 258	0
24	X	88/88 (100%)	1.16	18 (20%) 1 2	50, 106, 191, 346	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	Y	62/62 (100%)	0.53	7 (11%) 6 4	61, 141, 244, 287	0
26	Z	59/59 (100%)	1.42	15 (25%) 1 2	47, 102, 174, 342	0
27	1	30/30 (100%)	0.41	3 (10%) 8 5	161, 244, 282, 323	0
28	2	52/52 (100%)	0.58	9 (17%) 2 2	36, 93, 189, 273	0
29	3	44/44 (100%)	4.60	29 (65%) 0 1	151, 254, 304, 322	0
30	4	48/48 (100%)	1.71	22 (45%) 1 1	43, 66, 132, 297	0
31	5	63/63 (100%)	1.71	21 (33%) 1 1	47, 94, 171, 222	0
All	All	6197/6349 (97%)	0.66	851 (13%) 4 3	24, 100, 239, 453	0

All (851) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
29	3	16	CYS	20.2
29	3	43	CYS	15.3
15	O	59	LYS	14.1
15	O	60	GLY	11.3
29	3	15	GLU	10.8
29	3	49	HIS	10.5
7	G	97	ARG	10.4
15	O	58	LEU	10.0
21	U	62	GLU	9.3
29	3	42	TRP	9.3
29	3	41	PRO	9.3
29	3	44	ARG	9.1
15	O	61	ASN	9.1
15	O	65	VAL	8.8
7	G	95	ARG	8.8
1	A	1535	U	8.5
29	3	17	LYS	8.4
29	3	21	TYR	8.3
29	3	22	ALA	8.0
7	G	98	LEU	8.0
1	A	271(D)	U	7.9
9	I	5	ARG	7.8
29	3	40	CYS	7.7
29	3	14	THR	7.7
13	M	140	ALA	7.7
15	O	67	ARG	7.6
15	O	64	GLU	7.6
19	S	112	GLY	7.5

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Mol	Chain	Res	Type	RSRZ
7	G	96	ALA	7.5
22	V	190	GLU	7.5
7	G	41	MET	7.3
29	3	13	CYS	7.3
29	3	20	ASN	7.2
21	U	91	GLU	7.1
15	O	34	HIS	6.9
1	A	1741	C	6.8
15	O	62	LYS	6.8
7	G	55	PRO	6.7
15	O	57	LYS	6.7
13	M	141	GLN	6.6
6	F	13	GLU	6.6
7	G	40	GLU	6.6
29	3	19	ARG	6.5
15	O	68	GLN	6.5
12	L	102	ARG	6.4
21	U	40	GLU	6.3
8	H	128	LEU	6.3
1	A	1414	G	6.3
21	U	5	MET	6.3
21	U	88	LYS	6.2
21	U	68	HIS	6.2
8	H	127	VAL	6.0
1	A	2191	G	6.0
2	B	90	C	6.0
2	B	30	C	6.0
10	J	161	LEU	5.9
12	L	5	ASP	5.9
12	L	6	LEU	5.8
16	P	116	ALA	5.8
15	O	103	GLU	5.7
19	S	84	ARG	5.7
9	I	21	GLN	5.7
6	F	26	GLN	5.7
7	G	64	LEU	5.7
25	Y	9	GLN	5.6
1	A	653	C	5.6
7	G	39	PRO	5.6
19	S	37	ARG	5.6
15	O	97	ARG	5.6
6	F	33	ARG	5.6

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Mol	Chain	Res	Type	RSRZ
6	F	34	LEU	5.6
15	O	54	LEU	5.6
1	A	2833	G	5.6
21	U	9	LYS	5.5
15	O	22	GLY	5.5
8	H	108	THR	5.5
1	A	615	G	5.5
15	O	66	ALA	5.5
12	L	9	ASN	5.5
26	Z	34	GLU	5.5
1	A	1053	C	5.5
6	F	19	LEU	5.5
15	O	63	THR	5.4
1	A	1051	G	5.4
7	G	170	ARG	5.4
21	U	61	ILE	5.3
29	3	45	LYS	5.2
3	C	268	ARG	5.2
7	G	103	LEU	5.2
21	U	87	LYS	5.2
21	U	28	LYS	5.1
6	F	35	GLU	5.1
21	U	29	GLU	5.1
31	5	35	GLN	5.1
21	U	6	HIS	5.1
22	V	163	LEU	5.1
24	X	11	ARG	5.1
8	H	1	MET	5.1
9	I	22	GLY	5.1
21	U	26	LYS	5.0
5	E	44	ARG	5.0
5	E	96	ASP	5.0
4	D	203	LYS	5.0
6	F	11	TYR	5.0
7	G	101	ARG	5.0
9	I	15	GLU	5.0
21	U	50	ARG	5.0
1	A	9	U	5.0
21	U	36	ALA	5.0
29	3	18	ARG	4.9
22	V	73	GLN	4.9
29	3	52	VAL	4.9

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Mol	Chain	Res	Type	RSRZ
13	M	139	GLU	4.9
1	A	1920	C	4.9
15	O	33	LYS	4.9
29	3	47	THR	4.8
16	P	105	LEU	4.8
10	J	115	ALA	4.8
12	L	8	PRO	4.8
29	3	50	ARG	4.8
7	G	59	ARG	4.8
21	U	23	ARG	4.8
1	A	1052	C	4.8
22	V	179	ASP	4.8
21	U	67	LEU	4.8
1	A	229	A	4.8
1	A	2799	A	4.8
3	C	2	ALA	4.8
6	F	83	ARG	4.7
6	F	181	ARG	4.7
5	E	152	GLU	4.7
7	G	125	VAL	4.7
8	H	10	GLU	4.7
1	A	101	G	4.7
15	O	32	LEU	4.7
1	A	1026	U	4.7
1	A	1921	G	4.7
2	B	31	C	4.6
12	L	94	GLU	4.6
19	S	82	LEU	4.6
29	3	48	VAL	4.6
22	V	162	GLU	4.6
1	A	2190	G	4.5
15	O	107	GLU	4.5
1	A	2701	C	4.5
21	U	2	ARG	4.5
16	P	109	GLU	4.5
7	G	93	GLY	4.5
19	S	111	HIS	4.5
1	A	1460	A	4.5
22	V	77	ASP	4.5
14	N	72	ASP	4.4
2	B	51	G	4.4
21	U	35	TYR	4.4

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Mol	Chain	Res	Type	RSRZ
24	X	27	GLU	4.4
4	D	204	ALA	4.4
4	D	1	MET	4.4
6	F	21	ARG	4.4
8	H	109	ILE	4.3
2	B	88	C	4.3
15	O	83	LYS	4.3
20	T	26	TYR	4.3
1	A	1127	A	4.3
7	G	60	ARG	4.3
1	A	265	A	4.3
1	A	1906	G	4.3
10	J	56	LEU	4.3
26	Z	57	GLU	4.3
3	C	5	LYS	4.2
3	C	261	LYS	4.2
21	U	71	LYS	4.2
30	4	45	ALA	4.2
1	A	1754	C	4.2
31	5	25	MET	4.2
1	A	125	G	4.2
15	O	106	ARG	4.2
15	O	53	SER	4.2
6	F	162	THR	4.2
22	V	189	ALA	4.2
1	A	1494	A	4.2
8	H	37	VAL	4.2
1	A	1769	G	4.1
5	E	190	GLU	4.1
9	I	6	ASN	4.1
6	F	36	LYS	4.1
25	Y	12	GLU	4.1
15	O	102	ALA	4.1
1	A	2750	A	4.1
7	G	102	ALA	4.1
1	A	280	C	4.1
15	O	31	SER	4.1
21	U	14	LEU	4.1
1	A	1032	A	4.1
31	5	13	ARG	4.1
8	H	129	THR	4.1
7	G	132	ARG	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	654	U	4.0
6	F	14	GLU	4.0
1	A	2318	G	4.0
1	A	1642	G	4.0
23	W	40	GLN	4.0
30	4	9	ARG	4.0
16	P	106	SER	4.0
16	P	113	LYS	4.0
8	H	89	TYR	4.0
8	H	58	LEU	4.0
21	U	38	ILE	4.0
21	U	66	PRO	4.0
1	A	1644	C	4.0
8	H	38	LEU	4.0
6	F	51	ARG	3.9
16	P	115	ARG	3.9
10	J	116	THR	3.9
30	4	46	VAL	3.9
6	F	12	TYR	3.9
20	T	76	ARG	3.9
9	I	8	GLU	3.9
26	Z	55	ARG	3.9
9	I	20	ALA	3.9
21	U	22	GLY	3.9
16	P	94	ALA	3.8
6	F	32	PRO	3.8
1	A	2442	C	3.8
8	H	27	ARG	3.8
1	A	1544	C	3.8
1	A	1217	C	3.8
19	S	38	TYR	3.8
28	2	39	MET	3.8
1	A	945	A	3.8
9	I	9	LEU	3.8
16	P	95	ARG	3.8
22	V	31	ARG	3.8
10	J	111	GLU	3.8
1	A	1033	U	3.8
1	A	10	G	3.8
21	U	52	SER	3.8
26	Z	35	ARG	3.8
6	F	120	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
24	X	26	ARG	3.7
19	S	8	ARG	3.7
6	F	84	LYS	3.7
9	I	16	ASN	3.7
7	G	155	SER	3.7
16	P	108	ARG	3.7
28	2	26	THR	3.7
1	A	655	A	3.7
1	A	2378	A	3.7
19	S	26	GLY	3.7
22	V	80	ARG	3.7
16	P	93	ARG	3.7
1	A	830	G	3.7
2	B	89(A)	G	3.6
22	V	91	LEU	3.6
21	U	39	VAL	3.6
21	U	51	VAL	3.6
7	G	56	SER	3.6
21	U	41	GLY	3.6
1	A	1050	A	3.6
19	S	2	GLU	3.6
31	5	36	LYS	3.6
1	A	1574	C	3.6
1	A	2627	G	3.6
13	M	91	GLU	3.6
5	E	184	TYR	3.6
12	L	7	ARG	3.6
19	S	83	LYS	3.6
21	U	86	ARG	3.6
4	D	161	GLY	3.6
8	H	140	LEU	3.6
1	A	127	A	3.6
22	V	178	GLU	3.6
29	3	12	GLU	3.6
6	F	16	ARG	3.5
24	X	85	LEU	3.5
19	S	27	LYS	3.5
6	F	85	GLY	3.5
22	V	74	VAL	3.5
1	A	1415	U	3.5
26	Z	5	LYS	3.5
7	G	169	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
8	H	85	GLU	3.5
16	P	112	ARG	3.5
31	5	40	GLU	3.5
11	K	90	GLN	3.5
8	H	79	ILE	3.5
21	U	63	LYS	3.5
29	3	39	TYR	3.5
13	M	115	MET	3.4
1	A	1643	G	3.4
1	A	1600	C	3.4
1	A	2031	A	3.4
16	P	37	GLY	3.4
7	G	61	HIS	3.4
1	A	1886	C	3.4
15	O	21	THR	3.4
22	V	79	ARG	3.4
22	V	164	ALA	3.4
29	3	51	GLU	3.4
8	H	84	GLY	3.4
22	V	49	ARG	3.4
3	C	189	CYS	3.4
7	G	158	HIS	3.4
14	N	71	GLN	3.4
28	2	53	ALA	3.4
1	A	2702	U	3.4
12	L	138	LEU	3.4
28	2	27	PRO	3.4
6	F	171	ALA	3.4
5	E	188	ARG	3.4
10	J	143	LEU	3.4
6	F	173	LEU	3.4
21	U	8	LYS	3.4
1	A	1538	G	3.4
4	D	195	LEU	3.3
24	X	12	PRO	3.3
16	P	65	LYS	3.3
21	U	69	ALA	3.3
31	5	20	GLY	3.3
21	U	90	LEU	3.3
22	V	140	ASP	3.3
6	F	146	TYR	3.3
1	A	614	U	3.3

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Mol	Chain	Res	Type	RSRZ
3	C	267	SER	3.3
4	D	194	GLY	3.3
10	J	114	LEU	3.3
5	E	185	ASP	3.3
12	L	124	LYS	3.3
29	3	23	THR	3.3
16	P	64	ARG	3.3
31	5	31	HIS	3.3
2	B	87	G	3.3
6	F	20	ILE	3.3
30	4	38	GLY	3.2
1	A	1983	C	3.2
6	F	179	PRO	3.2
21	U	34	LYS	3.2
9	I	66	LEU	3.2
31	5	24	ALA	3.2
1	A	2356	C	3.2
1	A	224	G	3.2
21	U	4	LYS	3.2
1	A	1742	C	3.2
1	A	2805	G	3.2
21	U	32	PRO	3.2
25	Y	8	LYS	3.2
1	A	1454	U	3.2
1	A	126	A	3.2
19	S	1	MET	3.2
19	S	98	LYS	3.2
6	F	15	VAL	3.2
1	A	537	C	3.2
26	Z	7	LYS	3.2
22	V	81	ARG	3.2
4	D	200	GLU	3.2
22	V	75	ASN	3.2
19	S	39	THR	3.2
1	A	1435	G	3.2
22	V	84	GLU	3.2
24	X	19	GLN	3.2
10	J	64	ASP	3.1
6	F	49	ASP	3.1
15	O	56	LEU	3.1
1	A	2749	A	3.1
16	P	66	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
16	P	79	HIS	3.1
12	L	10	PRO	3.1
17	Q	70	ARG	3.1
6	F	86	MET	3.1
21	U	53	PRO	3.1
16	P	36	GLU	3.1
1	A	2062	A	3.1
1	A	11	G	3.1
3	C	150	LYS	3.1
14	N	102	GLU	3.1
22	V	55	HIS	3.1
3	C	262	ARG	3.1
7	G	105	LEU	3.1
1	A	2448	A	3.1
1	A	2804	C	3.1
1	A	2828	C	3.1
31	5	44	LYS	3.1
27	1	56	GLU	3.1
10	J	138	ARG	3.1
3	C	71	ASP	3.1
12	L	64	LYS	3.1
15	O	84	GLN	3.1
26	Z	36	VAL	3.0
15	O	52	SER	3.0
1	A	1534	G	3.0
3	C	188	GLU	3.0
6	F	178	PHE	3.0
7	G	94	TYR	3.0
28	2	25	LEU	3.0
30	4	48	LYS	3.0
21	U	25	GLY	3.0
21	U	72	VAL	3.0
8	H	72	LEU	3.0
9	I	18	GLU	3.0
1	A	898	C	3.0
8	H	114	LEU	3.0
1	A	1590	U	3.0
1	A	951	C	3.0
13	M	113	GLN	3.0
6	F	17	PRO	3.0
22	V	78	LYS	3.0
8	H	54	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
14	N	103	ARG	3.0
20	T	23	GLU	3.0
4	D	162	ALA	3.0
30	4	10	ARG	3.0
8	H	111	PRO	3.0
7	G	38	SER	3.0
16	P	114	LEU	3.0
30	4	41	ARG	3.0
15	O	80	LEU	3.0
6	F	18	GLU	3.0
6	F	172	LEU	2.9
1	A	2626	C	2.9
30	4	43	THR	2.9
9	I	19	ARG	2.9
1	A	829	A	2.9
10	J	160	LYS	2.9
14	N	22	ARG	2.9
10	J	110	LEU	2.9
28	2	24	ALA	2.9
2	B	50	G	2.9
10	J	52	LYS	2.9
26	Z	29	ARG	2.9
9	I	3	ASN	2.9
13	M	59	ARG	2.9
31	5	57	ARG	2.9
5	E	186	ILE	2.9
8	H	144	VAL	2.9
12	L	144	GLU	2.9
16	P	78	LEU	2.9
22	V	98	MET	2.9
20	T	25	LYS	2.9
19	S	23	LEU	2.9
12	L	61	ARG	2.9
21	U	24	VAL	2.9
3	C	264	LYS	2.9
1	A	867	C	2.9
1	A	1926	U	2.9
6	F	74	LYS	2.9
10	J	113	MET	2.9
27	1	39	ARG	2.9
21	U	15	VAL	2.8
20	T	75	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
31	5	54	GLU	2.8
3	C	258	LYS	2.8
31	5	34	TRP	2.8
13	M	60	ARG	2.8
22	V	99	TYR	2.8
9	I	12	THR	2.8
24	X	20	ARG	2.8
1	A	2827	C	2.8
19	S	97	LYS	2.8
25	Y	6	VAL	2.8
3	C	232	PRO	2.8
3	C	183	ARG	2.8
30	4	22	MET	2.8
15	O	108	GLY	2.8
19	S	9	TYR	2.8
8	H	2	LYS	2.8
14	N	42	LYS	2.8
7	G	65	HIS	2.8
1	A	1984	G	2.8
1	A	2379	G	2.8
4	D	8	LYS	2.8
19	S	36	LEU	2.8
9	I	11	ALA	2.8
19	S	31	GLU	2.8
1	A	1128	A	2.8
1	A	2421	G	2.8
3	C	260	ARG	2.8
7	G	133	VAL	2.7
8	H	137	PRO	2.7
10	J	117	HIS	2.7
22	V	180	VAL	2.7
5	E	95	ARG	2.7
8	H	8	PRO	2.7
21	U	37	VAL	2.7
1	A	273(E)	C	2.7
14	N	24	GLN	2.7
15	O	69	VAL	2.7
15	O	30	ARG	2.7
8	H	41	GLU	2.7
16	P	104	ASN	2.7
24	X	28	GLY	2.7
6	F	139	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
5	E	189	THR	2.7
3	C	272	ALA	2.7
19	S	7	ALA	2.7
30	4	47	ARG	2.7
6	F	168	GLU	2.7
10	J	71	MET	2.7
21	U	92	ASN	2.7
1	A	1770	G	2.7
31	5	51	ALA	2.7
23	W	42	GLY	2.7
1	A	2363	C	2.7
20	T	24	GLY	2.7
21	U	89	PHE	2.7
14	N	43	GLU	2.7
24	X	50	ARG	2.7
3	C	271	ILE	2.7
30	4	14	LYS	2.7
10	J	142	ARG	2.7
21	U	80	GLY	2.7
3	C	233	HIS	2.7
4	D	125	GLY	2.7
22	V	45	ASP	2.6
26	Z	1	MET	2.6
19	S	19	LEU	2.6
20	T	33	LYS	2.6
24	X	71	TYR	2.6
7	G	156	ALA	2.6
22	V	181	GLU	2.6
10	J	133	GLY	2.6
12	L	15	ARG	2.6
13	M	111	GLU	2.6
8	H	36	ALA	2.6
1	A	2518	A	2.6
1	A	2733	A	2.6
8	H	100	ALA	2.6
26	Z	27	GLY	2.6
1	A	283	A	2.6
1	A	1323	U	2.6
20	T	52	VAL	2.6
11	K	91	LEU	2.6
19	S	25	ARG	2.6
8	H	61	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
14	N	73	VAL	2.6
14	N	74	LYS	2.6
1	A	1242	A	2.6
22	V	32	HIS	2.6
1	A	2591	C	2.6
22	V	126	VAL	2.6
7	G	58	GLU	2.6
8	H	112	LYS	2.6
1	A	1930	G	2.6
5	E	45	ARG	2.6
22	V	92	SER	2.6
1	A	888	C	2.6
1	A	2700	C	2.6
10	J	84	ARG	2.6
8	H	115	ALA	2.6
1	A	225	A	2.6
1	A	1847	A	2.6
11	K	56	ASP	2.6
1	A	361	G	2.6
31	5	29	LYS	2.6
8	H	60	GLU	2.6
21	U	64	GLU	2.6
29	3	10	LEU	2.6
3	C	181	GLU	2.6
5	E	183	VAL	2.5
8	H	62	LYS	2.5
2	B	89(B)	A	2.5
1	A	128	C	2.5
1	A	1533	C	2.5
4	D	202	LYS	2.5
21	U	55	TYR	2.5
1	A	2602	A	2.5
8	H	125	GLU	2.5
29	3	38	LYS	2.5
19	S	40	ASN	2.5
3	C	182	LEU	2.5
31	5	41	ILE	2.5
6	F	73	ALA	2.5
1	A	2797	U	2.5
10	J	25	LYS	2.5
24	X	13	ILE	2.5
4	D	107	THR	2.5

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Mol	Chain	Res	Type	RSRZ
24	X	30	VAL	2.5
20	T	35	THR	2.5
5	E	66	PRO	2.5
12	L	110	TYR	2.5
14	N	70	LEU	2.5
10	J	137	ARG	2.5
1	A	1514	U	2.5
23	W	18	ALA	2.5
1	A	2625	G	2.5
7	G	106	THR	2.5
10	J	135	LEU	2.5
24	X	58	ILE	2.5
1	A	2275	C	2.5
20	T	82	GLN	2.5
22	V	3	TYR	2.5
16	P	62	THR	2.5
19	S	100	THR	2.5
30	4	11	LYS	2.5
10	J	66	THR	2.5
30	4	17	GLY	2.5
16	P	137	LYS	2.5
5	E	41	LEU	2.5
1	A	2331	G	2.5
6	F	161	THR	2.5
25	Y	4	SER	2.5
3	C	148	GLU	2.5
1	A	2377	A	2.5
1	A	90	U	2.5
22	V	159	PRO	2.4
1	A	1536	A	2.4
1	A	1938	A	2.4
1	A	2376	A	2.4
4	D	132	HIS	2.4
4	D	163	GLU	2.4
22	V	128	VAL	2.4
15	O	104	GLY	2.4
22	V	76	LEU	2.4
1	A	2752	C	2.4
1	A	50	U	2.4
1	A	1857	G	2.4
12	L	125	VAL	2.4
19	S	80	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
9	I	60	ARG	2.4
1	A	2537	U	2.4
22	V	156	LYS	2.4
4	D	15	PHE	2.4
30	4	42	LEU	2.4
1	A	362	U	2.4
2	B	58	A	2.4
1	A	2791	C	2.4
11	K	107	ARG	2.4
4	D	3	GLY	2.4
19	S	41	LYS	2.4
21	U	3	VAL	2.4
15	O	105	ALA	2.4
16	P	25	GLY	2.4
1	A	1768	U	2.4
12	L	39	LYS	2.4
4	D	164	ARG	2.4
6	F	22	ARG	2.4
10	J	134	PRO	2.4
16	P	110	ILE	2.4
28	2	23	HIS	2.4
1	A	1791	A	2.4
1	A	1931	U	2.4
6	F	28	VAL	2.4
16	P	1	MET	2.4
13	M	112	GLU	2.4
15	O	81	GLY	2.4
16	P	49	VAL	2.4
10	J	139	LEU	2.4
1	A	1856	G	2.4
10	J	140	PHE	2.4
30	4	36	GLN	2.4
5	E	176	LEU	2.4
7	G	116	GLU	2.4
11	K	106	LEU	2.4
19	S	24	ILE	2.4
3	C	266	SER	2.4
9	I	17	LEU	2.4
22	V	97	GLU	2.4
1	A	952	G	2.4
1	A	1753	G	2.4
9	I	61	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	890	A	2.4
1	A	2734	A	2.4
14	N	10	LEU	2.3
19	S	81	ALA	2.3
30	4	13	ALA	2.3
9	I	7	VAL	2.3
4	D	156	MET	2.3
5	E	181	LEU	2.3
13	M	17	LEU	2.3
14	N	21	TYR	2.3
24	X	18	ILE	2.3
1	A	2849	U	2.3
8	H	86	THR	2.3
25	Y	5	GLU	2.3
10	J	59	GLY	2.3
31	5	12	LYS	2.3
30	4	44	PRO	2.3
1	A	273(D)	C	2.3
10	J	92	GLN	2.3
1	A	273(F)	U	2.3
5	E	65	TRP	2.3
8	H	126	TYR	2.3
29	3	25	LYS	2.3
1	A	2703	C	2.3
22	V	160	GLY	2.3
12	L	97	PRO	2.3
22	V	114	GLY	2.3
15	O	43	GLU	2.3
1	A	961	C	2.3
10	J	30	LYS	2.3
19	S	99	ARG	2.3
21	U	73	ARG	2.3
20	T	53	LYS	2.3
1	A	1919	A	2.3
5	E	47	GLY	2.3
26	Z	26	LEU	2.3
3	C	149	PRO	2.3
30	4	12	ARG	2.3
1	A	1591	G	2.3
24	X	16	ASN	2.3
13	M	16	ARG	2.3
13	M	15	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
14	N	69	ASP	2.3
22	V	182	LYS	2.3
6	F	152	LEU	2.3
1	A	1929	G	2.3
30	4	32	LYS	2.3
28	2	28	PRO	2.3
1	A	2798	C	2.3
6	F	115	ARG	2.3
8	H	82	ARG	2.3
10	J	40	ASP	2.3
30	4	18	PHE	2.3
1	A	427	U	2.3
10	J	90	LEU	2.3
11	K	89	ASN	2.3
18	R	89	GLN	2.3
21	U	7	VAL	2.2
1	A	1434	A	2.2
12	L	149	GLU	2.2
16	P	107	ASP	2.2
1	A	807	U	2.2
1	A	831	G	2.2
8	H	7	GLU	2.2
20	T	5	TYR	2.2
1	A	2422	A	2.2
14	N	76	VAL	2.2
26	Z	54	VAL	2.2
1	A	1450	C	2.2
1	A	2248	C	2.2
8	H	9	LEU	2.2
1	A	1907	G	2.2
3	C	4	LYS	2.2
16	P	111	ARG	2.2
6	F	138	GLN	2.2
29	3	9	LEU	2.2
10	J	57	LEU	2.2
14	N	54	LEU	2.2
13	M	75	THR	2.2
3	C	231	HIS	2.2
14	N	25	ALA	2.2
1	A	281	G	2.2
1	A	528	A	2.2
1	A	2309	A	2.2

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Mol	Chain	Res	Type	RSRZ
3	C	270	ILE	2.2
31	5	58	ILE	2.2
27	1	55	PRO	2.2
24	X	15	ALA	2.2
11	K	65	THR	2.2
1	A	327	G	2.2
1	A	2802	G	2.2
12	L	45	LEU	2.2
1	A	2586	C	2.2
15	O	82	ILE	2.2
10	J	145	VAL	2.2
24	X	38	SER	2.2
30	4	28	ARG	2.2
1	A	738	G	2.2
19	S	43	GLY	2.2
1	A	456	C	2.2
4	D	135	HIS	2.2
16	P	101	PHE	2.2
1	A	508	G	2.2
1	A	1215	G	2.2
14	N	67	LEU	2.2
7	G	104	GLU	2.2
13	M	18	LYS	2.2
15	O	71	ARG	2.2
1	A	1573	G	2.2
5	E	19	GLU	2.1
16	P	74	ARG	2.1
31	5	14	VAL	2.1
1	A	226	G	2.1
1	A	493	G	2.1
14	N	44	LEU	2.1
31	5	52	LYS	2.1
14	N	66	VAL	2.1
14	N	75	LEU	2.1
8	H	43	ASN	2.1
14	N	45	ARG	2.1
26	Z	33	GLN	2.1
21	U	65	ALA	2.1
13	M	137	TYR	2.1
5	E	187	VAL	2.1
12	L	98	GLU	2.1
19	S	110	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
15	O	70	GLY	2.1
23	W	39	ARG	2.1
1	A	648	G	2.1
1	A	1216	G	2.1
1	A	1933	G	2.1
14	N	26	LYS	2.1
1	A	2317	C	2.1
3	C	226	MET	2.1
30	4	29	LYS	2.1
7	G	68	THR	2.1
1	A	1436	G	2.1
10	J	144	LYS	2.1
13	M	108	GLY	2.1
31	5	28	GLY	2.1
15	O	99	LYS	2.1
1	A	88	G	2.1
13	M	135	ASP	2.1
20	T	15	GLU	2.1
23	W	19	LYS	2.1
12	L	108	LYS	2.1
19	S	96	ILE	2.1
5	E	68	LYS	2.1
22	V	186	GLU	2.1
20	T	60	ARG	2.1
1	A	2538	C	2.1
10	J	136	GLY	2.1
1	A	504	U	2.1
12	L	137	LYS	2.1
17	Q	19	LYS	2.1
25	Y	13	ALA	2.1
14	N	77	ARG	2.1
1	A	899	A	2.1
1	A	2807	G	2.1
7	G	124	GLU	2.1
8	H	77	LEU	2.1
11	K	111	PHE	2.1
9	I	13	LEU	2.1
19	S	67	ASP	2.1
5	E	153	SER	2.0
6	F	23	PHE	2.0
6	F	141	PHE	2.0
12	L	62	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
21	U	31	LEU	2.0
1	A	569	U	2.0
4	D	57	LYS	2.0
15	O	19	LYS	2.0
5	E	37	VAL	2.0
8	H	64	GLU	2.0
2	B	67	G	2.0
28	2	30	LEU	2.0
31	5	50	LEU	2.0
1	A	1887	C	2.0
24	X	57	GLU	2.0
8	H	83	ALA	2.0
5	E	99	TYR	2.0
10	J	42	GLU	2.0
22	V	44	PHE	2.0
26	Z	37	LEU	2.0
20	T	34	ALA	2.0
12	L	142	GLY	2.0
23	W	20	ARG	2.0
1	A	2249	U	2.0
26	Z	38	GLU	2.0
22	V	50	GLN	2.0
14	N	68	ARG	2.0
8	H	26	ALA	2.0
21	U	27	VAL	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	A	3051	1/1	1.15	-	85,85,85,85	0
32	MG	A	3542	1/1	0.33	-	107,107,107,107	0
32	MG	A	3618	1/1	1.02	-	69,69,69,69	0
32	MG	6	128	1/1	0.14	-	99,99,99,99	0
32	MG	A	3063	1/1	0.57	-	60,60,60,60	0
32	MG	B	1086	1/1	0.38	-	96,96,96,96	0
32	MG	C	1142	1/1	0.25	-	90,90,90,90	0
32	MG	6	411	1/1	0.14	-	96,96,96,96	0
32	MG	A	3006	1/1	0.32	-	51,51,51,51	0
32	MG	A	3186	1/1	0.84	-	64,64,64,64	0
32	MG	A	3095	1/1	0.22	-	74,74,74,74	0
32	MG	F	703	1/1	0.16	-	122,122,122,122	0
32	MG	A	3395	1/1	0.55	-	136,136,136,136	0
32	MG	A	3155	1/1	0.36	-	87,87,87,87	0
32	MG	A	3639	1/1	0.40	-	53,53,53,53	0
32	MG	A	1	1/1	0.26	-	8,8,8,8	0
32	MG	C	274	1/1	0.32	-	89,89,89,89	0
32	MG	A	2964	1/1	0.59	-	47,47,47,47	0
32	MG	6	414	1/1	0.15	-	115,115,115,115	0
32	MG	A	3543	1/1	0.19	-	83,83,83,83	0
32	MG	A	3039	1/1	0.31	-	69,69,69,69	0
32	MG	A	3559	1/1	0.60	-	61,61,61,61	0
32	MG	A	2	1/1	0.49	-	12,12,12,12	0
32	MG	A	3393	1/1	0.60	-	93,93,93,93	0
32	MG	A	3309	1/1	0.50	-	69,69,69,69	0
32	MG	A	3219	1/1	0.14	-	61,61,61,61	0
32	MG	6	158	1/1	0.24	-	81,81,81,81	0
32	MG	A	3158	1/1	0.24	-	73,73,73,73	0
32	MG	A	2907	1/1	0.35	-	20,20,20,20	0
32	MG	A	3419	1/1	0.35	-	128,128,128,128	0
32	MG	6	889	1/1	0.76	-	78,78,78,78	0
32	MG	6	631	1/1	0.10	-	98,98,98,98	0
32	MG	A	3478	1/1	0.54	-	71,71,71,71	0
32	MG	A	2989	1/1	0.26	-	49,49,49,49	0
32	MG	A	3213	1/1	0.62	-	141,141,141,141	0
32	MG	6	1066	1/1	0.44	-	88,88,88,88	0
32	MG	A	3298	1/1	0.28	-	100,100,100,100	0
32	MG	A	3233	1/1	0.99	-	157,157,157,157	0
32	MG	A	3358	1/1	1.19	-	80,80,80,80	0
32	MG	A	3222	1/1	0.21	-	111,111,111,111	0
32	MG	A	3327	1/1	0.52	-	113,113,113,113	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3136	1/1	0.53	-	74,74,74,74	0
32	MG	A	3658	1/1	0.39	-	98,98,98,98	0
32	MG	A	3610	1/1	0.11	-	100,100,100,100	0
32	MG	6	918	1/1	0.37	-	91,91,91,91	0
32	MG	A	2933	1/1	0.19	-	30,30,30,30	0
32	MG	A	3058	1/1	0.51	-	85,85,85,85	0
32	MG	6	757	1/1	0.39	-	148,148,148,148	0
32	MG	A	3553	1/1	0.53	-	102,102,102,102	0
32	MG	A	3571	1/1	1.21	-	70,70,70,70	0
32	MG	A	3082	1/1	0.29	-	63,63,63,63	0
32	MG	A	3388	1/1	0.19	-	134,134,134,134	0
32	MG	A	3300	1/1	0.22	-	78,78,78,78	0
32	MG	A	3464	1/1	0.12	-	77,77,77,77	0
32	MG	A	2973	1/1	0.42	-	65,65,65,65	0
32	MG	A	3310	1/1	0.30	-	84,84,84,84	0
32	MG	6	925	1/1	0.17	-	92,92,92,92	0
32	MG	A	3029	1/1	0.18	-	50,50,50,50	0
32	MG	1	780	1/1	0.17	-	126,126,126,126	0
32	MG	A	3594	1/1	0.69	-	102,102,102,102	0
32	MG	A	3045	1/1	0.75	-	78,78,78,78	0
32	MG	A	3414	1/1	0.83	-	112,112,112,112	0
32	MG	A	3266	1/1	1.01	-	98,98,98,98	0
32	MG	A	3042	1/1	0.53	-	78,78,78,78	0
32	MG	A	3417	1/1	0.35	-	65,65,65,65	0
32	MG	A	3087	1/1	0.47	-	90,90,90,90	0
32	MG	A	2953	1/1	0.43	-	75,75,75,75	0
32	MG	6	185	1/1	0.30	-	48,48,48,48	0
32	MG	A	3590	1/1	0.35	-	77,77,77,77	0
32	MG	A	3221	1/1	0.20	-	90,90,90,90	0
32	MG	A	3556	1/1	0.57	-	59,59,59,59	0
32	MG	6	319	1/1	0.14	-	93,93,93,93	0
32	MG	A	168	1/1	0.54	-	77,77,77,77	0
32	MG	6	664	1/1	0.48	-	99,99,99,99	0
32	MG	A	3257	1/1	0.25	-	87,87,87,87	0
32	MG	A	2954	1/1	0.37	-	46,46,46,46	0
32	MG	6	190	1/1	0.30	-	96,96,96,96	0
32	MG	6	320	1/1	0.33	-	74,74,74,74	0
32	MG	M	608	1/1	0.47	-	85,85,85,85	0
32	MG	6	58	1/1	0.30	-	26,26,26,26	0
32	MG	A	3122	1/1	0.28	-	66,66,66,66	0
32	MG	B	171	1/1	0.54	-	74,74,74,74	0
32	MG	A	3451	1/1	0.38	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	321	1/1	0.50	-	78,78,78,78	0
32	MG	A	2967	1/1	0.48	-	76,76,76,76	0
32	MG	6	421	1/1	0.25	-	124,124,124,124	0
32	MG	A	3529	1/1	0.89	-	81,81,81,81	0
32	MG	A	3495	1/1	0.72	-	72,72,72,72	0
32	MG	6	382	1/1	0.62	-	64,64,64,64	0
32	MG	6	409	1/1	0.20	-	83,83,83,83	0
32	MG	A	3502	1/1	0.16	-	70,70,70,70	0
32	MG	A	3381	1/1	0.22	-	86,86,86,86	0
32	MG	P	695	1/1	0.20	-	84,84,84,84	0
32	MG	A	2950	1/1	0.28	-	73,73,73,73	0
32	MG	A	3105	1/1	0.15	-	70,70,70,70	0
32	MG	A	3524	1/1	0.15	-	74,74,74,74	0
32	MG	6	876	1/1	0.23	-	61,61,61,61	0
32	MG	A	3593	1/1	0.33	-	127,127,127,127	0
32	MG	A	3022	1/1	0.21	-	57,57,57,57	0
32	MG	A	3339	1/1	0.33	-	85,85,85,85	0
32	MG	A	3338	1/1	0.52	-	103,103,103,103	0
32	MG	A	2961	1/1	0.17	-	51,51,51,51	0
32	MG	A	3400	1/1	0.29	-	74,74,74,74	0
32	MG	A	3162	1/1	0.30	-	74,74,74,74	0
32	MG	6	709	1/1	0.15	-	105,105,105,105	0
32	MG	A	3638	1/1	0.32	-	82,82,82,82	0
32	MG	A	3600	1/1	0.50	-	52,52,52,52	0
32	MG	6	498	1/1	0.31	-	58,58,58,58	0
32	MG	A	157	1/1	0.15	-	52,52,52,52	0
32	MG	A	3341	1/1	0.52	-	62,62,62,62	0
32	MG	A	3578	1/1	0.21	-	126,126,126,126	0
32	MG	6	84	1/1	0.56	-	54,54,54,54	0
32	MG	A	3684	1/1	0.26	-	84,84,84,84	0
32	MG	6	473	1/1	0.10	-	87,87,87,87	0
32	MG	H	954	1/1	0.50	-	107,107,107,107	0
32	MG	6	1009	1/1	0.41	-	115,115,115,115	0
32	MG	A	3690	1/1	0.33	-	120,120,120,120	0
32	MG	A	3438	1/1	0.23	-	12,12,12,12	0
32	MG	A	3484	1/1	0.34	-	53,53,53,53	0
32	MG	6	187	1/1	0.10	-	37,37,37,37	0
32	MG	A	3236	1/1	0.54	-	85,85,85,85	0
32	MG	C	578	1/1	0.54	-	76,76,76,76	0
32	MG	A	3164	1/1	0.48	-	67,67,67,67	0
32	MG	A	3047	1/1	0.24	-	48,48,48,48	0
32	MG	A	3248	1/1	0.22	-	101,101,101,101	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3612	1/1	0.25	-	93,93,93,93	0
32	MG	6	836	1/1	0.27	-	58,58,58,58	0
32	MG	6	841	1/1	0.45	-	69,69,69,69	0
32	MG	A	891	1/1	0.43	-	72,72,72,72	0
32	MG	A	3252	1/1	0.54	-	64,64,64,64	0
32	MG	6	289	1/1	0.11	-	70,70,70,70	0
32	MG	6	596	1/1	2.67	-	119,119,119,119	0
32	MG	A	3369	1/1	0.67	-	74,74,74,74	0
32	MG	A	3032	1/1	0.81	-	65,65,65,65	0
32	MG	B	920	1/1	0.17	-	69,69,69,69	0
32	MG	A	2943	1/1	0.22	-	62,62,62,62	0
32	MG	6	660	1/1	0.30	-	88,88,88,88	0
32	MG	A	3406	1/1	1.44	-	106,106,106,106	0
32	MG	A	3356	1/1	0.51	-	72,72,72,72	0
32	MG	A	3220	1/1	0.26	-	42,42,42,42	0
32	MG	A	3672	1/1	0.53	-	107,107,107,107	0
32	MG	A	3496	1/1	0.32	-	60,60,60,60	0
32	MG	X	682	1/1	0.56	-	103,103,103,103	0
32	MG	6	502	1/1	0.26	-	76,76,76,76	0
32	MG	A	3373	1/1	0.24	-	114,114,114,114	0
32	MG	A	3205	1/1	0.39	-	79,79,79,79	0
32	MG	A	270	1/1	0.41	-	72,72,72,72	0
32	MG	A	3157	1/1	0.08	-	65,65,65,65	0
32	MG	A	2934	1/1	0.09	-	46,46,46,46	0
32	MG	A	3437	1/1	0.25	-	26,26,26,26	0
32	MG	A	3311	1/1	1.18	-	97,97,97,97	0
32	MG	A	3606	1/1	0.31	-	129,129,129,129	0
32	MG	6	1100	1/1	0.44	-	103,103,103,103	0
32	MG	6	342	1/1	0.53	-	90,90,90,90	0
32	MG	A	3	1/1	0.75	-	22,22,22,22	0
32	MG	A	3633	1/1	0.32	-	88,88,88,88	0
32	MG	A	3537	1/1	0.47	-	65,65,65,65	0
32	MG	6	1146	1/1	1.34	-	98,98,98,98	0
32	MG	A	2956	1/1	0.27	-	39,39,39,39	0
32	MG	A	3342	1/1	0.45	-	87,87,87,87	0
32	MG	A	3413	1/1	0.30	-	51,51,51,51	0
32	MG	A	3520	1/1	0.41	-	86,86,86,86	0
32	MG	6	256	1/1	0.40	-	102,102,102,102	0
32	MG	A	3307	1/1	1.53	-	56,56,56,56	0
32	MG	6	349	1/1	0.22	-	78,78,78,78	0
32	MG	A	3399	1/1	0.27	-	125,125,125,125	0
32	MG	6	485	1/1	0.10	-	105,105,105,105	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	2931	1/1	0.38	-	51,51,51,51	0
32	MG	A	2898	1/1	0.19	-	24,24,24,24	0
32	MG	A	3021	1/1	0.36	-	61,61,61,61	0
32	MG	J	939	1/1	0.12	-	89,89,89,89	0
32	MG	A	3512	1/1	0.14	-	81,81,81,81	0
32	MG	A	3320	1/1	0.37	-	98,98,98,98	0
32	MG	A	2948	1/1	0.27	-	45,45,45,45	0
32	MG	A	2903	1/1	0.57	-	33,33,33,33	0
32	MG	A	3354	1/1	0.91	-	85,85,85,85	0
32	MG	A	3098	1/1	0.51	-	72,72,72,72	0
32	MG	A	3161	1/1	0.43	-	127,127,127,127	0
32	MG	6	1122	1/1	0.14	-	75,75,75,75	0
32	MG	A	3199	1/1	0.33	-	70,70,70,70	0
32	MG	A	3583	1/1	0.09	-	87,87,87,87	0
32	MG	A	3100	1/1	0.91	-	64,64,64,64	0
32	MG	A	3230	1/1	0.33	-	49,49,49,49	0
32	MG	A	3319	1/1	1.66	-	71,71,71,71	0
32	MG	A	3595	1/1	0.21	-	105,105,105,105	0
32	MG	A	3367	1/1	0.24	-	131,131,131,131	0
32	MG	6	875	1/1	0.26	-	86,86,86,86	0
32	MG	A	3494	1/1	1.02	-	56,56,56,56	0
32	MG	S	316	1/1	0.22	-	52,52,52,52	0
32	MG	A	3398	1/1	0.09	-	108,108,108,108	0
32	MG	A	3507	1/1	0.26	-	67,67,67,67	0
32	MG	A	3509	1/1	0.49	-	67,67,67,67	0
32	MG	A	3090	1/1	0.94	-	74,74,74,74	0
32	MG	A	3624	1/1	1.20	-	75,75,75,75	0
32	MG	6	18	1/1	0.20	-	35,35,35,35	0
32	MG	A	3210	1/1	1.23	-	55,55,55,55	0
32	MG	A	3012	1/1	0.62	-	88,88,88,88	0
32	MG	A	169	1/1	0.41	-	69,69,69,69	0
32	MG	6	693	1/1	0.15	-	97,97,97,97	0
32	MG	A	3057	1/1	0.52	-	52,52,52,52	0
32	MG	A	3582	1/1	0.30	-	74,74,74,74	0
32	MG	A	2942	1/1	0.04	-	29,29,29,29	0
32	MG	A	3432	1/1	0.75	-	87,87,87,87	0
32	MG	A	2926	1/1	0.23	-	44,44,44,44	0
32	MG	A	3383	1/1	0.60	-	82,82,82,82	0
32	MG	A	3009	1/1	0.15	-	55,55,55,55	0
32	MG	6	729	1/1	0.28	-	104,104,104,104	0
32	MG	A	3440	1/1	0.16	-	19,19,19,19	0
32	MG	P	471	1/1	0.24	-	137,137,137,137	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	A	3297	1/1	1.11	-	157,157,157,157	0
32	MG	6	886	1/1	0.35	-	82,82,82,82	0
32	MG	A	3640	1/1	0.98	-	64,64,64,64	0
32	MG	A	3636	1/1	0.29	-	90,90,90,90	0
32	MG	A	3083	1/1	0.47	-	96,96,96,96	0
32	MG	A	2966	1/1	0.39	-	55,55,55,55	0
32	MG	A	3619	1/1	0.23	-	118,118,118,118	0
32	MG	A	3049	1/1	0.24	-	54,54,54,54	0
32	MG	A	3682	1/1	0.19	-	85,85,85,85	0
32	MG	A	3446	1/1	0.18	-	23,23,23,23	0
32	MG	A	3405	1/1	0.17	-	111,111,111,111	0
32	MG	A	3466	1/1	0.33	-	47,47,47,47	0
32	MG	6	1103	1/1	0.25	-	87,87,87,87	0
32	MG	B	1003	1/1	0.42	-	112,112,112,112	0
32	MG	A	3679	1/1	0.07	-	69,69,69,69	0
32	MG	A	3490	1/1	0.89	-	71,71,71,71	0
32	MG	A	3060	1/1	0.16	-	57,57,57,57	0
32	MG	A	3577	1/1	0.81	-	72,72,72,72	0
32	MG	6	846	1/1	0.18	-	71,71,71,71	0
32	MG	6	526	1/1	0.14	-	126,126,126,126	0
32	MG	6	199	1/1	0.75	-	54,54,54,54	0
32	MG	B	597	1/1	0.29	-	107,107,107,107	0
32	MG	A	3023	1/1	0.47	-	62,62,62,62	0
32	MG	A	538	1/1	0.82	-	81,81,81,81	0
32	MG	A	3066	1/1	0.34	-	104,104,104,104	0
32	MG	A	3317	1/1	0.38	-	179,179,179,179	0
32	MG	A	3129	1/1	0.13	-	88,88,88,88	0
32	MG	6	527	1/1	0.37	-	79,79,79,79	0
32	MG	A	3040	1/1	0.21	-	65,65,65,65	0
32	MG	6	363	1/1	0.83	-	91,91,91,91	0
32	MG	A	2962	1/1	0.24	-	38,38,38,38	0
32	MG	6	1083	1/1	0.41	-	70,70,70,70	0
32	MG	A	3384	1/1	0.14	-	85,85,85,85	0
32	MG	A	3598	1/1	0.32	-	97,97,97,97	0
32	MG	A	2902	1/1	0.20	-	17,17,17,17	0
32	MG	A	3227	1/1	0.50	-	54,54,54,54	0
32	MG	A	3681	1/1	0.82	-	72,72,72,72	0
32	MG	A	3362	1/1	0.59	-	76,76,76,76	0
32	MG	A	3187	1/1	1.01	-	91,91,91,91	0
32	MG	A	3139	1/1	0.32	-	62,62,62,62	0
32	MG	A	3389	1/1	1.01	-	84,84,84,84	0
32	MG	6	1098	1/1	0.12	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3101	1/1	0.20	-	65,65,65,65	0
32	MG	A	3159	1/1	0.57	-	43,43,43,43	0
32	MG	A	2957	1/1	0.64	-	51,51,51,51	0
32	MG	A	3527	1/1	0.51	-	100,100,100,100	0
32	MG	6	895	1/1	0.82	-	89,89,89,89	0
32	MG	A	2936	1/1	0.28	-	19,19,19,19	0
32	MG	6	686	1/1	0.50	-	80,80,80,80	0
32	MG	6	848	1/1	0.44	-	62,62,62,62	0
32	MG	A	3360	1/1	0.33	-	89,89,89,89	0
32	MG	6	885	1/1	0.40	-	106,106,106,106	0
32	MG	A	3450	1/1	0.21	-	26,26,26,26	0
32	MG	A	3135	1/1	0.39	-	148,148,148,148	0
32	MG	6	1139	1/1	0.42	-	114,114,114,114	0
32	MG	A	2905	1/1	0.49	-	27,27,27,27	0
32	MG	A	3024	1/1	0.22	-	63,63,63,63	0
32	MG	A	3067	1/1	0.25	-	73,73,73,73	0
32	MG	A	3648	1/1	0.42	-	98,98,98,98	0
32	MG	6	423	1/1	1.09	-	73,73,73,73	0
32	MG	6	975	1/1	1.18	-	74,74,74,74	0
32	MG	A	3065	1/1	0.48	-	55,55,55,55	0
32	MG	A	3386	1/1	0.32	-	93,93,93,93	0
32	MG	A	3335	1/1	1.33	-	87,87,87,87	0
32	MG	A	3426	1/1	1.04	-	111,111,111,111	0
32	MG	A	3292	1/1	0.26	-	126,126,126,126	0
32	MG	A	3688	1/1	0.73	-	92,92,92,92	0
32	MG	A	3329	1/1	0.41	-	66,66,66,66	0
32	MG	A	3079	1/1	0.23	-	72,72,72,72	0
32	MG	A	2912	1/1	0.50	-	45,45,45,45	0
32	MG	A	2917	1/1	0.53	-	48,48,48,48	0
32	MG	A	3068	1/1	0.33	-	43,43,43,43	0
32	MG	A	3008	1/1	0.20	-	45,45,45,45	0
32	MG	K	674	1/1	3.10	-	106,106,106,106	0
32	MG	A	3482	1/1	0.26	-	72,72,72,72	0
32	MG	6	110	1/1	0.39	-	56,56,56,56	0
32	MG	6	656	1/1	0.74	-	110,110,110,110	0
32	MG	A	3209	1/1	0.63	-	55,55,55,55	0
32	MG	A	3676	1/1	0.21	-	119,119,119,119	0
32	MG	A	3077	1/1	1.01	-	69,69,69,69	0
32	MG	A	3305	1/1	0.54	-	87,87,87,87	0
32	MG	A	3526	1/1	0.22	-	54,54,54,54	0
32	MG	A	2921	1/1	0.29	-	28,28,28,28	0
32	MG	A	3097	1/1	0.81	-	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3397	1/1	0.50	-	84,84,84,84	0
32	MG	A	3247	1/1	0.32	-	68,68,68,68	0
32	MG	6	1116	1/1	0.24	-	119,119,119,119	0
32	MG	A	3586	1/1	0.58	-	59,59,59,59	0
32	MG	A	3011	1/1	0.39	-	55,55,55,55	0
32	MG	A	3563	1/1	0.23	-	99,99,99,99	0
32	MG	A	2984	1/1	0.14	-	40,40,40,40	0
32	MG	6	478	1/1	0.08	-	84,84,84,84	0
32	MG	F	418	1/1	0.21	-	62,62,62,62	0
32	MG	6	508	1/1	0.07	-	63,63,63,63	0
32	MG	6	767	1/1	0.17	-	109,109,109,109	0
32	MG	A	3510	1/1	0.38	-	66,66,66,66	0
32	MG	A	3115	1/1	0.50	-	78,78,78,78	0
32	MG	6	1104	1/1	1.20	-	138,138,138,138	0
32	MG	A	3645	1/1	0.63	-	85,85,85,85	0
32	MG	A	2983	1/1	0.21	-	79,79,79,79	0
32	MG	A	3000	1/1	0.35	-	49,49,49,49	0
32	MG	A	3353	1/1	0.21	-	80,80,80,80	0
32	MG	A	3538	1/1	0.21	-	73,73,73,73	0
32	MG	A	3511	1/1	1.10	-	105,105,105,105	0
32	MG	K	434	1/1	0.50	-	114,114,114,114	0
32	MG	A	2951	1/1	0.44	-	63,63,63,63	0
32	MG	6	240	1/1	0.24	-	92,92,92,92	0
32	MG	6	772	1/1	0.30	-	101,101,101,101	0
32	MG	B	837	1/1	0.30	-	79,79,79,79	0
32	MG	A	2976	1/1	0.28	-	51,51,51,51	0
32	MG	A	3123	1/1	0.35	-	86,86,86,86	0
32	MG	A	2978	1/1	0.19	-	38,38,38,38	0
32	MG	A	3271	1/1	0.37	-	88,88,88,88	0
32	MG	6	663	1/1	0.89	-	121,121,121,121	0
32	MG	A	3516	1/1	0.44	-	89,89,89,89	0
32	MG	M	760	1/1	0.42	-	90,90,90,90	0
32	MG	A	3312	1/1	0.38	-	84,84,84,84	0
32	MG	6	1031	1/1	0.08	-	69,69,69,69	0
32	MG	A	3152	1/1	0.33	-	87,87,87,87	0
32	MG	A	3643	1/1	0.34	-	86,86,86,86	0
32	MG	A	3653	1/1	0.37	-	127,127,127,127	0
32	MG	A	3481	1/1	1.42	-	70,70,70,70	0
32	MG	B	1155	1/1	0.54	-	80,80,80,80	0
32	MG	A	3521	1/1	0.43	-	78,78,78,78	0
32	MG	6	1144	1/1	0.55	-	74,74,74,74	0
32	MG	A	3423	1/1	0.28	-	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3455	1/1	0.42	-	31,31,31,31	0
32	MG	A	3355	1/1	0.78	-	123,123,123,123	0
32	MG	A	3121	1/1	0.48	-	47,47,47,47	0
32	MG	B	481	1/1	0.12	-	67,67,67,67	0
32	MG	A	3439	1/1	0.46	-	21,21,21,21	0
32	MG	A	3599	1/1	0.37	-	77,77,77,77	0
32	MG	A	3424	1/1	1.27	-	67,67,67,67	0
32	MG	A	2930	1/1	0.22	-	56,56,56,56	0
32	MG	A	3330	1/1	0.47	-	65,65,65,65	0
32	MG	6	298	1/1	0.80	-	78,78,78,78	0
32	MG	A	3195	1/1	0.19	-	67,67,67,67	0
32	MG	6	195	1/1	0.13	-	89,89,89,89	0
32	MG	A	3392	1/1	0.15	-	103,103,103,103	0
32	MG	6	724	1/1	0.41	-	92,92,92,92	0
32	MG	A	3099	1/1	0.09	-	54,54,54,54	0
32	MG	6	148	1/1	0.15	-	86,86,86,86	0
32	MG	A	2945	1/1	0.32	-	68,68,68,68	0
32	MG	A	3225	1/1	1.29	-	97,97,97,97	0
32	MG	A	3404	1/1	0.90	-	90,90,90,90	0
32	MG	A	3278	1/1	0.41	-	95,95,95,95	0
32	MG	6	95	1/1	0.69	-	71,71,71,71	0
32	MG	A	3268	1/1	0.43	-	68,68,68,68	0
32	MG	A	3172	1/1	0.56	-	78,78,78,78	0
32	MG	A	3677	1/1	0.32	-	82,82,82,82	0
32	MG	6	176	1/1	0.18	-	123,123,123,123	0
32	MG	A	3622	1/1	0.22	-	65,65,65,65	0
32	MG	A	3321	1/1	0.81	-	109,109,109,109	0
32	MG	6	65	1/1	0.26	-	55,55,55,55	0
32	MG	6	668	1/1	0.15	-	91,91,91,91	0
32	MG	A	3237	1/1	0.53	-	79,79,79,79	0
32	MG	A	3014	1/1	0.55	-	88,88,88,88	0
32	MG	6	616	1/1	0.59	-	94,94,94,94	0
32	MG	A	3178	1/1	0.71	-	103,103,103,103	0
32	MG	6	243	1/1	0.66	-	56,56,56,56	0
32	MG	A	3246	1/1	0.28	-	88,88,88,88	0
32	MG	T	726	1/1	0.92	-	66,66,66,66	0
32	MG	6	870	1/1	0.14	-	94,94,94,94	0
32	MG	6	769	1/1	0.18	-	106,106,106,106	0
32	MG	A	3380	1/1	0.71	-	80,80,80,80	0
32	MG	A	3613	1/1	0.22	-	76,76,76,76	0
32	MG	6	260	1/1	0.21	-	99,99,99,99	0
32	MG	A	3588	1/1	0.26	-	142,142,142,142	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	2993	1/1	0.80	-	81,81,81,81	0
32	MG	A	3074	1/1	0.17	-	63,63,63,63	0
32	MG	A	3545	1/1	0.79	-	82,82,82,82	0
32	MG	A	3609	1/1	0.75	-	56,56,56,56	0
32	MG	6	905	1/1	0.76	-	76,76,76,76	0
32	MG	6	922	1/1	0.54	-	71,71,71,71	0
32	MG	A	2927	1/1	0.12	-	36,36,36,36	0
32	MG	A	3275	1/1	0.69	-	98,98,98,98	0
32	MG	A	3508	1/1	1.18	-	61,61,61,61	0
32	MG	A	3493	1/1	0.28	-	76,76,76,76	0
32	MG	A	3326	1/1	0.26	-	80,80,80,80	0
32	MG	A	3566	1/1	0.29	-	66,66,66,66	0
32	MG	A	3273	1/1	0.86	-	61,61,61,61	0
32	MG	A	974	1/1	0.29	-	75,75,75,75	0
32	MG	A	3492	1/1	0.57	-	71,71,71,71	0
32	MG	A	3295	1/1	0.64	-	58,58,58,58	0
32	MG	6	1150	1/1	1.28	-	110,110,110,110	0
32	MG	A	3314	1/1	0.11	-	79,79,79,79	0
32	MG	A	3119	1/1	0.30	-	98,98,98,98	0
32	MG	A	3096	1/1	0.54	-	72,72,72,72	0
32	MG	A	3256	1/1	0.29	-	107,107,107,107	0
32	MG	6	577	1/1	0.59	-	81,81,81,81	0
32	MG	6	1089	1/1	1.30	-	84,84,84,84	0
32	MG	A	3343	1/1	0.43	-	99,99,99,99	0
32	MG	6	46	1/1	0.14	-	62,62,62,62	0
32	MG	6	361	1/1	0.25	-	140,140,140,140	0
32	MG	A	3182	1/1	0.40	-	69,69,69,69	0
32	MG	6	1047	1/1	0.17	-	69,69,69,69	0
32	MG	A	3134	1/1	0.51	-	48,48,48,48	0
32	MG	6	692	1/1	0.10	-	111,111,111,111	0
32	MG	A	3621	1/1	0.97	-	101,101,101,101	0
32	MG	A	3368	1/1	0.95	-	80,80,80,80	0
32	MG	6	432	1/1	0.47	-	57,57,57,57	0
32	MG	A	3254	1/1	0.20	-	75,75,75,75	0
32	MG	N	989	1/1	0.64	-	78,78,78,78	0
32	MG	A	3555	1/1	0.44	-	81,81,81,81	0
32	MG	A	3028	1/1	1.14	-	92,92,92,92	0
32	MG	A	2980	1/1	0.33	-	50,50,50,50	0
32	MG	A	3322	1/1	0.23	-	168,168,168,168	0
32	MG	A	3239	1/1	0.41	-	164,164,164,164	0
32	MG	A	3144	1/1	0.34	-	50,50,50,50	0
32	MG	A	2909	1/1	0.31	-	6,6,6,6	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3370	1/1	0.33	-	58,58,58,58	0
32	MG	A	3539	1/1	0.55	-	79,79,79,79	0
32	MG	A	2960	1/1	0.36	-	43,43,43,43	0
32	MG	A	3177	1/1	0.61	-	73,73,73,73	0
32	MG	C	976	1/1	0.99	-	105,105,105,105	0
32	MG	6	585	1/1	0.54	-	112,112,112,112	0
32	MG	A	369	1/1	0.09	-	97,97,97,97	0
32	MG	A	3289	1/1	1.02	-	60,60,60,60	0
32	MG	A	3445	1/1	0.52	-	17,17,17,17	0
32	MG	6	354	1/1	0.23	-	101,101,101,101	0
32	MG	A	3601	1/1	0.28	-	105,105,105,105	0
32	MG	A	3651	1/1	0.63	-	76,76,76,76	0
32	MG	P	901	1/1	0.08	-	84,84,84,84	0
32	MG	A	3631	1/1	0.43	-	76,76,76,76	0
32	MG	A	3085	1/1	0.72	-	76,76,76,76	0
32	MG	A	3211	1/1	0.13	-	80,80,80,80	0
32	MG	A	3194	1/1	0.37	-	126,126,126,126	0
32	MG	6	27	1/1	0.13	-	37,37,37,37	0
32	MG	A	3501	1/1	0.43	-	79,79,79,79	0
32	MG	A	3061	1/1	0.19	-	63,63,63,63	0
32	MG	A	3132	1/1	0.64	-	91,91,91,91	0
32	MG	6	261	1/1	0.29	-	58,58,58,58	0
32	MG	6	464	1/1	0.51	-	77,77,77,77	0
32	MG	A	2944	1/1	0.12	-	65,65,65,65	0
32	MG	A	2914	1/1	0.17	-	17,17,17,17	0
32	MG	A	3530	1/1	0.12	-	50,50,50,50	0
32	MG	A	3316	1/1	0.26	-	103,103,103,103	0
32	MG	A	3176	1/1	0.07	-	85,85,85,85	0
32	MG	A	3201	1/1	0.18	-	86,86,86,86	0
32	MG	6	140	1/1	0.25	-	53,53,53,53	0
32	MG	6	227	1/1	0.20	-	63,63,63,63	0
32	MG	A	3635	1/1	0.38	-	91,91,91,91	0
32	MG	A	3579	1/1	0.46	-	69,69,69,69	0
32	MG	A	3226	1/1	0.60	-	73,73,73,73	0
32	MG	A	3103	1/1	0.45	-	69,69,69,69	0
32	MG	A	3269	1/1	0.24	-	67,67,67,67	0
32	MG	A	3415	1/1	0.50	-	90,90,90,90	0
32	MG	6	401	1/1	0.21	-	88,88,88,88	0
32	MG	A	3391	1/1	1.45	-	66,66,66,66	0
32	MG	A	3036	1/1	0.59	-	57,57,57,57	0
32	MG	C	619	1/1	0.92	-	82,82,82,82	0
32	MG	A	3548	1/1	0.47	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3659	1/1	1.07	-	92,92,92,92	0
32	MG	A	3281	1/1	0.94	-	83,83,83,83	0
32	MG	A	3632	1/1	0.21	-	145,145,145,145	0
32	MG	A	3519	1/1	0.77	-	64,64,64,64	0
32	MG	A	2904	1/1	0.52	-	19,19,19,19	0
32	MG	A	3138	1/1	0.81	-	123,123,123,123	0
32	MG	A	3546	1/1	0.31	-	95,95,95,95	0
32	MG	6	340	1/1	0.17	-	82,82,82,82	0
32	MG	A	3592	1/1	0.50	-	94,94,94,94	0
32	MG	A	3241	1/1	0.26	-	82,82,82,82	0
32	MG	A	3436	1/1	0.22	-	6,6,6,6	0
32	MG	6	395	1/1	0.24	-	90,90,90,90	0
32	MG	A	3263	1/1	0.30	-	93,93,93,93	0
32	MG	6	501	1/1	0.41	-	96,96,96,96	0
32	MG	A	3127	1/1	0.31	-	90,90,90,90	0
32	MG	A	3055	1/1	0.46	-	103,103,103,103	0
32	MG	A	3088	1/1	0.22	-	56,56,56,56	0
32	MG	A	3666	1/1	0.75	-	69,69,69,69	0
32	MG	A	3346	1/1	1.00	-	68,68,68,68	0
32	MG	U	1030	1/1	0.33	-	74,74,74,74	0
32	MG	A	3550	1/1	0.51	-	97,97,97,97	0
32	MG	A	3261	1/1	0.63	-	84,84,84,84	0
32	MG	A	3616	1/1	0.56	-	89,89,89,89	0
32	MG	A	3324	1/1	0.16	-	82,82,82,82	0
32	MG	A	3475	1/1	0.28	-	87,87,87,87	0
32	MG	6	1114	1/1	1.55	-	106,106,106,106	0
32	MG	A	3015	1/1	0.70	-	66,66,66,66	0
32	MG	A	3294	1/1	0.60	-	93,93,93,93	0
32	MG	A	3627	1/1	0.12	-	112,112,112,112	0
32	MG	A	3525	1/1	0.29	-	83,83,83,83	0
32	MG	A	3589	1/1	0.42	-	74,74,74,74	0
32	MG	P	287	1/1	0.61	-	80,80,80,80	0
32	MG	A	3214	1/1	0.43	-	86,86,86,86	0
32	MG	A	3255	1/1	0.09	-	53,53,53,53	0
32	MG	A	3670	1/1	0.38	-	122,122,122,122	0
32	MG	6	740	1/1	0.32	-	117,117,117,117	0
32	MG	A	3558	1/1	0.71	-	87,87,87,87	0
32	MG	A	3075	1/1	1.16	-	84,84,84,84	0
32	MG	A	2955	1/1	0.13	-	40,40,40,40	0
32	MG	A	3078	1/1	0.57	-	84,84,84,84	0
32	MG	A	3587	1/1	0.22	-	83,83,83,83	0
32	MG	A	2971	1/1	0.18	-	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3444	1/1	0.26	-	29,29,29,29	0
32	MG	6	517	1/1	0.40	-	105,105,105,105	0
32	MG	A	3106	1/1	0.47	-	91,91,91,91	0
32	MG	A	3223	1/1	0.94	-	64,64,64,64	0
32	MG	A	3035	1/1	0.80	-	58,58,58,58	0
32	MG	6	55	1/1	0.09	-	46,46,46,46	0
32	MG	A	3580	1/1	0.47	-	116,116,116,116	0
32	MG	U	280	1/1	0.35	-	70,70,70,70	0
32	MG	6	208	1/1	0.17	-	63,63,63,63	0
32	MG	A	3163	1/1	0.18	-	87,87,87,87	0
32	MG	6	400	1/1	0.94	-	75,75,75,75	0
32	MG	Y	438	1/1	0.40	-	110,110,110,110	0
32	MG	A	3016	1/1	0.90	-	83,83,83,83	0
32	MG	A	3487	1/1	0.33	-	69,69,69,69	0
32	MG	A	3465	1/1	0.35	-	30,30,30,30	0
32	MG	A	3642	1/1	0.21	-	102,102,102,102	0
32	MG	A	3680	1/1	0.47	-	123,123,123,123	0
32	MG	A	3131	1/1	0.68	-	62,62,62,62	0
32	MG	A	3363	1/1	0.54	-	154,154,154,154	0
32	MG	A	3409	1/1	0.72	-	78,78,78,78	0
32	MG	A	3585	1/1	0.39	-	62,62,62,62	0
32	MG	6	1110	1/1	0.56	-	81,81,81,81	0
32	MG	A	3081	1/1	0.15	-	67,67,67,67	0
32	MG	A	2920	1/1	0.16	-	25,25,25,25	0
32	MG	A	2998	1/1	1.04	-	96,96,96,96	0
32	MG	A	3086	1/1	0.29	-	57,57,57,57	0
32	MG	A	2959	1/1	0.35	-	34,34,34,34	0
32	MG	A	3313	1/1	0.61	-	73,73,73,73	0
32	MG	A	3513	1/1	0.61	-	90,90,90,90	0
32	MG	6	1056	1/1	0.09	-	126,126,126,126	0
32	MG	6	424	1/1	1.32	-	91,91,91,91	0
32	MG	B	551	1/1	0.40	-	82,82,82,82	0
32	MG	A	2977	1/1	0.33	-	56,56,56,56	0
32	MG	A	3348	1/1	0.25	-	77,77,77,77	0
32	MG	A	3193	1/1	0.89	-	107,107,107,107	0
32	MG	A	3421	1/1	0.35	-	83,83,83,83	0
32	MG	6	357	1/1	1.05	-	78,78,78,78	0
32	MG	A	3462	1/1	0.32	-	64,64,64,64	0
32	MG	6	114	1/1	0.15	-	71,71,71,71	0
32	MG	K	1004	1/1	0.67	-	158,158,158,158	0
32	MG	A	3026	1/1	1.19	-	76,76,76,76	0
32	MG	A	3153	1/1	0.28	-	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3002	1/1	0.47	-	61,61,61,61	0
32	MG	A	3347	1/1	0.14	-	91,91,91,91	0
32	MG	A	2970	1/1	0.21	-	60,60,60,60	0
32	MG	6	906	1/1	2.92	-	73,73,73,73	0
32	MG	A	3597	1/1	0.69	-	69,69,69,69	0
32	MG	6	854	1/1	1.21	-	80,80,80,80	0
32	MG	6	721	1/1	1.36	-	108,108,108,108	0
32	MG	6	953	1/1	0.62	-	75,75,75,75	0
32	MG	6	116	1/1	0.18	-	62,62,62,62	0
32	MG	A	3333	1/1	0.96	-	69,69,69,69	0
32	MG	6	738	1/1	0.15	-	89,89,89,89	0
32	MG	A	3359	1/1	0.39	-	81,81,81,81	0
32	MG	A	3259	1/1	1.16	-	104,104,104,104	0
32	MG	A	3412	1/1	0.26	-	86,86,86,86	0
32	MG	A	3033	1/1	0.33	-	72,72,72,72	0
32	MG	A	3148	1/1	0.56	-	70,70,70,70	0
32	MG	A	3262	1/1	0.34	-	104,104,104,104	0
32	MG	A	3518	1/1	0.14	-	90,90,90,90	0
32	MG	6	928	1/1	0.12	-	57,57,57,57	0
32	MG	A	3470	1/1	0.13	-	54,54,54,54	0
32	MG	6	566	1/1	0.66	-	111,111,111,111	0
32	MG	B	602	1/1	0.32	-	111,111,111,111	0
32	MG	A	3034	1/1	0.60	-	70,70,70,70	0
32	MG	A	3156	1/1	0.47	-	75,75,75,75	0
32	MG	A	3447	1/1	0.29	-	35,35,35,35	0
32	MG	A	3166	1/1	0.33	-	53,53,53,53	0
32	MG	A	3212	1/1	0.42	-	79,79,79,79	0
32	MG	A	3458	1/1	0.24	-	41,41,41,41	0
32	MG	6	731	1/1	0.08	-	123,123,123,123	0
32	MG	6	884	1/1	0.11	-	76,76,76,76	0
32	MG	V	642	1/1	0.34	-	98,98,98,98	0
32	MG	A	3443	1/1	0.28	-	42,42,42,42	0
32	MG	W	521	1/1	0.52	-	57,57,57,57	0
32	MG	A	3302	1/1	0.44	-	99,99,99,99	0
32	MG	A	3224	1/1	0.64	-	68,68,68,68	0
32	MG	A	3274	1/1	0.34	-	123,123,123,123	0
32	MG	A	3505	1/1	0.20	-	74,74,74,74	0
32	MG	A	3191	1/1	0.18	-	61,61,61,61	0
32	MG	A	3607	1/1	0.10	-	108,108,108,108	0
32	MG	A	3141	1/1	0.54	-	97,97,97,97	0
32	MG	A	2975	1/1	0.28	-	86,86,86,86	0
32	MG	A	2937	1/1	0.14	-	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3249	1/1	0.24	-	105,105,105,105	0
32	MG	A	3118	1/1	1.35	-	65,65,65,65	0
32	MG	A	3531	1/1	0.52	-	95,95,95,95	0
32	MG	A	3189	1/1	0.13	-	84,84,84,84	0
32	MG	A	3663	1/1	0.67	-	149,149,149,149	0
32	MG	A	3351	1/1	0.45	-	66,66,66,66	0
32	MG	C	273	1/1	0.31	-	60,60,60,60	0
32	MG	A	2915	1/1	0.24	-	38,38,38,38	0
32	MG	6	465	1/1	0.16	-	62,62,62,62	0
32	MG	A	3544	1/1	2.05	-	81,81,81,81	0
32	MG	A	3308	1/1	0.29	-	67,67,67,67	0
32	MG	6	1080	1/1	4.51	-	108,108,108,108	0
32	MG	A	3463	1/1	0.42	-	48,48,48,48	0
32	MG	A	3030	1/1	0.47	-	39,39,39,39	0
32	MG	A	3198	1/1	1.19	-	96,96,96,96	0
32	MG	6	638	1/1	0.20	-	98,98,98,98	0
32	MG	A	3569	1/1	0.65	-	67,67,67,67	0
32	MG	A	3641	1/1	1.12	-	67,67,67,67	0
32	MG	A	3349	1/1	0.29	-	107,107,107,107	0
32	MG	A	2901	1/1	0.22	-	16,16,16,16	0
32	MG	A	3184	1/1	0.31	-	89,89,89,89	0
32	MG	J	390	1/1	0.32	-	75,75,75,75	0
32	MG	A	3541	1/1	0.69	-	91,91,91,91	0
32	MG	A	3649	1/1	0.26	-	93,93,93,93	0
32	MG	6	385	1/1	1.44	-	64,64,64,64	0
32	MG	A	3567	1/1	0.79	-	77,77,77,77	0
32	MG	A	2985	1/1	0.59	-	50,50,50,50	0
32	MG	6	986	1/1	0.86	-	66,66,66,66	0
32	MG	P	850	1/1	0.16	-	69,69,69,69	0
32	MG	A	3318	1/1	0.37	-	106,106,106,106	0
32	MG	A	3175	1/1	0.64	-	85,85,85,85	0
32	MG	A	3046	1/1	0.78	-	62,62,62,62	0
32	MG	A	2918	1/1	0.10	-	12,12,12,12	0
32	MG	A	4	1/1	0.15	-	40,40,40,40	0
32	MG	A	2987	1/1	0.11	-	42,42,42,42	0
32	MG	A	3476	1/1	0.42	-	57,57,57,57	0
32	MG	6	82	1/1	0.14	-	67,67,67,67	0
32	MG	6	1060	1/1	0.59	-	79,79,79,79	0
32	MG	A	3498	1/1	0.80	-	53,53,53,53	0
32	MG	P	690	1/1	0.18	-	111,111,111,111	0
32	MG	A	3001	1/1	0.26	-	53,53,53,53	0
32	MG	A	3460	1/1	0.26	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3667	1/1	1.52	-	77,77,77,77	0
32	MG	A	3110	1/1	0.15	-	77,77,77,77	0
32	MG	A	3654	1/1	0.20	-	88,88,88,88	0
32	MG	B	333	1/1	0.20	-	102,102,102,102	0
32	MG	6	727	1/1	0.12	-	104,104,104,104	0
32	MG	6	428	1/1	0.47	-	88,88,88,88	0
32	MG	A	3620	1/1	0.86	-	62,62,62,62	0
32	MG	6	712	1/1	0.37	-	49,49,49,49	0
32	MG	A	2986	1/1	0.30	-	35,35,35,35	0
32	MG	A	3625	1/1	0.42	-	85,85,85,85	0
32	MG	A	3020	1/1	0.28	-	41,41,41,41	0
32	MG	A	3130	1/1	0.18	-	100,100,100,100	0
32	MG	A	3019	1/1	1.29	-	61,61,61,61	0
32	MG	A	3669	1/1	0.48	-	82,82,82,82	0
32	MG	A	3056	1/1	0.18	-	55,55,55,55	0
32	MG	A	3303	1/1	0.37	-	84,84,84,84	0
32	MG	A	3472	1/1	0.17	-	31,31,31,31	0
32	MG	6	410	1/1	0.09	-	71,71,71,71	0
32	MG	A	3488	1/1	0.92	-	79,79,79,79	0
32	MG	A	3491	1/1	0.64	-	40,40,40,40	0
32	MG	A	490	1/1	1.10	-	114,114,114,114	0
32	MG	6	386	1/1	0.14	-	65,65,65,65	0
32	MG	A	3197	1/1	0.62	-	70,70,70,70	0
32	MG	A	3154	1/1	0.23	-	86,86,86,86	0
32	MG	A	3629	1/1	1.85	-	89,89,89,89	0
32	MG	A	3584	1/1	0.44	-	58,58,58,58	0
32	MG	A	3048	1/1	0.65	-	110,110,110,110	0
32	MG	A	3280	1/1	0.34	-	68,68,68,68	0
32	MG	A	3695	1/1	1.06	-	97,97,97,97	0
32	MG	A	3113	1/1	0.26	-	40,40,40,40	0
32	MG	A	437	1/1	0.69	-	81,81,81,81	0
32	MG	E	210	1/1	0.33	-	75,75,75,75	0
32	MG	A	3378	1/1	0.72	-	123,123,123,123	0
32	MG	6	798	1/1	0.59	-	72,72,72,72	0
32	MG	6	593	1/1	0.86	-	140,140,140,140	0
32	MG	A	2916	1/1	0.23	-	13,13,13,13	0
32	MG	A	3169	1/1	0.56	-	79,79,79,79	0
32	MG	A	3125	1/1	0.29	-	61,61,61,61	0
32	MG	A	3287	1/1	0.24	-	60,60,60,60	0
32	MG	6	606	1/1	0.27	-	90,90,90,90	0
32	MG	B	367	1/1	0.50	-	108,108,108,108	0
32	MG	A	3207	1/1	0.54	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	2968	1/1	0.21	-	84,84,84,84	0
32	MG	6	1160	1/1	0.33	-	88,88,88,88	0
32	MG	A	3185	1/1	0.28	-	81,81,81,81	0
32	MG	A	3054	1/1	0.76	-	91,91,91,91	0
32	MG	A	3250	1/1	0.97	-	108,108,108,108	0
32	MG	A	3146	1/1	0.37	-	139,139,139,139	0
32	MG	A	2969	1/1	0.28	-	61,61,61,61	0
32	MG	A	3561	1/1	0.17	-	79,79,79,79	0
32	MG	B	1039	1/1	0.52	-	140,140,140,140	0
32	MG	B	700	1/1	0.71	-	154,154,154,154	0
32	MG	6	1127	1/1	0.23	-	108,108,108,108	0
32	MG	6	1027	1/1	0.83	-	70,70,70,70	0
32	MG	A	3010	1/1	0.28	-	54,54,54,54	0
32	MG	A	3228	1/1	0.79	-	56,56,56,56	0
32	MG	X	643	1/1	0.11	-	71,71,71,71	0
32	MG	A	3283	1/1	0.46	-	61,61,61,61	0
32	MG	A	3072	1/1	0.66	-	82,82,82,82	0
32	MG	A	2929	1/1	0.43	-	32,32,32,32	0
32	MG	A	3479	1/1	0.43	-	70,70,70,70	0
32	MG	6	763	1/1	0.22	-	106,106,106,106	0
32	MG	6	329	1/1	0.58	-	113,113,113,113	0
32	MG	A	3332	1/1	0.61	-	60,60,60,60	0
32	MG	6	515	1/1	2.12	-	101,101,101,101	0
32	MG	A	2991	1/1	0.86	-	57,57,57,57	0
32	MG	A	3084	1/1	0.38	-	65,65,65,65	0
32	MG	A	3027	1/1	0.45	-	62,62,62,62	0
32	MG	6	1090	1/1	0.15	-	86,86,86,86	0
32	MG	A	3070	1/1	0.41	-	38,38,38,38	0
32	MG	6	618	1/1	0.28	-	103,103,103,103	0
32	MG	A	3433	1/1	0.50	-	74,74,74,74	0
32	MG	A	3215	1/1	0.56	-	76,76,76,76	0
32	MG	A	3208	1/1	0.24	-	87,87,87,87	0
32	MG	A	3352	1/1	0.29	-	116,116,116,116	0
32	MG	B	553	1/1	0.39	-	85,85,85,85	0
32	MG	6	1065	1/1	0.20	-	71,71,71,71	0
32	MG	F	589	1/1	0.60	-	90,90,90,90	0
32	MG	6	142	1/1	0.15	-	88,88,88,88	0
32	MG	A	3108	1/1	0.35	-	73,73,73,73	0
32	MG	A	3296	1/1	0.37	-	84,84,84,84	0
32	MG	B	787	1/1	0.56	-	72,72,72,72	0
32	MG	A	3418	1/1	0.27	-	137,137,137,137	0
32	MG	A	3485	1/1	0.56	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3408	1/1	0.34	-	68,68,68,68	0
32	MG	A	3560	1/1	0.35	-	87,87,87,87	0
32	MG	A	3044	1/1	0.38	-	64,64,64,64	0
32	MG	A	3608	1/1	0.26	-	71,71,71,71	0
32	MG	A	3515	1/1	0.20	-	81,81,81,81	0
32	MG	A	3120	1/1	0.59	-	47,47,47,47	0
32	MG	6	281	1/1	0.23	-	51,51,51,51	0
32	MG	A	3457	1/1	0.80	-	47,47,47,47	0
32	MG	A	3245	1/1	0.35	-	60,60,60,60	0
32	MG	B	495	1/1	0.34	-	61,61,61,61	0
32	MG	A	3334	1/1	0.43	-	80,80,80,80	0
32	MG	A	3112	1/1	0.53	-	56,56,56,56	0
32	MG	6	561	1/1	0.08	-	68,68,68,68	0
32	MG	A	3174	1/1	0.48	-	67,67,67,67	0
32	MG	6	1070	1/1	1.73	-	90,90,90,90	0
32	MG	A	3441	1/1	0.51	-	29,29,29,29	0
32	MG	6	207	1/1	0.30	-	100,100,100,100	0
32	MG	A	3689	1/1	0.11	-	55,55,55,55	0
32	MG	A	3276	1/1	0.25	-	107,107,107,107	0
32	MG	A	3420	1/1	0.34	-	68,68,68,68	0
32	MG	A	3265	1/1	0.50	-	73,73,73,73	0
32	MG	A	3345	1/1	0.31	-	136,136,136,136	0
32	MG	6	513	1/1	0.12	-	66,66,66,66	0
32	MG	6	657	1/1	0.25	-	68,68,68,68	0
32	MG	A	3188	1/1	0.40	-	80,80,80,80	0
32	MG	V	1109	1/1	1.73	-	104,104,104,104	0
32	MG	A	3190	1/1	0.27	-	85,85,85,85	0
32	MG	6	540	1/1	0.31	-	71,71,71,71	0
32	MG	A	2949	1/1	0.11	-	55,55,55,55	0
32	MG	A	3229	1/1	0.49	-	64,64,64,64	0
32	MG	6	984	1/1	0.20	-	67,67,67,67	0
32	MG	A	3285	1/1	1.02	-	102,102,102,102	0
32	MG	6	781	1/1	0.25	-	112,112,112,112	0
32	MG	A	3430	1/1	0.53	-	115,115,115,115	0
32	MG	A	3325	1/1	0.81	-	86,86,86,86	0
32	MG	A	2988	1/1	0.23	-	69,69,69,69	0
32	MG	A	3557	1/1	0.41	-	67,67,67,67	0
32	MG	B	666	1/1	0.41	-	82,82,82,82	0
32	MG	6	506	1/1	0.38	-	103,103,103,103	0
32	MG	6	574	1/1	0.18	-	104,104,104,104	0
32	MG	A	3379	1/1	0.24	-	68,68,68,68	0
32	MG	A	3611	1/1	0.38	-	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	P	580	1/1	0.57	-	122,122,122,122	0
32	MG	A	3202	1/1	0.62	-	100,100,100,100	0
32	MG	A	3102	1/1	0.23	-	59,59,59,59	0
32	MG	6	489	1/1	0.30	-	98,98,98,98	0
32	MG	A	3365	1/1	0.29	-	113,113,113,113	0
32	MG	A	3536	1/1	0.83	-	67,67,67,67	0
32	MG	B	120	1/1	0.25	-	48,48,48,48	0
32	MG	A	3052	1/1	0.40	-	61,61,61,61	0
32	MG	A	3293	1/1	0.29	-	72,72,72,72	0
32	MG	6	311	1/1	0.25	-	54,54,54,54	0
32	MG	A	3449	1/1	0.26	-	36,36,36,36	0
32	MG	A	3683	1/1	0.77	-	97,97,97,97	0
32	MG	A	3357	1/1	0.18	-	33,33,33,33	0
32	MG	6	274	1/1	0.30	-	84,84,84,84	0
32	MG	6	790	1/1	0.89	-	106,106,106,106	0
32	MG	A	3540	1/1	0.65	-	65,65,65,65	0
32	MG	6	159	1/1	0.20	-	76,76,76,76	0
32	MG	A	3452	1/1	0.43	-	53,53,53,53	0
32	MG	A	3267	1/1	0.41	-	107,107,107,107	0
32	MG	6	398	1/1	0.14	-	140,140,140,140	0
32	MG	A	3570	1/1	0.20	-	91,91,91,91	0
32	MG	A	3304	1/1	0.20	-	109,109,109,109	0
32	MG	A	3500	1/1	0.28	-	67,67,67,67	0
32	MG	A	2941	1/1	0.66	-	37,37,37,37	0
32	MG	A	3547	1/1	0.34	-	83,83,83,83	0
32	MG	6	417	1/1	0.22	-	120,120,120,120	0
32	MG	A	3662	1/1	0.40	-	82,82,82,82	0
32	MG	6	710	1/1	0.30	-	108,108,108,108	0
32	MG	A	3234	1/1	0.68	-	69,69,69,69	0
32	MG	A	2935	1/1	0.15	-	31,31,31,31	0
32	MG	A	3180	1/1	0.95	-	72,72,72,72	0
32	MG	A	3340	1/1	0.43	-	125,125,125,125	0
32	MG	R	996	1/1	0.21	-	75,75,75,75	0
32	MG	A	3471	1/1	0.45	-	67,67,67,67	0
32	MG	A	3425	1/1	0.62	-	94,94,94,94	0
32	MG	6	447	1/1	0.26	-	56,56,56,56	0
32	MG	A	3290	1/1	0.39	-	71,71,71,71	0
32	MG	A	3007	1/1	0.41	-	21,21,21,21	0
32	MG	A	3665	1/1	0.11	-	67,67,67,67	0
32	MG	A	3372	1/1	1.04	-	76,76,76,76	0
32	MG	A	3165	1/1	0.53	-	71,71,71,71	0
32	MG	A	3004	1/1	0.49	-	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	1043	1/1	0.19	-	83,83,83,83	0
32	MG	6	545	1/1	0.16	-	107,107,107,107	0
32	MG	A	3565	1/1	0.69	-	90,90,90,90	0
32	MG	A	3416	1/1	0.47	-	49,49,49,49	0
32	MG	A	3605	1/1	0.53	-	81,81,81,81	0
32	MG	A	3374	1/1	0.78	-	123,123,123,123	0
32	MG	A	3337	1/1	0.24	-	78,78,78,78	0
32	MG	A	3390	1/1	0.78	-	66,66,66,66	0
32	MG	A	3647	1/1	0.69	-	88,88,88,88	0
32	MG	A	3660	1/1	0.70	-	86,86,86,86	0
32	MG	A	3532	1/1	0.74	-	88,88,88,88	0
32	MG	6	522	1/1	0.35	-	56,56,56,56	0
32	MG	A	3459	1/1	0.13	-	27,27,27,27	0
32	MG	6	394	1/1	0.19	-	108,108,108,108	0
32	MG	A	3534	1/1	0.67	-	99,99,99,99	0
32	MG	A	3168	1/1	0.29	-	74,74,74,74	0
32	MG	A	3554	1/1	0.47	-	76,76,76,76	0
32	MG	A	3552	1/1	0.96	-	89,89,89,89	0
32	MG	6	708	1/1	0.74	-	70,70,70,70	0
32	MG	A	3461	1/1	0.20	-	32,32,32,32	0
32	MG	A	2922	1/1	0.49	-	50,50,50,50	0
32	MG	A	2899	1/1	0.42	-	15,15,15,15	0
32	MG	A	3486	1/1	0.27	-	78,78,78,78	0
32	MG	6	271	1/1	0.19	-	79,79,79,79	0
32	MG	6	1040	1/1	0.36	-	91,91,91,91	0
32	MG	A	3137	1/1	0.26	-	99,99,99,99	0
32	MG	B	119	1/1	0.39	-	63,63,63,63	0
32	MG	A	2965	1/1	0.48	-	69,69,69,69	0
32	MG	6	131	1/1	0.69	-	58,58,58,58	0
32	MG	A	100	1/1	0.75	-	58,58,58,58	0
32	MG	A	3284	1/1	0.56	-	79,79,79,79	0
32	MG	A	3614	1/1	1.73	-	98,98,98,98	0
32	MG	A	3071	1/1	0.15	-	70,70,70,70	0
32	MG	6	143	1/1	0.07	-	59,59,59,59	0
32	MG	A	3301	1/1	0.90	-	63,63,63,63	0
32	MG	A	927	1/1	0.12	-	66,66,66,66	0
32	MG	C	609	1/1	1.16	-	128,128,128,128	0
32	MG	A	3517	1/1	0.49	-	68,68,68,68	0
32	MG	P	1102	1/1	0.38	-	86,86,86,86	0
32	MG	6	1073	1/1	0.10	-	79,79,79,79	0
32	MG	A	3576	1/1	0.56	-	104,104,104,104	0
32	MG	A	3535	1/1	0.06	-	107,107,107,107	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3306	1/1	0.28	-	71,71,71,71	0
32	MG	A	3596	1/1	0.34	-	83,83,83,83	0
32	MG	E	749	1/1	0.75	-	93,93,93,93	0
32	MG	A	3480	1/1	0.61	-	65,65,65,65	0
32	MG	A	3603	1/1	0.23	-	99,99,99,99	0
32	MG	A	3183	1/1	0.63	-	110,110,110,110	0
32	MG	A	3474	1/1	0.25	-	30,30,30,30	0
32	MG	A	3687	1/1	0.25	-	92,92,92,92	0
32	MG	A	3407	1/1	0.20	-	80,80,80,80	0
32	MG	A	3549	1/1	0.35	-	75,75,75,75	0
32	MG	A	3093	1/1	0.37	-	142,142,142,142	0
32	MG	A	3656	1/1	0.64	-	97,97,97,97	0
32	MG	A	3160	1/1	0.31	-	87,87,87,87	0
32	MG	A	3204	1/1	0.35	-	102,102,102,102	0
32	MG	A	3286	1/1	0.26	-	71,71,71,71	0
32	MG	A	3328	1/1	0.30	-	101,101,101,101	0
32	MG	A	3291	1/1	0.53	-	98,98,98,98	0
32	MG	6	279	1/1	0.68	-	122,122,122,122	0
32	MG	6	1123	1/1	0.49	-	107,107,107,107	0
32	MG	A	3581	1/1	0.41	-	67,67,67,67	0
32	MG	A	3692	1/1	0.24	-	72,72,72,72	0
32	MG	6	236	1/1	0.73	-	74,74,74,74	0
32	MG	A	3685	1/1	0.47	-	90,90,90,90	0
32	MG	A	3091	1/1	0.34	-	74,74,74,74	0
32	MG	A	3422	1/1	0.21	-	65,65,65,65	0
32	MG	A	3288	1/1	0.35	-	89,89,89,89	0
32	MG	A	3489	1/1	0.21	-	65,65,65,65	0
32	MG	A	3053	1/1	0.47	-	59,59,59,59	0
32	MG	6	1097	1/1	0.48	-	81,81,81,81	0
32	MG	O	1078	1/1	0.23	-	70,70,70,70	0
32	MG	6	467	1/1	1.70	-	78,78,78,78	0
32	MG	B	969	1/1	0.59	-	89,89,89,89	0
32	MG	Y	1156	1/1	0.77	-	95,95,95,95	0
32	MG	A	2994	1/1	0.18	-	75,75,75,75	0
32	MG	A	3456	1/1	0.67	-	46,46,46,46	0
32	MG	A	2938	1/1	0.59	-	47,47,47,47	0
32	MG	A	3503	1/1	0.69	-	75,75,75,75	0
32	MG	A	3506	1/1	0.61	-	81,81,81,81	0
32	MG	A	2999	1/1	0.20	-	55,55,55,55	0
32	MG	A	3623	1/1	0.84	-	80,80,80,80	0
32	MG	A	3572	1/1	0.71	-	74,74,74,74	0
32	MG	A	2972	1/1	0.14	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3630	1/1	0.77	-	96,96,96,96	0
32	MG	A	3258	1/1	0.15	-	53,53,53,53	0
32	MG	6	560	1/1	0.58	-	96,96,96,96	0
32	MG	6	1036	1/1	0.15	-	78,78,78,78	0
32	MG	A	3270	1/1	0.37	-	110,110,110,110	0
32	MG	A	365	1/1	0.89	-	86,86,86,86	0
32	MG	A	3575	1/1	0.89	-	146,146,146,146	0
32	MG	A	3299	1/1	0.78	-	87,87,87,87	0
32	MG	F	183	1/1	0.07	-	67,67,67,67	0
32	MG	A	3231	1/1	0.29	-	58,58,58,58	0
32	MG	P	594	1/1	0.23	-	96,96,96,96	0
32	MG	A	2946	1/1	0.46	-	53,53,53,53	0
32	MG	A	156	1/1	0.59	-	57,57,57,57	0
32	MG	A	3282	1/1	0.73	-	113,113,113,113	0
32	MG	A	3564	1/1	0.39	-	72,72,72,72	0
32	MG	A	2908	1/1	0.43	-	37,37,37,37	0
32	MG	A	3375	1/1	0.75	-	61,61,61,61	0
32	MG	A	3626	1/1	0.50	-	103,103,103,103	0
32	MG	A	3696	1/1	0.48	-	95,95,95,95	0
32	MG	6	191	1/1	0.21	-	62,62,62,62	0
32	MG	6	614	1/1	0.28	-	88,88,88,88	0
32	MG	A	3251	1/1	0.62	-	78,78,78,78	0
32	MG	A	3140	1/1	0.40	-	65,65,65,65	0
32	MG	A	3147	1/1	0.42	-	99,99,99,99	0
32	MG	A	3361	1/1	0.67	-	75,75,75,75	0
32	MG	A	3069	1/1	0.23	-	67,67,67,67	0
32	MG	Y	63	1/1	0.21	-	42,42,42,42	0
32	MG	A	3260	1/1	0.90	-	65,65,65,65	0
32	MG	6	679	1/1	0.64	-	118,118,118,118	0
32	MG	6	557	1/1	0.32	-	104,104,104,104	0
32	MG	6	375	1/1	1.42	-	109,109,109,109	0
32	MG	A	2982	1/1	0.37	-	54,54,54,54	0
32	MG	A	3171	1/1	0.53	-	62,62,62,62	0
32	MG	A	2963	1/1	0.22	-	51,51,51,51	0
32	MG	A	3253	1/1	1.01	-	92,92,92,92	0
32	MG	A	2923	1/1	0.15	-	62,62,62,62	0
32	MG	A	3041	1/1	0.15	-	58,58,58,58	0
32	MG	A	2906	1/1	0.21	-	24,24,24,24	0
32	MG	A	3674	1/1	0.45	-	68,68,68,68	0
32	MG	A	3402	1/1	0.61	-	83,83,83,83	0
32	MG	A	3591	1/1	1.34	-	107,107,107,107	0
32	MG	6	233	1/1	0.13	-	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3668	1/1	0.15	-	109,109,109,109	0
32	MG	A	3377	1/1	0.35	-	62,62,62,62	0
32	MG	6	469	1/1	0.32	-	86,86,86,86	0
32	MG	A	3117	1/1	0.46	-	61,61,61,61	0
32	MG	A	3336	1/1	0.44	-	77,77,77,77	0
32	MG	A	368	1/1	0.41	-	20,20,20,20	0
32	MG	6	867	1/1	0.21	-	97,97,97,97	0
32	MG	A	2932	1/1	0.60	-	47,47,47,47	0
32	MG	A	3634	1/1	0.49	-	107,107,107,107	0
32	MG	6	963	1/1	0.24	-	82,82,82,82	0
32	MG	A	141	1/1	0.42	-	71,71,71,71	0
32	MG	A	3092	1/1	0.41	-	72,72,72,72	0
32	MG	6	1005	1/1	0.66	-	91,91,91,91	0
32	MG	A	2911	1/1	0.18	-	14,14,14,14	0
32	MG	A	2981	1/1	0.24	-	43,43,43,43	0
32	MG	6	1111	1/1	0.20	-	84,84,84,84	0
32	MG	A	3109	1/1	0.18	-	85,85,85,85	0
32	MG	A	3469	1/1	0.31	-	46,46,46,46	0
32	MG	A	3650	1/1	1.00	-	113,113,113,113	0
32	MG	A	3376	1/1	0.28	-	108,108,108,108	0
32	MG	P	138	1/1	0.26	-	68,68,68,68	0
32	MG	A	2995	1/1	0.24	-	39,39,39,39	0
32	MG	A	3657	1/1	0.20	-	95,95,95,95	0
32	MG	A	3661	1/1	0.29	-	69,69,69,69	0
32	MG	6	1141	1/1	0.78	-	101,101,101,101	0
32	MG	A	3675	1/1	0.69	-	68,68,68,68	0
32	MG	6	604	1/1	0.13	-	116,116,116,116	0
32	MG	6	528	1/1	0.15	-	93,93,93,93	0
32	MG	A	3637	1/1	0.63	-	64,64,64,64	0
32	MG	6	961	1/1	0.09	-	71,71,71,71	0
32	MG	A	3429	1/1	0.27	-	72,72,72,72	0
32	MG	A	3200	1/1	0.69	-	96,96,96,96	0
32	MG	A	3005	1/1	0.15	-	73,73,73,73	0
32	MG	A	3080	1/1	0.61	-	123,123,123,123	0
32	MG	A	3240	1/1	0.33	-	109,109,109,109	0
32	MG	A	3522	1/1	0.24	-	77,77,77,77	0
32	MG	6	783	1/1	0.26	-	91,91,91,91	0
32	MG	6	294	1/1	0.11	-	93,93,93,93	0
32	MG	A	273	1/1	0.36	-	49,49,49,49	0
32	MG	6	743	1/1	0.90	-	119,119,119,119	0
32	MG	A	3497	1/1	0.75	-	90,90,90,90	0
32	MG	A	3025	1/1	0.13	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	559	1/1	0.63	-	89,89,89,89	0
32	MG	A	3038	1/1	0.84	-	73,73,73,73	0
32	MG	A	3218	1/1	0.59	-	59,59,59,59	0
32	MG	A	3145	1/1	0.77	-	79,79,79,79	0
32	MG	A	2974	1/1	0.66	-	69,69,69,69	0
32	MG	A	3217	1/1	0.51	-	54,54,54,54	0
32	MG	A	3167	1/1	0.26	-	119,119,119,119	0
32	MG	A	3617	1/1	0.20	-	78,78,78,78	0
32	MG	A	3216	1/1	0.16	-	97,97,97,97	0
32	MG	2	978	1/1	0.29	-	75,75,75,75	0
32	MG	2	183	1/1	0.18	-	27,27,27,27	0
32	MG	6	269	1/1	0.39	-	86,86,86,86	0
32	MG	A	3124	1/1	0.16	-	90,90,90,90	0
32	MG	A	160	1/1	0.46	-	76,76,76,76	0
32	MG	A	3431	1/1	1.11	-	85,85,85,85	0
32	MG	A	3411	1/1	0.23	-	79,79,79,79	0
32	MG	6	1013	1/1	0.17	-	77,77,77,77	0
32	MG	A	3173	1/1	0.35	-	68,68,68,68	0
32	MG	A	3644	1/1	0.20	-	151,151,151,151	0
32	MG	A	2940	1/1	0.28	-	37,37,37,37	0
32	MG	A	3181	1/1	0.48	-	90,90,90,90	0
32	MG	A	3126	1/1	0.38	-	64,64,64,64	0
32	MG	A	3128	1/1	1.27	-	95,95,95,95	0
32	MG	6	68	1/1	0.28	-	39,39,39,39	0
32	MG	6	203	1/1	0.11	-	66,66,66,66	0
32	MG	A	3107	1/1	0.46	-	95,95,95,95	0
32	MG	A	3272	1/1	0.13	-	85,85,85,85	0
32	MG	A	3453	1/1	0.39	-	39,39,39,39	0
32	MG	A	3442	1/1	0.33	-	38,38,38,38	0
32	MG	A	2947	1/1	0.17	-	59,59,59,59	0
32	MG	A	2979	1/1	0.23	-	44,44,44,44	0
32	MG	A	3403	1/1	0.43	-	85,85,85,85	0
32	MG	A	3232	1/1	0.32	-	62,62,62,62	0
32	MG	A	3076	1/1	0.40	-	57,57,57,57	0
32	MG	A	3031	1/1	0.44	-	94,94,94,94	0
32	MG	A	3196	1/1	1.17	-	68,68,68,68	0
32	MG	6	792	1/1	0.44	-	101,101,101,101	0
32	MG	6	623	1/1	0.46	-	98,98,98,98	0
32	MG	A	2997	1/1	0.44	-	65,65,65,65	0
32	MG	A	3350	1/1	0.19	-	95,95,95,95	0
32	MG	A	3652	1/1	0.81	-	105,105,105,105	0
32	MG	6	858	1/1	0.15	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3646	1/1	0.94	-	61,61,61,61	0
32	MG	6	514	1/1	1.62	-	173,173,173,173	0
32	MG	A	3604	1/1	0.71	-	79,79,79,79	0
32	MG	A	3551	1/1	0.79	-	80,80,80,80	0
32	MG	A	3628	1/1	0.27	-	93,93,93,93	0
32	MG	B	958	1/1	0.26	-	75,75,75,75	0
32	MG	P	603	1/1	0.20	-	86,86,86,86	0
32	MG	6	399	1/1	0.34	-	85,85,85,85	0
32	MG	A	3013	1/1	0.23	-	67,67,67,67	0
32	MG	A	3533	1/1	0.65	-	54,54,54,54	0
32	MG	V	704	1/1	0.75	-	75,75,75,75	0
32	MG	A	3528	1/1	0.30	-	87,87,87,87	0
32	MG	A	3094	1/1	0.13	-	25,25,25,25	0
32	MG	A	3062	1/1	0.31	-	87,87,87,87	0
32	MG	N	257	1/1	0.25	-	49,49,49,49	0
32	MG	A	3192	1/1	0.59	-	93,93,93,93	0
32	MG	A	2900	1/1	0.26	-	26,26,26,26	0
32	MG	6	383	1/1	0.20	-	71,71,71,71	0
32	MG	A	3396	1/1	0.40	-	95,95,95,95	0
32	MG	B	1099	1/1	0.54	-	98,98,98,98	0
32	MG	A	3114	1/1	0.28	-	87,87,87,87	0
32	MG	B	624	1/1	0.50	-	84,84,84,84	0
32	MG	A	3206	1/1	0.75	-	64,64,64,64	0
32	MG	K	219	1/1	0.08	-	77,77,77,77	0
32	MG	A	3323	1/1	0.27	-	101,101,101,101	0
32	MG	6	215	1/1	0.10	-	138,138,138,138	0
32	MG	6	717	1/1	0.17	-	113,113,113,113	0
32	MG	A	3467	1/1	0.33	-	48,48,48,48	0
32	MG	C	977	1/1	0.26	-	95,95,95,95	0
32	MG	B	407	1/1	0.75	-	125,125,125,125	0
32	MG	6	268	1/1	1.39	-	123,123,123,123	0
32	MG	B	1016	1/1	0.37	-	94,94,94,94	0
32	MG	A	166	1/1	0.47	-	80,80,80,80	0
32	MG	A	3568	1/1	0.21	-	64,64,64,64	0
32	MG	A	3104	1/1	0.65	-	76,76,76,76	0
32	MG	A	2952	1/1	0.33	-	49,49,49,49	0
32	MG	6	173	1/1	0.46	-	65,65,65,65	0
32	MG	A	3149	1/1	0.27	-	94,94,94,94	0
32	MG	6	284	1/1	0.69	-	78,78,78,78	0
32	MG	6	103	1/1	0.15	-	57,57,57,57	0
32	MG	A	3473	1/1	0.80	-	61,61,61,61	0
32	MG	3	737	1/1	0.31	-	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	2928	1/1	0.20	-	33,33,33,33	0
32	MG	A	2992	1/1	0.27	-	125,125,125,125	0
32	MG	A	1134	1/1	0.99	-	108,108,108,108	0
32	MG	A	3448	1/1	0.33	-	26,26,26,26	0
32	MG	A	3344	1/1	0.66	-	71,71,71,71	0
32	MG	A	3151	1/1	0.18	-	59,59,59,59	0
32	MG	A	3179	1/1	0.57	-	76,76,76,76	0
32	MG	J	494	1/1	0.56	-	69,69,69,69	0
32	MG	6	930	1/1	0.90	-	148,148,148,148	0
32	MG	A	3315	1/1	0.24	-	71,71,71,71	0
32	MG	A	170	1/1	0.28	-	57,57,57,57	0
32	MG	A	3691	1/1	0.38	-	112,112,112,112	0
32	MG	6	994	1/1	0.47	-	75,75,75,75	0
32	MG	A	3434	1/1	1.11	-	90,90,90,90	0
32	MG	A	2990	1/1	0.38	-	90,90,90,90	0
32	MG	A	3037	1/1	0.26	-	62,62,62,62	0
32	MG	A	3693	1/1	0.54	-	122,122,122,122	0
32	MG	A	137	1/1	0.21	-	73,73,73,73	0
32	MG	A	3387	1/1	0.55	-	125,125,125,125	0
32	MG	A	2958	1/1	0.35	-	54,54,54,54	0
32	MG	A	3468	1/1	0.73	-	80,80,80,80	0
32	MG	A	3064	1/1	0.59	-	68,68,68,68	0
32	MG	A	3073	1/1	0.29	-	53,53,53,53	0
32	MG	K	152	1/1	0.42	-	66,66,66,66	0
32	MG	6	565	1/1	0.28	-	112,112,112,112	0
32	MG	6	555	1/1	0.29	-	83,83,83,83	0
32	MG	6	678	1/1	0.64	-	87,87,87,87	0
32	MG	T	442	1/1	0.78	-	101,101,101,101	0
32	MG	C	1061	1/1	0.68	-	121,121,121,121	0
32	MG	A	3523	1/1	0.35	-	94,94,94,94	0
32	MG	A	3428	1/1	0.85	-	93,93,93,93	0
32	MG	6	534	1/1	0.25	-	104,104,104,104	0
32	MG	A	2939	1/1	0.28	-	56,56,56,56	0
32	MG	6	722	1/1	0.20	-	101,101,101,101	0
32	MG	A	5	1/1	0.54	-	19,19,19,19	0
32	MG	A	3602	1/1	0.57	-	119,119,119,119	0
32	MG	A	3238	1/1	0.35	-	95,95,95,95	0
32	MG	A	366	1/1	0.93	-	87,87,87,87	0
32	MG	A	3111	1/1	0.17	-	69,69,69,69	0
32	MG	A	3242	1/1	0.28	-	36,36,36,36	0
32	MG	A	3059	1/1	0.13	-	71,71,71,71	0
32	MG	A	3143	1/1	0.17	-	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	635	1/1	0.24	-	111,111,111,111	0
32	MG	A	3170	1/1	0.59	-	88,88,88,88	0
32	MG	A	3504	1/1	0.61	-	66,66,66,66	0
32	MG	A	3018	1/1	0.34	-	72,72,72,72	0
32	MG	I	766	1/1	0.70	-	109,109,109,109	0
32	MG	A	3483	1/1	0.88	-	67,67,67,67	0
32	MG	A	3514	1/1	0.28	-	94,94,94,94	0
32	MG	6	949	1/1	0.39	-	79,79,79,79	0
32	MG	B	463	1/1	0.13	-	111,111,111,111	0
32	MG	6	1072	1/1	0.26	-	77,77,77,77	0
32	MG	A	3477	1/1	0.29	-	58,58,58,58	0
32	MG	A	3562	1/1	0.28	-	95,95,95,95	0
32	MG	A	2924	1/1	0.49	-	47,47,47,47	0
32	MG	A	3003	1/1	0.22	-	98,98,98,98	0
32	MG	A	3203	1/1	0.30	-	67,67,67,67	0
32	MG	A	42	1/1	0.23	-	26,26,26,26	0
32	MG	P	531	1/1	0.17	-	103,103,103,103	0
32	MG	A	3364	1/1	1.72	-	130,130,130,130	0
32	MG	6	1074	1/1	0.15	-	129,129,129,129	0
32	MG	A	3410	1/1	0.97	-	88,88,88,88	0
32	MG	A	2925	1/1	0.23	-	49,49,49,49	0
32	MG	A	3655	1/1	0.19	-	114,114,114,114	0
32	MG	A	3385	1/1	0.26	-	66,66,66,66	0
32	MG	A	3499	1/1	0.29	-	73,73,73,73	0
32	MG	6	491	1/1	0.30	-	81,81,81,81	0
32	MG	A	3686	1/1	1.72	-	100,100,100,100	0
32	MG	A	3427	1/1	0.37	-	80,80,80,80	0
32	MG	A	3394	1/1	0.37	-	108,108,108,108	0
32	MG	A	3673	1/1	0.80	-	84,84,84,84	0
32	MG	A	3574	1/1	0.45	-	58,58,58,58	0
32	MG	A	3331	1/1	0.99	-	54,54,54,54	0
32	MG	A	3435	1/1	0.42	-	79,79,79,79	0
32	MG	A	167	1/1	0.28	-	76,76,76,76	0
32	MG	6	916	1/1	0.12	-	67,67,67,67	0
32	MG	6	35	1/1	0.16	-	65,65,65,65	0
32	MG	A	3279	1/1	0.69	-	91,91,91,91	0
32	MG	A	3573	1/1	0.31	-	40,40,40,40	0
32	MG	A	2913	1/1	0.16	-	24,24,24,24	0
32	MG	A	3694	1/1	1.50	-	75,75,75,75	0
32	MG	6	746	1/1	0.97	-	68,68,68,68	0
32	MG	A	2996	1/1	0.41	-	49,49,49,49	0
32	MG	A	3235	1/1	1.33	-	112,112,112,112	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3401	1/1	0.14	-	104,104,104,104	0
32	MG	6	449	1/1	0.59	-	92,92,92,92	0
32	MG	A	3678	1/1	0.28	-	89,89,89,89	0
32	MG	6	1075	1/1	0.38	-	113,113,113,113	0
32	MG	M	324	1/1	0.24	-	50,50,50,50	0
32	MG	A	3244	1/1	1.14	-	95,95,95,95	0
32	MG	A	3454	1/1	0.22	-	51,51,51,51	0
32	MG	A	3615	1/1	0.38	-	86,86,86,86	0
32	MG	A	3050	1/1	0.59	-	79,79,79,79	0
32	MG	A	3150	1/1	0.65	-	99,99,99,99	0
32	MG	A	2919	1/1	0.35	-	50,50,50,50	0
32	MG	A	3133	1/1	0.45	-	47,47,47,47	0
32	MG	A	3382	1/1	0.54	-	55,55,55,55	0
32	MG	A	3043	1/1	0.28	-	31,31,31,31	0
32	MG	A	3243	1/1	0.08	-	67,67,67,67	0
32	MG	A	3264	1/1	0.47	-	83,83,83,83	0
32	MG	6	675	1/1	0.12	-	118,118,118,118	0
32	MG	6	249	1/1	0.09	-	95,95,95,95	0
32	MG	6	444	1/1	1.38	-	84,84,84,84	0
32	MG	A	3089	1/1	0.12	-	79,79,79,79	0
32	MG	A	3664	1/1	0.35	-	63,63,63,63	0
32	MG	A	3366	1/1	0.13	-	107,107,107,107	0
32	MG	A	3371	1/1	0.61	-	108,108,108,108	0
32	MG	A	3116	1/1	0.39	-	60,60,60,60	0
32	MG	A	3142	1/1	0.46	-	70,70,70,70	0
32	MG	A	2910	1/1	0.82	-	43,43,43,43	0
32	MG	A	3017	1/1	0.27	-	68,68,68,68	0
32	MG	A	3671	1/1	0.57	-	92,92,92,92	0
32	MG	A	3277	1/1	0.42	-	100,100,100,100	0

6.5 Other polymers ⓘ

There are no such residues in this entry.