



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:51 PM UTC

PDB ID : 1J5E / pdb_00001j5e
Title : Structure of the Thermus thermophilus 30S Ribosomal Subunit
Authors : Wimberly, B.T.; Brodersen, D.E.; Clemons Jr., W.M.; Morgan-Warren, R.;
Carter, A.P.; Vornrhein, C.; Hartsch, T.; Ramakrishnan, V.
Deposited on : 2002-04-08
Resolution : 3.05 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

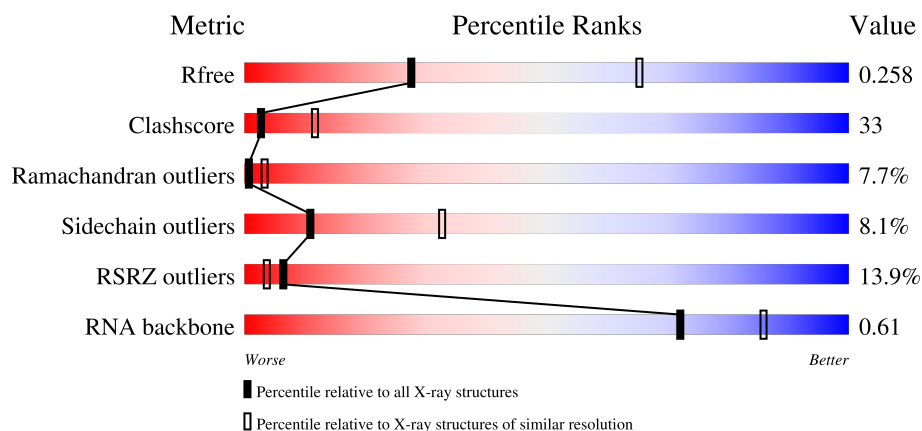
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)
RNA backbone	3983	1079 (3.30-2.82)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1522	9% 33% 52% 11% • •
2	B	256	17% 23% 51% 15% • 9%
3	C	239	15% 24% 44% 15% • 14%
4	D	208	18% 38% 53% 9%

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Mol	Chain	Length	Quality of chain
5	E	161	
6	F	101	
7	G	155	
8	H	138	
9	I	128	
10	J	104	
11	K	129	
12	L	135	
13	M	126	
14	N	60	
15	O	88	
16	P	88	
17	Q	104	
18	R	88	
19	S	92	
20	T	106	
21	V	26	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	UNX	A	100	-	-	-	X
22	UNX	A	1545	-	-	-	X
22	UNX	A	1546	-	-	-	X
22	UNX	A	1548	-	-	-	X
22	UNX	A	1549	-	-	-	X
22	UNX	A	1550	-	-	-	X
22	UNX	A	1552	-	-	-	X
22	UNX	A	1554	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	UNX	A	1555	-	-	-	X
22	UNX	A	1556	-	-	-	X
22	UNX	A	1557	-	-	-	X
22	UNX	A	1558	-	-	-	X
22	UNX	A	1559	-	-	-	X
22	UNX	A	1560	-	-	-	X
22	UNX	A	1561	-	-	-	X
22	UNX	A	1562	-	-	-	X
22	UNX	A	1563	-	-	-	X
22	UNX	A	1564	-	-	-	X
22	UNX	A	1565	-	-	-	X
22	UNX	A	1566	-	-	-	X
22	UNX	A	1568	-	-	-	X
22	UNX	A	1569	-	-	-	X
22	UNX	A	1570	-	-	-	X
22	UNX	A	1571	-	-	-	X
22	UNX	A	1572	-	-	-	X
22	UNX	A	1573	-	-	-	X
22	UNX	A	1574	-	-	-	X
22	UNX	A	1575	-	-	-	X
22	UNX	A	1576	-	-	-	X
22	UNX	A	1577	-	-	-	X
22	UNX	A	1578	-	-	-	X
22	UNX	A	1579	-	-	-	X
22	UNX	A	1580	-	-	-	X
22	UNX	A	1581	-	-	-	X
22	UNX	A	1582	-	-	-	X
22	UNX	A	1583	-	-	-	X
22	UNX	A	1584	-	-	-	X
22	UNX	A	1585	-	-	-	X
22	UNX	A	1586	-	-	-	X
22	UNX	A	1587	-	-	-	X
22	UNX	A	1588	-	-	-	X
22	UNX	A	1589	-	-	-	X
22	UNX	A	1590	-	-	-	X
22	UNX	A	1591	-	-	-	X
22	UNX	A	1592	-	-	-	X
22	UNX	A	1593	-	-	-	X
22	UNX	A	1594	-	-	-	X
22	UNX	A	1596	-	-	-	X
22	UNX	A	1597	-	-	-	X
22	UNX	A	1598	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	UNX	A	1599	-	-	-	X
22	UNX	A	1600	-	-	-	X
22	UNX	A	1601	-	-	-	X
22	UNX	A	1602	-	-	-	X
22	UNX	A	1603	-	-	-	X
22	UNX	A	1604	-	-	-	X
22	UNX	A	1605	-	-	-	X
22	UNX	A	1606	-	-	-	X
22	UNX	A	1607	-	-	-	X
22	UNX	A	1608	-	-	-	X
22	UNX	A	1609	-	-	-	X
22	UNX	A	1610	-	-	-	X
22	UNX	A	1612	-	-	-	X
22	UNX	A	1613	-	-	-	X
22	UNX	A	1614	-	-	-	X
22	UNX	A	1615	-	-	-	X
22	UNX	A	1617	-	-	-	X
22	UNX	A	1618	-	-	-	X
22	UNX	A	1619	-	-	-	X
22	UNX	A	1620	-	-	-	X
22	UNX	A	1621	-	-	-	X
22	UNX	A	1622	-	-	-	X
22	UNX	A	1623	-	-	-	X
22	UNX	A	1624	-	-	-	X
22	UNX	A	1625	-	-	-	X
22	UNX	A	1626	-	-	-	X
22	UNX	A	1627	-	-	-	X
22	UNX	A	1628	-	-	-	X
22	UNX	A	1629	-	-	-	X
22	UNX	A	1630	-	-	-	X
22	UNX	A	1631	-	-	-	X
22	UNX	A	1632	-	-	-	X
22	UNX	A	1633	-	-	-	X
22	UNX	A	1634	-	-	-	X
22	UNX	A	1635	-	-	-	X
22	UNX	A	1636	-	-	-	X
22	UNX	A	1637	-	-	-	X
22	UNX	A	1638	-	-	-	X
22	UNX	A	1639	-	-	-	X
22	UNX	A	1640	-	-	-	X
22	UNX	A	1641	-	-	-	X
22	UNX	A	1642	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	UNX	A	1643	-	-	-	X
22	UNX	A	1644	-	-	-	X
22	UNX	A	1645	-	-	-	X
22	UNX	A	1646	-	-	-	X
22	UNX	A	1647	-	-	-	X
22	UNX	A	1648	-	-	-	X
22	UNX	A	1649	-	-	-	X
22	UNX	A	1650	-	-	-	X
22	UNX	A	1651	-	-	-	X
22	UNX	A	1652	-	-	-	X
22	UNX	A	1653	-	-	-	X
22	UNX	A	1654	-	-	-	X
22	UNX	A	1655	-	-	-	X
22	UNX	A	1656	-	-	-	X
22	UNX	A	1657	-	-	-	X
22	UNX	A	1658	-	-	-	X
22	UNX	A	1659	-	-	-	X
22	UNX	A	1660	-	-	-	X
22	UNX	A	1661	-	-	-	X
22	UNX	A	1662	-	-	-	X
22	UNX	A	1663	-	-	-	X
22	UNX	A	1664	-	-	-	X
22	UNX	A	1665	-	-	-	X
22	UNX	A	1666	-	-	-	X
22	UNX	A	1667	-	-	-	X
22	UNX	A	1668	-	-	-	X
22	UNX	A	1669	-	-	-	X
22	UNX	A	1670	-	-	-	X
22	UNX	A	1671	-	-	-	X
22	UNX	A	1672	-	-	-	X
22	UNX	A	1673	-	-	-	X
22	UNX	A	1674	-	-	-	X
22	UNX	A	1675	-	-	-	X
22	UNX	A	1676	-	-	-	X
22	UNX	A	1677	-	-	-	X
22	UNX	A	1679	-	-	-	X
22	UNX	A	1680	-	-	-	X
22	UNX	A	1681	-	-	-	X
22	UNX	A	1682	-	-	-	X
22	UNX	A	1683	-	-	-	X
22	UNX	A	1684	-	-	-	X
22	UNX	A	1685	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	UNX	A	1686	-	-	-	X
22	UNX	A	1687	-	-	-	X
22	UNX	A	1688	-	-	-	X
22	UNX	A	1689	-	-	-	X
22	UNX	A	1690	-	-	-	X
22	UNX	A	1691	-	-	-	X
22	UNX	A	1692	-	-	-	X
22	UNX	A	1693	-	-	-	X
22	UNX	A	1694	-	-	-	X
22	UNX	A	1695	-	-	-	X
22	UNX	A	1696	-	-	-	X
22	UNX	A	1697	-	-	-	X
22	UNX	A	1698	-	-	-	X
22	UNX	A	1699	-	-	-	X
22	UNX	A	1700	-	-	-	X
22	UNX	A	1701	-	-	-	X
22	UNX	A	1702	-	-	-	X
22	UNX	A	1703	-	-	-	X
22	UNX	A	1704	-	-	-	X
22	UNX	A	1705	-	-	-	X
22	UNX	A	1706	-	-	-	X
22	UNX	A	1707	-	-	-	X
22	UNX	A	1708	-	-	-	X
22	UNX	A	1709	-	-	-	X
22	UNX	A	1710	-	-	-	X
22	UNX	A	1711	-	-	-	X
22	UNX	A	1712	-	-	-	X
22	UNX	A	1713	-	-	-	X
22	UNX	A	1714	-	-	-	X
22	UNX	A	1715	-	-	-	X
22	UNX	A	1716	-	-	-	X
22	UNX	A	1719	-	-	-	X
22	UNX	A	1720	-	-	-	X
22	UNX	A	1721	-	-	-	X
22	UNX	A	1722	-	-	-	X
22	UNX	A	1723	-	-	-	X
22	UNX	A	71	-	-	-	X
22	UNX	A	72	-	-	-	X
22	UNX	A	85	-	-	-	X
22	UNX	A	86	-	-	-	X
22	UNX	A	87	-	-	-	X
22	UNX	A	94	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	UNX	B	257	-	-	-	X
22	UNX	M	143	-	-	-	X

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 51933 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1513	Total	C	N	O	P	66	0	0
			32514	14472	6016	10513	1513			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	234	Total	C	N	O	S	0	0	0
			1900	1213	341	341	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	206	Total	C	N	O	S	0	0	0
			1612	1016	314	281	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	150	Total	C	N	O	S	0	0	0
			1146	724	217	201	4			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	S	0	0	0
			1011	639	198	174				

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	98	Total	C	N	O	S	0	0	0
			792	498	156	137	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	124	Total	C	N	O	S	0	0	0
			970	611	195	163	1			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	83	Total	C	N	O	S	0	0	0
			700	443	139	117	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	73	Total	C	N	O	0	0	0
			597	380	118	99			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	80	Total	C	N	O	S	0	0	0
			647	414	119	112	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	41	VAL	ILE	conflict	EMBL 11125386

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

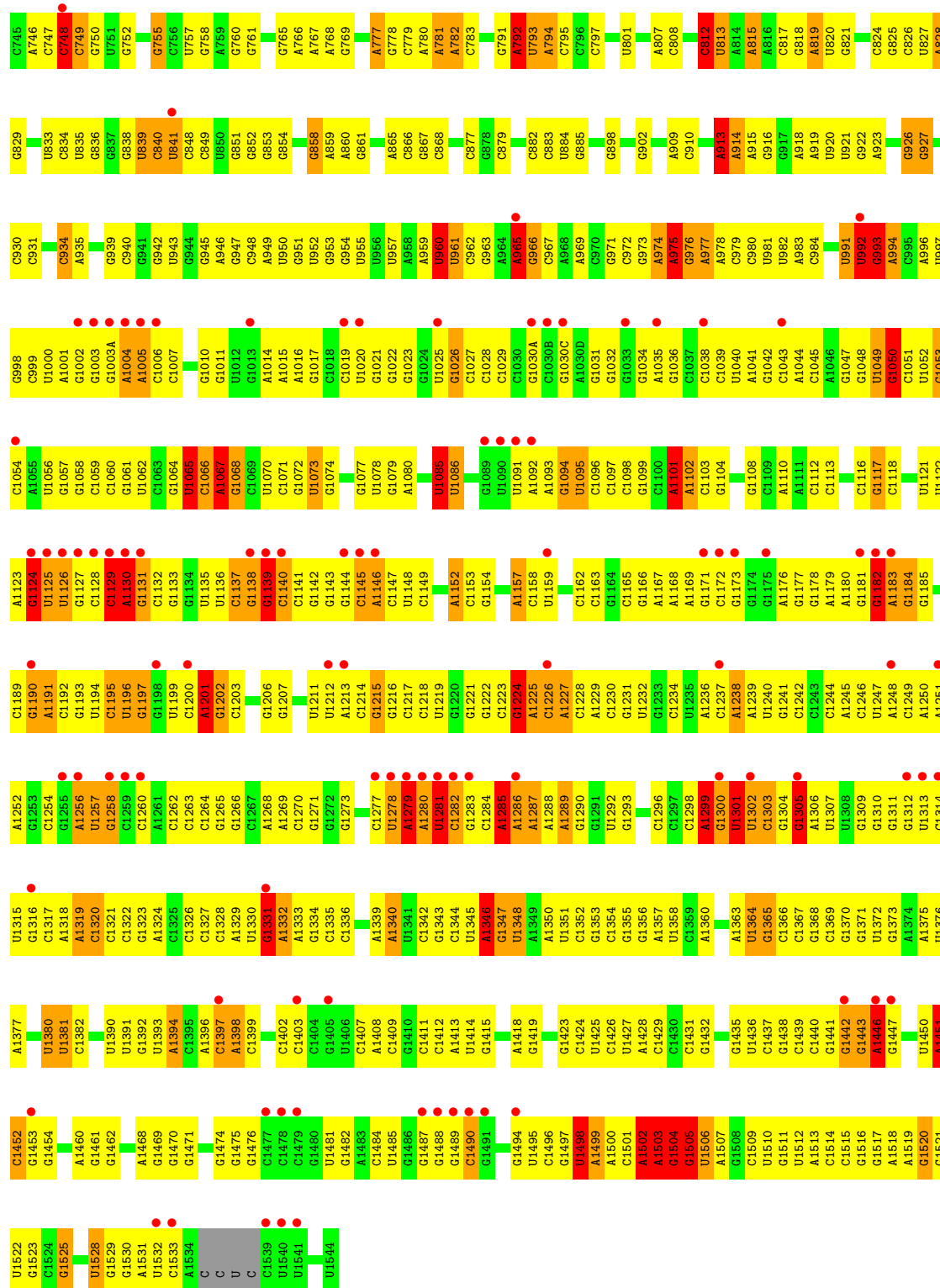
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	V	24	Total	C	N	O	0	0	0
			208	128	50	30			

- Molecule 22 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	186	Total	X	0	0
			186	186		
22	B	1	Total	X	0	0
			1	1		
22	M	1	Total	X	0	0
			1	1		

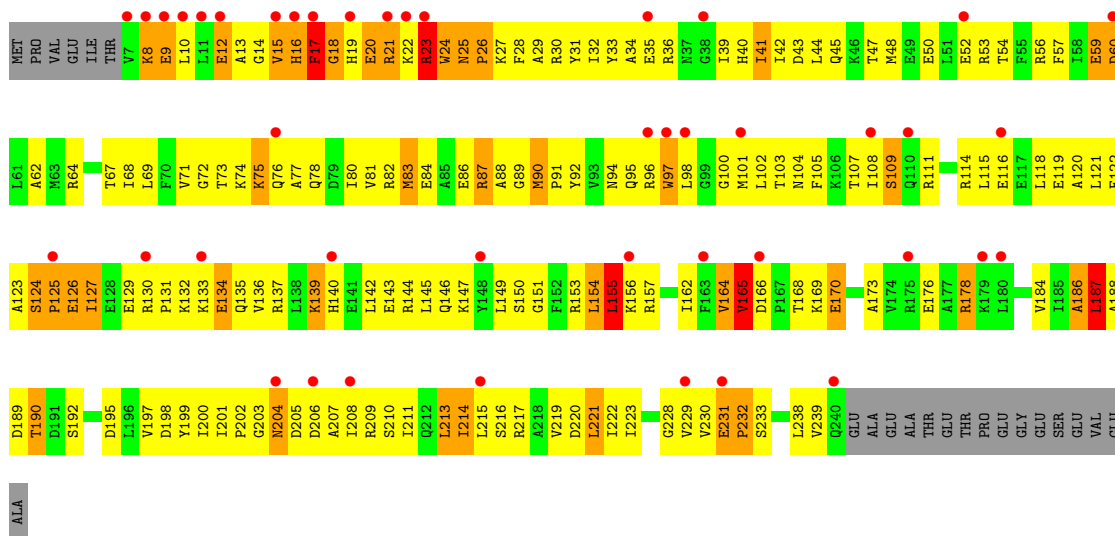
- Molecule 23 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

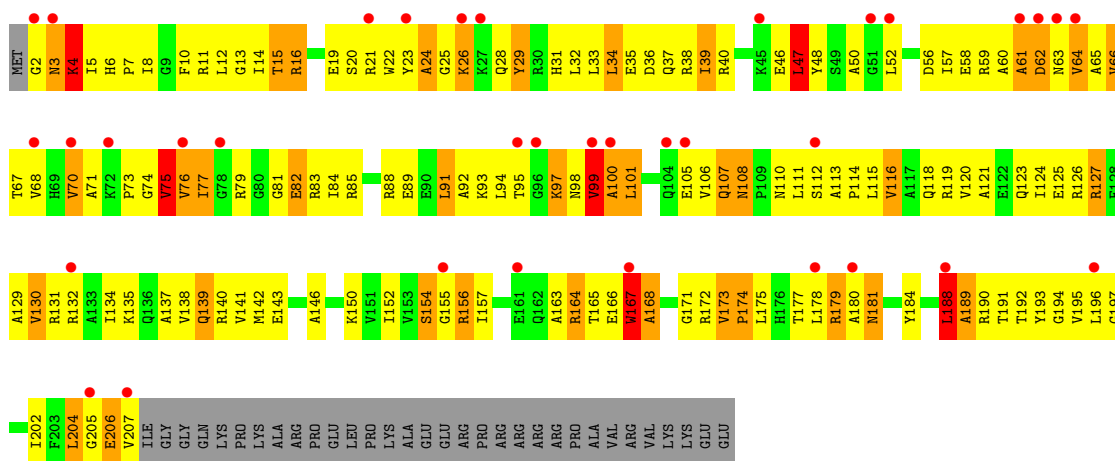
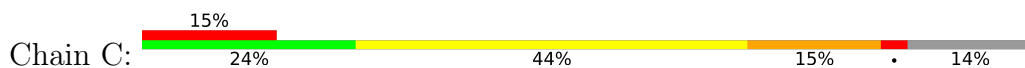


• Molecule 2: 30S RIBOSOMAL PROTEIN S2

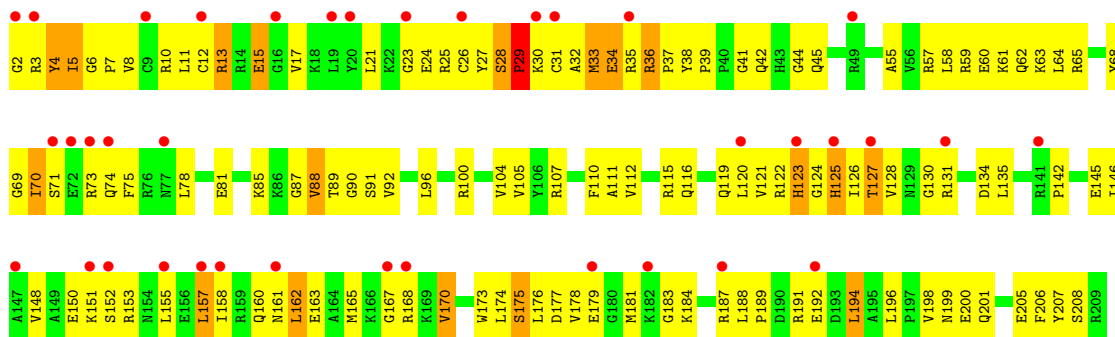
Chain B: 17% 23% 51% 15% 9%



• Molecule 3: 30S RIBOSOMAL PROTEIN S3

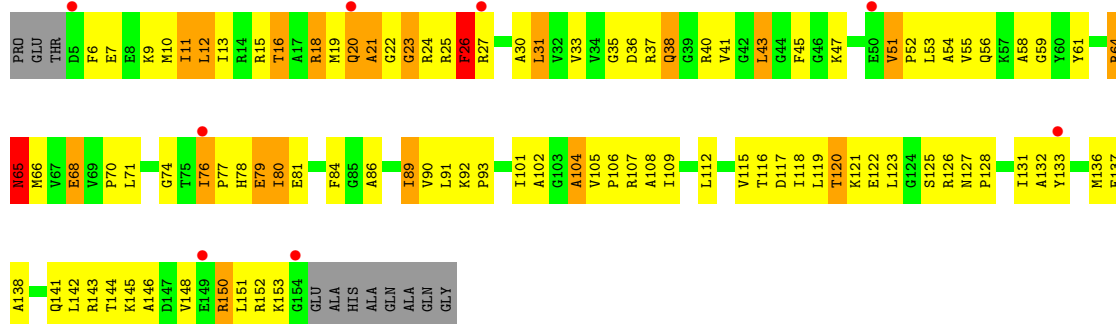


• Molecule 4: 30S RIBOSOMAL PROTEIN S4



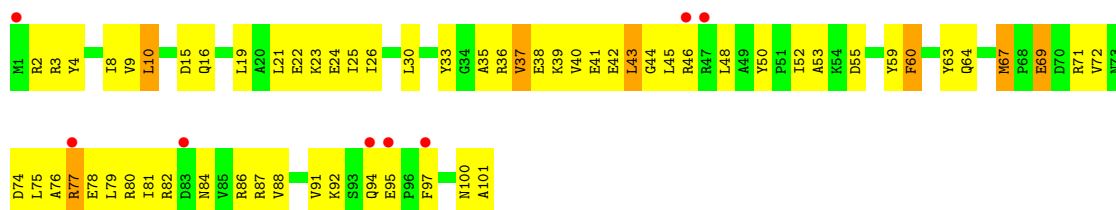
• Molecule 5: 30S RIBOSOMAL PROTEIN S5

Chain E: 



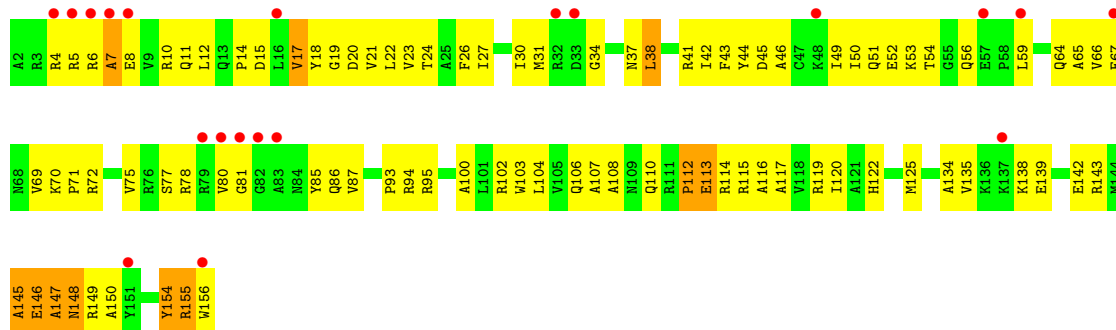
• Molecule 6: 30S RIBOSOMAL PROTEIN S6

Chain F: 



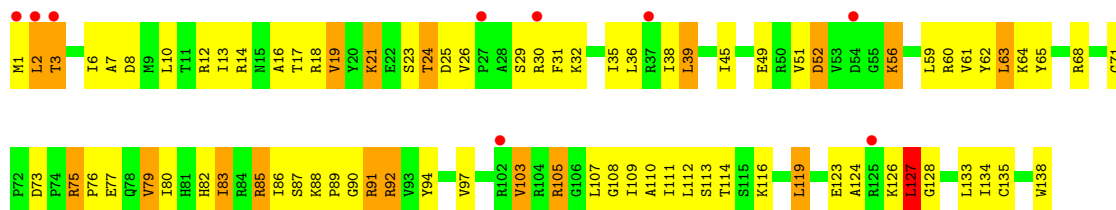
• Molecule 7: 30S RIBOSOMAL PROTEIN S7

Chain G: 

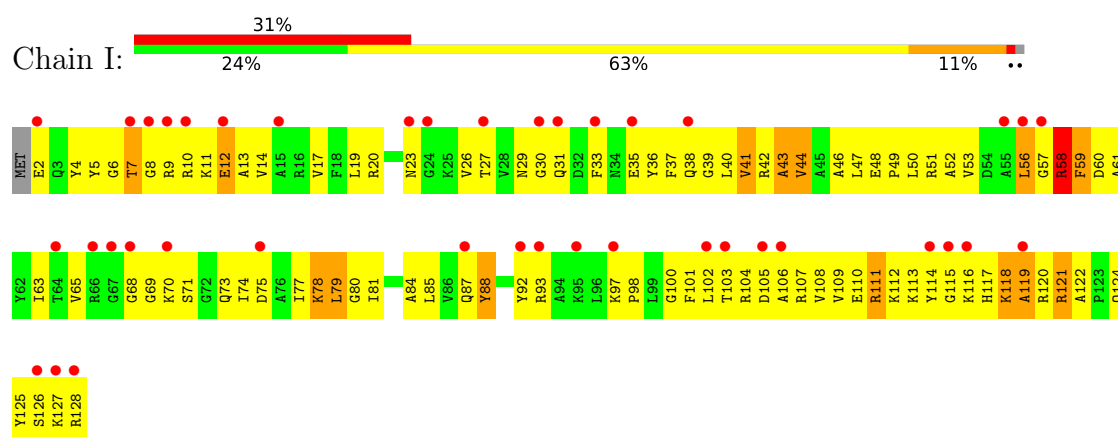


• Molecule 8: 30S RIBOSOMAL PROTEIN S8

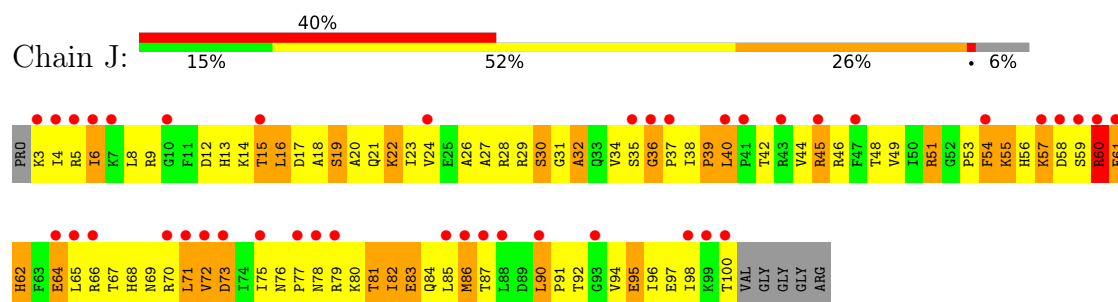
Chain H: 



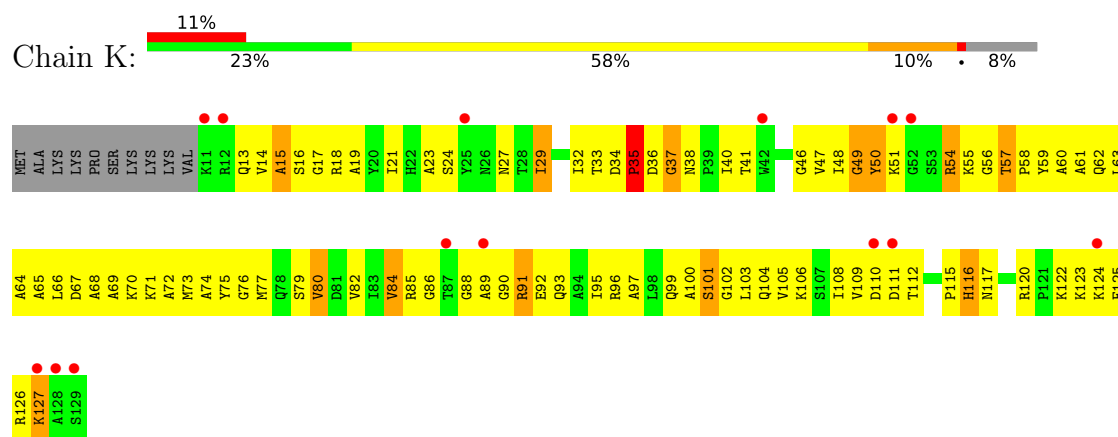
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



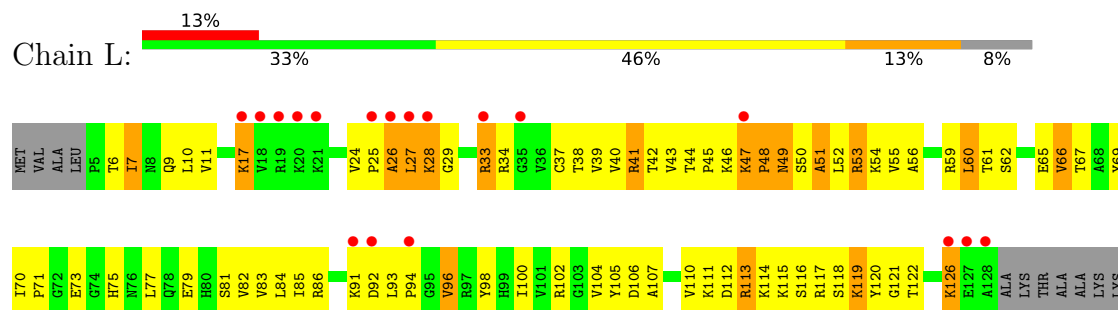
• Molecule 10: 30S RIBOSOMAL PROTEIN S10



• Molecule 11: 30S RIBOSOMAL PROTEIN S11

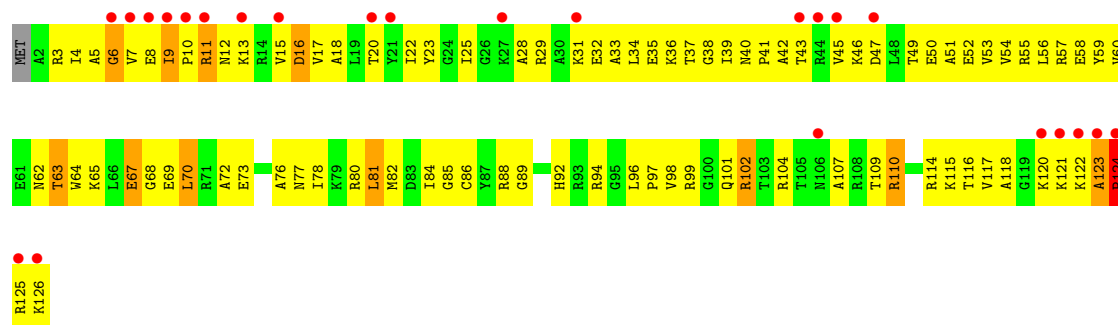


• Molecule 12: 30S RIBOSOMAL PROTEIN S12

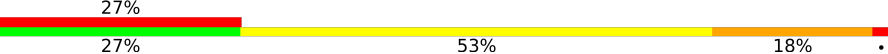


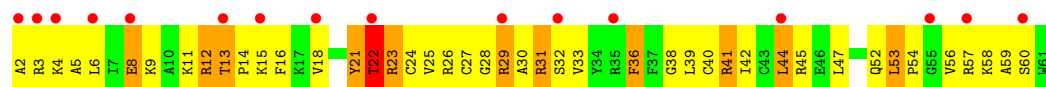
• Molecule 13: 30S RIBOSOMAL PROTEIN S13

Chain M: 



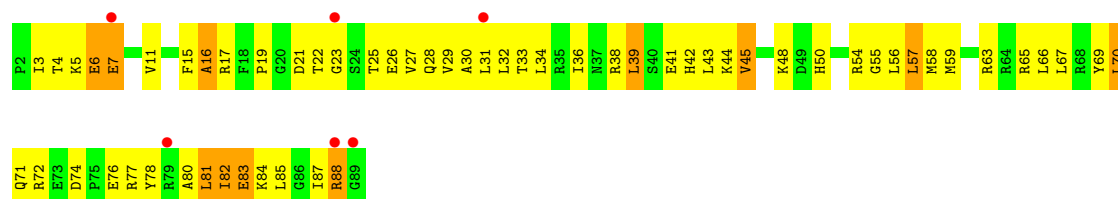
• Molecule 14: 30S RIBOSOMAL PROTEIN S14

Chain N: 



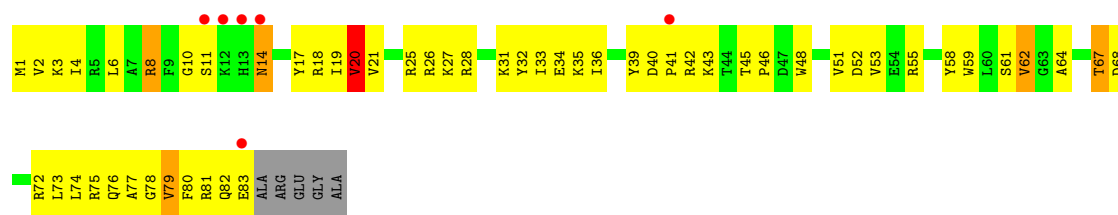
• Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain O: 



• Molecule 16: 30S RIBOSOMAL PROTEIN S16

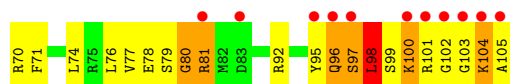
Chain P: 



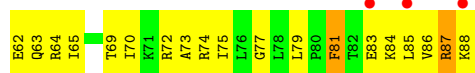
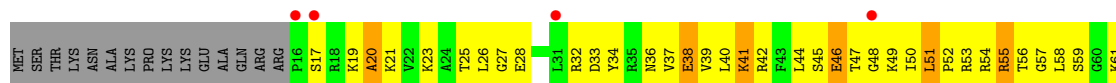
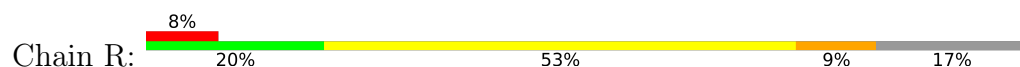
• Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain Q: 

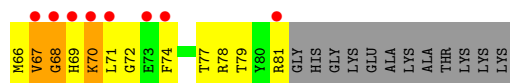
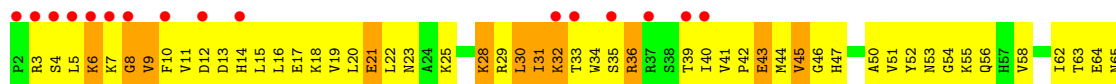
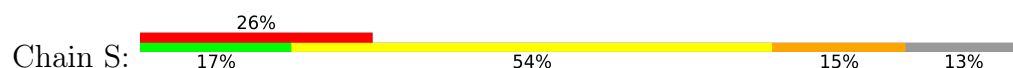




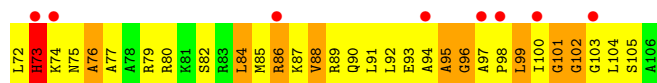
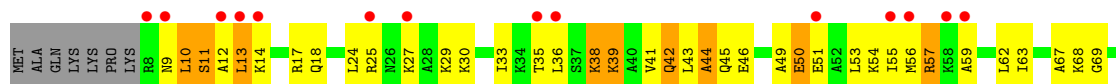
● Molecule 18: 30S RIBOSOMAL PROTEIN S18



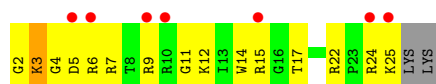
● Molecule 19: 30S RIBOSOMAL PROTEIN S19



● Molecule 20: 30S RIBOSOMAL PROTEIN S20



● Molecule 21: 30S RIBOSOMAL PROTEIN THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.38Å 401.38Å 175.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.76 – 3.05 59.76 – 3.05	Depositor EDS
% Data completeness (in resolution range)	94.0 (59.76-3.05) 94.0 (59.76-3.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 3.07Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.208 , 0.252 0.230 , 0.258	Depositor DCC
R_{free} test set	12919 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	68.0	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 76.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	51933	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.43	0/36393	0.73	82/56797 (0.1%)
2	B	0.45	0/1935	1.07	13/2609 (0.5%)
3	C	0.44	0/1636	1.01	9/2205 (0.4%)
4	D	0.44	0/1733	0.95	7/2318 (0.3%)
5	E	0.63	0/1162	1.19	10/1564 (0.6%)
6	F	0.41	0/856	0.95	3/1154 (0.3%)
7	G	0.42	0/1276	1.00	6/1709 (0.4%)
8	H	0.58	0/1136	1.13	9/1527 (0.6%)
9	I	0.41	0/1029	0.95	5/1378 (0.4%)
10	J	0.43	0/805	1.08	7/1082 (0.6%)
11	K	0.51	0/900	1.07	4/1213 (0.3%)
12	L	0.52	0/986	1.08	4/1320 (0.3%)
13	M	0.45	0/1008	0.99	2/1347 (0.1%)
14	N	0.44	0/501	1.21	7/664 (1.1%)
15	O	0.47	0/745	0.95	3/992 (0.3%)
16	P	0.51	0/716	1.17	8/963 (0.8%)
17	Q	0.54	0/870	1.07	2/1159 (0.2%)
18	R	0.43	0/603	0.96	4/799 (0.5%)
19	S	0.42	0/661	1.09	6/890 (0.7%)
20	T	0.50	0/764	1.12	7/1006 (0.7%)
21	V	0.49	0/212	0.87	0/277
All	All	0.44	0/55927	0.84	198/82973 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	2	40

There are no bond length outliers.

All (198) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	U	C2'-C3'-O3'	14.56	131.35	109.50
1	A	243	A	C2'-C3'-O3'	13.86	130.28	109.50
1	A	181	G	C2'-C3'-O3'	13.39	129.59	109.50
1	A	559	A	C2'-C3'-O3'	13.37	129.56	109.50
3	C	167	TRP	N-CA-C	12.81	119.28	108.78
12	L	26	ALA	N-CA-C	-11.86	99.57	113.21
1	A	1528	U	C2'-C3'-O3'	11.81	127.22	109.50
1	A	366	C	C2'-C3'-O3'	11.53	126.79	109.50
1	A	687	A	C2'-C3'-O3'	11.32	126.48	109.50
1	A	575	G	C2'-C3'-O3'	11.26	126.40	109.50
1	A	266	G	C2'-C3'-O3'	11.13	126.19	109.50
1	A	60	A	C2'-C3'-O3'	11.09	126.13	109.50
1	A	792	A	C2'-C3'-O3'	10.61	125.41	109.50
1	A	1528	U	C4'-C3'-O3'	10.58	125.27	109.40
20	T	13	LEU	N-CA-C	-9.98	100.24	111.82
11	K	37	GLY	N-CA-C	9.87	125.33	113.79
1	A	1067	A	C2'-C3'-O3'	9.83	124.25	109.50
5	E	23	GLY	N-CA-C	9.83	124.51	110.46
14	N	31	ARG	N-CA-C	9.73	124.20	111.75
1	A	115	G	C2'-C3'-O3'	9.69	124.03	109.50
1	A	372	C	C2'-C3'-O3'	9.60	123.89	109.50
1	A	7	G	C2'-C3'-O3'	9.57	123.85	109.50
1	A	181	G	C4'-C3'-O3'	9.34	123.42	109.40
14	N	8	GLU	N-CA-C	-9.09	101.72	113.17
15	O	45	VAL	N-CA-C	-9.05	96.44	109.29
1	A	428	G	C2'-C3'-O3'	9.04	123.06	109.50
1	A	1299	A	N9-C1'-C2'	8.78	125.17	112.00
2	B	13	ALA	N-CA-C	-8.73	102.53	113.01
1	A	1380	U	C2'-C3'-O3'	8.68	122.53	109.50
1	A	484	G	C2'-C3'-O3'	8.45	122.18	109.50
7	G	154	TYR	N-CA-C	-8.21	101.42	112.26
1	A	960	U	C2'-C3'-O3'	8.21	121.81	109.50
16	P	27	LYS	N-CA-C	-8.04	99.90	110.43
11	K	116	HIS	N-CA-C	-8.04	101.32	112.25
2	B	59	GLU	N-CA-C	-7.96	102.56	111.07
5	E	21	ALA	N-CA-C	-7.90	100.39	110.19
1	A	1224	G	C2'-C3'-O3'	7.81	121.21	109.50
1	A	559	A	C4'-C3'-O3'	7.76	121.04	109.40
2	B	190	THR	N-CA-C	7.75	121.67	111.75
7	G	145	ALA	N-CA-C	-7.66	99.78	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	147	ALA	N-CA-C	-7.56	103.43	114.39
1	A	913	A	C2'-C3'-O3'	7.53	120.79	109.50
2	B	154	LEU	N-CA-C	7.48	119.08	111.07
19	S	14	HIS	N-CA-C	-7.45	102.31	111.40
2	B	187	LEU	N-CA-C	-7.42	96.46	108.41
5	E	64	ARG	N-CA-C	-7.39	97.63	109.76
14	N	21	TYR	N-CA-C	7.37	120.31	107.49
1	A	1301	U	C2'-C3'-O3'	7.33	120.50	109.50
1	A	250	A	C2'-C3'-O3'	7.25	120.37	109.50
6	F	77	ARG	N-CA-C	-7.23	103.34	111.07
1	A	1364	U	C2'-C3'-O3'	7.17	120.26	109.50
1	A	1201	A	C2'-C3'-O3'	7.16	120.24	109.50
1	A	748	C	C2'-C3'-O3'	7.15	120.23	109.50
1	A	1503	A	C2'-C3'-O3'	7.14	120.21	109.50
5	E	20	GLN	N-CA-C	-7.12	98.53	109.14
1	A	5	U	C2'-C3'-O3'	7.11	120.16	109.50
18	R	81	PHE	N-CA-C	-7.10	104.75	113.41
1	A	1505	G	C2'-C3'-O3'	7.09	124.34	113.70
1	A	1335	C	C4'-C3'-O3'	-6.88	102.68	113.00
8	H	79	VAL	N-CA-C	-6.88	102.65	112.35
1	A	328	C	C2'-C3'-O3'	6.88	119.82	109.50
19	S	70	LYS	N-CA-C	6.85	119.80	108.49
12	L	119	LYS	N-CA-C	-6.79	99.24	110.17
1	A	1331	G	C2'-C3'-O3'	6.77	119.66	109.50
1	A	509	A	C2'-C3'-O3'	6.74	123.81	113.70
1	A	197	A	N9-C1'-C2'	6.72	124.09	114.00
4	D	33	MET	N-CA-C	-6.71	105.20	113.19
11	K	91	ARG	N-CA-C	-6.66	105.29	113.41
7	G	148	ASN	N-CA-C	-6.66	103.25	112.30
5	E	76	ILE	CA-C-N	6.65	126.60	119.28
5	E	76	ILE	C-N-CA	6.65	126.60	119.28
1	A	460	A	N9-C1'-C2'	6.64	121.96	112.00
5	E	7	GLU	N-CA-C	-6.62	101.61	110.55
20	T	44	ALA	N-CA-C	-6.60	104.08	111.28
1	A	965	A	C2'-C3'-O3'	6.59	119.38	109.50
2	B	105	PHE	N-CA-C	6.59	119.30	111.33
1	A	243	A	C4'-C3'-O3'	6.57	119.25	109.40
1	A	1065	U	C2'-C3'-O3'	6.54	119.32	109.50
3	C	167	TRP	CB-CA-C	-6.53	107.67	117.07
7	G	87	VAL	N-CA-C	6.52	114.24	108.63
1	A	1085	U	C2'-C3'-O3'	6.47	119.21	109.50
1	A	1281	U	C2'-C3'-O3'	6.45	119.18	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	26	PHE	N-CA-C	6.45	120.07	110.52
6	F	67	MET	N-CA-C	6.45	113.81	108.07
3	C	173	VAL	CA-C-N	6.44	127.89	119.84
3	C	173	VAL	C-N-CA	6.44	127.89	119.84
19	S	54	GLY	N-CA-C	-6.42	97.97	113.18
16	P	67	THR	N-CA-C	-6.40	102.04	110.43
8	H	87	SER	N-CA-C	-6.33	100.92	110.28
2	B	90	MET	N-CA-C	6.27	117.80	109.83
12	L	61	THR	N-CA-C	-6.26	105.61	113.18
12	L	66	VAL	N-CA-C	6.25	117.93	108.80
1	A	1124	G	N9-C1'-C2'	6.21	121.32	112.00
4	D	41	GLY	N-CA-C	6.20	120.48	112.68
3	C	93	LYS	N-CA-C	-6.18	105.80	113.15
1	A	119	A	C2'-C3'-O3'	6.14	118.72	109.50
1	A	60	A	C4'-C3'-O3'	6.13	118.60	109.40
17	Q	100	LYS	N-CA-C	-6.12	105.52	114.39
3	C	25	GLY	N-CA-C	6.11	119.71	110.18
1	A	63	C	C5'-C4'-C3'	-6.09	106.86	116.00
1	A	1129	C	C2'-C3'-O3'	6.04	118.56	109.50
1	A	533	A	C2'-C3'-O3'	6.02	118.54	109.50
1	A	115	G	N9-C1'-C2'	6.01	123.02	114.00
13	M	11	ARG	N-CA-C	5.97	118.26	109.24
20	T	88	VAL	N-CA-C	5.97	116.14	110.53
20	T	76	ALA	N-CA-C	-5.96	104.78	111.28
18	R	46	GLU	N-CA-C	-5.94	105.18	113.37
19	S	36	ARG	N-CA-C	-5.94	106.02	113.20
10	J	51	ARG	N-CA-C	5.91	117.42	110.97
4	D	12	CYS	N-CA-C	-5.90	104.03	111.11
10	J	81	THR	N-CA-C	-5.90	104.75	111.07
8	H	75	ARG	CA-C-N	5.89	125.85	119.78
8	H	75	ARG	C-N-CA	5.89	125.85	119.78
1	A	1504	G	C2'-C3'-O3'	5.87	118.30	109.50
1	A	413	G	C4'-C3'-O3'	-5.86	104.22	113.00
13	M	107	ALA	N-CA-C	-5.82	105.06	113.21
6	F	60	PHE	N-CA-C	5.81	118.94	109.59
16	P	77	ALA	N-CA-C	-5.81	106.81	112.97
1	A	701	C	C2'-C3'-O3'	5.80	118.20	109.50
16	P	25	ARG	N-CA-C	5.80	120.20	113.18
15	O	44	LYS	N-CA-C	-5.78	105.11	111.82
1	A	281	G	C2'-C3'-O3'	5.74	118.10	109.50
10	J	62	HIS	N-CA-C	5.73	119.15	109.76
1	A	1182	G	C2'-C3'-O3'	5.72	118.08	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1502	A	N9-C1'-C2'	5.68	122.52	114.00
1	A	993	G	C2'-C3'-O3'	5.67	118.00	109.50
1	A	389	A	C5'-C4'-C3'	5.66	124.49	116.00
4	D	11	LEU	N-CA-C	-5.66	104.73	111.69
1	A	413	G	N9-C1'-C2'	5.65	120.48	112.00
4	D	13	ARG	N-CA-C	5.65	117.12	111.07
9	I	63	ILE	N-CA-C	5.63	116.39	108.17
8	H	56	LYS	CA-C-N	5.62	125.90	119.83
8	H	56	LYS	C-N-CA	5.62	125.90	119.83
1	A	1285	A	C2'-C3'-O3'	5.61	117.92	109.50
19	S	34	TRP	N-CA-C	-5.61	106.20	113.16
20	T	69	GLY	N-CA-C	-5.60	104.01	112.41
2	B	45	GLN	N-CA-C	-5.60	105.28	111.71
2	B	23	ARG	N-CA-C	-5.52	99.03	110.80
1	A	812	C	C2'-C3'-O3'	5.52	117.78	109.50
2	B	186	ALA	N-CA-C	5.50	117.46	108.55
7	G	115	ARG	N-CA-C	5.50	117.70	108.96
5	E	51	VAL	CB-CA-C	-5.49	108.48	113.70
1	A	266	G	C5'-C4'-C3'	-5.49	106.97	115.20
14	N	38	GLY	N-CA-C	-5.47	108.08	115.36
3	C	99	VAL	N-CA-C	5.45	117.74	108.86
1	A	1200	C	C2'-C3'-O3'	-5.43	105.56	113.70
9	I	118	LYS	N-CA-C	5.42	116.81	110.41
16	P	20	VAL	N-CA-C	5.38	117.83	108.95
3	C	167	TRP	CA-C-O	5.37	121.05	117.94
4	D	28	SER	CA-C-N	5.37	126.55	119.84
4	D	28	SER	C-N-CA	5.37	126.55	119.84
14	N	53	LEU	CA-C-N	5.35	126.53	119.84
14	N	53	LEU	C-N-CA	5.35	126.53	119.84
15	O	5	LYS	N-CA-C	-5.34	105.45	111.28
20	T	38	LYS	N-CA-C	-5.33	105.15	110.97
1	A	687	A	C4'-C3'-O3'	5.33	117.40	109.40
1	A	1139	G	N9-C1'-C2'	5.32	119.99	112.00
1	A	1299	A	C4'-C3'-O3'	-5.32	105.02	113.00
1	A	975	A	C2'-C3'-O3'	5.31	117.47	109.50
5	E	11	ILE	N-CA-C	5.30	115.44	110.30
2	B	109	SER	N-CA-C	-5.28	105.20	111.69
1	A	661	G	C5'-C4'-C3'	-5.27	108.09	116.00
1	A	1346	A	C2'-C3'-O3'	5.27	117.41	109.50
3	C	4	LYS	N-CA-C	5.27	122.02	110.80
14	N	22	THR	N-CA-C	5.26	122.00	110.80
1	A	1050	G	C5'-C4'-C3'	5.25	123.88	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	T	75	ASN	N-CA-C	-5.25	106.83	113.18
11	K	88	GLY	N-CA-C	5.24	118.41	110.75
10	J	18	ALA	N-CA-C	-5.24	104.48	111.24
1	A	1279	A	N9-C1'-C2'	5.21	119.81	112.00
1	A	344	A	C2'-C3'-O3'	5.21	117.31	109.50
18	R	51	LEU	CA-C-N	5.20	125.18	120.03
18	R	51	LEU	C-N-CA	5.20	125.18	120.03
1	A	197	A	C2'-C3'-O3'	5.19	117.29	109.50
16	P	14	ASN	CA-C-N	5.19	125.11	119.76
16	P	14	ASN	C-N-CA	5.19	125.11	119.76
1	A	563	A	C4'-C3'-O3'	-5.18	105.23	113.00
1	A	1446	A	N9-C1'-C2'	5.17	119.76	112.00
9	I	61	ALA	N-CA-C	5.17	117.80	108.48
10	J	22	LYS	N-CA-C	-5.17	105.54	111.07
1	A	992	U	C2'-C3'-O3'	5.17	117.25	109.50
1	A	1305	G	N9-C1'-C2'	5.16	119.74	112.00
1	A	1195	C	C4'-C3'-O3'	-5.15	105.27	113.00
1	A	1101	A	C2'-C3'-O3'	5.14	117.22	109.50
2	B	134	GLU	N-CA-C	-5.14	106.69	113.12
1	A	1305	G	C4'-C3'-O3'	-5.10	105.35	113.00
9	I	87	GLN	N-CA-C	-5.10	105.72	111.28
8	H	135	CYS	N-CA-C	5.09	114.96	108.24
8	H	3	THR	N-CA-C	5.09	116.83	111.28
16	P	79	VAL	N-CA-C	-5.08	105.60	113.16
8	H	103	VAL	N-CA-C	5.07	116.21	109.37
19	S	21	GLU	N-CA-C	-5.06	105.89	111.71
9	I	59	PHE	CB-CA-C	-5.04	108.09	114.40
2	B	233	SER	N-CA-C	5.04	116.18	109.93
10	J	55	LYS	N-CA-C	5.04	118.58	109.32
10	J	60	ARG	N-CA-C	5.03	121.52	110.80
1	A	1451	A	C2'-C3'-O3'	5.03	117.04	109.50
17	Q	49	GLU	N-CA-C	-5.02	106.74	112.86

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	181	G	C3'
1	A	1528	U	C3'

All (40) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1073	U	Sidechain
1	A	1079	G	Sidechain
1	A	1085	U	Sidechain
1	A	1092	A	Sidechain
1	A	1130	A	Sidechain
1	A	1139	G	Sidechain
1	A	12	U	Sidechain
1	A	1281	U	Sidechain
1	A	1289	A	Sidechain
1	A	1293	G	Sidechain
1	A	1299	A	Sidechain
1	A	1301	U	Sidechain
1	A	1305	G	Sidechain
1	A	1340	A	Sidechain
1	A	1360	A	Sidechain
1	A	1506	U	Sidechain
1	A	1525	G	Sidechain
1	A	197	A	Sidechain
1	A	203	U	Sidechain
1	A	231	G	Sidechain
1	A	249	U	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	254	G	Sidechain
1	A	266	G	Sidechain
1	A	274	A	Sidechain
1	A	290	C	Sidechain
1	A	297	G	Sidechain
1	A	305	G	Sidechain
1	A	380	G	Sidechain
1	A	413	G	Sidechain
1	A	481	G	Sidechain
1	A	573	A	Sidechain
1	A	575	G	Sidechain
1	A	603	U	Sidechain
1	A	727	G	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain
1	A	982	U	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32514	0	16410	1123	0
2	B	1900	0	1951	236	1
3	C	1612	0	1677	238	0
4	D	1703	0	1764	157	0
5	E	1146	0	1207	113	0
6	F	843	0	857	76	0
7	G	1257	0	1296	97	0
8	H	1116	0	1177	71	0
9	I	1011	0	1043	118	0
10	J	792	0	835	133	0
11	K	885	0	904	92	0
12	L	970	0	1057	121	0
13	M	997	0	1072	124	0
14	N	492	0	529	76	0
15	O	734	0	771	62	0
16	P	700	0	720	59	0
17	Q	857	0	930	88	0
18	R	597	0	668	69	0
19	S	647	0	673	83	0
20	T	762	0	859	87	0
21	V	208	0	221	29	0
22	A	186	0	0	0	0
22	B	1	0	0	0	0
22	M	1	0	0	0	0
23	D	1	0	0	0	0
23	N	1	0	0	0	0
All	All	51933	0	36621	2952	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 33.

All (2952) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:41:ARG:HG2	12:L:42:THR:H	1.03	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.22	1.14
1:A:1443:G:H5''	1:A:1446:A:H5'	1.28	1.11
9:I:8:GLY:HA2	9:I:79:LEU:HD12	1.32	1.09
4:D:36:ARG:H	4:D:37:PRO:HD3	1.19	1.07
11:K:110:ASP:HB2	18:R:88:LYS:HD2	1.35	1.07
1:A:1489:G:H2'	1:A:1490:C:H5''	1.37	1.05
1:A:243:A:H4'	1:A:244:U:H5'	1.36	1.04
4:D:150:GLU:HG3	4:D:153:ARG:HH21	1.19	1.04
12:L:60:LEU:HD11	12:L:85:ILE:HD12	1.39	1.04
10:J:51:ARG:HB2	10:J:59:SER:HB3	1.34	1.03
20:T:39:LYS:HD2	20:T:55:ILE:HD13	1.41	1.02
13:M:49:THR:HG22	13:M:51:ALA:H	1.26	1.00
3:C:52:LEU:HD23	3:C:52:LEU:H	1.26	1.00
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.43	0.99
2:B:178:ARG:HH11	2:B:178:ARG:HG3	1.21	0.99
11:K:54:ARG:HB3	11:K:54:ARG:HH11	1.26	0.99
19:S:28:LYS:HG2	19:S:29:ARG:H	1.26	0.98
1:A:1116:C:H2'	1:A:1117:G:H5''	1.46	0.97
1:A:1057:G:H5''	3:C:154:SER:HB2	1.47	0.96
3:C:91:LEU:HD21	3:C:99:VAL:HG13	1.48	0.96
11:K:54:ARG:O	11:K:57:THR:HG22	1.66	0.95
1:A:1489:G:C2'	1:A:1490:C:H5''	1.96	0.94
10:J:31:GLY:HA2	10:J:78:ASN:HD22	1.32	0.94
3:C:14:ILE:HG22	3:C:15:THR:H	1.31	0.94
1:A:1190:G:OP1	3:C:4:LYS:HA	1.66	0.93
12:L:41:ARG:HG2	12:L:42:THR:N	1.83	0.93
6:F:94:GLN:HE21	18:R:32:ARG:HD3	1.32	0.93
19:S:31:ILE:HG22	19:S:32:LYS:H	1.34	0.93
17:Q:97:SER:HB2	17:Q:102:GLY:C	1.94	0.93
1:A:1256:A:H4'	1:A:1257:U:H5'	1.50	0.93
2:B:124:SER:HB2	2:B:125:PRO:HD2	1.49	0.93
12:L:75:HIS:HD2	12:L:77:LEU:H	1.05	0.92
1:A:1086:U:H3	1:A:1099:G:H22	1.08	0.92
16:P:58:TYR:O	16:P:61:SER:HB3	1.68	0.92
1:A:1137:C:H4'	1:A:1138:G:C2	2.05	0.92
13:M:40:ASN:HD22	13:M:41:PRO:CD	1.82	0.92
1:A:664:G:H22	1:A:741:G:H1	1.16	0.91
3:C:131:ARG:HG2	3:C:135:LYS:HE3	1.50	0.91
1:A:1305:G:HO2'	1:A:1306:A:H8	0.92	0.91
1:A:838:G:H2'	1:A:839:U:H5''	1.52	0.91
3:C:195:VAL:O	3:C:196:LEU:HD23	1.68	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1101:A:H4'	1:A:1102:A:O5'	1.65	0.90
5:E:81:GLU:HG2	5:E:90:VAL:HG22	1.52	0.90
9:I:70:LYS:O	9:I:74:ILE:HG13	1.72	0.90
1:A:1502:A:H2	1:A:1505:G:H1	1.20	0.90
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.51	0.90
1:A:1497:G:O2'	1:A:1498:U:H5'	1.71	0.89
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.51	0.89
2:B:91:PRO:HG2	2:B:155:LEU:HD23	1.54	0.89
10:J:8:LEU:HD21	10:J:96:ILE:HG12	1.54	0.88
2:B:59:GLU:HG2	2:B:221:LEU:HD11	1.51	0.88
12:L:25:PRO:C	12:L:27:LEU:H	1.79	0.87
4:D:36:ARG:N	4:D:37:PRO:HD3	1.88	0.87
1:A:1125:U:H3	10:J:5:ARG:HH21	1.18	0.86
4:D:150:GLU:HG3	4:D:153:ARG:NH2	1.90	0.86
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.57	0.86
1:A:1435:G:H2'	1:A:1436:U:C6	2.10	0.86
2:B:116:GLU:HG2	2:B:153:ARG:HH12	1.39	0.86
3:C:70:VAL:HG21	3:C:76:VAL:HG21	1.58	0.86
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.55	0.86
5:E:115:VAL:HG11	5:E:118:ILE:HG13	1.57	0.86
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.55	0.86
6:F:30:LEU:HD23	6:F:75:LEU:HD21	1.57	0.86
19:S:41:VAL:HG22	19:S:44:MET:HE3	1.56	0.85
1:A:1305:G:O2'	1:A:1306:A:H8	1.58	0.85
3:C:110:ASN:HD21	3:C:140:ARG:HB3	1.41	0.85
3:C:52:LEU:HD21	3:C:118:GLN:HE22	1.40	0.85
10:J:22:LYS:HE2	10:J:90:LEU:HD12	1.57	0.85
2:B:102:LEU:HD21	2:B:162:ILE:HD11	1.57	0.85
3:C:190:ARG:HB3	3:C:190:ARG:NH1	1.92	0.85
6:F:95:GLU:CD	6:F:95:GLU:H	1.85	0.84
1:A:1131:G:H1	1:A:1143:G:H21	1.22	0.84
13:M:50:GLU:O	13:M:54:VAL:HG23	1.77	0.84
10:J:49:VAL:HG13	14:N:41:ARG:HB2	1.57	0.84
1:A:250:A:H4'	1:A:251:G:O5'	1.76	0.84
3:C:64:VAL:HB	3:C:99:VAL:HB	1.59	0.84
13:M:3:ARG:HG2	13:M:9:ILE:HG23	1.56	0.84
1:A:1497:G:C2'	1:A:1498:U:H5'	2.08	0.84
1:A:141:A:H1'	1:A:182:U:O2	1.78	0.84
1:A:1064:G:H4'	1:A:1065:U:H5'	1.58	0.84
17:Q:27:PHE:CZ	17:Q:36:ILE:HD11	2.12	0.84
9:I:8:GLY:HA2	9:I:79:LEU:CD1	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:190:ARG:HB3	3:C:190:ARG:HH11	1.43	0.84
4:D:104:VAL:HG11	4:D:146:ILE:HD12	1.58	0.83
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.60	0.83
19:S:55:LYS:HG2	19:S:56:GLN:HE21	1.41	0.83
6:F:36:ARG:HH12	6:F:38:GLU:HG2	1.44	0.83
4:D:61:LYS:HD2	4:D:207:TYR:OH	1.78	0.83
3:C:172:ARG:HH12	3:C:174:PRO:HG3	1.43	0.83
1:A:135:C:O2	16:P:1:MET:HB2	1.78	0.83
1:A:1281:U:H5'	1:A:1282:C:H5	1.44	0.82
1:A:1356:G:H2'	1:A:1357:A:C8	2.15	0.82
3:C:191:THR:HG22	3:C:193:TYR:H	1.44	0.82
7:G:75:VAL:CG1	7:G:86:GLN:HB3	2.10	0.82
3:C:91:LEU:HD23	3:C:92:ALA:N	1.94	0.82
4:D:25:ARG:C	4:D:27:TYR:H	1.85	0.82
19:S:29:ARG:O	19:S:30:LEU:HB2	1.80	0.82
13:M:22:ILE:HD12	13:M:25:ILE:HD12	1.61	0.82
15:O:78:TYR:CZ	15:O:82:ILE:HD11	2.15	0.81
4:D:150:GLU:HA	4:D:153:ARG:HE	1.44	0.81
20:T:43:LEU:HD13	20:T:51:GLU:HG3	1.62	0.81
4:D:150:GLU:H	4:D:150:GLU:CD	1.86	0.81
3:C:8:ILE:HG23	3:C:16:ARG:HG2	1.60	0.81
13:M:78:ILE:HA	13:M:81:LEU:HD21	1.62	0.81
6:F:30:LEU:HB3	6:F:35:ALA:HB3	1.62	0.81
10:J:19:SER:HB2	10:J:91:PRO:HG3	1.60	0.81
17:Q:95:TYR:C	17:Q:97:SER:H	1.89	0.81
1:A:1060:C:C5	3:C:2:GLY:HA3	2.14	0.81
14:N:14:PRO:C	14:N:16:PHE:H	1.86	0.81
2:B:101:MET:HA	2:B:108:ILE:HD12	1.63	0.81
12:L:41:ARG:CG	12:L:42:THR:H	1.88	0.80
12:L:70:ILE:HD13	12:L:77:LEU:HD12	1.63	0.80
2:B:27:LYS:HD3	2:B:195:ASP:OD2	1.82	0.80
18:R:55:ARG:NH1	18:R:55:ARG:HB3	1.95	0.80
1:A:1285:A:H4'	1:A:1286:A:O5'	1.82	0.80
3:C:107:GLN:H	3:C:107:GLN:CD	1.88	0.80
1:A:673:G:H2'	1:A:674:G:C8	2.17	0.80
7:G:75:VAL:HG11	7:G:86:GLN:HB3	1.63	0.79
12:L:126:LYS:H	12:L:126:LYS:HD2	1.47	0.79
5:E:118:ILE:HG22	5:E:119:LEU:N	1.95	0.79
10:J:8:LEU:CD2	10:J:96:ILE:HG12	2.11	0.79
11:K:54:ARG:HB3	11:K:54:ARG:NH1	1.97	0.79
1:A:80:G:H3'	1:A:81:U:H5''	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:67:THR:HG22	12:L:96:VAL:HG13	1.63	0.79
12:L:28:LYS:HD2	12:L:33:ARG:HH22	1.47	0.79
2:B:8:LYS:O	2:B:9:GLU:HB2	1.81	0.79
20:T:54:LYS:HG3	20:T:100:ILE:CD1	2.13	0.79
1:A:1116:C:C2'	1:A:1117:G:H5''	2.12	0.78
1:A:1490:C:H6	1:A:1490:C:H5'	1.47	0.78
1:A:255:G:H1'	17:Q:16:GLN:NE2	1.97	0.78
2:B:132:LYS:HA	2:B:135:GLN:HB3	1.63	0.78
12:L:120:TYR:O	12:L:122:THR:HG23	1.83	0.78
3:C:15:THR:O	3:C:16:ARG:HB2	1.82	0.78
1:A:838:G:C2'	1:A:839:U:H5''	2.14	0.78
2:B:84:GLU:OE1	2:B:216:SER:HA	1.83	0.78
5:E:43:LEU:HD11	5:E:132:ALA:HB1	1.64	0.78
19:S:31:ILE:HG22	19:S:32:LYS:N	1.99	0.78
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.19	0.78
5:E:64:ARG:O	5:E:65:ASN:HB3	1.84	0.77
1:A:939:G:H5''	7:G:102:ARG:NH2	1.98	0.77
2:B:197:VAL:HB	2:B:200:ILE:HG12	1.66	0.77
15:O:17:ARG:HG3	15:O:17:ARG:HH11	1.49	0.77
1:A:1226:C:H4'	1:A:1227:A:OP1	1.84	0.77
3:C:150:LYS:HE2	3:C:152:ILE:HD11	1.66	0.77
7:G:66:VAL:HG12	7:G:70:LYS:HE3	1.65	0.77
1:A:761:G:H1'	17:Q:104:LYS:O	1.85	0.77
1:A:130:A:OP2	1:A:190(E):U:H2'	1.84	0.77
6:F:100:ASN:HD22	18:R:23:LYS:HG2	1.49	0.77
1:A:1250:A:H4'	9:I:68:GLY:H	1.47	0.77
1:A:243:A:C4'	1:A:244:U:H5'	2.13	0.77
3:C:110:ASN:O	3:C:111:LEU:HD23	1.85	0.77
6:F:86:ARG:O	6:F:87:ARG:HG2	1.85	0.77
9:I:118:LYS:O	9:I:119:ALA:HB3	1.85	0.77
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.64	0.77
1:A:839:U:H5'	1:A:840:C:H5	1.50	0.77
1:A:1152:A:H5''	10:J:13:HIS:CD2	2.19	0.77
1:A:1366:C:H2'	1:A:1367:C:H6	1.48	0.77
20:T:54:LYS:HG3	20:T:100:ILE:HD13	1.66	0.77
1:A:1236:A:H4'	1:A:1304:G:H4'	1.67	0.76
7:G:95:ARG:HG3	7:G:95:ARG:HH11	1.50	0.76
8:H:90:GLY:O	8:H:91:ARG:HB2	1.82	0.76
13:M:4:ILE:HG22	13:M:5:ALA:N	2.00	0.76
1:A:1256:A:N6	1:A:1278:U:H1'	2.00	0.76
2:B:57:PHE:O	2:B:60:ASP:HB3	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:97:SER:OG	17:Q:103:GLY:HA2	1.85	0.76
21:V:5:ASP:O	21:V:11:GLY:HA3	1.85	0.76
1:A:328:C:O2	1:A:328:C:H2'	1.85	0.76
3:C:19:GLU:HB3	3:C:40:ARG:HH21	1.50	0.76
2:B:139:LYS:O	2:B:143:GLU:HG2	1.86	0.76
20:T:14:LYS:O	20:T:18:GLN:HG3	1.86	0.76
16:P:74:LEU:O	16:P:79:VAL:HG23	1.85	0.76
1:A:761:G:H4'	17:Q:102:GLY:C	2.11	0.76
1:A:1025:U:H2'	1:A:1026:G:C8	2.21	0.76
2:B:36:ARG:HD2	2:B:41:ILE:HD12	1.68	0.75
10:J:82:ILE:O	10:J:86:MET:HB2	1.86	0.75
12:L:126:LYS:H	12:L:126:LYS:CD	1.96	0.75
3:C:50:ALA:HB1	3:C:70:VAL:HG11	1.68	0.75
19:S:16:LEU:O	19:S:19:VAL:HG12	1.87	0.75
3:C:116:VAL:HG21	3:C:202:ILE:HD11	1.68	0.75
10:J:96:ILE:HG22	10:J:97:GLU:H	1.52	0.75
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.51	0.75
12:L:48:PRO:HG2	12:L:49:ASN:H	1.52	0.75
1:A:80:G:H3'	1:A:81:U:C5'	2.16	0.75
1:A:351:G:H4'	1:A:352:C:OP1	1.85	0.75
1:A:839:U:H5'	1:A:840:C:C5	2.22	0.75
1:A:840:C:H5''	1:A:841:U:OP1	1.85	0.75
2:B:130:ARG:HH22	3:C:179:ARG:HH12	1.35	0.75
12:L:75:HIS:HD2	12:L:77:LEU:N	1.82	0.74
13:M:3:ARG:HA	13:M:8:GLU:O	1.86	0.74
1:A:1391:U:H2'	1:A:1392:G:C8	2.22	0.74
4:D:162:LEU:HD13	4:D:181:MET:HG2	1.67	0.74
13:M:88:ARG:HD2	19:S:3:ARG:HH21	1.50	0.74
1:A:1234:C:H5'	1:A:1365:G:OP1	1.86	0.74
2:B:72:GLY:HA3	2:B:81:VAL:HG21	1.69	0.74
19:S:40:ILE:HD13	19:S:62:ILE:HD13	1.68	0.74
1:A:1064:G:H4'	1:A:1065:U:C5'	2.18	0.74
15:O:33:THR:HG23	15:O:63:ARG:NH1	2.03	0.74
17:Q:95:TYR:O	17:Q:97:SER:N	2.19	0.74
19:S:17:GLU:O	19:S:21:GLU:HG3	1.87	0.74
1:A:579:G:H5'	1:A:728:A:H1'	1.69	0.74
2:B:16:HIS:NE2	2:B:214:ILE:HG12	2.02	0.74
2:B:77:ALA:HB2	2:B:211:ILE:CD1	2.10	0.74
3:C:52:LEU:HD23	3:C:52:LEU:N	2.02	0.74
1:A:1117:G:H4'	9:I:104:ARG:NH1	2.03	0.74
2:B:178:ARG:HG3	2:B:178:ARG:NH1	1.92	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:75:HIS:CD2	12:L:77:LEU:H	1.97	0.74
18:R:55:ARG:HB3	18:R:55:ARG:HH11	1.50	0.74
1:A:748:C:H1'	1:A:749:C:H5	1.53	0.74
6:F:69:GLU:HA	6:F:72:VAL:HG23	1.70	0.74
1:A:1125:U:H3	10:J:5:ARG:NH2	1.85	0.73
4:D:64:LEU:HD12	4:D:75:PHE:HZ	1.53	0.73
21:V:6:ARG:HD3	21:V:15:ARG:HH12	1.52	0.73
1:A:792:A:H4'	1:A:793:U:H5''	1.68	0.73
1:A:1279:A:H5''	1:A:1280:A:OP1	1.88	0.73
7:G:23:VAL:HG12	7:G:27:ILE:HD11	1.70	0.73
12:L:27:LEU:HG	12:L:28:LYS:H	1.53	0.73
2:B:23:ARG:NH1	2:B:24:TRP:N	2.35	0.73
9:I:44:VAL:HG13	9:I:51:ARG:HH22	1.52	0.73
3:C:52:LEU:H	3:C:52:LEU:CD2	2.00	0.73
12:L:27:LEU:O	12:L:29:GLY:N	2.21	0.73
1:A:992:U:H4'	1:A:993:G:O5'	1.86	0.73
1:A:1488:G:H2'	1:A:1489:G:C8	2.24	0.73
2:B:95:GLN:O	2:B:96:ARG:HD2	1.88	0.73
12:L:59:ARG:HD3	12:L:65:GLU:HG3	1.68	0.73
1:A:1412:C:H2'	1:A:1413:A:C8	2.24	0.73
2:B:91:PRO:HG3	2:B:154:LEU:HB2	1.69	0.73
3:C:13:GLY:HA3	14:N:57:ARG:HH21	1.54	0.73
6:F:26:ILE:HG21	6:F:63:TYR:HE2	1.54	0.73
2:B:23:ARG:HH11	2:B:24:TRP:N	1.86	0.72
2:B:116:GLU:HG2	2:B:153:ARG:NH1	2.04	0.72
8:H:1:MET:HG2	8:H:2:LEU:N	2.05	0.72
2:B:25:ASN:HD22	2:B:25:ASN:C	1.96	0.72
4:D:3:ARG:HH22	4:D:74:GLN:CD	1.97	0.72
1:A:434:U:H2'	1:A:435:C:C6	2.24	0.72
18:R:26:LEU:HD12	18:R:27:GLY:H	1.53	0.72
1:A:197:A:H4'	1:A:198:G:O5'	1.90	0.72
1:A:353:A:H5'	1:A:353:A:H8	1.53	0.72
1:A:161:A:H2'	1:A:162:A:C8	2.23	0.72
1:A:1152:A:H5''	10:J:13:HIS:HD2	1.53	0.72
10:J:39:PRO:O	10:J:40:LEU:HB2	1.89	0.72
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.23	0.72
20:T:10:LEU:O	20:T:12:ALA:N	2.22	0.72
1:A:877:C:O2	8:H:3:THR:HG21	1.89	0.72
1:A:1250:A:H4'	9:I:68:GLY:N	2.05	0.72
8:H:1:MET:HG2	8:H:2:LEU:H	1.54	0.72
11:K:84:VAL:HG11	11:K:95:ILE:HD11	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1148:U:H2'	1:A:1149:C:O4'	1.90	0.71
10:J:35:SER:HB2	10:J:72:VAL:O	1.90	0.71
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.70	0.71
18:R:45:SER:C	18:R:47:THR:H	1.97	0.71
1:A:501:C:H2'	1:A:502:G:H8	1.53	0.71
3:C:195:VAL:C	3:C:196:LEU:HD23	2.15	0.71
1:A:974:A:OP1	14:N:31:ARG:HG2	1.89	0.71
9:I:4:TYR:CE2	9:I:88:TYR:HA	2.24	0.71
18:R:33:ASP:OD2	18:R:36:ASN:HB2	1.90	0.71
1:A:1065:U:H4'	1:A:1066:C:O5'	1.89	0.71
1:A:977:A:H2'	1:A:978:A:H5''	1.72	0.71
1:A:1413:A:H2	1:A:1487:G:H22	1.39	0.71
10:J:45:ARG:HH22	14:N:36:PHE:HD2	1.36	0.71
1:A:344:A:H4'	1:A:345:C:OP2	1.91	0.71
9:I:111:ARG:HD3	9:I:112:LYS:N	2.06	0.71
1:A:1281:U:H5'	1:A:1282:C:C5	2.25	0.71
1:A:1343:G:H2'	1:A:1344:C:C6	2.26	0.71
5:E:43:LEU:HB2	5:E:136:MET:HE2	1.71	0.71
1:A:954:G:H5''	13:M:120:LYS:HD3	1.73	0.71
9:I:65:VAL:HG21	9:I:73:GLN:HB3	1.72	0.71
8:H:108:GLY:HA3	8:H:138:TRP:HB3	1.70	0.71
19:S:15:LEU:HD12	19:S:16:LEU:N	2.06	0.71
19:S:70:LYS:O	19:S:72:GLY:N	2.24	0.71
1:A:1411:C:H2'	1:A:1412:C:C6	2.26	0.70
3:C:7:PRO:HG2	3:C:184:TYR:HB2	1.73	0.70
1:A:706:A:C1'	11:K:29:ILE:HD11	2.21	0.70
1:A:818:G:C3'	1:A:819:A:H5''	2.21	0.70
4:D:30:LYS:C	4:D:32:ALA:H	1.97	0.70
5:E:102:ALA:HB1	5:E:120:THR:HG21	1.73	0.70
13:M:40:ASN:HB3	13:M:43:THR:HG23	1.72	0.70
1:A:537:G:OP1	12:L:113:ARG:NH2	2.24	0.70
1:A:706:A:O4'	11:K:29:ILE:HD11	1.91	0.70
1:A:1351:U:H2'	1:A:1352:C:H6	1.55	0.70
6:F:10:LEU:HD11	6:F:59:TYR:HD2	1.54	0.70
10:J:32:ALA:HB2	10:J:76:ASN:HD22	1.57	0.70
14:N:22:THR:HB	14:N:33:VAL:HG21	1.73	0.70
1:A:107:G:C2'	1:A:108:G:H5'	2.21	0.70
1:A:496:A:H4'	1:A:497:A:OP1	1.92	0.70
1:A:1489:G:C3'	1:A:1490:C:H5''	2.21	0.70
2:B:124:SER:HB2	2:B:125:PRO:CD	2.22	0.70
3:C:180:ALA:O	3:C:181:ASN:HB3	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:65:LEU:HD23	10:J:65:LEU:O	1.91	0.70
10:J:78:ASN:O	10:J:80:LYS:N	2.24	0.70
13:M:6:GLY:O	13:M:7:VAL:HG22	1.92	0.70
13:M:49:THR:HG22	13:M:51:ALA:N	2.02	0.70
1:A:1278:U:H5''	1:A:1279:A:C5'	2.21	0.70
4:D:36:ARG:H	4:D:37:PRO:CD	2.02	0.70
9:I:97:LYS:HG2	9:I:102:LEU:HD12	1.72	0.70
4:D:70:ILE:HD11	4:D:100:ARG:CZ	2.21	0.70
15:O:17:ARG:NH1	15:O:77:ARG:NH1	2.40	0.70
4:D:157:LEU:CD2	4:D:161:ASN:HD21	2.05	0.70
17:Q:45:HIS:HB2	17:Q:65:ILE:HD13	1.71	0.70
18:R:39:VAL:O	18:R:42:ARG:HB2	1.90	0.70
1:A:1168:A:H2'	1:A:1169:A:C8	2.27	0.70
4:D:28:SER:O	4:D:30:LYS:N	2.25	0.70
9:I:97:LYS:CG	9:I:102:LEU:HD12	2.22	0.70
10:J:30:SER:O	10:J:78:ASN:HB2	1.92	0.70
10:J:61:GLU:OE1	14:N:45:ARG:NH1	2.25	0.70
3:C:6:HIS:CD2	3:C:8:ILE:HB	2.27	0.69
13:M:81:LEU:O	13:M:86:CYS:HB3	1.92	0.69
1:A:438:G:H4'	1:A:439:A:OP1	1.90	0.69
4:D:150:GLU:CG	4:D:153:ARG:HH21	2.02	0.69
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.74	0.69
1:A:254:G:OP1	17:Q:67:LYS:O	2.10	0.69
1:A:954:G:C5'	13:M:120:LYS:HD3	2.23	0.69
13:M:40:ASN:HD22	13:M:41:PRO:HD2	1.56	0.69
3:C:52:LEU:HD21	3:C:118:GLN:NE2	2.07	0.69
13:M:81:LEU:HD23	13:M:81:LEU:H	1.56	0.69
19:S:62:ILE:HD12	19:S:66:MET:HG3	1.75	0.69
1:A:352:C:H4'	1:A:354:G:OP1	1.91	0.69
10:J:46:ARG:HH11	10:J:64:GLU:CB	2.05	0.69
12:L:55:VAL:HG12	12:L:56:ALA:H	1.57	0.69
1:A:1137:C:H4'	1:A:1138:G:N2	2.06	0.69
1:A:17:U:H2'	1:A:18:C:C6	2.28	0.69
1:A:1281:U:H4'	1:A:1282:C:OP2	1.92	0.69
3:C:52:LEU:CD2	3:C:118:GLN:HE22	2.05	0.69
4:D:199:ASN:ND2	4:D:201:GLN:HB2	2.08	0.69
10:J:30:SER:HB2	10:J:80:LYS:HB3	1.75	0.69
11:K:108:ILE:HB	18:R:87:ARG:O	1.91	0.69
13:M:11:ARG:HG2	13:M:12:ASN:N	2.07	0.69
1:A:392:G:H2'	1:A:393:A:H8	1.55	0.69
16:P:34:GLU:OE2	16:P:55:ARG:HD3	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:66:SER:O	17:Q:70:ARG:NH1	2.26	0.69
1:A:939:G:H5''	7:G:102:ARG:HH22	1.56	0.69
4:D:64:LEU:HD23	4:D:198:VAL:HG21	1.75	0.69
4:D:64:LEU:HD12	4:D:75:PHE:CZ	2.28	0.68
6:F:36:ARG:NH1	6:F:38:GLU:HG2	2.08	0.68
12:L:47:LYS:CB	12:L:48:PRO:CD	2.71	0.68
19:S:43:GLU:H	19:S:43:GLU:CD	2.00	0.68
21:V:6:ARG:CD	21:V:15:ARG:HH12	2.06	0.68
1:A:477:G:H2'	1:A:478:A:H8	1.56	0.68
10:J:42:THR:HG23	10:J:67:THR:O	1.93	0.68
17:Q:24:GLU:OE2	17:Q:37:LYS:HD3	1.92	0.68
1:A:1443:G:C5'	1:A:1446:A:H5'	2.15	0.68
2:B:187:LEU:HD12	2:B:205:ASP:HA	1.74	0.68
19:S:41:VAL:HG23	19:S:43:GLU:HG2	1.75	0.68
1:A:1141:C:H2'	1:A:1142:G:H8	1.57	0.68
12:L:25:PRO:C	12:L:27:LEU:N	2.52	0.68
1:A:731:G:OP1	1:A:766:A:H1'	1.94	0.68
1:A:1412:C:H2'	1:A:1413:A:H8	1.59	0.68
2:B:22:LYS:HD2	2:B:35:GLU:OE1	1.93	0.68
5:E:51:VAL:O	5:E:55:VAL:HG23	1.93	0.68
9:I:93:ARG:HD3	9:I:97:LYS:HE3	1.75	0.68
19:S:5:LEU:O	19:S:6:LYS:HB2	1.92	0.68
1:A:701:C:H5'	1:A:703:G:O4'	1.93	0.68
3:C:38:ARG:HH11	3:C:38:ARG:HG3	1.58	0.68
1:A:99:C:H2'	1:A:101:A:C8	2.28	0.68
1:A:382:A:H2'	1:A:383:A:C8	2.28	0.68
6:F:75:LEU:O	6:F:79:LEU:HG	1.94	0.68
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.75	0.68
4:D:151:LYS:N	4:D:151:LYS:HD2	2.08	0.68
6:F:100:ASN:ND2	18:R:23:LYS:HG2	2.08	0.68
9:I:26:VAL:HB	9:I:33:PHE:HB2	1.76	0.68
13:M:81:LEU:HD12	13:M:88:ARG:HD3	1.74	0.68
1:A:376:G:OP2	16:P:67:THR:HG21	1.94	0.68
1:A:948:C:OP1	13:M:109:THR:HG22	1.94	0.68
12:L:126:LYS:HD2	12:L:126:LYS:N	2.07	0.68
1:A:939:G:H2'	1:A:940:C:C6	2.27	0.68
1:A:1064:G:C4'	1:A:1065:U:H5'	2.23	0.68
15:O:55:GLY:O	15:O:59:MET:HG3	1.94	0.68
1:A:173:U:H5'	1:A:197:A:O4'	1.95	0.67
1:A:1016:A:H2'	1:A:1017:G:O4'	1.93	0.67
12:L:47:LYS:HB2	12:L:48:PRO:CD	2.23	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:40:ASN:HD22	13:M:41:PRO:N	1.91	0.67
18:R:45:SER:OG	18:R:49:LYS:HB2	1.94	0.67
2:B:18:GLY:HA2	2:B:42:ILE:H	1.59	0.67
3:C:82:GLU:O	3:C:85:ARG:HB3	1.94	0.67
1:A:1366:C:H2'	1:A:1367:C:C6	2.30	0.67
16:P:20:VAL:HG11	16:P:32:TYR:HB3	1.74	0.67
1:A:105:G:H2'	1:A:106:C:C6	2.29	0.67
1:A:328:C:H4'	1:A:329:A:O5'	1.94	0.67
3:C:179:ARG:HD3	3:C:206:GLU:HG2	1.76	0.67
1:A:31:G:N1	1:A:48:C:H5''	2.09	0.67
1:A:1112:C:O2	3:C:179:ARG:HB3	1.95	0.67
3:C:190:ARG:HH11	3:C:190:ARG:CB	2.07	0.67
1:A:915:A:H2'	1:A:916:G:H5'	1.76	0.67
1:A:1368:G:O2'	1:A:1369:C:H5'	1.95	0.67
4:D:151:LYS:HD2	4:D:151:LYS:H	1.60	0.67
18:R:26:LEU:HD21	18:R:39:VAL:CG2	2.25	0.67
1:A:371:G:O2'	1:A:372:C:H5'	1.95	0.67
13:M:33:ALA:HA	13:M:59:TYR:HE2	1.60	0.67
1:A:1057:G:O2'	1:A:1058:G:H5'	1.95	0.67
1:A:1502:A:H2	1:A:1505:G:N1	1.90	0.67
4:D:187:ARG:HH21	4:D:188:LEU:HD12	1.60	0.67
1:A:186:C:O3'	20:T:82:SER:HB3	1.95	0.67
3:C:130:VAL:HG21	3:C:157:ILE:HG23	1.75	0.67
1:A:686:U:HO2'	1:A:687:A:H8	1.40	0.66
1:A:748:C:H1'	1:A:749:C:C5	2.30	0.66
1:A:967:C:H4'	9:I:128:ARG:HG3	1.75	0.66
3:C:26:LYS:H	3:C:26:LYS:HD3	1.58	0.66
10:J:94:VAL:HG12	10:J:95:GLU:N	2.10	0.66
5:E:12:LEU:HD13	5:E:31:LEU:HB2	1.77	0.66
11:K:14:VAL:O	11:K:15:ALA:HB3	1.95	0.66
17:Q:76:LEU:C	17:Q:76:LEU:HD23	2.20	0.66
1:A:80:G:C3'	1:A:81:U:H5''	2.25	0.66
1:A:195:A:H4'	20:T:68:LYS:HE2	1.77	0.66
1:A:650:G:O2'	1:A:651:C:H5'	1.94	0.66
10:J:49:VAL:O	10:J:60:ARG:HA	1.95	0.66
11:K:66:LEU:HB3	11:K:70:LYS:HE3	1.78	0.66
15:O:33:THR:HG23	15:O:63:ARG:HH12	1.59	0.66
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.10	0.66
1:A:761:G:H5''	17:Q:102:GLY:HA3	1.78	0.66
4:D:32:ALA:C	4:D:34:GLU:H	2.04	0.66
13:M:65:LYS:HG3	13:M:69:GLU:OE2	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.59	0.66
1:A:662:G:H2'	1:A:663:A:C8	2.30	0.66
5:E:150:ARG:HG3	5:E:150:ARG:HH11	1.60	0.66
8:H:6:ILE:HD11	8:H:31:PHE:CD2	2.30	0.66
10:J:60:ARG:O	10:J:61:GLU:HB3	1.95	0.66
13:M:81:LEU:H	13:M:81:LEU:CD2	2.08	0.66
17:Q:97:SER:OG	17:Q:103:GLY:CA	2.44	0.66
2:B:71:VAL:O	2:B:165:VAL:HG23	1.96	0.66
3:C:107:GLN:H	3:C:107:GLN:NE2	1.94	0.66
7:G:85:TYR:HD1	7:G:154:TYR:HE1	1.42	0.66
9:I:10:ARG:HG2	9:I:75:ASP:HB2	1.77	0.66
19:S:33:THR:HG22	19:S:35:SER:H	1.60	0.66
1:A:353:A:H5'	1:A:353:A:C8	2.31	0.66
12:L:33:ARG:HD3	12:L:62:SER:HB3	1.77	0.66
14:N:14:PRO:HB2	14:N:16:PHE:O	1.95	0.66
1:A:266:G:O3'	17:Q:67:LYS:HB2	1.95	0.65
1:A:427:U:OP1	4:D:13:ARG:NH2	2.29	0.65
3:C:83:ARG:C	3:C:85:ARG:H	2.04	0.65
3:C:155:GLY:O	3:C:156:ARG:HB2	1.96	0.65
12:L:27:LEU:C	12:L:29:GLY:H	2.04	0.65
1:A:443:C:H2'	1:A:444:C:H6	1.61	0.65
1:A:1216:G:H5''	14:N:5:ALA:CB	2.27	0.65
11:K:14:VAL:HG21	11:K:40:ILE:HD11	1.77	0.65
18:R:47:THR:HG23	18:R:83:GLU:H	1.61	0.65
1:A:524:G:H2'	1:A:525:C:C6	2.31	0.65
5:E:80:ILE:HD11	5:E:91:LEU:HD12	1.76	0.65
13:M:34:LEU:HD13	13:M:41:PRO:HA	1.77	0.65
1:A:1278:U:H5''	1:A:1279:A:H5'	1.76	0.65
1:A:1495:U:H2'	1:A:1496:C:C6	2.31	0.65
2:B:15:VAL:CG2	2:B:209:ARG:HG3	2.26	0.65
2:B:18:GLY:HA3	2:B:41:ILE:HA	1.79	0.65
10:J:38:ILE:CG1	10:J:71:LEU:HB3	2.26	0.65
21:V:6:ARG:HD3	21:V:15:ARG:NH1	2.12	0.65
13:M:36:LYS:HD2	13:M:59:TYR:CZ	2.32	0.65
1:A:1224:G:H2'	19:S:78:ARG:HH22	1.62	0.65
1:A:1402:C:H2'	1:A:1403:C:O4'	1.97	0.65
1:A:1475:G:H2'	1:A:1476:G:H8	1.62	0.65
3:C:172:ARG:HB3	3:C:172:ARG:HH11	1.61	0.65
10:J:96:ILE:HG22	10:J:97:GLU:N	2.10	0.65
11:K:18:ARG:HB2	11:K:33:THR:HG23	1.78	0.65
12:L:27:LEU:C	12:L:29:GLY:N	2.54	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:86:ARG:HH11	12:L:86:ARG:HG3	1.61	0.65
19:S:17:GLU:HA	19:S:20:LEU:HD11	1.78	0.65
1:A:287:U:O2'	1:A:288:A:H5'	1.97	0.65
1:A:1425:U:H2'	1:A:1426:C:C6	2.31	0.65
3:C:172:ARG:HB3	3:C:172:ARG:NH1	2.11	0.65
5:E:40:ARG:HG2	5:E:68:GLU:OE2	1.96	0.65
15:O:29:VAL:HG12	15:O:85:LEU:CD1	2.26	0.65
19:S:28:LYS:HG2	19:S:29:ARG:N	2.06	0.65
1:A:403:C:O2'	1:A:404:U:H5'	1.97	0.65
1:A:677:U:H3	1:A:713:G:H22	1.45	0.65
1:A:1522:U:O2'	1:A:1523:G:H5'	1.96	0.65
5:E:15:ARG:HD2	5:E:15:ARG:O	1.96	0.65
7:G:50:ILE:O	7:G:54:THR:HB	1.96	0.65
13:M:33:ALA:HA	13:M:59:TYR:CE2	2.32	0.65
14:N:22:THR:CB	14:N:33:VAL:HG21	2.27	0.65
4:D:187:ARG:NH2	4:D:188:LEU:HD12	2.10	0.65
5:E:65:ASN:CG	5:E:65:ASN:O	2.40	0.65
6:F:94:GLN:NE2	18:R:32:ARG:HD3	2.09	0.65
6:F:100:ASN:HD22	18:R:23:LYS:CG	2.10	0.65
13:M:81:LEU:O	13:M:89:GLY:HA3	1.97	0.65
1:A:392:G:H2'	1:A:393:A:C8	2.32	0.64
6:F:67:MET:HE2	6:F:72:VAL:HG22	1.77	0.64
20:T:87:LYS:O	20:T:91:LEU:HD12	1.96	0.64
1:A:168:G:O2'	1:A:169:C:H5'	1.97	0.64
1:A:738:C:OP2	6:F:92:LYS:HE3	1.97	0.64
20:T:50:GLU:HG2	20:T:100:ILE:HG13	1.79	0.64
1:A:281:G:O2'	1:A:282:A:OP2	2.12	0.64
3:C:188:LEU:O	3:C:189:ALA:HB2	1.96	0.64
9:I:118:LYS:O	9:I:119:ALA:CB	2.45	0.64
1:A:203:U:H5''	1:A:204:U:OP1	1.97	0.64
1:A:397:A:H5'	1:A:398:C:OP1	1.98	0.64
1:A:765:G:H1	1:A:812:C:H2'	1.62	0.64
5:E:115:VAL:CG1	5:E:118:ILE:HG13	2.25	0.64
10:J:90:LEU:H	10:J:91:PRO:HD2	1.61	0.64
11:K:18:ARG:HB2	11:K:33:THR:CG2	2.28	0.64
20:T:85:MET:HE3	20:T:103:GLY:O	1.96	0.64
1:A:393:A:O2'	1:A:394:G:H5'	1.98	0.64
1:A:1040:U:H2'	1:A:1041:A:C8	2.33	0.64
3:C:112:SER:HB2	3:C:115:LEU:HD12	1.79	0.64
6:F:21:LEU:O	6:F:24:GLU:HB3	1.97	0.64
9:I:49:PRO:O	9:I:52:ALA:HB3	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:18:ARG:HD3	16:P:35:LYS:HE3	1.79	0.64
16:P:45:THR:HB	16:P:46:PRO:HD2	1.80	0.64
19:S:64:GLU:O	19:S:67:VAL:HG23	1.97	0.64
1:A:818:G:H3'	1:A:819:A:C5'	2.28	0.64
1:A:918:A:H2'	1:A:919:A:C8	2.32	0.64
5:E:79:GLU:HG3	5:E:93:PRO:HD2	1.79	0.64
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.33	0.64
19:S:40:ILE:HB	19:S:67:VAL:O	1.98	0.64
3:C:177:THR:CG2	3:C:180:ALA:HB2	2.28	0.64
11:K:40:ILE:HG22	11:K:41:THR:HG23	1.80	0.64
1:A:1142:G:H2'	1:A:1143:G:O4'	1.97	0.64
5:E:151:LEU:HD11	8:H:77:GLU:OE2	1.98	0.64
11:K:48:ILE:HG22	11:K:49:GLY:H	1.61	0.64
12:L:55:VAL:HG12	12:L:56:ALA:N	2.12	0.64
21:V:6:ARG:CD	21:V:15:ARG:NH1	2.61	0.64
1:A:922:G:H2'	1:A:923:A:C8	2.33	0.64
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.06	0.64
5:E:120:THR:CG2	5:E:121:LYS:N	2.61	0.64
11:K:74:ALA:C	11:K:76:GLY:H	2.06	0.64
2:B:215:LEU:O	2:B:219:VAL:HG23	1.97	0.64
3:C:64:VAL:HB	3:C:99:VAL:CB	2.27	0.64
17:Q:101:ARG:HA	17:Q:101:ARG:HE	1.62	0.64
19:S:44:MET:O	19:S:47:HIS:HB2	1.97	0.64
1:A:1153:C:H2'	1:A:1154:G:H8	1.62	0.63
1:A:1497:G:H2'	1:A:1498:U:H5'	1.78	0.63
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.78	0.63
9:I:48:GLU:N	9:I:49:PRO:HD2	2.13	0.63
12:L:110:VAL:O	12:L:122:THR:HG21	1.97	0.63
1:A:1020:U:H2'	1:A:1021:G:H8	1.63	0.63
1:A:1346:A:H2'	7:G:10:ARG:HH22	1.64	0.63
2:B:74:LYS:NZ	2:B:206:ASP:HA	2.13	0.63
2:B:95:GLN:OE1	2:B:95:GLN:HA	1.96	0.63
3:C:120:VAL:O	3:C:124:ILE:HG13	1.99	0.63
1:A:620:C:N1	4:D:135:LEU:HD13	2.12	0.63
1:A:1442:G:N3	1:A:1442:G:H2'	2.12	0.63
3:C:29:TYR:OH	14:N:54:PRO:HG2	1.98	0.63
4:D:70:ILE:HD11	4:D:100:ARG:NE	2.13	0.63
4:D:152:SER:HB3	4:D:155:LEU:HD12	1.80	0.63
1:A:1141:C:H2'	1:A:1142:G:C8	2.32	0.63
2:B:68:ILE:HB	2:B:90:MET:HE3	1.79	0.63
2:B:82:ARG:O	2:B:86:GLU:HG3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:131:ARG:H	4:D:131:ARG:HD2	1.62	0.63
9:I:111:ARG:HD3	9:I:112:LYS:C	2.24	0.63
1:A:243:A:H4'	1:A:244:U:C5'	2.22	0.63
1:A:1131:G:H1	1:A:1143:G:N2	1.95	0.63
1:A:1316:G:H4'	14:N:18:VAL:CG1	2.29	0.63
2:B:130:ARG:NH2	3:C:207:VAL:HG22	2.14	0.63
3:C:155:GLY:O	3:C:196:LEU:HD22	1.98	0.63
1:A:1026:G:H2'	1:A:1027:C:H5'	1.80	0.63
1:A:1053:G:C3'	1:A:1054:C:H5'	2.29	0.63
2:B:74:LYS:HZ1	2:B:206:ASP:HA	1.62	0.63
3:C:64:VAL:CB	3:C:99:VAL:HB	2.27	0.63
5:E:102:ALA:CB	5:E:120:THR:HG21	2.29	0.63
7:G:42:ILE:HG22	7:G:120:ILE:HD12	1.80	0.63
7:G:114:ARG:HG2	7:G:114:ARG:HH11	1.64	0.63
2:B:20:GLU:HG2	2:B:189:ASP:OD2	1.99	0.63
2:B:132:LYS:HG2	2:B:135:GLN:OE1	1.99	0.63
7:G:71:PRO:HD3	7:G:103:TRP:CZ3	2.33	0.63
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.37	0.63
19:S:39:THR:HA	19:S:70:LYS:HG2	1.81	0.63
1:A:405:U:H3'	1:A:406:G:H5'	1.80	0.63
3:C:3:ASN:C	3:C:4:LYS:HG2	2.23	0.63
3:C:50:ALA:O	3:C:70:VAL:HG12	1.99	0.63
5:E:150:ARG:HG3	5:E:150:ARG:NH1	2.14	0.63
16:P:8:ARG:HB2	16:P:28:ARG:NH1	2.14	0.63
1:A:448:A:H2'	1:A:449:C:H6	1.64	0.63
1:A:538:G:OP2	12:L:115:LYS:HG3	1.99	0.63
1:A:1132:C:H2'	1:A:1133:G:H8	1.64	0.63
1:A:1343:G:H1'	9:I:121:ARG:HH12	1.64	0.63
1:A:1347:G:O2'	1:A:1348:U:P	2.57	0.63
1:A:1347:G:C4	9:I:107:ARG:NH1	2.67	0.63
1:A:1487:G:O2'	1:A:1488:G:H5'	1.99	0.63
3:C:91:LEU:CD2	3:C:99:VAL:HG13	2.27	0.63
5:E:116:THR:HG23	5:E:117:ASP:OD2	1.98	0.63
13:M:82:MET:HE2	13:M:92:HIS:HB3	1.80	0.63
1:A:556:C:O2'	1:A:557:G:H5'	1.99	0.62
1:A:1238:A:H5'	1:A:1336:C:H41	1.64	0.62
2:B:73:THR:HB	2:B:170:GLU:OE2	1.99	0.62
15:O:17:ARG:CZ	15:O:77:ARG:HH11	2.11	0.62
1:A:1132:C:H2'	1:A:1133:G:C8	2.35	0.62
1:A:1189:C:OP1	10:J:51:ARG:NH2	2.29	0.62
1:A:1229:A:OP2	13:M:114:ARG:HD3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:184:VAL:N	2:B:198:ASP:OD2	2.32	0.62
12:L:43:VAL:HG12	12:L:44:THR:N	2.14	0.62
13:M:84:ILE:O	13:M:86:CYS:N	2.33	0.62
1:A:475:G:H2'	1:A:476:G:H8	1.63	0.62
1:A:1260:C:O5'	1:A:1284:C:H4'	1.99	0.62
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.80	0.62
1:A:976:G:OP1	14:N:32:SER:HA	1.98	0.62
1:A:1148:U:H4'	9:I:14:VAL:HG11	1.81	0.62
1:A:1225:A:H2'	1:A:1225:A:N3	2.14	0.62
3:C:60:ALA:O	3:C:61:ALA:HB2	2.00	0.62
3:C:177:THR:HG23	3:C:180:ALA:HB2	1.81	0.62
1:A:501:C:H2'	1:A:502:G:C8	2.34	0.62
1:A:113:G:H1'	1:A:354:G:H5'	1.80	0.62
1:A:1307:U:H5'	13:M:109:THR:HG21	1.81	0.62
1:A:1347:G:HO2'	1:A:1348:U:P	2.23	0.62
2:B:69:LEU:HD12	2:B:155:LEU:HD11	1.81	0.62
2:B:142:LEU:HD22	2:B:146:GLN:NE2	2.14	0.62
2:B:186:ALA:HB3	2:B:197:VAL:HG11	1.82	0.62
7:G:23:VAL:O	7:G:27:ILE:HG13	2.00	0.62
10:J:62:HIS:HB3	14:N:59:ALA:HB3	1.81	0.62
13:M:84:ILE:C	13:M:86:CYS:H	2.08	0.62
17:Q:69:LYS:C	17:Q:70:ARG:HD2	2.24	0.62
1:A:542:G:OP1	4:D:10:ARG:NH2	2.33	0.62
1:A:1392:G:O2'	1:A:1502:A:H5''	1.99	0.62
2:B:115:LEU:HG	2:B:153:ARG:NH2	2.14	0.62
1:A:216:G:H2'	1:A:217:C:C6	2.35	0.62
1:A:434:U:H2'	1:A:435:C:H6	1.64	0.62
2:B:23:ARG:NH1	2:B:23:ARG:C	2.58	0.62
4:D:30:LYS:C	4:D:32:ALA:N	2.58	0.62
4:D:148:VAL:CG1	4:D:158:ILE:HD13	2.30	0.62
5:E:120:THR:HG23	5:E:121:LYS:N	2.15	0.62
14:N:14:PRO:C	14:N:16:PHE:N	2.56	0.62
19:S:52:TYR:HA	19:S:56:GLN:O	1.99	0.62
20:T:43:LEU:HD12	20:T:55:ILE:HD12	1.81	0.62
20:T:56:MET:HE3	20:T:88:VAL:HG11	1.81	0.62
1:A:476:G:O2'	1:A:477:G:H5'	2.00	0.62
1:A:706:A:H1'	11:K:29:ILE:HD11	1.81	0.62
1:A:1176:A:H2'	1:A:1177:G:C8	2.35	0.62
1:A:1425:U:H2'	1:A:1426:C:H6	1.65	0.62
2:B:130:ARG:NH2	3:C:179:ARG:HH12	1.97	0.62
3:C:129:ALA:HB3	3:C:132:ARG:HD2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:19:LEU:O	9:I:20:ARG:HG3	1.99	0.62
1:A:959:A:H3'	1:A:960:U:H5''	1.82	0.62
5:E:80:ILE:CD1	5:E:91:LEU:HB2	2.30	0.62
7:G:139:GLU:O	7:G:143:ARG:HG3	2.00	0.62
7:G:155:ARG:O	7:G:156:TRP:HB3	1.99	0.62
1:A:1440:C:H2'	1:A:1441:G:H5'	1.82	0.61
4:D:61:LYS:NZ	4:D:62:GLN:HE21	1.98	0.61
20:T:50:GLU:HG3	20:T:99:LEU:HD12	1.82	0.61
1:A:193:C:H2'	1:A:194:C:C6	2.35	0.61
1:A:539:A:OP1	12:L:114:LYS:HE2	2.00	0.61
1:A:1370:G:O2'	1:A:1371:G:H5'	2.00	0.61
3:C:191:THR:HG22	3:C:192:THR:N	2.15	0.61
4:D:25:ARG:O	4:D:27:TYR:N	2.33	0.61
10:J:30:SER:OG	10:J:81:THR:HA	1.99	0.61
14:N:53:LEU:HB3	14:N:56:VAL:HG21	1.81	0.61
1:A:190(L):U:H3	20:T:105:SER:CB	2.12	0.61
2:B:12:GLU:C	2:B:14:GLY:H	2.07	0.61
2:B:80:ILE:HD11	2:B:208:ILE:HG23	1.81	0.61
5:E:115:VAL:HG11	5:E:118:ILE:CG1	2.28	0.61
7:G:78:ARG:HB2	7:G:156:TRP:CZ3	2.36	0.61
17:Q:21:VAL:HG21	17:Q:59:ILE:HD11	1.82	0.61
1:A:187:C:O2	20:T:105:SER:HB3	2.00	0.61
1:A:954:G:H21	1:A:1227:A:H62	1.49	0.61
1:A:1147:C:H4'	9:I:5:TYR:HE1	1.64	0.61
2:B:34:ALA:O	2:B:41:ILE:N	2.31	0.61
4:D:61:LYS:NZ	4:D:62:GLN:NE2	2.48	0.61
11:K:84:VAL:CG1	11:K:95:ILE:HD11	2.31	0.61
12:L:33:ARG:CD	12:L:62:SER:HB3	2.29	0.61
19:S:31:ILE:CG2	19:S:32:LYS:H	2.10	0.61
1:A:1178:G:P	9:I:97:LYS:HZ2	2.24	0.61
1:A:1182:G:H4'	1:A:1183:A:O5'	1.99	0.61
4:D:23:GLY:HA3	4:D:112:VAL:CG1	2.30	0.61
4:D:191:ARG:O	4:D:191:ARG:HD2	2.00	0.61
1:A:664:G:OP1	18:R:64:ARG:HD2	2.00	0.61
1:A:1329:A:P	13:M:28:ALA:HB3	2.41	0.61
7:G:38:LEU:HD12	7:G:38:LEU:O	2.01	0.61
9:I:44:VAL:HG12	9:I:51:ARG:HH12	1.66	0.61
1:A:386:C:O2'	1:A:387:U:H5'	2.00	0.61
2:B:115:LEU:O	2:B:119:GLU:HG3	2.00	0.61
16:P:4:ILE:HG13	16:P:64:ALA:HB1	1.83	0.61
1:A:1091:U:O2	1:A:1093:A:C8	2.54	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1484:C:H2'	1:A:1485:U:H6	1.65	0.61
2:B:88:ALA:C	2:B:90:MET:H	2.09	0.61
4:D:148:VAL:HG11	4:D:158:ILE:HG21	1.81	0.61
7:G:78:ARG:HB2	7:G:156:TRP:HZ3	1.65	0.61
17:Q:101:ARG:HA	17:Q:101:ARG:NE	2.16	0.61
1:A:551:U:H2'	1:A:552:U:H6	1.64	0.61
1:A:1053:G:C4'	1:A:1054:C:H5'	2.31	0.61
2:B:98:LEU:O	2:B:101:MET:HG3	2.01	0.61
3:C:191:THR:CG2	3:C:192:THR:N	2.64	0.61
9:I:4:TYR:CZ	9:I:88:TYR:HD1	2.17	0.61
20:T:54:LYS:HE3	20:T:100:ILE:HD11	1.82	0.61
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.36	0.61
1:A:1226:C:N4	13:M:104:ARG:HD2	2.16	0.61
1:A:1316:G:H4'	14:N:18:VAL:HG11	1.83	0.61
1:A:1475:G:H2'	1:A:1476:G:C8	2.36	0.61
3:C:13:GLY:HA3	14:N:57:ARG:NH2	2.14	0.61
4:D:162:LEU:CD1	4:D:181:MET:HE2	2.31	0.61
13:M:54:VAL:O	13:M:58:GLU:HG2	2.01	0.61
1:A:107:G:H2'	1:A:108:G:H5'	1.83	0.60
2:B:143:GLU:O	2:B:147:LYS:HG3	2.00	0.60
5:E:80:ILE:HD11	5:E:91:LEU:HB2	1.83	0.60
11:K:48:ILE:HG22	11:K:49:GLY:N	2.16	0.60
17:Q:76:LEU:HD23	17:Q:77:VAL:N	2.15	0.60
1:A:1147:C:H4'	9:I:5:TYR:CE1	2.36	0.60
4:D:157:LEU:HD22	4:D:161:ASN:ND2	2.16	0.60
13:M:40:ASN:ND2	13:M:41:PRO:HD2	2.16	0.60
15:O:29:VAL:HG12	15:O:85:LEU:HD11	1.82	0.60
1:A:812:C:O2'	1:A:813:U:OP2	2.17	0.60
2:B:33:TYR:O	2:B:34:ALA:HB2	2.02	0.60
3:C:47:LEU:HD23	3:C:68:VAL:HG11	1.83	0.60
10:J:46:ARG:HH11	10:J:64:GLU:HB3	1.65	0.60
10:J:71:LEU:O	10:J:72:VAL:HB	2.00	0.60
18:R:52:PRO:O	18:R:56:THR:HG23	2.00	0.60
1:A:112:G:N2	1:A:354:G:H5'	2.16	0.60
1:A:390:C:H2'	1:A:391:G:H8	1.66	0.60
1:A:425:G:O2'	1:A:426:G:H5'	2.02	0.60
7:G:72:ARG:HG2	7:G:142:GLU:OE1	2.02	0.60
19:S:13:ASP:HA	19:S:16:LEU:HB3	1.83	0.60
1:A:686:U:O2'	1:A:687:A:H8	1.84	0.60
3:C:20:SER:HB3	3:C:22:TRP:HE1	1.67	0.60
8:H:64:LYS:HG2	8:H:79:VAL:HG21	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:96:GLY:O	20:T:97:ALA:HB3	2.00	0.60
1:A:112:G:H21	1:A:354:G:H5'	1.65	0.60
1:A:390:C:O3'	16:P:28:ARG:NH2	2.34	0.60
1:A:1305:G:H5'	21:V:4:GLY:HA3	1.84	0.60
3:C:6:HIS:HD2	3:C:8:ILE:HB	1.66	0.60
5:E:76:ILE:HD13	5:E:142:LEU:HD11	1.84	0.60
7:G:42:ILE:HG23	7:G:117:ALA:HA	1.84	0.60
12:L:40:VAL:O	12:L:40:VAL:HG12	1.99	0.60
16:P:52:ASP:OD2	16:P:55:ARG:HG3	2.00	0.60
16:P:67:THR:HG22	16:P:68:ASP:N	2.15	0.60
2:B:122:PHE:HE2	2:B:139:LYS:HG2	1.65	0.60
3:C:26:LYS:HD3	3:C:26:LYS:N	2.17	0.60
10:J:30:SER:HB3	10:J:84:GLN:HE21	1.67	0.60
12:L:46:LYS:HG2	12:L:47:LYS:N	2.16	0.60
16:P:81:ARG:HG3	16:P:83:GLU:HG2	1.84	0.60
2:B:114:ARG:NH1	2:B:118:LEU:HD21	2.15	0.60
2:B:178:ARG:O	8:H:71:GLY:HA2	2.02	0.60
3:C:33:LEU:HD11	14:N:53:LEU:CD2	2.32	0.60
5:E:24:ARG:HG2	5:E:24:ARG:HH11	1.66	0.60
11:K:19:ALA:HB2	11:K:80:VAL:HG11	1.82	0.60
17:Q:104:LYS:O	17:Q:105:ALA:HB2	2.01	0.60
1:A:435:C:H2'	1:A:436:C:H6	1.67	0.60
2:B:140:HIS:O	2:B:143:GLU:HB2	2.01	0.60
3:C:47:LEU:H	3:C:47:LEU:CD1	2.15	0.60
11:K:69:ALA:O	11:K:73:MET:HG2	2.02	0.60
1:A:953:G:H1'	13:M:125:ARG:CB	2.31	0.60
1:A:1352:C:H2'	1:A:1353:G:C8	2.37	0.60
1:A:1381:U:O2'	1:A:1382:C:H5'	2.02	0.60
3:C:6:HIS:NE2	3:C:8:ILE:HD12	2.17	0.60
4:D:162:LEU:HD13	4:D:181:MET:HE2	1.82	0.60
6:F:10:LEU:CD1	6:F:59:TYR:HB3	2.29	0.60
12:L:28:LYS:HD2	12:L:33:ARG:HH12	1.65	0.60
13:M:10:PRO:O	13:M:45:VAL:HG11	2.01	0.60
1:A:449:C:O2	16:P:42:ARG:HD2	2.02	0.59
1:A:1306:A:N6	1:A:1331:G:H1'	2.17	0.59
1:A:1470:G:O2'	1:A:1471:G:H5'	2.02	0.59
3:C:79:ARG:HE	3:C:82:GLU:HG2	1.66	0.59
8:H:91:ARG:HG3	12:L:7:ILE:HG13	1.84	0.59
11:K:84:VAL:HG21	18:R:88:LYS:HD3	1.83	0.59
11:K:110:ASP:HB2	18:R:88:LYS:CD	2.20	0.59
14:N:11:LYS:O	14:N:13:THR:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:G:H2'	1:A:506:G:C8	2.37	0.59
1:A:1231:G:H5''	9:I:126:SER:CB	2.32	0.59
1:A:1376:U:H2'	1:A:1377:A:C8	2.36	0.59
9:I:93:ARG:NH1	9:I:97:LYS:NZ	2.51	0.59
14:N:24:CYS:HB3	14:N:28:GLY:H	1.66	0.59
15:O:11:VAL:HG21	15:O:34:LEU:HD12	1.83	0.59
1:A:996:A:H2'	1:A:997:U:C6	2.37	0.59
3:C:46:GLU:O	3:C:48:TYR:N	2.33	0.59
9:I:5:TYR:CD2	9:I:6:GLY:N	2.70	0.59
1:A:457:C:H2'	1:A:458:C:H6	1.67	0.59
1:A:1086:U:H3	1:A:1099:G:N2	1.91	0.59
1:A:1247:U:O2'	1:A:1248:A:H5'	2.02	0.59
20:T:57:ARG:HH21	20:T:100:ILE:CG2	2.16	0.59
1:A:839:U:O2	1:A:839:U:H2'	2.01	0.59
1:A:1130:A:H3'	1:A:1130:A:OP2	2.02	0.59
2:B:101:MET:CA	2:B:108:ILE:HD12	2.33	0.59
4:D:33:MET:O	4:D:37:PRO:HG3	2.02	0.59
5:E:118:ILE:CG2	5:E:119:LEU:N	2.65	0.59
13:M:94:ARG:HH22	19:S:81:ARG:NH1	2.00	0.59
1:A:109:A:H2'	1:A:326:G:N2	2.17	0.59
1:A:502:G:H4'	1:A:550:G:H4'	1.83	0.59
1:A:972:C:OP1	10:J:57:LYS:NZ	2.28	0.59
4:D:151:LYS:H	4:D:151:LYS:CD	2.16	0.59
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.66	0.59
12:L:28:LYS:HD2	12:L:33:ARG:NH2	2.17	0.59
13:M:125:ARG:HD2	13:M:125:ARG:C	2.27	0.59
1:A:513:C:O2'	1:A:514:C:H5'	2.03	0.59
1:A:736:C:H2'	1:A:737:A:C8	2.38	0.59
7:G:95:ARG:HG3	7:G:95:ARG:NH1	2.17	0.59
8:H:83:ILE:HG23	8:H:83:ILE:O	2.03	0.59
1:A:457:C:H2'	1:A:458:C:C6	2.38	0.59
1:A:560:U:H4'	1:A:561:U:H5''	1.83	0.59
2:B:120:ALA:O	2:B:124:SER:HB3	2.02	0.59
2:B:130:ARG:HD2	2:B:131:PRO:HD2	1.85	0.59
10:J:3:LYS:N	10:J:77:PRO:HD3	2.18	0.59
10:J:46:ARG:NH1	10:J:64:GLU:HG2	2.18	0.59
12:L:55:VAL:CG1	12:L:67:THR:HG23	2.33	0.59
1:A:390:C:H2'	1:A:391:G:C8	2.38	0.59
1:A:1251:A:H4'	9:I:12:GLU:OE2	2.02	0.59
7:G:122:HIS:HA	7:G:125:MET:HE3	1.85	0.59
16:P:51:VAL:O	16:P:51:VAL:HG12	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:G:P	12:L:115:LYS:HG3	2.43	0.58
1:A:812:C:HO2'	1:A:813:U:P	2.26	0.58
1:A:1347:G:O2'	1:A:1348:U:OP2	2.16	0.58
1:A:1490:C:H6	1:A:1490:C:C5'	2.13	0.58
3:C:14:ILE:O	3:C:16:ARG:N	2.35	0.58
7:G:51:GLN:OE1	7:G:51:GLN:HA	2.02	0.58
13:M:81:LEU:HD23	13:M:81:LEU:N	2.17	0.58
1:A:1441:G:H4'	1:A:1442:G:N7	2.18	0.58
1:A:1521:G:H2'	1:A:1522:U:C6	2.38	0.58
2:B:144:ARG:HG3	2:B:145:LEU:N	2.19	0.58
4:D:23:GLY:HA3	4:D:112:VAL:HG12	1.84	0.58
4:D:157:LEU:HD22	4:D:161:ASN:HD21	1.66	0.58
10:J:45:ARG:O	10:J:64:GLU:HA	2.03	0.58
10:J:60:ARG:HD2	10:J:60:ARG:N	2.17	0.58
14:N:8:GLU:O	14:N:11:LYS:HB2	2.02	0.58
1:A:255:G:H1'	17:Q:16:GLN:HE22	1.69	0.58
1:A:1072:G:H2'	1:A:1073:U:C6	2.38	0.58
6:F:3:ARG:HH21	6:F:64:GLN:NE2	2.01	0.58
10:J:82:ILE:O	10:J:82:ILE:HG22	2.03	0.58
12:L:24:VAL:O	12:L:24:VAL:HG12	2.03	0.58
18:R:86:VAL:O	18:R:87:ARG:HB2	2.03	0.58
1:A:39:G:O2'	1:A:40:C:H5'	2.03	0.58
1:A:60:A:H4'	1:A:61:G:O5'	2.03	0.58
1:A:991:U:O2'	1:A:992:U:H5'	2.02	0.58
1:A:1152:A:H5'	10:J:70:ARG:HH22	1.68	0.58
1:A:1316:G:N2	1:A:1318:A:H3'	2.18	0.58
2:B:10:LEU:HD23	2:B:48:MET:HG3	1.86	0.58
3:C:64:VAL:HB	3:C:99:VAL:CG2	2.33	0.58
9:I:11:LYS:O	9:I:11:LYS:HG2	2.03	0.58
9:I:79:LEU:HD23	9:I:101:PHE:O	2.02	0.58
14:N:9:LYS:HD3	14:N:9:LYS:C	2.28	0.58
1:A:976:G:OP2	1:A:1358:U:H1'	2.03	0.58
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.39	0.58
1:A:1182:G:O2'	1:A:1183:A:OP2	2.20	0.58
2:B:10:LEU:C	2:B:12:GLU:H	2.12	0.58
2:B:12:GLU:C	2:B:14:GLY:N	2.59	0.58
2:B:76:GLN:HG3	2:B:206:ASP:OD1	2.03	0.58
2:B:133:LYS:O	2:B:137:ARG:HG3	2.03	0.58
2:B:134:GLU:C	2:B:136:VAL:H	2.12	0.58
2:B:156:LYS:O	2:B:156:LYS:HD3	2.03	0.58
3:C:10:PHE:CZ	3:C:178:LEU:HD13	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:17:THR:HG22	8:H:63:LEU:HG	1.86	0.58
9:I:46:ALA:HB1	9:I:77:ILE:HG22	1.86	0.58
10:J:51:ARG:HB2	10:J:59:SER:CB	2.23	0.58
20:T:53:LEU:O	20:T:57:ARG:HD2	2.04	0.58
1:A:812:C:O2'	1:A:813:U:P	2.62	0.58
1:A:1054:C:OP1	1:A:1197:G:OP1	2.21	0.58
10:J:86:MET:HA	10:J:86:MET:HE3	1.85	0.58
15:O:17:ARG:NH1	15:O:77:ARG:HH11	2.01	0.58
15:O:87:ILE:O	15:O:88:ARG:HB2	2.04	0.58
1:A:411:A:N9	1:A:413:G:H1'	2.19	0.58
1:A:518:C:H5''	1:A:519:C:C6	2.38	0.58
1:A:761:G:C1'	17:Q:103:GLY:O	2.51	0.58
3:C:33:LEU:HD23	3:C:33:LEU:C	2.29	0.58
9:I:5:TYR:O	9:I:84:ALA:HA	2.03	0.58
13:M:94:ARG:NH2	19:S:81:ARG:HD3	2.19	0.58
1:A:376:G:P	16:P:67:THR:HG21	2.44	0.58
1:A:1117:G:H5'	1:A:1117:G:H8	1.66	0.58
3:C:10:PHE:CE2	3:C:178:LEU:HD13	2.38	0.58
12:L:92:ASP:O	12:L:94:PRO:HD3	2.04	0.58
13:M:40:ASN:ND2	13:M:41:PRO:CD	2.62	0.58
13:M:120:LYS:HE2	13:M:123:ALA:HB2	1.86	0.58
14:N:12:ARG:O	14:N:14:PRO:N	2.36	0.58
14:N:44:LEU:C	14:N:44:LEU:HD12	2.29	0.58
1:A:723:U:O2	1:A:723:U:H2'	2.04	0.58
1:A:818:G:C2'	1:A:819:A:H5''	2.34	0.58
2:B:115:LEU:HG	2:B:153:ARG:HH21	1.69	0.58
3:C:191:THR:HG21	3:C:193:TYR:CZ	2.39	0.58
4:D:32:ALA:C	4:D:34:GLU:N	2.60	0.58
9:I:23:ASN:HD22	9:I:23:ASN:C	2.12	0.58
10:J:15:THR:HG23	10:J:94:VAL:HG22	1.85	0.58
10:J:24:VAL:HG12	10:J:28:ARG:HE	1.68	0.58
1:A:765:G:H22	1:A:812:C:HO2'	1.51	0.58
5:E:122:GLU:O	5:E:123:LEU:HD23	2.03	0.58
11:K:109:VAL:HG13	18:R:85:LEU:O	2.04	0.58
12:L:85:ILE:HG23	12:L:98:TYR:HB3	1.86	0.58
1:A:1228:C:OP1	13:M:115:LYS:HG3	2.03	0.57
1:A:1498:U:H4'	1:A:1519:A:H2	1.69	0.57
2:B:16:HIS:NE2	2:B:214:ILE:CG1	2.66	0.57
9:I:7:THR:HG21	9:I:9:ARG:NH1	2.19	0.57
13:M:84:ILE:CG2	19:S:65:ASN:HD22	2.17	0.57
19:S:40:ILE:HG21	19:S:62:ILE:CD1	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:U:H4'	16:P:17:TYR:CE2	2.39	0.57
1:A:657:G:H4'	15:O:28:GLN:HG2	1.87	0.57
6:F:97:PHE:HB2	18:R:32:ARG:CZ	2.34	0.57
7:G:15:ASP:OD1	7:G:17:VAL:N	2.37	0.57
11:K:40:ILE:HG23	11:K:75:TYR:CD2	2.39	0.57
12:L:26:ALA:O	12:L:27:LEU:O	2.22	0.57
13:M:13:LYS:O	13:M:45:VAL:HG23	2.04	0.57
1:A:1095:U:H2'	1:A:1096:C:C6	2.39	0.57
9:I:17:VAL:HG21	9:I:80:GLY:HA3	1.86	0.57
16:P:17:TYR:HE1	16:P:41:PRO:HG2	1.69	0.57
20:T:10:LEU:HD12	20:T:12:ALA:HB3	1.85	0.57
1:A:346:G:C2'	1:A:347:G:H5'	2.34	0.57
13:M:31:LYS:O	13:M:35:GLU:HB2	2.05	0.57
14:N:24:CYS:HB3	14:N:28:GLY:N	2.20	0.57
1:A:757:U:H2'	1:A:758:G:O4'	2.03	0.57
1:A:860:A:H2'	1:A:861:G:O4'	2.03	0.57
1:A:1014:A:H2'	1:A:1015:A:C8	2.39	0.57
1:A:1015:A:H2'	1:A:1016:A:C8	2.40	0.57
1:A:1298:C:C4	7:G:114:ARG:HD3	2.40	0.57
3:C:121:ALA:O	3:C:125:GLU:HG3	2.04	0.57
4:D:7:PRO:HG2	4:D:10:ARG:HD2	1.87	0.57
8:H:29:SER:OG	8:H:32:LYS:HB2	2.04	0.57
8:H:91:ARG:HG2	12:L:7:ILE:HG21	1.87	0.57
9:I:9:ARG:HA	9:I:13:ALA:O	2.05	0.57
14:N:3:ARG:NH1	14:N:6:LEU:HD11	2.19	0.57
14:N:29:ARG:HG2	14:N:29:ARG:HH11	1.69	0.57
1:A:1241:G:H2'	1:A:1242:C:C6	2.39	0.57
1:A:1347:G:N2	1:A:1373:G:H2'	2.19	0.57
1:A:1504:G:H3'	1:A:1504:G:OP2	2.04	0.57
8:H:19:VAL:HG23	8:H:21:LYS:HD3	1.86	0.57
19:S:7:LYS:HG3	19:S:7:LYS:O	2.03	0.57
19:S:25:LYS:H	19:S:25:LYS:HD2	1.68	0.57
1:A:835:U:OP1	18:R:64:ARG:NH2	2.34	0.57
1:A:1414:U:O2'	1:A:1415:G:H5'	2.04	0.57
10:J:81:THR:C	10:J:83:GLU:H	2.10	0.57
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.05	0.57
18:R:47:THR:HG22	18:R:48:GLY:N	2.18	0.57
20:T:39:LYS:HD2	20:T:55:ILE:CD1	2.27	0.57
1:A:192:U:O2'	1:A:193:C:H5'	2.05	0.57
1:A:1044:A:C2'	1:A:1045:C:H5'	2.34	0.57
1:A:1305:G:N2	1:A:1331:G:O2'	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:15:VAL:HG11	2:B:209:ARG:C	2.30	0.57
2:B:223:ILE:HG21	2:B:230:VAL:CG2	2.35	0.57
4:D:35:ARG:O	4:D:36:ARG:HB2	2.04	0.57
8:H:103:VAL:HG21	8:H:110:ALA:HB2	1.87	0.57
12:L:82:VAL:N	12:L:106:ASP:OD1	2.34	0.57
13:M:49:THR:HB	13:M:52:GLU:HG3	1.86	0.57
1:A:1004:A:H5''	1:A:1025:U:C5	2.40	0.57
1:A:1152:A:H5'	10:J:70:ARG:NH2	2.19	0.57
1:A:1278:U:H5''	1:A:1279:A:O4'	2.04	0.57
3:C:91:LEU:HD11	3:C:99:VAL:HG13	1.87	0.57
5:E:80:ILE:HD12	5:E:80:ILE:O	2.05	0.57
12:L:47:LYS:CB	12:L:48:PRO:HD3	2.35	0.57
1:A:780:A:O2'	1:A:781:A:H5''	2.05	0.57
1:A:1040:U:H2'	1:A:1041:A:H8	1.70	0.57
2:B:209:ARG:HE	2:B:239:VAL:HG11	1.68	0.57
6:F:80:ARG:NH1	6:F:88:VAL:HB	2.19	0.57
14:N:3:ARG:O	14:N:4:LYS:C	2.48	0.57
17:Q:5:VAL:HG22	17:Q:60:ILE:HG12	1.87	0.57
19:S:5:LEU:O	19:S:6:LYS:CB	2.51	0.57
1:A:946:A:H2'	1:A:947:G:C8	2.40	0.56
1:A:1230:C:H1'	13:M:126:LYS:HA	1.86	0.56
1:A:1317:C:H2'	1:A:1318:A:O4'	2.04	0.56
1:A:1372:U:OP1	9:I:71:SER:HB3	2.04	0.56
3:C:29:TYR:CZ	14:N:54:PRO:HG2	2.40	0.56
3:C:84:ILE:O	3:C:88:ARG:HB2	2.05	0.56
8:H:123:GLU:O	8:H:127:LEU:HD23	2.05	0.56
13:M:13:LYS:HD3	13:M:17:VAL:HG11	1.86	0.56
1:A:129(A):G:O2'	1:A:190(E):U:H2'	2.05	0.56
1:A:1223:C:OP1	1:A:1224:G:H3'	2.04	0.56
15:O:3:ILE:HG22	15:O:7:GLU:HB3	1.86	0.56
15:O:41:GLU:OE2	15:O:41:GLU:HA	2.05	0.56
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.39	0.56
18:R:25:THR:O	18:R:26:LEU:HB2	2.04	0.56
19:S:28:LYS:CG	19:S:29:ARG:H	2.08	0.56
1:A:448:A:H2'	1:A:449:C:C6	2.40	0.56
1:A:915:A:C2'	1:A:916:G:H5'	2.35	0.56
1:A:1195:C:H3'	1:A:1196:U:C5'	2.35	0.56
1:A:1499:A:H1'	1:A:1520:G:H5'	1.87	0.56
2:B:98:LEU:HG	2:B:101:MET:HE3	1.87	0.56
2:B:126:GLU:HG2	2:B:129:GLU:OE1	2.05	0.56
3:C:83:ARG:C	3:C:85:ARG:N	2.63	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:12:LEU:HD22	5:E:12:LEU:C	2.30	0.56
9:I:39:GLY:O	9:I:40:LEU:HD23	2.05	0.56
10:J:4:ILE:HA	10:J:100:THR:HA	1.88	0.56
13:M:8:GLU:OE1	13:M:22:ILE:HG12	2.05	0.56
13:M:17:VAL:O	13:M:20:THR:HB	2.06	0.56
14:N:36:PHE:O	14:N:36:PHE:CD1	2.58	0.56
20:T:67:ALA:HA	20:T:73:HIS:H	1.70	0.56
1:A:1443:G:H5''	1:A:1446:A:C5'	2.19	0.56
2:B:47:THR:HA	2:B:202:PRO:HG2	1.87	0.56
3:C:188:LEU:HD13	3:C:195:VAL:HG13	1.86	0.56
6:F:2:ARG:CD	6:F:69:GLU:HG2	2.35	0.56
7:G:146:GLU:HA	7:G:149:ARG:HB2	1.87	0.56
8:H:60:ARG:HH11	8:H:60:ARG:HG3	1.70	0.56
9:I:93:ARG:NH1	9:I:97:LYS:HZ1	2.03	0.56
10:J:12:ASP:HB3	10:J:15:THR:HB	1.88	0.56
19:S:63:THR:HG22	19:S:64:GLU:H	1.71	0.56
1:A:818:G:H3'	1:A:819:A:H5''	1.87	0.56
1:A:1256:A:H61	1:A:1278:U:H1'	1.70	0.56
1:A:1257:U:H4'	1:A:1258:G:O5'	2.06	0.56
2:B:74:LYS:HZ1	2:B:206:ASP:CA	2.17	0.56
3:C:7:PRO:CG	3:C:184:TYR:HB2	2.35	0.56
13:M:15:VAL:HG23	13:M:43:THR:O	2.04	0.56
17:Q:26:GLN:HE21	17:Q:37:LYS:HE2	1.71	0.56
17:Q:59:ILE:CG2	17:Q:71:PHE:HB3	2.36	0.56
18:R:46:GLU:H	18:R:46:GLU:CD	2.14	0.56
1:A:477:G:H2'	1:A:478:A:C8	2.40	0.56
1:A:1028:C:H2'	1:A:1029:C:C6	2.40	0.56
1:A:1339:A:H2'	1:A:1340:A:O4'	2.06	0.56
1:A:1346:A:H4'	1:A:1347:G:O5'	2.06	0.56
3:C:32:LEU:HD23	3:C:32:LEU:O	2.05	0.56
3:C:33:LEU:HD23	3:C:33:LEU:O	2.04	0.56
4:D:6:GLY:O	4:D:8:VAL:HG23	2.06	0.56
4:D:176:LEU:HA	4:D:183:GLY:HA2	1.87	0.56
11:K:126:ARG:O	11:K:127:LYS:C	2.48	0.56
20:T:86:ARG:O	20:T:90:GLN:HG3	2.05	0.56
1:A:1053:G:H4'	1:A:1054:C:H5'	1.88	0.56
4:D:199:ASN:HD21	4:D:201:GLN:HB2	1.71	0.56
8:H:105:ARG:HG3	8:H:105:ARG:HH11	1.71	0.56
10:J:81:THR:O	10:J:85:LEU:HG	2.06	0.56
17:Q:67:LYS:O	17:Q:68:ARG:HB3	2.05	0.56
19:S:10:PHE:CD2	19:S:11:VAL:N	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:A:C4	1:A:413:G:H1'	2.41	0.56
1:A:438:G:C4'	1:A:439:A:OP1	2.53	0.56
1:A:1257:U:O2'	1:A:1258:G:OP2	2.21	0.56
13:M:117:VAL:HG12	13:M:118:ALA:H	1.70	0.56
18:R:53:ARG:HD3	18:R:63:GLN:CB	2.36	0.56
19:S:10:PHE:CD2	19:S:10:PHE:C	2.83	0.56
1:A:187:C:H1'	20:T:85:MET:HE2	1.88	0.56
1:A:1216:G:H5''	14:N:5:ALA:HB1	1.88	0.56
3:C:3:ASN:ND2	3:C:4:LYS:HE2	2.21	0.56
4:D:24:GLU:HG2	4:D:25:ARG:N	2.21	0.56
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.88	0.56
5:E:118:ILE:HG22	5:E:119:LEU:H	1.67	0.56
19:S:40:ILE:HG21	19:S:62:ILE:HD11	1.88	0.56
1:A:1044:A:H2'	1:A:1045:C:C5'	2.36	0.56
10:J:22:LYS:CE	10:J:90:LEU:HD12	2.33	0.56
13:M:40:ASN:ND2	13:M:42:ALA:H	2.04	0.56
17:Q:103:GLY:O	17:Q:104:LYS:O	2.24	0.56
1:A:166:G:O2'	1:A:167:G:H5'	2.06	0.55
1:A:1326:C:OP1	21:V:12:LYS:NZ	2.37	0.55
2:B:21:ARG:HG3	2:B:23:ARG:HD2	1.88	0.55
4:D:148:VAL:HG11	4:D:158:ILE:HD13	1.88	0.55
16:P:26:ARG:HD2	16:P:31:LYS:O	2.06	0.55
1:A:1042:G:O2'	1:A:1043:C:H5'	2.05	0.55
4:D:24:GLU:H	4:D:112:VAL:CG1	2.19	0.55
7:G:116:ALA:HA	7:G:119:ARG:NH2	2.21	0.55
12:L:50:SER:O	12:L:51:ALA:HB2	2.05	0.55
20:T:35:THR:O	20:T:39:LYS:HB2	2.06	0.55
20:T:94:ALA:O	20:T:95:ALA:HB3	2.06	0.55
1:A:518:C:O2'	12:L:50:SER:HB3	2.06	0.55
1:A:1202:G:O2'	1:A:1203:C:H5'	2.06	0.55
3:C:33:LEU:HD11	14:N:53:LEU:HD22	1.87	0.55
1:A:505:G:H2'	1:A:506:G:H8	1.69	0.55
1:A:1251:A:H2'	1:A:1252:A:C8	2.41	0.55
2:B:17:PHE:CD1	2:B:17:PHE:C	2.85	0.55
2:B:23:ARG:HD3	2:B:23:ARG:N	2.22	0.55
3:C:38:ARG:HB3	3:C:94:LEU:HD21	1.88	0.55
3:C:108:ASN:C	3:C:110:ASN:H	2.12	0.55
4:D:61:LYS:HZ2	4:D:62:GLN:HE21	1.55	0.55
8:H:126:LYS:C	8:H:128:GLY:H	2.14	0.55
10:J:24:VAL:HG21	10:J:37:PRO:HD3	1.88	0.55
12:L:43:VAL:HG12	12:L:44:THR:H	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:65:LYS:HE3	13:M:69:GLU:OE2	2.07	0.55
1:A:1193:G:O2'	1:A:1194:U:H5'	2.07	0.55
1:A:1236:A:H2'	1:A:1237:C:C6	2.41	0.55
1:A:1268:A:H2'	1:A:1269:A:C8	2.41	0.55
2:B:15:VAL:HG22	2:B:209:ARG:HG3	1.88	0.55
2:B:67:THR:HG22	2:B:68:ILE:N	2.21	0.55
6:F:69:GLU:HA	6:F:72:VAL:CG2	2.37	0.55
12:L:47:LYS:HB2	12:L:48:PRO:HD2	1.88	0.55
16:P:81:ARG:CG	16:P:83:GLU:HG2	2.36	0.55
1:A:490:G:H2'	1:A:491:G:H8	1.72	0.55
1:A:760:G:C2	17:Q:103:GLY:O	2.60	0.55
1:A:761:G:O4'	17:Q:103:GLY:O	2.25	0.55
1:A:1006:C:H2'	1:A:1007:C:H6	1.72	0.55
4:D:107:ARG:HH21	4:D:194:LEU:HD12	1.70	0.55
18:R:86:VAL:O	18:R:87:ARG:CB	2.55	0.55
1:A:620:C:H2'	1:A:621:A:O4'	2.07	0.55
1:A:818:G:C3'	1:A:819:A:C5'	2.83	0.55
1:A:1460:A:H2'	1:A:1461:G:O4'	2.07	0.55
4:D:177:ASP:OD1	4:D:179:GLU:HB2	2.07	0.55
6:F:46:ARG:HB2	6:F:60:PHE:HE1	1.71	0.55
6:F:76:ALA:O	6:F:80:ARG:HG3	2.06	0.55
10:J:49:VAL:HG11	14:N:41:ARG:O	2.07	0.55
13:M:37:THR:HG22	13:M:37:THR:O	2.07	0.55
1:A:437:U:O2'	4:D:123:HIS:CD2	2.60	0.55
1:A:954:G:H2'	1:A:955:U:C6	2.42	0.55
9:I:7:THR:HG22	9:I:8:GLY:N	2.22	0.55
1:A:227:G:O2'	16:P:62:VAL:HG11	2.05	0.55
1:A:551:U:H2'	1:A:552:U:C6	2.41	0.55
1:A:1066:C:O2'	1:A:1067:A:H5'	2.07	0.55
1:A:1442:G:H21	1:A:1446:A:H5''	1.72	0.55
17:Q:68:ARG:N	17:Q:70:ARG:NH1	2.55	0.55
20:T:67:ALA:HB2	20:T:77:ALA:HB2	1.88	0.55
20:T:82:SER:O	20:T:86:ARG:HB2	2.06	0.55
1:A:186:C:O2	20:T:85:MET:HE1	2.06	0.55
1:A:761:G:H1'	17:Q:103:GLY:O	2.06	0.55
1:A:1333:A:H2'	1:A:1334:G:O4'	2.07	0.55
3:C:138:VAL:HG21	3:C:168:ALA:HB1	1.89	0.55
3:C:181:ASN:HD21	3:C:204:LEU:HD12	1.72	0.55
9:I:47:LEU:C	9:I:49:PRO:HD2	2.32	0.55
10:J:51:ARG:H	10:J:59:SER:HB2	1.72	0.55
15:O:87:ILE:O	15:O:88:ARG:CB	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:C:H2'	1:A:194:C:H6	1.72	0.54
1:A:532:A:H2'	1:A:533:A:H5''	1.89	0.54
2:B:17:PHE:C	2:B:17:PHE:HD1	2.14	0.54
2:B:75:LYS:O	2:B:75:LYS:HD3	2.08	0.54
3:C:37:GLN:NE2	14:N:52:GLN:OE1	2.40	0.54
6:F:25:ILE:HD12	6:F:82:ARG:HD2	1.88	0.54
1:A:26:A:N6	1:A:558:G:H1'	2.21	0.54
1:A:54:C:H2'	1:A:352:C:H41	1.71	0.54
1:A:190(F):G:H4'	1:A:190(G):G:OP2	2.07	0.54
1:A:195:A:H4'	20:T:68:LYS:CE	2.38	0.54
1:A:939:G:H2'	1:A:940:C:H6	1.71	0.54
1:A:977:A:C2'	1:A:978:A:H5''	2.38	0.54
1:A:1319:A:H5'	1:A:1320:C:OP1	2.06	0.54
2:B:17:PHE:CD1	2:B:18:GLY:N	2.75	0.54
2:B:33:TYR:HB2	2:B:43:ASP:HB2	1.89	0.54
3:C:112:SER:CB	3:C:115:LEU:HD12	2.36	0.54
5:E:21:ALA:O	5:E:23:GLY:N	2.40	0.54
8:H:36:LEU:HD12	8:H:59:LEU:HD13	1.88	0.54
8:H:56:LYS:HD2	8:H:56:LYS:N	2.23	0.54
13:M:5:ALA:O	13:M:6:GLY:C	2.51	0.54
1:A:130:A:C8	17:Q:63:ARG:HG3	2.42	0.54
1:A:967:C:C4'	9:I:128:ARG:HG3	2.37	0.54
2:B:17:PHE:HD1	2:B:18:GLY:N	2.04	0.54
2:B:33:TYR:HB3	2:B:41:ILE:O	2.08	0.54
7:G:116:ALA:HA	7:G:119:ARG:CZ	2.37	0.54
15:O:32:LEU:O	15:O:36:ILE:HG13	2.06	0.54
17:Q:79:SER:O	17:Q:80:GLY:O	2.25	0.54
3:C:150:LYS:CE	3:C:152:ILE:HD11	2.38	0.54
5:E:15:ARG:O	5:E:27:ARG:O	2.25	0.54
5:E:137:GLU:O	5:E:141:GLN:HG3	2.07	0.54
7:G:69:VAL:HG12	7:G:100:ALA:HA	1.90	0.54
13:M:60:VAL:O	13:M:63:THR:HG22	2.07	0.54
1:A:425:G:H4'	4:D:45:GLN:HE22	1.73	0.54
1:A:743:U:H2'	1:A:744:C:C6	2.43	0.54
1:A:1128:C:H2'	1:A:1129:C:H5''	1.90	0.54
1:A:1320:C:N3	19:S:36:ARG:HG3	2.23	0.54
3:C:58:GLU:H	3:C:65:ALA:HB3	1.72	0.54
6:F:4:TYR:OH	6:F:69:GLU:HB3	2.07	0.54
7:G:113:GLU:HG2	7:G:119:ARG:HG2	1.90	0.54
13:M:29:ARG:HB3	13:M:64:TRP:CH2	2.42	0.54
15:O:27:VAL:O	15:O:31:LEU:HD13	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:21:VAL:O	16:P:33:ILE:HB	2.07	0.54
7:G:18:TYR:CE2	7:G:59:LEU:HB2	2.42	0.54
9:I:85:LEU:O	9:I:92:TYR:HD1	1.91	0.54
10:J:3:LYS:N	10:J:75:ILE:HA	2.22	0.54
17:Q:18:THR:HG23	17:Q:69:LYS:HE3	1.88	0.54
17:Q:67:LYS:CA	17:Q:70:ARG:HH12	2.21	0.54
1:A:429:U:H2'	4:D:25:ARG:HH12	1.73	0.54
1:A:960:U:H5'	1:A:960:U:O2	2.08	0.54
3:C:77:ILE:HG22	3:C:81:GLY:HA2	1.90	0.54
7:G:138:LYS:HE2	7:G:142:GLU:OE1	2.08	0.54
10:J:31:GLY:HA2	10:J:78:ASN:ND2	2.12	0.54
13:M:94:ARG:HH22	19:S:81:ARG:HH11	1.54	0.54
1:A:190:C:H2'	1:A:190(A):C:C6	2.43	0.54
1:A:750:G:H1'	15:O:22:THR:OG1	2.08	0.54
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.23	0.54
2:B:187:LEU:HD23	2:B:214:ILE:HG21	1.90	0.54
4:D:160:GLN:O	4:D:163:GLU:HB3	2.08	0.54
6:F:26:ILE:HG21	6:F:63:TYR:CE2	2.40	0.54
13:M:53:VAL:O	13:M:57:ARG:HB2	2.08	0.54
16:P:42:ARG:O	16:P:43:LYS:C	2.51	0.54
20:T:72:LEU:HD21	20:T:80:ARG:CZ	2.38	0.54
1:A:35:G:H2'	1:A:36:C:C6	2.43	0.54
1:A:429:U:H2'	4:D:25:ARG:NH1	2.22	0.54
1:A:983:A:H5'	1:A:984:C:OP2	2.07	0.54
1:A:1351:U:H2'	1:A:1352:C:C6	2.40	0.54
2:B:142:LEU:HD22	2:B:146:GLN:HE22	1.73	0.54
5:E:104:ALA:O	5:E:105:VAL:C	2.49	0.54
9:I:81:ILE:O	9:I:85:LEU:HB2	2.08	0.54
1:A:281:G:O2'	1:A:282:A:P	2.65	0.54
1:A:1222:G:P	19:S:77:THR:HG21	2.48	0.54
1:A:1318:A:H4'	19:S:10:PHE:CE1	2.42	0.54
1:A:1494:G:O2'	1:A:1495:U:H5'	2.08	0.54
1:A:1516:G:H2'	1:A:1518:A:OP2	2.08	0.54
3:C:116:VAL:O	3:C:120:VAL:HG23	2.07	0.54
1:A:299:G:H2'	1:A:300:A:C8	2.43	0.53
1:A:475:G:H2'	1:A:476:G:C8	2.43	0.53
4:D:126:ILE:HG22	4:D:127:THR:N	2.23	0.53
8:H:119:LEU:HD12	8:H:124:ALA:HA	1.90	0.53
16:P:43:LYS:HB3	16:P:48:TRP:CD1	2.43	0.53
1:A:639:G:O2'	1:A:640:A:H5'	2.08	0.53
1:A:957:U:H4'	19:S:79:THR:HB	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1218:C:H2'	1:A:1219:U:C6	2.42	0.53
1:A:1347:G:C2'	1:A:1348:U:OP2	2.56	0.53
3:C:174:PRO:HB2	3:C:177:THR:HG22	1.89	0.53
5:E:101:ILE:O	5:E:120:THR:HB	2.08	0.53
7:G:44:TYR:HE1	9:I:41:VAL:HG11	1.72	0.53
9:I:97:LYS:O	9:I:100:GLY:N	2.36	0.53
10:J:27:ALA:C	10:J:29:ARG:H	2.15	0.53
11:K:14:VAL:O	11:K:15:ALA:CB	2.57	0.53
15:O:70:LEU:HD11	15:O:77:ARG:HB2	1.89	0.53
16:P:11:SER:OG	16:P:14:ASN:HB3	2.08	0.53
1:A:33:A:H2'	1:A:34:C:H6	1.73	0.53
1:A:1003:G:C2	1:A:1003(A):G:C6	2.96	0.53
2:B:18:GLY:CA	2:B:42:ILE:H	2.20	0.53
9:I:17:VAL:HG11	9:I:81:ILE:HA	1.90	0.53
12:L:46:LYS:CG	12:L:47:LYS:N	2.71	0.53
19:S:51:VAL:HG12	19:S:52:TYR:N	2.23	0.53
1:A:190(L):U:H3	20:T:105:SER:HG	1.56	0.53
1:A:1117:G:H4'	9:I:104:ARG:HH11	1.72	0.53
1:A:1402:C:O2	1:A:1500:A:N1	2.41	0.53
2:B:97:TRP:CH2	2:B:176:GLU:CD	2.85	0.53
3:C:113:ALA:HB3	3:C:114:PRO:HD3	1.90	0.53
14:N:44:LEU:HD12	14:N:44:LEU:O	2.08	0.53
1:A:33:A:H2'	1:A:34:C:C6	2.44	0.53
1:A:101:A:O2'	1:A:102:G:H5'	2.07	0.53
1:A:382:A:H2'	1:A:383:A:H8	1.70	0.53
1:A:386:C:C2'	1:A:387:U:H5'	2.39	0.53
1:A:979:C:H2'	1:A:980:C:H5'	1.91	0.53
1:A:1286:A:H5''	21:V:25:LYS:HZ2	1.73	0.53
7:G:6:ARG:O	7:G:7:ALA:C	2.52	0.53
7:G:42:ILE:CG2	7:G:120:ILE:HD12	2.39	0.53
7:G:71:PRO:HD3	7:G:103:TRP:HZ3	1.74	0.53
12:L:28:LYS:O	12:L:29:GLY:C	2.51	0.53
1:A:300:A:H2'	1:A:301:G:O4'	2.08	0.53
1:A:959:A:C2	1:A:1222:G:O4'	2.61	0.53
1:A:1003:G:N2	1:A:1039:C:C2	2.77	0.53
1:A:1121:U:H2'	1:A:1122:U:H6	1.73	0.53
1:A:1305:G:O2'	1:A:1306:A:C8	2.44	0.53
8:H:80:ILE:O	8:H:80:ILE:HG22	2.08	0.53
9:I:48:GLU:OE1	9:I:51:ARG:HD2	2.09	0.53
10:J:38:ILE:HG13	10:J:71:LEU:HB3	1.90	0.53
13:M:8:GLU:OE1	13:M:22:ILE:HA	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:27:PHE:CE1	17:Q:36:ILE:HD11	2.42	0.53
18:R:36:ASN:CG	18:R:39:VAL:HG12	2.34	0.53
1:A:407:G:O2'	4:D:116:GLN:HG3	2.08	0.53
1:A:818:G:O2'	1:A:819:A:H5''	2.08	0.53
1:A:1157:A:H4'	1:A:1158:C:O5'	2.08	0.53
5:E:18:ARG:HG2	5:E:19:MET:N	2.23	0.53
5:E:76:ILE:O	5:E:93:PRO:HB3	2.07	0.53
8:H:8:ASP:O	8:H:12:ARG:HG3	2.08	0.53
13:M:102:ARG:NH1	13:M:102:ARG:HB2	2.24	0.53
16:P:19:ILE:HG22	16:P:36:ILE:HG13	1.90	0.53
18:R:61:LYS:O	18:R:65:ILE:HG13	2.08	0.53
19:S:42:PRO:O	19:S:45:VAL:HG23	2.09	0.53
20:T:38:LYS:O	20:T:39:LYS:C	2.51	0.53
21:V:9:ARG:NH1	21:V:22:ARG:HA	2.23	0.53
1:A:187:C:C2	20:T:105:SER:HB3	2.43	0.53
1:A:518:C:HO2'	12:L:50:SER:HB3	1.74	0.53
1:A:1068:G:OP2	1:A:1068:G:H8	1.91	0.53
2:B:23:ARG:O	2:B:24:TRP:O	2.27	0.53
3:C:91:LEU:HD21	3:C:99:VAL:CG1	2.30	0.53
3:C:130:VAL:O	3:C:134:ILE:HG13	2.07	0.53
12:L:53:ARG:HG2	12:L:69:TYR:HE1	1.73	0.53
12:L:55:VAL:HG11	12:L:67:THR:HG23	1.91	0.53
13:M:11:ARG:CG	13:M:12:ASN:N	2.72	0.53
20:T:76:ALA:O	20:T:80:ARG:HG2	2.09	0.53
1:A:623:C:O2'	1:A:624:C:H5'	2.09	0.53
1:A:1305:G:OP1	21:V:2:GLY:N	2.42	0.53
1:A:1426:C:H2'	1:A:1427:U:C6	2.44	0.53
2:B:124:SER:O	2:B:127:ILE:HG13	2.08	0.53
2:B:166:ASP:OD2	2:B:169:LYS:HB2	2.09	0.53
3:C:32:LEU:HD21	3:C:59:ARG:HD2	1.91	0.53
4:D:6:GLY:O	4:D:7:PRO:C	2.50	0.53
5:E:20:GLN:C	5:E:21:ALA:O	2.51	0.53
9:I:31:GLN:HB3	9:I:35:GLU:HB3	1.91	0.53
10:J:44:VAL:HG22	10:J:66:ARG:HB3	1.91	0.53
20:T:93:GLU:HA	20:T:93:GLU:OE2	2.09	0.53
1:A:101:A:H2'	1:A:102:G:H8	1.74	0.53
1:A:148:G:H2'	1:A:149:A:H8	1.74	0.53
1:A:373:A:O2'	1:A:374:A:H5'	2.09	0.53
1:A:528:C:H41	12:L:49:ASN:ND2	2.06	0.53
1:A:1184:G:H2'	1:A:1185:G:H8	1.73	0.53
7:G:69:VAL:HG21	7:G:104:LEU:HD21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:23:ASN:C	9:I:23:ASN:ND2	2.66	0.53
1:A:188:C:H4'	20:T:89:ARG:NH1	2.25	0.52
1:A:370:C:O2'	1:A:371:G:H5'	2.09	0.52
1:A:1006:C:H2'	1:A:1007:C:C6	2.44	0.52
6:F:75:LEU:C	6:F:75:LEU:HD13	2.34	0.52
1:A:246:A:N6	1:A:281:G:H1'	2.24	0.52
1:A:252:U:H2'	1:A:253:U:C6	2.44	0.52
1:A:1038:C:H2'	1:A:1039:C:C6	2.43	0.52
2:B:32:ILE:HD13	2:B:40:HIS:CD2	2.44	0.52
3:C:92:ALA:C	3:C:94:LEU:H	2.17	0.52
5:E:31:LEU:HD22	5:E:43:LEU:CD2	2.39	0.52
12:L:47:LYS:HB3	12:L:48:PRO:HD3	1.91	0.52
14:N:33:VAL:HA	14:N:40:CYS:HA	1.91	0.52
1:A:761:G:C5'	17:Q:102:GLY:HA3	2.39	0.52
1:A:1423:G:O2'	1:A:1424:C:H5'	2.09	0.52
2:B:213:LEU:C	2:B:213:LEU:CD2	2.83	0.52
3:C:14:ILE:HG22	3:C:15:THR:N	2.12	0.52
3:C:23:TYR:CD2	3:C:24:ALA:N	2.78	0.52
12:L:55:VAL:HG11	12:L:67:THR:CG2	2.39	0.52
13:M:102:ARG:HB2	13:M:102:ARG:HH11	1.75	0.52
20:T:50:GLU:O	20:T:100:ILE:HD12	2.09	0.52
1:A:621:A:H2'	1:A:622:A:C8	2.44	0.52
1:A:684:A:H1'	11:K:38:ASN:HB3	1.91	0.52
1:A:922:G:N3	1:A:1398:A:H2	2.07	0.52
1:A:1128:C:H1'	1:A:1146:A:H61	1.75	0.52
2:B:23:ARG:HH11	2:B:23:ARG:C	2.16	0.52
5:E:12:LEU:CD1	5:E:31:LEU:HB2	2.39	0.52
6:F:10:LEU:HD11	6:F:59:TYR:CD2	2.41	0.52
11:K:13:GLN:HA	11:K:75:TYR:O	2.08	0.52
13:M:86:CYS:SG	13:M:88:ARG:HB3	2.49	0.52
1:A:103:C:P	20:T:17:ARG:HH11	2.32	0.52
1:A:401:C:H1'	1:A:622:A:H1'	1.91	0.52
1:A:1038:C:H2'	1:A:1039:C:H6	1.74	0.52
1:A:1513:A:H2'	1:A:1514:C:C6	2.44	0.52
3:C:22:TRP:CZ2	14:N:54:PRO:HG3	2.44	0.52
4:D:65:ARG:HB2	4:D:75:PHE:CE1	2.45	0.52
6:F:43:LEU:H	6:F:43:LEU:CD2	2.23	0.52
8:H:14:ARG:O	8:H:18:ARG:HD3	2.10	0.52
13:M:117:VAL:HG12	13:M:118:ALA:N	2.24	0.52
19:S:13:ASP:O	19:S:17:GLU:HG2	2.10	0.52
20:T:43:LEU:CD1	20:T:55:ILE:HD12	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:G:O2'	1:A:116:A:OP2	2.22	0.52
1:A:953:G:H2'	1:A:954:G:O4'	2.09	0.52
1:A:1397:C:H4'	1:A:1398:A:OP2	2.09	0.52
3:C:70:VAL:O	3:C:106:VAL:HG23	2.09	0.52
4:D:104:VAL:HG11	4:D:146:ILE:CD1	2.37	0.52
5:E:80:ILE:HD13	5:E:138:ALA:HB1	1.90	0.52
21:V:17:THR:O	21:V:22:ARG:HD3	2.10	0.52
21:V:24:ARG:O	21:V:25:LYS:HB2	2.10	0.52
1:A:1428:A:H2'	1:A:1429:C:C6	2.44	0.52
3:C:107:GLN:CD	3:C:107:GLN:N	2.64	0.52
3:C:154:SER:O	3:C:165:THR:HA	2.09	0.52
5:E:74:GLY:HA3	5:E:116:THR:HG22	1.92	0.52
6:F:67:MET:CE	6:F:72:VAL:HA	2.40	0.52
11:K:17:GLY:O	11:K:80:VAL:HA	2.09	0.52
18:R:19:LYS:O	18:R:20:ALA:HB2	2.10	0.52
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.91	0.52
19:S:50:ALA:HA	19:S:58:VAL:O	2.10	0.52
1:A:142:G:O2'	1:A:196:A:N1	2.40	0.52
1:A:190(E):U:O2'	17:Q:63:ARG:NH2	2.43	0.52
1:A:791:G:H2'	1:A:792:A:H5'	1.91	0.52
1:A:1202:G:H2'	1:A:1203:C:O4'	2.10	0.52
1:A:1424:C:O2'	1:A:1425:U:H5'	2.09	0.52
2:B:73:THR:HG23	2:B:95:GLN:O	2.09	0.52
6:F:3:ARG:NH2	6:F:64:GLN:NE2	2.57	0.52
6:F:53:ALA:C	6:F:55:ASP:H	2.18	0.52
8:H:25:ASP:OD1	8:H:60:ARG:HD3	2.09	0.52
9:I:9:ARG:HG2	9:I:14:VAL:HG22	1.92	0.52
11:K:77:MET:HE3	11:K:80:VAL:HG22	1.91	0.52
14:N:12:ARG:O	14:N:13:THR:C	2.52	0.52
15:O:36:ILE:HA	15:O:59:MET:HE3	1.91	0.52
20:T:41:VAL:O	20:T:45:GLN:HB2	2.10	0.52
1:A:115:G:H1'	1:A:116:A:N7	2.24	0.52
1:A:605:U:O2'	1:A:606:G:H5'	2.10	0.52
1:A:1167:A:H2'	1:A:1168:A:C8	2.45	0.52
1:A:1451:A:O2'	1:A:1452:C:OP1	2.26	0.52
1:A:1481:U:O2'	1:A:1482:G:H5'	2.09	0.52
3:C:130:VAL:HG12	3:C:134:ILE:HD11	1.91	0.52
4:D:170:VAL:CG1	4:D:174:LEU:HB2	2.39	0.52
16:P:20:VAL:CG1	16:P:32:TYR:HB3	2.40	0.52
1:A:148:G:H2'	1:A:149:A:C8	2.45	0.52
1:A:357:G:O2'	1:A:358:U:H5'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1021:G:C2'	1:A:1022:G:H5'	2.40	0.52
4:D:158:ILE:HG22	4:D:181:MET:HE2	1.92	0.52
6:F:8:ILE:HD11	6:F:79:LEU:HD13	1.92	0.52
11:K:27:ASN:HA	11:K:56:GLY:HA2	1.92	0.52
11:K:62:GLN:HG3	11:K:97:ALA:HB2	1.92	0.52
13:M:73:GLU:O	13:M:76:ALA:HB3	2.09	0.52
13:M:78:ILE:HA	13:M:81:LEU:CD2	2.38	0.52
18:R:88:LYS:OXT	18:R:88:LYS:HG2	2.10	0.52
21:V:24:ARG:O	21:V:25:LYS:CB	2.58	0.52
1:A:443:C:H2'	1:A:444:C:C6	2.43	0.51
1:A:1241:G:H2'	1:A:1242:C:H6	1.75	0.51
1:A:1511:G:H2'	1:A:1512:U:O4'	2.09	0.51
2:B:215:LEU:O	2:B:216:SER:C	2.52	0.51
3:C:20:SER:HB3	3:C:22:TRP:NE1	2.25	0.51
3:C:139:GLN:HA	3:C:139:GLN:NE2	2.25	0.51
8:H:24:THR:HG23	8:H:61:VAL:HB	1.92	0.51
9:I:44:VAL:HG13	9:I:51:ARG:NH2	2.24	0.51
9:I:115:GLY:HA2	10:J:58:ASP:OD1	2.10	0.51
10:J:22:LYS:NZ	10:J:91:PRO:HD3	2.25	0.51
12:L:42:THR:HG21	12:L:52:LEU:HB3	1.91	0.51
13:M:88:ARG:HG3	13:M:98:VAL:CG1	2.40	0.51
17:Q:96:GLN:O	17:Q:96:GLN:CD	2.54	0.51
1:A:452:A:H4'	16:P:72:ARG:NH2	2.25	0.51
1:A:738:C:P	6:F:92:LYS:HE3	2.50	0.51
1:A:921:U:O2'	5:E:19:MET:O	2.28	0.51
1:A:1329:A:O2'	1:A:1330:U:H5'	2.11	0.51
2:B:130:ARG:HH22	3:C:179:ARG:NH1	2.05	0.51
3:C:134:ILE:HG21	3:C:167:TRP:O	2.11	0.51
1:A:163:C:O2'	1:A:164:U:H5'	2.10	0.51
1:A:794:A:H2'	1:A:795:C:C6	2.45	0.51
1:A:1221:G:O3'	19:S:77:THR:HG21	2.10	0.51
1:A:1525:G:P	11:K:120:ARG:HH22	2.32	0.51
2:B:126:GLU:O	2:B:129:GLU:HB2	2.11	0.51
3:C:94:LEU:HD22	3:C:95:THR:HG23	1.92	0.51
3:C:97:LYS:O	3:C:98:ASN:HB3	2.10	0.51
5:E:15:ARG:O	5:E:16:THR:O	2.28	0.51
5:E:40:ARG:HG2	5:E:40:ARG:HH11	1.76	0.51
7:G:156:TRP:OXT	7:G:156:TRP:HD1	1.93	0.51
10:J:20:ALA:O	10:J:24:VAL:HG23	2.11	0.51
10:J:39:PRO:O	10:J:40:LEU:CB	2.57	0.51
17:Q:97:SER:O	17:Q:98:LEU:C	2.54	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:G:H1'	1:A:550:G:H5'	1.91	0.51
1:A:527:G:O2'	1:A:535:A:N1	2.33	0.51
1:A:560:U:O2'	1:A:561:U:OP2	2.27	0.51
1:A:1003(A):G:N1	1:A:1004:A:H1'	2.25	0.51
1:A:1094:G:H5''	1:A:1095:U:H5	1.75	0.51
1:A:1191:A:H2'	1:A:1192:C:C6	2.45	0.51
3:C:84:ILE:O	3:C:84:ILE:HG12	2.10	0.51
5:E:13:ILE:HG22	5:E:30:ALA:CB	2.40	0.51
6:F:69:GLU:OE1	6:F:69:GLU:N	2.44	0.51
12:L:119:LYS:O	12:L:120:TYR:HB2	2.11	0.51
14:N:21:TYR:HE2	14:N:23:ARG:NE	2.09	0.51
19:S:53:ASN:HB2	19:S:56:GLN:H	1.74	0.51
1:A:190(L):U:H3	20:T:105:SER:HB2	1.75	0.51
1:A:580:U:H2'	1:A:581:G:O4'	2.11	0.51
4:D:24:GLU:O	4:D:25:ARG:HB3	2.10	0.51
7:G:102:ARG:O	7:G:106:GLN:HG3	2.11	0.51
10:J:23:ILE:N	10:J:23:ILE:HD12	2.26	0.51
10:J:69:ASN:O	10:J:70:ARG:HD3	2.11	0.51
14:N:57:ARG:HG2	14:N:58:LYS:H	1.75	0.51
1:A:828:A:H2'	1:A:829:G:O4'	2.10	0.51
1:A:1059:C:O2'	1:A:1060:C:H5'	2.11	0.51
1:A:1346:A:C4	7:G:10:ARG:NH2	2.78	0.51
1:A:1468:A:H2'	1:A:1469:G:O4'	2.09	0.51
1:A:1518:A:H2'	1:A:1519:A:C8	2.45	0.51
3:C:61:ALA:O	3:C:63:ASN:N	2.44	0.51
3:C:137:ALA:HA	3:C:140:ARG:NH1	2.26	0.51
4:D:87:GLY:O	4:D:88:VAL:C	2.53	0.51
5:E:127:ASN:O	5:E:128:PRO:C	2.53	0.51
5:E:144:THR:C	5:E:146:ALA:N	2.67	0.51
9:I:125:TYR:CD2	9:I:125:TYR:N	2.79	0.51
9:I:127:LYS:N	9:I:127:LYS:HD2	2.25	0.51
17:Q:45:HIS:HB2	17:Q:65:ILE:CD1	2.37	0.51
17:Q:45:HIS:CB	17:Q:65:ILE:HD13	2.39	0.51
19:S:81:ARG:O	19:S:81:ARG:HG2	2.11	0.51
1:A:187:C:C1'	20:T:85:MET:HE2	2.40	0.51
1:A:478:A:O2'	1:A:479:C:H5'	2.11	0.51
1:A:791:G:H2'	1:A:792:A:C5'	2.40	0.51
1:A:808:C:OP1	15:O:48:LYS:HE3	2.11	0.51
1:A:922:G:H5'	5:E:19:MET:O	2.11	0.51
1:A:1021:G:H2'	1:A:1022:G:O4'	2.11	0.51
1:A:1126:U:OP2	1:A:1281:U:O2	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:26:PRO:O	2:B:29:ALA:HB2	2.10	0.51
3:C:34:LEU:HD23	3:C:34:LEU:O	2.10	0.51
8:H:49:GLU:HG2	8:H:62:TYR:HE2	1.75	0.51
14:N:28:GLY:O	14:N:30:ALA:N	2.43	0.51
17:Q:15:MET:HE1	17:Q:43:LEU:HD22	1.92	0.51
19:S:45:VAL:HG12	19:S:46:GLY:N	2.26	0.51
1:A:760:G:N1	17:Q:104:LYS:O	2.43	0.51
1:A:992:U:O2'	1:A:993:G:OP2	2.26	0.51
1:A:1085:U:O3'	1:A:1086:U:C6	2.64	0.51
2:B:144:ARG:O	2:B:147:LYS:N	2.42	0.51
3:C:139:GLN:CA	3:C:139:GLN:HE21	2.23	0.51
5:E:115:VAL:HG12	5:E:116:THR:N	2.24	0.51
1:A:7:G:H5'	1:A:298:A:O4'	2.11	0.51
1:A:160:A:H1'	1:A:344:A:C5	2.46	0.51
1:A:1152:A:H2'	1:A:1153:C:C6	2.45	0.51
1:A:1262:C:H42	1:A:1273:G:H1	1.59	0.51
2:B:19:HIS:NE2	2:B:206:ASP:HB3	2.26	0.51
2:B:53:ARG:NH1	2:B:53:ARG:HG2	2.26	0.51
2:B:96:ARG:O	2:B:98:LEU:HD23	2.11	0.51
5:E:61:TYR:O	5:E:64:ARG:O	2.29	0.51
5:E:89:ILE:HD13	5:E:90:VAL:H	1.75	0.51
5:E:92:LYS:HB3	5:E:119:LEU:HB2	1.93	0.51
9:I:27:THR:HG23	9:I:30:GLY:O	2.11	0.51
9:I:44:VAL:CG1	9:I:51:ARG:HH12	2.23	0.51
12:L:28:LYS:CD	12:L:33:ARG:HH12	2.24	0.51
1:A:112:G:H21	1:A:354:G:C5'	2.24	0.51
1:A:1162:C:H2'	1:A:1163:C:C6	2.46	0.51
2:B:97:TRP:CZ2	2:B:102:LEU:HD13	2.45	0.51
4:D:81:GLU:O	4:D:85:LYS:HG3	2.11	0.51
6:F:9:VAL:HG22	6:F:60:PHE:CE2	2.46	0.51
6:F:43:LEU:H	6:F:43:LEU:HD22	1.76	0.51
12:L:53:ARG:NH1	12:L:92:ASP:OD2	2.42	0.51
1:A:149:A:O2'	1:A:150:C:H5'	2.11	0.50
1:A:650:G:C2'	1:A:651:C:H5'	2.40	0.50
1:A:1097:C:H2'	1:A:1098:C:C6	2.45	0.50
1:A:1190:G:O2'	1:A:1191:A:P	2.69	0.50
1:A:1396:A:H4'	1:A:1397:C:H5''	1.93	0.50
3:C:188:LEU:CD1	3:C:195:VAL:HG13	2.41	0.50
11:K:32:ILE:CG2	11:K:77:MET:HE2	2.42	0.50
21:V:6:ARG:HD2	21:V:15:ARG:NH1	2.25	0.50
1:A:659:U:O2'	1:A:660:G:H5'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:853:G:O2'	1:A:854:G:H5'	2.11	0.50
1:A:1035:A:H2'	1:A:1036:G:H8	1.76	0.50
1:A:1440:C:C2'	1:A:1441:G:H5'	2.41	0.50
3:C:58:GLU:O	3:C:59:ARG:HG2	2.11	0.50
3:C:112:SER:O	3:C:116:VAL:HG23	2.11	0.50
5:E:11:ILE:HB	5:E:31:LEU:HB3	1.93	0.50
6:F:19:LEU:C	6:F:19:LEU:HD23	2.36	0.50
10:J:27:ALA:HB1	10:J:81:THR:HG23	1.92	0.50
10:J:71:LEU:O	10:J:72:VAL:CB	2.60	0.50
14:N:29:ARG:O	14:N:33:VAL:HG13	2.11	0.50
1:A:1418:A:H2'	1:A:1419:G:O4'	2.12	0.50
4:D:29:PRO:C	4:D:30:LYS:HG3	2.35	0.50
9:I:17:VAL:CG2	9:I:80:GLY:HA3	2.41	0.50
12:L:115:LYS:O	12:L:117:ARG:N	2.37	0.50
13:M:77:ASN:O	13:M:80:ARG:HB3	2.10	0.50
14:N:22:THR:OG1	14:N:33:VAL:HG21	2.11	0.50
1:A:824:C:H2'	1:A:825:G:H8	1.76	0.50
1:A:1021:G:C2	1:A:1022:G:H1'	2.45	0.50
1:A:1283:G:O2'	1:A:1284:C:H5'	2.11	0.50
2:B:53:ARG:HG2	2:B:53:ARG:HH11	1.76	0.50
2:B:88:ALA:O	2:B:90:MET:N	2.45	0.50
2:B:121:LEU:O	2:B:127:ILE:HG12	2.11	0.50
2:B:221:LEU:O	2:B:221:LEU:HD13	2.11	0.50
3:C:47:LEU:CD1	3:C:47:LEU:N	2.74	0.50
4:D:151:LYS:N	4:D:151:LYS:CD	2.75	0.50
5:E:21:ALA:C	5:E:23:GLY:H	2.19	0.50
7:G:69:VAL:HG12	7:G:69:VAL:O	2.12	0.50
21:V:2:GLY:C	21:V:4:GLY:N	2.69	0.50
1:A:222:U:H2'	1:A:223:U:C6	2.47	0.50
1:A:325:A:H2'	1:A:326:G:O4'	2.12	0.50
1:A:839:U:O2	1:A:839:U:C2'	2.59	0.50
1:A:1179:A:H2'	1:A:1180:A:O4'	2.11	0.50
1:A:1278:U:C5'	1:A:1279:A:O4'	2.59	0.50
1:A:1310:G:O2'	1:A:1311:G:H5'	2.12	0.50
2:B:186:ALA:HB3	2:B:197:VAL:CG1	2.41	0.50
3:C:177:THR:HG23	3:C:177:THR:O	2.10	0.50
5:E:121:LYS:HE3	5:E:123:LEU:HD21	1.93	0.50
9:I:46:ALA:HA	9:I:78:LYS:HB2	1.93	0.50
9:I:112:LYS:C	9:I:112:LYS:HD3	2.37	0.50
1:A:556:C:C2'	1:A:557:G:H5'	2.40	0.50
1:A:792:A:H4'	1:A:793:U:C5'	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:960:U:H1'	1:A:1223:C:H5'	1.93	0.50
1:A:999:C:H2'	1:A:1000:U:C6	2.45	0.50
1:A:1136:U:H5''	1:A:1137:C:OP2	2.12	0.50
1:A:1305:G:C8	1:A:1305:G:OP2	2.64	0.50
2:B:33:TYR:HB3	2:B:41:ILE:HG22	1.93	0.50
2:B:44:LEU:HA	2:B:47:THR:OG1	2.12	0.50
2:B:124:SER:CB	2:B:125:PRO:HD2	2.32	0.50
2:B:132:LYS:O	2:B:136:VAL:HG23	2.12	0.50
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.93	0.50
6:F:38:GLU:O	6:F:39:LYS:HB3	2.12	0.50
12:L:46:LYS:O	12:L:47:LYS:C	2.54	0.50
18:R:45:SER:C	18:R:47:THR:N	2.65	0.50
1:A:217:C:O2'	1:A:218:C:H5'	2.12	0.50
1:A:746:A:O2'	1:A:747:C:H5'	2.11	0.50
1:A:1025:U:OP1	1:A:1025:U:H4'	2.11	0.50
1:A:1044:A:H2'	1:A:1045:C:H5'	1.92	0.50
1:A:1096:C:H2'	1:A:1097:C:H6	1.77	0.50
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.45	0.50
1:A:1305:G:C5'	21:V:4:GLY:HA3	2.41	0.50
3:C:178:LEU:O	3:C:179:ARG:CB	2.60	0.50
4:D:3:ARG:NH2	4:D:74:GLN:OE1	2.43	0.50
4:D:8:VAL:HG11	4:D:21:LEU:HB3	1.94	0.50
9:I:10:ARG:HG2	9:I:75:ASP:CB	2.41	0.50
9:I:120:ARG:O	9:I:121:ARG:C	2.54	0.50
10:J:3:LYS:HA	10:J:75:ILE:HA	1.94	0.50
17:Q:27:PHE:HB2	17:Q:28:PRO:HD2	1.94	0.50
17:Q:97:SER:HB2	17:Q:103:GLY:N	2.26	0.50
1:A:1074:G:O3'	2:B:103:THR:HG22	2.12	0.50
1:A:1306:A:H2'	1:A:1307:U:O4'	2.12	0.50
3:C:79:ARG:HG2	3:C:82:GLU:HG2	1.92	0.50
4:D:8:VAL:HG13	4:D:21:LEU:HD13	1.93	0.50
9:I:19:LEU:C	9:I:20:ARG:HG3	2.37	0.50
11:K:74:ALA:C	11:K:76:GLY:N	2.69	0.50
12:L:46:LYS:HG2	12:L:47:LYS:HG3	1.93	0.50
17:Q:10:VAL:O	17:Q:53:LEU:HD12	2.12	0.50
17:Q:45:HIS:NE2	17:Q:47:PRO:HG3	2.27	0.50
1:A:136:C:H2'	1:A:137:C:H6	1.77	0.50
1:A:179:A:H2'	1:A:180:U:C6	2.46	0.50
1:A:255:G:O6	1:A:266:G:O6	2.29	0.50
1:A:959:A:H2'	1:A:960:U:O4'	2.12	0.50
1:A:1498:U:H4'	1:A:1519:A:C2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1499:A:O2'	1:A:1500:A:H5'	2.12	0.50
2:B:69:LEU:C	2:B:69:LEU:HD23	2.36	0.50
4:D:126:ILE:CG2	4:D:127:THR:N	2.75	0.50
7:G:38:LEU:O	7:G:42:ILE:HG13	2.12	0.50
8:H:38:ILE:N	8:H:38:ILE:HD12	2.27	0.50
11:K:23:ALA:CB	11:K:91:ARG:HB2	2.42	0.50
11:K:82:VAL:HG23	11:K:105:VAL:HG13	1.93	0.50
20:T:101:GLY:O	20:T:102:GLY:O	2.30	0.50
1:A:89:C:H2'	1:A:90:U:O4'	2.12	0.49
1:A:430:A:C2'	1:A:431:A:H5'	2.42	0.49
1:A:865:A:H5'	1:A:1078:U:O4	2.12	0.49
1:A:1165:C:O2'	1:A:1166:G:H5'	2.12	0.49
1:A:1181:G:O2'	1:A:1184:G:H5'	2.11	0.49
3:C:139:GLN:O	3:C:143:GLU:N	2.37	0.49
3:C:167:TRP:O	3:C:168:ALA:HB3	2.10	0.49
7:G:18:TYR:HD2	7:G:59:LEU:HD22	1.76	0.49
13:M:84:ILE:C	13:M:86:CYS:N	2.70	0.49
14:N:15:LYS:HB3	14:N:16:PHE:CD1	2.47	0.49
15:O:3:ILE:CG2	15:O:7:GLU:HB3	2.41	0.49
17:Q:26:GLN:O	17:Q:27:PHE:HB3	2.12	0.49
18:R:87:ARG:HG2	18:R:87:ARG:HH11	1.76	0.49
1:A:1323:G:H2'	1:A:1324:A:C8	2.47	0.49
2:B:30:ARG:HG3	2:B:31:TYR:CD2	2.48	0.49
3:C:47:LEU:N	3:C:47:LEU:HD12	2.27	0.49
3:C:171:GLY:O	3:C:173:VAL:HG23	2.12	0.49
3:C:172:ARG:HH12	3:C:174:PRO:CG	2.22	0.49
5:E:31:LEU:HD22	5:E:43:LEU:HD21	1.94	0.49
7:G:108:ALA:O	7:G:119:ARG:HB3	2.12	0.49
8:H:113:SER:HB2	8:H:134:ILE:CD1	2.29	0.49
10:J:60:ARG:O	10:J:61:GLU:CB	2.61	0.49
11:K:48:ILE:HD13	11:K:63:LEU:HB3	1.93	0.49
11:K:51:LYS:O	11:K:55:LYS:HE3	2.11	0.49
12:L:45:PRO:HD3	12:L:51:ALA:O	2.11	0.49
1:A:129(A):G:O2'	1:A:130:A:OP2	2.28	0.49
1:A:204:U:H4'	1:A:216:G:O5'	2.12	0.49
1:A:489:C:H2'	1:A:490:G:H8	1.77	0.49
1:A:521:G:O2'	1:A:522:C:H5'	2.12	0.49
1:A:625:G:H2'	1:A:626:U:C6	2.47	0.49
1:A:1085:U:O3'	1:A:1086:U:H6	1.95	0.49
1:A:1102:A:H2'	1:A:1103:C:C6	2.46	0.49
1:A:1301:U:O2'	1:A:1302:U:OP1	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1365:G:O2'	1:A:1366:C:H5'	2.12	0.49
9:I:36:TYR:HD2	9:I:37:PHE:CE2	2.30	0.49
11:K:65:ALA:HB3	11:K:97:ALA:HB3	1.93	0.49
11:K:124:LYS:HD2	11:K:125:PHE:CE1	2.48	0.49
12:L:48:PRO:HG2	12:L:49:ASN:N	2.26	0.49
1:A:218:C:H2'	1:A:219:C:C6	2.47	0.49
1:A:245:C:O2	1:A:283:C:N3	2.46	0.49
1:A:647:C:H2'	1:A:648:A:H8	1.78	0.49
1:A:834:C:H2'	1:A:835:U:C6	2.48	0.49
1:A:1057:G:H5''	3:C:154:SER:CB	2.30	0.49
1:A:1172:C:O2'	1:A:1173:G:H5'	2.11	0.49
1:A:1256:A:C4'	1:A:1257:U:H5'	2.35	0.49
1:A:1366:C:C2	1:A:1367:C:C5	3.00	0.49
2:B:124:SER:CB	2:B:125:PRO:CD	2.90	0.49
2:B:206:ASP:O	2:B:207:ALA:HB3	2.11	0.49
3:C:38:ARG:HG3	3:C:38:ARG:NH1	2.26	0.49
4:D:7:PRO:CG	4:D:10:ARG:HD2	2.43	0.49
12:L:45:PRO:HB2	12:L:49:ASN:O	2.13	0.49
13:M:80:ARG:C	13:M:82:MET:H	2.20	0.49
15:O:4:THR:HB	15:O:6:GLU:HG2	1.93	0.49
15:O:36:ILE:HA	15:O:59:MET:CE	2.42	0.49
15:O:39:LEU:HD12	15:O:59:MET:HE2	1.93	0.49
1:A:218:C:H2'	1:A:219:C:H6	1.76	0.49
3:C:14:ILE:CG2	3:C:15:THR:H	2.11	0.49
4:D:38:TYR:CE1	4:D:45:GLN:HG3	2.48	0.49
4:D:78:LEU:HD22	4:D:96:LEU:HB3	1.94	0.49
5:E:13:ILE:HG13	5:E:13:ILE:O	2.11	0.49
15:O:17:ARG:HG3	15:O:17:ARG:NH1	2.23	0.49
1:A:190:C:H2'	1:A:190(A):C:H6	1.76	0.49
2:B:168:THR:OG1	2:B:192:SER:HB3	2.12	0.49
6:F:43:LEU:HD22	6:F:43:LEU:N	2.27	0.49
6:F:100:ASN:O	18:R:28:GLU:HG3	2.13	0.49
13:M:94:ARG:CZ	19:S:81:ARG:HD3	2.43	0.49
15:O:34:LEU:O	15:O:34:LEU:HD23	2.12	0.49
1:A:149:A:H2'	1:A:150:C:C6	2.48	0.49
1:A:265:G:O2'	1:A:266:G:H5'	2.13	0.49
1:A:491:G:H2'	1:A:492:G:H8	1.77	0.49
1:A:659:U:H2'	1:A:660:G:O4'	2.13	0.49
2:B:35:GLU:HA	2:B:39:ILE:O	2.13	0.49
2:B:97:TRP:CH2	2:B:173:ALA:HA	2.47	0.49
2:B:102:LEU:CD2	2:B:162:ILE:HD11	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:180:ALA:O	3:C:181:ASN:CB	2.61	0.49
3:C:191:THR:HG22	3:C:193:TYR:N	2.23	0.49
7:G:85:TYR:CD1	7:G:154:TYR:HE1	2.28	0.49
10:J:16:LEU:HD23	10:J:94:VAL:HG22	1.95	0.49
11:K:48:ILE:HD11	11:K:64:ALA:HA	1.95	0.49
11:K:85:ARG:HH11	11:K:85:ARG:HG3	1.77	0.49
17:Q:78:GLU:HG3	17:Q:78:GLU:O	2.12	0.49
1:A:346:G:H2'	1:A:347:G:H5'	1.94	0.49
1:A:586:C:O2'	1:A:587:G:H5'	2.12	0.49
1:A:1153:C:H2'	1:A:1154:G:C8	2.46	0.49
1:A:1181:G:H4'	1:A:1184:G:H5'	1.94	0.49
1:A:1305:G:H22	1:A:1331:G:H2'	1.77	0.49
1:A:1503:A:O2'	1:A:1504:G:OP1	2.29	0.49
2:B:144:ARG:HG3	2:B:145:LEU:H	1.77	0.49
3:C:3:ASN:HD22	3:C:4:LYS:HG2	1.78	0.49
4:D:157:LEU:CD2	4:D:161:ASN:ND2	2.74	0.49
8:H:65:TYR:HA	8:H:79:VAL:HG23	1.94	0.49
10:J:32:ALA:HB2	10:J:76:ASN:HB2	1.94	0.49
15:O:30:ALA:HA	15:O:85:LEU:HD21	1.94	0.49
18:R:34:TYR:HA	18:R:69:THR:HG23	1.93	0.49
20:T:89:ARG:HE	20:T:104:LEU:HD22	1.78	0.49
1:A:269:C:H2'	1:A:270:A:C8	2.48	0.49
1:A:393:A:C2	1:A:394:G:C8	3.00	0.49
1:A:1162:C:H2'	1:A:1163:C:H6	1.78	0.49
1:A:1194:U:O2'	1:A:1195:C:H5'	2.12	0.49
1:A:1250:A:H2'	1:A:1251:A:C8	2.47	0.49
1:A:1346:A:H1'	1:A:1348:U:C5	2.47	0.49
1:A:1505:G:C8	1:A:1505:G:H3'	2.48	0.49
3:C:116:VAL:O	3:C:119:ARG:HB3	2.13	0.49
5:E:36:ASP:O	5:E:37:ARG:HB2	2.13	0.49
5:E:84:PHE:CE2	5:E:133:TYR:HD1	2.31	0.49
7:G:85:TYR:HD1	7:G:154:TYR:CE1	2.27	0.49
8:H:60:ARG:HG3	8:H:60:ARG:NH1	2.28	0.49
11:K:79:SER:OG	11:K:106:LYS:HG2	2.12	0.49
1:A:1121:U:H2'	1:A:1122:U:C6	2.48	0.49
1:A:1129:C:O2'	1:A:1130:A:OP2	2.24	0.49
1:A:1238:A:N7	1:A:1303:C:H1'	2.28	0.49
1:A:1279:A:O2'	1:A:1282:C:N4	2.46	0.49
1:A:1413:A:O2'	1:A:1414:U:H5'	2.12	0.49
2:B:213:LEU:C	2:B:213:LEU:HD23	2.37	0.49
8:H:13:ILE:O	8:H:17:THR:HG23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:51:VAL:O	16:P:51:VAL:CG1	2.60	0.49
16:P:52:ASP:OD2	16:P:55:ARG:HB2	2.13	0.49
19:S:5:LEU:HD11	19:S:70:LYS:NZ	2.28	0.49
1:A:178:C:O2'	1:A:179:A:H5'	2.14	0.48
1:A:624:C:O2'	1:A:625:G:H5'	2.13	0.48
1:A:722:A:H4'	1:A:723:U:C5	2.48	0.48
1:A:1070:U:O2'	1:A:1071:C:H5'	2.13	0.48
1:A:1222:G:OP1	19:S:77:THR:HG21	2.13	0.48
1:A:1230:C:O2'	1:A:1231:G:H5'	2.13	0.48
2:B:17:PHE:HA	2:B:44:LEU:HD21	1.95	0.48
7:G:156:TRP:OXT	7:G:156:TRP:CD1	2.66	0.48
9:I:50:LEU:C	9:I:52:ALA:N	2.69	0.48
11:K:110:ASP:OD2	18:R:88:LYS:NZ	2.45	0.48
12:L:27:LEU:HG	12:L:28:LYS:N	2.25	0.48
13:M:78:ILE:O	13:M:82:MET:HB2	2.12	0.48
1:A:220:G:O2'	1:A:221:C:H5'	2.12	0.48
1:A:407:G:H5''	4:D:115:ARG:HB3	1.96	0.48
1:A:974:A:OP2	14:N:41:ARG:NH1	2.45	0.48
1:A:1369:C:H2'	1:A:1370:G:C8	2.48	0.48
2:B:188:ALA:O	2:B:202:PRO:HA	2.13	0.48
2:B:204:ASN:ND2	2:B:206:ASP:H	2.11	0.48
4:D:196:LEU:C	4:D:198:VAL:H	2.21	0.48
8:H:103:VAL:CG2	8:H:110:ALA:HB2	2.43	0.48
10:J:38:ILE:HG13	10:J:71:LEU:CB	2.43	0.48
10:J:45:ARG:NH2	14:N:36:PHE:CD2	2.81	0.48
1:A:960:U:O2'	1:A:1223:C:H4'	2.13	0.48
1:A:1102:A:H2'	1:A:1103:C:H6	1.77	0.48
1:A:1347:G:N7	9:I:10:ARG:NH2	2.61	0.48
2:B:25:ASN:O	2:B:27:LYS:N	2.47	0.48
2:B:178:ARG:NH2	8:H:68:ARG:NH2	2.62	0.48
3:C:79:ARG:C	3:C:81:GLY:H	2.21	0.48
4:D:31:CYS:C	4:D:33:MET:H	2.21	0.48
6:F:48:LEU:HD13	6:F:52:ILE:HG13	1.95	0.48
16:P:1:MET:HE3	16:P:3:LYS:HG2	1.94	0.48
17:Q:12:SER:HB3	17:Q:20:THR:HB	1.95	0.48
1:A:279:A:H5''	1:A:280:C:H3'	1.94	0.48
3:C:173:VAL:N	3:C:174:PRO:CD	2.76	0.48
4:D:127:THR:CG2	4:D:128:VAL:N	2.75	0.48
12:L:42:THR:CG2	12:L:52:LEU:HB3	2.44	0.48
12:L:83:VAL:HG22	12:L:84:LEU:N	2.28	0.48
18:R:36:ASN:HD22	18:R:38:GLU:HG2	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:39:THR:HG22	19:S:40:ILE:N	2.28	0.48
1:A:261:U:OP2	20:T:79:ARG:NH2	2.46	0.48
1:A:538:G:O2'	1:A:539:A:H5'	2.13	0.48
1:A:954:G:H2'	1:A:955:U:H6	1.78	0.48
1:A:1195:C:H2'	1:A:1197:G:H5'	1.96	0.48
3:C:179:ARG:HD2	3:C:179:ARG:C	2.37	0.48
4:D:119:GLN:HG2	4:D:123:HIS:CD2	2.47	0.48
7:G:138:LYS:HD3	7:G:138:LYS:C	2.39	0.48
10:J:6:ILE:HG23	10:J:98:ILE:HG12	1.94	0.48
12:L:83:VAL:HG21	12:L:100:ILE:HD13	1.95	0.48
17:Q:56:VAL:HG12	17:Q:77:VAL:HB	1.95	0.48
1:A:61:G:H2'	1:A:62:U:O4'	2.13	0.48
1:A:942:G:O2'	1:A:943:U:H5'	2.12	0.48
3:C:138:VAL:O	3:C:142:MET:HB2	2.13	0.48
4:D:57:ARG:NH2	4:D:205:GLU:OE2	2.46	0.48
9:I:65:VAL:HG13	9:I:65:VAL:O	2.13	0.48
10:J:39:PRO:HA	10:J:70:ARG:HH11	1.78	0.48
10:J:65:LEU:O	10:J:65:LEU:CD2	2.59	0.48
11:K:86:GLY:H	11:K:112:THR:HG23	1.79	0.48
15:O:25:THR:HG21	15:O:70:LEU:HD23	1.94	0.48
1:A:31:G:H1	1:A:48:C:H5''	1.77	0.48
1:A:337:C:H2'	1:A:338:A:C8	2.49	0.48
1:A:600:C:OP1	8:H:97:VAL:HG12	2.13	0.48
1:A:1181:G:H4'	1:A:1184:G:C4'	2.43	0.48
1:A:1298:C:C5	7:G:114:ARG:HD3	2.48	0.48
1:A:1329:A:C2'	1:A:1330:U:H5'	2.43	0.48
2:B:12:GLU:HG2	2:B:213:LEU:HD11	1.95	0.48
2:B:111:ARG:HB3	2:B:149:LEU:HD11	1.95	0.48
3:C:23:TYR:O	3:C:24:ALA:HB2	2.14	0.48
5:E:51:VAL:O	5:E:54:ALA:HB3	2.13	0.48
6:F:46:ARG:HB2	6:F:60:PHE:CE1	2.48	0.48
7:G:112:PRO:O	7:G:113:GLU:C	2.57	0.48
11:K:60:ALA:O	11:K:61:ALA:C	2.56	0.48
12:L:119:LYS:O	12:L:120:TYR:CB	2.62	0.48
16:P:52:ASP:CG	16:P:52:ASP:O	2.57	0.48
18:R:28:GLU:OE1	18:R:28:GLU:N	2.46	0.48
18:R:46:GLU:CD	18:R:46:GLU:N	2.72	0.48
18:R:47:THR:HA	18:R:83:GLU:HB2	1.96	0.48
1:A:184:G:H2'	1:A:185:A:H8	1.77	0.48
1:A:555:C:H2'	1:A:556:C:C6	2.48	0.48
1:A:559:A:P	5:E:126:ARG:HH22	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:A:C2	1:A:801:U:C5	3.02	0.48
1:A:1047:G:H5'	14:N:4:LYS:HD2	1.96	0.48
1:A:1056:U:O2'	1:A:1057:G:H5'	2.14	0.48
1:A:1342:C:O2'	1:A:1343:G:H5'	2.13	0.48
4:D:3:ARG:O	4:D:5:ILE:HG13	2.13	0.48
4:D:36:ARG:N	4:D:37:PRO:CD	2.65	0.48
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.96	0.48
9:I:111:ARG:HG3	9:I:111:ARG:NH1	2.28	0.48
16:P:6:LEU:HB3	16:P:17:TYR:CD2	2.49	0.48
17:Q:95:TYR:C	17:Q:97:SER:N	2.58	0.48
18:R:39:VAL:HG13	18:R:40:LEU:N	2.28	0.48
19:S:32:LYS:HG3	19:S:32:LYS:O	2.13	0.48
1:A:421:U:H5'	1:A:422:C:C5	2.48	0.48
1:A:1127:G:N2	1:A:1147:C:N4	2.62	0.48
1:A:1347:G:H3'	9:I:108:VAL:O	2.14	0.48
2:B:187:LEU:CD2	2:B:214:ILE:HG13	2.44	0.48
5:E:148:VAL:O	5:E:152:ARG:HG3	2.14	0.48
7:G:64:GLN:O	7:G:67:GLU:HB3	2.14	0.48
10:J:94:VAL:HG12	10:J:95:GLU:H	1.76	0.48
15:O:41:GLU:O	15:O:42:HIS:C	2.57	0.48
17:Q:17:LYS:HA	17:Q:46:ASP:O	2.14	0.48
1:A:620:C:C2	4:D:135:LEU:HD13	2.49	0.48
1:A:731:G:H5'	1:A:766:A:H4'	1.94	0.48
1:A:825:G:H2'	1:A:826:C:H6	1.78	0.48
2:B:230:VAL:HG13	2:B:231:GLU:OE2	2.13	0.48
4:D:200:GLU:OE1	4:D:200:GLU:N	2.46	0.48
9:I:117:HIS:HB2	9:I:121:ARG:HD2	1.95	0.48
11:K:58:PRO:HB2	11:K:93:GLN:HG3	1.95	0.48
12:L:53:ARG:HG2	12:L:93:LEU:HD11	1.95	0.48
18:R:53:ARG:HD3	18:R:63:GLN:HB3	1.95	0.48
1:A:155:C:H2'	1:A:156:G:H8	1.79	0.47
1:A:657:G:O2'	1:A:658:G:H5'	2.13	0.47
1:A:848:C:H2'	1:A:849:C:C6	2.49	0.47
1:A:1394:A:C5	1:A:1501:C:H4'	2.49	0.47
4:D:174:LEU:O	4:D:175:SER:HB3	2.13	0.47
12:L:53:ARG:HB3	12:L:93:LEU:HD11	1.94	0.47
12:L:110:VAL:O	12:L:122:THR:CG2	2.62	0.47
1:A:190(I):G:O2'	1:A:190(J):U:H5'	2.14	0.47
1:A:528:C:H5'	1:A:535:A:C6	2.49	0.47
1:A:613:C:O2'	1:A:614:A:H5'	2.14	0.47
1:A:625:G:H2'	1:A:626:U:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:760:G:O6	17:Q:105:ALA:HB2	2.14	0.47
1:A:1051:C:O2'	1:A:1052:U:H5'	2.13	0.47
1:A:1488:G:H2'	1:A:1489:G:H8	1.77	0.47
3:C:100:ALA:O	3:C:101:LEU:HB2	2.14	0.47
5:E:71:LEU:HD21	5:E:115:VAL:HG22	1.96	0.47
12:L:86:ARG:HG3	12:L:86:ARG:NH1	2.28	0.47
17:Q:68:ARG:O	17:Q:69:LYS:HB2	2.13	0.47
1:A:513:C:H2'	1:A:514:C:C6	2.49	0.47
1:A:1057:G:C2'	1:A:1058:G:H5'	2.44	0.47
3:C:8:ILE:O	3:C:11:ARG:N	2.47	0.47
12:L:34:ARG:HG3	12:L:34:ARG:O	2.13	0.47
20:T:59:ALA:O	20:T:63:ILE:HG13	2.14	0.47
1:A:41:G:H2'	1:A:42:G:C8	2.49	0.47
1:A:560:U:O5'	1:A:560:U:H6	1.98	0.47
1:A:666:G:H5'	1:A:726:C:H1'	1.96	0.47
1:A:1497:G:H2'	1:A:1498:U:C5'	2.42	0.47
2:B:15:VAL:HG12	2:B:210:SER:HB2	1.97	0.47
2:B:59:GLU:O	2:B:60:ASP:C	2.57	0.47
2:B:125:PRO:C	2:B:127:ILE:H	2.22	0.47
9:I:111:ARG:HG3	9:I:111:ARG:HH11	1.80	0.47
12:L:26:ALA:C	12:L:27:LEU:O	2.57	0.47
19:S:10:PHE:HE2	19:S:12:ASP:OD1	1.97	0.47
1:A:19:C:H2'	1:A:20:U:H6	1.80	0.47
1:A:51:A:H4'	1:A:52:G:C5'	2.45	0.47
2:B:108:ILE:O	2:B:108:ILE:HG22	2.13	0.47
2:B:115:LEU:O	2:B:115:LEU:HD12	2.13	0.47
3:C:35:GLU:O	3:C:38:ARG:N	2.47	0.47
7:G:21:VAL:HG23	7:G:22:LEU:N	2.29	0.47
7:G:65:ALA:O	7:G:66:VAL:C	2.58	0.47
7:G:77:SER:O	7:G:156:TRP:HZ3	1.98	0.47
13:M:39:ILE:CD1	13:M:56:LEU:HG	2.44	0.47
17:Q:97:SER:CB	17:Q:102:GLY:C	2.78	0.47
20:T:29:LYS:O	20:T:33:ILE:HG13	2.14	0.47
20:T:42:GLN:NE2	20:T:42:GLN:O	2.47	0.47
20:T:94:ALA:O	20:T:95:ALA:CB	2.63	0.47
1:A:51:A:H4'	1:A:52:G:O5'	2.15	0.47
1:A:1074:G:O2'	1:A:1101:A:N1	2.45	0.47
1:A:1286:A:H5''	21:V:25:LYS:NZ	2.29	0.47
2:B:75:LYS:HE3	2:B:78:GLN:OE1	2.14	0.47
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.49	0.47
6:F:67:MET:HE2	6:F:72:VAL:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:54:THR:HG22	7:G:56:GLN:H	1.80	0.47
7:G:75:VAL:CG1	7:G:86:GLN:HE21	2.27	0.47
10:J:27:ALA:HB2	10:J:85:LEU:HD21	1.96	0.47
14:N:53:LEU:HB3	14:N:56:VAL:CG2	2.45	0.47
1:A:187:C:N3	20:T:105:SER:HB3	2.30	0.47
1:A:435:C:O2'	1:A:436:C:H5'	2.15	0.47
1:A:768:A:H2'	1:A:769:G:O4'	2.14	0.47
1:A:913:A:O2'	1:A:914:A:P	2.73	0.47
1:A:998:G:O2'	1:A:999:C:H5'	2.15	0.47
1:A:1123:A:O3'	10:J:36:GLY:HA3	2.15	0.47
1:A:1202:G:O4'	14:N:29:ARG:HD3	2.14	0.47
1:A:1292:U:P	7:G:41:ARG:HH22	2.36	0.47
2:B:53:ARG:NH1	2:B:199:TYR:CD2	2.82	0.47
2:B:178:ARG:HH22	8:H:68:ARG:NH2	2.12	0.47
3:C:131:ARG:HA	3:C:134:ILE:HD12	1.96	0.47
3:C:139:GLN:NE2	3:C:139:GLN:CA	2.78	0.47
4:D:24:GLU:CG	4:D:25:ARG:N	2.77	0.47
4:D:105:VAL:HG13	4:D:110:PHE:HB2	1.95	0.47
5:E:68:GLU:O	5:E:70:PRO:HD3	2.15	0.47
7:G:46:ALA:O	7:G:50:ILE:HG13	2.15	0.47
10:J:30:SER:CB	10:J:80:LYS:HB3	2.45	0.47
11:K:33:THR:OG1	11:K:37:GLY:C	2.58	0.47
11:K:72:ALA:HB1	11:K:77:MET:HG3	1.97	0.47
12:L:28:LYS:HD2	12:L:33:ARG:NH1	2.29	0.47
13:M:49:THR:CG2	13:M:51:ALA:H	2.13	0.47
16:P:43:LYS:HG2	16:P:48:TRP:CE2	2.50	0.47
19:S:15:LEU:O	19:S:19:VAL:N	2.48	0.47
21:V:3:LYS:HB3	21:V:14:TRP:CD1	2.50	0.47
1:A:180:U:H2'	1:A:181:G:H5'	1.96	0.47
1:A:606:G:H2'	1:A:631:G:N2	2.30	0.47
1:A:1194:U:H2'	1:A:1195:C:C6	2.50	0.47
1:A:1286:A:H2'	1:A:1287:A:H4'	1.96	0.47
1:A:1515:C:H2'	1:A:1516:G:C8	2.50	0.47
3:C:167:TRP:O	3:C:168:ALA:CB	2.63	0.47
4:D:163:GLU:C	4:D:165:MET:N	2.72	0.47
7:G:23:VAL:HG12	7:G:27:ILE:CD1	2.41	0.47
10:J:94:VAL:CG1	10:J:95:GLU:N	2.77	0.47
15:O:77:ARG:O	15:O:80:ALA:HB3	2.15	0.47
1:A:190(H):G:O2'	1:A:190(I):G:H5'	2.14	0.47
1:A:1001:A:H2'	1:A:1002:G:H8	1.79	0.47
1:A:1231:G:H4'	9:I:126:SER:OG	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1240:U:P	7:G:116:ALA:HB2	2.55	0.47
1:A:1245:A:H2'	1:A:1246:C:C6	2.50	0.47
1:A:1300:G:O2'	1:A:1301:U:H6	1.98	0.47
1:A:1326:C:H5''	21:V:12:LYS:NZ	2.30	0.47
1:A:1367:C:H4'	10:J:48:THR:HG21	1.97	0.47
1:A:1510:U:H2'	1:A:1511:G:C8	2.50	0.47
2:B:18:GLY:CA	2:B:41:ILE:HA	2.44	0.47
3:C:79:ARG:HG2	3:C:82:GLU:CG	2.45	0.47
4:D:162:LEU:HD13	4:D:181:MET:CG	2.42	0.47
5:E:92:LYS:O	5:E:118:ILE:HG23	2.15	0.47
6:F:2:ARG:NE	6:F:69:GLU:HG2	2.29	0.47
6:F:95:GLU:CD	6:F:95:GLU:N	2.65	0.47
8:H:126:LYS:C	8:H:128:GLY:N	2.73	0.47
9:I:48:GLU:N	9:I:49:PRO:CD	2.77	0.47
12:L:54:LYS:N	12:L:54:LYS:HD2	2.30	0.47
16:P:51:VAL:O	16:P:52:ASP:C	2.58	0.47
20:T:50:GLU:HG3	20:T:99:LEU:CD1	2.45	0.47
1:A:184:G:C4'	1:A:224:C:H4'	2.44	0.47
1:A:517:G:H5'	1:A:519:C:C2	2.50	0.47
1:A:633:G:H2'	1:A:634:C:C6	2.49	0.47
1:A:926:G:H2'	1:A:1505:G:N3	2.30	0.47
1:A:1051:C:H2'	1:A:1052:U:H6	1.80	0.47
1:A:1232:U:H5''	9:I:124:GLN:O	2.14	0.47
1:A:1262:C:H2'	1:A:1263:C:H6	1.79	0.47
2:B:62:ALA:C	2:B:64:ARG:H	2.23	0.47
10:J:22:LYS:HE2	10:J:90:LEU:HB2	1.97	0.47
11:K:80:VAL:HG21	11:K:103:LEU:HD13	1.97	0.47
19:S:15:LEU:HD12	19:S:16:LEU:H	1.77	0.47
20:T:11:SER:C	20:T:13:LEU:H	2.22	0.47
1:A:321:A:O2'	1:A:322:C:H5'	2.15	0.46
1:A:1004:A:N6	1:A:1035:A:H62	2.13	0.46
2:B:50:GLU:HB3	2:B:200:ILE:O	2.15	0.46
3:C:64:VAL:CG2	3:C:99:VAL:HB	2.45	0.46
5:E:107:ARG:HG2	5:E:108:ALA:N	2.29	0.46
6:F:2:ARG:HD2	6:F:69:GLU:HG2	1.96	0.46
13:M:82:MET:CE	13:M:92:HIS:HB3	2.44	0.46
17:Q:66:SER:OG	17:Q:69:LYS:HB3	2.15	0.46
1:A:190(L):U:N3	20:T:105:SER:OG	2.45	0.46
1:A:542:G:H2'	1:A:543:C:H6	1.80	0.46
1:A:781:A:H2'	1:A:782:A:H5'	1.98	0.46
1:A:952:U:O2'	1:A:953:G:H5'	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1320:C:H2'	1:A:1321:C:O4'	2.16	0.46
1:A:1392:G:H21	1:A:1502:A:H8	1.61	0.46
1:A:1481:U:H2'	1:A:1482:G:O4'	2.15	0.46
3:C:130:VAL:CG2	3:C:157:ILE:HG23	2.41	0.46
3:C:173:VAL:O	3:C:173:VAL:HG12	2.14	0.46
5:E:18:ARG:HG2	5:E:19:MET:H	1.81	0.46
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.49	0.46
12:L:82:VAL:O	12:L:106:ASP:HB2	2.15	0.46
13:M:97:PRO:HB2	13:M:101:GLN:OE1	2.14	0.46
15:O:66:LEU:O	15:O:69:TYR:HB3	2.15	0.46
1:A:5:U:O2'	1:A:6:G:P	2.73	0.46
1:A:458:C:H2'	1:A:459:G:H8	1.80	0.46
1:A:1238:A:H5'	1:A:1336:C:N4	2.29	0.46
1:A:1442:G:N2	1:A:1446:A:C8	2.80	0.46
2:B:15:VAL:CG1	2:B:209:ARG:HG3	2.46	0.46
3:C:154:SER:OG	3:C:155:GLY:N	2.48	0.46
3:C:167:TRP:HB3	3:C:168:ALA:H	1.32	0.46
4:D:111:ALA:HB1	4:D:116:GLN:HB3	1.96	0.46
7:G:15:ASP:O	7:G:19:GLY:HA2	2.16	0.46
9:I:33:PHE:CE2	9:I:47:LEU:HD11	2.51	0.46
9:I:104:ARG:O	9:I:105:ASP:C	2.59	0.46
12:L:59:ARG:NH1	12:L:65:GLU:HG2	2.31	0.46
12:L:77:LEU:HD21	12:L:107:ALA:HB2	1.97	0.46
13:M:36:LYS:C	13:M:38:GLY:H	2.24	0.46
13:M:62:ASN:O	13:M:63:THR:HB	2.16	0.46
15:O:83:GLU:C	15:O:83:GLU:OE1	2.58	0.46
1:A:41:G:H2'	1:A:42:G:H8	1.80	0.46
1:A:624:C:H2'	1:A:625:G:H8	1.81	0.46
1:A:934:C:C4	1:A:1345:U:C5	3.04	0.46
1:A:976:G:C8	1:A:1358:U:C2	3.04	0.46
1:A:1367:C:H5'	10:J:60:ARG:NH1	2.31	0.46
1:A:1496:C:H2'	1:A:1497:G:O4'	2.16	0.46
2:B:42:ILE:HD12	2:B:203:GLY:HA2	1.97	0.46
4:D:39:PRO:HG2	4:D:44:GLY:HA2	1.97	0.46
11:K:34:ASP:O	11:K:36:ASP:N	2.48	0.46
11:K:50:TYR:HD1	11:K:60:ALA:HB2	1.80	0.46
12:L:37:CYS:O	12:L:79:GLU:O	2.34	0.46
13:M:46:LYS:HG3	13:M:47:ASP:N	2.30	0.46
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.97	0.46
18:R:36:ASN:ND2	18:R:38:GLU:HG2	2.29	0.46
1:A:103:C:OP2	20:T:17:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:83:MET:HG3	2:B:238:LEU:CD1	2.46	0.46
7:G:154:TYR:O	7:G:156:TRP:N	2.49	0.46
8:H:92:ARG:HG2	8:H:94:TYR:OH	2.16	0.46
10:J:24:VAL:CG1	10:J:28:ARG:HE	2.29	0.46
10:J:96:ILE:CG2	10:J:97:GLU:H	2.25	0.46
11:K:48:ILE:O	11:K:49:GLY:C	2.59	0.46
18:R:59:SER:OG	18:R:62:GLU:HG3	2.15	0.46
1:A:132:C:O2'	1:A:133:U:H5'	2.15	0.46
1:A:279:A:C6	17:Q:98:LEU:HD13	2.51	0.46
1:A:390:C:H6	1:A:390:C:O5'	1.99	0.46
1:A:707:C:OP1	11:K:85:ARG:NH1	2.49	0.46
1:A:743:U:H2'	1:A:744:C:H6	1.79	0.46
1:A:828:A:H5''	1:A:859:A:C2	2.51	0.46
1:A:834:C:H2'	1:A:835:U:H6	1.79	0.46
1:A:951:G:O2'	1:A:952:U:H5'	2.15	0.46
1:A:1277:C:C2'	1:A:1278:U:H5'	2.46	0.46
1:A:1301:U:O2'	1:A:1302:U:P	2.74	0.46
3:C:21:ARG:NH2	3:C:56:ASP:OD2	2.48	0.46
3:C:164:ARG:HB3	3:C:164:ARG:HH11	1.80	0.46
5:E:33:VAL:HG11	5:E:109:ILE:HA	1.96	0.46
7:G:20:ASP:OD1	7:G:22:LEU:HB3	2.15	0.46
7:G:135:VAL:O	7:G:139:GLU:HG3	2.15	0.46
10:J:49:VAL:CG1	14:N:41:ARG:HB2	2.38	0.46
11:K:16:SER:O	11:K:35:PRO:HD3	2.16	0.46
11:K:59:TYR:O	11:K:62:GLN:HB3	2.15	0.46
12:L:38:THR:HG22	12:L:39:VAL:HG23	1.97	0.46
13:M:5:ALA:O	13:M:8:GLU:N	2.45	0.46
15:O:34:LEU:HD23	15:O:34:LEU:C	2.40	0.46
19:S:22:LEU:CD1	19:S:31:ILE:HD11	2.46	0.46
20:T:67:ALA:O	20:T:73:HIS:ND1	2.47	0.46
1:A:1044:A:O2'	1:A:1045:C:H5'	2.15	0.46
1:A:1152:A:O2'	1:A:1153:C:H5'	2.16	0.46
1:A:1171:G:H2'	1:A:1172:C:C6	2.51	0.46
1:A:1190:G:HO2'	1:A:1191:A:P	2.39	0.46
1:A:1394:A:C6	1:A:1501:C:H4'	2.50	0.46
1:A:1474:G:O2'	1:A:1475:G:H5'	2.15	0.46
2:B:10:LEU:C	2:B:12:GLU:N	2.72	0.46
2:B:32:ILE:HG21	2:B:40:HIS:HD2	1.81	0.46
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.69	0.46
2:B:134:GLU:C	2:B:136:VAL:N	2.71	0.46
2:B:178:ARG:NH1	2:B:178:ARG:CG	2.67	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:173:TRP:CD2	4:D:189:PRO:HB3	2.51	0.46
7:G:107:ALA:O	7:G:110:GLN:HB2	2.16	0.46
8:H:6:ILE:HD12	8:H:35:ILE:HD12	1.97	0.46
10:J:48:THR:OG1	10:J:62:HIS:CD2	2.69	0.46
10:J:53:PRO:O	10:J:54:PHE:O	2.34	0.46
11:K:54:ARG:H	11:K:54:ARG:HG2	1.47	0.46
11:K:84:VAL:HG23	11:K:109:VAL:O	2.16	0.46
12:L:60:LEU:HD21	12:L:66:VAL:HG22	1.97	0.46
21:V:2:GLY:O	21:V:4:GLY:N	2.49	0.46
1:A:92:C:O2'	1:A:93:G:H5'	2.15	0.46
1:A:129(A):G:O2'	1:A:190(E):U:H5''	2.16	0.46
1:A:160:A:H1'	1:A:344:A:N7	2.31	0.46
1:A:1238:A:OP1	1:A:1336:C:H5	1.98	0.46
1:A:1300:G:O2'	1:A:1301:U:P	2.73	0.46
2:B:228:GLY:O	2:B:229:VAL:C	2.58	0.46
3:C:23:TYR:CG	3:C:24:ALA:N	2.84	0.46
3:C:129:ALA:HB3	3:C:132:ARG:CD	2.45	0.46
3:C:174:PRO:O	3:C:177:THR:HG22	2.15	0.46
4:D:162:LEU:HD13	4:D:181:MET:CE	2.46	0.46
5:E:121:LYS:HE3	5:E:123:LEU:CD2	2.46	0.46
8:H:23:SER:OG	8:H:60:ARG:HD2	2.15	0.46
10:J:62:HIS:CB	14:N:59:ALA:HB3	2.45	0.46
12:L:46:LYS:CG	12:L:47:LYS:H	2.29	0.46
14:N:12:ARG:O	14:N:14:PRO:HD3	2.16	0.46
1:A:70:G:H2'	1:A:73:C:C6	2.51	0.46
1:A:458:C:H2'	1:A:459:G:O4'	2.16	0.46
1:A:518:C:H5''	1:A:519:C:H6	1.78	0.46
1:A:1049:U:H4'	1:A:1050:G:OP2	2.16	0.46
1:A:1049:U:H1'	1:A:1201:A:N7	2.31	0.46
1:A:1221:G:O2'	1:A:1222:G:H5'	2.15	0.46
1:A:1237:C:H2'	1:A:1336:C:C5	2.51	0.46
2:B:22:LYS:O	2:B:23:ARG:HG3	2.16	0.46
2:B:78:GLN:O	2:B:94:ASN:OD1	2.33	0.46
3:C:108:ASN:C	3:C:110:ASN:N	2.73	0.46
4:D:152:SER:HA	4:D:155:LEU:HG	1.97	0.46
5:E:144:THR:O	5:E:145:LYS:C	2.59	0.46
6:F:44:GLY:HA2	6:F:59:TYR:CE1	2.51	0.46
9:I:97:LYS:HG3	9:I:102:LEU:HD12	1.96	0.46
11:K:100:ALA:O	11:K:101:SER:C	2.58	0.46
12:L:48:PRO:CG	12:L:49:ASN:H	2.25	0.46
12:L:71:PRO:O	12:L:102:ARG:HD2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:37:THR:HG23	13:M:55:ARG:CB	2.46	0.46
19:S:18:LYS:HG2	19:S:18:LYS:O	2.16	0.46
20:T:63:ILE:HG23	20:T:72:LEU:CD1	2.46	0.46
1:A:151:A:H2'	1:A:152:A:O4'	2.15	0.46
1:A:690:G:H2'	1:A:691:G:O4'	2.15	0.46
1:A:947:G:H2'	1:A:948:C:O4'	2.15	0.46
1:A:1158:C:N3	1:A:1181:G:N2	2.61	0.46
1:A:1390:U:H2'	1:A:1391:U:C6	2.51	0.46
1:A:1461:G:O2'	1:A:1462:G:H5'	2.16	0.46
1:A:1515:C:H2'	1:A:1516:G:H8	1.81	0.46
8:H:116:LYS:NZ	8:H:127:LEU:HD12	2.31	0.46
9:I:48:GLU:OE1	9:I:48:GLU:HA	2.16	0.46
11:K:93:GLN:HE21	11:K:96:ARG:NH2	2.13	0.46
1:A:421:U:H5'	1:A:422:C:H5	1.80	0.45
1:A:877:C:H5''	8:H:88:LYS:HD3	1.97	0.45
1:A:1039:C:O2'	1:A:1040:U:H5'	2.16	0.45
1:A:1225:A:H5'	1:A:1226:C:OP2	2.16	0.45
1:A:1230:C:O2'	13:M:126:LYS:HA	2.16	0.45
1:A:1230:C:H2'	1:A:1231:G:H8	1.81	0.45
1:A:1256:A:O2'	1:A:1257:U:P	2.74	0.45
1:A:1296:C:H4'	1:A:1302:U:C5	2.51	0.45
1:A:1515:C:O2'	1:A:1516:G:H5'	2.16	0.45
2:B:52:GLU:O	2:B:56:ARG:HB2	2.17	0.45
3:C:131:ARG:O	3:C:135:LYS:HG3	2.16	0.45
4:D:145:GLU:HG2	4:D:184:LYS:HE2	1.96	0.45
5:E:15:ARG:NE	5:E:26:PHE:CD2	2.84	0.45
8:H:45:ILE:O	8:H:45:ILE:HG13	2.16	0.45
16:P:72:ARG:O	16:P:72:ARG:HG2	2.16	0.45
1:A:58:C:O2'	1:A:59:A:H5'	2.16	0.45
1:A:242:C:H2'	1:A:243:A:H5'	1.98	0.45
1:A:513:C:H2'	1:A:514:C:H6	1.80	0.45
1:A:909:A:H2'	1:A:910:C:O4'	2.16	0.45
1:A:1131:G:H2'	1:A:1132:C:C6	2.51	0.45
1:A:1202:G:C2'	1:A:1203:C:H5'	2.46	0.45
1:A:1250:A:H4'	9:I:68:GLY:CA	2.47	0.45
1:A:1532:U:O5'	1:A:1532:U:H6	1.99	0.45
2:B:129:GLU:O	2:B:130:ARG:HB2	2.15	0.45
3:C:157:ILE:HD11	3:C:166:GLU:HB2	1.97	0.45
4:D:61:LYS:HZ1	4:D:62:GLN:NE2	2.14	0.45
6:F:101:ALA:HB2	18:R:28:GLU:HB3	1.97	0.45
7:G:75:VAL:HG12	7:G:86:GLN:HE21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:59:TYR:O	13:M:63:THR:HB	2.16	0.45
14:N:21:TYR:HE2	14:N:23:ARG:HE	1.63	0.45
14:N:39:LEU:CD1	14:N:47:LEU:HD12	2.46	0.45
17:Q:80:GLY:O	17:Q:81:ARG:HB3	2.15	0.45
1:A:755:G:H1'	8:H:1:MET:HE3	1.97	0.45
1:A:882:C:O2'	1:A:883:C:H5'	2.16	0.45
1:A:975:A:H4'	1:A:976:G:OP2	2.16	0.45
1:A:1196:U:H4'	1:A:1197:G:OP2	2.15	0.45
1:A:1305:G:N2	1:A:1331:G:C2'	2.79	0.45
1:A:1318:A:H4'	19:S:10:PHE:CD1	2.51	0.45
2:B:19:HIS:HD2	2:B:189:ASP:OD2	1.99	0.45
2:B:95:GLN:C	2:B:96:ARG:HD2	2.40	0.45
2:B:142:LEU:HB3	2:B:146:GLN:HE22	1.80	0.45
3:C:99:VAL:CG2	3:C:100:ALA:N	2.80	0.45
4:D:63:LYS:O	4:D:64:LEU:C	2.58	0.45
4:D:121:VAL:O	4:D:134:ASP:HA	2.16	0.45
5:E:15:ARG:CD	5:E:26:PHE:CD2	2.99	0.45
5:E:35:GLY:HA3	5:E:112:LEU:HB3	1.97	0.45
8:H:114:THR:C	8:H:116:LYS:H	2.22	0.45
10:J:4:ILE:HG12	10:J:100:THR:CB	2.47	0.45
10:J:8:LEU:HD12	10:J:20:ALA:HB2	1.97	0.45
10:J:51:ARG:HG3	10:J:60:ARG:O	2.17	0.45
11:K:40:ILE:HG23	11:K:75:TYR:CE2	2.51	0.45
11:K:115:PRO:C	11:K:117:ASN:H	2.25	0.45
13:M:49:THR:O	13:M:53:VAL:HG23	2.16	0.45
13:M:51:ALA:O	13:M:55:ARG:HG3	2.16	0.45
14:N:26:ARG:NH1	14:N:47:LEU:HD21	2.32	0.45
1:A:190(B):C:H2'	1:A:190(C):C:O4'	2.17	0.45
1:A:808:C:OP2	15:O:48:LYS:HE2	2.17	0.45
1:A:920:U:H2'	1:A:921:U:C6	2.51	0.45
1:A:975:A:H4'	1:A:976:G:H5'	1.97	0.45
1:A:1216:G:H5''	14:N:5:ALA:HB2	1.99	0.45
1:A:1309:G:N7	13:M:99:ARG:NH2	2.61	0.45
1:A:1435:G:H2'	1:A:1436:U:H6	1.69	0.45
3:C:126:ARG:C	3:C:127:ARG:HG3	2.42	0.45
4:D:4:TYR:O	4:D:5:ILE:HB	2.17	0.45
4:D:78:LEU:HA	4:D:78:LEU:HD23	1.78	0.45
4:D:130:GLY:O	4:D:131:ARG:C	2.58	0.45
5:E:102:ALA:HB2	5:E:120:THR:CB	2.46	0.45
5:E:115:VAL:HG11	5:E:118:ILE:CD1	2.46	0.45
9:I:85:LEU:O	9:I:92:TYR:CD1	2.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:71:GLN:O	15:O:72:ARG:C	2.59	0.45
19:S:63:THR:HG22	19:S:64:GLU:N	2.32	0.45
1:A:113:G:H1'	1:A:354:G:C5'	2.46	0.45
1:A:260:G:O2'	1:A:261:U:H5'	2.16	0.45
1:A:686:U:O4	1:A:703:G:H1'	2.17	0.45
1:A:848:C:H2'	1:A:849:C:H6	1.80	0.45
1:A:1044:A:H2'	1:A:1045:C:C4'	2.46	0.45
1:A:1305:G:C5'	21:V:4:GLY:C	2.90	0.45
1:A:1501:C:OP2	1:A:1504:G:H2'	2.17	0.45
2:B:223:ILE:HG21	2:B:230:VAL:HG23	1.99	0.45
6:F:33:TYR:HB2	6:F:75:LEU:HD23	1.98	0.45
7:G:77:SER:O	7:G:156:TRP:CZ3	2.69	0.45
10:J:54:PHE:O	10:J:55:LYS:HG2	2.17	0.45
18:R:41:LYS:O	18:R:41:LYS:HG2	2.13	0.45
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.51	0.45
19:S:20:LEU:O	19:S:23:ASN:HB2	2.15	0.45
1:A:28:G:O2'	1:A:296:U:OP1	2.33	0.45
1:A:255:G:H1'	17:Q:16:GLN:HE21	1.77	0.45
1:A:439:A:C4	1:A:497:A:C2	3.04	0.45
1:A:533:A:O2'	1:A:534:U:P	2.75	0.45
1:A:797:C:OP1	11:K:124:LYS:HG3	2.17	0.45
1:A:826:C:H2'	1:A:827:U:H6	1.82	0.45
1:A:1019:C:O2'	1:A:1020:U:H5'	2.17	0.45
1:A:1489:G:H2'	1:A:1490:C:C5'	2.27	0.45
2:B:23:ARG:CZ	2:B:23:ARG:HB2	2.47	0.45
2:B:71:VAL:HB	2:B:164:VAL:HG23	1.99	0.45
2:B:137:ARG:O	2:B:140:HIS:HB2	2.16	0.45
4:D:142:PRO:HG2	4:D:187:ARG:NH1	2.32	0.45
5:E:102:ALA:HB2	5:E:120:THR:HB	1.97	0.45
9:I:121:ARG:HG2	9:I:121:ARG:HH11	1.81	0.45
14:N:25:VAL:O	14:N:25:VAL:HG13	2.16	0.45
16:P:20:VAL:CG1	16:P:21:VAL:N	2.76	0.45
18:R:58:LEU:HD22	18:R:62:GLU:HB3	1.99	0.45
19:S:67:VAL:O	19:S:69:HIS:N	2.49	0.45
20:T:42:GLN:O	20:T:45:GLN:HB3	2.16	0.45
1:A:319:G:O2'	1:A:320:C:H5'	2.16	0.45
1:A:474:G:O2'	1:A:475:G:H5'	2.16	0.45
1:A:627:G:O2'	1:A:628:G:H5'	2.17	0.45
1:A:820:U:H4'	1:A:821:G:OP2	2.15	0.45
1:A:976:G:C8	1:A:1358:U:O2	2.70	0.45
1:A:1044:A:H2'	1:A:1045:C:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1279:A:O2'	1:A:1281:U:OP2	2.33	0.45
1:A:1331:G:O2'	1:A:1332:A:OP2	2.31	0.45
2:B:16:HIS:CE1	2:B:210:SER:HG	2.35	0.45
3:C:108:ASN:OD1	3:C:110:ASN:HB2	2.16	0.45
7:G:38:LEU:HD11	7:G:42:ILE:HD11	1.99	0.45
9:I:36:TYR:CD2	9:I:37:PHE:CE2	3.04	0.45
12:L:117:ARG:HD2	12:L:122:THR:OG1	2.17	0.45
14:N:12:ARG:O	14:N:14:PRO:CD	2.65	0.45
16:P:82:GLN:O	16:P:83:GLU:C	2.59	0.45
18:R:47:THR:HG22	18:R:48:GLY:H	1.79	0.45
1:A:22:G:H4'	1:A:885:G:C8	2.51	0.45
1:A:75:G:O2'	1:A:76:C:H5'	2.17	0.45
1:A:197:A:H1'	1:A:198:G:O4'	2.17	0.45
1:A:258:G:H2'	1:A:259:G:H8	1.82	0.45
1:A:645:C:O2'	1:A:646:U:H5'	2.16	0.45
1:A:1060:C:C4	3:C:2:GLY:HA3	2.52	0.45
1:A:1108:G:H4'	1:A:1191:A:O4'	2.17	0.45
1:A:1206:G:C6	1:A:1207:G:C5	3.05	0.45
2:B:100:GLY:O	2:B:104:ASN:N	2.44	0.45
3:C:60:ALA:O	3:C:61:ALA:CB	2.63	0.45
3:C:204:LEU:O	3:C:205:GLY:C	2.59	0.45
4:D:3:ARG:NE	4:D:71:SER:HB3	2.31	0.45
5:E:45:PHE:CD2	5:E:47:LYS:HE3	2.52	0.45
7:G:18:TYR:CD2	7:G:59:LEU:HB2	2.52	0.45
9:I:40:LEU:O	9:I:42:ARG:N	2.50	0.45
10:J:29:ARG:C	10:J:84:GLN:HE22	2.25	0.45
13:M:9:ILE:HD12	13:M:9:ILE:N	2.32	0.45
17:Q:104:LYS:HB3	17:Q:105:ALA:H	1.48	0.45
1:A:411:A:C6	1:A:429:U:C4	3.04	0.45
1:A:452:A:O2'	1:A:453:A:O4'	2.34	0.45
1:A:735:C:O2'	1:A:736:C:H5'	2.17	0.45
1:A:1300:G:O2'	1:A:1301:U:C6	2.70	0.45
1:A:1450:U:H2'	1:A:1452:C:C5	2.52	0.45
2:B:25:ASN:HD22	2:B:27:LYS:H	1.65	0.45
2:B:178:ARG:NH2	8:H:68:ARG:HH22	2.14	0.45
3:C:113:ALA:N	3:C:114:PRO:CD	2.80	0.45
7:G:12:LEU:HD12	7:G:12:LEU:N	2.32	0.45
10:J:27:ALA:CB	10:J:81:THR:HG23	2.47	0.45
10:J:30:SER:CB	10:J:84:GLN:HE21	2.29	0.45
12:L:85:ILE:HG23	12:L:98:TYR:CB	2.46	0.45
14:N:29:ARG:HB3	14:N:40:CYS:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:18:THR:HG23	17:Q:69:LYS:CE	2.47	0.45
17:Q:81:ARG:HG3	17:Q:81:ARG:O	2.17	0.45
18:R:70:ILE:O	18:R:74:ARG:HG3	2.17	0.45
19:S:72:GLY:C	19:S:74:PHE:H	2.25	0.45
1:A:173:U:H5''	1:A:197:A:H5'	1.99	0.45
1:A:188:C:C4'	20:T:89:ARG:NH1	2.80	0.45
1:A:403:C:H2'	1:A:404:U:H6	1.81	0.45
1:A:485:G:C2'	1:A:486:U:OP2	2.65	0.45
1:A:509:A:H5''	4:D:55:ALA:HB2	1.99	0.45
1:A:583:A:H2'	1:A:584:G:O4'	2.17	0.45
1:A:600:C:O2'	1:A:601:C:H5'	2.17	0.45
1:A:718:G:H4'	11:K:117:ASN:HD21	1.81	0.45
1:A:1254:C:OP1	10:J:45:ARG:HD3	2.17	0.45
1:A:1353:G:H2'	1:A:1354:C:H6	1.82	0.45
1:A:1484:C:H2'	1:A:1485:U:C6	2.49	0.45
2:B:88:ALA:C	2:B:90:MET:N	2.71	0.45
2:B:92:TYR:CE1	2:B:151:GLY:HA3	2.51	0.45
3:C:95:THR:C	3:C:97:LYS:N	2.73	0.45
3:C:123:GLN:HE22	3:C:140:ARG:HH22	1.65	0.45
11:K:69:ALA:O	11:K:70:LYS:C	2.60	0.45
15:O:48:LYS:O	15:O:50:HIS:N	2.50	0.45
20:T:100:ILE:C	20:T:102:GLY:N	2.74	0.45
1:A:45:U:H2'	1:A:46:G:C8	2.53	0.44
1:A:1005:A:H2'	1:A:1006:C:O4'	2.17	0.44
1:A:1074:G:O3'	2:B:103:THR:CG2	2.65	0.44
1:A:1347:G:C5	9:I:107:ARG:NH1	2.85	0.44
3:C:188:LEU:O	3:C:189:ALA:CB	2.59	0.44
5:E:13:ILE:HG22	5:E:30:ALA:HB2	1.99	0.44
9:I:117:HIS:C	9:I:118:LYS:HG3	2.41	0.44
11:K:23:ALA:HB2	11:K:91:ARG:HB2	1.99	0.44
13:M:110:ARG:HG2	13:M:110:ARG:HH11	1.82	0.44
16:P:20:VAL:CG1	16:P:32:TYR:CB	2.95	0.44
16:P:55:ARG:O	16:P:58:TYR:HB3	2.17	0.44
1:A:384:G:H2'	1:A:385:C:C6	2.53	0.44
1:A:662:G:H2'	1:A:663:A:H8	1.79	0.44
1:A:981:U:H5'	14:N:21:TYR:CE1	2.53	0.44
1:A:1266:G:N2	1:A:1269:A:OP2	2.49	0.44
1:A:1372:U:O2'	1:A:1373:G:H5'	2.18	0.44
1:A:1503:A:O2'	1:A:1504:G:P	2.75	0.44
2:B:107:THR:C	2:B:109:SER:N	2.75	0.44
3:C:28:GLN:O	3:C:31:HIS:N	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:8:VAL:HG21	4:D:115:ARG:CZ	2.46	0.44
5:E:80:ILE:CD1	5:E:91:LEU:HD12	2.46	0.44
7:G:143:ARG:O	7:G:145:ALA:O	2.34	0.44
10:J:68:HIS:N	10:J:68:HIS:CD2	2.85	0.44
13:M:84:ILE:HG13	13:M:86:CYS:HB2	2.00	0.44
13:M:84:ILE:HG21	19:S:65:ASN:HD22	1.81	0.44
14:N:23:ARG:HD3	14:N:30:ALA:HB2	1.99	0.44
15:O:87:ILE:CG2	15:O:88:ARG:N	2.80	0.44
1:A:691:G:O2'	1:A:797:C:H4'	2.17	0.44
1:A:792:A:H1'	1:A:794:A:N7	2.31	0.44
1:A:865:A:H2'	1:A:866:C:C6	2.53	0.44
1:A:950:U:H2'	1:A:951:G:C8	2.52	0.44
1:A:1097:C:H2'	1:A:1098:C:H6	1.82	0.44
1:A:1263:C:H2'	1:A:1264:C:H6	1.83	0.44
3:C:11:ARG:NH1	3:C:177:THR:O	2.50	0.44
3:C:46:GLU:C	3:C:48:TYR:H	2.22	0.44
5:E:119:LEU:HD23	5:E:119:LEU:HA	1.84	0.44
5:E:143:ARG:NH1	8:H:77:GLU:CD	2.75	0.44
6:F:40:VAL:CG2	6:F:41:GLU:N	2.80	0.44
9:I:103:THR:HG22	9:I:104:ARG:N	2.31	0.44
10:J:8:LEU:CD1	10:J:20:ALA:HB2	2.48	0.44
10:J:46:ARG:NH1	10:J:64:GLU:CG	2.80	0.44
10:J:85:LEU:O	10:J:87:THR:N	2.50	0.44
16:P:20:VAL:HG13	16:P:21:VAL:N	2.32	0.44
16:P:43:LYS:HA	16:P:48:TRP:HB3	2.00	0.44
20:T:24:LEU:HD12	20:T:24:LEU:O	2.17	0.44
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.52	0.44
1:A:644:G:O2'	1:A:645:C:H5'	2.17	0.44
1:A:807:A:H2'	1:A:808:C:C6	2.52	0.44
1:A:975:A:O5'	1:A:976:G:H5'	2.17	0.44
1:A:1289:A:H2'	1:A:1290:G:H5'	2.00	0.44
1:A:1299:A:C8	1:A:1301:U:H1'	2.53	0.44
2:B:54:THR:O	2:B:57:PHE:HB3	2.18	0.44
3:C:6:HIS:CD2	3:C:8:ILE:H	2.36	0.44
8:H:114:THR:C	8:H:116:LYS:N	2.75	0.44
9:I:46:ALA:O	9:I:49:PRO:HD2	2.17	0.44
10:J:3:LYS:CA	10:J:75:ILE:HA	2.48	0.44
14:N:9:LYS:HG3	14:N:21:TYR:O	2.17	0.44
17:Q:68:ARG:H	17:Q:70:ARG:NH1	2.15	0.44
17:Q:104:LYS:O	17:Q:105:ALA:CB	2.65	0.44
20:T:30:LYS:O	20:T:33:ILE:HB	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:100:ILE:O	20:T:102:GLY:N	2.50	0.44
1:A:389:A:H2'	1:A:390:C:C5'	2.48	0.44
1:A:393:A:C2'	1:A:394:G:H5'	2.47	0.44
1:A:460:A:N7	1:A:462:G:C6	2.85	0.44
1:A:663:A:H5''	18:R:61:LYS:HE3	1.99	0.44
1:A:1319:A:H5''	19:S:5:LEU:HD21	1.98	0.44
4:D:24:GLU:CG	4:D:25:ARG:H	2.31	0.44
7:G:145:ALA:C	7:G:147:ALA:H	2.25	0.44
10:J:72:VAL:O	10:J:73:ASP:HB2	2.18	0.44
11:K:51:LYS:O	11:K:55:LYS:CE	2.65	0.44
13:M:34:LEU:HD13	13:M:41:PRO:CA	2.45	0.44
13:M:39:ILE:HD12	13:M:56:LEU:HG	1.98	0.44
15:O:82:ILE:O	15:O:83:GLU:C	2.61	0.44
19:S:45:VAL:C	19:S:47:HIS:H	2.25	0.44
20:T:42:GLN:HA	20:T:45:GLN:HB2	1.99	0.44
1:A:50:A:N6	1:A:361:G:H4'	2.33	0.44
1:A:321:A:H2'	1:A:322:C:C6	2.52	0.44
1:A:532:A:H2'	1:A:533:A:C5'	2.48	0.44
1:A:962:C:H2'	1:A:963:G:O4'	2.18	0.44
1:A:1391:U:H2'	1:A:1392:G:H8	1.74	0.44
3:C:12:LEU:HD23	3:C:12:LEU:HA	1.76	0.44
7:G:95:ARG:NH1	7:G:95:ARG:CG	2.80	0.44
9:I:50:LEU:C	9:I:52:ALA:H	2.26	0.44
10:J:6:ILE:O	10:J:71:LEU:O	2.35	0.44
10:J:30:SER:HB3	10:J:84:GLN:NE2	2.31	0.44
13:M:110:ARG:HH11	13:M:110:ARG:CG	2.31	0.44
18:R:25:THR:O	18:R:25:THR:HG22	2.17	0.44
1:A:927:G:H4'	1:A:1503:A:N7	2.32	0.44
1:A:1010:G:O2'	1:A:1011:G:H5'	2.18	0.44
1:A:1095:U:H2'	1:A:1096:C:H6	1.83	0.44
4:D:8:VAL:HG11	4:D:21:LEU:CB	2.47	0.44
9:I:10:ARG:O	9:I:11:LYS:C	2.60	0.44
9:I:121:ARG:C	9:I:121:ARG:HD3	2.42	0.44
11:K:95:ILE:HD13	11:K:108:ILE:HG21	1.99	0.44
13:M:120:LYS:HE2	13:M:123:ALA:CB	2.47	0.44
17:Q:76:LEU:C	17:Q:76:LEU:CD2	2.90	0.44
20:T:63:ILE:HD13	20:T:80:ARG:CB	2.48	0.44
1:A:116:A:H2'	1:A:117:G:O4'	2.17	0.44
1:A:397:A:H3'	1:A:397:A:N3	2.32	0.44
1:A:540:G:H2'	1:A:541:G:O4'	2.18	0.44
1:A:755:G:OP2	15:O:65:ARG:HD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1152:A:H2'	1:A:1153:C:H6	1.83	0.44
1:A:1440:C:H2'	1:A:1441:G:C5'	2.48	0.44
2:B:219:VAL:O	2:B:220:ASP:C	2.61	0.44
5:E:36:ASP:OD2	5:E:40:ARG:HD3	2.18	0.44
8:H:7:ALA:HB2	8:H:85:ARG:HD2	1.99	0.44
8:H:73:ASP:OD2	8:H:75:ARG:HB2	2.18	0.44
8:H:103:VAL:HG21	8:H:109:ILE:O	2.18	0.44
9:I:93:ARG:CD	9:I:97:LYS:HE3	2.47	0.44
10:J:81:THR:C	10:J:83:GLU:N	2.76	0.44
12:L:111:LYS:O	12:L:112:ASP:HB2	2.18	0.44
13:M:80:ARG:C	13:M:82:MET:N	2.73	0.44
16:P:6:LEU:HB3	16:P:17:TYR:HD2	1.81	0.44
16:P:39:TYR:CZ	16:P:41:PRO:HA	2.52	0.44
20:T:72:LEU:O	20:T:73:HIS:O	2.35	0.44
1:A:582:U:O4'	17:Q:105:ALA:HA	2.17	0.44
1:A:665:A:H2'	1:A:725:G:N2	2.33	0.44
1:A:953:G:H1'	13:M:125:ARG:HB3	1.99	0.44
1:A:1231:G:OP1	9:I:127:LYS:NZ	2.50	0.44
1:A:1288:A:O4'	1:A:1353:G:H4'	2.18	0.44
1:A:1314:C:OP2	19:S:6:LYS:CD	2.66	0.44
3:C:188:LEU:HD22	3:C:188:LEU:HA	1.79	0.44
5:E:78:HIS:HD2	8:H:107:LEU:HD12	1.83	0.44
6:F:22:GLU:OE2	6:F:84:ASN:HB2	2.18	0.44
10:J:75:ILE:HG22	10:J:76:ASN:N	2.32	0.44
12:L:70:ILE:CD1	12:L:77:LEU:HD12	2.42	0.44
13:M:123:ALA:O	13:M:124:PRO:C	2.60	0.44
15:O:27:VAL:O	15:O:28:GLN:C	2.61	0.44
15:O:29:VAL:HG11	15:O:67:LEU:HD21	2.00	0.44
19:S:10:PHE:C	19:S:10:PHE:HD2	2.26	0.44
1:A:80:G:C2'	1:A:81:U:H5''	2.48	0.43
1:A:104:G:N7	20:T:14:LYS:NZ	2.63	0.43
1:A:677:U:O2	1:A:777:A:O2'	2.33	0.43
1:A:1131:G:H2'	1:A:1132:C:H6	1.82	0.43
1:A:1229:A:H2'	1:A:1230:C:H6	1.83	0.43
1:A:1314:C:H2'	1:A:1315:U:C6	2.53	0.43
1:A:1533:C:O2	1:A:1533:C:H2'	2.17	0.43
2:B:107:THR:C	2:B:109:SER:H	2.25	0.43
4:D:10:ARG:HH11	4:D:10:ARG:HG3	1.83	0.43
7:G:78:ARG:HG2	7:G:80:VAL:HG23	1.99	0.43
9:I:69:GLY:O	9:I:73:GLN:HG3	2.18	0.43
15:O:54:ARG:O	15:O:58:MET:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:15:ARG:O	21:V:17:THR:HG23	2.18	0.43
1:A:192:U:H1'	20:T:103:GLY:HA2	1.99	0.43
1:A:409:G:OP1	4:D:24:GLU:O	2.36	0.43
1:A:1051:C:H2'	1:A:1052:U:C6	2.53	0.43
1:A:1128:C:O2'	1:A:1130:A:C8	2.62	0.43
2:B:92:TYR:CD1	2:B:151:GLY:HA3	2.53	0.43
2:B:204:ASN:HD22	2:B:206:ASP:H	1.66	0.43
3:C:99:VAL:HG22	3:C:100:ALA:O	2.18	0.43
3:C:134:ILE:HG22	3:C:168:ALA:CB	2.48	0.43
4:D:55:ALA:O	4:D:59:ARG:HG2	2.19	0.43
4:D:178:VAL:O	4:D:178:VAL:HG12	2.18	0.43
5:E:118:ILE:CG2	5:E:119:LEU:H	2.27	0.43
7:G:108:ALA:O	7:G:119:ARG:HD2	2.18	0.43
11:K:50:TYR:N	11:K:50:TYR:CD2	2.84	0.43
16:P:20:VAL:HG13	16:P:32:TYR:HB2	2.00	0.43
18:R:37:VAL:O	18:R:41:LYS:HB3	2.18	0.43
1:A:253:U:H2'	1:A:254:G:C8	2.53	0.43
1:A:363:A:O2'	1:A:364:A:H5'	2.18	0.43
1:A:564:C:H5'	12:L:10:LEU:HD13	2.01	0.43
1:A:718:G:C8	11:K:116:HIS:HB3	2.53	0.43
1:A:838:G:C3'	1:A:839:U:H5''	2.48	0.43
1:A:1113:C:H1'	3:C:178:LEU:HD21	1.99	0.43
1:A:1497:G:C2'	1:A:1498:U:C5'	2.87	0.43
2:B:119:GLU:OE1	2:B:153:ARG:NH2	2.51	0.43
3:C:19:GLU:HB3	3:C:40:ARG:NH2	2.25	0.43
3:C:123:GLN:HE22	3:C:140:ARG:NH2	2.16	0.43
4:D:24:GLU:HG2	4:D:25:ARG:H	1.82	0.43
4:D:61:LYS:HZ2	4:D:62:GLN:NE2	2.13	0.43
7:G:24:THR:HA	7:G:27:ILE:HD12	2.00	0.43
8:H:16:ALA:O	8:H:21:LYS:HG2	2.18	0.43
11:K:85:ARG:HG3	11:K:85:ARG:NH1	2.33	0.43
11:K:100:ALA:O	11:K:102:GLY:N	2.51	0.43
16:P:67:THR:CG2	16:P:68:ASP:N	2.82	0.43
1:A:267:C:H2'	1:A:268:C:C6	2.53	0.43
1:A:430:A:H2'	1:A:431:A:H5'	1.99	0.43
1:A:1053:G:O2'	1:A:1199:U:H5	2.01	0.43
2:B:10:LEU:CD2	2:B:48:MET:HE2	2.48	0.43
2:B:83:MET:HG3	2:B:238:LEU:HD11	2.00	0.43
3:C:188:LEU:HD13	3:C:189:ALA:H	1.83	0.43
5:E:143:ARG:HD3	5:E:143:ARG:HA	1.71	0.43
6:F:15:ASP:O	6:F:16:GLN:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:86:ILE:HD12	8:H:133:LEU:HD22	2.00	0.43
10:J:56:HIS:O	10:J:58:ASP:N	2.52	0.43
12:L:7:ILE:O	12:L:11:VAL:HG23	2.18	0.43
1:A:16:A:O2'	1:A:17:U:H5'	2.18	0.43
1:A:383:A:H2'	1:A:384:G:H5'	1.99	0.43
1:A:618:C:N3	1:A:622:A:N6	2.67	0.43
1:A:1031:G:H2'	1:A:1032:G:H8	1.83	0.43
1:A:1152:A:OP1	10:J:13:HIS:HB2	2.19	0.43
1:A:1286:A:H4'	21:V:25:LYS:HE3	2.01	0.43
2:B:17:PHE:H	2:B:44:LEU:HD21	1.83	0.43
2:B:146:GLN:O	2:B:150:SER:HB3	2.18	0.43
3:C:82:GLU:CD	3:C:82:GLU:C	2.87	0.43
4:D:15:GLU:C	4:D:17:VAL:N	2.76	0.43
12:L:60:LEU:CD2	12:L:66:VAL:HG22	2.49	0.43
13:M:23:TYR:CE2	13:M:70:LEU:HD13	2.53	0.43
15:O:17:ARG:HH11	15:O:17:ARG:CG	2.26	0.43
16:P:75:ARG:O	16:P:78:GLY:N	2.49	0.43
18:R:26:LEU:HD21	18:R:39:VAL:HG23	2.00	0.43
19:S:12:ASP:HB2	19:S:35:SER:OG	2.19	0.43
20:T:50:GLU:HG2	20:T:100:ILE:CG1	2.47	0.43
1:A:137:C:O2'	1:A:138:G:H5'	2.17	0.43
1:A:143:A:H2	1:A:220:G:H22	1.66	0.43
1:A:436:C:H2'	1:A:437:U:C6	2.53	0.43
1:A:437:U:O2'	4:D:123:HIS:HD2	2.02	0.43
1:A:502:G:C1'	1:A:550:G:H5'	2.49	0.43
1:A:640:A:C2'	1:A:641:U:H5'	2.48	0.43
1:A:765:G:N2	1:A:812:C:O2'	2.51	0.43
1:A:961:U:C2'	1:A:962:C:H5'	2.48	0.43
1:A:1125:U:H5''	1:A:1126:U:H5	1.83	0.43
1:A:1305:G:N2	1:A:1331:G:HO2'	2.16	0.43
1:A:1346:A:C4	7:G:10:ARG:CZ	3.02	0.43
2:B:28:PHE:CD2	2:B:190:THR:HA	2.54	0.43
3:C:70:VAL:HG12	3:C:71:ALA:H	1.84	0.43
4:D:25:ARG:HH21	4:D:30:LYS:HD3	1.82	0.43
4:D:198:VAL:HG12	4:D:199:ASN:N	2.33	0.43
7:G:75:VAL:HG13	7:G:86:GLN:HB3	1.94	0.43
11:K:127:LYS:HD3	11:K:127:LYS:HA	1.78	0.43
15:O:15:PHE:O	15:O:16:ALA:C	2.61	0.43
19:S:8:GLY:O	19:S:9:VAL:C	2.62	0.43
1:A:433:C:O2'	1:A:434:U:H5'	2.18	0.43
1:A:448:A:C4	1:A:487:A:C2	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:628:G:H2'	1:A:629:G:H8	1.84	0.43
1:A:851:G:H2'	1:A:852:G:H8	1.84	0.43
1:A:1399:C:C2	1:A:1502:A:N6	2.86	0.43
2:B:14:GLY:C	2:B:15:VAL:HG23	2.44	0.43
2:B:41:ILE:O	2:B:41:ILE:HG22	2.19	0.43
2:B:90:MET:HA	2:B:91:PRO:HD3	1.70	0.43
2:B:130:ARG:HH22	3:C:207:VAL:HG22	1.82	0.43
3:C:116:VAL:HG11	3:C:141:VAL:HG21	2.01	0.43
3:C:191:THR:HB	3:C:194:GLY:O	2.18	0.43
3:C:193:TYR:HE1	3:C:196:LEU:HD11	1.83	0.43
4:D:127:THR:HG23	4:D:128:VAL:N	2.34	0.43
5:E:6:PHE:CZ	5:E:66:MET:HE2	2.53	0.43
9:I:56:LEU:HB3	9:I:57:GLY:H	1.74	0.43
9:I:106:ALA:O	9:I:108:VAL:HG23	2.19	0.43
16:P:40:ASP:HB3	16:P:48:TRP:HB2	2.00	0.43
17:Q:97:SER:O	17:Q:98:LEU:HD12	2.19	0.43
20:T:63:ILE:HD13	20:T:80:ARG:HB3	2.01	0.43
1:A:254:G:O2'	1:A:255:G:H5'	2.18	0.43
1:A:487:A:H2'	1:A:488:C:O4'	2.19	0.43
1:A:552:U:H4'	12:L:86:ARG:O	2.19	0.43
1:A:652:U:H2'	1:A:752:G:N1	2.33	0.43
1:A:718:G:H1'	11:K:116:HIS:HA	2.00	0.43
1:A:730:G:C5	1:A:731:G:H1'	2.54	0.43
1:A:913:A:O2'	1:A:914:A:OP2	2.36	0.43
1:A:991:U:O2	1:A:993:G:H8	2.02	0.43
1:A:1064:G:H1'	1:A:1190:G:H21	1.84	0.43
1:A:1135:U:H6	1:A:1135:U:O5'	2.01	0.43
1:A:1305:G:H5''	21:V:4:GLY:C	2.43	0.43
1:A:1376:U:H2'	1:A:1377:A:H8	1.80	0.43
2:B:137:ARG:HA	2:B:140:HIS:HD2	1.84	0.43
4:D:120:LEU:HD23	4:D:125:HIS:CD2	2.54	0.43
5:E:105:VAL:HB	5:E:106:PRO:CD	2.40	0.43
11:K:46:GLY:O	11:K:47:VAL:C	2.62	0.43
11:K:77:MET:CE	11:K:80:VAL:HG22	2.48	0.43
14:N:14:PRO:O	14:N:16:PHE:N	2.44	0.43
15:O:78:TYR:CE2	15:O:82:ILE:HD11	2.53	0.43
16:P:80:PHE:O	16:P:81:ARG:C	2.60	0.43
19:S:3:ARG:O	19:S:4:SER:HB3	2.18	0.43
1:A:157:G:O2'	1:A:158:G:H5'	2.18	0.43
1:A:782:A:H2'	1:A:783:C:O4'	2.19	0.43
1:A:1004:A:H5''	1:A:1025:U:C4	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1441:G:H4'	1:A:1442:G:C8	2.54	0.43
1:A:1504:G:OP1	1:A:1507:A:H4'	2.19	0.43
3:C:7:PRO:HG2	3:C:184:TYR:CB	2.45	0.43
6:F:77:ARG:O	6:F:81:ILE:HG13	2.18	0.43
7:G:148:ASN:C	7:G:150:ALA:H	2.26	0.43
10:J:46:ARG:HH11	10:J:64:GLU:CG	2.31	0.43
13:M:33:ALA:HB2	13:M:64:TRP:CH2	2.54	0.43
17:Q:60:ILE:HD13	17:Q:61:GLU:N	2.34	0.43
19:S:40:ILE:HG23	19:S:44:MET:SD	2.59	0.43
1:A:359:U:O2'	1:A:360:A:H5'	2.18	0.43
1:A:718:G:H4'	11:K:117:ASN:ND2	2.34	0.43
1:A:719:C:O2	18:R:50:ILE:HG13	2.19	0.43
1:A:858:G:O2'	1:A:859:A:H5'	2.18	0.43
1:A:960:U:O2	1:A:960:U:H2'	2.18	0.43
1:A:1126:U:H2'	1:A:1127:G:O4'	2.19	0.43
1:A:1262:C:H2'	1:A:1263:C:C6	2.54	0.43
1:A:1270:C:H4'	1:A:1313:U:O2'	2.19	0.43
1:A:1288:A:H1'	1:A:1353:G:O4'	2.18	0.43
1:A:1331:G:O2'	1:A:1332:A:P	2.76	0.43
1:A:1438:G:H2'	1:A:1439:C:C6	2.54	0.43
2:B:74:LYS:HD2	2:B:166:ASP:HB2	2.00	0.43
3:C:28:GLN:O	3:C:29:TYR:C	2.62	0.43
4:D:104:VAL:O	4:D:105:VAL:C	2.59	0.43
5:E:40:ARG:NH1	5:E:68:GLU:OE1	2.51	0.43
8:H:68:ARG:HG2	8:H:68:ARG:HH11	1.84	0.43
9:I:78:LYS:HD3	9:I:101:PHE:CD2	2.54	0.43
16:P:4:ILE:HG23	16:P:36:ILE:HD11	2.01	0.43
16:P:39:TYR:CD2	16:P:73:LEU:HD11	2.54	0.43
17:Q:45:HIS:CD2	17:Q:47:PRO:HG3	2.54	0.43
19:S:25:LYS:HD2	19:S:25:LYS:N	2.34	0.43
21:V:2:GLY:C	21:V:4:GLY:H	2.26	0.43
1:A:176:C:H2'	1:A:177:C:H6	1.83	0.42
1:A:247:G:OP2	17:Q:100:LYS:HG3	2.19	0.42
1:A:370:C:C2'	1:A:371:G:H5'	2.48	0.42
1:A:636:U:H2'	1:A:637:G:C8	2.54	0.42
1:A:942:G:C2	1:A:943:U:C6	3.07	0.42
1:A:994:A:N7	1:A:1216:G:H4'	2.34	0.42
1:A:1104:G:OP1	2:B:111:ARG:HD2	2.18	0.42
1:A:1217:C:O2'	1:A:1218:C:H5'	2.19	0.42
1:A:1305:G:H22	1:A:1331:G:C2'	2.32	0.42
1:A:1397:C:O2'	1:A:1398:A:P	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:11:ARG:O	3:C:14:ILE:O	2.36	0.42
3:C:134:ILE:HD13	3:C:166:GLU:HB3	2.01	0.42
3:C:191:THR:HG21	3:C:193:TYR:CE1	2.53	0.42
5:E:16:THR:HG23	5:E:27:ARG:O	2.19	0.42
5:E:115:VAL:CG1	5:E:116:THR:N	2.82	0.42
9:I:78:LYS:HE2	9:I:78:LYS:HB3	1.87	0.42
9:I:97:LYS:HB2	9:I:98:PRO:HD3	2.01	0.42
10:J:17:ASP:O	10:J:21:GLN:HB2	2.19	0.42
10:J:32:ALA:HB2	10:J:75:ILE:O	2.19	0.42
10:J:55:LYS:O	10:J:56:HIS:HB2	2.19	0.42
11:K:104:GLN:OE1	11:K:106:LYS:HE2	2.19	0.42
12:L:27:LEU:O	12:L:28:LYS:C	2.63	0.42
19:S:20:LEU:HD12	19:S:21:GLU:N	2.34	0.42
1:A:413:G:N2	1:A:428:G:H1'	2.34	0.42
1:A:451:A:N6	1:A:480:U:H2'	2.33	0.42
1:A:647:C:H2'	1:A:648:A:C8	2.54	0.42
3:C:74:GLY:O	3:C:75:VAL:C	2.62	0.42
4:D:8:VAL:CG1	4:D:21:LEU:HD13	2.49	0.42
5:E:24:ARG:HG2	5:E:24:ARG:NH1	2.32	0.42
5:E:80:ILE:HD12	5:E:80:ILE:H	1.84	0.42
10:J:53:PRO:O	10:J:54:PHE:C	2.62	0.42
11:K:21:ILE:HD12	11:K:95:ILE:HG12	2.00	0.42
1:A:80:G:H2'	1:A:81:U:H5''	2.01	0.42
1:A:243:A:N6	1:A:281:G:O2'	2.51	0.42
1:A:418:C:H2'	1:A:419:C:H6	1.84	0.42
1:A:512:U:H1'	4:D:42:GLN:OE1	2.19	0.42
1:A:522:C:O2'	1:A:523:A:H5'	2.19	0.42
1:A:545:C:O2'	1:A:549:C:OP1	2.37	0.42
1:A:640:A:O2'	1:A:641:U:H5'	2.20	0.42
1:A:1126:U:H2'	1:A:1127:G:H8	1.84	0.42
1:A:1157:A:O4'	1:A:1158:C:C2	2.72	0.42
1:A:1347:G:HO2'	1:A:1373:G:H1	1.66	0.42
2:B:25:ASN:C	2:B:25:ASN:ND2	2.68	0.42
2:B:43:ASP:C	2:B:43:ASP:OD1	2.61	0.42
3:C:50:ALA:O	3:C:70:VAL:CG1	2.67	0.42
6:F:75:LEU:O	6:F:75:LEU:HD13	2.18	0.42
7:G:31:MET:SD	7:G:34:GLY:HA2	2.60	0.42
12:L:33:ARG:HD2	12:L:62:SER:HB3	2.01	0.42
17:Q:59:ILE:CG2	17:Q:71:PHE:CD1	3.02	0.42
1:A:160:A:H2'	1:A:161:A:O4'	2.18	0.42
1:A:162:A:H2'	1:A:163:C:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:U:O4	1:A:223:U:H1'	2.20	0.42
1:A:409:G:H2'	1:A:410:G:O4'	2.18	0.42
1:A:1230:C:H1'	13:M:125:ARG:O	2.19	0.42
6:F:19:LEU:HD21	6:F:23:LYS:HD2	2.01	0.42
10:J:12:ASP:OD1	10:J:14:LYS:N	2.50	0.42
13:M:7:VAL:O	13:M:7:VAL:HG23	2.18	0.42
14:N:23:ARG:C	14:N:33:VAL:HG11	2.44	0.42
15:O:39:LEU:HD12	15:O:59:MET:CE	2.48	0.42
1:A:833:U:H2'	1:A:834:C:C6	2.55	0.42
1:A:839:U:C5'	1:A:840:C:H5	2.27	0.42
1:A:942:G:H2'	1:A:943:U:H6	1.84	0.42
1:A:1057:G:H4'	3:C:197:GLY:H	1.85	0.42
1:A:1060:C:O2'	1:A:1061:G:H5'	2.18	0.42
1:A:1129:C:O2'	1:A:1130:A:P	2.78	0.42
1:A:1346:A:C8	7:G:10:ARG:NH2	2.87	0.42
3:C:14:ILE:O	3:C:15:THR:C	2.62	0.42
4:D:25:ARG:C	4:D:27:TYR:N	2.55	0.42
6:F:30:LEU:HB3	6:F:35:ALA:CB	2.41	0.42
10:J:22:LYS:HZ3	10:J:91:PRO:HD3	1.84	0.42
11:K:93:GLN:NE2	11:K:96:ARG:NH2	2.67	0.42
14:N:12:ARG:C	14:N:14:PRO:HD3	2.44	0.42
16:P:76:GLN:C	16:P:78:GLY:H	2.28	0.42
20:T:10:LEU:C	20:T:12:ALA:H	2.26	0.42
21:V:9:ARG:HH11	21:V:22:ARG:HA	1.85	0.42
1:A:173:U:C5'	1:A:197:A:O4'	2.65	0.42
1:A:523:A:C2	12:L:91:LYS:HB3	2.54	0.42
1:A:825:G:H2'	1:A:826:C:C6	2.53	0.42
1:A:977:A:H2'	1:A:978:A:C5'	2.45	0.42
1:A:1181:G:O2'	1:A:1182:G:H5'	2.19	0.42
1:A:1244:C:O2'	1:A:1245:A:H5'	2.19	0.42
1:A:1353:G:H2'	1:A:1354:C:C6	2.54	0.42
2:B:17:PHE:CA	2:B:44:LEU:HD21	2.49	0.42
2:B:73:THR:O	2:B:74:LYS:C	2.61	0.42
2:B:187:LEU:HD21	2:B:214:ILE:HG13	2.00	0.42
3:C:23:TYR:OH	10:J:9:ARG:HD3	2.20	0.42
4:D:70:ILE:HD11	4:D:100:ARG:CD	2.49	0.42
6:F:40:VAL:HG22	6:F:41:GLU:N	2.34	0.42
7:G:15:ASP:OD2	7:G:23:VAL:HG11	2.19	0.42
8:H:75:ARG:HA	8:H:76:PRO:HD3	1.70	0.42
10:J:32:ALA:CB	10:J:76:ASN:HD22	2.30	0.42
11:K:57:THR:OG1	11:K:58:PRO:HD2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:41:ARG:CB	12:L:41:ARG:NH1	2.82	0.42
12:L:41:ARG:HB3	12:L:41:ARG:HH11	1.84	0.42
19:S:41:VAL:HB	19:S:43:GLU:OE2	2.20	0.42
1:A:169:C:O2'	1:A:170:U:H5'	2.19	0.42
1:A:397:A:H5'	1:A:398:C:P	2.60	0.42
1:A:562:C:O2'	12:L:17:LYS:HE3	2.20	0.42
1:A:974:A:P	14:N:41:ARG:HH12	2.42	0.42
1:A:1202:G:C2	14:N:42:ILE:HG21	2.55	0.42
1:A:1327:C:O2'	1:A:1328:C:H5'	2.19	0.42
2:B:14:GLY:C	2:B:15:VAL:CG2	2.92	0.42
2:B:22:LYS:HD2	2:B:35:GLU:CD	2.45	0.42
3:C:64:VAL:HG12	3:C:65:ALA:H	1.84	0.42
6:F:100:ASN:ND2	18:R:23:LYS:O	2.52	0.42
7:G:38:LEU:HD12	7:G:42:ILE:HG13	2.00	0.42
9:I:110:GLU:HG2	9:I:113:LYS:NZ	2.35	0.42
13:M:96:LEU:HB3	13:M:97:PRO:HD2	2.01	0.42
15:O:38:ARG:O	15:O:41:GLU:HB3	2.20	0.42
1:A:418:C:H2'	1:A:419:C:C6	2.54	0.42
1:A:502:G:H2'	1:A:503:C:H6	1.84	0.42
1:A:1271:G:H5'	1:A:1314:C:OP1	2.20	0.42
1:A:1277:C:H1'	1:A:1282:C:O2	2.20	0.42
1:A:1505:G:H3'	1:A:1505:G:H8	1.85	0.42
2:B:8:LYS:O	2:B:9:GLU:CB	2.60	0.42
2:B:87:ARG:NH2	2:B:220:ASP:OD1	2.51	0.42
2:B:187:LEU:HA	2:B:201:ILE:HB	2.02	0.42
4:D:25:ARG:HA	4:D:28:SER:OG	2.19	0.42
4:D:60:GLU:OE1	4:D:60:GLU:HA	2.19	0.42
18:R:48:GLY:O	18:R:74:ARG:NH2	2.41	0.42
1:A:252:U:O2'	1:A:275:G:N2	2.53	0.42
1:A:413:G:H22	1:A:428:G:H1'	1.85	0.42
1:A:528:C:H41	12:L:49:ASN:CG	2.28	0.42
1:A:602:A:C2	1:A:637:G:C2	3.08	0.42
1:A:815:A:N6	1:A:1509:C:H1'	2.35	0.42
1:A:825:G:O2'	1:A:826:C:H5'	2.20	0.42
1:A:930:C:O2'	1:A:931:C:H5'	2.20	0.42
1:A:951:G:C6	1:A:1231:G:C6	3.08	0.42
1:A:965:A:O2'	1:A:966:G:C5'	2.67	0.42
1:A:965:A:C2	13:M:124:PRO:HB2	2.55	0.42
1:A:1056:U:H5'	3:C:163:ALA:HB2	2.02	0.42
1:A:1091:U:O2	1:A:1093:A:H8	2.03	0.42
1:A:1375:A:OP1	7:G:12:LEU:HD21	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:LYS:HB2	2:B:9:GLU:H	1.58	0.42
4:D:8:VAL:CG1	4:D:21:LEU:CD1	2.98	0.42
4:D:89:THR:O	4:D:90:GLY:C	2.61	0.42
5:E:43:LEU:N	5:E:136:MET:HE2	2.35	0.42
5:E:80:ILE:HD12	5:E:91:LEU:HB2	2.00	0.42
5:E:131:ILE:HD13	5:E:131:ILE:HA	1.93	0.42
6:F:45:LEU:O	6:F:46:ARG:HG2	2.20	0.42
11:K:86:GLY:H	11:K:112:THR:CG2	2.32	0.42
13:M:16:ASP:O	13:M:17:VAL:C	2.63	0.42
18:R:17:SER:HB2	18:R:54:ARG:HH21	1.85	0.42
20:T:54:LYS:HA	20:T:57:ARG:HD3	2.02	0.42
1:A:145:G:O2'	1:A:146:G:H5'	2.20	0.42
1:A:373:A:H2'	1:A:374:A:H8	1.85	0.42
1:A:521:G:OP1	12:L:73:GLU:O	2.38	0.42
1:A:584:G:H2'	1:A:585:G:C8	2.54	0.42
1:A:974:A:OP1	1:A:974:A:H8	2.03	0.42
1:A:1260:C:H4'	1:A:1284:C:H5'	2.01	0.42
1:A:1306:A:O2'	13:M:109:THR:HG21	2.19	0.42
1:A:1531:A:O5'	1:A:1531:A:H8	2.03	0.42
3:C:134:ILE:HG22	3:C:168:ALA:HB3	2.01	0.42
3:C:139:GLN:O	3:C:140:ARG:C	2.62	0.42
5:E:21:ALA:C	5:E:23:GLY:N	2.77	0.42
5:E:24:ARG:O	5:E:25:ARG:HG2	2.20	0.42
7:G:38:LEU:HD12	7:G:38:LEU:C	2.45	0.42
9:I:56:LEU:O	9:I:58:ARG:N	2.49	0.42
11:K:32:ILE:HG21	11:K:77:MET:HE2	2.01	0.42
11:K:111:ASP:CG	18:R:84:LYS:HE2	2.45	0.42
17:Q:40:LYS:HD3	17:Q:42:TYR:OH	2.20	0.42
17:Q:63:ARG:O	17:Q:64:PRO:C	2.63	0.42
17:Q:95:TYR:N	17:Q:95:TYR:CD1	2.88	0.42
18:R:51:LEU:HA	18:R:52:PRO:HD3	1.80	0.42
20:T:42:GLN:O	20:T:46:GLU:HG3	2.19	0.42
20:T:53:LEU:HD13	20:T:101:GLY:N	2.35	0.42
21:V:7:ARG:O	21:V:7:ARG:HG3	2.19	0.42
1:A:490:G:H2'	1:A:491:G:C8	2.54	0.41
1:A:761:G:O2'	17:Q:104:LYS:HA	2.20	0.41
1:A:767:A:H2'	1:A:768:A:O4'	2.20	0.41
1:A:1060:C:OP1	14:N:45:ARG:NH2	2.53	0.41
1:A:1264:C:H2'	1:A:1265:G:C8	2.54	0.41
1:A:1407:C:H2'	1:A:1408:A:H8	1.85	0.41
2:B:23:ARG:C	2:B:24:TRP:HD1	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:127:ILE:C	2:B:129:GLU:H	2.28	0.41
3:C:38:ARG:CB	3:C:94:LEU:HD21	2.50	0.41
3:C:77:ILE:CG2	3:C:81:GLY:HA2	2.50	0.41
4:D:205:GLU:O	4:D:208:SER:HB2	2.20	0.41
6:F:42:GLU:C	6:F:44:GLY:N	2.78	0.41
6:F:48:LEU:HD13	6:F:52:ILE:CG1	2.50	0.41
7:G:93:PRO:HG2	7:G:94:ARG:H	1.85	0.41
8:H:6:ILE:O	8:H:10:LEU:HG	2.20	0.41
9:I:120:ARG:O	9:I:122:ALA:N	2.53	0.41
13:M:115:LYS:HZ2	13:M:115:LYS:HB3	1.86	0.41
20:T:80:ARG:O	20:T:84:LEU:HB2	2.20	0.41
1:A:867:G:O2'	1:A:868:C:H5'	2.20	0.41
1:A:961:U:O2'	1:A:962:C:H5'	2.20	0.41
1:A:1034:G:O2'	1:A:1035:A:H5'	2.20	0.41
1:A:1061:G:C2'	1:A:1062:U:H5'	2.50	0.41
1:A:1239:A:C4	1:A:1298:C:N4	2.88	0.41
1:A:1346:A:C5	7:G:10:ARG:CZ	3.02	0.41
1:A:1426:C:H2'	1:A:1427:U:H6	1.84	0.41
2:B:116:GLU:CG	2:B:153:ARG:NH1	2.80	0.41
3:C:61:ALA:O	3:C:62:ASP:C	2.63	0.41
3:C:112:SER:HB2	3:C:115:LEU:HB2	2.01	0.41
3:C:206:GLU:O	3:C:207:VAL:C	2.63	0.41
5:E:36:ASP:OD1	5:E:38:GLN:N	2.39	0.41
7:G:155:ARG:O	7:G:156:TRP:CB	2.64	0.41
9:I:59:PHE:HB3	9:I:60:ASP:H	1.56	0.41
12:L:104:VAL:HG12	12:L:105:TYR:CD1	2.55	0.41
13:M:40:ASN:ND2	13:M:41:PRO:N	2.64	0.41
13:M:67:GLU:HB3	13:M:68:GLY:H	1.58	0.41
1:A:184:G:O4'	1:A:224:C:H4'	2.19	0.41
1:A:489:C:H2'	1:A:490:G:C8	2.54	0.41
1:A:550:G:O2'	1:A:551:U:H5'	2.20	0.41
1:A:628:G:O2'	1:A:629:G:H5'	2.20	0.41
1:A:1137:C:H4'	1:A:1138:G:N1	2.33	0.41
1:A:1264:C:H2'	1:A:1265:G:H8	1.85	0.41
2:B:165:VAL:O	2:B:187:LEU:O	2.38	0.41
4:D:24:GLU:H	4:D:112:VAL:HG11	1.85	0.41
8:H:51:VAL:CG1	8:H:52:ASP:N	2.82	0.41
8:H:108:GLY:CA	8:H:138:TRP:HB3	2.46	0.41
10:J:80:LYS:HA	10:J:83:GLU:HB2	2.03	0.41
15:O:87:ILE:HG22	15:O:88:ARG:N	2.34	0.41
16:P:19:ILE:HG22	16:P:36:ILE:CG1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:C:C6	1:A:365:U:H2'	2.56	0.41
1:A:547:A:H4'	1:A:548:G:O5'	2.19	0.41
1:A:619:U:N3	4:D:134:ASP:OD1	2.52	0.41
1:A:778:G:O2'	1:A:779:C:H5'	2.19	0.41
1:A:1077:G:N2	1:A:1080:A:OP2	2.50	0.41
1:A:1094:G:OP2	1:A:1095:U:C5	2.74	0.41
1:A:1127:G:N2	1:A:1144:G:N2	2.69	0.41
1:A:1213:A:N1	1:A:1215:G:H1'	2.35	0.41
1:A:1262:C:N4	1:A:1273:G:H1	2.18	0.41
1:A:1352:C:OP1	21:V:3:LYS:NZ	2.51	0.41
3:C:70:VAL:O	3:C:106:VAL:N	2.51	0.41
4:D:148:VAL:HG13	4:D:158:ILE:HD13	2.01	0.41
9:I:42:ARG:O	9:I:43:ALA:C	2.63	0.41
13:M:32:GLU:O	13:M:35:GLU:N	2.53	0.41
20:T:57:ARG:HE	20:T:100:ILE:HG21	1.84	0.41
1:A:67:C:O2'	1:A:171:A:H1'	2.20	0.41
1:A:546:G:OP1	4:D:73:ARG:HB2	2.21	0.41
1:A:1126:U:P	1:A:1126:U:H6	2.43	0.41
1:A:1311:G:H2'	1:A:1312:G:O4'	2.20	0.41
1:A:1322:C:OP1	19:S:78:ARG:NH2	2.54	0.41
1:A:1350:A:C6	1:A:1351:U:N3	2.89	0.41
1:A:1371:G:H2'	1:A:1372:U:H6	1.86	0.41
1:A:1393:U:O4'	1:A:1502:A:H5'	2.20	0.41
2:B:142:LEU:O	2:B:143:GLU:C	2.63	0.41
3:C:73:PRO:HD3	3:C:105:GLU:HG3	2.03	0.41
3:C:179:ARG:O	3:C:179:ARG:CG	2.69	0.41
4:D:23:GLY:HA3	4:D:112:VAL:HG13	2.02	0.41
7:G:69:VAL:O	7:G:69:VAL:CG1	2.68	0.41
8:H:126:LYS:O	8:H:128:GLY:N	2.54	0.41
10:J:3:LYS:CG	10:J:75:ILE:HG23	2.50	0.41
12:L:55:VAL:CG1	12:L:67:THR:CG2	2.97	0.41
12:L:117:ARG:O	12:L:118:SER:C	2.64	0.41
18:R:44:LEU:HD23	18:R:44:LEU:HA	1.89	0.41
1:A:625:G:O2'	1:A:626:U:H5'	2.20	0.41
1:A:1145:C:O2'	1:A:1146:A:O5'	2.39	0.41
1:A:1195:C:H3'	1:A:1196:U:H5''	2.02	0.41
1:A:1228:C:H4'	13:M:116:THR:HA	2.02	0.41
1:A:1292:U:P	7:G:41:ARG:NH2	2.94	0.41
1:A:1453:G:H2'	1:A:1454:G:O4'	2.21	0.41
2:B:22:LYS:C	2:B:23:ARG:HG3	2.45	0.41
2:B:90:MET:HE2	2:B:222:ILE:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:58:ALA:O	5:E:59:GLY:C	2.63	0.41
5:E:86:ALA:C	5:E:125:SER:HB3	2.45	0.41
7:G:45:ASP:O	7:G:49:ILE:HG13	2.20	0.41
10:J:3:LYS:HG3	10:J:75:ILE:HG23	2.02	0.41
11:K:65:ALA:O	11:K:68:ALA:HB3	2.20	0.41
15:O:70:LEU:HD12	15:O:78:TYR:HB2	2.01	0.41
16:P:4:ILE:CG1	16:P:64:ALA:HB1	2.49	0.41
1:A:43:C:H2'	1:A:44:G:O4'	2.21	0.41
1:A:736:C:H2'	1:A:737:A:H8	1.83	0.41
1:A:769:G:H4'	1:A:1513:A:H4'	2.02	0.41
1:A:976:G:OP1	14:N:31:ARG:O	2.39	0.41
1:A:1030(A):G:H21	1:A:1030(C):G:H3'	1.84	0.41
5:E:51:VAL:HB	5:E:52:PRO:CD	2.37	0.41
10:J:75:ILE:O	10:J:76:ASN:HB2	2.21	0.41
11:K:86:GLY:N	11:K:112:THR:HG23	2.35	0.41
11:K:99:GLN:HG2	11:K:105:VAL:HG21	2.02	0.41
12:L:60:LEU:HD21	12:L:66:VAL:CG2	2.50	0.41
12:L:83:VAL:HG22	12:L:84:LEU:H	1.86	0.41
17:Q:95:TYR:N	17:Q:95:TYR:HD1	2.18	0.41
20:T:86:ARG:O	20:T:87:LYS:C	2.62	0.41
1:A:107:G:O2'	1:A:108:G:H5'	2.19	0.41
1:A:439:A:N6	1:A:497:A:H1'	2.35	0.41
1:A:519:C:H2'	1:A:520:A:C8	2.56	0.41
1:A:866:C:H2'	1:A:867:G:O4'	2.20	0.41
1:A:913:A:O2'	1:A:914:A:O4'	2.26	0.41
1:A:913:A:H1'	1:A:914:A:O4'	2.21	0.41
1:A:1053:G:C3'	1:A:1054:C:C5'	2.99	0.41
1:A:1203:C:OP1	14:N:2:ALA:HB3	2.20	0.41
1:A:1390:U:H2'	1:A:1391:U:H6	1.86	0.41
1:A:1431:C:H2'	1:A:1432:G:O4'	2.21	0.41
1:A:1460:A:P	20:T:27:LYS:NZ	2.94	0.41
3:C:47:LEU:H	3:C:47:LEU:HD13	1.83	0.41
6:F:48:LEU:HD13	6:F:52:ILE:HD12	2.03	0.41
7:G:23:VAL:HG13	7:G:43:PHE:CE2	2.56	0.41
8:H:82:HIS:O	8:H:83:ILE:HB	2.21	0.41
10:J:53:PRO:HA	14:N:41:ARG:HH21	1.85	0.41
13:M:4:ILE:HG22	13:M:5:ALA:H	1.84	0.41
16:P:43:LYS:HA	16:P:48:TRP:CB	2.51	0.41
18:R:21:LYS:HG3	18:R:57:GLY:CA	2.51	0.41
1:A:134:A:H1'	1:A:325:A:C5	2.56	0.41
1:A:382:A:C2	1:A:383:A:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:C:H2'	1:A:437:U:H6	1.86	0.41
1:A:570:G:H1'	1:A:820:U:C4	2.56	0.41
1:A:692:U:O2	1:A:695:A:C8	2.73	0.41
1:A:836:G:C6	1:A:851:G:C6	3.09	0.41
1:A:1057:G:H2'	1:A:1058:G:O4'	2.20	0.41
1:A:1116:C:O2'	9:I:108:VAL:HG21	2.21	0.41
1:A:1118:C:H1'	1:A:1179:A:C4	2.56	0.41
1:A:1191:A:H2'	1:A:1192:C:H6	1.84	0.41
1:A:1231:G:H5''	9:I:126:SER:HB3	2.01	0.41
1:A:1286:A:H2'	1:A:1287:A:O5'	2.21	0.41
1:A:1495:U:H2'	1:A:1496:C:H6	1.83	0.41
2:B:14:GLY:O	2:B:15:VAL:HG22	2.21	0.41
2:B:15:VAL:HG11	2:B:210:SER:N	2.36	0.41
2:B:134:GLU:HG2	2:B:137:ARG:HH21	1.86	0.41
3:C:57:ILE:O	3:C:57:ILE:HG22	2.20	0.41
3:C:67:THR:O	3:C:67:THR:HG22	2.21	0.41
3:C:89:GLU:C	3:C:91:LEU:N	2.76	0.41
4:D:124:GLY:C	4:D:126:ILE:H	2.29	0.41
4:D:167:GLY:O	4:D:168:ARG:C	2.63	0.41
5:E:40:ARG:NH1	5:E:68:GLU:OE2	2.49	0.41
5:E:118:ILE:HD13	5:E:118:ILE:HG21	1.74	0.41
5:E:152:ARG:NH2	8:H:107:LEU:O	2.54	0.41
6:F:33:TYR:HA	6:F:71:ARG:NH2	2.36	0.41
9:I:108:VAL:HG12	9:I:109:VAL:N	2.36	0.41
9:I:110:GLU:OE2	9:I:113:LYS:NZ	2.53	0.41
9:I:114:TYR:C	9:I:116:LYS:H	2.29	0.41
10:J:28:ARG:C	10:J:29:ARG:HG3	2.46	0.41
11:K:67:ASP:OD2	11:K:71:LYS:HE3	2.21	0.41
11:K:95:ILE:O	11:K:95:ILE:HG22	2.20	0.41
12:L:27:LEU:HB3	12:L:62:SER:HB2	2.03	0.41
12:L:28:LYS:CG	12:L:33:ARG:HH12	2.34	0.41
12:L:46:LYS:NZ	12:L:47:LYS:HE3	2.36	0.41
12:L:53:ARG:CB	12:L:93:LEU:HD11	2.50	0.41
12:L:55:VAL:CG1	12:L:56:ALA:N	2.83	0.41
13:M:78:ILE:CA	13:M:81:LEU:HD21	2.43	0.41
15:O:34:LEU:C	15:O:34:LEU:CD2	2.94	0.41
16:P:1:MET:HE1	16:P:3:LYS:HE2	2.02	0.41
19:S:5:LEU:HD23	19:S:5:LEU:HA	1.88	0.41
19:S:16:LEU:O	19:S:20:LEU:HG	2.21	0.41
20:T:43:LEU:HD13	20:T:51:GLU:CG	2.43	0.41
20:T:44:ALA:HB2	20:T:88:VAL:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:53:LEU:C	20:T:57:ARG:HD2	2.46	0.41
1:A:19:C:O2'	1:A:20:U:H5'	2.20	0.41
1:A:750:G:N3	15:O:23:GLY:HA3	2.36	0.41
1:A:883:C:O2'	1:A:884:U:H5'	2.21	0.41
1:A:919:A:O2'	1:A:920:U:H5'	2.22	0.41
1:A:1096:C:H2'	1:A:1097:C:C6	2.56	0.41
1:A:1331:G:HO2'	1:A:1332:A:P	2.44	0.41
2:B:53:ARG:NH1	2:B:199:TYR:HD2	2.19	0.41
2:B:60:ASP:O	2:B:64:ARG:HB2	2.20	0.41
2:B:125:PRO:HG2	2:B:126:GLU:H	1.86	0.41
2:B:130:ARG:HB3	2:B:134:GLU:OE1	2.20	0.41
3:C:79:ARG:NE	3:C:82:GLU:HG2	2.34	0.41
3:C:174:PRO:HB2	3:C:177:THR:CG2	2.50	0.41
3:C:191:THR:HG21	3:C:193:TYR:CE2	2.56	0.41
4:D:62:GLN:HE22	4:D:65:ARG:NH1	2.18	0.41
5:E:9:LYS:HG3	5:E:112:LEU:HD11	2.03	0.41
6:F:78:GLU:HA	6:F:81:ILE:CD1	2.51	0.41
6:F:91:VAL:HG13	18:R:72:ARG:NH2	2.36	0.41
8:H:39:LEU:HD13	8:H:39:LEU:HA	1.86	0.41
10:J:15:THR:HG23	10:J:94:VAL:CG2	2.49	0.41
15:O:26:GLU:HG3	15:O:81:LEU:HG	2.02	0.41
15:O:74:ASP:OD1	15:O:76:GLU:HB3	2.21	0.41
17:Q:97:SER:O	17:Q:99:SER:N	2.53	0.41
18:R:44:LEU:HD22	18:R:48:GLY:O	2.21	0.41
1:A:502:G:H2'	1:A:503:C:C6	2.56	0.40
1:A:637:G:O2'	1:A:638:G:H5'	2.21	0.40
1:A:642:A:C2	8:H:113:SER:O	2.74	0.40
1:A:948:C:O2'	1:A:949:A:H5'	2.21	0.40
1:A:952:U:H2'	1:A:953:G:H8	1.85	0.40
1:A:953:G:H1'	13:M:125:ARG:HA	2.03	0.40
1:A:1028:C:H2'	1:A:1029:C:H6	1.84	0.40
1:A:1110:A:O5'	1:A:1110:A:H8	2.04	0.40
1:A:1138:G:N1	1:A:1140:C:C2	2.89	0.40
1:A:1257:U:H4'	1:A:1258:G:C5'	2.50	0.40
1:A:1263:C:H2'	1:A:1264:C:C6	2.56	0.40
1:A:1372:U:H5''	9:I:71:SER:CB	2.51	0.40
1:A:1392:G:H2'	1:A:1393:U:H6	1.86	0.40
1:A:1402:C:H2'	1:A:1403:C:H6	1.85	0.40
1:A:1437:C:H2'	1:A:1438:G:H8	1.86	0.40
4:D:68:TYR:O	4:D:69:GLY:C	2.63	0.40
4:D:91:SER:O	4:D:92:VAL:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:194:LEU:HD22	4:D:194:LEU:N	2.36	0.40
6:F:74:ASP:O	6:F:75:LEU:C	2.64	0.40
8:H:29:SER:O	8:H:30:ARG:C	2.64	0.40
10:J:23:ILE:N	10:J:23:ILE:CD1	2.85	0.40
13:M:96:LEU:O	13:M:110:ARG:NH1	2.54	0.40
15:O:43:LEU:C	15:O:45:VAL:O	2.64	0.40
15:O:81:LEU:HD22	15:O:85:LEU:HD12	2.03	0.40
16:P:34:GLU:HG2	16:P:35:LYS:N	2.36	0.40
18:R:26:LEU:CD1	18:R:27:GLY:H	2.29	0.40
20:T:36:LEU:HD12	20:T:62:LEU:HD12	2.03	0.40
20:T:68:LYS:HD2	20:T:68:LYS:HA	1.92	0.40
1:A:671:G:H2'	1:A:672:U:O4'	2.21	0.40
1:A:965:A:O2'	1:A:966:G:P	2.80	0.40
1:A:1112:C:N3	3:C:178:LEU:N	2.62	0.40
1:A:1355:G:O2'	1:A:1356:G:H5'	2.21	0.40
3:C:77:ILE:O	3:C:83:ARG:HB3	2.21	0.40
4:D:58:LEU:HD23	4:D:206:PHE:CE1	2.57	0.40
7:G:41:ARG:O	7:G:42:ILE:C	2.64	0.40
7:G:104:LEU:HD23	7:G:134:ALA:HB1	2.03	0.40
11:K:122:LYS:O	11:K:123:LYS:C	2.63	0.40
13:M:37:THR:HG23	13:M:55:ARG:HB2	2.03	0.40
15:O:57:LEU:HD12	15:O:57:LEU:HA	1.86	0.40
1:A:176:C:H2'	1:A:177:C:C6	2.56	0.40
1:A:335:C:H2'	1:A:336:C:H6	1.86	0.40
1:A:458:C:H2'	1:A:459:G:C8	2.57	0.40
1:A:1326:C:H5''	21:V:12:LYS:HZ1	1.85	0.40
1:A:1428:A:H2'	1:A:1429:C:O4'	2.22	0.40
2:B:14:GLY:O	2:B:15:VAL:CG2	2.69	0.40
2:B:21:ARG:H	2:B:21:ARG:HG2	1.72	0.40
2:B:130:ARG:NH2	3:C:207:VAL:CG2	2.82	0.40
2:B:156:LYS:HD3	2:B:156:LYS:C	2.45	0.40
2:B:217:ARG:C	2:B:219:VAL:N	2.78	0.40
3:C:65:ALA:O	3:C:66:VAL:HB	2.21	0.40
4:D:8:VAL:C	4:D:10:ARG:N	2.79	0.40
4:D:196:LEU:C	4:D:198:VAL:N	2.79	0.40
5:E:76:ILE:HG23	5:E:77:PRO:HD2	2.04	0.40
6:F:30:LEU:CB	6:F:35:ALA:HB3	2.41	0.40
8:H:19:VAL:CG2	8:H:21:LYS:HD3	2.52	0.40
8:H:89:PRO:HA	8:H:92:ARG:NH1	2.37	0.40
10:J:59:SER:O	10:J:60:ARG:HB2	2.21	0.40
10:J:65:LEU:HD12	14:N:56:VAL:HG22	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:39:LEU:HD11	14:N:47:LEU:HD12	2.02	0.40
15:O:70:LEU:O	15:O:71:GLN:C	2.64	0.40
15:O:74:ASP:CG	15:O:77:ARG:HG3	2.46	0.40
17:Q:6:LEU:O	17:Q:58:GLU:HA	2.21	0.40
1:A:155:C:H2'	1:A:156:G:C8	2.57	0.40
1:A:359:U:H2'	1:A:360:A:C8	2.57	0.40
1:A:567:G:H2'	1:A:568:G:O4'	2.21	0.40
1:A:973:G:H8	1:A:973:G:O5'	2.05	0.40
1:A:1298:C:H2'	7:G:114:ARG:HH12	1.86	0.40
1:A:1372:U:H5''	9:I:71:SER:HB2	2.04	0.40
2:B:154:LEU:O	2:B:155:LEU:C	2.65	0.40
3:C:13:GLY:O	3:C:14:ILE:HD13	2.22	0.40
3:C:33:LEU:C	3:C:33:LEU:CD2	2.94	0.40
3:C:35:GLU:O	3:C:36:ASP:C	2.64	0.40
3:C:39:ILE:HG22	3:C:40:ARG:N	2.37	0.40
5:E:66:MET:HE3	5:E:66:MET:HB3	1.98	0.40
8:H:111:ILE:O	8:H:134:ILE:HB	2.20	0.40
10:J:44:VAL:HG11	10:J:46:ARG:NH1	2.37	0.40
13:M:63:THR:HG23	13:M:64:TRP:CD2	2.56	0.40
13:M:69:GLU:O	13:M:72:ALA:HB3	2.21	0.40
1:A:16:A:C2'	1:A:17:U:H5'	2.52	0.40
1:A:103:C:P	20:T:17:ARG:NH1	2.95	0.40
1:A:182:U:OP2	1:A:183:G:C8	2.74	0.40
1:A:330:C:H6	1:A:330:C:H5''	1.86	0.40
1:A:547:A:OP2	4:D:2:GLY:N	2.54	0.40
1:A:715:A:H2'	1:A:716:A:C8	2.57	0.40
1:A:939:G:C6	1:A:940:C:N4	2.89	0.40
1:A:1003(A):G:H2'	1:A:1004:A:H4'	2.03	0.40
1:A:1124:G:C8	1:A:1145:C:C5	3.09	0.40
1:A:1408:A:O2'	1:A:1409:C:H5'	2.21	0.40
2:B:208:ILE:O	2:B:209:ARG:C	2.64	0.40
2:B:216:SER:OG	2:B:217:ARG:N	2.55	0.40
3:C:70:VAL:C	3:C:106:VAL:HG23	2.46	0.40
3:C:126:ARG:O	3:C:127:ARG:HB2	2.22	0.40
5:E:118:ILE:HG22	5:E:119:LEU:O	2.21	0.40
6:F:48:LEU:HD13	6:F:52:ILE:CD1	2.51	0.40
14:N:29:ARG:HH11	14:N:29:ARG:CG	2.32	0.40
17:Q:92:ARG:O	17:Q:95:TYR:HB2	2.22	0.40
19:S:67:VAL:HG12	19:S:68:GLY:N	2.35	0.40
20:T:92:LEU:O	20:T:96:GLY:HA3	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:157:ARG:NH1	2:B:157:ARG:NH1[7_555]	1.70	0.50

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	232/256 (91%)	174 (75%)	34 (15%)	24 (10%)	0	2
3	C	204/239 (85%)	135 (66%)	40 (20%)	29 (14%)	0	0
4	D	206/208 (99%)	166 (81%)	31 (15%)	9 (4%)	2	9
5	E	148/161 (92%)	130 (88%)	13 (9%)	5 (3%)	3	13
6	F	99/101 (98%)	79 (80%)	19 (19%)	1 (1%)	12	37
7	G	153/155 (99%)	127 (83%)	16 (10%)	10 (6%)	1	5
8	H	136/138 (99%)	125 (92%)	7 (5%)	4 (3%)	3	16
9	I	125/128 (98%)	88 (70%)	27 (22%)	10 (8%)	1	3
10	J	96/104 (92%)	59 (62%)	20 (21%)	17 (18%)	0	0
11	K	117/129 (91%)	88 (75%)	20 (17%)	9 (8%)	1	3
12	L	122/135 (90%)	98 (80%)	15 (12%)	9 (7%)	1	4
13	M	123/126 (98%)	88 (72%)	27 (22%)	8 (6%)	1	5
14	N	58/60 (97%)	40 (69%)	11 (19%)	7 (12%)	0	1
15	O	86/88 (98%)	70 (81%)	11 (13%)	5 (6%)	1	6
16	P	81/88 (92%)	65 (80%)	15 (18%)	1 (1%)	10	32
17	Q	102/104 (98%)	84 (82%)	10 (10%)	8 (8%)	1	3
18	R	71/88 (81%)	62 (87%)	7 (10%)	2 (3%)	4	16
19	S	78/92 (85%)	49 (63%)	18 (23%)	11 (14%)	0	0
20	T	97/106 (92%)	65 (67%)	20 (21%)	12 (12%)	0	1
21	V	22/26 (85%)	19 (86%)	2 (9%)	1 (4%)	2	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2356/2532 (93%)	1811 (77%)	363 (15%)	182 (8%)	1	3

All (182) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	9	GLU
2	B	15	VAL
2	B	16	HIS
2	B	17	PHE
2	B	21	ARG
2	B	24	TRP
3	C	4	LYS
3	C	15	THR
3	C	16	ARG
3	C	26	LYS
3	C	47	LEU
3	C	61	ALA
3	C	62	ASP
3	C	97	LYS
3	C	101	LEU
3	C	146	ALA
3	C	154	SER
3	C	179	ARG
3	C	189	ALA
4	D	29	PRO
4	D	36	ARG
5	E	16	THR
5	E	153	LYS
7	G	7	ALA
7	G	155	ARG
8	H	24	THR
8	H	83	ILE
8	H	91	ARG
9	I	88	TYR
10	J	32	ALA
10	J	39	PRO
10	J	54	PHE
10	J	57	LYS
10	J	79	ARG
10	J	86	MET
11	K	57	THR
11	K	127	LYS

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Mol	Chain	Res	Type
12	L	27	LEU
12	L	28	LYS
12	L	47	LYS
13	M	63	THR
13	M	67	GLU
13	M	121	LYS
13	M	122	LYS
13	M	124	PRO
14	N	22	THR
14	N	29	ARG
15	O	88	ARG
17	Q	69	LYS
17	Q	80	GLY
17	Q	81	ARG
17	Q	96	GLN
17	Q	98	LEU
17	Q	104	LYS
18	R	87	ARG
19	S	6	LYS
19	S	71	LEU
20	T	11	SER
20	T	73	HIS
2	B	8	LYS
2	B	18	GLY
2	B	20	GLU
2	B	97	TRP
2	B	123	ALA
2	B	232	PRO
3	C	29	TYR
3	C	156	ARG
3	C	168	ALA
3	C	181	ASN
3	C	206	GLU
4	D	4	TYR
4	D	26	CYS
4	D	88	VAL
4	D	125	HIS
5	E	22	GLY
5	E	104	ALA
6	F	37	VAL
7	G	52	GLU
9	I	41	VAL

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Mol	Chain	Res	Type
9	I	58	ARG
10	J	30	SER
10	J	34	VAL
10	J	40	LEU
10	J	72	VAL
11	K	15	ALA
11	K	49	GLY
11	K	50	TYR
11	K	89	ALA
12	L	41	ARG
12	L	48	PRO
12	L	51	ALA
12	L	116	SER
12	L	121	GLY
13	M	6	GLY
13	M	85	GLY
16	P	10	GLY
18	R	20	ALA
19	S	9	VAL
19	S	45	VAL
19	S	67	VAL
19	S	68	GLY
20	T	9	ASN
20	T	49	ALA
20	T	95	ALA
20	T	99	LEU
20	T	102	GLY
2	B	26	PRO
2	B	60	ASP
2	B	83	MET
2	B	89	GLY
2	B	204	ASN
4	D	175	SER
5	E	65	ASN
7	G	5	ARG
8	H	127	LEU
9	I	56	LEU
10	J	19	SER
10	J	60	ARG
10	J	61	GLU
10	J	90	LEU
11	K	35	PRO

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Mol	Chain	Res	Type
11	K	101	SER
12	L	49	ASN
14	N	13	THR
14	N	23	ARG
17	Q	97	SER
19	S	28	LYS
19	S	30	LEU
19	S	32	LYS
20	T	74	LYS
2	B	126	GLU
2	B	165	VAL
3	C	39	ILE
3	C	100	ALA
3	C	188	LEU
7	G	4	ARG
7	G	81	GLY
7	G	112	PRO
9	I	7	THR
9	I	12	GLU
9	I	119	ALA
13	M	123	ALA
14	N	12	ARG
14	N	60	SER
15	O	16	ALA
17	Q	33	GLY
20	T	50	GLU
21	V	3	LYS
2	B	155	LEU
3	C	24	ALA
3	C	66	VAL
3	C	127	ARG
4	D	123	HIS
7	G	53	LYS
9	I	121	ARG
14	N	36	PHE
15	O	84	LYS
19	S	31	ILE
2	B	127	ILE
3	C	108	ASN
3	C	174	PRO
4	D	5	ILE
9	I	43	ALA

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Mol	Chain	Res	Type
10	J	26	ALA
2	B	124	SER
2	B	214	ILE
7	G	14	PRO
10	J	82	ILE
20	T	98	PRO
2	B	125	PRO
3	C	76	VAL
3	C	77	ILE
7	G	17	VAL
10	J	36	GLY
15	O	82	ILE
9	I	44	VAL
19	S	8	GLY
20	T	101	GLY
15	O	19	PRO
20	T	96	GLY
3	C	75	VAL
11	K	90	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	202/220 (92%)	184 (91%)	18 (9%)	9	29
3	C	160/188 (85%)	141 (88%)	19 (12%)	5	18
4	D	180/180 (100%)	169 (94%)	11 (6%)	17	42
5	E	115/122 (94%)	98 (85%)	17 (15%)	3	11
6	F	90/90 (100%)	86 (96%)	4 (4%)	25	53
7	G	126/126 (100%)	120 (95%)	6 (5%)	23	50
8	H	119/119 (100%)	106 (89%)	13 (11%)	6	21
9	I	98/99 (99%)	90 (92%)	8 (8%)	10	32
10	J	87/91 (96%)	78 (90%)	9 (10%)	7	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K	90/99 (91%)	83 (92%)	7 (8%)	11	34
12	L	104/111 (94%)	95 (91%)	9 (9%)	9	30
13	M	100/101 (99%)	93 (93%)	7 (7%)	14	38
14	N	49/49 (100%)	47 (96%)	2 (4%)	27	55
15	O	79/79 (100%)	72 (91%)	7 (9%)	9	29
16	P	72/74 (97%)	67 (93%)	5 (7%)	14	38
17	Q	96/96 (100%)	90 (94%)	6 (6%)	16	41
18	R	64/77 (83%)	60 (94%)	4 (6%)	16	41
19	S	71/79 (90%)	70 (99%)	1 (1%)	59	73
20	T	76/82 (93%)	68 (90%)	8 (10%)	6	23
21	V	19/21 (90%)	19 (100%)	0	100	100
All	All	1997/2103 (95%)	1836 (92%)	161 (8%)	11	33

All (161) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	12	GLU
2	B	17	PHE
2	B	23	ARG
2	B	25	ASN
2	B	41	ILE
2	B	75	LYS
2	B	87	ARG
2	B	139	LYS
2	B	155	LEU
2	B	164	VAL
2	B	165	VAL
2	B	170	GLU
2	B	178	ARG
2	B	187	LEU
2	B	213	LEU
2	B	221	LEU
2	B	231	GLU
2	B	232	PRO
3	C	3	ASN
3	C	5	ILE
3	C	34	LEU
3	C	47	LEU

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Mol	Chain	Res	Type
3	C	64	VAL
3	C	70	VAL
3	C	75	VAL
3	C	82	GLU
3	C	91	LEU
3	C	99	VAL
3	C	107	GLN
3	C	116	VAL
3	C	130	VAL
3	C	139	GLN
3	C	164	ARG
3	C	167	TRP
3	C	175	LEU
3	C	188	LEU
3	C	204	LEU
4	D	15	GLU
4	D	29	PRO
4	D	34	GLU
4	D	70	ILE
4	D	122	ARG
4	D	127	THR
4	D	157	LEU
4	D	162	LEU
4	D	170	VAL
4	D	192	GLU
4	D	194	LEU
5	E	10	MET
5	E	12	LEU
5	E	18	ARG
5	E	26	PHE
5	E	31	LEU
5	E	38	GLN
5	E	41	VAL
5	E	43	LEU
5	E	53	LEU
5	E	56	GLN
5	E	65	ASN
5	E	68	GLU
5	E	79	GLU
5	E	80	ILE
5	E	89	ILE
5	E	120	THR

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Mol	Chain	Res	Type
5	E	150	ARG
6	F	10	LEU
6	F	37	VAL
6	F	43	LEU
6	F	69	GLU
7	G	8	GLU
7	G	11	GLN
7	G	37	ASN
7	G	38	LEU
7	G	113	GLU
7	G	146	GLU
8	H	2	LEU
8	H	19	VAL
8	H	21	LYS
8	H	26	VAL
8	H	39	LEU
8	H	52	ASP
8	H	63	LEU
8	H	85	ARG
8	H	92	ARG
8	H	105	ARG
8	H	112	LEU
8	H	119	LEU
8	H	127	LEU
9	I	2	GLU
9	I	29	ASN
9	I	38	GLN
9	I	53	VAL
9	I	58	ARG
9	I	78	LYS
9	I	79	LEU
9	I	111	ARG
10	J	6	ILE
10	J	15	THR
10	J	16	LEU
10	J	45	ARG
10	J	64	GLU
10	J	71	LEU
10	J	73	ASP
10	J	83	GLU
10	J	95	GLU
11	K	24	SER

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Mol	Chain	Res	Type
11	K	29	ILE
11	K	35	PRO
11	K	54	ARG
11	K	80	VAL
11	K	84	VAL
11	K	92	GLU
12	L	7	ILE
12	L	17	LYS
12	L	33	ARG
12	L	53	ARG
12	L	60	LEU
12	L	81	SER
12	L	96	VAL
12	L	113	ARG
12	L	126	LYS
13	M	9	ILE
13	M	16	ASP
13	M	70	LEU
13	M	81	LEU
13	M	102	ARG
13	M	110	ARG
13	M	124	PRO
14	N	41	ARG
14	N	44	LEU
15	O	6	GLU
15	O	7	GLU
15	O	39	LEU
15	O	57	LEU
15	O	70	LEU
15	O	81	LEU
15	O	83	GLU
16	P	2	VAL
16	P	8	ARG
16	P	20	VAL
16	P	53	VAL
16	P	62	VAL
17	Q	34	LYS
17	Q	38	ARG
17	Q	60	ILE
17	Q	68	ARG
17	Q	74	LEU
17	Q	98	LEU

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Mol	Chain	Res	Type
18	R	38	GLU
18	R	41	LYS
18	R	55	ARG
18	R	75	ILE
19	S	43	GLU
20	T	10	LEU
20	T	25	ARG
20	T	39	LYS
20	T	42	GLN
20	T	57	ARG
20	T	73	HIS
20	T	84	LEU
20	T	86	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (61) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	19	HIS
2	B	25	ASN
2	B	40	HIS
2	B	94	ASN
2	B	146	GLN
2	B	204	ASN
2	B	240	GLN
3	C	3	ASN
3	C	6	HIS
3	C	31	HIS
3	C	69	HIS
3	C	104	GLN
3	C	107	GLN
3	C	110	ASN
3	C	118	GLN
3	C	123	GLN
3	C	139	GLN
3	C	181	ASN
4	D	45	GLN
4	D	62	GLN
4	D	123	HIS
4	D	161	ASN
4	D	199	ASN
5	E	38	GLN
5	E	65	ASN

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Mol	Chain	Res	Type
5	E	73	ASN
6	F	18	GLN
6	F	27	GLN
6	F	32	ASN
6	F	57	GLN
6	F	64	GLN
6	F	94	GLN
6	F	100	ASN
7	G	37	ASN
7	G	86	GLN
7	G	106	GLN
9	I	23	ASN
9	I	73	GLN
10	J	56	HIS
10	J	69	ASN
10	J	76	ASN
10	J	78	ASN
10	J	84	GLN
11	K	22	HIS
11	K	62	GLN
11	K	93	GLN
11	K	117	ASN
12	L	8	ASN
12	L	49	ASN
12	L	75	HIS
13	M	12	ASN
13	M	40	ASN
13	M	62	ASN
15	O	13	GLN
15	O	37	ASN
17	Q	16	GLN
17	Q	26	GLN
18	R	36	ASN
19	S	14	HIS
19	S	56	GLN
20	T	42	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1512/1522 (99%)	221 (14%)	88 (5%)

All (221) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	48	C
1	A	49	U
1	A	51	A
1	A	52	G
1	A	61	G
1	A	81	U
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	182	U
1	A	190(D)	U
1	A	190(E)	U
1	A	190(F)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	282	A
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A

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Mol	Chain	Res	Type
1	A	330	C
1	A	332	G
1	A	344	A
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C
1	A	412	A
1	A	413	G
1	A	421	U
1	A	428	G
1	A	429	U
1	A	430	A
1	A	439	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	481	G
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	527	G
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A

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Mol	Chain	Res	Type
1	A	575	G
1	A	576	G
1	A	577	G
1	A	588	G
1	A	653	A
1	A	665	A
1	A	686	U
1	A	687	A
1	A	688	G
1	A	702	A
1	A	703	G
1	A	718	G
1	A	723	U
1	A	731	G
1	A	749	C
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	793	U
1	A	794	A
1	A	813	U
1	A	815	A
1	A	817	C
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	858	G
1	A	902	G
1	A	913	A
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A

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Mol	Chain	Res	Type
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1005	A
1	A	1023	G
1	A	1026	G
1	A	1050	G
1	A	1053	G
1	A	1065	U
1	A	1066	C
1	A	1067	A
1	A	1068	G
1	A	1085	U
1	A	1086	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1145	C
1	A	1146	A
1	A	1152	A
1	A	1157	A
1	A	1159	U
1	A	1183	A

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Mol	Chain	Res	Type
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1211	U
1	A	1212	U
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1238	A
1	A	1257	U
1	A	1258	G
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1299	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1320	C
1	A	1332	A
1	A	1347	G
1	A	1348	U
1	A	1363	A
1	A	1364	U
1	A	1365	G
1	A	1381	U
1	A	1394	A
1	A	1398	A
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1447	G

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Mol	Chain	Res	Type
1	A	1452	C
1	A	1490	C
1	A	1499	A
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G

All (88) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	7	G
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	202	U
1	A	203	U
1	A	204	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	281	G
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C

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Mol	Chain	Res	Type
1	A	428	G
1	A	429	U
1	A	438	G
1	A	484	G
1	A	496	A
1	A	497	A
1	A	509	A
1	A	518	C
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	701	C
1	A	748	C
1	A	792	A
1	A	812	C
1	A	840	C
1	A	913	A
1	A	960	U
1	A	965	A
1	A	975	A
1	A	976	G
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1085	U
1	A	1101	A
1	A	1129	C
1	A	1145	C
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1214	C
1	A	1224	G
1	A	1226	C
1	A	1256	A
1	A	1257	U

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Mol	Chain	Res	Type
1	A	1278	U
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1319	A
1	A	1331	G
1	A	1346	A
1	A	1347	G
1	A	1364	U
1	A	1380	U
1	A	1397	C
1	A	1451	A
1	A	1498	U
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1528	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 190 ligands modelled in this entry, 188 are unknown and 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	1510/1522 (99%)	0.62	141 (9%) 14 7	28, 59, 140, 201	0
2	B	234/256 (91%)	1.08	43 (18%) 3 2	31, 77, 150, 191	0
3	C	206/239 (86%)	1.04	35 (16%) 4 2	35, 77, 131, 153	0
4	D	208/208 (100%)	0.98	37 (17%) 4 2	32, 64, 114, 169	0
5	E	150/161 (93%)	0.36	8 (5%) 32 16	26, 48, 86, 139	0
6	F	101/101 (100%)	0.80	8 (7%) 18 9	47, 84, 120, 138	0
7	G	155/155 (100%)	0.84	20 (12%) 7 4	38, 72, 122, 156	0
8	H	138/138 (100%)	0.29	9 (6%) 25 12	19, 45, 78, 131	0
9	I	127/128 (99%)	1.45	40 (31%) 1 1	36, 85, 129, 175	0
10	J	98/104 (94%)	1.95	42 (42%) 0 0	41, 106, 158, 190	0
11	K	119/129 (92%)	0.83	14 (11%) 9 5	34, 59, 105, 175	0
12	L	124/135 (91%)	0.86	18 (14%) 6 3	25, 60, 113, 162	0
13	M	125/126 (99%)	1.25	24 (19%) 3 1	46, 79, 138, 189	0
14	N	60/60 (100%)	1.51	16 (26%) 1 1	39, 72, 108, 148	0
15	O	88/88 (100%)	0.47	6 (6%) 23 11	31, 60, 114, 182	0
16	P	83/88 (94%)	0.69	6 (7%) 21 11	31, 53, 74, 138	0
17	Q	104/104 (100%)	0.84	16 (15%) 5 2	32, 55, 128, 201	0
18	R	73/88 (82%)	0.79	7 (9%) 13 7	37, 68, 137, 186	0
19	S	80/92 (86%)	1.85	24 (30%) 1 1	54, 95, 153, 187	0
20	T	99/106 (93%)	1.30	22 (22%) 2 1	29, 60, 115, 187	0
21	V	24/26 (92%)	1.61	7 (29%) 1 1	36, 66, 103, 129	0
All	All	3906/4054 (96%)	0.84	543 (13%) 6 4	19, 64, 135, 201	0

All (543) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	G	5	ARG	11.0
19	S	3	ARG	10.1
13	M	124	PRO	9.8
13	M	123	ALA	9.4
1	A	1126	U	7.5
2	B	16	HIS	7.4
17	Q	101	ARG	7.2
17	Q	104	LYS	7.1
5	E	154	GLY	7.0
19	S	4	SER	6.9
17	Q	103	GLY	6.9
1	A	1491	G	6.6
11	K	129	SER	6.6
21	V	25	LYS	6.5
4	D	19	LEU	6.4
7	G	4	ARG	6.4
19	S	33	THR	6.4
20	T	103	GLY	6.4
1	A	1533	C	6.2
4	D	31	CYS	6.2
11	K	89	ALA	6.1
7	G	8	GLU	6.1
10	J	57	LYS	5.9
1	A	202	U	5.9
21	V	6	ARG	5.9
20	T	74	LYS	5.8
20	T	9	ASN	5.8
13	M	125	ARG	5.7
5	E	5	ASP	5.6
10	J	43	ARG	5.5
2	B	7	VAL	5.5
4	D	3	ARG	5.4
12	L	28	LYS	5.4
1	A	481	G	5.3
1	A	1002	G	5.3
15	O	7	GLU	5.3
1	A	1446	A	5.3
7	G	16	LEU	5.3
19	S	37	ARG	5.3
11	K	127	LYS	5.3
17	Q	102	GLY	5.3
20	T	12	ALA	5.3
1	A	81	U	5.2

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Mol	Chain	Res	Type	RSRZ
11	K	11	LYS	5.1
12	L	19	ARG	5.1
19	S	2	PRO	5.0
1	A	1490	C	5.0
10	J	71	LEU	4.9
1	A	1129	C	4.9
10	J	45	ARG	4.9
1	A	1280	A	4.9
19	S	6	LYS	4.9
19	S	68	GLY	4.8
1	A	1281	U	4.8
12	L	128	ALA	4.8
1	A	1127	G	4.8
1	A	1182	G	4.8
1	A	532	A	4.8
8	H	1	MET	4.8
13	M	13	LYS	4.8
9	I	8	GLY	4.7
1	A	841	U	4.7
2	B	133	LYS	4.7
1	A	1539	C	4.7
17	Q	13	ASP	4.7
17	Q	100	LYS	4.7
20	T	58	LYS	4.7
10	J	75	ILE	4.6
12	L	47	LYS	4.6
16	P	12	LYS	4.6
7	G	82	GLY	4.6
10	J	5	ARG	4.6
4	D	9	CYS	4.6
6	F	95	GLU	4.5
1	A	458	C	4.5
1	A	1124	G	4.5
1	A	1054	C	4.5
1	A	1145	C	4.5
1	A	1139	G	4.5
9	I	7	THR	4.5
13	M	122	LYS	4.4
2	B	96	ARG	4.4
1	A	1003	G	4.4
4	D	35	ARG	4.4
10	J	78	ASN	4.4

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Mol	Chain	Res	Type	RSRZ
13	M	9	ILE	4.3
2	B	229	VAL	4.3
1	A	1125	U	4.2
1	A	1144	G	4.2
3	C	167	TRP	4.2
13	M	126	LYS	4.2
13	M	7	VAL	4.2
20	T	36	LEU	4.2
10	J	37	PRO	4.2
1	A	723	U	4.2
2	B	206	ASP	4.2
18	R	17	SER	4.2
19	S	35	SER	4.1
18	R	16	PRO	4.1
18	R	31	LEU	4.1
1	A	1020	U	4.1
9	I	56	LEU	4.1
1	A	1282	C	4.0
1	A	1279	A	4.0
4	D	73	ARG	4.0
21	V	24	ARG	4.0
2	B	21	ARG	4.0
7	G	79	ARG	4.0
1	A	349	A	4.0
1	A	1283	G	3.9
1	A	1212	U	3.9
1	A	1540	U	3.9
13	M	10	PRO	3.9
4	D	71	SER	3.9
9	I	126	SER	3.9
7	G	81	GLY	3.8
9	I	27	THR	3.8
19	S	69	HIS	3.8
13	M	11	ARG	3.8
1	A	1181	G	3.8
1	A	1255	G	3.8
14	N	13	THR	3.8
10	J	73	ASP	3.7
10	J	72	VAL	3.7
4	D	141	ARG	3.7
11	K	111	ASP	3.7
13	M	6	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
19	S	5	LEU	3.7
4	D	49	ARG	3.7
18	R	48	GLY	3.7
4	D	16	GLY	3.7
3	C	68	VAL	3.6
4	D	192	GLU	3.6
4	D	23	GLY	3.6
14	N	2	ALA	3.6
13	M	21	TYR	3.6
1	A	1006	C	3.5
1	A	1403	C	3.5
21	V	5	ASP	3.5
1	A	306	G	3.5
1	A	1198	G	3.5
14	N	3	ARG	3.5
11	K	42	TRP	3.5
1	A	1300	G	3.5
10	J	100	THR	3.5
1	A	412	A	3.5
1	A	494	G	3.5
10	J	66	ARG	3.5
13	M	121	LYS	3.4
20	T	73	HIS	3.4
2	B	156	LYS	3.4
1	A	1314	C	3.4
2	B	175	ARG	3.4
9	I	64	THR	3.4
4	D	123	HIS	3.4
2	B	166	ASP	3.4
10	J	65	LEU	3.4
4	D	151	LYS	3.4
10	J	59	SER	3.4
19	S	67	VAL	3.4
2	B	38	GLY	3.4
1	A	1183	A	3.3
1	A	457	C	3.3
10	J	93	GLY	3.3
13	M	8	GLU	3.3
19	S	81	ARG	3.3
10	J	3	LYS	3.3
11	K	12	ARG	3.3
11	K	110	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	415	A	3.3
3	C	178	LEU	3.2
1	A	1442	G	3.2
9	I	92	TYR	3.2
3	C	72	LYS	3.2
9	I	97	LYS	3.2
12	L	18	VAL	3.2
20	T	55	ILE	3.2
9	I	119	ALA	3.2
3	C	2	GLY	3.2
14	N	8	GLU	3.2
11	K	25	TYR	3.2
1	A	351	G	3.2
1	A	1258	G	3.2
1	A	1259	C	3.2
1	A	1260	C	3.2
2	B	17	PHE	3.2
19	S	74	PHE	3.2
4	D	158	ILE	3.2
2	B	12	GLU	3.1
9	I	9	ARG	3.1
2	B	8	LYS	3.1
3	C	61	ALA	3.1
19	S	12	ASP	3.1
4	D	131	ARG	3.1
4	D	152	SER	3.1
10	J	90	LEU	3.1
14	N	32	SER	3.1
16	P	83	GLU	3.1
2	B	11	LEU	3.1
19	S	39	THR	3.1
1	A	1019	C	3.1
10	J	79	ARG	3.1
20	T	25	ARG	3.1
16	P	14	ASN	3.1
12	L	26	ALA	3.1
3	C	26	LYS	3.1
9	I	2	GLU	3.1
18	R	83	GLU	3.1
19	S	73	GLU	3.1
4	D	26	CYS	3.1
1	A	1003(A)	G	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	1138	G	3.0
4	D	167	GLY	3.0
17	Q	68	ARG	3.0
7	G	156	TRP	3.0
20	T	51	GLU	3.0
2	B	125	PRO	3.0
10	J	40	LEU	3.0
1	A	1278	U	3.0
7	G	7	ALA	3.0
7	G	80	VAL	3.0
3	C	52	LEU	3.0
4	D	157	LEU	3.0
1	A	1013	G	3.0
10	J	47	PHE	3.0
15	O	31	LEU	3.0
20	T	13	LEU	3.0
3	C	132	ARG	3.0
4	D	187	ARG	3.0
9	I	66	ARG	3.0
10	J	10	GLY	3.0
19	S	14	HIS	3.0
2	B	9	GLU	2.9
1	A	1213	A	2.9
1	A	1200	C	2.9
10	J	64	GLU	2.9
3	C	51	GLY	2.9
2	B	98	LEU	2.9
8	H	2	LEU	2.9
1	A	443	C	2.9
20	T	59	ALA	2.9
20	T	97	ALA	2.9
14	N	44	LEU	2.9
9	I	70	LYS	2.9
12	L	20	LYS	2.9
12	L	91	LYS	2.9
13	M	31	LYS	2.9
1	A	459	G	2.9
1	A	1453	G	2.9
1	A	1237	C	2.9
1	A	1541	U	2.9
20	T	8	ARG	2.9
5	E	50	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
3	C	207	VAL	2.9
19	S	7	LYS	2.9
17	Q	96	GLN	2.8
13	M	15	VAL	2.8
10	J	70	ARG	2.8
3	C	205	GLY	2.8
13	M	120	LYS	2.8
7	G	151	TYR	2.8
14	N	6	LEU	2.8
9	I	106	ALA	2.8
11	K	128	ALA	2.8
1	A	182	U	2.8
1	A	1405	G	2.8
7	G	57	GLU	2.8
4	D	120	LEU	2.8
10	J	6	ILE	2.8
19	S	70	LYS	2.8
1	A	1248	A	2.8
1	A	1033	G	2.8
1	A	1038	C	2.8
1	A	1190	G	2.8
1	A	1447	G	2.8
3	C	95	THR	2.8
3	C	96	GLY	2.8
9	I	10	ARG	2.8
1	A	413	G	2.8
10	J	77	PRO	2.8
11	K	52	GLY	2.7
8	H	37	ARG	2.7
2	B	179	LYS	2.7
8	H	3	THR	2.7
1	A	266	G	2.7
12	L	92	ASP	2.7
13	M	44	ARG	2.7
6	F	94	GLN	2.7
16	P	41	PRO	2.7
12	L	127	GLU	2.7
9	I	115	GLY	2.7
14	N	60	SER	2.7
1	A	748	C	2.7
1	A	1131	G	2.7
21	V	9	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	460	A	2.7
20	T	98	PRO	2.7
10	J	87	THR	2.7
1	A	1005	A	2.6
3	C	104	GLN	2.6
9	I	116	LYS	2.6
1	A	1478	C	2.6
2	B	97	TRP	2.6
2	B	148	TYR	2.6
1	A	1089	G	2.6
2	B	23	ARG	2.6
4	D	2	GLY	2.6
3	C	161	GLU	2.6
2	B	10	LEU	2.6
4	D	147	ALA	2.6
10	J	7	LYS	2.6
10	J	98	ILE	2.6
6	F	1	MET	2.6
19	S	32	LYS	2.6
2	B	76	GLN	2.6
3	C	3	ASN	2.6
3	C	99	VAL	2.6
20	T	94	ALA	2.6
9	I	95	LYS	2.6
1	A	1477	C	2.6
3	C	155	GLY	2.6
3	C	196	LEU	2.6
5	E	149	GLU	2.6
11	K	87	THR	2.6
13	M	43	THR	2.6
1	A	350	G	2.6
1	A	1173	G	2.6
1	A	1286	A	2.6
9	I	30	GLY	2.6
9	I	75	ASP	2.6
15	O	23	GLY	2.6
1	A	341	C	2.6
2	B	35	GLU	2.6
9	I	128	ARG	2.6
11	K	51	LYS	2.6
12	L	33	ARG	2.6
2	B	108	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1313	U	2.5
12	L	94	PRO	2.5
10	J	36	GLY	2.5
4	D	155	LEU	2.5
18	R	85	LEU	2.5
3	C	62	ASP	2.5
5	E	27	ARG	2.5
20	T	27	LYS	2.5
1	A	1489	G	2.5
1	A	1043	C	2.5
15	O	89	GLY	2.5
9	I	87	GLN	2.5
1	A	1091	U	2.5
12	L	17	LYS	2.5
1	A	88	A	2.5
1	A	1030(B)	C	2.5
10	J	86	MET	2.5
2	B	204	ASN	2.5
20	T	35	THR	2.5
6	F	77	ARG	2.5
10	J	60	ARG	2.5
21	V	10	ARG	2.5
9	I	67	GLY	2.5
13	M	45	VAL	2.5
20	T	100	ILE	2.4
2	B	163	PHE	2.4
19	S	10	PHE	2.4
3	C	63	ASN	2.4
4	D	182	LYS	2.4
13	M	47	ASP	2.4
1	A	396	G	2.4
9	I	24	GLY	2.4
19	S	8	GLY	2.4
16	P	11	SER	2.4
5	E	133	TYR	2.4
1	A	1140	C	2.4
9	I	55	ALA	2.4
1	A	1488	G	2.4
9	I	38	GLN	2.4
12	L	35	GLY	2.4
7	G	137	LYS	2.4
1	A	401	C	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	992	U	2.4
10	J	85	LEU	2.4
1	A	1175	G	2.4
14	N	18	VAL	2.4
3	C	78	GLY	2.4
7	G	33	ASP	2.4
17	Q	105	ALA	2.4
7	G	48	LYS	2.4
13	M	27	LYS	2.4
20	T	56	MET	2.4
2	B	240	GLN	2.4
7	G	59	LEU	2.4
1	A	414	A	2.4
9	I	35	GLU	2.4
1	A	486	U	2.4
1	A	1172	C	2.3
14	N	22	THR	2.3
17	Q	14	LYS	2.3
14	N	57	ARG	2.3
3	C	188	LEU	2.3
19	S	71	LEU	2.3
11	K	124	LYS	2.3
14	N	15	LYS	2.3
20	T	86	ARG	2.3
16	P	13	HIS	2.3
1	A	1090	U	2.3
17	Q	95	TYR	2.3
8	H	54	ASP	2.3
4	D	74	GLN	2.3
18	R	88	LYS	2.3
2	B	52	GLU	2.3
4	D	179	GLU	2.3
1	A	217	C	2.3
2	B	130	ARG	2.3
4	D	168	ARG	2.3
6	F	46	ARG	2.3
14	N	29	ARG	2.3
3	C	100	ALA	2.3
9	I	15	ALA	2.3
2	B	215	LEU	2.3
1	A	438	G	2.3
1	A	1312	G	2.3

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Mol	Chain	Res	Type	RSRZ
4	D	161	ASN	2.3
13	M	106	ASN	2.3
1	A	487	A	2.3
1	A	965	A	2.3
2	B	116	GLU	2.3
5	E	76	ILE	2.3
14	N	55	GLY	2.3
9	I	102	LEU	2.3
17	Q	97	SER	2.3
9	I	23	ASN	2.3
6	F	47	ARG	2.3
15	O	79	ARG	2.3
6	F	83	ASP	2.3
1	A	1030(C)	G	2.2
1	A	1487	G	2.2
1	A	1004	A	2.2
10	J	99	LYS	2.2
1	A	456	C	2.2
7	G	32	ARG	2.2
3	C	76	VAL	2.2
9	I	12	GLU	2.2
9	I	105	ASP	2.2
12	L	27	LEU	2.2
6	F	97	PHE	2.2
9	I	127	LYS	2.2
1	A	1532	U	2.2
3	C	64	VAL	2.2
4	D	12	CYS	2.2
2	B	180	LEU	2.2
3	C	180	ALA	2.2
4	D	30	LYS	2.2
9	I	33	PHE	2.2
7	G	6	ARG	2.2
4	D	125	HIS	2.2
9	I	103	THR	2.2
1	A	495	U	2.2
1	A	1025	U	2.2
1	A	1251	A	2.2
1	A	1256	A	2.2
1	A	1494	G	2.2
2	B	101	MET	2.2
7	G	83	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
3	C	27	LYS	2.2
12	L	21	LYS	2.2
4	D	20	TYR	2.2
10	J	4	ILE	2.2
10	J	35	SER	2.2
10	J	88	LEU	2.2
17	Q	22	LEU	2.2
1	A	203	U	2.2
1	A	204	U	2.2
8	H	27	PRO	2.2
1	A	452	A	2.2
1	A	442	C	2.1
1	A	1226	C	2.1
14	N	4	LYS	2.1
20	T	14	LYS	2.1
3	C	21	ARG	2.1
7	G	67	GLU	2.1
10	J	61	GLU	2.1
9	I	57	GLY	2.1
14	N	35	ARG	2.1
10	J	54	PHE	2.1
1	A	1302	U	2.1
10	J	58	ASP	2.1
2	B	15	VAL	2.1
3	C	23	TYR	2.1
1	A	44	G	2.1
1	A	158	G	2.1
1	A	183	G	2.1
1	A	1316	G	2.1
8	H	30	ARG	2.1
9	I	31	GLN	2.1
3	C	112	SER	2.1
9	I	68	GLY	2.1
1	A	1159	U	2.1
17	Q	52	LYS	2.1
17	Q	81	ARG	2.1
1	A	733	A	2.1
1	A	1092	A	2.1
1	A	1130	A	2.1
1	A	1146	A	2.1
1	A	181	G	2.1
1	A	1128	C	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1397	C	2.1
13	M	20	THR	2.1
3	C	105	GLU	2.1
4	D	72	GLU	2.1
10	J	41	PRO	2.1
12	L	25	PRO	2.1
10	J	24	VAL	2.1
2	B	19	HIS	2.1
8	H	102	ARG	2.1
21	V	15	ARG	2.1
4	D	127	THR	2.1
1	A	447	G	2.1
1	A	1030(A)	G	2.1
1	A	1171	G	2.1
1	A	1305	G	2.1
1	A	1331	G	2.1
5	E	20	GLN	2.1
2	B	22	LYS	2.0
3	C	45	LYS	2.0
2	B	208	ILE	2.0
4	D	77	ASN	2.0
8	H	125	ARG	2.0
9	I	114	TYR	2.0
2	B	231	GLU	2.0
1	A	1277	C	2.0
12	L	126	LYS	2.0
2	B	140	HIS	2.0
10	J	15	THR	2.0
2	B	60	ASP	2.0
17	Q	83	ASP	2.0
2	B	110	GLN	2.0
1	A	440	A	2.0
1	A	1035	A	2.0
3	C	70	VAL	2.0
9	I	93	ARG	2.0
15	O	88	ARG	2.0
19	S	40	ILE	2.0
1	A	1479	C	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 oligosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	UNX	A	1695	1/1	-0.91	0.90	57,57,57,57	1
22	UNX	A	1635	1/1	-0.81	0.62	57,57,57,57	1
22	UNX	A	1632	1/1	-0.76	0.70	57,57,57,57	1
22	UNX	A	1646	1/1	-0.53	1.05	57,57,57,57	1
22	UNX	A	1719	1/1	-0.43	0.98	57,57,57,57	1
22	UNX	A	1716	1/1	-0.41	1.16	57,57,57,57	1
22	UNX	A	1641	1/1	-0.40	0.89	57,57,57,57	1
22	UNX	A	1683	1/1	-0.39	0.90	57,57,57,57	1
22	UNX	A	1634	1/1	-0.38	0.83	57,57,57,57	1
22	UNX	A	1636	1/1	-0.34	0.92	57,57,57,57	1
22	UNX	A	1589	1/1	-0.32	0.72	57,57,57,57	1
22	UNX	A	1673	1/1	-0.31	0.83	57,57,57,57	1
22	UNX	A	1588	1/1	-0.30	0.74	57,57,57,57	1
22	UNX	A	1703	1/1	-0.29	0.93	57,57,57,57	1
22	UNX	A	1603	1/1	-0.22	0.81	57,57,57,57	1
22	UNX	A	1628	1/1	-0.22	2.87	57,57,57,57	1
22	UNX	A	1649	1/1	-0.22	1.05	57,57,57,57	1
22	UNX	A	1585	1/1	-0.21	1.13	57,57,57,57	1
22	UNX	A	1568	1/1	-0.21	0.67	57,57,57,57	1
22	UNX	A	1584	1/1	-0.20	0.72	57,57,57,57	1
22	UNX	A	1704	1/1	-0.20	0.85	57,57,57,57	1
22	UNX	A	1629	1/1	-0.20	0.84	57,57,57,57	1
22	UNX	A	1639	1/1	-0.20	1.91	57,57,57,57	1
22	UNX	A	1680	1/1	-0.16	1.13	57,57,57,57	1
22	UNX	A	1665	1/1	-0.13	0.90	57,57,57,57	1
22	UNX	A	1601	1/1	-0.12	1.14	57,57,57,57	1
22	UNX	A	1700	1/1	-0.11	0.85	57,57,57,57	1
22	UNX	M	143	1/1	-0.11	0.70	57,57,57,57	1
22	UNX	A	1705	1/1	-0.10	1.23	57,57,57,57	1
22	UNX	A	1689	1/1	-0.10	1.78	57,57,57,57	1
22	UNX	A	1609	1/1	-0.09	0.79	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
22	UNX	A	1640	1/1	-0.09	1.82	57,57,57,57	1
22	UNX	A	1711	1/1	-0.08	1.12	57,57,57,57	1
22	UNX	A	1648	1/1	-0.07	0.79	57,57,57,57	1
22	UNX	A	1677	1/1	-0.07	0.82	57,57,57,57	1
22	UNX	A	94	1/1	-0.06	0.87	57,57,57,57	1
22	UNX	A	1668	1/1	-0.05	1.09	57,57,57,57	1
22	UNX	A	1620	1/1	-0.05	1.03	57,57,57,57	1
22	UNX	A	1625	1/1	-0.05	1.07	57,57,57,57	1
22	UNX	A	1656	1/1	-0.04	1.09	57,57,57,57	1
22	UNX	A	1651	1/1	-0.04	0.74	57,57,57,57	1
22	UNX	A	1715	1/1	-0.04	2.34	57,57,57,57	1
22	UNX	A	1621	1/1	-0.03	1.01	57,57,57,57	1
22	UNX	A	1637	1/1	-0.02	0.89	57,57,57,57	1
22	UNX	A	1561	1/1	-0.02	1.32	57,57,57,57	1
22	UNX	A	1650	1/1	-0.00	1.01	57,57,57,57	1
22	UNX	A	1694	1/1	-0.00	0.96	57,57,57,57	1
22	UNX	A	1697	1/1	0.01	1.20	57,57,57,57	1
22	UNX	A	1633	1/1	0.02	0.98	57,57,57,57	1
22	UNX	A	1615	1/1	0.02	0.88	57,57,57,57	1
22	UNX	A	1612	1/1	0.02	0.75	57,57,57,57	1
22	UNX	A	1672	1/1	0.03	0.82	57,57,57,57	1
22	UNX	A	1714	1/1	0.03	0.80	57,57,57,57	1
22	UNX	A	1571	1/1	0.04	1.12	57,57,57,57	1
22	UNX	A	1685	1/1	0.05	0.82	57,57,57,57	1
22	UNX	A	1619	1/1	0.05	1.16	57,57,57,57	1
22	UNX	A	1679	1/1	0.05	1.05	57,57,57,57	1
22	UNX	A	1592	1/1	0.06	1.25	57,57,57,57	0
22	UNX	A	1602	1/1	0.06	0.83	57,57,57,57	1
22	UNX	A	1630	1/1	0.06	0.84	57,57,57,57	1
22	UNX	A	1702	1/1	0.07	1.01	57,57,57,57	1
22	UNX	A	1610	1/1	0.08	1.15	57,57,57,57	1
22	UNX	A	1570	1/1	0.08	0.93	57,57,57,57	1
22	UNX	A	1662	1/1	0.10	1.50	57,57,57,57	1
22	UNX	A	1666	1/1	0.11	0.95	57,57,57,57	1
22	UNX	A	1652	1/1	0.11	0.73	57,57,57,57	1
22	UNX	A	1572	1/1	0.11	0.80	57,57,57,57	1
22	UNX	A	1596	1/1	0.13	0.94	57,57,57,57	1
22	UNX	A	1631	1/1	0.15	1.27	57,57,57,57	1
22	UNX	A	1600	1/1	0.16	0.90	57,57,57,57	1
22	UNX	A	1582	1/1	0.18	0.87	57,57,57,57	1
22	UNX	A	1608	1/1	0.19	0.90	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	UNX	A	1675	1/1	0.19	1.63	57,57,57,57	1
22	UNX	A	1669	1/1	0.21	0.83	57,57,57,57	1
22	UNX	A	1618	1/1	0.21	1.06	57,57,57,57	1
22	UNX	A	1577	1/1	0.21	0.71	57,57,57,57	1
22	UNX	A	1617	1/1	0.21	1.05	57,57,57,57	1
22	UNX	B	257	1/1	0.23	0.50	57,57,57,57	1
22	UNX	A	1604	1/1	0.23	0.87	57,57,57,57	1
22	UNX	A	1706	1/1	0.24	1.08	57,57,57,57	1
22	UNX	A	1701	1/1	0.25	1.32	57,57,57,57	1
22	UNX	A	1698	1/1	0.26	1.30	57,57,57,57	1
22	UNX	A	71	1/1	0.28	1.00	57,57,57,57	1
22	UNX	A	1667	1/1	0.29	0.90	57,57,57,57	1
22	UNX	A	1643	1/1	0.29	1.14	57,57,57,57	1
22	UNX	A	1613	1/1	0.31	2.18	57,57,57,57	1
22	UNX	A	1627	1/1	0.31	0.72	57,57,57,57	1
22	UNX	A	1624	1/1	0.31	0.89	57,57,57,57	1
22	UNX	A	1664	1/1	0.32	1.27	57,57,57,57	1
22	UNX	A	1655	1/1	0.33	0.96	57,57,57,57	1
22	UNX	A	1653	1/1	0.34	0.71	57,57,57,57	1
22	UNX	A	1696	1/1	0.34	1.14	57,57,57,57	1
22	UNX	A	1569	1/1	0.34	0.89	57,57,57,57	1
22	UNX	A	1699	1/1	0.35	1.19	57,57,57,57	1
22	UNX	A	1663	1/1	0.37	1.64	57,57,57,57	1
22	UNX	A	100	1/1	0.37	0.67	57,57,57,57	1
22	UNX	A	1546	1/1	0.38	0.84	57,57,57,57	0
22	UNX	A	1606	1/1	0.39	0.94	57,57,57,57	1
22	UNX	A	1598	1/1	0.39	0.87	57,57,57,57	1
22	UNX	A	1691	1/1	0.40	1.77	57,57,57,57	1
22	UNX	A	1670	1/1	0.40	1.25	57,57,57,57	1
22	UNX	A	1661	1/1	0.40	1.25	57,57,57,57	1
22	UNX	A	1591	1/1	0.41	0.87	57,57,57,57	1
22	UNX	A	1713	1/1	0.42	1.57	57,57,57,57	1
22	UNX	A	1622	1/1	0.43	1.15	57,57,57,57	1
22	UNX	A	1644	1/1	0.44	0.79	57,57,57,57	1
22	UNX	A	1638	1/1	0.44	1.46	57,57,57,57	1
22	UNX	A	1658	1/1	0.44	1.43	57,57,57,57	1
22	UNX	A	1654	1/1	0.44	0.89	57,57,57,57	1
22	UNX	A	1578	1/1	0.45	1.14	57,57,57,57	1
22	UNX	A	1597	1/1	0.45	1.88	57,57,57,57	1
22	UNX	A	1614	1/1	0.45	1.06	57,57,57,57	1
22	UNX	A	1573	1/1	0.45	1.26	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	UNX	A	1626	1/1	0.47	1.07	57,57,57,57	1
22	UNX	A	1593	1/1	0.47	0.95	57,57,57,57	1
22	UNX	A	1563	1/1	0.47	1.07	57,57,57,57	1
22	UNX	A	1684	1/1	0.48	1.50	57,57,57,57	1
22	UNX	A	1707	1/1	0.49	1.09	57,57,57,57	1
22	UNX	A	1552	1/1	0.49	0.82	57,57,57,57	1
22	UNX	A	1579	1/1	0.49	1.31	57,57,57,57	1
22	UNX	A	1709	1/1	0.50	1.04	57,57,57,57	1
22	UNX	A	1576	1/1	0.50	1.34	57,57,57,57	1
22	UNX	A	1607	1/1	0.50	0.77	57,57,57,57	1
22	UNX	A	1712	1/1	0.51	1.10	57,57,57,57	1
22	UNX	A	72	1/1	0.51	1.38	57,57,57,57	1
22	UNX	A	1560	1/1	0.52	0.71	57,57,57,57	1
22	UNX	A	1710	1/1	0.53	1.27	57,57,57,57	1
22	UNX	A	1545	1/1	0.53	0.81	57,57,57,57	0
22	UNX	A	1605	1/1	0.54	0.94	57,57,57,57	1
22	UNX	A	1723	1/1	0.55	0.99	55,55,55,55	1
22	UNX	A	1687	1/1	0.55	1.17	57,57,57,57	1
22	UNX	A	1690	1/1	0.55	1.33	57,57,57,57	1
22	UNX	A	1566	1/1	0.56	0.91	57,57,57,57	1
22	UNX	A	1660	1/1	0.56	1.18	57,57,57,57	1
22	UNX	A	1720	1/1	0.56	1.05	57,57,57,57	1
22	UNX	A	1590	1/1	0.57	0.92	57,57,57,57	1
22	UNX	A	1692	1/1	0.58	0.79	57,57,57,57	1
22	UNX	A	1586	1/1	0.58	1.08	57,57,57,57	1
22	UNX	A	1674	1/1	0.59	1.24	57,57,57,57	1
22	UNX	A	1688	1/1	0.59	0.88	57,57,57,57	1
22	UNX	A	1671	1/1	0.59	1.22	57,57,57,57	1
22	UNX	A	87	1/1	0.60	0.90	57,57,57,57	1
22	UNX	A	1557	1/1	0.60	1.30	57,57,57,57	1
22	UNX	A	1583	1/1	0.61	1.52	57,57,57,57	1
22	UNX	A	1558	1/1	0.61	1.08	57,57,57,57	1
22	UNX	A	1721	1/1	0.61	1.26	57,57,57,57	1
22	UNX	A	1599	1/1	0.62	1.04	57,57,57,57	1
22	UNX	A	1565	1/1	0.62	0.84	57,57,57,57	1
22	UNX	A	86	1/1	0.63	0.72	57,57,57,57	1
22	UNX	A	1681	1/1	0.63	1.22	57,57,57,57	1
22	UNX	A	1682	1/1	0.63	1.07	57,57,57,57	1
22	UNX	A	1642	1/1	0.63	0.93	57,57,57,57	1
22	UNX	A	1574	1/1	0.63	0.91	57,57,57,57	1
22	UNX	A	1559	1/1	0.64	0.90	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	UNX	A	1686	1/1	0.65	1.19	57,57,57,57	1
22	UNX	A	1693	1/1	0.65	0.80	57,57,57,57	1
22	UNX	A	1575	1/1	0.65	0.85	57,57,57,57	1
22	UNX	A	1562	1/1	0.67	1.03	57,57,57,57	1
22	UNX	A	85	1/1	0.67	1.23	57,57,57,57	1
22	UNX	A	1580	1/1	0.67	1.18	57,57,57,57	1
22	UNX	A	1676	1/1	0.67	1.16	57,57,57,57	1
22	UNX	A	1549	1/1	0.68	1.04	57,57,57,57	1
22	UNX	A	1645	1/1	0.68	1.15	57,57,57,57	1
22	UNX	A	1708	1/1	0.69	1.24	57,57,57,57	1
22	UNX	A	1623	1/1	0.69	0.75	57,57,57,57	1
22	UNX	A	1555	1/1	0.69	0.86	57,57,57,57	0
22	UNX	A	1556	1/1	0.70	0.99	57,57,57,57	1
22	UNX	A	1554	1/1	0.70	0.66	57,57,57,57	0
22	UNX	A	1647	1/1	0.70	1.58	57,57,57,57	1
22	UNX	A	1581	1/1	0.71	1.00	57,57,57,57	1
22	UNX	A	1564	1/1	0.72	1.17	57,57,57,57	1
22	UNX	A	1587	1/1	0.72	0.98	57,57,57,57	1
22	UNX	A	1657	1/1	0.72	1.06	57,57,57,57	1
22	UNX	A	1659	1/1	0.73	1.52	57,57,57,57	1
22	UNX	A	1550	1/1	0.73	0.88	57,57,57,57	1
22	UNX	A	1722	1/1	0.73	0.92	55,55,55,55	1
22	UNX	A	1594	1/1	0.75	1.05	57,57,57,57	1
22	UNX	A	1548	1/1	0.77	0.72	57,57,57,57	0
22	UNX	A	1678	1/1	0.80	1.36	57,57,57,57	1
22	UNX	A	1595	1/1	0.80	1.25	57,57,57,57	1
22	UNX	A	1567	1/1	0.81	0.94	57,57,57,57	1
22	UNX	A	1717	1/1	0.81	0.78	57,57,57,57	1
22	UNX	A	1611	1/1	0.81	1.06	57,57,57,57	1
22	UNX	A	1553	1/1	0.82	1.13	57,57,57,57	1
22	UNX	A	1616	1/1	0.83	0.86	57,57,57,57	1
22	UNX	A	1547	1/1	0.83	0.66	57,57,57,57	0
22	UNX	A	1551	1/1	0.86	0.78	57,57,57,57	1
22	UNX	A	1718	1/1	0.90	0.32	57,57,57,57	1
23	ZN	D	306	1/1	0.91	0.38	67,67,67,67	0
23	ZN	N	307	1/1	0.99	0.04	67,67,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.