



Full wwPDB X-ray Structure Validation Report i

Feb 27, 2014 – 03:35 PM GMT

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

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

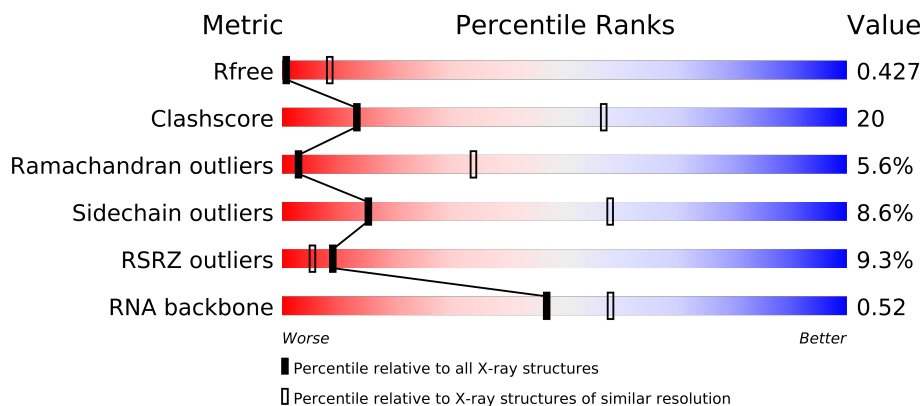
The following versions of software and data (see [references](#)) were used in the production of this report:

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

1 Overall quality at a glance

The reported resolution of this entry is 3.50 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

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

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Mol	Chain	Length	Quality of chain
12	L	146	
13	M	136	
14	N	117	
15	O	98	
16	P	137	
17	Q	116	
18	R	101	
19	S	112	
20	T	92	
21	U	100	
22	V	188	
23	W	76	
24	X	88	
25	Y	62	
26	Z	59	
27	1	30	
28	2	52	
29	3	44	
30	4	48	
31	5	63	

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 89771 atoms, of which 0 are hydrogen and 0 are deuterium.

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

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	P	12	Total	Mg	0	0
			12	12		
32	K	12	Total	Mg	0	0
			12	12		
32	B	43	Total	Mg	0	0
			43	43		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	6	330	Total Mg 330 330	0	0
32	W	1	Total Mg 1 1	0	0
32	N	1	Total Mg 1 1	0	0
32	X	3	Total Mg 3 3	0	0
32	2	3	Total Mg 3 3	0	0
32	S	2	Total Mg 2 2	0	0
32	J	6	Total Mg 6 6	0	0
32	E	3	Total Mg 3 3	0	0
32	V	4	Total Mg 4 4	0	0
32	A	1038	Total Mg 1038 1038	0	0
32	5	1	Total Mg 1 1	0	0
32	M	1	Total Mg 1 1	0	0
32	1	1	Total Mg 1 1	0	0
32	D	6	Total Mg 6 6	0	0
32	I	1	Total Mg 1 1	0	0
32	4	3	Total Mg 3 3	0	0
32	U	1	Total Mg 1 1	0	0
32	L	3	Total Mg 3 3	0	0
32	G	3	Total Mg 3 3	0	0
32	Q	2	Total Mg 2 2	0	0
32	C	8	Total Mg 8 8	0	0

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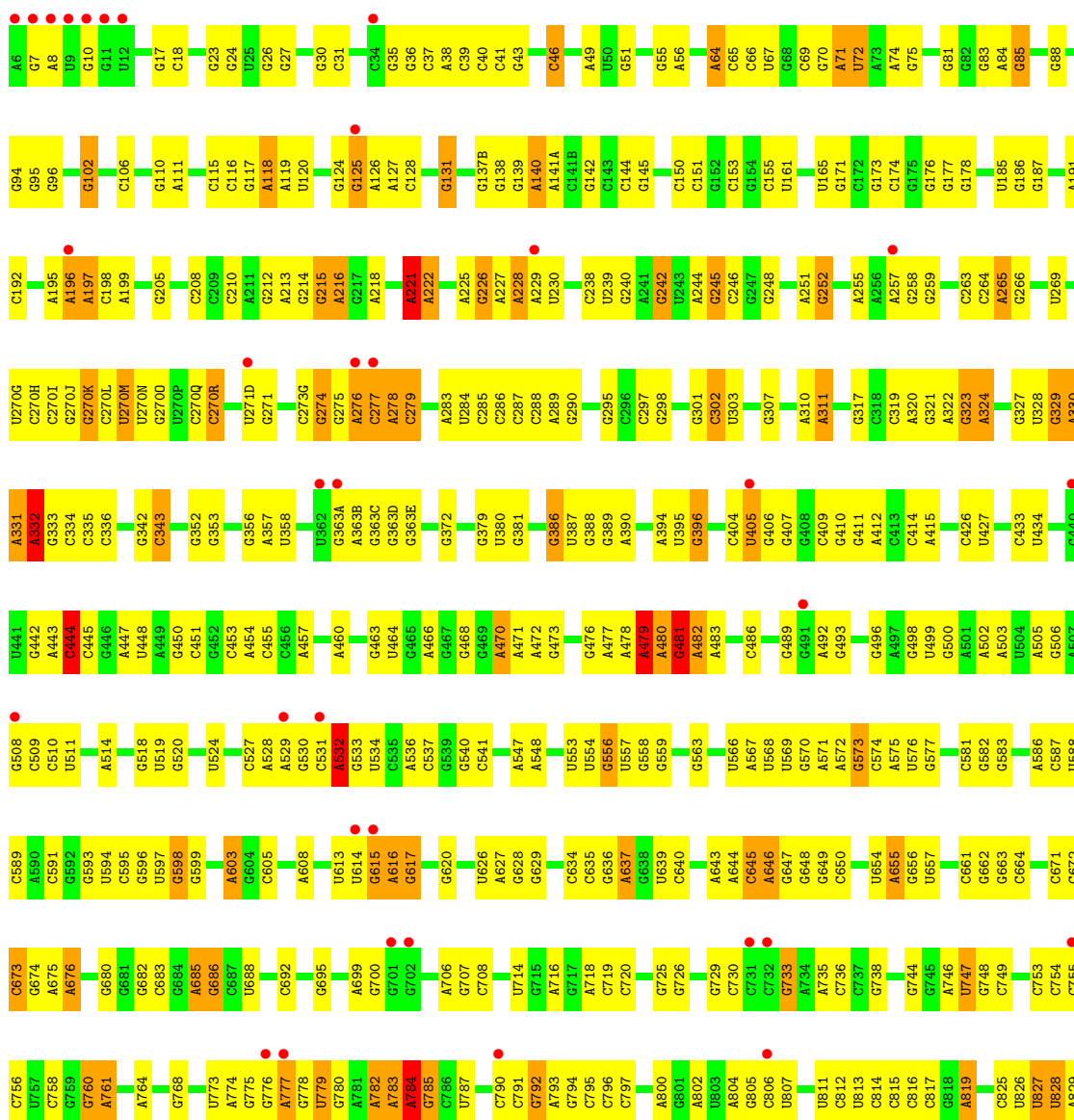
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	O	1	Total 1	Mg 1	0	0
32	Y	2	Total 2	Mg 2	0	0
32	F	4	Total 4	Mg 4	0	0

3 Residue-property plots

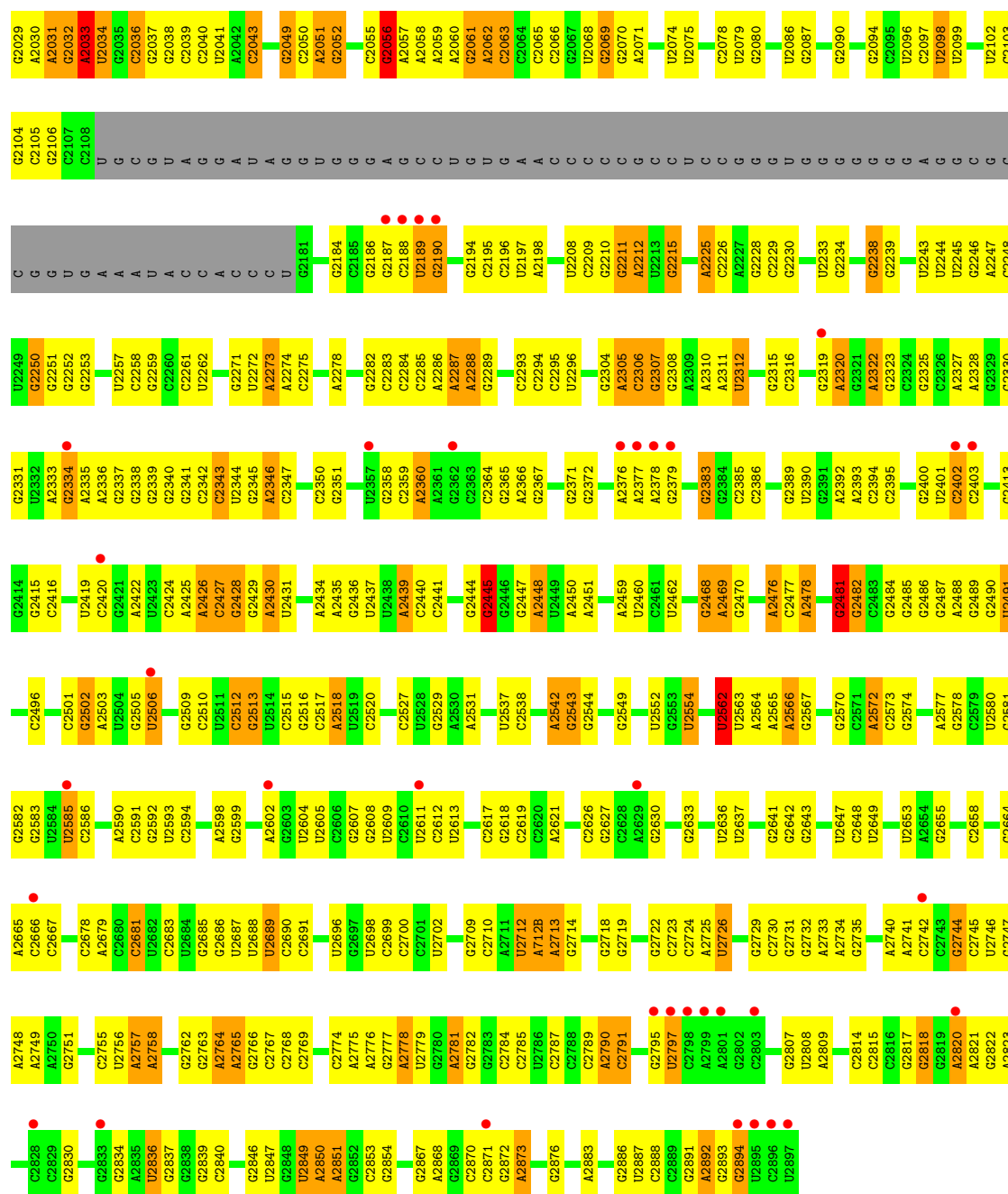
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

- Molecule 1: 23S ribosomal RNA

Chain A:

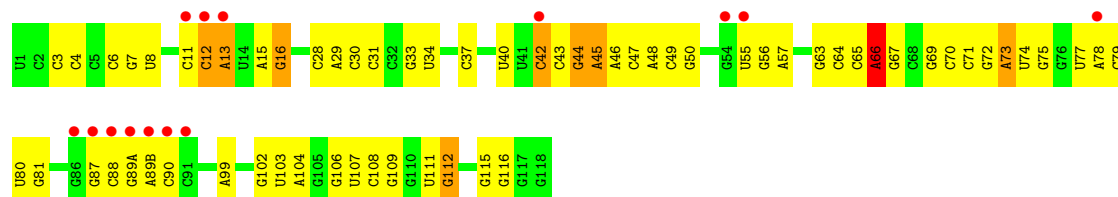






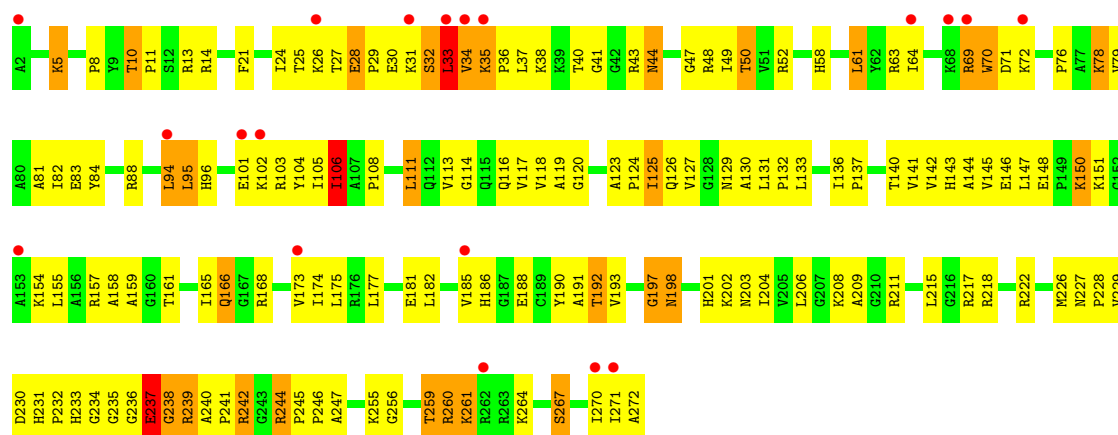
• Molecule 2: 5S ribosomal RNA

Chain B:



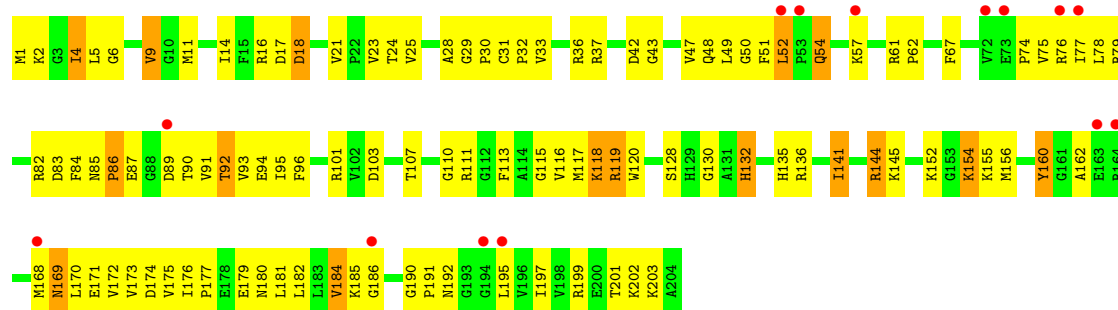
• Molecule 3: 50S ribosomal protein L2

Chain C:



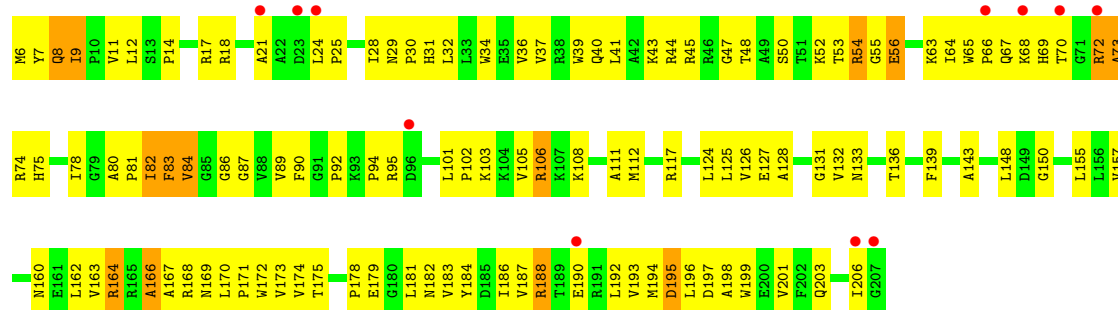
• Molecule 4: 50S ribosomal protein L3

Chain D:



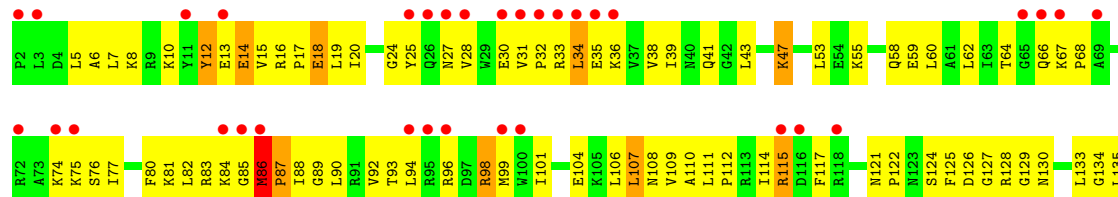
• Molecule 5: 50S ribosomal protein L4

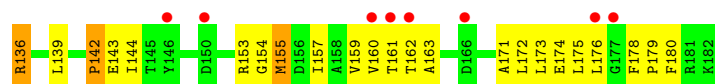
Chain E:



• Molecule 6: 50S ribosomal protein L5

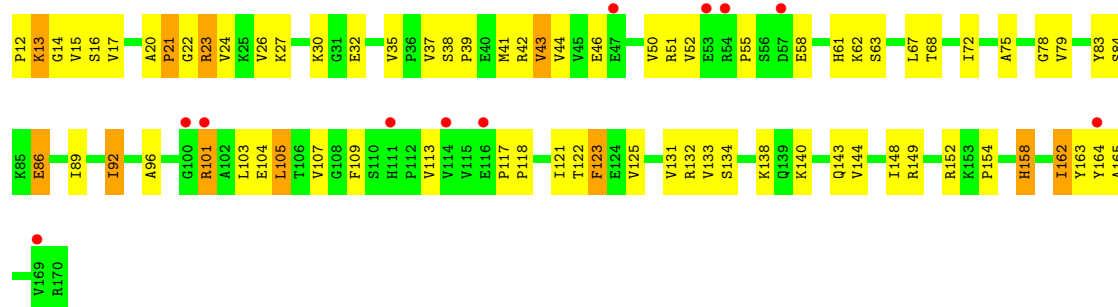
Chain F:





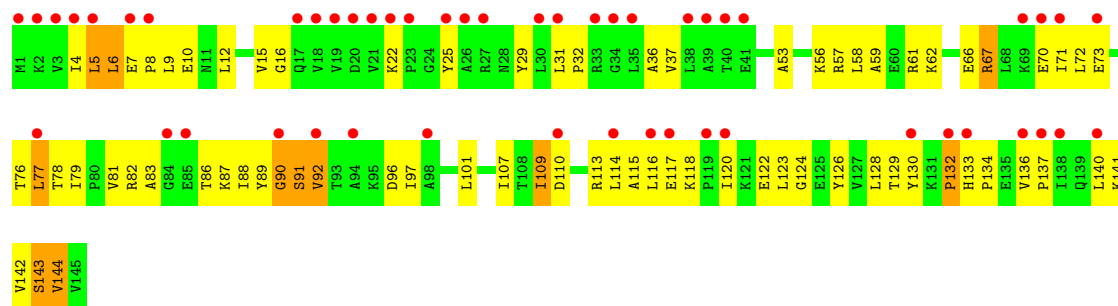
- Molecule 7: 50S ribosomal protein L6

Chain G:



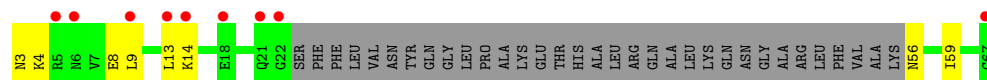
- Molecule 8: 50S ribosomal protein L9

Chain H:



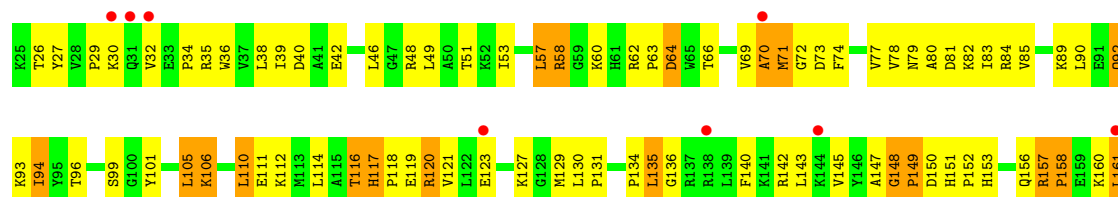
- Molecule 9: 50S ribosomal protein L10

Chain I:



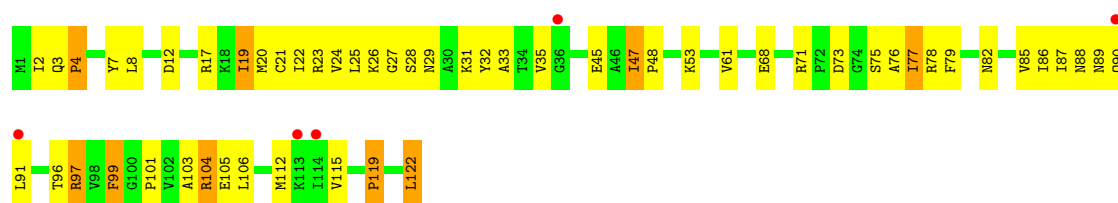
- Molecule 10: 50S ribosomal protein L13

Chain J:



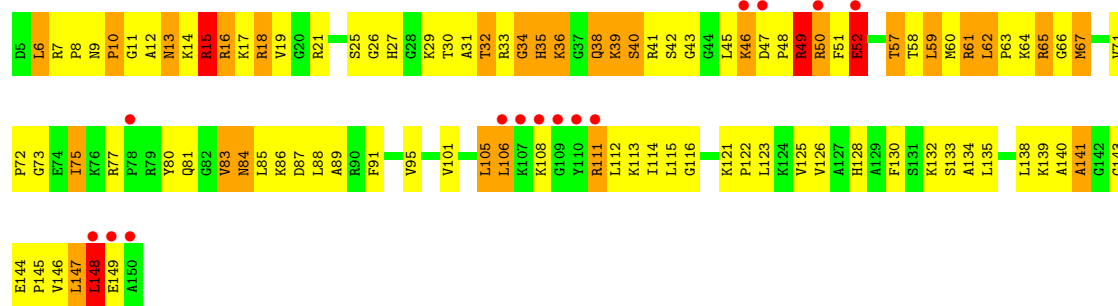
- Molecule 11: 50S ribosomal protein L14

Chain K:



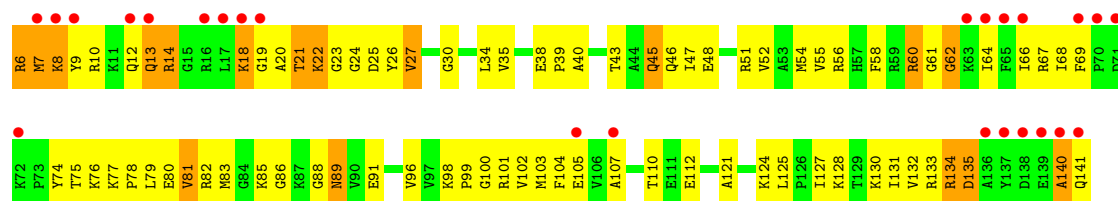
- Molecule 12: 50S ribosomal protein L15

Chain L:



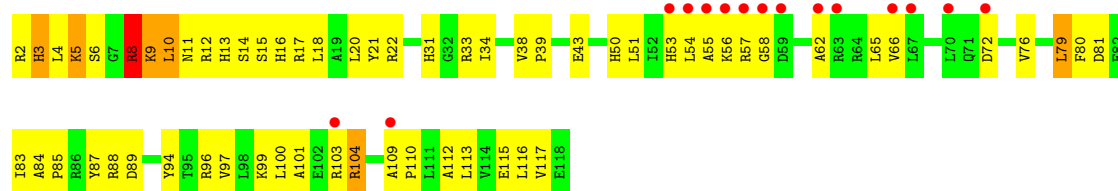
- Molecule 13: 50S ribosomal protein L16

Chain M:



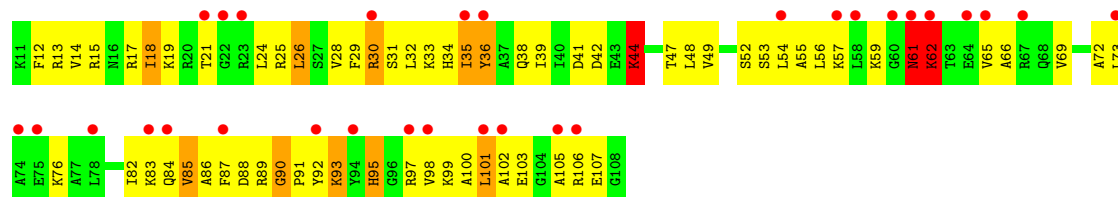
- Molecule 14: 50S ribosomal protein L17

Chain N:



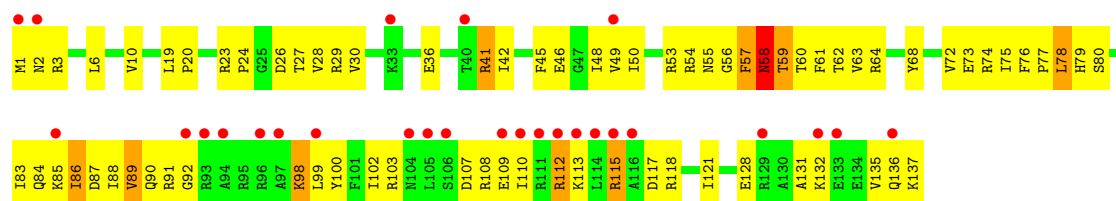
- Molecule 15: 50S ribosomal protein L18

Chain O:



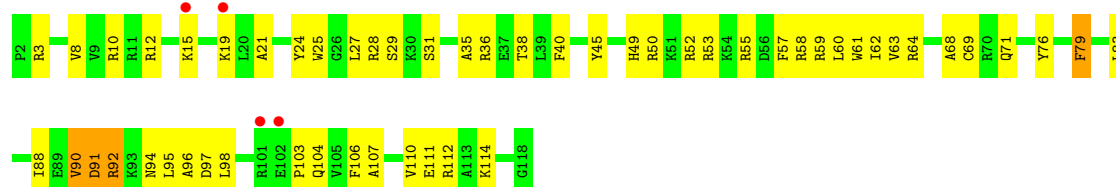
- Molecule 16: 50S ribosomal protein L19

Chain P: 



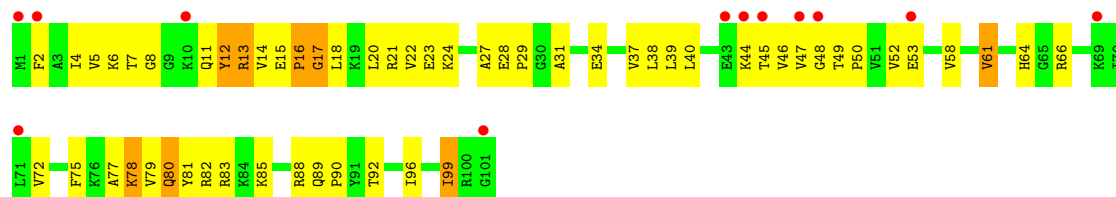
- Molecule 17: 50S ribosomal protein L20

Chain Q: 



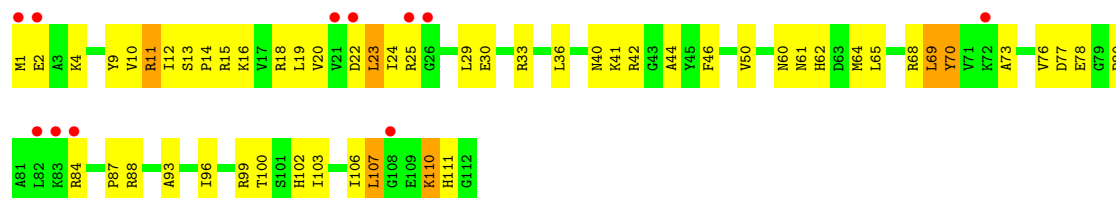
- Molecule 18: 50S ribosomal protein L21

Chain R: 



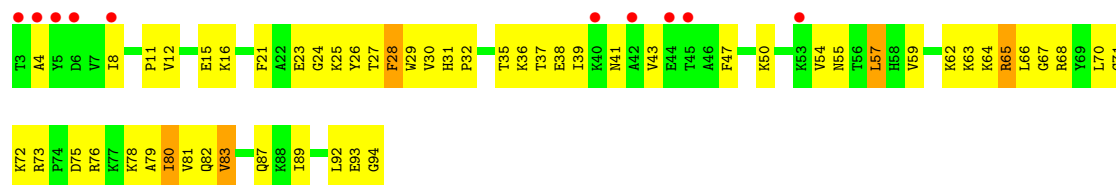
- Molecule 19: 50S ribosomal protein L22

Chain S: 



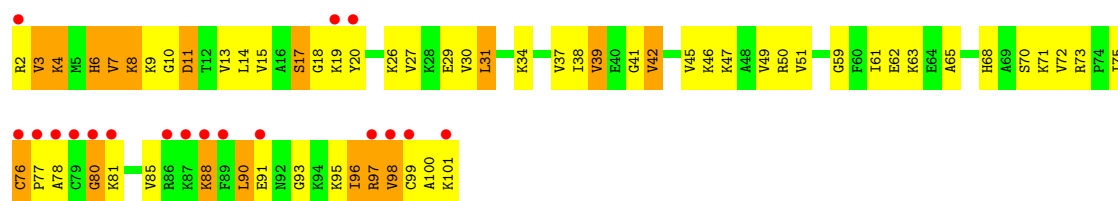
- Molecule 20: 50S ribosomal protein L23

Chain T: 



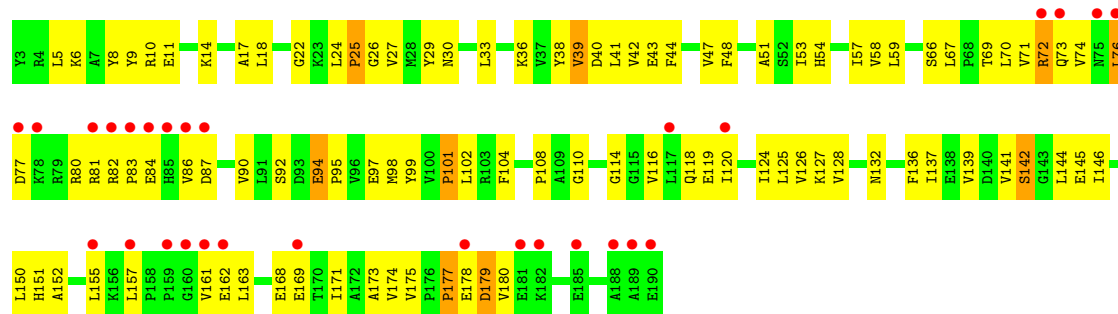
- Molecule 21: 50S ribosomal protein L24

Chain U: 



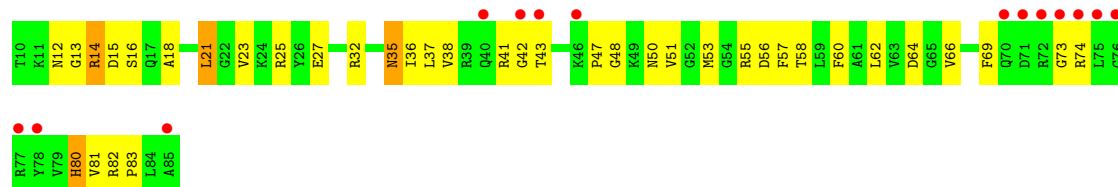
• Molecule 22: 50S ribosomal protein L25

Chain V:



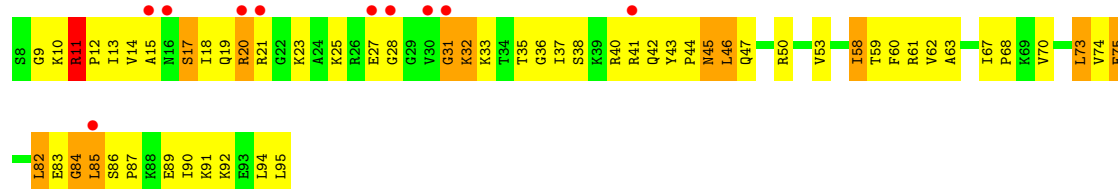
• Molecule 23: 50S ribosomal protein L27

Chain W:



• Molecule 24: 50S ribosomal protein L28

Chain X:



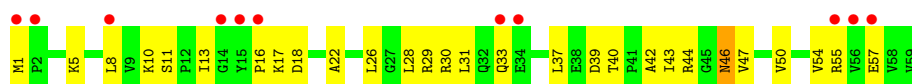
• Molecule 25: 50S ribosomal protein L29

Chain Y:



• Molecule 26: 50S ribosomal protein L30

Chain Z:



- Molecule 27: 50S ribosomal protein L31

Chain 1:



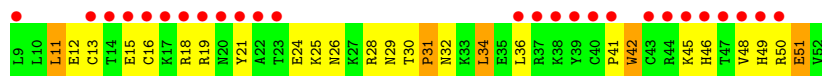
- Molecule 28: 50S ribosomal protein L32

Chain 2:



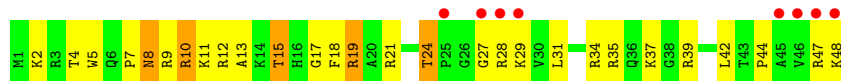
- Molecule 29: 50S ribosomal protein L33

Chain 3:



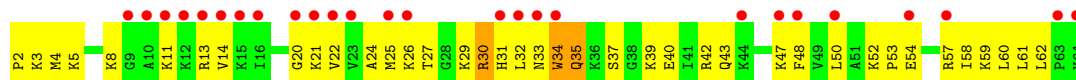
- Molecule 30: 50S ribosomal protein L34

Chain 4:



- Molecule 31: 50S ribosomal protein L35

Chain 5:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.94Å 455.59Å 618.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.50 60.01 – 3.49	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-3.50) 99.6 (60.01-3.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 3.49Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.233 , 0.264 0.429 , 0.427	Depositor DCC
R_{free} test set	7390 reflections (0.99%)	DCC
Wilson B-factor (Å ²)	106.2	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 46.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	1 of 746568 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.66	EDS
Total number of atoms	89771	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

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

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.54	0/66575	1.04	119/103930 (0.1%)
2	B	0.44	0/2853	0.93	2/4451 (0.0%)
3	C	0.34	0/2155	0.52	0/2905
4	D	0.27	0/1597	0.48	0/2153
5	E	0.31	0/1622	0.47	0/2194
6	F	0.23	0/1500	0.42	0/2017
7	G	0.24	0/1246	0.43	0/1682
8	H	0.31	0/1148	0.47	0/1552
9	I	0.22	0/252	0.38	0/333
10	J	0.27	0/1124	0.47	0/1515
11	K	0.28	0/942	0.49	0/1268
12	L	0.32	0/1131	0.57	0/1504
13	M	0.30	0/1099	0.50	0/1468
14	N	0.27	0/974	0.45	0/1302
15	O	0.24	0/779	0.42	0/1036
16	P	0.27	0/1158	0.44	0/1544
17	Q	0.31	0/970	0.47	0/1290
18	R	0.29	0/790	0.46	0/1057
19	S	0.30	0/902	0.50	0/1209
20	T	0.33	0/740	0.50	0/993
21	U	0.26	0/789	0.45	0/1051
22	V	0.23	0/1524	0.45	0/2068
23	W	0.27	0/613	0.43	0/816
24	X	0.31	0/702	0.57	0/932
25	Y	0.31	0/523	0.54	0/690
26	Z	0.24	0/473	0.41	0/634
27	1	0.20	0/229	0.38	0/309
28	2	0.28	0/419	0.51	0/567
29	3	0.21	0/388	0.40	0/518
30	4	0.38	0/427	0.53	0/561
31	5	0.32	0/516	0.51	0/679
All	All	0.48	0/96160	0.93	121/144228 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	F	0	1
12	L	0	1
All	All	0	2

There are no bond length outliers.

All (121) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	676	A	C1'-O4'-C4'	-9.79	102.07	109.90
1	A	1786	A	C1'-O4'-C4'	-9.78	102.07	109.90
1	A	945	A	C1'-O4'-C4'	-9.73	102.11	109.90
1	A	945	A	O4'-C1'-N9	9.13	115.50	108.20
1	A	2818	G	C1'-O4'-C4'	-9.09	102.63	109.90
1	A	265	A	C3'-C2'-C1'	-8.72	94.53	101.50
1	A	761	A	N1-C6-N6	8.67	123.80	118.60
1	A	748	G	C1'-O4'-C4'	-8.53	103.08	109.90
1	A	221	A	P-O3'-C3'	8.12	129.45	119.70
1	A	1786	A	C3'-C2'-C1'	-8.09	95.03	101.50
1	A	1614	A	C1'-O4'-C4'	-7.70	103.74	109.90
1	A	1937	A	P-O3'-C3'	7.66	128.89	119.70
1	A	933	A	O4'-C1'-N9	7.51	114.21	108.20
1	A	481	G	P-O3'-C3'	7.49	128.69	119.70
1	A	945	A	C3'-C2'-C1'	-7.42	95.56	101.50
1	A	1022	G	P-O3'-C3'	7.13	128.26	119.70
1	A	242	G	C3'-C2'-C1'	-7.02	95.88	101.50
1	A	1395	A	C1'-O4'-C4'	-6.94	104.35	109.90
1	A	1698	A	C3'-C2'-C1'	-6.84	96.03	101.50
1	A	989	G	C1'-O4'-C4'	-6.84	104.43	109.90
1	A	332	A	P-O3'-C3'	6.82	127.88	119.70
1	A	1545	A	C1'-O4'-C4'	-6.63	104.60	109.90
1	A	131	G	C1'-O4'-C4'	-6.62	104.60	109.90
1	A	1558	A	P-O3'-C3'	6.57	127.59	119.70
1	A	2506	U	O4'-C1'-N1	6.54	113.44	108.20
1	A	1542	G	P-O3'-C3'	6.54	127.55	119.70
1	A	1266	G	C3'-C2'-C1'	-6.50	96.30	101.50
1	A	372	G	O4'-C1'-N9	6.48	113.38	108.20
1	A	2049	G	C1'-O4'-C4'	-6.47	104.72	109.90
1	A	2445	G	C4'-C3'-C2'	-6.47	96.13	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2447	G	P-O3'-C3'	6.47	127.46	119.70
1	A	783	A	C3'-C2'-C1'	-6.45	96.34	101.50
1	A	1427	A	P-O3'-C3'	6.39	127.37	119.70
1	A	933	A	C4'-C3'-C2'	-6.38	96.22	102.60
1	A	1385	G	C3'-C2'-C1'	-6.37	96.41	101.50
1	A	1698	A	C1'-O4'-C4'	-6.36	104.81	109.90
1	A	783	A	C2-N3-C4	-6.35	107.43	110.60
1	A	1608	A	C1'-O4'-C4'	-6.30	104.86	109.90
1	A	761	A	C6-C5-N7	-6.29	127.90	132.30
1	A	933	A	C1'-O4'-C4'	-6.24	104.91	109.90
1	A	1984	G	C4'-C3'-C2'	-6.23	96.37	102.60
1	A	131	G	O4'-C4'-C3'	-6.19	97.81	104.00
1	A	1046	A	C5-C6-N1	-6.19	114.60	117.70
1	A	1496	A	O4'-C1'-N9	6.17	113.14	108.20
1	A	2225	A	P-O3'-C3'	6.16	127.09	119.70
1	A	859	G	C3'-C2'-C1'	-6.14	96.59	101.50
1	A	1379	A	P-O3'-C3'	6.13	127.05	119.70
1	A	450	G	C5-C6-N1	-6.09	108.45	111.50
1	A	791	C	C3'-C2'-C1'	-6.08	96.63	101.50
1	A	1021	A	C3'-C2'-C1'	-6.08	96.63	101.50
1	A	673	C	C4'-C3'-C2'	-6.08	96.52	102.60
1	A	1786	A	N9-C1'-C2'	6.04	121.85	114.00
1	A	2033	A	P-O3'-C3'	6.04	126.94	119.70
1	A	783	A	N1-C6-N6	6.02	122.21	118.60
1	A	760	G	C4'-C3'-C2'	-6.01	96.59	102.60
1	A	2613	U	C3'-C2'-C1'	-6.00	96.70	101.50
1	A	686	G	O4'-C1'-N9	5.96	112.96	108.20
1	A	2481	G	P-O3'-C3'	5.93	126.82	119.70
1	A	2562	U	C4'-C3'-C2'	-5.89	96.70	102.60
1	A	2049	G	C4'-C3'-C2'	-5.79	96.81	102.60
1	A	825	C	C4'-C3'-C2'	-5.78	96.83	102.60
1	A	807	U	C4'-C3'-C2'	-5.76	96.84	102.60
1	A	2098	U	P-O3'-C3'	5.72	126.56	119.70
1	A	733	G	O4'-C1'-N9	-5.70	103.64	108.20
1	A	1761	C	C1'-O4'-C4'	-5.67	105.36	109.90
1	A	444	C	C4'-C3'-C2'	-5.66	96.94	102.60
1	A	761	A	N7-C8-N9	5.66	116.63	113.80
1	A	680	G	O4'-C1'-N9	-5.65	103.68	108.20
1	A	2512	C	C4'-C3'-C2'	-5.65	96.95	102.60
1	A	2056	G	N3-C4-N9	-5.63	122.62	126.00
1	A	2278	A	C1'-O4'-C4'	-5.58	105.44	109.90
1	A	783	A	C5-N7-C8	-5.58	101.11	103.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	66	A	P-O3'-C3'	5.57	126.39	119.70
1	A	2428	G	P-O3'-C3'	5.57	126.39	119.70
1	A	989	G	O4'-C1'-N9	5.53	112.62	108.20
1	A	974(B)	C	C3'-C2'-C1'	-5.51	97.10	101.50
1	A	95	G	C4'-C3'-C2'	-5.50	97.11	102.60
1	A	1255	U	C1'-O4'-C4'	-5.49	105.51	109.90
1	A	940	G	C4'-C3'-C2'	-5.48	97.12	102.60
1	A	450	G	C4-C5-C6	5.47	122.08	118.80
1	A	85	G	C3'-C2'-C1'	-5.46	97.13	101.50
1	A	1275	A	C3'-C2'-C1'	-5.45	97.14	101.50
1	A	938	G	C4'-C3'-C2'	-5.43	97.17	102.60
1	A	527	C	O4'-C1'-N1	5.40	112.52	108.20
1	A	407	G	C4'-C3'-C2'	-5.39	97.21	102.60
1	A	479	A	C1'-O4'-C4'	-5.39	105.59	109.90
1	A	1786	A	O4'-C1'-C2'	-5.38	100.42	105.80
1	A	2052	G	C4'-C3'-C2'	-5.37	97.23	102.60
1	A	226	G	C3'-C2'-C1'	-5.35	97.22	101.50
1	A	2789	C	C1'-O4'-C4'	-5.35	105.62	109.90
1	A	761	A	C5-C6-N1	-5.30	115.05	117.70
1	A	2689	U	P-O3'-C3'	5.29	126.05	119.70
1	A	1162	G	C4'-C3'-C2'	-5.29	97.31	102.60
1	A	1616	A	O4'-C1'-N9	5.28	112.43	108.20
1	A	210	C	C6-N1-C2	5.27	122.41	120.30
1	A	532	A	C1'-O4'-C4'	-5.24	105.71	109.90
1	A	1613	G	C4'-C3'-C2'	-5.21	97.39	102.60
1	A	974(B)	C	O4'-C1'-C2'	-5.21	100.59	105.80
1	A	1855	G	C4'-C3'-C2'	-5.20	97.40	102.60
1	A	1012	U	C3'-C2'-C1'	-5.18	97.36	101.50
1	A	444	C	C1'-O4'-C4'	-5.17	105.77	109.90
1	A	784	A	C3'-C2'-C1'	5.14	105.61	101.50
1	A	1559	G	C1'-O4'-C4'	-5.13	105.79	109.90
1	A	2056	G	C4'-C3'-C2'	-5.13	97.47	102.60
1	A	208	C	C6-N1-C2	5.13	122.35	120.30
1	A	692	C	C4'-C3'-C2'	-5.13	97.47	102.60
1	A	463	G	C4'-C3'-C2'	-5.12	97.48	102.60
1	A	807	U	O4'-C4'-C3'	-5.12	98.88	104.00
1	A	2744	G	C4'-C3'-C2'	-5.12	97.48	102.60
1	A	1504	C	N1-C1'-C2'	-5.11	106.37	112.00
1	A	933	A	O4'-C4'-C3'	-5.11	98.89	104.00
1	A	1267	U	P-O3'-C3'	5.11	125.83	119.70
1	A	2681	C	C3'-C2'-C1'	-5.09	97.43	101.50
1	A	1496	A	C1'-O4'-C4'	-5.09	105.83	109.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	738	G	C1'-O4'-C4'	-5.06	105.85	109.90
2	B	42	C	C1'-O4'-C4'	-5.06	105.85	109.90
1	A	1022	G	C3'-C2'-C1'	5.05	105.54	101.50
1	A	324	A	C4'-C3'-C2'	-5.04	97.56	102.60
1	A	1929	G	C3'-C2'-C1'	-5.03	97.48	101.50
1	A	672	C	C4'-C3'-C2'	-5.02	97.58	102.60
1	A	1743	G	C4'-C3'-C2'	-5.01	97.59	102.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

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

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	59442	0	29966	1293	0
2	B	2551	0	1295	53	0
3	C	2105	0	2182	212	0
4	D	1564	0	1629	112	0
5	E	1587	0	1632	106	0
6	F	1475	0	1537	109	0
7	G	1223	0	1282	66	0
8	H	1133	0	1220	80	0
9	I	254	0	275	8	0
10	J	1097	0	1168	83	0
11	K	932	0	994	55	0
12	L	1114	0	1187	169	0
13	M	1079	0	1127	99	0
14	N	960	0	1021	71	0
15	O	771	0	832	70	0
16	P	1144	0	1211	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Q	953	0	1013	71	0
18	R	779	0	852	73	0
19	S	891	0	951	52	0
20	T	726	0	778	59	0
21	U	776	0	870	76	0
22	V	1492	0	1513	92	0
23	W	605	0	628	38	0
24	X	695	0	764	68	0
25	Y	521	0	575	45	0
26	Z	468	0	523	24	0
27	1	226	0	225	17	0
28	2	405	0	420	29	0
29	3	381	0	391	26	0
30	4	419	0	467	32	0
31	5	508	0	576	55	0
32	1	1	0	0	0	0
32	2	3	0	0	0	0
32	4	3	0	0	0	0
32	5	1	0	0	0	0
32	6	330	0	0	0	0
32	A	1038	0	0	0	0
32	B	43	0	0	0	0
32	C	8	0	0	0	0
32	D	6	0	0	0	0
32	E	3	0	0	0	0
32	F	4	0	0	0	0
32	G	3	0	0	0	0
32	I	1	0	0	0	0
32	J	6	0	0	0	0
32	K	12	0	0	0	0
32	L	3	0	0	0	0
32	M	1	0	0	0	0
32	N	1	0	0	0	0
32	O	1	0	0	0	0
32	P	12	0	0	0	0
32	Q	2	0	0	0	0
32	S	2	0	0	0	0
32	U	1	0	0	0	0
32	V	4	0	0	0	0
32	W	1	0	0	0	0
32	X	3	0	0	0	0
32	Y	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	89771	0	59104	3032	0

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

All (3032) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2015:A:H1'	28:2:2:ALA:HA	1.33	1.08
12:L:33:ARG:HG3	12:L:36:LYS:HD3	1.33	1.08
12:L:49:ARG:HG2	12:L:50:ARG:H	1.18	1.06
12:L:128:HIS:HA	12:L:147:LEU:HB3	1.30	1.06
23:W:23:VAL:HA	23:W:38:VAL:HG22	1.37	1.03
10:J:70:ALA:HB2	10:J:135:LEU:HD12	1.41	1.03
15:O:24:LEU:HD12	15:O:84:GLN:HB3	1.38	1.02
17:Q:92:ARG:HB2	17:Q:92:ARG:HH11	1.24	1.01
3:C:242:ARG:HD3	3:C:242:ARG:H	1.23	0.99
8:H:92:VAL:HG13	8:H:120:ILE:HB	1.42	0.99
21:U:8:LYS:H	21:U:8:LYS:HZ2	1.07	0.98
1:A:2681:C:H5	1:A:2725:A:H62	0.99	0.98
1:A:2781:A:H5'	1:A:2782:G:H5'	1.46	0.98
1:A:1163:G:H2'	1:A:1164:G:H5''	1.46	0.97
20:T:11:PRO:HA	20:T:28:PHE:HB3	1.47	0.95
1:A:2068:U:H3	1:A:2430:A:H2	1.13	0.95
22:V:18:LEU:HD23	22:V:25:PRO:HG3	1.49	0.95
1:A:780:G:H21	1:A:783:A:H62	1.15	0.94
1:A:1899:G:H21	1:A:1902:C:H41	1.07	0.94
10:J:42:GLU:HA	10:J:82:LYS:HB3	1.50	0.93
1:A:1046:A:N3	9:I:4:LYS:HD3	1.84	0.92
13:M:22:LYS:HE2	13:M:22:LYS:HA	1.50	0.92
10:J:157:ARG:H	10:J:158:PRO:HD3	1.30	0.92
1:A:1021:A:H3'	1:A:1021:A:C8	2.05	0.91
12:L:50:ARG:HB2	31:5:60:LEU:HD11	1.49	0.91
6:F:60:LEU:HD11	6:F:92:VAL:HG11	1.52	0.91
12:L:49:ARG:HG2	12:L:50:ARG:N	1.84	0.91
1:A:1019:U:HO2'	1:A:1021:A:H2	0.95	0.91
12:L:114:ILE:HD11	12:L:130:PHE:CD1	2.05	0.91
1:A:2420:C:OP1	31:5:34:TRP:HA	1.71	0.90
1:A:587:C:H42	12:L:33:ARG:HG2	1.35	0.90
7:G:16:SER:HB2	7:G:27:LYS:HB2	1.52	0.90
11:K:3:GLN:HB2	11:K:4:PRO:HD2	1.53	0.90
1:A:547:A:H2'	1:A:548:A:C8	2.07	0.90
25:Y:2:LYS:HA	25:Y:5:GLU:CD	1.90	0.90

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1021:A:H3'	1:A:1021:A:H8	1.32	0.90
1:A:2426:A:H3'	1:A:2427:C:H5''	1.54	0.89
21:U:81:LYS:HD2	21:U:96:ILE:HD12	1.54	0.89
1:A:761:A:O5'	1:A:761:A:H8	1.56	0.89
27:1:50:THR:HG22	27:1:51:TYR:H	1.37	0.89
1:A:996:A:H4'	17:Q:92:ARG:NH1	1.87	0.88
7:G:101:ARG:HE	7:G:101:ARG:H	1.18	0.88
1:A:954:G:H5''	13:M:13:GLN:HG3	1.54	0.88
1:A:2331:G:H4'	23:W:43:THR:H	1.36	0.88
1:A:886:C:H2'	1:A:887:A:H4'	1.53	0.88
1:A:197:A:H8	1:A:197:A:H5'	1.36	0.88
25:Y:17:SER:HB3	25:Y:18:PRO:HD3	1.57	0.87
19:S:24:ILE:HG21	19:S:36:LEU:HD21	1.56	0.87
1:A:142:G:H4'	20:T:35:THR:HG21	1.55	0.87
28:2:35:GLU:HB2	28:2:49:CYS:SG	2.15	0.87
1:A:857:C:H4'	23:W:23:VAL:HG21	1.55	0.86
1:A:1899:G:H21	1:A:1902:C:N4	1.73	0.86
5:E:67:GLN:O	5:E:67:GLN:HG3	1.74	0.85
17:Q:88:ILE:HB	17:Q:90:VAL:HG12	1.58	0.85
15:O:35:ILE:HG12	15:O:101:LEU:HD21	1.57	0.85
27:1:59:VAL:HG12	27:1:60:GLU:H	1.40	0.85
11:K:119:PRO:HB2	16:P:68:TYR:HE1	1.41	0.85
1:A:2681:C:H5	1:A:2725:A:N6	1.74	0.85
20:T:35:THR:O	20:T:39:ILE:HG12	1.76	0.85
8:H:5:LEU:HD23	8:H:5:LEU:H	1.40	0.85
21:U:2:ARG:HG2	21:U:3:VAL:HG23	1.59	0.85
6:F:41:GLN:HG2	6:F:155:MET:HB3	1.59	0.84
1:A:2712:U:H1'	1:A:712(B):A:C8	2.12	0.84
12:L:41:ARG:HH22	12:L:45:LEU:HB2	1.43	0.84
1:A:2426:A:H3'	1:A:2427:C:C5'	2.08	0.84
24:X:11:ARG:HB3	24:X:12:PRO:HD2	1.60	0.84
1:A:2744:G:H21	7:G:143:GLN:HE22	1.23	0.84
12:L:45:LEU:HD23	12:L:46:LYS:H	1.43	0.84
7:G:89:ILE:HG12	7:G:162:ILE:HG22	1.58	0.83
1:A:245:G:H5'	12:L:73:GLY:HA2	1.59	0.83
1:A:270(J):G:HO2'	1:A:270(K):G:H8	1.24	0.83
23:W:35:ASN:HD22	23:W:35:ASN:H	1.25	0.83
16:P:26:ASP:HB2	16:P:91:ARG:HA	1.61	0.83
6:F:55:LYS:HD2	6:F:58:GLN:HE21	1.42	0.83
4:D:91:VAL:HB	4:D:95:ILE:HD11	1.60	0.83
19:S:13:SER:HB3	19:S:16:LYS:HD2	1.59	0.83
1:A:848:G:H2'	1:A:849:A:C8	2.13	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2439:A:H5'	1:A:2439:A:C8	2.14	0.83
22:V:97:GLU:HB3	22:V:125:LEU:HD21	1.61	0.83
21:U:45:VAL:HG22	21:U:62:GLU:HB3	1.59	0.82
3:C:159:ALA:HB1	3:C:198:ASN:O	1.78	0.82
21:U:8:LYS:N	21:U:8:LYS:HZ2	1.77	0.82
1:A:676:A:H8	1:A:2069:G:H21	1.25	0.82
1:A:2327:A:H2'	1:A:2328:A:C8	2.15	0.82
12:L:89:ALA:HB1	12:L:121:LYS:HD3	1.62	0.82
7:G:92:ILE:HD12	7:G:92:ILE:H	1.45	0.82
3:C:133:LEU:HD23	3:C:136:ILE:HD12	1.61	0.81
1:A:2400:G:H4'	29:3:19:ARG:HD3	1.61	0.81
3:C:25:THR:O	3:C:27:THR:HG22	1.80	0.81
21:U:88:LYS:HE2	21:U:93:GLY:HA3	1.62	0.81
1:A:1899:G:N2	1:A:1902:C:H41	1.79	0.81
21:U:78:ALA:HB3	21:U:81:LYS:HE3	1.62	0.81
14:N:54:LEU:HD11	14:N:65:LEU:HD23	1.60	0.81
31:5:54:GLU:HA	31:5:57:ARG:HH12	1.46	0.81
21:U:81:LYS:HD3	21:U:97:ARG:HB3	1.63	0.81
13:M:81:VAL:HG12	13:M:82:ARG:HG2	1.62	0.81
7:G:162:ILE:HD13	7:G:162:ILE:H	1.45	0.81
6:F:109:VAL:HG11	6:F:142:PRO:HG3	1.62	0.81
8:H:71:ILE:HG23	8:H:72:LEU:HD22	1.63	0.81
1:A:1813:G:H1'	3:C:50:THR:HG21	1.63	0.81
1:A:947:G:H2'	1:A:948:G:H5''	1.63	0.80
5:E:41:LEU:HA	5:E:44:ARG:HD3	1.62	0.80
1:A:1658:C:OP1	4:D:132:HIS:ND1	2.15	0.80
1:A:947:G:C2'	1:A:948:G:H5''	2.11	0.80
11:K:119:PRO:HB2	16:P:68:TYR:CE1	2.16	0.80
8:H:62:LYS:HB2	8:H:133:HIS:CE1	2.18	0.79
1:A:2873:A:C2	14:N:6:SER:HB2	2.17	0.79
20:T:29:TRP:CZ3	20:T:78:LYS:HG3	2.16	0.79
30:4:8:ASN:ND2	30:4:11:LYS:H	1.79	0.79
1:A:2025:C:H2'	1:A:2026:C:C6	2.18	0.79
1:A:948:G:H8	1:A:948:G:H5'	1.47	0.79
22:V:77:ASP:HB2	22:V:84:GLU:HG3	1.63	0.79
3:C:264:LYS:O	3:C:267:SER:HB2	1.83	0.79
12:L:6:LEU:HD23	12:L:6:LEU:H	1.46	0.79
23:W:35:ASN:ND2	23:W:35:ASN:H	1.81	0.79
1:A:996:A:H4'	17:Q:92:ARG:HH12	1.45	0.78
1:A:1021:A:H62	1:A:1141:U:H3	1.31	0.78
17:Q:92:ARG:HB2	17:Q:92:ARG:NH1	1.97	0.78
13:M:75:THR:HA	13:M:88:GLY:HA2	1.64	0.78

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:65:TRP:CZ3	5:E:75:HIS:HD2	2.01	0.78
1:A:125:G:H4'	1:A:126:A:OP2	1.82	0.78
12:L:36:LYS:HG3	12:L:41:ARG:HB2	1.63	0.78
6:F:66:GLN:HG2	6:F:67:LYS:H	1.48	0.78
15:O:49:VAL:HG12	15:O:73:LEU:HD23	1.65	0.78
25:Y:16:LEU:HB2	25:Y:20:GLU:HG3	1.63	0.78
15:O:24:LEU:O	15:O:86:ALA:HB3	1.82	0.78
26:Z:8:LEU:HD12	26:Z:31:LEU:HA	1.66	0.78
1:A:773:U:C4'	3:C:47:GLY:HA3	2.14	0.78
20:T:63:LYS:NZ	20:T:72:LYS:HB3	1.99	0.78
1:A:1006:C:O2	10:J:129:MET:HG2	1.83	0.77
1:A:587:C:N3	12:L:33:ARG:HD2	2.00	0.77
12:L:122:PRO:HA	12:L:141:ALA:O	1.84	0.77
1:A:2210:G:N3	1:A:2210:G:H3'	1.99	0.77
1:A:1311:G:H5'	1:A:1311:G:H8	1.48	0.77
3:C:33:LEU:H	3:C:33:LEU:HD23	1.50	0.77
1:A:1579:A:H5'	1:A:1579:A:H8	1.47	0.77
5:E:53:THR:HG23	5:E:55:GLY:H	1.49	0.77
19:S:1:MET:HE2	19:S:2:GLU:H	1.50	0.77
17:Q:83:LEU:HG	17:Q:88:ILE:HD11	1.65	0.77
13:M:75:THR:HA	13:M:88:GLY:CA	2.15	0.77
3:C:30:GLU:CD	3:C:63:ARG:HE	1.87	0.77
1:A:1175:U:H2'	1:A:1176:G:H8	1.50	0.77
17:Q:24:TYR:HB2	17:Q:29:SER:HB3	1.65	0.77
3:C:71:ASP:HB3	3:C:103:ARG:HH22	1.49	0.77
16:P:27:THR:HG23	16:P:89:VAL:HG13	1.66	0.76
1:A:2394:C:OP1	12:L:63:PRO:HD2	1.85	0.76
15:O:103:GLU:O	15:O:107:GLU:HG2	1.84	0.76
1:A:2637:U:H5''	4:D:82:ARG:NH2	2.00	0.76
30:4:12:ARG:NH2	30:4:44:PRO:HB3	2.00	0.76
21:U:27:VAL:HG12	21:U:39:VAL:HG22	1.68	0.76
4:D:201:THR:HG22	4:D:202:LYS:H	1.50	0.76
18:R:4:ILE:HB	18:R:39:LEU:HB2	1.68	0.76
1:A:1510:A:H2'	1:A:1511:A:C8	2.21	0.76
21:U:31:LEU:HD23	21:U:31:LEU:H	1.50	0.76
1:A:140:A:H8	1:A:1408:C:HO2'	1.34	0.76
1:A:1210:A:H5''	1:A:1210:A:H8	1.51	0.76
1:A:773:U:H4'	3:C:47:GLY:HA3	1.68	0.75
25:Y:39:ALA:HA	25:Y:45:SER:HB3	1.67	0.75
1:A:2377:A:H2'	1:A:2378:A:C8	2.20	0.75
12:L:115:LEU:HA	12:L:134:ALA:HB2	1.69	0.75
12:L:45:LEU:HD23	12:L:46:LYS:N	2.01	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2542:A:N3	1:A:2542:A:H5''	2.01	0.75
4:D:52:LEU:H	4:D:52:LEU:HD12	1.50	0.75
30:4:8:ASN:C	30:4:8:ASN:HD22	1.90	0.75
4:D:201:THR:HG22	4:D:202:LYS:N	2.01	0.75
1:A:603:A:N1	1:A:655:A:H1'	2.02	0.75
1:A:528:A:H8	1:A:528:A:H3'	1.52	0.75
10:J:66:THR:H	10:J:71:MET:HE3	1.52	0.75
14:N:10:LEU:HB2	14:N:17:ARG:HE	1.52	0.75
1:A:343:C:H5'	1:A:343:C:H6	1.49	0.74
4:D:117:MET:HE1	4:D:136:ARG:HA	1.69	0.74
10:J:57:LEU:O	10:J:72:GLY:HA3	1.87	0.74
4:D:2:LYS:HD3	4:D:95:ILE:HG22	1.67	0.74
6:F:28:VAL:O	6:F:31:VAL:HG12	1.88	0.74
1:A:2039:C:H2'	1:A:2040:C:H6	1.52	0.74
3:C:244:ARG:HG3	3:C:245:PRO:HD2	1.68	0.74
1:A:2056:G:N2	28:2:4:HIS:O	2.20	0.74
1:A:547:A:H2'	1:A:548:A:H8	1.51	0.74
1:A:674:G:H1'	5:E:74:ARG:HD3	1.69	0.74
1:A:2427:C:H5'	1:A:2427:C:H6	1.52	0.74
14:N:10:LEU:HB2	14:N:17:ARG:NE	2.03	0.74
11:K:71:ARG:HH12	16:P:74:ARG:HH22	1.32	0.74
13:M:8:LYS:HG3	13:M:9:TYR:H	1.51	0.74
20:T:30:VAL:HG11	20:T:39:ILE:HD12	1.69	0.74
1:A:2287:A:O2'	1:A:2288:A:H5''	1.88	0.74
20:T:15:GLU:H	20:T:15:GLU:CD	1.91	0.74
8:H:83:ALA:HB2	8:H:88:ILE:HD13	1.68	0.74
16:P:84:GLN:HG3	16:P:85:LYS:HG3	1.70	0.74
12:L:26:GLY:HA2	12:L:30:THR:HG23	1.69	0.73
12:L:33:ARG:CG	12:L:36:LYS:HD3	2.13	0.73
10:J:157:ARG:H	10:J:158:PRO:CD	2.01	0.73
20:T:50:LYS:H	20:T:87:GLN:HE22	1.34	0.73
1:A:1314:C:H6	1:A:1314:C:H5'	1.53	0.73
10:J:157:ARG:N	10:J:158:PRO:HD3	2.03	0.73
8:H:82:ARG:HB3	8:H:89:TYR:HB2	1.70	0.73
1:A:2025:C:H2'	1:A:2026:C:H6	1.53	0.73
2:B:43:C:H4'	6:F:98:ARG:HH12	1.52	0.73
6:F:86:MET:SD	6:F:87:PRO:HD3	2.29	0.73
22:V:126:VAL:HG12	22:V:163:LEU:HA	1.71	0.73
1:A:528:A:H2	1:A:2043:C:H4'	1.52	0.73
2:B:13:A:N7	2:B:70:C:H4'	2.04	0.73
3:C:147:LEU:HD13	3:C:155:LEU:HD11	1.69	0.73
4:D:51:PHE:HD1	4:D:52:LEU:HG	1.53	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:77:ILE:HG22	6:F:80:PHE:H	1.54	0.73
7:G:35:VAL:HG21	7:G:75:ALA:HB2	1.70	0.73
1:A:1678:G:O5'	1:A:1678:G:H8	1.72	0.73
15:O:30:ARG:HB3	15:O:35:ILE:HD13	1.72	0.72
1:A:2469:A:H2	1:A:2481:G:H21	1.34	0.72
12:L:29:LYS:N	12:L:29:LYS:HD2	2.04	0.72
21:U:71:LYS:NZ	21:U:71:LYS:HB2	2.04	0.72
4:D:154:LYS:HA	4:D:154:LYS:HE3	1.71	0.72
21:U:96:ILE:HD11	21:U:99:CYS:HB2	1.70	0.72
3:C:30:GLU:HG3	3:C:63:ARG:NH2	2.04	0.72
1:A:1210:A:C8	1:A:1210:A:H5''	2.24	0.72
1:A:848:G:C4	1:A:933:A:H8	2.07	0.72
22:V:48:PHE:HA	22:V:51:ALA:HB3	1.71	0.72
1:A:1405:U:H2'	1:A:1406:U:C6	2.25	0.72
31:5:57:ARG:HB2	31:5:57:ARG:NH1	2.05	0.72
12:L:59:LEU:HA	12:L:61:ARG:NE	2.04	0.72
24:X:17:SER:HB3	24:X:44:PRO:HD3	1.70	0.72
18:R:66:ARG:HD2	18:R:88:ARG:CZ	2.20	0.72
3:C:242:ARG:N	3:C:242:ARG:HD3	2.00	0.72
25:Y:2:LYS:H	25:Y:2:LYS:CD	2.03	0.72
11:K:35:VAL:HG11	11:K:103:ALA:HB3	1.69	0.72
1:A:106:C:H1'	21:U:2:ARG:HE	1.52	0.72
5:E:160:ASN:OD1	5:E:163:VAL:HG23	1.90	0.72
13:M:43:THR:HB	13:M:45:GLN:HE21	1.55	0.71
1:A:1019:U:H3	1:A:114(B):A:H62	1.37	0.71
4:D:179:GLU:HB3	4:D:181:LEU:HD23	1.72	0.71
1:A:1516:U:H2'	1:A:1517:G:H8	1.55	0.71
1:A:2075:U:H2'	1:A:2238:G:N2	2.06	0.71
1:A:1429:G:H2'	1:A:1430:C:C6	2.25	0.71
31:5:26:LYS:HA	31:5:48:PHE:HE2	1.55	0.71
20:T:63:LYS:HD2	20:T:72:LYS:HA	1.71	0.71
5:E:139:PHE:HB2	5:E:166:ALA:HB1	1.73	0.71
1:A:2415:G:H4'	12:L:66:GLY:CA	2.20	0.71
3:C:35:LYS:HG3	3:C:104:TYR:CE2	2.26	0.71
9:I:14:LYS:HE2	9:I:14:LYS:HA	1.71	0.71
1:A:1336:A:H2'	1:A:1337:G:H8	1.55	0.71
26:Z:43:ILE:O	26:Z:47:VAL:HG23	1.91	0.71
1:A:556:G:H2'	1:A:557:U:C6	2.26	0.71
6:F:83:ARG:HG3	6:F:84:LYS:H	1.54	0.71
15:O:34:HIS:HA	15:O:54:LEU:HD23	1.72	0.71
18:R:5:VAL:HG23	18:R:37:VAL:HG23	1.71	0.71
1:A:197:A:H5'	1:A:197:A:C8	2.24	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:16:ARG:HE	12:L:17:LYS:N	1.88	0.71
1:A:1343:G:H5'	1:A:1343:G:C8	2.26	0.71
13:M:75:THR:HG21	13:M:85:LYS:NZ	2.06	0.71
3:C:227:ASN:HB3	3:C:228:PRO:HD2	1.72	0.71
8:H:9:LEU:HB3	8:H:12:LEU:HD23	1.73	0.71
1:A:1541:U:H3'	1:A:1542:G:O3'	1.91	0.70
17:Q:15:LYS:O	17:Q:19:LYS:HG3	1.91	0.70
24:X:50:ARG:HG2	24:X:59:THR:HG22	1.73	0.70
1:A:1021:A:C3'	1:A:1021:A:C8	2.73	0.70
1:A:2392:A:H2	1:A:2424:C:H42	1.39	0.70
3:C:155:LEU:HD23	3:C:177:LEU:HD21	1.72	0.70
3:C:118:VAL:HG22	3:C:119:ALA:H	1.54	0.70
3:C:27:THR:O	3:C:27:THR:HG23	1.91	0.70
30:4:11:LYS:O	30:4:15:THR:HG23	1.89	0.70
1:A:860:U:H5	1:A:917:A:N7	1.89	0.70
1:A:322:A:H3'	5:E:169:ASN:ND2	2.06	0.70
1:A:806:C:OP2	12:L:39:LYS:HD2	1.90	0.70
22:V:108:PRO:HG3	22:V:141:VAL:HG22	1.73	0.70
6:F:19:LEU:HD11	6:F:172:LEU:HD13	1.73	0.70
8:H:76:THR:HG22	8:H:141:LYS:HD3	1.74	0.70
3:C:144:ALA:HB3	3:C:192:THR:HG23	1.73	0.70
22:V:104:PHE:HA	22:V:139:VAL:HB	1.73	0.70
27:1:38:ALA:HA	27:1:55:PRO:HA	1.71	0.70
10:J:90:LEU:HD12	10:J:90:LEU:H	1.54	0.70
1:A:2036:C:H6	1:A:2036:C:H5'	1.56	0.70
1:A:1899:G:N2	1:A:1902:C:N4	2.38	0.70
29:3:15:GLU:OE2	29:3:18:ARG:HD2	1.92	0.70
1:A:2261:C:C6	23:W:16:SER:HB3	2.25	0.70
1:A:1657:C:H2'	1:A:1658:C:H6	1.54	0.70
25:Y:16:LEU:O	25:Y:20:GLU:HB2	1.92	0.70
1:A:2543:G:H8	1:A:2543:G:H5'	1.57	0.70
1:A:528:A:C8	1:A:528:A:H3'	2.26	0.70
5:E:155:LEU:HD23	5:E:186:ILE:HD13	1.72	0.70
1:A:2740:A:H2'	1:A:2741:A:C8	2.26	0.70
12:L:49:ARG:CG	12:L:50:ARG:N	2.53	0.69
24:X:27:GLU:HB2	24:X:33:LYS:HA	1.74	0.69
15:O:90:GLY:O	15:O:92:TYR:N	2.25	0.69
26:Z:8:LEU:CD1	26:Z:31:LEU:HD12	2.22	0.69
30:4:5:TRP:NE1	30:4:7:PRO:HG3	2.07	0.69
7:G:17:VAL:HG22	7:G:26:VAL:HG22	1.74	0.69
7:G:43:VAL:HA	7:G:52:VAL:HG22	1.73	0.69
3:C:186:HIS:HD2	3:C:188:GLU:H	1.38	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1418:G:H8	1:A:1418:G:O5'	1.74	0.69
20:T:27:THR:HB	20:T:80:ILE:HB	1.74	0.69
12:L:64:LYS:HB2	31:5:25:MET:HG3	1.73	0.69
1:A:1311:G:H5'	1:A:1311:G:C8	2.27	0.69
8:H:110:ASP:HB2	8:H:113:ARG:HG2	1.72	0.69
6:F:121:ASN:HD22	6:F:122:PRO:HD2	1.56	0.69
22:V:163:LEU:HD23	22:V:163:LEU:H	1.56	0.69
1:A:1174:A:H3'	1:A:1175:U:H5''	1.73	0.69
1:A:796:C:H2'	1:A:797:C:C6	2.27	0.69
8:H:56:LYS:HA	8:H:59:ALA:HB3	1.74	0.69
1:A:1046:A:H3'	1:A:1047:G:H5''	1.75	0.69
8:H:78:THR:HA	8:H:143:SER:HB3	1.75	0.69
29:3:42:TRP:HA	29:3:42:TRP:CE3	2.25	0.69
24:X:83:GLU:HG2	24:X:84:GLY:H	1.57	0.69
28:2:45:VAL:HG12	28:2:46:CYS:H	1.58	0.69
1:A:2287:A:H62	1:A:2344:U:H3	1.38	0.69
8:H:79:ILE:HB	8:H:144:VAL:HA	1.73	0.69
16:P:26:ASP:CB	16:P:91:ARG:HA	2.22	0.69
1:A:2415:G:H4'	12:L:66:GLY:HA3	1.75	0.69
1:A:1778:U:H2'	1:A:1784:A:N6	2.07	0.69
3:C:238:GLY:O	3:C:239:ARG:C	2.32	0.68
13:M:60:ARG:H	22:V:179:ASP:HB2	1.57	0.68
3:C:155:LEU:HD23	3:C:177:LEU:CD2	2.23	0.68
1:A:1516:U:H2'	1:A:1517:G:C8	2.28	0.68
13:M:24:GLY:HA2	13:M:101:ARG:HA	1.75	0.68
17:Q:90:VAL:HG13	17:Q:91:ASP:H	1.58	0.68
6:F:7:LEU:HD23	6:F:10:LYS:HD2	1.74	0.68
24:X:11:ARG:HB3	24:X:12:PRO:CD	2.23	0.68
12:L:59:LEU:HA	12:L:61:ARG:CZ	2.24	0.68
2:B:79:C:H2'	2:B:80:U:O4'	1.94	0.68
1:A:1542:G:H1'	1:A:1543:A:C4	2.28	0.68
1:A:2068:U:N3	1:A:2430:A:H2	1.90	0.68
20:T:50:LYS:H	20:T:87:GLN:NE2	1.90	0.68
1:A:2023:G:H5'	1:A:2617:C:H4'	1.75	0.68
1:A:1826:G:H4'	3:C:242:ARG:HE	1.59	0.68
29:3:36:LEU:H	29:3:36:LEU:HD23	1.58	0.68
3:C:201:HIS:O	3:C:204:ILE:HG13	1.94	0.68
30:4:35:ARG:HG3	30:4:42:LEU:HD11	1.76	0.68
3:C:148:GLU:HB2	3:C:151:LYS:HD2	1.75	0.68
1:A:591:C:O2	31:5:2:PRO:HA	1.93	0.68
29:3:42:TRP:HA	29:3:42:TRP:HE3	1.58	0.68
19:S:18:ARG:HG2	19:S:76:VAL:CG1	2.24	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:973:A:OP2	18:R:78:LYS:NZ	2.23	0.68
1:A:673:C:H5''	5:E:81:PRO:HD2	1.75	0.67
1:A:1544:C:H3'	1:A:1545:A:H5'	1.75	0.67
8:H:87:LYS:HA	8:H:122:GLU:HA	1.76	0.67
3:C:96:HIS:HD2	3:C:102:LYS:HG2	1.58	0.67
1:A:141(A):A:H8	1:A:1595:G:H21	1.40	0.67
22:V:136:PHE:C	22:V:137:ILE:HD12	2.15	0.67
1:A:185:U:H2'	1:A:186:G:C8	2.29	0.67
25:Y:46:GLN:O	25:Y:47:ASN:HB2	1.93	0.67
2:B:66:A:H61	2:B:107:U:H2'	1.59	0.67
5:E:8:GLN:HA	5:E:21:ALA:HA	1.77	0.67
1:A:65:C:H2'	1:A:66:C:H6	1.60	0.67
1:A:587:C:N4	12:L:33:ARG:HG2	2.09	0.67
1:A:760:G:H2'	1:A:761:A:H5'	1.77	0.67
17:Q:50:ARG:HH22	18:R:72:VAL:HG12	1.58	0.67
1:A:2056:G:N3	1:A:2056:G:H2'	2.08	0.67
1:A:1046:A:H1'	9:I:4:LYS:CD	2.23	0.67
1:A:245:G:H2'	1:A:246:C:H6	1.59	0.67
17:Q:55:ARG:HA	17:Q:58:ARG:HD2	1.76	0.67
1:A:480:A:OP2	21:U:46:LYS:HE2	1.95	0.67
10:J:66:THR:HB	10:J:69:VAL:HG12	1.76	0.67
1:A:1316:U:H2'	1:A:1317:A:C8	2.29	0.67
2:B:55:U:H4'	6:F:27:ASN:HD21	1.59	0.67
1:A:443:A:H2'	5:E:45:ARG:HH12	1.60	0.67
12:L:62:LEU:HD11	31:5:27:THR:HA	1.76	0.66
1:A:954:G:H5''	13:M:13:GLN:CG	2.25	0.66
3:C:69:ARG:HH21	3:C:130:ALA:HB2	1.59	0.66
31:5:39:LYS:O	31:5:43:GLN:HG2	1.96	0.66
1:A:1348:G:H2'	1:A:1349:A:H5''	1.77	0.66
4:D:30:PRO:HD3	4:D:180:ASN:ND2	2.10	0.66
22:V:24:LEU:HB2	22:V:41:LEU:HD23	1.77	0.66
1:A:1794:U:H2'	1:A:1795:C:H6	1.59	0.66
10:J:118:PRO:O	10:J:121:VAL:HG22	1.94	0.66
21:U:8:LYS:NZ	21:U:8:LYS:H	1.89	0.66
6:F:98:ARG:H	6:F:98:ARG:HD2	1.59	0.66
1:A:588:U:H2'	1:A:589:C:C6	2.30	0.66
1:A:1175:U:H2'	1:A:1176:G:C8	2.29	0.66
1:A:528:A:C2	1:A:2043:C:H4'	2.31	0.66
12:L:146:VAL:HG22	12:L:147:LEU:H	1.57	0.66
1:A:1163:G:C2'	1:A:1164:G:H5''	2.23	0.66
21:U:42:VAL:HG12	21:U:65:ALA:HB3	1.78	0.66
3:C:217:ARG:HH11	3:C:217:ARG:HG2	1.60	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:148:LEU:HD13	12:L:148:LEU:H	1.59	0.66
20:T:26:TYR:HB3	20:T:92:LEU:HD13	1.77	0.66
23:W:37:LEU:O	23:W:38:VAL:HG23	1.96	0.66
1:A:251:A:C5	1:A:252:G:H1'	2.31	0.66
10:J:36:TRP:HB2	10:J:156:GLN:HB2	1.76	0.66
3:C:94:LEU:HB2	3:C:104:TYR:HE1	1.60	0.66
8:H:92:VAL:HA	8:H:96:ASP:OD2	1.96	0.65
3:C:270:ILE:O	3:C:271:ILE:HG13	1.96	0.65
1:A:2359:C:H2'	1:A:2360:A:C8	2.31	0.65
12:L:111:ARG:HG3	12:L:128:HIS:CG	2.30	0.65
1:A:675:A:H4'	5:E:67:GLN:NE2	2.12	0.65
1:A:270(G):U:H2'	1:A:270(H):C:C6	2.31	0.65
4:D:92:THR:HB	4:D:94:GLU:HG2	1.78	0.65
1:A:948:G:H5'	1:A:948:G:C8	2.31	0.65
11:K:103:ALA:HB1	11:K:105:GLU:OE1	1.97	0.65
2:B:74:U:H2'	2:B:75:G:C8	2.32	0.65
1:A:1332:G:C8	1:A:1332:G:H5'	2.32	0.65
12:L:41:ARG:NH2	12:L:45:LEU:HD12	2.12	0.65
17:Q:110:VAL:O	17:Q:114:LYS:HG2	1.97	0.65
18:R:49:THR:HB	18:R:50:PRO:HD2	1.78	0.65
1:A:1336:A:H2'	1:A:1337:G:C8	2.30	0.65
6:F:32:PRO:HB2	6:F:172:LEU:HD22	1.77	0.65
1:A:389:G:O6	12:L:71:VAL:HG23	1.97	0.65
1:A:1858:G:H1'	1:A:1884:A:N6	2.11	0.65
5:E:103:LYS:HA	5:E:106:ARG:HG3	1.77	0.65
1:A:2822:G:H2'	1:A:2823:A:H5''	1.77	0.65
1:A:733:G:N7	1:A:761:A:C6	2.64	0.65
15:O:99:LYS:O	15:O:103:GLU:HB2	1.96	0.65
1:A:1607:C:H4'	1:A:1608:A:O5'	1.97	0.65
1:A:2599:G:C8	3:C:237:GLU:HG3	2.32	0.65
18:R:22:VAL:HG12	18:R:23:GLU:N	2.10	0.65
31:5:22:VAL:HB	31:5:54:GLU:HG2	1.77	0.65
1:A:342:G:C2'	1:A:343:C:H5''	2.26	0.65
1:A:343:C:C6	1:A:343:C:H5'	2.32	0.65
1:A:910:A:H62	13:M:12:GLN:HA	1.62	0.65
1:A:811:U:O2	1:A:1250:G:H2'	1.97	0.65
3:C:244:ARG:HG3	3:C:245:PRO:CD	2.26	0.65
3:C:10:THR:HG23	3:C:13:ARG:CB	2.27	0.65
1:A:330:A:C2	1:A:1210:A:H2'	2.33	0.64
8:H:6:LEU:H	8:H:6:LEU:HD23	1.63	0.64
1:A:2637:U:H5''	4:D:82:ARG:HH21	1.61	0.64
1:A:661:C:O3'	12:L:18:ARG:HG2	1.98	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:9:ASN:N	12:L:10:PRO:HD3	2.12	0.64
24:X:10:LYS:O	24:X:11:ARG:HG2	1.97	0.64
29:3:11:LEU:HG	29:3:26:ASN:HB2	1.78	0.64
7:G:55:PRO:HG2	7:G:61:HIS:HD2	1.62	0.64
3:C:131:LEU:CD1	3:C:136:ILE:HG12	2.28	0.64
1:A:1652:A:OP1	14:N:9:LYS:HE3	1.98	0.64
1:A:663:G:H5''	12:L:21:ARG:HD3	1.80	0.64
5:E:102:PRO:HB2	5:E:105:VAL:HG23	1.80	0.64
1:A:81:G:H21	21:U:2:ARG:NH2	1.96	0.64
25:Y:6:VAL:O	25:Y:10:LEU:HG	1.97	0.64
1:A:1614:A:N6	19:S:87:PRO:HA	2.11	0.64
1:A:2271:G:OP1	23:W:18:ALA:HB1	1.96	0.64
10:J:135:LEU:HD23	10:J:136:GLY:N	2.12	0.64
8:H:82:ARG:HB3	8:H:89:TYR:CB	2.27	0.64
2:B:13:A:H5'	23:W:74:ARG:HH21	1.62	0.64
1:A:860:U:C5	1:A:917:A:N7	2.66	0.64
1:A:2506:U:H5	1:A:2583:G:H1	1.44	0.64
10:J:36:TRP:HB2	10:J:156:GLN:CB	2.28	0.64
7:G:149:ARG:HA	7:G:162:ILE:CG1	2.28	0.64
5:E:139:PHE:CB	5:E:166:ALA:HB1	2.28	0.64
14:N:79:LEU:HD23	14:N:83:ILE:HB	1.79	0.64
14:N:38:VAL:HB	14:N:39:PRO:HD3	1.78	0.64
1:A:2402:C:H5'	1:A:2403:C:OP2	1.97	0.64
26:Z:5:LYS:HB3	26:Z:57:GLU:HB2	1.79	0.64
4:D:51:PHE:H	4:D:75:VAL:HB	1.60	0.64
14:N:9:LYS:O	14:N:10:LEU:HG	1.97	0.64
3:C:78:LYS:HD3	3:C:114:GLY:HA2	1.80	0.64
7:G:101:ARG:NE	7:G:101:ARG:H	1.93	0.64
15:O:66:ALA:HB1	15:O:101:LEU:HD22	1.80	0.63
10:J:112:LYS:O	10:J:116:THR:HG22	1.98	0.63
1:A:2687:U:C4	1:A:2688:U:C5	2.86	0.63
15:O:31:SER:HB3	15:O:34:HIS:HB2	1.79	0.63
4:D:119:ARG:HD3	4:D:120:TRP:CE2	2.33	0.63
1:A:1803:A:H5''	1:A:1804:C:OP2	1.98	0.63
24:X:86:SER:O	24:X:90:ILE:HG12	1.98	0.63
13:M:83:MET:O	13:M:83:MET:HG3	1.97	0.63
1:A:1694:C:C5'	1:A:1694:C:H6	2.11	0.63
1:A:1657:C:H2'	1:A:1658:C:C6	2.33	0.63
1:A:126:A:OP2	30:4:19:ARG:HB2	1.97	0.63
1:A:1434:A:H2'	1:A:1435:G:C8	2.34	0.63
13:M:6:ARG:O	13:M:7:MET:HB2	1.98	0.63
1:A:140:A:H8	1:A:1408:C:O2'	1.81	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:586:A:H5'	5:E:89:VAL:HG21	1.78	0.63
13:M:20:ALA:HB1	13:M:99:PRO:O	1.98	0.63
3:C:158:ALA:HB3	3:C:161:THR:HG21	1.80	0.63
1:A:637:A:O5'	12:L:116:GLY:HA2	1.98	0.63
3:C:186:HIS:CD2	3:C:188:GLU:H	2.16	0.63
1:A:1937:A:O2'	1:A:1938:A:H5'	1.98	0.63
17:Q:92:ARG:HD3	17:Q:94:ASN:HB3	1.79	0.63
1:A:2401:U:H2'	1:A:2402:C:H5''	1.80	0.63
24:X:19:GLN:HG2	24:X:41:ARG:HB2	1.80	0.63
1:A:2062:A:O2'	1:A:2063:C:H5'	1.98	0.63
13:M:110:THR:HB	13:M:112:GLU:OE1	1.98	0.63
15:O:24:LEU:HD13	15:O:82:ILE:HG23	1.81	0.63
18:R:39:LEU:HD12	18:R:47:VAL:HG11	1.81	0.63
1:A:2873:A:N3	14:N:6:SER:HB2	2.14	0.63
1:A:1210:A:H4'	1:A:1211:U:O5'	1.99	0.63
15:O:33:LYS:HD3	15:O:33:LYS:O	1.97	0.63
1:A:2350:C:H5''	31:5:42:ARG:HD3	1.81	0.63
1:A:1437:C:H2'	1:A:1438:U:C6	2.34	0.63
1:A:7:G:H2'	1:A:8:A:H8	1.64	0.63
3:C:5:LYS:HD2	3:C:5:LYS:N	2.14	0.63
1:A:1694:C:H5''	1:A:1694:C:H6	1.62	0.63
4:D:36:ARG:NH1	4:D:86:PRO:HD2	2.14	0.63
18:R:38:LEU:O	18:R:39:LEU:HD13	1.99	0.63
18:R:40:LEU:HD23	18:R:47:VAL:HG23	1.80	0.63
24:X:13:ILE:HD11	24:X:15:ALA:HB2	1.80	0.63
3:C:61:LEU:O	3:C:63:ARG:NH1	2.31	0.63
14:N:10:LEU:CB	14:N:17:ARG:HE	2.12	0.63
1:A:2724:C:OP1	4:D:118:LYS:HE3	1.98	0.63
1:A:1309:G:H3'	30:4:9:ARG:HH12	1.64	0.63
7:G:101:ARG:N	7:G:101:ARG:HE	1.93	0.62
11:K:71:ARG:NH1	16:P:74:ARG:HH22	1.95	0.62
3:C:142:VAL:HG23	3:C:192:THR:O	1.98	0.62
5:E:170:LEU:HD12	5:E:171:PRO:HD2	1.81	0.62
1:A:2777:G:H5''	1:A:2778:A:H5'	1.80	0.62
1:A:1388:G:H2'	1:A:1389:G:H8	1.64	0.62
21:U:50:ARG:HD3	21:U:51:VAL:H	1.64	0.62
30:4:8:ASN:ND2	30:4:8:ASN:C	2.53	0.62
1:A:1314:C:H5'	1:A:1314:C:C6	2.34	0.62
1:A:65:C:H2'	1:A:66:C:C6	2.34	0.62
3:C:95:LEU:HD12	3:C:95:LEU:O	1.98	0.62
1:A:747:U:OP2	28:2:3:LYS:HD3	1.99	0.62
5:E:31:HIS:HB2	12:L:13:ASN:HB3	1.80	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:14:LYS:O	12:L:15:ARG:HB2	1.99	0.62
12:L:30:THR:HG22	12:L:31:ALA:N	2.15	0.62
1:A:1316:U:H2'	1:A:1317:A:H8	1.64	0.62
1:A:1389:G:H2'	1:A:1390:U:C6	2.34	0.62
1:A:2078:C:H2'	1:A:2079:U:H6	1.64	0.62
20:T:64:LYS:HG2	20:T:65:ARG:H	1.64	0.62
1:A:1022:G:H8	10:J:92:GLN:NE2	1.96	0.62
12:L:62:LEU:N	12:L:62:LEU:HD13	2.14	0.62
11:K:20:MET:HG2	11:K:21:CYS:O	2.00	0.62
5:E:178:PRO:HB3	5:E:201:VAL:HG11	1.82	0.62
3:C:79:VAL:HG21	3:C:111:LEU:HD11	1.80	0.62
3:C:206:LEU:O	3:C:211:ARG:HD3	2.00	0.62
17:Q:90:VAL:HG23	18:R:39:LEU:HB3	1.81	0.62
20:T:63:LYS:HZ1	20:T:72:LYS:HB3	1.63	0.62
4:D:9:VAL:HG22	4:D:25:VAL:HB	1.81	0.62
1:A:1794:U:H2'	1:A:1795:C:C6	2.35	0.62
24:X:25:LYS:HG2	24:X:35:THR:HG22	1.80	0.62
10:J:127:LYS:HB2	10:J:140:PHE:CE1	2.33	0.62
1:A:2210:G:H21	1:A:2211:G:H5'	1.64	0.62
21:U:90:LEU:HG	21:U:91:GLU:N	2.15	0.62
1:A:2307:G:H2'	1:A:2308:G:H5'	1.81	0.62
11:K:104:ARG:HB3	11:K:104:ARG:HH11	1.65	0.62
23:W:23:VAL:HA	23:W:38:VAL:CG2	2.24	0.62
1:A:1529:A:H62	1:A:1542:G:N2	1.98	0.62
22:V:69:THR:HG22	22:V:90:VAL:HG22	1.82	0.62
11:K:2:ILE:HD11	11:K:82:ASN:HD22	1.64	0.62
7:G:68:THR:O	7:G:72:ILE:HG12	2.00	0.62
24:X:46:LEU:O	24:X:46:LEU:HD23	2.00	0.62
1:A:1542:G:H4'	1:A:1543:A:O5'	2.00	0.62
22:V:102:LEU:HD23	22:V:137:ILE:HB	1.80	0.62
20:T:59:VAL:HB	20:T:76:ARG:HG3	1.81	0.62
7:G:84:SER:HA	7:G:133:VAL:O	2.00	0.62
17:Q:92:ARG:HD2	17:Q:95:LEU:HG	1.81	0.62
4:D:132:HIS:HA	4:D:135:HIS:NE2	2.15	0.62
24:X:27:GLU:HB3	24:X:33:LYS:HG3	1.82	0.62
17:Q:21:ALA:CB	17:Q:35:ALA:HB1	2.30	0.62
1:A:38:A:H2'	1:A:39:C:C6	2.34	0.62
1:A:492:A:H2'	1:A:493:G:O4'	2.00	0.62
1:A:664:C:H4'	1:A:941:A:OP1	2.00	0.61
28:2:40:LYS:CE	28:2:46:CYS:HB3	2.29	0.61
1:A:1343:G:H5'	1:A:1343:G:H8	1.64	0.61
24:X:27:GLU:CB	24:X:33:LYS:HA	2.30	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:779:U:H5'	3:C:49:ILE:HD11	1.82	0.61
1:A:1007:C:O2'	10:J:131:PRO:HA	1.99	0.61
2:B:50:G:OP2	15:O:62:LYS:HD3	2.00	0.61
21:U:8:LYS:HE2	21:U:37:VAL:HG11	1.81	0.61
1:A:2393:A:C5'	12:L:62:LEU:HD12	2.31	0.61
1:A:860:U:O2'	1:A:861:A:H5'	1.99	0.61
12:L:71:VAL:HB	12:L:72:PRO:HD3	1.82	0.61
24:X:19:GLN:HE21	24:X:41:ARG:HE	1.48	0.61
1:A:2787:C:H1'	4:D:62:PRO:HG3	1.81	0.61
1:A:2346:A:H5''	1:A:2383:G:H1'	1.82	0.61
1:A:2502:G:H5'	1:A:2503:A:H5''	1.81	0.61
10:J:57:LEU:HD21	10:J:143:LEU:HB2	1.82	0.61
8:H:126:TYR:H	8:H:142:VAL:HB	1.65	0.61
4:D:132:HIS:CD2	4:D:135:HIS:NE2	2.68	0.61
12:L:16:ARG:NH1	12:L:18:ARG:HG3	2.16	0.61
1:A:729:G:C5	3:C:208:LYS:HB2	2.36	0.61
11:K:47:ILE:HG13	11:K:48:PRO:HD2	1.82	0.61
1:A:639:U:H2'	1:A:640:C:C6	2.35	0.61
2:B:11:C:H3'	2:B:12:C:H6	1.65	0.61
1:A:2593:U:H2'	1:A:2594:C:C6	2.36	0.61
13:M:38:GLU:HB2	13:M:127:ILE:HG23	1.83	0.61
13:M:38:GLU:O	13:M:127:ILE:HD13	2.01	0.61
1:A:1408:C:C2	1:A:1595:G:N2	2.69	0.61
14:N:17:ARG:HG3	14:N:18:LEU:N	2.14	0.61
26:Z:1:MET:SD	26:Z:40:THR:HA	2.41	0.61
16:P:41:ARG:HD2	16:P:42:ILE:H	1.66	0.61
16:P:50:ILE:HA	16:P:99:LEU:HD11	1.82	0.61
21:U:76:CYS:HB3	21:U:77:PRO:HD2	1.81	0.61
1:A:2294:C:H2'	1:A:2295:C:H6	1.66	0.61
1:A:774:A:H2	1:A:787:U:HO2'	1.47	0.61
1:A:780:G:H21	1:A:783:A:N6	1.94	0.61
25:Y:2:LYS:H	25:Y:2:LYS:HD2	1.65	0.61
28:2:40:LYS:HE2	28:2:46:CYS:HB3	1.81	0.61
3:C:44:ASN:HB3	3:C:50:THR:HG21	1.82	0.61
19:S:78:GLU:OE2	19:S:99:ARG:HD3	2.00	0.61
14:N:84:ALA:HB3	14:N:85:PRO:HD3	1.83	0.61
20:T:70:LEU:HD23	20:T:71:GLY:N	2.13	0.61
14:N:4:LEU:HG	14:N:4:LEU:O	2.00	0.61
3:C:267:SER:O	3:C:270:ILE:HG13	2.01	0.61
12:L:140:ALA:O	12:L:141:ALA:HB2	2.00	0.61
6:F:10:LYS:O	6:F:14:GLU:HB3	2.00	0.61
16:P:98:LYS:HB3	16:P:100:TYR:CE1	2.36	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:4:ILE:CG1	4:D:28:ALA:HB1	2.31	0.61
1:A:2562:U:H1'	11:K:23:ARG:NH1	2.15	0.61
1:A:2393:A:H5''	12:L:62:LEU:HB3	1.83	0.61
3:C:30:GLU:HG3	3:C:63:ARG:HH21	1.64	0.61
1:A:1678:G:N2	1:A:1989:G:H22	1.98	0.61
1:A:1543:A:H5'	1:A:1544:C:OP2	2.00	0.61
10:J:62:ARG:NH2	10:J:64:ASP:HB2	2.16	0.61
12:L:91:PHE:CE2	12:L:95:VAL:HG12	2.35	0.61
3:C:21:PHE:O	3:C:24:ILE:HG22	2.01	0.61
1:A:1021:A:O2'	1:A:1123:C:H5''	2.01	0.61
3:C:25:THR:HG22	3:C:82:ILE:O	2.00	0.61
1:A:674:G:H2'	1:A:804:A:H61	1.66	0.61
1:A:1429:G:H2'	1:A:1430:C:H6	1.65	0.61
21:U:76:CYS:CB	21:U:77:PRO:HD2	2.31	0.61
3:C:70:TRP:CZ2	3:C:150:LYS:HA	2.36	0.61
19:S:65:LEU:HB2	19:S:68:ARG:HG2	1.83	0.61
25:Y:17:SER:HB3	25:Y:18:PRO:CD	2.30	0.61
8:H:83:ALA:HB3	8:H:123:LEU:HD12	1.82	0.61
22:V:58:VAL:HA	22:V:67:LEU:O	2.01	0.61
19:S:29:LEU:HD22	19:S:69:LEU:HD11	1.81	0.61
1:A:2075:U:H2'	1:A:2238:G:H22	1.64	0.60
1:A:185:U:H2'	1:A:186:G:H8	1.63	0.60
1:A:2186:G:H2'	1:A:2187:G:H8	1.65	0.60
5:E:83:PHE:O	5:E:84:VAL:C	2.40	0.60
1:A:242:G:C8	31:5:5:LYS:HG2	2.35	0.60
10:J:80:ALA:O	10:J:83:ILE:HG13	2.01	0.60
5:E:199:TRP:O	5:E:203:GLN:HG2	2.00	0.60
13:M:30:GLY:HA2	13:M:107:ALA:HB2	1.83	0.60
1:A:1587:A:H2'	1:A:1588:C:C6	2.37	0.60
5:E:164:ARG:HG3	5:E:175:THR:OG1	2.00	0.60
1:A:996:A:C4'	17:Q:92:ARG:HH12	2.13	0.60
1:A:795:C:H2'	1:A:796:C:H6	1.65	0.60
8:H:90:GLY:O	8:H:91:SER:HB2	2.00	0.60
1:A:1953:A:H2	1:A:2549:G:N3	1.98	0.60
1:A:214:G:H1'	1:A:216:A:O2'	2.00	0.60
1:A:85:G:H5''	1:A:85:G:H8	1.65	0.60
11:K:3:GLN:CB	11:K:4:PRO:HD2	2.27	0.60
31:5:22:VAL:HB	31:5:54:GLU:CG	2.31	0.60
20:T:8:ILE:H	20:T:8:ILE:HD12	1.64	0.60
1:A:510:C:H2'	1:A:511:U:O4'	2.00	0.60
1:A:2850:A:C8	1:A:2850:A:H5'	2.36	0.60
3:C:34:VAL:O	3:C:35:LYS:HD3	2.01	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:51:PHE:CD1	4:D:52:LEU:HG	2.36	0.60
24:X:73:LEU:HD21	24:X:94:LEU:HG	1.83	0.60
1:A:2653:U:H3	1:A:2667:C:H42	1.50	0.60
12:L:57:THR:HG23	12:L:59:LEU:CB	2.31	0.60
1:A:342:G:H2'	1:A:343:C:H5''	1.82	0.60
1:A:83:G:H22	1:A:102:G:H2'	1.65	0.60
4:D:32:PRO:HA	4:D:90:THR:HG22	1.83	0.60
1:A:955:C:OP1	13:M:85:LYS:HE2	2.00	0.60
1:A:1568:G:P	3:C:63:ARG:HH22	2.24	0.60
24:X:31:GLY:O	24:X:32:LYS:HB2	2.01	0.60
1:A:1156:A:H4'	1:A:1157:G:OP2	2.02	0.60
24:X:67:ILE:N	24:X:68:PRO:HD2	2.15	0.60
21:U:71:LYS:HB2	21:U:71:LYS:HZ2	1.67	0.60
1:A:273(G):C:H2'	1:A:274:G:H5''	1.84	0.60
12:L:38:GLN:HG3	12:L:39:LYS:H	1.66	0.60
13:M:76:LYS:N	13:M:88:GLY:HA2	2.17	0.60
1:A:153:C:OP1	24:X:92:LYS:HE2	2.02	0.60
1:A:2893:G:H5''	1:A:2894:G:O4'	2.02	0.60
14:N:11:ASN:OD1	14:N:12:ARG:N	2.32	0.60
1:A:839:U:H2'	1:A:840:C:C6	2.37	0.60
1:A:1603:A:C8	1:A:1603:A:H5'	2.37	0.60
1:A:1980:G:H3'	1:A:1981:A:H5''	1.84	0.60
3:C:28:GLU:HB3	3:C:29:PRO:HD3	1.83	0.60
6:F:83:ARG:HG3	6:F:84:LYS:N	2.16	0.59
24:X:19:GLN:NE2	24:X:41:ARG:HE	2.00	0.59
1:A:426:C:H2'	1:A:427:U:H6	1.67	0.59
1:A:656:G:H2'	1:A:657:U:O4'	2.02	0.59
1:A:1046:A:H1'	9:I:4:LYS:HD3	1.83	0.59
1:A:2038:G:H2'	1:A:2039:C:C6	2.36	0.59
1:A:476:G:H4'	1:A:502:A:N1	2.17	0.59
11:K:53:LYS:N	11:K:53:LYS:HD2	2.17	0.59
4:D:50:GLY:HA3	4:D:75:VAL:HG11	1.83	0.59
1:A:2074:U:H2'	1:A:2075:U:C6	2.38	0.59
1:A:1540:G:H2'	1:A:1541:U:O4'	2.02	0.59
1:A:1264:G:OP1	28:2:19:ARG:NH2	2.34	0.59
3:C:108:PRO:HG3	3:C:143:HIS:CE1	2.37	0.59
1:A:942:G:H5'	12:L:35:HIS:HB2	1.85	0.59
25:Y:13:ALA:O	25:Y:17:SER:HA	2.02	0.59
1:A:2712:U:H1'	1:A:712(B):A:H8	1.66	0.59
1:A:185:U:H4'	1:A:218:A:H4'	1.83	0.59
10:J:117:HIS:CE1	10:J:120:ARG:HE	2.19	0.59
30:4:21:ARG:HB3	30:4:31:LEU:HD21	1.83	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:12:TYR:OH	18:R:22:VAL:HG13	2.02	0.59
20:T:12:VAL:HG12	20:T:28:PHE:HA	1.84	0.59
10:J:39:ILE:HG22	10:J:40:ASP:O	2.03	0.59
13:M:141:GLN:HG2	22:V:72:ARG:HA	1.84	0.59
3:C:35:LYS:HE3	3:C:104:TYR:CD2	2.37	0.59
31:5:57:ARG:HH11	31:5:57:ARG:HB2	1.66	0.59
12:L:57:THR:HG23	12:L:59:LEU:HB2	1.85	0.59
14:N:18:LEU:HD11	14:N:22:ARG:CZ	2.32	0.59
4:D:173:VAL:HG12	4:D:174:ASP:H	1.66	0.59
2:B:87:G:H21	2:B:89(B):A:H62	1.51	0.59
1:A:2577:A:H5''	1:A:2578:G:H5'	1.82	0.59
1:A:1291:C:H2'	1:A:1292:U:C6	2.37	0.59
18:R:81:TYR:C	18:R:82:ARG:HG3	2.21	0.59
8:H:92:VAL:HG21	8:H:97:ILE:HD11	1.84	0.59
2:B:13:A:H5'	23:W:74:ARG:NH2	2.18	0.59
1:A:779:U:OP1	3:C:49:ILE:HG13	2.02	0.59
10:J:119:GLU:O	10:J:123:GLU:HG3	2.02	0.59
1:A:1358:G:O2'	1:A:1359:A:H5''	2.01	0.59
25:Y:38:GLN:HB3	25:Y:44:LEU:HB3	1.84	0.59
1:A:295:G:H4'	21:U:2:ARG:NH1	2.17	0.59
3:C:30:GLU:CG	3:C:63:ARG:HH21	2.16	0.59
5:E:181:LEU:HD22	5:E:186:ILE:HD11	1.85	0.59
17:Q:50:ARG:NH2	18:R:72:VAL:HG12	2.17	0.59
4:D:36:ARG:HH12	4:D:86:PRO:HD2	1.68	0.59
1:A:1799:G:H8	3:C:181:GLU:CD	2.05	0.59
1:A:1993:U:H4'	4:D:128:SER:HB3	1.83	0.59
21:U:13:VAL:HG11	21:U:72:VAL:HB	1.83	0.59
6:F:60:LEU:HD11	6:F:92:VAL:CG1	2.31	0.59
1:A:1311:G:H8	1:A:1311:G:C5'	2.13	0.59
25:Y:38:GLN:O	25:Y:41:ILE:HG12	2.03	0.59
1:A:2815:C:O2'	28:2:43:HIS:HD2	1.86	0.59
1:A:1566:A:O2'	1:A:1567:A:H5'	2.03	0.59
1:A:674:G:C1'	5:E:74:ARG:HD3	2.33	0.59
1:A:2468:G:H22	1:A:2481:G:H2'	1.67	0.59
5:E:150:GLY:HA2	5:E:172:TRP:CE3	2.37	0.59
1:A:784:A:C5	3:C:229:VAL:HG21	2.37	0.59
1:A:826:U:O2	1:A:832:G:C2	2.56	0.59
25:Y:2:LYS:N	25:Y:2:LYS:HD2	2.18	0.59
27:1:50:THR:HG22	27:1:51:TYR:N	2.15	0.59
1:A:2607:G:H2'	1:A:2608:G:O4'	2.03	0.59
22:V:14:LYS:HB2	22:V:17:ALA:HB3	1.85	0.59
23:W:21:LEU:HD12	23:W:21:LEU:H	1.68	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:760:G:C2'	1:A:761:A:H5'	2.32	0.58
1:A:835:A:OP1	31:5:52:LYS:HG2	2.03	0.58
30:4:34:ARG:HD2	30:4:39:ARG:HG3	1.85	0.58
20:T:47:PHE:HB3	20:T:89:ILE:HD12	1.83	0.58
16:P:20:PRO:HD2	16:P:86:ILE:HG23	1.84	0.58
24:X:37:ILE:CG2	24:X:38:SER:N	2.66	0.58
16:P:132:LYS:O	16:P:136:GLN:HG3	2.02	0.58
11:K:122:LEU:HD13	16:P:72:VAL:HG11	1.83	0.58
25:Y:24:LEU:HD22	25:Y:60:LEU:HD13	1.86	0.58
3:C:11:PRO:C	3:C:13:ARG:H	2.07	0.58
1:A:414:C:H2'	1:A:415:A:C8	2.38	0.58
18:R:38:LEU:HD23	18:R:39:LEU:N	2.18	0.58
26:Z:8:LEU:HB2	26:Z:28:LEU:HD23	1.85	0.58
1:A:1434:A:H2'	1:A:1435:G:H8	1.68	0.58
1:A:1478:G:O2'	1:A:1558:A:H2	1.86	0.58
1:A:2776:A:H4'	1:A:2777:G:H5''	1.84	0.58
4:D:1:MET:HB3	4:D:83:ASP:O	2.02	0.58
7:G:13:LYS:HE2	7:G:14:GLY:H	1.66	0.58
1:A:603:A:H61	1:A:655:A:H1'	1.68	0.58
1:A:2476:A:H2'	1:A:2476:A:N3	2.17	0.58
3:C:8:PRO:HB3	3:C:14:ARG:CB	2.33	0.58
1:A:1161:C:O2'	18:R:8:GLY:HA2	2.04	0.58
1:A:886:C:C2'	1:A:887:A:H4'	2.31	0.58
14:N:4:LEU:C	14:N:6:SER:H	2.05	0.58
1:A:528:A:C3'	1:A:528:A:C8	2.87	0.58
8:H:123:LEU:HD23	8:H:124:GLY:N	2.18	0.58
1:A:1952:A:C5	11:K:22:ILE:HD12	2.39	0.58
19:S:40:ASN:O	19:S:41:LYS:HG2	2.04	0.58
17:Q:95:LEU:O	17:Q:98:LEU:HG	2.04	0.58
1:A:2392:A:OP1	31:5:32:LEU:HB3	2.04	0.58
1:A:71:A:C2	20:T:31:HIS:HE1	2.22	0.58
4:D:132:HIS:CG	4:D:135:HIS:NE2	2.71	0.58
1:A:558:G:OP1	10:J:134:PRO:HD2	2.03	0.58
3:C:130:ALA:HB2	3:C:192:THR:HB	1.86	0.58
1:A:795:C:H2'	1:A:796:C:C6	2.37	0.58
1:A:7:G:H2'	1:A:8:A:C8	2.37	0.58
1:A:966:G:H2'	1:A:967:C:H6	1.67	0.58
8:H:53:ALA:O	8:H:57:ARG:HB2	2.03	0.58
4:D:92:THR:O	4:D:95:ILE:HG13	2.03	0.58
2:B:70:C:H2'	2:B:71:C:H6	1.68	0.58
1:A:1378:A:O2'	1:A:1379:A:H3'	2.03	0.58
13:M:66:ILE:HG22	13:M:104:PHE:CD2	2.39	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:36:LYS:HB3	6:F:160:VAL:HB	1.84	0.58
12:L:128:HIS:HA	12:L:147:LEU:CB	2.21	0.58
1:A:270(J):G:O2'	1:A:270(K):G:H8	1.87	0.58
6:F:114:ILE:HG23	6:F:115:ARG:HD2	1.84	0.58
9:I:4:LYS:HG2	9:I:8:GLU:HG3	1.85	0.58
3:C:31:LYS:O	3:C:36:PRO:HD3	2.03	0.58
1:A:2039:C:H2'	1:A:2040:C:C6	2.35	0.58
8:H:113:ARG:HB2	8:H:130:TYR:CE1	2.38	0.58
7:G:55:PRO:HG2	7:G:61:HIS:CD2	2.38	0.58
15:O:52:SER:HB2	15:O:56:LEU:HB2	1.85	0.58
11:K:86:ILE:H	11:K:86:ILE:HD12	1.68	0.58
25:Y:16:LEU:HB2	25:Y:20:GLU:CG	2.34	0.58
5:E:53:THR:HG22	5:E:56:GLU:CD	2.23	0.58
22:V:24:LEU:HD21	22:V:86:VAL:CG2	2.33	0.58
1:A:814:C:C5	12:L:27:HIS:NE2	2.72	0.58
31:5:37:SER:OG	31:5:40:GLU:HG2	2.04	0.58
1:A:114(B):A:H4'	10:J:48:ARG:HH22	1.69	0.57
14:N:101:ALA:HB2	28:2:44:THR:HG21	1.86	0.57
1:A:245:G:O6	31:5:8:LYS:HE3	2.04	0.57
1:A:2439:A:C5'	1:A:2439:A:C8	2.86	0.57
5:E:80:ALA:O	5:E:83:PHE:HB2	2.04	0.57
1:A:83:G:N2	1:A:102:G:H2'	2.18	0.57
20:T:57:LEU:HD12	20:T:57:LEU:N	2.19	0.57
18:R:28:GLU:HB2	18:R:31:ALA:HB2	1.85	0.57
1:A:278:A:H4'	1:A:279:C:OP1	2.04	0.57
24:X:83:GLU:HG2	24:X:84:GLY:N	2.17	0.57
1:A:1331:A:HO2'	1:A:1332:G:H8	1.51	0.57
4:D:84:PHE:CZ	4:D:86:PRO:HG3	2.39	0.57
1:A:1275:A:C8	14:N:16:HIS:CD2	2.92	0.57
1:A:1504:C:HO2'	1:A:1505:C:P	2.26	0.57
1:A:2633:G:O2'	4:D:61:ARG:HD3	2.05	0.57
1:A:534:U:O2'	17:Q:49:HIS:HD2	1.87	0.57
3:C:246:PRO:HD2	3:C:255:LYS:HD3	1.86	0.57
6:F:47:LYS:HG3	6:F:82:LEU:HD22	1.85	0.57
12:L:18:ARG:CZ	12:L:18:ARG:HB3	2.33	0.57
1:A:2243:U:H2'	1:A:2244:U:C6	2.39	0.57
1:A:929:G:H8	1:A:929:G:O5'	1.88	0.57
29:3:11:LEU:HD11	29:3:51:GLU:HG3	1.87	0.57
1:A:572:A:C2	1:A:2033:A:C2	2.93	0.57
1:A:1579:A:H5'	1:A:1579:A:C8	2.35	0.57
4:D:5:LEU:HB2	4:D:51:PHE:CD2	2.39	0.57
29:3:11:LEU:HD13	29:3:12:GLU:N	2.19	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:164:ARG:O	5:E:168:ARG:HB2	2.05	0.57
29:3:13:CYS:SG	29:3:24:GLU:HG3	2.45	0.57
1:A:2647:U:H2'	1:A:2648:C:C6	2.40	0.57
7:G:20:ALA:HB1	7:G:21:PRO:HD2	1.87	0.57
24:X:58:ILE:HD11	24:X:91:LYS:HG2	1.85	0.57
2:B:30:C:OP2	15:O:32:LEU:HD11	2.04	0.57
1:A:2790:A:H2'	1:A:2791:C:H5''	1.87	0.57
18:R:64:HIS:CD2	18:R:92:THR:HG22	2.39	0.57
21:U:8:LYS:NZ	21:U:8:LYS:N	2.51	0.57
31:5:54:GLU:HA	31:5:57:ARG:NH1	2.19	0.57
8:H:113:ARG:HB2	8:H:130:TYR:CZ	2.39	0.57
1:A:1331:A:O2'	1:A:1332:G:H8	1.88	0.57
1:A:1154:G:H8	1:A:1154:G:O5'	1.88	0.57
5:E:195:ASP:OD2	5:E:197:ASP:HB3	2.05	0.57
3:C:231:HIS:CG	3:C:232:PRO:HD2	2.39	0.57
1:A:2104:G:H2'	1:A:2105:C:C6	2.39	0.57
24:X:27:GLU:CD	24:X:33:LYS:HE3	2.24	0.57
1:A:832:G:OP1	12:L:40:SER:HB3	2.05	0.57
6:F:136:ARG:O	6:F:154:GLY:HA2	2.05	0.57
20:T:26:TYR:O	20:T:81:VAL:HG22	2.04	0.57
1:A:1360:A:H5'	1:A:1361:G:OP2	2.05	0.57
1:A:1544:C:H3'	1:A:1545:A:C5'	2.34	0.57
3:C:8:PRO:HB3	3:C:14:ARG:HB3	1.87	0.57
20:T:12:VAL:HG12	20:T:27:THR:O	2.05	0.57
31:5:53:PRO:HB2	31:5:57:ARG:HH21	1.70	0.57
5:E:52:LYS:HB3	5:E:56:GLU:O	2.04	0.57
4:D:33:VAL:HG12	4:D:89:ASP:O	2.04	0.57
1:A:46:C:OP2	1:A:215:G:H2'	2.05	0.57
1:A:319:C:H2'	1:A:320:A:C8	2.40	0.57
1:A:581:C:OP1	17:Q:31:SER:HB2	2.05	0.57
1:A:301:G:C4	1:A:302:C:C5	2.93	0.57
1:A:2563:U:O2	1:A:2565:A:H8	1.86	0.57
20:T:31:HIS:ND1	20:T:32:PRO:HD2	2.19	0.56
1:A:330:A:H2	1:A:1210:A:H2'	1.70	0.56
1:A:2376:A:N6	15:O:89:ARG:HD2	2.20	0.56
1:A:2078:C:H2'	1:A:2079:U:C6	2.38	0.56
12:L:135:LEU:O	12:L:139:LYS:HB2	2.04	0.56
12:L:111:ARG:HG3	12:L:128:HIS:CB	2.36	0.56
5:E:203:GLN:HA	5:E:206:ILE:O	2.05	0.56
17:Q:36:ARG:HG2	17:Q:40:PHE:CE1	2.40	0.56
25:Y:21:LEU:HD23	25:Y:22:GLU:N	2.19	0.56
2:B:37:C:H2'	15:O:95:HIS:HE1	1.70	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:68:ALA:O	17:Q:71:GLN:HB3	2.04	0.56
5:E:192:LEU:HD21	5:E:194:MET:CE	2.36	0.56
1:A:1495:A:H2'	1:A:1496:A:N3	2.20	0.56
1:A:747:U:C4	28:2:2:ALA:N	2.74	0.56
1:A:806:C:O2'	1:A:2445:G:H4'	2.05	0.56
3:C:233:HIS:CE1	3:C:247:ALA:H	2.23	0.56
1:A:1046:A:C3'	1:A:1047:G:H5''	2.35	0.56
6:F:5:LEU:HD21	27:1:50:THR:HG23	1.87	0.56
22:V:24:LEU:HD21	22:V:86:VAL:HG21	1.87	0.56
11:K:104:ARG:NH1	11:K:104:ARG:HB3	2.20	0.56
12:L:125:VAL:O	12:L:145:PRO:HD2	2.05	0.56
20:T:8:ILE:HD12	20:T:8:ILE:N	2.20	0.56
1:A:319:C:H2'	1:A:320:A:H8	1.71	0.56
25:Y:23:LYS:O	25:Y:27:GLU:HG3	2.05	0.56
3:C:44:ASN:HB3	3:C:50:THR:CG2	2.36	0.56
1:A:1430:C:H2'	1:A:1431:U:C6	2.40	0.56
1:A:2305:A:H5''	6:F:134:GLY:HA3	1.87	0.56
1:A:1966:A:H4'	1:A:1967:C:OP1	2.04	0.56
1:A:1373:A:H2'	1:A:1374:G:O4'	2.06	0.56
2:B:8:U:H5''	15:O:15:ARG:HH22	1.71	0.56
25:Y:2:LYS:N	25:Y:2:LYS:CD	2.69	0.56
4:D:67:PHE:HE2	4:D:75:VAL:HG22	1.70	0.56
12:L:143:GLY:O	12:L:145:PRO:HD3	2.05	0.56
1:A:1187:G:H5''	18:R:81:TYR:CE2	2.41	0.56
1:A:2496:C:OP1	13:M:81:VAL:HG13	2.05	0.56
1:A:911:A:C6	13:M:9:TYR:HE1	2.24	0.56
14:N:51:LEU:HD22	14:N:66:VAL:HG13	1.88	0.56
31:5:14:VAL:HG13	31:5:22:VAL:HG13	1.88	0.56
3:C:182:LEU:O	3:C:271:ILE:HD12	2.06	0.56
1:A:1311:G:C8	1:A:1311:G:C5'	2.87	0.56
2:B:43:C:H2'	2:B:44:G:H5''	1.86	0.56
1:A:1541:U:H3'	1:A:1542:G:C3'	2.35	0.56
1:A:1434:A:H61	1:A:1558:A:N6	2.03	0.56
7:G:121:ILE:HD11	7:G:140:LYS:HD3	1.87	0.56
1:A:2746:U:H2'	1:A:2747:G:H5'	1.86	0.56
22:V:95:PRO:HB2	22:V:127:LYS:HE3	1.88	0.56
10:J:148:GLY:HA3	10:J:149:PRO:O	2.04	0.56
10:J:151:HIS:HD2	10:J:152:PRO:O	1.89	0.56
1:A:1241:A:N3	1:A:1241:A:H5'	2.21	0.56
1:A:2058:A:N6	1:A:2059:A:N6	2.54	0.56
16:P:28:VAL:HA	16:P:89:VAL:HG12	1.88	0.56
30:4:37:LYS:HD3	30:4:39:ARG:HE	1.71	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:40:ALA:HB3	13:M:127:ILE:HD11	1.87	0.56
14:N:13:HIS:CE1	14:N:16:HIS:HB2	2.39	0.56
5:E:184:TYR:CE2	5:E:188:ARG:HD2	2.40	0.56
1:A:626:U:O2	12:L:105:LEU:HB3	2.04	0.56
1:A:1005:C:O2'	10:J:51:THR:HG21	2.06	0.56
1:A:828:U:H4'	1:A:831:G:N1	2.21	0.56
16:P:117:ASP:O	16:P:121:ILE:HG13	2.05	0.56
13:M:58:PHE:O	13:M:58:PHE:CD1	2.59	0.56
1:A:2233:U:H2'	1:A:2234:G:C8	2.41	0.56
27:1:48:ILE:H	27:1:48:ILE:HD12	1.69	0.56
12:L:33:ARG:O	12:L:34:GLY:C	2.44	0.56
15:O:35:ILE:CG1	15:O:101:LEU:HD21	2.34	0.56
1:A:2036:C:C6	1:A:2036:C:H5'	2.38	0.56
15:O:26:LEU:O	15:O:88:ASP:HB3	2.06	0.56
18:R:77:ALA:O	18:R:79:VAL:N	2.39	0.56
29:3:11:LEU:HB2	29:3:26:ASN:H	1.70	0.56
1:A:2294:C:H2'	1:A:2295:C:C6	2.41	0.56
6:F:110:ALA:O	6:F:114:ILE:HG13	2.05	0.56
1:A:999:U:H5''	1:A:1154:G:O6	2.05	0.56
21:U:96:ILE:HG23	21:U:101:LYS:O	2.06	0.56
28:2:33:CYS:SG	28:2:40:LYS:HE3	2.46	0.56
15:O:49:VAL:HG13	15:O:76:LYS:HD2	1.87	0.56
16:P:48:ILE:H	16:P:48:ILE:HD12	1.70	0.56
14:N:9:LYS:C	14:N:10:LEU:HG	2.26	0.56
1:A:706:A:H2'	1:A:707:G:O4'	2.07	0.56
3:C:126:GLN:O	3:C:193:VAL:HG11	2.05	0.56
19:S:73:ALA:O	19:S:106:ILE:HG12	2.05	0.56
3:C:271:ILE:O	3:C:272:ALA:HB3	2.06	0.55
1:A:2036:C:H6	1:A:2036:C:C5'	2.18	0.55
2:B:111:U:H2'	2:B:112:G:H8	1.70	0.55
1:A:1996:C:OP1	11:K:31:LYS:HE3	2.06	0.55
1:A:442:G:H1'	5:E:48:THR:HG21	1.88	0.55
12:L:114:ILE:O	12:L:114:ILE:HD12	2.05	0.55
31:5:52:LYS:N	31:5:53:PRO:HD2	2.20	0.55
1:A:2210:G:N2	1:A:2211:G:H5'	2.21	0.55
24:X:27:GLU:CB	24:X:33:LYS:HG3	2.37	0.55
10:J:62:ARG:HH21	10:J:64:ASP:HB2	1.70	0.55
1:A:1588:C:H2'	1:A:1589:C:H6	1.71	0.55
1:A:221:A:H4'	1:A:222:A:O5'	2.06	0.55
22:V:8:TYR:HB2	22:V:38:TYR:CZ	2.41	0.55
3:C:242:ARG:CD	3:C:242:ARG:H	2.08	0.55
12:L:18:ARG:NH1	12:L:18:ARG:HB3	2.22	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:173:LEU:HD23	6:F:176:LEU:HD12	1.88	0.55
1:A:64:A:O2'	20:T:71:GLY:HA3	2.06	0.55
1:A:278:A:H2'	1:A:279:C:O4'	2.06	0.55
17:Q:104:GLN:HB3	18:R:44:LYS:HZ1	1.71	0.55
16:P:80:SER:HB3	16:P:83:ILE:HG13	1.88	0.55
17:Q:92:ARG:HG2	18:R:11:GLN:NE2	2.21	0.55
21:U:45:VAL:HA	21:U:62:GLU:HA	1.87	0.55
1:A:343:C:C5'	1:A:343:C:H6	2.18	0.55
2:B:11:C:H3'	2:B:12:C:C6	2.41	0.55
16:P:19:LEU:HD13	16:P:78:LEU:HD22	1.89	0.55
26:Z:11:SER:OG	26:Z:13:ILE:HG12	2.06	0.55
12:L:115:LEU:HA	12:L:134:ALA:CB	2.36	0.55
25:Y:2:LYS:HA	25:Y:5:GLU:OE2	2.07	0.55
1:A:195:A:OP1	12:L:46:LYS:HE2	2.07	0.55
21:U:7:VAL:HB	21:U:8:LYS:HZ2	1.71	0.55
1:A:1046:A:H1'	9:I:4:LYS:HD2	1.89	0.55
26:Z:1:MET:HA	26:Z:39:ASP:HB3	1.88	0.55
8:H:12:LEU:H	8:H:12:LEU:HD22	1.71	0.55
2:B:104:A:O4'	22:V:29:TYR:HE1	1.90	0.55
1:A:2892:A:H2'	1:A:2893:G:H5'	1.87	0.55
14:N:88:ARG:HG3	14:N:89:ASP:OD1	2.07	0.55
23:W:51:VAL:N	23:W:62:LEU:HD12	2.22	0.55
1:A:1639:U:H2'	1:A:1640:C:H5''	1.89	0.55
1:A:55:G:H2'	1:A:56:A:H8	1.72	0.55
10:J:42:GLU:HA	10:J:82:LYS:CB	2.32	0.55
30:4:8:ASN:HD21	30:4:11:LYS:H	1.52	0.55
1:A:1173:G:H1'	1:A:1177:A:H61	1.71	0.55
3:C:71:ASP:HB3	3:C:103:ARG:NH2	2.20	0.55
13:M:112:GLU:H	13:M:112:GLU:CD	2.10	0.55
16:P:57:PHE:O	16:P:59:THR:N	2.39	0.55
24:X:23:LYS:HB3	24:X:37:ILE:HG12	1.87	0.55
4:D:67:PHE:CE2	4:D:75:VAL:HG22	2.41	0.55
1:A:1292:U:H2'	1:A:1293:C:C6	2.42	0.55
7:G:44:VAL:O	7:G:50:VAL:HG13	2.07	0.55
12:L:33:ARG:HG3	12:L:36:LYS:CD	2.22	0.55
1:A:1826:G:H4'	3:C:242:ARG:NE	2.22	0.55
1:A:676:A:H2	1:A:802:A:H61	1.54	0.55
1:A:1188:U:O2'	1:A:1189:A:H5'	2.06	0.55
1:A:1276:A:O2'	14:N:16:HIS:HE1	1.90	0.55
6:F:81:LYS:O	6:F:82:LEU:HD23	2.06	0.55
13:M:75:THR:HA	13:M:88:GLY:HA3	1.88	0.55
26:Z:26:LEU:HB2	26:Z:28:LEU:HD13	1.89	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:45:GLN:H	13:M:45:GLN:CD	2.10	0.55
1:A:1448:G:H2'	1:A:149(B):A:C8	2.41	0.55
1:A:1833:U:H2'	1:A:1834:U:H6	1.70	0.55
3:C:217:ARG:HG2	3:C:217:ARG:NH1	2.19	0.54
14:N:12:ARG:HD3	14:N:16:HIS:ND1	2.23	0.54
1:A:2102:U:H2'	1:A:2103:C:C6	2.43	0.54
20:T:28:PHE:HE2	20:T:92:LEU:HD11	1.71	0.54
1:A:2393:A:H5'	12:L:62:LEU:HD12	1.89	0.54
13:M:140:ALA:HB3	22:V:53:ILE:HD13	1.89	0.54
11:K:68:GLU:HB3	11:K:78:ARG:HB2	1.90	0.54
10:J:90:LEU:O	10:J:111:GLU:HG3	2.07	0.54
8:H:114:LEU:HD21	8:H:128:LEU:HD13	1.89	0.54
1:A:1614:A:H62	19:S:93:ALA:HB2	1.72	0.54
19:S:4:LYS:HG2	19:S:106:ILE:HG22	1.89	0.54
13:M:26:TYR:HA	22:V:81:ARG:HH21	1.72	0.54
3:C:25:THR:HG21	3:C:81:ALA:HB1	1.89	0.54
1:A:1257:C:H4'	5:E:83:PHE:CE2	2.42	0.54
5:E:192:LEU:HD23	5:E:193:VAL:N	2.22	0.54
11:K:73:ASP:OD1	11:K:75:SER:HB3	2.07	0.54
5:E:32:LEU:C	5:E:32:LEU:HD23	2.28	0.54
1:A:2014:A:H2'	1:A:2015:A:C8	2.43	0.54
1:A:910:A:C4	13:M:13:GLN:NE2	2.74	0.54
16:P:59:THR:O	16:P:78:LEU:HB2	2.07	0.54
5:E:183:VAL:O	5:E:187:VAL:HG23	2.08	0.54
12:L:112:LEU:HD23	12:L:113:LYS:N	2.22	0.54
18:R:6:LYS:O	18:R:37:VAL:HG21	2.08	0.54
8:H:92:VAL:HG23	8:H:96:ASP:HB2	1.90	0.54
12:L:64:LYS:HD2	31:5:25:MET:SD	2.48	0.54
1:A:819:A:C4	1:A:1189:A:C2	2.95	0.54
1:A:966:G:H2'	1:A:967:C:C6	2.41	0.54
1:A:919:G:H5'	2:B:81:G:H1'	1.89	0.54
11:K:96:THR:O	11:K:97:ARG:C	2.46	0.54
1:A:2749:A:H4'	7:G:62:LYS:HB3	1.89	0.54
25:Y:11:GLU:OE1	25:Y:11:GLU:N	2.40	0.54
7:G:27:LYS:HG2	7:G:32:GLU:HB2	1.90	0.54
13:M:141:GLN:HA	22:V:71:VAL:O	2.08	0.54
22:V:74:VAL:O	22:V:76:LEU:HD12	2.07	0.54
5:E:63:LYS:HE3	5:E:75:HIS:O	2.08	0.54
11:K:103:ALA:O	11:K:106:LEU:HD13	2.07	0.54
1:A:2774:C:H2'	1:A:2775:A:O4'	2.06	0.54
1:A:2744:G:H21	7:G:143:GLN:NE2	2.00	0.54
31:5:52:LYS:H	31:5:53:PRO:HD2	1.73	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:529:A:H62	1:A:2041:U:H3	1.54	0.54
1:A:276:A:H3'	1:A:277:C:H5''	1.89	0.54
1:A:1819:A:H4'	1:A:1820:U:H5''	1.88	0.54
1:A:2726:U:H5'	1:A:2726:U:O2	2.08	0.54
3:C:125:ILE:HD12	3:C:125:ILE:H	1.72	0.54
1:A:2393:A:H5''	12:L:62:LEU:HD12	1.90	0.54
3:C:123:ALA:HB3	3:C:131:LEU:HD23	1.88	0.54
1:A:947:G:N2	1:A:971:C:C2	2.76	0.54
7:G:121:ILE:HD11	7:G:140:LYS:HB3	1.90	0.54
22:V:110:GLY:HA3	22:V:174:VAL:HG11	1.90	0.54
1:A:2293:C:H4'	15:O:93:LYS:NZ	2.23	0.54
1:A:1647:G:OP2	1:A:1647:G:H3'	2.06	0.54
17:Q:79:PHE:HE1	17:Q:83:LEU:HD21	1.72	0.54
21:U:37:VAL:HG21	21:U:72:VAL:HG21	1.89	0.54
1:A:2744:G:N2	7:G:143:GLN:HE22	1.99	0.54
26:Z:17:LYS:HD3	26:Z:17:LYS:C	2.28	0.54
1:A:2422:A:N7	31:5:31:HIS:CE1	2.76	0.54
27:1:59:VAL:HG12	27:1:60:GLU:N	2.19	0.54
8:H:77:LEU:HD11	8:H:101:LEU:HB2	1.90	0.54
11:K:2:ILE:HG12	11:K:8:LEU:HD11	1.88	0.54
21:U:76:CYS:SG	21:U:77:PRO:HD2	2.48	0.54
7:G:109:PHE:CE1	7:G:152:ARG:HD3	2.43	0.54
1:A:605:C:H1'	1:A:657:U:O2'	2.08	0.54
1:A:137(B):G:H2'	1:A:139:G:N7	2.22	0.54
1:A:614:U:H4'	1:A:615:G:H5''	1.90	0.54
17:Q:92:ARG:CD	17:Q:94:ASN:HB3	2.38	0.53
3:C:25:THR:HG21	3:C:81:ALA:CB	2.37	0.53
3:C:71:ASP:CB	3:C:103:ARG:HH22	2.20	0.53
15:O:87:PHE:CE2	15:O:89:ARG:HA	2.43	0.53
2:B:40:U:H6	2:B:40:U:O5'	1.92	0.53
18:R:22:VAL:HG12	18:R:23:GLU:H	1.73	0.53
3:C:233:HIS:HE1	3:C:247:ALA:H	1.56	0.53
12:L:58:THR:C	12:L:60:MET:H	2.12	0.53
30:4:8:ASN:ND2	30:4:11:LYS:N	2.54	0.53
15:O:34:HIS:ND1	15:O:54:LEU:HB2	2.22	0.53
8:H:76:THR:HA	8:H:141:LYS:HB2	1.89	0.53
25:Y:46:GLN:HA	25:Y:46:GLN:OE1	2.09	0.53
4:D:47:VAL:HG21	4:D:86:PRO:HD3	1.90	0.53
5:E:192:LEU:HD21	5:E:194:MET:HE3	1.90	0.53
1:A:17:G:H4'	17:Q:25:TRP:CH2	2.42	0.53
5:E:36:VAL:O	5:E:40:GLN:HG3	2.07	0.53
12:L:132:LYS:HD2	12:L:132:LYS:N	2.21	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:84:ASN:HB3	12:L:86:LYS:HG2	1.90	0.53
31:5:34:TRP:CG	31:5:35:GLN:N	2.76	0.53
4:D:25:VAL:HG12	4:D:181:LEU:HD12	1.91	0.53
8:H:130:TYR:CD2	8:H:132:PRO:HG3	2.43	0.53
1:A:2186:G:H2'	1:A:2187:G:C8	2.42	0.53
1:A:581:C:H2'	1:A:582:G:H8	1.74	0.53
1:A:2814:C:O2'	28:2:29:ILE:HG13	2.08	0.53
1:A:1655:A:H1'	4:D:113:PHE:CD2	2.43	0.53
20:T:23:GLU:HG3	20:T:24:GLY:H	1.73	0.53
1:A:2481:G:O2'	1:A:2482:G:P	2.65	0.53
1:A:2401:U:C2'	1:A:2402:C:H5''	2.39	0.53
6:F:96:ARG:O	6:F:99:MET:HB3	2.09	0.53
4:D:111:ARG:HD2	4:D:160:TYR:CE1	2.44	0.53
14:N:104:ARG:NH1	14:N:109:ALA:HB3	2.24	0.53
6:F:32:PRO:HA	6:F:162:THR:OG1	2.09	0.53
1:A:814:C:O2'	1:A:815:C:H5'	2.08	0.53
21:U:59:GLY:C	21:U:61:ILE:H	2.11	0.53
14:N:96:ARG:HH22	14:N:117:VAL:HG23	1.73	0.53
1:A:1932:A:H3'	1:A:1933:G:H8	1.73	0.53
1:A:483:A:H4'	21:U:49:VAL:HG23	1.89	0.53
2:B:49:C:OP1	15:O:97:ARG:HG3	2.08	0.53
1:A:1266:G:H5''	28:2:23:HIS:NE2	2.23	0.53
12:L:62:LEU:H	12:L:62:LEU:HD22	1.74	0.53
31:5:50:LEU:HB2	31:5:54:GLU:HG3	1.90	0.53
22:V:108:PRO:HA	22:V:142:SER:O	2.07	0.53
17:Q:58:ARG:O	17:Q:62:ILE:HG12	2.08	0.53
1:A:1309:G:H3'	30:4:9:ARG:NH1	2.22	0.53
12:L:27:HIS:HE1	18:R:83:ARG:HH12	1.56	0.53
1:A:1692:U:O2'	1:A:1693:U:H2'	2.09	0.53
1:A:1862:G:H2'	1:A:1863:G:H8	1.73	0.53
10:J:157:ARG:N	10:J:158:PRO:CD	2.65	0.53
4:D:33:VAL:HG23	4:D:47:VAL:HG13	1.91	0.53
3:C:72:LYS:HE3	3:C:101:GLU:HG2	1.91	0.53
19:S:103:ILE:H	19:S:103:ILE:HD12	1.74	0.53
1:A:1386:C:H2'	1:A:1387:C:H6	1.74	0.53
1:A:1386:C:H2'	1:A:1387:C:C6	2.44	0.53
1:A:2394:C:H2'	1:A:2395:C:C6	2.44	0.53
7:G:149:ARG:HA	7:G:162:ILE:HG12	1.90	0.53
22:V:76:LEU:H	22:V:76:LEU:HD12	1.73	0.53
3:C:131:LEU:HA	3:C:190:TYR:CE2	2.43	0.53
21:U:11:ASP:O	21:U:26:LYS:HA	2.09	0.53
1:A:2543:G:H2'	1:A:2544:G:C8	2.44	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:322:A:H3'	5:E:169:ASN:HD21	1.72	0.53
1:A:597:U:O2'	12:L:15:ARG:HG2	2.09	0.53
1:A:2648:C:H2'	1:A:2649:U:C6	2.43	0.53
16:P:1:MET:O	16:P:3:ARG:N	2.40	0.53
24:X:45:ASN:ND2	24:X:47:GLN:HE21	2.07	0.53
1:A:127:A:H5''	1:A:128:C:O4'	2.09	0.53
27:1:42:CYS:SG	27:1:46:ASN:HB3	2.49	0.53
3:C:132:PRO:HD3	3:C:190:TYR:CZ	2.44	0.53
1:A:2822:G:O6	14:N:4:LEU:HD23	2.08	0.53
12:L:17:LYS:O	12:L:19:VAL:HG22	2.09	0.53
1:A:1614:A:H61	19:S:88:ARG:H	1.55	0.53
15:O:41:ASP:OD2	15:O:44:LYS:HD3	2.09	0.53
22:V:118:GLN:HB2	22:V:173:ALA:O	2.09	0.53
19:S:110:LYS:HG3	19:S:111:HIS:ND1	2.24	0.53
1:A:2731:G:C6	1:A:2732:G:O6	2.62	0.53
18:R:38:LEU:HD22	18:R:52:VAL:HG11	1.91	0.53
1:A:1164:G:H8	1:A:1164:G:C5'	2.22	0.53
1:A:637:A:OP1	12:L:133:SER:HB3	2.09	0.53
6:F:107:LEU:HA	6:F:111:LEU:HD12	1.91	0.53
1:A:948:G:H8	1:A:948:G:C5'	2.18	0.53
1:A:323:G:H5'	5:E:169:ASN:HD21	1.73	0.53
8:H:117:GLU:HG3	8:H:118:LYS:N	2.24	0.53
1:A:2010:G:H5''	19:S:42:ARG:HB2	1.91	0.53
1:A:486:C:H4'	19:S:60:ASN:HD22	1.74	0.53
20:T:39:ILE:O	20:T:43:VAL:HG12	2.09	0.52
1:A:1510:A:H2'	1:A:1511:A:H8	1.71	0.52
14:N:10:LEU:HD22	14:N:17:ARG:CD	2.39	0.52
23:W:48:GLY:HA3	23:W:80:HIS:ND1	2.24	0.52
1:A:263:C:H2'	1:A:264:C:O4'	2.09	0.52
1:A:176:G:O2'	1:A:177:G:H5'	2.09	0.52
8:H:77:LEU:HG	8:H:101:LEU:HD13	1.91	0.52
1:A:2358:G:C6	1:A:2359:C:C4	2.97	0.52
1:A:2271:G:H2'	1:A:2272:U:C6	2.44	0.52
6:F:47:LYS:HG3	6:F:82:LEU:CD2	2.38	0.52
1:A:593:G:O2'	31:5:62:LEU:HD13	2.09	0.52
17:Q:88:ILE:HG13	17:Q:88:ILE:O	2.09	0.52
1:A:1022:G:H8	10:J:92:GLN:HE22	1.56	0.52
1:A:2517:C:C6	1:A:2542:A:C2	2.96	0.52
1:A:775:G:C4	1:A:794:G:C8	2.97	0.52
1:A:568:U:O4	18:R:78:LYS:NZ	2.40	0.52
13:M:58:PHE:HD1	13:M:58:PHE:O	1.92	0.52
22:V:94:GLU:H	22:V:94:GLU:CD	2.12	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:78:PRO:O	13:M:79:LEU:HB2	2.09	0.52
15:O:49:VAL:HG11	15:O:73:LEU:HA	1.92	0.52
11:K:68:GLU:H	11:K:68:GLU:CD	2.12	0.52
1:A:779:U:P	3:C:49:ILE:HG13	2.49	0.52
21:U:90:LEU:HG	21:U:91:GLU:HG2	1.91	0.52
30:4:21:ARG:HB3	30:4:31:LEU:CD2	2.40	0.52
16:P:57:PHE:HE2	16:P:79:HIS:HB2	1.74	0.52
17:Q:49:HIS:HA	17:Q:52:ARG:HB2	1.92	0.52
22:V:5:LEU:HB3	22:V:59:LEU:HD23	1.92	0.52
1:A:1826:G:OP1	3:C:233:HIS:HD2	1.92	0.52
12:L:62:LEU:CD2	31:5:25:MET:HB2	2.38	0.52
1:A:2439:A:H8	1:A:2439:A:C5'	2.22	0.52
5:E:53:THR:HG23	5:E:55:GLY:N	2.19	0.52
5:E:34:TRP:HB2	12:L:10:PRO:O	2.10	0.52
12:L:143:GLY:C	12:L:145:PRO:HD3	2.29	0.52
11:K:112:MET:HA	11:K:115:VAL:HG22	1.91	0.52
6:F:139:LEU:HA	6:F:144:ILE:HG21	1.91	0.52
12:L:88:LEU:HD22	12:L:114:ILE:HG21	1.90	0.52
1:A:959:A:O2'	1:A:960:A:H5'	2.10	0.52
16:P:26:ASP:HB2	16:P:90:GLN:O	2.09	0.52
25:Y:39:ALA:HA	25:Y:45:SER:CB	2.39	0.52
13:M:60:ARG:H	22:V:179:ASP:CB	2.22	0.52
8:H:6:LEU:HA	8:H:15:VAL:HG13	1.90	0.52
18:R:15:GLU:HB3	18:R:16:PRO:HD2	1.92	0.52
1:A:871:U:H4'	13:M:69:PHE:CE2	2.45	0.52
1:A:195:A:H61	1:A:198:C:H3'	1.75	0.52
15:O:35:ILE:O	15:O:53:SER:HB2	2.10	0.52
27:1:46:ASN:HB2	27:1:64:LYS:HB2	1.90	0.52
1:A:270(L):C:H2'	1:A:270(M):U:H5''	1.91	0.52
12:L:16:ARG:C	12:L:16:ARG:HE	2.13	0.52
3:C:204:ILE:HD12	3:C:204:ILE:O	2.10	0.52
1:A:830:G:H4'	1:A:831:G:OP2	2.09	0.52
1:A:144:C:H2'	1:A:145:G:C8	2.45	0.52
1:A:298:G:P	21:U:85:VAL:HG22	2.49	0.52
1:A:553:U:O2'	1:A:554:U:H5'	2.10	0.52
1:A:1592:C:H2'	1:A:1593:G:H8	1.75	0.52
5:E:18:ARG:O	5:E:18:ARG:HG3	2.09	0.52
17:Q:92:ARG:NH2	18:R:11:GLN:H	2.07	0.52
13:M:81:VAL:CG1	13:M:82:ARG:HG2	2.37	0.52
4:D:101:ARG:HD3	4:D:169:ASN:ND2	2.24	0.52
4:D:201:THR:CG2	4:D:202:LYS:N	2.72	0.52
21:U:31:LEU:HD23	21:U:31:LEU:N	2.23	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:556:G:H2'	1:A:557:U:H6	1.70	0.52
1:A:2688:U:O2	1:A:2688:U:H3'	2.09	0.52
18:R:28:GLU:HB2	18:R:31:ALA:CB	2.39	0.52
13:M:58:PHE:CD1	13:M:61:GLY:HA3	2.45	0.52
19:S:46:PHE:O	19:S:50:VAL:HG12	2.09	0.52
4:D:172:VAL:HG13	4:D:182:LEU:HD11	1.90	0.52
19:S:80:PRO:O	19:S:100:THR:HG22	2.10	0.52
3:C:166:GLN:HE21	3:C:166:GLN:CA	2.22	0.52
12:L:52:GLU:OE1	12:L:52:GLU:HA	2.10	0.52
10:J:135:LEU:HD23	10:J:136:GLY:H	1.75	0.52
20:T:30:VAL:HG12	20:T:31:HIS:N	2.24	0.52
1:A:2210:G:H21	1:A:2211:G:C5'	2.22	0.52
1:A:1568:G:OP2	3:C:63:ARG:NH2	2.43	0.52
1:A:1173:G:H3'	1:A:1174:A:C5'	2.40	0.52
1:A:661:C:H2'	1:A:662:G:C8	2.45	0.52
30:4:34:ARG:HB3	30:4:42:LEU:HD22	1.92	0.52
1:A:1980:G:H3'	1:A:1981:A:C5'	2.40	0.52
1:A:2305:A:C2	6:F:154:GLY:HA3	2.44	0.52
1:A:1495:A:H2'	1:A:1495:A:N3	2.25	0.52
15:O:15:ARG:O	15:O:19:LYS:HG3	2.10	0.52
1:A:2258:C:H4'	1:A:2259:G:OP2	2.10	0.52
1:A:2371:G:O2'	29:3:45:LYS:HB3	2.10	0.52
1:A:848:G:C4	1:A:933:A:C8	2.95	0.52
1:A:588:U:H1'	5:E:90:PHE:CD1	2.45	0.52
1:A:2305:A:H3'	1:A:2306:C:H5''	1.92	0.52
19:S:19:LEU:HB3	28:2:25:LEU:CD1	2.41	0.52
1:A:1790:C:O2'	3:C:209:ALA:HB2	2.10	0.52
29:3:30:THR:HG22	29:3:31:PRO:HD2	1.92	0.52
13:M:52:VAL:O	13:M:56:ARG:HB2	2.10	0.52
13:M:54:MET:HG2	13:M:64:ILE:HD13	1.91	0.52
17:Q:92:ARG:HD2	17:Q:95:LEU:CG	2.38	0.51
8:H:92:VAL:HG22	8:H:120:ILE:HD12	1.92	0.51
12:L:58:THR:C	12:L:61:ARG:HE	2.13	0.51
1:A:2415:G:H4'	12:L:66:GLY:HA2	1.92	0.51
8:H:142:VAL:HG12	8:H:143:SER:H	1.74	0.51
1:A:2747:G:O6	1:A:2755:C:H5''	2.10	0.51
1:A:2729:G:H2'	1:A:2730:C:C6	2.45	0.51
19:S:84:ARG:HB2	19:S:96:ILE:HG22	1.92	0.51
11:K:24:VAL:HG23	11:K:33:ALA:HB2	1.92	0.51
1:A:2320:A:H2'	1:A:2320:A:N3	2.25	0.51
1:A:2094:G:N2	1:A:2196:C:H1'	2.25	0.51
5:E:82:ILE:O	5:E:82:ILE:HG13	2.09	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2056:G:N2	1:A:2057:A:H1'	2.25	0.51
24:X:13:ILE:HG23	24:X:14:VAL:H	1.75	0.51
14:N:10:LEU:HB2	14:N:17:ARG:CZ	2.40	0.51
22:V:104:PHE:HB3	22:V:141:VAL:HG11	1.93	0.51
11:K:2:ILE:CG1	11:K:8:LEU:HD11	2.40	0.51
1:A:2105:C:H2'	1:A:2106:G:C8	2.45	0.51
1:A:1973:G:H2'	1:A:1974:C:H6	1.75	0.51
1:A:2188:C:H2'	1:A:2189:U:O4'	2.10	0.51
1:A:1444:G:H2'	1:A:1445:C:C5	2.46	0.51
1:A:144(B):A:H5''	1:A:1445:C:H5	1.75	0.51
1:A:2032:G:O2'	4:D:145:LYS:HE2	2.09	0.51
1:A:1028:A:N6	1:A:1125:G:H2'	2.25	0.51
1:A:2378:A:H2'	15:O:21:THR:HG21	1.92	0.51
14:N:21:TYR:HE2	14:N:43:GLU:HB3	1.75	0.51
6:F:74:LYS:HA	6:F:74:LYS:HE3	1.92	0.51
2:B:71:C:C2	2:B:72:G:C8	2.98	0.51
8:H:142:VAL:HG12	8:H:143:SER:N	2.26	0.51
16:P:6:LEU:O	16:P:10:VAL:HG23	2.10	0.51
1:A:2252:G:H2'	1:A:2253:G:H8	1.76	0.51
25:Y:12:GLU:C	25:Y:14:ARG:H	2.13	0.51
20:T:15:GLU:N	20:T:15:GLU:CD	2.62	0.51
6:F:85:GLY:C	6:F:86:MET:HG3	2.31	0.51
8:H:116:LEU:HD22	8:H:128:LEU:HD21	1.91	0.51
8:H:86:THR:O	8:H:122:GLU:HG3	2.11	0.51
17:Q:8:VAL:HG11	17:Q:12:ARG:CZ	2.39	0.51
1:A:1010:A:H1'	1:A:1153:C:H1'	1.93	0.51
12:L:85:LEU:H	12:L:85:LEU:HD23	1.75	0.51
1:A:310:A:OP1	21:U:18:GLY:HA2	2.11	0.51
1:A:1541:U:H3'	1:A:1542:G:H3'	1.93	0.51
5:E:182:ASN:O	5:E:186:ILE:HG12	2.11	0.51
24:X:27:GLU:HB2	24:X:32:LYS:O	2.11	0.51
8:H:101:LEU:HG	8:H:107:ILE:HG23	1.92	0.51
6:F:134:GLY:C	6:F:135:LEU:HD12	2.30	0.51
1:A:320:A:H2'	5:E:136:THR:HG21	1.91	0.51
1:A:915:C:H2'	1:A:916:G:C8	2.46	0.51
1:A:1206:G:C6	1:A:1207:C:C4	2.98	0.51
1:A:498:G:N3	21:U:47:LYS:HE3	2.25	0.51
13:M:75:THR:CA	13:M:88:GLY:HA2	2.39	0.51
24:X:11:ARG:HB2	24:X:13:ILE:HG22	1.93	0.51
1:A:1335:U:H2'	1:A:1336:A:H8	1.76	0.51
1:A:389:G:C6	12:L:71:VAL:HG23	2.45	0.51
1:A:1187:G:O5'	1:A:1187:G:H8	1.94	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2537:U:H2'	1:A:2538:C:H6	1.75	0.51
12:L:75:ILE:HD13	12:L:77:ARG:NE	2.25	0.51
3:C:244:ARG:HG3	3:C:245:PRO:N	2.25	0.51
1:A:588:U:C2	5:E:90:PHE:CE1	2.98	0.51
1:A:2893:G:H3'	1:A:2894:G:H5'	1.93	0.51
30:4:24:THR:O	30:4:28:ARG:HG3	2.11	0.51
1:A:23:G:H2'	1:A:24:G:H8	1.75	0.51
15:O:38:GLN:HB3	15:O:47:THR:CG2	2.40	0.51
25:Y:14:ARG:HA	25:Y:17:SER:HB2	1.93	0.51
31:5:50:LEU:HD13	31:5:57:ARG:CZ	2.40	0.51
1:A:1404:C:O2'	1:A:1405:U:H5'	2.10	0.51
1:A:917:A:H2'	1:A:918:A:O4'	2.10	0.51
20:T:89:ILE:O	20:T:93:GLU:HG2	2.11	0.51
12:L:138:LEU:HD11	12:L:144:GLU:HB3	1.93	0.51
1:A:1817:G:OP1	3:C:88:ARG:NH2	2.43	0.51
1:A:719:C:H2'	1:A:720:C:H6	1.75	0.51
1:A:49:A:H5''	1:A:51:G:O4'	2.10	0.51
13:M:74:TYR:CD2	13:M:91:GLU:HB2	2.46	0.51
31:5:53:PRO:HB2	31:5:57:ARG:NH2	2.26	0.51
14:N:17:ARG:O	14:N:20:LEU:HB3	2.11	0.51
3:C:118:VAL:HG22	3:C:119:ALA:N	2.25	0.51
15:O:26:LEU:HG	15:O:39:ILE:CD1	2.40	0.51
8:H:4:ILE:HD11	8:H:16:GLY:HA2	1.92	0.51
2:B:30:C:H2'	2:B:31:C:H5'	1.93	0.51
1:A:2698:U:H2'	1:A:2699:C:C6	2.46	0.51
13:M:68:ILE:HG23	13:M:103:MET:HA	1.92	0.51
1:A:2795:G:H3'	1:A:2797:U:C5'	2.41	0.51
12:L:147:LEU:HD13	12:L:148:LEU:O	2.11	0.51
21:U:95:LYS:HG2	21:U:100:ALA:HA	1.92	0.51
13:M:75:THR:HG21	13:M:85:LYS:HZ1	1.74	0.51
8:H:72:LEU:HD12	8:H:140:LEU:HD13	1.92	0.51
11:K:2:ILE:CD1	11:K:82:ASN:HD22	2.23	0.51
13:M:48:GLU:O	13:M:52:VAL:HG12	2.11	0.51
17:Q:8:VAL:HG11	17:Q:12:ARG:NE	2.26	0.51
14:N:72:ASP:O	14:N:76:VAL:HG12	2.10	0.51
1:A:1809:A:H2'	1:A:1810:A:C8	2.46	0.51
1:A:1680:U:O2	1:A:1763:G:H3'	2.11	0.51
1:A:566:U:H2'	1:A:567:A:O4'	2.11	0.51
2:B:63:G:H2'	2:B:64:C:C6	2.46	0.51
3:C:37:LEU:HD12	3:C:38:LYS:H	1.75	0.51
18:R:13:ARG:HD2	18:R:13:ARG:C	2.31	0.51
3:C:238:GLY:O	3:C:240:ALA:N	2.44	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:955:C:OP2	13:M:14:ARG:HD2	2.11	0.50
13:M:8:LYS:O	13:M:9:TYR:HB3	2.11	0.50
20:T:30:VAL:HG11	20:T:39:ILE:CD1	2.38	0.50
24:X:62:VAL:HG22	24:X:63:ALA:N	2.26	0.50
3:C:131:LEU:HD11	3:C:136:ILE:HG12	1.92	0.50
1:A:628:G:H2'	1:A:629:G:H8	1.75	0.50
1:A:1537:C:H2'	1:A:1538:G:O4'	2.11	0.50
1:A:1178:C:H2'	1:A:1179:C:H6	1.75	0.50
1:A:2419:U:O4	31:5:30:ARG:CZ	2.60	0.50
1:A:1929:G:N3	1:A:1929:G:H5''	2.26	0.50
1:A:960:A:H61	13:M:82:ARG:HH21	1.60	0.50
1:A:675:A:H4'	5:E:67:GLN:HE21	1.76	0.50
1:A:390:A:C6	12:L:71:VAL:HG21	2.46	0.50
1:A:646:A:H5'	1:A:646:A:N3	2.27	0.50
21:U:20:TYR:CE1	21:U:42:VAL:HA	2.46	0.50
1:A:2777:G:C5'	1:A:2778:A:H5'	2.42	0.50
10:J:127:LYS:HA	10:J:130:LEU:HD12	1.93	0.50
1:A:814:C:H5	12:L:27:HIS:NE2	2.09	0.50
6:F:133:LEU:HD21	6:F:157:ILE:HG13	1.93	0.50
1:A:150:C:H2'	1:A:151:C:C6	2.46	0.50
5:E:179:GLU:CD	5:E:179:GLU:H	2.13	0.50
17:Q:88:ILE:HB	17:Q:90:VAL:CG1	2.35	0.50
17:Q:112:ARG:HH21	18:R:46:VAL:HG21	1.76	0.50
1:A:1813:G:H1'	3:C:50:THR:CG2	2.37	0.50
15:O:26:LEU:HD13	15:O:87:PHE:HD1	1.76	0.50
8:H:107:ILE:HG13	8:H:109:ILE:HG23	1.92	0.50
16:P:57:PHE:CG	16:P:58:ASN:N	2.80	0.50
22:V:39:VAL:HG21	22:V:44:PHE:CD2	2.47	0.50
10:J:49:LEU:O	10:J:53:ILE:HG13	2.11	0.50
1:A:2335:A:C8	1:A:2337:G:C5	3.00	0.50
1:A:1165:U:H2'	1:A:1166:C:C6	2.47	0.50
1:A:2641:G:H5''	10:J:99:SER:HB3	1.94	0.50
1:A:379:G:N2	24:X:20:ARG:HH12	2.09	0.50
22:V:27:VAL:HG22	22:V:36:LYS:HA	1.93	0.50
1:A:780:G:N2	1:A:783:A:H62	1.96	0.50
15:O:30:ARG:C	15:O:30:ARG:HD2	2.32	0.50
6:F:74:LYS:HE2	6:F:84:LYS:HE3	1.94	0.50
15:O:25:ARG:HD2	15:O:88:ASP:OD1	2.12	0.50
3:C:43:ARG:HB2	3:C:48:ARG:O	2.10	0.50
1:A:628:G:H2'	1:A:629:G:C8	2.47	0.50
1:A:2462:U:H1'	1:A:2491:U:O4	2.10	0.50
1:A:576:U:H2'	1:A:577:G:C8	2.46	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1056:G:H8	1:A:1056:G:O5'	1.94	0.50
17:Q:90:VAL:HG13	17:Q:91:ASP:N	2.26	0.50
21:U:14:LEU:HD23	21:U:15:VAL:N	2.26	0.50
20:T:11:PRO:HG3	25:Y:37:PHE:CE2	2.46	0.50
22:V:125:LEU:HD23	22:V:126:VAL:N	2.27	0.50
10:J:57:LEU:HD11	10:J:142:ARG:HB2	1.93	0.50
7:G:46:GLU:HG3	7:G:51:ARG:NE	2.26	0.50
15:O:36:TYR:CD1	15:O:36:TYR:N	2.79	0.50
1:A:1824:G:OP1	3:C:52:ARG:HD3	2.11	0.50
5:E:29:ASN:H	5:E:112:MET:CE	2.25	0.50
1:A:363(D):G:H2'	1:A:363(E):G:H8	1.77	0.50
8:H:31:LEU:HB3	8:H:32:PRO:HD3	1.94	0.50
1:A:2758:A:C4	7:G:67:LEU:HD21	2.47	0.50
15:O:69:VAL:O	15:O:72:ALA:HB3	2.11	0.50
7:G:92:ILE:N	7:G:92:ILE:HD12	2.21	0.50
3:C:132:PRO:HG3	3:C:190:TYR:CE1	2.46	0.50
14:N:10:LEU:CB	14:N:17:ARG:NE	2.73	0.50
1:A:557:U:H2'	1:A:558:G:H8	1.76	0.50
1:A:518:G:H4'	19:S:18:ARG:NH1	2.26	0.50
8:H:6:LEU:N	8:H:6:LEU:HD23	2.25	0.50
1:A:774:A:H2	1:A:787:U:O2'	1.95	0.50
18:R:81:TYR:O	18:R:82:ARG:HG3	2.12	0.50
1:A:1567:A:H2'	3:C:84:TYR:HE2	1.76	0.50
1:A:2846:G:H2'	1:A:2847:U:O4'	2.12	0.50
17:Q:95:LEU:HD11	18:R:12:TYR:HA	1.93	0.50
20:T:63:LYS:HZ2	20:T:72:LYS:HB3	1.77	0.50
1:A:1405:U:H2'	1:A:1406:U:H6	1.75	0.50
6:F:25:TYR:CD1	6:F:30:GLU:HB3	2.47	0.50
3:C:150:LYS:HA	3:C:150:LYS:HE3	1.94	0.50
1:A:1602:U:H3'	1:A:1603:A:H5''	1.94	0.50
1:A:1504:C:O2'	1:A:1505:C:H6	1.95	0.50
1:A:2244:U:O2'	1:A:2245:U:H5'	2.11	0.50
5:E:28:ILE:O	5:E:30:PRO:HD3	2.11	0.50
6:F:16:ARG:O	6:F:20:ILE:HG12	2.12	0.50
7:G:23:ARG:N	7:G:23:ARG:HD3	2.27	0.50
17:Q:106:PHE:O	17:Q:110:VAL:HG23	2.12	0.50
1:A:2246:G:H2'	1:A:2247:A:C8	2.47	0.50
12:L:83:VAL:O	12:L:114:ILE:HA	2.11	0.50
1:A:37:C:H2'	1:A:38:A:C8	2.47	0.50
1:A:2572:A:H62	4:D:145:LYS:HG3	1.77	0.50
16:P:107:ASP:O	16:P:110:ILE:HG22	2.11	0.50
1:A:1341:U:O4	20:T:16:LYS:HE2	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:81:ALA:HB3	3:C:94:LEU:HB3	1.93	0.50
1:A:860:U:O2	1:A:860:U:O4'	2.30	0.50
16:P:100:TYR:HD2	16:P:103:ARG:NH2	2.10	0.50
1:A:1603:A:H8	1:A:1603:A:H5'	1.77	0.50
16:P:54:ARG:HA	16:P:59:THR:OG1	2.12	0.50
6:F:130:ASN:OD1	6:F:160:VAL:HA	2.11	0.50
1:A:1344:G:H4'	1:A:1384:A:C5	2.47	0.50
21:U:29:GLU:HB3	21:U:38:ILE:HB	1.94	0.50
1:A:2050:C:H1'	4:D:156:MET:HE1	1.93	0.50
17:Q:60:LEU:HD23	17:Q:60:LEU:C	2.32	0.50
4:D:9:VAL:HG13	4:D:25:VAL:O	2.11	0.49
1:A:661:C:H4'	12:L:16:ARG:CD	2.42	0.49
8:H:77:LEU:O	8:H:143:SER:HB3	2.12	0.49
24:X:90:ILE:O	24:X:94:LEU:HB2	2.12	0.49
1:A:1486:A:N6	1:A:1504:C:H42	2.10	0.49
3:C:72:LYS:CE	3:C:101:GLU:HG2	2.42	0.49
1:A:2208:U:O2'	1:A:2209:C:H5'	2.12	0.49
9:I:9:LEU:O	9:I:13:LEU:HG	2.12	0.49
1:A:1111:A:N3	1:A:1112:G:H1'	2.27	0.49
17:Q:79:PHE:C	17:Q:79:PHE:CD1	2.86	0.49
1:A:1161:C:O2'	18:R:23:GLU:HG2	2.11	0.49
1:A:114(B):A:N3	1:A:1144:G:C8	2.80	0.49
1:A:2392:A:H2	1:A:2424:C:N4	2.08	0.49
4:D:51:PHE:HB3	4:D:52:LEU:HD12	1.94	0.49
3:C:244:ARG:HB2	3:C:244:ARG:HH11	1.77	0.49
8:H:82:ARG:HG2	8:H:89:TYR:CD1	2.47	0.49
2:B:71:C:C4	2:B:72:G:N7	2.80	0.49
4:D:120:TRP:CD1	4:D:155:LYS:HB3	2.47	0.49
11:K:24:VAL:CG2	11:K:33:ALA:HB2	2.41	0.49
18:R:14:VAL:HG13	18:R:96:ILE:HG13	1.94	0.49
1:A:270(Q):C:HO2'	1:A:270(R):C:H6	1.58	0.49
1:A:2853:C:H2'	1:A:2854:G:H8	1.77	0.49
6:F:153:ARG:HB3	6:F:153:ARG:NH1	2.27	0.49
11:K:61:VAL:HG13	11:K:61:VAL:O	2.11	0.49
1:A:827:U:O2	1:A:2246:G:H4'	2.12	0.49
1:A:114(B):A:C4	1:A:1144:G:N7	2.80	0.49
1:A:603:A:H61	1:A:655:A:C1'	2.25	0.49
1:A:1431:U:H2'	1:A:1432:C:C6	2.47	0.49
13:M:60:ARG:N	22:V:179:ASP:HB2	2.27	0.49
1:A:1478:G:H2'	1:A:1479:G:H8	1.77	0.49
1:A:2335:A:H2'	15:O:13:ARG:HH22	1.77	0.49
1:A:165:U:H2'	1:A:171:G:O4'	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:903:C:H2'	1:A:904:C:C6	2.47	0.49
1:A:1971:A:C4	3:C:241:PRO:HG3	2.47	0.49
31:5:14:VAL:CG1	31:5:22:VAL:HG13	2.42	0.49
15:O:14:VAL:O	15:O:18:ILE:HG12	2.13	0.49
1:A:2516:G:C6	1:A:2517:C:N4	2.80	0.49
4:D:117:MET:CE	4:D:136:ARG:HA	2.41	0.49
1:A:2481:G:HO2'	1:A:2482:G:P	2.35	0.49
5:E:155:LEU:CD2	5:E:186:ILE:HD13	2.40	0.49
7:G:51:ARG:O	7:G:52:VAL:HG23	2.13	0.49
29:3:36:LEU:HB3	29:3:50:ARG:NH1	2.27	0.49
2:B:75:G:N1	2:B:102:G:N2	2.60	0.49
3:C:10:THR:HG23	3:C:13:ARG:HB2	1.94	0.49
1:A:2894:G:H2'	1:A:2894:G:N3	2.27	0.49
1:A:966:G:C4	1:A:967:C:C5	3.00	0.49
1:A:1486:A:C6	1:A:1504:C:N4	2.80	0.49
19:S:12:ILE:HD12	19:S:46:PHE:CE2	2.48	0.49
29:3:16:CYS:SG	29:3:48:VAL:HG23	2.53	0.49
10:J:77:VAL:HB	10:J:145:VAL:HG22	1.93	0.49
1:A:41:C:H2'	1:A:43:G:O4'	2.11	0.49
1:A:471:A:H2'	1:A:472:A:O4'	2.12	0.49
1:A:855:G:H2'	1:A:856:C:C6	2.47	0.49
16:P:24:PRO:HA	16:P:49:VAL:HG13	1.93	0.49
1:A:2439:A:H8	1:A:2439:A:H5'	1.70	0.49
7:G:92:ILE:CD1	7:G:92:ILE:H	2.21	0.49
4:D:201:THR:O	4:D:202:LYS:HD3	2.13	0.49
1:A:1478:G:HO2'	1:A:1558:A:H2	1.61	0.49
1:A:596:G:C6	1:A:597:U:C4	3.01	0.49
21:U:90:LEU:HG	21:U:91:GLU:H	1.76	0.49
1:A:2340:G:H2'	1:A:2341:G:H8	1.77	0.49
1:A:1354:A:C8	1:A:1355:G:C8	3.01	0.49
1:A:1963:U:H2'	1:A:1963:U:O2	2.13	0.49
28:2:33:CYS:SG	28:2:49:CYS:SG	3.07	0.49
1:A:322:A:OP2	5:E:169:ASN:HB2	2.12	0.49
1:A:1188:U:C2'	1:A:1189:A:H5'	2.42	0.49
1:A:1608:A:HO2'	1:A:1610:A:P	2.35	0.49
14:N:81:ASP:O	14:N:85:PRO:HG2	2.12	0.49
12:L:126:VAL:HA	12:L:145:PRO:HB2	1.95	0.49
1:A:144:C:H2'	1:A:145:G:H8	1.77	0.49
1:A:69:C:H2'	1:A:70:G:C8	2.47	0.49
1:A:118:A:N3	1:A:178:G:H1'	2.27	0.49
12:L:32:THR:OG1	12:L:36:LYS:HB3	2.13	0.49
23:W:37:LEU:HG	23:W:60:PHE:HA	1.95	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:603:A:N6	1:A:655:A:H1'	2.28	0.49
6:F:98:ARG:O	6:F:101:ILE:HG12	2.12	0.49
1:A:405:U:H3'	1:A:406:G:H5'	1.95	0.49
1:A:1887:C:H3'	1:A:1888:G:H5''	1.95	0.49
1:A:258:G:H2'	1:A:259:G:H8	1.78	0.49
1:A:289:A:H2'	1:A:290:G:O4'	2.13	0.49
11:K:88:ASN:OD1	11:K:89:ASN:N	2.46	0.49
1:A:2784:C:H2'	1:A:2785:C:C6	2.47	0.49
1:A:116:C:H2'	1:A:117:G:C8	2.47	0.49
1:A:943:U:OP2	12:L:38:GLN:CD	2.51	0.49
12:L:35:HIS:O	12:L:36:LYS:HB2	2.13	0.49
1:A:1022:G:O2'	1:A:1023:U:OP2	2.28	0.49
4:D:169:ASN:ND2	4:D:201:THR:HG21	2.28	0.49
1:A:2365:G:O6	31:5:39:LYS:HE3	2.13	0.49
3:C:10:THR:HG23	3:C:13:ARG:HB3	1.93	0.49
29:3:11:LEU:HD21	29:3:51:GLU:CD	2.33	0.49
29:3:13:CYS:O	29:3:21:TYR:HA	2.13	0.49
22:V:82:ARG:HG2	22:V:83:PRO:HD2	1.95	0.49
1:A:2512:C:H5''	1:A:2513:G:OP2	2.13	0.49
23:W:53:MET:HA	23:W:58:THR:O	2.12	0.49
1:A:1027:A:C2	1:A:2488:A:H5'	2.47	0.49
14:N:50:HIS:O	14:N:54:LEU:HB2	2.13	0.49
1:A:1171:G:H2'	1:A:1173:G:O4'	2.13	0.49
6:F:86:MET:H	6:F:87:PRO:CD	2.26	0.49
1:A:1517:G:H2'	1:A:1518:C:C6	2.48	0.49
1:A:1495:A:H2'	1:A:1496:A:C2	2.48	0.49
1:A:466:A:N3	1:A:683:C:H1'	2.28	0.49
8:H:115:ALA:HB3	8:H:129:THR:O	2.12	0.49
17:Q:79:PHE:HD1	17:Q:79:PHE:C	2.16	0.49
18:R:47:VAL:HG13	18:R:52:VAL:N	2.27	0.49
3:C:242:ARG:CD	3:C:242:ARG:N	2.71	0.49
13:M:76:LYS:H	13:M:88:GLY:HA2	1.76	0.49
3:C:31:LYS:HE3	3:C:33:LEU:HD21	1.94	0.49
4:D:201:THR:CG2	4:D:202:LYS:H	2.22	0.49
10:J:66:THR:N	10:J:71:MET:HE3	2.22	0.49
3:C:70:TRP:CH2	3:C:150:LYS:HA	2.48	0.49
11:K:79:PHE:HD2	16:P:72:VAL:HG22	1.78	0.49
1:A:69:C:O2'	1:A:70:G:H5'	2.13	0.49
4:D:14:ILE:HD12	4:D:14:ILE:C	2.33	0.49
10:J:58:ARG:C	10:J:60:LYS:H	2.15	0.49
1:A:634:C:H2'	1:A:635:C:C6	2.48	0.49
28:2:3:LYS:HD2	28:2:3:LYS:N	2.28	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:733:G:H8	1:A:733:G:O5'	1.96	0.48
21:U:2:ARG:C	21:U:4:LYS:H	2.17	0.48
23:W:32:ARG:C	23:W:35:ASN:HD21	2.15	0.48
6:F:173:LEU:HA	6:F:176:LEU:HD12	1.93	0.48
1:A:1437:C:H2'	1:A:1438:U:H6	1.75	0.48
1:A:784:A:N7	3:C:229:VAL:HG21	2.27	0.48
5:E:12:LEU:HB2	5:E:124:LEU:HD11	1.94	0.48
1:A:2795:G:H3'	1:A:2797:U:H5''	1.95	0.48
1:A:2436:G:C5	1:A:2437:U:C5	3.01	0.48
1:A:329:G:H1	21:U:19:LYS:HE3	1.78	0.48
1:A:1615:C:O2'	1:A:1616:A:H5'	2.13	0.48
1:A:114(B):A:C4	1:A:1144:G:C8	3.01	0.48
22:V:99:TYR:CE2	22:V:125:LEU:HD12	2.48	0.48
13:M:43:THR:OG1	13:M:46:GLN:HG3	2.13	0.48
1:A:1937:A:N7	1:A:1939:U:H2'	2.27	0.48
1:A:380:U:O2	24:X:20:ARG:NH2	2.46	0.48
1:A:718:A:O5'	1:A:718:A:H8	1.96	0.48
12:L:114:ILE:CD1	12:L:130:PHE:CD1	2.90	0.48
1:A:270(H):C:H2'	1:A:270(I):C:H6	1.77	0.48
6:F:55:LYS:O	6:F:59:GLU:HG3	2.13	0.48
1:A:124:G:N7	30:4:19:ARG:NH2	2.61	0.48
1:A:2516:G:O6	1:A:2517:C:N4	2.47	0.48
8:H:88:ILE:CG2	8:H:89:TYR:N	2.76	0.48
21:U:76:CYS:CB	21:U:77:PRO:CD	2.91	0.48
1:A:1953:A:C2	1:A:2549:G:N3	2.79	0.48
1:A:1567:A:H5''	3:C:58:HIS:CD2	2.48	0.48
22:V:10:ARG:HH21	22:V:26:GLY:H	1.62	0.48
4:D:31:CYS:HB3	4:D:49:LEU:HB3	1.95	0.48
1:A:1001:A:H2'	1:A:1002:G:O4'	2.13	0.48
1:A:496:G:H1'	19:S:61:ASN:ND2	2.29	0.48
25:Y:10:LEU:O	25:Y:13:ALA:HB3	2.13	0.48
19:S:24:ILE:HG21	19:S:36:LEU:CD2	2.37	0.48
1:A:2741:A:H2'	1:A:2742:C:O4'	2.13	0.48
17:Q:62:ILE:HD12	17:Q:76:TYR:CE1	2.49	0.48
1:A:1614:A:C6	19:S:87:PRO:HA	2.48	0.48
1:A:363(A):G:H2'	1:A:363(B):A:H8	1.78	0.48
1:A:2815:C:O2'	28:2:43:HIS:CD2	2.64	0.48
1:A:826:U:C5	1:A:828:U:H1'	2.49	0.48
1:A:1995:U:H3'	1:A:1996:C:H2'	1.96	0.48
14:N:103:ARG:HH12	14:N:110:PRO:HG3	1.79	0.48
1:A:2590:A:C2	1:A:2605:U:C2	3.02	0.48
12:L:36:LYS:HG3	12:L:41:ARG:CB	2.40	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:956:G:N2	1:A:959:A:H3'	2.29	0.48
26:Z:8:LEU:HA	26:Z:54:VAL:HG12	1.96	0.48
11:K:71:ARG:HH12	16:P:74:ARG:NH2	2.08	0.48
1:A:2286:A:H4'	1:A:2287:A:O4'	2.14	0.48
1:A:481:G:O2'	1:A:482:A:P	2.71	0.48
1:A:481:G:H1'	1:A:506:G:N2	2.27	0.48
1:A:768:G:O2'	1:A:1379:A:N6	2.46	0.48
1:A:1051:G:H2'	1:A:1052:C:C6	2.49	0.48
11:K:12:ASP:OD1	11:K:85:VAL:HG13	2.12	0.48
1:A:1289:C:H2'	1:A:1290:C:H6	1.79	0.48
1:A:747:U:O2	1:A:2014:A:H1'	2.13	0.48
12:L:85:LEU:HA	12:L:88:LEU:CB	2.43	0.48
16:P:46:GLU:OE2	16:P:89:VAL:HG11	2.14	0.48
1:A:948:G:OP1	1:A:962:G:OP1	2.32	0.48
1:A:2517:C:C5	1:A:2542:A:C2	3.02	0.48
16:P:58:ASN:HD22	16:P:58:ASN:C	2.17	0.48
5:E:126:VAL:O	5:E:196:LEU:HG	2.13	0.48
1:A:920:G:H2'	1:A:921:G:H8	1.79	0.48
1:A:2090:G:H21	24:X:45:ASN:ND2	2.10	0.48
22:V:10:ARG:HB3	22:V:36:LYS:HB3	1.94	0.48
1:A:1040:C:H2'	1:A:1041:C:C6	2.49	0.48
1:A:2366:A:H2'	1:A:2367:G:O4'	2.14	0.48
1:A:1239:G:O2'	1:A:1240:U:H5'	2.13	0.48
13:M:23:GLY:HA3	13:M:98:LYS:HB2	1.95	0.48
7:G:30:LYS:HB2	7:G:79:VAL:HA	1.94	0.48
1:A:754:C:H2'	1:A:755:C:C6	2.48	0.48
1:A:1689:A:H62	1:A:1698:A:H2	1.60	0.48
10:J:160:LYS:CD	10:J:161:LEU:H	2.27	0.48
2:B:46:A:H2'	2:B:47:C:C6	2.48	0.48
6:F:143:GLU:CD	6:F:143:GLU:H	2.17	0.48
18:R:49:THR:HB	18:R:50:PRO:CD	2.43	0.48
6:F:60:LEU:O	6:F:64:THR:HG22	2.12	0.48
21:U:81:LYS:CD	21:U:97:ARG:HB3	2.39	0.48
3:C:25:THR:HG21	3:C:81:ALA:CA	2.43	0.48
1:A:2484:G:H5''	13:M:45:GLN:HB2	1.95	0.48
19:S:14:PRO:O	19:S:15:ARG:C	2.52	0.48
1:A:1478:G:N3	1:A:1479:G:C8	2.82	0.48
24:X:19:GLN:HA	24:X:41:ARG:HA	1.96	0.48
1:A:1390:U:O2'	1:A:1391:U:H5'	2.13	0.48
10:J:80:ALA:HB3	10:J:147:ALA:HB2	1.94	0.48
1:A:2892:A:N6	1:A:2893:G:C2	2.81	0.48
1:A:1357:U:H2'	1:A:1358:G:O4'	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:380:U:O2'	24:X:20:ARG:HB3	2.13	0.48
1:A:2784:C:H2'	1:A:2785:C:H6	1.79	0.48
15:O:85:VAL:HG11	15:O:106:ARG:HD2	1.95	0.48
3:C:105:ILE:CG1	3:C:106:ILE:HD12	2.43	0.48
1:A:2840:C:H4'	14:N:53:HIS:CD2	2.49	0.48
1:A:1709:U:C2	1:A:1750:G:C2	3.01	0.48
31:5:11:LYS:C	31:5:11:LYS:HD3	2.34	0.48
23:W:50:ASN:HD22	23:W:83:PRO:HD3	1.77	0.48
22:V:119:GLU:HG3	22:V:119:GLU:O	2.14	0.48
1:A:196:A:N3	1:A:196:A:H2'	2.28	0.48
1:A:2056:G:N2	1:A:2057:A:C1'	2.77	0.48
20:T:54:VAL:C	20:T:55:ASN:HD22	2.17	0.48
31:5:33:ASN:ND2	31:5:34:TRP:H	2.11	0.48
3:C:25:THR:O	3:C:25:THR:HG23	2.14	0.48
6:F:77:ILE:HG22	6:F:80:PHE:N	2.25	0.48
26:Z:40:THR:O	26:Z:44:ARG:HG3	2.14	0.48
15:O:39:ILE:O	15:O:48:LEU:HD13	2.14	0.48
3:C:79:VAL:O	3:C:113:VAL:HG13	2.14	0.48
12:L:95:VAL:HG23	12:L:125:VAL:HA	1.95	0.48
22:V:5:LEU:HD23	22:V:6:LYS:N	2.29	0.48
1:A:380:U:H1'	24:X:20:ARG:NH1	2.29	0.48
8:H:66:GLU:HB3	8:H:67:ARG:NH1	2.28	0.48
1:A:714:U:O2	1:A:716:A:C8	2.67	0.48
3:C:40:THR:HG22	3:C:41:GLY:N	2.28	0.48
23:W:66:VAL:O	23:W:81:VAL:HA	2.13	0.48
1:A:1504:C:O2'	1:A:1505:C:O5'	2.31	0.48
14:N:87:TYR:HE1	14:N:117:VAL:HG13	1.79	0.48
3:C:72:LYS:HE3	3:C:101:GLU:CB	2.44	0.48
1:A:270(Q):C:O2'	1:A:270(R):C:H6	1.97	0.48
23:W:27:GLU:HB2	23:W:69:PHE:HD1	1.79	0.48
1:A:356:G:H2'	1:A:357:A:C8	2.49	0.48
17:Q:107:ALA:O	17:Q:111:GLU:HG2	2.13	0.48
2:B:28:C:H2'	2:B:29:A:O4'	2.14	0.48
31:5:29:LYS:HB3	31:5:29:LYS:NZ	2.29	0.48
1:A:954:G:C5	1:A:955:C:C5	3.01	0.48
15:O:34:HIS:CG	15:O:54:LEU:HB2	2.49	0.48
8:H:109:ILE:HD13	8:H:109:ILE:N	2.29	0.48
14:N:97:VAL:HA	14:N:113:LEU:O	2.14	0.48
22:V:81:ARG:O	22:V:82:ARG:HB2	2.13	0.48
1:A:1973:G:H2'	1:A:1974:C:C6	2.49	0.48
1:A:2252:G:H2'	1:A:2253:G:C8	2.49	0.48
1:A:2537:U:H2'	1:A:2538:C:C6	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:649:G:H2'	1:A:650:C:C6	2.49	0.48
28:2:3:LYS:O	28:2:4:HIS:C	2.52	0.47
1:A:587:C:C5	1:A:671:C:H1'	2.49	0.47
18:R:47:VAL:HG12	18:R:49:THR:O	2.13	0.47
1:A:761:A:O5'	1:A:761:A:C8	2.48	0.47
20:T:30:VAL:HG21	20:T:79:ALA:HB3	1.96	0.47
16:P:27:THR:HA	16:P:48:ILE:HA	1.96	0.47
21:U:10:GLY:HA2	21:U:27:VAL:HG23	1.95	0.47
4:D:101:ARG:HG2	4:D:171:GLU:HA	1.96	0.47
4:D:171:GLU:HG2	4:D:185:LYS:HG2	1.96	0.47
1:A:1317:A:N6	1:A:1336:A:N6	2.62	0.47
15:O:89:ARG:O	15:O:90:GLY:O	2.31	0.47
1:A:598:G:H5'	12:L:15:ARG:CB	2.44	0.47
1:A:226:G:N2	1:A:228:A:H62	2.12	0.47
1:A:2476:A:C2	1:A:2477:C:C6	3.02	0.47
12:L:135:LEU:HD13	12:L:135:LEU:O	2.14	0.47
16:P:60:THR:HG22	16:P:77:PRO:HA	1.96	0.47
1:A:409:C:O2'	1:A:410:G:H5'	2.14	0.47
1:A:1198:U:O2	1:A:1249:U:H1'	2.14	0.47
10:J:63:PRO:O	17:Q:64:ARG:HD2	2.14	0.47
1:A:909:A:H2'	1:A:912:C:H5	1.79	0.47
1:A:1971:A:C5	3:C:241:PRO:HG3	2.48	0.47
6:F:92:VAL:O	6:F:92:VAL:HG13	2.15	0.47
4:D:5:LEU:HB2	4:D:51:PHE:HD2	1.77	0.47
1:A:603:A:C6	1:A:655:A:H1'	2.50	0.47
18:R:79:VAL:O	18:R:79:VAL:HG12	2.14	0.47
8:H:6:LEU:HD23	8:H:36:ALA:HA	1.96	0.47
1:A:1308:A:N6	1:A:1309:G:C2	2.83	0.47
1:A:2593:U:H2'	1:A:2594:C:H6	1.79	0.47
8:H:57:ARG:O	8:H:61:ARG:HG3	2.14	0.47
23:W:12:ASN:O	23:W:14:ARG:HB2	2.14	0.47
1:A:2552:U:H2'	1:A:2554:U:OP2	2.14	0.47
7:G:154:PRO:HB3	7:G:163:TYR:CE2	2.49	0.47
1:A:2822:G:H8	1:A:2822:G:O5'	1.97	0.47
4:D:103:ASP:OD1	4:D:201:THR:HG23	2.15	0.47
1:A:1509:A:H4'	1:A:1510:A:C1'	2.44	0.47
1:A:2542:A:C8	1:A:2544:G:O6	2.67	0.47
8:H:78:THR:HA	8:H:143:SER:CB	2.41	0.47
1:A:919:G:H2'	1:A:920:G:C8	2.50	0.47
1:A:903:C:H2'	1:A:904:C:H6	1.79	0.47
4:D:78:LEU:N	4:D:78:LEU:HD23	2.29	0.47
18:R:99:ILE:HD13	18:R:99:ILE:N	2.28	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1411:C:H2'	1:A:1412:A:C8	2.50	0.47
1:A:2056:G:C2'	1:A:2056:G:N3	2.77	0.47
13:M:81:VAL:HG12	13:M:82:ARG:N	2.29	0.47
3:C:25:THR:O	3:C:27:THR:N	2.48	0.47
1:A:2038:G:H2'	1:A:2039:C:H6	1.78	0.47
3:C:69:ARG:HH12	3:C:117:VAL:CG2	2.26	0.47
1:A:94:G:H21	25:Y:47:ASN:ND2	2.12	0.47
1:A:1478:G:O2'	1:A:1558:A:C2	2.67	0.47
24:X:19:GLN:HG2	24:X:41:ARG:CB	2.45	0.47
13:M:39:PRO:O	13:M:40:ALA:HB2	2.14	0.47
8:H:58:LEU:HD23	8:H:61:ARG:HD2	1.96	0.47
5:E:125:LEU:HB3	5:E:196:LEU:HD23	1.95	0.47
1:A:2699:C:H2'	1:A:2700:C:O4'	2.14	0.47
14:N:53:HIS:O	14:N:56:LYS:HB3	2.14	0.47
1:A:1709:U:H2'	1:A:1710:C:C6	2.49	0.47
1:A:1936:A:OP1	1:A:1936:A:H3'	2.14	0.47
1:A:451:C:H41	1:A:453:C:H3'	1.78	0.47
4:D:152:LYS:HE2	4:D:152:LYS:HB3	1.72	0.47
28:2:4:HIS:HB2	28:2:5:PRO:CD	2.45	0.47
1:A:1827:C:H2'	1:A:1828:G:O4'	2.14	0.47
1:A:124:G:C5	30:4:19:ARG:NH2	2.82	0.47
1:A:1578:U:H2'	1:A:1579:A:H5''	1.95	0.47
1:A:1431:U:H2'	1:A:1432:C:H6	1.80	0.47
8:H:12:LEU:N	8:H:12:LEU:HD22	2.29	0.47
1:A:2687:U:C4	1:A:2688:U:H5	2.30	0.47
1:A:2630:G:H1'	1:A:2894:G:H1'	1.97	0.47
1:A:320:A:H5''	1:A:321:G:OP1	2.15	0.47
1:A:2846:G:H2'	1:A:2847:U:C6	2.50	0.47
1:A:2247:A:H2'	1:A:2248:C:C6	2.49	0.47
1:A:1658:C:OP1	4:D:132:HIS:O	2.33	0.47
1:A:775:G:C5	1:A:794:G:C8	3.02	0.47
2:B:106:G:C6	2:B:107:U:C4	3.03	0.47
1:A:1030:G:OP2	13:M:128:LYS:HE3	2.14	0.47
4:D:4:ILE:HG12	4:D:28:ALA:HB1	1.95	0.47
3:C:108:PRO:CG	3:C:143:HIS:CE1	2.97	0.47
19:S:4:LYS:HG2	19:S:106:ILE:CG2	2.44	0.47
2:B:111:U:HO2'	2:B:112:G:H8	1.59	0.47
14:N:87:TYR:OH	14:N:116:LEU:HB3	2.15	0.47
14:N:96:ARG:NH2	14:N:117:VAL:HG23	2.30	0.47
16:P:109:GLU:HA	16:P:112:ARG:HG3	1.97	0.47
4:D:54:GLN:HB2	4:D:74:PRO:O	2.15	0.47
1:A:2887:U:H2'	1:A:2888:C:H6	1.80	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1900:A:N1	1:A:1970:A:C6	2.83	0.47
21:U:13:VAL:HG13	21:U:73:ARG:O	2.14	0.47
31:5:32:LEU:HD23	31:5:33:ASN:H	1.80	0.47
16:P:27:THR:CG2	16:P:90:GLN:HB3	2.44	0.47
14:N:54:LEU:HD23	14:N:62:ALA:HB1	1.95	0.47
12:L:6:LEU:N	12:L:6:LEU:HD23	2.23	0.47
1:A:2469:A:H5'	1:A:2470:G:OP2	2.15	0.47
13:M:6:ARG:N	13:M:6:ARG:HE	2.13	0.47
10:J:127:LYS:HB2	10:J:140:PHE:HE1	1.77	0.47
1:A:2564:A:OP1	1:A:2648:C:H4'	2.14	0.47
24:X:58:ILE:HD11	24:X:91:LYS:CG	2.44	0.47
1:A:1639:U:H4'	1:A:2699:C:H4'	1.96	0.47
1:A:1833:U:C2	1:A:1834:U:C6	3.01	0.47
19:S:22:ASP:HA	19:S:25:ARG:HH12	1.79	0.47
1:A:816:C:O2'	1:A:817:C:H5'	2.15	0.47
1:A:1449:G:H2'	1:A:1450:C:C6	2.50	0.47
6:F:104:GLU:O	6:F:108:ASN:HB2	2.15	0.47
19:S:62:HIS:O	19:S:64:MET:HG3	2.14	0.47
1:A:2751:G:H2'	1:A:2751:G:N3	2.30	0.47
2:B:78:A:C2	2:B:99:A:C4	3.02	0.47
19:S:20:VAL:O	19:S:23:LEU:HB2	2.14	0.47
3:C:259:THR:O	3:C:260:ARG:HB2	2.15	0.47
4:D:176:ILE:O	4:D:176:ILE:HG22	2.15	0.47
10:J:30:LYS:O	10:J:32:VAL:HG23	2.15	0.47
12:L:50:ARG:HD3	12:L:51:PHE:HB2	1.97	0.47
24:X:11:ARG:HD2	24:X:60:PHE:HD2	1.79	0.47
1:A:270(L):C:H6	1:A:270(L):C:O5'	1.98	0.47
14:N:10:LEU:HB2	14:N:17:ARG:NH2	2.30	0.47
8:H:79:ILE:HG22	8:H:81:VAL:CG2	2.45	0.47
1:A:322:A:P	5:E:169:ASN:HB2	2.55	0.47
6:F:6:ALA:HB1	6:F:10:LYS:HE3	1.97	0.47
1:A:2730:C:O2'	1:A:2731:G:H5'	2.14	0.47
5:E:29:ASN:H	5:E:112:MET:HE1	1.79	0.47
19:S:20:VAL:HG11	19:S:44:ALA:HA	1.97	0.47
1:A:433:C:H2'	1:A:434:U:C6	2.50	0.47
1:A:2190:G:H8	1:A:2190:G:H5'	1.79	0.47
18:R:6:LYS:HA	18:R:11:GLN:HB3	1.97	0.47
3:C:33:LEU:O	3:C:35:LYS:N	2.48	0.47
1:A:125:G:H5'	30:4:19:ARG:HG3	1.96	0.47
4:D:5:LEU:C	4:D:51:PHE:HE2	2.18	0.47
15:O:90:GLY:O	15:O:92:TYR:CD1	2.68	0.47
1:A:2850:A:H2'	1:A:2851:A:C8	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:966:G:C6	1:A:967:C:N4	2.82	0.47
18:R:24:LYS:HA	18:R:92:THR:HG23	1.96	0.47
5:E:37:VAL:HG13	5:E:184:TYR:HD1	1.80	0.47
1:A:649:G:C5	1:A:650:C:C4	3.03	0.47
1:A:244:A:C2	1:A:255:A:C4	3.03	0.47
28:2:4:HIS:HB2	28:2:5:PRO:HD3	1.97	0.47
12:L:38:GLN:HG3	12:L:41:ARG:HG2	1.96	0.47
12:L:62:LEU:HA	12:L:63:PRO:HD3	1.78	0.47
3:C:136:ILE:O	3:C:168:ARG:NH2	2.48	0.47
12:L:61:ARG:HH11	31:5:13:ARG:HD2	1.80	0.47
3:C:43:ARG:HB2	3:C:49:ILE:HA	1.97	0.47
13:M:35:VAL:HA	13:M:101:ARG:O	2.14	0.47
7:G:123:PHE:HA	7:G:133:VAL:HA	1.97	0.47
21:U:76:CYS:O	21:U:77:PRO:C	2.53	0.47
2:B:8:U:H5''	15:O:15:ARG:NH2	2.29	0.47
1:A:2730:C:H4'	4:D:168:MET:O	2.14	0.47
18:R:99:ILE:HD13	18:R:99:ILE:H	1.80	0.47
23:W:42:GLY:HA2	23:W:57:PHE:CD2	2.50	0.47
1:A:2836:U:C4	1:A:2883:A:N6	2.83	0.47
1:A:2836:U:H2'	1:A:2837:G:C8	2.49	0.47
1:A:536:A:H2'	1:A:537:C:C6	2.50	0.47
25:Y:52:ASP:O	25:Y:56:GLN:HB2	2.14	0.47
5:E:132:VAL:HG23	5:E:133:ASN:N	2.30	0.47
20:T:66:LEU:HD23	20:T:67:GLY:N	2.29	0.47
23:W:32:ARG:CB	23:W:35:ASN:HD21	2.28	0.46
12:L:57:THR:CG2	12:L:59:LEU:HB2	2.45	0.46
6:F:109:VAL:C	6:F:112:PRO:HD2	2.35	0.46
1:A:773:U:H4'	3:C:47:GLY:CA	2.40	0.46
8:H:82:ARG:HD2	8:H:89:TYR:CD2	2.50	0.46
3:C:147:LEU:HD13	3:C:155:LEU:CD1	2.43	0.46
3:C:154:LYS:C	3:C:155:LEU:HD12	2.35	0.46
1:A:661:C:H4'	12:L:16:ARG:HD2	1.96	0.46
1:A:2272:U:H5''	1:A:2273:A:OP1	2.15	0.46
16:P:30:VAL:HG12	16:P:86:ILE:CG1	2.45	0.46
1:A:1952:A:C4	11:K:22:ILE:HD12	2.49	0.46
1:A:636:G:OP1	12:L:132:LYS:HD3	2.15	0.46
4:D:49:LEU:O	4:D:78:LEU:HA	2.14	0.46
4:D:175:VAL:O	4:D:177:PRO:HD3	2.15	0.46
6:F:174:GLU:HG2	6:F:180:PHE:HD1	1.81	0.46
6:F:38:VAL:HG22	6:F:93:THR:HG23	1.97	0.46
18:R:22:VAL:CG1	18:R:23:GLU:N	2.76	0.46
1:A:71:A:C2	20:T:31:HIS:CE1	3.03	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:25:THR:HG21	3:C:81:ALA:HA	1.96	0.46
1:A:2027:G:H2'	1:A:2028:U:O4'	2.15	0.46
1:A:661:C:H4'	12:L:18:ARG:HG2	1.96	0.46
1:A:242:G:N7	31:5:5:LYS:HG2	2.30	0.46
9:I:56:ASN:HA	9:I:59:ILE:HD12	1.98	0.46
18:R:20:LEU:HD12	18:R:21:ARG:H	1.81	0.46
11:K:76:ALA:HB3	16:P:75:ILE:HB	1.97	0.46
1:A:532:A:C8	1:A:2021:C:C5	3.04	0.46
16:P:29:ARG:HA	16:P:45:PHE:O	2.15	0.46
31:5:60:LEU:C	31:5:62:LEU:H	2.18	0.46
24:X:11:ARG:HB2	24:X:13:ILE:CG2	2.46	0.46
3:C:35:LYS:HA	3:C:35:LYS:HD2	1.62	0.46
8:H:83:ALA:CB	8:H:123:LEU:HD12	2.45	0.46
3:C:76:PRO:CB	3:C:116:GLN:HE21	2.28	0.46
5:E:83:PHE:O	5:E:86:GLY:N	2.44	0.46
1:A:448:U:H1'	5:E:84:VAL:CG2	2.45	0.46
1:A:2745:C:C4	1:A:2746:U:C4	3.03	0.46
1:A:380:U:O2'	24:X:20:ARG:HG2	2.15	0.46
8:H:31:LEU:HD13	8:H:37:VAL:HA	1.98	0.46
1:A:2590:A:O2'	1:A:2591:C:H5'	2.15	0.46
1:A:2887:U:H2'	1:A:2888:C:C6	2.50	0.46
1:A:2627:G:H8	1:A:2627:G:O5'	1.98	0.46
1:A:110:G:C2	1:A:111:A:C8	3.03	0.46
18:R:75:PHE:C	18:R:75:PHE:CD1	2.89	0.46
12:L:80:TYR:CE1	12:L:111:ARG:HG2	2.50	0.46
3:C:31:LYS:HA	3:C:31:LYS:HD2	1.67	0.46
1:A:2543:G:C8	1:A:2543:G:H5'	2.43	0.46
6:F:53:LEU:CD1	6:F:88:ILE:HG12	2.46	0.46
1:A:307:G:N1	1:A:310:A:OP2	2.49	0.46
24:X:27:GLU:HG3	24:X:33:LYS:CD	2.45	0.46
22:V:22:GLY:O	22:V:41:LEU:HG	2.15	0.46
1:A:2599:G:N7	3:C:237:GLU:HG3	2.31	0.46
1:A:1588:C:H2'	1:A:1589:C:C6	2.50	0.46
1:A:2320:A:C8	1:A:2333:A:N6	2.83	0.46
1:A:2846:G:H2'	1:A:2847:U:H6	1.81	0.46
1:A:69:C:H2'	1:A:70:G:H8	1.81	0.46
22:V:54:HIS:HB3	22:V:101:PRO:HD3	1.98	0.46
10:J:34:PRO:HB3	10:J:74:PHE:CE1	2.50	0.46
1:A:2228:G:C6	1:A:2229:C:C4	3.03	0.46
1:A:394:A:O2'	1:A:395:U:H5'	2.15	0.46
10:J:92:GLN:O	10:J:94:ILE:HG13	2.15	0.46
6:F:64:THR:HG23	6:F:66:GLN:N	2.31	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:84:ASN:HA	12:L:115:LEU:O	2.16	0.46
25:Y:1:MET:SD	25:Y:1:MET:O	2.73	0.46
1:A:245:G:H2'	1:A:246:C:C6	2.44	0.46
12:L:16:ARG:CZ	12:L:18:ARG:HG3	2.45	0.46
6:F:15:VAL:O	6:F:19:LEU:HG	2.16	0.46
25:Y:41:ILE:HD11	25:Y:44:LEU:HD12	1.96	0.46
14:N:33:ARG:HG3	14:N:115:GLU:HG3	1.98	0.46
5:E:54:ARG:HA	5:E:87:GLY:HA3	1.97	0.46
20:T:26:TYR:HE1	20:T:83:VAL:HG21	1.80	0.46
1:A:1019:U:H3	1:A:114(B):A:N6	2.10	0.46
1:A:1173:G:H3'	1:A:1174:A:H5''	1.97	0.46
8:H:83:ALA:CA	8:H:89:TYR:HD1	2.28	0.46
1:A:1448:G:H21	1:A:1529:A:H2	1.63	0.46
7:G:58:GLU:HB2	7:G:61:HIS:ND1	2.30	0.46
7:G:103:LEU:HD22	7:G:123:PHE:CE1	2.50	0.46
1:A:2667:C:H1'	7:G:109:PHE:HD2	1.81	0.46
26:Z:55:ARG:HD3	26:Z:55:ARG:HA	1.65	0.46
28:2:18:ALA:O	28:2:21:SER:HB2	2.16	0.46
1:A:1762:A:H8	1:A:1762:A:O5'	1.97	0.46
1:A:96:G:H4'	25:Y:48:HIS:CD2	2.51	0.46
1:A:836:G:H2'	1:A:837:C:C6	2.51	0.46
5:E:143:ALA:HB1	5:E:148:LEU:HB2	1.97	0.46
1:A:1164:G:C8	1:A:1164:G:C5'	2.99	0.46
3:C:132:PRO:HD3	3:C:190:TYR:CE2	2.51	0.46
5:E:63:LYS:HG2	5:E:65:TRP:O	2.15	0.46
1:A:2287:A:C6	1:A:2289:G:C4	3.02	0.46
6:F:86:MET:O	6:F:87:PRO:O	2.33	0.46
3:C:130:ALA:HA	3:C:192:THR:HA	1.96	0.46
18:R:77:ALA:C	18:R:79:VAL:H	2.19	0.46
1:A:2273:A:H2'	1:A:2274:A:C8	2.51	0.46
1:A:2582:G:C2	1:A:2583:G:C8	3.03	0.46
11:K:79:PHE:CD2	16:P:72:VAL:HG22	2.50	0.46
17:Q:28:ARG:HG3	17:Q:38:THR:OG1	2.15	0.46
13:M:47:ILE:HG22	13:M:48:GLU:N	2.30	0.46
1:A:2012:G:O2'	19:S:96:ILE:HD11	2.16	0.46
23:W:50:ASN:ND2	23:W:83:PRO:HD3	2.30	0.46
18:R:34:GLU:HG3	18:R:58:VAL:HG22	1.98	0.46
1:A:286:C:H2'	1:A:287:C:H6	1.81	0.46
19:S:9:TYR:H	19:S:102:HIS:CD2	2.34	0.46
1:A:1121:C:H6	1:A:1121:C:O5'	1.99	0.46
10:J:81:ASP:N	10:J:81:ASP:OD1	2.49	0.46
1:A:1632:A:O5'	1:A:1632:A:H8	1.99	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:60:LEU:C	6:F:60:LEU:HD13	2.36	0.46
29:3:25:LYS:HD3	31:5:34:TRP:CZ3	2.50	0.46
15:O:49:VAL:CG1	15:O:76:LYS:HB2	2.46	0.46
27:1:57:ILE:HG22	27:1:59:VAL:CG2	2.46	0.46
6:F:88:ILE:HG13	6:F:89:GLY:N	2.31	0.46
1:A:558:G:H2'	1:A:559:G:H8	1.80	0.46
1:A:1348:G:C2'	1:A:1349:A:H5''	2.45	0.46
5:E:198:ALA:O	5:E:201:VAL:HG12	2.16	0.46
1:A:36:G:N1	1:A:445:C:C4	2.84	0.46
1:A:1178:C:H2'	1:A:1179:C:C6	2.51	0.46
1:A:1354:A:H2'	1:A:1355:G:O4'	2.16	0.46
19:S:9:TYR:H	19:S:102:HIS:HD2	1.62	0.46
17:Q:69:CYS:CB	17:Q:79:PHE:HD2	2.29	0.46
20:T:25:LYS:HE3	20:T:82:GLN:OE1	2.16	0.46
1:A:958:U:H5'	13:M:14:ARG:NH1	2.31	0.46
14:N:21:TYR:CE2	14:N:43:GLU:HB3	2.50	0.46
1:A:2039:C:C2	1:A:2040:C:C5	3.04	0.46
1:A:478:A:C6	1:A:480:A:C6	3.03	0.46
1:A:1654:A:OP2	14:N:3:HIS:NE2	2.49	0.46
6:F:81:LYS:C	6:F:82:LEU:HD23	2.37	0.46
5:E:28:ILE:HA	5:E:112:MET:HE3	1.97	0.46
4:D:190:GLY:HA2	4:D:191:PRO:HD3	1.75	0.46
1:A:1252:G:C2	1:A:1253:A:C2	3.04	0.46
5:E:70:THR:HG23	5:E:72:ARG:H	1.81	0.46
1:A:2315:G:H2'	1:A:2316:C:C6	2.51	0.46
1:A:2527:C:O5'	1:A:2527:C:H6	1.98	0.46
25:Y:59:ARG:HG2	25:Y:59:ARG:H	1.59	0.46
17:Q:69:CYS:SG	17:Q:79:PHE:HD2	2.39	0.46
22:V:71:VAL:HG11	22:V:74:VAL:CG2	2.46	0.46
1:A:863:A:OP1	13:M:21:THR:HB	2.16	0.46
16:P:20:PRO:CD	16:P:86:ILE:HG23	2.45	0.46
1:A:414:C:H2'	1:A:415:A:H8	1.80	0.46
6:F:128:ARG:HH21	6:F:130:ASN:HD21	1.63	0.46
19:S:10:VAL:O	19:S:12:ILE:N	2.49	0.46
1:A:356:G:H2'	1:A:357:A:H8	1.81	0.46
23:W:12:ASN:O	23:W:14:ARG:N	2.49	0.46
1:A:2830:G:N3	1:A:2883:A:H2	2.14	0.46
22:V:54:HIS:CG	22:V:101:PRO:HG3	2.51	0.46
1:A:239:U:O2'	1:A:240:G:H5'	2.15	0.46
7:G:24:VAL:HG23	7:G:37:VAL:HG21	1.98	0.46
1:A:1748:G:H2'	1:A:1749:A:C8	2.51	0.46
1:A:1487:G:H2'	1:A:1488:G:H8	1.80	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:56:G:H4'	2:B:57:A:C8	2.50	0.46
5:E:167:ALA:HB1	5:E:173:VAL:HG11	1.97	0.46
25:Y:33:MET:O	25:Y:37:PHE:HB2	2.15	0.45
12:L:65:ARG:H	12:L:65:ARG:HD2	1.81	0.45
21:U:11:ASP:H	21:U:27:VAL:CG2	2.29	0.45
1:A:1210:A:C5'	1:A:1210:A:H8	2.26	0.45
29:3:34:LEU:HD23	29:3:36:LEU:HD22	1.98	0.45
13:M:66:ILE:HG22	13:M:104:PHE:HD2	1.80	0.45
5:E:11:VAL:HG13	5:E:196:LEU:HD21	1.97	0.45
5:E:157:VAL:HB	5:E:194:MET:HB3	1.97	0.45
24:X:45:ASN:HD21	24:X:47:GLN:NE2	2.15	0.45
3:C:174:ILE:N	3:C:174:ILE:HD12	2.31	0.45
1:A:1010:A:H1'	1:A:1153:C:C1'	2.46	0.45
23:W:14:ARG:O	23:W:15:ASP:HB2	2.16	0.45
14:N:31:HIS:HB2	14:N:34:ILE:HD11	1.97	0.45
1:A:943:U:OP1	12:L:38:GLN:HB3	2.16	0.45
1:A:1826:G:H2'	1:A:1827:C:C6	2.52	0.45
1:A:1970:A:H4'	1:A:1971:A:OP1	2.15	0.45
21:U:13:VAL:CG1	21:U:72:VAL:HB	2.47	0.45
21:U:15:VAL:HG22	21:U:72:VAL:HG12	1.98	0.45
1:A:1022:G:N2	1:A:114(B):A:C2	2.84	0.45
21:U:88:LYS:HE2	21:U:93:GLY:CA	2.42	0.45
1:A:1006:C:H5'	10:J:51:THR:HG23	1.98	0.45
12:L:30:THR:HG22	12:L:31:ALA:H	1.79	0.45
3:C:228:PRO:HD3	3:C:234:GLY:O	2.16	0.45
3:C:76:PRO:HB3	3:C:116:GLN:HE21	1.81	0.45
1:A:2359:C:H2'	1:A:2360:A:H8	1.81	0.45
3:C:5:LYS:H	3:C:5:LYS:HD2	1.80	0.45
1:A:581:C:H2'	1:A:582:G:C8	2.51	0.45
1:A:357:A:H2'	1:A:358:U:C6	2.51	0.45
1:A:532:A:N1	1:A:2020:A:H1'	2.30	0.45
1:A:2722:G:H4'	14:N:5:LYS:HB3	1.97	0.45
1:A:2655:G:N2	1:A:2664:G:C5	2.84	0.45
1:A:1270:C:H5''	1:A:1271:G:O5'	2.16	0.45
1:A:868:U:C4	1:A:869:G:N7	2.85	0.45
2:B:6:C:C2	2:B:115:G:N2	2.84	0.45
1:A:388:G:OP1	24:X:33:LYS:HB3	2.16	0.45
1:A:1331:A:O2'	1:A:1332:G:C8	2.68	0.45
1:A:2346:A:H5''	1:A:2383:G:C1'	2.45	0.45
1:A:301:G:H5'	1:A:334:C:O2'	2.15	0.45
1:A:919:G:C5'	2:B:81:G:H1'	2.47	0.45
6:F:174:GLU:HG2	6:F:180:PHE:CD1	2.51	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:969:U:H2'	1:A:970:C:C6	2.52	0.45
21:U:68:HIS:ND1	21:U:70:SER:HB3	2.31	0.45
10:J:105:LEU:O	10:J:106:LYS:C	2.55	0.45
1:A:519:U:H2'	1:A:520:G:H8	1.82	0.45
1:A:1461:G:O2'	1:A:1462:C:H5'	2.16	0.45
1:A:2015:A:N3	28:2:2:ALA:N	2.64	0.45
1:A:1021:A:H2'	1:A:1023:U:H5'	1.97	0.45
12:L:85:LEU:HA	12:L:88:LEU:HB2	1.98	0.45
31:5:54:GLU:O	31:5:58:ILE:HG12	2.16	0.45
1:A:2033:A:O2'	1:A:2034:U:P	2.74	0.45
26:Z:28:LEU:HA	26:Z:33:GLN:OE1	2.16	0.45
12:L:140:ALA:O	12:L:141:ALA:CB	2.63	0.45
21:U:9:LYS:O	21:U:27:VAL:HG21	2.17	0.45
11:K:71:ARG:HH21	11:K:77:ILE:HG21	1.80	0.45
12:L:12:ALA:HB1	12:L:16:ARG:HB2	1.98	0.45
1:A:861:A:H2'	1:A:862:G:O4'	2.17	0.45
1:A:2261:C:H3'	23:W:16:SER:CB	2.46	0.45
18:R:78:LYS:HG3	18:R:79:VAL:HG23	1.98	0.45
1:A:2271:G:H2'	1:A:2272:U:H6	1.81	0.45
1:A:2563:U:H4'	11:K:28:SER:HA	1.99	0.45
1:A:2259:G:C2	1:A:2282:G:N1	2.84	0.45
1:A:2094:G:P	8:H:22:LYS:HD2	2.57	0.45
6:F:39:ILE:HG12	6:F:157:ILE:HG22	1.98	0.45
16:P:63:VAL:O	16:P:73:GLU:HA	2.16	0.45
1:A:2734:A:C8	1:A:2735:G:C8	3.05	0.45
1:A:2531:A:H2	1:A:2658:C:O2	1.99	0.45
1:A:1954:G:N2	1:A:1956:U:H3	2.14	0.45
1:A:2764:A:N7	1:A:2766:G:C6	2.84	0.45
1:A:1208:C:C4	1:A:1209:G:N7	2.85	0.45
10:J:101:TYR:CD1	10:J:101:TYR:N	2.85	0.45
1:A:1733:G:H8	1:A:1733:G:O5'	2.00	0.45
17:Q:92:ARG:HG2	18:R:11:GLN:CD	2.37	0.45
3:C:27:THR:O	3:C:27:THR:CG2	2.63	0.45
3:C:32:SER:O	3:C:33:LEU:O	2.35	0.45
1:A:639:U:H2'	1:A:640:C:H6	1.81	0.45
1:A:1587:A:H2'	1:A:1588:C:H6	1.81	0.45
1:A:813:U:H2'	1:A:814:C:C6	2.52	0.45
1:A:2306:C:H4'	6:F:136:ARG:HH22	1.82	0.45
5:E:124:LEU:HD12	5:E:125:LEU:N	2.31	0.45
5:E:29:ASN:N	5:E:112:MET:HE1	2.32	0.45
1:A:1871:A:H2'	1:A:1872:A:C8	2.51	0.45
1:A:1229:G:H2'	1:A:1230:C:C6	2.51	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1506:C:H2'	1:A:1508:A:C8	2.50	0.45
1:A:1599:C:OP2	20:T:36:LYS:HD3	2.17	0.45
1:A:1826:G:H2'	1:A:1827:C:H6	1.81	0.45
15:O:72:ALA:O	15:O:76:LYS:HG3	2.17	0.45
16:P:27:THR:HG22	16:P:90:GLN:HB3	1.99	0.45
12:L:57:THR:HG23	12:L:59:LEU:HB3	1.97	0.45
5:E:53:THR:C	5:E:55:GLY:N	2.70	0.45
1:A:479:A:HO2'	1:A:481:G:H8	1.61	0.45
16:P:50:ILE:HA	16:P:99:LEU:CD1	2.46	0.45
1:A:2807:G:C6	1:A:2893:G:O6	2.69	0.45
1:A:2815:C:O2'	28:2:42:PRO:HB2	2.16	0.45
12:L:27:HIS:CE1	18:R:83:ARG:HH12	2.34	0.45
11:K:31:LYS:HB3	11:K:32:TYR:CE1	2.51	0.45
17:Q:104:GLN:HB3	18:R:44:LYS:NZ	2.32	0.45
1:A:499:U:C4'	21:U:47:LYS:HZ1	2.30	0.45
1:A:2334:G:H4'	1:A:2335:A:OP2	2.17	0.45
1:A:116:C:O2'	1:A:117:G:H5'	2.17	0.45
1:A:1272:A:O2'	1:A:1273:U:H5'	2.17	0.45
1:A:1599:C:H2'	1:A:1600:C:C6	2.52	0.45
4:D:37:ARG:HD3	4:D:42:ASP:OD1	2.17	0.45
4:D:203:LYS:O	4:D:203:LYS:HD2	2.17	0.45
1:A:996:A:H4'	17:Q:92:ARG:CZ	2.44	0.45
1:A:1971:A:N3	3:C:239:ARG:O	2.49	0.45
1:A:1022:G:C6	1:A:1140:C:C4	3.04	0.45
6:F:41:GLN:HG2	6:F:155:MET:CB	2.37	0.45
1:A:2210:G:C3'	1:A:2210:G:N3	2.77	0.45
7:G:46:GLU:HG3	7:G:51:ARG:CD	2.47	0.45
1:A:644:A:C2	1:A:646:A:C4	3.05	0.45
1:A:1188:U:H4'	18:R:79:VAL:HG13	1.99	0.45
1:A:1804:C:O5'	1:A:1804:C:H6	1.99	0.45
1:A:1694:C:C6	1:A:1694:C:C5'	2.96	0.45
3:C:211:ARG:O	3:C:215:LEU:HG	2.16	0.45
11:K:22:ILE:HA	11:K:22:ILE:HD13	1.77	0.45
1:A:2817:G:H21	1:A:2836:U:H1'	1.82	0.45
10:J:26:THR:HG22	10:J:27:TYR:N	2.31	0.45
10:J:93:LYS:HB3	10:J:110:LEU:HB2	1.99	0.45
25:Y:31:GLU:O	25:Y:35:LEU:HB2	2.17	0.45
22:V:152:ALA:N	22:V:169:GLU:O	2.48	0.45
1:A:1850:G:C6	1:A:1851:U:C4	3.05	0.45
16:P:115:ARG:HG2	16:P:115:ARG:H	1.53	0.45
18:R:38:LEU:C	18:R:39:LEU:HD22	2.36	0.45
1:A:2394:C:H2'	1:A:2395:C:H6	1.81	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:6:GLY:HA2	4:D:51:PHE:CZ	2.51	0.45
11:K:77:ILE:HD13	11:K:78:ARG:N	2.31	0.45
1:A:661:C:H2'	1:A:662:G:H8	1.82	0.45
1:A:643:A:C2	1:A:644:A:C4	3.05	0.45
29:3:34:LEU:N	29:3:34:LEU:HD13	2.32	0.45
20:T:64:LYS:HG2	20:T:65:ARG:N	2.30	0.45
21:U:75:ILE:HG12	21:U:76:CYS:N	2.32	0.45
15:O:38:GLN:HB3	15:O:47:THR:HG23	1.98	0.45
1:A:380:U:H4'	24:X:21:ARG:O	2.17	0.45
24:X:21:ARG:HA	24:X:21:ARG:HD3	1.86	0.45
1:A:1615:C:C6	1:A:1617:C:C5	3.04	0.45
4:D:78:LEU:C	4:D:79:ARG:HD2	2.36	0.45
1:A:2515:C:H1'	1:A:2570:G:N2	2.32	0.45
1:A:1326:U:O2'	1:A:1327:C:H5'	2.17	0.45
4:D:24:THR:HB	4:D:186:GLY:O	2.17	0.45
12:L:128:HIS:HB3	12:L:147:LEU:HD23	1.97	0.45
5:E:160:ASN:ND2	5:E:162:LEU:H	2.15	0.45
5:E:89:VAL:HG12	5:E:90:PHE:CD2	2.52	0.45
3:C:70:TRP:C	3:C:70:TRP:CD1	2.90	0.45
7:G:13:LYS:HE2	7:G:14:GLY:N	2.32	0.45
22:V:8:TYR:HB2	22:V:38:TYR:CE2	2.52	0.45
1:A:311:A:C8	1:A:332:A:C5	3.05	0.45
1:A:2748:A:C2	1:A:2757:A:C4	3.04	0.45
12:L:39:LYS:HD3	12:L:39:LYS:HA	1.71	0.45
10:J:42:GLU:O	10:J:42:GLU:HG3	2.17	0.45
1:A:637:A:OP2	12:L:115:LEU:HB2	2.16	0.45
1:A:846:C:C2	1:A:847:U:C5	3.05	0.45
31:5:14:VAL:HG22	31:5:24:ALA:HB2	1.99	0.45
12:L:16:ARG:NH2	12:L:18:ARG:H	2.15	0.45
10:J:116:THR:O	10:J:118:PRO:HD3	2.17	0.45
1:A:2346:A:C2	1:A:2383:G:C2	3.05	0.45
3:C:108:PRO:HB3	3:C:143:HIS:CE1	2.52	0.45
5:E:192:LEU:HD23	5:E:192:LEU:C	2.37	0.45
1:A:155:C:H2'	1:A:161:U:H5'	1.99	0.45
1:A:1600:C:O2'	1:A:1601:G:H5'	2.17	0.45
1:A:1427:A:H4'	1:A:1428:C:O5'	2.17	0.45
3:C:124:PRO:HG2	3:C:129:ASN:ND2	2.32	0.45
29:3:41:PRO:HG3	29:3:49:HIS:HE1	1.82	0.45
13:M:51:ARG:O	13:M:55:VAL:HG13	2.18	0.45
3:C:218:ARG:HG3	3:C:218:ARG:HH11	1.82	0.45
20:T:55:ASN:HB2	20:T:80:ILE:HG23	1.99	0.44
13:M:22:LYS:CE	13:M:22:LYS:HA	2.35	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:81:LYS:NZ	21:U:99:CYS:SG	2.90	0.44
1:A:2250:G:C4	13:M:82:ARG:HG3	2.52	0.44
16:P:88:ILE:HG13	16:P:89:VAL:N	2.31	0.44
26:Z:26:LEU:HB2	26:Z:28:LEU:CD1	2.47	0.44
1:A:1578:U:C2'	1:A:1579:A:H5''	2.47	0.44
1:A:2287:A:C4	1:A:2289:G:C8	3.04	0.44
1:A:662:G:OP1	12:L:18:ARG:HD2	2.17	0.44
1:A:1448:G:N2	1:A:149(B):A:N6	2.66	0.44
6:F:125:PHE:C	6:F:127:GLY:H	2.19	0.44
1:A:644:A:O2'	1:A:645:C:H5''	2.17	0.44
3:C:11:PRO:C	3:C:13:ARG:N	2.70	0.44
7:G:105:LEU:N	7:G:105:LEU:HD13	2.31	0.44
22:V:58:VAL:HG11	22:V:66:SER:HB2	1.98	0.44
1:A:2666:C:H3'	1:A:2667:C:C6	2.52	0.44
1:A:813:U:O2'	1:A:1225:G:H1'	2.17	0.44
6:F:16:ARG:HB3	6:F:17:PRO:HD3	1.98	0.44
1:A:404:C:H4'	1:A:405:U:H5'	1.99	0.44
7:G:122:THR:O	7:G:134:SER:HB2	2.16	0.44
19:S:70:TYR:O	19:S:107:LEU:HA	2.17	0.44
27:1:46:ASN:HB2	27:1:64:LYS:CB	2.47	0.44
1:A:2712:U:O2'	1:A:712(B):A:P	2.75	0.44
13:M:141:GLN:HE21	22:V:72:ARG:HG2	1.82	0.44
1:A:744:G:OP1	4:D:132:HIS:HB2	2.18	0.44
1:A:572:A:H5''	1:A:573:G:OP2	2.16	0.44
1:A:1652:A:H2'	1:A:1653:G:O4'	2.18	0.44
22:V:137:ILE:N	22:V:137:ILE:HD12	2.33	0.44
24:X:90:ILE:O	24:X:94:LEU:N	2.50	0.44
4:D:118:LYS:NZ	14:N:2:ARG:HH22	2.15	0.44
16:P:98:LYS:HB3	16:P:100:TYR:HE1	1.82	0.44
7:G:20:ALA:HB1	7:G:21:PRO:CD	2.47	0.44
7:G:22:GLY:C	7:G:23:ARG:HD3	2.38	0.44
1:A:1797:C:O2'	3:C:259:THR:HG23	2.17	0.44
27:1:40:ILE:O	27:1:47:VAL:HA	2.17	0.44
12:L:67:MET:HA	12:L:67:MET:HE3	1.99	0.44
1:A:783:A:H3'	1:A:783:A:C8	2.52	0.44
19:S:1:MET:HG3	19:S:2:GLU:N	2.32	0.44
3:C:30:GLU:HG3	3:C:63:ARG:CZ	2.47	0.44
6:F:25:TYR:CZ	6:F:32:PRO:HD3	2.51	0.44
8:H:128:LEU:HG	8:H:142:VAL:CG2	2.48	0.44
10:J:114:LEU:HA	10:J:118:PRO:HB3	1.99	0.44
1:A:1478:G:C2	1:A:1479:G:C8	3.05	0.44
4:D:4:ILE:CG2	4:D:96:PHE:HE1	2.29	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:62:ARG:NE	10:J:64:ASP:HB2	2.32	0.44
1:A:226:G:N2	1:A:227:A:C2	2.84	0.44
1:A:1378:A:H4'	1:A:1379:A:OP1	2.17	0.44
1:A:753:C:H2'	1:A:754:C:H6	1.82	0.44
31:5:11:LYS:HB2	31:5:61:LEU:HD22	2.00	0.44
1:A:792:G:H5''	1:A:793:A:H5'	1.98	0.44
20:T:24:GLY:O	20:T:83:VAL:HG22	2.17	0.44
6:F:58:GLN:O	6:F:62:LEU:HD13	2.17	0.44
4:D:91:VAL:HB	4:D:95:ILE:CD1	2.39	0.44
14:N:54:LEU:HD22	14:N:66:VAL:HG23	1.99	0.44
6:F:106:LEU:HB3	6:F:107:LEU:HD23	1.99	0.44
1:A:2027:G:C2	1:A:2028:U:H1'	2.53	0.44
14:N:9:LYS:HD3	14:N:43:GLU:OE1	2.18	0.44
8:H:114:LEU:HA	8:H:130:TYR:HD1	1.83	0.44
1:A:2598:A:H5''	3:C:235:GLY:HA2	1.98	0.44
1:A:828:U:O2	1:A:828:U:H3'	2.18	0.44
16:P:30:VAL:HG12	16:P:86:ILE:HG12	1.99	0.44
23:W:51:VAL:HG21	23:W:80:HIS:HA	2.00	0.44
1:A:1536:A:H5''	1:A:1537:C:OP2	2.17	0.44
22:V:10:ARG:HG2	22:V:11:GLU:N	2.32	0.44
3:C:260:ARG:O	3:C:261:LYS:C	2.55	0.44
16:P:62:THR:HG22	16:P:75:ILE:HG13	1.98	0.44
1:A:2501:C:H6	1:A:2501:C:H2'	1.56	0.44
1:A:2330:G:O2'	23:W:41:ARG:HB2	2.18	0.44
1:A:616:A:C4'	1:A:617:G:OP1	2.66	0.44
7:G:12:PRO:O	7:G:15:VAL:HG22	2.18	0.44
1:A:1916:A:H2'	1:A:1917:U:O4'	2.18	0.44
3:C:175:LEU:HD12	3:C:185:VAL:HG21	1.98	0.44
8:H:7:GLU:OE1	8:H:8:PRO:HD2	2.17	0.44
12:L:38:GLN:CG	12:L:39:LYS:H	2.28	0.44
15:O:98:VAL:O	15:O:101:LEU:HB2	2.18	0.44
13:M:141:GLN:N	22:V:53:ILE:HB	2.33	0.44
1:A:1174:A:H3'	1:A:1175:U:C5'	2.46	0.44
14:N:10:LEU:HD23	14:N:21:TYR:OH	2.18	0.44
1:A:2484:G:C2	1:A:2485:G:C8	3.06	0.44
6:F:172:LEU:O	6:F:176:LEU:HG	2.18	0.44
21:U:90:LEU:N	21:U:90:LEU:HD23	2.33	0.44
5:E:124:LEU:HB3	5:E:193:VAL:HG22	1.98	0.44
16:P:110:ILE:HD12	16:P:110:ILE:HA	1.85	0.44
17:Q:60:LEU:O	17:Q:60:LEU:HD23	2.16	0.44
1:A:2364:C:H1'	23:W:36:ILE:HD11	2.00	0.44
1:A:613:U:H4'	1:A:616:A:N6	2.33	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:225:A:O2'	1:A:257:A:H4'	2.17	0.44
1:A:2767:C:H2'	1:A:2768:C:H6	1.83	0.44
7:G:38:SER:HB2	7:G:41:MET:HG3	1.99	0.44
5:E:50:SER:HA	5:E:92:PRO:O	2.17	0.44
1:A:1668:A:H4'	1:A:1669:A:O5'	2.18	0.44
21:U:63:LYS:HE3	21:U:63:LYS:HB2	1.81	0.44
10:J:156:GLN:O	10:J:157:ARG:HB2	2.16	0.44
1:A:2285:C:H41	29:3:25:LYS:NZ	2.16	0.44
1:A:956:G:OP1	13:M:86:GLY:N	2.48	0.44
25:Y:16:LEU:N	25:Y:16:LEU:HD22	2.33	0.44
26:Z:46:ASN:HD22	26:Z:46:ASN:HA	1.66	0.44
1:A:2543:G:H2'	1:A:2544:G:O4'	2.17	0.44
3:C:142:VAL:HG23	3:C:192:THR:C	2.38	0.44
1:A:794:G:C5	1:A:795:C:C4	3.06	0.44
1:A:186:G:H2'	1:A:187:G:H8	1.82	0.44
25:Y:46:GLN:O	25:Y:47:ASN:CB	2.60	0.44
1:A:2850:A:H8	1:A:2850:A:H5'	1.80	0.44
1:A:2666:C:H3'	1:A:2667:C:H6	1.82	0.44
6:F:126:ASP:OD2	6:F:130:ASN:HB2	2.18	0.44
8:H:25:TYR:O	8:H:29:TYR:HB3	2.18	0.44
10:J:161:LEU:N	10:J:161:LEU:HD23	2.32	0.44
4:D:21:VAL:HG12	4:D:23:VAL:HG13	1.98	0.44
1:A:212:G:O2'	1:A:213:A:H5'	2.18	0.44
1:A:2580:U:H4'	4:D:130:GLY:HA2	1.99	0.44
18:R:27:ALA:HB3	18:R:61:VAL:HG11	1.99	0.44
3:C:120:GLY:O	3:C:131:LEU:HB3	2.17	0.44
24:X:43:TYR:HA	24:X:44:PRO:HD3	1.77	0.44
3:C:69:ARG:HH12	3:C:117:VAL:HG21	1.82	0.44
24:X:27:GLU:HG2	24:X:28:GLY:N	2.31	0.44
1:A:2376:A:H61	15:O:89:ARG:HG3	1.83	0.44
1:A:464:U:H4'	30:4:5:TRP:CZ3	2.53	0.44
18:R:72:VAL:HG22	18:R:85:LYS:O	2.18	0.44
4:D:47:VAL:HG23	4:D:84:PHE:O	2.17	0.44
25:Y:24:LEU:HD23	25:Y:24:LEU:O	2.18	0.44
1:A:534:U:O2'	17:Q:49:HIS:CD2	2.69	0.44
1:A:2647:U:H2'	1:A:2648:C:H6	1.82	0.44
22:V:5:LEU:HD21	22:V:39:VAL:HB	2.00	0.44
1:A:1833:U:C2	1:A:1834:U:C5	3.06	0.44
1:A:1655:A:O2'	4:D:115:GLY:HA2	2.18	0.44
22:V:92:SER:HB2	22:V:94:GLU:OE2	2.17	0.44
16:P:107:ASP:OD2	16:P:109:GLU:HB2	2.18	0.44
4:D:77:ILE:HG22	4:D:78:LEU:N	2.33	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:238:C:O2'	1:A:608:A:H1'	2.17	0.44
1:A:994:C:OP1	17:Q:53:ARG:NH2	2.51	0.44
26:Z:16:PRO:HB2	26:Z:18:ASP:OD1	2.18	0.44
17:Q:79:PHE:HE2	17:Q:106:PHE:CZ	2.36	0.44
18:R:7:THR:HG23	18:R:22:VAL:HG11	1.99	0.44
6:F:5:LEU:O	6:F:8:LYS:HB3	2.18	0.44
20:T:35:THR:HB	20:T:38:GLU:H	1.82	0.44
22:V:163:LEU:CD2	22:V:163:LEU:H	2.29	0.44
3:C:35:LYS:O	3:C:64:ILE:HD12	2.18	0.44
3:C:33:LEU:O	3:C:36:PRO:HD2	2.18	0.44
3:C:83:GLU:OE1	3:C:104:TYR:OH	2.31	0.44
1:A:528:A:H2	1:A:2043:C:C4'	2.28	0.44
1:A:557:U:H2'	1:A:558:G:C8	2.52	0.44
10:J:62:ARG:CZ	10:J:64:ASP:HB2	2.47	0.44
1:A:301:G:C6	1:A:317:G:C6	3.06	0.44
25:Y:19:VAL:HG12	25:Y:23:LYS:HE3	2.00	0.44
22:V:110:GLY:HA2	22:V:146:ILE:HG23	1.99	0.44
22:V:118:GLN:HG3	22:V:175:VAL:HG13	1.99	0.44
30:4:24:THR:HG23	30:4:27:GLY:HA3	1.99	0.44
4:D:176:ILE:HD12	4:D:176:ILE:N	2.33	0.44
1:A:2722:G:H2'	1:A:2723:C:C6	2.53	0.44
1:A:2768:C:C4	1:A:2769:C:C5	3.06	0.44
1:A:851:U:O2'	26:Z:42:ALA:O	2.34	0.44
1:A:637:A:C5'	12:L:116:GLY:HA2	2.48	0.44
12:L:85:LEU:HD21	12:L:116:GLY:O	2.17	0.44
3:C:132:PRO:HA	3:C:190:TYR:HA	2.00	0.44
3:C:271:ILE:O	3:C:272:ALA:CB	2.65	0.44
16:P:74:ARG:HD3	16:P:76:PHE:CE2	2.53	0.44
15:O:26:LEU:HG	15:O:39:ILE:HD11	2.00	0.44
2:B:79:C:H6	2:B:79:C:O5'	2.01	0.44
2:B:65:C:O2'	2:B:66:A:H5'	2.18	0.44
10:J:116:THR:HG23	10:J:117:HIS:N	2.33	0.44
1:A:2562:U:H1'	11:K:23:ARG:HH12	1.81	0.44
1:A:2850:A:H5''	1:A:2868:A:C2	2.52	0.44
1:A:2809:A:C6	1:A:2892:A:C8	3.05	0.44
1:A:826:U:H2'	1:A:828:U:O4'	2.18	0.44
15:O:36:TYR:HD1	15:O:36:TYR:H	1.64	0.44
1:A:855:G:H2'	1:A:856:C:H6	1.83	0.44
1:A:1798:U:H5''	3:C:259:THR:O	2.17	0.44
7:G:38:SER:HB2	7:G:41:MET:CG	2.48	0.44
1:A:1717:G:C6	1:A:1743:G:C6	3.06	0.44
1:A:2574:G:H8	1:A:2574:G:O5'	2.01	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1191:G:OP1	12:L:35:HIS:CD2	2.71	0.43
8:H:9:LEU:HB2	8:H:12:LEU:HB2	2.00	0.43
7:G:42:ARG:O	7:G:52:VAL:HA	2.18	0.43
8:H:15:VAL:HG12	8:H:16:GLY:N	2.32	0.43
1:A:2777:G:H4'	1:A:2778:A:H5'	2.00	0.43
1:A:514:A:H1'	1:A:581:C:O2'	2.18	0.43
1:A:265:A:C8	1:A:266:G:H1'	2.53	0.43
1:A:150:C:H2'	1:A:151:C:H6	1.82	0.43
1:A:2839:G:C5	1:A:2840:C:C4	3.06	0.43
5:E:50:SER:HB2	5:E:94:PRO:HD3	1.99	0.43
1:A:843:G:C8	1:A:843:G:H5''	2.53	0.43
30:4:13:ALA:O	30:4:17:GLY:HA3	2.18	0.43
1:A:251:A:H5''	12:L:51:PHE:CE1	2.52	0.43
18:R:45:THR:O	18:R:46:VAL:C	2.56	0.43
21:U:14:LEU:C	21:U:14:LEU:HD23	2.38	0.43
31:5:25:MET:SD	31:5:47:LYS:HG2	2.58	0.43
13:M:85:LYS:HG3	13:M:86:GLY:N	2.32	0.43
7:G:149:ARG:HD2	7:G:164:TYR:HE1	1.82	0.43
7:G:86:GLU:HG2	7:G:164:TYR:O	2.18	0.43
16:P:26:ASP:OD1	16:P:26:ASP:O	2.36	0.43
14:N:8:ARG:CZ	14:N:43:GLU:HG3	2.48	0.43
10:J:57:LEU:CD1	10:J:142:ARG:HB2	2.48	0.43
1:A:1678:G:O5'	1:A:1678:G:C8	2.62	0.43
1:A:1317:A:C6	1:A:1318:C:C4	3.05	0.43
1:A:1335:U:H2'	1:A:1336:A:C8	2.53	0.43
26:Z:40:THR:OG1	26:Z:43:ILE:HG12	2.19	0.43
22:V:141:VAL:HA	22:V:144:LEU:HD23	2.00	0.43
13:M:101:ARG:HG3	13:M:102:VAL:N	2.33	0.43
29:3:11:LEU:HD13	29:3:12:GLU:H	1.83	0.43
21:U:76:CYS:HB3	21:U:77:PRO:CD	2.48	0.43
23:W:56:ASP:O	23:W:57:PHE:HB2	2.19	0.43
20:T:62:LYS:O	20:T:73:ARG:HB2	2.17	0.43
1:A:1483:G:H2'	1:A:1484:G:C8	2.53	0.43
4:D:192:ASN:N	4:D:192:ASN:HD22	2.16	0.43
24:X:75:GLU:OE1	24:X:75:GLU:HA	2.18	0.43
1:A:833:U:H5''	12:L:48:PRO:HB2	1.98	0.43
17:Q:90:VAL:O	17:Q:92:ARG:N	2.52	0.43
6:F:66:GLN:NE2	6:F:94:LEU:HB3	2.33	0.43
26:Z:22:ALA:O	26:Z:26:LEU:HG	2.18	0.43
6:F:84:LYS:HG3	6:F:85:GLY:H	1.83	0.43
10:J:116:THR:OG1	10:J:117:HIS:N	2.51	0.43
1:A:598:G:H2'	1:A:599:G:O4'	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:145:VAL:HG12	3:C:146:GLU:O	2.17	0.43
1:A:102:G:H8	1:A:102:G:H5'	1.82	0.43
1:A:1291:C:H2'	1:A:1292:U:H6	1.81	0.43
18:R:28:GLU:OE1	18:R:31:ALA:HB2	2.18	0.43
1:A:221:A:N7	1:A:266:G:C5	2.86	0.43
16:P:77:PRO:HB2	16:P:80:SER:HB2	2.01	0.43
1:A:1655:A:H1'	4:D:113:PHE:CE2	2.53	0.43
1:A:1655:A:H4'	4:D:115:GLY:N	2.34	0.43
1:A:363(C):G:H2'	1:A:363(D):G:H8	1.84	0.43
1:A:1750:G:H2'	1:A:1751:C:C6	2.53	0.43
23:W:14:ARG:HE	23:W:14:ARG:HB2	1.50	0.43
1:A:286:C:C2	1:A:287:C:C5	3.07	0.43
10:J:78:VAL:O	10:J:79:ASN:HB2	2.18	0.43
1:A:708:C:H6	1:A:708:C:O5'	2.01	0.43
12:L:65:ARG:N	12:L:65:ARG:HD2	2.33	0.43
23:W:32:ARG:CA	23:W:35:ASN:HD21	2.32	0.43
26:Z:26:LEU:HD21	26:Z:46:ASN:HB3	2.00	0.43
3:C:102:LYS:C	3:C:103:ARG:HG2	2.37	0.43
15:O:18:ILE:HA	15:O:21:THR:OG1	2.18	0.43
5:E:181:LEU:CD2	5:E:186:ILE:HD11	2.47	0.43
1:A:390:A:C5	12:L:71:VAL:HG21	2.52	0.43
1:A:777:A:O2'	1:A:778:G:H5'	2.17	0.43
2:B:73:A:H3'	2:B:74:U:C6	2.54	0.43
12:L:8:PRO:C	12:L:10:PRO:HD3	2.39	0.43
4:D:36:ARG:HD3	4:D:85:ASN:HD21	1.84	0.43
11:K:47:ILE:HD12	11:K:47:ILE:HA	1.88	0.43
1:A:510:C:OP1	1:A:511:U:OP2	2.36	0.43
10:J:149:PRO:O	10:J:150:ASP:HB2	2.19	0.43
13:M:61:GLY:O	22:V:177:PRO:HA	2.19	0.43
1:A:405:U:H3'	1:A:406:G:C5'	2.48	0.43
18:R:61:VAL:HG23	18:R:61:VAL:O	2.19	0.43
26:Z:30:ARG:H	26:Z:30:ARG:HG2	1.63	0.43
12:L:48:PRO:O	12:L:49:ARG:C	2.57	0.43
1:A:1825:A:H2'	1:A:1826:G:C8	2.54	0.43
1:A:1826:G:C6	1:A:1827:C:C4	3.06	0.43
20:T:21:PHE:CD2	20:T:26:TYR:HD2	2.36	0.43
1:A:142:G:H1'	20:T:37:THR:HG21	2.01	0.43
1:A:71:A:OP1	1:A:72:U:H2'	2.18	0.43
21:U:4:LYS:HD3	21:U:4:LYS:H	1.83	0.43
8:H:72:LEU:HD12	8:H:140:LEU:CD1	2.48	0.43
1:A:2037:G:H2'	1:A:2038:G:C8	2.53	0.43
4:D:86:PRO:HB2	4:D:87:GLU:H	1.42	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:96:ALA:CB	7:G:105:LEU:HB3	2.48	0.43
1:A:36:G:C5	1:A:37:C:C5	3.06	0.43
1:A:2061:G:H5''	1:A:2503:A:C2	2.53	0.43
1:A:2572:A:C8	4:D:144:ARG:HB3	2.53	0.43
6:F:16:ARG:HB3	6:F:17:PRO:CD	2.49	0.43
23:W:27:GLU:HB2	23:W:69:PHE:CD1	2.54	0.43
1:A:1851:U:H2'	1:A:1852:C:H6	1.83	0.43
13:M:134:ARG:O	13:M:135:ASP:HB2	2.17	0.43
1:A:1416:G:HO2'	1:A:1417:C:H5	1.61	0.43
1:A:454:A:H4'	1:A:455:C:OP2	2.19	0.43
1:A:1563:G:H2'	1:A:1564:C:H6	1.83	0.43
1:A:685:A:H1'	1:A:688:U:O4	2.18	0.43
1:A:2867:G:C5	16:P:23:ARG:NH1	2.87	0.43
11:K:99:PHE:CD1	11:K:99:PHE:N	2.85	0.43
12:L:47:ASP:HB3	12:L:48:PRO:CA	2.49	0.43
25:Y:9:GLN:O	25:Y:12:GLU:HB3	2.18	0.43
3:C:25:THR:HG23	3:C:27:THR:HG22	2.00	0.43
1:A:744:G:OP1	4:D:132:HIS:CB	2.67	0.43
2:B:102:G:H1'	22:V:73:GLN:HE22	1.83	0.43
1:A:39:C:H2'	1:A:40:C:C6	2.53	0.43
21:U:75:ILE:HG13	21:U:80:GLY:H	1.83	0.43
3:C:146:GLU:OE2	3:C:150:LYS:N	2.51	0.43
14:N:11:ASN:O	14:N:12:ARG:HB2	2.18	0.43
1:A:426:C:C2	1:A:427:U:C5	3.07	0.43
1:A:17:G:H2'	1:A:18:C:C6	2.53	0.43
1:A:379:G:N2	24:X:20:ARG:NH1	2.66	0.43
2:B:45:A:H2'	2:B:45:A:N3	2.34	0.43
1:A:1464:C:H2'	1:A:1465:G:C8	2.53	0.43
17:Q:112:ARG:NH2	18:R:46:VAL:HG21	2.34	0.43
8:H:92:VAL:HG22	8:H:92:VAL:O	2.19	0.43
10:J:38:LEU:HD13	10:J:39:ILE:N	2.33	0.43
1:A:2025:C:C2	1:A:2026:C:C5	3.07	0.43
1:A:1579:A:H2'	1:A:1580:A:C8	2.54	0.43
4:D:170:LEU:HB3	4:D:184:VAL:HG12	1.99	0.43
13:M:24:GLY:HA2	13:M:101:ARG:CA	2.47	0.43
1:A:1567:A:C8	3:C:84:TYR:CE2	3.07	0.43
16:P:19:LEU:HA	16:P:20:PRO:HD3	1.74	0.43
16:P:56:GLY:O	16:P:59:THR:HG22	2.18	0.43
6:F:128:ARG:HG2	6:F:129:GLY:H	1.84	0.43
27:1:48:ILE:N	27:1:48:ILE:HD12	2.33	0.43
3:C:72:LYS:HE3	3:C:101:GLU:HB3	2.00	0.43
1:A:2590:A:H2'	1:A:2591:C:C6	2.54	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:616:A:H4'	1:A:617:G:OP1	2.18	0.43
1:A:2450:A:O2'	1:A:2451:A:H5'	2.18	0.43
1:A:2389:G:H5''	1:A:2390:U:H5'	2.01	0.43
13:M:130:LYS:HG2	13:M:131:ILE:N	2.33	0.43
1:A:2678:C:H2'	1:A:2679:A:H8	1.83	0.43
1:A:1620:G:O2'	30:4:2:LYS:HG2	2.18	0.43
22:V:150:LEU:HD23	22:V:151:HIS:N	2.33	0.43
14:N:55:ALA:HA	14:N:80:PHE:CE1	2.53	0.43
22:V:70:LEU:HD23	22:V:70:LEU:N	2.34	0.43
12:L:50:ARG:HB2	31:5:60:LEU:CD1	2.35	0.43
12:L:50:ARG:HB3	31:5:60:LEU:HD21	2.00	0.43
6:F:8:LYS:O	6:F:12:TYR:HD1	2.02	0.43
23:W:43:THR:HG22	23:W:43:THR:O	2.19	0.43
22:V:71:VAL:HA	22:V:87:ASP:O	2.19	0.43
1:A:2026:C:C2	1:A:2027:G:C8	3.07	0.43
1:A:214:G:O2'	1:A:215:G:O4'	2.33	0.43
15:O:93:LYS:HA	15:O:93:LYS:HE3	2.01	0.43
17:Q:25:TRP:O	17:Q:28:ARG:HB3	2.19	0.43
1:A:2050:C:H2'	1:A:2051:A:C8	2.54	0.43
1:A:1796:U:H2'	1:A:1797:C:C6	2.53	0.43
1:A:2509:G:C5	1:A:2510:C:C5	3.06	0.43
1:A:587:C:C6	1:A:671:C:H1'	2.54	0.43
17:Q:79:PHE:HE1	17:Q:83:LEU:CD2	2.31	0.43
3:C:222:ARG:HE	3:C:222:ARG:HB2	1.70	0.43
27:1:64:LYS:HA	27:1:64:LYS:HE3	2.00	0.43
6:F:55:LYS:HD2	6:F:58:GLN:NE2	2.21	0.43
3:C:35:LYS:HB3	3:C:36:PRO:HD3	2.00	0.43
31:5:21:LYS:HA	31:5:54:GLU:OE2	2.19	0.43
14:N:4:LEU:C	14:N:6:SER:N	2.72	0.43
1:A:330:A:O2'	1:A:331:A:C8	2.72	0.43
1:A:1678:G:H22	1:A:1989:G:H22	1.64	0.43
1:A:795:C:O2'	1:A:796:C:H5'	2.18	0.43
1:A:448:U:H1'	5:E:84:VAL:HG21	2.01	0.43
1:A:2563:U:O2	1:A:2565:A:C8	2.71	0.43
12:L:105:LEU:H	12:L:105:LEU:HD12	1.83	0.43
1:A:1028:A:N3	1:A:2486:G:O2'	2.38	0.43
1:A:1536:A:O5'	1:A:1536:A:H8	2.02	0.43
4:D:93:VAL:HG21	4:D:177:PRO:HA	1.99	0.43
1:A:2086:U:H2'	1:A:2087:G:C8	2.54	0.43
1:A:2585:U:H4'	1:A:2586:C:OP1	2.17	0.43
1:A:2683:C:OP1	16:P:53:ARG:NH2	2.51	0.43
7:G:86:GLU:CD	7:G:86:GLU:H	2.22	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:848:G:N9	1:A:933:A:H8	2.17	0.43
22:V:51:ALA:HB1	22:V:57:ILE:HD11	2.01	0.43
6:F:161:THR:HG21	6:F:172:LEU:HD23	2.01	0.43
2:B:106:G:O2'	2:B:107:U:H5'	2.19	0.43
18:R:72:VAL:CG2	18:R:85:LYS:HB3	2.48	0.43
14:N:2:ARG:HB3	14:N:3:HIS:CE1	2.54	0.43
11:K:86:ILE:HD12	11:K:86:ILE:N	2.31	0.43
1:A:1996:C:H5	11:K:32:TYR:OH	2.02	0.43
29:3:30:THR:CG2	29:3:31:PRO:HD2	2.48	0.43
1:A:2591:C:H2'	1:A:2592:G:C8	2.54	0.43
19:S:70:TYR:HD2	19:S:70:TYR:H	1.66	0.43
1:A:533:G:N3	17:Q:45:TYR:CE1	2.87	0.43
5:E:117:ARG:HD2	5:E:190:GLU:O	2.18	0.43
22:V:128:VAL:CG2	22:V:132:ASN:HB2	2.49	0.43
3:C:140:THR:O	3:C:165:ILE:HD12	2.19	0.43
10:J:85:VAL:HG22	10:J:89:LYS:HG3	2.01	0.43
12:L:101:VAL:HG23	12:L:108:LYS:H	1.84	0.43
1:A:1576:U:C2	1:A:1577:C:C5	3.07	0.43
1:A:944:G:H5''	1:A:945:A:C5'	2.49	0.43
1:A:783:A:C3'	1:A:783:A:C8	3.00	0.42
28:2:33:CYS:HB2	28:2:34:PRO:HD2	2.01	0.42
24:X:11:ARG:NH1	24:X:61:ARG:H	2.17	0.42
3:C:33:LEU:HD23	3:C:33:LEU:N	2.25	0.42
1:A:2286:A:C8	1:A:2287:A:N6	2.87	0.42
8:H:114:LEU:HA	8:H:130:TYR:CD1	2.54	0.42
1:A:775:G:C2	1:A:777:A:N6	2.86	0.42
7:G:107:VAL:HG23	7:G:109:PHE:CE1	2.54	0.42
20:T:93:GLU:O	20:T:94:GLY:C	2.57	0.42
1:A:2243:U:H2'	1:A:2244:U:H6	1.84	0.42
19:S:10:VAL:HG21	19:S:103:ILE:HD13	2.01	0.42
10:J:160:LYS:HD2	10:J:161:LEU:H	1.83	0.42
1:A:2723:C:O5'	1:A:2723:C:H6	2.02	0.42
10:J:27:TYR:O	10:J:29:PRO:HD3	2.19	0.42
3:C:226:MET:HB3	3:C:230:ASP:HB2	2.00	0.42
1:A:195:A:H4'	1:A:251:A:O2'	2.20	0.42
1:A:142:G:H1'	20:T:37:THR:CG2	2.49	0.42
3:C:31:LYS:HG3	3:C:33:LEU:HG	2.01	0.42
3:C:33:LEU:HB2	3:C:34:VAL:H	1.64	0.42
12:L:57:THR:C	12:L:59:LEU:H	2.21	0.42
12:L:6:LEU:H	12:L:6:LEU:CD2	2.26	0.42
15:O:100:ALA:HA	15:O:103:GLU:HB3	2.00	0.42
1:A:141(A):A:C8	1:A:1408:C:H1'	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:10:LEU:HD22	14:N:17:ARG:HD3	2.01	0.42
5:E:139:PHE:HB2	5:E:166:ALA:CB	2.48	0.42
1:A:66:C:H2'	1:A:67:U:H6	1.84	0.42
1:A:811:U:H3'	12:L:25:SER:O	2.19	0.42
1:A:500:G:N2	1:A:502:A:H2'	2.34	0.42
24:X:45:ASN:HD21	24:X:47:GLN:HE21	1.67	0.42
19:S:84:ARG:HB2	19:S:96:ILE:CG2	2.49	0.42
1:A:816:C:H2'	1:A:817:C:H6	1.84	0.42
1:A:1599:C:H2'	1:A:1600:C:H6	1.84	0.42
3:C:202:LYS:HG3	3:C:203:ASN:OD1	2.19	0.42
1:A:1526:G:H2'	1:A:1527:G:C8	2.54	0.42
1:A:993:G:H1'	18:R:89:GLN:OE1	2.19	0.42
4:D:110:GLY:HA2	4:D:162:ALA:HB2	2.02	0.42
1:A:735:A:H3'	1:A:736:C:C6	2.53	0.42
1:A:1683:C:H2'	1:A:1684:C:C6	2.54	0.42
1:A:1581:G:H2'	1:A:1582:C:O4'	2.19	0.42
18:R:40:LEU:H	18:R:47:VAL:CG2	2.33	0.42
10:J:40:ASP:OD1	10:J:42:GLU:HG2	2.20	0.42
4:D:91:VAL:CB	4:D:95:ILE:HD11	2.42	0.42
13:M:141:GLN:OXT	22:V:98:MET:HE3	2.19	0.42
31:5:53:PRO:C	31:5:57:ARG:NH2	2.73	0.42
1:A:2037:G:C6	1:A:2038:G:C6	3.06	0.42
1:A:2287:A:C2	1:A:2289:G:C8	3.07	0.42
1:A:598:G:H5'	12:L:15:ARG:CG	2.50	0.42
11:K:7:TYR:CE1	11:K:20:MET:HB2	2.54	0.42
20:T:70:LEU:C	20:T:70:LEU:HD23	2.39	0.42
14:N:104:ARG:HH11	14:N:104:ARG:HB2	1.85	0.42
1:A:1344:G:H5'	1:A:1384:A:C6	2.55	0.42
1:A:755:C:H2'	1:A:756:C:C6	2.54	0.42
1:A:909:A:C4	1:A:912:C:C5	3.07	0.42
1:A:571:A:C8	1:A:2030:A:N6	2.87	0.42
1:A:1831:G:C5	1:A:1832:C:C5	3.07	0.42
1:A:2891:G:H8	1:A:2891:G:O5'	2.02	0.42
2:B:16:G:C6	2:B:69:G:C2	3.07	0.42
25:Y:15:LYS:HA	25:Y:15:LYS:HE2	2.00	0.42
21:U:6:HIS:O	21:U:7:VAL:O	2.37	0.42
1:A:114(B):A:O2'	1:A:1143:A:H3'	2.19	0.42
1:A:910:A:C6	1:A:911:A:C6	3.08	0.42
5:E:65:TRP:HZ3	5:E:75:HIS:HD2	1.60	0.42
26:Z:50:VAL:O	26:Z:54:VAL:HG22	2.19	0.42
1:A:1006:C:C2	1:A:1138:G:N2	2.87	0.42
1:A:1493:C:C4	1:A:2210:G:O2'	2.73	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1541:U:C3'	1:A:1542:G:O3'	2.65	0.42
18:R:77:ALA:C	18:R:79:VAL:N	2.73	0.42
1:A:2777:G:H3'	1:A:2777:G:H8	1.85	0.42
1:A:102:G:H5''	1:A:102:G:C8	2.55	0.42
6:F:129:GLY:HA3	6:F:163:ALA:HB3	2.01	0.42
1:A:1494:A:HO2'	1:A:1495:A:P	2.42	0.42
22:V:6:LYS:HG3	22:V:8:TYR:CZ	2.54	0.42
1:A:55:G:H2'	1:A:56:A:C8	2.54	0.42
31:5:29:LYS:HG2	31:5:29:LYS:O	2.19	0.42
1:A:2820:A:O4'	14:N:5:LYS:HG3	2.18	0.42
1:A:1399:C:O2'	1:A:1400:G:H5'	2.17	0.42
4:D:197:ILE:HD11	4:D:199:ARG:HE	1.84	0.42
1:A:1414:G:C4	1:A:1415:U:C5	3.07	0.42
1:A:2096:U:H2'	1:A:2097:C:C6	2.55	0.42
6:F:178:PHE:HA	6:F:179:PRO:HD3	1.79	0.42
1:A:2212:A:HO2'	1:A:2215:G:C1'	2.32	0.42
1:A:1285:G:C5	1:A:1329:U:C4	3.07	0.42
4:D:17:ASP:OD1	4:D:18:ASP:N	2.53	0.42
28:2:9:LYS:HD3	28:2:9:LYS:HA	1.88	0.42
22:V:48:PHE:CE2	22:V:71:VAL:HG21	2.55	0.42
1:A:947:G:H2'	1:A:948:G:C5'	2.43	0.42
1:A:2516:G:C6	1:A:2517:C:C4	3.07	0.42
8:H:82:ARG:HB3	8:H:89:TYR:CG	2.55	0.42
1:A:646:A:H2'	1:A:647:G:O4'	2.20	0.42
4:D:4:ILE:HG13	4:D:28:ALA:HB1	2.01	0.42
1:A:2850:A:H2'	1:A:2851:A:O4'	2.19	0.42
1:A:1265:A:H3'	28:2:19:ARG:NH1	2.35	0.42
1:A:1495:A:N3	1:A:1496:A:C2	2.87	0.42
1:A:2196:C:O2'	1:A:2197:U:H5'	2.19	0.42
13:M:68:ILE:HD13	13:M:103:MET:HG3	2.02	0.42
1:A:1324:G:H4'	1:A:1616:A:C2	2.54	0.42
4:D:11:MET:CB	4:D:24:THR:HA	2.49	0.42
1:A:1546:A:H2'	1:A:154(B):C:O4'	2.20	0.42
1:A:1759:A:C8	1:A:2696:U:H1'	2.54	0.42
1:A:1828:G:OP2	3:C:239:ARG:NH2	2.53	0.42
13:M:75:THR:HG21	13:M:85:LYS:HZ2	1.82	0.42
20:T:30:VAL:HG12	20:T:31:HIS:H	1.84	0.42
13:M:141:GLN:NE2	22:V:72:ARG:HG2	2.35	0.42
1:A:1310:G:C3'	1:A:1311:G:H5''	2.49	0.42
1:A:1310:G:H2'	1:A:1311:G:H5''	2.00	0.42
4:D:101:ARG:HB3	4:D:169:ASN:HD22	1.83	0.42
1:A:778:G:C5	1:A:779:U:C4	3.07	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:94:G:N3	25:Y:47:ASN:ND2	2.67	0.42
12:L:9:ASN:N	12:L:10:PRO:CD	2.81	0.42
1:A:85:G:H5''	1:A:85:G:C8	2.50	0.42
1:A:840:C:H2'	1:A:841:A:C8	2.54	0.42
6:F:115:ARG:CD	6:F:115:ARG:H	2.30	0.42
3:C:126:GLN:HG2	3:C:127:VAL:H	1.85	0.42
1:A:2749:A:H1'	7:G:63:SER:OG	2.20	0.42
1:A:297:C:H2'	1:A:298:G:O4'	2.20	0.42
4:D:107:THR:O	4:D:190:GLY:HA2	2.20	0.42
1:A:2618:G:C6	1:A:2619:C:C4	3.07	0.42
1:A:2070:G:H2'	1:A:2071:A:O4'	2.19	0.42
1:A:648:G:O4'	1:A:2351:G:H5''	2.20	0.42
1:A:1918:A:O2'	1:A:1920:C:N4	2.53	0.42
1:A:2870:C:H2'	1:A:2871:C:O4'	2.20	0.42
13:M:62:GLY:HA2	22:V:116:VAL:HG22	2.02	0.42
1:A:2322:A:H3'	1:A:2323:G:H8	1.83	0.42
11:K:19:ILE:HD13	11:K:19:ILE:H	1.84	0.42
12:L:86:LYS:HG3	12:L:87:ASP:N	2.34	0.42
3:C:32:SER:HA	3:C:36:PRO:HG2	2.01	0.42
6:F:111:LEU:N	6:F:112:PRO:CD	2.83	0.42
8:H:133:HIS:HA	8:H:134:PRO:HD3	1.90	0.42
8:H:88:ILE:HG13	8:H:144:VAL:HG11	2.02	0.42
12:L:30:THR:CG2	12:L:31:ALA:N	2.80	0.42
14:N:100:LEU:HD21	14:N:113:LEU:HB2	2.01	0.42
1:A:839:U:H2'	1:A:840:C:H6	1.82	0.42
19:S:4:LYS:HA	19:S:106:ILE:HG22	2.01	0.42
1:A:919:G:H2'	1:A:920:G:H8	1.85	0.42
1:A:628:G:C6	1:A:636:G:C2	3.07	0.42
3:C:166:GLN:HB2	3:C:174:ILE:HG22	2.00	0.42
1:A:1040:C:H2'	1:A:1041:C:H6	1.85	0.42
1:A:433:C:O2'	1:A:434:U:H5'	2.19	0.42
1:A:1695:G:N2	1:A:1696:G:C8	2.88	0.42
17:Q:57:PHE:HB3	17:Q:61:TRP:CZ2	2.55	0.42
19:S:30:GLU:HA	19:S:33:ARG:HD2	2.01	0.42
1:A:191:A:H2'	1:A:192:C:C6	2.55	0.42
1:A:460:A:C6	1:A:470:A:C8	3.08	0.42
2:B:3:C:H2'	2:B:4:C:C6	2.55	0.42
28:2:13:LYS:HB3	28:2:13:LYS:HE2	1.85	0.42
1:A:2444:G:C6	1:A:2445:G:C5	3.07	0.42
12:L:51:PHE:HB3	12:L:52:GLU:H	1.76	0.42
3:C:222:ARG:HH12	3:C:239:ARG:CZ	2.33	0.42
1:A:114(B):A:C2	1:A:1144:G:C8	3.08	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:Y:2:LYS:HD3	25:Y:2:LYS:H	1.84	0.42
13:M:81:VAL:HG12	13:M:82:ARG:CG	2.41	0.42
1:A:573:G:O2'	1:A:574:C:H3'	2.20	0.42
21:U:27:VAL:O	21:U:27:VAL:HG23	2.19	0.42
4:D:171:GLU:HG2	4:D:185:LYS:CG	2.50	0.42
1:A:2468:G:HO2'	1:A:2469:A:P	2.41	0.42
1:A:479:A:H4'	1:A:480:A:O5'	2.20	0.42
1:A:1349:A:N6	1:A:1598:C:H42	2.17	0.42
1:A:2477:C:HO2'	1:A:2478:A:P	2.43	0.42
1:A:2341:G:H2'	1:A:2342:C:C6	2.54	0.42
23:W:82:ARG:HA	23:W:83:PRO:HD2	1.91	0.42
3:C:261:LYS:HB2	3:C:261:LYS:NZ	2.35	0.42
7:G:144:VAL:O	7:G:148:ILE:HG12	2.20	0.42
1:A:335:C:C2	1:A:336:C:C5	3.08	0.42
10:J:35:ARG:O	10:J:73:ASP:HB3	2.20	0.42
1:A:173:G:H2'	1:A:174:C:C6	2.54	0.42
30:4:47:ARG:O	30:4:48:LYS:HB2	2.19	0.42
1:A:924:C:H2'	1:A:925:C:C6	2.54	0.42
17:Q:92:ARG:CD	17:Q:95:LEU:H	2.32	0.42
17:Q:92:ARG:HH21	18:R:11:GLN:H	1.67	0.42
20:T:26:TYR:CE1	20:T:83:VAL:HG21	2.55	0.42
1:A:2247:A:H2'	1:A:2248:C:H6	1.83	0.42
1:A:2262:U:H4'	1:A:2328:A:C2	2.55	0.42
3:C:35:LYS:CB	3:C:36:PRO:HD3	2.50	0.42
3:C:35:LYS:HG3	3:C:104:TYR:CD2	2.55	0.42
3:C:76:PRO:HA	3:C:118:VAL:HG23	2.02	0.42
1:A:2809:A:N6	1:A:2892:A:C8	2.88	0.42
24:X:37:ILE:HG23	24:X:38:SER:N	2.35	0.42
25:Y:21:LEU:CD2	25:Y:22:GLU:HG3	2.50	0.42
1:A:1862:G:H2'	1:A:1863:G:C8	2.53	0.42
13:M:74:TYR:O	13:M:89:ASN:N	2.52	0.42
3:C:105:ILE:HG12	3:C:106:ILE:HD12	2.02	0.42
11:K:17:ARG:HB2	11:K:45:GLU:HG3	2.01	0.42
17:Q:59:ARG:O	17:Q:63:VAL:HG23	2.20	0.42
1:A:1726:G:C2	1:A:1735:U:O2	2.73	0.42
22:V:157:LEU:N	22:V:157:LEU:HD12	2.34	0.42
1:A:1140:C:OP1	10:J:46:LEU:HB3	2.20	0.42
31:5:33:ASN:ND2	31:5:34:TRP:N	2.67	0.42
27:1:50:THR:CG2	27:1:51:TYR:H	2.14	0.42
20:T:31:HIS:HA	20:T:32:PRO:HD3	1.97	0.42
15:O:49:VAL:HG13	15:O:76:LYS:HB2	2.02	0.42
3:C:197:GLY:O	3:C:198:ASN:C	2.58	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:94:LEU:HB2	3:C:104:TYR:CE1	2.47	0.42
1:A:2028:U:O4	1:A:2033:A:OP1	2.38	0.42
6:F:161:THR:HG21	6:F:172:LEU:CD2	2.50	0.42
1:A:907:U:O2'	13:M:101:ARG:NH2	2.49	0.42
1:A:595:C:H2'	1:A:596:G:O4'	2.20	0.42
1:A:1602:U:H3'	1:A:1603:A:C5'	2.50	0.42
1:A:56:A:C2	1:A:115:C:O2	2.73	0.42
8:H:29:TYR:C	8:H:32:PRO:HD2	2.40	0.42
1:A:912:C:C2	1:A:913:U:C5	3.08	0.42
1:A:2886:G:H2'	1:A:2887:U:H6	1.84	0.42
19:S:107:LEU:N	19:S:107:LEU:CD1	2.83	0.42
22:V:40:ASP:OD1	22:V:42:VAL:HG12	2.19	0.42
6:F:34:LEU:HD21	6:F:159:VAL:HG21	2.02	0.42
1:A:699:A:H4'	1:A:1634:A:N7	2.34	0.42
16:P:131:ALA:O	16:P:135:VAL:HG23	2.20	0.42
1:A:284:U:H2'	1:A:285:C:C6	2.55	0.42
7:G:78:GLY:HA2	7:G:83:TYR:CE1	2.54	0.42
30:4:18:PHE:CD2	30:4:18:PHE:C	2.93	0.42
1:A:2284:C:O5'	1:A:2284:C:H6	2.03	0.42
15:O:28:VAL:HG13	15:O:35:ILE:HD11	2.02	0.41
27:1:42:CYS:HA	27:1:59:VAL:C	2.41	0.41
1:A:270(K):G:H2'	1:A:270(L):C:O4'	2.20	0.41
3:C:35:LYS:HZ1	3:C:104:TYR:H	1.68	0.41
4:D:116:VAL:HG13	4:D:117:MET:N	2.34	0.41
16:P:61:PHE:CZ	16:P:76:PHE:HB2	2.54	0.41
1:A:1543:A:C8	1:A:1543:A:H3'	2.55	0.41
1:A:65:C:O2'	1:A:66:C:H5'	2.20	0.41
3:C:235:GLY:O	3:C:237:GLU:N	2.48	0.41
1:A:363(A):G:H2'	1:A:363(B):A:C8	2.54	0.41
16:P:128:GLU:O	16:P:132:LYS:HG3	2.19	0.41
6:F:114:ILE:HB	6:F:117:PHE:HB2	2.02	0.41
17:Q:28:ARG:CG	17:Q:38:THR:OG1	2.68	0.41
19:S:12:ILE:HD12	19:S:46:PHE:HE2	1.85	0.41
1:A:2230:G:H1'	24:X:45:ASN:HB2	2.02	0.41
1:A:2846:G:C5	1:A:2847:U:C5	3.08	0.41
1:A:1284:A:H2'	1:A:1285:G:O4'	2.19	0.41
13:M:121:ALA:HA	13:M:124:LYS:HG3	2.02	0.41
1:A:725:G:C6	1:A:726:G:N1	2.88	0.41
11:K:90:GLN:O	11:K:91:LEU:HB2	2.20	0.41
21:U:95:LYS:HB3	21:U:99:CYS:O	2.19	0.41
24:X:11:ARG:HH11	24:X:60:PHE:HA	1.85	0.41
3:C:27:THR:CG2	3:C:83:GLU:HG2	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:14:SER:HA	14:N:17:ARG:HG2	2.02	0.41
1:A:342:G:O2'	1:A:343:C:H5''	2.20	0.41
1:A:1518:C:O2'	1:A:1519:G:H5'	2.20	0.41
22:V:179:ASP:CG	22:V:180:VAL:N	2.74	0.41
22:V:24:LEU:HD21	22:V:86:VAL:HG23	2.01	0.41
1:A:1388:G:N3	1:A:1389:G:C8	2.89	0.41
1:A:2849:U:H4'	1:A:2868:A:C2	2.55	0.41
1:A:2809:A:N1	1:A:2892:A:C4	2.88	0.41
1:A:828:U:C5	1:A:829:A:N6	2.88	0.41
22:V:9:TYR:O	22:V:38:TYR:HE2	2.03	0.41
1:A:1926:U:O2	1:A:1929:G:C2	2.73	0.41
1:A:1465:G:C2	1:A:1466:G:C8	3.08	0.41
15:O:102:ALA:HA	15:O:105:ALA:HB3	2.02	0.41
1:A:2194:G:H2'	1:A:2195:C:H6	1.85	0.41
1:A:2304:G:H1	1:A:2312:U:H3	1.67	0.41
1:A:1688:U:O2	1:A:1700:A:H8	2.03	0.41
1:A:2518:A:H5'	1:A:2518:A:C8	2.55	0.41
1:A:1502:C:H6	1:A:1502:C:O5'	2.04	0.41
1:A:2057:A:H2'	1:A:2058:A:O4'	2.20	0.41
20:T:24:GLY:HA3	20:T:82:GLN:HE22	1.85	0.41
1:A:125:G:H5'	30:4:19:ARG:CG	2.50	0.41
6:F:53:LEU:HD13	6:F:88:ILE:HG12	2.02	0.41
1:A:558:G:P	10:J:134:PRO:HD2	2.61	0.41
10:J:90:LEU:CD1	10:J:90:LEU:H	2.30	0.41
22:V:102:LEU:HD21	22:V:124:ILE:HD11	2.01	0.41
1:A:588:U:H2'	1:A:589:C:H6	1.81	0.41
1:A:2686:G:C5	1:A:2687:U:C4	3.08	0.41
1:A:1939:U:OP1	1:A:2604:U:O2'	2.36	0.41
30:4:21:ARG:CB	30:4:31:LEU:HD21	2.50	0.41
24:X:23:LYS:O	24:X:23:LYS:HG3	2.20	0.41
16:P:64:ARG:HA	16:P:72:VAL:O	2.20	0.41
1:A:486:C:H4'	19:S:60:ASN:ND2	2.35	0.41
1:A:1028:A:H61	1:A:1125:G:H2'	1.84	0.41
23:W:36:ILE:HG23	23:W:58:THR:HG23	2.03	0.41
1:A:1464:C:O2	1:A:1528:A:H2	2.03	0.41
1:A:1682:G:H2'	1:A:1683:C:C6	2.55	0.41
1:A:2718:G:H2'	1:A:2719:G:C8	2.55	0.41
1:A:1328:G:H2'	1:A:1330:C:C5	2.55	0.41
1:A:1998:G:H2'	1:A:1999:C:C6	2.56	0.41
1:A:396:G:H1'	24:X:42:GLN:OE1	2.20	0.41
12:L:36:LYS:O	12:L:38:GLN:HG2	2.20	0.41
22:V:97:GLU:O	22:V:98:MET:HB3	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:572:A:H2'	1:A:573:G:O4'	2.20	0.41
1:A:2542:A:H8	1:A:2544:G:O6	2.03	0.41
15:O:31:SER:HB3	15:O:34:HIS:H	1.84	0.41
6:F:122:PRO:O	6:F:125:PHE:HD1	2.03	0.41
24:X:84:GLY:O	24:X:85:LEU:C	2.58	0.41
6:F:115:ARG:HD2	6:F:115:ARG:N	2.35	0.41
1:A:2050:C:H1'	4:D:156:MET:CE	2.49	0.41
1:A:1414:G:C5	1:A:1415:U:C5	3.08	0.41
1:A:1396:U:O2	1:A:1396:U:H2'	2.18	0.41
13:M:18:LYS:HB3	13:M:19:GLY:H	1.62	0.41
1:A:1214:A:H2'	1:A:1215:G:O4'	2.20	0.41
1:A:2029:G:H2'	1:A:2031:A:OP1	2.20	0.41
1:A:1022:G:C5	1:A:1140:C:N4	2.88	0.41
6:F:5:LEU:HA	6:F:5:LEU:HD23	1.84	0.41
20:T:30:VAL:HG21	20:T:79:ALA:CB	2.50	0.41
28:2:44:THR:HG22	28:2:45:VAL:N	2.36	0.41
15:O:65:VAL:O	15:O:69:VAL:HG12	2.20	0.41
3:C:136:ILE:HA	3:C:137:PRO:HD3	1.96	0.41
1:A:971:C:H2'	1:A:972:G:H5'	2.03	0.41
3:C:61:LEU:HA	3:C:61:LEU:HD12	1.84	0.41
1:A:330:A:O2'	1:A:331:A:H8	2.04	0.41
21:U:17:SER:CB	21:U:71:LYS:HD2	2.50	0.41
1:A:1543:A:H8	1:A:1543:A:H3'	1.85	0.41
6:F:171:ALA:O	6:F:175:LEU:HG	2.20	0.41
5:E:155:LEU:HA	5:E:174:VAL:HG23	2.03	0.41
1:A:1612:C:O3'	30:4:5:TRP:HD1	2.03	0.41
7:G:105:LEU:HD22	7:G:113:VAL:HB	2.02	0.41
16:P:100:TYR:C	16:P:102:ILE:N	2.73	0.41
1:A:1951:U:O2	1:A:1953:A:H8	2.02	0.41
1:A:1276:A:H5''	1:A:1276:A:H8	1.85	0.41
3:C:108:PRO:HG3	3:C:143:HIS:NE2	2.35	0.41
13:M:104:PHE:HE1	13:M:125:LEU:HD11	1.84	0.41
1:A:302:C:H2'	1:A:303:U:C6	2.56	0.41
1:A:302:C:O2'	1:A:303:U:H5'	2.21	0.41
1:A:1494:A:H4'	1:A:1495:A:OP1	2.21	0.41
10:J:151:HIS:CD2	10:J:152:PRO:O	2.73	0.41
22:V:38:TYR:CD1	22:V:38:TYR:O	2.73	0.41
1:A:719:C:H2'	1:A:720:C:C6	2.53	0.41
1:A:1170:G:N2	1:A:1180:C:C2	2.89	0.41
1:A:30:G:C5	1:A:31:C:C4	3.09	0.41
1:A:1109:C:H2'	1:A:1110:G:O4'	2.20	0.41
18:R:22:VAL:CG1	18:R:23:GLU:H	2.33	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2422:A:C5	1:A:2424:C:C4	3.09	0.41
1:A:2416:C:OP1	12:L:64:LYS:O	2.39	0.41
24:X:11:ARG:HG3	24:X:62:VAL:HA	2.02	0.41
8:H:82:ARG:C	8:H:89:TYR:HB2	2.41	0.41
2:B:72:G:N2	2:B:103:U:C5	2.88	0.41
6:F:32:PRO:CB	6:F:172:LEU:HD22	2.49	0.41
6:F:15:VAL:HG22	6:F:175:LEU:HB3	2.03	0.41
29:3:34:LEU:HD13	29:3:34:LEU:H	1.86	0.41
1:A:477:A:H2'	1:A:478:A:C8	2.54	0.41
1:A:2777:G:C4'	1:A:2778:A:H5'	2.50	0.41
13:M:127:ILE:HG22	13:M:128:LYS:N	2.35	0.41
5:E:150:GLY:HA2	5:E:172:TRP:CD2	2.55	0.41
1:A:1952:A:C2	11:K:22:ILE:HG23	2.56	0.41
6:F:128:ARG:HH21	6:F:130:ASN:ND2	2.17	0.41
13:M:26:TYR:O	13:M:26:TYR:CD1	2.73	0.41
1:A:2257:U:O2'	1:A:2258:C:H5'	2.21	0.41
3:C:37:LEU:HD12	3:C:38:LYS:N	2.36	0.41
7:G:83:TYR:CZ	7:G:138:LYS:HG3	2.55	0.41
1:A:1232:G:H2'	1:A:1233:C:H6	1.85	0.41
1:A:979:G:H3'	1:A:980:A:H5''	2.02	0.41
5:E:6:MET:HB3	5:E:7:TYR:H	1.55	0.41
1:A:1818:U:H2'	3:C:157:ARG:HG3	2.02	0.41
1:A:1676:A:N6	1:A:1677:A:C6	2.88	0.41
14:N:99:LYS:HB3	14:N:99:LYS:HE3	1.86	0.41
21:U:97:ARG:O	21:U:97:ARG:HG2	2.21	0.41
1:A:956:G:H22	1:A:959:A:H3'	1.85	0.41
19:S:24:ILE:CG2	19:S:36:LEU:HD21	2.39	0.41
1:A:846:C:H4'	1:A:847:U:O5'	2.20	0.41
1:A:773:U:C5'	3:C:47:GLY:HA3	2.51	0.41
1:A:310:A:OP1	21:U:17:SER:O	2.38	0.41
6:F:13:GLU:O	6:F:14:GLU:HB2	2.19	0.41
2:B:106:G:C5	2:B:107:U:C5	3.08	0.41
12:L:7:ARG:O	12:L:10:PRO:HD3	2.21	0.41
1:A:426:C:C2	1:A:427:U:C6	3.09	0.41
5:E:12:LEU:HD13	5:E:17:ARG:HG2	2.03	0.41
1:A:1496:A:C8	1:A:1498:C:N3	2.88	0.41
16:P:3:ARG:HD2	16:P:6:LEU:HD23	2.03	0.41
1:A:2296:U:O4	15:O:13:ARG:NH2	2.50	0.41
1:A:1050:A:H2'	1:A:1051:G:C8	2.55	0.41
3:C:105:ILE:HG13	3:C:106:ILE:HD12	2.02	0.41
1:A:1798:U:C5'	3:C:259:THR:O	2.69	0.41
1:A:335:C:H2'	1:A:336:C:C6	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1676:A:H2'	1:A:1677:A:O4'	2.20	0.41
1:A:1248:G:C5	17:Q:3:ARG:HB2	2.55	0.41
1:A:1648:C:H2'	1:A:1649:G:O5'	2.20	0.41
6:F:66:GLN:HG2	6:F:67:LYS:N	2.26	0.41
6:F:41:GLN:HB3	6:F:43:LEU:HD13	2.03	0.41
31:5:13:ARG:HG3	31:5:14:VAL:HG23	2.02	0.41
15:O:17:ARG:HG2	15:O:18:ILE:HD13	2.02	0.41
1:A:1447:G:N3	1:A:1545:A:H2	2.18	0.41
1:A:861:A:C2	1:A:917:A:C4	3.09	0.41
19:S:14:PRO:O	19:S:18:ARG:HG3	2.21	0.41
13:M:20:ALA:O	13:M:21:THR:O	2.39	0.41
1:A:1257:C:H4'	5:E:83:PHE:CD2	2.56	0.41
1:A:2306:C:H4'	6:F:136:ARG:NH2	2.35	0.41
1:A:161:U:O2	1:A:165:U:O4	2.39	0.41
1:A:288:C:O2'	1:A:289:A:H5'	2.20	0.41
4:D:76:ARG:HG2	4:D:77:ILE:HG13	2.03	0.41
1:A:1271:G:O3'	1:A:1272:A:H4'	2.21	0.41
13:M:34:LEU:HD12	13:M:130:LYS:O	2.21	0.41
1:A:489:G:C5	1:A:1284:A:C2	3.09	0.41
1:A:1696:G:C6	1:A:1697:G:C4	3.08	0.41
1:A:1024:G:H8	1:A:1024:G:O5'	2.03	0.41
2:B:116:G:H4'	15:O:55:ALA:O	2.21	0.41
22:V:30:ASN:OD1	22:V:33:LEU:N	2.53	0.41
2:B:33:G:O2'	2:B:34:U:H5'	2.20	0.41
2:B:7:G:H5''	15:O:29:PHE:CD2	2.55	0.41
12:L:47:ASP:HB3	12:L:48:PRO:HA	2.01	0.41
31:5:59:LYS:HA	31:5:62:LEU:HD11	2.03	0.41
1:A:593:G:C6	1:A:594:U:C4	3.09	0.41
18:R:4:ILE:HG22	18:R:5:VAL:N	2.36	0.41
1:A:2247:A:O2'	1:A:2248:C:H5'	2.20	0.41
1:A:827:U:H2'	1:A:2068:U:C2	2.56	0.41
6:F:5:LEU:HD21	27:1:50:THR:CG2	2.50	0.41
1:A:71:A:H4'	1:A:72:U:H5''	2.03	0.41
8:H:5:LEU:H	8:H:5:LEU:CD2	2.18	0.41
1:A:2712:U:O2'	1:A:2713:A:H5'	2.21	0.41
1:A:270(H):C:H2'	1:A:270(I):C:C6	2.56	0.41
14:N:4:LEU:CG	14:N:4:LEU:O	2.66	0.41
30:4:8:ASN:HD21	30:4:10:ARG:HB3	1.86	0.41
1:A:2024:G:H2'	1:A:2025:C:H6	1.86	0.41
3:C:270:ILE:C	3:C:271:ILE:HG13	2.40	0.41
1:A:1006:C:H1'	10:J:129:MET:HG2	2.02	0.41
1:A:2636:U:H2'	1:A:2637:U:H6	1.86	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:57:LEU:HA	10:J:57:LEU:HD13	1.73	0.41
21:U:17:SER:HB2	21:U:71:LYS:HD2	2.02	0.41
6:F:18:GLU:HB3	6:F:175:LEU:HD13	2.03	0.41
5:E:181:LEU:HD23	5:E:181:LEU:HA	1.93	0.41
13:M:24:GLY:HA2	13:M:100:GLY:C	2.41	0.41
1:A:468:G:N7	30:4:39:ARG:NH2	2.69	0.41
2:B:74:U:H2'	2:B:75:G:H8	1.83	0.41
1:A:1332:G:N2	1:A:1609:A:O2'	2.54	0.41
3:C:235:GLY:C	3:C:237:GLU:H	2.24	0.41
24:X:37:ILE:HG22	24:X:38:SER:N	2.36	0.41
1:A:2476:A:N1	1:A:2477:C:C4	2.88	0.41
16:P:118:ARG:HA	16:P:121:ILE:HD12	2.03	0.41
5:E:40:GLN:O	5:E:43:LYS:HG2	2.21	0.41
14:N:104:ARG:CB	14:N:104:ARG:HH11	2.33	0.41
14:N:116:LEU:HA	14:N:116:LEU:HD23	1.79	0.41
14:N:94:TYR:O	14:N:117:VAL:HG12	2.20	0.41
1:A:1790:C:H5''	1:A:1791:A:P	2.61	0.41
18:R:17:GLY:HA2	18:R:96:ILE:O	2.21	0.41
19:S:22:ASP:HA	19:S:25:ARG:NH1	2.36	0.41
1:A:2817:G:H21	1:A:2836:U:C1'	2.33	0.41
1:A:2836:U:H2'	1:A:2837:G:H8	1.86	0.41
1:A:1748:G:H2'	1:A:1749:A:H8	1.84	0.41
1:A:2765:A:H5'	1:A:2766:G:OP2	2.21	0.41
1:A:2658:C:H4'	7:G:158:HIS:CE1	2.56	0.41
3:C:140:THR:HG22	3:C:141:VAL:N	2.36	0.41
1:A:924:C:H2'	1:A:925:C:H6	1.86	0.41
1:A:699:A:H2'	1:A:700:G:O4'	2.20	0.41
21:U:34:LYS:HE2	21:U:34:LYS:HB3	1.80	0.41
22:V:43:GLU:O	22:V:47:VAL:HG23	2.21	0.41
1:A:2709:G:O2'	1:A:2710:C:H5'	2.20	0.41
1:A:26:G:C6	1:A:27:G:N1	2.89	0.41
5:E:14:PRO:HD3	5:E:128:ALA:HB2	2.02	0.41
1:A:583:G:OP2	17:Q:10:ARG:HD2	2.21	0.41
1:A:997:G:O2'	1:A:998:C:H5'	2.21	0.41
1:A:2019:A:H5''	17:Q:27:LEU:HD12	2.03	0.41
1:A:1221:C:H2'	1:A:122(A):C:C6	2.56	0.41
1:A:447:A:C5	1:A:473:G:C5	3.09	0.41
22:V:155:LEU:HD21	22:V:171:ILE:HG13	2.02	0.41
26:Z:37:LEU:HA	26:Z:37:LEU:HD23	1.95	0.41
4:D:141:ILE:HG13	4:D:141:ILE:O	2.21	0.41
18:R:40:LEU:C	18:R:45:THR:HB	2.41	0.41
6:F:60:LEU:HD12	6:F:68:PRO:HB3	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:O:66:ALA:HA	15:O:69:VAL:HG12	2.03	0.41
1:A:948:G:C5'	1:A:948:G:C8	3.00	0.41
14:N:14:SER:O	14:N:15:SER:C	2.59	0.41
6:F:87:PRO:O	6:F:88:ILE:HB	2.21	0.41
4:D:181:LEU:HA	4:D:181:LEU:HD13	1.70	0.41
1:A:1334:G:C6	1:A:1335:U:C4	3.09	0.41
1:A:643:A:O2'	1:A:644:A:H5'	2.21	0.41
1:A:1778:U:H2'	1:A:1784:A:H62	1.83	0.41
14:N:100:LEU:HD23	14:N:112:ALA:HA	2.02	0.41
15:O:61:ASN:O	15:O:62:LYS:C	2.59	0.41
5:E:111:ALA:HB2	5:E:206:ILE:HD12	2.03	0.41
13:M:132:VAL:HG11	22:V:81:ARG:NH1	2.36	0.41
1:A:1647:G:H3'	1:A:1647:G:P	2.61	0.41
1:A:2013:A:H4'	19:S:96:ILE:HD12	2.03	0.41
6:F:16:ARG:N	6:F:17:PRO:HD2	2.36	0.41
1:A:1198:U:H2'	1:A:1199:U:C6	2.56	0.41
1:A:1229:G:H2'	1:A:1230:C:H6	1.86	0.41
1:A:945:A:O2'	1:A:946:G:H4'	2.21	0.41
5:E:24:LEU:HA	5:E:25:PRO:HD3	1.86	0.41
1:A:2459:A:C4	1:A:2460:U:C6	3.09	0.41
1:A:540:G:C4	1:A:541:C:C5	3.09	0.41
1:A:1368:G:C2	1:A:1369:G:C8	3.09	0.41
24:X:70:VAL:O	24:X:74:VAL:HG23	2.20	0.41
1:A:885:C:O5'	1:A:885:C:H6	2.04	0.41
5:E:9:ILE:H	5:E:9:ILE:HD13	1.86	0.41
16:P:137:LYS:HD2	16:P:137:LYS:N	2.36	0.41
1:A:941:A:H4'	12:L:35:HIS:CD2	2.56	0.40
21:U:30:VAL:HG13	21:U:37:VAL:HG12	2.03	0.40
3:C:133:LEU:HB3	3:C:173:VAL:HG11	2.02	0.40
1:A:2343:C:O2'	1:A:2344:U:H5'	2.21	0.40
11:K:106:LEU:N	11:K:106:LEU:HD12	2.36	0.40
3:C:118:VAL:HG13	3:C:119:ALA:N	2.37	0.40
13:M:60:ARG:HB2	13:M:60:ARG:HH11	1.86	0.40
2:B:73:A:C4	2:B:104:A:C2	3.09	0.40
12:L:21:ARG:H	12:L:21:ARG:HG2	1.73	0.40
3:C:79:VAL:HG11	3:C:111:LEU:CD1	2.51	0.40
7:G:104:GLU:HA	7:G:113:VAL:O	2.22	0.40
1:A:784:A:H5'	1:A:785:G:OP1	2.20	0.40
1:A:524:U:O2'	1:A:554:U:H4'	2.21	0.40
15:O:38:GLN:HB3	15:O:47:THR:HG21	2.03	0.40
8:H:66:GLU:O	8:H:70:GLU:HG2	2.20	0.40
1:A:2626:C:H2'	1:A:2627:G:O4'	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:47:GLY:O	5:E:94:PRO:HB3	2.21	0.40
18:R:89:GLN:HA	18:R:90:PRO:HD3	1.80	0.40
1:A:2642:G:O2'	1:A:2643:G:H5'	2.21	0.40
5:E:39:TRP:CD1	5:E:101:LEU:HB2	2.57	0.40
1:A:2762:G:O2'	1:A:2763:G:H5'	2.21	0.40
1:A:386:G:H4'	1:A:387:U:OP2	2.21	0.40
1:A:1532:C:O5'	1:A:1532:C:H6	2.04	0.40
18:R:6:LYS:HG3	18:R:6:LYS:O	2.21	0.40
1:A:2685:G:N3	1:A:2725:A:C2	2.89	0.40
21:U:97:ARG:HD3	21:U:98:VAL:HG12	2.04	0.40
13:M:81:VAL:O	13:M:82:ARG:HD3	2.21	0.40
24:X:10:LYS:O	24:X:11:ARG:CG	2.67	0.40
7:G:86:GLU:HB3	7:G:132:ARG:NH1	2.37	0.40
3:C:131:LEU:HD12	3:C:136:ILE:HG12	2.02	0.40
22:V:144:LEU:HD22	22:V:144:LEU:N	2.36	0.40
1:A:388:G:C4	1:A:390:A:C6	3.10	0.40
12:L:126:VAL:HG22	12:L:145:PRO:HB2	2.02	0.40
22:V:161:VAL:HG12	22:V:162:GLU:N	2.35	0.40
1:A:1639:U:C2'	1:A:1640:C:H5''	2.51	0.40
1:A:2293:C:H4'	15:O:93:LYS:HZ2	1.87	0.40
22:V:118:GLN:HB2	22:V:173:ALA:C	2.42	0.40
1:A:1289:C:H2'	1:A:1290:C:C6	2.55	0.40
1:A:451:C:N4	1:A:453:C:H3'	2.36	0.40
1:A:1270:C:H5''	1:A:1271:G:C5'	2.52	0.40
1:A:570:G:H2'	1:A:2030:A:C5	2.55	0.40
13:M:67:ARG:HD2	13:M:105:GLU:OE2	2.21	0.40
20:T:41:ASN:HD22	20:T:41:ASN:N	2.19	0.40
24:X:82:LEU:HD12	24:X:82:LEU:N	2.36	0.40
17:Q:83:LEU:HD12	17:Q:83:LEU:N	2.36	0.40
1:A:2246:G:H2'	1:A:2247:A:H8	1.87	0.40
4:D:184:VAL:HG12	4:D:185:LYS:H	1.86	0.40
1:A:1509:A:H4'	1:A:1510:A:N9	2.36	0.40
2:B:70:C:H2'	2:B:71:C:C6	2.52	0.40
1:A:643:A:OP1	29:3:42:TRP:NE1	2.54	0.40
6:F:7:LEU:HA	6:F:10:LYS:HD2	2.03	0.40
19:S:18:ARG:NH1	19:S:76:VAL:HG13	2.36	0.40
7:G:103:LEU:HG	7:G:105:LEU:CD1	2.51	0.40
10:J:83:ILE:HG22	10:J:84:ARG:O	2.21	0.40
1:A:656:G:H8	1:A:656:G:O5'	2.05	0.40
1:A:830:G:C4	1:A:2448:A:C6	3.09	0.40
22:V:127:LYS:HB3	22:V:162:GLU:CG	2.51	0.40
13:M:77:LYS:HA	13:M:78:PRO:HD3	1.73	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:175:LEU:HA	3:C:175:LEU:HD23	1.95	0.40
1:A:327:G:C2	1:A:328:U:C2	3.10	0.40
1:A:2386:C:H4'	23:W:55:ARG:O	2.21	0.40
7:G:117:PRO:HA	7:G:118:PRO:HD2	1.93	0.40
29:3:25:LYS:HD3	31:5:34:TRP:CH2	2.56	0.40
25:Y:1:MET:SD	25:Y:5:GLU:OE2	2.80	0.40
1:A:270(I):C:O2'	1:A:270(J):G:H5'	2.22	0.40
22:V:71:VAL:HG11	22:V:74:VAL:HG23	2.02	0.40
12:L:57:THR:C	12:L:59:LEU:N	2.75	0.40
1:A:1408:C:N3	1:A:1595:G:C2	2.89	0.40
1:A:1211:U:H4'	1:A:1212:G:OP2	2.22	0.40
11:K:71:ARG:NH2	11:K:77:ILE:HG21	2.37	0.40
8:H:83:ALA:N	8:H:89:TYR:HD1	2.20	0.40
1:A:2484:G:H2'	1:A:2485:G:H8	1.86	0.40
8:H:130:TYR:HD2	8:H:132:PRO:HG3	1.83	0.40
1:A:443:A:H1'	1:A:1201:C:O4'	2.21	0.40
10:J:117:HIS:HA	10:J:118:PRO:HD2	1.98	0.40
24:X:35:THR:HB	24:X:36:GLY:H	1.54	0.40
16:P:3:ARG:NH1	16:P:6:LEU:HD23	2.37	0.40
1:A:2230:G:H1'	24:X:45:ASN:CB	2.51	0.40
5:E:72:ARG:O	5:E:73:ALA:O	2.39	0.40
1:A:1401:G:H2'	1:A:1402:C:C6	2.57	0.40
8:H:136:VAL:N	8:H:137:PRO:HD3	2.37	0.40
1:A:2338:G:C2	1:A:2339:G:C8	3.10	0.40
1:A:991:C:C5	1:A:1185:C:C4	3.09	0.40
1:A:2065:C:H2'	1:A:2066:C:C6	2.56	0.40
13:M:80:GLU:HA	13:M:80:GLU:OE2	2.21	0.40
5:E:108:LYS:HD3	5:E:108:LYS:HA	1.94	0.40
5:E:64:ILE:HA	5:E:64:ILE:HD12	1.81	0.40
12:L:106:LEU:HD22	12:L:106:LEU:HA	1.86	0.40
17:Q:91:ASP:OD2	17:Q:96:ALA:HB2	2.22	0.40
1:A:782:A:H5'	1:A:783:A:C2	2.57	0.40
10:J:157:ARG:HG2	10:J:157:ARG:O	2.21	0.40
12:L:114:ILE:HD11	12:L:130:PHE:CG	2.54	0.40
12:L:64:LYS:O	12:L:65:ARG:C	2.59	0.40
16:P:26:ASP:HB3	16:P:92:GLY:H	1.86	0.40
12:L:122:PRO:O	12:L:123:LEU:HB3	2.21	0.40
1:A:2287:A:C5	1:A:2289:G:C5	3.10	0.40
6:F:87:PRO:HB2	6:F:88:ILE:H	1.65	0.40
15:O:26:LEU:HB3	15:O:87:PHE:HA	2.03	0.40
14:N:38:VAL:HG22	14:N:112:ALA:HB2	2.04	0.40
1:A:7:G:H2'	1:A:8:A:O4'	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:444:C:H2'	1:A:445:C:H6	1.86	0.40
10:J:64:ASP:N	10:J:64:ASP:OD1	2.54	0.40
19:S:29:LEU:HD22	19:S:69:LEU:CD1	2.49	0.40
1:A:758:C:O2	1:A:1981:A:H2	2.04	0.40
1:A:319:C:C2	1:A:320:A:C8	3.08	0.40
1:A:2565:A:H5''	1:A:2566:A:OP2	2.22	0.40
13:M:27:VAL:H	22:V:81:ARG:NH2	2.20	0.40
22:V:145:GLU:HG3	22:V:146:ILE:N	2.37	0.40
2:B:48:A:H2'	2:B:49:C:C6	2.57	0.40
1:A:380:U:H2'	1:A:381:G:H8	1.87	0.40
1:A:1710:C:O2'	1:A:1711:C:H5'	2.22	0.40
1:A:1750:G:H2'	1:A:1751:C:H6	1.87	0.40
1:A:1961:C:O2'	1:A:1962:C:H5'	2.22	0.40
7:G:125:VAL:HG22	7:G:131:VAL:HG22	2.03	0.40
1:A:2489:G:C6	1:A:2490:G:N1	2.89	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	269/271 (99%)	218 (81%)	33 (12%)	18 (7%)	2	28
4	D	202/204 (99%)	167 (83%)	29 (14%)	6 (3%)	7	53
5	E	200/202 (99%)	165 (82%)	28 (14%)	7 (4%)	6	50
6	F	179/181 (99%)	133 (74%)	37 (21%)	9 (5%)	3	37
7	G	157/159 (99%)	125 (80%)	28 (18%)	4 (2%)	9	57
8	H	143/145 (99%)	109 (76%)	28 (20%)	6 (4%)	4	43
9	I	28/65 (43%)	27 (96%)	1 (4%)	0	100	100
10	J	135/137 (98%)	108 (80%)	19 (14%)	8 (6%)	2	32
11	K	120/122 (98%)	107 (89%)	6 (5%)	7 (6%)	3	32
12	L	144/146 (99%)	92 (64%)	37 (26%)	15 (10%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	M	134/136 (98%)	97 (72%)	24 (18%)	13 (10%)	1	16
14	N	115/117 (98%)	97 (84%)	14 (12%)	4 (4%)	6	50
15	O	96/98 (98%)	65 (68%)	18 (19%)	13 (14%)	0	8
16	P	135/137 (98%)	99 (73%)	30 (22%)	6 (4%)	4	41
17	Q	114/116 (98%)	99 (87%)	13 (11%)	2 (2%)	13	65
18	R	99/101 (98%)	71 (72%)	19 (19%)	9 (9%)	1	18
19	S	110/112 (98%)	94 (86%)	14 (13%)	2 (2%)	13	65
20	T	90/92 (98%)	82 (91%)	7 (8%)	1 (1%)	21	77
21	U	98/100 (98%)	63 (64%)	23 (24%)	12 (12%)	1	11
22	V	186/188 (99%)	140 (75%)	36 (19%)	10 (5%)	3	35
23	W	74/76 (97%)	57 (77%)	14 (19%)	3 (4%)	4	44
24	X	86/88 (98%)	57 (66%)	20 (23%)	9 (10%)	1	14
25	Y	60/62 (97%)	49 (82%)	8 (13%)	3 (5%)	3	37
26	Z	57/59 (97%)	51 (90%)	5 (9%)	1 (2%)	13	65
27	1	28/30 (93%)	15 (54%)	10 (36%)	3 (11%)	1	13
28	2	50/52 (96%)	40 (80%)	6 (12%)	4 (8%)	1	21
29	3	42/44 (96%)	35 (83%)	2 (5%)	5 (12%)	1	11
30	4	46/48 (96%)	41 (89%)	5 (11%)	0	100	100
31	5	61/63 (97%)	44 (72%)	13 (21%)	4 (7%)	2	28
All	All	3258/3351 (97%)	2547 (78%)	527 (16%)	184 (6%)	3	34

All (184) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	26	LYS
3	C	33	LEU
3	C	35	LYS
3	C	237	GLU
3	C	239	ARG
3	C	260	ARG
4	D	16	ARG
5	E	73	ALA
6	F	87	PRO
7	G	92	ILE
7	G	165	ALA

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Mol	Chain	Res	Type
8	H	91	SER
10	J	116	THR
10	J	149	PRO
10	J	157	ARG
12	L	15	ARG
12	L	36	LYS
12	L	46	LYS
12	L	59	LEU
12	L	141	ALA
13	M	8	LYS
13	M	21	THR
15	O	12	PHE
15	O	59	LYS
15	O	62	LYS
15	O	90	GLY
15	O	91	PRO
16	P	58	ASN
16	P	115	ARG
18	R	53	GLU
18	R	78	LYS
19	S	110	LYS
21	U	3	VAL
21	U	7	VAL
22	V	178	GLU
23	W	47	PRO
24	X	11	ARG
25	Y	47	ASN
28	2	35	GLU
29	3	28	ARG
3	C	34	VAL
3	C	69	ARG
3	C	70	TRP
3	C	106	ILE
3	C	125	ILE
3	C	197	GLY
4	D	86	PRO
5	E	84	VAL
6	F	14	GLU
6	F	24	GLY
6	F	86	MET
8	H	10	GLU
8	H	90	GLY

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Mol	Chain	Res	Type
10	J	106	LYS
10	J	153	HIS
12	L	11	GLY
12	L	34	GLY
12	L	149	GLU
13	M	7	MET
13	M	10	ARG
13	M	18	LYS
13	M	62	GLY
14	N	3	HIS
14	N	57	ARG
15	O	35	ILE
15	O	44	LYS
15	O	57	LYS
16	P	2	ASN
21	U	17	SER
21	U	42	VAL
21	U	80	GLY
21	U	98	VAL
22	V	120	ILE
22	V	177	PRO
22	V	179	ASP
23	W	13	GLY
23	W	73	GLY
24	X	85	LEU
28	2	4	HIS
31	5	3	LYS
4	D	18	ASP
5	E	68	LYS
5	E	166	ALA
7	G	21	PRO
8	H	143	SER
10	J	148	GLY
11	K	4	PRO
11	K	26	LYS
11	K	97	ARG
12	L	18	ARG
12	L	42	SER
12	L	49	ARG
12	L	148	LEU
14	N	58	GLY
15	O	85	VAL

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Mol	Chain	Res	Type
15	O	95	HIS
16	P	36	GLU
16	P	57	PHE
18	R	17	GLY
18	R	29	PRO
18	R	80	GLN
21	U	88	LYS
21	U	96	ILE
22	V	114	GLY
22	V	168	GLU
24	X	9	GLY
24	X	31	GLY
24	X	32	LYS
25	Y	17	SER
27	1	44	CYS
27	1	62	CYS
29	3	31	PRO
29	3	46	HIS
31	5	34	TRP
31	5	35	GLN
3	C	32	SER
3	C	238	GLY
3	C	256	GLY
4	D	43	GLY
5	E	127	GLU
6	F	35	GLU
6	F	124	SER
8	H	132	PRO
10	J	70	ALA
11	K	29	ASN
12	L	65	ARG
13	M	81	VAL
13	M	133	ARG
13	M	134	ARG
13	M	140	ALA
14	N	8	ARG
15	O	83	LYS
15	O	101	LEU
17	Q	91	ASP
18	R	2	PHE
19	S	11	ARG
20	T	4	ALA

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Mol	Chain	Res	Type
21	U	39	VAL
21	U	90	LEU
22	V	80	ARG
22	V	142	SER
25	Y	15	LYS
26	Z	29	ARG
27	1	54	LYS
28	2	45	VAL
29	3	32	ASN
29	3	51	GLU
31	5	20	GLY
3	C	191	ALA
3	C	198	ASN
6	F	12	TYR
13	M	25	ASP
15	O	61	ASN
16	P	55	ASN
18	R	48	GLY
24	X	53	VAL
24	X	84	GLY
24	X	87	PRO
4	D	29	GLY
6	F	136	ARG
6	F	142	PRO
7	G	39	PRO
12	L	43	GLY
13	M	27	VAL
21	U	11	ASP
3	C	236	GLY
11	K	27	GLY
12	L	10	PRO
24	X	58	ILE
5	E	131	GLY
13	M	96	VAL
18	R	61	VAL
4	D	4	ILE
11	K	101	PRO
17	Q	90	VAL
18	R	16	PRO
22	V	101	PRO
10	J	158	PRO
11	K	119	PRO

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Mol	Chain	Res	Type
22	V	39	VAL
28	2	46	CYS
5	E	82	ILE
8	H	144	VAL
21	U	41	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	
3	C	213/213 (100%)	192 (90%)	21 (10%)	11	49
4	D	165/165 (100%)	149 (90%)	16 (10%)	12	50
5	E	161/161 (100%)	147 (91%)	14 (9%)	15	57
6	F	155/155 (100%)	144 (93%)	11 (7%)	21	67
7	G	132/132 (100%)	123 (93%)	9 (7%)	22	70
8	H	122/122 (100%)	115 (94%)	7 (6%)	29	76
9	I	27/53 (51%)	26 (96%)	1 (4%)	45	86
10	J	116/116 (100%)	103 (89%)	13 (11%)	9	41
11	K	100/100 (100%)	92 (92%)	8 (8%)	17	61
12	L	112/112 (100%)	87 (78%)	25 (22%)	1	8
13	M	106/106 (100%)	98 (92%)	8 (8%)	19	65
14	N	100/100 (100%)	94 (94%)	6 (6%)	27	74
15	O	77/77 (100%)	68 (88%)	9 (12%)	8	38
16	P	121/121 (100%)	110 (91%)	11 (9%)	14	54
17	Q	92/92 (100%)	88 (96%)	4 (4%)	40	84
18	R	82/82 (100%)	77 (94%)	5 (6%)	26	73
19	S	91/91 (100%)	85 (93%)	6 (7%)	24	71
20	T	74/74 (100%)	67 (90%)	7 (10%)	12	51
21	U	84/84 (100%)	78 (93%)	6 (7%)	21	67
22	V	163/163 (100%)	159 (98%)	4 (2%)	60	91
23	W	61/61 (100%)	55 (90%)	6 (10%)	12	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	X	73/73 (100%)	61 (84%)	12 (16%)	3	20
25	Y	58/58 (100%)	51 (88%)	7 (12%)	7	36
26	Z	51/51 (100%)	49 (96%)	2 (4%)	43	85
27	1	27/27 (100%)	24 (89%)	3 (11%)	9	42
28	2	45/45 (100%)	43 (96%)	2 (4%)	39	83
29	3	43/43 (100%)	39 (91%)	4 (9%)	13	53
30	4	41/41 (100%)	34 (83%)	7 (17%)	3	18
31	5	53/53 (100%)	51 (96%)	2 (4%)	44	85
All	All	2745/2771 (99%)	2509 (91%)	236 (9%)	15	58

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

Mol	Chain	Res	Type
3	C	5	LYS
3	C	10	THR
3	C	28	GLU
3	C	33	LEU
3	C	44	ASN
3	C	50	THR
3	C	61	LEU
3	C	78	LYS
3	C	94	LEU
3	C	95	LEU
3	C	106	ILE
3	C	111	LEU
3	C	150	LYS
3	C	166	GLN
3	C	192	THR
3	C	237	GLU
3	C	242	ARG
3	C	244	ARG
3	C	259	THR
3	C	261	LYS
3	C	267	SER
4	D	9	VAL
4	D	48	GLN
4	D	52	LEU
4	D	54	GLN
4	D	57	LYS

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Mol	Chain	Res	Type
4	D	92	THR
4	D	118	LYS
4	D	119	ARG
4	D	132	HIS
4	D	141	ILE
4	D	144	ARG
4	D	154	LYS
4	D	160	TYR
4	D	169	ASN
4	D	184	VAL
4	D	195	LEU
5	E	8	GLN
5	E	9	ILE
5	E	54	ARG
5	E	56	GLU
5	E	66	PRO
5	E	69	HIS
5	E	72	ARG
5	E	78	ILE
5	E	83	PHE
5	E	95	ARG
5	E	106	ARG
5	E	164	ARG
5	E	188	ARG
5	E	195	ASP
6	F	18	GLU
6	F	33	ARG
6	F	34	LEU
6	F	47	LYS
6	F	76	SER
6	F	86	MET
6	F	90	LEU
6	F	98	ARG
6	F	107	LEU
6	F	115	ARG
6	F	155	MET
7	G	13	LYS
7	G	23	ARG
7	G	43	VAL
7	G	86	GLU
7	G	101	ARG
7	G	105	LEU

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Mol	Chain	Res	Type
7	G	123	PHE
7	G	158	HIS
7	G	162	ILE
8	H	5	LEU
8	H	6	LEU
8	H	67	ARG
8	H	73	GLU
8	H	77	LEU
8	H	92	VAL
8	H	109	ILE
9	I	3	ASN
10	J	57	LEU
10	J	58	ARG
10	J	64	ASP
10	J	71	MET
10	J	92	GLN
10	J	94	ILE
10	J	96	THR
10	J	105	LEU
10	J	110	LEU
10	J	117	HIS
10	J	120	ARG
10	J	135	LEU
10	J	161	LEU
11	K	19	ILE
11	K	25	LEU
11	K	47	ILE
11	K	77	ILE
11	K	87	ILE
11	K	99	PHE
11	K	104	ARG
11	K	122	LEU
12	L	6	LEU
12	L	13	ASN
12	L	15	ARG
12	L	16	ARG
12	L	32	THR
12	L	35	HIS
12	L	38	GLN
12	L	39	LYS
12	L	40	SER
12	L	49	ARG

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Mol	Chain	Res	Type
12	L	50	ARG
12	L	52	GLU
12	L	57	THR
12	L	61	ARG
12	L	62	LEU
12	L	67	MET
12	L	75	ILE
12	L	81	GLN
12	L	83	VAL
12	L	84	ASN
12	L	105	LEU
12	L	106	LEU
12	L	111	ARG
12	L	147	LEU
12	L	148	LEU
13	M	6	ARG
13	M	13	GLN
13	M	14	ARG
13	M	22	LYS
13	M	45	GLN
13	M	60	ARG
13	M	89	ASN
13	M	135	ASP
14	N	5	LYS
14	N	8	ARG
14	N	9	LYS
14	N	10	LEU
14	N	79	LEU
14	N	104	ARG
15	O	18	ILE
15	O	26	LEU
15	O	30	ARG
15	O	36	TYR
15	O	42	ASP
15	O	44	LYS
15	O	61	ASN
15	O	62	LYS
15	O	93	LYS
16	P	41	ARG
16	P	58	ASN
16	P	59	THR
16	P	78	LEU

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Mol	Chain	Res	Type
16	P	86	ILE
16	P	87	ASP
16	P	89	VAL
16	P	98	LYS
16	P	108	ARG
16	P	112	ARG
16	P	113	LYS
17	Q	79	PHE
17	Q	92	ARG
17	Q	97	ASP
17	Q	103	PRO
18	R	12	TYR
18	R	13	ARG
18	R	18	LEU
18	R	80	GLN
18	R	99	ILE
19	S	11	ARG
19	S	23	LEU
19	S	69	LEU
19	S	70	TYR
19	S	77	ASP
19	S	107	LEU
20	T	28	PHE
20	T	57	LEU
20	T	65	ARG
20	T	68	ARG
20	T	75	ASP
20	T	80	ILE
20	T	83	VAL
21	U	4	LYS
21	U	6	HIS
21	U	8	LYS
21	U	31	LEU
21	U	76	CYS
21	U	97	ARG
22	V	25	PRO
22	V	72	ARG
22	V	76	LEU
22	V	94	GLU
23	W	14	ARG
23	W	21	LEU
23	W	25	ARG

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Mol	Chain	Res	Type
23	W	35	ASN
23	W	64	ASP
23	W	80	HIS
24	X	11	ARG
24	X	17	SER
24	X	18	ILE
24	X	20	ARG
24	X	40	ARG
24	X	45	ASN
24	X	46	LEU
24	X	73	LEU
24	X	75	GLU
24	X	82	LEU
24	X	89	GLU
24	X	95	LEU
25	Y	2	LYS
25	Y	21	LEU
25	Y	37	PHE
25	Y	53	LEU
25	Y	56	GLN
25	Y	59	ARG
25	Y	61	LEU
26	Z	10	LYS
26	Z	46	ASN
27	1	46	ASN
27	1	49	GLU
27	1	60	GLU
28	2	3	LYS
28	2	23	HIS
29	3	11	LEU
29	3	29	ASN
29	3	34	LEU
29	3	42	TRP
30	4	4	THR
30	4	8	ASN
30	4	10	ARG
30	4	15	THR
30	4	19	ARG
30	4	24	THR
30	4	29	LYS
31	5	4	MET
31	5	30	ARG

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

Mol	Chain	Res	Type
3	C	58	HIS
3	C	87	ASN
3	C	96	HIS
3	C	116	GLN
3	C	126	GLN
3	C	166	GLN
3	C	186	HIS
3	C	198	ASN
3	C	227	ASN
3	C	233	HIS
4	D	60	ASN
4	D	66	HIS
4	D	129	HIS
4	D	143	ASN
4	D	169	ASN
4	D	192	ASN
5	E	67	GLN
5	E	69	HIS
5	E	75	HIS
5	E	169	ASN
6	F	27	ASN
6	F	58	GLN
6	F	66	GLN
6	F	108	ASN
6	F	121	ASN
7	G	143	GLN
7	G	147	ASN
8	H	133	HIS
9	I	3	ASN
9	I	6	ASN
10	J	79	ASN
10	J	151	HIS
10	J	154	GLN
11	K	89	ASN
12	L	13	ASN
12	L	27	HIS
12	L	35	HIS
12	L	38	GLN
12	L	81	GLN
13	M	13	GLN
13	M	45	GLN

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Mol	Chain	Res	Type
13	M	141	GLN
14	N	13	HIS
14	N	16	HIS
14	N	61	HIS
14	N	71	GLN
14	N	91	GLN
15	O	61	ASN
15	O	95	HIS
16	P	43	GLN
16	P	58	ASN
16	P	79	HIS
16	P	84	GLN
16	P	90	GLN
17	Q	49	HIS
17	Q	72	HIS
19	S	34	ASN
19	S	57	ASN
19	S	61	ASN
19	S	102	HIS
20	T	31	HIS
20	T	41	ASN
20	T	55	ASN
20	T	87	GLN
21	U	6	HIS
22	V	118	GLN
23	W	35	ASN
23	W	50	ASN
23	W	70	GLN
24	X	19	GLN
24	X	45	ASN
24	X	56	GLN
24	X	66	HIS
25	Y	47	ASN
26	Z	19	GLN
26	Z	46	ASN
26	Z	52	HIS
27	1	46	ASN
28	2	43	HIS
29	3	29	ASN
30	4	8	ASN
30	4	36	GLN
31	5	31	HIS

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Mol	Chain	Res	Type
31	5	33	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2757/2879 (95%)	407 (14%)	70 (2%)
2	B	118/119 (99%)	16 (13%)	1 (0%)
All	All	2875/2998 (95%)	423 (14%)	71 (2%)

All (423) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	G
1	A	35	G
1	A	46	C
1	A	64	A
1	A	71	A
1	A	72	U
1	A	74	A
1	A	75	G
1	A	84	A
1	A	88	G
1	A	102	G
1	A	118	A
1	A	119	A
1	A	120	U
1	A	125	G
1	A	131	G
1	A	138	G
1	A	140	A
1	A	196	A
1	A	197	A
1	A	199	A
1	A	205	G
1	A	215	G
1	A	216	A
1	A	221	A
1	A	222	A
1	A	228	A
1	A	229	A
1	A	230	U

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Mol	Chain	Res	Type
1	A	245	G
1	A	248	G
1	A	252	G
1	A	269	U
1	A	270(K)	G
1	A	270(M)	U
1	A	270(N)	U
1	A	270(O)	G
1	A	270(R)	C
1	A	271(D)	U
1	A	271	G
1	A	274	G
1	A	275	G
1	A	276	A
1	A	277	C
1	A	278	A
1	A	279	C
1	A	283	A
1	A	302	C
1	A	311	A
1	A	323	G
1	A	324	A
1	A	329	G
1	A	330	A
1	A	332	A
1	A	333	G
1	A	343	C
1	A	352	G
1	A	353	G
1	A	386	G
1	A	396	G
1	A	405	U
1	A	411	G
1	A	412	A
1	A	444	C
1	A	457	A
1	A	470	A
1	A	480	A
1	A	481	G
1	A	482	A
1	A	505	A
1	A	508	G

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Mol	Chain	Res	Type
1	A	509	C
1	A	530	G
1	A	531	C
1	A	532	A
1	A	556	G
1	A	563	G
1	A	569	U
1	A	573	G
1	A	575	A
1	A	598	G
1	A	603	A
1	A	615	G
1	A	617	G
1	A	620	G
1	A	627	A
1	A	637	A
1	A	645	C
1	A	646	A
1	A	654	U
1	A	655	A
1	A	686	G
1	A	695	G
1	A	730	C
1	A	746	A
1	A	747	U
1	A	749	C
1	A	764	A
1	A	776	G
1	A	777	A
1	A	779	U
1	A	782	A
1	A	784	A
1	A	785	G
1	A	790	C
1	A	792	G
1	A	800	A
1	A	805	G
1	A	812	C
1	A	819	A
1	A	827	U
1	A	828	U
1	A	846	C

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Mol	Chain	Res	Type
1	A	847	U
1	A	859	G
1	A	887	A
1	A	889	C
1	A	890	A
1	A	896	A
1	A	897	C
1	A	910	A
1	A	917	A
1	A	931	G
1	A	932	G
1	A	941	A
1	A	945	A
1	A	946	G
1	A	948	G
1	A	959	A
1	A	961	C
1	A	973	A
1	A	974(A)	G
1	A	974(B)	C
1	A	975	G
1	A	983	A
1	A	989	G
1	A	990	A
1	A	996	A
1	A	1011	G
1	A	1012	U
1	A	1013	C
1	A	1022	G
1	A	1023	U
1	A	1025	G
1	A	1026	U
1	A	1033	U
1	A	1047	G
1	A	1112	G
1	A	1126	A
1	A	1129	A
1	A	1130	U
1	A	1135	C
1	A	1136	G
1	A	1139	G
1	A	114(B)	A

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Mol	Chain	Res	Type
1	A	1144	G
1	A	1155	A
1	A	1164	G
1	A	1174	A
1	A	1175	U
1	A	1205	U
1	A	1210	A
1	A	1211	U
1	A	1220	A
1	A	1221	C
1	A	1227	G
1	A	1241	A
1	A	1242	A
1	A	1249	U
1	A	1250	G
1	A	1253	A
1	A	1256	G
1	A	1271	G
1	A	1272	A
1	A	1300	U
1	A	1301	A
1	A	1309	G
1	A	1312	U
1	A	1314	C
1	A	1329	U
1	A	1343	G
1	A	1345	C
1	A	1349	A
1	A	1352	U
1	A	1359	A
1	A	1360	A
1	A	1365	A
1	A	1368	G
1	A	1378	A
1	A	1379	A
1	A	1380	G
1	A	1384	A
1	A	1385	G
1	A	1386	C
1	A	1396	U
1	A	1416	G
1	A	1417	C

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Mol	Chain	Res	Type
1	A	1420	U
1	A	1427	A
1	A	1428	C
1	A	144(B)	A
1	A	1453	A
1	A	1455	G
1	A	1467	C
1	A	1483	G
1	A	1490	A
1	A	1493	C
1	A	1494	A
1	A	1495	A
1	A	1497	U
1	A	1505	C
1	A	1509	A
1	A	1510	A
1	A	1542	G
1	A	1543	A
1	A	1544	C
1	A	1545	A
1	A	1558	A
1	A	1559	G
1	A	1569	A
1	A	1579	A
1	A	1585	C
1	A	1586	A
1	A	1598	C
1	A	1603	A
1	A	1604	C
1	A	1609	A
1	A	1610	A
1	A	1617	C
1	A	1618	A
1	A	1640	C
1	A	1647	G
1	A	1648	C
1	A	1673	U
1	A	1674	G
1	A	1694	C
1	A	1695	G
1	A	1696	G
1	A	1729	A

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Mol	Chain	Res	Type
1	A	1763	G
1	A	1764	G
1	A	1773	A
1	A	1776	G
1	A	1786	A
1	A	1791	A
1	A	1800	C
1	A	1801	G
1	A	1803	A
1	A	1811	G
1	A	1816	G
1	A	1829	A
1	A	1838	C
1	A	1839	G
1	A	1847	A
1	A	1888	G
1	A	1889	A
1	A	1902	C
1	A	1903	G
1	A	1906	G
1	A	1913	A
1	A	1914	C
1	A	1929	G
1	A	1930	G
1	A	1936	A
1	A	1938	A
1	A	1939	U
1	A	1955	U
1	A	1963	U
1	A	1966	A
1	A	1967	C
1	A	1970	A
1	A	1971	A
1	A	1972	A
1	A	1982	C
1	A	1991	U
1	A	1992	G
1	A	1993	U
1	A	1997	G
1	A	2004	G
1	A	2023	G
1	A	2031	A

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Mol	Chain	Res	Type
1	A	2032	G
1	A	2033	A
1	A	2034	U
1	A	2036	C
1	A	2043	C
1	A	2049	G
1	A	2052	G
1	A	2055	C
1	A	2056	G
1	A	2060	A
1	A	2061	G
1	A	2062	A
1	A	2063	C
1	A	2069	G
1	A	2080	G
1	A	2099	U
1	A	2184	G
1	A	2189	U
1	A	2190	G
1	A	2198	A
1	A	2211	G
1	A	2212	A
1	A	2215	G
1	A	2225	A
1	A	2226	C
1	A	2238	G
1	A	2239	G
1	A	2251	G
1	A	2273	A
1	A	2275	C
1	A	2283	C
1	A	2287	A
1	A	2288	A
1	A	2305	A
1	A	2306	C
1	A	2307	G
1	A	2310	A
1	A	2311	A
1	A	2312	U
1	A	2319	G
1	A	2320	A
1	A	2322	A

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Mol	Chain	Res	Type
1	A	2325	G
1	A	2334	G
1	A	2336	A
1	A	2343	C
1	A	2345	G
1	A	2346	A
1	A	2347	C
1	A	2360	A
1	A	2372	G
1	A	2379	G
1	A	2383	G
1	A	2385	C
1	A	2402	C
1	A	2413	G
1	A	2425	A
1	A	2427	C
1	A	2428	G
1	A	2429	G
1	A	2430	A
1	A	2431	U
1	A	2434	A
1	A	2435	A
1	A	2439	A
1	A	2440	C
1	A	2441	C
1	A	2445	G
1	A	2448	A
1	A	2469	A
1	A	2476	A
1	A	2478	A
1	A	2482	G
1	A	2487	G
1	A	2491	U
1	A	2502	G
1	A	2505	G
1	A	2513	G
1	A	2518	A
1	A	2520	C
1	A	2529	G
1	A	2542	A
1	A	2543	G
1	A	2554	U

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Mol	Chain	Res	Type
1	A	2562	U
1	A	2566	A
1	A	2567	G
1	A	2572	A
1	A	2573	C
1	A	2602	A
1	A	2609	U
1	A	2611	U
1	A	2612	C
1	A	2621	A
1	A	2665	A
1	A	2690	C
1	A	2691	C
1	A	2702	U
1	A	2712	U
1	A	712(B)	A
1	A	2713	A
1	A	2714	G
1	A	2726	U
1	A	2733	A
1	A	2757	A
1	A	2758	A
1	A	2764	A
1	A	2765	A
1	A	2778	A
1	A	2779	U
1	A	2781	A
1	A	2790	A
1	A	2791	C
1	A	2797	U
1	A	2808	U
1	A	2818	G
1	A	2820	A
1	A	2821	A
1	A	2834	G
1	A	2836	U
1	A	2850	A
1	A	2851	A
1	A	2872	G
1	A	2876	G
1	A	2892	A
1	A	2894	G

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Mol	Chain	Res	Type
2	B	12	C
2	B	13	A
2	B	15	A
2	B	16	G
2	B	42	C
2	B	44	G
2	B	45	A
2	B	67	G
2	B	73	A
2	B	77	U
2	B	88	C
2	B	89(A)	G
2	B	90	C
2	B	108	C
2	B	109	G
2	B	112	G

All (71) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	102	G
1	A	119	A
1	A	120	U
1	A	131	G
1	A	199	A
1	A	221	A
1	A	278	A
1	A	331	A
1	A	332	A
1	A	343	C
1	A	479	A
1	A	481	G
1	A	503	A
1	A	616	A
1	A	682	G
1	A	685	A
1	A	746	A
1	A	764	A
1	A	776	G
1	A	846	C
1	A	858	U
1	A	859	G

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Mol	Chain	Res	Type
1	A	933	A
1	A	945	A
1	A	948	G
1	A	961	C
1	A	974(A)	G
1	A	989	G
1	A	1022	G
1	A	1157	G
1	A	1210	A
1	A	1221	C
1	A	1253	A
1	A	1311	G
1	A	1314	C
1	A	1343	G
1	A	1378	A
1	A	1379	A
1	A	1427	A
1	A	1494	A
1	A	1542	G
1	A	1558	A
1	A	1579	A
1	A	1603	A
1	A	1608	A
1	A	1694	C
1	A	1800	C
1	A	1929	G
1	A	1930	G
1	A	1937	A
1	A	1980	G
1	A	2033	A
1	A	2051	A
1	A	2062	A
1	A	2098	U
1	A	2225	A
1	A	2250	G
1	A	2311	A
1	A	2426	A
1	A	2427	C
1	A	2439	A
1	A	2468	G
1	A	2481	G
1	A	2581	G

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Mol	Chain	Res	Type
1	A	2585	U
1	A	2689	U
1	A	2756	U
1	A	2849	U
1	A	2850	A
1	A	2873	A
2	B	66	A

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 1495 ligands modelled in this entry, 1495 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	2760/2879 (95%)	0.03	112 (4%) 35 15	33, 77, 196, 377	0
2	B	119/119 (100%)	0.53	14 (11%) 5 4	87, 132, 198, 274	0
3	C	271/271 (100%)	0.42	19 (7%) 16 7	26, 72, 144, 220	0
4	D	204/204 (100%)	0.39	14 (6%) 17 7	36, 90, 189, 305	0
5	E	202/202 (100%)	0.35	11 (5%) 25 10	20, 85, 182, 249	0
6	F	181/181 (100%)	1.07	41 (22%) 1 2	109, 198, 281, 324	0
7	G	159/159 (100%)	0.48	11 (6%) 17 7	61, 117, 190, 269	0
8	H	145/145 (100%)	1.52	50 (34%) 1 1	60, 210, 372, 482	0
9	I	32/65 (49%)	1.66	9 (28%) 1 1	176, 235, 294, 325	0
10	J	137/137 (100%)	0.70	8 (5%) 22 9	55, 101, 170, 219	0
11	K	122/122 (100%)	0.35	5 (4%) 35 15	41, 90, 153, 251	0
12	L	146/146 (100%)	0.68	14 (9%) 8 5	27, 111, 207, 324	0
13	M	136/136 (100%)	0.88	25 (18%) 2 2	46, 106, 199, 388	0
14	N	117/117 (100%)	0.68	15 (12%) 4 3	41, 89, 173, 285	0
15	O	98/98 (100%)	1.41	30 (30%) 1 1	80, 148, 221, 299	0
16	P	137/137 (100%)	0.94	27 (19%) 2 2	60, 119, 249, 299	0
17	Q	116/116 (100%)	0.14	4 (3%) 43 19	34, 84, 154, 205	0
18	R	101/101 (100%)	0.65	12 (11%) 5 4	52, 132, 197, 321	0
19	S	112/112 (100%)	0.80	11 (9%) 8 5	40, 72, 166, 277	0
20	T	92/92 (100%)	0.66	10 (10%) 6 4	41, 78, 161, 204	0
21	U	100/100 (100%)	1.00	18 (18%) 2 2	49, 119, 264, 373	0
22	V	188/188 (100%)	0.70	29 (15%) 3 3	67, 154, 220, 254	0
23	W	76/76 (100%)	0.80	14 (18%) 2 2	54, 101, 167, 254	0
24	X	88/88 (100%)	0.72	10 (11%) 6 4	31, 83, 196, 340	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	Y	62/62 (100%)	0.83	10 (16%) 2 2	45, 99, 224, 304	0
26	Z	59/59 (100%)	0.89	11 (18%) 2 2	45, 102, 189, 335	0
27	1	30/30 (100%)	0.77	2 (6%) 17 8	187, 262, 306, 326	0
28	2	52/52 (100%)	0.07	2 (3%) 38 17	24, 93, 214, 262	0
29	3	44/44 (100%)	3.30	26 (59%) 0 1	191, 247, 298, 313	0
30	4	48/48 (100%)	0.69	8 (16%) 2 2	23, 45, 122, 217	0
31	5	63/63 (100%)	1.50	26 (41%) 1 1	43, 92, 170, 209	0
All	All	6197/6349 (97%)	0.43	598 (9%) 9 5	20, 91, 234, 482	0

All (598) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	10	G	14.5
29	3	47	THR	10.9
26	Z	1	MET	9.6
12	L	150	ALA	9.2
1	A	11	G	8.9
1	A	9	U	8.8
29	3	49	HIS	8.6
13	M	141	GLN	8.3
2	B	88	C	8.2
16	P	115	ARG	7.9
12	L	149	GLU	7.8
5	E	207	GLY	7.7
1	A	2378	A	7.6
29	3	36	LEU	7.4
9	I	5	ARG	7.4
21	U	76	CYS	7.4
1	A	6	A	7.3
29	3	50	ARG	7.1
21	U	79	CYS	7.0
22	V	73	GLN	6.9
1	A	2402	C	6.8
29	3	18	ARG	6.8
29	3	15	GLU	6.7
6	F	25	TYR	6.6
13	M	140	ALA	6.6
8	H	132	PRO	6.6
22	V	181	GLU	6.5
29	3	20	ASN	6.4

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Mol	Chain	Res	Type	RSRZ
29	3	21	TYR	6.4
1	A	8	A	6.4
29	3	43	CYS	6.2
1	A	2801	A	6.2
2	B	11	C	6.1
8	H	4	ILE	6.1
19	S	1	MET	6.1
1	A	1741	C	6.1
8	H	1	MET	6.1
1	A	2895	U	5.9
1	A	2602	A	5.9
1	A	508	G	5.9
1	A	1420	U	5.7
8	H	94	ALA	5.7
15	O	106	ARG	5.6
22	V	189	ALA	5.5
1	A	1847	A	5.3
10	J	161	LEU	5.3
1	A	896	A	5.3
21	U	78	ALA	5.2
8	H	71	ILE	5.2
6	F	34	LEU	5.2
16	P	111	ARG	5.2
6	F	116	ASP	5.1
8	H	70	GLU	5.1
29	3	38	LYS	5.1
19	S	2	GLU	4.9
16	P	93	ARG	4.9
2	B	12	C	4.9
1	A	405	U	4.8
8	H	22	LYS	4.8
6	F	35	GLU	4.8
9	I	22	GLY	4.8
29	3	37	ARG	4.8
22	V	178	GLU	4.8
15	O	22	GLY	4.8
29	3	14	THR	4.8
15	O	61	ASN	4.8
1	A	2187	G	4.7
16	P	129	ARG	4.7
12	L	110	TYR	4.7
16	P	114	LEU	4.7

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Mol	Chain	Res	Type	RSRZ
16	P	113	LYS	4.6
6	F	30	GLU	4.6
29	3	48	VAL	4.6
6	F	26	GLN	4.6
13	M	139	GLU	4.5
21	U	89	PHE	4.5
1	A	12	U	4.5
1	A	776	G	4.5
1	A	2797	U	4.5
12	L	111	ARG	4.5
8	H	130	TYR	4.5
1	A	950	G	4.4
21	U	77	PRO	4.4
1	A	1026	U	4.4
15	O	21	THR	4.4
19	S	72	LYS	4.4
6	F	85	GLY	4.3
9	I	14	LYS	4.3
18	R	43	GLU	4.3
3	C	2	ALA	4.3
13	M	64	ILE	4.3
29	3	22	ALA	4.3
6	F	176	LEU	4.2
12	L	108	LYS	4.2
14	N	54	LEU	4.2
1	A	2897	U	4.2
26	Z	34	GLU	4.2
29	3	19	ARG	4.2
6	F	118	ARG	4.2
8	H	21	VAL	4.2
31	5	10	ALA	4.1
1	A	2379	G	4.1
16	P	112	ARG	4.1
9	I	21	GLN	4.1
14	N	57	ARG	4.1
6	F	86	MET	4.1
1	A	2188	C	4.1
18	R	101	GLY	4.0
22	V	117	LEU	4.0
14	N	58	GLY	4.0
13	M	137	TYR	4.0
11	K	90	GLN	4.0

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Mol	Chain	Res	Type	RSRZ
29	3	41	PRO	4.0
15	O	102	ALA	4.0
22	V	85	HIS	4.0
29	3	17	LYS	4.0
1	A	968	G	3.9
10	J	31	GLN	3.9
26	Z	55	ARG	3.9
1	A	7	G	3.9
1	A	2896	C	3.9
4	D	73	GLU	3.9
22	V	185	GLU	3.9
25	Y	15	LYS	3.9
1	A	701	G	3.9
29	3	16	CYS	3.9
15	O	60	GLY	3.9
23	W	71	ASP	3.9
22	V	77	ASP	3.8
8	H	18	VAL	3.8
1	A	2894	G	3.8
16	P	94	ALA	3.8
9	I	18	GLU	3.8
15	O	105	ALA	3.8
6	F	94	LEU	3.8
28	2	48	GLU	3.8
1	A	888	C	3.8
6	F	161	THR	3.8
8	H	2	LYS	3.8
23	W	72	ARG	3.8
1	A	702	G	3.8
10	J	30	LYS	3.8
8	H	20	ASP	3.7
13	M	65	PHE	3.7
25	Y	8	LYS	3.7
1	A	1963	U	3.7
22	V	157	LEU	3.7
22	V	72	ARG	3.7
23	W	76	GLY	3.7
6	F	95	ARG	3.7
1	A	2376	A	3.6
8	H	77	LEU	3.6
22	V	162	GLU	3.6
14	N	59	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
8	H	69	LYS	3.6
8	H	19	VAL	3.6
7	G	53	GLU	3.6
3	C	26	LYS	3.6
8	H	92	VAL	3.6
9	I	6	ASN	3.6
21	U	86	ARG	3.5
29	3	44	ARG	3.5
1	A	1183	G	3.5
2	B	13	A	3.5
2	B	87	G	3.5
8	H	3	VAL	3.5
15	O	87	PHE	3.5
25	Y	31	GLU	3.5
1	A	1174	A	3.5
31	5	21	LYS	3.5
3	C	185	VAL	3.4
22	V	84	GLU	3.4
2	B	89(B)	A	3.4
15	O	58	LEU	3.4
15	O	92	TYR	3.4
29	3	23	THR	3.4
1	A	363(A)	G	3.4
17	Q	102	GLU	3.4
6	F	2	PRO	3.4
1	A	277	C	3.4
21	U	81	LYS	3.4
22	V	75	ASN	3.4
24	X	28	GLY	3.4
15	O	30	ARG	3.4
16	P	96	ARG	3.4
7	G	116	GLU	3.3
6	F	65	GLY	3.3
16	P	136	GLN	3.3
1	A	2377	A	3.3
6	F	13	GLU	3.3
6	F	32	PRO	3.3
16	P	1	MET	3.3
16	P	132	LYS	3.3
4	D	57	LYS	3.3
16	P	109	GLU	3.3
6	F	33	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
29	3	9	LEU	3.3
1	A	271(D)	U	3.2
1	A	614	U	3.2
6	F	74	LYS	3.2
8	H	140	LEU	3.2
6	F	28	VAL	3.2
6	F	72	ARG	3.2
6	F	31	VAL	3.2
1	A	1742	C	3.2
12	L	106	LEU	3.2
25	Y	56	GLN	3.2
2	B	91	C	3.2
1	A	1631	A	3.2
13	M	72	LYS	3.2
1	A	362	U	3.2
13	M	136	ALA	3.2
24	X	27	GLU	3.1
25	Y	9	GLN	3.1
14	N	62	ALA	3.1
22	V	182	LYS	3.1
8	H	120	ILE	3.1
8	H	5	LEU	3.1
6	F	150	ASP	3.1
18	R	48	GLY	3.1
2	B	89(A)	G	3.1
8	H	23	PRO	3.1
10	J	70	ALA	3.1
17	Q	101	ARG	3.1
8	H	41	GLU	3.1
8	H	137	PRO	3.1
1	A	1421	G	3.1
1	A	2798	C	3.1
22	V	160	GLY	3.1
16	P	116	ALA	3.1
13	M	63	LYS	3.1
19	S	25	ARG	3.1
20	T	3	THR	3.1
1	A	1032	A	3.0
31	5	47	LYS	3.0
1	A	2828	C	3.0
3	C	271	ILE	3.0
23	W	85	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	2803	C	3.0
19	S	84	ARG	3.0
10	J	32	VAL	3.0
22	V	82	ARG	3.0
31	5	15	LYS	3.0
26	Z	2	PRO	3.0
6	F	3	LEU	3.0
25	Y	3	LEU	3.0
1	A	2833	G	3.0
8	H	114	LEU	3.0
21	U	87	LYS	3.0
1	A	1591	G	3.0
1	A	2334	G	3.0
3	C	35	LYS	3.0
21	U	2	ARG	3.0
8	H	25	TYR	2.9
15	O	64	GLU	2.9
1	A	529	A	2.9
9	I	67	GLY	2.9
5	E	23	ASP	2.9
13	M	138	ASP	2.9
12	L	107	LYS	2.9
21	U	101	LYS	2.9
13	M	17	LEU	2.9
1	A	969	U	2.9
31	5	44	LYS	2.9
21	U	99	CYS	2.9
4	D	72	VAL	2.9
8	H	39	ALA	2.9
18	R	1	MET	2.9
1	A	1128	A	2.9
1	A	1632	A	2.9
24	X	31	GLY	2.9
5	E	24	LEU	2.9
6	F	146	TYR	2.9
23	W	40	GLN	2.9
22	V	169	GLU	2.9
6	F	11	TYR	2.9
1	A	2799	A	2.8
1	A	1273	U	2.8
14	N	67	LEU	2.8
22	V	81	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
23	W	78	TYR	2.8
1	A	1218	C	2.8
1	A	2420	C	2.8
7	G	57	ASP	2.8
12	L	47	ASP	2.8
22	V	188	ALA	2.8
1	A	732	C	2.8
31	5	64	TYR	2.8
21	U	88	LYS	2.8
19	S	26	GLY	2.8
24	X	16	ASN	2.8
1	A	615	G	2.8
21	U	19	LYS	2.8
31	5	26	LYS	2.8
1	A	2666	C	2.8
16	P	106	SER	2.8
1	A	440	G	2.8
16	P	104	ASN	2.8
3	C	34	VAL	2.7
22	V	161	VAL	2.7
22	V	87	ASP	2.7
2	B	42	C	2.7
26	Z	14	GLY	2.7
24	X	15	ALA	2.7
29	3	39	TYR	2.7
1	A	1460	A	2.7
8	H	35	LEU	2.7
23	W	43	THR	2.7
1	A	2629	A	2.7
2	B	78	A	2.7
20	T	44	GLU	2.7
6	F	75	LYS	2.7
31	5	54	GLU	2.7
31	5	25	MET	2.7
6	F	99	MET	2.7
7	G	101	ARG	2.7
15	O	67	ARG	2.7
1	A	1124	C	2.7
1	A	2871	C	2.7
7	G	100	GLY	2.7
8	H	85	GLU	2.7
22	V	76	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
21	U	91	GLU	2.7
7	G	47	GLU	2.7
1	A	1186	G	2.7
2	B	54	G	2.7
12	L	109	GLY	2.7
7	G	164	TYR	2.7
24	X	85	LEU	2.7
31	5	16	ILE	2.7
15	O	57	LYS	2.6
1	A	1166	C	2.6
29	3	13	CYS	2.6
15	O	97	ARG	2.6
1	A	2362	G	2.6
19	S	108	GLY	2.6
3	C	101	GLU	2.6
13	M	16	ARG	2.6
5	E	66	PRO	2.6
2	B	86	G	2.6
13	M	69	PHE	2.6
3	C	102	LYS	2.6
30	4	25	PRO	2.6
14	N	53	HIS	2.6
19	S	22	ASP	2.6
6	F	67	LYS	2.6
13	M	70	PRO	2.6
15	O	23	ARG	2.6
18	R	2	PHE	2.6
13	M	71	ASP	2.6
18	R	47	VAL	2.6
6	F	160	VAL	2.6
5	E	70	THR	2.6
13	M	66	ILE	2.6
25	Y	4	SER	2.6
1	A	1494	A	2.6
7	G	169	VAL	2.5
26	Z	16	PRO	2.5
1	A	34	C	2.5
8	H	31	LEU	2.5
12	L	52	GLU	2.5
4	D	76	ARG	2.5
5	E	68	LYS	2.5
4	D	164	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
31	5	11	LYS	2.5
3	C	68	LYS	2.5
23	W	42	GLY	2.5
16	P	133	GLU	2.5
22	V	190	GLU	2.5
25	Y	30	ARG	2.5
15	O	94	TYR	2.5
8	H	136	VAL	2.5
8	H	90	GLY	2.5
1	A	196	A	2.5
3	C	31	LYS	2.5
18	R	10	LYS	2.5
20	T	40	LYS	2.5
12	L	148	LEU	2.5
30	4	47	ARG	2.5
25	Y	16	LEU	2.5
1	A	898	C	2.5
7	G	54	ARG	2.5
15	O	74	ALA	2.5
1	A	2506	U	2.5
19	S	82	LEU	2.5
21	U	80	GLY	2.5
14	N	109	ALA	2.5
1	A	2357	U	2.5
8	H	117	GLU	2.5
31	5	20	GLY	2.5
6	F	36	LYS	2.5
23	W	74	ARG	2.5
23	W	75	LEU	2.5
5	E	190	GLU	2.4
3	C	33	LEU	2.4
8	H	7	GLU	2.4
13	M	19	GLY	2.4
29	3	40	CYS	2.4
1	A	276	A	2.4
1	A	1848	A	2.4
1	A	2585	U	2.4
6	F	84	LYS	2.4
5	E	72	ARG	2.4
13	M	18	LYS	2.4
21	U	20	TYR	2.4
31	5	63	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	2189	U	2.4
7	G	111	HIS	2.4
8	H	17	GLN	2.4
6	F	96	ARG	2.4
2	B	90	C	2.4
15	O	75	GLU	2.4
1	A	731	C	2.4
8	H	33	ARG	2.4
8	H	98	ALA	2.4
10	J	138	ARG	2.4
8	H	84	GLY	2.4
6	F	115	ARG	2.4
6	F	69	ALA	2.4
8	H	119	PRO	2.4
11	K	91	LEU	2.4
2	B	55	U	2.4
6	F	162	THR	2.4
18	R	69	LYS	2.4
15	O	78	LEU	2.4
23	W	73	GLY	2.4
1	A	1373	A	2.4
4	D	53	PRO	2.3
16	P	2	ASN	2.3
16	P	33	LYS	2.3
23	W	70	GLN	2.3
31	5	34	TRP	2.3
15	O	35	ILE	2.3
4	D	89	ASP	2.3
24	X	41	ARG	2.3
15	O	83	LYS	2.3
22	V	155	LEU	2.3
1	A	951	C	2.3
8	H	27	ARG	2.3
10	J	144	LYS	2.3
18	R	44	LYS	2.3
16	P	110	ILE	2.3
20	T	8	ILE	2.3
1	A	755	C	2.3
12	L	50	ARG	2.3
16	P	49	VAL	2.3
31	5	22	VAL	2.3
14	N	55	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
27	1	65	CYS	2.3
12	L	46	LYS	2.3
30	4	46	VAL	2.3
8	H	40	THR	2.3
15	O	98	VAL	2.3
31	5	13	ARG	2.3
5	E	206	ILE	2.3
11	K	114	ILE	2.3
31	5	33	ASN	2.3
9	I	9	LEU	2.3
10	J	123	GLU	2.3
25	Y	60	LEU	2.3
18	R	45	THR	2.3
3	C	94	LEU	2.3
15	O	36	TYR	2.3
1	A	531	C	2.3
1	A	1544	C	2.3
17	Q	15	LYS	2.3
16	P	105	LEU	2.3
3	C	270	ILE	2.3
4	D	195	LEU	2.3
13	M	107	ALA	2.3
30	4	28	ARG	2.3
16	P	97	ALA	2.3
5	E	96	ASP	2.3
1	A	2403	C	2.3
14	N	63	ARG	2.3
15	O	73	LEU	2.3
20	T	53	LYS	2.3
31	5	48	PHE	2.3
14	N	72	ASP	2.3
31	5	57	ARG	2.2
8	H	73	GLU	2.2
3	C	72	LYS	2.2
1	A	491	G	2.2
13	M	105	GLU	2.2
20	T	45	THR	2.2
18	R	53	GLU	2.2
22	V	120	ILE	2.2
15	O	62	LYS	2.2
20	T	4	ALA	2.2
16	P	92	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
14	N	66	VAL	2.2
19	S	21	VAL	2.2
1	A	2611	U	2.2
6	F	66	GLN	2.2
31	5	14	VAL	2.2
1	A	125	G	2.2
4	D	52	LEU	2.2
13	M	13	GLN	2.2
1	A	872	A	2.2
8	H	116	LEU	2.2
19	S	83	LYS	2.2
13	M	9	TYR	2.2
1	A	229	A	2.2
9	I	13	LEU	2.2
1	A	2319	G	2.2
8	H	38	LEU	2.2
16	P	99	LEU	2.2
22	V	86	VAL	2.2
7	G	114	VAL	2.2
13	M	8	LYS	2.2
30	4	48	LYS	2.2
1	A	989	G	2.2
4	D	163	GLU	2.2
1	A	1490	A	2.2
6	F	177	GLY	2.2
1	A	2742	C	2.2
3	C	64	ILE	2.2
31	5	9	GLY	2.2
31	5	23	VAL	2.2
28	2	37	LYS	2.2
15	O	54	LEU	2.2
1	A	806	C	2.2
22	V	83	PRO	2.2
26	Z	57	GLU	2.2
27	1	56	GLU	2.2
16	P	40	THR	2.2
21	U	97	ARG	2.2
23	W	77	ARG	2.2
1	A	967	C	2.1
22	V	78	LYS	2.1
31	5	32	LEU	2.1
1	A	2190	G	2.1

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Mol	Chain	Res	Type	RSRZ
15	O	84	GLN	2.1
3	C	153	ALA	2.1
31	5	50	LEU	2.1
24	X	20	ARG	2.1
4	D	194	GLY	2.1
8	H	34	GLY	2.1
1	A	1642	G	2.1
24	X	30	VAL	2.1
5	E	21	ALA	2.1
15	O	101	LEU	2.1
16	P	85	LYS	2.1
3	C	69	ARG	2.1
3	C	262	ARG	2.1
26	Z	33	GLN	2.1
1	A	790	C	2.1
6	F	166	ASP	2.1
8	H	133	HIS	2.1
20	T	5	TYR	2.1
30	4	45	ALA	2.1
4	D	186	GLY	2.1
21	U	98	VAL	2.1
26	Z	15	TYR	2.1
1	A	1127	A	2.1
8	H	30	LEU	2.1
18	R	71	LEU	2.1
11	K	113	LYS	2.1
31	5	12	LYS	2.1
1	A	914	C	2.1
4	D	77	ILE	2.1
31	5	31	HIS	2.1
17	Q	19	LYS	2.1
29	3	46	HIS	2.1
1	A	1167	U	2.1
13	M	7	MET	2.1
20	T	42	ALA	2.1
12	L	78	PRO	2.1
13	M	12	GLN	2.1
1	A	257	A	2.1
1	A	777	A	2.1
1	A	2820	A	2.1
8	H	26	ALA	2.1
22	V	159	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	964	C	2.1
26	Z	8	LEU	2.1
1	A	866	A	2.1
8	H	110	ASP	2.1
26	Z	56	VAL	2.1
1	A	1590	U	2.1
30	4	29	LYS	2.0
15	O	65	VAL	2.0
24	X	21	ARG	2.0
6	F	27	ASN	2.0
14	N	70	LEU	2.0
29	3	45	LYS	2.0
14	N	103	ARG	2.0
20	T	6	ASP	2.0
6	F	100	TRP	2.0
23	W	46	LYS	2.0
1	A	2795	G	2.0
11	K	36	GLY	2.0
30	4	27	GLY	2.0
8	H	138	ILE	2.0
3	C	173	VAL	2.0
4	D	168	MET	2.0
8	H	8	PRO	2.0
14	N	56	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3494	1/1	0.38	-	124,124,124,124	0
32	MG	S	325	1/1	1.22	-	98,98,98,98	0
32	MG	A	3026	1/1	0.59	-	80,80,80,80	0
32	MG	A	3416	1/1	0.14	-	101,101,101,101	0
32	MG	A	3369	1/1	0.13	-	78,78,78,78	0
32	MG	A	3459	1/1	0.56	-	97,97,97,97	0
32	MG	A	3631	1/1	0.08	-	121,121,121,121	0
32	MG	A	3230	1/1	0.49	-	69,69,69,69	0
32	MG	A	3062	1/1	0.18	-	50,50,50,50	0
32	MG	A	3760	1/1	0.37	-	84,84,84,84	0
32	MG	A	3347	1/1	1.26	-	89,89,89,89	0
32	MG	6	992	1/1	0.21	-	98,98,98,98	0
32	MG	A	3563	1/1	0.11	-	82,82,82,82	0
32	MG	A	3606	1/1	0.39	-	96,96,96,96	0
32	MG	G	597	1/1	0.20	-	108,108,108,108	0
32	MG	6	593	1/1	0.40	-	121,121,121,121	0
32	MG	K	1243	1/1	0.50	-	86,86,86,86	0
32	MG	A	3254	1/1	0.66	-	138,138,138,138	0
32	MG	6	698	1/1	0.48	-	69,69,69,69	0
32	MG	A	3177	1/1	0.56	-	62,62,62,62	0
32	MG	6	351	1/1	2.82	-	158,158,158,158	0
32	MG	A	3267	1/1	0.34	-	86,86,86,86	0
32	MG	6	485	1/1	0.16	-	83,83,83,83	0
32	MG	A	3314	1/1	0.39	-	95,95,95,95	0
32	MG	A	3900	1/1	0.08	-	78,78,78,78	0
32	MG	P	1266	1/1	0.66	-	80,80,80,80	0
32	MG	A	3439	1/1	0.33	-	54,54,54,54	0
32	MG	A	367	1/1	0.91	-	71,71,71,71	0
32	MG	A	3663	1/1	0.18	-	26,26,26,26	0
32	MG	6	1082	1/1	0.45	-	93,93,93,93	0
32	MG	A	3098	1/1	0.37	-	50,50,50,50	0
32	MG	A	3456	1/1	0.65	-	74,74,74,74	0
32	MG	A	2911	1/1	0.17	-	12,12,12,12	0
32	MG	A	3818	1/1	0.52	-	109,109,109,109	0
32	MG	A	3109	1/1	0.32	-	50,50,50,50	0
32	MG	A	3867	1/1	0.43	-	120,120,120,120	0
32	MG	A	3097	1/1	0.16	-	69,69,69,69	0
32	MG	A	3871	1/1	0.19	-	77,77,77,77	0
32	MG	6	1086	1/1	0.66	-	64,64,64,64	0
32	MG	6	1112	1/1	1.09	-	96,96,96,96	0
32	MG	6	1395	1/1	0.37	-	137,137,137,137	0
32	MG	A	2935	1/1	0.62	-	25,25,25,25	0
32	MG	A	3478	1/1	0.43	-	104,104,104,104	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	1452	1/1	0.77	-	63,63,63,63	0
32	MG	A	3753	1/1	1.03	-	106,106,106,106	0
32	MG	A	3462	1/1	0.25	-	93,93,93,93	0
32	MG	A	3685	1/1	0.33	-	98,98,98,98	0
32	MG	A	3249	1/1	0.42	-	90,90,90,90	0
32	MG	A	3853	1/1	0.67	-	52,52,52,52	0
32	MG	A	3366	1/1	2.72	-	92,92,92,92	0
32	MG	A	3841	1/1	0.20	-	72,72,72,72	0
32	MG	B	122	1/1	0.14	-	56,56,56,56	0
32	MG	6	651	1/1	0.11	-	91,91,91,91	0
32	MG	6	522	1/1	1.16	-	113,113,113,113	0
32	MG	A	3493	1/1	0.09	-	119,119,119,119	0
32	MG	A	3813	1/1	0.19	-	67,67,67,67	0
32	MG	L	151	1/1	0.07	-	7,7,7,7	0
32	MG	A	3476	1/1	0.23	-	127,127,127,127	0
32	MG	A	3690	1/1	0.52	-	81,81,81,81	0
32	MG	A	3868	1/1	0.12	-	96,96,96,96	0
32	MG	A	3201	1/1	0.07	-	59,59,59,59	0
32	MG	A	2917	1/1	0.43	-	34,34,34,34	0
32	MG	6	582	1/1	0.21	-	89,89,89,89	0
32	MG	A	3574	1/1	0.93	-	148,148,148,148	0
32	MG	D	837	1/1	0.86	-	52,52,52,52	0
32	MG	B	825	1/1	1.23	-	95,95,95,95	0
32	MG	A	3517	1/1	1.18	-	70,70,70,70	0
32	MG	A	3671	1/1	0.62	-	54,54,54,54	0
32	MG	A	3535	1/1	0.28	-	73,73,73,73	0
32	MG	A	3148	1/1	0.38	-	42,42,42,42	0
32	MG	A	3736	1/1	0.20	-	75,75,75,75	0
32	MG	A	3377	1/1	0.21	-	49,49,49,49	0
32	MG	A	3354	1/1	0.18	-	83,83,83,83	0
32	MG	D	389	1/1	0.08	-	61,61,61,61	0
32	MG	A	3191	1/1	0.39	-	97,97,97,97	0
32	MG	A	3442	1/1	0.24	-	125,125,125,125	0
32	MG	6	523	1/1	0.34	-	140,140,140,140	0
32	MG	A	3687	1/1	0.84	-	75,75,75,75	0
32	MG	A	3214	1/1	0.81	-	86,86,86,86	0
32	MG	A	3081	1/1	0.21	-	46,46,46,46	0
32	MG	A	3450	1/1	0.20	-	73,73,73,73	0
32	MG	A	3104	1/1	0.26	-	66,66,66,66	0
32	MG	A	3726	1/1	0.28	-	56,56,56,56	0
32	MG	A	3858	1/1	0.31	-	79,79,79,79	0
32	MG	A	3512	1/1	0.69	-	93,93,93,93	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3695	1/1	0.50	-	69,69,69,69	0
32	MG	A	3261	1/1	0.27	-	82,82,82,82	0
32	MG	A	3595	1/1	0.28	-	96,96,96,96	0
32	MG	A	3434	1/1	0.33	-	89,89,89,89	0
32	MG	A	2899	1/1	0.45	-	17,17,17,17	0
32	MG	A	3114	1/1	0.43	-	36,36,36,36	0
32	MG	A	3499	1/1	0.52	-	99,99,99,99	0
32	MG	A	3453	1/1	0.67	-	81,81,81,81	0
32	MG	A	3806	1/1	0.35	-	74,74,74,74	0
32	MG	A	3213	1/1	0.56	-	55,55,55,55	0
32	MG	A	3160	1/1	0.37	-	56,56,56,56	0
32	MG	A	3382	1/1	0.23	-	76,76,76,76	0
32	MG	A	3754	1/1	0.49	-	88,88,88,88	0
32	MG	A	3842	1/1	0.12	-	70,70,70,70	0
32	MG	A	3700	1/1	0.23	-	92,92,92,92	0
32	MG	A	2910	1/1	0.31	-	25,25,25,25	0
32	MG	A	3431	1/1	1.15	-	94,94,94,94	0
32	MG	A	3607	1/1	0.35	-	51,51,51,51	0
32	MG	A	3070	1/1	0.43	-	120,120,120,120	0
32	MG	A	3482	1/1	0.27	-	81,81,81,81	0
32	MG	A	3298	1/1	0.45	-	83,83,83,83	0
32	MG	N	874	1/1	0.10	-	88,88,88,88	0
32	MG	6	530	1/1	0.22	-	106,106,106,106	0
32	MG	A	3391	1/1	0.55	-	102,102,102,102	0
32	MG	A	2919	1/1	0.16	-	18,18,18,18	0
32	MG	A	3758	1/1	0.33	-	60,60,60,60	0
32	MG	A	3569	1/1	0.18	-	91,91,91,91	0
32	MG	A	3429	1/1	0.27	-	79,79,79,79	0
32	MG	A	3811	1/1	0.73	-	81,81,81,81	0
32	MG	A	3164	1/1	0.55	-	73,73,73,73	0
32	MG	A	3621	1/1	0.51	-	64,64,64,64	0
32	MG	B	396	1/1	0.13	-	92,92,92,92	0
32	MG	A	3501	1/1	0.28	-	59,59,59,59	0
32	MG	6	767	1/1	0.32	-	79,79,79,79	0
32	MG	6	1492	1/1	0.13	-	119,119,119,119	0
32	MG	A	3635	1/1	0.44	-	103,103,103,103	0
32	MG	6	584	1/1	0.24	-	103,103,103,103	0
32	MG	A	3204	1/1	1.31	-	73,73,73,73	0
32	MG	A	3247	1/1	0.42	-	67,67,67,67	0
32	MG	6	151	1/1	0.15	-	68,68,68,68	0
32	MG	6	461	1/1	0.20	-	74,74,74,74	0
32	MG	B	119	1/1	0.28	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	137	1/1	0.49	-	90,90,90,90	0
32	MG	6	322	1/1	0.25	-	78,78,78,78	0
32	MG	A	3645	1/1	0.41	-	92,92,92,92	0
32	MG	A	3480	1/1	0.65	-	61,61,61,61	0
32	MG	6	372	1/1	0.23	-	104,104,104,104	0
32	MG	A	3195	1/1	0.26	-	94,94,94,94	0
32	MG	A	3139	1/1	0.43	-	60,60,60,60	0
32	MG	A	3355	1/1	0.78	-	96,96,96,96	0
32	MG	A	3819	1/1	0.54	-	104,104,104,104	0
32	MG	6	1193	1/1	0.14	-	75,75,75,75	0
32	MG	A	3038	1/1	0.25	-	50,50,50,50	0
32	MG	A	3654	1/1	0.29	-	101,101,101,101	0
32	MG	A	3851	1/1	0.20	-	186,186,186,186	0
32	MG	A	2923	1/1	0.30	-	21,21,21,21	0
32	MG	A	3011	1/1	0.22	-	38,38,38,38	0
32	MG	A	3046	1/1	0.18	-	39,39,39,39	0
32	MG	A	3005	1/1	0.15	-	36,36,36,36	0
32	MG	B	1025	1/1	1.17	-	114,114,114,114	0
32	MG	A	3084	1/1	0.26	-	67,67,67,67	0
32	MG	A	2957	1/1	0.09	-	32,32,32,32	0
32	MG	6	1198	1/1	0.37	-	74,74,74,74	0
32	MG	A	3619	1/1	0.76	-	59,59,59,59	0
32	MG	A	2954	1/1	0.12	-	33,33,33,33	0
32	MG	A	2968	1/1	0.17	-	60,60,60,60	0
32	MG	A	3581	1/1	0.16	-	77,77,77,77	0
32	MG	A	2955	1/1	0.22	-	58,58,58,58	0
32	MG	6	979	1/1	0.17	-	92,92,92,92	0
32	MG	A	3719	1/1	0.22	-	76,76,76,76	0
32	MG	A	3723	1/1	0.33	-	96,96,96,96	0
32	MG	A	3022	1/1	0.63	-	58,58,58,58	0
32	MG	A	3327	1/1	0.44	-	70,70,70,70	0
32	MG	A	3568	1/1	1.46	-	68,68,68,68	0
32	MG	K	633	1/1	0.21	-	73,73,73,73	0
32	MG	A	3412	1/1	0.28	-	86,86,86,86	0
32	MG	A	3306	1/1	0.23	-	94,94,94,94	0
32	MG	A	3187	1/1	0.14	-	46,46,46,46	0
32	MG	A	369	1/1	0.28	-	63,63,63,63	0
32	MG	A	3634	1/1	0.35	-	99,99,99,99	0
32	MG	A	3111	1/1	0.17	-	61,61,61,61	0
32	MG	A	2946	1/1	0.12	-	48,48,48,48	0
32	MG	6	501	1/1	0.93	-	129,129,129,129	0
32	MG	6	330	1/1	0.12	-	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	2906	1/1	0.39	-	23,23,23,23	0
32	MG	W	1311	1/1	0.43	-	56,56,56,56	0
32	MG	A	3095	1/1	0.22	-	49,49,49,49	0
32	MG	A	3749	1/1	0.13	-	138,138,138,138	0
32	MG	6	276	1/1	0.12	-	98,98,98,98	0
32	MG	A	3283	1/1	0.51	-	73,73,73,73	0
32	MG	A	618	1/1	0.19	-	81,81,81,81	0
32	MG	A	3385	1/1	0.46	-	51,51,51,51	0
32	MG	6	1444	1/1	2.85	-	125,125,125,125	0
32	MG	A	2997	1/1	0.44	-	51,51,51,51	0
32	MG	A	3228	1/1	0.46	-	56,56,56,56	0
32	MG	A	3225	1/1	0.64	-	59,59,59,59	0
32	MG	6	972	1/1	1.64	-	90,90,90,90	0
32	MG	6	309	1/1	0.16	-	95,95,95,95	0
32	MG	A	3372	1/1	0.61	-	44,44,44,44	0
32	MG	A	3320	1/1	0.16	-	103,103,103,103	0
32	MG	6	1018	1/1	0.16	-	95,95,95,95	0
32	MG	A	2916	1/1	0.40	-	68,68,68,68	0
32	MG	A	3404	1/1	0.83	-	79,79,79,79	0
32	MG	A	3072	1/1	0.45	-	68,68,68,68	0
32	MG	A	2924	1/1	0.37	-	24,24,24,24	0
32	MG	A	3367	1/1	0.41	-	53,53,53,53	0
32	MG	A	3824	1/1	0.29	-	63,63,63,63	0
32	MG	A	3105	1/1	0.21	-	66,66,66,66	0
32	MG	6	1004	1/1	0.24	-	94,94,94,94	0
32	MG	A	3640	1/1	0.26	-	88,88,88,88	0
32	MG	A	3415	1/1	1.87	-	66,66,66,66	0
32	MG	A	3447	1/1	0.48	-	72,72,72,72	0
32	MG	6	319	1/1	0.15	-	133,133,133,133	0
32	MG	A	3126	1/1	0.81	-	29,29,29,29	0
32	MG	F	1019	1/1	3.28	-	103,103,103,103	0
32	MG	6	220	1/1	0.56	-	93,93,93,93	0
32	MG	A	3734	1/1	0.51	-	74,74,74,74	0
32	MG	A	3319	1/1	0.26	-	96,96,96,96	0
32	MG	A	3540	1/1	3.47	-	164,164,164,164	0
32	MG	6	360	1/1	0.42	-	128,128,128,128	0
32	MG	6	1314	1/1	0.73	-	99,99,99,99	0
32	MG	B	1042	1/1	0.58	-	117,117,117,117	0
32	MG	6	628	1/1	0.74	-	90,90,90,90	0
32	MG	A	3485	1/1	0.44	-	78,78,78,78	0
32	MG	6	1261	1/1	0.42	-	107,107,107,107	0
32	MG	A	3549	1/1	0.20	-	92,92,92,92	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	449	1/1	0.16	-	109,109,109,109	0
32	MG	A	3886	1/1	0.16	-	94,94,94,94	0
32	MG	A	3368	1/1	0.27	-	90,90,90,90	0
32	MG	J	1390	1/1	1.81	-	91,91,91,91	0
32	MG	A	3326	1/1	0.13	-	46,46,46,46	0
32	MG	A	3744	1/1	0.22	-	65,65,65,65	0
32	MG	6	271	1/1	0.65	-	78,78,78,78	0
32	MG	A	3613	1/1	0.42	-	61,61,61,61	0
32	MG	A	3321	1/1	0.29	-	100,100,100,100	0
32	MG	A	3632	1/1	1.19	-	76,76,76,76	0
32	MG	A	3679	1/1	0.29	-	36,36,36,36	0
32	MG	A	3788	1/1	0.26	-	80,80,80,80	0
32	MG	S	1480	1/1	1.10	-	62,62,62,62	0
32	MG	A	3103	1/1	0.34	-	91,91,91,91	0
32	MG	A	2987	1/1	0.44	-	54,54,54,54	0
32	MG	A	3207	1/1	0.15	-	79,79,79,79	0
32	MG	A	3414	1/1	0.33	-	55,55,55,55	0
32	MG	6	748	1/1	0.26	-	123,123,123,123	0
32	MG	A	3394	1/1	0.36	-	75,75,75,75	0
32	MG	6	244	1/1	0.82	-	82,82,82,82	0
32	MG	A	3500	1/1	0.47	-	102,102,102,102	0
32	MG	A	3551	1/1	0.61	-	66,66,66,66	0
32	MG	6	590	1/1	0.22	-	78,78,78,78	0
32	MG	A	3669	1/1	0.21	-	23,23,23,23	0
32	MG	B	120	1/1	0.19	-	33,33,33,33	0
32	MG	6	1115	1/1	0.07	-	76,76,76,76	0
32	MG	A	3468	1/1	0.97	-	83,83,83,83	0
32	MG	A	3108	1/1	0.24	-	31,31,31,31	0
32	MG	A	3664	1/1	0.09	-	24,24,24,24	0
32	MG	B	1054	1/1	0.10	-	84,84,84,84	0
32	MG	A	3384	1/1	0.14	-	124,124,124,124	0
32	MG	A	2969	1/1	0.28	-	50,50,50,50	0
32	MG	6	1020	1/1	0.13	-	109,109,109,109	0
32	MG	6	1441	1/1	0.28	-	73,73,73,73	0
32	MG	B	240	1/1	0.17	-	58,58,58,58	0
32	MG	A	3764	1/1	0.07	-	77,77,77,77	0
32	MG	C	273	1/1	0.28	-	67,67,67,67	0
32	MG	6	952	1/1	2.61	-	131,131,131,131	0
32	MG	A	2936	1/1	0.45	-	29,29,29,29	0
32	MG	A	3554	1/1	0.19	-	76,76,76,76	0
32	MG	A	3360	1/1	0.30	-	75,75,75,75	0
32	MG	D	835	1/1	2.05	-	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	6	647	1/1	0.15	-	117,117,117,117	0
32	MG	6	1267	1/1	0.88	-	87,87,87,87	0
32	MG	A	3353	1/1	0.65	-	169,169,169,169	0
32	MG	6	1277	1/1	0.45	-	109,109,109,109	0
32	MG	V	508	1/1	0.22	-	90,90,90,90	0
32	MG	A	3505	1/1	0.56	-	95,95,95,95	0
32	MG	A	3340	1/1	0.52	-	88,88,88,88	0
32	MG	A	3778	1/1	0.30	-	78,78,78,78	0
32	MG	6	1385	1/1	0.16	-	70,70,70,70	0
32	MG	6	246	1/1	0.39	-	59,59,59,59	0
32	MG	A	158	1/1	0.20	-	72,72,72,72	0
32	MG	A	3799	1/1	0.86	-	73,73,73,73	0
32	MG	6	660	1/1	0.40	-	69,69,69,69	0
32	MG	A	3576	1/1	0.23	-	83,83,83,83	0
32	MG	C	980	1/1	0.10	-	79,79,79,79	0
32	MG	A	3585	1/1	0.68	-	78,78,78,78	0
32	MG	A	3153	1/1	0.24	-	113,113,113,113	0
32	MG	6	636	1/1	0.61	-	108,108,108,108	0
32	MG	A	3389	1/1	0.50	-	84,84,84,84	0
32	MG	A	3346	1/1	0.33	-	95,95,95,95	0
32	MG	A	2998	1/1	0.19	-	38,38,38,38	0
32	MG	A	2992	1/1	0.36	-	69,69,69,69	0
32	MG	A	3407	1/1	0.23	-	108,108,108,108	0
32	MG	A	3245	1/1	0.78	-	65,65,65,65	0
32	MG	A	3040	1/1	0.38	-	72,72,72,72	0
32	MG	A	3837	1/1	0.25	-	83,83,83,83	0
32	MG	A	3751	1/1	0.10	-	109,109,109,109	0
32	MG	A	3809	1/1	0.26	-	90,90,90,90	0
32	MG	A	3161	1/1	0.10	-	93,93,93,93	0
32	MG	A	2979	1/1	0.32	-	40,40,40,40	0
32	MG	A	3596	1/1	0.49	-	80,80,80,80	0
32	MG	A	3863	1/1	0.22	-	100,100,100,100	0
32	MG	A	3464	1/1	0.26	-	95,95,95,95	0
32	MG	A	3832	1/1	0.48	-	101,101,101,101	0
32	MG	6	1117	1/1	0.68	-	84,84,84,84	0
32	MG	A	3628	1/1	1.08	-	81,81,81,81	0
32	MG	6	1335	1/1	0.23	-	116,116,116,116	0
32	MG	A	3573	1/1	0.27	-	128,128,128,128	0
32	MG	6	542	1/1	0.24	-	147,147,147,147	0
32	MG	6	1423	1/1	0.20	-	107,107,107,107	0
32	MG	A	3706	1/1	0.35	-	59,59,59,59	0
32	MG	A	3001	1/1	0.35	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3762	1/1	0.53	-	97,97,97,97	0
32	MG	B	831	1/1	0.38	-	72,72,72,72	0
32	MG	A	3451	1/1	0.22	-	99,99,99,99	0
32	MG	A	3722	1/1	0.24	-	61,61,61,61	0
32	MG	A	3786	1/1	0.47	-	121,121,121,121	0
32	MG	A	3779	1/1	0.64	-	90,90,90,90	0
32	MG	A	3666	1/1	0.45	-	52,52,52,52	0
32	MG	A	2904	1/1	0.21	-	19,19,19,19	0
32	MG	6	286	1/1	0.21	-	59,59,59,59	0
32	MG	A	3398	1/1	0.29	-	75,75,75,75	0
32	MG	A	3402	1/1	0.25	-	95,95,95,95	0
32	MG	A	3290	1/1	0.14	-	104,104,104,104	0
32	MG	A	3829	1/1	0.23	-	104,104,104,104	0
32	MG	B	339	1/1	0.31	-	103,103,103,103	0
32	MG	A	3586	1/1	0.36	-	36,36,36,36	0
32	MG	A	3890	1/1	0.20	-	52,52,52,52	0
32	MG	C	970	1/1	0.46	-	164,164,164,164	0
32	MG	6	883	1/1	0.11	-	92,92,92,92	0
32	MG	A	3761	1/1	0.78	-	76,76,76,76	0
32	MG	A	2934	1/1	0.15	-	5,5,5,5	0
32	MG	A	3068	1/1	0.98	-	67,67,67,67	0
32	MG	A	3163	1/1	0.28	-	88,88,88,88	0
32	MG	6	712	1/1	0.76	-	77,77,77,77	0
32	MG	A	3255	1/1	0.71	-	127,127,127,127	0
32	MG	A	3466	1/1	0.32	-	86,86,86,86	0
32	MG	A	3885	1/1	0.40	-	94,94,94,94	0
32	MG	A	2974	1/1	0.29	-	12,12,12,12	0
32	MG	A	2	1/1	0.30	-	17,17,17,17	0
32	MG	6	1152	1/1	0.17	-	126,126,126,126	0
32	MG	6	310	1/1	0.42	-	96,96,96,96	0
32	MG	6	432	1/1	0.18	-	63,63,63,63	0
32	MG	6	235	1/1	0.15	-	99,99,99,99	0
32	MG	A	3527	1/1	0.31	-	102,102,102,102	0
32	MG	A	2932	1/1	0.69	-	31,31,31,31	0
32	MG	A	3735	1/1	0.30	-	63,63,63,63	0
32	MG	A	4	1/1	0.12	-	16,16,16,16	0
32	MG	6	595	1/1	0.10	-	69,69,69,69	0
32	MG	6	1199	1/1	0.18	-	78,78,78,78	0
32	MG	A	2995	1/1	0.16	-	52,52,52,52	0
32	MG	A	3266	1/1	0.42	-	92,92,92,92	0
32	MG	A	3692	1/1	0.36	-	133,133,133,133	0
32	MG	A	2993	1/1	0.16	-	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3781	1/1	0.61	-	59,59,59,59	0
32	MG	A	2959	1/1	0.23	-	34,34,34,34	0
32	MG	A	3609	1/1	0.35	-	90,90,90,90	0
32	MG	A	3436	1/1	0.31	-	101,101,101,101	0
32	MG	A	3006	1/1	0.43	-	48,48,48,48	0
32	MG	6	1058	1/1	0.25	-	104,104,104,104	0
32	MG	E	1089	1/1	0.21	-	81,81,81,81	0
32	MG	K	929	1/1	0.22	-	109,109,109,109	0
32	MG	6	1445	1/1	0.58	-	106,106,106,106	0
32	MG	A	3198	1/1	0.17	-	93,93,93,93	0
32	MG	A	3446	1/1	0.13	-	92,92,92,92	0
32	MG	A	3358	1/1	0.92	-	78,78,78,78	0
32	MG	A	2903	1/1	0.37	-	11,11,11,11	0
32	MG	A	3176	1/1	0.46	-	69,69,69,69	0
32	MG	A	3045	1/1	0.32	-	56,56,56,56	0
32	MG	A	3288	1/1	0.55	-	76,76,76,76	0
32	MG	A	2908	1/1	0.30	-	15,15,15,15	0
32	MG	6	288	1/1	0.18	-	133,133,133,133	0
32	MG	6	745	1/1	0.15	-	77,77,77,77	0
32	MG	A	3674	1/1	0.35	-	51,51,51,51	0
32	MG	A	3896	1/1	0.22	-	86,86,86,86	0
32	MG	A	1	1/1	0.38	-	9,9,9,9	0
32	MG	A	3793	1/1	0.29	-	100,100,100,100	0
32	MG	A	3096	1/1	0.85	-	87,87,87,87	0
32	MG	6	1296	1/1	0.10	-	97,97,97,97	0
32	MG	A	3004	1/1	0.76	-	72,72,72,72	0
32	MG	6	907	1/1	0.11	-	107,107,107,107	0
32	MG	A	3192	1/1	0.44	-	89,89,89,89	0
32	MG	A	3816	1/1	0.26	-	63,63,63,63	0
32	MG	6	1233	1/1	0.84	-	87,87,87,87	0
32	MG	A	3175	1/1	0.28	-	73,73,73,73	0
32	MG	6	1392	1/1	0.13	-	95,95,95,95	0
32	MG	4	1024	1/1	0.19	-	55,55,55,55	0
32	MG	B	765	1/1	0.22	-	82,82,82,82	0
32	MG	A	3166	1/1	0.15	-	102,102,102,102	0
32	MG	A	3649	1/1	0.28	-	97,97,97,97	0
32	MG	A	3420	1/1	0.20	-	110,110,110,110	0
32	MG	A	3117	1/1	0.19	-	85,85,85,85	0
32	MG	6	155	1/1	0.07	-	66,66,66,66	0
32	MG	A	3597	1/1	0.57	-	162,162,162,162	0
32	MG	A	3352	1/1	0.52	-	70,70,70,70	0
32	MG	A	3222	1/1	0.40	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3030	1/1	0.41	-	76,76,76,76	0
32	MG	4	1468	1/1	0.92	-	76,76,76,76	0
32	MG	A	3232	1/1	0.33	-	59,59,59,59	0
32	MG	6	779	1/1	0.10	-	94,94,94,94	0
32	MG	6	1487	1/1	0.11	-	86,86,86,86	0
32	MG	A	3677	1/1	0.26	-	59,59,59,59	0
32	MG	A	3770	1/1	0.36	-	99,99,99,99	0
32	MG	6	649	1/1	0.87	-	100,100,100,100	0
32	MG	A	3359	1/1	0.19	-	74,74,74,74	0
32	MG	6	393	1/1	0.37	-	61,61,61,61	0
32	MG	A	2912	1/1	0.23	-	14,14,14,14	0
32	MG	D	415	1/1	0.20	-	70,70,70,70	0
32	MG	6	331	1/1	0.26	-	60,60,60,60	0
32	MG	A	3592	1/1	0.30	-	85,85,85,85	0
32	MG	6	783	1/1	0.43	-	93,93,93,93	0
32	MG	A	2909	1/1	0.15	-	71,71,71,71	0
32	MG	A	3243	1/1	0.74	-	70,70,70,70	0
32	MG	6	627	1/1	0.72	-	78,78,78,78	0
32	MG	A	3901	1/1	0.24	-	90,90,90,90	0
32	MG	B	1436	1/1	0.09	-	113,113,113,113	0
32	MG	A	3708	1/1	0.33	-	69,69,69,69	0
32	MG	A	3665	1/1	0.17	-	13,13,13,13	0
32	MG	A	3123	1/1	0.98	-	69,69,69,69	0
32	MG	A	3275	1/1	0.35	-	79,79,79,79	0
32	MG	A	3667	1/1	0.60	-	40,40,40,40	0
32	MG	A	3042	1/1	0.50	-	25,25,25,25	0
32	MG	A	3065	1/1	0.48	-	48,48,48,48	0
32	MG	A	3322	1/1	0.46	-	90,90,90,90	0
32	MG	A	3289	1/1	0.71	-	72,72,72,72	0
32	MG	A	3197	1/1	0.18	-	92,92,92,92	0
32	MG	A	3295	1/1	0.45	-	99,99,99,99	0
32	MG	A	3399	1/1	0.56	-	66,66,66,66	0
32	MG	6	959	1/1	1.06	-	123,123,123,123	0
32	MG	6	608	1/1	1.57	-	124,124,124,124	0
32	MG	6	968	1/1	1.01	-	88,88,88,88	0
32	MG	A	3259	1/1	0.17	-	109,109,109,109	0
32	MG	A	3893	1/1	0.47	-	114,114,114,114	0
32	MG	A	3015	1/1	0.54	-	128,128,128,128	0
32	MG	A	2967	1/1	0.38	-	50,50,50,50	0
32	MG	A	3386	1/1	0.48	-	76,76,76,76	0
32	MG	A	3725	1/1	0.24	-	96,96,96,96	0
32	MG	4	1066	1/1	1.23	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3529	1/1	0.37	-	74,74,74,74	0
32	MG	A	3315	1/1	0.14	-	66,66,66,66	0
32	MG	6	951	1/1	0.13	-	79,79,79,79	0
32	MG	A	3129	1/1	0.85	-	50,50,50,50	0
32	MG	6	738	1/1	0.27	-	105,105,105,105	0
32	MG	A	3484	1/1	0.71	-	87,87,87,87	0
32	MG	A	3425	1/1	0.16	-	113,113,113,113	0
32	MG	A	3180	1/1	0.24	-	74,74,74,74	0
32	MG	A	3741	1/1	0.11	-	96,96,96,96	0
32	MG	A	3393	1/1	0.20	-	110,110,110,110	0
32	MG	6	821	1/1	0.88	-	87,87,87,87	0
32	MG	B	423	1/1	0.26	-	113,113,113,113	0
32	MG	A	3827	1/1	0.88	-	40,40,40,40	0
32	MG	A	3872	1/1	0.61	-	73,73,73,73	0
32	MG	A	3017	1/1	0.19	-	23,23,23,23	0
32	MG	A	3525	1/1	1.42	-	73,73,73,73	0
32	MG	A	3337	1/1	0.58	-	97,97,97,97	0
32	MG	A	2901	1/1	0.53	-	22,22,22,22	0
32	MG	A	3473	1/1	0.39	-	97,97,97,97	0
32	MG	6	1161	1/1	0.15	-	76,76,76,76	0
32	MG	A	3055	1/1	0.32	-	64,64,64,64	0
32	MG	A	3300	1/1	0.32	-	54,54,54,54	0
32	MG	C	1387	1/1	0.23	-	104,104,104,104	0
32	MG	A	3082	1/1	0.27	-	67,67,67,67	0
32	MG	A	3263	1/1	0.25	-	87,87,87,87	0
32	MG	A	3578	1/1	0.65	-	85,85,85,85	0
32	MG	A	3024	1/1	0.35	-	73,73,73,73	0
32	MG	A	3542	1/1	0.34	-	61,61,61,61	0
32	MG	A	3050	1/1	0.46	-	126,126,126,126	0
32	MG	A	3587	1/1	0.53	-	90,90,90,90	0
32	MG	A	3060	1/1	0.11	-	69,69,69,69	0
32	MG	A	3272	1/1	0.27	-	62,62,62,62	0
32	MG	A	3299	1/1	0.31	-	127,127,127,127	0
32	MG	6	965	1/1	0.94	-	117,117,117,117	0
32	MG	A	927	1/1	0.18	-	80,80,80,80	0
32	MG	A	3335	1/1	1.05	-	112,112,112,112	0
32	MG	6	567	1/1	0.69	-	123,123,123,123	0
32	MG	A	3454	1/1	0.69	-	80,80,80,80	0
32	MG	A	3610	1/1	0.32	-	114,114,114,114	0
32	MG	A	3242	1/1	0.21	-	52,52,52,52	0
32	MG	6	746	1/1	0.15	-	72,72,72,72	0
32	MG	A	3636	1/1	0.51	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	A	3392	1/1	0.53	-	77,77,77,77	0
32	MG	A	3766	1/1	0.33	-	84,84,84,84	0
32	MG	A	3438	1/1	0.69	-	120,120,120,120	0
32	MG	6	324	1/1	1.34	-	100,100,100,100	0
32	MG	A	3388	1/1	0.19	-	82,82,82,82	0
32	MG	A	3122	1/1	0.10	-	114,114,114,114	0
32	MG	6	622	1/1	0.18	-	112,112,112,112	0
32	MG	A	3169	1/1	0.68	-	76,76,76,76	0
32	MG	U	1345	1/1	0.29	-	84,84,84,84	0
32	MG	A	3697	1/1	0.19	-	85,85,85,85	0
32	MG	6	811	1/1	0.14	-	132,132,132,132	0
32	MG	A	3791	1/1	0.25	-	97,97,97,97	0
32	MG	A	3882	1/1	0.47	-	55,55,55,55	0
32	MG	6	1083	1/1	1.38	-	68,68,68,68	0
32	MG	A	3234	1/1	0.58	-	85,85,85,85	0
32	MG	6	867	1/1	0.29	-	105,105,105,105	0
32	MG	A	3009	1/1	0.32	-	33,33,33,33	0
32	MG	A	168	1/1	0.29	-	59,59,59,59	0
32	MG	A	3496	1/1	0.26	-	102,102,102,102	0
32	MG	A	3031	1/1	0.37	-	76,76,76,76	0
32	MG	A	2938	1/1	0.52	-	37,37,37,37	0
32	MG	A	3557	1/1	0.37	-	87,87,87,87	0
32	MG	A	3312	1/1	0.25	-	65,65,65,65	0
32	MG	A	3731	1/1	0.55	-	86,86,86,86	0
32	MG	B	1287	1/1	0.20	-	84,84,84,84	0
32	MG	A	2978	1/1	0.28	-	22,22,22,22	0
32	MG	A	3310	1/1	0.38	-	80,80,80,80	0
32	MG	6	957	1/1	0.21	-	61,61,61,61	0
32	MG	A	3390	1/1	0.43	-	76,76,76,76	0
32	MG	A	3227	1/1	0.86	-	64,64,64,64	0
32	MG	A	3740	1/1	1.02	-	96,96,96,96	0
32	MG	6	1075	1/1	0.29	-	118,118,118,118	0
32	MG	A	3481	1/1	0.55	-	82,82,82,82	0
32	MG	A	3413	1/1	0.52	-	60,60,60,60	0
32	MG	6	1463	1/1	0.78	-	97,97,97,97	0
32	MG	6	381	1/1	0.25	-	137,137,137,137	0
32	MG	A	3178	1/1	0.16	-	49,49,49,49	0
32	MG	A	366	1/1	0.97	-	78,78,78,78	0
32	MG	A	3605	1/1	0.11	-	113,113,113,113	0
32	MG	A	3504	1/1	0.28	-	98,98,98,98	0
32	MG	A	3418	1/1	0.41	-	65,65,65,65	0
32	MG	A	3409	1/1	1.15	-	110,110,110,110	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3075	1/1	1.12	-	71,71,71,71	0
32	MG	6	1428	1/1	0.68	-	88,88,88,88	0
32	MG	A	3344	1/1	0.19	-	70,70,70,70	0
32	MG	6	611	1/1	0.34	-	82,82,82,82	0
32	MG	A	3364	1/1	0.15	-	98,98,98,98	0
32	MG	A	2990	1/1	0.33	-	46,46,46,46	0
32	MG	A	3843	1/1	0.27	-	92,92,92,92	0
32	MG	A	3831	1/1	0.26	-	67,67,67,67	0
32	MG	A	3873	1/1	0.71	-	60,60,60,60	0
32	MG	A	3257	1/1	0.67	-	43,43,43,43	0
32	MG	6	850	1/1	0.28	-	99,99,99,99	0
32	MG	A	3641	1/1	0.65	-	45,45,45,45	0
32	MG	B	471	1/1	0.46	-	101,101,101,101	0
32	MG	6	766	1/1	0.13	-	97,97,97,97	0
32	MG	A	365	1/1	0.66	-	105,105,105,105	0
32	MG	A	3472	1/1	0.12	-	117,117,117,117	0
32	MG	A	2907	1/1	0.46	-	49,49,49,49	0
32	MG	6	596	1/1	1.36	-	118,118,118,118	0
32	MG	A	490	1/1	1.02	-	70,70,70,70	0
32	MG	A	3106	1/1	0.51	-	58,58,58,58	0
32	MG	I	585	1/1	0.21	-	104,104,104,104	0
32	MG	A	3825	1/1	0.32	-	108,108,108,108	0
32	MG	A	3618	1/1	0.20	-	86,86,86,86	0
32	MG	D	935	1/1	0.39	-	107,107,107,107	0
32	MG	6	1322	1/1	0.86	-	122,122,122,122	0
32	MG	A	3311	1/1	0.74	-	110,110,110,110	0
32	MG	A	3194	1/1	0.59	-	56,56,56,56	0
32	MG	A	3602	1/1	0.48	-	100,100,100,100	0
32	MG	B	233	1/1	0.31	-	63,63,63,63	0
32	MG	A	3756	1/1	0.47	-	81,81,81,81	0
32	MG	A	3342	1/1	0.55	-	67,67,67,67	0
32	MG	A	3173	1/1	0.31	-	114,114,114,114	0
32	MG	A	3661	1/1	0.43	-	15,15,15,15	0
32	MG	6	565	1/1	0.67	-	108,108,108,108	0
32	MG	A	3502	1/1	0.35	-	63,63,63,63	0
32	MG	A	3817	1/1	0.35	-	108,108,108,108	0
32	MG	A	3277	1/1	0.46	-	76,76,76,76	0
32	MG	A	3627	1/1	1.31	-	113,113,113,113	0
32	MG	6	820	1/1	0.23	-	131,131,131,131	0
32	MG	6	579	1/1	0.39	-	107,107,107,107	0
32	MG	A	3100	1/1	0.56	-	88,88,88,88	0
32	MG	A	3165	1/1	0.44	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	6	531	1/1	0.17	-	102,102,102,102	0
32	MG	A	3074	1/1	0.45	-	71,71,71,71	0
32	MG	B	417	1/1	0.29	-	85,85,85,85	0
32	MG	A	3772	1/1	0.60	-	104,104,104,104	0
32	MG	A	3689	1/1	1.18	-	137,137,137,137	0
32	MG	A	3332	1/1	2.05	-	58,58,58,58	0
32	MG	6	489	1/1	0.20	-	123,123,123,123	0
32	MG	A	3709	1/1	0.20	-	82,82,82,82	0
32	MG	A	3252	1/1	0.29	-	55,55,55,55	0
32	MG	A	3808	1/1	0.30	-	172,172,172,172	0
32	MG	A	3110	1/1	0.20	-	74,74,74,74	0
32	MG	6	1153	1/1	0.29	-	82,82,82,82	0
32	MG	6	833	1/1	0.49	-	111,111,111,111	0
32	MG	A	3724	1/1	0.72	-	88,88,88,88	0
32	MG	A	3864	1/1	0.27	-	94,94,94,94	0
32	MG	A	3801	1/1	0.47	-	90,90,90,90	0
32	MG	A	3604	1/1	0.67	-	79,79,79,79	0
32	MG	6	205	1/1	0.45	-	51,51,51,51	0
32	MG	B	1226	1/1	0.35	-	105,105,105,105	0
32	MG	J	1176	1/1	0.43	-	32,32,32,32	0
32	MG	2	298	1/1	1.07	-	78,78,78,78	0
32	MG	A	3487	1/1	0.36	-	130,130,130,130	0
32	MG	A	3528	1/1	0.11	-	102,102,102,102	0
32	MG	A	3737	1/1	0.28	-	92,92,92,92	0
32	MG	A	2928	1/1	0.18	-	42,42,42,42	0
32	MG	A	3469	1/1	0.64	-	69,69,69,69	0
32	MG	A	3583	1/1	0.66	-	91,91,91,91	0
32	MG	A	3904	1/1	0.36	-	53,53,53,53	0
32	MG	A	3334	1/1	0.51	-	75,75,75,75	0
32	MG	A	2958	1/1	0.71	-	45,45,45,45	0
32	MG	A	3244	1/1	1.12	-	71,71,71,71	0
32	MG	A	3840	1/1	0.84	-	123,123,123,123	0
32	MG	A	3156	1/1	0.22	-	73,73,73,73	0
32	MG	A	3091	1/1	0.13	-	78,78,78,78	0
32	MG	6	911	1/1	0.31	-	97,97,97,97	0
32	MG	6	296	1/1	0.56	-	80,80,80,80	0
32	MG	A	3339	1/1	0.73	-	75,75,75,75	0
32	MG	6	759	1/1	1.45	-	112,112,112,112	0
32	MG	A	3143	1/1	0.51	-	33,33,33,33	0
32	MG	A	2930	1/1	0.34	-	7,7,7,7	0
32	MG	6	1459	1/1	0.25	-	99,99,99,99	0
32	MG	A	3624	1/1	0.68	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	A	3328	1/1	0.47	-	88,88,88,88	0
32	MG	A	3807	1/1	0.51	-	98,98,98,98	0
32	MG	6	786	1/1	0.17	-	76,76,76,76	0
32	MG	A	3891	1/1	0.57	-	74,74,74,74	0
32	MG	C	1488	1/1	0.24	-	67,67,67,67	0
32	MG	A	3511	1/1	0.26	-	96,96,96,96	0
32	MG	A	169	1/1	0.15	-	45,45,45,45	0
32	MG	A	3652	1/1	0.25	-	56,56,56,56	0
32	MG	A	2920	1/1	0.27	-	31,31,31,31	0
32	MG	A	3647	1/1	1.87	-	102,102,102,102	0
32	MG	A	3146	1/1	0.32	-	52,52,52,52	0
32	MG	B	953	1/1	0.37	-	88,88,88,88	0
32	MG	6	612	1/1	0.83	-	49,49,49,49	0
32	MG	6	236	1/1	0.22	-	84,84,84,84	0
32	MG	A	3053	1/1	0.24	-	114,114,114,114	0
32	MG	A	2953	1/1	0.32	-	42,42,42,42	0
32	MG	A	3658	1/1	0.47	-	106,106,106,106	0
32	MG	6	1060	1/1	0.21	-	101,101,101,101	0
32	MG	A	3707	1/1	1.11	-	58,58,58,58	0
32	MG	J	726	1/1	1.71	-	126,126,126,126	0
32	MG	A	3656	1/1	0.41	-	111,111,111,111	0
32	MG	6	352	1/1	0.13	-	80,80,80,80	0
32	MG	A	3823	1/1	0.61	-	101,101,101,101	0
32	MG	A	3073	1/1	0.23	-	67,67,67,67	0
32	MG	6	652	1/1	0.34	-	88,88,88,88	0
32	MG	6	380	1/1	0.18	-	51,51,51,51	0
32	MG	A	2921	1/1	0.29	-	21,21,21,21	0
32	MG	6	445	1/1	0.63	-	72,72,72,72	0
32	MG	A	3028	1/1	0.27	-	44,44,44,44	0
32	MG	A	3151	1/1	0.28	-	70,70,70,70	0
32	MG	A	3256	1/1	0.24	-	85,85,85,85	0
32	MG	6	1350	1/1	0.33	-	89,89,89,89	0
32	MG	V	680	1/1	0.38	-	115,115,115,115	0
32	MG	A	2939	1/1	0.48	-	21,21,21,21	0
32	MG	6	991	1/1	1.07	-	108,108,108,108	0
32	MG	6	150	1/1	0.26	-	76,76,76,76	0
32	MG	A	3720	1/1	0.24	-	82,82,82,82	0
32	MG	A	3144	1/1	0.82	-	50,50,50,50	0
32	MG	6	293	1/1	0.33	-	79,79,79,79	0
32	MG	A	3865	1/1	0.38	-	103,103,103,103	0
32	MG	A	3000	1/1	0.37	-	60,60,60,60	0
32	MG	A	3203	1/1	0.12	-	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3226	1/1	0.42	-	75,75,75,75	0
32	MG	J	1440	1/1	0.80	-	135,135,135,135	0
32	MG	A	3423	1/1	0.33	-	79,79,79,79	0
32	MG	A	3676	1/1	0.62	-	51,51,51,51	0
32	MG	6	239	1/1	0.07	-	93,93,93,93	0
32	MG	A	3548	1/1	0.20	-	107,107,107,107	0
32	MG	A	3579	1/1	0.43	-	60,60,60,60	0
32	MG	A	3800	1/1	1.09	-	102,102,102,102	0
32	MG	A	3171	1/1	0.25	-	54,54,54,54	0
32	MG	A	2949	1/1	0.35	-	44,44,44,44	0
32	MG	A	3856	1/1	0.54	-	130,130,130,130	0
32	MG	A	3174	1/1	0.49	-	69,69,69,69	0
32	MG	6	1007	1/1	0.16	-	136,136,136,136	0
32	MG	1	338	1/1	0.22	-	80,80,80,80	0
32	MG	6	1093	1/1	0.45	-	125,125,125,125	0
32	MG	A	3681	1/1	0.54	-	23,23,23,23	0
32	MG	6	689	1/1	0.66	-	97,97,97,97	0
32	MG	A	157	1/1	0.21	-	43,43,43,43	0
32	MG	6	1367	1/1	1.19	-	102,102,102,102	0
32	MG	A	3467	1/1	0.35	-	88,88,88,88	0
32	MG	6	653	1/1	0.63	-	80,80,80,80	0
32	MG	A	3296	1/1	0.37	-	152,152,152,152	0
32	MG	6	65	1/1	0.33	-	54,54,54,54	0
32	MG	6	815	1/1	0.23	-	125,125,125,125	0
32	MG	A	3688	1/1	0.42	-	109,109,109,109	0
32	MG	K	758	1/1	0.42	-	98,98,98,98	0
32	MG	A	2972	1/1	0.13	-	23,23,23,23	0
32	MG	6	606	1/1	0.50	-	116,116,116,116	0
32	MG	A	3491	1/1	0.61	-	63,63,63,63	0
32	MG	6	467	1/1	2.71	-	115,115,115,115	0
32	MG	A	3580	1/1	1.20	-	95,95,95,95	0
32	MG	A	3894	1/1	0.12	-	124,124,124,124	0
32	MG	A	3794	1/1	0.35	-	103,103,103,103	0
32	MG	A	3713	1/1	1.10	-	67,67,67,67	0
32	MG	6	1172	1/1	0.37	-	74,74,74,74	0
32	MG	A	3325	1/1	0.12	-	53,53,53,53	0
32	MG	6	159	1/1	0.74	-	70,70,70,70	0
32	MG	6	1391	1/1	0.17	-	66,66,66,66	0
32	MG	A	3617	1/1	0.27	-	58,58,58,58	0
32	MG	A	2965	1/1	0.77	-	38,38,38,38	0
32	MG	B	599	1/1	0.07	-	113,113,113,113	0
32	MG	A	3710	1/1	0.36	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	2927	1/1	0.31	-	23,23,23,23	0
32	MG	6	566	1/1	0.11	-	92,92,92,92	0
32	MG	A	3016	1/1	1.21	-	68,68,68,68	0
32	MG	A	3550	1/1	0.92	-	101,101,101,101	0
32	MG	A	3047	1/1	0.69	-	77,77,77,77	0
32	MG	A	3253	1/1	0.26	-	78,78,78,78	0
32	MG	A	3286	1/1	0.30	-	107,107,107,107	0
32	MG	A	3570	1/1	0.22	-	136,136,136,136	0
32	MG	A	3206	1/1	0.46	-	59,59,59,59	0
32	MG	A	3608	1/1	0.26	-	47,47,47,47	0
32	MG	A	3848	1/1	0.31	-	60,60,60,60	0
32	MG	A	3125	1/1	0.43	-	57,57,57,57	0
32	MG	6	1317	1/1	1.23	-	145,145,145,145	0
32	MG	B	1011	1/1	0.74	-	134,134,134,134	0
32	MG	A	3380	1/1	0.41	-	84,84,84,84	0
32	MG	A	3199	1/1	0.39	-	64,64,64,64	0
32	MG	A	3279	1/1	0.45	-	104,104,104,104	0
32	MG	6	675	1/1	0.29	-	77,77,77,77	0
32	MG	A	3131	1/1	0.40	-	61,61,61,61	0
32	MG	A	3248	1/1	0.26	-	87,87,87,87	0
32	MG	6	1183	1/1	0.13	-	86,86,86,86	0
32	MG	6	713	1/1	0.13	-	89,89,89,89	0
32	MG	A	3168	1/1	0.73	-	46,46,46,46	0
32	MG	G	1421	1/1	0.27	-	98,98,98,98	0
32	MG	A	3044	1/1	0.50	-	79,79,79,79	0
32	MG	A	3815	1/1	0.48	-	67,67,67,67	0
32	MG	A	3090	1/1	0.19	-	49,49,49,49	0
32	MG	A	3881	1/1	0.26	-	105,105,105,105	0
32	MG	A	3850	1/1	0.39	-	50,50,50,50	0
32	MG	A	3010	1/1	0.13	-	47,47,47,47	0
32	MG	6	1181	1/1	0.17	-	75,75,75,75	0
32	MG	6	1415	1/1	0.46	-	98,98,98,98	0
32	MG	6	1265	1/1	0.46	-	130,130,130,130	0
32	MG	A	3460	1/1	0.60	-	93,93,93,93	0
32	MG	B	414	1/1	0.33	-	65,65,65,65	0
32	MG	A	3743	1/1	0.72	-	78,78,78,78	0
32	MG	A	3133	1/1	0.28	-	61,61,61,61	0
32	MG	6	1114	1/1	0.33	-	94,94,94,94	0
32	MG	A	3205	1/1	0.33	-	91,91,91,91	0
32	MG	A	3642	1/1	0.48	-	104,104,104,104	0
32	MG	A	3088	1/1	0.25	-	55,55,55,55	0
32	MG	6	1404	1/1	0.61	-	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	1017	1/1	0.14	-	123,123,123,123	0
32	MG	A	3440	1/1	0.54	-	52,52,52,52	0
32	MG	6	1061	1/1	0.16	-	113,113,113,113	0
32	MG	A	3120	1/1	0.11	-	63,63,63,63	0
32	MG	A	3615	1/1	0.22	-	124,124,124,124	0
32	MG	A	2922	1/1	0.41	-	34,34,34,34	0
32	MG	P	1476	1/1	0.69	-	87,87,87,87	0
32	MG	6	1049	1/1	0.29	-	167,167,167,167	0
32	MG	A	3338	1/1	1.20	-	77,77,77,77	0
32	MG	A	3524	1/1	0.22	-	68,68,68,68	0
32	MG	2	430	1/1	0.17	-	42,42,42,42	0
32	MG	A	3510	1/1	0.23	-	99,99,99,99	0
32	MG	A	3795	1/1	0.34	-	57,57,57,57	0
32	MG	A	3755	1/1	0.39	-	83,83,83,83	0
32	MG	A	3489	1/1	0.32	-	77,77,77,77	0
32	MG	6	476	1/1	0.17	-	80,80,80,80	0
32	MG	A	3080	1/1	0.70	-	56,56,56,56	0
32	MG	A	3876	1/1	0.65	-	95,95,95,95	0
32	MG	B	1482	1/1	1.22	-	101,101,101,101	0
32	MG	A	2952	1/1	0.10	-	31,31,31,31	0
32	MG	A	3769	1/1	0.63	-	73,73,73,73	0
32	MG	6	1012	1/1	0.63	-	92,92,92,92	0
32	MG	A	3014	1/1	0.60	-	47,47,47,47	0
32	MG	6	1427	1/1	1.13	-	87,87,87,87	0
32	MG	6	495	1/1	0.36	-	76,76,76,76	0
32	MG	A	3260	1/1	0.11	-	108,108,108,108	0
32	MG	A	3838	1/1	0.27	-	72,72,72,72	0
32	MG	A	3136	1/1	0.23	-	31,31,31,31	0
32	MG	A	3419	1/1	0.38	-	60,60,60,60	0
32	MG	A	3033	1/1	0.58	-	74,74,74,74	0
32	MG	A	3869	1/1	0.43	-	125,125,125,125	0
32	MG	A	3748	1/1	1.43	-	88,88,88,88	0
32	MG	A	3087	1/1	0.62	-	59,59,59,59	0
32	MG	A	3158	1/1	0.94	-	67,67,67,67	0
32	MG	A	3410	1/1	0.66	-	48,48,48,48	0
32	MG	6	1398	1/1	0.62	-	83,83,83,83	0
32	MG	A	3555	1/1	0.48	-	93,93,93,93	0
32	MG	A	3417	1/1	1.03	-	72,72,72,72	0
32	MG	A	3083	1/1	0.33	-	47,47,47,47	0
32	MG	6	722	1/1	0.40	-	88,88,88,88	0
32	MG	J	853	1/1	1.08	-	84,84,84,84	0
32	MG	A	3571	1/1	0.24	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3785	1/1	0.81	-	79,79,79,79	0
32	MG	6	484	1/1	0.54	-	75,75,75,75	0
32	MG	V	1289	1/1	0.88	-	96,96,96,96	0
32	MG	6	776	1/1	0.34	-	118,118,118,118	0
32	MG	B	1068	1/1	0.17	-	67,67,67,67	0
32	MG	6	791	1/1	0.40	-	80,80,80,80	0
32	MG	A	3560	1/1	0.25	-	56,56,56,56	0
32	MG	A	3653	1/1	0.34	-	89,89,89,89	0
32	MG	A	3262	1/1	0.17	-	99,99,99,99	0
32	MG	A	3803	1/1	1.13	-	58,58,58,58	0
32	MG	A	3236	1/1	0.44	-	57,57,57,57	0
32	MG	A	3718	1/1	1.01	-	64,64,64,64	0
32	MG	6	1224	1/1	0.13	-	97,97,97,97	0
32	MG	A	3796	1/1	0.32	-	80,80,80,80	0
32	MG	6	277	1/1	0.36	-	98,98,98,98	0
32	MG	D	262	1/1	0.25	-	39,39,39,39	0
32	MG	A	3064	1/1	0.28	-	33,33,33,33	0
32	MG	A	100	1/1	0.39	-	23,23,23,23	0
32	MG	A	3603	1/1	0.11	-	154,154,154,154	0
32	MG	A	3830	1/1	0.58	-	80,80,80,80	0
32	MG	A	3884	1/1	0.23	-	132,132,132,132	0
32	MG	A	2915	1/1	0.18	-	12,12,12,12	0
32	MG	A	3874	1/1	0.24	-	111,111,111,111	0
32	MG	A	3588	1/1	0.98	-	72,72,72,72	0
32	MG	6	756	1/1	0.21	-	125,125,125,125	0
32	MG	A	3273	1/1	0.61	-	69,69,69,69	0
32	MG	A	3544	1/1	0.64	-	93,93,93,93	0
32	MG	6	973	1/1	0.40	-	109,109,109,109	0
32	MG	A	3678	1/1	0.33	-	60,60,60,60	0
32	MG	A	3680	1/1	0.51	-	57,57,57,57	0
32	MG	A	1134	1/1	0.93	-	50,50,50,50	0
32	MG	A	3116	1/1	0.42	-	76,76,76,76	0
32	MG	K	894	1/1	0.57	-	92,92,92,92	0
32	MG	A	3777	1/1	0.14	-	94,94,94,94	0
32	MG	A	3892	1/1	0.26	-	80,80,80,80	0
32	MG	A	3432	1/1	0.24	-	84,84,84,84	0
32	MG	B	1256	1/1	0.38	-	91,91,91,91	0
32	MG	6	654	1/1	0.55	-	77,77,77,77	0
32	MG	6	465	1/1	0.22	-	92,92,92,92	0
32	MG	A	3623	1/1	1.17	-	103,103,103,103	0
32	MG	A	3124	1/1	0.09	-	114,114,114,114	0
32	MG	6	524	1/1	0.62	-	122,122,122,122	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3519	1/1	0.38	-	148,148,148,148	0
32	MG	A	166	1/1	0.16	-	81,81,81,81	0
32	MG	A	3705	1/1	0.25	-	78,78,78,78	0
32	MG	A	3147	1/1	0.24	-	33,33,33,33	0
32	MG	A	3572	1/1	0.23	-	110,110,110,110	0
32	MG	A	363	1/1	0.49	-	54,54,54,54	0
32	MG	A	3562	1/1	0.15	-	115,115,115,115	0
32	MG	A	2981	1/1	0.33	-	28,28,28,28	0
32	MG	A	3134	1/1	0.49	-	69,69,69,69	0
32	MG	A	3712	1/1	0.47	-	50,50,50,50	0
32	MG	A	3293	1/1	0.27	-	67,67,67,67	0
32	MG	A	3898	1/1	0.58	-	58,58,58,58	0
32	MG	6	364	1/1	0.47	-	85,85,85,85	0
32	MG	6	1333	1/1	0.36	-	74,74,74,74	0
32	MG	A	3265	1/1	1.04	-	116,116,116,116	0
32	MG	A	3424	1/1	0.21	-	90,90,90,90	0
32	MG	A	555	1/1	0.47	-	102,102,102,102	0
32	MG	A	3113	1/1	0.65	-	59,59,59,59	0
32	MG	6	872	1/1	0.23	-	125,125,125,125	0
32	MG	A	3020	1/1	0.40	-	83,83,83,83	0
32	MG	6	926	1/1	0.15	-	89,89,89,89	0
32	MG	A	3188	1/1	0.21	-	76,76,76,76	0
32	MG	A	3483	1/1	0.52	-	120,120,120,120	0
32	MG	A	3211	1/1	0.28	-	112,112,112,112	0
32	MG	6	1202	1/1	0.57	-	114,114,114,114	0
32	MG	A	3052	1/1	0.15	-	61,61,61,61	0
32	MG	A	2900	1/1	0.45	-	20,20,20,20	0
32	MG	A	2925	1/1	0.32	-	25,25,25,25	0
32	MG	P	836	1/1	0.27	-	109,109,109,109	0
32	MG	A	3179	1/1	0.40	-	86,86,86,86	0
32	MG	6	473	1/1	0.41	-	95,95,95,95	0
32	MG	A	3836	1/1	0.39	-	95,95,95,95	0
32	MG	6	988	1/1	0.64	-	76,76,76,76	0
32	MG	K	798	1/1	1.68	-	94,94,94,94	0
32	MG	A	3061	1/1	0.67	-	43,43,43,43	0
32	MG	A	3611	1/1	0.48	-	125,125,125,125	0
32	MG	A	3240	1/1	0.25	-	70,70,70,70	0
32	MG	A	3673	1/1	0.51	-	55,55,55,55	0
32	MG	6	928	1/1	0.35	-	91,91,91,91	0
32	MG	A	3780	1/1	0.44	-	61,61,61,61	0
32	MG	C	535	1/1	0.25	-	131,131,131,131	0
32	MG	O	847	1/1	0.15	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3094	1/1	0.38	-	58,58,58,58	0
32	MG	A	3638	1/1	1.28	-	83,83,83,83	0
32	MG	A	3648	1/1	0.28	-	106,106,106,106	0
32	MG	A	3140	1/1	0.53	-	56,56,56,56	0
32	MG	6	1139	1/1	0.54	-	63,63,63,63	0
32	MG	A	3057	1/1	0.05	-	85,85,85,85	0
32	MG	A	3835	1/1	0.83	-	96,96,96,96	0
32	MG	A	3193	1/1	0.53	-	43,43,43,43	0
32	MG	A	3291	1/1	0.27	-	46,46,46,46	0
32	MG	A	3590	1/1	0.64	-	85,85,85,85	0
32	MG	A	141	1/1	0.18	-	35,35,35,35	0
32	MG	A	3849	1/1	0.16	-	87,87,87,87	0
32	MG	A	2948	1/1	0.27	-	45,45,45,45	0
32	MG	A	3189	1/1	0.26	-	67,67,67,67	0
32	MG	A	3231	1/1	0.27	-	76,76,76,76	0
32	MG	A	3371	1/1	0.40	-	63,63,63,63	0
32	MG	A	3089	1/1	0.65	-	46,46,46,46	0
32	MG	A	3721	1/1	0.70	-	92,92,92,92	0
32	MG	B	916	1/1	0.13	-	73,73,73,73	0
32	MG	A	3246	1/1	0.14	-	48,48,48,48	0
32	MG	B	646	1/1	0.43	-	75,75,75,75	0
32	MG	6	1356	1/1	0.16	-	137,137,137,137	0
32	MG	A	3093	1/1	0.45	-	50,50,50,50	0
32	MG	6	908	1/1	0.23	-	47,47,47,47	0
32	MG	A	3172	1/1	0.61	-	82,82,82,82	0
32	MG	A	3750	1/1	0.50	-	67,67,67,67	0
32	MG	B	444	1/1	0.14	-	72,72,72,72	0
32	MG	A	3523	1/1	0.15	-	30,30,30,30	0
32	MG	6	644	1/1	0.17	-	102,102,102,102	0
32	MG	A	3552	1/1	0.12	-	81,81,81,81	0
32	MG	A	3121	1/1	0.65	-	62,62,62,62	0
32	MG	A	3170	1/1	0.29	-	38,38,38,38	0
32	MG	A	3883	1/1	0.40	-	78,78,78,78	0
32	MG	6	1299	1/1	0.88	-	58,58,58,58	0
32	MG	A	3159	1/1	0.34	-	54,54,54,54	0
32	MG	6	1399	1/1	1.54	-	136,136,136,136	0
32	MG	A	3241	1/1	0.31	-	77,77,77,77	0
32	MG	A	3305	1/1	0.22	-	58,58,58,58	0
32	MG	6	447	1/1	0.27	-	63,63,63,63	0
32	MG	6	1358	1/1	0.23	-	80,80,80,80	0
32	MG	A	3448	1/1	0.57	-	137,137,137,137	0
32	MG	A	5	1/1	0.41	-	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	1223	1/1	0.20	-	80,80,80,80	0
32	MG	A	3422	1/1	0.64	-	62,62,62,62	0
32	MG	L	1464	1/1	0.48	-	66,66,66,66	0
32	MG	A	3387	1/1	0.59	-	72,72,72,72	0
32	MG	6	735	1/1	0.77	-	65,65,65,65	0
32	MG	A	3079	1/1	0.28	-	127,127,127,127	0
32	MG	A	3553	1/1	0.21	-	93,93,93,93	0
32	MG	6	219	1/1	0.40	-	77,77,77,77	0
32	MG	A	3703	1/1	0.42	-	50,50,50,50	0
32	MG	6	134	1/1	0.21	-	66,66,66,66	0
32	MG	A	3662	1/1	0.25	-	22,22,22,22	0
32	MG	A	3691	1/1	0.52	-	59,59,59,59	0
32	MG	A	3051	1/1	0.06	-	127,127,127,127	0
32	MG	E	208	1/1	0.48	-	32,32,32,32	0
32	MG	A	3783	1/1	0.48	-	76,76,76,76	0
32	MG	A	3309	1/1	0.65	-	38,38,38,38	0
32	MG	A	3492	1/1	0.09	-	21,21,21,21	0
32	MG	A	2988	1/1	0.07	-	26,26,26,26	0
32	MG	A	3396	1/1	0.52	-	124,124,124,124	0
32	MG	P	860	1/1	0.34	-	72,72,72,72	0
32	MG	A	3294	1/1	0.15	-	85,85,85,85	0
32	MG	A	3541	1/1	0.27	-	87,87,87,87	0
32	MG	6	1354	1/1	0.51	-	99,99,99,99	0
32	MG	A	3655	1/1	0.25	-	73,73,73,73	0
32	MG	A	2913	1/1	0.15	-	32,32,32,32	0
32	MG	A	3670	1/1	0.62	-	45,45,45,45	0
32	MG	A	3699	1/1	0.62	-	46,46,46,46	0
32	MG	A	3049	1/1	0.33	-	129,129,129,129	0
32	MG	A	3490	1/1	0.26	-	69,69,69,69	0
32	MG	A	2986	1/1	0.31	-	47,47,47,47	0
32	MG	K	232	1/1	0.20	-	87,87,87,87	0
32	MG	A	3739	1/1	0.89	-	41,41,41,41	0
32	MG	A	3054	1/1	0.87	-	91,91,91,91	0
32	MG	6	771	1/1	0.14	-	93,93,93,93	0
32	MG	A	2999	1/1	0.49	-	41,41,41,41	0
32	MG	6	413	1/1	0.34	-	79,79,79,79	0
32	MG	A	3229	1/1	0.40	-	126,126,126,126	0
32	MG	Q	887	1/1	0.32	-	97,97,97,97	0
32	MG	A	3155	1/1	0.53	-	59,59,59,59	0
32	MG	A	3307	1/1	0.47	-	96,96,96,96	0
32	MG	6	453	1/1	0.51	-	63,63,63,63	0
32	MG	B	312	1/1	0.06	-	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3152	1/1	0.41	-	30,30,30,30	0
32	MG	A	2991	1/1	0.27	-	36,36,36,36	0
32	MG	A	3220	1/1	0.28	-	81,81,81,81	0
32	MG	6	1163	1/1	0.84	-	83,83,83,83	0
32	MG	A	3577	1/1	0.94	-	81,81,81,81	0
32	MG	B	479	1/1	0.31	-	93,93,93,93	0
32	MG	F	1279	1/1	0.85	-	70,70,70,70	0
32	MG	6	737	1/1	0.83	-	95,95,95,95	0
32	MG	A	3702	1/1	0.42	-	58,58,58,58	0
32	MG	A	3239	1/1	0.20	-	111,111,111,111	0
32	MG	A	3696	1/1	0.24	-	80,80,80,80	0
32	MG	6	962	1/1	0.14	-	97,97,97,97	0
32	MG	A	3128	1/1	0.47	-	40,40,40,40	0
32	MG	B	202	1/1	0.33	-	78,78,78,78	0
32	MG	C	1286	1/1	0.39	-	80,80,80,80	0
32	MG	A	3812	1/1	1.02	-	77,77,77,77	0
32	MG	A	3251	1/1	0.31	-	73,73,73,73	0
32	MG	A	3316	1/1	1.24	-	81,81,81,81	0
32	MG	A	273	1/1	0.51	-	51,51,51,51	0
32	MG	A	3421	1/1	0.31	-	63,63,63,63	0
32	MG	Y	63	1/1	0.09	-	12,12,12,12	0
32	MG	A	3810	1/1	0.39	-	80,80,80,80	0
32	MG	A	3209	1/1	0.25	-	98,98,98,98	0
32	MG	6	1438	1/1	0.89	-	85,85,85,85	0
32	MG	A	3742	1/1	0.66	-	57,57,57,57	0
32	MG	A	3594	1/1	0.36	-	73,73,73,73	0
32	MG	6	891	1/1	0.60	-	181,181,181,181	0
32	MG	A	3682	1/1	0.63	-	61,61,61,61	0
32	MG	A	3711	1/1	0.18	-	57,57,57,57	0
32	MG	A	3854	1/1	0.39	-	76,76,76,76	0
32	MG	A	3150	1/1	0.65	-	53,53,53,53	0
32	MG	A	3495	1/1	0.55	-	66,66,66,66	0
32	MG	A	3757	1/1	0.39	-	61,61,61,61	0
32	MG	C	1130	1/1	0.24	-	58,58,58,58	0
32	MG	A	3507	1/1	0.18	-	51,51,51,51	0
32	MG	A	3474	1/1	0.58	-	79,79,79,79	0
32	MG	G	1270	1/1	0.25	-	102,102,102,102	0
32	MG	A	3403	1/1	0.54	-	56,56,56,56	0
32	MG	6	320	1/1	0.79	-	117,117,117,117	0
32	MG	A	2989	1/1	0.43	-	32,32,32,32	0
32	MG	A	3313	1/1	0.28	-	78,78,78,78	0
32	MG	A	2982	1/1	0.29	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3792	1/1	0.61	-	97,97,97,97	0
32	MG	A	3145	1/1	0.47	-	70,70,70,70	0
32	MG	A	3463	1/1	0.67	-	86,86,86,86	0
32	MG	A	3274	1/1	0.55	-	71,71,71,71	0
32	MG	A	3839	1/1	0.83	-	84,84,84,84	0
32	MG	A	3058	1/1	0.34	-	49,49,49,49	0
32	MG	A	3714	1/1	0.84	-	70,70,70,70	0
32	MG	6	1178	1/1	0.77	-	135,135,135,135	0
32	MG	6	241	1/1	0.14	-	49,49,49,49	0
32	MG	A	3465	1/1	0.21	-	61,61,61,61	0
32	MG	6	1379	1/1	0.24	-	144,144,144,144	0
32	MG	6	1244	1/1	0.29	-	76,76,76,76	0
32	MG	6	854	1/1	1.13	-	100,100,100,100	0
32	MG	A	3650	1/1	0.18	-	63,63,63,63	0
32	MG	A	3822	1/1	0.27	-	56,56,56,56	0
32	MG	6	1346	1/1	0.55	-	95,95,95,95	0
32	MG	A	3405	1/1	0.39	-	67,67,67,67	0
32	MG	A	3370	1/1	0.34	-	80,80,80,80	0
32	MG	6	1037	1/1	0.82	-	96,96,96,96	0
32	MG	6	177	1/1	0.78	-	84,84,84,84	0
32	MG	J	504	1/1	0.81	-	61,61,61,61	0
32	MG	6	517	1/1	0.06	-	83,83,83,83	0
32	MG	6	318	1/1	0.10	-	87,87,87,87	0
32	MG	6	411	1/1	0.23	-	90,90,90,90	0
32	MG	B	468	1/1	0.64	-	103,103,103,103	0
32	MG	A	3365	1/1	0.10	-	99,99,99,99	0
32	MG	A	3219	1/1	0.57	-	88,88,88,88	0
32	MG	A	3532	1/1	1.54	-	147,147,147,147	0
32	MG	A	2984	1/1	0.17	-	36,36,36,36	0
32	MG	A	3185	1/1	0.31	-	108,108,108,108	0
32	MG	6	313	1/1	0.13	-	111,111,111,111	0
32	MG	A	3329	1/1	0.81	-	76,76,76,76	0
32	MG	6	681	1/1	0.34	-	117,117,117,117	0
32	MG	A	3304	1/1	0.51	-	105,105,105,105	0
32	MG	6	559	1/1	0.44	-	76,76,76,76	0
32	MG	A	3356	1/1	0.48	-	107,107,107,107	0
32	MG	A	3752	1/1	1.37	-	65,65,65,65	0
32	MG	A	3157	1/1	0.92	-	58,58,58,58	0
32	MG	A	3591	1/1	0.33	-	152,152,152,152	0
32	MG	6	751	1/1	0.20	-	67,67,67,67	0
32	MG	6	684	1/1	0.23	-	71,71,71,71	0
32	MG	A	3130	1/1	0.49	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	A	3497	1/1	0.23	-	97,97,97,97	0
32	MG	A	3646	1/1	0.24	-	84,84,84,84	0
32	MG	A	3250	1/1	0.28	-	57,57,57,57	0
32	MG	K	374	1/1	0.80	-	86,86,86,86	0
32	MG	A	3343	1/1	0.14	-	83,83,83,83	0
32	MG	A	3101	1/1	0.26	-	65,65,65,65	0
32	MG	6	1341	1/1	0.27	-	88,88,88,88	0
32	MG	A	3897	1/1	0.23	-	98,98,98,98	0
32	MG	A	3518	1/1	0.30	-	70,70,70,70	0
32	MG	A	3857	1/1	0.19	-	59,59,59,59	0
32	MG	A	3378	1/1	0.08	-	92,92,92,92	0
32	MG	A	3534	1/1	1.75	-	87,87,87,87	0
32	MG	6	163	1/1	0.22	-	94,94,94,94	0
32	MG	A	2944	1/1	0.53	-	25,25,25,25	0
32	MG	A	3069	1/1	0.10	-	68,68,68,68	0
32	MG	A	3875	1/1	0.89	-	135,135,135,135	0
32	MG	6	1187	1/1	0.14	-	75,75,75,75	0
32	MG	6	1263	1/1	0.24	-	97,97,97,97	0
32	MG	A	3567	1/1	1.06	-	82,82,82,82	0
32	MG	A	3037	1/1	0.34	-	60,60,60,60	0
32	MG	A	3626	1/1	0.54	-	128,128,128,128	0
32	MG	A	3013	1/1	0.35	-	48,48,48,48	0
32	MG	A	3426	1/1	0.12	-	96,96,96,96	0
32	MG	A	3233	1/1	0.09	-	59,59,59,59	0
32	MG	6	946	1/1	0.19	-	96,96,96,96	0
32	MG	A	3184	1/1	0.27	-	65,65,65,65	0
32	MG	6	1200	1/1	0.19	-	113,113,113,113	0
32	MG	A	2994	1/1	0.09	-	25,25,25,25	0
32	MG	A	3210	1/1	0.40	-	73,73,73,73	0
32	MG	A	3859	1/1	0.66	-	70,70,70,70	0
32	MG	A	3866	1/1	0.68	-	85,85,85,85	0
32	MG	A	3488	1/1	0.31	-	76,76,76,76	0
32	MG	A	3190	1/1	0.42	-	53,53,53,53	0
32	MG	A	3433	1/1	0.36	-	67,67,67,67	0
32	MG	A	3008	1/1	0.19	-	52,52,52,52	0
32	MG	A	3099	1/1	0.45	-	54,54,54,54	0
32	MG	A	3509	1/1	0.29	-	108,108,108,108	0
32	MG	A	3745	1/1	0.45	-	70,70,70,70	0
32	MG	A	3533	1/1	0.21	-	77,77,77,77	0
32	MG	A	3582	1/1	0.60	-	97,97,97,97	0
32	MG	A	3543	1/1	0.88	-	71,71,71,71	0
32	MG	A	3657	1/1	0.61	-	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	6	586	1/1	0.09	-	109,109,109,109	0
32	MG	6	1205	1/1	0.21	-	115,115,115,115	0
32	MG	A	3486	1/1	0.28	-	48,48,48,48	0
32	MG	6	725	1/1	0.19	-	114,114,114,114	0
32	MG	A	3086	1/1	0.62	-	72,72,72,72	0
32	MG	6	624	1/1	0.18	-	76,76,76,76	0
32	MG	A	2943	1/1	0.71	-	56,56,56,56	0
32	MG	A	2975	1/1	0.27	-	40,40,40,40	0
32	MG	6	275	1/1	0.62	-	99,99,99,99	0
32	MG	6	1355	1/1	0.18	-	84,84,84,84	0
32	MG	K	1268	1/1	0.34	-	73,73,73,73	0
32	MG	A	3351	1/1	0.34	-	76,76,76,76	0
32	MG	A	3717	1/1	0.74	-	63,63,63,63	0
32	MG	A	3428	1/1	0.38	-	71,71,71,71	0
32	MG	P	1318	1/1	0.34	-	87,87,87,87	0
32	MG	A	3137	1/1	0.43	-	86,86,86,86	0
32	MG	6	656	1/1	0.37	-	141,141,141,141	0
32	MG	A	3513	1/1	0.42	-	91,91,91,91	0
32	MG	B	687	1/1	0.19	-	98,98,98,98	0
32	MG	A	2914	1/1	0.43	-	37,37,37,37	0
32	MG	6	1191	1/1	0.19	-	105,105,105,105	0
32	MG	6	801	1/1	0.38	-	94,94,94,94	0
32	MG	A	3324	1/1	0.33	-	90,90,90,90	0
32	MG	A	3821	1/1	0.40	-	92,92,92,92	0
32	MG	6	995	1/1	0.41	-	83,83,83,83	0
32	MG	A	2964	1/1	0.18	-	29,29,29,29	0
32	MG	A	2977	1/1	0.38	-	52,52,52,52	0
32	MG	A	3683	1/1	0.44	-	69,69,69,69	0
32	MG	A	3903	1/1	0.91	-	104,104,104,104	0
32	MG	6	1031	1/1	0.54	-	135,135,135,135	0
32	MG	A	3521	1/1	0.42	-	52,52,52,52	0
32	MG	A	3238	1/1	0.36	-	80,80,80,80	0
32	MG	A	3531	1/1	0.38	-	101,101,101,101	0
32	MG	A	3805	1/1	0.28	-	37,37,37,37	0
32	MG	A	3441	1/1	0.49	-	79,79,79,79	0
32	MG	A	3701	1/1	0.47	-	60,60,60,60	0
32	MG	A	3895	1/1	0.72	-	104,104,104,104	0
32	MG	A	3879	1/1	0.67	-	81,81,81,81	0
32	MG	A	3802	1/1	0.35	-	79,79,79,79	0
32	MG	A	3216	1/1	0.29	-	54,54,54,54	0
32	MG	A	3430	1/1	0.17	-	103,103,103,103	0
32	MG	A	3716	1/1	0.44	-	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3285	1/1	0.23	-	36,36,36,36	0
32	MG	A	3516	1/1	0.37	-	101,101,101,101	0
32	MG	A	2950	1/1	0.39	-	40,40,40,40	0
32	MG	A	437	1/1	0.18	-	139,139,139,139	0
32	MG	A	3297	1/1	0.38	-	84,84,84,84	0
32	MG	A	3826	1/1	0.23	-	90,90,90,90	0
32	MG	A	3789	1/1	0.19	-	89,89,89,89	0
32	MG	A	3852	1/1	0.72	-	74,74,74,74	0
32	MG	A	3138	1/1	0.24	-	94,94,94,94	0
32	MG	A	3212	1/1	0.33	-	83,83,83,83	0
32	MG	A	3400	1/1	0.17	-	127,127,127,127	0
32	MG	A	3593	1/1	0.49	-	99,99,99,99	0
32	MG	6	71	1/1	0.56	-	57,57,57,57	0
32	MG	A	3888	1/1	0.83	-	105,105,105,105	0
32	MG	A	3847	1/1	0.18	-	102,102,102,102	0
32	MG	A	3215	1/1	0.36	-	43,43,43,43	0
32	MG	A	3302	1/1	0.10	-	130,130,130,130	0
32	MG	A	3059	1/1	1.14	-	80,80,80,80	0
32	MG	6	1185	1/1	0.30	-	99,99,99,99	0
32	MG	A	3612	1/1	0.20	-	58,58,58,58	0
32	MG	A	3427	1/1	0.60	-	85,85,85,85	0
32	MG	A	3336	1/1	0.32	-	78,78,78,78	0
32	MG	B	731	1/1	0.58	-	137,137,137,137	0
32	MG	6	251	1/1	0.25	-	85,85,85,85	0
32	MG	6	539	1/1	0.18	-	107,107,107,107	0
32	MG	6	1363	1/1	0.17	-	87,87,87,87	0
32	MG	6	1371	1/1	0.69	-	100,100,100,100	0
32	MG	6	1310	1/1	0.15	-	84,84,84,84	0
32	MG	A	3323	1/1	0.80	-	88,88,88,88	0
32	MG	A	2976	1/1	0.31	-	39,39,39,39	0
32	MG	A	3375	1/1	0.64	-	78,78,78,78	0
32	MG	6	1473	1/1	0.89	-	93,93,93,93	0
32	MG	A	3514	1/1	0.23	-	97,97,97,97	0
32	MG	6	299	1/1	0.14	-	115,115,115,115	0
32	MG	A	974	1/1	0.69	-	80,80,80,80	0
32	MG	6	932	1/1	0.07	-	112,112,112,112	0
32	MG	A	3200	1/1	0.30	-	75,75,75,75	0
32	MG	A	3056	1/1	0.17	-	61,61,61,61	0
32	MG	A	3546	1/1	0.73	-	60,60,60,60	0
32	MG	A	3820	1/1	0.96	-	114,114,114,114	0
32	MG	A	3112	1/1	0.46	-	38,38,38,38	0
32	MG	A	3406	1/1	0.38	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3025	1/1	0.88	-	79,79,79,79	0
32	MG	6	1469	1/1	0.47	-	110,110,110,110	0
32	MG	A	3522	1/1	0.56	-	159,159,159,159	0
32	MG	A	3264	1/1	0.24	-	94,94,94,94	0
32	MG	A	3107	1/1	0.31	-	52,52,52,52	0
32	MG	A	2983	1/1	0.44	-	20,20,20,20	0
32	MG	A	3790	1/1	0.28	-	60,60,60,60	0
32	MG	A	3397	1/1	0.54	-	80,80,80,80	0
32	MG	A	3738	1/1	0.42	-	84,84,84,84	0
32	MG	6	294	1/1	0.67	-	70,70,70,70	0
32	MG	A	3349	1/1	0.35	-	105,105,105,105	0
32	MG	A	2963	1/1	0.27	-	39,39,39,39	0
32	MG	6	456	1/1	0.09	-	80,80,80,80	0
32	MG	K	221	1/1	0.14	-	94,94,94,94	0
32	MG	A	3520	1/1	0.31	-	64,64,64,64	0
32	MG	A	3282	1/1	0.18	-	57,57,57,57	0
32	MG	A	3012	1/1	0.36	-	60,60,60,60	0
32	MG	6	1105	1/1	0.55	-	71,71,71,71	0
32	MG	A	2945	1/1	0.65	-	46,46,46,46	0
32	MG	A	3556	1/1	0.26	-	65,65,65,65	0
32	MG	X	885	1/1	0.26	-	91,91,91,91	0
32	MG	A	2960	1/1	0.13	-	39,39,39,39	0
32	MG	6	463	1/1	0.10	-	65,65,65,65	0
32	MG	A	3727	1/1	0.30	-	74,74,74,74	0
32	MG	A	3331	1/1	0.52	-	120,120,120,120	0
32	MG	A	3270	1/1	0.35	-	38,38,38,38	0
32	MG	A	3102	1/1	0.07	-	84,84,84,84	0
32	MG	A	3280	1/1	0.32	-	44,44,44,44	0
32	MG	6	778	1/1	0.17	-	98,98,98,98	0
32	MG	6	1026	1/1	0.52	-	78,78,78,78	0
32	MG	6	1067	1/1	0.22	-	107,107,107,107	0
32	MG	A	3565	1/1	0.47	-	115,115,115,115	0
32	MG	A	3395	1/1	0.44	-	78,78,78,78	0
32	MG	A	3142	1/1	0.40	-	43,43,43,43	0
32	MG	A	3672	1/1	0.56	-	60,60,60,60	0
32	MG	A	3202	1/1	0.31	-	34,34,34,34	0
32	MG	A	3018	1/1	0.35	-	58,58,58,58	0
32	MG	6	1300	1/1	1.13	-	118,118,118,118	0
32	MG	A	3224	1/1	0.41	-	64,64,64,64	0
32	MG	A	3776	1/1	0.15	-	109,109,109,109	0
32	MG	6	1087	1/1	0.47	-	96,96,96,96	0
32	MG	A	3471	1/1	0.32	-	105,105,105,105	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	2966	1/1	0.12	-	37,37,37,37	0
32	MG	6	732	1/1	0.31	-	90,90,90,90	0
32	MG	A	3629	1/1	0.37	-	74,74,74,74	0
32	MG	6	1485	1/1	0.21	-	98,98,98,98	0
32	MG	A	3584	1/1	0.21	-	87,87,87,87	0
32	MG	A	3566	1/1	0.54	-	65,65,65,65	0
32	MG	A	3545	1/1	0.21	-	106,106,106,106	0
32	MG	6	829	1/1	0.20	-	133,133,133,133	0
32	MG	6	419	1/1	0.44	-	81,81,81,81	0
32	MG	A	3620	1/1	0.50	-	91,91,91,91	0
32	MG	A	2933	1/1	0.50	-	54,54,54,54	0
32	MG	6	551	1/1	5.51	-	169,169,169,169	0
32	MG	A	2996	1/1	0.26	-	62,62,62,62	0
32	MG	6	1056	1/1	0.17	-	103,103,103,103	0
32	MG	A	3887	1/1	0.56	-	91,91,91,91	0
32	MG	A	3763	1/1	0.77	-	134,134,134,134	0
32	MG	A	3759	1/1	0.29	-	81,81,81,81	0
32	MG	A	3614	1/1	1.35	-	113,113,113,113	0
32	MG	A	3686	1/1	0.91	-	71,71,71,71	0
32	MG	A	3019	1/1	0.57	-	80,80,80,80	0
32	MG	A	3287	1/1	0.59	-	70,70,70,70	0
32	MG	A	3537	1/1	0.18	-	85,85,85,85	0
32	MG	6	1389	1/1	0.20	-	87,87,87,87	0
32	MG	A	3693	1/1	0.41	-	61,61,61,61	0
32	MG	A	2985	1/1	0.52	-	60,60,60,60	0
32	MG	A	2971	1/1	0.57	-	49,49,49,49	0
32	MG	A	3303	1/1	0.51	-	78,78,78,78	0
32	MG	A	3844	1/1	0.45	-	61,61,61,61	0
32	MG	A	368	1/1	0.17	-	96,96,96,96	0
32	MG	6	481	1/1	0.62	-	65,65,65,65	0
32	MG	A	3002	1/1	0.44	-	50,50,50,50	0
32	MG	6	1005	1/1	0.52	-	103,103,103,103	0
32	MG	B	930	1/1	0.27	-	104,104,104,104	0
32	MG	P	379	1/1	0.30	-	106,106,106,106	0
32	MG	6	119	1/1	0.25	-	121,121,121,121	0
32	MG	A	3902	1/1	1.20	-	119,119,119,119	0
32	MG	6	1203	1/1	1.21	-	127,127,127,127	0
32	MG	A	3066	1/1	0.22	-	51,51,51,51	0
32	MG	A	3539	1/1	0.16	-	104,104,104,104	0
32	MG	A	3039	1/1	0.23	-	63,63,63,63	0
32	MG	A	3149	1/1	0.19	-	106,106,106,106	0
32	MG	6	1458	1/1	2.52	-	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3181	1/1	0.75	-	83,83,83,83	0
32	MG	A	3376	1/1	0.32	-	84,84,84,84	0
32	MG	6	282	1/1	0.23	-	101,101,101,101	0
32	MG	A	3730	1/1	0.35	-	68,68,68,68	0
32	MG	A	3186	1/1	0.41	-	97,97,97,97	0
32	MG	A	2961	1/1	0.33	-	34,34,34,34	0
32	MG	A	3330	1/1	0.14	-	123,123,123,123	0
32	MG	A	3162	1/1	0.34	-	84,84,84,84	0
32	MG	A	3132	1/1	0.24	-	67,67,67,67	0
32	MG	A	270	1/1	0.33	-	93,93,93,93	0
32	MG	6	403	1/1	0.43	-	70,70,70,70	0
32	MG	A	3728	1/1	0.41	-	70,70,70,70	0
32	MG	A	2980	1/1	0.29	-	41,41,41,41	0
32	MG	A	3258	1/1	0.26	-	51,51,51,51	0
32	MG	6	1021	1/1	0.48	-	134,134,134,134	0
32	MG	A	3357	1/1	0.24	-	69,69,69,69	0
32	MG	A	3633	1/1	0.43	-	128,128,128,128	0
32	MG	A	3341	1/1	0.68	-	68,68,68,68	0
32	MG	A	3515	1/1	0.40	-	105,105,105,105	0
32	MG	6	795	1/1	0.25	-	139,139,139,139	0
32	MG	A	3575	1/1	0.14	-	92,92,92,92	0
32	MG	A	3461	1/1	0.46	-	121,121,121,121	0
32	MG	A	3127	1/1	0.17	-	81,81,81,81	0
32	MG	A	3643	1/1	0.81	-	90,90,90,90	0
32	MG	6	1412	1/1	0.22	-	92,92,92,92	0
32	MG	6	1450	1/1	0.31	-	91,91,91,91	0
32	MG	A	3437	1/1	0.68	-	64,64,64,64	0
32	MG	A	3768	1/1	0.69	-	133,133,133,133	0
32	MG	A	3118	1/1	0.26	-	93,93,93,93	0
32	MG	B	1375	1/1	0.23	-	107,107,107,107	0
32	MG	A	3589	1/1	0.32	-	93,93,93,93	0
32	MG	Q	742	1/1	0.49	-	57,57,57,57	0
32	MG	6	317	1/1	0.34	-	111,111,111,111	0
32	MG	6	845	1/1	0.24	-	94,94,94,94	0
32	MG	A	3600	1/1	0.41	-	119,119,119,119	0
32	MG	A	3071	1/1	0.29	-	65,65,65,65	0
32	MG	A	3444	1/1	0.50	-	59,59,59,59	0
32	MG	6	301	1/1	0.17	-	94,94,94,94	0
32	MG	A	3154	1/1	0.34	-	83,83,83,83	0
32	MG	6	1301	1/1	0.21	-	105,105,105,105	0
32	MG	6	1288	1/1	1.49	-	138,138,138,138	0
32	MG	2	1189	1/1	0.44	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3845	1/1	0.14	-	116,116,116,116	0
32	MG	A	3828	1/1	0.19	-	106,106,106,106	0
32	MG	A	3732	1/1	0.40	-	75,75,75,75	0
32	MG	A	3141	1/1	0.29	-	76,76,76,76	0
32	MG	A	3833	1/1	1.21	-	79,79,79,79	0
32	MG	6	617	1/1	0.28	-	76,76,76,76	0
32	MG	A	3401	1/1	0.65	-	100,100,100,100	0
32	MG	6	518	1/1	0.27	-	114,114,114,114	0
32	MG	A	3558	1/1	0.36	-	53,53,53,53	0
32	MG	A	3746	1/1	0.47	-	84,84,84,84	0
32	MG	A	3775	1/1	0.49	-	64,64,64,64	0
32	MG	A	3694	1/1	0.56	-	83,83,83,83	0
32	MG	A	3782	1/1	1.29	-	87,87,87,87	0
32	MG	6	1374	1/1	0.33	-	81,81,81,81	0
32	MG	A	3880	1/1	0.66	-	80,80,80,80	0
32	MG	A	3374	1/1	0.28	-	68,68,68,68	0
32	MG	A	2931	1/1	0.12	-	21,21,21,21	0
32	MG	A	156	1/1	0.66	-	89,89,89,89	0
32	MG	A	3675	1/1	0.58	-	66,66,66,66	0
32	MG	A	3085	1/1	0.13	-	68,68,68,68	0
32	MG	6	1053	1/1	0.37	-	129,129,129,129	0
32	MG	A	3077	1/1	0.42	-	71,71,71,71	0
32	MG	A	3063	1/1	0.12	-	78,78,78,78	0
32	MG	A	3630	1/1	0.43	-	74,74,74,74	0
32	MG	A	3684	1/1	0.31	-	65,65,65,65	0
32	MG	6	1251	1/1	0.69	-	112,112,112,112	0
32	MG	A	3373	1/1	0.39	-	107,107,107,107	0
32	MG	A	3452	1/1	0.39	-	79,79,79,79	0
32	MG	A	3278	1/1	0.23	-	104,104,104,104	0
32	MG	A	3862	1/1	0.73	-	103,103,103,103	0
32	MG	A	3784	1/1	0.48	-	74,74,74,74	0
32	MG	A	2956	1/1	0.16	-	37,37,37,37	0
32	MG	P	1132	1/1	0.39	-	76,76,76,76	0
32	MG	A	3361	1/1	0.34	-	83,83,83,83	0
32	MG	M	1400	1/1	1.56	-	106,106,106,106	0
32	MG	A	3622	1/1	0.41	-	103,103,103,103	0
32	MG	A	3616	1/1	0.19	-	108,108,108,108	0
32	MG	A	42	1/1	0.38	-	21,21,21,21	0
32	MG	B	609	1/1	0.24	-	73,73,73,73	0
32	MG	6	868	1/1	0.17	-	94,94,94,94	0
32	MG	A	3007	1/1	0.82	-	52,52,52,52	0
32	MG	6	1206	1/1	0.21	-	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3877	1/1	0.28	-	117,117,117,117	0
32	MG	A	2962	1/1	0.56	-	36,36,36,36	0
32	MG	A	2929	1/1	0.24	-	43,43,43,43	0
32	MG	A	170	1/1	0.36	-	39,39,39,39	0
32	MG	A	3598	1/1	0.24	-	68,68,68,68	0
32	MG	A	3032	1/1	0.32	-	37,37,37,37	0
32	MG	A	3455	1/1	0.17	-	37,37,37,37	0
32	MG	A	3457	1/1	0.52	-	87,87,87,87	0
32	MG	A	3408	1/1	0.22	-	109,109,109,109	0
32	MG	A	3530	1/1	0.10	-	133,133,133,133	0
32	MG	A	3834	1/1	0.32	-	88,88,88,88	0
32	MG	K	744	1/1	0.50	-	69,69,69,69	0
32	MG	A	3435	1/1	0.23	-	97,97,97,97	0
32	MG	6	1195	1/1	0.32	-	109,109,109,109	0
32	MG	B	1417	1/1	0.20	-	90,90,90,90	0
32	MG	A	3363	1/1	0.37	-	97,97,97,97	0
32	MG	A	3217	1/1	0.19	-	59,59,59,59	0
32	MG	A	3281	1/1	0.28	-	61,61,61,61	0
32	MG	A	3183	1/1	0.49	-	46,46,46,46	0
32	MG	A	3506	1/1	0.49	-	62,62,62,62	0
32	MG	A	3034	1/1	0.45	-	51,51,51,51	0
32	MG	A	3774	1/1	0.54	-	105,105,105,105	0
32	MG	6	817	1/1	0.67	-	122,122,122,122	0
32	MG	F	1362	1/1	0.19	-	129,129,129,129	0
32	MG	A	2940	1/1	0.30	-	52,52,52,52	0
32	MG	6	1394	1/1	3.09	-	102,102,102,102	0
32	MG	A	3814	1/1	0.43	-	55,55,55,55	0
32	MG	6	1276	1/1	0.30	-	135,135,135,135	0
32	MG	A	3235	1/1	0.24	-	100,100,100,100	0
32	MG	A	2941	1/1	0.18	-	43,43,43,43	0
32	MG	6	50	1/1	0.23	-	60,60,60,60	0
32	MG	A	3237	1/1	0.24	-	92,92,92,92	0
32	MG	6	332	1/1	0.28	-	94,94,94,94	0
32	MG	A	3268	1/1	0.27	-	59,59,59,59	0
32	MG	B	1359	1/1	0.52	-	74,74,74,74	0
32	MG	6	295	1/1	0.22	-	94,94,94,94	0
32	MG	A	3048	1/1	0.29	-	55,55,55,55	0
32	MG	A	2918	1/1	0.23	-	25,25,25,25	0
32	MG	A	3659	1/1	0.39	-	73,73,73,73	0
32	MG	A	3704	1/1	0.18	-	41,41,41,41	0
32	MG	A	3747	1/1	0.29	-	79,79,79,79	0
32	MG	A	3041	1/1	0.11	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	3899	1/1	1.03	-	55,55,55,55	0
32	MG	A	3076	1/1	0.12	-	83,83,83,83	0
32	MG	P	1041	1/1	0.18	-	90,90,90,90	0
32	MG	A	3167	1/1	0.19	-	50,50,50,50	0
32	MG	A	2951	1/1	0.97	-	43,43,43,43	0
32	MG	6	1014	1/1	0.20	-	76,76,76,76	0
32	MG	A	3715	1/1	0.73	-	96,96,96,96	0
32	MG	A	3733	1/1	0.12	-	54,54,54,54	0
32	MG	A	3458	1/1	0.22	-	81,81,81,81	0
32	MG	6	1324	1/1	0.25	-	97,97,97,97	0
32	MG	A	3547	1/1	0.38	-	83,83,83,83	0
32	MG	A	3729	1/1	0.66	-	60,60,60,60	0
32	MG	P	1483	1/1	0.21	-	124,124,124,124	0
32	MG	A	3846	1/1	0.58	-	84,84,84,84	0
32	MG	A	3798	1/1	0.14	-	123,123,123,123	0
32	MG	A	2942	1/1	0.37	-	33,33,33,33	0
32	MG	A	3878	1/1	0.34	-	86,86,86,86	0
32	MG	6	800	1/1	0.78	-	76,76,76,76	0
32	MG	6	784	1/1	0.69	-	104,104,104,104	0
32	MG	B	1410	1/1	0.86	-	123,123,123,123	0
32	MG	6	478	1/1	0.17	-	79,79,79,79	0
32	MG	A	3135	1/1	0.12	-	100,100,100,100	0
32	MG	6	1240	1/1	0.13	-	98,98,98,98	0
32	MG	6	607	1/1	0.63	-	85,85,85,85	0
32	MG	A	2905	1/1	0.76	-	21,21,21,21	0
32	MG	6	167	1/1	0.42	-	104,104,104,104	0
32	MG	A	2898	1/1	0.33	-	16,16,16,16	0
32	MG	A	3445	1/1	0.32	-	71,71,71,71	0
32	MG	6	642	1/1	0.69	-	93,93,93,93	0
32	MG	A	3639	1/1	0.54	-	115,115,115,115	0
32	MG	A	3773	1/1	0.21	-	47,47,47,47	0
32	MG	A	3301	1/1	0.71	-	95,95,95,95	0
32	MG	A	3	1/1	0.12	-	16,16,16,16	0
32	MG	6	788	1/1	1.95	-	203,203,203,203	0
32	MG	A	3023	1/1	0.48	-	74,74,74,74	0
32	MG	A	3021	1/1	0.41	-	53,53,53,53	0
32	MG	A	3381	1/1	0.41	-	69,69,69,69	0
32	MG	A	3350	1/1	0.59	-	79,79,79,79	0
32	MG	A	3698	1/1	0.49	-	47,47,47,47	0
32	MG	A	3269	1/1	0.79	-	99,99,99,99	0
32	MG	A	3383	1/1	0.52	-	121,121,121,121	0
32	MG	A	3559	1/1	0.67	-	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	2973	1/1	0.11	-	16,16,16,16	0
32	MG	A	2926	1/1	0.19	-	13,13,13,13	0
32	MG	A	3651	1/1	0.94	-	123,123,123,123	0
32	MG	A	3119	1/1	0.16	-	68,68,68,68	0
32	MG	6	1433	1/1	0.10	-	89,89,89,89	0
32	MG	6	460	1/1	0.81	-	130,130,130,130	0
32	MG	A	160	1/1	0.35	-	44,44,44,44	0
32	MG	A	3271	1/1	0.22	-	85,85,85,85	0
32	MG	F	942	1/1	0.54	-	159,159,159,159	0
32	MG	6	764	1/1	0.18	-	99,99,99,99	0
32	MG	A	2902	1/1	0.40	-	38,38,38,38	0
32	MG	A	3787	1/1	0.56	-	89,89,89,89	0
32	MG	A	3092	1/1	0.35	-	75,75,75,75	0
32	MG	6	940	1/1	0.24	-	99,99,99,99	0
32	MG	A	3625	1/1	0.47	-	79,79,79,79	0
32	MG	V	1091	1/1	1.06	-	128,128,128,128	0
32	MG	A	3035	1/1	0.68	-	43,43,43,43	0
32	MG	A	3797	1/1	0.68	-	64,64,64,64	0
32	MG	P	664	1/1	0.49	-	115,115,115,115	0
32	MG	A	3196	1/1	0.26	-	74,74,74,74	0
32	MG	A	3221	1/1	0.15	-	67,67,67,67	0
32	MG	A	3644	1/1	0.76	-	93,93,93,93	0
32	MG	A	3292	1/1	0.56	-	87,87,87,87	0
32	MG	A	3470	1/1	0.33	-	133,133,133,133	0
32	MG	A	3078	1/1	0.78	-	59,59,59,59	0
32	MG	6	290	1/1	0.87	-	79,79,79,79	0
32	MG	A	3348	1/1	0.45	-	121,121,121,121	0
32	MG	6	1036	1/1	0.38	-	58,58,58,58	0
32	MG	A	3564	1/1	0.58	-	110,110,110,110	0
32	MG	6	435	1/1	0.23	-	66,66,66,66	0
32	MG	K	538	1/1	0.55	-	60,60,60,60	0
32	MG	A	3526	1/1	0.31	-	73,73,73,73	0
32	MG	6	806	1/1	0.21	-	103,103,103,103	0
32	MG	6	679	1/1	0.87	-	87,87,87,87	0
32	MG	A	3508	1/1	0.44	-	87,87,87,87	0
32	MG	6	1073	1/1	0.11	-	87,87,87,87	0
32	MG	A	2947	1/1	0.35	-	41,41,41,41	0
32	MG	6	1344	1/1	4.19	-	117,117,117,117	0
32	MG	6	1332	1/1	0.13	-	127,127,127,127	0
32	MG	A	3318	1/1	0.25	-	85,85,85,85	0
32	MG	A	3276	1/1	0.51	-	65,65,65,65	0
32	MG	A	3860	1/1	1.19	-	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	B	121	1/1	0.22	-	69,69,69,69	0
32	MG	X	598	1/1	0.46	-	103,103,103,103	0
32	MG	6	805	1/1	0.20	-	95,95,95,95	0
32	MG	A	3362	1/1	0.74	-	73,73,73,73	0
32	MG	A	3027	1/1	0.51	-	79,79,79,79	0
32	MG	5	1113	1/1	0.97	-	71,71,71,71	0
32	MG	A	3036	1/1	0.20	-	89,89,89,89	0
32	MG	A	3536	1/1	0.72	-	84,84,84,84	0
32	MG	A	3115	1/1	0.11	-	64,64,64,64	0
32	MG	6	373	1/1	0.09	-	77,77,77,77	0
32	MG	6	1455	1/1	1.72	-	96,96,96,96	0
32	MG	E	257	1/1	0.17	-	83,83,83,83	0
32	MG	A	3067	1/1	1.26	-	83,83,83,83	0
32	MG	A	3345	1/1	0.11	-	116,116,116,116	0
32	MG	A	3498	1/1	0.21	-	70,70,70,70	0
32	MG	6	1079	1/1	0.37	-	107,107,107,107	0
32	MG	A	2937	1/1	0.24	-	25,25,25,25	0
32	MG	P	969	1/1	0.59	-	89,89,89,89	0
32	MG	A	3599	1/1	0.14	-	85,85,85,85	0
32	MG	A	3503	1/1	0.71	-	111,111,111,111	0
32	MG	A	3443	1/1	0.91	-	60,60,60,60	0
32	MG	6	1434	1/1	1.17	-	98,98,98,98	0
32	MG	B	1306	1/1	0.57	-	109,109,109,109	0
32	MG	L	958	1/1	0.18	-	146,146,146,146	0
32	MG	6	1290	1/1	0.13	-	109,109,109,109	0
32	MG	6	1062	1/1	1.28	-	111,111,111,111	0
32	MG	A	3284	1/1	1.15	-	66,66,66,66	0
32	MG	A	3804	1/1	0.36	-	114,114,114,114	0
32	MG	A	3308	1/1	0.79	-	77,77,77,77	0
32	MG	6	348	1/1	0.38	-	100,100,100,100	0
32	MG	A	3379	1/1	0.37	-	112,112,112,112	0
32	MG	A	3767	1/1	0.33	-	91,91,91,91	0
32	MG	P	869	1/1	0.72	-	110,110,110,110	0
32	MG	A	3479	1/1	0.29	-	95,95,95,95	0
32	MG	A	3182	1/1	0.10	-	84,84,84,84	0
32	MG	A	3411	1/1	0.48	-	68,68,68,68	0
32	MG	A	3765	1/1	0.20	-	136,136,136,136	0
32	MG	A	3333	1/1	0.44	-	59,59,59,59	0
32	MG	A	3601	1/1	0.17	-	130,130,130,130	0
32	MG	A	3218	1/1	0.31	-	80,80,80,80	0
32	MG	6	1308	1/1	0.96	-	100,100,100,100	0
32	MG	A	2970	1/1	1.54	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	6	1340	1/1	0.23	-	76,76,76,76	0
32	MG	A	3861	1/1	0.57	-	113,113,113,113	0
32	MG	A	3223	1/1	0.10	-	82,82,82,82	0
32	MG	A	3538	1/1	2.27	-	107,107,107,107	0
32	MG	A	3029	1/1	0.23	-	70,70,70,70	0
32	MG	A	3043	1/1	1.50	-	62,62,62,62	0
32	MG	A	3475	1/1	1.23	-	83,83,83,83	0
32	MG	A	3208	1/1	0.20	-	60,60,60,60	0
32	MG	A	3771	1/1	0.28	-	84,84,84,84	0
32	MG	A	3561	1/1	0.32	-	97,97,97,97	0
32	MG	A	3889	1/1	0.33	-	89,89,89,89	0
32	MG	Y	1214	1/1	0.55	-	69,69,69,69	0
32	MG	A	3637	1/1	0.37	-	129,129,129,129	0
32	MG	A	3003	1/1	0.18	-	54,54,54,54	0
32	MG	6	376	1/1	1.28	-	76,76,76,76	0
32	MG	A	3660	1/1	0.42	-	12,12,12,12	0
32	MG	6	410	1/1	0.20	-	93,93,93,93	0
32	MG	A	3870	1/1	0.31	-	66,66,66,66	0
32	MG	A	3477	1/1	0.28	-	89,89,89,89	0
32	MG	X	1313	1/1	0.45	-	60,60,60,60	0
32	MG	A	3317	1/1	0.36	-	79,79,79,79	0
32	MG	A	3449	1/1	0.82	-	57,57,57,57	0
32	MG	A	3668	1/1	0.33	-	75,75,75,75	0
32	MG	A	3855	1/1	0.37	-	78,78,78,78	0

6.5 Other polymers ⓘ

There are no such residues in this entry.