



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2026 – 07:25 PM UTC

PDB ID : 5J4D / pdb_00005j4d
Title : E. coli release factor 1 bound to the 70S ribosome in response to a pseudouridylated stop codon
Authors : Svidritskiy, E.; Korostelev, A.A.
Deposited on : 2016-03-31
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

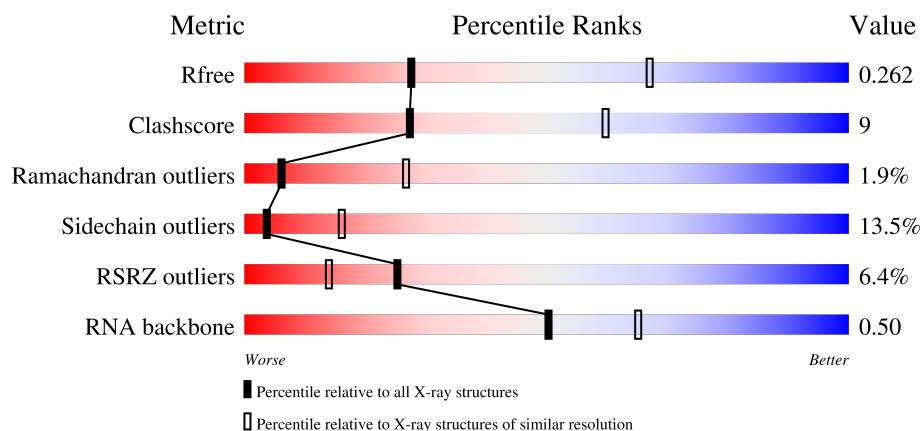
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)
RNA backbone	3983	1022 (3.32-2.88)

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

Mol	Chain	Length	Quality of chain
1	A	1507	3% 59% 35% 6%
1	FB	1507	4% 60% 34% 6%
2	B	2880	3% 64% 29% 7%
2	GB	2880	4% 63% 30% 7%

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Mol	Chain	Length	Quality of chain
3	C	120	
3	HB	120	
4	D	77	
4	IA	77	
4	IB	77	
4	NC	77	
5	E	275	
5	JB	275	
6	F	206	
6	KB	206	
7	G	205	
7	LB	205	
8	H	182	
8	MB	182	
9	I	180	
9	NB	180	
10	J	148	
10	OB	148	
11	K	140	
11	PB	140	
12	L	122	
12	QB	122	
13	M	150	
13	RB	150	
14	N	141	

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Mol	Chain	Length	Quality of chain
14	SB	141	4% 64% 32% .
15	O	118	% 64% 31% 5%
15	TB	118	7% 66% 29% 5%
16	P	112	9% 61% 29% 8% .
16	UB	112	12% 61% 30% 7% .
17	Q	146	% 61% 29% . 6%
17	VB	146	2% 63% 27% . 6%
18	R	118	70% 24% 5% .
18	WB	118	2% 67% 28% . .
19	S	101	67% 29% .
19	XB	101	4% 66% 31% .
20	T	113	68% 26% 5% .
20	YB	113	7% 70% 25% . .
21	U	96	2% 76% 19% . .
21	ZB	96	9% 75% 19% 5% .
22	AC	110	25% 61% 35% . .
22	V	110	2% 59% 36% . .
23	BC	206	6% 59% 28% 5% 8%
23	W	206	3% 61% 26% 5% 8%
24	CC	85	14% 72% 20% 7% .
24	X	85	12% 80% 12% 7% .
25	DC	98	5% 66% 26% 7% .
25	Y	98	5% 66% 27% 6% .
26	EC	72	21% 62% 29% 6% .
26	Z	72	3% 60% 31% 7% .

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Mol	Chain	Length	Quality of chain
27	AA	60	
27	FC	60	
28	BA	71	
28	GC	71	
29	CA	60	
29	HC	60	
30	DA	54	
30	IC	54	
31	EA	49	
31	JC	49	
32	FA	65	
32	KC	65	
33	GA	37	
33	LC	37	
34	HA	27	
34	MC	27	
35	JA	368	
35	OC	368	
36	KA	256	
36	PC	256	
37	LA	239	
37	QC	239	
38	MA	209	
38	RC	209	
39	NA	162	

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Mol	Chain	Length	Quality of chain
39	SC	162	
40	OA	101	
40	TC	101	
41	PA	156	
41	UC	156	
42	QA	138	
42	VC	138	
43	RA	128	
43	WC	128	
44	SA	105	
44	XC	105	
45	TA	129	
45	YC	129	
46	UA	132	
46	ZC	132	
47	AD	126	
47	VA	126	
48	BD	61	
48	WA	61	
49	CD	89	
49	XA	89	
50	DD	88	
50	YA	88	
51	ED	105	
51	ZA	105	

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Mol	Chain	Length	Quality of chain
52	AB	88	
52	FD	88	
53	BB	93	
53	GD	93	
54	CB	106	
54	HD	106	
55	DB	27	
55	ID	27	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	A	1610	-	-	-	X
56	MG	A	1621	-	-	-	X
56	MG	A	1630	-	-	-	X
56	MG	A	1631	-	-	-	X
56	MG	A	1666	-	-	-	X
56	MG	A	1669	-	-	-	X
56	MG	A	1672	-	-	-	X
56	MG	A	1709	-	-	-	X
56	MG	A	1730	-	-	-	X
56	MG	A	1792	-	-	-	X
56	MG	A	1799	-	-	-	X
56	MG	A	1804	-	-	-	X
56	MG	A	1833	-	-	-	X
56	MG	A	1845	-	-	-	X
56	MG	A	1874	-	-	-	X
56	MG	A	1878	-	-	-	X
56	MG	B	2942	-	-	-	X
56	MG	B	3782	-	-	-	X
56	MG	B	3826	-	-	-	X
56	MG	B	3834	-	-	-	X
56	MG	FB	1615	-	-	-	X
56	MG	FB	1631	-	-	-	X
56	MG	FB	1633	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	FB	1636	-	-	-	X
56	MG	FB	1642	-	-	-	X
56	MG	FB	1686	-	-	-	X
56	MG	FB	1704	-	-	-	X
56	MG	FB	1758	-	-	-	X
56	MG	FB	1862	-	-	-	X
56	MG	FB	1911	-	-	-	X
56	MG	FB	1917	-	-	-	X
56	MG	FB	1939	-	-	-	X
56	MG	GB	2907	-	-	-	X
56	MG	GB	2919	-	-	-	X
56	MG	GB	2921	-	-	-	X
56	MG	GB	2947	-	-	-	X
56	MG	GB	2951	-	-	-	X
56	MG	GB	2971	-	-	-	X
56	MG	GB	3001	-	-	-	X
56	MG	GB	3016	-	-	-	X
56	MG	GB	3022	-	-	-	X
56	MG	GB	3117	-	-	-	X
56	MG	GB	3188	-	-	-	X
56	MG	GB	3293	-	-	-	X
56	MG	GB	3376	-	-	-	X
56	MG	HB	207	-	-	-	X
56	MG	HB	221	-	-	-	X
56	MG	MB	203	-	-	-	X
56	MG	RA	202	-	-	-	X
56	MG	RA	203	-	-	-	X
56	MG	SA	201	-	-	-	X
56	MG	WA	101	-	-	-	X
56	MG	XC	201	-	-	-	X

2 Entry composition [i](#)

There are 57 unique types of molecules in this entry. The entry contains 300991 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1507	Total	C	N	O	P	0	0	0
			32394	14424	5998	10465	1507			
1	FB	1507	Total	C	N	O	P	0	0	0
			32394	14424	5998	10465	1507			

- Molecule 2 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	2880	Total	C	N	O	P	0	0	0
			62031	27612	11589	19950	2880			
2	GB	2880	Total	C	N	O	P	0	0	0
			62031	27612	11589	19950	2880			

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	120	Total	C	N	O	P	0	0	0
			2576	1146	476	834	120			
3	HB	120	Total	C	N	O	P	0	0	0
			2576	1146	476	834	120			

- Molecule 4 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	77	Total	C	N	O	P	S	0	0	0
			1642	734	297	534	76	1			
4	IA	77	Total	C	N	O	P	S	0	0	0
			1642	734	297	534	76	1			
4	IB	77	Total	C	N	O	P	S	0	0	0
			1642	734	297	534	76	1			
4	NC	77	Total	C	N	O	P	S	0	0	0
			1642	734	297	534	76	1			

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	275	Total	C	N	O	S	0	0	0
			2145	1353	428	361	3			
5	JB	275	Total	C	N	O	S	0	0	0
			2145	1353	428	361	3			

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	204	Total	C	N	O	S	0	0	0
			1563	988	299	270	6			
6	KB	204	Total	C	N	O	S	0	0	0
			1563	988	299	270	6			

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	202	Total	C	N	O	S	0	0	0
			1586	1011	297	275	3			
7	LB	202	Total	C	N	O	S	0	0	0
			1586	1011	297	275	3			

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	181	Total	C	N	O	S	0	0	0
			1471	940	267	260	4			
8	MB	181	Total	C	N	O	S	0	0	0
			1471	940	267	260	4			

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
9	NB	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	146	Total	C	N	O	S	0	0	0
			1137	727	201	208	1			
10	OB	146	Total	C	N	O	S	0	0	0
			1137	727	201	208	1			

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			
11	PB	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	122	Total	C	N	O	S	0	0	0
			932	587	171	170	4			
12	QB	122	Total	C	N	O	S	0	0	0
			932	587	171	170	4			

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	150	Total	C	N	O	S	0	0	0
			1145	712	232	198	3			
13	RB	150	Total	C	N	O	S	0	0	0
			1145	712	232	198	3			

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	141	Total	C	N	O	S	0	0	0
			1121	715	212	187	7			
14	SB	141	Total	C	N	O	S	0	0	0
			1121	715	212	187	7			

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	TB	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	110	Total	C	N	O		0	0	0
			877	553	175	149				
16	UB	110	Total	C	N	O		0	0	0
			877	553	175	149				

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	137	Total	C	N	O	S	0	0	0
			1143	713	234	195	1			
17	VB	137	Total	C	N	O	S	0	0	0
			1143	713	234	195	1			

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	117	Total	C	N	O	S	0	0	0
			964	610	202	151	1			
18	WB	117	Total	C	N	O	S	0	0	0
			964	610	202	151	1			

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	112	Total	C	N	O	S	0	0	0
			890	560	175	153	2			
20	YB	112	Total	C	N	O	S	0	0	0
			890	560	175	153	2			

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
21	ZB	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	107	Total	C	N	O	S	0	0	0
			814	523	154	131	6			
22	AC	107	Total	C	N	O	S	0	0	0
			814	523	154	131	6			

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	189	Total	C	N	O	S	0	0	0
			1495	953	266	273	3			
23	BC	189	Total	C	N	O	S	0	0	0
			1495	953	266	273	3			

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	X	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			
24	CC	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	Y	97	Total	C	N	O	S	0	0	0
			761	478	151	131	1			
25	DC	97	Total	C	N	O	S	0	0	0
			761	478	151	131	1			

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Z	70	Total	C	N	O	S	0	0	0
			592	368	119	103	2			
26	EC	70	Total	C	N	O	S	0	0	0
			592	368	119	103	2			

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	AA	60	Total	C	N	O	S	0	0	0
			477	303	91	82	1			
27	FC	60	Total	C	N	O	S	0	0	0
			477	303	91	82	1			

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BA	69	Total	C	N	O	S	0	0	0
			552	349	99	99	5			
28	GC	69	Total	C	N	O	S	0	0	0
			552	349	99	99	5			

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	CA	59	Total	C	N	O	S	0	0	0
			460	290	90	75	5			
29	HC	59	Total	C	N	O	S	0	0	0
			460	290	90	75	5			

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	DA	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
30	IC	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	EA	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	JC	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	FA	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
32	KC	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	GA	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
33	LC	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 34 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	HA	11	Total	C	N	O	P	0	0	0
			220	98	44	67	11			
34	MC	11	Total	C	N	O	P	0	0	0
			220	98	44	67	11			

- Molecule 35 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	JA	258	Total	C	N	O	S	0	0	0
			2005	1227	380	390	8			
35	OC	258	Total	C	N	O	S	0	0	0
			2005	1227	380	390	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JA	361	LEU	-	expression tag	UNP P0A7I0
JA	362	GLU	-	expression tag	UNP P0A7I0
JA	363	HIS	-	expression tag	UNP P0A7I0
JA	364	HIS	-	expression tag	UNP P0A7I0

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Chain	Residue	Modelled	Actual	Comment	Reference
JA	365	HIS	-	expression tag	UNP P0A7I0
JA	366	HIS	-	expression tag	UNP P0A7I0
JA	367	HIS	-	expression tag	UNP P0A7I0
JA	368	HIS	-	expression tag	UNP P0A7I0
OC	361	LEU	-	expression tag	UNP P0A7I0
OC	362	GLU	-	expression tag	UNP P0A7I0
OC	363	HIS	-	expression tag	UNP P0A7I0
OC	364	HIS	-	expression tag	UNP P0A7I0
OC	365	HIS	-	expression tag	UNP P0A7I0
OC	366	HIS	-	expression tag	UNP P0A7I0
OC	367	HIS	-	expression tag	UNP P0A7I0
OC	368	HIS	-	expression tag	UNP P0A7I0

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	KA	234	Total	C	N	O	S	0	0	0
			1900	1213	341	341	5			
36	PC	234	Total	C	N	O	S	0	0	0
			1900	1213	341	341	5			

- Molecule 37 is a protein called 30S ribosomal protein S3.

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

- Molecule 38 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	MA	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
38	RC	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	NA	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	SC	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	OA	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
40	TC	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	PA	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
41	UC	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	QA	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
42	VC	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 43 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
43	RA	127	Total	C	N	O	0	0	0
			1011	639	198	174			
43	WC	127	Total	C	N	O	0	0	0
			1011	639	198	174			

- Molecule 44 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	SA	98	Total	C	N	O	S	0	0	0
			794	499	156	138	1			
44	XC	98	Total	C	N	O	S	0	0	0
			794	499	156	138	1			

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	TA	116	Total	C	N	O	S	0	0	0
			864	537	164	160	3			
45	YC	116	Total	C	N	O	S	0	0	0
			864	537	164	160	3			

- Molecule 46 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	UA	122	Total	C	N	O	S	0	0	0
			958	604	193	159	2			
46	ZC	122	Total	C	N	O	S	0	0	0
			958	604	193	159	2			

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	VA	117	Total	C	N	O	S	0	0	0
			933	577	192	162	2			
47	AD	117	Total	C	N	O	S	0	0	0
			933	577	192	162	2			

- Molecule 48 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 49 is a protein called 30S ribosomal protein S15.

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

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	YA	83	Total	C	N	O	S	0	0	0
			700	443	139	117	1			
50	DD	83	Total	C	N	O	S	0	0	0
			700	443	139	117	1			

- Molecule 51 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	ZA	99	Total	C	N	O	S	0	0	0
			823	528	152	141	2			
51	ED	99	Total	C	N	O	S	0	0	0
			823	528	152	141	2			

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
52	AB	70	Total	C	N	O	0	0	0
			574	367	112	95			
52	FD	70	Total	C	N	O	0	0	0
			574	367	112	95			

- Molecule 53 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	BB	83	Total	C	N	O	S	0	0	0
			665	424	124	115	2			
53	GD	83	Total	C	N	O	S	0	0	0
			665	424	124	115	2			

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	CB	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			
54	HD	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

- Molecule 55 is a protein called 30S ribosomal protein Thx.

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

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

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	A	287	Total	Mg	0	0
			287	287		
56	B	944	Total	Mg	0	0
			944	944		
56	C	44	Total	Mg	0	0
			44	44		
56	D	2	Total	Mg	0	0
			2	2		
56	E	10	Total	Mg	0	0
			10	10		
56	F	15	Total	Mg	0	0
			15	15		
56	G	11	Total	Mg	0	0
			11	11		
56	H	3	Total	Mg	0	0
			3	3		
56	I	7	Total	Mg	0	0
			7	7		
56	J	3	Total	Mg	0	0
			3	3		
56	K	9	Total	Mg	0	0
			9	9		
56	L	5	Total	Mg	0	0
			5	5		
56	M	8	Total	Mg	0	0
			8	8		
56	N	6	Total	Mg	0	0
			6	6		
56	O	3	Total	Mg	0	0
			3	3		
56	P	4	Total	Mg	0	0
			4	4		
56	Q	4	Total	Mg	0	0
			4	4		
56	R	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	S	8	Total 8	Mg 8	0	0
56	T	5	Total 5	Mg 5	0	0
56	U	2	Total 2	Mg 2	0	0
56	W	8	Total 8	Mg 8	0	0
56	X	8	Total 8	Mg 8	0	0
56	Y	5	Total 5	Mg 5	0	0
56	Z	3	Total 3	Mg 3	0	0
56	AA	4	Total 4	Mg 4	0	0
56	BA	3	Total 3	Mg 3	0	0
56	CA	3	Total 3	Mg 3	0	0
56	DA	3	Total 3	Mg 3	0	0
56	EA	2	Total 2	Mg 2	0	0
56	FA	4	Total 4	Mg 4	0	0
56	GA	1	Total 1	Mg 1	0	0
56	HA	2	Total 2	Mg 2	0	0
56	IA	21	Total 21	Mg 21	0	0
56	JA	13	Total 13	Mg 13	0	0
56	KA	4	Total 4	Mg 4	0	0
56	LA	2	Total 2	Mg 2	0	0
56	MA	5	Total 5	Mg 5	0	0
56	NA	3	Total 3	Mg 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	OA	4	Total 4	Mg 4	0	0
56	PA	3	Total 3	Mg 3	0	0
56	QA	2	Total 2	Mg 2	0	0
56	RA	4	Total 4	Mg 4	0	0
56	SA	3	Total 3	Mg 3	0	0
56	TA	1	Total 1	Mg 1	0	0
56	UA	3	Total 3	Mg 3	0	0
56	VA	3	Total 3	Mg 3	0	0
56	WA	1	Total 1	Mg 1	0	0
56	XA	3	Total 3	Mg 3	0	0
56	YA	1	Total 1	Mg 1	0	0
56	ZA	3	Total 3	Mg 3	0	0
56	BB	1	Total 1	Mg 1	0	0
56	CB	1	Total 1	Mg 1	0	0
56	DB	1	Total 1	Mg 1	0	0
56	FB	349	Total 349	Mg 349	0	0
56	GB	812	Total 812	Mg 812	0	0
56	HB	32	Total 32	Mg 32	0	0
56	IB	5	Total 5	Mg 5	0	0
56	JB	13	Total 13	Mg 13	0	0
56	KB	4	Total 4	Mg 4	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	LB	5	Total 5	Mg 5	0	0
56	MB	7	Total 7	Mg 7	0	0
56	NB	3	Total 3	Mg 3	0	0
56	OB	2	Total 2	Mg 2	0	0
56	PB	4	Total 4	Mg 4	0	0
56	QB	6	Total 6	Mg 6	0	0
56	RB	6	Total 6	Mg 6	0	0
56	SB	4	Total 4	Mg 4	0	0
56	TB	4	Total 4	Mg 4	0	0
56	UB	1	Total 1	Mg 1	0	0
56	VB	8	Total 8	Mg 8	0	0
56	WB	3	Total 3	Mg 3	0	0
56	XB	4	Total 4	Mg 4	0	0
56	YB	7	Total 7	Mg 7	0	0
56	ZB	1	Total 1	Mg 1	0	0
56	BC	9	Total 9	Mg 9	0	0
56	CC	2	Total 2	Mg 2	0	0
56	DC	3	Total 3	Mg 3	0	0
56	EC	4	Total 4	Mg 4	0	0
56	FC	1	Total 1	Mg 1	0	0
56	GC	2	Total 2	Mg 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	HC	2	Total 2	Mg 2	0	0
56	KC	5	Total 5	Mg 5	0	0
56	MC	1	Total 1	Mg 1	0	0
56	NC	14	Total 14	Mg 14	0	0
56	OC	7	Total 7	Mg 7	0	0
56	PC	5	Total 5	Mg 5	0	0
56	QC	4	Total 4	Mg 4	0	0
56	RC	11	Total 11	Mg 11	0	0
56	SC	7	Total 7	Mg 7	0	0
56	TC	1	Total 1	Mg 1	0	0
56	UC	2	Total 2	Mg 2	0	0
56	VC	2	Total 2	Mg 2	0	0
56	WC	2	Total 2	Mg 2	0	0
56	XC	2	Total 2	Mg 2	0	0
56	YC	6	Total 6	Mg 6	0	0
56	ZC	2	Total 2	Mg 2	0	0
56	AD	1	Total 1	Mg 1	0	0
56	CD	3	Total 3	Mg 3	0	0
56	DD	1	Total 1	Mg 1	0	0
56	ED	2	Total 2	Mg 2	0	0
56	GD	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	HD	1	Total	Mg	0	0
			1	1		

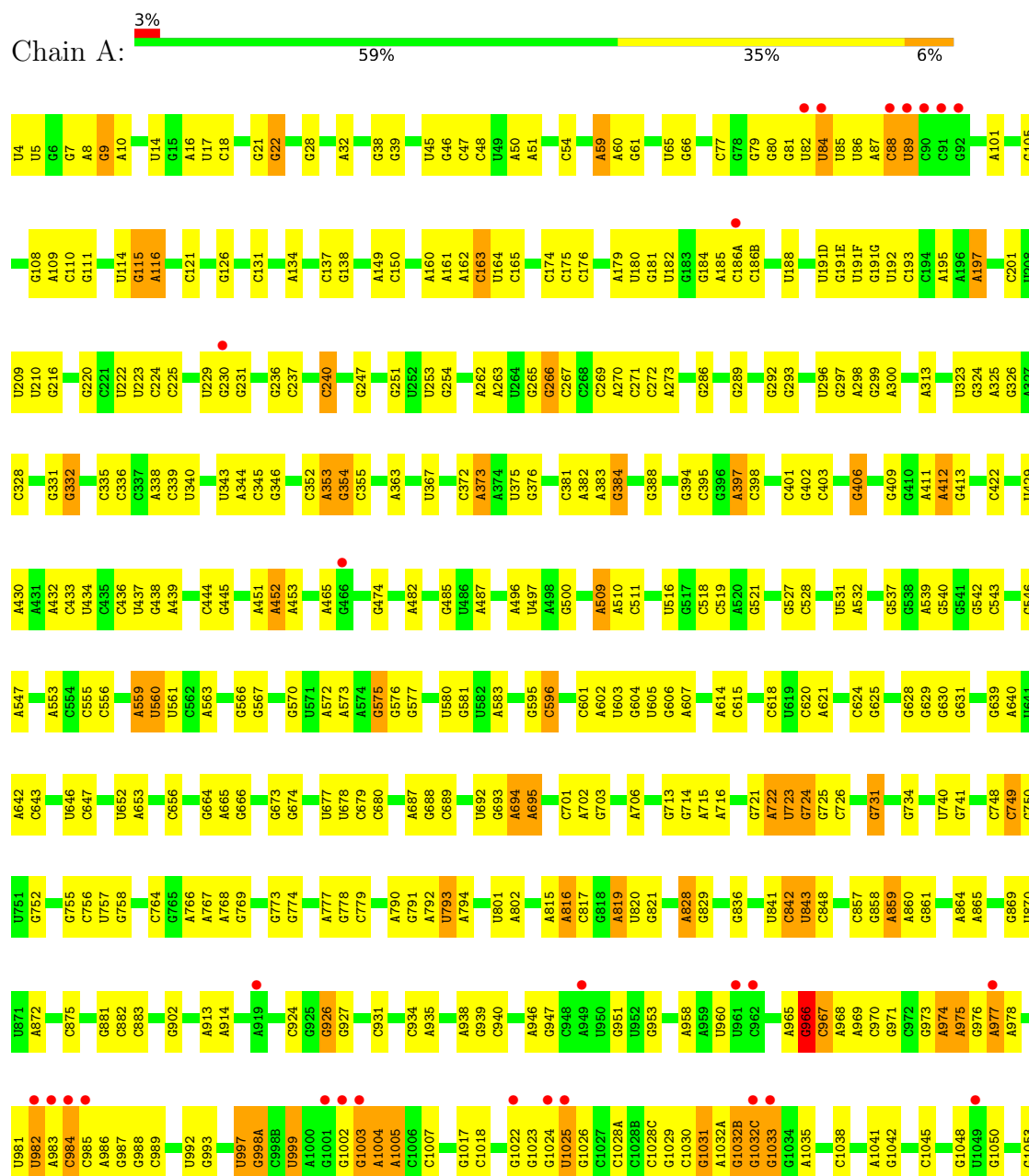
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

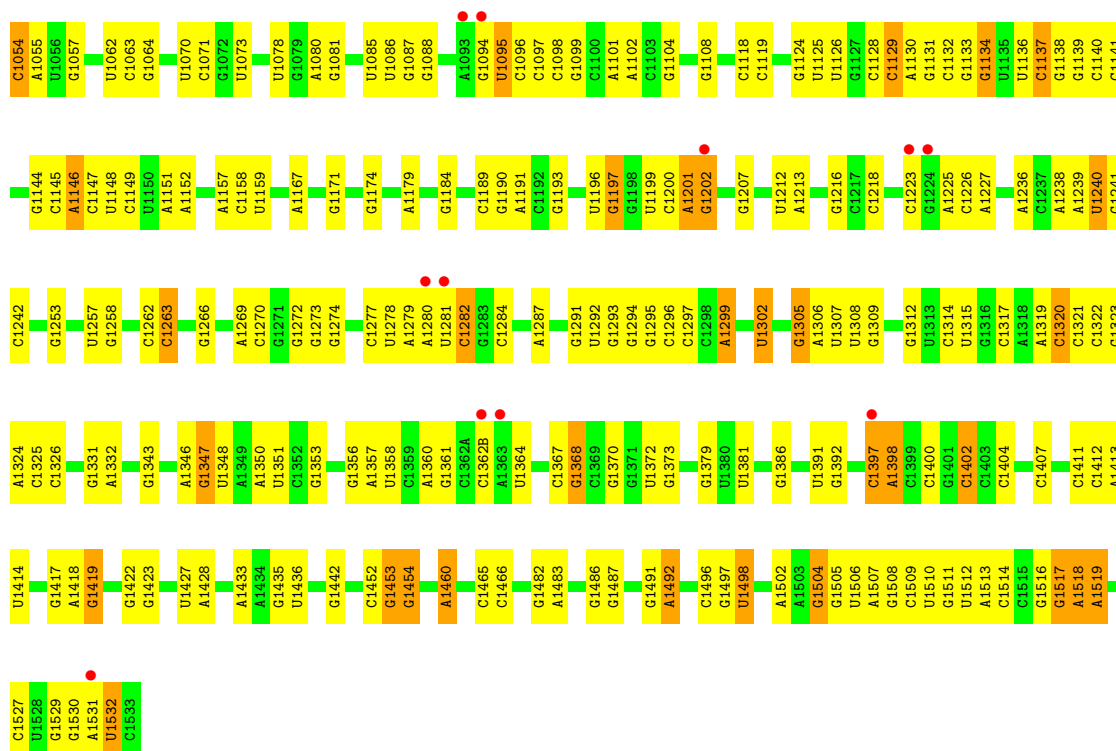
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	V	1	Total	Zn	0	0
			1	1		
57	BA	1	Total	Zn	0	0
			1	1		
57	CA	1	Total	Zn	0	0
			1	1		
57	DA	1	Total	Zn	0	0
			1	1		
57	GA	1	Total	Zn	0	0
			1	1		
57	AC	1	Total	Zn	0	0
			1	1		
57	GC	1	Total	Zn	0	0
			1	1		
57	HC	1	Total	Zn	0	0
			1	1		
57	IC	1	Total	Zn	0	0
			1	1		
57	LC	1	Total	Zn	0	0
			1	1		

3 Residue-property plots

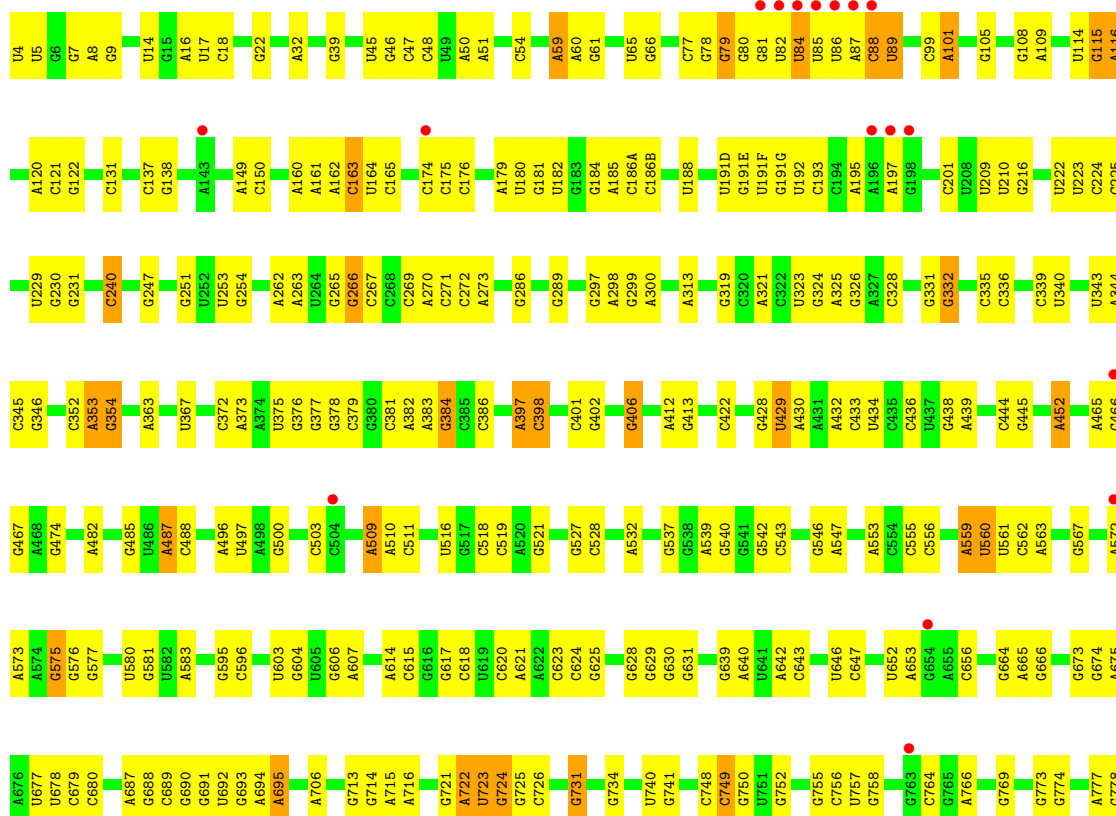
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

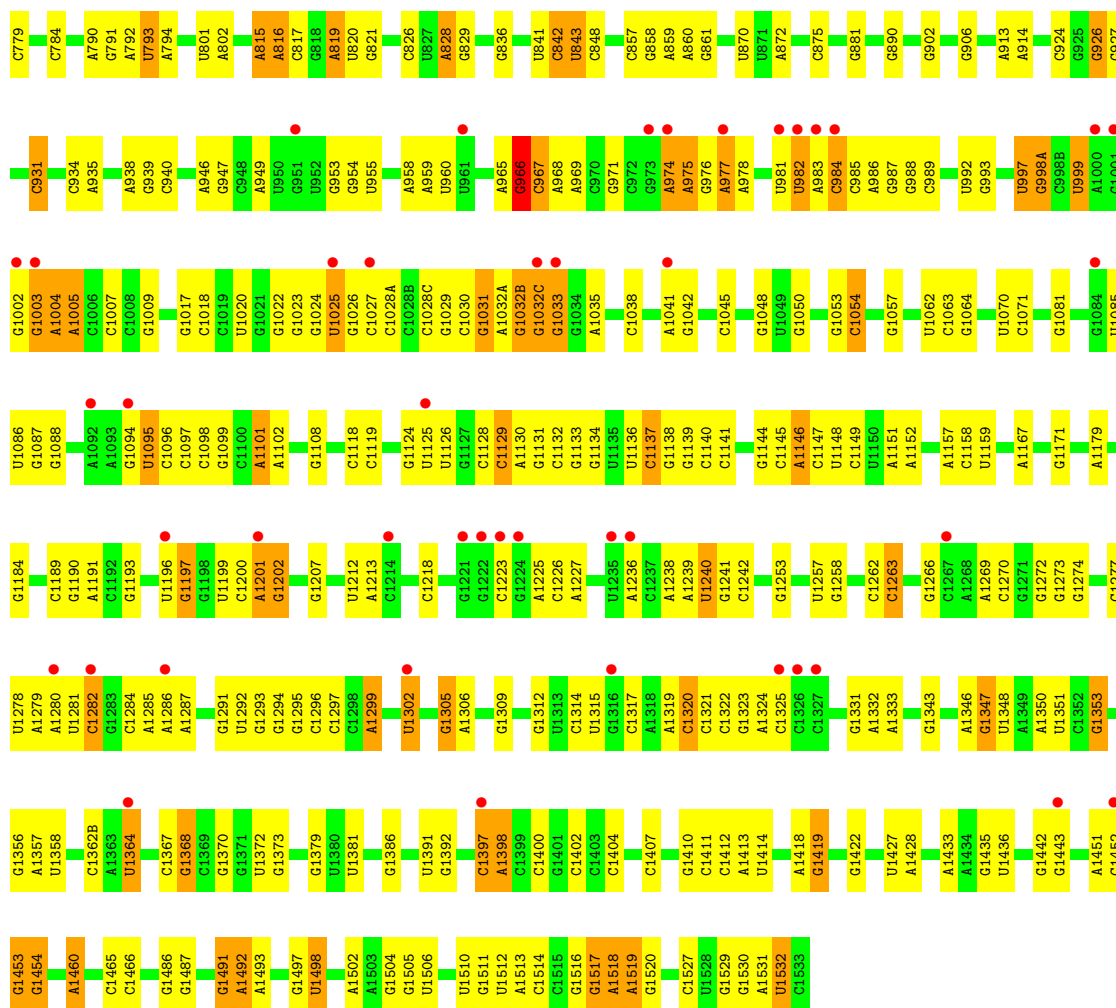
• Molecule 1: 16S ribosomal RNA



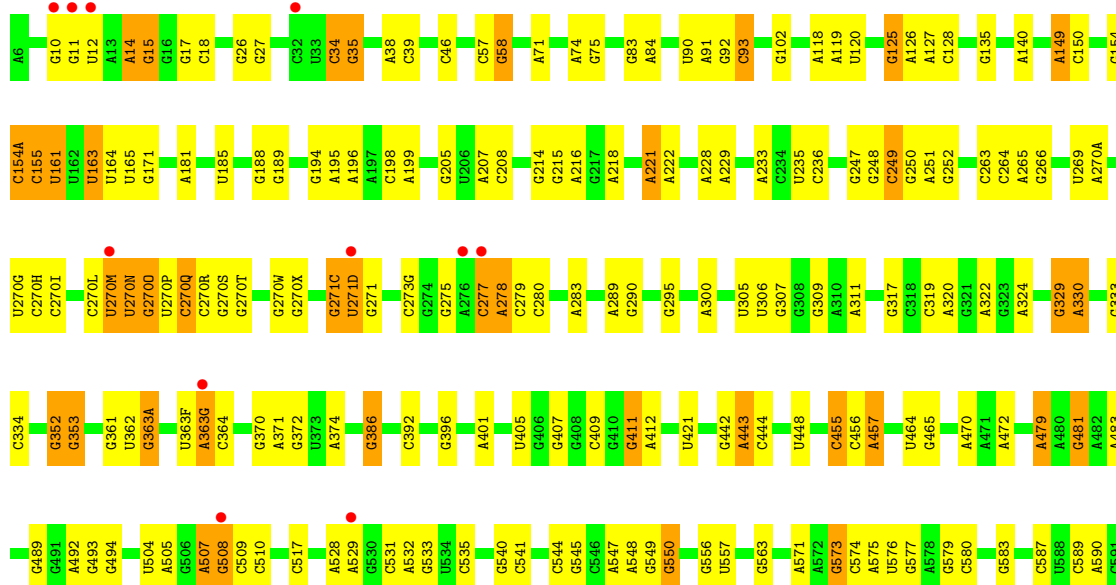


• Molecule 1: 16S ribosomal RNA

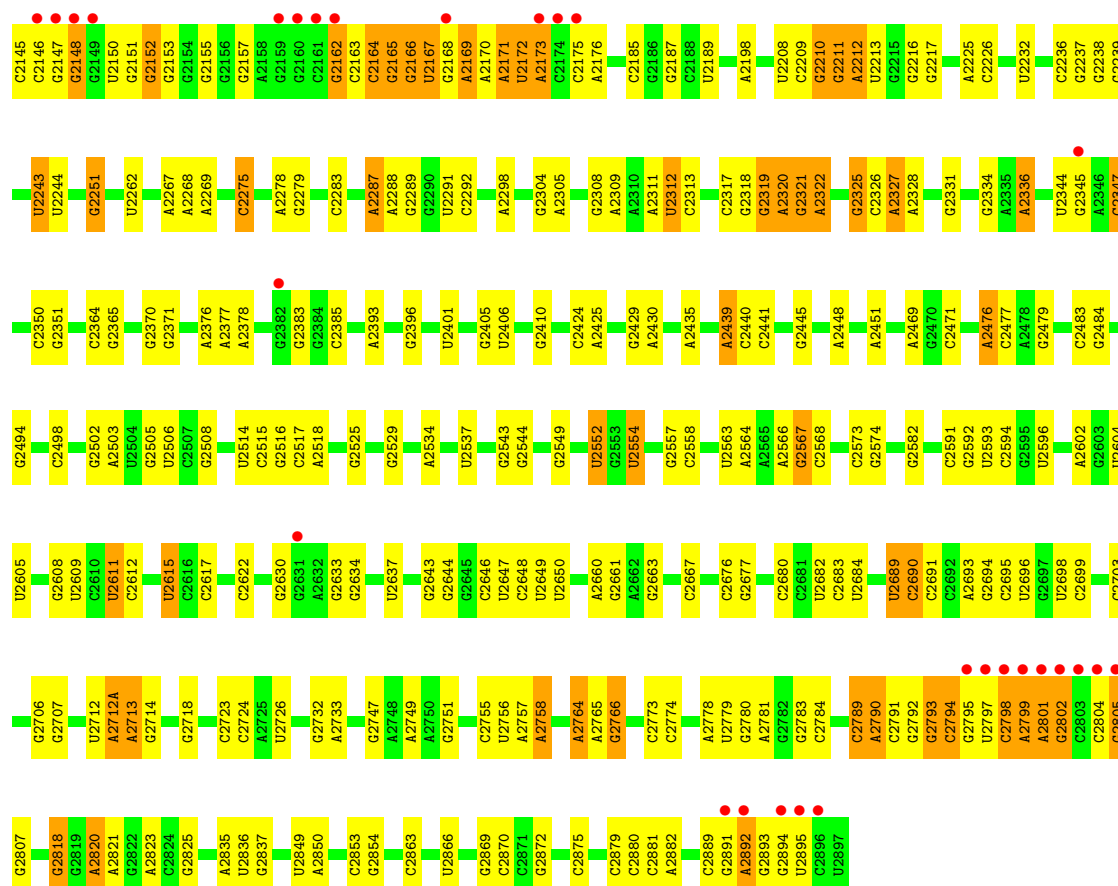




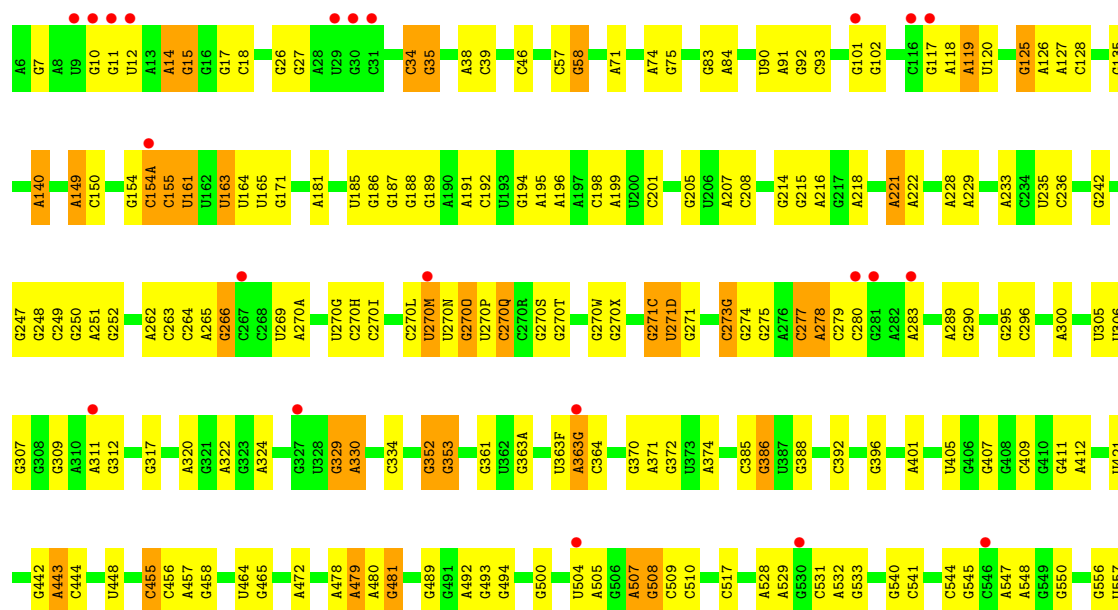
• Molecule 2: 25S ribosomal RNA

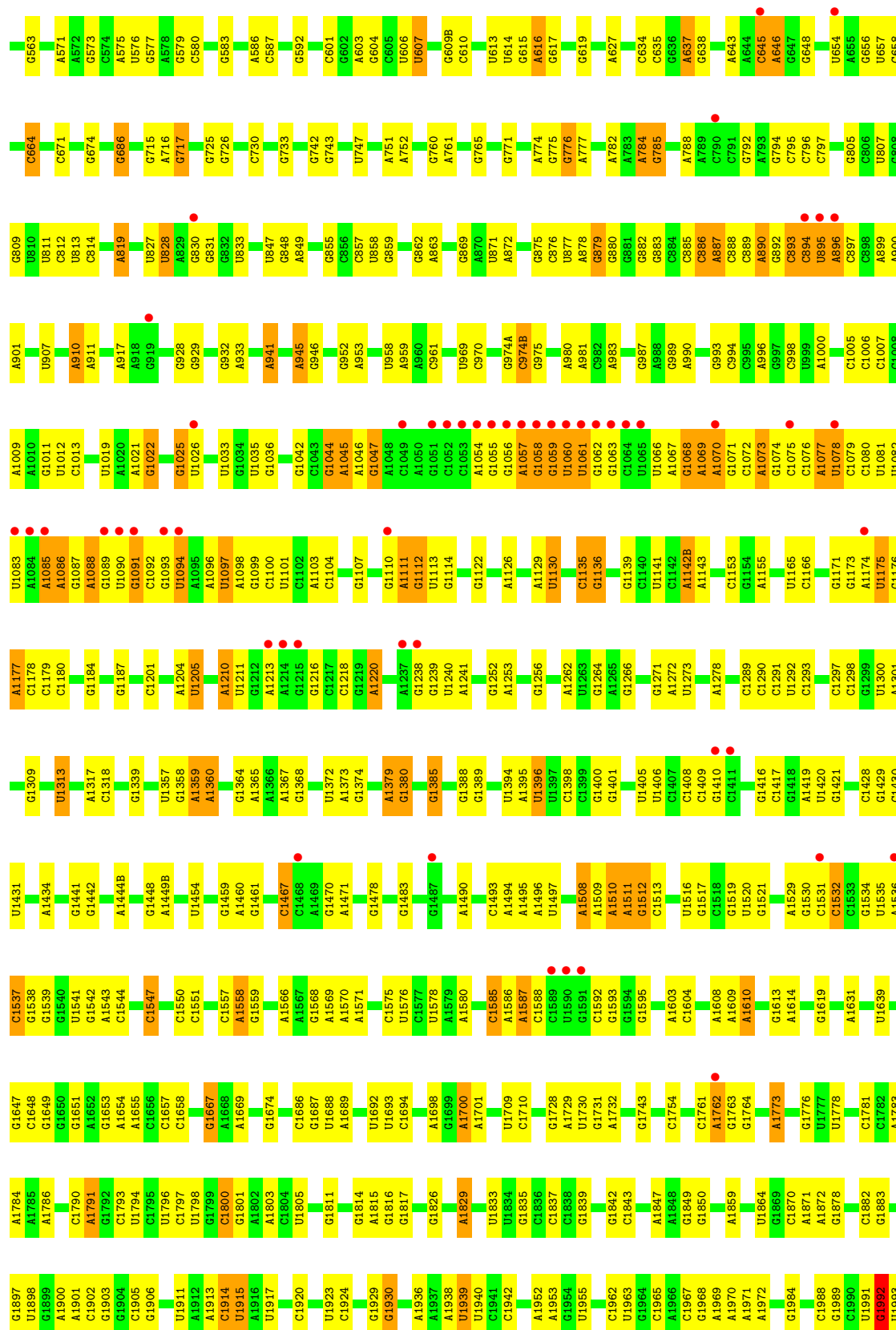


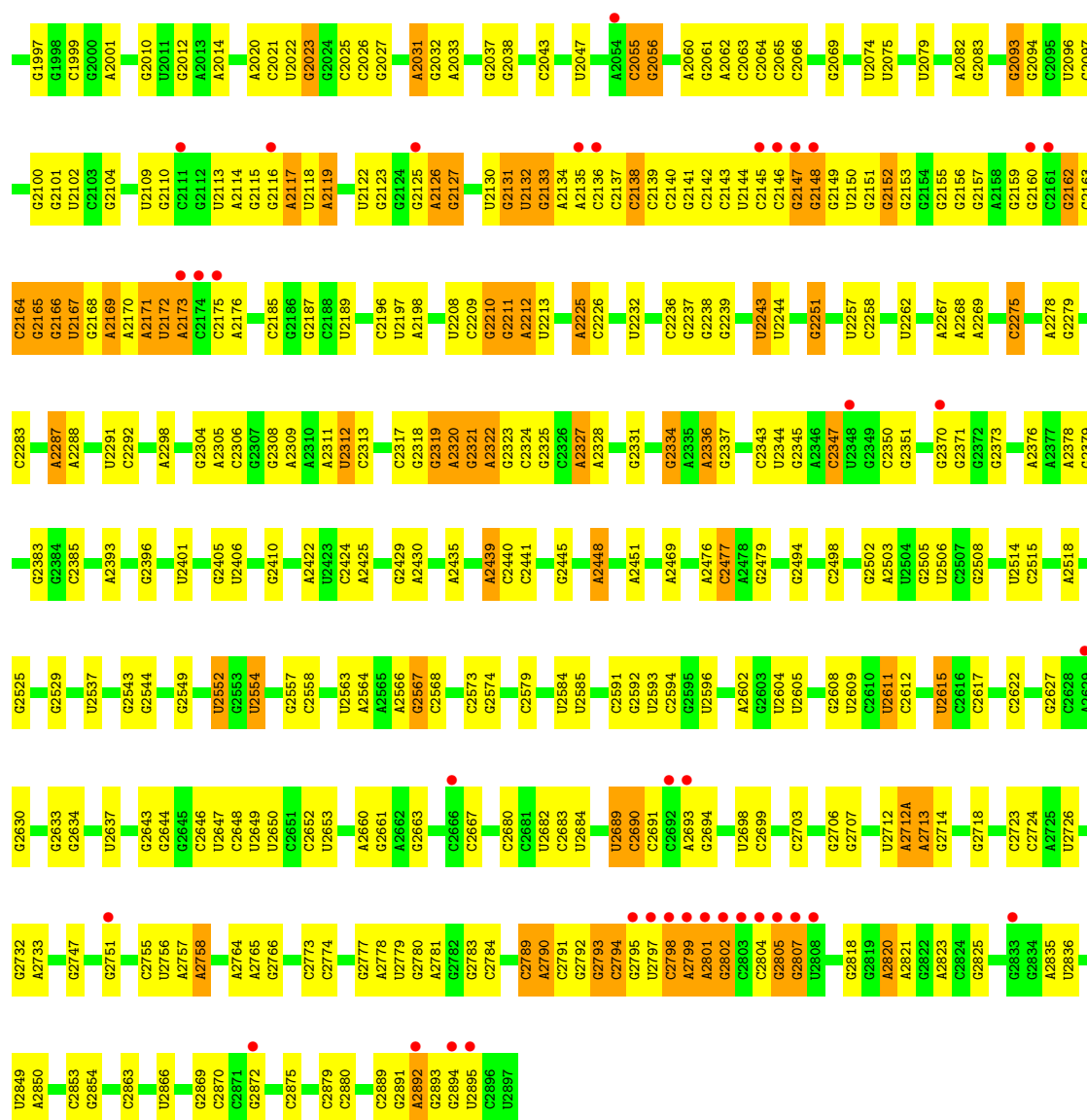
A2060	A1952	C1843	G1728	C1585	G1491	G1385	A1241	G1122	G1056	A959	G859	G742	G592
G2061	A1953	A1847	A1729	A1586	G1492	G1388	A1245	A1126	A1057	A960	U860	G743	C601
C2062	G1954	A1848	G1730	A1587	A1493	G1389	G1245	A1129	G1058	C961	G861	G602	A603
C2064	U1955	G1849	A1732	C1588	A1496	G1394	G1252	A1130	G1059	U969	A863	U747	G604
C2065	C1958	G1850	G1743	C1592	U1497	U1394	A1263	U1130	U1061	C970	G869	A751	C605
C2066	C1962	A1859	C1754	G1593	A1508	U1396	G1256	C1135	G1062	G974A	A870	A752	U606
G2069	U1963	U1864	C1761	G1594	A1509	U1397	G1262	G1136	C1064	C974B	U871	G765	U607
U2079	G1965	G1869	A1763	A1509	A1510	C1398	A1263	G1139	U1065	G975	A872	G610	G609B
A2082	C1966	A1870	G1763	A1503	A1511	C1399	U1263	G1140	A1067	A983	C876	G768	C610
G2083	C1967	A1871	G1764	G1512	G1512	G1400	G1264	U1141	G1068	G987	A878	G771	G615
C2088	G1968	A1872	G1764	C1513	C1513	G1401	A1265	G1142	A1069	A988	G879	A774	A616
U2089	A1969	A1609	G1769	A1608	U1516	U1405	G1266	A1142B	A1070	G989	G880	G775	G617
A1970	A1970	A1610	A1773	A1610	G1517	U1406	G1271	A1143	C1072	A990	G881	G776	G619
A1971	G1882	A1614	C1776	A1614	G1518	C1407	A1272	C1153	A1073	G983	C884	A777	A627
A1972	G1883	A1631	G1777	A1631	G1519	C1408	U1273	G1154	G1074	A996	C885	A782	C634
C2097	C1892	C1776	U1777	C1642	G1522	C1409	C1289	A1155	C1075	G997	C886	A783	C635
G2100	G1897	U1778	U1778	C1648	G1523	G1416	C1290	U1165	U1082	C1005	C887	A784	C636
G2101	C1898	C1781	C1781	C1648	G1530	C1417	C1291	C1166	U1078	C998	G888	G785	G636
U2102	G1899	C1782	A1783	C1648	C1532	G1418	C1293	G1170	C1079	U999	C889	A637	A637
C2103	A1900	G1786	A1786	G1642	C1533	A1419	C1297	G1171	U1081	A1000	A890	A788	G638
G2104	A1901	A1788	A1788	G1642	C1534	U1420	C1298	G1173	U1082	C1006	C892	A789	A643
C1902	C1902	A1788	A1788	C1648	G1535	G1421	C1299	A1174	U1083	C1007	C893	G792	A643
U1993	U1993	A1788	A1788	C1648	G1536	C1428	G1299	U1175	A1084	C1008	C894	G792	A643
G1997	G1997	A1788	A1788	C1648	G1537	C1429	G1300	G1176	A1085	U995	C895	C796	C645
C2111	C2111	A1788	A1788	C1648	C1538	C1430	A1301	A1177	U1086	A1009	A896	C797	A646
G2112	G2112	A1788	A1788	C1648	G1539	C1431	G1309	C1178	G1087	A1010	C897	G647	G647
U2113	U2113	A1788	A1788	C1648	G1540	U1431	G1309	C1180	G1088	C998	C998	G805	U654
A2114	A2114	A1788	A1788	C1648	G1541	A1434	U1313	G1184	U1090	A900	A901	U807	A655
G2115	G2115	A1788	A1788	C1648	G1542	G1441	A1317	G1187	U1091	U1019	U907	U811	G656
G2116	G2116	A1788	A1788	C1648	G1543	G1442	C1318	G1187	G1093	A1020	A1021	C812	G657
A2117	A2117	A1788	A1788	C1648	G1544	G1443	C1318	C1201	U1094	G1022	A911	U813	C658
C2006	C2006	A1788	A1788	C1648	G1545	A1444B	G1339	U1205	A1095	G1025	A917	C914	C664
G2012	G2012	A1788	A1788	C1648	G1546	G1448	C1345	A1204	U1097	U1026	A917	A819	C671
A2013	A2013	A1788	A1788	C1648	G1547	U1448	G1346	U1205	U1098	G1026	A917	A819	C671
A2014	A2014	A1788	A1788	C1648	G1548	U1449	G1346	U1205	U1099	G1026	A917	A819	C671
G2125	G2125	A1788	A1788	C1648	G1549	U1450	G1346	U1205	U1100	G1026	A917	A819	C671
A2126	A2126	A1788	A1788	C1648	G1550	U1451	G1346	U1205	U1101	G1026	A917	A819	C671
G2127	G2127	A1788	A1788	C1648	G1551	U1452	G1346	U1205	U1102	G1026	A917	A819	C671
U2130	U2130	A1788	A1788	C1648	G1552	U1453	G1346	U1205	U1103	G1026	A917	A819	C671
G2131	G2131	A1788	A1788	C1648	G1553	U1454	G1346	U1205	U1104	G1026	A917	A819	C671
U2132	U2132	A1788	A1788	C1648	G1554	U1455	G1346	U1205	U1105	G1026	A917	A819	C671
G2133	G2133	A1788	A1788	C1648	G1555	U1456	G1346	U1205	U1106	G1026	A917	A819	C671
A2134	A2134	A1788	A1788	C1648	G1556	U1457	G1346	U1205	U1107	G1026	A917	A819	C671
A2135	A2135	A1788	A1788	C1648	G1557	U1458	G1346	U1205	U1108	G1026	A917	A819	C671
C2136	C2136	A1788	A1788	C1648	G1558	U1459	G1346	U1205	U1109	G1026	A917	A819	C671
C2137	C2137	A1788	A1788	C1648	G1559	U1460	G1346	U1205	U1110	G1026	A917	A819	C671
C2138	C2138	A1788	A1788	C1648	G1560	U1461	G1346	U1205	U1111	G1026	A917	A819	C671
C2139	C2139	A1788	A1788	C1648	G1561	U1462	G1346	U1205	U1112	G1026	A917	A819	C671
C2140	C2140	A1788	A1788	C1648	G1562	U1463	G1346	U1205	U1113	G1026	A917	A819	C671
C2141	C2141	A1788	A1788	C1648	G1563	U1464	G1346	U1205	U1114	G1026	A917	A819	C671
G2142	G2142	A1788	A1788	C1648	G1564	U1465	G1346	U1205	U1115	G1026	A917	A819	C671
C2143	C2143	A1788	A1788	C1648	G1565	U1466	G1346	U1205	U1116	G1026	A917	A819	C671
U2144	U2144	A1788	A1788	C1648	G1566	U1467	G1346	U1205	U1117	G1026	A917	A819	C671



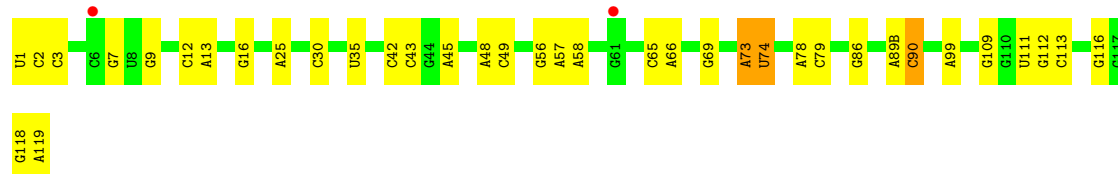
• Molecule 2: 25S ribosomal RNA





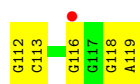


• Molecule 3: 5S ribosomal RNA

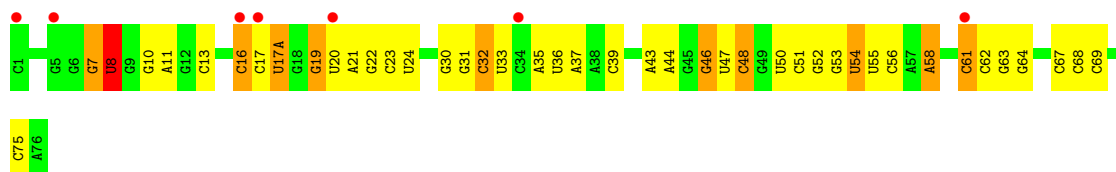
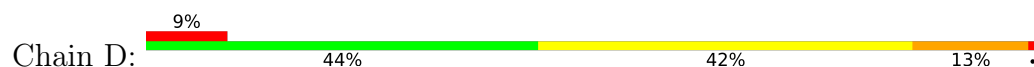


• Molecule 3: 5S ribosomal RNA





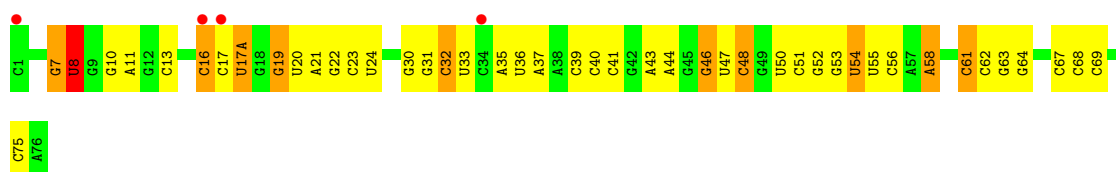
• Molecule 4: tRNA



• Molecule 4: tRNA



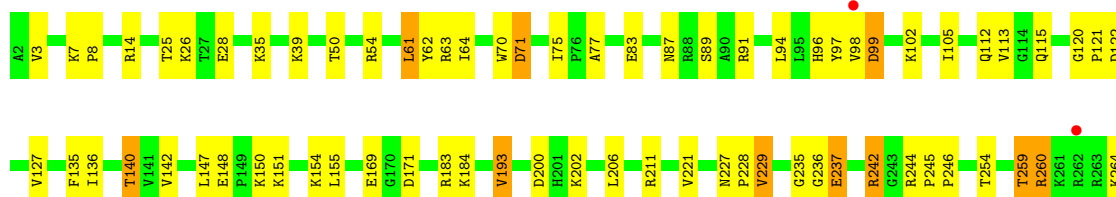
• Molecule 4: tRNA

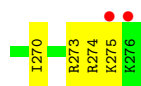


• Molecule 4: tRNA

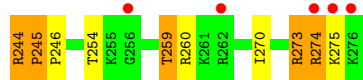
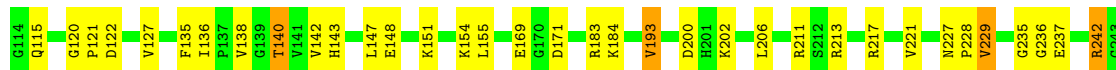
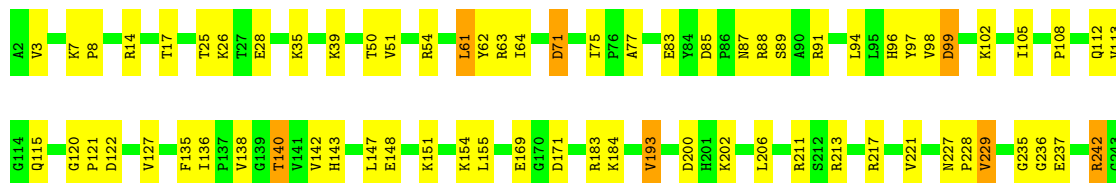
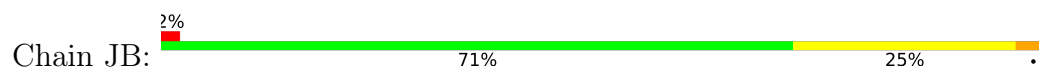


• Molecule 5: 50S ribosomal protein L2





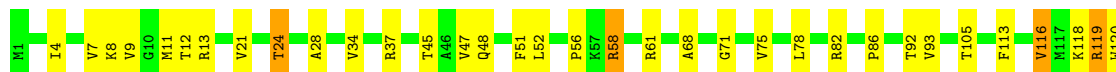
• Molecule 5: 50S ribosomal protein L2



• Molecule 6: 50S ribosomal protein L3



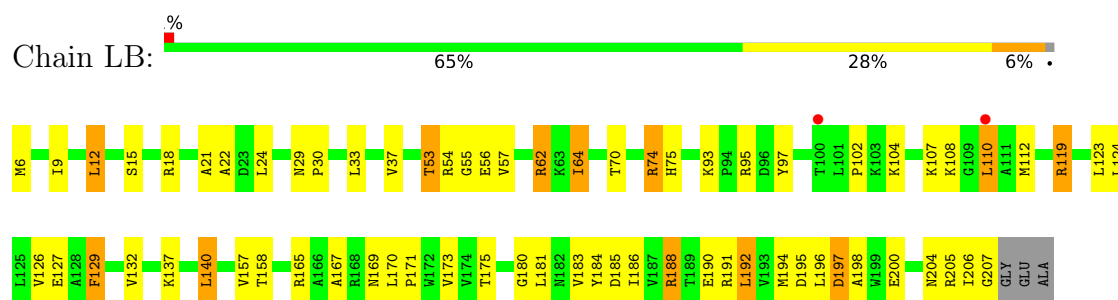
• Molecule 6: 50S ribosomal protein L3



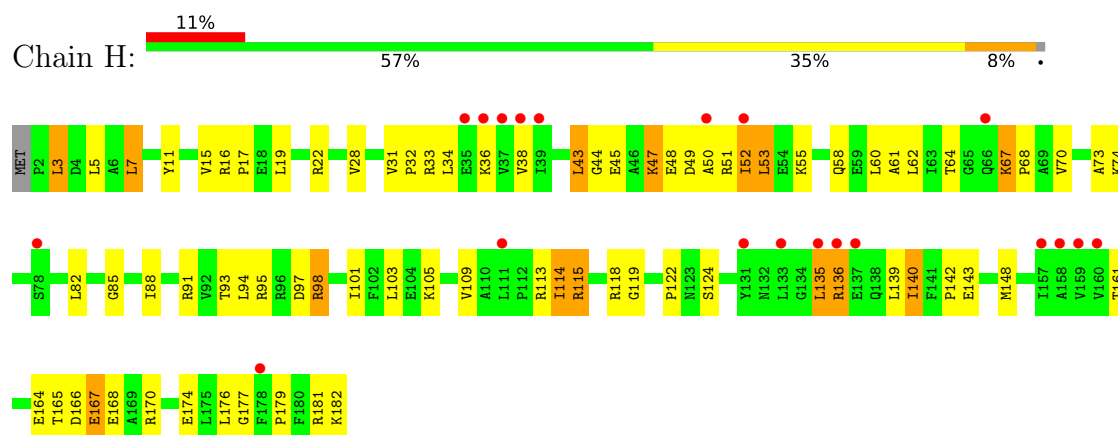
• Molecule 7: 50S ribosomal protein L4



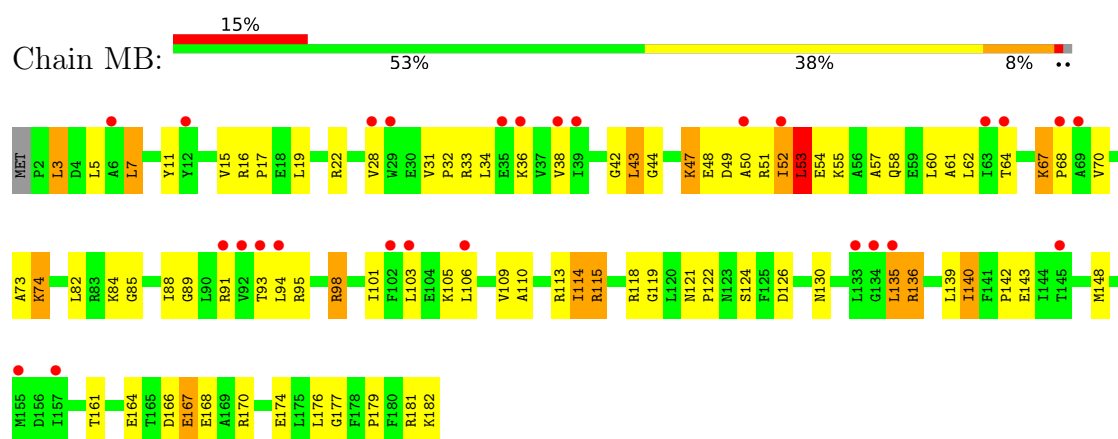
• Molecule 7: 50S ribosomal protein L4



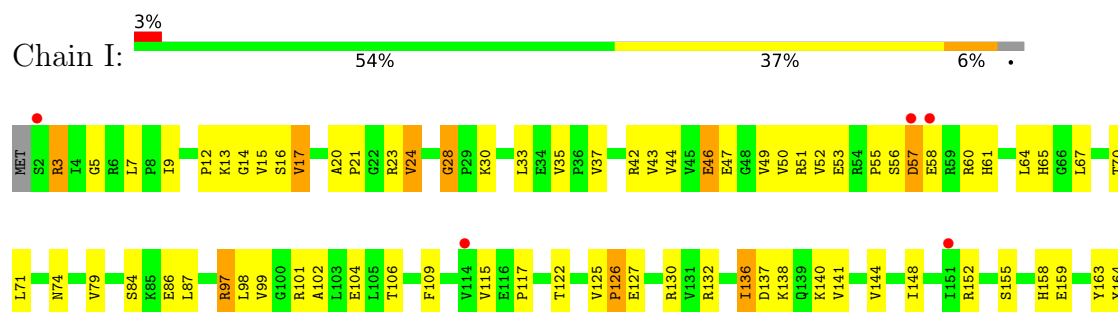
• Molecule 8: 50S ribosomal protein L5



• Molecule 8: 50S ribosomal protein L5

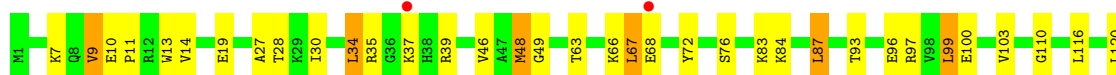
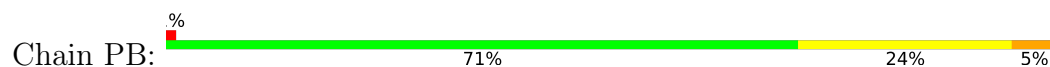


• Molecule 9: 50S ribosomal protein L6





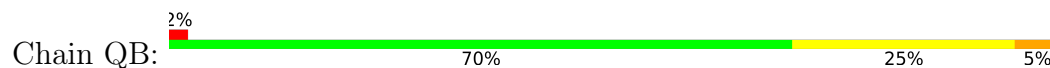
- Molecule 11: 50S ribosomal protein L13



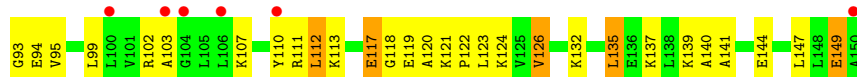
- Molecule 12: 50S ribosomal protein L14



- Molecule 12: 50S ribosomal protein L14

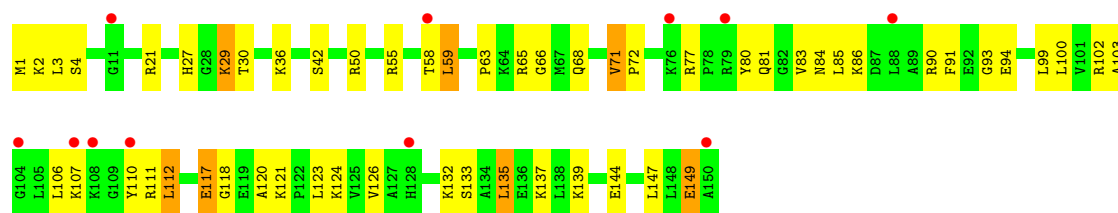


- Molecule 13: 50S ribosomal protein L15

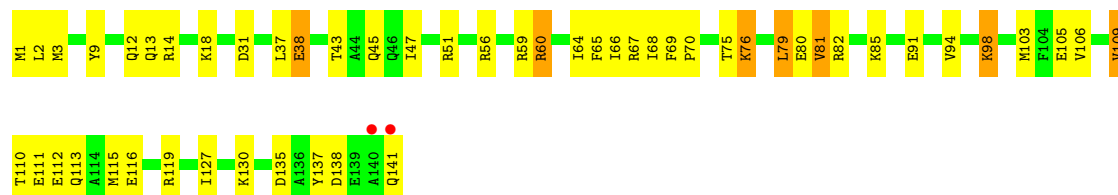


- Molecule 13: 50S ribosomal protein L15

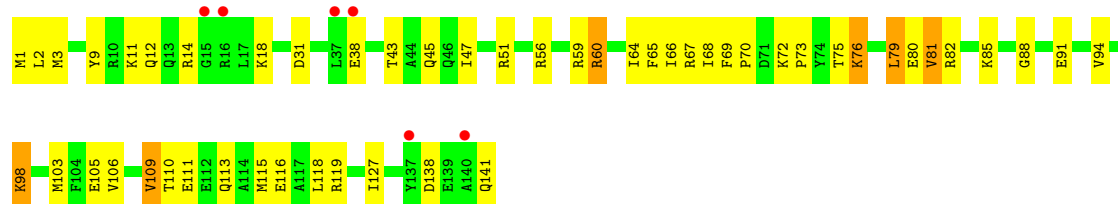




• Molecule 14: 50S ribosomal protein L16



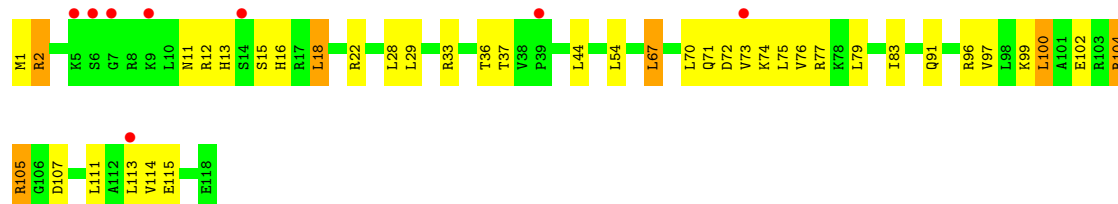
• Molecule 14: 50S ribosomal protein L16



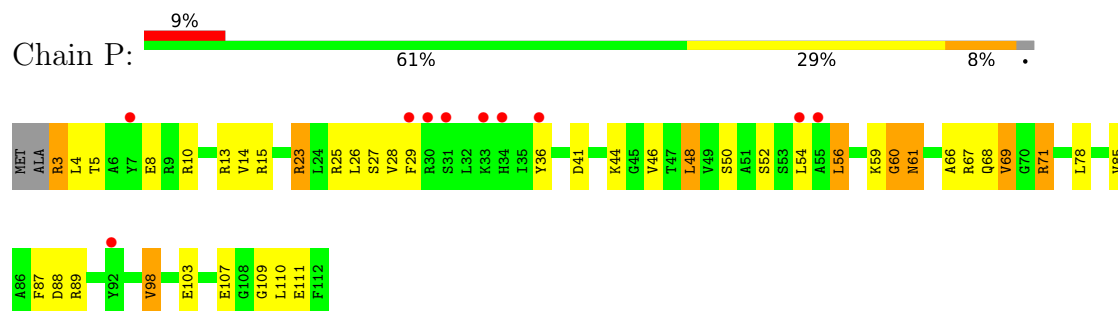
• Molecule 15: 50S ribosomal protein L17



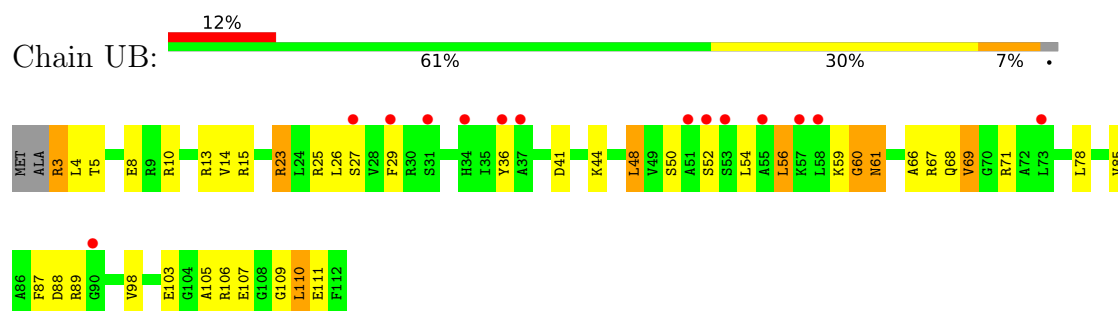
• Molecule 15: 50S ribosomal protein L17



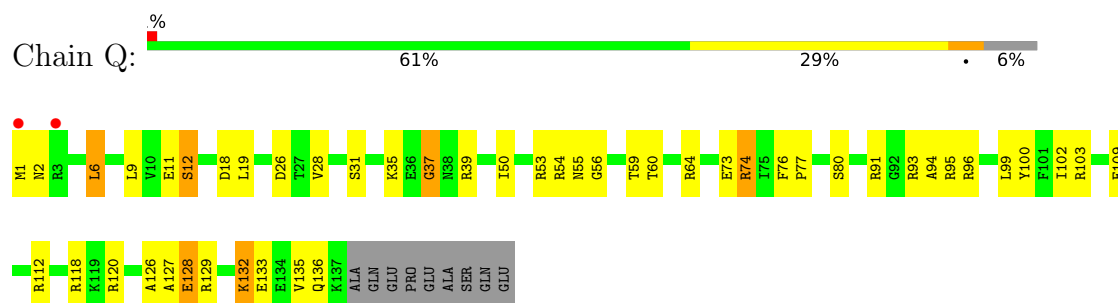
- Molecule 16: 50S ribosomal protein L18



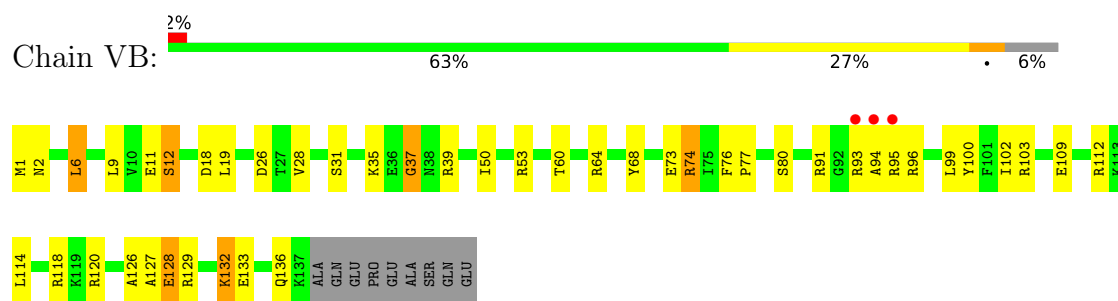
- Molecule 16: 50S ribosomal protein L18



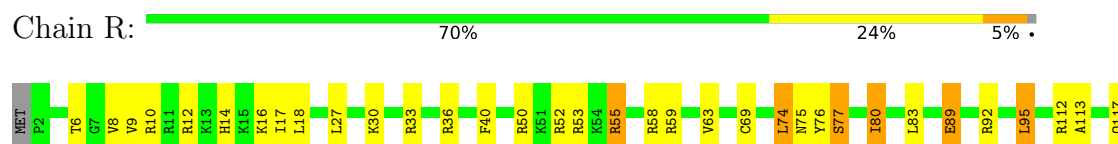
- Molecule 17: 50S ribosomal protein L19



- Molecule 17: 50S ribosomal protein L19



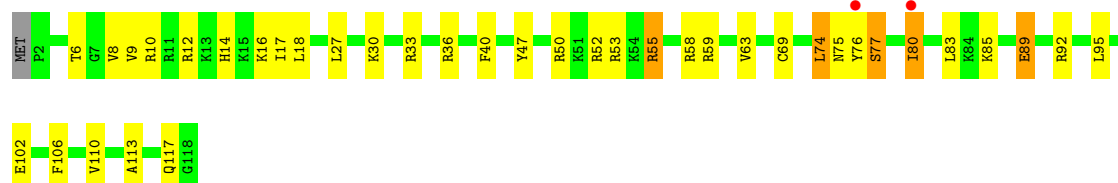
- Molecule 18: 50S ribosomal protein L20



G118

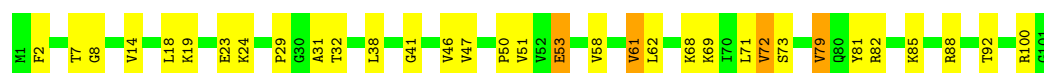
- Molecule 18: 50S ribosomal protein L20

Chain WB: 



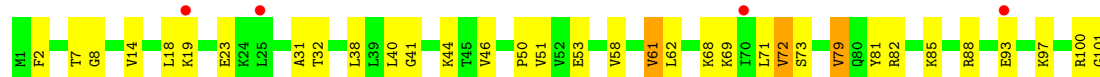
- Molecule 19: 50S ribosomal protein L21

Chain S: 



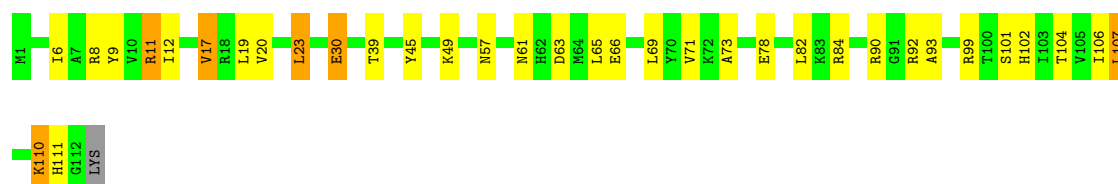
- Molecule 19: 50S ribosomal protein L21

Chain XB: 



- Molecule 20: 50S ribosomal protein L22

Chain T: 

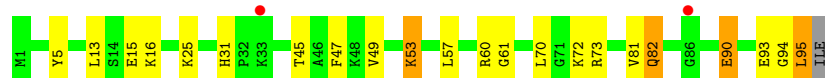
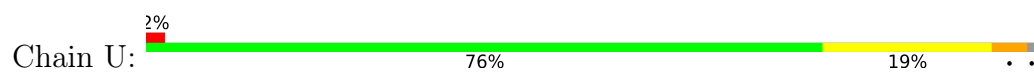


- Molecule 20: 50S ribosomal protein L22

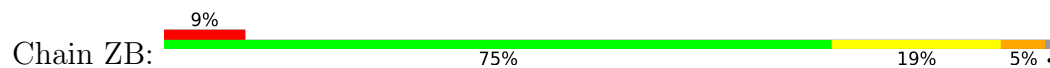
Chain YB: 



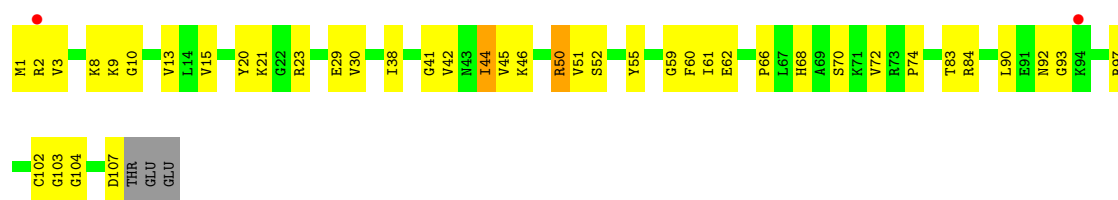
- Molecule 21: 50S ribosomal protein L23



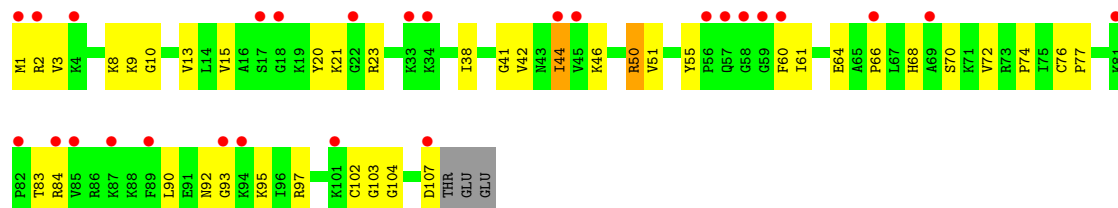
- Molecule 21: 50S ribosomal protein L23



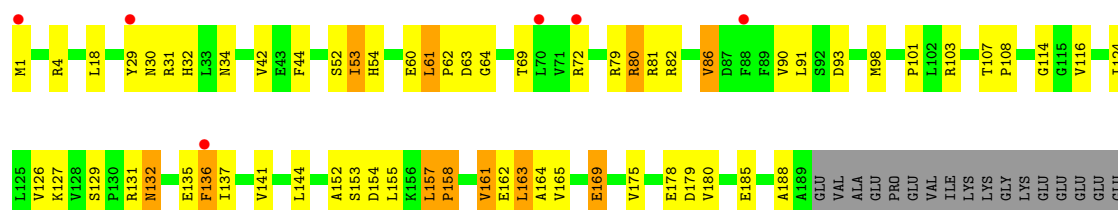
- Molecule 22: 50S ribosomal protein L24



- Molecule 22: 50S ribosomal protein L24

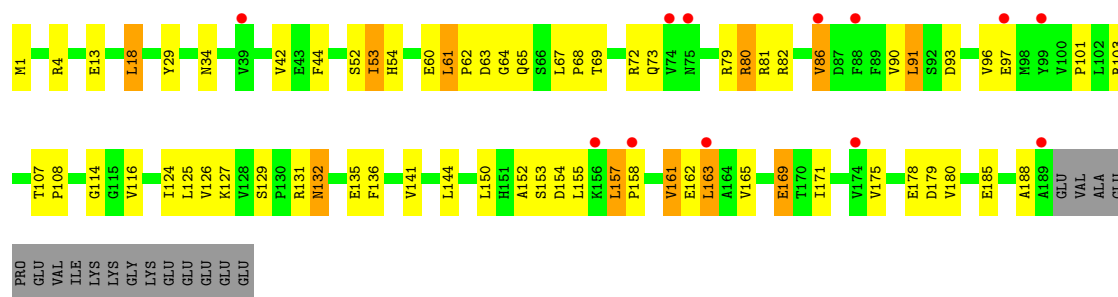


- Molecule 23: 50S ribosomal protein L25

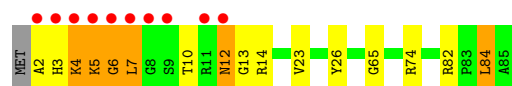
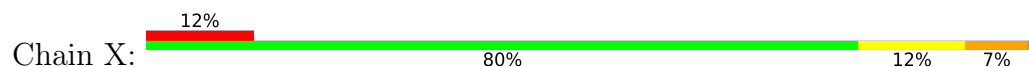


- Molecule 23: 50S ribosomal protein L25

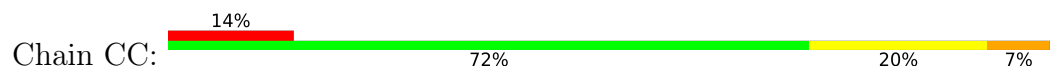




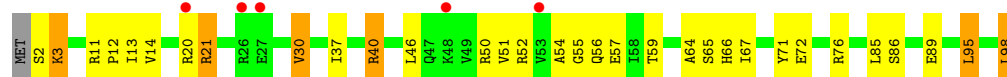
- Molecule 24: 50S ribosomal protein L27



- Molecule 24: 50S ribosomal protein L27



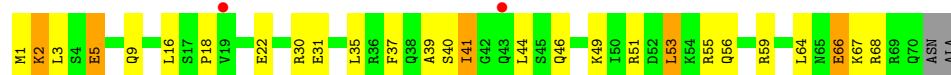
- Molecule 25: 50S ribosomal protein L28



- Molecule 25: 50S ribosomal protein L28

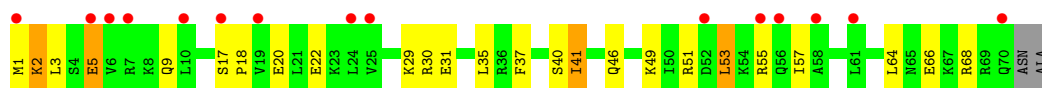


- Molecule 26: 50S ribosomal protein L29



- Molecule 26: 50S ribosomal protein L29





- Molecule 27: 50S ribosomal protein L30

Chain AA: 63% 32% 5%



- Molecule 27: 50S ribosomal protein L30

Chain FC: 2% 67% 27% 7%



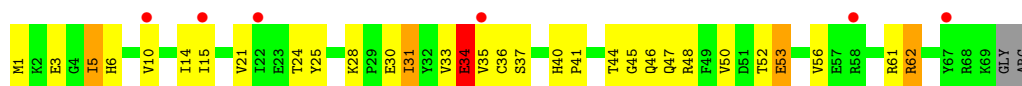
- Molecule 28: 50S ribosomal protein L31

Chain BA: 4% 52% 37% 7% ..



- Molecule 28: 50S ribosomal protein L31

Chain GC: 8% 54% 37% 6% ..



- Molecule 29: 50S ribosomal protein L32

Chain CA: 73% 23% ..



- Molecule 29: 50S ribosomal protein L32

Chain HC: 2% 75% 22% ..



- Molecule 30: 50S ribosomal protein L33

Chain DA:  54% 35% 9% .



- Molecule 30: 50S ribosomal protein L33

Chain IC:  4% 54% 35% 9% .



- Molecule 31: 50S ribosomal protein L34

Chain EA:  2% 67% 29% ..



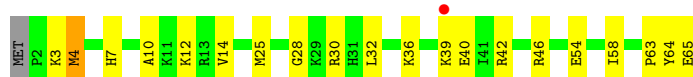
- Molecule 31: 50S ribosomal protein L34

Chain JC:  78% 18% ..



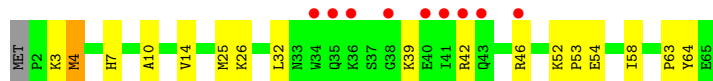
- Molecule 32: 50S ribosomal protein L35

Chain FA:  2% 68% 29% ..



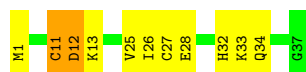
- Molecule 32: 50S ribosomal protein L35

Chain KC:  14% 72% 25% ..

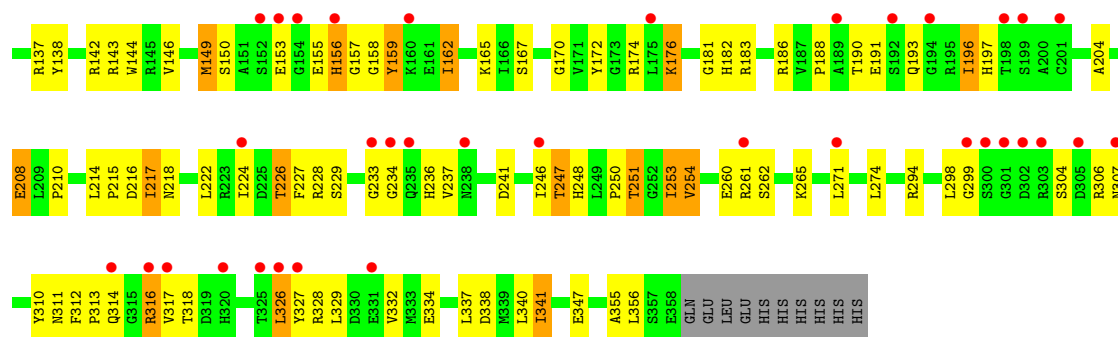


- Molecule 33: 50S ribosomal protein L36

Chain GA:  70% 24% 5%

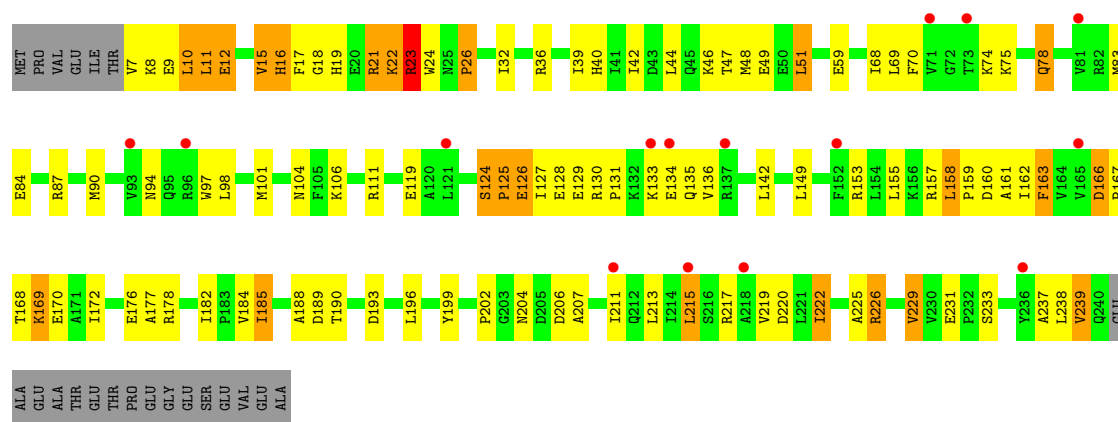


- Molecule 33: 50S ribosomal protein L36



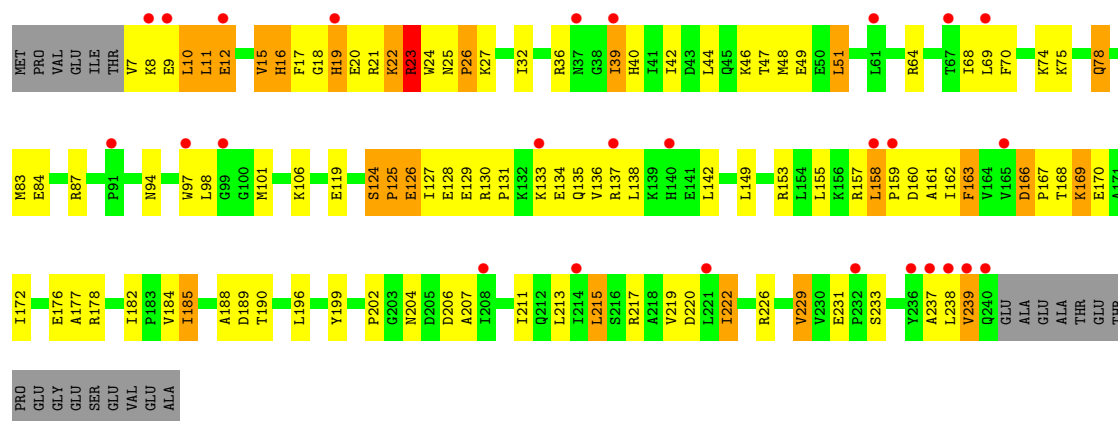
• Molecule 36: 30S ribosomal protein S2

Chain KA: 6% 50% 32% 9% 9%



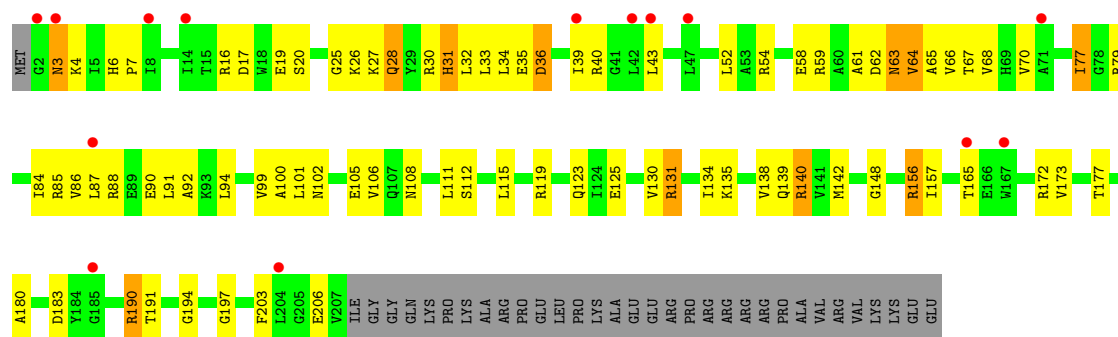
• Molecule 36: 30S ribosomal protein S2

Chain PC: 11% 50% 32% 9% 9%

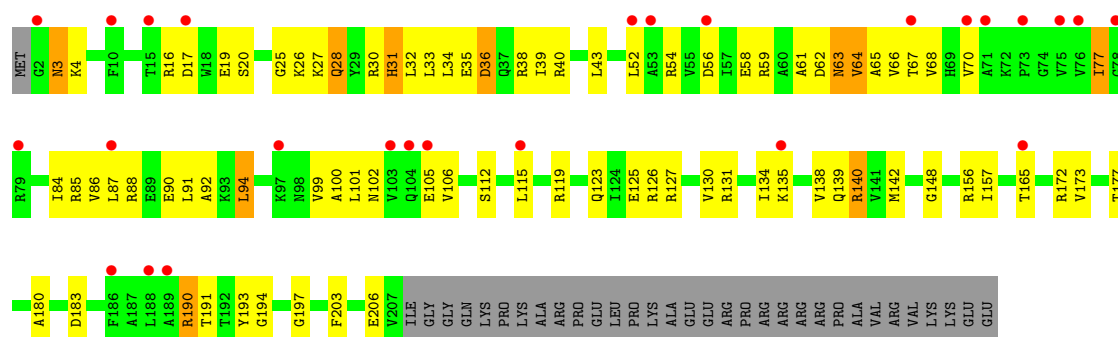


• Molecule 37: 30S ribosomal protein S3

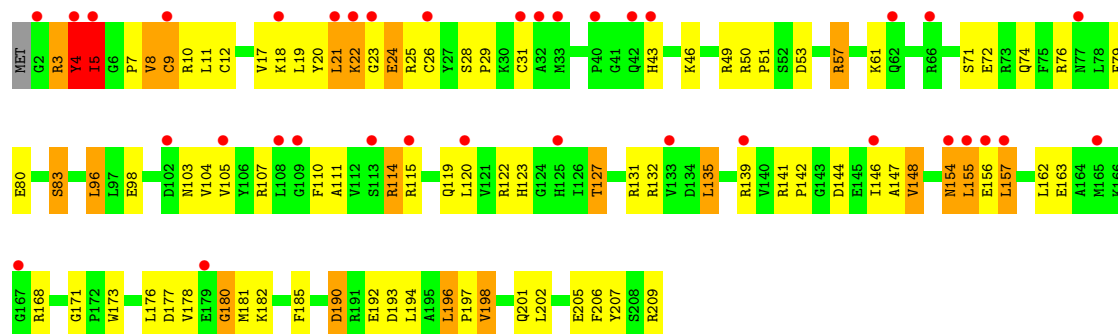
Chain LA: 6% 52% 30% 5% 14%



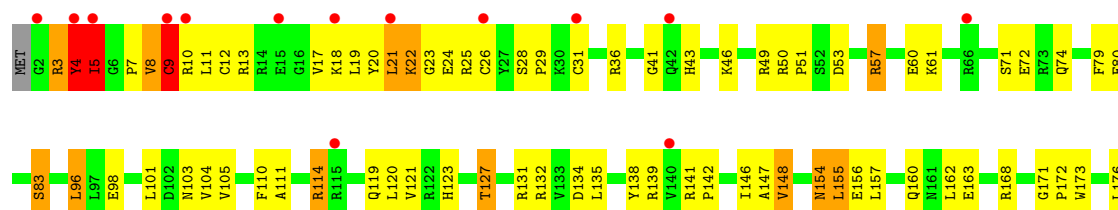
• Molecule 37: 30S ribosomal protein S3



• Molecule 38: 30S ribosomal protein S4

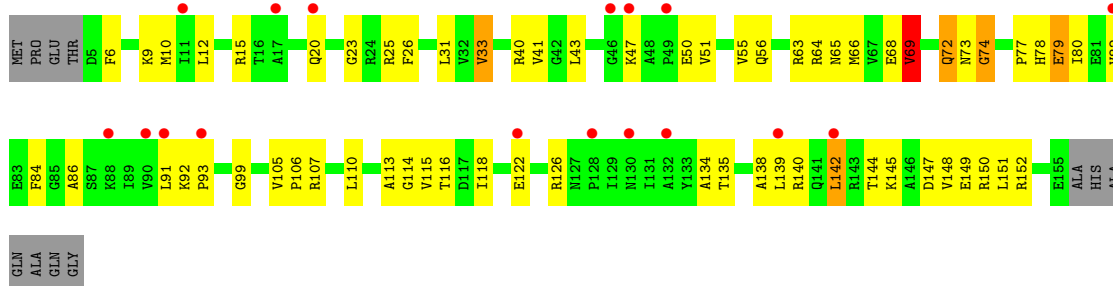


• Molecule 38: 30S ribosomal protein S4

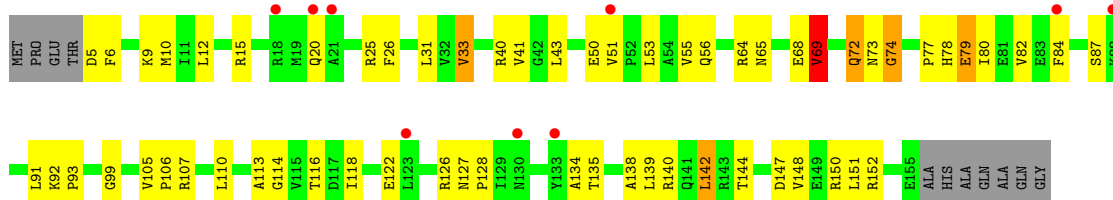




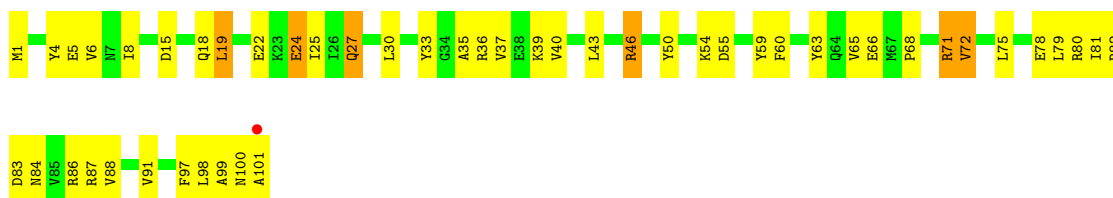
• Molecule 39: 30S ribosomal protein S5



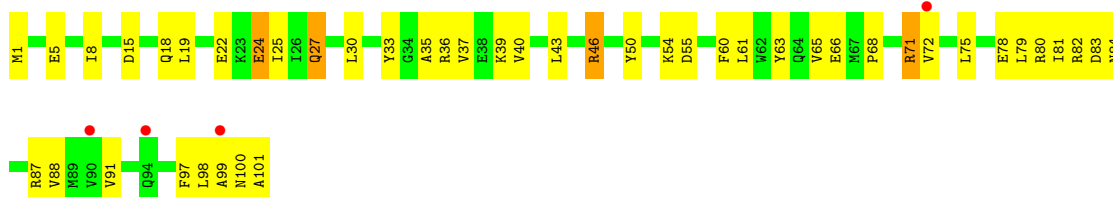
• Molecule 39: 30S ribosomal protein S5



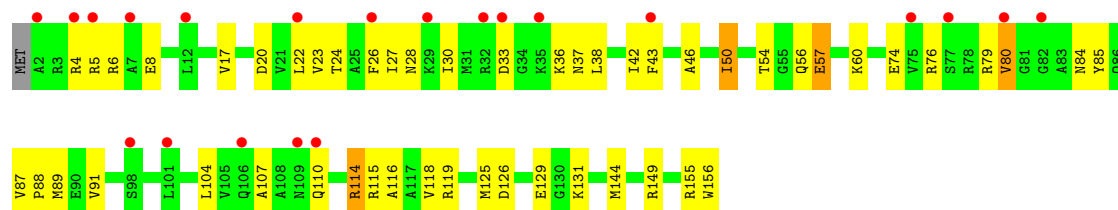
• Molecule 40: 30S ribosomal protein S6



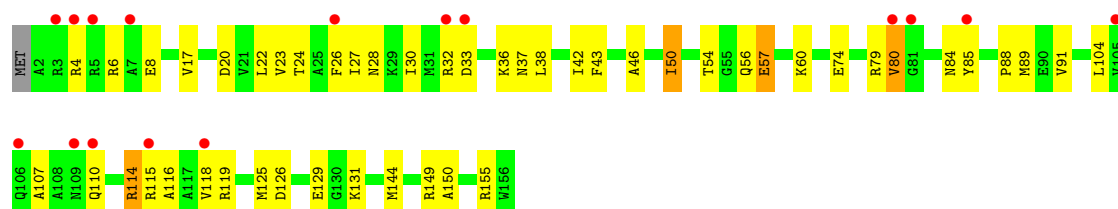
• Molecule 40: 30S ribosomal protein S6



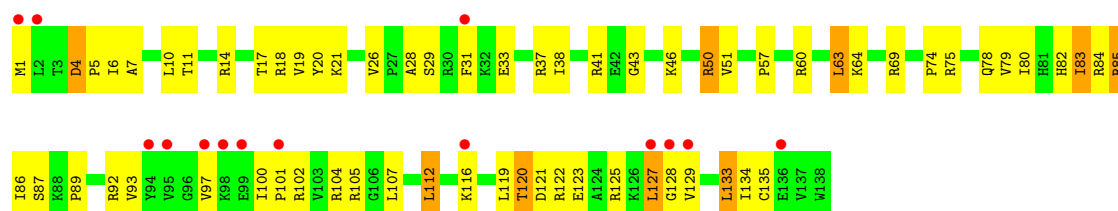
• Molecule 41: 30S ribosomal protein S7



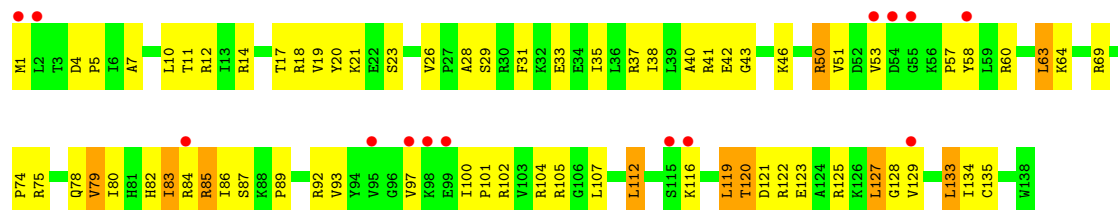
- Molecule 41: 30S ribosomal protein S7



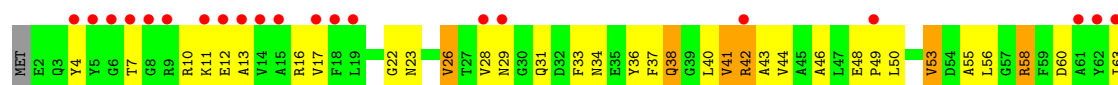
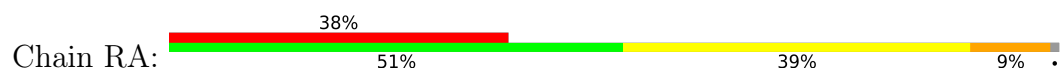
- Molecule 42: 30S ribosomal protein S8

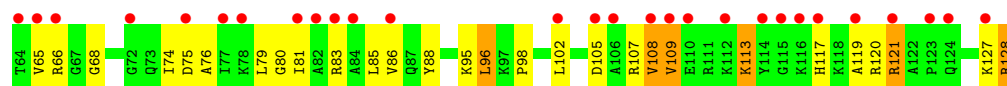


- Molecule 42: 30S ribosomal protein S8



- Molecule 43: 30S ribosomal protein S9

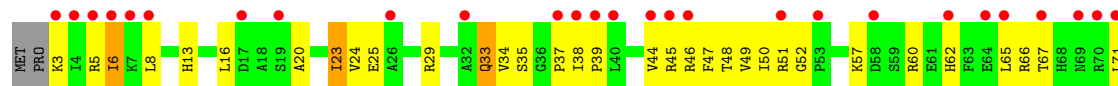




- Molecule 43: 30S ribosomal protein S9



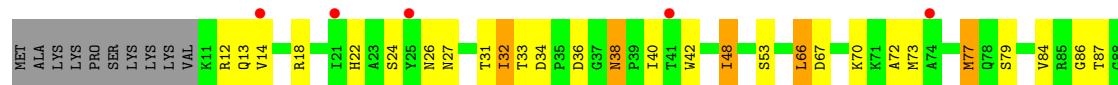
- Molecule 44: 30S ribosomal protein S10



- Molecule 44: 30S ribosomal protein S10

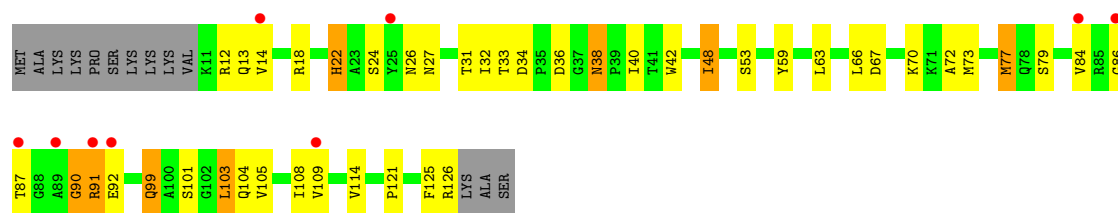


- Molecule 45: 30S ribosomal protein S11

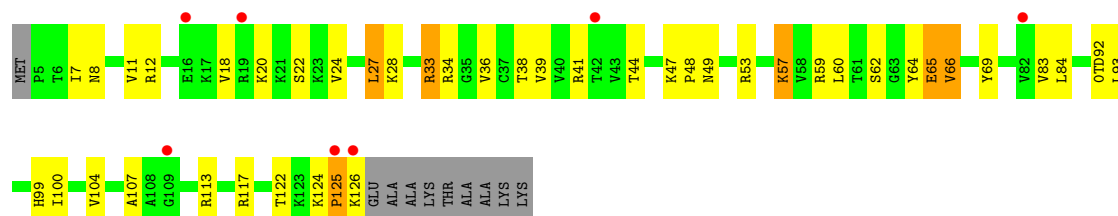


- Molecule 45: 30S ribosomal protein S11

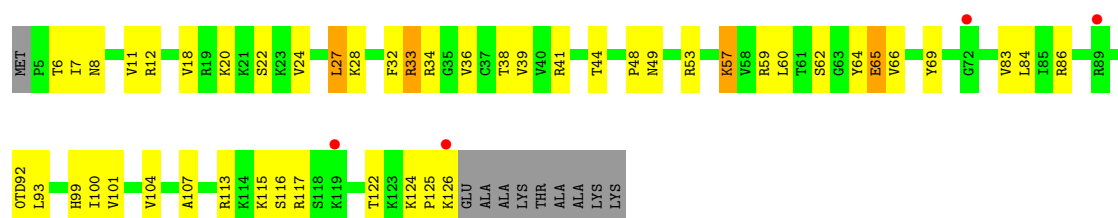




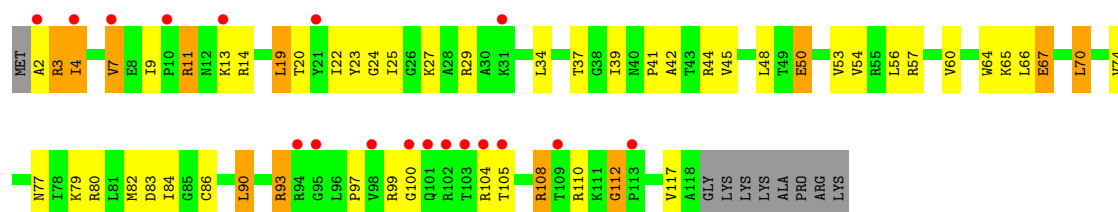
• Molecule 46: 30S ribosomal protein S12



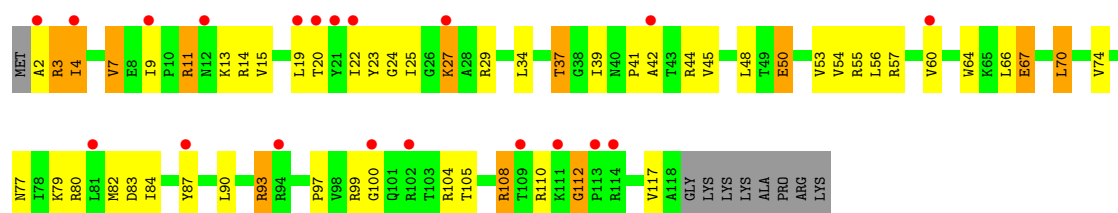
• Molecule 46: 30S ribosomal protein S12



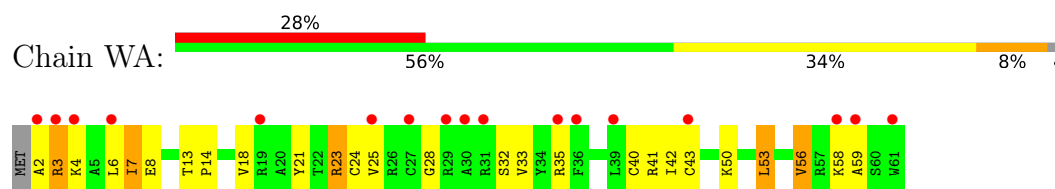
• Molecule 47: 30S ribosomal protein S13



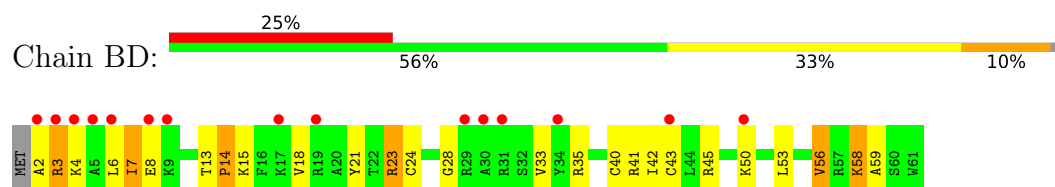
• Molecule 47: 30S ribosomal protein S13



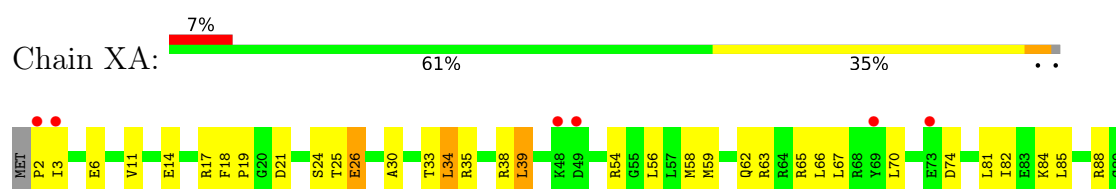
- Molecule 48: 30S ribosomal protein S14 type Z



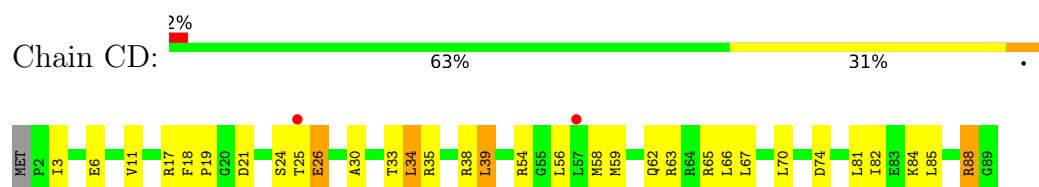
- Molecule 48: 30S ribosomal protein S14 type Z



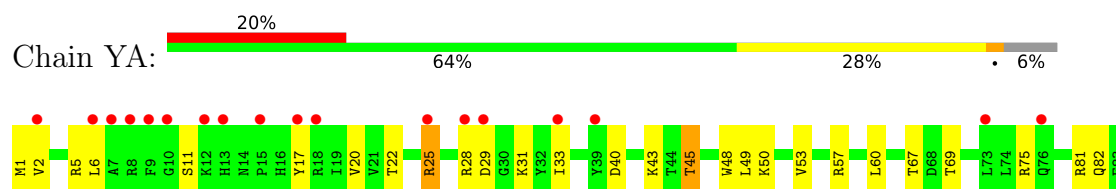
- Molecule 49: 30S ribosomal protein S15



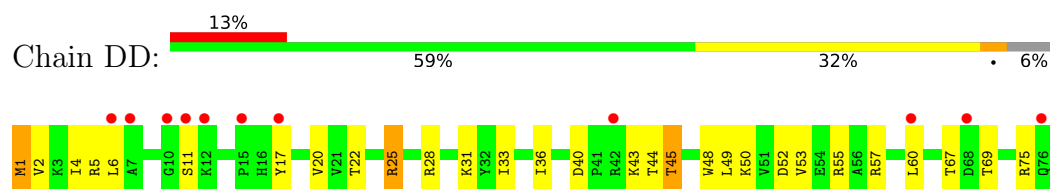
- Molecule 49: 30S ribosomal protein S15



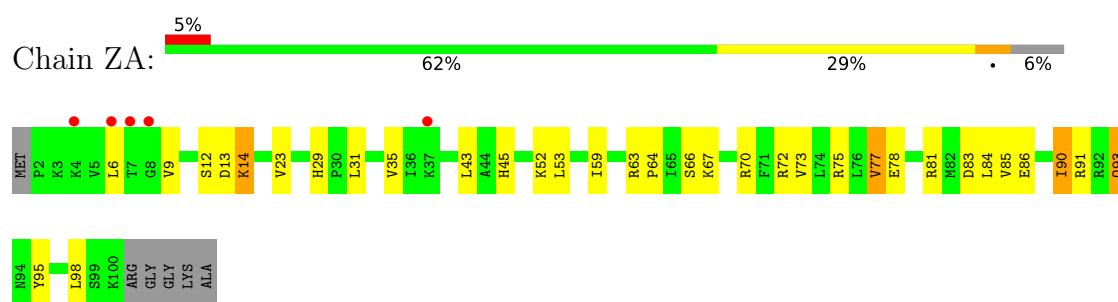
- Molecule 50: 30S ribosomal protein S16



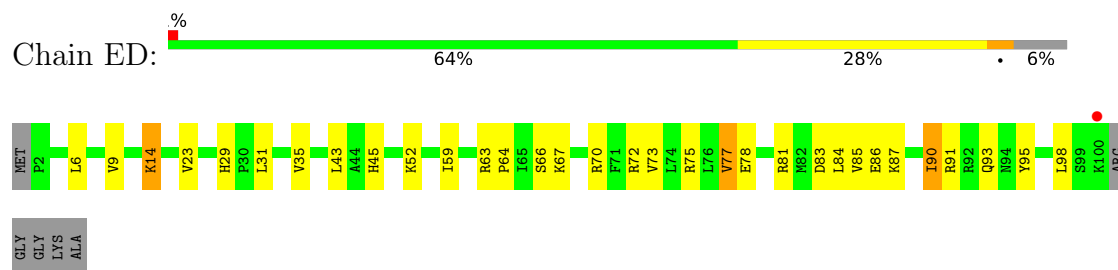
- Molecule 50: 30S ribosomal protein S16



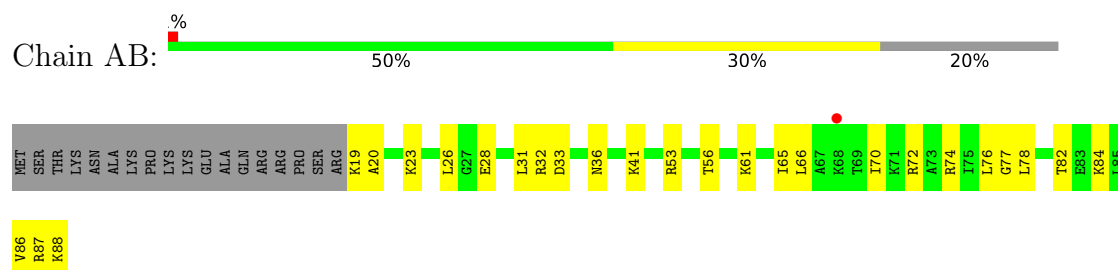
- Molecule 51: 30S ribosomal protein S17



- Molecule 51: 30S ribosomal protein S17



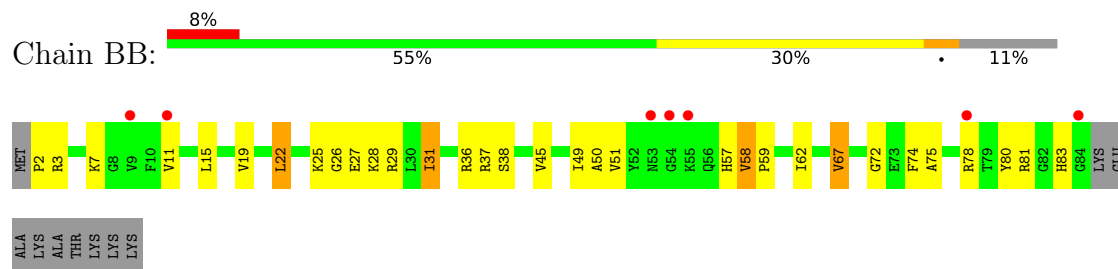
- Molecule 52: 30S ribosomal protein S18



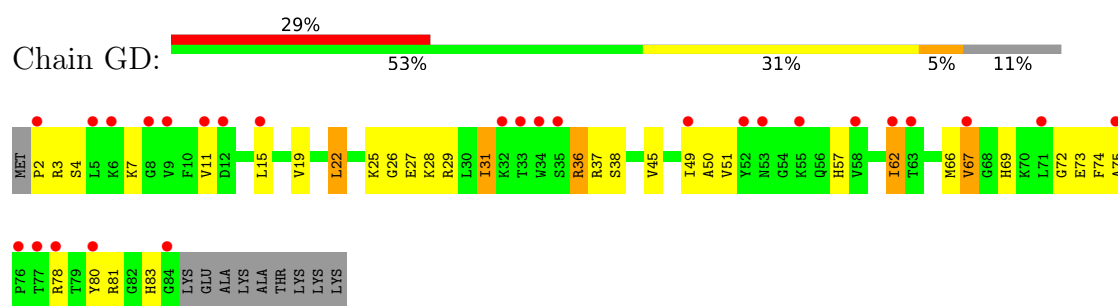
- Molecule 52: 30S ribosomal protein S18



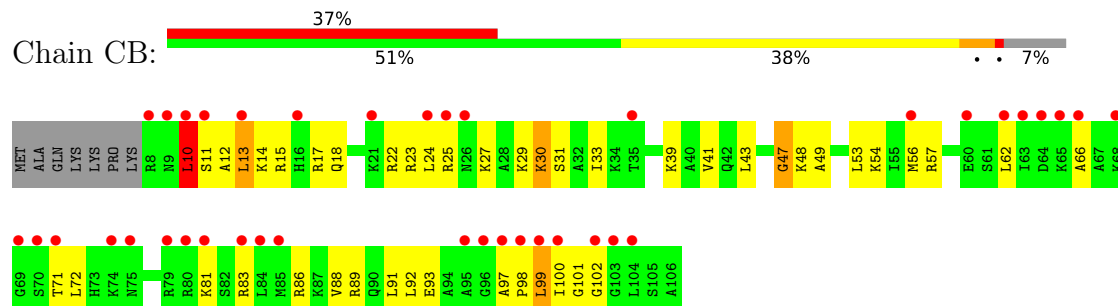
- Molecule 53: 30S ribosomal protein S19



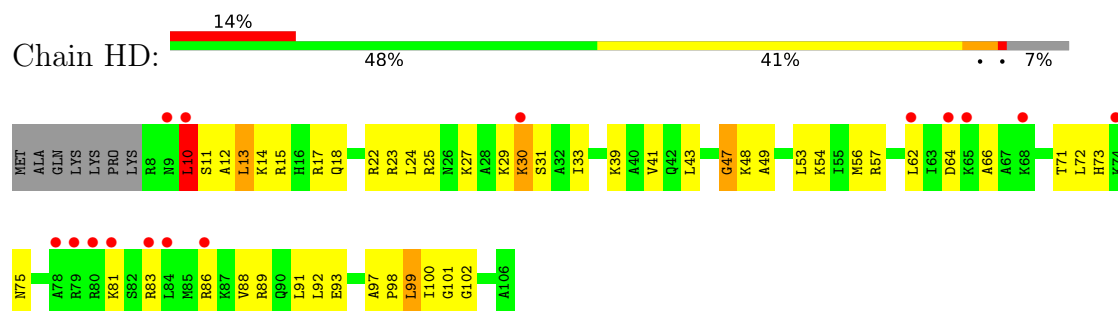
- Molecule 53: 30S ribosomal protein S19



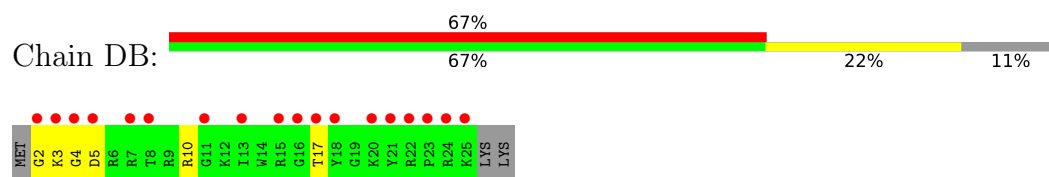
- Molecule 54: 30S ribosomal protein S20



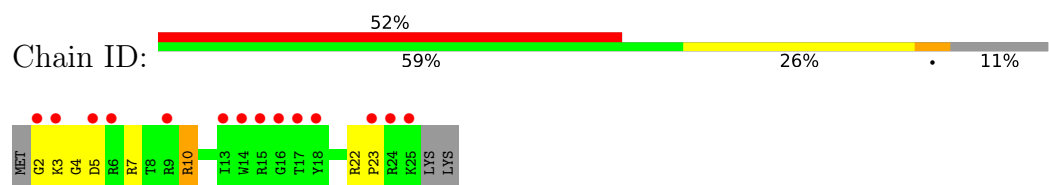
- Molecule 54: 30S ribosomal protein S20



- Molecule 55: 30S ribosomal protein Thx



- Molecule 55: 30S ribosomal protein Thx



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.54Å 454.40Å 619.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.98 – 3.10 49.98 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.98-3.10) 100.0 (49.98-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.06 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.221 , 0.256 0.232 , 0.262	Depositor DCC
R_{free} test set	23533 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	74.6	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 56.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	300991	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 0TD, OMG, MA6, 2MG, 2MU, 7MG, PSU, UR3, 4OC, 4SU, 5MC, 2MA, M2G, ZN, MG, 5MU

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	0.29	0/35961	0.43	0/56125
1	FB	0.31	0/35961	0.44	0/56125
2	B	0.46	0/69214	0.55	1/108048 (0.0%)
2	GB	0.38	0/69214	0.51	1/108048 (0.0%)
3	C	0.33	0/2881	0.44	0/4494
3	HB	0.27	0/2881	0.40	0/4494
4	D	0.25	1/1744 (0.1%)	0.35	0/2719
4	IA	0.35	1/1744 (0.1%)	0.45	0/2719
4	IB	0.26	1/1744 (0.1%)	0.35	0/2719
4	NC	0.33	0/1744	0.43	0/2719
5	E	0.78	0/2195	1.01	7/2955 (0.2%)
5	JB	0.68	0/2195	0.98	8/2955 (0.3%)
6	F	0.67	0/1596	0.97	2/2153 (0.1%)
6	KB	0.60	0/1596	0.93	2/2153 (0.1%)
7	G	0.69	0/1621	0.96	1/2194 (0.0%)
7	LB	0.59	0/1621	0.92	1/2194 (0.0%)
8	H	0.48	0/1496	0.86	2/2013 (0.1%)
8	MB	0.42	0/1496	0.87	3/2013 (0.1%)
9	I	0.58	0/1356	0.94	3/1834 (0.2%)
9	NB	0.42	0/1356	0.89	2/1834 (0.1%)
10	J	0.54	0/1152	0.91	4/1559 (0.3%)
10	OB	0.50	0/1152	0.89	1/1559 (0.1%)
11	K	0.64	0/1148	0.92	3/1547 (0.2%)
11	PB	0.52	0/1148	0.87	2/1547 (0.1%)
12	L	0.64	0/942	0.92	2/1268 (0.2%)
12	QB	0.59	0/942	0.90	2/1268 (0.2%)
13	M	0.63	0/1162	0.91	0/1544
13	RB	0.56	0/1162	0.88	0/1544
14	N	0.71	0/1142	0.92	0/1525
14	SB	0.59	0/1142	0.89	0/1525
15	O	0.63	0/982	0.86	1/1312 (0.1%)
15	TB	0.55	0/982	0.84	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	P	0.48	0/887	0.83	0/1180
16	UB	0.42	0/887	0.82	0/1180
17	Q	0.58	0/1157	0.85	0/1544
17	VB	0.52	0/1157	0.85	0/1544
18	R	0.71	0/982	0.89	1/1306 (0.1%)
18	WB	0.59	0/982	0.84	1/1306 (0.1%)
19	S	0.64	0/790	0.93	0/1057
19	XB	0.53	0/790	0.88	0/1057
20	T	0.74	0/901	0.90	0/1209
20	YB	0.65	0/901	0.87	0/1209
21	U	0.68	0/764	0.90	2/1025 (0.2%)
21	ZB	0.58	0/764	0.88	2/1025 (0.2%)
22	AC	0.56	0/827	0.87	0/1103
22	V	0.65	0/827	0.89	0/1103
23	BC	0.48	0/1527	0.88	2/2073 (0.1%)
23	W	0.54	0/1527	0.89	3/2073 (0.1%)
24	CC	0.59	0/671	0.93	1/892 (0.1%)
24	X	0.71	0/671	0.94	0/892
25	DC	0.59	0/768	0.91	1/1021 (0.1%)
25	Y	0.69	0/768	0.96	0/1021
26	EC	0.55	0/594	0.78	0/785
26	Z	0.72	0/594	0.83	1/785 (0.1%)
27	AA	0.70	0/482	0.96	2/646 (0.3%)
27	FC	0.56	0/482	0.96	3/646 (0.5%)
28	BA	0.49	0/565	0.80	0/761
28	GC	0.51	0/565	0.80	0/761
29	CA	0.68	0/474	0.93	2/640 (0.3%)
29	HC	0.59	0/474	0.85	0/640
30	DA	0.59	0/460	0.88	2/613 (0.3%)
30	IC	0.54	0/460	0.86	2/613 (0.3%)
31	EA	0.93	0/426	0.92	0/561
31	JC	0.72	0/426	0.86	0/561
32	FA	0.74	0/525	0.88	1/691 (0.1%)
32	KC	0.61	0/525	0.80	0/691
33	GA	0.67	0/310	1.01	1/407 (0.2%)
33	LC	0.51	0/310	0.95	1/407 (0.2%)
34	HA	0.44	0/225	0.46	0/348
34	MC	0.41	0/225	0.48	0/348
35	JA	0.52	0/2037	0.90	9/2746 (0.3%)
35	OC	0.49	0/2037	0.89	7/2746 (0.3%)
36	KA	0.44	0/1935	0.86	5/2609 (0.2%)
36	PC	0.46	0/1935	0.86	4/2609 (0.2%)
37	LA	0.42	0/1636	0.81	0/2205

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
37	QC	0.43	0/1636	0.81	0/2205
38	MA	0.50	0/1733	0.87	4/2318 (0.2%)
38	RC	0.57	0/1733	0.89	3/2318 (0.1%)
39	NA	0.51	0/1171	0.91	3/1576 (0.2%)
39	SC	0.56	0/1171	0.91	3/1576 (0.2%)
40	OA	0.55	0/856	0.84	0/1154
40	TC	0.49	0/856	0.83	0/1154
41	PA	0.43	0/1276	0.78	0/1709
41	UC	0.41	0/1276	0.79	0/1709
42	QA	0.48	0/1136	0.88	2/1527 (0.1%)
42	VC	0.48	0/1136	0.88	1/1527 (0.1%)
43	RA	0.41	0/1029	0.79	0/1378
43	WC	0.41	0/1029	0.80	0/1378
44	SA	0.44	0/807	0.81	2/1085 (0.2%)
44	XC	0.44	0/807	0.81	2/1085 (0.2%)
45	TA	0.53	0/879	0.89	2/1187 (0.2%)
45	YC	0.53	0/879	0.87	2/1187 (0.2%)
46	UA	0.53	0/963	0.87	0/1287
46	ZC	0.53	0/963	0.85	0/1287
47	AD	0.39	0/943	0.90	3/1265 (0.2%)
47	VA	0.40	0/943	0.91	3/1265 (0.2%)
48	BD	0.39	0/501	0.83	0/664
48	WA	0.37	0/501	0.84	2/664 (0.3%)
49	CD	0.52	0/745	0.83	2/992 (0.2%)
49	XA	0.52	0/745	0.82	2/992 (0.2%)
50	DD	0.51	0/716	0.76	0/963
50	YA	0.44	0/716	0.75	0/963
51	ED	0.51	0/836	0.76	0/1117
51	ZA	0.49	0/836	0.77	0/1117
52	AB	0.53	0/579	0.85	0/768
52	FD	0.53	0/579	0.85	0/768
53	BB	0.37	0/680	0.88	3/915 (0.3%)
53	GD	0.36	0/680	0.88	1/915 (0.1%)
54	CB	0.44	0/764	0.84	0/1006
54	HD	0.49	0/764	0.84	0/1006
55	DB	0.40	0/212	0.84	0/277
55	ID	0.38	0/212	0.80	0/277
All	All	0.44	3/322210 (0.0%)	0.62	141/481238 (0.0%)

All (3) bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	IB	8	4SU	O3'-P	5.87	1.62	1.56
4	D	8	4SU	O3'-P	5.36	1.61	1.56
4	IA	8	4SU	O3'-P	5.01	1.61	1.56

All (141) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1992	G	C2'-C3'-O3'	7.78	121.17	109.50
2	GB	1992	G	C2'-C3'-O3'	7.71	121.07	109.50
47	VA	112	GLY	CA-C-N	7.69	127.74	119.89
47	VA	112	GLY	C-N-CA	7.69	127.74	119.89
10	OB	136	VAL	N-CA-C	7.68	114.55	107.56
47	AD	112	GLY	CA-C-N	7.47	127.51	119.89
47	AD	112	GLY	C-N-CA	7.47	127.51	119.89
5	JB	244	ARG	CA-C-N	-7.36	112.80	120.38
5	JB	244	ARG	C-N-CA	-7.36	112.80	120.38
38	MA	180	GLY	N-CA-C	-7.08	104.23	112.73
5	E	120	GLY	CA-C-N	7.07	128.68	119.84
5	E	120	GLY	C-N-CA	7.07	128.68	119.84
5	E	244	ARG	CA-C-N	-6.76	113.42	120.38
5	E	244	ARG	C-N-CA	-6.76	113.42	120.38
18	R	9	VAL	N-CA-C	6.70	116.85	110.42
36	PC	166	ASP	CA-C-N	6.68	126.27	119.19
36	PC	166	ASP	C-N-CA	6.68	126.27	119.19
6	F	125	GLY	CA-C-N	6.65	126.88	119.90
6	F	125	GLY	C-N-CA	6.65	126.88	119.90
36	KA	166	ASP	CA-C-N	6.57	126.15	119.19
36	KA	166	ASP	C-N-CA	6.57	126.15	119.19
10	J	136	VAL	N-CA-C	6.38	113.36	107.56
5	JB	120	GLY	CA-C-N	6.37	127.81	119.84
5	JB	120	GLY	C-N-CA	6.37	127.81	119.84
5	JB	245	PRO	CA-C-N	6.30	127.71	119.84
5	JB	245	PRO	C-N-CA	6.30	127.71	119.84
9	NB	28	GLY	CA-C-N	6.28	125.50	118.97
9	NB	28	GLY	C-N-CA	6.28	125.50	118.97
11	K	110	GLY	CA-C-N	6.21	127.61	119.84
11	K	110	GLY	C-N-CA	6.21	127.61	119.84
6	KB	125	GLY	CA-C-N	6.21	126.42	119.90
6	KB	125	GLY	C-N-CA	6.21	126.42	119.90
11	PB	110	GLY	CA-C-N	6.14	127.51	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	PB	110	GLY	C-N-CA	6.14	127.51	119.84
47	VA	67	GLU	CB-CA-C	-6.11	109.54	116.63
7	G	9	ILE	N-CA-C	6.11	113.93	107.76
9	I	28	GLY	CA-C-N	6.08	125.30	118.97
9	I	28	GLY	C-N-CA	6.08	125.30	118.97
30	IC	30	THR	CA-C-N	6.05	125.75	119.64
30	IC	30	THR	C-N-CA	6.05	125.75	119.64
47	AD	67	GLU	CB-CA-C	-6.04	109.62	116.63
8	MB	44	GLY	N-CA-C	-6.03	107.38	115.21
5	E	245	PRO	CA-C-N	6.00	127.34	119.84
5	E	245	PRO	C-N-CA	6.00	127.34	119.84
36	PC	11	LEU	N-CA-C	-5.98	105.24	112.54
27	AA	11	SER	CA-C-N	5.97	126.08	119.87
27	AA	11	SER	C-N-CA	5.97	126.08	119.87
39	NA	69	VAL	CA-C-N	5.97	127.30	119.84
39	NA	69	VAL	C-N-CA	5.97	127.30	119.84
39	SC	69	VAL	CA-C-N	5.91	127.22	119.84
39	SC	69	VAL	C-N-CA	5.91	127.22	119.84
9	I	9	ILE	N-CA-C	5.86	112.89	107.56
33	LC	13	LYS	N-CA-C	-5.84	106.11	113.18
35	OC	158	GLY	CA-C-N	5.83	132.19	121.70
35	OC	158	GLY	C-N-CA	5.83	132.19	121.70
35	JA	158	GLY	CA-C-N	5.82	132.18	121.70
35	JA	158	GLY	C-N-CA	5.82	132.18	121.70
38	RC	180	GLY	N-CA-C	-5.79	105.78	112.73
36	KA	11	LEU	N-CA-C	-5.69	105.60	112.54
18	WB	9	VAL	N-CA-C	5.64	115.83	110.42
10	J	124	GLY	N-CA-C	5.60	119.17	110.88
8	H	44	GLY	N-CA-C	-5.59	107.94	115.21
45	TA	38	ASN	CA-C-N	5.59	125.50	119.85
45	TA	38	ASN	C-N-CA	5.59	125.50	119.85
21	U	31	HIS	CA-C-N	5.58	125.94	119.47
21	U	31	HIS	C-N-CA	5.58	125.94	119.47
49	CD	74	ASP	CA-C-N	5.53	125.89	119.47
49	CD	74	ASP	C-N-CA	5.53	125.89	119.47
35	JA	103	LYS	N-CA-C	5.49	117.93	110.35
36	KA	193	ASP	CA-C-N	5.49	125.10	119.56
36	KA	193	ASP	C-N-CA	5.49	125.10	119.56
53	BB	58	VAL	N-CA-C	5.48	113.30	107.76
30	DA	30	THR	CA-C-N	5.47	125.17	119.64
30	DA	30	THR	C-N-CA	5.47	125.17	119.64
27	FC	11	SER	CA-C-N	5.46	125.55	119.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	FC	11	SER	C-N-CA	5.46	125.55	119.87
35	OC	104	ASP	CA-C-N	-5.46	113.02	119.84
35	OC	104	ASP	C-N-CA	-5.46	113.02	119.84
38	RC	9	CYS	N-CA-C	-5.45	106.58	113.18
5	E	237	GLU	N-CA-C	-5.45	101.10	109.76
23	W	107	THR	CA-C-N	5.42	125.42	119.89
23	W	107	THR	C-N-CA	5.42	125.42	119.89
35	OC	108	GLU	N-CA-C	-5.39	105.40	112.41
38	RC	5	ILE	N-CA-C	5.39	120.55	109.34
38	MA	5	ILE	N-CA-C	5.36	120.49	109.34
42	QA	4	ASP	CA-C-N	5.33	124.84	119.19
42	QA	4	ASP	C-N-CA	5.33	124.84	119.19
12	L	118	ALA	CA-C-N	5.33	124.84	119.19
12	L	118	ALA	C-N-CA	5.33	124.84	119.19
35	JA	108	GLU	N-CA-C	-5.31	105.50	112.41
21	ZB	31	HIS	CA-C-N	5.30	125.62	119.47
21	ZB	31	HIS	C-N-CA	5.30	125.62	119.47
35	JA	104	ASP	CA-C-N	-5.28	113.24	119.84
35	JA	104	ASP	C-N-CA	-5.28	113.24	119.84
35	JA	160	LYS	N-CA-C	-5.27	106.85	113.28
33	GA	13	LYS	N-CA-C	-5.27	106.69	113.23
35	OC	217	ILE	N-CA-C	5.26	116.09	111.56
26	Z	66	GLU	N-CA-C	-5.26	105.72	111.82
38	MA	171	GLY	CA-C-N	5.25	125.56	119.47
38	MA	171	GLY	C-N-CA	5.25	125.56	119.47
42	VC	79	VAL	N-CA-C	-5.23	107.31	111.81
48	WA	53	LEU	CA-C-N	5.23	125.48	119.83
48	WA	53	LEU	C-N-CA	5.23	125.48	119.83
12	QB	118	ALA	CA-C-N	5.23	124.73	119.19
12	QB	118	ALA	C-N-CA	5.23	124.73	119.19
23	BC	107	THR	CA-C-N	5.23	125.22	119.89
23	BC	107	THR	C-N-CA	5.23	125.22	119.89
49	XA	74	ASP	CA-C-N	5.21	125.51	119.47
49	XA	74	ASP	C-N-CA	5.21	125.51	119.47
7	LB	9	ILE	N-CA-C	5.19	113.01	107.76
44	XC	52	GLY	CA-C-N	5.19	125.27	119.87
44	XC	52	GLY	C-N-CA	5.19	125.27	119.87
44	SA	52	GLY	CA-C-N	5.19	125.27	119.87
44	SA	52	GLY	C-N-CA	5.19	125.27	119.87
24	CC	38	VAL	N-CA-C	5.19	115.38	108.27
39	NA	114	GLY	N-CA-C	-5.17	108.09	115.64
53	BB	58	VAL	CA-C-N	5.14	124.90	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	BB	58	VAL	C-N-CA	5.14	124.90	119.76
8	H	45	GLU	N-CA-C	-5.13	106.85	113.01
27	FC	56	VAL	N-CA-C	5.13	115.24	107.75
10	J	110	ASP	CA-C-N	5.13	126.25	119.84
10	J	110	ASP	C-N-CA	5.13	126.25	119.84
35	JA	217	ILE	N-CA-C	5.12	115.96	111.56
11	K	71	ILE	N-CA-C	5.10	115.32	107.77
32	FA	64	TYR	N-CA-C	-5.10	106.65	112.92
36	PC	19	HIS	N-CA-C	5.09	116.03	108.60
35	JA	356	LEU	N-CA-C	-5.08	106.91	114.64
53	GD	36	ARG	N-CA-C	-5.07	107.14	113.38
8	MB	89	GLY	N-CA-C	5.07	117.88	110.38
35	OC	103	LYS	N-CA-C	5.06	117.33	110.35
15	O	38	VAL	CB-CA-C	-5.06	107.37	114.00
39	SC	114	GLY	N-CA-C	-5.06	108.25	115.64
29	CA	40	LYS	CA-C-N	-5.04	115.19	120.38
29	CA	40	LYS	C-N-CA	-5.04	115.19	120.38
5	JB	85	ASP	CA-C-N	5.04	124.65	119.56
5	JB	85	ASP	C-N-CA	5.04	124.65	119.56
45	YC	38	ASN	CA-C-N	5.04	124.94	119.85
45	YC	38	ASN	C-N-CA	5.04	124.94	119.85
23	W	158	PRO	O-C-N	5.04	123.63	121.31
8	MB	53	LEU	N-CA-C	-5.02	107.15	113.28
25	DC	67	ILE	CB-CA-C	-5.02	108.93	113.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32394	0	16367	379	0
1	FB	32394	0	16366	357	0
2	B	62031	0	31273	586	0
2	GB	62031	0	31269	594	0
3	C	2576	0	1305	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	HB	2576	0	1305	18	0
4	D	1642	0	841	29	0
4	IA	1642	0	841	23	0
4	IB	1642	0	840	29	0
4	NC	1642	0	841	15	0
5	E	2145	0	2234	44	0
5	JB	2145	0	2234	52	0
6	F	1563	0	1629	36	0
6	KB	1563	0	1629	34	0
7	G	1586	0	1632	46	0
7	LB	1586	0	1632	41	0
8	H	1471	0	1526	53	0
8	MB	1471	0	1526	56	0
9	I	1330	0	1407	44	0
9	NB	1330	0	1407	42	0
10	J	1137	0	1225	47	0
10	OB	1137	0	1225	43	0
11	K	1121	0	1195	19	0
11	PB	1121	0	1195	24	0
12	L	932	0	994	23	0
12	QB	932	0	993	19	0
13	M	1145	0	1228	54	0
13	RB	1145	0	1228	44	0
14	N	1121	0	1179	40	0
14	SB	1121	0	1179	38	0
15	O	968	0	1032	28	0
15	TB	968	0	1033	29	0
16	P	877	0	938	31	0
16	UB	877	0	938	28	0
17	Q	1143	0	1211	42	0
17	VB	1143	0	1211	44	0
18	R	964	0	1022	20	0
18	WB	964	0	1022	23	0
19	S	779	0	852	13	0
19	XB	779	0	852	14	0
20	T	890	0	951	23	0
20	YB	890	0	951	21	0
21	U	750	0	814	10	0
21	ZB	750	0	814	11	0
22	AC	814	0	904	20	0
22	V	814	0	904	24	0
23	BC	1495	0	1521	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	W	1495	0	1521	36	0
24	CC	662	0	688	20	0
24	X	662	0	688	19	0
25	DC	761	0	837	23	0
25	Y	761	0	837	25	0
26	EC	592	0	654	16	0
26	Z	592	0	654	16	0
27	AA	477	0	529	14	0
27	FC	477	0	529	14	0
28	BA	552	0	537	22	0
28	GC	552	0	537	18	0
29	CA	460	0	480	10	0
29	HC	460	0	480	11	0
30	DA	453	0	473	13	0
30	IC	453	0	473	13	0
31	EA	418	0	467	15	0
31	JC	418	0	467	13	0
32	FA	517	0	582	16	0
32	KC	517	0	582	11	0
33	GA	307	0	335	6	0
33	LC	307	0	335	6	0
34	HA	220	0	108	7	0
34	MC	220	0	108	7	0
35	JA	2005	0	1964	61	0
35	OC	2005	0	1964	58	0
36	KA	1900	0	1951	70	0
36	PC	1900	0	1951	74	0
37	LA	1612	0	1677	50	0
37	QC	1612	0	1676	52	0
38	MA	1703	0	1767	73	0
38	RC	1703	0	1766	68	0
39	NA	1155	0	1213	34	0
39	SC	1155	0	1213	30	0
40	OA	843	0	857	35	0
40	TC	843	0	857	32	0
41	PA	1257	0	1296	30	0
41	UC	1257	0	1296	30	0
42	QA	1116	0	1177	53	0
42	VC	1116	0	1177	55	0
43	RA	1011	0	1043	46	0
43	WC	1011	0	1043	47	0
44	SA	794	0	840	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	XC	794	0	840	35	0
45	TA	864	0	881	32	0
45	YC	864	0	881	35	0
46	UA	958	0	1047	31	0
46	ZC	958	0	1047	31	0
47	AD	933	0	992	43	0
47	VA	933	0	992	47	0
48	BD	492	0	533	21	0
48	WA	492	0	533	20	0
49	CD	734	0	771	23	0
49	XA	734	0	771	24	0
50	DD	700	0	720	19	0
50	YA	700	0	720	14	0
51	ED	823	0	893	18	0
51	ZA	823	0	893	21	0
52	AB	574	0	644	17	0
52	FD	574	0	644	19	0
53	BB	665	0	686	19	0
53	GD	665	0	686	20	0
54	CB	762	0	859	34	0
54	HD	762	0	859	35	0
55	DB	208	0	221	5	0
55	ID	208	0	221	5	0
56	A	287	0	0	0	0
56	AA	4	0	0	0	0
56	AD	1	0	0	0	0
56	B	944	0	0	0	0
56	BA	3	0	0	0	0
56	BB	1	0	0	0	0
56	BC	9	0	0	0	0
56	C	44	0	0	0	0
56	CA	3	0	0	0	0
56	CB	1	0	0	0	0
56	CC	2	0	0	0	0
56	CD	3	0	0	0	0
56	D	2	0	0	0	0
56	DA	3	0	0	0	0
56	DB	1	0	0	0	0
56	DC	3	0	0	0	0
56	DD	1	0	0	0	0
56	E	10	0	0	0	0
56	EA	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	EC	4	0	0	0	0
56	ED	2	0	0	0	0
56	F	15	0	0	0	0
56	FA	4	0	0	0	0
56	FB	349	0	0	0	0
56	FC	1	0	0	0	0
56	G	11	0	0	0	0
56	GA	1	0	0	0	0
56	GB	812	0	0	0	0
56	GC	2	0	0	0	0
56	GD	1	0	0	0	0
56	H	3	0	0	0	0
56	HA	2	0	0	0	0
56	HB	32	0	0	0	0
56	HC	2	0	0	0	0
56	HD	1	0	0	0	0
56	I	7	0	0	0	0
56	IA	21	0	0	0	0
56	IB	5	0	0	0	0
56	J	3	0	0	0	0
56	JA	13	0	0	0	0
56	JB	13	0	0	0	0
56	K	9	0	0	0	0
56	KA	4	0	0	0	0
56	KB	4	0	0	0	0
56	KC	5	0	0	0	0
56	L	5	0	0	0	0
56	LA	2	0	0	0	0
56	LB	5	0	0	0	0
56	M	8	0	0	0	0
56	MA	5	0	0	0	0
56	MB	7	0	0	0	0
56	MC	1	0	0	0	0
56	N	6	0	0	0	0
56	NA	3	0	0	0	0
56	NB	3	0	0	0	0
56	NC	14	0	0	0	0
56	O	3	0	0	0	0
56	OA	4	0	0	0	0
56	OB	2	0	0	0	0
56	OC	7	0	0	0	0
56	P	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	PA	3	0	0	0	0
56	PB	4	0	0	0	0
56	PC	5	0	0	0	0
56	Q	4	0	0	0	0
56	QA	2	0	0	0	0
56	QB	6	0	0	0	0
56	QC	4	0	0	0	0
56	R	2	0	0	0	0
56	RA	4	0	0	0	0
56	RB	6	0	0	0	0
56	RC	11	0	0	0	0
56	S	8	0	0	0	0
56	SA	3	0	0	0	0
56	SB	4	0	0	0	0
56	SC	7	0	0	0	0
56	T	5	0	0	0	0
56	TA	1	0	0	0	0
56	TB	4	0	0	0	0
56	TC	1	0	0	0	0
56	U	2	0	0	0	0
56	UA	3	0	0	0	0
56	UB	1	0	0	0	0
56	UC	2	0	0	0	0
56	VA	3	0	0	0	0
56	VB	8	0	0	0	0
56	VC	2	0	0	0	0
56	W	8	0	0	0	0
56	WA	1	0	0	0	0
56	WB	3	0	0	0	0
56	WC	2	0	0	0	0
56	X	8	0	0	0	0
56	XA	3	0	0	0	0
56	XB	4	0	0	0	0
56	XC	2	0	0	0	0
56	Y	5	0	0	0	0
56	YA	1	0	0	0	0
56	YB	7	0	0	0	0
56	YC	6	0	0	0	0
56	Z	3	0	0	0	0
56	ZA	3	0	0	0	0
56	ZB	1	0	0	0	0
56	ZC	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	AC	1	0	0	0	0
57	BA	1	0	0	0	0
57	CA	1	0	0	0	0
57	DA	1	0	0	0	0
57	GA	1	0	0	0	0
57	GC	1	0	0	0	0
57	HC	1	0	0	0	0
57	IC	1	0	0	0	0
57	LC	1	0	0	0	0
57	V	1	0	0	0	0
All	All	300991	0	203678	4460	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (4460) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:RC:9:CYS:SG	38:RC:18:LYS:NZ	2.06	1.28
38:MA:9:CYS:SG	38:MA:18:LYS:NZ	2.09	1.26
38:MA:18:LYS:NZ	38:MA:26:CYS:SG	2.12	1.20
38:RC:18:LYS:NZ	38:RC:26:CYS:SG	2.15	1.20
42:VC:50:ARG:HB3	42:VC:50:ARG:HH11	1.21	1.03
42:QA:50:ARG:HB3	42:QA:50:ARG:HH11	1.22	1.02
2:GB:1019:U:HO2'	2:GB:1021:A:H2	1.02	1.01
2:B:84:A:OP2	22:V:8:LYS:NZ	1.95	1.00
8:MB:98:ARG:HH11	8:MB:98:ARG:HG3	1.26	0.99
1:A:1309:G:OP2	47:VA:99:ARG:NH1	1.97	0.97
15:O:105:ARG:HG2	15:O:105:ARG:HH11	1.27	0.97
15:TB:105:ARG:HG2	15:TB:105:ARG:HH11	1.26	0.97
2:GB:2133:G:HO2'	2:GB:2157:G:H1	1.09	0.96
8:H:98:ARG:HH11	8:H:98:ARG:HG3	1.26	0.96
1:FB:176:C:OP1	54:HD:29:LYS:NZ	1.98	0.96
11:K:123:TYR:HH	11:K:130:HIS:HE2	1.07	0.95
1:FB:1309:G:OP2	47:AD:99:ARG:NH1	1.98	0.94
2:GB:84:A:OP2	22:AC:8:LYS:NZ	2.01	0.94
2:B:2298:A:H62	2:B:2318:G:H8	1.14	0.93
29:CA:16:ARG:HG2	29:CA:16:ARG:HH11	1.34	0.93
14:SB:85:LYS:HD3	24:CC:7:LEU:HD22	1.51	0.92
2:B:2133:G:HO2'	2:B:2157:G:H1	0.98	0.92
2:B:1019:U:HO2'	2:B:1021:A:H2	1.02	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:C:OP1	54:CB:29:LYS:NZ	2.03	0.91
11:PB:123:TYR:HH	11:PB:130:HIS:HE2	1.09	0.91
12:L:35:VAL:HG11	12:L:103:ALA:HB3	1.53	0.91
35:OC:153:GLU:HA	35:OC:159:TYR:H	1.35	0.91
35:JA:153:GLU:HA	35:JA:159:TYR:H	1.36	0.91
2:GB:2298:A:H62	2:GB:2318:G:H8	1.10	0.91
29:HC:16:ARG:NH1	29:HC:17:ASP:OD1	2.03	0.91
38:RC:18:LYS:NZ	38:RC:31:CYS:SG	2.43	0.91
23:W:79:ARG:HD2	23:W:80:ARG:HH11	1.36	0.90
2:GB:1798:U:H5'	5:JB:259:THR:HG22	1.51	0.90
12:QB:35:VAL:HG11	12:QB:103:ALA:HB3	1.52	0.88
16:P:3:ARG:HH11	16:P:3:ARG:HA	1.36	0.88
43:RA:55:ALA:HB1	43:RA:58:ARG:HB2	1.54	0.88
43:WC:55:ALA:HB1	43:WC:58:ARG:HB2	1.56	0.88
2:B:1359:A:H2	2:B:1372:U:H3	1.22	0.88
23:BC:79:ARG:HD2	23:BC:80:ARG:HH11	1.39	0.88
16:UB:3:ARG:HH11	16:UB:3:ARG:HA	1.36	0.87
14:N:85:LYS:HD3	24:X:7:LEU:HD22	1.58	0.86
8:MB:136:ARG:HE	8:MB:136:ARG:H	1.23	0.86
2:B:1798:U:H5'	5:E:259:THR:HG22	1.54	0.86
1:FB:1266:G:N2	1:FB:1269:A:OP2	2.09	0.86
21:U:60:ARG:NH1	31:EA:47:ARG:HH22	1.73	0.86
29:HC:16:ARG:HG2	29:HC:16:ARG:HH11	1.40	0.86
2:GB:1359:A:H2	2:GB:1372:U:H3	1.23	0.86
38:MA:18:LYS:NZ	38:MA:31:CYS:SG	2.48	0.86
44:SA:33:GLN:HG2	44:SA:75:ILE:HG22	1.58	0.86
1:A:1266:G:N2	1:A:1269:A:OP2	2.09	0.85
54:HD:100:ILE:HG12	54:HD:102:GLY:H	1.42	0.85
1:A:542:G:OP1	38:MA:10:ARG:NH2	2.09	0.85
47:VA:3:ARG:HG2	47:VA:3:ARG:HH11	1.40	0.85
2:B:2469:A:H4'	14:N:56:ARG:HG2	1.58	0.85
2:B:1530:G:H1	2:B:1541:U:H3	1.25	0.84
2:B:1216:G:OP2	18:R:12:ARG:NH2	2.10	0.84
30:DA:12:GLU:OE1	30:DA:19:ARG:NH1	2.09	0.84
30:IC:12:GLU:OE1	30:IC:19:ARG:NH1	2.11	0.84
36:KA:87:ARG:NH1	36:KA:233:SER:HB2	1.93	0.84
29:CA:16:ARG:NH1	29:CA:17:ASP:OD1	2.10	0.84
2:GB:1530:G:H1	2:GB:1541:U:H3	1.25	0.83
2:B:1761:C:H5'	2:B:1762:A:OP2	1.78	0.83
2:GB:2637:U:OP1	6:KB:82:ARG:NH1	2.11	0.83
36:PC:87:ARG:NH1	36:PC:233:SER:HB2	1.94	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:VC:69:ARG:NH1	42:VC:75:ARG:O	2.13	0.82
44:XC:33:GLN:HG2	44:XC:75:ILE:HG22	1.60	0.82
40:TC:46:ARG:HB3	40:TC:46:ARG:HH11	1.44	0.82
2:GB:2287:A:H62	2:GB:2344:U:H3	1.27	0.82
8:H:136:ARG:HE	8:H:136:ARG:H	1.24	0.82
36:PC:155:LEU:HD21	36:PC:159:PRO:HD3	1.61	0.82
39:SC:78:HIS:HD1	42:VC:104:ARG:HD2	1.45	0.82
2:B:1379:A:H4'	2:B:1380:G:OP2	1.77	0.82
8:H:170:ARG:NH1	8:H:174:GLU:OE2	2.12	0.81
42:QA:69:ARG:NH1	42:QA:75:ARG:O	2.12	0.81
36:KA:155:LEU:HD21	36:KA:159:PRO:HD3	1.60	0.81
2:GB:1761:C:H5'	2:GB:1762:A:OP2	1.79	0.81
37:QC:77:ILE:HA	37:QC:84:ILE:HB	1.62	0.81
2:GB:1216:G:OP2	18:WB:12:ARG:NH2	2.12	0.81
22:V:102:CYS:SG	22:V:103:GLY:N	2.53	0.81
2:B:847:U:O4	2:B:933:A:N6	2.14	0.80
47:AD:3:ARG:HG2	47:AD:3:ARG:HH11	1.44	0.80
2:GB:1379:A:H4'	2:GB:1380:G:OP2	1.79	0.80
8:MB:170:ARG:NH1	8:MB:174:GLU:OE2	2.12	0.80
2:GB:2319:G:H22	16:UB:3:ARG:NH1	1.80	0.80
2:GB:847:U:O4	2:GB:933:A:N6	2.13	0.80
6:F:47:VAL:HG11	6:F:86:PRO:HD2	1.65	0.79
36:PC:9:GLU:HG3	36:PC:217:ARG:NH1	1.97	0.79
41:UC:57:GLU:H	41:UC:60:LYS:HZ3	1.30	0.79
38:RC:18:LYS:HZ3	38:RC:31:CYS:HG	1.26	0.79
2:B:2287:A:H62	2:B:2344:U:H3	1.28	0.79
2:B:993:G:OP1	18:R:50:ARG:NH2	2.16	0.79
2:B:2637:U:OP1	6:F:82:ARG:NH1	2.16	0.79
36:KA:130:ARG:NH1	36:KA:134:GLU:HB3	1.98	0.79
40:OA:46:ARG:HB3	40:OA:46:ARG:HH11	1.48	0.79
7:G:119:ARG:HH11	7:G:119:ARG:HB2	1.48	0.79
1:FB:1295:G:O2'	47:AD:14:ARG:NH1	2.16	0.79
2:GB:819:A:OP2	2:GB:1187:G:N2	2.14	0.79
2:B:2319:G:H22	16:P:3:ARG:NH1	1.81	0.79
7:LB:119:ARG:HH11	7:LB:119:ARG:HB2	1.46	0.79
1:FB:706:A:H4'	45:YC:22:HIS:HD2	1.48	0.78
8:H:115:ARG:HD3	47:VA:7:VAL:HG22	1.65	0.78
37:LA:77:ILE:HA	37:LA:84:ILE:HB	1.63	0.78
2:GB:1264:G:OP1	29:HC:19:ARG:NH2	2.16	0.78
40:TC:46:ARG:HB3	40:TC:46:ARG:NH1	1.99	0.78
9:I:137:ASP:HB3	9:I:140:LYS:HE2	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:KB:47:VAL:HG11	6:KB:86:PRO:HD2	1.65	0.78
1:FB:656:C:H4'	49:CD:62:GLN:HE22	1.47	0.78
2:GB:1204:A:H2	2:GB:1241:A:H62	1.32	0.78
41:PA:57:GLU:H	41:PA:60:LYS:HZ3	1.32	0.78
4:IA:76:A:H3'	35:JA:234:GLY:HA3	1.66	0.77
1:A:1295:G:O2'	47:VA:14:ARG:NH1	2.17	0.77
36:KA:9:GLU:HG3	36:KA:217:ARG:NH1	1.98	0.77
51:ZA:66:SER:O	51:ZA:70:ARG:NH1	2.17	0.77
36:PC:9:GLU:HG3	36:PC:217:ARG:HH12	1.50	0.77
2:GB:320:A:OP2	7:LB:137:LYS:HE2	1.84	0.77
2:B:1262:A:N3	29:CA:10:LYS:NZ	2.33	0.77
54:CB:100:ILE:HG12	54:CB:102:GLY:H	1.47	0.77
2:GB:2469:A:H4'	14:SB:56:ARG:HG2	1.65	0.77
4:IB:30:G:H21	41:UC:144:MET:HE1	1.49	0.77
39:NA:78:HIS:HD1	42:QA:104:ARG:HD2	1.49	0.77
42:QA:10:LEU:HD22	42:QA:83:ILE:HD11	1.65	0.77
43:RA:117:HIS:HB2	43:RA:121:ARG:HG2	1.67	0.77
21:ZB:60:ARG:NH1	31:JC:47:ARG:HH22	1.83	0.77
42:VC:50:ARG:HB3	42:VC:50:ARG:NH1	1.98	0.77
9:I:56:SER:OG	9:I:57:ASP:N	2.17	0.77
2:GB:1262:A:N3	29:HC:10:LYS:NZ	2.33	0.77
36:PC:130:ARG:NH1	36:PC:134:GLU:HB3	1.99	0.77
2:B:1264:G:OP1	29:CA:19:ARG:NH2	2.16	0.76
5:E:71:ASP:N	5:E:71:ASP:OD2	2.16	0.76
16:P:15:ARG:NH1	16:P:25:ARG:HH21	1.83	0.76
42:QA:50:ARG:HB3	42:QA:50:ARG:NH1	1.97	0.76
2:B:1434:A:H61	2:B:1558:A:H62	1.30	0.76
38:RC:7:PRO:HB2	38:RC:10:ARG:HD2	1.66	0.76
2:B:648:G:H21	32:FA:46:ARG:HH12	1.34	0.76
38:MA:7:PRO:HB2	38:MA:10:ARG:HD2	1.68	0.76
2:B:2792:G:H1	2:B:2805:G:H1'	1.49	0.76
8:MB:5:LEU:HD22	8:MB:101:ILE:HD11	1.67	0.76
8:H:98:ARG:HH11	8:H:98:ARG:CG	1.98	0.75
2:GB:1434:A:H61	2:GB:1558:A:H62	1.32	0.75
8:H:5:LEU:HD22	8:H:101:ILE:HD11	1.68	0.75
35:OC:233:GLY:HA3	35:OC:237:VAL:HB	1.69	0.75
4:NC:19:G:H4'	4:NC:20:U:OP2	1.84	0.75
2:GB:2792:G:H1	2:GB:2805:G:H1'	1.51	0.75
46:ZC:39:VAL:HG12	46:ZC:57:LYS:HB2	1.68	0.75
1:A:656:C:H4'	49:XA:62:GLN:HE22	1.50	0.75
47:AD:3:ARG:HH12	47:AD:9:ILE:HG12	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:MB:98:ARG:HH11	8:MB:98:ARG:CG	1.99	0.75
4:IA:19:G:H4'	4:IA:20:U:OP2	1.86	0.75
42:VC:10:LEU:HD22	42:VC:83:ILE:HD11	1.67	0.75
38:RC:127:THR:HA	38:RC:132:ARG:HA	1.69	0.74
5:JB:71:ASP:OD2	5:JB:71:ASP:N	2.19	0.74
49:CD:18:PHE:HB2	49:CD:19:PRO:HD2	1.69	0.74
2:GB:797:C:OP2	7:LB:62:ARG:HG3	1.86	0.74
15:O:12:ARG:HH11	15:O:12:ARG:HG3	1.53	0.74
36:KA:9:GLU:HG3	36:KA:217:ARG:HH12	1.51	0.74
5:E:112:GLN:HB2	5:E:115:GLN:HB3	1.70	0.74
16:P:3:ARG:HA	16:P:3:ARG:NH1	2.03	0.74
16:UB:15:ARG:NH1	16:UB:25:ARG:HH21	1.86	0.74
15:TB:105:ARG:HG2	15:TB:105:ARG:NH1	2.01	0.73
5:E:35:LYS:HD3	5:E:64:ILE:HD11	1.69	0.73
7:G:185:ASP:HA	7:G:188:ARG:HD2	1.69	0.73
23:W:93:ASP:HB2	23:W:131:ARG:HH22	1.54	0.73
2:B:1060:U:O2'	2:B:1061:U:OP2	2.06	0.73
38:RC:173:TRP:CD1	38:RC:173:TRP:H	2.05	0.73
38:MA:127:THR:HA	38:MA:132:ARG:HA	1.70	0.73
46:UA:33:ARG:HE	46:UA:62:SER:HB3	1.52	0.73
53:GD:22:LEU:HD21	53:GD:29:ARG:HB2	1.71	0.73
2:GB:1055:G:N2	2:GB:1104:C:O2	2.22	0.73
9:NB:56:SER:OG	9:NB:57:ASP:N	2.22	0.73
47:AD:54:VAL:HA	47:AD:57:ARG:NH1	2.04	0.73
2:B:2210:G:H3'	2:B:2211:G:C8	2.24	0.73
40:OA:46:ARG:HB3	40:OA:46:ARG:NH1	2.03	0.73
49:XA:18:PHE:HB2	49:XA:19:PRO:HD2	1.71	0.73
35:OC:142:ARG:NH2	35:OC:174:ARG:HH11	1.87	0.73
43:WC:117:HIS:HB2	43:WC:121:ARG:HG2	1.69	0.73
53:BB:36:ARG:NH2	53:BB:75:ALA:O	2.22	0.73
1:FB:1024:G:N7	1:FB:1025:U:O2'	2.22	0.73
47:VA:13:LYS:HA	47:VA:44:ARG:HH11	1.53	0.73
2:B:797:C:OP2	7:G:62:ARG:HG3	1.89	0.72
2:B:1204:A:H2	2:B:1241:A:H62	1.35	0.72
4:IB:50:U:H3	4:IB:64:G:H1	1.36	0.72
50:DD:22:THR:HA	50:DD:33:ILE:HG12	1.71	0.72
50:YA:22:THR:HA	50:YA:33:ILE:HG12	1.72	0.72
53:BB:22:LEU:HD21	53:BB:29:ARG:HB2	1.70	0.72
2:GB:2138:C:N3	2:GB:2153:G:N2	2.34	0.72
22:AC:102:CYS:SG	22:AC:103:GLY:N	2.62	0.72
2:B:363(F):U:H3'	2:B:363(G):A:H8	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:VB:100:TYR:HB3	17:VB:103:ARG:HH11	1.55	0.72
46:UA:39:VAL:HG12	46:UA:57:LYS:HB2	1.70	0.72
15:TB:13:HIS:CD2	15:TB:16:HIS:H	2.07	0.72
47:VA:3:ARG:HH12	47:VA:9:ILE:HG12	1.53	0.72
47:VA:54:VAL:HA	47:VA:57:ARG:NH1	2.05	0.72
1:FB:1356:G:H2'	1:FB:1357:A:C8	2.24	0.72
1:A:1356:G:H2'	1:A:1357:A:C8	2.25	0.72
17:VB:74:ARG:HG2	17:VB:74:ARG:HH11	1.53	0.72
2:B:2138:C:N3	2:B:2153:G:N2	2.33	0.72
2:GB:2210:G:H3'	2:GB:2211:G:C8	2.24	0.72
35:OC:188:PRO:HG2	35:OC:191:GLU:HB2	1.71	0.72
9:I:130:ARG:HH12	9:I:132:ARG:HH21	1.35	0.72
35:JA:233:GLY:HA3	35:JA:237:VAL:HB	1.72	0.71
1:FB:1453:G:H4'	1:FB:1454:G:OP2	1.90	0.71
6:KB:128:SER:OG	6:KB:129:HIS:N	2.20	0.71
35:OC:107:ASP:HB3	35:OC:109:ARG:HG2	1.72	0.71
15:TB:12:ARG:HH11	15:TB:12:ARG:HG3	1.55	0.71
17:VB:129:ARG:HA	17:VB:132:LYS:NZ	2.04	0.71
16:UB:3:ARG:HA	16:UB:3:ARG:NH1	2.04	0.71
23:BC:93:ASP:HB2	23:BC:131:ARG:HH22	1.55	0.71
47:VA:3:ARG:HH11	47:VA:3:ARG:CG	2.04	0.71
2:B:547:A:H3'	2:B:548:A:C8	2.25	0.71
2:B:1055:G:N2	2:B:1104:C:O2	2.24	0.71
17:Q:129:ARG:HA	17:Q:132:LYS:NZ	2.04	0.71
2:GB:547:A:H3'	2:GB:548:A:C8	2.25	0.71
4:D:50:U:H3	4:D:64:G:H1	1.36	0.71
35:JA:188:PRO:HG2	35:JA:191:GLU:HB2	1.72	0.71
45:YC:79:SER:HA	45:YC:104:GLN:HB3	1.73	0.71
6:F:61:ARG:HG2	6:F:61:ARG:HH11	1.56	0.71
37:LA:139:GLN:HG3	37:LA:140:ARG:NH1	2.05	0.71
47:AD:13:LYS:HA	47:AD:44:ARG:HH11	1.56	0.71
2:B:1815:A:P	5:E:54:ARG:HH22	2.14	0.70
45:TA:79:SER:HA	45:TA:104:GLN:HB3	1.73	0.70
2:GB:993:G:OP1	18:WB:50:ARG:NH2	2.24	0.70
2:GB:1092:C:O2	2:GB:1099:G:N2	2.24	0.70
53:BB:11:VAL:HG23	53:BB:38:SER:HB2	1.73	0.70
2:GB:1761:C:H3'	2:GB:1762:A:H5''	1.72	0.70
36:PC:74:LYS:NZ	36:PC:166:ASP:HB2	2.07	0.70
23:W:79:ARG:HD2	23:W:80:ARG:NH1	2.07	0.70
36:KA:74:LYS:NZ	36:KA:166:ASP:HB2	2.07	0.70
38:MA:173:TRP:CD1	38:MA:173:TRP:H	2.08	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:JA:107:ASP:HB3	35:JA:109:ARG:HG2	1.73	0.70
1:FB:1381:U:H1'	41:UC:79:ARG:HG2	1.72	0.70
5:JB:112:GLN:HB2	5:JB:115:GLN:HB3	1.72	0.70
51:ED:66:SER:O	51:ED:70:ARG:NH1	2.24	0.70
38:MA:96:LEU:HG	38:MA:139:ARG:HH12	1.57	0.70
6:KB:61:ARG:HH11	6:KB:61:ARG:HG2	1.57	0.70
9:NB:137:ASP:HB3	9:NB:140:LYS:HE2	1.73	0.70
15:O:105:ARG:HG2	15:O:105:ARG:NH1	2.02	0.69
41:PA:57:GLU:N	41:PA:60:LYS:HZ3	1.89	0.69
37:QC:139:GLN:HG3	37:QC:140:ARG:NH1	2.07	0.69
17:Q:100:TYR:HB3	17:Q:103:ARG:HH11	1.56	0.69
38:MA:18:LYS:HD3	38:MA:31:CYS:SG	2.32	0.69
42:VC:86:ILE:HG21	42:VC:133:LEU:HD13	1.73	0.69
10:OB:10:GLU:N	10:OB:10:GLU:OE2	2.24	0.69
53:GD:11:VAL:HG23	53:GD:38:SER:HB2	1.74	0.69
1:A:1064:G:O2'	1:A:1190:G:N2	2.25	0.69
2:B:833:U:O2	13:M:55:ARG:NH2	2.25	0.69
1:FB:1028(A):C:O2	1:FB:1033:G:N2	2.19	0.69
46:ZC:33:ARG:HE	46:ZC:62:SER:HB3	1.58	0.69
53:GD:36:ARG:NH2	53:GD:75:ALA:O	2.26	0.69
39:SC:40:ARG:NH1	39:SC:68:GLU:HB2	2.08	0.69
2:B:1689:A:H62	2:B:1698:A:H2	1.40	0.69
1:A:1381:U:H1'	41:PA:79:ARG:HG2	1.74	0.69
17:Q:60:THR:HG22	17:Q:77:PRO:HA	1.74	0.69
25:Y:52:ARG:NH1	25:Y:57:GLU:HB2	2.07	0.69
33:GA:11:CYS:SG	33:GA:12:ASP:N	2.66	0.69
2:GB:10:G:O2'	2:GB:2801:A:N7	2.25	0.69
36:PC:162:ILE:HD11	36:PC:184:VAL:HG22	1.74	0.69
1:A:953:G:H5'	1:A:965:A:H61	1.57	0.69
17:Q:91:ARG:HG2	17:Q:91:ARG:HH11	1.58	0.69
2:GB:1669:A:O2'	2:GB:2549:G:OP1	2.11	0.69
2:B:307:G:H21	2:B:330:A:H62	1.41	0.69
2:B:1092:C:O2	2:B:1099:G:N2	2.26	0.69
9:I:159:GLU:HG3	9:I:169:VAL:HG11	1.75	0.69
2:GB:833:U:O2	13:RB:55:ARG:NH2	2.26	0.69
2:GB:1815:A:P	5:JB:54:ARG:HH22	2.15	0.69
25:DC:52:ARG:NH1	25:DC:57:GLU:HB2	2.09	0.69
1:FB:677:U:H3	1:FB:713:G:H22	1.41	0.68
5:E:75:ILE:HD13	5:E:99:ASP:OD2	1.94	0.68
5:E:142:VAL:HG23	5:E:193:VAL:HA	1.75	0.68
2:GB:1060:U:O2'	2:GB:1061:U:OP2	2.10	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:MB:113:ARG:HH12	8:MB:142:PRO:HA	1.59	0.68
13:RB:85:LEU:HD13	13:RB:120:ALA:HB2	1.75	0.68
9:NB:130:ARG:HH12	9:NB:132:ARG:HH21	1.41	0.68
17:VB:60:THR:HG22	17:VB:77:PRO:HA	1.74	0.68
38:RC:96:LEU:HG	38:RC:139:ARG:HH12	1.58	0.68
41:UC:20:ASP:OD2	41:UC:22:LEU:HB3	1.92	0.68
41:UC:57:GLU:N	41:UC:60:LYS:HZ3	1.90	0.68
1:A:677:U:H3	1:A:713:G:H22	1.41	0.68
2:GB:1173:G:H2'	2:GB:1175:U:H5''	1.74	0.68
5:JB:35:LYS:HD3	5:JB:64:ILE:HD11	1.74	0.68
2:B:1173:G:H2'	2:B:1175:U:H5''	1.74	0.68
49:CD:35:ARG:HG3	49:CD:35:ARG:HH11	1.59	0.68
2:B:1021:A:H62	2:B:1141:U:H3	1.42	0.68
2:B:2131:G:H4'	2:B:2132:U:OP2	1.94	0.68
35:JA:142:ARG:NH2	35:JA:174:ARG:HH11	1.90	0.68
49:XA:35:ARG:HH11	49:XA:35:ARG:HG3	1.59	0.68
1:FB:542:G:OP1	38:RC:10:ARG:NH2	2.27	0.68
2:GB:2104:G:H1	2:GB:2185:C:H42	1.42	0.68
2:B:1669:A:O2'	2:B:2549:G:OP1	2.12	0.68
2:B:2163:C:H5'	2:B:2165:G:H21	1.59	0.68
8:MB:73:ALA:HB3	8:MB:85:GLY:H	1.57	0.68
35:OC:116:ARG:HD2	35:OC:298:LEU:HD21	1.75	0.68
38:RC:190:ASP:OD2	38:RC:190:ASP:N	2.25	0.68
41:UC:126:ASP:HA	41:UC:129:GLU:HB2	1.76	0.68
1:A:664:G:H22	1:A:741:G:H1	1.42	0.67
1:A:1024:G:N7	1:A:1025:U:O2'	2.23	0.67
2:GB:363(F):U:H3'	2:GB:363(G):A:H8	1.59	0.67
7:LB:185:ASP:HA	7:LB:188:ARG:HD2	1.75	0.67
37:QC:70:VAL:O	37:QC:106:VAL:N	2.27	0.67
38:MA:18:LYS:HZ3	38:MA:31:CYS:HG	1.40	0.67
2:GB:1398:C:O3'	21:ZB:25:LYS:NZ	2.26	0.67
33:LC:11:CYS:SG	33:LC:12:ASP:N	2.67	0.67
36:PC:18:GLY:HA2	36:PC:42:ILE:HG13	1.75	0.67
14:N:138:ASP:OD1	23:W:81:ARG:NH1	2.27	0.67
36:KA:18:GLY:HA2	36:KA:42:ILE:HG13	1.76	0.67
2:GB:1021:A:H62	2:GB:1141:U:H3	1.42	0.67
47:AD:3:ARG:HH11	47:AD:3:ARG:CG	2.07	0.67
1:A:1453:G:H4'	1:A:1454:G:OP2	1.94	0.67
12:L:115:VAL:HG13	12:L:121:VAL:HG21	1.77	0.67
42:QA:7:ALA:HB2	42:QA:85:ARG:HD2	1.74	0.67
47:VA:3:ARG:HG2	47:VA:4:ILE:HG22	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:91:A:H2'	2:B:92:G:H8	1.59	0.67
39:NA:40:ARG:NH1	39:NA:68:GLU:HB2	2.09	0.67
2:GB:155:C:H5	2:GB:171:G:H22	1.42	0.67
32:KC:39:LYS:HA	32:KC:42:ARG:NH1	2.10	0.67
2:B:1385:G:O2'	2:B:1396:U:O2	2.12	0.67
47:AD:3:ARG:HH11	47:AD:4:ILE:HG22	1.60	0.67
2:B:155:C:H5	2:B:171:G:H22	1.42	0.67
38:MA:26:CYS:HA	38:MA:31:CYS:HB2	1.76	0.67
1:FB:664:G:H22	1:FB:741:G:H1	1.40	0.67
12:QB:115:VAL:HG13	12:QB:121:VAL:HG21	1.77	0.67
35:JA:107:ASP:HB2	35:JA:172:TYR:HD1	1.58	0.67
35:JA:224:ILE:HG12	35:JA:246:ILE:HG12	1.77	0.67
41:PA:126:ASP:HA	41:PA:129:GLU:HB2	1.77	0.67
43:RA:96:LEU:H	43:RA:98:PRO:HD2	1.60	0.67
2:GB:1689:A:H62	2:GB:1698:A:H2	1.41	0.67
7:LB:157:VAL:HB	7:LB:194:MET:HG2	1.76	0.67
2:B:1019:U:H3	2:B:1142(B):A:H62	1.41	0.67
2:B:1754:C:OP1	17:Q:96:ARG:NH1	2.28	0.67
1:FB:1422:G:H5''	12:QB:48:PRO:HB3	1.77	0.67
2:GB:1754:C:OP1	17:VB:96:ARG:NH1	2.28	0.67
2:GB:2126:A:H4'	2:GB:2127:G:H5'	1.76	0.67
5:JB:75:ILE:HD13	5:JB:99:ASP:OD2	1.95	0.67
7:LB:12:LEU:HG	7:LB:124:LEU:HD11	1.76	0.67
8:MB:115:ARG:HD3	47:AD:7:VAL:HG22	1.77	0.67
2:B:11:G:H2'	2:B:12:U:H5'	1.77	0.67
2:B:645:C:H4'	2:B:646:A:OP2	1.93	0.67
11:K:123:TYR:OH	11:K:130:HIS:NE2	2.17	0.67
2:GB:2143:C:O2	2:GB:2148:G:N2	2.27	0.67
4:NC:76:A:H3'	35:OC:234:GLY:HA3	1.77	0.67
49:CD:39:LEU:HD12	49:CD:56:LEU:HB2	1.75	0.67
17:Q:74:ARG:HG2	17:Q:74:ARG:HH11	1.59	0.66
37:LA:27:LYS:HG3	37:LA:28:GLN:HG3	1.78	0.66
2:GB:1044:G:H5'	2:GB:1045:A:OP2	1.95	0.66
1:FB:1454:G:OP1	54:HD:39:LYS:NZ	2.24	0.66
2:GB:2131:G:H4'	2:GB:2132:U:OP2	1.93	0.66
5:JB:142:VAL:HG23	5:JB:193:VAL:HA	1.77	0.66
41:PA:20:ASP:OD2	41:PA:22:LEU:HB3	1.95	0.66
47:VA:3:ARG:HH11	47:VA:4:ILE:HG22	1.60	0.66
8:H:113:ARG:HH12	8:H:142:PRO:HA	1.59	0.66
1:A:630:G:H5'	1:A:631:G:OP2	1.95	0.66
27:AA:3:ARG:HH11	27:AA:60:GLU:HB2	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:SA:80:LYS:HA	44:SA:83:GLU:HB2	1.78	0.66
37:QC:20:SER:OG	37:QC:40:ARG:NH2	2.28	0.66
43:WC:96:LEU:H	43:WC:98:PRO:HD2	1.60	0.66
2:B:2267:A:H5''	2:B:2268:A:H5'	1.77	0.66
42:VC:7:ALA:HB2	42:VC:85:ARG:HD2	1.77	0.66
1:A:1028(A):C:O2	1:A:1033:G:N2	2.19	0.66
32:FA:39:LYS:HA	32:FA:42:ARG:NH1	2.11	0.66
1:FB:630:G:H5'	1:FB:631:G:OP2	1.96	0.66
1:FB:1064:G:O2'	1:FB:1190:G:N2	2.28	0.66
2:GB:1358:G:O2'	2:GB:1373:A:N6	2.27	0.66
35:OC:107:ASP:HB2	35:OC:172:TYR:HD1	1.59	0.66
38:RC:18:LYS:HD3	38:RC:31:CYS:SG	2.36	0.66
38:RC:154:ASN:N	38:RC:154:ASN:OD1	2.27	0.66
47:AD:3:ARG:HG2	47:AD:4:ILE:HG22	1.77	0.66
36:KA:24:TRP:CD1	36:KA:24:TRP:H	2.14	0.66
1:FB:953:G:H5'	1:FB:965:A:H61	1.61	0.66
2:B:1044:G:H5'	2:B:1045:A:OP2	1.96	0.66
2:GB:1019:U:H3	2:GB:1142(B):A:H62	1.44	0.66
2:B:2104:G:H1	2:B:2185:C:H42	1.44	0.66
2:GB:2508:G:OP1	35:OC:228:ARG:NH2	2.25	0.66
1:A:706:A:H4'	45:TA:22:HIS:HD2	1.61	0.65
14:N:109:VAL:HG13	14:N:113:GLN:HB3	1.78	0.65
38:MA:3:ARG:HD2	38:MA:5:ILE:HG23	1.77	0.65
1:A:1454:G:OP1	54:CB:39:LYS:NZ	2.27	0.65
2:B:2126:A:H4'	2:B:2127:G:H5'	1.77	0.65
17:Q:133:GLU:OE2	17:Q:133:GLU:N	2.28	0.65
35:JA:116:ARG:HD2	35:JA:298:LEU:HD21	1.77	0.65
2:GB:2163:C:H5'	2:GB:2165:G:H21	1.62	0.65
14:SB:109:VAL:HG13	14:SB:113:GLN:HB3	1.78	0.65
2:B:10:G:O2'	2:B:2801:A:N7	2.28	0.65
2:B:127:A:H5''	2:B:128:C:C6	2.31	0.65
38:MA:154:ASN:OD1	38:MA:154:ASN:N	2.28	0.65
1:FB:1130:A:H2'	1:FB:1131:G:C8	2.31	0.65
2:GB:771:G:OP1	31:JC:10:ARG:NH1	2.29	0.65
2:B:2291:U:H2'	2:B:2292:C:C6	2.30	0.65
2:B:2784:C:H1'	6:F:37:ARG:HH12	1.61	0.65
8:H:167:GLU:N	8:H:167:GLU:OE2	2.30	0.65
36:KA:162:ILE:HD11	36:KA:184:VAL:HG22	1.77	0.65
2:GB:155:C:H41	2:GB:171:G:H1	1.45	0.65
49:CD:56:LEU:HA	49:CD:59:MET:HE3	1.79	0.65
42:VC:89:PRO:HA	42:VC:92:ARG:HH12	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:10:GLU:N	10:J:10:GLU:OE2	2.29	0.65
25:Y:86:SER:N	25:Y:89:GLU:OE2	2.21	0.65
1:FB:723:U:O2'	1:FB:724:G:O5'	2.15	0.65
16:P:78:LEU:HD11	16:P:109:GLY:HA3	1.79	0.65
42:QA:86:ILE:HG21	42:QA:133:LEU:HD13	1.78	0.65
48:WA:24:CYS:HB3	48:WA:28:GLY:H	1.62	0.65
2:B:1761:C:H3'	2:B:1762:A:H5''	1.77	0.65
2:GB:11:G:H2'	2:GB:12:U:H5'	1.79	0.65
36:PC:23:ARG:NH1	36:PC:23:ARG:HB2	2.11	0.65
2:B:1398:C:O3'	21:U:25:LYS:NZ	2.30	0.65
2:B:1803:A:O2'	5:E:259:THR:HG21	1.97	0.65
1:FB:1130:A:H2'	1:FB:1131:G:H8	1.62	0.65
1:A:1130:A:H2'	1:A:1131:G:C8	2.32	0.65
2:B:155:C:H41	2:B:171:G:H1	1.43	0.65
15:O:67:LEU:HD22	15:O:76:VAL:HG21	1.78	0.65
36:PC:24:TRP:CD1	36:PC:24:TRP:H	2.14	0.65
1:A:1498:UR3:OP2	34:HA:16:A:O2'	2.15	0.64
3:C:13:A:N1	3:C:69:G:O2'	2.30	0.64
1:FB:820:U:H4'	1:FB:821:G:OP2	1.97	0.64
2:GB:127:A:H5''	2:GB:128:C:C6	2.32	0.64
2:GB:2287:A:N6	2:GB:2344:U:H3	1.96	0.64
6:KB:24:THR:HG23	6:KB:184:VAL:HG23	1.78	0.64
44:XC:80:LYS:HA	44:XC:83:GLU:HB2	1.78	0.64
8:H:73:ALA:HB3	8:H:85:GLY:H	1.63	0.64
37:LA:64:VAL:HG22	37:LA:99:VAL:HA	1.78	0.64
2:GB:91:A:H2'	2:GB:92:G:H8	1.61	0.64
7:LB:64:ILE:HD11	7:LB:75:HIS:HB2	1.79	0.64
7:LB:167:ALA:HB1	7:LB:173:VAL:HG11	1.79	0.64
36:PC:69:LEU:HB3	36:PC:162:ILE:HG22	1.79	0.64
15:O:104:ARG:NH1	15:O:107:ASP:OD2	2.30	0.64
37:LA:70:VAL:O	37:LA:106:VAL:N	2.28	0.64
2:GB:2291:U:H2'	2:GB:2292:C:C6	2.33	0.64
35:OC:224:ILE:HG12	35:OC:246:ILE:HG12	1.80	0.64
3:C:57:A:OP2	3:C:58:A:OP2	2.16	0.64
2:GB:2267:A:H5''	2:GB:2268:A:H5'	1.80	0.64
16:P:3:ARG:HH11	16:P:3:ARG:CA	2.07	0.64
2:GB:307:G:H21	2:GB:330:A:H62	1.44	0.64
38:RC:3:ARG:HD2	38:RC:5:ILE:HG23	1.78	0.64
4:D:31:G:H1	4:D:39:C:H42	1.45	0.64
24:X:6:GLY:HA3	4:IA:1:C:O2	1.97	0.64
1:FB:1412:C:H2'	1:FB:1413:A:C8	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:HB:57:A:OP2	3:HB:58:A:OP2	2.15	0.64
10:OB:118:LYS:NZ	10:OB:121:LYS:HG3	2.12	0.64
13:M:77:ARG:NH1	13:M:77:ARG:HB2	2.12	0.64
53:BB:50:ALA:HB1	53:BB:57:HIS:HB3	1.78	0.64
37:QC:58:GLU:HB3	44:XC:92:THR:HG21	1.80	0.64
49:XA:39:LEU:HD12	49:XA:56:LEU:HB2	1.78	0.64
2:GB:140:A:H8	2:GB:1408:C:HO2'	1.43	0.64
23:BC:80:ARG:HB3	23:BC:82:ARG:NH1	2.13	0.64
53:GD:50:ALA:HB1	53:GD:57:HIS:HB3	1.78	0.64
6:KB:48:GLN:HG2	6:KB:78:LEU:HD12	1.79	0.64
16:UB:3:ARG:HH11	16:UB:3:ARG:CA	2.08	0.64
38:RC:201:GLN:NE2	39:SC:116:THR:O	2.31	0.64
2:B:140:A:H8	2:B:1408:C:HO2'	1.45	0.64
47:VA:54:VAL:HA	47:VA:57:ARG:HH12	1.62	0.64
2:B:2445:G:OP1	7:G:74:ARG:NH2	2.30	0.63
6:F:24:THR:HG23	6:F:184:VAL:HG23	1.80	0.63
37:LA:20:SER:OG	37:LA:40:ARG:NH2	2.31	0.63
9:NB:159:GLU:HG3	9:NB:169:VAL:HG11	1.79	0.63
1:A:8:A:C6	38:MA:209:ARG:HB2	2.33	0.63
40:OA:46:ARG:HB2	40:OA:60:PHE:CE1	2.34	0.63
54:CB:43:LEU:O	54:CB:47:GLY:N	2.30	0.63
7:LB:197:ASP:OD1	7:LB:197:ASP:N	2.29	0.63
37:QC:27:LYS:HG3	37:QC:28:GLN:HG3	1.78	0.63
9:NB:24:VAL:HG13	9:NB:35:VAL:HB	1.81	0.63
1:A:1422:G:H5''	12:L:48:PRO:HB3	1.81	0.63
47:VA:34:LEU:HD13	47:VA:41:PRO:HA	1.80	0.63
47:VA:108:ARG:NH1	47:VA:112:GLY:O	2.32	0.63
12:QB:19:ILE:HG22	12:QB:43:VAL:HA	1.80	0.63
16:UB:78:LEU:HD11	16:UB:109:GLY:HA3	1.79	0.63
38:RC:178:VAL:O	38:RC:180:GLY:N	2.31	0.63
38:MA:190:ASP:OD2	38:MA:190:ASP:N	2.31	0.63
47:VA:24:GLY:HA3	47:VA:66:LEU:HD23	1.81	0.63
2:GB:648:G:H21	32:KC:46:ARG:HH12	1.43	0.63
2:GB:1047:G:H2'	2:GB:1110:G:H1	1.63	0.63
3:HB:13:A:N1	3:HB:69:G:O2'	2.30	0.63
2:B:1047:G:H2'	2:B:1110:G:H1	1.63	0.63
6:F:128:SER:OG	6:F:129:HIS:N	2.28	0.63
36:KA:74:LYS:HZ2	36:KA:166:ASP:HB2	1.64	0.63
44:XC:13:HIS:HA	44:XC:16:LEU:HB3	1.81	0.63
2:B:1864:U:OP1	2:B:2410:G:O2'	2.14	0.63
13:RB:77:ARG:NH1	13:RB:77:ARG:HB2	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:TC:68:PRO:HG2	40:TC:71:ARG:HH21	1.64	0.63
48:BD:24:CYS:HB3	48:BD:28:GLY:H	1.64	0.63
1:FB:1460:A:OP2	54:HD:27:LYS:NZ	2.28	0.63
17:VB:133:GLU:N	17:VB:133:GLU:OE2	2.31	0.63
1:A:723:U:O2'	1:A:724:G:O5'	2.15	0.63
28:GC:36:CYS:SG	28:GC:37:SER:N	2.70	0.63
38:RC:98:GLU:OE2	38:RC:103:ASN:ND2	2.31	0.63
1:A:1379:G:OP1	41:PA:6:ARG:NH1	2.31	0.62
2:B:771:G:OP1	31:EA:10:ARG:NH1	2.30	0.62
23:W:80:ARG:HB3	23:W:82:ARG:NH1	2.13	0.62
36:KA:69:LEU:HB3	36:KA:162:ILE:HG22	1.79	0.62
2:GB:2210:G:H3'	2:GB:2211:G:N7	2.15	0.62
16:UB:67:ARG:NH1	16:UB:103:GLU:OE1	2.32	0.62
47:AD:54:VAL:HA	47:AD:57:ARG:HH12	1.62	0.62
55:ID:2:GLY:O	55:ID:4:GLY:N	2.32	0.62
38:MA:79:PHE:O	38:MA:83:SER:OG	2.16	0.62
49:XA:56:LEU:HA	49:XA:59:MET:HE3	1.81	0.62
35:OC:262:SER:HB3	35:OC:265:LYS:HB2	1.79	0.62
1:A:820:U:H4'	1:A:821:G:OP2	1.97	0.62
1:A:1130:A:H2'	1:A:1131:G:H8	1.65	0.62
1:A:1412:C:H2'	1:A:1413:A:C8	2.34	0.62
13:M:85:LEU:HD13	13:M:120:ALA:HB2	1.80	0.62
51:ED:6:LEU:HD23	51:ED:23:VAL:HG11	1.81	0.62
2:B:1434:A:H61	2:B:1558:A:N6	1.96	0.62
2:B:2143:C:O2	2:B:2148:G:N2	2.28	0.62
15:O:18:LEU:HD21	15:O:22:ARG:NH1	2.15	0.62
17:Q:129:ARG:HA	17:Q:132:LYS:HZ1	1.63	0.62
36:KA:124:SER:H	36:KA:125:PRO:HD2	1.64	0.62
2:GB:2784:C:H1'	6:KB:37:ARG:HH12	1.63	0.62
39:NA:122:GLU:O	39:NA:126:ARG:NE	2.24	0.62
14:SB:138:ASP:OD1	23:BC:81:ARG:NH1	2.33	0.62
7:G:157:VAL:HB	7:G:194:MET:HG2	1.81	0.62
36:KA:23:ARG:NH1	36:KA:23:ARG:HB2	2.15	0.62
11:PB:46:VAL:HG23	11:PB:48:MET:HG2	1.80	0.62
23:BC:79:ARG:HD2	23:BC:80:ARG:NH1	2.11	0.62
2:B:1364:G:OP2	25:Y:3:LYS:HG3	1.99	0.62
13:M:99:LEU:HD23	13:M:102:ARG:HH21	1.65	0.62
55:DB:2:GLY:O	55:DB:4:GLY:N	2.33	0.62
37:QC:64:VAL:HG22	37:QC:99:VAL:HA	1.81	0.62
22:V:83:THR:OG1	22:V:84:ARG:N	2.26	0.62
23:W:127:LYS:HB2	23:W:162:GLU:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:6:GLY:HA3	4:IA:1:C:H1'	1.80	0.62
38:MA:178:VAL:O	38:MA:180:GLY:N	2.32	0.62
1:A:1348:U:H4'	43:RA:120:ARG:HG3	1.80	0.62
2:B:1184:G:H5''	27:AA:29:ARG:HD3	1.81	0.62
7:G:167:ALA:HB1	7:G:173:VAL:HG11	1.80	0.62
1:FB:1379:G:OP1	41:UC:6:ARG:NH1	2.33	0.62
2:GB:2698:U:H2'	2:GB:2699:C:C6	2.34	0.62
2:B:34:C:O2'	2:B:35:G:OP1	2.18	0.62
2:B:2210:G:H3'	2:B:2211:G:N7	2.15	0.62
7:G:197:ASP:OD1	7:G:197:ASP:N	2.33	0.62
15:TB:67:LEU:HD22	15:TB:76:VAL:HG21	1.81	0.62
23:BC:157:LEU:HD23	23:BC:161:VAL:HG12	1.81	0.62
31:JC:34:ARG:HG2	31:JC:34:ARG:HH11	1.65	0.62
38:RC:9:CYS:HG	38:RC:31:CYS:HG	1.46	0.62
2:B:634:C:H2'	2:B:635:C:C6	2.35	0.61
7:G:12:LEU:HG	7:G:124:LEU:HD11	1.82	0.61
2:GB:1385:G:O2'	2:GB:1396:U:O2	2.16	0.61
8:MB:136:ARG:H	8:MB:136:ARG:NE	1.95	0.61
15:TB:97:VAL:HG22	15:TB:114:VAL:HG22	1.82	0.61
23:W:157:LEU:HD23	23:W:161:VAL:HG12	1.83	0.61
37:LA:16:ARG:NH2	37:LA:183:ASP:OD1	2.33	0.61
1:FB:1348:U:H4'	43:WC:120:ARG:HG3	1.81	0.61
22:AC:44:ILE:HD13	22:AC:44:ILE:H	1.64	0.61
42:VC:89:PRO:HA	42:VC:92:ARG:NH1	2.15	0.61
1:A:559:A:H4'	1:A:560:U:H3'	1.81	0.61
37:LA:31:HIS:HA	37:LA:34:LEU:HB3	1.82	0.61
17:VB:74:ARG:HG2	17:VB:74:ARG:NH1	2.14	0.61
47:AD:24:GLY:HA3	47:AD:66:LEU:HD23	1.81	0.61
5:E:122:ASP:N	5:E:122:ASP:OD1	2.28	0.61
10:J:91:SER:O	10:J:93:THR:N	2.33	0.61
22:V:50:ARG:HH11	22:V:50:ARG:HB2	1.66	0.61
36:KA:24:TRP:H	36:KA:24:TRP:HD1	1.49	0.61
1:FB:1531:A:OP2	1:FB:1532:U:H5	1.84	0.61
2:GB:1058:G:N2	2:GB:1087:G:OP2	2.32	0.61
4:IB:31:G:H1	4:IB:39:C:H42	1.46	0.61
38:RC:168:ARG:HH11	38:RC:168:ARG:HG3	1.65	0.61
6:F:48:GLN:HG2	6:F:78:LEU:HD12	1.81	0.61
44:SA:13:HIS:HA	44:SA:16:LEU:HB3	1.82	0.61
2:GB:322:A:OP2	7:LB:169:ASN:HB2	2.01	0.61
1:A:191(G):G:O2'	54:CB:101:GLY:O	2.19	0.61
16:P:67:ARG:NH1	16:P:103:GLU:OE1	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:QA:89:PRO:HA	42:QA:92:ARG:HH12	1.66	0.61
1:FB:17:U:H2'	1:FB:18:C:C6	2.36	0.61
2:GB:2508:G:P	35:OC:228:ARG:HH22	2.24	0.61
2:B:1058:G:N2	2:B:1087:G:OP2	2.34	0.61
2:B:1252:G:N3	18:R:33:ARG:HD2	2.16	0.61
38:MA:98:GLU:OE2	38:MA:103:ASN:ND2	2.33	0.61
38:RC:26:CYS:HA	38:RC:31:CYS:HB2	1.81	0.61
38:RC:103:ASN:OD1	38:RC:114:ARG:NH2	2.33	0.61
40:TC:46:ARG:HH11	40:TC:46:ARG:CB	2.12	0.61
47:AD:34:LEU:HD13	47:AD:41:PRO:HA	1.82	0.61
54:HD:43:LEU:O	54:HD:47:GLY:N	2.32	0.61
28:BA:36:CYS:SG	28:BA:37:SER:N	2.69	0.61
44:SA:34:VAL:HA	44:SA:74:ILE:HG22	1.82	0.61
2:B:270(Q):C:OP2	2:B:270(Q):C:H6	1.83	0.61
2:GB:1184:G:H5''	27:FC:29:ARG:HD3	1.83	0.61
38:MA:168:ARG:HH11	38:MA:168:ARG:HG3	1.65	0.61
1:FB:1314:C:N4	53:GD:2:PRO:O	2.34	0.61
1:A:1022:G:C2	1:A:1023:G:H1'	2.36	0.60
2:GB:2168:G:O2'	2:GB:2170:A:N7	2.33	0.60
8:MB:136:ARG:HE	8:MB:136:ARG:N	1.98	0.60
36:PC:24:TRP:H	36:PC:24:TRP:HD1	1.48	0.60
2:B:819:A:OP2	2:B:1187:G:N2	2.21	0.60
54:CB:98:PRO:O	54:CB:100:ILE:N	2.33	0.60
1:FB:1022:G:C2	1:FB:1023:G:H1'	2.36	0.60
2:GB:645:C:H4'	2:GB:646:A:OP2	2.00	0.60
6:KB:105:THR:OG1	6:KB:199:ARG:NH2	2.34	0.60
45:YC:67:ASP:HA	45:YC:70:LYS:HE2	1.83	0.60
49:CD:17:ARG:HD3	49:CD:26:GLU:OE2	2.01	0.60
4:D:30:G:H21	41:PA:144:MET:HE1	1.67	0.60
9:I:56:SER:HB3	9:I:61:HIS:ND1	2.16	0.60
15:O:97:VAL:HG22	15:O:114:VAL:HG22	1.83	0.60
21:U:60:ARG:NH1	31:EA:47:ARG:NH2	2.49	0.60
14:SB:51:ARG:HG3	14:SB:66:ILE:HD11	1.84	0.60
37:QC:16:ARG:NH2	37:QC:183:ASP:OD1	2.35	0.60
54:HD:98:PRO:O	54:HD:100:ILE:N	2.33	0.60
1:A:1323:G:H2'	1:A:1324:A:C8	2.36	0.60
8:H:136:ARG:H	8:H:136:ARG:NE	1.97	0.60
27:FC:3:ARG:HH11	27:FC:60:GLU:HB2	1.65	0.60
36:PC:124:SER:H	36:PC:125:PRO:HD2	1.65	0.60
1:A:363:A:OP2	46:UA:34:ARG:HD3	2.02	0.60
1:A:1367:C:H5'	44:SA:60:ARG:NH1	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:634:C:H2'	2:GB:635:C:C6	2.36	0.60
17:VB:100:TYR:CD1	17:VB:103:ARG:NH1	2.69	0.60
23:BC:127:LYS:HB2	23:BC:162:GLU:HB2	1.83	0.60
37:QC:31:HIS:HA	37:QC:34:LEU:HB3	1.83	0.60
44:XC:62:HIS:HB3	48:BD:59:ALA:HB3	1.82	0.60
1:A:17:U:H2'	1:A:18:C:C6	2.37	0.60
2:B:1094:U:H1'	2:B:1096:A:C8	2.37	0.60
2:B:1177:A:H2'	2:B:1178:C:O4'	2.02	0.60
2:B:2115:G:N2	2:B:2119:A:OP1	2.33	0.60
14:N:43:THR:HA	14:N:94:VAL:HG12	1.83	0.60
1:FB:184:G:H2'	1:FB:185:A:H8	1.65	0.60
1:FB:1367:C:H5'	44:XC:60:ARG:NH1	2.16	0.60
10:OB:83:ALA:HA	10:OB:88:ILE:HG12	1.82	0.60
37:QC:59:ARG:NH1	37:QC:64:VAL:HG12	2.17	0.60
1:A:1367:C:H4'	44:SA:48:THR:HG21	1.84	0.60
37:LA:58:GLU:HB3	44:SA:92:THR:HG21	1.83	0.60
42:QA:116:LYS:HD2	42:QA:129:VAL:HG11	1.84	0.60
1:FB:559:A:H4'	1:FB:560:U:H3'	1.81	0.60
2:GB:1252:G:N3	18:WB:33:ARG:HD2	2.16	0.60
2:GB:2023:G:H5'	2:GB:2617:C:H4'	1.82	0.60
22:AC:83:THR:OG1	22:AC:84:ARG:N	2.32	0.60
1:A:116:A:H61	1:A:313:A:H1'	1.67	0.60
19:S:58:VAL:HG21	19:S:100:ARG:HH21	1.66	0.60
2:GB:1177:A:H2'	2:GB:1178:C:O4'	2.01	0.60
36:PC:74:LYS:HZ2	36:PC:166:ASP:HB2	1.67	0.60
2:B:2168:G:O2'	2:B:2170:A:N7	2.33	0.60
37:LA:52:LEU:HD13	37:LA:68:VAL:HG13	1.84	0.60
7:LB:119:ARG:HB2	7:LB:119:ARG:NH1	2.16	0.60
1:FB:1367:C:H4'	44:XC:48:THR:HG21	1.83	0.60
8:MB:11:TYR:HA	8:MB:15:VAL:HB	1.84	0.60
33:LC:11:CYS:HB3	33:LC:32:HIS:CE1	2.37	0.60
13:M:91:PHE:O	13:M:121:LYS:NZ	2.33	0.59
13:M:118:GLY:O	13:M:137:LYS:NZ	2.31	0.59
27:AA:1:MET:HE3	27:AA:39:ASP:HB3	1.84	0.59
33:GA:11:CYS:HB3	33:GA:32:HIS:CE1	2.37	0.59
34:HA:14:A:H3'	34:HA:15:A:C8	2.37	0.59
36:KA:19:HIS:HD2	36:KA:189:ASP:OD2	1.85	0.59
37:LA:131:ARG:NH1	39:NA:50:GLU:HG3	2.17	0.59
2:GB:1864:U:OP1	2:GB:2410:G:O2'	2.14	0.59
22:AC:23:ARG:NH2	22:AC:41:GLY:O	2.35	0.59
1:A:1492:A:N6	46:UA:48:PRO:O	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:64:ILE:HD11	7:G:75:HIS:HB2	1.84	0.59
8:H:11:TYR:HA	8:H:15:VAL:HB	1.84	0.59
9:I:24:VAL:HG13	9:I:35:VAL:HB	1.83	0.59
10:J:93:THR:HG23	10:J:95:LYS:H	1.65	0.59
14:N:116:GLU:OE2	14:N:119:ARG:NE	2.32	0.59
49:XA:33:THR:HG21	49:XA:85:LEU:HD22	1.83	0.59
2:GB:507:A:O2'	2:GB:508:G:OP2	2.18	0.59
49:CD:33:THR:HG21	49:CD:85:LEU:HD22	1.83	0.59
1:A:1314:C:N4	53:BB:2:PRO:O	2.36	0.59
29:CA:16:ARG:HG2	29:CA:16:ARG:NH1	2.11	0.59
1:FB:164:U:H2'	1:FB:165:C:C6	2.36	0.59
2:GB:1364:G:OP2	25:DC:3:LYS:HG3	2.02	0.59
10:OB:83:ALA:HA	10:OB:88:ILE:HG21	1.84	0.59
33:LC:25:VAL:HB	33:LC:34:GLN:HB2	1.83	0.59
40:TC:33:TYR:HD1	40:TC:71:ARG:HG2	1.67	0.59
1:A:403:C:O2'	38:MA:122:ARG:NH2	2.35	0.59
2:B:1358:G:O2'	2:B:1373:A:N6	2.34	0.59
1:FB:773:G:O3'	5:JB:202:LYS:NZ	2.28	0.59
8:MB:167:GLU:N	8:MB:167:GLU:OE2	2.35	0.59
15:TB:13:HIS:HD2	15:TB:16:HIS:H	1.49	0.59
42:VC:85:ARG:HD3	42:VC:87:SER:O	2.02	0.59
43:WC:105:ASP:OD2	43:WC:107:ARG:HG2	2.02	0.59
1:A:184:G:H2'	1:A:185:A:H8	1.67	0.59
1:A:1531:A:OP2	1:A:1532:U:H5	1.84	0.59
20:T:110:LYS:NZ	20:T:111:HIS:H	2.00	0.59
35:JA:262:SER:HB3	35:JA:265:LYS:HB2	1.84	0.59
1:FB:116:A:H61	1:FB:313:A:H1'	1.66	0.59
1:FB:692:U:O4	45:YC:26:ASN:ND2	2.35	0.59
1:FB:1498:UR3:OP2	34:MC:16:A:O2'	2.20	0.59
1:FB:1516:G:N1	1:FB:1519:MA6:OP2	2.36	0.59
2:GB:270(M):U:O2'	2:GB:270(O):G:N2	2.35	0.59
2:GB:2393:A:H5''	13:RB:63:PRO:HB3	1.84	0.59
40:TC:46:ARG:HB2	40:TC:60:PHE:CE1	2.38	0.59
47:AD:108:ARG:NH1	47:AD:112:GLY:O	2.35	0.59
54:HD:10:LEU:HD12	54:HD:12:ALA:H	1.68	0.59
2:B:2393:A:H5''	13:M:63:PRO:HB3	1.83	0.59
14:SB:43:THR:HA	14:SB:94:VAL:HG12	1.85	0.59
15:TB:100:LEU:HD11	15:TB:113:LEU:HD23	1.85	0.59
35:OC:182:HIS:HB3	35:OC:310:TYR:HE1	1.67	0.59
2:B:606:U:OP2	7:G:104:LYS:HE3	2.03	0.59
8:H:11:TYR:CZ	8:H:16:ARG:HD3	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:15:ARG:HG2	16:P:88:ASP:OD2	2.03	0.59
28:BA:44:THR:O	28:BA:46:GLN:N	2.35	0.59
28:BA:56:VAL:HG22	28:BA:61:ARG:HA	1.84	0.59
43:RA:95:LYS:H	43:RA:98:PRO:HG2	1.67	0.59
49:XA:3:ILE:HD13	49:XA:34:LEU:HD23	1.84	0.59
2:GB:1803:A:O2'	5:JB:259:THR:HG21	2.02	0.59
7:LB:107:LYS:NZ	7:LB:207:GLY:H	2.01	0.59
36:PC:19:HIS:HD2	36:PC:189:ASP:OD2	1.85	0.59
33:GA:27:CYS:SG	33:GA:28:GLU:N	2.75	0.59
1:FB:1005:A:N6	1:FB:1024:G:O2'	2.36	0.59
2:GB:1113:U:H2'	2:GB:1114:G:H8	1.66	0.59
13:RB:81:GLN:OE1	13:RB:107:LYS:N	2.32	0.59
18:WB:36:ARG:HD3	18:WB:40:PHE:CZ	2.38	0.59
37:QC:67:THR:HA	37:QC:102:ASN:HB3	1.83	0.59
14:N:82:ARG:NH1	24:X:4:LYS:HB2	2.18	0.59
1:FB:1320:C:N3	53:GD:36:ARG:HD3	2.18	0.59
2:GB:1022:G:O6	11:PB:66:LYS:NZ	2.36	0.59
5:JB:122:ASP:N	5:JB:122:ASP:OD1	2.31	0.59
12:QB:75:SER:HB2	17:VB:74:ARG:HH12	1.67	0.59
13:RB:99:LEU:HD23	13:RB:102:ARG:HH21	1.68	0.59
31:JC:34:ARG:HG2	31:JC:34:ARG:NH1	2.18	0.59
2:B:270(M):U:O2'	2:B:270(O):G:N2	2.35	0.59
2:B:784:A:C5	5:E:229:VAL:HG21	2.38	0.59
2:B:1022:G:O6	11:K:66:LYS:NZ	2.34	0.59
2:B:1091:G:N2	2:B:1100:C:O2'	2.36	0.59
35:JA:126:LEU:HG	35:JA:157:GLY:H	1.67	0.59
40:OA:33:TYR:HD1	40:OA:71:ARG:HG2	1.67	0.59
40:OA:68:PRO:HG2	40:OA:71:ARG:HH21	1.68	0.59
14:SB:82:ARG:NH1	24:CC:4:LYS:HB2	2.18	0.59
37:QC:85:ARG:HG2	37:QC:88:ARG:NH2	2.18	0.59
2:B:154(A):C:O2'	2:B:155:C:N3	2.36	0.58
10:J:83:ALA:HA	10:J:88:ILE:HG21	1.84	0.58
2:GB:1291:C:H2'	2:GB:1292:U:H6	1.68	0.58
25:DC:86:SER:N	25:DC:89:GLU:OE2	2.23	0.58
37:LA:67:THR:HA	37:LA:102:ASN:HB3	1.85	0.58
52:AB:33:ASP:OD2	52:AB:36:ASN:HB2	2.03	0.58
2:GB:140:A:H8	2:GB:1408:C:O2'	1.87	0.58
2:GB:1786:A:H1'	2:GB:1938:A:N6	2.17	0.58
2:B:2139:C:H3'	2:B:2140:C:C6	2.38	0.58
18:R:59:ARG:O	18:R:63:VAL:HG23	2.03	0.58
20:T:8:ARG:HB2	20:T:102:HIS:ND1	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:363:A:OP2	46:ZC:34:ARG:HD3	2.03	0.58
2:GB:616:A:C4	7:LB:180:GLY:HA2	2.39	0.58
2:GB:2115:G:N2	2:GB:2119:A:OP1	2.35	0.58
2:GB:2232:U:P	25:DC:40:ARG:HH22	2.26	0.58
2:B:185:U:H4'	2:B:218:A:H4'	1.85	0.58
5:E:148:GLU:HB2	5:E:151:LYS:HD2	1.85	0.58
6:F:105:THR:OG1	6:F:199:ARG:NH2	2.36	0.58
43:RA:11:LYS:O	43:RA:13:ALA:N	2.32	0.58
43:RA:26:VAL:HB	43:RA:33:PHE:HB2	1.85	0.58
1:FB:191(G):G:O2'	54:HD:101:GLY:O	2.21	0.58
1:FB:266:G:H3'	51:ED:67:LYS:HB2	1.85	0.58
2:GB:880:G:H1	2:GB:897:C:H42	1.49	0.58
2:GB:2445:G:OP1	7:LB:74:ARG:NH2	2.37	0.58
8:MB:115:ARG:NH1	47:AD:2:ALA:HB2	2.18	0.58
22:AC:50:ARG:HB2	22:AC:50:ARG:HH11	1.68	0.58
28:GC:56:VAL:HG22	28:GC:61:ARG:HA	1.85	0.58
2:B:1045:A:H1'	2:B:1047:G:H1'	1.85	0.58
2:B:2023:G:H5'	2:B:2617:C:H4'	1.85	0.58
2:B:2698:U:H2'	2:B:2699:C:C6	2.37	0.58
12:L:19:ILE:HG22	12:L:43:VAL:HA	1.86	0.58
14:N:65:PHE:HB2	14:N:105:GLU:HB2	1.85	0.58
28:BA:62:ARG:NH1	28:BA:62:ARG:HA	2.18	0.58
36:KA:48:MET:HA	36:KA:51:LEU:HB2	1.85	0.58
37:LA:59:ARG:NH1	37:LA:64:VAL:HG12	2.18	0.58
40:OA:46:ARG:HH11	40:OA:46:ARG:CB	2.14	0.58
1:FB:1124:G:N7	1:FB:1145:C:O2'	2.36	0.58
22:AC:92:ASN:OD1	22:AC:93:GLY:N	2.37	0.58
35:OC:126:LEU:HG	35:OC:157:GLY:H	1.69	0.58
36:PC:185:ILE:HG23	36:PC:199:TYR:HB2	1.86	0.58
44:XC:34:VAL:HA	44:XC:74:ILE:HG22	1.84	0.58
45:YC:31:THR:HG22	45:YC:42:TRP:HB2	1.86	0.58
2:B:2151:G:N2	2:B:2152:G:O6	2.37	0.58
2:B:2166:G:N7	2:B:2168:G:N2	2.51	0.58
33:GA:25:VAL:HB	33:GA:34:GLN:HB2	1.84	0.58
47:VA:11:ARG:HA	47:VA:45:VAL:HB	1.85	0.58
8:MB:122:PRO:HG2	8:MB:182:LYS:HG2	1.86	0.58
12:QB:45:GLU:HA	12:QB:54:GLU:OE2	2.04	0.58
14:SB:47:ILE:HD12	14:SB:70:PRO:HG3	1.84	0.58
28:GC:44:THR:O	28:GC:46:GLN:N	2.37	0.58
47:AD:11:ARG:HA	47:AD:45:VAL:HB	1.84	0.58
2:B:885:C:N4	2:B:886:C:O2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1653:G:H5''	15:O:2:ARG:HD3	1.86	0.58
28:BA:62:ARG:HA	28:BA:62:ARG:CZ	2.33	0.58
1:FB:1368:G:H4'	44:XC:46:ARG:NH1	2.18	0.58
2:GB:885:C:N4	2:GB:886:C:O2	2.36	0.58
8:MB:50:ALA:HB1	8:MB:52:ILE:HG13	1.86	0.58
19:XB:72:VAL:HG13	19:XB:85:LYS:HB3	1.84	0.58
36:PC:74:LYS:HE3	36:PC:206:ASP:HA	1.86	0.58
2:B:896:A:H4'	2:B:896:A:OP2	2.04	0.58
2:B:2792:G:H2'	2:B:2793:G:C8	2.39	0.58
8:H:50:ALA:HB1	8:H:52:ILE:HG13	1.85	0.58
14:N:76:LYS:HB3	14:N:91:GLU:HG3	1.85	0.58
24:X:12:ASN:HA	24:X:14:ARG:NH2	2.19	0.58
35:JA:226:THR:HG23	35:JA:241:ASP:HB3	1.86	0.58
1:FB:1343:G:O2'	43:WC:121:ARG:NH1	2.36	0.58
1:FB:1353:G:OP1	55:ID:10:ARG:NH1	2.37	0.58
8:MB:11:TYR:CZ	8:MB:16:ARG:HD3	2.38	0.58
18:WB:59:ARG:O	18:WB:63:VAL:HG23	2.04	0.58
36:PC:32:ILE:HD11	36:PC:40:HIS:HB3	1.86	0.58
37:QC:130:VAL:O	37:QC:134:ILE:HG12	2.04	0.58
47:AD:82:MET:HE3	47:AD:93:ARG:HG2	1.86	0.58
2:B:2138:C:H42	2:B:2153:G:H1	1.50	0.58
13:M:124:LYS:HE2	13:M:144:GLU:OE2	2.03	0.58
14:N:67:ARG:NH1	14:N:105:GLU:OE2	2.35	0.58
2:GB:2139:C:H3'	2:GB:2140:C:C6	2.39	0.58
16:UB:41:ASP:HB2	16:UB:48:LEU:HD21	1.86	0.58
37:QC:65:ALA:HA	37:QC:100:ALA:HB3	1.86	0.58
39:SC:77:PRO:HG2	39:SC:78:HIS:CD2	2.38	0.58
1:A:1320:C:N3	53:BB:36:ARG:HD3	2.18	0.58
2:B:1045:A:O2'	2:B:1047:G:N3	2.33	0.58
31:EA:47:ARG:HB3	31:EA:47:ARG:HH11	1.67	0.58
42:QA:89:PRO:HA	42:QA:92:ARG:NH1	2.19	0.58
1:FB:429:U:OP2	38:RC:36:ARG:NH2	2.37	0.58
2:GB:479:A:N3	2:GB:481:G:H5''	2.18	0.58
2:GB:1060:U:H5''	2:GB:1061:U:H3'	1.86	0.58
1:A:692:U:O4	45:TA:26:ASN:ND2	2.37	0.57
38:MA:103:ASN:OD1	38:MA:114:ARG:NH2	2.36	0.57
42:QA:85:ARG:HD3	42:QA:87:SER:O	2.04	0.57
2:GB:1532:C:H42	2:GB:1539:G:H1	1.52	0.57
1:A:537:G:OP1	46:UA:113:ARG:NH2	2.30	0.57
1:A:740:U:OP1	49:XA:38:ARG:HD3	2.04	0.57
1:FB:1291:G:O2'	43:WC:38:GLN:OE1	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:1025:G:C4	2:GB:1135:C:H1'	2.39	0.57
38:RC:9:CYS:HG	38:RC:18:LYS:NZ	2.00	0.57
2:B:1113:U:H2'	2:B:1114:G:H8	1.68	0.57
2:B:2317:C:H2'	2:B:2318:G:H5'	1.84	0.57
10:J:118:LYS:NZ	10:J:121:LYS:HG3	2.18	0.57
49:XA:25:THR:HG21	49:XA:70:LEU:HB2	1.87	0.57
1:FB:1493:A:N3	35:OC:119:THR:HG23	2.18	0.57
2:GB:2552:2MU:H2'	2:GB:2554:U:OP2	2.04	0.57
9:NB:56:SER:HB3	9:NB:61:HIS:ND1	2.19	0.57
17:VB:129:ARG:HA	17:VB:132:LYS:HZ1	1.68	0.57
43:WC:83:ARG:HG2	43:WC:102:LEU:HD23	1.85	0.57
52:FD:33:ASP:OD2	52:FD:36:ASN:HB2	2.04	0.57
1:A:1291:G:O2'	43:RA:38:GLN:OE1	2.22	0.57
16:P:41:ASP:HB2	16:P:48:LEU:HD21	1.85	0.57
37:LA:65:ALA:HA	37:LA:100:ALA:HB3	1.86	0.57
47:VA:82:MET:HE3	47:VA:93:ARG:HG2	1.85	0.57
1:FB:452:A:OP1	50:DD:43:LYS:NZ	2.37	0.57
2:GB:185:U:H4'	2:GB:218:A:H4'	1.85	0.57
2:GB:774:A:H2'	2:GB:774:A:N3	2.19	0.57
2:GB:2232:U:OP2	25:DC:40:ARG:NH2	2.36	0.57
37:QC:52:LEU:HD13	37:QC:68:VAL:HG13	1.86	0.57
43:WC:26:VAL:HB	43:WC:33:PHE:HB2	1.86	0.57
51:ED:59:ILE:HG22	51:ED:73:VAL:HA	1.87	0.57
2:B:784:A:H5'	2:B:785:G:OP1	2.05	0.57
17:Q:73:GLU:OE1	17:Q:103:ARG:NH2	2.37	0.57
17:Q:74:ARG:HG2	17:Q:74:ARG:NH1	2.20	0.57
20:T:110:LYS:HZ2	20:T:111:HIS:H	1.51	0.57
35:JA:138:TYR:HE1	35:JA:338:ASP:OD2	1.86	0.57
39:NA:110:LEU:HD13	39:NA:118:ILE:HD13	1.85	0.57
40:OA:33:TYR:CE2	40:OA:78:GLU:HG3	2.39	0.57
43:RA:17:VAL:HG11	43:RA:81:ILE:HG12	1.85	0.57
1:FB:790:A:OP1	4:NC:38:A:O2'	2.21	0.57
1:FB:1323:G:H2'	1:FB:1324:A:C8	2.39	0.57
2:GB:1094:U:H1'	2:GB:1096:A:C8	2.40	0.57
2:GB:2317:C:H2'	2:GB:2318:G:H5'	1.87	0.57
2:GB:2494:G:O2'	14:SB:80:GLU:HA	2.03	0.57
8:MB:61:ALA:HB2	8:MB:68:PRO:HD3	1.87	0.57
17:VB:91:ARG:HG2	17:VB:91:ARG:HH11	1.68	0.57
39:SC:122:GLU:O	39:SC:126:ARG:NE	2.26	0.57
2:B:479:A:N3	2:B:481:G:H5''	2.20	0.57
8:H:67:LYS:H	28:BA:6:HIS:CE1	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:20:ALA:HB3	9:I:23:ARG:HG3	1.86	0.57
11:K:46:VAL:HG23	11:K:48:MET:HG2	1.85	0.57
15:O:100:LEU:HD11	15:O:113:LEU:HD23	1.87	0.57
2:GB:1339:G:H5''	21:ZB:16:LYS:HD3	1.87	0.57
2:GB:2680:C:H5'	6:KB:189:PRO:HA	1.87	0.57
1:A:1368:G:H4'	44:SA:46:ARG:NH1	2.19	0.57
2:B:686:G:O5'	31:EA:11:LYS:NZ	2.38	0.57
2:B:1077:A:H3'	2:B:1078:U:H4'	1.85	0.57
2:B:2287:A:N6	2:B:2344:U:H3	1.99	0.57
2:B:2784:C:H1'	6:F:37:ARG:NH1	2.19	0.57
6:F:61:ARG:HG2	6:F:61:ARG:NH1	2.20	0.57
17:Q:74:ARG:HD3	17:Q:76:PHE:CZ	2.39	0.57
16:UB:15:ARG:HG2	16:UB:88:ASP:OD2	2.04	0.57
22:V:44:ILE:H	22:V:44:ILE:HD13	1.67	0.57
25:Y:95:LEU:HD12	25:Y:98:LEU:HD12	1.86	0.57
2:GB:2166:G:N7	2:GB:2168:G:N2	2.52	0.57
13:RB:2:LYS:HB3	13:RB:2:LYS:NZ	2.20	0.57
23:BC:4:ARG:NH1	23:BC:60:GLU:HG2	2.20	0.57
38:RC:9:CYS:SG	38:RC:26:CYS:SG	3.03	0.57
45:YC:99:GLN:HE21	52:FD:88:LYS:NZ	2.03	0.57
49:CD:88:ARG:NH2	49:CD:88:ARG:HB3	2.20	0.57
1:A:452:A:OP1	50:YA:43:LYS:NZ	2.38	0.57
1:A:1124:G:N7	1:A:1145:C:O2'	2.37	0.57
2:B:2021:C:OP1	29:CA:12:SER:OG	2.23	0.57
8:H:122:PRO:HG2	8:H:182:LYS:HG2	1.86	0.57
36:KA:32:ILE:HD11	36:KA:40:HIS:HB3	1.87	0.57
36:KA:74:LYS:HE3	36:KA:206:ASP:HA	1.86	0.57
43:RA:83:ARG:HG2	43:RA:102:LEU:HD23	1.86	0.57
47:VA:22:ILE:HD12	47:VA:25:ILE:HD12	1.87	0.57
1:FB:1158:C:O2'	36:PC:133:LYS:NZ	2.38	0.57
10:OB:61:ARG:HD3	10:OB:64:GLU:OE2	2.04	0.57
42:VC:112:LEU:HA	42:VC:134:ILE:HG12	1.87	0.57
43:WC:17:VAL:HG11	43:WC:81:ILE:HG12	1.85	0.57
1:A:999:U:H3	1:A:1041:A:H62	1.52	0.57
13:M:71:VAL:HG22	13:M:72:PRO:HA	1.86	0.57
20:T:30:GLU:OE2	20:T:30:GLU:HA	2.04	0.57
23:W:4:ARG:NH1	23:W:60:GLU:HG2	2.19	0.57
24:X:2:ALA:HA	35:JA:236:HIS:CE1	2.39	0.57
37:LA:85:ARG:HG2	37:LA:88:ARG:NH2	2.20	0.57
47:VA:14:ARG:HE	47:VA:42:ALA:HA	1.69	0.57
1:FB:706:A:H5''	45:YC:22:HIS:CD2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:270(Q):C:OP2	2:GB:270(Q):C:H6	1.87	0.57
2:GB:796:C:H2'	2:GB:797:C:C6	2.40	0.57
5:JB:148:GLU:HB2	5:JB:151:LYS:HD2	1.87	0.57
10:OB:57:ARG:HB3	10:OB:61:ARG:HH22	1.70	0.57
1:A:1005:A:N6	1:A:1024:G:O2'	2.37	0.56
2:B:1291:C:H2'	2:B:1292:U:H6	1.70	0.56
2:B:2795:G:H1'	2:B:2802:G:N2	2.20	0.56
8:H:61:ALA:HB2	8:H:68:PRO:HD3	1.87	0.56
36:KA:97:TRP:HH2	36:KA:176:GLU:OE2	1.87	0.56
41:PA:74:GLU:HG2	41:PA:91:VAL:HG22	1.87	0.56
1:FB:539:A:H2'	1:FB:540:G:C8	2.40	0.56
2:GB:34:C:O2'	2:GB:35:G:OP1	2.22	0.56
2:GB:896:A:OP2	2:GB:896:A:H4'	2.04	0.56
2:GB:1045:A:O2'	2:GB:1047:G:N3	2.32	0.56
2:GB:1667:G:O2'	2:GB:1991:U:O4	2.19	0.56
8:MB:19:LEU:HD13	8:MB:32:PRO:HG2	1.86	0.56
9:NB:20:ALA:HB3	9:NB:23:ARG:HG3	1.86	0.56
14:SB:60:ARG:NH2	23:BC:114:GLY:HA3	2.20	0.56
36:PC:126:GLU:HA	36:PC:129:GLU:OE2	2.04	0.56
42:VC:116:LYS:HD2	42:VC:129:VAL:HG11	1.86	0.56
2:B:1800:C:OP2	5:E:183:ARG:NH2	2.38	0.56
2:B:2508:G:OP1	35:JA:228:ARG:NH2	2.36	0.56
2:B:2680:C:H5'	6:F:189:PRO:HA	1.87	0.56
17:Q:100:TYR:CD1	17:Q:103:ARG:NH1	2.73	0.56
36:KA:46:LYS:HA	36:KA:49:GLU:HB3	1.87	0.56
4:IB:21:A:O4'	4:IB:48:C:N4	2.38	0.56
28:GC:62:ARG:HA	28:GC:62:ARG:CZ	2.35	0.56
38:RC:201:GLN:HE21	39:SC:99:GLY:HA2	1.70	0.56
2:B:2552:2MU:H6	2:B:2552:2MU:O5'	2.06	0.56
4:D:43:A:H2'	4:D:44:A:C8	2.41	0.56
8:H:148:MET:HE1	28:BA:28:LYS:NZ	2.21	0.56
10:J:1:MET:N	10:J:21:VAL:O	2.38	0.56
10:J:61:ARG:HD3	10:J:64:GLU:OE2	2.05	0.56
18:R:69:CYS:HB3	18:R:74:LEU:O	2.05	0.56
36:KA:126:GLU:HA	36:KA:129:GLU:OE2	2.04	0.56
39:NA:139:LEU:HA	39:NA:142:LEU:HD22	1.87	0.56
1:FB:222:U:H2'	1:FB:223:U:C6	2.40	0.56
1:FB:537:G:OP1	46:ZC:113:ARG:NH2	2.29	0.56
1:FB:1004:A:N6	1:FB:1026:G:OP2	2.37	0.56
2:GB:2792:G:H2'	2:GB:2793:G:C8	2.40	0.56
5:JB:96:HIS:CD2	5:JB:102:LYS:HG2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:MC:14:A:H3'	34:MC:15:A:C8	2.40	0.56
36:PC:47:THR:HA	36:PC:202:PRO:HG2	1.88	0.56
1:A:1003:G:H2'	1:A:1004:A:H4'	1.87	0.56
39:NA:77:PRO:HG2	39:NA:78:HIS:CD2	2.41	0.56
49:XA:17:ARG:HD3	49:XA:26:GLU:OE2	2.06	0.56
54:CB:30:LYS:HB2	54:CB:30:LYS:NZ	2.19	0.56
2:GB:154:G:H2'	2:GB:155:C:O2	2.06	0.56
2:GB:270(M):U:H3'	2:GB:270(M):U:OP2	2.05	0.56
2:GB:2543:G:H2'	2:GB:2544:G:C8	2.40	0.56
15:TB:18:LEU:HD21	15:TB:22:ARG:NH1	2.19	0.56
54:HD:30:LYS:HB2	54:HD:30:LYS:NZ	2.21	0.56
4:D:21:A:O4'	4:D:48:C:N4	2.38	0.56
12:L:75:SER:HB2	17:Q:74:ARG:HH12	1.70	0.56
24:X:12:ASN:HA	24:X:14:ARG:HH21	1.70	0.56
43:RA:50:LEU:HA	43:RA:53:VAL:HG22	1.88	0.56
1:FB:1086:U:H3	1:FB:1099:G:H22	1.53	0.56
2:GB:882:G:O6	2:GB:894:C:N4	2.38	0.56
2:GB:2138:C:H42	2:GB:2153:G:H1	1.51	0.56
9:NB:60:ARG:NH1	9:NB:60:ARG:HB3	2.21	0.56
39:SC:9:LYS:HB3	39:SC:33:VAL:HG13	1.87	0.56
2:B:2139:C:H3'	2:B:2140:C:H6	1.70	0.56
10:J:62:LYS:HD2	10:J:135:GLU:OE2	2.06	0.56
14:N:51:ARG:HG3	14:N:66:ILE:HD11	1.88	0.56
37:LA:130:VAL:O	37:LA:134:ILE:HG12	2.06	0.56
40:OA:15:ASP:OD1	40:OA:18:GLN:N	2.26	0.56
49:XA:82:ILE:HD12	49:XA:88:ARG:NH2	2.19	0.56
1:FB:740:U:OP1	49:CD:38:ARG:HD3	2.04	0.56
2:GB:784:A:H5'	2:GB:785:G:OP1	2.06	0.56
2:GB:1077:A:H3'	2:GB:1078:U:H4'	1.86	0.56
2:GB:2795:G:H1'	2:GB:2802:G:N2	2.20	0.56
8:MB:148:MET:HE1	28:GC:28:LYS:NZ	2.21	0.56
20:YB:8:ARG:HB2	20:YB:102:HIS:ND1	2.20	0.56
36:PC:46:LYS:HA	36:PC:49:GLU:HB3	1.87	0.56
39:SC:31:LEU:HD22	39:SC:43:LEU:HD11	1.88	0.56
39:SC:105:VAL:HB	39:SC:106:PRO:HD3	1.88	0.56
1:A:1422:G:O3'	12:L:49:ARG:NH1	2.37	0.56
2:B:84:A:P	22:V:8:LYS:HZ2	2.21	0.56
2:B:2552:2MU:H2'	2:B:2554:U:OP2	2.05	0.56
9:I:109:PHE:CE1	9:I:152:ARG:NH1	2.73	0.56
23:W:80:ARG:HG2	23:W:82:ARG:HH22	1.71	0.56
44:SA:62:HIS:HB3	48:WA:59:ALA:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:299:G:H2'	1:FB:300:A:C8	2.40	0.56
2:GB:1434:A:H61	2:GB:1558:A:N6	2.00	0.56
13:RB:71:VAL:HG22	13:RB:72:PRO:HA	1.86	0.56
13:RB:91:PHE:O	13:RB:121:LYS:NZ	2.38	0.56
17:VB:73:GLU:OE1	17:VB:103:ARG:NH2	2.39	0.56
4:NC:23:C:H2'	4:NC:24:U:C6	2.41	0.56
36:PC:48:MET:HA	36:PC:51:LEU:HB2	1.86	0.56
39:SC:110:LEU:HD13	39:SC:118:ILE:HD13	1.88	0.56
42:VC:28:ALA:HB3	42:VC:57:PRO:HB2	1.86	0.56
43:WC:50:LEU:HA	43:WC:53:VAL:HG22	1.88	0.56
1:A:706:A:H4'	45:TA:22:HIS:CD2	2.40	0.56
2:B:880:G:H1	2:B:897:C:H42	1.54	0.56
2:B:1532:C:H42	2:B:1539:G:H1	1.53	0.56
7:G:107:LYS:NZ	7:G:207:GLY:H	2.03	0.56
1:FB:624:C:H2'	1:FB:625:G:H8	1.71	0.56
1:FB:1118:C:H1'	1:FB:1179:A:C5	2.41	0.56
1:FB:1492:A:N6	46:ZC:48:PRO:O	2.38	0.56
15:TB:12:ARG:HG3	15:TB:12:ARG:NH1	2.20	0.56
36:PC:97:TRP:HH2	36:PC:176:GLU:OE2	1.89	0.56
49:CD:35:ARG:HG3	49:CD:35:ARG:NH1	2.21	0.56
2:B:2724:C:OP1	6:F:118:LYS:NZ	2.39	0.56
6:F:12:THR:HG21	17:Q:11:GLU:OE2	2.05	0.56
46:UA:117:ARG:HB3	46:UA:122:THR:HB	1.87	0.56
1:FB:999:U:H3	1:FB:1041:A:H62	1.53	0.56
1:FB:1005:A:H1'	1:FB:1026:G:H1	1.71	0.56
1:FB:1167:A:H8	1:FB:1167:A:OP1	1.88	0.56
2:GB:784:A:C5	5:JB:229:VAL:HG21	2.40	0.56
2:GB:1019:U:OP1	2:GB:1035:U:O2'	2.21	0.56
2:GB:2139:C:H3'	2:GB:2140:C:H6	1.71	0.56
22:AC:15:VAL:HG21	22:AC:42:VAL:HG11	1.88	0.56
1:A:164:U:H2'	1:A:165:C:C6	2.41	0.56
1:A:773:G:O3'	5:E:202:LYS:NZ	2.38	0.56
1:A:973:G:OP1	44:SA:57:LYS:NZ	2.29	0.56
2:B:882:G:O6	2:B:894:C:N4	2.38	0.56
2:B:1025:G:C4	2:B:1135:C:H1'	2.41	0.56
23:W:4:ARG:HH11	23:W:60:GLU:HG2	1.69	0.56
36:KA:47:THR:HA	36:KA:202:PRO:HG2	1.87	0.56
2:GB:606:U:OP2	7:LB:104:LYS:HE3	2.06	0.56
8:MB:67:LYS:H	28:GC:6:HIS:CE1	2.23	0.56
9:NB:136:ILE:H	9:NB:136:ILE:HD12	1.71	0.56
11:PB:13:TRP:CE2	11:PB:133:GLN:HG2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:YB:30:GLU:HA	20:YB:30:GLU:OE2	2.05	0.56
45:YC:18:ARG:HH21	45:YC:36:ASP:C	2.14	0.56
51:ED:86:GLU:O	51:ED:90:ILE:HG22	2.06	0.56
1:A:652:U:O4	1:A:752:G:O2'	2.20	0.55
2:B:857:C:H4'	24:X:23:VAL:HG21	1.88	0.55
2:B:1786:A:H1'	2:B:1938:A:N6	2.21	0.55
2:B:2439:A:H5'	2:B:2439:A:C8	2.41	0.55
7:G:184:TYR:O	7:G:188:ARG:HG3	2.05	0.55
39:NA:9:LYS:HB3	39:NA:33:VAL:HG13	1.88	0.55
4:IB:17:C:OP2	4:IB:17(A):U:O2'	2.24	0.55
17:VB:77:PRO:HB2	17:VB:80:SER:HB2	1.87	0.55
25:DC:95:LEU:HD12	25:DC:98:LEU:HD12	1.89	0.55
38:RC:18:LYS:CE	38:RC:26:CYS:SG	2.94	0.55
1:A:982:U:OP2	48:WA:23:ARG:NH2	2.39	0.55
7:G:119:ARG:HB2	7:G:119:ARG:NH1	2.19	0.55
9:I:136:ILE:H	9:I:136:ILE:HD12	1.72	0.55
6:KB:61:ARG:HG2	6:KB:61:ARG:NH1	2.21	0.55
8:MB:98:ARG:HG3	8:MB:98:ARG:NH1	2.05	0.55
19:XB:58:VAL:HG21	19:XB:100:ARG:HH21	1.71	0.55
46:ZC:83:VAL:HG21	46:ZC:100:ILE:HD13	1.86	0.55
49:CD:3:ILE:HD13	49:CD:34:LEU:HD23	1.88	0.55
54:HD:13:LEU:O	54:HD:17:ARG:HG3	2.07	0.55
1:A:108:G:N1	54:CB:15:ARG:HG2	2.21	0.55
2:B:2347:C:OP1	30:DA:38:LYS:NZ	2.39	0.55
2:B:2543:G:H2'	2:B:2544:G:C8	2.41	0.55
5:E:26:LYS:HD3	5:E:83:GLU:OE2	2.06	0.55
6:F:11:MET:HG2	6:F:24:THR:HB	1.88	0.55
22:V:15:VAL:HG21	22:V:42:VAL:HG11	1.87	0.55
22:V:92:ASN:OD1	22:V:93:GLY:N	2.39	0.55
42:QA:51:VAL:HG11	42:QA:60:ARG:HH12	1.70	0.55
1:FB:1269:A:N1	1:FB:1312:G:O2'	2.37	0.55
23:BC:80:ARG:HG2	23:BC:82:ARG:HH22	1.72	0.55
49:CD:25:THR:HG21	49:CD:70:LEU:HB2	1.89	0.55
2:B:751:A:H5'	20:T:90:ARG:HA	1.89	0.55
2:B:2327:A:H2'	2:B:2328:A:C8	2.40	0.55
36:KA:161:ALA:HB1	36:KA:185:ILE:HD11	1.88	0.55
43:RA:10:ARG:HG3	43:RA:105:ASP:HB3	1.88	0.55
1:FB:1005:A:H1'	1:FB:1026:G:N1	2.22	0.55
37:QC:148:GLY:HA3	37:QC:172:ARG:O	2.07	0.55
38:RC:12:CYS:SG	38:RC:18:LYS:HE3	2.46	0.55
38:RC:142:PRO:HA	38:RC:185:PHE:HD2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:330:A:H2	2:B:1210:A:H2'	1.71	0.55
39:NA:15:ARG:HD2	39:NA:26:PHE:CG	2.41	0.55
2:GB:2096:U:H2'	2:GB:2097:C:C6	2.41	0.55
22:AC:46:LYS:HG2	22:AC:60:PHE:CD1	2.42	0.55
1:A:266:G:H3'	51:ZA:67:LYS:HB2	1.87	0.55
1:A:981:U:H5'	48:WA:21:TYR:CE2	2.42	0.55
1:A:1080:A:OP1	39:NA:47:LYS:HD3	2.07	0.55
1:A:1423:G:P	12:L:49:ARG:HH12	2.29	0.55
2:B:320:A:OP2	7:G:137:LYS:HE2	2.07	0.55
2:B:1069:A:N7	2:B:1073:A:N6	2.49	0.55
10:J:27:ARG:HD2	25:Y:71:TYR:CE2	2.42	0.55
14:N:60:ARG:NH2	23:W:114:GLY:HA3	2.21	0.55
51:ZA:59:ILE:HG22	51:ZA:73:VAL:HA	1.88	0.55
1:FB:344:A:H4'	1:FB:345:C:OP2	2.06	0.55
2:GB:1021:A:C8	2:GB:1021:A:H3'	2.42	0.55
2:GB:1091:G:N2	2:GB:1100:C:O2'	2.40	0.55
15:TB:104:ARG:NH1	15:TB:107:ASP:OD2	2.38	0.55
17:VB:74:ARG:HD3	17:VB:76:PHE:CZ	2.40	0.55
40:TC:101:ALA:OXT	52:FD:28:GLU:HB2	2.07	0.55
42:VC:11:THR:HG23	42:VC:14:ARG:NH1	2.22	0.55
49:CD:82:ILE:HD12	49:CD:88:ARG:NH2	2.22	0.55
1:A:1516:G:N1	1:A:1519:MA6:OP2	2.39	0.55
36:KA:84:GLU:HB3	36:KA:219:VAL:HG21	1.88	0.55
54:CB:10:LEU:HD12	54:CB:12:ALA:H	1.71	0.55
2:GB:2376:A:N6	16:UB:89:ARG:HD3	2.22	0.55
1:A:865:A:H5'	1:A:1078:U:C4	2.42	0.55
1:A:1269:A:N1	1:A:1312:G:O2'	2.37	0.55
2:B:363(F):U:H3'	2:B:363(G):A:C8	2.38	0.55
12:L:1:MET:HE3	12:L:32:TYR:CE2	2.41	0.55
35:JA:116:ARG:HH11	35:JA:298:LEU:HD21	1.72	0.55
35:JA:248:HIS:HB3	35:JA:253:ILE:HG23	1.89	0.55
45:TA:31:THR:HG22	45:TA:42:TRP:HB2	1.88	0.55
1:FB:7:G:H5'	1:FB:298:A:O4'	2.06	0.55
1:FB:706:A:H4'	45:YC:22:HIS:CD2	2.35	0.55
2:GB:330:A:H2	2:GB:1210:A:H2'	1.70	0.55
18:WB:69:CYS:HB3	18:WB:74:LEU:O	2.07	0.55
43:WC:95:LYS:H	43:WC:98:PRO:HG2	1.72	0.55
1:A:1147:C:O2'	43:RA:16:ARG:HD2	2.06	0.55
2:B:1339:G:H5''	21:U:16:LYS:HD3	1.88	0.55
2:B:2171:A:O2'	2:B:2172:U:H5''	2.06	0.55
2:B:2376:A:N6	16:P:89:ARG:HD3	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:101:ARG:HH11	9:I:122:THR:HG23	1.71	0.55
11:K:13:TRP:CE2	11:K:133:GLN:HG2	2.42	0.55
36:KA:185:ILE:HG23	36:KA:199:TYR:HB2	1.88	0.55
41:PA:28:ASN:OD1	41:PA:36:LYS:NZ	2.39	0.55
42:QA:11:THR:HG23	42:QA:14:ARG:NH1	2.22	0.55
2:GB:1021:A:H8	2:GB:1022:G:H5''	1.72	0.55
2:GB:1045:A:H1'	2:GB:1047:G:H1'	1.88	0.55
2:GB:2313:C:H4'	8:MB:91:ARG:HG3	1.88	0.55
2:GB:2327:A:H2'	2:GB:2328:A:C8	2.42	0.55
10:OB:91:SER:O	10:OB:93:THR:N	2.40	0.55
24:CC:6:GLY:HA3	4:NC:1:C:O2	2.07	0.55
35:OC:248:HIS:HB2	35:OC:274:LEU:HD11	1.87	0.55
51:ED:52:LYS:NZ	51:ED:52:LYS:HB3	2.22	0.55
54:HD:56:MET:HG3	54:HD:88:VAL:HG21	1.89	0.55
2:B:154:G:H2'	2:B:155:C:O2	2.07	0.55
2:B:1939:5MU:OP1	2:B:2604:U:O2'	2.22	0.55
2:B:2304:G:H22	2:B:2312:U:H3	1.54	0.55
8:H:19:LEU:HD13	8:H:32:PRO:HG2	1.88	0.55
31:EA:34:ARG:HG2	31:EA:34:ARG:HH11	1.70	0.55
35:JA:247:THR:HG23	35:JA:254:VAL:HG22	1.89	0.55
42:QA:28:ALA:HB3	42:QA:57:PRO:HB2	1.89	0.55
45:TA:67:ASP:HA	45:TA:70:LYS:HE2	1.89	0.55
2:GB:2171:A:O2'	2:GB:2172:U:H5''	2.06	0.55
13:RB:93:GLY:H	13:RB:123:LEU:HD22	1.72	0.55
13:RB:124:LYS:HE2	13:RB:144:GLU:OE2	2.06	0.55
28:GC:24:THR:OG1	28:GC:25:TYR:N	2.39	0.55
28:GC:62:ARG:HA	28:GC:62:ARG:NH1	2.21	0.55
1:A:59:A:H3'	1:A:331:G:H22	1.72	0.54
1:A:1005:A:H1'	1:A:1026:G:H1	1.71	0.54
2:B:1060:U:H5''	2:B:1061:U:H3'	1.88	0.54
14:N:116:GLU:OE2	14:N:119:ARG:NH2	2.40	0.54
46:UA:24:VAL:HB	46:UA:27:LEU:HD22	1.89	0.54
48:WA:21:TYR:HE1	48:WA:23:ARG:NH1	2.05	0.54
1:FB:474:G:OP2	50:DD:75:ARG:NH1	2.40	0.54
1:FB:646:U:H2'	1:FB:647:C:C6	2.43	0.54
2:GB:1085:A:O2'	2:GB:1104:C:O2'	2.25	0.54
6:KB:12:THR:HG21	17:VB:11:GLU:OE2	2.07	0.54
10:OB:38:LEU:HB3	10:OB:40:THR:HG23	1.87	0.54
42:VC:51:VAL:HG11	42:VC:60:ARG:HH12	1.72	0.54
49:XA:21:ASP:OD2	49:XA:24:SER:HB3	2.08	0.54
1:FB:1003:G:H2'	1:FB:1004:A:H4'	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:154(A):C:O2'	2:GB:155:C:N3	2.40	0.54
10:OB:76:THR:HG22	10:OB:141:LYS:HD2	1.90	0.54
10:OB:133:HIS:CE1	10:OB:135:GLU:HB3	2.42	0.54
23:BC:4:ARG:HH11	23:BC:60:GLU:HG2	1.70	0.54
36:PC:23:ARG:HB2	36:PC:23:ARG:HH11	1.68	0.54
41:UC:74:GLU:HG2	41:UC:91:VAL:HG22	1.88	0.54
2:B:1019:U:OP1	2:B:1035:U:O2'	2.23	0.54
7:G:116:ASP:OD2	13:M:1:MET:N	2.36	0.54
13:M:81:GLN:OE1	13:M:107:LYS:N	2.32	0.54
15:O:12:ARG:HG3	15:O:12:ARG:NH1	2.20	0.54
35:JA:248:HIS:HB2	35:JA:274:LEU:HD11	1.89	0.54
2:GB:2439:A:H5'	2:GB:2439:A:C8	2.42	0.54
4:IB:52:G:H1	4:IB:62:C:H42	1.55	0.54
14:SB:81:VAL:HG12	24:CC:5:LYS:HD2	1.89	0.54
27:FC:1:MET:HE3	27:FC:39:ASP:HB3	1.89	0.54
49:CD:21:ASP:OD2	49:CD:24:SER:HB3	2.07	0.54
1:FB:723:U:H1'	1:FB:724:G:OP1	2.08	0.54
2:GB:1796:U:H2'	2:GB:1797:C:C6	2.42	0.54
2:GB:2151:G:N2	2:GB:2152:G:O6	2.40	0.54
1:A:222:U:H2'	1:A:223:U:C6	2.43	0.54
1:A:1358:U:OP1	48:WA:35:ARG:HG2	2.07	0.54
2:B:277:C:H4'	2:B:278:A:OP2	2.08	0.54
2:B:1358:G:O2'	2:B:1359:A:H5''	2.07	0.54
31:EA:34:ARG:HG2	31:EA:34:ARG:NH1	2.22	0.54
39:NA:105:VAL:HB	39:NA:106:PRO:HD3	1.88	0.54
40:OA:101:ALA:OXT	52:AB:28:GLU:HB2	2.07	0.54
1:FB:179:A:H2'	1:FB:180:U:H6	1.72	0.54
1:FB:180:U:H2'	1:FB:181:G:H5'	1.90	0.54
1:FB:1347:G:C8	43:WC:107:ARG:HG3	2.43	0.54
2:GB:1728:G:H8	2:GB:1732:A:H62	1.55	0.54
13:RB:94:GLU:OE2	13:RB:124:LYS:HD2	2.07	0.54
24:CC:12:ASN:HA	24:CC:14:ARG:NH2	2.23	0.54
30:IC:34:LEU:H	30:IC:51:GLU:HB2	1.72	0.54
39:SC:20:GLN:HG2	39:SC:25:ARG:HD2	1.89	0.54
1:A:109:A:C6	1:A:326:G:C6	2.96	0.54
22:V:46:LYS:HG2	22:V:60:PHE:CD1	2.42	0.54
31:EA:47:ARG:HB3	31:EA:47:ARG:NH1	2.22	0.54
37:LA:61:ALA:O	37:LA:63:ASN:ND2	2.40	0.54
38:MA:9:CYS:SG	38:MA:26:CYS:SG	3.06	0.54
1:FB:1358:U:OP1	48:BD:35:ARG:HG2	2.07	0.54
2:GB:207:A:H2'	2:GB:208:C:O4'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:2208:U:H2'	2:GB:2209:C:C6	2.43	0.54
14:SB:65:PHE:HB2	14:SB:105:GLU:HB2	1.90	0.54
21:ZB:90:GLU:HA	21:ZB:93:GLU:HG2	1.89	0.54
2:B:2115:G:H4'	2:B:2167:U:C2	2.43	0.54
9:I:3:ARG:NH1	9:I:3:ARG:HA	2.23	0.54
12:L:45:GLU:HA	12:L:54:GLU:OE2	2.06	0.54
22:V:38:ILE:HD11	22:V:66:PRO:HG3	1.88	0.54
23:W:185:GLU:HA	23:W:188:ALA:HB3	1.90	0.54
36:KA:131:PRO:HB2	36:KA:134:GLU:HG2	1.90	0.54
43:RA:105:ASP:OD2	43:RA:107:ARG:HG2	2.07	0.54
1:FB:109:A:C6	1:FB:326:G:C6	2.95	0.54
1:FB:673:G:H2'	1:FB:674:G:C8	2.43	0.54
2:GB:1011:G:OP1	18:WB:77:SER:HB2	2.07	0.54
2:GB:1805:U:O2	5:JB:50:THR:HB	2.07	0.54
2:GB:2593:U:H2'	2:GB:2594:C:C6	2.42	0.54
9:NB:164:TYR:HB2	9:NB:167:GLU:HB2	1.89	0.54
25:DC:40:ARG:C	25:DC:40:ARG:HD3	2.32	0.54
1:A:224:C:H2'	1:A:225:C:C6	2.42	0.54
1:A:1118:C:H1'	1:A:1179:A:C5	2.43	0.54
2:B:507:A:O2'	2:B:508:G:OP2	2.24	0.54
9:I:28:GLY:HA3	9:I:79:VAL:HB	1.90	0.54
19:S:72:VAL:HG13	19:S:85:LYS:HB3	1.88	0.54
26:Z:2:LYS:H	26:Z:2:LYS:HD3	1.73	0.54
42:QA:112:LEU:HA	42:QA:134:ILE:HG12	1.89	0.54
43:RA:29:ASN:N	43:RA:63:ILE:O	2.32	0.54
1:FB:108:G:N1	54:HD:15:ARG:HG2	2.23	0.54
44:XC:6:ILE:HD11	44:XC:72:VAL:HB	1.90	0.54
46:ZC:28:LYS:NZ	46:ZC:64:TYR:HE2	2.05	0.54
1:A:646:U:H2'	1:A:647:C:C6	2.43	0.54
8:H:113:ARG:NH2	8:H:139:LEU:O	2.41	0.54
38:MA:196:LEU:O	38:MA:198:VAL:N	2.39	0.54
2:GB:1069:A:N7	2:GB:1073:A:N6	2.50	0.54
2:GB:2875:C:O2'	17:VB:2:ASN:OD1	2.25	0.54
11:PB:35:ARG:HA	11:PB:116:LEU:HD13	1.90	0.54
13:RB:124:LYS:HG3	13:RB:144:GLU:OE2	2.08	0.54
42:VC:11:THR:HG23	42:VC:14:ARG:HH12	1.71	0.54
44:XC:50:ILE:HB	48:BD:41:ARG:NH1	2.22	0.54
1:A:7:G:H5'	1:A:298:A:O4'	2.07	0.54
1:A:1005:A:H1'	1:A:1026:G:N1	2.22	0.54
1:A:1226:C:H4'	53:BB:80:TYR:CZ	2.42	0.54
1:A:1253:G:H1	1:A:1284:C:H42	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1347:G:C8	43:RA:107:ARG:HG3	2.43	0.54
2:B:2096:U:H2'	2:B:2097:C:C6	2.42	0.54
36:KA:78:GLN:OE1	36:KA:94:ASN:ND2	2.41	0.54
37:LA:33:LEU:HD21	48:WA:53:LEU:HD22	1.90	0.54
49:XA:30:ALA:HA	49:XA:85:LEU:HD11	1.90	0.54
1:FB:1147:C:O2'	43:WC:16:ARG:HD2	2.07	0.54
2:GB:848:G:O6	2:GB:929:G:H2'	2.07	0.54
2:GB:2347:C:OP1	30:IC:38:LYS:NZ	2.41	0.54
3:HB:86:G:H1	3:HB:90:C:H42	1.55	0.54
47:AD:54:VAL:HG22	47:AD:57:ARG:HH12	1.73	0.54
1:A:721:G:H4'	1:A:722:A:O4'	2.07	0.53
1:A:723:U:H1'	1:A:724:G:OP1	2.08	0.53
2:B:34:C:HO2'	2:B:35:G:P	2.30	0.53
2:B:2494:G:O2'	14:N:80:GLU:HA	2.07	0.53
9:I:60:ARG:NH1	9:I:60:ARG:HB3	2.22	0.53
1:FB:1133:G:H1	1:FB:1141:C:N4	2.07	0.53
2:GB:887:A:H1'	2:GB:890:A:H61	1.73	0.53
12:QB:98:VAL:HG22	12:QB:118:ALA:HA	1.91	0.53
14:SB:1:MET:SD	14:SB:45:GLN:NE2	2.81	0.53
43:WC:29:ASN:N	43:WC:63:ILE:O	2.29	0.53
55:ID:2:GLY:C	55:ID:4:GLY:H	2.15	0.53
1:A:624:C:H2'	1:A:625:G:H8	1.73	0.53
2:B:443:A:H1'	2:B:1201:C:O4'	2.07	0.53
2:B:975:G:H1'	2:B:990:A:C2	2.43	0.53
2:B:2208:U:H2'	2:B:2209:C:C6	2.42	0.53
11:K:138:LEU:HD13	11:K:139:GLU:H	1.73	0.53
34:HA:19:PSU:N3	35:JA:120:GLY:O	2.41	0.53
1:FB:59:A:H3'	1:FB:331:G:H22	1.73	0.53
2:GB:270(T):G:OP1	25:DC:76:ARG:NH1	2.40	0.53
2:GB:556:G:H2'	2:GB:557:U:C6	2.43	0.53
14:SB:18:LYS:O	14:SB:98:LYS:NZ	2.39	0.53
23:BC:185:GLU:HA	23:BC:188:ALA:HB3	1.90	0.53
38:RC:196:LEU:O	38:RC:198:VAL:N	2.39	0.53
43:WC:28:VAL:HG22	43:WC:63:ILE:HD12	1.89	0.53
2:B:1728:G:H8	2:B:1732:A:H62	1.54	0.53
25:Y:72:GLU:O	25:Y:76:ARG:HG3	2.08	0.53
4:IA:35:A:OP2	43:RA:128:ARG:NH1	2.42	0.53
36:KA:24:TRP:CZ3	36:KA:26:PRO:HA	2.43	0.53
38:MA:9:CYS:HG	38:MA:18:LYS:HZ2	1.54	0.53
42:QA:11:THR:HG23	42:QA:14:ARG:HH12	1.73	0.53
55:DB:2:GLY:C	55:DB:4:GLY:H	2.16	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:224:C:H2'	1:FB:225:C:C6	2.43	0.53
1:FB:666:G:H5'	1:FB:726:C:H1'	1.90	0.53
2:GB:1011:G:OP1	18:WB:75:ASN:HB2	2.09	0.53
14:SB:67:ARG:NH1	14:SB:105:GLU:OE2	2.40	0.53
33:LC:27:CYS:SG	33:LC:28:GLU:N	2.81	0.53
42:VC:4:ASP:OD2	42:VC:85:ARG:NE	2.41	0.53
51:ED:83:ASP:O	51:ED:86:GLU:HB2	2.08	0.53
2:B:289:A:H2'	2:B:290:G:O4'	2.08	0.53
2:B:1803:A:HO2'	5:E:259:THR:HG21	1.73	0.53
2:B:2804:C:H2'	2:B:2805:G:O4'	2.07	0.53
28:BA:24:THR:OG1	28:BA:25:TYR:N	2.41	0.53
2:GB:277:C:H4'	2:GB:278:A:OP2	2.09	0.53
2:GB:1130:U:O2	6:KB:149:ARG:NH2	2.42	0.53
8:MB:55:LYS:O	8:MB:58:GLN:HG3	2.08	0.53
24:CC:6:GLY:HA3	4:NC:1:C:H1'	1.89	0.53
35:OC:248:HIS:HB3	35:OC:253:ILE:HG23	1.91	0.53
37:QC:177:THR:HG22	37:QC:180:ALA:H	1.74	0.53
40:TC:99:ALA:O	52:FD:28:GLU:HG3	2.09	0.53
46:ZC:117:ARG:HB3	46:ZC:122:THR:HB	1.90	0.53
1:A:1189:C:OP1	44:SA:51:ARG:NH2	2.39	0.53
2:B:601:C:OP1	7:G:108:LYS:HE3	2.08	0.53
5:E:96:HIS:CD2	5:E:102:LYS:HG2	2.43	0.53
10:J:38:LEU:HB3	10:J:40:THR:HG23	1.91	0.53
17:Q:77:PRO:HB2	17:Q:80:SER:HB2	1.91	0.53
30:DA:34:LEU:H	30:DA:51:GLU:HB2	1.73	0.53
45:TA:18:ARG:HH21	45:TA:36:ASP:C	2.16	0.53
1:FB:652:U:O4	1:FB:752:G:O2'	2.21	0.53
1:FB:706:A:C5'	45:YC:22:HIS:HD2	2.22	0.53
1:FB:981:U:H5'	48:BD:21:TYR:CE2	2.44	0.53
2:GB:295:G:H4'	22:AC:1:MET:HE3	1.90	0.53
2:GB:1113:U:H2'	2:GB:1114:G:C8	2.43	0.53
26:EC:37:PHE:O	26:EC:41:ILE:HG13	2.09	0.53
46:ZC:24:VAL:HB	46:ZC:27:LEU:HD22	1.91	0.53
1:A:474:G:OP2	50:YA:75:ARG:NH1	2.41	0.53
2:B:307:G:N2	2:B:309:G:H3'	2.24	0.53
2:B:1113:U:H2'	2:B:1114:G:C8	2.44	0.53
2:B:2313:C:H4'	8:H:91:ARG:HG3	1.90	0.53
35:JA:311:ASN:HB3	35:JA:316:ARG:HG2	1.91	0.53
36:KA:23:ARG:HB2	36:KA:23:ARG:HH11	1.73	0.53
49:XA:88:ARG:NH2	49:XA:88:ARG:HB3	2.24	0.53
2:GB:2784:C:H1'	6:KB:37:ARG:NH1	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:IB:43:A:H2'	4:IB:44:A:C8	2.43	0.53
34:MC:19:PSU:N3	35:OC:120:GLY:O	2.41	0.53
35:OC:311:ASN:HB3	35:OC:316:ARG:HG2	1.90	0.53
46:ZC:8:ASN:O	46:ZC:12:ARG:HG3	2.09	0.53
47:AD:22:ILE:HD12	47:AD:25:ILE:HD12	1.88	0.53
49:CD:62:GLN:OE1	49:CD:65:ARG:NH1	2.41	0.53
52:FD:70:ILE:O	52:FD:74:ARG:HG3	2.09	0.53
1:A:1167:A:H8	1:A:1167:A:OP1	1.91	0.53
1:A:1423:G:OP1	12:L:49:ARG:NH2	2.36	0.53
2:B:270(T):G:OP1	25:Y:76:ARG:NH1	2.41	0.53
2:B:2232:U:OP2	25:Y:40:ARG:NH2	2.41	0.53
10:J:118:LYS:NZ	10:J:119:PRO:O	2.42	0.53
13:M:94:GLU:OE2	13:M:124:LYS:HD2	2.09	0.53
13:M:124:LYS:HG3	13:M:144:GLU:OE2	2.09	0.53
23:W:29:TYR:HB3	23:W:34:ASN:HD22	1.73	0.53
36:KA:68:ILE:HG12	36:KA:161:ALA:HB3	1.90	0.53
43:RA:4:TYR:HB3	43:RA:88:TYR:HB2	1.90	0.53
1:FB:185:A:N3	54:HD:81:LYS:NZ	2.57	0.53
1:FB:519:C:OP1	35:OC:183:ARG:NH1	2.42	0.53
2:GB:83:G:N2	2:GB:102:G:H1'	2.24	0.53
2:GB:289:A:H2'	2:GB:290:G:O4'	2.09	0.53
14:SB:76:LYS:HB3	14:SB:91:GLU:HG3	1.91	0.53
20:YB:110:LYS:NZ	20:YB:111:HIS:H	2.06	0.53
35:OC:116:ARG:HH11	35:OC:298:LEU:HD21	1.74	0.53
1:A:1129:C:H5''	43:RA:16:ARG:HH22	1.74	0.53
2:B:848:G:O6	2:B:929:G:H2'	2.09	0.53
2:B:887:A:H1'	2:B:890:A:H61	1.74	0.53
2:B:1805:U:O2	5:E:50:THR:HB	2.08	0.53
8:H:3:LEU:HD13	8:H:5:LEU:HD21	1.90	0.53
25:Y:50:ARG:HD2	25:Y:57:GLU:OE2	2.07	0.53
26:Z:22:GLU:OE2	26:Z:68:ARG:NH2	2.41	0.53
4:IA:33:U:OP2	43:RA:128:ARG:NH2	2.42	0.53
36:PC:84:GLU:HB3	36:PC:219:VAL:HG21	1.90	0.53
39:SC:15:ARG:HD2	39:SC:26:PHE:CG	2.44	0.53
1:A:1086:U:H3	1:A:1099:G:H22	1.57	0.53
2:B:2021:C:H4'	2:B:2022:U:OP2	2.09	0.53
10:J:133:HIS:CE1	10:J:135:GLU:HB3	2.44	0.53
38:MA:201:GLN:NE2	39:NA:116:THR:O	2.42	0.53
44:SA:35:SER:HB3	44:SA:73:ASP:OD2	2.09	0.53
49:XA:35:ARG:HG3	49:XA:35:ARG:NH1	2.20	0.53
49:XA:62:GLN:OE1	49:XA:65:ARG:NH1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:982:U:OP2	48:BD:23:ARG:NH2	2.42	0.53
12:QB:1:MET:HE3	12:QB:32:TYR:CE2	2.44	0.53
38:RC:71:SER:HB3	38:RC:74:GLN:HG3	1.91	0.53
1:A:706:A:N3	45:TA:31:THR:HG21	2.24	0.53
1:A:1133:G:H1	1:A:1141:C:N4	2.07	0.53
1:A:1460:A:OP2	54:CB:27:LYS:NZ	2.31	0.53
2:B:83:G:N2	2:B:102:G:H1'	2.24	0.53
2:B:556:G:H2'	2:B:557:U:C6	2.44	0.53
2:B:2648:C:H2'	2:B:2649:U:C6	2.44	0.53
42:QA:17:THR:HG22	42:QA:63:LEU:HG	1.91	0.53
46:UA:83:VAL:HG21	46:UA:100:ILE:HD13	1.90	0.53
51:ZA:6:LEU:HD23	51:ZA:23:VAL:HG11	1.91	0.53
2:GB:857:C:H4'	24:CC:23:VAL:HG21	1.90	0.53
4:IB:16:C:H5'	4:IB:17:C:H5	1.73	0.53
17:VB:100:TYR:HD1	17:VB:103:ARG:NH1	2.06	0.53
35:OC:109:ARG:NH1	35:OC:210:PRO:HD3	2.24	0.53
39:SC:139:LEU:HA	39:SC:142:LEU:HD22	1.90	0.53
40:TC:33:TYR:CE2	40:TC:78:GLU:HG3	2.44	0.53
44:XC:6:ILE:HG22	44:XC:98:ILE:HG22	1.91	0.53
1:A:666:G:H5'	1:A:726:C:H1'	1.91	0.52
2:B:848:G:H2'	2:B:849:A:C8	2.45	0.52
2:B:2789:C:O3'	2:B:2790:A:H4'	2.09	0.52
13:M:2:LYS:NZ	13:M:4:SER:OG	2.40	0.52
54:CB:13:LEU:O	54:CB:17:ARG:HG3	2.07	0.52
1:FB:269:C:H2'	1:FB:270:A:C8	2.44	0.52
1:FB:542:G:H5'	38:RC:41:GLY:HA3	1.91	0.52
1:FB:580:U:H2'	1:FB:581:G:O4'	2.09	0.52
2:GB:751:A:H5'	20:YB:90:ARG:HA	1.91	0.52
2:GB:2370:G:C6	2:GB:2371:G:C6	2.97	0.52
2:GB:2405:G:OP1	13:RB:77:ARG:NH2	2.41	0.52
4:IB:19:G:H1	4:IB:56:C:H42	1.56	0.52
35:OC:326:LEU:HD13	35:OC:328:ARG:NH1	2.24	0.52
37:QC:61:ALA:O	37:QC:63:ASN:ND2	2.42	0.52
1:A:269:C:H2'	1:A:270:A:C8	2.44	0.52
2:B:363(G):A:H1'	2:B:364:C:H5	1.74	0.52
26:Z:1:MET:HE1	26:Z:9:GLN:HG3	1.91	0.52
42:QA:51:VAL:HG11	42:QA:60:ARG:NH1	2.25	0.52
43:RA:28:VAL:HG22	43:RA:63:ILE:HD12	1.90	0.52
1:FB:614:A:H2'	1:FB:615:C:C6	2.45	0.52
2:GB:300:A:H2'	2:GB:334:C:H1'	1.91	0.52
2:GB:2552:2MU:H6	2:GB:2552:2MU:O5'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:OB:118:LYS:HZ1	10:OB:121:LYS:HG3	1.74	0.52
38:RC:18:LYS:NZ	38:RC:31:CYS:HG	2.00	0.52
50:DD:53:VAL:HG12	50:DD:57:ARG:HH11	1.73	0.52
1:A:1118:C:H2'	1:A:1119:C:C6	2.45	0.52
5:E:26:LYS:HB3	5:E:83:GLU:HG2	1.92	0.52
10:J:57:ARG:HB3	10:J:61:ARG:HH22	1.73	0.52
12:L:98:VAL:HG22	12:L:118:ALA:HA	1.92	0.52
38:MA:155:LEU:HD13	38:MA:156:GLU:N	2.25	0.52
45:TA:12:ARG:HG2	45:TA:13:GLN:HG2	1.92	0.52
1:FB:706:A:C4'	45:YC:22:HIS:HD2	2.20	0.52
35:OC:226:THR:HG23	35:OC:241:ASP:HB3	1.91	0.52
37:QC:61:ALA:O	37:QC:63:ASN:N	2.39	0.52
1:A:344:A:H4'	1:A:345:C:OP2	2.10	0.52
1:A:642:A:H2'	1:A:643:C:C6	2.45	0.52
1:A:693:G:H2'	1:A:694:A:C8	2.45	0.52
2:B:2079:U:OP1	25:Y:21:ARG:NH2	2.42	0.52
10:J:88:ILE:HD12	10:J:89:TYR:H	1.73	0.52
17:Q:94:ALA:HB1	17:Q:99:LEU:HD21	1.91	0.52
23:W:124:ILE:HD11	23:W:165:VAL:HG21	1.91	0.52
42:QA:4:ASP:OD2	42:QA:85:ARG:NE	2.42	0.52
1:FB:1391:U:H2'	1:FB:1392:G:C8	2.45	0.52
10:OB:93:THR:HG23	10:OB:95:LYS:H	1.74	0.52
1:A:353:A:H5'	1:A:353:A:H8	1.75	0.52
1:A:383:A:C5	1:A:384:G:H1'	2.44	0.52
2:B:774:A:H2'	2:B:774:A:N3	2.24	0.52
2:B:2232:U:P	25:Y:40:ARG:HH22	2.32	0.52
7:G:53:THR:HG22	7:G:56:GLU:HG3	1.91	0.52
14:N:47:ILE:HD12	14:N:70:PRO:HG3	1.92	0.52
1:FB:1129:C:H5''	43:WC:16:ARG:HH22	1.74	0.52
2:GB:307:G:N2	2:GB:309:G:H3'	2.25	0.52
24:CC:12:ASN:HA	24:CC:14:ARG:HH21	1.75	0.52
36:PC:166:ASP:HB3	36:PC:169:LYS:HB3	1.91	0.52
47:AD:14:ARG:HE	47:AD:42:ALA:HA	1.73	0.52
2:B:545:G:H21	2:B:548:A:H62	1.58	0.52
2:B:1047:G:H2'	2:B:1110:G:N1	2.25	0.52
2:B:1657:C:H2'	2:B:1658:C:H6	1.75	0.52
7:G:127:GLU:HB3	7:G:196:LEU:HD12	1.91	0.52
9:I:17:VAL:HG11	9:I:50:VAL:HG21	1.92	0.52
2:GB:2648:C:H2'	2:GB:2649:U:C6	2.44	0.52
5:JB:26:LYS:HD3	5:JB:83:GLU:OE2	2.10	0.52
27:FC:3:ARG:NH1	27:FC:60:GLU:OE1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:PC:131:PRO:HB2	36:PC:134:GLU:HG2	1.90	0.52
1:A:180:U:H2'	1:A:181:G:H5'	1.92	0.52
1:A:958:A:N3	1:A:985:C:O2'	2.43	0.52
2:B:140:A:H8	2:B:1408:C:O2'	1.91	0.52
2:B:550:G:O2'	2:B:1220:A:N3	2.39	0.52
2:B:1067:A:OP1	2:B:1068:G:N2	2.43	0.52
9:I:55:PRO:HG2	9:I:61:HIS:CE1	2.45	0.52
51:ZA:86:GLU:O	51:ZA:90:ILE:HG22	2.09	0.52
2:GB:2804:C:H2'	2:GB:2805:G:O4'	2.09	0.52
5:JB:62:TYR:HA	5:JB:87:ASN:ND2	2.24	0.52
29:HC:32:PRO:HG3	29:HC:39:MET:HE1	1.92	0.52
4:NC:33:U:OP2	43:WC:128:ARG:NH2	2.43	0.52
38:RC:176:LEU:HD12	38:RC:182:LYS:O	2.09	0.52
39:SC:78:HIS:ND1	42:VC:104:ARG:HD2	2.19	0.52
1:A:299:G:H2'	1:A:300:A:C8	2.45	0.52
2:B:270(M):U:H3'	2:B:270(M):U:OP2	2.10	0.52
8:H:136:ARG:HE	8:H:136:ARG:N	2.01	0.52
34:HA:14:A:H3'	34:HA:15:A:H8	1.74	0.52
44:SA:5:ARG:HG3	44:SA:73:ASP:HB3	1.90	0.52
44:SA:8:LEU:HG	44:SA:96:ILE:HG23	1.91	0.52
2:GB:320:A:H4'	2:GB:322:A:N7	2.25	0.52
2:GB:1709:U:H2'	2:GB:1710:C:C6	2.45	0.52
14:SB:60:ARG:HA	23:BC:178:GLU:O	2.10	0.52
36:PC:78:GLN:OE1	36:PC:94:ASN:ND2	2.42	0.52
37:QC:119:ARG:O	37:QC:123:GLN:HG3	2.09	0.52
42:VC:17:THR:HG22	42:VC:63:LEU:HG	1.91	0.52
45:YC:12:ARG:HG2	45:YC:13:GLN:HG2	1.91	0.52
1:A:539:A:H2'	1:A:540:G:C8	2.44	0.52
1:A:1397:C:O2'	1:A:1398:A:OP1	2.27	0.52
1:A:1496:C:H4'	2:B:1920:4OC:O2'	2.09	0.52
2:B:1568:G:P	5:E:63:ARG:HH22	2.33	0.52
2:B:1796:U:H2'	2:B:1797:C:C6	2.45	0.52
18:R:36:ARG:HD3	18:R:40:PHE:CZ	2.45	0.52
21:U:90:GLU:HA	21:U:93:GLU:HG2	1.92	0.52
36:KA:98:LEU:H	36:KA:101:MET:HE3	1.74	0.52
38:MA:50:ARG:HD3	38:MA:51:PRO:HD2	1.92	0.52
42:QA:92:ARG:HG2	42:QA:92:ARG:HH11	1.75	0.52
1:FB:706:A:C5'	45:YC:22:HIS:CD2	2.93	0.52
2:GB:1047:G:H2'	2:GB:1110:G:N1	2.25	0.52
2:GB:1490:A:O2'	5:JB:99:ASP:OD1	2.22	0.52
2:GB:2564:A:OP1	2:GB:2648:C:H4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:PC:24:TRP:CZ3	36:PC:26:PRO:HA	2.45	0.52
38:RC:43:HIS:CE1	38:RC:46:LYS:HZ2	2.27	0.52
40:TC:36:ARG:NH2	40:TC:66:GLU:OE1	2.41	0.52
44:XC:35:SER:HB3	44:XC:73:ASP:OD2	2.10	0.52
1:A:179:A:H2'	1:A:180:U:H6	1.74	0.52
1:A:531:U:H2'	35:JA:314:GLN:NE2	2.24	0.52
2:B:26:G:C6	2:B:27:G:N1	2.78	0.52
4:D:17:C:OP2	4:D:17(A):U:O2'	2.26	0.52
38:MA:71:SER:HB3	38:MA:74:GLN:HG3	1.92	0.52
44:SA:50:ILE:HB	48:WA:41:ARG:NH1	2.25	0.52
2:GB:848:G:H2'	2:GB:849:A:C8	2.45	0.52
7:LB:127:GLU:HB3	7:LB:196:LEU:HD12	1.91	0.52
9:NB:28:GLY:HA3	9:NB:79:VAL:HB	1.92	0.52
40:TC:1:MET:HE3	40:TC:66:GLU:HG2	1.91	0.52
44:XC:45:ARG:HG3	44:XC:47:PHE:HE2	1.75	0.52
48:BD:21:TYR:HE1	48:BD:23:ARG:NH1	2.08	0.52
1:A:731:G:OP1	1:A:766:A:H1'	2.09	0.51
3:C:16:G:N2	3:C:69:G:H1'	2.25	0.51
8:H:113:ARG:NH1	8:H:142:PRO:HA	2.25	0.51
10:J:83:ALA:HA	10:J:88:ILE:HG12	1.92	0.51
14:N:18:LYS:O	14:N:98:LYS:NZ	2.39	0.51
20:T:65:LEU:HD12	20:T:66:GLU:H	1.75	0.51
35:JA:109:ARG:NH1	35:JA:210:PRO:HD3	2.25	0.51
37:LA:58:GLU:HB2	37:LA:65:ALA:HB3	1.92	0.51
1:FB:1003:G:H1	1:FB:1038:C:H42	1.58	0.51
2:GB:1510:A:H2'	2:GB:1511:A:C8	2.45	0.51
2:GB:2115:G:H4'	2:GB:2167:U:C2	2.44	0.51
2:GB:2591:C:H2'	2:GB:2592:G:C8	2.45	0.51
13:RB:118:GLY:O	13:RB:137:LYS:NZ	2.34	0.51
13:RB:149:GLU:HA	13:RB:149:GLU:OE2	2.07	0.51
36:PC:161:ALA:HB1	36:PC:185:ILE:HD11	1.91	0.51
41:UC:115:ARG:O	41:UC:118:VAL:HB	2.11	0.51
1:A:509:A:N3	1:A:543:C:O2'	2.37	0.51
2:B:1405:U:H2'	2:B:1406:U:C6	2.45	0.51
4:D:16:C:H5'	4:D:17:C:H5	1.74	0.51
13:M:2:LYS:NZ	13:M:2:LYS:HB3	2.25	0.51
41:PA:57:GLU:H	41:PA:60:LYS:NZ	2.04	0.51
45:TA:99:GLN:HE21	52:AB:88:LYS:NZ	2.08	0.51
13:RB:81:GLN:HB2	13:RB:110:TYR:CD1	2.45	0.51
43:WC:10:ARG:HG3	43:WC:105:ASP:HB3	1.93	0.51
49:CD:88:ARG:HB3	49:CD:88:ARG:HH21	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:HD:54:LYS:HA	54:HD:57:ARG:NH1	2.25	0.51
1:A:595:G:H1'	1:A:596:C:H5	1.76	0.51
1:A:614:A:H2'	1:A:615:C:C6	2.45	0.51
1:A:1343:G:O2'	43:RA:121:ARG:NH1	2.42	0.51
1:A:1368:G:H4'	44:SA:46:ARG:HH11	1.76	0.51
2:B:2168:G:H2'	2:B:2169:A:H3'	1.93	0.51
6:F:174:ASP:OD1	6:F:175:VAL:N	2.43	0.51
37:LA:88:ARG:HD3	37:LA:101:LEU:HD22	1.91	0.51
37:LA:148:GLY:HA3	37:LA:172:ARG:O	2.10	0.51
38:MA:61:LYS:HD2	38:MA:207:TYR:OH	2.10	0.51
51:ZA:83:ASP:O	51:ZA:86:GLU:HB2	2.10	0.51
1:FB:1189:C:OP1	44:XC:51:ARG:NH2	2.40	0.51
1:FB:1226:C:H4'	53:GD:80:TYR:CZ	2.44	0.51
2:GB:363(G):A:H1'	2:GB:364:C:H5	1.74	0.51
2:GB:911:A:H2'	14:SB:9:TYR:OH	2.10	0.51
17:VB:18:ASP:OD1	17:VB:18:ASP:N	2.44	0.51
1:A:1128:C:H5''	43:RA:66:ARG:NH1	2.26	0.51
1:A:1350:A:O2'	41:PA:33:ASP:OD1	2.28	0.51
2:B:300:A:H2'	2:B:334:C:H1'	1.93	0.51
2:B:1021:A:H8	2:B:1022:G:H5''	1.75	0.51
2:B:1709:U:H2'	2:B:1710:C:C6	2.45	0.51
7:G:53:THR:HG23	7:G:55:GLY:H	1.75	0.51
13:M:93:GLY:H	13:M:123:LEU:HD22	1.76	0.51
13:M:140:ALA:HA	2:GB:928:G:H5'	1.92	0.51
14:N:37:LEU:HD21	14:N:130:LYS:HD3	1.92	0.51
36:KA:211:ILE:O	36:KA:215:LEU:HB2	2.10	0.51
38:MA:142:PRO:HA	38:MA:185:PHE:HD2	1.75	0.51
39:NA:78:HIS:ND1	42:QA:104:ARG:HD2	2.21	0.51
45:TA:121:PRO:HG2	45:TA:126:ARG:HG3	1.92	0.51
1:FB:323:U:H2'	1:FB:324:G:O4'	2.10	0.51
1:FB:679:C:H2'	1:FB:680:C:C6	2.46	0.51
1:FB:1517:G:H3'	1:FB:1518:MA6:H8	1.92	0.51
2:GB:1359:A:H2	2:GB:1372:U:N3	2.01	0.51
2:GB:1394:U:H4'	2:GB:1603:A:H4'	1.93	0.51
26:EC:1:MET:HG2	26:EC:5:GLU:HB3	1.91	0.51
29:HC:16:ARG:NH1	29:HC:16:ARG:HG2	2.16	0.51
35:OC:204:ALA:HB2	35:OC:298:LEU:HD13	1.92	0.51
37:QC:88:ARG:HD3	37:QC:101:LEU:HD22	1.91	0.51
7:G:192:LEU:HD13	7:G:194:MET:HE2	1.92	0.51
10:J:14:ASP:OD1	10:J:15:VAL:N	2.43	0.51
15:O:12:ARG:HD3	15:O:16:HIS:CD2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:MA:28:SER:HB2	38:MA:29:PRO:HD2	1.93	0.51
42:QA:85:ARG:NH1	42:QA:87:SER:O	2.43	0.51
43:RA:10:ARG:HD2	43:RA:75:ASP:HB2	1.93	0.51
1:FB:714:G:H2'	1:FB:715:A:C8	2.44	0.51
8:MB:34:LEU:HD23	8:MB:161:THR:HG22	1.91	0.51
11:PB:99:LEU:O	11:PB:103:VAL:HG23	2.11	0.51
26:EC:22:GLU:OE2	26:EC:68:ARG:NH2	2.44	0.51
1:A:108:G:C6	54:CB:15:ARG:HG2	2.46	0.51
1:A:580:U:H2'	1:A:581:G:O4'	2.11	0.51
1:A:1418:A:H5''	1:A:1419:G:OP2	2.11	0.51
2:B:295:G:O5'	22:V:1:MET:HG3	2.11	0.51
2:B:1011:G:OP1	18:R:75:ASN:HB2	2.11	0.51
7:G:33:LEU:HD11	7:G:112:MET:HB3	1.92	0.51
11:K:99:LEU:O	11:K:103:VAL:HG23	2.09	0.51
13:M:149:GLU:OE2	13:M:149:GLU:HA	2.09	0.51
22:V:23:ARG:NH2	22:V:41:GLY:O	2.43	0.51
35:JA:326:LEU:HD13	35:JA:328:ARG:NH1	2.25	0.51
40:OA:1:MET:HE3	40:OA:66:GLU:HG2	1.92	0.51
1:FB:406:G:H1	1:FB:436:C:H42	1.59	0.51
1:FB:721:G:H4'	1:FB:722:A:O4'	2.10	0.51
2:GB:2168:G:H2'	2:GB:2169:A:H3'	1.92	0.51
3:HB:43:C:H5''	28:GC:1:MET:HG3	1.93	0.51
6:KB:34:VAL:HG21	6:KB:78:LEU:HD11	1.92	0.51
7:LB:184:TYR:O	7:LB:188:ARG:HG3	2.10	0.51
8:MB:3:LEU:HD13	8:MB:5:LEU:HD21	1.91	0.51
36:PC:68:ILE:HG12	36:PC:161:ALA:HB3	1.91	0.51
38:RC:79:PHE:O	38:RC:83:SER:OG	2.23	0.51
45:YC:91:ARG:HB3	45:YC:92:GLU:OE2	2.10	0.51
1:A:673:G:H2'	1:A:674:G:C8	2.46	0.51
2:B:370:G:H4'	2:B:371:A:OP2	2.10	0.51
4:D:52:G:H1	4:D:62:C:H42	1.58	0.51
4:D:53:G:N2	4:D:61:C:O2	2.42	0.51
8:H:55:LYS:O	8:H:58:GLN:HG3	2.11	0.51
9:I:12:PRO:O	9:I:15:VAL:HG22	2.11	0.51
36:KA:166:ASP:HB3	36:KA:169:LYS:HB3	1.93	0.51
40:OA:99:ALA:O	52:AB:28:GLU:HG3	2.11	0.51
2:GB:1266:G:O2'	2:GB:2012:G:O6	2.26	0.51
11:PB:34:LEU:O	11:PB:49:GLY:HA3	2.11	0.51
31:JC:47:ARG:NH1	31:JC:47:ARG:HB3	2.26	0.51
36:PC:211:ILE:O	36:PC:215:LEU:HB2	2.11	0.51
38:RC:168:ARG:HG3	38:RC:168:ARG:NH1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:XC:8:LEU:HG	44:XC:96:ILE:HG23	1.91	0.51
1:A:674:G:OP1	40:OA:87:ARG:NH2	2.42	0.51
2:B:1021:A:C8	2:B:1021:A:H3'	2.46	0.51
2:B:1364:G:P	25:Y:3:LYS:HG3	2.50	0.51
8:H:34:LEU:HD23	8:H:161:THR:HG22	1.93	0.51
38:MA:18:LYS:CE	38:MA:26:CYS:SG	2.96	0.51
39:NA:148:VAL:HG21	42:QA:107:LEU:HD22	1.93	0.51
48:WA:40:CYS:SG	48:WA:43:CYS:SG	3.08	0.51
51:ZA:52:LYS:NZ	51:ZA:52:LYS:HB3	2.26	0.51
1:FB:108:G:C6	54:HD:15:ARG:HG2	2.46	0.51
1:FB:595:G:H1'	1:FB:596:C:H5	1.75	0.51
2:GB:443:A:H1'	2:GB:1201:C:O4'	2.10	0.51
2:GB:1604:C:O2'	2:GB:1610:A:N1	2.41	0.51
2:GB:1783:A:H5'	2:GB:2608:G:H4'	1.93	0.51
4:IB:53:G:N2	4:IB:61:C:O2	2.43	0.51
9:NB:3:ARG:NH1	9:NB:3:ARG:HA	2.26	0.51
10:OB:14:ASP:OD1	10:OB:15:VAL:N	2.43	0.51
10:OB:62:LYS:HD2	10:OB:135:GLU:OE2	2.11	0.51
16:UB:52:SER:O	16:UB:56:LEU:HB2	2.11	0.51
17:VB:127:ALA:O	17:VB:129:ARG:N	2.42	0.51
26:EC:46:GLN:HB2	26:EC:49:LYS:HE3	1.93	0.51
40:TC:97:PHE:HB2	52:FD:32:ARG:NH1	2.25	0.51
43:WC:4:TYR:HB3	43:WC:88:TYR:HB2	1.92	0.51
44:XC:5:ARG:HD3	44:XC:71:LEU:HD11	1.93	0.51
1:A:815:A:N3	1:A:1527:C:O2'	2.37	0.51
2:B:857:C:H1'	24:X:26:TYR:HE1	1.75	0.51
9:I:164:TYR:HB2	9:I:167:GLU:HB2	1.91	0.51
26:Z:1:MET:HG2	26:Z:5:GLU:HB3	1.92	0.51
1:FB:376:G:H5''	50:DD:5:ARG:HD2	1.93	0.51
1:FB:678:U:H2'	1:FB:679:C:C6	2.46	0.51
1:FB:987:G:H2'	1:FB:988:G:C8	2.46	0.51
1:FB:1118:C:H2'	1:FB:1119:C:C6	2.46	0.51
2:GB:252:G:OP1	13:RB:50:ARG:NH1	2.43	0.51
2:GB:507:A:HO2'	2:GB:508:G:P	2.33	0.51
2:GB:2021:C:H4'	2:GB:2022:U:OP2	2.10	0.51
22:AC:38:ILE:HD11	22:AC:66:PRO:HG3	1.93	0.51
38:RC:50:ARG:HD3	38:RC:51:PRO:HD2	1.92	0.51
51:ED:14:LYS:N	51:ED:14:LYS:HE3	2.26	0.51
1:A:185:A:N3	54:CB:81:LYS:NZ	2.58	0.51
1:A:987:G:H2'	1:A:988:G:C8	2.46	0.51
2:B:271(C):G:O2'	2:B:421:U:OP2	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:35:ARG:HA	11:K:116:LEU:HD13	1.92	0.51
54:CB:56:MET:HG3	54:CB:88:VAL:HG21	1.93	0.51
1:FB:1057:G:H4'	37:QC:197:GLY:H	1.76	0.51
2:GB:34:C:HO2'	2:GB:35:G:P	2.34	0.51
2:GB:1790:C:H5''	2:GB:1791:A:OP1	2.10	0.51
4:IB:8:4SU:O2'	4:IB:46:G:N2	2.37	0.51
9:NB:109:PHE:CE1	9:NB:152:ARG:NH1	2.78	0.51
19:XB:44:LYS:NZ	19:XB:101:GLY:OXT	2.35	0.51
36:PC:130:ARG:HG2	36:PC:131:PRO:HD2	1.93	0.51
38:RC:192:GLU:H	38:RC:192:GLU:CD	2.19	0.51
2:B:1171:G:N2	2:B:1178:C:N3	2.58	0.50
2:B:1394:U:H4'	2:B:1603:A:H4'	1.93	0.50
45:TA:77:MET:HG2	45:TA:103:LEU:HD21	1.94	0.50
48:WA:41:ARG:NH1	48:WA:42:ILE:HD11	2.26	0.50
2:GB:363(F):U:H3'	2:GB:363(G):A:C8	2.41	0.50
2:GB:1882:C:H2'	2:GB:1883:G:O4'	2.12	0.50
2:GB:2724:C:OP1	6:KB:118:LYS:NZ	2.39	0.50
40:TC:15:ASP:OD1	40:TC:18:GLN:N	2.26	0.50
47:AD:3:ARG:NH1	47:AD:4:ILE:HG22	2.26	0.50
50:DD:40:ASP:HB3	50:DD:48:TRP:HB2	1.92	0.50
1:A:983:A:H5'	1:A:984:C:OP2	2.11	0.50
2:B:998:C:OP2	18:R:58:ARG:NH2	2.37	0.50
2:B:2370:G:C6	2:B:2371:G:C6	2.99	0.50
44:SA:6:ILE:HD11	44:SA:72:VAL:HB	1.92	0.50
51:ZA:14:LYS:N	51:ZA:14:LYS:HE3	2.26	0.50
1:FB:642:A:H2'	1:FB:643:C:C6	2.46	0.50
2:GB:892:G:H2'	2:GB:893:C:H4'	1.93	0.50
2:GB:1826:G:H4'	5:JB:242:ARG:HH21	1.75	0.50
2:GB:2892:A:H2'	2:GB:2893:G:O4'	2.11	0.50
4:IB:54:5MU:HN3	4:IB:58:A:H62	1.58	0.50
34:MC:13:A:H2'	34:MC:14:A:H4'	1.93	0.50
1:A:28:G:O2'	1:A:296:U:OP1	2.25	0.50
2:B:309:G:N3	2:B:329:G:O2'	2.44	0.50
2:B:2591:C:H2'	2:B:2592:G:C8	2.47	0.50
9:I:86:GLU:HG2	9:I:132:ARG:HG3	1.93	0.50
10:J:31:LEU:HD11	10:J:38:LEU:HG	1.94	0.50
28:BA:48:ARG:HE	28:BA:52:THR:HA	1.76	0.50
36:KA:19:HIS:CD2	36:KA:189:ASP:OD2	2.64	0.50
2:GB:1171:G:N2	2:GB:1178:C:N3	2.57	0.50
2:GB:1495:A:H2'	2:GB:1496:A:C8	2.47	0.50
9:NB:55:PRO:HG2	9:NB:61:HIS:CE1	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:PC:163:PHE:CD2	36:PC:185:ILE:HB	2.47	0.50
1:A:430:A:OP2	38:MA:8:VAL:HG12	2.12	0.50
1:A:987:G:H1	1:A:1218:C:H42	1.59	0.50
2:B:1359:A:H2	2:B:1372:U:N3	2.00	0.50
2:B:1536:A:H5''	2:B:1537:C:C5	2.46	0.50
2:B:1592:C:H2'	2:B:1593:G:C8	2.46	0.50
2:B:2243:U:H2'	2:B:2244:U:C6	2.47	0.50
2:B:2312:U:H5'	8:H:88:ILE:HD11	1.93	0.50
6:F:116:VAL:HG13	6:F:122:PHE:HB2	1.93	0.50
15:O:36:THR:HG22	15:O:37:THR:N	2.26	0.50
15:O:79:LEU:HA	15:O:83:ILE:HD12	1.94	0.50
37:LA:180:ALA:HB1	37:LA:203:PHE:CE1	2.46	0.50
44:SA:3:LYS:NZ	44:SA:75:ILE:O	2.42	0.50
45:TA:90:GLY:O	45:TA:92:GLU:N	2.44	0.50
1:FB:656:C:H4'	49:CD:62:GLN:NE2	2.20	0.50
1:FB:1128:C:H5''	43:WC:66:ARG:NH1	2.26	0.50
2:GB:975:G:H1'	2:GB:990:A:C2	2.46	0.50
23:BC:124:ILE:HD11	23:BC:165:VAL:HG21	1.94	0.50
40:TC:30:LEU:HB3	40:TC:35:ALA:HB3	1.93	0.50
45:YC:87:THR:HA	45:YC:91:ARG:HD2	1.94	0.50
2:B:747:U:O2	2:B:2014:A:H1'	2.12	0.50
2:B:796:C:H2'	2:B:797:C:C6	2.46	0.50
12:L:36:GLY:HA3	12:L:109:LYS:HG3	1.94	0.50
38:MA:12:CYS:SG	38:MA:18:LYS:HE3	2.51	0.50
47:VA:54:VAL:HG22	47:VA:57:ARG:HH12	1.76	0.50
47:VA:70:LEU:O	47:VA:74:VAL:HG23	2.11	0.50
1:FB:555:C:H2'	1:FB:556:C:C6	2.46	0.50
2:GB:609(B):G:N2	2:GB:619:G:H1'	2.26	0.50
2:GB:1557:C:H5''	2:GB:1558:A:OP2	2.12	0.50
5:JB:206:LEU:HD22	5:JB:211:ARG:HG2	1.93	0.50
37:QC:58:GLU:HB2	37:QC:65:ALA:HB3	1.94	0.50
44:XC:5:ARG:HG3	44:XC:73:ASP:HB3	1.92	0.50
1:A:406:G:H1	1:A:436:C:H42	1.60	0.50
1:A:1104:G:O5'	36:KA:111:ARG:HD2	2.11	0.50
1:A:1414:U:H3	1:A:1486:G:H1	1.60	0.50
2:B:540:G:H2'	2:B:541:C:C6	2.47	0.50
2:B:1570:A:H2'	2:B:1571:A:C8	2.47	0.50
2:B:2892:A:H2'	2:B:2893:G:O4'	2.12	0.50
4:D:19:G:H1	4:D:56:C:H42	1.57	0.50
8:H:115:ARG:NH1	47:VA:2:ALA:HB2	2.26	0.50
13:M:59:LEU:HD23	32:FA:58:ILE:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:NA:20:GLN:HG2	39:NA:25:ARG:HD2	1.93	0.50
46:UA:38:THR:OG1	46:UA:57:LYS:HB3	2.11	0.50
1:FB:272:C:H2'	1:FB:273:A:H8	1.76	0.50
1:FB:1253:G:H1	1:FB:1284:C:H42	1.57	0.50
2:GB:194:G:H2'	2:GB:195:A:O4'	2.11	0.50
2:GB:1364:G:P	25:DC:3:LYS:HG3	2.52	0.50
6:KB:11:MET:HG2	6:KB:24:THR:HB	1.93	0.50
43:WC:86:VAL:HG11	43:WC:102:LEU:HD11	1.93	0.50
48:BD:41:ARG:NH1	48:BD:42:ILE:HD11	2.26	0.50
1:A:335:C:O2'	1:A:1433:A:N3	2.40	0.50
1:A:1124:G:H1	1:A:1149:C:H42	1.60	0.50
2:B:270(R):C:HO2'	10:J:42:SER:HG	1.60	0.50
2:B:1495:A:H2'	2:B:1496:A:C8	2.45	0.50
2:B:2508:G:P	35:JA:228:ARG:HH22	2.34	0.50
16:P:52:SER:O	16:P:56:LEU:HB2	2.12	0.50
44:SA:44:VAL:HG22	44:SA:66:ARG:HG2	1.94	0.50
50:YA:53:VAL:HG12	50:YA:57:ARG:HH11	1.77	0.50
1:FB:769:G:H4'	1:FB:1513:A:H4'	1.94	0.50
2:GB:161:U:H2'	2:GB:163:U:OP2	2.11	0.50
2:GB:686:G:N2	2:GB:788:A:H61	2.10	0.50
2:GB:889:C:O2'	2:GB:890:A:O4'	2.30	0.50
2:GB:1409:C:H2'	2:GB:1410:G:C8	2.46	0.50
7:LB:192:LEU:HD13	7:LB:194:MET:HE2	1.92	0.50
11:PB:9:VAL:HG21	11:PB:39:ARG:HH22	1.76	0.50
25:DC:72:GLU:O	25:DC:76:ARG:HG3	2.12	0.50
26:EC:2:LYS:HD3	26:EC:2:LYS:H	1.76	0.50
42:VC:20:TYR:HE2	42:VC:75:ARG:HD2	1.77	0.50
4:D:8:4SU:O2'	4:D:46:G:N2	2.36	0.50
10:J:76:THR:HG22	10:J:141:LYS:HD2	1.92	0.50
19:S:2:PHE:CZ	19:S:41:GLY:HA3	2.46	0.50
46:UA:8:ASN:O	46:UA:12:ARG:HG3	2.11	0.50
46:UA:28:LYS:NZ	46:UA:64:TYR:HE2	2.09	0.50
1:FB:353:A:H5'	1:FB:353:A:H8	1.75	0.50
1:FB:500:G:H5'	46:ZC:124:LYS:HZ2	1.77	0.50
2:GB:958:U:H5'	14:SB:14:ARG:HD3	1.94	0.50
2:GB:1914:C:OP2	2:GB:1915:5MU:H72	2.11	0.50
13:RB:2:LYS:NZ	13:RB:4:SER:OG	2.44	0.50
20:YB:82:LEU:HD22	20:YB:84:ARG:NH2	2.27	0.50
23:BC:52:SER:OG	23:BC:53:ILE:N	2.44	0.50
28:GC:48:ARG:HE	28:GC:52:THR:HA	1.77	0.50
48:BD:40:CYS:SG	48:BD:43:CYS:SG	3.09	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:575:G:OP1	1:A:575:G:H4'	2.12	0.50
1:A:1004:A:N6	1:A:1026:G:OP2	2.40	0.50
1:A:1517:G:H3'	1:A:1518:MA6:H8	1.93	0.50
2:B:517:C:OP1	29:CA:16:ARG:NH2	2.44	0.50
2:B:1292:U:H2'	2:B:1293:C:C6	2.47	0.50
2:B:2141:G:N2	2:B:2151:G:H1'	2.26	0.50
2:B:2405:G:OP1	13:M:77:ARG:NH2	2.45	0.50
4:IB:30:G:N2	41:UC:144:MET:HE1	2.23	0.50
23:BC:29:TYR:HB3	23:BC:34:ASN:HD22	1.76	0.50
37:QC:180:ALA:HB1	37:QC:203:PHE:CE1	2.46	0.50
44:XC:3:LYS:NZ	44:XC:75:ILE:O	2.43	0.50
47:AD:23:TYR:HB3	47:AD:67:GLU:HA	1.94	0.50
1:A:865:A:H5'	1:A:1078:U:O4	2.12	0.49
1:A:1132:C:H2'	1:A:1133:G:H8	1.76	0.49
2:B:969:U:H2'	2:B:970:C:C6	2.47	0.49
37:LA:119:ARG:O	37:LA:123:GLN:HG3	2.12	0.49
45:TA:91:ARG:HB3	45:TA:92:GLU:OE2	2.11	0.49
1:FB:383:A:C5	1:FB:384:G:H1'	2.47	0.49
1:FB:706:A:N3	45:YC:31:THR:HG21	2.27	0.49
1:FB:1443:G:O6	2:GB:2863:C:H5''	2.11	0.49
2:GB:270(G):U:H2'	2:GB:270(H):C:C6	2.47	0.49
6:KB:45:THR:O	6:KB:82:ARG:HD2	2.12	0.49
8:MB:113:ARG:NH1	8:MB:142:PRO:HA	2.25	0.49
9:NB:101:ARG:HH11	9:NB:122:THR:HG23	1.75	0.49
35:OC:165:LYS:NZ	35:OC:208:GLU:HG3	2.27	0.49
35:OC:247:THR:HG23	35:OC:254:VAL:HG22	1.93	0.49
36:PC:74:LYS:HZ3	36:PC:166:ASP:HB2	1.77	0.49
1:A:603:U:H2'	1:A:604:G:C8	2.48	0.49
1:A:679:C:H2'	1:A:680:C:C6	2.47	0.49
2:B:1510:A:H2'	2:B:1511:A:C8	2.46	0.49
2:B:1557:C:H5''	2:B:1558:A:OP2	2.12	0.49
2:B:2350:C:H2'	2:B:2351:G:O4'	2.13	0.49
2:B:2792:G:H2'	2:B:2793:G:H8	1.77	0.49
4:D:75:C:H5'	25:Y:30:VAL:HG21	1.93	0.49
21:U:61:GLY:HA3	21:U:73:ARG:O	2.12	0.49
38:MA:192:GLU:H	38:MA:192:GLU:CD	2.20	0.49
40:OA:24:GLU:HA	40:OA:24:GLU:OE2	2.12	0.49
54:CB:30:LYS:HB2	54:CB:30:LYS:HZ1	1.77	0.49
1:FB:966:M2G:HM13	1:FB:967:5MC:H1'	1.94	0.49
1:FB:1347:G:N2	1:FB:1373:G:H2'	2.27	0.49
2:GB:1800:C:OP2	5:JB:183:ARG:NH2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LB:53:THR:CG2	7:LB:55:GLY:H	2.24	0.49
8:MB:113:ARG:NH2	8:MB:139:LEU:O	2.45	0.49
14:SB:116:GLU:OE2	14:SB:119:ARG:NE	2.42	0.49
38:RC:61:LYS:HD2	38:RC:207:TYR:OH	2.11	0.49
42:VC:51:VAL:HG11	42:VC:60:ARG:NH1	2.27	0.49
1:A:500:G:H5'	46:UA:124:LYS:NZ	2.27	0.49
1:A:1003:G:H1	1:A:1038:C:H42	1.60	0.49
2:B:609(B):G:N2	2:B:619:G:H1'	2.27	0.49
3:C:7:G:H5'	16:P:29:PHE:CD2	2.48	0.49
13:M:65:ARG:HG3	13:M:66:GLY:N	2.26	0.49
23:W:155:LEU:O	23:W:157:LEU:HD12	2.11	0.49
25:Y:65:SER:OG	25:Y:66:HIS:ND1	2.37	0.49
40:OA:30:LEU:HB3	40:OA:35:ALA:HB3	1.94	0.49
42:QA:82:HIS:NE2	42:QA:84:ARG:HD2	2.27	0.49
43:RA:86:VAL:HG11	43:RA:102:LEU:HD11	1.94	0.49
2:GB:1358:G:O2'	2:GB:1359:A:H5''	2.13	0.49
2:GB:1692:U:H2'	2:GB:1694:C:C5	2.47	0.49
2:GB:1754:C:P	17:VB:96:ARG:HH12	2.35	0.49
2:GB:2563:U:H4'	12:QB:28:SER:HA	1.94	0.49
2:GB:2789:C:O3'	2:GB:2790:A:H4'	2.11	0.49
6:KB:119:ARG:HG2	6:KB:120:TRP:CE2	2.48	0.49
9:NB:17:VAL:HG11	9:NB:50:VAL:HG21	1.94	0.49
20:YB:57:ASN:O	20:YB:61:ASN:HB2	2.13	0.49
35:OC:196:ILE:HD13	35:OC:313:PRO:HG2	1.95	0.49
40:TC:68:PRO:HG2	40:TC:71:ARG:NH2	2.26	0.49
42:VC:82:HIS:NE2	42:VC:84:ARG:HD2	2.27	0.49
44:XC:44:VAL:HG22	44:XC:66:ARG:HG2	1.93	0.49
46:ZC:11:VAL:HG13	51:ED:29:HIS:HD2	1.76	0.49
54:HD:30:LYS:HA	54:HD:33:ILE:HG12	1.94	0.49
1:A:437:U:H5'	38:MA:155:LEU:HD11	1.93	0.49
2:B:889:C:O2'	2:B:890:A:O4'	2.31	0.49
10:J:101:LEU:HG	10:J:107:ILE:HG12	1.95	0.49
35:JA:182:HIS:HB3	35:JA:310:TYR:HE1	1.77	0.49
36:KA:163:PHE:CD2	36:KA:185:ILE:HB	2.47	0.49
37:LA:33:LEU:HA	37:LA:36:ASP:HB2	1.94	0.49
49:XA:54:ARG:O	49:XA:58:MET:HG3	2.11	0.49
50:YA:40:ASP:HB3	50:YA:48:TRP:HB2	1.93	0.49
1:FB:335:C:O2'	1:FB:1433:A:N3	2.41	0.49
2:GB:1059:G:H2'	2:GB:1059:G:N3	2.27	0.49
2:GB:1292:U:H2'	2:GB:1293:C:C6	2.47	0.49
2:GB:2564:A:C2	2:GB:2647:U:H4'	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:QB:24:VAL:HB	12:QB:33:ALA:HB2	1.94	0.49
17:VB:9:LEU:O	17:VB:12:SER:OG	2.26	0.49
19:XB:14:VAL:HG12	19:XB:18:LEU:HD23	1.93	0.49
36:PC:157:ARG:O	36:PC:158:LEU:HB3	2.11	0.49
53:GD:31:ILE:HG13	53:GD:49:ILE:HG23	1.94	0.49
1:A:769:G:H4'	1:A:1513:A:H4'	1.94	0.49
1:A:1356:G:H2'	1:A:1357:A:H8	1.77	0.49
2:B:776:G:H4'	2:B:777:A:O5'	2.13	0.49
2:B:1179:C:H2'	2:B:1180:C:C6	2.48	0.49
2:B:2334:G:O6	24:X:74:ARG:NH2	2.45	0.49
2:B:2646:C:OP2	2:B:2732:G:O2'	2.30	0.49
2:B:2794:C:H42	2:B:2802:G:H1	1.59	0.49
3:C:43:C:H5''	28:BA:1:MET:HG3	1.94	0.49
25:Y:2:SER:HB3	25:Y:46:LEU:HD12	1.94	0.49
42:QA:51:VAL:HG21	42:QA:60:ARG:HH11	1.77	0.49
47:VA:3:ARG:CG	47:VA:3:ARG:NH1	2.70	0.49
1:FB:272:C:H2'	1:FB:273:A:C8	2.47	0.49
1:FB:987:G:H1	1:FB:1218:C:H42	1.58	0.49
2:GB:1021:A:H3'	2:GB:1021:A:H8	1.77	0.49
6:KB:174:ASP:OD1	6:KB:175:VAL:N	2.46	0.49
7:LB:33:LEU:HD11	7:LB:112:MET:HB3	1.93	0.49
7:LB:181:LEU:HD11	7:LB:186:ILE:HD11	1.95	0.49
7:LB:195:ASP:HB3	7:LB:198:ALA:H	1.78	0.49
30:IC:15:GLU:HG3	30:IC:47:THR:HG23	1.93	0.49
31:JC:5:TRP:NE1	31:JC:7:PRO:HG3	2.26	0.49
36:PC:19:HIS:CD2	36:PC:189:ASP:OD2	2.65	0.49
36:PC:44:LEU:H	36:PC:44:LEU:HD12	1.76	0.49
45:YC:99:GLN:HE21	52:FD:88:LYS:HZ1	1.58	0.49
1:A:801:U:H2'	1:A:802:A:H8	1.77	0.49
1:A:1347:G:N2	1:A:1373:G:H2'	2.27	0.49
2:B:1778:U:H2'	2:B:1784:A:N6	2.27	0.49
2:B:2055:C:H5'	2:B:2056:G:O5'	2.11	0.49
2:B:2563:U:H4'	12:L:28:SER:HA	1.93	0.49
2:B:2564:A:C2	2:B:2647:U:H4'	2.47	0.49
3:C:7:G:H4'	16:P:29:PHE:HB2	1.94	0.49
36:KA:7:VAL:HB	36:KA:8:LYS:HD2	1.95	0.49
38:MA:168:ARG:HG3	38:MA:168:ARG:NH1	2.28	0.49
41:PA:115:ARG:O	41:PA:118:VAL:HB	2.12	0.49
47:VA:3:ARG:NH1	47:VA:4:ILE:HG22	2.26	0.49
1:FB:1412:C:H2'	1:FB:1413:A:H8	1.77	0.49
2:GB:309:G:N3	2:GB:329:G:O2'	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:TB:96:ARG:NH1	15:TB:115:GLU:OE2	2.46	0.49
30:IC:6:ARG:NH1	30:IC:26:ASN:HB2	2.28	0.49
41:UC:23:VAL:O	41:UC:27:ILE:HG13	2.13	0.49
43:WC:10:ARG:HD2	43:WC:75:ASP:HB2	1.92	0.49
1:A:1320:C:H2'	1:A:1321:C:O4'	2.13	0.49
2:B:14:A:H5''	2:B:15:G:OP2	2.13	0.49
2:B:2031:A:C6	2:B:2498:C:H1'	2.48	0.49
24:X:5:LYS:NZ	35:JA:262:SER:OG	2.45	0.49
36:KA:167:PRO:HG2	36:KA:188:ALA:HB2	1.95	0.49
38:MA:43:HIS:CE1	38:MA:46:LYS:HZ2	2.29	0.49
43:RA:50:LEU:HD12	43:RA:56:LEU:HD12	1.94	0.49
51:ZA:95:TYR:HA	51:ZA:98:LEU:HD12	1.94	0.49
1:FB:977:A:H2'	1:FB:978:A:H5''	1.94	0.49
1:FB:1397:C:O2'	1:FB:1398:A:OP1	2.28	0.49
2:GB:271(C):G:H4'	2:GB:271(D):U:H5''	1.94	0.49
2:GB:857:C:H1'	24:CC:26:TYR:HE1	1.77	0.49
2:GB:1187:G:H5''	19:XB:81:TYR:CE1	2.47	0.49
2:GB:1570:A:H2'	2:GB:1571:A:C8	2.48	0.49
2:GB:1778:U:H2'	2:GB:1784:A:N6	2.27	0.49
3:HB:7:G:H4'	16:UB:29:PHE:HB2	1.94	0.49
26:EC:18:PRO:O	26:EC:22:GLU:HG3	2.13	0.49
31:JC:47:ARG:HB3	31:JC:47:ARG:HH11	1.76	0.49
38:RC:111:ALA:HB2	38:RC:120:LEU:HD12	1.95	0.49
38:RC:155:LEU:HD13	38:RC:156:GLU:N	2.28	0.49
42:VC:122:ARG:HA	42:VC:125:ARG:HD2	1.94	0.49
46:ZC:7:ILE:O	46:ZC:11:VAL:HG23	2.13	0.49
46:ZC:38:THR:OG1	46:ZC:57:LYS:HB3	2.12	0.49
1:A:714:G:H2'	1:A:715:A:C8	2.47	0.49
2:B:1266:G:O2'	2:B:2012:G:O6	2.27	0.49
2:B:1359:A:H2'	2:B:1360:A:H5'	1.95	0.49
2:B:2082:A:H2'	2:B:2083:G:O4'	2.13	0.49
6:F:119:ARG:HG2	6:F:120:TRP:CE2	2.47	0.49
7:G:95:ARG:HD3	7:G:97:TYR:CZ	2.47	0.49
20:T:20:VAL:O	20:T:23:LEU:HB2	2.12	0.49
20:T:82:LEU:HD22	20:T:84:ARG:NH2	2.28	0.49
36:KA:177:ALA:HB1	36:KA:182:ILE:HB	1.95	0.49
37:LA:61:ALA:O	37:LA:63:ASN:N	2.43	0.49
1:FB:801:U:H2'	1:FB:802:A:H8	1.78	0.49
2:GB:857:C:N4	2:GB:858:U:O4	2.46	0.49
2:GB:2622:C:O2'	2:GB:2825:G:N7	2.45	0.49
2:GB:2747:G:OP1	9:NB:138:LYS:NZ	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:EC:35:LEU:HD12	26:EC:53:LEU:HD12	1.95	0.49
26:EC:64:LEU:O	26:EC:68:ARG:HG2	2.13	0.49
38:RC:57:ARG:HB3	38:RC:206:PHE:HB2	1.94	0.49
2:B:1085:A:O2'	2:B:1104:C:O2'	2.27	0.49
2:B:1508:A:H3'	2:B:1509:A:C8	2.47	0.49
2:B:1754:C:P	17:Q:96:ARG:HH12	2.36	0.49
5:E:112:GLN:O	5:E:115:GLN:HG2	2.12	0.49
13:M:29:LYS:HB3	13:M:30:THR:H	1.47	0.49
18:R:14:HIS:O	18:R:18:LEU:HD12	2.13	0.49
44:SA:6:ILE:HG22	44:SA:98:ILE:HG22	1.94	0.49
48:WA:2:ALA:HA	48:WA:6:LEU:HD13	1.94	0.49
54:CB:54:LYS:HA	54:CB:57:ARG:NH1	2.28	0.49
1:FB:137:C:H2'	1:FB:138:G:H8	1.77	0.49
1:FB:959:A:O2'	1:FB:984:C:O2'	2.25	0.49
1:FB:983:A:H5'	1:FB:984:C:OP2	2.13	0.49
1:FB:1025:U:H5'	1:FB:1026:G:H5'	1.95	0.49
2:GB:540:G:H2'	2:GB:541:C:C6	2.47	0.49
2:GB:1111:A:N3	2:GB:1112:G:H1'	2.27	0.49
2:GB:2849:U:OP2	17:VB:95:ARG:NH1	2.45	0.49
17:VB:94:ALA:HB1	17:VB:99:LEU:HD21	1.95	0.49
46:ZC:60:LEU:HD21	46:ZC:66:VAL:HG22	1.95	0.49
1:A:323:U:H2'	1:A:324:G:O4'	2.12	0.49
2:B:1516:U:H2'	2:B:1517:G:H8	1.78	0.49
12:L:2:ILE:HD12	12:L:6:THR:HG21	1.93	0.49
18:R:52:ARG:HA	18:R:55:ARG:HG3	1.94	0.49
30:DA:15:GLU:HG3	30:DA:47:THR:HG23	1.94	0.49
37:LA:177:THR:HG22	37:LA:180:ALA:H	1.78	0.49
40:OA:97:PHE:HB2	52:AB:32:ARG:NH1	2.28	0.49
1:FB:674:G:OP1	40:TC:87:ARG:NH2	2.45	0.49
1:FB:1062:U:H2'	1:FB:1063:C:C6	2.48	0.49
2:GB:1430:C:H2'	2:GB:1431:U:C6	2.48	0.49
2:GB:2779:U:OP1	2:GB:2780:G:H2'	2.12	0.49
45:YC:121:PRO:HG2	45:YC:126:ARG:HG3	1.94	0.49
46:ZC:69:TYR:HD2	46:ZC:99:HIS:CD2	2.30	0.49
1:A:1073:U:O2'	36:KA:104:ASN:OD1	2.27	0.48
2:B:1882:C:H2'	2:B:1883:G:O4'	2.13	0.48
4:D:51:C:H2'	4:D:52:G:C8	2.48	0.48
6:F:174:ASP:HB3	6:F:183:LEU:HD22	1.95	0.48
12:L:24:VAL:HB	12:L:33:ALA:HB2	1.95	0.48
14:N:64:ILE:HG13	23:W:178:GLU:HG3	1.95	0.48
17:Q:109:GLU:HG2	17:Q:112:ARG:NH2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:ZA:45:HIS:HB3	51:ZA:72:ARG:HG2	1.95	0.48
1:FB:1124:G:H1	1:FB:1149:C:H42	1.61	0.48
2:GB:2150:U:H2'	2:GB:2151:G:H8	1.78	0.48
25:DC:95:LEU:O	25:DC:98:LEU:HB2	2.13	0.48
45:YC:90:GLY:O	45:YC:92:GLU:N	2.46	0.48
47:AD:108:ARG:O	47:AD:112:GLY:N	2.46	0.48
1:A:38:G:H22	1:A:397:A:H5''	1.78	0.48
1:A:500:G:H5'	46:UA:124:LYS:HZ2	1.78	0.48
1:A:1025:U:H5'	1:A:1026:G:H5'	1.94	0.48
2:B:154(A):C:H2'	2:B:161:U:C5	2.48	0.48
2:B:492:A:H2'	2:B:493:G:O4'	2.13	0.48
2:B:987:G:O2'	2:B:1000:A:N3	2.44	0.48
2:B:1187:G:H5''	19:S:81:TYR:CE1	2.49	0.48
2:B:2150:U:H2'	2:B:2151:G:H8	1.78	0.48
44:SA:5:ARG:HD3	44:SA:71:LEU:HD11	1.95	0.48
44:SA:20:ALA:O	44:SA:23:ILE:HG22	2.13	0.48
1:FB:1510:U:H2'	1:FB:1511:G:C8	2.48	0.48
2:GB:576:U:H2'	2:GB:577:G:C8	2.49	0.48
2:GB:1067:A:OP1	2:GB:1068:G:N2	2.45	0.48
2:GB:1508:A:H3'	2:GB:1509:A:C8	2.48	0.48
2:GB:1532:C:H42	2:GB:1539:G:H22	1.62	0.48
37:QC:180:ALA:HA	37:QC:206:GLU:HA	1.95	0.48
38:RC:25:ARG:O	38:RC:28:SER:OG	2.21	0.48
40:TC:50:TYR:CE2	52:FD:77:GLY:HA2	2.48	0.48
43:WC:121:ARG:HH11	43:WC:121:ARG:HB2	1.78	0.48
1:A:397:A:H3'	1:A:397:A:N3	2.28	0.48
1:A:437:U:OP1	38:MA:155:LEU:HD21	2.13	0.48
1:A:966:M2G:HM13	1:A:967:5MC:H1'	1.95	0.48
1:A:1057:G:H4'	37:LA:197:GLY:H	1.77	0.48
1:A:1085:U:H3'	1:A:1086:U:C6	2.48	0.48
1:A:1412:C:H2'	1:A:1413:A:H8	1.78	0.48
1:A:1510:U:H2'	1:A:1511:G:C8	2.48	0.48
6:F:7:VAL:HG23	6:F:51:PHE:HE2	1.77	0.48
6:F:34:VAL:HG21	6:F:78:LEU:HD11	1.95	0.48
15:O:70:LEU:O	15:O:72:ASP:N	2.45	0.48
17:Q:18:ASP:OD1	17:Q:18:ASP:N	2.44	0.48
19:S:14:VAL:HG12	19:S:18:LEU:HD23	1.96	0.48
35:JA:172:TYR:O	35:JA:176:LYS:HB2	2.13	0.48
39:NA:31:LEU:HD22	39:NA:43:LEU:HD11	1.95	0.48
39:NA:147:ASP:OD2	39:NA:150:ARG:NH2	2.46	0.48
1:FB:1003:G:H1	1:FB:1038:C:N4	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:686:G:O5'	31:JC:11:LYS:NZ	2.46	0.48
2:GB:2115:G:H2'	2:GB:2117:A:N7	2.29	0.48
10:OB:118:LYS:NZ	10:OB:119:PRO:O	2.46	0.48
18:WB:113:ALA:O	18:WB:117:GLN:HG2	2.12	0.48
37:QC:180:ALA:HB1	37:QC:203:PHE:HE1	1.78	0.48
39:SC:84:PHE:HB3	39:SC:134:ALA:HB2	1.95	0.48
44:XC:20:ALA:O	44:XC:23:ILE:HG22	2.13	0.48
1:A:977:A:H2'	1:A:978:A:H5'	1.94	0.48
2:B:1309:G:H4'	31:EA:7:PRO:HB2	1.95	0.48
11:K:9:VAL:HG21	11:K:39:ARG:HH22	1.79	0.48
16:P:60:GLY:O	16:P:61:ASN:HB3	2.14	0.48
37:LA:180:ALA:HB1	37:LA:203:PHE:HE1	1.78	0.48
40:OA:80:ARG:HE	40:OA:88:VAL:HB	1.77	0.48
53:BB:31:ILE:HG13	53:BB:49:ILE:HG23	1.94	0.48
2:GB:2208:U:H4'	5:JB:151:LYS:HG2	1.94	0.48
12:QB:36:GLY:HA3	12:QB:109:LYS:HG3	1.94	0.48
16:UB:4:LEU:HD23	16:UB:8:GLU:OE2	2.13	0.48
17:VB:132:LYS:NZ	17:VB:132:LYS:HB2	2.27	0.48
36:PC:167:PRO:HG2	36:PC:188:ALA:HB2	1.95	0.48
1:A:946:A:H2'	1:A:947:G:C8	2.48	0.48
2:B:1467:C:OP2	2:B:1547:C:H5	1.96	0.48
13:M:77:ARG:HB2	13:M:77:ARG:HH11	1.76	0.48
13:M:83:VAL:HG12	13:M:112:LEU:HD21	1.96	0.48
17:Q:127:ALA:O	17:Q:129:ARG:N	2.43	0.48
1:FB:8:A:C6	38:RC:209:ARG:HB2	2.48	0.48
1:FB:191(D):U:H2'	1:FB:191(E):G:C8	2.49	0.48
2:GB:263:C:H2'	2:GB:264:C:O4'	2.13	0.48
2:GB:271(C):G:O2'	2:GB:421:U:OP2	2.18	0.48
2:GB:929:G:H8	2:GB:929:G:O5'	1.96	0.48
2:GB:1657:C:H2'	2:GB:1658:C:H6	1.78	0.48
3:HB:7:G:H5'	16:UB:29:PHE:CD2	2.49	0.48
5:JB:246:PRO:O	5:JB:254:THR:HG22	2.12	0.48
14:SB:111:GLU:O	14:SB:115:MET:HG2	2.13	0.48
15:TB:1:MET:HB2	15:TB:1:MET:HE3	1.78	0.48
15:TB:36:THR:HG22	15:TB:37:THR:N	2.29	0.48
21:ZB:44:GLU:OE1	21:ZB:50:LYS:HD2	2.13	0.48
40:TC:27:GLN:HA	40:TC:30:LEU:HD12	1.95	0.48
45:YC:77:MET:HG2	45:YC:103:LEU:HD21	1.95	0.48
2:B:207:A:H2'	2:B:208:C:O4'	2.12	0.48
2:B:540:G:H2'	2:B:541:C:H6	1.79	0.48
2:B:892:G:H2'	2:B:893:C:H4'	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1011:G:OP1	18:R:77:SER:HB2	2.13	0.48
2:B:1692:U:H2'	2:B:1694:C:C5	2.48	0.48
2:B:2345:G:OP2	30:DA:38:LYS:HD3	2.14	0.48
2:B:2693:A:H2'	2:B:2694:G:C8	2.48	0.48
5:E:62:TYR:HA	5:E:87:ASN:ND2	2.29	0.48
8:H:113:ARG:HD2	28:BA:33:VAL:HG13	1.96	0.48
9:I:56:SER:OG	9:I:58:GLU:HG2	2.14	0.48
15:O:33:ARG:HD2	15:O:113:LEU:HD13	1.94	0.48
20:T:57:ASN:O	20:T:61:ASN:HB2	2.13	0.48
20:T:82:LEU:HD22	20:T:84:ARG:HH22	1.79	0.48
26:Z:51:ARG:O	26:Z:55:ARG:HG2	2.14	0.48
32:FA:4:MET:HE2	32:FA:63:PRO:HG3	1.95	0.48
38:MA:9:CYS:HG	38:MA:18:LYS:NZ	2.05	0.48
38:MA:176:LEU:HD12	38:MA:182:LYS:O	2.13	0.48
51:ZA:78:GLU:OE2	51:ZA:81:ARG:HD3	2.13	0.48
1:FB:149:A:H2'	1:FB:150:C:C6	2.49	0.48
1:FB:500:G:H5'	46:ZC:124:LYS:NZ	2.29	0.48
1:FB:1085:U:H3'	1:FB:1086:U:C6	2.48	0.48
1:FB:1414:U:H3	1:FB:1486:G:H1	1.62	0.48
2:GB:295:G:O5'	22:AC:1:MET:HG3	2.14	0.48
2:GB:969:U:H2'	2:GB:970:C:C6	2.48	0.48
2:GB:1060:U:C5'	2:GB:1061:U:H3'	2.43	0.48
2:GB:2211:G:H2'	2:GB:2212:A:C2	2.49	0.48
5:JB:112:GLN:O	5:JB:115:GLN:HG2	2.13	0.48
9:NB:12:PRO:O	9:NB:15:VAL:HG22	2.14	0.48
10:OB:31:LEU:HD11	10:OB:38:LEU:HG	1.95	0.48
22:AC:15:VAL:HG11	22:AC:20:TYR:HB2	1.94	0.48
35:OC:172:TYR:O	35:OC:176:LYS:HB2	2.13	0.48
37:QC:191:THR:OG1	37:QC:194:GLY:O	2.22	0.48
41:UC:28:ASN:OD1	41:UC:36:LYS:NZ	2.43	0.48
42:VC:51:VAL:HG21	42:VC:60:ARG:HH11	1.77	0.48
47:AD:29:ARG:NH1	47:AD:64:TRP:CG	2.81	0.48
1:A:192:U:H2'	1:A:193:C:C6	2.49	0.48
1:A:1070:U:H2'	1:A:1071:C:C6	2.48	0.48
1:A:1241:G:H2'	1:A:1242:C:C6	2.49	0.48
2:B:1059:G:H2'	2:B:1059:G:N3	2.29	0.48
2:B:1085:A:OP2	2:B:1085:A:H8	1.97	0.48
6:F:4:ILE:HD13	6:F:28:ALA:HB1	1.95	0.48
19:S:69:LYS:HA	19:S:88:ARG:HG2	1.96	0.48
20:T:73:ALA:HB3	20:T:106:ILE:HB	1.95	0.48
35:JA:337:LEU:O	35:JA:341:ILE:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:MA:57:ARG:HB3	38:MA:206:PHE:HB2	1.96	0.48
41:PA:38:LEU:O	41:PA:42:ILE:HG13	2.13	0.48
42:QA:20:TYR:HE2	42:QA:75:ARG:HD2	1.78	0.48
1:FB:603:U:H2'	1:FB:604:G:C8	2.48	0.48
1:FB:816:A:OP2	1:FB:1527:C:H5'	2.13	0.48
2:GB:987:G:O2'	2:GB:1000:A:N3	2.44	0.48
2:GB:1441:G:H2'	2:GB:1442:G:H8	1.79	0.48
30:IC:13:CYS:SG	30:IC:47:THR:HG21	2.54	0.48
40:TC:75:LEU:O	40:TC:79:LEU:HG	2.14	0.48
42:VC:101:PRO:HG3	42:VC:133:LEU:HD11	1.96	0.48
49:CD:30:ALA:HA	49:CD:85:LEU:HD11	1.95	0.48
1:A:323:U:O3'	54:CB:22:ARG:HD3	2.14	0.48
1:A:1048:G:OP1	48:WA:3:ARG:HB3	2.14	0.48
2:B:270(G):U:H2'	2:B:270(H):C:C6	2.48	0.48
2:B:374:A:C2	2:B:401:A:C4	3.02	0.48
2:B:1345:C:OP2	2:B:1346:G:OP2	2.32	0.48
2:B:1585:C:H4'	2:B:1586:A:OP2	2.14	0.48
4:D:54:5MU:HN3	4:D:58:A:H62	1.60	0.48
15:O:36:THR:HG22	15:O:37:THR:H	1.78	0.48
16:P:10:ARG:HG2	16:P:13:ARG:NH2	2.29	0.48
43:RA:76:ALA:O	43:RA:80:GLY:N	2.45	0.48
52:AB:61:LYS:O	52:AB:65:ILE:HG13	2.14	0.48
2:GB:848:G:N9	2:GB:933:A:H8	2.12	0.48
2:GB:1289:C:H2'	2:GB:1290:C:H6	1.79	0.48
6:KB:7:VAL:HG23	6:KB:51:PHE:HE2	1.77	0.48
7:LB:107:LYS:HD2	7:LB:206:ILE:HA	1.95	0.48
9:NB:86:GLU:HG2	9:NB:132:ARG:HG3	1.95	0.48
1:A:1054:C:N3	34:HA:22:A:N6	2.62	0.48
2:B:161:U:H2'	2:B:163:U:OP2	2.14	0.48
2:B:271(C):G:H4'	2:B:271(D):U:H5''	1.95	0.48
2:B:576:U:H2'	2:B:577:G:C8	2.48	0.48
2:B:1130:U:O2	6:F:149:ARG:NH2	2.47	0.48
2:B:2646:C:H2'	2:B:2647:U:O4'	2.13	0.48
10:J:110:ASP:OD1	10:J:112:LYS:HE3	2.14	0.48
14:N:60:ARG:HA	23:W:178:GLU:O	2.14	0.48
24:X:2:ALA:HB3	4:IA:76:A:H62	1.78	0.48
38:MA:127:THR:HG23	38:MA:147:ALA:HB3	1.95	0.48
43:RA:42:ARG:HE	43:RA:42:ARG:HB2	1.57	0.48
43:RA:121:ARG:HB2	43:RA:121:ARG:HH11	1.78	0.48
1:FB:270:A:H2'	1:FB:271:C:C6	2.49	0.48
1:FB:1031:G:H8	1:FB:1032(B):G:H1	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:1070:U:H2'	1:FB:1071:C:C6	2.48	0.48
2:GB:125:G:H4'	2:GB:126:A:OP2	2.13	0.48
7:LB:95:ARG:HD3	7:LB:97:TYR:CZ	2.49	0.48
10:OB:6:LEU:HG	10:OB:36:ALA:HA	1.96	0.48
11:PB:30:ILE:HG22	11:PB:34:LEU:HD22	1.96	0.48
13:RB:83:VAL:HG12	13:RB:112:LEU:HD21	1.94	0.48
17:VB:129:ARG:HA	17:VB:132:LYS:HZ3	1.76	0.48
35:OC:214:LEU:O	35:OC:216:ASP:N	2.47	0.48
2:B:900:A:H2'	2:B:901:A:O4'	2.14	0.48
2:B:1902:C:H5'	5:E:246:PRO:HD3	1.96	0.48
2:B:2114:A:H2	2:B:2171:A:H61	1.62	0.48
2:B:2115:G:H2'	2:B:2117:A:N7	2.29	0.48
2:B:2593:U:H2'	2:B:2594:C:C6	2.49	0.48
2:B:2875:C:O2'	17:Q:2:ASN:OD1	2.26	0.48
5:E:136:ILE:HG22	5:E:140:THR:OG1	2.14	0.48
8:H:7:LEU:HD22	8:H:176:LEU:HD22	1.96	0.48
13:M:81:GLN:HB2	13:M:110:TYR:CD1	2.49	0.48
21:U:53:LYS:HG2	21:U:82:GLN:HB3	1.96	0.48
1:FB:881:G:OP2	46:ZC:12:ARG:NH2	2.47	0.48
2:GB:370:G:H4'	2:GB:371:A:OP2	2.14	0.48
2:GB:607:U:OP1	7:LB:102:PRO:HA	2.14	0.48
2:GB:1058:G:N2	2:GB:1080:C:H42	2.11	0.48
2:GB:1179:C:H2'	2:GB:1180:C:C6	2.48	0.48
2:GB:1448:G:H4'	2:GB:1543:A:OP1	2.14	0.48
2:GB:1798:U:H5'	5:JB:259:THR:CG2	2.34	0.48
2:GB:2114:A:H2	2:GB:2171:A:H61	1.62	0.48
2:GB:2243:U:H2'	2:GB:2244:U:C6	2.48	0.48
8:MB:113:ARG:HD2	28:GC:33:VAL:HG13	1.94	0.48
13:RB:2:LYS:HB3	13:RB:2:LYS:HZ3	1.79	0.48
32:KC:54:GLU:O	32:KC:58:ILE:HG13	2.14	0.48
1:A:137:C:H2'	1:A:138:G:H8	1.79	0.47
1:A:1031:G:H8	1:A:1032(B):G:H1	1.62	0.47
2:B:1587:A:H2'	2:B:1588:C:H6	1.79	0.47
9:I:60:ARG:O	9:I:64:LEU:HG	2.14	0.47
39:NA:31:LEU:HD23	39:NA:31:LEU:HA	1.72	0.47
1:FB:59:A:H1'	1:FB:354:G:N2	2.30	0.47
1:FB:693:G:H2'	1:FB:694:A:C8	2.48	0.47
1:FB:938:A:C6	1:FB:939:G:C5	3.02	0.47
1:FB:1314:C:H2'	1:FB:1315:U:C6	2.49	0.47
2:GB:492:A:H2'	2:GB:493:G:O4'	2.13	0.47
3:HB:16:G:N2	3:HB:69:G:H1'	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:JB:274:ARG:HH11	5:JB:274:ARG:HG2	1.79	0.47
10:OB:118:LYS:HE2	10:OB:121:LYS:HE3	1.95	0.47
28:GC:14:ILE:HG12	28:GC:31:ILE:HG13	1.96	0.47
35:OC:138:TYR:HE1	35:OC:338:ASP:OD2	1.97	0.47
43:WC:11:LYS:O	43:WC:13:ALA:N	2.35	0.47
45:YC:108:ILE:HB	52:FD:87:ARG:HB3	1.96	0.47
46:ZC:53:ARG:HG3	46:ZC:93:LEU:HD21	1.96	0.47
1:A:857:C:H2'	1:A:858:G:O4'	2.14	0.47
1:A:1158:C:O2'	36:KA:133:LYS:NZ	2.47	0.47
2:B:1111:A:N3	2:B:1112:G:H1'	2.30	0.47
2:B:2564:A:OP1	2:B:2648:C:H4'	2.14	0.47
23:W:54:HIS:ND1	23:W:101:PRO:HG3	2.29	0.47
30:DA:14:THR:O	30:DA:17:LYS:NZ	2.48	0.47
39:NA:84:PHE:HB3	39:NA:134:ALA:HB2	1.95	0.47
47:VA:23:TYR:HB3	47:VA:67:GLU:HA	1.95	0.47
47:VA:29:ARG:NH1	47:VA:64:TRP:CG	2.82	0.47
1:FB:1132:C:H2'	1:FB:1133:G:H8	1.78	0.47
2:GB:154(A):C:H2'	2:GB:161:U:C5	2.49	0.47
2:GB:674:G:P	7:LB:54:ARG:HH22	2.38	0.47
2:GB:998:C:OP2	18:WB:58:ARG:NH2	2.41	0.47
2:GB:1007:C:OP1	11:PB:35:ARG:NH1	2.48	0.47
2:GB:1516:U:H2'	2:GB:1517:G:H8	1.79	0.47
2:GB:2082:A:H2'	2:GB:2083:G:O4'	2.14	0.47
2:GB:2567:G:H2'	2:GB:2568:C:C6	2.49	0.47
2:GB:2850:A:OP2	2:GB:2866:U:H5	1.97	0.47
8:MB:166:ASP:O	8:MB:170:ARG:N	2.40	0.47
10:OB:110:ASP:HB3	10:OB:113:ARG:HG2	1.96	0.47
23:BC:54:HIS:CG	23:BC:101:PRO:HG3	2.49	0.47
23:BC:54:HIS:ND1	23:BC:101:PRO:HG3	2.29	0.47
38:RC:26:CYS:SG	38:RC:31:CYS:SG	3.12	0.47
38:RC:53:ASP:O	38:RC:57:ARG:HD2	2.13	0.47
42:VC:64:LYS:HG3	42:VC:79:VAL:HG21	1.95	0.47
2:B:1430:C:H2'	2:B:1431:U:C6	2.49	0.47
3:C:42:C:O2	8:H:93:THR:N	2.39	0.47
10:J:69:LYS:NZ	10:J:73:GLU:OE2	2.44	0.47
23:W:54:HIS:CG	23:W:101:PRO:HG3	2.50	0.47
25:Y:95:LEU:O	25:Y:98:LEU:HB2	2.14	0.47
26:Z:37:PHE:O	26:Z:40:SER:HB3	2.14	0.47
40:OA:36:ARG:NH2	40:OA:66:GLU:OE1	2.46	0.47
1:FB:1241:G:H2'	1:FB:1242:C:C6	2.50	0.47
1:FB:1356:G:H2'	1:FB:1357:A:H8	1.75	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:1309:G:H4'	31:JC:7:PRO:HB2	1.96	0.47
2:GB:1939:5MU:OP1	2:GB:2604:U:O2'	2.28	0.47
10:OB:1:MET:N	10:OB:21:VAL:O	2.43	0.47
13:RB:135:LEU:HD13	13:RB:139:LYS:HD2	1.95	0.47
15:TB:12:ARG:HD3	15:TB:16:HIS:CD2	2.48	0.47
15:TB:70:LEU:O	15:TB:72:ASP:N	2.47	0.47
37:QC:85:ARG:HG2	37:QC:88:ARG:HH21	1.79	0.47
38:RC:148:VAL:HG12	38:RC:181:MET:O	2.15	0.47
1:A:939:G:H2'	1:A:940:C:C6	2.49	0.47
1:A:1007:C:H42	1:A:1022:G:H1	1.63	0.47
1:A:1278:U:H5''	1:A:1279:A:O4'	2.14	0.47
2:B:1914:C:OP2	2:B:1915:5MU:H72	2.13	0.47
2:B:2163:C:H5'	2:B:2164:C:OP2	2.15	0.47
2:B:2747:G:OP1	9:I:138:LYS:NZ	2.41	0.47
2:B:2849:U:OP2	17:Q:95:ARG:NH1	2.47	0.47
4:D:32:5MC:H2'	4:D:33:U:O4'	2.13	0.47
13:M:135:LEU:HD13	13:M:139:LYS:HD2	1.96	0.47
23:W:158:PRO:O	23:W:161:VAL:HB	2.15	0.47
32:FA:54:GLU:O	32:FA:58:ILE:HG13	2.13	0.47
36:KA:44:LEU:H	36:KA:44:LEU:HD12	1.80	0.47
36:KA:130:ARG:HG2	36:KA:131:PRO:HD2	1.95	0.47
38:MA:201:GLN:HE21	39:NA:99:GLY:HA2	1.78	0.47
43:RA:48:GLU:N	43:RA:49:PRO:HD2	2.29	0.47
1:FB:240:C:H42	1:FB:286:G:H1	1.63	0.47
1:FB:985:C:H2'	1:FB:986:A:C8	2.48	0.47
1:FB:1070:U:H2'	1:FB:1071:C:H6	1.79	0.47
1:FB:1278:U:H5''	1:FB:1279:A:O4'	2.14	0.47
2:GB:880:G:H1	2:GB:897:C:N4	2.12	0.47
2:GB:2869:G:H2'	2:GB:2870:C:O4'	2.14	0.47
9:NB:60:ARG:O	9:NB:64:LEU:HG	2.15	0.47
9:NB:126:PRO:HB2	9:NB:127:GLU:H	1.58	0.47
13:RB:84:ASN:HB2	13:RB:86:LYS:HG2	1.96	0.47
14:SB:110:THR:OG1	14:SB:113:GLN:HB2	2.15	0.47
24:CC:2:ALA:HB3	4:NC:76:A:H62	1.80	0.47
25:DC:64:ALA:HA	25:DC:67:ILE:HG13	1.97	0.47
34:MC:20:A:N6	35:OC:190:THR:OG1	2.46	0.47
36:PC:7:VAL:HB	36:PC:8:LYS:HD2	1.96	0.47
1:A:401:C:O2'	1:A:621:A:N3	2.43	0.47
1:A:974:A:H8	1:A:974:A:OP1	1.98	0.47
1:A:1070:U:H2'	1:A:1071:C:H6	1.79	0.47
2:B:249:C:O2	32:FA:12:LYS:NZ	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1058:G:N2	2:B:1080:C:H42	2.12	0.47
2:B:1550:C:H2'	2:B:1551:C:H6	1.79	0.47
2:B:2693:A:H2'	2:B:2694:G:H8	1.79	0.47
4:D:68:C:H2'	4:D:69:C:H6	1.79	0.47
25:Y:11:ARG:HB2	25:Y:12:PRO:HD2	1.95	0.47
30:DA:6:ARG:NH1	30:DA:26:ASN:HB2	2.28	0.47
34:HA:13:A:H2'	34:HA:14:A:H4'	1.96	0.47
38:MA:111:ALA:HB2	38:MA:120:LEU:HD12	1.96	0.47
39:NA:79:GLU:CD	39:NA:79:GLU:H	2.22	0.47
43:RA:34:ASN:O	43:RA:38:GLN:HB3	2.13	0.47
44:SA:49:VAL:HG23	48:WA:41:ARG:HB2	1.96	0.47
2:GB:586:A:N1	2:GB:809:G:O2'	2.41	0.47
2:GB:1313:U:H2'	2:GB:1610:A:C2	2.50	0.47
2:GB:2794:C:H42	2:GB:2802:G:H1	1.61	0.47
26:EC:1:MET:HE1	26:EC:9:GLN:HG3	1.96	0.47
38:RC:21:LEU:O	38:RC:22:LYS:HB2	2.13	0.47
38:RC:105:VAL:HG13	38:RC:110:PHE:HB2	1.95	0.47
41:UC:57:GLU:H	41:UC:60:LYS:NZ	2.05	0.47
43:WC:34:ASN:O	43:WC:38:GLN:HB3	2.13	0.47
44:XC:57:LYS:HG3	44:XC:60:ARG:HH21	1.79	0.47
49:CD:26:GLU:HG3	49:CD:81:LEU:HD22	1.96	0.47
1:A:1003:G:H1	1:A:1038:C:N4	2.12	0.47
1:A:1017:G:H2'	1:A:1018:C:C6	2.50	0.47
2:B:194:G:H2'	2:B:195:A:O4'	2.13	0.47
2:B:2798:C:H5''	2:B:2799:A:OP2	2.15	0.47
9:I:97:ARG:O	9:I:97:ARG:HD3	2.14	0.47
16:P:68:GLN:HG2	16:P:71:ARG:HH21	1.79	0.47
17:Q:100:TYR:HD1	17:Q:103:ARG:NH1	2.12	0.47
20:T:78:GLU:CD	20:T:99:ARG:HH11	2.22	0.47
23:W:152:ALA:C	23:W:154:ASP:H	2.23	0.47
34:HA:20:A:N6	35:JA:190:THR:OG1	2.46	0.47
38:MA:8:VAL:HA	38:MA:11:LEU:HD13	1.97	0.47
46:UA:7:ILE:O	46:UA:11:VAL:HG23	2.14	0.47
2:GB:540:G:H2'	2:GB:541:C:H6	1.80	0.47
3:HB:112:G:H2'	3:HB:113:C:C6	2.50	0.47
37:QC:77:ILE:HG23	37:QC:84:ILE:HD12	1.96	0.47
42:VC:121:ASP:N	42:VC:121:ASP:OD1	2.47	0.47
46:ZC:11:VAL:HG13	51:ED:29:HIS:CD2	2.50	0.47
48:BD:2:ALA:HA	48:BD:6:LEU:HD13	1.95	0.47
2:B:1165:U:H2'	2:B:1166:C:C6	2.50	0.47
2:B:1826:G:H4'	5:E:242:ARG:HH21	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2695:C:H2'	2:B:2696:U:C6	2.50	0.47
2:B:2850:A:OP2	2:B:2866:U:H5	1.98	0.47
25:Y:40:ARG:C	25:Y:40:ARG:HD3	2.40	0.47
26:Z:46:GLN:HB2	26:Z:49:LYS:HE3	1.97	0.47
27:AA:29:ARG:NH1	27:AA:29:ARG:HB2	2.30	0.47
29:CA:32:PRO:HG3	29:CA:39:MET:HE1	1.96	0.47
36:KA:97:TRP:CH2	36:KA:176:GLU:OE2	2.68	0.47
37:LA:191:THR:OG1	37:LA:194:GLY:O	2.22	0.47
38:MA:18:LYS:NZ	38:MA:31:CYS:HG	2.06	0.47
38:MA:196:LEU:HD12	38:MA:196:LEU:HA	1.81	0.47
40:OA:27:GLN:HA	40:OA:30:LEU:HD12	1.95	0.47
46:UA:11:VAL:HG13	51:ZA:29:HIS:HD2	1.80	0.47
46:UA:28:LYS:HZ3	46:UA:64:TYR:HE2	1.61	0.47
1:FB:509:A:N3	1:FB:543:C:O2'	2.38	0.47
1:FB:1017:G:H2'	1:FB:1018:C:C6	2.50	0.47
1:FB:1368:G:H4'	44:XC:46:ARG:HH11	1.77	0.47
1:FB:1418:A:H5''	1:FB:1419:G:OP2	2.14	0.47
2:GB:1085:A:OP2	2:GB:1085:A:H8	1.98	0.47
2:GB:2021:C:OP1	29:HC:12:SER:OG	2.28	0.47
2:GB:2141:G:N2	2:GB:2151:G:H1'	2.30	0.47
2:GB:2792:G:H2'	2:GB:2793:G:H8	1.78	0.47
2:GB:2889:C:H2'	2:GB:2891:G:O4'	2.14	0.47
3:HB:42:C:O2	8:MB:93:THR:N	2.38	0.47
5:JB:228:PRO:HD3	5:JB:235:GLY:CA	2.45	0.47
7:LB:53:THR:HG23	7:LB:55:GLY:H	1.79	0.47
9:NB:102:ALA:HA	9:NB:117:PRO:HD3	1.97	0.47
9:NB:140:LYS:HE2	9:NB:140:LYS:HB3	1.68	0.47
11:PB:39:ARG:HH21	11:PB:48:MET:HE2	1.80	0.47
13:RB:65:ARG:HG3	13:RB:66:GLY:N	2.29	0.47
14:SB:60:ARG:HA	23:BC:179:ASP:HA	1.96	0.47
14:SB:116:GLU:OE2	14:SB:119:ARG:NH2	2.45	0.47
20:YB:20:VAL:O	20:YB:23:LEU:HB2	2.15	0.47
4:NC:65:C:H2'	4:NC:66:C:H6	1.80	0.47
35:OC:104:ASP:CG	35:OC:105:PRO:HD2	2.40	0.47
35:OC:134:MET:SD	35:OC:337:LEU:HD21	2.54	0.47
35:OC:314:GLN:HB2	35:OC:316:ARG:HD2	1.96	0.47
42:VC:125:ARG:NH1	42:VC:125:ARG:HG2	2.30	0.47
51:ED:45:HIS:HB3	51:ED:72:ARG:HG2	1.95	0.47
54:HD:23:ARG:NH1	54:HD:24:LEU:HD22	2.30	0.47
1:A:149:A:H2'	1:A:150:C:C6	2.50	0.47
1:A:620:C:C2	38:MA:135:LEU:HG	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:G:H2'	1:A:640:A:H8	1.79	0.47
2:B:91:A:C4	2:B:92:G:C8	3.03	0.47
2:B:1520:U:H2'	2:B:1521:G:O4'	2.15	0.47
2:B:1592:C:H2'	2:B:1593:G:H8	1.78	0.47
11:K:39:ARG:HH21	11:K:48:MET:HE2	1.80	0.47
13:M:63:PRO:HB2	32:FA:30:ARG:HH21	1.79	0.47
17:Q:132:LYS:HG2	17:Q:136:GLN:HE21	1.80	0.47
36:KA:157:ARG:O	36:KA:158:LEU:HB3	2.13	0.47
38:MA:105:VAL:HG13	38:MA:110:PHE:HB2	1.95	0.47
52:AB:70:ILE:O	52:AB:74:ARG:HG3	2.15	0.47
1:FB:1226:C:N4	47:AD:104:ARG:HD2	2.30	0.47
1:FB:1240:U:H4'	41:UC:38:LEU:HD21	1.95	0.47
2:GB:1448:G:O2'	2:GB:1529:A:N1	2.48	0.47
2:GB:1550:C:H2'	2:GB:1551:C:H6	1.80	0.47
2:GB:1587:A:H2'	2:GB:1588:C:C6	2.50	0.47
2:GB:1587:A:H2'	2:GB:1588:C:H6	1.79	0.47
2:GB:1639:U:H4'	2:GB:2699:C:H4'	1.97	0.47
2:GB:2031:A:C6	2:GB:2498:C:H1'	2.50	0.47
4:IB:8:4SU:H2'	4:IB:13:C:H42	1.80	0.47
9:NB:13:LYS:HA	9:NB:14:GLY:HA2	1.60	0.47
19:XB:69:LYS:HA	19:XB:88:ARG:HG2	1.96	0.47
37:QC:19:GLU:HG2	37:QC:54:ARG:CZ	2.45	0.47
54:HD:14:LYS:O	54:HD:18:GLN:HG3	2.15	0.47
1:A:272:C:H2'	1:A:273:A:H8	1.79	0.47
2:B:643:A:C8	30:DA:44:ARG:NH1	2.82	0.47
2:B:911:A:H2'	14:N:9:TYR:OH	2.15	0.47
5:E:206:LEU:HD22	5:E:211:ARG:HG2	1.97	0.47
6:F:45:THR:O	6:F:82:ARG:HD2	2.15	0.47
16:P:15:ARG:NH1	16:P:88:ASP:OD2	2.47	0.47
37:LA:180:ALA:HA	37:LA:206:GLU:HA	1.97	0.47
41:PA:129:GLU:OE1	41:PA:131:LYS:NZ	2.38	0.47
42:QA:121:ASP:OD1	42:QA:121:ASP:N	2.48	0.47
45:TA:34:ASP:OD1	45:TA:38:ASN:HB2	2.15	0.47
1:FB:432:A:H3'	1:FB:433:C:C6	2.50	0.47
2:GB:455:C:N3	2:GB:472:A:H2'	2.30	0.47
2:GB:2055:C:H5'	2:GB:2056:G:O5'	2.14	0.47
4:IB:51:C:H2'	4:IB:52:G:C8	2.50	0.47
5:JB:136:ILE:HG22	5:JB:140:THR:OG1	2.15	0.47
15:TB:36:THR:HG22	15:TB:37:THR:H	1.80	0.47
16:UB:10:ARG:O	16:UB:14:VAL:HG12	2.15	0.47
23:BC:152:ALA:C	23:BC:154:ASP:H	2.23	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:SC:31:LEU:HD23	39:SC:31:LEU:HA	1.71	0.47
39:SC:79:GLU:H	39:SC:79:GLU:CD	2.23	0.47
42:VC:92:ARG:HG2	42:VC:92:ARG:HH11	1.79	0.47
50:DD:1:MET:SD	50:DD:1:MET:N	2.80	0.47
1:A:756:C:H2'	1:A:757:U:O4'	2.14	0.47
1:A:1460:A:P	54:CB:27:LYS:HZ2	2.37	0.47
2:B:811:U:H2'	13:M:21:ARG:HA	1.97	0.47
5:E:8:PRO:HB3	5:E:14:ARG:HB2	1.96	0.47
35:JA:115:VAL:HG12	35:JA:162:ILE:HG22	1.97	0.47
36:KA:21:ARG:O	36:KA:23:ARG:N	2.47	0.47
37:LA:135:LYS:HA	37:LA:138:VAL:HG12	1.97	0.47
38:MA:18:LYS:HG3	38:MA:20:TYR:H	1.79	0.47
42:QA:101:PRO:HG3	42:QA:133:LEU:HD11	1.96	0.47
54:CB:30:LYS:HA	54:CB:33:ILE:HG12	1.96	0.47
1:FB:1314:C:OP2	53:GD:4:SER:OG	2.28	0.47
2:GB:1405:U:H2'	2:GB:1406:U:C6	2.49	0.47
2:GB:2114:A:H2	2:GB:2171:A:N6	2.13	0.47
2:GB:2306:C:N4	8:MB:42:GLY:O	2.42	0.47
2:GB:2557:G:H2'	2:GB:2558:C:C6	2.50	0.47
2:GB:2646:C:OP2	2:GB:2732:G:O2'	2.31	0.47
6:KB:4:ILE:HD13	6:KB:28:ALA:HB1	1.96	0.47
6:KB:78:LEU:HD13	6:KB:78:LEU:HA	1.81	0.47
8:MB:114:ILE:HG22	8:MB:140:ILE:HG12	1.96	0.47
11:PB:34:LEU:HD21	11:PB:120:LEU:HB2	1.97	0.47
14:SB:79:LEU:HD13	14:SB:80:GLU:HG3	1.97	0.47
45:YC:86:GLY:O	45:YC:91:ARG:NH1	2.41	0.47
47:AD:14:ARG:HG3	47:AD:44:ARG:CZ	2.45	0.47
1:A:191(D):U:H2'	1:A:191(E):G:C8	2.50	0.46
1:A:474:G:H5'	50:YA:81:ARG:HG2	1.97	0.46
1:A:519:C:OP2	35:JA:304:SER:HB3	2.15	0.46
1:A:678:U:H2'	1:A:679:C:C6	2.50	0.46
2:B:1923:U:H2'	2:B:1924:C:C6	2.51	0.46
25:Y:54:ALA:C	25:Y:56:GLN:H	2.23	0.46
27:AA:30:ARG:HH11	27:AA:30:ARG:HG3	1.79	0.46
42:QA:123:GLU:O	42:QA:127:LEU:HD22	2.15	0.46
1:FB:192:U:H2'	1:FB:193:C:C6	2.50	0.46
1:FB:757:U:H2'	1:FB:758:G:O4'	2.15	0.46
2:GB:583:G:OP2	18:WB:10:ARG:HD2	2.15	0.46
2:GB:1070:A:N6	2:GB:1097:U:O2'	2.47	0.46
2:GB:1400:G:H2'	2:GB:1401:G:C8	2.50	0.46
2:GB:1653:G:H5''	15:TB:2:ARG:HD3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:2758:A:C4	9:NB:67:LEU:HD21	2.50	0.46
3:HB:1:U:OP2	3:HB:1:U:C6	2.67	0.46
5:JB:8:PRO:HB3	5:JB:14:ARG:HB2	1.97	0.46
20:YB:73:ALA:HB3	20:YB:106:ILE:HB	1.97	0.46
23:BC:155:LEU:O	23:BC:157:LEU:HD12	2.15	0.46
36:PC:177:ALA:HB1	36:PC:182:ILE:HB	1.97	0.46
44:XC:67:THR:O	44:XC:67:THR:OG1	2.32	0.46
45:YC:121:PRO:HB2	45:YC:125:PHE:HB2	1.97	0.46
47:AD:66:LEU:C	47:AD:70:LEU:HB2	2.40	0.46
1:A:1367:C:H5'	44:SA:60:ARG:HH12	1.79	0.46
2:B:278:A:H2'	2:B:279:C:O4'	2.16	0.46
2:B:280:C:C2	2:B:361:G:N2	2.83	0.46
2:B:295:G:H4'	22:V:1:MET:HE3	1.96	0.46
2:B:1073:A:H5''	2:B:1074:G:C8	2.51	0.46
2:B:1409:C:H2'	2:B:1410:G:C8	2.50	0.46
2:B:1790:C:H5''	2:B:1791:A:OP1	2.14	0.46
2:B:2622:C:O2'	2:B:2825:G:N7	2.46	0.46
7:G:110:LEU:HD21	7:G:181:LEU:HG	1.96	0.46
11:K:30:ILE:HG22	11:K:34:LEU:HD22	1.97	0.46
35:JA:214:LEU:O	35:JA:216:ASP:N	2.48	0.46
44:SA:25:GLU:OE2	44:SA:25:GLU:N	2.46	0.46
49:XA:26:GLU:HG3	49:XA:81:LEU:HD22	1.96	0.46
1:FB:731:G:OP1	1:FB:766:A:H1'	2.16	0.46
1:FB:1511:G:H2'	1:FB:1512:U:O4'	2.15	0.46
2:GB:1291:C:H2'	2:GB:1292:U:C6	2.49	0.46
2:GB:1317:A:H2'	2:GB:1318:C:C6	2.50	0.46
9:NB:126:PRO:HG2	9:NB:130:ARG:CZ	2.45	0.46
35:OC:149:MET:HE2	35:OC:149:MET:HB3	1.76	0.46
36:PC:220:ASP:C	36:PC:222:ILE:H	2.23	0.46
44:XC:49:VAL:HG23	48:BD:41:ARG:HB2	1.96	0.46
54:HD:53:LEU:O	54:HD:57:ARG:HG3	2.14	0.46
1:A:4:U:O4	42:QA:105:ARG:HG3	2.16	0.46
1:A:126:G:OP1	1:A:605:U:O2'	2.32	0.46
1:A:174:C:H2'	1:A:175:C:C6	2.51	0.46
1:A:528:C:H41	46:UA:49:ASN:CG	2.23	0.46
2:B:1060:U:C5'	2:B:1061:U:H3'	2.45	0.46
2:B:1870:C:H2'	2:B:1871:A:O4'	2.16	0.46
38:MA:177:ASP:OD1	38:MA:180:GLY:HA3	2.15	0.46
44:SA:45:ARG:HG3	44:SA:47:PHE:HE2	1.79	0.46
1:FB:397:A:H5'	1:FB:398:C:OP1	2.15	0.46
1:FB:939:G:H2'	1:FB:940:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:1460:A:P	54:HD:27:LYS:NZ	2.88	0.46
2:GB:1441:G:H2'	2:GB:1442:G:C8	2.51	0.46
2:GB:2350:C:H2'	2:GB:2351:G:O4'	2.15	0.46
2:GB:2863:C:OP1	17:VB:93:ARG:NH1	2.48	0.46
4:IB:75:C:H5'	25:DC:30:VAL:HG21	1.97	0.46
6:KB:24:THR:HG22	6:KB:186:GLY:O	2.15	0.46
21:ZB:53:LYS:HG2	21:ZB:82:GLN:HB3	1.97	0.46
23:BC:69:THR:HG22	23:BC:90:VAL:HA	1.97	0.46
39:SC:147:ASP:OD2	39:SC:150:ARG:NH2	2.48	0.46
42:VC:87:SER:HA	42:VC:93:VAL:HG23	1.98	0.46
54:HD:73:HIS:ND1	54:HD:75:ASN:OD1	2.47	0.46
1:A:272:C:H2'	1:A:273:A:C8	2.50	0.46
1:A:1277:C:H1'	1:A:1282:C:H1'	1.97	0.46
1:A:1452:C:O5'	1:A:1452:C:H6	1.98	0.46
2:B:270(A):A:H1'	2:B:370:G:C2	2.51	0.46
2:B:1313:U:H2'	2:B:1610:A:C2	2.50	0.46
2:B:1511:A:C8	2:B:1512:G:C8	3.02	0.46
7:G:107:LYS:HZ1	7:G:207:GLY:H	1.62	0.46
11:K:72:TYR:HE2	11:K:87:LEU:HG	1.81	0.46
13:M:86:LYS:HB3	13:M:118:GLY:HA3	1.98	0.46
24:X:65:GLY:HA2	24:X:84:LEU:HG	1.98	0.46
4:IA:23:C:H2'	4:IA:24:U:C6	2.50	0.46
35:JA:196:ILE:HD13	35:JA:313:PRO:HG2	1.96	0.46
39:NA:107:ARG:HG3	39:NA:107:ARG:HH11	1.80	0.46
42:QA:51:VAL:HG21	42:QA:60:ARG:NH1	2.30	0.46
43:RA:127:LYS:NZ	43:RA:127:LYS:HB3	2.30	0.46
46:UA:83:VAL:HG23	46:UA:107:ALA:HB2	1.96	0.46
54:CB:53:LEU:O	54:CB:57:ARG:HG3	2.15	0.46
1:FB:1320:C:H2'	1:FB:1321:C:O4'	2.15	0.46
1:FB:1427:U:H2'	1:FB:1428:A:C8	2.50	0.46
2:GB:270(W):G:H2'	2:GB:270(X):G:H8	1.80	0.46
2:GB:1568:G:P	5:JB:63:ARG:HH22	2.38	0.46
4:IB:32:5MC:H2'	4:IB:33:U:O4'	2.15	0.46
5:JB:147:LEU:HD13	5:JB:155:LEU:HD11	1.96	0.46
7:LB:53:THR:HG22	7:LB:56:GLU:HG3	1.98	0.46
34:MC:14:A:H3'	34:MC:15:A:H8	1.79	0.46
35:OC:156:HIS:HA	35:OC:157:GLY:HA2	1.73	0.46
36:PC:98:LEU:H	36:PC:101:MET:HE3	1.80	0.46
37:QC:33:LEU:HA	37:QC:36:ASP:HB2	1.97	0.46
37:QC:35:GLU:O	37:QC:39:ILE:HG13	2.15	0.46
38:RC:8:VAL:HA	38:RC:11:LEU:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:SC:152:ARG:HB3	42:VC:43:GLY:HA3	1.97	0.46
1:A:8:A:N6	38:MA:209:ARG:HB2	2.30	0.46
1:A:1513:A:H2'	1:A:1514:C:C6	2.50	0.46
2:B:2126:A:O3'	2:B:2127:G:H8	1.98	0.46
8:H:50:ALA:C	8:H:52:ILE:H	2.23	0.46
14:N:110:THR:OG1	14:N:113:GLN:HB2	2.15	0.46
15:O:72:ASP:HB3	15:O:75:LEU:HB3	1.98	0.46
36:KA:97:TRP:HH2	36:KA:176:GLU:CD	2.24	0.46
42:QA:125:ARG:HG2	42:QA:125:ARG:NH1	2.31	0.46
47:VA:50:GLU:HA	47:VA:53:VAL:HB	1.98	0.46
1:FB:45:U:H2'	1:FB:46:G:C8	2.50	0.46
1:FB:756:C:H2'	1:FB:757:U:O4'	2.16	0.46
1:FB:857:C:H2'	1:FB:858:G:O4'	2.14	0.46
1:FB:1314:C:H2'	1:FB:1315:U:H6	1.80	0.46
2:GB:601:C:OP1	7:LB:108:LYS:HE3	2.16	0.46
2:GB:1213:A:N3	2:GB:1238:G:O2'	2.42	0.46
2:GB:1536:A:H5''	2:GB:1537:C:C5	2.51	0.46
2:GB:2163:C:H5'	2:GB:2164:C:OP2	2.15	0.46
2:GB:2646:C:H2'	2:GB:2647:U:O4'	2.15	0.46
2:GB:2684:U:OP1	17:VB:53:ARG:HD3	2.15	0.46
4:IB:68:C:H2'	4:IB:69:C:H6	1.80	0.46
16:UB:10:ARG:HG2	16:UB:13:ARG:NH2	2.31	0.46
38:RC:196:LEU:HA	38:RC:197:PRO:HD3	1.81	0.46
40:TC:91:VAL:HG11	52:FD:72:ARG:NH1	2.31	0.46
51:ED:95:TYR:HA	51:ED:98:LEU:HD12	1.97	0.46
1:A:953:G:N7	47:VA:104:ARG:NH2	2.59	0.46
1:A:1418:A:H2	2:B:1948:G:N3	2.13	0.46
1:A:1427:U:H2'	1:A:1428:A:C8	2.50	0.46
2:B:1364:G:C8	25:Y:3:LYS:HD2	2.50	0.46
2:B:1490:A:H8	2:B:1490:A:O5'	1.99	0.46
2:B:1587:A:H2'	2:B:1588:C:C6	2.50	0.46
2:B:2275:C:O2	14:N:85:LYS:HG3	2.15	0.46
3:C:86:G:H1	3:C:90:C:H42	1.64	0.46
7:G:107:LYS:HD2	7:G:206:ILE:HA	1.98	0.46
27:AA:7:LYS:HB2	27:AA:34:GLU:HG2	1.97	0.46
27:AA:23:LEU:HD13	27:AA:50:VAL:HG11	1.98	0.46
40:OA:46:ARG:HB2	40:OA:60:PHE:HE1	1.79	0.46
40:OA:78:GLU:O	40:OA:81:ILE:HG22	2.16	0.46
42:QA:38:ILE:HD13	42:QA:120:THR:HG22	1.98	0.46
48:WA:4:LYS:O	48:WA:7:ILE:HG22	2.16	0.46
54:CB:30:LYS:NZ	54:CB:30:LYS:CB	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:397:A:H3'	1:FB:397:A:N3	2.30	0.46
1:FB:401:C:O2'	1:FB:621:A:N3	2.46	0.46
2:GB:195:A:H61	2:GB:198:C:H3'	1.81	0.46
2:GB:550:G:O2'	2:GB:1220:A:N3	2.40	0.46
2:GB:1057:A:H5''	2:GB:1086:A:H2	1.81	0.46
2:GB:1176:G:H3'	2:GB:1177:A:C8	2.51	0.46
2:GB:2065:C:H2'	2:GB:2066:C:C6	2.50	0.46
4:IB:31:G:H1	4:IB:39:C:N4	2.13	0.46
5:JB:17:THR:O	5:JB:211:ARG:NH2	2.43	0.46
6:KB:181:LEU:HD21	17:VB:6:LEU:HD12	1.97	0.46
11:PB:72:TYR:HE2	11:PB:87:LEU:HG	1.81	0.46
25:DC:11:ARG:HB2	25:DC:12:PRO:HD2	1.98	0.46
38:RC:127:THR:HG23	38:RC:147:ALA:HB3	1.96	0.46
40:TC:22:GLU:OE2	40:TC:84:ASN:HB2	2.16	0.46
41:UC:79:ARG:HD2	41:UC:80:VAL:N	2.30	0.46
47:AD:70:LEU:O	47:AD:74:VAL:HG23	2.16	0.46
1:A:1095:U:H2'	1:A:1096:C:C6	2.50	0.46
2:B:674:G:O2'	7:G:74:ARG:HD3	2.16	0.46
2:B:1187:G:H8	2:B:1187:G:O5'	1.98	0.46
2:B:1367:A:N7	2:B:1368:G:H1'	2.31	0.46
2:B:1532:C:H42	2:B:1539:G:H22	1.62	0.46
2:B:2114:A:H2	2:B:2171:A:N6	2.14	0.46
2:B:2889:C:H2'	2:B:2891:G:O4'	2.16	0.46
4:D:31:G:H1	4:D:39:C:N4	2.12	0.46
5:E:228:PRO:HD3	5:E:235:GLY:CA	2.46	0.46
6:F:119:ARG:HG2	6:F:120:TRP:NE1	2.30	0.46
7:G:53:THR:CG2	7:G:55:GLY:H	2.28	0.46
8:H:177:GLY:O	8:H:179:PRO:HD3	2.16	0.46
38:MA:21:LEU:O	38:MA:22:LYS:HB2	2.15	0.46
45:TA:99:GLN:HE21	52:AB:88:LYS:HZ1	1.64	0.46
50:YA:45:THR:O	50:YA:48:TRP:HD1	1.99	0.46
1:FB:639:G:H2'	1:FB:640:A:H8	1.80	0.46
2:GB:247:G:H4'	2:GB:386:G:C5	2.51	0.46
2:GB:1520:U:H2'	2:GB:1521:G:O4'	2.15	0.46
2:GB:2660:A:H2'	2:GB:2661:G:O4'	2.16	0.46
4:IB:23:C:H2'	4:IB:24:U:C6	2.50	0.46
6:KB:116:VAL:HG13	6:KB:122:PHE:HB2	1.97	0.46
41:UC:38:LEU:O	41:UC:42:ILE:HG13	2.15	0.46
44:XC:51:ARG:O	48:BD:45:ARG:NH1	2.48	0.46
1:A:376:G:H5''	50:YA:5:ARG:HD2	1.97	0.46
1:A:620:C:H2'	1:A:621:A:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:790:A:C6	1:A:791:G:C6	3.04	0.46
1:A:1201:A:H1'	1:A:1202:G:OP2	2.16	0.46
2:B:235:U:H2'	2:B:236:C:C6	2.51	0.46
2:B:742:G:H2'	2:B:743:G:C8	2.51	0.46
2:B:1021:A:H8	2:B:1021:A:H3'	1.81	0.46
10:J:7:GLU:HG3	10:J:8:PRO:HD2	1.98	0.46
10:J:83:ALA:HA	10:J:88:ILE:CG2	2.46	0.46
37:LA:92:ALA:HB2	37:LA:99:VAL:HG22	1.98	0.46
44:SA:57:LYS:HG3	44:SA:60:ARG:HH21	1.80	0.46
1:FB:81:G:H2'	1:FB:82:U:C6	2.51	0.46
2:GB:1153:C:OP1	18:WB:92:ARG:NH2	2.47	0.46
2:GB:1833:U:O2'	2:GB:1969:A:N1	2.40	0.46
10:OB:130:TYR:CE2	10:OB:132:PRO:HB3	2.51	0.46
19:XB:2:PHE:CZ	19:XB:41:GLY:HA3	2.50	0.46
21:ZB:61:GLY:HA3	21:ZB:73:ARG:O	2.16	0.46
26:EC:51:ARG:O	26:EC:55:ARG:HG2	2.16	0.46
27:FC:30:ARG:HG3	27:FC:30:ARG:HH11	1.81	0.46
36:PC:10:LEU:HA	36:PC:12:GLU:HG3	1.98	0.46
40:TC:80:ARG:HE	40:TC:88:VAL:HB	1.81	0.46
41:UC:23:VAL:HG13	41:UC:43:PHE:CE2	2.49	0.46
42:VC:51:VAL:HG21	42:VC:60:ARG:NH1	2.30	0.46
44:XC:24:VAL:HG13	44:XC:34:VAL:HG11	1.97	0.46
1:A:382:A:H2'	1:A:383:A:H8	1.81	0.46
1:A:790:A:OP1	4:IA:38:A:O2'	2.30	0.46
1:A:1465:C:H2'	1:A:1466:C:O4'	2.16	0.46
2:B:263:C:H2'	2:B:264:C:O4'	2.15	0.46
2:B:857:C:N4	2:B:858:U:O4	2.49	0.46
7:G:195:ASP:HB3	7:G:198:ALA:H	1.81	0.46
14:N:79:LEU:HD13	14:N:80:GLU:HG3	1.98	0.46
17:Q:54:ARG:HA	17:Q:59:THR:OG1	2.16	0.46
22:V:51:VAL:HA	22:V:55:TYR:O	2.16	0.46
23:W:79:ARG:HB3	23:W:80:ARG:HD3	1.97	0.46
4:IA:66:C:H2'	4:IA:67:C:C6	2.51	0.46
43:RA:22:GLY:HA3	43:RA:60:ASP:CG	2.41	0.46
54:CB:14:LYS:O	54:CB:18:GLN:HG3	2.16	0.46
1:FB:444:C:H2'	1:FB:445:G:H8	1.81	0.46
1:FB:474:G:H5'	50:DD:81:ARG:HG2	1.96	0.46
1:FB:1032(B):G:H2'	1:FB:1032(C):G:O4'	2.16	0.46
2:GB:2312:U:H5'	8:MB:88:ILE:HD11	1.98	0.46
13:RB:86:LYS:HB3	13:RB:118:GLY:HA3	1.98	0.46
27:FC:29:ARG:HB2	27:FC:29:ARG:NH1	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:RC:28:SER:HB2	38:RC:29:PRO:HD2	1.97	0.46
43:WC:48:GLU:N	43:WC:49:PRO:HD2	2.31	0.46
47:AD:3:ARG:CG	47:AD:3:ARG:NH1	2.73	0.46
54:HD:30:LYS:NZ	54:HD:30:LYS:CB	2.78	0.46
1:A:1032(B):G:H2'	1:A:1032(C):G:O4'	2.16	0.46
1:A:1314:C:H2'	1:A:1315:U:C6	2.51	0.46
1:A:1372:U:H2'	1:A:1373:G:O4'	2.16	0.46
2:B:2764:A:N7	2:B:2766:G:C6	2.84	0.46
12:L:25:LEU:HA	12:L:25:LEU:HD23	1.70	0.46
18:R:113:ALA:O	18:R:117:GLN:HG2	2.16	0.46
23:W:169:GLU:OE2	23:W:169:GLU:HA	2.16	0.46
28:BA:34:GLU:HB2	28:BA:35:VAL:H	1.53	0.46
30:DA:2:ALA:HB1	30:DA:6:ARG:O	2.16	0.46
36:KA:10:LEU:HG	36:KA:48:MET:SD	2.56	0.46
36:KA:178:ARG:HD2	36:KA:196:LEU:O	2.16	0.46
40:OA:75:LEU:O	40:OA:79:LEU:HG	2.16	0.46
51:ZA:43:LEU:HA	51:ZA:43:LEU:HD23	1.62	0.46
54:CB:23:ARG:NH1	54:CB:24:LEU:HD22	2.31	0.46
1:FB:382:A:H2'	1:FB:383:A:H8	1.81	0.46
1:FB:1452:C:O5'	1:FB:1452:C:H6	1.99	0.46
2:GB:747:U:O2	2:GB:2014:A:H1'	2.16	0.46
2:GB:862:G:H2'	2:GB:863:A:O4'	2.16	0.46
2:GB:2649:U:H2'	2:GB:2650:U:C6	2.51	0.46
2:GB:2693:A:H2'	2:GB:2694:G:C8	2.51	0.46
7:LB:140:LEU:HD12	7:LB:140:LEU:HA	1.65	0.46
10:OB:88:ILE:HD12	10:OB:89:TYR:H	1.80	0.46
11:PB:27:ALA:HB1	11:PB:103:VAL:HG22	1.97	0.46
12:QB:2:ILE:HD12	12:QB:6:THR:HG21	1.97	0.46
27:FC:23:LEU:HD13	27:FC:50:VAL:HG11	1.99	0.46
37:QC:33:LEU:HD21	48:BD:53:LEU:HD22	1.98	0.46
38:RC:177:ASP:OD2	38:RC:182:LYS:HG3	2.16	0.46
43:WC:50:LEU:HD12	43:WC:56:LEU:HD12	1.97	0.46
48:BD:4:LYS:O	48:BD:7:ILE:HG22	2.16	0.46
1:A:816:A:OP2	1:A:1527:C:H5'	2.16	0.45
1:A:1097:C:H2'	1:A:1098:C:C6	2.51	0.45
2:B:270(W):G:H2'	2:B:270(X):G:H8	1.81	0.45
2:B:929:G:H8	2:B:929:G:O5'	1.99	0.45
2:B:974(B):C:OP2	2:B:974(B):C:H4'	2.16	0.45
2:B:1988:C:H2'	2:B:1989:G:O4'	2.16	0.45
4:D:8:4SU:H2'	4:D:13:C:H42	1.82	0.45
9:I:52:VAL:O	9:I:65:HIS:NE2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:144:VAL:O	9:I:148:ILE:HG12	2.16	0.45
14:N:60:ARG:HA	23:W:179:ASP:HA	1.97	0.45
22:V:68:HIS:ND1	22:V:70:SER:HB3	2.31	0.45
27:AA:10:LYS:HB3	27:AA:53:LEU:HA	1.98	0.45
28:BA:14:ILE:HG12	28:BA:31:ILE:HG13	1.97	0.45
31:EA:5:TRP:NE1	31:EA:7:PRO:HG3	2.31	0.45
37:LA:85:ARG:HG2	37:LA:88:ARG:HH21	1.79	0.45
38:MA:177:ASP:OD2	38:MA:182:LYS:HG3	2.17	0.45
1:FB:1007:C:H42	1:FB:1022:G:H1	1.63	0.45
2:GB:686:G:H21	2:GB:788:A:H61	1.62	0.45
2:GB:871:U:H2'	2:GB:872:A:C8	2.51	0.45
2:GB:1297:C:H2'	2:GB:1298:C:H6	1.82	0.45
2:GB:1478:G:O2'	2:GB:1558:A:C2	2.69	0.45
2:GB:1814:G:H4'	5:JB:51:VAL:HG21	1.98	0.45
2:GB:1988:C:H2'	2:GB:1989:G:O4'	2.16	0.45
2:GB:2094:G:H5'	10:OB:25:TYR:CD1	2.51	0.45
2:GB:2798:C:H5''	2:GB:2799:A:OP2	2.16	0.45
7:LB:129:PHE:HB2	7:LB:132:VAL:HG21	1.97	0.45
10:OB:83:ALA:HA	10:OB:88:ILE:CG2	2.46	0.45
13:RB:77:ARG:HB2	13:RB:77:ARG:HH11	1.80	0.45
16:UB:60:GLY:O	16:UB:61:ASN:HB3	2.15	0.45
24:CC:2:ALA:N	35:OC:261:ARG:HD3	2.31	0.45
35:OC:115:VAL:HG12	35:OC:162:ILE:HG22	1.98	0.45
1:A:749:C:H2'	1:A:750:G:H8	1.81	0.45
1:A:1305:G:N2	1:A:1331:G:H1'	2.32	0.45
1:A:1312:G:N2	1:A:1325:C:O2	2.49	0.45
2:B:455:C:N3	2:B:472:A:H2'	2.31	0.45
2:B:1057:A:H5''	2:B:1086:A:H2	1.80	0.45
4:D:68:C:H2'	4:D:69:C:C6	2.51	0.45
6:F:56:PRO:C	6:F:58:ARG:H	2.25	0.45
36:KA:126:GLU:CD	36:KA:130:ARG:HB2	2.41	0.45
1:FB:1053:G:N7	1:FB:1200:C:H5'	2.31	0.45
1:FB:1223:C:P	53:GD:78:ARG:HH21	2.40	0.45
2:GB:606:U:H4'	2:GB:658:C:H4'	1.98	0.45
2:GB:776:G:H4'	2:GB:777:A:O5'	2.16	0.45
2:GB:2304:G:H22	2:GB:2312:U:H3	1.61	0.45
5:JB:121:PRO:HB3	5:JB:135:PHE:CE2	2.52	0.45
24:CC:56:ASP:O	24:CC:57:PHE:HB2	2.16	0.45
28:GC:15:ILE:HG12	28:GC:21:VAL:HG22	1.98	0.45
36:PC:98:LEU:HG	36:PC:101:MET:HE3	1.98	0.45
40:TC:22:GLU:OE1	40:TC:82:ARG:NH2	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:819:A:H4'	1:A:820:U:OP2	2.16	0.45
1:A:1005:A:H2	1:A:1024:G:H21	1.63	0.45
2:B:17:G:H2'	2:B:18:C:C6	2.51	0.45
2:B:443:A:N7	7:G:45:ARG:HG2	2.32	0.45
2:B:1441:G:H2'	2:B:1442:G:C8	2.52	0.45
2:B:1441:G:H2'	2:B:1442:G:H8	1.81	0.45
2:B:1754:C:P	17:Q:96:ARG:NH1	2.90	0.45
2:B:2319:G:O6	16:P:4:LEU:HD12	2.15	0.45
3:C:112:G:H2'	3:C:113:C:C6	2.51	0.45
10:J:8:PRO:HG3	10:J:15:VAL:HG12	1.98	0.45
17:Q:132:LYS:NZ	17:Q:132:LYS:HB2	2.31	0.45
28:BA:15:ILE:HG12	28:BA:21:VAL:HG13	1.99	0.45
35:JA:134:MET:SD	35:JA:337:LEU:HD21	2.56	0.45
40:OA:50:TYR:CE2	52:AB:77:GLY:HA2	2.51	0.45
41:PA:79:ARG:HD2	41:PA:80:VAL:N	2.32	0.45
44:SA:65:LEU:HB2	48:WA:56:VAL:HG13	1.99	0.45
51:ZA:14:LYS:HE3	51:ZA:14:LYS:H	1.80	0.45
1:FB:620:C:H2'	1:FB:621:A:O4'	2.16	0.45
1:FB:931:C:H42	1:FB:1386:G:H1	1.65	0.45
1:FB:997:U:H2'	1:FB:998(A):G:O4'	2.17	0.45
1:FB:1312:G:N2	1:FB:1325:C:O2	2.49	0.45
2:GB:547:A:C3'	2:GB:548:A:C8	2.97	0.45
2:GB:879:G:H22	2:GB:899:A:H1'	1.81	0.45
2:GB:2345:G:OP2	30:IC:38:LYS:HD3	2.17	0.45
10:OB:54:GLN:HA	10:OB:57:ARG:HH11	1.81	0.45
20:YB:65:LEU:HD12	20:YB:66:GLU:H	1.81	0.45
25:DC:2:SER:HB3	25:DC:46:LEU:HD12	1.97	0.45
31:JC:34:ARG:HH11	31:JC:34:ARG:CG	2.27	0.45
36:PC:178:ARG:HD2	36:PC:196:LEU:O	2.17	0.45
39:SC:107:ARG:HH11	39:SC:107:ARG:HG3	1.81	0.45
43:WC:108:VAL:HG12	43:WC:109:VAL:H	1.81	0.45
1:A:59:A:H1'	1:A:354:G:N2	2.32	0.45
1:A:270:A:H2'	1:A:271:C:C6	2.51	0.45
1:A:1492:A:H5'	46:UA:47:LYS:HD2	1.99	0.45
2:B:320:A:H4'	2:B:322:A:N7	2.32	0.45
2:B:1007:C:OP1	11:K:35:ARG:NH1	2.50	0.45
2:B:1317:A:H2'	2:B:1318:C:C6	2.52	0.45
2:B:1639:U:H4'	2:B:2699:C:H4'	1.98	0.45
2:B:2649:U:H2'	2:B:2650:U:C6	2.51	0.45
7:G:64:ILE:H	7:G:64:ILE:HG13	1.46	0.45
9:I:3:ARG:NH2	9:I:5:GLY:H	2.13	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:2:LEU:O	14:N:3:MET:HB3	2.16	0.45
16:P:10:ARG:O	16:P:14:VAL:HG12	2.17	0.45
20:T:65:LEU:HD12	20:T:66:GLU:N	2.32	0.45
36:KA:163:PHE:HD2	36:KA:163:PHE:HA	1.64	0.45
41:PA:23:VAL:HG13	41:PA:43:PHE:CE2	2.52	0.45
1:FB:1097:C:H2'	1:FB:1098:C:C6	2.52	0.45
2:GB:270(A):A:H1'	2:GB:370:G:C2	2.52	0.45
2:GB:2064:C:H2'	2:GB:2065:C:C6	2.51	0.45
16:UB:68:GLN:HG2	16:UB:71:ARG:HH21	1.82	0.45
20:YB:82:LEU:HD22	20:YB:84:ARG:HH22	1.82	0.45
36:PC:12:GLU:HA	36:PC:15:VAL:HG22	1.98	0.45
42:VC:38:ILE:HD13	42:VC:120:THR:HG22	1.98	0.45
47:AD:66:LEU:HA	47:AD:70:LEU:HD12	1.97	0.45
1:A:555:C:H2'	1:A:556:C:C6	2.51	0.45
2:B:306:U:H2'	2:B:307:G:O4'	2.16	0.45
2:B:547:A:H8	2:B:547:A:O5'	1.99	0.45
2:B:648:G:H21	32:FA:46:ARG:NH1	2.07	0.45
2:B:725:G:C6	2:B:726:G:N1	2.85	0.45
2:B:2869:G:H2'	2:B:2870:C:O4'	2.17	0.45
9:I:126:PRO:HG2	9:I:130:ARG:CZ	2.46	0.45
25:Y:64:ALA:HA	25:Y:67:ILE:HG13	1.98	0.45
41:PA:116:ALA:HA	41:PA:119:ARG:NH1	2.32	0.45
53:BB:29:ARG:NH1	53:BB:29:ARG:HA	2.32	0.45
54:CB:23:ARG:HH11	54:CB:24:LEU:HD22	1.80	0.45
1:FB:174:C:H2'	1:FB:175:C:C6	2.52	0.45
1:FB:528:C:H41	46:ZC:49:ASN:CG	2.24	0.45
2:GB:742:G:H2'	2:GB:743:G:C8	2.50	0.45
2:GB:1999:C:H4'	2:GB:2723:C:O2	2.17	0.45
8:MB:135:LEU:HD12	8:MB:136:ARG:HH21	1.81	0.45
36:PC:19:HIS:NE2	36:PC:206:ASP:HB2	2.32	0.45
36:PC:97:TRP:CH2	36:PC:176:GLU:OE2	2.69	0.45
38:RC:4:TYR:HD2	38:RC:4:TYR:HA	1.70	0.45
38:RC:18:LYS:HG3	38:RC:20:TYR:H	1.82	0.45
51:ED:78:GLU:OE2	51:ED:81:ARG:HD3	2.17	0.45
54:HD:23:ARG:HH11	54:HD:24:LEU:HD22	1.81	0.45
2:B:489:G:N7	20:T:49:LYS:NZ	2.65	0.45
2:B:2208:U:H4'	5:E:151:LYS:HG2	1.97	0.45
2:B:2749:A:OP1	9:I:3:ARG:NH1	2.30	0.45
10:J:43:ASN:N	10:J:43:ASN:OD1	2.50	0.45
17:Q:91:ARG:HG2	17:Q:91:ARG:NH1	2.27	0.45
22:V:9:LYS:HA	22:V:10:GLY:HA2	1.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:15:ILE:HG12	28:BA:21:VAL:HG22	1.98	0.45
36:KA:10:LEU:HA	36:KA:12:GLU:HG3	1.97	0.45
39:NA:144:THR:O	39:NA:148:VAL:HG23	2.17	0.45
40:OA:22:GLU:OE2	40:OA:84:ASN:HB2	2.16	0.45
40:OA:40:VAL:HG22	40:OA:63:TYR:CD1	2.51	0.45
42:QA:37:ARG:O	42:QA:41:ARG:HG2	2.17	0.45
46:UA:11:VAL:HG13	51:ZA:29:HIS:CD2	2.52	0.45
46:UA:53:ARG:HG3	46:UA:93:LEU:HD21	1.99	0.45
1:FB:4:U:O4	42:VC:105:ARG:HG3	2.17	0.45
1:FB:1435:G:H2'	1:FB:1436:U:C6	2.51	0.45
2:GB:330:A:H2	2:GB:1210:A:C2'	2.29	0.45
2:GB:1056:G:H1'	2:GB:1103:A:N6	2.31	0.45
2:GB:1511:A:C8	2:GB:1512:G:C8	3.05	0.45
5:JB:169:GLU:OE2	5:JB:184:LYS:HE2	2.17	0.45
8:MB:98:ARG:CG	8:MB:98:ARG:NH1	2.67	0.45
10:OB:64:GLU:HG3	10:OB:67:ARG:NH1	2.32	0.45
15:TB:79:LEU:HA	15:TB:83:ILE:HD12	1.98	0.45
17:VB:26:ASP:OD1	17:VB:120:ARG:NH2	2.46	0.45
28:GC:15:ILE:HG12	28:GC:21:VAL:HG13	1.98	0.45
4:NC:66:C:H2'	4:NC:67:C:C6	2.52	0.45
1:A:229:U:H2'	1:A:230:G:O4'	2.17	0.45
1:A:432:A:H3'	1:A:433:C:C6	2.52	0.45
2:B:579:G:H2'	2:B:580:C:C6	2.52	0.45
2:B:1448:G:H4'	2:B:1543:A:OP1	2.16	0.45
5:E:169:GLU:OE2	5:E:184:LYS:HE2	2.17	0.45
6:F:8:LYS:NZ	6:F:188:VAL:O	2.46	0.45
13:M:2:LYS:HB3	13:M:2:LYS:HZ3	1.81	0.45
13:M:80:TYR:CD1	13:M:111:ARG:HB2	2.52	0.45
14:N:1:MET:SD	14:N:45:GLN:NE2	2.90	0.45
36:KA:74:LYS:HZ3	36:KA:166:ASP:HB2	1.80	0.45
41:PA:107:ALA:HA	41:PA:110:GLN:HG2	1.99	0.45
47:VA:66:LEU:C	47:VA:70:LEU:HB2	2.42	0.45
48:WA:21:TYR:CE1	48:WA:23:ARG:NH1	2.83	0.45
1:FB:1095:U:H2'	1:FB:1096:C:C6	2.51	0.45
1:FB:1277:C:H1'	1:FB:1282:C:H1'	1.98	0.45
2:GB:1009:A:OP2	11:PB:37:LYS:NZ	2.50	0.45
2:GB:1073:A:H5''	2:GB:1074:G:C8	2.51	0.45
2:GB:1448:G:H5''	2:GB:1543:A:OP2	2.17	0.45
2:GB:2126:A:O3'	2:GB:2127:G:H8	1.98	0.45
2:GB:2334:G:O6	24:CC:74:ARG:NH2	2.49	0.45
8:MB:7:LEU:HD22	8:MB:176:LEU:HD22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:MB:16:ARG:HB2	8:MB:17:PRO:HD3	1.99	0.45
10:OB:8:PRO:HG3	10:OB:15:VAL:HG12	1.99	0.45
23:BC:108:PRO:HG3	23:BC:141:VAL:HG22	1.98	0.45
36:PC:70:PHE:CE1	36:PC:163:PHE:HD1	2.34	0.45
43:WC:76:ALA:O	43:WC:80:GLY:N	2.47	0.45
49:CD:54:ARG:O	49:CD:58:MET:HG3	2.17	0.45
1:A:339:C:H2'	1:A:340:U:H6	1.82	0.45
1:A:563:A:N7	1:A:567:G:H1'	2.31	0.45
2:B:606:U:H4'	2:B:658:C:H4'	1.99	0.45
2:B:607:U:OP1	7:G:102:PRO:HA	2.17	0.45
2:B:1899:G:H2'	2:B:1899:G:N3	2.32	0.45
11:K:34:LEU:HD21	11:K:120:LEU:HB2	1.99	0.45
20:T:71:VAL:HA	20:T:107:LEU:HD12	1.99	0.45
43:RA:7:THR:HB	43:RA:83:ARG:HH21	1.81	0.45
45:TA:87:THR:HA	45:TA:91:ARG:HD2	1.99	0.45
47:VA:66:LEU:HA	47:VA:70:LEU:HD12	1.97	0.45
1:FB:429:U:OP1	38:RC:13:ARG:NH1	2.49	0.45
1:FB:819:A:H4'	1:FB:820:U:OP2	2.16	0.45
2:GB:252:G:P	13:RB:50:ARG:HH12	2.39	0.45
7:LB:129:PHE:HB2	7:LB:132:VAL:CG2	2.47	0.45
10:OB:29:TYR:CE1	10:OB:33:ARG:NH1	2.84	0.45
21:ZB:60:ARG:NH1	31:JC:47:ARG:NH2	2.59	0.45
36:PC:127:ILE:HG23	36:PC:135:GLN:HB2	1.99	0.45
43:WC:127:LYS:NZ	43:WC:127:LYS:HB3	2.32	0.45
1:A:1511:G:H2'	1:A:1512:U:O4'	2.15	0.45
2:B:1176:G:H3'	2:B:1177:A:C8	2.52	0.45
2:B:1478:G:O2'	2:B:1558:A:C2	2.70	0.45
2:B:1897:G:H2'	2:B:1898:U:O4'	2.17	0.45
2:B:2895:U:O5'	2:B:2895:U:H6	1.99	0.45
7:G:65:TRP:HB2	7:G:66:PRO:HD2	1.98	0.45
7:G:108:LYS:O	7:G:112:MET:HB2	2.16	0.45
23:W:108:PRO:HG3	23:W:141:VAL:HG22	1.98	0.45
35:JA:108:GLU:HB2	35:JA:170:GLY:HA2	1.99	0.45
38:MA:98:GLU:OE1	38:MA:107:ARG:NH2	2.49	0.45
1:FB:624:C:H2'	1:FB:625:G:C8	2.52	0.45
1:FB:1005:A:H2	1:FB:1024:G:H21	1.65	0.45
2:GB:637:A:OP1	13:RB:133:SER:OG	2.32	0.45
2:GB:1176:G:H8	2:GB:1177:A:C8	2.35	0.45
2:GB:2615:U:C2	29:HC:7:PRO:HA	2.52	0.45
5:JB:25:THR:HG21	5:JB:113:VAL:HG21	1.99	0.45
7:LB:107:LYS:HZ1	7:LB:207:GLY:H	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:VB:132:LYS:HG2	17:VB:136:GLN:HE21	1.81	0.45
30:IC:9:LEU:HA	30:IC:54:ILE:HB	1.98	0.45
36:PC:229:VAL:HB	36:PC:231:GLU:OE2	2.17	0.45
37:QC:130:VAL:HG21	37:QC:157:ILE:HG23	1.99	0.45
42:VC:100:ILE:O	42:VC:125:ARG:NH2	2.50	0.45
46:ZC:59:ARG:HD3	46:ZC:65:GLU:HG2	1.98	0.45
1:A:162:A:C5	1:A:163:C:H1'	2.52	0.45
1:A:325:A:H2'	1:A:326:G:O4'	2.17	0.45
1:A:985:C:H2'	1:A:986:A:C8	2.52	0.45
1:A:1273:G:H2'	1:A:1274:G:O4'	2.17	0.45
2:B:1056:G:H1'	2:B:1103:A:N6	2.32	0.45
2:B:1173:G:O2'	2:B:1177:A:N6	2.50	0.45
2:B:1289:C:H2'	2:B:1290:C:H6	1.82	0.45
2:B:1783:A:H5'	2:B:2608:G:H4'	1.99	0.45
2:B:2660:A:H2'	2:B:2661:G:O4'	2.16	0.45
8:H:98:ARG:HG3	8:H:98:ARG:NH1	2.06	0.45
9:I:13:LYS:HA	9:I:14:GLY:HA2	1.62	0.45
13:M:122:PRO:HB3	13:M:141:ALA:O	2.17	0.45
26:Z:2:LYS:HE2	26:Z:5:GLU:HG3	1.99	0.45
32:FA:28:GLY:O	32:FA:36:LYS:NZ	2.49	0.45
35:JA:165:LYS:NZ	35:JA:208:GLU:HG3	2.31	0.45
37:LA:19:GLU:HG2	37:LA:54:ARG:CZ	2.46	0.45
38:MA:53:ASP:O	38:MA:57:ARG:HD2	2.16	0.45
44:SA:24:VAL:HG13	44:SA:34:VAL:HG11	1.99	0.45
54:CB:89:ARG:O	54:CB:93:GLU:HG2	2.17	0.45
2:GB:2133:G:HO2'	2:GB:2157:G:N2	2.14	0.45
2:GB:2805:G:N2	2:GB:2807:G:O6	2.50	0.45
7:LB:110:LEU:HD21	7:LB:181:LEU:HG	1.99	0.45
15:TB:13:HIS:NE2	15:TB:16:HIS:HB2	2.31	0.45
37:QC:135:LYS:HA	37:QC:138:VAL:HG12	1.98	0.45
46:ZC:84:LEU:HD22	46:ZC:104:VAL:HG11	1.99	0.45
54:HD:66:ALA:HB3	54:HD:72:LEU:HD12	1.99	0.45
54:HD:89:ARG:O	54:HD:93:GLU:HG2	2.17	0.45
1:A:4:U:H4'	1:A:5:U:OP2	2.17	0.44
1:A:792:A:H4'	1:A:793:U:O5'	2.16	0.44
1:A:967:5MC:H2'	1:A:968:A:C8	2.52	0.44
1:A:1053:G:N7	1:A:1200:C:H5'	2.32	0.44
1:A:1240:U:H4'	41:PA:38:LEU:HD21	1.98	0.44
1:A:1391:U:H2'	1:A:1392:G:C8	2.52	0.44
2:B:686:G:N2	2:B:788:A:H61	2.15	0.44
2:B:752:A:O5'	31:EA:1:MET:HE1	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1153:C:OP1	18:R:92:ARG:NH2	2.45	0.44
6:F:154:LYS:HA	6:F:154:LYS:HD3	1.83	0.44
7:G:188:ARG:HB3	13:M:3:LEU:HD22	1.98	0.44
8:H:15:VAL:HG21	8:H:176:LEU:HD23	1.99	0.44
11:K:10:GLU:CD	11:K:11:PRO:HD2	2.41	0.44
18:R:89:GLU:OE2	19:S:50:PRO:HB3	2.17	0.44
25:Y:20:ARG:HG2	25:Y:20:ARG:HH11	1.82	0.44
28:BA:62:ARG:HB3	28:BA:63:TYR:H	1.56	0.44
30:DA:9:LEU:HA	30:DA:54:ILE:HB	1.99	0.44
35:JA:137:ARG:NH1	35:JA:334:GLU:HG3	2.32	0.44
37:LA:125:GLU:HG2	37:LA:190:ARG:O	2.17	0.44
46:UA:27:LEU:HD12	46:UA:27:LEU:HA	1.77	0.44
2:GB:14:A:H5''	2:GB:15:G:OP2	2.18	0.44
2:GB:165:U:H2'	2:GB:171:G:O4'	2.17	0.44
2:GB:1532:C:N4	2:GB:1539:G:H22	2.15	0.44
2:GB:1914:C:O2'	35:OC:294:ARG:HD2	2.17	0.44
4:IB:68:C:H2'	4:IB:69:C:C6	2.51	0.44
7:LB:108:LYS:O	7:LB:112:MET:HB2	2.17	0.44
9:NB:52:VAL:O	9:NB:65:HIS:NE2	2.50	0.44
10:OB:101:LEU:HG	10:OB:107:ILE:HG12	1.98	0.44
25:DC:50:ARG:HD2	25:DC:57:GLU:OE2	2.16	0.44
4:NC:35:A:OP2	43:WC:128:ARG:NH1	2.49	0.44
41:UC:88:PRO:HG2	41:UC:149:ARG:HA	1.98	0.44
48:BD:21:TYR:CE1	48:BD:23:ARG:NH1	2.85	0.44
54:HD:47:GLY:HA2	54:HD:48:LYS:C	2.42	0.44
1:A:1306:A:H1'	1:A:1332:A:C2	2.52	0.44
1:A:1460:A:P	54:CB:27:LYS:NZ	2.91	0.44
2:B:251:A:C5	2:B:252:G:H1'	2.52	0.44
2:B:969:U:O3'	27:AA:14:GLY:HA2	2.17	0.44
2:B:1176:G:H8	2:B:1177:A:C8	2.34	0.44
10:J:6:LEU:HG	10:J:36:ALA:HA	1.98	0.44
13:M:84:ASN:HB2	13:M:86:LYS:HG2	1.99	0.44
14:N:81:VAL:HG12	24:X:5:LYS:HD2	1.99	0.44
17:Q:100:TYR:HB3	17:Q:103:ARG:NH1	2.29	0.44
23:W:62:PRO:C	23:W:64:GLY:H	2.25	0.44
37:LA:43:LEU:HD11	37:LA:66:VAL:HG11	1.98	0.44
45:TA:32:ILE:HD12	45:TA:72:ALA:HB2	1.99	0.44
47:VA:79:LYS:HE3	47:VA:83:ASP:OD2	2.18	0.44
1:FB:162:A:C5	1:FB:163:C:H1'	2.51	0.44
1:FB:184:G:H2'	1:FB:185:A:C8	2.49	0.44
1:FB:325:A:H2'	1:FB:326:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:546:G:P	38:RC:72:GLU:HB3	2.57	0.44
1:FB:1239:A:H62	1:FB:1299:A:H62	1.65	0.44
2:GB:305:U:H2'	2:GB:306:U:C6	2.52	0.44
2:GB:910:A:H62	14:SB:12:GLN:HA	1.82	0.44
2:GB:1173:G:O2'	2:GB:1177:A:N6	2.50	0.44
2:GB:1614:A:C2	20:YB:93:ALA:HB2	2.52	0.44
2:GB:1897:G:H2'	2:GB:1898:U:O4'	2.17	0.44
2:GB:2378:A:H4'	16:UB:23:ARG:NH1	2.32	0.44
8:MB:51:ARG:C	8:MB:53:LEU:H	2.26	0.44
13:RB:85:LEU:HD12	13:RB:137:LYS:HD2	1.99	0.44
15:TB:13:HIS:CD2	15:TB:13:HIS:C	2.94	0.44
16:UB:66:ALA:O	16:UB:69:VAL:HG13	2.16	0.44
18:WB:89:GLU:OE2	19:XB:50:PRO:HB3	2.16	0.44
30:IC:14:THR:O	30:IC:17:LYS:NZ	2.50	0.44
35:OC:337:LEU:O	35:OC:341:ILE:HG23	2.17	0.44
36:PC:97:TRP:HH2	36:PC:176:GLU:CD	2.25	0.44
1:A:409:G:OP1	38:MA:24:GLU:N	2.51	0.44
1:A:757:U:H2'	1:A:758:G:O4'	2.17	0.44
1:A:1314:C:H2'	1:A:1315:U:H6	1.82	0.44
2:B:270(N):U:OP2	2:B:270(N):U:H6	2.00	0.44
2:B:862:G:H2'	2:B:863:A:O4'	2.17	0.44
2:B:1999:C:H4'	2:B:2723:C:O2	2.17	0.44
6:F:24:THR:HG22	6:F:186:GLY:O	2.17	0.44
10:J:118:LYS:HE2	10:J:121:LYS:HE3	1.98	0.44
36:KA:16:HIS:O	36:KA:18:GLY:N	2.51	0.44
36:KA:220:ASP:C	36:KA:222:ILE:H	2.24	0.44
42:QA:6:ILE:HD11	42:QA:31:PHE:HD2	1.82	0.44
49:XA:88:ARG:HB3	49:XA:88:ARG:HH21	1.81	0.44
2:GB:278:A:H2'	2:GB:279:C:O4'	2.17	0.44
2:GB:517:C:OP1	29:HC:16:ARG:NH2	2.50	0.44
2:GB:848:G:N3	2:GB:933:A:H1'	2.32	0.44
2:GB:952:G:C6	2:GB:953:A:N7	2.85	0.44
2:GB:1359:A:H2'	2:GB:1360:A:H5'	1.98	0.44
2:GB:2236:C:H2'	2:GB:2237:G:O4'	2.18	0.44
26:EC:2:LYS:HE2	26:EC:5:GLU:HG3	1.98	0.44
53:GD:15:LEU:O	53:GD:19:VAL:HG23	2.18	0.44
2:B:252:G:OP1	13:M:50:ARG:NH1	2.49	0.44
2:B:270(S):G:H2'	2:B:270(T):G:C8	2.52	0.44
2:B:2064:C:H2'	2:B:2065:C:C6	2.53	0.44
3:C:1:U:OP2	3:C:1:U:C6	2.71	0.44
4:D:23:C:H2'	4:D:24:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:JA:204:ALA:HB2	35:JA:298:LEU:HD13	1.99	0.44
1:FB:1367:C:H5'	44:XC:60:ARG:HH12	1.79	0.44
2:GB:1467:C:OP2	2:GB:1547:C:H5	2.01	0.44
2:GB:1991:U:H2'	2:GB:1992:G:H5''	1.99	0.44
2:GB:2343:C:HO2'	2:GB:2373:G:HO2'	1.64	0.44
3:HB:65:C:O2'	3:HB:66:A:OP1	2.35	0.44
3:HB:116:G:H4'	16:UB:54:LEU:HG	1.99	0.44
39:SC:148:VAL:HG21	42:VC:107:LEU:HD22	2.00	0.44
54:HD:100:ILE:HG12	54:HD:102:GLY:N	2.22	0.44
1:A:59:A:H5''	1:A:60:A:H5''	2.00	0.44
1:A:926:G:C6	1:A:1505:G:C6	3.06	0.44
1:A:938:A:C6	1:A:939:G:C5	3.05	0.44
2:B:768:G:O2'	2:B:1379:A:N1	2.46	0.44
2:B:1009:A:OP2	11:K:37:LYS:NZ	2.51	0.44
2:B:1992:G:O2'	2:B:1993:U:OP2	2.32	0.44
2:B:2643:G:H2'	2:B:2644:G:O4'	2.18	0.44
35:JA:312:PHE:CD1	35:JA:329:LEU:HD21	2.53	0.44
40:OA:68:PRO:HG2	40:OA:71:ARG:NH2	2.31	0.44
43:RA:13:ALA:HB2	43:RA:68:GLY:HA3	1.98	0.44
43:RA:108:VAL:HG12	43:RA:109:VAL:H	1.82	0.44
1:FB:958:A:N3	1:FB:985:C:O2'	2.46	0.44
1:FB:1087:G:H2'	1:FB:1088:G:C8	2.52	0.44
1:FB:1306:A:H1'	1:FB:1332:A:C2	2.52	0.44
1:FB:1498:UR3:O2'	34:MC:17:U:OP1	2.27	0.44
2:GB:716:A:C2	2:GB:717:G:H1'	2.52	0.44
2:GB:882:G:H2'	2:GB:883:G:C8	2.52	0.44
2:GB:1278:A:OP1	15:TB:36:THR:HG23	2.17	0.44
2:GB:1592:C:H2'	2:GB:1593:G:C8	2.52	0.44
2:GB:2123:G:N2	2:GB:2175:C:O2	2.45	0.44
10:OB:43:ASN:N	10:OB:43:ASN:OD1	2.51	0.44
17:VB:6:LEU:HD13	17:VB:6:LEU:HA	1.87	0.44
18:WB:8:VAL:HG22	18:WB:12:ARG:HG3	2.00	0.44
25:DC:7:ILE:HD13	25:DC:98:LEU:HD11	1.98	0.44
30:IC:23:THR:OG1	30:IC:24:GLU:N	2.46	0.44
4:NC:32:5MC:HM52	4:NC:33:U:O4	2.18	0.44
35:OC:186:ARG:HA	35:OC:313:PRO:HD3	1.99	0.44
53:GD:19:VAL:HA	53:GD:22:LEU:HD12	1.99	0.44
54:HD:83:ARG:HA	54:HD:86:ARG:HD3	1.99	0.44
1:A:353:A:H5'	1:A:353:A:C8	2.53	0.44
1:A:715:A:H2'	1:A:716:A:C8	2.52	0.44
2:B:330:A:H2	2:B:1210:A:C2'	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:848:G:N3	2:B:933:A:H1'	2.32	0.44
2:B:2001:A:H4'	2:B:2689:U:O2'	2.16	0.44
2:B:2141:G:C2	2:B:2151:G:H1'	2.53	0.44
6:F:111:ARG:HA	15:O:1:MET:SD	2.57	0.44
9:I:42:ARG:HB3	9:I:53:GLU:HB2	1.98	0.44
11:K:27:ALA:HB1	11:K:103:VAL:HG22	1.99	0.44
4:IA:65:C:H2'	4:IA:66:C:H6	1.82	0.44
38:MA:104:VAL:HG11	38:MA:146:ILE:HG13	1.98	0.44
46:UA:69:TYR:HD2	46:UA:99:HIS:CD2	2.36	0.44
49:XA:63:ARG:HG2	49:XA:67:LEU:HD12	1.98	0.44
1:FB:88:C:H2'	1:FB:89:U:C6	2.52	0.44
1:FB:715:A:H2'	1:FB:716:A:C8	2.52	0.44
1:FB:946:A:H2'	1:FB:947:G:C8	2.52	0.44
1:FB:1124:G:H5''	44:XC:35:SER:OG	2.17	0.44
2:GB:374:A:C2	2:GB:401:A:C4	3.05	0.44
2:GB:1005:C:H2'	2:GB:1006:C:C6	2.53	0.44
8:MB:109:VAL:HG13	28:GC:33:VAL:HG21	1.99	0.44
27:FC:10:LYS:HB3	27:FC:53:LEU:HA	2.00	0.44
42:VC:86:ILE:HG12	42:VC:135:CYS:HA	1.99	0.44
47:AD:50:GLU:HA	47:AD:53:VAL:HB	2.00	0.44
51:ED:14:LYS:HE3	51:ED:14:LYS:H	1.82	0.44
2:B:38:A:H2'	2:B:39:C:C6	2.53	0.44
2:B:1070:A:N6	2:B:1097:U:O2'	2.48	0.44
8:H:16:ARG:HB2	8:H:17:PRO:HD3	2.00	0.44
15:O:96:ARG:NH1	15:O:115:GLU:OE2	2.49	0.44
23:W:129:SER:HB3	23:W:132:ASN:HD21	1.83	0.44
41:PA:79:ARG:CD	41:PA:80:VAL:H	2.31	0.44
43:RA:113:LYS:NZ	43:RA:119:ALA:O	2.51	0.44
45:TA:108:ILE:HB	52:AB:87:ARG:HB3	1.99	0.44
46:UA:7:ILE:HD13	46:UA:7:ILE:HA	1.91	0.44
48:WA:50:LYS:HD2	48:WA:50:LYS:HA	1.84	0.44
1:FB:1272:G:C2	1:FB:1273:G:H1'	2.53	0.44
1:FB:1452:C:H2'	1:FB:1453:G:H5''	2.00	0.44
2:GB:900:A:H2'	2:GB:901:A:O4'	2.17	0.44
2:GB:981:A:N1	2:GB:2027:G:O2'	2.45	0.44
2:GB:2135:A:N6	2:GB:2155:G:H1	2.15	0.44
2:GB:2667:C:H1'	9:NB:109:PHE:CD1	2.53	0.44
4:IB:7:G:N2	4:IB:67:C:O2	2.51	0.44
4:IB:67:C:H2'	4:IB:68:C:C6	2.53	0.44
12:QB:64:ARG:O	12:QB:82:ASN:HA	2.18	0.44
18:WB:102:GLU:HG3	19:XB:2:PHE:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CC:29:GLN:HE21	24:CC:29:GLN:HB3	1.68	0.44
26:EC:17:SER:N	26:EC:20:GLU:OE1	2.30	0.44
36:PC:166:ASP:HA	36:PC:167:PRO:HD3	1.72	0.44
37:QC:43:LEU:HD11	37:QC:66:VAL:HG11	1.99	0.44
46:ZC:83:VAL:HG23	46:ZC:107:ALA:HB2	1.99	0.44
1:A:82:U:O5'	1:A:84:U:H5''	2.18	0.44
1:A:114:U:H2'	1:A:115:G:C8	2.53	0.44
1:A:1062:U:H2'	1:A:1063:C:C6	2.53	0.44
2:B:149:A:H2'	2:B:150:C:O4'	2.18	0.44
2:B:195:A:H61	2:B:198:C:H3'	1.83	0.44
2:B:307:G:H21	2:B:330:A:N6	2.10	0.44
2:B:547:A:C3'	2:B:548:A:C8	2.97	0.44
2:B:828:U:H4'	2:B:831:G:N1	2.33	0.44
2:B:1388:G:H2'	2:B:1389:G:H8	1.83	0.44
2:B:2236:C:H2'	2:B:2237:G:O4'	2.17	0.44
2:B:2758:A:C4	9:I:67:LEU:HD21	2.53	0.44
4:D:17:C:H3'	4:D:17(A):U:H2'	1.99	0.44
10:J:4:ILE:HA	10:J:17:GLN:O	2.18	0.44
10:J:110:ASP:HB3	10:J:113:ARG:HG2	1.99	0.44
12:L:34:THR:OG1	12:L:35:VAL:N	2.46	0.44
16:P:4:LEU:HD23	16:P:8:GLU:OE2	2.18	0.44
35:JA:314:GLN:HB2	35:JA:316:ARG:HD2	1.99	0.44
39:NA:80:ILE:HD11	39:NA:138:ALA:HB1	2.00	0.44
1:FB:860:A:H2'	1:FB:861:G:O4'	2.18	0.44
1:FB:1273:G:H2'	1:FB:1274:G:O4'	2.17	0.44
2:GB:752:A:O5'	31:JC:1:MET:HE1	2.18	0.44
2:GB:1870:C:H2'	2:GB:1871:A:O4'	2.18	0.44
13:RB:50:ARG:HH21	32:KC:7:HIS:CD2	2.36	0.44
13:RB:59:LEU:HD23	32:KC:58:ILE:HD13	1.98	0.44
4:NC:35:A:H2'	4:NC:36:U:H6	1.83	0.44
36:PC:24:TRP:CD1	36:PC:24:TRP:N	2.84	0.44
1:A:1124:G:H5''	44:SA:35:SER:OG	2.18	0.44
1:A:1226:C:N4	47:VA:104:ARG:HD2	2.32	0.44
2:B:270(H):C:H2'	2:B:270(I):C:C6	2.53	0.44
2:B:861:A:O3'	14:N:18:LYS:NZ	2.51	0.44
2:B:1291:C:H2'	2:B:1292:U:C6	2.52	0.44
6:F:97:LYS:HG2	6:F:100:GLU:OE2	2.17	0.44
9:I:140:LYS:HE2	9:I:140:LYS:HB3	1.68	0.44
12:L:10:VAL:HG13	12:L:17:ARG:C	2.42	0.44
14:N:135:ASP:HB3	14:N:137:TYR:H	1.83	0.44
20:T:6:ILE:HG12	20:T:104:THR:OG1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:69:THR:HG22	23:W:90:VAL:HA	1.99	0.44
4:IA:32:5MC:HM52	4:IA:33:U:O4	2.18	0.44
38:MA:5:ILE:H	38:MA:5:ILE:HG13	1.55	0.44
1:FB:553:A:H5''	46:ZC:24:VAL:HG21	1.99	0.44
1:FB:749:C:H2'	1:FB:750:G:H8	1.82	0.44
2:GB:1408:C:H2'	2:GB:1409:C:C6	2.52	0.44
2:GB:2611:U:C4	29:HC:3:LYS:HG2	2.52	0.44
11:PB:138:LEU:HD13	11:PB:139:GLU:H	1.83	0.44
13:RB:93:GLY:N	13:RB:123:LEU:HD22	2.33	0.44
18:WB:52:ARG:HA	18:WB:55:ARG:HG3	2.00	0.44
21:ZB:5:TYR:CE1	26:EC:30:ARG:HG3	2.53	0.44
23:BC:61:LEU:HB3	23:BC:63:ASP:OD1	2.18	0.44
24:CC:7:LEU:O	4:NC:1:C:O2'	2.34	0.44
35:OC:316:ARG:HE	35:OC:316:ARG:HB3	1.54	0.44
37:QC:112:SER:HB3	37:QC:115:LEU:HD12	2.00	0.44
49:CD:11:VAL:HG21	49:CD:34:LEU:HD13	2.00	0.44
1:A:343:U:H2'	1:A:345:C:C5	2.53	0.43
1:A:689:C:OP1	45:TA:27:ASN:ND2	2.48	0.43
1:A:997:U:H2'	1:A:998(A):G:O4'	2.18	0.43
1:A:1508:G:H2'	1:A:1509:C:H6	1.84	0.43
2:B:305:U:H2'	2:B:306:U:C6	2.52	0.43
2:B:807:U:OP1	13:M:36:LYS:NZ	2.46	0.43
2:B:910:A:H62	14:N:12:GLN:HA	1.82	0.43
9:I:102:ALA:HA	9:I:117:PRO:HD3	2.00	0.43
10:J:29:TYR:CE1	10:J:33:ARG:NH1	2.86	0.43
14:N:111:GLU:O	14:N:115:MET:HG2	2.18	0.43
42:QA:100:ILE:O	42:QA:125:ARG:NH2	2.51	0.43
1:FB:438:G:H4'	38:RC:123:HIS:CD2	2.53	0.43
1:FB:575:G:OP1	1:FB:575:G:H4'	2.18	0.43
1:FB:1118:C:H2'	1:FB:1119:C:H6	1.83	0.43
1:FB:1201:A:H1'	1:FB:1202:G:OP2	2.18	0.43
1:FB:1350:A:O2'	41:UC:33:ASP:OD1	2.33	0.43
2:GB:235:U:H2'	2:GB:236:C:C6	2.52	0.43
2:GB:664:C:H4'	2:GB:941:A:OP1	2.17	0.43
2:GB:1842:G:H2'	2:GB:1843:C:C6	2.53	0.43
2:GB:2451:A:H5'	24:CC:3:HIS:HE2	1.83	0.43
13:RB:63:PRO:HG2	32:KC:25:MET:HB2	2.00	0.43
14:SB:69:PHE:HA	14:SB:70:PRO:HD3	1.75	0.43
22:AC:9:LYS:HA	22:AC:10:GLY:HA2	1.61	0.43
22:AC:102:CYS:SG	22:AC:104:GLY:N	2.78	0.43
36:PC:64:ARG:HH11	36:PC:64:ARG:HG3	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:QC:86:VAL:O	37:QC:90:GLU:HG2	2.17	0.43
53:GD:22:LEU:HD23	53:GD:26:GLY:O	2.18	0.43
55:ID:22:ARG:HA	55:ID:23:PRO:HD2	1.91	0.43
1:A:375:U:O2	50:YA:28:ARG:NH2	2.51	0.43
1:A:706:A:H5''	45:TA:22:HIS:CD2	2.53	0.43
1:A:1144:G:N2	1:A:1146:A:H62	2.16	0.43
1:A:1435:G:H2'	1:A:1436:U:C6	2.53	0.43
2:B:583:G:OP2	18:R:10:ARG:HD2	2.18	0.43
2:B:832:G:H5'	13:M:45:LEU:HD21	2.00	0.43
2:B:1688:U:O2	2:B:1700:A:H5'	2.17	0.43
2:B:1790:C:H2'	2:B:1791:A:C5	2.52	0.43
2:B:1800:C:OP1	5:E:264:LYS:NZ	2.44	0.43
4:D:7:G:N2	4:D:67:C:O2	2.51	0.43
5:E:25:THR:HG21	5:E:113:VAL:HG21	2.00	0.43
7:G:132:VAL:HG23	7:G:132:VAL:O	2.17	0.43
8:H:166:ASP:O	8:H:170:ARG:N	2.42	0.43
11:K:97:ARG:HA	11:K:100:GLU:HB2	2.01	0.43
35:JA:248:HIS:CE1	35:JA:250:PRO:HD2	2.53	0.43
36:KA:70:PHE:CE1	36:KA:163:PHE:HD1	2.36	0.43
37:LA:112:SER:HB3	37:LA:115:LEU:HD12	2.00	0.43
42:QA:87:SER:HA	42:QA:93:VAL:HG23	2.00	0.43
53:BB:15:LEU:O	53:BB:19:VAL:HG23	2.18	0.43
1:FB:606:G:H2'	1:FB:631:G:N2	2.32	0.43
1:FB:689:C:OP1	45:YC:27:ASN:ND2	2.47	0.43
2:GB:280:C:C2	2:GB:361:G:N2	2.86	0.43
2:GB:969:U:O3'	27:FC:14:GLY:HA2	2.18	0.43
2:GB:1686:C:H2'	2:GB:1687:G:O4'	2.18	0.43
2:GB:2693:A:H2'	2:GB:2694:G:H8	1.82	0.43
6:KB:119:ARG:HG2	6:KB:120:TRP:NE1	2.33	0.43
8:MB:50:ALA:C	8:MB:52:ILE:H	2.25	0.43
13:RB:59:LEU:HD21	32:KC:10:ALA:HA	2.00	0.43
15:TB:72:ASP:HB3	15:TB:75:LEU:HB3	2.00	0.43
17:VB:114:LEU:HD23	17:VB:114:LEU:HA	1.89	0.43
19:XB:97:LYS:HA	19:XB:97:LYS:HD2	1.80	0.43
42:VC:97:VAL:HG21	42:VC:128:GLY:HA2	1.99	0.43
45:YC:24:SER:HB2	45:YC:27:ASN:H	1.83	0.43
48:BD:53:LEU:O	48:BD:56:VAL:HG23	2.18	0.43
1:A:1272:G:C2	1:A:1273:G:H1'	2.53	0.43
2:B:636:G:N7	13:M:113:LYS:HE2	2.34	0.43
2:B:2706:G:H2'	2:B:2707:G:O4'	2.19	0.43
2:B:2779:U:OP1	2:B:2780:G:H2'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2853:C:H2'	2:B:2854:G:C8	2.53	0.43
2:B:2863:C:OP1	17:Q:93:ARG:NH1	2.51	0.43
8:H:103:LEU:HD23	8:H:103:LEU:HA	1.85	0.43
9:I:101:ARG:NH1	9:I:122:THR:HG23	2.31	0.43
21:U:94:GLY:HA3	21:U:95:LEU:C	2.44	0.43
26:Z:35:LEU:HD12	26:Z:53:LEU:HD12	2.01	0.43
35:JA:181:GLY:O	35:JA:307:ASN:HB2	2.18	0.43
35:JA:186:ARG:HA	35:JA:313:PRO:HD3	1.99	0.43
35:JA:251:THR:HB	35:JA:253:ILE:HG22	2.00	0.43
37:LA:77:ILE:HG23	37:LA:84:ILE:HD12	2.01	0.43
39:NA:92:LYS:HA	39:NA:93:PRO:HD3	1.89	0.43
42:QA:122:ARG:HA	42:QA:125:ARG:HD2	1.99	0.43
46:UA:60:LEU:HD21	46:UA:66:VAL:HG22	1.99	0.43
1:FB:801:U:H2'	1:FB:802:A:C8	2.52	0.43
1:FB:975:A:H5'	1:FB:975:A:H8	1.82	0.43
1:FB:1054:C:OP2	1:FB:1197:G:OP2	2.36	0.43
1:FB:1451:A:H8	1:FB:1452:C:O4'	2.01	0.43
2:GB:306:U:H2'	2:GB:307:G:O4'	2.18	0.43
2:GB:448:U:O4	2:GB:583:G:H1'	2.17	0.43
2:GB:1165:U:H2'	2:GB:1166:C:C6	2.52	0.43
2:GB:1693:U:O2'	5:JB:14:ARG:NH2	2.51	0.43
2:GB:1754:C:P	17:VB:96:ARG:NH1	2.91	0.43
2:GB:2712(A):A:H5''	2:GB:2713:A:OP2	2.18	0.43
9:NB:70:THR:HG22	9:NB:74:ASN:OD1	2.18	0.43
14:SB:2:LEU:HB2	14:SB:70:PRO:HG2	2.00	0.43
14:SB:64:ILE:HG13	23:BC:178:GLU:HG3	2.00	0.43
16:UB:15:ARG:NH1	16:UB:88:ASP:OD2	2.50	0.43
35:OC:108:GLU:HB2	35:OC:170:GLY:HA2	1.99	0.43
35:OC:317:VAL:HB	35:OC:329:LEU:HD13	1.99	0.43
41:UC:79:ARG:CD	41:UC:80:VAL:H	2.30	0.43
47:AD:27:LYS:HB2	47:AD:27:LYS:HE2	1.86	0.43
47:AD:45:VAL:O	47:AD:48:LEU:HB2	2.18	0.43
47:AD:79:LYS:HE3	47:AD:83:ASP:OD2	2.18	0.43
52:FD:35:ARG:HB2	52:FD:35:ARG:HH11	1.84	0.43
1:A:858:G:O6	1:A:869:G:H3'	2.18	0.43
1:A:1087:G:H2'	1:A:1088:G:C8	2.53	0.43
2:B:84:A:P	22:V:8:LYS:NZ	2.87	0.43
2:B:362:U:O2'	2:B:363(A):G:H5''	2.18	0.43
2:B:1035:U:H2'	2:B:1036:G:C8	2.52	0.43
2:B:1429:G:H2'	2:B:1430:C:C6	2.53	0.43
2:B:1448:G:O2'	2:B:1529:A:N1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2123:G:N2	2:B:2175:C:O2	2.46	0.43
2:B:2135:A:N6	2:B:2155:G:H1	2.16	0.43
2:B:2168:G:C8	2:B:2170:A:OP2	2.71	0.43
3:C:113:C:O2'	16:P:46:VAL:HG23	2.18	0.43
6:F:24:THR:HG21	6:F:188:VAL:HG23	1.99	0.43
8:H:3:LEU:HB3	8:H:97:ASP:OD2	2.18	0.43
8:H:148:MET:HE1	28:BA:28:LYS:HZ3	1.82	0.43
9:I:21:PRO:O	9:I:23:ARG:HG2	2.18	0.43
23:W:30:ASN:O	23:W:32:HIS:N	2.51	0.43
28:BA:5:ILE:HG13	28:BA:6:HIS:CD2	2.53	0.43
36:KA:12:GLU:HA	36:KA:15:VAL:HG22	2.00	0.43
37:LA:86:VAL:O	37:LA:90:GLU:HG2	2.19	0.43
39:NA:152:ARG:HB3	42:QA:43:GLY:HA3	1.99	0.43
41:PA:23:VAL:O	41:PA:27:ILE:HG13	2.18	0.43
41:PA:88:PRO:HG2	41:PA:149:ARG:HA	1.99	0.43
43:RA:46:ALA:HB2	43:RA:74:ILE:HG23	2.00	0.43
47:VA:39:ILE:HG13	47:VA:56:LEU:HD22	1.99	0.43
48:WA:53:LEU:O	48:WA:56:VAL:HG23	2.18	0.43
1:FB:114:U:H2'	1:FB:115:G:C8	2.54	0.43
1:FB:375:U:O2	50:DD:28:ARG:NH2	2.50	0.43
1:FB:1465:C:H2'	1:FB:1466:C:O4'	2.19	0.43
2:GB:38:A:H2'	2:GB:39:C:C6	2.53	0.43
2:GB:270(M):U:H3'	2:GB:270(M):U:P	2.58	0.43
2:GB:545:G:H21	2:GB:548:A:H62	1.66	0.43
2:GB:1429:G:H2'	2:GB:1430:C:C6	2.53	0.43
2:GB:1790:C:H2'	2:GB:1791:A:C5	2.53	0.43
2:GB:2853:C:H2'	2:GB:2854:G:C8	2.53	0.43
4:IB:17:C:H3'	4:IB:17(A):U:H2'	1.99	0.43
4:IB:63:G:H2'	4:IB:64:G:C8	2.52	0.43
5:JB:77:ALA:HB2	5:JB:97:TYR:CD1	2.54	0.43
7:LB:132:VAL:HG23	7:LB:132:VAL:O	2.18	0.43
14:SB:67:ARG:HH11	14:SB:67:ARG:HG3	1.83	0.43
19:XB:40:LEU:HD23	19:XB:40:LEU:HA	1.81	0.43
36:PC:70:PHE:HE1	36:PC:163:PHE:HD1	1.67	0.43
37:QC:92:ALA:HB2	37:QC:99:VAL:HG22	2.01	0.43
42:VC:37:ARG:O	42:VC:41:ARG:HG2	2.19	0.43
42:VC:119:LEU:HD12	42:VC:123:GLU:HB2	1.99	0.43
43:WC:7:THR:HB	43:WC:83:ARG:HH21	1.83	0.43
52:FD:61:LYS:O	52:FD:65:ILE:HG13	2.17	0.43
1:A:45:U:H2'	1:A:46:G:C8	2.54	0.43
1:A:546:G:P	38:MA:72:GLU:HB3	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:859:A:H2'	1:A:860:A:O4'	2.18	0.43
2:B:882:G:H2'	2:B:883:G:C8	2.54	0.43
2:B:1093:G:H2'	2:B:1093:G:N3	2.33	0.43
2:B:2251:OMG:HM23	2:B:2251:OMG:H1'	1.65	0.43
7:G:116:ASP:OD2	13:M:1:MET:HB2	2.18	0.43
8:H:16:ARG:HD2	8:H:31:VAL:HG11	1.99	0.43
8:H:47:LYS:HG3	8:H:48:GLU:H	1.83	0.43
10:J:133:HIS:HA	10:J:134:PRO:HD3	1.81	0.43
37:LA:58:GLU:O	37:LA:65:ALA:N	2.51	0.43
41:PA:26:PHE:O	41:PA:30:ILE:HG13	2.19	0.43
47:VA:14:ARG:NE	47:VA:42:ALA:HA	2.32	0.43
47:VA:86:CYS:O	47:VA:90:LEU:HD22	2.19	0.43
1:FB:1147:C:HO2'	43:WC:5:TYR:HH	1.66	0.43
1:FB:1262:C:H2'	1:FB:1263:C:C6	2.54	0.43
2:GB:17:G:H2'	2:GB:18:C:C6	2.54	0.43
2:GB:587:C:C6	2:GB:671:C:H1'	2.54	0.43
2:GB:760:G:H2'	2:GB:761:A:O4'	2.19	0.43
2:GB:1688:U:O2	2:GB:1700:A:H5'	2.18	0.43
2:GB:1901:A:N3	2:GB:1901:A:H2'	2.33	0.43
2:GB:2010:G:H5''	20:YB:42:ARG:HB2	2.00	0.43
2:GB:2025:C:H2'	2:GB:2026:C:C6	2.53	0.43
2:GB:2079:U:OP1	25:DC:21:ARG:NH2	2.52	0.43
2:GB:2805:G:N2	2:GB:2807:G:N7	2.66	0.43
6:KB:56:PRO:C	6:KB:58:ARG:H	2.26	0.43
8:MB:47:LYS:HG3	8:MB:48:GLU:H	1.83	0.43
16:UB:27:SER:HA	16:UB:88:ASP:HB3	2.00	0.43
40:TC:78:GLU:O	40:TC:81:ILE:HG22	2.19	0.43
43:WC:33:PHE:CE1	43:WC:37:PHE:HD2	2.36	0.43
50:DD:45:THR:O	50:DD:48:TRP:HD1	2.02	0.43
1:A:297:G:N2	1:A:300:A:OP2	2.45	0.43
2:B:189:G:OP2	25:Y:14:VAL:HG21	2.19	0.43
2:B:448:U:O4	2:B:583:G:H1'	2.18	0.43
2:B:879:G:H22	2:B:899:A:H1'	1.83	0.43
2:B:1108:U:C4	2:B:1109:C:C4	3.07	0.43
2:B:2320:A:H2'	2:B:2320:A:N3	2.32	0.43
3:C:73:A:C6	3:C:74:U:C2	3.06	0.43
5:E:246:PRO:O	5:E:254:THR:HG22	2.18	0.43
8:H:11:TYR:OH	8:H:16:ARG:HD3	2.18	0.43
17:Q:128:GLU:O	17:Q:132:LYS:NZ	2.51	0.43
18:R:112:ARG:NH1	19:S:47:VAL:HB	2.34	0.43
35:JA:109:ARG:HD3	35:JA:208:GLU:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:LA:130:VAL:HG21	37:LA:157:ILE:HG23	2.01	0.43
38:MA:25:ARG:O	38:MA:28:SER:OG	2.21	0.43
39:NA:72:GLN:C	39:NA:74:GLY:H	2.27	0.43
40:OA:91:VAL:HG11	52:AB:72:ARG:NH1	2.33	0.43
54:CB:98:PRO:C	54:CB:100:ILE:H	2.25	0.43
1:FB:695:A:OP2	45:YC:53:SER:HB2	2.18	0.43
1:FB:875:C:O2'	42:VC:14:ARG:NH1	2.48	0.43
1:FB:974:A:H8	1:FB:974:A:OP1	2.01	0.43
2:GB:149:A:H2'	2:GB:150:C:O4'	2.18	0.43
2:GB:275:G:H8	2:GB:275:G:O5'	2.01	0.43
2:GB:458:G:O2'	31:JC:39:ARG:HD3	2.17	0.43
2:GB:811:U:H2'	13:RB:21:ARG:HA	2.01	0.43
2:GB:2144:U:O2'	2:GB:2147:G:O6	2.25	0.43
2:GB:2514:U:H2'	2:GB:2515:C:C6	2.54	0.43
2:GB:2895:U:O5'	2:GB:2895:U:H6	2.01	0.43
8:MB:16:ARG:HD2	8:MB:31:VAL:HG11	1.99	0.43
8:MB:74:LYS:O	8:MB:84:LYS:HG3	2.18	0.43
13:RB:107:LYS:O	13:RB:110:TYR:HB2	2.19	0.43
17:VB:128:GLU:O	17:VB:132:LYS:NZ	2.50	0.43
20:YB:23:LEU:HD12	20:YB:23:LEU:HA	1.86	0.43
27:FC:7:LYS:HB2	27:FC:34:GLU:HG2	2.01	0.43
35:OC:137:ARG:NH1	35:OC:334:GLU:HG3	2.33	0.43
36:PC:69:LEU:O	36:PC:163:PHE:N	2.46	0.43
41:UC:26:PHE:O	41:UC:30:ILE:HG13	2.19	0.43
1:A:1073:U:H3	1:A:1102:A:H61	1.66	0.43
2:B:275:G:O5'	2:B:275:G:H8	2.01	0.43
2:B:464:U:H2'	2:B:465:G:O4'	2.19	0.43
2:B:2211:G:H2'	2:B:2212:A:C2	2.53	0.43
8:H:36:LYS:HD3	8:H:95:ARG:NH1	2.33	0.43
8:H:109:VAL:HG13	28:BA:33:VAL:HG21	2.00	0.43
46:UA:124:LYS:HA	46:UA:125:PRO:HD3	1.73	0.43
52:AB:19:LYS:HB3	52:AB:20:ALA:H	1.66	0.43
1:FB:82:U:O5'	1:FB:84:U:H5''	2.19	0.43
1:FB:790:A:C6	1:FB:791:G:C6	3.06	0.43
1:FB:949:A:H1'	1:FB:1364:U:H3	1.82	0.43
2:GB:201:C:O2'	2:GB:251:A:N1	2.50	0.43
2:GB:464:U:H2'	2:GB:465:G:O4'	2.19	0.43
2:GB:489:G:N7	20:YB:49:LYS:NZ	2.65	0.43
2:GB:579:G:H2'	2:GB:580:C:C6	2.54	0.43
2:GB:813:U:H2'	2:GB:814:C:C6	2.54	0.43
2:GB:876:C:H2'	2:GB:877:U:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:1952:A:C6	2:GB:1953:A:N1	2.86	0.43
2:GB:2780:G:H4'	2:GB:2781:A:OP2	2.18	0.43
9:NB:42:ARG:HB3	9:NB:53:GLU:HB2	2.01	0.43
10:OB:7:GLU:HG3	10:OB:8:PRO:HD2	2.00	0.43
13:RB:80:TYR:CD1	13:RB:111:ARG:HB2	2.53	0.43
18:WB:106:PHE:O	18:WB:110:VAL:HG23	2.19	0.43
28:GC:34:GLU:HB2	28:GC:35:VAL:H	1.53	0.43
30:IC:34:LEU:HA	30:IC:34:LEU:HD23	1.76	0.43
36:PC:16:HIS:O	36:PC:18:GLY:N	2.52	0.43
37:QC:191:THR:C	37:QC:193:TYR:H	2.27	0.43
40:TC:24:GLU:HA	40:TC:24:GLU:OE2	2.17	0.43
43:WC:22:GLY:HA3	43:WC:60:ASP:CG	2.43	0.43
47:AD:39:ILE:HG13	47:AD:56:LEU:HD22	2.01	0.43
50:DD:53:VAL:CG1	50:DD:57:ARG:HH11	2.31	0.43
1:A:1054:C:OP2	1:A:1197:G:OP2	2.36	0.43
1:A:1174:G:OP1	41:PA:5:ARG:NH2	2.52	0.43
2:B:589:C:H2'	2:B:590:A:C8	2.54	0.43
2:B:686:G:H21	2:B:788:A:H61	1.66	0.43
2:B:700:G:O6	2:B:733:G:N2	2.52	0.43
2:B:1815:A:OP2	5:E:54:ARG:NH2	2.50	0.43
2:B:2514:U:H2'	2:B:2515:C:C6	2.54	0.43
3:C:116:G:H4'	16:P:54:LEU:HG	2.01	0.43
12:L:68:GLU:HB3	12:L:78:ARG:NH1	2.34	0.43
13:M:63:PRO:HG2	32:FA:25:MET:HB2	1.99	0.43
17:Q:35:LYS:HE2	17:Q:37:GLY:O	2.18	0.43
21:U:5:TYR:CE1	26:Z:30:ARG:HG3	2.54	0.43
26:Z:37:PHE:O	26:Z:41:ILE:HG13	2.18	0.43
37:LA:34:LEU:HD13	48:WA:25:VAL:HB	2.01	0.43
41:PA:76:ARG:HD3	41:PA:156:TRP:HZ2	1.83	0.43
42:QA:19:VAL:HG23	42:QA:21:LYS:HG2	2.01	0.43
47:VA:14:ARG:HG3	47:VA:44:ARG:CZ	2.49	0.43
1:FB:99:C:H2'	1:FB:101:A:C8	2.53	0.43
1:FB:731:G:H5'	1:FB:766:A:H4'	2.00	0.43
2:GB:1093:G:H2'	2:GB:1093:G:N3	2.34	0.43
2:GB:1205:U:C4	7:LB:171:PRO:HA	2.53	0.43
2:GB:1357:U:H2'	2:GB:1358:G:O4'	2.18	0.43
2:GB:1693:U:OP2	2:GB:1694:C:H5	2.01	0.43
2:GB:2022:U:O2'	2:GB:2617:C:H5'	2.19	0.43
13:RB:29:LYS:HB3	13:RB:30:THR:H	1.41	0.43
35:OC:142:ARG:NH2	35:OC:174:ARG:NH1	2.63	0.43
37:QC:54:ARG:NE	37:QC:56:ASP:OD2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:UC:129:GLU:OE1	41:UC:131:LYS:NZ	2.43	0.43
41:UC:150:ALA:HA	45:YC:59:TYR:HB3	2.00	0.43
48:BD:15:LYS:NZ	48:BD:15:LYS:HB3	2.34	0.43
51:ED:43:LEU:HA	51:ED:43:LEU:HD23	1.64	0.43
54:HD:30:LYS:HB2	54:HD:30:LYS:HZ1	1.84	0.43
1:A:801:U:H2'	1:A:802:A:C8	2.53	0.43
1:A:1223:C:P	53:BB:78:ARG:HH21	2.42	0.43
1:A:1326:C:OP1	55:DB:17:THR:OG1	2.33	0.43
1:A:1517:G:H1'	2:B:1919:A:O3'	2.18	0.43
2:B:1060:U:H4'	2:B:1061:U:O5'	2.18	0.43
2:B:1532:C:N4	2:B:1539:G:H22	2.17	0.43
2:B:2344:U:O2'	30:DA:36:LEU:HD22	2.18	0.43
4:D:67:C:H2'	4:D:68:C:C6	2.53	0.43
8:H:51:ARG:C	8:H:53:LEU:H	2.27	0.43
16:P:3:ARG:NH1	16:P:4:LEU:H	2.16	0.43
24:X:2:ALA:N	35:JA:261:ARG:HD3	2.34	0.43
32:FA:65:GLU:OE2	32:FA:65:GLU:HA	2.19	0.43
4:IA:47:U:H5''	4:IA:48:C:H5'	2.01	0.43
47:VA:108:ARG:O	47:VA:112:GLY:N	2.51	0.43
50:YA:49:LEU:HD12	50:YA:50:LYS:H	1.84	0.43
1:FB:229:U:H2'	1:FB:230:G:O4'	2.19	0.43
1:FB:815:A:N3	1:FB:1527:C:O2'	2.41	0.43
1:FB:1502:A:C8	1:FB:1505:G:N2	2.87	0.43
2:GB:90:U:H1'	2:GB:91:A:C8	2.54	0.43
2:GB:2667:C:H1'	9:NB:109:PHE:HD1	1.84	0.43
2:GB:2706:G:H2'	2:GB:2707:G:O4'	2.18	0.43
3:HB:73:A:C4	3:HB:104:A:C2	3.07	0.43
8:MB:164:GLU:HB2	8:MB:168:GLU:OE2	2.19	0.43
9:NB:3:ARG:HA	9:NB:3:ARG:HH11	1.84	0.43
10:OB:110:ASP:HB3	10:OB:113:ARG:CG	2.49	0.43
11:PB:97:ARG:HA	11:PB:100:GLU:HB2	2.00	0.43
17:VB:100:TYR:HD1	17:VB:103:ARG:HH12	1.59	0.43
20:YB:11:ARG:HD3	20:YB:82:LEU:HD12	2.01	0.43
36:PC:126:GLU:CD	36:PC:130:ARG:HB2	2.43	0.43
41:UC:79:ARG:HD2	41:UC:80:VAL:H	1.84	0.43
43:WC:13:ALA:HB2	43:WC:68:GLY:HA3	1.99	0.43
45:YC:48:ILE:HD12	45:YC:48:ILE:HA	1.71	0.43
1:A:81:G:H2'	1:A:82:U:C6	2.54	0.43
1:A:1118:C:H2'	1:A:1119:C:H6	1.82	0.43
2:B:1245:G:OP1	13:M:13:ASN:ND2	2.52	0.43
2:B:2783:G:H2'	2:B:2784:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:64:THR:HB	8:H:94:LEU:HD21	2.00	0.43
9:I:87:LEU:HD23	9:I:164:TYR:HA	2.01	0.43
9:I:98:LEU:HG	9:I:125:VAL:HG23	2.00	0.43
10:J:26:ALA:O	10:J:31:LEU:HB2	2.19	0.43
26:Z:18:PRO:O	26:Z:22:GLU:HG3	2.19	0.43
28:BA:50:VAL:O	47:VA:65:LYS:NZ	2.37	0.43
33:GA:1:MET:HE2	33:GA:33:LYS:HE3	2.00	0.43
41:PA:37:ASN:OD1	43:RA:41:VAL:HG22	2.18	0.43
51:ZA:13:ASP:OD2	51:ZA:53:LEU:HB2	2.19	0.43
1:FB:265:G:H5'	51:ED:64:PRO:O	2.19	0.43
1:FB:946:A:O2'	1:FB:1333:A:N3	2.43	0.43
2:GB:264:C:O2'	2:GB:265:A:H2'	2.19	0.43
2:GB:807:U:OP1	13:RB:36:LYS:NZ	2.40	0.43
2:GB:887:A:H1'	2:GB:890:A:N6	2.34	0.43
2:GB:974(B):C:OP2	2:GB:974(B):C:H4'	2.18	0.43
2:GB:994:C:OP1	18:WB:53:ARG:NH2	2.52	0.43
2:GB:1021:A:C8	2:GB:1022:G:H5''	2.54	0.43
2:GB:1367:A:N7	2:GB:1368:G:H1'	2.34	0.43
2:GB:1519:G:H2'	2:GB:1520:U:O4'	2.19	0.43
2:GB:1923:U:H2'	2:GB:1924:C:C6	2.54	0.43
6:KB:24:THR:HG21	6:KB:188:VAL:HG23	2.00	0.43
7:LB:64:ILE:H	7:LB:64:ILE:HG13	1.44	0.43
10:OB:101:LEU:HD23	10:OB:109:ILE:HG12	2.00	0.43
11:PB:7:LYS:HA	11:PB:7:LYS:HD3	1.75	0.43
23:BC:67:LEU:HA	23:BC:68:PRO:HD2	1.91	0.43
28:GC:5:ILE:HG13	28:GC:6:HIS:CD2	2.54	0.43
35:OC:312:PHE:CD1	35:OC:329:LEU:HD21	2.54	0.43
36:PC:21:ARG:O	36:PC:23:ARG:N	2.52	0.43
43:WC:42:ARG:HE	43:WC:42:ARG:HB2	1.57	0.43
46:ZC:28:LYS:HZ3	46:ZC:64:TYR:HE2	1.67	0.43
50:DD:25:ARG:H	50:DD:25:ARG:HG2	1.53	0.43
53:GD:69:HIS:HB3	53:GD:73:GLU:OE2	2.18	0.43
1:A:160:A:H2'	1:A:161:A:O4'	2.18	0.42
1:A:240:C:H42	1:A:286:G:H1	1.67	0.42
1:A:1411:C:H2'	1:A:1412:C:C6	2.54	0.42
2:B:1641:A:H2'	2:B:1642:G:O4'	2.19	0.42
2:B:1998:G:O2'	2:B:2724:C:O2'	2.33	0.42
2:B:2611:U:C4	29:CA:3:LYS:HG2	2.53	0.42
8:H:114:ILE:HG22	8:H:140:ILE:HG12	2.02	0.42
13:M:19:VAL:HA	13:M:27:HIS:HB2	2.01	0.42
13:M:85:LEU:HD12	13:M:137:LYS:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:27:SER:HA	16:P:88:ASP:HB3	2.01	0.42
35:JA:104:ASP:CG	35:JA:105:PRO:HD2	2.44	0.42
38:MA:192:GLU:OE2	38:MA:192:GLU:N	2.37	0.42
40:OA:4:TYR:CZ	40:OA:72:VAL:HG11	2.54	0.42
44:SA:25:GLU:H	44:SA:25:GLU:CD	2.27	0.42
45:TA:66:LEU:O	45:TA:70:LYS:HG3	2.19	0.42
54:CB:49:ALA:HB3	54:CB:99:LEU:HB2	2.00	0.42
2:GB:26:G:C6	2:GB:27:G:N1	2.86	0.42
2:GB:270(H):C:H2'	2:GB:270(I):C:C6	2.54	0.42
2:GB:2093:G:C6	2:GB:2225:A:C8	3.07	0.42
4:IB:67:C:H2'	4:IB:68:C:H6	1.84	0.42
14:SB:38:GLU:HG3	14:SB:127:ILE:HB	2.02	0.42
14:SB:68:ILE:HG23	14:SB:103:MET:HA	2.01	0.42
18:WB:47:TYR:HA	18:WB:50:ARG:NH2	2.34	0.42
25:DC:54:ALA:C	25:DC:56:GLN:H	2.26	0.42
39:SC:50:GLU:HB2	39:SC:53:LEU:HD13	2.00	0.42
44:XC:38:ILE:HA	44:XC:39:PRO:HD3	1.82	0.42
1:A:8:A:N6	38:MA:205:GLU:O	2.52	0.42
1:A:262:A:C6	1:A:263:A:C6	3.07	0.42
1:A:553:A:H5''	46:UA:24:VAL:HG21	2.01	0.42
2:B:165:U:H2'	2:B:171:G:O4'	2.19	0.42
2:B:637:A:H4'	2:B:638:G:O5'	2.19	0.42
2:B:876:C:H2'	2:B:877:U:O4'	2.19	0.42
2:B:880:G:H1	2:B:897:C:N4	2.17	0.42
2:B:1170:G:N2	2:B:1180:C:C2	2.87	0.42
2:B:2557:G:H2'	2:B:2558:C:C6	2.53	0.42
7:G:123:LEU:HD13	7:G:192:LEU:HB3	2.01	0.42
7:G:140:LEU:HA	7:G:140:LEU:HD12	1.63	0.42
10:J:54:GLN:HA	10:J:57:ARG:HH11	1.84	0.42
10:J:123:LEU:HD12	10:J:123:LEU:HA	1.93	0.42
13:M:47:ASP:HA	13:M:48:PRO:HD2	1.95	0.42
28:BA:34:GLU:HG3	47:VA:3:ARG:HA	2.01	0.42
35:JA:328:ARG:NH1	35:JA:339:MET:HB3	2.34	0.42
36:KA:19:HIS:NE2	36:KA:206:ASP:HB2	2.34	0.42
37:LA:6:HIS:HA	37:LA:7:PRO:HD3	1.93	0.42
44:SA:37:PRO:HA	44:SA:72:VAL:HG22	2.01	0.42
45:TA:111:ASP:CG	52:AB:84:LYS:HE2	2.44	0.42
1:FB:4:U:H4'	1:FB:5:U:OP2	2.19	0.42
1:FB:433:C:H2'	1:FB:434:U:C6	2.53	0.42
1:FB:988:G:C2	1:FB:989:C:H1'	2.55	0.42
2:GB:592:G:H4'	32:KC:3:LYS:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:945:A:C4	2:GB:2448:A:C2	3.07	0.42
2:GB:1651:G:N7	15:TB:11:ASN:ND2	2.64	0.42
2:GB:2378:A:C5	2:GB:2379:G:H1'	2.54	0.42
2:GB:2633:G:H2'	2:GB:2634:G:O4'	2.18	0.42
5:JB:61:LEU:HD13	5:JB:61:LEU:HA	1.82	0.42
9:NB:87:LEU:HD23	9:NB:164:TYR:HA	2.01	0.42
10:OB:90:GLY:C	10:OB:92:VAL:H	2.27	0.42
20:YB:71:VAL:HA	20:YB:107:LEU:HD12	2.01	0.42
32:KC:4:MET:HE2	32:KC:63:PRO:HG3	2.00	0.42
35:OC:251:THR:HB	35:OC:253:ILE:HG22	2.01	0.42
36:PC:47:THR:O	36:PC:51:LEU:N	2.52	0.42
38:RC:8:VAL:O	38:RC:11:LEU:HB2	2.18	0.42
38:RC:171:GLY:HA2	38:RC:172:PRO:HD3	1.88	0.42
39:SC:78:HIS:CE1	42:VC:104:ARG:NH1	2.87	0.42
44:XC:23:ILE:HD12	44:XC:23:ILE:HA	1.81	0.42
52:FD:76:LEU:HD13	52:FD:76:LEU:HA	1.80	0.42
1:A:843:U:C5	1:A:848:C:H1'	2.54	0.42
1:A:1262:C:H2'	1:A:1263:C:C6	2.54	0.42
2:B:544:C:H2'	2:B:545:G:O4'	2.19	0.42
2:B:1651:G:N7	15:O:11:ASN:ND2	2.67	0.42
5:E:206:LEU:HD23	5:E:206:LEU:HA	1.73	0.42
7:G:122:LYS:HB3	7:G:191:ARG:HG2	2.02	0.42
20:T:12:ILE:O	20:T:101:SER:OG	2.37	0.42
22:V:13:VAL:HG12	22:V:74:PRO:HA	2.01	0.42
22:V:102:CYS:SG	22:V:104:GLY:N	2.77	0.42
35:JA:102:PRO:HB2	35:JA:103:LYS:H	1.64	0.42
39:NA:63:ARG:O	39:NA:66:MET:HG2	2.19	0.42
39:NA:145:LYS:O	39:NA:149:GLU:HG3	2.20	0.42
41:PA:114:ARG:H	41:PA:114:ARG:HG2	1.61	0.42
45:TA:24:SER:HB2	45:TA:27:ASN:H	1.83	0.42
49:XA:2:PRO:HB2	49:XA:3:ILE:H	1.65	0.42
50:YA:6:LEU:HG	50:YA:17:TYR:HB3	2.00	0.42
54:CB:66:ALA:HB3	54:CB:72:LEU:HD12	2.00	0.42
1:FB:924:C:O2'	1:FB:1502:A:N1	2.43	0.42
1:FB:1513:A:H2'	1:FB:1514:C:C6	2.54	0.42
2:GB:392:C:H5''	2:GB:409:C:H5''	2.02	0.42
2:GB:1902:C:H5'	5:JB:246:PRO:HD3	1.99	0.42
2:GB:1930:G:O2'	2:GB:1968:G:O6	2.28	0.42
2:GB:2196:C:O2'	2:GB:2197:U:H5'	2.18	0.42
2:GB:2262:U:H4'	2:GB:2328:A:C2	2.54	0.42
5:JB:244:ARG:HB2	5:JB:245:PRO:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:MB:119:GLY:HA3	8:MB:181:ARG:HA	2.01	0.42
9:NB:60:ARG:HB3	9:NB:60:ARG:HH11	1.84	0.42
12:QB:119:PRO:HB2	17:VB:68:TYR:CD2	2.55	0.42
19:XB:68:LYS:H	19:XB:68:LYS:HG2	1.70	0.42
20:YB:34:ASN:ND2	29:HC:39:MET:HG3	2.35	0.42
25:DC:20:ARG:HG2	25:DC:20:ARG:HH11	1.84	0.42
1:A:134:A:N6	50:YA:25:ARG:NH1	2.68	0.42
2:B:155:C:H6	2:B:155:C:H2'	1.65	0.42
2:B:952:G:C6	2:B:953:A:N7	2.87	0.42
2:B:2747:G:O6	2:B:2755:C:H5''	2.20	0.42
17:Q:50:ILE:HD13	17:Q:64:ARG:HB2	2.00	0.42
26:Z:64:LEU:O	26:Z:68:ARG:HG2	2.20	0.42
4:IA:35:A:H2'	4:IA:36:U:H6	1.83	0.42
35:JA:138:TYR:CZ	35:JA:142:ARG:HD2	2.55	0.42
40:OA:5:GLU:HA	40:OA:63:TYR:O	2.19	0.42
51:ZA:12:SER:HA	51:ZA:14:LYS:NZ	2.35	0.42
55:DB:2:GLY:C	55:DB:4:GLY:N	2.78	0.42
1:FB:262:A:C6	1:FB:263:A:C6	3.07	0.42
1:FB:1125:U:O2'	1:FB:1126:U:O5'	2.33	0.42
2:GB:1585:C:H4'	2:GB:1586:A:OP2	2.20	0.42
2:GB:2074:U:H2'	2:GB:2075:U:C6	2.55	0.42
2:GB:2579:C:H4'	6:KB:134:ILE:HG12	2.00	0.42
9:NB:118:PRO:HG2	9:NB:121:ILE:HG13	1.99	0.42
14:SB:79:LEU:HD23	14:SB:79:LEU:HA	1.81	0.42
15:TB:33:ARG:HD2	15:TB:113:LEU:HD13	2.02	0.42
21:ZB:31:HIS:HA	21:ZB:32:PRO:HD3	1.89	0.42
35:OC:109:ARG:HD3	35:OC:208:GLU:O	2.19	0.42
35:OC:181:GLY:O	35:OC:307:ASN:HB2	2.19	0.42
38:RC:192:GLU:OE2	38:RC:192:GLU:N	2.39	0.42
42:VC:4:ASP:HA	42:VC:5:PRO:HD2	1.92	0.42
45:YC:34:ASP:OD1	45:YC:38:ASN:HB2	2.19	0.42
52:FD:66:LEU:O	52:FD:70:ILE:HG13	2.20	0.42
1:A:186(A):C:H2'	1:A:186(B):C:C6	2.54	0.42
1:A:701:C:OP1	1:A:702:A:O2'	2.33	0.42
2:B:264:C:O2'	2:B:265:A:H2'	2.19	0.42
2:B:535:C:O3'	18:R:53:ARG:NH1	2.50	0.42
2:B:715:G:H2'	2:B:716:A:C8	2.53	0.42
2:B:879:G:H2'	2:B:880:G:H8	1.84	0.42
2:B:1063:G:N1	2:B:1088:A:N1	2.68	0.42
2:B:1297:C:H2'	2:B:1298:C:H6	1.84	0.42
2:B:1539:G:H2'	2:B:1540:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1668:A:H4'	2:B:1669:A:O5'	2.20	0.42
2:B:1849:G:H2'	2:B:1850:G:H8	1.84	0.42
2:B:2690:C:N4	2:B:2713:A:H1'	2.34	0.42
2:B:2820:A:OP2	15:O:2:ARG:NH2	2.52	0.42
3:C:3:C:C2	3:C:118:G:C2	3.07	0.42
3:C:42:C:OP1	8:H:67:LYS:HE2	2.20	0.42
10:J:14:ASP:OD1	10:J:15:VAL:HG12	2.19	0.42
13:M:59:LEU:CD1	13:M:60:MET:HE2	2.50	0.42
22:V:52:SER:HG	22:V:55:TYR:H	1.66	0.42
30:DA:4:GLU:H	30:DA:4:GLU:HG2	1.72	0.42
35:JA:317:VAL:HB	35:JA:329:LEU:HD13	2.00	0.42
40:OA:86:ARG:O	40:OA:87:ARG:HG2	2.19	0.42
43:RA:28:VAL:HB	43:RA:36:TYR:HD2	1.84	0.42
47:VA:3:ARG:NH1	47:VA:3:ARG:HB3	2.35	0.42
49:XA:21:ASP:CG	49:XA:24:SER:HB3	2.44	0.42
1:FB:160:A:H2'	1:FB:161:A:O4'	2.18	0.42
1:FB:343:U:H2'	1:FB:345:C:C5	2.55	0.42
1:FB:432:A:H3'	1:FB:433:C:H6	1.85	0.42
1:FB:563:A:N7	1:FB:567:G:H1'	2.35	0.42
1:FB:987:G:H2'	1:FB:988:G:H8	1.82	0.42
1:FB:1133:G:H1	1:FB:1141:C:H42	1.68	0.42
1:FB:1291:G:C6	1:FB:1292:U:C4	3.07	0.42
1:FB:1411:C:H2'	1:FB:1412:C:C6	2.54	0.42
2:GB:478:A:N1	2:GB:500:G:H4'	2.35	0.42
2:GB:1793:C:H2'	2:GB:1794:U:C6	2.55	0.42
2:GB:2141:G:C2	2:GB:2151:G:H1'	2.54	0.42
2:GB:2156:G:H2'	2:GB:2157:G:C5	2.55	0.42
2:GB:2479:G:H5''	2:GB:2537:U:O4'	2.19	0.42
2:GB:2850:A:OP2	2:GB:2866:U:C5	2.72	0.42
10:OB:40:THR:OG1	10:OB:43:ASN:OD1	2.36	0.42
17:VB:35:LYS:HE2	17:VB:37:GLY:O	2.19	0.42
18:WB:76:TYR:CZ	18:WB:80:ILE:HG13	2.54	0.42
22:AC:13:VAL:HG12	22:AC:74:PRO:HA	2.00	0.42
24:CC:70:GLN:HG2	24:CC:72:ARG:HG3	2.00	0.42
36:PC:137:ARG:NH1	36:PC:138:LEU:HG	2.34	0.42
38:RC:21:LEU:H	38:RC:21:LEU:HG	1.60	0.42
42:VC:46:LYS:HG3	42:VC:64:LYS:HB3	2.00	0.42
42:VC:86:ILE:HG13	42:VC:133:LEU:HD22	2.00	0.42
46:ZC:84:LEU:HD23	46:ZC:101:VAL:HG21	2.01	0.42
47:AD:87:TYR:H	53:GD:73:GLU:HG2	1.85	0.42
48:BD:50:LYS:HD2	48:BD:50:LYS:HA	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:GD:62:ILE:HA	53:GD:66:MET:SD	2.60	0.42
54:HD:25:ARG:O	54:HD:29:LYS:HG3	2.19	0.42
55:ID:5:ASP:O	55:ID:7:ARG:N	2.47	0.42
1:A:881:G:OP2	46:UA:12:ARG:NH2	2.53	0.42
2:B:319:C:C2	2:B:333:G:N2	2.88	0.42
2:B:871:U:H2'	2:B:872:A:C8	2.54	0.42
2:B:910:A:C5	14:N:13:GLN:HG3	2.55	0.42
2:B:1471:A:C6	2:B:1522:G:C2	3.07	0.42
2:B:1693:U:O2'	5:E:14:ARG:NH2	2.53	0.42
2:B:1833:U:O2'	2:B:1969:A:N1	2.45	0.42
2:B:2676:C:H2'	2:B:2677:G:H8	1.83	0.42
3:C:78:A:C2	3:C:99:A:C4	3.07	0.42
5:E:61:LEU:HD13	5:E:61:LEU:HA	1.81	0.42
8:H:115:ARG:NH2	47:VA:7:VAL:HG13	2.34	0.42
12:L:64:ARG:O	12:L:82:ASN:HA	2.20	0.42
17:Q:129:ARG:HA	17:Q:132:LYS:HZ3	1.84	0.42
26:Z:16:LEU:O	26:Z:67:LYS:HE3	2.20	0.42
40:OA:19:LEU:HD21	40:OA:59:TYR:CE1	2.55	0.42
40:OA:37:VAL:HA	40:OA:65:VAL:HG12	2.00	0.42
42:QA:119:LEU:HD12	42:QA:123:GLU:HB2	2.00	0.42
43:RA:33:PHE:CE1	43:RA:37:PHE:HD2	2.37	0.42
53:BB:58:VAL:HA	53:BB:59:PRO:HD3	1.77	0.42
1:FB:81:G:H2'	1:FB:82:U:C5	2.55	0.42
1:FB:466:G:H4'	1:FB:467:G:OP2	2.19	0.42
1:FB:968:A:H8	1:FB:968:A:OP1	2.03	0.42
1:FB:1004:A:H61	1:FB:1026:G:P	2.41	0.42
1:FB:1144:G:N2	1:FB:1146:A:H62	2.17	0.42
1:FB:1305:G:N2	1:FB:1331:G:H1'	2.34	0.42
2:GB:1187:G:H8	2:GB:1187:G:O5'	2.02	0.42
6:KB:68:ALA:O	6:KB:71:GLY:N	2.53	0.42
11:PB:10:GLU:CD	11:PB:11:PRO:HD2	2.44	0.42
23:BC:13:GLU:HB2	23:BC:18:LEU:HD11	2.01	0.42
35:OC:248:HIS:CE1	35:OC:250:PRO:HD2	2.54	0.42
39:SC:72:GLN:C	39:SC:74:GLY:H	2.26	0.42
40:TC:60:PHE:CZ	52:FD:78:LEU:HD21	2.54	0.42
42:VC:123:GLU:O	42:VC:127:LEU:HD22	2.19	0.42
43:WC:113:LYS:N	43:WC:113:LYS:HD3	2.35	0.42
43:WC:113:LYS:NZ	43:WC:119:ALA:O	2.53	0.42
51:ED:84:LEU:HD23	51:ED:84:LEU:HA	1.82	0.42
1:A:628:G:H2'	1:A:629:G:O4'	2.20	0.42
1:A:656:C:H4'	49:XA:62:GLN:NE2	2.24	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:592:G:O2'	32:FA:4:MET:HB2	2.20	0.42
2:B:830:G:H4'	2:B:831:G:OP2	2.20	0.42
2:B:887:A:H1'	2:B:890:A:N6	2.35	0.42
2:B:2025:C:H2'	2:B:2026:C:C6	2.55	0.42
10:J:101:LEU:HD23	10:J:109:ILE:HG12	2.02	0.42
14:N:82:ARG:HH11	24:X:4:LYS:HB2	1.83	0.42
14:N:109:VAL:HG22	14:N:113:GLN:OE1	2.19	0.42
17:Q:26:ASP:OD1	17:Q:120:ARG:NH2	2.47	0.42
36:KA:229:VAL:HB	36:KA:231:GLU:OE2	2.20	0.42
37:LA:131:ARG:NH1	37:LA:135:LYS:HE2	2.34	0.42
39:NA:78:HIS:CE1	42:QA:104:ARG:NH1	2.88	0.42
42:QA:64:LYS:HG3	42:QA:79:VAL:HG21	2.01	0.42
50:YA:25:ARG:H	50:YA:25:ARG:HG2	1.54	0.42
1:FB:353:A:H5'	1:FB:353:A:C8	2.54	0.42
1:FB:539:A:OP2	46:ZC:115:LYS:NZ	2.52	0.42
1:FB:791:G:C6	1:FB:792:A:N7	2.88	0.42
1:FB:1137:C:H4'	1:FB:1138:G:C2	2.54	0.42
2:GB:1060:U:H4'	2:GB:1061:U:O5'	2.20	0.42
2:GB:2037:G:C6	2:GB:2038:G:C6	3.08	0.42
2:GB:2319:G:O6	16:UB:4:LEU:HD12	2.20	0.42
2:GB:2320:A:H2'	2:GB:2320:A:N3	2.34	0.42
2:GB:2690:C:N4	2:GB:2713:A:H1'	2.35	0.42
6:KB:174:ASP:HB3	6:KB:183:LEU:HD22	2.01	0.42
6:KB:181:LEU:HA	6:KB:181:LEU:HD12	1.79	0.42
8:MB:54:GLU:HA	8:MB:57:ALA:HB3	2.01	0.42
8:MB:166:ASP:O	8:MB:170:ARG:HB2	2.20	0.42
16:UB:3:ARG:NH1	16:UB:4:LEU:H	2.17	0.42
21:ZB:94:GLY:HA3	21:ZB:95:LEU:C	2.44	0.42
24:CC:2:ALA:HA	35:OC:236:HIS:CE1	2.54	0.42
36:PC:106:LYS:HE2	36:PC:106:LYS:HB3	1.92	0.42
37:QC:30:ARG:NH1	37:QC:31:HIS:CD2	2.88	0.42
38:RC:104:VAL:HG11	38:RC:146:ILE:HG13	2.01	0.42
41:UC:37:ASN:OD1	43:WC:41:VAL:HG22	2.19	0.42
1:A:14:U:H2'	1:A:16:A:OP2	2.20	0.42
1:A:184:G:H2'	1:A:185:A:C8	2.51	0.42
1:A:197:A:N1	1:A:220:G:O2'	2.47	0.42
1:A:601:C:H2'	1:A:602:A:C8	2.54	0.42
2:B:1510:A:C8	2:B:1511:A:C8	3.07	0.42
2:B:1541:U:H2'	2:B:1542:G:O4'	2.19	0.42
2:B:1769:G:O2'	2:B:1958:C:OP1	2.33	0.42
5:E:77:ALA:HB2	5:E:97:TYR:CD1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:129:PHE:HB2	7:G:132:VAL:HG21	2.01	0.42
8:H:165:THR:OG1	8:H:166:ASP:N	2.53	0.42
10:J:64:GLU:HG3	10:J:67:ARG:NH1	2.34	0.42
10:J:67:ARG:HG3	10:J:68:LEU:HD12	2.01	0.42
16:P:26:LEU:HD22	16:P:87:PHE:CE1	2.55	0.42
38:MA:148:VAL:HG12	38:MA:181:MET:O	2.20	0.42
1:FB:377:G:H1	1:FB:386:C:H42	1.68	0.42
2:GB:307:G:H21	2:GB:330:A:N6	2.12	0.42
2:GB:875:G:H2'	2:GB:876:C:O4'	2.20	0.42
2:GB:980:A:C4	2:GB:1136:G:O4'	2.73	0.42
2:GB:1409:C:H2'	2:GB:1410:G:H8	1.84	0.42
2:GB:1541:U:H2'	2:GB:1542:G:O4'	2.19	0.42
2:GB:1592:C:H2'	2:GB:1593:G:H8	1.83	0.42
2:GB:2168:G:C8	2:GB:2170:A:OP2	2.73	0.42
2:GB:2747:G:O6	2:GB:2755:C:H5''	2.19	0.42
7:LB:185:ASP:OD1	7:LB:188:ARG:NH1	2.53	0.42
8:MB:64:THR:HB	8:MB:94:LEU:HD21	2.01	0.42
17:VB:109:GLU:HG2	17:VB:112:ARG:NH2	2.34	0.42
36:PC:10:LEU:HG	36:PC:48:MET:SD	2.59	0.42
36:PC:219:VAL:HA	36:PC:222:ILE:HB	2.01	0.42
40:TC:5:GLU:HA	40:TC:63:TYR:O	2.20	0.42
40:TC:100:ASN:OD1	52:FD:23:LYS:HG2	2.19	0.42
42:VC:23:SER:OG	42:VC:60:ARG:HG3	2.20	0.42
42:VC:31:PHE:O	42:VC:35:ILE:HG13	2.19	0.42
1:A:21:G:H2'	1:A:22:G:C8	2.55	0.42
1:A:433:C:H2'	1:A:434:U:C6	2.55	0.42
1:A:882:C:O2'	1:A:883:C:H5'	2.20	0.42
1:A:1277:C:O2'	1:A:1279:A:H1'	2.19	0.42
1:A:1452:C:H2'	1:A:1453:G:H5''	2.01	0.42
2:B:609(B):G:H2'	2:B:610:C:C6	2.55	0.42
2:B:813:U:H2'	2:B:814:C:C6	2.54	0.42
2:B:1657:C:H2'	2:B:1658:C:C6	2.52	0.42
2:B:2317:C:C2'	2:B:2318:G:H5'	2.48	0.42
4:D:7:G:H5''	4:D:8:4SU:H5	2.01	0.42
4:D:63:G:H2'	4:D:64:G:C8	2.55	0.42
9:I:155:SER:HB3	9:I:158:HIS:O	2.19	0.42
10:J:109:ILE:H	10:J:109:ILE:HG13	1.80	0.42
11:K:99:LEU:HD23	11:K:99:LEU:HA	1.87	0.42
15:O:1:MET:HE3	15:O:1:MET:HB2	1.81	0.42
16:P:26:LEU:HD22	16:P:87:PHE:HE1	1.85	0.42
18:R:95:LEU:HD13	18:R:95:LEU:HA	1.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:KA:69:LEU:O	36:KA:163:PHE:N	2.45	0.42
42:QA:4:ASP:HA	42:QA:5:PRO:HD2	1.88	0.42
44:SA:38:ILE:HA	44:SA:39:PRO:HD3	1.82	0.42
46:UA:84:LEU:HD22	46:UA:104:VAL:HG11	2.02	0.42
47:VA:97:PRO:HA	47:VA:110:ARG:HG3	2.01	0.42
54:CB:47:GLY:HA2	54:CB:48:LYS:C	2.44	0.42
54:CB:83:ARG:HA	54:CB:86:ARG:HD3	2.02	0.42
1:FB:381:C:H2'	1:FB:382:A:O4'	2.20	0.42
2:GB:296:C:O3'	22:AC:95:LYS:NZ	2.53	0.42
2:GB:1490:A:H8	2:GB:1490:A:O5'	2.03	0.42
2:GB:1510:A:C8	2:GB:1511:A:C8	3.08	0.42
2:GB:1575:C:H2'	2:GB:1576:U:O4'	2.20	0.42
2:GB:2275:C:O2	14:SB:85:LYS:HG3	2.19	0.42
4:IB:10:G:H2'	4:IB:11:A:H8	1.84	0.42
10:OB:67:ARG:HG3	10:OB:68:LEU:HD12	2.01	0.42
18:WB:80:ILE:HD13	18:WB:80:ILE:HA	1.76	0.42
32:KC:52:LYS:HB3	32:KC:53:PRO:HD3	2.02	0.42
4:NC:35:A:H2'	4:NC:36:U:C6	2.55	0.42
36:PC:178:ARG:NH2	42:VC:74:PRO:HB3	2.34	0.42
39:SC:69:VAL:HG11	39:SC:113:ALA:HB1	2.02	0.42
1:A:38:G:N1	1:A:397:A:OP1	2.51	0.42
1:A:236:G:H2'	1:A:237:C:O4'	2.20	0.42
1:A:452:A:O2'	1:A:453:A:H8	2.03	0.42
2:B:573:G:O2'	2:B:574:C:H3'	2.20	0.42
2:B:616:A:C4	7:G:180:GLY:HA2	2.55	0.42
2:B:1252:G:C2	2:B:1253:A:C2	3.08	0.42
2:B:1901:A:H2'	2:B:1901:A:N3	2.35	0.42
2:B:2287:A:C4	2:B:2289:G:C8	3.08	0.42
25:Y:50:ARG:HG2	25:Y:59:THR:HB	2.02	0.42
4:IA:47:U:OP2	4:IA:47:U:H6	2.02	0.42
37:LA:138:VAL:O	37:LA:142:MET:HB2	2.20	0.42
39:NA:20:GLN:O	39:NA:23:GLY:N	2.43	0.42
42:QA:97:VAL:HG21	42:QA:128:GLY:HA2	2.02	0.42
46:UA:59:ARG:HD3	46:UA:65:GLU:HG2	2.02	0.42
47:VA:20:THR:C	47:VA:22:ILE:H	2.27	0.42
49:XA:11:VAL:HG21	49:XA:34:LEU:HD13	2.01	0.42
54:CB:25:ARG:O	54:CB:29:LYS:HG3	2.19	0.42
1:FB:603:U:H2'	1:FB:604:G:H8	1.85	0.42
1:FB:967:5MC:H2'	1:FB:968:A:C8	2.54	0.42
1:FB:1350:A:C6	1:FB:1351:U:C4	3.08	0.42
2:GB:330:A:C2	2:GB:1210:A:H2'	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:643:A:C8	30:IC:44:ARG:NH1	2.88	0.42
2:GB:1141:U:H2'	11:PB:63:THR:HG21	2.01	0.42
2:GB:2159:G:H2'	2:GB:2160:G:C8	2.55	0.42
2:GB:2298:A:N6	2:GB:2318:G:H8	1.94	0.42
8:MB:121:ASN:HA	8:MB:122:PRO:HD3	1.91	0.42
8:MB:121:ASN:ND2	8:MB:181:ARG:HH22	2.17	0.42
10:OB:48:GLU:O	10:OB:52:ARG:HB2	2.20	0.42
14:SB:2:LEU:O	14:SB:3:MET:HB3	2.20	0.42
19:XB:8:GLY:HA3	19:XB:23:GLU:HB2	2.01	0.42
33:LC:1:MET:HE2	33:LC:33:LYS:HE3	2.02	0.42
36:PC:25:ASN:O	36:PC:27:LYS:N	2.53	0.42
48:BD:14:PRO:HB2	48:BD:15:LYS:H	1.56	0.42
49:CD:63:ARG:HG2	49:CD:67:LEU:HD12	2.01	0.42
53:GD:36:ARG:HB2	53:GD:72:GLY:HA3	2.01	0.42
54:HD:88:VAL:O	54:HD:92:LEU:HB2	2.20	0.42
1:A:444:C:H2'	1:A:445:G:H8	1.85	0.41
1:A:583:A:H61	1:A:758:G:H1'	1.85	0.41
1:A:624:C:H2'	1:A:625:G:C8	2.54	0.41
1:A:828:A:H2'	1:A:829:G:O4'	2.19	0.41
1:A:924:C:O2'	1:A:1502:A:N1	2.44	0.41
1:A:1226:C:H4'	53:BB:80:TYR:OH	2.19	0.41
2:B:1005:C:H2'	2:B:1006:C:C6	2.54	0.41
2:B:1614:A:C2	20:T:93:ALA:HB2	2.55	0.41
2:B:2325:G:H5''	2:B:2326:C:OP2	2.20	0.41
2:B:2378:A:H4'	16:P:23:ARG:NH1	2.35	0.41
2:B:2712:U:H1'	2:B:2712(A):A:C8	2.55	0.41
2:B:2773:C:H2'	2:B:2774:C:H6	1.85	0.41
4:D:67:C:H2'	4:D:68:C:H6	1.84	0.41
6:F:78:LEU:HA	6:F:78:LEU:HD13	1.79	0.41
8:H:135:LEU:HD12	8:H:136:ARG:HH21	1.84	0.41
8:H:164:GLU:HB2	8:H:168:GLU:OE2	2.20	0.41
19:S:29:PRO:HA	19:S:61:VAL:HG22	2.02	0.41
22:V:15:VAL:HG11	22:V:20:TYR:HB2	2.01	0.41
23:W:61:LEU:HB3	23:W:63:ASP:OD1	2.20	0.41
25:Y:85:LEU:HD23	25:Y:89:GLU:HB3	2.02	0.41
27:AA:3:ARG:NH1	27:AA:60:GLU:OE1	2.53	0.41
4:IA:35:A:H2'	4:IA:36:U:C6	2.55	0.41
38:MA:4:TYR:HD2	38:MA:4:TYR:HA	1.70	0.41
39:NA:69:VAL:HG11	39:NA:113:ALA:HB1	2.02	0.41
43:RA:11:LYS:C	43:RA:13:ALA:H	2.26	0.41
45:TA:86:GLY:O	45:TA:91:ARG:NH1	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:TA:121:PRO:HB2	45:TA:125:PHE:HB2	2.01	0.41
53:BB:22:LEU:HD23	53:BB:26:GLY:O	2.20	0.41
1:FB:14:U:H2'	1:FB:16:A:OP2	2.20	0.41
1:FB:628:G:H2'	1:FB:629:G:O4'	2.19	0.41
1:FB:784:C:H4'	2:GB:1837:C:OP1	2.20	0.41
1:FB:1048:G:OP1	48:BD:3:ARG:HB3	2.19	0.41
1:FB:1372:U:H2'	1:FB:1373:G:O4'	2.20	0.41
2:GB:1063:G:N1	2:GB:1088:A:N1	2.68	0.41
2:GB:1388:G:H2'	2:GB:1389:G:H8	1.85	0.41
9:NB:11:VAL:HG13	9:NB:15:VAL:HG23	2.02	0.41
18:WB:14:HIS:O	18:WB:18:LEU:HD12	2.19	0.41
20:YB:13:SER:HA	20:YB:14:PRO:HD3	1.90	0.41
26:EC:41:ILE:HG13	26:EC:41:ILE:H	1.57	0.41
35:OC:182:HIS:HB3	35:OC:310:TYR:CE1	2.50	0.41
39:SC:80:ILE:HD11	39:SC:138:ALA:HB1	2.00	0.41
40:TC:37:VAL:HA	40:TC:65:VAL:HG12	2.01	0.41
41:UC:107:ALA:HA	41:UC:110:GLN:HG2	2.01	0.41
43:WC:53:VAL:HG11	43:WC:85:LEU:HD13	2.01	0.41
44:XC:61:GLU:HG3	48:BD:58:LYS:HE3	2.01	0.41
1:A:88:C:H2'	1:A:89:U:C6	2.54	0.41
1:A:332:G:OP2	54:CB:10:LEU:HG	2.21	0.41
1:A:603:U:H2'	1:A:604:G:H8	1.84	0.41
1:A:864:A:H5'	39:NA:86:ALA:HB2	2.02	0.41
1:A:951:G:N3	1:A:970:C:O2'	2.50	0.41
1:A:1291:G:C6	1:A:1292:U:C4	3.09	0.41
1:A:1293:G:H2'	1:A:1294:G:C8	2.56	0.41
2:B:352:G:H4'	2:B:353:G:OP2	2.20	0.41
2:B:411:G:C5	13:M:72:PRO:HB3	2.56	0.41
2:B:958:U:H5'	14:N:14:ARG:HD3	2.02	0.41
2:B:1519:G:H2'	2:B:1520:U:O4'	2.20	0.41
2:B:1798:U:H5'	5:E:259:THR:CG2	2.38	0.41
2:B:1850:G:H1	2:B:1892:C:H42	1.68	0.41
2:B:2088:G:C6	2:B:2089:U:C4	3.08	0.41
2:B:2364:C:H2'	2:B:2365:G:O4'	2.20	0.41
9:I:70:THR:HG22	9:I:74:ASN:OD1	2.20	0.41
10:J:57:ARG:H	10:J:57:ARG:HG3	1.71	0.41
10:J:110:ASP:HA	10:J:111:PRO:HD2	1.86	0.41
15:O:74:LYS:HB2	15:O:74:LYS:HE2	1.90	0.41
31:EA:3:ARG:HA	31:EA:3:ARG:HD3	1.74	0.41
36:KA:59:GLU:HG3	36:KA:225:ALA:HB2	2.01	0.41
42:QA:50:ARG:H	42:QA:50:ARG:HG2	1.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:DB:2:GLY:N	55:DB:5:ASP:HB2	2.35	0.41
1:FB:562:C:H4'	1:FB:563:A:O5'	2.20	0.41
2:GB:186:G:H2'	2:GB:187:G:H8	1.85	0.41
2:GB:742:G:H2'	2:GB:743:G:H8	1.85	0.41
2:GB:784:A:C6	5:JB:229:VAL:HG21	2.55	0.41
2:GB:2162:G:H1'	2:GB:2173:A:H1'	2.02	0.41
8:MB:103:LEU:HD23	8:MB:103:LEU:HA	1.88	0.41
23:BC:150:LEU:HD12	23:BC:171:ILE:HB	2.02	0.41
39:SC:40:ARG:CZ	39:SC:68:GLU:HB2	2.49	0.41
39:SC:92:LYS:HA	39:SC:93:PRO:HD3	1.88	0.41
40:TC:46:ARG:HB2	40:TC:60:PHE:HE1	1.82	0.41
41:UC:46:ALA:O	41:UC:50:ILE:HG13	2.20	0.41
43:WC:28:VAL:HB	43:WC:36:TYR:HD2	1.85	0.41
47:AD:14:ARG:NE	47:AD:42:ALA:HA	2.35	0.41
47:AD:97:PRO:HA	47:AD:110:ARG:HG3	2.01	0.41
1:A:1350:A:C6	1:A:1351:U:C4	3.09	0.41
2:B:392:C:H5''	2:B:409:C:H5''	2.02	0.41
2:B:587:C:C6	2:B:671:C:H1'	2.56	0.41
2:B:716:A:C2	2:B:717:G:H1'	2.55	0.41
2:B:1773:A:C5	2:B:1829:A:H1'	2.55	0.41
2:B:1842:G:H2'	2:B:1843:C:C6	2.55	0.41
2:B:2567:G:H2'	2:B:2568:C:C6	2.56	0.41
2:B:2615:U:C2	29:CA:7:PRO:HA	2.55	0.41
2:B:2780:G:H4'	2:B:2781:A:OP2	2.19	0.41
13:M:119:GLU:HB2	27:FC:1:MET:N	2.35	0.41
14:N:69:PHE:HA	14:N:70:PRO:HD3	1.76	0.41
16:P:41:ASP:OD2	16:P:44:LYS:HG3	2.19	0.41
27:AA:26:LEU:HD23	27:AA:26:LEU:HA	1.85	0.41
32:FA:36:LYS:HD3	32:FA:40:GLU:OE2	2.21	0.41
36:KA:166:ASP:HA	36:KA:167:PRO:HD3	1.74	0.41
36:KA:215:LEU:O	36:KA:219:VAL:HG23	2.20	0.41
42:QA:125:ARG:HG2	42:QA:125:ARG:HH11	1.85	0.41
44:SA:25:GLU:O	44:SA:29:ARG:HG3	2.20	0.41
1:FB:623:C:H6	1:FB:623:C:O5'	2.03	0.41
2:GB:270(S):G:H2'	2:GB:270(T):G:C8	2.54	0.41
2:GB:1613:G:C2	2:GB:1619:G:C5	3.08	0.41
2:GB:1800:C:OP1	5:JB:260:ARG:NH2	2.53	0.41
9:NB:3:ARG:NH2	9:NB:5:GLY:H	2.18	0.41
10:OB:110:ASP:OD1	10:OB:112:LYS:HE3	2.20	0.41
12:QB:25:LEU:HD23	12:QB:25:LEU:HA	1.71	0.41
16:UB:26:LEU:HD22	16:UB:87:PHE:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:VB:126:ALA:HA	17:VB:129:ARG:CZ	2.49	0.41
26:EC:37:PHE:O	26:EC:40:SER:HB3	2.19	0.41
27:FC:1:MET:HA	27:FC:2:PRO:HD2	1.92	0.41
37:QC:125:GLU:HG2	37:QC:190:ARG:O	2.19	0.41
42:VC:53:VAL:HB	42:VC:58:TYR:CD2	2.56	0.41
47:AD:20:THR:C	47:AD:22:ILE:H	2.28	0.41
49:CD:21:ASP:CG	49:CD:24:SER:HB3	2.44	0.41
54:HD:49:ALA:HB3	54:HD:99:LEU:HB2	2.02	0.41
1:A:432:A:H2'	1:A:433:C:O4'	2.20	0.41
1:A:695:A:OP2	45:TA:53:SER:HB2	2.20	0.41
1:A:1055:A:H2'	37:LA:156:ARG:HD2	2.02	0.41
2:B:330:A:C2	2:B:1210:A:H2'	2.54	0.41
2:B:1406:U:H2'	2:B:1407:C:C6	2.55	0.41
2:B:1800:C:OP1	5:E:260:ARG:NH2	2.52	0.41
2:B:1964:G:O2'	2:B:1967:C:OP2	2.35	0.41
2:B:2101:G:C5	2:B:2102:U:C4	3.09	0.41
2:B:2216:G:H2'	2:B:2217:G:H8	1.85	0.41
2:B:2331:G:O2'	2:B:2336:A:N1	2.42	0.41
2:B:2695:C:H2'	2:B:2696:U:H6	1.85	0.41
2:B:2818:G:O2'	2:B:2837:G:H5'	2.20	0.41
4:D:10:G:H2'	4:D:11:A:H8	1.85	0.41
4:D:51:C:O2	4:D:64:G:N2	2.53	0.41
9:I:52:VAL:HG23	9:I:65:HIS:CD2	2.56	0.41
9:I:60:ARG:HB3	9:I:60:ARG:HH11	1.86	0.41
23:W:31:ARG:H	23:W:31:ARG:HG2	1.68	0.41
27:AA:3:ARG:HB2	27:AA:60:GLU:HB2	2.03	0.41
35:JA:131:LEU:HA	35:JA:134:MET:HG2	2.03	0.41
35:JA:131:LEU:O	35:JA:134:MET:HG3	2.20	0.41
38:MA:8:VAL:HB	38:MA:115:ARG:NH1	2.35	0.41
38:MA:8:VAL:O	38:MA:11:LEU:HB2	2.20	0.41
39:NA:113:ALA:HB3	39:NA:115:VAL:HG23	2.03	0.41
45:TA:77:MET:HE2	45:TA:77:MET:HB2	1.91	0.41
1:FB:59:A:H5''	1:FB:60:A:H5''	2.03	0.41
1:FB:78:G:H2'	1:FB:79:G:O4'	2.21	0.41
1:FB:149:A:H2'	1:FB:150:C:H6	1.85	0.41
1:FB:339:C:H2'	1:FB:340:U:H6	1.84	0.41
1:FB:487:A:H5''	1:FB:488:C:OP2	2.20	0.41
1:FB:828:A:H2'	1:FB:829:G:O4'	2.19	0.41
2:GB:1297:C:H2'	2:GB:1298:C:C6	2.55	0.41
2:GB:1470:G:H8	2:GB:1470:G:O5'	2.03	0.41
2:GB:2251:OMG:HM23	2:GB:2251:OMG:HI'	1.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:2319:G:H3'	2:GB:2319:G:OP1	2.20	0.41
5:JB:26:LYS:HB3	5:JB:83:GLU:HG2	2.03	0.41
9:NB:101:ARG:HG3	9:NB:117:PRO:HG3	2.02	0.41
14:SB:72:LYS:HA	14:SB:73:PRO:HD3	1.87	0.41
22:AC:68:HIS:ND1	22:AC:70:SER:HB3	2.35	0.41
23:BC:61:LEU:HB2	23:BC:65:GLN:HB2	2.02	0.41
23:BC:129:SER:HB3	23:BC:132:ASN:HD21	1.85	0.41
28:GC:40:HIS:HA	28:GC:41:PRO:HD2	1.86	0.41
38:RC:12:CYS:SG	38:RC:18:LYS:CE	3.08	0.41
1:A:339:C:H2'	1:A:340:U:C6	2.55	0.41
1:A:375:U:H4'	50:YA:17:TYR:CE1	2.56	0.41
1:A:606:G:H2'	1:A:631:G:N2	2.35	0.41
1:A:778:G:H8	1:A:778:G:O5'	2.04	0.41
1:A:841:U:O2'	1:A:842:C:OP1	2.36	0.41
1:A:1239:A:H62	1:A:1299:A:H62	1.68	0.41
2:B:1952:A:C6	2:B:1953:A:N1	2.89	0.41
2:B:2479:G:H5''	2:B:2537:U:O4'	2.20	0.41
2:B:2633:G:H2'	2:B:2634:G:O4'	2.20	0.41
6:F:68:ALA:O	6:F:71:GLY:N	2.53	0.41
16:P:56:LEU:HD22	16:P:56:LEU:HA	1.88	0.41
17:Q:6:LEU:HD13	17:Q:6:LEU:HA	1.82	0.41
31:EA:26:GLY:O	31:EA:30:VAL:HG23	2.20	0.41
35:JA:103:LYS:O	35:JA:104:ASP:HB2	2.20	0.41
36:KA:90:MET:HE3	36:KA:226:ARG:HH12	1.85	0.41
36:KA:178:ARG:NH2	42:QA:74:PRO:HB3	2.35	0.41
1:FB:253:U:H2'	1:FB:254:G:C8	2.56	0.41
1:FB:428:G:O4'	1:FB:430:A:C8	2.73	0.41
2:GB:251:A:C5	2:GB:252:G:H1'	2.55	0.41
2:GB:637:A:H4'	2:GB:638:G:O5'	2.21	0.41
2:GB:1289:C:H2'	2:GB:1290:C:C6	2.55	0.41
2:GB:1373:A:H2'	2:GB:1374:G:O4'	2.21	0.41
2:GB:1773:A:C5	2:GB:1829:A:H1'	2.55	0.41
3:HB:30:C:H2'	3:HB:31:C:H5'	2.03	0.41
4:IB:8:4SU:H1'	4:IB:48:C:O2	2.21	0.41
5:JB:227:ASN:HB3	5:JB:228:PRO:HD2	2.03	0.41
9:NB:101:ARG:NH1	9:NB:122:THR:HG23	2.35	0.41
11:PB:35:ARG:HG2	11:PB:35:ARG:HH11	1.86	0.41
20:YB:110:LYS:HZ3	20:YB:111:HIS:H	1.67	0.41
38:RC:177:ASP:OD1	38:RC:180:GLY:HA3	2.20	0.41
40:TC:40:VAL:HG22	40:TC:63:TYR:CD1	2.55	0.41
42:VC:85:ARG:NH1	42:VC:87:SER:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:ZC:59:ARG:HH11	46:ZC:65:GLU:HG3	1.84	0.41
47:AD:37:THR:O	47:AD:55:ARG:NH1	2.48	0.41
53:GD:29:ARG:NH1	53:GD:29:ARG:HA	2.35	0.41
1:A:253:U:H2'	1:A:254:G:C8	2.56	0.41
1:A:373:A:O2'	1:A:451:A:N7	2.54	0.41
1:A:382:A:H2'	1:A:383:A:C8	2.55	0.41
2:B:57:C:H2'	2:B:58:G:O4'	2.20	0.41
2:B:481:G:C2	2:B:507:A:C4	3.08	0.41
2:B:751:A:C6	2:B:789:A:C5	3.09	0.41
2:B:807:U:OP2	13:M:41:ARG:NH2	2.54	0.41
2:B:848:G:N9	2:B:933:A:H8	2.17	0.41
2:B:895:U:H5'	2:B:896:A:OP1	2.21	0.41
2:B:1935:G:H1'	2:B:1964:G:N2	2.36	0.41
2:B:2005:A:H5''	2:B:2006:C:OP2	2.20	0.41
10:J:31:LEU:HD21	10:J:37:VAL:HA	2.03	0.41
19:S:31:ALA:O	19:S:61:VAL:HG12	2.21	0.41
4:IA:35:A:P	43:RA:128:ARG:HH11	2.43	0.41
4:IA:47:U:H6	4:IA:47:U:P	2.44	0.41
4:IA:76:A:O2'	35:JA:235:GLN:HB2	2.20	0.41
37:LA:35:GLU:O	37:LA:39:ILE:HG13	2.21	0.41
40:OA:60:PHE:CZ	52:AB:78:LEU:HD21	2.54	0.41
53:BB:3:ARG:NH1	53:BB:7:LYS:HD3	2.36	0.41
53:BB:19:VAL:HA	53:BB:22:LEU:HD12	2.02	0.41
1:FB:382:A:H2'	1:FB:383:A:C8	2.56	0.41
1:FB:503:C:OP2	46:ZC:116:SER:OG	2.34	0.41
1:FB:617:G:H4'	50:DD:44:THR:O	2.21	0.41
1:FB:630:G:H3'	1:FB:631:G:H8	1.85	0.41
1:FB:675:A:O2'	45:YC:114:VAL:O	2.34	0.41
1:FB:1277:C:O2'	1:FB:1279:A:H1'	2.20	0.41
2:GB:7:G:H4'	11:PB:13:TRP:CH2	2.56	0.41
2:GB:117:G:C6	2:GB:119:A:C6	3.08	0.41
2:GB:544:C:H2'	2:GB:545:G:O4'	2.21	0.41
2:GB:637:A:H8	13:RB:117:GLU:HG3	1.86	0.41
2:GB:828:U:H4'	2:GB:831:G:N1	2.35	0.41
2:GB:2321:G:H5'	2:GB:2322:A:OP2	2.20	0.41
2:GB:2643:G:H2'	2:GB:2644:G:O4'	2.20	0.41
2:GB:2712:U:H1'	2:GB:2712(A):A:C8	2.56	0.41
4:IB:40:C:H2'	4:IB:41:C:H6	1.85	0.41
8:MB:11:TYR:OH	8:MB:16:ARG:HD3	2.20	0.41
10:OB:6:LEU:HD11	10:OB:37:VAL:HB	2.03	0.41
10:OB:26:ALA:O	10:OB:31:LEU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:QB:64:ARG:NH1	12:QB:81:ASP:OD1	2.54	0.41
15:TB:70:LEU:C	15:TB:72:ASP:H	2.29	0.41
17:VB:100:TYR:HB3	17:VB:103:ARG:NH1	2.29	0.41
25:DC:73:LEU:HB3	25:DC:94:LEU:HD22	2.02	0.41
40:TC:8:ILE:HB	40:TC:61:LEU:HB2	2.03	0.41
41:UC:116:ALA:HA	41:UC:119:ARG:NH1	2.36	0.41
44:XC:25:GLU:OE2	44:XC:25:GLU:N	2.51	0.41
52:FD:73:ALA:HB3	52:FD:79:LEU:HD12	2.02	0.41
1:A:987:G:H2'	1:A:988:G:H8	1.82	0.41
1:A:1125:U:O2'	1:A:1126:U:O5'	2.35	0.41
1:A:1216:G:OP1	48:WA:2:ALA:N	2.53	0.41
2:B:221:A:H61	2:B:265:A:H8	1.69	0.41
2:B:1472:A:H61	2:B:1521:G:H1'	1.85	0.41
2:B:2483:C:H2'	2:B:2484:G:O4'	2.21	0.41
5:E:121:PRO:HB3	5:E:135:PHE:CE2	2.56	0.41
10:J:90:GLY:C	10:J:92:VAL:H	2.28	0.41
17:Q:126:ALA:HA	17:Q:129:ARG:CZ	2.51	0.41
20:T:11:ARG:HD3	20:T:82:LEU:HD12	2.02	0.41
22:V:45:VAL:O	22:V:62:GLU:HA	2.20	0.41
36:KA:70:PHE:HE1	36:KA:163:PHE:HD1	1.68	0.41
37:LA:30:ARG:NH1	37:LA:31:HIS:CD2	2.89	0.41
40:OA:6:VAL:HG12	40:OA:8:ILE:HD11	2.03	0.41
40:OA:22:GLU:OE1	40:OA:82:ARG:NH2	2.54	0.41
41:PA:87:VAL:HA	41:PA:88:PRO:HD3	1.86	0.41
52:AB:66:LEU:O	52:AB:70:ILE:HG13	2.21	0.41
1:FB:120:A:O2'	1:FB:122:G:OP1	2.32	0.41
1:FB:191(E):G:H2'	1:FB:191(F):U:C6	2.56	0.41
1:FB:375:U:H4'	50:DD:17:TYR:CE1	2.56	0.41
1:FB:378:G:C6	1:FB:379:C:C4	3.08	0.41
2:GB:385:C:O2'	2:GB:388:G:N2	2.53	0.41
2:GB:656:G:H2'	2:GB:657:U:C6	2.55	0.41
2:GB:879:G:H2'	2:GB:880:G:H8	1.85	0.41
2:GB:1454:U:OP1	15:TB:77:ARG:NH1	2.53	0.41
2:GB:2451:A:H5'	24:CC:3:HIS:NE2	2.36	0.41
2:GB:2893:G:O5'	2:GB:2893:G:H8	2.04	0.41
5:JB:108:PRO:HB3	5:JB:143:HIS:HE1	1.85	0.41
5:JB:213:ARG:HD2	5:JB:217:ARG:O	2.20	0.41
5:JB:273:ARG:HB3	5:JB:273:ARG:HH11	1.85	0.41
9:NB:9:ILE:HA	9:NB:10:PRO:HD2	1.91	0.41
14:SB:118:LEU:HD23	14:SB:118:LEU:HA	1.92	0.41
24:CC:65:GLY:HA2	24:CC:84:LEU:HG	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:WC:40:LEU:HB2	43:WC:43:ALA:HB2	2.02	0.41
45:YC:79:SER:HA	45:YC:104:GLN:CB	2.46	0.41
50:DD:4:ILE:HG23	50:DD:36:ILE:HD11	2.02	0.41
50:DD:55:ARG:HD2	50:DD:55:ARG:HA	1.83	0.41
1:A:706:A:C5'	45:TA:22:HIS:CD2	3.03	0.41
1:A:1004:A:H61	1:A:1026:G:P	2.43	0.41
1:A:1128:C:H4'	1:A:1148:U:O2	2.20	0.41
1:A:1417:G:O2'	1:A:1483:A:N6	2.53	0.41
1:A:1504:G:OP1	1:A:1507:A:H4'	2.20	0.41
2:B:221:A:N6	2:B:265:A:H8	2.18	0.41
2:B:1289:C:H2'	2:B:1290:C:C6	2.56	0.41
2:B:1586:A:C2'	2:B:1587:A:H5'	2.50	0.41
2:B:1686:C:H2'	2:B:1687:G:O4'	2.21	0.41
8:H:119:GLY:HA3	8:H:181:ARG:HA	2.03	0.41
13:M:83:VAL:CG1	13:M:112:LEU:HD21	2.51	0.41
14:N:2:LEU:HB2	14:N:70:PRO:HG2	2.01	0.41
18:R:76:TYR:CZ	18:R:80:ILE:HG13	2.56	0.41
23:W:98:MET:HE3	23:W:98:MET:HB2	1.94	0.41
27:AA:35:ARG:HH21	27:AA:37:LEU:HD21	1.86	0.41
28:BA:40:HIS:HA	28:BA:41:PRO:HD2	1.87	0.41
31:EA:34:ARG:HH11	31:EA:34:ARG:CG	2.31	0.41
36:KA:217:ARG:HD3	36:KA:217:ARG:HA	1.90	0.41
47:VA:84:ILE:HB	53:BB:74:PHE:HE1	1.86	0.41
53:BB:29:ARG:HA	53:BB:29:ARG:HH11	1.86	0.41
1:FB:335:C:H2'	1:FB:336:C:C6	2.55	0.41
1:FB:1101:A:H4'	1:FB:1102:A:O5'	2.21	0.41
2:GB:479:A:H1'	2:GB:480:A:H5''	2.02	0.41
7:LB:123:LEU:HD13	7:LB:192:LEU:HB3	2.03	0.41
8:MB:106:LEU:HA	8:MB:110:ALA:HB3	2.03	0.41
9:NB:144:VAL:O	9:NB:148:ILE:HG12	2.20	0.41
12:QB:105:GLU:OE1	12:QB:105:GLU:N	2.50	0.41
20:YB:45:TYR:CZ	20:YB:49:LYS:HE3	2.55	0.41
23:BC:4:ARG:HD3	23:BC:60:GLU:OE2	2.21	0.41
23:BC:169:GLU:OE2	23:BC:169:GLU:HA	2.20	0.41
35:OC:271:LEU:HD23	35:OC:271:LEU:HA	1.95	0.41
36:PC:87:ARG:CZ	36:PC:233:SER:HB2	2.51	0.41
36:PC:163:PHE:HD2	36:PC:163:PHE:HA	1.63	0.41
37:QC:38:ARG:HD2	37:QC:94:LEU:HD11	2.02	0.41
44:XC:15:THR:HB	44:XC:91:PRO:HG3	2.03	0.41
45:YC:77:MET:HE2	45:YC:77:MET:HB2	1.90	0.41
53:GD:3:ARG:NH1	53:GD:7:LYS:HD3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:G:H5'	51:ZA:64:PRO:O	2.21	0.41
1:A:335:C:H2'	1:A:336:C:C6	2.55	0.41
1:A:355:C:O2'	1:A:388:G:N3	2.50	0.41
1:A:381:C:H2'	1:A:382:A:O4'	2.21	0.41
1:A:570:G:H1'	1:A:820:U:C4	2.55	0.41
1:A:860:A:H2'	1:A:861:G:O4'	2.21	0.41
1:A:1031:G:C8	1:A:1032(B):G:N1	2.88	0.41
1:A:1137:C:H4'	1:A:1138:G:C2	2.56	0.41
1:A:1296:C:H4'	1:A:1302:U:C5	2.56	0.41
1:A:1360:A:H2'	1:A:1361:G:O4'	2.21	0.41
1:A:1502:A:C8	1:A:1505:G:N2	2.88	0.41
2:B:90:U:H1'	2:B:91:A:C8	2.56	0.41
2:B:125:G:H4'	2:B:126:A:OP2	2.21	0.41
2:B:247:G:H4'	2:B:386:G:C5	2.55	0.41
2:B:270(W):G:C4	2:B:270(X):G:C8	3.09	0.41
2:B:483:A:O2'	22:V:59:GLY:N	2.53	0.41
2:B:637:A:H8	13:M:117:GLU:HG3	1.86	0.41
2:B:656:G:H2'	2:B:657:U:C6	2.56	0.41
2:B:1454:U:OP1	15:O:77:ARG:NH1	2.50	0.41
2:B:2022:U:O2'	2:B:2617:C:H5'	2.21	0.41
2:B:2684:U:OP1	17:Q:53:ARG:HD3	2.21	0.41
2:B:2850:A:OP2	2:B:2866:U:C5	2.74	0.41
5:E:147:LEU:HD13	5:E:155:LEU:HD11	2.02	0.41
7:G:120:GLU:HB3	7:G:122:LYS:HG2	2.03	0.41
12:L:63:VAL:HG12	12:L:106:LEU:HD11	2.03	0.41
13:M:50:ARG:HH21	32:FA:7:HIS:CD2	2.39	0.41
14:N:68:ILE:HG23	14:N:103:MET:HA	2.03	0.41
15:O:45:ARG:HE	15:O:45:ARG:HB3	1.52	0.41
15:O:70:LEU:C	15:O:72:ASP:H	2.29	0.41
15:O:104:ARG:HG2	15:O:111:LEU:HD21	2.02	0.41
19:S:8:GLY:HA3	19:S:23:GLU:HB2	2.03	0.41
20:T:9:TYR:H	20:T:102:HIS:CE1	2.39	0.41
20:T:45:TYR:CZ	20:T:49:LYS:HE3	2.56	0.41
22:V:29:GLU:HG2	22:V:30:VAL:N	2.36	0.41
23:W:44:PHE:CE1	23:W:86:VAL:HG11	2.55	0.41
24:X:2:ALA:HB3	4:IA:76:A:N6	2.36	0.41
38:MA:144:ASP:N	38:MA:144:ASP:OD1	2.54	0.41
41:PA:46:ALA:O	41:PA:50:ILE:HG13	2.21	0.41
42:QA:46:LYS:HG3	42:QA:64:LYS:HB3	2.03	0.41
43:RA:53:VAL:HG11	43:RA:85:LEU:HD13	2.01	0.41
45:TA:34:ASP:OD2	45:TA:36:ASP:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:UA:59:ARG:HH11	46:UA:65:GLU:HG3	1.85	0.41
47:VA:60:VAL:HG13	47:VA:64:TRP:CE3	2.56	0.41
52:AB:53:ARG:HA	52:AB:56:THR:OG1	2.21	0.41
1:FB:323:U:O3'	54:HD:22:ARG:HD3	2.21	0.41
1:FB:433:C:H2'	1:FB:434:U:H6	1.86	0.41
1:FB:778:G:H2'	1:FB:779:C:O4'	2.21	0.41
1:FB:890:G:O2'	1:FB:906:G:O6	2.35	0.41
1:FB:1009:G:N2	1:FB:1020:U:O2	2.41	0.41
1:FB:1191:A:OP1	37:QC:4:LYS:HG3	2.20	0.41
1:FB:1293:G:H2'	1:FB:1294:G:C8	2.56	0.41
1:FB:1296:C:H4'	1:FB:1302:U:C5	2.56	0.41
2:GB:57:C:H2'	2:GB:58:G:O4'	2.21	0.41
2:GB:733:G:O6	2:GB:761:A:C8	2.73	0.41
2:GB:1021:A:C8	2:GB:1021:A:C3'	3.02	0.41
2:GB:2047:U:O2'	2:GB:2823:A:N1	2.49	0.41
2:GB:2331:G:O2'	2:GB:2336:A:N1	2.41	0.41
2:GB:2344:U:O2'	30:IC:36:LEU:HD22	2.21	0.41
2:GB:2652:C:H2'	2:GB:2653:U:O4'	2.21	0.41
2:GB:2853:C:H2'	2:GB:2854:G:H8	1.86	0.41
8:MB:177:GLY:O	8:MB:179:PRO:HD3	2.20	0.41
13:RB:106:LEU:HD13	13:RB:112:LEU:HD23	2.03	0.41
14:SB:11:LYS:NZ	14:SB:88:GLY:O	2.48	0.41
17:VB:50:ILE:HD13	17:VB:64:ARG:HB2	2.03	0.41
17:VB:132:LYS:NZ	17:VB:132:LYS:CB	2.84	0.41
17:VB:132:LYS:HB2	17:VB:132:LYS:HZ2	1.85	0.41
19:XB:31:ALA:O	19:XB:61:VAL:HG12	2.21	0.41
23:BC:79:ARG:HB3	23:BC:80:ARG:HD3	2.02	0.41
23:BC:97:GLU:HB3	23:BC:125:LEU:HD11	2.03	0.41
23:BC:158:PRO:O	23:BC:161:VAL:HB	2.20	0.41
35:OC:103:LYS:O	35:OC:104:ASP:HB2	2.20	0.41
37:QC:138:VAL:O	37:QC:142:MET:HB2	2.21	0.41
37:QC:191:THR:HB	37:QC:193:TYR:CE2	2.56	0.41
38:RC:101:LEU:HB2	38:RC:138:TYR:HB3	2.03	0.41
39:SC:127:ASN:HA	39:SC:128:PRO:HD2	1.93	0.41
42:VC:40:ALA:C	42:VC:42:GLU:H	2.29	0.41
45:YC:101:SER:OG	45:YC:103:LEU:HB2	2.21	0.41
52:FD:41:LYS:HE2	52:FD:41:LYS:HB3	1.82	0.41
1:A:1418:A:N6	1:A:1482:G:O2'	2.53	0.41
2:B:457:A:N6	2:B:470:A:H5''	2.36	0.41
2:B:1235:G:C2	2:B:1236:G:N2	2.89	0.41
2:B:2065:C:H2'	2:B:2066:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:48:A:H2'	3:C:49:C:C6	2.56	0.41
7:G:196:LEU:HA	7:G:196:LEU:HD23	1.83	0.41
10:J:72:LEU:HD21	10:J:107:ILE:CD1	2.51	0.41
13:M:59:LEU:HD21	32:FA:10:ALA:HA	2.03	0.41
13:M:93:GLY:N	13:M:123:LEU:HD22	2.35	0.41
13:M:95:VAL:O	13:M:126:VAL:HG23	2.21	0.41
19:S:2:PHE:CD1	19:S:2:PHE:C	2.98	0.41
35:JA:125:ALA:O	35:JA:158:GLY:HA3	2.21	0.41
35:JA:278:ILE:HG13	35:JA:279:HIS:N	2.35	0.41
40:OA:100:ASN:OD1	52:AB:23:LYS:HG2	2.21	0.41
51:ZA:90:ILE:O	51:ZA:93:GLN:HG2	2.22	0.41
1:FB:186(A):C:H2'	1:FB:186(B):C:C6	2.56	0.41
1:FB:332:G:OP2	54:HD:10:LEU:HG	2.21	0.41
1:FB:949:A:H1'	1:FB:1364:U:N3	2.36	0.41
1:FB:954:G:H2'	1:FB:955:U:C6	2.56	0.41
2:GB:794:G:H2'	2:GB:795:C:C6	2.56	0.41
2:GB:1239:G:H2'	2:GB:1240:U:O4'	2.21	0.41
2:GB:1814:G:C4'	5:JB:51:VAL:HG21	2.51	0.41
12:QB:68:GLU:HB3	12:QB:78:ARG:NH1	2.36	0.41
25:DC:65:SER:OG	25:DC:66:HIS:ND1	2.41	0.41
35:OC:138:TYR:CZ	35:OC:142:ARG:HD2	2.56	0.41
36:PC:134:GLU:OE2	36:PC:134:GLU:HA	2.21	0.41
37:QC:126:ARG:C	37:QC:127:ARG:HG2	2.46	0.41
38:RC:60:GLU:HG3	38:RC:198:VAL:HG23	2.03	0.41
42:VC:19:VAL:HG23	42:VC:21:LYS:HG2	2.03	0.41
45:YC:32:ILE:HD12	45:YC:72:ALA:HB2	2.02	0.41
47:AD:84:ILE:HB	53:GD:74:PHE:HE1	1.86	0.41
50:DD:52:ASP:OD2	50:DD:55:ARG:HG2	2.20	0.41
52:FD:53:ARG:C	52:FD:55:ARG:H	2.29	0.41
1:A:174:C:H2'	1:A:175:C:H6	1.85	0.40
1:A:411:A:H2'	1:A:412:A:H4'	2.03	0.40
1:A:433:C:H2'	1:A:434:U:H6	1.86	0.40
1:A:778:G:H2'	1:A:779:C:O4'	2.21	0.40
1:A:875:C:O2'	42:QA:14:ARG:NH1	2.49	0.40
1:A:1134:G:OP2	1:A:1134:G:H8	2.04	0.40
1:A:1262:C:H42	1:A:1273:G:H1	1.69	0.40
2:B:1490:A:H4'	2:B:1491:G:OP2	2.21	0.40
2:B:2319:G:H3'	2:B:2319:G:OP1	2.21	0.40
2:B:2516:G:C6	2:B:2517:C:C4	3.09	0.40
2:B:2667:C:H1'	9:I:109:PHE:CD1	2.55	0.40
6:F:37:ARG:HA	6:F:42:ASP:OD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:185:ASP:OD1	7:G:188:ARG:NH1	2.55	0.40
12:L:111:PHE:O	12:L:115:VAL:HG23	2.20	0.40
12:L:118:ALA:HA	12:L:119:PRO:HD3	1.80	0.40
14:N:38:GLU:HG3	14:N:127:ILE:HB	2.02	0.40
21:U:47:PHE:O	21:U:49:VAL:HG13	2.21	0.40
33:GA:27:CYS:HB3	33:GA:32:HIS:HB2	2.03	0.40
4:IA:21:A:HO2'	4:IA:22:G:H8	1.67	0.40
35:JA:354:ALA:HA	35:JA:358:GLU:HB3	2.03	0.40
36:KA:47:THR:O	36:KA:51:LEU:N	2.53	0.40
38:MA:155:LEU:HD13	38:MA:157:LEU:H	1.86	0.40
38:MA:190:ASP:O	38:MA:193:ASP:HB2	2.21	0.40
42:QA:86:ILE:HG12	42:QA:135:CYS:HA	2.03	0.40
43:RA:40:LEU:HB2	43:RA:43:ALA:HB2	2.03	0.40
1:FB:792:A:H4'	1:FB:793:U:O5'	2.21	0.40
2:GB:191:A:H2'	2:GB:192:C:C6	2.57	0.40
2:GB:262:A:H2'	2:GB:263:C:O4'	2.21	0.40
2:GB:1035:U:H2'	2:GB:1036:G:C8	2.55	0.40
2:GB:1849:G:H2'	2:GB:1850:G:H8	1.86	0.40
2:GB:2001:A:H4'	2:GB:2689:U:O2'	2.21	0.40
2:GB:2783:G:H2'	2:GB:2784:C:C6	2.55	0.40
5:JB:273:ARG:HB3	5:JB:273:ARG:NH1	2.36	0.40
10:OB:57:ARG:HA	10:OB:60:GLU:HB3	2.03	0.40
10:OB:72:LEU:HD21	10:OB:107:ILE:CD1	2.52	0.40
13:RB:100:LEU:HD23	13:RB:100:LEU:HA	1.86	0.40
15:TB:74:LYS:HE2	15:TB:74:LYS:HB2	1.91	0.40
37:QC:88:ARG:HD3	37:QC:101:LEU:HB3	2.03	0.40
38:RC:121:VAL:O	38:RC:134:ASP:HA	2.21	0.40
1:A:110:C:H2'	1:A:111:G:O4'	2.21	0.40
1:A:394:G:H2'	1:A:395:C:C6	2.56	0.40
1:A:1307:U:H2'	1:A:1308:U:O4'	2.21	0.40
1:A:1422:G:H2'	1:A:1423:G:C8	2.56	0.40
2:B:92:G:H2'	2:B:93:C:C6	2.56	0.40
2:B:270(Q):C:H2'	2:B:270(R):C:H6	1.85	0.40
2:B:674:G:H1'	7:G:74:ARG:HD3	2.03	0.40
2:B:1693:U:OP2	2:B:1694:C:H5	2.05	0.40
2:B:1782:C:O2	2:B:2608:G:O2'	2.37	0.40
2:B:1923:U:H2'	2:B:1924:C:H6	1.86	0.40
2:B:2047:U:O2'	2:B:2823:A:N1	2.48	0.40
2:B:2162:G:H1'	2:B:2173:A:H1'	2.02	0.40
2:B:2262:U:H4'	2:B:2328:A:C2	2.56	0.40
2:B:2377:A:H2'	2:B:2378:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2451:A:H5'	24:X:3:HIS:HE2	1.86	0.40
2:B:2881:C:H2'	2:B:2882:A:O4'	2.21	0.40
4:D:58:A:N6	4:D:61:C:C2	2.90	0.40
9:I:3:ARG:HA	9:I:3:ARG:HH11	1.84	0.40
9:I:163:TYR:CE1	9:I:169:VAL:HG13	2.56	0.40
16:P:28:VAL:HG11	16:P:98:VAL:HG13	2.04	0.40
31:EA:35:ARG:HG3	31:EA:42:LEU:HD21	2.04	0.40
36:KA:127:ILE:HG23	36:KA:135:GLN:HB2	2.02	0.40
45:TA:48:ILE:HD12	45:TA:48:ILE:HA	1.71	0.40
51:ZA:12:SER:HA	51:ZA:14:LYS:HZ2	1.86	0.40
1:FB:432:A:H2'	1:FB:433:C:O4'	2.21	0.40
1:FB:1240:U:C2	41:UC:32:ARG:HD2	2.56	0.40
1:FB:1285:A:H4'	1:FB:1286:A:O5'	2.22	0.40
1:FB:1519:MA6:H5''	1:FB:1520:G:OP2	2.22	0.40
2:GB:91:A:C4	2:GB:92:G:C8	3.09	0.40
2:GB:221:A:N6	2:GB:265:A:H8	2.19	0.40
2:GB:242:G:H5''	32:KC:64:TYR:CE2	2.56	0.40
2:GB:320:A:H4'	2:GB:322:A:C8	2.56	0.40
2:GB:895:U:H5'	2:GB:896:A:OP1	2.21	0.40
2:GB:2257:U:O2'	2:GB:2258:C:H5'	2.21	0.40
2:GB:2336:A:H3'	2:GB:2337:G:H8	1.86	0.40
2:GB:2477:C:O2	33:LC:4:ARG:NH2	2.39	0.40
5:JB:62:TYR:HA	5:JB:87:ASN:HD21	1.84	0.40
5:JB:246:PRO:C	5:JB:254:THR:HG22	2.46	0.40
6:KB:8:LYS:NZ	6:KB:188:VAL:O	2.47	0.40
7:LB:29:ASN:HA	7:LB:30:PRO:HD2	1.99	0.40
8:MB:36:LYS:HD3	8:MB:95:ARG:NH1	2.36	0.40
9:NB:155:SER:HB3	9:NB:158:HIS:O	2.20	0.40
10:OB:4:ILE:HA	10:OB:17:GLN:O	2.22	0.40
12:QB:75:SER:HB2	17:VB:74:ARG:NH1	2.34	0.40
13:RB:83:VAL:CG1	13:RB:112:LEU:HD21	2.50	0.40
18:WB:85:LYS:HB3	18:WB:85:LYS:HE3	1.92	0.40
23:BC:91:LEU:HD12	23:BC:96:VAL:HG11	2.02	0.40
36:PC:20:GLU:O	36:PC:39:ILE:HG22	2.21	0.40
37:QC:58:GLU:O	37:QC:65:ALA:N	2.53	0.40
41:UC:114:ARG:H	41:UC:114:ARG:HG2	1.63	0.40
43:WC:46:ALA:HB2	43:WC:74:ILE:HG23	2.01	0.40
45:YC:59:TYR:CZ	45:YC:63:LEU:HD11	2.56	0.40
46:ZC:32:PHE:CD1	46:ZC:86:ARG:HB3	2.56	0.40
51:ED:84:LEU:O	51:ED:87:LYS:HG3	2.21	0.40
1:A:931:C:H42	1:A:1386:G:H1	1.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:973:G:H3'	1:A:974:A:H5''	2.03	0.40
1:A:1191:A:OP1	37:LA:4:LYS:HG3	2.21	0.40
2:B:592:G:H4'	32:FA:3:LYS:HB2	2.03	0.40
2:B:784:A:C6	5:E:229:VAL:HG21	2.56	0.40
2:B:1575:C:H2'	2:B:1576:U:O4'	2.20	0.40
2:B:2321:G:H5'	2:B:2322:A:OP2	2.21	0.40
2:B:2471:C:N4	2:B:2476:A:O2'	2.53	0.40
2:B:2582:G:H2'	2:B:2582:G:N3	2.37	0.40
3:C:78:A:H2'	3:C:79:C:O4'	2.21	0.40
5:E:70:TRP:CH2	5:E:150:LYS:HG3	2.55	0.40
6:F:181:LEU:HD21	17:Q:6:LEU:HD12	2.03	0.40
10:J:80:PRO:HA	10:J:145:VAL:HG23	2.02	0.40
17:Q:55:ASN:H	17:Q:59:THR:HB	1.86	0.40
18:R:8:VAL:HG22	18:R:12:ARG:HG3	2.04	0.40
19:S:24:LYS:HA	19:S:92:THR:OG1	2.21	0.40
23:W:162:GLU:O	23:W:164:ALA:N	2.54	0.40
27:AA:59:VAL:HB	27:AA:60:GLU:H	1.66	0.40
30:DA:47:THR:HG22	30:DA:48:VAL:O	2.20	0.40
35:JA:351:ASP:O	35:JA:355:ALA:HB2	2.21	0.40
41:PA:79:ARG:HD2	41:PA:80:VAL:H	1.86	0.40
42:QA:120:THR:HG23	42:QA:123:GLU:CD	2.47	0.40
44:SA:77:PRO:HB2	44:SA:78:ASN:H	1.71	0.40
45:TA:66:LEU:HD22	45:TA:66:LEU:HA	1.80	0.40
47:VA:19:LEU:HD13	47:VA:19:LEU:HA	1.80	0.40
47:VA:45:VAL:O	47:VA:48:LEU:HB2	2.20	0.40
51:ZA:84:LEU:HD23	51:ZA:84:LEU:HA	1.87	0.40
54:CB:88:VAL:O	54:CB:92:LEU:HB2	2.20	0.40
1:FB:690:G:H2'	1:FB:691:G:O4'	2.21	0.40
1:FB:826:C:H5'	42:VC:12:ARG:NH2	2.36	0.40
1:FB:926:G:C6	1:FB:1505:G:C6	3.09	0.40
1:FB:1031:G:C8	1:FB:1032(B):G:N1	2.89	0.40
2:GB:265:A:H1'	2:GB:266:G:O4'	2.21	0.40
2:GB:725:G:C6	2:GB:726:G:N1	2.90	0.40
2:GB:2323:G:H2'	2:GB:2324:C:O4'	2.21	0.40
3:HB:3:C:C2	3:HB:118:G:C2	3.09	0.40
3:HB:73:A:C6	3:HB:74:U:C2	3.10	0.40
13:RB:1:MET:HE2	13:RB:1:MET:HB2	1.92	0.40
20:YB:78:GLU:CD	20:YB:99:ARG:HH11	2.29	0.40
23:BC:62:PRO:C	23:BC:64:GLY:H	2.28	0.40
36:PC:215:LEU:O	36:PC:219:VAL:HG23	2.21	0.40
42:VC:120:THR:HG23	42:VC:123:GLU:OE2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:WC:11:LYS:C	43:WC:13:ALA:H	2.26	0.40
54:HD:64:ASP:OD2	54:HD:81:LYS:HD3	2.20	0.40
1:A:9:G:H2'	1:A:10:A:C8	2.56	0.40
1:A:292:G:N7	1:A:293:G:H1'	2.36	0.40
1:A:338:A:C6	1:A:339:C:C4	3.10	0.40
1:A:438:G:H4'	38:MA:123:HIS:CD2	2.57	0.40
1:A:560:U:H5'	1:A:566:G:N2	2.36	0.40
1:A:988:G:C2	1:A:989:C:H1'	2.56	0.40
2:B:1400:G:H2'	2:B:1401:G:C8	2.56	0.40
2:B:1448:G:H5''	2:B:1543:A:OP2	2.22	0.40
2:B:2723:C:OP2	6:F:109:LYS:NZ	2.55	0.40
5:E:227:ASN:HB3	5:E:228:PRO:HD2	2.03	0.40
9:I:46:GLU:OE1	9:I:51:ARG:NE	2.53	0.40
10:J:88:ILE:HD12	10:J:89:TYR:N	2.36	0.40
14:N:112:GLU:HG2	14:N:113:GLN:N	2.37	0.40
16:P:66:ALA:O	16:P:69:VAL:HG13	2.22	0.40
17:Q:9:LEU:O	17:Q:12:SER:OG	2.33	0.40
23:W:52:SER:OG	23:W:53:ILE:N	2.53	0.40
26:Z:39:ALA:HA	26:Z:44:LEU:HB3	2.03	0.40
4:IA:24:U:H2'	4:IA:25:C:O4'	2.22	0.40
37:LA:108:ASN:HB3	37:LA:111:LEU:HD12	2.04	0.40
44:SA:23:ILE:HD12	44:SA:23:ILE:HA	1.79	0.40
53:BB:36:ARG:HB2	53:BB:72:GLY:HA3	2.04	0.40
1:FB:841:U:O2'	1:FB:842:C:OP1	2.35	0.40
1:FB:843:U:C5	1:FB:848:C:H1'	2.55	0.40
1:FB:1128:C:H4'	1:FB:1148:U:O2	2.21	0.40
2:GB:101:G:H4'	2:GB:102:G:OP2	2.21	0.40
2:GB:273(G):C:H2'	2:GB:274:G:O4'	2.21	0.40
2:GB:352:G:H4'	2:GB:353:G:OP2	2.21	0.40
2:GB:613:U:H2'	2:GB:614:U:O4'	2.21	0.40
2:GB:715:G:H2'	2:GB:716:A:C8	2.57	0.40
2:GB:830:G:H4'	2:GB:831:G:OP2	2.22	0.40
2:GB:1655:A:H1'	6:KB:113:PHE:CD2	2.57	0.40
2:GB:2773:C:H2'	2:GB:2774:C:H6	1.87	0.40
2:GB:2820:A:OP2	15:TB:2:ARG:NH2	2.54	0.40
3:HB:48:A:H2'	3:HB:49:C:C6	2.57	0.40
8:MB:126:ASP:HB2	8:MB:130:ASN:O	2.22	0.40
11:PB:67:LEU:HD13	11:PB:67:LEU:HA	1.90	0.40
16:UB:105:ALA:O	16:UB:110:LEU:HB2	2.21	0.40
22:AC:51:VAL:HA	22:AC:55:TYR:O	2.21	0.40
22:AC:76:CYS:HA	22:AC:77:PRO:HD2	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:FC:26:LEU:HD23	27:FC:26:LEU:HA	1.93	0.40
27:FC:59:VAL:O	27:FC:60:GLU:HB3	2.21	0.40
35:OC:227:PHE:HA	35:OC:241:ASP:OD2	2.22	0.40
37:QC:28:GLN:HA	37:QC:31:HIS:CE1	2.56	0.40
37:QC:139:GLN:HG3	37:QC:140:ARG:HH12	1.86	0.40
47:AD:60:VAL:HG13	47:AD:64:TRP:CE3	2.57	0.40
50:DD:6:LEU:HG	50:DD:17:TYR:HB3	2.03	0.40
50:DD:49:LEU:HD12	50:DD:50:LYS:H	1.86	0.40
1:A:191(E):G:H2'	1:A:191(F):U:C6	2.57	0.40
1:A:767:A:H2'	1:A:768:A:O4'	2.22	0.40
1:A:975:A:H8	1:A:975:A:H5'	1.85	0.40
1:A:1128:C:C5'	43:RA:66:ARG:HH12	2.35	0.40
1:A:1308:U:H3'	47:VA:99:ARG:NH1	2.36	0.40
2:B:17:G:H2'	2:B:18:C:H6	1.85	0.40
2:B:1357:U:H2'	2:B:1358:G:O4'	2.21	0.40
2:B:2893:G:O5'	2:B:2893:G:H8	2.05	0.40
7:G:60:SER:OG	7:G:61:GLY:N	2.54	0.40
15:O:59:ASP:OD2	15:O:61:HIS:HB3	2.21	0.40
17:Q:56:GLY:O	17:Q:59:THR:HG22	2.22	0.40
20:T:12:ILE:HD13	20:T:17:VAL:HG22	2.03	0.40
20:T:69:LEU:HA	20:T:69:LEU:HD23	1.83	0.40
23:W:136:PHE:O	23:W:137:ILE:HD13	2.21	0.40
24:X:7:LEU:O	4:IA:1:C:O2'	2.39	0.40
26:Z:56:GLN:HA	26:Z:59:ARG:NH1	2.37	0.40
35:JA:146:VAL:HG23	35:JA:164:ALA:HB1	2.03	0.40
36:KA:106:LYS:HE2	36:KA:106:LYS:HB3	1.93	0.40
38:MA:76:ARG:HA	38:MA:76:ARG:HD2	1.83	0.40
42:QA:86:ILE:HG13	42:QA:133:LEU:HD22	2.04	0.40
1:FB:297:G:N2	1:FB:300:A:OP2	2.44	0.40
1:FB:583:A:H61	1:FB:758:G:H1'	1.87	0.40
1:FB:1128:C:C5'	43:WC:66:ARG:HH12	2.35	0.40
1:FB:1410:G:C2	1:FB:1491:G:C2	3.09	0.40
2:GB:189:G:OP2	25:DC:14:VAL:HG21	2.22	0.40
2:GB:547:A:N7	2:GB:548:A:C6	2.90	0.40
2:GB:609(B):G:H2'	2:GB:610:C:C6	2.56	0.40
2:GB:879:G:N2	2:GB:899:A:H1'	2.36	0.40
2:GB:1817:G:OP1	5:JB:88:ARG:NH2	2.47	0.40
2:GB:2101:G:C5	2:GB:2102:U:C4	3.09	0.40
2:GB:2109:U:H5'	2:GB:2149:G:H21	1.87	0.40
2:GB:2152:G:H3'	2:GB:2153:G:H8	1.87	0.40
2:GB:2584:U:H2'	2:GB:2585:U:H2'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GB:2627:G:N2	2:GB:2777:G:OP2	2.55	0.40
3:HB:75:G:H22	23:BC:73:GLN:HE21	1.70	0.40
11:PB:35:ARG:NH1	11:PB:35:ARG:HG2	2.37	0.40
16:UB:41:ASP:OD2	16:UB:44:LYS:HG3	2.21	0.40
23:BC:44:PHE:CE1	23:BC:86:VAL:HG11	2.56	0.40
26:EC:29:LYS:HG2	26:EC:57:ILE:HD13	2.04	0.40
39:SC:144:THR:O	39:SC:148:VAL:HG23	2.22	0.40
44:XC:55:LYS:HB3	44:XC:56:HIS:H	1.74	0.40
47:AD:11:ARG:C	47:AD:13:LYS:H	2.29	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	
5	E	273/275 (99%)	252 (92%)	20 (7%)	1 (0%)	30	61
5	JB	273/275 (99%)	250 (92%)	22 (8%)	1 (0%)	30	61
6	F	202/206 (98%)	188 (93%)	12 (6%)	2 (1%)	12	41
6	KB	202/206 (98%)	189 (94%)	11 (5%)	2 (1%)	12	41
7	G	200/205 (98%)	184 (92%)	14 (7%)	2 (1%)	12	41
7	LB	200/205 (98%)	182 (91%)	16 (8%)	2 (1%)	12	41
8	H	179/182 (98%)	156 (87%)	19 (11%)	4 (2%)	5	24
8	MB	179/182 (98%)	157 (88%)	18 (10%)	4 (2%)	5	24
9	I	172/180 (96%)	155 (90%)	16 (9%)	1 (1%)	21	52
9	NB	172/180 (96%)	155 (90%)	16 (9%)	1 (1%)	21	52
10	J	144/148 (97%)	128 (89%)	12 (8%)	4 (3%)	4	20
10	OB	144/148 (97%)	128 (89%)	12 (8%)	4 (3%)	4	20
11	K	138/140 (99%)	129 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	PB	138/140 (99%)	128 (93%)	10 (7%)	0	100	100
12	L	120/122 (98%)	108 (90%)	10 (8%)	2 (2%)	7	30
12	QB	120/122 (98%)	109 (91%)	10 (8%)	1 (1%)	16	47
13	M	148/150 (99%)	134 (90%)	13 (9%)	1 (1%)	18	49
13	RB	148/150 (99%)	134 (90%)	13 (9%)	1 (1%)	18	49
14	N	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	18	49
14	SB	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	18	49
15	O	116/118 (98%)	109 (94%)	5 (4%)	2 (2%)	7	30
15	TB	116/118 (98%)	108 (93%)	6 (5%)	2 (2%)	7	30
16	P	108/112 (96%)	96 (89%)	10 (9%)	2 (2%)	6	27
16	UB	108/112 (96%)	96 (89%)	10 (9%)	2 (2%)	6	27
17	Q	135/146 (92%)	122 (90%)	10 (7%)	3 (2%)	5	24
17	VB	135/146 (92%)	122 (90%)	11 (8%)	2 (2%)	8	32
18	R	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
18	WB	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
19	S	99/101 (98%)	92 (93%)	5 (5%)	2 (2%)	6	25
19	XB	99/101 (98%)	92 (93%)	6 (6%)	1 (1%)	12	41
20	T	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
20	YB	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
21	U	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
21	ZB	93/96 (97%)	90 (97%)	3 (3%)	0	100	100
22	AC	105/110 (96%)	93 (89%)	12 (11%)	0	100	100
22	V	105/110 (96%)	95 (90%)	10 (10%)	0	100	100
23	BC	187/206 (91%)	167 (89%)	16 (9%)	4 (2%)	5	25
23	W	187/206 (91%)	167 (89%)	16 (9%)	4 (2%)	5	25
24	CC	82/85 (96%)	75 (92%)	4 (5%)	3 (4%)	2	15
24	X	82/85 (96%)	75 (92%)	4 (5%)	3 (4%)	2	15
25	DC	95/98 (97%)	88 (93%)	6 (6%)	1 (1%)	11	39
25	Y	95/98 (97%)	88 (93%)	5 (5%)	2 (2%)	5	25
26	EC	68/72 (94%)	65 (96%)	3 (4%)	0	100	100
26	Z	68/72 (94%)	65 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	AA	58/60 (97%)	54 (93%)	3 (5%)	1 (2%)	7	30
27	FC	58/60 (97%)	53 (91%)	4 (7%)	1 (2%)	7	30
28	BA	67/71 (94%)	45 (67%)	16 (24%)	6 (9%)	0	3
28	GC	67/71 (94%)	45 (67%)	16 (24%)	6 (9%)	0	3
29	CA	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
29	HC	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
30	DA	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
30	IC	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
31	EA	46/49 (94%)	46 (100%)	0	0	100	100
31	JC	46/49 (94%)	46 (100%)	0	0	100	100
32	FA	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
32	KC	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
33	GA	35/37 (95%)	32 (91%)	1 (3%)	2 (6%)	1	8
33	LC	35/37 (95%)	32 (91%)	2 (6%)	1 (3%)	3	19
35	JA	256/368 (70%)	215 (84%)	32 (12%)	9 (4%)	3	16
35	OC	256/368 (70%)	218 (85%)	28 (11%)	10 (4%)	2	14
36	KA	232/256 (91%)	191 (82%)	24 (10%)	17 (7%)	1	5
36	PC	232/256 (91%)	190 (82%)	25 (11%)	17 (7%)	1	5
37	LA	204/239 (85%)	181 (89%)	18 (9%)	5 (2%)	4	21
37	QC	204/239 (85%)	179 (88%)	20 (10%)	5 (2%)	4	21
38	MA	206/209 (99%)	184 (89%)	17 (8%)	5 (2%)	4	22
38	RC	206/209 (99%)	182 (88%)	19 (9%)	5 (2%)	4	22
39	NA	149/162 (92%)	132 (89%)	14 (9%)	3 (2%)	6	25
39	SC	149/162 (92%)	132 (89%)	14 (9%)	3 (2%)	6	25
40	OA	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
40	TC	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
41	PA	153/156 (98%)	139 (91%)	9 (6%)	5 (3%)	3	17
41	UC	153/156 (98%)	137 (90%)	11 (7%)	5 (3%)	3	17
42	QA	136/138 (99%)	126 (93%)	10 (7%)	0	100	100
42	VC	136/138 (99%)	124 (91%)	12 (9%)	0	100	100
43	RA	125/128 (98%)	109 (87%)	14 (11%)	2 (2%)	7	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	WC	125/128 (98%)	111 (89%)	13 (10%)	1 (1%)	16	47
44	SA	96/105 (91%)	81 (84%)	12 (12%)	3 (3%)	3	18
44	XC	96/105 (91%)	81 (84%)	12 (12%)	3 (3%)	3	18
45	TA	114/129 (88%)	103 (90%)	8 (7%)	3 (3%)	4	21
45	YC	114/129 (88%)	104 (91%)	7 (6%)	3 (3%)	4	21
46	UA	119/132 (90%)	104 (87%)	13 (11%)	2 (2%)	7	30
46	ZC	119/132 (90%)	105 (88%)	12 (10%)	2 (2%)	7	30
47	AD	115/126 (91%)	101 (88%)	13 (11%)	1 (1%)	14	44
47	VA	115/126 (91%)	100 (87%)	14 (12%)	1 (1%)	14	44
48	BD	58/61 (95%)	50 (86%)	6 (10%)	2 (3%)	3	16
48	WA	58/61 (95%)	50 (86%)	6 (10%)	2 (3%)	3	16
49	CD	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	10	37
49	XA	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	10	37
50	DD	81/88 (92%)	75 (93%)	6 (7%)	0	100	100
50	YA	81/88 (92%)	75 (93%)	6 (7%)	0	100	100
51	ED	97/105 (92%)	86 (89%)	9 (9%)	2 (2%)	5	25
51	ZA	97/105 (92%)	87 (90%)	8 (8%)	2 (2%)	5	25
52	AB	68/88 (77%)	60 (88%)	7 (10%)	1 (2%)	8	32
52	FD	68/88 (77%)	61 (90%)	5 (7%)	2 (3%)	3	19
53	BB	81/93 (87%)	70 (86%)	7 (9%)	4 (5%)	1	11
53	GD	81/93 (87%)	70 (86%)	7 (9%)	4 (5%)	1	11
54	CB	97/106 (92%)	83 (86%)	9 (9%)	5 (5%)	1	10
54	HD	97/106 (92%)	82 (84%)	10 (10%)	5 (5%)	1	10
55	DB	22/27 (82%)	17 (77%)	4 (18%)	1 (4%)	2	12
55	ID	22/27 (82%)	18 (82%)	3 (14%)	1 (4%)	2	12
All	All	11996/12852 (93%)	10786 (90%)	982 (8%)	228 (2%)	6	27

All (228) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	47	LYS
9	I	126	PRO
10	J	92	VAL

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Mol	Chain	Res	Type
14	N	60	ARG
15	O	2	ARG
24	X	4	LYS
25	Y	3	LYS
28	BA	45	GLY
28	BA	50	VAL
35	JA	104	ASP
36	KA	17	PHE
36	KA	36	ARG
36	KA	125	PRO
36	KA	128	GLU
38	MA	4	TYR
38	MA	5	ILE
44	SA	77	PRO
45	TA	91	ARG
54	CB	99	LEU
55	DB	3	LYS
8	MB	43	LEU
8	MB	47	LYS
9	NB	126	PRO
10	OB	89	TYR
10	OB	92	VAL
14	SB	60	ARG
15	TB	2	ARG
24	CC	4	LYS
25	DC	3	LYS
28	GC	45	GLY
28	GC	50	VAL
35	OC	104	ASP
36	PC	17	PHE
36	PC	36	ARG
36	PC	125	PRO
36	PC	128	GLU
38	RC	4	TYR
38	RC	5	ILE
44	XC	77	PRO
45	YC	91	ARG
54	HD	99	LEU
55	ID	3	LYS
6	F	58	ARG
8	H	43	LEU
10	J	88	ILE

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Mol	Chain	Res	Type
10	J	89	TYR
23	W	163	LEU
28	BA	47	GLN
35	JA	102	PRO
35	JA	159	TYR
35	JA	193	GLN
36	KA	22	LYS
36	KA	78	GLN
36	KA	124	SER
36	KA	126	GLU
36	KA	226	ARG
37	LA	26	LYS
37	LA	156	ARG
39	NA	65	ASN
41	PA	4	ARG
41	PA	17	VAL
46	UA	22	SER
46	UA	125	PRO
47	VA	100	GLY
48	WA	3	ARG
48	WA	14	PRO
6	KB	58	ARG
10	OB	88	ILE
23	BC	163	LEU
28	GC	47	GLN
35	OC	102	PRO
35	OC	159	TYR
35	OC	193	GLN
36	PC	22	LYS
36	PC	78	GLN
36	PC	124	SER
36	PC	204	ASN
36	PC	226	ARG
37	QC	26	LYS
37	QC	156	ARG
39	SC	65	ASN
41	UC	4	ARG
41	UC	17	VAL
46	ZC	125	PRO
47	AD	100	GLY
48	BD	3	ARG
48	BD	14	PRO

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Mol	Chain	Res	Type
6	F	52	LEU
7	G	21	ALA
7	G	22	ALA
10	J	85	GLU
13	M	103	ALA
15	O	71	GLN
17	Q	12	SER
17	Q	37	GLY
19	S	79	VAL
23	W	153	SER
28	BA	34	GLU
33	GA	11	CYS
35	JA	299	GLY
36	KA	204	ASN
36	KA	207	ALA
36	KA	237	ALA
39	NA	74	GLY
41	PA	54	THR
41	PA	85	TYR
43	RA	96	LEU
44	SA	33	GLN
44	SA	78	ASN
51	ZA	77	VAL
53	BB	81	ARG
54	CB	11	SER
6	KB	52	LEU
7	LB	22	ALA
10	OB	85	GLU
13	RB	103	ALA
15	TB	71	GLN
17	VB	12	SER
17	VB	37	GLY
23	BC	153	SER
28	GC	34	GLU
35	OC	218	ASN
35	OC	299	GLY
36	PC	23	ARG
36	PC	126	GLU
36	PC	237	ALA
37	QC	62	ASP
39	SC	6	PHE
39	SC	74	GLY

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Mol	Chain	Res	Type
41	UC	54	THR
41	UC	85	TYR
43	WC	96	LEU
44	XC	33	GLN
44	XC	78	ASN
46	ZC	22	SER
53	GD	81	ARG
16	P	60	GLY
23	W	157	LEU
35	JA	144	TRP
35	JA	218	ASN
36	KA	23	ARG
36	KA	26	PRO
36	KA	158	LEU
37	LA	3	ASN
37	LA	62	ASP
39	NA	6	PHE
52	AB	41	LYS
53	BB	45	VAL
54	CB	10	LEU
54	CB	47	GLY
54	CB	97	ALA
7	LB	21	ALA
12	QB	111	PHE
16	UB	60	GLY
19	XB	79	VAL
23	BC	157	LEU
33	LC	11	CYS
35	OC	144	TRP
36	PC	158	LEU
36	PC	207	ALA
37	QC	3	ASN
51	ED	77	VAL
54	HD	11	SER
54	HD	97	ALA
8	H	52	ILE
8	H	124	SER
12	L	5	GLN
16	P	61	ASN
19	S	53	GLU
28	BA	53	GLU
33	GA	12	ASP

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Mol	Chain	Res	Type
35	JA	143	ARG
35	JA	215	PRO
38	MA	22	LYS
38	MA	23	GLY
43	RA	12	GLU
45	TA	90	GLY
49	XA	14	GLU
51	ZA	31	LEU
8	MB	52	ILE
8	MB	124	SER
16	UB	61	ASN
23	BC	135	GLU
24	CC	13	GLY
28	GC	53	GLU
35	OC	143	ARG
35	OC	215	PRO
36	PC	26	PRO
38	RC	22	LYS
45	YC	90	GLY
51	ED	31	LEU
52	FD	41	LYS
52	FD	59	SER
53	GD	27	GLU
53	GD	45	VAL
54	HD	10	LEU
54	HD	47	GLY
23	W	135	GLU
24	X	13	GLY
36	KA	239	VAL
41	PA	80	VAL
45	TA	105	VAL
53	BB	27	GLU
35	OC	355	ALA
36	PC	239	VAL
38	RC	23	GLY
41	UC	80	VAL
45	YC	105	VAL
49	CD	88	ARG
5	E	236	GLY
12	L	27	GLY
24	X	6	GLY
28	BA	5	ILE

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Mol	Chain	Res	Type
36	KA	15	VAL
38	MA	197	PRO
36	PC	15	VAL
27	AA	59	VAL
37	LA	25	GLY
5	JB	236	GLY
27	FC	59	VAL
28	GC	5	ILE
53	BB	67	VAL
24	CC	6	GLY
37	QC	25	GLY
38	RC	197	PRO
53	GD	67	VAL
17	Q	135	VAL
25	Y	55	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	
5	E	217/217 (100%)	189 (87%)	28 (13%)	4	18
5	JB	217/217 (100%)	189 (87%)	28 (13%)	4	18
6	F	165/166 (99%)	145 (88%)	20 (12%)	5	20
6	KB	165/166 (99%)	146 (88%)	19 (12%)	5	23
7	G	161/162 (99%)	131 (81%)	30 (19%)	1	8
7	LB	161/162 (99%)	130 (81%)	31 (19%)	1	7
8	H	154/156 (99%)	129 (84%)	25 (16%)	2	11
8	MB	154/156 (99%)	129 (84%)	25 (16%)	2	11
9	I	144/148 (97%)	119 (83%)	25 (17%)	2	9
9	NB	144/148 (97%)	119 (83%)	25 (17%)	2	9
10	J	122/124 (98%)	89 (73%)	33 (27%)	0	2
10	OB	122/124 (98%)	91 (75%)	31 (25%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K	119/119 (100%)	101 (85%)	18 (15%)	3	13
11	PB	119/119 (100%)	103 (87%)	16 (13%)	4	17
12	L	100/100 (100%)	87 (87%)	13 (13%)	4	18
12	QB	100/100 (100%)	88 (88%)	12 (12%)	5	21
13	M	116/116 (100%)	101 (87%)	15 (13%)	4	18
13	RB	116/116 (100%)	100 (86%)	16 (14%)	3	15
14	N	111/111 (100%)	100 (90%)	11 (10%)	7	29
14	SB	111/111 (100%)	101 (91%)	10 (9%)	9	33
15	O	101/101 (100%)	88 (87%)	13 (13%)	4	18
15	TB	101/101 (100%)	86 (85%)	15 (15%)	3	13
16	P	87/88 (99%)	72 (83%)	15 (17%)	2	10
16	UB	87/88 (99%)	72 (83%)	15 (17%)	2	10
17	Q	121/128 (94%)	110 (91%)	11 (9%)	9	32
17	VB	121/128 (94%)	110 (91%)	11 (9%)	9	32
18	R	93/94 (99%)	81 (87%)	12 (13%)	4	18
18	WB	93/94 (99%)	81 (87%)	12 (13%)	4	18
19	S	82/82 (100%)	67 (82%)	15 (18%)	2	8
19	XB	82/82 (100%)	67 (82%)	15 (18%)	2	8
20	T	91/92 (99%)	81 (89%)	10 (11%)	6	24
20	YB	91/92 (99%)	81 (89%)	10 (11%)	6	24
21	U	77/78 (99%)	66 (86%)	11 (14%)	3	14
21	ZB	77/78 (99%)	66 (86%)	11 (14%)	3	14
22	AC	87/91 (96%)	76 (87%)	11 (13%)	4	19
22	V	87/91 (96%)	77 (88%)	10 (12%)	5	23
23	BC	163/179 (91%)	143 (88%)	20 (12%)	4	20
23	W	163/179 (91%)	143 (88%)	20 (12%)	4	20
24	CC	66/67 (98%)	59 (89%)	7 (11%)	6	26
24	X	66/67 (98%)	60 (91%)	6 (9%)	9	32
25	DC	81/83 (98%)	72 (89%)	9 (11%)	6	24
25	Y	81/83 (98%)	73 (90%)	8 (10%)	7	29
26	EC	66/67 (98%)	59 (89%)	7 (11%)	6	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	Z	66/67 (98%)	59 (89%)	7 (11%)	6	26
27	AA	52/52 (100%)	46 (88%)	6 (12%)	5	23
27	FC	52/52 (100%)	47 (90%)	5 (10%)	8	30
28	BA	59/63 (94%)	52 (88%)	7 (12%)	5	21
28	GC	59/63 (94%)	52 (88%)	7 (12%)	5	21
29	CA	51/52 (98%)	45 (88%)	6 (12%)	5	21
29	HC	51/52 (98%)	45 (88%)	6 (12%)	5	21
30	DA	51/52 (98%)	41 (80%)	10 (20%)	1	6
30	IC	51/52 (98%)	41 (80%)	10 (20%)	1	6
31	EA	41/42 (98%)	37 (90%)	4 (10%)	7	29
31	JC	41/42 (98%)	38 (93%)	3 (7%)	13	40
32	FA	54/55 (98%)	51 (94%)	3 (6%)	19	49
32	KC	54/55 (98%)	50 (93%)	4 (7%)	13	40
33	GA	34/34 (100%)	33 (97%)	1 (3%)	37	66
33	LC	34/34 (100%)	33 (97%)	1 (3%)	37	66
35	JA	209/308 (68%)	175 (84%)	34 (16%)	2	11
35	OC	209/308 (68%)	176 (84%)	33 (16%)	2	12
36	KA	202/220 (92%)	172 (85%)	30 (15%)	3	13
36	PC	202/220 (92%)	173 (86%)	29 (14%)	3	14
37	LA	160/188 (85%)	141 (88%)	19 (12%)	5	21
37	QC	160/188 (85%)	142 (89%)	18 (11%)	5	23
38	MA	180/181 (99%)	149 (83%)	31 (17%)	2	10
38	RC	180/181 (99%)	150 (83%)	30 (17%)	2	10
39	NA	116/123 (94%)	98 (84%)	18 (16%)	2	12
39	SC	116/123 (94%)	96 (83%)	20 (17%)	2	10
40	OA	90/90 (100%)	77 (86%)	13 (14%)	3	14
40	TC	90/90 (100%)	77 (86%)	13 (14%)	3	14
41	PA	126/127 (99%)	115 (91%)	11 (9%)	9	34
41	UC	126/127 (99%)	115 (91%)	11 (9%)	9	34
42	QA	119/119 (100%)	103 (87%)	16 (13%)	4	17
42	VC	119/119 (100%)	102 (86%)	17 (14%)	3	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	RA	98/99 (99%)	82 (84%)	16 (16%)	2	11
43	WC	98/99 (99%)	83 (85%)	15 (15%)	3	12
44	SA	88/92 (96%)	82 (93%)	6 (7%)	14	42
44	XC	88/92 (96%)	82 (93%)	6 (7%)	14	42
45	TA	88/99 (89%)	77 (88%)	11 (12%)	4	19
45	YC	88/99 (89%)	76 (86%)	12 (14%)	3	16
46	UA	102/108 (94%)	91 (89%)	11 (11%)	6	25
46	ZC	102/108 (94%)	91 (89%)	11 (11%)	6	25
47	AD	94/101 (93%)	77 (82%)	17 (18%)	2	8
47	VA	94/101 (93%)	78 (83%)	16 (17%)	2	10
48	BD	49/50 (98%)	41 (84%)	8 (16%)	2	11
48	WA	49/50 (98%)	40 (82%)	9 (18%)	1	8
49	CD	79/80 (99%)	73 (92%)	6 (8%)	12	39
49	XA	79/80 (99%)	73 (92%)	6 (8%)	12	39
50	DD	72/74 (97%)	61 (85%)	11 (15%)	3	12
50	YA	72/74 (97%)	60 (83%)	12 (17%)	2	10
51	ED	94/97 (97%)	84 (89%)	10 (11%)	6	26
51	ZA	94/97 (97%)	84 (89%)	10 (11%)	6	26
52	AB	61/77 (79%)	56 (92%)	5 (8%)	10	36
52	FD	61/77 (79%)	57 (93%)	4 (7%)	15	43
53	BB	72/80 (90%)	63 (88%)	9 (12%)	4	19
53	GD	72/80 (90%)	63 (88%)	9 (12%)	4	19
54	CB	76/82 (93%)	68 (90%)	8 (10%)	6	26
54	HD	76/82 (93%)	68 (90%)	8 (10%)	6	26
55	DB	19/22 (86%)	18 (95%)	1 (5%)	20	51
55	ID	19/22 (86%)	18 (95%)	1 (5%)	20	51
All	All	10120/10672 (95%)	8754 (86%)	1366 (14%)	4	16

All (1366) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	3	VAL
5	E	7	LYS

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Mol	Chain	Res	Type
5	E	28	GLU
5	E	39	LYS
5	E	61	LEU
5	E	71	ASP
5	E	89	SER
5	E	91	ARG
5	E	94	LEU
5	E	98	VAL
5	E	99	ASP
5	E	105	ILE
5	E	127	VAL
5	E	140	THR
5	E	154	LYS
5	E	171	ASP
5	E	193	VAL
5	E	200	ASP
5	E	221	VAL
5	E	229	VAL
5	E	237	GLU
5	E	242	ARG
5	E	259	THR
5	E	260	ARG
5	E	270	ILE
5	E	273	ARG
5	E	274	ARG
5	E	275	LYS
6	F	9	VAL
6	F	13	ARG
6	F	21	VAL
6	F	24	THR
6	F	75	VAL
6	F	78	LEU
6	F	92	THR
6	F	93	VAL
6	F	116	VAL
6	F	119	ARG
6	F	128	SER
6	F	154	LYS
6	F	170	LEU
6	F	173	VAL
6	F	175	VAL
6	F	178	GLU

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Mol	Chain	Res	Type
6	F	181	LEU
6	F	182	LEU
6	F	185	LYS
6	F	192	ASN
7	G	6	MET
7	G	12	LEU
7	G	15	SER
7	G	18	ARG
7	G	24	LEU
7	G	37	VAL
7	G	53	THR
7	G	57	VAL
7	G	62	ARG
7	G	64	ILE
7	G	70	THR
7	G	74	ARG
7	G	93	LYS
7	G	110	LEU
7	G	119	ARG
7	G	126	VAL
7	G	129	PHE
7	G	140	LEU
7	G	158	THR
7	G	170	LEU
7	G	175	THR
7	G	183	VAL
7	G	188	ARG
7	G	190	GLU
7	G	191	ARG
7	G	192	LEU
7	G	197	ASP
7	G	200	GLU
7	G	204	ASN
7	G	205	ARG
8	H	3	LEU
8	H	7	LEU
8	H	22	ARG
8	H	28	VAL
8	H	33	ARG
8	H	38	VAL
8	H	43	LEU
8	H	49	ASP

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Mol	Chain	Res	Type
8	H	53	LEU
8	H	60	LEU
8	H	62	LEU
8	H	67	LYS
8	H	70	VAL
8	H	74	LYS
8	H	82	LEU
8	H	98	ARG
8	H	105	LYS
8	H	114	ILE
8	H	115	ARG
8	H	118	ARG
8	H	135	LEU
8	H	136	ARG
8	H	140	ILE
8	H	143	GLU
8	H	167	GLU
9	I	3	ARG
9	I	7	LEU
9	I	16	SER
9	I	17	VAL
9	I	24	VAL
9	I	30	LYS
9	I	33	LEU
9	I	37	VAL
9	I	43	VAL
9	I	44	VAL
9	I	46	GLU
9	I	47	GLU
9	I	49	VAL
9	I	57	ASP
9	I	71	LEU
9	I	84	SER
9	I	97	ARG
9	I	99	VAL
9	I	104	GLU
9	I	106	THR
9	I	115	VAL
9	I	127	GLU
9	I	136	ILE
9	I	141	VAL
9	I	169	VAL

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Mol	Chain	Res	Type
10	J	4	ILE
10	J	9	LEU
10	J	18	VAL
10	J	19	VAL
10	J	21	VAL
10	J	31	LEU
10	J	37	VAL
10	J	43	ASN
10	J	44	LEU
10	J	57	ARG
10	J	74	ASN
10	J	77	LEU
10	J	86	THR
10	J	88	ILE
10	J	89	TYR
10	J	92	VAL
10	J	99	GLU
10	J	107	ILE
10	J	108	THR
10	J	109	ILE
10	J	112	LYS
10	J	113	ARG
10	J	118	LYS
10	J	122	GLU
10	J	123	LEU
10	J	125	GLU
10	J	127	VAL
10	J	129	THR
10	J	131	LYS
10	J	136	VAL
10	J	140	LEU
10	J	144	VAL
10	J	145	VAL
11	K	9	VAL
11	K	14	VAL
11	K	15	LEU
11	K	19	GLU
11	K	28	THR
11	K	34	LEU
11	K	48	MET
11	K	67	LEU
11	K	68	GLU

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Mol	Chain	Res	Type
11	K	76	SER
11	K	83	LYS
11	K	84	LYS
11	K	87	LEU
11	K	93	THR
11	K	96	GLU
11	K	99	LEU
11	K	112	LEU
11	K	138	LEU
12	L	10	VAL
12	L	20	MET
12	L	24	VAL
12	L	32	TYR
12	L	45	GLU
12	L	53	LYS
12	L	61	VAL
12	L	66	LYS
12	L	69	VAL
12	L	70	LYS
12	L	78	ARG
12	L	98	VAL
12	L	116	SER
13	M	3	LEU
13	M	29	LYS
13	M	42	SER
13	M	58	THR
13	M	68	GLN
13	M	71	VAL
13	M	75	ILE
13	M	90	ARG
13	M	112	LEU
13	M	117	GLU
13	M	126	VAL
13	M	132	LYS
13	M	135	LEU
13	M	147	LEU
13	M	149	GLU
14	N	31	ASP
14	N	38	GLU
14	N	59	ARG
14	N	75	THR
14	N	76	LYS

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Mol	Chain	Res	Type
14	N	79	LEU
14	N	81	VAL
14	N	98	LYS
14	N	106	VAL
14	N	109	VAL
14	N	141	GLN
15	O	15	SER
15	O	18	LEU
15	O	28	LEU
15	O	29	LEU
15	O	44	LEU
15	O	67	LEU
15	O	73	VAL
15	O	91	GLN
15	O	99	LYS
15	O	100	LEU
15	O	102	GLU
15	O	105	ARG
15	O	111	LEU
16	P	3	ARG
16	P	5	THR
16	P	23	ARG
16	P	36	TYR
16	P	48	LEU
16	P	50	SER
16	P	56	LEU
16	P	59	LYS
16	P	69	VAL
16	P	71	ARG
16	P	85	VAL
16	P	98	VAL
16	P	107	GLU
16	P	110	LEU
16	P	111	GLU
17	Q	1	MET
17	Q	6	LEU
17	Q	19	LEU
17	Q	28	VAL
17	Q	31	SER
17	Q	39	ARG
17	Q	74	ARG
17	Q	102	ILE

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Mol	Chain	Res	Type
17	Q	118	ARG
17	Q	128	GLU
17	Q	132	LYS
18	R	6	THR
18	R	16	LYS
18	R	17	ILE
18	R	27	LEU
18	R	30	LYS
18	R	55	ARG
18	R	74	LEU
18	R	77	SER
18	R	80	ILE
18	R	83	LEU
18	R	89	GLU
18	R	95	LEU
19	S	7	THR
19	S	19	LYS
19	S	32	THR
19	S	38	LEU
19	S	46	VAL
19	S	51	VAL
19	S	53	GLU
19	S	61	VAL
19	S	62	LEU
19	S	68	LYS
19	S	71	LEU
19	S	72	VAL
19	S	73	SER
19	S	79	VAL
19	S	82	ARG
20	T	11	ARG
20	T	17	VAL
20	T	19	LEU
20	T	23	LEU
20	T	30	GLU
20	T	39	THR
20	T	63	ASP
20	T	92	ARG
20	T	107	LEU
20	T	110	LYS
21	U	13	LEU
21	U	15	GLU

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Mol	Chain	Res	Type
21	U	45	THR
21	U	53	LYS
21	U	57	LEU
21	U	70	LEU
21	U	72	LYS
21	U	81	VAL
21	U	82	GLN
21	U	90	GLU
21	U	95	LEU
22	V	2	ARG
22	V	3	VAL
22	V	21	LYS
22	V	44	ILE
22	V	50	ARG
22	V	61	ILE
22	V	72	VAL
22	V	90	LEU
22	V	97	ARG
22	V	107	ASP
23	W	1	MET
23	W	18	LEU
23	W	42	VAL
23	W	53	ILE
23	W	61	LEU
23	W	72	ARG
23	W	80	ARG
23	W	86	VAL
23	W	91	LEU
23	W	103	ARG
23	W	116	VAL
23	W	126	VAL
23	W	132	ASN
23	W	136	PHE
23	W	144	LEU
23	W	161	VAL
23	W	163	LEU
23	W	169	GLU
23	W	175	VAL
23	W	180	VAL
24	X	5	LYS
24	X	7	LEU
24	X	10	THR

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Mol	Chain	Res	Type
24	X	12	ASN
24	X	82	ARG
24	X	84	LEU
25	Y	13	ILE
25	Y	21	ARG
25	Y	30	VAL
25	Y	37	ILE
25	Y	40	ARG
25	Y	51	VAL
25	Y	95	LEU
25	Y	98	LEU
26	Z	2	LYS
26	Z	3	LEU
26	Z	5	GLU
26	Z	31	GLU
26	Z	41	ILE
26	Z	53	LEU
26	Z	66	GLU
27	AA	3	ARG
27	AA	6	VAL
27	AA	18	ASP
27	AA	23	LEU
27	AA	54	VAL
27	AA	56	VAL
28	BA	3	GLU
28	BA	10	VAL
28	BA	30	GLU
28	BA	31	ILE
28	BA	34	GLU
28	BA	53	GLU
28	BA	62	ARG
29	CA	6	VAL
29	CA	16	ARG
29	CA	26	THR
29	CA	29	ILE
29	CA	48	GLU
29	CA	55	ARG
30	DA	4	GLU
30	DA	5	VAL
30	DA	13	CYS
30	DA	14	THR
30	DA	19	ARG

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Mol	Chain	Res	Type
30	DA	24	GLU
30	DA	30	THR
30	DA	35	GLU
30	DA	48	VAL
30	DA	52	VAL
31	EA	4	THR
31	EA	11	LYS
31	EA	24	THR
31	EA	43	THR
32	FA	4	MET
32	FA	14	VAL
32	FA	32	LEU
33	GA	26	ILE
35	JA	119	THR
35	JA	134	MET
35	JA	146	VAL
35	JA	149	MET
35	JA	150	SER
35	JA	155	GLU
35	JA	156	HIS
35	JA	162	ILE
35	JA	167	SER
35	JA	176	LYS
35	JA	196	ILE
35	JA	197	HIS
35	JA	208	GLU
35	JA	217	ILE
35	JA	222	LEU
35	JA	226	THR
35	JA	229	SER
35	JA	247	THR
35	JA	251	THR
35	JA	253	ILE
35	JA	254	VAL
35	JA	260	GLU
35	JA	304	SER
35	JA	306	ARG
35	JA	316	ARG
35	JA	318	THR
35	JA	326	LEU
35	JA	327	TYR
35	JA	328	ARG

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Mol	Chain	Res	Type
35	JA	332	VAL
35	JA	340	LEU
35	JA	341	ILE
35	JA	347	GLU
35	JA	356	LEU
36	KA	10	LEU
36	KA	11	LEU
36	KA	12	GLU
36	KA	16	HIS
36	KA	21	ARG
36	KA	22	LYS
36	KA	23	ARG
36	KA	39	ILE
36	KA	51	LEU
36	KA	75	LYS
36	KA	83	MET
36	KA	119	GLU
36	KA	136	VAL
36	KA	142	LEU
36	KA	149	LEU
36	KA	153	ARG
36	KA	160	ASP
36	KA	163	PHE
36	KA	168	THR
36	KA	169	LYS
36	KA	170	GLU
36	KA	172	ILE
36	KA	185	ILE
36	KA	190	THR
36	KA	213	LEU
36	KA	215	LEU
36	KA	222	ILE
36	KA	229	VAL
36	KA	238	LEU
36	KA	239	VAL
37	LA	3	ASN
37	LA	17	ASP
37	LA	28	GLN
37	LA	31	HIS
37	LA	32	LEU
37	LA	36	ASP
37	LA	63	ASN

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Mol	Chain	Res	Type
37	LA	64	VAL
37	LA	77	ILE
37	LA	79	ARG
37	LA	87	LEU
37	LA	91	LEU
37	LA	94	LEU
37	LA	105	GLU
37	LA	131	ARG
37	LA	140	ARG
37	LA	165	THR
37	LA	173	VAL
37	LA	190	ARG
38	MA	3	ARG
38	MA	4	TYR
38	MA	5	ILE
38	MA	8	VAL
38	MA	9	CYS
38	MA	17	VAL
38	MA	19	LEU
38	MA	21	LEU
38	MA	24	GLU
38	MA	49	ARG
38	MA	57	ARG
38	MA	80	GLU
38	MA	83	SER
38	MA	96	LEU
38	MA	114	ARG
38	MA	119	GLN
38	MA	127	THR
38	MA	131	ARG
38	MA	135	LEU
38	MA	141	ARG
38	MA	148	VAL
38	MA	154	ASN
38	MA	155	LEU
38	MA	157	LEU
38	MA	162	LEU
38	MA	163	GLU
38	MA	190	ASP
38	MA	194	LEU
38	MA	196	LEU
38	MA	198	VAL

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Mol	Chain	Res	Type
38	MA	202	LEU
39	NA	10	MET
39	NA	12	LEU
39	NA	33	VAL
39	NA	41	VAL
39	NA	51	VAL
39	NA	55	VAL
39	NA	56	GLN
39	NA	64	ARG
39	NA	69	VAL
39	NA	72	GLN
39	NA	73	ASN
39	NA	79	GLU
39	NA	82	VAL
39	NA	91	LEU
39	NA	135	THR
39	NA	140	ARG
39	NA	142	LEU
39	NA	151	LEU
40	OA	19	LEU
40	OA	24	GLU
40	OA	25	ILE
40	OA	27	GLN
40	OA	39	LYS
40	OA	43	LEU
40	OA	46	ARG
40	OA	54	LYS
40	OA	55	ASP
40	OA	71	ARG
40	OA	72	VAL
40	OA	83	ASP
40	OA	98	LEU
41	PA	8	GLU
41	PA	24	THR
41	PA	50	ILE
41	PA	56	GLN
41	PA	57	GLU
41	PA	84	ASN
41	PA	89	MET
41	PA	104	LEU
41	PA	114	ARG
41	PA	125	MET

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Mol	Chain	Res	Type
41	PA	155	ARG
42	QA	1	MET
42	QA	18	ARG
42	QA	26	VAL
42	QA	29	SER
42	QA	33	GLU
42	QA	50	ARG
42	QA	63	LEU
42	QA	78	GLN
42	QA	80	ILE
42	QA	83	ILE
42	QA	85	ARG
42	QA	102	ARG
42	QA	112	LEU
42	QA	120	THR
42	QA	127	LEU
42	QA	133	LEU
43	RA	23	ASN
43	RA	26	VAL
43	RA	31	GLN
43	RA	38	GLN
43	RA	41	VAL
43	RA	42	ARG
43	RA	44	VAL
43	RA	53	VAL
43	RA	58	ARG
43	RA	65	VAL
43	RA	79	LEU
43	RA	108	VAL
43	RA	109	VAL
43	RA	113	LYS
43	RA	121	ARG
43	RA	128	ARG
44	SA	6	ILE
44	SA	23	ILE
44	SA	67	THR
44	SA	80	LYS
44	SA	95	GLU
44	SA	96	ILE
45	TA	14	VAL
45	TA	32	ILE
45	TA	33	THR

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Mol	Chain	Res	Type
45	TA	40	ILE
45	TA	48	ILE
45	TA	66	LEU
45	TA	73	MET
45	TA	77	MET
45	TA	84	VAL
45	TA	99	GLN
45	TA	103	LEU
46	UA	18	VAL
46	UA	20	LYS
46	UA	27	LEU
46	UA	33	ARG
46	UA	36	VAL
46	UA	41	ARG
46	UA	44	THR
46	UA	57	LYS
46	UA	65	GLU
46	UA	66	VAL
46	UA	126	LYS
47	VA	3	ARG
47	VA	4	ILE
47	VA	7	VAL
47	VA	11	ARG
47	VA	19	LEU
47	VA	27	LYS
47	VA	37	THR
47	VA	50	GLU
47	VA	70	LEU
47	VA	77	ASN
47	VA	80	ARG
47	VA	90	LEU
47	VA	93	ARG
47	VA	105	THR
47	VA	108	ARG
47	VA	117	VAL
48	WA	7	ILE
48	WA	8	GLU
48	WA	13	THR
48	WA	18	VAL
48	WA	23	ARG
48	WA	32	SER
48	WA	33	VAL

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Mol	Chain	Res	Type
48	WA	56	VAL
48	WA	58	LYS
49	XA	6	GLU
49	XA	26	GLU
49	XA	34	LEU
49	XA	39	LEU
49	XA	66	LEU
49	XA	84	LYS
50	YA	1	MET
50	YA	2	VAL
50	YA	11	SER
50	YA	20	VAL
50	YA	25	ARG
50	YA	29	ASP
50	YA	31	LYS
50	YA	45	THR
50	YA	60	LEU
50	YA	67	THR
50	YA	69	THR
50	YA	82	GLN
51	ZA	9	VAL
51	ZA	14	LYS
51	ZA	35	VAL
51	ZA	63	ARG
51	ZA	75	ARG
51	ZA	77	VAL
51	ZA	85	VAL
51	ZA	90	ILE
51	ZA	91	ARG
51	ZA	93	GLN
52	AB	26	LEU
52	AB	31	LEU
52	AB	76	LEU
52	AB	82	THR
52	AB	86	VAL
53	BB	22	LEU
53	BB	25	LYS
53	BB	28	LYS
53	BB	31	ILE
53	BB	37	ARG
53	BB	51	VAL
53	BB	62	ILE

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Mol	Chain	Res	Type
53	BB	67	VAL
53	BB	83	HIS
54	CB	10	LEU
54	CB	13	LEU
54	CB	30	LYS
54	CB	31	SER
54	CB	41	VAL
54	CB	62	LEU
54	CB	71	THR
54	CB	91	LEU
55	DB	10	ARG
5	JB	3	VAL
5	JB	7	LYS
5	JB	28	GLU
5	JB	39	LYS
5	JB	61	LEU
5	JB	71	ASP
5	JB	89	SER
5	JB	91	ARG
5	JB	94	LEU
5	JB	98	VAL
5	JB	99	ASP
5	JB	105	ILE
5	JB	127	VAL
5	JB	138	VAL
5	JB	140	THR
5	JB	154	LYS
5	JB	171	ASP
5	JB	193	VAL
5	JB	200	ASP
5	JB	221	VAL
5	JB	229	VAL
5	JB	237	GLU
5	JB	242	ARG
5	JB	259	THR
5	JB	270	ILE
5	JB	273	ARG
5	JB	274	ARG
5	JB	275	LYS
6	KB	9	VAL
6	KB	13	ARG
6	KB	21	VAL

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Mol	Chain	Res	Type
6	KB	24	THR
6	KB	75	VAL
6	KB	92	THR
6	KB	93	VAL
6	KB	116	VAL
6	KB	119	ARG
6	KB	128	SER
6	KB	134	ILE
6	KB	154	LYS
6	KB	170	LEU
6	KB	175	VAL
6	KB	178	GLU
6	KB	181	LEU
6	KB	182	LEU
6	KB	185	LYS
6	KB	192	ASN
7	LB	6	MET
7	LB	12	LEU
7	LB	15	SER
7	LB	18	ARG
7	LB	24	LEU
7	LB	37	VAL
7	LB	53	THR
7	LB	57	VAL
7	LB	62	ARG
7	LB	64	ILE
7	LB	70	THR
7	LB	74	ARG
7	LB	93	LYS
7	LB	110	LEU
7	LB	119	ARG
7	LB	126	VAL
7	LB	129	PHE
7	LB	140	LEU
7	LB	158	THR
7	LB	165	ARG
7	LB	170	LEU
7	LB	175	THR
7	LB	183	VAL
7	LB	188	ARG
7	LB	190	GLU
7	LB	191	ARG

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Mol	Chain	Res	Type
7	LB	192	LEU
7	LB	197	ASP
7	LB	200	GLU
7	LB	204	ASN
7	LB	205	ARG
8	MB	3	LEU
8	MB	7	LEU
8	MB	22	ARG
8	MB	28	VAL
8	MB	33	ARG
8	MB	38	VAL
8	MB	43	LEU
8	MB	49	ASP
8	MB	53	LEU
8	MB	60	LEU
8	MB	62	LEU
8	MB	67	LYS
8	MB	70	VAL
8	MB	74	LYS
8	MB	82	LEU
8	MB	98	ARG
8	MB	105	LYS
8	MB	114	ILE
8	MB	115	ARG
8	MB	118	ARG
8	MB	135	LEU
8	MB	136	ARG
8	MB	140	ILE
8	MB	143	GLU
8	MB	167	GLU
9	NB	3	ARG
9	NB	7	LEU
9	NB	16	SER
9	NB	17	VAL
9	NB	24	VAL
9	NB	30	LYS
9	NB	33	LEU
9	NB	37	VAL
9	NB	43	VAL
9	NB	44	VAL
9	NB	46	GLU
9	NB	47	GLU

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Mol	Chain	Res	Type
9	NB	49	VAL
9	NB	57	ASP
9	NB	71	LEU
9	NB	84	SER
9	NB	97	ARG
9	NB	99	VAL
9	NB	104	GLU
9	NB	106	THR
9	NB	115	VAL
9	NB	127	GLU
9	NB	136	ILE
9	NB	141	VAL
9	NB	169	VAL
10	OB	4	ILE
10	OB	9	LEU
10	OB	18	VAL
10	OB	19	VAL
10	OB	31	LEU
10	OB	43	ASN
10	OB	44	LEU
10	OB	57	ARG
10	OB	74	ASN
10	OB	77	LEU
10	OB	86	THR
10	OB	88	ILE
10	OB	89	TYR
10	OB	92	VAL
10	OB	99	GLU
10	OB	107	ILE
10	OB	108	THR
10	OB	109	ILE
10	OB	112	LYS
10	OB	113	ARG
10	OB	118	LYS
10	OB	122	GLU
10	OB	123	LEU
10	OB	125	GLU
10	OB	127	VAL
10	OB	129	THR
10	OB	131	LYS
10	OB	136	VAL
10	OB	140	LEU

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Mol	Chain	Res	Type
10	OB	144	VAL
10	OB	145	VAL
11	PB	9	VAL
11	PB	14	VAL
11	PB	19	GLU
11	PB	28	THR
11	PB	34	LEU
11	PB	48	MET
11	PB	67	LEU
11	PB	68	GLU
11	PB	76	SER
11	PB	83	LYS
11	PB	84	LYS
11	PB	87	LEU
11	PB	93	THR
11	PB	96	GLU
11	PB	99	LEU
11	PB	138	LEU
12	QB	10	VAL
12	QB	20	MET
12	QB	24	VAL
12	QB	32	TYR
12	QB	45	GLU
12	QB	61	VAL
12	QB	66	LYS
12	QB	69	VAL
12	QB	70	LYS
12	QB	78	ARG
12	QB	98	VAL
12	QB	116	SER
13	RB	3	LEU
13	RB	27	HIS
13	RB	29	LYS
13	RB	42	SER
13	RB	58	THR
13	RB	59	LEU
13	RB	68	GLN
13	RB	71	VAL
13	RB	90	ARG
13	RB	112	LEU
13	RB	117	GLU
13	RB	126	VAL

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Mol	Chain	Res	Type
13	RB	132	LYS
13	RB	135	LEU
13	RB	147	LEU
13	RB	149	GLU
14	SB	31	ASP
14	SB	59	ARG
14	SB	75	THR
14	SB	76	LYS
14	SB	79	LEU
14	SB	81	VAL
14	SB	98	LYS
14	SB	106	VAL
14	SB	109	VAL
14	SB	141	GLN
15	TB	15	SER
15	TB	18	LEU
15	TB	28	LEU
15	TB	29	LEU
15	TB	44	LEU
15	TB	54	LEU
15	TB	67	LEU
15	TB	73	VAL
15	TB	91	GLN
15	TB	99	LYS
15	TB	100	LEU
15	TB	102	GLU
15	TB	104	ARG
15	TB	105	ARG
15	TB	111	LEU
16	UB	3	ARG
16	UB	5	THR
16	UB	23	ARG
16	UB	36	TYR
16	UB	48	LEU
16	UB	50	SER
16	UB	56	LEU
16	UB	59	LYS
16	UB	69	VAL
16	UB	85	VAL
16	UB	98	VAL
16	UB	106	ARG
16	UB	107	GLU

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Mol	Chain	Res	Type
16	UB	110	LEU
16	UB	111	GLU
17	VB	1	MET
17	VB	6	LEU
17	VB	19	LEU
17	VB	28	VAL
17	VB	31	SER
17	VB	39	ARG
17	VB	74	ARG
17	VB	102	ILE
17	VB	118	ARG
17	VB	128	GLU
17	VB	132	LYS
18	WB	6	THR
18	WB	16	LYS
18	WB	17	ILE
18	WB	27	LEU
18	WB	30	LYS
18	WB	55	ARG
18	WB	74	LEU
18	WB	77	SER
18	WB	80	ILE
18	WB	83	LEU
18	WB	89	GLU
18	WB	95	LEU
19	XB	7	THR
19	XB	19	LYS
19	XB	32	THR
19	XB	38	LEU
19	XB	46	VAL
19	XB	51	VAL
19	XB	53	GLU
19	XB	61	VAL
19	XB	62	LEU
19	XB	71	LEU
19	XB	72	VAL
19	XB	73	SER
19	XB	79	VAL
19	XB	82	ARG
19	XB	93	GLU
20	YB	11	ARG
20	YB	17	VAL

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Mol	Chain	Res	Type
20	YB	19	LEU
20	YB	23	LEU
20	YB	30	GLU
20	YB	39	THR
20	YB	63	ASP
20	YB	92	ARG
20	YB	107	LEU
20	YB	110	LYS
21	ZB	13	LEU
21	ZB	15	GLU
21	ZB	45	THR
21	ZB	53	LYS
21	ZB	57	LEU
21	ZB	70	LEU
21	ZB	72	LYS
21	ZB	81	VAL
21	ZB	82	GLN
21	ZB	90	GLU
21	ZB	95	LEU
22	AC	2	ARG
22	AC	3	VAL
22	AC	21	LYS
22	AC	44	ILE
22	AC	50	ARG
22	AC	61	ILE
22	AC	64	GLU
22	AC	72	VAL
22	AC	90	LEU
22	AC	97	ARG
22	AC	107	ASP
23	BC	1	MET
23	BC	18	LEU
23	BC	42	VAL
23	BC	53	ILE
23	BC	61	LEU
23	BC	72	ARG
23	BC	80	ARG
23	BC	86	VAL
23	BC	91	LEU
23	BC	103	ARG
23	BC	116	VAL
23	BC	126	VAL

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Mol	Chain	Res	Type
23	BC	132	ASN
23	BC	136	PHE
23	BC	144	LEU
23	BC	161	VAL
23	BC	163	LEU
23	BC	169	GLU
23	BC	175	VAL
23	BC	180	VAL
24	CC	5	LYS
24	CC	7	LEU
24	CC	10	THR
24	CC	12	ASN
24	CC	68	GLU
24	CC	82	ARG
24	CC	84	LEU
25	DC	13	ILE
25	DC	21	ARG
25	DC	30	VAL
25	DC	37	ILE
25	DC	40	ARG
25	DC	51	VAL
25	DC	59	THR
25	DC	95	LEU
25	DC	98	LEU
26	EC	2	LYS
26	EC	3	LEU
26	EC	5	GLU
26	EC	31	GLU
26	EC	41	ILE
26	EC	53	LEU
26	EC	66	GLU
27	FC	3	ARG
27	FC	6	VAL
27	FC	23	LEU
27	FC	54	VAL
27	FC	56	VAL
28	GC	3	GLU
28	GC	10	VAL
28	GC	30	GLU
28	GC	31	ILE
28	GC	34	GLU
28	GC	53	GLU

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Mol	Chain	Res	Type
28	GC	62	ARG
29	HC	6	VAL
29	HC	16	ARG
29	HC	26	THR
29	HC	29	ILE
29	HC	48	GLU
29	HC	55	ARG
30	IC	4	GLU
30	IC	5	VAL
30	IC	13	CYS
30	IC	14	THR
30	IC	19	ARG
30	IC	24	GLU
30	IC	30	THR
30	IC	35	GLU
30	IC	48	VAL
30	IC	52	VAL
31	JC	4	THR
31	JC	11	LYS
31	JC	24	THR
32	KC	4	MET
32	KC	14	VAL
32	KC	26	LYS
32	KC	32	LEU
33	LC	26	ILE
35	OC	119	THR
35	OC	134	MET
35	OC	146	VAL
35	OC	149	MET
35	OC	150	SER
35	OC	155	GLU
35	OC	156	HIS
35	OC	162	ILE
35	OC	167	SER
35	OC	176	LYS
35	OC	196	ILE
35	OC	197	HIS
35	OC	208	GLU
35	OC	217	ILE
35	OC	222	LEU
35	OC	226	THR
35	OC	229	SER

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Mol	Chain	Res	Type
35	OC	247	THR
35	OC	251	THR
35	OC	253	ILE
35	OC	254	VAL
35	OC	260	GLU
35	OC	304	SER
35	OC	306	ARG
35	OC	316	ARG
35	OC	318	THR
35	OC	326	LEU
35	OC	327	TYR
35	OC	332	VAL
35	OC	340	LEU
35	OC	341	ILE
35	OC	347	GLU
35	OC	356	LEU
36	PC	10	LEU
36	PC	11	LEU
36	PC	12	GLU
36	PC	16	HIS
36	PC	22	LYS
36	PC	23	ARG
36	PC	39	ILE
36	PC	51	LEU
36	PC	75	LYS
36	PC	83	MET
36	PC	119	GLU
36	PC	136	VAL
36	PC	142	LEU
36	PC	149	LEU
36	PC	153	ARG
36	PC	160	ASP
36	PC	163	PHE
36	PC	168	THR
36	PC	169	LYS
36	PC	170	GLU
36	PC	172	ILE
36	PC	185	ILE
36	PC	190	THR
36	PC	213	LEU
36	PC	215	LEU
36	PC	222	ILE

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Mol	Chain	Res	Type
36	PC	229	VAL
36	PC	238	LEU
36	PC	239	VAL
37	QC	3	ASN
37	QC	17	ASP
37	QC	28	GLN
37	QC	31	HIS
37	QC	32	LEU
37	QC	36	ASP
37	QC	63	ASN
37	QC	64	VAL
37	QC	77	ILE
37	QC	87	LEU
37	QC	91	LEU
37	QC	94	LEU
37	QC	105	GLU
37	QC	131	ARG
37	QC	140	ARG
37	QC	165	THR
37	QC	173	VAL
37	QC	190	ARG
38	RC	3	ARG
38	RC	4	TYR
38	RC	5	ILE
38	RC	8	VAL
38	RC	9	CYS
38	RC	17	VAL
38	RC	19	LEU
38	RC	21	LEU
38	RC	24	GLU
38	RC	49	ARG
38	RC	57	ARG
38	RC	80	GLU
38	RC	83	SER
38	RC	96	LEU
38	RC	114	ARG
38	RC	119	GLN
38	RC	127	THR
38	RC	131	ARG
38	RC	135	LEU
38	RC	141	ARG
38	RC	148	VAL

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Mol	Chain	Res	Type
38	RC	154	ASN
38	RC	155	LEU
38	RC	157	LEU
38	RC	160	GLN
38	RC	162	LEU
38	RC	163	GLU
38	RC	190	ASP
38	RC	194	LEU
38	RC	202	LEU
39	SC	5	ASP
39	SC	10	MET
39	SC	12	LEU
39	SC	33	VAL
39	SC	41	VAL
39	SC	51	VAL
39	SC	55	VAL
39	SC	56	GLN
39	SC	64	ARG
39	SC	69	VAL
39	SC	72	GLN
39	SC	73	ASN
39	SC	79	GLU
39	SC	82	VAL
39	SC	87	SER
39	SC	91	LEU
39	SC	135	THR
39	SC	140	ARG
39	SC	142	LEU
39	SC	151	LEU
40	TC	19	LEU
40	TC	24	GLU
40	TC	25	ILE
40	TC	27	GLN
40	TC	39	LYS
40	TC	43	LEU
40	TC	46	ARG
40	TC	54	LYS
40	TC	55	ASP
40	TC	71	ARG
40	TC	72	VAL
40	TC	83	ASP
40	TC	98	LEU

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Mol	Chain	Res	Type
41	UC	8	GLU
41	UC	24	THR
41	UC	50	ILE
41	UC	56	GLN
41	UC	57	GLU
41	UC	84	ASN
41	UC	89	MET
41	UC	104	LEU
41	UC	114	ARG
41	UC	125	MET
41	UC	155	ARG
42	VC	1	MET
42	VC	18	ARG
42	VC	26	VAL
42	VC	29	SER
42	VC	33	GLU
42	VC	50	ARG
42	VC	63	LEU
42	VC	78	GLN
42	VC	80	ILE
42	VC	83	ILE
42	VC	85	ARG
42	VC	102	ARG
42	VC	112	LEU
42	VC	119	LEU
42	VC	120	THR
42	VC	127	LEU
42	VC	133	LEU
43	WC	23	ASN
43	WC	26	VAL
43	WC	31	GLN
43	WC	38	GLN
43	WC	41	VAL
43	WC	42	ARG
43	WC	44	VAL
43	WC	58	ARG
43	WC	65	VAL
43	WC	79	LEU
43	WC	108	VAL
43	WC	109	VAL
43	WC	113	LYS
43	WC	121	ARG

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Mol	Chain	Res	Type
43	WC	128	ARG
44	XC	6	ILE
44	XC	23	ILE
44	XC	67	THR
44	XC	80	LYS
44	XC	95	GLU
44	XC	96	ILE
45	YC	14	VAL
45	YC	22	HIS
45	YC	33	THR
45	YC	40	ILE
45	YC	48	ILE
45	YC	66	LEU
45	YC	73	MET
45	YC	77	MET
45	YC	84	VAL
45	YC	99	GLN
45	YC	103	LEU
45	YC	109	VAL
46	ZC	6	THR
46	ZC	18	VAL
46	ZC	20	LYS
46	ZC	27	LEU
46	ZC	33	ARG
46	ZC	36	VAL
46	ZC	41	ARG
46	ZC	44	THR
46	ZC	57	LYS
46	ZC	65	GLU
46	ZC	126	LYS
47	AD	3	ARG
47	AD	4	ILE
47	AD	7	VAL
47	AD	11	ARG
47	AD	15	VAL
47	AD	19	LEU
47	AD	27	LYS
47	AD	37	THR
47	AD	50	GLU
47	AD	70	LEU
47	AD	77	ASN
47	AD	80	ARG

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Mol	Chain	Res	Type
47	AD	90	LEU
47	AD	93	ARG
47	AD	105	THR
47	AD	108	ARG
47	AD	117	VAL
48	BD	7	ILE
48	BD	8	GLU
48	BD	13	THR
48	BD	18	VAL
48	BD	23	ARG
48	BD	33	VAL
48	BD	56	VAL
48	BD	58	LYS
49	CD	6	GLU
49	CD	26	GLU
49	CD	34	LEU
49	CD	39	LEU
49	CD	66	LEU
49	CD	84	LYS
50	DD	1	MET
50	DD	2	VAL
50	DD	11	SER
50	DD	20	VAL
50	DD	25	ARG
50	DD	31	LYS
50	DD	45	THR
50	DD	60	LEU
50	DD	67	THR
50	DD	69	THR
50	DD	82	GLN
51	ED	9	VAL
51	ED	14	LYS
51	ED	35	VAL
51	ED	63	ARG
51	ED	75	ARG
51	ED	77	VAL
51	ED	85	VAL
51	ED	90	ILE
51	ED	91	ARG
51	ED	93	GLN
52	FD	26	LEU
52	FD	31	LEU

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Mol	Chain	Res	Type
52	FD	76	LEU
52	FD	82	THR
53	GD	22	LEU
53	GD	25	LYS
53	GD	28	LYS
53	GD	31	ILE
53	GD	37	ARG
53	GD	51	VAL
53	GD	62	ILE
53	GD	67	VAL
53	GD	83	HIS
54	HD	10	LEU
54	HD	13	LEU
54	HD	30	LYS
54	HD	31	SER
54	HD	41	VAL
54	HD	62	LEU
54	HD	71	THR
54	HD	91	LEU
55	ID	10	ARG

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

Mol	Chain	Res	Type
5	E	166	GLN
6	F	85	ASN
7	G	29	ASN
7	G	203	GLN
8	H	123	ASN
8	H	132	ASN
10	J	74	ASN
11	K	131	GLN
12	L	89	ASN
15	O	61	HIS
17	Q	84	GLN
18	R	94	ASN
18	R	117	GLN
23	W	34	ASN
23	W	55	HIS
23	W	73	GLN
27	AA	32	GLN
28	BA	20	ASN

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Mol	Chain	Res	Type
35	JA	263	GLN
35	JA	352	GLN
36	KA	19	HIS
36	KA	78	GLN
36	KA	94	ASN
37	LA	31	HIS
37	LA	108	ASN
38	MA	45	GLN
41	PA	86	GLN
41	PA	122	HIS
41	PA	148	ASN
43	RA	3	GLN
43	RA	117	HIS
44	SA	76	ASN
45	TA	22	HIS
45	TA	26	ASN
45	TA	99	GLN
47	VA	101	GLN
53	BB	69	HIS
7	LB	29	ASN
7	LB	75	HIS
7	LB	203	GLN
8	MB	132	ASN
10	OB	74	ASN
11	PB	94	HIS
11	PB	131	GLN
12	QB	3	GLN
12	QB	89	ASN
13	RB	70	GLN
15	TB	13	HIS
17	VB	84	GLN
18	WB	94	ASN
18	WB	117	GLN
23	BC	34	ASN
23	BC	55	HIS
23	BC	73	GLN
27	FC	32	GLN
28	GC	20	ASN
35	OC	263	GLN
36	PC	19	HIS
36	PC	78	GLN
36	PC	94	ASN

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Mol	Chain	Res	Type
37	QC	31	HIS
37	QC	108	ASN
38	RC	42	GLN
40	TC	13	ASN
41	UC	122	HIS
41	UC	148	ASN
43	WC	3	GLN
43	WC	117	HIS
44	XC	76	ASN
45	YC	22	HIS
45	YC	26	ASN
45	YC	99	GLN
47	AD	101	GLN
53	GD	69	HIS
54	HD	42	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1505/1507 (99%)	228 (15%)	11 (0%)
1	FB	1505/1507 (99%)	229 (15%)	11 (0%)
2	B	2879/2880 (99%)	475 (16%)	24 (0%)
2	GB	2879/2880 (99%)	475 (16%)	21 (0%)
3	C	119/120 (99%)	16 (13%)	1 (0%)
3	HB	119/120 (99%)	16 (13%)	1 (0%)
34	HA	9/27 (33%)	4 (44%)	0
34	MC	9/27 (33%)	4 (44%)	0
4	D	76/77 (98%)	15 (19%)	0
4	IA	76/77 (98%)	7 (9%)	1 (1%)
4	IB	76/77 (98%)	15 (19%)	0
4	NC	76/77 (98%)	7 (9%)	1 (1%)
All	All	9328/9376 (99%)	1491 (15%)	71 (0%)

All (1491) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	22	G
1	A	32	A
1	A	39	G
1	A	47	C

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Mol	Chain	Res	Type
1	A	48	C
1	A	50	A
1	A	51	A
1	A	54	C
1	A	59	A
1	A	61	G
1	A	65	U
1	A	66	G
1	A	77	C
1	A	79	G
1	A	80	G
1	A	84	U
1	A	85	U
1	A	86	U
1	A	87	A
1	A	88	C
1	A	89	U
1	A	101	A
1	A	105	G
1	A	115	G
1	A	116	A
1	A	121	C
1	A	131	C
1	A	163	C
1	A	182	U
1	A	188	U
1	A	195	A
1	A	197	A
1	A	201	C
1	A	209	U
1	A	210	U
1	A	216	G
1	A	231	G
1	A	240	C
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	289	G
1	A	328	C
1	A	332	G
1	A	346	G

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Mol	Chain	Res	Type
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	372	C
1	A	373	A
1	A	384	G
1	A	397	A
1	A	398	C
1	A	402	G
1	A	406	G
1	A	412	A
1	A	413	G
1	A	422	C
1	A	429	U
1	A	439	A
1	A	452	A
1	A	465	A
1	A	482	A
1	A	485	G
1	A	487	A
1	A	496	A
1	A	497	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	521	G
1	A	532	A
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	596	C
1	A	607	A
1	A	618	C
1	A	653	A

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Mol	Chain	Res	Type
1	A	665	A
1	A	687	A
1	A	688	G
1	A	694	A
1	A	695	A
1	A	703	G
1	A	722	A
1	A	723	U
1	A	724	G
1	A	725	G
1	A	731	G
1	A	734	G
1	A	748	C
1	A	749	C
1	A	755	G
1	A	764	C
1	A	774	G
1	A	777	A
1	A	793	U
1	A	794	A
1	A	816	A
1	A	817	C
1	A	819	A
1	A	828	A
1	A	836	G
1	A	842	C
1	A	843	U
1	A	859	A
1	A	870	U
1	A	872	A
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	966	M2G
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A

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Mol	Chain	Res	Type
1	A	976	G
1	A	977	A
1	A	982	U
1	A	984	C
1	A	992	U
1	A	993	G
1	A	997	U
1	A	998(A)	G
1	A	999	U
1	A	1002	G
1	A	1003	G
1	A	1004	A
1	A	1005	A
1	A	1025	U
1	A	1028(C)	C
1	A	1029	G
1	A	1030	C
1	A	1031	G
1	A	1032(A)	A
1	A	1032(B)	G
1	A	1032(C)	G
1	A	1033	G
1	A	1035	A
1	A	1042	G
1	A	1045	C
1	A	1050	G
1	A	1054	C
1	A	1081	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1108	G
1	A	1129	C
1	A	1134	G
1	A	1136	U
1	A	1137	C
1	A	1139	G
1	A	1140	C
1	A	1146	A
1	A	1151	A
1	A	1152	A
1	A	1157	A

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Mol	Chain	Res	Type
1	A	1159	U
1	A	1171	G
1	A	1184	G
1	A	1193	G
1	A	1196	U
1	A	1197	G
1	A	1199	U
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1225	A
1	A	1227	A
1	A	1236	A
1	A	1238	A
1	A	1240	U
1	A	1257	U
1	A	1258	G
1	A	1263	C
1	A	1270	C
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1287	A
1	A	1297	C
1	A	1299	A
1	A	1302	U
1	A	1305	G
1	A	1317	C
1	A	1319	A
1	A	1320	C
1	A	1322	C
1	A	1346	A
1	A	1347	G
1	A	1353	G
1	A	1362(B)	C
1	A	1364	U
1	A	1368	G
1	A	1370	G
1	A	1397	C
1	A	1398	A
1	A	1402	4OC
1	A	1419	G

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Mol	Chain	Res	Type
1	A	1442	G
1	A	1453	G
1	A	1454	G
1	A	1460	A
1	A	1487	G
1	A	1492	A
1	A	1497	G
1	A	1504	G
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G
1	A	1532	U
2	B	14	A
2	B	15	G
2	B	34	C
2	B	35	G
2	B	46	C
2	B	58	G
2	B	71	A
2	B	74	A
2	B	75	G
2	B	93	C
2	B	118	A
2	B	119	A
2	B	120	U
2	B	125	G
2	B	135	G
2	B	149	A
2	B	154(A)	C
2	B	155	C
2	B	161	U
2	B	163	U
2	B	164	U
2	B	181	A
2	B	188	G
2	B	196	A
2	B	199	A
2	B	205	G
2	B	214	G
2	B	215	G
2	B	216	A

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Mol	Chain	Res	Type
2	B	221	A
2	B	222	A
2	B	228	A
2	B	229	A
2	B	233	A
2	B	248	G
2	B	249	C
2	B	250	G
2	B	266	G
2	B	269	U
2	B	270(L)	C
2	B	270(M)	U
2	B	270(N)	U
2	B	270(O)	G
2	B	270(P)	U
2	B	270(Q)	C
2	B	271(C)	G
2	B	271(D)	U
2	B	271	G
2	B	273(G)	C
2	B	278	A
2	B	283	A
2	B	311	A
2	B	317	G
2	B	324	A
2	B	329	G
2	B	330	A
2	B	352	G
2	B	353	G
2	B	363(A)	G
2	B	363(G)	A
2	B	372	G
2	B	386	G
2	B	396	G
2	B	405	U
2	B	407	G
2	B	411	G
2	B	412	A
2	B	442	G
2	B	443	A
2	B	444	C
2	B	455	C

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Mol	Chain	Res	Type
2	B	456	C
2	B	457	A
2	B	479	A
2	B	481	G
2	B	494	G
2	B	504	U
2	B	505	A
2	B	508	G
2	B	509	C
2	B	510	C
2	B	529	A
2	B	531	C
2	B	532	A
2	B	533	G
2	B	549	G
2	B	550	G
2	B	563	G
2	B	571	A
2	B	573	G
2	B	575	A
2	B	603	A
2	B	604	G
2	B	607	U
2	B	615	G
2	B	616	A
2	B	617	G
2	B	627	A
2	B	637	A
2	B	645	C
2	B	646	A
2	B	654	U
2	B	655	A
2	B	664	C
2	B	686	G
2	B	717	G
2	B	730	C
2	B	765	G
2	B	775	G
2	B	776	G
2	B	782	A
2	B	784	A
2	B	785	G

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Mol	Chain	Res	Type
2	B	792	G
2	B	805	G
2	B	812	C
2	B	819	A
2	B	827	U
2	B	828	U
2	B	855	G
2	B	859	G
2	B	869	G
2	B	878	A
2	B	879	G
2	B	886	C
2	B	887	A
2	B	888	C
2	B	890	A
2	B	893	C
2	B	894	C
2	B	895	U
2	B	896	A
2	B	907	U
2	B	910	A
2	B	917	A
2	B	932	G
2	B	941	A
2	B	945	A
2	B	946	G
2	B	959	A
2	B	961	C
2	B	974(A)	G
2	B	974(B)	C
2	B	983	A
2	B	989	G
2	B	990	A
2	B	996	A
2	B	1012	U
2	B	1013	C
2	B	1022	G
2	B	1025	G
2	B	1026	U
2	B	1033	U
2	B	1039	G
2	B	1042	G

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Mol	Chain	Res	Type
2	B	1044	G
2	B	1045	A
2	B	1046	A
2	B	1047	G
2	B	1054	A
2	B	1057	A
2	B	1058	G
2	B	1059	G
2	B	1060	U
2	B	1061	U
2	B	1062	G
2	B	1066	U
2	B	1068	G
2	B	1069	A
2	B	1070	A
2	B	1071	G
2	B	1072	C
2	B	1073	A
2	B	1075	C
2	B	1076	C
2	B	1077	A
2	B	1078	U
2	B	1079	C
2	B	1081	U
2	B	1082	U
2	B	1083	U
2	B	1085	A
2	B	1086	A
2	B	1088	A
2	B	1089	G
2	B	1090	U
2	B	1091	G
2	B	1094	U
2	B	1097	U
2	B	1098	A
2	B	1101	U
2	B	1107	G
2	B	1111	A
2	B	1112	G
2	B	1122	G
2	B	1126	A
2	B	1129	A

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Mol	Chain	Res	Type
2	B	1130	U
2	B	1135	C
2	B	1136	G
2	B	1139	G
2	B	1142(B)	A
2	B	1143	A
2	B	1155	A
2	B	1174	A
2	B	1175	U
2	B	1177	A
2	B	1205	U
2	B	1210	A
2	B	1211	U
2	B	1218	C
2	B	1220	A
2	B	1253	A
2	B	1256	G
2	B	1271	G
2	B	1272	A
2	B	1273	U
2	B	1300	U
2	B	1301	A
2	B	1313	U
2	B	1359	A
2	B	1360	A
2	B	1365	A
2	B	1380	G
2	B	1385	G
2	B	1395	A
2	B	1416	G
2	B	1417	C
2	B	1419	A
2	B	1420	U
2	B	1421	G
2	B	1428	C
2	B	1444(B)	A
2	B	1449(B)	A
2	B	1459	G
2	B	1460	A
2	B	1461	G
2	B	1467	C
2	B	1471	A

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Mol	Chain	Res	Type
2	B	1483	G
2	B	1493	C
2	B	1494	A
2	B	1497	U
2	B	1508	A
2	B	1510	A
2	B	1511	A
2	B	1512	G
2	B	1513	C
2	B	1532	C
2	B	1534	G
2	B	1535	U
2	B	1537	C
2	B	1538	G
2	B	1544	C
2	B	1547	C
2	B	1558	A
2	B	1559	G
2	B	1566	A
2	B	1569	A
2	B	1578	U
2	B	1585	C
2	B	1587	A
2	B	1595	G
2	B	1608	A
2	B	1609	A
2	B	1610	A
2	B	1631	A
2	B	1647	G
2	B	1648	C
2	B	1654	A
2	B	1667	G
2	B	1674	G
2	B	1693	U
2	B	1700	A
2	B	1701	A
2	B	1729	A
2	B	1730	U
2	B	1731	G
2	B	1743	G
2	B	1762	A
2	B	1763	G

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Mol	Chain	Res	Type
2	B	1764	G
2	B	1773	A
2	B	1776	G
2	B	1781	C
2	B	1791	A
2	B	1800	C
2	B	1801	G
2	B	1811	G
2	B	1816	G
2	B	1829	A
2	B	1835	G
2	B	1839	G
2	B	1847	A
2	B	1859	A
2	B	1872	A
2	B	1878	G
2	B	1900	A
2	B	1903	G
2	B	1905	C
2	B	1906	G
2	B	1913	A
2	B	1914	C
2	B	1921	G
2	B	1929	G
2	B	1930	G
2	B	1936	A
2	B	1940	U
2	B	1955	U
2	B	1963	U
2	B	1965	C
2	B	1967	C
2	B	1970	A
2	B	1971	A
2	B	1972	A
2	B	1984	G
2	B	1992	G
2	B	1993	U
2	B	1997	G
2	B	2020	A
2	B	2023	G
2	B	2031	A
2	B	2032	G

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Mol	Chain	Res	Type
2	B	2033	A
2	B	2043	C
2	B	2055	C
2	B	2056	G
2	B	2060	A
2	B	2061	G
2	B	2062	A
2	B	2069	G
2	B	2100	G
2	B	2110	G
2	B	2113	U
2	B	2116	G
2	B	2117	A
2	B	2118	U
2	B	2119	A
2	B	2122	U
2	B	2125	G
2	B	2126	A
2	B	2127	G
2	B	2130	U
2	B	2131	G
2	B	2132	U
2	B	2133	G
2	B	2134	A
2	B	2136	C
2	B	2137	C
2	B	2138	C
2	B	2142	C
2	B	2145	C
2	B	2146	C
2	B	2147	G
2	B	2148	G
2	B	2152	G
2	B	2162	G
2	B	2164	C
2	B	2165	G
2	B	2166	G
2	B	2167	U
2	B	2169	A
2	B	2171	A
2	B	2172	U
2	B	2173	A

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Mol	Chain	Res	Type
2	B	2176	A
2	B	2187	G
2	B	2189	U
2	B	2198	A
2	B	2210	G
2	B	2211	G
2	B	2212	A
2	B	2213	U
2	B	2225	A
2	B	2226	C
2	B	2238	G
2	B	2239	G
2	B	2243	U
2	B	2269	A
2	B	2275	C
2	B	2278	A
2	B	2279	G
2	B	2283	C
2	B	2287	A
2	B	2288	A
2	B	2305	A
2	B	2308	G
2	B	2309	A
2	B	2311	A
2	B	2312	U
2	B	2319	G
2	B	2320	A
2	B	2321	G
2	B	2322	A
2	B	2325	G
2	B	2327	A
2	B	2336	A
2	B	2347	C
2	B	2383	G
2	B	2385	C
2	B	2396	G
2	B	2401	U
2	B	2406	U
2	B	2424	C
2	B	2425	A
2	B	2429	G
2	B	2430	A

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Mol	Chain	Res	Type
2	B	2435	A
2	B	2439	A
2	B	2440	C
2	B	2441	C
2	B	2448	A
2	B	2476	A
2	B	2477	C
2	B	2502	G
2	B	2505	G
2	B	2506	U
2	B	2518	A
2	B	2525	G
2	B	2529	G
2	B	2534	A
2	B	2554	U
2	B	2566	A
2	B	2567	G
2	B	2573	C
2	B	2574	G
2	B	2596	U
2	B	2602	A
2	B	2609	U
2	B	2611	U
2	B	2612	C
2	B	2615	U
2	B	2630	G
2	B	2663	G
2	B	2682	U
2	B	2683	C
2	B	2689	U
2	B	2690	C
2	B	2691	C
2	B	2703	C
2	B	2712(A)	A
2	B	2713	A
2	B	2714	G
2	B	2718	G
2	B	2726	U
2	B	2733	A
2	B	2751	G
2	B	2757	A
2	B	2758	A

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Mol	Chain	Res	Type
2	B	2764	A
2	B	2765	A
2	B	2766	G
2	B	2778	A
2	B	2789	C
2	B	2790	A
2	B	2791	C
2	B	2793	G
2	B	2794	C
2	B	2797	U
2	B	2798	C
2	B	2799	A
2	B	2801	A
2	B	2802	G
2	B	2805	G
2	B	2807	G
2	B	2818	G
2	B	2820	A
2	B	2821	A
2	B	2835	A
2	B	2836	U
2	B	2872	G
2	B	2879	C
2	B	2880	C
2	B	2892	A
2	B	2894	G
3	C	2	C
3	C	9	G
3	C	12	C
3	C	25	A
3	C	30	C
3	C	35	U
3	C	45	A
3	C	56	G
3	C	66	A
3	C	73	A
3	C	74	U
3	C	89(B)	A
3	C	90	C
3	C	109	G
3	C	111	U
3	C	119	A

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Mol	Chain	Res	Type
4	D	7	G
4	D	8	4SU
4	D	16	C
4	D	17(A)	U
4	D	19	G
4	D	20	U
4	D	22	G
4	D	35	A
4	D	36	U
4	D	37	A
4	D	46	G
4	D	47	U
4	D	48	C
4	D	58	A
4	D	61	C
34	HA	14	A
34	HA	16	A
34	HA	21	A
34	HA	22	A
4	IA	10	G
4	IA	18	G
4	IA	20	U
4	IA	47	U
4	IA	48	C
4	IA	52	G
4	IA	76	A
1	FB	9	G
1	FB	22	G
1	FB	32	A
1	FB	39	G
1	FB	47	C
1	FB	48	C
1	FB	50	A
1	FB	51	A
1	FB	54	C
1	FB	59	A
1	FB	61	G
1	FB	65	U
1	FB	66	G
1	FB	77	C
1	FB	79	G
1	FB	80	G

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Mol	Chain	Res	Type
1	FB	84	U
1	FB	85	U
1	FB	86	U
1	FB	87	A
1	FB	88	C
1	FB	89	U
1	FB	101	A
1	FB	105	G
1	FB	115	G
1	FB	116	A
1	FB	121	C
1	FB	131	C
1	FB	163	C
1	FB	182	U
1	FB	188	U
1	FB	195	A
1	FB	197	A
1	FB	201	C
1	FB	209	U
1	FB	210	U
1	FB	216	G
1	FB	231	G
1	FB	240	C
1	FB	247	G
1	FB	251	G
1	FB	266	G
1	FB	267	C
1	FB	289	G
1	FB	319	G
1	FB	321	A
1	FB	328	C
1	FB	332	G
1	FB	346	G
1	FB	352	C
1	FB	353	A
1	FB	354	G
1	FB	367	U
1	FB	372	C
1	FB	373	A
1	FB	384	G
1	FB	397	A
1	FB	398	C

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Mol	Chain	Res	Type
1	FB	402	G
1	FB	406	G
1	FB	412	A
1	FB	413	G
1	FB	422	C
1	FB	429	U
1	FB	439	A
1	FB	452	A
1	FB	465	A
1	FB	482	A
1	FB	485	G
1	FB	487	A
1	FB	496	A
1	FB	497	U
1	FB	509	A
1	FB	510	A
1	FB	511	C
1	FB	518	C
1	FB	521	G
1	FB	532	A
1	FB	547	A
1	FB	559	A
1	FB	560	U
1	FB	561	U
1	FB	572	A
1	FB	573	A
1	FB	575	G
1	FB	576	G
1	FB	577	G
1	FB	607	A
1	FB	618	C
1	FB	653	A
1	FB	665	A
1	FB	687	A
1	FB	688	G
1	FB	695	A
1	FB	722	A
1	FB	723	U
1	FB	724	G
1	FB	725	G
1	FB	731	G
1	FB	734	G

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Mol	Chain	Res	Type
1	FB	748	C
1	FB	749	C
1	FB	755	G
1	FB	764	C
1	FB	774	G
1	FB	777	A
1	FB	793	U
1	FB	794	A
1	FB	815	A
1	FB	816	A
1	FB	817	C
1	FB	819	A
1	FB	828	A
1	FB	836	G
1	FB	842	C
1	FB	843	U
1	FB	859	A
1	FB	870	U
1	FB	872	A
1	FB	902	G
1	FB	914	A
1	FB	926	G
1	FB	927	G
1	FB	931	C
1	FB	934	C
1	FB	935	A
1	FB	960	U
1	FB	966	M2G
1	FB	969	A
1	FB	971	G
1	FB	974	A
1	FB	975	A
1	FB	976	G
1	FB	977	A
1	FB	982	U
1	FB	984	C
1	FB	992	U
1	FB	993	G
1	FB	997	U
1	FB	998(A)	G
1	FB	999	U
1	FB	1002	G

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Mol	Chain	Res	Type
1	FB	1003	G
1	FB	1004	A
1	FB	1005	A
1	FB	1025	U
1	FB	1027	C
1	FB	1028(C)	C
1	FB	1029	G
1	FB	1030	C
1	FB	1031	G
1	FB	1032(A)	A
1	FB	1032(B)	G
1	FB	1032(C)	G
1	FB	1033	G
1	FB	1035	A
1	FB	1042	G
1	FB	1045	C
1	FB	1050	G
1	FB	1054	C
1	FB	1081	G
1	FB	1094	G
1	FB	1095	U
1	FB	1101	A
1	FB	1108	G
1	FB	1129	C
1	FB	1134	G
1	FB	1136	U
1	FB	1137	C
1	FB	1139	G
1	FB	1140	C
1	FB	1146	A
1	FB	1151	A
1	FB	1152	A
1	FB	1157	A
1	FB	1159	U
1	FB	1171	G
1	FB	1184	G
1	FB	1193	G
1	FB	1196	U
1	FB	1197	G
1	FB	1199	U
1	FB	1202	G
1	FB	1212	U

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Mol	Chain	Res	Type
1	FB	1213	A
1	FB	1225	A
1	FB	1227	A
1	FB	1236	A
1	FB	1238	A
1	FB	1240	U
1	FB	1257	U
1	FB	1258	G
1	FB	1263	C
1	FB	1270	C
1	FB	1280	A
1	FB	1281	U
1	FB	1282	C
1	FB	1287	A
1	FB	1297	C
1	FB	1299	A
1	FB	1302	U
1	FB	1305	G
1	FB	1317	C
1	FB	1319	A
1	FB	1320	C
1	FB	1322	C
1	FB	1346	A
1	FB	1347	G
1	FB	1353	G
1	FB	1362(B)	C
1	FB	1364	U
1	FB	1368	G
1	FB	1370	G
1	FB	1397	C
1	FB	1398	A
1	FB	1419	G
1	FB	1442	G
1	FB	1453	G
1	FB	1454	G
1	FB	1460	A
1	FB	1487	G
1	FB	1492	A
1	FB	1497	G
1	FB	1504	G
1	FB	1506	U
1	FB	1517	G

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Mol	Chain	Res	Type
1	FB	1529	G
1	FB	1530	G
1	FB	1532	U
2	GB	14	A
2	GB	15	G
2	GB	34	C
2	GB	35	G
2	GB	46	C
2	GB	58	G
2	GB	71	A
2	GB	74	A
2	GB	75	G
2	GB	93	C
2	GB	118	A
2	GB	119	A
2	GB	120	U
2	GB	125	G
2	GB	135	G
2	GB	140	A
2	GB	149	A
2	GB	154(A)	C
2	GB	155	C
2	GB	161	U
2	GB	163	U
2	GB	164	U
2	GB	181	A
2	GB	188	G
2	GB	196	A
2	GB	199	A
2	GB	205	G
2	GB	214	G
2	GB	215	G
2	GB	216	A
2	GB	221	A
2	GB	222	A
2	GB	228	A
2	GB	229	A
2	GB	233	A
2	GB	248	G
2	GB	249	C
2	GB	250	G
2	GB	266	G

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Mol	Chain	Res	Type
2	GB	269	U
2	GB	270(L)	C
2	GB	270(M)	U
2	GB	270(N)	U
2	GB	270(O)	G
2	GB	270(P)	U
2	GB	270(Q)	C
2	GB	271(C)	G
2	GB	271(D)	U
2	GB	271	G
2	GB	273(G)	C
2	GB	278	A
2	GB	283	A
2	GB	311	A
2	GB	312	G
2	GB	317	G
2	GB	324	A
2	GB	329	G
2	GB	330	A
2	GB	352	G
2	GB	353	G
2	GB	363(A)	G
2	GB	363(G)	A
2	GB	372	G
2	GB	386	G
2	GB	396	G
2	GB	405	U
2	GB	407	G
2	GB	411	G
2	GB	412	A
2	GB	442	G
2	GB	443	A
2	GB	444	C
2	GB	455	C
2	GB	456	C
2	GB	457	A
2	GB	479	A
2	GB	481	G
2	GB	494	G
2	GB	504	U
2	GB	505	A
2	GB	508	G

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Mol	Chain	Res	Type
2	GB	509	C
2	GB	510	C
2	GB	529	A
2	GB	531	C
2	GB	532	A
2	GB	533	G
2	GB	563	G
2	GB	571	A
2	GB	573	G
2	GB	575	A
2	GB	603	A
2	GB	604	G
2	GB	607	U
2	GB	615	G
2	GB	616	A
2	GB	617	G
2	GB	627	A
2	GB	637	A
2	GB	645	C
2	GB	646	A
2	GB	654	U
2	GB	664	C
2	GB	686	G
2	GB	717	G
2	GB	730	C
2	GB	765	G
2	GB	775	G
2	GB	776	G
2	GB	782	A
2	GB	784	A
2	GB	785	G
2	GB	792	G
2	GB	805	G
2	GB	812	C
2	GB	819	A
2	GB	827	U
2	GB	828	U
2	GB	855	G
2	GB	859	G
2	GB	869	G
2	GB	878	A
2	GB	879	G

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Mol	Chain	Res	Type
2	GB	886	C
2	GB	887	A
2	GB	888	C
2	GB	890	A
2	GB	893	C
2	GB	894	C
2	GB	895	U
2	GB	896	A
2	GB	907	U
2	GB	910	A
2	GB	917	A
2	GB	932	G
2	GB	941	A
2	GB	945	A
2	GB	946	G
2	GB	959	A
2	GB	961	C
2	GB	974(A)	G
2	GB	974(B)	C
2	GB	983	A
2	GB	989	G
2	GB	996	A
2	GB	1012	U
2	GB	1013	C
2	GB	1022	G
2	GB	1025	G
2	GB	1026	U
2	GB	1033	U
2	GB	1042	G
2	GB	1044	G
2	GB	1045	A
2	GB	1046	A
2	GB	1047	G
2	GB	1054	A
2	GB	1057	A
2	GB	1058	G
2	GB	1059	G
2	GB	1060	U
2	GB	1061	U
2	GB	1062	G
2	GB	1066	U
2	GB	1068	G

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Mol	Chain	Res	Type
2	GB	1069	A
2	GB	1070	A
2	GB	1071	G
2	GB	1072	C
2	GB	1073	A
2	GB	1075	C
2	GB	1076	C
2	GB	1077	A
2	GB	1078	U
2	GB	1079	C
2	GB	1081	U
2	GB	1082	U
2	GB	1083	U
2	GB	1085	A
2	GB	1086	A
2	GB	1088	A
2	GB	1089	G
2	GB	1090	U
2	GB	1091	G
2	GB	1094	U
2	GB	1097	U
2	GB	1098	A
2	GB	1101	U
2	GB	1107	G
2	GB	1111	A
2	GB	1112	G
2	GB	1122	G
2	GB	1126	A
2	GB	1129	A
2	GB	1130	U
2	GB	1135	C
2	GB	1136	G
2	GB	1139	G
2	GB	1142(B)	A
2	GB	1143	A
2	GB	1155	A
2	GB	1174	A
2	GB	1175	U
2	GB	1177	A
2	GB	1205	U
2	GB	1210	A
2	GB	1211	U

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Mol	Chain	Res	Type
2	GB	1218	C
2	GB	1220	A
2	GB	1253	A
2	GB	1256	G
2	GB	1271	G
2	GB	1272	A
2	GB	1273	U
2	GB	1300	U
2	GB	1301	A
2	GB	1313	U
2	GB	1359	A
2	GB	1360	A
2	GB	1365	A
2	GB	1380	G
2	GB	1385	G
2	GB	1395	A
2	GB	1416	G
2	GB	1417	C
2	GB	1419	A
2	GB	1420	U
2	GB	1421	G
2	GB	1428	C
2	GB	1444(B)	A
2	GB	1449(B)	A
2	GB	1459	G
2	GB	1460	A
2	GB	1461	G
2	GB	1467	C
2	GB	1471	A
2	GB	1483	G
2	GB	1493	C
2	GB	1494	A
2	GB	1497	U
2	GB	1508	A
2	GB	1510	A
2	GB	1511	A
2	GB	1512	G
2	GB	1513	C
2	GB	1532	C
2	GB	1534	G
2	GB	1535	U
2	GB	1537	C

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Mol	Chain	Res	Type
2	GB	1538	G
2	GB	1544	C
2	GB	1547	C
2	GB	1558	A
2	GB	1559	G
2	GB	1566	A
2	GB	1569	A
2	GB	1578	U
2	GB	1580	A
2	GB	1585	C
2	GB	1587	A
2	GB	1595	G
2	GB	1608	A
2	GB	1609	A
2	GB	1610	A
2	GB	1631	A
2	GB	1647	G
2	GB	1648	C
2	GB	1649	G
2	GB	1654	A
2	GB	1667	G
2	GB	1674	G
2	GB	1700	A
2	GB	1701	A
2	GB	1729	A
2	GB	1730	U
2	GB	1731	G
2	GB	1743	G
2	GB	1762	A
2	GB	1763	G
2	GB	1764	G
2	GB	1773	A
2	GB	1776	G
2	GB	1781	C
2	GB	1791	A
2	GB	1800	C
2	GB	1801	G
2	GB	1811	G
2	GB	1816	G
2	GB	1829	A
2	GB	1835	G
2	GB	1839	G

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Mol	Chain	Res	Type
2	GB	1847	A
2	GB	1859	A
2	GB	1872	A
2	GB	1878	G
2	GB	1900	A
2	GB	1903	G
2	GB	1905	C
2	GB	1906	G
2	GB	1913	A
2	GB	1914	C
2	GB	1929	G
2	GB	1930	G
2	GB	1936	A
2	GB	1940	U
2	GB	1955	U
2	GB	1963	U
2	GB	1965	C
2	GB	1967	C
2	GB	1970	A
2	GB	1971	A
2	GB	1972	A
2	GB	1984	G
2	GB	1992	G
2	GB	1993	U
2	GB	1997	G
2	GB	2020	A
2	GB	2023	G
2	GB	2031	A
2	GB	2032	G
2	GB	2033	A
2	GB	2043	C
2	GB	2055	C
2	GB	2056	G
2	GB	2060	A
2	GB	2061	G
2	GB	2062	A
2	GB	2063	C
2	GB	2069	G
2	GB	2093	G
2	GB	2100	G
2	GB	2110	G
2	GB	2113	U

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Mol	Chain	Res	Type
2	GB	2116	G
2	GB	2117	A
2	GB	2118	U
2	GB	2119	A
2	GB	2122	U
2	GB	2125	G
2	GB	2126	A
2	GB	2127	G
2	GB	2130	U
2	GB	2131	G
2	GB	2132	U
2	GB	2133	G
2	GB	2134	A
2	GB	2136	C
2	GB	2137	C
2	GB	2138	C
2	GB	2142	C
2	GB	2145	C
2	GB	2146	C
2	GB	2147	G
2	GB	2148	G
2	GB	2152	G
2	GB	2162	G
2	GB	2164	C
2	GB	2165	G
2	GB	2166	G
2	GB	2167	U
2	GB	2169	A
2	GB	2171	A
2	GB	2172	U
2	GB	2173	A
2	GB	2176	A
2	GB	2187	G
2	GB	2189	U
2	GB	2198	A
2	GB	2210	G
2	GB	2211	G
2	GB	2212	A
2	GB	2213	U
2	GB	2225	A
2	GB	2226	C
2	GB	2238	G

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Mol	Chain	Res	Type
2	GB	2239	G
2	GB	2243	U
2	GB	2269	A
2	GB	2275	C
2	GB	2278	A
2	GB	2279	G
2	GB	2283	C
2	GB	2287	A
2	GB	2288	A
2	GB	2305	A
2	GB	2308	G
2	GB	2309	A
2	GB	2311	A
2	GB	2312	U
2	GB	2319	G
2	GB	2320	A
2	GB	2321	G
2	GB	2322	A
2	GB	2325	G
2	GB	2327	A
2	GB	2334	G
2	GB	2336	A
2	GB	2347	C
2	GB	2383	G
2	GB	2385	C
2	GB	2396	G
2	GB	2401	U
2	GB	2406	U
2	GB	2422	A
2	GB	2424	C
2	GB	2425	A
2	GB	2429	G
2	GB	2430	A
2	GB	2435	A
2	GB	2439	A
2	GB	2440	C
2	GB	2441	C
2	GB	2448	A
2	GB	2476	A
2	GB	2477	C
2	GB	2502	G
2	GB	2505	G

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Mol	Chain	Res	Type
2	GB	2506	U
2	GB	2518	A
2	GB	2525	G
2	GB	2529	G
2	GB	2554	U
2	GB	2566	A
2	GB	2567	G
2	GB	2573	C
2	GB	2574	G
2	GB	2596	U
2	GB	2602	A
2	GB	2609	U
2	GB	2611	U
2	GB	2612	C
2	GB	2615	U
2	GB	2630	G
2	GB	2663	G
2	GB	2682	U
2	GB	2683	C
2	GB	2689	U
2	GB	2690	C
2	GB	2691	C
2	GB	2703	C
2	GB	2712(A)	A
2	GB	2713	A
2	GB	2714	G
2	GB	2718	G
2	GB	2726	U
2	GB	2733	A
2	GB	2751	G
2	GB	2757	A
2	GB	2758	A
2	GB	2764	A
2	GB	2765	A
2	GB	2766	G
2	GB	2778	A
2	GB	2789	C
2	GB	2790	A
2	GB	2791	C
2	GB	2793	G
2	GB	2794	C
2	GB	2797	U

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Mol	Chain	Res	Type
2	GB	2798	C
2	GB	2799	A
2	GB	2801	A
2	GB	2802	G
2	GB	2805	G
2	GB	2807	G
2	GB	2818	G
2	GB	2820	A
2	GB	2821	A
2	GB	2835	A
2	GB	2836	U
2	GB	2872	G
2	GB	2879	C
2	GB	2880	C
2	GB	2892	A
2	GB	2894	G
3	HB	2	C
3	HB	9	G
3	HB	12	C
3	HB	25	A
3	HB	30	C
3	HB	35	U
3	HB	45	A
3	HB	56	G
3	HB	66	A
3	HB	73	A
3	HB	74	U
3	HB	89(B)	A
3	HB	90	C
3	HB	109	G
3	HB	111	U
3	HB	119	A
4	IB	7	G
4	IB	8	4SU
4	IB	16	C
4	IB	17(A)	U
4	IB	19	G
4	IB	20	U
4	IB	22	G
4	IB	35	A
4	IB	36	U
4	IB	37	A

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Mol	Chain	Res	Type
4	IB	46	G
4	IB	47	U
4	IB	48	C
4	IB	58	A
4	IB	61	C
34	MC	14	A
34	MC	16	A
34	MC	21	A
34	MC	22	A
4	NC	10	G
4	NC	18	G
4	NC	20	U
4	NC	47	U
4	NC	48	C
4	NC	52	G
4	NC	76	A

All (71) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	115	G
1	A	509	A
1	A	560	U
1	A	687	A
1	A	723	U
1	A	748	C
1	A	793	U
1	A	842	C
1	A	913	A
1	A	1201	A
1	A	1491	G
2	B	34	C
2	B	196	A
2	B	277	C
2	B	507	A
2	B	528	A
2	B	645	C
2	B	774	A
2	B	784	A
2	B	893	C
2	B	974(A)	G
2	B	1060	U

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Mol	Chain	Res	Type
2	B	1210	A
2	B	1379	A
2	B	1396	U
2	B	1420	U
2	B	1531	C
2	B	1608	A
2	B	1992	G
2	B	2062	A
2	B	2136	C
2	B	2439	A
2	B	2518	A
2	B	2611	U
2	B	2756	U
3	C	65	C
4	IA	19	G
1	FB	115	G
1	FB	509	A
1	FB	560	U
1	FB	687	A
1	FB	723	U
1	FB	748	C
1	FB	793	U
1	FB	842	C
1	FB	913	A
1	FB	1201	A
1	FB	1491	G
2	GB	34	C
2	GB	277	C
2	GB	507	A
2	GB	528	A
2	GB	645	C
2	GB	784	A
2	GB	893	C
2	GB	974(A)	G
2	GB	1060	U
2	GB	1210	A
2	GB	1379	A
2	GB	1396	U
2	GB	1420	U
2	GB	1531	C
2	GB	1608	A
2	GB	1992	G

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Mol	Chain	Res	Type
2	GB	2062	A
2	GB	2136	C
2	GB	2439	A
2	GB	2611	U
2	GB	2756	U
3	HB	65	C
4	NC	19	G

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

66 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	PSU	IA	55	4	18,21,22	1.71	2 (11%)	21,30,33	1.85	4 (19%)
2	PSU	GB	2605	2	18,21,22	1.58	3 (16%)	21,30,33	1.59	5 (23%)
1	2MG	A	1207	1	23,26,27	2.24	3 (13%)	33,38,41	2.05	10 (30%)
2	OMG	GB	2251	4,2	23,26,27	2.01	3 (13%)	32,38,41	1.93	9 (28%)
1	5MC	A	1400	1	19,22,23	2.60	4 (21%)	26,32,35	1.09	2 (7%)
1	M2G	FB	966	1	24,27,28	2.23	4 (16%)	33,40,43	1.91	8 (24%)
2	4OC	GB	1920	2	19,22,24	1.13	1 (5%)	25,31,35	1.07	1 (4%)
2	4OC	B	1920	56,2	19,22,24	1.12	1 (5%)	25,31,35	1.11	1 (4%)
1	5MC	FB	1407	1	19,22,23	2.75	4 (21%)	26,32,35	1.06	2 (7%)
1	MA6	A	1519	1	23,26,27	1.57	4 (17%)	33,38,41	2.12	10 (30%)
2	PSU	GB	1911	2	18,21,22	1.63	2 (11%)	21,30,33	1.89	6 (28%)
1	5MC	FB	1400	1	19,22,23	2.53	4 (21%)	26,32,35	1.01	2 (7%)
2	2MA	B	2503	2	22,25,26	1.73	4 (18%)	32,37,40	2.14	7 (21%)
4	5MU	D	54	4	19,22,23	2.08	3 (15%)	27,32,35	2.01	7 (25%)
4	5MC	IB	32	4	19,22,23	2.66	5 (26%)	26,32,35	1.04	2 (7%)
46	0TD	ZC	92	46	8,9,10	2.80	2 (25%)	6,11,13	2.59	3 (50%)
2	5MU	GB	1939	56,2	19,22,23	2.27	3 (15%)	27,32,35	2.57	7 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PSU	NC	55	4	18,21,22	1.85	3 (16%)	21,30,33	1.69	2 (9%)
2	OMG	B	2251	4,2	23,26,27	2.08	3 (13%)	32,38,41	1.99	9 (28%)
2	2MU	B	2552	56,2	19,22,24	2.68	7 (36%)	25,31,36	2.43	8 (32%)
1	MA6	FB	1519	1	23,26,27	1.44	3 (13%)	33,38,41	2.18	11 (33%)
2	PSU	GB	1917	2	18,21,22	1.76	2 (11%)	21,30,33	1.87	5 (23%)
2	5MC	GB	1962	2	19,22,23	2.82	5 (26%)	26,32,35	1.09	2 (7%)
2	PSU	B	1911	2	18,21,22	1.66	2 (11%)	21,30,33	1.63	4 (19%)
1	PSU	FB	516	1	18,21,22	1.52	2 (11%)	21,30,33	1.60	4 (19%)
4	4SU	D	8	4	18,21,22	5.79	1 (5%)	25,30,33	0.67	0
1	2MG	FB	1207	1	23,26,27	2.20	3 (13%)	33,38,41	2.06	10 (30%)
4	5MU	IB	54	4	19,22,23	2.08	3 (15%)	27,32,35	2.02	8 (29%)
1	UR3	A	1498	1,56	19,22,23	1.73	1 (5%)	26,32,35	1.61	3 (11%)
1	M2G	A	966	1	24,27,28	2.31	4 (16%)	33,40,43	1.93	8 (24%)
2	2MA	GB	2503	2	22,25,26	1.81	5 (22%)	32,37,40	2.09	8 (25%)
4	5MC	D	32	4	19,22,23	2.71	5 (26%)	26,32,35	0.97	2 (7%)
2	5MU	B	1939	56,2	19,22,23	2.11	2 (10%)	27,32,35	2.51	8 (29%)
2	5MC	B	1942	56,2	19,22,23	2.81	4 (21%)	26,32,35	1.37	4 (15%)
4	5MC	NC	32	4	19,22,23	2.60	4 (21%)	26,32,35	1.20	3 (11%)
4	5MU	IA	54	4,56	19,22,23	2.09	3 (15%)	27,32,35	2.19	10 (37%)
1	5MC	A	1404	1	19,22,23	2.75	4 (21%)	26,32,35	1.24	2 (7%)
1	7MG	A	527	1,56	23,26,27	2.96	7 (30%)	27,39,42	2.12	9 (33%)
4	4SU	IB	8	4	18,21,22	5.86	1 (5%)	25,30,33	0.63	0
1	UR3	FB	1498	1,56	19,22,23	1.75	1 (5%)	26,32,35	1.62	3 (11%)
1	PSU	A	516	1	18,21,22	1.52	2 (11%)	21,30,33	1.66	5 (23%)
2	5MU	GB	1915	2	19,22,23	2.10	3 (15%)	27,32,35	2.13	7 (25%)
2	2MU	GB	2552	56,2	19,22,24	2.55	3 (15%)	25,31,36	2.26	8 (32%)
1	5MC	FB	1404	1	19,22,23	2.96	4 (21%)	26,32,35	1.20	2 (7%)
1	4OC	A	1402	1	20,23,24	1.16	2 (10%)	25,32,35	1.04	1 (4%)
2	PSU	B	1917	2	18,21,22	1.63	2 (11%)	21,30,33	1.76	5 (23%)
4	PSU	D	55	4	18,21,22	1.77	3 (16%)	21,30,33	1.61	2 (9%)
2	5MC	B	1962	56,2	19,22,23	2.83	4 (21%)	26,32,35	1.25	2 (7%)
2	5MU	B	1915	2	19,22,23	1.98	3 (15%)	27,32,35	2.45	5 (18%)
1	MA6	A	1518	1	23,26,27	1.47	3 (13%)	33,38,41	2.19	9 (27%)
2	PSU	B	2605	2	18,21,22	1.59	2 (11%)	21,30,33	1.71	4 (19%)
4	5MC	IA	32	4	19,22,23	2.53	4 (21%)	26,32,35	1.17	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	A	967	1	19,22,23	2.76	5 (26%)	26,32,35	1.10	1 (3%)
4	5MU	NC	54	4	19,22,23	2.12	3 (15%)	27,32,35	2.07	9 (33%)
46	0TD	UA	92	46	8,9,10	2.32	2 (25%)	6,11,13	2.62	3 (50%)
34	PSU	MC	19	34,56	18,21,22	1.68	2 (11%)	21,30,33	1.89	7 (33%)
2	5MC	GB	1942	2	19,22,23	2.70	4 (21%)	26,32,35	1.47	4 (15%)
1	7MG	FB	527	1	23,26,27	2.95	7 (30%)	27,39,42	2.14	10 (37%)
1	4OC	FB	1402	1,56	20,23,24	1.07	2 (10%)	25,32,35	1.11	3 (12%)
1	5MC	A	1407	1	19,22,23	2.64	4 (21%)	26,32,35	1.16	2 (7%)
1	5MC	FB	967	1	19,22,23	2.41	5 (26%)	26,32,35	1.16	3 (11%)
1	MA6	FB	1518	1	23,26,27	1.50	2 (8%)	33,38,41	2.10	9 (27%)
4	4SU	NC	8	4	18,21,22	5.77	1 (5%)	25,30,33	0.97	1 (4%)
34	PSU	HA	19	34	18,21,22	1.64	2 (11%)	21,30,33	1.93	6 (28%)
4	PSU	IB	55	4	18,21,22	1.73	3 (16%)	21,30,33	1.61	3 (14%)
4	4SU	IA	8	4	18,21,22	5.80	1 (5%)	25,30,33	0.94	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PSU	IA	55	4	-	0/7/25/26	0/2/2/2
2	PSU	GB	2605	2	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
2	OMG	GB	2251	4,2	-	1/9/27/28	0/3/3/3
1	5MC	A	1400	1	-	1/7/25/26	0/2/2/2
1	M2G	FB	966	1	-	0/11/29/30	0/3/3/3
2	4OC	GB	1920	2	-	0/9/27/30	0/2/2/2
2	4OC	B	1920	56,2	-	1/9/27/30	0/2/2/2
1	5MC	FB	1407	1	-	0/7/25/26	0/2/2/2
1	MA6	A	1519	1	-	4/11/29/30	0/3/3/3
2	PSU	GB	1911	2	-	0/7/25/26	0/2/2/2
1	5MC	FB	1400	1	-	1/7/25/26	0/2/2/2
2	2MA	B	2503	2	-	1/7/25/26	0/3/3/3
4	5MU	D	54	4	-	0/7/25/26	0/2/2/2
4	5MC	IB	32	4	-	0/7/25/26	0/2/2/2
46	0TD	ZC	92	46	-	2/7/12/14	-
2	5MU	GB	1939	56,2	-	0/7/25/26	0/2/2/2
4	PSU	NC	55	4	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	B	2251	4,2	-	1/9/27/28	0/3/3/3
2	2MU	B	2552	56,2	-	2/9/27/28	0/2/2/2
1	MA6	FB	1519	1	-	4/11/29/30	0/3/3/3
2	PSU	GB	1917	2	-	0/7/25/26	0/2/2/2
2	5MC	GB	1962	2	-	2/7/25/26	0/2/2/2
2	PSU	B	1911	2	-	0/7/25/26	0/2/2/2
1	PSU	FB	516	1	-	0/7/25/26	0/2/2/2
4	4SU	D	8	4	-	0/7/25/26	0/2/2/2
1	2MG	FB	1207	1	-	0/9/27/28	0/3/3/3
4	5MU	IB	54	4	-	0/7/25/26	0/2/2/2
1	UR3	A	1498	1,56	-	0/7/25/26	0/2/2/2
1	M2G	A	966	1	-	0/11/29/30	0/3/3/3
2	2MA	GB	2503	2	-	1/7/25/26	0/3/3/3
4	5MC	D	32	4	-	0/7/25/26	0/2/2/2
2	5MU	B	1939	56,2	-	0/7/25/26	0/2/2/2
2	5MC	B	1942	56,2	-	0/7/25/26	0/2/2/2
4	5MC	NC	32	4	-	0/7/25/26	0/2/2/2
4	5MU	IA	54	4,56	-	0/7/25/26	0/2/2/2
1	5MC	A	1404	1	-	0/7/25/26	0/2/2/2
1	7MG	A	527	1,56	-	1/7/37/38	0/3/3/3
4	4SU	IB	8	4	-	0/7/25/26	0/2/2/2
1	UR3	FB	1498	1,56	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1	-	0/7/25/26	0/2/2/2
2	5MU	GB	1915	2	-	0/7/25/26	0/2/2/2
2	2MU	GB	2552	56,2	-	2/9/27/28	0/2/2/2
1	5MC	FB	1404	1	-	0/7/25/26	0/2/2/2
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
2	PSU	B	1917	2	-	0/7/25/26	0/2/2/2
4	PSU	D	55	4	-	0/7/25/26	0/2/2/2
2	5MC	B	1962	56,2	-	2/7/25/26	0/2/2/2
2	5MU	B	1915	2	-	0/7/25/26	0/2/2/2
1	MA6	A	1518	1	-	0/11/29/30	0/3/3/3
2	PSU	B	2605	2	-	0/7/25/26	0/2/2/2
4	5MC	IA	32	4	-	0/7/25/26	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
4	5MU	NC	54	4	-	0/7/25/26	0/2/2/2
46	0TD	UA	92	46	-	2/7/12/14	-
34	PSU	MC	19	34,56	-	0/7/25/26	0/2/2/2
2	5MC	GB	1942	2	-	0/7/25/26	0/2/2/2
1	7MG	FB	527	1	-	1/7/37/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	4OC	FB	1402	1,56	-	2/9/29/30	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	5MC	FB	967	1	-	0/7/25/26	0/2/2/2
1	MA6	FB	1518	1	-	0/11/29/30	0/3/3/3
4	4SU	NC	8	4	-	0/7/25/26	0/2/2/2
34	PSU	HA	19	34	-	0/7/25/26	0/2/2/2
4	PSU	IB	55	4	-	0/7/25/26	0/2/2/2
4	4SU	IA	8	4	-	0/7/25/26	0/2/2/2

All (205) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	IB	8	4SU	C4-S4	-24.80	1.24	1.68
4	IA	8	4SU	C4-S4	-24.51	1.24	1.68
4	D	8	4SU	C4-S4	-24.49	1.24	1.68
4	NC	8	4SU	C4-S4	-24.42	1.25	1.68
1	FB	1404	5MC	C5-C4	-10.88	1.35	1.44
2	B	1962	5MC	C5-C4	-10.38	1.36	1.44
2	B	1942	5MC	C5-C4	-10.27	1.36	1.44
1	A	527	7MG	O6-C6	10.18	1.42	1.23
1	FB	1407	5MC	C5-C4	-10.06	1.36	1.44
1	FB	527	7MG	O6-C6	10.04	1.42	1.23
2	GB	1962	5MC	C5-C4	-9.99	1.36	1.44
1	A	967	5MC	C5-C4	-9.69	1.36	1.44
2	GB	1942	5MC	C5-C4	-9.42	1.37	1.44
1	A	1404	5MC	C5-C4	-9.36	1.37	1.44
4	D	32	5MC	C5-C4	-9.32	1.37	1.44
1	A	1407	5MC	C5-C4	-9.25	1.37	1.44
1	A	1207	2MG	O6-C6	9.07	1.40	1.23
1	A	966	M2G	O6-C6	9.04	1.40	1.23
4	IB	32	5MC	C5-C4	-9.01	1.37	1.44
1	FB	1207	2MG	O6-C6	8.89	1.40	1.23
1	A	1400	5MC	C5-C4	-8.85	1.37	1.44
1	FB	966	M2G	O6-C6	8.79	1.40	1.23
4	NC	32	5MC	C5-C4	-8.79	1.37	1.44
1	FB	1400	5MC	C5-C4	-8.77	1.37	1.44
2	GB	2552	2MU	O4-C4	8.21	1.40	1.24
2	B	2552	2MU	O4-C4	8.15	1.40	1.24
4	IA	32	5MC	C5-C4	-7.99	1.38	1.44
2	B	2251	OMG	O6-C6	7.93	1.38	1.23
2	GB	2251	OMG	O6-C6	7.83	1.38	1.23
1	FB	967	5MC	C5-C4	-7.63	1.38	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	FB	527	7MG	C5-N7	7.04	1.44	1.35
4	NC	54	5MU	O4-C4	7.02	1.36	1.23
1	FB	1498	UR3	O4-C4	6.80	1.38	1.23
1	A	527	7MG	C5-N7	6.78	1.44	1.35
1	A	1498	UR3	O4-C4	6.75	1.38	1.23
4	IA	54	5MU	O4-C4	6.63	1.36	1.23
2	GB	1939	5MU	C4-C5	-6.59	1.34	1.44
4	D	54	5MU	O4-C4	6.32	1.35	1.23
4	IB	54	5MU	O4-C4	6.16	1.35	1.23
2	GB	1939	5MU	O4-C4	6.16	1.35	1.23
2	B	1939	5MU	C4-C5	-6.08	1.34	1.44
2	B	1939	5MU	O4-C4	6.04	1.35	1.23
2	GB	1915	5MU	O4-C4	5.96	1.34	1.23
2	B	1915	5MU	C4-C5	-5.93	1.35	1.44
4	NC	55	PSU	C6-C5	5.90	1.41	1.35
46	ZC	92	0TD	CB-CA	-5.82	1.52	1.54
2	GB	1915	5MU	C4-C5	-5.78	1.35	1.44
4	D	55	PSU	C6-C5	5.74	1.41	1.35
4	IB	55	PSU	C6-C5	5.68	1.41	1.35
2	GB	1917	PSU	C6-C5	5.67	1.41	1.35
4	IA	55	PSU	C6-C5	5.57	1.41	1.35
4	IB	54	5MU	C4-C5	-5.56	1.35	1.44
34	MC	19	PSU	C6-C5	5.49	1.41	1.35
34	HA	19	PSU	C6-C5	5.46	1.41	1.35
2	B	2503	2MA	C8-N7	5.42	1.42	1.31
2	B	1911	PSU	C6-C5	5.42	1.41	1.35
2	GB	2503	2MA	C8-N7	5.41	1.42	1.31
4	D	54	5MU	C4-C5	-5.39	1.36	1.44
2	B	1915	5MU	O4-C4	5.18	1.33	1.23
2	B	1917	PSU	C6-C5	5.17	1.41	1.35
2	B	2552	2MU	C3'-C2'	-5.10	1.41	1.53
1	A	966	M2G	C2-N2	5.09	1.44	1.35
4	IA	54	5MU	C4-C5	-5.04	1.36	1.44
2	GB	1911	PSU	C6-C5	5.02	1.40	1.35
2	GB	2552	2MU	C3'-C2'	-4.93	1.42	1.53
4	NC	54	5MU	C4-C5	-4.88	1.36	1.44
2	GB	2605	PSU	C6-C5	4.87	1.40	1.35
2	B	2605	PSU	C6-C5	4.75	1.40	1.35
1	FB	966	M2G	C2-N2	4.71	1.43	1.35
1	A	516	PSU	C6-C5	4.65	1.40	1.35
1	FB	516	PSU	C6-C5	4.60	1.40	1.35
1	A	1519	MA6	C6-N6	4.45	1.49	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	IA	32	5MC	C6-C5	4.44	1.41	1.34
4	IA	32	5MC	C4-N4	4.43	1.45	1.34
1	A	1404	5MC	C4-N4	4.41	1.45	1.34
4	NC	32	5MC	C4-N4	4.34	1.45	1.34
1	FB	1518	MA6	C6-N6	4.31	1.48	1.36
1	A	1400	5MC	C6-C5	4.29	1.41	1.34
1	FB	967	5MC	C4-N4	4.28	1.45	1.34
46	ZC	92	0TD	CB-SB	-4.25	1.78	1.82
46	UA	92	0TD	CB-CA	-4.25	1.53	1.54
4	D	32	5MC	C4-N4	4.24	1.45	1.34
4	D	32	5MC	C6-C5	4.19	1.41	1.34
4	IB	32	5MC	C6-C5	4.19	1.41	1.34
4	IB	32	5MC	C4-N4	4.18	1.44	1.34
4	NC	32	5MC	C6-C5	4.17	1.41	1.34
1	A	1404	5MC	C6-C5	4.07	1.41	1.34
2	B	2503	2MA	C2-N1	4.06	1.41	1.34
1	A	1400	5MC	C4-N4	4.05	1.44	1.34
1	A	967	5MC	C4-N4	4.04	1.44	1.34
2	GB	1962	5MC	C4-N4	4.01	1.44	1.34
2	B	1962	5MC	C4-N4	3.97	1.44	1.34
1	A	1207	2MG	C2-N2	3.96	1.41	1.33
1	A	1518	MA6	C6-N6	3.95	1.47	1.36
2	GB	1942	5MC	C4-N4	3.95	1.44	1.34
2	B	1962	5MC	C6-N1	-3.95	1.31	1.38
1	FB	1400	5MC	C4-N4	3.93	1.44	1.34
1	FB	1519	MA6	C6-N6	3.93	1.47	1.36
1	FB	1404	5MC	C4-N4	3.92	1.44	1.34
1	A	1518	MA6	C4-N3	3.91	1.41	1.34
2	GB	1942	5MC	C6-N1	-3.91	1.31	1.38
1	A	1407	5MC	C6-C5	3.88	1.40	1.34
2	GB	2503	2MA	C2-N1	3.87	1.40	1.34
1	A	1519	MA6	C4-N3	3.87	1.41	1.34
1	FB	1207	2MG	C2-N2	3.87	1.41	1.33
1	FB	1518	MA6	C4-N3	3.83	1.41	1.34
46	UA	92	0TD	CB-SB	-3.80	1.78	1.82
2	B	1942	5MC	C4-N4	3.77	1.43	1.34
1	FB	1404	5MC	C6-C5	3.74	1.40	1.34
2	GB	2251	OMG	C2-N2	3.73	1.42	1.34
1	A	1407	5MC	C4-N4	3.72	1.43	1.34
2	B	2251	OMG	C2-N2	3.72	1.42	1.34
1	FB	1407	5MC	C4-N4	3.72	1.43	1.34
1	FB	1519	MA6	C4-N3	3.66	1.41	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	FB	967	5MC	C6-C5	3.65	1.40	1.34
2	GB	1962	5MC	C6-N1	-3.65	1.31	1.38
1	A	527	7MG	C2-N2	3.63	1.42	1.34
1	A	967	5MC	C6-C5	3.61	1.40	1.34
2	B	1942	5MC	C6-N1	-3.61	1.31	1.38
1	FB	1404	5MC	C6-N1	-3.54	1.32	1.38
1	FB	1407	5MC	C6-C5	3.52	1.40	1.34
1	FB	1400	5MC	C6-C5	3.51	1.40	1.34
2	GB	1920	4OC	C4-N4	3.50	1.42	1.33
1	A	1404	5MC	C6-N1	-3.45	1.32	1.38
2	GB	1962	5MC	C6-C5	3.41	1.40	1.34
1	A	967	5MC	C6-N1	-3.41	1.32	1.38
1	FB	527	7MG	C8-N9	-3.40	1.43	1.45
1	FB	1407	5MC	C6-N1	-3.40	1.32	1.38
1	A	1407	5MC	C6-N1	-3.37	1.32	1.38
1	FB	967	5MC	C6-N1	-3.35	1.32	1.38
2	B	1920	4OC	C4-N4	3.34	1.42	1.33
2	B	1942	5MC	C6-C5	3.30	1.40	1.34
1	A	1402	4OC	C4-N4	3.27	1.42	1.36
1	A	527	7MG	C4-N9	3.26	1.41	1.37
2	B	2605	PSU	C6-N1	3.23	1.41	1.36
1	FB	527	7MG	C2-N2	3.20	1.41	1.34
2	GB	1942	5MC	C6-C5	3.17	1.39	1.34
4	IA	32	5MC	C6-N1	-3.14	1.32	1.38
4	D	55	PSU	C6-N1	3.14	1.41	1.36
1	FB	1400	5MC	C6-N1	-3.12	1.32	1.38
1	FB	527	7MG	C4-N9	3.12	1.41	1.37
4	NC	32	5MC	C6-N1	-3.10	1.32	1.38
1	FB	1402	4OC	C4-N4	3.07	1.42	1.36
1	A	527	7MG	C8-N9	-3.07	1.43	1.45
4	NC	55	PSU	C6-N1	3.06	1.41	1.36
4	IB	32	5MC	C6-N1	-3.02	1.32	1.38
4	D	32	5MC	C6-N1	-2.95	1.33	1.38
4	IB	55	PSU	C6-N1	2.95	1.41	1.36
2	B	2552	2MU	O3'-C3'	-2.90	1.35	1.43
2	GB	2503	2MA	C5-C4	2.86	1.44	1.39
2	GB	1911	PSU	C6-N1	2.86	1.41	1.36
2	GB	2605	PSU	C6-N1	2.85	1.41	1.36
2	B	2251	OMG	C6-N1	-2.85	1.33	1.38
2	GB	1917	PSU	C6-N1	2.85	1.41	1.36
34	MC	19	PSU	C6-N1	2.78	1.40	1.36
1	A	1402	4OC	C4-N3	2.69	1.37	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C6-N1	-2.68	1.33	1.38
1	A	1400	5MC	C6-N1	-2.67	1.33	1.38
1	FB	527	7MG	C6-N1	-2.66	1.33	1.38
1	FB	1402	4OC	C4-N3	2.65	1.37	1.32
2	B	1917	PSU	C6-N1	2.65	1.40	1.36
4	IB	54	5MU	C6-C5	2.64	1.38	1.34
1	A	1207	2MG	C2-N3	2.64	1.37	1.32
4	IA	55	PSU	C6-N1	2.64	1.40	1.36
1	A	516	PSU	C6-N1	2.62	1.40	1.36
2	B	1962	5MC	C6-C5	2.61	1.38	1.34
1	FB	966	M2G	C4-N3	2.59	1.40	1.34
2	GB	1915	5MU	C6-C5	2.58	1.38	1.34
2	B	1911	PSU	C6-N1	2.58	1.40	1.36
2	GB	2251	OMG	C6-N1	-2.57	1.34	1.38
2	GB	1939	5MU	C2-N1	-2.56	1.34	1.38
2	GB	2503	2MA	C6-N6	2.56	1.40	1.34
1	FB	1519	MA6	C2-N1	2.55	1.38	1.33
2	B	2503	2MA	C5-C4	2.52	1.43	1.39
1	A	966	M2G	C4-N3	2.52	1.40	1.34
2	B	2552	2MU	C3'-C4'	-2.51	1.46	1.53
4	D	54	5MU	C6-C5	2.51	1.38	1.34
1	FB	516	PSU	C6-N1	2.48	1.40	1.36
2	GB	2552	2MU	O3'-C3'	-2.47	1.36	1.43
2	B	2552	2MU	O4'-C4'	-2.45	1.39	1.45
1	FB	1207	2MG	C2-N3	2.39	1.36	1.32
2	B	1915	5MU	C6-C5	2.38	1.38	1.34
2	B	2552	2MU	C4-N3	-2.35	1.34	1.38
2	GB	2503	2MA	C4-N9	2.35	1.42	1.37
4	IA	54	5MU	C6-C5	2.33	1.38	1.34
1	A	527	7MG	C2-N3	2.31	1.38	1.33
34	HA	19	PSU	C6-N1	2.30	1.40	1.36
2	B	2552	2MU	C5'-C4'	-2.29	1.44	1.51
1	FB	527	7MG	C2-N3	2.29	1.38	1.33
2	GB	2605	PSU	C1'-C5	2.28	1.55	1.50
4	NC	54	5MU	C6-C5	2.26	1.38	1.34
1	A	967	5MC	C4-N3	2.26	1.37	1.34
1	FB	967	5MC	C4-N3	2.25	1.37	1.34
4	IB	55	PSU	C1'-C5	2.21	1.55	1.50
1	A	1519	MA6	C2-N1	2.19	1.37	1.33
4	IB	32	5MC	C4-N3	2.15	1.37	1.34
1	A	1518	MA6	C6-N1	2.15	1.38	1.34
4	D	55	PSU	C1'-C5	2.14	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2503	2MA	C4-N9	2.13	1.42	1.37
4	D	32	5MC	C4-N3	2.06	1.37	1.34
1	FB	966	M2G	C6-N1	-2.05	1.35	1.38
1	A	966	M2G	C2-N3	2.05	1.37	1.32
1	A	1519	MA6	C6-N1	2.05	1.38	1.34
4	NC	55	PSU	C2-N1	2.03	1.39	1.36
2	GB	1962	5MC	C4-N3	2.03	1.37	1.34

All (323) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2503	2MA	C5-C4-N3	-8.03	118.72	127.18
2	B	1915	5MU	C5-C4-N3	7.39	121.75	115.32
2	GB	2503	2MA	C5-C4-N3	-6.81	120.00	127.18
1	FB	966	M2G	C5-C4-N3	-6.39	118.21	128.39
2	GB	1939	5MU	C4-N3-C2	-6.31	119.06	127.34
1	A	966	M2G	C5-C4-N3	-6.31	118.35	128.39
2	B	2251	OMG	C5-C4-N3	-6.04	118.77	128.39
2	B	1939	5MU	C4-N3-C2	-6.03	119.44	127.34
2	B	1915	5MU	C4-N3-C2	-5.98	119.50	127.34
1	A	1207	2MG	C2-N3-C4	5.87	119.35	112.00
1	FB	1498	UR3	C4-N3-C2	-5.85	119.87	124.58
1	A	1518	MA6	N1-C2-N3	-5.82	119.77	128.58
1	FB	1207	2MG	C2-N3-C4	5.80	119.26	112.00
2	B	2552	2MU	C4-N3-C2	-5.72	119.51	126.61
2	GB	2251	OMG	C5-C4-N3	-5.66	119.38	128.39
1	A	1498	UR3	C4-N3-C2	-5.63	120.05	124.58
2	GB	1939	5MU	O4-C4-C5	-5.54	118.58	124.92
2	GB	1915	5MU	C5-C4-N3	5.50	120.11	115.32
2	B	1939	5MU	C5-C4-N3	5.38	120.00	115.32
1	FB	1518	MA6	N1-C2-N3	-5.28	120.58	128.58
2	GB	2552	2MU	C4-N3-C2	-5.28	120.06	126.61
1	FB	1519	MA6	C5-C4-N3	-5.28	119.45	126.72
1	A	527	7MG	C2-N3-C4	5.19	121.24	112.30
1	A	966	M2G	N9-C4-N3	5.14	136.23	125.95
1	FB	966	M2G	N9-C4-N3	5.12	136.19	125.95
2	GB	1915	5MU	C4-N3-C2	-5.08	120.67	127.34
2	GB	1939	5MU	C5-C4-N3	5.04	119.71	115.32
1	FB	1207	2MG	C5-C4-N3	-5.01	120.42	128.39
1	A	1519	MA6	C5-C4-N3	-4.98	119.86	126.72
4	IA	54	5MU	C4-N3-C2	-4.98	120.81	127.34
1	A	1207	2MG	C5-C4-N3	-4.95	120.51	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	HA	19	PSU	N1-C2-N3	4.95	120.39	115.17
2	B	1915	5MU	O4-C4-C5	-4.92	119.28	124.92
4	D	54	5MU	C5-C4-N3	4.80	119.49	115.32
34	MC	19	PSU	N1-C2-N3	4.78	120.21	115.17
2	GB	1939	5MU	C5-C6-N1	-4.77	118.14	123.31
1	FB	527	7MG	C5-C6-N1	4.76	119.32	110.94
2	B	1939	5MU	O4-C4-C5	-4.76	119.47	124.92
1	FB	527	7MG	C2-N3-C4	4.75	120.47	112.30
46	UA	92	0TD	CSB-SB-CB	4.73	110.86	102.36
46	ZC	92	0TD	CSB-SB-CB	4.72	110.86	102.36
4	IB	54	5MU	C5-C4-N3	4.72	119.43	115.32
4	IB	54	5MU	C4-N3-C2	-4.70	121.17	127.34
4	D	54	5MU	C4-N3-C2	-4.70	121.18	127.34
2	GB	2552	2MU	O2'-C2'-C1'	4.69	117.89	108.99
4	NC	54	5MU	C4-N3-C2	-4.69	121.20	127.34
1	FB	1519	MA6	C4-C5-N7	-4.67	105.25	110.58
2	B	1939	5MU	C5-C6-N1	-4.66	118.25	123.31
4	IA	54	5MU	N3-C2-N1	4.53	120.78	114.89
1	A	527	7MG	C5-C6-N1	4.52	118.90	110.94
1	A	1518	MA6	C5-C4-N3	-4.52	120.50	126.72
2	B	2251	OMG	C2-N3-C4	4.50	120.05	112.30
2	B	2605	PSU	C4-N3-C2	-4.50	120.18	126.37
2	GB	1911	PSU	N1-C2-N3	4.46	119.88	115.17
2	B	2552	2MU	N3-C2-N1	4.44	120.67	114.89
4	IA	55	PSU	N1-C2-N3	4.42	119.83	115.17
2	GB	1917	PSU	N1-C2-N3	4.41	119.82	115.17
2	B	1917	PSU	N1-C2-N3	4.37	119.77	115.17
1	FB	1518	MA6	C5-C4-N3	-4.35	120.73	126.72
2	GB	1911	PSU	C4-N3-C2	-4.33	120.40	126.37
1	A	1519	MA6	N1-C2-N3	-4.33	122.03	128.58
2	GB	1939	5MU	N3-C2-N1	4.30	120.48	114.89
1	A	516	PSU	C4-N3-C2	-4.26	120.50	126.37
2	B	2503	2MA	N3-C4-N9	4.25	132.38	126.99
2	GB	2251	OMG	C2-N3-C4	4.24	119.61	112.30
1	FB	1518	MA6	C2-N1-C6	4.24	122.19	111.83
2	B	2552	2MU	O2'-C2'-C1'	4.23	117.02	108.99
1	A	1518	MA6	C2-N1-C6	4.22	122.14	111.83
2	B	1962	5MC	C5-C6-N1	-4.16	118.79	123.31
2	GB	1917	PSU	C4-N3-C2	-4.16	120.65	126.37
2	GB	1915	5MU	C5-C6-N1	-4.15	118.81	123.31
4	IA	55	PSU	C4-N3-C2	-4.14	120.67	126.37
2	B	1915	5MU	C5-C6-N1	-4.13	118.83	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	FB	1519	MA6	C5-N7-C8	4.09	109.87	103.45
34	MC	19	PSU	C4-N3-C2	-4.08	120.74	126.37
2	GB	1939	5MU	O2-C2-N1	-4.08	117.49	122.80
2	B	2552	2MU	C5-C4-N3	4.07	120.51	114.80
4	D	55	PSU	C4-N3-C2	-4.05	120.79	126.37
2	B	1911	PSU	N1-C2-N3	4.05	119.44	115.17
4	NC	55	PSU	N1-C2-N3	4.04	119.42	115.17
2	GB	2605	PSU	C4-N3-C2	-4.03	120.82	126.37
1	FB	1519	MA6	N9-C8-N7	-4.03	108.22	113.94
4	NC	55	PSU	C4-N3-C2	-4.02	120.83	126.37
2	GB	1939	5MU	C6-C5-C4	4.00	121.32	118.02
4	IB	55	PSU	N1-C2-N3	4.00	119.38	115.17
2	B	1915	5MU	N3-C2-N1	4.00	120.09	114.89
2	GB	1915	5MU	O4-C4-C5	-3.99	120.35	124.92
4	IA	54	5MU	C5M-C5-C6	-3.98	117.46	122.85
1	A	1518	MA6	N9-C8-N7	-3.98	108.29	113.94
2	GB	2503	2MA	C4-C5-N7	-3.97	106.04	110.58
4	D	55	PSU	N1-C2-N3	3.96	119.34	115.17
4	IB	54	5MU	N3-C2-N1	3.95	120.04	114.89
1	A	1519	MA6	C4-C5-N7	-3.95	106.06	110.58
4	IB	55	PSU	C4-N3-C2	-3.95	120.93	126.37
4	IB	54	5MU	O4-C4-C5	-3.93	120.42	124.92
4	NC	54	5MU	C5-C4-N3	3.92	118.73	115.32
1	FB	527	7MG	N9-C4-N3	3.91	131.20	125.46
1	FB	1518	MA6	N9-C8-N7	-3.90	108.41	113.94
34	HA	19	PSU	C4-N3-C2	-3.89	121.01	126.37
2	GB	2503	2MA	N6-C6-N1	3.88	122.27	117.03
2	B	1939	5MU	C6-C5-C4	3.88	121.22	118.02
2	B	1939	5MU	N3-C2-N1	3.85	119.90	114.89
2	GB	1915	5MU	N3-C2-N1	3.84	119.89	114.89
1	FB	516	PSU	C4-N3-C2	-3.84	121.08	126.37
4	NC	54	5MU	N3-C2-N1	3.82	119.86	114.89
4	D	54	5MU	O4-C4-C5	-3.80	120.57	124.92
1	A	1519	MA6	C2-N1-C6	3.80	121.11	111.83
2	B	2552	2MU	C2'-C1'-N1	-3.79	107.04	114.24
1	A	1519	MA6	N9-C8-N7	-3.79	108.56	113.94
1	FB	1400	5MC	C5-C6-N1	-3.77	119.22	123.31
2	GB	2552	2MU	C5-C4-N3	3.76	120.06	114.80
2	B	2503	2MA	C4-C5-N7	-3.75	106.30	110.58
2	GB	2251	OMG	N9-C4-N3	3.74	133.44	125.95
1	A	1518	MA6	C2-N3-C4	3.74	120.96	111.83
2	GB	1942	5MC	C5-C6-N1	-3.73	119.26	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1519	MA6	C5-N7-C8	3.73	109.31	103.45
4	D	54	5MU	N3-C2-N1	3.72	119.74	114.89
2	B	1917	PSU	C4-N3-C2	-3.69	121.29	126.37
2	B	2251	OMG	N9-C4-N3	3.69	133.33	125.95
1	FB	967	5MC	C5-C6-N1	-3.68	119.31	123.31
2	GB	2503	2MA	N3-C4-N9	3.67	131.65	126.99
1	A	527	7MG	N9-C4-N3	3.67	130.83	125.46
4	IA	54	5MU	C5-C4-N3	3.64	118.48	115.32
1	A	1400	5MC	C5-C6-N1	-3.63	119.38	123.31
2	GB	2552	2MU	N3-C2-N1	3.62	119.61	114.89
2	B	2605	PSU	N1-C2-N3	3.61	118.97	115.17
4	NC	32	5MC	C5-C6-N1	-3.59	119.41	123.31
1	A	1498	UR3	C5-C4-N3	3.59	119.77	115.04
1	A	966	M2G	C2-N3-C4	3.56	119.10	112.51
1	A	527	7MG	C5-C4-N3	-3.55	121.47	128.13
1	A	516	PSU	N1-C2-N3	3.54	118.90	115.17
4	NC	54	5MU	C5M-C5-C6	-3.53	118.08	122.85
2	GB	2503	2MA	C5-N7-C8	3.52	108.98	103.45
1	A	1407	5MC	C5-C6-N1	-3.51	119.50	123.31
2	GB	2552	2MU	C2'-C1'-N1	-3.49	107.61	114.24
2	B	1942	5MC	C5-C6-N1	-3.46	119.56	123.31
2	B	1920	4OC	CM2-O2'-C2'	3.43	123.27	114.47
1	FB	1518	MA6	C2-N3-C4	3.42	120.19	111.83
2	GB	1962	5MC	C5-C6-N1	-3.42	119.60	123.31
2	B	1939	5MU	C5M-C5-C6	-3.42	118.22	122.85
1	FB	966	M2G	C2-N3-C4	3.41	118.83	112.51
4	IA	32	5MC	C5-C6-N1	-3.41	119.61	123.31
1	A	967	5MC	C5-C6-N1	-3.41	119.61	123.31
1	FB	1498	UR3	C5-C4-N3	3.40	119.52	115.04
4	NC	54	5MU	O4-C4-C5	-3.39	121.03	124.92
1	FB	1519	MA6	N1-C2-N3	-3.39	123.45	128.58
2	B	1911	PSU	C4-N3-C2	-3.39	121.70	126.37
1	FB	1404	5MC	C5-C6-N1	-3.39	119.64	123.31
2	B	2552	2MU	O2-C2-N1	-3.38	118.39	122.80
1	FB	527	7MG	O6-C6-C5	-3.38	119.32	127.62
1	FB	527	7MG	C5-C4-N3	-3.37	121.81	128.13
1	A	1519	MA6	C2-N3-C4	3.36	120.04	111.83
1	FB	527	7MG	C6-C5-C4	-3.35	116.50	122.40
1	A	1207	2MG	N1-C2-N2	3.35	119.98	116.56
2	B	1939	5MU	O2-C2-N1	-3.33	118.46	122.80
1	FB	516	PSU	N1-C2-N3	3.33	118.68	115.17
2	GB	2503	2MA	N9-C8-N7	-3.33	109.21	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	GB	1920	4OC	CM2-O2'-C2'	3.32	123.01	114.47
1	A	1404	5MC	C5-C6-N1	-3.32	119.71	123.31
2	GB	2552	2MU	O4-C4-C5	-3.31	119.45	125.16
2	GB	1942	5MC	C1'-N1-C6	-3.29	115.73	121.15
1	A	1518	MA6	C5-N7-C8	3.28	108.60	103.45
4	IA	54	5MU	C6-C5-C4	3.27	120.72	118.02
34	HA	19	PSU	O2-C2-N1	-3.27	119.42	122.79
2	B	2552	2MU	O4-C4-C5	-3.24	119.57	125.16
1	FB	1519	MA6	C2-N1-C6	3.24	119.74	111.83
1	FB	1518	MA6	C5-N7-C8	3.24	108.54	103.45
1	FB	1207	2MG	N1-C2-N2	3.22	119.85	116.56
1	A	1518	MA6	C4-N9-C8	3.17	109.07	105.74
4	IA	55	PSU	O2-C2-N1	-3.17	119.52	122.79
2	GB	2605	PSU	N1-C2-N3	3.15	118.49	115.17
1	A	1518	MA6	C4-C5-N7	-3.14	106.99	110.58
2	B	2251	OMG	N9-C8-N7	-3.14	107.58	113.40
1	A	527	7MG	C6-C5-C4	-3.14	116.88	122.40
1	FB	1519	MA6	N3-C4-N9	3.13	132.50	127.17
4	IA	54	5MU	C5-C6-N1	-3.12	119.93	123.31
34	MC	19	PSU	O2-C2-N1	-3.11	119.58	122.79
1	A	1518	MA6	N3-C4-N9	3.11	132.45	127.17
1	FB	1518	MA6	C4-N9-C8	3.10	108.99	105.74
1	FB	1407	5MC	C5-C6-N1	-3.09	119.96	123.31
2	GB	1942	5MC	CM5-C5-C6	-3.07	118.70	122.85
1	A	966	M2G	N9-C8-N7	-3.06	107.72	113.40
1	FB	1518	MA6	C4-C5-N7	-3.06	107.09	110.58
2	GB	2552	2MU	O2-C2-N1	-3.06	118.82	122.80
1	FB	1207	2MG	C2-N1-C6	-3.05	120.87	124.55
1	FB	516	PSU	O2-C2-N1	-3.03	119.66	122.79
4	NC	54	5MU	C5-C6-N1	-3.02	120.03	123.31
1	FB	1518	MA6	N3-C4-N9	3.01	132.29	127.17
1	A	1519	MA6	N3-C4-N9	3.01	132.29	127.17
1	FB	1519	MA6	C4-C5-C6	2.99	119.00	115.91
1	FB	1519	MA6	C2-N3-C4	2.97	119.08	111.83
4	IB	32	5MC	C5-C6-N1	-2.97	120.09	123.31
1	A	1404	5MC	C5-C4-N3	-2.97	118.71	121.75
2	B	1942	5MC	C1'-N1-C6	-2.97	116.27	121.15
1	A	527	7MG	O6-C6-C5	-2.94	120.40	127.62
4	D	54	5MU	C5-C6-N1	-2.94	120.12	123.31
1	FB	1207	2MG	N9-C8-N7	-2.94	107.96	113.40
1	FB	1207	2MG	C4-C5-N7	-2.92	106.05	110.67
1	A	1207	2MG	N9-C8-N7	-2.90	108.03	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	HA	19	PSU	C6-C5-C4	2.90	120.13	118.17
1	A	1207	2MG	C4-C5-N7	-2.89	106.10	110.67
46	UA	92	0TD	OD2-CG-CB	2.88	119.37	113.15
4	IA	54	5MU	C5M-C5-C4	2.85	121.82	118.78
1	FB	527	7MG	N2-C2-N1	2.84	122.75	116.76
2	B	2503	2MA	C5-C4-N9	2.83	108.90	105.81
2	B	2503	2MA	C5-N7-C8	2.83	107.90	103.45
2	B	1911	PSU	C6-N1-C2	-2.82	120.07	122.69
1	FB	1207	2MG	C6-C5-N7	2.81	135.40	130.29
1	A	527	7MG	N2-C2-N1	2.80	122.68	116.76
2	B	2552	2MU	C6'-O2'-C2'	2.80	121.66	114.47
46	ZC	92	0TD	OD2-CG-CB	2.78	119.15	113.15
2	GB	2251	OMG	N9-C8-N7	-2.77	108.27	113.40
1	A	1207	2MG	C6-C5-N7	2.77	135.33	130.29
2	B	2251	OMG	C8-N7-C5	2.76	109.18	104.26
1	A	966	M2G	O6-C6-C5	-2.76	119.25	126.53
1	FB	966	M2G	O6-C6-C5	-2.75	119.27	126.53
4	NC	54	5MU	C6-C5-C4	2.74	120.28	118.02
2	GB	1917	PSU	C6-C5-C4	2.73	120.02	118.17
1	FB	1519	MA6	C4-N9-C8	2.73	108.61	105.74
2	B	1942	5MC	CM5-C5-C6	-2.73	119.16	122.85
4	IB	54	5MU	C5-C6-N1	-2.73	120.35	123.31
1	A	516	PSU	O2-C2-N1	-2.73	119.97	122.79
1	FB	966	M2G	N9-C8-N7	-2.71	108.37	113.40
1	A	1207	2MG	C2-N1-C6	-2.71	121.27	124.55
4	IA	54	5MU	O2-C2-N1	-2.71	119.27	122.80
2	GB	1915	5MU	C6-C5-C4	2.68	120.23	118.02
4	NC	54	5MU	C5M-C5-C4	2.68	121.65	118.78
2	GB	1911	PSU	C6-N1-C2	-2.67	120.22	122.69
2	GB	1911	PSU	O2-C2-N1	-2.66	120.04	122.79
1	A	527	7MG	N1-C2-N3	-2.65	118.47	123.32
2	GB	2251	OMG	C2-N1-C6	-2.64	120.32	125.11
2	B	1962	5MC	CM5-C5-C6	-2.62	119.30	122.85
34	MC	19	PSU	C6-C5-C4	2.62	119.94	118.17
4	IA	32	5MC	C5-C4-N3	-2.59	119.10	121.75
2	B	2605	PSU	C5-C6-N1	-2.59	118.54	122.14
4	D	32	5MC	C5-C4-N3	-2.57	119.12	121.75
1	A	1207	2MG	N9-C4-N3	2.57	131.09	125.95
4	NC	32	5MC	C5-C4-N3	-2.57	119.12	121.75
1	FB	527	7MG	C4-C5-N7	2.56	108.40	105.38
1	A	527	7MG	C4-C5-N7	2.56	108.40	105.38
1	A	1207	2MG	C8-N7-C5	2.56	108.81	104.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	FB	1207	2MG	N9-C4-N3	2.55	131.06	125.95
1	FB	1402	4OC	C6-C5-C4	2.55	120.07	117.00
2	B	2503	2MA	N9-C8-N7	-2.55	110.32	113.94
2	GB	1917	PSU	O2-C2-N1	-2.55	120.16	122.79
1	FB	1404	5MC	C5-C4-N3	-2.55	119.14	121.75
1	FB	1207	2MG	C8-N7-C5	2.54	108.79	104.26
2	GB	2251	OMG	O6-C6-C5	-2.54	119.82	126.53
4	D	32	5MC	C5-C6-N1	-2.54	120.56	123.31
4	IA	32	5MC	O2-C2-N3	-2.53	118.34	122.33
4	D	54	5MU	C5M-C5-C6	-2.52	119.44	122.85
1	A	1498	UR3	C1'-N1-C2	2.51	121.15	117.04
2	GB	2552	2MU	C6'-O2'-C2'	2.49	120.87	114.47
4	IA	54	5MU	O4-C4-C5	-2.48	122.08	124.92
46	UA	92	0TD	OD2-CG-OD1	-2.48	118.45	124.08
34	HA	19	PSU	C6-N1-C2	-2.48	120.39	122.69
4	NC	32	5MC	O2-C2-N3	-2.47	118.43	122.33
2	B	2251	OMG	C2-N1-C6	-2.47	120.63	125.11
46	ZC	92	0TD	OD2-CG-OD1	-2.47	118.47	124.08
2	GB	2605	PSU	O4-C4-C5	-2.45	117.91	124.01
2	B	2503	2MA	N6-C6-N1	2.44	120.33	117.03
2	B	2251	OMG	C4-C5-N7	-2.43	106.82	110.67
1	A	1402	4OC	C6-C5-C4	2.40	119.89	117.00
4	IB	32	5MC	C5-C4-N3	-2.37	119.33	121.75
2	B	1917	PSU	O2-C2-N1	-2.37	120.35	122.79
2	GB	2251	OMG	CM2-O2'-C2'	2.36	120.54	114.47
1	A	1519	MA6	C4-N9-C8	2.36	108.21	105.74
2	GB	2251	OMG	C5-C6-N1	2.34	119.20	113.25
2	GB	1942	5MC	O2-C2-N3	-2.33	118.66	122.33
2	GB	2503	2MA	C5-C4-N9	2.32	108.34	105.81
2	B	1917	PSU	C6-N1-C2	-2.30	120.56	122.69
1	A	966	M2G	C5-C6-N1	2.30	119.10	113.25
1	FB	966	M2G	C5-C6-N1	2.29	119.09	113.25
2	GB	2605	PSU	C5-C4-N3	2.29	121.59	116.55
4	IB	54	5MU	C6-C5-C4	2.28	119.90	118.02
1	A	966	M2G	C8-N9-C4	2.26	110.26	106.03
1	FB	527	7MG	N1-C2-N3	-2.25	119.20	123.32
1	A	1407	5MC	O2-C2-N3	-2.23	118.81	122.33
2	B	2605	PSU	C5-C4-N3	2.23	121.47	116.55
2	GB	1917	PSU	C5-C6-N1	-2.23	119.05	122.14
4	IB	54	5MU	C5M-C5-C6	-2.22	119.84	122.85
1	FB	967	5MC	CM5-C5-C6	-2.22	119.85	122.85
1	FB	967	5MC	C1'-N1-C6	-2.22	117.50	121.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1942	5MC	O2-C2-N3	-2.21	118.84	122.33
4	IB	54	5MU	C6-N1-C2	-2.21	119.10	121.30
1	A	966	M2G	C8-N7-C5	2.20	108.18	104.26
4	D	54	5MU	C6-C5-C4	2.20	119.83	118.02
1	FB	516	PSU	O4'-C1'-C2'	2.20	108.19	105.15
1	FB	1407	5MC	O2-C2-N3	-2.20	118.87	122.33
1	FB	1400	5MC	CM5-C5-C6	-2.18	119.90	122.85
1	FB	1207	2MG	C5-C6-N1	2.18	118.79	113.25
1	A	516	PSU	O4'-C1'-C2'	2.17	108.15	105.15
2	B	2251	OMG	C5-C6-N1	2.17	118.77	113.25
2	GB	1962	5MC	C5-C4-N3	-2.17	119.53	121.75
34	MC	19	PSU	C6-N1-C2	-2.16	120.68	122.69
1	A	516	PSU	C5-C6-N1	-2.16	119.15	122.14
2	GB	2251	OMG	C8-N7-C5	2.15	108.09	104.26
1	A	1400	5MC	O2-C2-N3	-2.15	118.95	122.33
1	A	1519	MA6	C4-C5-C6	2.14	118.12	115.91
2	B	2251	OMG	O6-C6-C5	-2.14	120.89	126.53
1	A	1207	2MG	C5-C6-N1	2.13	118.69	113.25
2	GB	2503	2MA	C6-C5-C4	2.12	120.07	117.18
2	B	1911	PSU	O4'-C1'-C2'	2.11	108.06	105.15
1	FB	1498	UR3	C1'-N1-C2	2.09	120.46	117.04
1	FB	966	M2G	CM2-N2-CM1	2.07	122.49	115.87
1	FB	1519	MA6	C5-C4-N9	2.06	108.05	105.81
2	B	1917	PSU	C6-C5-C4	2.05	119.56	118.17
4	IA	55	PSU	C6-C5-C4	2.05	119.56	118.17
2	GB	1911	PSU	C6-C5-C4	2.05	119.56	118.17
1	FB	1402	4OC	C5-C6-N1	-2.04	118.52	121.84
2	GB	1915	5MU	O2-C2-N1	-2.04	120.14	122.80
1	FB	527	7MG	C6-C5-N7	2.04	135.09	131.93
34	HA	19	PSU	O4'-C1'-C2'	2.04	107.97	105.15
2	GB	1911	PSU	O4-C4-C5	-2.04	118.94	124.01
4	IB	55	PSU	O2-C2-N1	-2.04	120.69	122.79
2	GB	2605	PSU	C5-C6-N1	-2.03	119.32	122.14
4	IA	54	5MU	C6-N1-C2	-2.03	119.28	121.30
4	NC	54	5MU	O2-C2-N1	-2.03	120.16	122.80
34	MC	19	PSU	O4'-C1'-C2'	2.03	107.96	105.15
1	FB	1402	4OC	C2'-C1'-N1	-2.02	110.40	114.24
1	FB	966	M2G	C8-N9-C4	2.02	109.81	106.03
34	MC	19	PSU	C5-C6-N1	-2.02	119.34	122.14
4	NC	8	4SU	C6-N1-C2	-2.01	118.55	121.00

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2251	OMG	C1'-C2'-O2'-CM2
2	B	2552	2MU	C1'-C2'-O2'-C6'
2	GB	2251	OMG	C1'-C2'-O2'-CM2
2	GB	2552	2MU	C1'-C2'-O2'-C6'
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	1519	MA6	O4'-C4'-C5'-O5'
1	FB	1402	4OC	O4'-C4'-C5'-O5'
1	FB	1519	MA6	O4'-C4'-C5'-O5'
2	B	1962	5MC	O4'-C4'-C5'-O5'
1	A	1519	MA6	C3'-C4'-C5'-O5'
1	FB	1519	MA6	C3'-C4'-C5'-O5'
1	A	1402	4OC	C3'-C4'-C5'-O5'
1	FB	1402	4OC	C3'-C4'-C5'-O5'
2	GB	1962	5MC	O4'-C4'-C5'-O5'
2	B	1962	5MC	C3'-C4'-C5'-O5'
1	FB	1519	MA6	C5-C6-N6-C9
46	UA	92	0TD	CG-CB-SB-CSB
46	ZC	92	0TD	CG-CB-SB-CSB
46	UA	92	0TD	SB-CB-CG-OD1
46	ZC	92	0TD	SB-CB-CG-OD1
1	A	1519	MA6	C5-C6-N6-C9
2	B	2552	2MU	O4'-C4'-C5'-O5'
2	GB	2552	2MU	O4'-C4'-C5'-O5'
1	FB	527	7MG	C3'-C4'-C5'-O5'
1	A	527	7MG	C3'-C4'-C5'-O5'
1	FB	1519	MA6	C4'-C5'-O5'-P
2	GB	1962	5MC	C3'-C4'-C5'-O5'
1	A	1519	MA6	C4'-C5'-O5'-P
2	B	2503	2MA	C4'-C5'-O5'-P
1	A	1400	5MC	O4'-C4'-C5'-O5'
2	GB	2503	2MA	C4'-C5'-O5'-P
2	B	1920	4OC	C2'-C1'-N1-C2
1	FB	1400	5MC	O4'-C4'-C5'-O5'

There are no ring outliers.

29 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	GB	2251	OMG	1	0
1	FB	966	M2G	1	0
2	B	1920	4OC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1519	MA6	1	0
4	D	54	5MU	1	0
4	IB	32	5MC	1	0
2	GB	1939	5MU	1	0
2	B	2251	OMG	1	0
2	B	2552	2MU	2	0
1	FB	1519	MA6	2	0
4	D	8	4SU	3	0
4	IB	54	5MU	1	0
1	A	1498	UR3	1	0
1	A	966	M2G	1	0
4	D	32	5MC	1	0
2	B	1939	5MU	1	0
4	NC	32	5MC	1	0
4	IB	8	4SU	3	0
1	FB	1498	UR3	2	0
2	GB	1915	5MU	1	0
2	GB	2552	2MU	2	0
2	B	1915	5MU	1	0
1	A	1518	MA6	1	0
4	IA	32	5MC	1	0
1	A	967	5MC	2	0
34	MC	19	PSU	1	0
1	FB	967	5MC	2	0
1	FB	1518	MA6	1	0
34	HA	19	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2903 ligands modelled in this entry, 2903 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	1495/1507 (99%)	0.17	39 (2%) 57 36	52, 100, 166, 256	0
1	FB	1495/1507 (99%)	0.37	61 (4%) 41 23	57, 88, 151, 209	0
2	B	2869/2880 (99%)	-0.23	74 (2%) 57 36	36, 55, 145, 201	0
2	GB	2869/2880 (99%)	0.23	113 (3%) 43 24	47, 73, 172, 242	0
3	C	120/120 (100%)	0.15	2 (1%) 69 48	63, 83, 96, 117	0
3	HB	120/120 (100%)	0.68	9 (7%) 20 11	80, 111, 128, 144	0
4	D	73/77 (94%)	0.56	7 (9%) 13 7	67, 157, 172, 174	0
4	IA	73/77 (94%)	-0.05	1 (1%) 73 53	52, 84, 91, 100	0
4	IB	73/77 (94%)	0.57	4 (5%) 30 16	79, 164, 182, 186	0
4	NC	73/77 (94%)	-0.12	1 (1%) 73 53	61, 89, 100, 105	0
5	E	275/275 (100%)	-0.12	4 (1%) 72 52	36, 50, 58, 66	0
5	JB	275/275 (100%)	0.16	5 (1%) 67 47	45, 64, 74, 85	0
6	F	204/206 (99%)	0.13	5 (2%) 58 37	39, 60, 79, 86	0
6	KB	204/206 (99%)	0.44	1 (0%) 87 73	53, 77, 97, 107	0
7	G	202/205 (98%)	-0.12	0 100 100	34, 59, 78, 86	0
7	LB	202/205 (98%)	0.28	2 (0%) 79 61	50, 78, 91, 101	0
8	H	181/182 (99%)	0.77	20 (11%) 10 5	85, 91, 111, 119	0
8	MB	181/182 (99%)	1.11	27 (14%) 5 3	99, 119, 132, 135	0
9	I	174/180 (96%)	0.19	5 (2%) 53 32	64, 72, 78, 91	0
9	NB	174/180 (96%)	1.38	29 (16%) 4 2	109, 147, 163, 169	0
10	J	146/148 (98%)	0.85	13 (8%) 15 8	64, 96, 111, 113	0
10	OB	146/148 (98%)	1.52	36 (24%) 2 1	86, 120, 129, 130	0
11	K	140/140 (100%)	-0.00	1 (0%) 84 68	44, 56, 75, 77	0
11	PB	140/140 (100%)	0.53	2 (1%) 73 53	64, 82, 99, 103	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
12	L	122/122 (100%)	-0.07	0 100 100	50, 59, 68, 71	0
12	QB	122/122 (100%)	0.15	2 (1%) 70 49	59, 69, 75, 79	0
13	M	150/150 (100%)	0.35	8 (5%) 32 17	36, 64, 87, 90	0
13	RB	150/150 (100%)	0.68	11 (7%) 21 11	50, 79, 105, 107	0
14	N	141/141 (100%)	0.13	2 (1%) 73 53	48, 59, 72, 80	0
14	SB	141/141 (100%)	0.48	6 (4%) 40 22	63, 82, 97, 103	0
15	O	118/118 (100%)	0.17	1 (0%) 82 65	47, 60, 73, 78	0
15	TB	118/118 (100%)	0.85	8 (6%) 23 12	62, 76, 83, 87	0
16	P	110/112 (98%)	0.58	10 (9%) 15 8	72, 80, 87, 89	0
16	UB	110/112 (98%)	1.19	14 (12%) 8 4	91, 106, 113, 116	0
17	Q	137/146 (93%)	0.17	2 (1%) 72 52	59, 68, 119, 142	0
17	VB	137/146 (93%)	0.28	3 (2%) 62 41	69, 79, 108, 117	0
18	R	117/118 (99%)	-0.04	0 100 100	39, 52, 63, 67	0
18	WB	117/118 (99%)	0.53	2 (1%) 69 48	55, 77, 90, 93	0
19	S	101/101 (100%)	-0.08	0 100 100	40, 60, 67, 71	0
19	XB	101/101 (100%)	0.44	4 (3%) 42 23	56, 84, 94, 99	0
20	T	112/113 (99%)	-0.14	0 100 100	39, 49, 66, 80	0
20	YB	112/113 (99%)	0.58	8 (7%) 22 12	54, 68, 87, 100	0
21	U	95/96 (98%)	0.12	2 (2%) 63 42	49, 56, 66, 74	0
21	ZB	95/96 (98%)	0.88	9 (9%) 14 7	71, 84, 95, 97	0
22	AC	107/110 (97%)	1.64	27 (25%) 1 1	82, 90, 101, 103	0
22	V	107/110 (97%)	0.29	2 (1%) 66 45	55, 63, 76, 82	0
23	BC	189/206 (91%)	0.76	12 (6%) 26 14	89, 108, 118, 121	0
23	W	189/206 (91%)	0.43	6 (3%) 50 30	65, 83, 93, 96	0
24	CC	84/85 (98%)	0.89	12 (14%) 6 3	72, 78, 89, 93	0
24	X	84/85 (98%)	0.57	10 (11%) 9 5	52, 59, 72, 77	0
25	DC	97/98 (98%)	0.67	5 (5%) 33 17	56, 73, 108, 115	0
25	Y	97/98 (98%)	0.32	5 (5%) 33 17	43, 56, 88, 95	0
26	EC	70/72 (97%)	1.32	15 (21%) 2 1	88, 95, 103, 107	0
26	Z	70/72 (97%)	0.43	2 (2%) 53 32	57, 63, 68, 77	0
27	AA	60/60 (100%)	0.21	0 100 100	47, 58, 74, 87	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
27	FC	60/60 (100%)	0.45	1 (1%) 69 48	69, 78, 88, 92	0
28	BA	69/71 (97%)	0.74	3 (4%) 40 22	119, 124, 142, 145	0
28	GC	69/71 (97%)	0.97	6 (8%) 16 9	135, 143, 153, 154	0
29	CA	59/60 (98%)	-0.03	0 100 100	36, 58, 68, 71	0
29	HC	59/60 (98%)	0.30	1 (1%) 69 48	53, 77, 85, 87	0
30	DA	53/54 (98%)	0.32	0 100 100	61, 66, 69, 70	0
30	IC	53/54 (98%)	0.47	2 (3%) 44 25	74, 82, 85, 87	0
31	EA	48/49 (97%)	-0.01	1 (2%) 63 42	38, 40, 47, 52	0
31	JC	48/49 (97%)	0.33	0 100 100	53, 57, 64, 71	0
32	FA	64/65 (98%)	0.21	1 (1%) 70 49	43, 49, 58, 59	0
32	KC	64/65 (98%)	0.81	9 (14%) 6 3	58, 65, 74, 74	0
33	GA	37/37 (100%)	0.34	0 100 100	55, 61, 67, 69	0
33	LC	37/37 (100%)	1.22	6 (16%) 4 2	85, 96, 105, 112	0
34	HA	10/27 (37%)	1.46	3 (30%) 1 1	81, 92, 108, 109	0
34	MC	10/27 (37%)	1.12	2 (20%) 3 1	89, 94, 109, 110	0
35	JA	258/368 (70%)	0.59	19 (7%) 20 11	61, 96, 121, 135	0
35	OC	258/368 (70%)	0.90	38 (14%) 6 3	88, 105, 134, 141	0
36	KA	234/256 (91%)	0.87	15 (6%) 25 14	109, 125, 145, 157	0
36	PC	234/256 (91%)	0.89	27 (11%) 9 5	101, 123, 139, 163	0
37	LA	206/239 (86%)	0.73	14 (6%) 23 12	104, 117, 133, 134	0
37	QC	206/239 (86%)	0.98	26 (12%) 8 4	100, 115, 131, 132	0
38	MA	208/209 (99%)	1.20	36 (17%) 4 2	89, 104, 113, 118	0
38	RC	208/209 (99%)	0.67	14 (6%) 24 13	74, 81, 88, 92	0
39	NA	151/162 (93%)	0.94	17 (11%) 10 5	82, 95, 103, 111	0
39	SC	151/162 (93%)	0.61	9 (5%) 27 15	73, 85, 92, 105	0
40	OA	101/101 (100%)	0.42	1 (0%) 79 61	75, 83, 91, 103	0
40	TC	101/101 (100%)	0.50	4 (3%) 42 23	87, 95, 100, 110	0
41	PA	155/156 (99%)	1.00	21 (13%) 7 4	103, 113, 119, 122	0
41	UC	155/156 (99%)	0.89	16 (10%) 12 6	102, 111, 118, 120	0
42	QA	138/138 (100%)	0.86	14 (10%) 12 6	83, 97, 104, 109	0
42	VC	138/138 (100%)	0.65	14 (10%) 12 6	73, 87, 95, 101	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
43	RA	127/128 (99%)	1.76	49 (38%) 1 0	90, 141, 148, 151	0
43	WC	127/128 (99%)	1.38	26 (20%) 2 1	88, 135, 144, 148	0
44	SA	98/105 (93%)	1.85	37 (37%) 1 0	101, 144, 156, 156	0
44	XC	98/105 (93%)	1.65	27 (27%) 1 1	103, 139, 151, 153	0
45	TA	116/129 (89%)	0.77	9 (7%) 19 10	66, 84, 93, 97	0
45	YC	116/129 (89%)	0.71	9 (7%) 19 10	69, 90, 96, 103	0
46	UA	121/132 (91%)	0.67	7 (5%) 29 16	74, 79, 88, 93	0
46	ZC	121/132 (91%)	0.26	4 (3%) 49 29	67, 73, 80, 84	0
47	AD	117/126 (92%)	1.30	20 (17%) 4 2	98, 137, 141, 143	0
47	VA	117/126 (92%)	1.11	18 (15%) 5 2	94, 125, 130, 131	0
48	BD	60/61 (98%)	1.58	15 (25%) 2 1	108, 116, 133, 134	0
48	WA	60/61 (98%)	1.61	17 (28%) 1 1	110, 119, 127, 128	0
49	CD	88/89 (98%)	0.30	2 (2%) 61 39	70, 86, 94, 96	0
49	XA	88/89 (98%)	0.61	6 (6%) 23 12	66, 85, 94, 96	0
50	DD	83/88 (94%)	0.78	11 (13%) 7 4	73, 80, 94, 111	0
50	YA	83/88 (94%)	1.57	18 (21%) 2 1	96, 109, 126, 143	0
51	ED	99/105 (94%)	0.41	1 (1%) 79 61	69, 81, 87, 90	0
51	ZA	99/105 (94%)	0.60	5 (5%) 33 18	72, 88, 93, 94	0
52	AB	70/88 (79%)	0.39	1 (1%) 73 53	77, 88, 98, 101	0
52	FD	70/88 (79%)	0.56	5 (7%) 22 12	84, 94, 104, 109	0
53	BB	83/93 (89%)	1.11	7 (8%) 17 9	104, 130, 136, 138	0
53	GD	83/93 (89%)	1.65	27 (32%) 1 0	111, 139, 144, 146	0
54	CB	99/106 (93%)	1.79	39 (39%) 1 0	97, 111, 126, 128	0
54	HD	99/106 (93%)	1.06	15 (15%) 5 3	79, 97, 112, 114	0
55	DB	24/27 (88%)	2.87	18 (75%) 0 0	113, 123, 127, 132	0
55	ID	24/27 (88%)	2.31	14 (58%) 0 0	118, 127, 133, 138	0
All	All	21476/22228 (96%)	0.42	1376 (6%) 25 14	34, 82, 143, 256	0

All (1376) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
48	WA	2	ALA	9.7
1	FB	1001	G	8.5

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Mol	Chain	Res	Type	RSRZ
10	OB	83	ALA	7.7
44	XC	73	ASP	7.7
26	EC	1	MET	7.5
2	GB	2799	A	7.4
9	NB	68	THR	7.3
48	BD	2	ALA	7.2
24	X	3	HIS	7.0
2	B	2160	G	6.9
24	CC	3	HIS	6.7
50	YA	8	ARG	6.6
36	PC	12	GLU	6.5
55	DB	25	LYS	6.4
15	TB	7	GLY	6.4
49	XA	69	TYR	6.4
50	YA	17	TYR	6.3
24	X	4	LYS	6.3
38	RC	9	CYS	6.3
2	B	1537	C	6.2
8	MB	69	ALA	6.2
2	B	277	C	6.2
16	UB	34	HIS	6.1
54	CB	64	ASP	6.1
41	PA	32	ARG	6.0
16	UB	52	SER	6.0
38	MA	31	CYS	5.9
24	CC	4	LYS	5.9
2	B	2161	C	5.8
38	MA	9	CYS	5.8
47	AD	102	ARG	5.8
38	RC	4	TYR	5.8
44	XC	38	ILE	5.8
44	XC	72	VAL	5.7
1	FB	84	U	5.6
10	OB	31	LEU	5.6
2	B	2799	A	5.6
47	VA	102	ARG	5.6
1	FB	1002	G	5.6
22	AC	56	PRO	5.6
54	CB	80	ARG	5.5
38	RC	42	GLN	5.5
43	RA	127	LYS	5.5
43	RA	17	VAL	5.5

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Mol	Chain	Res	Type	RSRZ
14	N	141	GLN	5.5
2	B	1536	A	5.4
36	PC	238	LEU	5.4
54	CB	9	ASN	5.4
38	RC	2	GLY	5.4
1	FB	1000	A	5.3
16	UB	36	TYR	5.3
22	AC	59	GLY	5.3
35	OC	301	GLY	5.3
44	SA	6	ILE	5.3
10	J	89	TYR	5.3
2	GB	2798	C	5.3
9	NB	71	LEU	5.2
44	SA	71	LEU	5.2
44	SA	72	VAL	5.2
38	MA	26	CYS	5.2
54	CB	60	GLU	5.2
24	CC	8	GLY	5.2
54	CB	70	SER	5.2
9	NB	64	LEU	5.1
2	B	276	A	5.1
53	GD	34	TRP	5.1
2	B	1058	G	5.1
8	MB	157	ILE	5.1
38	MA	42	GLN	5.0
38	MA	4	TYR	5.0
44	XC	71	LEU	5.0
48	BD	31	ARG	5.0
21	ZB	6	ASP	5.0
41	UC	33	ASP	5.0
20	YB	97	LYS	5.0
55	ID	25	LYS	5.0
53	GD	33	THR	4.9
43	RA	7	THR	4.9
1	FB	977	A	4.9
43	RA	5	TYR	4.8
2	B	2136	C	4.8
24	CC	2	ALA	4.8
43	RA	66	ARG	4.8
8	H	39	ILE	4.8
45	YC	87	THR	4.8
32	KC	38	GLY	4.8

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Mol	Chain	Res	Type	RSRZ
47	AD	19	LEU	4.8
2	B	2801	A	4.7
38	RC	26	CYS	4.7
13	M	110	TYR	4.7
35	OC	300	SER	4.7
43	RA	18	PHE	4.7
38	RC	31	CYS	4.6
2	GB	2802	G	4.6
2	GB	1084	A	4.6
2	B	2798	C	4.6
44	SA	69	ASN	4.6
42	QA	1	MET	4.6
1	FB	81	G	4.6
9	I	2	SER	4.6
10	OB	38	LEU	4.6
44	SA	8	LEU	4.6
2	GB	1060	U	4.5
10	J	33	ARG	4.5
22	AC	57	GLN	4.5
1	FB	1224	G	4.5
9	NB	52	VAL	4.5
45	TA	25	TYR	4.5
40	TC	99	ALA	4.5
1	FB	974	A	4.5
54	CB	11	SER	4.5
54	CB	81	LYS	4.5
43	WC	3	GLN	4.5
53	GD	9	VAL	4.5
10	OB	39	ALA	4.5
8	MB	35	GLU	4.5
15	TB	14	SER	4.4
44	XC	37	PRO	4.4
48	WA	6	LEU	4.4
43	RA	11	LYS	4.4
2	GB	11	G	4.4
47	AD	87	TYR	4.4
43	WC	19	LEU	4.4
8	H	35	GLU	4.3
43	RA	6	GLY	4.3
10	OB	81	VAL	4.3
2	B	2892	A	4.3
16	P	29	PHE	4.3

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Mol	Chain	Res	Type	RSRZ
54	HD	81	LYS	4.3
10	OB	90	GLY	4.3
47	VA	104	ARG	4.3
37	QC	103	VAL	4.3
16	UB	55	ALA	4.3
35	OC	316	ARG	4.3
10	OB	28	ASN	4.3
35	JA	182	HIS	4.2
55	DB	16	GLY	4.2
55	ID	2	GLY	4.2
8	H	133	LEU	4.2
35	OC	326	LEU	4.2
2	B	1055	G	4.2
2	GB	546	C	4.2
2	GB	2805	G	4.2
38	MA	2	GLY	4.2
41	UC	85	TYR	4.2
8	H	160	VAL	4.2
36	PC	239	VAL	4.2
2	GB	2801	A	4.2
34	MC	13	A	4.2
1	A	984	C	4.2
3	HB	5	C	4.2
47	AD	27	LYS	4.2
10	OB	40	THR	4.2
50	YA	9	PHE	4.1
55	DB	5	ASP	4.1
1	A	977	A	4.1
2	B	1762	A	4.1
6	F	151	TYR	4.1
35	OC	119	THR	4.1
42	VC	1	MET	4.1
50	YA	7	ALA	4.1
43	WC	7	THR	4.1
1	FB	983	A	4.1
10	OB	34	GLY	4.1
1	A	985	C	4.1
24	X	9	SER	4.1
36	KA	133	LYS	4.1
24	X	5	LYS	4.0
10	OB	36	ALA	4.0
9	I	57	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
15	TB	6	SER	4.0
41	UC	110	GLN	4.0
50	YA	15	PRO	4.0
2	B	12	U	4.0
43	RA	108	VAL	4.0
44	XC	36	GLY	4.0
43	WC	18	PHE	4.0
45	YC	86	GLY	4.0
2	B	2803	C	4.0
26	EC	19	VAL	3.9
42	QA	129	VAL	3.9
22	AC	58	GLY	3.9
24	CC	10	THR	3.9
50	YA	39	TYR	3.9
51	ZA	6	LEU	3.9
54	CB	10	LEU	3.9
53	GD	77	THR	3.9
13	RB	11	GLY	3.9
8	MB	102	PHE	3.9
1	A	1223	C	3.9
44	SA	7	LYS	3.9
10	J	35	LEU	3.9
43	RA	9	ARG	3.9
55	DB	15	ARG	3.9
50	YA	13	HIS	3.9
39	SC	21	ALA	3.9
8	MB	39	ILE	3.9
22	AC	89	PHE	3.9
2	GB	2173	A	3.8
34	HA	15	A	3.8
54	CB	83	ARG	3.8
28	GC	22	ILE	3.8
43	WC	9	ARG	3.8
24	X	8	GLY	3.8
25	DC	36	GLY	3.8
41	PA	33	ASP	3.8
10	J	92	VAL	3.8
54	CB	74	LYS	3.8
2	GB	1026	U	3.8
8	MB	93	THR	3.8
28	GC	58	ARG	3.8
2	GB	1215	G	3.8

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Mol	Chain	Res	Type	RSRZ
24	X	2	ALA	3.8
38	MA	18	LYS	3.8
43	WC	66	ARG	3.8
2	B	1535	U	3.8
2	B	2895	U	3.8
2	B	2896	C	3.7
4	D	34	C	3.7
54	CB	63	ILE	3.7
22	AC	60	PHE	3.7
2	GB	2629	A	3.7
35	OC	302	ASP	3.7
1	FB	1003	G	3.7
2	GB	1058	G	3.7
35	OC	198	THR	3.7
4	IB	1	C	3.7
22	AC	85	VAL	3.7
54	HD	86	ARG	3.7
9	NB	67	LEU	3.7
39	SC	88	LYS	3.7
44	XC	35	SER	3.7
55	DB	17	THR	3.7
5	E	262	ARG	3.7
10	OB	6	LEU	3.7
6	KB	151	TYR	3.6
1	FB	87	A	3.6
2	GB	2161	C	3.6
35	JA	194	GLY	3.6
43	RA	72	GLY	3.6
55	DB	2	GLY	3.6
9	NB	40	GLU	3.6
41	PA	5	ARG	3.6
10	OB	35	LEU	3.6
2	GB	1083	U	3.6
44	SA	99	LYS	3.6
54	HD	74	LYS	3.6
53	GD	75	ALA	3.6
10	OB	41	GLU	3.6
21	ZB	1	MET	3.6
44	SA	4	ILE	3.6
39	SC	20	GLN	3.6
9	NB	60	ARG	3.6
44	SA	70	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
41	PA	22	LEU	3.6
1	FB	1223	C	3.6
37	QC	10	PHE	3.6
37	LA	2	GLY	3.6
8	H	159	VAL	3.6
17	VB	94	ALA	3.6
37	QC	53	ALA	3.6
54	CB	84	LEU	3.6
1	A	1002	G	3.5
1	FB	1032(C)	G	3.5
22	AC	84	ARG	3.5
1	A	1362(B)	C	3.5
50	YA	2	VAL	3.5
9	NB	85	LYS	3.5
41	PA	109	ASN	3.5
53	GD	80	TYR	3.5
35	JA	301	GLY	3.5
21	ZB	33	LYS	3.5
50	YA	6	LEU	3.5
2	GB	10	G	3.5
42	VC	99	GLU	3.5
25	Y	26	ARG	3.5
41	UC	5	ARG	3.5
53	BB	78	ARG	3.5
35	OC	201	CYS	3.5
55	ID	17	THR	3.5
32	KC	43	GLN	3.5
44	SA	93	GLY	3.5
44	XC	5	ARG	3.5
2	B	2148	G	3.5
45	TA	74	ALA	3.5
2	GB	12	U	3.5
10	J	90	GLY	3.5
41	PA	82	GLY	3.5
42	VC	95	VAL	3.5
38	MA	21	LEU	3.5
47	AD	113	PRO	3.5
2	GB	1590	U	3.5
35	OC	327	TYR	3.4
55	DB	20	LYS	3.4
45	TA	14	VAL	3.4
13	M	104	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
53	GD	84	GLY	3.4
55	DB	11	GLY	3.4
8	MB	91	ARG	3.4
38	RC	18	LYS	3.4
48	BD	17	LYS	3.4
43	RA	102	LEU	3.4
44	SA	65	LEU	3.4
37	QC	67	THR	3.4
43	RA	64	THR	3.4
16	P	30	ARG	3.4
18	WB	80	ILE	3.4
15	TB	9	LYS	3.4
2	GB	1762	A	3.4
30	IC	39	TYR	3.4
10	J	146	ALA	3.4
53	GD	76	PRO	3.4
2	B	508	G	3.4
32	KC	40	GLU	3.4
10	OB	92	VAL	3.4
45	YC	14	VAL	3.4
41	PA	2	ALA	3.4
1	FB	1280	A	3.4
9	NB	61	HIS	3.4
2	GB	2136	C	3.4
3	HB	6	C	3.4
5	JB	262	ARG	3.4
36	PC	165	VAL	3.4
41	UC	115	ARG	3.4
50	YA	10	GLY	3.4
2	GB	1214	A	3.3
2	GB	2693	A	3.3
2	GB	2111	C	3.3
10	OB	37	VAL	3.3
41	PA	29	LYS	3.3
52	FD	68	LYS	3.3
44	SA	39	PRO	3.3
2	GB	30	G	3.3
39	SC	130	ASN	3.3
43	RA	65	VAL	3.3
2	B	1214	A	3.3
8	MB	12	TYR	3.3
37	QC	2	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
32	KC	46	ARG	3.3
45	YC	92	GLU	3.3
1	FB	1094	G	3.3
2	B	1538	G	3.3
2	GB	1062	G	3.3
2	GB	1063	G	3.3
10	J	29	TYR	3.3
22	AC	82	PRO	3.3
2	GB	2895	U	3.3
41	PA	106	GLN	3.3
47	VA	105	THR	3.3
43	RA	14	VAL	3.3
10	OB	89	TYR	3.3
3	HB	116	G	3.3
54	CB	71	THR	3.3
8	MB	36	LYS	3.3
4	IB	16	C	3.3
49	XA	3	ILE	3.3
24	CC	9	SER	3.2
23	BC	163	LEU	3.2
24	CC	7	LEU	3.2
42	VC	2	LEU	3.2
26	Z	43	GLN	3.2
32	KC	35	GLN	3.2
2	B	1084	A	3.2
21	U	33	LYS	3.2
1	FB	82	U	3.2
2	B	1056	G	3.2
2	B	2162	G	3.2
9	NB	43	VAL	3.2
1	FB	1326	C	3.2
2	GB	2804	C	3.2
10	OB	115	ALA	3.2
53	GD	32	LYS	3.2
52	FD	31	LEU	3.2
16	P	92	TYR	3.2
45	YC	25	TYR	3.2
43	WC	108	VAL	3.2
2	GB	1085	A	3.2
1	A	1202	G	3.2
2	GB	1055	G	3.2
2	GB	2160	G	3.2

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Mol	Chain	Res	Type	RSRZ
1	FB	1397	C	3.2
37	LA	87	LEU	3.2
16	P	36	TYR	3.2
42	VC	97	VAL	3.2
43	WC	109	VAL	3.2
10	OB	1	MET	3.2
16	UB	53	SER	3.2
43	RA	81	ILE	3.2
55	DB	18	TYR	3.1
2	GB	2894	G	3.1
39	SC	18	ARG	3.1
32	KC	41	ILE	3.1
33	LC	8	LYS	3.1
35	OC	160	LYS	3.1
54	CB	68	LYS	3.1
8	MB	64	THR	3.1
9	I	58	GLU	3.1
16	UB	29	PHE	3.1
53	GD	52	TYR	3.1
5	JB	276	LYS	3.1
48	WA	30	ALA	3.1
13	M	106	LEU	3.1
5	JB	256	GLY	3.1
48	WA	29	ARG	3.1
8	MB	52	ILE	3.1
43	RA	112	LYS	3.1
47	AD	12	ASN	3.1
48	BD	30	ALA	3.1
20	YB	112	GLY	3.1
2	GB	2803	C	3.1
37	QC	70	VAL	3.1
16	P	33	LYS	3.1
41	PA	35	LYS	3.1
2	B	1061	U	3.1
53	BB	84	GLY	3.1
43	WC	121	ARG	3.1
23	BC	39	VAL	3.1
53	BB	55	LYS	3.1
36	PC	232	PRO	3.1
38	MA	33	MET	3.1
43	RA	123	PRO	3.1
4	IB	34	C	3.0

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Mol	Chain	Res	Type	RSRZ
43	RA	119	ALA	3.0
2	B	2894	G	3.0
33	LC	37	GLY	3.0
2	GB	1094	U	3.0
47	AD	60	VAL	3.0
39	NA	122	GLU	3.0
23	W	29	TYR	3.0
21	ZB	9	LEU	3.0
2	GB	1054	A	3.0
2	GB	2135	A	3.0
33	LC	18	ARG	3.0
39	NA	130	ASN	3.0
35	OC	314	GLN	3.0
8	MB	92	VAL	3.0
9	NB	168	PRO	3.0
2	B	2147	G	3.0
38	MA	120	LEU	3.0
23	BC	189	ALA	3.0
38	MA	66	ARG	3.0
41	UC	32	ARG	3.0
48	BD	3	ARG	3.0
55	ID	15	ARG	3.0
16	UB	57	LYS	3.0
37	QC	104	GLN	3.0
38	MA	109	GLY	3.0
42	QA	98	LYS	3.0
46	ZC	126	LYS	3.0
2	B	2135	A	3.0
2	GB	1174	A	3.0
2	GB	1536	A	3.0
44	SA	67	THR	3.0
2	B	2146	C	3.0
2	B	2174	C	3.0
2	GB	1064	C	3.0
42	QA	2	LEU	3.0
28	BA	58	ARG	3.0
22	AC	33	LYS	3.0
42	QA	116	LYS	3.0
55	ID	3	LYS	3.0
6	F	9	VAL	3.0
44	XC	34	VAL	3.0
53	BB	9	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
47	AD	109	THR	3.0
44	SA	38	ILE	3.0
24	X	7	LEU	3.0
43	RA	12	GLU	3.0
34	HA	13	A	3.0
44	XC	43	ARG	3.0
12	QB	28	SER	3.0
3	C	6	C	3.0
4	D	1	C	3.0
26	EC	6	VAL	3.0
9	NB	9	ILE	3.0
35	OC	175	LEU	2.9
41	PA	101	LEU	2.9
2	B	1534	G	2.9
26	EC	58	ALA	2.9
1	A	1280	A	2.9
2	B	1057	A	2.9
37	LA	185	GLY	2.9
42	VC	54	ASP	2.9
37	LA	8	ILE	2.9
47	VA	113	PRO	2.9
53	GD	2	PRO	2.9
55	DB	3	LYS	2.9
40	OA	101	ALA	2.9
43	WC	65	VAL	2.9
51	ZA	8	GLY	2.9
53	GD	62	ILE	2.9
55	DB	13	ILE	2.9
22	V	2	ARG	2.9
10	J	121	LYS	2.9
1	A	91	C	2.9
2	B	32	C	2.9
2	GB	2174	C	2.9
4	D	17	C	2.9
10	OB	119	PRO	2.9
39	NA	128	PRO	2.9
1	A	82	U	2.9
2	B	270(M)	U	2.9
2	B	1065	U	2.9
2	GB	654	U	2.9
42	VC	129	VAL	2.9
35	JA	300	SER	2.9

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Mol	Chain	Res	Type	RSRZ
38	RC	10	ARG	2.9
52	FD	85	LEU	2.9
54	CB	85	MET	2.9
43	RA	116	LYS	2.9
1	FB	1222	G	2.9
2	B	11	G	2.9
2	B	2159	G	2.9
42	QA	99	GLU	2.9
1	A	919	A	2.9
22	AC	93	GLY	2.9
42	VC	55	GLY	2.9
10	J	88	ILE	2.9
17	Q	1	MET	2.9
5	JB	275	LYS	2.9
42	VC	116	LYS	2.9
53	GD	5	LEU	2.9
8	H	50	ALA	2.9
53	GD	63	THR	2.9
13	RB	79	ARG	2.9
55	DB	21	TYR	2.9
2	B	2802	G	2.9
10	OB	45	LYS	2.9
39	SC	123	LEU	2.9
44	SA	62	HIS	2.8
1	FB	961	U	2.8
1	FB	1235	U	2.8
38	MA	113	SER	2.8
55	ID	5	ASP	2.8
47	VA	10	PRO	2.8
55	ID	23	PRO	2.8
20	YB	82	LEU	2.8
47	AD	22	ILE	2.8
36	KA	218	ALA	2.8
54	CB	97	ALA	2.8
1	FB	1025	U	2.8
1	FB	1443	G	2.8
2	GB	2833	G	2.8
50	YA	29	ASP	2.8
1	A	1397	C	2.8
44	SA	94	VAL	2.8
55	ID	24	ARG	2.8
15	TB	5	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
42	VC	98	LYS	2.8
41	PA	7	ALA	2.8
26	EC	55	ARG	2.8
48	BD	29	ARG	2.8
13	RB	58	THR	2.8
51	ZA	7	THR	2.8
54	CB	35	THR	2.8
2	B	1070	A	2.8
1	A	1025	U	2.8
36	PC	221	LEU	2.8
22	AC	18	GLY	2.8
1	A	1001	G	2.8
43	RA	124	GLN	2.8
44	XC	44	VAL	2.8
43	WC	12	GLU	2.8
44	SA	95	GLU	2.8
55	DB	8	THR	2.8
37	QC	186	PHE	2.8
55	ID	16	GLY	2.8
35	OC	307	ASN	2.8
9	NB	170	ARG	2.8
50	YA	25	ARG	2.8
1	A	90	C	2.8
2	GB	1093	G	2.8
23	W	88	PHE	2.7
33	LC	21	GLY	2.7
21	ZB	31	HIS	2.7
35	OC	156	HIS	2.7
13	RB	76	LYS	2.7
22	AC	69	ALA	2.7
23	BC	156	LYS	2.7
25	Y	48	LYS	2.7
43	RA	13	ALA	2.7
50	DD	7	ALA	2.7
2	B	1213	A	2.7
2	GB	9	U	2.7
2	GB	504	U	2.7
8	MB	68	PRO	2.7
3	HB	28	C	2.7
26	EC	5	GLU	2.7
37	LA	14	ILE	2.7
42	QA	128	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
55	ID	14	TRP	2.7
1	A	1094	G	2.7
1	FB	466	G	2.7
2	GB	117	G	2.7
10	OB	82	ARG	2.7
37	LA	3	ASN	2.7
44	SA	3	LYS	2.7
48	WA	4	LYS	2.7
50	YA	12	LYS	2.7
53	GD	53	ASN	2.7
53	GD	55	LYS	2.7
49	CD	57	LEU	2.7
53	GD	15	LEU	2.7
1	A	982	U	2.7
43	RA	8	GLY	2.7
19	XB	19	LYS	2.7
1	FB	1327	C	2.7
2	GB	1589	C	2.7
2	GB	2175	C	2.7
18	WB	76	TYR	2.7
8	MB	135	LEU	2.7
1	A	230	G	2.7
1	FB	1033	G	2.7
50	DD	76	GLN	2.7
43	RA	63	ILE	2.7
22	AC	1	MET	2.7
23	W	72	ARG	2.7
46	UA	42	THR	2.7
48	WA	31	ARG	2.7
43	WC	116	LYS	2.7
35	JA	200	ALA	2.7
43	RA	62	TYR	2.7
55	ID	18	TYR	2.7
9	NB	50	VAL	2.7
43	WC	86	VAL	2.7
1	FB	1267	C	2.7
35	JA	352	GLN	2.7
35	JA	339	MET	2.7
53	GD	78	ARG	2.7
11	PB	37	LYS	2.7
19	XB	93	GLU	2.7
35	OC	194	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
39	NA	88	LYS	2.7
47	VA	103	THR	2.7
1	A	1022	G	2.7
1	FB	1084	G	2.7
2	B	1238	G	2.7
2	GB	2370	G	2.7
2	GB	2872	G	2.7
43	WC	62	TYR	2.7
10	OB	32	PRO	2.6
8	MB	155	MET	2.6
34	HA	22	A	2.6
41	PA	43	PHE	2.6
41	PA	110	GLN	2.6
44	SA	96	ILE	2.6
54	CB	79	ARG	2.6
54	CB	65	LYS	2.6
9	NB	7	LEU	2.6
43	RA	114	TYR	2.6
38	MA	125	HIS	2.6
2	GB	919	G	2.6
2	GB	2795	G	2.6
3	HB	18	G	2.6
20	YB	95	ILE	2.6
44	XC	58	ASP	2.6
45	TA	21	ILE	2.6
35	OC	235	GLN	2.6
54	CB	75	ASN	2.6
54	HD	9	ASN	2.6
2	GB	1057	A	2.6
8	MB	106	LEU	2.6
13	RB	150	ALA	2.6
21	ZB	95	LEU	2.6
36	KA	215	LEU	2.6
44	XC	32	ALA	2.6
2	GB	894	C	2.6
4	D	16	C	2.6
10	OB	109	ILE	2.6
44	SA	45	ARG	2.6
45	YC	91	ARG	2.6
47	VA	31	LYS	2.6
9	NB	174	GLY	2.6
2	GB	270(M)	U	2.6

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Mol	Chain	Res	Type	RSRZ
2	GB	2348	U	2.6
36	KA	134	GLU	2.6
39	NA	132	ALA	2.6
41	PA	80	VAL	2.6
43	RA	15	ALA	2.6
42	VC	58	TYR	2.6
53	GD	35	SER	2.6
23	BC	88	PHE	2.6
2	GB	267	C	2.6
2	GB	1049	C	2.6
8	H	135	LEU	2.6
49	XA	73	GLU	2.6
14	SB	140	ALA	2.6
26	EC	25	VAL	2.6
1	A	1049	U	2.6
2	GB	1061	U	2.6
8	H	136	ARG	2.6
38	RC	115	ARG	2.6
47	AD	94	ARG	2.6
48	BD	19	ARG	2.6
55	DB	24	ARG	2.6
10	OB	4	ILE	2.6
19	XB	70	ILE	2.6
1	A	1003	G	2.6
1	A	1032(C)	G	2.6
2	B	10	G	2.6
2	B	1099	G	2.6
2	B	2345	G	2.6
36	PC	159	PRO	2.6
55	DB	23	PRO	2.6
26	EC	56	GLN	2.6
26	EC	70	GLN	2.6
34	MC	15	A	2.6
44	XC	10	GLY	2.6
46	UA	109	GLY	2.6
23	BC	75	ASN	2.6
38	MA	77	ASN	2.6
50	DD	68	ASP	2.6
53	BB	53	ASN	2.6
32	KC	42	ARG	2.6
36	KA	137	ARG	2.6
43	RA	82	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
52	AB	68	LYS	2.6
1	A	84	U	2.5
16	P	34	HIS	2.5
23	BC	99	TYR	2.5
35	JA	357	SER	2.5
42	VC	115	SER	2.5
13	RB	104	GLY	2.5
36	PC	240	GLN	2.5
24	CC	75	LEU	2.5
36	PC	61	LEU	2.5
1	A	1224	G	2.5
8	H	36	LYS	2.5
26	EC	7	ARG	2.5
35	JA	330	ASP	2.5
35	OC	261	ARG	2.5
43	RA	121	ARG	2.5
47	AD	114	ARG	2.5
52	FD	22	VAL	2.5
2	GB	363(G)	A	2.5
2	GB	2892	A	2.5
47	AD	2	ALA	2.5
10	OB	88	ILE	2.5
44	SA	74	ILE	2.5
2	B	2804	C	2.5
2	GB	116	C	2.5
20	YB	99	ARG	2.5
38	MA	133	VAL	2.5
39	NA	82	VAL	2.5
22	AC	107	ASP	2.5
36	PC	237	ALA	2.5
44	SA	17	ASP	2.5
44	SA	75	ILE	2.5
43	WC	64	THR	2.5
14	SB	137	TYR	2.5
21	ZB	5	TYR	2.5
35	OC	320	HIS	2.5
9	NB	175	LYS	2.5
22	AC	4	LYS	2.5
22	AC	94	LYS	2.5
35	OC	303	ARG	2.5
37	QC	115	LEU	2.5
41	UC	3	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
48	WA	3	ARG	2.5
55	DB	22	ARG	2.5
9	NB	17	VAL	2.5
37	QC	76	VAL	2.5
41	UC	80	VAL	2.5
37	LA	71	ALA	2.5
37	QC	189	ALA	2.5
26	EC	52	ASP	2.5
47	AD	9	ILE	2.5
50	YA	33	ILE	2.5
21	ZB	60	ARG	2.5
22	AC	81	LYS	2.5
26	EC	24	LEU	2.5
38	MA	115	ARG	2.5
43	RA	19	LEU	2.5
44	SA	46	ARG	2.5
50	YA	18	ARG	2.5
54	CB	104	LEU	2.5
23	BC	174	VAL	2.5
38	MA	62	GLN	2.5
41	UC	105	VAL	2.5
4	D	5	G	2.5
2	GB	31	C	2.5
2	GB	2666	C	2.5
3	HB	27	C	2.5
4	IB	17	C	2.5
23	W	136	PHE	2.5
36	KA	152	PHE	2.5
1	FB	86	U	2.5
2	GB	2797	U	2.5
35	JA	160	LYS	2.5
8	MB	103	LEU	2.5
13	M	79	ARG	2.5
36	KA	96	ARG	2.5
38	MA	22	LYS	2.5
22	AC	66	PRO	2.5
48	WA	39	LEU	2.5
54	HD	62	LEU	2.5
54	HD	83	ARG	2.5
54	HD	84	LEU	2.5
38	MA	43	HIS	2.5
43	RA	117	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
42	QA	97	VAL	2.5
45	YC	84	VAL	2.5
47	VA	101	GLN	2.5
6	F	77	ILE	2.4
26	EC	17	SER	2.4
28	GC	15	ILE	2.4
1	FB	1092	A	2.4
1	FB	1286	A	2.4
23	BC	97	GLU	2.4
44	SA	64	GLU	2.4
25	DC	48	LYS	2.4
29	HC	8	LYS	2.4
43	WC	16	ARG	2.4
44	XC	45	ARG	2.4
54	CB	26	ASN	2.4
1	A	1024	G	2.4
37	QC	15	THR	2.4
47	AD	20	THR	2.4
1	FB	984	C	2.4
2	B	2382	G	2.4
2	B	2805	G	2.4
2	GB	530	G	2.4
1	FB	982	U	2.4
2	GB	1090	U	2.4
35	JA	264	HIS	2.4
12	QB	27	GLY	2.4
24	X	6	GLY	2.4
41	UC	118	VAL	2.4
50	DD	10	GLY	2.4
16	P	55	ALA	2.4
23	W	1	MET	2.4
41	PA	26	PHE	2.4
16	UB	58	LEU	2.4
36	PC	69	LEU	2.4
1	A	1363	A	2.4
1	A	1531	A	2.4
1	FB	1041	A	2.4
1	FB	1201	A	2.4
39	NA	49	PRO	2.4
22	AC	22	GLY	2.4
25	DC	53	VAL	2.4
28	GC	10	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
35	OC	115	VAL	2.4
44	SA	44	VAL	2.4
2	GB	280	C	2.4
8	MB	63	ILE	2.4
36	PC	208	ILE	2.4
45	TA	89	ALA	2.4
54	HD	78	ALA	2.4
55	DB	7	ARG	2.4
23	BC	158	PRO	2.4
35	OC	325	THR	2.4
36	PC	91	PRO	2.4
46	UA	125	PRO	2.4
37	QC	56	ASP	2.4
47	VA	100	GLY	2.4
47	AD	100	GLY	2.4
8	MB	50	ALA	2.4
1	A	983	A	2.4
38	RC	5	ILE	2.4
5	E	276	LYS	2.4
39	NA	20	GLN	2.4
46	UA	19	ARG	2.4
41	UC	26	PHE	2.4
1	FB	981	U	2.4
1	FB	1214	C	2.4
2	B	271(D)	U	2.4
35	OC	271	LEU	2.4
37	QC	52	LEU	2.4
37	QC	188	LEU	2.4
38	RC	21	LEU	2.4
41	PA	12	LEU	2.4
44	SA	40	LEU	2.4
53	GD	71	LEU	2.4
1	A	92	G	2.4
1	A	466	G	2.4
1	FB	951	G	2.4
1	FB	1221	G	2.4
1	FB	1316	G	2.4
2	GB	281	G	2.4
2	GB	2148	G	2.4
9	NB	108	GLY	2.4
35	OC	118	GLY	2.4
36	PC	140	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
20	YB	96	ILE	2.4
33	LC	17	ILE	2.4
35	JA	327	TYR	2.4
44	XC	6	ILE	2.4
44	XC	74	ILE	2.4
45	YC	89	ALA	2.4
47	VA	2	ALA	2.4
13	RB	108	LYS	2.4
22	AC	34	LYS	2.4
46	ZC	119	LYS	2.4
35	JA	306	ARG	2.4
41	UC	4	ARG	2.4
26	EC	10	LEU	2.4
54	HD	10	LEU	2.4
1	A	1093	A	2.4
2	B	1237	A	2.4
16	UB	31	SER	2.4
1	FB	1302	U	2.4
2	GB	2808	U	2.4
8	MB	38	VAL	2.4
36	KA	71	VAL	2.4
37	QC	75	VAL	2.4
39	SC	51	VAL	2.4
42	QA	95	VAL	2.4
2	B	1092	C	2.3
8	H	157	ILE	2.3
16	UB	37	ALA	2.3
38	MA	154	ASN	2.3
46	UA	126	LYS	2.3
47	VA	4	ILE	2.3
48	BD	50	LYS	2.3
1	FB	654	G	2.3
2	GB	1110	G	2.3
2	GB	2807	G	2.3
11	K	8	GLN	2.3
10	OB	145	VAL	2.3
28	GC	35	VAL	2.3
36	KA	165	VAL	2.3
45	YC	109	VAL	2.3
53	BB	11	VAL	2.3
43	WC	123	PRO	2.3
37	QC	97	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
5	JB	274	ARG	2.3
38	MA	23	GLY	2.3
39	NA	46	GLY	2.3
10	OB	97	ILE	2.3
44	XC	100	THR	2.3
54	CB	25	ARG	2.3
36	KA	236	TYR	2.3
39	SC	133	TYR	2.3
41	UC	106	GLN	2.3
42	QA	31	PHE	2.3
25	Y	27	GLU	2.3
38	MA	156	GLU	2.3
1	FB	763	G	2.3
2	B	2795	G	2.3
2	GB	101	G	2.3
2	GB	2116	G	2.3
5	E	98	VAL	2.3
24	CC	5	LYS	2.3
50	DD	12	LYS	2.3
15	TB	39	PRO	2.3
55	ID	9	ARG	2.3
35	OC	152	SER	2.3
35	OC	199	SER	2.3
38	MA	167	GLY	2.3
41	PA	77	SER	2.3
43	RA	115	GLY	2.3
54	CB	96	GLY	2.3
50	DD	17	TYR	2.3
23	W	70	LEU	2.3
35	JA	305	ASP	2.3
2	GB	1065	U	2.3
38	RC	15	GLU	2.3
42	QA	101	PRO	2.3
44	SA	37	PRO	2.3
41	UC	81	GLY	2.3
47	VA	95	GLY	2.3
10	J	94	ALA	2.3
35	OC	189	ALA	2.3
54	CB	56	MET	2.3
13	M	4	SER	2.3
35	OC	192	SER	2.3
2	B	2125	G	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	2168	G	2.3
2	GB	1091	G	2.3
2	GB	2147	G	2.3
2	GB	2751	G	2.3
8	H	66	GLN	2.3
51	ZA	37	LYS	2.3
54	HD	68	LYS	2.3
2	GB	2054	A	2.3
9	NB	114	VAL	2.3
38	MA	105	VAL	2.3
42	VC	53	VAL	2.3
43	RA	109	VAL	2.3
43	RA	110	GLU	2.3
46	UA	16	GLU	2.3
48	WA	25	VAL	2.3
48	WA	35	ARG	2.3
1	A	961	U	2.3
2	B	654	U	2.3
10	J	97	ILE	2.3
44	XC	4	ILE	2.3
44	XC	75	ILE	2.3
13	M	150	ALA	2.3
46	ZC	72	GLY	2.3
54	CB	95	ALA	2.3
2	GB	1053	C	2.3
2	GB	1411	C	2.3
2	GB	1531	C	2.3
2	GB	2692	C	2.3
4	D	61	C	2.3
13	M	100	LEU	2.3
44	SA	19	SER	2.3
8	H	131	TYR	2.3
10	J	25	TYR	2.3
22	AC	101	LYS	2.3
32	KC	36	LYS	2.3
36	PC	37	ASN	2.3
41	UC	109	ASN	2.3
43	RA	29	ASN	2.3
43	RA	78	LYS	2.3
48	BD	43	CYS	2.3
43	RA	83	ARG	2.3
55	ID	6	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
8	H	37	VAL	2.3
43	RA	86	VAL	2.3
8	H	137	GLU	2.2
2	B	2116	G	2.2
28	BA	22	ILE	2.2
8	MB	6	ALA	2.2
38	MA	32	ALA	2.2
1	FB	1364	U	2.2
2	B	896	A	2.2
2	B	2797	U	2.2
2	GB	283	A	2.2
2	GB	895	U	2.2
10	J	47	LEU	2.2
10	OB	47	LEU	2.2
37	LA	47	LEU	2.2
38	MA	155	LEU	2.2
48	BD	6	LEU	2.2
54	CB	99	LEU	2.2
37	LA	167	TRP	2.2
35	JA	197	HIS	2.2
16	P	31	SER	2.2
20	YB	98	LYS	2.2
1	A	88	C	2.2
2	GB	1052	C	2.2
43	WC	93	ARG	2.2
46	ZC	89	ARG	2.2
54	HD	80	ARG	2.2
24	X	12	ASN	2.2
6	F	127	ASP	2.2
35	OC	305	ASP	2.2
54	HD	64	ASP	2.2
36	KA	211	ILE	2.2
44	SA	98	ILE	2.2
25	DC	82	LEU	2.2
54	CB	66	ALA	2.2
55	DB	4	GLY	2.2
48	WA	61	TRP	2.2
1	A	1033	G	2.2
2	B	920	G	2.2
2	GB	1059	G	2.2
39	NA	47	LYS	2.2
44	XC	42	THR	2.2

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Mol	Chain	Res	Type	RSRZ
51	ED	100	LYS	2.2
54	CB	21	LYS	2.2
16	P	7	TYR	2.2
17	VB	95	ARG	2.2
44	XC	70	ARG	2.2
1	A	949	A	2.2
1	FB	1236	A	2.2
2	B	1054	A	2.2
2	GB	1237	A	2.2
43	WC	87	GLN	2.2
38	MA	146	ILE	2.2
48	WA	27	CYS	2.2
55	ID	13	ILE	2.2
1	FB	88	C	2.2
1	FB	1282	C	2.2
2	B	2111	C	2.2
3	HB	4	C	2.2
14	N	140	ALA	2.2
14	SB	37	LEU	2.2
37	LA	42	LEU	2.2
38	MA	102	ASP	2.2
35	OC	299	GLY	2.2
43	RA	84	ALA	2.2
43	RA	106	ALA	2.2
47	AD	42	ALA	2.2
54	CB	103	GLY	2.2
10	OB	131	LYS	2.2
13	RB	107	LYS	2.2
44	XC	3	LYS	2.2
54	HD	30	LYS	2.2
8	H	178	PHE	2.2
36	PC	67	THR	2.2
13	RB	110	TYR	2.2
8	H	78	SER	2.2
1	FB	1125	U	2.2
2	B	1026	U	2.2
50	YA	76	GLN	2.2
9	NB	4	ILE	2.2
35	OC	224	ILE	2.2
2	GB	327	G	2.2
2	GB	1238	G	2.2
7	LB	110	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
10	OB	123	LEU	2.2
35	JA	153	GLU	2.2
47	AD	81	LEU	2.2
50	YA	73	LEU	2.2
38	MA	40	PRO	2.2
44	SA	32	ALA	2.2
44	SA	53	PRO	2.2
54	CB	102	GLY	2.2
44	SA	58	ASP	2.2
48	BD	9	LYS	2.2
49	XA	49	ASP	2.2
10	OB	33	ARG	2.2
24	X	11	ARG	2.2
41	PA	4	ARG	2.2
44	SA	5	ARG	2.2
45	TA	91	ARG	2.2
50	DD	42	ARG	2.2
54	CB	8	ARG	2.2
1	A	962	C	2.2
2	B	2175	C	2.2
4	IA	1	C	2.2
32	KC	34	TRP	2.2
13	RB	128	HIS	2.2
41	PA	75	VAL	2.2
47	VA	98	VAL	2.2
53	GD	67	VAL	2.2
16	UB	27	SER	2.2
25	DC	18	ILE	2.2
35	JA	304	SER	2.2
35	OC	246	ILE	2.2
37	LA	39	ILE	2.2
43	RA	77	ILE	2.2
44	SA	82	ILE	2.2
50	DD	11	SER	2.2
10	OB	44	LEU	2.2
37	LA	43	LEU	2.2
11	PB	68	GLU	2.2
30	IC	20	ASN	2.2
43	WC	11	LYS	2.2
43	WC	43	ALA	2.2
1	A	89	U	2.2
2	GB	29	U	2.2

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Mol	Chain	Res	Type	RSRZ
8	MB	134	GLY	2.2
21	ZB	32	PRO	2.2
32	FA	39	LYS	2.2
1	FB	196	A	2.2
2	GB	1070	A	2.2
1	FB	973	G	2.2
8	MB	28	VAL	2.1
9	I	114	VAL	2.1
15	TB	73	VAL	2.1
23	BC	74	VAL	2.1
36	KA	93	VAL	2.1
43	WC	41	VAL	2.1
49	CD	25	THR	2.1
28	GC	67	TYR	2.1
1	FB	504	C	2.1
2	B	1100	C	2.1
2	GB	790	C	2.1
2	GB	1075	C	2.1
2	GB	2146	C	2.1
3	HB	62	C	2.1
8	H	52	ILE	2.1
8	MB	133	LEU	2.1
15	TB	113	LEU	2.1
16	P	54	LEU	2.1
36	KA	121	LEU	2.1
40	TC	94	GLN	2.1
54	CB	13	LEU	2.1
6	F	204	ALA	2.1
9	NB	110	SER	2.1
13	M	103	ALA	2.1
17	Q	3	ARG	2.1
20	YB	78	GLU	2.1
35	JA	331	GLU	2.1
38	MA	139	ARG	2.1
48	BD	8	GLU	2.1
50	DD	15	PRO	2.1
1	A	1281	U	2.1
2	GB	1078	U	2.1
9	NB	35	VAL	2.1
54	CB	16	HIS	2.1
2	GB	896	A	2.1
36	PC	158	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
47	AD	111	LYS	2.1
48	BD	4	LYS	2.1
1	FB	198	G	2.1
2	GB	830	G	2.1
2	GB	1410	G	2.1
14	SB	38	GLU	2.1
21	U	86	GLY	2.1
35	OC	153	GLU	2.1
35	OC	233	GLY	2.1
54	CB	69	GLY	2.1
1	FB	1325	C	2.1
39	NA	90	VAL	2.1
53	GD	12	ASP	2.1
5	E	275	LYS	2.1
13	RB	88	LEU	2.1
16	UB	73	LEU	2.1
37	LA	204	LEU	2.1
42	QA	127	LEU	2.1
44	XC	99	LYS	2.1
47	VA	13	LYS	2.1
47	VA	109	THR	2.1
54	HD	65	LYS	2.1
14	SB	16	ARG	2.1
50	YA	28	ARG	2.1
8	H	158	ALA	2.1
39	NA	17	ALA	2.1
44	XC	20	ALA	2.1
1	FB	143	A	2.1
1	FB	197	A	2.1
2	B	1783	A	2.1
36	PC	9	GLU	2.1
37	QC	73	PRO	2.1
37	QC	105	GLU	2.1
54	CB	98	PRO	2.1
41	PA	98	SER	2.1
44	XC	69	ASN	2.1
2	GB	1051	G	2.1
2	GB	1056	G	2.1
3	HB	7	G	2.1
36	KA	81	VAL	2.1
40	TC	90	VAL	2.1
2	GB	645	C	2.1

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Mol	Chain	Res	Type	RSRZ
8	MB	29	TRP	2.1
22	AC	87	LYS	2.1
27	FC	20	LYS	2.1
9	I	151	ILE	2.1
19	XB	25	LEU	2.1
36	PC	19	HIS	2.1
39	NA	91	LEU	2.1
39	NA	142	LEU	2.1
53	GD	49	ILE	2.1
22	AC	2	ARG	2.1
10	OB	29	TYR	2.1
44	XC	48	THR	2.1
54	HD	79	ARG	2.1
38	MA	165	MET	2.1
33	LC	5	ALA	2.1
43	RA	61	ALA	2.1
48	WA	59	ALA	2.1
1	FB	85	U	2.1
43	WC	73	GLN	2.1
10	OB	16	GLY	2.1
14	SB	15	GLY	2.1
15	O	7	GLY	2.1
16	UB	90	GLY	2.1
36	PC	99	GLY	2.1
53	BB	54	GLY	2.1
9	NB	10	PRO	2.1
9	NB	118	PRO	2.1
43	WC	2	GLU	2.1
49	XA	2	PRO	2.1
23	BC	86	VAL	2.1
28	BA	33	VAL	2.1
35	OC	317	VAL	2.1
37	QC	135	LYS	2.1
49	XA	48	LYS	2.1
51	ZA	4	LYS	2.1
9	NB	72	ILE	2.1
9	NB	87	LEU	2.1
22	AC	44	ILE	2.1
24	CC	11	ARG	2.1
26	EC	61	LEU	2.1
36	PC	39	ILE	2.1
36	PC	214	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
37	QC	79	ARG	2.1
48	WA	19	ARG	2.1
37	QC	17	ASP	2.1
7	LB	100	THR	2.1
36	KA	73	THR	2.1
37	LA	165	THR	2.1
1	A	186(A)	C	2.1
2	B	2149	G	2.1
2	GB	1487	G	2.1
44	SA	26	ALA	2.1
24	CC	6	GLY	2.1
35	OC	331	GLU	2.1
39	SC	84	PHE	2.1
1	FB	1196	U	2.0
25	Y	53	VAL	2.0
36	PC	8	LYS	2.0
36	PC	133	LYS	2.0
40	TC	72	VAL	2.0
47	VA	7	VAL	2.0
48	WA	58	LYS	2.0
52	FD	23	LYS	2.0
53	GD	11	VAL	2.0
9	NB	152	ARG	2.0
17	VB	93	ARG	2.0
24	CC	74	ARG	2.0
35	OC	238	ASN	2.0
37	QC	87	LEU	2.0
38	MA	108	LEU	2.0
43	RA	42	ARG	2.0
44	SA	51	ARG	2.0
47	VA	94	ARG	2.0
50	DD	6	LEU	2.0
54	CB	24	LEU	2.0
36	PC	97	TRP	2.0
1	FB	572	A	2.0
2	B	363(G)	A	2.0
2	B	2173	A	2.0
2	GB	311	A	2.0
2	GB	1213	A	2.0
10	OB	146	ALA	2.0
35	JA	104	ASP	2.0
36	PC	236	TYR	2.0

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Mol	Chain	Res	Type	RSRZ
37	QC	71	ALA	2.0
37	QC	165	THR	2.0
41	UC	7	ALA	2.0
43	RA	75	ASP	2.0
45	TA	41	THR	2.0
47	VA	21	TYR	2.0
45	TA	119	CYS	2.0
48	BD	5	ALA	2.0
35	OC	154	GLY	2.0
45	TA	118	GLY	2.0
48	WA	36	PHE	2.0
53	GD	8	GLY	2.0
43	RA	49	PRO	2.0
43	WC	49	PRO	2.0
1	FB	174	C	2.0
1	FB	1027	C	2.0
1	FB	1452	C	2.0
2	GB	2145	C	2.0
22	V	94	LYS	2.0
22	AC	45	VAL	2.0
26	Z	19	VAL	2.0
43	RA	28	VAL	2.0
2	B	1062	G	2.0
2	B	2631	G	2.0
2	B	2891	G	2.0
2	GB	1089	G	2.0
2	GB	1591	G	2.0
2	GB	2125	G	2.0
3	C	61	G	2.0
8	H	111	LEU	2.0
31	EA	23	ARG	2.0
36	PC	137	ARG	2.0
38	MA	157	LEU	2.0
39	NA	139	LEU	2.0
50	DD	60	LEU	2.0
54	CB	62	LEU	2.0
22	AC	17	SER	2.0
38	MA	5	ILE	2.0
54	CB	100	ILE	2.0
2	B	1105	U	2.0
4	D	20	U	2.0
8	MB	145	THR	2.0

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Mol	Chain	Res	Type	RSRZ
10	OB	26	ALA	2.0
16	UB	51	ALA	2.0
42	QA	94	TYR	2.0
43	RA	4	TYR	2.0
47	AD	21	TYR	2.0
48	BD	34	TYR	2.0
43	RA	105	ASP	2.0
9	NB	123	PHE	2.0
35	OC	234	GLY	2.0
37	QC	78	GLY	2.0
48	WA	43	CYS	2.0
39	NA	93	PRO	2.0
53	GD	6	LYS	2.0
2	B	529	A	2.0
8	H	38	VAL	2.0
38	MA	179	GLU	2.0
42	QA	136	GLU	2.0
25	Y	20	ARG	2.0
38	RC	66	ARG	2.0
38	RC	140	VAL	2.0
42	VC	84	ARG	2.0
43	WC	83	ARG	2.0
46	UA	82	VAL	2.0
53	GD	58	VAL	2.0
8	MB	94	LEU	2.0
39	NA	11	ILE	2.0
47	AD	4	ILE	2.0
2	GB	154(A)	C	2.0
2	GB	1468	C	2.0
4	NC	1	C	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	PSU	IB	55	20/21	0.61	0.15	182,183,184,184	0
4	4SU	D	8	20/21	0.62	0.11	163,164,165,165	0
4	5MU	IB	54	21/22	0.68	0.13	180,181,182,183	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	PSU	D	55	20/21	0.69	0.11	168,169,171,171	0
4	5MU	D	54	21/22	0.70	0.12	167,167,169,169	0
4	4SU	IB	8	20/21	0.71	0.10	169,170,170,170	0
4	5MC	D	32	21/22	0.75	0.14	139,139,139,139	0
4	5MU	NC	54	21/22	0.84	0.17	97,98,100,100	0
34	PSU	HA	19	20/21	0.85	0.13	87,87,88,88	0
1	PSU	A	516	20/21	0.87	0.11	90,92,95,95	0
1	2MG	A	1207	24/25	0.88	0.10	107,110,114,115	0
4	5MC	IA	32	21/22	0.88	0.12	84,84,85,85	0
4	5MU	IA	54	21/22	0.88	0.16	86,88,90,90	0
4	PSU	IA	55	20/21	0.88	0.13	87,88,90,90	0
1	2MG	FB	1207	24/25	0.88	0.11	108,110,113,114	0
34	PSU	MC	19	20/21	0.88	0.12	91,91,91,91	0
4	5MC	IB	32	21/22	0.89	0.11	147,147,148,148	0
4	PSU	NC	55	20/21	0.89	0.10	97,98,99,99	0
1	PSU	FB	516	20/21	0.90	0.10	83,84,87,87	0
1	5MC	FB	967	21/22	0.90	0.13	88,89,91,92	0
46	0TD	ZC	92	10/11	0.90	0.16	77,78,78,78	0
46	0TD	UA	92	10/11	0.90	0.19	81,81,81,81	0
2	PSU	GB	1911	20/21	0.90	0.11	72,75,76,77	0
1	7MG	FB	527	24/25	0.91	0.12	74,75,76,77	0
2	5MU	B	1915	21/22	0.91	0.09	75,77,79,79	0
4	5MC	NC	32	21/22	0.91	0.11	85,86,86,86	0
1	5MC	A	1400	21/22	0.91	0.12	80,82,85,86	0
1	4OC	A	1402	22/23	0.92	0.11	72,73,75,75	0
4	4SU	IA	8	20/21	0.92	0.10	84,86,86,87	0
1	M2G	FB	966	25/26	0.92	0.12	86,88,90,91	0
2	PSU	GB	1917	20/21	0.92	0.08	77,79,81,82	0
2	2MA	GB	2503	23/24	0.92	0.12	51,52,53,53	0
2	5MU	GB	1915	21/22	0.93	0.07	88,89,91,92	0
4	4SU	NC	8	20/21	0.93	0.08	89,91,92,92	0
1	5MC	FB	1400	21/22	0.93	0.11	78,80,82,83	0
2	PSU	B	1911	20/21	0.93	0.11	63,65,67,67	0
1	4OC	FB	1402	22/23	0.94	0.10	73,74,75,75	0
2	PSU	B	1917	20/21	0.94	0.08	64,66,68,69	0
2	4OC	GB	1920	21/23	0.94	0.09	70,72,73,74	0
2	2MU	GB	2552	21/23	0.95	0.09	56,57,58,58	0
2	PSU	GB	2605	20/21	0.95	0.09	51,52,52,53	0
1	5MC	A	1404	21/22	0.95	0.09	64,66,67,67	0
1	5MC	FB	1404	21/22	0.95	0.11	65,66,66,66	0
1	UR3	FB	1498	21/22	0.95	0.12	70,70,71,71	0
1	MA6	FB	1519	24/25	0.95	0.10	63,65,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	4OC	B	1920	21/23	0.95	0.10	61,63,64,65	0
2	5MU	B	1939	21/22	0.95	0.11	44,45,46,46	0
1	5MC	A	1407	21/22	0.95	0.10	64,65,67,68	0
1	M2G	A	966	25/26	0.95	0.11	88,90,91,92	0
2	5MC	GB	1942	21/22	0.95	0.09	59,60,61,62	0
2	OMG	GB	2251	24/25	0.95	0.10	57,58,60,60	0
1	7MG	A	527	24/25	0.95	0.10	79,81,83,84	0
1	MA6	A	1519	24/25	0.96	0.09	60,63,64,64	0
1	5MC	A	967	21/22	0.96	0.08	90,91,93,93	0
2	5MU	GB	1939	21/22	0.96	0.11	53,54,54,55	0
1	UR3	A	1498	21/22	0.96	0.09	67,68,69,69	0
2	5MC	GB	1962	21/22	0.96	0.09	58,59,60,61	0
1	5MC	FB	1407	21/22	0.96	0.09	69,70,71,71	0
2	5MC	B	1942	21/22	0.96	0.08	49,50,51,51	0
2	OMG	B	2251	24/25	0.96	0.09	44,44,45,45	0
2	2MA	B	2503	23/24	0.96	0.09	37,38,38,38	0
2	PSU	B	2605	20/21	0.96	0.09	41,42,43,43	0
1	MA6	FB	1518	24/25	0.97	0.10	63,64,66,66	0
2	2MU	B	2552	21/23	0.97	0.09	45,46,47,47	0
1	MA6	A	1518	24/25	0.97	0.08	59,62,63,63	0
2	5MC	B	1962	21/22	0.97	0.07	50,52,53,54	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3443	1/1	-0.70	0.30	176,176,176,176	0
56	MG	GB	3517	1/1	-0.67	0.31	219,219,219,219	0
56	MG	GB	3441	1/1	-0.55	0.30	155,155,155,155	0
56	MG	B	3402	1/1	-0.54	0.34	179,179,179,179	0
56	MG	GB	3293	1/1	-0.52	0.44	190,190,190,190	0
56	MG	B	3782	1/1	-0.51	0.44	175,175,175,175	0
56	MG	B	3798	1/1	-0.46	0.34	157,157,157,157	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3449	1/1	-0.41	0.33	197,197,197,197	0
56	MG	B	3669	1/1	-0.39	0.29	146,146,146,146	0
56	MG	B	3721	1/1	-0.35	0.39	147,147,147,147	0
56	MG	GB	3478	1/1	-0.34	0.31	187,187,187,187	0
56	MG	B	3493	1/1	-0.34	0.36	182,182,182,182	0
56	MG	GB	3393	1/1	-0.33	0.27	192,192,192,192	0
56	MG	IB	104	1/1	-0.31	0.27	163,163,163,163	0
56	MG	GB	3585	1/1	-0.30	0.30	158,158,158,158	0
56	MG	B	3496	1/1	-0.30	0.19	167,167,167,167	0
56	MG	GB	3472	1/1	-0.28	0.39	189,189,189,189	0
56	MG	GB	3188	1/1	-0.27	0.45	179,179,179,179	0
56	MG	GB	3504	1/1	-0.26	0.22	195,195,195,195	0
56	MG	FB	1695	1/1	-0.17	0.38	156,156,156,156	0
56	MG	A	1877	1/1	-0.14	0.23	167,167,167,167	0
56	MG	GC	103	1/1	-0.12	0.36	135,135,135,135	0
56	MG	A	1792	1/1	-0.11	0.42	132,132,132,132	0
56	MG	GB	3663	1/1	-0.11	0.31	206,206,206,206	0
56	MG	A	1702	1/1	-0.10	0.30	147,147,147,147	0
56	MG	B	3648	1/1	-0.10	0.29	146,146,146,146	0
56	MG	FB	1811	1/1	-0.09	0.29	143,143,143,143	0
56	MG	HB	216	1/1	-0.05	0.29	136,136,136,136	0
56	MG	GB	3261	1/1	-0.04	0.19	134,134,134,134	0
56	MG	A	1870	1/1	-0.04	0.24	123,123,123,123	0
56	MG	GB	3383	1/1	-0.04	0.34	191,191,191,191	0
56	MG	GB	3193	1/1	-0.03	0.28	141,141,141,141	0
56	MG	A	1804	1/1	-0.02	0.43	136,136,136,136	0
56	MG	GB	3209	1/1	-0.01	0.26	133,133,133,133	0
56	MG	B	3413	1/1	0.00	0.24	140,140,140,140	0
56	MG	B	3636	1/1	0.01	0.37	171,171,171,171	0
56	MG	B	3353	1/1	0.01	0.32	173,173,173,173	0
56	MG	B	3615	1/1	0.03	0.39	159,159,159,159	0
56	MG	B	3298	1/1	0.04	0.31	168,168,168,168	0
56	MG	GB	2947	1/1	0.05	0.52	109,109,109,109	0
56	MG	FB	1876	1/1	0.06	0.20	170,170,170,170	0
56	MG	FB	1871	1/1	0.06	0.36	114,114,114,114	0
56	MG	GB	3229	1/1	0.07	0.34	120,120,120,120	0
56	MG	A	1874	1/1	0.07	0.41	126,126,126,126	0
56	MG	A	1765	1/1	0.08	0.27	152,152,152,152	0
56	MG	FB	1686	1/1	0.08	0.43	124,124,124,124	0
56	MG	GB	3586	1/1	0.10	0.27	187,187,187,187	0
56	MG	HB	208	1/1	0.11	0.26	126,126,126,126	0
56	MG	GB	3207	1/1	0.11	0.24	126,126,126,126	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3467	1/1	0.12	0.23	120,120,120,120	0
56	MG	KA	303	1/1	0.12	0.19	130,130,130,130	0
56	MG	B	3667	1/1	0.12	0.25	145,145,145,145	0
56	MG	FB	1727	1/1	0.14	0.34	141,141,141,141	0
56	MG	B	3389	1/1	0.14	0.32	124,124,124,124	0
56	MG	GB	3459	1/1	0.15	0.21	140,140,140,140	0
56	MG	FB	1906	1/1	0.16	0.36	136,136,136,136	0
56	MG	FB	1767	1/1	0.18	0.21	121,121,121,121	0
56	MG	FB	1647	1/1	0.18	0.25	143,143,143,143	0
56	MG	A	1642	1/1	0.19	0.37	125,125,125,125	0
56	MG	B	3515	1/1	0.20	0.36	167,167,167,167	0
56	MG	B	3749	1/1	0.21	0.25	130,130,130,130	0
56	MG	IB	103	1/1	0.21	0.14	146,146,146,146	0
56	MG	FB	1870	1/1	0.22	0.18	127,127,127,127	0
56	MG	A	1731	1/1	0.22	0.24	134,134,134,134	0
56	MG	GB	3001	1/1	0.22	0.45	111,111,111,111	0
56	MG	FB	1826	1/1	0.22	0.20	143,143,143,143	0
56	MG	GB	3221	1/1	0.23	0.36	164,164,164,164	0
56	MG	FB	1786	1/1	0.24	0.27	119,119,119,119	0
56	MG	GB	3314	1/1	0.24	0.28	140,140,140,140	0
56	MG	B	3791	1/1	0.24	0.27	139,139,139,139	0
56	MG	FB	1931	1/1	0.24	0.24	144,144,144,144	0
56	MG	FB	1821	1/1	0.24	0.17	135,135,135,135	0
56	MG	A	1875	1/1	0.25	0.33	126,126,126,126	0
56	MG	FB	1917	1/1	0.25	0.45	110,110,110,110	0
56	MG	FB	1709	1/1	0.26	0.39	130,130,130,130	0
56	MG	B	3701	1/1	0.26	0.28	115,115,115,115	0
56	MG	A	1669	1/1	0.26	0.59	114,114,114,114	0
56	MG	GB	3286	1/1	0.27	0.38	125,125,125,125	0
56	MG	QC	303	1/1	0.27	0.30	120,120,120,120	0
56	MG	GB	3230	1/1	0.28	0.31	110,110,110,110	0
56	MG	B	3445	1/1	0.28	0.30	116,116,116,116	0
56	MG	XC	201	1/1	0.28	0.40	112,112,112,112	0
56	MG	GB	3476	1/1	0.29	0.35	130,130,130,130	0
56	MG	GB	3270	1/1	0.29	0.26	97,97,97,97	0
56	MG	PC	303	1/1	0.30	0.24	133,133,133,133	0
56	MG	A	1845	1/1	0.30	0.46	107,107,107,107	0
56	MG	B	3787	1/1	0.30	0.24	132,132,132,132	0
56	MG	B	3834	1/1	0.31	0.54	165,165,165,165	0
56	MG	GB	3356	1/1	0.31	0.14	134,134,134,134	0
56	MG	FB	1862	1/1	0.31	0.44	118,118,118,118	0
56	MG	D	102	1/1	0.31	0.25	153,153,153,153	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3139	1/1	0.32	0.33	125,125,125,125	0
56	MG	LA	302	1/1	0.32	0.20	119,119,119,119	0
56	MG	FB	1861	1/1	0.33	0.21	119,119,119,119	0
56	MG	OC	407	1/1	0.33	0.20	109,109,109,109	0
56	MG	HB	217	1/1	0.33	0.39	111,111,111,111	0
56	MG	B	3795	1/1	0.33	0.27	151,151,151,151	0
56	MG	B	3685	1/1	0.33	0.34	117,117,117,117	0
56	MG	OB	202	1/1	0.35	0.17	115,115,115,115	0
56	MG	B	3342	1/1	0.35	0.17	115,115,115,115	0
56	MG	GB	3651	1/1	0.35	0.18	130,130,130,130	0
56	MG	GB	3255	1/1	0.36	0.23	100,100,100,100	0
56	MG	FB	1919	1/1	0.36	0.27	126,126,126,126	0
56	MG	A	1760	1/1	0.36	0.38	136,136,136,136	0
56	MG	HB	207	1/1	0.37	0.47	107,107,107,107	0
56	MG	B	3818	1/1	0.37	0.23	177,177,177,177	0
56	MG	FB	1806	1/1	0.39	0.23	135,135,135,135	0
56	MG	RA	201	1/1	0.39	0.39	123,123,123,123	0
56	MG	PC	302	1/1	0.39	0.32	104,104,104,104	0
56	MG	B	3677	1/1	0.40	0.16	149,149,149,149	0
56	MG	A	1882	1/1	0.41	0.32	104,104,104,104	0
56	MG	B	3606	1/1	0.41	0.26	125,125,125,125	0
56	MG	B	3586	1/1	0.42	0.24	116,116,116,116	0
56	MG	GB	3666	1/1	0.42	0.30	125,125,125,125	0
56	MG	A	1746	1/1	0.42	0.27	141,141,141,141	0
56	MG	KA	302	1/1	0.42	0.24	123,123,123,123	0
56	MG	GB	3662	1/1	0.42	0.22	117,117,117,117	0
56	MG	FB	1613	1/1	0.43	0.38	80,80,80,80	0
56	MG	SA	201	1/1	0.43	0.53	120,120,120,120	0
56	MG	PC	301	1/1	0.44	0.31	115,115,115,115	0
56	MG	NB	201	1/1	0.44	0.39	130,130,130,130	0
56	MG	FB	1792	1/1	0.44	0.21	165,165,165,165	0
56	MG	A	1885	1/1	0.44	0.22	135,135,135,135	0
56	MG	GB	3465	1/1	0.44	0.25	114,114,114,114	0
56	MG	FB	1673	1/1	0.45	0.38	113,113,113,113	0
56	MG	NB	202	1/1	0.45	0.28	120,120,120,120	0
56	MG	GB	3426	1/1	0.45	0.34	117,117,117,117	0
56	MG	B	3166	1/1	0.45	0.33	93,93,93,93	0
56	MG	WA	101	1/1	0.45	0.44	109,109,109,109	0
56	MG	HB	221	1/1	0.46	0.41	114,114,114,114	0
56	MG	GB	3324	1/1	0.47	0.25	105,105,105,105	0
56	MG	OC	402	1/1	0.47	0.22	110,110,110,110	0
56	MG	A	1785	1/1	0.48	0.25	107,107,107,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	GB	3540	1/1	0.48	0.36	115,115,115,115	0
56	MG	PC	304	1/1	0.48	0.16	135,135,135,135	0
56	MG	FB	1732	1/1	0.48	0.34	105,105,105,105	0
56	MG	GC	102	1/1	0.48	0.21	127,127,127,127	0
56	MG	SC	205	1/1	0.49	0.13	99,99,99,99	0
56	MG	FB	1943	1/1	0.49	0.22	105,105,105,105	0
56	MG	BC	306	1/1	0.50	0.13	108,108,108,108	0
56	MG	RA	202	1/1	0.50	0.58	117,117,117,117	0
56	MG	GD	101	1/1	0.50	0.40	99,99,99,99	0
56	MG	FB	1663	1/1	0.51	0.24	156,156,156,156	0
56	MG	MB	204	1/1	0.51	0.24	115,115,115,115	0
56	MG	FB	1925	1/1	0.51	0.11	147,147,147,147	0
56	MG	GB	3632	1/1	0.52	0.21	130,130,130,130	0
56	MG	A	1824	1/1	0.52	0.23	111,111,111,111	0
56	MG	OC	403	1/1	0.52	0.20	112,112,112,112	0
56	MG	FB	1885	1/1	0.52	0.38	115,115,115,115	0
56	MG	MC	101	1/1	0.53	0.38	94,94,94,94	0
56	MG	B	3291	1/1	0.53	0.19	109,109,109,109	0
56	MG	WC	202	1/1	0.53	0.23	121,121,121,121	0
56	MG	GB	3445	1/1	0.53	0.21	122,122,122,122	0
56	MG	FB	1631	1/1	0.53	0.46	96,96,96,96	0
56	MG	B	3485	1/1	0.54	0.23	117,117,117,117	0
56	MG	A	1724	1/1	0.54	0.35	68,68,68,68	0
56	MG	A	1688	1/1	0.54	0.33	82,82,82,82	0
56	MG	NA	201	1/1	0.54	0.33	100,100,100,100	0
56	MG	FB	1915	1/1	0.55	0.16	87,87,87,87	0
56	MG	B	3629	1/1	0.55	0.20	125,125,125,125	0
56	MG	GB	3086	1/1	0.55	0.30	107,107,107,107	0
56	MG	GB	2945	1/1	0.55	0.31	92,92,92,92	0
56	MG	A	1613	1/1	0.56	0.18	79,79,79,79	0
56	MG	A	1801	1/1	0.56	0.11	97,97,97,97	0
56	MG	FB	1918	1/1	0.56	0.17	92,92,92,92	0
56	MG	B	3707	1/1	0.56	0.13	113,113,113,113	0
56	MG	GB	3218	1/1	0.56	0.26	61,61,61,61	0
56	MG	A	1710	1/1	0.56	0.19	135,135,135,135	0
56	MG	GB	3299	1/1	0.56	0.14	134,134,134,134	0
56	MG	B	3411	1/1	0.56	0.17	78,78,78,78	0
56	MG	HB	204	1/1	0.56	0.33	91,91,91,91	0
56	MG	HB	210	1/1	0.57	0.22	114,114,114,114	0
56	MG	FB	1791	1/1	0.57	0.28	105,105,105,105	0
56	MG	A	1799	1/1	0.57	0.40	118,118,118,118	0
56	MG	HB	218	1/1	0.57	0.29	116,116,116,116	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	A	1631	1/1	0.57	0.55	98,98,98,98	0
56	MG	HB	230	1/1	0.57	0.18	131,131,131,131	0
56	MG	FB	1807	1/1	0.57	0.32	97,97,97,97	0
56	MG	VA	203	1/1	0.58	0.39	102,102,102,102	0
56	MG	BC	302	1/1	0.58	0.24	109,109,109,109	0
56	MG	QA	202	1/1	0.58	0.18	100,100,100,100	0
56	MG	FB	1741	1/1	0.58	0.27	127,127,127,127	0
56	MG	B	3541	1/1	0.58	0.20	120,120,120,120	0
56	MG	BA	104	1/1	0.58	0.21	105,105,105,105	0
56	MG	GB	2944	1/1	0.58	0.34	90,90,90,90	0
56	MG	A	1851	1/1	0.58	0.17	117,117,117,117	0
56	MG	FB	1724	1/1	0.58	0.21	142,142,142,142	0
56	MG	FB	1678	1/1	0.59	0.25	70,70,70,70	0
56	MG	A	1621	1/1	0.59	0.42	85,85,85,85	0
56	MG	RA	204	1/1	0.59	0.11	137,137,137,137	0
56	MG	BC	305	1/1	0.59	0.23	110,110,110,110	0
56	MG	B	3279	1/1	0.59	0.24	75,75,75,75	0
56	MG	GB	3675	1/1	0.59	0.19	134,134,134,134	0
56	MG	B	3550	1/1	0.59	0.21	147,147,147,147	0
56	MG	A	1864	1/1	0.59	0.15	138,138,138,138	0
56	MG	GB	3220	1/1	0.59	0.26	121,121,121,121	0
56	MG	GB	3420	1/1	0.59	0.33	99,99,99,99	0
56	MG	A	1686	1/1	0.60	0.21	87,87,87,87	0
56	MG	GB	3227	1/1	0.60	0.27	95,95,95,95	0
56	MG	VA	202	1/1	0.60	0.28	100,100,100,100	0
56	MG	FB	1697	1/1	0.60	0.38	94,94,94,94	0
56	MG	GB	3452	1/1	0.60	0.24	74,74,74,74	0
56	MG	A	1828	1/1	0.60	0.25	106,106,106,106	0
56	MG	GB	3357	1/1	0.60	0.17	152,152,152,152	0
56	MG	GB	3361	1/1	0.60	0.22	91,91,91,91	0
56	MG	B	3796	1/1	0.60	0.23	113,113,113,113	0
56	MG	A	1737	1/1	0.60	0.24	106,106,106,106	0
56	MG	GB	3101	1/1	0.60	0.35	115,115,115,115	0
56	MG	GB	3705	1/1	0.61	0.32	104,104,104,104	0
56	MG	A	1749	1/1	0.61	0.32	110,110,110,110	0
56	MG	HB	206	1/1	0.61	0.30	118,118,118,118	0
56	MG	FB	1869	1/1	0.61	0.23	109,109,109,109	0
56	MG	XA	101	1/1	0.61	0.09	86,86,86,86	0
56	MG	GB	3607	1/1	0.61	0.25	111,111,111,111	0
56	MG	FB	1899	1/1	0.61	0.25	86,86,86,86	0
56	MG	C	239	1/1	0.62	0.17	87,87,87,87	0
56	MG	D	101	1/1	0.62	0.30	100,100,100,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	B	3405	1/1	0.62	0.18	124,124,124,124	0
56	MG	GB	3059	1/1	0.62	0.40	91,91,91,91	0
56	MG	QC	301	1/1	0.62	0.28	97,97,97,97	0
56	MG	MB	203	1/1	0.62	0.47	116,116,116,116	0
56	MG	VA	201	1/1	0.62	0.22	123,123,123,123	0
56	MG	A	1872	1/1	0.62	0.20	111,111,111,111	0
56	MG	B	3023	1/1	0.62	0.26	75,75,75,75	0
56	MG	GB	3170	1/1	0.62	0.23	77,77,77,77	0
56	MG	GB	3622	1/1	0.63	0.29	105,105,105,105	0
56	MG	A	1713	1/1	0.63	0.31	88,88,88,88	0
56	MG	B	3574	1/1	0.63	0.15	117,117,117,117	0
56	MG	A	1725	1/1	0.63	0.32	114,114,114,114	0
56	MG	A	1812	1/1	0.63	0.32	128,128,128,128	0
56	MG	B	3674	1/1	0.63	0.14	131,131,131,131	0
56	MG	FB	1720	1/1	0.63	0.23	81,81,81,81	0
56	MG	GB	3338	1/1	0.63	0.13	71,71,71,71	0
56	MG	GB	3250	1/1	0.63	0.23	77,77,77,77	0
56	MG	A	1815	1/1	0.63	0.21	108,108,108,108	0
56	MG	A	1778	1/1	0.63	0.32	104,104,104,104	0
56	MG	HB	222	1/1	0.64	0.23	108,108,108,108	0
56	MG	GB	3668	1/1	0.64	0.34	68,68,68,68	0
56	MG	GB	3531	1/1	0.64	0.21	106,106,106,106	0
56	MG	FB	1758	1/1	0.64	0.42	129,129,129,129	0
56	MG	HB	203	1/1	0.64	0.27	101,101,101,101	0
56	MG	A	1833	1/1	0.64	0.54	116,116,116,116	0
56	MG	FB	1864	1/1	0.64	0.22	103,103,103,103	0
56	MG	A	1696	1/1	0.64	0.23	157,157,157,157	0
56	MG	GB	3084	1/1	0.64	0.27	79,79,79,79	0
56	MG	GB	3424	1/1	0.64	0.17	128,128,128,128	0
56	MG	FB	1717	1/1	0.64	0.35	74,74,74,74	0
56	MG	B	3634	1/1	0.64	0.26	106,106,106,106	0
56	MG	GB	3219	1/1	0.64	0.26	85,85,85,85	0
56	MG	GB	3447	1/1	0.64	0.18	199,199,199,199	0
56	MG	PA	202	1/1	0.65	0.23	102,102,102,102	0
56	MG	FB	1902	1/1	0.65	0.18	132,132,132,132	0
56	MG	GB	2943	1/1	0.65	0.38	92,92,92,92	0
56	MG	W	304	1/1	0.65	0.20	82,82,82,82	0
56	MG	ZA	201	1/1	0.65	0.24	85,85,85,85	0
56	MG	GB	3592	1/1	0.65	0.21	116,116,116,116	0
56	MG	A	1670	1/1	0.65	0.22	122,122,122,122	0
56	MG	B	3554	1/1	0.65	0.14	60,60,60,60	0
56	MG	FB	1835	1/1	0.65	0.21	104,104,104,104	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	RA	203	1/1	0.65	0.59	119,119,119,119	0
56	MG	YC	206	1/1	0.65	0.18	88,88,88,88	0
56	MG	GB	3656	1/1	0.65	0.16	93,93,93,93	0
56	MG	A	1757	1/1	0.66	0.20	118,118,118,118	0
56	MG	GB	3528	1/1	0.66	0.13	79,79,79,79	0
56	MG	GB	3243	1/1	0.66	0.30	93,93,93,93	0
56	MG	FB	1753	1/1	0.66	0.29	92,92,92,92	0
56	MG	FB	1939	1/1	0.66	0.43	98,98,98,98	0
56	MG	FB	1730	1/1	0.66	0.18	78,78,78,78	0
56	MG	EC	103	1/1	0.66	0.15	90,90,90,90	0
56	MG	IB	102	1/1	0.66	0.20	112,112,112,112	0
56	MG	IA	108	1/1	0.66	0.28	82,82,82,82	0
56	MG	GB	3423	1/1	0.66	0.23	75,75,75,75	0
56	MG	HB	213	1/1	0.66	0.19	122,122,122,122	0
56	MG	HB	214	1/1	0.66	0.34	107,107,107,107	0
56	MG	HB	211	1/1	0.67	0.26	87,87,87,87	0
56	MG	GB	3614	1/1	0.67	0.14	139,139,139,139	0
56	MG	FB	1800	1/1	0.67	0.31	92,92,92,92	0
56	MG	GB	3257	1/1	0.67	0.18	86,86,86,86	0
56	MG	FB	1868	1/1	0.67	0.33	87,87,87,87	0
56	MG	GB	3654	1/1	0.67	0.19	72,72,72,72	0
56	MG	GB	3419	1/1	0.67	0.08	74,74,74,74	0
56	MG	JA	412	1/1	0.67	0.13	107,107,107,107	0
56	MG	B	3590	1/1	0.67	0.28	95,95,95,95	0
56	MG	A	1677	1/1	0.67	0.27	105,105,105,105	0
56	MG	GB	3298	1/1	0.67	0.27	80,80,80,80	0
56	MG	A	1719	1/1	0.67	0.20	101,101,101,101	0
56	MG	FB	1722	1/1	0.67	0.16	101,101,101,101	0
56	MG	A	1610	1/1	0.67	0.41	78,78,78,78	0
56	MG	GB	2940	1/1	0.67	0.32	79,79,79,79	0
56	MG	GB	3589	1/1	0.67	0.25	94,94,94,94	0
56	MG	A	1800	1/1	0.67	0.23	132,132,132,132	0
56	MG	GB	3596	1/1	0.67	0.38	90,90,90,90	0
56	MG	SA	202	1/1	0.67	0.38	125,125,125,125	0
56	MG	GB	3626	1/1	0.68	0.17	81,81,81,81	0
56	MG	FB	1938	1/1	0.68	0.13	104,104,104,104	0
56	MG	A	1727	1/1	0.68	0.31	92,92,92,92	0
56	MG	FB	1940	1/1	0.68	0.19	94,94,94,94	0
56	MG	C	240	1/1	0.68	0.19	75,75,75,75	0
56	MG	A	1722	1/1	0.68	0.25	98,98,98,98	0
56	MG	A	1789	1/1	0.68	0.18	87,87,87,87	0
56	MG	H	201	1/1	0.68	0.22	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	P	201	1/1	0.68	0.12	82,82,82,82	0
56	MG	A	1813	1/1	0.68	0.13	89,89,89,89	0
56	MG	BC	307	1/1	0.68	0.24	104,104,104,104	0
56	MG	EC	101	1/1	0.68	0.18	95,95,95,95	0
56	MG	GB	3682	1/1	0.68	0.21	77,77,77,77	0
56	MG	B	3378	1/1	0.68	0.20	111,111,111,111	0
56	MG	GB	3022	1/1	0.68	0.43	63,63,63,63	0
56	MG	GB	3039	1/1	0.68	0.28	52,52,52,52	0
56	MG	DA	104	1/1	0.68	0.11	71,71,71,71	0
56	MG	B	3644	1/1	0.68	0.17	146,146,146,146	0
56	MG	JA	410	1/1	0.68	0.10	96,96,96,96	0
56	MG	B	2991	1/1	0.68	0.30	56,56,56,56	0
56	MG	B	3792	1/1	0.68	0.18	100,100,100,100	0
56	MG	FB	1616	1/1	0.68	0.30	87,87,87,87	0
56	MG	A	1715	1/1	0.68	0.17	102,102,102,102	0
56	MG	FB	1633	1/1	0.68	0.44	68,68,68,68	0
56	MG	A	1714	1/1	0.68	0.38	97,97,97,97	0
56	MG	GB	3385	1/1	0.68	0.25	98,98,98,98	0
56	MG	UC	202	1/1	0.68	0.23	105,105,105,105	0
56	MG	B	3188	1/1	0.68	0.29	74,74,74,74	0
56	MG	PA	201	1/1	0.68	0.12	99,99,99,99	0
56	MG	B	3235	1/1	0.68	0.23	72,72,72,72	0
56	MG	A	1773	1/1	0.68	0.36	88,88,88,88	0
56	MG	FB	1896	1/1	0.69	0.15	82,82,82,82	0
56	MG	GB	2923	1/1	0.69	0.34	62,62,62,62	0
56	MG	B	3283	1/1	0.69	0.25	92,92,92,92	0
56	MG	GB	3281	1/1	0.69	0.16	72,72,72,72	0
56	MG	NC	103	1/1	0.69	0.23	84,84,84,84	0
56	MG	A	1803	1/1	0.69	0.16	103,103,103,103	0
56	MG	A	1745	1/1	0.69	0.24	78,78,78,78	0
56	MG	A	1775	1/1	0.69	0.22	96,96,96,96	0
56	MG	B	3349	1/1	0.69	0.26	132,132,132,132	0
56	MG	B	3778	1/1	0.69	0.22	67,67,67,67	0
56	MG	B	3241	1/1	0.69	0.14	77,77,77,77	0
56	MG	GB	3602	1/1	0.69	0.17	75,75,75,75	0
56	MG	FB	1748	1/1	0.69	0.22	116,116,116,116	0
56	MG	NA	202	1/1	0.69	0.24	101,101,101,101	0
56	MG	YB	203	1/1	0.69	0.19	86,86,86,86	0
56	MG	UC	201	1/1	0.69	0.28	105,105,105,105	0
56	MG	FB	1932	1/1	0.69	0.24	89,89,89,89	0
56	MG	A	1649	1/1	0.69	0.29	101,101,101,101	0
56	MG	GB	3362	1/1	0.69	0.24	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1891	1/1	0.69	0.17	132,132,132,132	0
56	MG	FB	1893	1/1	0.69	0.31	86,86,86,86	0
56	MG	A	1747	1/1	0.70	0.12	104,104,104,104	0
56	MG	GB	3224	1/1	0.70	0.26	61,61,61,61	0
56	MG	XA	102	1/1	0.70	0.19	88,88,88,88	0
56	MG	IA	118	1/1	0.70	0.09	67,67,67,67	0
56	MG	UB	201	1/1	0.70	0.27	99,99,99,99	0
56	MG	MA	303	1/1	0.70	0.20	101,101,101,101	0
56	MG	GB	3142	1/1	0.70	0.22	50,50,50,50	0
56	MG	FB	1793	1/1	0.70	0.38	98,98,98,98	0
56	MG	A	1668	1/1	0.70	0.39	80,80,80,80	0
56	MG	FB	1629	1/1	0.70	0.36	66,66,66,66	0
56	MG	FB	1740	1/1	0.70	0.20	96,96,96,96	0
56	MG	B	3009	1/1	0.70	0.28	72,72,72,72	0
56	MG	FB	1703	1/1	0.70	0.24	86,86,86,86	0
56	MG	A	1808	1/1	0.70	0.24	94,94,94,94	0
56	MG	FB	1646	1/1	0.70	0.25	81,81,81,81	0
56	MG	GB	3487	1/1	0.70	0.16	79,79,79,79	0
56	MG	GB	3194	1/1	0.71	0.15	62,62,62,62	0
56	MG	A	1630	1/1	0.71	0.48	88,88,88,88	0
56	MG	GB	3394	1/1	0.71	0.16	77,77,77,77	0
56	MG	GB	3006	1/1	0.71	0.34	83,83,83,83	0
56	MG	A	1859	1/1	0.71	0.33	90,90,90,90	0
56	MG	FB	1747	1/1	0.71	0.24	101,101,101,101	0
56	MG	JA	408	1/1	0.71	0.24	97,97,97,97	0
56	MG	GB	3701	1/1	0.71	0.19	70,70,70,70	0
56	MG	Y	104	1/1	0.71	0.16	71,71,71,71	0
56	MG	GB	3300	1/1	0.71	0.13	90,90,90,90	0
56	MG	C	208	1/1	0.71	0.29	81,81,81,81	0
56	MG	NA	203	1/1	0.71	0.13	98,98,98,98	0
56	MG	GB	3111	1/1	0.71	0.33	66,66,66,66	0
56	MG	GB	3351	1/1	0.71	0.26	83,83,83,83	0
56	MG	GB	3353	1/1	0.71	0.24	68,68,68,68	0
56	MG	FB	1779	1/1	0.71	0.17	88,88,88,88	0
56	MG	FB	1920	1/1	0.71	0.18	70,70,70,70	0
56	MG	FB	1643	1/1	0.71	0.32	94,94,94,94	0
56	MG	A	1676	1/1	0.71	0.28	80,80,80,80	0
56	MG	GB	2995	1/1	0.71	0.16	58,58,58,58	0
56	MG	A	1708	1/1	0.72	0.32	79,79,79,79	0
56	MG	B	3418	1/1	0.72	0.26	76,76,76,76	0
56	MG	WB	203	1/1	0.72	0.14	87,87,87,87	0
56	MG	A	1816	1/1	0.72	0.23	108,108,108,108	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	A	1849	1/1	0.72	0.36	88,88,88,88	0
56	MG	A	1850	1/1	0.72	0.20	117,117,117,117	0
56	MG	W	303	1/1	0.72	0.15	87,87,87,87	0
56	MG	B	3280	1/1	0.72	0.24	87,87,87,87	0
56	MG	A	1695	1/1	0.72	0.21	71,71,71,71	0
56	MG	GB	2971	1/1	0.72	0.54	93,93,93,93	0
56	MG	GB	2982	1/1	0.72	0.17	67,67,67,67	0
56	MG	FB	1615	1/1	0.72	0.40	87,87,87,87	0
56	MG	HC	103	1/1	0.72	0.10	90,90,90,90	0
56	MG	B	3807	1/1	0.72	0.19	92,92,92,92	0
56	MG	QA	201	1/1	0.72	0.14	106,106,106,106	0
56	MG	B	3039	1/1	0.72	0.30	50,50,50,50	0
56	MG	B	3540	1/1	0.72	0.12	85,85,85,85	0
56	MG	GB	3599	1/1	0.72	0.23	101,101,101,101	0
56	MG	IA	109	1/1	0.72	0.10	79,79,79,79	0
56	MG	GB	3065	1/1	0.72	0.38	95,95,95,95	0
56	MG	FB	1837	1/1	0.72	0.35	91,91,91,91	0
56	MG	A	1743	1/1	0.72	0.13	80,80,80,80	0
56	MG	GB	3265	1/1	0.72	0.36	100,100,100,100	0
56	MG	C	231	1/1	0.72	0.21	89,89,89,89	0
56	MG	C	233	1/1	0.72	0.30	84,84,84,84	0
56	MG	GB	3652	1/1	0.72	0.08	73,73,73,73	0
56	MG	KB	301	1/1	0.72	0.35	62,62,62,62	0
56	MG	GB	3117	1/1	0.72	0.41	82,82,82,82	0
56	MG	B	3547	1/1	0.72	0.13	90,90,90,90	0
56	MG	FB	1755	1/1	0.72	0.13	70,70,70,70	0
56	MG	GB	3162	1/1	0.72	0.26	101,101,101,101	0
56	MG	GB	3095	1/1	0.73	0.29	63,63,63,63	0
56	MG	A	1712	1/1	0.73	0.24	76,76,76,76	0
56	MG	FB	1628	1/1	0.73	0.34	81,81,81,81	0
56	MG	FB	1911	1/1	0.73	0.40	110,110,110,110	0
56	MG	FB	1704	1/1	0.73	0.45	93,93,93,93	0
56	MG	BC	309	1/1	0.73	0.26	98,98,98,98	0
56	MG	GB	3603	1/1	0.73	0.19	101,101,101,101	0
56	MG	GB	3462	1/1	0.73	0.18	101,101,101,101	0
56	MG	A	1648	1/1	0.73	0.39	100,100,100,100	0
56	MG	A	1612	1/1	0.73	0.23	54,54,54,54	0
56	MG	HB	215	1/1	0.73	0.23	109,109,109,109	0
56	MG	A	1672	1/1	0.73	0.66	105,105,105,105	0
56	MG	A	1837	1/1	0.73	0.22	124,124,124,124	0
56	MG	A	1709	1/1	0.73	0.46	83,83,83,83	0
56	MG	A	1740	1/1	0.73	0.20	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	MG	GB	3202	1/1	0.73	0.21	101,101,101,101	0
56	MG	A	1795	1/1	0.73	0.23	110,110,110,110	0
56	MG	GB	3657	1/1	0.73	0.14	101,101,101,101	0
56	MG	I	204	1/1	0.73	0.12	68,68,68,68	0
56	MG	B	3762	1/1	0.73	0.10	71,71,71,71	0
56	MG	GB	3533	1/1	0.73	0.14	93,93,93,93	0
56	MG	FB	1681	1/1	0.73	0.30	99,99,99,99	0
56	MG	GB	3674	1/1	0.73	0.12	84,84,84,84	0
56	MG	GB	3549	1/1	0.73	0.34	86,86,86,86	0
56	MG	GB	3553	1/1	0.73	0.09	86,86,86,86	0
56	MG	GB	3696	1/1	0.73	0.15	72,72,72,72	0
56	MG	P	202	1/1	0.73	0.11	94,94,94,94	0
56	MG	VB	202	1/1	0.73	0.19	80,80,80,80	0
56	MG	A	1615	1/1	0.73	0.40	89,89,89,89	0
56	MG	GB	3179	1/1	0.74	0.24	69,69,69,69	0
56	MG	GB	3541	1/1	0.74	0.20	64,64,64,64	0
56	MG	FB	1814	1/1	0.74	0.13	78,78,78,78	0
56	MG	GB	3703	1/1	0.74	0.11	70,70,70,70	0
56	MG	A	1666	1/1	0.74	0.42	80,80,80,80	0
56	MG	GB	3562	1/1	0.74	0.08	57,57,57,57	0
56	MG	FB	1824	1/1	0.74	0.21	70,70,70,70	0
56	MG	A	1682	1/1	0.74	0.20	98,98,98,98	0
56	MG	A	1878	1/1	0.74	0.44	101,101,101,101	0
56	MG	B	3823	1/1	0.74	0.06	92,92,92,92	0
56	MG	FB	1843	1/1	0.74	0.09	85,85,85,85	0
56	MG	A	1685	1/1	0.74	0.14	76,76,76,76	0
56	MG	A	1605	1/1	0.74	0.27	67,67,67,67	0
56	MG	FB	1605	1/1	0.74	0.25	70,70,70,70	0
56	MG	B	2942	1/1	0.74	0.43	58,58,58,58	0
56	MG	NC	101	1/1	0.74	0.26	85,85,85,85	0
56	MG	A	1852	1/1	0.74	0.24	96,96,96,96	0
56	MG	NC	111	1/1	0.74	0.16	87,87,87,87	0
56	MG	B	3328	1/1	0.74	0.22	72,72,72,72	0
56	MG	GB	3358	1/1	0.74	0.11	87,87,87,87	0
56	MG	A	1673	1/1	0.74	0.27	75,75,75,75	0
56	MG	A	1830	1/1	0.74	0.14	67,67,67,67	0
56	MG	GB	3489	1/1	0.74	0.21	65,65,65,65	0
56	MG	GB	3498	1/1	0.74	0.13	74,74,74,74	0
56	MG	A	1831	1/1	0.74	0.25	96,96,96,96	0
56	MG	B	3151	1/1	0.74	0.22	55,55,55,55	0
56	MG	GB	3524	1/1	0.74	0.16	83,83,83,83	0
56	MG	RC	308	1/1	0.74	0.13	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	MB	202	1/1	0.74	0.25	110,110,110,110	0
56	MG	A	1607	1/1	0.74	0.39	76,76,76,76	0
56	MG	TA	201	1/1	0.74	0.18	92,92,92,92	0
56	MG	MB	206	1/1	0.74	0.16	127,127,127,127	0
56	MG	A	1744	1/1	0.74	0.14	87,87,87,87	0
56	MG	XC	202	1/1	0.74	0.32	113,113,113,113	0
56	MG	GB	3535	1/1	0.74	0.19	83,83,83,83	0
56	MG	GB	3537	1/1	0.74	0.12	93,93,93,93	0
56	MG	GB	3519	1/1	0.75	0.19	85,85,85,85	0
56	MG	A	1788	1/1	0.75	0.15	76,76,76,76	0
56	MG	A	1829	1/1	0.75	0.25	109,109,109,109	0
56	MG	FB	1726	1/1	0.75	0.36	94,94,94,94	0
56	MG	GB	3689	1/1	0.75	0.17	67,67,67,67	0
56	MG	B	3525	1/1	0.75	0.23	64,64,64,64	0
56	MG	A	1753	1/1	0.75	0.36	84,84,84,84	0
56	MG	FB	1815	1/1	0.75	0.20	79,79,79,79	0
56	MG	GB	3389	1/1	0.75	0.16	74,74,74,74	0
56	MG	HB	202	1/1	0.75	0.19	79,79,79,79	0
56	MG	B	3799	1/1	0.75	0.10	89,89,89,89	0
56	MG	GB	3033	1/1	0.75	0.28	79,79,79,79	0
56	MG	A	1678	1/1	0.75	0.31	97,97,97,97	0
56	MG	GB	3048	1/1	0.75	0.19	64,64,64,64	0
56	MG	GB	3571	1/1	0.75	0.13	66,66,66,66	0
56	MG	B	3432	1/1	0.75	0.22	68,68,68,68	0
56	MG	FB	1832	1/1	0.75	0.27	76,76,76,76	0
56	MG	HB	212	1/1	0.75	0.23	85,85,85,85	0
56	MG	B	3758	1/1	0.75	0.19	80,80,80,80	0
56	MG	B	3827	1/1	0.75	0.09	64,64,64,64	0
56	MG	GB	3442	1/1	0.75	0.14	194,194,194,194	0
56	MG	A	1700	1/1	0.75	0.29	82,82,82,82	0
56	MG	FB	1848	1/1	0.75	0.35	76,76,76,76	0
56	MG	FB	1687	1/1	0.75	0.23	109,109,109,109	0
56	MG	FB	1933	1/1	0.75	0.29	126,126,126,126	0
56	MG	AA	104	1/1	0.75	0.16	75,75,75,75	0
56	MG	FB	1766	1/1	0.75	0.40	84,84,84,84	0
56	MG	GB	3146	1/1	0.75	0.19	67,67,67,67	0
56	MG	QC	304	1/1	0.75	0.18	104,104,104,104	0
56	MG	GB	3160	1/1	0.75	0.29	89,89,89,89	0
56	MG	C	201	1/1	0.75	0.23	67,67,67,67	0
56	MG	A	1751	1/1	0.75	0.37	86,86,86,86	0
56	MG	IA	103	1/1	0.75	0.22	76,76,76,76	0
56	MG	B	3567	1/1	0.75	0.20	106,106,106,106	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3344	1/1	0.75	0.19	77,77,77,77	0
56	MG	B	3392	1/1	0.75	0.20	78,78,78,78	0
56	MG	FB	1884	1/1	0.75	0.15	87,87,87,87	0
56	MG	AD	201	1/1	0.75	0.11	80,80,80,80	0
56	MG	B	3307	1/1	0.75	0.15	81,81,81,81	0
56	MG	FB	1768	1/1	0.76	0.12	80,80,80,80	0
56	MG	FB	1941	1/1	0.76	0.35	89,89,89,89	0
56	MG	A	1764	1/1	0.76	0.33	85,85,85,85	0
56	MG	GB	2919	1/1	0.76	0.42	66,66,66,66	0
56	MG	F	311	1/1	0.76	0.07	59,59,59,59	0
56	MG	FB	1602	1/1	0.76	0.32	66,66,66,66	0
56	MG	GB	3375	1/1	0.76	0.22	76,76,76,76	0
56	MG	GB	3508	1/1	0.76	0.20	78,78,78,78	0
56	MG	GB	3240	1/1	0.76	0.21	106,106,106,106	0
56	MG	B	3790	1/1	0.76	0.21	62,62,62,62	0
56	MG	B	2967	1/1	0.76	0.35	53,53,53,53	0
56	MG	FB	1614	1/1	0.76	0.25	70,70,70,70	0
56	MG	NC	104	1/1	0.76	0.24	93,93,93,93	0
56	MG	HB	226	1/1	0.76	0.24	105,105,105,105	0
56	MG	B	3810	1/1	0.76	0.15	59,59,59,59	0
56	MG	GB	2951	1/1	0.76	0.40	71,71,71,71	0
56	MG	OC	405	1/1	0.76	0.23	91,91,91,91	0
56	MG	A	1782	1/1	0.76	0.18	130,130,130,130	0
56	MG	FB	1620	1/1	0.76	0.27	67,67,67,67	0
56	MG	C	237	1/1	0.76	0.12	83,83,83,83	0
56	MG	A	1690	1/1	0.76	0.19	94,94,94,94	0
56	MG	B	3826	1/1	0.76	0.43	97,97,97,97	0
56	MG	GB	3016	1/1	0.76	0.42	76,76,76,76	0
56	MG	KA	301	1/1	0.76	0.24	118,118,118,118	0
56	MG	MB	207	1/1	0.76	0.20	105,105,105,105	0
56	MG	FB	1936	1/1	0.76	0.27	87,87,87,87	0
56	MG	RC	310	1/1	0.76	0.25	83,83,83,83	0
56	MG	GB	3576	1/1	0.76	0.30	70,70,70,70	0
56	MG	SC	206	1/1	0.76	0.23	93,93,93,93	0
56	MG	B	3519	1/1	0.76	0.33	50,50,50,50	0
56	MG	SB	201	1/1	0.76	0.28	77,77,77,77	0
56	MG	GB	3317	1/1	0.76	0.15	70,70,70,70	0
56	MG	GB	3041	1/1	0.76	0.19	93,93,93,93	0
56	MG	GB	3210	1/1	0.76	0.20	77,77,77,77	0
56	MG	FB	1644	1/1	0.76	0.22	81,81,81,81	0
56	MG	GB	3058	1/1	0.76	0.20	49,49,49,49	0
56	MG	CD	103	1/1	0.76	0.24	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BC	304	1/1	0.76	0.24	91,91,91,91	0
56	MG	GB	3378	1/1	0.77	0.12	74,74,74,74	0
56	MG	GB	3685	1/1	0.77	0.28	70,70,70,70	0
56	MG	XB	204	1/1	0.77	0.06	97,97,97,97	0
56	MG	GB	3235	1/1	0.77	0.12	57,57,57,57	0
56	MG	GB	3092	1/1	0.77	0.32	87,87,87,87	0
56	MG	FB	1718	1/1	0.77	0.15	66,66,66,66	0
56	MG	GB	2921	1/1	0.77	0.51	72,72,72,72	0
56	MG	B	3490	1/1	0.77	0.10	44,44,44,44	0
56	MG	GB	3706	1/1	0.77	0.24	83,83,83,83	0
56	MG	GB	3395	1/1	0.77	0.18	81,81,81,81	0
56	MG	IA	117	1/1	0.77	0.21	81,81,81,81	0
56	MG	GB	3555	1/1	0.77	0.14	72,72,72,72	0
56	MG	GB	3556	1/1	0.77	0.27	77,77,77,77	0
56	MG	B	3695	1/1	0.77	0.12	71,71,71,71	0
56	MG	B	3391	1/1	0.77	0.10	56,56,56,56	0
56	MG	FB	1642	1/1	0.77	0.52	104,104,104,104	0
56	MG	B	3592	1/1	0.77	0.14	73,73,73,73	0
56	MG	F	308	1/1	0.77	0.27	58,58,58,58	0
56	MG	A	1717	1/1	0.77	0.30	86,86,86,86	0
56	MG	A	1787	1/1	0.77	0.13	77,77,77,77	0
56	MG	GB	3446	1/1	0.77	0.18	75,75,75,75	0
56	MG	GB	2991	1/1	0.77	0.28	63,63,63,63	0
56	MG	A	1769	1/1	0.77	0.20	85,85,85,85	0
56	MG	FB	1665	1/1	0.77	0.37	70,70,70,70	0
56	MG	B	3170	1/1	0.77	0.26	62,62,62,62	0
56	MG	A	1667	1/1	0.77	0.32	82,82,82,82	0
56	MG	GB	3329	1/1	0.77	0.23	85,85,85,85	0
56	MG	MA	304	1/1	0.77	0.14	96,96,96,96	0
56	MG	GB	3630	1/1	0.77	0.21	75,75,75,75	0
56	MG	A	1819	1/1	0.77	0.23	82,82,82,82	0
56	MG	B	2993	1/1	0.77	0.27	47,47,47,47	0
56	MG	C	205	1/1	0.77	0.31	68,68,68,68	0
56	MG	B	3273	1/1	0.77	0.33	76,76,76,76	0
56	MG	C	218	1/1	0.77	0.20	66,66,66,66	0
56	MG	A	1858	1/1	0.77	0.29	100,100,100,100	0
56	MG	GB	3659	1/1	0.77	0.34	80,80,80,80	0
56	MG	GB	3360	1/1	0.77	0.20	84,84,84,84	0
56	MG	B	3461	1/1	0.77	0.09	56,56,56,56	0
56	MG	A	1809	1/1	0.77	0.40	97,97,97,97	0
56	MG	NB	203	1/1	0.77	0.20	92,92,92,92	0
56	MG	GB	3373	1/1	0.77	0.27	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	2907	1/1	0.77	0.45	60,60,60,60	0
56	MG	SB	204	1/1	0.77	0.18	81,81,81,81	0
56	MG	GB	3376	1/1	0.77	0.40	90,90,90,90	0
56	MG	Y	103	1/1	0.78	0.09	74,74,74,74	0
56	MG	GB	3604	1/1	0.78	0.28	64,64,64,64	0
56	MG	FB	1699	1/1	0.78	0.18	86,86,86,86	0
56	MG	GB	3611	1/1	0.78	0.12	77,77,77,77	0
56	MG	FB	1701	1/1	0.78	0.37	68,68,68,68	0
56	MG	GB	3618	1/1	0.78	0.09	109,109,109,109	0
56	MG	B	3056	1/1	0.78	0.15	49,49,49,49	0
56	MG	B	3375	1/1	0.78	0.33	79,79,79,79	0
56	MG	FB	1706	1/1	0.78	0.31	69,69,69,69	0
56	MG	FB	1846	1/1	0.78	0.15	73,73,73,73	0
56	MG	GB	3633	1/1	0.78	0.28	74,74,74,74	0
56	MG	A	1776	1/1	0.78	0.22	78,78,78,78	0
56	MG	FB	1853	1/1	0.78	0.18	126,126,126,126	0
56	MG	A	1777	1/1	0.78	0.17	91,91,91,91	0
56	MG	A	1636	1/1	0.78	0.36	82,82,82,82	0
56	MG	A	1659	1/1	0.78	0.23	87,87,87,87	0
56	MG	A	1741	1/1	0.78	0.28	73,73,73,73	0
56	MG	A	1637	1/1	0.78	0.24	67,67,67,67	0
56	MG	B	3560	1/1	0.78	0.24	114,114,114,114	0
56	MG	JA	405	1/1	0.78	0.34	91,91,91,91	0
56	MG	C	212	1/1	0.78	0.18	62,62,62,62	0
56	MG	A	1811	1/1	0.78	0.24	76,76,76,76	0
56	MG	GB	3027	1/1	0.78	0.24	74,74,74,74	0
56	MG	GB	3676	1/1	0.78	0.17	88,88,88,88	0
56	MG	GB	3030	1/1	0.78	0.40	88,88,88,88	0
56	MG	C	222	1/1	0.78	0.10	105,105,105,105	0
56	MG	FB	1888	1/1	0.78	0.31	82,82,82,82	0
56	MG	A	1620	1/1	0.78	0.22	93,93,93,93	0
56	MG	A	1646	1/1	0.78	0.26	74,74,74,74	0
56	MG	A	1814	1/1	0.78	0.14	92,92,92,92	0
56	MG	B	3767	1/1	0.78	0.10	60,60,60,60	0
56	MG	FB	1901	1/1	0.78	0.21	75,75,75,75	0
56	MG	GB	3711	1/1	0.78	0.17	77,77,77,77	0
56	MG	GB	3319	1/1	0.78	0.18	84,84,84,84	0
56	MG	A	1693	1/1	0.78	0.28	79,79,79,79	0
56	MG	B	3593	1/1	0.78	0.08	78,78,78,78	0
56	MG	FB	1908	1/1	0.78	0.29	65,65,65,65	0
56	MG	B	3596	1/1	0.78	0.09	55,55,55,55	0
56	MG	B	3297	1/1	0.78	0.18	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3102	1/1	0.78	0.24	50,50,50,50	0
56	MG	F	309	1/1	0.78	0.14	38,38,38,38	0
56	MG	QC	302	1/1	0.78	0.36	103,103,103,103	0
56	MG	FB	1769	1/1	0.78	0.23	91,91,91,91	0
56	MG	GB	3136	1/1	0.78	0.30	71,71,71,71	0
56	MG	RC	304	1/1	0.78	0.15	80,80,80,80	0
56	MG	OA	202	1/1	0.78	0.27	78,78,78,78	0
56	MG	A	1856	1/1	0.78	0.26	87,87,87,87	0
56	MG	F	315	1/1	0.78	0.13	67,67,67,67	0
56	MG	B	3617	1/1	0.78	0.16	54,54,54,54	0
56	MG	FB	1671	1/1	0.78	0.24	87,87,87,87	0
56	MG	B	3627	1/1	0.78	0.12	56,56,56,56	0
56	MG	FB	1677	1/1	0.78	0.33	67,67,67,67	0
56	MG	GB	3587	1/1	0.78	0.27	101,101,101,101	0
56	MG	A	1609	1/1	0.78	0.29	55,55,55,55	0
56	MG	B	3010	1/1	0.78	0.33	77,77,77,77	0
56	MG	W	302	1/1	0.78	0.10	70,70,70,70	0
56	MG	A	1797	1/1	0.78	0.10	90,90,90,90	0
56	MG	A	1679	1/1	0.78	0.23	95,95,95,95	0
56	MG	B	3785	1/1	0.79	0.21	61,61,61,61	0
56	MG	RB	204	1/1	0.79	0.10	98,98,98,98	0
56	MG	A	1619	1/1	0.79	0.18	61,61,61,61	0
56	MG	GB	3182	1/1	0.79	0.20	88,88,88,88	0
56	MG	GB	3511	1/1	0.79	0.28	82,82,82,82	0
56	MG	GB	3183	1/1	0.79	0.07	61,61,61,61	0
56	MG	A	1655	1/1	0.79	0.25	66,66,66,66	0
56	MG	XB	202	1/1	0.79	0.15	76,76,76,76	0
56	MG	GB	3521	1/1	0.79	0.25	76,76,76,76	0
56	MG	GB	3192	1/1	0.79	0.11	49,49,49,49	0
56	MG	GB	3004	1/1	0.79	0.23	60,60,60,60	0
56	MG	BC	303	1/1	0.79	0.09	106,106,106,106	0
56	MG	FB	1630	1/1	0.79	0.22	64,64,64,64	0
56	MG	A	1611	1/1	0.79	0.24	96,96,96,96	0
56	MG	B	3293	1/1	0.79	0.14	82,82,82,82	0
56	MG	GB	3025	1/1	0.79	0.39	64,64,64,64	0
56	MG	GB	3369	1/1	0.79	0.17	90,90,90,90	0
56	MG	FB	1929	1/1	0.79	0.19	94,94,94,94	0
56	MG	FB	1636	1/1	0.79	0.58	98,98,98,98	0
56	MG	MA	305	1/1	0.79	0.19	103,103,103,103	0
56	MG	GB	3554	1/1	0.79	0.15	71,71,71,71	0
56	MG	B	3294	1/1	0.79	0.27	75,75,75,75	0
56	MG	FB	1772	1/1	0.79	0.24	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	A	1634	1/1	0.79	0.28	72,72,72,72	0
56	MG	FB	1714	1/1	0.79	0.25	66,66,66,66	0
56	MG	A	1608	1/1	0.79	0.30	55,55,55,55	0
56	MG	NC	105	1/1	0.79	0.21	94,94,94,94	0
56	MG	GB	3064	1/1	0.79	0.29	72,72,72,72	0
56	MG	H	202	1/1	0.79	0.10	89,89,89,89	0
56	MG	H	203	1/1	0.79	0.12	89,89,89,89	0
56	MG	FB	1664	1/1	0.79	0.24	85,85,85,85	0
56	MG	GB	3245	1/1	0.79	0.29	76,76,76,76	0
56	MG	GB	3088	1/1	0.79	0.24	60,60,60,60	0
56	MG	FB	1803	1/1	0.79	0.31	84,84,84,84	0
56	MG	FB	1804	1/1	0.79	0.26	81,81,81,81	0
56	MG	A	1730	1/1	0.79	0.44	81,81,81,81	0
56	MG	HB	219	1/1	0.79	0.13	94,94,94,94	0
56	MG	A	1794	1/1	0.79	0.29	73,73,73,73	0
56	MG	GB	3269	1/1	0.79	0.21	77,77,77,77	0
56	MG	B	3412	1/1	0.79	0.15	57,57,57,57	0
56	MG	U	101	1/1	0.79	0.16	56,56,56,56	0
56	MG	GB	3122	1/1	0.79	0.23	76,76,76,76	0
56	MG	GB	3135	1/1	0.79	0.20	61,61,61,61	0
56	MG	B	3276	1/1	0.79	0.18	68,68,68,68	0
56	MG	JB	306	1/1	0.79	0.12	69,69,69,69	0
56	MG	GB	3137	1/1	0.79	0.26	66,66,66,66	0
56	MG	FB	1733	1/1	0.79	0.30	62,62,62,62	0
56	MG	FB	1822	1/1	0.79	0.27	73,73,73,73	0
56	MG	GB	3648	1/1	0.79	0.12	88,88,88,88	0
56	MG	FB	1679	1/1	0.79	0.28	81,81,81,81	0
56	MG	A	1694	1/1	0.79	0.19	90,90,90,90	0
56	MG	GB	3482	1/1	0.79	0.20	77,77,77,77	0
56	MG	GB	2983	1/1	0.79	0.20	69,69,69,69	0
56	MG	GB	3328	1/1	0.79	0.21	75,75,75,75	0
56	MG	FB	1895	1/1	0.80	0.11	73,73,73,73	0
56	MG	KA	304	1/1	0.80	0.24	109,109,109,109	0
56	MG	GB	3323	1/1	0.80	0.25	71,71,71,71	0
56	MG	GB	3077	1/1	0.80	0.26	68,68,68,68	0
56	MG	FB	1637	1/1	0.80	0.33	64,64,64,64	0
56	MG	GB	3085	1/1	0.80	0.19	60,60,60,60	0
56	MG	A	1784	1/1	0.80	0.23	85,85,85,85	0
56	MG	B	3426	1/1	0.80	0.20	57,57,57,57	0
56	MG	GB	3578	1/1	0.80	0.15	92,92,92,92	0
56	MG	A	1770	1/1	0.80	0.21	139,139,139,139	0
56	MG	B	3436	1/1	0.80	0.11	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	A	1643	1/1	0.80	0.24	70,70,70,70	0
56	MG	FB	1651	1/1	0.80	0.33	90,90,90,90	0
56	MG	FB	1775	1/1	0.80	0.16	83,83,83,83	0
56	MG	FB	1777	1/1	0.80	0.21	97,97,97,97	0
56	MG	GB	3597	1/1	0.80	0.14	80,80,80,80	0
56	MG	B	3113	1/1	0.80	0.17	65,65,65,65	0
56	MG	PB	201	1/1	0.80	0.18	93,93,93,93	0
56	MG	B	3455	1/1	0.80	0.28	47,47,47,47	0
56	MG	B	3457	1/1	0.80	0.09	66,66,66,66	0
56	MG	B	3118	1/1	0.80	0.31	96,96,96,96	0
56	MG	GB	3606	1/1	0.80	0.20	75,75,75,75	0
56	MG	I	205	1/1	0.80	0.08	69,69,69,69	0
56	MG	L	203	1/1	0.80	0.17	71,71,71,71	0
56	MG	A	1625	1/1	0.80	0.27	66,66,66,66	0
56	MG	A	1687	1/1	0.80	0.23	84,84,84,84	0
56	MG	P	204	1/1	0.80	0.13	77,77,77,77	0
56	MG	B	2927	1/1	0.80	0.35	50,50,50,50	0
56	MG	B	3815	1/1	0.80	0.13	61,61,61,61	0
56	MG	A	1699	1/1	0.80	0.24	92,92,92,92	0
56	MG	B	3656	1/1	0.80	0.19	59,59,59,59	0
56	MG	FB	1819	1/1	0.80	0.13	71,71,71,71	0
56	MG	X	106	1/1	0.80	0.10	63,63,63,63	0
56	MG	B	3499	1/1	0.80	0.12	48,48,48,48	0
56	MG	B	3503	1/1	0.80	0.21	77,77,77,77	0
56	MG	GB	3425	1/1	0.80	0.24	58,58,58,58	0
56	MG	FC	101	1/1	0.80	0.14	87,87,87,87	0
56	MG	GB	2933	1/1	0.80	0.44	63,63,63,63	0
56	MG	B	3214	1/1	0.80	0.28	83,83,83,83	0
56	MG	B	3371	1/1	0.80	0.15	133,133,133,133	0
56	MG	C	203	1/1	0.80	0.24	79,79,79,79	0
56	MG	B	3222	1/1	0.80	0.20	50,50,50,50	0
56	MG	FB	1840	1/1	0.80	0.10	110,110,110,110	0
56	MG	FB	1716	1/1	0.80	0.24	82,82,82,82	0
56	MG	B	2949	1/1	0.80	0.20	45,45,45,45	0
56	MG	ZA	202	1/1	0.80	0.20	87,87,87,87	0
56	MG	OC	401	1/1	0.80	0.28	68,68,68,68	0
56	MG	C	209	1/1	0.80	0.22	62,62,62,62	0
56	MG	FB	1855	1/1	0.80	0.13	68,68,68,68	0
56	MG	GB	2993	1/1	0.80	0.12	71,71,71,71	0
56	MG	IA	114	1/1	0.80	0.11	71,71,71,71	0
56	MG	FB	1723	1/1	0.80	0.30	86,86,86,86	0
56	MG	A	1840	1/1	0.80	0.17	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1866	1/1	0.80	0.10	94,94,94,94	0
56	MG	GB	3249	1/1	0.80	0.12	68,68,68,68	0
56	MG	GB	3007	1/1	0.80	0.34	73,73,73,73	0
56	MG	GB	3253	1/1	0.80	0.36	76,76,76,76	0
56	MG	B	3267	1/1	0.80	0.10	61,61,61,61	0
56	MG	JA	401	1/1	0.80	0.28	52,52,52,52	0
56	MG	FB	1729	1/1	0.80	0.26	72,72,72,72	0
56	MG	B	3719	1/1	0.80	0.22	79,79,79,79	0
56	MG	GB	3028	1/1	0.80	0.22	71,71,71,71	0
56	MG	A	1868	1/1	0.80	0.12	71,71,71,71	0
56	MG	FB	1877	1/1	0.80	0.20	80,80,80,80	0
56	MG	A	1768	1/1	0.80	0.28	84,84,84,84	0
56	MG	GB	3530	1/1	0.80	0.13	85,85,85,85	0
56	MG	GB	3289	1/1	0.80	0.27	63,63,63,63	0
56	MG	A	1847	1/1	0.80	0.23	93,93,93,93	0
56	MG	A	1755	1/1	0.80	0.18	71,71,71,71	0
56	MG	GB	3049	1/1	0.80	0.31	61,61,61,61	0
56	MG	B	3014	1/1	0.80	0.15	56,56,56,56	0
56	MG	B	3287	1/1	0.80	0.17	40,40,40,40	0
56	MG	GB	3548	1/1	0.80	0.14	68,68,68,68	0
56	MG	C	244	1/1	0.81	0.11	65,65,65,65	0
56	MG	B	3320	1/1	0.81	0.27	64,64,64,64	0
56	MG	FB	1721	1/1	0.81	0.23	76,76,76,76	0
56	MG	B	3688	1/1	0.81	0.08	60,60,60,60	0
56	MG	GB	3655	1/1	0.81	0.12	59,59,59,59	0
56	MG	B	3691	1/1	0.81	0.17	92,92,92,92	0
56	MG	B	3511	1/1	0.81	0.14	65,65,65,65	0
56	MG	B	3604	1/1	0.81	0.14	60,60,60,60	0
56	MG	F	312	1/1	0.81	0.20	77,77,77,77	0
56	MG	JA	403	1/1	0.81	0.20	47,47,47,47	0
56	MG	VB	207	1/1	0.81	0.10	83,83,83,83	0
56	MG	B	3704	1/1	0.81	0.10	69,69,69,69	0
56	MG	A	1821	1/1	0.81	0.19	77,77,77,77	0
56	MG	FB	1668	1/1	0.81	0.30	82,82,82,82	0
56	MG	GB	3529	1/1	0.81	0.17	107,107,107,107	0
56	MG	B	3609	1/1	0.81	0.13	44,44,44,44	0
56	MG	GB	3038	1/1	0.81	0.17	71,71,71,71	0
56	MG	B	3268	1/1	0.81	0.30	70,70,70,70	0
56	MG	FB	1742	1/1	0.81	0.35	67,67,67,67	0
56	MG	GB	3692	1/1	0.81	0.18	81,81,81,81	0
56	MG	B	3746	1/1	0.81	0.17	68,68,68,68	0
56	MG	B	3137	1/1	0.81	0.16	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	A	1866	1/1	0.81	0.17	95,95,95,95	0
56	MG	A	1606	1/1	0.81	0.26	95,95,95,95	0
56	MG	A	1783	1/1	0.81	0.18	111,111,111,111	0
56	MG	A	1853	1/1	0.81	0.21	99,99,99,99	0
56	MG	FB	1688	1/1	0.81	0.19	64,64,64,64	0
56	MG	FB	1689	1/1	0.81	0.16	66,66,66,66	0
56	MG	FB	1865	1/1	0.81	0.41	71,71,71,71	0
56	MG	GB	3410	1/1	0.81	0.35	76,76,76,76	0
56	MG	NC	102	1/1	0.81	0.17	65,65,65,65	0
56	MG	GB	2914	1/1	0.81	0.37	58,58,58,58	0
56	MG	C	211	1/1	0.81	0.28	83,83,83,83	0
56	MG	HB	209	1/1	0.81	0.11	81,81,81,81	0
56	MG	B	3199	1/1	0.81	0.22	55,55,55,55	0
56	MG	GB	3584	1/1	0.81	0.17	71,71,71,71	0
56	MG	C	214	1/1	0.81	0.13	79,79,79,79	0
56	MG	FB	1776	1/1	0.81	0.14	67,67,67,67	0
56	MG	B	3203	1/1	0.81	0.21	57,57,57,57	0
56	MG	FB	1872	1/1	0.81	0.11	87,87,87,87	0
56	MG	FB	1624	1/1	0.81	0.30	66,66,66,66	0
56	MG	GB	3120	1/1	0.81	0.22	79,79,79,79	0
56	MG	GB	3121	1/1	0.81	0.29	62,62,62,62	0
56	MG	FB	1785	1/1	0.81	0.13	87,87,87,87	0
56	MG	GB	3601	1/1	0.81	0.22	58,58,58,58	0
56	MG	B	3211	1/1	0.81	0.22	65,65,65,65	0
56	MG	GB	3451	1/1	0.81	0.12	79,79,79,79	0
56	MG	HB	228	1/1	0.81	0.24	81,81,81,81	0
56	MG	A	1671	1/1	0.81	0.20	94,94,94,94	0
56	MG	A	1711	1/1	0.81	0.33	95,95,95,95	0
56	MG	B	3071	1/1	0.81	0.40	58,58,58,58	0
56	MG	GB	3463	1/1	0.81	0.23	66,66,66,66	0
56	MG	IB	105	1/1	0.81	0.24	117,117,117,117	0
56	MG	A	1780	1/1	0.81	0.14	83,83,83,83	0
56	MG	GB	3308	1/1	0.81	0.13	61,61,61,61	0
56	MG	VC	201	1/1	0.81	0.47	77,77,77,77	0
56	MG	LB	304	1/1	0.81	0.16	83,83,83,83	0
56	MG	GB	3468	1/1	0.81	0.20	86,86,86,86	0
56	MG	GB	3143	1/1	0.81	0.23	78,78,78,78	0
56	MG	GB	3473	1/1	0.81	0.12	76,76,76,76	0
56	MG	ZC	202	1/1	0.81	0.14	75,75,75,75	0
56	MG	MB	205	1/1	0.81	0.13	122,122,122,122	0
56	MG	GB	2985	1/1	0.81	0.24	58,58,58,58	0
56	MG	B	3683	1/1	0.81	0.15	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3568	1/1	0.82	0.26	66,66,66,66	0
56	MG	FB	1894	1/1	0.82	0.23	70,70,70,70	0
56	MG	GB	3184	1/1	0.82	0.21	61,61,61,61	0
56	MG	GB	3185	1/1	0.82	0.18	67,67,67,67	0
56	MG	FB	1794	1/1	0.82	0.29	85,85,85,85	0
56	MG	B	3434	1/1	0.82	0.14	75,75,75,75	0
56	MG	FB	1632	1/1	0.82	0.37	69,69,69,69	0
56	MG	BA	103	1/1	0.82	0.08	107,107,107,107	0
56	MG	GB	3020	1/1	0.82	0.22	60,60,60,60	0
56	MG	A	1887	1/1	0.82	0.38	87,87,87,87	0
56	MG	B	3339	1/1	0.82	0.11	60,60,60,60	0
56	MG	B	2919	1/1	0.82	0.27	52,52,52,52	0
56	MG	GB	3409	1/1	0.82	0.16	70,70,70,70	0
56	MG	B	3262	1/1	0.82	0.14	45,45,45,45	0
56	MG	GB	3029	1/1	0.82	0.28	75,75,75,75	0
56	MG	B	3351	1/1	0.82	0.18	77,77,77,77	0
56	MG	B	2921	1/1	0.82	0.25	42,42,42,42	0
56	MG	IA	116	1/1	0.82	0.32	84,84,84,84	0
56	MG	B	3077	1/1	0.82	0.23	45,45,45,45	0
56	MG	FB	1659	1/1	0.82	0.33	69,69,69,69	0
56	MG	GB	3431	1/1	0.82	0.19	76,76,76,76	0
56	MG	GB	3438	1/1	0.82	0.20	52,52,52,52	0
56	MG	GB	3621	1/1	0.82	0.15	64,64,64,64	0
56	MG	B	3098	1/1	0.82	0.12	46,46,46,46	0
56	MG	UA	201	1/1	0.82	0.17	75,75,75,75	0
56	MG	GB	3444	1/1	0.82	0.18	78,78,78,78	0
56	MG	GB	3237	1/1	0.82	0.25	93,93,93,93	0
56	MG	GB	3238	1/1	0.82	0.28	76,76,76,76	0
56	MG	YB	202	1/1	0.82	0.13	71,71,71,71	0
56	MG	A	1763	1/1	0.82	0.29	109,109,109,109	0
56	MG	YB	206	1/1	0.82	0.15	70,70,70,70	0
56	MG	FB	1836	1/1	0.82	0.09	66,66,66,66	0
56	MG	A	1718	1/1	0.82	0.24	64,64,64,64	0
56	MG	A	1834	1/1	0.82	0.12	82,82,82,82	0
56	MG	B	3738	1/1	0.82	0.14	55,55,55,55	0
56	MG	GB	3083	1/1	0.82	0.26	70,70,70,70	0
56	MG	B	3616	1/1	0.82	0.12	95,95,95,95	0
56	MG	GB	3658	1/1	0.82	0.10	95,95,95,95	0
56	MG	B	2959	1/1	0.82	0.22	84,84,84,84	0
56	MG	GB	3661	1/1	0.82	0.14	66,66,66,66	0
56	MG	B	3400	1/1	0.82	0.10	43,43,43,43	0
56	MG	GB	3087	1/1	0.82	0.35	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	2964	1/1	0.82	0.25	55,55,55,55	0
56	MG	A	1656	1/1	0.82	0.45	100,100,100,100	0
56	MG	GB	3475	1/1	0.82	0.20	79,79,79,79	0
56	MG	GB	3272	1/1	0.82	0.18	62,62,62,62	0
56	MG	GB	3278	1/1	0.82	0.29	75,75,75,75	0
56	MG	FB	1764	1/1	0.82	0.35	82,82,82,82	0
56	MG	FB	1863	1/1	0.82	0.23	72,72,72,72	0
56	MG	A	1838	1/1	0.82	0.15	106,106,106,106	0
56	MG	NC	108	1/1	0.82	0.09	81,81,81,81	0
56	MG	GB	3107	1/1	0.82	0.26	81,81,81,81	0
56	MG	C	213	1/1	0.82	0.07	72,72,72,72	0
56	MG	GB	3507	1/1	0.82	0.12	109,109,109,109	0
56	MG	GB	2932	1/1	0.82	0.50	68,68,68,68	0
56	MG	GB	3704	1/1	0.82	0.12	86,86,86,86	0
56	MG	MA	301	1/1	0.82	0.27	97,97,97,97	0
56	MG	GB	2939	1/1	0.82	0.29	64,64,64,64	0
56	MG	GB	3311	1/1	0.82	0.25	64,64,64,64	0
56	MG	A	1601	1/1	0.82	0.29	56,56,56,56	0
56	MG	FB	1696	1/1	0.82	0.29	85,85,85,85	0
56	MG	GB	3527	1/1	0.82	0.16	81,81,81,81	0
56	MG	A	1733	1/1	0.82	0.34	100,100,100,100	0
56	MG	B	3651	1/1	0.82	0.23	74,74,74,74	0
56	MG	FB	1700	1/1	0.82	0.35	73,73,73,73	0
56	MG	FB	1874	1/1	0.82	0.12	69,69,69,69	0
56	MG	W	308	1/1	0.82	0.08	73,73,73,73	0
56	MG	GB	3337	1/1	0.82	0.20	58,58,58,58	0
56	MG	SC	202	1/1	0.82	0.26	92,92,92,92	0
56	MG	FB	1782	1/1	0.82	0.24	91,91,91,91	0
56	MG	GB	3152	1/1	0.82	0.19	74,74,74,74	0
56	MG	GB	3154	1/1	0.82	0.16	61,61,61,61	0
56	MG	FB	1702	1/1	0.82	0.17	81,81,81,81	0
56	MG	FB	1625	1/1	0.82	0.33	78,78,78,78	0
56	MG	GB	3167	1/1	0.82	0.37	82,82,82,82	0
56	MG	A	1716	1/1	0.82	0.21	78,78,78,78	0
56	MG	GB	3174	1/1	0.82	0.20	64,64,64,64	0
56	MG	A	1641	1/1	0.82	0.22	79,79,79,79	0
56	MG	GB	3558	1/1	0.82	0.07	98,98,98,98	0
56	MG	A	1886	1/1	0.82	0.24	78,78,78,78	0
56	MG	HB	227	1/1	0.82	0.10	99,99,99,99	0
56	MG	GB	3567	1/1	0.82	0.12	52,52,52,52	0
56	MG	GB	3474	1/1	0.83	0.18	69,69,69,69	0
56	MG	B	2946	1/1	0.83	0.34	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3647	1/1	0.83	0.16	77,77,77,77	0
56	MG	B	2947	1/1	0.83	0.20	40,40,40,40	0
56	MG	HA	101	1/1	0.83	0.31	77,77,77,77	0
56	MG	GB	3481	1/1	0.83	0.12	64,64,64,64	0
56	MG	B	3376	1/1	0.83	0.12	133,133,133,133	0
56	MG	GB	3181	1/1	0.83	0.16	64,64,64,64	0
56	MG	IA	106	1/1	0.83	0.22	82,82,82,82	0
56	MG	GB	3497	1/1	0.83	0.19	59,59,59,59	0
56	MG	FB	1850	1/1	0.83	0.08	89,89,89,89	0
56	MG	GB	3334	1/1	0.83	0.17	109,109,109,109	0
56	MG	VB	203	1/1	0.83	0.16	79,79,79,79	0
56	MG	B	3172	1/1	0.83	0.22	59,59,59,59	0
56	MG	A	1635	1/1	0.83	0.26	104,104,104,104	0
56	MG	GB	3339	1/1	0.83	0.10	67,67,67,67	0
56	MG	GB	3187	1/1	0.83	0.11	55,55,55,55	0
56	MG	YB	201	1/1	0.83	0.31	72,72,72,72	0
56	MG	FB	1773	1/1	0.83	0.37	78,78,78,78	0
56	MG	B	3189	1/1	0.83	0.19	59,59,59,59	0
56	MG	YB	204	1/1	0.83	0.12	78,78,78,78	0
56	MG	A	1618	1/1	0.83	0.27	80,80,80,80	0
56	MG	FB	1638	1/1	0.83	0.25	60,60,60,60	0
56	MG	GB	3197	1/1	0.83	0.18	100,100,100,100	0
56	MG	GB	3683	1/1	0.83	0.16	64,64,64,64	0
56	MG	B	3398	1/1	0.83	0.23	64,64,64,64	0
56	MG	GB	3051	1/1	0.83	0.34	67,67,67,67	0
56	MG	B	3065	1/1	0.83	0.28	63,63,63,63	0
56	MG	K	206	1/1	0.83	0.09	73,73,73,73	0
56	MG	A	1822	1/1	0.83	0.24	72,72,72,72	0
56	MG	GB	2917	1/1	0.83	0.31	46,46,46,46	0
56	MG	B	3073	1/1	0.83	0.28	62,62,62,62	0
56	MG	A	1652	1/1	0.83	0.30	70,70,70,70	0
56	MG	GB	3223	1/1	0.83	0.08	81,81,81,81	0
56	MG	GB	3709	1/1	0.83	0.20	74,74,74,74	0
56	MG	P	203	1/1	0.83	0.29	75,75,75,75	0
56	MG	GB	3386	1/1	0.83	0.09	76,76,76,76	0
56	MG	GB	2925	1/1	0.83	0.24	54,54,54,54	0
56	MG	B	2973	1/1	0.83	0.20	41,41,41,41	0
56	MG	HB	205	1/1	0.83	0.31	74,74,74,74	0
56	MG	FB	1795	1/1	0.83	0.24	61,61,61,61	0
56	MG	FB	1796	1/1	0.83	0.10	79,79,79,79	0
56	MG	GB	3090	1/1	0.83	0.28	67,67,67,67	0
56	MG	FB	1878	1/1	0.83	0.18	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1880	1/1	0.83	0.20	74,74,74,74	0
56	MG	B	3105	1/1	0.83	0.11	78,78,78,78	0
56	MG	A	1604	1/1	0.83	0.30	73,73,73,73	0
56	MG	GB	3104	1/1	0.83	0.12	65,65,65,65	0
56	MG	C	236	1/1	0.83	0.28	77,77,77,77	0
56	MG	A	1732	1/1	0.83	0.18	56,56,56,56	0
56	MG	GB	3429	1/1	0.83	0.11	49,49,49,49	0
56	MG	GB	2964	1/1	0.83	0.27	59,59,59,59	0
56	MG	B	3708	1/1	0.83	0.20	71,71,71,71	0
56	MG	GB	3259	1/1	0.83	0.17	70,70,70,70	0
56	MG	GB	3260	1/1	0.83	0.16	59,59,59,59	0
56	MG	B	3711	1/1	0.83	0.11	64,64,64,64	0
56	MG	HB	225	1/1	0.83	0.19	96,96,96,96	0
56	MG	GB	3598	1/1	0.83	0.21	78,78,78,78	0
56	MG	B	3130	1/1	0.83	0.42	80,80,80,80	0
56	MG	GB	3123	1/1	0.83	0.16	62,62,62,62	0
56	MG	GB	3130	1/1	0.83	0.23	60,60,60,60	0
56	MG	A	1723	1/1	0.83	0.17	79,79,79,79	0
56	MG	Z	103	1/1	0.83	0.28	74,74,74,74	0
56	MG	FB	1684	1/1	0.83	0.31	79,79,79,79	0
56	MG	B	3722	1/1	0.83	0.11	44,44,44,44	0
56	MG	WC	201	1/1	0.83	0.14	121,121,121,121	0
56	MG	JB	305	1/1	0.83	0.12	76,76,76,76	0
56	MG	BA	102	1/1	0.83	0.13	83,83,83,83	0
56	MG	FB	1622	1/1	0.83	0.27	74,74,74,74	0
56	MG	GB	3005	1/1	0.83	0.26	61,61,61,61	0
56	MG	ZC	201	1/1	0.83	0.08	70,70,70,70	0
56	MG	FB	1752	1/1	0.83	0.33	96,96,96,96	0
56	MG	A	1639	1/1	0.83	0.18	61,61,61,61	0
56	MG	CD	102	1/1	0.83	0.18	75,75,75,75	0
56	MG	GB	3009	1/1	0.83	0.29	62,62,62,62	0
56	MG	FB	1694	1/1	0.83	0.05	81,81,81,81	0
56	MG	B	3463	1/1	0.84	0.16	65,65,65,65	0
56	MG	B	3465	1/1	0.84	0.14	91,91,91,91	0
56	MG	KB	302	1/1	0.84	0.11	75,75,75,75	0
56	MG	FB	1942	1/1	0.84	0.13	72,72,72,72	0
56	MG	MB	201	1/1	0.84	0.23	111,111,111,111	0
56	MG	A	1697	1/1	0.84	0.36	78,78,78,78	0
56	MG	FB	1944	1/1	0.84	0.09	78,78,78,78	0
56	MG	GB	3608	1/1	0.84	0.14	68,68,68,68	0
56	MG	FB	1948	1/1	0.84	0.30	116,116,116,116	0
56	MG	B	3201	1/1	0.84	0.20	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	A	1790	1/1	0.84	0.13	65,65,65,65	0
56	MG	FB	1857	1/1	0.84	0.50	82,82,82,82	0
56	MG	GB	3256	1/1	0.84	0.26	72,72,72,72	0
56	MG	FB	1765	1/1	0.84	0.14	77,77,77,77	0
56	MG	A	1681	1/1	0.84	0.23	69,69,69,69	0
56	MG	GB	3453	1/1	0.84	0.08	85,85,85,85	0
56	MG	QB	201	1/1	0.84	0.24	73,73,73,73	0
56	MG	I	201	1/1	0.84	0.13	77,77,77,77	0
56	MG	GB	3103	1/1	0.84	0.15	70,70,70,70	0
56	MG	I	202	1/1	0.84	0.22	70,70,70,70	0
56	MG	TB	203	1/1	0.84	0.15	66,66,66,66	0
56	MG	GB	3105	1/1	0.84	0.38	73,73,73,73	0
56	MG	GB	2926	1/1	0.84	0.19	69,69,69,69	0
56	MG	B	3835	1/1	0.84	0.10	80,80,80,80	0
56	MG	B	3212	1/1	0.84	0.21	52,52,52,52	0
56	MG	GB	3119	1/1	0.84	0.13	59,59,59,59	0
56	MG	B	2912	1/1	0.84	0.42	59,59,59,59	0
56	MG	A	1629	1/1	0.84	0.20	67,67,67,67	0
56	MG	JA	413	1/1	0.84	0.31	97,97,97,97	0
56	MG	N	203	1/1	0.84	0.06	70,70,70,70	0
56	MG	B	3633	1/1	0.84	0.25	63,63,63,63	0
56	MG	B	3308	1/1	0.84	0.23	50,50,50,50	0
56	MG	GB	2950	1/1	0.84	0.32	60,60,60,60	0
56	MG	B	3314	1/1	0.84	0.08	44,44,44,44	0
56	MG	GB	3672	1/1	0.84	0.24	68,68,68,68	0
56	MG	GB	3673	1/1	0.84	0.29	50,50,50,50	0
56	MG	B	3000	1/1	0.84	0.20	70,70,70,70	0
56	MG	Q	203	1/1	0.84	0.10	78,78,78,78	0
56	MG	MA	302	1/1	0.84	0.19	105,105,105,105	0
56	MG	GB	3505	1/1	0.84	0.08	81,81,81,81	0
56	MG	FB	1882	1/1	0.84	0.07	77,77,77,77	0
56	MG	EC	102	1/1	0.84	0.13	91,91,91,91	0
56	MG	FB	1708	1/1	0.84	0.25	73,73,73,73	0
56	MG	A	1844	1/1	0.84	0.22	89,89,89,89	0
56	MG	GB	3159	1/1	0.84	0.38	81,81,81,81	0
56	MG	FB	1887	1/1	0.84	0.22	65,65,65,65	0
56	MG	GB	3700	1/1	0.84	0.09	61,61,61,61	0
56	MG	B	3134	1/1	0.84	0.21	56,56,56,56	0
56	MG	GB	2997	1/1	0.84	0.26	68,68,68,68	0
56	MG	GB	3000	1/1	0.84	0.24	67,67,67,67	0
56	MG	A	1684	1/1	0.84	0.15	67,67,67,67	0
56	MG	GB	3345	1/1	0.84	0.19	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1798	1/1	0.84	0.40	79,79,79,79	0
56	MG	B	3549	1/1	0.84	0.10	51,51,51,51	0
56	MG	W	305	1/1	0.84	0.09	67,67,67,67	0
56	MG	C	230	1/1	0.84	0.22	69,69,69,69	0
56	MG	B	3433	1/1	0.84	0.17	101,101,101,101	0
56	MG	FB	1900	1/1	0.84	0.07	56,56,56,56	0
56	MG	GB	3019	1/1	0.84	0.23	49,49,49,49	0
56	MG	FB	1641	1/1	0.84	0.23	61,61,61,61	0
56	MG	GB	3364	1/1	0.84	0.12	70,70,70,70	0
56	MG	B	2929	1/1	0.84	0.25	47,47,47,47	0
56	MG	B	3271	1/1	0.84	0.23	68,68,68,68	0
56	MG	PA	203	1/1	0.84	0.14	92,92,92,92	0
56	MG	GB	3196	1/1	0.84	0.21	63,63,63,63	0
56	MG	GB	3377	1/1	0.84	0.26	72,72,72,72	0
56	MG	A	1602	1/1	0.84	0.36	69,69,69,69	0
56	MG	A	1863	1/1	0.84	0.17	93,93,93,93	0
56	MG	RC	302	1/1	0.84	0.35	77,77,77,77	0
56	MG	A	1879	1/1	0.84	0.12	65,65,65,65	0
56	MG	FB	1823	1/1	0.84	0.18	87,87,87,87	0
56	MG	B	3456	1/1	0.84	0.10	50,50,50,50	0
56	MG	GB	3214	1/1	0.84	0.26	64,64,64,64	0
56	MG	GB	3582	1/1	0.84	0.16	68,68,68,68	0
56	MG	FB	1825	1/1	0.84	0.18	86,86,86,86	0
56	MG	SC	207	1/1	0.84	0.19	85,85,85,85	0
56	MG	HB	224	1/1	0.84	0.09	118,118,118,118	0
56	MG	B	3801	1/1	0.84	0.11	74,74,74,74	0
56	MG	GB	3400	1/1	0.84	0.23	71,71,71,71	0
56	MG	FB	1831	1/1	0.84	0.24	81,81,81,81	0
56	MG	FB	1739	1/1	0.84	0.26	70,70,70,70	0
56	MG	B	3804	1/1	0.84	0.09	51,51,51,51	0
56	MG	IB	101	1/1	0.84	0.21	89,89,89,89	0
56	MG	GA	102	1/1	0.84	0.08	67,67,67,67	0
56	MG	F	302	1/1	0.84	0.09	79,79,79,79	0
56	MG	GB	3062	1/1	0.84	0.35	61,61,61,61	0
56	MG	A	1881	1/1	0.84	0.17	128,128,128,128	0
56	MG	JB	303	1/1	0.84	0.11	71,71,71,71	0
56	MG	JB	304	1/1	0.84	0.10	76,76,76,76	0
56	MG	A	1772	1/1	0.84	0.09	143,143,143,143	0
56	MG	GB	3002	1/1	0.85	0.50	88,88,88,88	0
56	MG	FB	1608	1/1	0.85	0.32	72,72,72,72	0
56	MG	FB	1611	1/1	0.85	0.34	63,63,63,63	0
56	MG	B	3563	1/1	0.85	0.11	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3369	1/1	0.85	0.16	69,69,69,69	0
56	MG	B	3573	1/1	0.85	0.13	57,57,57,57	0
56	MG	HA	102	1/1	0.85	0.40	69,69,69,69	0
56	MG	GB	3488	1/1	0.85	0.19	78,78,78,78	0
56	MG	C	225	1/1	0.85	0.13	83,83,83,83	0
56	MG	GB	3493	1/1	0.85	0.11	62,62,62,62	0
56	MG	FB	1737	1/1	0.85	0.20	61,61,61,61	0
56	MG	B	3089	1/1	0.85	0.38	67,67,67,67	0
56	MG	IA	107	1/1	0.85	0.13	76,76,76,76	0
56	MG	B	3720	1/1	0.85	0.07	59,59,59,59	0
56	MG	FB	1626	1/1	0.85	0.14	72,72,72,72	0
56	MG	B	3454	1/1	0.85	0.12	67,67,67,67	0
56	MG	B	3196	1/1	0.85	0.36	80,80,80,80	0
56	MG	GB	3514	1/1	0.85	0.11	67,67,67,67	0
56	MG	IA	115	1/1	0.85	0.27	73,73,73,73	0
56	MG	A	1841	1/1	0.85	0.18	67,67,67,67	0
56	MG	FB	1886	1/1	0.85	0.16	82,82,82,82	0
56	MG	FB	1754	1/1	0.85	0.27	86,86,86,86	0
56	MG	B	3100	1/1	0.85	0.25	46,46,46,46	0
56	MG	FB	1889	1/1	0.85	0.19	69,69,69,69	0
56	MG	GB	3050	1/1	0.85	0.21	70,70,70,70	0
56	MG	B	3747	1/1	0.85	0.30	74,74,74,74	0
56	MG	A	1793	1/1	0.85	0.14	116,116,116,116	0
56	MG	A	1640	1/1	0.85	0.15	76,76,76,76	0
56	MG	B	2925	1/1	0.85	0.30	52,52,52,52	0
56	MG	FB	1639	1/1	0.85	0.20	72,72,72,72	0
56	MG	JB	308	1/1	0.85	0.11	73,73,73,73	0
56	MG	JB	310	1/1	0.85	0.15	64,64,64,64	0
56	MG	B	3607	1/1	0.85	0.07	59,59,59,59	0
56	MG	GB	3070	1/1	0.85	0.19	63,63,63,63	0
56	MG	GB	3544	1/1	0.85	0.16	70,70,70,70	0
56	MG	GB	3547	1/1	0.85	0.50	67,67,67,67	0
56	MG	B	3467	1/1	0.85	0.10	50,50,50,50	0
56	MG	GB	3301	1/1	0.85	0.11	55,55,55,55	0
56	MG	B	3470	1/1	0.85	0.14	71,71,71,71	0
56	MG	GB	3309	1/1	0.85	0.29	57,57,57,57	0
56	MG	GB	3310	1/1	0.85	0.14	69,69,69,69	0
56	MG	B	3038	1/1	0.85	0.21	48,48,48,48	0
56	MG	B	3786	1/1	0.85	0.18	68,68,68,68	0
56	MG	FB	1907	1/1	0.85	0.21	115,115,115,115	0
56	MG	B	3486	1/1	0.85	0.16	51,51,51,51	0
56	MG	G	3206	1/1	0.85	0.18	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1654	1/1	0.85	0.21	56,56,56,56	0
56	MG	PB	202	1/1	0.85	0.12	89,89,89,89	0
56	MG	FB	1780	1/1	0.85	0.16	85,85,85,85	0
56	MG	FB	1655	1/1	0.85	0.27	63,63,63,63	0
56	MG	GB	3331	1/1	0.85	0.15	61,61,61,61	0
56	MG	G	3211	1/1	0.85	0.11	60,60,60,60	0
56	MG	GB	3335	1/1	0.85	0.18	54,54,54,54	0
56	MG	LA	301	1/1	0.85	0.26	109,109,109,109	0
56	MG	FB	1788	1/1	0.85	0.12	76,76,76,76	0
56	MG	FB	1790	1/1	0.85	0.14	63,63,63,63	0
56	MG	VB	205	1/1	0.85	0.16	70,70,70,70	0
56	MG	GB	3340	1/1	0.85	0.13	66,66,66,66	0
56	MG	B	3788	1/1	0.85	0.18	56,56,56,56	0
56	MG	B	3619	1/1	0.85	0.10	70,70,70,70	0
56	MG	GB	3346	1/1	0.85	0.35	66,66,66,66	0
56	MG	FB	1667	1/1	0.85	0.18	65,65,65,65	0
56	MG	FB	1935	1/1	0.85	0.17	71,71,71,71	0
56	MG	B	3217	1/1	0.85	0.18	54,54,54,54	0
56	MG	B	3218	1/1	0.85	0.13	61,61,61,61	0
56	MG	A	1654	1/1	0.85	0.30	83,83,83,83	0
56	MG	FB	1797	1/1	0.85	0.16	81,81,81,81	0
56	MG	FB	1676	1/1	0.85	0.19	74,74,74,74	0
56	MG	B	3136	1/1	0.85	0.17	43,43,43,43	0
56	MG	B	3797	1/1	0.85	0.12	60,60,60,60	0
56	MG	GB	3613	1/1	0.85	0.08	57,57,57,57	0
56	MG	I	206	1/1	0.85	0.09	74,74,74,74	0
56	MG	FB	1946	1/1	0.85	0.17	70,70,70,70	0
56	MG	B	3050	1/1	0.85	0.18	42,42,42,42	0
56	MG	B	3637	1/1	0.85	0.26	62,62,62,62	0
56	MG	B	3638	1/1	0.85	0.25	61,61,61,61	0
56	MG	B	3505	1/1	0.85	0.08	51,51,51,51	0
56	MG	GB	3380	1/1	0.85	0.12	57,57,57,57	0
56	MG	GB	3382	1/1	0.85	0.16	72,72,72,72	0
56	MG	GB	3635	1/1	0.85	0.19	78,78,78,78	0
56	MG	B	2971	1/1	0.85	0.21	51,51,51,51	0
56	MG	B	3649	1/1	0.85	0.10	104,104,104,104	0
56	MG	GB	3155	1/1	0.85	0.32	89,89,89,89	0
56	MG	B	3512	1/1	0.85	0.17	71,71,71,71	0
56	MG	GB	3653	1/1	0.85	0.34	78,78,78,78	0
56	MG	B	3335	1/1	0.85	0.13	78,78,78,78	0
56	MG	NC	106	1/1	0.85	0.14	77,77,77,77	0
56	MG	S	208	1/1	0.85	0.13	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3164	1/1	0.85	0.33	46,46,46,46	0
56	MG	B	3662	1/1	0.85	0.08	65,65,65,65	0
56	MG	GB	3169	1/1	0.85	0.10	54,54,54,54	0
56	MG	B	3824	1/1	0.85	0.12	68,68,68,68	0
56	MG	GB	3411	1/1	0.85	0.10	67,67,67,67	0
56	MG	GB	3414	1/1	0.85	0.21	75,75,75,75	0
56	MG	B	3421	1/1	0.85	0.13	80,80,80,80	0
56	MG	GB	3178	1/1	0.85	0.18	50,50,50,50	0
56	MG	B	3423	1/1	0.85	0.13	43,43,43,43	0
56	MG	B	3539	1/1	0.85	0.13	51,51,51,51	0
56	MG	PC	305	1/1	0.85	0.11	96,96,96,96	0
56	MG	W	306	1/1	0.85	0.13	77,77,77,77	0
56	MG	B	3424	1/1	0.85	0.19	57,57,57,57	0
56	MG	B	3681	1/1	0.85	0.36	71,71,71,71	0
56	MG	FB	1838	1/1	0.85	0.10	76,76,76,76	0
56	MG	A	1658	1/1	0.85	0.17	87,87,87,87	0
56	MG	RC	303	1/1	0.85	0.24	75,75,75,75	0
56	MG	GB	2955	1/1	0.85	0.31	69,69,69,69	0
56	MG	GB	3190	1/1	0.85	0.25	71,71,71,71	0
56	MG	GB	3688	1/1	0.85	0.17	74,74,74,74	0
56	MG	GB	2963	1/1	0.85	0.31	59,59,59,59	0
56	MG	B	3169	1/1	0.85	0.16	47,47,47,47	0
56	MG	GB	2968	1/1	0.85	0.39	69,69,69,69	0
56	MG	GB	3697	1/1	0.85	0.31	69,69,69,69	0
56	MG	FB	1845	1/1	0.85	0.20	74,74,74,74	0
56	MG	GB	2979	1/1	0.85	0.24	52,52,52,52	0
56	MG	Z	102	1/1	0.85	0.21	67,67,67,67	0
56	MG	B	2937	1/1	0.85	0.32	50,50,50,50	0
56	MG	YA	101	1/1	0.85	0.38	98,98,98,98	0
56	MG	A	1771	1/1	0.85	0.11	80,80,80,80	0
56	MG	GB	2992	1/1	0.85	0.21	64,64,64,64	0
56	MG	GB	3710	1/1	0.85	0.29	61,61,61,61	0
56	MG	FB	1719	1/1	0.85	0.18	67,67,67,67	0
56	MG	A	1738	1/1	0.85	0.19	86,86,86,86	0
56	MG	CB	201	1/1	0.85	0.21	94,94,94,94	0
56	MG	GB	2999	1/1	0.85	0.23	67,67,67,67	0
56	MG	B	3555	1/1	0.85	0.15	54,54,54,54	0
56	MG	ED	201	1/1	0.85	0.22	83,83,83,83	0
56	MG	B	3440	1/1	0.85	0.12	59,59,59,59	0
56	MG	GB	2972	1/1	0.86	0.28	51,51,51,51	0
56	MG	FB	1757	1/1	0.86	0.17	101,101,101,101	0
56	MG	GB	3359	1/1	0.86	0.13	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	HB	231	1/1	0.86	0.26	79,79,79,79	0
56	MG	S	202	1/1	0.86	0.12	63,63,63,63	0
56	MG	GB	3566	1/1	0.86	0.27	66,66,66,66	0
56	MG	FB	1653	1/1	0.86	0.23	65,65,65,65	0
56	MG	B	3739	1/1	0.86	0.13	53,53,53,53	0
56	MG	B	3119	1/1	0.86	0.34	69,69,69,69	0
56	MG	GB	3575	1/1	0.86	0.08	72,72,72,72	0
56	MG	OA	203	1/1	0.86	0.09	62,62,62,62	0
56	MG	FB	1662	1/1	0.86	0.34	66,66,66,66	0
56	MG	GB	3579	1/1	0.86	0.08	65,65,65,65	0
56	MG	GB	2994	1/1	0.86	0.33	74,74,74,74	0
56	MG	B	3064	1/1	0.86	0.25	52,52,52,52	0
56	MG	B	3532	1/1	0.86	0.15	95,95,95,95	0
56	MG	B	3752	1/1	0.86	0.07	53,53,53,53	0
56	MG	B	3358	1/1	0.86	0.28	96,96,96,96	0
56	MG	C	219	1/1	0.86	0.33	81,81,81,81	0
56	MG	B	3761	1/1	0.86	0.13	53,53,53,53	0
56	MG	B	3133	1/1	0.86	0.19	50,50,50,50	0
56	MG	C	229	1/1	0.86	0.27	80,80,80,80	0
56	MG	GB	3387	1/1	0.86	0.17	66,66,66,66	0
56	MG	A	1843	1/1	0.86	0.45	89,89,89,89	0
56	MG	B	3205	1/1	0.86	0.10	68,68,68,68	0
56	MG	A	1661	1/1	0.86	0.27	64,64,64,64	0
56	MG	GB	3010	1/1	0.86	0.24	67,67,67,67	0
56	MG	A	1692	1/1	0.86	0.23	63,63,63,63	0
56	MG	GB	3404	1/1	0.86	0.18	64,64,64,64	0
56	MG	GB	3407	1/1	0.86	0.10	54,54,54,54	0
56	MG	GB	3018	1/1	0.86	0.32	73,73,73,73	0
56	MG	B	3384	1/1	0.86	0.10	55,55,55,55	0
56	MG	QB	202	1/1	0.86	0.15	66,66,66,66	0
56	MG	RB	201	1/1	0.86	0.08	71,71,71,71	0
56	MG	B	2963	1/1	0.86	0.23	49,49,49,49	0
56	MG	B	3390	1/1	0.86	0.12	72,72,72,72	0
56	MG	B	3162	1/1	0.86	0.15	43,43,43,43	0
56	MG	B	3295	1/1	0.86	0.10	55,55,55,55	0
56	MG	GB	3422	1/1	0.86	0.17	64,64,64,64	0
56	MG	GB	3625	1/1	0.86	0.07	78,78,78,78	0
56	MG	FB	1904	1/1	0.86	0.13	60,60,60,60	0
56	MG	GB	3629	1/1	0.86	0.22	57,57,57,57	0
56	MG	FB	1905	1/1	0.86	0.28	70,70,70,70	0
56	MG	B	3296	1/1	0.86	0.12	55,55,55,55	0
56	MG	B	3794	1/1	0.86	0.12	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3226	1/1	0.86	0.14	67,67,67,67	0
56	MG	GB	3639	1/1	0.86	0.22	71,71,71,71	0
56	MG	GB	3640	1/1	0.86	0.16	96,96,96,96	0
56	MG	GB	3645	1/1	0.86	0.10	71,71,71,71	0
56	MG	GB	3430	1/1	0.86	0.34	75,75,75,75	0
56	MG	IA	102	1/1	0.86	0.22	81,81,81,81	0
56	MG	ZB	101	1/1	0.86	0.23	78,78,78,78	0
56	MG	BC	301	1/1	0.86	0.21	85,85,85,85	0
56	MG	B	3675	1/1	0.86	0.16	60,60,60,60	0
56	MG	A	1664	1/1	0.86	0.25	73,73,73,73	0
56	MG	B	3678	1/1	0.86	0.17	57,57,57,57	0
56	MG	FB	1601	1/1	0.86	0.17	88,88,88,88	0
56	MG	FB	1805	1/1	0.86	0.25	74,74,74,74	0
56	MG	B	3578	1/1	0.86	0.09	54,54,54,54	0
56	MG	FB	1604	1/1	0.86	0.42	67,67,67,67	0
56	MG	CC	101	1/1	0.86	0.33	66,66,66,66	0
56	MG	GB	3448	1/1	0.86	0.23	48,48,48,48	0
56	MG	FB	1926	1/1	0.86	0.24	85,85,85,85	0
56	MG	B	3484	1/1	0.86	0.12	50,50,50,50	0
56	MG	IA	112	1/1	0.86	0.23	83,83,83,83	0
56	MG	A	1873	1/1	0.86	0.15	80,80,80,80	0
56	MG	A	1622	1/1	0.86	0.23	73,73,73,73	0
56	MG	FB	1712	1/1	0.86	0.20	78,78,78,78	0
56	MG	GB	3079	1/1	0.86	0.21	62,62,62,62	0
56	MG	B	3689	1/1	0.86	0.09	50,50,50,50	0
56	MG	A	1689	1/1	0.86	0.07	56,56,56,56	0
56	MG	B	3248	1/1	0.86	0.31	84,84,84,84	0
56	MG	IA	121	1/1	0.86	0.09	79,79,79,79	0
56	MG	GB	3266	1/1	0.86	0.15	57,57,57,57	0
56	MG	B	3183	1/1	0.86	0.23	57,57,57,57	0
56	MG	FB	1827	1/1	0.86	0.10	71,71,71,71	0
56	MG	GB	3686	1/1	0.86	0.46	65,65,65,65	0
56	MG	NC	112	1/1	0.86	0.24	76,76,76,76	0
56	MG	FB	1829	1/1	0.86	0.10	69,69,69,69	0
56	MG	B	3263	1/1	0.86	0.19	69,69,69,69	0
56	MG	GB	3093	1/1	0.86	0.23	58,58,58,58	0
56	MG	GB	3094	1/1	0.86	0.21	54,54,54,54	0
56	MG	JA	404	1/1	0.86	0.14	83,83,83,83	0
56	MG	GB	3292	1/1	0.86	0.19	86,86,86,86	0
56	MG	B	3331	1/1	0.86	0.17	49,49,49,49	0
56	MG	B	3266	1/1	0.86	0.12	54,54,54,54	0
56	MG	B	3610	1/1	0.86	0.26	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	2915	1/1	0.86	0.36	52,52,52,52	0
56	MG	I	207	1/1	0.86	0.11	70,70,70,70	0
56	MG	J	202	1/1	0.86	0.12	79,79,79,79	0
56	MG	GB	3109	1/1	0.86	0.20	63,63,63,63	0
56	MG	FB	1842	1/1	0.86	0.09	73,73,73,73	0
56	MG	B	3508	1/1	0.86	0.14	65,65,65,65	0
56	MG	K	209	1/1	0.86	0.07	67,67,67,67	0
56	MG	FB	1634	1/1	0.86	0.28	80,80,80,80	0
56	MG	B	2984	1/1	0.86	0.26	58,58,58,58	0
56	MG	GB	3321	1/1	0.86	0.22	61,61,61,61	0
56	MG	FB	1849	1/1	0.86	0.13	65,65,65,65	0
56	MG	GB	3526	1/1	0.86	0.22	80,80,80,80	0
56	MG	FB	1735	1/1	0.86	0.09	85,85,85,85	0
56	MG	GB	3124	1/1	0.86	0.16	79,79,79,79	0
56	MG	FB	1852	1/1	0.86	0.09	76,76,76,76	0
56	MG	GB	3131	1/1	0.86	0.25	71,71,71,71	0
56	MG	L	204	1/1	0.86	0.10	60,60,60,60	0
56	MG	B	3839	1/1	0.86	0.14	50,50,50,50	0
56	MG	O	203	1/1	0.86	0.18	65,65,65,65	0
56	MG	A	1704	1/1	0.86	0.24	65,65,65,65	0
56	MG	B	3191	1/1	0.86	0.23	59,59,59,59	0
56	MG	B	3732	1/1	0.86	0.13	57,57,57,57	0
56	MG	C	207	1/1	0.86	0.21	57,57,57,57	0
56	MG	B	3518	1/1	0.86	0.27	56,56,56,56	0
56	MG	R	202	1/1	0.86	0.18	49,49,49,49	0
56	MG	HB	223	1/1	0.86	0.17	85,85,85,85	0
56	MG	FB	1649	1/1	0.86	0.31	62,62,62,62	0
56	MG	GB	2970	1/1	0.86	0.28	52,52,52,52	0
56	MG	ED	202	1/1	0.86	0.31	72,72,72,72	0
56	MG	FB	1650	1/1	0.86	0.30	66,66,66,66	0
56	MG	B	3419	1/1	0.87	0.12	54,54,54,54	0
56	MG	B	3725	1/1	0.87	0.07	53,53,53,53	0
56	MG	GB	3631	1/1	0.87	0.09	60,60,60,60	0
56	MG	B	3228	1/1	0.87	0.18	58,58,58,58	0
56	MG	FB	1603	1/1	0.87	0.31	60,60,60,60	0
56	MG	GB	3634	1/1	0.87	0.19	63,63,63,63	0
56	MG	FB	1923	1/1	0.87	0.26	67,67,67,67	0
56	MG	GB	3636	1/1	0.87	0.17	75,75,75,75	0
56	MG	GB	3471	1/1	0.87	0.21	64,64,64,64	0
56	MG	OB	201	1/1	0.87	0.17	102,102,102,102	0
56	MG	FB	1924	1/1	0.87	0.12	71,71,71,71	0
56	MG	GB	3642	1/1	0.87	0.13	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3008	1/1	0.87	0.25	62,62,62,62	0
56	MG	B	3323	1/1	0.87	0.23	83,83,83,83	0
56	MG	FB	1683	1/1	0.87	0.25	75,75,75,75	0
56	MG	QB	205	1/1	0.87	0.16	68,68,68,68	0
56	MG	GB	3012	1/1	0.87	0.21	52,52,52,52	0
56	MG	FB	1927	1/1	0.87	0.25	69,69,69,69	0
56	MG	N	202	1/1	0.87	0.06	71,71,71,71	0
56	MG	B	3230	1/1	0.87	0.11	59,59,59,59	0
56	MG	A	1820	1/1	0.87	0.25	93,93,93,93	0
56	MG	A	1860	1/1	0.87	0.41	81,81,81,81	0
56	MG	B	3060	1/1	0.87	0.19	53,53,53,53	0
56	MG	FB	1851	1/1	0.87	0.14	70,70,70,70	0
56	MG	FB	1771	1/1	0.87	0.22	83,83,83,83	0
56	MG	A	1626	1/1	0.87	0.37	63,63,63,63	0
56	MG	WB	202	1/1	0.87	0.17	80,80,80,80	0
56	MG	GB	3501	1/1	0.87	0.09	77,77,77,77	0
56	MG	B	3754	1/1	0.87	0.15	57,57,57,57	0
56	MG	C	216	1/1	0.87	0.20	80,80,80,80	0
56	MG	FB	1859	1/1	0.87	0.14	83,83,83,83	0
56	MG	B	3435	1/1	0.87	0.11	63,63,63,63	0
56	MG	GB	3510	1/1	0.87	0.21	73,73,73,73	0
56	MG	GB	3352	1/1	0.87	0.23	67,67,67,67	0
56	MG	YB	205	1/1	0.87	0.11	57,57,57,57	0
56	MG	A	1662	1/1	0.87	0.29	95,95,95,95	0
56	MG	GB	3191	1/1	0.87	0.17	68,68,68,68	0
56	MG	GB	3679	1/1	0.87	0.12	72,72,72,72	0
56	MG	GB	3518	1/1	0.87	0.20	96,96,96,96	0
56	MG	GB	3047	1/1	0.87	0.18	59,59,59,59	0
56	MG	GB	3684	1/1	0.87	0.11	66,66,66,66	0
56	MG	FB	1778	1/1	0.87	0.38	83,83,83,83	0
56	MG	B	3066	1/1	0.87	0.29	55,55,55,55	0
56	MG	FB	1949	1/1	0.87	0.11	82,82,82,82	0
56	MG	GB	2905	1/1	0.87	0.51	62,62,62,62	0
56	MG	A	1865	1/1	0.87	0.20	77,77,77,77	0
56	MG	DC	102	1/1	0.87	0.21	78,78,78,78	0
56	MG	W	301	1/1	0.87	0.22	73,73,73,73	0
56	MG	GB	3061	1/1	0.87	0.25	62,62,62,62	0
56	MG	B	3777	1/1	0.87	0.11	50,50,50,50	0
56	MG	GB	3374	1/1	0.87	0.15	62,62,62,62	0
56	MG	B	3178	1/1	0.87	0.21	43,43,43,43	0
56	MG	B	3452	1/1	0.87	0.27	82,82,82,82	0
56	MG	A	1758	1/1	0.87	0.12	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	KC	104	1/1	0.87	0.11	60,60,60,60	0
56	MG	B	3664	1/1	0.87	0.11	54,54,54,54	0
56	MG	B	3370	1/1	0.87	0.17	64,64,64,64	0
56	MG	FB	1875	1/1	0.87	0.17	72,72,72,72	0
56	MG	B	3562	1/1	0.87	0.16	73,73,73,73	0
56	MG	HB	201	1/1	0.87	0.48	78,78,78,78	0
56	MG	X	108	1/1	0.87	0.22	53,53,53,53	0
56	MG	GB	3550	1/1	0.87	0.23	61,61,61,61	0
56	MG	A	1827	1/1	0.87	0.17	85,85,85,85	0
56	MG	A	1869	1/1	0.87	0.23	79,79,79,79	0
56	MG	FB	1881	1/1	0.87	0.27	68,68,68,68	0
56	MG	GB	3233	1/1	0.87	0.17	65,65,65,65	0
56	MG	B	3096	1/1	0.87	0.24	54,54,54,54	0
56	MG	A	1810	1/1	0.87	0.20	75,75,75,75	0
56	MG	GB	3564	1/1	0.87	0.21	70,70,70,70	0
56	MG	GB	3399	1/1	0.87	0.14	54,54,54,54	0
56	MG	A	1663	1/1	0.87	0.12	63,63,63,63	0
56	MG	B	3200	1/1	0.87	0.31	66,66,66,66	0
56	MG	B	3589	1/1	0.87	0.11	60,60,60,60	0
56	MG	B	3687	1/1	0.87	0.14	52,52,52,52	0
56	MG	GB	3248	1/1	0.87	0.20	60,60,60,60	0
56	MG	B	3104	1/1	0.87	0.21	70,70,70,70	0
56	MG	GB	3412	1/1	0.87	0.25	75,75,75,75	0
56	MG	B	3007	1/1	0.87	0.24	51,51,51,51	0
56	MG	FB	1728	1/1	0.87	0.39	81,81,81,81	0
56	MG	G	3204	1/1	0.87	0.07	49,49,49,49	0
56	MG	A	1762	1/1	0.87	0.28	93,93,93,93	0
56	MG	A	1651	1/1	0.87	0.35	97,97,97,97	0
56	MG	RC	306	1/1	0.87	0.16	81,81,81,81	0
56	MG	GB	3258	1/1	0.87	0.11	74,74,74,74	0
56	MG	B	3599	1/1	0.87	0.16	69,69,69,69	0
56	MG	SC	201	1/1	0.87	0.38	70,70,70,70	0
56	MG	GB	3113	1/1	0.87	0.14	69,69,69,69	0
56	MG	GB	3115	1/1	0.87	0.24	61,61,61,61	0
56	MG	GB	2980	1/1	0.87	0.17	43,43,43,43	0
56	MG	B	3012	1/1	0.87	0.25	51,51,51,51	0
56	MG	A	1728	1/1	0.87	0.30	61,61,61,61	0
56	MG	GB	3439	1/1	0.87	0.16	74,74,74,74	0
56	MG	A	1674	1/1	0.87	0.28	65,65,65,65	0
56	MG	GB	2987	1/1	0.87	0.18	48,48,48,48	0
56	MG	B	3710	1/1	0.87	0.11	69,69,69,69	0
56	MG	A	1802	1/1	0.87	0.28	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3126	1/1	0.87	0.20	53,53,53,53	0
56	MG	YC	203	1/1	0.87	0.15	82,82,82,82	0
56	MG	B	3712	1/1	0.87	0.09	59,59,59,59	0
56	MG	FB	1743	1/1	0.87	0.20	84,84,84,84	0
56	MG	A	1675	1/1	0.87	0.31	74,74,74,74	0
56	MG	FB	1909	1/1	0.87	0.13	72,72,72,72	0
56	MG	JB	313	1/1	0.87	0.12	68,68,68,68	0
56	MG	B	3312	1/1	0.87	0.14	53,53,53,53	0
56	MG	DD	101	1/1	0.87	0.13	71,71,71,71	0
56	MG	GB	3138	1/1	0.87	0.35	67,67,67,67	0
56	MG	GB	3457	1/1	0.87	0.17	80,80,80,80	0
56	MG	B	3224	1/1	0.87	0.12	52,52,52,52	0
56	MG	B	3386	1/1	0.88	0.08	101,101,101,101	0
56	MG	B	3387	1/1	0.88	0.21	60,60,60,60	0
56	MG	B	3595	1/1	0.88	0.17	75,75,75,75	0
56	MG	FB	1783	1/1	0.88	0.27	79,79,79,79	0
56	MG	B	3018	1/1	0.88	0.26	50,50,50,50	0
56	MG	GB	3347	1/1	0.88	0.23	66,66,66,66	0
56	MG	B	3479	1/1	0.88	0.17	39,39,39,39	0
56	MG	GB	2998	1/1	0.88	0.18	55,55,55,55	0
56	MG	B	3483	1/1	0.88	0.12	48,48,48,48	0
56	MG	GB	3355	1/1	0.88	0.17	69,69,69,69	0
56	MG	B	2917	1/1	0.88	0.42	46,46,46,46	0
56	MG	B	3129	1/1	0.88	0.23	54,54,54,54	0
56	MG	X	103	1/1	0.88	0.35	64,64,64,64	0
56	MG	X	104	1/1	0.88	0.19	51,51,51,51	0
56	MG	GB	3560	1/1	0.88	0.22	60,60,60,60	0
56	MG	GB	3561	1/1	0.88	0.14	68,68,68,68	0
56	MG	A	1706	1/1	0.88	0.34	88,88,88,88	0
56	MG	UA	203	1/1	0.88	0.12	74,74,74,74	0
56	MG	B	3395	1/1	0.88	0.12	58,58,58,58	0
56	MG	FB	1690	1/1	0.88	0.20	69,69,69,69	0
56	MG	B	2965	1/1	0.88	0.25	45,45,45,45	0
56	MG	GB	3372	1/1	0.88	0.17	81,81,81,81	0
56	MG	GB	3572	1/1	0.88	0.24	67,67,67,67	0
56	MG	C	226	1/1	0.88	0.09	89,89,89,89	0
56	MG	Z	101	1/1	0.88	0.20	76,76,76,76	0
56	MG	GB	3577	1/1	0.88	0.14	91,91,91,91	0
56	MG	A	1748	1/1	0.88	0.14	76,76,76,76	0
56	MG	FB	1912	1/1	0.88	0.22	73,73,73,73	0
56	MG	FB	1698	1/1	0.88	0.16	82,82,82,82	0
56	MG	B	3302	1/1	0.88	0.17	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3379	1/1	0.88	0.24	64,64,64,64	0
56	MG	B	3753	1/1	0.88	0.23	75,75,75,75	0
56	MG	B	2969	1/1	0.88	0.29	57,57,57,57	0
56	MG	GB	3588	1/1	0.88	0.14	69,69,69,69	0
56	MG	B	3406	1/1	0.88	0.09	55,55,55,55	0
56	MG	A	1836	1/1	0.88	0.20	105,105,105,105	0
56	MG	GB	3593	1/1	0.88	0.29	53,53,53,53	0
56	MG	B	3139	1/1	0.88	0.11	47,47,47,47	0
56	MG	B	3146	1/1	0.88	0.19	48,48,48,48	0
56	MG	GB	3203	1/1	0.88	0.21	60,60,60,60	0
56	MG	B	3063	1/1	0.88	0.16	44,44,44,44	0
56	MG	GB	3034	1/1	0.88	0.34	63,63,63,63	0
56	MG	B	3517	1/1	0.88	0.16	53,53,53,53	0
56	MG	B	3152	1/1	0.88	0.26	56,56,56,56	0
56	MG	A	1823	1/1	0.88	0.13	54,54,54,54	0
56	MG	GB	3402	1/1	0.88	0.24	66,66,66,66	0
56	MG	TB	204	1/1	0.88	0.34	73,73,73,73	0
56	MG	GB	3044	1/1	0.88	0.32	57,57,57,57	0
56	MG	FB	1609	1/1	0.88	0.25	64,64,64,64	0
56	MG	GB	3408	1/1	0.88	0.17	55,55,55,55	0
56	MG	F	303	1/1	0.88	0.17	71,71,71,71	0
56	MG	GB	3222	1/1	0.88	0.22	60,60,60,60	0
56	MG	VB	208	1/1	0.88	0.11	74,74,74,74	0
56	MG	GB	3616	1/1	0.88	0.11	81,81,81,81	0
56	MG	GB	3617	1/1	0.88	0.21	67,67,67,67	0
56	MG	B	2976	1/1	0.88	0.29	44,44,44,44	0
56	MG	B	2983	1/1	0.88	0.21	50,50,50,50	0
56	MG	A	1645	1/1	0.88	0.13	75,75,75,75	0
56	MG	GB	3415	1/1	0.88	0.25	55,55,55,55	0
56	MG	GB	3055	1/1	0.88	0.23	64,64,64,64	0
56	MG	GB	3228	1/1	0.88	0.12	62,62,62,62	0
56	MG	GB	3056	1/1	0.88	0.25	57,57,57,57	0
56	MG	B	3428	1/1	0.88	0.17	48,48,48,48	0
56	MG	B	3429	1/1	0.88	0.19	46,46,46,46	0
56	MG	B	3544	1/1	0.88	0.17	85,85,85,85	0
56	MG	GB	3236	1/1	0.88	0.25	74,74,74,74	0
56	MG	B	3341	1/1	0.88	0.24	58,58,58,58	0
56	MG	FB	1839	1/1	0.88	0.30	78,78,78,78	0
56	MG	G	3208	1/1	0.88	0.16	58,58,58,58	0
56	MG	GB	3434	1/1	0.88	0.17	63,63,63,63	0
56	MG	GB	3437	1/1	0.88	0.30	70,70,70,70	0
56	MG	GB	3067	1/1	0.88	0.15	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3068	1/1	0.88	0.16	66,66,66,66	0
56	MG	CC	102	1/1	0.88	0.17	77,77,77,77	0
56	MG	GB	3440	1/1	0.88	0.14	80,80,80,80	0
56	MG	GB	3649	1/1	0.88	0.17	70,70,70,70	0
56	MG	GB	3247	1/1	0.88	0.25	62,62,62,62	0
56	MG	B	3668	1/1	0.88	0.07	63,63,63,63	0
56	MG	IA	120	1/1	0.88	0.17	85,85,85,85	0
56	MG	B	2986	1/1	0.88	0.17	37,37,37,37	0
56	MG	GB	3251	1/1	0.88	0.11	55,55,55,55	0
56	MG	A	1759	1/1	0.88	0.32	62,62,62,62	0
56	MG	KC	102	1/1	0.88	0.17	61,61,61,61	0
56	MG	A	1805	1/1	0.88	0.32	87,87,87,87	0
56	MG	B	3186	1/1	0.88	0.20	48,48,48,48	0
56	MG	B	3559	1/1	0.88	0.17	63,63,63,63	0
56	MG	B	3679	1/1	0.88	0.13	66,66,66,66	0
56	MG	FB	1635	1/1	0.88	0.30	78,78,78,78	0
56	MG	GB	3455	1/1	0.88	0.12	64,64,64,64	0
56	MG	B	3680	1/1	0.88	0.18	52,52,52,52	0
56	MG	JA	411	1/1	0.88	0.25	100,100,100,100	0
56	MG	GB	3263	1/1	0.88	0.18	77,77,77,77	0
56	MG	FB	1856	1/1	0.88	0.12	100,100,100,100	0
56	MG	A	1616	1/1	0.88	0.24	74,74,74,74	0
56	MG	B	3368	1/1	0.88	0.18	57,57,57,57	0
56	MG	GB	3097	1/1	0.88	0.18	57,57,57,57	0
56	MG	B	3816	1/1	0.88	0.16	60,60,60,60	0
56	MG	OC	404	1/1	0.88	0.08	97,97,97,97	0
56	MG	A	1742	1/1	0.88	0.25	66,66,66,66	0
56	MG	GB	3280	1/1	0.88	0.18	84,84,84,84	0
56	MG	B	2904	1/1	0.88	0.28	46,46,46,46	0
56	MG	B	3570	1/1	0.88	0.11	65,65,65,65	0
56	MG	GB	3288	1/1	0.88	0.13	73,73,73,73	0
56	MG	GB	3477	1/1	0.88	0.09	60,60,60,60	0
56	MG	B	3825	1/1	0.88	0.13	55,55,55,55	0
56	MG	M	204	1/1	0.88	0.14	69,69,69,69	0
56	MG	GB	2946	1/1	0.88	0.30	52,52,52,52	0
56	MG	GB	3486	1/1	0.88	0.21	68,68,68,68	0
56	MG	GB	3294	1/1	0.88	0.21	64,64,64,64	0
56	MG	B	3571	1/1	0.88	0.17	66,66,66,66	0
56	MG	GB	3702	1/1	0.88	0.08	53,53,53,53	0
56	MG	A	1754	1/1	0.88	0.41	90,90,90,90	0
56	MG	GB	3491	1/1	0.88	0.27	55,55,55,55	0
56	MG	FB	1760	1/1	0.88	0.38	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	RC	309	1/1	0.88	0.09	77,77,77,77	0
56	MG	GB	2952	1/1	0.88	0.28	63,63,63,63	0
56	MG	GB	3307	1/1	0.88	0.14	51,51,51,51	0
56	MG	GB	3499	1/1	0.88	0.16	61,61,61,61	0
56	MG	SC	204	1/1	0.88	0.17	81,81,81,81	0
56	MG	N	206	1/1	0.88	0.10	69,69,69,69	0
56	MG	GB	2961	1/1	0.88	0.31	64,64,64,64	0
56	MG	B	3832	1/1	0.88	0.06	59,59,59,59	0
56	MG	B	2961	1/1	0.88	0.19	38,38,38,38	0
56	MG	GB	3312	1/1	0.88	0.21	73,73,73,73	0
56	MG	B	2962	1/1	0.88	0.28	43,43,43,43	0
56	MG	FB	1657	1/1	0.88	0.34	62,62,62,62	0
56	MG	GB	3512	1/1	0.88	0.11	67,67,67,67	0
56	MG	B	3583	1/1	0.88	0.07	73,73,73,73	0
56	MG	B	3844	1/1	0.88	0.10	53,53,53,53	0
56	MG	GB	2973	1/1	0.88	0.22	50,50,50,50	0
56	MG	GB	3132	1/1	0.88	0.18	65,65,65,65	0
56	MG	GB	3325	1/1	0.88	0.16	54,54,54,54	0
56	MG	B	3584	1/1	0.88	0.07	46,46,46,46	0
56	MG	B	3289	1/1	0.88	0.13	38,38,38,38	0
56	MG	GB	3330	1/1	0.88	0.11	79,79,79,79	0
56	MG	OA	204	1/1	0.88	0.09	82,82,82,82	0
56	MG	B	3381	1/1	0.88	0.16	77,77,77,77	0
56	MG	B	3115	1/1	0.88	0.13	39,39,39,39	0
56	MG	GB	2986	1/1	0.88	0.34	49,49,49,49	0
56	MG	FB	1669	1/1	0.88	0.24	67,67,67,67	0
56	MG	B	3650	1/1	0.89	0.19	58,58,58,58	0
56	MG	FB	1674	1/1	0.89	0.20	69,69,69,69	0
56	MG	FB	1675	1/1	0.89	0.35	72,72,72,72	0
56	MG	B	2934	1/1	0.89	0.41	62,62,62,62	0
56	MG	B	3270	1/1	0.89	0.20	56,56,56,56	0
56	MG	FB	1810	1/1	0.89	0.23	71,71,71,71	0
56	MG	K	201	1/1	0.89	0.28	58,58,58,58	0
56	MG	A	1883	1/1	0.89	0.14	79,79,79,79	0
56	MG	GB	3098	1/1	0.89	0.15	68,68,68,68	0
56	MG	FB	1947	1/1	0.89	0.17	73,73,73,73	0
56	MG	B	3663	1/1	0.89	0.09	51,51,51,51	0
56	MG	L	202	1/1	0.89	0.11	58,58,58,58	0
56	MG	B	3354	1/1	0.89	0.08	48,48,48,48	0
56	MG	A	1647	1/1	0.89	0.15	82,82,82,82	0
56	MG	GB	2911	1/1	0.89	0.35	45,45,45,45	0
56	MG	GB	2912	1/1	0.89	0.39	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	2913	1/1	0.89	0.21	63,63,63,63	0
56	MG	A	1644	1/1	0.89	0.24	62,62,62,62	0
56	MG	GB	3114	1/1	0.89	0.29	69,69,69,69	0
56	MG	B	3278	1/1	0.89	0.18	54,54,54,54	0
56	MG	HB	232	1/1	0.89	0.34	84,84,84,84	0
56	MG	B	3197	1/1	0.89	0.23	53,53,53,53	0
56	MG	GB	3536	1/1	0.89	0.17	67,67,67,67	0
56	MG	GB	3118	1/1	0.89	0.20	56,56,56,56	0
56	MG	B	3441	1/1	0.89	0.21	49,49,49,49	0
56	MG	O	201	1/1	0.89	0.06	76,76,76,76	0
56	MG	GB	3543	1/1	0.89	0.11	55,55,55,55	0
56	MG	FB	1828	1/1	0.89	0.20	70,70,70,70	0
56	MG	A	1848	1/1	0.89	0.30	70,70,70,70	0
56	MG	B	3373	1/1	0.89	0.10	50,50,50,50	0
56	MG	JB	307	1/1	0.89	0.13	63,63,63,63	0
56	MG	GB	2927	1/1	0.89	0.29	62,62,62,62	0
56	MG	B	3447	1/1	0.89	0.18	63,63,63,63	0
56	MG	GB	3129	1/1	0.89	0.25	65,65,65,65	0
56	MG	FB	1834	1/1	0.89	0.32	68,68,68,68	0
56	MG	GB	2934	1/1	0.89	0.27	60,60,60,60	0
56	MG	LB	303	1/1	0.89	0.22	53,53,53,53	0
56	MG	A	1861	1/1	0.89	0.10	92,92,92,92	0
56	MG	B	3453	1/1	0.89	0.12	44,44,44,44	0
56	MG	Q	202	1/1	0.89	0.17	74,74,74,74	0
56	MG	B	2911	1/1	0.89	0.30	48,48,48,48	0
56	MG	R	201	1/1	0.89	0.12	54,54,54,54	0
56	MG	A	1729	1/1	0.89	0.20	63,63,63,63	0
56	MG	UA	202	1/1	0.89	0.25	79,79,79,79	0
56	MG	B	3135	1/1	0.89	0.14	48,48,48,48	0
56	MG	FB	1844	1/1	0.89	0.21	81,81,81,81	0
56	MG	GB	3570	1/1	0.89	0.07	82,82,82,82	0
56	MG	GB	3151	1/1	0.89	0.20	70,70,70,70	0
56	MG	B	3209	1/1	0.89	0.14	51,51,51,51	0
56	MG	T	203	1/1	0.89	0.09	58,58,58,58	0
56	MG	B	3833	1/1	0.89	0.18	48,48,48,48	0
56	MG	GB	3366	1/1	0.89	0.15	65,65,65,65	0
56	MG	GB	3367	1/1	0.89	0.24	76,76,76,76	0
56	MG	GB	3156	1/1	0.89	0.20	46,46,46,46	0
56	MG	GB	2962	1/1	0.89	0.21	61,61,61,61	0
56	MG	GB	3583	1/1	0.89	0.25	68,68,68,68	0
56	MG	B	3385	1/1	0.89	0.13	59,59,59,59	0
56	MG	B	3003	1/1	0.89	0.22	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3694	1/1	0.89	0.30	54,54,54,54	0
56	MG	B	3842	1/1	0.89	0.12	60,60,60,60	0
56	MG	A	1817	1/1	0.89	0.09	66,66,66,66	0
56	MG	FB	1854	1/1	0.89	0.23	86,86,86,86	0
56	MG	GB	3173	1/1	0.89	0.12	80,80,80,80	0
56	MG	B	3698	1/1	0.89	0.10	77,77,77,77	0
56	MG	GB	3381	1/1	0.89	0.26	66,66,66,66	0
56	MG	A	1739	1/1	0.89	0.16	59,59,59,59	0
56	MG	X	101	1/1	0.89	0.25	58,58,58,58	0
56	MG	A	1633	1/1	0.89	0.29	86,86,86,86	0
56	MG	C	206	1/1	0.89	0.20	54,54,54,54	0
56	MG	X	105	1/1	0.89	0.17	55,55,55,55	0
56	MG	GB	3388	1/1	0.89	0.21	64,64,64,64	0
56	MG	B	3706	1/1	0.89	0.16	50,50,50,50	0
56	MG	B	3472	1/1	0.89	0.14	55,55,55,55	0
56	MG	B	3591	1/1	0.89	0.23	61,61,61,61	0
56	MG	FB	1610	1/1	0.89	0.34	68,68,68,68	0
56	MG	GB	3609	1/1	0.89	0.19	73,73,73,73	0
56	MG	FB	1867	1/1	0.89	0.15	82,82,82,82	0
56	MG	YB	207	1/1	0.89	0.11	79,79,79,79	0
56	MG	FB	1731	1/1	0.89	0.15	70,70,70,70	0
56	MG	B	3150	1/1	0.89	0.19	53,53,53,53	0
56	MG	GB	3403	1/1	0.89	0.42	65,65,65,65	0
56	MG	A	1880	1/1	0.89	0.21	77,77,77,77	0
56	MG	GB	3405	1/1	0.89	0.15	70,70,70,70	0
56	MG	B	3093	1/1	0.89	0.28	54,54,54,54	0
56	MG	B	3396	1/1	0.89	0.21	49,49,49,49	0
56	MG	A	1698	1/1	0.89	0.33	77,77,77,77	0
56	MG	FB	1618	1/1	0.89	0.41	67,67,67,67	0
56	MG	B	3310	1/1	0.89	0.20	56,56,56,56	0
56	MG	GB	3205	1/1	0.89	0.30	71,71,71,71	0
56	MG	GB	3003	1/1	0.89	0.32	55,55,55,55	0
56	MG	B	2928	1/1	0.89	0.23	39,39,39,39	0
56	MG	B	3723	1/1	0.89	0.11	67,67,67,67	0
56	MG	B	3494	1/1	0.89	0.19	70,70,70,70	0
56	MG	B	3729	1/1	0.89	0.09	93,93,93,93	0
56	MG	B	3495	1/1	0.89	0.11	46,46,46,46	0
56	MG	GB	3638	1/1	0.89	0.39	66,66,66,66	0
56	MG	B	3099	1/1	0.89	0.16	37,37,37,37	0
56	MG	B	3614	1/1	0.89	0.16	50,50,50,50	0
56	MG	B	3744	1/1	0.89	0.09	48,48,48,48	0
56	MG	GB	3643	1/1	0.89	0.18	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3427	1/1	0.89	0.17	61,61,61,61	0
56	MG	IA	105	1/1	0.89	0.23	80,80,80,80	0
56	MG	C	234	1/1	0.89	0.07	65,65,65,65	0
56	MG	B	3239	1/1	0.89	0.13	64,64,64,64	0
56	MG	GB	3432	1/1	0.89	0.31	49,49,49,49	0
56	MG	FB	1761	1/1	0.89	0.12	72,72,72,72	0
56	MG	GB	3021	1/1	0.89	0.19	56,56,56,56	0
56	MG	B	3408	1/1	0.89	0.20	55,55,55,55	0
56	MG	B	3409	1/1	0.89	0.17	105,105,105,105	0
56	MG	NC	113	1/1	0.89	0.08	80,80,80,80	0
56	MG	IA	110	1/1	0.89	0.18	83,83,83,83	0
56	MG	GB	3234	1/1	0.89	0.26	57,57,57,57	0
56	MG	B	3322	1/1	0.89	0.17	46,46,46,46	0
56	MG	C	243	1/1	0.89	0.15	57,57,57,57	0
56	MG	B	3624	1/1	0.89	0.11	66,66,66,66	0
56	MG	A	1603	1/1	0.89	0.21	78,78,78,78	0
56	MG	GB	3239	1/1	0.89	0.10	54,54,54,54	0
56	MG	B	3101	1/1	0.89	0.31	47,47,47,47	0
56	MG	GB	3242	1/1	0.89	0.13	65,65,65,65	0
56	MG	GB	3450	1/1	0.89	0.19	77,77,77,77	0
56	MG	E	310	1/1	0.89	0.08	57,57,57,57	0
56	MG	FB	1774	1/1	0.89	0.18	67,67,67,67	0
56	MG	GB	3040	1/1	0.89	0.30	48,48,48,48	0
56	MG	B	3630	1/1	0.89	0.08	39,39,39,39	0
56	MG	GB	3678	1/1	0.89	0.12	87,87,87,87	0
56	MG	RC	301	1/1	0.89	0.36	69,69,69,69	0
56	MG	B	3031	1/1	0.89	0.19	54,54,54,54	0
56	MG	FB	1648	1/1	0.89	0.30	57,57,57,57	0
56	MG	B	3763	1/1	0.89	0.11	56,56,56,56	0
56	MG	B	3180	1/1	0.89	0.20	58,58,58,58	0
56	MG	B	3769	1/1	0.89	0.07	69,69,69,69	0
56	MG	B	3771	1/1	0.89	0.11	47,47,47,47	0
56	MG	B	3773	1/1	0.89	0.10	99,99,99,99	0
56	MG	GB	3469	1/1	0.89	0.16	65,65,65,65	0
56	MG	B	3776	1/1	0.89	0.10	62,62,62,62	0
56	MG	SC	203	1/1	0.89	0.25	85,85,85,85	0
56	MG	B	3635	1/1	0.89	0.12	56,56,56,56	0
56	MG	B	3265	1/1	0.89	0.21	62,62,62,62	0
56	MG	FB	1661	1/1	0.89	0.19	66,66,66,66	0
56	MG	B	3781	1/1	0.89	0.11	69,69,69,69	0
56	MG	GB	3264	1/1	0.89	0.08	71,71,71,71	0
56	MG	B	3340	1/1	0.89	0.07	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3032	1/1	0.89	0.22	43,43,43,43	0
56	MG	GB	3480	1/1	0.89	0.15	70,70,70,70	0
56	MG	GB	3066	1/1	0.89	0.25	55,55,55,55	0
56	MG	GB	3707	1/1	0.89	0.34	42,42,42,42	0
56	MG	B	3640	1/1	0.89	0.11	53,53,53,53	0
56	MG	GB	3483	1/1	0.89	0.21	78,78,78,78	0
56	MG	YC	204	1/1	0.89	0.15	94,94,94,94	0
56	MG	B	3529	1/1	0.89	0.24	43,43,43,43	0
56	MG	FB	1930	1/1	0.89	0.14	68,68,68,68	0
56	MG	B	3645	1/1	0.89	0.11	70,70,70,70	0
56	MG	B	3106	1/1	0.89	0.25	58,58,58,58	0
56	MG	GB	3282	1/1	0.89	0.11	70,70,70,70	0
56	MG	GB	3283	1/1	0.89	0.20	73,73,73,73	0
56	MG	B	3533	1/1	0.89	0.13	60,60,60,60	0
56	MG	FB	1934	1/1	0.89	0.13	82,82,82,82	0
56	MG	FB	1672	1/1	0.89	0.23	60,60,60,60	0
56	MG	FB	1802	1/1	0.89	0.19	64,64,64,64	0
56	MG	GB	2967	1/1	0.90	0.28	61,61,61,61	0
56	MG	B	3444	1/1	0.90	0.10	52,52,52,52	0
56	MG	HB	220	1/1	0.90	0.14	92,92,92,92	0
56	MG	B	3026	1/1	0.90	0.08	40,40,40,40	0
56	MG	B	2906	1/1	0.90	0.31	29,29,29,29	0
56	MG	B	3272	1/1	0.90	0.18	63,63,63,63	0
56	MG	FB	1759	1/1	0.90	0.28	66,66,66,66	0
56	MG	GB	2976	1/1	0.90	0.26	52,52,52,52	0
56	MG	GB	3153	1/1	0.90	0.12	59,59,59,59	0
56	MG	B	2907	1/1	0.90	0.30	41,41,41,41	0
56	MG	A	1650	1/1	0.90	0.12	86,86,86,86	0
56	MG	GB	3354	1/1	0.90	0.30	81,81,81,81	0
56	MG	A	1701	1/1	0.90	0.31	56,56,56,56	0
56	MG	GB	3157	1/1	0.90	0.14	68,68,68,68	0
56	MG	B	3800	1/1	0.90	0.10	52,52,52,52	0
56	MG	B	2956	1/1	0.90	0.32	49,49,49,49	0
56	MG	B	2992	1/1	0.90	0.13	38,38,38,38	0
56	MG	B	3806	1/1	0.90	0.10	58,58,58,58	0
56	MG	GB	3165	1/1	0.90	0.25	66,66,66,66	0
56	MG	JB	302	1/1	0.90	0.13	63,63,63,63	0
56	MG	FB	1883	1/1	0.90	0.08	70,70,70,70	0
56	MG	K	204	1/1	0.90	0.11	65,65,65,65	0
56	MG	FB	1770	1/1	0.90	0.26	93,93,93,93	0
56	MG	B	3682	1/1	0.90	0.15	67,67,67,67	0
56	MG	GB	3563	1/1	0.90	0.13	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	K	208	1/1	0.90	0.06	71,71,71,71	0
56	MG	GB	3565	1/1	0.90	0.12	60,60,60,60	0
56	MG	GB	3177	1/1	0.90	0.34	58,58,58,58	0
56	MG	GB	2996	1/1	0.90	0.41	57,57,57,57	0
56	MG	B	3575	1/1	0.90	0.19	69,69,69,69	0
56	MG	KB	303	1/1	0.90	0.16	79,79,79,79	0
56	MG	LB	302	1/1	0.90	0.26	61,61,61,61	0
56	MG	B	3814	1/1	0.90	0.25	38,38,38,38	0
56	MG	B	3576	1/1	0.90	0.14	69,69,69,69	0
56	MG	LB	305	1/1	0.90	0.20	55,55,55,55	0
56	MG	A	1807	1/1	0.90	0.13	87,87,87,87	0
56	MG	GB	3574	1/1	0.90	0.07	83,83,83,83	0
56	MG	B	3131	1/1	0.90	0.18	57,57,57,57	0
56	MG	FB	1666	1/1	0.90	0.24	66,66,66,66	0
56	MG	B	2998	1/1	0.90	0.22	47,47,47,47	0
56	MG	FB	1897	1/1	0.90	0.25	67,67,67,67	0
56	MG	FB	1898	1/1	0.90	0.13	70,70,70,70	0
56	MG	B	3690	1/1	0.90	0.18	59,59,59,59	0
56	MG	GB	3384	1/1	0.90	0.19	63,63,63,63	0
56	MG	A	1638	1/1	0.90	0.20	61,61,61,61	0
56	MG	B	3292	1/1	0.90	0.15	50,50,50,50	0
56	MG	O	202	1/1	0.90	0.13	70,70,70,70	0
56	MG	A	1628	1/1	0.90	0.36	77,77,77,77	0
56	MG	B	3474	1/1	0.90	0.09	41,41,41,41	0
56	MG	PB	203	1/1	0.90	0.11	91,91,91,91	0
56	MG	GB	3199	1/1	0.90	0.16	67,67,67,67	0
56	MG	GB	3201	1/1	0.90	0.30	57,57,57,57	0
56	MG	QB	203	1/1	0.90	0.15	69,69,69,69	0
56	MG	FB	1789	1/1	0.90	0.10	69,69,69,69	0
56	MG	B	3476	1/1	0.90	0.16	67,67,67,67	0
56	MG	A	1855	1/1	0.90	0.15	89,89,89,89	0
56	MG	B	3008	1/1	0.90	0.26	80,80,80,80	0
56	MG	SB	202	1/1	0.90	0.27	80,80,80,80	0
56	MG	FB	1910	1/1	0.90	0.17	78,78,78,78	0
56	MG	A	1653	1/1	0.90	0.31	74,74,74,74	0
56	MG	GB	3212	1/1	0.90	0.30	55,55,55,55	0
56	MG	B	3597	1/1	0.90	0.09	49,49,49,49	0
56	MG	GB	3217	1/1	0.90	0.13	65,65,65,65	0
56	MG	GB	3026	1/1	0.90	0.16	54,54,54,54	0
56	MG	B	3144	1/1	0.90	0.13	40,40,40,40	0
56	MG	B	3600	1/1	0.90	0.07	54,54,54,54	0
56	MG	B	3216	1/1	0.90	0.22	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	WB	201	1/1	0.90	0.11	80,80,80,80	0
56	MG	FB	1685	1/1	0.90	0.14	61,61,61,61	0
56	MG	GB	3612	1/1	0.90	0.12	71,71,71,71	0
56	MG	S	207	1/1	0.90	0.23	49,49,49,49	0
56	MG	GB	3417	1/1	0.90	0.07	66,66,66,66	0
56	MG	B	3716	1/1	0.90	0.17	65,65,65,65	0
56	MG	B	3605	1/1	0.90	0.21	57,57,57,57	0
56	MG	A	1734	1/1	0.90	0.30	72,72,72,72	0
56	MG	B	3306	1/1	0.90	0.07	44,44,44,44	0
56	MG	FB	1693	1/1	0.90	0.32	66,66,66,66	0
56	MG	GB	3623	1/1	0.90	0.12	63,63,63,63	0
56	MG	B	3608	1/1	0.90	0.12	63,63,63,63	0
56	MG	B	3401	1/1	0.90	0.08	46,46,46,46	0
56	MG	B	3148	1/1	0.90	0.14	67,67,67,67	0
56	MG	FB	1813	1/1	0.90	0.09	69,69,69,69	0
56	MG	B	3149	1/1	0.90	0.14	42,42,42,42	0
56	MG	A	1846	1/1	0.90	0.15	57,57,57,57	0
56	MG	GB	3054	1/1	0.90	0.23	56,56,56,56	0
56	MG	B	3736	1/1	0.90	0.11	52,52,52,52	0
56	MG	B	3501	1/1	0.90	0.12	48,48,48,48	0
56	MG	B	3407	1/1	0.90	0.10	72,72,72,72	0
56	MG	B	3226	1/1	0.90	0.22	64,64,64,64	0
56	MG	C	224	1/1	0.90	0.14	74,74,74,74	0
56	MG	B	3621	1/1	0.90	0.14	49,49,49,49	0
56	MG	A	1761	1/1	0.90	0.22	74,74,74,74	0
56	MG	B	3625	1/1	0.90	0.24	58,58,58,58	0
56	MG	B	3094	1/1	0.90	0.19	51,51,51,51	0
56	MG	FB	1710	1/1	0.90	0.29	67,67,67,67	0
56	MG	FB	1830	1/1	0.90	0.27	69,69,69,69	0
56	MG	B	3154	1/1	0.90	0.14	58,58,58,58	0
56	MG	GB	3073	1/1	0.90	0.13	64,64,64,64	0
56	MG	GB	3075	1/1	0.90	0.21	65,65,65,65	0
56	MG	C	232	1/1	0.90	0.07	82,82,82,82	0
56	MG	GB	2904	1/1	0.90	0.47	57,57,57,57	0
56	MG	GB	3080	1/1	0.90	0.13	58,58,58,58	0
56	MG	GB	3454	1/1	0.90	0.08	77,77,77,77	0
56	MG	GB	3082	1/1	0.90	0.20	53,53,53,53	0
56	MG	FB	1833	1/1	0.90	0.20	62,62,62,62	0
56	MG	GB	3458	1/1	0.90	0.06	95,95,95,95	0
56	MG	GB	2906	1/1	0.90	0.32	53,53,53,53	0
56	MG	GB	3461	1/1	0.90	0.23	76,76,76,76	0
56	MG	NC	110	1/1	0.90	0.15	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3095	1/1	0.90	0.22	56,56,56,56	0
56	MG	B	3016	1/1	0.90	0.26	76,76,76,76	0
56	MG	B	3247	1/1	0.90	0.09	62,62,62,62	0
56	MG	B	3167	1/1	0.90	0.12	44,44,44,44	0
56	MG	GB	3271	1/1	0.90	0.33	84,84,84,84	0
56	MG	B	3250	1/1	0.90	0.08	42,42,42,42	0
56	MG	GB	3470	1/1	0.90	0.21	73,73,73,73	0
56	MG	DA	103	1/1	0.90	0.07	68,68,68,68	0
56	MG	B	3258	1/1	0.90	0.15	49,49,49,49	0
56	MG	GB	2918	1/1	0.90	0.35	56,56,56,56	0
56	MG	B	3530	1/1	0.90	0.10	58,58,58,58	0
56	MG	A	1707	1/1	0.90	0.29	79,79,79,79	0
56	MG	B	3019	1/1	0.90	0.27	51,51,51,51	0
56	MG	GB	3099	1/1	0.90	0.23	48,48,48,48	0
56	MG	FB	1621	1/1	0.90	0.25	74,74,74,74	0
56	MG	GB	3687	1/1	0.90	0.08	72,72,72,72	0
56	MG	B	3347	1/1	0.90	0.19	54,54,54,54	0
56	MG	E	303	1/1	0.90	0.15	62,62,62,62	0
56	MG	GB	2928	1/1	0.90	0.51	77,77,77,77	0
56	MG	GB	3695	1/1	0.90	0.16	75,75,75,75	0
56	MG	B	3022	1/1	0.90	0.23	45,45,45,45	0
56	MG	B	2940	1/1	0.90	0.14	33,33,33,33	0
56	MG	GB	3698	1/1	0.90	0.13	68,68,68,68	0
56	MG	GB	3699	1/1	0.90	0.16	57,57,57,57	0
56	MG	B	3780	1/1	0.90	0.15	70,70,70,70	0
56	MG	GB	2935	1/1	0.90	0.19	50,50,50,50	0
56	MG	GB	3304	1/1	0.90	0.35	58,58,58,58	0
56	MG	GB	3306	1/1	0.90	0.21	57,57,57,57	0
56	MG	GB	2936	1/1	0.90	0.29	54,54,54,54	0
56	MG	GB	3496	1/1	0.90	0.10	70,70,70,70	0
56	MG	B	3024	1/1	0.90	0.14	40,40,40,40	0
56	MG	B	3181	1/1	0.90	0.20	57,57,57,57	0
56	MG	GB	3116	1/1	0.90	0.25	66,66,66,66	0
56	MG	F	310	1/1	0.90	0.08	69,69,69,69	0
56	MG	B	3655	1/1	0.90	0.19	46,46,46,46	0
56	MG	B	3356	1/1	0.90	0.17	50,50,50,50	0
56	MG	VC	202	1/1	0.90	0.18	75,75,75,75	0
56	MG	B	3269	1/1	0.90	0.09	52,52,52,52	0
56	MG	B	3553	1/1	0.90	0.16	59,59,59,59	0
56	MG	B	3789	1/1	0.90	0.20	46,46,46,46	0
56	MG	FB	1744	1/1	0.90	0.18	55,55,55,55	0
56	MG	YC	202	1/1	0.90	0.11	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1745	1/1	0.90	0.14	67,67,67,67	0
56	MG	GB	2953	1/1	0.90	0.24	56,56,56,56	0
56	MG	YC	205	1/1	0.90	0.19	66,66,66,66	0
56	MG	GB	3516	1/1	0.90	0.15	63,63,63,63	0
56	MG	G	3207	1/1	0.90	0.14	36,36,36,36	0
56	MG	GB	2958	1/1	0.90	0.39	65,65,65,65	0
56	MG	GB	2960	1/1	0.90	0.22	63,63,63,63	0
56	MG	B	3361	1/1	0.90	0.14	72,72,72,72	0
56	MG	GB	3332	1/1	0.90	0.13	64,64,64,64	0
56	MG	FB	1750	1/1	0.90	0.32	70,70,70,70	0
56	MG	G	3210	1/1	0.90	0.16	62,62,62,62	0
56	MG	GB	3336	1/1	0.90	0.14	68,68,68,68	0
56	MG	B	3365	1/1	0.90	0.10	73,73,73,73	0
57	ZN	GC	101	1/1	0.90	0.09	149,149,149,149	0
56	MG	GB	3053	1/1	0.91	0.12	53,53,53,53	0
56	MG	ZA	203	1/1	0.91	0.31	91,91,91,91	0
56	MG	B	3035	1/1	0.91	0.20	63,63,63,63	0
56	MG	B	3568	1/1	0.91	0.09	53,53,53,53	0
56	MG	B	3768	1/1	0.91	0.11	41,41,41,41	0
56	MG	B	3658	1/1	0.91	0.13	54,54,54,54	0
56	MG	Y	101	1/1	0.91	0.12	49,49,49,49	0
56	MG	A	1832	1/1	0.91	0.15	67,67,67,67	0
56	MG	B	2933	1/1	0.91	0.14	52,52,52,52	0
56	MG	C	238	1/1	0.91	0.09	91,91,91,91	0
56	MG	B	3774	1/1	0.91	0.12	46,46,46,46	0
56	MG	JB	311	1/1	0.91	0.17	63,63,63,63	0
56	MG	GB	3580	1/1	0.91	0.13	74,74,74,74	0
56	MG	B	3318	1/1	0.91	0.22	49,49,49,49	0
56	MG	B	3042	1/1	0.91	0.30	53,53,53,53	0
56	MG	GB	3406	1/1	0.91	0.15	59,59,59,59	0
56	MG	GB	3069	1/1	0.91	0.30	59,59,59,59	0
56	MG	B	3321	1/1	0.91	0.31	60,60,60,60	0
56	MG	B	3259	1/1	0.91	0.08	38,38,38,38	0
56	MG	B	3577	1/1	0.91	0.07	66,66,66,66	0
56	MG	B	3261	1/1	0.91	0.23	50,50,50,50	0
56	MG	GB	2922	1/1	0.91	0.38	63,63,63,63	0
56	MG	GB	3413	1/1	0.91	0.10	58,58,58,58	0
56	MG	B	3676	1/1	0.91	0.09	55,55,55,55	0
56	MG	GB	3081	1/1	0.91	0.20	51,51,51,51	0
56	MG	GB	3416	1/1	0.91	0.18	61,61,61,61	0
56	MG	B	3004	1/1	0.91	0.30	43,43,43,43	0
56	MG	GB	3600	1/1	0.91	0.31	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3006	1/1	0.91	0.24	53,53,53,53	0
56	MG	GB	3244	1/1	0.91	0.17	52,52,52,52	0
56	MG	FB	1623	1/1	0.91	0.27	53,53,53,53	0
56	MG	B	3487	1/1	0.91	0.09	81,81,81,81	0
56	MG	B	3264	1/1	0.91	0.23	70,70,70,70	0
56	MG	FB	1736	1/1	0.91	0.18	58,58,58,58	0
56	MG	B	3337	1/1	0.91	0.11	46,46,46,46	0
56	MG	PB	204	1/1	0.91	0.05	95,95,95,95	0
56	MG	GB	3089	1/1	0.91	0.16	66,66,66,66	0
56	MG	FB	1627	1/1	0.91	0.28	75,75,75,75	0
56	MG	B	3120	1/1	0.91	0.33	56,56,56,56	0
56	MG	B	3057	1/1	0.91	0.09	61,61,61,61	0
56	MG	A	1752	1/1	0.91	0.15	67,67,67,67	0
56	MG	RB	202	1/1	0.91	0.15	77,77,77,77	0
56	MG	GB	2941	1/1	0.91	0.26	53,53,53,53	0
56	MG	GB	3096	1/1	0.91	0.23	56,56,56,56	0
56	MG	GB	2942	1/1	0.91	0.31	54,54,54,54	0
56	MG	SB	203	1/1	0.91	0.23	73,73,73,73	0
56	MG	GB	3619	1/1	0.91	0.08	75,75,75,75	0
56	MG	GB	3620	1/1	0.91	0.21	69,69,69,69	0
56	MG	B	3192	1/1	0.91	0.31	58,58,58,58	0
56	MG	B	3345	1/1	0.91	0.16	72,72,72,72	0
56	MG	B	3062	1/1	0.91	0.19	40,40,40,40	0
56	MG	GB	3624	1/1	0.91	0.14	65,65,65,65	0
56	MG	VB	204	1/1	0.91	0.12	74,74,74,74	0
56	MG	B	2966	1/1	0.91	0.32	60,60,60,60	0
56	MG	GB	3443	1/1	0.91	0.17	69,69,69,69	0
56	MG	IA	113	1/1	0.91	0.20	71,71,71,71	0
56	MG	GB	3267	1/1	0.91	0.21	74,74,74,74	0
56	MG	GB	2948	1/1	0.91	0.26	51,51,51,51	0
56	MG	FB	1749	1/1	0.91	0.13	111,111,111,111	0
56	MG	A	1842	1/1	0.91	0.07	67,67,67,67	0
56	MG	B	2938	1/1	0.91	0.26	55,55,55,55	0
56	MG	A	1884	1/1	0.91	0.20	60,60,60,60	0
56	MG	GB	3112	1/1	0.91	0.13	64,64,64,64	0
56	MG	B	3202	1/1	0.91	0.25	64,64,64,64	0
56	MG	FB	1640	1/1	0.91	0.23	64,64,64,64	0
56	MG	B	3699	1/1	0.91	0.21	49,49,49,49	0
56	MG	B	3013	1/1	0.91	0.23	50,50,50,50	0
56	MG	B	3809	1/1	0.91	0.18	66,66,66,66	0
56	MG	B	3703	1/1	0.91	0.11	59,59,59,59	0
56	MG	A	1876	1/1	0.91	0.10	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3207	1/1	0.91	0.08	41,41,41,41	0
56	MG	B	3521	1/1	0.91	0.15	73,73,73,73	0
56	MG	GB	3297	1/1	0.91	0.40	67,67,67,67	0
56	MG	JA	406	1/1	0.91	0.06	87,87,87,87	0
56	MG	B	3817	1/1	0.91	0.09	46,46,46,46	0
56	MG	B	3612	1/1	0.91	0.11	59,59,59,59	0
56	MG	BC	308	1/1	0.91	0.13	104,104,104,104	0
56	MG	B	3141	1/1	0.91	0.14	44,44,44,44	0
56	MG	GB	3303	1/1	0.91	0.15	61,61,61,61	0
56	MG	GB	2974	1/1	0.91	0.22	49,49,49,49	0
56	MG	K	205	1/1	0.91	0.10	56,56,56,56	0
56	MG	B	3528	1/1	0.91	0.07	43,43,43,43	0
56	MG	K	207	1/1	0.91	0.15	67,67,67,67	0
56	MG	GB	3134	1/1	0.91	0.20	61,61,61,61	0
56	MG	B	2920	1/1	0.91	0.33	44,44,44,44	0
56	MG	B	3714	1/1	0.91	0.14	52,52,52,52	0
56	MG	B	3438	1/1	0.91	0.19	63,63,63,63	0
56	MG	GB	3313	1/1	0.91	0.13	56,56,56,56	0
56	MG	KC	101	1/1	0.91	0.19	58,58,58,58	0
56	MG	B	3717	1/1	0.91	0.09	52,52,52,52	0
56	MG	B	3080	1/1	0.91	0.13	66,66,66,66	0
56	MG	M	201	1/1	0.91	0.18	44,44,44,44	0
56	MG	GB	3320	1/1	0.91	0.12	60,60,60,60	0
56	MG	B	3087	1/1	0.91	0.22	53,53,53,53	0
56	MG	GB	3144	1/1	0.91	0.11	57,57,57,57	0
56	MG	GB	3680	1/1	0.91	0.18	60,60,60,60	0
56	MG	B	3537	1/1	0.91	0.11	46,46,46,46	0
56	MG	A	1767	1/1	0.91	0.09	77,77,77,77	0
56	MG	NC	107	1/1	0.91	0.07	96,96,96,96	0
56	MG	GB	3326	1/1	0.91	0.09	60,60,60,60	0
56	MG	GB	3495	1/1	0.91	0.12	72,72,72,72	0
56	MG	GB	3327	1/1	0.91	0.08	76,76,76,76	0
56	MG	B	3374	1/1	0.91	0.07	61,61,61,61	0
56	MG	B	3724	1/1	0.91	0.09	48,48,48,48	0
56	MG	B	3628	1/1	0.91	0.15	61,61,61,61	0
56	MG	FB	1787	1/1	0.91	0.30	77,77,77,77	0
56	MG	GB	3694	1/1	0.91	0.12	61,61,61,61	0
56	MG	GB	3502	1/1	0.91	0.08	53,53,53,53	0
56	MG	C	202	1/1	0.91	0.30	59,59,59,59	0
56	MG	GB	3333	1/1	0.91	0.31	66,66,66,66	0
56	MG	OA	201	1/1	0.91	0.18	72,72,72,72	0
56	MG	B	2922	1/1	0.91	0.25	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	2923	1/1	0.91	0.27	40,40,40,40	0
56	MG	GB	3161	1/1	0.91	0.29	73,73,73,73	0
56	MG	B	3733	1/1	0.91	0.07	54,54,54,54	0
56	MG	GB	3163	1/1	0.91	0.15	74,74,74,74	0
56	MG	GB	3515	1/1	0.91	0.26	76,76,76,76	0
56	MG	B	3545	1/1	0.91	0.05	74,74,74,74	0
56	MG	B	3737	1/1	0.91	0.08	62,62,62,62	0
56	MG	B	2958	1/1	0.91	0.32	49,49,49,49	0
56	MG	A	1720	1/1	0.91	0.30	72,72,72,72	0
56	MG	FB	1913	1/1	0.91	0.19	72,72,72,72	0
56	MG	B	3159	1/1	0.91	0.20	47,47,47,47	0
56	MG	FB	1916	1/1	0.91	0.10	73,73,73,73	0
56	MG	A	1703	1/1	0.91	0.13	61,61,61,61	0
56	MG	FB	1799	1/1	0.91	0.30	71,71,71,71	0
56	MG	S	203	1/1	0.91	0.14	57,57,57,57	0
56	MG	GB	3180	1/1	0.91	0.32	68,68,68,68	0
56	MG	FB	1801	1/1	0.91	0.16	75,75,75,75	0
56	MG	S	204	1/1	0.91	0.12	60,60,60,60	0
56	MG	GB	3534	1/1	0.91	0.22	59,59,59,59	0
56	MG	B	3027	1/1	0.91	0.16	42,42,42,42	0
56	MG	B	3748	1/1	0.91	0.20	65,65,65,65	0
56	MG	GB	3023	1/1	0.91	0.31	51,51,51,51	0
56	MG	TC	201	1/1	0.91	0.07	79,79,79,79	0
56	MG	B	3303	1/1	0.91	0.09	41,41,41,41	0
56	MG	GB	3363	1/1	0.91	0.12	75,75,75,75	0
56	MG	FB	1691	1/1	0.91	0.23	74,74,74,74	0
56	MG	FB	1692	1/1	0.91	0.17	67,67,67,67	0
56	MG	GB	3545	1/1	0.91	0.21	77,77,77,77	0
56	MG	SA	203	1/1	0.91	0.22	109,109,109,109	0
56	MG	T	204	1/1	0.91	0.06	56,56,56,56	0
56	MG	T	205	1/1	0.91	0.09	58,58,58,58	0
56	MG	GB	3031	1/1	0.91	0.24	60,60,60,60	0
56	MG	B	3028	1/1	0.91	0.40	50,50,50,50	0
56	MG	C	220	1/1	0.91	0.06	83,83,83,83	0
56	MG	FB	1817	1/1	0.91	0.22	62,62,62,62	0
56	MG	C	221	1/1	0.91	0.23	70,70,70,70	0
56	MG	B	3462	1/1	0.91	0.11	41,41,41,41	0
56	MG	GB	3559	1/1	0.91	0.17	72,72,72,72	0
56	MG	B	3561	1/1	0.91	0.20	52,52,52,52	0
56	MG	B	3755	1/1	0.91	0.06	61,61,61,61	0
56	MG	HB	229	1/1	0.91	0.10	100,100,100,100	0
56	MG	B	2995	1/1	0.91	0.16	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	W	307	1/1	0.91	0.06	87,87,87,87	0
56	MG	C	227	1/1	0.91	0.12	64,64,64,64	0
56	MG	A	1627	1/1	0.91	0.37	73,73,73,73	0
56	MG	B	3565	1/1	0.91	0.12	49,49,49,49	0
56	MG	GB	3552	1/1	0.92	0.09	68,68,68,68	0
56	MG	A	1624	1/1	0.92	0.19	63,63,63,63	0
56	MG	GB	3368	1/1	0.92	0.12	70,70,70,70	0
56	MG	B	3082	1/1	0.92	0.22	44,44,44,44	0
56	MG	GB	3189	1/1	0.92	0.12	64,64,64,64	0
56	MG	GB	3557	1/1	0.92	0.16	76,76,76,76	0
56	MG	B	3382	1/1	0.92	0.15	54,54,54,54	0
56	MG	B	3693	1/1	0.92	0.07	51,51,51,51	0
56	MG	B	3580	1/1	0.92	0.10	58,58,58,58	0
56	MG	B	3582	1/1	0.92	0.09	46,46,46,46	0
56	MG	B	3025	1/1	0.92	0.17	47,47,47,47	0
56	MG	B	2931	1/1	0.92	0.23	39,39,39,39	0
56	MG	B	3477	1/1	0.92	0.06	43,43,43,43	0
56	MG	B	3090	1/1	0.92	0.10	53,53,53,53	0
56	MG	GB	3200	1/1	0.92	0.43	63,63,63,63	0
56	MG	B	3830	1/1	0.92	0.12	60,60,60,60	0
56	MG	B	2932	1/1	0.92	0.24	52,52,52,52	0
56	MG	JB	309	1/1	0.92	0.14	69,69,69,69	0
56	MG	GB	3569	1/1	0.92	0.24	55,55,55,55	0
56	MG	GB	3035	1/1	0.92	0.10	65,65,65,65	0
56	MG	GB	3036	1/1	0.92	0.22	58,58,58,58	0
56	MG	GB	3206	1/1	0.92	0.16	64,64,64,64	0
56	MG	B	3299	1/1	0.92	0.14	45,45,45,45	0
56	MG	B	3301	1/1	0.92	0.10	49,49,49,49	0
56	MG	KB	304	1/1	0.92	0.05	82,82,82,82	0
56	MG	B	3223	1/1	0.92	0.35	65,65,65,65	0
56	MG	GB	3391	1/1	0.92	0.19	60,60,60,60	0
56	MG	GB	3392	1/1	0.92	0.29	56,56,56,56	0
56	MG	B	3153	1/1	0.92	0.21	42,42,42,42	0
56	MG	B	3394	1/1	0.92	0.10	52,52,52,52	0
56	MG	FB	1808	1/1	0.92	0.12	66,66,66,66	0
56	MG	B	3492	1/1	0.92	0.07	75,75,75,75	0
56	MG	B	3305	1/1	0.92	0.15	49,49,49,49	0
56	MG	B	2915	1/1	0.92	0.26	57,57,57,57	0
56	MG	B	3397	1/1	0.92	0.19	52,52,52,52	0
56	MG	A	1614	1/1	0.92	0.31	52,52,52,52	0
56	MG	B	3498	1/1	0.92	0.24	60,60,60,60	0
56	MG	B	3160	1/1	0.92	0.15	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1820	1/1	0.92	0.20	85,85,85,85	0
56	MG	B	3500	1/1	0.92	0.06	52,52,52,52	0
56	MG	B	2918	1/1	0.92	0.28	43,43,43,43	0
56	MG	B	3311	1/1	0.92	0.10	46,46,46,46	0
56	MG	GB	2901	1/1	0.92	0.17	58,58,58,58	0
56	MG	GB	3063	1/1	0.92	0.09	53,53,53,53	0
56	MG	B	3504	1/1	0.92	0.09	45,45,45,45	0
56	MG	B	3163	1/1	0.92	0.11	49,49,49,49	0
56	MG	B	3507	1/1	0.92	0.09	42,42,42,42	0
56	MG	A	1680	1/1	0.92	0.31	75,75,75,75	0
56	MG	GB	2910	1/1	0.92	0.31	48,48,48,48	0
56	MG	QB	206	1/1	0.92	0.14	63,63,63,63	0
56	MG	GB	3418	1/1	0.92	0.11	58,58,58,58	0
56	MG	B	3734	1/1	0.92	0.09	69,69,69,69	0
56	MG	B	3315	1/1	0.92	0.13	43,43,43,43	0
56	MG	GB	3071	1/1	0.92	0.18	56,56,56,56	0
56	MG	B	3618	1/1	0.92	0.11	43,43,43,43	0
56	MG	B	3317	1/1	0.92	0.13	55,55,55,55	0
56	MG	B	3244	1/1	0.92	0.23	53,53,53,53	0
56	MG	TB	201	1/1	0.92	0.16	66,66,66,66	0
56	MG	TB	202	1/1	0.92	0.13	72,72,72,72	0
56	MG	GB	2916	1/1	0.92	0.17	51,51,51,51	0
56	MG	GB	3615	1/1	0.92	0.20	76,76,76,76	0
56	MG	FB	1713	1/1	0.92	0.29	75,75,75,75	0
56	MG	B	3623	1/1	0.92	0.12	64,64,64,64	0
56	MG	FB	1715	1/1	0.92	0.26	82,82,82,82	0
56	MG	BB	101	1/1	0.92	0.15	127,127,127,127	0
56	MG	B	3319	1/1	0.92	0.15	47,47,47,47	0
56	MG	B	3246	1/1	0.92	0.11	47,47,47,47	0
56	MG	GB	2924	1/1	0.92	0.29	51,51,51,51	0
56	MG	B	3037	1/1	0.92	0.19	52,52,52,52	0
56	MG	B	3417	1/1	0.92	0.09	57,57,57,57	0
56	MG	FB	1841	1/1	0.92	0.13	85,85,85,85	0
56	MG	B	3750	1/1	0.92	0.17	57,57,57,57	0
56	MG	XB	203	1/1	0.92	0.23	79,79,79,79	0
56	MG	GB	3628	1/1	0.92	0.11	73,73,73,73	0
56	MG	B	3005	1/1	0.92	0.23	45,45,45,45	0
56	MG	A	1756	1/1	0.92	0.14	66,66,66,66	0
56	MG	B	3257	1/1	0.92	0.21	54,54,54,54	0
56	MG	B	3041	1/1	0.92	0.10	39,39,39,39	0
56	MG	B	3756	1/1	0.92	0.10	59,59,59,59	0
56	MG	B	3334	1/1	0.92	0.09	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3268	1/1	0.92	0.34	42,42,42,42	0
56	MG	B	3177	1/1	0.92	0.10	47,47,47,47	0
56	MG	GB	3637	1/1	0.92	0.07	49,49,49,49	0
56	MG	AA	103	1/1	0.92	0.14	59,59,59,59	0
56	MG	B	3536	1/1	0.92	0.11	38,38,38,38	0
56	MG	FB	1617	1/1	0.92	0.33	59,59,59,59	0
56	MG	A	1657	1/1	0.92	0.48	90,90,90,90	0
56	MG	C	241	1/1	0.92	0.14	81,81,81,81	0
56	MG	B	3047	1/1	0.92	0.21	42,42,42,42	0
56	MG	GB	3646	1/1	0.92	0.07	75,75,75,75	0
56	MG	CA	104	1/1	0.92	0.08	65,65,65,65	0
56	MG	FB	1858	1/1	0.92	0.06	97,97,97,97	0
56	MG	GB	3110	1/1	0.92	0.16	72,72,72,72	0
56	MG	DC	101	1/1	0.92	0.13	60,60,60,60	0
56	MG	GB	3650	1/1	0.92	0.13	57,57,57,57	0
56	MG	GB	2949	1/1	0.92	0.40	52,52,52,52	0
56	MG	FB	1738	1/1	0.92	0.34	69,69,69,69	0
56	MG	B	3049	1/1	0.92	0.28	40,40,40,40	0
56	MG	B	2970	1/1	0.92	0.19	36,36,36,36	0
56	MG	GB	3466	1/1	0.92	0.08	80,80,80,80	0
56	MG	FA	102	1/1	0.92	0.17	58,58,58,58	0
56	MG	GB	2954	1/1	0.92	0.36	50,50,50,50	0
56	MG	FA	104	1/1	0.92	0.09	49,49,49,49	0
56	MG	GB	2956	1/1	0.92	0.23	47,47,47,47	0
56	MG	B	3542	1/1	0.92	0.06	66,66,66,66	0
56	MG	B	3184	1/1	0.92	0.12	46,46,46,46	0
56	MG	GB	3302	1/1	0.92	0.18	47,47,47,47	0
56	MG	E	308	1/1	0.92	0.21	52,52,52,52	0
56	MG	GB	3667	1/1	0.92	0.15	54,54,54,54	0
56	MG	FB	1746	1/1	0.92	0.05	63,63,63,63	0
56	MG	IA	101	1/1	0.92	0.12	67,67,67,67	0
56	MG	B	3116	1/1	0.92	0.09	49,49,49,49	0
56	MG	GB	3125	1/1	0.92	0.23	62,62,62,62	0
56	MG	GB	2965	1/1	0.92	0.20	54,54,54,54	0
56	MG	F	301	1/1	0.92	0.18	46,46,46,46	0
56	MG	B	2944	1/1	0.92	0.33	44,44,44,44	0
56	MG	FB	1751	1/1	0.92	0.16	83,83,83,83	0
56	MG	B	3652	1/1	0.92	0.18	56,56,56,56	0
56	MG	GB	3133	1/1	0.92	0.27	69,69,69,69	0
56	MG	GB	3316	1/1	0.92	0.06	73,73,73,73	0
56	MG	B	3654	1/1	0.92	0.12	66,66,66,66	0
56	MG	GB	3490	1/1	0.92	0.13	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3437	1/1	0.92	0.08	39,39,39,39	0
56	MG	A	1691	1/1	0.92	0.11	61,61,61,61	0
56	MG	B	3551	1/1	0.92	0.13	51,51,51,51	0
56	MG	GB	3322	1/1	0.92	0.20	56,56,56,56	0
56	MG	B	3660	1/1	0.92	0.10	54,54,54,54	0
56	MG	GB	3693	1/1	0.92	0.07	69,69,69,69	0
56	MG	B	3059	1/1	0.92	0.11	43,43,43,43	0
56	MG	GB	3140	1/1	0.92	0.25	74,74,74,74	0
56	MG	GB	2981	1/1	0.92	0.24	50,50,50,50	0
56	MG	B	2975	1/1	0.92	0.34	49,49,49,49	0
56	MG	G	3205	1/1	0.92	0.08	40,40,40,40	0
56	MG	B	3195	1/1	0.92	0.13	52,52,52,52	0
56	MG	GB	3506	1/1	0.92	0.25	71,71,71,71	0
56	MG	B	3665	1/1	0.92	0.22	56,56,56,56	0
56	MG	B	3557	1/1	0.92	0.12	47,47,47,47	0
56	MG	RC	305	1/1	0.92	0.08	75,75,75,75	0
56	MG	GB	3509	1/1	0.92	0.15	75,75,75,75	0
56	MG	B	3061	1/1	0.92	0.35	58,58,58,58	0
56	MG	A	1867	1/1	0.92	0.13	64,64,64,64	0
56	MG	B	3793	1/1	0.92	0.09	81,81,81,81	0
56	MG	RC	311	1/1	0.92	0.10	78,78,78,78	0
56	MG	B	3132	1/1	0.92	0.23	46,46,46,46	0
56	MG	B	3362	1/1	0.92	0.20	66,66,66,66	0
56	MG	B	2978	1/1	0.92	0.16	44,44,44,44	0
56	MG	B	3564	1/1	0.92	0.08	52,52,52,52	0
56	MG	JA	407	1/1	0.92	0.16	61,61,61,61	0
56	MG	FB	1656	1/1	0.92	0.31	70,70,70,70	0
56	MG	GB	3341	1/1	0.92	0.10	54,54,54,54	0
56	MG	B	3015	1/1	0.92	0.19	49,49,49,49	0
56	MG	B	3566	1/1	0.92	0.17	60,60,60,60	0
56	MG	B	2981	1/1	0.92	0.18	41,41,41,41	0
56	MG	GB	3166	1/1	0.92	0.21	52,52,52,52	0
56	MG	GB	3349	1/1	0.92	0.21	51,51,51,51	0
56	MG	GB	3350	1/1	0.92	0.21	61,61,61,61	0
56	MG	A	1779	1/1	0.92	0.31	82,82,82,82	0
56	MG	GB	3532	1/1	0.92	0.11	70,70,70,70	0
56	MG	B	3802	1/1	0.92	0.06	77,77,77,77	0
56	MG	YC	201	1/1	0.92	0.14	68,68,68,68	0
56	MG	FB	1781	1/1	0.92	0.16	90,90,90,90	0
56	MG	B	3803	1/1	0.92	0.13	58,58,58,58	0
56	MG	K	202	1/1	0.92	0.04	63,63,63,63	0
56	MG	FB	1784	1/1	0.92	0.14	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3538	1/1	0.92	0.13	58,58,58,58	0
56	MG	B	2955	1/1	0.92	0.13	46,46,46,46	0
56	MG	B	3288	1/1	0.92	0.09	59,59,59,59	0
56	MG	A	1806	1/1	0.92	0.12	56,56,56,56	0
56	MG	CD	101	1/1	0.92	0.32	77,77,77,77	0
56	MG	GB	3015	1/1	0.92	0.22	54,54,54,54	0
56	MG	B	3076	1/1	0.92	0.20	45,45,45,45	0
56	MG	GB	3546	1/1	0.92	0.06	63,63,63,63	0
56	MG	FB	1670	1/1	0.92	0.42	74,74,74,74	0
56	MG	FB	1914	1/1	0.92	0.10	63,63,63,63	0
56	MG	A	1798	1/1	0.92	0.17	70,70,70,70	0
56	MG	GB	3186	1/1	0.92	0.10	63,63,63,63	0
56	MG	B	3601	1/1	0.93	0.14	53,53,53,53	0
56	MG	B	3070	1/1	0.93	0.08	47,47,47,47	0
56	MG	GB	3479	1/1	0.93	0.12	66,66,66,66	0
56	MG	G	3203	1/1	0.93	0.16	42,42,42,42	0
56	MG	B	3514	1/1	0.93	0.06	55,55,55,55	0
56	MG	B	3175	1/1	0.93	0.28	60,60,60,60	0
56	MG	B	3232	1/1	0.93	0.13	57,57,57,57	0
56	MG	B	3705	1/1	0.93	0.12	49,49,49,49	0
56	MG	B	3367	1/1	0.93	0.13	63,63,63,63	0
56	MG	B	2910	1/1	0.93	0.21	34,34,34,34	0
56	MG	B	3520	1/1	0.93	0.09	64,64,64,64	0
56	MG	GB	3060	1/1	0.93	0.23	61,61,61,61	0
56	MG	B	3237	1/1	0.93	0.11	45,45,45,45	0
56	MG	GB	3198	1/1	0.93	0.32	59,59,59,59	0
56	MG	B	3811	1/1	0.93	0.08	48,48,48,48	0
56	MG	B	3812	1/1	0.93	0.05	62,62,62,62	0
56	MG	GB	3644	1/1	0.93	0.08	77,77,77,77	0
56	MG	B	3813	1/1	0.93	0.11	52,52,52,52	0
56	MG	B	3524	1/1	0.93	0.14	48,48,48,48	0
56	MG	FB	1860	1/1	0.93	0.16	89,89,89,89	0
56	MG	GB	3204	1/1	0.93	0.17	53,53,53,53	0
56	MG	I	203	1/1	0.93	0.10	68,68,68,68	0
56	MG	B	3125	1/1	0.93	0.33	60,60,60,60	0
56	MG	B	3072	1/1	0.93	0.06	46,46,46,46	0
56	MG	B	3715	1/1	0.93	0.08	64,64,64,64	0
56	MG	GB	2937	1/1	0.93	0.20	49,49,49,49	0
56	MG	GB	3211	1/1	0.93	0.12	61,61,61,61	0
56	MG	GB	2938	1/1	0.93	0.27	45,45,45,45	0
56	MG	B	2939	1/1	0.93	0.33	48,48,48,48	0
56	MG	J	201	1/1	0.93	0.08	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3820	1/1	0.93	0.12	54,54,54,54	0
56	MG	GB	3513	1/1	0.93	0.08	49,49,49,49	0
56	MG	GB	3660	1/1	0.93	0.30	46,46,46,46	0
56	MG	B	3074	1/1	0.93	0.21	36,36,36,36	0
56	MG	B	3718	1/1	0.93	0.12	54,54,54,54	0
56	MG	FB	1762	1/1	0.93	0.16	69,69,69,69	0
56	MG	GB	3665	1/1	0.93	0.08	61,61,61,61	0
56	MG	FB	1763	1/1	0.93	0.18	67,67,67,67	0
56	MG	JA	409	1/1	0.93	0.34	89,89,89,89	0
56	MG	B	3531	1/1	0.93	0.12	42,42,42,42	0
56	MG	GB	3669	1/1	0.93	0.17	57,57,57,57	0
56	MG	GB	3520	1/1	0.93	0.12	73,73,73,73	0
56	MG	B	3075	1/1	0.93	0.17	42,42,42,42	0
56	MG	A	1781	1/1	0.93	0.14	95,95,95,95	0
56	MG	GB	3525	1/1	0.93	0.11	79,79,79,79	0
56	MG	B	3828	1/1	0.93	0.08	66,66,66,66	0
56	MG	GB	3677	1/1	0.93	0.24	60,60,60,60	0
56	MG	FB	1660	1/1	0.93	0.30	70,70,70,70	0
56	MG	B	3829	1/1	0.93	0.05	46,46,46,46	0
56	MG	GB	3231	1/1	0.93	0.13	60,60,60,60	0
56	MG	GB	3681	1/1	0.93	0.09	60,60,60,60	0
56	MG	GB	3091	1/1	0.93	0.27	57,57,57,57	0
56	MG	B	3535	1/1	0.93	0.08	60,60,60,60	0
56	MG	B	2941	1/1	0.93	0.27	49,49,49,49	0
56	MG	B	3379	1/1	0.93	0.19	52,52,52,52	0
56	MG	B	3448	1/1	0.93	0.08	58,58,58,58	0
56	MG	B	3449	1/1	0.93	0.17	46,46,46,46	0
56	MG	B	3837	1/1	0.93	0.12	50,50,50,50	0
56	MG	M	208	1/1	0.93	0.13	44,44,44,44	0
56	MG	GB	3690	1/1	0.93	0.11	64,64,64,64	0
56	MG	N	201	1/1	0.93	0.28	51,51,51,51	0
56	MG	GB	3539	1/1	0.93	0.16	68,68,68,68	0
56	MG	GB	3100	1/1	0.93	0.15	58,58,58,58	0
56	MG	B	3838	1/1	0.93	0.14	54,54,54,54	0
56	MG	FB	1890	1/1	0.93	0.07	60,60,60,60	0
56	MG	B	3252	1/1	0.93	0.10	45,45,45,45	0
56	MG	GB	3396	1/1	0.93	0.26	71,71,71,71	0
56	MG	N	204	1/1	0.93	0.11	61,61,61,61	0
56	MG	B	3840	1/1	0.93	0.18	48,48,48,48	0
56	MG	KC	103	1/1	0.93	0.29	64,64,64,64	0
56	MG	GB	2969	1/1	0.93	0.18	53,53,53,53	0
56	MG	B	3841	1/1	0.93	0.16	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3252	1/1	0.93	0.13	59,59,59,59	0
56	MG	GB	3551	1/1	0.93	0.10	96,96,96,96	0
56	MG	B	3079	1/1	0.93	0.20	48,48,48,48	0
56	MG	B	3383	1/1	0.93	0.13	47,47,47,47	0
56	MG	A	1721	1/1	0.93	0.07	97,97,97,97	0
56	MG	B	2914	1/1	0.93	0.26	47,47,47,47	0
56	MG	B	3260	1/1	0.93	0.20	47,47,47,47	0
56	MG	GB	2978	1/1	0.93	0.22	58,58,58,58	0
56	MG	NC	109	1/1	0.93	0.06	89,89,89,89	0
56	MG	B	3458	1/1	0.93	0.10	41,41,41,41	0
56	MG	B	3741	1/1	0.93	0.09	47,47,47,47	0
56	MG	FB	1903	1/1	0.93	0.06	76,76,76,76	0
56	MG	B	3193	1/1	0.93	0.09	54,54,54,54	0
56	MG	NC	114	1/1	0.93	0.14	64,64,64,64	0
56	MG	B	3388	1/1	0.93	0.14	55,55,55,55	0
56	MG	B	3138	1/1	0.93	0.23	63,63,63,63	0
56	MG	B	3646	1/1	0.93	0.11	54,54,54,54	0
56	MG	B	3464	1/1	0.93	0.09	48,48,48,48	0
56	MG	B	3043	1/1	0.93	0.22	54,54,54,54	0
56	MG	OC	406	1/1	0.93	0.10	70,70,70,70	0
56	MG	B	3466	1/1	0.93	0.07	51,51,51,51	0
56	MG	B	3045	1/1	0.93	0.29	43,43,43,43	0
56	MG	GB	3127	1/1	0.93	0.15	68,68,68,68	0
56	MG	B	3468	1/1	0.93	0.10	57,57,57,57	0
56	MG	B	3198	1/1	0.93	0.17	47,47,47,47	0
56	MG	A	1862	1/1	0.93	0.19	60,60,60,60	0
56	MG	GB	3573	1/1	0.93	0.07	69,69,69,69	0
56	MG	B	3757	1/1	0.93	0.10	53,53,53,53	0
56	MG	U	102	1/1	0.93	0.20	55,55,55,55	0
56	MG	B	3473	1/1	0.93	0.14	51,51,51,51	0
56	MG	B	3048	1/1	0.93	0.26	45,45,45,45	0
56	MG	B	3017	1/1	0.93	0.21	51,51,51,51	0
56	MG	GB	3433	1/1	0.93	0.08	65,65,65,65	0
56	MG	B	3661	1/1	0.93	0.10	51,51,51,51	0
56	MG	GB	3435	1/1	0.93	0.09	53,53,53,53	0
56	MG	B	3324	1/1	0.93	0.19	44,44,44,44	0
56	MG	B	3325	1/1	0.93	0.12	53,53,53,53	0
56	MG	B	3481	1/1	0.93	0.05	54,54,54,54	0
56	MG	GB	3141	1/1	0.93	0.17	49,49,49,49	0
56	MG	B	2994	1/1	0.93	0.28	58,58,58,58	0
56	MG	B	3572	1/1	0.93	0.26	66,66,66,66	0
56	MG	FB	1928	1/1	0.93	0.21	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	2968	1/1	0.93	0.24	53,53,53,53	0
56	MG	GB	3150	1/1	0.93	0.08	46,46,46,46	0
56	MG	GB	3594	1/1	0.93	0.11	68,68,68,68	0
56	MG	B	3204	1/1	0.93	0.08	40,40,40,40	0
56	MG	B	2916	1/1	0.93	0.27	36,36,36,36	0
56	MG	GB	3014	1/1	0.93	0.29	64,64,64,64	0
56	MG	B	2901	1/1	0.93	0.17	49,49,49,49	0
56	MG	B	3488	1/1	0.93	0.09	57,57,57,57	0
56	MG	B	3275	1/1	0.93	0.23	49,49,49,49	0
56	MG	B	3001	1/1	0.93	0.16	37,37,37,37	0
56	MG	B	3783	1/1	0.93	0.18	50,50,50,50	0
56	MG	A	1786	1/1	0.93	0.23	59,59,59,59	0
56	MG	B	3157	1/1	0.93	0.14	44,44,44,44	0
56	MG	B	2972	1/1	0.93	0.27	45,45,45,45	0
56	MG	A	1665	1/1	0.93	0.30	66,66,66,66	0
56	MG	E	301	1/1	0.93	0.12	52,52,52,52	0
56	MG	B	3415	1/1	0.93	0.12	42,42,42,42	0
56	MG	A	1818	1/1	0.93	0.13	65,65,65,65	0
56	MG	B	3107	1/1	0.93	0.22	56,56,56,56	0
56	MG	FB	1725	1/1	0.93	0.16	68,68,68,68	0
56	MG	B	3352	1/1	0.93	0.21	53,53,53,53	0
56	MG	DA	102	1/1	0.93	0.20	62,62,62,62	0
56	MG	B	3420	1/1	0.93	0.13	43,43,43,43	0
56	MG	GB	2902	1/1	0.93	0.57	51,51,51,51	0
56	MG	B	2909	1/1	0.93	0.31	33,33,33,33	0
56	MG	F	305	1/1	0.93	0.16	58,58,58,58	0
56	MG	F	306	1/1	0.93	0.14	60,60,60,60	0
56	MG	B	2960	1/1	0.93	0.13	47,47,47,47	0
56	MG	B	3355	1/1	0.93	0.09	55,55,55,55	0
56	MG	B	3067	1/1	0.93	0.33	50,50,50,50	0
56	MG	B	3068	1/1	0.93	0.14	43,43,43,43	0
56	MG	GB	3108	1/1	0.94	0.17	54,54,54,54	0
56	MG	A	1857	1/1	0.94	0.12	69,69,69,69	0
56	MG	B	3742	1/1	0.94	0.12	54,54,54,54	0
56	MG	FB	1892	1/1	0.94	0.14	68,68,68,68	0
56	MG	L	205	1/1	0.94	0.14	61,61,61,61	0
56	MG	B	3284	1/1	0.94	0.27	72,72,72,72	0
56	MG	B	2977	1/1	0.94	0.32	53,53,53,53	0
56	MG	M	205	1/1	0.94	0.11	45,45,45,45	0
56	MG	A	1705	1/1	0.94	0.17	66,66,66,66	0
56	MG	GB	2975	1/1	0.94	0.33	61,61,61,61	0
56	MG	B	3229	1/1	0.94	0.14	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3182	1/1	0.94	0.26	50,50,50,50	0
56	MG	GB	3275	1/1	0.94	0.13	61,61,61,61	0
56	MG	GB	3276	1/1	0.94	0.08	79,79,79,79	0
56	MG	GB	3277	1/1	0.94	0.13	54,54,54,54	0
56	MG	B	3653	1/1	0.94	0.10	56,56,56,56	0
56	MG	GB	3279	1/1	0.94	0.20	69,69,69,69	0
56	MG	B	3231	1/1	0.94	0.25	47,47,47,47	0
56	MG	B	3569	1/1	0.94	0.08	61,61,61,61	0
56	MG	B	2979	1/1	0.94	0.15	43,43,43,43	0
56	MG	B	3657	1/1	0.94	0.14	45,45,45,45	0
56	MG	GB	3284	1/1	0.94	0.23	64,64,64,64	0
56	MG	GB	3285	1/1	0.94	0.20	52,52,52,52	0
56	MG	B	3030	1/1	0.94	0.28	59,59,59,59	0
56	MG	B	3185	1/1	0.94	0.12	45,45,45,45	0
56	MG	B	2980	1/1	0.94	0.26	54,54,54,54	0
56	MG	GB	3291	1/1	0.94	0.12	73,73,73,73	0
56	MG	GB	2988	1/1	0.94	0.23	50,50,50,50	0
56	MG	C	215	1/1	0.94	0.14	58,58,58,58	0
56	MG	RB	203	1/1	0.94	0.27	57,57,57,57	0
56	MG	B	3760	1/1	0.94	0.13	65,65,65,65	0
56	MG	GB	3295	1/1	0.94	0.07	65,65,65,65	0
56	MG	GB	3296	1/1	0.94	0.09	65,65,65,65	0
56	MG	C	217	1/1	0.94	0.22	60,60,60,60	0
56	MG	B	3497	1/1	0.94	0.10	52,52,52,52	0
56	MG	FB	1682	1/1	0.94	0.30	64,64,64,64	0
56	MG	A	1683	1/1	0.94	0.29	80,80,80,80	0
56	MG	B	3140	1/1	0.94	0.19	54,54,54,54	0
56	MG	B	3766	1/1	0.94	0.20	42,42,42,42	0
56	MG	B	3364	1/1	0.94	0.09	37,37,37,37	0
56	MG	B	3666	1/1	0.94	0.20	41,41,41,41	0
56	MG	GB	3641	1/1	0.94	0.10	64,64,64,64	0
56	MG	GB	3305	1/1	0.94	0.26	49,49,49,49	0
56	MG	S	205	1/1	0.94	0.08	54,54,54,54	0
56	MG	B	2948	1/1	0.94	0.23	43,43,43,43	0
56	MG	B	3770	1/1	0.94	0.07	65,65,65,65	0
56	MG	FB	1921	1/1	0.94	0.12	78,78,78,78	0
56	MG	B	3143	1/1	0.94	0.11	39,39,39,39	0
56	MG	GB	3145	1/1	0.94	0.33	65,65,65,65	0
56	MG	B	2913	1/1	0.94	0.28	38,38,38,38	0
56	MG	GB	3147	1/1	0.94	0.09	54,54,54,54	0
56	MG	GB	3149	1/1	0.94	0.23	58,58,58,58	0
56	MG	B	3670	1/1	0.94	0.07	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3249	1/1	0.94	0.07	43,43,43,43	0
56	MG	B	3194	1/1	0.94	0.18	53,53,53,53	0
56	MG	B	3585	1/1	0.94	0.14	49,49,49,49	0
56	MG	B	3779	1/1	0.94	0.08	58,58,58,58	0
56	MG	B	2952	1/1	0.94	0.21	46,46,46,46	0
56	MG	B	3253	1/1	0.94	0.13	53,53,53,53	0
56	MG	B	3102	1/1	0.94	0.20	46,46,46,46	0
56	MG	GB	3494	1/1	0.94	0.13	67,67,67,67	0
56	MG	B	3309	1/1	0.94	0.17	56,56,56,56	0
56	MG	B	3442	1/1	0.94	0.04	58,58,58,58	0
56	MG	B	2902	1/1	0.94	0.35	35,35,35,35	0
56	MG	C	242	1/1	0.94	0.07	86,86,86,86	0
56	MG	FB	1705	1/1	0.94	0.24	60,60,60,60	0
56	MG	GB	3500	1/1	0.94	0.17	57,57,57,57	0
56	MG	B	3594	1/1	0.94	0.10	56,56,56,56	0
56	MG	B	3377	1/1	0.94	0.09	44,44,44,44	0
56	MG	GB	3670	1/1	0.94	0.08	52,52,52,52	0
56	MG	B	3686	1/1	0.94	0.16	43,43,43,43	0
56	MG	B	3040	1/1	0.94	0.20	41,41,41,41	0
56	MG	GB	3168	1/1	0.94	0.28	61,61,61,61	0
56	MG	DC	103	1/1	0.94	0.18	76,76,76,76	0
56	MG	B	2924	1/1	0.94	0.27	35,35,35,35	0
56	MG	DB	101	1/1	0.94	0.22	119,119,119,119	0
56	MG	GB	3171	1/1	0.94	0.18	63,63,63,63	0
56	MG	B	3598	1/1	0.94	0.07	62,62,62,62	0
56	MG	E	305	1/1	0.94	0.10	50,50,50,50	0
56	MG	GB	3176	1/1	0.94	0.16	51,51,51,51	0
56	MG	GB	3032	1/1	0.94	0.15	54,54,54,54	0
56	MG	B	2957	1/1	0.94	0.17	45,45,45,45	0
56	MG	Y	105	1/1	0.94	0.07	52,52,52,52	0
56	MG	B	3523	1/1	0.94	0.10	54,54,54,54	0
56	MG	FB	1606	1/1	0.94	0.35	57,57,57,57	0
56	MG	KC	105	1/1	0.94	0.21	73,73,73,73	0
56	MG	FB	1607	1/1	0.94	0.34	58,58,58,58	0
56	MG	B	3110	1/1	0.94	0.22	48,48,48,48	0
56	MG	B	3603	1/1	0.94	0.12	48,48,48,48	0
56	MG	B	3451	1/1	0.94	0.07	53,53,53,53	0
56	MG	GB	3043	1/1	0.94	0.19	52,52,52,52	0
56	MG	F	304	1/1	0.94	0.08	49,49,49,49	0
56	MG	GB	3045	1/1	0.94	0.25	51,51,51,51	0
56	MG	GB	3046	1/1	0.94	0.26	55,55,55,55	0
56	MG	FB	1612	1/1	0.94	0.30	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3527	1/1	0.94	0.15	52,52,52,52	0
56	MG	B	3316	1/1	0.94	0.14	35,35,35,35	0
56	MG	A	1825	1/1	0.94	0.10	56,56,56,56	0
56	MG	CA	103	1/1	0.94	0.21	49,49,49,49	0
56	MG	GB	3052	1/1	0.94	0.24	55,55,55,55	0
56	MG	B	3702	1/1	0.94	0.13	86,86,86,86	0
56	MG	A	1660	1/1	0.94	0.13	60,60,60,60	0
56	MG	FB	1619	1/1	0.94	0.35	58,58,58,58	0
56	MG	B	2997	1/1	0.94	0.24	42,42,42,42	0
56	MG	GB	3057	1/1	0.94	0.11	44,44,44,44	0
56	MG	FB	1734	1/1	0.94	0.17	65,65,65,65	0
56	MG	A	1796	1/1	0.94	0.10	61,61,61,61	0
56	MG	F	314	1/1	0.94	0.23	39,39,39,39	0
56	MG	GB	3542	1/1	0.94	0.09	112,112,112,112	0
56	MG	B	3611	1/1	0.94	0.10	48,48,48,48	0
56	MG	B	2974	1/1	0.94	0.17	39,39,39,39	0
56	MG	B	3808	1/1	0.94	0.06	50,50,50,50	0
56	MG	GB	3208	1/1	0.94	0.09	53,53,53,53	0
56	MG	B	3208	1/1	0.94	0.20	47,47,47,47	0
56	MG	B	3709	1/1	0.94	0.13	64,64,64,64	0
56	MG	GB	2929	1/1	0.94	0.22	46,46,46,46	0
56	MG	GB	2930	1/1	0.94	0.41	64,64,64,64	0
56	MG	A	1766	1/1	0.94	0.09	103,103,103,103	0
56	MG	GB	3216	1/1	0.94	0.33	60,60,60,60	0
56	MG	B	3121	1/1	0.94	0.21	43,43,43,43	0
56	MG	B	3051	1/1	0.94	0.31	40,40,40,40	0
56	MG	B	3127	1/1	0.94	0.18	55,55,55,55	0
56	MG	GB	3072	1/1	0.94	0.19	49,49,49,49	0
56	MG	B	3329	1/1	0.94	0.12	47,47,47,47	0
56	MG	GB	3074	1/1	0.94	0.20	59,59,59,59	0
56	MG	B	3330	1/1	0.94	0.08	41,41,41,41	0
56	MG	GB	3076	1/1	0.94	0.17	59,59,59,59	0
56	MG	B	3543	1/1	0.94	0.07	44,44,44,44	0
56	MG	GB	3078	1/1	0.94	0.31	64,64,64,64	0
56	MG	B	3215	1/1	0.94	0.23	47,47,47,47	0
56	MG	IA	111	1/1	0.94	0.19	49,49,49,49	0
56	MG	GB	3397	1/1	0.94	0.29	60,60,60,60	0
56	MG	B	3332	1/1	0.94	0.11	65,65,65,65	0
56	MG	B	3626	1/1	0.94	0.09	54,54,54,54	0
56	MG	B	3546	1/1	0.94	0.07	47,47,47,47	0
56	MG	B	3469	1/1	0.94	0.25	60,60,60,60	0
56	MG	B	3333	1/1	0.94	0.07	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1756	1/1	0.94	0.24	68,68,68,68	0
56	MG	B	3081	1/1	0.94	0.21	44,44,44,44	0
56	MG	B	3055	1/1	0.94	0.21	37,37,37,37	0
56	MG	IA	119	1/1	0.94	0.05	73,73,73,73	0
56	MG	FB	1645	1/1	0.94	0.16	56,56,56,56	0
56	MG	B	3726	1/1	0.94	0.16	50,50,50,50	0
56	MG	B	3727	1/1	0.94	0.13	49,49,49,49	0
56	MG	FB	1879	1/1	0.94	0.16	78,78,78,78	0
56	MG	B	3277	1/1	0.94	0.10	51,51,51,51	0
56	MG	GB	3246	1/1	0.94	0.16	79,79,79,79	0
56	MG	K	203	1/1	0.94	0.12	73,73,73,73	0
56	MG	B	3338	1/1	0.94	0.09	47,47,47,47	0
56	MG	GB	2957	1/1	0.94	0.31	51,51,51,51	0
56	MG	B	3174	1/1	0.94	0.16	42,42,42,42	0
56	MG	GB	2959	1/1	0.94	0.25	56,56,56,56	0
56	MG	B	3478	1/1	0.94	0.10	50,50,50,50	0
56	MG	B	3558	1/1	0.94	0.14	64,64,64,64	0
56	MG	B	3002	1/1	0.94	0.19	38,38,38,38	0
56	MG	B	3088	1/1	0.94	0.11	50,50,50,50	0
56	MG	L	201	1/1	0.94	0.13	54,54,54,54	0
56	MG	B	3410	1/1	0.94	0.15	49,49,49,49	0
56	MG	GB	2966	1/1	0.94	0.30	56,56,56,56	0
57	ZN	BA	101	1/1	0.94	0.11	131,131,131,131	0
56	MG	GB	3428	1/1	0.94	0.20	59,59,59,59	0
56	MG	B	3647	1/1	0.95	0.09	48,48,48,48	0
56	MG	B	2953	1/1	0.95	0.23	37,37,37,37	0
56	MG	GB	3401	1/1	0.95	0.09	68,68,68,68	0
56	MG	E	302	1/1	0.95	0.16	52,52,52,52	0
56	MG	FB	1873	1/1	0.95	0.09	107,107,107,107	0
56	MG	GB	3664	1/1	0.95	0.11	58,58,58,58	0
56	MG	B	3805	1/1	0.95	0.08	54,54,54,54	0
56	MG	E	304	1/1	0.95	0.09	55,55,55,55	0
56	MG	B	3233	1/1	0.95	0.14	51,51,51,51	0
56	MG	B	3516	1/1	0.95	0.15	57,57,57,57	0
56	MG	B	3579	1/1	0.95	0.08	47,47,47,47	0
56	MG	B	3091	1/1	0.95	0.16	36,36,36,36	0
56	MG	GB	3671	1/1	0.95	0.08	82,82,82,82	0
56	MG	VB	201	1/1	0.95	0.16	74,74,74,74	0
56	MG	B	3730	1/1	0.95	0.05	55,55,55,55	0
56	MG	FB	1680	1/1	0.95	0.17	87,87,87,87	0
56	MG	GB	3287	1/1	0.95	0.21	62,62,62,62	0
56	MG	B	3731	1/1	0.95	0.09	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3092	1/1	0.95	0.18	44,44,44,44	0
56	MG	B	3290	1/1	0.95	0.20	51,51,51,51	0
56	MG	B	3238	1/1	0.95	0.09	44,44,44,44	0
56	MG	B	3735	1/1	0.95	0.06	71,71,71,71	0
56	MG	B	3069	1/1	0.95	0.21	40,40,40,40	0
56	MG	B	2954	1/1	0.95	0.19	42,42,42,42	0
56	MG	Y	102	1/1	0.95	0.18	54,54,54,54	0
56	MG	GB	3421	1/1	0.95	0.07	77,77,77,77	0
56	MG	B	3587	1/1	0.95	0.05	62,62,62,62	0
56	MG	B	3588	1/1	0.95	0.05	46,46,46,46	0
56	MG	F	313	1/1	0.95	0.22	49,49,49,49	0
56	MG	B	3822	1/1	0.95	0.24	44,44,44,44	0
56	MG	B	3740	1/1	0.95	0.18	70,70,70,70	0
56	MG	B	3460	1/1	0.95	0.11	43,43,43,43	0
56	MG	AA	101	1/1	0.95	0.23	59,59,59,59	0
56	MG	GB	3691	1/1	0.95	0.09	71,71,71,71	0
56	MG	B	3242	1/1	0.95	0.16	49,49,49,49	0
56	MG	B	3743	1/1	0.95	0.07	52,52,52,52	0
56	MG	B	3343	1/1	0.95	0.12	56,56,56,56	0
56	MG	B	3745	1/1	0.95	0.10	56,56,56,56	0
56	MG	B	3344	1/1	0.95	0.29	49,49,49,49	0
56	MG	G	3209	1/1	0.95	0.24	48,48,48,48	0
56	MG	B	3155	1/1	0.95	0.10	43,43,43,43	0
56	MG	B	3346	1/1	0.95	0.13	45,45,45,45	0
56	MG	B	3156	1/1	0.95	0.19	50,50,50,50	0
56	MG	B	3348	1/1	0.95	0.15	55,55,55,55	0
56	MG	EA	101	1/1	0.95	0.30	45,45,45,45	0
56	MG	B	3751	1/1	0.95	0.10	48,48,48,48	0
56	MG	GB	3195	1/1	0.95	0.10	52,52,52,52	0
56	MG	B	3836	1/1	0.95	0.24	46,46,46,46	0
56	MG	B	3126	1/1	0.95	0.10	43,43,43,43	0
56	MG	FB	1711	1/1	0.95	0.16	69,69,69,69	0
56	MG	GB	3708	1/1	0.95	0.11	71,71,71,71	0
56	MG	EC	104	1/1	0.95	0.18	79,79,79,79	0
56	MG	B	3158	1/1	0.95	0.14	50,50,50,50	0
56	MG	B	3034	1/1	0.95	0.21	55,55,55,55	0
56	MG	B	3128	1/1	0.95	0.08	33,33,33,33	0
56	MG	GB	3712	1/1	0.95	0.07	66,66,66,66	0
56	MG	B	3538	1/1	0.95	0.14	57,57,57,57	0
56	MG	B	3602	1/1	0.95	0.07	54,54,54,54	0
56	MG	IA	104	1/1	0.95	0.13	44,44,44,44	0
56	MG	GB	3581	1/1	0.95	0.10	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	FB	1818	1/1	0.95	0.06	83,83,83,83	0
56	MG	B	3843	1/1	0.95	0.07	49,49,49,49	0
56	MG	B	3161	1/1	0.95	0.11	38,38,38,38	0
56	MG	B	3053	1/1	0.95	0.14	46,46,46,46	0
56	MG	FB	1922	1/1	0.95	0.07	83,83,83,83	0
56	MG	B	3414	1/1	0.95	0.09	47,47,47,47	0
56	MG	B	3304	1/1	0.95	0.15	43,43,43,43	0
56	MG	GB	3460	1/1	0.95	0.06	63,63,63,63	0
56	MG	B	3416	1/1	0.95	0.20	37,37,37,37	0
56	MG	B	3765	1/1	0.95	0.07	50,50,50,50	0
56	MG	B	3256	1/1	0.95	0.10	38,38,38,38	0
56	MG	B	3480	1/1	0.95	0.05	44,44,44,44	0
56	MG	GB	2990	1/1	0.95	0.37	63,63,63,63	0
56	MG	B	3360	1/1	0.95	0.07	43,43,43,43	0
56	MG	C	210	1/1	0.95	0.41	75,75,75,75	0
56	MG	GB	3343	1/1	0.95	0.06	57,57,57,57	0
56	MG	B	3097	1/1	0.95	0.33	54,54,54,54	0
56	MG	B	3548	1/1	0.95	0.04	44,44,44,44	0
56	MG	B	2987	1/1	0.95	0.19	34,34,34,34	0
56	MG	B	3772	1/1	0.95	0.11	57,57,57,57	0
56	MG	GB	3605	1/1	0.95	0.08	61,61,61,61	0
56	MG	GB	3348	1/1	0.95	0.12	59,59,59,59	0
56	MG	B	3036	1/1	0.95	0.27	45,45,45,45	0
56	MG	B	3206	1/1	0.95	0.15	44,44,44,44	0
56	MG	FB	1937	1/1	0.95	0.30	65,65,65,65	0
56	MG	M	202	1/1	0.95	0.10	58,58,58,58	0
56	MG	B	2988	1/1	0.95	0.24	38,38,38,38	0
56	MG	B	2990	1/1	0.95	0.22	41,41,41,41	0
56	MG	B	3171	1/1	0.95	0.12	48,48,48,48	0
56	MG	B	3620	1/1	0.95	0.07	50,50,50,50	0
56	MG	A	1871	1/1	0.95	0.11	85,85,85,85	0
56	MG	GB	3484	1/1	0.95	0.08	60,60,60,60	0
56	MG	B	3622	1/1	0.95	0.08	55,55,55,55	0
56	MG	FB	1945	1/1	0.95	0.07	68,68,68,68	0
56	MG	C	223	1/1	0.95	0.14	56,56,56,56	0
56	MG	A	1750	1/1	0.95	0.11	80,80,80,80	0
56	MG	A	1623	1/1	0.95	0.19	67,67,67,67	0
56	MG	GB	3241	1/1	0.95	0.28	74,74,74,74	0
56	MG	A	1835	1/1	0.95	0.07	70,70,70,70	0
56	MG	GB	3013	1/1	0.95	0.24	56,56,56,56	0
56	MG	B	2926	1/1	0.95	0.30	36,36,36,36	0
56	MG	GB	3627	1/1	0.95	0.07	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	C	228	1/1	0.95	0.05	76,76,76,76	0
56	MG	JB	312	1/1	0.95	0.07	62,62,62,62	0
56	MG	GB	2903	1/1	0.95	0.28	36,36,36,36	0
56	MG	GB	3371	1/1	0.95	0.10	56,56,56,56	0
56	MG	GB	3128	1/1	0.95	0.32	58,58,58,58	0
56	MG	GB	3017	1/1	0.95	0.19	56,56,56,56	0
56	MG	B	3179	1/1	0.95	0.18	47,47,47,47	0
56	MG	LB	301	1/1	0.95	0.13	60,60,60,60	0
56	MG	B	3108	1/1	0.95	0.13	35,35,35,35	0
56	MG	B	3221	1/1	0.95	0.13	53,53,53,53	0
56	MG	FB	1652	1/1	0.95	0.42	70,70,70,70	0
56	MG	B	3084	1/1	0.95	0.27	42,42,42,42	0
56	MG	B	3631	1/1	0.95	0.17	50,50,50,50	0
56	MG	GB	3024	1/1	0.95	0.23	57,57,57,57	0
56	MG	Q	204	1/1	0.95	0.09	74,74,74,74	0
56	MG	B	3142	1/1	0.95	0.12	46,46,46,46	0
56	MG	B	3112	1/1	0.95	0.09	49,49,49,49	0
56	MG	S	201	1/1	0.95	0.14	63,63,63,63	0
56	MG	B	3225	1/1	0.95	0.19	46,46,46,46	0
56	MG	GB	3262	1/1	0.95	0.16	50,50,50,50	0
56	MG	A	1617	1/1	0.95	0.31	59,59,59,59	0
56	MG	A	1726	1/1	0.95	0.19	73,73,73,73	0
56	MG	A	1791	1/1	0.95	0.20	59,59,59,59	0
56	MG	GB	3390	1/1	0.95	0.08	47,47,47,47	0
56	MG	GB	2920	1/1	0.95	0.41	57,57,57,57	0
56	MG	S	206	1/1	0.95	0.05	57,57,57,57	0
56	MG	B	3510	1/1	0.95	0.08	45,45,45,45	0
56	MG	GB	3522	1/1	0.95	0.10	71,71,71,71	0
56	MG	B	3641	1/1	0.95	0.11	50,50,50,50	0
56	MG	B	3187	1/1	0.95	0.11	59,59,59,59	0
56	MG	B	3117	1/1	0.95	0.28	48,48,48,48	0
56	MG	QB	204	1/1	0.95	0.12	65,65,65,65	0
56	MG	B	3513	1/1	0.95	0.14	53,53,53,53	0
56	MG	GB	3398	1/1	0.95	0.12	63,63,63,63	0
56	MG	B	2903	1/1	0.96	0.36	35,35,35,35	0
56	MG	XB	201	1/1	0.96	0.17	55,55,55,55	0
56	MG	B	3357	1/1	0.96	0.06	54,54,54,54	0
56	MG	B	3078	1/1	0.96	0.16	43,43,43,43	0
56	MG	GB	3595	1/1	0.96	0.14	74,74,74,74	0
56	MG	B	3696	1/1	0.96	0.10	52,52,52,52	0
56	MG	B	3697	1/1	0.96	0.09	56,56,56,56	0
56	MG	GB	3485	1/1	0.96	0.08	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	GB	3273	1/1	0.96	0.07	54,54,54,54	0
56	MG	GB	3274	1/1	0.96	0.29	73,73,73,73	0
56	MG	B	3103	1/1	0.96	0.17	51,51,51,51	0
56	MG	B	3632	1/1	0.96	0.14	64,64,64,64	0
56	MG	X	107	1/1	0.96	0.12	72,72,72,72	0
56	MG	GB	3172	1/1	0.96	0.15	57,57,57,57	0
56	MG	B	3522	1/1	0.96	0.12	49,49,49,49	0
56	MG	A	1854	1/1	0.96	0.08	75,75,75,75	0
56	MG	B	2985	1/1	0.96	0.25	46,46,46,46	0
56	MG	GB	2977	1/1	0.96	0.22	52,52,52,52	0
56	MG	B	3775	1/1	0.96	0.08	42,42,42,42	0
56	MG	B	3164	1/1	0.96	0.11	46,46,46,46	0
56	MG	B	3581	1/1	0.96	0.08	46,46,46,46	0
56	MG	B	3526	1/1	0.96	0.31	49,49,49,49	0
56	MG	B	3639	1/1	0.96	0.13	46,46,46,46	0
56	MG	B	3165	1/1	0.96	0.13	46,46,46,46	0
56	MG	FB	1847	1/1	0.96	0.14	67,67,67,67	0
56	MG	GB	3290	1/1	0.96	0.28	48,48,48,48	0
56	MG	B	2945	1/1	0.96	0.19	47,47,47,47	0
56	MG	B	3642	1/1	0.96	0.04	52,52,52,52	0
56	MG	B	3643	1/1	0.96	0.06	56,56,56,56	0
56	MG	GB	2989	1/1	0.96	0.33	59,59,59,59	0
56	MG	B	2905	1/1	0.96	0.12	45,45,45,45	0
56	MG	B	2935	1/1	0.96	0.33	44,44,44,44	0
56	MG	J	203	1/1	0.96	0.27	80,80,80,80	0
56	MG	CA	102	1/1	0.96	0.19	52,52,52,52	0
56	MG	HC	102	1/1	0.96	0.08	62,62,62,62	0
56	MG	B	3109	1/1	0.96	0.25	53,53,53,53	0
56	MG	B	3086	1/1	0.96	0.18	43,43,43,43	0
56	MG	B	3372	1/1	0.96	0.08	40,40,40,40	0
56	MG	XA	103	1/1	0.96	0.13	72,72,72,72	0
56	MG	B	3326	1/1	0.96	0.18	44,44,44,44	0
56	MG	B	3327	1/1	0.96	0.04	43,43,43,43	0
56	MG	B	3243	1/1	0.96	0.14	43,43,43,43	0
56	MG	EA	102	1/1	0.96	0.07	44,44,44,44	0
56	MG	FA	101	1/1	0.96	0.06	54,54,54,54	0
56	MG	GB	3523	1/1	0.96	0.19	61,61,61,61	0
56	MG	B	2936	1/1	0.96	0.26	34,34,34,34	0
56	MG	FA	103	1/1	0.96	0.09	48,48,48,48	0
56	MG	GB	2908	1/1	0.96	0.30	44,44,44,44	0
56	MG	B	3482	1/1	0.96	0.10	47,47,47,47	0
56	MG	A	1826	1/1	0.96	0.11	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3114	1/1	0.96	0.18	49,49,49,49	0
56	MG	B	3176	1/1	0.96	0.15	53,53,53,53	0
56	MG	B	3380	1/1	0.96	0.07	51,51,51,51	0
56	MG	GB	3011	1/1	0.96	0.17	54,54,54,54	0
56	MG	GB	3318	1/1	0.96	0.14	54,54,54,54	0
56	MG	B	3044	1/1	0.96	0.12	40,40,40,40	0
56	MG	B	3728	1/1	0.96	0.09	50,50,50,50	0
56	MG	B	3659	1/1	0.96	0.06	52,52,52,52	0
56	MG	B	2950	1/1	0.96	0.23	62,62,62,62	0
56	MG	B	3251	1/1	0.96	0.28	53,53,53,53	0
56	MG	B	3336	1/1	0.96	0.26	60,60,60,60	0
56	MG	M	207	1/1	0.96	0.21	51,51,51,51	0
56	MG	C	235	1/1	0.96	0.08	73,73,73,73	0
56	MG	B	3046	1/1	0.96	0.13	34,34,34,34	0
56	MG	B	2951	1/1	0.96	0.40	43,43,43,43	0
56	MG	B	3255	1/1	0.96	0.10	48,48,48,48	0
56	MG	B	3213	1/1	0.96	0.12	48,48,48,48	0
56	MG	GB	3436	1/1	0.96	0.12	71,71,71,71	0
56	MG	N	205	1/1	0.96	0.07	65,65,65,65	0
56	MG	A	1632	1/1	0.96	0.40	65,65,65,65	0
56	MG	FB	1707	1/1	0.96	0.24	69,69,69,69	0
56	MG	B	3300	1/1	0.96	0.21	50,50,50,50	0
56	MG	GB	2931	1/1	0.96	0.22	47,47,47,47	0
56	MG	B	3011	1/1	0.96	0.28	55,55,55,55	0
56	MG	B	3556	1/1	0.96	0.21	45,45,45,45	0
56	MG	B	3671	1/1	0.96	0.13	46,46,46,46	0
56	MG	B	3672	1/1	0.96	0.08	52,52,52,52	0
56	MG	B	3673	1/1	0.96	0.10	50,50,50,50	0
56	MG	B	2908	1/1	0.96	0.22	42,42,42,42	0
56	MG	JA	402	1/1	0.96	0.22	54,54,54,54	0
56	MG	B	3393	1/1	0.96	0.10	46,46,46,46	0
56	MG	B	3613	1/1	0.96	0.21	55,55,55,55	0
56	MG	B	3122	1/1	0.96	0.26	46,46,46,46	0
56	MG	B	3821	1/1	0.96	0.11	53,53,53,53	0
56	MG	E	306	1/1	0.96	0.11	51,51,51,51	0
56	MG	E	307	1/1	0.96	0.08	55,55,55,55	0
56	MG	FB	1809	1/1	0.96	0.14	63,63,63,63	0
56	MG	GB	3456	1/1	0.96	0.20	68,68,68,68	0
56	MG	B	3450	1/1	0.96	0.10	63,63,63,63	0
56	MG	B	3124	1/1	0.96	0.15	44,44,44,44	0
56	MG	FB	1812	1/1	0.96	0.06	70,70,70,70	0
56	MG	B	3219	1/1	0.96	0.16	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3220	1/1	0.96	0.14	46,46,46,46	0
56	MG	B	3509	1/1	0.96	0.06	52,52,52,52	0
56	MG	GB	3148	1/1	0.96	0.30	59,59,59,59	0
56	MG	RB	205	1/1	0.96	0.14	55,55,55,55	0
56	MG	RB	206	1/1	0.96	0.12	59,59,59,59	0
56	MG	GB	3464	1/1	0.96	0.11	83,83,83,83	0
56	MG	FB	1816	1/1	0.96	0.07	75,75,75,75	0
56	MG	B	2996	1/1	0.96	0.20	38,38,38,38	0
56	MG	B	3684	1/1	0.96	0.06	61,61,61,61	0
56	MG	B	3399	1/1	0.96	0.24	53,53,53,53	0
56	MG	F	307	1/1	0.96	0.07	70,70,70,70	0
56	MG	B	3052	1/1	0.96	0.23	47,47,47,47	0
56	MG	B	2930	1/1	0.96	0.20	34,34,34,34	0
56	MG	GB	3365	1/1	0.96	0.26	60,60,60,60	0
56	MG	B	3054	1/1	0.96	0.33	58,58,58,58	0
56	MG	B	3759	1/1	0.96	0.12	47,47,47,47	0
56	MG	B	3459	1/1	0.96	0.08	46,46,46,46	0
56	MG	B	3190	1/1	0.96	0.21	57,57,57,57	0
56	MG	A	1735	1/1	0.96	0.30	69,69,69,69	0
56	MG	VB	206	1/1	0.96	0.05	69,69,69,69	0
56	MG	B	3692	1/1	0.96	0.11	51,51,51,51	0
56	MG	G	3202	1/1	0.96	0.20	34,34,34,34	0
56	MG	HD	201	1/1	0.96	0.10	79,79,79,79	0
56	MG	GB	3590	1/1	0.96	0.09	76,76,76,76	0
56	MG	GB	3591	1/1	0.96	0.14	71,71,71,71	0
56	MG	B	3403	1/1	0.97	0.06	50,50,50,50	0
56	MG	B	3404	1/1	0.97	0.12	47,47,47,47	0
56	MG	GB	3225	1/1	0.97	0.06	65,65,65,65	0
56	MG	B	3020	1/1	0.97	0.24	37,37,37,37	0
56	MG	B	3359	1/1	0.97	0.23	63,63,63,63	0
56	MG	B	3021	1/1	0.97	0.19	43,43,43,43	0
56	MG	GB	3342	1/1	0.97	0.06	45,45,45,45	0
56	MG	GB	3175	1/1	0.97	0.08	52,52,52,52	0
56	MG	B	3029	1/1	0.97	0.18	41,41,41,41	0
56	MG	C	204	1/1	0.97	0.24	54,54,54,54	0
56	MG	GB	3232	1/1	0.97	0.16	61,61,61,61	0
56	MG	B	3111	1/1	0.97	0.17	33,33,33,33	0
56	MG	A	1774	1/1	0.97	0.06	106,106,106,106	0
56	MG	GB	2984	1/1	0.97	0.26	66,66,66,66	0
56	MG	A	1839	1/1	0.97	0.08	85,85,85,85	0
56	MG	B	3502	1/1	0.97	0.06	48,48,48,48	0
56	MG	B	3366	1/1	0.97	0.17	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	B	3168	1/1	0.97	0.10	35,35,35,35	0
56	MG	AA	102	1/1	0.97	0.04	59,59,59,59	0
56	MG	Q	201	1/1	0.97	0.20	62,62,62,62	0
56	MG	B	2989	1/1	0.97	0.24	53,53,53,53	0
56	MG	B	3506	1/1	0.97	0.07	46,46,46,46	0
56	MG	RC	307	1/1	0.97	0.06	85,85,85,85	0
56	MG	B	3234	1/1	0.97	0.08	51,51,51,51	0
56	MG	GB	3042	1/1	0.97	0.28	54,54,54,54	0
56	MG	B	3475	1/1	0.97	0.23	46,46,46,46	0
56	MG	B	3784	1/1	0.97	0.09	44,44,44,44	0
56	MG	B	3446	1/1	0.97	0.06	42,42,42,42	0
56	MG	E	309	1/1	0.97	0.04	53,53,53,53	0
56	MG	B	3147	1/1	0.97	0.10	52,52,52,52	0
56	MG	B	3236	1/1	0.97	0.26	44,44,44,44	0
56	MG	B	3254	1/1	0.97	0.12	61,61,61,61	0
56	MG	B	3350	1/1	0.97	0.05	40,40,40,40	0
56	MG	GB	3254	1/1	0.97	0.08	62,62,62,62	0
56	MG	GB	2909	1/1	0.97	0.31	38,38,38,38	0
56	MG	B	3058	1/1	0.97	0.35	48,48,48,48	0
56	MG	B	3313	1/1	0.97	0.12	49,49,49,49	0
56	MG	B	3422	1/1	0.97	0.08	66,66,66,66	0
56	MG	GB	3315	1/1	0.97	0.04	51,51,51,51	0
56	MG	GB	3610	1/1	0.97	0.07	78,78,78,78	0
56	MG	B	2943	1/1	0.97	0.18	37,37,37,37	0
56	MG	B	3831	1/1	0.97	0.14	43,43,43,43	0
56	MG	B	3552	1/1	0.97	0.10	46,46,46,46	0
56	MG	GB	3106	1/1	0.97	0.32	66,66,66,66	0
56	MG	B	3274	1/1	0.97	0.13	54,54,54,54	0
56	MG	B	3210	1/1	0.97	0.12	54,54,54,54	0
56	MG	GB	3158	1/1	0.97	0.07	52,52,52,52	0
56	MG	B	3240	1/1	0.97	0.12	51,51,51,51	0
56	MG	B	2999	1/1	0.97	0.20	35,35,35,35	0
56	MG	B	3489	1/1	0.97	0.17	40,40,40,40	0
56	MG	GB	3213	1/1	0.97	0.06	59,59,59,59	0
56	MG	GB	3503	1/1	0.97	0.13	52,52,52,52	0
56	MG	B	3764	1/1	0.97	0.09	48,48,48,48	0
56	MG	GB	3215	1/1	0.97	0.18	55,55,55,55	0
56	MG	M	203	1/1	0.97	0.18	43,43,43,43	0
56	MG	G	3201	1/1	0.97	0.14	36,36,36,36	0
56	MG	B	3430	1/1	0.97	0.11	46,46,46,46	0
56	MG	FB	1658	1/1	0.97	0.08	72,72,72,72	0
56	MG	M	206	1/1	0.97	0.23	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	JB	301	1/1	0.97	0.19	45,45,45,45	0
56	MG	B	3491	1/1	0.97	0.12	48,48,48,48	0
57	ZN	AC	201	1/1	0.97	0.05	100,100,100,100	0
56	MG	B	3431	1/1	0.97	0.06	47,47,47,47	0
56	MG	B	3282	1/1	0.98	0.12	50,50,50,50	0
56	MG	B	3227	1/1	0.98	0.09	44,44,44,44	0
56	MG	B	3173	1/1	0.98	0.06	40,40,40,40	0
56	MG	B	3700	1/1	0.98	0.06	46,46,46,46	0
56	MG	B	3285	1/1	0.98	0.06	42,42,42,42	0
56	MG	B	3286	1/1	0.98	0.06	41,41,41,41	0
56	MG	B	3471	1/1	0.98	0.07	49,49,49,49	0
56	MG	B	3819	1/1	0.98	0.09	56,56,56,56	0
56	MG	B	3439	1/1	0.98	0.11	49,49,49,49	0
56	MG	B	3123	1/1	0.98	0.11	33,33,33,33	0
56	MG	GB	3492	1/1	0.98	0.06	70,70,70,70	0
56	MG	B	3425	1/1	0.98	0.17	47,47,47,47	0
56	MG	X	102	1/1	0.98	0.18	50,50,50,50	0
56	MG	B	2982	1/1	0.98	0.18	42,42,42,42	0
56	MG	B	3427	1/1	0.98	0.05	47,47,47,47	0
56	MG	B	3245	1/1	0.98	0.18	52,52,52,52	0
56	MG	B	3145	1/1	0.98	0.06	43,43,43,43	0
56	MG	B	3363	1/1	0.98	0.06	44,44,44,44	0
56	MG	B	3085	1/1	0.98	0.05	38,38,38,38	0
56	MG	T	201	1/1	0.98	0.13	42,42,42,42	0
56	MG	T	202	1/1	0.98	0.07	45,45,45,45	0
56	MG	B	3083	1/1	0.98	0.32	40,40,40,40	0
56	MG	B	3281	1/1	0.98	0.20	53,53,53,53	0
56	MG	B	3534	1/1	0.98	0.04	45,45,45,45	0
56	MG	B	3033	1/1	0.99	0.28	50,50,50,50	0
56	MG	GB	3037	1/1	0.99	0.07	52,52,52,52	0
56	MG	GB	3370	1/1	0.99	0.09	65,65,65,65	0
57	ZN	CA	101	1/1	0.99	0.03	62,62,62,62	0
57	ZN	DA	101	1/1	0.99	0.02	71,71,71,71	0
57	ZN	GA	101	1/1	0.99	0.03	70,70,70,70	0
56	MG	A	1736	1/1	0.99	0.04	53,53,53,53	0
56	MG	B	3713	1/1	0.99	0.06	46,46,46,46	0
57	ZN	HC	101	1/1	0.99	0.03	86,86,86,86	0
57	ZN	IC	101	1/1	0.99	0.04	91,91,91,91	0
57	ZN	V	501	1/1	1.00	0.04	72,72,72,72	0
57	ZN	LC	101	1/1	1.00	0.02	97,97,97,97	0

6.5 Other polymers [i](#)

There are no such residues in this entry.