



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:57 AM GMT

PDB ID : 3G71
Title : Co-crystal structure of Bruceantin bound to the large ribosomal subunit
Authors : Gurel, G.; Blaha, G.; Moore, P.B.; Steitz, T.A.
Deposited on : 2009-02-09
Resolution : 2.85 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

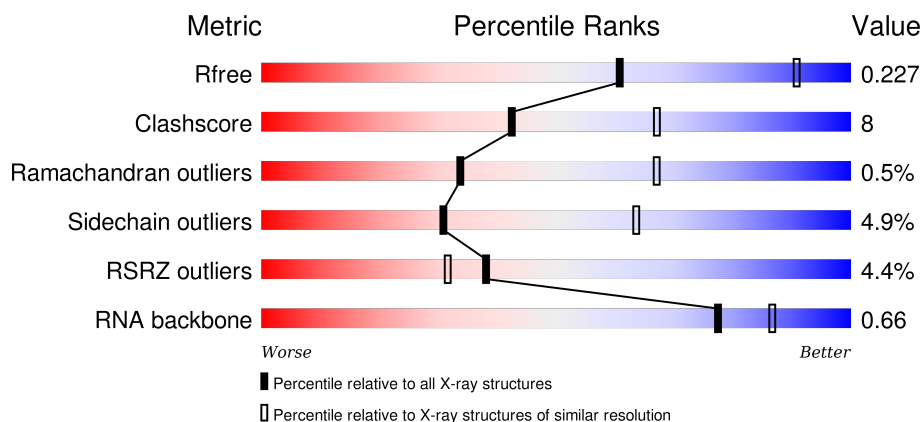
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	91344	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)
RNA backbone	2183	1020 (3.22-2.50)

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

Mol	Chain	Length	Quality of chain
1	0	2923	<div> <div>6%</div> <div>54% 34% 5% 6%</div> </div>
2	A	237	<div> <div>6%</div> <div>84% 14% .</div> </div>
3	B	337	<div> <div>85% 14% .</div> </div>
4	C	246	<div> <div>84% 13% .</div> </div>

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Mol	Chain	Length	Quality of chain
5	D	177	
6	E	172	
7	F	119	
8	G	348	
9	H	177	
10	I	70	
11	J	142	
12	K	132	
13	L	165	
14	M	194	
15	N	186	
16	O	115	
17	P	143	
18	Q	95	
19	R	150	
20	S	81	
21	T	119	
22	U	53	
23	V	65	
24	W	154	
25	X	82	
26	Y	142	
27	Z	73	
28	1	56	
29	2	50	

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Mol	Chain	Length	Quality of chain
30	3	92	
31	9	122	

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
32	MG	0	8002	-	-	-	X
32	MG	0	8004	-	-	-	X
32	MG	0	8006	-	-	-	X
32	MG	0	8008	-	-	-	X
32	MG	0	8009	-	-	-	X
32	MG	0	8011	-	-	-	X
32	MG	0	8012	-	-	-	X
32	MG	0	8014	-	-	-	X
32	MG	0	8028	-	-	-	X
32	MG	0	8041	-	-	-	X
32	MG	0	8043	-	-	-	X
32	MG	0	8047	-	-	-	X
32	MG	0	8062	-	-	-	X
32	MG	0	8067	-	-	-	X
32	MG	0	8070	-	-	-	X
32	MG	0	8072	-	-	-	X
32	MG	9	8040	-	-	-	X
33	K	0	8402	-	-	-	X
34	NA	0	8504	-	-	-	X
34	NA	0	8511	-	-	-	X
34	NA	0	8519	-	-	-	X
34	NA	0	8521	-	-	-	X
34	NA	0	8522	-	-	-	X
34	NA	0	8523	-	-	-	X
34	NA	0	8527	-	-	-	X
34	NA	0	8528	-	-	-	X
34	NA	0	8530	-	-	-	X
34	NA	0	8534	-	-	-	X
34	NA	0	8535	-	-	-	X
34	NA	0	8537	-	-	-	X
34	NA	0	8542	-	-	-	X
34	NA	0	8547	-	-	-	X
34	NA	0	8553	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
34	NA	0	8555	-	-	-	X
34	NA	0	8556	-	-	-	X
34	NA	0	8558	-	-	-	X
34	NA	0	8559	-	-	-	X
34	NA	0	8560	-	-	-	X
34	NA	0	8562	-	-	-	X
34	NA	0	8563	-	-	-	X
34	NA	0	8564	-	-	-	X
34	NA	0	8565	-	-	-	X
34	NA	0	8568	-	-	-	X
34	NA	0	8575	-	-	-	X
34	NA	9	8572	-	-	-	X
34	NA	M	8539	-	-	-	X
35	CL	0	8815	-	-	-	X
35	CL	0	8816	-	-	-	X
36	SR	0	8902	-	-	-	X
36	SR	0	8903	-	-	-	X
36	SR	0	8904	-	-	-	X
36	SR	0	8908	-	-	-	X
36	SR	0	8949	-	-	-	X
36	SR	B	8987	-	-	-	X
37	WIN	0	9101	-	-	-	X

2 Entry composition

There are 39 unique types of molecules in this entry. The entry contains 99174 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	0	0
			59021	26349	10873	19054	2745			

- Molecule 2 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	237	Total	C	N	O	S	0	0	0
			1754	1072	352	325	5			

- Molecule 3 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

- Molecule 4 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	246	Total	C	N	O	S	0	0	0
			1860	1130	345	384	1			

- Molecule 5 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	140	Total	C	N	O	S	0	0	0
			1094	685	195	210	4			

- Molecule 6 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	E	172	Total	C	N	O	S	0	0	0
			1358	840	224	290	4			

- Molecule 7 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	F	119	Total	C	N	O	S	0	0	0
			890	551	141	197	1			

- Molecule 8 is a protein called 50S ribosomal protein L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	G	29	Total	C	N	O	S	0	0	0
			240	149	39	51	1			

- Molecule 9 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	H	160	Total	C	N	O	S	0	0	0
			1282	798	240	238	6			

- Molecule 10 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	I	70	Total	C	N	O	S	0	0	0
			520	323	81	115	1			

- Molecule 11 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	J	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 12 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	K	132	Total	C	N	O	S	0	0	0
			994	609	189	192	4			

- Molecule 13 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	L	145	Total	C	N	O		0	0	0
			1118	670	222	226				

- Molecule 14 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	M	194	Total	C	N	O	S	0	0	0
			1559	943	333	282	1			

- Molecule 15 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	N	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 16 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	O	115	Total	C	N	O		0	0	0
			865	529	161	175				

- Molecule 17 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	P	143	Total	C	N	O		0	0	0
			1137	683	229	225				

- Molecule 18 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	Q	95	Total	C	N	O		0	0	0
			735	450	141	144				

- Molecule 19 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	R	150	Total	C	N	O	S	0	0	0
			1150	713	209	224	4			

- Molecule 20 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	S	81	Total	C	N	O	S	0	0	0
			642	389	111	139	3			

- Molecule 21 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	T	119	Total	C	N	O	0	0	0
			950	568	180	202			

- Molecule 22 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	U	53	Total	C	N	O	S	0	0	0
			411	244	75	87	5			

- Molecule 23 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	V	65	Total	C	N	O	S	0	0	0
			500	304	94	101	1			

- Molecule 24 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	W	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 25 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	X	82	Total	C	N	O	S	0	0	0
			655	402	129	123	1			

- Molecule 26 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
26	Y	142	Total	C	N	O	0	0	0
			1131	686	228	217			

- Molecule 27 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Z	73	Total	C	N	O	S	0	0	0
			574	343	113	113	5			

- Molecule 28 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 29 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 30 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 31 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	0	85	Total	Mg	0	0
			85	85		
32	9	2	Total	Mg	0	0
			2	2		
32	K	1	Total	Mg	0	0
			1	1		
32	B	1	Total	Mg	0	0
			1	1		
32	A	1	Total	Mg	0	0
			1	1		
32	T	1	Total	Mg	0	0
			1	1		
32	2	1	Total	Mg	0	0
			1	1		
32	Y	1	Total	Mg	0	0
			1	1		

- Molecule 33 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	0	2	Total K 2 2	0	0

- Molecule 34 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	0	66	Total Na 66 66	0	0
34	J	1	Total Na 1 1	0	0
34	Q	1	Total Na 1 1	0	0
34	H	1	Total Na 1 1	0	0
34	C	1	Total Na 1 1	0	0
34	R	1	Total Na 1 1	0	0
34	9	2	Total Na 2 2	0	0
34	S	1	Total Na 1 1	0	0
34	M	1	Total Na 1 1	0	0

- Molecule 35 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	0	9	Total Cl 9 9	0	0
35	J	3	Total Cl 3 3	0	0
35	K	1	Total Cl 1 1	0	0
35	B	1	Total Cl 1 1	0	0
35	A	1	Total Cl 1 1	0	0
35	N	1	Total Cl 1 1	0	0
35	O	1	Total Cl 1 1	0	0
35	R	1	Total Cl 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	Y	1	Total	Cl	0	0
			1	1		
35	L	1	Total	Cl	0	0
			1	1		
35	3	1	Total	Cl	0	0
			1	1		
35	M	1	Total	Cl	0	0
			1	1		

- Molecule 36 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	95	Total	Sr	0	0
			95	95		
36	1	1	Total	Sr	0	0
			1	1		
36	B	2	Total	Sr	0	0
			2	2		
36	3	2	Total	Sr	0	0
			2	2		
36	A	2	Total	Sr	0	0
			2	2		
36	R	1	Total	Sr	0	0
			1	1		
36	9	3	Total	Sr	0	0
			3	3		
36	S	1	Total	Sr	0	0
			1	1		
36	F	1	Total	Sr	0	0
			1	1		

- Molecule 37 is METHYL (5BETA,7ALPHA,9BETA,10ALPHA,11ALPHA,12ALPHA,13BETA,15ALPHA)-15-{[(2E)-3,4-DIMETHYLPENT-2-ENOYL]OXY}-3,11,12-TRIHYDROXY-2,16-DIOXO-13,20-EPOXYPICRAS-3-EN-21-OATE (three-letter code: WIN) (formula: C₂₈H₃₆O₁₁).

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
39	C	171	Total 171	O 171	0	0
39	D	45	Total 45	O 45	0	0
39	E	40	Total 40	O 40	0	0
39	F	25	Total 25	O 25	0	0
39	G	18	Total 18	O 18	0	0
39	H	62	Total 62	O 62	0	0
39	I	5	Total 5	O 5	0	0
39	J	52	Total 52	O 52	0	0
39	K	53	Total 53	O 53	0	0
39	L	79	Total 79	O 79	0	0
39	M	128	Total 128	O 128	0	0
39	N	62	Total 62	O 62	0	0
39	O	40	Total 40	O 40	0	0
39	P	65	Total 65	O 65	0	0
39	Q	43	Total 43	O 43	0	0
39	R	77	Total 77	O 77	0	0
39	S	28	Total 28	O 28	0	0
39	T	32	Total 32	O 32	0	0
39	U	27	Total 27	O 27	0	0
39	V	12	Total 12	O 12	0	0
39	W	65	Total 65	O 65	0	0

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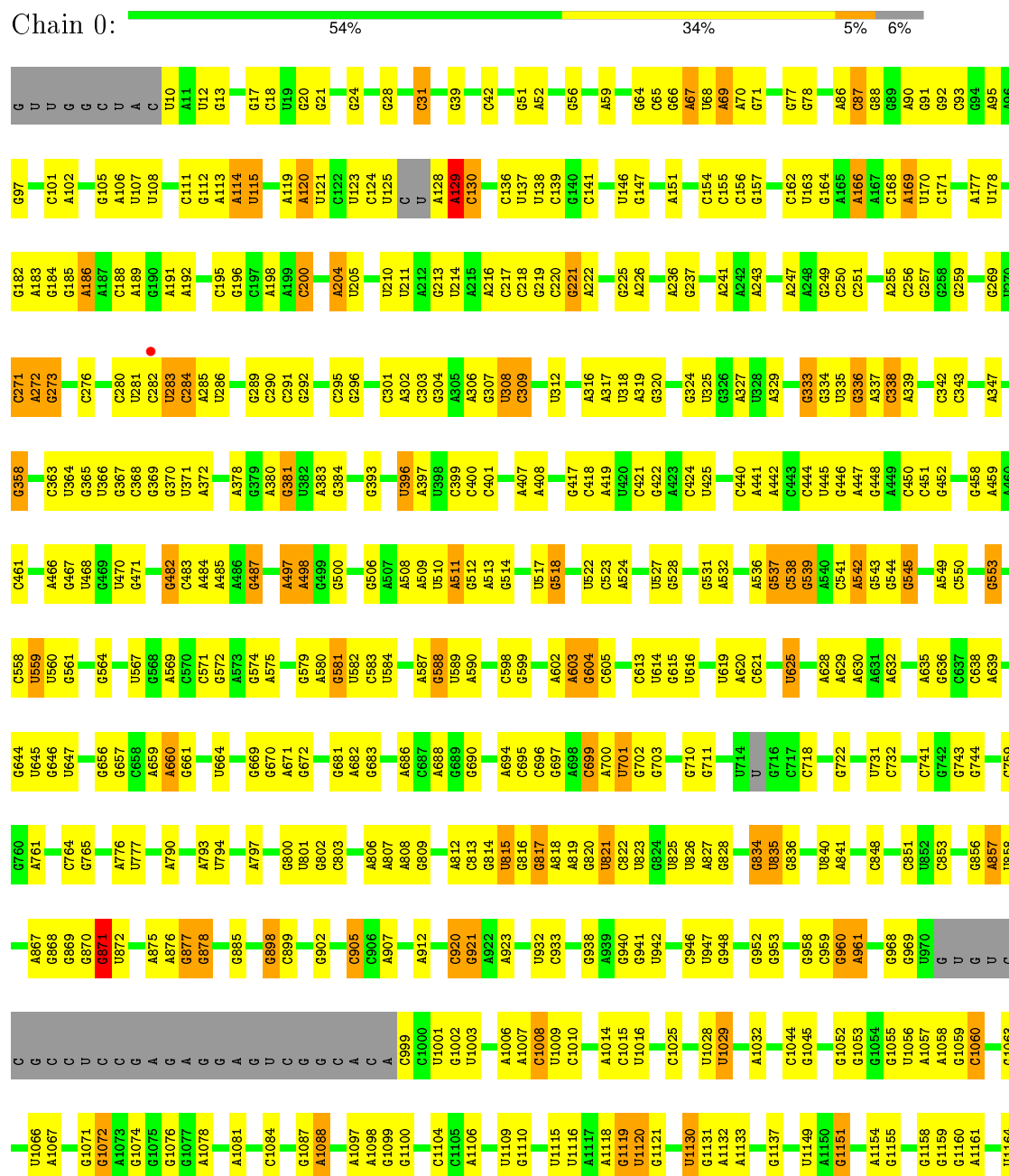
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
39	X	20	Total 20	O 20	0	0
39	Y	94	Total 94	O 94	0	0
39	Z	28	Total 28	O 28	0	0
39	1	52	Total 52	O 52	0	0
39	2	39	Total 39	O 39	0	0
39	3	66	Total 66	O 66	0	0
39	9	149	Total 149	O 149	0	0

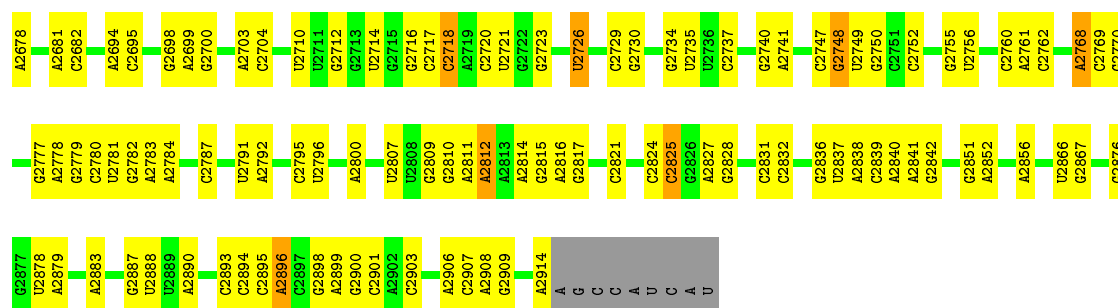
3 Residue-property plots

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

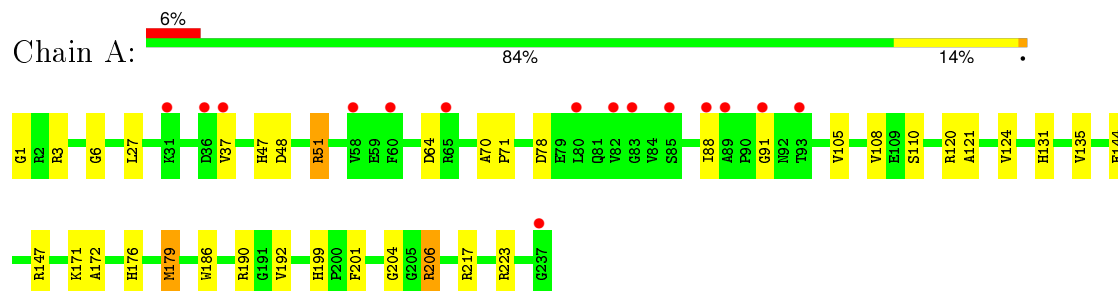
• Molecule 1: 23S ribosomal RNA



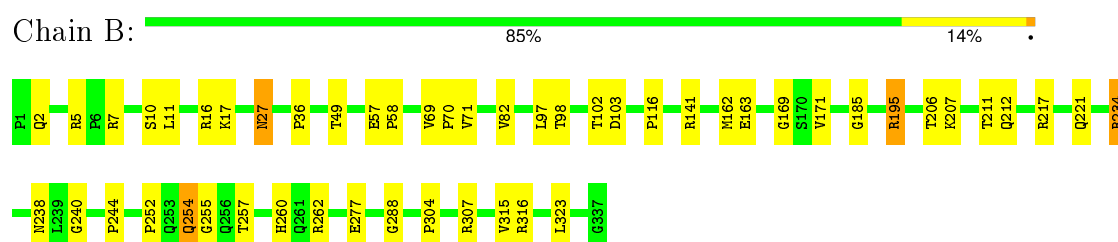




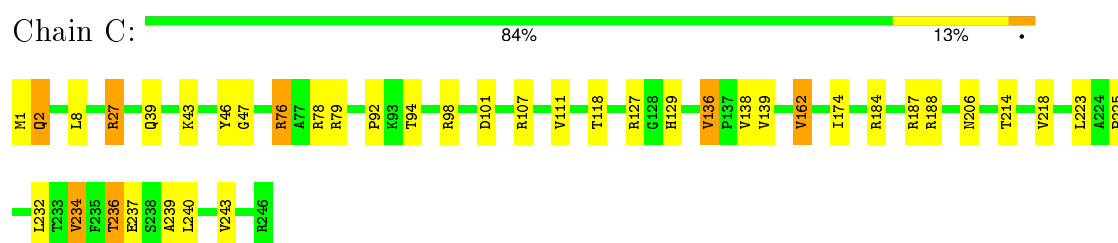
• Molecule 2: 50S ribosomal protein L2P



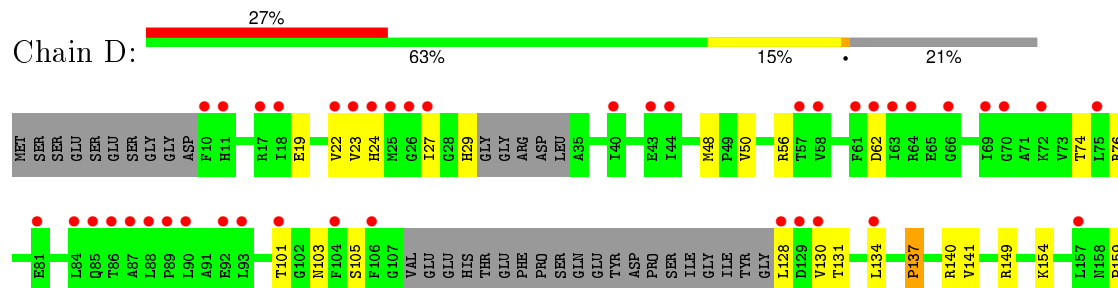
• Molecule 3: 50S ribosomal protein L3P

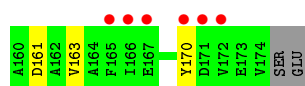


• Molecule 4: 50S ribosomal protein L4P

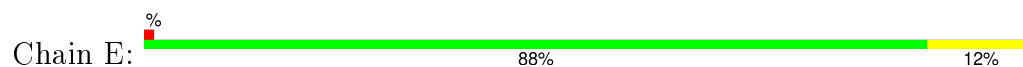


• Molecule 5: 50S ribosomal protein L5P

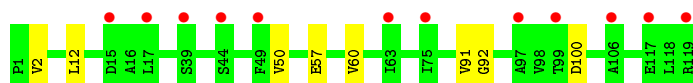
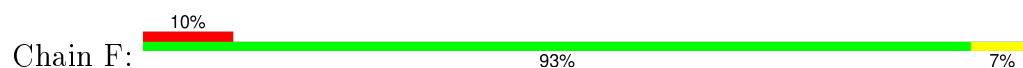




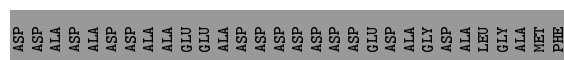
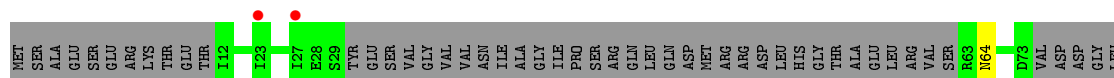
- Molecule 6: 50S ribosomal protein L6P



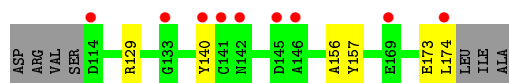
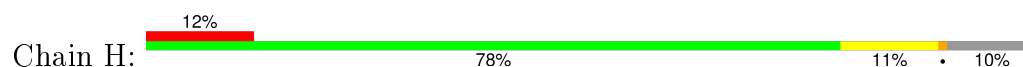
- Molecule 7: 50S ribosomal protein L7Ae



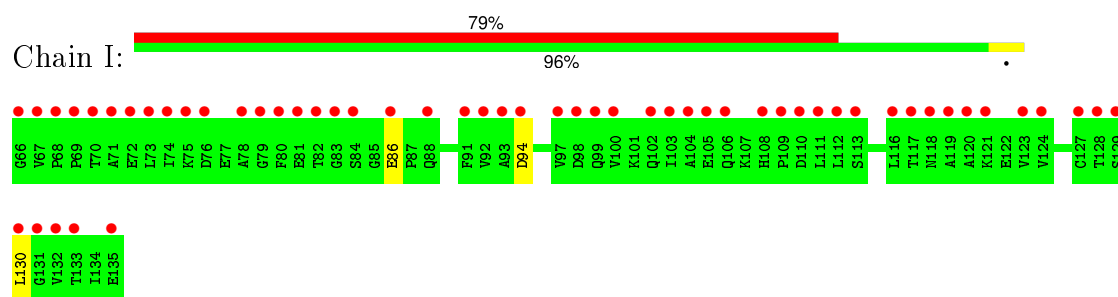
- Molecule 8: 50S ribosomal protein L10E



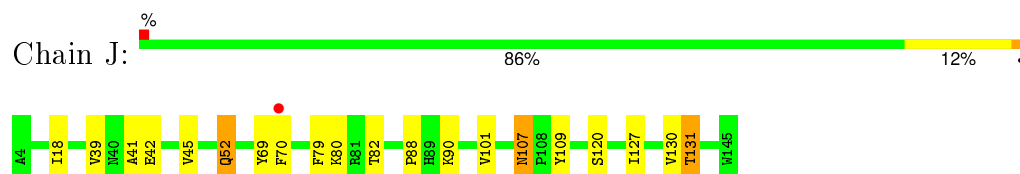
- Molecule 9: 50S ribosomal protein L10e



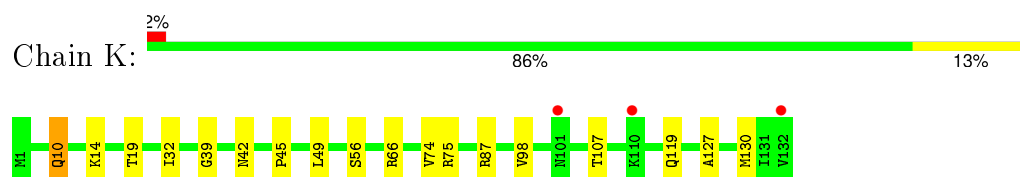
- Molecule 10: 50S ribosomal protein L11P



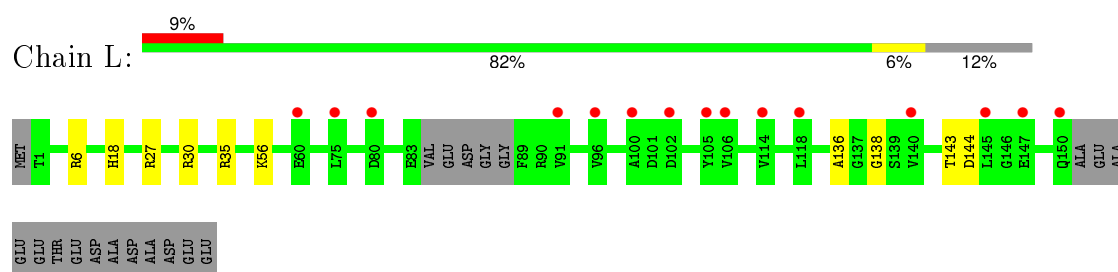
- Molecule 11: 50S ribosomal protein L13P



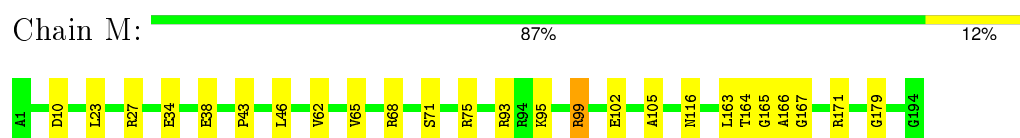
- Molecule 12: 50S ribosomal protein L14P



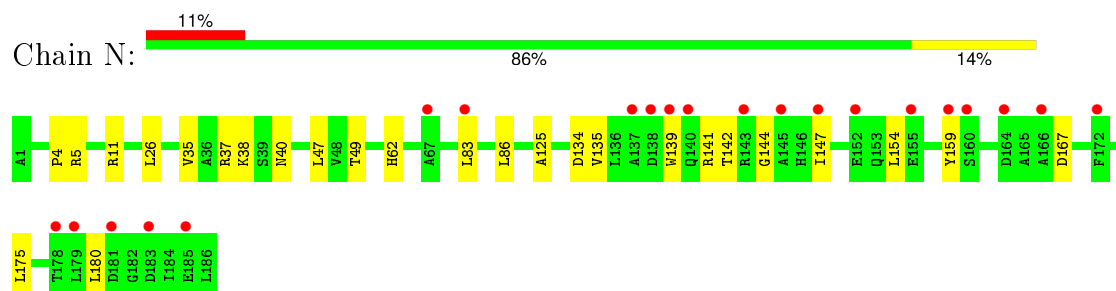
- Molecule 13: 50S ribosomal protein L15P




- Molecule 14: 50S ribosomal protein L15e



- Molecule 15: 50S ribosomal protein L18P




- Molecule 16: 50S ribosomal protein L18e

Chain O:  90% 9%




- Molecule 17: 50S ribosomal protein L19e

Chain P:  87% 13%




- Molecule 18: 50S ribosomal protein L21e

Chain Q:  87% 12%




- Molecule 19: 50S ribosomal protein L22P

Chain R:  89% 9%




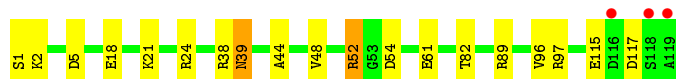
- Molecule 20: 50S ribosomal protein L23P

Chain S:  88% 12%



- Molecule 21: 50S ribosomal protein L24P

Chain T:  84% 14%

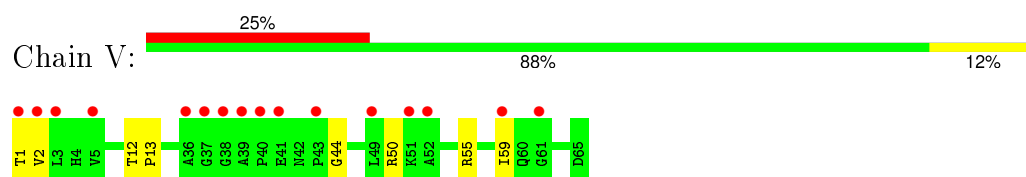


- Molecule 22: 50S ribosomal protein L24e

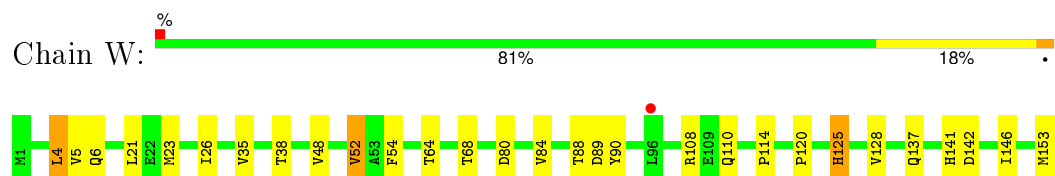
Chain U:  91% 9%



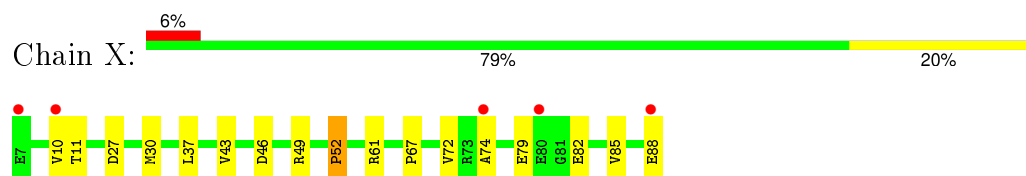
- Molecule 23: 50S ribosomal protein L29P



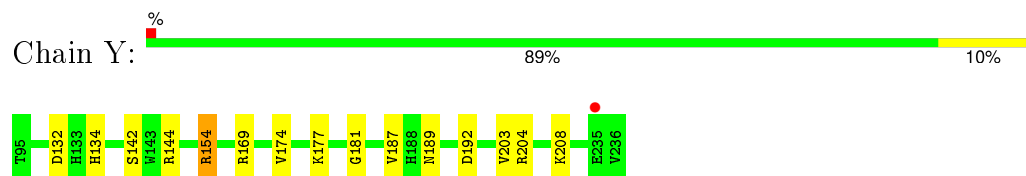
- Molecule 24: 50S ribosomal protein L30P



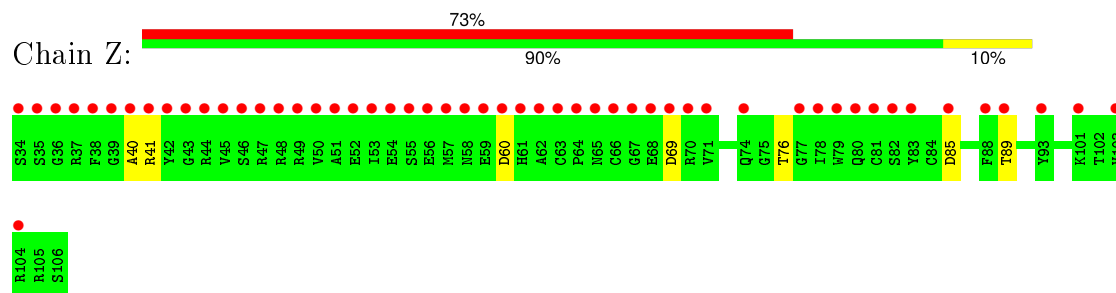
- Molecule 25: 50S ribosomal protein L31e



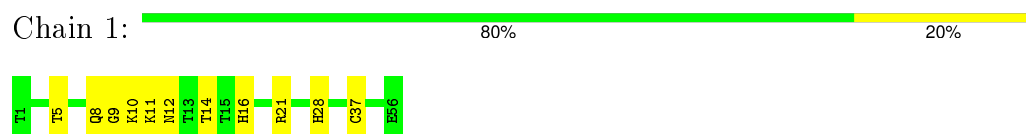
- Molecule 26: 50S ribosomal protein L32e



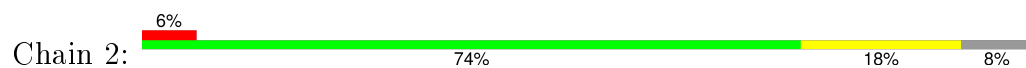
- Molecule 27: 50S ribosomal protein L37Ae



- Molecule 28: 50S ribosomal protein L37e

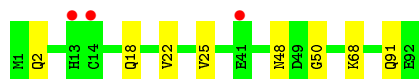
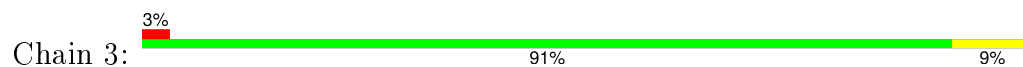


- Molecule 29: 50S ribosomal protein L39e

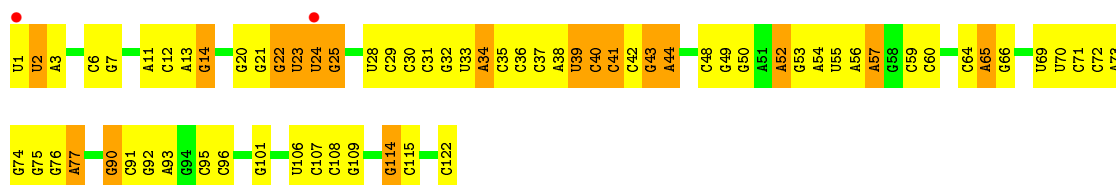
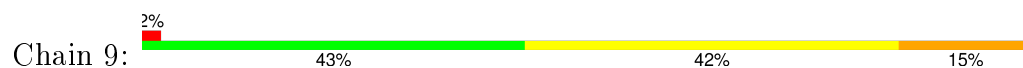




- Molecule 30: 50S ribosomal protein L44E



- Molecule 31: 5S ribosomal RNA



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	212.21Å 299.54Å 574.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.76 – 2.85 85.61 – 2.40	Depositor EDS
% Data completeness (in resolution range)	91.2 (49.76-2.85) 91.0 (85.61-2.40)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.186 , 0.233 0.182 , 0.227	Depositor DCC
R_{free} test set	4137 reflections (1.09%)	DCC
Wilson B-factor (Å ²)	58.3	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 80.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 667142 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99174	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.57% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, OMG, CL, SR, NA, K, UR3, CD, OMU, WIN, 1MA, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.39	0/65958	0.68	10/102869 (0.0%)
2	A	0.51	1/1787 (0.1%)	0.76	0/2408
3	B	0.53	0/2690	0.77	0/3652
4	C	0.56	0/1885	0.79	0/2552
5	D	0.63	0/1111	0.71	2/1498 (0.1%)
6	E	0.60	0/1383	0.68	0/1880
7	F	0.54	0/901	0.70	0/1224
8	G	0.50	0/241	0.66	0/324
9	H	0.61	0/1302	0.76	0/1743
10	I	0.58	0/527	0.63	0/716
11	J	0.62	0/1136	0.73	0/1530
12	K	0.49	0/1004	0.80	0/1351
13	L	0.52	0/1130	0.74	0/1509
14	M	0.51	0/1583	0.74	0/2116
15	N	0.55	0/1474	0.75	0/1999
16	O	0.50	0/874	0.72	1/1181 (0.1%)
17	P	0.53	0/1148	0.66	0/1528
18	Q	0.51	0/749	0.75	0/1005
19	R	0.57	0/1173	0.76	0/1578
20	S	0.54	0/649	0.65	0/875
21	T	0.47	0/958	0.76	1/1289 (0.1%)
22	U	0.58	0/418	0.68	0/562
23	V	0.43	0/503	0.68	0/675
24	W	0.52	0/1219	0.77	1/1655 (0.1%)
25	X	0.52	0/665	0.75	0/895
26	Y	0.51	0/1147	0.72	0/1536
27	Z	0.68	0/585	0.71	0/781
28	1	0.55	0/438	0.73	0/578
29	2	0.45	0/401	0.70	0/529
30	3	0.56	0/771	0.67	0/1024
31	9	0.33	0/2904	0.69	1/4526 (0.0%)
All	All	0.44	1/98714 (0.0%)	0.70	16/147588 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	31
24	W	0	1
31	9	0	1
All	All	0	33

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	192	VAL	CB-CG1	-5.05	1.42	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	871	G	C5'-C4'-O4'	-7.01	100.69	109.10
1	0	2726	U	N1-C1'-C2'	5.93	121.71	114.00
1	0	1942	A	C5'-C4'-C3'	5.70	125.13	116.00
1	0	1504	A	C1'-O4'-C4'	-5.67	105.36	109.90
31	9	39	U	N1-C1'-C2'	5.64	121.34	114.00
1	0	1504	A	N9-C1'-C2'	5.62	121.30	114.00
21	T	52	ARG	N-CA-C	5.46	125.75	111.00
16	O	66	GLY	N-CA-C	5.40	126.60	113.10
1	0	2316	G	C5'-C4'-C3'	-5.27	107.57	116.00
1	0	129	A	C2'-C3'-O3'	5.25	122.11	113.70
1	0	1165	G	C5'-C4'-O4'	5.24	115.39	109.10
1	0	1120	U	C5'-C4'-C3'	-5.20	107.68	116.00
5	D	170	TYR	N-CA-C	5.11	124.81	111.00
24	W	4	LEU	CA-CB-CG	5.10	127.04	115.30
1	0	1819	G	C5'-C4'-C3'	5.07	124.12	116.00
5	D	137	PRO	N-CA-C	5.05	125.23	112.10

There are no chirality outliers.

All (33) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1078	A	Sidechain
1	0	1260	G	Sidechain
1	0	1635	U	Sidechain

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Mol	Chain	Res	Type	Group
1	0	1749	U	Sidechain
1	0	1819	G	Sidechain
1	0	1829	A	Sidechain
1	0	1848	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	1972	U	Sidechain
1	0	221	G	Sidechain
1	0	2308	U	Sidechain
1	0	2465	A	Sidechain
1	0	2493	C	Sidechain
1	0	2503	A	Sidechain
1	0	2607	U	Sidechain
1	0	2673	U	Sidechain
1	0	2842	G	Sidechain
1	0	333	G	Sidechain
1	0	396	U	Sidechain
1	0	458	G	Sidechain
1	0	471	G	Sidechain
1	0	482	G	Sidechain
1	0	518	G	Sidechain
1	0	619	U	Sidechain
1	0	625	U	Sidechain
1	0	722	G	Sidechain
1	0	815	U	Sidechain
1	0	817	G	Sidechain
1	0	818	A	Sidechain
1	0	867	A	Sidechain
31	9	90	G	Sidechain
24	W	90	TYR	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	59021	0	29812	1012	0
2	A	1754	0	1766	26	0
3	B	2625	0	2533	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	1860	0	1813	23	0
5	D	1094	0	1085	14	0
6	E	1358	0	1266	10	0
7	F	890	0	843	2	0
8	G	240	0	231	1	0
9	H	1282	0	1292	14	0
10	I	520	0	500	2	0
11	J	1120	0	1098	16	0
12	K	994	0	1027	12	0
13	L	1118	0	1076	9	0
14	M	1559	0	1573	15	0
15	N	1445	0	1401	14	0
16	O	865	0	873	8	0
17	P	1137	0	1123	12	0
18	Q	735	0	729	7	0
19	R	1150	0	1122	11	0
20	S	642	0	605	6	0
21	T	950	0	924	9	0
22	U	411	0	364	3	0
23	V	500	0	511	6	0
24	W	1196	0	1137	20	0
25	X	655	0	653	7	0
26	Y	1131	0	1133	12	0
27	Z	574	0	534	6	0
28	1	431	0	426	10	0
29	2	396	0	413	8	0
30	3	755	0	729	5	0
31	9	2599	0	1325	77	0
32	0	85	0	0	0	0
32	2	1	0	0	0	0
32	9	2	0	0	0	0
32	A	1	0	0	0	0
32	B	1	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	2	0	0	0	0
34	0	66	0	0	0	0
34	9	2	0	0	0	0
34	C	1	0	0	0	0
34	H	1	0	0	0	0
34	J	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	M	1	0	0	0	0
34	Q	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
35	0	9	0	0	0	0
35	3	1	0	0	0	0
35	A	1	0	0	0	0
35	B	1	0	0	0	0
35	J	3	0	0	1	0
35	K	1	0	0	1	0
35	L	1	0	0	0	0
35	M	1	0	0	0	0
35	N	1	0	0	0	0
35	O	1	0	0	0	0
35	R	1	0	0	0	0
35	Y	1	0	0	0	0
36	0	95	0	0	0	0
36	1	1	0	0	0	0
36	3	2	0	0	0	0
36	9	3	0	0	0	0
36	A	2	0	0	0	0
36	B	2	0	0	0	0
36	F	1	0	0	0	0
36	R	1	0	0	0	0
36	S	1	0	0	0	0
37	0	39	0	36	13	0
38	1	1	0	0	0	0
38	3	1	0	0	0	0
38	O	1	0	0	0	0
38	U	1	0	0	0	0
38	Z	1	0	0	0	0
39	0	5993	0	0	125	0
39	1	52	0	0	0	0
39	2	39	0	0	0	0
39	3	66	0	0	0	0
39	9	149	0	0	7	0
39	A	107	0	0	3	0
39	B	146	0	0	1	0
39	C	171	0	0	5	0
39	D	45	0	0	0	0
39	E	40	0	0	0	0
39	F	25	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	G	18	0	0	0	0
39	H	62	0	0	2	0
39	I	5	0	0	1	0
39	J	52	0	0	1	0
39	K	53	0	0	0	0
39	L	79	0	0	3	0
39	M	128	0	0	0	0
39	N	62	0	0	0	0
39	O	40	0	0	2	0
39	P	65	0	0	0	0
39	Q	43	0	0	0	0
39	R	77	0	0	1	0
39	S	28	0	0	0	0
39	T	32	0	0	0	0
39	U	27	0	0	0	0
39	V	12	0	0	0	0
39	W	65	0	0	1	0
39	X	20	0	0	0	0
39	Y	94	0	0	3	0
39	Z	28	0	0	1	0
All	All	99174	0	59953	1243	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 8.

All (1243) 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)
1:0:871:G:H8	1:0:871:G:H5'	1.10	1.15
1:0:1160:G:H5'	1:0:1161:A:H5'	1.26	1.12
1:0:871:G:C8	1:0:871:G:H5'	1.88	1.08
31:9:76:G:H3'	31:9:77:A:H5''	1.36	1.05
31:9:56:A:H2'	31:9:57:A:H5''	1.37	1.04
1:0:156:C:H5''	14:M:171:ARG:HD3	1.43	0.99
1:0:1701:A:H4'	1:0:1702:U:H5''	1.49	0.94
1:0:656:G:H5'	16:O:3:THR:HG22	1.48	0.94
1:0:542:A:H5'	1:0:542:A:H8	1.33	0.93
1:0:1242:A:H5'	11:J:82:THR:HG23	1.47	0.93
1:0:545:G:H8	1:0:545:G:H5'	1.31	0.93
1:0:2540:G:H4'	37:0:9101:WIN:H1O	1.50	0.91
1:0:870:G:H2'	1:0:871:G:H5''	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2717:C:C2'	1:0:2718:C:H5''	2.02	0.90
15:N:37:ARG:NH1	31:9:6:C:H5''	1.87	0.90
1:0:1666:C:C2'	1:0:1667:A:H5''	2.02	0.90
1:0:2506:A:HO2'	1:0:2507:G:H8	0.94	0.89
1:0:381:G:H5''	39:0:2945:HOH:O	1.74	0.86
12:K:10:GLN:H	12:K:10:GLN:HE21	1.18	0.86
1:0:1603:A:H5'	1:0:1605:G:O4'	1.74	0.86
17:P:115:SER:H	17:P:118:GLN:HE21	1.22	0.86
1:0:1474:C:H6	1:0:1474:C:H5'	1.40	0.85
1:0:2586:U:H3	1:0:2592:G:H22	1.22	0.85
1:0:1119:G:H2'	11:J:52:GLN:NE2	1.92	0.85
1:0:1160:G:C5'	1:0:1161:A:H5'	2.06	0.84
1:0:2812:A:H2	1:0:2814:A:H62	1.26	0.84
1:0:1160:G:H5'	1:0:1161:A:C5'	2.06	0.84
1:0:2717:C:H2'	1:0:2718:C:H5''	1.57	0.84
1:0:1372:A:H3'	39:0:6923:HOH:O	1.76	0.84
1:0:541:C:H2'	1:0:542:A:H5''	1.59	0.83
1:0:877:G:H5'	1:0:878:G:OP1	1.79	0.83
1:0:1205:U:H2'	1:0:1206:U:H5''	1.59	0.82
1:0:1593:C:H5'	17:P:116:SER:O	1.79	0.82
1:0:823:U:H3'	39:0:3123:HOH:O	1.78	0.82
1:0:2487:C:C2	37:0:9101:WIN:H1F	2.15	0.82
1:0:1666:C:H2'	1:0:1667:A:H5''	1.61	0.82
31:9:29:C:H2'	31:9:30:C:H5'	1.62	0.81
1:0:657:G:OP1	4:C:27:ARG:NH2	2.14	0.81
1:0:506:G:H22	1:0:509:A:C5'	1.94	0.81
31:9:56:A:C2'	31:9:57:A:H5''	2.11	0.81
1:0:506:G:H22	1:0:509:A:H5''	1.46	0.79
1:0:1118:A:H3'	1:0:1118:A:H8	1.47	0.79
1:0:500:G:H21	19:R:98:ASN:HD21	1.26	0.79
1:0:541:C:C2'	1:0:542:A:H5''	2.13	0.78
1:0:1205:U:H2'	1:0:1206:U:C5'	2.12	0.78
1:0:1835:U:H5	1:0:1840:A:N7	1.81	0.78
1:0:1118:A:H62	1:0:1244:U:H3	1.29	0.78
1:0:1118:A:H3'	1:0:1118:A:C8	2.19	0.77
1:0:2637:A:H5'	39:0:3948:HOH:O	1.84	0.77
1:0:157:G:H4'	14:M:95:LYS:HE2	1.66	0.77
1:0:1666:C:O2'	1:0:1667:A:H5''	1.83	0.77
1:0:871:G:H8	1:0:871:G:C5'	1.96	0.77
1:0:1300:G:H1'	39:0:3448:HOH:O	1.83	0.77
1:0:2756:U:H3	1:0:2896:A:H2	1.33	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1474:C:C6	1:0:1474:C:H5'	2.20	0.76
1:0:1684:A:H1'	29:2:43:ARG:HH22	1.49	0.76
1:0:2533:C:H5'	1:0:2533:C:H6	1.50	0.76
1:0:870:G:C2'	1:0:871:G:H5''	2.16	0.75
1:0:1116:U:HO2'	1:0:1118:A:H2	1.31	0.75
31:9:24:U:H3'	31:9:25:G:H5'	1.67	0.75
1:0:545:G:C8	1:0:545:G:H5'	2.17	0.75
1:0:681:G:N3	1:0:681:G:H5'	2.01	0.75
1:0:2506:A:O2'	1:0:2507:G:H8	1.70	0.75
1:0:1667:A:H8	1:0:1667:A:H5'	1.52	0.75
1:0:1701:A:H5'	39:0:5659:HOH:O	1.86	0.74
1:0:1116:U:H3	1:0:1246:A:H62	1.31	0.74
19:R:8:ALA:HB1	19:R:13:THR:HG21	1.70	0.74
31:9:73:A:H61	31:9:108:C:H42	1.33	0.74
31:9:92:G:H2'	31:9:93:A:C8	2.22	0.73
21:T:24:ARG:HH21	21:T:39:ASN:HD22	1.35	0.73
1:0:1666:C:H2'	1:0:1667:A:C5'	2.18	0.73
1:0:2005:G:H3'	1:0:2005:G:OP2	1.89	0.73
1:0:1206:U:H6	1:0:1206:U:H5'	1.54	0.73
1:0:2420:G:O2'	1:0:2421:G:H5'	1.89	0.73
1:0:281:U:H2'	1:0:282:C:O4'	1.89	0.72
1:0:2717:C:O2'	1:0:2718:C:H5''	1.89	0.72
1:0:182:G:H5'	39:0:4102:HOH:O	1.90	0.72
1:0:559:U:H5'	1:0:559:U:H6	1.55	0.71
1:0:2291:A:C8	1:0:2309:C:H5'	2.25	0.71
1:0:2578:G:H5'	1:0:2578:G:H8	1.55	0.71
1:0:544:G:H2'	1:0:545:G:H5''	1.73	0.71
31:9:14:G:H5'	31:9:14:G:H8	1.56	0.70
1:0:12:U:H2'	1:0:13:G:H5'	1.74	0.70
1:0:1116:U:O2'	1:0:1118:A:H2	1.74	0.69
1:0:1701:A:H4'	1:0:1702:U:C5'	2.21	0.69
1:0:541:C:H2'	1:0:542:A:C5'	2.22	0.69
1:0:1278:A:H4'	1:0:1279:U:C4	2.28	0.69
1:0:2635:A:O2'	1:0:2636:C:H5'	1.93	0.69
1:0:450:C:OP1	4:C:184:ARG:NH2	2.24	0.69
1:0:542:A:H5'	1:0:542:A:C8	2.22	0.69
1:0:853:C:H3'	39:0:3276:HOH:O	1.91	0.69
1:0:1834:C:H2'	1:0:1840:A:N6	2.07	0.68
1:0:93:C:H5''	23:V:1:THR:HB	1.74	0.68
1:0:603:A:H5''	1:0:604:G:OP1	1.93	0.68
1:0:2769:C:C2'	1:0:2770:G:H5'	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2502:C:H2'	1:0:2503:A:H5'	1.76	0.68
1:0:2768:A:H2'	1:0:2769:C:O4'	1.93	0.67
1:0:1189:A:H1'	1:0:1209:C:O4'	1.94	0.67
1:0:2716:G:H5''	3:B:206:THR:HG21	1.74	0.67
1:0:1119:G:H2'	11:J:52:GLN:HE22	1.58	0.67
3:B:238:ASN:HD22	3:B:240:GLY:H	1.43	0.67
1:0:1632:A:H2'	1:0:1633:C:H5'	1.76	0.67
1:0:2502:C:C2'	1:0:2503:A:H5'	2.25	0.67
3:B:221:GLN:HE22	12:K:42:ASN:HD22	1.41	0.67
1:0:1119:G:N2	1:0:1246:A:C2	2.60	0.67
1:0:20:G:H21	19:R:117:HIS:HD2	1.41	0.66
1:0:1625:U:H4'	39:0:3427:HOH:O	1.94	0.66
1:0:1189:A:H1'	1:0:1209:C:C1'	2.24	0.66
1:0:188:C:H5''	14:M:163:LEU:HD21	1.77	0.66
1:0:1377:C:H6	1:0:1377:C:H5'	1.61	0.66
1:0:2908:A:H2'	1:0:2909:G:O4'	1.96	0.66
39:0:4058:HOH:O	35:K:8812:CL:CL	2.50	0.65
1:0:2443:C:H1'	13:L:56:LYS:HE3	1.76	0.65
1:0:2468:A:H61	30:3:48:ASN:HD21	1.44	0.65
1:0:2320:U:H4'	1:0:2321:A:O4'	1.97	0.65
15:N:141:ARG:HH21	31:9:48:C:H4'	1.59	0.65
1:0:671:A:O2'	1:0:672:G:H2'	1.97	0.65
1:0:2710:U:H1'	39:0:7520:HOH:O	1.96	0.65
31:9:49:G:O2'	31:9:50:G:H5'	1.97	0.65
1:0:1973:A:H2'	1:0:1974:G:O4'	1.96	0.65
25:X:37:LEU:HD13	25:X:85:VAL:HG21	1.79	0.65
1:0:308:U:H5'	1:0:309:C:OP1	1.96	0.65
1:0:821:U:H2'	1:0:822:C:H6	1.61	0.65
1:0:544:G:C2'	1:0:545:G:H5''	2.27	0.64
31:9:39:U:H1'	31:9:44:A:H61	1.61	0.64
24:W:137:GLN:HE21	24:W:141:HIS:HE1	1.45	0.64
1:0:871:G:C8	1:0:871:G:C5'	2.74	0.64
1:0:136:C:H2'	1:0:137:U:O4'	1.97	0.64
1:0:1181:A:H2'	1:0:1182:C:H5'	1.78	0.64
1:0:1184:C:H1'	39:0:7308:HOH:O	1.98	0.64
31:9:75:G:H1	31:9:106:U:H3	1.45	0.64
31:9:3:A:N6	31:9:22:G:H1'	2.13	0.64
1:0:1947:G:H2'	1:0:1948:G:H8	1.63	0.64
1:0:1183:C:N4	1:0:1184:C:H41	1.94	0.64
1:0:2827:A:H2'	1:0:2828:G:O4'	1.97	0.64
1:0:2787:C:H5	39:0:3383:HOH:O	1.81	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:3:2:GLN:HE21	30:3:91:GLN:HE21	1.45	0.63
1:0:371:U:H2'	1:0:372:A:H8	1.63	0.63
1:0:1641:A:H2'	1:0:1642:A:H5'	1.80	0.63
1:0:2491:G:H1'	39:0:6473:HOH:O	1.97	0.63
1:0:1166:A:H1'	1:0:1192:A:C2	2.33	0.63
1:0:1165:G:H4'	1:0:1174:A:O2'	1.99	0.63
31:9:7:G:H5'	39:9:5071:HOH:O	1.98	0.63
1:0:2896:A:H5''	39:0:5399:HOH:O	1.99	0.62
14:M:164:THR:HG22	14:M:166:ALA:H	1.63	0.62
1:0:2533:C:C6	1:0:2533:C:H5'	2.33	0.62
39:0:4183:HOH:O	12:K:39:GLY:HA2	1.99	0.62
1:0:482:G:H4'	1:0:508:A:N1	2.15	0.62
1:0:272:A:H5'	1:0:273:G:OP2	1.99	0.62
1:0:2419:U:H5''	1:0:2420:G:H5'	1.81	0.62
1:0:1835:U:C5	1:0:1840:A:N7	2.67	0.62
1:0:1886:A:H4'	39:Z:395:HOH:O	1.99	0.62
15:N:141:ARG:NH2	31:9:48:C:H4'	2.15	0.62
1:0:1762:C:H2'	1:0:1763:C:H6	1.64	0.62
1:0:2748:G:H2'	39:0:7410:HOH:O	2.00	0.62
1:0:2486:A:H3'	39:0:3735:HOH:O	1.99	0.62
31:9:1:U:H4'	31:9:3:A:OP1	1.99	0.61
1:0:1800:G:H1'	17:P:88:GLN:NE2	2.15	0.61
1:0:1819:G:H5'	39:0:3491:HOH:O	1.99	0.61
24:W:4:LEU:HD23	24:W:54:PHE:HB3	1.81	0.61
1:0:2401:A:H2'	1:0:2402:A:C8	2.35	0.61
1:0:285:A:H2'	1:0:286:U:O4'	2.00	0.61
1:0:440:C:H2'	1:0:441:A:C8	2.36	0.61
1:0:56:G:H5''	23:V:50:ARG:NH1	2.15	0.61
16:O:32:ARG:HE	16:O:35:LYS:HD2	1.66	0.61
1:0:1741:U:H5'	1:0:1742:A:OP1	2.00	0.61
31:9:76:G:H3'	31:9:77:A:C5'	2.22	0.61
1:0:282:C:H1'	1:0:368:C:N4	2.15	0.61
1:0:820:G:H3'	39:0:6936:HOH:O	2.01	0.61
1:0:656:G:H1'	39:C:7042:HOH:O	2.00	0.60
1:0:1201:C:H5''	39:0:5584:HOH:O	1.99	0.60
24:W:88:THR:HG23	24:W:110:GLN:HB3	1.83	0.60
1:0:1528:A:H2'	1:0:1529:G:O4'	2.00	0.60
1:0:553:G:P	26:Y:204:ARG:HH22	2.24	0.60
1:0:1015:C:H2'	1:0:1016:U:H6	1.66	0.60
1:0:1097:A:H5''	24:W:125:HIS:NE2	2.16	0.60
1:0:558:C:C2'	1:0:559:U:H5''	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1187:U:O2'	1:0:1189:A:H2	1.83	0.60
1:0:1213:C:O2'	1:0:1214:G:H5'	2.02	0.60
1:0:2054:A:N3	19:R:128:ARG:NH2	2.49	0.60
1:0:1189:A:H3'	39:0:7609:HOH:O	2.02	0.60
1:0:1209:C:H2'	1:0:1210:G:H8	1.65	0.60
31:9:12:C:H5'	31:9:70:U:O4'	2.00	0.60
1:0:2472:C:O2'	1:0:2634:G:H4'	2.01	0.60
31:9:24:U:H3'	31:9:25:G:C5'	2.31	0.60
1:0:814:G:H4'	39:0:7240:HOH:O	2.01	0.60
15:N:11:ARG:HD3	31:9:114:G:O6	2.02	0.59
1:0:2426:G:H1'	39:0:5391:HOH:O	2.01	0.59
1:0:1972:U:H2'	1:0:1973:A:H5'	1.85	0.59
1:0:1166:A:H61	1:0:1180:U:H3	1.50	0.59
1:0:2563:U:H2'	1:0:2565:C:O5'	2.02	0.59
1:0:282:C:O2'	1:0:283:U:H5'	2.02	0.59
1:0:399:C:H5'	14:M:179:GLY:O	2.03	0.59
7:F:91:VAL:HG12	7:F:92:GLY:H	1.68	0.59
1:0:1120:U:H5''	1:0:1120:U:C6	2.38	0.59
1:0:338:C:H4'	4:C:174:ILE:CD1	2.32	0.59
4:C:127:ARG:NH2	4:C:225:PRO:HG2	2.18	0.59
1:0:2712:G:H5'	39:0:4183:HOH:O	2.02	0.59
1:0:2851:G:O2'	1:0:2852:A:H5'	2.03	0.59
31:9:13:A:O2'	31:9:14:G:H5''	2.02	0.58
1:0:2616:G:H1'	39:0:8327:HOH:O	2.03	0.58
1:0:2781:U:H1'	6:E:139:GLU:OE2	2.03	0.58
31:9:39:U:H3'	31:9:40:C:H5''	1.85	0.58
1:0:56:G:H5''	23:V:50:ARG:HH12	1.67	0.58
1:0:2252:A:C5	1:0:2253:G:H1'	2.38	0.58
1:0:1446:U:H2'	20:S:55:GLN:NE2	2.17	0.58
1:0:558:C:O2'	1:0:559:U:H5''	2.03	0.58
1:0:1189:A:H1'	1:0:1209:C:H1'	1.84	0.58
1:0:2241:C:H2'	1:0:2242:U:C6	2.38	0.58
1:0:2270:G:H4'	2:A:223:ARG:NH1	2.18	0.58
1:0:2721:U:H4'	12:K:87:ARG:HG3	1.83	0.58
1:0:1328:A:OP1	26:Y:169:ARG:HD2	2.03	0.58
1:0:1363:G:P	4:C:76:ARG:HH22	2.26	0.58
1:0:821:U:H2'	1:0:822:C:C6	2.39	0.58
1:0:902:G:N7	13:L:18:HIS:HD2	2.02	0.58
1:0:1165:G:H1'	1:0:1174:A:H1'	1.85	0.58
1:0:67:A:H5''	1:0:69:A:C8	2.39	0.58
1:0:960:G:H4'	39:0:7253:HOH:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1790:C:H2'	1:0:1791:U:H6	1.68	0.58
1:0:1441:G:O2'	1:0:1442:A:H5'	2.04	0.58
1:0:1679:C:H5'	39:0:4173:HOH:O	2.04	0.58
1:0:2524:G:H21	1:0:2526:C:N4	2.02	0.58
1:0:2783:A:H3'	39:0:4201:HOH:O	2.03	0.58
24:W:137:GLN:HE21	24:W:141:HIS:CE1	2.21	0.58
29:2:40:ARG:HD2	29:2:47:THR:HG22	1.84	0.58
1:0:1973:A:H5'	1:0:1973:A:H8	1.68	0.57
1:0:2894:C:O2'	1:0:2895:C:H5'	2.04	0.57
1:0:952:G:N3	1:0:2302:A:H2'	2.19	0.57
3:B:36:PRO:HG3	3:B:169:GLY:H	1.68	0.57
22:U:39:ASN:ND2	22:U:44:ARG:HH11	2.02	0.57
1:0:1118:A:C8	1:0:1118:A:C3'	2.83	0.57
1:0:2670:G:O2'	1:0:2671:U:H5'	2.03	0.57
1:0:1733:A:H4'	3:B:212:GLN:HA	1.85	0.57
1:0:1419:U:H2'	1:0:1685:A:C2	2.39	0.57
1:0:2769:C:H2'	1:0:2770:G:O4'	2.04	0.57
1:0:2769:C:H2'	1:0:2770:G:H5'	1.85	0.57
1:0:407:A:H5'	39:0:5296:HOH:O	2.04	0.57
31:9:14:G:H5'	31:9:14:G:C8	2.38	0.57
1:0:2769:C:O2'	1:0:2770:G:H5'	2.04	0.57
1:0:1441:G:H1'	39:0:7717:HOH:O	2.03	0.57
5:D:154:LYS:HD2	5:D:154:LYS:H	1.69	0.57
5:D:140:ARG:HB3	31:9:29:C:H5"	1.86	0.57
1:0:1994:A:P	12:K:66:ARG:HH22	2.28	0.57
31:9:55:U:H4'	31:9:56:A:C8	2.39	0.57
1:0:1015:C:H2'	1:0:1016:U:C6	2.40	0.57
1:0:1838:U:O2'	1:0:2644:C:H5'	2.05	0.57
1:0:2780:C:H1'	6:E:143:GLN:HE21	1.69	0.57
1:0:1166:A:P	1:0:1174:A:H4'	2.44	0.57
1:0:1819:G:H2'	1:0:1820:G:H4'	1.86	0.57
1:0:68:U:O2'	1:0:69:A:H5"	2.05	0.57
1:0:2365:G:H4'	18:Q:45:PRO:O	2.05	0.57
1:0:1667:A:C8	1:0:1667:A:H5'	2.37	0.57
1:0:2781:U:O2'	1:0:2782:G:H5'	2.04	0.57
1:0:1008:C:H5"	9:H:19:ARG:HH12	1.68	0.57
1:0:2900:G:H2'	1:0:2901:C:O4'	2.05	0.56
17:P:115:SER:H	17:P:118:GLN:NE2	1.99	0.56
1:0:1132:A:N6	1:0:1229:C:H2'	2.20	0.56
1:0:625:U:H3'	39:0:7631:HOH:O	2.04	0.56
1:0:969:G:H1	1:0:999:C:H42	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2534:C:H1'	39:0:8179:HOH:O	2.04	0.56
1:0:65:C:O2'	1:0:66:G:H5'	2.04	0.56
1:0:119:A:H2'	1:0:120:A:H5''	1.86	0.56
1:0:794:U:H3	1:0:819:A:H61	1.54	0.56
1:0:560:U:H2'	1:0:561:G:H8	1.69	0.56
1:0:95:A:H5''	1:0:97:G:O4'	2.05	0.56
31:9:38:A:H2'	31:9:39:U:C6	2.41	0.56
1:0:69:A:H5'	1:0:69:A:H8	1.69	0.56
25:X:61:ARG:HH12	25:X:67:PRO:HD3	1.70	0.56
1:0:2755:G:H1'	39:0:3447:HOH:O	2.06	0.56
1:0:797:A:N6	1:0:816:G:H1'	2.20	0.56
1:0:1279:U:O2	1:0:1279:U:H2'	2.05	0.56
1:0:2032:U:H5'	39:0:3222:HOH:O	2.04	0.56
5:D:103:ASN:HD22	5:D:134:LEU:H	1.54	0.56
1:0:2760:C:H5''	39:0:4329:HOH:O	2.06	0.56
1:0:2756:U:N3	1:0:2896:A:H2	2.02	0.56
15:N:144:GLY:O	15:N:147:ILE:HG22	2.05	0.56
1:0:1634:G:H3'	39:0:8650:HOH:O	2.06	0.56
1:0:441:A:H1'	1:0:442:A:N7	2.21	0.55
1:0:162:C:H2'	1:0:163:U:H5'	1.88	0.55
1:0:1845:A:OP2	2:A:190:ARG:NH1	2.39	0.55
1:0:731:U:H2'	1:0:732:C:C6	2.41	0.55
1:0:1205:U:C2'	1:0:1206:U:H5''	2.34	0.55
4:C:139:VAL:HG13	39:C:6251:HOH:O	2.06	0.55
1:0:1330:A:H5''	39:Y:7277:HOH:O	2.06	0.55
1:0:613:C:H2'	1:0:614:U:H6	1.71	0.55
1:0:196:G:H2'	39:0:6170:HOH:O	2.05	0.55
1:0:2769:C:H2'	1:0:2770:G:C5'	2.36	0.55
1:0:2597:U:H1'	39:0:4058:HOH:O	2.05	0.55
31:9:55:U:H4'	31:9:56:A:H8	1.71	0.55
31:9:29:C:C2'	31:9:30:C:H5'	2.33	0.55
1:0:1654:U:H2'	2:A:47:HIS:HD2	1.71	0.55
1:0:1422:U:H2'	1:0:1423:C:C6	2.41	0.55
1:0:1497:G:H4'	1:0:1627:G:O2'	2.07	0.55
1:0:1701:A:H5''	1:0:1702:U:H3'	1.88	0.55
5:D:76:ARG:NH2	31:9:44:A:H1'	2.21	0.55
31:9:95:C:O2'	31:9:96:C:H5'	2.06	0.55
1:0:317:A:OP1	21:T:52:ARG:O	2.24	0.55
1:0:776:A:OP1	28:1:28:HIS:HE1	1.89	0.55
1:0:306:A:P	21:T:38:ARG:HH21	2.30	0.55
1:0:31:C:H2'	39:0:7619:HOH:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:559:U:H5'	1:0:559:U:C6	2.40	0.55
1:0:1182:C:H1'	1:0:1192:A:H8	1.71	0.55
1:0:371:U:H2'	1:0:372:A:C8	2.42	0.55
9:H:72:ALA:HB2	9:H:156:ALA:HB2	1.87	0.55
1:0:468:U:H3'	39:0:7448:HOH:O	2.05	0.55
1:0:2509:A:H2'	1:0:2510:C:O4'	2.07	0.55
9:H:59:GLN:HE21	9:H:129:ARG:HE	1.55	0.55
1:0:2613:G:O2'	1:0:2614:C:H5'	2.07	0.55
4:C:162:VAL:HG22	4:C:232:LEU:HD21	1.89	0.55
1:0:1364:G:H1'	39:0:3619:HOH:O	2.06	0.55
1:0:1118:A:H8	1:0:1119:G:H5''	1.71	0.55
1:0:1632:A:C2'	1:0:1633:C:H5'	2.37	0.55
1:0:1173:A:H4'	1:0:1174:A:C8	2.41	0.55
1:0:588:G:O6	24:W:154:ARG:NH1	2.40	0.55
1:0:625:U:H5''	1:0:1044:C:N4	2.22	0.55
1:0:2050:G:H5''	19:R:80:TYR:O	2.06	0.55
1:0:1741:U:O2'	1:0:2723:G:H4'	2.07	0.54
1:0:1527:A:H1'	1:0:1528:A:C8	2.42	0.54
11:J:41:ALA:HB3	39:J:5907:HOH:O	2.06	0.54
1:0:1979:G:H2'	39:0:3969:HOH:O	2.07	0.54
1:0:2064:U:H5'	1:0:2652:U:H4'	1.89	0.54
16:O:38:ARG:NH1	39:O:7674:HOH:O	2.40	0.54
1:0:69:A:H5'	1:0:69:A:C8	2.43	0.54
1:0:1677:U:OP2	29:2:8:LYS:NZ	2.39	0.54
2:A:48:ASP:HB3	39:A:5706:HOH:O	2.07	0.54
1:0:121:U:OP2	29:2:10:ARG:NH2	2.38	0.54
24:W:21:LEU:HD21	24:W:48:VAL:HG11	1.89	0.54
1:0:841:A:H5''	39:0:6534:HOH:O	2.07	0.54
1:0:1191:A:H2	1:0:1206:U:H3	1.56	0.54
1:0:1790:C:H2'	1:0:1791:U:C6	2.42	0.54
1:0:1855:G:H4'	1:0:1856:C:O5'	2.07	0.54
1:0:128:A:O2'	1:0:129:A:H5'	2.07	0.54
31:9:92:G:H2'	31:9:93:A:H8	1.70	0.54
1:0:2524:G:H21	1:0:2526:C:H41	1.56	0.54
1:0:1787:C:H4'	1:0:2883:A:O4'	2.07	0.54
1:0:836:G:H5''	39:0:3971:HOH:O	2.07	0.54
1:0:2435:U:H1'	39:0:4462:HOH:O	2.07	0.54
1:0:1053:G:OP1	9:H:15:PRO:HG3	2.08	0.54
1:0:2672:C:H1'	39:0:6210:HOH:O	2.07	0.54
1:0:1762:C:H2'	1:0:1763:C:C6	2.43	0.54
1:0:2505:G:O2'	1:0:2506:A:H5'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2779:G:H21	6:E:143:GLN:NE2	2.06	0.54
1:0:1594:C:O2'	1:0:1607:A:H4'	2.08	0.54
1:0:2414:A:H2'	1:0:2415:A:C8	2.42	0.54
1:0:90:A:H2'	1:0:91:G:O4'	2.08	0.54
1:0:10:U:O4	1:0:532:A:OP2	2.25	0.54
1:0:2878:U:H2'	1:0:2879:A:O4'	2.08	0.54
37:0:9101:WIN:H1FB	37:0:9101:WIN:H1OA	1.89	0.53
1:0:506:G:H22	1:0:509:A:H5'	1.69	0.53
1:0:1921:A:O2'	1:0:1922:A:H5'	2.07	0.53
29:2:41:HIS:H	29:2:45:ASN:HD22	1.56	0.53
1:0:1206:U:H2'	1:0:1207:A:O4'	2.08	0.53
1:0:1972:U:H2'	1:0:1973:A:C5'	2.39	0.53
1:0:2700:G:H3'	39:0:8266:HOH:O	2.08	0.53
1:0:694:A:H2'	1:0:695:C:H5'	1.90	0.53
2:A:121:ALA:O	2:A:124:VAL:HG22	2.08	0.53
6:E:95:VAL:HG11	6:E:131:LEU:HD11	1.90	0.53
1:0:2487:C:C6	37:0:9101:WIN:O1K	2.61	0.53
1:0:1119:G:H8	11:J:52:GLN:HE22	1.55	0.53
20:S:33:SER:O	20:S:37:VAL:HG23	2.07	0.53
31:9:64:C:H2'	31:9:65:A:H5'	1.91	0.53
1:0:445:U:H2'	1:0:446:G:H8	1.72	0.53
1:0:1119:G:H22	1:0:1246:A:H2	1.51	0.53
31:9:23:U:O2'	31:9:24:U:H4'	2.09	0.53
1:0:558:C:H2'	1:0:559:U:C5'	2.38	0.53
5:D:103:ASN:ND2	5:D:134:LEU:H	2.07	0.53
1:0:87:C:H2'	29:2:28:LYS:O	2.08	0.53
1:0:1477:C:H5'	1:0:1868:G:C5'	2.38	0.53
1:0:2445:U:H2'	1:0:2446:G:C8	2.43	0.53
1:0:316:A:N3	1:0:336:G:O2'	2.38	0.53
2:A:179:MET:HG2	2:A:186:TRP:HB2	1.91	0.53
1:0:1947:G:H2'	1:0:1948:G:C8	2.43	0.53
1:0:2111:G:H1'	39:0:3082:HOH:O	2.07	0.53
1:0:2344:G:N3	1:0:2344:G:H2'	2.23	0.53
31:9:2:U:OP2	31:9:3:A:H5'	2.08	0.53
1:0:1878:G:O2'	1:0:1879:U:OP2	2.27	0.53
1:0:1299:G:O6	13:L:6:ARG:HD3	2.08	0.53
1:0:635:A:H2'	1:0:636:G:H5''	1.90	0.53
1:0:447:A:O2'	1:0:448:G:H5'	2.09	0.53
1:0:848:C:H5'	39:0:7034:HOH:O	2.09	0.53
1:0:2795:C:O2'	1:0:2796:U:H5'	2.09	0.53
1:0:947:U:O2'	1:0:948:G:H5'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:71:C:H2'	31:9:72:C:H6	1.74	0.53
1:0:407:A:H2'	1:0:408:A:C8	2.44	0.53
1:0:450:C:H4'	4:C:46:TYR:CE1	2.43	0.52
1:0:1803:C:H2'	1:0:1804:A:C8	2.44	0.52
1:0:195:C:H2'	1:0:196:G:H5'	1.90	0.52
13:L:136:ALA:HB3	39:L:6166:HOH:O	2.07	0.52
1:0:1603:A:H5''	1:0:1605:G:H5'	1.91	0.52
1:0:1181:A:C2'	1:0:1182:C:H5'	2.39	0.52
1:0:2364:A:H5''	18:Q:15:LYS:HD3	1.91	0.52
1:0:2387:U:H2'	1:0:2388:C:C6	2.44	0.52
6:E:137:ASP:O	6:E:141:VAL:HG23	2.10	0.52
1:0:1375:A:C2'	1:0:1376:G:H5'	2.39	0.52
1:0:2103:A:H2'	1:0:2104:C:H5'	1.90	0.52
1:0:1180:U:H4'	10:I:86:GLU:HG2	1.91	0.52
39:0:6217:HOH:O	21:T:38:ARG:NH1	2.42	0.52
1:0:1268:C:H2'	1:0:1269:G:H8	1.74	0.52
1:0:790:A:H1'	1:0:1710:A:H2'	1.91	0.52
1:0:2039:A:OP2	3:B:234:ARG:NH2	2.43	0.52
1:0:1427:A:H61	1:0:1440:U:H1'	1.73	0.52
31:9:34:A:H2'	31:9:35:C:O4'	2.10	0.52
1:0:1333:U:H2'	1:0:1334:C:C6	2.44	0.52
1:0:247:A:H2'	39:0:8680:HOH:O	2.09	0.52
37:0:9101:WIN:H1A	37:0:9101:WIN:H1BA	1.92	0.52
1:0:10:U:O4	1:0:531:G:H2'	2.10	0.52
11:J:127:ILE:HG22	35:J:8801:CL:CL	2.46	0.52
30:3:25:VAL:HG22	30:3:68:LYS:HG3	1.91	0.52
1:0:522:U:O2'	1:0:1366:C:H5'	2.09	0.52
3:B:217:ARG:HG3	3:B:257:THR:HG22	1.92	0.52
28:1:8:GLN:HE22	28:1:11:LYS:NZ	2.08	0.52
1:0:1596:U:H2'	1:0:1598:A:OP2	2.10	0.52
1:0:2542:C:H1'	39:0:6378:HOH:O	2.08	0.52
1:0:303:C:H2'	1:0:304:G:O4'	2.10	0.52
1:0:2717:C:H2'	1:0:2718:C:C5'	2.34	0.52
1:0:821:U:H3'	39:0:8455:HOH:O	2.10	0.52
1:0:2248:C:H3'	39:0:4476:HOH:O	2.10	0.52
1:0:2256:G:O2'	1:0:2257:G:H5'	2.10	0.52
1:0:1060:C:H6	1:0:1060:C:H5'	1.75	0.52
1:0:1167:G:H2'	1:0:1168:C:C6	2.45	0.52
3:B:221:GLN:HE22	12:K:42:ASN:ND2	2.08	0.52
30:3:2:GLN:HE21	30:3:91:GLN:NE2	2.07	0.52
1:0:249:G:O2'	1:0:250:C:H5'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:141:VAL:HG21	31:9:57:A:H8	1.75	0.51
1:0:564:G:H1'	39:0:5694:HOH:O	2.10	0.51
1:0:1928:C:H2'	1:0:1929:G:O4'	2.10	0.51
1:0:2584:G:H4'	39:0:6824:HOH:O	2.09	0.51
1:0:1175:G:H1'	1:0:1193:A:H2'	1.92	0.51
1:0:1940:C:H4'	39:0:7130:HOH:O	2.10	0.51
4:C:118:THR:O	4:C:136:VAL:HG13	2.09	0.51
13:L:143:THR:HG22	13:L:144:ASP:H	1.75	0.51
1:0:497:A:H2'	1:0:498:A:C5'	2.40	0.51
1:0:1444:G:H5''	20:S:11:THR:HG22	1.92	0.51
1:0:1313:A:H5'	26:Y:208:LYS:O	2.10	0.51
1:0:1205:U:H2'	1:0:1206:U:H5'	1.91	0.51
1:0:2271:G:N3	1:0:2271:G:H2'	2.24	0.51
1:0:2271:G:H5'	39:A:3548:HOH:O	2.09	0.51
1:0:154:C:H2'	1:0:155:C:H6	1.76	0.51
1:0:905:C:H3'	39:0:4139:HOH:O	2.10	0.51
1:0:105:G:O2'	1:0:106:A:H5'	2.11	0.51
1:0:1183:C:H41	1:0:1192:A:P	2.34	0.51
1:0:2597:U:H2'	1:0:2598:U:H5'	1.91	0.51
1:0:200:C:H2'	39:0:8130:HOH:O	2.11	0.51
1:0:1010:C:H4'	15:N:4:PRO:HB2	1.93	0.51
1:0:1856:C:H5'	1:0:1858:A:O4'	2.11	0.51
1:0:1299:G:N7	13:L:6:ARG:NH1	2.59	0.51
1:0:2088:C:H1'	1:0:2841:A:N1	2.26	0.51
14:M:99:ARG:HD2	14:M:167:GLY:HA2	1.93	0.51
1:0:958:G:H2'	1:0:959:C:C6	2.45	0.51
1:0:1566:C:H2'	1:0:1567:G:C8	2.46	0.51
1:0:2353:A:H4'	1:0:2354:A:O5'	2.10	0.51
1:0:1029:U:O2'	1:0:1273:C:OP1	2.26	0.51
27:Z:60:ASP:HB3	27:Z:69:ASP:HB3	1.93	0.51
1:0:2510:C:H42	1:0:2564:G:H22	1.58	0.51
1:0:1634:G:H2'	1:0:1635:U:C6	2.46	0.51
24:W:64:THR:O	24:W:68:THR:HG22	2.11	0.51
1:0:1391:G:H2'	1:0:1392:A:H5'	1.93	0.51
1:0:527:U:H2'	1:0:528:G:C8	2.46	0.51
1:0:364:U:H2'	1:0:365:G:O4'	2.11	0.51
1:0:1234:U:N3	3:B:244:PRO:HB3	2.25	0.50
1:0:1636:G:O2'	1:0:1637:A:H5'	2.10	0.50
1:0:1603:A:C5'	1:0:1605:G:H5'	2.41	0.50
31:9:90:G:H3'	39:9:2357:HOH:O	2.10	0.50
1:0:1755:A:H2'	1:0:1756:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:17:ASP:HB3	20:S:23:LYS:HB2	1.93	0.50
1:0:1130:U:H4'	39:0:5437:HOH:O	2.11	0.50
2:A:199:HIS:HD2	2:A:201:PHE:H	1.59	0.50
1:0:1118:A:C8	1:0:1119:G:H5''	2.45	0.50
7:F:2:VAL:HG22	7:F:57:GLU:OE1	2.11	0.50
1:0:1525:G:H5'	1:0:1526:A:OP2	2.11	0.50
1:0:2002:C:H2'	1:0:2003:U:H5'	1.94	0.50
1:0:1864:C:C5	14:M:75:ARG:NH1	2.79	0.50
1:0:1980:U:O2	1:0:2008:U:H4'	2.10	0.50
1:0:280:C:H2'	1:0:281:U:O4'	2.11	0.50
1:0:10:U:H6	1:0:10:U:H3'	1.76	0.50
1:0:1189:A:O2'	1:0:1208:C:H2'	2.12	0.50
1:0:1413:A:H2'	1:0:1414:A:O4'	2.12	0.50
1:0:324:G:O2'	1:0:325:U:H5'	2.12	0.50
1:0:899:C:H5'	39:0:7471:HOH:O	2.11	0.50
1:0:656:G:H5'	16:O:3:THR:CG2	2.33	0.50
1:0:2467:A:O2'	1:0:2468:A:H2'	2.11	0.50
1:0:441:A:H8	1:0:441:A:O5'	1.95	0.50
1:0:338:C:H4'	4:C:174:ILE:HD11	1.94	0.50
1:0:1566:C:H2'	1:0:1567:G:H8	1.76	0.50
1:0:485:A:N3	1:0:487:G:H5''	2.27	0.50
1:0:1406:A:H4'	1:0:1407:A:H5''	1.92	0.50
1:0:2081:A:H4'	11:J:69:TYR:CE1	2.47	0.50
1:0:1116:U:O2'	1:0:1118:A:C2	2.50	0.50
1:0:380:A:H2'	39:0:6974:HOH:O	2.11	0.50
1:0:1066:U:H2'	1:0:1067:A:C8	2.47	0.50
1:0:2659:U:H5''	39:0:8896:HOH:O	2.11	0.50
1:0:2511:A:H2'	1:0:2512:U:O4'	2.12	0.50
1:0:1377:C:H5'	1:0:1377:C:C6	2.45	0.50
1:0:2898:G:H4'	3:B:288:GLY:HA2	1.94	0.50
1:0:2135:A:O2'	1:0:2136:G:H5'	2.12	0.50
1:0:969:G:H1	1:0:999:C:N4	2.10	0.49
1:0:1878:G:H1'	39:0:5431:HOH:O	2.12	0.49
1:0:1864:C:H5	14:M:75:ARG:NH1	2.10	0.49
1:0:2703:A:H2'	1:0:2704:C:H6	1.77	0.49
1:0:536:A:H3'	39:0:3958:HOH:O	2.11	0.49
1:0:1589:G:H22	1:0:1605:G:H1'	1.77	0.49
1:0:319:A:H4'	1:0:338:C:C5	2.47	0.49
1:0:2415:A:H2'	1:0:2416:G:H5'	1.93	0.49
1:0:920:C:H4'	1:0:921:G:C2	2.47	0.49
1:0:2345:A:H3'	1:0:2346:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:711:G:H1'	39:0:6793:HOH:O	2.11	0.49
1:0:170:U:H2'	1:0:171:C:H5'	1.94	0.49
1:0:21:G:H4'	19:R:2:ILE:HG22	1.93	0.49
1:0:1644:C:H2'	1:0:1645:U:H6	1.77	0.49
31:9:114:G:H2'	31:9:115:C:C6	2.48	0.49
1:0:941:G:C5	1:0:942:U:C4	3.00	0.49
1:0:1307:A:H2'	1:0:1308:A:C8	2.47	0.49
1:0:2521:A:OP2	9:H:6:ALA:HB3	2.11	0.49
1:0:857:A:H4'	2:A:176:HIS:CD2	2.46	0.49
1:0:459:A:H4'	39:0:4687:HOH:O	2.12	0.49
13:L:138:GLY:HA3	39:L:4360:HOH:O	2.11	0.49
1:0:500:G:H21	19:R:98:ASN:ND2	2.05	0.49
1:0:2720:C:O2	12:K:87:ARG:NH2	2.45	0.49
1:0:797:A:H61	1:0:816:G:H1'	1.77	0.49
1:0:451:C:O2'	1:0:452:G:H5'	2.12	0.49
1:0:2103:A:N6	37:0:9101:WIN:O1G	2.41	0.49
1:0:2538:A:H1'	37:0:9101:WIN:O1M	2.12	0.49
1:0:2578:G:C8	1:0:2578:G:H5'	2.43	0.49
1:0:2781:U:C2'	1:0:2782:G:H5'	2.42	0.49
1:0:1115:U:O2'	1:0:1116:U:H5'	2.11	0.49
1:0:2807:U:P	3:B:27:ASN:HD21	2.34	0.49
1:0:1172:G:H5''	39:0:7015:HOH:O	2.12	0.49
1:0:932:U:H2'	1:0:933:C:C6	2.48	0.49
1:0:660:A:H4'	1:0:661:G:O5'	2.13	0.49
1:0:2072:G:H3'	1:0:2073:G:C5'	2.43	0.49
1:0:1181:A:H2'	1:0:1182:C:C5'	2.42	0.49
31:9:64:C:C2'	31:9:65:A:H5'	2.43	0.49
1:0:1398:G:O2'	1:0:1399:A:H5'	2.13	0.49
14:M:23:LEU:HD13	14:M:27:ARG:HH21	1.78	0.49
1:0:1244:U:OP1	11:J:18:ILE:HD13	2.13	0.49
1:0:281:U:O2'	1:0:282:C:H5'	2.13	0.49
1:0:941:G:O2'	1:0:942:U:H5'	2.12	0.49
1:0:2325:U:O2'	1:0:2411:C:H1'	2.13	0.49
1:0:2821:C:H4'	3:B:116:PRO:HG3	1.95	0.49
1:0:1453:G:H2'	1:0:1454:U:O4'	2.13	0.49
1:0:2498:C:O2'	1:0:2499:U:H5'	2.12	0.49
1:0:2510:C:H5'	1:0:2511:A:OP2	2.13	0.49
31:9:73:A:H61	31:9:108:C:N4	2.06	0.49
1:0:2032:U:H2'	1:0:2033:G:C5'	2.43	0.49
1:0:2524:G:N2	1:0:2526:C:H41	2.11	0.49
1:0:2729:C:O2'	1:0:2730:G:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:28:G:H1'	39:0:3446:HOH:O	2.13	0.49
1:0:1589:G:N2	1:0:1605:G:H1'	2.27	0.49
1:0:669:G:O2'	1:0:670:G:H5'	2.12	0.49
4:C:127:ARG:HD3	4:C:129:HIS:HE1	1.77	0.49
1:0:1423:C:O2'	1:0:1424:A:H5'	2.13	0.49
1:0:946:C:H2'	1:0:947:U:C6	2.47	0.49
1:0:250:C:O2'	1:0:251:C:H5'	2.13	0.49
1:0:1603:A:H5'	1:0:1605:G:C4'	2.43	0.48
1:0:12:U:C2'	1:0:13:G:H5'	2.42	0.48
1:0:1735:C:OP2	3:B:234:ARG:HG3	2.13	0.48
1:0:1333:U:H2'	1:0:1334:C:H6	1.78	0.48
1:0:2887:G:H2'	1:0:2888:U:C6	2.47	0.48
1:0:589:U:H2'	1:0:590:A:H8	1.78	0.48
8:G:64:ASN:HD22	8:G:64:ASN:N	2.10	0.48
1:0:1980:U:O2'	1:0:1981:A:H5'	2.13	0.48
39:0:7291:HOH:O	3:B:211:THR:HG21	2.12	0.48
15:N:40:ASN:ND2	31:9:28:U:H5''	2.28	0.48
14:M:102:GLU:OE1	14:M:164:THR:HG21	2.13	0.48
1:0:271:C:H41	1:0:378:A:H2	1.61	0.48
1:0:2269:C:H2'	1:0:2270:G:H5'	1.95	0.48
1:0:64:G:H2'	1:0:65:C:O4'	2.13	0.48
1:0:1495:C:H1'	1:0:1573:A:H1'	1.94	0.48
1:0:130:C:H2'	39:0:7324:HOH:O	2.13	0.48
1:0:2375:A:H2'	1:0:2376:C:C6	2.47	0.48
31:9:107:C:H5	39:9:3167:HOH:O	1.96	0.48
31:9:73:A:N6	31:9:108:C:H42	2.06	0.48
1:0:1120:U:H5'	1:0:1121:G:OP2	2.12	0.48
1:0:583:C:H2'	1:0:584:U:H6	1.78	0.48
37:0:9101:WIN:O1L	37:0:9101:WIN:H1FA	2.14	0.48
31:9:107:C:O2'	31:9:108:C:H5'	2.14	0.48
1:0:1058:A:H2'	1:0:1060:C:H5''	1.95	0.48
24:W:108:ARG:HH21	24:W:114:PRO:HG2	1.79	0.48
1:0:1797:A:H4'	1:0:1798:C:C5	2.49	0.48
1:0:2563:U:O2'	1:0:2564:G:H3'	2.13	0.48
1:0:2768:A:O2'	1:0:2769:C:H5'	2.12	0.48
1:0:137:U:H2'	1:0:139:C:C5	2.49	0.48
1:0:120:A:H2'	1:0:120:A:N3	2.28	0.48
1:0:210:U:H2'	1:0:211:U:C6	2.48	0.48
1:0:659:A:H5''	39:0:6799:HOH:O	2.13	0.48
1:0:24:G:N2	1:0:518:G:H1'	2.29	0.48
14:M:34:GLU:HB3	14:M:38:GLU:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1250:C:O2'	1:0:1251:C:H5'	2.13	0.48
1:0:2893:C:O2'	1:0:2894:C:H5'	2.13	0.48
1:0:816:G:H5'	1:0:1598:A:H4'	1.95	0.48
1:0:961:A:H4'	39:0:6342:HOH:O	2.13	0.48
19:R:40:ALA:O	19:R:44:VAL:HG23	2.14	0.48
1:0:1714:C:O2'	1:0:1715:C:H5'	2.13	0.48
1:0:2717:C:OP1	3:B:207:LYS:HG3	2.13	0.48
1:0:2507:G:H2'	1:0:2510:C:H42	1.78	0.48
1:0:2072:G:C6	1:0:2533:C:H1'	2.49	0.48
1:0:368:C:H2'	1:0:369:G:H5'	1.96	0.48
1:0:1209:C:H2'	1:0:1210:G:C8	2.49	0.48
1:0:1183:C:H42	1:0:1184:C:H41	1.62	0.48
1:0:2269:C:C2'	1:0:2270:G:H5'	2.44	0.48
1:0:1268:C:H2'	1:0:1269:G:C8	2.48	0.48
1:0:107:U:H2'	1:0:108:U:H5'	1.96	0.48
1:0:1104:C:H4'	11:J:88:PRO:HD3	1.96	0.48
1:0:2839:C:H2'	1:0:2840:A:H5''	1.94	0.48
1:0:2540:G:H4'	37:0:9101:WIN:C1O	2.35	0.48
1:0:2718:C:H6	1:0:2718:C:H5'	1.79	0.48
1:0:1603:A:H5''	1:0:1604:G:H3'	1.95	0.48
1:0:877:G:C5'	1:0:878:G:OP1	2.58	0.48
3:B:212:GLN:HB2	3:B:257:THR:HG21	1.96	0.48
1:0:301:C:H2'	1:0:302:A:H8	1.79	0.48
1:0:292:G:H2'	1:0:358:G:N2	2.28	0.48
1:0:2379:G:H5'	1:0:2381:C:O4'	2.14	0.48
5:D:159:PRO:O	5:D:163:VAL:HG23	2.14	0.48
1:0:2073:G:H5''	39:0:8581:HOH:O	2.14	0.48
1:0:1641:A:C2'	1:0:1642:A:H5'	2.44	0.48
1:0:2270:G:H4'	2:A:223:ARG:HH12	1.79	0.48
1:0:214:U:H5'	39:0:5454:HOH:O	2.14	0.48
1:0:710:G:H1'	39:O:1484:HOH:O	2.14	0.48
1:0:812:A:H2'	1:0:813:C:C6	2.48	0.48
1:0:1845:A:P	2:A:190:ARG:HH11	2.37	0.47
1:0:1289:C:O2'	1:0:1290:G:H5'	2.14	0.47
1:0:621:C:H5'	26:Y:132:ASP:OD2	2.14	0.47
1:0:2487:C:O2	37:0:9101:WIN:H1F	2.13	0.47
1:0:1185:U:H2'	1:0:1186:C:C6	2.49	0.47
1:0:123:U:H2'	1:0:124:C:C6	2.49	0.47
31:9:42:C:H5'	31:9:43:G:OP2	2.14	0.47
1:0:1477:C:O2'	1:0:1478:U:H5'	2.14	0.47
1:0:226:A:H1'	1:0:393:G:C5	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1568:G:O2'	1:0:1569:U:H5'	2.14	0.47
1:0:2090:G:H2'	1:0:2091:G:C8	2.49	0.47
19:R:39:THR:HG23	19:R:107:GLU:O	2.14	0.47
1:0:1903:U:O2'	1:0:1904:A:N7	2.46	0.47
14:M:43:PRO:HG3	14:M:62:VAL:HG21	1.96	0.47
1:0:1559:A:H4'	39:0:5067:HOH:O	2.14	0.47
1:0:189:A:OP1	14:M:171:ARG:NH2	2.46	0.47
1:0:2100:A:H5'	39:C:7192:HOH:O	2.14	0.47
1:0:1419:U:H5'	1:0:1420:C:OP2	2.15	0.47
1:0:1014:A:H2'	1:0:1015:C:H5'	1.94	0.47
1:0:816:G:C6	1:0:817:G:N1	2.82	0.47
1:0:834:G:H3'	1:0:835:U:H4'	1.97	0.47
1:0:1681:G:H5''	1:0:1682:A:H5'	1.96	0.47
26:Y:177:LYS:HD3	26:Y:181:GLY:O	2.15	0.47
12:K:32:ILE:HD11	12:K:56:SER:HB3	1.96	0.47
1:0:1815:A:H2'	1:0:1816:C:O4'	2.14	0.47
1:0:1370:G:H5''	39:R:4608:HOH:O	2.14	0.47
1:0:1484:G:H3'	39:0:7776:HOH:O	2.15	0.47
1:0:960:G:H3'	1:0:960:G:N3	2.28	0.47
1:0:1028:U:H1'	39:0:8330:HOH:O	2.14	0.47
23:V:55:ARG:O	23:V:59:ILE:HG12	2.15	0.47
1:0:1071:G:H4'	26:Y:154:ARG:NH2	2.30	0.47
1:0:1861:C:H4'	2:A:6:GLY:O	2.15	0.47
11:J:107:ASN:HD22	11:J:109:TYR:H	1.61	0.47
1:0:2437:A:H2'	1:0:2438:G:C8	2.50	0.47
1:0:1415:G:H5'	28:1:12:ASN:O	2.14	0.47
1:0:2598:U:O2	1:0:2600:A:H8	1.98	0.47
1:0:2134:G:N2	1:0:2242:U:C2	2.82	0.47
1:0:571:C:H6	1:0:571:C:O5'	1.96	0.47
1:0:2509:A:OP2	1:0:2510:C:H5	1.98	0.47
1:0:960:G:N3	1:0:960:G:C2'	2.77	0.47
1:0:307:G:H3'	39:0:6217:HOH:O	2.14	0.47
1:0:1056:U:H2'	1:0:1057:A:O4'	2.14	0.47
1:0:2587:OMU:H2'	1:0:2589:U:H5''	1.97	0.47
1:0:396:U:H1'	39:0:7529:HOH:O	2.14	0.47
1:0:2389:U:H4'	18:Q:53:HIS:CD2	2.48	0.47
1:0:2372:A:H2'	1:0:2373:U:C6	2.50	0.47
1:0:1120:U:H6	1:0:1120:U:H5''	1.78	0.47
1:0:1496:A:H5'	1:0:1572:A:H1'	1.96	0.47
1:0:2338:G:H1'	5:D:105:SER:OG	2.15	0.47
1:0:2737:C:OP2	17:P:61:ARG:NH2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:366:U:H2'	1:0:367:G:O4'	2.14	0.47
1:0:1666:C:C2'	1:0:1667:A:C5'	2.80	0.47
1:0:470:U:O2'	28:1:16:HIS:HD2	1.98	0.47
1:0:421:C:H2'	1:0:422:G:H8	1.80	0.47
1:0:1503:U:H2'	1:0:1504:A:O4'	2.14	0.47
39:0:5919:HOH:O	6:E:31:ARG:NH1	2.43	0.47
1:0:1409:G:C2	1:0:1410:G:C8	3.03	0.47
1:0:2281:C:C2'	1:0:2282:U:H5'	2.44	0.47
1:0:1342:C:C2'	1:0:1343:C:H5'	2.45	0.47
1:0:506:G:N2	1:0:509:A:H5''	2.24	0.46
1:0:2005:G:O2'	1:0:2008:U:OP2	2.33	0.46
1:0:821:U:H4'	27:Z:41:ARG:HH12	1.80	0.46
1:0:2241:C:O2'	1:0:2242:U:H5'	2.16	0.46
1:0:2445:U:H2'	1:0:2446:G:H8	1.78	0.46
1:0:1130:U:H5'	39:0:7596:HOH:O	2.14	0.46
1:0:396:U:O2'	1:0:418:C:H4'	2.14	0.46
1:0:690:G:H4'	1:0:741:C:O2	2.15	0.46
31:9:20:G:O2'	31:9:21:G:H5'	2.15	0.46
1:0:558:C:H2'	1:0:559:U:H5''	1.96	0.46
1:0:2598:U:O2	1:0:2600:A:C8	2.69	0.46
31:9:39:U:H3	31:9:42:C:H5''	1.81	0.46
1:0:1735:C:O2'	1:0:1736:A:H5'	2.15	0.46
1:0:946:C:H2'	1:0:947:U:H6	1.81	0.46
1:0:1427:A:H61	1:0:1440:U:C1'	2.28	0.46
1:0:2541:U:H4'	39:0:4427:HOH:O	2.15	0.46
6:E:116:THR:HG22	6:E:151:LEU:HD22	1.96	0.46
1:0:1363:G:OP1	4:C:76:ARG:NH2	2.48	0.46
1:0:1942:A:O2'	1:0:1943:C:H5'	2.15	0.46
1:0:213:G:N2	1:0:225:G:H2'	2.31	0.46
1:0:2382:A:H5'	39:0:3538:HOH:O	2.14	0.46
1:0:1773:G:C8	27:Z:40:ALA:HA	2.50	0.46
1:0:2668:G:H2'	1:0:2669:U:C6	2.50	0.46
1:0:1052:G:H2'	1:0:1052:G:N3	2.30	0.46
1:0:1201:C:H2'	1:0:1202:A:H5'	1.97	0.46
1:0:2326:C:H4'	1:0:2412:G:H4'	1.98	0.46
1:0:2594:C:O2'	1:0:2595:U:H5'	2.15	0.46
1:0:2348:C:H5'	5:D:22:VAL:HG11	1.97	0.46
1:0:2866:U:H4'	1:0:2867:G:H5'	1.96	0.46
1:0:1545:C:H2'	1:0:1546:G:O4'	2.16	0.46
1:0:2100:A:C2	37:0:9101:WIN:H1DB	2.51	0.46
1:0:1158:G:O2'	1:0:1159:G:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1422:U:H2'	1:0:1423:C:H6	1.78	0.46
1:0:1025:C:H5'	24:W:23:MET:O	2.15	0.46
1:0:216:A:O2'	1:0:217:C:H5'	2.15	0.46
1:0:146:U:O2'	1:0:147:G:H5'	2.16	0.46
1:0:512:G:O3'	1:0:513:A:H8	1.99	0.46
1:0:1063:G:H5''	39:0:6221:HOH:O	2.16	0.46
1:0:700:A:H5''	1:0:701:U:H5'	1.97	0.46
1:0:256:C:H2'	1:0:257:G:O4'	2.16	0.46
1:0:164:G:H3'	39:0:8328:HOH:O	2.16	0.46
1:0:2392:C:H4'	39:0:9136:HOH:O	2.15	0.46
15:N:159:TYR:HE1	31:9:50:G:H5''	1.80	0.46
24:W:4:LEU:HD22	24:W:52:VAL:HG21	1.97	0.46
1:0:2851:G:C2'	1:0:2852:A:H5'	2.45	0.46
1:0:517:U:H2'	1:0:518:G:H5'	1.97	0.46
1:0:255:A:H2'	1:0:256:C:C6	2.49	0.46
4:C:1:MET:HG2	4:C:2:GLN:H	1.81	0.46
1:0:2638:G:H5'	39:0:3790:HOH:O	2.15	0.46
1:0:1384:C:H5'	25:X:30:MET:HG2	1.96	0.46
9:H:49:GLN:HE21	9:H:140:TYR:HE2	1.63	0.46
1:0:2629:C:H41	2:A:206:ARG:HH21	1.64	0.46
1:0:2896:A:N3	1:0:2896:A:H2'	2.31	0.46
1:0:2899:A:O2'	1:0:2900:G:H5'	2.16	0.46
1:0:682:A:H2'	1:0:683:G:O4'	2.15	0.46
3:B:17:LYS:O	3:B:260:HIS:HD2	1.99	0.46
1:0:1919:A:H4'	39:0:3679:HOH:O	2.16	0.46
1:0:2548:C:H5'	3:B:252:PRO:HD2	1.98	0.46
1:0:236:A:H8	1:0:236:A:OP1	1.99	0.46
1:0:1667:A:H2'	1:0:1668:U:C6	2.50	0.46
31:9:29:C:H2'	31:9:30:C:C5'	2.40	0.46
20:S:11:THR:H	20:S:14:ALA:HB3	1.79	0.46
2:A:199:HIS:CD2	2:A:201:PHE:H	2.33	0.46
1:0:602:A:O2'	1:0:605:C:H4'	2.15	0.46
1:0:800:G:H2'	1:0:801:U:C6	2.50	0.46
1:0:183:A:O2'	1:0:184:G:H5'	2.16	0.46
1:0:1769:C:O2'	1:0:1770:U:H5'	2.15	0.46
1:0:523:C:H2'	1:0:524:A:C8	2.51	0.46
1:0:1716:A:H4'	17:P:55:LYS:HD3	1.97	0.46
1:0:101:C:H2'	1:0:102:A:C8	2.51	0.46
1:0:1834:C:H2'	1:0:1840:A:H62	1.80	0.45
31:9:108:C:O2'	31:9:109:G:H5'	2.17	0.45
1:0:960:G:H2'	1:0:960:G:N3	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1314:U:H5''	1:0:1316:G:O4'	2.16	0.45
17:P:105:LEU:HD21	17:P:137:LEU:HD11	1.98	0.45
1:0:168:C:O5'	1:0:168:C:H6	1.98	0.45
1:0:1731:C:H1'	39:0:5883:HOH:O	2.16	0.45
1:0:466:A:H2'	1:0:467:G:O4'	2.16	0.45
1:0:1160:G:H5'	1:0:1161:A:C4'	2.46	0.45
1:0:2505:G:C2'	1:0:2506:A:H5'	2.46	0.45
1:0:1204:C:H2'	1:0:1205:U:O4'	2.16	0.45
1:0:364:U:H2'	1:0:365:G:C8	2.51	0.45
1:0:1562:C:O2	1:0:1562:C:H2'	2.16	0.45
1:0:702:G:O2'	1:0:703:G:H5'	2.17	0.45
4:C:47:GLY:HA2	4:C:92:PRO:HB2	1.97	0.45
1:0:2300:A:H4'	1:0:2301:A:O5'	2.16	0.45
1:0:2064:U:H4'	1:0:2653:A:OP1	2.16	0.45
1:0:834:G:H4'	1:0:835:U:OP2	2.15	0.45
1:0:2348:C:H1'	5:D:131:THR:HG21	1.96	0.45
1:0:1007:A:H2'	9:H:22:TYR:CZ	2.52	0.45
1:0:204:A:H2'	1:0:205:U:H5'	1.98	0.45
31:9:31:C:H2'	31:9:32:G:O4'	2.17	0.45
1:0:1500:U:P	17:P:41:ARG:HH22	2.39	0.45
1:0:1593:C:OP1	17:P:117:SER:HB3	2.16	0.45
1:0:820:G:C5	2:A:171:LYS:HB2	2.51	0.45
25:X:61:ARG:NH1	25:X:67:PRO:HD3	2.31	0.45
1:0:2256:G:C2'	1:0:2257:G:H5'	2.47	0.45
1:0:1362:U:H5'	39:0:7682:HOH:O	2.16	0.45
1:0:657:G:P	4:C:27:ARG:HH22	2.40	0.45
1:0:2269:C:H2'	1:0:2270:G:C5'	2.46	0.45
1:0:1131:G:C6	1:0:1230:A:C4	3.04	0.45
12:K:74:VAL:HG12	12:K:75:ARG:HG3	1.97	0.45
1:0:2694:A:H4'	6:E:91:PHE:CE1	2.51	0.45
3:B:238:ASN:HD22	3:B:240:GLY:N	2.12	0.45
1:0:1375:A:H2'	1:0:1376:G:H5'	1.99	0.45
1:0:1687:C:O2	28:1:9:GLY:HA2	2.17	0.45
3:B:315:VAL:HG23	3:B:316:ARG:HG2	1.99	0.45
13:L:30:ARG:NH1	39:L:165:HOH:O	2.48	0.45
1:0:1706:G:C6	1:0:1707:G:C6	3.05	0.45
1:0:1220:U:H4'	9:H:174:LEU:HD21	1.98	0.45
1:0:2740:G:H2'	1:0:2741:A:O4'	2.16	0.45
1:0:51:G:O2'	1:0:52:A:H5'	2.17	0.45
26:Y:144:ARG:NH1	39:Y:4909:HOH:O	2.49	0.45
1:0:569:A:H5''	1:0:587:A:N1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:59:A:H5'	39:0:2959:HOH:O	2.16	0.45
1:0:558:C:H2'	1:0:559:U:H5'	1.99	0.45
1:0:1202:A:H2'	1:0:1203:G:H5'	1.98	0.45
1:0:527:U:H2'	1:0:528:G:H8	1.81	0.45
1:0:221:G:H2'	1:0:222:A:C8	2.51	0.45
24:W:6:GLN:HB2	24:W:26:ILE:HD11	1.99	0.45
1:0:243:A:H61	1:0:269:G:C1'	2.30	0.45
31:9:22:G:H5'	31:9:23:U:OP1	2.17	0.45
1:0:363:C:O2'	1:0:364:U:H5'	2.17	0.45
1:0:334:G:H2'	1:0:335:U:O4'	2.16	0.45
1:0:1616:A:H5''	1:0:1617:C:OP1	2.17	0.45
4:C:188:ARG:HD3	39:C:2507:HOH:O	2.15	0.45
1:0:664:U:O4	1:0:681:G:H5''	2.16	0.45
1:0:820:G:OP1	27:Z:41:ARG:NH2	2.50	0.45
1:0:1439:C:H5''	29:2:41:HIS:HE1	1.82	0.45
1:0:1375:A:O2'	1:0:1376:G:H5'	2.17	0.45
31:9:36:C:C5	31:9:37:C:C5	3.05	0.45
1:0:1149:U:H5''	1:0:1151:G:O4'	2.17	0.45
1:0:2083:A:N6	11:J:90:LYS:HE3	2.32	0.45
1:0:1849:G:H1'	1:0:2011:A:N1	2.32	0.45
1:0:1937:U:O2'	1:0:1938:G:H5'	2.17	0.45
1:0:558:C:C2'	1:0:559:U:C5'	2.95	0.44
1:0:2291:A:N9	1:0:2309:C:H5'	2.32	0.44
1:0:1783:A:O2'	1:0:1784:U:H5'	2.17	0.44
1:0:424:C:H2'	1:0:425:U:C6	2.51	0.44
20:S:51:GLN:HE21	20:S:53:ASN:HD21	1.64	0.44
1:0:646:G:H2'	1:0:647:U:C6	2.51	0.44
5:D:141:VAL:HG21	31:9:57:A:C8	2.52	0.44
15:N:37:ARG:NH1	31:9:6:C:OP1	2.45	0.44
1:0:319:A:H4'	1:0:338:C:C4	2.52	0.44
1:0:2241:C:H2'	1:0:2242:U:H6	1.79	0.44
1:0:711:G:C2	1:0:718:C:C2	3.06	0.44
1:0:1398:G:H2'	1:0:1399:A:C8	2.52	0.44
1:0:1249:U:H2'	1:0:1250:C:C6	2.52	0.44
1:0:1447:U:H3'	1:0:1506:U:O2	2.16	0.44
1:0:1506:U:H6	1:0:1506:U:H5'	1.82	0.44
1:0:807:A:O2'	1:0:808:A:H5'	2.18	0.44
1:0:538:C:OP2	26:Y:134:HIS:HE1	2.00	0.44
1:0:629:A:H2'	1:0:630:A:O4'	2.17	0.44
1:0:2121:G:O2'	1:0:2122:C:H5'	2.16	0.44
1:0:2510:C:H42	1:0:2564:G:N2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:968:G:O2'	1:0:969:G:H5'	2.17	0.44
1:0:583:C:H2'	1:0:584:U:C6	2.53	0.44
19:R:39:THR:HG22	19:R:42:GLU:H	1.83	0.44
1:0:1768:C:H2'	1:0:1769:C:O4'	2.18	0.44
1:0:793:A:H5''	17:P:83:LYS:HG2	1.99	0.44
1:0:383:A:H2'	1:0:384:G:O4'	2.18	0.44
1:0:1098:A:H2'	1:0:1099:G:O4'	2.17	0.44
1:0:2004:U:H4'	39:0:4302:HOH:O	2.18	0.44
1:0:2678:A:H4'	39:0:6889:HOH:O	2.18	0.44
1:0:483:C:C4	1:0:484:A:C6	3.06	0.44
31:9:3:A:OP2	31:9:25:G:N2	2.51	0.44
1:0:2831:C:C2'	1:0:2832:C:H5'	2.48	0.44
1:0:1634:G:H2'	1:0:1635:U:H6	1.82	0.44
1:0:1626:A:H2'	1:0:1627:G:C5'	2.48	0.44
1:0:2256:G:H2'	1:0:2257:G:C5'	2.48	0.44
5:D:22:VAL:HG22	5:D:74:THR:HG22	2.00	0.44
1:0:645:U:O2	1:0:761:A:H2	2.01	0.44
24:W:80:ASP:O	24:W:84:VAL:HG23	2.18	0.44
1:0:802:G:O2'	1:0:803:C:H5'	2.17	0.44
1:0:282:C:HO2'	1:0:368:C:N4	2.15	0.44
28:1:8:GLN:HE22	28:1:11:LYS:HZ2	1.65	0.44
31:9:52:A:H2'	31:9:53:G:O4'	2.18	0.44
3:B:254:GLN:HG2	3:B:255:GLY:N	2.32	0.44
1:0:1622:G:H2'	1:0:1623:C:H5'	1.98	0.44
1:0:1445:G:N2	1:0:1678:A:H1'	2.33	0.44
1:0:177:A:H2'	1:0:178:U:O4'	2.17	0.44
1:0:2105:C:H2'	1:0:2106:C:C6	2.52	0.44
12:K:14:LYS:HB2	12:K:45:PRO:HG2	1.99	0.44
31:9:2:U:OP2	31:9:2:U:H4'	2.18	0.44
23:V:1:THR:HG23	23:V:2:VAL:HG23	2.00	0.44
24:W:48:VAL:HG12	24:W:52:VAL:HB	1.98	0.44
1:0:1197:G:H1'	1:0:1203:G:N2	2.33	0.44
1:0:815:U:O2'	1:0:1598:A:H4'	2.17	0.44
1:0:2838:A:OP1	3:B:307:ARG:NH2	2.50	0.44
1:0:1535:G:H2'	1:0:1536:C:C6	2.53	0.44
1:0:628:1MA:H4'	39:0:7268:HOH:O	2.18	0.44
1:0:1994:A:OP1	12:K:66:ARG:NH2	2.51	0.44
1:0:1439:C:O5'	1:0:1439:C:H6	2.00	0.44
1:0:920:C:H5''	1:0:921:G:O5'	2.18	0.44
1:0:517:U:C2'	1:0:518:G:H5'	2.47	0.44
13:L:27:ARG:HH21	13:L:30:ARG:HG2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1311:G:C2	1:0:1312:G:C8	3.06	0.44
1:0:1664:A:H8	1:0:1664:A:OP1	2.01	0.44
1:0:1666:C:H2'	1:0:1667:A:H5'	1.97	0.44
1:0:271:C:H4'	1:0:272:A:OP1	2.17	0.44
1:0:1330:A:C5'	39:Y:7277:HOH:O	2.65	0.44
1:0:333:G:O2'	1:0:334:G:H5'	2.18	0.44
1:0:2626:C:H2'	1:0:2627:G:C8	2.53	0.44
1:0:1515:A:H2'	1:0:1516:U:C6	2.53	0.44
1:0:2094:G:O6	1:0:2649:A:H2	2.00	0.44
31:9:59:C:H2'	31:9:60:C:C6	2.52	0.44
1:0:2824:C:H5''	1:0:2825:C:H5'	1.99	0.44
2:A:51:ARG:NH1	2:A:120:ARG:O	2.51	0.44
1:0:2041:G:O2'	1:0:2042:U:H5'	2.17	0.44
2:A:70:ALA:HB1	27:Z:89:THR:HG21	2.00	0.44
1:0:445:U:H2'	1:0:446:G:C8	2.52	0.44
1:0:1170:U:H2'	1:0:1172:G:OP2	2.18	0.44
1:0:2281:C:H2'	1:0:2282:U:H5'	2.00	0.44
1:0:1587:U:H2'	1:0:1588:G:O4'	2.17	0.44
1:0:2809:G:H2'	1:0:2810:G:O4'	2.18	0.44
1:0:1088:A:C6	1:0:1291:A:H1'	2.53	0.44
39:0:2979:HOH:O	28:1:10:LYS:HG3	2.18	0.44
1:0:39:G:N2	1:0:444:C:C2	2.86	0.44
1:0:1844:C:O5'	1:0:1844:C:H6	2.01	0.44
1:0:1592:G:O2'	1:0:1593:C:O5'	2.36	0.43
1:0:2502:C:H2'	1:0:2503:A:C5'	2.47	0.43
1:0:2634:G:OP2	2:A:204:GLY:N	2.48	0.43
1:0:851:C:O2	1:0:2022:A:H2	2.01	0.43
1:0:764:C:H2'	1:0:765:G:O4'	2.18	0.43
1:0:638:C:H2'	1:0:639:A:C8	2.53	0.43
1:0:2856:A:H4'	25:X:11:THR:HB	1.99	0.43
1:0:1119:G:H8	11:J:52:GLN:NE2	2.16	0.43
1:0:241:A:C2	1:0:378:A:H4'	2.53	0.43
24:W:125:HIS:HE1	39:W:3071:HOH:O	2.01	0.43
1:0:635:A:H2	39:0:3734:HOH:O	2.00	0.43
1:0:1544:U:H2'	1:0:1545:C:C6	2.54	0.43
1:0:1361:C:H2'	1:0:1362:U:C6	2.53	0.43
3:B:141:ARG:HD2	3:B:163:GLU:OE2	2.18	0.43
1:0:1321:A:H2'	1:0:1322:G:C8	2.53	0.43
1:0:169:A:H5''	39:0:5578:HOH:O	2.18	0.43
1:0:2831:C:H2'	1:0:2832:C:H5'	2.00	0.43
1:0:1654:U:H2'	2:A:47:HIS:CD2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:101:C:H2'	1:0:102:A:H8	1.84	0.43
1:0:329:A:OP2	4:C:206:ASN:HB2	2.17	0.43
1:0:1003:U:H4'	9:H:91:ARG:O	2.18	0.43
1:0:1759:A:N3	1:0:1818:C:H2'	2.33	0.43
1:0:1595:G:O2'	1:0:1596:U:H5'	2.19	0.43
1:0:694:A:C2'	1:0:695:C:H5'	2.48	0.43
1:0:1406:A:H4'	1:0:1407:A:C5'	2.48	0.43
1:0:2438:G:H2'	1:0:2439:C:O4'	2.18	0.43
1:0:2649:A:H5'	1:0:2649:A:H8	1.83	0.43
1:0:111:C:O2'	1:0:112:G:H5'	2.18	0.43
6:E:112:ALA:HA	6:E:113:PRO:HD3	1.90	0.43
28:1:21:ARG:HD2	28:1:37:CYS:SG	2.57	0.43
15:N:83:LEU:HD13	15:N:175:LEU:HD23	2.00	0.43
1:0:2783:A:H2'	1:0:2784:A:C8	2.53	0.43
1:0:1734:C:OP1	3:B:234:ARG:HD3	2.19	0.43
1:0:419:A:H1'	1:0:1921:A:C2	2.53	0.43
1:0:106:A:H2'	1:0:107:U:O4'	2.19	0.43
1:0:1881:A:OP1	2:A:199:HIS:HE1	2.02	0.43
1:0:1883:U:H5'	1:0:2012:U:OP2	2.19	0.43
1:0:289:G:O2'	1:0:290:C:H5'	2.19	0.43
1:0:2698:G:H2'	1:0:2699:A:C8	2.54	0.43
1:0:2488:A:H1'	39:0:3241:HOH:O	2.19	0.43
31:9:49:G:H5''	39:9:4707:HOH:O	2.19	0.43
25:X:74:ALA:HB2	25:X:85:VAL:HG13	2.01	0.43
1:0:820:G:H5'	1:0:821:U:H5'	1.99	0.43
1:0:271:C:C2	1:0:273:G:O4'	2.72	0.43
1:0:1626:A:H2'	1:0:1627:G:H5'	2.00	0.43
1:0:1427:A:N6	1:0:1440:U:H1'	2.33	0.43
1:0:1504:A:H4'	1:0:1506:U:C5	2.53	0.43
1:0:312:U:C2	1:0:320:G:N2	2.87	0.43
1:0:92:G:H4'	23:V:44:GLY:HA3	1.99	0.43
1:0:2676:C:H4'	11:J:70:PHE:CE1	2.54	0.43
1:0:2633:A:H5'	39:0:5222:HOH:O	2.18	0.43
1:0:2507:G:H2'	1:0:2510:C:N4	2.33	0.43
1:0:2591:C:H2'	1:0:2592:G:O4'	2.19	0.43
31:9:3:A:H2	31:9:21:G:N3	2.17	0.43
1:0:1439:C:H5''	29:2:41:HIS:CE1	2.52	0.43
1:0:1622:G:C2'	1:0:1623:C:H5'	2.48	0.43
1:0:111:C:H2'	1:0:112:G:O4'	2.18	0.43
1:0:1211:G:H2'	1:0:1212:C:C6	2.53	0.43
1:0:2114:C:OP1	2:A:1:GLY:HA2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2073:G:OP2	1:0:2490:A:H5'	2.19	0.43
1:0:2716:G:H5'	3:B:262:ARG:HG3	2.00	0.43
1:0:138:U:OP2	1:0:139:C:H5	2.01	0.43
1:0:1184:C:O2'	1:0:1185:U:OP2	2.30	0.43
1:0:1846:U:O2'	2:A:172:ALA:HB2	2.17	0.43
1:0:1571:G:H1'	1:0:1627:G:N2	2.34	0.43
1:0:447:A:P	21:T:1:SER:HB2	2.59	0.43
15:N:4:PRO:HG3	31:9:69:U:OP1	2.19	0.43
1:0:2115:U:H2'	1:0:2116:U:C6	2.53	0.43
1:0:1294:A:H2'	1:0:1295:G:O4'	2.18	0.43
1:0:42:C:H1'	39:0:3438:HOH:O	2.18	0.43
1:0:1202:A:C2'	1:0:1203:G:H5'	2.49	0.43
1:0:661:G:C5	1:0:686:A:C2	3.07	0.43
1:0:571:C:H2'	1:0:572:G:O4'	2.18	0.43
1:0:1200:A:H3'	39:0:4912:HOH:O	2.18	0.43
1:0:1001:U:O2'	1:0:1002:G:H5'	2.19	0.43
1:0:2837:U:H2'	39:0:6433:HOH:O	2.17	0.43
1:0:1592:G:H2'	1:0:1593:C:C6	2.54	0.43
1:0:2070:G:H2'	1:0:2072:G:OP1	2.18	0.43
1:0:2781:U:H2'	1:0:2782:G:C5'	2.48	0.43
1:0:836:G:H1'	39:0:7509:HOH:O	2.18	0.43
1:0:2266:A:H2'	1:0:2267:G:C8	2.54	0.43
1:0:1482:A:O2'	1:0:1483:C:H5'	2.18	0.43
1:0:369:G:H2'	1:0:370:G:H8	1.84	0.42
1:0:1845:A:O2'	1:0:1846:U:H5'	2.19	0.42
1:0:2438:G:H5'	39:0:5494:HOH:O	2.18	0.42
1:0:255:A:H2'	1:0:256:C:H6	1.84	0.42
11:J:42:GLU:O	11:J:131:THR:HG23	2.19	0.42
1:0:699:C:C2	1:0:743:G:N2	2.87	0.42
1:0:1966:U:H2'	1:0:1967:U:C6	2.54	0.42
1:0:696:C:H2'	1:0:697:G:O4'	2.19	0.42
1:0:2566:A:H2	1:0:2695:C:O2	2.02	0.42
1:0:2102:G:C2	1:0:2104:C:C4	3.08	0.42
1:0:1119:G:N2	1:0:1246:A:N1	2.67	0.42
1:0:1205:U:C2'	1:0:1206:U:C5'	2.89	0.42
31:9:1:U:O2'	31:9:3:A:H5''	2.19	0.42
1:0:1803:C:H2'	1:0:1804:A:H8	1.83	0.42
1:0:1421:C:O2'	1:0:1422:U:H5'	2.19	0.42
1:0:1562:C:N4	39:0:5067:HOH:O	2.52	0.42
1:0:538:C:H5''	1:0:539:G:C8	2.53	0.42
1:0:912:A:C4	1:0:1294:A:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1381:A:N3	1:0:1382:G:H1'	2.34	0.42
1:0:1795:G:H2'	1:0:1796:A:O4'	2.19	0.42
1:0:2816:A:H5''	1:0:2817:G:H5'	2.01	0.42
1:0:1613:C:H2'	1:0:1614:G:O4'	2.18	0.42
1:0:1386:G:O2'	1:0:1387:G:H5'	2.19	0.42
1:0:1434:A:H2'	1:0:1436:C:C5	2.54	0.42
1:0:1245:C:O5'	1:0:1245:C:H6	2.02	0.42
1:0:2045:G:H2'	1:0:2046:G:O4'	2.19	0.42
31:9:91:C:H2'	31:9:92:G:O4'	2.19	0.42
1:0:1407:A:O2'	1:0:1408:U:H3'	2.19	0.42
1:0:166:A:O2'	1:0:898:G:O6	2.36	0.42
1:0:615:G:H2'	1:0:616:U:C6	2.54	0.42
1:0:2487:C:H2'	1:0:2488:A:O4'	2.18	0.42
1:0:2252:A:H2'	1:0:2253:G:O4'	2.19	0.42
1:0:1010:C:OP1	15:N:5:ARG:NH1	2.53	0.42
1:0:1130:U:H2'	1:0:1131:G:O4'	2.18	0.42
1:0:2239:C:H2'	1:0:2240:U:C6	2.54	0.42
4:C:218:VAL:HG12	39:C:5065:HOH:O	2.19	0.42
1:0:1968:A:H2'	1:0:1969:A:C8	2.55	0.42
1:0:2079:G:H2'	1:0:2080:G:O4'	2.19	0.42
1:0:2546:U:H4'	39:B:3923:HOH:O	2.20	0.42
18:Q:19:ARG:HH21	31:9:11:A:P	2.42	0.42
1:0:276:C:O5'	1:0:276:C:H6	2.03	0.42
1:0:1393:A:H2'	1:0:1394:C:C6	2.54	0.42
1:0:308:U:C4	1:0:342:C:H1'	2.54	0.42
16:O:32:ARG:HH21	16:O:35:LYS:NZ	2.17	0.42
1:0:1992:U:H2'	1:0:1994:A:OP2	2.19	0.42
1:0:2039:A:H4'	1:0:2760:C:O2'	2.20	0.42
1:0:2345:A:H3'	1:0:2346:C:H6	1.83	0.42
1:0:524:A:H5''	19:R:29:LYS:HD3	2.00	0.42
1:0:1761:U:H5'	17:P:81:LYS:O	2.20	0.42
26:Y:187:VAL:HG23	26:Y:192:ASP:HB2	2.00	0.42
1:0:295:C:H2'	1:0:296:G:O4'	2.20	0.42
1:0:1396:C:H1'	17:P:1:THR:O	2.19	0.42
1:0:542:A:H2'	1:0:543:G:O4'	2.19	0.42
30:3:48:ASN:ND2	30:3:50:GLY:H	2.17	0.42
1:0:670:G:H2'	1:0:671:A:C8	2.54	0.42
14:M:164:THR:HG22	14:M:165:GLY:N	2.34	0.42
1:0:272:A:H3'	39:0:7395:HOH:O	2.19	0.42
1:0:812:A:H2'	1:0:813:C:O4'	2.19	0.42
1:0:2589:U:H2'	1:0:2590:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:470:U:O2'	28:1:16:HIS:CD2	2.72	0.42
1:0:699:C:C2	1:0:744:G:C2	3.07	0.42
1:0:567:U:O5'	1:0:567:U:H6	2.02	0.42
1:0:876:A:N3	1:0:876:A:H2'	2.34	0.42
1:0:2777:G:O2'	1:0:2778:A:H5'	2.20	0.42
15:N:35:VAL:HG11	31:9:6:C:H4'	2.01	0.42
1:0:342:C:H2'	1:0:343:C:H6	1.84	0.42
1:0:1181:A:N1	1:0:1192:A:O2'	2.42	0.42
1:0:1788:U:C2	1:0:1805:G:N2	2.88	0.42
1:0:958:G:H2'	1:0:959:C:H6	1.84	0.42
1:0:2649:A:H5'	1:0:2649:A:C8	2.55	0.42
1:0:1211:G:H2'	1:0:1212:C:H6	1.83	0.42
1:0:1218:U:H2'	1:0:1219:U:C6	2.54	0.42
1:0:1055:G:OP2	9:H:99:ARG:NH1	2.53	0.42
21:T:18:GLU:O	21:T:21:LYS:HG2	2.20	0.42
9:H:69:ARG:HD3	39:H:6314:HOH:O	2.20	0.42
1:0:1463:U:H2'	1:0:1464:C:C6	2.55	0.42
1:0:574:G:O2'	1:0:575:A:H5'	2.20	0.42
1:0:447:A:OP1	21:T:2:LYS:HG2	2.20	0.42
1:0:204:A:C2'	1:0:205:U:H5'	2.49	0.42
2:A:70:ALA:HA	2:A:71:PRO:HD3	1.88	0.42
1:0:113:A:H2'	1:0:115:U:O4	2.20	0.42
11:J:80:LYS:HE3	11:J:101:VAL:O	2.20	0.42
1:0:825:U:H5''	1:0:826:U:OP1	2.19	0.42
1:0:1576:G:H2'	1:0:1577:U:C6	2.55	0.42
1:0:2419:U:H5''	1:0:2420:G:C5'	2.50	0.42
1:0:482:G:O4'	1:0:511:A:C2	2.72	0.42
1:0:1819:G:H2'	1:0:1820:G:C5'	2.50	0.42
1:0:1202:A:H2'	1:0:1203:G:C5'	2.50	0.42
1:0:907:A:H4'	1:0:1328:A:C2	2.55	0.42
1:0:210:U:H2'	1:0:211:U:H6	1.84	0.42
1:0:1099:G:H2'	1:0:1100:G:O4'	2.20	0.42
2:A:71:PRO:HG2	2:A:91:GLY:HA2	2.02	0.42
1:0:1154:A:H2'	1:0:1155:G:C8	2.55	0.42
1:0:1074:G:H4'	1:0:1260:G:C6	2.54	0.42
1:0:138:U:OP1	1:0:259:G:H5'	2.20	0.42
1:0:1789:G:H2'	1:0:1790:C:O5'	2.20	0.42
1:0:2416:G:H2'	1:0:2417:C:C6	2.55	0.42
1:0:1878:G:O2'	1:0:1879:U:P	2.78	0.42
1:0:812:A:H1'	39:0:8714:HOH:O	2.19	0.42
1:0:1682:A:H5''	39:0:4695:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1706:G:C5	1:0:1707:G:C6	3.08	0.42
1:0:1873:G:H3'	39:0:4169:HOH:O	2.19	0.42
1:0:1556:G:O2'	1:0:1557:G:H5'	2.19	0.42
31:9:56:A:C3'	31:9:57:A:H5''	2.50	0.41
1:0:2039:A:H2'	1:0:2040:C:C6	2.54	0.41
1:0:1942:A:H4'	39:A:241:HOH:O	2.19	0.41
1:0:581:G:O2'	1:0:582:U:H5'	2.20	0.41
16:O:73:ASP:HA	16:O:92:VAL:O	2.20	0.41
1:0:218:C:C5	1:0:220:C:C4	3.07	0.41
1:0:17:G:H2'	1:0:18:C:C6	2.56	0.41
1:0:185:G:H4'	1:0:186:A:H4'	2.02	0.41
1:0:2564:G:OP2	1:0:2565:C:H5''	2.20	0.41
1:0:2533:C:H6	1:0:2533:C:C5'	2.27	0.41
1:0:1819:G:H2'	1:0:1820:G:C4'	2.50	0.41
9:H:59:GLN:NE2	9:H:129:ARG:HE	2.15	0.41
1:0:1855:G:H8	2:A:144:GLU:OE2	2.04	0.41
1:0:2583:A:H5'	39:0:6007:HOH:O	2.21	0.41
1:0:2540:G:O2'	37:0:9101:WIN:H2G	2.20	0.41
1:0:283:U:H5	1:0:284:C:C4	2.37	0.41
1:0:1166:A:OP1	1:0:1174:A:H4'	2.19	0.41
1:0:1268:C:O2'	1:0:1269:G:H5'	2.20	0.41
1:0:107:U:C2'	1:0:108:U:H5'	2.51	0.41
1:0:1098:A:OP1	24:W:128:VAL:HG22	2.20	0.41
9:H:31:ILE:HG23	39:H:6314:HOH:O	2.19	0.41
18:Q:25:PRO:HA	18:Q:26:PRO:HD3	1.87	0.41
4:C:107:ARG:O	4:C:111:VAL:HG23	2.20	0.41
1:0:1909:A:H2'	1:0:1910:A:C8	2.56	0.41
31:9:39:U:H3'	31:9:40:C:C5'	2.49	0.41
1:0:1741:U:C4	1:0:2033:G:C8	3.08	0.41
1:0:1014:A:H5''	31:9:101:G:O2'	2.20	0.41
1:0:2251:G:H2'	1:0:2252:A:C8	2.54	0.41
1:0:2354:A:C2	1:0:2367:A:C8	3.09	0.41
1:0:710:G:OP1	16:O:24:ALA:HB3	2.21	0.41
1:0:168:C:H5'	1:0:2277:U:OP1	2.21	0.41
16:O:70:LEU:O	16:O:92:VAL:HG21	2.21	0.41
1:0:1766:U:O2	1:0:1778:A:H5'	2.21	0.41
22:U:14:GLU:O	22:U:17:THR:HB	2.20	0.41
1:0:2016:U:H2'	1:0:2017:U:O4'	2.20	0.41
1:0:2103:A:H2'	1:0:2104:C:C5'	2.51	0.41
1:0:2538:A:O2'	37:0:9101:WIN:H1AB	2.21	0.41
1:0:317:A:H4'	39:0:8457:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2087:C:O2'	1:0:2088:C:H5'	2.20	0.41
1:0:1706:G:C6	1:0:1707:G:N1	2.88	0.41
1:0:2815:G:N7	11:J:80:LYS:NZ	2.69	0.41
4:C:138:VAL:O	4:C:234:VAL:HA	2.21	0.41
1:0:2714:U:H4'	3:B:10:SER:HB2	2.02	0.41
1:0:2473:U:O3'	1:0:2474:A:H3'	2.20	0.41
12:K:130:MET:SD	22:U:25:ASP:O	2.78	0.41
4:C:39:GLN:O	4:C:43:LYS:HD3	2.20	0.41
31:9:28:U:H2'	31:9:29:C:C6	2.55	0.41
1:0:1684:A:O2'	1:0:1685:A:H5''	2.20	0.41
24:W:137:GLN:NE2	24:W:141:HIS:HE1	2.14	0.41
24:W:48:VAL:HG12	24:W:48:VAL:O	2.20	0.41
1:0:2092:G:H2'	1:0:2613:G:OP1	2.21	0.41
1:0:2265:U:H2'	1:0:2266:A:C8	2.55	0.41
18:Q:25:PRO:HB2	39:9:4350:HOH:O	2.19	0.41
1:0:125:U:H2'	39:0:8451:HOH:O	2.21	0.41
1:0:2906:A:H5'	1:0:2907:C:O4'	2.20	0.41
1:0:1306:U:H5''	4:C:184:ARG:HD2	2.03	0.41
3:B:304:PRO:HD2	3:B:307:ARG:NE	2.36	0.41
9:H:70:LEU:O	9:H:74:ARG:HB2	2.20	0.41
1:0:1688:G:O2'	28:1:5:THR:HG23	2.20	0.41
1:0:2515:C:H2'	1:0:2516:G:O4'	2.21	0.41
1:0:318:U:H5'	1:0:339:A:N3	2.36	0.41
4:C:236:THR:HG22	4:C:239:ALA:H	1.86	0.41
1:0:2734:G:O2'	1:0:2735:U:H5'	2.21	0.41
1:0:1456:C:H2'	1:0:1457:U:C6	2.55	0.41
1:0:2664:A:OP1	1:0:2664:A:H8	2.03	0.41
1:0:579:G:H2'	1:0:580:A:C8	2.56	0.41
1:0:559:U:H2'	1:0:560:U:O4'	2.20	0.41
1:0:1973:A:H5'	1:0:1973:A:C8	2.53	0.41
1:0:1736:A:H1'	39:0:7468:HOH:O	2.20	0.41
1:0:1624:A:H5'	1:0:1626:A:O4'	2.21	0.41
1:0:1290:G:H3'	39:0:4115:HOH:O	2.20	0.41
1:0:2326:C:H4'	1:0:2412:G:C4'	2.51	0.41
1:0:806:A:H2'	1:0:807:A:O4'	2.21	0.41
1:0:185:G:H4'	1:0:186:A:OP1	2.21	0.41
1:0:400:C:O2'	1:0:401:C:H5'	2.21	0.41
1:0:1076:G:C2	1:0:1084:C:C2	3.09	0.41
14:M:65:VAL:HG21	14:M:105:ALA:HB2	2.03	0.41
1:0:549:A:O2'	1:0:550:C:H5'	2.21	0.41
1:0:2812:A:C2	1:0:2814:A:N6	2.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:282:C:H1'	1:0:368:C:H41	1.83	0.41
1:0:1631:A:H2'	1:0:1632:A:C8	2.56	0.41
1:0:1165:G:O3'	1:0:1174:A:H4'	2.20	0.41
1:0:1185:U:H5'	39:0:7308:HOH:O	2.21	0.41
1:0:1762:C:O2'	1:0:1763:C:H5'	2.20	0.41
1:0:10:U:C6	1:0:10:U:H3'	2.56	0.41
31:9:35:C:H5''	39:9:4078:HOH:O	2.20	0.41
1:0:1167:G:H4'	10:I:130:LEU:HD21	2.03	0.41
1:0:291:C:H2'	1:0:292:G:O4'	2.21	0.41
1:0:2089:A:O2'	1:0:2090:G:H5'	2.21	0.41
1:0:327:A:H4'	1:0:329:A:C8	2.56	0.41
1:0:318:U:H5'	1:0:339:A:C4	2.56	0.41
3:B:102:THR:HB	3:B:103:ASP:H	1.71	0.41
1:0:1383:U:H5'	25:X:27:ASP:OD1	2.21	0.41
5:D:23:VAL:HG12	5:D:130:VAL:HG22	2.02	0.41
1:0:2908:A:O5'	1:0:2908:A:H8	2.04	0.41
24:W:88:THR:HG22	24:W:89:ASP:H	1.86	0.41
3:B:10:SER:O	3:B:16:ARG:NH1	2.53	0.41
3:B:69:VAL:HA	3:B:70:PRO:HD3	1.92	0.41
1:0:1652:C:H4'	27:Z:76:THR:HG21	2.03	0.41
1:0:940:G:O2'	1:0:1032:A:N1	2.52	0.41
1:0:2074:A:H1'	39:0:6299:HOH:O	2.21	0.41
1:0:2385:G:H2'	1:0:2386:U:C6	2.56	0.41
1:0:1811:A:C2	1:0:2752:C:H1'	2.56	0.41
1:0:2481:G:H5''	39:0:3267:HOH:O	2.20	0.41
1:0:2047:C:H5'	39:0:6092:HOH:O	2.21	0.41
1:0:1159:G:H21	1:0:1189:A:H8	1.69	0.40
1:0:2672:C:H2'	1:0:2673:U:H6	1.85	0.40
1:0:2548:C:OP2	3:B:5:ARG:NH2	2.54	0.40
1:0:2121:G:H1'	39:0:3302:HOH:O	2.20	0.40
1:0:1778:A:H2'	1:0:1779:A:H5'	2.03	0.40
1:0:856:G:H2'	39:0:4459:HOH:O	2.22	0.40
3:B:195:ARG:HG2	3:B:323:LEU:HD22	2.02	0.40
31:9:54:A:O2'	31:9:55:U:H5'	2.21	0.40
31:9:73:A:H2'	31:9:74:G:O4'	2.20	0.40
1:0:283:U:H5	1:0:284:C:N3	2.18	0.40
1:0:1972:U:C2'	1:0:1973:A:C5'	3.00	0.40
1:0:304:G:H1'	1:0:347:A:N6	2.36	0.40
1:0:2002:C:C2'	1:0:2003:U:H5'	2.51	0.40
1:0:1072:G:OP2	26:Y:154:ARG:NH2	2.55	0.40
1:0:1342:C:O2'	1:0:1343:C:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:134:HIS:H	26:Y:134:HIS:CD2	2.39	0.40
1:0:383:A:H4'	39:0:4330:HOH:O	2.21	0.40
1:0:327:A:H4'	1:0:329:A:N7	2.37	0.40
1:0:2114:C:O2'	1:0:2115:U:H5'	2.21	0.40
2:A:135:VAL:HG11	2:A:147:ARG:NH2	2.36	0.40
18:Q:47:VAL:HA	18:Q:48:PRO:HD3	1.94	0.40
24:W:5:VAL:HG11	24:W:153:MET:CE	2.52	0.40
1:0:1183:C:H5	1:0:1192:A:OP1	2.03	0.40
1:0:1804:A:H2'	1:0:1805:G:C8	2.56	0.40
1:0:10:U:C4	1:0:532:A:C8	3.10	0.40
15:N:86:LEU:HD12	15:N:125:ALA:HB2	2.03	0.40
3:B:57:GLU:HA	3:B:58:PRO:HD2	1.98	0.40
1:0:282:C:O2'	1:0:283:U:C5'	2.70	0.40
1:0:308:U:H5'	21:T:97:ARG:NH2	2.36	0.40
1:0:137:U:OP1	1:0:259:G:O2'	2.40	0.40
1:0:1016:U:H1'	39:0:8342:HOH:O	2.20	0.40
1:0:1788:U:O2'	1:0:1789:G:H5'	2.22	0.40
1:0:1008:C:O2'	1:0:1009:U:H5'	2.21	0.40
1:0:1132:A:H2'	1:0:1133:A:C8	2.57	0.40
1:0:1361:C:H2'	1:0:1362:U:H6	1.86	0.40
1:0:537:G:O4'	1:0:538:C:C5	2.75	0.40
1:0:598:C:H2'	1:0:599:G:H8	1.86	0.40
6:E:49:ILE:HD11	6:E:69:ILE:HD12	2.02	0.40
1:0:1812:G:H4'	1:0:1814:G:O4'	2.22	0.40
1:0:1175:G:H1'	1:0:1193:A:C2'	2.51	0.40
1:0:2401:A:H2'	1:0:2402:A:H8	1.82	0.40
1:0:1594:C:O2'	1:0:1595:G:H5'	2.22	0.40
1:0:827:A:H2'	1:0:828:G:O4'	2.22	0.40
1:0:316:A:H5'	21:T:54:ASP:OD2	2.22	0.40
1:0:1167:G:H1'	39:I:6825:HOH:O	2.21	0.40
1:0:2629:C:N4	2:A:206:ARG:HH21	2.18	0.40
1:0:1211:G:O2'	1:0:1212:C:H5'	2.22	0.40
1:0:113:A:OP2	1:0:114:A:H2'	2.21	0.40
5:D:48:MET:HB3	31:9:41:C:H4'	2.04	0.40
1:0:77:G:C2'	1:0:78:G:H5'	2.51	0.40
1:0:1657:A:H2'	1:0:1658:A:C8	2.56	0.40
31:9:33:U:H2'	39:9:3797:HOH:O	2.20	0.40
1:0:1331:G:OP2	26:Y:142:SER:OG	2.33	0.40
1:0:1257:C:O2'	1:0:1258:G:H5'	2.22	0.40
1:0:1537:C:H1'	39:0:6076:HOH:O	2.22	0.40
1:0:2245:C:H6	1:0:2245:C:O5'	2.04	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	
2	A	235/237 (99%)	218 (93%)	14 (6%)	3 (1%)	15	42
3	B	335/337 (99%)	307 (92%)	26 (8%)	2 (1%)	30	63
4	C	244/246 (99%)	224 (92%)	18 (7%)	2 (1%)	24	56
5	D	134/177 (76%)	121 (90%)	10 (8%)	3 (2%)	8	27
6	E	170/172 (99%)	161 (95%)	9 (5%)	0	100	100
7	F	117/119 (98%)	109 (93%)	7 (6%)	1 (1%)	21	52
8	G	25/348 (7%)	25 (100%)	0	0	100	100
9	H	156/177 (88%)	150 (96%)	5 (3%)	1 (1%)	30	63
10	I	68/70 (97%)	58 (85%)	10 (15%)	0	100	100
11	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
12	K	130/132 (98%)	125 (96%)	4 (3%)	1 (1%)	24	56
13	L	141/165 (86%)	127 (90%)	14 (10%)	0	100	100
14	M	192/194 (99%)	187 (97%)	4 (2%)	1 (0%)	34	67
15	N	184/186 (99%)	173 (94%)	8 (4%)	3 (2%)	12	36
16	O	113/115 (98%)	111 (98%)	2 (2%)	0	100	100
17	P	141/143 (99%)	139 (99%)	2 (1%)	0	100	100
18	Q	93/95 (98%)	88 (95%)	4 (4%)	1 (1%)	17	47
19	R	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
20	S	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
21	T	117/119 (98%)	111 (95%)	5 (4%)	1 (1%)	21	52
22	U	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
23	V	63/65 (97%)	61 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	W	152/154 (99%)	148 (97%)	4 (3%)	0	100	100
25	X	80/82 (98%)	77 (96%)	2 (2%)	1 (1%)	15	42
26	Y	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
27	Z	71/73 (97%)	65 (92%)	6 (8%)	0	100	100
28	1	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
29	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
30	3	90/92 (98%)	88 (98%)	2 (2%)	0	100	100
All	All	3705/4172 (89%)	3503 (94%)	182 (5%)	20 (0%)	34	67

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	37	VAL
5	D	137	PRO
15	N	154	LEU
15	N	139	TRP
3	B	2	GLN
5	D	56	ARG
12	K	127	ALA
15	N	167	ASP
2	A	27	LEU
3	B	185	GLY
4	C	8	LEU
7	F	100	ASP
14	M	71	SER
9	H	19	ARG
21	T	44	ALA
4	C	79	ARG
5	D	27	ILE
18	Q	18	PRO
2	A	88	ILE
25	X	52	PRO

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	179/179 (100%)	168 (94%)	11 (6%)	23	52
3	B	282/282 (100%)	268 (95%)	14 (5%)	30	62
4	C	193/193 (100%)	176 (91%)	17 (9%)	12	33
5	D	117/148 (79%)	108 (92%)	9 (8%)	16	39
6	E	152/152 (100%)	146 (96%)	6 (4%)	39	73
7	F	93/93 (100%)	90 (97%)	3 (3%)	46	79
8	G	27/282 (10%)	27 (100%)	0	100	100
9	H	134/145 (92%)	128 (96%)	6 (4%)	34	67
10	I	58/58 (100%)	57 (98%)	1 (2%)	68	89
11	J	118/118 (100%)	110 (93%)	8 (7%)	20	46
12	K	106/106 (100%)	100 (94%)	6 (6%)	25	56
13	L	113/127 (89%)	112 (99%)	1 (1%)	84	95
14	M	158/158 (100%)	152 (96%)	6 (4%)	40	74
15	N	149/149 (100%)	140 (94%)	9 (6%)	24	53
16	O	93/93 (100%)	90 (97%)	3 (3%)	46	79
17	P	113/113 (100%)	108 (96%)	5 (4%)	35	68
18	Q	79/79 (100%)	75 (95%)	4 (5%)	29	62
19	R	117/117 (100%)	112 (96%)	5 (4%)	35	69
20	S	71/71 (100%)	70 (99%)	1 (1%)	74	91
21	T	105/105 (100%)	96 (91%)	9 (9%)	13	34
22	U	44/44 (100%)	44 (100%)	0	100	100
23	V	51/51 (100%)	49 (96%)	2 (4%)	39	73
24	W	130/130 (100%)	123 (95%)	7 (5%)	27	59
25	X	66/66 (100%)	57 (86%)	9 (14%)	5	12
26	Y	120/120 (100%)	116 (97%)	4 (3%)	45	78
27	Z	60/60 (100%)	59 (98%)	1 (2%)	68	89
28	1	46/46 (100%)	45 (98%)	1 (2%)	60	86
29	2	42/46 (91%)	41 (98%)	1 (2%)	57	84
30	3	79/79 (100%)	77 (98%)	2 (2%)	55	84
All	All	3095/3410 (91%)	2944 (95%)	151 (5%)	31	63

All (151) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	3	ARG
2	A	51	ARG
2	A	64	ASP
2	A	78	ASP
2	A	105	VAL
2	A	108	VAL
2	A	110	SER
2	A	131	HIS
2	A	179	MET
2	A	206	ARG
2	A	217	ARG
3	B	7	ARG
3	B	11	LEU
3	B	27	ASN
3	B	49	THR
3	B	71	VAL
3	B	82	VAL
3	B	97	LEU
3	B	98	THR
3	B	162	MET
3	B	171	VAL
3	B	195	ARG
3	B	234	ARG
3	B	254	GLN
3	B	277	GLU
4	C	2	GLN
4	C	27	ARG
4	C	76	ARG
4	C	78	ARG
4	C	94	THR
4	C	98	ARG
4	C	101	ASP
4	C	136	VAL
4	C	162	VAL
4	C	187	ARG
4	C	214	THR
4	C	223	LEU
4	C	234	VAL
4	C	236	THR
4	C	237	GLU
4	C	240	LEU
4	C	243	VAL

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Mol	Chain	Res	Type
5	D	19	GLU
5	D	24	HIS
5	D	29	HIS
5	D	50	VAL
5	D	62	ASP
5	D	101	THR
5	D	128	LEU
5	D	149	ARG
5	D	161	ASP
6	E	16	ASP
6	E	36	PRO
6	E	61	THR
6	E	102	VAL
6	E	156	ASP
6	E	164	ASP
7	F	12	LEU
7	F	50	VAL
7	F	60	VAL
9	H	62	HIS
9	H	65	LEU
9	H	87	LYS
9	H	91	ARG
9	H	157	TYR
9	H	173	GLU
10	I	94	ASP
11	J	39	VAL
11	J	45	VAL
11	J	52	GLN
11	J	79	PHE
11	J	107	ASN
11	J	120	SER
11	J	130	VAL
11	J	131	THR
12	K	10	GLN
12	K	19	THR
12	K	49	LEU
12	K	98	VAL
12	K	107	THR
12	K	119	GLN
13	L	35	ARG
14	M	10	ASP
14	M	46	LEU

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Mol	Chain	Res	Type
14	M	68	ARG
14	M	93	ARG
14	M	99	ARG
14	M	116	ASN
15	N	26	LEU
15	N	38	LYS
15	N	47	LEU
15	N	49	THR
15	N	62	HIS
15	N	134	ASP
15	N	135	VAL
15	N	142	THR
15	N	180	LEU
16	O	3	THR
16	O	25	VAL
16	O	80	ASP
17	P	13	VAL
17	P	21	VAL
17	P	52	LYS
17	P	91	LYS
17	P	98	ILE
18	Q	11	ARG
18	Q	16	ASN
18	Q	18	PRO
18	Q	57	ASP
19	R	13	THR
19	R	39	THR
19	R	119	VAL
19	R	125	ARG
19	R	132	ARG
20	S	81	ILE
21	T	5	ASP
21	T	39	ASN
21	T	48	VAL
21	T	61	GLU
21	T	82	THR
21	T	89	ARG
21	T	96	VAL
21	T	115	GLU
21	T	117	ASP
23	V	12	THR
23	V	13	PRO

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Mol	Chain	Res	Type
24	W	35	VAL
24	W	38	THR
24	W	52	VAL
24	W	120	PRO
24	W	125	HIS
24	W	142	ASP
24	W	146	ILE
25	X	10	VAL
25	X	43	VAL
25	X	46	ASP
25	X	49	ARG
25	X	52	PRO
25	X	72	VAL
25	X	79	GLU
25	X	82	GLU
25	X	88	GLU
26	Y	154	ARG
26	Y	174	VAL
26	Y	189	ASN
26	Y	203	VAL
27	Z	85	ASP
28	1	14	THR
29	2	18	ASN
30	3	18	GLN
30	3	22	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (66) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	47	HIS
2	A	176	HIS
2	A	199	HIS
3	B	27	ASN
3	B	145	HIS
3	B	238	ASN
3	B	260	HIS
3	B	320	GLN
3	B	332	ASN
4	C	2	GLN
4	C	67	GLN
4	C	73	GLN
4	C	129	HIS

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Mol	Chain	Res	Type
5	D	103	ASN
6	E	143	GLN
8	G	64	ASN
9	H	49	GLN
9	H	59	GLN
10	I	102	GLN
11	J	52	GLN
11	J	107	ASN
12	K	10	GLN
12	K	42	ASN
13	L	18	HIS
13	L	41	HIS
14	M	24	GLN
14	M	58	GLN
14	M	137	ASN
14	M	170	ASN
15	N	40	ASN
15	N	107	ASN
17	P	50	GLN
17	P	66	GLN
17	P	88	GLN
17	P	89	ASN
17	P	118	GLN
18	Q	40	HIS
19	R	94	ASN
19	R	98	ASN
19	R	117	HIS
19	R	123	GLN
20	S	51	GLN
20	S	55	GLN
21	T	39	ASN
22	U	39	ASN
22	U	48	ASN
23	V	60	GLN
24	W	110	GLN
24	W	119	HIS
24	W	125	HIS
24	W	141	HIS
25	X	23	HIS
26	Y	119	GLN
26	Y	129	ASN
26	Y	134	HIS

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Mol	Chain	Res	Type
26	Y	189	ASN
28	1	8	GLN
28	1	16	HIS
28	1	28	HIS
29	2	16	ASN
29	2	18	ASN
29	2	41	HIS
29	2	45	ASN
30	3	2	GLN
30	3	30	GLN
30	3	48	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2745/2923 (93%)	238 (8%)	26 (0%)
31	9	121/122 (99%)	17 (14%)	1 (0%)
All	All	2866/3045 (94%)	255 (8%)	27 (0%)

All (255) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G
1	0	86	A
1	0	87	C
1	0	88	G
1	0	114	A
1	0	115	U
1	0	120	A
1	0	130	C
1	0	141	C
1	0	151	A
1	0	166	A
1	0	169	A
1	0	186	A
1	0	191	A
1	0	192	A

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Mol	Chain	Res	Type
1	0	198	A
1	0	200	C
1	0	204	A
1	0	219	G
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U
1	0	284	C
1	0	308	U
1	0	309	C
1	0	336	G
1	0	337	A
1	0	358	G
1	0	381	G
1	0	397	A
1	0	417	G
1	0	461	C
1	0	487	G
1	0	497	A
1	0	498	A
1	0	510	U
1	0	511	A
1	0	514	G
1	0	537	G
1	0	538	C
1	0	539	G
1	0	542	A
1	0	545	G
1	0	553	G
1	0	559	U
1	0	581	G
1	0	588	G
1	0	604	G
1	0	620	A
1	0	632	A
1	0	644	G
1	0	660	A
1	0	688	A
1	0	701	U
1	0	759	C

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Mol	Chain	Res	Type
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U
1	0	840	U
1	0	857	A
1	0	858	U
1	0	868	G
1	0	869	G
1	0	871	G
1	0	872	U
1	0	875	A
1	0	877	G
1	0	878	G
1	0	885	G
1	0	898	G
1	0	905	C
1	0	920	C
1	0	921	G
1	0	923	A
1	0	938	G
1	0	953	G
1	0	960	G
1	0	961	A
1	0	1006	A
1	0	1008	C
1	0	1029	U
1	0	1045	G
1	0	1059	G
1	0	1060	C
1	0	1072	G
1	0	1081	A
1	0	1087	G
1	0	1088	A
1	0	1106	A
1	0	1109	U
1	0	1110	G
1	0	1119	G
1	0	1130	U
1	0	1137	G
1	0	1151	G
1	0	1164	U

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Mol	Chain	Res	Type
1	0	1165	G
1	0	1166	A
1	0	1174	A
1	0	1175	G
1	0	1185	U
1	0	1193	A
1	0	1205	U
1	0	1206	U
1	0	1216	G
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1279	U
1	0	1289	C
1	0	1331	G
1	0	1342	C
1	0	1353	C
1	0	1357	A
1	0	1360	C
1	0	1377	C
1	0	1378	G
1	0	1407	A
1	0	1409	G
1	0	1474	C
1	0	1485	A
1	0	1505	U
1	0	1506	U
1	0	1524	U
1	0	1525	G
1	0	1526	A
1	0	1535	G
1	0	1592	G
1	0	1617	C
1	0	1625	U
1	0	1626	A
1	0	1634	G
1	0	1656	A
1	0	1667	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1692	C

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Mol	Chain	Res	Type
1	0	1701	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1730	G
1	0	1731	C
1	0	1752	G
1	0	1778	A
1	0	1798	C
1	0	1819	G
1	0	1820	G
1	0	1829	A
1	0	1856	C
1	0	1879	U
1	0	1919	A
1	0	1942	A
1	0	1965	C
1	0	1971	G
1	0	1973	A
1	0	1978	A
1	0	1980	U
1	0	1996	U
1	0	2006	C
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G
1	0	2033	G
1	0	2034	U
1	0	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2110	G
1	0	2133	U
1	0	2243	C
1	0	2258	A
1	0	2271	G
1	0	2291	A

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Mol	Chain	Res	Type
1	0	2317	C
1	0	2320	U
1	0	2321	A
1	0	2345	A
1	0	2354	A
1	0	2361	A
1	0	2369	A
1	0	2379	G
1	0	2422	U
1	0	2462	G
1	0	2476	C
1	0	2480	G
1	0	2483	A
1	0	2507	G
1	0	2509	A
1	0	2511	A
1	0	2533	C
1	0	2537	G
1	0	2541	U
1	0	2553	A
1	0	2564	G
1	0	2589	U
1	0	2601	A
1	0	2602	G
1	0	2608	C
1	0	2613	G
1	0	2638	G
1	0	2645	U
1	0	2649	A
1	0	2664	A
1	0	2676	C
1	0	2681	A
1	0	2682	C
1	0	2726	U
1	0	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2762	C
1	0	2768	A
1	0	2792	A
1	0	2800	A

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Mol	Chain	Res	Type
1	0	2811	A
1	0	2812	A
1	0	2825	C
1	0	2836	G
1	0	2876	G
1	0	2890	A
1	0	2896	A
1	0	2903	C
1	0	2914	A
31	9	2	U
31	9	14	G
31	9	22	G
31	9	23	U
31	9	24	U
31	9	25	G
31	9	34	A
31	9	40	C
31	9	41	C
31	9	43	G
31	9	44	A
31	9	52	A
31	9	57	A
31	9	66	G
31	9	77	A
31	9	114	G
31	9	122	C

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	129	A
1	0	338	C
1	0	603	A
1	0	644	G
1	0	699	C
1	0	834	G
1	0	857	A
1	0	871	G
1	0	877	G
1	0	898	G
1	0	1165	G
1	0	1237	U

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Mol	Chain	Res	Type
1	0	1246	A
1	0	1352	A
1	0	1377	C
1	0	1474	C
1	0	1667	A
1	0	1684	A
1	0	1979	G
1	0	2467	A
1	0	2526	C
1	0	2536	C
1	0	2649	A
1	0	2718	C
1	0	2761	A
1	0	2791	U
31	9	65	A

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

5 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	$\# Z > 2$
1	OMU	0	2587	1,34	12,22,23	1.04	1 (8%)	19,31,34	3.15	2 (10%)
1	OMG	0	2588	1	17,26,27	1.02	1 (5%)	21,38,41	2.54	3 (14%)
1	UR3	0	2619	1	12,22,23	0.81	0	16,32,35	0.75	0
1	PSU	0	2621	1	13,21,22	1.68	2 (15%)	18,30,33	6.19	4 (22%)
1	1MA	0	628	1,34	14,25,26	1.03	1 (7%)	15,37,40	1.19	1 (6%)

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
1	OMU	0	2587	1,34	-	0/5/27/28	0/2/2/2
1	OMG	0	2588	1	-	0/5/27/28	0/3/3/3
1	UR3	0	2619	1	-	0/3/25/26	0/2/2/2
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	1MA	0	628	1,34	-	0/3/25/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C5-C1'	-5.13	1.47	1.52
1	0	2587	OMU	C4-N3	2.29	1.37	1.33
1	0	2621	PSU	C4-N3	2.51	1.37	1.33
1	0	628	1MA	C6-N6	2.75	1.34	1.29
1	0	2588	OMG	C6-N1	3.15	1.39	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	N1-C2-N3	-21.74	114.46	128.33
1	0	2588	OMG	C5-C6-N1	-8.73	111.66	123.59
1	0	628	1MA	C2-N3-C4	-3.66	110.73	116.40
1	0	2587	OMU	C5-C4-N3	-3.25	114.79	123.12
1	0	2588	OMG	N3-C2-N1	-2.32	123.91	127.44
1	0	2621	PSU	C5-C1'-C2'	-2.13	111.74	115.52
1	0	2621	PSU	C6-N1-C2	2.67	119.76	115.47
1	0	2588	OMG	C6-N1-C2	6.65	125.17	115.94
1	0	2587	OMU	C4-N3-C2	13.16	127.17	114.14
1	0	2621	PSU	C4-N3-C2	13.89	127.25	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2587	OMU	1	0
1	0	628	1MA	1	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 306 ligands modelled in this entry, 305 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
37	WIN	0	9101	-	38,43,43	1.88	8 (21%)	50,71,71	3.76	26 (52%)

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
37	WIN	0	9101	-	-	0/20/110/110	0/3/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	0	9101	WIN	C2B-C1X	-3.96	1.40	1.46
37	0	9101	WIN	C1N-C1W	-2.84	1.39	1.47
37	0	9101	WIN	C1B-C1V	2.10	1.54	1.50
37	0	9101	WIN	O1U-C2G	2.45	1.49	1.46
37	0	9101	WIN	O1U-C1Z	2.55	1.38	1.34
37	0	9101	WIN	C1C-C1Y	3.38	1.56	1.50
37	0	9101	WIN	C1N-C1V	5.00	1.41	1.33
37	0	9101	WIN	C2M-C2G	5.19	1.61	1.53

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	0	9101	WIN	C2F-O1T-C1W	-9.24	104.94	116.93
37	0	9101	WIN	C1C-C1Y-C2B	-7.22	113.13	122.11
37	0	9101	WIN	O1U-C1Z-C2F	-6.84	106.04	118.40
37	0	9101	WIN	O1J-C2A-C2L	-5.97	111.90	123.59
37	0	9101	WIN	O1T-C1W-O1G	-4.99	115.53	123.30
37	0	9101	WIN	O1H-C1X-C1P	-4.91	111.59	120.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	0	9101	WIN	C1O-C2M-C2K	-4.81	92.00	100.97
37	0	9101	WIN	O1U-C2G-C1Q	-4.76	96.58	105.00
37	0	9101	WIN	O1K-C2B-C1Y	-3.86	116.56	122.06
37	0	9101	WIN	C2H-C1Q-C2G	-3.34	102.67	111.48
37	0	9101	WIN	O1L-C2D-C2J	-3.00	101.83	111.83
37	0	9101	WIN	C1F-C2I-C2J	-2.71	106.07	113.04
37	0	9101	WIN	O1S-C1O-C2M	-2.40	103.02	105.83
37	0	9101	WIN	O1I-C1Z-C2F	-2.09	118.54	122.06
37	0	9101	WIN	O1K-C2B-C1X	2.14	120.02	115.79
37	0	9101	WIN	C2I-C2J-C2D	2.36	120.98	115.24
37	0	9101	WIN	C1F-C2I-C2H	2.81	114.87	109.96
37	0	9101	WIN	C2M-C2J-C2D	2.90	116.06	110.08
37	0	9101	WIN	C1A-O1R-C2A	3.33	121.87	116.00
37	0	9101	WIN	C1Q-C2G-C2M	4.74	121.06	113.99
37	0	9101	WIN	C1C-C1Y-C2H	5.05	130.28	116.45
37	0	9101	WIN	C1V-C1N-C1W	5.50	142.36	126.99
37	0	9101	WIN	C2I-C2H-C1Y	5.55	120.23	112.16
37	0	9101	WIN	O1U-C1Z-O1I	5.98	127.45	118.51
37	0	9101	WIN	C1O-C2M-C2G	6.15	123.74	112.83
37	0	9101	WIN	O1R-C2A-C2L	8.97	125.14	111.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
37	0	9101	WIN	13	0

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	0	2749/2923 (94%)	-0.61	6 (0%) 95 95	24, 56, 105, 182	0
2	A	237/237 (100%)	0.08	15 (6%) 23 17	35, 71, 114, 133	0
3	B	337/337 (100%)	-0.42	0 100 100	34, 65, 95, 108	0
4	C	246/246 (100%)	-0.41	0 100 100	31, 56, 80, 91	0
5	D	140/177 (79%)	1.48	48 (34%) 0 0	80, 120, 142, 152	0
6	E	172/172 (100%)	-0.14	1 (0%) 90 89	55, 81, 105, 112	0
7	F	119/119 (100%)	0.66	12 (10%) 9 5	64, 90, 122, 137	0
8	G	29/348 (8%)	0.85	2 (6%) 20 14	89, 109, 116, 119	0
9	H	160/177 (90%)	0.66	22 (13%) 4 2	57, 84, 120, 128	0
10	I	70/70 (100%)	3.89	55 (78%) 0 0	142, 164, 183, 184	0
11	J	142/142 (100%)	-0.42	1 (0%) 89 88	47, 60, 82, 104	0
12	K	132/132 (100%)	-0.42	3 (2%) 64 59	44, 61, 86, 91	0
13	L	145/165 (87%)	0.45	15 (10%) 9 5	35, 87, 131, 142	0
14	M	194/194 (100%)	-0.42	0 100 100	38, 55, 75, 82	0
15	N	186/186 (100%)	0.39	21 (11%) 7 4	55, 83, 139, 146	0
16	O	115/115 (100%)	-0.40	0 100 100	43, 66, 84, 88	0
17	P	143/143 (100%)	-0.25	1 (0%) 89 88	50, 70, 86, 94	0
18	Q	95/95 (100%)	-0.50	0 100 100	49, 60, 76, 89	0
19	R	150/150 (100%)	-0.56	0 100 100	38, 56, 78, 84	0
20	S	81/81 (100%)	0.01	2 (2%) 61 56	56, 76, 100, 108	0
21	T	119/119 (100%)	-0.04	3 (2%) 61 56	48, 71, 100, 127	0
22	U	53/53 (100%)	-0.27	0 100 100	56, 72, 95, 102	0
23	V	65/65 (100%)	1.54	16 (24%) 1 0	66, 94, 137, 144	0
24	W	154/154 (100%)	-0.45	1 (0%) 90 89	44, 60, 79, 90	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	X	82/82 (100%)	-0.07	5 (6%) 25 18	55, 71, 97, 111	0
26	Y	142/142 (100%)	-0.57	1 (0%) 89 88	31, 53, 80, 102	0
27	Z	73/73 (100%)	4.60	53 (72%) 0 0	99, 132, 149, 150	0
28	1	56/56 (100%)	-0.47	0 100 100	33, 41, 52, 62	0
29	2	46/50 (92%)	0.05	3 (6%) 22 16	48, 79, 112, 122	0
30	3	92/92 (100%)	0.31	3 (3%) 50 43	58, 85, 99, 109	0
31	9	122/122 (100%)	-0.77	2 (1%) 74 72	46, 78, 108, 156	0
All	All	6646/7217 (92%)	-0.20	291 (4%) 38 31	24, 64, 122, 184	0

All (291) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
27	Z	58	ASN	18.5
27	Z	46	SER	18.5
27	Z	35	SER	17.2
23	V	1	THR	14.5
10	I	74	ILE	14.1
27	Z	50	VAL	14.0
27	Z	43	GLY	11.3
27	Z	55	SER	10.7
23	V	39	ALA	10.6
27	Z	53	ILE	10.2
10	I	128	THR	9.9
27	Z	45	VAL	9.6
27	Z	47	ARG	9.5
27	Z	42	TYR	9.3
5	D	63	ILE	8.9
27	Z	69	ASP	8.6
27	Z	44	ARG	8.4
27	Z	59	GLU	8.0
10	I	70	THR	8.0
23	V	40	PRO	7.8
27	Z	38	PHE	7.8
10	I	72	GLU	7.4
27	Z	49	ARG	7.3
27	Z	34	SER	7.1
10	I	104	ALA	6.8
10	I	83	GLY	6.7
10	I	97	VAL	6.7
27	Z	54	GLU	6.6

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Mol	Chain	Res	Type	RSRZ
15	N	166	ALA	6.6
10	I	71	ALA	6.6
27	Z	57	MET	6.3
27	Z	48	ARG	6.3
10	I	102	GLN	6.2
10	I	132	VAL	6.0
10	I	66	GLY	5.9
10	I	106	GLN	5.9
5	D	88	LEU	5.7
27	Z	51	ALA	5.7
10	I	91	PHE	5.6
10	I	93	ALA	5.5
23	V	43	PRO	5.5
10	I	100	VAL	5.5
27	Z	68	GLU	5.5
5	D	69	ILE	5.4
2	A	85	SER	5.3
10	I	105	GLU	5.2
10	I	79	GLY	5.2
10	I	111	LEU	5.2
10	I	99	GLN	5.1
10	I	108	HIS	5.1
5	D	57	THR	5.1
7	F	106	ALA	5.1
2	A	37	VAL	5.1
27	Z	82	SER	5.0
5	D	90	LEU	5.0
10	I	73	LEU	4.9
5	D	27	ILE	4.7
27	Z	81	CYS	4.7
20	S	81	ILE	4.7
5	D	172	VAL	4.7
5	D	10	PHE	4.6
10	I	112	LEU	4.6
5	D	89	PRO	4.6
10	I	80	PHE	4.6
5	D	18	ILE	4.6
27	Z	62	ALA	4.5
10	I	127	CYS	4.5
5	D	44	ILE	4.5
27	Z	52	GLU	4.5
27	Z	40	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
9	H	141	CYS	4.4
5	D	25	MET	4.4
5	D	87	ALA	4.4
13	L	60	GLU	4.3
5	D	26	GLY	4.3
27	Z	56	GLU	4.3
27	Z	39	GLY	4.3
10	I	92	VAL	4.3
21	T	119	ALA	4.2
27	Z	78	ILE	4.2
27	Z	36	GLY	4.2
10	I	116	LEU	4.2
27	Z	60	ASP	4.2
23	V	38	GLY	4.1
10	I	110	ASP	4.1
13	L	80	ASP	4.1
10	I	113	SER	4.1
10	I	88	GLN	4.1
27	Z	37	ARG	4.1
10	I	69	PRO	4.0
5	D	85	GLN	4.0
7	F	49	PHE	4.0
10	I	130	LEU	3.9
27	Z	70	ARG	3.9
27	Z	83	TYR	3.9
15	N	145	ALA	3.9
5	D	40	ILE	3.9
27	Z	77	GLY	3.9
2	A	237	GLY	3.9
10	I	94	ASP	3.8
5	D	61	PHE	3.8
27	Z	63	CYS	3.8
10	I	98	ASP	3.8
10	I	109	PRO	3.8
13	L	106	VAL	3.8
10	I	75	LYS	3.7
27	Z	67	GLY	3.7
10	I	78	ALA	3.7
5	D	134	LEU	3.6
5	D	130	VAL	3.6
10	I	117	THR	3.6
9	H	40	GLN	3.6

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Mol	Chain	Res	Type	RSRZ
7	F	99	THR	3.6
15	N	185	GLU	3.6
2	A	80	LEU	3.6
10	I	103	ILE	3.6
8	G	23	ILE	3.6
27	Z	64	PRO	3.6
15	N	179	LEU	3.6
10	I	81	GLU	3.6
2	A	82	VAL	3.6
10	I	124	VAL	3.5
10	I	84	SER	3.5
15	N	178	THR	3.5
7	F	75	ILE	3.5
9	H	77	ILE	3.5
27	Z	79	TRP	3.5
2	A	31	LYS	3.5
15	N	147	ILE	3.4
13	L	91	VAL	3.4
10	I	76	ASP	3.4
10	I	121	LYS	3.4
9	H	146	ALA	3.4
5	D	128	LEU	3.4
9	H	86	TYR	3.4
9	H	90	LEU	3.4
9	H	133	GLY	3.3
27	Z	66	CYS	3.3
5	D	92	GLU	3.3
27	Z	41	ARG	3.3
27	Z	61	HIS	3.3
29	2	49	GLU	3.3
27	Z	93	TYR	3.3
27	Z	80	GLN	3.3
5	D	104	PHE	3.2
31	9	1	U	3.2
26	Y	235	GLU	3.2
7	F	15	ASP	3.2
5	D	64	ARG	3.2
27	Z	89	THR	3.2
2	A	83	GLY	3.2
5	D	170	TYR	3.2
1	0	1172	G	3.1
5	D	106	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
7	F	119	ARG	3.1
29	2	39	ARG	3.1
5	D	58	VAL	3.0
5	D	84	LEU	3.0
10	I	120	ALA	3.0
23	V	2	VAL	3.0
29	2	48	ASP	3.0
5	D	86	THR	3.0
10	I	86	GLU	3.0
5	D	22	VAL	3.0
13	L	147	GLU	2.9
2	A	88	ILE	2.9
7	F	44	SER	2.9
13	L	96	VAL	2.9
2	A	60	PHE	2.9
15	N	155	GLU	2.9
5	D	62	ASP	2.9
9	H	76	LEU	2.9
25	X	80	GLU	2.9
15	N	138	ASP	2.9
8	G	27	ILE	2.9
9	H	174	LEU	2.9
23	V	59	ILE	2.8
5	D	81	GLU	2.8
25	X	88	GLU	2.8
9	H	35	LYS	2.8
5	D	166	ILE	2.8
2	A	65	ARG	2.8
23	V	51	LYS	2.8
9	H	114	ASP	2.8
1	0	282	C	2.8
13	L	102	ASP	2.8
23	V	41	GLU	2.8
23	V	52	ALA	2.8
15	N	160	SER	2.7
13	L	75	LEU	2.7
5	D	75	LEU	2.7
21	T	116	ASP	2.7
9	H	48	VAL	2.7
21	T	118	SER	2.7
15	N	172	PHE	2.7
10	I	67	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
10	I	135	GLU	2.7
23	V	37	GLY	2.7
13	L	114	VAL	2.7
11	J	70	PHE	2.6
24	W	96	LEU	2.6
9	H	145	ASP	2.6
2	A	58	VAL	2.6
7	F	17	LEU	2.6
13	L	100	ALA	2.6
25	X	10	VAL	2.6
30	3	14	CYS	2.6
9	H	37	GLY	2.6
10	I	82	THR	2.6
27	Z	104	ARG	2.6
2	A	91	GLY	2.6
5	D	66	GLY	2.5
27	Z	85	ASP	2.5
12	K	132	VAL	2.5
5	D	23	VAL	2.5
5	D	43	GLU	2.5
10	I	68	PRO	2.5
13	L	118	LEU	2.5
6	E	10	ASP	2.5
10	I	118	ASN	2.5
10	I	131	GLY	2.5
15	N	140	GLN	2.4
5	D	70	GLY	2.4
10	I	123	VAL	2.4
27	Z	88	PHE	2.4
13	L	140	VAL	2.4
15	N	137	ALA	2.3
27	Z	101	LYS	2.3
15	N	181	ASP	2.3
27	Z	71	VAL	2.3
5	D	11	HIS	2.3
7	F	97	ALA	2.3
9	H	169	GLU	2.3
12	K	110	LYS	2.3
9	H	89	THR	2.3
15	N	183	ASP	2.3
2	A	36	ASP	2.3
13	L	150	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
5	D	157	LEU	2.3
15	N	83	LEU	2.3
23	V	3	LEU	2.3
31	9	24	U	2.3
7	F	117	GLU	2.3
9	H	87	LYS	2.2
1	0	1199	A	2.2
25	X	7	GLU	2.2
15	N	139	TRP	2.2
27	Z	74	GLN	2.2
13	L	105	TYR	2.2
15	N	152	GLU	2.2
1	0	1198	U	2.2
5	D	171	ASP	2.2
15	N	164	ASP	2.2
1	0	1948	G	2.2
5	D	93	LEU	2.2
10	I	129	SER	2.1
30	3	41	GLU	2.1
27	Z	65	ASN	2.1
1	0	1171	A	2.1
2	A	93	THR	2.1
9	H	66	GLU	2.1
15	N	159	TYR	2.1
17	P	71	TYR	2.1
5	D	72	LYS	2.1
5	D	167	GLU	2.1
20	S	76	GLU	2.1
2	A	89	ALA	2.1
10	I	119	ALA	2.1
9	H	140	TYR	2.1
23	V	36	ALA	2.1
5	D	101	THR	2.1
5	D	129	ASP	2.1
10	I	133	THR	2.1
12	K	101	ASN	2.1
9	H	85	ASP	2.1
7	F	63	ILE	2.1
23	V	5	VAL	2.1
25	X	74	ALA	2.1
23	V	61	GLY	2.0
30	3	13	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
9	H	142	ASN	2.0
5	D	17	ARG	2.0
5	D	165	PHE	2.0
13	L	145	LEU	2.0
23	V	49	LEU	2.0
15	N	67	ALA	2.0
7	F	39	SER	2.0
15	N	143	ARG	2.0
5	D	24	HIS	2.0
9	H	50	ILE	2.0
27	Z	103	VAL	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å ²)	Q<0.9
1	1MA	0	628	23/24	0.98	0.15	-	34,36,38,39	0
1	OMG	0	2588	24/25	0.99	0.12	-	42,44,46,48	0
1	OMU	0	2587	21/22	0.99	0.10	-	43,44,46,48	0
1	UR3	0	2619	21/22	0.98	0.14	-	45,48,51,54	0
1	PSU	0	2621	20/21	0.98	0.12	-	30,35,50,51	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(\AA^2)	Q<0.9
34	NA	0	8565	1/1	0.81	1.92	146.34	100,100,100,100	0
34	NA	0	8547	1/1	0.95	0.88	54.24	71,71,71,71	0
34	NA	0	8542	1/1	0.80	0.70	51.61	62,62,62,62	0
34	NA	0	8556	1/1	0.50	1.47	51.44	68,68,68,68	0
34	NA	0	8564	1/1	0.98	0.66	49.96	95,95,95,95	0
34	NA	0	8562	1/1	0.89	0.62	31.79	82,82,82,82	0
34	NA	0	8519	1/1	0.96	0.33	27.51	50,50,50,50	0
34	NA	0	8527	1/1	0.68	0.56	26.32	86,86,86,86	0
34	NA	0	8535	1/1	0.85	0.38	25.04	63,63,63,63	0
34	NA	9	8572	1/1	0.49	0.50	24.43	117,117,117,117	0
32	MG	9	8040	1/1	0.70	0.36	23.68	97,97,97,97	0
34	NA	0	8555	1/1	0.81	0.58	20.53	53,53,53,53	0
34	NA	0	8558	1/1	0.87	0.50	18.32	63,63,63,63	0
32	MG	0	8072	1/1	0.70	0.31	17.80	82,82,82,82	0
33	K	0	8402	1/1	0.89	0.46	15.10	90,90,90,90	0
36	SR	0	8903	1/1	1.00	0.21	14.91	66,66,66,66	0
34	NA	0	8553	1/1	0.87	0.42	13.88	69,69,69,69	0
34	NA	0	8559	1/1	0.73	0.25	12.73	95,95,95,95	0
36	SR	0	8949	1/1	0.66	0.20	11.90	146,146,146,146	0
32	MG	0	8009	1/1	0.99	0.35	11.25	42,42,42,42	0
32	MG	0	8047	1/1	0.89	0.39	10.97	71,71,71,71	0
34	NA	0	8504	1/1	0.68	0.34	10.50	46,46,46,46	0
32	MG	0	8070	1/1	0.98	0.28	10.27	64,64,64,64	0
34	NA	0	8560	1/1	0.67	0.54	10.15	97,97,97,97	0
34	NA	0	8575	1/1	0.95	0.27	9.71	87,87,87,87	0
34	NA	0	8511	1/1	0.87	0.22	8.93	67,67,67,67	0
36	SR	B	8987	1/1	0.76	0.54	8.91	200,200,200,200	0
34	NA	0	8530	1/1	0.90	0.30	8.26	60,60,60,60	0
36	SR	0	8908	1/1	0.81	0.29	8.10	175,175,175,175	0
37	WIN	0	9101	39/39	0.83	0.33	7.92	125,127,128,129	0
32	MG	0	8041	1/1	0.95	0.23	7.56	32,32,32,32	0
32	MG	0	8028	1/1	0.99	0.25	7.51	30,30,30,30	0
34	NA	0	8563	1/1	0.71	0.24	6.64	82,82,82,82	0
32	MG	0	8014	1/1	0.97	0.20	6.51	33,33,33,33	0
34	NA	0	8534	1/1	0.95	0.26	6.37	47,47,47,47	0
34	NA	0	8537	1/1	0.87	0.21	6.34	50,50,50,50	0
34	NA	M	8539	1/1	0.97	0.29	6.16	53,53,53,53	0
32	MG	0	8067	1/1	0.98	0.26	5.95	34,34,34,34	0
32	MG	0	8062	1/1	0.82	0.28	5.78	61,61,61,61	0
35	CL	0	8815	1/1	0.89	0.14	5.33	83,83,83,83	0
34	NA	0	8521	1/1	0.94	0.26	4.88	71,71,71,71	0
34	NA	0	8522	1/1	0.56	0.14	4.48	108,108,108,108	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
36	SR	0	8904	1/1	0.97	0.20	4.45	64,64,64,64	0
32	MG	0	8006	1/1	0.81	0.17	3.60	33,33,33,33	0
32	MG	0	8012	1/1	0.98	0.20	3.59	26,26,26,26	0
32	MG	0	8011	1/1	0.98	0.24	3.39	30,30,30,30	0
35	CL	0	8816	1/1	0.98	0.22	3.07	75,75,75,75	0
32	MG	0	8008	1/1	0.98	0.16	3.05	32,32,32,32	0
36	SR	0	8902	1/1	0.89	0.17	2.86	70,70,70,70	0
34	NA	0	8568	1/1	0.87	0.22	2.75	57,57,57,57	0
34	NA	0	8523	1/1	0.77	0.16	2.60	65,65,65,65	0
32	MG	0	8004	1/1	0.99	0.17	2.50	29,29,29,29	0
34	NA	0	8528	1/1	0.93	0.17	2.41	60,60,60,60	0
32	MG	0	8043	1/1	0.92	0.16	2.33	58,58,58,58	0
32	MG	0	8002	1/1	0.89	0.18	2.08	26,26,26,26	0
34	NA	0	8533	1/1	0.89	0.15	1.87	72,72,72,72	0
32	MG	0	8050	1/1	0.71	0.19	1.75	74,74,74,74	0
36	SR	0	8962	1/1	0.88	0.18	1.65	180,180,180,180	0
32	MG	0	8055	1/1	0.99	0.20	1.36	49,49,49,49	0
32	MG	0	8084	1/1	0.88	0.14	1.29	36,36,36,36	0
32	MG	A	8051	1/1	0.88	0.29	1.21	98,98,98,98	0
32	MG	0	8088	1/1	0.98	0.18	1.13	46,46,46,46	0
36	SR	A	8930	1/1	0.82	0.26	0.98	169,169,169,169	0
34	NA	C	8503	1/1	0.54	0.25	0.85	46,46,46,46	0
38	CD	1	8702	1/1	0.99	0.14	0.79	72,72,72,72	0
32	MG	0	8075	1/1	0.72	0.11	0.65	58,58,58,58	0
32	MG	0	8001	1/1	0.94	0.15	0.61	26,26,26,26	0
32	MG	0	8003	1/1	0.98	0.15	0.60	35,35,35,35	0
35	CL	O	8808	1/1	0.97	0.20	0.28	79,79,79,79	0
34	NA	0	8569	1/1	0.98	0.16	0.23	61,61,61,61	0
32	MG	B	8042	1/1	0.98	0.13	0.18	62,62,62,62	0
34	NA	J	8538	1/1	0.85	0.21	0.04	67,67,67,67	0
36	SR	0	8943	1/1	0.84	0.10	-0.03	95,95,95,95	0
34	NA	Q	8540	1/1	0.87	0.13	-0.28	58,58,58,58	0
34	NA	0	8520	1/1	0.90	0.10	-0.36	55,55,55,55	0
34	NA	0	8515	1/1	0.82	0.15	-0.37	50,50,50,50	0
38	CD	U	8701	1/1	1.00	0.12	-0.37	71,71,71,71	0
36	SR	0	8972	1/1	0.68	0.14	-0.45	164,164,164,164	0
35	CL	K	8812	1/1	0.98	0.11	-0.69	57,57,57,57	0
35	CL	0	8805	1/1	0.97	0.10	-0.78	76,76,76,76	0
32	MG	0	8021	1/1	0.98	0.10	-0.80	43,43,43,43	0
36	SR	0	8910	1/1	0.71	0.11	-0.95	106,106,106,106	0
36	SR	A	8929	1/1	0.89	0.09	-0.98	142,142,142,142	0
36	SR	0	8969	1/1	0.84	0.14	-0.99	173,173,173,173	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	0	8034	1/1	0.93	0.14	-1.05	47,47,47,47	0
36	SR	0	8975	1/1	0.90	0.07	-1.10	154,154,154,154	0
35	CL	L	8810	1/1	0.94	0.09	-1.11	69,69,69,69	0
36	SR	0	8935	1/1	0.98	0.09	-1.23	93,93,93,93	0
32	MG	0	8045	1/1	0.95	0.08	-1.26	30,30,30,30	0
35	CL	J	8821	1/1	0.96	0.09	-1.36	78,78,78,78	0
32	MG	0	8058	1/1	0.97	0.07	-1.46	23,23,23,23	0
36	SR	0	8992	1/1	0.94	0.11	-1.80	137,137,137,137	0
34	NA	0	8545	1/1	0.95	0.14	-2.03	48,48,48,48	0
32	MG	0	8025	1/1	0.97	0.10	-2.12	37,37,37,37	0
32	MG	0	8010	1/1	0.98	0.11	-2.26	34,34,34,34	0
32	MG	Y	8086	1/1	0.97	0.10	-2.42	55,55,55,55	0
36	SR	0	8985	1/1	0.95	0.05	-2.44	148,148,148,148	0
38	CD	3	8704	1/1	0.99	0.06	-2.46	94,94,94,94	0
32	MG	0	8087	1/1	0.96	0.13	-2.59	36,36,36,36	0
36	SR	0	8984	1/1	0.75	0.07	-2.66	143,143,143,143	0
35	CL	B	8819	1/1	0.98	0.10	-2.78	57,57,57,57	0
32	MG	0	8052	1/1	0.84	0.06	-2.84	58,58,58,58	0
32	MG	T	8057	1/1	0.92	0.04	-2.92	72,72,72,72	0
36	SR	0	8970	1/1	0.93	0.06	-3.08	135,135,135,135	0
35	CL	3	8804	1/1	0.74	0.07	-3.26	76,76,76,76	0
36	SR	0	8936	1/1	0.98	0.07	-3.32	108,108,108,108	0
32	MG	0	8065	1/1	0.97	0.07	-3.78	41,41,41,41	0
38	CD	Z	8703	1/1	0.92	0.06	-3.80	172,172,172,172	0
35	CL	M	8818	1/1	0.98	0.04	-3.88	49,49,49,49	0
32	MG	0	8013	1/1	0.92	0.06	-4.27	30,30,30,30	0
34	NA	0	8557	1/1	0.80	0.04	-6.57	74,74,74,74	0
32	MG	0	8044	1/1	0.94	0.05	-6.61	55,55,55,55	0
34	NA	0	8517	1/1	0.97	0.10	-9.75	36,36,36,36	0
36	SR	9	8978	1/1	0.78	0.11	-	169,169,169,169	0
36	SR	0	9001	1/1	0.72	0.16	-	184,184,184,184	0
36	SR	0	8957	1/1	0.92	0.21	-	200,200,200,200	0
36	SR	0	8964	1/1	0.80	0.10	-	139,139,139,139	0
36	SR	0	8967	1/1	0.96	0.04	-	147,147,147,147	0
32	MG	0	8022	1/1	0.99	0.17	-	37,37,37,37	0
36	SR	0	8986	1/1	0.85	0.48	-	200,200,200,200	0
32	MG	0	8046	1/1	0.97	0.18	-	53,53,53,53	0
32	MG	0	8079	1/1	0.92	0.30	-	67,67,67,67	0
36	SR	R	8912	1/1	0.99	0.19	-	93,93,93,93	0
34	NA	0	8502	1/1	0.68	0.20	-	66,66,66,66	0
34	NA	0	8561	1/1	0.86	0.65	-	90,90,90,90	0
32	MG	0	8031	1/1	0.93	0.34	-	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
34	NA	0	8505	1/1	0.88	1.07	-	44,44,44,44	0
32	MG	0	8032	1/1	0.95	0.06	-	42,42,42,42	0
32	MG	0	8007	1/1	0.97	0.19	-	40,40,40,40	0
34	NA	0	8548	1/1	0.76	0.29	-	67,67,67,67	0
34	NA	0	8546	1/1	0.94	0.73	-	85,85,85,85	0
36	SR	0	8909	1/1	0.87	0.17	-	99,99,99,99	0
32	MG	0	8038	1/1	0.77	0.09	-	70,70,70,70	0
36	SR	0	8995	1/1	0.78	0.14	-	142,142,142,142	0
36	SR	0	9008	1/1	0.75	0.24	-	111,111,111,111	0
32	MG	0	8071	1/1	0.93	0.12	-	71,71,71,71	0
32	MG	0	8016	1/1	0.96	0.16	-	30,30,30,30	0
36	SR	0	8911	1/1	0.99	0.08	-	95,95,95,95	0
32	MG	0	8026	1/1	0.99	0.12	-	55,55,55,55	0
35	CL	0	8817	1/1	0.98	0.05	-	68,68,68,68	0
32	MG	0	8063	1/1	0.87	0.22	-	80,80,80,80	0
32	MG	0	8020	1/1	0.91	0.16	-	57,57,57,57	0
36	SR	0	8906	1/1	0.99	0.23	-	67,67,67,67	0
35	CL	0	8813	1/1	0.98	0.02	-	54,54,54,54	0
32	MG	2	8060	1/1	0.92	0.10	-	65,65,65,65	0
32	MG	0	8082	1/1	0.90	0.30	-	81,81,81,81	0
34	NA	0	8529	1/1	0.76	0.07	-	50,50,50,50	0
34	NA	0	8526	1/1	0.94	0.12	-	45,45,45,45	0
36	SR	9	9003	1/1	0.45	0.06	-	187,187,187,187	0
32	MG	0	8039	1/1	0.86	0.22	-	63,63,63,63	0
32	MG	0	8085	1/1	0.88	0.11	-	69,69,69,69	0
36	SR	0	8965	1/1	0.74	0.11	-	151,151,151,151	0
32	MG	0	8024	1/1	0.94	0.20	-	54,54,54,54	0
34	NA	0	8550	1/1	0.82	0.49	-	59,59,59,59	0
34	NA	0	8501	1/1	0.84	0.18	-	54,54,54,54	0
32	MG	0	8076	1/1	0.96	0.10	-	38,38,38,38	0
32	MG	0	8093	1/1	0.97	0.07	-	45,45,45,45	0
36	SR	3	8932	1/1	0.96	0.10	-	94,94,94,94	0
34	NA	0	8544	1/1	0.90	0.19	-	73,73,73,73	0
32	MG	0	8005	1/1	0.96	0.23	-	35,35,35,35	0
36	SR	0	8981	1/1	0.87	0.21	-	158,158,158,158	0
36	SR	S	8961	1/1	0.83	0.12	-	145,145,145,145	0
36	SR	0	8959	1/1	0.65	0.25	-	181,181,181,181	0
36	SR	0	8937	1/1	0.86	0.33	-	125,125,125,125	0
36	SR	0	8976	1/1	0.68	0.23	-	200,200,200,200	0
36	SR	0	8920	1/1	0.83	0.57	-	185,185,185,185	0
35	CL	0	8811	1/1	0.96	0.11	-	72,72,72,72	0
32	MG	0	8048	1/1	0.96	0.23	-	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
34	NA	0	8552	1/1	0.96	0.27	-	80,80,80,80	0
32	MG	0	8019	1/1	0.94	0.23	-	30,30,30,30	0
36	SR	0	8993	1/1	0.96	0.05	-	178,178,178,178	0
34	NA	0	8541	1/1	0.93	0.34	-	70,70,70,70	0
34	NA	0	8512	1/1	0.91	0.30	-	48,48,48,48	0
34	NA	0	8513	1/1	0.96	0.33	-	56,56,56,56	0
32	MG	0	8030	1/1	0.78	0.33	-	79,79,79,79	0
38	CD	O	8705	1/1	0.98	0.06	-	105,105,105,105	0
36	SR	0	8918	1/1	0.99	0.14	-	94,94,94,94	0
36	SR	1	8952	1/1	0.92	0.16	-	93,93,93,93	0
34	NA	R	8532	1/1	0.87	0.11	-	59,59,59,59	0
36	SR	0	8968	1/1	0.83	0.06	-	165,165,165,165	0
32	MG	0	8090	1/1	-0.01	0.56	-	121,121,121,121	0
32	MG	0	8018	1/1	0.88	0.28	-	54,54,54,54	0
36	SR	0	8953	1/1	0.99	0.19	-	164,164,164,164	0
36	SR	0	8917	1/1	0.56	0.22	-	151,151,151,151	0
36	SR	0	9007	1/1	0.96	0.69	-	199,199,199,199	0
36	SR	0	8947	1/1	0.96	0.25	-	200,200,200,200	0
36	SR	0	8933	1/1	0.63	0.09	-	143,143,143,143	0
36	SR	9	8980	1/1	0.78	0.05	-	175,175,175,175	0
36	SR	0	8974	1/1	0.95	0.22	-	179,179,179,179	0
32	MG	0	8089	1/1	0.65	0.16	-	64,64,64,64	0
36	SR	0	8928	1/1	0.70	0.09	-	151,151,151,151	0
36	SR	0	8991	1/1	0.71	0.26	-	195,195,195,195	0
36	SR	0	8983	1/1	0.62	0.12	-	199,199,199,199	0
35	CL	Y	8820	1/1	0.98	0.05	-	46,46,46,46	0
36	SR	0	8925	1/1	0.98	0.11	-	95,95,95,95	0
32	MG	0	8035	1/1	0.96	0.19	-	70,70,70,70	0
34	NA	0	8516	1/1	0.93	0.15	-	37,37,37,37	0
36	SR	0	8956	1/1	0.78	0.10	-	187,187,187,187	0
32	MG	0	8061	1/1	0.96	0.22	-	36,36,36,36	0
32	MG	0	8036	1/1	0.93	0.12	-	60,60,60,60	0
36	SR	0	8926	1/1	0.97	0.12	-	142,142,142,142	0
32	MG	0	8027	1/1	0.85	0.17	-	47,47,47,47	0
34	NA	0	8551	1/1	0.96	0.20	-	60,60,60,60	0
34	NA	0	8536	1/1	0.82	0.06	-	65,65,65,65	0
36	SR	0	8988	1/1	0.89	0.12	-	158,158,158,158	0
36	SR	0	8989	1/1	0.87	0.17	-	185,185,185,185	0
36	SR	0	8998	1/1	0.54	0.24	-	175,175,175,175	0
36	SR	0	8982	1/1	0.62	0.96	-	200,200,200,200	0
32	MG	0	8069	1/1	0.82	0.19	-	49,49,49,49	0
32	MG	0	8033	1/1	0.95	0.20	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
36	SR	0	8955	1/1	0.72	0.10	-	198,198,198,198	0
36	SR	0	8940	1/1	0.96	0.10	-	94,94,94,94	0
32	MG	0	8078	1/1	0.93	0.29	-	54,54,54,54	0
36	SR	0	8915	1/1	0.67	0.10	-	136,136,136,136	0
34	NA	0	8571	1/1	0.86	0.30	-	98,98,98,98	0
32	MG	0	8080	1/1	0.88	0.30	-	87,87,87,87	0
34	NA	0	8509	1/1	0.90	0.27	-	77,77,77,77	0
32	MG	0	8073	1/1	0.95	0.08	-	80,80,80,80	0
32	MG	0	8083	1/1	0.99	0.27	-	74,74,74,74	0
33	K	0	8401	1/1	0.78	0.89	-	123,123,123,123	0
36	SR	0	8922	1/1	0.81	0.28	-	156,156,156,156	0
36	SR	0	8960	1/1	0.94	0.10	-	151,151,151,151	0
34	NA	0	8567	1/1	0.88	0.51	-	87,87,87,87	0
36	SR	0	8905	1/1	0.99	0.26	-	73,73,73,73	0
36	SR	F	9005	1/1	0.93	0.04	-	149,149,149,149	0
36	SR	0	8979	1/1	0.93	0.10	-	195,195,195,195	0
36	SR	0	8938	1/1	0.62	0.06	-	191,191,191,191	0
36	SR	0	8946	1/1	0.96	0.17	-	129,129,129,129	0
36	SR	0	8971	1/1	0.89	0.06	-	185,185,185,185	0
36	SR	0	8944	1/1	0.34	0.16	-	178,178,178,178	0
32	MG	0	8092	1/1	0.82	0.10	-	80,80,80,80	0
36	SR	0	8919	1/1	0.93	0.08	-	179,179,179,179	0
34	NA	0	8554	1/1	0.43	0.43	-	70,70,70,70	0
36	SR	0	8924	1/1	0.77	0.21	-	149,149,149,149	0
36	SR	0	8934	1/1	0.85	0.32	-	166,166,166,166	0
32	MG	0	8066	1/1	0.87	0.34	-	88,88,88,88	0
34	NA	0	8525	1/1	0.36	0.27	-	93,93,93,93	0
36	SR	0	8966	1/1	0.49	0.14	-	120,120,120,120	0
34	NA	0	8573	1/1	0.89	0.13	-	87,87,87,87	0
34	NA	0	8507	1/1	0.90	0.17	-	46,46,46,46	0
36	SR	0	8916	1/1	0.88	0.10	-	129,129,129,129	0
32	MG	0	8068	1/1	0.92	0.09	-	67,67,67,67	0
35	CL	A	8809	1/1	0.94	0.31	-	96,96,96,96	0
36	SR	3	8999	1/1	0.98	0.10	-	140,140,140,140	0
32	MG	0	8015	1/1	0.98	0.14	-	33,33,33,33	0
35	CL	R	8806	1/1	1.00	0.11	-	55,55,55,55	0
34	NA	0	8508	1/1	0.91	0.20	-	63,63,63,63	0
36	SR	0	9006	1/1	0.56	0.57	-	200,200,200,200	0
35	CL	J	8802	1/1	0.98	0.08	-	79,79,79,79	0
36	SR	0	8914	1/1	0.91	0.30	-	127,127,127,127	0
34	NA	0	8531	1/1	0.75	0.23	-	50,50,50,50	0
32	MG	0	8023	1/1	0.96	0.20	-	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	0	8017	1/1	0.98	0.08	-	34,34,34,34	0
32	MG	0	8056	1/1	0.95	0.15	-	62,62,62,62	0
34	NA	9	8543	1/1	0.96	0.17	-	57,57,57,57	0
32	MG	0	8077	1/1	0.98	0.06	-	43,43,43,43	0
34	NA	0	8514	1/1	0.89	0.71	-	54,54,54,54	0
34	NA	0	8566	1/1	0.75	0.59	-	59,59,59,59	0
32	MG	0	8037	1/1	0.84	0.16	-	80,80,80,80	0
32	MG	0	8029	1/1	0.96	0.17	-	69,69,69,69	0
32	MG	0	8091	1/1	0.60	0.13	-	89,89,89,89	0
36	SR	0	8990	1/1	0.90	0.11	-	116,116,116,116	0
36	SR	0	9000	1/1	0.76	0.20	-	200,200,200,200	0
32	MG	9	8074	1/1	0.95	0.14	-	101,101,101,101	0
36	SR	0	8994	1/1	0.80	0.40	-	199,199,199,199	0
36	SR	0	8901	1/1	0.85	0.14	-	96,96,96,96	0
35	CL	0	8822	1/1	0.97	0.35	-	86,86,86,86	0
35	CL	N	8807	1/1	0.97	0.17	-	72,72,72,72	0
36	SR	0	8997	1/1	0.80	1.16	-	200,200,200,200	0
36	SR	0	8941	1/1	0.59	0.23	-	131,131,131,131	0
36	SR	B	8950	1/1	0.75	0.12	-	119,119,119,119	0
32	MG	0	8064	1/1	0.93	0.18	-	51,51,51,51	0
36	SR	0	8996	1/1	0.63	0.47	-	200,200,200,200	0
34	NA	S	8510	1/1	0.97	0.15	-	50,50,50,50	0
35	CL	J	8801	1/1	0.93	0.09	-	82,82,82,82	0
34	NA	H	8518	1/1	0.76	0.50	-	95,95,95,95	0
36	SR	0	8927	1/1	0.97	0.11	-	167,167,167,167	0
35	CL	0	8814	1/1	0.97	0.09	-	66,66,66,66	0
36	SR	0	8923	1/1	0.91	0.15	-	112,112,112,112	0
36	SR	0	8954	1/1	0.87	0.11	-	109,109,109,109	0
36	SR	0	8977	1/1	0.11	0.06	-	197,197,197,197	0
36	SR	0	8939	1/1	0.93	0.06	-	145,145,145,145	0
36	SR	0	9004	1/1	0.95	0.47	-	200,200,200,200	0
36	SR	0	8931	1/1	0.92	0.09	-	136,136,136,136	0
36	SR	0	9002	1/1	0.84	0.15	-	183,183,183,183	0
36	SR	0	8973	1/1	0.97	0.11	-	141,141,141,141	0
34	NA	0	8506	1/1	0.52	0.22	-	76,76,76,76	0
35	CL	0	8803	1/1	0.95	0.07	-	62,62,62,62	0
36	SR	0	8921	1/1	0.94	0.11	-	99,99,99,99	0
36	SR	0	8913	1/1	0.54	0.82	-	200,200,200,200	0
36	SR	0	8945	1/1	0.95	0.07	-	131,131,131,131	0
36	SR	0	8907	1/1	1.00	0.14	-	62,62,62,62	0
32	MG	0	8059	1/1	0.91	0.12	-	52,52,52,52	0
32	MG	0	8049	1/1	0.93	0.53	-	116,116,116,116	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
36	SR	0	8948	1/1	0.93	0.16	-	122,122,122,122	0
34	NA	0	8549	1/1	0.76	0.91	-	60,60,60,60	0
34	NA	0	8574	1/1	0.93	0.40	-	69,69,69,69	0
32	MG	K	8054	1/1	0.82	0.21	-	47,47,47,47	0
34	NA	0	8570	1/1	0.96	0.08	-	59,59,59,59	0
34	NA	0	8524	1/1	0.55	0.62	-	73,73,73,73	0
36	SR	0	8958	1/1	0.76	0.12	-	121,121,121,121	0
36	SR	0	8963	1/1	0.96	0.08	-	133,133,133,133	0
36	SR	0	8942	1/1	0.75	0.18	-	144,144,144,144	0
36	SR	0	8951	1/1	0.77	0.05	-	149,149,149,149	0
32	MG	0	8053	1/1	0.88	0.06	-	69,69,69,69	0
32	MG	0	8081	1/1	0.94	0.17	-	81,81,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.