



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 04:16 PM GMT

PDB ID : 3CCV  
Title : Structure of Anisomycin resistant 50S Ribosomal Subunit: 23S rRNA mutation G2616A  
Authors : Blaha, G.; Gurel, G.  
Deposited on : 2008-02-26  
Resolution : 2.90 Å(reported)

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

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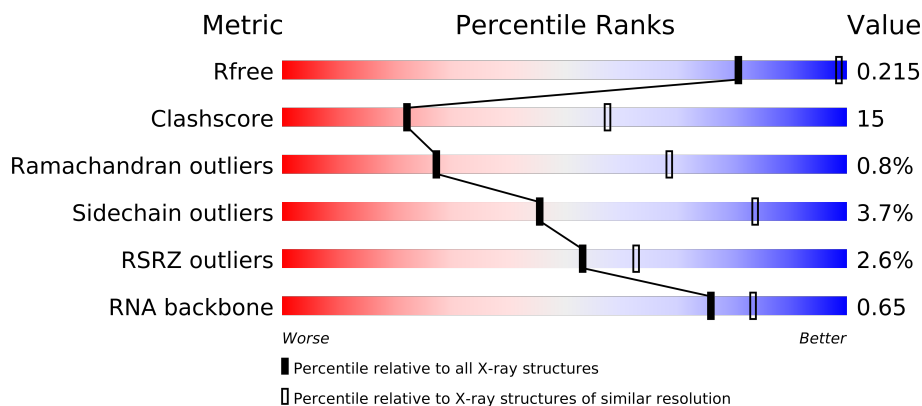
The following versions of software and data (see [references](#)) were used in the production of this report:

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

# 1 Overall quality at a glance

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)
RNA backbone	1838	1055 (3.40-2.40)

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

Mol	Chain	Length	Quality of chain
1	A	240	
2	B	338	
3	C	246	
4	D	177	
5	E	178	
6	F	120	
7	G	348	
8	H	177	
9	I	162	
10	J	145	
11	K	132	

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Mol	Chain	Length	Quality of chain
12	L	165	
13	M	196	
14	N	187	
15	O	116	
16	P	149	
17	Q	96	
18	R	155	
19	S	85	
20	T	120	
21	U	67	
22	V	71	
23	W	154	
24	X	92	
25	Y	241	
26	Z	116	
27	1	57	
28	2	50	
29	3	92	
30	0	2923	
31	9	122	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
32	MG	0	8003	-	X
32	MG	0	8004	-	X
32	MG	0	8009	-	X
32	MG	0	8014	-	X
32	MG	0	8016	-	X
32	MG	0	8022	-	X
32	MG	0	8026	-	X
32	MG	0	8028	-	X
32	MG	0	8029	-	X
32	MG	0	8030	-	X
32	MG	0	8037	-	X
32	MG	0	8039	-	X
32	MG	0	8040	-	X
32	MG	0	8041	-	X
32	MG	0	8047	-	X
32	MG	0	8048	-	X
32	MG	0	8049	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
32	MG	0	8055	-	X
32	MG	0	8061	-	X
32	MG	0	8063	-	X
32	MG	0	8066	-	X
32	MG	0	8067	-	X
32	MG	0	8071	-	X
32	MG	0	8072	-	X
32	MG	0	8078	-	X
32	MG	0	8080	-	X
32	MG	0	8081	-	X
32	MG	0	8084	-	X
32	MG	0	8090	-	X
32	MG	9	8074	-	X
32	MG	A	8051	-	X
34	NA	0	8501	-	X
34	NA	0	8505	-	X
34	NA	0	8506	-	X
34	NA	0	8509	-	X
34	NA	0	8512	-	X
34	NA	0	8513	-	X
34	NA	0	8514	-	X
34	NA	0	8518	-	X
34	NA	0	8521	-	X
34	NA	0	8522	-	X
34	NA	0	8524	-	X
34	NA	0	8525	-	X
34	NA	0	8527	-	X
34	NA	0	8528	-	X
34	NA	0	8530	-	X
34	NA	0	8535	-	X
34	NA	0	8537	-	X
34	NA	0	8541	-	X
34	NA	0	8542	-	X
34	NA	0	8546	-	X
34	NA	0	8547	-	X
34	NA	0	8548	-	X
34	NA	0	8549	-	X
34	NA	0	8550	-	X
34	NA	0	8551	-	X
34	NA	0	8552	-	X
34	NA	0	8553	-	X
34	NA	0	8554	-	X

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Mol	Type	Chain	Res	Geometry	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	8561	-	X
34	NA	0	8562	-	X
34	NA	0	8563	-	X
34	NA	0	8564	-	X
34	NA	0	8565	-	X
34	NA	0	8566	-	X
34	NA	0	8567	-	X
34	NA	0	8568	-	X
34	NA	0	8573	-	X
34	NA	0	8574	-	X
34	NA	0	8575	-	X
34	NA	9	8572	-	X
35	CL	0	8816	-	X
35	CL	0	8822	-	X
36	SR	0	8903	-	X
36	SR	0	8904	-	X
36	SR	0	8905	-	X
36	SR	0	8909	-	X
36	SR	0	8914	-	X
36	SR	0	8924	-	X
36	SR	0	8925	-	X
36	SR	0	8937	-	X
36	SR	0	8955	-	X
36	SR	0	8957	-	X
36	SR	0	8962	-	X
36	SR	0	8969	-	X
36	SR	0	8976	-	X
36	SR	0	8979	-	X
36	SR	0	8982	-	X
36	SR	0	8986	-	X
36	SR	0	8994	-	X
36	SR	0	8996	-	X
36	SR	0	8997	-	X
36	SR	0	9001	-	X
36	SR	0	9004	-	X
36	SR	0	9007	-	X
36	SR	B	8987	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
36	SR	R	8912	-	X
36	SR	Y	9002	-	X

## 2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99121 atoms, of which 0 are hydrogen and 0 are deuterium.

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

- Molecule 1 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	0	0	0
			1753	1072	352	324	5			

- Molecule 2 is a protein called 50S ribosomal protein L3P.

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

- Molecule 3 is a protein called 50S ribosomal protein L4P.

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

- Molecule 4 is a protein called 50S ribosomal protein L5P.

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

- Molecule 5 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	172	Total	C	N	O	S	0	0	0
			1357	840	224	289	4			

- Molecule 6 is a protein called 50S ribosomal protein L7Ae.

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

- Molecule 7 is a protein called 50S ribosomal protein L10E.

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

- Molecule 8 is a protein called 50S ribosomal protein L10e.

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

- Molecule 9 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	70	Total	C	N	O	S	0	0	0
			519	323	81	114	1			

- Molecule 10 is a protein called 50S ribosomal protein L13P.

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

- Molecule 11 is a protein called 50S ribosomal protein L14P.

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

- Molecule 12 is a protein called 50S ribosomal protein L15P.

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

- Molecule 13 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	194	Total	C	N	O	S	0	0	0
			1558	943	333	281	1			

- Molecule 14 is a protein called 50S ribosomal protein L18P.



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

- Molecule 15 is a protein called 50S ribosomal protein L18e.

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

- Molecule 16 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	143	Total	C	N	O		0	0	0
			1136	683	229	224				

- Molecule 17 is a protein called 50S ribosomal protein L21e.

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

- Molecule 18 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	150	Total	C	N	O	S	0	0	0
			1149	713	209	223	4			

- Molecule 19 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	0
			641	389	111	138	3			

- Molecule 20 is a protein called 50S ribosomal protein L24P.

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

- Molecule 21 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	53	Total	C	N	O	S	0	0	0
			410	244	75	86	5			

- Molecule 22 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	65	Total	C	N	O	S	0	0	0
			499	304	94	100	1			

- Molecule 23 is a protein called 50S ribosomal protein L30P.

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

- Molecule 24 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	X	82	Total	C	N	O	S	0	0	0
			654	402	129	122	1			

- Molecule 25 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	Y	142	Total	C	N	O		0	0	0
			1130	686	228	216				

- Molecule 26 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Z	73	Total	C	N	O	S	0	0	0
			573	343	113	112	5			

- Molecule 27 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 28 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 29 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 30 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	0	2754	Total	C	N	O	P	0	0	0
			59019	26349	10873	19052	2745			

- 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	87	Total	Mg	0	0
			87	87		
32	Y	1	Total	Mg	0	0
			1	1		
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	9	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	67	Total Na 67 67	0	0
34	J	1	Total Na 1 1	0	0
34	Q	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	10	Total Cl 10 10	0	0
35	J	3	Total Cl 3 3	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
35	Y	1	Total Cl 1 1	0	0
35	L	1	Total Cl 1 1	0	0

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	94	Total 94	Sr 94	0	0
36	Y	1	Total 1	Sr 1	0	0
36	B	2	Total 2	Sr 2	0	0
36	1	2	Total 2	Sr 2	0	0
36	A	3	Total 3	Sr 3	0	0
36	3	1	Total 1	Sr 1	0	0
36	R	1	Total 1	Sr 1	0	0
36	9	2	Total 2	Sr 2	0	0
36	S	1	Total 1	Sr 1	0	0
36	F	1	Total 1	Sr 1	0	0

- Molecule 37 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	O	1	Total 1	Cd 1	0	0
37	Z	1	Total 1	Cd 1	0	0
37	1	1	Total 1	Cd 1	0	0
37	3	1	Total 1	Cd 1	0	0
37	U	1	Total 1	Cd 1	0	0

- Molecule 38 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
38	0	5910	Total O 5910 5910	0	0
38	9	142	Total O 142 142	0	0
38	A	112	Total O 112 112	0	0
38	B	149	Total O 149 149	0	0
38	C	185	Total O 185 185	0	0
38	D	49	Total O 49 49	0	0
38	E	45	Total O 45 45	0	0
38	F	26	Total O 26 26	0	0
38	G	17	Total O 17 17	0	0
38	H	67	Total O 67 67	0	0
38	I	8	Total O 8 8	0	0
38	J	51	Total O 51 51	0	0
38	K	51	Total O 51 51	0	0
38	L	89	Total O 89 89	0	0
38	M	133	Total O 133 133	0	0
38	N	61	Total O 61 61	0	0
38	O	39	Total O 39 39	0	0
38	P	62	Total O 62 62	0	0
38	Q	45	Total O 45 45	0	0
38	R	81	Total O 81 81	0	0
38	S	32	Total O 32 32	0	0

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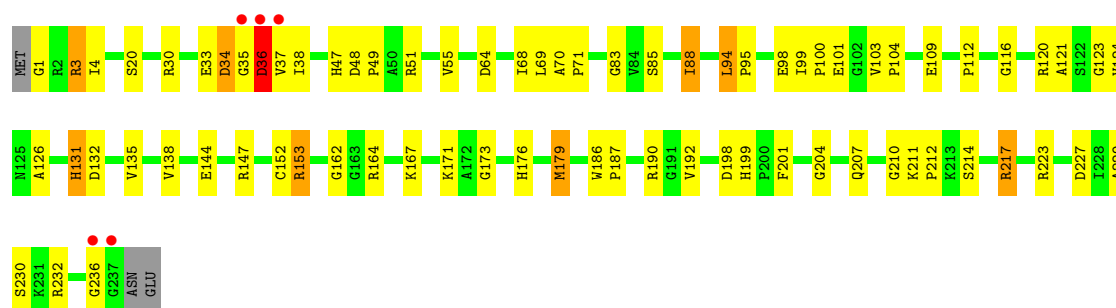
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	T	35	Total	O	0	0
			35	35		
38	U	29	Total	O	0	0
			29	29		
38	V	15	Total	O	0	0
			15	15		
38	W	67	Total	O	0	0
			67	67		
38	X	26	Total	O	0	0
			26	26		
38	Y	98	Total	O	0	0
			98	98		
38	Z	32	Total	O	0	0
			32	32		
38	1	54	Total	O	0	0
			54	54		
38	2	44	Total	O	0	0
			44	44		
38	3	69	Total	O	0	0
			69	69		

### 3 Residue-property plots

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

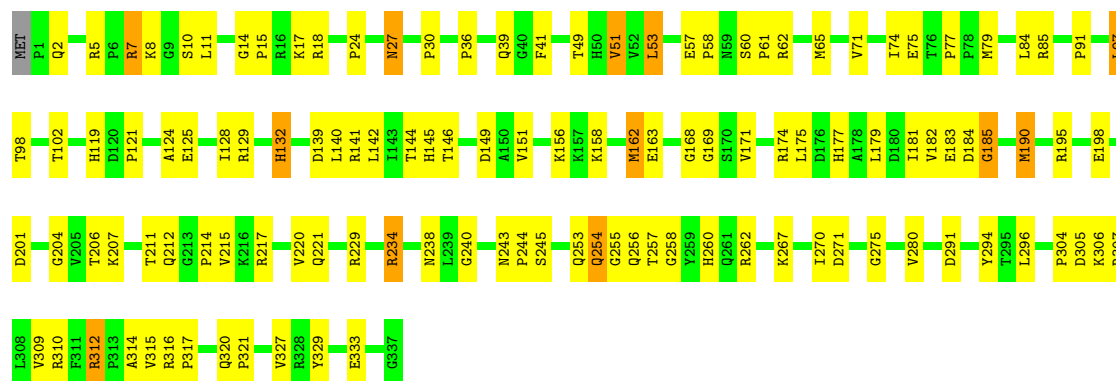
- Molecule 1: 50S ribosomal protein L2P

Chain A: 



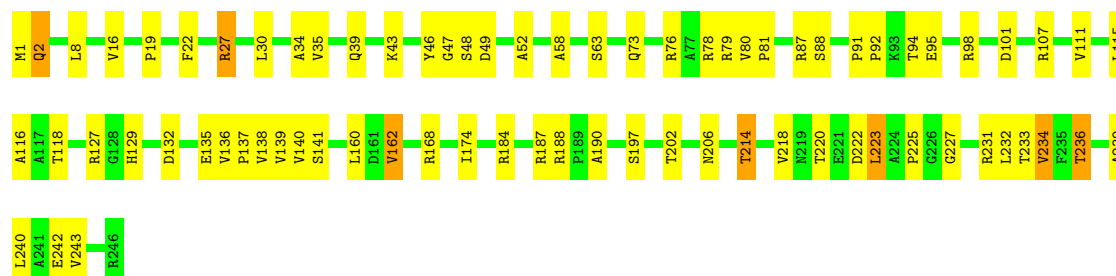
- Molecule 2: 50S ribosomal protein L3P

Chain B: 



- Molecule 3: 50S ribosomal protein L4P

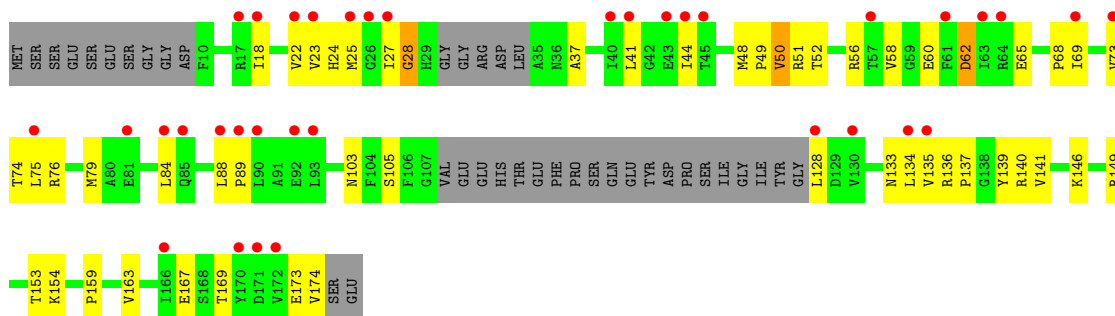
Chain C: 





- Molecule 4: 50S ribosomal protein L5P

Chain D:



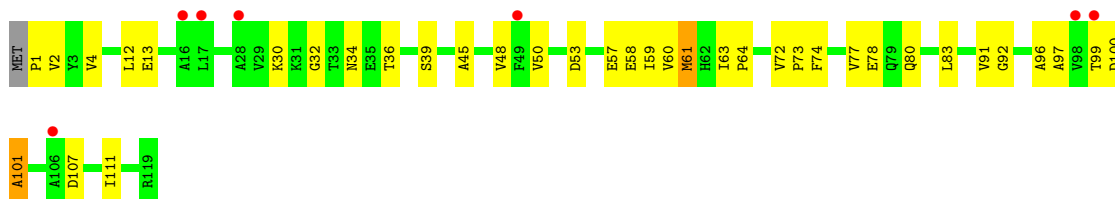
- Molecule 5: 50S ribosomal protein L6P

Chain E:



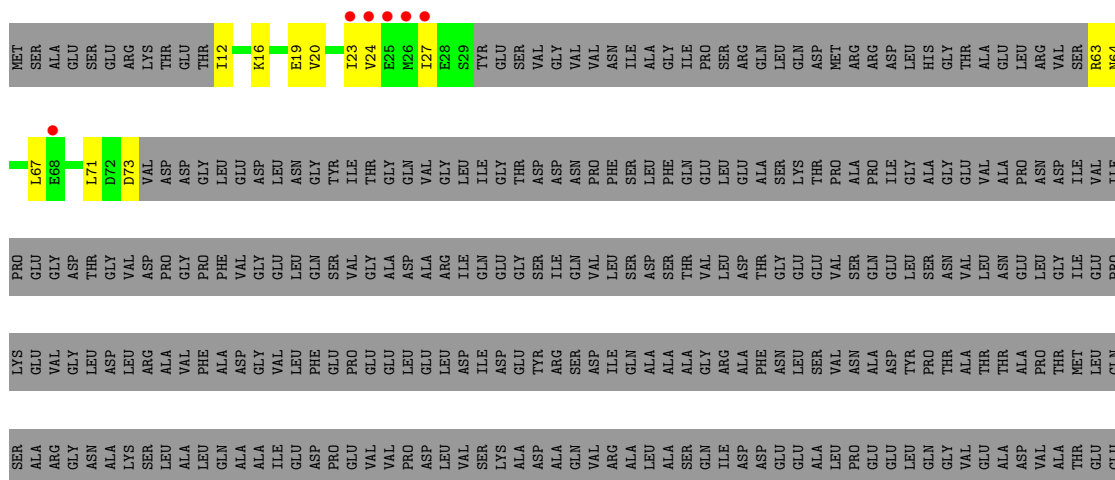
- Molecule 6: 50S ribosomal protein L7Ae

Chain F:



- Molecule 7: 50S ribosomal protein L10E

Chain G:



PRO	THR	ASP	ASP	GLN	ASP	ASP	ASP	THR	ALA	SER	GLU	ASP	ASP	ALA	ASP	ALA	ASP	ASP	ALA	ALA	GLU	GLU	ALA	ASP	ASP	ASP	ASP	ASP	ASP	GLU	GLU	ALA	GLY	ASP	ALA	LEU	GLY	ALA	MET	PHF
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- Molecule 8: 50S ribosomal protein L10e

Chain H:

[illegible]

- Molecule 9: 50S ribosomal protein L11P

Chain I:

Al20	Al21	Al22	Al23	Al24	Al25	Al26	Al27	Al28	Al29	Al30	Al31	Al32	Al33	Al34	Al35	Al36	Al37	Al38	Al39	Al40	Al41	Al42	Al43	Al44	Al45	Al46	Al47	Al48	Al49	Al50	Al51	Al52	Al53	Al54	Al55	Al56	Al57	Al58	Al59	Al60	Al61	Al62	Al63	Al64	Al65	Al66	Al67	Al68	Al69	Al70	Al71	Al72	Al73	Al74	Al75	Al76	Al77	Al78	Al79	Al80	Al81	Al82	Al83	Al84	Al85	Al86	Al87	Al88	Al89	Al90	Al91	Al92	Al93	Al94	Al95	Al96	Al97	Al98	Al99	Al100	Al101	Al102	Al103	Al104	Al105	Al106	Al107	Al108	Al109	Al110	Al111	Al112	Al113	Al114	Al115	Al116	Al117	Al118	Al119	Al120	Al121	Al122	Al123	Al124	Al125	Al126	Al127	Al128	Al129	Al130	Al131	Al132	Al133	Al134	Al135	Al136	Al137	Al138	Al139	Al140	Al141	Al142	Al143	Al144	Al145	Al146	Al147	Al148	Al149	Al150	Al151	Al152	Al153	Al154	Al155	Al156	Al157	Al158	Al159	Al160	Al161	Al162	Al163	Al164	Al165	Al166	Al167	Al168	Al169	Al170	Al171	Al172	Al173	Al174	Al175	Al176	Al177	Al178	Al179	Al180	Al181	Al182	Al183	Al184	Al185	Al186	Al187	Al188	Al189	Al190	Al191	Al192	Al193	Al194	Al195	Al196	Al197	Al198	Al199	Al200	Al201	Al202	Al203	Al204	Al205	Al206	Al207	Al208	Al209	Al210	Al211	Al212	Al213	Al214	Al215	Al216	Al217	Al218	Al219	Al220	Al221	Al222	Al223	Al224	Al225	Al226	Al227	Al228	Al229	Al230	Al231	Al232	Al233	Al234	Al235	Al236	Al237	Al238	Al239	Al240	Al241	Al242	Al243	Al244	Al245	Al246	Al247	Al248	Al249	Al250	Al251	Al252	Al253	Al254	Al255	Al256	Al257	Al258	Al259	Al260	Al261	Al262	Al263	Al264	Al265	Al266	Al267	Al268	Al269	Al270	Al271	Al272	Al273	Al274	Al275	Al276	Al277	Al278	Al279	Al280	Al281	Al282	Al283	Al284	Al285	Al286	Al287	Al288	Al289	Al290	Al291	Al292	Al293	Al294	Al295	Al296	Al297	Al298	Al299	Al300	Al301	Al302	Al303	Al304	Al305	Al306	Al307	Al308	Al309	Al310	Al311	Al312	Al313	Al314	Al315	Al316	Al317	Al318	Al319	Al320	Al321	Al322	Al323	Al324	Al325	Al326	Al327	Al328	Al329	Al330	Al331	Al332	Al333	Al334	Al335	Al336	Al337	Al338	Al339	Al340	Al341	Al342	Al343	Al344	Al345	Al346	Al347	Al348	Al349	Al350	Al351	Al352	Al353	Al354	Al355	Al356	Al357	Al358	Al359	Al360	Al361	Al362	Al363	Al364	Al365	Al366	Al367	Al368	Al369	Al370	Al371	Al372	Al373	Al374	Al375	Al376	Al377	Al378	Al379	Al380	Al381	Al382	Al383	Al384	Al385	Al386	Al387	Al388	Al389	Al390	Al391	Al392	Al393	Al394	Al395	Al396	Al397	Al398	Al399	Al400	Al401	Al402	Al403	Al404	Al405	Al406	Al407	Al408	Al409	Al410	Al411	Al412	Al413	Al414	Al415	Al416	Al417	Al418	Al419	Al420	Al421	Al422	Al423	Al424	Al425	Al426	Al427	Al428	Al429	Al430	Al431	Al432	Al433	Al434	Al435	Al436	Al437	Al438	Al439	Al440	Al441	Al442	Al443	Al444	Al445	Al446	Al447	Al448	Al449	Al450	Al451	Al452	Al453	Al454	Al455	Al456	Al457	Al458	Al459	Al460	Al461	Al462	Al463	Al464	Al465	Al466	Al467	Al468	Al469	Al470	Al471	Al472	Al473	Al474	Al475	Al476	Al477	Al478	Al479	Al480	Al481	Al482	Al
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- Molecule 10: 50S ribosomal protein L13P

Chain J: 

[illegible]

- Molecule 11: 50S ribosomal protein L14P

Chain K: 

A118	A125	A126	A127	A128	A129	M130	M131	M132	M1	L4	V8	T9	Q10	K14	C20	R27	E28	L29	I32	S33	V34	G39	T40	K41	M42	P45	K46	A47	G48	L49	V55	S56	R66	V74	R75	K78	P79	I80	R81	R82	R87	V96	I97	V98	E102	L109	I113	A114	R115	E116
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- Molecule 12: 50S ribosomal protein L15P

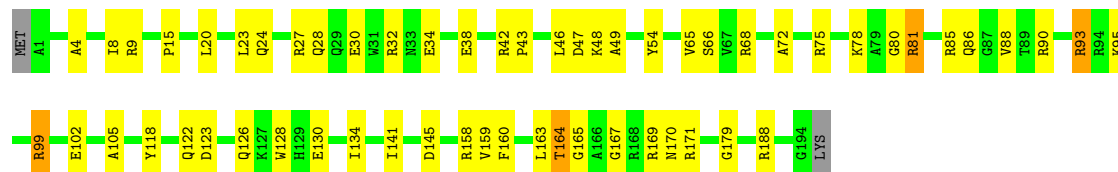
Chain L: 

The heatmap displays the relative frequency of various amino acids across 48 different protein classes. The columns represent amino acids, labeled from MET to Y105. The rows represent protein classes, labeled from T1 to Y105. The color intensity indicates the frequency, with a scale from blue (low) to red (high). Notable features include a strong red signal for Lysine (K) in classes T1 through R6, and a strong red signal for Aspartic Acid (D) in classes D80 and D92.



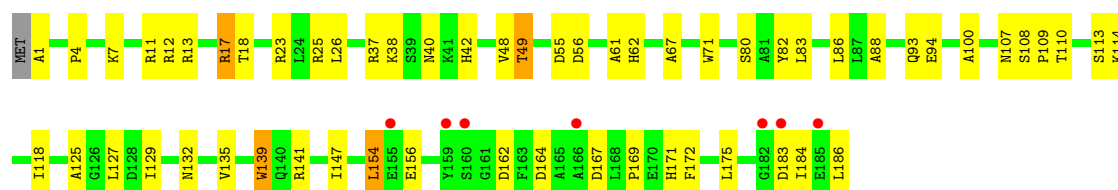
- Molecule 13: 50S ribosomal protein L15e

Chain M:



- Molecule 14: 50S ribosomal protein L18P

Chain N:



- Molecule 15: 50S ribosomal protein L18e

Chain O:



- Molecule 16: 50S ribosomal protein L19e

Chain P:



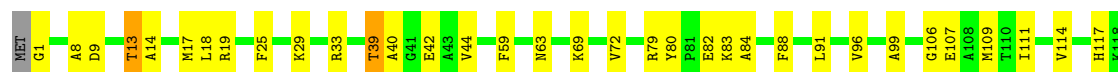
- Molecule 17: 50S ribosomal protein L21e

Chain Q:



- Molecule 18: 50S ribosomal protein L22P

Chain R:





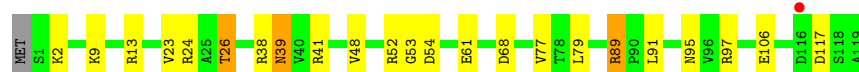
- Molecule 19: 50S ribosomal protein L23P

Chain S:



- Molecule 20: 50S ribosomal protein L24P

Chain T:



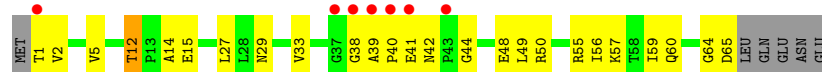
- Molecule 21: 50S ribosomal protein L24e

Chain U:



- Molecule 22: 50S ribosomal protein L29P

Chain V:



- Molecule 23: 50S ribosomal protein L30P

Chain W:



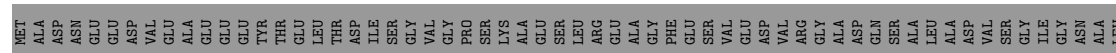
- Molecule 24: 50S ribosomal protein L31e

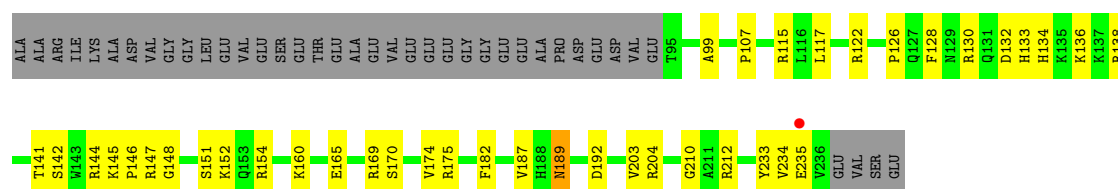
Chain X:



- Molecule 25: 50S ribosomal protein L32e

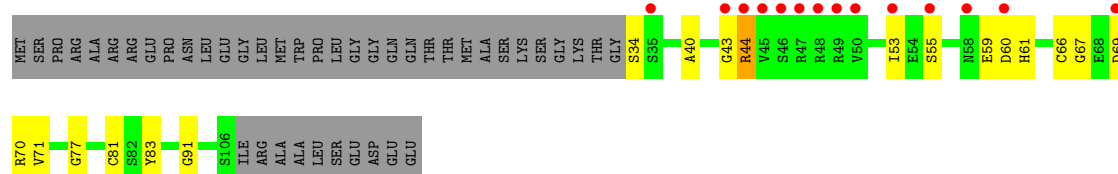
Chain Y:





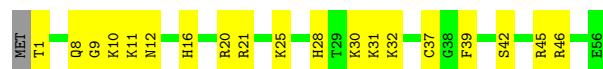
- Molecule 26: 50S ribosomal protein L37Ae

Chain Z:



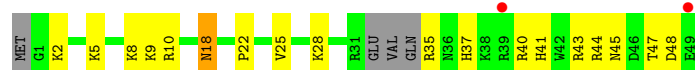
- Molecule 27: 50S ribosomal protein L37e

Chain 1:



- Molecule 28: 50S ribosomal protein L39e

Chain 2:



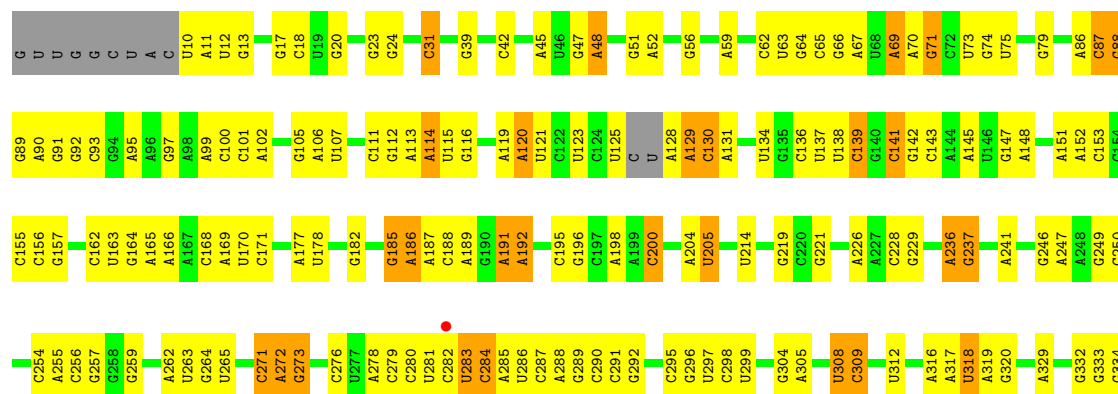
- Molecule 29: 50S ribosomal protein L44E

Chain 3:



- Molecule 30: 23S RIBOSOMAL RNA

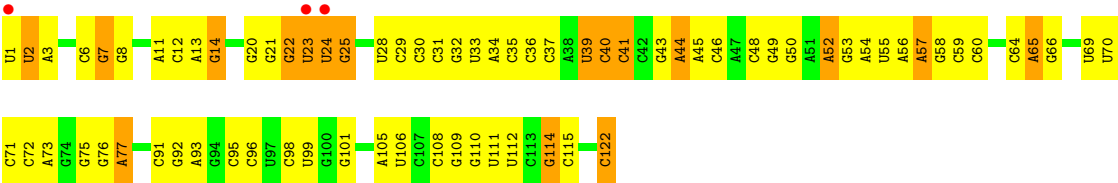
Chain 0:



A1559	G1472	G1386	G1214	A1150	U1056	C	A875	A790	G689	G604	U522	U425	U335
	U1473	G1387	A1215	A1151	A1057	C	A876	A791	G690	C505	C523	G336	
	C1474	G1390	G1217	A1152	A1058	G	G877	G792	A694	G613	A524	C427	
	C1477	A1392	G1218	A1154	G1059	C	G878	U794	C695	U614	U527	C432	C338
		A1393	U1219	G1155	C1060	U	A882	G795	C699	A620	G528	C433	A339
		C1394	U1220	G1158	U1066	C		A797	A700	C921	A532	C342	
	C1395	G1221	A1067		C	G884	G702	G622	A441	C343			
	C1396	G1224	G1160	G1072	G	U701	U623	A442	C344				
	A1398	C1225	A1161	A1073	A	G703	C536	G345					
	A1399	U1310	G1162	G1074	G	C704	C537	U346	U347				
C1400	G1311	G1163	G1075	G	C705	C538	A347						
C1494	G1312	A1230	G1076	G	G807	C539	U349						
	A1313	G1165	G1077	A	A808	A540	A447						
	U1495	G1166	G1078	G	G809	C541	C448						
U1577	A1406	U1314	U1294	A1166	G1078	G710	A449						
	A1407	G1315	G1167	A1079	U	G810	A542	C450					
C1583	A1408	G1316	U1237	C1168	C1080	C	A631	G358					
C1584	G1409	G1238	G1239	A1081	A1081	C	A632	U359					
C1585	A1501	A1321	G1238	U1169	C	A632	G543	A360					
	A1502	G1322	G1239	U1170	G	A632	G544	C361					
G1587	U1503	G1322	U1170	C1084	G	A632	G545	G362					
A1588	A1504	G1322	G1171	C1084	G	A632	G545	G363					
A1589	U1505	G1327	G1172	G1087	A	A632	G545	U364					
C1686	U1506	U1418	A1173	A1088	C	A632	G545	G365					
	G1592	U1419	C1245	A1174	A	A632	G545	U366					
C1593	U1511	G1331	G1175	A1097	C999	A632	G545	G367					
C1594	U1512	C1332	A1246	A1098	C1000	A632	G545	C368					
G1603	C1520	U1249	U1180	G1099	U1001	A632	G545	G369					
G1605	U1516	C1251	A1181	G1102	U1002	A632	G545	U370					
A1606	C1517	G1339	C1182	C1103	U1003	A632	G545	G371					
	U1517	U1339	C1183	A1006	A	A632	G545	U372					
G1706	C1520	C1341	U1185	U1109	C1008	A632	G545	G373					
A1604	C1521	A1342	U1186	G1110	U1008	A632	G545	A378					
G1605	A1522	C1343	C1187	C1101	C1010	A632	G545	G379					
A1711	U1523	A1434	U1261	U1116	A1013	A632	G545	A380					
	C1524	U1435	U1266	A1188	A1014	A632	G545	G381					
C1713	A1526	C1353	U1267	A1117	A1014	A632	G545	G393					
G1613	U1527	C1360	G1190	U1118	C1015	A632	G545	G394					
A1615	G1441	U1441	A1191	G1119	U1016	A632	G545	A395					
A1616	A1528	G1269	A1192	U1120	U1016	A632	G545	U396					
C1617	U1529	A1442	A1193	G1121	G1021	A632	G545	A397					
U1722	G1535	G1364	C1273	A1194	A1022	A632	G545	U398					
	C1536	A1444	A1274	C1127	C1023	A632	G545	C399					
G1622	U1537	C1366	C1275	U1128	G1024	A632	G545	A407					
A1624	U1447	U1447	A1199	C1129	A1014	A632	G545	A408					
U1625	C1451	U1371	A1200	U1130	G1027	A632	G545	G413					
A1626	A1626	U1371	U1278	G1131	U1028	A632	G545	A415					
G1731	U1544	C1456	C1281	A1202	U1029	A632	G545	G416					
A1632	U1544	U1457	G1373	G1203	U1041	A632	G545	C417					
C1633	G1546	A1287	C1374	U1205	G1044	A632	G545	A418					
A1634	U1461	C1377	U1286	U1206	C1044	A632	G545	C419					
U1635	C1378	U1461	U1288	A1207	G1045	A632	G545	U420					
G1636	A1462	C1378	C1289	C1208	C1051	A632	G545	G421					
A1637	C1463	U1379	G1290	C1209	G1052	A632	G545	C424					
U1741	C1464	U1380	A1291	G1210	G1053	A632	G545	A425					
	G1552	U1384	C1212	G1211	G1054	A632	G545	C426					
A1641	A1470	C1384	A1294	C1212	C1054	A632	G545	A427					
A1642	A1471	C1385	C1295	C1212	C1054	A632	G545	C428					



Chain 9: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	211.75Å 299.01Å 574.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.99 – 2.90 85.44 – 2.40	Depositor EDS
% Data completeness (in resolution range)	93.5 (49.99-2.90) 93.6 (85.44-2.40)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.175 , 0.225 0.170 , 0.215	Depositor DCC
$R_{free}$ test set	3577 reflections (0.98%)	DCC
Wilson B-factor (Å <sup>2</sup> )	47.7	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 40.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 667149 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	99121	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, OMG, CL, SR, NA, K, CD, OMU, UR3, 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	A	0.32	0/1786	0.64	0/2408
2	B	0.32	0/2690	0.65	0/3652
3	C	0.36	0/1885	0.63	0/2552
4	D	0.33	0/1111	0.56	0/1498
5	E	0.33	0/1382	0.57	0/1880
6	F	0.33	0/901	0.57	0/1224
7	G	0.32	0/241	0.49	0/324
8	H	0.34	0/1302	0.65	0/1743
9	I	0.29	0/526	0.50	0/716
10	J	0.36	0/1136	0.60	0/1530
11	K	0.36	0/1004	0.68	0/1351
12	L	0.35	0/1130	0.66	0/1509
13	M	0.34	0/1582	0.62	0/2116
14	N	0.30	0/1474	0.63	0/1999
15	O	0.34	0/874	0.59	0/1181
16	P	0.32	0/1147	0.51	0/1528
17	Q	0.34	0/749	0.67	0/1005
18	R	1.26	7/1172 (0.6%)	1.10	6/1578 (0.4%)
19	S	0.33	0/648	0.57	0/875
20	T	0.33	0/958	0.64	0/1289
21	U	0.33	0/417	0.56	0/562
22	V	0.32	0/502	0.53	0/675
23	W	0.35	0/1219	0.62	0/1655
24	X	0.34	0/664	0.59	0/895
25	Y	0.35	0/1146	0.61	0/1536
26	Z	0.36	0/584	0.61	0/781
27	1	0.39	0/438	0.60	0/578
28	2	0.33	0/401	0.56	0/529
29	3	0.34	0/771	0.56	0/1024
30	0	0.38	0/65956	0.69	13/102865 (0.0%)
31	9	0.32	0/2904	0.68	1/4526 (0.0%)
All	All	0.39	7/98700 (0.0%)	0.67	20/147584 (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
18	R	1	0
23	W	0	1
30	0	0	29
All	All	1	30

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	R	150	PRO	CB-CG	27.44	2.87	1.50
18	R	150	PRO	CA-C	-18.09	1.16	1.52
18	R	150	PRO	CG-CD	13.93	1.96	1.50
18	R	150	PRO	C-O	11.89	1.47	1.23
18	R	150	PRO	N-CA	11.37	1.66	1.47
18	R	150	PRO	N-CD	10.70	1.62	1.47
18	R	150	PRO	CA-CB	7.62	1.68	1.53

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	R	150	PRO	CB-CA-C	-22.52	55.71	112.00
18	R	150	PRO	N-CA-C	-19.33	61.85	112.10
18	R	150	PRO	CA-N-CD	12.27	128.87	111.70
18	R	150	PRO	N-CA-CB	11.00	116.50	103.30
18	R	150	PRO	CA-C-O	-8.51	99.79	120.20
18	R	150	PRO	CA-CB-CG	-6.15	92.32	104.00
30	0	1942	A	C5'-C4'-C3'	6.08	125.73	116.00
30	0	2316	G	C5'-C4'-C3'	-5.93	106.52	116.00
31	9	39	U	N1-C1'-C2'	5.87	121.63	114.00
30	0	1504	A	N9-C1'-C2'	5.86	121.62	114.00
30	0	1504	A	C1'-O4'-C4'	-5.83	105.24	109.90
30	0	1120	U	C5'-C4'-C3'	-5.56	107.11	116.00
30	0	2726	U	N1-C1'-C2'	5.45	121.08	114.00
30	0	871	G	C5'-C4'-O4'	-5.44	102.57	109.10
30	0	2313	C	C5'-C4'-O4'	5.34	115.51	109.10
30	0	1165	G	C1'-O4'-C4'	-5.32	105.64	109.90
30	0	2467	A	C1'-O4'-C4'	-5.22	105.72	109.90
30	0	1592	G	N9-C1'-C2'	5.21	120.78	114.00
30	0	1829	A	N9-C1'-C2'	-5.19	106.29	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	841	A	C1'-O4'-C4'	-5.16	105.77	109.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
18	R	150	PRO	CA

All (30) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	0	1078	A	Sidechain
30	0	1237	U	Sidechain
30	0	1430	G	Sidechain
30	0	1819	G	Sidechain
30	0	1829	A	Sidechain
30	0	1863	G	Sidechain
30	0	1877	G	Sidechain
30	0	1878	G	Sidechain
30	0	205	U	Sidechain
30	0	221	G	Sidechain
30	0	2308	U	Sidechain
30	0	2313	C	Sidechain
30	0	246	G	Sidechain
30	0	2465	A	Sidechain
30	0	2493	C	Sidechain
30	0	2503	A	Sidechain
30	0	2506	A	Sidechain
30	0	2607	U	Sidechain
30	0	2673	U	Sidechain
30	0	2842	G	Sidechain
30	0	396	U	Sidechain
30	0	458	G	Sidechain
30	0	48	A	Sidechain
30	0	482	G	Sidechain
30	0	518	G	Sidechain
30	0	795	G	Sidechain
30	0	817	G	Sidechain
30	0	868	G	Sidechain
30	0	952	G	Sidechain
23	W	90	TYR	Sidechain

## 5.2 Close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1753	0	1766	74	0
2	B	2625	0	2532	108	0
3	C	1860	0	1813	56	0
4	D	1094	0	1085	38	0
5	E	1357	0	1266	34	0
6	F	890	0	843	28	0
7	G	240	0	231	9	0
8	H	1282	0	1292	39	0
9	I	519	0	500	20	0
10	J	1120	0	1098	43	0
11	K	994	0	1027	40	0
12	L	1118	0	1076	37	0
13	M	1558	0	1573	52	0
14	N	1445	0	1401	54	0
15	O	865	0	873	23	0
16	P	1136	0	1123	25	0
17	Q	735	0	729	18	0
18	R	1149	0	1122	40	0
19	S	641	0	605	14	0
20	T	950	0	924	22	0
21	U	410	0	364	16	0
22	V	499	0	511	20	0
23	W	1196	0	1137	66	0
24	X	654	0	653	23	0
25	Y	1130	0	1133	40	0
26	Z	573	0	531	15	0
27	1	431	0	426	25	0
28	2	396	0	413	18	0
29	3	755	0	728	15	0
30	0	59019	0	29809	1374	0
31	9	2599	0	1325	96	0
32	0	87	0	0	0	0
32	9	1	0	0	0	0
32	A	1	0	0	0	0
32	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	67	0	0	0	0
34	9	2	0	0	0	0
34	C	1	0	0	0	0
34	J	1	0	0	0	0
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	10	0	0	1	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	2	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	94	0	0	0	0
36	1	2	0	0	0	0
36	3	1	0	0	0	0
36	9	2	0	0	0	0
36	A	3	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
36	Y	1	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5910	0	0	205	0
38	1	54	0	0	6	0
38	2	44	0	0	1	0
38	3	69	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	9	142	0	0	10	0
38	A	112	0	0	7	0
38	B	149	0	0	13	0
38	C	185	0	0	17	0
38	D	49	0	0	4	0
38	E	45	0	0	4	0
38	F	26	0	0	3	0
38	G	17	0	0	0	0
38	H	67	0	0	4	0
38	I	8	0	0	1	0
38	J	51	0	0	2	0
38	K	51	0	0	2	0
38	L	89	0	0	8	0
38	M	133	0	0	4	0
38	N	61	0	0	7	0
38	O	39	0	0	3	0
38	P	62	0	0	1	0
38	Q	45	0	0	2	0
38	R	81	0	0	3	0
38	S	32	0	0	3	0
38	T	35	0	0	3	0
38	U	29	0	0	2	0
38	V	15	0	0	2	0
38	W	67	0	0	6	0
38	X	26	0	0	4	0
38	Y	98	0	0	5	0
38	Z	32	0	0	1	0
All	All	99121	0	59909	2240	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 15.

All (2240) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:150:PRO:CG	18:R:150:PRO:CD	1.96	1.43
30:0:1160:G:C5'	30:0:1161:A:H5'	1.74	1.18
30:0:871:G:C8	30:0:871:G:H5'	1.80	1.15
30:0:1160:G:H5'	30:0:1161:A:C5'	1.74	1.15
30:0:871:G:H8	30:0:871:G:H5'	1.07	1.11
14:N:37:ARG:NH1	31:9:6:C:H5''	1.63	1.09
30:0:1559:A:H1'	38:0:5862:HOH:O	1.53	1.08
18:R:150:PRO:CG	18:R:150:PRO:C	2.22	1.08

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1205:U:H2'	30:0:1206:U:H5''	1.31	1.07
30:0:2717:C:C2'	30:0:2718:C:H5''	1.84	1.07
30:0:1701:A:H4'	30:0:1702:U:H5''	1.38	1.05
30:0:2717:C:H2'	30:0:2718:C:H5''	1.34	1.05
31:9:56:A:C2'	31:9:57:A:H5''	1.86	1.05
31:9:56:A:H2'	31:9:57:A:H5''	1.08	1.03
15:O:3:THR:HG22	30:0:656:G:H5'	1.37	1.02
30:0:2291:A:C8	30:0:2309:C:H5'	1.95	1.02
31:9:76:G:H3'	31:9:77:A:H5''	1.41	1.00
10:J:82:THR:HG23	30:0:1242:A:H5'	1.41	0.98
30:0:1666:C:O2'	30:0:1667:A:H5''	1.64	0.98
30:0:282:C:H1'	30:0:368:C:N4	1.79	0.98
30:0:1474:C:H6	30:0:1474:C:H5'	1.29	0.97
30:0:545:G:H8	30:0:545:G:H5'	1.24	0.97
13:M:171:ARG:HD3	30:0:156:C:H5''	1.44	0.96
30:0:1187:U:HO2'	30:0:1189:A:H2	0.98	0.96
30:0:870:G:H2'	30:0:871:G:H5''	1.48	0.95
30:0:1625:U:H4'	38:0:4666:HOH:O	1.67	0.95
30:0:871:G:H8	30:0:871:G:C5'	1.81	0.94
11:K:10:GLN:H	11:K:10:GLN:HE21	1.06	0.93
4:D:154:LYS:HD2	4:D:154:LYS:H	1.34	0.93
30:0:1205:U:H2'	30:0:1206:U:C5'	1.99	0.93
10:J:52:GLN:NE2	30:0:1119:G:H2'	1.82	0.92
30:0:2812:A:H2	30:0:2814:A:H62	1.11	0.92
30:0:1116:U:O2'	30:0:1118:A:H2	1.51	0.92
30:0:542:A:H5'	30:0:542:A:H8	1.35	0.92
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.10	0.92
11:K:29:LEU:HB3	11:K:55:VAL:HG11	1.49	0.92
30:0:506:G:H22	30:0:509:A:C5'	1.82	0.92
3:C:236:THR:HG22	3:C:239:ALA:H	1.31	0.91
30:0:2010:A:H2'	38:0:5957:HOH:O	1.69	0.91
30:0:2533:C:H5'	30:0:2533:C:H6	1.34	0.90
30:0:1184:C:H1'	38:0:7462:HOH:O	1.71	0.90
30:0:69:A:H5'	30:0:69:A:C8	2.07	0.90
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.54	0.90
30:0:1603:A:H5'	30:0:1605:G:O4'	1.71	0.90
30:0:877:G:H5'	30:0:878:G:OP1	1.72	0.90
16:P:115:SER:H	16:P:118:GLN:HE21	1.18	0.90
15:O:3:THR:CG2	30:0:656:G:H5'	2.02	0.89
30:0:381:G:H5''	38:0:4318:HOH:O	1.72	0.89
30:0:853:C:H3'	38:0:4550:HOH:O	1.72	0.89
30:0:2908:A:H2'	30:0:2909:G:O4'	1.73	0.89

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1474:C:C6	30:0:1474:C:H5'	2.09	0.88
30:0:282:C:O2'	30:0:283:U:H5'	1.73	0.88
30:0:2541:U:H5'	30:0:2541:U:H6	1.37	0.88
30:0:541:C:H2'	30:0:542:A:H5''	1.55	0.88
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.18	0.88
30:0:272:A:H3'	38:0:7525:HOH:O	1.74	0.88
30:0:541:C:C2'	30:0:542:A:H5''	2.04	0.88
30:0:69:A:H5'	30:0:69:A:H8	1.39	0.87
30:0:1878:G:H1'	38:0:6119:HOH:O	1.74	0.87
30:0:2783:A:H3'	38:0:5234:HOH:O	1.75	0.87
2:B:238:ASN:HD22	2:B:240:GLY:H	1.22	0.87
30:0:1667:A:H8	30:0:1667:A:H5'	1.39	0.86
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.57	0.86
30:0:1835:U:H5	30:0:1840:A:N7	1.74	0.86
30:0:1118:A:H3'	30:0:1118:A:H8	1.39	0.86
18:R:99:ALA:HB1	18:R:109:MET:HE1	1.58	0.85
30:0:2644:C:O2'	30:0:2645:U:H5'	1.76	0.85
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.58	0.85
2:B:36:PRO:HA	2:B:168:GLY:HA3	1.58	0.85
30:0:1205:U:C2'	30:0:1206:U:H5''	2.06	0.85
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.59	0.85
30:0:1979:G:H2'	38:0:3289:HOH:O	1.73	0.85
28:2:18:ASN:HD21	28:2:40:ARG:H	1.24	0.84
30:0:1118:A:H3'	30:0:1118:A:C8	2.11	0.84
14:N:37:ARG:HH12	31:9:6:C:H5''	1.43	0.84
30:0:1666:C:C2'	30:0:1667:A:H5''	2.07	0.84
30:0:2506:A:O2'	30:0:2507:G:H8	1.59	0.84
30:0:1372:A:H3'	38:0:7186:HOH:O	1.78	0.84
3:C:1:MET:HG2	3:C:2:GLN:H	1.42	0.84
31:9:92:G:H2'	31:9:93:A:C8	2.13	0.84
30:0:2769:C:C2'	30:0:2770:G:H5'	2.08	0.84
30:0:1183:C:N4	30:0:1184:C:H41	1.76	0.83
30:0:182:G:H5'	38:0:5160:HOH:O	1.79	0.83
31:9:29:C:H2'	31:9:30:C:H5'	1.60	0.83
30:0:2635:A:O2'	30:0:2636:C:H5'	1.79	0.83
14:N:83:LEU:HD13	14:N:175:LEU:HD23	1.59	0.83
30:0:559:U:H5'	30:0:559:U:H6	1.43	0.83
30:0:506:G:H22	30:0:509:A:H5'	1.44	0.82
30:0:1119:G:H22	30:0:1246:A:H2	1.25	0.82
23:W:88:THR:HB	38:W:6679:HOH:O	1.78	0.82
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.25	0.82
30:0:1701:A:H5'	38:0:6284:HOH:O	1.80	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:545:G:C8	30:0:545:G:H5'	2.12	0.82
1:A:94:LEU:HD12	1:A:98:GLU:HB2	1.62	0.81
30:0:2586:U:H3	30:0:2592:G:H22	1.26	0.81
31:9:14:G:H5'	31:9:14:G:H8	1.45	0.81
11:K:39:GLY:HA2	38:0:5223:HOH:O	1.79	0.81
30:0:2502:C:C2'	30:0:2503:A:H5'	2.11	0.81
18:R:8:ALA:HB1	18:R:13:THR:HG21	1.63	0.81
30:0:2502:C:H2'	30:0:2503:A:H5'	1.61	0.81
30:0:2506:A:HO2'	30:0:2507:G:H8	0.83	0.81
2:B:201:ASP:HB2	2:B:312:ARG:HD2	1.62	0.81
30:0:1119:G:N2	30:0:1246:A:C2	2.48	0.80
30:0:1175:G:H1'	30:0:1193:A:H2'	1.63	0.80
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.46	0.80
8:H:59:GLN:NE2	8:H:129:ARG:HE	1.77	0.80
30:0:2896:A:H5''	38:0:6099:HOH:O	1.81	0.80
30:0:363:C:H1'	38:0:5282:HOH:O	1.82	0.80
30:0:1206:U:H6	30:0:1206:U:H5'	1.45	0.80
30:0:283:U:H5	30:0:284:C:N3	1.79	0.80
30:0:1160:G:H5'	30:0:1161:A:H5'	0.87	0.80
28:2:41:HIS:H	28:2:45:ASN:HD22	1.29	0.80
30:0:1973:A:H8	30:0:1973:A:H5'	1.45	0.80
30:0:603:A:H5''	30:0:604:G:OP1	1.81	0.80
30:0:1603:A:H5''	30:0:1605:G:H5'	1.63	0.79
30:0:541:C:H2'	30:0:542:A:C5'	2.12	0.79
23:W:72:PRO:HG2	23:W:77:ALA:HB3	1.64	0.79
10:J:70:PHE:CE1	30:0:2676:C:H4'	2.17	0.78
30:0:281:U:O2'	30:0:282:C:H5'	1.83	0.78
27:1:1:THR:HA	38:0:9358:HOH:O	1.83	0.78
30:0:2644:C:H2'	38:0:4596:HOH:O	1.83	0.78
14:N:113:SER:HB2	38:N:8855:HOH:O	1.82	0.78
15:O:47:ARG:HG3	15:O:47:ARG:HH11	1.47	0.78
21:U:9:CYS:HA	21:U:52:THR:HG22	1.64	0.78
30:0:1183:C:H42	30:0:1184:C:H41	1.32	0.78
30:0:2795:C:O2'	30:0:2796:U:H5'	1.83	0.78
3:C:115:LEU:HD13	3:C:223:LEU:HD21	1.63	0.78
30:0:1189:A:H1'	30:0:1209:C:O4'	1.84	0.78
23:W:84:VAL:HG12	38:W:6679:HOH:O	1.84	0.78
30:0:236:A:H4'	30:0:237:G:H5'	1.66	0.78
30:0:558:C:O2'	30:0:559:U:H5''	1.84	0.77
30:0:2748:G:H5'	38:0:7537:HOH:O	1.83	0.77
30:0:1300:G:H1'	38:0:4684:HOH:O	1.83	0.77
16:P:117:SER:HB3	30:0:1593:C:OP1	1.84	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1116:U:H3	30:0:1246:A:H62	1.31	0.77
30:0:2769:C:O2'	30:0:2770:G:H5'	1.83	0.77
2:B:179:LEU:O	2:B:183:GLU:HG2	1.84	0.77
12:L:133:VAL:HA	38:L:8876:HOH:O	1.84	0.77
30:0:871:G:C8	30:0:871:G:C5'	2.60	0.77
30:0:1183:C:H2'	38:0:6244:HOH:O	1.85	0.77
10:J:127:ILE:HG22	35:J:8801:CL:CL	2.22	0.77
31:9:49:G:H5''	38:9:9087:HOH:O	1.84	0.77
30:0:2578:G:H5'	30:0:2578:G:H8	1.51	0.76
2:B:206:THR:HG21	30:0:2716:G:H5''	1.68	0.76
29:3:25:VAL:HG22	29:3:68:LYS:HG3	1.65	0.76
14:N:141:ARG:HH21	31:9:48:C:H4'	1.50	0.76
30:0:1209:C:H2'	30:0:1210:G:H8	1.51	0.76
30:0:192:A:H5'	38:0:7639:HOH:O	1.86	0.76
8:H:29:SER:HA	8:H:62:HIS:HD2	1.50	0.76
30:0:2533:C:C6	30:0:2533:C:H5'	2.20	0.75
23:W:4:LEU:HD23	23:W:54:PHE:HB3	1.69	0.75
30:0:2748:G:H1'	38:0:7896:HOH:O	1.85	0.75
30:0:567:U:H5''	38:0:5289:HOH:O	1.87	0.75
30:0:1189:A:H1'	30:0:1209:C:C1'	2.15	0.75
30:0:506:G:H22	30:0:509:A:H5''	1.51	0.75
30:0:847:C:H4'	38:0:3748:HOH:O	1.87	0.75
30:0:1790:C:H2'	30:0:1791:U:H6	1.52	0.75
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.15	0.74
30:0:1701:A:H4'	30:0:1702:U:C5'	2.17	0.74
30:0:1120:U:H5'	30:0:1121:G:OP2	1.86	0.74
1:A:35:GLY:O	1:A:36:ASP:HB3	1.86	0.74
30:0:558:C:C2'	30:0:559:U:H5''	2.17	0.74
30:0:1666:C:H2'	30:0:1667:A:C5'	2.16	0.74
30:0:2487:C:H5	38:0:4889:HOH:O	1.71	0.74
3:C:127:ARG:NH2	3:C:225:PRO:HG2	2.03	0.74
30:0:1080:C:H4'	30:0:1081:A:OP1	1.87	0.74
13:M:102:GLU:OE1	13:M:164:THR:HG21	1.88	0.74
30:0:870:G:C2'	30:0:871:G:H5''	2.16	0.74
30:0:2717:C:H2'	30:0:2718:C:C5'	2.14	0.74
30:0:2637:A:H4'	38:0:6063:HOH:O	1.87	0.74
30:0:544:G:H2'	30:0:545:G:H5''	1.70	0.73
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.70	0.73
30:0:1441:G:O2'	30:0:1442:A:H5'	1.88	0.73
26:Z:61:HIS:HB2	26:Z:71:VAL:HB	1.70	0.73
30:0:1189:A:H3'	38:0:7676:HOH:O	1.86	0.73
3:C:47:GLY:HA2	3:C:92:PRO:HB2	1.71	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:2541:U:H5'	30:0:2541:U:C6	2.23	0.73
30:0:2787:C:H5	38:0:4633:HOH:O	1.72	0.73
30:0:2717:C:O2'	30:0:2718:C:H5''	1.89	0.73
30:0:1641:A:H2'	30:0:1642:A:H5'	1.69	0.73
30:0:1666:C:H2'	30:0:1667:A:H5'	1.71	0.73
30:0:2679:G:H2'	30:0:2681:A:OP2	1.89	0.73
30:0:2524:G:H21	30:0:2526:C:N4	1.86	0.73
14:N:49:THR:HG22	14:N:56:ASP:HB2	1.70	0.73
30:0:1701:A:H5''	30:0:1702:U:H3'	1.71	0.73
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.70	0.73
22:V:1:THR:HG23	22:V:2:VAL:H	1.54	0.73
30:0:271:C:H41	30:0:378:A:H2	1.33	0.73
30:0:2420:G:O2'	30:0:2421:G:H5'	1.88	0.73
30:0:396:U:H1'	38:0:7622:HOH:O	1.88	0.72
30:0:1118:A:H62	30:0:1244:U:H3	1.36	0.72
30:0:1525:G:H5'	30:0:1526:A:OP2	1.89	0.72
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.71	0.72
30:0:2102:G:H2'	38:0:7763:HOH:O	1.87	0.72
4:D:103:ASN:ND2	4:D:134:LEU:H	1.88	0.72
30:0:827:A:H1'	38:0:6214:HOH:O	1.89	0.72
30:0:2254:G:H1'	38:0:5534:HOH:O	1.89	0.72
30:0:2644:C:HO2'	30:0:2645:U:H6	1.36	0.71
30:0:1632:A:H2'	30:0:1633:C:H5'	1.72	0.71
30:0:1441:G:H1'	38:0:7761:HOH:O	1.90	0.71
18:R:25:PHE:CE2	18:R:29:LYS:HE2	2.25	0.71
30:0:280:C:H2'	30:0:281:U:O4'	1.91	0.71
30:0:2769:C:H2'	30:0:2770:G:H5'	1.73	0.71
3:C:139:VAL:HG13	38:C:8659:HOH:O	1.90	0.71
13:M:95:LYS:HE2	30:0:157:G:H4'	1.73	0.71
30:0:281:U:H2'	30:0:282:C:O4'	1.91	0.71
30:0:2491:G:H1'	38:0:6868:HOH:O	1.90	0.70
30:0:2577:A:H8	38:0:9598:HOH:O	1.74	0.70
30:0:31:C:H4'	38:0:7421:HOH:O	1.91	0.70
30:0:1730:G:H5'	30:0:1731:C:C5	2.27	0.70
30:0:2505:G:O2'	30:0:2506:A:H5'	1.92	0.70
30:0:2756:U:H3	30:0:2896:A:H2	1.35	0.70
4:D:105:SER:OG	30:0:2338:G:H1'	1.90	0.70
13:M:134:ILE:HG23	13:M:141:ILE:HD13	1.74	0.70
5:E:100:ASP:HB2	38:E:2789:HOH:O	1.92	0.70
30:0:2812:A:H1'	38:0:5787:HOH:O	1.92	0.70
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.57	0.70
30:0:2073:G:OP2	30:0:2490:A:H5'	1.92	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:51:ARG:HB2	38:A:9063:HOH:O	1.91	0.70
13:M:171:ARG:CD	30:0:156:C:H5''	2.20	0.69
30:0:1838:U:O2'	30:0:2644:C:H5'	1.92	0.69
26:Z:81:CYS:SG	26:Z:83:TYR:HB3	2.32	0.69
11:K:14:LYS:HB2	11:K:45:PRO:HG2	1.74	0.69
38:C:8676:HOH:O	30:0:2100:A:H5'	1.92	0.69
30:0:2135:A:O2'	30:0:2136:G:H5'	1.92	0.69
2:B:212:GLN:HB2	2:B:257:THR:HG21	1.74	0.69
30:0:285:A:H2'	30:0:286:U:O4'	1.92	0.69
30:0:2004:U:H4'	38:0:5307:HOH:O	1.92	0.69
30:0:1634:G:H3'	38:0:3891:HOH:O	1.93	0.69
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.03	0.69
30:0:558:C:H2'	30:0:559:U:C5'	2.23	0.69
30:0:681:G:N3	30:0:681:G:H5'	2.08	0.69
30:0:2670:G:O2'	30:0:2671:U:H5'	1.92	0.69
30:0:1666:C:C2'	30:0:1667:A:C5'	2.70	0.69
30:0:1451:C:H5'	30:0:1505:U:C5	2.28	0.69
24:X:61:ARG:HH12	24:X:67:PRO:HD3	1.57	0.69
30:0:1377:C:H6	30:0:1377:C:H5'	1.58	0.69
23:W:137:GLN:NE2	23:W:141:HIS:HE1	1.88	0.69
30:0:1835:U:C5	30:0:1840:A:N7	2.59	0.69
21:U:56:ARG:NH2	30:0:2890:A:H1'	2.08	0.68
10:J:19:MET:HE3	10:J:132:LEU:HD21	1.73	0.68
30:0:2563:U:H2'	30:0:2565:C:O5'	1.93	0.68
24:X:78:GLU:HB3	38:X:5564:HOH:O	1.94	0.68
30:0:1667:A:C8	30:0:1667:A:H5'	2.27	0.68
16:P:115:SER:H	16:P:118:GLN:NE2	1.88	0.68
30:0:960:G:H2'	30:0:960:G:N3	2.09	0.68
30:0:2851:G:O2'	30:0:2852:A:H5'	1.94	0.68
30:0:2005:G:H3'	30:0:2005:G:OP2	1.94	0.68
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.08	0.68
30:0:812:A:H1'	38:0:3955:HOH:O	1.93	0.68
21:U:47:ARG:HG3	38:U:4381:HOH:O	1.94	0.68
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.76	0.68
30:0:138:U:H5''	30:0:139:C:OP2	1.94	0.68
1:A:199:HIS:HD2	1:A:201:PHE:H	1.41	0.68
30:0:2111:G:H1'	38:0:9049:HOH:O	1.93	0.68
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.75	0.68
30:0:564:G:H1'	38:0:6310:HOH:O	1.92	0.68
30:0:1528:A:H2'	30:0:1529:G:O4'	1.94	0.68
20:T:2:LYS:HG2	30:0:447:A:OP1	1.93	0.68
30:0:2659:U:H5''	38:0:4123:HOH:O	1.93	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1730:G:H5''	30:0:1731:C:H6	1.59	0.67
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.75	0.67
30:0:2827:A:H2'	30:0:2828:G:O4'	1.94	0.67
24:X:76:ARG:HH11	24:X:76:ARG:HG3	1.60	0.67
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.74	0.67
11:K:87:ARG:HG3	30:0:2721:U:H4'	1.76	0.67
18:R:150:PRO:O	18:R:150:PRO:CG	2.42	0.67
30:0:1562:C:O2	30:0:1562:C:H2'	1.94	0.67
30:0:1182:C:H1'	30:0:1192:A:H8	1.60	0.67
3:C:236:THR:HA	38:C:8662:HOH:O	1.95	0.67
30:0:299:U:H5'	38:0:7336:HOH:O	1.93	0.67
14:N:37:ARG:NH1	31:9:6:C:C5'	2.52	0.67
3:C:236:THR:HG22	3:C:239:ALA:N	2.09	0.67
30:0:544:G:C2'	30:0:545:G:H5''	2.24	0.67
23:W:80:ASP:O	23:W:84:VAL:HG23	1.94	0.67
30:0:130:C:H2'	38:0:3158:HOH:O	1.95	0.67
29:3:48:ASN:HD21	30:0:2468:A:H61	1.43	0.67
31:9:75:G:H1	31:9:106:U:H3	1.42	0.67
10:J:18:ILE:HD13	30:0:1244:U:OP1	1.95	0.67
30:0:2852:A:H5''	38:0:5236:HOH:O	1.94	0.67
30:0:292:G:H2'	30:0:358:G:N2	2.10	0.66
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.77	0.66
3:C:27:ARG:NH2	30:0:657:G:OP1	2.29	0.66
9:I:86:GLU:HG2	30:0:1180:U:H4'	1.76	0.66
30:0:1159:G:H21	30:0:1189:A:H8	1.42	0.66
22:V:42:ASN:HB3	38:V:7247:HOH:O	1.95	0.66
25:Y:169:ARG:HD2	30:0:1328:A:OP1	1.95	0.66
30:0:2524:G:H21	30:0:2526:C:H41	1.44	0.66
30:0:1189:A:O2'	30:0:1208:C:H2'	1.96	0.66
30:0:848:C:H5'	38:0:7271:HOH:O	1.94	0.66
35:0:8813:CL:CL	38:0:4684:HOH:O	2.51	0.66
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.59	0.66
31:9:23:U:O2'	31:9:24:U:H4'	1.96	0.66
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.60	0.66
30:0:1118:A:C8	30:0:1118:A:C3'	2.75	0.66
14:N:110:THR:HB	14:N:113:SER:OG	1.95	0.66
30:0:1834:C:H2'	30:0:1840:A:N6	2.10	0.66
31:9:92:G:H2'	31:9:93:A:H8	1.61	0.65
26:Z:34:SER:HA	30:0:797:A:H5'	1.76	0.65
30:0:441:A:H1'	30:0:442:A:N7	2.12	0.65
30:0:2812:A:C2	30:0:2814:A:N6	2.62	0.65
10:J:70:PHE:HE1	30:0:2676:C:H4'	1.61	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:W:59:GLN:HE22	23:W:98:PHE:HB2	1.62	0.65
14:N:38:LYS:HE2	14:N:107:ASN:ND2	2.11	0.65
13:M:164:THR:HG22	13:M:167:GLY:H	1.59	0.65
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.78	0.65
30:0:482:G:H4'	30:0:508:A:N1	2.12	0.65
30:0:2755:G:H1'	38:0:4683:HOH:O	1.97	0.65
3:C:140:VAL:HB	38:C:8662:HOH:O	1.97	0.65
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.78	0.65
30:0:2878:U:H2'	30:0:2879:A:O4'	1.96	0.65
6:F:96:ALA:HA	38:F:3111:HOH:O	1.96	0.65
5:E:20:ILE:HD11	5:E:40:VAL:HG11	1.79	0.65
30:0:2769:C:H2'	30:0:2770:G:C5'	2.25	0.65
30:0:2748:G:H2'	38:0:7537:HOH:O	1.96	0.65
31:9:14:G:H5'	31:9:14:G:C8	2.30	0.65
2:B:217:ARG:HG3	2:B:257:THR:HG22	1.79	0.65
30:0:841:A:H5''	38:0:6907:HOH:O	1.96	0.65
30:0:1741:U:H5'	30:0:1742:A:OP1	1.96	0.65
30:0:1477:C:H5'	30:0:1868:G:C5'	2.27	0.65
30:0:2559:C:H4'	38:0:7254:HOH:O	1.97	0.65
6:F:63:ILE:HB	6:F:64:PRO:HD3	1.78	0.65
30:0:1278:A:H4'	30:0:1279:U:C4	2.32	0.65
30:0:558:C:H2'	30:0:559:U:H5'	1.79	0.64
30:0:2756:U:N3	30:0:2896:A:H2	1.95	0.64
30:0:1649:G:H1'	38:0:5533:HOH:O	1.97	0.64
30:0:2768:A:H2'	30:0:2769:C:O4'	1.96	0.64
30:0:711:G:H1'	38:0:7093:HOH:O	1.96	0.64
3:C:184:ARG:NH2	30:0:450:C:OP1	2.30	0.64
12:L:57:VAL:HG21	30:0:2443:C:H5'	1.80	0.64
19:S:43:GLU:HB3	38:S:8989:HOH:O	1.97	0.64
2:B:307:ARG:HG3	2:B:307:ARG:HH11	1.61	0.64
30:0:308:U:H5'	30:0:309:C:OP1	1.96	0.64
10:J:41:ALA:HB3	38:J:5907:HOH:O	1.96	0.64
4:D:25:MET:HE3	4:D:37:ALA:HB1	1.77	0.64
30:0:2256:G:O2'	30:0:2257:G:H5'	1.98	0.64
30:0:1166:A:H61	30:0:1180:U:H3	1.45	0.64
23:W:26:ILE:HB	38:W:5420:HOH:O	1.96	0.64
30:0:1741:U:O2'	30:0:2723:G:H4'	1.98	0.64
30:0:2894:C:O2'	30:0:2895:C:H5'	1.98	0.64
2:B:98:THR:HG22	30:0:2820:A:OP1	1.98	0.64
38:Z:8707:HOH:O	30:0:1886:A:H4'	1.97	0.64
12:L:114:VAL:HG11	38:L:8876:HOH:O	1.97	0.64
12:L:56:LYS:HE3	30:0:2443:C:H1'	1.80	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:41:PHE:HA	2:B:79:MET:HE2	1.80	0.64
9:I:73:LEU:HD12	9:I:107:LYS:NZ	2.13	0.64
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.33	0.64
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.33	0.64
10:J:82:THR:CG2	30:0:1242:A:H5'	2.21	0.64
30:0:1603:A:C5'	30:0:1605:G:H5'	2.28	0.64
24:X:74:ALA:HB2	24:X:85:VAL:HG13	1.80	0.64
30:0:559:U:H5'	30:0:559:U:C6	2.29	0.64
11:K:66:ARG:HH22	30:0:1994:A:P	2.21	0.64
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.33	0.63
4:D:23:VAL:HG22	4:D:73:VAL:HB	1.80	0.63
30:0:1790:C:H2'	30:0:1791:U:C6	2.32	0.63
3:C:174:ILE:HD11	30:0:338:C:H4'	1.80	0.63
30:0:1183:C:N3	30:0:1184:C:C5	2.67	0.63
2:B:320:GLN:HE21	2:B:321:PRO:HD2	1.63	0.63
31:9:49:G:H2'	31:9:50:G:O4'	1.98	0.63
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.28	0.63
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.46	0.63
13:M:86:GLN:NE2	30:0:2274:A:H1'	2.14	0.63
12:L:18:HIS:HD2	30:0:902:G:N7	1.97	0.63
30:0:542:A:C8	30:0:542:A:H5'	2.24	0.63
30:0:1187:U:H2'	38:0:6893:HOH:O	1.99	0.63
30:0:1189:A:H1'	30:0:1209:C:H1'	1.79	0.63
30:0:71:G:H8	38:0:3908:HOH:O	1.81	0.63
30:0:123:U:H5'	38:0:6657:HOH:O	1.97	0.63
38:N:8844:HOH:O	31:9:7:G:H5'	1.98	0.63
30:0:247:A:H2'	38:0:3920:HOH:O	1.99	0.63
2:B:254:GLN:HG2	2:B:255:GLY:N	2.14	0.63
5:E:137:ASP:O	5:E:141:VAL:HG23	1.99	0.63
17:Q:25:PRO:HB2	38:Q:4350:HOH:O	1.99	0.62
30:0:2345:A:H3'	30:0:2346:C:C6	2.34	0.62
9:I:126:THR:O	9:I:130:LEU:HG	1.99	0.62
30:0:1973:A:H5'	30:0:1973:A:C8	2.32	0.62
30:0:2637:A:H5'	38:0:4930:HOH:O	1.99	0.62
30:0:200:C:H2'	38:0:3440:HOH:O	1.97	0.62
30:0:2426:G:H1'	38:0:6092:HOH:O	1.98	0.62
30:0:1632:A:C2'	30:0:1633:C:H5'	2.29	0.62
3:C:174:ILE:CD1	30:0:338:C:H4'	2.30	0.62
30:0:2481:G:H5'	38:0:4543:HOH:O	1.98	0.62
30:0:1249:U:H2'	30:0:1250:C:C6	2.34	0.62
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.29	0.62
4:D:159:PRO:O	4:D:163:VAL:HG23	2.00	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:371:U:H2'	30:0:372:A:H8	1.65	0.62
30:0:2320:U:H4'	30:0:2321:A:O4'	1.99	0.62
30:0:2478:U:O2'	30:0:2479:A:H5'	1.99	0.62
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.27	0.62
30:0:1730:G:C5'	30:0:1731:C:C6	2.82	0.62
28:2:35:ARG:HB2	38:2:2691:HOH:O	1.98	0.62
30:0:583:C:H2'	30:0:584:U:H6	1.64	0.62
30:0:1132:A:N6	30:0:1229:C:H2'	2.14	0.62
15:O:25:VAL:HG12	30:0:709:G:O2'	1.99	0.62
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.81	0.62
30:0:960:G:N3	30:0:960:G:C2'	2.63	0.62
8:H:59:GLN:HE21	8:H:129:ARG:NE	1.95	0.62
30:0:2541:U:H6	30:0:2541:U:C5'	2.09	0.61
30:0:2644:C:O2'	30:0:2645:U:H6	1.83	0.61
30:0:1942:A:H3'	38:0:7346:HOH:O	1.99	0.61
30:0:363:C:O2'	30:0:364:U:H5'	2.00	0.61
6:F:91:VAL:HG12	6:F:92:GLY:N	2.15	0.61
16:P:59:ARG:HH22	16:P:66:GLN:NE2	1.98	0.61
31:9:39:U:H1'	31:9:44:A:H61	1.65	0.61
19:S:17:ASP:HB3	19:S:23:LYS:HB2	1.81	0.61
31:9:58:G:C8	31:9:59:C:C5	2.88	0.61
10:J:131:THR:HB	10:J:134:GLU:HG3	1.81	0.61
9:I:130:LEU:HD22	30:0:1167:G:H4'	1.82	0.61
30:0:2241:C:O2'	30:0:2242:U:H5'	2.00	0.61
5:E:91:PHE:HE1	30:0:2694:A:H4'	1.63	0.61
14:N:67:ALA:HA	14:N:71:TRP:HB3	1.80	0.61
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.29	0.61
30:0:2768:A:O2'	30:0:2769:C:H5'	2.00	0.61
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.64	0.61
30:0:1172:G:H1'	38:0:4974:HOH:O	2.01	0.61
30:0:635:A:H2'	30:0:636:G:H5''	1.82	0.61
30:0:1474:C:C5'	30:0:1474:C:H6	2.07	0.61
13:M:72:ALA:HB2	13:M:93:ARG:HG2	1.81	0.61
23:W:4:LEU:CD2	23:W:54:PHE:HB3	2.31	0.61
1:A:109:GLU:HG2	1:A:116:GLY:H	1.65	0.61
30:0:1185:U:H5'	38:0:7462:HOH:O	1.99	0.61
11:K:10:GLN:N	11:K:10:GLN:HE21	1.89	0.61
30:0:558:C:C2'	30:0:559:U:C5'	2.79	0.61
23:W:88:THR:HG23	23:W:110:GLN:HB3	1.81	0.61
30:0:2604:A:H5'	38:0:5788:HOH:O	2.01	0.61
4:D:22:VAL:HG22	4:D:74:THR:HG22	1.83	0.61
29:3:15:ASN:O	30:0:2408:A:H4'	2.01	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:1:MET:HG2	3:C:2:GLN:N	2.15	0.61
30:0:407:A:H5'	38:0:6024:HOH:O	2.00	0.61
11:K:49:LEU:HD23	11:K:80:ILE:HD13	1.83	0.61
1:A:36:ASP:O	1:A:38:ILE:N	2.33	0.61
12:L:6:ARG:HD3	30:0:1299:G:O6	1.99	0.61
20:T:61:GLU:HG2	38:T:3851:HOH:O	1.98	0.61
5:E:143:GLN:HE21	30:0:2780:C:H1'	1.66	0.61
30:0:1202:A:C2'	30:0:1203:G:H5'	2.31	0.60
23:W:125:HIS:HE1	38:W:3071:HOH:O	1.84	0.60
30:0:1377:C:H5'	30:0:1377:C:C6	2.36	0.60
26:Z:34:SER:CB	30:0:797:A:H4'	2.30	0.60
30:0:2781:U:C2'	30:0:2782:G:H5'	2.31	0.60
30:0:514:G:H4'	38:0:5644:HOH:O	2.00	0.60
17:Q:21:ARG:HH12	30:0:2353:A:H1'	1.66	0.60
27:1:8:GLN:HE22	27:1:11:LYS:NZ	1.98	0.60
30:0:969:G:H1	30:0:999:C:N4	1.98	0.60
23:W:141:HIS:HB2	23:W:146:ILE:HG12	1.84	0.60
5:E:91:PHE:CE1	30:0:2694:A:H4'	2.36	0.60
30:0:644:G:N3	30:0:644:G:H5'	2.16	0.60
30:0:2414:A:H2'	30:0:2415:A:C8	2.35	0.60
9:I:112:LEU:HD11	30:0:1162:G:H1'	1.83	0.60
4:D:173:GLU:HG3	4:D:174:VAL:HG23	1.84	0.60
30:0:1819:G:H2'	30:0:1820:G:H4'	1.81	0.60
1:A:199:HIS:CD2	1:A:201:PHE:H	2.18	0.60
30:0:120:A:H2'	30:0:120:A:N3	2.16	0.60
17:Q:15:LYS:HD3	30:0:2364:A:H5''	1.83	0.60
25:Y:204:ARG:HH22	30:0:553:G:P	2.25	0.60
30:0:1202:A:O2'	30:0:1203:G:H5'	2.01	0.60
30:0:1730:G:H5''	30:0:1731:C:C6	2.36	0.60
10:J:39:VAL:HG22	10:J:106:GLY:O	2.01	0.60
30:0:920:C:H5''	30:0:921:G:O5'	2.02	0.60
30:0:1342:C:C2'	30:0:1343:C:H5'	2.30	0.60
30:0:625:U:H5''	30:0:1044:C:N4	2.16	0.60
2:B:71:VAL:HG11	2:B:296:LEU:HB3	1.81	0.60
14:N:7:LYS:HE3	17:Q:21:ARG:O	2.01	0.60
30:0:746:A:H5'	38:0:5514:HOH:O	2.02	0.60
26:Z:40:ALA:HA	30:0:1773:G:C8	2.37	0.60
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.02	0.60
18:R:39:THR:HG22	18:R:42:GLU:H	1.67	0.60
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.41	0.60
14:N:40:ASN:ND2	31:9:28:U:H5''	2.17	0.60
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.32	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1393:A:H2'	30:0:1394:C:C6	2.37	0.60
30:0:2869:G:H2'	30:0:2870:C:C6	2.36	0.60
18:R:128:ARG:NH2	30:0:2054:A:N3	2.50	0.59
30:0:669:G:O2'	30:0:670:G:H5'	2.02	0.59
27:1:16:HIS:HD2	30:0:470:U:O2'	1.83	0.59
30:0:2524:G:N2	30:0:2526:C:H41	2.00	0.59
30:0:31:C:H2'	38:0:7684:HOH:O	2.02	0.59
30:0:515:C:H5''	38:0:5644:HOH:O	2.01	0.59
30:0:283:U:C5	30:0:284:C:N3	2.67	0.59
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.83	0.59
30:0:1457:U:H5	38:0:7872:HOH:O	1.84	0.59
20:T:9:LYS:HD3	38:0:3750:HOH:O	2.02	0.59
30:0:128:A:O2'	30:0:129:A:H5'	2.02	0.59
18:R:39:THR:HG23	18:R:107:GLU:O	2.02	0.59
12:L:41:HIS:CD2	30:0:926:A:O2'	2.56	0.59
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.84	0.59
9:I:120:ALA:O	9:I:124:VAL:HG23	2.02	0.59
30:0:2498:C:O2'	30:0:2499:U:H5'	2.02	0.59
30:0:2756:U:N3	30:0:2896:A:C2	2.63	0.59
30:0:1425:G:O2'	30:0:1426:C:H5'	2.02	0.59
2:B:156:LYS:HB3	30:0:2846:C:H4'	1.84	0.59
30:0:2403:C:H5'	38:0:6025:HOH:O	2.02	0.59
2:B:36:PRO:HG3	2:B:169:GLY:H	1.67	0.59
31:9:13:A:O2'	31:9:14:G:H5''	2.03	0.59
13:M:24:GLN:NE2	13:M:27:ARG:HH11	2.01	0.59
30:0:1183:C:H42	30:0:1184:C:N4	2.00	0.59
18:R:99:ALA:HB1	18:R:109:MET:CE	2.30	0.59
2:B:51:VAL:HG13	2:B:53:LEU:HD13	1.83	0.59
30:0:1268:C:O2'	30:0:1269:G:H5'	2.01	0.59
12:L:134:GLU:HG3	38:L:8857:HOH:O	2.03	0.59
30:0:2505:G:C2'	30:0:2506:A:H5'	2.33	0.59
1:A:99:ILE:O	1:A:131:HIS:HE1	1.86	0.59
30:0:2419:U:H5''	30:0:2420:G:H5'	1.83	0.59
30:0:1426:C:H2'	38:0:9591:HOH:O	2.03	0.59
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.84	0.59
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.38	0.59
20:T:9:LYS:HB2	38:0:7421:HOH:O	2.01	0.59
2:B:294:TYR:HE2	38:B:9117:HOH:O	1.85	0.59
31:9:2:U:OP2	31:9:3:A:H5'	2.03	0.58
27:1:28:HIS:HE1	30:0:776:A:OP1	1.86	0.58
30:0:807:A:O2'	30:0:808:A:H5'	2.03	0.58
30:0:2637:A:C5'	38:0:4930:HOH:O	2.50	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:9:LYS:HE3	20:T:13:ARG:NH1	2.18	0.58
30:0:2781:U:H2'	30:0:2782:G:H5'	1.84	0.58
30:0:2344:G:N3	30:0:2344:G:H2'	2.18	0.58
30:0:2900:G:H2'	30:0:2901:C:O4'	2.03	0.58
18:R:29:LYS:HD3	30:0:524:A:H5''	1.85	0.58
1:A:48:ASP:HB3	38:A:9063:HOH:O	2.02	0.58
11:K:8:VAL:HG13	11:K:80:ILE:HG22	1.84	0.58
6:F:58:GLU:CD	13:M:27:ARG:HH22	2.06	0.58
30:0:1201:C:H5''	38:0:6233:HOH:O	2.02	0.58
11:K:32:ILE:HD11	11:K:56:SER:HB3	1.84	0.58
23:W:52:VAL:HG22	23:W:53:ALA:H	1.68	0.58
31:9:1:U:H5''	31:9:3:A:OP1	2.03	0.58
22:V:44:GLY:HA3	30:0:92:G:H4'	1.85	0.58
30:0:1942:A:O2'	30:0:1943:C:H5'	2.03	0.58
30:0:1230:A:OP1	30:0:1230:A:H8	1.85	0.58
15:O:42:GLU:HB2	38:O:2176:HOH:O	2.02	0.58
14:N:11:ARG:HD3	31:9:114:G:O6	2.03	0.58
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.85	0.58
4:D:25:MET:HE2	4:D:41:LEU:HG	1.85	0.58
30:0:485:A:N3	30:0:487:G:H5''	2.19	0.58
30:0:2335:C:H2'	30:0:2336:G:C8	2.38	0.58
30:0:2533:C:H6	30:0:2533:C:C5'	2.12	0.58
14:N:141:ARG:NH2	31:9:48:C:H4'	2.19	0.58
18:R:18:LEU:HG	18:R:91:LEU:HD13	1.86	0.58
30:0:1649:G:O2'	30:0:1650:C:H5'	2.04	0.58
30:0:1211:G:H2'	30:0:1212:C:H6	1.69	0.58
12:L:30:ARG:HD3	30:0:164:G:H4'	1.86	0.58
2:B:162:MET:CE	2:B:310:ARG:HD3	2.33	0.58
20:T:41:ARG:HG2	20:T:41:ARG:HH11	1.66	0.58
30:0:1015:C:H2'	30:0:1016:U:H6	1.67	0.58
14:N:61:ALA:HB3	14:N:88:ALA:HB2	1.85	0.58
30:0:2802:C:H2'	30:0:2803:C:H6	1.68	0.58
30:0:2445:U:H2'	30:0:2446:G:C8	2.39	0.58
13:M:179:GLY:O	30:0:399:C:H5'	2.04	0.58
1:A:212:PRO:HB2	38:A:9024:HOH:O	2.04	0.58
30:0:2032:U:H2'	30:0:2033:G:C5'	2.34	0.58
13:M:163:LEU:HD21	30:0:188:C:H5''	1.86	0.58
2:B:145:HIS:HD2	2:B:146:THR:O	1.87	0.58
30:0:1165:G:O2'	30:0:1174:A:H1'	2.04	0.57
30:0:1207:A:C8	30:0:1208:C:C5	2.92	0.57
30:0:1856:C:H5'	30:0:1858:A:O4'	2.04	0.57
1:A:55:VAL:HG23	1:A:68:ILE:O	2.04	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1947:G:N2	30:0:1966:U:C2	2.71	0.57
30:0:1596:U:H2'	30:0:1598:A:OP2	2.03	0.57
9:I:110:ASP:O	30:0:1163:G:H5'	2.04	0.57
30:0:1181:A:H2'	30:0:1182:C:H5'	1.86	0.57
30:0:1819:G:H2'	30:0:1820:G:C5'	2.34	0.57
30:0:1015:C:H2'	30:0:1016:U:C6	2.39	0.57
30:0:2472:C:O2'	30:0:2634:G:H4'	2.03	0.57
30:0:705:C:H2'	30:0:705:C:O2	2.04	0.57
30:0:1903:U:O2'	30:0:1904:A:N7	2.38	0.57
30:0:2851:G:C2'	30:0:2852:A:H5'	2.34	0.57
30:0:1477:C:O2'	30:0:1478:U:H5'	2.04	0.57
30:0:1307:A:H2'	30:0:1308:A:C8	2.39	0.57
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.86	0.57
21:U:17:THR:HG22	21:U:18:GLY:N	2.18	0.57
30:0:1463:U:H2'	30:0:1464:C:C6	2.39	0.57
22:V:1:THR:HB	30:0:93:C:H5''	1.86	0.57
22:V:38:GLY:O	22:V:41:GLU:HG3	2.05	0.57
30:0:2251:G:H2'	30:0:2252:A:C8	2.40	0.57
30:0:2415:A:H2'	30:0:2416:G:H5'	1.86	0.57
30:0:255:A:H2'	30:0:256:C:H6	1.68	0.57
30:0:264:G:H1'	30:0:265:U:H5	1.70	0.57
2:B:125:GLU:O	2:B:129:ARG:HG3	2.04	0.57
30:0:2689:A:H2'	30:0:2690:U:H5'	1.87	0.57
30:0:1138:G:H4'	38:0:5706:HOH:O	2.03	0.57
30:0:876:A:N3	30:0:876:A:H2'	2.19	0.57
30:0:1588:G:C6	30:0:1589:G:N1	2.73	0.57
1:A:47:HIS:CD2	30:0:1654:U:H2'	2.39	0.57
9:I:130:LEU:CD2	30:0:1167:G:H4'	2.35	0.57
30:0:941:G:C5	30:0:942:U:C4	2.93	0.57
30:0:1174:A:C5	30:0:1201:C:H4'	2.39	0.57
30:0:2291:A:N9	30:0:2309:C:H5'	2.19	0.57
30:0:1603:A:H5'	30:0:1605:G:C4'	2.34	0.57
30:0:2509:A:H2'	30:0:2510:C:O4'	2.05	0.57
38:B:9100:HOH:O	30:0:2672:C:H1'	2.05	0.57
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.34	0.57
30:0:2134:G:N2	30:0:2242:U:C2	2.73	0.57
30:0:1044:C:H5''	38:0:9025:HOH:O	2.05	0.57
1:A:121:ALA:O	1:A:124:VAL:HG22	2.05	0.57
30:0:823:U:H3'	38:0:4446:HOH:O	2.03	0.57
31:9:22:G:H5'	31:9:23:U:OP1	2.05	0.57
2:B:140:LEU:HA	38:B:9048:HOH:O	2.05	0.57
30:0:694:A:H2'	30:0:695:C:H5'	1.86	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:P:54:LYS:HB2	30:0:1717:A:H5''	1.87	0.57
30:0:834:G:H3'	30:0:835:U:H4'	1.87	0.56
5:E:132:THR:HB	38:E:2227:HOH:O	2.05	0.56
30:0:821:U:H3'	38:0:3765:HOH:O	2.05	0.56
30:0:821:U:H2'	30:0:822:C:H6	1.70	0.56
30:0:2710:U:H1'	38:0:7616:HOH:O	2.04	0.56
3:C:188:ARG:HD3	38:C:8564:HOH:O	2.05	0.56
31:9:29:C:C2'	31:9:30:C:H5'	2.33	0.56
30:0:1641:A:C2'	30:0:1642:A:H5'	2.35	0.56
4:D:25:MET:CE	4:D:37:ALA:HB1	2.35	0.56
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.34	0.56
30:0:952:G:N3	30:0:2302:A:H2'	2.20	0.56
30:0:671:A:O2'	30:0:672:G:H2'	2.05	0.56
30:0:1135:G:H5'	38:0:5927:HOH:O	2.05	0.56
10:J:74:ARG:O	10:J:78:ILE:HG12	2.05	0.56
17:Q:19:ARG:HH21	31:9:11:A:P	2.27	0.56
23:W:88:THR:HG22	23:W:90:TYR:HD1	1.69	0.56
30:0:308:U:C4	30:0:342:C:H1'	2.41	0.56
17:Q:28:ARG:HG2	38:Q:4350:HOH:O	2.04	0.56
30:0:1160:G:O2'	30:0:1190:G:H1'	2.06	0.56
30:0:1279:U:O2	30:0:1279:U:H2'	2.05	0.56
5:E:143:GLN:NE2	30:0:2779:G:H21	2.04	0.56
27:I:20:ARG:HG2	30:0:111:C:O2'	2.06	0.56
30:0:316:A:N3	30:0:336:G:O2'	2.37	0.56
8:H:26:ILE:HA	8:H:123:ILE:HG21	1.87	0.56
30:0:2256:G:H2'	30:0:2257:G:C5'	2.35	0.56
25:Y:187:VAL:HG23	25:Y:192:ASP:HB2	1.87	0.56
31:9:76:G:C3'	31:9:77:A:H5''	2.28	0.56
23:W:139:GLY:O	23:W:141:HIS:HD2	1.89	0.56
9:I:108:HIS:H	9:I:109:PRO:HD2	1.71	0.56
24:X:23:HIS:HE1	30:0:2044:G:OP1	1.88	0.56
30:0:10:U:O4	30:0:532:A:OP2	2.23	0.56
30:0:282:C:O2'	30:0:283:U:C5'	2.50	0.56
23:W:125:HIS:NE2	30:0:1097:A:H5''	2.21	0.56
30:0:1592:G:H2'	30:0:1593:C:C6	2.41	0.56
1:A:36:ASP:HB2	1:A:85:SER:H	1.71	0.56
3:C:129:HIS:HE1	3:C:231:ARG:HA	1.71	0.56
17:Q:26:PRO:O	17:Q:30:VAL:HG23	2.05	0.56
30:0:2880:A:H2'	30:0:2881:C:H5'	1.88	0.56
30:0:1768:C:H2'	30:0:1769:C:O4'	2.06	0.56
6:F:39:SER:HB3	6:F:45:ALA:HB2	1.88	0.56
14:N:37:ARG:NH1	31:9:6:C:OP1	2.38	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:99:ARG:CD	13:M:167:GLY:HA2	2.33	0.56
2:B:85:ARG:NH1	38:B:9100:HOH:O	2.39	0.56
14:N:169:PRO:O	14:N:172:PHE:HB3	2.06	0.56
31:9:64:C:C2'	31:9:65:A:H5'	2.36	0.56
28:2:8:LYS:NZ	30:0:1677:U:OP2	2.37	0.56
24:X:43:VAL:HG11	24:X:82:GLU:HA	1.88	0.56
30:0:1118:A:H8	30:0:1119:G:H5''	1.71	0.55
30:0:816:G:C6	30:0:817:G:N1	2.74	0.55
31:9:64:C:H2'	31:9:65:A:H5'	1.88	0.55
30:0:2703:A:H2'	30:0:2704:C:H6	1.71	0.55
2:B:27:ASN:H	2:B:27:ASN:HD22	1.54	0.55
19:S:76:GLU:HB3	38:S:8991:HOH:O	2.05	0.55
30:0:1163:G:H1	30:0:1184:C:N4	2.03	0.55
30:0:1588:G:C6	30:0:1589:G:C6	2.94	0.55
30:0:2645:U:OP2	30:0:2645:U:C6	2.60	0.55
30:0:2802:C:H2'	30:0:2803:C:C6	2.41	0.55
30:0:1595:G:O2'	30:0:1596:U:H5'	2.06	0.55
30:0:2269:C:C2'	30:0:2270:G:H5'	2.37	0.55
8:H:48:VAL:HA	8:H:170:ARG:O	2.05	0.55
30:0:1119:G:N2	30:0:1246:A:H2	1.97	0.55
30:0:1477:C:H5'	30:0:1868:G:H5''	1.88	0.55
30:0:2256:G:C2'	30:0:2257:G:H5'	2.35	0.55
28:2:10:ARG:NH2	30:0:121:U:OP2	2.40	0.55
30:0:1878:G:O2'	30:0:1879:U:C6	2.58	0.55
23:W:88:THR:HG22	23:W:89:ASP:H	1.71	0.55
31:9:39:U:H3'	31:9:40:C:H5''	1.88	0.55
30:0:407:A:H3'	38:0:4460:HOH:O	2.06	0.55
5:E:84:MET:HG2	5:E:168:ILE:HA	1.88	0.55
30:0:735:C:H2'	30:0:736:A:H5'	1.87	0.55
18:R:96:VAL:HG13	18:R:106:GLY:HA3	1.88	0.55
30:0:652:G:H8	38:0:3009:HOH:O	1.89	0.55
9:I:111:LEU:HD23	30:0:1163:G:H4'	1.88	0.55
30:0:272:A:H5'	30:0:273:G:OP2	2.07	0.55
30:0:1377:C:C5'	30:0:1377:C:H6	2.18	0.55
2:B:234:ARG:HG3	30:0:1735:C:OP2	2.06	0.55
30:0:2626:C:H2'	30:0:2627:G:C8	2.42	0.55
1:A:33:GLU:CD	1:A:33:GLU:H	2.10	0.55
30:0:810:G:H2'	30:0:811:C:C6	2.42	0.55
2:B:275:GLY:O	2:B:291:ASP:HA	2.07	0.55
4:D:154:LYS:HD2	4:D:154:LYS:N	2.15	0.55
30:0:877:G:C5'	30:0:878:G:OP1	2.52	0.55
28:2:18:ASN:ND2	28:2:40:ARG:H	2.01	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:W:88:THR:HG23	23:W:110:GLN:HE21	1.71	0.55
31:9:49:G:O2'	31:9:50:G:H5'	2.07	0.55
31:9:39:U:H1'	31:9:44:A:N6	2.21	0.55
27:1:46:ARG:HA	38:1:8971:HOH:O	2.05	0.55
31:9:12:C:H5'	31:9:70:U:O4'	2.06	0.55
30:0:581:G:O2'	30:0:582:U:H5'	2.06	0.55
1:A:223:ARG:HD2	30:0:2272:G:OP1	2.07	0.55
22:V:50:ARG:HH12	30:0:56:G:H5''	1.70	0.55
38:O:7674:HOH:O	30:0:935:G:H5'	2.05	0.55
13:M:99:ARG:HD2	13:M:167:GLY:CA	2.35	0.55
31:9:91:C:H2'	31:9:92:G:O4'	2.07	0.55
31:9:28:U:H2'	31:9:29:C:C6	2.41	0.55
30:0:2502:C:H2'	30:0:2503:A:C5'	2.36	0.55
23:W:38:THR:HG22	23:W:39:ASP:N	2.22	0.55
17:Q:40:HIS:HE1	30:0:949:U:O2'	1.90	0.55
30:0:1174:A:C6	30:0:1201:C:H4'	2.42	0.54
30:0:1209:C:H2'	30:0:1210:G:C8	2.36	0.54
30:0:271:C:C2	30:0:273:G:O4'	2.60	0.54
30:0:567:U:H5''	38:0:6401:HOH:O	2.06	0.54
31:9:1:U:H4'	31:9:3:A:OP1	2.07	0.54
22:V:50:ARG:NH1	30:0:56:G:H5''	2.22	0.54
30:0:2697:A:H2'	30:0:2698:G:O4'	2.07	0.54
13:M:34:GLU:HB3	13:M:38:GLU:HG3	1.89	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.07	0.54
30:0:2718:C:H6	30:0:2718:C:H5'	1.73	0.54
15:O:47:ARG:HG3	15:O:47:ARG:NH1	2.19	0.54
2:B:162:MET:HE3	2:B:310:ARG:HD3	1.89	0.54
30:0:204:A:H2'	30:0:205:U:H5'	1.88	0.54
30:0:2616:A:H4'	30:0:2617:G:OP1	2.06	0.54
30:0:1291:A:H2	38:0:5292:HOH:O	1.89	0.54
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.89	0.54
30:0:1172:G:H5''	38:0:7257:HOH:O	2.07	0.54
30:0:999:C:O2'	30:0:1000:C:H5'	2.07	0.54
27:1:9:GLY:HA2	30:0:1687:C:O2	2.07	0.54
23:W:154:ARG:NH1	30:0:588:G:O6	2.40	0.54
21:U:9:CYS:HA	21:U:52:THR:CG2	2.35	0.54
30:0:2564:G:OP2	30:0:2565:C:H5''	2.06	0.54
21:U:17:THR:HG22	21:U:18:GLY:H	1.72	0.54
30:0:1484:G:H2'	38:0:9103:HOH:O	2.08	0.54
13:M:99:ARG:HE	13:M:170:ASN:HD22	1.55	0.54
2:B:304:PRO:HD2	2:B:307:ARG:NE	2.22	0.54
11:K:27:ARG:HD2	38:K:3442:HOH:O	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:7:LEU:HD12	30:0:2424:U:H1'	1.89	0.54
2:B:267:LYS:HD3	38:0:9562:HOH:O	2.06	0.54
30:0:1559:A:OP2	30:0:1559:A:H8	1.88	0.54
30:0:1175:G:H1'	30:0:1193:A:C2'	2.36	0.54
14:N:80:SER:HB2	38:N:8833:HOH:O	2.07	0.54
30:0:1766:U:O2	30:0:1778:A:H5'	2.08	0.54
8:H:168:VAL:HG13	38:H:213:HOH:O	2.08	0.54
15:O:37:ARG:HD2	30:0:656:G:OP2	2.08	0.54
2:B:79:MET:HE1	38:B:9092:HOH:O	2.07	0.54
30:0:65:C:O2'	30:0:66:G:H5'	2.07	0.54
18:R:14:ALA:HB3	18:R:147:LEU:HB2	1.89	0.54
30:0:1183:C:C2	30:0:1184:C:C5	2.96	0.54
21:U:46:ALA:HB1	21:U:52:THR:HG21	1.89	0.54
27:1:37:CYS:SG	27:1:39:PHE:HB2	2.48	0.54
30:0:1131:G:C6	30:0:1230:A:C4	2.96	0.54
5:E:154:ILE:HD11	5:E:157:LYS:HE2	1.90	0.54
30:0:958:G:H2'	30:0:959:C:C6	2.42	0.54
19:S:33:SER:O	19:S:37:VAL:HG23	2.08	0.54
2:B:211:THR:HG23	30:0:2840:A:OP1	2.08	0.54
8:H:64:SER:OG	30:0:2520:G:H5'	2.07	0.54
5:E:10:ASP:HA	38:E:6017:HOH:O	2.06	0.54
6:F:58:GLU:HB3	13:M:8:ILE:HG23	1.90	0.54
30:0:2269:C:O2'	30:0:2270:G:H5'	2.07	0.54
14:N:132:ASN:O	14:N:135:VAL:HG12	2.08	0.54
7:G:20:VAL:O	7:G:24:VAL:HG23	2.08	0.54
31:9:34:A:H2'	31:9:35:C:O4'	2.08	0.53
30:0:420:U:H2'	30:0:421:C:C6	2.44	0.53
30:0:549:A:O2'	30:0:550:C:H5'	2.08	0.53
30:0:2070:G:H2'	30:0:2072:G:OP1	2.08	0.53
30:0:1730:G:H5'	30:0:1731:C:H5	1.73	0.53
31:9:1:U:O3'	31:9:3:A:H5''	2.08	0.53
30:0:2345:A:H3'	30:0:2346:C:H6	1.71	0.53
13:M:23:LEU:HD13	13:M:27:ARG:NH2	2.23	0.53
30:0:2705:U:H2'	30:0:2706:A:C8	2.43	0.53
30:0:961:A:H4'	38:0:6768:HOH:O	2.07	0.53
30:0:90:A:H2'	30:0:91:G:O4'	2.08	0.53
13:M:28:GLN:O	13:M:32:ARG:HG3	2.08	0.53
8:H:61:ARG:HG3	8:H:61:ARG:HH11	1.73	0.53
23:W:125:HIS:HB2	23:W:137:GLN:HG2	1.90	0.53
30:0:1505:U:H1'	38:0:7584:HOH:O	2.07	0.53
2:B:41:PHE:HB3	2:B:190:MET:HE3	1.89	0.53
30:0:255:A:H2'	30:0:256:C:C6	2.44	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:V:55:ARG:O	22:V:59:ILE:HG12	2.08	0.53
3:C:95:GLU:HG3	38:C:8688:HOH:O	2.07	0.53
5:E:68:HIS:O	5:E:72:MET:HG3	2.09	0.53
11:K:4:LEU:HD22	11:K:116:GLU:HB3	1.90	0.53
30:0:2826:G:C6	30:0:2913:A:N6	2.75	0.53
30:0:1615:A:H5'	38:0:4180:HOH:O	2.09	0.53
30:0:1622:G:H2'	30:0:1623:C:H5'	1.90	0.53
10:J:19:MET:HE3	10:J:132:LEU:HD11	1.89	0.53
14:N:114:LYS:O	14:N:118:ILE:HG13	2.07	0.53
12:L:41:HIS:HD2	30:0:926:A:O2'	1.90	0.53
8:H:27:PRO:HD3	8:H:123:ILE:HG22	1.91	0.53
8:H:174:LEU:HD21	30:0:1220:U:H4'	1.89	0.53
13:M:188:ARG:HD3	30:0:155:C:OP2	2.08	0.53
30:0:297:U:H2'	30:0:298:C:C6	2.43	0.53
30:0:484:A:N1	30:0:506:G:H4'	2.23	0.53
30:0:1838:U:H3'	38:0:5521:HOH:O	2.09	0.53
31:9:20:G:O2'	31:9:21:G:H5'	2.08	0.53
30:0:2597:U:H2'	30:0:2598:U:H5'	1.90	0.53
30:0:318:U:H5'	30:0:339:A:C2	2.44	0.53
30:0:2243:C:H5''	38:0:3745:HOH:O	2.07	0.53
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.43	0.53
30:0:281:U:C2'	30:0:282:C:H5'	2.39	0.53
30:0:1878:G:O2'	30:0:1879:U:P	2.67	0.53
2:B:7:ARG:HG2	2:B:7:ARG:HH11	1.72	0.53
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.09	0.53
30:0:2371:G:H5'	38:0:5010:HOH:O	2.07	0.53
13:M:164:THR:HB	38:M:8819:HOH:O	2.08	0.53
30:0:1972:U:H2'	30:0:1973:A:C5'	2.38	0.53
30:0:1592:G:H2'	30:0:1593:C:H6	1.71	0.53
31:9:24:U:H3'	31:9:25:G:C5'	2.39	0.53
30:0:319:A:H4'	30:0:338:C:C4	2.44	0.53
30:0:1483:C:O2'	30:0:1484:G:H5'	2.09	0.53
5:E:69:ILE:HA	5:E:72:MET:CE	2.39	0.53
30:0:1921:A:O2'	30:0:1922:A:H5'	2.09	0.53
28:2:28:LYS:O	30:0:87:C:H2'	2.09	0.53
30:0:506:G:N2	30:0:509:A:H5''	2.22	0.53
14:N:38:LYS:HE2	14:N:107:ASN:HD21	1.72	0.53
30:0:256:C:H2'	30:0:257:G:O4'	2.09	0.53
30:0:2301:A:H5''	30:0:2302:A:H5'	1.91	0.53
30:0:1202:A:H2'	30:0:1203:G:C5'	2.39	0.53
28:2:41:HIS:HD2	28:2:44:ARG:H	1.56	0.53
15:O:44:ASN:OD1	15:O:65:LEU:HB2	2.07	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1795:G:H2'	30:0:1796:A:O4'	2.09	0.53
30:0:522:U:O2'	30:0:1366:C:H5'	2.08	0.53
30:0:396:U:O2'	30:0:418:C:H4'	2.08	0.52
30:0:1342:C:H2'	30:0:1343:C:H5'	1.91	0.52
27:1:45:ARG:NH2	38:1:8976:HOH:O	2.38	0.52
22:V:39:ALA:N	22:V:40:PRO:HD2	2.24	0.52
30:0:413:G:H2'	30:0:414:C:C6	2.44	0.52
30:0:1535:G:H2'	30:0:1536:C:C6	2.44	0.52
3:C:63:SER:OG	30:0:2101:A:H2'	2.09	0.52
30:0:1201:C:H2'	30:0:1202:A:H5'	1.91	0.52
30:0:1603:A:C5'	30:0:1605:G:O4'	2.53	0.52
30:0:1878:G:C1'	38:0:6119:HOH:O	2.42	0.52
30:0:2507:G:H2'	30:0:2510:C:H42	1.74	0.52
12:L:37:LYS:HE2	30:0:2466:G:OP2	2.09	0.52
9:I:121:LYS:HB3	30:0:1184:C:H4'	1.90	0.52
23:W:4:LEU:HD22	23:W:52:VAL:HG21	1.90	0.52
3:C:2:GLN:HB3	38:C:8534:HOH:O	2.09	0.52
30:0:1268:C:H2'	30:0:1269:G:H8	1.75	0.52
28:2:22:PRO:HG2	28:2:25:VAL:HG23	1.90	0.52
30:0:1213:C:O2'	30:0:1214:G:H5'	2.10	0.52
22:V:64:GLY:O	22:V:65:ASP:HB2	2.08	0.52
3:C:218:VAL:HG12	38:C:8634:HOH:O	2.08	0.52
25:Y:134:HIS:HE1	30:0:538:C:OP2	1.92	0.52
8:H:69:ARG:HD3	38:H:233:HOH:O	2.10	0.52
31:9:56:A:H2'	31:9:57:A:C5'	2.05	0.52
30:0:613:C:H2'	30:0:614:U:H6	1.75	0.52
28:2:40:ARG:HD2	28:2:47:THR:HG22	1.91	0.52
1:A:101:GLU:OE2	1:A:131:HIS:HB2	2.10	0.52
30:0:1855:G:H4'	30:0:1856:C:O5'	2.09	0.52
5:E:3:VAL:HG22	5:E:49:ILE:HB	1.90	0.52
18:R:33:ARG:NH1	38:R:8946:HOH:O	2.43	0.52
13:M:75:ARG:HH11	30:0:1864:C:H5	1.56	0.52
30:0:1183:C:O2	30:0:1183:C:H2'	2.08	0.52
30:0:137:U:H2'	30:0:139:C:C5	2.45	0.52
1:A:186:TRP:CG	1:A:187:PRO:HA	2.45	0.52
30:0:2300:A:H4'	30:0:2301:A:O5'	2.10	0.52
14:N:93:GLN:HE21	14:N:93:GLN:HA	1.74	0.52
25:Y:235:GLU:H	25:Y:235:GLU:CD	2.11	0.52
30:0:1679:C:H5'	38:0:9325:HOH:O	2.08	0.52
30:0:2613:G:O2'	30:0:2614:C:H5'	2.09	0.52
30:0:2433:A:H2'	30:0:2434:A:C8	2.44	0.52
30:0:1497:G:H4'	30:0:1627:G:O2'	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:80:TRP:O	5:E:134:SER:HA	2.09	0.52
23:W:119:HIS:HD2	23:W:120:PRO:O	1.93	0.52
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.89	0.52
30:0:2445:U:H2'	30:0:2446:G:H8	1.74	0.52
13:M:30:GLU:O	13:M:34:GLU:HG3	2.10	0.52
25:Y:146:PRO:O	25:Y:154:ARG:HG3	2.10	0.52
12:L:148:GLU:HA	38:L:8875:HOH:O	2.08	0.52
30:0:2469:A:H1'	38:0:3237:HOH:O	2.08	0.52
2:B:238:ASN:HD22	2:B:240:GLY:N	2.00	0.52
30:0:603:A:H1'	30:0:605:C:C2	2.44	0.52
30:0:2256:G:H2'	30:0:2257:G:H5'	1.92	0.52
2:B:320:GLN:NE2	2:B:321:PRO:HD2	2.24	0.52
5:E:143:GLN:NE2	30:0:2780:C:H1'	2.25	0.52
30:0:2781:U:O2'	30:0:2782:G:H5'	2.08	0.52
27:1:8:GLN:HE22	27:1:11:LYS:HZ2	1.58	0.52
30:0:1342:C:O2'	30:0:1343:C:H5'	2.09	0.52
3:C:107:ARG:O	3:C:111:VAL:HG23	2.10	0.52
2:B:8:LYS:HG3	2:B:220:VAL:HG12	1.92	0.52
30:0:1309:U:O2'	30:0:1310:U:H5'	2.10	0.52
25:Y:170:SER:OG	25:Y:175:ARG:HG3	2.09	0.52
18:R:117:HIS:HD2	30:0:20:G:H21	1.56	0.52
20:T:38:ARG:NH1	38:T:6217:HOH:O	2.42	0.52
30:0:1202:A:H2'	30:0:1203:G:H5'	1.91	0.52
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.88	0.52
30:0:1527:A:H1'	30:0:1528:A:C8	2.45	0.52
4:D:52:THR:HG21	30:0:2346:C:O2'	2.10	0.52
2:B:271:ASP:HB3	2:B:296:LEU:HD12	1.91	0.52
16:P:58:SER:HB3	38:0:5627:HOH:O	2.10	0.52
25:Y:142:SER:OG	30:0:1331:G:OP2	2.27	0.52
31:9:52:A:O2'	31:9:53:G:H5'	2.10	0.52
31:9:110:G:C5	31:9:111:U:C5	2.97	0.52
30:0:905:C:H3'	38:0:5190:HOH:O	2.08	0.52
30:0:2587:OMU:H2'	30:0:2589:U:H5''	1.92	0.52
30:0:645:U:O2	30:0:761:A:H2	1.92	0.52
30:0:1207:A:C8	30:0:1208:C:C6	2.98	0.52
2:B:207:LYS:HG3	30:0:2717:C:OP1	2.10	0.52
16:P:115:SER:N	16:P:118:GLN:HE21	1.97	0.52
30:0:559:U:H6	30:0:559:U:C5'	2.17	0.52
21:U:9:CYS:CA	21:U:52:THR:HG22	2.39	0.52
30:0:1477:C:C5'	30:0:1868:G:H5''	2.39	0.52
2:B:158:LYS:HD3	30:0:2846:C:OP1	2.10	0.52
1:A:171:LYS:HB2	30:0:820:G:C5	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:2269:C:H2'	30:0:2270:G:C5'	2.40	0.52
6:F:57:GLU:O	6:F:61:MET:HG3	2.09	0.52
12:L:143:THR:HG21	38:L:8841:HOH:O	2.09	0.52
30:0:2836:G:H1'	38:0:6838:HOH:O	2.09	0.52
30:0:1825:U:O2'	30:0:1826:C:H5'	2.10	0.52
9:I:69:PRO:HA	30:0:1164:U:OP1	2.10	0.52
30:0:2072:G:C6	30:0:2533:C:H1'	2.45	0.52
2:B:41:PHE:HB3	2:B:190:MET:CE	2.40	0.52
30:0:2781:U:H2'	30:0:2782:G:C5'	2.39	0.52
24:X:43:VAL:HG12	24:X:44:ASP:N	2.25	0.52
30:0:538:C:H5''	30:0:539:G:C8	2.45	0.52
30:0:1857:A:H5''	38:0:6701:HOH:O	2.10	0.52
18:R:40:ALA:O	18:R:44:VAL:HG23	2.10	0.52
30:0:177:A:H2'	30:0:178:U:O4'	2.09	0.52
30:0:1636:G:O2'	30:0:1637:A:H5'	2.09	0.52
15:O:3:THR:HG22	30:0:656:G:C5'	2.26	0.51
30:0:1589:G:H4'	38:0:6857:HOH:O	2.10	0.51
30:0:2830:U:O2'	30:0:2831:C:H5'	2.09	0.51
30:0:1419:U:H2'	30:0:1685:A:C2	2.45	0.51
4:D:65:GLU:HA	38:D:6752:HOH:O	2.09	0.51
30:0:912:A:C4	30:0:1294:A:C2	2.97	0.51
30:0:12:U:H2'	30:0:13:G:H5'	1.92	0.51
30:0:1165:G:H4'	30:0:1174:A:O2'	2.10	0.51
30:0:1762:C:H2'	30:0:1763:C:H6	1.76	0.51
30:0:497:A:H2'	30:0:498:A:C5'	2.41	0.51
30:0:24:G:N2	30:0:518:G:H1'	2.25	0.51
30:0:1058:A:H2'	30:0:1060:C:H5''	1.91	0.51
11:K:82:ARG:NH2	11:K:115:ARG:HG2	2.26	0.51
30:0:1188:A:C6	30:0:1189:A:C6	2.98	0.51
30:0:558:C:H2'	30:0:559:U:H5''	1.87	0.51
1:A:51:ARG:NH1	1:A:120:ARG:O	2.43	0.51
31:9:52:A:H2'	31:9:53:G:O4'	2.09	0.51
30:0:661:G:C5	30:0:686:A:C2	2.99	0.51
27:1:25:LYS:HD2	28:2:48:ASP:HA	1.92	0.51
30:0:2435:U:H1'	38:0:5428:HOH:O	2.11	0.51
1:A:210:GLY:HA3	38:A:9046:HOH:O	2.08	0.51
30:0:304:G:H1'	30:0:347:A:N6	2.25	0.51
30:0:2064:U:H5'	30:0:2652:U:H4'	1.93	0.51
29:3:70:ARG:HB3	38:3:8997:HOH:O	2.09	0.51
30:0:1976:G:H1'	30:0:2005:G:N2	2.26	0.51
11:K:74:VAL:HG11	11:K:113:ILE:HG12	1.91	0.51
30:0:119:A:H2'	30:0:120:A:H5''	1.92	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:2689:A:C2'	30:0:2690:U:H5'	2.39	0.51
20:T:68:ASP:HB2	38:0:5658:HOH:O	2.10	0.51
30:0:1565:C:O2'	30:0:1566:C:H5'	2.10	0.51
23:W:21:LEU:HD21	23:W:48:VAL:CG1	2.39	0.51
30:0:64:G:H2'	30:0:65:C:O4'	2.11	0.51
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.76	0.51
30:0:380:A:H2'	38:0:7225:HOH:O	2.10	0.51
29:3:3:MET:O	29:3:90:PHE:HA	2.10	0.51
30:0:2421:G:H3'	30:0:2422:U:H5''	1.92	0.51
30:0:2421:G:H3'	30:0:2422:U:C5'	2.40	0.51
30:0:204:A:C2'	30:0:205:U:H5'	2.40	0.51
5:E:69:ILE:HA	5:E:72:MET:HE2	1.91	0.51
30:0:677:C:O2'	30:0:678:G:H5'	2.10	0.51
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.40	0.51
30:0:42:C:H1'	38:0:4676:HOH:O	2.10	0.51
24:X:85:VAL:HG12	24:X:86:GLU:N	2.26	0.51
30:0:1730:G:C5'	30:0:1731:C:H6	2.23	0.51
8:H:61:ARG:HG3	38:0:4972:HOH:O	2.10	0.51
25:Y:133:HIS:HD2	38:Y:9065:HOH:O	1.93	0.51
10:J:26:VAL:HG13	10:J:36:VAL:HG11	1.93	0.51
2:B:212:GLN:HA	30:0:1733:A:H4'	1.91	0.51
6:F:50:VAL:HG13	6:F:60:VAL:HG11	1.92	0.51
20:T:97:ARG:NH2	30:0:309:C:OP1	2.44	0.51
30:0:407:A:H8	38:0:4460:HOH:O	1.94	0.51
30:0:537:G:O4'	30:0:538:C:C5	2.64	0.51
30:0:589:U:H2'	30:0:590:A:H8	1.75	0.51
18:R:59:PHE:O	18:R:63:ASN:HB3	2.11	0.51
30:0:2105:C:H2'	30:0:2106:C:C6	2.46	0.51
30:0:1925:G:O2'	30:0:1926:G:H5'	2.11	0.51
30:0:1622:G:C2'	30:0:1623:C:H5'	2.41	0.51
3:C:214:THR:HG23	38:C:8648:HOH:O	2.10	0.51
7:G:12:ILE:HG23	38:0:5457:HOH:O	2.09	0.51
8:H:22:TYR:CZ	30:0:1007:A:H2'	2.46	0.51
14:N:110:THR:HB	14:N:113:SER:HG	1.74	0.51
23:W:119:HIS:HE1	38:0:9554:HOH:O	1.93	0.51
30:0:1819:G:H2'	30:0:1820:G:C4'	2.41	0.51
30:0:1482:A:O2'	30:0:1483:C:H5'	2.11	0.51
7:G:64:ASN:N	7:G:64:ASN:HD22	2.09	0.51
30:0:1252:A:H2'	30:0:1253:C:O4'	2.11	0.51
12:L:92:ASP:HA	12:L:121:ILE:HB	1.91	0.51
30:0:1205:U:C2'	30:0:1206:U:C5'	2.77	0.50
30:0:2717:C:C2'	30:0:2718:C:C5'	2.75	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:567:U:C5'	38:0:6401:HOH:O	2.59	0.50
25:Y:187:VAL:HG23	25:Y:192:ASP:HB3	1.92	0.50
12:L:143:THR:HG22	12:L:144:ASP:N	2.27	0.50
30:0:1321:A:H2'	30:0:1322:G:C8	2.47	0.50
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.44	0.50
16:P:83:LYS:HG2	30:0:793:A:H5''	1.93	0.50
30:0:1173:A:H4'	30:0:1174:A:C8	2.45	0.50
30:0:1191:A:C2	30:0:1207:A:C2	2.99	0.50
30:0:2769:C:H2'	30:0:2770:G:O4'	2.11	0.50
30:0:1684:A:O2'	30:0:1685:A:H5''	2.12	0.50
30:0:1778:A:H2'	30:0:1779:A:H5'	1.92	0.50
30:0:1762:C:O2'	30:0:1763:C:H5'	2.12	0.50
13:M:90:ARG:NH2	30:0:2266:A:OP2	2.44	0.50
30:0:939:A:N1	30:0:1027:G:O2'	2.40	0.50
30:0:1386:G:O2'	30:0:1387:G:H5'	2.12	0.50
2:B:132:HIS:NE2	2:B:171:VAL:HG23	2.27	0.50
30:0:1915:U:O2'	30:0:1916:C:H5'	2.11	0.50
25:Y:212:ARG:HD2	38:Y:9085:HOH:O	2.09	0.50
30:0:1158:G:O2'	30:0:1159:G:H5'	2.11	0.50
30:0:1667:A:H2'	30:0:1668:U:C6	2.45	0.50
4:D:103:ASN:HD22	4:D:134:LEU:H	1.59	0.50
30:0:711:G:C2	30:0:718:C:C2	3.00	0.50
30:0:940:G:C5	30:0:1027:G:C2	3.00	0.50
12:L:97:VAL:HG12	12:L:98:GLU:O	2.12	0.50
1:A:112:PRO:HD3	1:A:152:CYS:SG	2.51	0.50
6:F:53:ASP:OD1	6:F:80:GLN:HB2	2.11	0.50
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.92	0.50
30:0:2385:G:H2'	30:0:2386:U:C6	2.47	0.50
2:B:102:THR:HG21	2:B:182:VAL:O	2.11	0.50
21:U:6:CYS:HB2	21:U:32:CYS:HB3	1.93	0.50
2:B:62:ARG:HA	2:B:65:MET:CE	2.41	0.50
30:0:1187:U:O2'	30:0:1189:A:H2	1.79	0.50
31:9:3:A:H2	31:9:21:G:N3	2.09	0.50
15:O:25:VAL:HG23	15:O:26:TRP:N	2.27	0.50
30:0:1130:U:H2'	30:0:1131:G:O4'	2.11	0.50
30:0:2250:G:N2	30:0:2251:G:H1'	2.27	0.50
30:0:735:C:C2'	30:0:736:A:H5'	2.41	0.50
21:U:39:ASN:ND2	21:U:44:ARG:HH11	2.08	0.50
30:0:1304:U:H2'	30:0:1305:C:C6	2.46	0.50
23:W:43:GLY:HA3	30:0:945:U:O2'	2.11	0.50
30:0:2089:A:O2'	30:0:2090:G:H5'	2.11	0.50
30:0:2667:G:H1'	30:0:2914:A:N3	2.26	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
38:M:8837:HOH:O	30:0:169:A:H5''	2.12	0.50
18:R:132:ARG:HG2	18:R:133:ALA:N	2.24	0.50
30:0:2584:G:H4'	38:0:7115:HOH:O	2.10	0.50
18:R:150:PRO:CG	18:R:150:PRO:CB	2.87	0.50
30:0:282:C:H1'	30:0:368:C:H41	1.71	0.50
30:0:559:U:C5	30:0:560:U:C5	3.00	0.50
30:0:2724:U:H2'	30:0:2725:G:O4'	2.11	0.50
30:0:17:G:H2'	30:0:18:C:C6	2.47	0.50
3:C:22:PHE:HA	3:C:116:ALA:HA	1.92	0.50
9:I:89:GLU:OE2	30:0:1181:A:H5'	2.11	0.50
31:9:55:U:H5'	38:9:9135:HOH:O	2.11	0.50
30:0:69:A:C8	30:0:69:A:C5'	2.90	0.50
10:J:19:MET:CE	10:J:132:LEU:HD11	2.41	0.50
1:A:33:GLU:O	1:A:34:ASP:HB2	2.10	0.50
17:Q:95:GLU:HA	30:0:949:U:H4'	1.93	0.50
25:Y:151:SER:HB3	25:Y:154:ARG:HB2	1.92	0.50
3:C:79:ARG:O	3:C:87:ARG:HG2	2.11	0.50
30:0:1333:U:H2'	30:0:1334:C:C6	2.47	0.50
30:0:332:G:O2'	30:0:333:G:H5'	2.12	0.50
26:Z:34:SER:HB3	30:0:797:A:H4'	1.93	0.50
1:A:109:GLU:HG2	1:A:116:GLY:N	2.26	0.50
10:J:107:ASN:HD22	10:J:109:TYR:H	1.58	0.50
30:0:2710:U:H2'	30:0:2711:U:C6	2.46	0.50
5:E:154:ILE:HD11	5:E:157:LYS:HB2	1.92	0.50
30:0:1200:A:H3'	38:0:5754:HOH:O	2.11	0.50
30:0:1422:U:H2'	30:0:1423:C:C6	2.47	0.50
30:0:2372:A:H2'	30:0:2373:U:H6	1.77	0.50
12:L:67:ARG:HB2	12:L:112:GLY:HA3	1.93	0.50
30:0:1170:U:H2'	30:0:1172:G:OP2	2.11	0.50
30:0:920:C:H4'	30:0:921:G:C2	2.45	0.50
30:0:2252:A:C5	30:0:2253:G:H1'	2.47	0.50
30:0:1762:C:H2'	30:0:1763:C:C6	2.47	0.50
30:0:1380:U:H5'	38:0:9218:HOH:O	2.12	0.50
30:0:638:C:H2'	30:0:639:A:C8	2.47	0.50
31:9:24:U:H3'	31:9:25:G:H5'	1.94	0.50
22:V:12:THR:HG23	22:V:14:ALA:H	1.77	0.50
30:0:876:A:N3	30:0:876:A:C2'	2.75	0.50
2:B:258:GLY:H	2:B:260:HIS:CE1	2.29	0.50
31:9:55:U:H4'	31:9:56:A:C8	2.47	0.49
11:K:55:VAL:HG12	11:K:56:SER:N	2.27	0.49
30:0:136:C:H2'	30:0:137:U:O4'	2.12	0.49
6:F:91:VAL:HG11	30:0:262:A:OP2	2.11	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:49:LEU:CD2	11:K:80:ILE:HD13	2.42	0.49
30:0:2871:G:H2'	30:0:2872:U:C6	2.47	0.49
23:W:13:MET:HE3	23:W:17:ILE:HG22	1.93	0.49
4:D:50:VAL:HG13	31:9:41:C:O4'	2.12	0.49
30:0:1165:G:O2'	30:0:1174:A:C1'	2.60	0.49
30:0:1211:G:H2'	30:0:1212:C:C6	2.47	0.49
30:0:488:U:H2'	38:0:4004:HOH:O	2.12	0.49
8:H:34:HIS:HD2	8:H:90:LEU:O	1.95	0.49
12:L:34:GLY:HA3	12:L:38:HIS:CE1	2.46	0.49
30:0:2534:C:H1'	38:0:3491:HOH:O	2.11	0.49
23:W:61:THR:HG23	23:W:151:GLU:HG3	1.94	0.49
30:0:1186:C:N4	30:0:1187:U:C4	2.81	0.49
30:0:559:U:H2'	30:0:560:U:O4'	2.12	0.49
18:R:9:ASP:O	18:R:13:THR:HB	2.11	0.49
18:R:18:LEU:HD12	18:R:143:VAL:CG1	2.42	0.49
4:D:76:ARG:NE	31:9:44:A:O4'	2.44	0.49
2:B:91:PRO:HA	10:J:144:THR:OG1	2.12	0.49
30:0:790:A:H1'	30:0:1710:A:H2'	1.94	0.49
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.13	0.49
25:Y:115:ARG:HH21	30:0:1266:U:H4'	1.76	0.49
38:R:8953:HOH:O	30:0:1370:G:H5''	2.12	0.49
13:M:99:ARG:HE	13:M:170:ASN:ND2	2.10	0.49
30:0:69:A:H8	30:0:69:A:C5'	2.17	0.49
14:N:71:TRP:CE3	14:N:175:LEU:HD22	2.47	0.49
30:0:1972:U:C2'	30:0:1973:A:H5''	2.42	0.49
18:R:128:ARG:NH2	30:0:2054:A:C2	2.80	0.49
30:0:1309:U:C2'	30:0:1310:U:H5'	2.43	0.49
30:0:1524:U:OP1	30:0:1524:U:H4'	2.12	0.49
30:0:947:U:O2'	30:0:948:G:H5'	2.13	0.49
8:H:39:LYS:HA	8:H:87:LYS:NZ	2.27	0.49
2:B:244:PRO:HB3	30:0:1234:U:N3	2.27	0.49
30:0:1515:A:H2'	30:0:1516:U:C6	2.48	0.49
30:0:1286:A:H5''	30:0:1287:A:OP1	2.13	0.49
30:0:1193:A:C2	30:0:1194:A:N6	2.80	0.49
30:0:483:C:C4	30:0:484:A:C6	3.01	0.49
14:N:1:ALA:HB2	31:9:14:G:O2'	2.13	0.49
5:E:139:GLU:OE2	30:0:2781:U:H1'	2.13	0.49
30:0:968:G:C2	30:0:1001:U:O2	2.66	0.49
30:0:2326:C:H4'	30:0:2412:G:C4'	2.43	0.49
24:X:30:MET:HG2	30:0:1384:C:H5'	1.94	0.49
30:0:1119:G:N2	30:0:1246:A:N1	2.60	0.49
1:A:211:LYS:HB3	1:A:212:PRO:CD	2.38	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1278:A:H2'	30:0:1280:A:C8	2.48	0.49
30:0:920:C:H5'	30:0:921:G:C4	2.48	0.49
30:0:1245:C:O5'	30:0:1245:C:H6	1.96	0.49
30:0:1056:U:H2'	30:0:1057:A:O4'	2.12	0.49
5:E:126:ILE:HB	5:E:131:LEU:HD23	1.94	0.49
31:9:56:A:C3'	31:9:57:A:H5''	2.42	0.49
30:0:2541:U:O2'	30:0:2542:C:H5'	2.13	0.49
30:0:371:U:H2'	30:0:372:A:C8	2.47	0.49
30:0:2269:C:H2'	30:0:2270:G:H5'	1.94	0.49
2:B:17:LYS:O	2:B:260:HIS:HD2	1.95	0.49
11:K:34:VAL:HG22	11:K:47:ALA:HB2	1.94	0.49
30:0:899:C:H5'	38:0:3199:HOH:O	2.13	0.49
30:0:1706:G:H1'	30:0:1712:A:H61	1.78	0.49
19:S:57:THR:HG22	19:S:58:MET:N	2.28	0.49
11:K:130:MET:SD	21:U:25:ASP:O	2.70	0.49
30:0:1909:A:N1	30:0:2128:G:H1'	2.27	0.49
9:I:73:LEU:HD12	9:I:107:LYS:HZ1	1.76	0.49
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.13	0.49
1:A:179:MET:HG2	1:A:186:TRP:CB	2.43	0.49
30:0:2869:G:H2'	30:0:2870:C:H6	1.78	0.49
14:N:17:ARG:HH11	14:N:17:ARG:HB3	1.78	0.49
30:0:1849:G:H1'	30:0:2011:A:N1	2.28	0.49
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.12	0.49
6:F:107:ASP:O	6:F:111:ILE:HG13	2.12	0.49
1:A:94:LEU:HG	1:A:99:ILE:CD1	2.43	0.49
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.94	0.49
3:C:127:ARG:CZ	3:C:225:PRO:HG2	2.42	0.49
25:Y:169:ARG:HD3	30:0:1328:A:C8	2.47	0.49
2:B:307:ARG:HG3	2:B:307:ARG:NH1	2.28	0.49
15:O:24:ALA:HB3	30:0:710:G:OP1	2.13	0.49
1:A:190:ARG:NH2	1:A:207:GLN:OE1	2.45	0.49
30:0:2121:G:O2'	30:0:2122:C:H5'	2.13	0.49
30:0:2512:U:H4'	30:0:2514:U:O4	2.12	0.49
2:B:206:THR:HG21	30:0:2716:G:C5'	2.40	0.49
30:0:2271:G:N3	30:0:2271:G:H2'	2.28	0.49
30:0:226:A:H1'	30:0:393:G:C5	2.48	0.49
30:0:1506:U:H6	30:0:1506:U:H5'	1.77	0.49
30:0:1066:U:H2'	30:0:1067:A:C8	2.48	0.49
20:T:53:GLY:HA3	38:0:6800:HOH:O	2.12	0.49
14:N:4:PRO:HG3	31:9:69:U:OP1	2.13	0.49
3:C:34:ALA:HB3	3:C:220:THR:HG21	1.94	0.49
13:M:78:LYS:HD3	38:0:7679:HOH:O	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:167:GLY:O	13:M:171:ARG:HG3	2.13	0.48
30:0:1118:A:C8	30:0:1119:G:H5''	2.48	0.48
30:0:2645:U:H1'	38:0:9305:HOH:O	2.13	0.48
30:0:191:A:C4	30:0:237:G:N7	2.81	0.48
30:0:2836:G:H5''	38:0:5165:HOH:O	2.12	0.48
19:S:57:THR:HG23	38:S:8979:HOH:O	2.11	0.48
30:0:2664:A:OP1	30:0:2664:A:H8	1.96	0.48
19:S:11:THR:H	19:S:14:ALA:HB3	1.77	0.48
30:0:1545:C:H2'	30:0:1546:G:O4'	2.13	0.48
30:0:1116:U:O2'	30:0:1118:A:C2	2.39	0.48
30:0:1972:U:H2'	30:0:1973:A:H5''	1.94	0.48
31:9:3:A:OP2	31:9:25:G:N2	2.45	0.48
30:0:1477:C:H5'	30:0:1868:G:H5'	1.94	0.48
30:0:2379:G:N7	30:0:2408:A:N1	2.61	0.48
30:0:2326:C:H4'	30:0:2412:G:H4'	1.95	0.48
30:0:1447:U:H3'	30:0:1506:U:O2	2.13	0.48
3:C:58:ALA:HA	3:C:73:GLN:HE21	1.78	0.48
30:0:2329:C:O2'	30:0:2330:U:H5'	2.13	0.48
17:Q:53:HIS:CD2	30:0:2389:U:H4'	2.48	0.48
4:D:141:VAL:HG21	31:9:57:A:H8	1.78	0.48
23:W:4:LEU:O	23:W:32:CYS:HA	2.13	0.48
30:0:2102:G:H1'	30:0:2103:A:N7	2.29	0.48
30:0:447:A:O2'	30:0:448:G:H5'	2.13	0.48
30:0:10:U:C4	30:0:532:A:C8	3.01	0.48
30:0:1013:A:H1'	38:0:9158:HOH:O	2.13	0.48
30:0:2816:A:H5''	30:0:2817:G:H5'	1.96	0.48
30:0:59:A:H5'	38:0:4330:HOH:O	2.12	0.48
3:C:43:LYS:HG2	30:0:449:A:N7	2.28	0.48
30:0:1185:U:H2'	30:0:1186:C:C6	2.48	0.48
30:0:1667:A:C2	30:0:1668:U:C2	3.02	0.48
23:W:139:GLY:O	23:W:141:HIS:CD2	2.66	0.48
30:0:1589:G:N2	30:0:1605:G:H1'	2.27	0.48
16:P:115:SER:OG	16:P:118:GLN:HG3	2.13	0.48
30:0:2420:G:H2'	30:0:2421:G:H8	1.79	0.48
10:J:74:ARG:HB3	10:J:74:ARG:HH11	1.77	0.48
12:L:34:GLY:HA2	38:0:5408:HOH:O	2.12	0.48
2:B:139:ASP:HB2	38:B:8995:HOH:O	2.12	0.48
13:M:171:ARG:NH2	30:0:189:A:OP1	2.47	0.48
30:0:541:C:O2'	30:0:542:A:H5''	2.14	0.48
23:W:88:THR:HG22	23:W:90:TYR:CD1	2.48	0.48
1:A:95:PRO:HG2	1:A:98:GLU:HG2	1.96	0.48
30:0:2493:C:O2	30:0:2493:C:H2'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:119:HIS:O	2:B:121:PRO:HD3	2.13	0.48
30:0:699:C:H6	30:0:744:G:O4'	1.96	0.48
30:0:228:C:H2'	30:0:229:G:H5'	1.94	0.48
6:F:30:LYS:HE2	6:F:99:THR:HG21	1.94	0.48
30:0:1520:G:C6	30:0:1521:C:N4	2.82	0.48
30:0:1522:A:C2	30:0:1665:G:C6	3.02	0.48
30:0:2374:G:H2'	30:0:2375:A:C8	2.48	0.48
30:0:2372:A:H2'	30:0:2373:U:C6	2.48	0.48
16:P:1:THR:O	30:0:1396:C:H1'	2.14	0.48
30:0:499:G:O2'	30:0:500:G:H5'	2.13	0.48
30:0:536:A:H3'	38:0:5049:HOH:O	2.14	0.48
30:0:1029:U:O2'	30:0:1273:C:OP1	2.27	0.48
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.13	0.48
5:E:101:GLU:HB2	5:E:116:THR:O	2.14	0.48
30:0:834:G:H4'	30:0:835:U:OP2	2.13	0.48
27:1:45:ARG:HB3	38:1:8967:HOH:O	2.14	0.48
30:0:1594:C:O2'	30:0:1607:A:H4'	2.13	0.48
30:0:346:U:H4'	38:0:6842:HOH:O	2.13	0.48
30:0:2387:U:H2'	30:0:2388:C:C6	2.48	0.48
1:A:1:GLY:HA2	30:0:2114:C:OP1	2.13	0.48
30:0:1739:G:O2'	30:0:1740:U:H5'	2.13	0.48
30:0:291:C:H2'	30:0:292:G:O4'	2.14	0.48
31:9:1:U:C4'	31:9:3:A:OP1	2.60	0.48
30:0:1130:U:H5'	38:0:7668:HOH:O	2.13	0.48
30:0:1314:U:H5''	30:0:1316:G:O4'	2.13	0.48
31:9:45:A:C5	31:9:46:C:C5	3.02	0.48
30:0:312:U:C2	30:0:320:G:N2	2.82	0.48
1:A:3:ARG:HD3	30:0:870:G:OP2	2.13	0.48
30:0:545:G:H8	30:0:545:G:C5'	2.12	0.48
30:0:289:G:O2'	30:0:290:C:H5'	2.14	0.48
30:0:2255:A:O2'	30:0:2256:G:H5'	2.14	0.48
30:0:304:G:H1'	30:0:347:A:H61	1.78	0.48
1:A:126:ALA:HB1	1:A:138:VAL:CG1	2.44	0.48
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.94	0.48
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.29	0.48
30:0:1593:C:H1'	38:0:6105:HOH:O	2.14	0.48
10:J:107:ASN:C	10:J:107:ASN:HD22	2.16	0.48
30:0:625:U:H3'	38:0:3250:HOH:O	2.13	0.48
30:0:820:G:H5'	30:0:821:U:H5'	1.95	0.48
30:0:2840:A:H3'	38:0:7643:HOH:O	2.13	0.48
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.44	0.48
30:0:2090:G:H2'	30:0:2091:G:C8	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1423:C:O2'	30:0:1424:A:H5'	2.14	0.48
23:W:68:THR:HG23	23:W:69:ARG:HG2	1.96	0.48
27:1:12:ASN:O	30:0:1415:G:H5'	2.14	0.48
30:0:466:A:H2'	30:0:467:G:O4'	2.13	0.48
30:0:541:C:C2'	30:0:542:A:C5'	2.79	0.47
23:W:122:ARG:NH2	38:0:5289:HOH:O	2.46	0.47
30:0:736:A:H2'	30:0:737:A:O4'	2.14	0.47
31:9:110:G:C6	31:9:111:U:C5	3.02	0.47
30:0:106:A:H2'	30:0:107:U:O4'	2.14	0.47
30:0:1028:U:H1'	38:0:3639:HOH:O	2.14	0.47
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.14	0.47
30:0:559:U:C3'	30:0:559:U:C6	2.97	0.47
30:0:602:A:O2'	30:0:605:C:H4'	2.13	0.47
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.29	0.47
30:0:1787:C:H4'	30:0:2883:A:O4'	2.14	0.47
4:D:51:ARG:NH1	4:D:68:PRO:HB3	2.29	0.47
16:P:87:ARG:HG2	38:P:185:HOH:O	2.14	0.47
30:0:722:G:H22	30:0:938:G:P	2.37	0.47
30:0:185:G:O3'	30:0:186:A:H4'	2.14	0.47
30:0:1181:A:H2'	30:0:1182:C:C5'	2.44	0.47
30:0:1181:A:C2'	30:0:1182:C:H5'	2.43	0.47
30:0:2541:U:H3'	38:0:9060:HOH:O	2.14	0.47
8:H:158:ASN:ND2	30:0:2502:C:H4'	2.30	0.47
30:0:1562:C:O2	30:0:1562:C:C2'	2.61	0.47
30:0:2134:G:C6	30:0:2258:A:C8	3.02	0.47
30:0:1456:C:H2'	30:0:1457:U:C6	2.49	0.47
22:V:12:THR:HG22	22:V:15:GLU:H	1.77	0.47
30:0:2032:U:O2'	30:0:2033:G:H5''	2.14	0.47
30:0:2266:A:H2'	30:0:2267:G:C8	2.49	0.47
30:0:946:C:O2'	30:0:947:U:H5'	2.14	0.47
14:N:100:ALA:O	14:N:129:ILE:HG23	2.13	0.47
6:F:59:ILE:CD1	30:0:263:U:C2	2.98	0.47
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.49	0.47
30:0:1890:U:H4'	30:0:2010:A:C6	2.50	0.47
30:0:1588:G:C5	30:0:1589:G:C6	3.03	0.47
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.50	0.47
30:0:968:G:O2'	30:0:969:G:H5'	2.14	0.47
31:9:71:C:H2'	31:9:72:C:H6	1.79	0.47
30:0:1183:C:N3	30:0:1184:C:N4	2.62	0.47
30:0:1206:U:H2'	30:0:1207:A:O4'	2.14	0.47
30:0:2712:G:O2'	30:0:2713:G:H5'	2.14	0.47
30:0:2000:G:O2'	30:0:2001:G:H5'	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:2001:G:O2'	30:0:2002:C:H5'	2.14	0.47
31:9:65:A:N6	31:9:112:U:C6	2.82	0.47
8:H:31:ILE:HD11	8:H:65:LEU:HD23	1.96	0.47
23:W:64:THR:O	23:W:68:THR:HG22	2.14	0.47
30:0:168:C:O5'	30:0:168:C:H6	1.97	0.47
30:0:305:A:C5	30:0:329:A:C2	3.03	0.47
30:0:1137:G:H1'	38:0:3876:HOH:O	2.14	0.47
1:A:217:ARG:HG2	1:A:229:ALA:HB2	1.96	0.47
25:Y:210:GLY:H	30:0:1313:A:H5''	1.78	0.47
30:0:138:U:OP2	30:0:139:C:H5	1.98	0.47
11:K:81:ARG:HD3	11:K:87:ARG:NH2	2.30	0.47
30:0:2335:C:H2'	30:0:2336:G:H8	1.78	0.47
30:0:1406:A:H4'	30:0:1407:A:H5''	1.96	0.47
30:0:1153:C:N3	30:0:2786:G:O6	2.48	0.47
30:0:1823:G:O2'	30:0:1824:C:H5'	2.14	0.47
30:0:283:U:C5	30:0:284:C:C4	3.03	0.47
11:K:29:LEU:HB3	11:K:55:VAL:CG1	2.32	0.47
30:0:560:U:H2'	30:0:561:G:H8	1.79	0.47
11:K:41:LYS:O	11:K:42:ASN:HB2	2.15	0.47
26:Z:70:ARG:HD3	26:Z:83:TYR:HB2	1.95	0.47
20:T:26:THR:HA	20:T:39:ASN:HB3	1.95	0.47
11:K:74:VAL:HG12	11:K:75:ARG:HG3	1.95	0.47
16:P:59:ARG:O	16:P:63:ARG:HG3	2.15	0.47
30:0:969:G:H1	30:0:999:C:H42	1.61	0.47
29:3:28:GLY:HA3	30:0:2435:U:OP1	2.15	0.47
21:U:44:ARG:HB3	38:U:3805:HOH:O	2.13	0.47
25:Y:136:LYS:HE2	25:Y:138:ARG:NH1	2.28	0.47
30:0:2871:G:H2'	30:0:2872:U:H6	1.79	0.47
23:W:13:MET:HE1	23:W:18:GLN:HA	1.95	0.47
1:A:217:ARG:NH2	30:0:1853:C:O2'	2.48	0.47
30:0:2239:C:O2'	30:0:2240:U:H5'	2.14	0.47
30:0:1400:C:O2'	30:0:1401:G:H5'	2.15	0.47
30:0:2361:A:H2'	30:0:2362:A:C8	2.49	0.47
30:0:527:U:H2'	30:0:528:G:C8	2.49	0.47
30:0:2074:A:H2'	38:0:3533:HOH:O	2.14	0.47
30:0:2649:A:H5'	30:0:2649:A:C8	2.50	0.47
19:S:77:VAL:O	19:S:80:ARG:HG2	2.15	0.47
30:0:844:A:C6	30:0:882:A:C6	3.03	0.47
30:0:814:G:H4'	38:0:3130:HOH:O	2.15	0.47
30:0:1548:U:O2'	30:0:1549:C:H5'	2.14	0.47
30:0:853:C:H2'	30:0:854:G:O4'	2.14	0.47
30:0:2506:A:N6	30:0:2511:A:O2'	2.43	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:221:GLN:HE22	11:K:42:ASN:ND2	2.04	0.47
30:0:1904:A:H2'	30:0:1905:U:O4'	2.15	0.47
30:0:810:G:H2'	30:0:811:C:H6	1.79	0.47
30:0:249:G:O2'	30:0:250:C:H5'	2.15	0.47
18:R:122:GLN:HB3	18:R:138:SER:HB2	1.95	0.47
30:0:1942:A:H2'	30:0:1943:C:H6	1.79	0.47
10:J:127:ILE:CG2	35:J:8801:CL:CL	2.96	0.47
14:N:147:ILE:HB	38:9:9087:HOH:O	2.15	0.47
30:0:1377:C:H1'	38:0:9039:HOH:O	2.15	0.47
30:0:290:C:O2'	30:0:291:C:H5'	2.14	0.47
30:0:1014:A:H2'	30:0:1015:C:H5'	1.96	0.47
25:Y:144:ARG:CZ	38:Y:9096:HOH:O	2.62	0.47
2:B:212:GLN:HB2	2:B:257:THR:CG2	2.44	0.47
2:B:144:THR:HB	38:B:9092:HOH:O	2.14	0.47
11:K:113:ILE:HD12	11:K:128:ALA:HB2	1.96	0.47
10:J:6:PHE:HB3	10:J:109:TYR:OH	2.15	0.47
27:1:28:HIS:CD2	27:1:31:LYS:HG3	2.50	0.47
30:0:2649:A:H5'	30:0:2649:A:H8	1.79	0.47
14:N:139:TRP:CE3	14:N:139:TRP:HA	2.50	0.47
30:0:1970:G:H2'	30:0:1970:G:N3	2.30	0.47
14:N:162:ASP:HA	38:N:8830:HOH:O	2.15	0.47
16:P:114:LEU:HA	16:P:118:GLN:NE2	2.30	0.46
30:0:364:U:H2'	30:0:365:G:O4'	2.15	0.46
31:9:3:A:C2	31:9:21:G:N3	2.83	0.46
10:J:131:THR:HG22	10:J:133:GLY:N	2.30	0.46
12:L:27:ARG:HH21	12:L:30:ARG:HG2	1.80	0.46
30:0:17:G:H2'	30:0:18:C:H6	1.79	0.46
30:0:254:C:O2	30:0:254:C:H2'	2.14	0.46
30:0:1149:U:C5	30:0:1215:A:C5	3.04	0.46
16:P:91:LYS:O	16:P:95:GLU:HG3	2.15	0.46
3:C:168:ARG:NH2	3:C:190:ALA:O	2.48	0.46
30:0:1760:G:H5'	30:0:1818:C:O2'	2.15	0.46
31:9:76:G:H3'	31:9:77:A:C5'	2.28	0.46
25:Y:189:ASN:ND2	25:Y:192:ASP:H	2.13	0.46
27:1:16:HIS:HE1	30:0:775:G:OP1	1.98	0.46
27:1:42:SER:HB2	38:1:8956:HOH:O	2.14	0.46
18:R:111:ILE:HG23	18:R:145:LEU:CD1	2.46	0.46
30:0:1379:A:H1'	38:0:9689:HOH:O	2.15	0.46
30:0:1244:U:H4'	30:0:1246:A:O4'	2.16	0.46
30:0:1940:C:H4'	38:0:7346:HOH:O	2.16	0.46
26:Z:70:ARG:CD	26:Z:83:TYR:HB2	2.45	0.46
31:9:1:U:O3'	31:9:3:A:C5'	2.63	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1820:G:C6	30:0:2030:A:C2	3.04	0.46
15:O:65:LEU:HD13	30:0:746:A:C6	2.51	0.46
12:L:30:ARG:NH2	38:L:8823:HOH:O	2.44	0.46
23:W:13:MET:CE	23:W:17:ILE:HG22	2.46	0.46
13:M:169:ARG:NH2	38:M:8849:HOH:O	2.48	0.46
30:0:162:C:H2'	30:0:163:U:H5'	1.97	0.46
30:0:2858:U:H2'	30:0:2859:C:O4'	2.15	0.46
30:0:2578:G:C8	30:0:2578:G:H5'	2.39	0.46
27:1:16:HIS:CD2	30:0:470:U:O2'	2.67	0.46
30:0:1268:C:H2'	30:0:1269:G:C8	2.50	0.46
30:0:1921:A:C6	30:0:1922:A:C2	3.04	0.46
30:0:2064:U:H4'	30:0:2653:A:OP1	2.14	0.46
30:0:764:C:H2'	30:0:765:G:O4'	2.15	0.46
25:Y:117:LEU:HA	25:Y:174:VAL:HG11	1.98	0.46
30:0:95:A:H5''	30:0:97:G:O4'	2.14	0.46
30:0:1511:U:O2'	30:0:1512:G:H5'	2.15	0.46
30:0:152:A:H2'	30:0:153:C:C6	2.50	0.46
30:0:2783:A:H2'	30:0:2784:A:C8	2.50	0.46
27:1:1:THR:HB	38:0:7140:HOH:O	2.15	0.46
1:A:36:ASP:CB	1:A:85:SER:H	2.29	0.46
30:0:2420:G:H2'	30:0:2421:G:C8	2.51	0.46
31:9:58:G:H3'	31:9:59:C:C6	2.49	0.46
30:0:255:A:C5	30:0:256:C:C4	3.04	0.46
15:O:38:ARG:NH1	38:O:7674:HOH:O	2.48	0.46
30:0:2839:C:H2'	30:0:2840:A:H5''	1.96	0.46
3:C:39:GLN:O	3:C:43:LYS:HD3	2.16	0.46
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.79	0.46
30:0:1021:G:O2'	30:0:1022:A:H5'	2.16	0.46
31:9:33:U:H2'	38:9:9066:HOH:O	2.15	0.46
30:0:89:G:H4'	38:0:4766:HOH:O	2.16	0.46
10:J:54:VAL:HG11	10:J:138:THR:HG21	1.96	0.46
30:0:1339:G:C6	30:0:1340:G:N1	2.84	0.46
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.16	0.46
30:0:282:C:C2'	30:0:283:U:H5'	2.45	0.46
23:W:125:HIS:CE1	30:0:1097:A:H5''	2.51	0.46
28:2:44:ARG:HD3	38:0:6937:HOH:O	2.15	0.46
30:0:1845:A:O2'	30:0:1846:U:H5'	2.15	0.46
30:0:2617:G:H2'	30:0:2617:G:N3	2.30	0.46
3:C:19:PRO:HG2	3:C:22:PHE:CE1	2.50	0.46
30:0:125:U:H2'	38:0:3761:HOH:O	2.15	0.46
3:C:132:ASP:HB3	38:C:8567:HOH:O	2.16	0.46
30:0:1087:G:H4'	30:0:1088:A:OP1	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:280:VAL:HG13	2:B:333:GLU:O	2.16	0.46
30:0:1166:A:N3	30:0:1166:A:H2'	2.31	0.46
30:0:1878:G:O2'	30:0:1879:U:OP2	2.33	0.46
30:0:1840:A:H4'	30:0:1841:C:O5'	2.16	0.46
3:C:46:TYR:CE1	30:0:450:C:H4'	2.50	0.46
4:D:52:THR:CG2	30:0:2346:C:H4'	2.45	0.46
30:0:407:A:H2'	30:0:408:A:C8	2.51	0.46
30:0:1044:C:H5	38:0:6604:HOH:O	1.98	0.46
30:0:704:C:H2'	30:0:705:C:H6	1.81	0.46
7:G:16:LYS:O	7:G:20:VAL:HG23	2.16	0.46
2:B:260:HIS:HE1	38:0:5167:HOH:O	1.97	0.46
2:B:314:ALA:HB3	2:B:317:PRO:HG3	1.98	0.46
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.48	0.46
24:X:85:VAL:HG12	24:X:86:GLU:H	1.80	0.46
30:0:1730:G:C5'	30:0:1731:C:C5	2.95	0.46
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.98	0.46
5:E:143:GLN:HE22	30:0:2779:G:H21	1.63	0.46
30:0:2353:A:H4'	30:0:2354:A:O5'	2.16	0.46
30:0:2032:U:H2'	30:0:2033:G:H5'	1.97	0.46
23:W:10:GLU:HB2	23:W:18:GLN:NE2	2.31	0.46
19:S:45:TYR:O	19:S:80:ARG:NH2	2.49	0.46
13:M:159:VAL:HG13	13:M:160:PHE:N	2.31	0.46
3:C:48:SER:HB3	30:0:1352:A:N1	2.31	0.46
13:M:81:ARG:HG3	13:M:85:ARG:HB2	1.97	0.46
13:M:65:VAL:HG21	13:M:105:ALA:HB2	1.98	0.46
30:0:1834:C:H2'	30:0:1840:A:H62	1.81	0.46
11:K:74:VAL:HG13	11:K:113:ILE:HG12	1.98	0.46
19:S:56:ASN:O	28:2:8:LYS:NZ	2.47	0.46
13:M:145:ASP:HB2	38:M:8864:HOH:O	2.15	0.46
30:0:862:U:H2'	30:0:863:G:H8	1.80	0.46
30:0:772:G:H2'	30:0:773:A:O4'	2.16	0.46
30:0:1052:G:H2'	30:0:1052:G:N3	2.30	0.46
3:C:197:SER:HB3	38:C:8579:HOH:O	2.16	0.46
30:0:2002:C:H2'	30:0:2003:U:H5'	1.97	0.46
30:0:2250:G:H2'	30:0:2251:G:O4'	2.16	0.46
30:0:699:C:H2'	30:0:744:G:N3	2.31	0.46
30:0:571:C:H6	30:0:571:C:O5'	1.99	0.46
30:0:2594:C:O2'	30:0:2595:U:H5'	2.16	0.46
14:N:94:GLU:HG3	14:N:186:LEU:HD12	1.98	0.46
31:9:36:C:C5	31:9:37:C:C5	3.04	0.46
2:B:329:TYR:CE2	21:U:15:PRO:HG2	2.51	0.46
30:0:2906:A:H5'	30:0:2907:C:O4'	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:424:C:H2'	30:0:425:U:C6	2.51	0.46
3:C:233:THR:HG22	3:C:234:VAL:N	2.31	0.46
30:0:2505:G:H2'	30:0:2506:A:H5'	1.97	0.45
1:A:94:LEU:HG	1:A:99:ILE:HD11	1.97	0.45
3:C:27:ARG:HG2	3:C:30:LEU:HG	1.98	0.45
10:J:75:PRO:HG2	10:J:105:LEU:CD2	2.45	0.45
12:L:18:HIS:CD2	30:0:902:G:N7	2.82	0.45
31:9:58:G:H3'	31:9:59:C:C5	2.51	0.45
10:J:39:VAL:HG22	10:J:107:ASN:HA	1.98	0.45
1:A:223:ARG:NH1	30:0:2270:G:H4'	2.31	0.45
8:H:91:ARG:O	30:0:1003:U:H4'	2.16	0.45
4:D:75:LEU:HD22	4:D:79:MET:HB3	1.98	0.45
7:G:23:ILE:O	7:G:27:ILE:HG13	2.16	0.45
30:0:1154:A:H2'	30:0:1155:G:C8	2.51	0.45
6:F:48:VAL:CG2	6:F:74:PHE:HB3	2.46	0.45
30:0:1181:A:N1	30:0:1192:A:O2'	2.42	0.45
23:W:24:LEU:O	23:W:26:ILE:HG22	2.16	0.45
30:0:559:U:H3'	30:0:559:U:C6	2.51	0.45
30:0:2756:U:C2	30:0:2896:A:H2	2.33	0.45
30:0:1080:C:O5'	30:0:1080:C:H6	1.99	0.45
30:0:1626:A:H2'	30:0:1627:G:C5'	2.47	0.45
13:M:9:ARG:HD2	30:0:380:A:OP2	2.15	0.45
7:G:67:LEU:O	7:G:71:LEU:HG	2.15	0.45
2:B:305:ASP:O	2:B:306:LYS:HB2	2.17	0.45
3:C:118:THR:HG22	3:C:137:PRO:HB3	1.96	0.45
30:0:2473:U:O3'	30:0:2474:A:H3'	2.16	0.45
30:0:2112:A:H2'	30:0:2113:G:C8	2.51	0.45
30:0:1185:U:C5'	38:0:7462:HOH:O	2.62	0.45
2:B:36:PRO:CA	2:B:168:GLY:HA3	2.40	0.45
30:0:2506:A:O2'	30:0:2507:G:O5'	2.35	0.45
30:0:2511:A:H2'	30:0:2512:U:O4'	2.16	0.45
30:0:366:U:H2'	30:0:367:G:O4'	2.16	0.45
12:L:18:HIS:HB3	38:0:9150:HOH:O	2.15	0.45
31:9:114:G:H2'	31:9:115:C:C6	2.52	0.45
30:0:2825:C:H4'	30:0:2826:G:O5'	2.16	0.45
8:H:31:ILE:HG23	38:H:233:HOH:O	2.16	0.45
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.51	0.45
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.98	0.45
11:K:114:ALA:HB3	11:K:117:VAL:HG23	1.99	0.45
31:9:55:U:H4'	31:9:56:A:H8	1.81	0.45
3:C:129:HIS:CE1	3:C:232:LEU:H	2.35	0.45
30:0:816:G:H5'	30:0:1598:A:H4'	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:27:ASN:HD21	30:0:2807:U:P	2.39	0.45
19:S:37:VAL:O	19:S:41:VAL:HG23	2.16	0.45
30:0:297:U:H2'	30:0:298:C:H6	1.80	0.45
12:L:67:ARG:O	12:L:71:GLU:HG3	2.17	0.45
30:0:1850:U:H2'	30:0:1851:G:H8	1.80	0.45
30:0:214:U:H5'	38:0:6139:HOH:O	2.15	0.45
25:Y:148:GLY:HA3	30:0:622:G:P	2.56	0.45
30:0:1182:C:C1'	30:0:1192:A:H8	2.28	0.45
10:J:52:GLN:HE22	30:0:1119:G:H8	1.65	0.45
30:0:513:A:N3	38:0:3653:HOH:O	2.36	0.45
30:0:2250:G:C2	30:0:2251:G:H1'	2.50	0.45
20:T:54:ASP:OD2	30:0:316:A:H5'	2.16	0.45
4:D:140:ARG:HG3	4:D:140:ARG:HH11	1.80	0.45
15:O:21:SER:OG	15:O:106:PRO:HB2	2.15	0.45
17:Q:32:GLU:O	17:Q:93:ARG:NH2	2.50	0.45
1:A:164:ARG:NH2	30:0:1877:G:OP1	2.49	0.45
30:0:702:G:O2'	30:0:703:G:H5'	2.16	0.45
30:0:432:G:O2'	30:0:433:C:H5'	2.16	0.45
30:0:2740:G:H2'	30:0:2741:A:O4'	2.16	0.45
25:Y:122:ARG:NH2	38:Y:9019:HOH:O	2.49	0.45
30:0:2644:C:H4'	38:0:9154:HOH:O	2.16	0.45
30:0:1789:G:H2'	30:0:1790:C:O5'	2.16	0.45
10:J:19:MET:HE1	10:J:79:PHE:HA	1.98	0.45
4:D:49:PRO:HA	4:D:73:VAL:HG22	1.99	0.45
30:0:652:G:H2'	30:0:653:U:O4'	2.16	0.45
30:0:101:C:H2'	30:0:102:A:C8	2.51	0.45
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.51	0.45
30:0:2439:C:H5'	38:0:5486:HOH:O	2.17	0.45
30:0:2637:A:H5'	38:0:9275:HOH:O	2.16	0.45
30:0:2415:A:C2'	30:0:2416:G:H5'	2.46	0.45
12:L:30:ARG:HD2	30:0:164:G:H5''	1.99	0.45
30:0:1198:U:C6	30:0:1200:A:OP2	2.70	0.45
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.99	0.45
20:T:79:LEU:HG	20:T:89:ARG:HB2	1.98	0.45
24:X:25:ARG:HD2	38:X:5356:HOH:O	2.17	0.45
30:0:415:A:O2'	30:0:416:G:H5'	2.17	0.45
30:0:1209:C:C2	30:0:1210:G:C8	3.05	0.45
13:M:164:THR:CG2	13:M:165:GLY:N	2.79	0.45
23:W:122:ARG:HH11	23:W:122:ARG:HG3	1.81	0.45
12:L:57:VAL:HG12	12:L:57:VAL:O	2.17	0.45
6:F:91:VAL:HG12	6:F:92:GLY:H	1.79	0.45
30:0:1015:C:O5'	30:0:1015:C:H6	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:2032:U:C2'	30:0:2033:G:C5'	2.95	0.45
30:0:2324:G:N2	30:0:2377:U:H1'	2.32	0.45
30:0:113:A:OP2	30:0:114:A:H2'	2.17	0.45
2:B:256:GLN:HG2	38:B:9125:HOH:O	2.16	0.45
30:0:2566:A:C2	30:0:2696:G:O4'	2.70	0.45
30:0:281:U:HO2'	30:0:282:C:H5'	1.80	0.45
30:0:1117:A:C2	30:0:1244:U:C2	3.05	0.45
23:W:119:HIS:CG	38:0:5289:HOH:O	2.70	0.45
4:D:48:MET:HB3	31:9:41:C:H4'	1.99	0.45
30:0:2361:A:H8	30:0:2361:A:H5'	1.82	0.45
12:L:150:GLN:HB3	38:L:8872:HOH:O	2.16	0.45
30:0:1006:A:N1	30:0:2311:A:H1'	2.31	0.45
30:0:690:G:H4'	30:0:741:C:O2	2.17	0.45
1:A:232:ARG:NH2	1:A:236:GLY:O	2.50	0.45
23:W:11:VAL:O	23:W:12:ASN:HB2	2.17	0.45
14:N:154:LEU:C	14:N:156:GLU:H	2.18	0.45
30:0:587:A:H5''	38:0:7285:HOH:O	2.16	0.45
16:P:36:THR:O	16:P:39:ASP:HB2	2.17	0.45
15:O:35:LYS:HD3	38:0:4615:HOH:O	2.17	0.45
1:A:211:LYS:HB2	38:A:9077:HOH:O	2.16	0.45
30:0:1543:G:N1	30:0:1641:A:OP2	2.40	0.45
1:A:192:VAL:HG12	1:A:207:GLN:HB3	1.99	0.45
30:0:1171:A:H2'	30:0:1172:G:H5'	1.98	0.45
30:0:737:A:H2'	30:0:738:G:O4'	2.17	0.45
2:B:215:VAL:HA	2:B:220:VAL:HG22	1.98	0.45
30:0:629:A:H2'	30:0:630:A:O4'	2.17	0.45
2:B:214:PRO:HD2	38:0:9075:HOH:O	2.15	0.45
2:B:229:ARG:HD2	38:0:9108:HOH:O	2.17	0.45
3:C:49:ASP:HB3	3:C:52:ALA:HB2	1.99	0.45
30:0:1163:G:H2'	30:0:1164:U:C5	2.52	0.44
30:0:1188:A:N6	30:0:1189:A:N6	2.65	0.44
18:R:29:LYS:HD2	38:R:8943:HOH:O	2.16	0.44
9:I:112:LEU:HG	30:0:1162:G:O2'	2.17	0.44
31:9:35:C:H5''	38:9:9076:HOH:O	2.17	0.44
30:0:2114:C:O2'	30:0:2115:U:H5'	2.17	0.44
30:0:105:G:O2'	30:0:106:A:H5'	2.17	0.44
24:X:25:ARG:HD3	24:X:64:ALA:O	2.16	0.44
30:0:2325:U:O2'	30:0:2411:C:H1'	2.16	0.44
30:0:1224:G:H2'	30:0:1225:C:C6	2.51	0.44
2:B:177:HIS:O	2:B:181:ILE:HG13	2.17	0.44
3:C:138:VAL:HG11	3:C:160:LEU:HD13	1.98	0.44
30:0:541:C:H2'	30:0:542:A:H5'	1.91	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1592:G:O2'	30:0:1593:C:O5'	2.35	0.44
8:H:30:LYS:H	8:H:62:HIS:CD2	2.35	0.44
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.46	0.44
2:B:217:ARG:CG	2:B:257:THR:HG22	2.47	0.44
30:0:137:U:OP1	30:0:259:G:O2'	2.33	0.44
30:0:1992:U:H2'	30:0:1994:A:OP2	2.17	0.44
30:0:820:G:O2'	30:0:856:G:H4'	2.18	0.44
27:1:25:LYS:O	27:1:25:LYS:HG2	2.18	0.44
30:0:699:C:C2	30:0:743:G:N2	2.85	0.44
30:0:1398:G:O2'	30:0:1399:A:H5'	2.18	0.44
16:P:55:LYS:HG2	16:P:56:GLY:N	2.31	0.44
24:X:21:PRO:HG2	24:X:24:LYS:HD3	1.99	0.44
12:L:33:ALA:HB3	38:L:8896:HOH:O	2.16	0.44
30:0:1501:A:H4'	38:0:5597:HOH:O	2.17	0.44
30:0:134:U:C2	30:0:145:A:C2	3.06	0.44
12:L:14:GLY:O	30:0:1295:G:H5''	2.17	0.44
30:0:727:G:H3'	30:0:728:C:H6	1.82	0.44
30:0:195:C:H2'	30:0:196:G:H5'	1.99	0.44
30:0:1206:U:C5'	30:0:1206:U:H6	2.22	0.44
30:0:1702:U:H1'	38:0:5772:HOH:O	2.18	0.44
30:0:283:U:H5	30:0:284:C:C4	2.33	0.44
30:0:2509:A:OP2	30:0:2510:C:H5	2.00	0.44
15:O:25:VAL:CG1	30:0:710:G:H5'	2.48	0.44
30:0:660:A:H4'	30:0:661:G:O5'	2.18	0.44
2:B:243:ASN:HA	2:B:244:PRO:C	2.38	0.44
30:0:1583:U:H2'	30:0:1584:C:O4'	2.18	0.44
6:F:101:ALA:HA	38:F:5413:HOH:O	2.16	0.44
30:0:2753:G:O2'	30:0:2754:G:H5'	2.18	0.44
24:X:73:ARG:NH1	24:X:88:GLU:HB2	2.33	0.44
2:B:198:GLU:HA	38:B:9126:HOH:O	2.17	0.44
30:0:1166:A:OP1	30:0:1174:A:H4'	2.16	0.44
30:0:2003:U:H4'	30:0:2004:U:H5	1.83	0.44
30:0:1249:U:H2'	30:0:1250:C:H6	1.79	0.44
30:0:999:C:H2'	30:0:1000:C:O4'	2.17	0.44
2:B:253:GLN:OE1	30:0:2090:G:N2	2.51	0.44
30:0:790:A:H2'	30:0:791:A:O4'	2.18	0.44
25:Y:210:GLY:N	30:0:1313:A:H5''	2.33	0.44
30:0:2245:C:H6	30:0:2245:C:O5'	2.00	0.44
10:J:45:VAL:HG11	10:J:121:LEU:HD22	1.99	0.44
28:2:37:HIS:CE1	30:0:462:A:C8	3.06	0.44
30:0:535:G:C5	30:0:2063:U:C4	3.05	0.44
30:0:295:C:H2'	30:0:296:G:O4'	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1714:C:O2'	30:0:1715:C:H5'	2.17	0.44
30:0:2401:A:H2'	30:0:2402:A:C8	2.52	0.44
26:Z:77:GLY:HA2	26:Z:91:GLY:O	2.17	0.44
30:0:1163:G:N2	38:0:4726:HOH:O	2.49	0.44
30:0:1183:C:H41	30:0:1192:A:P	2.40	0.44
30:0:545:G:C8	30:0:545:G:C5'	2.94	0.44
1:A:199:HIS:HE1	30:0:1881:A:OP1	2.01	0.44
10:J:130:VAL:HG12	10:J:131:THR:N	2.33	0.44
1:A:144:GLU:OE2	30:0:1855:G:H8	2.00	0.44
30:0:694:A:C2'	30:0:695:C:H5'	2.47	0.44
12:L:4:LYS:HE2	30:0:645:U:OP2	2.18	0.44
30:0:73:U:O2'	30:0:74:G:H5'	2.18	0.44
8:H:76:LEU:HD21	8:H:149:VAL:HA	1.98	0.44
3:C:80:VAL:HA	3:C:81:PRO:HD3	1.84	0.44
30:0:1434:A:H2'	30:0:1436:C:C5	2.52	0.44
17:Q:1:PRO:HA	30:0:2299:G:O6	2.17	0.44
30:0:1163:G:C2	30:0:1184:C:N3	2.86	0.44
30:0:1191:A:H2	30:0:1206:U:H3	1.64	0.44
31:9:31:C:H2'	31:9:32:G:O4'	2.18	0.44
26:Z:44:ARG:HB2	30:0:1886:A:O2'	2.18	0.44
11:K:66:ARG:HH12	30:0:1992:U:H3'	1.82	0.44
30:0:2846:C:H4'	38:0:5080:HOH:O	2.18	0.44
16:P:120:ARG:NH1	30:0:1594:C:C5	2.86	0.44
30:0:1755:A:H2'	30:0:1756:G:O4'	2.18	0.44
30:0:758:A:H2'	30:0:759:C:O4'	2.17	0.44
30:0:1871:U:O4'	30:0:1873:G:C8	2.71	0.44
1:A:167:LYS:HB2	26:Z:53:ILE:HD13	1.99	0.44
30:0:1444:G:O2'	30:0:1502:A:N1	2.41	0.44
30:0:1805:G:O2'	30:0:1806:G:H5'	2.17	0.44
9:I:87:PRO:HD2	30:0:1180:U:O2'	2.17	0.44
30:0:241:A:N1	30:0:378:A:H4'	2.33	0.44
30:0:506:G:N2	30:0:509:A:C5'	2.66	0.44
11:K:41:LYS:HA	30:0:2582:G:O3'	2.18	0.44
30:0:1972:U:H2'	30:0:1973:A:H5'	1.99	0.44
30:0:603:A:H4'	30:0:604:G:O5'	2.17	0.44
30:0:2104:C:O2	30:0:2485:A:N1	2.51	0.44
31:9:1:U:C5'	31:9:3:A:OP1	2.65	0.44
30:0:2895:C:H2'	38:0:9570:HOH:O	2.18	0.44
2:B:51:VAL:CG1	2:B:53:LEU:HD13	2.46	0.44
30:0:2064:U:H5'	30:0:2652:U:O3'	2.18	0.44
15:O:32:ARG:HD3	15:O:32:ARG:O	2.17	0.44
29:3:11:CYS:HB2	29:3:20:HIS:CE1	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:75:GLU:OE2	2:B:151:VAL:HG13	2.18	0.44
25:Y:165:GLU:HB3	38:0:6704:HOH:O	2.17	0.44
19:S:55:GLN:NE2	30:0:1446:U:H2'	2.32	0.44
30:0:1702:U:H5'	38:0:3421:HOH:O	2.16	0.44
1:A:95:PRO:HA	1:A:153:ARG:HA	2.00	0.44
30:0:512:G:O3'	30:0:513:A:H8	2.00	0.44
30:0:1051:C:H2'	30:0:1052:G:O4'	2.18	0.44
14:N:108:SER:HA	14:N:109:PRO:HD3	1.75	0.44
30:0:574:G:O2'	30:0:575:A:H5'	2.18	0.44
30:0:1143:G:C6	30:0:1221:G:C6	3.06	0.44
4:D:62:ASP:HA	38:D:4233:HOH:O	2.18	0.44
7:G:63:ARG:NH1	30:0:1151:G:OP1	2.51	0.44
30:0:731:U:H2'	30:0:732:C:C6	2.53	0.44
8:H:57:THR:HG23	8:H:131:GLN:HA	2.00	0.44
30:0:1116:U:HO2'	30:0:1118:A:H2	0.68	0.44
30:0:2908:A:O5'	30:0:2908:A:H8	2.00	0.44
30:0:2073:G:H5''	38:0:3823:HOH:O	2.17	0.44
13:M:86:GLN:HE22	30:0:2274:A:H1'	1.83	0.44
25:Y:189:ASN:HD22	25:Y:189:ASN:C	2.21	0.44
31:9:39:U:C2'	31:9:40:C:OP1	2.66	0.44
30:0:1819:G:C2'	30:0:1820:G:H5'	2.47	0.44
20:T:23:VAL:HG23	20:T:41:ARG:HG3	1.98	0.44
30:0:2249:G:C2	30:0:2253:G:C6	3.06	0.44
30:0:2328:U:C4	30:0:2329:C:C5	3.06	0.44
9:I:101:LYS:O	9:I:105:GLU:HG3	2.18	0.44
2:B:124:ALA:O	2:B:128:ILE:HG13	2.18	0.44
30:0:494:C:H2'	30:0:496:G:OP2	2.17	0.44
30:0:2891:A:C2	30:0:2892:G:C4	3.06	0.44
30:0:596:C:H2'	30:0:597:A:C8	2.52	0.44
30:0:596:C:H2'	30:0:597:A:H8	1.83	0.44
3:C:16:VAL:HG21	38:C:8641:HOH:O	2.17	0.44
9:I:87:PRO:HB3	38:I:6825:HOH:O	2.18	0.43
30:0:1586:G:O2'	30:0:1587:U:H5'	2.18	0.43
2:B:315:VAL:HG23	2:B:316:ARG:HG2	2.00	0.43
30:0:2896:A:N3	30:0:2896:A:H2'	2.32	0.43
1:A:223:ARG:NH1	38:A:8985:HOH:O	2.50	0.43
30:0:2662:G:N3	30:0:2816:A:H2	2.16	0.43
30:0:276:C:O5'	30:0:276:C:H6	2.01	0.43
30:0:2515:C:H2'	30:0:2516:G:O4'	2.18	0.43
30:0:2544:G:H2'	30:0:2545:U:O4'	2.18	0.43
16:P:81:LYS:HG2	38:0:9538:HOH:O	2.18	0.43
16:P:105:LEU:HD21	16:P:137:LEU:HD11	1.99	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:88:G:H5'	30:0:88:G:H8	1.83	0.43
30:0:2314:G:C2'	30:0:2315:C:H5'	2.48	0.43
30:0:506:G:N2	30:0:509:A:H5'	2.23	0.43
30:0:2524:G:H5''	38:0:4731:HOH:O	2.18	0.43
30:0:482:G:O4'	30:0:511:A:C2	2.70	0.43
14:N:18:THR:HG21	38:N:8844:HOH:O	2.17	0.43
10:J:131:THR:HG22	10:J:133:GLY:H	1.82	0.43
30:0:2705:U:H2'	30:0:2706:A:H8	1.82	0.43
30:0:1504:A:H5'	38:0:4414:HOH:O	2.18	0.43
30:0:1568:G:O2'	30:0:1569:U:H5'	2.18	0.43
30:0:1797:A:H2'	30:0:1799:G:O5'	2.18	0.43
3:C:88:SER:HB3	3:C:91:PRO:HB3	2.01	0.43
10:J:135:ILE:O	10:J:139:LEU:HG	2.18	0.43
30:0:1996:U:O2'	30:0:1997:A:H5'	2.18	0.43
2:B:24:PRO:HG2	2:B:204:GLY:HA2	2.00	0.43
30:0:1163:G:N2	30:0:1184:C:N3	2.66	0.43
11:K:20:CYS:HB2	11:K:29:LEU:HG	1.99	0.43
23:W:21:LEU:O	23:W:26:ILE:HG23	2.19	0.43
30:0:960:G:H3'	30:0:960:G:N3	2.33	0.43
11:K:74:VAL:HG21	11:K:96:VAL:HG23	1.99	0.43
30:0:1167:G:H2'	30:0:1168:C:O4'	2.18	0.43
30:0:806:A:H2'	30:0:807:A:O4'	2.19	0.43
30:0:398:U:H2'	30:0:399:C:C6	2.53	0.43
30:0:875:A:H5'	30:0:876:A:N7	2.33	0.43
2:B:215:VAL:HB	38:B:9086:HOH:O	2.18	0.43
30:0:2115:U:H2'	30:0:2116:U:C6	2.53	0.43
30:0:629:A:C2	30:0:2074:A:C2	3.06	0.43
8:H:91:ARG:NH1	8:H:138:THR:OG1	2.47	0.43
13:M:123:ASP:OD1	13:M:126:GLN:HG2	2.18	0.43
30:0:2887:G:H2'	30:0:2888:U:C6	2.53	0.43
30:0:675:U:H2'	30:0:676:C:H5'	2.00	0.43
38:3:8961:HOH:O	30:0:2382:A:H5'	2.17	0.43
30:0:1538:C:O2'	30:0:1539:U:H5'	2.17	0.43
2:B:185:GLY:HA2	38:B:9099:HOH:O	2.17	0.43
20:T:52:ARG:O	30:0:317:A:OP1	2.35	0.43
23:W:115:THR:HG23	38:W:5420:HOH:O	2.19	0.43
30:0:2653:A:H2'	30:0:2654:C:C6	2.54	0.43
15:O:105:ASN:HD21	15:O:109:SER:N	2.16	0.43
30:0:2067:A:H2'	30:0:2068:G:O4'	2.18	0.43
30:0:1079:A:H4'	30:0:2078:U:H5'	2.00	0.43
19:S:49:VAL:HG13	19:S:66:VAL:HG13	2.00	0.43
8:H:46:TYR:HA	8:H:47:PRO:HD3	1.81	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:368:C:H2'	30:0:369:G:H5'	2.00	0.43
30:0:1890:U:H1'	38:0:5957:HOH:O	2.18	0.43
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.83	0.43
30:0:255:A:C5	30:0:256:C:C5	3.06	0.43
30:0:2265:U:H2'	30:0:2266:A:C8	2.53	0.43
30:0:1333:U:H2'	30:0:1334:C:H6	1.83	0.43
5:E:126:ILE:HB	5:E:131:LEU:CD2	2.48	0.43
30:0:699:C:C6	30:0:744:G:O4'	2.71	0.43
30:0:2543:G:O3'	30:0:2590:U:H5'	2.19	0.43
30:0:1127:C:C5	30:0:1128:U:C4	3.06	0.43
28:2:5:LYS:O	28:2:9:LYS:HG3	2.18	0.43
30:0:445:U:H2'	30:0:446:G:H8	1.84	0.43
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.19	0.43
6:F:77:VAL:HG21	6:F:83:LEU:HD13	1.99	0.43
26:Z:55:SER:O	26:Z:59:GLU:HG3	2.17	0.43
30:0:2072:G:N2	38:0:6868:HOH:O	2.51	0.43
14:N:38:LYS:HD2	14:N:114:LYS:HE3	2.01	0.43
4:D:41:LEU:HA	4:D:44:ILE:HG22	2.00	0.43
30:0:1425:G:C2'	30:0:1426:C:H5'	2.48	0.43
30:0:2403:C:H2'	30:0:2404:G:O5'	2.18	0.43
30:0:821:U:H2'	30:0:822:C:C6	2.50	0.43
21:U:6:CYS:HA	21:U:13:ILE:HD11	2.01	0.43
23:W:117:ARG:HD3	30:0:1287:A:O4'	2.19	0.43
30:0:1850:U:O4'	30:0:1941:A:C2	2.71	0.43
16:P:134:VAL:O	16:P:137:LEU:HB3	2.19	0.43
12:L:125:PHE:CE1	12:L:140:VAL:HG13	2.54	0.43
30:0:565:A:C6	30:0:566:A:C6	3.07	0.43
30:0:426:G:H2'	30:0:427:C:O4'	2.18	0.43
31:9:98:C:O2'	31:9:99:U:H5'	2.19	0.43
30:0:1250:C:O2'	30:0:1251:C:H5'	2.18	0.43
6:F:91:VAL:CG1	6:F:92:GLY:N	2.81	0.43
12:L:6:ARG:NH1	30:0:1299:G:N7	2.66	0.43
30:0:1819:G:O2'	30:0:1820:G:H5'	2.18	0.43
30:0:1773:G:N2	30:0:1774:G:C8	2.86	0.43
30:0:807:A:H2'	30:0:808:A:O4'	2.19	0.43
2:B:5:ARG:NH1	30:0:2547:C:OP2	2.52	0.43
25:Y:107:PRO:HB3	25:Y:182:PHE:CD2	2.53	0.43
30:0:1427:A:H61	30:0:1440:U:H1'	1.82	0.43
1:A:123:GLY:HA3	1:A:162:GLY:HA2	1.99	0.43
23:W:130:HIS:O	23:W:136:GLY:HA3	2.18	0.43
30:0:170:U:H2'	30:0:171:C:H5'	1.98	0.43
30:0:1474:C:C5'	30:0:1474:C:C6	2.90	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1634:G:H2'	30:0:1635:U:C6	2.53	0.43
24:X:76:ARG:NH1	24:X:76:ARG:HG3	2.31	0.43
31:9:105:A:H2'	31:9:106:U:O4'	2.18	0.43
30:0:2256:G:C2'	30:0:2257:G:C5'	2.97	0.43
26:Z:43:GLY:HA2	30:0:1771:U:O2	2.19	0.43
30:0:163:U:O3'	30:0:896:C:H4'	2.19	0.43
30:0:2543:G:H2'	30:0:2544:G:O4'	2.18	0.43
30:0:684:G:H2'	30:0:685:C:C6	2.54	0.43
23:W:107:LEU:O	23:W:112:LEU:HB2	2.18	0.43
31:9:54:A:C2	31:9:55:U:N3	2.87	0.43
30:0:2661:U:H3	30:0:2812:A:H62	1.65	0.43
30:0:1167:G:C2	30:0:1168:C:C2	3.07	0.43
30:0:1463:U:H2'	30:0:1464:C:H6	1.83	0.43
30:0:111:C:O2'	30:0:112:G:H5'	2.19	0.43
5:E:11:VAL:HG12	5:E:12:ASP:N	2.34	0.43
5:E:19:ASP:HA	5:E:31:ARG:O	2.19	0.43
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.54	0.43
22:V:29:ASN:O	22:V:33:VAL:HG23	2.18	0.43
30:0:544:G:C3'	30:0:545:G:H5''	2.48	0.43
1:A:101:GLU:HG2	38:A:9034:HOH:O	2.18	0.43
11:K:87:ARG:NH1	38:K:4066:HOH:O	2.47	0.43
22:V:56:ILE:O	22:V:60:GLN:HG3	2.19	0.43
25:Y:189:ASN:ND2	25:Y:192:ASP:N	2.66	0.43
30:0:111:C:C2'	30:0:112:G:H5'	2.49	0.43
24:X:71:ARG:HD2	38:X:7542:HOH:O	2.18	0.43
12:L:33:ALA:HB2	30:0:165:A:H5''	1.99	0.43
30:0:1023:C:O2'	30:0:1024:G:H5'	2.19	0.43
30:0:1517:C:O2	30:0:1670:A:C2	2.72	0.43
30:0:1682:A:H5''	38:0:9456:HOH:O	2.19	0.43
30:0:2079:G:H2'	30:0:2080:G:O4'	2.19	0.43
30:0:2540:G:H5''	38:0:4662:HOH:O	2.19	0.43
30:0:2757:A:H2'	30:0:2758:G:O4'	2.18	0.43
14:N:37:ARG:HH11	31:9:6:C:H5''	1.71	0.42
30:0:2102:G:C2'	38:0:7763:HOH:O	2.59	0.42
10:J:107:ASN:ND2	10:J:109:TYR:H	2.16	0.42
30:0:920:C:H4'	30:0:921:G:N2	2.34	0.42
27:1:28:HIS:HD2	27:1:30:LYS:H	1.65	0.42
30:0:699:C:C2	30:0:744:G:C2	3.06	0.42
7:G:19:GLU:O	7:G:23:ILE:HG13	2.19	0.42
30:0:702:G:C2	30:0:703:G:C8	3.07	0.42
30:0:1503:U:H2'	30:0:1504:A:O4'	2.19	0.42
26:Z:66:CYS:SG	26:Z:67:GLY:N	2.92	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:2692:G:HO2'	30:0:2693:U:P	2.41	0.42
30:0:1576:G:H2'	30:0:1577:U:O4'	2.19	0.42
30:0:2610:U:H3'	38:0:7521:HOH:O	2.18	0.42
30:0:2668:G:H2'	30:0:2669:U:C6	2.54	0.42
30:0:1461:U:H2'	30:0:1462:C:C6	2.54	0.42
30:0:1166:A:H1'	30:0:1192:A:C2	2.55	0.42
30:0:1181:A:C2	30:0:1192:A:C8	3.06	0.42
23:W:4:LEU:HD13	23:W:52:VAL:HG21	2.01	0.42
18:R:106:GLY:HA2	18:R:109:MET:HE3	2.00	0.42
30:0:2635:A:C2'	30:0:2636:C:H5'	2.49	0.42
29:3:48:ASN:ND2	29:3:50:GLY:H	2.17	0.42
1:A:190:ARG:HD2	30:0:1884:G:O6	2.18	0.42
30:0:512:G:H5''	30:0:515:C:H1'	2.00	0.42
30:0:2054:A:H5'	38:0:4901:HOH:O	2.18	0.42
30:0:705:C:C2'	30:0:705:C:O2	2.67	0.42
30:0:946:C:H2'	30:0:947:U:H6	1.83	0.42
11:K:34:VAL:CG2	11:K:47:ALA:HB2	2.49	0.42
30:0:62:C:C4	30:0:63:U:C4	3.07	0.42
30:0:682:A:H2'	30:0:683:G:O4'	2.18	0.42
30:0:142:G:O2'	30:0:143:C:H5'	2.18	0.42
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.52	0.42
14:N:164:ASP:OD1	14:N:167:ASP:HA	2.19	0.42
30:0:343:C:O2'	30:0:344:C:H5'	2.19	0.42
12:L:61:ALA:HB2	12:L:105:TYR:CZ	2.54	0.42
1:A:4:ILE:HG22	1:A:198:ASP:O	2.19	0.42
30:0:2646:G:C5	30:0:2647:C:C5	3.07	0.42
24:X:72:VAL:HG22	24:X:85:VAL:HG12	2.01	0.42
3:C:46:TYR:CE2	3:C:98:ARG:NH1	2.87	0.42
17:Q:18:PRO:O	17:Q:21:ARG:HB2	2.19	0.42
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.83	0.42
30:0:729:C:C2	30:0:743:G:C2	3.07	0.42
23:W:65:VAL:HA	23:W:68:THR:HG22	2.00	0.42
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.34	0.42
5:E:21:THR:HG23	5:E:30:THR:OG1	2.18	0.42
30:0:2809:G:H2'	30:0:2810:G:O4'	2.20	0.42
31:9:108:C:H2'	31:9:109:G:C8	2.53	0.42
30:0:2657:G:O2'	30:0:2842:G:N7	2.47	0.42
31:9:95:C:O2'	31:9:96:C:H5'	2.20	0.42
3:C:140:VAL:HG12	3:C:141:SER:N	2.34	0.42
23:W:88:THR:CG2	23:W:90:TYR:HD1	2.31	0.42
13:M:93:ARG:HD2	30:0:1470:A:OP1	2.19	0.42
30:0:1298:U:H2'	30:0:1299:G:C8	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:39:VAL:CG2	10:J:107:ASN:HA	2.49	0.42
2:B:53:LEU:HD21	2:B:270:ILE:HD12	2.00	0.42
30:0:1947:G:H2'	30:0:1948:G:H8	1.84	0.42
8:H:123:ILE:HD12	8:H:123:ILE:N	2.34	0.42
24:X:43:VAL:HG12	24:X:44:ASP:H	1.83	0.42
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.33	0.42
25:Y:154:ARG:NH2	30:0:1072:G:OP2	2.53	0.42
30:0:622:G:O2'	30:0:623:U:H5'	2.20	0.42
18:R:17:MET:HE3	18:R:19:ARG:NH2	2.34	0.42
25:Y:152:LYS:CB	25:Y:160:LYS:HG3	2.49	0.42
8:H:141:CYS:HB2	38:H:197:HOH:O	2.20	0.42
30:0:349:U:O2'	30:0:350:G:H5'	2.19	0.42
30:0:51:G:O2'	30:0:52:A:H5'	2.20	0.42
14:N:42:HIS:CG	14:N:62:HIS:HE1	2.37	0.42
30:0:48:A:N1	30:0:148:A:O2'	2.43	0.42
14:N:71:TRP:HB2	38:N:8836:HOH:O	2.19	0.42
18:R:18:LEU:HD12	18:R:143:VAL:HG11	2.01	0.42
12:L:53:ARG:NH2	12:L:57:VAL:HG12	2.34	0.42
4:D:135:VAL:HG22	4:D:136:ARG:N	2.34	0.42
30:0:2316:G:H4'	38:0:6092:HOH:O	2.19	0.42
1:A:186:TRP:CD1	1:A:187:PRO:HA	2.55	0.42
30:0:2626:C:H2'	30:0:2627:G:H8	1.84	0.42
25:Y:130:ARG:HB2	25:Y:142:SER:O	2.18	0.42
30:0:1706:G:C6	30:0:1707:G:C6	3.08	0.42
6:F:99:THR:HG23	6:F:99:THR:O	2.19	0.42
30:0:2237:G:H1'	38:0:4856:HOH:O	2.18	0.42
30:0:2429:A:H4'	38:0:7729:HOH:O	2.19	0.42
2:B:84:LEU:HD23	2:B:142:LEU:HD23	2.02	0.42
30:0:1416:G:C2'	30:0:1417:G:H5'	2.50	0.42
3:C:35:VAL:HG21	3:C:227:GLY:HA2	2.01	0.42
30:0:1616:A:H5''	30:0:1617:C:OP1	2.19	0.42
13:M:49:ALA:C	13:M:54:TYR:HB3	2.39	0.42
30:0:39:G:N2	30:0:444:C:C2	2.88	0.42
9:I:118:ASN:HB3	30:0:1185:U:H5''	2.01	0.42
30:0:1973:A:H2'	30:0:1974:G:O4'	2.19	0.42
30:0:567:U:O5'	30:0:567:U:H6	2.03	0.42
1:A:36:ASP:HA	1:A:83:GLY:HA3	2.01	0.42
30:0:2002:C:C2'	30:0:2003:U:H5'	2.49	0.42
30:0:2004:U:H6	30:0:2004:U:P	2.43	0.42
30:0:664:U:O4	30:0:681:G:H5''	2.20	0.42
30:0:2709:G:N2	38:0:7616:HOH:O	2.51	0.42
30:0:2883:A:H2'	30:0:2884:G:O4'	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1850:U:H2'	30:0:1851:G:C8	2.55	0.42
30:0:2751:C:H2'	30:0:2752:C:H6	1.84	0.42
30:0:360:A:H2'	30:0:361:C:O4'	2.19	0.42
30:0:1098:A:H2'	30:0:1099:G:O4'	2.19	0.42
30:0:851:C:O2	30:0:2022:A:H2	2.03	0.42
2:B:60:SER:HA	2:B:61:PRO:HD3	1.87	0.42
30:0:2645:U:O2'	30:0:2646:G:P	2.78	0.42
30:0:1942:A:H2'	30:0:1943:C:C6	2.55	0.42
30:0:236:A:H4'	30:0:237:G:OP1	2.19	0.42
1:A:88:ILE:HG22	1:A:88:ILE:O	2.20	0.42
30:0:128:A:H3'	30:0:128:A:C8	2.54	0.42
30:0:130:C:H5'	38:0:5216:HOH:O	2.19	0.42
30:0:187:A:H3'	30:0:188:C:C6	2.55	0.42
30:0:1058:A:H2'	30:0:1060:C:C5'	2.50	0.42
10:J:22:VAL:O	10:J:26:VAL:HG23	2.20	0.42
2:B:102:THR:HG23	2:B:182:VAL:HG12	2.02	0.42
2:B:258:GLY:HA2	38:0:4005:HOH:O	2.20	0.42
2:B:18:ARG:HG3	2:B:256:GLN:HG3	2.02	0.42
5:E:7:ILE:HG22	5:E:45:ASP:O	2.19	0.42
28:2:2:LYS:HG3	30:0:1486:A:C5	2.54	0.42
30:0:1139:U:H2'	30:0:1140:C:C6	2.54	0.42
30:0:417:G:P	38:0:7414:HOH:O	2.77	0.42
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.20	0.42
13:M:42:ARG:HA	13:M:43:PRO:HD3	1.87	0.42
18:R:84:ALA:O	18:R:88:PHE:HD1	2.02	0.42
30:0:2761:A:C4	30:0:2763:G:C8	3.07	0.42
30:0:1917:G:C6	30:0:1918:U:C4	3.07	0.42
30:0:1191:A:N3	30:0:1207:A:C2	2.87	0.42
3:C:236:THR:HG21	38:C:8579:HOH:O	2.20	0.42
5:E:60:SER:OG	30:0:2784:A:H1'	2.20	0.42
31:9:31:C:C2	31:9:50:G:N2	2.88	0.42
30:0:309:C:O2	30:0:309:C:H2'	2.19	0.42
20:T:24:ARG:HH21	20:T:39:ASN:ND2	2.16	0.42
30:0:1214:G:H4'	38:0:4747:HOH:O	2.19	0.42
30:0:1060:C:H6	30:0:1060:C:H5'	1.85	0.42
25:Y:138:ARG:HD3	30:0:638:C:OP2	2.20	0.42
5:E:11:VAL:HG13	5:E:23:GLU:O	2.19	0.42
23:W:44:MET:CE	30:0:944:G:H21	2.33	0.42
3:C:242:GLU:HB2	38:C:8587:HOH:O	2.19	0.42
30:0:1907:U:O2'	30:0:1908:G:H5'	2.20	0.42
15:O:29:VAL:HG11	15:O:98:LEU:HD21	2.01	0.42
27:1:10:LYS:HG3	38:1:8981:HOH:O	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:377:C:H5	38:0:3302:HOH:O	2.01	0.42
30:0:1159:G:H1	30:0:1208:C:H42	1.68	0.42
30:0:241:A:C2	30:0:378:A:H4'	2.54	0.42
30:0:1789:G:C2'	30:0:1790:C:O5'	2.68	0.42
1:A:103:VAL:HA	1:A:104:PRO:HD3	1.86	0.42
30:0:1008:C:O2'	30:0:1009:U:H5'	2.20	0.42
30:0:999:C:C2'	30:0:1000:C:H5'	2.49	0.42
30:0:1903:U:O2'	30:0:1904:A:C8	2.68	0.42
3:C:95:GLU:CD	3:C:95:GLU:H	2.23	0.42
30:0:1520:G:C6	30:0:1521:C:C4	3.07	0.42
13:M:80:GLY:O	13:M:81:ARG:HD3	2.20	0.42
30:0:569:A:H5''	30:0:587:A:N1	2.35	0.42
8:H:139:ALA:HB3	8:H:149:VAL:HG21	2.02	0.42
13:M:122:GLN:HB2	13:M:126:GLN:O	2.20	0.42
31:9:73:A:N1	31:9:108:C:O2	2.53	0.42
14:N:82:TYR:CD2	14:N:82:TYR:C	2.93	0.42
13:M:15:PRO:HA	13:M:20:LEU:HD23	2.02	0.42
15:O:39:THR:O	15:O:115:ARG:NH2	2.53	0.42
4:D:167:GLU:C	4:D:169:THR:H	2.23	0.42
30:0:365:G:C6	30:0:366:U:C4	3.08	0.42
22:V:1:THR:CG2	22:V:2:VAL:H	2.25	0.42
30:0:1130:U:H2'	30:0:1131:G:C4'	2.50	0.42
13:M:158:ARG:HB2	13:M:163:LEU:HB2	2.02	0.42
10:J:74:ARG:NH1	10:J:76:ASP:HB2	2.35	0.42
30:0:699:C:C6	30:0:744:G:C4	3.08	0.42
3:C:206:ASN:HB2	30:0:329:A:OP2	2.20	0.42
30:0:2739:A:C6	30:0:2740:G:C5	3.08	0.42
5:E:7:ILE:HA	5:E:8:PRO:HD3	1.95	0.42
30:0:2553:A:H2'	30:0:2553:A:N3	2.35	0.42
25:Y:141:THR:HG23	38:Y:9073:HOH:O	2.19	0.42
23:W:29:VAL:O	23:W:30:ASN:HB2	2.19	0.42
30:0:1494:A:C4	30:0:1495:C:C5	3.08	0.42
14:N:171:HIS:CE1	38:N:8861:HOH:O	2.71	0.42
18:R:69:LYS:HB2	18:R:72:VAL:HG23	2.02	0.42
30:0:1373:G:H4'	38:0:5286:HOH:O	2.20	0.42
30:0:1183:C:N3	30:0:1184:C:C4	2.88	0.41
30:0:1207:A:N6	38:0:5631:HOH:O	2.53	0.41
30:0:2541:U:H5''	38:0:5398:HOH:O	2.20	0.41
30:0:1878:G:O2'	30:0:1879:U:H6	2.03	0.41
30:0:116:G:H1'	30:0:129:A:N3	2.35	0.41
30:0:2256:G:H2'	30:0:2257:G:O5'	2.19	0.41
30:0:2425:A:H5'	30:0:2426:G:OP2	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1771:U:O2'	30:0:1773:G:N7	2.52	0.41
20:T:41:ARG:NH1	20:T:41:ARG:HG2	2.34	0.41
30:0:941:G:C6	30:0:942:U:C4	3.08	0.41
30:0:2616:A:C4'	30:0:2617:G:OP1	2.67	0.41
30:0:2587:OMU:H6	30:0:2587:OMU:O5'	2.19	0.41
30:0:1926:G:H2'	30:0:1927:A:C8	2.55	0.41
30:0:939:A:C2	30:0:1027:G:N3	2.88	0.41
24:X:30:MET:HE1	24:X:58:ALA:HB3	2.02	0.41
30:0:424:C:H2'	30:0:425:U:H6	1.85	0.41
2:B:24:PRO:CG	2:B:204:GLY:HA2	2.49	0.41
6:F:83:LEU:HA	6:F:83:LEU:HD12	1.91	0.41
30:0:1416:G:H2'	30:0:1417:G:H5'	2.01	0.41
30:0:1574:C:H6	30:0:1574:C:O5'	2.03	0.41
2:B:14:GLY:HA2	2:B:15:PRO:C	2.39	0.41
30:0:1375:A:C2'	30:0:1376:G:H5'	2.50	0.41
30:0:45:A:N6	30:0:147:G:C4	2.88	0.41
30:0:1202:A:H2'	30:0:1203:G:O4'	2.20	0.41
30:0:2509:A:OP2	30:0:2510:C:C5	2.73	0.41
30:0:2591:C:H2'	30:0:2592:G:O4'	2.20	0.41
31:9:2:U:C1'	38:9:9099:HOH:O	2.67	0.41
31:9:2:U:H1'	38:9:9099:HOH:O	2.19	0.41
11:K:109:LEU:CD1	11:K:113:ILE:HD11	2.50	0.41
30:0:1001:U:O2'	30:0:1002:G:H5'	2.20	0.41
27:1:28:HIS:CE1	27:1:31:LYS:HE2	2.56	0.41
30:0:803:C:O2'	30:0:804:C:H5'	2.21	0.41
30:0:2611:G:H5'	30:0:2613:G:C8	2.55	0.41
8:H:102:LYS:HD3	8:H:122:LYS:HD3	2.02	0.41
30:0:131:A:OP2	30:0:141:C:H5	2.03	0.41
30:0:2866:U:H4'	30:0:2867:G:H5'	2.01	0.41
30:0:1191:A:H2'	30:0:1193:A:H5'	2.02	0.41
23:W:125:HIS:CD2	23:W:127:GLY:H	2.38	0.41
1:A:212:PRO:HA	30:0:1943:C:O4'	2.19	0.41
25:Y:189:ASN:HD22	25:Y:192:ASP:H	1.67	0.41
14:N:25:ARG:HG2	30:0:2416:G:O2'	2.20	0.41
4:D:58:VAL:HG12	4:D:60:GLU:HG2	2.01	0.41
2:B:102:THR:CG2	2:B:182:VAL:HG12	2.50	0.41
2:B:62:ARG:HA	2:B:65:MET:HE3	2.02	0.41
30:0:2361:A:H2'	30:0:2362:A:O4'	2.20	0.41
30:0:862:U:H2'	30:0:863:G:C8	2.55	0.41
30:0:2438:G:H2'	30:0:2439:C:C6	2.55	0.41
24:X:73:ARG:HH12	24:X:88:GLU:HB2	1.85	0.41
23:W:73:LEU:HA	23:W:73:LEU:HD12	1.77	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1391:G:H2'	30:0:1392:A:H5'	2.02	0.41
30:0:1946:C:H2'	30:0:1971:G:C8	2.55	0.41
30:0:2729:C:O2'	30:0:2730:G:H5'	2.19	0.41
30:0:1940:C:H1'	38:0:9375:HOH:O	2.20	0.41
3:C:240:LEU:HB2	38:C:8659:HOH:O	2.20	0.41
20:T:26:THR:HG23	20:T:97:ARG:HG3	2.02	0.41
10:J:75:PRO:HD3	10:J:136:SER:OG	2.20	0.41
22:V:44:GLY:O	22:V:48:GLU:HG2	2.21	0.41
30:0:2880:A:C2'	30:0:2881:C:H5'	2.50	0.41
15:O:38:ARG:HD3	30:0:654:A:OP2	2.20	0.41
17:Q:7:LEU:HD12	30:0:2424:U:C1'	2.50	0.41
14:N:4:PRO:HB2	30:0:1010:C:H4'	2.02	0.41
30:0:1398:G:H2'	30:0:1399:A:C8	2.55	0.41
30:0:1576:G:H2'	30:0:1577:U:C6	2.55	0.41
30:0:1613:C:H2'	30:0:1614:G:O4'	2.20	0.41
29:3:69:TYR:HB2	29:3:78:HIS:CE1	2.55	0.41
30:0:23:G:H1'	30:0:520:A:N6	2.36	0.41
21:U:23:HIS:NE2	21:U:29:THR:OG1	2.41	0.41
14:N:147:ILE:HD12	38:9:9087:HOH:O	2.20	0.41
31:9:2:U:OP2	31:9:2:U:H4'	2.21	0.41
30:0:370:G:N2	30:0:371:U:C2	2.89	0.41
1:A:187:PRO:HB2	30:0:1845:A:O3'	2.20	0.41
18:R:39:THR:HB	18:R:42:GLU:HG3	2.02	0.41
23:W:38:THR:HG22	23:W:39:ASP:H	1.86	0.41
30:0:1327:G:C6	30:0:1331:G:C6	3.09	0.41
30:0:946:C:H2'	30:0:947:U:C6	2.54	0.41
30:0:2737:C:H2'	38:0:6141:HOH:O	2.21	0.41
1:A:214:SER:HA	1:A:227:ASP:O	2.21	0.41
6:F:72:VAL:HA	6:F:73:PRO:HD3	1.86	0.41
30:0:2506:A:H62	30:0:2511:A:HO2'	1.66	0.41
29:3:38:ARG:HD2	30:0:396:U:OP2	2.20	0.41
1:A:48:ASP:HA	1:A:49:PRO:HD3	1.92	0.41
6:F:32:GLY:N	38:F:3111:HOH:O	2.53	0.41
13:M:24:GLN:HA	13:M:24:GLN:NE2	2.35	0.41
19:S:57:THR:C	19:S:59:ASP:H	2.24	0.41
25:Y:145:LYS:O	25:Y:147:ARG:HG2	2.20	0.41
8:H:92:LYS:HG3	8:H:130:VAL:HG22	2.02	0.41
30:0:1311:G:C2	30:0:1312:G:C8	3.08	0.41
30:0:1471:A:H2'	30:0:1472:C:C6	2.55	0.41
30:0:659:A:H5''	38:0:7096:HOH:O	2.19	0.41
30:0:334:G:H2'	30:0:335:U:O4'	2.20	0.41
4:D:88:LEU:HB2	4:D:89:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1259:A:N1	30:0:1261:A:H1'	2.35	0.41
30:0:2088:C:H1'	30:0:2841:A:N1	2.36	0.41
18:R:80:TYR:O	30:0:2050:G:H5''	2.20	0.41
38:D:7597:HOH:O	31:9:56:A:H2	2.04	0.41
10:J:52:GLN:NE2	30:0:1119:G:H8	2.18	0.41
30:0:2526:C:H3'	30:0:2526:C:H6	1.85	0.41
30:0:2102:G:N2	30:0:2104:C:C6	2.89	0.41
30:0:2480:G:O2'	30:0:2481:G:H5'	2.21	0.41
24:X:43:VAL:HG12	24:X:47:ALA:HB3	2.01	0.41
25:Y:151:SER:HB3	25:Y:154:ARG:CB	2.50	0.41
30:0:517:U:C2'	30:0:518:G:H5'	2.50	0.41
2:B:174:ARG:HA	2:B:177:HIS:HB3	2.03	0.41
29:3:69:TYR:CZ	29:3:80:ARG:HD2	2.55	0.41
8:H:157:TYR:C	8:H:157:TYR:CD1	2.94	0.41
18:R:114:VAL:HG13	18:R:114:VAL:O	2.21	0.41
20:T:77:VAL:HG11	20:T:91:LEU:HD11	2.03	0.41
1:A:20:SER:HB3	30:0:1872:C:H5	1.85	0.41
30:0:99:A:C8	30:0:100:C:C5	3.08	0.41
30:0:2083:A:H3'	38:0:7573:HOH:O	2.20	0.41
17:Q:66:LYS:HB2	17:Q:70:ALA:O	2.20	0.41
30:0:1982:C:H2'	30:0:1983:C:O4'	2.20	0.41
6:F:1:PRO:H3	6:F:4:VAL:HG23	1.86	0.41
11:K:78:LYS:HA	11:K:79:PRO:HD3	1.94	0.41
30:0:1076:G:C2	30:0:1084:C:C2	3.08	0.41
16:P:18:LYS:O	16:P:21:VAL:HG13	2.20	0.41
30:0:2764:C:H2'	30:0:2765:C:H6	1.84	0.41
29:3:91:GLN:O	29:3:92:GLU:HB2	2.20	0.41
30:0:1896:G:C6	30:0:1897:U:C4	3.09	0.41
31:9:1:U:O3'	31:9:3:A:OP1	2.39	0.41
6:F:50:VAL:CG2	6:F:63:ILE:HG21	2.51	0.41
2:B:97:LEU:O	2:B:98:THR:HG23	2.21	0.41
2:B:53:LEU:HD11	2:B:327:VAL:HG22	2.02	0.41
30:0:10:U:O4	30:0:532:A:H8	2.04	0.41
30:0:1626:A:C2'	30:0:1627:G:H5'	2.51	0.41
30:0:79:G:N2	30:0:97:G:H1'	2.36	0.41
30:0:2607:U:H4'	38:0:9440:HOH:O	2.21	0.41
18:R:1:GLY:HA2	18:R:119:VAL:HG21	2.02	0.41
15:O:14:LEU:CD2	15:O:102:ILE:HD11	2.51	0.41
30:0:626:U:C4	30:0:627:G:C6	3.08	0.41
30:0:278:A:C6	30:0:279:C:C4	3.09	0.41
23:W:80:ASP:HB2	38:W:3312:HOH:O	2.21	0.41
30:0:1632:A:C3'	30:0:1633:C:H5'	2.51	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:812:A:H2'	30:0:813:C:C6	2.55	0.41
30:0:812:A:H2'	30:0:813:C:O4'	2.21	0.41
14:N:38:LYS:HB2	14:N:38:LYS:HE3	1.81	0.41
16:P:59:ARG:HH22	16:P:66:GLN:HE22	1.69	0.41
27:1:28:HIS:O	27:1:32:LYS:N	2.47	0.41
30:0:393:G:C6	30:0:394:G:C6	3.09	0.41
30:0:1406:A:H4'	30:0:1407:A:C5'	2.51	0.41
30:0:196:G:H1'	30:0:198:A:N7	2.35	0.41
4:D:88:LEU:N	4:D:89:PRO:CD	2.83	0.41
15:O:14:LEU:HD23	15:O:102:ILE:HD11	2.03	0.41
5:E:166:VAL:HG12	38:E:3134:HOH:O	2.21	0.41
30:0:1783:A:O2'	30:0:1784:U:H5'	2.21	0.41
2:B:10:SER:HB2	30:0:2714:U:H4'	2.02	0.41
30:0:1552:G:H2'	30:0:1553:C:C6	2.56	0.41
30:0:1275:C:N3	30:0:1281:C:N4	2.69	0.41
30:0:287:C:H2'	30:0:288:A:C8	2.56	0.41
30:0:1964:U:O2	30:0:1964:U:H2'	2.21	0.41
30:0:1445:G:N2	30:0:1678:A:H1'	2.36	0.41
30:0:1074:G:H4'	30:0:1260:G:C6	2.56	0.41
30:0:1184:C:O2'	30:0:1185:U:OP2	2.34	0.41
30:0:1587:U:H2'	30:0:1588:G:O4'	2.21	0.41
30:0:1641:A:H2'	30:0:1642:A:C5'	2.45	0.41
2:B:85:ARG:NH1	30:0:2671:U:O2	2.54	0.41
10:J:105:LEU:HD23	38:J:5907:HOH:O	2.21	0.41
31:9:58:G:N7	31:9:59:C:C4	2.89	0.41
17:Q:50:GLY:HA2	38:0:6025:HOH:O	2.20	0.41
1:A:204:GLY:N	30:0:2634:G:OP2	2.53	0.41
2:B:211:THR:HG21	38:0:7451:HOH:O	2.21	0.41
5:E:49:ILE:HD11	5:E:69:ILE:HD12	2.03	0.41
30:0:1712:A:H2'	30:0:1713:G:O4'	2.20	0.41
30:0:74:G:O2'	30:0:75:U:H5'	2.20	0.41
30:0:2842:G:H2'	30:0:2843:A:H5'	2.02	0.41
18:R:79:ARG:HB3	30:0:2050:G:OP1	2.21	0.41
30:0:1084:C:H6	30:0:1084:C:O5'	2.04	0.41
2:B:57:GLU:HA	2:B:58:PRO:HD2	1.91	0.41
30:0:1930:A:H2'	30:0:1931:A:C8	2.55	0.41
30:0:1743:G:H1'	38:0:4892:HOH:O	2.20	0.41
8:H:100:GLU:HB3	8:H:124:VAL:HG11	2.02	0.41
30:0:594:C:C4	30:0:595:U:C4	3.09	0.41
30:0:2804:C:H2'	30:0:2805:A:O4'	2.21	0.41
14:N:13:ARG:NH1	30:0:2368:A:C6	2.89	0.41
30:0:2277:U:O2'	30:0:2278:U:H5'	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:1363:G:H2'	30:0:1364:G:C8	2.56	0.41
21:U:33:SER:O	21:U:37:GLU:HG3	2.21	0.41
30:0:2072:G:O2'	30:0:2489:G:N2	2.53	0.40
12:L:129:ALA:O	12:L:133:VAL:HG23	2.21	0.40
29:3:38:ARG:HH11	30:0:396:U:P	2.43	0.40
4:D:25:MET:HE2	4:D:41:LEU:CG	2.50	0.40
1:A:190:ARG:NH1	30:0:1845:A:OP2	2.54	0.40
30:0:2617:G:C2	30:0:2618:G:C8	3.09	0.40
30:0:11:A:H5'	30:0:12:U:OP2	2.20	0.40
3:C:214:THR:HG21	38:C:8608:HOH:O	2.20	0.40
12:L:121:ILE:HG12	12:L:141:GLU:HB2	2.04	0.40
30:0:228:C:C2'	30:0:229:G:H5'	2.51	0.40
30:0:1760:G:C2	30:0:1813:U:O4'	2.74	0.40
30:0:1041:U:H4'	30:0:1295:G:H5'	2.03	0.40
30:0:1917:G:C5	30:0:1918:U:C4	3.09	0.40
22:V:5:VAL:HG23	38:V:2271:HOH:O	2.20	0.40
29:3:79:LEU:HD13	30:0:2457:U:H1'	2.04	0.40
4:D:18:ILE:HD13	4:D:84:LEU:HD12	2.03	0.40
18:R:82:GLU:HG3	18:R:83:LYS:N	2.35	0.40
22:V:27:LEU:HA	22:V:49:LEU:HD13	2.02	0.40
30:0:2712:G:H5'	38:0:5223:HOH:O	2.20	0.40
30:0:2712:G:P	38:0:5223:HOH:O	2.80	0.40
30:0:2820:A:H2'	30:0:2821:C:C6	2.55	0.40
30:0:1819:G:C2'	30:0:1820:G:C5'	2.99	0.40
2:B:310:ARG:HD2	38:B:9115:HOH:O	2.21	0.40
30:0:1014:A:H5''	31:9:101:G:O2'	2.21	0.40
30:0:42:C:H3'	38:0:4165:HOH:O	2.21	0.40
30:0:17:G:O2'	30:0:18:C:H5'	2.20	0.40
30:0:844:A:C6	30:0:882:A:C5	3.08	0.40
30:0:1215:A:O3'	30:0:1216:G:C4'	2.69	0.40
30:0:79:G:H22	30:0:97:G:H1'	1.86	0.40
2:B:75:GLU:C	2:B:77:PRO:HD3	2.42	0.40
14:N:23:ARG:HH11	14:N:23:ARG:HG2	1.87	0.40
30:0:2791:U:H1'	30:0:2792:A:H5''	2.03	0.40
16:P:14:LEU:HD13	16:P:51:ALA:HB2	2.03	0.40
1:A:173:GLY:O	1:A:176:HIS:HB3	2.21	0.40
2:B:30:PRO:HB2	2:B:39:GLN:NE2	2.36	0.40
30:0:1183:C:O2	30:0:1183:C:C2'	2.70	0.40
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.43	0.40
30:0:2004:U:H2'	30:0:2005:G:OP1	2.22	0.40
30:0:2819:C:H2'	30:0:2820:A:C8	2.55	0.40
30:0:2252:A:H2'	30:0:2253:G:H5'	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:7:ARG:CG	2:B:7:ARG:HH11	2.35	0.40
14:N:93:GLN:NE2	14:N:93:GLN:HA	2.35	0.40
30:0:1624:A:H5'	30:0:1626:A:O4'	2.20	0.40
30:0:517:U:H2'	30:0:518:G:H5'	2.03	0.40
30:0:47:G:N3	30:0:114:A:C2	2.90	0.40
30:0:1102:C:H5	38:0:3487:HOH:O	2.04	0.40
30:0:2039:A:H4'	30:0:2760:C:O2'	2.22	0.40
30:0:2897:C:H2'	30:0:2898:G:H8	1.85	0.40
3:C:135:GLU:HB3	38:C:8582:HOH:O	2.20	0.40
30:0:2550:U:O2'	30:0:2551:C:H5'	2.20	0.40
13:M:118:TYR:CZ	13:M:130:GLU:HB2	2.56	0.40
23:W:88:THR:HG22	23:W:89:ASP:N	2.34	0.40
1:A:132:ASP:HB3	1:A:135:VAL:H	1.87	0.40
30:0:129:A:H4'	30:0:130:C:OP1	2.21	0.40
31:9:59:C:H2'	31:9:60:C:C6	2.56	0.40
30:0:694:A:H4'	30:0:2441:U:OP1	2.21	0.40
7:G:64:ASN:N	7:G:64:ASN:ND2	2.69	0.40
30:0:1544:U:H2'	30:0:1545:C:H6	1.87	0.40
25:Y:126:PRO:HG2	25:Y:128:PHE:CZ	2.56	0.40
30:0:249:G:H2'	30:0:250:C:H6	1.86	0.40
30:0:101:C:H2'	30:0:102:A:H8	1.87	0.40
20:T:52:ARG:HB2	20:T:95:ASN:HB3	2.02	0.40
30:0:445:U:H2'	30:0:446:G:C8	2.57	0.40
30:0:2758:G:H2'	30:0:2759:C:C6	2.56	0.40
30:0:1139:U:H2'	30:0:1140:C:H6	1.85	0.40
27:1:10:LYS:N	38:1:8981:HOH:O	2.50	0.40
1:A:230:SER:HB2	30:0:1852:A:H4'	2.04	0.40
2:B:245:SER:HB3	30:0:2094:G:H4'	2.02	0.40
13:M:47:ASP:CG	13:M:48:LYS:N	2.75	0.40
31:9:122:C:C6	38:9:9043:HOH:O	2.71	0.40
30:0:272:A:N1	30:0:369:G:H5''	2.36	0.40
30:0:1116:U:C2'	30:0:1118:A:C2	3.05	0.40
30:0:2491:G:C1'	38:0:6868:HOH:O	2.59	0.40
30:0:1589:G:H22	30:0:1605:G:H1'	1.85	0.40
4:D:146:LYS:NZ	14:N:107:ASN:ND2	2.70	0.40
13:M:24:GLN:HE22	13:M:27:ARG:HH11	1.68	0.40
1:A:171:LYS:HB2	30:0:820:G:C6	2.57	0.40
30:0:951:A:O2'	30:0:952:G:H5'	2.21	0.40
31:9:65:A:C6	31:9:112:U:C5	3.10	0.40
5:E:84:MET:HE1	5:E:148:ILE:HD12	2.04	0.40
30:0:2824:C:H5''	30:0:2825:C:H5'	2.03	0.40
30:0:517:U:H1'	38:0:7571:HOH:O	2.20	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:0:2327:A:H2'	30:0:2328:U:O4'	2.21	0.40
30:0:1472:C:H6	30:0:1472:C:O5'	2.04	0.40
30:0:1217:G:C2	30:0:1218:U:C2	3.09	0.40
23:W:5:VAL:HG11	23:W:153:MET:CE	2.52	0.40
2:B:149:ASP:HB2	38:B:9049:HOH:O	2.21	0.40
31:9:8:G:H5'	38:9:9103:HOH:O	2.21	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	
1	A	235/240 (98%)	212 (90%)	19 (8%)	4 (2%)	14	45
2	B	335/338 (99%)	308 (92%)	24 (7%)	3 (1%)	25	66
3	C	244/246 (99%)	228 (93%)	15 (6%)	1 (0%)	43	82
4	D	134/177 (76%)	112 (84%)	18 (13%)	4 (3%)	7	27
5	E	170/178 (96%)	162 (95%)	8 (5%)	0	100	100
6	F	117/120 (98%)	106 (91%)	8 (7%)	3 (3%)	8	32
7	G	25/348 (7%)	24 (96%)	1 (4%)	0	100	100
8	H	156/177 (88%)	144 (92%)	10 (6%)	2 (1%)	18	54
9	I	68/162 (42%)	55 (81%)	11 (16%)	2 (3%)	7	28
10	J	140/145 (97%)	131 (94%)	9 (6%)	0	100	100
11	K	130/132 (98%)	123 (95%)	6 (5%)	1 (1%)	27	68
12	L	141/165 (86%)	126 (89%)	12 (8%)	3 (2%)	11	39
13	M	192/196 (98%)	185 (96%)	6 (3%)	1 (0%)	38	79
14	N	184/187 (98%)	169 (92%)	11 (6%)	4 (2%)	10	37
15	O	113/116 (97%)	109 (96%)	4 (4%)	0	100	100
16	P	141/149 (95%)	138 (98%)	3 (2%)	0	100	100
17	Q	93/96 (97%)	87 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	R	148/155 (96%)	140 (95%)	8 (5%)	0	100	100
19	S	79/85 (93%)	76 (96%)	3 (4%)	0	100	100
20	T	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
21	U	51/67 (76%)	46 (90%)	5 (10%)	0	100	100
22	V	63/71 (89%)	59 (94%)	4 (6%)	0	100	100
23	W	152/154 (99%)	146 (96%)	6 (4%)	0	100	100
24	X	80/92 (87%)	74 (92%)	5 (6%)	1 (1%)	18	54
25	Y	140/241 (58%)	138 (99%)	2 (1%)	0	100	100
26	Z	71/116 (61%)	63 (89%)	7 (10%)	1 (1%)	16	52
27	1	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
28	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
29	3	90/92 (98%)	87 (97%)	2 (2%)	1 (1%)	21	60
All	All	3705/4472 (83%)	3451 (93%)	223 (6%)	31 (1%)	27	68

All (31) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	VAL
4	D	137	PRO
6	F	101	ALA
14	N	154	LEU
14	N	183	ASP
14	N	184	ILE
1	A	34	ASP
4	D	27	ILE
12	L	80	ASP
12	L	149	ARG
24	X	70	ILE
26	Z	44	ARG
1	A	36	ASP
1	A	88	ILE
2	B	2	GLN
3	C	8	LEU
6	F	100	ASP
8	H	19	ARG
11	K	127	ALA
12	L	21	ARG
14	N	139	TRP

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Mol	Chain	Res	Type
2	B	184	ASP
4	D	56	ARG
2	B	185	GLY
6	F	61	MET
9	I	108	HIS
9	I	83	GLY
29	3	56	PRO
8	H	171	GLY
4	D	28	GLY
13	M	88	VAL

### 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	
1	A	179/182 (98%)	169 (94%)	10 (6%)	30	66
2	B	282/283 (100%)	267 (95%)	15 (5%)	32	70
3	C	193/193 (100%)	177 (92%)	16 (8%)	16	43
4	D	117/148 (79%)	112 (96%)	5 (4%)	40	78
5	E	152/156 (97%)	149 (98%)	3 (2%)	68	92
6	F	93/94 (99%)	92 (99%)	1 (1%)	84	97
7	G	27/282 (10%)	26 (96%)	1 (4%)	45	84
8	H	134/145 (92%)	128 (96%)	6 (4%)	38	77
9	I	58/130 (45%)	58 (100%)	0	100	100
10	J	118/121 (98%)	111 (94%)	7 (6%)	28	64
11	K	106/106 (100%)	105 (99%)	1 (1%)	87	97
12	L	113/127 (89%)	107 (95%)	6 (5%)	32	70
13	M	158/160 (99%)	152 (96%)	6 (4%)	44	83
14	N	149/150 (99%)	145 (97%)	4 (3%)	57	90
15	O	93/94 (99%)	93 (100%)	0	100	100
16	P	113/117 (97%)	110 (97%)	3 (3%)	57	90
17	Q	79/80 (99%)	77 (98%)	2 (2%)	60	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	R	117/122 (96%)	112 (96%)	5 (4%)	40	78
19	S	71/74 (96%)	71 (100%)	0	100	100
20	T	105/106 (99%)	100 (95%)	5 (5%)	35	74
21	U	44/53 (83%)	43 (98%)	1 (2%)	63	92
22	V	51/57 (90%)	50 (98%)	1 (2%)	68	92
23	W	130/130 (100%)	124 (95%)	6 (5%)	37	76
24	X	66/74 (89%)	59 (89%)	7 (11%)	10	28
25	Y	120/196 (61%)	118 (98%)	2 (2%)	73	94
26	Z	60/94 (64%)	60 (100%)	0	100	100
27	1	46/47 (98%)	46 (100%)	0	100	100
28	2	42/46 (91%)	41 (98%)	1 (2%)	61	91
29	3	79/79 (100%)	78 (99%)	1 (1%)	80	96
All	All	3095/3646 (85%)	2980 (96%)	115 (4%)	45	84

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	30	ARG
1	A	36	ASP
1	A	64	ASP
1	A	69	LEU
1	A	94	LEU
1	A	131	HIS
1	A	153	ARG
1	A	179	MET
1	A	217	ARG
2	B	7	ARG
2	B	11	LEU
2	B	27	ASN
2	B	49	THR
2	B	51	VAL
2	B	53	LEU
2	B	97	LEU
2	B	132	HIS
2	B	162	MET
2	B	175	LEU
2	B	190	MET

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Mol	Chain	Res	Type
2	B	195	ARG
2	B	234	ARG
2	B	254	GLN
2	B	312	ARG
3	C	2	GLN
3	C	27	ARG
3	C	76	ARG
3	C	78	ARG
3	C	94	THR
3	C	101	ASP
3	C	136	VAL
3	C	162	VAL
3	C	187	ARG
3	C	202	THR
3	C	214	THR
3	C	222	ASP
3	C	223	LEU
3	C	234	VAL
3	C	236	THR
3	C	243	VAL
4	D	24	HIS
4	D	50	VAL
4	D	62	ASP
4	D	149	ARG
4	D	153	THR
5	E	16	ASP
5	E	155	ASN
5	E	156	ASP
6	F	12	LEU
7	G	73	ASP
8	H	62	HIS
8	H	65	LEU
8	H	87	LYS
8	H	91	ARG
8	H	157	TYR
8	H	173	GLU
10	J	39	VAL
10	J	45	VAL
10	J	46	ILE
10	J	52	GLN
10	J	74	ARG
10	J	79	PHE

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Mol	Chain	Res	Type
10	J	107	ASN
11	K	10	GLN
12	L	35	ARG
12	L	80	ASP
12	L	99	GLU
12	L	101	ASP
12	L	104	ASP
12	L	114	VAL
13	M	46	LEU
13	M	68	ARG
13	M	81	ARG
13	M	93	ARG
13	M	99	ARG
13	M	164	THR
14	N	17	ARG
14	N	26	LEU
14	N	49	THR
14	N	127	LEU
16	P	52	LYS
16	P	91	LYS
16	P	98	ILE
17	Q	11	ARG
17	Q	95	GLU
18	R	13	THR
18	R	39	THR
18	R	125	ARG
18	R	132	ARG
18	R	143	VAL
20	T	26	THR
20	T	39	ASN
20	T	48	VAL
20	T	89	ARG
20	T	117	ASP
21	U	52	THR
22	V	12	THR
23	W	4	LEU
23	W	73	LEU
23	W	76	ASP
23	W	108	ARG
23	W	142	ASP
23	W	146	ILE
24	X	12	ILE

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Mol	Chain	Res	Type
24	X	27	ASP
24	X	46	ASP
24	X	72	VAL
24	X	79	GLU
24	X	82	GLU
24	X	88	GLU
25	Y	189	ASN
25	Y	203	VAL
28	2	18	ASN
29	3	56	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (76) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	199	HIS
2	B	2	GLN
2	B	27	ASN
2	B	145	HIS
2	B	221	GLN
2	B	238	ASN
2	B	260	HIS
2	B	320	GLN
2	B	332	ASN
3	C	73	GLN
3	C	129	HIS
3	C	163	HIS
4	D	103	ASN
4	D	133	ASN
5	E	143	GLN
7	G	64	ASN
8	H	34	HIS
8	H	59	GLN
8	H	62	HIS
9	I	106	GLN
10	J	52	GLN
10	J	107	ASN
11	K	10	GLN
11	K	44	HIS
12	L	18	HIS
12	L	41	HIS
12	L	116	HIS

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Mol	Chain	Res	Type
13	M	24	GLN
13	M	58	GLN
13	M	137	ASN
13	M	170	ASN
14	N	21	HIS
14	N	40	ASN
14	N	93	GLN
14	N	107	ASN
16	P	50	GLN
16	P	66	GLN
16	P	73	HIS
16	P	89	ASN
16	P	118	GLN
17	Q	16	ASN
17	Q	40	HIS
18	R	22	GLN
18	R	61	GLN
18	R	94	ASN
18	R	98	ASN
18	R	113	HIS
18	R	117	HIS
18	R	122	GLN
18	R	123	GLN
19	S	9	HIS
19	S	44	GLN
20	T	39	ASN
21	U	39	ASN
22	V	60	GLN
23	W	28	HIS
23	W	59	GLN
23	W	87	HIS
23	W	110	GLN
23	W	119	HIS
23	W	125	HIS
23	W	141	HIS
24	X	23	HIS
25	Y	134	HIS
25	Y	189	ASN
26	Z	61	HIS
27	1	8	GLN
27	1	16	HIS
27	1	28	HIS

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Mol	Chain	Res	Type
28	2	16	ASN
28	2	18	ASN
28	2	41	HIS
28	2	45	ASN
29	3	2	GLN
29	3	48	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	0	2745/2923 (93%)	238 (8%)	25 (0%)
31	9	121/122 (99%)	17 (14%)	2 (1%)
All	All	2866/3045 (94%)	255 (8%)	27 (0%)

All (255) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	0	31	C
30	0	67	A
30	0	69	A
30	0	70	A
30	0	71	G
30	0	86	A
30	0	87	C
30	0	88	G
30	0	114	A
30	0	115	U
30	0	120	A
30	0	130	C
30	0	139	C
30	0	141	C
30	0	151	A
30	0	166	A
30	0	185	G
30	0	186	A
30	0	191	A
30	0	192	A
30	0	200	C
30	0	219	G
30	0	236	A
30	0	237	G

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Mol	Chain	Res	Type
30	0	271	C
30	0	272	A
30	0	273	G
30	0	283	U
30	0	284	C
30	0	308	U
30	0	309	C
30	0	318	U
30	0	336	G
30	0	337	A
30	0	358	G
30	0	368	C
30	0	381	G
30	0	397	A
30	0	417	G
30	0	461	C
30	0	487	G
30	0	498	A
30	0	510	U
30	0	511	A
30	0	514	G
30	0	537	G
30	0	538	C
30	0	539	G
30	0	542	A
30	0	545	G
30	0	553	G
30	0	559	U
30	0	588	G
30	0	604	G
30	0	620	A
30	0	632	A
30	0	644	G
30	0	660	A
30	0	688	A
30	0	701	U
30	0	759	C
30	0	777	U
30	0	809	G
30	0	821	U
30	0	835	U
30	0	840	U

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Mol	Chain	Res	Type
30	0	857	A
30	0	858	U
30	0	868	G
30	0	869	G
30	0	871	G
30	0	872	U
30	0	875	A
30	0	877	G
30	0	878	G
30	0	884	C
30	0	885	G
30	0	898	G
30	0	905	C
30	0	920	C
30	0	921	G
30	0	923	A
30	0	953	G
30	0	960	G
30	0	961	A
30	0	1006	A
30	0	1008	C
30	0	1029	U
30	0	1045	G
30	0	1059	G
30	0	1060	C
30	0	1072	G
30	0	1081	A
30	0	1088	A
30	0	1109	U
30	0	1110	G
30	0	1119	G
30	0	1130	U
30	0	1137	G
30	0	1161	A
30	0	1164	U
30	0	1165	G
30	0	1166	A
30	0	1174	A
30	0	1175	G
30	0	1185	U
30	0	1192	A
30	0	1193	A

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Mol	Chain	Res	Type
30	0	1206	U
30	0	1208	C
30	0	1216	G
30	0	1237	U
30	0	1238	C
30	0	1239	G
30	0	1242	A
30	0	1279	U
30	0	1289	C
30	0	1331	G
30	0	1342	C
30	0	1353	C
30	0	1360	C
30	0	1377	C
30	0	1378	G
30	0	1407	A
30	0	1409	G
30	0	1474	C
30	0	1505	U
30	0	1506	U
30	0	1524	U
30	0	1525	G
30	0	1526	A
30	0	1559	A
30	0	1592	G
30	0	1625	U
30	0	1626	A
30	0	1634	G
30	0	1656	A
30	0	1667	A
30	0	1682	A
30	0	1684	A
30	0	1685	A
30	0	1692	C
30	0	1701	A
30	0	1722	U
30	0	1723	G
30	0	1725	C
30	0	1731	C
30	0	1752	G
30	0	1778	A
30	0	1798	C

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Mol	Chain	Res	Type
30	0	1819	G
30	0	1820	G
30	0	1829	A
30	0	1856	C
30	0	1879	U
30	0	1919	A
30	0	1942	A
30	0	1965	C
30	0	1971	G
30	0	1973	A
30	0	1979	G
30	0	1996	U
30	0	2004	U
30	0	2008	U
30	0	2011	A
30	0	2012	U
30	0	2013	G
30	0	2033	G
30	0	2034	U
30	0	2064	U
30	0	2072	G
30	0	2073	G
30	0	2074	A
30	0	2096	A
30	0	2101	A
30	0	2102	G
30	0	2103	A
30	0	2110	G
30	0	2243	C
30	0	2258	A
30	0	2271	G
30	0	2272	G
30	0	2291	A
30	0	2317	C
30	0	2321	A
30	0	2345	A
30	0	2354	A
30	0	2361	A
30	0	2369	A
30	0	2379	G
30	0	2422	U
30	0	2462	G

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Mol	Chain	Res	Type
30	0	2465	A
30	0	2467	A
30	0	2476	C
30	0	2483	A
30	0	2507	G
30	0	2509	A
30	0	2511	A
30	0	2533	C
30	0	2537	G
30	0	2540	G
30	0	2541	U
30	0	2553	A
30	0	2564	G
30	0	2570	G
30	0	2589	U
30	0	2601	A
30	0	2602	G
30	0	2608	C
30	0	2611	G
30	0	2613	G
30	0	2617	G
30	0	2634	G
30	0	2638	G
30	0	2645	U
30	0	2649	A
30	0	2650	U
30	0	2664	A
30	0	2681	A
30	0	2682	C
30	0	2726	U
30	0	2747	C
30	0	2748	G
30	0	2749	U
30	0	2750	G
30	0	2762	C
30	0	2768	A
30	0	2800	A
30	0	2811	A
30	0	2812	A
30	0	2825	C
30	0	2852	A
30	0	2876	G

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Mol	Chain	Res	Type
30	0	2890	A
30	0	2896	A
30	0	2903	C
30	0	2914	A
31	9	2	U
31	9	7	G
31	9	14	G
31	9	22	G
31	9	23	U
31	9	24	U
31	9	25	G
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
30	0	69	A
30	0	129	A
30	0	603	A
30	0	644	G
30	0	699	C
30	0	834	G
30	0	857	A
30	0	871	G
30	0	877	G
30	0	1080	C
30	0	1237	U
30	0	1246	A
30	0	1352	A
30	0	1474	C
30	0	1506	U
30	0	1692	C
30	0	1730	G

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Mol	Chain	Res	Type
30	0	2313	C
30	0	2467	A
30	0	2536	C
30	0	2616	A
30	0	2649	A
30	0	2718	C
30	0	2726	U
30	0	2761	A
31	9	43	G
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	$\# Z  > 2$
30	OMU	0	2587	30	20,22,23	0.79	1 (5%)	24,31,34	0.74	0
30	OMG	0	2588	30	24,26,27	0.78	0	32,38,41	5.25	3 (9%)
30	UR3	0	2619	30	20,22,23	0.82	1 (5%)	23,32,35	0.82	0
30	PSU	0	2621	30	19,21,22	1.21	3 (15%)	23,30,33	1.12	2 (8%)
30	1MA	0	628	30	23,25,26	0.83	0	32,37,40	0.96	1 (3%)

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
30	OMU	0	2587	30	-	0/8/27/28	0/2/2/2
30	OMG	0	2588	30	-	0/10/27/28	0/1/3/3
30	UR3	0	2619	30	-	0/6/25/26	0/2/2/2
30	PSU	0	2621	30	-	0/8/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	1MA	0	628	30	-	1/8/25/26	0/1/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C2-N1	3.00	1.43	1.37
30	0	2587	OMU	P-OP1	2.59	1.49	1.46
30	0	2621	PSU	P-OP1	2.36	1.49	1.46
30	0	2619	UR3	P-OP1	2.25	1.49	1.46
30	0	2621	PSU	C6-N1	2.19	1.34	1.32

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2588	OMG	C6-C5-N7	-29.11	130.22	134.14
30	0	2588	OMG	C6-N1-C2	3.29	125.26	119.51
30	0	628	1MA	C2-N3-C4	-3.23	110.71	116.23
30	0	2588	OMG	C2-N3-C4	-2.38	111.75	115.09
30	0	2621	PSU	C5-C1'-C2'	-2.34	111.48	115.61
30	0	2621	PSU	C5-C4-N3	-2.16	114.92	118.86

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	0	628	1MA	C2'-C1'-N9-C8

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 305 ligands modelled in this entry, 305 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	237/240 (98%)	-0.46	5 (2%) 60 69	25, 49, 89, 109	0
2	B	337/338 (99%)	-0.58	0 100 100	27, 54, 81, 92	0
3	C	246/246 (100%)	-0.66	0 100 100	22, 42, 65, 77	0
4	D	140/177 (79%)	1.06	35 (25%) 1 2	65, 101, 125, 137	0
5	E	172/178 (96%)	-0.29	1 (0%) 86 91	45, 71, 92, 97	0
6	F	119/120 (99%)	0.12	7 (5%) 22 25	48, 69, 99, 116	0
7	G	29/348 (8%)	1.02	6 (20%) 1 2	76, 95, 103, 106	0
8	H	160/177 (90%)	-0.21	5 (3%) 47 55	41, 59, 97, 103	0
9	I	70/162 (43%)	3.14	49 (70%) 0 0	127, 146, 165, 166	0
10	J	142/145 (97%)	-0.64	0 100 100	38, 51, 72, 91	0
11	K	132/132 (100%)	-0.76	0 100 100	35, 50, 74, 84	0
12	L	145/165 (87%)	-0.12	3 (2%) 60 69	25, 64, 110, 127	0
13	M	194/196 (98%)	-0.75	0 100 100	28, 40, 57, 65	0
14	N	186/187 (99%)	-0.09	7 (3%) 38 45	41, 66, 114, 123	0
15	O	115/116 (99%)	-0.51	0 100 100	34, 53, 72, 76	0
16	P	143/149 (95%)	-0.60	0 100 100	37, 54, 69, 79	0
17	Q	95/96 (98%)	-0.61	0 100 100	36, 46, 62, 76	0
18	R	150/155 (96%)	-0.74	0 100 100	30, 44, 65, 81	0
19	S	81/85 (95%)	-0.39	1 (1%) 75 83	41, 56, 78, 89	0
20	T	119/120 (99%)	-0.49	1 (0%) 83 89	39, 54, 83, 110	0
21	U	53/67 (79%)	-0.58	1 (1%) 64 72	42, 55, 75, 83	0
22	V	65/71 (91%)	0.39	7 (10%) 6 8	44, 70, 119, 125	0
23	W	154/154 (100%)	-0.53	0 100 100	36, 50, 67, 80	0
24	X	82/92 (89%)	-0.30	3 (3%) 39 47	43, 61, 86, 101	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	Y	142/241 (58%)	-0.71	1 (0%) 84 90	24, 42, 67, 88	0
26	Z	73/116 (62%)	0.67	14 (19%) 2 2	55, 77, 92, 98	0
27	1	56/57 (98%)	-0.70	0 100 100	25, 30, 37, 43	0
28	2	46/50 (92%)	-0.16	2 (4%) 34 40	31, 61, 91, 101	0
29	3	92/92 (100%)	-0.29	0 100 100	36, 63, 77, 90	0
30	0	2754/2923 (94%)	-0.49	22 (0%) 83 89	19, 44, 88, 164	0
31	9	122/122 (100%)	-0.52	3 (2%) 54 64	37, 67, 89, 147	0
All	All	6651/7517 (88%)	-0.39	173 (2%) 53 63	19, 51, 100, 166	0

All (173) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
22	V	39	ALA	9.6
9	I	74	ILE	8.7
22	V	40	PRO	8.4
26	Z	46	SER	7.9
4	D	63	ILE	7.1
9	I	70	THR	7.1
31	9	1	U	7.0
9	I	72	GLU	6.7
9	I	71	ALA	6.5
9	I	108	HIS	6.1
4	D	57	THR	6.1
9	I	104	ALA	5.9
9	I	128	THR	5.8
9	I	66	GLY	5.8
9	I	113	SER	5.7
9	I	102	GLN	5.6
9	I	93	ALA	5.5
14	N	166	ALA	5.4
9	I	76	ASP	5.2
9	I	79	GLY	5.1
9	I	99	GLN	4.9
9	I	100	VAL	4.8
9	I	112	LEU	4.8
9	I	97	VAL	4.8
4	D	85	GLN	4.5
26	Z	44	ARG	4.5
9	I	91	PHE	4.4
26	Z	50	VAL	4.3

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Mol	Chain	Res	Type	RSRZ
9	I	109	PRO	4.3
9	I	106	GLN	4.3
26	Z	45	VAL	4.3
9	I	92	VAL	4.2
9	I	80	PHE	4.2
9	I	132	VAL	4.2
9	I	69	PRO	4.1
22	V	1	THR	4.1
4	D	90	LEU	4.0
1	A	37	VAL	4.0
31	9	24	U	4.0
30	0	1172	G	4.0
30	0	1198	U	3.9
9	I	111	LEU	3.9
4	D	44	ILE	3.9
9	I	67	VAL	3.9
9	I	88	GLN	3.9
4	D	18	ILE	3.9
19	S	81	ILE	3.8
22	V	43	PRO	3.8
9	I	83	GLY	3.7
30	0	735	C	3.7
30	0	1199	A	3.7
26	Z	58	ASN	3.7
26	Z	35	SER	3.7
4	D	89	PRO	3.7
28	2	49	GLU	3.5
4	D	17	ARG	3.5
26	Z	48	ARG	3.5
25	Y	235	GLU	3.5
6	F	106	ALA	3.5
30	0	2645	U	3.4
22	V	38	GLY	3.4
9	I	73	LEU	3.3
7	G	27	ILE	3.3
9	I	98	ASP	3.3
4	D	61	PHE	3.2
1	A	237	GLY	3.2
4	D	75	LEU	3.2
4	D	92	GLU	3.2
6	F	98	VAL	3.2
4	D	64	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
9	I	110	ASP	3.1
9	I	116	LEU	3.1
6	F	28	ALA	3.1
30	0	970	U	3.1
9	I	82	THR	3.1
4	D	170	TYR	3.0
24	X	80	GLU	3.0
14	N	155	GLU	3.0
4	D	26	GLY	3.0
28	2	39	ARG	3.0
4	D	27	ILE	3.0
4	D	73	VAL	2.9
4	D	81	GLU	2.9
30	0	1200	A	2.9
24	X	71	ARG	2.9
7	G	26	MET	2.9
26	Z	55	SER	2.9
9	I	78	ALA	2.9
24	X	88	GLU	2.9
4	D	69	ILE	2.9
4	D	171	ASP	2.8
14	N	183	ASP	2.8
30	0	1202	A	2.8
9	I	103	ILE	2.7
9	I	86	GLU	2.7
9	I	95	LEU	2.7
12	L	80	ASP	2.7
26	Z	49	ARG	2.7
9	I	84	SER	2.7
26	Z	43	GLY	2.7
7	G	25	GLU	2.7
4	D	166	ILE	2.6
26	Z	53	ILE	2.6
14	N	185	GLU	2.6
4	D	172	VAL	2.6
6	F	99	THR	2.5
9	I	105	GLU	2.5
4	D	41	LEU	2.5
9	I	114	TYR	2.5
8	H	40	GLN	2.5
22	V	41	GLU	2.5
30	0	2237	G	2.5

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Mol	Chain	Res	Type	RSRZ
4	D	93	LEU	2.5
30	0	282	C	2.5
4	D	135	VAL	2.5
9	I	121	LYS	2.5
30	0	2637	A	2.5
30	0	960	G	2.4
7	G	24	VAL	2.4
9	I	81	GLU	2.4
4	D	84	LEU	2.4
30	0	1163	G	2.4
30	0	1203	G	2.4
12	L	81	VAL	2.3
8	H	81	GLY	2.3
5	E	100	ASP	2.3
4	D	40	ILE	2.3
31	9	23	U	2.3
30	0	1177	A	2.3
9	I	75	LYS	2.3
26	Z	60	ASP	2.3
14	N	182	GLY	2.3
9	I	94	ASP	2.3
21	U	47	ARG	2.3
30	0	1279	U	2.3
4	D	88	LEU	2.3
4	D	45	THR	2.3
7	G	23	ILE	2.3
26	Z	69	ASP	2.3
1	A	236	GLY	2.3
9	I	133	THR	2.3
9	I	118	ASN	2.3
26	Z	47	ARG	2.3
8	H	86	TYR	2.2
8	H	174	LEU	2.2
7	G	68	GLU	2.2
9	I	101	LYS	2.2
4	D	134	LEU	2.2
4	D	25	MET	2.2
4	D	22	VAL	2.2
30	0	1204	C	2.2
14	N	160	SER	2.1
4	D	43	GLU	2.1
30	0	1169	U	2.1

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Mol	Chain	Res	Type	RSRZ
20	T	116	ASP	2.1
22	V	37	GLY	2.1
30	0	1173	A	2.1
1	A	35	GLY	2.1
6	F	16	ALA	2.1
14	N	159	TYR	2.1
12	L	60	GLU	2.1
30	0	1171	A	2.1
6	F	49	PHE	2.1
4	D	23	VAL	2.1
30	0	1165	G	2.1
1	A	36	ASP	2.1
4	D	130	VAL	2.1
8	H	76	LEU	2.1
6	F	17	LEU	2.0
9	I	117	THR	2.0
30	0	1170	U	2.0
4	D	128	LEU	2.0
9	I	130	LEU	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
30	1MA	0	628	23/24	0.16	1.44	28,29,31,32	0
30	UR3	0	2619	21/22	0.12	0.21	45,48,53,54	0
30	OMU	0	2587	21/22	0.11	-0.37	32,36,38,39	0
30	PSU	0	2621	20/21	0.13	-0.63	26,30,50,51	0
30	OMG	0	2588	24/25	0.11	-2.38	30,35,38,40	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
34	NA	0	8561	1/1	0.77	107.28	77,77,77,77	0
32	MG	0	8078	1/1	0.45	84.33	76,76,76,76	0
34	NA	0	8554	1/1	0.92	82.94	69,69,69,69	0
34	NA	0	8505	1/1	0.70	68.93	34,34,34,34	0
35	CL	0	8822	1/1	0.48	59.09	83,83,83,83	0
36	SR	0	8982	1/1	0.91	56.53	197,197,197,197	0
36	SR	0	8997	1/1	0.56	51.81	194,194,194,194	0
36	SR	0	9004	1/1	1.21	46.89	200,200,200,200	0
34	NA	0	8547	1/1	0.81	45.67	60,60,60,60	0
34	NA	0	8535	1/1	0.32	35.69	55,55,55,55	0
34	NA	0	8514	1/1	0.39	31.81	48,48,48,48	0
34	NA	0	8560	1/1	0.66	31.23	85,85,85,85	0
36	SR	0	8994	1/1	0.31	30.19	192,192,192,192	0
34	NA	0	8509	1/1	0.20	28.68	63,63,63,63	0
34	NA	0	8562	1/1	0.36	28.38	55,55,55,55	0
34	NA	0	8546	1/1	0.84	25.35	82,82,82,82	0
34	NA	0	8566	1/1	0.48	24.45	71,71,71,71	0
36	SR	0	8996	1/1	0.59	24.18	200,200,200,200	0
34	NA	0	8522	1/1	0.23	20.74	67,67,67,67	0
36	SR	0	8986	1/1	0.26	18.85	200,200,200,200	0
34	NA	0	8556	1/1	0.82	18.28	55,55,55,55	0
34	NA	0	8574	1/1	0.33	17.96	52,52,52,52	0
32	MG	0	8049	1/1	0.27	17.50	58,58,58,58	0
34	NA	0	8568	1/1	0.51	17.11	36,36,36,36	0
34	NA	0	8512	1/1	0.31	16.19	45,45,45,45	0
34	NA	0	8563	1/1	0.42	15.92	67,67,67,67	0
32	MG	0	8030	1/1	0.38	15.34	72,72,72,72	0
34	NA	0	8555	1/1	0.42	15.33	53,53,53,53	0
34	NA	0	8524	1/1	0.22	14.82	52,52,52,52	0
34	NA	0	8506	1/1	0.19	14.50	63,63,63,63	0
32	MG	0	8066	1/1	0.28	13.29	80,80,80,80	0
34	NA	0	8550	1/1	0.25	12.92	53,53,53,53	0
34	NA	0	8525	1/1	0.25	12.29	83,83,83,83	0
34	NA	0	8559	1/1	0.19	12.03	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
36	SR	B	8987	1/1	0.57	11.94	200,200,200,200	0
34	NA	0	8553	1/1	0.29	11.48	52,52,52,52	0
32	MG	0	8039	1/1	0.28	11.44	67,67,67,67	0
34	NA	0	8541	1/1	0.29	10.73	61,61,61,61	0
34	NA	9	8572	1/1	0.27	9.82	80,80,80,80	0
34	NA	0	8542	1/1	0.22	9.44	48,48,48,48	0
32	MG	0	8041	1/1	0.21	8.99	29,29,29,29	0
36	SR	0	8962	1/1	0.21	8.96	155,155,155,155	0
36	SR	0	8976	1/1	0.29	8.94	194,194,194,194	0
36	SR	0	8903	1/1	0.16	8.83	53,53,53,53	0
34	NA	0	8551	1/1	0.22	8.61	38,38,38,38	0
32	MG	0	8071	1/1	0.18	8.54	50,50,50,50	0
34	NA	0	8558	1/1	0.35	8.39	45,45,45,45	0
34	NA	0	8528	1/1	0.23	8.31	44,44,44,44	0
34	NA	0	8565	1/1	0.20	8.23	57,57,57,57	0
36	SR	0	9007	1/1	0.22	8.02	191,191,191,191	0
36	SR	0	8914	1/1	0.27	7.83	121,121,121,121	0
32	MG	0	8040	1/1	0.18	7.80	80,80,80,80	0
34	NA	0	8518	1/1	0.34	7.70	82,82,82,82	0
34	NA	0	8549	1/1	0.21	7.59	51,51,51,51	0
32	MG	0	8072	1/1	0.18	6.93	43,43,43,43	0
34	NA	0	8573	1/1	0.17	6.93	61,61,61,61	0
34	NA	0	8567	1/1	0.24	6.77	72,72,72,72	0
32	MG	0	8047	1/1	0.27	6.66	50,50,50,50	0
36	SR	0	8937	1/1	0.20	6.64	102,102,102,102	0
32	MG	0	8009	1/1	0.22	6.59	28,28,28,28	0
36	SR	0	8924	1/1	0.17	6.55	133,133,133,133	0
34	NA	0	8548	1/1	0.14	6.43	42,42,42,42	0
36	SR	Y	9002	1/1	0.14	6.14	188,188,188,188	0
32	MG	9	8074	1/1	0.16	5.87	75,75,75,75	0
35	CL	0	8816	1/1	0.30	5.86	67,67,67,67	0
36	SR	0	8905	1/1	0.24	5.81	69,69,69,69	0
36	SR	0	8925	1/1	0.12	5.80	87,87,87,87	0
32	MG	0	8067	1/1	0.25	5.63	50,50,50,50	0
32	MG	0	8055	1/1	0.19	5.51	30,30,30,30	0
32	MG	0	8029	1/1	0.17	5.37	46,46,46,46	0
36	SR	0	8909	1/1	0.15	5.26	86,86,86,86	0
34	NA	0	8530	1/1	0.20	5.15	41,41,41,41	0
36	SR	0	9001	1/1	0.20	4.95	176,176,176,176	0
32	MG	0	8090	1/1	0.19	4.82	55,55,55,55	0
34	NA	0	8552	1/1	0.25	4.77	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
36	SR	0	8957	1/1	0.21	4.52	200,200,200,200	0
32	MG	0	8081	1/1	0.15	4.17	74,74,74,74	0
32	MG	0	8016	1/1	0.23	3.95	50,50,50,50	0
32	MG	0	8048	1/1	0.17	3.90	22,22,22,22	0
34	NA	0	8521	1/1	0.20	3.79	50,50,50,50	0
36	SR	0	8904	1/1	0.18	3.58	55,55,55,55	0
34	NA	0	8501	1/1	0.14	3.50	33,33,33,33	0
34	NA	0	8513	1/1	0.23	3.47	42,42,42,42	0
32	MG	0	8014	1/1	0.16	3.45	21,21,21,21	0
32	MG	0	8037	1/1	0.12	3.30	59,59,59,59	0
36	SR	R	8912	1/1	0.16	3.23	83,83,83,83	0
32	MG	0	8063	1/1	0.18	3.20	90,90,90,90	0
36	SR	0	8969	1/1	0.18	3.02	164,164,164,164	0
32	MG	0	8080	1/1	0.18	3.01	66,66,66,66	0
32	MG	A	8051	1/1	0.29	2.94	60,60,60,60	0
34	NA	0	8564	1/1	0.15	2.86	70,70,70,70	0
32	MG	0	8022	1/1	0.14	2.84	31,31,31,31	0
32	MG	0	8004	1/1	0.17	2.81	25,25,25,25	0
34	NA	0	8575	1/1	0.17	2.72	83,83,83,83	0
34	NA	0	8527	1/1	0.17	2.71	47,47,47,47	0
32	MG	0	8003	1/1	0.17	2.69	26,26,26,26	0
34	NA	0	8537	1/1	0.13	2.60	38,38,38,38	0
32	MG	0	8028	1/1	0.17	2.38	24,24,24,24	0
32	MG	0	8026	1/1	0.12	2.29	33,33,33,33	0
36	SR	0	8979	1/1	0.16	2.10	198,198,198,198	0
32	MG	0	8061	1/1	0.19	2.09	25,25,25,25	0
36	SR	0	8955	1/1	0.12	2.02	198,198,198,198	0
32	MG	0	8084	1/1	0.13	2.01	29,29,29,29	0
34	NA	0	8545	1/1	0.16	1.97	38,38,38,38	0
32	MG	0	8069	1/1	0.20	1.96	57,57,57,57	0
32	MG	0	8023	1/1	0.15	1.95	26,26,26,26	0
34	NA	0	8531	1/1	0.12	1.95	41,41,41,41	0
34	NA	0	8508	1/1	0.14	1.87	43,43,43,43	0
32	MG	0	8045	1/1	0.12	1.83	35,35,35,35	0
36	SR	0	8991	1/1	0.15	1.71	186,186,186,186	0
32	MG	0	8017	1/1	0.17	1.64	23,23,23,23	0
32	MG	0	8062	1/1	0.18	1.48	44,44,44,44	0
36	SR	0	8946	1/1	0.16	1.39	99,99,99,99	0
32	MG	0	8046	1/1	0.16	1.37	44,44,44,44	0
36	SR	0	8958	1/1	0.11	1.36	97,97,97,97	0
36	SR	0	8926	1/1	0.10	1.28	122,122,122,122	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
32	MG	0	8088	1/1	0.16	1.18	32,32,32,32	0
32	MG	0	8015	1/1	0.13	1.04	31,31,31,31	0
32	MG	0	8085	1/1	0.13	0.91	80,80,80,80	0
34	NA	0	8515	1/1	0.17	0.84	35,35,35,35	0
32	MG	0	8008	1/1	0.12	0.83	24,24,24,24	0
32	MG	0	8031	1/1	0.12	0.72	57,57,57,57	0
32	MG	0	8021	1/1	0.11	0.61	32,32,32,32	0
32	MG	B	8042	1/1	0.12	0.61	44,44,44,44	0
34	NA	0	8504	1/1	0.15	0.61	31,31,31,31	0
34	NA	0	8520	1/1	0.11	0.61	40,40,40,40	0
36	SR	0	8906	1/1	0.18	0.56	53,53,53,53	0
34	NA	0	8519	1/1	0.15	0.53	39,39,39,39	0
36	SR	0	8918	1/1	0.12	0.51	79,79,79,79	0
34	NA	0	8557	1/1	0.09	0.44	57,57,57,57	0
33	K	0	8401	1/1	0.16	0.39	93,93,93,93	0
36	SR	0	8936	1/1	0.12	0.34	91,91,91,91	0
32	MG	0	8070	1/1	0.12	0.30	43,43,43,43	0
34	NA	0	8507	1/1	0.14	0.29	32,32,32,32	0
32	MG	0	8073	1/1	0.10	0.17	74,74,74,74	0
34	NA	0	8571	1/1	0.09	0.16	61,61,61,61	0
32	MG	0	8056	1/1	0.12	0.15	41,41,41,41	0
34	NA	0	8534	1/1	0.21	0.15	64,64,64,64	0
32	MG	K	8054	1/1	0.13	0.13	37,37,37,37	0
36	SR	0	8953	1/1	0.15	0.11	160,160,160,160	0
36	SR	0	8964	1/1	0.10	0.06	124,124,124,124	0
32	MG	0	8019	1/1	0.14	0.06	19,19,19,19	0
36	SR	3	8932	1/1	0.12	0.03	74,74,74,74	0
35	CL	J	8801	1/1	0.15	-0.01	71,71,71,71	0
37	CD	1	8702	1/1	0.12	-0.05	60,60,60,60	0
36	SR	0	8981	1/1	0.12	-0.11	171,171,171,171	0
32	MG	0	8006	1/1	0.12	-0.12	21,21,21,21	0
32	MG	0	8043	1/1	0.10	-0.12	43,43,43,43	0
34	NA	0	8544	1/1	0.11	-0.15	60,60,60,60	0
32	MG	0	8060	1/1	0.09	-0.19	43,43,43,43	0
32	MG	0	8018	1/1	0.11	-0.23	27,27,27,27	0
36	SR	0	8938	1/1	0.08	-0.27	165,165,165,165	0
36	SR	0	8933	1/1	0.12	-0.29	141,141,141,141	0
32	MG	0	8020	1/1	0.09	-0.30	36,36,36,36	0
36	SR	0	8947	1/1	0.14	-0.35	162,162,162,162	0
36	SR	0	8922	1/1	0.14	-0.36	155,155,155,155	0
36	SR	0	8915	1/1	0.10	-0.44	110,110,110,110	0
32	MG	0	8001	1/1	0.12	-0.44	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
34	NA	9	8543	1/1	0.17	-0.48	44,44,44,44	0
36	SR	0	8984	1/1	0.10	-0.48	114,114,114,114	0
32	MG	0	8005	1/1	0.17	-0.48	31,31,31,31	0
34	NA	0	8533	1/1	0.11	-0.49	55,55,55,55	0
35	CL	O	8808	1/1	0.15	-0.51	73,73,73,73	0
32	MG	0	8025	1/1	0.12	-0.51	27,27,27,27	0
34	NA	0	8570	1/1	0.09	-0.54	48,48,48,48	0
32	MG	0	8079	1/1	0.12	-0.54	39,39,39,39	0
36	SR	0	8972	1/1	0.11	-0.55	127,127,127,127	0
32	MG	0	8024	1/1	0.14	-0.57	52,52,52,52	0
36	SR	0	8990	1/1	0.13	-0.63	173,173,173,173	0
34	NA	Q	8540	1/1	0.10	-0.64	58,58,58,58	0
32	MG	0	8035	1/1	0.10	-0.69	43,43,43,43	0
32	MG	0	8082	1/1	0.14	-0.70	73,73,73,73	0
36	SR	1	8952	1/1	0.13	-0.74	79,79,79,79	0
32	MG	0	8076	1/1	0.12	-0.78	39,39,39,39	0
34	NA	0	8511	1/1	0.10	-0.78	56,56,56,56	0
36	SR	0	8907	1/1	0.10	-0.78	43,43,43,43	0
36	SR	F	9005	1/1	0.08	-0.82	132,132,132,132	0
34	NA	M	8539	1/1	0.10	-0.82	26,26,26,26	0
36	SR	0	8921	1/1	0.11	-0.84	77,77,77,77	0
32	MG	0	8010	1/1	0.14	-0.85	48,48,48,48	0
36	SR	0	8948	1/1	0.10	-0.90	88,88,88,88	0
36	SR	0	8993	1/1	0.07	-0.90	173,173,173,173	0
32	MG	0	8011	1/1	0.14	-0.92	23,23,23,23	0
32	MG	0	8083	1/1	0.09	-0.93	37,37,37,37	0
36	SR	0	8956	1/1	0.07	-1.01	138,138,138,138	0
37	CD	U	8701	1/1	0.09	-1.02	62,62,62,62	0
32	MG	0	8012	1/1	0.13	-1.02	22,22,22,22	0
36	SR	0	8954	1/1	0.09	-1.03	100,100,100,100	0
36	SR	B	8950	1/1	0.14	-1.03	114,114,114,114	0
36	SR	0	8934	1/1	0.11	-1.13	117,117,117,117	0
35	CL	J	8802	1/1	0.10	-1.14	66,66,66,66	0
36	SR	0	8944	1/1	0.10	-1.15	175,175,175,175	0
34	NA	0	8523	1/1	0.10	-1.17	46,46,46,46	0
36	SR	0	8998	1/1	0.12	-1.21	172,172,172,172	0
34	NA	0	8517	1/1	0.12	-1.22	46,46,46,46	0
36	SR	0	8988	1/1	0.10	-1.22	162,162,162,162	0
36	SR	A	8929	1/1	0.08	-1.23	130,130,130,130	0
35	CL	J	8821	1/1	0.07	-1.27	60,60,60,60	0
32	MG	0	8058	1/1	0.07	-1.34	16,16,16,16	0
32	MG	0	8059	1/1	0.08	-1.38	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
36	SR	0	8985	1/1	0.08	-1.39	124,124,124,124	0
36	SR	0	8943	1/1	0.08	-1.43	99,99,99,99	0
36	SR	0	8941	1/1	0.14	-1.53	104,104,104,104	0
35	CL	M	8818	1/1	0.07	-1.55	44,44,44,44	0
32	MG	0	8064	1/1	0.11	-1.63	41,41,41,41	0
36	SR	0	8927	1/1	0.10	-1.65	170,170,170,170	0
34	NA	J	8538	1/1	0.05	-1.70	43,43,43,43	0
32	MG	T	8057	1/1	0.09	-1.72	66,66,66,66	0
36	SR	0	8931	1/1	0.09	-1.73	110,110,110,110	0
36	SR	0	8908	1/1	0.10	-1.76	83,83,83,83	0
36	SR	0	8935	1/1	0.09	-1.80	80,80,80,80	0
37	CD	Z	8703	1/1	0.06	-1.81	83,83,83,83	0
32	MG	0	8002	1/1	0.12	-1.82	30,30,30,30	0
36	SR	0	8923	1/1	0.10	-1.83	87,87,87,87	0
36	SR	0	8911	1/1	0.07	-1.84	75,75,75,75	0
36	SR	0	8940	1/1	0.10	-1.86	78,78,78,78	0
34	NA	0	8502	1/1	0.09	-1.90	51,51,51,51	0
36	SR	0	8939	1/1	0.03	-1.93	145,145,145,145	0
36	SR	0	8966	1/1	0.08	-1.95	100,100,100,100	0
36	SR	A	8977	1/1	0.05	-1.95	154,154,154,154	0
32	MG	0	8053	1/1	0.05	-1.96	38,38,38,38	0
36	SR	1	8913	1/1	0.10	-1.99	91,91,91,91	0
36	SR	0	8975	1/1	0.07	-2.00	137,137,137,137	0
36	SR	0	8902	1/1	0.13	-2.03	37,37,37,37	0
35	CL	3	8804	1/1	0.08	-2.06	58,58,58,58	0
36	SR	A	8930	1/1	0.04	-2.07	110,110,110,110	0
34	NA	0	8529	1/1	0.04	-2.10	39,39,39,39	0
37	CD	3	8704	1/1	0.05	-2.15	76,76,76,76	0
34	NA	C	8503	1/1	0.07	-2.18	27,27,27,27	0
34	NA	R	8532	1/1	0.06	-2.24	45,45,45,45	0
36	SR	0	8999	1/1	0.06	-2.31	93,93,93,93	0
36	SR	0	8959	1/1	0.08	-2.34	159,159,159,159	0
35	CL	0	8812	1/1	0.06	-2.35	45,45,45,45	0
32	MG	0	8036	1/1	0.06	-2.43	46,46,46,46	0
37	CD	O	8705	1/1	0.08	-2.43	84,84,84,84	0
36	SR	0	8974	1/1	0.12	-2.46	158,158,158,158	0
36	SR	0	9008	1/1	0.12	-2.47	84,84,84,84	0
32	MG	0	8068	1/1	0.07	-2.48	52,52,52,52	0
35	CL	0	8811	1/1	0.06	-2.55	63,63,63,63	0
35	CL	N	8807	1/1	0.08	-2.60	71,71,71,71	0
32	MG	0	8038	1/1	0.11	-2.60	66,66,66,66	0
36	SR	0	8917	1/1	0.08	-2.65	111,111,111,111	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
35	CL	R	8806	1/1	0.09	-2.72	47,47,47,47	0
32	MG	0	8050	1/1	0.11	-2.86	28,28,28,28	0
35	CL	0	8817	1/1	0.07	-2.89	51,51,51,51	0
32	MG	0	8091	1/1	0.07	-2.90	51,51,51,51	0
36	SR	9	9003	1/1	0.07	-2.91	171,171,171,171	0
35	CL	0	8805	1/1	0.07	-2.99	53,53,53,53	0
32	MG	0	8033	1/1	0.07	-3.00	49,49,49,49	0
35	CL	0	8803	1/1	0.07	-3.06	52,52,52,52	0
35	CL	A	8809	1/1	0.07	-3.33	65,65,65,65	0
32	MG	0	8077	1/1	0.05	-3.49	35,35,35,35	0
35	CL	B	8819	1/1	0.10	-3.50	51,51,51,51	0
35	CL	0	8813	1/1	0.06	-3.51	46,46,46,46	0
36	SR	9	8980	1/1	0.08	-3.56	158,158,158,158	0
36	SR	0	9000	1/1	0.06	-3.56	165,165,165,165	0
36	SR	0	8951	1/1	0.03	-3.64	144,144,144,144	0
36	SR	0	8960	1/1	0.04	-3.66	134,134,134,134	0
32	MG	0	8044	1/1	0.07	-3.95	45,45,45,45	0
35	CL	Y	8820	1/1	0.06	-4.01	40,40,40,40	0
32	MG	0	8007	1/1	0.10	-4.23	43,43,43,43	0
36	SR	0	8901	1/1	0.09	-4.28	84,84,84,84	0
33	K	0	8402	1/1	0.07	-4.31	67,67,67,67	0
36	SR	0	8949	1/1	0.08	-4.40	104,104,104,104	0
34	NA	0	8526	1/1	0.04	-4.41	39,39,39,39	0
36	SR	0	8978	1/1	0.05	-4.53	119,119,119,119	0
32	MG	0	8027	1/1	0.06	-4.61	31,31,31,31	0
36	SR	0	8910	1/1	0.06	-4.75	99,99,99,99	0
36	SR	0	8971	1/1	0.05	-4.78	175,175,175,175	0
32	MG	0	8075	1/1	0.04	-4.82	39,39,39,39	0
35	CL	L	8810	1/1	0.05	-4.89	52,52,52,52	0
36	SR	0	8920	1/1	0.05	-4.91	112,112,112,112	0
32	MG	0	8034	1/1	0.06	-4.93	38,38,38,38	0
32	MG	0	8092	1/1	0.07	-4.95	66,66,66,66	0
34	NA	0	8569	1/1	0.09	-5.01	44,44,44,44	0
32	MG	0	8032	1/1	0.04	-5.05	44,44,44,44	0
36	SR	0	8992	1/1	0.06	-5.08	133,133,133,133	0
36	SR	0	8928	1/1	0.06	-5.08	139,139,139,139	0
36	SR	0	8919	1/1	0.10	-5.11	178,178,178,178	0
32	MG	0	8052	1/1	0.04	-5.13	39,39,39,39	0
36	SR	0	8968	1/1	0.05	-5.16	161,161,161,161	0
35	CL	0	8815	1/1	0.07	-5.24	67,67,67,67	0
36	SR	S	8961	1/1	0.05	-5.45	128,128,128,128	0
32	MG	0	8065	1/1	0.05	-5.71	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
36	SR	0	8983	1/1	0.07	-6.28	177,177,177,177	0
36	SR	0	8916	1/1	0.05	-6.41	104,104,104,104	0
32	MG	Y	8086	1/1	0.05	-6.50	35,35,35,35	0
34	NA	0	8516	1/1	0.10	-6.60	45,45,45,45	0
36	SR	0	8965	1/1	0.07	-6.64	121,121,121,121	0
35	CL	0	8814	1/1	0.10	-6.73	50,50,50,50	0
36	SR	0	8945	1/1	0.06	-6.73	107,107,107,107	0
36	SR	0	8989	1/1	0.06	-6.75	159,159,159,159	0
36	SR	0	8970	1/1	0.02	-6.80	123,123,123,123	0
36	SR	0	8995	1/1	0.07	-6.91	136,136,136,136	0
34	NA	S	8510	1/1	0.06	-7.15	27,27,27,27	0
32	MG	0	8087	1/1	0.08	-8.20	31,31,31,31	0
32	MG	0	8013	1/1	0.04	-8.84	21,21,21,21	0
36	SR	0	8967	1/1	0.02	-9.02	131,131,131,131	0
36	SR	0	8942	1/1	0.06	-9.70	115,115,115,115	0
32	MG	0	8093	1/1	0.04	-9.77	27,27,27,27	0
34	NA	0	8536	1/1	0.06	-12.53	47,47,47,47	0
36	SR	0	8973	1/1	0.07	-14.20	121,121,121,121	0
36	SR	0	8963	1/1	0.04	-25.67	131,131,131,131	0
32	MG	0	8089	1/1	0.07	-	42,42,42,42	0
36	SR	0	9006	1/1	1.89	-	200,200,200,200	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.