



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 05:22 AM GMT

PDB ID : 1VQ8
Title : The structure of CCDA-PHE-CAP-BIO and the antibiotic sparsomycin bound to the large ribosomal subunit of haloarcula marismortui
Authors : Schmeing, T.M.; Steitz, T.A.
Deposited on : 2004-12-16
Resolution : 2.20 Å(reported)

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

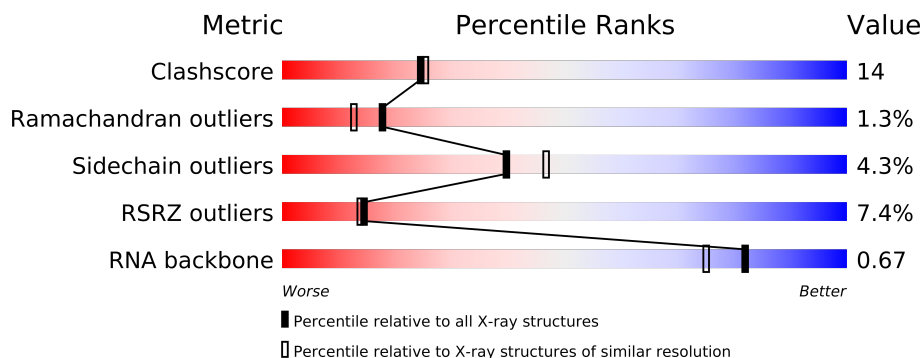
The following versions of software and data (see [references](#)) were used in the production of this report:

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

1 Overall quality at a glance

The reported resolution of this entry is 2.20 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))
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)
RNA backbone	1838	1120 (3.00-1.40)

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 ≥ 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	0	2922	
2	9	122	
3	4	5	
4	A	240	
5	B	338	
6	C	246	
7	D	177	
8	E	178	
9	F	120	
10	G	348	
11	H	171	
12	J	145	
13	K	132	
14	L	165	

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Mol	Chain	Length	Quality of chain
15	M	194	
16	N	187	
17	O	116	
18	P	149	
19	Q	96	
20	R	155	
21	S	85	
22	T	120	
23	U	66	
24	V	71	
25	W	154	
26	X	92	
27	Y	241	
28	Z	83	
29	1	57	
30	2	50	
31	3	92	
32	I	162	

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

Mol	Type	Chain	Res	Geometry	Electron density
33	MG	0	8001	-	X
33	MG	0	8008	-	X
33	MG	0	8012	-	X
33	MG	0	8013	-	X
33	MG	0	8014	-	X
33	MG	0	8017	-	X
33	MG	0	8021	-	X
33	MG	0	8022	-	X
33	MG	0	8024	-	X
33	MG	0	8025	-	X
33	MG	0	8026	-	X
33	MG	0	8027	-	X
33	MG	0	8029	-	X
33	MG	0	8038	-	X
33	MG	0	8040	-	X
33	MG	0	8047	-	X
33	MG	0	8050	-	X
33	MG	0	8051	-	X
33	MG	0	8052	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
33	MG	0	8056	-	X
33	MG	0	8057	-	X
33	MG	0	8059	-	X
33	MG	0	8060	-	X
33	MG	0	8061	-	X
33	MG	0	8065	-	X
33	MG	0	8070	-	X
33	MG	0	8072	-	X
33	MG	0	8079	-	X
33	MG	0	8080	-	X
33	MG	0	8082	-	X
33	MG	0	8084	-	X
33	MG	0	8085	-	X
33	MG	0	8089	-	X
33	MG	0	8091	-	X
33	MG	0	8092	-	X
33	MG	0	8094	-	X
33	MG	0	8103	-	X
33	MG	0	8108	-	X
33	MG	0	8110	-	X
33	MG	0	8114	-	X
33	MG	9	8095	-	X
33	MG	K	8069	-	X
34	K	0	9001	-	X
35	NA	0	9101	-	X
35	NA	0	9102	-	X
35	NA	0	9106	-	X
35	NA	0	9107	-	X
35	NA	0	9111	-	X
35	NA	0	9113	-	X
35	NA	0	9115	-	X
35	NA	0	9116	-	X
35	NA	0	9118	-	X
35	NA	0	9122	-	X
35	NA	0	9125	-	X
35	NA	0	9127	-	X
35	NA	0	9128	-	X
35	NA	0	9129	-	X
35	NA	0	9140	-	X
35	NA	0	9141	-	X
35	NA	0	9149	-	X
35	NA	0	9152	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
35	NA	0	9154	-	X
35	NA	0	9155	-	X
35	NA	0	9157	-	X
35	NA	0	9158	-	X
35	NA	0	9159	-	X
35	NA	0	9164	-	X
35	NA	0	9167	-	X
35	NA	0	9168	-	X
35	NA	0	9169	-	X
35	NA	0	9170	-	X
35	NA	0	9172	-	X
35	NA	0	9173	-	X
35	NA	0	9174	-	X
35	NA	0	9175	-	X
35	NA	0	9177	-	X
35	NA	0	9178	-	X
35	NA	0	9179	-	X
35	NA	0	9182	-	X
35	NA	0	9184	-	X
35	NA	0	9185	-	X
35	NA	9	9183	-	X
35	NA	B	9161	-	X
35	NA	S	9112	-	X
36	CL	0	9316	-	X
36	CL	0	9322	-	X
36	CL	B	9319	-	X
37	SR	0	9406	-	X
37	SR	0	9407	-	X
37	SR	0	9408	-	X
37	SR	0	9410	-	X
37	SR	0	9411	-	X
37	SR	0	9412	-	X
37	SR	0	9415	-	X
37	SR	0	9416	-	X
37	SR	0	9420	-	X
37	SR	0	9424	-	X
37	SR	0	9427	-	X
37	SR	0	9430	-	X
37	SR	0	9432	-	X
37	SR	0	9433	-	X
37	SR	0	9482	-	X
37	SR	0	9500	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
37	SR	O	9501	-	X
37	SR	O	9539	-	X
37	SR	O	9547	-	X
37	SR	O	9601	-	X
37	SR	O	9626	-	X
37	SR	B	9521	-	X
37	SR	L	9409	-	X
39	CD	O	9205	-	X

2 Entry composition

There are 40 unique types of molecules in this entry. The entry contains 99035 atoms, of which 0 are hydrogen and 0 are deuterium.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	0	0
			59021	26350	10878	19048	2745			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	9	122	Total	C	N	O	P	0	0	0
			2600	1160	472	847	121			

- Molecule 3 is a RNA chain called 5'-R(*CP*CP*(DA)*(PHE)*(ACA))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	4	5	Total	C	N	O	P	0	0	0
			73	40	12	19	2			

- Molecule 4 is a protein called 50S ribosomal protein L2P.

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

- Molecule 5 is a protein called 50S ribosomal protein L3P.

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

- Molecule 6 is a protein called 50S ribosomal protein L4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	246	Total	C	N	O	S	0	0	0
			1859	1131	344	383	1			

- Molecule 7 is a protein called 50S ribosomal protein L5P.

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

- Molecule 8 is a protein called 50S ribosomal protein L6P.

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

- Molecule 9 is a protein called 50S ribosomal protein L7AE.

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

- Molecule 10 is a protein called ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG.

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

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	H	160	Total	C	N	O	S	0	0	0
			1266	785	237	238	6			

- Molecule 12 is a protein called 50S ribosomal protein L13P.

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

- Molecule 13 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	132	Total	C	N	O	S	0	0	0
			992	609	187	192	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	44	LEU	HIS	CONFLICT	UNP P22450

- Molecule 14 is a protein called 50S ribosomal protein L15P.

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

- Molecule 15 is a protein called 50S Ribosomal Protein L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	194	Total	C	N	O	S	0	0	0
			1560	943	332	284	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	CONFLICT	GB 55231501
M	194	ALA	GLY	CONFLICT	GB 55231501

- Molecule 16 is a protein called 50S ribosomal protein L18P.

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

- Molecule 17 is a protein called 50S ribosomal protein L18e.

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

- Molecule 18 is a protein called 50S ribosomal protein L19E.

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

- Molecule 19 is a protein called 50S ribosomal protein L21e.

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

- Molecule 20 is a protein called 50S ribosomal protein L22P.

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

- Molecule 21 is a protein called 50S ribosomal protein L23P.

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

- Molecule 22 is a protein called 50S ribosomal protein L24P.

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

- Molecule 23 is a protein called 50S ribosomal protein L24E.

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

- Molecule 24 is a protein called 50S ribosomal protein L29P.

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

- Molecule 25 is a protein called 50S ribosomal protein L30P.

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

- Molecule 26 is a protein called 50S ribosomal protein L31e.

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

- Molecule 27 is a protein called 50S ribosomal protein L32E.

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

- Molecule 28 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Z	73	Total	C	N	O	S	0	0	0
			578	346	116	111	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	SER	CONFLICT	GB 55231162

- Molecule 29 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 30 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 31 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L11P.

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

- Molecule 33 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	88	Total	Mg	0	0
			88	88		
33	Y	1	Total	Mg	0	0
			1	1		
33	K	1	Total	Mg	0	0
			1	1		
33	A	1	Total	Mg	0	0
			1	1		
33	T	1	Total	Mg	0	0
			1	1		
33	4	1	Total	Mg	0	0
			1	1		
33	9	1	Total	Mg	0	0
			1	1		

- Molecule 34 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	2	Total	K	0	0
			2	2		

- Molecule 35 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	65	Total	Na	0	0
			65	65		
35	J	1	Total	Na	0	0
			1	1		
35	Q	1	Total	Na	0	0
			1	1		
35	D	1	Total	Na	0	0
			1	1		
35	B	1	Total	Na	0	0
			1	1		
35	C	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	R	2	Total 2	Na 2	0	0
35	9	1	Total 1	Na 1	0	0
35	S	1	Total 1	Na 1	0	0
35	M	1	Total 1	Na 1	0	0

- Molecule 36 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	10	Total 10	Cl 10	0	0
36	J	3	Total 3	Cl 3	0	0
36	B	1	Total 1	Cl 1	0	0
36	A	1	Total 1	Cl 1	0	0
36	N	1	Total 1	Cl 1	0	0
36	O	1	Total 1	Cl 1	0	0
36	R	1	Total 1	Cl 1	0	0
36	Y	1	Total 1	Cl 1	0	0
36	L	1	Total 1	Cl 1	0	0
36	3	1	Total 1	Cl 1	0	0
36	M	1	Total 1	Cl 1	0	0

- Molecule 37 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

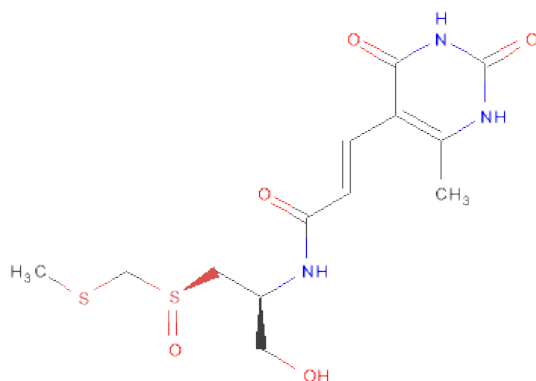
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	0	98	Total 98	Sr 98	0	0
37	1	2	Total 2	Sr 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	H	1	Total 1	Sr 1	0	0
37	B	2	Total 2	Sr 2	0	0
37	3	1	Total 1	Sr 1	0	0
37	A	3	Total 3	Sr 3	0	0
37	R	1	Total 1	Sr 1	0	0
37	9	3	Total 3	Sr 3	0	0
37	L	1	Total 1	Sr 1	0	0
37	S	1	Total 1	Sr 1	0	0
37	F	1	Total 1	Sr 1	0	0

- Molecule 38 is SPARSOMYCIN (three-letter code: SPS) (formula: $C_{13}H_{19}N_3O_5S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
38	4	1	Total 23	C 13	N 3	O 5	S 2	0	0

- Molecule 39 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
39	O	1	Total Cd 1 1	0	0
39	Z	1	Total Cd 1 1	0	0
39	1	1	Total Cd 1 1	0	0
39	3	1	Total Cd 1 1	0	0
39	U	1	Total Cd 1 1	0	0

- Molecule 40 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
40	0	5743	Total O 5743 5743	0	0
40	9	136	Total O 136 136	0	0
40	4	2	Total O 2 2	0	0
40	A	120	Total O 120 120	0	0
40	B	135	Total O 135 135	0	0
40	C	172	Total O 172 172	0	0
40	D	48	Total O 48 48	0	0
40	E	42	Total O 42 42	0	0
40	F	27	Total O 27 27	0	0
40	G	16	Total O 16 16	0	0
40	H	71	Total O 71 71	0	0
40	J	51	Total O 51 51	0	0
40	K	58	Total O 58 58	0	0
40	L	87	Total O 87 87	0	0
40	M	127	Total O 127 127	0	0

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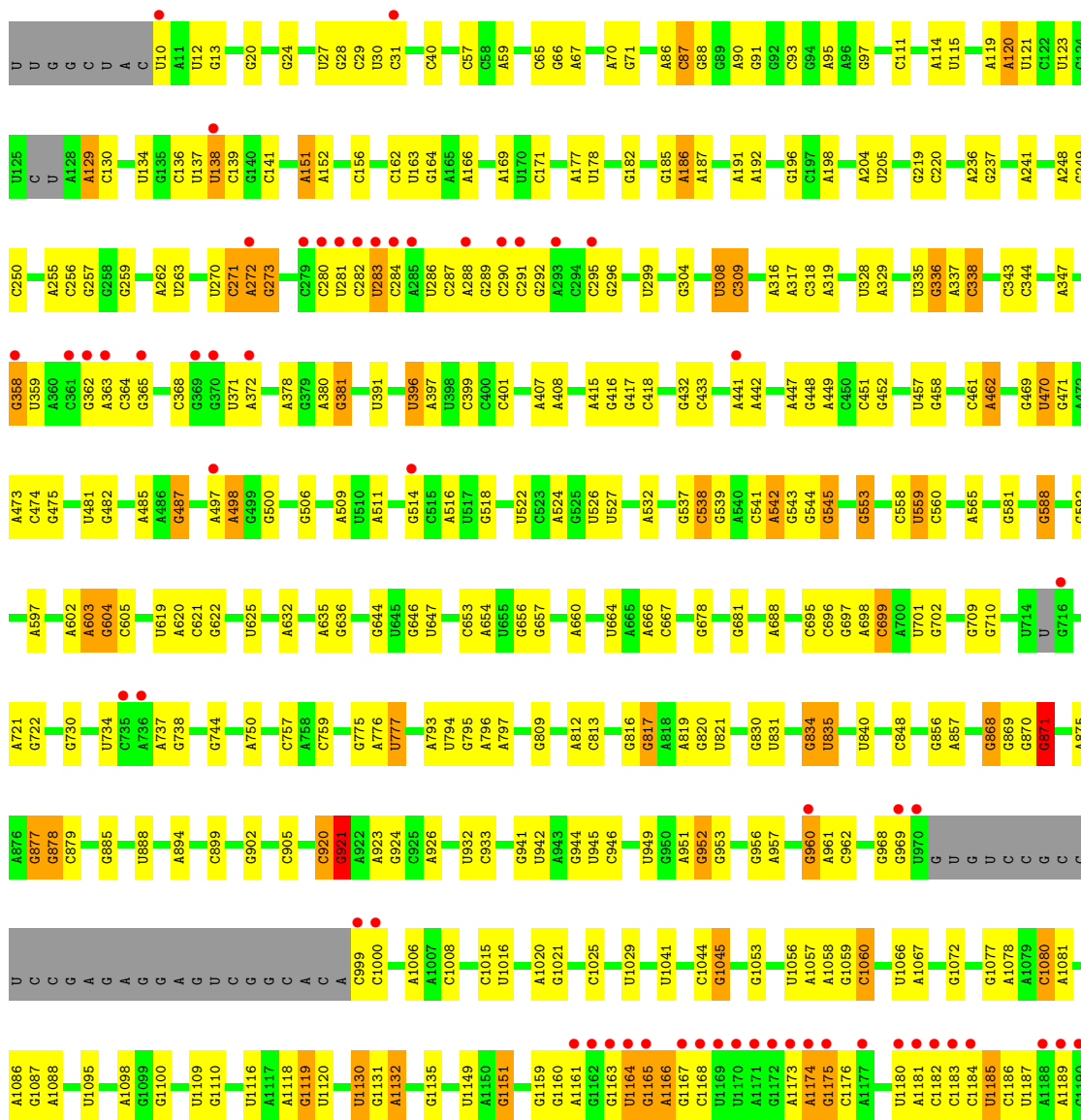
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
40	N	59	Total	O	0	0
			59	59		
40	O	41	Total	O	0	0
			41	41		
40	P	64	Total	O	0	0
			64	64		
40	Q	58	Total	O	0	0
			58	58		
40	R	85	Total	O	0	0
			85	85		
40	S	30	Total	O	0	0
			30	30		
40	T	36	Total	O	0	0
			36	36		
40	U	28	Total	O	0	0
			28	28		
40	V	15	Total	O	0	0
			15	15		
40	W	68	Total	O	0	0
			68	68		
40	X	23	Total	O	0	0
			23	23		
40	Y	95	Total	O	0	0
			95	95		
40	Z	35	Total	O	0	0
			35	35		
40	1	50	Total	O	0	0
			50	50		
40	2	35	Total	O	0	0
			35	35		
40	3	76	Total	O	0	0
			76	76		
40	I	10	Total	O	0	0
			10	10		

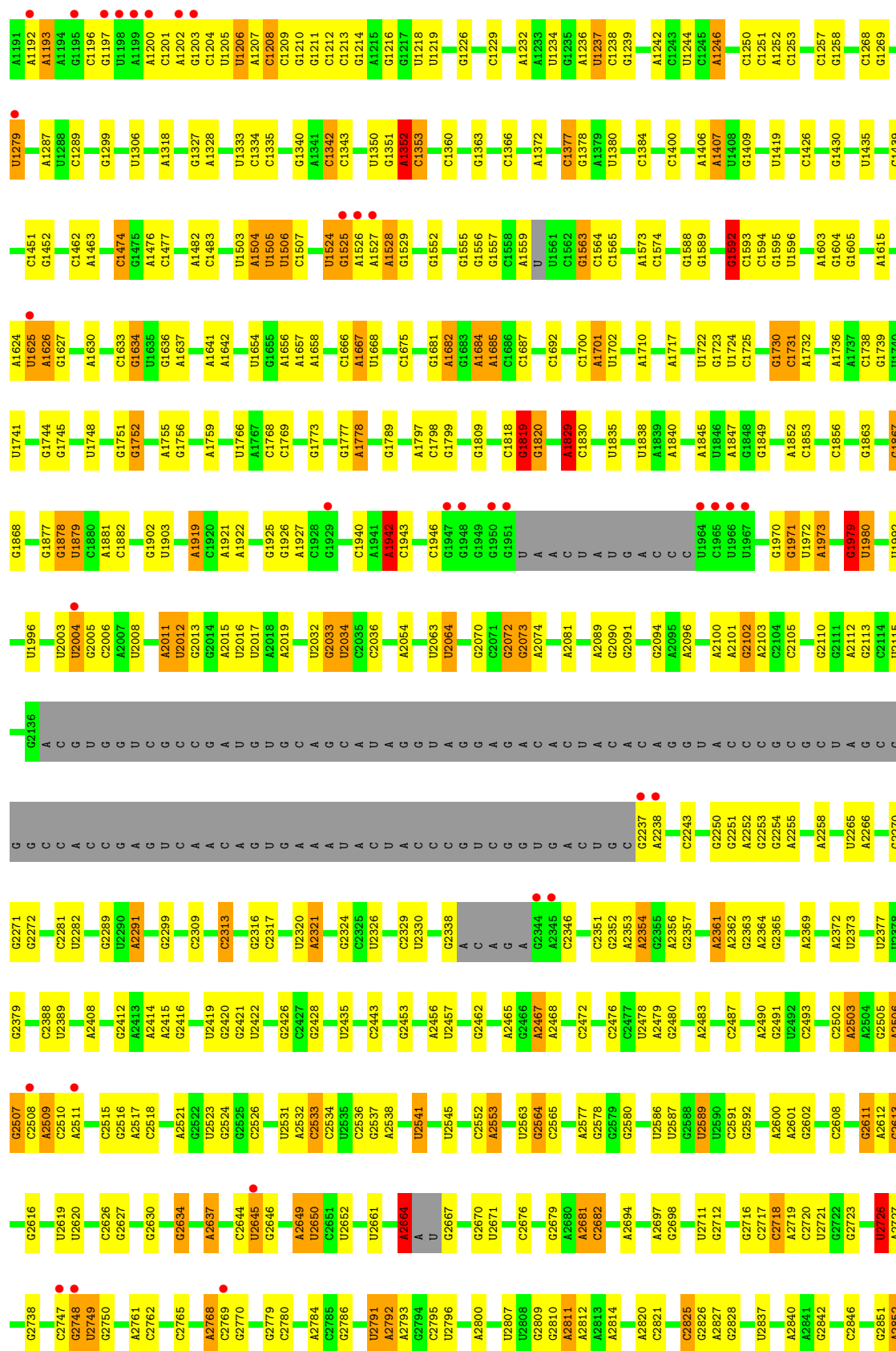
3 Residue-property plots

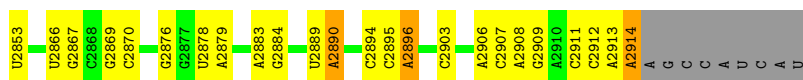
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

- Molecule 1: 23S ribosomal rna

Chain 0: 







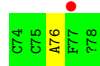
• Molecule 2: 5S ribosomal RNA

Chain 9:



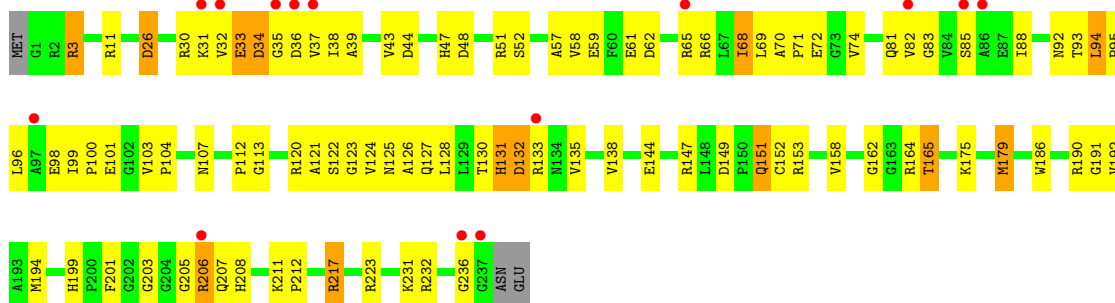
• Molecule 3: 5'-R(*CP*CP*(DA)*(PHE)*(ACA))-3'

Chain 4:



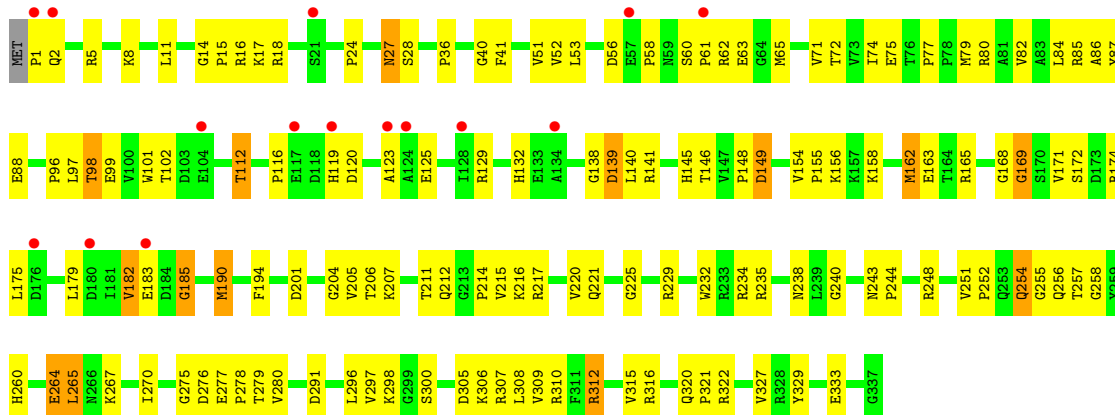
• Molecule 4: 50S ribosomal protein L2P

Chain A:



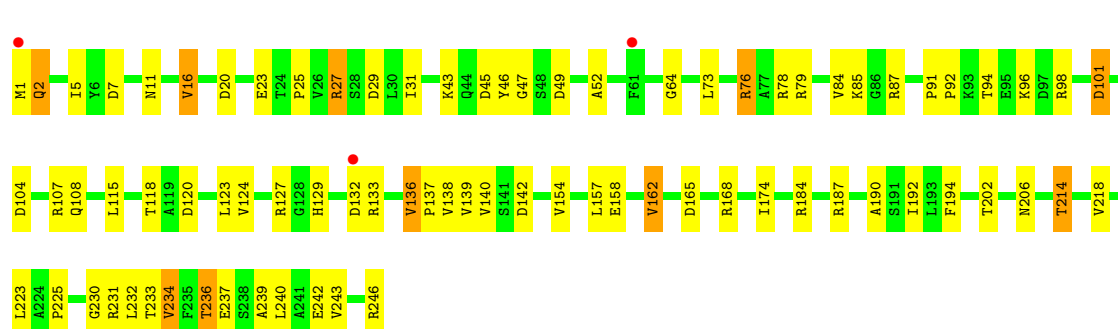
• Molecule 5: 50S ribosomal protein L3P

Chain B:



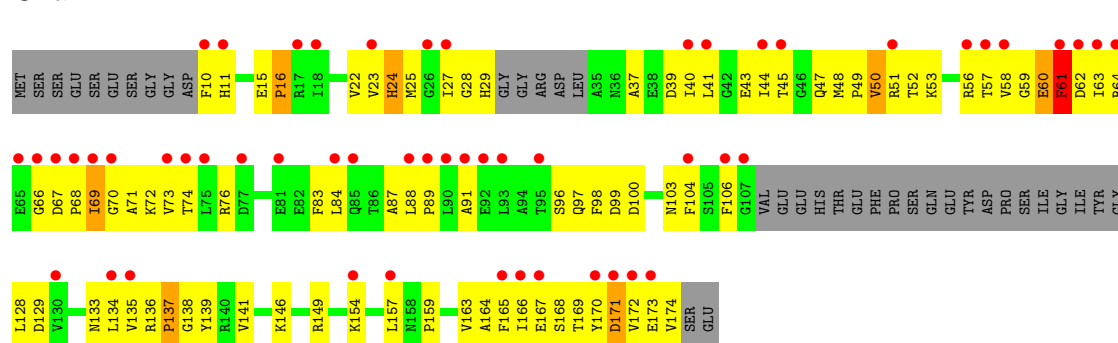
• Molecule 6: 50S ribosomal protein L4E

Chain C:



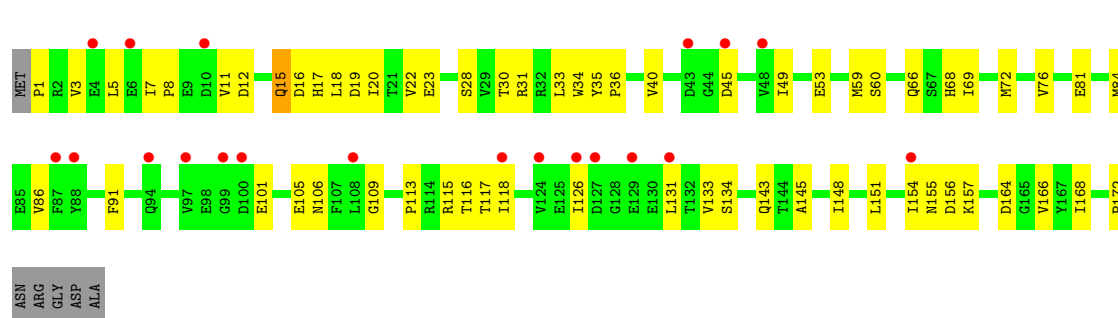
- Molecule 7: 50S ribosomal protein L5P

Chain D:



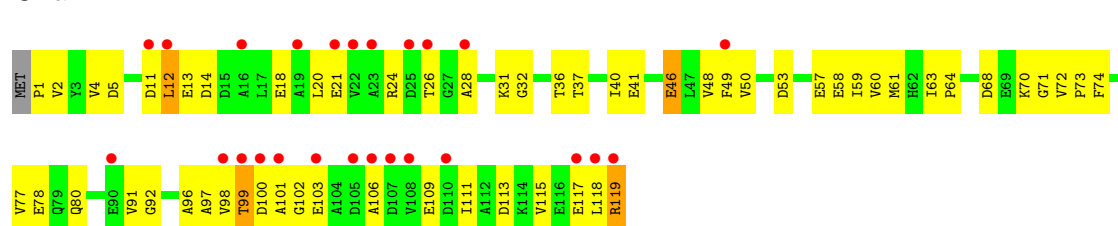
- Molecule 8: 50S ribosomal protein L6P

Chain E:



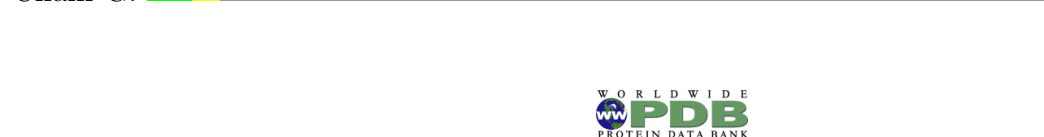
- Molecule 9: 50S ribosomal protein L7AE

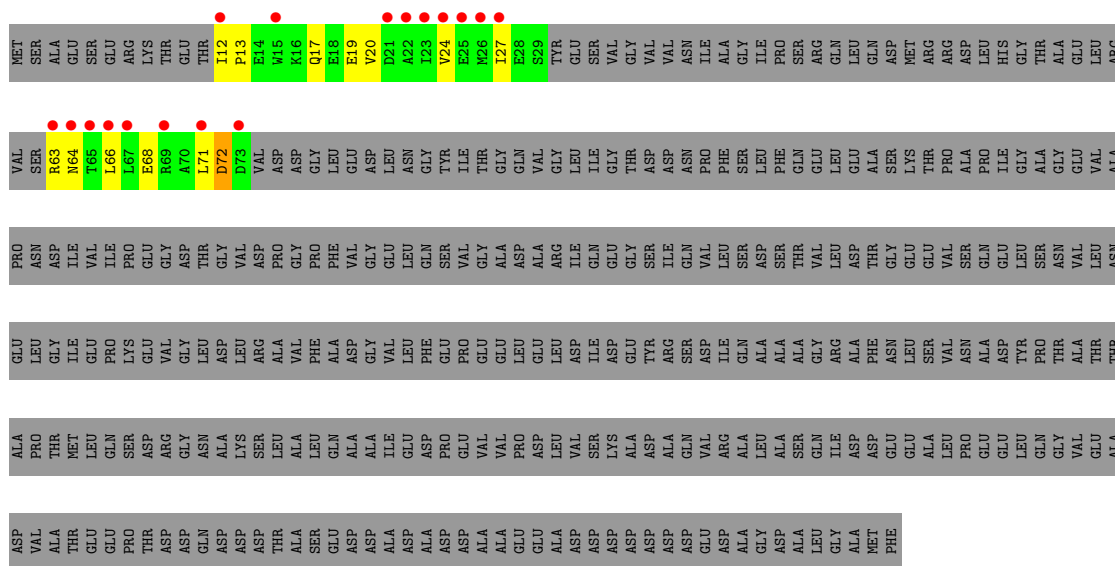
Chain F:



- Molecule 10: ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG

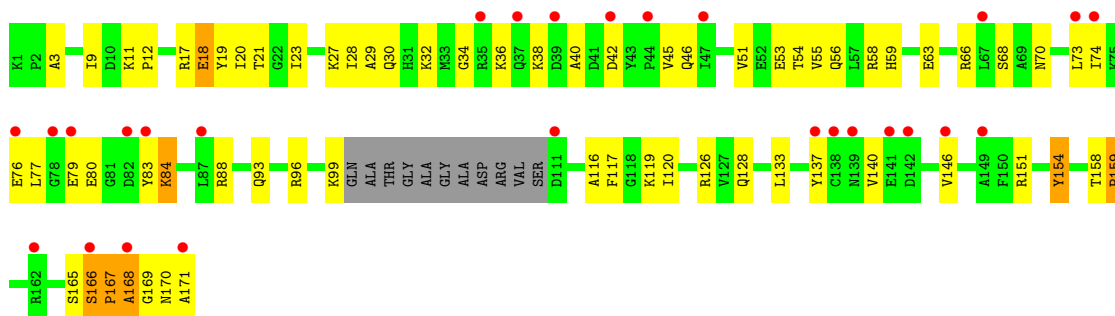
Chain G:





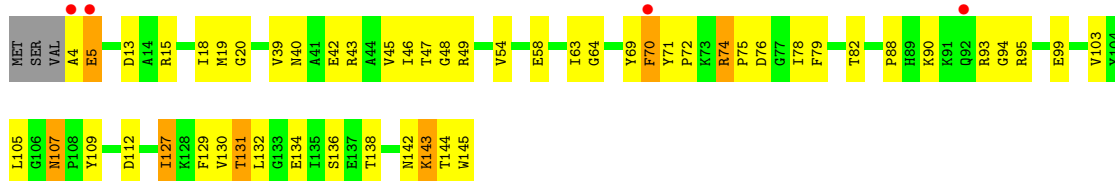
- Molecule 11: 50S RIBOSOMAL PROTEIN L10E

Chain H:



- Molecule 12: 50S ribosomal protein L13P

Chain J:



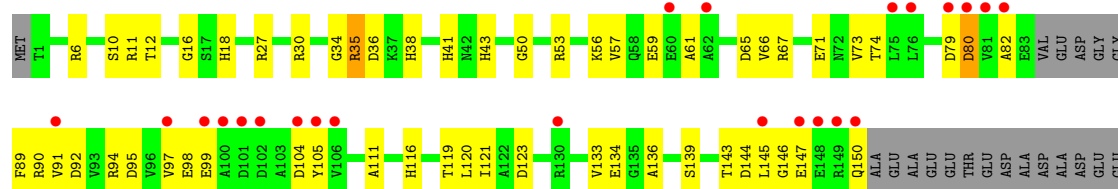
- Molecule 13: 50S ribosomal protein L14P

Chain K:



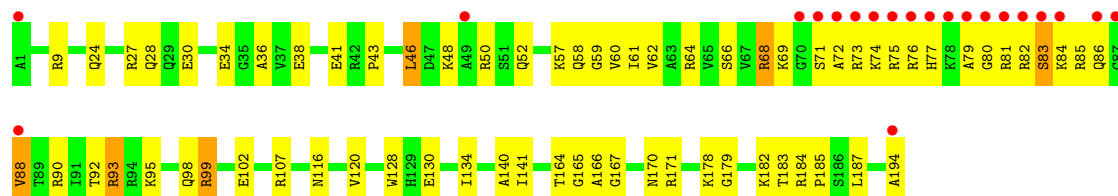
- Molecule 14: 50S ribosomal protein L15P

Chain L: 



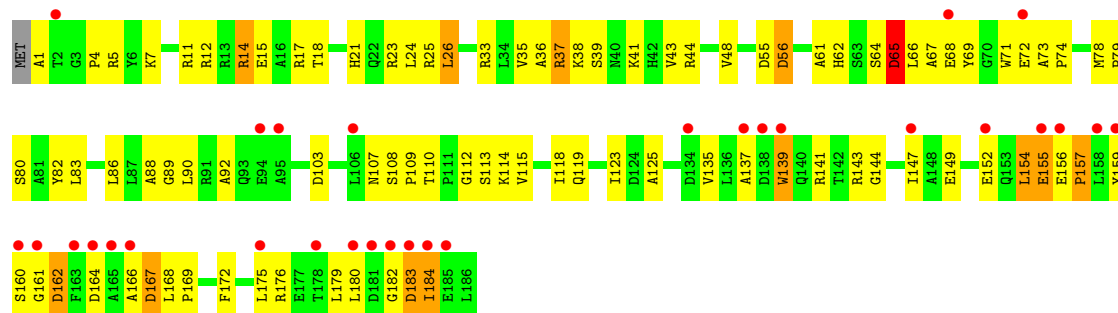
- Molecule 15: 50S Ribosomal Protein L15E

Chain M: 



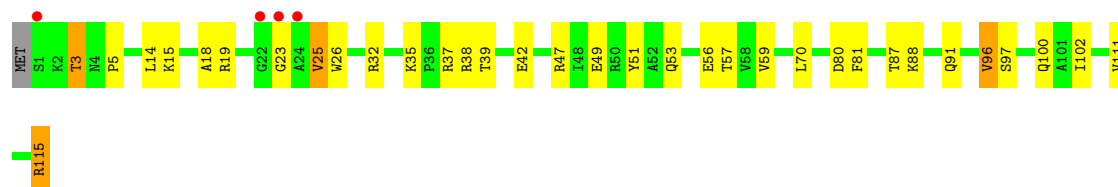
- Molecule 16: 50S ribosomal protein L18P

Chain N: 



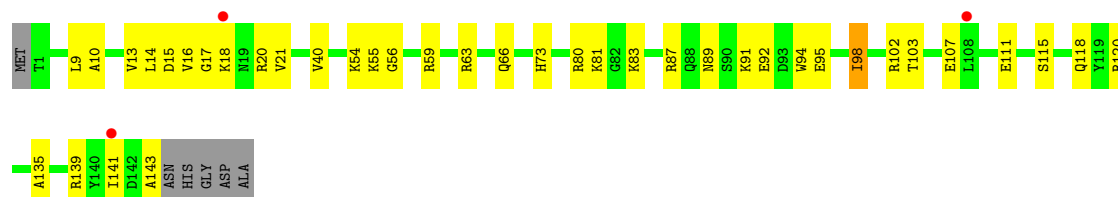
- Molecule 17: 50S ribosomal protein L18e

Chain O: 



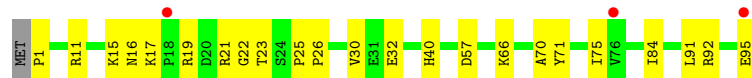
- Molecule 18: 50S ribosomal protein L19E

Chain P: 



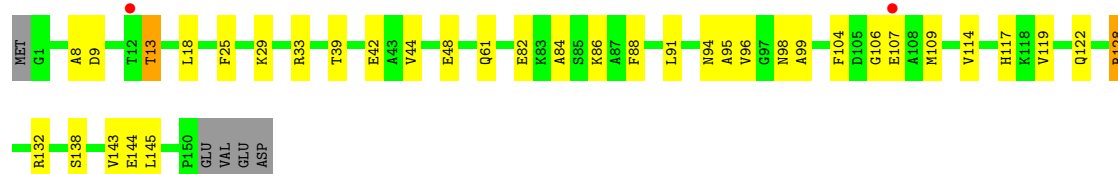
- Molecule 19: 50S ribosomal protein L21e

Chain Q: 



- Molecule 20: 50S ribosomal protein L22P

Chain R: 



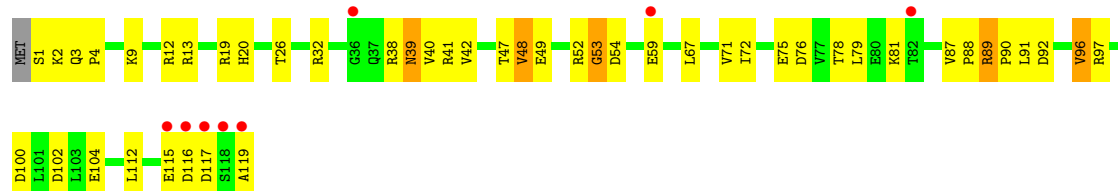
- Molecule 21: 50S ribosomal protein L23P

Chain S: 



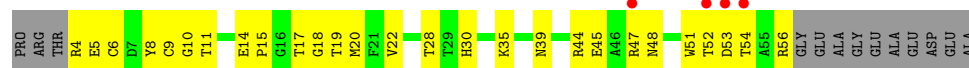
- Molecule 22: 50S ribosomal protein L24P

Chain T: 



- Molecule 23: 50S ribosomal protein L24E

Chain U: 



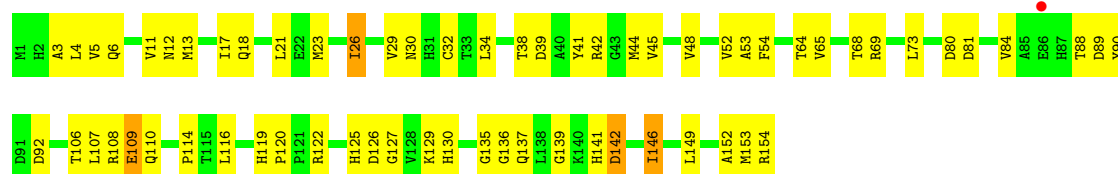
- Molecule 24: 50S ribosomal protein L29P

Chain V: 



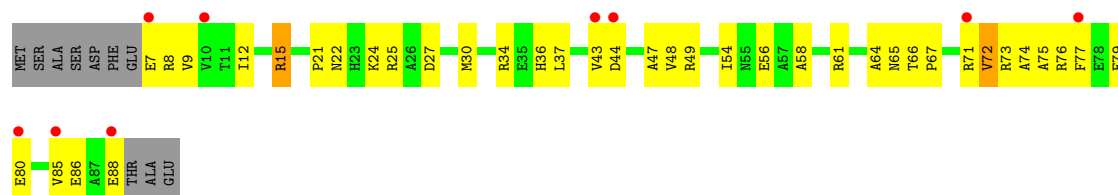
- Molecule 25: 50S ribosomal protein L30P

Chain W: 



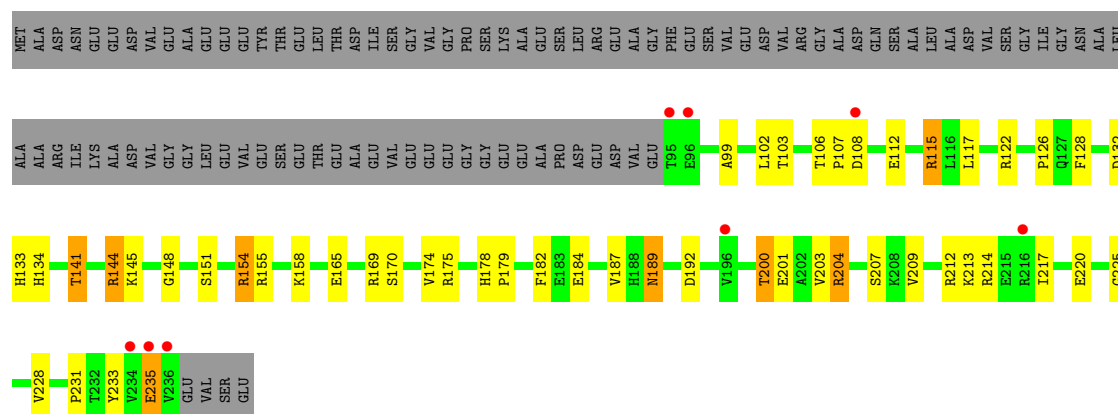
- Molecule 26: 50S ribosomal protein L31e

Chain X:



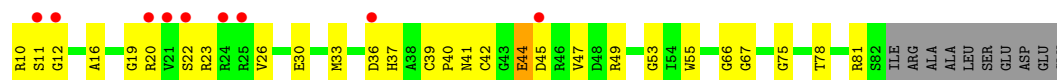
- Molecule 27: 50S ribosomal protein L32E

Chain Y:



- Molecule 28: 50S ribosomal protein L37Ae

Chain Z:



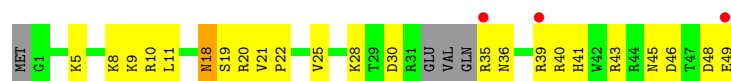
- Molecule 29: 50S ribosomal protein L37e

Chain 1:

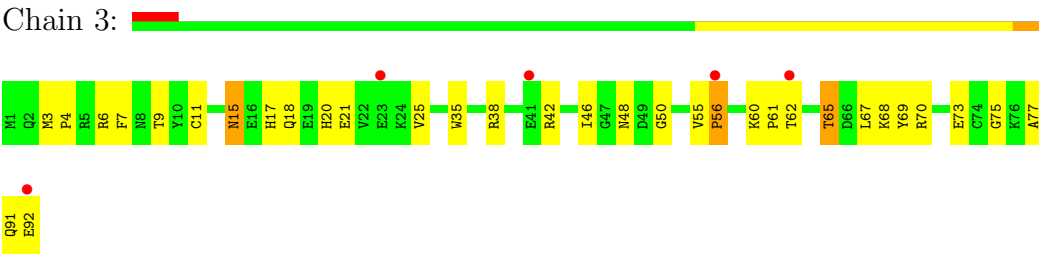


- Molecule 30: 50S ribosomal protein L39e

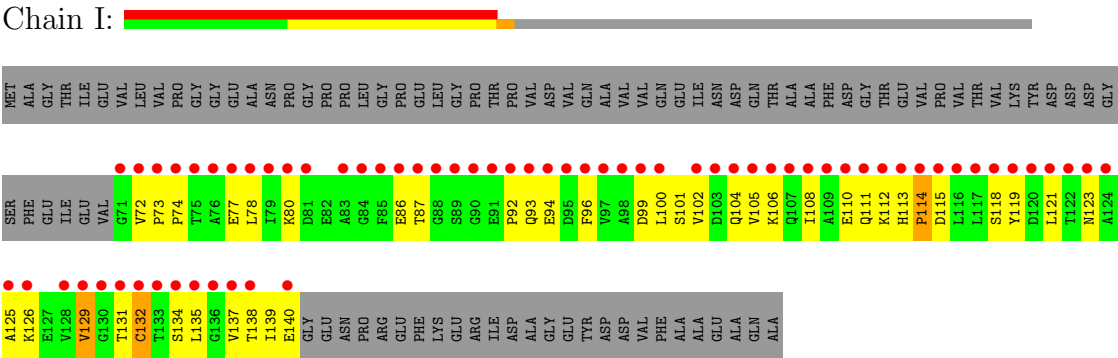
Chain 2:



● Molecule 31: 50S ribosomal protein L44E



● Molecule 32: 50S RIBOSOMAL PROTEIN L11P



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	211.52Å 298.48Å 574.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 49.75 – 2.20	Depositor EDS
% Data completeness (in resolution range)	90.1 (50.00-2.20) 90.0 (49.75-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.220 , 0.247 0.217 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 903877 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	99035	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ACA, OMG, CL, SR, NA, K, SPS, MG, 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	0	0.39	0/65959	0.70	26/102870 (0.0%)
2	9	0.36	0/2905	0.72	1/4528 (0.0%)
3	4	0.54	0/75	0.62	0/110
4	A	0.34	0/1786	0.67	0/2408
5	B	0.34	0/2690	0.66	0/3652
6	C	0.37	0/1884	0.65	0/2551
7	D	0.31	0/1111	0.56	0/1498
8	E	0.34	0/1382	0.58	0/1880
9	F	0.34	0/901	0.56	0/1224
10	G	0.29	0/241	0.46	0/324
11	H	0.34	0/1287	0.64	0/1725
12	J	0.35	0/1136	0.60	0/1530
13	K	0.35	0/1001	0.67	0/1347
14	L	0.34	0/1130	0.67	0/1509
15	M	0.34	0/1584	0.62	0/2119
16	N	0.29	0/1474	0.61	0/1999
17	O	0.33	0/874	0.60	0/1181
18	P	0.34	0/1147	0.57	0/1528
19	Q	0.35	0/749	0.70	1/1005 (0.1%)
20	R	0.36	0/1172	0.67	1/1578 (0.1%)
21	S	0.33	0/648	0.58	0/875
22	T	0.31	0/958	0.61	0/1289
23	U	0.34	0/417	0.56	0/562
24	V	0.28	0/502	0.54	0/675
25	W	0.34	0/1219	0.61	0/1655
26	X	0.33	0/664	0.58	0/895
27	Y	0.35	0/1146	0.65	0/1536
28	Z	0.36	0/589	0.64	0/787
29	1	0.42	0/438	0.66	0/578
30	2	0.35	0/401	0.63	0/529
31	3	0.37	0/771	0.59	0/1024
32	I	0.31	0/526	0.54	0/716

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.37	0/98767	0.68	29/147687 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	1	51
2	9	0	2
All	All	1	53

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1563	G	C2'-C3'-O3'	9.87	131.21	109.50
1	0	871	G	C5'-C4'-O4'	-7.88	99.64	109.10
1	0	1942	A	C5'-C4'-C3'	7.22	127.56	116.00
1	0	1979	G	C2'-C3'-O3'	6.97	124.85	113.70
1	0	1819	G	C5'-C4'-C3'	6.93	127.09	116.00
2	9	3039	U	N1-C1'-C2'	6.83	122.89	114.00
1	0	1592	G	N9-C1'-C2'	6.57	122.54	114.00
1	0	1504	A	C1'-O4'-C4'	-6.28	104.88	109.90
1	0	1819	G	C1'-O4'-C4'	-6.23	104.92	109.90
1	0	777	U	O4'-C1'-N1	6.21	113.17	108.20
1	0	2313	C	C5'-C4'-O4'	5.93	116.21	109.10
1	0	1819	G	C4'-C3'-C2'	-5.71	96.89	102.60
1	0	2467	A	C1'-O4'-C4'	-5.63	105.39	109.90
1	0	2291	A	N9-C1'-C2'	5.63	121.32	114.00
1	0	1352	A	N9-C1'-C2'	5.37	120.98	114.00
1	0	2726	U	N1-C1'-C2'	5.37	120.98	114.00
1	0	1615	A	C5'-C4'-C3'	5.35	124.56	116.00
1	0	129	A	C2'-C3'-O3'	5.31	122.19	113.70
20	R	128	ARG	NE-CZ-NH2	-5.29	117.66	120.30
19	Q	17	LYS	N-CA-C	-5.26	96.81	111.00
1	0	1559	A	C2'-C3'-O3'	5.26	122.11	113.70
1	0	1352	A	OP1-P-O3'	5.24	116.73	105.20
1	0	1504	A	N9-C1'-C2'	5.24	120.81	114.00
1	0	1352	A	C2'-C3'-O3'	5.22	122.06	113.70
1	0	1942	A	C1'-O4'-C4'	-5.22	105.72	109.90
1	0	1452	G	C5'-C4'-C3'	-5.18	107.71	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	921	G	N9-C1'-C2'	5.18	120.73	114.00
1	0	1504	A	O4'-C4'-C3'	-5.02	98.98	104.00
1	0	2664	A	N9-C1'-C2'	5.02	120.53	114.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	0	1563	G	C3'

All (53) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1078	A	Sidechain
1	0	1080	C	Sidechain
1	0	1132	A	Sidechain
1	0	1327	G	Sidechain
1	0	1340	G	Sidechain
1	0	1430	G	Sidechain
1	0	1592	G	Sidechain
1	0	1744	G	Sidechain
1	0	1777	G	Sidechain
1	0	1809	G	Sidechain
1	0	1819	G	Sidechain
1	0	182	G	Sidechain
1	0	1829	A	Sidechain
1	0	1845	A	Sidechain
1	0	1863	G	Sidechain
1	0	1867	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	1970	G	Sidechain
1	0	2036	C	Sidechain
1	0	2115	U	Sidechain
1	0	2316	G	Sidechain
1	0	24	G	Sidechain
1	0	2465	A	Sidechain
1	0	2493	C	Sidechain
1	0	2503	A	Sidechain
1	0	2506	A	Sidechain
1	0	2552	C	Sidechain
1	0	2564	G	Sidechain
1	0	2616	G	Sidechain

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Mol	Chain	Res	Type	Group
1	0	2630	G	Sidechain
1	0	2664	A	Sidechain
1	0	270	U	Sidechain
1	0	2793	A	Sidechain
1	0	2811	A	Sidechain
1	0	2842	G	Sidechain
1	0	396	U	Sidechain
1	0	458	G	Sidechain
1	0	462	A	Sidechain
1	0	469	G	Sidechain
1	0	470	U	Sidechain
1	0	471	G	Sidechain
1	0	482	G	Sidechain
1	0	518	G	Sidechain
1	0	619	U	Sidechain
1	0	722	G	Sidechain
1	0	795	G	Sidechain
1	0	817	G	Sidechain
1	0	868	G	Sidechain
1	0	888	U	Sidechain
1	0	952	G	Sidechain
2	9	3039	U	Sidechain
2	9	3065	A	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	0	59021	0	29811	707	0
2	9	2600	0	1326	58	0
3	4	73	0	44	2	0
4	A	1753	0	1766	110	0
5	B	2625	0	2532	139	0
6	C	1859	0	1816	86	0
7	D	1094	0	1085	83	0
8	E	1357	0	1266	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	F	890	0	843	55	0
10	G	240	0	231	12	0
11	H	1266	0	1268	63	0
12	J	1120	0	1098	62	0
13	K	992	0	1031	57	0
14	L	1118	0	1076	61	0
15	M	1560	0	1567	73	0
16	N	1445	0	1401	96	0
17	O	865	0	873	39	0
18	P	1136	0	1123	38	0
19	Q	735	0	729	19	0
20	R	1149	0	1122	39	0
21	S	641	0	605	20	0
22	T	950	0	923	56	0
23	U	410	0	364	31	0
24	V	499	0	511	43	0
25	W	1196	0	1137	77	0
26	X	654	0	653	39	0
27	Y	1130	0	1133	56	0
28	Z	578	0	539	24	0
29	1	431	0	426	21	0
30	2	396	0	413	26	0
31	3	755	0	728	33	0
32	I	519	0	500	45	0
33	0	88	0	0	0	0
33	4	1	0	0	0	0
33	9	1	0	0	0	0
33	A	1	0	0	0	0
33	K	1	0	0	0	0
33	T	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	2	0	0	0	0
35	0	65	0	0	0	0
35	9	1	0	0	0	0
35	B	1	0	0	0	0
35	C	1	0	0	0	0
35	D	1	0	0	0	0
35	J	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	2	0	0	0	0
35	S	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	0	10	0	0	0	0
36	3	1	0	0	0	0
36	A	1	0	0	0	0
36	B	1	0	0	0	0
36	J	3	0	0	1	0
36	L	1	0	0	0	0
36	M	1	0	0	0	0
36	N	1	0	0	0	0
36	O	1	0	0	0	0
36	R	1	0	0	0	0
36	Y	1	0	0	0	0
37	0	98	0	0	0	0
37	1	2	0	0	0	0
37	3	1	0	0	0	0
37	9	3	0	0	0	0
37	A	3	0	0	0	0
37	B	2	0	0	0	0
37	F	1	0	0	0	0
37	H	1	0	0	0	0
37	L	1	0	0	0	0
37	R	1	0	0	0	0
37	S	1	0	0	0	0
38	4	23	0	19	4	0
39	1	1	0	0	0	0
39	3	1	0	0	0	0
39	O	1	0	0	0	0
39	U	1	0	0	0	0
39	Z	1	0	0	0	0
40	0	5743	0	0	113	0
40	1	50	0	0	1	0
40	2	35	0	0	3	0
40	3	76	0	0	5	0
40	4	2	0	0	1	0
40	9	136	0	0	4	0
40	A	120	0	0	11	0
40	B	135	0	0	23	0
40	C	172	0	0	14	0
40	D	48	0	0	5	0
40	E	42	0	0	1	0
40	F	27	0	0	4	0
40	G	16	0	0	1	0
40	H	71	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	I	10	0	0	0	0
40	J	51	0	0	4	0
40	K	58	0	0	5	0
40	L	87	0	0	10	0
40	M	127	0	0	6	0
40	N	59	0	0	8	0
40	O	41	0	0	6	0
40	P	64	0	0	1	0
40	Q	58	0	0	2	0
40	R	85	0	0	4	0
40	S	30	0	0	1	0
40	T	36	0	0	4	0
40	U	28	0	0	2	0
40	V	15	0	0	1	0
40	W	68	0	0	4	0
40	X	23	0	0	4	0
40	Y	95	0	0	9	0
40	Z	35	0	0	2	0
All	All	99035	0	59959	2109	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 14.

All (2109) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:V:12:THR:HG22	24:V:15:GLU:HG3	1.28	1.10
26:X:37:LEU:HD13	26:X:85:VAL:HG21	1.31	1.10
6:C:236:THR:HG22	6:C:239:ALA:H	1.10	1.09
25:W:21:LEU:HD21	25:W:48:VAL:HG11	1.28	1.08
22:T:71:VAL:HG11	22:T:90:PRO:HB3	1.36	1.06
25:W:6:GLN:HB2	25:W:26:ILE:HD11	1.37	1.06
13:K:29:LEU:HB3	13:K:55:VAL:HG11	1.39	1.04
5:B:264:GLU:HG2	5:B:267:LYS:HE2	1.41	1.00
1:O:156:C:H5''	15:M:171:ARG:HD3	1.44	1.00
2:9:3076:G:H3'	2:9:3077:A:H5''	1.42	0.99
5:B:162:MET:HE2	5:B:310:ARG:HD3	1.44	0.98
1:O:289:G:H22	1:O:363:A:H2	1.04	0.98
1:O:1160:G:H5'	1:O:1161:A:H5'	1.47	0.97
25:W:4:LEU:HD22	25:W:52:VAL:HG21	1.47	0.97
25:W:137:GLN:HE21	25:W:141:HIS:HE1	1.11	0.95
5:B:86:ALA:HA	40:B:9578:HOH:O	1.66	0.95
13:K:74:VAL:HG11	13:K:113:ILE:HG12	1.47	0.94

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:B:238:ASN:HD22	5:B:240:GLY:H	1.10	0.94
5:B:307:ARG:HH11	5:B:307:ARG:HG3	1.31	0.94
7:D:58:VAL:HB	7:D:62:ASP:HB3	1.49	0.93
9:F:91:VAL:HG12	9:F:92:GLY:H	1.34	0.93
18:P:115:SER:H	18:P:118:GLN:HE21	1.11	0.93
22:T:9:LYS:HE3	22:T:13:ARG:NH1	1.82	0.93
15:M:99:ARG:HH21	15:M:170:ASN:HD22	1.10	0.93
13:K:10:GLN:H	13:K:10:GLN:NE2	1.64	0.93
1:0:1242:A:H5'	12:J:82:THR:HG23	1.50	0.93
21:S:51:GLN:HE21	21:S:53:ASN:HD21	1.09	0.93
1:0:1701:A:H4'	1:0:1702:U:H5''	1.50	0.92
5:B:140:LEU:HA	40:B:9578:HOH:O	1.71	0.91
1:0:656:G:H5'	17:O:3:THR:HG22	1.53	0.90
1:0:1166:A:H61	1:0:1180:U:H3	1.18	0.90
13:K:10:GLN:N	13:K:10:GLN:HE21	1.69	0.89
16:N:113:SER:HB2	40:N:9354:HOH:O	1.73	0.89
25:W:6:GLN:HB2	25:W:26:ILE:CD1	2.02	0.89
25:W:21:LEU:HD22	25:W:26:ILE:HD13	1.52	0.89
4:A:153:ARG:HH11	4:A:153:ARG:HB2	1.38	0.88
1:0:871:G:C8	1:0:871:G:H5'	2.09	0.88
9:F:46:GLU:OE1	9:F:100:ASP:HA	1.71	0.88
1:0:1372:A:H3'	40:0:7650:HOH:O	1.73	0.88
1:0:2840:A:OP1	5:B:211:THR:HG23	1.73	0.88
13:K:81:ARG:HB2	13:K:87:ARG:HH11	1.38	0.88
20:R:8:ALA:HB1	20:R:13:THR:HG21	1.55	0.88
1:0:542:A:H5'	1:0:542:A:H8	1.39	0.87
1:0:1474:C:H6	1:0:1474:C:H5'	1.39	0.87
5:B:36:PRO:HA	5:B:168:GLY:HA3	1.56	0.87
6:C:127:ARG:NH2	6:C:225:PRO:HG2	1.89	0.87
29:1:25:LYS:HD2	30:2:49:GLU:H	1.40	0.87
13:K:10:GLN:H	13:K:10:GLN:HE21	0.87	0.86
13:K:107:THR:HG22	13:K:108:GLU:HG3	1.54	0.86
13:K:39:GLY:HA2	40:K:4183:HOH:O	1.74	0.86
1:0:2812:A:H2	1:0:2814:A:H62	1.17	0.86
1:0:288:A:H61	1:0:364:C:H42	1.19	0.86
2:9:3056:A:H2'	2:9:3057:A:H5''	1.56	0.86
13:K:4:LEU:HD22	13:K:116:GLU:HB3	1.57	0.86
1:0:1973:A:H5'	1:0:1973:A:H8	1.41	0.86
12:J:93:ARG:HH11	12:J:93:ARG:HB3	1.37	0.85
7:D:28:GLY:HA2	7:D:69:ILE:HG23	1.59	0.85
1:0:541:C:H2'	1:0:542:A:H5''	1.59	0.85
1:0:1206:U:H6	1:0:1206:U:H5'	1.40	0.85

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2586:U:H3	1:0:2592:G:H22	1.26	0.84
8:E:20:ILE:HD11	8:E:40:VAL:HG11	1.59	0.84
6:C:236:THR:HG22	6:C:239:ALA:N	1.92	0.84
1:0:2506:A:O2'	1:0:2507:G:H8	1.61	0.83
20:R:25:PHE:CE2	20:R:29:LYS:HE2	2.11	0.83
1:0:2748:G:H5'	40:0:7982:HOH:O	1.77	0.83
1:0:2506:A:HO2'	1:0:2507:G:H8	0.85	0.83
8:E:36:PRO:HD3	12:J:127:ILE:HD12	1.60	0.83
1:0:1835:U:H5	1:0:1840:A:N7	1.77	0.83
1:0:1603:A:H5'	1:0:1605:G:O4'	1.77	0.83
4:A:211:LYS:HG2	4:A:212:PRO:HD2	1.59	0.83
4:A:192:VAL:HB	40:A:9579:HOH:O	1.78	0.82
6:C:236:THR:CG2	6:C:239:ALA:H	1.91	0.82
1:0:2534:C:H1'	40:0:4078:HOH:O	1.80	0.82
13:K:81:ARG:HB2	13:K:87:ARG:NH1	1.94	0.82
16:N:144:GLY:O	16:N:147:ILE:HG22	1.80	0.81
16:N:7:LYS:HE3	19:Q:21:ARG:O	1.80	0.81
1:0:2054:A:N3	20:R:128:ARG:NH2	2.29	0.81
1:0:1041:U:H5'	40:L:9495:HOH:O	1.80	0.81
7:D:136:ARG:HH12	7:D:157:LEU:HA	1.43	0.81
25:W:88:THR:HB	40:W:6679:HOH:O	1.79	0.81
1:0:1116:U:O2'	1:0:1118:A:H2	1.64	0.81
13:K:14:LYS:HB2	13:K:45:PRO:HG2	1.63	0.81
15:M:107:ARG:HH11	15:M:107:ARG:HG3	1.44	0.81
6:C:1:MET:HG2	6:C:2:GLN:H	1.45	0.80
40:0:5382:HOH:O	12:J:47:THR:HB	1.81	0.80
5:B:212:GLN:HB2	5:B:257:THR:HG21	1.63	0.80
1:0:2717:C:C2'	1:0:2718:C:H5''	2.12	0.80
27:Y:200:THR:HG22	27:Y:201:GLU:HG3	1.62	0.80
1:0:541:C:C2'	1:0:542:A:H5''	2.12	0.80
1:0:545:G:H8	1:0:545:G:H5'	1.45	0.80
15:M:80:GLY:O	15:M:81:ARG:HD2	1.81	0.79
27:Y:235:GLU:H	27:Y:235:GLU:CD	1.85	0.79
22:T:71:VAL:HG11	22:T:90:PRO:CB	2.11	0.79
15:M:102:GLU:OE1	15:M:164:THR:HG21	1.82	0.79
5:B:162:MET:HE1	5:B:308:LEU:HD21	1.61	0.79
1:0:2780:C:H1'	8:E:143:GLN:HE21	1.48	0.79
18:P:115:SER:H	18:P:118:GLN:NE2	1.80	0.79
1:0:111:C:O2'	29:1:20:ARG:HG2	1.82	0.79
25:W:137:GLN:HE21	25:W:141:HIS:CE1	2.00	0.79
6:C:139:VAL:HG13	40:C:9249:HOH:O	1.82	0.79
17:O:32:ARG:HE	17:O:35:LYS:HD2	1.46	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:9:3029:C:H2'	2:9:3030:C:H5'	1.65	0.79
4:A:192:VAL:HG22	40:A:9617:HOH:O	1.80	0.79
7:D:25:MET:HE2	7:D:41:LEU:HG	1.64	0.78
1:0:2003:U:H4'	1:0:2004:U:H5	1.49	0.78
13:K:74:VAL:HG13	13:K:113:ILE:HG23	1.62	0.78
5:B:162:MET:CE	5:B:310:ARG:HD3	2.12	0.78
1:0:1878:G:H1'	40:0:6629:HOH:O	1.82	0.78
1:0:870:G:H2'	1:0:871:G:H5''	1.65	0.78
6:C:5:ILE:HD11	6:C:16:VAL:CG2	2.13	0.78
1:0:93:C:H5''	24:V:1:THR:HB	1.65	0.78
11:H:27:LYS:H	11:H:59:HIS:HD2	1.32	0.77
15:M:134:ILE:HG23	15:M:141:ILE:HD13	1.66	0.77
7:D:172:VAL:HG12	7:D:173:GLU:H	1.49	0.77
12:J:19:MET:HE3	12:J:132:LEU:HD21	1.66	0.77
25:W:125:HIS:HD2	25:W:127:GLY:H	1.32	0.77
1:0:2541:U:H4'	40:0:5938:HOH:O	1.83	0.77
1:0:871:G:C8	1:0:871:G:C5'	2.68	0.77
1:0:797:A:H5'	28:Z:10:ARG:N	1.99	0.77
4:A:192:VAL:CG1	4:A:207:GLN:HB3	2.15	0.77
6:C:27:ARG:HG3	6:C:29:ASP:OD1	1.85	0.77
6:C:47:GLY:HA2	6:C:92:PRO:HB2	1.67	0.76
1:0:871:G:H8	1:0:871:G:C5'	1.96	0.76
4:A:192:VAL:HG12	4:A:207:GLN:HB3	1.67	0.76
27:Y:154:ARG:HH12	27:Y:155:ARG:HG2	1.49	0.76
11:H:21:THR:O	11:H:120:ILE:HD12	1.85	0.76
1:0:796:A:HO2'	28:Z:10:ARG:N	1.83	0.76
32:I:99:ASP:OD1	32:I:138:THR:HB	1.84	0.76
4:A:35:GLY:O	4:A:36:ASP:HB3	1.84	0.76
27:Y:151:SER:O	27:Y:155:ARG:HG3	1.86	0.76
22:T:49:GLU:HB3	22:T:59:GLU:HG2	1.68	0.76
16:N:83:LEU:HD13	16:N:175:LEU:HD23	1.67	0.76
1:0:1377:C:H6	1:0:1377:C:H5'	1.50	0.76
1:0:289:G:N2	1:0:363:A:H2	1.83	0.76
18:P:115:SER:OG	18:P:118:GLN:HG3	1.85	0.76
6:C:5:ILE:HD11	6:C:16:VAL:HG22	1.68	0.76
1:0:2851:G:C2'	1:0:2852:A:H5'	2.15	0.76
1:0:481:U:H5''	40:0:6177:HOH:O	1.85	0.75
9:F:50:VAL:HG13	9:F:60:VAL:HG11	1.68	0.75
22:T:41:ARG:HG2	22:T:41:ARG:HH11	1.50	0.75
25:W:88:THR:HG23	25:W:110:GLN:NE2	2.01	0.75
12:J:75:PRO:HG2	12:J:105:LEU:HD21	1.67	0.75
18:P:91:LYS:O	18:P:95:GLU:HG3	1.86	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:M:99:ARG:NH2	15:M:170:ASN:HD22	1.83	0.75
1:0:2890:A:H1'	23:U:56:ARG:NH2	2.02	0.74
13:K:29:LEU:HB3	13:K:55:VAL:CG1	2.17	0.74
40:9:4707:HOH:O	16:N:147:ILE:HD12	1.87	0.74
16:N:11:ARG:HG3	16:N:14:ARG:HH12	1.51	0.74
5:B:190:MET:HE2	5:B:194:PHE:HD1	1.52	0.74
24:V:12:THR:HG22	24:V:15:GLU:CG	2.13	0.74
4:A:191:GLY:HA2	4:A:194:MET:HE2	1.69	0.74
13:K:74:VAL:CG1	13:K:113:ILE:HG12	2.15	0.74
4:A:153:ARG:NH1	4:A:153:ARG:HB2	2.01	0.74
4:A:191:GLY:HA2	4:A:194:MET:CE	2.18	0.74
1:0:1667:A:H8	1:0:1667:A:H5'	1.52	0.74
1:0:506:G:H22	1:0:509:A:C5'	2.01	0.74
1:0:2717:C:H2'	1:0:2718:C:H5''	1.69	0.74
16:N:11:ARG:HG3	16:N:14:ARG:NH1	2.03	0.74
1:0:1751:G:H2'	1:0:1752:G:H5''	1.69	0.74
31:3:6:ARG:NH1	31:3:21:GLU:HG3	2.02	0.74
25:W:21:LEU:CD2	25:W:48:VAL:HG11	2.13	0.74
6:C:2:GLN:HB3	40:C:9189:HOH:O	1.86	0.74
7:D:154:LYS:HD2	7:D:154:LYS:H	1.52	0.74
1:0:1160:G:C5'	1:0:1161:A:H5'	2.18	0.74
9:F:91:VAL:HG12	9:F:92:GLY:N	2.01	0.74
9:F:96:ALA:HA	40:F:3111:HOH:O	1.88	0.74
1:0:1119:G:N2	1:0:1246:A:C2	2.55	0.73
26:X:54:ILE:HD11	26:X:85:VAL:HG12	1.69	0.73
13:K:81:ARG:HD3	13:K:87:ARG:NH1	2.03	0.73
32:I:102:VAL:HG12	32:I:106:LYS:HE3	1.68	0.73
1:0:280:C:H2'	1:0:281:U:O4'	1.89	0.73
1:0:1118:A:H62	1:0:1244:U:H3	1.36	0.73
1:0:544:G:H2'	1:0:545:G:H5''	1.70	0.73
20:R:18:LEU:HD12	20:R:143:VAL:HG11	1.69	0.73
40:0:9966:HOH:O	29:1:1:THR:HA	1.88	0.73
1:0:871:G:H8	1:0:871:G:H5'	1.52	0.73
1:0:1205:U:H2'	1:0:1206:U:H5''	1.71	0.73
13:K:32:ILE:HD11	13:K:56:SER:HB3	1.70	0.73
4:A:51:ARG:HB2	40:A:9592:HOH:O	1.89	0.72
28:Z:11:SER:HB3	28:Z:23:ARG:HB2	1.71	0.72
1:0:1206:U:H2'	1:0:1207:A:O4'	1.89	0.72
4:A:199:HIS:HD2	4:A:201:PHE:H	1.38	0.72
6:C:78:ARG:HG3	6:C:78:ARG:HH11	1.54	0.72
14:L:73:VAL:HG23	14:L:74:THR:H	1.55	0.72
1:0:1116:U:HO2'	1:0:1118:A:H2	0.80	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:69:LEU:HD23	4:A:107:ASN:HB2	1.70	0.72
12:J:74:ARG:NH1	12:J:76:ASP:HB2	2.04	0.72
32:I:74:PRO:HG2	32:I:77:GLU:OE1	1.89	0.72
4:A:48:ASP:HB3	40:A:9592:HOH:O	1.90	0.72
10:G:12:ILE:N	10:G:13:PRO:HD3	2.04	0.72
24:V:20:LEU:HD22	24:V:60:GLN:HE22	1.55	0.72
31:3:38:ARG:HB3	31:3:42:ARG:HH12	1.55	0.71
1:0:2644:C:H2'	40:0:7574:HOH:O	1.90	0.71
1:0:1175:G:H1'	1:0:1193:A:H2'	1.70	0.71
25:W:4:LEU:HD23	25:W:54:PHE:HB3	1.72	0.71
30:2:41:HIS:H	30:2:45:ASN:HD22	1.37	0.71
11:H:46:GLN:HB3	11:H:167:PRO:HD2	1.72	0.71
17:O:32:ARG:HH21	17:O:35:LYS:HZ2	1.38	0.71
5:B:18:ARG:HG3	5:B:256:GLN:HG3	1.72	0.71
1:0:902:G:N7	14:L:18:HIS:HD2	1.88	0.71
7:D:135:VAL:HG21	7:D:139:TYR:CD1	2.26	0.71
1:0:2346:C:O2'	7:D:52:THR:HG21	1.89	0.71
40:0:7900:HOH:O	5:B:211:THR:HG21	1.91	0.71
12:J:74:ARG:HB3	12:J:74:ARG:HH11	1.55	0.71
1:0:2716:G:H5''	5:B:206:THR:HG21	1.73	0.71
7:D:58:VAL:HG12	7:D:60:GLU:HG2	1.71	0.71
1:0:1244:U:OP1	12:J:18:ILE:HD13	1.91	0.71
1:0:474:C:O3'	6:C:73:LEU:HD21	1.91	0.71
5:B:16:ARG:NH1	40:B:9610:HOH:O	2.23	0.71
16:N:80:SER:HB2	40:N:9332:HOH:O	1.91	0.71
11:H:154:TYR:HB2	40:H:9557:HOH:O	1.91	0.71
25:W:13:MET:CE	25:W:17:ILE:HG22	2.20	0.70
1:0:1700:C:H5''	1:0:1701:A:OP2	1.91	0.70
21:S:51:GLN:NE2	21:S:53:ASN:HD21	1.87	0.70
1:0:541:C:H2'	1:0:542:A:C5'	2.22	0.70
29:1:8:GLN:HE22	29:1:11:LYS:NZ	1.89	0.70
4:A:100:PRO:HG2	4:A:103:VAL:HG21	1.74	0.70
1:0:1189:A:H3'	40:0:8198:HOH:O	1.91	0.70
1:0:559:U:H5'	1:0:559:U:H6	1.55	0.70
2:9:3014:G:H8	2:9:3014:G:H5'	1.56	0.70
1:0:1118:A:H3'	1:0:1118:A:H8	1.56	0.70
26:X:37:LEU:CD1	26:X:85:VAL:HG21	2.15	0.70
1:0:1166:A:H1'	1:0:1192:A:C2	2.27	0.70
25:W:125:HIS:CD2	25:W:127:GLY:H	2.10	0.70
20:R:18:LEU:HB2	20:R:143:VAL:CG1	2.22	0.70
5:B:201:ASP:HB2	5:B:312:ARG:HD2	1.74	0.70
4:A:82:VAL:HG13	4:A:93:THR:HB	1.74	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:R:99:ALA:HB1	20:R:109:MET:HE1	1.71	0.70
25:W:52:VAL:HG22	25:W:53:ALA:H	1.56	0.69
1:0:1183:C:N4	1:0:1184:C:H41	1.89	0.69
1:0:1118:A:C8	1:0:1118:A:H3'	2.27	0.69
9:F:58:GLU:CD	15:M:27:ARG:HH22	1.94	0.69
1:0:1666:C:H2'	1:0:1667:A:H5'	1.73	0.69
5:B:51:VAL:CG2	5:B:327:VAL:HG13	2.23	0.69
13:K:109:LEU:HD13	13:K:113:ILE:HD11	1.74	0.69
1:0:381:G:H5''	40:M:9371:HOH:O	1.91	0.69
1:0:2468:A:H61	31:3:48:ASN:HD21	1.40	0.69
1:0:1116:U:H3	1:0:1246:A:H62	1.40	0.69
9:F:58:GLU:OE1	15:M:27:ARG:NH2	2.25	0.69
5:B:112:THR:HG23	5:B:158:LYS:NZ	2.07	0.69
15:M:164:THR:HG22	15:M:166:ALA:H	1.57	0.69
11:H:166:SER:HB3	11:H:167:PRO:HD3	1.74	0.69
27:Y:189:ASN:HA	27:Y:217:ILE:HD11	1.75	0.69
22:T:9:LYS:HE3	22:T:13:ARG:HH11	1.53	0.69
6:C:1:MET:HG2	6:C:2:GLN:N	2.08	0.69
20:R:18:LEU:HB2	20:R:143:VAL:HG12	1.74	0.69
22:T:115:GLU:HG3	22:T:116:ASP:N	2.08	0.69
21:S:51:GLN:HE21	21:S:53:ASN:ND2	1.87	0.69
28:Z:11:SER:CB	28:Z:23:ARG:HB2	2.23	0.68
18:P:80:ARG:HG2	18:P:87:ARG:CZ	2.23	0.68
1:0:1165:G:H1'	1:0:1174:A:H1'	1.74	0.68
5:B:264:GLU:HG2	5:B:267:LYS:CE	2.20	0.68
4:A:153:ARG:CB	4:A:153:ARG:HH11	2.06	0.68
24:V:1:THR:HG23	24:V:2:VAL:H	1.57	0.68
40:0:5995:HOH:O	10:G:12:ILE:HA	1.91	0.68
22:T:26:THR:HA	22:T:39:ASN:HB3	1.76	0.68
1:0:560:C:H42	1:0:597:A:H61	1.41	0.68
5:B:51:VAL:HG23	5:B:329:TYR:O	1.94	0.68
14:L:35:ARG:HB2	14:L:35:ARG:HH11	1.58	0.68
1:0:2807:U:P	5:B:27:ASN:HD21	2.16	0.68
15:M:164:THR:HG22	15:M:166:ALA:N	2.08	0.68
23:U:17:THR:HG22	23:U:18:GLY:N	2.08	0.68
24:V:12:THR:CG2	24:V:15:GLU:HG3	2.16	0.68
17:O:32:ARG:NE	17:O:35:LYS:HD2	2.08	0.68
1:0:506:G:H22	1:0:509:A:H5''	1.57	0.68
7:D:39:ASP:O	7:D:43:GLU:HG3	1.94	0.68
24:V:39:ALA:C	24:V:41:GLU:H	1.97	0.68
8:E:15:GLN:HG2	8:E:19:ASP:O	1.94	0.68
1:0:316:A:H5'	22:T:54:ASP:OD2	1.94	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1168:C:H5''	32:I:87:THR:HG23	1.74	0.68
25:W:149:LEU:HG	25:W:153:MET:HE2	1.76	0.68
16:N:48:VAL:CG1	16:N:55:ASP:HB3	2.24	0.68
32:I:78:LEU:HD12	32:I:112:LYS:NZ	2.09	0.68
5:B:125:GLU:O	5:B:129:ARG:HG3	1.94	0.68
24:V:43:PRO:O	24:V:46:ILE:HG22	1.94	0.67
16:N:154:LEU:HG	16:N:155:GLU:H	1.59	0.67
16:N:110:THR:HB	16:N:113:SER:OG	1.93	0.67
18:P:59:ARG:NH2	18:P:66:GLN:HE22	1.93	0.67
1:0:328:U:O4'	6:C:202:THR:HG22	1.93	0.67
15:M:187:LEU:CD2	15:M:194:ALA:HB3	2.24	0.67
1:0:87:C:H2'	30:2:28:LYS:O	1.94	0.67
6:C:132:ASP:HB3	40:C:9166:HOH:O	1.94	0.67
1:0:2005:G:H3'	1:0:2005:G:OP2	1.95	0.67
1:0:1730:G:H5'	1:0:1731:C:C5	2.29	0.67
1:0:1973:A:H5'	1:0:1973:A:C8	2.28	0.67
5:B:221:GLN:HE22	13:K:42:ASN:HD22	1.40	0.67
18:P:103:THR:O	18:P:107:GLU:HG3	1.93	0.67
26:X:30:MET:HE1	26:X:58:ALA:HB3	1.77	0.67
27:Y:187:VAL:HG23	27:Y:192:ASP:CB	2.25	0.67
1:0:2003:U:H4'	1:0:2004:U:C5	2.29	0.67
27:Y:187:VAL:HG23	27:Y:192:ASP:HB2	1.74	0.67
4:A:57:ALA:HB1	4:A:65:ARG:HE	1.59	0.67
1:0:2578:G:H5'	1:0:2578:G:H8	1.58	0.67
8:E:15:GLN:HG3	8:E:20:ILE:HG12	1.75	0.67
11:H:27:LYS:N	11:H:59:HIS:HD2	1.91	0.67
14:L:143:THR:HG22	14:L:144:ASP:N	2.10	0.67
23:U:52:THR:HG22	23:U:54:THR:N	2.10	0.67
1:0:962:C:H1'	16:N:5:ARG:NH1	2.10	0.67
16:N:164:ASP:CG	16:N:167:ASP:HA	2.15	0.67
7:D:25:MET:HE1	7:D:37:ALA:HB1	1.77	0.66
1:0:282:C:O2'	1:0:283:U:H5'	1.95	0.66
26:X:71:ARG:HB3	26:X:88:GLU:OE1	1.95	0.66
15:M:107:ARG:NH1	15:M:107:ARG:HG3	2.08	0.66
1:0:1165:G:H4'	1:0:1174:A:O2'	1.95	0.66
22:T:49:GLU:CB	22:T:59:GLU:HG2	2.25	0.66
1:0:1159:G:H21	1:0:1189:A:H8	1.42	0.66
1:0:2718:C:H6	1:0:2718:C:H5'	1.60	0.66
15:M:134:ILE:CG2	15:M:141:ILE:HD13	2.26	0.66
1:0:1201:C:H2'	1:0:1202:A:H5'	1.76	0.66
31:3:25:VAL:HG22	31:3:68:LYS:HG3	1.78	0.66
5:B:179:LEU:O	5:B:183:GLU:HG2	1.94	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:W:21:LEU:O	25:W:26:ILE:HG23	1.95	0.66
1:0:1701:A:H4'	1:0:1702:U:C5'	2.23	0.66
1:0:524:A:H5''	20:R:29:LYS:HD3	1.77	0.66
17:O:14:LEU:HG	17:O:102:ILE:HD11	1.76	0.66
1:0:447:A:P	22:T:1:SER:HB2	2.35	0.66
22:T:71:VAL:HG12	22:T:72:ILE:N	2.11	0.66
1:0:1838:U:O2'	1:0:2644:C:H5'	1.96	0.66
1:0:681:G:N3	1:0:681:G:H5'	2.11	0.66
13:K:49:LEU:HD12	13:K:80:ILE:HG21	1.77	0.66
1:0:1299:G:O6	14:L:6:ARG:HD3	1.96	0.66
1:0:2505:G:O2'	1:0:2506:A:H5'	1.96	0.66
5:B:254:GLN:HG2	5:B:255:GLY:N	2.10	0.66
15:M:183:THR:HG22	15:M:194:ALA:HB1	1.77	0.65
14:L:133:VAL:HA	40:L:9475:HOH:O	1.96	0.65
25:W:88:THR:HG22	25:W:89:ASP:N	2.11	0.65
28:Z:22:SER:O	28:Z:26:VAL:HG23	1.96	0.65
14:L:53:ARG:NH2	14:L:57:VAL:HG12	2.10	0.65
9:F:14:ASP:O	9:F:18:GLU:HG3	1.96	0.65
11:H:46:GLN:HE21	11:H:137:TYR:HE2	1.42	0.65
1:0:1187:U:HO2'	1:0:1189:A:H2	1.45	0.65
16:N:33:ARG:NH1	16:N:103:ASP:OD2	2.28	0.65
1:0:291:C:H2'	1:0:292:G:O4'	1.95	0.65
27:Y:144:ARG:CZ	40:Y:9411:HOH:O	2.44	0.65
32:I:132:CYS:HB3	32:I:137:VAL:HB	1.77	0.65
40:0:6989:HOH:O	27:Y:141:THR:HG23	1.97	0.65
4:A:211:LYS:CG	4:A:212:PRO:HD2	2.27	0.65
17:O:32:ARG:HD3	17:O:32:ARG:O	1.97	0.65
27:Y:144:ARG:HH11	27:Y:144:ARG:CG	2.10	0.65
25:W:108:ARG:HH21	25:W:114:PRO:HG2	1.61	0.65
1:0:2480:G:H3'	40:0:4750:HOH:O	1.96	0.65
1:0:2769:C:H2'	1:0:2770:G:O4'	1.97	0.65
4:A:199:HIS:CD2	4:A:201:PHE:H	2.15	0.64
1:0:1919:A:H4'	40:0:5395:HOH:O	1.97	0.64
1:0:544:G:C2'	1:0:545:G:H5''	2.26	0.64
1:0:470:U:O2'	29:1:16:HIS:HD2	1.79	0.64
25:W:80:ASP:O	25:W:84:VAL:HG23	1.97	0.64
12:J:75:PRO:HD3	12:J:136:SER:OG	1.96	0.64
1:0:2694:A:H4'	8:E:91:PHE:CE1	2.33	0.64
20:R:18:LEU:HD12	20:R:143:VAL:CG1	2.28	0.64
26:X:72:VAL:HG13	26:X:85:VAL:HG13	1.79	0.64
5:B:238:ASN:ND2	5:B:240:GLY:H	1.90	0.64
7:D:138:GLY:N	40:D:7597:HOH:O	2.31	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2270:G:H4'	4:A:223:ARG:HH12	1.61	0.64
5:B:297:VAL:HB	40:B:9599:HOH:O	1.97	0.64
13:K:62:PRO:HG3	13:K:65:ARG:HH21	1.63	0.64
1:0:1183:C:H2'	40:0:6750:HOH:O	1.98	0.64
24:V:39:ALA:N	24:V:40:PRO:HD2	2.12	0.64
2:9:3056:A:C2'	2:9:3057:A:H5''	2.26	0.64
1:0:281:U:H2'	1:0:282:C:O4'	1.97	0.64
1:0:949:U:H4'	19:Q:95:GLU:HA	1.80	0.64
29:1:21:ARG:HD2	29:1:37:CYS:SG	2.37	0.64
4:A:203:GLY:HA2	40:A:9536:HOH:O	1.97	0.64
1:0:1184:C:H1'	40:0:7910:HOH:O	1.98	0.64
1:0:2507:G:H2'	1:0:2510:C:H42	1.61	0.64
25:W:130:HIS:O	25:W:136:GLY:HA3	1.98	0.64
1:0:1666:C:O2'	1:0:1667:A:H5''	1.97	0.64
11:H:166:SER:CB	11:H:167:PRO:CD	2.75	0.64
17:O:57:THR:O	17:O:111:VAL:HG23	1.97	0.64
30:2:20:ARG:HD2	30:2:39:ARG:NH2	2.12	0.64
5:B:307:ARG:NH1	5:B:307:ARG:HG3	2.05	0.64
7:D:64:ARG:NE	7:D:67:ASP:HB3	2.13	0.64
30:2:20:ARG:HD2	30:2:39:ARG:HH21	1.62	0.64
6:C:118:THR:HG22	6:C:137:PRO:HB3	1.79	0.64
1:0:1160:G:H5'	1:0:1161:A:C5'	2.23	0.63
32:I:125:ALA:O	32:I:129:VAL:HG23	1.96	0.63
5:B:238:ASN:HD22	5:B:240:GLY:N	1.90	0.63
13:K:115:ARG:HG3	13:K:116:GLU:N	2.13	0.63
1:0:2851:G:H2'	1:0:2852:A:H5'	1.79	0.63
1:0:123:U:H5'	40:0:7139:HOH:O	1.99	0.63
27:Y:165:GLU:HB3	40:Y:9393:HOH:O	1.97	0.63
12:J:131:THR:HG22	12:J:134:GLU:H	1.63	0.63
25:W:81:ASP:OD1	25:W:92:ASP:HB2	1.98	0.63
28:Z:53:GLY:HA2	28:Z:67:GLY:O	1.99	0.63
25:W:48:VAL:O	25:W:48:VAL:HG12	1.98	0.63
4:A:36:ASP:HA	4:A:83:GLY:HA3	1.80	0.63
1:0:1184:C:H4'	32:I:126:LYS:HB3	1.80	0.63
1:0:1377:C:H5'	1:0:1377:C:C6	2.33	0.63
6:C:194:PHE:CD2	6:C:234:VAL:HG11	2.33	0.63
15:M:99:ARG:HH21	15:M:170:ASN:ND2	1.89	0.63
1:0:558:C:H2'	1:0:559:U:H5'	1.80	0.63
24:V:55:ARG:O	24:V:59:ILE:HG12	1.99	0.63
9:F:48:VAL:HG12	9:F:97:ALA:HB2	1.79	0.63
8:E:31:ARG:NH1	8:E:68:HIS:CG	2.67	0.63
2:9:3004:G:H21	16:N:44:ARG:NH1	1.97	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:N:139:TRP:HA	16:N:139:TRP:CE3	2.33	0.63
4:A:33:GLU:O	4:A:34:ASP:HB2	1.98	0.63
8:E:20:ILE:CD1	8:E:40:VAL:HG11	2.29	0.63
1:0:1116:U:O2'	1:0:1118:A:C2	2.45	0.63
1:0:380:A:OP2	15:M:9:ARG:HD2	1.99	0.63
28:Z:37:HIS:HB2	28:Z:47:VAL:HB	1.81	0.63
32:I:110:GLU:HA	32:I:113:HIS:CE1	2.34	0.63
2:9:3013:A:O2'	2:9:3014:G:H5''	1.99	0.63
15:M:24:GLN:O	15:M:28:GLN:HG3	1.99	0.62
10:G:27:ILE:HD13	10:G:71:LEU:HD23	1.81	0.62
23:U:45:GLU:HB2	23:U:48:ASN:HD22	1.64	0.62
4:A:33:GLU:CD	4:A:33:GLU:H	2.03	0.62
11:H:166:SER:HB3	11:H:167:PRO:CD	2.29	0.62
26:X:21:PRO:HG2	26:X:24:LYS:HD3	1.79	0.62
1:0:1053:G:OP1	11:H:12:PRO:HG3	1.98	0.62
1:0:1426:C:H2'	40:0:3201:HOH:O	1.97	0.62
1:0:1333:U:H2'	1:0:1334:C:C6	2.35	0.62
14:L:104:ASP:HB2	40:L:9465:HOH:O	1.99	0.62
1:0:1552:G:N2	1:0:1634:G:H1'	2.13	0.62
26:X:15:ARG:HB3	26:X:15:ARG:HH11	1.64	0.62
1:0:343:C:O2'	1:0:344:C:H5'	1.99	0.62
6:C:162:VAL:HG22	6:C:232:LEU:HD21	1.80	0.62
25:W:88:THR:HG22	25:W:89:ASP:H	1.64	0.62
7:D:172:VAL:HG12	7:D:173:GLU:N	2.14	0.62
25:W:13:MET:HE3	25:W:17:ILE:HG22	1.79	0.62
5:B:329:TYR:CE2	23:U:15:PRO:HG2	2.35	0.62
11:H:58:ARG:HG3	11:H:58:ARG:HH11	1.63	0.62
18:P:9:LEU:O	18:P:13:VAL:HG12	1.98	0.62
4:A:194:MET:HE1	4:A:199:HIS:HB2	1.81	0.62
1:0:282:C:H1'	1:0:368:C:N4	2.14	0.62
1:0:2878:U:H2'	1:0:2879:A:O4'	1.99	0.62
1:0:960:G:H4'	40:0:7877:HOH:O	1.99	0.62
4:A:131:HIS:O	4:A:132:ASP:HB2	2.00	0.62
2:9:3069:U:OP1	16:N:4:PRO:HG3	2.00	0.62
7:D:58:VAL:CG1	7:D:60:GLU:HG2	2.30	0.62
1:0:656:G:H5'	17:O:3:THR:CG2	2.28	0.62
1:0:1118:A:H8	1:0:1119:G:H5''	1.65	0.62
1:0:120:A:H5'	29:1:20:ARG:HH21	1.64	0.62
20:R:106:GLY:HA2	20:R:109:MET:HE3	1.80	0.62
15:M:69:LYS:O	15:M:73:ARG:NH2	2.32	0.62
1:0:797:A:C4'	28:Z:10:ARG:N	2.63	0.62
20:R:99:ALA:HB1	20:R:109:MET:CE	2.30	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:E:31:ARG:HH12	8:E:68:HIS:CD2	2.18	0.62
1:0:2073:G:OP2	1:0:2490:A:H5'	1.98	0.62
1:0:2649:A:H5'	1:0:2649:A:H8	1.64	0.62
5:B:88:GLU:HB3	5:B:97:LEU:HD12	1.82	0.62
22:T:112:LEU:CD2	22:T:119:ALA:HB3	2.29	0.62
22:T:32:ARG:NH1	22:T:38:ARG:HH12	1.98	0.62
18:P:115:SER:N	18:P:118:GLN:HE21	1.92	0.62
1:0:1474:C:C6	1:0:1474:C:H5'	2.28	0.62
1:0:2768:A:H2'	1:0:2769:C:C6	2.35	0.62
1:0:877:G:H5'	1:0:878:G:OP1	2.00	0.62
1:0:338:C:H4'	6:C:174:ILE:CD1	2.30	0.62
25:W:84:VAL:HG12	40:W:6679:HOH:O	1.99	0.61
1:0:2769:C:C2'	1:0:2770:G:H5'	2.30	0.61
16:N:139:TRP:HA	16:N:139:TRP:HE3	1.65	0.61
1:0:960:G:N3	1:0:960:G:H3'	2.15	0.61
1:0:2533:C:H5'	1:0:2533:C:H6	1.65	0.61
5:B:58:PRO:HA	5:B:63:GLU:OE2	1.99	0.61
1:0:545:G:C8	1:0:545:G:H5'	2.31	0.61
14:L:35:ARG:HB2	14:L:35:ARG:NH1	2.15	0.61
22:T:38:ARG:NH1	40:T:6217:HOH:O	2.33	0.61
13:K:75:ARG:HD3	13:K:112:PRO:O	2.00	0.61
11:H:63:GLU:HA	40:H:9545:HOH:O	2.00	0.61
25:W:137:GLN:NE2	25:W:141:HIS:HE1	1.91	0.61
9:F:50:VAL:CG1	9:F:60:VAL:HG11	2.30	0.61
1:0:1926:G:H2'	1:0:1927:A:C8	2.35	0.61
7:D:23:VAL:HG21	7:D:45:THR:HG21	1.81	0.61
1:0:542:A:H5'	1:0:542:A:C8	2.28	0.61
1:0:1882:C:OP1	4:A:192:VAL:HG23	2.01	0.61
1:0:1119:G:H22	1:0:1246:A:H2	1.43	0.61
1:0:164:G:H4'	14:L:30:ARG:HD3	1.83	0.61
1:0:625:U:H5''	1:0:1044:C:N4	2.15	0.61
17:O:32:ARG:HB2	40:O:4656:HOH:O	2.01	0.61
4:A:88:ILE:HD13	4:A:100:PRO:HD3	1.81	0.61
1:0:316:A:N3	1:0:336:G:O2'	2.32	0.61
8:E:68:HIS:O	8:E:72:MET:HG3	1.99	0.61
7:D:149:ARG:HH12	16:N:15:GLU:HA	1.65	0.61
5:B:72:THR:HB	40:B:9599:HOH:O	1.99	0.61
20:R:44:VAL:O	20:R:48:GLU:HG3	1.99	0.61
25:W:68:THR:HG23	25:W:69:ARG:HG2	1.81	0.61
1:0:1205:U:C2'	1:0:1206:U:H5''	2.30	0.61
7:D:25:MET:SD	7:D:40:ILE:HD11	2.40	0.61
1:0:1189:A:O2'	1:0:1208:C:H2'	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:R:9:ASP:O	20:R:13:THR:HB	2.00	0.61
8:E:101:GLU:HB2	8:E:116:THR:O	2.00	0.61
21:S:57:THR:HG22	21:S:58:MET:N	2.15	0.61
40:0:6053:HOH:O	5:B:298:LYS:HG2	2.00	0.61
13:K:34:VAL:CG2	13:K:47:ALA:HB2	2.30	0.61
7:D:51:ARG:HH11	7:D:68:PRO:HB3	1.65	0.61
5:B:154:VAL:HG12	5:B:156:LYS:HG2	1.83	0.61
1:0:1058:A:H2'	1:0:1060:C:H5''	1.82	0.61
21:S:10:VAL:HG11	24:V:36:ALA:HA	1.83	0.61
1:0:2649:A:H5'	1:0:2649:A:C8	2.36	0.61
7:D:23:VAL:HG22	7:D:73:VAL:HB	1.81	0.61
30:2:22:PRO:HG2	30:2:25:VAL:HG23	1.82	0.61
9:F:37:THR:O	9:F:41:GLU:HG3	2.01	0.61
12:J:19:MET:CE	12:J:132:LEU:HD11	2.31	0.60
5:B:190:MET:HE2	5:B:194:PHE:CD1	2.36	0.60
30:2:22:PRO:HG2	30:2:25:VAL:CG2	2.31	0.60
1:0:656:G:C5'	17:O:3:THR:HG22	2.29	0.60
7:D:22:VAL:HG22	7:D:74:THR:HG22	1.82	0.60
5:B:71:VAL:HG11	5:B:296:LEU:HD22	1.82	0.60
12:J:76:ASP:HA	40:J:5907:HOH:O	2.00	0.60
16:N:164:ASP:OD1	16:N:167:ASP:HA	2.02	0.60
1:0:2426:G:H1'	40:0:6602:HOH:O	1.99	0.60
9:F:1:PRO:H3	9:F:4:VAL:HG23	1.66	0.60
1:0:553:G:P	27:Y:204:ARG:HH22	2.24	0.60
1:0:2270:G:H4'	4:A:223:ARG:NH1	2.17	0.60
1:0:1946:C:H2'	1:0:1971:G:C8	2.36	0.60
4:A:194:MET:CE	4:A:199:HIS:HB2	2.32	0.60
26:X:9:VAL:HG22	26:X:88:GLU:OE2	2.01	0.60
16:N:86:LEU:HD12	16:N:125:ALA:HB2	1.83	0.60
5:B:217:ARG:HG3	5:B:257:THR:HG22	1.82	0.60
12:J:74:ARG:O	12:J:78:ILE:HG12	2.02	0.60
14:L:143:THR:HG22	14:L:144:ASP:H	1.67	0.60
16:N:12:ARG:HD3	16:N:18:THR:OG1	2.02	0.60
2:9:3020:G:O2'	2:9:3021:G:H5'	2.01	0.60
25:W:139:GLY:O	25:W:141:HIS:HD2	1.85	0.60
4:A:33:GLU:CD	4:A:33:GLU:N	2.55	0.60
11:H:30:GLN:H	11:H:66:ARG:NH1	1.99	0.60
29:1:10:LYS:HG3	40:1:9489:HOH:O	2.00	0.60
21:S:73:ASP:OD1	21:S:76:GLU:HG3	2.01	0.60
12:J:75:PRO:HG2	12:J:105:LEU:CD2	2.31	0.60
4:A:88:ILE:HG22	4:A:88:ILE:O	2.02	0.60
1:0:1159:G:H1	1:0:1208:C:H42	1.50	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:B:8:LYS:HG3	5:B:220:VAL:HG12	1.84	0.60
5:B:275:GLY:O	5:B:291:ASP:HA	2.01	0.60
26:X:72:VAL:HG13	26:X:85:VAL:CG1	2.32	0.60
23:U:14:GLU:O	23:U:17:THR:HB	2.02	0.60
23:U:17:THR:CG2	23:U:18:GLY:N	2.64	0.60
23:U:45:GLU:HB2	23:U:48:ASN:ND2	2.16	0.60
13:K:34:VAL:HG22	13:K:47:ALA:HB2	1.83	0.60
1:0:1451:C:H5'	1:0:1505:U:C5	2.37	0.60
1:0:635:A:H2'	1:0:636:G:H5''	1.83	0.60
9:F:99:THR:O	9:F:100:ASP:HB2	2.01	0.60
1:0:1205:U:H2'	1:0:1206:U:C5'	2.32	0.60
27:Y:144:ARG:HH11	27:Y:144:ARG:HG3	1.67	0.60
2:9:3040:C:N4	7:D:53:LYS:HE3	2.17	0.60
1:0:396:U:O2'	1:0:418:C:H4'	2.02	0.59
1:0:2896:A:N3	1:0:2896:A:H2'	2.17	0.59
1:0:2524:G:H21	1:0:2526:C:H41	1.48	0.59
4:A:179:MET:HG2	4:A:186:TRP:CB	2.32	0.59
1:0:2064:U:H5'	1:0:2652:U:H4'	1.83	0.59
1:0:1181:A:H5'	32:I:94:GLU:OE2	2.02	0.59
1:0:1119:G:OP2	12:J:49:ARG:HD3	2.02	0.59
1:0:2851:G:O2'	1:0:2852:A:H5'	2.01	0.59
9:F:2:VAL:HG22	9:F:57:GLU:OE1	2.03	0.59
1:0:2820:A:OP1	5:B:98:THR:HG22	2.03	0.59
27:Y:212:ARG:HD2	40:Y:9401:HOH:O	2.01	0.59
1:0:1182:C:H1'	1:0:1192:A:H8	1.68	0.59
1:0:2443:C:H5'	14:L:57:VAL:HG21	1.83	0.59
7:D:170:TYR:O	7:D:171:ASP:HB3	2.02	0.59
40:0:7995:HOH:O	31:3:60:LYS:HG3	2.02	0.59
5:B:85:ARG:NH1	40:B:9626:HOH:O	2.35	0.59
14:L:67:ARG:O	14:L:71:GLU:HG3	2.03	0.59
1:0:2726:U:O2'	26:X:22:ASN:ND2	2.35	0.59
2:9:3029:C:C2'	2:9:3030:C:H5'	2.33	0.59
9:F:63:ILE:HB	9:F:64:PRO:HD3	1.85	0.59
11:H:56:GLN:HE22	11:H:93:GLN:HG2	1.67	0.59
9:F:12:LEU:HD21	9:F:111:ILE:HG23	1.83	0.59
1:0:1766:U:O2	1:0:1778:A:H5'	2.03	0.59
26:X:12:ILE:HD12	26:X:36:HIS:ND1	2.17	0.59
17:O:39:THR:O	17:O:115:ARG:NH2	2.33	0.59
32:I:92:PRO:C	32:I:94:GLU:H	2.06	0.59
5:B:145:HIS:HD2	5:B:146:THR:O	1.86	0.59
14:L:36:ASP:HB2	40:L:9437:HOH:O	2.02	0.59
5:B:141:ARG:HG2	5:B:165:ARG:HA	1.84	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:391:U:OP2	15:M:84:LYS:NZ	2.35	0.59
12:J:74:ARG:HH12	12:J:76:ASP:HB2	1.64	0.59
1:0:2644:C:O2'	1:0:2645:U:H5'	2.03	0.59
1:0:2765:C:H4'	40:0:6053:HOH:O	2.02	0.59
1:0:2827:A:H2'	1:0:2828:G:O4'	2.03	0.59
1:0:2338:G:H2'	7:D:129:ASP:OD1	2.03	0.59
1:0:2291:A:C8	1:0:2309:C:H5'	2.38	0.59
1:0:516:A:H5'	40:0:6177:HOH:O	2.03	0.59
1:0:2072:G:H4'	40:0:4372:HOH:O	2.02	0.58
40:0:9737:HOH:O	15:M:82:ARG:HD2	2.01	0.58
8:E:23:GLU:HG2	8:E:28:SER:HB3	1.85	0.58
29:1:56:GLU:HG2	29:1:56:GLU:OXT	2.03	0.58
25:W:88:THR:HG22	25:W:90:TYR:HD1	1.68	0.58
25:W:88:THR:HG23	25:W:110:GLN:HE21	1.65	0.58
32:I:102:VAL:O	32:I:106:LYS:HG3	2.03	0.58
1:0:1201:C:H5''	40:0:6739:HOH:O	2.03	0.58
1:0:2419:U:H5''	1:0:2420:G:H5'	1.84	0.58
4:A:190:ARG:NH2	4:A:207:GLN:OE1	2.36	0.58
7:D:41:LEU:HA	7:D:44:ILE:HG22	1.85	0.58
29:1:8:GLN:HE22	29:1:11:LYS:HZ2	1.51	0.58
4:A:179:MET:HA	4:A:179:MET:CE	2.33	0.58
16:N:162:ASP:HA	40:N:9327:HOH:O	2.02	0.58
16:N:143:ARG:HH21	16:N:169:PRO:HB2	1.69	0.58
7:D:49:PRO:HB3	7:D:73:VAL:HG22	1.84	0.58
1:0:2524:G:H21	1:0:2526:C:H5	1.49	0.58
1:0:138:U:H5''	1:0:139:C:OP2	2.03	0.58
18:P:135:ALA:HB1	18:P:139:ARG:HH12	1.67	0.58
32:I:78:LEU:HD12	32:I:112:LYS:HZ2	1.66	0.58
1:0:2420:G:O2'	1:0:2421:G:H5'	2.04	0.58
12:J:107:ASN:HD22	12:J:107:ASN:C	2.07	0.58
12:J:107:ASN:ND2	12:J:109:TYR:H	2.01	0.58
5:B:305:ASP:O	5:B:306:LYS:HB2	2.04	0.58
26:X:76:ARG:HH11	26:X:76:ARG:HG3	1.67	0.58
32:I:110:GLU:HA	32:I:113:HIS:NE2	2.18	0.58
2:9:3039:U:H1'	2:9:3044:A:H61	1.68	0.58
16:N:69:TYR:HE2	16:N:184:ILE:HG13	1.68	0.58
1:0:263:U:O4'	9:F:59:ILE:HD13	2.03	0.58
24:V:39:ALA:N	24:V:40:PRO:CD	2.66	0.58
2:9:3051:A:H5'	16:N:160:SER:CB	2.34	0.58
31:3:65:THR:HG22	31:3:67:LEU:HG	1.85	0.58
13:K:4:LEU:CD2	13:K:116:GLU:HB3	2.32	0.58
31:3:70:ARG:HB3	40:3:9510:HOH:O	2.04	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:I:113:HIS:N	32:I:114:PRO:HD2	2.18	0.58
6:C:78:ARG:HG3	6:C:78:ARG:NH1	2.19	0.58
14:L:57:VAL:HG12	14:L:57:VAL:O	2.04	0.58
8:E:116:THR:HG22	8:E:151:LEU:HD22	1.85	0.58
1:O:621:C:H5'	27:Y:132:ASP:OD2	2.03	0.58
4:A:121:ALA:O	4:A:124:VAL:HG22	2.03	0.58
1:O:797:A:C5'	28:Z:10:ARG:N	2.67	0.58
9:F:58:GLU:HA	9:F:61:MET:HG3	1.85	0.58
1:O:1168:C:H5''	32:I:87:THR:CG2	2.34	0.58
1:O:1384:C:H5'	26:X:30:MET:HG2	1.85	0.58
1:O:1687:C:O2	29:1:9:GLY:HA2	2.04	0.58
7:D:136:ARG:NH1	7:D:157:LEU:HA	2.16	0.58
1:O:657:G:OP1	6:C:27:ARG:NH2	2.29	0.58
1:O:441:A:H1'	1:O:442:A:N7	2.19	0.58
27:Y:189:ASN:HD22	27:Y:189:ASN:C	2.07	0.57
1:O:1730:G:H5''	1:O:1731:C:H6	1.69	0.57
1:O:2795:C:O2'	1:O:2796:U:H5'	2.04	0.57
1:O:121:U:OP2	30:2:10:ARG:NH2	2.33	0.57
1:O:2908:A:H2'	1:O:2909:G:O4'	2.02	0.57
31:3:3:MET:HG3	31:3:4:PRO:HD2	1.85	0.57
5:B:162:MET:HE2	5:B:310:ARG:CD	2.28	0.57
32:I:118:SER:HB2	32:I:123:ASN:HB2	1.87	0.57
13:K:81:ARG:HD3	13:K:87:ARG:CZ	2.34	0.57
1:O:1943:C:H4'	4:A:211:LYS:O	2.05	0.57
1:O:506:G:H22	1:O:509:A:H5'	1.69	0.57
1:O:2769:C:O2'	1:O:2770:G:H5'	2.04	0.57
9:F:48:VAL:HG12	9:F:97:ALA:CB	2.33	0.57
1:O:2237:G:H1'	1:O:2238:A:C8	2.40	0.57
2:9:3018:U:H2'	2:9:3019:G:H8	1.70	0.57
5:B:175:LEU:O	5:B:175:LEU:HD23	2.05	0.57
5:B:62:ARG:HA	5:B:65:MET:CE	2.34	0.57
2:9:3014:G:H5'	2:9:3014:G:C8	2.39	0.57
9:F:13:GLU:OE1	9:F:77:VAL:HG13	2.05	0.57
6:C:79:ARG:O	6:C:87:ARG:HG2	2.04	0.57
23:U:47:ARG:HG3	40:U:4381:HOH:O	2.03	0.57
16:N:23:ARG:HG2	16:N:23:ARG:HH11	1.69	0.57
25:W:26:ILE:HB	40:W:5420:HOH:O	2.03	0.57
32:I:139:ILE:HG22	32:I:140:GLU:N	2.20	0.57
11:H:40:ALA:HB1	11:H:137:TYR:CE2	2.40	0.57
26:X:43:VAL:HG12	26:X:44:ASP:N	2.19	0.57
5:B:102:THR:HG21	5:B:182:VAL:O	2.04	0.57
4:A:95:PRO:HG2	4:A:98:GLU:HG2	1.86	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:C:129:HIS:HD2	6:C:165:ASP:OD2	1.88	0.57
6:C:127:ARG:HD3	6:C:129:HIS:HE1	1.68	0.57
1:O:2694:A:H4'	8:E:91:PHE:HE1	1.69	0.57
1:O:1634:G:H3'	40:O:4466:HOH:O	2.04	0.57
1:O:20:G:H21	20:R:117:HIS:HD2	1.52	0.57
5:B:96:PRO:HG3	40:B:9626:HOH:O	2.02	0.57
1:O:2676:C:H4'	12:J:70:PHE:CD1	2.39	0.57
10:G:64:ASN:N	10:G:64:ASN:HD22	2.01	0.57
6:C:140:VAL:HB	40:C:9252:HOH:O	2.04	0.57
1:O:1180:U:O2'	32:I:92:PRO:HD2	2.05	0.57
22:T:41:ARG:NH1	22:T:41:ARG:HG2	2.19	0.57
1:O:1189:A:H1'	1:O:1209:C:O4'	2.04	0.57
15:M:24:GLN:NE2	15:M:27:ARG:HH11	2.03	0.57
5:B:17:LYS:O	5:B:260:HIS:HD2	1.86	0.57
6:C:127:ARG:CZ	6:C:225:PRO:HG2	2.35	0.57
6:C:129:HIS:CE1	6:C:231:ARG:HA	2.40	0.57
27:Y:154:ARG:HH11	27:Y:154:ARG:HB3	1.69	0.57
16:N:61:ALA:HB3	16:N:88:ALA:HB2	1.87	0.57
21:S:77:VAL:O	21:S:80:ARG:HG2	2.05	0.57
20:R:39:THR:HG22	20:R:107:GLU:O	2.05	0.57
28:Z:19:GLY:O	28:Z:23:ARG:HG2	2.05	0.57
40:O:4931:HOH:O	15:M:83:SER:HB3	2.04	0.57
11:H:170:ASN:HD22	11:H:170:ASN:N	2.01	0.57
2:9:3041:C:O4'	7:D:50:VAL:HG13	2.05	0.56
6:C:242:GLU:HB2	40:C:9186:HOH:O	2.05	0.56
1:O:256:C:H2'	1:O:257:G:O4'	2.05	0.56
25:W:5:VAL:O	25:W:52:VAL:HG23	2.04	0.56
7:D:59:GLY:O	7:D:61:PHE:N	2.38	0.56
1:O:2779:G:H21	8:E:143:GLN:NE2	2.03	0.56
31:3:3:MET:O	31:3:90:PHE:HA	2.05	0.56
25:W:4:LEU:O	25:W:32:CYS:HA	2.05	0.56
16:N:115:VAL:HG22	40:N:9354:HOH:O	2.05	0.56
15:M:107:ARG:NH1	40:M:9378:HOH:O	2.38	0.56
1:O:2717:C:O2'	1:O:2718:C:H5''	2.05	0.56
1:O:1730:G:C5'	1:O:1731:C:C6	2.87	0.56
24:V:64:GLY:O	24:V:65:ASP:HB2	2.03	0.56
1:O:2524:G:N2	1:O:2526:C:H41	2.03	0.56
1:O:2912:C:H2'	1:O:2913:A:O4'	2.05	0.56
1:O:500:G:H21	20:R:98:ASN:HD21	1.51	0.56
5:B:267:LYS:HE3	5:B:300:SER:O	2.05	0.56
4:A:113:GLY:HA2	4:A:153:ARG:NH2	2.20	0.56
8:E:20:ILE:HD12	8:E:33:LEU:HD12	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:M:187:LEU:HD23	15:M:194:ALA:HB3	1.86	0.56
23:U:4:ARG:HH11	23:U:4:ARG:HG2	1.71	0.56
25:W:4:LEU:HD11	25:W:45:VAL:HG12	1.88	0.56
1:0:871:G:H8	1:0:871:G:H5''	1.70	0.56
20:R:18:LEU:HG	20:R:91:LEU:HD13	1.87	0.56
2:9:3051:A:H5'	16:N:160:SER:HB3	1.87	0.56
11:H:76:GLU:C	11:H:77:LEU:HD23	2.26	0.56
1:0:1681:G:H5''	1:0:1682:A:H5'	1.87	0.56
1:0:2105:C:H5'	40:4:7933:HOH:O	2.05	0.56
13:K:55:VAL:HG12	13:K:56:SER:N	2.20	0.56
12:J:74:ARG:NH1	12:J:105:LEU:HD11	2.21	0.56
9:F:50:VAL:HG21	9:F:63:ILE:HG21	1.88	0.56
22:T:48:VAL:HG22	22:T:96:VAL:HG22	1.87	0.56
1:0:737:A:H2'	1:0:738:G:O4'	2.05	0.56
4:A:206:ARG:HD3	4:A:206:ARG:H	1.71	0.56
12:J:93:ARG:NH1	12:J:93:ARG:HB3	2.17	0.56
14:L:79:ASP:HB2	40:L:9459:HOH:O	2.06	0.56
25:W:52:VAL:HG22	25:W:53:ALA:N	2.20	0.56
30:2:48:ASP:O	30:2:49:GLU:HB2	2.05	0.56
27:Y:154:ARG:NH1	27:Y:155:ARG:HG2	2.19	0.56
11:H:20:ILE:HG23	11:H:120:ILE:HD11	1.87	0.56
16:N:11:ARG:O	16:N:15:GLU:HG3	2.06	0.56
1:0:1595:G:O2'	1:0:1596:U:H5'	2.06	0.56
7:D:57:THR:HG23	7:D:63:ILE:HA	1.88	0.56
1:0:2563:U:H2'	1:0:2565:C:O5'	2.05	0.56
5:B:40:GLY:HA3	40:B:9637:HOH:O	2.04	0.56
27:Y:126:PRO:HG2	27:Y:128:PHE:CE1	2.41	0.56
29:1:25:LYS:HD2	30:2:49:GLU:N	2.18	0.56
9:F:58:GLU:HA	9:F:61:MET:HE2	1.88	0.56
1:0:1592:G:O2'	1:0:1593:C:O4'	2.24	0.56
1:0:1878:G:O2'	1:0:1879:U:OP2	2.24	0.55
4:A:135:VAL:HG21	4:A:147:ARG:NH1	2.20	0.55
1:0:95:A:H5''	1:0:97:G:O4'	2.06	0.55
31:3:62:THR:HB	40:3:9487:HOH:O	2.05	0.55
4:A:123:GLY:HA3	4:A:162:GLY:HA2	1.86	0.55
1:0:2721:U:H4'	13:K:87:ARG:HG3	1.88	0.55
8:E:34:TRP:O	12:J:127:ILE:HD11	2.06	0.55
16:N:149:GLU:O	16:N:152:GLU:HB3	2.05	0.55
1:0:2320:U:H4'	1:0:2321:A:O4'	2.06	0.55
24:V:11:MET:HB3	24:V:15:GLU:HB2	1.88	0.55
40:0:6753:HOH:O	23:U:56:ARG:HB3	2.05	0.55
16:N:154:LEU:O	16:N:155:GLU:HB2	2.06	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:2453:G:H5''	40:L:9442:HOH:O	2.04	0.55
6:C:236:THR:HG21	40:C:9178:HOH:O	2.05	0.55
2:9:3076:G:C3'	2:9:3077:A:H5''	2.27	0.55
28:Z:10:ARG:HA	40:Z:9215:HOH:O	2.06	0.55
32:I:112:LYS:C	32:I:114:PRO:HD2	2.27	0.55
14:L:80:ASP:CB	14:L:90:ARG:HB3	2.36	0.55
16:N:183:ASP:O	16:N:184:ILE:O	2.25	0.55
2:9:3041:C:H4'	7:D:48:MET:HB3	1.88	0.55
1:O:248:A:H5'	1:O:249:G:OP2	2.07	0.55
22:T:40:VAL:HG22	22:T:41:ARG:N	2.22	0.55
10:G:12:ILE:N	10:G:13:PRO:CD	2.69	0.55
24:V:56:ILE:O	24:V:60:GLN:HG3	2.05	0.55
12:J:70:PHE:CG	12:J:70:PHE:O	2.60	0.55
19:Q:25:PRO:HB2	40:Q:4350:HOH:O	2.07	0.55
5:B:120:ASP:OD2	5:B:123:ALA:HB2	2.07	0.55
7:D:44:ILE:HG12	7:D:83:PHE:HE1	1.72	0.55
1:O:1209:C:H2'	1:O:1210:G:H8	1.71	0.55
1:O:558:C:O2'	1:O:559:U:H5''	2.06	0.55
2:9:3014:G:O2'	16:N:1:ALA:HB2	2.05	0.55
5:B:112:THR:HG23	5:B:158:LYS:HZ1	1.71	0.55
25:W:64:THR:O	25:W:68:THR:HG22	2.06	0.55
5:B:84:LEU:HB2	5:B:182:VAL:HG21	1.89	0.55
1:O:1200:A:H4'	40:O:7793:HOH:O	2.07	0.55
19:Q:32:GLU:HA	19:Q:71:TYR:OH	2.06	0.55
18:P:111:GLU:HG2	18:P:111:GLU:O	2.06	0.55
1:O:870:G:C2'	1:O:871:G:H5''	2.35	0.55
14:L:136:ALA:HB3	40:L:9475:HOH:O	2.06	0.55
1:O:2072:G:C6	1:O:2533:C:H1'	2.42	0.55
16:N:89:GLY:O	16:N:92:ALA:HB3	2.07	0.55
11:H:171:ALA:HA	40:H:9535:HOH:O	2.06	0.55
12:J:75:PRO:HB3	12:J:132:LEU:HB3	1.89	0.55
1:O:2645:U:OP2	1:O:2645:U:C6	2.59	0.55
25:W:13:MET:HE1	25:W:18:GLN:HA	1.89	0.55
14:L:91:VAL:HG13	14:L:120:LEU:HD23	1.88	0.55
1:O:2521:A:OP2	11:H:3:ALA:HB3	2.07	0.55
5:B:185:GLY:HA2	40:B:9625:HOH:O	2.05	0.55
1:O:272:A:H5'	1:O:273:G:OP2	2.07	0.55
2:9:3057:A:H8	7:D:141:VAL:HG21	1.72	0.55
24:V:1:THR:HG23	24:V:2:VAL:N	2.22	0.55
22:T:49:GLU:OE2	22:T:97:ARG:HD2	2.07	0.55
30:2:36:ASN:HB3	30:2:39:ARG:HG3	1.89	0.55
5:B:62:ARG:HA	5:B:65:MET:HE2	1.88	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:C:214:THR:HG23	40:C:9237:HOH:O	2.06	0.55
1:O:1236:A:C8	12:J:63:ILE:HD11	2.41	0.55
15:M:79:ALA:HB3	15:M:81:ARG:NH1	2.22	0.55
24:V:42:ASN:HB3	40:V:7247:HOH:O	2.06	0.55
40:O:9698:HOH:O	5:B:214:PRO:HD2	2.06	0.55
1:O:2502:C:C2'	1:O:2503:A:H5'	2.36	0.55
40:O:3147:HOH:O	18:P:81:LYS:HG2	2.06	0.55
1:O:2365:G:H5''	40:Q:6597:HOH:O	2.06	0.55
15:M:68:ARG:HD3	15:M:68:ARG:O	2.08	0.54
1:O:2524:G:H21	1:O:2526:C:N4	2.04	0.54
9:F:13:GLU:OE2	9:F:78:GLU:HG2	2.07	0.54
1:O:1406:A:H4'	1:O:1407:A:H5''	1.88	0.54
1:O:1528:A:H2'	1:O:1529:G:O4'	2.07	0.54
17:O:59:VAL:CG2	17:O:111:VAL:HG21	2.37	0.54
5:B:97:LEU:O	5:B:98:THR:HG23	2.06	0.54
5:B:5:ARG:HH11	5:B:8:LYS:HE2	1.72	0.54
8:E:22:VAL:HG12	8:E:76:VAL:HG11	1.89	0.54
1:O:485:A:N3	1:O:487:G:H5''	2.22	0.54
1:O:2416:G:O2'	16:N:25:ARG:HG2	2.06	0.54
4:A:107:ASN:OD1	4:A:120:ARG:HD2	2.07	0.54
1:O:949:U:C4'	19:Q:95:GLU:HA	2.37	0.54
8:E:31:ARG:HH12	8:E:68:HIS:CG	2.25	0.54
21:S:57:THR:CG2	21:S:58:MET:N	2.69	0.54
25:W:41:TYR:HA	25:W:44:MET:HE3	1.88	0.54
5:B:321:PRO:HA	40:B:9646:HOH:O	2.07	0.54
9:F:31:LYS:HE3	40:F:2623:HOH:O	2.06	0.54
32:I:134:SER:O	32:I:135:LEU:HD23	2.07	0.54
18:P:16:VAL:HG12	18:P:17:GLY:N	2.23	0.54
4:A:34:ASP:OD1	4:A:35:GLY:N	2.41	0.54
17:O:59:VAL:HG23	17:O:111:VAL:CG2	2.37	0.54
1:O:1067:A:H5'	40:O:4901:HOH:O	2.06	0.54
1:O:2717:C:OP1	5:B:207:LYS:HG3	2.08	0.54
24:V:56:ILE:HG22	24:V:60:GLN:HE21	1.72	0.54
4:A:101:GLU:OE2	4:A:131:HIS:HB2	2.08	0.54
11:H:79:GLU:C	11:H:80:GLU:HG3	2.28	0.54
32:I:72:VAL:HG11	32:I:111:GLN:O	2.07	0.54
25:W:65:VAL:HG12	25:W:116:LEU:HD13	1.89	0.54
1:O:2670:G:O2'	1:O:2671:U:H5'	2.07	0.54
1:O:2720:C:O2	13:K:87:ARG:NH2	2.41	0.54
1:O:2748:G:OP1	1:O:2749:U:H5''	2.07	0.54
7:D:104:PHE:CE2	7:D:166:ILE:HD13	2.42	0.54
18:P:98:ILE:HD13	18:P:98:ILE:O	2.08	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:9:3029:C:O3'	7:D:138:GLY:HA2	2.07	0.54
1:0:2866:U:H4'	1:0:2867:G:H5'	1.89	0.54
1:0:656:G:OP2	17:O:37:ARG:HD2	2.08	0.54
12:J:93:ARG:HH11	12:J:93:ARG:CB	2.13	0.54
1:0:1667:A:H2'	1:0:1668:U:C6	2.43	0.54
40:0:3309:HOH:O	5:B:254:GLN:HG3	2.08	0.54
11:H:169:GLY:C	11:H:170:ASN:HD22	2.11	0.54
5:B:321:PRO:HG3	40:B:9595:HOH:O	2.08	0.54
15:M:66:SER:HB3	15:M:128:TRP:CD1	2.43	0.54
2:9:3114:G:O6	16:N:11:ARG:HD3	2.07	0.54
1:0:1853:C:OP1	4:A:231:LYS:HG3	2.08	0.54
1:0:12:U:H2'	1:0:13:G:H5'	1.90	0.54
1:0:834:G:H4'	1:0:835:U:OP2	2.08	0.54
1:0:2894:C:O2'	1:0:2895:C:H5'	2.07	0.54
1:0:151:A:H2'	1:0:152:A:O4'	2.07	0.54
14:L:80:ASP:HB2	14:L:90:ARG:O	2.06	0.53
15:M:58:GLN:HG3	40:M:9405:HOH:O	2.07	0.53
1:0:1902:G:H2'	1:0:1903:U:O4'	2.08	0.53
1:0:1641:A:H2'	1:0:1642:A:H5'	1.90	0.53
1:0:286:U:H2'	1:0:287:C:C6	2.43	0.53
1:0:757:C:OP1	14:L:27:ARG:HD2	2.07	0.53
1:0:1335:C:OP2	27:Y:207:SER:HB3	2.08	0.53
8:E:154:ILE:HD11	8:E:157:LYS:HB2	1.89	0.53
6:C:236:THR:HA	40:C:9252:HOH:O	2.07	0.53
1:0:156:C:H5''	15:M:171:ARG:CD	2.27	0.53
9:F:60:VAL:HG12	9:F:60:VAL:O	2.09	0.53
1:0:1189:A:H1'	1:0:1209:C:C1'	2.38	0.53
4:A:94:LEU:N	4:A:94:LEU:HD23	2.24	0.53
16:N:86:LEU:HD21	16:N:180:LEU:CD1	2.38	0.53
14:L:150:GLN:HB3	40:L:9471:HOH:O	2.08	0.53
5:B:139:ASP:HB3	40:B:9552:HOH:O	2.08	0.53
1:0:558:C:H2'	1:0:559:U:C5'	2.38	0.53
6:C:194:PHE:HA	6:C:234:VAL:HG13	1.91	0.53
1:0:709:G:O2'	17:O:25:VAL:CG1	2.56	0.53
1:0:1819:G:H2'	1:0:1820:G:H4'	1.89	0.53
22:T:47:THR:HB	22:T:100:ASP:HB3	1.90	0.53
8:E:145:ALA:HB1	8:E:168:ILE:CD1	2.38	0.53
5:B:310:ARG:HD2	40:B:9587:HOH:O	2.08	0.53
5:B:41:PHE:CD1	5:B:79:MET:HE2	2.42	0.53
16:N:164:ASP:OD2	16:N:167:ASP:HA	2.09	0.53
16:N:169:PRO:O	16:N:172:PHE:HB3	2.09	0.53
1:0:40:C:H4'	40:0:7476:HOH:O	2.08	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2711:U:H1'	40:0:4024:HOH:O	2.08	0.53
4:A:165:THR:HG22	40:A:9604:HOH:O	2.09	0.53
10:G:20:VAL:O	10:G:24:VAL:HG23	2.08	0.53
23:U:5:GLU:HG2	23:U:10:GLY:O	2.07	0.53
25:W:88:THR:HG23	25:W:110:GLN:HB3	1.91	0.53
15:M:77:HIS:HD2	15:M:79:ALA:O	1.91	0.53
6:C:20:ASP:O	6:C:23:GLU:HB2	2.08	0.53
1:0:793:A:H5''	18:P:83:LYS:HG2	1.91	0.53
20:R:122:GLN:HB3	20:R:138:SER:HB2	1.89	0.53
1:0:1555:G:H4'	1:0:1630:A:H2	1.73	0.53
15:M:60:VAL:C	15:M:61:ILE:HD12	2.28	0.53
15:M:167:GLY:O	15:M:171:ARG:HG3	2.09	0.53
31:3:70:ARG:HG2	31:3:70:ARG:HH11	1.74	0.53
13:K:58:THR:HG22	13:K:59:LYS:HG3	1.90	0.53
1:0:1363:G:OP1	6:C:76:ARG:NH2	2.42	0.53
4:A:164:ARG:CZ	40:A:9572:HOH:O	2.56	0.53
22:T:9:LYS:CE	22:T:13:ARG:NH1	2.65	0.53
32:I:138:THR:HG22	32:I:139:ILE:H	1.74	0.53
18:P:10:ALA:HA	18:P:13:VAL:CG1	2.38	0.53
1:0:1476:A:O2'	1:0:1477:C:H5'	2.08	0.53
1:0:538:C:OP2	27:Y:134:HIS:HE1	1.91	0.53
5:B:264:GLU:CG	5:B:267:LYS:HE2	2.29	0.53
1:0:2812:A:C2	1:0:2814:A:N6	2.65	0.53
1:0:1118:A:C8	1:0:1119:G:H5''	2.44	0.53
8:E:20:ILE:CD1	8:E:33:LEU:HD12	2.39	0.52
8:E:3:VAL:HG22	8:E:49:ILE:HB	1.91	0.52
15:M:30:GLU:O	15:M:34:GLU:HG3	2.09	0.52
1:0:2541:U:H5'	1:0:2541:U:H6	1.74	0.52
32:I:99:ASP:O	32:I:100:LEU:HD23	2.09	0.52
1:0:1666:C:H2'	1:0:1667:A:C5'	2.37	0.52
1:0:1730:G:H5'	1:0:1731:C:H5	1.74	0.52
22:T:19:ARG:HD3	22:T:67:LEU:O	2.09	0.52
25:W:38:THR:HG22	25:W:39:ASP:N	2.24	0.52
2:9:3049:G:O2'	2:9:3050:G:H5'	2.10	0.52
1:0:1626:A:H2'	1:0:1627:G:O4'	2.08	0.52
1:0:1268:C:O2'	27:Y:169:ARG:HB2	2.09	0.52
1:0:288:A:H2'	1:0:289:G:C8	2.43	0.52
32:I:105:VAL:HG11	32:I:129:VAL:CG2	2.39	0.52
18:P:98:ILE:HD12	18:P:102:ARG:NE	2.24	0.52
1:0:951:A:C2'	1:0:952:G:H5'	2.39	0.52
6:C:84:VAL:HG12	6:C:85:LYS:HG2	1.92	0.52
17:O:87:THR:O	17:O:91:GLN:HG3	2.08	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1352:A:O2'	1:0:1353:C:OP1	2.24	0.52
27:Y:106:THR:HG23	27:Y:107:PRO:HD2	1.90	0.52
1:0:1166:A:H1'	1:0:1192:A:N3	2.25	0.52
14:L:90:ARG:NH2	14:L:121:ILE:HD11	2.23	0.52
25:W:88:THR:HG22	25:W:90:TYR:CD1	2.45	0.52
27:Y:235:GLU:CD	27:Y:235:GLU:N	2.59	0.52
1:0:1878:G:O2'	1:0:1879:U:C6	2.60	0.52
2:9:3008:G:O6	16:N:11:ARG:NH1	2.42	0.52
1:0:949:U:O2'	19:Q:40:HIS:HE1	1.93	0.52
5:B:232:TRP:CD1	5:B:235:ARG:HD2	2.44	0.52
5:B:232:TRP:HD1	5:B:235:ARG:HD2	1.74	0.52
19:Q:75:ILE:HD13	19:Q:84:ILE:HD11	1.91	0.52
14:L:134:GLU:HG3	40:L:9458:HOH:O	2.10	0.52
1:0:1878:G:O2'	1:0:1879:U:P	2.68	0.52
12:J:19:MET:HE3	12:J:132:LEU:HD11	1.91	0.52
1:0:2032:U:H2'	1:0:2033:G:C5'	2.40	0.52
6:C:233:THR:HG22	6:C:234:VAL:N	2.25	0.52
22:T:32:ARG:NH1	22:T:38:ARG:NH1	2.56	0.52
1:0:894:A:N1	6:C:87:ARG:NH2	2.57	0.52
15:M:57:LYS:HE2	15:M:140:ALA:O	2.10	0.52
7:D:134:LEU:HD11	7:D:166:ILE:HD11	1.90	0.52
14:L:73:VAL:HG23	14:L:74:THR:N	2.25	0.52
14:L:92:ASP:HB3	14:L:95:ASP:OD2	2.10	0.52
4:A:217:ARG:CG	4:A:217:ARG:HH11	2.23	0.52
1:0:750:A:O3'	6:C:101:ASP:HB2	2.09	0.52
27:Y:117:LEU:HA	27:Y:174:VAL:HG11	1.92	0.52
1:0:2626:C:H2'	1:0:2627:G:C8	2.45	0.52
1:0:364:C:H2'	1:0:365:G:O4'	2.10	0.52
1:0:848:C:H5'	40:0:7728:HOH:O	2.09	0.52
32:I:114:PRO:HG2	32:I:115:ASP:H	1.75	0.52
1:0:2346:C:O5'	1:0:2346:C:H6	1.93	0.52
1:0:1187:U:O2'	1:0:1189:A:H2	1.91	0.52
14:L:119:THR:HG23	14:L:139:SER:OG	2.10	0.52
16:N:72:GLU:HG2	16:N:72:GLU:O	2.10	0.52
15:M:98:GLN:O	15:M:102:GLU:HG3	2.10	0.51
40:0:7093:HOH:O	27:Y:155:ARG:HD2	2.08	0.51
1:0:2415:A:N3	16:N:26:LEU:HD13	2.25	0.51
1:0:1738:C:H1'	40:0:7770:HOH:O	2.10	0.51
8:E:35:TYR:HA	12:J:127:ILE:CD1	2.41	0.51
25:W:149:LEU:HG	25:W:153:MET:CE	2.40	0.51
14:L:92:ASP:HA	14:L:121:ILE:HB	1.92	0.51
1:0:962:C:H1'	16:N:5:ARG:HH12	1.75	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:128:LEU:HD21	4:A:131:HIS:HE1	1.75	0.51
1:0:1060:C:H6	1:0:1060:C:H5'	1.76	0.51
2:9:3042:C:O2	7:D:76:ARG:NH1	2.43	0.51
1:0:1328:A:OP1	27:Y:169:ARG:HD2	2.10	0.51
1:0:2081:A:H4'	12:J:69:TYR:CE1	2.45	0.51
16:N:154:LEU:O	16:N:155:GLU:CB	2.58	0.51
27:Y:144:ARG:CG	27:Y:144:ARG:NH1	2.71	0.51
9:F:48:VAL:HG23	9:F:74:PHE:CB	2.40	0.51
11:H:116:ALA:O	11:H:117:PHE:C	2.49	0.51
1:0:1242:A:C5'	12:J:82:THR:HG23	2.31	0.51
1:0:1181:A:N1	1:0:1192:A:O2'	2.40	0.51
1:0:2064:U:H5'	1:0:2652:U:O3'	2.10	0.51
5:B:258:GLY:H	5:B:260:HIS:CE1	2.28	0.51
8:E:154:ILE:HG13	8:E:156:ASP:OD1	2.10	0.51
2:9:3049:G:C2'	2:9:3050:G:H5'	2.41	0.51
1:0:920:C:H5''	1:0:921:G:O5'	2.10	0.51
28:Z:42:CYS:SG	28:Z:44:GLU:HB2	2.51	0.51
27:Y:112:GLU:OE1	27:Y:112:GLU:HA	2.10	0.51
8:E:11:VAL:HG12	8:E:12:ASP:N	2.24	0.51
13:K:74:VAL:HG11	13:K:113:ILE:CG1	2.32	0.51
15:M:71:SER:O	15:M:73:ARG:NH1	2.43	0.51
20:R:39:THR:HB	20:R:42:GLU:HG3	1.93	0.51
9:F:53:ASP:OD1	9:F:80:GLN:HB2	2.11	0.51
13:K:125:ALA:C	13:K:127:ALA:H	2.13	0.51
9:F:28:ALA:CB	9:F:99:THR:HG23	2.41	0.51
32:I:113:HIS:N	32:I:114:PRO:CD	2.73	0.51
1:0:2769:C:H2'	1:0:2770:G:C5'	2.40	0.51
8:E:23:GLU:HG2	8:E:28:SER:CB	2.41	0.51
11:H:170:ASN:ND2	11:H:170:ASN:N	2.59	0.51
6:C:154:VAL:O	6:C:158:GLU:HG3	2.11	0.51
24:V:25:THR:HG22	24:V:29:ASN:HD21	1.75	0.51
1:0:2505:G:C2'	1:0:2506:A:H5'	2.41	0.51
28:Z:26:VAL:O	28:Z:30:GLU:HG3	2.10	0.51
6:C:136:VAL:HG22	6:C:137:PRO:HA	1.93	0.51
9:F:48:VAL:HG23	9:F:74:PHE:HB3	1.93	0.51
15:M:34:GLU:HB3	15:M:38:GLU:HG3	1.91	0.51
1:0:1594:C:OP2	18:P:120:ARG:HD2	2.10	0.51
1:0:1234:U:N3	5:B:244:PRO:HB3	2.26	0.51
7:D:128:LEU:HB2	40:D:6007:HOH:O	2.11	0.51
9:F:91:VAL:CG1	9:F:92:GLY:H	2.14	0.51
1:0:2712:G:H5'	40:K:4183:HOH:O	2.11	0.51
1:0:1730:G:C5'	1:0:1731:C:H6	2.23	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:H:56:GLN:NE2	11:H:126:ARG:HE	2.09	0.51
27:Y:99:ALA:HB2	27:Y:233:TYR:CZ	2.46	0.51
12:J:88:PRO:O	12:J:94:GLY:HA3	2.11	0.51
14:L:65:ASP:CG	14:L:111:ALA:HB3	2.31	0.51
15:M:64:ARG:HD2	40:M:9384:HOH:O	2.09	0.51
25:W:5:VAL:O	25:W:52:VAL:CG2	2.59	0.51
1:O:1701:A:H5''	1:O:1702:U:H3'	1.93	0.51
1:O:475:G:OP1	6:C:73:LEU:CD2	2.58	0.51
5:B:254:GLN:HG2	5:B:255:GLY:H	1.76	0.51
25:W:38:THR:O	25:W:42:ARG:HB2	2.10	0.51
5:B:215:VAL:HB	5:B:234:ARG:HH12	1.76	0.51
1:O:1400:C:H4'	26:X:56:GLU:HG2	1.92	0.51
1:O:1351:G:OP1	6:C:96:LYS:NZ	2.39	0.51
1:O:299:U:H5'	40:O:7789:HOH:O	2.11	0.51
20:R:82:GLU:O	20:R:86:LYS:HG3	2.11	0.51
8:E:35:TYR:HA	12:J:127:ILE:HD12	1.93	0.51
1:O:328:U:O4'	6:C:202:THR:CG2	2.59	0.51
9:F:36:THR:HG23	9:F:97:ALA:HB2	1.92	0.51
12:J:4:ALA:O	12:J:5:GLU:HB2	2.11	0.51
1:O:2456:A:H2'	1:O:2457:U:C6	2.46	0.51
2:9:3002:U:OP2	2:9:3003:A:H5'	2.10	0.51
14:L:145:LEU:O	14:L:145:LEU:HD23	2.10	0.51
1:O:134:U:H6	1:O:134:U:H5''	1.75	0.51
25:W:139:GLY:O	25:W:141:HIS:CD2	2.63	0.50
1:O:2718:C:H5'	1:O:2718:C:C6	2.44	0.50
23:U:9:CYS:HA	23:U:52:THR:HG23	1.93	0.50
8:E:49:ILE:HD11	8:E:69:ILE:HD12	1.92	0.50
12:J:107:ASN:HD22	12:J:109:TYR:H	1.58	0.50
27:Y:112:GLU:CD	27:Y:115:ARG:NH1	2.64	0.50
1:O:1218:U:H2'	1:O:1219:U:C6	2.46	0.50
1:O:776:A:OP1	29:1:28:HIS:HE1	1.95	0.50
15:M:72:ALA:HB2	15:M:93:ARG:HG2	1.93	0.50
5:B:41:PHE:CD2	5:B:190:MET:HE3	2.47	0.50
1:O:2896:A:H5''	40:X:5399:HOH:O	2.10	0.50
32:I:101:SER:H	32:I:104:GLN:NE2	2.09	0.50
17:O:42:GLU:HB2	40:O:2176:HOH:O	2.10	0.50
40:9:1361:HOH:O	16:N:41:LYS:HE3	2.10	0.50
1:O:588:G:O6	25:W:154:ARG:NH1	2.45	0.50
1:O:1462:C:H2'	1:O:1463:A:C8	2.47	0.50
1:O:870:G:OP2	4:A:3:ARG:HD3	2.12	0.50
1:O:2661:U:H3	1:O:2812:A:H62	1.60	0.50
2:9:3057:A:C8	7:D:141:VAL:HG21	2.46	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:36:ASP:C	4:A:38:ILE:H	2.15	0.50
23:U:9:CYS:O	23:U:52:THR:HG23	2.11	0.50
32:I:105:VAL:HG11	32:I:129:VAL:HG22	1.92	0.50
1:0:945:U:H2'	1:0:946:C:C6	2.46	0.50
4:A:192:VAL:HG11	4:A:207:GLN:HB3	1.93	0.50
1:0:2487:C:H1'	40:0:5938:HOH:O	2.10	0.50
14:L:143:THR:O	14:L:147:GLU:HG3	2.10	0.50
14:L:104:ASP:O	14:L:105:TYR:HB3	2.11	0.50
1:0:241:A:C2	1:0:378:A:H4'	2.47	0.50
1:0:2414:A:H2'	1:0:2415:A:C8	2.47	0.50
17:O:53:GLN:HE21	17:O:56:GLU:CD	2.15	0.50
1:0:407:A:H2'	1:0:408:A:C8	2.47	0.50
6:C:236:THR:HG22	6:C:239:ALA:CB	2.41	0.50
22:T:71:VAL:CG1	22:T:72:ILE:N	2.74	0.50
15:M:164:THR:CG2	15:M:165:GLY:N	2.74	0.50
5:B:307:ARG:HB3	40:B:9642:HOH:O	2.11	0.50
1:0:2726:U:O2	1:0:2749:U:O5'	2.30	0.50
7:D:25:MET:HE1	7:D:37:ALA:O	2.11	0.50
32:I:138:THR:HG22	32:I:139:ILE:N	2.26	0.50
1:0:447:A:OP2	22:T:1:SER:HB2	2.11	0.50
11:H:38:LYS:HE2	11:H:42:ASP:HB2	1.93	0.50
20:R:119:VAL:HG12	20:R:119:VAL:O	2.11	0.50
5:B:162:MET:CE	5:B:308:LEU:HD21	2.36	0.50
5:B:16:ARG:NH2	40:B:9557:HOH:O	2.39	0.50
1:0:1350:U:H2'	1:0:1351:G:O4'	2.11	0.50
15:M:41:GLU:HG3	40:M:9344:HOH:O	2.12	0.50
15:M:48:LYS:O	15:M:52:GLN:HG3	2.12	0.50
4:A:39:ALA:HB3	4:A:61:GLU:OE2	2.11	0.50
1:0:2507:G:H2'	1:0:2510:C:N4	2.27	0.50
12:J:47:THR:HG22	12:J:48:GLY:N	2.26	0.50
1:0:119:A:H2'	1:0:120:A:H5''	1.93	0.50
9:F:50:VAL:CG2	9:F:63:ILE:HG21	2.41	0.50
13:K:28:GLU:HB3	13:K:59:LYS:HB2	1.93	0.50
31:3:35:TRP:HB2	40:3:9493:HOH:O	2.12	0.50
1:0:2265:U:H2'	1:0:2266:A:C8	2.47	0.50
21:S:33:SER:O	21:S:37:VAL:HG23	2.10	0.50
13:K:132:VAL:HG11	23:U:22:VAL:HG22	1.93	0.50
4:A:191:GLY:HA2	4:A:194:MET:HE3	1.91	0.50
7:D:136:ARG:HB3	7:D:137:PRO:HD2	1.93	0.50
1:0:292:G:H2'	1:0:358:G:N2	2.27	0.50
40:0:3164:HOH:O	25:W:119:HIS:HE1	1.95	0.50
1:0:2524:G:N2	1:0:2526:C:H5	2.10	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1477:C:H5'	1:0:1868:G:C5'	2.41	0.50
11:H:158:THR:HB	11:H:159:PRO:HD3	1.94	0.50
16:N:36:ALA:O	16:N:37:ARG:HD2	2.12	0.50
12:J:13:ASP:OD1	12:J:15:ARG:HB3	2.12	0.50
8:E:20:ILE:HD11	8:E:40:VAL:CG1	2.39	0.50
7:D:25:MET:CE	7:D:41:LEU:HG	2.38	0.50
10:G:12:ILE:HD12	40:G:692:HOH:O	2.11	0.50
1:0:65:C:O2'	1:0:66:G:H5'	2.12	0.50
6:C:104:ASP:O	6:C:108:GLN:HG3	2.12	0.50
40:0:5157:HOH:O	4:A:206:ARG:HD3	2.11	0.49
27:Y:115:ARG:NE	40:Y:9356:HOH:O	2.45	0.49
17:O:97:SER:OG	17:O:100:GLN:HG3	2.12	0.49
8:E:7:ILE:HG22	8:E:45:ASP:O	2.11	0.49
21:S:29:ASP:OD1	21:S:31:ARG:NH1	2.45	0.49
18:P:141:ILE:C	18:P:143:ALA:H	2.14	0.49
20:R:84:ALA:O	20:R:88:PHE:HD1	1.95	0.49
2:9:3023:U:O2'	2:9:3024:U:H4'	2.12	0.49
8:E:166:VAL:HG12	40:E:3134:HOH:O	2.12	0.49
5:B:212:GLN:HB2	5:B:257:THR:CG2	2.38	0.49
7:D:25:MET:CE	7:D:40:ILE:HD11	2.42	0.49
32:I:74:PRO:C	32:I:112:LYS:HZ1	2.14	0.49
24:V:39:ALA:O	24:V:41:GLU:N	2.44	0.49
1:0:2072:G:H3'	1:0:2073:G:C5'	2.42	0.49
16:N:114:LYS:O	16:N:118:ILE:HG13	2.12	0.49
1:0:1279:U:O2	1:0:1279:U:H2'	2.12	0.49
11:H:27:LYS:H	11:H:59:HIS:CD2	2.20	0.49
1:0:2541:U:C2	1:0:2619:UR3:H3U2	2.47	0.49
20:R:104:PHE:HB3	20:R:109:MET:HE1	1.94	0.49
28:Z:30:GLU:HG2	28:Z:33:MET:HE3	1.95	0.49
22:T:38:ARG:HG3	22:T:38:ARG:HH11	1.77	0.49
1:0:2911:C:O2'	1:0:2912:C:H5'	2.12	0.49
1:0:944:G:H21	25:W:44:MET:CE	2.26	0.49
27:Y:203:VAL:CG1	27:Y:228:VAL:HG22	2.42	0.49
6:C:236:THR:H	6:C:239:ALA:HB3	1.77	0.49
20:R:29:LYS:NZ	40:R:9451:HOH:O	2.45	0.49
1:0:2889:U:H4'	1:0:2890:A:H5'	1.95	0.49
11:H:58:ARG:HG3	11:H:58:ARG:NH1	2.27	0.49
4:A:232:ARG:NH2	4:A:236:GLY:O	2.37	0.49
29:1:25:LYS:O	29:1:25:LYS:HG2	2.12	0.49
11:H:45:VAL:HA	11:H:167:PRO:O	2.12	0.49
6:C:118:THR:O	6:C:136:VAL:HG13	2.11	0.49
16:N:179:LEU:HD23	16:N:184:ILE:HD12	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1200:A:H3'	40:0:6281:HOH:O	2.11	0.49
1:0:2502:C:H2'	1:0:2503:A:H5'	1.95	0.49
1:0:926:A:O2'	14:L:41:HIS:HD2	1.96	0.49
1:0:309:C:OP1	22:T:97:ARG:NH2	2.39	0.49
1:0:2346:C:H4'	7:D:52:THR:CG2	2.42	0.49
14:L:144:ASP:HA	14:L:147:GLU:OE1	2.11	0.49
1:0:1592:G:H2'	1:0:1593:C:C6	2.48	0.49
5:B:320:GLN:HE21	5:B:321:PRO:HD2	1.77	0.49
4:A:217:ARG:HH11	4:A:217:ARG:HG3	1.76	0.49
1:0:678:G:OP2	6:C:107:ARG:NH2	2.45	0.49
7:D:24:HIS:HB2	7:D:72:LYS:CB	2.43	0.49
21:S:8:PRO:HD2	24:V:32:ALA:HA	1.95	0.49
12:J:142:ASN:O	12:J:144:THR:N	2.46	0.49
1:0:2100:A:H4'	6:C:64:GLY:O	2.12	0.49
1:0:1118:A:C8	1:0:1118:A:C3'	2.90	0.49
6:C:27:ARG:O	6:C:31:ILE:HG13	2.13	0.49
11:H:46:GLN:NE2	11:H:137:TYR:HE2	2.08	0.49
13:K:62:PRO:HG3	13:K:65:ARG:NH2	2.26	0.49
27:Y:145:LYS:HE2	40:Y:9405:HOH:O	2.11	0.49
2:9:3052:A:O2'	2:9:3053:G:H5'	2.13	0.49
12:J:45:VAL:HG22	12:J:46:ILE:N	2.27	0.49
8:E:81:GLU:HG2	8:E:134:SER:CB	2.42	0.49
1:0:820:G:O2'	1:0:856:G:H4'	2.13	0.49
16:N:110:THR:HB	16:N:113:SER:HG	1.75	0.49
1:0:1666:C:C2'	1:0:1667:A:C5'	2.91	0.49
7:D:24:HIS:HB2	7:D:72:LYS:HB3	1.94	0.49
1:0:542:A:H2'	1:0:543:G:O4'	2.12	0.49
22:T:112:LEU:HD23	22:T:119:ALA:HB3	1.93	0.49
9:F:111:ILE:O	9:F:115:VAL:HG23	2.13	0.49
7:D:50:VAL:O	7:D:71:ALA:HA	2.13	0.49
16:N:82:TYR:OH	16:N:176:ARG:NH1	2.46	0.49
20:R:132:ARG:NH2	40:R:9494:HOH:O	2.46	0.49
1:0:797:A:H4'	28:Z:10:ARG:N	2.28	0.49
1:0:775:G:OP1	29:1:16:HIS:HE1	1.96	0.49
30:2:35:ARG:HB2	40:2:2691:HOH:O	2.11	0.49
1:0:2090:G:H2'	1:0:2091:G:C8	2.47	0.49
5:B:265:LEU:HD21	5:B:316:ARG:HD3	1.95	0.49
1:0:2846:C:H4'	40:0:5619:HOH:O	2.11	0.49
1:0:1506:U:H6	1:0:1506:U:H5'	1.78	0.49
22:T:71:VAL:HG13	22:T:91:LEU:O	2.13	0.48
40:0:4331:HOH:O	22:T:9:LYS:HD3	2.13	0.48
16:N:167:ASP:C	16:N:168:LEU:HG	2.34	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:V:64:GLY:O	24:V:65:ASP:CB	2.60	0.48
8:E:69:ILE:HA	8:E:72:MET:CE	2.43	0.48
18:P:10:ALA:HA	18:P:13:VAL:HG12	1.94	0.48
16:N:36:ALA:C	16:N:37:ARG:HD2	2.34	0.48
22:T:89:ARG:O	22:T:89:ARG:HG3	2.13	0.48
6:C:246:ARG:NH1	40:C:9174:HOH:O	2.45	0.48
1:O:1119:G:N2	1:O:1246:A:N1	2.61	0.48
17:O:14:LEU:CG	17:O:102:ILE:HD11	2.43	0.48
1:O:920:C:H4'	1:O:921:G:C2	2.49	0.48
1:O:999:C:H2'	1:O:1000:C:O4'	2.12	0.48
7:D:25:MET:CE	7:D:37:ALA:HB1	2.42	0.48
5:B:190:MET:CE	5:B:194:PHE:CD1	2.96	0.48
1:O:475:G:OP1	6:C:73:LEU:HD22	2.12	0.48
27:Y:126:PRO:HG2	27:Y:128:PHE:CZ	2.49	0.48
4:A:52:SER:HB2	4:A:164:ARG:HH11	1.78	0.48
6:C:104:ASP:HA	6:C:107:ARG:NH1	2.27	0.48
28:Z:36:ASP:HB3	28:Z:45:ASP:O	2.13	0.48
1:O:2408:A:H4'	31:3:15:ASN:O	2.13	0.48
1:O:1183:C:H5	1:O:1192:A:OP1	1.96	0.48
1:O:319:A:H4'	1:O:338:C:C5	2.48	0.48
1:O:1527:A:H1'	1:O:1528:A:C8	2.48	0.48
1:O:2508:C:H2'	40:O:7232:HOH:O	2.12	0.48
1:O:2102:G:H5''	1:O:2538:A:C2	2.48	0.48
26:X:34:ARG:NH1	26:X:48:VAL:O	2.46	0.48
24:V:39:ALA:C	24:V:41:GLU:N	2.65	0.48
6:C:157:LEU:HD22	6:C:162:VAL:CG1	2.43	0.48
22:T:38:ARG:HG3	22:T:38:ARG:NH1	2.29	0.48
16:N:36:ALA:HB1	16:N:118:ILE:HD12	1.96	0.48
1:O:2509:A:H2'	1:O:2510:C:O4'	2.13	0.48
16:N:69:TYR:CE2	16:N:184:ILE:HG13	2.49	0.48
16:N:73:ALA:N	40:N:9360:HOH:O	2.45	0.48
1:O:1921:A:O2'	1:O:1922:A:H5'	2.14	0.48
11:H:34:GLY:HA3	11:H:84:LYS:HA	1.95	0.48
17:O:80:ASP:OD1	17:O:81:PHE:N	2.45	0.48
1:O:2472:C:O2'	1:O:2634:G:H4'	2.13	0.48
26:X:7:GLU:HA	26:X:74:ALA:O	2.14	0.48
15:M:59:GLY:HA3	15:M:141:ILE:HD12	1.95	0.48
15:M:24:GLN:HA	15:M:24:GLN:NE2	2.28	0.48
12:J:131:THR:HB	12:J:134:GLU:OE1	2.14	0.48
1:O:2032:U:H2'	1:O:2033:G:H5'	1.94	0.48
1:O:666:A:H2'	1:O:667:C:O4'	2.14	0.48
13:K:27:ARG:HD2	40:K:4747:HOH:O	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:72:GLU:HG3	28:Z:66:GLY:HA2	1.95	0.48
14:L:10:SER:O	14:L:11:ARG:HB3	2.14	0.48
5:B:56:ASP:HB3	5:B:322:ARG:HE	1.79	0.48
9:F:60:VAL:O	9:F:60:VAL:CG1	2.61	0.48
12:J:107:ASN:HD21	12:J:109:TYR:HB2	1.78	0.48
25:W:65:VAL:CG1	25:W:116:LEU:HD13	2.42	0.48
18:P:98:ILE:HD12	18:P:102:ARG:CZ	2.43	0.48
1:O:969:G:H1	1:O:999:C:H42	1.62	0.48
1:O:2883:A:H2'	1:O:2884:G:O4'	2.14	0.48
14:L:97:VAL:HG12	14:L:98:GLU:O	2.13	0.48
14:L:123:ASP:O	14:L:146:GLY:HA2	2.13	0.48
15:M:184:ARG:HG3	15:M:185:PRO:HA	1.96	0.48
1:O:1724:U:H5''	40:O:4309:HOH:O	2.12	0.48
9:F:46:GLU:O	9:F:73:PRO:HD2	2.14	0.48
15:M:182:LYS:O	15:M:194:ALA:HB2	2.14	0.48
6:C:84:VAL:O	6:C:85:LYS:HB2	2.14	0.48
1:O:653:C:H2'	1:O:654:A:C8	2.48	0.48
21:S:56:ASN:O	30:2:8:LYS:NZ	2.42	0.48
1:O:2587:OMU:H6	1:O:2587:OMU:O5'	2.13	0.48
1:O:1739:G:H1'	1:O:2726:U:O4	2.13	0.48
24:V:1:THR:CG2	24:V:2:VAL:H	2.20	0.48
1:O:558:C:C2'	1:O:559:U:H5''	2.44	0.48
14:L:91:VAL:CG1	14:L:120:LEU:HD23	2.43	0.48
1:O:2769:C:H2'	1:O:2770:G:H5'	1.95	0.48
24:V:8:ILE:HG21	24:V:59:ILE:HG13	1.96	0.48
11:H:3:ALA:HA	11:H:58:ARG:NH1	2.28	0.48
40:O:5826:HOH:O	25:W:122:ARG:NH2	2.41	0.48
17:O:96:VAL:HG13	17:O:100:GLN:HB2	1.96	0.48
1:O:1789:G:O6	18:P:73:HIS:HE1	1.97	0.48
8:E:5:LEU:HD21	8:E:66:GLN:HG3	1.95	0.48
16:N:64:SER:C	16:N:66:LEU:H	2.17	0.48
25:W:142:ASP:HB2	40:W:2729:HOH:O	2.14	0.48
1:O:1603:A:H5''	1:O:1605:G:H5'	1.96	0.47
15:M:79:ALA:HB3	15:M:81:ARG:HH12	1.79	0.47
1:O:2852:A:H5''	40:O:5770:HOH:O	2.14	0.47
5:B:41:PHE:CG	5:B:190:MET:HE3	2.49	0.47
14:L:61:ALA:HB2	14:L:105:TYR:CZ	2.49	0.47
1:O:1044:C:H5''	40:O:9649:HOH:O	2.13	0.47
15:M:43:PRO:HG3	15:M:62:VAL:HG21	1.95	0.47
1:O:1736:A:H1'	40:O:8086:HOH:O	2.14	0.47
13:K:14:LYS:HG3	13:K:32:ILE:O	2.13	0.47
5:B:267:LYS:HD2	40:B:9530:HOH:O	2.13	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:R:106:GLY:HA2	20:R:109:MET:CE	2.44	0.47
14:L:35:ARG:HD3	14:L:35:ARG:C	2.35	0.47
1:0:2895:C:H4'	40:X:4132:HOH:O	2.13	0.47
2:9:3048:C:H4'	16:N:141:ARG:HH21	1.79	0.47
1:0:2112:A:H2'	1:0:2113:G:C8	2.49	0.47
13:K:55:VAL:CG1	13:K:56:SER:N	2.77	0.47
1:0:2812:A:N7	40:0:7959:HOH:O	2.35	0.47
1:0:2749:U:H5'	40:0:8433:HOH:O	2.13	0.47
27:Y:154:ARG:HH12	27:Y:155:ARG:CG	2.21	0.47
1:0:1730:G:H5''	1:0:1731:C:C6	2.49	0.47
5:B:58:PRO:HA	5:B:63:GLU:CD	2.34	0.47
22:T:81:LYS:HD2	22:T:87:VAL:HG11	1.96	0.47
4:A:149:ASP:OD1	4:A:151:GLN:HB2	2.14	0.47
26:X:74:ALA:CB	26:X:85:VAL:HG22	2.44	0.47
1:0:1972:U:H2'	1:0:1973:A:C5'	2.44	0.47
31:3:11:CYS:HB2	31:3:20:HIS:CE1	2.50	0.47
5:B:51:VAL:HG22	5:B:52:VAL:N	2.29	0.47
1:0:2611:G:H5'	1:0:2613:G:C8	2.49	0.47
32:I:106:LYS:O	32:I:110:GLU:HG3	2.14	0.47
1:0:558:C:C2'	1:0:559:U:C5'	2.93	0.47
16:N:152:GLU:C	16:N:154:LEU:H	2.16	0.47
17:O:59:VAL:HG21	17:O:111:VAL:HG21	1.94	0.47
12:J:130:VAL:HG12	12:J:131:THR:N	2.30	0.47
1:0:317:A:OP1	22:T:52:ARG:O	2.33	0.47
6:C:133:ARG:HG3	6:C:133:ARG:HH11	1.79	0.47
40:0:7351:HOH:O	15:M:178:LYS:HB2	2.14	0.47
5:B:53:LEU:HD21	5:B:270:ILE:HD12	1.97	0.47
23:U:11:THR:HG22	23:U:53:ASP:OD2	2.15	0.47
1:0:2717:C:H2'	1:0:2718:C:C5'	2.40	0.47
16:N:166:ALA:O	16:N:167:ASP:O	2.33	0.47
11:H:29:ALA:HB3	11:H:66:ARG:HH12	1.80	0.47
5:B:5:ARG:NH1	5:B:8:LYS:HE2	2.30	0.47
2:9:3018:U:H2'	2:9:3019:G:C8	2.50	0.47
1:0:2906:A:H5'	1:0:2907:C:O4'	2.15	0.47
1:0:2545:U:OP2	5:B:2:GLN:NE2	2.47	0.47
1:0:1979:G:O2'	1:0:1980:U:OP1	2.27	0.47
6:C:25:PRO:HG2	40:C:9125:HOH:O	2.14	0.47
1:0:2681:A:H4'	1:0:2682:C:H5'	1.97	0.47
1:0:1185:U:H2'	1:0:1186:C:C6	2.48	0.47
40:0:3822:HOH:O	32:I:92:PRO:HD3	2.13	0.47
1:0:1881:A:OP1	4:A:199:HIS:HE1	1.97	0.47
23:U:52:THR:HG22	23:U:54:THR:H	1.77	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:L:80:ASP:HB2	14:L:90:ARG:HB3	1.96	0.47
1:O:2443:C:H1'	14:L:56:LYS:HE3	1.97	0.47
27:Y:184:GLU:OE1	27:Y:204:ARG:NH1	2.48	0.47
11:H:56:GLN:HE21	11:H:126:ARG:HE	1.61	0.47
1:O:2421:G:H4'	40:O:5324:HOH:O	2.13	0.47
1:O:1406:A:H4'	1:O:1407:A:C5'	2.45	0.47
14:L:98:GLU:O	14:L:99:GLU:HB2	2.15	0.47
24:V:5:VAL:CG1	24:V:9:ARG:NH1	2.78	0.47
6:C:218:VAL:N	40:C:9225:HOH:O	2.48	0.47
1:O:185:G:H4'	1:O:186:A:H4'	1.96	0.47
26:X:25:ARG:HD2	40:X:5356:HOH:O	2.15	0.47
2:9:3059:C:H2'	2:9:3060:C:C6	2.50	0.47
8:E:106:ASN:ND2	8:E:109:GLY:HA2	2.30	0.47
7:D:84:LEU:HA	7:D:87:ALA:HB3	1.97	0.47
13:K:98:VAL:HG22	13:K:102:GLU:C	2.35	0.47
1:O:29:C:C2'	1:O:30:U:H5'	2.44	0.47
7:D:146:LYS:NZ	16:N:107:ASN:HD21	2.13	0.47
5:B:41:PHE:HB3	5:B:190:MET:HE1	1.97	0.47
14:L:53:ARG:HH22	14:L:57:VAL:HG12	1.80	0.47
1:O:2503:A:P	11:H:151:ARG:HH22	2.38	0.47
32:I:131:THR:O	32:I:135:LEU:HG	2.15	0.47
1:O:710:G:H5'	17:O:25:VAL:HG13	1.97	0.47
6:C:133:ARG:NE	6:C:138:VAL:HG22	2.29	0.47
1:O:932:U:H2'	1:O:933:C:C6	2.50	0.47
1:O:1992:U:OP2	13:K:66:ARG:HD2	2.14	0.47
9:F:118:LEU:O	9:F:119:ARG:HB3	2.15	0.47
27:Y:187:VAL:HG23	27:Y:192:ASP:HB3	1.96	0.47
1:O:1066:U:H2'	1:O:1067:A:C8	2.49	0.47
27:Y:99:ALA:HB2	27:Y:233:TYR:CE2	2.50	0.47
6:C:133:ARG:HE	6:C:138:VAL:HG22	1.79	0.47
13:K:101:ASN:O	13:K:102:GLU:HB2	2.15	0.47
31:3:55:VAL:HG22	40:3:9444:HOH:O	2.15	0.47
26:X:61:ARG:HB2	26:X:65:ASN:HB2	1.97	0.47
26:X:66:THR:HG23	26:X:67:PRO:HD2	1.96	0.47
1:O:475:G:C5'	6:C:73:LEU:HD23	2.45	0.47
1:O:1853:C:O2'	4:A:217:ARG:NH2	2.49	0.47
29:1:28:HIS:CD2	29:1:30:LYS:HB2	2.50	0.47
16:N:37:ARG:NE	40:N:9330:HOH:O	2.47	0.47
12:J:43:ARG:HG2	40:J:5361:HOH:O	2.15	0.47
2:9:3091:C:H2'	2:9:3092:G:O4'	2.15	0.47
4:A:36:ASP:HB2	4:A:85:SER:H	1.79	0.46
1:O:1667:A:C8	1:O:1667:A:H5'	2.41	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:3:42:ARG:HH11	31:3:42:ARG:HG3	1.80	0.46
20:R:104:PHE:CB	20:R:109:MET:HE1	2.45	0.46
5:B:87:TYR:O	5:B:138:GLY:N	2.34	0.46
16:N:119:GLN:O	16:N:123:ILE:HG13	2.15	0.46
8:E:1:PRO:HG2	8:E:59:MET:SD	2.56	0.46
18:P:89:ASN:HB3	18:P:92:GLU:HB2	1.96	0.46
40:O:5274:HOH:O	16:N:21:HIS:HD2	1.97	0.46
8:E:126:ILE:HB	8:E:131:LEU:CD2	2.46	0.46
8:E:84:MET:HE1	8:E:148:ILE:HD12	1.97	0.46
17:O:47:ARG:HG3	17:O:47:ARG:HH11	1.80	0.46
26:X:85:VAL:HG12	26:X:86:GLU:N	2.30	0.46
25:W:88:THR:CG2	25:W:89:ASP:H	2.28	0.46
32:I:139:ILE:CG2	32:I:140:GLU:N	2.78	0.46
40:O:3549:HOH:O	6:C:78:ARG:HD3	2.15	0.46
1:O:447:A:OP1	22:T:2:LYS:HG2	2.15	0.46
1:O:1333:U:H2'	1:O:1334:C:H6	1.80	0.46
11:H:30:GLN:H	11:H:66:ARG:HH11	1.63	0.46
10:G:64:ASN:N	10:G:64:ASN:ND2	2.63	0.46
2:9:3001:U:H5'	2:9:3121:C:O2	2.15	0.46
16:N:78:MET:HB2	16:N:79:PRO:HD3	1.97	0.46
7:D:154:LYS:H	7:D:154:LYS:CD	2.24	0.46
1:O:57:C:H5'	24:V:46:ILE:HG21	1.98	0.46
16:N:167:ASP:O	16:N:168:LEU:HG	2.15	0.46
25:W:122:ARG:HG3	25:W:152:ALA:O	2.14	0.46
2:9:3039:U:H1'	2:9:3044:A:N6	2.30	0.46
31:3:60:LYS:HG3	31:3:61:PRO:HD2	1.96	0.46
30:2:5:LYS:O	30:2:9:LYS:HG3	2.15	0.46
15:M:68:ARG:NH2	15:M:73:ARG:HD3	2.31	0.46
5:B:305:ASP:O	5:B:306:LYS:CB	2.63	0.46
1:O:500:G:O2'	20:R:94:ASN:ND2	2.48	0.46
5:B:243:ASN:HA	5:B:244:PRO:C	2.36	0.46
20:R:119:VAL:O	20:R:119:VAL:CG1	2.63	0.46
1:O:1211:G:O2'	1:O:1212:C:H5'	2.16	0.46
4:A:71:PRO:HD2	4:A:74:VAL:HG21	1.98	0.46
17:O:88:LYS:HD3	40:O:7061:HOH:O	2.15	0.46
23:U:20:MET:CE	23:U:30:HIS:NE2	2.79	0.46
2:9:3029:C:H2'	2:9:3030:C:C5'	2.42	0.46
22:T:40:VAL:HG22	22:T:41:ARG:H	1.81	0.46
29:1:8:GLN:HE22	29:1:11:LYS:HZ1	1.62	0.46
17:O:14:LEU:CD2	17:O:102:ILE:HD11	2.46	0.46
4:A:132:ASP:OD1	4:A:133:ARG:N	2.49	0.46
4:A:70:ALA:HA	4:A:71:PRO:HD3	1.76	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:F:21:GLU:O	9:F:24:ARG:HG3	2.15	0.46
20:R:33:ARG:NH1	40:R:9454:HOH:O	2.40	0.46
1:O:399:C:H5'	15:M:179:GLY:O	2.15	0.46
4:A:58:VAL:HG21	4:A:68:ILE:HD12	1.98	0.46
3:4:76:DA:H5''	38:4:9701:SPS:C6	2.45	0.46
14:L:143:THR:CG2	14:L:144:ASP:N	2.78	0.46
14:L:120:LEU:HD12	14:L:133:VAL:HG21	1.97	0.46
17:O:26:TRP:HA	17:O:26:TRP:CE3	2.50	0.46
1:O:1717:A:H5''	18:P:54:LYS:HB2	1.97	0.46
1:O:2019:A:H5'	40:O:5087:HOH:O	2.16	0.46
1:O:462:A:H2'	40:O:5427:HOH:O	2.15	0.46
1:O:622:G:P	27:Y:148:GLY:HA3	2.55	0.46
5:B:312:ARG:HD3	5:B:315:VAL:HG13	1.97	0.46
5:B:51:VAL:HG23	5:B:327:VAL:HG13	1.97	0.46
23:U:17:THR:CG2	23:U:18:GLY:H	2.27	0.46
26:X:9:VAL:HG13	26:X:88:GLU:OE2	2.15	0.46
1:O:1299:G:H5'	40:O:4642:HOH:O	2.15	0.46
15:M:90:ARG:HB2	31:3:46:ILE:HD11	1.98	0.46
25:W:29:VAL:O	25:W:30:ASN:HB2	2.16	0.46
4:A:96:LEU:HG	4:A:152:CYS:O	2.16	0.46
13:K:114:ALA:HB3	13:K:117:VAL:HG23	1.96	0.46
31:3:18:GLN:OE1	31:3:73:GLU:HB3	2.15	0.46
15:M:95:LYS:HA	15:M:170:ASN:HD21	1.81	0.46
25:W:88:THR:CG2	25:W:90:TYR:HD1	2.27	0.46
31:3:69:TYR:O	31:3:77:ALA:HA	2.16	0.46
1:O:57:C:H5'	24:V:46:ILE:CG2	2.46	0.46
1:O:951:A:O2'	1:O:952:G:H5'	2.16	0.46
11:H:18:GLU:HG3	11:H:19:TYR:CE1	2.51	0.46
1:O:2837:U:H2'	40:O:7315:HOH:O	2.14	0.46
4:A:66:ARG:HH11	4:A:66:ARG:HB2	1.80	0.46
5:B:140:LEU:HD23	40:B:9578:HOH:O	2.16	0.46
22:T:41:ARG:NH1	22:T:42:VAL:O	2.49	0.46
27:Y:144:ARG:NH1	40:Y:9377:HOH:O	2.49	0.46
1:O:834:G:H3'	1:O:835:U:H4'	1.98	0.46
17:O:25:VAL:HG23	40:O:3062:HOH:O	2.16	0.46
2:9:3006:C:H4'	16:N:35:VAL:HG11	1.98	0.46
26:X:25:ARG:NH2	40:X:5740:HOH:O	2.48	0.46
4:A:126:ALA:HB1	4:A:138:VAL:CG1	2.46	0.46
1:O:1940:C:H4'	40:O:7797:HOH:O	2.14	0.46
1:O:204:A:C2'	1:O:205:U:H5'	2.46	0.46
4:A:125:ASN:HB3	4:A:158:VAL:HG12	1.98	0.46
1:O:432:G:O2'	1:O:433:C:H5'	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:451:C:O2'	1:0:452:G:H5'	2.15	0.46
2:9:3028:U:H2'	2:9:3029:C:C6	2.51	0.46
27:Y:151:SER:HB3	27:Y:154:ARG:HB3	1.98	0.46
1:0:1202:A:H2'	1:0:1203:G:O4'	2.16	0.46
14:L:144:ASP:O	14:L:147:GLU:HB2	2.16	0.46
38:4:9701:SPS:O1	38:4:9701:SPS:H91	2.16	0.46
17:O:26:TRP:HA	17:O:26:TRP:HE3	1.80	0.46
11:H:73:LEU:HD21	11:H:146:VAL:HA	1.98	0.46
5:B:41:PHE:CG	5:B:79:MET:HE2	2.51	0.45
1:0:1167:G:H2'	1:0:1168:C:O4'	2.16	0.45
1:0:1730:G:H5'	1:0:1731:C:C6	2.50	0.45
23:U:52:THR:CG2	23:U:54:THR:HB	2.46	0.45
1:0:664:U:O4	1:0:681:G:H5"	2.16	0.45
5:B:71:VAL:CG1	5:B:296:LEU:HD22	2.46	0.45
18:P:135:ALA:HB1	18:P:139:ARG:NH1	2.31	0.45
15:M:66:SER:HB3	15:M:128:TRP:NE1	2.31	0.45
5:B:138:GLY:O	5:B:139:ASP:O	2.34	0.45
20:R:82:GLU:OE1	20:R:86:LYS:HE3	2.16	0.45
8:E:81:GLU:HG2	8:E:134:SER:HB3	1.97	0.45
8:E:81:GLU:O	8:E:172:PRO:HD3	2.16	0.45
1:0:2679:G:H2'	1:0:2681:A:OP2	2.15	0.45
1:0:1086:A:C6	25:W:11:VAL:HG11	2.51	0.45
1:0:2531:U:O2'	1:0:2532:A:H5'	2.16	0.45
1:0:1419:U:H2'	1:0:1685:A:C2	2.52	0.45
7:D:159:PRO:O	7:D:163:VAL:HG23	2.17	0.45
4:A:36:ASP:O	4:A:36:ASP:CG	2.54	0.45
1:0:1165:G:O3'	1:0:1174:A:H4'	2.16	0.45
1:0:136:C:H2'	1:0:137:U:O4'	2.15	0.45
26:X:76:ARG:O	26:X:77:PHE:HB3	2.16	0.45
18:P:16:VAL:HG13	18:P:20:ARG:NH1	2.31	0.45
9:F:26:THR:HG21	9:F:103:GLU:HG3	1.97	0.45
1:0:415:A:O2'	1:0:416:G:H5'	2.17	0.45
1:0:2825:C:H4'	1:0:2826:G:O5'	2.15	0.45
25:W:88:THR:CG2	25:W:89:ASP:N	2.78	0.45
23:U:14:GLU:OE1	23:U:15:PRO:HD2	2.17	0.45
16:N:33:ARG:NH2	40:N:9350:HOH:O	2.50	0.45
1:0:249:G:O2'	1:0:250:C:H5'	2.17	0.45
27:Y:106:THR:CG2	27:Y:107:PRO:HD2	2.47	0.45
1:0:1847:A:OP1	4:A:175:LYS:HG3	2.16	0.45
1:0:1135:G:H5'	40:0:6446:HOH:O	2.16	0.45
9:F:20:LEU:HB2	9:F:49:PHE:CZ	2.51	0.45
1:0:1829:A:H2'	1:0:1830:C:H5'	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:L:89:PHE:CD1	14:L:89:PHE:N	2.85	0.45
1:O:289:G:H5'	40:O:5159:HOH:O	2.17	0.45
15:M:107:ARG:CG	15:M:107:ARG:NH1	2.78	0.45
1:O:2619:UR3:H2'	1:O:2620:U:C6	2.51	0.45
8:E:101:GLU:HA	8:E:118:ILE:HG13	1.97	0.45
23:U:20:MET:CG	23:U:28:THR:HG23	2.47	0.45
8:E:16:ASP:O	8:E:17:HIS:HB2	2.15	0.45
12:J:54:VAL:HG11	12:J:138:THR:HG21	1.99	0.45
6:C:124:VAL:HA	6:C:230:GLY:O	2.16	0.45
22:T:12:ARG:NH1	40:T:3035:HOH:O	2.49	0.45
2:9:3005:G:OP1	16:N:17:ARG:NH2	2.50	0.45
15:M:164:THR:CG2	15:M:166:ALA:H	2.27	0.45
13:K:109:LEU:CD1	13:K:113:ILE:HD11	2.46	0.45
12:J:103:VAL:HG12	40:J:5907:HOH:O	2.16	0.45
17:O:59:VAL:CG2	17:O:111:VAL:CG2	2.95	0.45
7:D:51:ARG:HD3	40:D:7636:HOH:O	2.16	0.45
1:O:734:U:H1'	1:O:737:A:N6	2.32	0.45
24:V:25:THR:HG22	24:V:29:ASN:ND2	2.32	0.45
9:F:102:GLY:O	9:F:103:GLU:HB2	2.16	0.45
40:O:9834:HOH:O	4:A:11:ARG:HD3	2.17	0.45
23:U:6:CYS:C	23:U:8:TYR:H	2.19	0.45
20:R:25:PHE:CZ	20:R:29:LYS:HE2	2.50	0.45
5:B:217:ARG:HG3	5:B:257:THR:CG2	2.47	0.45
7:D:167:GLU:C	7:D:169:THR:H	2.20	0.45
16:N:86:LEU:O	16:N:90:LEU:HG	2.15	0.45
14:L:66:VAL:HG23	14:L:67:ARG:N	2.31	0.45
26:X:43:VAL:CG1	26:X:47:ALA:HB3	2.45	0.45
1:O:2697:A:H2'	1:O:2698:G:O4'	2.17	0.45
1:O:1130:U:H2'	1:O:1131:G:O4'	2.17	0.45
1:O:1624:A:H4'	1:O:1625:U:H5'	1.99	0.45
6:C:168:ARG:NH2	6:C:190:ALA:O	2.50	0.45
1:O:371:U:H2'	1:O:372:A:H8	1.80	0.45
22:T:71:VAL:CG1	22:T:90:PRO:HB3	2.25	0.45
25:W:3:ALA:O	25:W:54:PHE:HA	2.17	0.45
1:O:2506:A:O2'	1:O:2507:G:O5'	2.35	0.45
15:M:81:ARG:HG2	15:M:85:ARG:O	2.16	0.45
26:X:30:MET:HB2	26:X:30:MET:HE3	1.76	0.45
26:X:73:ARG:NH1	26:X:88:GLU:HG2	2.32	0.45
40:O:5514:HOH:O	11:H:58:ARG:HG3	2.16	0.45
1:O:2289:G:H21	1:O:2291:A:H2	1.62	0.45
4:A:122:SER:O	4:A:124:VAL:HG13	2.17	0.45
1:O:1745:G:H22	1:O:2033:G:H5'	1.82	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:968:G:O2'	1:0:969:G:H5'	2.17	0.45
1:0:2356:A:H2'	1:0:2357:G:O4'	2.16	0.45
1:0:1149:U:H5''	1:0:1151:G:O4'	2.17	0.45
9:F:68:ASP:C	9:F:70:LYS:H	2.20	0.45
6:C:236:THR:O	6:C:237:GLU:C	2.54	0.45
24:V:38:GLY:C	24:V:40:PRO:HD2	2.36	0.45
23:U:9:CYS:CA	23:U:52:THR:HG23	2.47	0.45
6:C:233:THR:HG22	6:C:234:VAL:H	1.82	0.45
8:E:69:ILE:HA	8:E:72:MET:HE3	1.97	0.45
4:A:130:THR:HG22	4:A:131:HIS:O	2.17	0.45
5:B:80:ARG:HB2	5:B:145:HIS:CE1	2.52	0.45
1:0:1741:U:H3'	40:0:3369:HOH:O	2.16	0.45
1:0:497:A:H2'	1:0:498:A:C5'	2.47	0.45
1:0:59:A:H5'	40:0:4886:HOH:O	2.15	0.45
7:D:60:GLU:O	7:D:61:PHE:C	2.55	0.45
1:0:1180:U:H1'	40:0:3822:HOH:O	2.17	0.45
31:3:75:GLY:HA2	40:3:9510:HOH:O	2.16	0.45
4:A:88:ILE:HD13	4:A:100:PRO:CD	2.46	0.45
5:B:254:GLN:NE2	40:B:9588:HOH:O	2.49	0.45
30:2:20:ARG:HG3	30:2:21:VAL:N	2.31	0.45
4:A:66:ARG:HH11	4:A:66:ARG:CB	2.29	0.45
1:0:1151:G:OP1	10:G:63:ARG:NH1	2.50	0.45
1:0:1654:U:H2'	4:A:47:HIS:HD2	1.82	0.45
13:K:119:GLN:O	13:K:119:GLN:HG2	2.17	0.45
1:0:120:A:H2'	1:0:120:A:N3	2.32	0.45
31:3:38:ARG:CB	31:3:42:ARG:HH12	2.25	0.45
4:A:128:LEU:HD21	4:A:131:HIS:CE1	2.51	0.45
1:0:2073:G:H5''	40:0:4398:HOH:O	2.16	0.45
7:D:170:TYR:O	7:D:171:ASP:CB	2.65	0.45
1:0:968:G:H1'	11:H:32:LYS:HD2	1.98	0.45
1:0:2329:C:O2'	1:0:2330:U:H5'	2.17	0.45
7:D:10:PHE:CD1	7:D:11:HIS:N	2.85	0.45
13:K:87:ARG:NH1	40:K:4066:HOH:O	2.49	0.44
1:0:2591:C:H2'	1:0:2592:G:O4'	2.17	0.44
1:0:1603:A:C5'	1:0:1605:G:H5'	2.47	0.44
12:J:19:MET:HE2	12:J:132:LEU:HD11	1.98	0.44
6:C:157:LEU:HD22	6:C:162:VAL:HG11	1.98	0.44
18:P:13:VAL:HG11	18:P:40:VAL:CG1	2.47	0.44
11:H:29:ALA:C	11:H:30:GLN:HG3	2.38	0.44
1:0:2415:A:H2'	1:0:2416:G:H5'	1.98	0.44
26:X:25:ARG:HD3	26:X:64:ALA:O	2.17	0.44
1:0:1942:A:H3'	40:0:7797:HOH:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:N:74:PRO:HG2	16:N:159:TYR:CE1	2.52	0.44
1:0:1056:U:H2'	1:0:1057:A:O4'	2.16	0.44
9:F:109:GLU:HG2	9:F:113:ASP:OD2	2.17	0.44
18:P:18:LYS:O	18:P:21:VAL:HG13	2.17	0.44
6:C:142:ASP:OD1	6:C:236:THR:HG23	2.16	0.44
5:B:168:GLY:O	5:B:169:GLY:O	2.36	0.44
1:0:1835:U:C5	1:0:1840:A:N7	2.69	0.44
7:D:154:LYS:HD2	7:D:154:LYS:N	2.26	0.44
1:0:1435:U:H5'	40:0:3201:HOH:O	2.16	0.44
26:X:12:ILE:HD12	26:X:36:HIS:CG	2.52	0.44
2:9:3051:A:H5'	16:N:160:SER:HB2	1.99	0.44
2:9:3052:A:H2'	2:9:3053:G:O4'	2.17	0.44
9:F:117:GLU:C	9:F:119:ARG:H	2.21	0.44
10:G:19:GLU:HG2	10:G:66:LEU:HD13	1.99	0.44
2:9:3064:C:C2'	2:9:3065:A:H5'	2.48	0.44
1:0:1250:C:O2'	1:0:1251:C:H5'	2.16	0.44
7:D:91:ALA:HB2	7:D:106:PHE:CD2	2.52	0.44
5:B:277:GLU:N	5:B:278:PRO:HD2	2.32	0.44
6:C:49:ASP:HB3	6:C:52:ALA:HB2	1.99	0.44
22:T:53:GLY:HA3	40:T:6384:HOH:O	2.17	0.44
5:B:60:SER:HA	5:B:61:PRO:HD3	1.86	0.44
1:0:1166:A:N6	1:0:1180:U:H3	2.00	0.44
1:0:1972:U:H2'	1:0:1973:A:H5''	1.98	0.44
8:E:116:THR:CG2	8:E:151:LEU:HD22	2.47	0.44
27:Y:107:PRO:HD3	27:Y:182:PHE:CE1	2.52	0.44
1:0:2456:A:H2'	1:0:2457:U:H6	1.83	0.44
6:C:246:ARG:NH1	6:C:246:ARG:HB3	2.32	0.44
1:0:1768:C:H2'	1:0:1769:C:O4'	2.17	0.44
1:0:1684:A:H1'	30:2:43:ARG:HH22	1.83	0.44
10:G:68:GLU:O	10:G:72:ASP:HB2	2.18	0.44
31:3:91:GLN:O	31:3:92:GLU:HB2	2.17	0.44
2:9:3108:C:O2'	2:9:3109:G:H5'	2.16	0.44
16:N:108:SER:HA	16:N:109:PRO:HD3	1.82	0.44
18:P:115:SER:HG	18:P:118:GLN:HG3	1.81	0.44
15:M:95:LYS:HD2	15:M:99:ARG:HG2	1.98	0.44
7:D:66:GLY:O	7:D:67:ASP:HB3	2.17	0.44
7:D:173:GLU:OE1	7:D:174:VAL:HG23	2.18	0.44
1:0:447:A:OP1	22:T:1:SER:HB2	2.17	0.44
4:A:99:ILE:O	4:A:131:HIS:CE1	2.70	0.44
1:0:2073:G:H3'	40:0:4398:HOH:O	2.18	0.44
12:J:63:ILE:CG2	12:J:64:GLY:N	2.79	0.44
4:A:164:ARG:NE	40:A:9572:HOH:O	2.50	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2361:A:H2'	1:0:2362:A:C8	2.51	0.44
1:0:177:A:H2'	1:0:178:U:O4'	2.16	0.44
17:O:38:ARG:NH1	40:O:7674:HOH:O	2.50	0.44
40:0:9644:HOH:O	14:L:30:ARG:HD2	2.16	0.44
8:E:101:GLU:HB3	8:E:117:THR:HA	2.00	0.44
19:Q:25:PRO:HA	19:Q:26:PRO:HD3	1.83	0.44
1:0:794:U:H3	1:0:819:A:H61	1.64	0.44
1:0:2364:A:H5''	19:Q:15:LYS:HD3	2.00	0.44
16:N:112:GLY:HA2	16:N:137:ALA:N	2.32	0.44
15:M:86:GLN:O	15:M:88:VAL:HG23	2.16	0.44
5:B:36:PRO:HB3	5:B:174:ARG:CB	2.47	0.44
16:N:168:LEU:HA	16:N:169:PRO:HD3	1.77	0.44
25:W:119:HIS:HD2	25:W:120:PRO:O	2.00	0.44
23:U:4:ARG:NH1	23:U:4:ARG:HG2	2.31	0.44
11:H:76:GLU:O	11:H:77:LEU:HD23	2.16	0.44
14:L:145:LEU:C	14:L:145:LEU:HD23	2.37	0.44
2:9:3092:G:H2'	2:9:3093:A:C8	2.53	0.44
6:C:7:ASP:OD1	6:C:11:ASN:N	2.50	0.44
5:B:74:ILE:HD13	5:B:309:VAL:HG21	2.00	0.44
27:Y:178:HIS:CG	27:Y:179:PRO:HD2	2.53	0.44
32:I:93:GLN:HA	32:I:96:PHE:HE2	1.83	0.44
1:0:602:A:O2'	1:0:605:C:H4'	2.17	0.44
5:B:24:PRO:CG	5:B:204:GLY:HA2	2.48	0.44
24:V:20:LEU:HD11	24:V:53:ILE:HG23	2.00	0.44
28:Z:30:GLU:HA	28:Z:33:MET:HE3	1.99	0.44
11:H:66:ARG:HD3	40:H:9545:HOH:O	2.18	0.44
21:S:57:THR:HG22	21:S:59:ASP:H	1.81	0.44
20:R:39:THR:CG2	20:R:107:GLU:O	2.66	0.44
1:0:2791:U:H1'	1:0:2792:A:H5''	1.99	0.44
1:0:1025:C:H5'	25:W:23:MET:O	2.17	0.44
5:B:225:GLY:HA3	40:B:9567:HOH:O	2.18	0.44
18:P:63:ARG:NH2	40:P:190:HOH:O	2.51	0.44
1:0:220:C:H1'	40:0:6282:HOH:O	2.17	0.44
5:B:14:GLY:HA2	5:B:15:PRO:C	2.37	0.44
1:0:1098:A:O3'	25:W:129:LYS:HE2	2.18	0.44
1:0:1120:U:H5''	1:0:1120:U:C6	2.53	0.44
1:0:236:A:H8	1:0:236:A:OP1	2.01	0.44
1:0:1182:C:H1'	1:0:1192:A:C8	2.50	0.44
1:0:111:C:HO2'	29:1:20:ARG:HG2	1.76	0.44
1:0:1751:G:C2'	1:0:1752:G:H5''	2.42	0.44
8:E:101:GLU:OE2	8:E:115:ARG:HD3	2.17	0.44
4:A:135:VAL:HG13	4:A:135:VAL:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1476:A:O2'	1:0:1868:G:H5'	2.18	0.44
1:0:2506:A:O2'	1:0:2507:G:P	2.76	0.44
1:0:1926:G:H2'	1:0:1927:A:H8	1.82	0.44
40:0:5826:HOH:O	25:W:119:HIS:CG	2.71	0.44
21:S:57:THR:HG23	40:S:9487:HOH:O	2.17	0.44
19:Q:75:ILE:HD13	19:Q:84:ILE:CD1	2.48	0.44
1:0:407:A:H5'	40:0:6540:HOH:O	2.17	0.44
1:0:1852:A:H5''	4:A:232:ARG:O	2.18	0.44
1:0:926:A:O2'	14:L:41:HIS:CD2	2.71	0.44
1:0:335:U:H4'	22:T:92:ASP:OD2	2.18	0.44
11:H:96:ARG:NH2	40:H:9498:HOH:O	2.50	0.44
14:L:34:GLY:HA3	14:L:38:HIS:CE1	2.53	0.44
1:0:90:A:H2'	1:0:91:G:O4'	2.18	0.44
27:Y:209:VAL:HG12	27:Y:214:ARG:HG3	1.99	0.44
24:V:12:THR:HG23	24:V:14:ALA:H	1.82	0.43
5:B:162:MET:HG3	5:B:310:ARG:HD3	2.00	0.43
30:2:48:ASP:O	30:2:49:GLU:CB	2.65	0.43
20:R:18:LEU:HB2	20:R:143:VAL:HG13	1.98	0.43
1:0:1203:G:O2'	1:0:1204:C:H5'	2.17	0.43
9:F:11:ASP:O	9:F:14:ASP:HB2	2.17	0.43
40:0:5006:HOH:O	30:2:39:ARG:HG2	2.18	0.43
11:H:99:LYS:HD3	11:H:119:LYS:HD3	1.98	0.43
20:R:95:ALA:HB2	20:R:145:LEU:HD23	2.00	0.43
1:0:2254:G:O2'	1:0:2255:A:H5'	2.18	0.43
15:M:36:ALA:HB1	40:M:9353:HOH:O	2.17	0.43
1:0:1252:A:H2'	1:0:1253:C:O4'	2.17	0.43
4:A:26:ASP:O	4:A:26:ASP:OD1	2.36	0.43
25:W:141:HIS:HB2	25:W:146:ILE:HG12	2.00	0.43
1:0:262:A:OP2	9:F:91:VAL:HG11	2.18	0.43
12:J:132:LEU:HA	12:J:132:LEU:HD23	1.89	0.43
1:0:1163:G:H2'	1:0:1164:U:C5	2.52	0.43
20:R:96:VAL:HG13	20:R:106:GLY:HA3	2.00	0.43
7:D:51:ARG:NH1	7:D:68:PRO:HB3	2.32	0.43
1:0:263:U:C2	9:F:59:ILE:HD12	2.53	0.43
26:X:43:VAL:CG1	26:X:44:ASP:N	2.81	0.43
40:9:3472:HOH:O	16:N:41:LYS:HD3	2.17	0.43
1:0:1306:U:OP1	6:C:184:ARG:HD2	2.18	0.43
6:C:46:TYR:CE2	6:C:98:ARG:NH1	2.86	0.43
1:0:2491:G:H1'	40:0:7345:HOH:O	2.17	0.43
5:B:205:VAL:O	5:B:307:ARG:NE	2.49	0.43
1:0:1972:U:C2'	1:0:1973:A:H5''	2.48	0.43
9:F:32:GLY:N	40:F:3111:HOH:O	2.50	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:137:U:H2'	1:0:139:C:C5	2.53	0.43
9:F:49:PHE:HE1	9:F:98:VAL:HG23	1.84	0.43
1:0:699:C:H2'	1:0:744:G:O4'	2.18	0.43
1:0:449:A:N7	6:C:43:LYS:HG2	2.33	0.43
1:0:196:G:H1'	1:0:198:A:N7	2.34	0.43
13:K:30:LYS:O	13:K:55:VAL:HG13	2.18	0.43
25:W:110:GLN:NE2	25:W:110:GLN:HA	2.34	0.43
1:0:1132:A:N6	1:0:1229:C:H2'	2.33	0.43
1:0:2649:A:O4'	1:0:2650:U:H5	2.01	0.43
1:0:1406:A:H5'	1:0:1407:A:C8	2.54	0.43
1:0:921:G:H4'	1:0:924:G:N1	2.33	0.43
1:0:1218:U:H2'	1:0:1219:U:H6	1.82	0.43
1:0:371:U:H2'	1:0:372:A:C8	2.53	0.43
1:0:1015:C:H2'	1:0:1016:U:C6	2.53	0.43
1:0:1342:C:O2'	1:0:1343:C:H5'	2.18	0.43
1:0:1206:U:C6	1:0:1206:U:H5'	2.33	0.43
4:A:201:PHE:HB3	40:A:9617:HOH:O	2.18	0.43
1:0:93:C:H5''	24:V:1:THR:CB	2.43	0.43
1:0:1838:U:H1'	1:0:2644:C:O4'	2.18	0.43
4:A:65:ARG:HH11	4:A:65:ARG:HG2	1.83	0.43
14:L:94:ARG:NH1	14:L:143:THR:HG21	2.34	0.43
40:0:3297:HOH:O	15:M:82:ARG:HA	2.17	0.43
1:0:308:U:C2	22:T:52:ARG:NH2	2.87	0.43
1:0:1211:G:H2'	1:0:1212:C:H6	1.83	0.43
12:J:54:VAL:O	12:J:58:GLU:HG3	2.18	0.43
1:0:830:G:O2'	1:0:831:U:H5'	2.18	0.43
1:0:2515:C:C2'	1:0:2516:G:H5'	2.48	0.43
1:0:1503:U:H2'	1:0:1504:A:O4'	2.19	0.43
1:0:2372:A:H2'	1:0:2373:U:C6	2.54	0.43
1:0:544:G:C3'	1:0:545:G:H5''	2.49	0.43
11:H:56:GLN:NE2	11:H:93:GLN:HG2	2.31	0.43
1:0:2676:C:H4'	12:J:70:PHE:HD1	1.83	0.43
1:0:1268:C:O2'	1:0:1269:G:H5'	2.18	0.43
1:0:945:U:H2'	1:0:946:C:H6	1.83	0.43
6:C:184:ARG:HB3	40:C:9167:HOH:O	2.18	0.43
25:W:106:THR:OG1	25:W:109:GLU:HB2	2.19	0.43
16:N:156:GLU:O	16:N:157:PRO:C	2.57	0.43
23:U:35:LYS:HE2	23:U:51:TRP:CZ2	2.53	0.43
6:C:120:ASP:C	6:C:120:ASP:OD1	2.57	0.43
8:E:18:LEU:HD13	8:E:34:TRP:CG	2.53	0.43
1:0:1603:A:H5'	1:0:1605:G:C4'	2.48	0.43
1:0:2645:U:OP2	1:0:2645:U:H6	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1439:C:OP1	30:2:41:HIS:HE1	2.02	0.43
1:0:1189:A:H1'	1:0:1209:C:H1'	1.99	0.43
5:B:51:VAL:HG21	5:B:327:VAL:HG13	1.99	0.43
1:0:1201:C:C2'	1:0:1202:A:H5'	2.44	0.43
2:9:3044:A:H2'	2:9:3045:A:O4'	2.19	0.43
12:J:43:ARG:NH1	40:J:5361:HOH:O	2.52	0.43
25:W:11:VAL:O	25:W:12:ASN:HB2	2.18	0.43
1:0:1482:A:O2'	1:0:1483:C:H5'	2.19	0.43
5:B:248:ARG:NH2	40:B:9527:HOH:O	2.44	0.43
21:S:38:ALA:O	21:S:42:GLU:HG3	2.18	0.43
5:B:132:HIS:CE1	5:B:171:VAL:HG21	2.54	0.43
25:W:26:ILE:O	25:W:26:ILE:HG12	2.17	0.43
1:0:2346:C:O3'	7:D:52:THR:HG23	2.19	0.43
1:0:559:U:H5'	1:0:559:U:C6	2.44	0.43
16:N:143:ARG:HE	16:N:143:ARG:HB3	1.65	0.43
24:V:8:ILE:CG2	24:V:59:ILE:HG13	2.49	0.43
40:0:7250:HOH:O	16:N:4:PRO:HD2	2.18	0.43
1:0:271:C:H41	1:0:378:A:H2	1.62	0.43
13:K:125:ALA:O	13:K:127:ALA:N	2.47	0.43
29:1:28:HIS:CD2	29:1:31:LYS:HG3	2.53	0.43
6:C:45:ASP:OD2	6:C:98:ARG:HD2	2.19	0.43
1:0:1213:C:O2'	1:0:1214:G:H5'	2.19	0.43
1:0:2250:G:OP1	4:A:31:LYS:HD3	2.19	0.43
1:0:10:U:O4	1:0:532:A:OP2	2.37	0.43
19:Q:30:VAL:O	19:Q:30:VAL:HG12	2.18	0.43
11:H:83:TYR:C	11:H:83:TYR:CD1	2.92	0.43
1:0:1206:U:C5'	1:0:1206:U:H6	2.21	0.43
7:D:172:VAL:CG1	7:D:173:GLU:H	2.26	0.43
22:T:20:HIS:HB3	22:T:41:ARG:HD2	2.00	0.43
1:0:1175:G:H2'	1:0:1176:C:O4'	2.19	0.43
1:0:2032:U:C2'	1:0:2033:G:H5''	2.49	0.43
2:9:3006:C:OP1	16:N:37:ARG:CZ	2.67	0.43
22:T:78:THR:HB	22:T:87:VAL:O	2.19	0.43
4:A:66:ARG:NH1	4:A:66:ARG:CB	2.81	0.43
40:0:4961:HOH:O	4:A:11:ARG:CZ	2.66	0.43
22:T:88:PRO:HB3	40:T:6320:HOH:O	2.19	0.43
1:0:329:A:OP2	6:C:206:ASN:HB2	2.19	0.43
1:0:812:A:H2'	1:0:813:C:C6	2.54	0.43
27:Y:151:SER:HB3	27:Y:154:ARG:CB	2.49	0.43
22:T:49:GLU:HB3	22:T:59:GLU:CG	2.44	0.43
14:L:92:ASP:OD1	14:L:94:ARG:HB2	2.18	0.43
30:2:19:SER:O	30:2:36:ASN:ND2	2.43	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1044:C:H3'	1:0:1045:G:H5''	2.01	0.43
12:J:39:VAL:CG1	12:J:40:ASN:N	2.82	0.43
4:A:217:ARG:NH1	4:A:217:ARG:CG	2.79	0.43
15:M:61:ILE:N	15:M:61:ILE:HD12	2.33	0.43
16:N:43:VAL:HG13	16:N:118:ILE:HD11	2.01	0.43
6:C:98:ARG:NH1	40:C:9161:HOH:O	2.51	0.43
1:0:1755:A:H2'	1:0:1756:G:O4'	2.19	0.43
8:E:105:GLU:HG2	8:E:113:PRO:HB3	2.01	0.43
13:K:13:GLU:OE1	13:K:44:LEU:HD12	2.19	0.43
1:0:1377:C:H1'	40:0:7728:HOH:O	2.18	0.42
12:J:130:VAL:HG12	12:J:131:THR:H	1.84	0.42
13:K:34:VAL:HG21	13:K:47:ALA:HB2	2.00	0.42
31:3:65:THR:HG23	31:3:88:LEU:HD22	2.00	0.42
1:0:793:A:C5'	18:P:83:LYS:HG2	2.49	0.42
2:9:3001:U:O3'	2:9:3003:A:H5''	2.19	0.42
22:T:75:GLU:O	22:T:76:ASP:HB2	2.19	0.42
1:0:2435:U:H1'	40:0:5968:HOH:O	2.19	0.42
5:B:101:TRP:HB2	5:B:119:HIS:CD2	2.54	0.42
32:I:80:LYS:HD3	32:I:86:GLU:O	2.18	0.42
13:K:63:GLU:HB2	40:K:6344:HOH:O	2.19	0.42
1:0:603:A:H5''	1:0:604:G:OP1	2.18	0.42
1:0:1196:C:H2'	1:0:1197:G:O4'	2.18	0.42
28:Z:75:GLY:O	28:Z:78:THR:HB	2.18	0.42
7:D:62:ASP:HA	40:D:4233:HOH:O	2.17	0.42
1:0:1186:C:H5''	32:I:119:TYR:CE1	2.54	0.42
9:F:28:ALA:HB3	9:F:99:THR:O	2.19	0.42
31:3:70:ARG:HG3	31:3:77:ALA:HB2	2.01	0.42
1:0:1189:A:HO2'	1:0:1208:C:H2'	1.82	0.42
9:F:40:ILE:HD11	9:F:48:VAL:HG11	2.00	0.42
11:H:3:ALA:HA	11:H:58:ARG:HH12	1.84	0.42
1:0:2428:G:N7	31:3:60:LYS:NZ	2.65	0.42
16:N:67:ALA:O	16:N:69:TYR:N	2.52	0.42
21:S:37:VAL:O	21:S:41:VAL:HG23	2.18	0.42
1:0:1226:G:H5'	40:0:5079:HOH:O	2.19	0.42
1:0:565:A:OP2	1:0:592:G:N1	2.49	0.42
26:X:7:GLU:HA	26:X:75:ALA:HA	2.01	0.42
40:0:7872:HOH:O	22:T:9:LYS:HB2	2.18	0.42
4:A:192:VAL:HG12	4:A:207:GLN:CB	2.41	0.42
1:0:1174:A:C5	1:0:1201:C:H4'	2.54	0.42
13:K:49:LEU:HD12	13:K:80:ILE:HD13	2.01	0.42
7:D:23:VAL:O	7:D:23:VAL:HG23	2.19	0.42
27:Y:107:PRO:HB3	27:Y:182:PHE:CE2	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:Q:75:ILE:CD1	19:Q:84:ILE:HD11	2.50	0.42
9:F:5:ASP:O	9:F:119:ARG:NH1	2.52	0.42
1:0:2251:G:H2'	1:0:2252:A:C8	2.54	0.42
1:0:2353:A:H4'	1:0:2354:A:O5'	2.17	0.42
15:M:46:LEU:HD22	15:M:50:ARG:HG3	2.02	0.42
1:0:2015:A:H2'	1:0:2016:U:O4'	2.19	0.42
25:W:73:LEU:HA	25:W:73:LEU:HD12	1.89	0.42
26:X:74:ALA:HB2	26:X:85:VAL:HG22	2.02	0.42
25:W:48:VAL:CG1	25:W:48:VAL:O	2.67	0.42
1:0:362:G:H2'	1:0:363:A:C8	2.54	0.42
4:A:88:ILE:CD1	4:A:100:PRO:HD3	2.45	0.42
22:T:115:GLU:CG	22:T:116:ASP:N	2.79	0.42
14:L:143:THR:CG2	14:L:144:ASP:H	2.32	0.42
4:A:94:LEU:HG	4:A:99:ILE:HD11	2.00	0.42
1:0:1925:G:O2'	1:0:1926:G:H5'	2.20	0.42
16:N:35:VAL:HG12	16:N:37:ARG:HD3	2.01	0.42
1:0:2478:U:O2'	1:0:2479:A:H5'	2.20	0.42
7:D:67:ASP:O	7:D:69:ILE:HG13	2.20	0.42
24:V:1:THR:OG1	24:V:2:VAL:N	2.52	0.42
31:3:20:HIS:HA	31:3:70:ARG:O	2.20	0.42
32:I:113:HIS:HE1	32:I:121:LEU:HD22	1.82	0.42
7:D:52:THR:HB	7:D:70:GLY:C	2.39	0.42
30:2:19:SER:HB3	40:2:4479:HOH:O	2.20	0.42
24:V:16:ARG:NH2	24:V:63:GLU:HG3	2.35	0.42
1:0:137:U:OP1	1:0:259:G:O2'	2.37	0.42
16:N:182:GLY:O	16:N:183:ASP:C	2.57	0.42
1:0:1476:A:H1'	1:0:1867:G:O2'	2.19	0.42
12:J:45:VAL:CG2	12:J:129:PHE:CD1	3.03	0.42
1:0:2587:OMU:H2'	1:0:2589:U:H5''	2.01	0.42
14:L:12:THR:HG21	14:L:16:GLY:O	2.18	0.42
30:2:49:GLU:HB2	40:2:131:HOH:O	2.20	0.42
24:V:16:ARG:NH1	24:V:65:ASP:O	2.53	0.42
24:V:42:ASN:O	24:V:44:GLY:N	2.52	0.42
17:O:18:ALA:HB2	17:O:26:TRP:HB2	2.01	0.42
7:D:10:PHE:CG	7:D:11:HIS:N	2.87	0.42
20:R:114:VAL:HA	20:R:144:GLU:O	2.19	0.42
17:O:49:GLU:OE1	17:O:70:LEU:HD12	2.19	0.42
25:W:34:LEU:HD12	25:W:107:LEU:HD11	2.01	0.42
9:F:106:ALA:HB3	40:F:6617:HOH:O	2.18	0.42
21:S:6:LYS:O	21:S:7:HIS:HB3	2.20	0.42
2:9:3107:C:H5	40:9:3167:HOH:O	2.02	0.42
1:0:1185:U:H4'	32:I:123:ASN:HB3	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:B:16:ARG:NE	40:B:9557:HOH:O	2.28	0.42
1:0:1159:G:H1	1:0:1208:C:N4	2.16	0.42
1:0:87:C:C2	30:2:30:ASP:OD2	2.73	0.42
8:E:22:VAL:O	8:E:28:SER:HA	2.20	0.42
25:W:38:THR:HG22	25:W:39:ASP:H	1.84	0.42
1:0:204:A:H2'	1:0:205:U:H5'	2.01	0.42
1:0:1654:U:H2'	4:A:47:HIS:CD2	2.55	0.42
1:0:1588:G:C6	1:0:1589:G:N1	2.88	0.42
18:P:55:LYS:HG2	18:P:56:GLY:N	2.34	0.42
1:0:2809:G:H2'	1:0:2810:G:O4'	2.19	0.42
1:0:2667:G:H1'	1:0:2914:A:N3	2.34	0.42
1:0:2577:A:H5'	40:0:8264:HOH:O	2.18	0.42
1:0:646:G:H2'	1:0:647:U:C6	2.55	0.42
15:M:164:THR:HG22	15:M:167:GLY:H	1.85	0.42
1:0:1185:U:H5'	40:0:7910:HOH:O	2.20	0.42
40:0:6241:HOH:O	13:K:87:ARG:CZ	2.68	0.42
1:0:1603:A:H5''	1:0:1604:G:H3'	2.02	0.42
1:0:2780:C:C1'	8:E:143:GLN:HE21	2.25	0.42
31:3:6:ARG:HA	31:3:20:HIS:O	2.20	0.42
1:0:171:C:OP2	15:M:84:LYS:HG3	2.19	0.42
26:X:43:VAL:HG12	26:X:47:ALA:HB3	2.00	0.42
5:B:234:ARG:NH1	40:B:9612:HOH:O	2.52	0.42
18:P:89:ASN:OD1	18:P:92:GLU:HB2	2.19	0.42
15:M:76:ARG:HG3	15:M:88:VAL:HG21	2.02	0.42
1:0:2324:G:N2	1:0:2377:U:H1'	2.35	0.42
4:A:81:GLN:N	4:A:92:ASN:OD1	2.42	0.42
30:2:18:ASN:ND2	30:2:40:ARG:H	2.17	0.42
27:Y:122:ARG:NH2	40:Y:9336:HOH:O	2.52	0.42
13:K:74:VAL:HG12	13:K:74:VAL:O	2.18	0.42
26:X:30:MET:CE	26:X:58:ALA:HB3	2.48	0.42
2:9:3039:U:H3'	2:9:3040:C:H5''	2.01	0.42
13:K:118:ALA:HB1	13:K:125:ALA:CB	2.50	0.42
23:U:20:MET:HE3	23:U:30:HIS:NE2	2.35	0.42
1:0:1573:A:H2'	1:0:1574:C:O4'	2.19	0.42
11:H:88:ARG:HG2	11:H:133:LEU:O	2.20	0.42
40:0:3426:HOH:O	5:B:252:PRO:HD3	2.20	0.42
1:0:2011:A:H4'	1:0:2012:U:O5'	2.20	0.42
1:0:1759:A:N3	1:0:1818:C:H2'	2.35	0.42
22:T:3:GLN:HA	22:T:4:PRO:HD3	1.85	0.42
4:A:95:PRO:HA	4:A:153:ARG:HA	2.02	0.42
4:A:207:GLN:O	4:A:208:HIS:HB3	2.20	0.42
16:N:154:LEU:CG	16:N:155:GLU:H	2.25	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:223:ARG:NE	40:A:9559:HOH:O	2.52	0.42
11:H:28:ILE:HA	11:H:63:GLU:OE1	2.20	0.42
1:O:737:A:H3'	1:O:737:A:C8	2.55	0.42
29:1:28:HIS:O	29:1:32:LYS:N	2.45	0.42
9:F:70:LYS:C	9:F:72:VAL:H	2.23	0.42
1:O:879:C:H5	40:O:3763:HOH:O	2.03	0.42
1:O:2034:U:H4'	40:O:6439:HOH:O	2.20	0.42
7:D:99:ASP:HB3	7:D:103:ASN:H	1.85	0.42
27:Y:133:HIS:HD2	40:Y:9384:HOH:O	2.03	0.42
1:O:295:C:H2'	1:O:296:G:O4'	2.19	0.42
23:U:44:ARG:HB3	40:U:3805:HOH:O	2.19	0.42
1:O:1174:A:C6	1:O:1201:C:H4'	2.55	0.41
1:O:2523:U:O2'	1:O:2524:G:H5'	2.20	0.41
1:O:2089:A:O2'	1:O:2090:G:H5'	2.20	0.41
5:B:1:PRO:O	5:B:2:GLN:HB2	2.20	0.41
11:H:146:VAL:HG22	40:H:9542:HOH:O	2.20	0.41
21:S:11:THR:H	21:S:14:ALA:HB3	1.83	0.41
7:D:15:GLU:HA	7:D:16:PRO:HD3	1.83	0.41
22:T:102:ASP:OD1	22:T:104:GLU:HG3	2.20	0.41
15:M:120:VAL:HG11	15:M:130:GLU:HG3	2.01	0.41
8:E:20:ILE:O	8:E:30:THR:HA	2.20	0.41
20:R:61:GLN:NE2	40:R:9451:HOH:O	2.53	0.41
16:N:152:GLU:C	16:N:154:LEU:N	2.74	0.41
1:O:2768:A:O2'	1:O:2769:C:O4'	2.33	0.41
24:V:59:ILE:O	24:V:63:GLU:HG2	2.20	0.41
18:P:14:LEU:O	18:P:16:VAL:HG23	2.20	0.41
4:A:112:PRO:HD3	4:A:152:CYS:SG	2.60	0.41
20:R:114:VAL:HG13	20:R:114:VAL:O	2.20	0.41
1:O:941:G:C5	1:O:942:U:C4	3.09	0.41
1:O:1748:U:H4'	40:O:7963:HOH:O	2.19	0.41
1:O:1507:C:H4'	40:O:4185:HOH:O	2.20	0.41
40:O:4417:HOH:O	11:H:11:LYS:HE2	2.20	0.41
1:O:304:G:H1'	1:O:347:A:N6	2.34	0.41
1:O:1257:C:H2'	1:O:1258:G:O4'	2.20	0.41
12:J:143:LYS:HG3	12:J:145:TRP:CE2	2.55	0.41
1:O:2869:G:H2'	1:O:2870:C:O4'	2.20	0.41
26:X:72:VAL:CG1	26:X:85:VAL:CG1	2.98	0.41
2:9:3056:A:C3'	2:9:3057:A:H5''	2.50	0.41
7:D:167:GLU:OE2	7:D:173:GLU:HB3	2.20	0.41
6:C:27:ARG:HD2	17:O:5:PRO:HD2	2.02	0.41
2:9:3004:G:O2'	16:N:44:ARG:NH2	2.53	0.41
1:O:380:A:H2'	40:O:7686:HOH:O	2.19	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:271:C:O2	1:0:273:G:H5''	2.19	0.41
29:1:28:HIS:HD2	29:1:30:LYS:H	1.68	0.41
22:T:79:LEU:HG	22:T:89:ARG:HB2	2.02	0.41
8:E:1:PRO:HD2	8:E:53:GLU:O	2.20	0.41
23:U:19:THR:HG22	23:U:20:MET:N	2.35	0.41
1:0:2637:A:H5''	38:4:9701:SPS:O3	2.19	0.41
18:P:55:LYS:CG	18:P:56:GLY:N	2.82	0.41
1:0:2363:G:O2'	19:Q:11:ARG:HG3	2.20	0.41
4:A:43:VAL:O	4:A:44:ASP:HB2	2.20	0.41
11:H:51:VAL:CG1	11:H:53:GLU:O	2.68	0.41
15:M:183:THR:CG2	15:M:194:ALA:HB1	2.46	0.41
1:0:447:A:O2'	1:0:448:G:H5'	2.20	0.41
1:0:2769:C:C2'	1:0:2770:G:C5'	2.98	0.41
1:0:2338:G:OP1	7:D:97:GLN:HG2	2.20	0.41
16:N:67:ALA:C	16:N:69:TYR:H	2.23	0.41
1:0:2453:G:H4'	14:L:50:GLY:C	2.40	0.41
1:0:1236:A:H2'	1:0:1237:U:O4'	2.20	0.41
18:P:98:ILE:CD1	18:P:102:ARG:NE	2.84	0.41
8:E:81:GLU:HA	8:E:133:VAL:O	2.20	0.41
1:0:1741:U:O2'	1:0:2723:G:H4'	2.20	0.41
1:0:1849:G:H1'	1:0:2011:A:N1	2.35	0.41
1:0:2580:G:N3	1:0:2600:A:H2	2.18	0.41
7:D:27:ILE:HB	40:D:5858:HOH:O	2.19	0.41
16:N:62:HIS:HB3	16:N:65:ASP:OD1	2.20	0.41
1:0:2784:A:H1'	8:E:60:SER:OG	2.20	0.41
1:0:1524:U:HO2'	1:0:1525:G:P	2.44	0.41
1:0:522:U:O2'	1:0:1366:C:H5'	2.19	0.41
18:P:15:ASP:O	18:P:15:ASP:OD1	2.39	0.41
28:Z:10:ARG:C	28:Z:12:GLY:H	2.23	0.41
1:0:1666:C:C2'	1:0:1667:A:H5''	2.50	0.41
10:G:12:ILE:HG22	10:G:17:GLN:NE2	2.36	0.41
5:B:154:VAL:HA	5:B:155:PRO:HD3	1.88	0.41
21:S:10:VAL:HG11	24:V:36:ALA:CA	2.49	0.41
12:J:39:VAL:HG11	12:J:107:ASN:CG	2.41	0.41
26:X:76:ARG:NH1	26:X:76:ARG:HG3	2.35	0.41
1:0:1675:C:H5''	30:2:5:LYS:HD2	2.03	0.41
4:A:43:VAL:HG21	4:A:59:GLU:HG3	2.01	0.41
1:0:1020:A:H2'	1:0:1021:G:C8	2.56	0.41
1:0:1773:G:C8	28:Z:16:ALA:HA	2.56	0.41
1:0:1657:A:H2'	1:0:1658:A:C8	2.55	0.41
1:0:899:C:H5'	40:0:3789:HOH:O	2.21	0.41
1:0:1565:C:O4'	1:0:2738:G:H1'	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:162:C:H2'	1:0:163:U:H5'	2.02	0.41
1:0:697:G:H4'	1:0:730:G:O3'	2.21	0.41
15:M:74:LYS:HE3	15:M:75:ARG:O	2.20	0.41
11:H:140:VAL:HG12	11:H:140:VAL:O	2.21	0.41
4:A:30:ARG:HB3	4:A:30:ARG:HE	1.69	0.41
22:T:115:GLU:HG3	22:T:116:ASP:H	1.81	0.41
1:0:290:C:O2'	1:0:291:C:H5'	2.20	0.41
12:J:42:GLU:O	12:J:131:THR:HG23	2.20	0.41
1:0:625:U:H5''	1:0:1044:C:H41	1.86	0.41
1:0:2428:G:H5'	40:0:7132:HOH:O	2.21	0.41
16:N:24:LEU:HD13	19:Q:26:PRO:HB3	2.03	0.41
1:0:2253:G:O2'	1:0:2254:G:H5'	2.21	0.41
1:0:1318:A:H4'	1:0:1343:C:H4'	2.02	0.41
40:0:6789:HOH:O	27:Y:158:LYS:HD3	2.19	0.41
1:0:2351:C:H2'	1:0:2352:G:O4'	2.20	0.41
31:3:7:PHE:CE1	31:3:9:THR:HB	2.56	0.41
27:Y:102:LEU:HD11	27:Y:225:GLY:HA2	2.02	0.41
27:Y:213:LYS:HE3	27:Y:213:LYS:HB2	1.85	0.41
7:D:60:GLU:O	7:D:60:GLU:HG3	2.21	0.41
7:D:135:VAL:HG22	7:D:136:ARG:H	1.86	0.41
24:V:1:THR:O	24:V:2:VAL:C	2.59	0.41
7:D:166:ILE:O	7:D:169:THR:N	2.54	0.41
26:X:73:ARG:NH1	26:X:73:ARG:HB2	2.35	0.41
1:0:1299:G:N2	40:0:5231:HOH:O	2.53	0.41
9:F:48:VAL:CG2	9:F:74:PHE:HB3	2.51	0.41
40:0:5826:HOH:O	25:W:69:ARG:NH2	2.54	0.41
15:M:82:ARG:O	15:M:84:LYS:N	2.53	0.41
11:H:36:LYS:HA	11:H:84:LYS:NZ	2.36	0.41
23:U:39:ASN:ND2	23:U:44:ARG:HH11	2.18	0.41
19:Q:22:GLY:O	19:Q:23:THR:C	2.58	0.41
1:0:2517:A:H2'	1:0:2518:C:O4'	2.21	0.41
40:0:9728:HOH:O	5:B:229:ARG:HD2	2.20	0.41
1:0:695:C:H2'	1:0:696:C:C6	2.55	0.41
11:H:17:ARG:HD3	11:H:23:ILE:HD12	2.03	0.41
1:0:2388:C:H2'	1:0:2389:U:O4'	2.21	0.41
1:0:2299:G:O6	19:Q:1:PRO:HA	2.21	0.41
5:B:276:ASP:O	5:B:279:THR:HG22	2.20	0.41
5:B:280:VAL:HG13	5:B:333:GLU:O	2.21	0.41
13:K:7:ASP:OD2	13:K:81:ARG:NH2	2.54	0.41
13:K:82:ARG:NH2	13:K:115:ARG:HG2	2.36	0.41
8:E:20:ILE:HD12	8:E:33:LEU:CD1	2.49	0.41
27:Y:148:GLY:O	27:Y:154:ARG:HD3	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:3:38:ARG:HB3	31:3:42:ARG:NH1	2.31	0.41
1:0:1173:A:H4'	1:0:1174:A:C8	2.56	0.41
14:L:80:ASP:HB3	14:L:90:ARG:HB3	2.02	0.41
4:A:223:ARG:CZ	40:A:9559:HOH:O	2.69	0.41
21:S:57:THR:HG22	21:S:59:ASP:N	2.34	0.41
1:0:1505:U:H1'	40:0:8100:HOH:O	2.20	0.41
5:B:146:THR:C	5:B:148:PRO:HD3	2.41	0.41
15:M:82:ARG:O	15:M:83:SER:C	2.59	0.41
1:0:2515:C:H2'	1:0:2516:G:C5'	2.51	0.41
16:N:71:TRP:HB2	40:N:9335:HOH:O	2.19	0.41
12:J:95:ARG:HG2	12:J:99:GLU:OE2	2.21	0.41
1:0:359:U:H3'	40:0:6290:HOH:O	2.20	0.41
28:Z:49:ARG:HB2	28:Z:55:TRP:CZ3	2.56	0.41
1:0:1636:G:O2'	1:0:1637:A:H5'	2.20	0.41
1:0:1556:G:O2'	1:0:1557:G:H5'	2.21	0.41
32:I:118:SER:CB	32:I:123:ASN:HB2	2.50	0.41
11:H:167:PRO:O	11:H:168:ALA:HB2	2.21	0.41
9:F:57:GLU:O	9:F:61:MET:HG3	2.21	0.41
14:L:59:GLU:HB3	40:L:9465:HOH:O	2.20	0.41
6:C:162:VAL:HG13	6:C:192:ILE:HD11	2.02	0.41
22:T:32:ARG:HH12	22:T:38:ARG:HH12	1.66	0.41
1:0:1095:U:O2	25:W:120:PRO:HG2	2.21	0.41
5:B:141:ARG:HD2	5:B:163:GLU:OE2	2.21	0.41
5:B:62:ARG:HA	5:B:65:MET:HE3	2.03	0.41
1:0:255:A:H2'	1:0:256:C:C6	2.56	0.41
28:Z:39:CYS:HA	28:Z:40:PRO:HD3	1.95	0.41
13:K:118:ALA:HB1	13:K:125:ALA:HB2	2.03	0.41
6:C:133:ARG:NH1	40:C:9214:HOH:O	2.53	0.41
16:N:38:LYS:HD3	16:N:107:ASN:ND2	2.36	0.41
3:4:76:DA:H8	38:4:9701:SPS:H81	1.85	0.41
5:B:171:VAL:HG23	5:B:172:SER:N	2.36	0.41
5:B:75:GLU:C	5:B:77:PRO:HD3	2.40	0.41
1:0:721:A:H4'	17:O:51:TYR:CD1	2.55	0.41
4:A:104:PRO:HG3	4:A:127:GLN:OE1	2.21	0.41
30:2:11:LEU:HA	30:2:11:LEU:HD23	1.90	0.41
19:Q:66:LYS:HB2	19:Q:70:ALA:O	2.21	0.41
1:0:2281:C:C2'	1:0:2282:U:H5'	2.50	0.41
11:H:9:ILE:HD12	11:H:54:THR:HG22	2.03	0.41
11:H:54:THR:HG23	11:H:128:GLN:HA	2.03	0.41
2:9:3118:C:H4'	16:N:56:ASP:OD1	2.21	0.41
25:W:6:GLN:CB	25:W:26:ILE:HD11	2.27	0.41
5:B:84:LEU:O	5:B:99:GLU:HA	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:I:72:VAL:CG1	32:I:73:PRO:HD2	2.51	0.41
22:T:81:LYS:HD2	22:T:87:VAL:CG1	2.52	0.41
1:O:2016:U:H2'	1:O:2017:U:C6	2.55	0.41
12:J:71:TYR:CD1	12:J:72:PRO:HD2	2.56	0.41
7:D:88:LEU:N	7:D:89:PRO:CD	2.84	0.41
2:9:3011:A:P	19:Q:19:ARG:HH21	2.43	0.41
1:O:2553:A:H2'	1:O:2553:A:N3	2.35	0.41
7:D:28:GLY:O	7:D:29:HIS:HB3	2.21	0.40
7:D:40:ILE:HG13	7:D:41:LEU:N	2.36	0.40
31:3:70:ARG:CG	31:3:77:ALA:HB2	2.51	0.40
1:O:1163:G:H5'	32:I:115:ASP:O	2.21	0.40
32:I:78:LEU:CD1	32:I:112:LYS:HZ2	2.32	0.40
27:Y:144:ARG:NH2	40:Y:9411:HOH:O	2.51	0.40
1:O:1132:A:N3	1:O:2521:A:O2'	2.49	0.40
1:O:2094:G:O6	1:O:2649:A:H2	2.04	0.40
5:B:320:GLN:HA	5:B:321:PRO:HD3	1.95	0.40
28:Z:39:CYS:O	28:Z:42:CYS:O	2.40	0.40
1:O:819:A:H5''	40:Z:9220:HOH:O	2.20	0.40
1:O:526:U:H2'	1:O:527:U:C6	2.56	0.40
17:O:15:LYS:HD3	17:O:19:ARG:NH2	2.36	0.40
32:I:108:ILE:C	32:I:110:GLU:H	2.24	0.40
1:O:1176:C:H3'	40:O:5396:HOH:O	2.22	0.40
2:9:3044:A:O4'	7:D:76:ARG:NE	2.55	0.40
1:O:2421:G:H2'	40:O:4646:HOH:O	2.20	0.40
1:O:2908:A:H2'	1:O:2909:G:C4'	2.51	0.40
16:N:23:ARG:HG2	16:N:23:ARG:NH1	2.34	0.40
18:P:94:TRP:CZ2	18:P:98:ILE:HG13	2.56	0.40
17:O:23:GLY:C	40:O:3062:HOH:O	2.59	0.40
17:O:81:PHE:N	17:O:81:PHE:CD1	2.89	0.40
5:B:24:PRO:HG3	5:B:204:GLY:HA2	2.03	0.40
1:O:2515:C:H2'	1:O:2516:G:H5'	2.03	0.40
11:H:54:THR:O	11:H:55:VAL:HG13	2.21	0.40
12:J:90:LYS:HB2	36:J:9302:CL:CL	2.57	0.40
1:O:1797:A:H2'	1:O:1799:G:O5'	2.22	0.40
1:O:2821:C:H4'	5:B:116:PRO:HG3	2.03	0.40
1:O:27:U:H2'	1:O:28:G:O4'	2.21	0.40
24:V:12:THR:OG1	24:V:13:PRO:HD2	2.20	0.40
2:9:3028:U:P	16:N:39:SER:OG	2.80	0.40
11:H:165:SER:OG	11:H:168:ALA:HB3	2.21	0.40
1:O:2070:G:H2'	1:O:2072:G:OP1	2.22	0.40
1:O:338:C:H4'	6:C:174:ILE:HD11	2.02	0.40
12:J:107:ASN:ND2	12:J:107:ASN:C	2.73	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:432:G:H2'	1:0:433:C:H6	1.86	0.40
1:0:1342:C:C2'	1:0:1343:C:H5'	2.51	0.40
1:0:2612:A:H4'	40:0:4260:HOH:O	2.21	0.40
5:B:149:ASP:HB2	40:B:9579:HOH:O	2.21	0.40
27:Y:170:SER:OG	27:Y:175:ARG:HG3	2.21	0.40
1:0:1077:G:H2'	1:0:1080:C:H42	1.86	0.40
7:D:165:PHE:O	7:D:168:SER:HB3	2.22	0.40
6:C:123:LEU:HD23	6:C:123:LEU:HA	1.84	0.40
24:V:12:THR:HG23	24:V:14:ALA:N	2.36	0.40
1:0:1242:A:O3'	12:J:20:GLY:HA3	2.22	0.40
4:A:36:ASP:O	4:A:38:ILE:N	2.48	0.40
14:L:73:VAL:HG21	14:L:116:HIS:CD2	2.57	0.40
5:B:102:THR:CG2	5:B:182:VAL:HG12	2.51	0.40
1:0:920:C:H5'	1:0:921:G:C4	2.56	0.40
8:E:7:ILE:HA	8:E:8:PRO:HD3	1.95	0.40
31:3:17:HIS:O	31:3:18:GLN:HG3	2.22	0.40
1:0:2326:U:H4'	1:0:2412:G:H4'	2.04	0.40
1:0:956:G:H2'	1:0:957:A:O4'	2.21	0.40
25:W:126:ASP:HB3	25:W:135:GLY:O	2.21	0.40
2:9:3095:C:O2'	2:9:3096:C:H5'	2.22	0.40
1:0:1380:U:O4	1:0:2748:G:H1'	2.22	0.40
4:A:32:VAL:HG12	4:A:34:ASP:N	2.36	0.40
1:0:559:U:H2'	1:0:560:C:O4'	2.22	0.40
31:3:48:ASN:ND2	31:3:50:GLY:H	2.20	0.40
23:U:52:THR:HG21	23:U:54:THR:HB	2.03	0.40
6:C:194:PHE:CE2	6:C:234:VAL:HG11	2.56	0.40
1:0:2896:A:C2'	1:0:2896:A:N3	2.84	0.40
1:0:1504:A:H5'	40:0:4966:HOH:O	2.20	0.40
11:H:70:ASN:O	11:H:74:ILE:HG13	2.21	0.40
40:0:4664:HOH:O	5:B:216:LYS:HE2	2.20	0.40
1:0:401:C:O2'	15:M:92:THR:HB	2.22	0.40
7:D:96:SER:C	7:D:98:PHE:H	2.24	0.40
19:Q:91:LEU:C	19:Q:92:ARG:HG2	2.41	0.40
1:0:816:G:C6	1:0:817:G:N1	2.90	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	
4	A	235/240 (98%)	210 (89%)	21 (9%)	4 (2%)	14	8
5	B	335/338 (99%)	312 (93%)	19 (6%)	4 (1%)	19	14
6	C	244/246 (99%)	226 (93%)	18 (7%)	0	100	100
7	D	134/177 (76%)	103 (77%)	23 (17%)	8 (6%)	2	1
8	E	170/178 (96%)	163 (96%)	7 (4%)	0	100	100
9	F	117/120 (98%)	102 (87%)	13 (11%)	2 (2%)	14	8
10	G	25/348 (7%)	25 (100%)	0	0	100	100
11	H	156/171 (91%)	140 (90%)	13 (8%)	3 (2%)	12	7
12	J	140/145 (97%)	132 (94%)	6 (4%)	2 (1%)	16	12
13	K	130/132 (98%)	121 (93%)	8 (6%)	1 (1%)	27	24
14	L	141/165 (86%)	118 (84%)	21 (15%)	2 (1%)	16	12
15	M	192/194 (99%)	181 (94%)	9 (5%)	2 (1%)	22	18
16	N	184/187 (98%)	161 (88%)	13 (7%)	10 (5%)	3	1
17	O	113/116 (97%)	108 (96%)	5 (4%)	0	100	100
18	P	141/149 (95%)	134 (95%)	7 (5%)	0	100	100
19	Q	93/96 (97%)	88 (95%)	5 (5%)	0	100	100
20	R	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
21	S	79/85 (93%)	74 (94%)	5 (6%)	0	100	100
22	T	117/120 (98%)	111 (95%)	5 (4%)	1 (1%)	25	21
23	U	51/66 (77%)	48 (94%)	3 (6%)	0	100	100
24	V	63/71 (89%)	57 (90%)	3 (5%)	3 (5%)	4	1
25	W	152/154 (99%)	149 (98%)	3 (2%)	0	100	100
26	X	80/92 (87%)	72 (90%)	8 (10%)	0	100	100
27	Y	140/241 (58%)	138 (99%)	2 (1%)	0	100	100
28	Z	71/83 (86%)	62 (87%)	6 (8%)	3 (4%)	4	1
29	1	54/57 (95%)	52 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
31	3	90/92 (98%)	87 (97%)	2 (2%)	1 (1%)	21	16
32	I	68/162 (42%)	54 (79%)	11 (16%)	3 (4%)	4	1
All	All	3705/4430 (84%)	3410 (92%)	246 (7%)	49 (1%)	18	13

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	37	VAL
5	B	139	ASP
9	F	101	ALA
11	H	166	SER
11	H	168	ALA
14	L	80	ASP
16	N	154	LEU
16	N	167	ASP
16	N	183	ASP
16	N	184	ILE
28	Z	81	ARG
4	A	34	ASP
5	B	169	GLY
7	D	16	PRO
7	D	60	GLU
7	D	61	PHE
15	M	83	SER
16	N	155	GLU
16	N	162	ASP
28	Z	20	ARG
32	I	132	CYS
5	B	185	GLY
7	D	56	ARG
7	D	137	PRO
7	D	164	ALA
7	D	171	ASP
12	J	143	LYS
16	N	65	ASP
16	N	68	GLU
24	V	43	PRO
28	Z	41	ASN
13	K	126	SER
14	L	82	ALA

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Mol	Chain	Res	Type
31	3	56	PRO
32	I	114	PRO
4	A	132	ASP
4	A	205	GLY
12	J	5	GLU
22	T	53	GLY
7	D	69	ILE
9	F	71	GLY
24	V	40	PRO
32	I	129	VAL
5	B	182	VAL
16	N	157	PRO
16	N	161	GLY
11	H	167	PRO
15	M	88	VAL
24	V	2	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	
4	A	179/182 (98%)	166 (93%)	13 (7%)	20	20
5	B	282/283 (100%)	268 (95%)	14 (5%)	34	39
6	C	193/193 (100%)	176 (91%)	17 (9%)	14	13
7	D	117/148 (79%)	111 (95%)	6 (5%)	33	38
8	E	152/156 (97%)	148 (97%)	4 (3%)	59	70
9	F	93/94 (99%)	89 (96%)	4 (4%)	40	47
10	G	27/283 (10%)	26 (96%)	1 (4%)	45	54
11	H	132/138 (96%)	127 (96%)	5 (4%)	44	53
12	J	118/121 (98%)	111 (94%)	7 (6%)	28	30
13	K	106/106 (100%)	100 (94%)	6 (6%)	29	32
14	L	113/127 (89%)	111 (98%)	2 (2%)	71	82
15	M	158/158 (100%)	153 (97%)	5 (3%)	51	62
16	N	149/150 (99%)	142 (95%)	7 (5%)	36	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	O	93/94 (99%)	89 (96%)	4 (4%)	40	47
18	P	113/117 (97%)	112 (99%)	1 (1%)	87	94
19	Q	79/80 (99%)	77 (98%)	2 (2%)	60	71
20	R	117/122 (96%)	116 (99%)	1 (1%)	87	94
21	S	71/74 (96%)	71 (100%)	0	100	100
22	T	105/106 (99%)	100 (95%)	5 (5%)	35	41
23	U	44/52 (85%)	44 (100%)	0	100	100
24	V	51/57 (90%)	50 (98%)	1 (2%)	68	79
25	W	130/130 (100%)	126 (97%)	4 (3%)	52	63
26	X	66/74 (89%)	59 (89%)	7 (11%)	10	8
27	Y	120/196 (61%)	108 (90%)	12 (10%)	11	10
28	Z	60/68 (88%)	59 (98%)	1 (2%)	73	84
29	1	46/47 (98%)	46 (100%)	0	100	100
30	2	42/46 (91%)	40 (95%)	2 (5%)	35	41
31	3	79/79 (100%)	76 (96%)	3 (4%)	44	53
32	I	58/130 (45%)	58 (100%)	0	100	100
All	All	3093/3611 (86%)	2959 (96%)	134 (4%)	40	47

All (134) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	3	ARG
4	A	26	ASP
4	A	33	GLU
4	A	62	ASP
4	A	68	ILE
4	A	94	LEU
4	A	131	HIS
4	A	144	GLU
4	A	151	GLN
4	A	165	THR
4	A	179	MET
4	A	206	ARG
4	A	217	ARG
5	B	11	LEU
5	B	27	ASN

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Mol	Chain	Res	Type
5	B	28	SER
5	B	82	VAL
5	B	98	THR
5	B	112	THR
5	B	149	ASP
5	B	162	MET
5	B	190	MET
5	B	251	VAL
5	B	254	GLN
5	B	264	GLU
5	B	265	LEU
5	B	312	ARG
6	C	2	GLN
6	C	16	VAL
6	C	27	ARG
6	C	76	ARG
6	C	91	PRO
6	C	94	THR
6	C	101	ASP
6	C	115	LEU
6	C	136	VAL
6	C	162	VAL
6	C	187	ARG
6	C	214	THR
6	C	223	LEU
6	C	234	VAL
6	C	236	THR
6	C	240	LEU
6	C	243	VAL
7	D	24	HIS
7	D	47	GLN
7	D	50	VAL
7	D	61	PHE
7	D	100	ASP
7	D	133	ASN
8	E	15	GLN
8	E	86	VAL
8	E	155	ASN
8	E	164	ASP
9	F	12	LEU
9	F	46	GLU
9	F	99	THR

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Mol	Chain	Res	Type
9	F	119	ARG
10	G	72	ASP
11	H	18	GLU
11	H	68	SER
11	H	84	LYS
11	H	154	TYR
11	H	159	PRO
12	J	70	PHE
12	J	74	ARG
12	J	79	PHE
12	J	107	ASN
12	J	112	ASP
12	J	127	ILE
12	J	131	THR
13	K	4	LEU
13	K	10	GLN
13	K	84	ASP
13	K	98	VAL
13	K	100	GLU
13	K	107	THR
14	L	35	ARG
14	L	43	HIS
15	M	46	LEU
15	M	68	ARG
15	M	93	ARG
15	M	99	ARG
15	M	116	ASN
16	N	14	ARG
16	N	26	LEU
16	N	37	ARG
16	N	56	ASP
16	N	65	ASP
16	N	135	VAL
16	N	139	TRP
17	O	3	THR
17	O	25	VAL
17	O	96	VAL
17	O	115	ARG
18	P	98	ILE
19	Q	16	ASN
19	Q	57	ASP
20	R	13	THR

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Mol	Chain	Res	Type
22	T	39	ASN
22	T	48	VAL
22	T	89	ARG
22	T	96	VAL
22	T	117	ASP
24	V	65	ASP
25	W	26	ILE
25	W	109	GLU
25	W	142	ASP
25	W	146	ILE
26	X	8	ARG
26	X	15	ARG
26	X	27	ASP
26	X	49	ARG
26	X	72	VAL
26	X	79	GLU
26	X	80	GLU
27	Y	103	THR
27	Y	108	ASP
27	Y	115	ARG
27	Y	141	THR
27	Y	144	ARG
27	Y	154	ARG
27	Y	189	ASN
27	Y	200	THR
27	Y	204	ARG
27	Y	220	GLU
27	Y	231	PRO
27	Y	235	GLU
28	Z	44	GLU
30	2	18	ASN
30	2	46	ASP
31	3	15	ASN
31	3	56	PRO
31	3	65	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (85) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	5	GLN
4	A	199	HIS
5	B	2	GLN

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Mol	Chain	Res	Type
5	B	27	ASN
5	B	145	HIS
5	B	191	ASN
5	B	221	GLN
5	B	238	ASN
5	B	256	GLN
5	B	260	HIS
5	B	320	GLN
5	B	332	ASN
6	C	11	ASN
6	C	39	GLN
6	C	129	HIS
6	C	163	HIS
7	D	47	GLN
7	D	103	ASN
7	D	133	ASN
8	E	106	ASN
8	E	143	GLN
10	G	17	GLN
10	G	64	ASN
11	H	56	GLN
11	H	59	HIS
11	H	70	ASN
11	H	132	GLN
11	H	170	ASN
12	J	25	GLN
12	J	107	ASN
12	J	126	ASN
13	K	10	GLN
14	L	18	HIS
14	L	41	HIS
14	L	42	ASN
14	L	43	HIS
15	M	24	GLN
15	M	58	GLN
15	M	77	HIS
15	M	143	ASN
15	M	170	ASN
16	N	107	ASN
17	O	53	GLN
17	O	100	GLN
18	P	50	GLN

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Mol	Chain	Res	Type
18	P	66	GLN
18	P	73	HIS
18	P	88	GLN
18	P	118	GLN
19	Q	16	ASN
19	Q	40	HIS
20	R	61	GLN
20	R	94	ASN
20	R	98	ASN
20	R	113	HIS
20	R	117	HIS
21	S	44	GLN
21	S	53	ASN
22	T	39	ASN
23	U	39	ASN
23	U	48	ASN
24	V	29	ASN
24	V	60	GLN
25	W	12	ASN
25	W	110	GLN
25	W	119	HIS
25	W	125	HIS
25	W	141	HIS
26	X	22	ASN
26	X	23	HIS
27	Y	133	HIS
27	Y	134	HIS
27	Y	149	GLN
27	Y	189	ASN
29	1	8	GLN
29	1	16	HIS
29	1	28	HIS
30	2	16	ASN
30	2	18	ASN
30	2	41	HIS
30	2	45	ASN
31	3	30	GLN
31	3	48	ASN
32	I	93	GLN
32	I	113	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2745/2922 (93%)	237 (8%)	36 (1%)
2	9	121/122 (99%)	16 (13%)	2 (1%)
3	4	1/5 (20%)	0	0
All	All	2867/3049 (94%)	253 (8%)	38 (1%)

All (253) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	67	A
1	0	70	A
1	0	71	G
1	0	86	A
1	0	87	C
1	0	88	G
1	0	114	A
1	0	115	U
1	0	120	A
1	0	130	C
1	0	138	U
1	0	141	C
1	0	151	A
1	0	166	A
1	0	186	A
1	0	187	A
1	0	191	A
1	0	192	A
1	0	219	G
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U
1	0	284	C
1	0	308	U
1	0	309	C
1	0	318	C
1	0	336	G
1	0	337	A
1	0	358	G
1	0	381	G
1	0	397	A
1	0	417	G

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Mol	Chain	Res	Type
1	0	457	U
1	0	461	C
1	0	473	A
1	0	487	G
1	0	498	A
1	0	511	A
1	0	514	G
1	0	537	G
1	0	538	C
1	0	539	G
1	0	542	A
1	0	545	G
1	0	553	G
1	0	559	U
1	0	581	G
1	0	588	G
1	0	604	G
1	0	620	A
1	0	632	A
1	0	644	G
1	0	660	A
1	0	688	A
1	0	698	A
1	0	701	U
1	0	702	G
1	0	759	C
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U
1	0	840	U
1	0	868	G
1	0	869	G
1	0	871	G
1	0	875	A
1	0	877	G
1	0	878	G
1	0	885	G
1	0	905	C
1	0	920	C
1	0	921	G
1	0	923	A

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Mol	Chain	Res	Type
1	0	953	G
1	0	960	G
1	0	961	A
1	0	1006	A
1	0	1008	C
1	0	1029	U
1	0	1045	G
1	0	1059	G
1	0	1060	C
1	0	1072	G
1	0	1081	A
1	0	1087	G
1	0	1088	A
1	0	1100	G
1	0	1109	U
1	0	1110	G
1	0	1119	G
1	0	1130	U
1	0	1151	G
1	0	1164	U
1	0	1165	G
1	0	1166	A
1	0	1174	A
1	0	1175	G
1	0	1185	U
1	0	1193	A
1	0	1206	U
1	0	1208	C
1	0	1216	G
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1279	U
1	0	1287	A
1	0	1289	C
1	0	1342	C
1	0	1353	C
1	0	1360	C
1	0	1377	C
1	0	1378	G
1	0	1407	A
1	0	1409	G

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Mol	Chain	Res	Type
1	0	1474	C
1	0	1505	U
1	0	1506	U
1	0	1524	U
1	0	1525	G
1	0	1526	A
1	0	1528	A
1	0	1564	C
1	0	1592	G
1	0	1625	U
1	0	1626	A
1	0	1633	C
1	0	1634	G
1	0	1656	A
1	0	1667	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1692	C
1	0	1701	A
1	0	1710	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1731	C
1	0	1732	A
1	0	1752	G
1	0	1778	A
1	0	1798	C
1	0	1819	G
1	0	1820	G
1	0	1829	A
1	0	1856	C
1	0	1879	U
1	0	1919	A
1	0	1942	A
1	0	1971	G
1	0	1973	A
1	0	1979	G
1	0	1980	U
1	0	1996	U
1	0	2004	U

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Mol	Chain	Res	Type
1	0	2006	C
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G
1	0	2033	G
1	0	2034	U
1	0	2063	U
1	0	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2103	A
1	0	2110	G
1	0	2243	C
1	0	2258	A
1	0	2271	G
1	0	2272	G
1	0	2317	C
1	0	2321	A
1	0	2354	A
1	0	2361	A
1	0	2369	A
1	0	2379	G
1	0	2422	U
1	0	2462	G
1	0	2476	C
1	0	2483	A
1	0	2507	G
1	0	2509	A
1	0	2511	A
1	0	2533	C
1	0	2537	G
1	0	2541	U
1	0	2553	A
1	0	2564	G
1	0	2589	U
1	0	2601	A
1	0	2602	G

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Mol	Chain	Res	Type
1	0	2608	C
1	0	2611	G
1	0	2613	G
1	0	2634	G
1	0	2637	A
1	0	2645	U
1	0	2646	G
1	0	2649	A
1	0	2650	U
1	0	2664	A
1	0	2681	A
1	0	2682	C
1	0	2718	C
1	0	2719	A
1	0	2726	U
1	0	2727	A
1	0	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2762	C
1	0	2768	A
1	0	2786	G
1	0	2792	A
1	0	2800	A
1	0	2811	A
1	0	2825	C
1	0	2852	A
1	0	2853	U
1	0	2876	G
1	0	2890	A
1	0	2896	A
1	0	2903	C
1	0	2914	A
2	9	3002	U
2	9	3014	G
2	9	3022	G
2	9	3023	U
2	9	3024	U
2	9	3025	G
2	9	3039	U
2	9	3041	C

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Mol	Chain	Res	Type
2	9	3043	G
2	9	3044	A
2	9	3052	A
2	9	3057	A
2	9	3066	G
2	9	3077	A
2	9	3114	G
2	9	3122	C

All (38) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	87	C
1	0	129	A
1	0	169	A
1	0	338	C
1	0	603	A
1	0	644	G
1	0	699	C
1	0	834	G
1	0	857	A
1	0	871	G
1	0	877	G
1	0	1165	G
1	0	1232	A
1	0	1237	U
1	0	1246	A
1	0	1352	A
1	0	1506	U
1	0	1563	G
1	0	1684	A
1	0	1685	A
1	0	1692	C
1	0	1730	G
1	0	1856	C
1	0	1942	A
1	0	1973	A
1	0	1979	G
1	0	2011	A
1	0	2313	C
1	0	2467	A
1	0	2536	C

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Mol	Chain	Res	Type
1	0	2649	A
1	0	2718	C
1	0	2726	U
1	0	2761	A
1	0	2791	U
1	0	2852	A
2	9	3055	U
2	9	3065	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMU	0	2587	1	20,22,23	0.87	1 (5%)	24,31,34	0.78	0
1	OMG	0	2588	1	24,26,27	0.85	1 (4%)	32,38,41	4.98	3 (9%)
1	UR3	0	2619	1	20,22,23	0.82	0	23,32,35	0.86	0
1	PSU	0	2621	1	19,21,22	1.33	3 (15%)	23,30,33	1.04	1 (4%)
1	1MA	0	628	1,35	23,25,26	0.92	1 (4%)	32,37,40	1.01	2 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	0	2587	1	-	0/8/27/28	0/2/2/2
1	OMG	0	2588	1	-	0/10/27/28	0/1/3/3
1	UR3	0	2619	1	-	0/6/25/26	0/2/2/2
1	PSU	0	2621	1	-	0/8/25/26	0/2/2/2
1	1MA	0	628	1,35	-	1/8/25/26	0/1/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C6-N1	3.30	1.35	1.32
1	0	2621	PSU	C2-N1	3.08	1.43	1.37
1	0	2587	OMU	P-OP1	2.84	1.50	1.46
1	0	2621	PSU	P-OP1	2.44	1.49	1.46
1	0	2588	OMG	P-OP1	2.19	1.49	1.46
1	0	628	1MA	P-OP1	2.15	1.49	1.46

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2588	OMG	C6-C5-N7	-27.58	130.43	134.14
1	0	2588	OMG	C6-N1-C2	3.24	125.17	119.51
1	0	628	1MA	C2-N3-C4	-3.19	110.78	116.23
1	0	2621	PSU	C5-C4-N3	-2.25	114.76	118.86
1	0	2588	OMG	C2-N3-C4	-2.22	111.97	115.09
1	0	628	1MA	CM1-N1-C6	2.03	123.37	120.56

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	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 313 ligands modelled in this entry, 312 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	SPS	4	9701	33	23,23,23	1.32	3 (13%)	25,30,30	2.01	2 (8%)

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
38	SPS	4	9701	33	-	1/17/18/18	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	4	9701	SPS	C1-C6	3.76	1.53	1.43
38	4	9701	SPS	C9-C10	-2.89	1.41	1.48
38	4	9701	SPS	O15-S15	-2.15	1.43	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	4	9701	SPS	C7-C5-C6	-7.47	121.67	126.94
38	4	9701	SPS	C6-C5-N4	4.71	119.52	117.31

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
38	4	9701	SPS	S15-C16-S17-C18

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2754/2922 (94%)	-0.15	91 (3%) 44 45	19, 43, 76, 127	0
2	9	122/122 (100%)	0.13	6 (4%) 28 28	39, 58, 76, 127	0
3	4	5/5 (100%)	0.95	1 (20%) 2 1	52, 54, 58, 58	0
4	A	237/240 (98%)	0.42	14 (5%) 22 21	26, 45, 70, 85	0
5	B	337/338 (99%)	0.27	15 (4%) 32 32	27, 47, 65, 73	0
6	C	246/246 (100%)	-0.03	3 (1%) 75 76	26, 44, 61, 69	0
7	D	140/177 (79%)	1.95	54 (38%) 1 0	51, 74, 102, 109	0
8	E	172/178 (96%)	0.74	20 (11%) 5 5	40, 57, 69, 74	0
9	F	119/120 (99%)	1.05	25 (21%) 1 1	45, 62, 82, 87	0
10	G	29/348 (8%)	2.53	17 (58%) 0 0	59, 77, 83, 86	0
11	H	160/171 (93%)	0.73	27 (16%) 2 2	41, 54, 79, 83	0
12	J	142/145 (97%)	0.05	4 (2%) 50 51	36, 45, 58, 71	0
13	K	132/132 (100%)	-0.12	2 (1%) 70 71	32, 43, 59, 64	0
14	L	145/165 (87%)	0.70	23 (15%) 3 2	26, 56, 90, 100	0
15	M	194/194 (100%)	0.52	21 (10%) 6 6	32, 42, 65, 70	0
16	N	186/187 (99%)	0.95	30 (16%) 2 2	42, 56, 89, 94	0
17	O	115/116 (99%)	0.15	4 (3%) 42 42	37, 50, 60, 65	0
18	P	143/149 (95%)	0.11	3 (2%) 60 61	35, 47, 57, 66	0
19	Q	95/96 (98%)	0.18	3 (3%) 45 46	39, 45, 56, 67	0
20	R	150/155 (96%)	-0.02	2 (1%) 74 74	29, 41, 56, 64	0
21	S	81/85 (95%)	0.31	6 (7%) 14 14	39, 52, 66, 79	0
22	T	119/120 (99%)	0.56	8 (6%) 17 17	38, 50, 70, 92	0
23	U	53/66 (80%)	0.27	4 (7%) 14 13	38, 47, 61, 69	0
24	V	65/71 (91%)	1.80	16 (24%) 1 1	46, 64, 93, 97	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	154/154 (100%)	0.04	1 (0%) 86 88	36, 47, 60, 68	0
26	X	82/92 (89%)	0.47	9 (10%) 6 6	39, 50, 69, 85	0
27	Y	142/241 (58%)	0.24	8 (5%) 24 23	28, 41, 59, 73	0
28	Z	73/83 (87%)	0.61	9 (12%) 5 4	43, 58, 70, 76	0
29	1	56/57 (98%)	-0.36	0 100 100	25, 32, 39, 48	0
30	2	46/50 (92%)	0.44	3 (6%) 18 18	31, 49, 62, 71	0
31	3	92/92 (100%)	0.32	5 (5%) 25 25	34, 51, 60, 70	0
32	I	70/162 (43%)	5.71	66 (94%) 0 0	90, 102, 117, 118	0
All	All	6656/7479 (88%)	0.26	500 (7%) 14 13	19, 47, 79, 127	0

All (500) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
32	I	71	GLY	17.7
7	D	63	ILE	16.3
16	N	166	ALA	14.8
24	V	1	THR	14.7
32	I	133	THR	13.6
32	I	76	ALA	12.5
32	I	79	ILE	11.5
32	I	118	SER	11.5
24	V	40	PRO	11.2
32	I	85	PHE	10.8
24	V	39	ALA	10.4
32	I	77	GLU	10.3
32	I	75	THR	10.1
7	D	57	THR	9.8
32	I	137	VAL	9.0
32	I	116	LEU	9.0
15	M	70	GLY	8.6
16	N	165	ALA	8.3
7	D	61	PHE	8.3
32	I	81	ASP	8.2
1	0	282	C	8.0
32	I	96	PHE	7.9
4	A	237	GLY	7.8
32	I	121	LEU	7.7
32	I	109	ALA	7.6
7	D	10	PHE	7.5

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Mol	Chain	Res	Type	RSRZ
32	I	105	VAL	7.5
32	I	132	CYS	7.4
32	I	88	GLY	7.4
32	I	87	THR	7.2
1	0	1951	G	7.1
32	I	129	VAL	7.1
32	I	113	HIS	7.0
2	9	3001	U	7.0
32	I	78	LEU	7.0
32	I	91	GLU	6.9
32	I	107	GLN	6.8
32	I	125	ALA	6.8
1	0	497	A	6.8
32	I	126	LYS	6.7
22	T	119	ALA	6.6
32	I	108	ILE	6.5
7	D	90	LEU	6.5
24	V	38	GLY	6.5
32	I	102	VAL	6.4
10	G	26	MET	6.3
4	A	37	VAL	6.3
1	0	1199	A	6.3
30	2	49	GLU	6.2
2	9	3002	U	6.1
32	I	86	GLU	6.0
32	I	111	GLN	6.0
32	I	134	SER	5.9
32	I	119	TYR	5.8
32	I	122	THR	5.7
7	D	93	LEU	5.7
32	I	93	GLN	5.7
1	0	1202	A	5.7
2	9	3024	U	5.6
7	D	170	TYR	5.5
1	0	1173	A	5.5
32	I	114	PRO	5.5
32	I	104	GLN	5.4
10	G	23	ILE	5.4
21	S	81	ILE	5.4
7	D	44	ILE	5.3
32	I	89	SER	5.2
16	N	180	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
13	K	132	VAL	5.1
10	G	27	ILE	5.1
9	F	28	ALA	5.1
26	X	88	GLU	5.1
22	T	117	ASP	5.1
32	I	98	ALA	5.1
32	I	117	LEU	5.1
32	I	97	VAL	5.1
14	L	91	VAL	5.0
22	T	116	ASP	5.0
1	0	1172	G	5.0
22	T	118	SER	5.0
1	0	514	G	4.9
26	X	80	GLU	4.9
12	J	70	PHE	4.9
32	I	136	GLY	4.8
5	B	1	PRO	4.8
14	L	81	VAL	4.8
2	9	3023	U	4.8
1	0	284	C	4.8
8	E	45	ASP	4.8
28	Z	22	SER	4.8
32	I	138	THR	4.7
1	0	280	C	4.7
32	I	84	GLY	4.7
16	N	68	GLU	4.7
30	2	35	ARG	4.6
24	V	37	GLY	4.6
1	0	1192	A	4.6
1	0	1177	A	4.6
17	O	22	GLY	4.6
8	E	100	ASP	4.6
11	H	171	ALA	4.6
15	M	71	SER	4.5
7	D	66	GLY	4.5
24	V	43	PRO	4.5
9	F	99	THR	4.5
7	D	92	GLU	4.4
32	I	74	PRO	4.4
32	I	83	ALA	4.4
7	D	88	LEU	4.4
16	N	95	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
1	0	960	G	4.3
1	0	1200	A	4.3
7	D	107	GLY	4.3
4	A	236	GLY	4.3
1	0	1965	C	4.3
1	0	735	C	4.3
10	G	69	ARG	4.3
7	D	172	VAL	4.2
28	Z	11	SER	4.2
7	D	166	ILE	4.2
10	G	71	LEU	4.2
1	0	2508	C	4.2
1	0	1171	A	4.2
1	0	2004	U	4.2
9	F	118	LEU	4.2
9	F	22	VAL	4.1
16	N	184	ILE	4.1
1	0	1948	G	4.1
24	V	36	ALA	4.1
1	0	999	C	4.1
14	L	80	ASP	4.1
15	M	79	ALA	4.1
1	0	970	U	4.1
7	D	91	ALA	4.0
7	D	11	HIS	4.0
1	0	285	A	4.0
1	0	2344	G	4.0
32	I	72	VAL	4.0
23	U	47	ARG	4.0
11	H	73	LEU	4.0
8	E	10	ASP	4.0
7	D	171	ASP	4.0
4	A	133	ARG	4.0
7	D	64	ARG	4.0
7	D	62	ASP	3.9
1	0	1525	G	3.9
1	0	1950	G	3.9
1	0	2237	G	3.9
32	I	80	LYS	3.9
32	I	120	ASP	3.9
4	A	36	ASP	3.9
7	D	135	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
27	Y	235	GLU	3.9
28	Z	20	ARG	3.9
16	N	160	SER	3.8
9	F	117	GLU	3.8
13	K	118	ALA	3.8
32	I	99	ASP	3.8
1	0	1168	C	3.8
1	0	283	U	3.8
1	0	1169	U	3.8
9	F	119	ARG	3.8
24	V	8	ILE	3.8
9	F	101	ALA	3.7
15	M	74	LYS	3.7
14	L	105	TYR	3.7
7	D	27	ILE	3.7
27	Y	95	THR	3.7
2	9	3122	C	3.7
9	F	100	ASP	3.7
16	N	158	LEU	3.7
27	Y	236	VAL	3.7
16	N	163	PHE	3.7
16	N	185	GLU	3.7
7	D	69	ILE	3.7
15	M	75	ARG	3.6
9	F	105	ASP	3.6
7	D	134	LEU	3.6
14	L	76	LEU	3.6
8	E	6	GLU	3.6
8	E	124	VAL	3.6
16	N	181	ASP	3.6
1	0	1182	C	3.6
22	T	115	GLU	3.6
24	V	41	GLU	3.6
16	N	155	GLU	3.6
1	0	10	U	3.6
7	D	85	GLN	3.5
22	T	82	THR	3.5
16	N	147	ILE	3.5
1	0	1164	U	3.5
16	N	134	ASP	3.5
1	0	2511	A	3.5
15	M	86	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
7	D	89	PRO	3.5
19	Q	95	GLU	3.5
1	0	1198	U	3.4
1	0	369	G	3.4
1	0	1181	A	3.4
11	H	168	ALA	3.4
32	I	123	ASN	3.4
32	I	124	ALA	3.4
5	B	2	GLN	3.4
14	L	97	VAL	3.4
15	M	80	GLY	3.4
1	0	2769	C	3.4
1	0	138	U	3.4
32	I	94	GLU	3.4
14	L	75	LEU	3.4
4	A	35	GLY	3.4
7	D	106	PHE	3.4
31	3	92	GLU	3.3
1	0	2238	A	3.3
1	0	1966	U	3.3
4	A	31	LYS	3.3
21	S	20	PHE	3.3
7	D	95	THR	3.3
15	M	84	LYS	3.3
16	N	159	TYR	3.3
16	N	175	LEU	3.3
24	V	59	ILE	3.3
1	0	1163	G	3.3
11	H	74	ILE	3.3
32	I	103	ASP	3.3
5	B	183	GLU	3.3
10	G	66	LEU	3.3
8	E	126	ILE	3.2
19	Q	18	PRO	3.2
11	H	78	GLY	3.2
1	0	370	G	3.2
1	0	1162	G	3.2
1	0	1165	G	3.2
28	Z	36	ASP	3.2
28	Z	24	ARG	3.2
17	O	1	SER	3.2
11	H	146	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
15	M	88	VAL	3.2
4	A	97	ALA	3.2
11	H	111	ASP	3.2
7	D	173	GLU	3.2
1	O	969	G	3.2
10	G	12	ILE	3.2
10	G	22	ALA	3.1
11	H	83	TYR	3.1
16	N	2	THR	3.1
26	X	71	ARG	3.1
18	P	18	LYS	3.1
9	F	103	GLU	3.1
14	L	106	VAL	3.1
26	X	85	VAL	3.1
32	I	106	LYS	3.1
1	O	272	A	3.1
32	I	90	GLY	3.1
1	O	1203	G	3.1
5	B	123	ALA	3.1
7	D	130	VAL	3.1
14	L	60	GLU	3.1
32	I	92	PRO	3.1
7	D	56	ARG	3.1
9	F	107	ASP	3.1
1	O	361	C	3.1
1	O	1183	C	3.1
9	F	25	ASP	3.1
1	O	288	A	3.0
24	V	5	VAL	3.0
16	N	161	GLY	3.0
9	F	106	ALA	3.0
14	L	148	GLU	3.0
1	O	362	G	3.0
7	D	81	GLU	3.0
32	I	110	GLU	3.0
1	O	281	U	3.0
9	F	98	VAL	3.0
10	G	65	THR	3.0
16	N	178	THR	3.0
11	H	162	ARG	3.0
14	L	147	GLU	3.0
28	Z	21	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
8	E	154	ILE	2.9
7	D	104	PHE	2.9
16	N	94	GLU	2.9
10	G	24	VAL	2.9
12	J	4	ALA	2.9
15	M	87	GLY	2.9
14	L	62	ALA	2.9
9	F	90	GLU	2.9
10	G	15	TRP	2.9
32	I	135	LEU	2.9
11	H	37	GLN	2.9
1	0	1967	U	2.9
7	D	51	ARG	2.8
11	H	35	ARG	2.8
14	L	79	ASP	2.8
25	W	86	GLU	2.8
1	0	372	A	2.8
7	D	75	LEU	2.8
1	0	2748	G	2.8
26	X	77	PHE	2.8
16	N	183	ASP	2.8
31	3	41	GLU	2.8
15	M	76	ARG	2.8
27	Y	216	ARG	2.8
16	N	182	GLY	2.8
6	C	61	PHE	2.8
19	Q	76	VAL	2.8
32	I	100	LEU	2.8
1	0	1161	A	2.8
1	0	2345	A	2.8
7	D	154	LYS	2.8
5	B	104	GLU	2.8
14	L	99	GLU	2.8
14	L	150	GLN	2.8
7	D	18	ILE	2.8
1	0	358	G	2.8
28	Z	12	GLY	2.8
14	L	145	LEU	2.8
9	F	108	VAL	2.7
1	0	1625	U	2.7
7	D	65	GLU	2.7
14	L	100	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	0	1174	A	2.7
7	D	41	LEU	2.7
32	I	130	GLY	2.7
11	H	166	SER	2.7
5	B	119	HIS	2.7
1	0	1180	U	2.7
21	S	78	ALA	2.7
11	H	82	ASP	2.7
15	M	81	ARG	2.7
24	V	2	VAL	2.7
1	0	441	A	2.7
1	0	295	C	2.7
8	E	87	PHE	2.7
1	0	1190	G	2.6
11	H	141	GLU	2.6
24	V	63	GLU	2.6
1	0	1170	U	2.6
17	O	23	GLY	2.6
1	0	736	A	2.6
7	D	40	ILE	2.6
15	M	77	HIS	2.6
26	X	7	GLU	2.6
1	0	1000	C	2.6
1	0	2645	U	2.6
9	F	26	THR	2.6
11	H	79	GLU	2.6
11	H	142	ASP	2.6
14	L	82	ALA	2.6
32	I	112	LYS	2.6
7	D	68	PRO	2.6
8	E	88	TYR	2.6
16	N	156	GLU	2.6
7	D	73	VAL	2.6
24	V	3	LEU	2.6
1	0	1175	G	2.6
1	0	1947	G	2.6
27	Y	96	GLU	2.6
4	A	82	VAL	2.6
26	X	10	VAL	2.6
14	L	101	ASP	2.5
4	A	85	SER	2.5
1	0	1929	G	2.5

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Mol	Chain	Res	Type	RSRZ
7	D	67	ASP	2.5
8	E	99	GLY	2.5
9	F	16	ALA	2.5
9	F	21	GLU	2.5
3	4	77	PHE	2.5
7	D	45	THR	2.5
8	E	94	GLN	2.5
10	G	73	ASP	2.5
4	A	32	VAL	2.5
27	Y	108	ASP	2.5
1	0	2747	C	2.5
7	D	26	GLY	2.5
15	M	1	ALA	2.5
15	M	194	ALA	2.5
7	D	74	THR	2.5
15	M	73	ARG	2.5
1	0	1184	C	2.5
16	N	137	ALA	2.5
16	N	138	ASP	2.5
14	L	149	ARG	2.5
5	B	117	GLU	2.5
7	D	77	ASP	2.5
11	H	39	ASP	2.5
24	V	10	ASP	2.5
11	H	149	ALA	2.4
1	0	279	C	2.4
5	B	57	GLU	2.4
5	B	180	ASP	2.4
32	I	131	THR	2.4
9	F	11	ASP	2.4
1	0	716	G	2.4
1	0	1167	G	2.4
1	0	1279	U	2.4
4	A	65	ARG	2.4
11	H	47	ILE	2.4
31	3	56	PRO	2.4
9	F	23	ALA	2.4
8	E	129	GLU	2.4
10	G	21	ASP	2.4
14	L	104	ASP	2.4
16	N	72	GLU	2.4
8	E	118	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
10	G	67	LEU	2.3
26	X	44	ASP	2.3
7	D	167	GLU	2.3
21	S	70	GLU	2.3
7	D	157	LEU	2.3
5	B	134	ALA	2.3
32	I	128	VAL	2.3
28	Z	45	ASP	2.3
7	D	70	GLY	2.3
2	9	3072	C	2.3
8	E	43	ASP	2.3
8	E	127	ASP	2.3
4	A	206	ARG	2.3
7	D	23	VAL	2.3
15	M	49	ALA	2.3
15	M	72	ALA	2.3
23	U	53	ASP	2.3
15	M	82	ARG	2.3
11	H	87	LEU	2.3
16	N	164	ASP	2.3
21	S	45	TYR	2.3
1	0	1189	A	2.3
22	T	59	GLU	2.3
1	0	293	A	2.2
31	3	62	THR	2.2
28	Z	25	ARG	2.2
10	G	64	ASN	2.2
7	D	58	VAL	2.2
26	X	43	VAL	2.2
32	I	115	ASP	2.2
1	0	365	G	2.2
1	0	1195	G	2.2
7	D	84	LEU	2.2
12	J	5	GLU	2.2
1	0	291	C	2.2
31	3	23	GLU	2.2
27	Y	234	VAL	2.2
11	H	139	ASN	2.2
18	P	141	ILE	2.2
16	N	139	TRP	2.2
7	D	165	PHE	2.2
9	F	49	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
12	J	92	GLN	2.2
14	L	130	ARG	2.2
15	M	78	LYS	2.2
23	U	54	THR	2.2
24	V	14	ALA	2.2
1	0	1527	A	2.2
6	C	1	MET	2.2
8	E	131	LEU	2.2
5	B	21	SER	2.2
8	E	97	VAL	2.2
11	H	138	CYS	2.2
1	0	31	C	2.1
9	F	12	LEU	2.1
15	M	83	SER	2.1
30	2	39	ARG	2.1
9	F	110	ASP	2.1
14	L	102	ASP	2.1
32	I	95	ASP	2.1
5	B	61	PRO	2.1
20	R	12	THR	2.1
10	G	63	ARG	2.1
16	N	152	GLU	2.1
4	A	86	ALA	2.1
11	H	137	TYR	2.1
5	B	124	ALA	2.1
17	O	24	ALA	2.1
16	N	106	LEU	2.1
11	H	76	GLU	2.1
21	S	2	TRP	2.1
8	E	48	VAL	2.1
27	Y	196	VAL	2.1
1	0	363	A	2.1
1	0	1526	A	2.1
5	B	128	ILE	2.1
10	G	25	GLU	2.1
7	D	17	ARG	2.1
1	0	290	C	2.1
32	I	73	PRO	2.1
1	0	1964	U	2.1
9	F	19	ALA	2.1
8	E	108	LEU	2.0
11	H	67	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
18	P	108	LEU	2.0
8	E	4	GLU	2.0
1	0	1197	G	2.0
32	I	140	GLU	2.0
5	B	176	ASP	2.0
6	C	132	ASP	2.0
23	U	52	THR	2.0
20	R	107	GLU	2.0
22	T	36	GLY	2.0
1	0	1188	A	2.0
11	H	42	ASP	2.0
11	H	44	PRO	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	OMU	0	2587	21/22	0.12	1.48	30,35,36,37	0
1	OMG	0	2588	24/25	0.11	-0.23	30,34,36,38	0
1	UR3	0	2619	21/22	0.12	-0.37	34,38,41,43	0
1	PSU	0	2621	20/21	0.12	-0.86	31,33,38,38	0
1	1MA	0	628	23/24	0.12	-0.95	28,32,33,34	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	9111	1/1	0.23	315.81	59,59,59,59	0
37	SR	0	9601	1/1	0.59	241.00	191,191,191,191	0
33	MG	0	8094	1/1	0.45	78.93	83,83,83,83	0
37	SR	0	9500	1/1	1.75	68.38	197,197,197,197	0
35	NA	0	9125	1/1	0.80	61.44	93,93,93,93	0
35	NA	0	9179	1/1	0.56	60.59	89,89,89,89	0
33	MG	0	8082	1/1	0.23	43.00	82,82,82,82	0
33	MG	0	8108	1/1	0.28	39.56	81,81,81,81	0
33	MG	0	8024	1/1	0.84	37.94	74,74,74,74	0
35	NA	0	9152	1/1	0.30	33.47	64,64,64,64	0
35	NA	0	9170	1/1	0.42	32.15	72,72,72,72	0
35	NA	0	9122	1/1	0.44	30.53	77,77,77,77	0
34	K	0	9001	1/1	0.27	29.70	84,84,84,84	0
35	NA	0	9102	1/1	0.36	29.07	61,61,61,61	0
35	NA	0	9178	1/1	0.49	25.14	52,52,52,52	0
37	SR	B	9521	1/1	0.82	23.69	185,185,185,185	0
37	SR	0	9547	1/1	0.27	22.44	166,166,166,166	0
35	NA	9	9183	1/1	0.40	21.66	77,77,77,77	0
33	MG	0	8025	1/1	0.31	21.14	24,24,24,24	0
35	NA	B	9161	1/1	0.34	20.65	62,62,62,62	0
37	SR	0	9539	1/1	0.44	19.50	145,145,145,145	0
35	NA	0	9169	1/1	0.62	18.35	90,90,90,90	0
35	NA	0	9173	1/1	0.25	18.23	59,59,59,59	0
33	MG	0	8092	1/1	0.64	17.91	80,80,80,80	0
33	MG	0	8014	1/1	0.28	17.74	67,67,67,67	0
33	MG	0	8013	1/1	0.37	17.63	14,14,14,14	0
33	MG	0	8022	1/1	0.53	17.39	63,63,63,63	0
35	NA	0	9185	1/1	0.36	16.16	52,52,52,52	0
35	NA	0	9168	1/1	0.17	16.09	66,66,66,66	0
37	SR	0	9410	1/1	0.19	16.02	45,45,45,45	0
35	NA	0	9158	1/1	0.35	15.87	55,55,55,55	0
35	NA	S	9112	1/1	0.79	15.76	75,75,75,75	0
33	MG	0	8008	1/1	0.22	15.70	16,16,16,16	0
37	SR	0	9626	1/1	0.33	15.05	127,127,127,127	0
33	MG	0	8038	1/1	0.24	13.85	18,18,18,18	0
33	MG	0	8089	1/1	0.17	12.68	54,54,54,54	0
35	NA	0	9172	1/1	0.40	12.59	76,76,76,76	0
35	NA	0	9164	1/1	0.28	12.55	60,60,60,60	0
33	MG	0	8001	1/1	0.20	12.40	23,23,23,23	0
33	MG	0	8047	1/1	0.31	12.33	85,85,85,85	0
33	MG	0	8114	1/1	0.29	11.86	71,71,71,71	0
37	SR	0	9408	1/1	0.20	11.67	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
39	CD	O	9205	1/1	0.43	11.66	197,197,197,197	0
37	SR	0	9406	1/1	0.21	11.35	43,43,43,43	0
35	NA	0	9157	1/1	0.18	11.27	37,37,37,37	0
35	NA	0	9113	1/1	0.21	10.95	64,64,64,64	0
35	NA	0	9184	1/1	0.25	10.60	73,73,73,73	0
35	NA	0	9177	1/1	0.33	10.48	71,71,71,71	0
35	NA	0	9107	1/1	0.22	10.06	54,54,54,54	0
37	SR	0	9411	1/1	0.18	9.74	46,46,46,46	0
33	MG	0	8050	1/1	0.24	9.72	88,88,88,88	0
33	MG	0	8085	1/1	0.22	9.69	67,67,67,67	0
33	MG	0	8065	1/1	0.57	9.29	93,93,93,93	0
35	NA	0	9129	1/1	0.21	9.06	74,74,74,74	0
33	MG	0	8051	1/1	0.17	8.87	23,23,23,23	0
37	SR	0	9482	1/1	0.19	8.64	115,115,115,115	0
35	NA	0	9175	1/1	0.20	8.57	47,47,47,47	0
36	CL	0	9322	1/1	0.18	8.22	51,51,51,51	0
33	MG	0	8084	1/1	0.26	8.18	61,61,61,61	0
33	MG	0	8012	1/1	0.24	8.16	37,37,37,37	0
33	MG	0	8021	1/1	0.23	7.91	56,56,56,56	0
33	MG	0	8052	1/1	0.21	7.71	74,74,74,74	0
33	MG	0	8057	1/1	0.27	7.56	77,77,77,77	0
35	NA	0	9140	1/1	0.28	7.30	63,63,63,63	0
33	MG	0	8027	1/1	0.21	7.05	35,35,35,35	0
35	NA	0	9106	1/1	0.17	7.01	35,35,35,35	0
37	SR	L	9409	1/1	0.19	6.97	49,49,49,49	0
35	NA	0	9182	1/1	0.23	6.66	63,63,63,63	0
35	NA	0	9118	1/1	0.20	6.57	49,49,49,49	0
37	SR	0	9407	1/1	0.16	6.52	46,46,46,46	0
37	SR	0	9432	1/1	0.13	6.30	61,61,61,61	0
35	NA	0	9154	1/1	0.19	5.99	57,57,57,57	0
35	NA	0	9167	1/1	0.12	5.81	49,49,49,49	0
33	MG	0	8059	1/1	0.18	5.63	48,48,48,48	0
35	NA	0	9101	1/1	0.17	5.43	45,45,45,45	0
33	MG	0	8056	1/1	0.23	5.42	54,54,54,54	0
33	MG	K	8069	1/1	0.20	5.42	24,24,24,24	0
33	MG	0	8070	1/1	0.15	5.12	21,21,21,21	0
33	MG	0	8103	1/1	0.16	5.06	62,62,62,62	0
35	NA	0	9128	1/1	0.13	5.06	39,39,39,39	0
33	MG	0	8061	1/1	0.15	5.01	75,75,75,75	0
37	SR	0	9412	1/1	0.15	4.95	48,48,48,48	0
36	CL	B	9319	1/1	0.23	4.80	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	9115	1/1	0.15	4.43	35,35,35,35	0
33	MG	0	8029	1/1	0.19	4.38	26,26,26,26	0
33	MG	0	8017	1/1	0.13	4.10	23,23,23,23	0
36	CL	0	9316	1/1	0.27	3.82	69,69,69,69	0
35	NA	0	9149	1/1	0.16	3.80	43,43,43,43	0
35	NA	0	9116	1/1	0.17	3.77	46,46,46,46	0
33	MG	0	8072	1/1	0.16	3.70	70,70,70,70	0
33	MG	9	8095	1/1	0.19	3.59	48,48,48,48	0
33	MG	0	8060	1/1	0.20	3.54	76,76,76,76	0
35	NA	0	9127	1/1	0.16	3.38	57,57,57,57	0
37	SR	0	9420	1/1	0.16	3.36	65,65,65,65	0
33	MG	0	8080	1/1	0.17	3.31	46,46,46,46	0
33	MG	0	8026	1/1	0.14	3.17	28,28,28,28	0
33	MG	0	8091	1/1	0.13	3.08	64,64,64,64	0
37	SR	0	9501	1/1	0.20	3.01	196,196,196,196	0
33	MG	0	8110	1/1	0.17	3.00	44,44,44,44	0
33	MG	0	8079	1/1	0.14	2.99	28,28,28,28	0
35	NA	0	9159	1/1	0.18	2.87	46,46,46,46	0
35	NA	0	9141	1/1	0.13	2.85	70,70,70,70	0
37	SR	0	9415	1/1	0.12	2.41	54,54,54,54	0
37	SR	0	9424	1/1	0.16	2.34	46,46,46,46	0
35	NA	0	9174	1/1	0.13	2.32	61,61,61,61	0
33	MG	0	8040	1/1	0.24	2.26	69,69,69,69	0
37	SR	0	9416	1/1	0.15	2.22	47,47,47,47	0
35	NA	0	9155	1/1	0.28	2.14	52,52,52,52	0
37	SR	0	9430	1/1	0.15	2.10	46,46,46,46	0
37	SR	0	9427	1/1	0.12	2.08	54,54,54,54	0
37	SR	0	9433	1/1	0.11	2.07	68,68,68,68	0
35	NA	0	9163	1/1	0.16	1.99	58,58,58,58	0
33	MG	0	8020	1/1	0.17	1.85	36,36,36,36	0
37	SR	R	9418	1/1	0.15	1.80	54,54,54,54	0
35	NA	0	9181	1/1	0.12	1.79	52,52,52,52	0
35	NA	0	9120	1/1	0.14	1.69	55,55,55,55	0
37	SR	1	9419	1/1	0.14	1.65	43,43,43,43	0
37	SR	F	9595	1/1	0.16	1.62	92,92,92,92	0
33	MG	0	8058	1/1	0.19	1.47	39,39,39,39	0
35	NA	0	9165	1/1	0.22	1.39	44,44,44,44	0
37	SR	0	9434	1/1	0.12	1.23	59,59,59,59	0
33	MG	0	8074	1/1	0.21	1.19	20,20,20,20	0
33	MG	0	8045	1/1	0.16	1.17	84,84,84,84	0
33	MG	0	8107	1/1	0.15	1.13	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	MG	0	8097	1/1	0.14	1.12	57,57,57,57	0
35	NA	0	9171	1/1	0.11	1.05	66,66,66,66	0
37	SR	0	9414	1/1	0.13	0.97	54,54,54,54	0
37	SR	0	9423	1/1	0.11	0.82	51,51,51,51	0
37	SR	0	9467	1/1	0.11	0.82	71,71,71,71	0
35	NA	0	9124	1/1	0.14	0.74	53,53,53,53	0
37	SR	S	9470	1/1	0.13	0.74	91,91,91,91	0
33	MG	0	8090	1/1	0.17	0.73	68,68,68,68	0
37	SR	0	9465	1/1	0.10	0.70	98,98,98,98	0
35	NA	0	9186	1/1	0.13	0.65	67,67,67,67	0
33	MG	0	8063	1/1	0.14	0.64	64,64,64,64	0
35	NA	C	9104	1/1	0.17	0.60	31,31,31,31	0
35	NA	0	9114	1/1	0.14	0.60	56,56,56,56	0
33	MG	0	8055	1/1	0.15	0.58	83,83,83,83	0
35	NA	0	9132	1/1	0.13	0.57	54,54,54,54	0
33	MG	0	8054	1/1	0.12	0.56	55,55,55,55	0
37	SR	0	9515	1/1	0.13	0.53	88,88,88,88	0
37	SR	0	9457	1/1	0.11	0.53	49,49,49,49	0
33	MG	0	8115	1/1	0.13	0.50	55,55,55,55	0
33	MG	0	8041	1/1	0.12	0.47	51,51,51,51	0
33	MG	0	8101	1/1	0.11	0.46	59,59,59,59	0
37	SR	0	9417	1/1	0.14	0.37	53,53,53,53	0
39	CD	U	9201	1/1	0.13	0.36	59,59,59,59	0
38	SPS	4	9701	23/23	0.17	0.30	49,53,67,71	0
35	NA	0	9110	1/1	0.11	0.29	45,45,45,45	0
37	SR	H	9486	1/1	0.12	0.18	107,107,107,107	0
33	MG	0	8099	1/1	0.12	0.18	62,62,62,62	0
33	MG	0	8015	1/1	0.12	0.16	29,29,29,29	0
36	CL	M	9318	1/1	0.17	0.13	40,40,40,40	0
35	NA	0	9160	1/1	0.11	0.12	36,36,36,36	0
37	SR	0	9451	1/1	0.12	0.07	64,64,64,64	0
37	SR	0	9452	1/1	0.13	0.04	105,105,105,105	0
37	SR	A	9437	1/1	0.13	-0.06	61,61,61,61	0
35	NA	0	9126	1/1	0.11	-0.06	52,52,52,52	0
35	NA	0	9139	1/1	0.15	-0.11	57,57,57,57	0
39	CD	Z	9203	1/1	0.14	-0.15	59,59,59,59	0
35	NA	D	9151	1/1	0.26	-0.15	62,62,62,62	0
33	MG	0	8002	1/1	0.12	-0.24	29,29,29,29	0
35	NA	0	9117	1/1	0.12	-0.27	32,32,32,32	0
33	MG	0	8004	1/1	0.10	-0.27	26,26,26,26	0
35	NA	Q	9148	1/1	0.17	-0.29	51,51,51,51	0
37	SR	0	9413	1/1	0.14	-0.31	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	9150	1/1	0.13	-0.35	47,47,47,47	0
37	SR	0	9422	1/1	0.11	-0.37	55,55,55,55	0
33	MG	A	8066	1/1	0.12	-0.43	53,53,53,53	0
37	SR	9	9588	1/1	0.12	-0.43	118,118,118,118	0
37	SR	0	9537	1/1	0.10	-0.48	136,136,136,136	0
36	CL	0	9314	1/1	0.12	-0.53	43,43,43,43	0
35	NA	0	9162	1/1	0.11	-0.56	49,49,49,49	0
35	NA	0	9156	1/1	0.12	-0.57	55,55,55,55	0
37	SR	1	9460	1/1	0.13	-0.61	51,51,51,51	0
37	SR	0	9530	1/1	0.11	-0.62	102,102,102,102	0
33	MG	0	8068	1/1	0.12	-0.62	41,41,41,41	0
37	SR	0	9428	1/1	0.11	-0.67	49,49,49,49	0
37	SR	A	9497	1/1	0.09	-0.67	78,78,78,78	0
37	SR	0	9560	1/1	0.09	-0.70	88,88,88,88	0
37	SR	0	9421	1/1	0.10	-0.71	65,65,65,65	0
36	CL	J	9301	1/1	0.09	-0.74	46,46,46,46	0
34	K	0	9002	1/1	0.10	-0.77	78,78,78,78	0
39	CD	3	9204	1/1	0.08	-0.79	59,59,59,59	0
37	SR	0	9475	1/1	0.09	-0.80	76,76,76,76	0
36	CL	J	9321	1/1	0.10	-0.82	64,64,64,64	0
37	SR	0	9509	1/1	0.11	-0.82	83,83,83,83	0
35	NA	M	9147	1/1	0.11	-0.84	43,43,43,43	0
37	SR	0	9440	1/1	0.06	-0.88	61,61,61,61	0
35	NA	R	9137	1/1	0.10	-0.93	33,33,33,33	0
33	MG	0	8093	1/1	0.12	-0.96	45,45,45,45	0
35	NA	0	9130	1/1	0.10	-1.01	47,47,47,47	0
33	MG	0	8104	1/1	0.11	-1.03	49,49,49,49	0
37	SR	0	9545	1/1	0.04	-1.09	72,72,72,72	0
37	SR	0	9462	1/1	0.12	-1.10	64,64,64,64	0
36	CL	O	9308	1/1	0.09	-1.11	59,59,59,59	0
35	NA	R	9138	1/1	0.08	-1.11	58,58,58,58	0
36	CL	0	9311	1/1	0.10	-1.11	61,61,61,61	0
33	MG	T	8073	1/1	0.14	-1.16	41,41,41,41	0
35	NA	0	9166	1/1	0.09	-1.20	68,68,68,68	0
33	MG	0	8096	1/1	0.10	-1.21	40,40,40,40	0
37	SR	0	9445	1/1	0.09	-1.25	55,55,55,55	0
35	NA	J	9146	1/1	0.07	-1.26	51,51,51,51	0
37	SR	0	9488	1/1	0.10	-1.26	72,72,72,72	0
37	SR	0	9431	1/1	0.12	-1.27	56,56,56,56	0
37	SR	0	9443	1/1	0.10	-1.30	54,54,54,54	0
33	MG	0	8102	1/1	0.08	-1.35	66,66,66,66	0
37	SR	0	9590	1/1	0.10	-1.36	117,117,117,117	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	9131	1/1	0.10	-1.38	45,45,45,45	0
37	SR	0	9534	1/1	0.10	-1.40	95,95,95,95	0
33	MG	4	8118	1/1	0.11	-1.40	45,45,45,45	0
37	SR	0	9504	1/1	0.09	-1.44	88,88,88,88	0
37	SR	0	9444	1/1	0.12	-1.45	50,50,50,50	0
37	SR	0	9474	1/1	0.07	-1.47	71,71,71,71	0
33	MG	0	8046	1/1	0.07	-1.55	37,37,37,37	0
37	SR	0	9484	1/1	0.10	-1.57	134,134,134,134	0
37	SR	0	9450	1/1	0.07	-1.61	60,60,60,60	0
37	SR	0	9442	1/1	0.12	-1.63	59,59,59,59	0
37	SR	0	9517	1/1	0.07	-1.65	92,92,92,92	0
33	MG	0	8076	1/1	0.10	-1.65	51,51,51,51	0
36	CL	0	9312	1/1	0.08	-1.66	47,47,47,47	0
39	CD	1	9202	1/1	0.07	-1.80	55,55,55,55	0
37	SR	0	9585	1/1	0.09	-1.88	83,83,83,83	0
37	SR	0	9532	1/1	0.08	-1.90	115,115,115,115	0
33	MG	0	8117	1/1	0.11	-1.91	39,39,39,39	0
37	SR	0	9429	1/1	0.10	-1.98	64,64,64,64	0
36	CL	L	9310	1/1	0.08	-1.98	47,47,47,47	0
37	SR	0	9490	1/1	0.07	-1.98	101,101,101,101	0
37	SR	0	9568	1/1	0.10	-1.99	70,70,70,70	0
37	SR	0	9448	1/1	0.08	-2.05	59,59,59,59	0
33	MG	0	8028	1/1	0.10	-2.08	31,31,31,31	0
33	MG	0	8106	1/1	0.06	-2.19	47,47,47,47	0
37	SR	3	9439	1/1	0.07	-2.19	64,64,64,64	0
37	SR	0	9468	1/1	0.06	-2.27	97,97,97,97	0
36	CL	N	9307	1/1	0.11	-2.32	60,60,60,60	0
36	CL	J	9302	1/1	0.06	-2.39	54,54,54,54	0
37	SR	0	9449	1/1	0.09	-2.44	57,57,57,57	0
33	MG	0	8116	1/1	0.06	-2.45	51,51,51,51	0
36	CL	Y	9320	1/1	0.09	-2.47	40,40,40,40	0
37	SR	0	9478	1/1	0.07	-2.48	69,69,69,69	0
35	NA	0	9108	1/1	0.08	-2.51	31,31,31,31	0
33	MG	0	8044	1/1	0.07	-2.55	35,35,35,35	0
35	NA	0	9134	1/1	0.04	-2.60	42,42,42,42	0
33	MG	0	8067	1/1	0.09	-2.62	33,33,33,33	0
37	SR	0	9453	1/1	0.08	-2.63	68,68,68,68	0
37	SR	0	9438	1/1	0.07	-2.83	61,61,61,61	0
37	SR	0	9447	1/1	0.09	-2.89	62,62,62,62	0
36	CL	R	9306	1/1	0.08	-2.92	43,43,43,43	0
33	MG	0	8112	1/1	0.07	-2.95	45,45,45,45	0
33	MG	0	8036	1/1	0.08	-3.02	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
37	SR	0	9446	1/1	0.08	-3.07	78,78,78,78	0
35	NA	0	9136	1/1	0.08	-3.16	30,30,30,30	0
37	SR	0	9508	1/1	0.08	-3.26	78,78,78,78	0
33	MG	0	8037	1/1	0.06	-3.27	39,39,39,39	0
36	CL	A	9309	1/1	0.07	-3.31	56,56,56,56	0
37	SR	0	9405	1/1	0.06	-3.32	80,80,80,80	0
37	SR	0	9483	1/1	0.07	-3.43	69,69,69,69	0
33	MG	0	8088	1/1	0.06	-3.48	43,43,43,43	0
37	SR	0	9529	1/1	0.09	-3.54	136,136,136,136	0
37	SR	0	9456	1/1	0.07	-3.64	64,64,64,64	0
33	MG	0	8003	1/1	0.10	-3.66	26,26,26,26	0
33	MG	0	8098	1/1	0.08	-3.68	45,45,45,45	0
36	CL	0	9305	1/1	0.05	-3.77	50,50,50,50	0
37	SR	A	9436	1/1	0.03	-3.78	68,68,68,68	0
37	SR	0	9466	1/1	0.05	-3.84	89,89,89,89	0
37	SR	0	9566	1/1	0.06	-3.85	92,92,92,92	0
37	SR	0	9426	1/1	0.07	-4.00	64,64,64,64	0
35	NA	0	9143	1/1	0.06	-4.01	37,37,37,37	0
33	MG	0	8019	1/1	0.06	-4.01	47,47,47,47	0
36	CL	3	9304	1/1	0.06	-4.02	65,65,65,65	0
37	SR	0	9441	1/1	0.08	-4.07	57,57,57,57	0
33	MG	0	8042	1/1	0.07	-4.12	57,57,57,57	0
37	SR	0	9489	1/1	0.04	-4.18	85,85,85,85	0
33	MG	0	8031	1/1	0.06	-4.18	51,51,51,51	0
36	CL	0	9317	1/1	0.06	-4.28	48,48,48,48	0
37	SR	0	9473	1/1	0.05	-4.38	69,69,69,69	0
33	MG	0	8005	1/1	0.08	-4.42	29,29,29,29	0
33	MG	0	8030	1/1	0.05	-4.45	37,37,37,37	0
37	SR	0	9461	1/1	0.03	-4.51	71,71,71,71	0
37	SR	0	9435	1/1	0.07	-4.52	68,68,68,68	0
37	SR	0	9459	1/1	0.06	-4.57	95,95,95,95	0
37	SR	0	9495	1/1	0.08	-4.84	85,85,85,85	0
33	MG	0	8009	1/1	0.04	-4.90	31,31,31,31	0
37	SR	0	9629	1/1	0.08	-4.92	68,68,68,68	0
37	SR	0	9505	1/1	0.07	-4.95	97,97,97,97	0
37	SR	9	9503	1/1	0.04	-4.96	102,102,102,102	0
37	SR	0	9498	1/1	0.05	-5.03	61,61,61,61	0
37	SR	B	9458	1/1	0.06	-5.13	64,64,64,64	0
37	SR	0	9506	1/1	0.05	-5.26	74,74,74,74	0
33	MG	0	8039	1/1	0.06	-5.29	61,61,61,61	0
33	MG	Y	8109	1/1	0.04	-5.31	35,35,35,35	0
37	SR	0	9477	1/1	0.08	-5.31	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
37	SR	0	9455	1/1	0.08	-5.37	61,61,61,61	0
36	CL	0	9313	1/1	0.05	-5.43	47,47,47,47	0
33	MG	0	8032	1/1	0.07	-5.75	33,33,33,33	0
33	MG	0	8113	1/1	0.11	-5.98	49,49,49,49	0
33	MG	0	8043	1/1	0.07	-6.39	50,50,50,50	0
37	SR	0	9464	1/1	0.06	-6.70	79,79,79,79	0
35	NA	0	9135	1/1	0.07	-6.72	39,39,39,39	0
37	SR	0	9581	1/1	0.06	-6.73	110,110,110,110	0
36	CL	0	9315	1/1	0.08	-7.13	53,53,53,53	0
37	SR	0	9522	1/1	0.05	-7.24	98,98,98,98	0
35	NA	0	9105	1/1	0.03	-7.31	33,33,33,33	0
33	MG	0	8075	1/1	0.04	-7.42	43,43,43,43	0
33	MG	0	8083	1/1	0.10	-7.78	53,53,53,53	0
37	SR	0	9425	1/1	0.06	-8.43	108,108,108,108	0
37	SR	9	9481	1/1	0.07	-9.57	82,82,82,82	0
35	NA	0	9123	1/1	0.06	-10.14	39,39,39,39	0
37	SR	0	9480	1/1	0.03	-14.43	82,82,82,82	0
37	SR	0	9570	1/1	0.04	-15.40	92,92,92,92	0
37	SR	0	9454	1/1	0.05	-15.48	71,71,71,71	0
36	CL	0	9303	1/1	0.07	-18.45	43,43,43,43	0
37	SR	0	9469	1/1	0.04	-26.19	83,83,83,83	0

6.5 Other polymers ⓘ

There are no such residues in this entry.