



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 08:19 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 X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

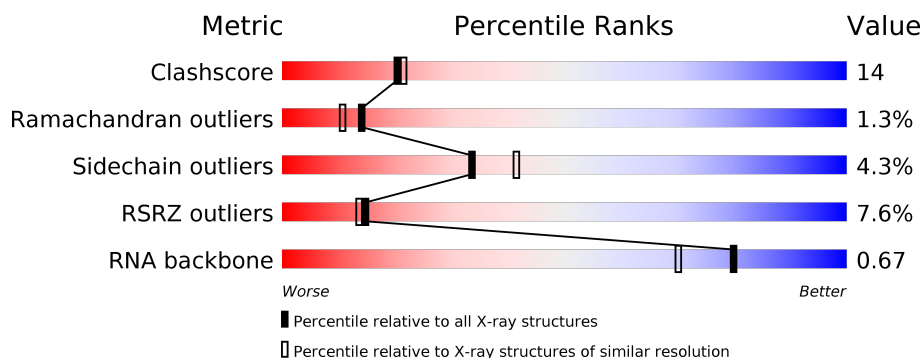
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)
RNA backbone	2435	1007 (2.74-1.66)

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

Mol	Chain	Length	Quality of chain
1	0	2922	<div> <div>3%</div> <div>66% 24% 6%</div> </div>
2	9	122	<div> <div>5%</div> <div>54% 36% 9%</div> </div>
3	4	5	<div> <div>20%</div> <div>80% 20%</div> </div>
4	A	240	<div> <div>6%</div> <div>58% 35% 5%</div> </div>
5	B	338	<div> <div>3%</div> <div>58% 38%</div> </div>
6	C	246	<div> <div>%</div> <div>67% 28%</div> </div>

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Mol	Chain	Length	Quality of chain
7	D	177	
8	E	178	
9	F	120	
10	G	348	
11	H	171	
12	J	145	
13	K	132	
14	L	165	
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	

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Mol	Chain	Length	Quality of chain
32	I	162	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
33	MG	0	8001	-	-	-	X
33	MG	0	8008	-	-	-	X
33	MG	0	8012	-	-	-	X
33	MG	0	8013	-	-	-	X
33	MG	0	8017	-	-	-	X
33	MG	0	8021	-	-	-	X
33	MG	0	8038	-	-	-	X
33	MG	0	8052	-	-	-	X
33	MG	0	8056	-	-	-	X
33	MG	0	8060	-	-	-	X
33	MG	0	8065	-	-	-	X
33	MG	0	8080	-	-	-	X
33	MG	0	8110	-	-	-	X
33	MG	K	8069	-	-	-	X
35	NA	0	9118	-	-	-	X
35	NA	0	9120	-	-	-	X
35	NA	0	9125	-	-	-	X
35	NA	0	9127	-	-	-	X
35	NA	0	9150	-	-	-	X
35	NA	0	9156	-	-	-	X
35	NA	0	9159	-	-	-	X
35	NA	0	9164	-	-	-	X
35	NA	0	9168	-	-	-	X
35	NA	0	9169	-	-	-	X
35	NA	0	9171	-	-	-	X
35	NA	0	9172	-	-	-	X
35	NA	0	9173	-	-	-	X
35	NA	0	9177	-	-	-	X
35	NA	0	9178	-	-	-	X
35	NA	0	9185	-	-	-	X
35	NA	9	9183	-	-	-	X
35	NA	B	9161	-	-	-	X
36	CL	0	9316	-	-	-	X
36	CL	B	9319	-	-	-	X
37	SR	0	9406	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
37	SR	0	9407	-	-	-	X
37	SR	0	9410	-	-	-	X
37	SR	0	9416	-	-	-	X
37	SR	0	9424	-	-	-	X
37	SR	0	9482	-	-	-	X
37	SR	0	9500	-	-	-	X
37	SR	B	9521	-	-	-	X
37	SR	L	9409	-	-	-	X
37	SR	R	9418	-	-	-	X

## 2 Entry composition

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	0	0
			59021	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			
			735	450	141	144	0	0	0

- 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		
			1149	713	209	223	4	0	0

- 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		
			641	389	111	138	3	0	0

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

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

- 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		
			410	244	75	86	5	0	0

- 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		
			499	304	94	100	1	0	0

- 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		
			1196	737	209	244	6	0	0

- 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).

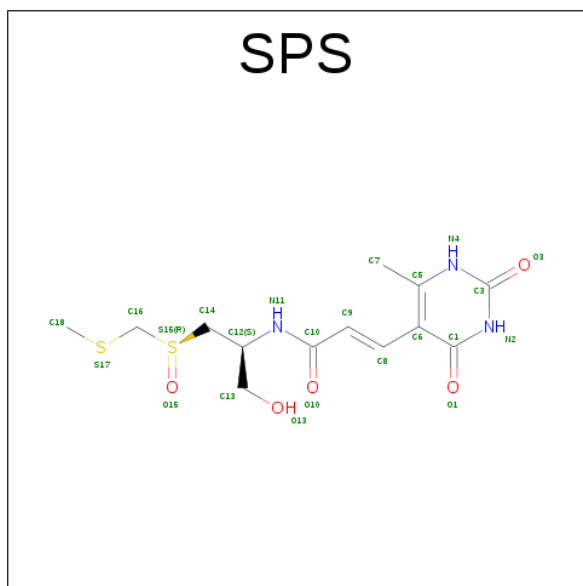
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	0	98	Total 98	Sr 98	0	0
37	1	2	Total 2	Sr 2	0	0

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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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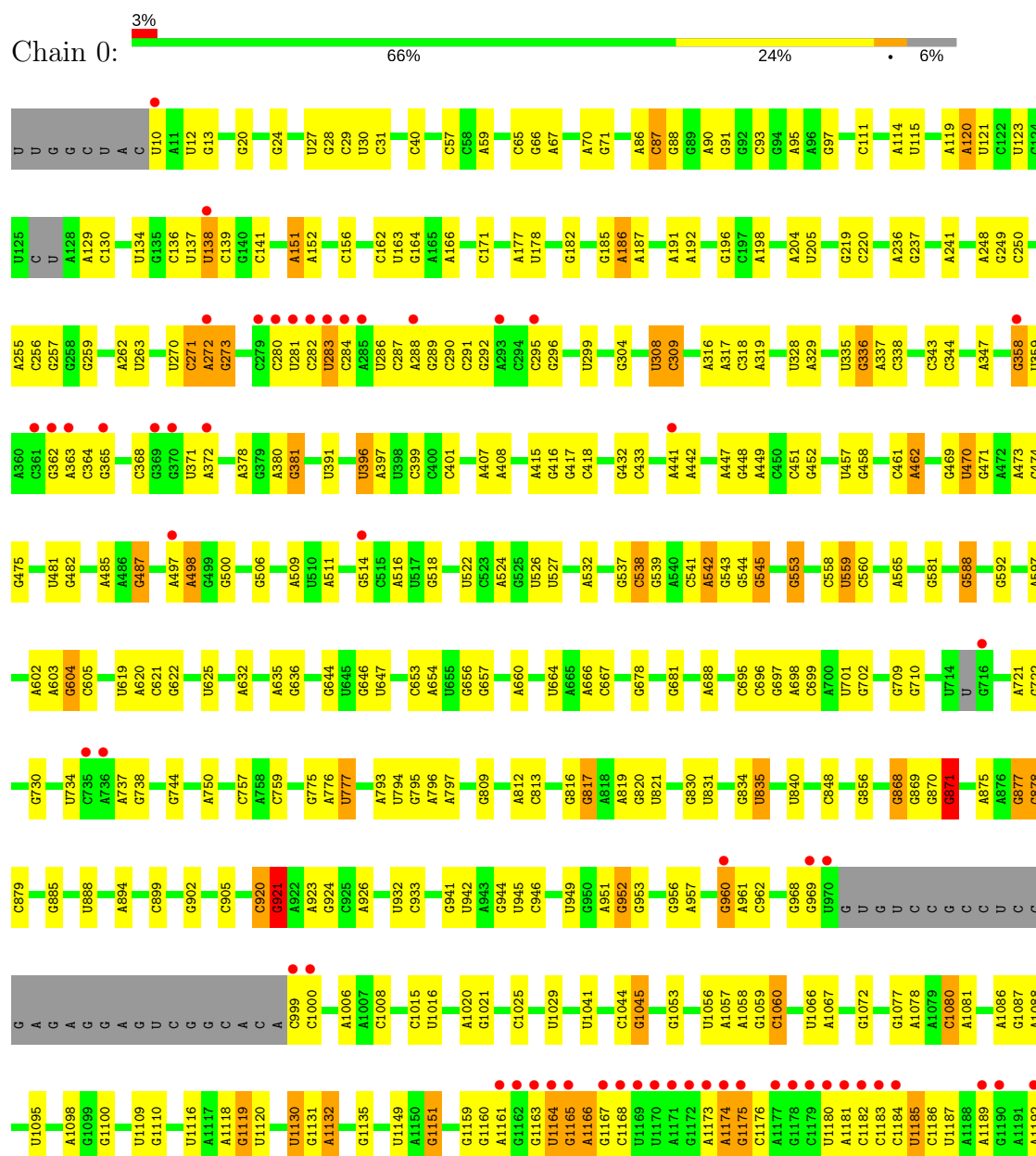
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
40	N	59	Total	O	0	0
			59	59		
40	O	41	Total	O	0	0
			41	41		
40	P	64	Total	O	0	0
			64	64		
40	Q	58	Total	O	0	0
			58	58		
40	R	85	Total	O	0	0
			85	85		
40	S	30	Total	O	0	0
			30	30		
40	T	36	Total	O	0	0
			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 [i](#)

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

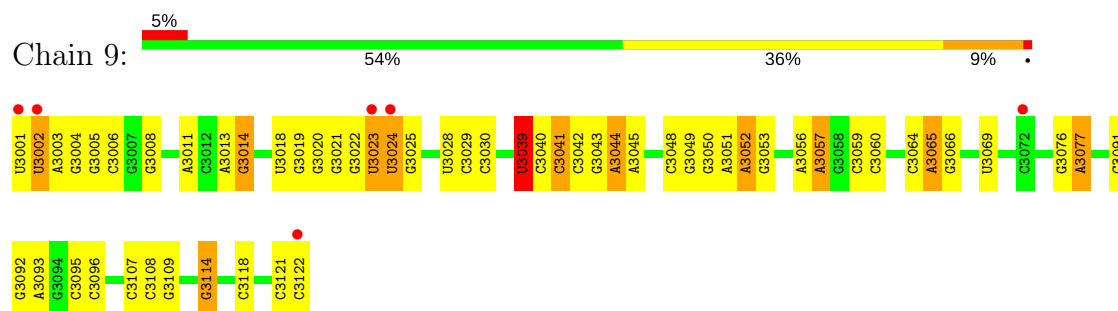
- Molecule 1: 23S ribosomal rna



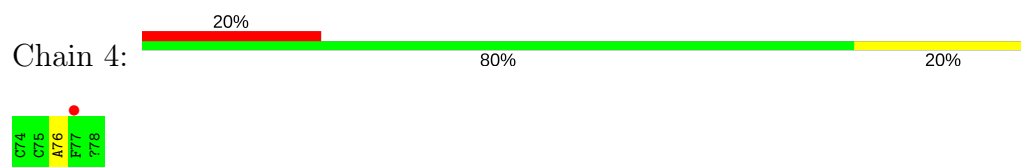


C2868	C2869	C2870	C2876	C2877	C2878	C2879	C2883	C2884	C2889	C2890	C2894	C2895	C2896	C2903	A2906	C2907	A2908	C2909	A2910	C2911	C2912	A2913	A2914	A	G	C	C	C	A	U
C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777
C2509	C2510	C2511	C2515	C2516	C2517	C2518	C2521	C2522	C2523	C2524	C2525	C2526	C2527	C2528	C2529	C2530	C2531	C2532	C2533	C2534	C2535	C2536	C2537	C2538	C2539	C2540	C2541	C2542	C2543	C2544
C2388	C2389	C2390	C2391	C2392	C2393	C2394	C2395	C2396	C2397	C2398	C2399	C2400	C2401	C2402	C2403	C2404	C2405	C2406	C2407	C2408	C2409	C2410	C2411	C2412	C2413	C2414	C2415	C2416	C2417	C2418
C2281	C2282	C2283	C2284	C2285	C2286	C2287	C2288	C2289	C2290	C2291	C2292	C2293	C2294	C2295	C2296	C2297	C2298	C2299	C2300	C2301	C2302	C2303	C2304	C2305	C2306	C2307	C2308	C2309	C2310	C2311
C	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
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G1213	G121																													

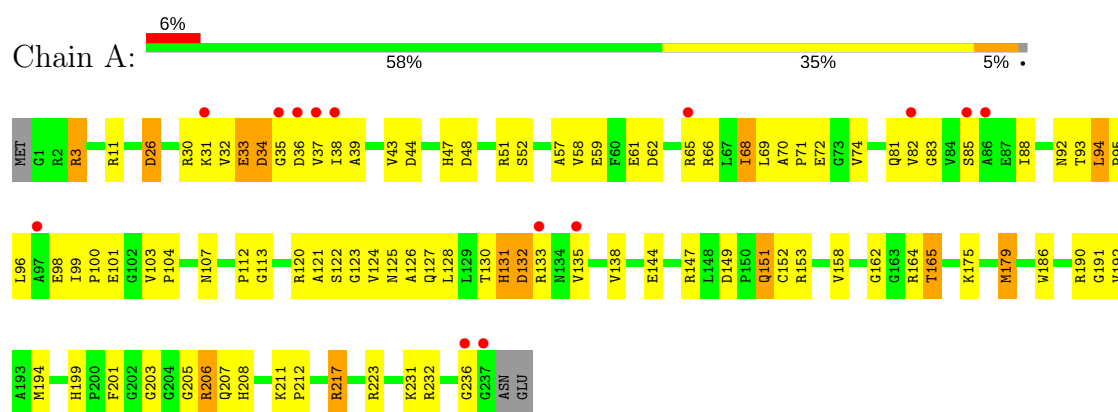
- Molecule 2: 5S ribosomal RNA



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



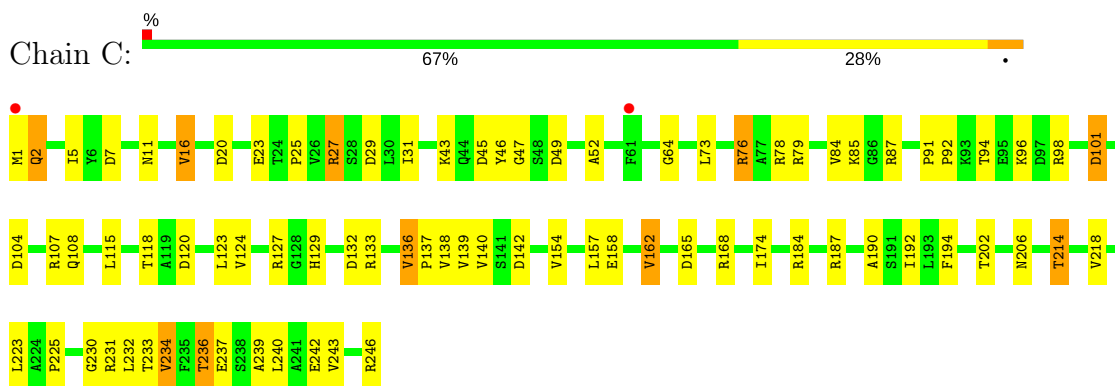
- Molecule 4: 50S ribosomal protein L2P



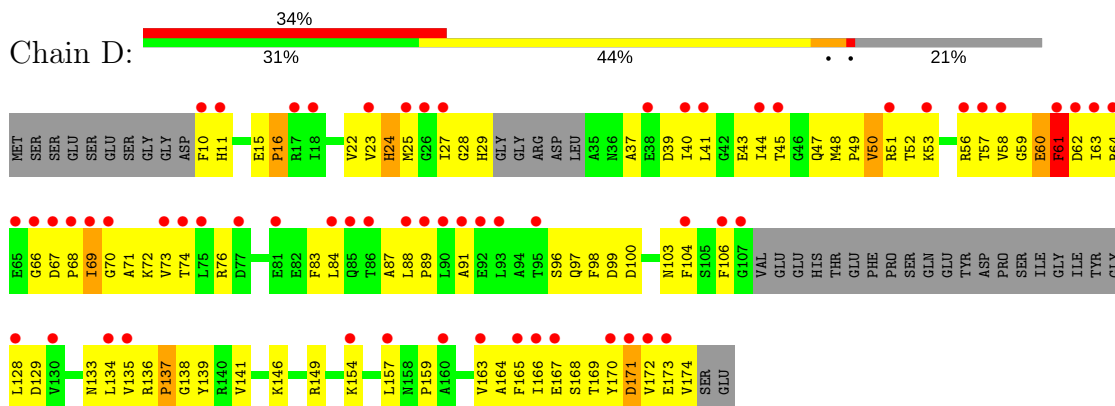
- Molecule 5: 50S ribosomal protein L3P



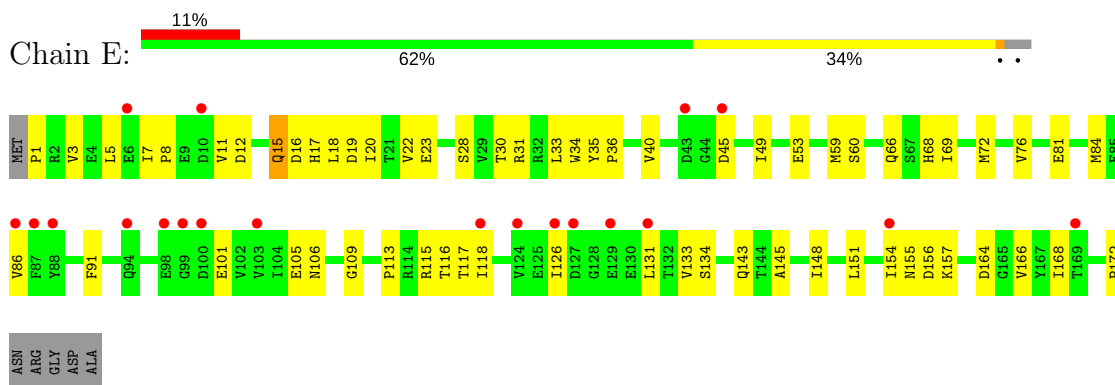
- Molecule 6: 50S ribosomal protein L4E



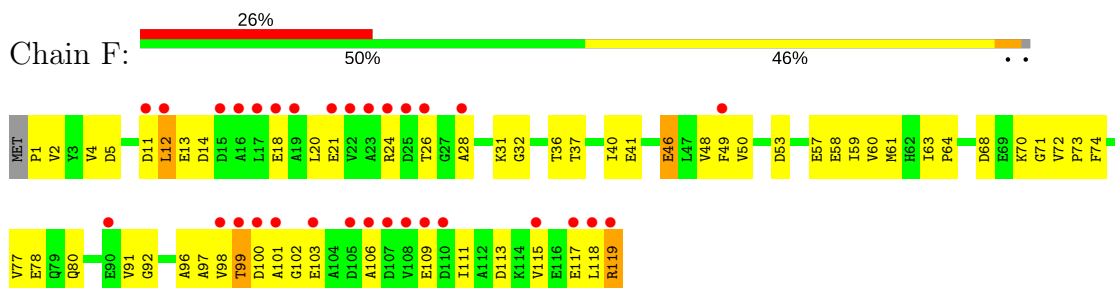
- Molecule 7: 50S ribosomal protein L5P



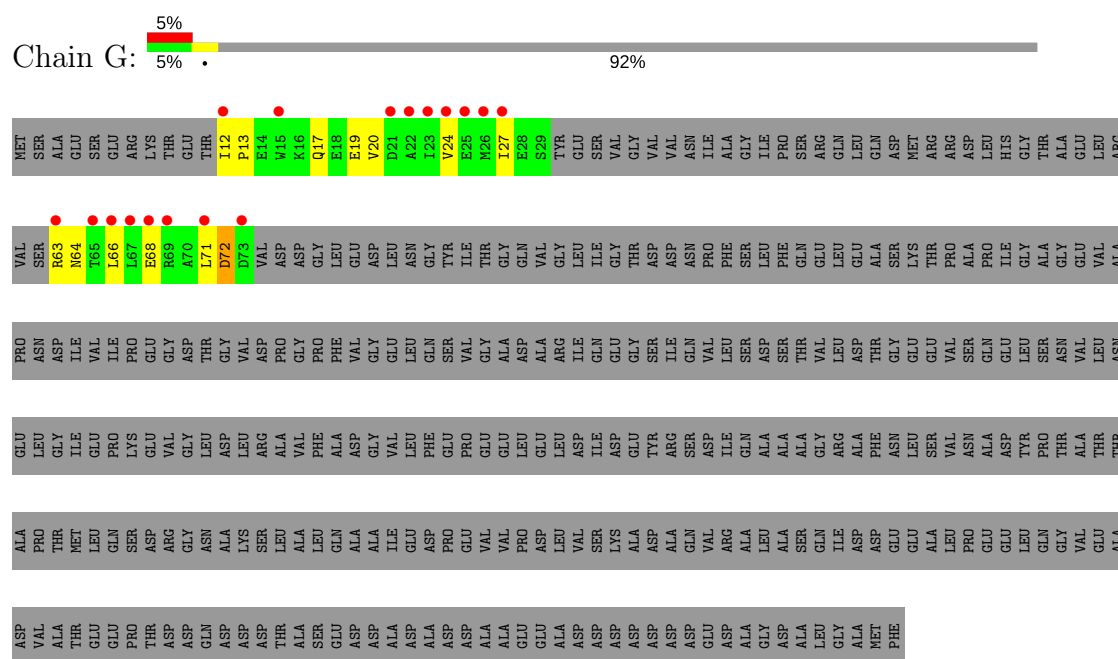
- Molecule 8: 50S ribosomal protein L6P



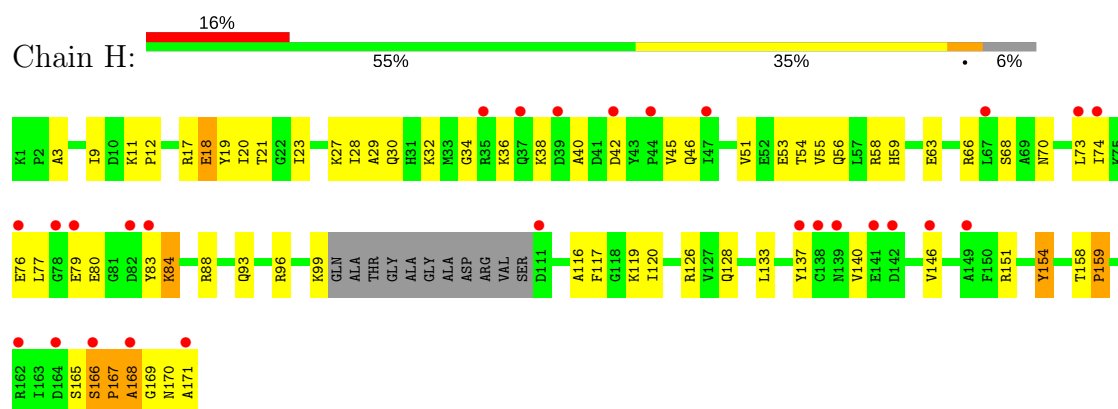
- Molecule 9: 50S ribosomal protein L7AE



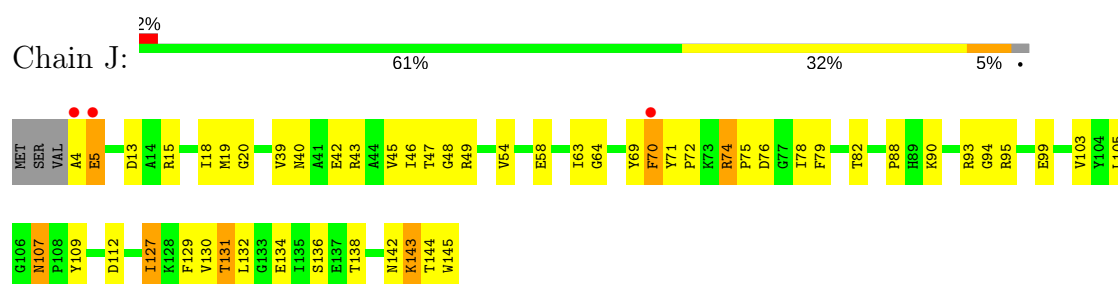
• Molecule 10: ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG



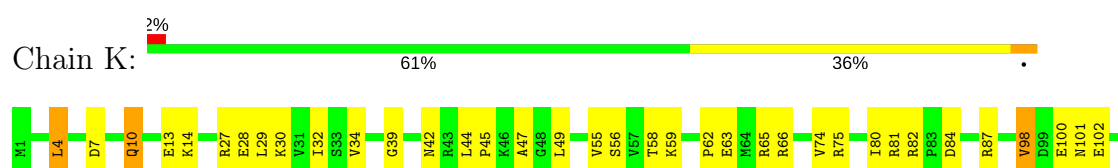
- Molecule 11: 50S RIBOSOMAL PROTEIN L10E

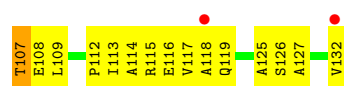


- Molecule 12: 50S ribosomal protein L13P



- Molecule 13: 50S ribosomal protein L14P





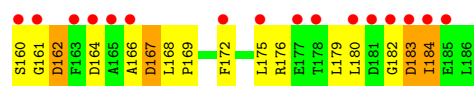
- Molecule 14: 50S ribosomal protein L15P



- Molecule 15: 50S Ribosomal Protein L15E



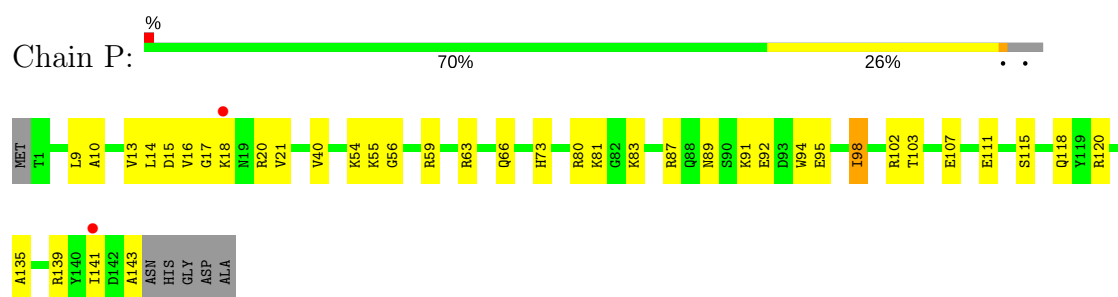
- Molecule 16: 50S ribosomal protein L18P



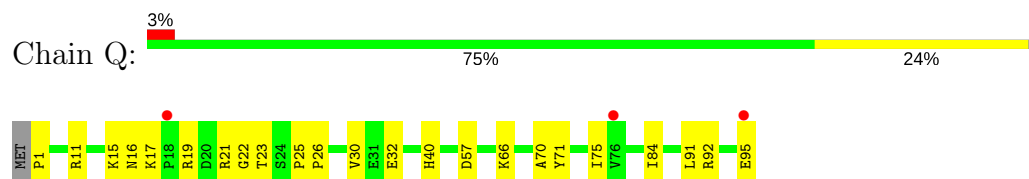
- Molecule 17: 50S ribosomal protein L18e



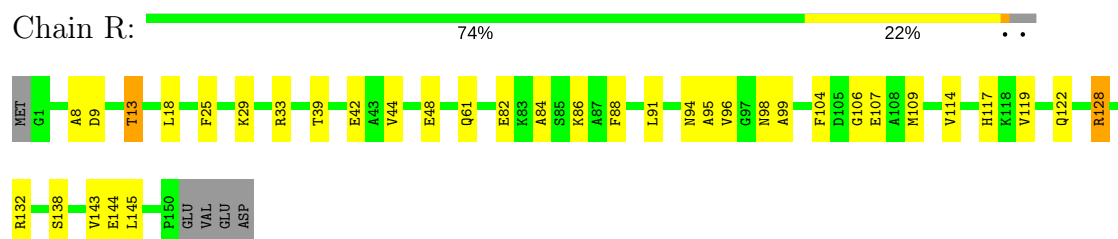
- Molecule 18: 50S ribosomal protein L19E



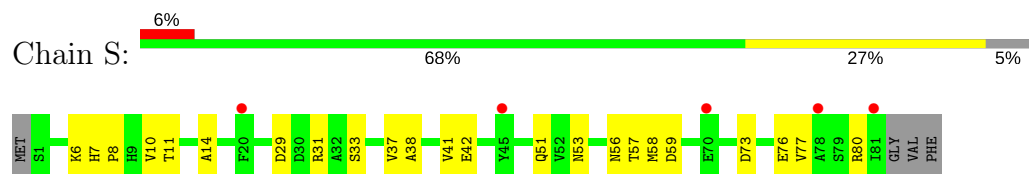
- Molecule 19: 50S ribosomal protein L21e



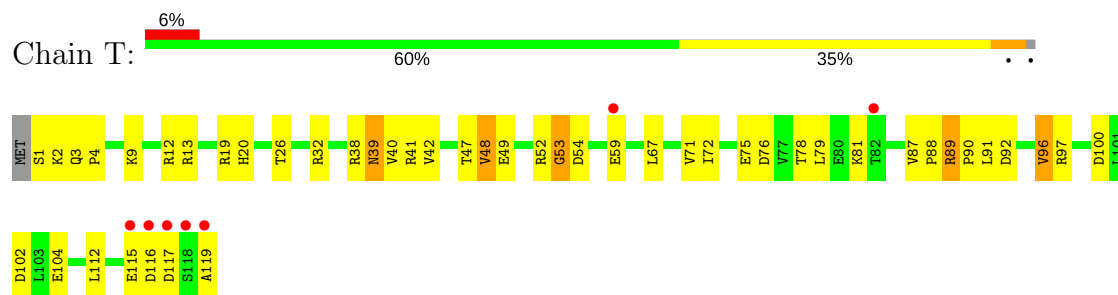
- Molecule 20: 50S ribosomal protein L22P



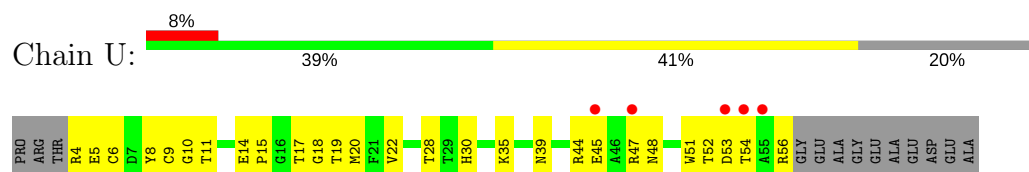
- Molecule 21: 50S ribosomal protein L23P



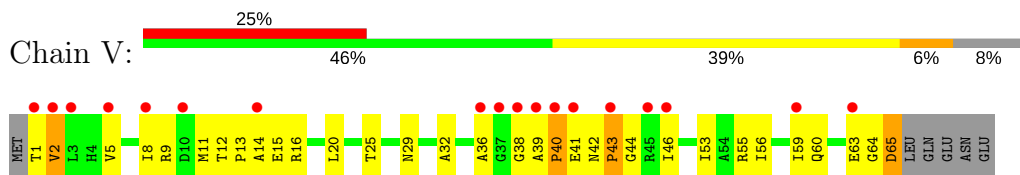
- Molecule 22: 50S ribosomal protein L24P



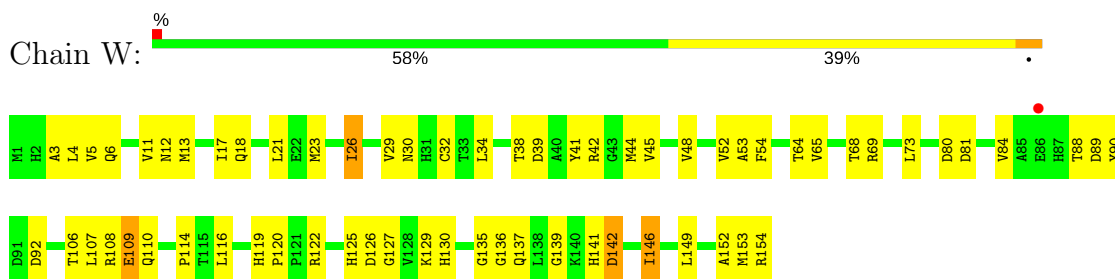
- Molecule 23: 50S ribosomal protein L24E



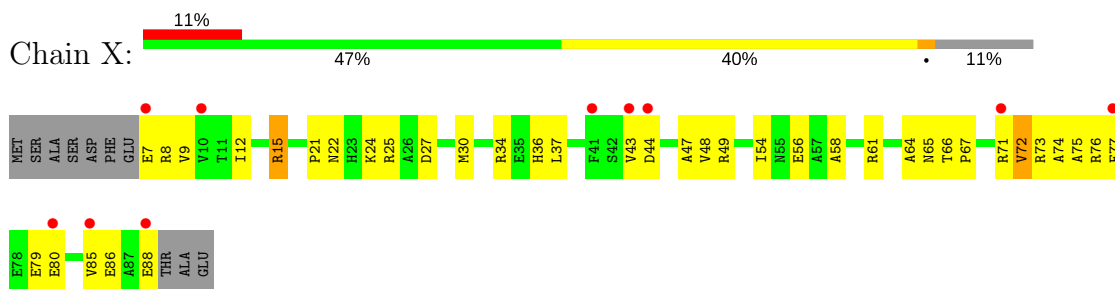
- Molecule 24: 50S ribosomal protein L29P



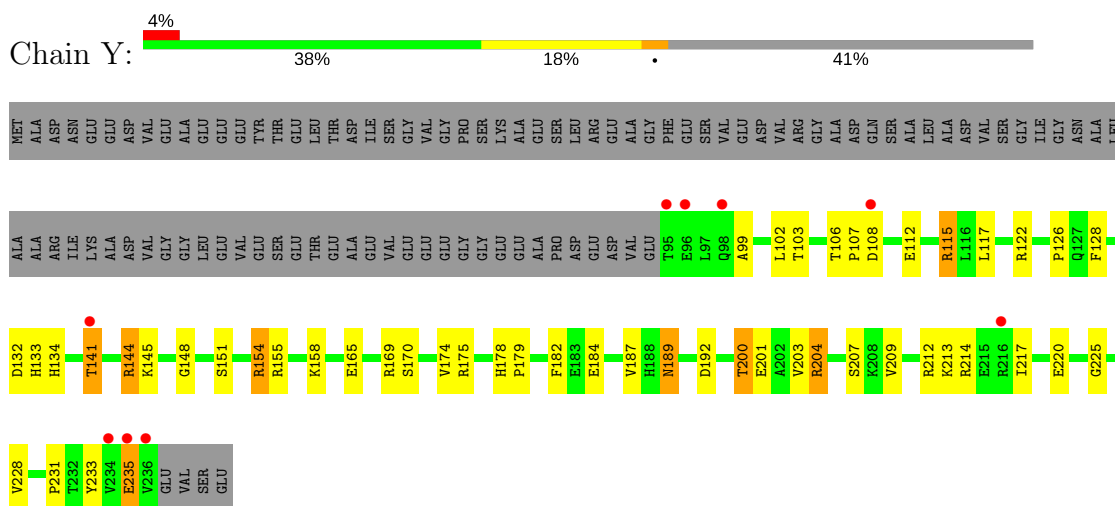
- Molecule 25: 50S ribosomal protein L30P



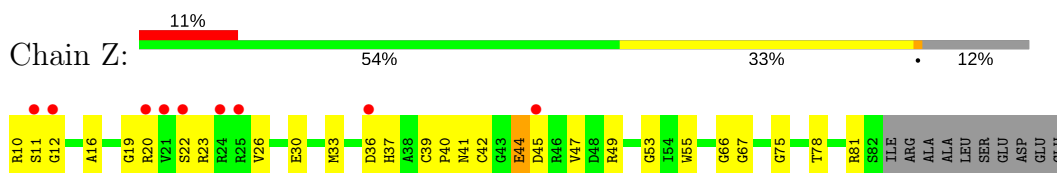
- Molecule 26: 50S ribosomal protein L31e



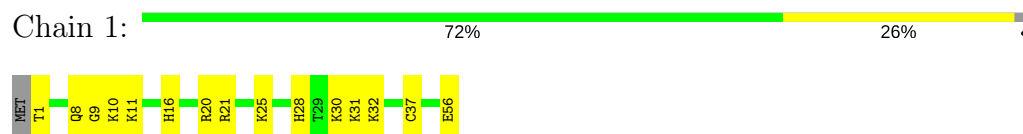
- Molecule 27: 50S ribosomal protein L32E



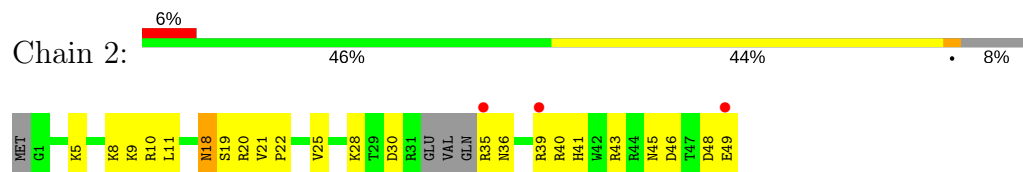
- Molecule 28: 50S ribosomal protein L37Ae



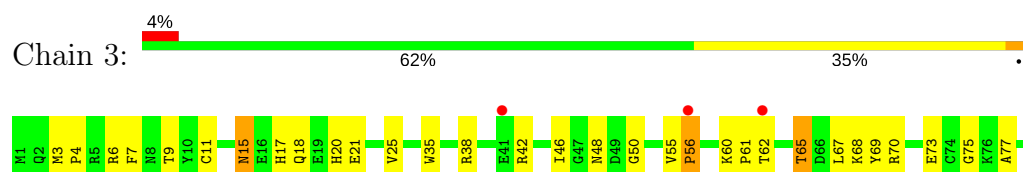
- Molecule 29: 50S ribosomal protein L37e



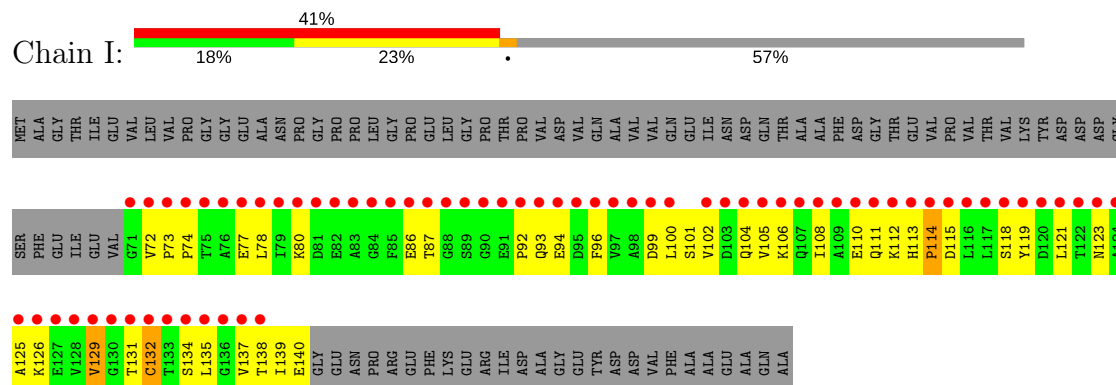
- Molecule 30: 50S ribosomal protein L39e



- 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, $\alpha$ , $\beta$ , $\gamma$	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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	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 <sup>2</sup> )	41.8	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 51.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	99035	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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.*

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

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	59021	0	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
9	F	890	0	843	55	0
10	G	240	0	231	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
36	0	10	0	0	0	0
36	3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
40	I	10	0	0	0	0
40	J	51	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (2109) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:0:156: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
1:0:289:G:H22	1:0:363:A:H2	1.04	0.98
5:B:162:MET:HE2	5:B:310:ARG:HD3	1.44	0.98
1:0:1160:G:H5'	1:0:1161: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	Interatomic distance (Å)	Clash overlap (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
13:K:10:GLN:H	13:K:10:GLN:NE2	1.64	0.93
15:M:99:ARG:HH21	15:M:170:ASN:HD22	1.10	0.93
1:O: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:O:1701:A:H4'	1:O:1702:U:H5''	1.50	0.92
5:B:140:LEU:HA	40:B:9578:HOH:O	1.71	0.91
1:O:656:G:H5'	17:O:3:THR:HG22	1.53	0.90
1:O:1166:A:H61	1:O: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:21:LEU:HD22	25:W:26:ILE:HD13	1.52	0.89
25:W:6:GLN:HB2	25:W:26:ILE:CD1	2.02	0.89
4:A:153:ARG:HH11	4:A:153:ARG:HB2	1.38	0.88
1:O:871:G:C8	1:O:871:G:H5'	2.09	0.88
1:O:1372:A:H3'	40:O:7650:HOH:O	1.73	0.88
9:F:46:GLU:OE1	9:F:100:ASP:HA	1.71	0.88
1:O: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:O:1474:C:H6	1:O:1474:C:H5'	1.39	0.87
1:O:542:A:H5'	1:O:542:A:H8	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:107:THR:HG22	13:K:108:GLU:HG3	1.54	0.86
13:K:10:GLN:H	13:K:10:GLN:HE21	0.87	0.86
13:K:39:GLY:HA2	40:K:4183:HOH:O	1.74	0.86
1:O:2812:A:H2	1:O:2814:A:H62	1.17	0.86
1:O:288:A:H61	1:O: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:O:1973:A:H5'	1:O: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:O:1206:U:H6	1:O:1206:U:H5'	1.40	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:541:C:H2'	1:0:542:A:H5''	1.59	0.85
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
1:0:1835:U:H5	1:0:1840:A:N7	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
1:0:1603: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
1:0:2534:C:H1'	40:0:4078:HOH:O	1.80	0.82
6:C:236:THR:CG2	6:C:239:ALA:H	1.91	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
1:0:1041:U:H5'	40:L:9495:HOH:O	1.80	0.81
1:0:2054:A:N3	20:R:128:ARG:NH2	2.29	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
1:0:2717:C:C2'	1:0:2718:C:H5''	2.12	0.80
5:B:212:GLN:HB2	5:B:257:THR:HG21	1.63	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
1:0:2780:C:H1'	8:E:143:GLN:HE21	1.48	0.79
5:B:162:MET:HE1	5:B:308:LEU:HD21	1.61	0.79
15:M:102:GLU:OE1	15:M:164:THR:HG21	1.82	0.79
22:T:71:VAL:HG11	22:T:90:PRO:CB	2.11	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
2:9:3029:C:H2'	2:9:3030:C:H5'	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
25:W:137:GLN:HE21	25:W:141:HIS:CE1	2.00	0.79
4:A:192:VAL:HG22	40:A:9617:HOH:O	1.80	0.79
1:O:2003:U:H4'	1:O:2004:U:H5	1.49	0.78
7:D:25:MET:HE2	7:D:41:LEU:HG	1.64	0.78
13:K:74:VAL:HG13	13:K:113:ILE:HG23	1.62	0.78
1:O:1878:G:H1'	40:O:6629:HOH:O	1.82	0.78
5:B:162:MET:CE	5:B:310:ARG:HD3	2.12	0.78
1:O:870:G:H2'	1:O:871:G:H5''	1.65	0.78
6:C:5:ILE:HD11	6:C:16:VAL:CG2	2.13	0.78
1:O: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:O:2541:U:H4'	40:O:5938:HOH:O	1.83	0.77
1:O:871:G:C8	1:O:871:G:C5'	2.68	0.77
1:O: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:O:871:G:H8	1:O: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:O:796:A:HO2'	28:Z:10:ARG:N	1.83	0.76
4:A:35:GLY:O	4:A:36:ASP:HB3	1.84	0.76
32:I:99:ASP:OD1	32:I:138:THR:HB	1.84	0.76
22:T:49:GLU:HB3	22:T:59:GLU:HG2	1.68	0.76
27:Y:151:SER:O	27:Y:155:ARG:HG3	1.86	0.76
1:O:1377:C:H6	1:O:1377:C:H5'	1.50	0.76
16:N:83:LEU:HD13	16:N:175:LEU:HD23	1.67	0.76
1:O:289:G:N2	1:O:363:A:H2	1.83	0.76
18:P:115:SER:OG	18:P:118:GLN:HG3	1.85	0.76
1:O:2851:G:C2'	1:O:2852:A:H5'	2.15	0.76
6:C:5:ILE:HD11	6:C:16:VAL:HG22	1.68	0.76
1:O:481:U:H5''	40:O: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:75:PRO:HG2	12:J:105:LEU:HD21	1.67	0.75
25:W:88:THR:HG23	25:W:110:GLN:NE2	2.01	0.75
18:P:91:LYS:O	18:P:95:GLU:HG3	1.86	0.75
15:M:99:ARG:NH2	15:M:170:ASN:HD22	1.83	0.75
1:O:2890:A:H1'	23:U:56:ARG:NH2	2.02	0.74
5:B:190:MET:HE2	5:B:194:PHE:HD1	1.52	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
4:A:191:GLY:HA2	4:A:194:MET:HE2	1.69	0.74
24:V:12:THR:HG22	24:V:15:GLU:CG	2.13	0.74
1:O:1667:A:H8	1:O:1667:A:H5'	1.52	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
13:K:74:VAL:CG1	13:K:113:ILE:HG12	2.15	0.74
1:O:506:G:H22	1:O:509:A:C5'	2.01	0.74
1:O:1751:G:H2'	1:O:1752:G:H5''	1.69	0.74
1:O:2717:C:H2'	1:O:2718:C:H5''	1.69	0.74
31:3:6:ARG:NH1	31:3:21:GLU:HG3	2.02	0.74
16:N:11:ARG:HG3	16:N:14:ARG:NH1	2.03	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
25:W:21:LEU:CD2	25:W:48:VAL:HG11	2.13	0.74
1:O:1160:G:C5'	1:O: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:O:1119:G:N2	1:O:1246:A:C2	2.55	0.73
32:I:102:VAL:HG12	32:I:106:LYS:HE3	1.68	0.73
13:K:81:ARG:HD3	13:K:87:ARG:NH1	2.03	0.73
26:X:54:ILE:HD11	26:X:85:VAL:HG12	1.69	0.73
1:O:280:C:H2'	1:O:281:U:O4'	1.89	0.73
1:O:1118:A:H62	1:O:1244:U:H3	1.36	0.73
1:O:544:G:H2'	1:O:545:G:H5''	1.70	0.73
40:O:9966:HOH:O	29:1:1:THR:HA	1.88	0.73
20:R:18:LEU:HD12	20:R:143:VAL:HG11	1.69	0.73
1:O:871:G:H8	1:O:871:G:H5'	1.52	0.73
1:O:1205:U:H2'	1:O: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:O:1206:U:H2'	1:O:1207:A:O4'	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:O:1116:U:HO2'	1:O:1118:A:H2	0.80	0.72
4:A:69:LEU:HD23	4:A:107:ASN:HB2	1.70	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
32:I:74:PRO:HG2	32:I:77:GLU:OE1	1.89	0.72
12:J:74:ARG:NH1	12:J:76:ASP:HB2	2.04	0.72
24:V:20:LEU:HD22	24:V:60:GLN:HE22	1.55	0.72
1:O:1175:G:H1'	1:O:1193:A:H2'	1.70	0.71
1:O:2644:C:H2'	40:O:7574:HOH:O	1.90	0.71
31:3:38:ARG:HB3	31:3:42:ARG:HH12	1.55	0.71
30:2:41:HIS:H	30:2:45:ASN:HD22	1.37	0.71
25:W:4:LEU:HD23	25:W:54:PHE:HB3	1.72	0.71
11:H:46:GLN:HB3	11:H:167:PRO:HD2	1.72	0.71
5:B:18:ARG:HG3	5:B:256:GLN:HG3	1.72	0.71
1:O:902:G:N7	14:L:18:HIS:HD2	1.88	0.71
17:O:32:ARG:HH21	17:O:35:LYS:HZ2	1.38	0.71
1:O:2346:C:O2'	7:D:52:THR:HG21	1.89	0.71
7:D:135:VAL:HG21	7:D:139:TYR:CD1	2.26	0.71
1:O:2716:G:H5''	5:B:206:THR:HG21	1.73	0.71
40:O: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
5:B:16:ARG:NH1	40:B:9610:HOH:O	2.23	0.71
1:O:474:C:O3'	6:C:73:LEU:HD21	1.91	0.71
7:D:58:VAL:HG12	7:D:60:GLU:HG2	1.71	0.71
1:O:1244:U:OP1	12:J:18:ILE:HD13	1.91	0.71
11:H:154:TYR:HB2	40:H:9557:HOH:O	1.91	0.71
16:N:80:SER:HB2	40:N:9332:HOH:O	1.91	0.71
25:W:13:MET:CE	25:W:17:ILE:HG22	2.20	0.70
1:O:1700:C:H5''	1:O:1701:A:OP2	1.91	0.70
21:S:51:GLN:NE2	21:S:53:ASN:HD21	1.87	0.70
1:O:541:C:H2'	1:O: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:O:1189:A:H3'	40:O:8198:HOH:O	1.91	0.70
1:O:559:U:H5'	1:O:559:U:H6	1.55	0.70
2:9:3014:G:H8	2:9:3014:G:H5'	1.56	0.70
1:O:1118:A:H3'	1:O:1118:A:H8	1.56	0.70
1:O:1166:A:H1'	1:O:1192:A:C2	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:82:VAL:HG13	4:A:93:THR:HB	1.74	0.70
5:B:201:ASP:HB2	5:B:312:ARG:HD2	1.74	0.70
20:R:18:LEU:HB2	20:R:143:VAL:CG1	2.22	0.70
20:R:99:ALA:HB1	20:R:109:MET:HE1	1.71	0.70
25:W:125:HIS:CD2	25:W:127:GLY:H	2.10	0.70
26:X:37:LEU:CD1	26:X:85:VAL:HG21	2.15	0.70
1:0:1118:A:C8	1:0:1118:A:H3'	2.27	0.69
1:0:1183:C:N4	1:0:1184:C:H41	1.89	0.69
25:W:52:VAL:HG22	25:W:53:ALA:H	1.56	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
1:0:381:G:H5''	40:M:9371:HOH:O	1.91	0.69
13:K:109:LEU:HD13	13:K:113:ILE:HD11	1.74	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
5:B:112:THR:HG23	5:B:158:LYS:NZ	2.07	0.69
9:F:58:GLU:OE1	15:M:27:ARG:NH2	2.25	0.69
11:H:166:SER:HB3	11:H:167:PRO:HD3	1.74	0.69
15:M:164:THR:HG22	15:M:166:ALA:H	1.57	0.69
27:Y:189:ASN:HA	27:Y:217:ILE:HD11	1.75	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
22:T:9:LYS:HE3	22:T:13:ARG:HH11	1.53	0.69
21:S:51:GLN:HE21	21:S:53:ASN:ND2	1.87	0.69
18:P:80:ARG:HG2	18:P:87:ARG:CZ	2.23	0.68
28:Z:11:SER:CB	28:Z:23:ARG:HB2	2.23	0.68
1:0:1165:G:H1'	1:0:1174:A:H1'	1.74	0.68
4:A:153:ARG:CB	4:A:153:ARG:HH11	2.06	0.68
5:B:264:GLU:HG2	5:B:267:LYS:CE	2.20	0.68
40:O: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
24:V:1:THR:HG23	24:V:2:VAL:H	1.57	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
1:0:506:G:H22	1:0:509:A:H5''	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:39:ASP:O	7:D:43:GLU:HG3	1.94	0.68
17:O:32:ARG:NE	17:O:35:LYS:HD2	2.08	0.68
24:V:12:THR:CG2	24:V:15:GLU:HG3	2.16	0.68
24:V:39:ALA:C	24:V:41:GLU:H	1.97	0.68
1:O:316:A:H5'	22:T:54:ASP:OD2	1.94	0.68
8:E:15:GLN:HG2	8:E:19:ASP:O	1.94	0.68
1:O:1168:C:H5''	32:I:87:THR:HG23	1.74	0.68
16:N:48:VAL:CG1	16:N:55:ASP:HB3	2.24	0.68
25:W:149:LEU:HG	25:W:153:MET:HE2	1.76	0.68
5:B:125:GLU:O	5:B:129:ARG:HG3	1.94	0.68
32:I:78:LEU:HD12	32:I:112:LYS:NZ	2.09	0.68
16:N:154:LEU:HG	16:N:155:GLU:H	1.59	0.67
24:V:43:PRO:O	24:V:46:ILE:HG22	1.94	0.67
1:O: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
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:O:2005:G:H3'	1:O:2005:G:OP2	1.95	0.67
1:O: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:O:1730:G:H5'	1:O:1731:C:C5	2.29	0.67
1:O:1973:A:H5'	1:O: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:O:2003:U:H4'	1:O:2004:U:C5	2.29	0.67
4:A:57:ALA:HB1	4:A:65:ARG:HE	1.59	0.67
27:Y:187:VAL:HG23	27:Y:192:ASP:HB2	1.74	0.67
1:O:2578:G:H5'	1:O: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:O: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
1:O:282:C:O2'	1:O:283:U:H5'	1.95	0.66
7:D:25:MET:HE1	7:D:37:ALA:HB1	1.77	0.66
26:X:71:ARG:HB3	26:X:88:GLU:OE1	1.95	0.66
1:O:1165:G:H4'	1:O:1174:A:O2'	1.95	0.66
15:M:107:ARG:NH1	15:M:107:ARG:HG3	2.08	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1159:G:H21	1:0:1189:A:H8	1.42	0.66
22:T:49:GLU:CB	22:T:59:GLU:HG2	2.25	0.66
1:0:1201:C:H2'	1:0:1202:A:H5'	1.76	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
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
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
25:W:21:LEU:O	25:W:26:ILE:HG23	1.95	0.66
1:0:1299:G:O6	14:L:6:ARG:HD3	1.96	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
22:T:71:VAL:HG12	22:T:72:ILE:N	2.11	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
14:L:133:VAL:HA	40:L:9475:HOH:O	1.96	0.65
15:M:183:THR:HG22	15:M:194:ALA:HB1	1.77	0.65
14:L:53:ARG:NH2	14:L:57:VAL:HG12	2.10	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
9:F:14:ASP:O	9:F:18:GLU:HG3	1.96	0.65
1:0:1187:U:HO2'	1:0:1189:A:H2	1.45	0.65
11:H:46:GLN:HE21	11:H:137:TYR:HE2	1.42	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
32:I:132:CYS:HB3	32:I:137:VAL:HB	1.77	0.65
27:Y:144:ARG:CZ	40:Y:9411:HOH:O	2.44	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
25:W:108:ARG:HH21	25:W:114:PRO:HG2	1.61	0.65
27:Y:144:ARG:HH11	27:Y:144:ARG:CG	2.10	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
1:0:1919:A:H4'	40:0:5395:HOH:O	1.97	0.64
4:A:199:HIS:CD2	4:A:201:PHE:H	2.15	0.64
1:0:544:G:C2'	1:0:545:G:H5''	2.26	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:470:U:O2'	29:1:16:HIS:HD2	1.79	0.64
1:0:2694:A:H4'	8:E:91:PHE:CE1	2.33	0.64
12:J:75:PRO:HD3	12:J:136:SER:OG	1.96	0.64
25:W:80:ASP:O	25:W:84:VAL:HG23	1.97	0.64
20:R:18:LEU:HD12	20:R:143:VAL:CG1	2.28	0.64
1:0:2270:G:H4'	4:A:223:ARG:HH12	1.61	0.64
5:B:238:ASN:ND2	5:B:240:GLY:H	1.90	0.64
5:B:297:VAL:HB	40:B:9599:HOH:O	1.97	0.64
7:D:138:GLY:N	40:D:7597:HOH:O	2.31	0.64
13:K:62:PRO:HG3	13:K:65:ARG:HH21	1.63	0.64
26:X:72:VAL:HG13	26:X:85:VAL:HG13	1.79	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
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
2:9:3056:A:C2'	2:9:3057:A:H5''	2.26	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
30:2:20:ARG:HD2	30:2:39:ARG:NH2	2.12	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:HH21	1.62	0.64
5:B:307:ARG:NH1	5:B:307:ARG:HG3	2.05	0.64
6:C:118:THR:HG22	6:C:137:PRO:HB3	1.79	0.64
7:D:64:ARG:NE	7:D:67:ASP:HB3	2.13	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
1:0:123:U:H5'	40:0:7139:HOH:O	1.99	0.63
1:0:2851:G:H2'	1:0:2852:A:H5'	1.79	0.63
5:B:238:ASN:HD22	5:B:240:GLY:N	1.90	0.63
12:J:131:THR:HG22	12:J:134:GLU:H	1.63	0.63
13:K:115:ARG:HG3	13:K:116:GLU:N	2.13	0.63
25:W:81:ASP:OD1	25:W:92:ASP:HB2	1.98	0.63
27:Y:165:GLU:HB3	40:Y:9393:HOH:O	1.97	0.63
28:Z:53:GLY:HA2	28:Z:67:GLY:O	1.99	0.63
25:W:48:VAL:HG12	25:W:48:VAL:O	1.98	0.63
4:A:36:ASP:HA	4:A:83:GLY:HA3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:0:1184:C:H4'	32:I:126:LYS:HB3	1.80	0.63
1:0:558:C:H2'	1:0:559:U:H5'	1.80	0.63
8:E:31:ARG:NH1	8:E:68:HIS:CG	2.67	0.63
9:F:48:VAL:HG12	9:F:97:ALA:HB2	1.79	0.63
15:M:99:ARG:HH21	15:M:170:ASN:ND2	1.89	0.63
16:N:139:TRP:HA	16:N:139:TRP:CE3	2.33	0.63
2:9:3004:G:H21	16:N:44:ARG:NH1	1.97	0.63
24:V:55:ARG:O	24:V:59:ILE:HG12	1.99	0.63
4:A:33:GLU:O	4:A:34:ASP:HB2	1.98	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
8:E:20:ILE:CD1	8:E:40:VAL:HG11	2.29	0.63
28:Z:37:HIS:HB2	28:Z:47:VAL:HB	1.81	0.63
2:9:3013:A:O2'	2:9:3014:G:H5''	1.99	0.63
32:I:110:GLU:HA	32:I:113:HIS:CE1	2.34	0.63
10:G:27:ILE:HD13	10:G:71:LEU:HD23	1.81	0.62
15:M:24:GLN:O	15:M:28:GLN:HG3	1.99	0.62
23:U:45:GLU:HB2	23:U:48:ASN:HD22	1.64	0.62
1:0:1053:G:OP1	11:H:12:PRO:HG3	1.98	0.62
1:0:1333:U:H2'	1:0:1334:C:C6	2.35	0.62
1:0:1426:C:H2'	40:0:3201:HOH:O	1.97	0.62
1:0:1552:G:N2	1:0:1634:G:H1'	2.13	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
14:L:104:ASP:HB2	40:L:9465:HOH:O	1.99	0.62
26:X:15:ARG:HB3	26:X:15:ARG:HH11	1.64	0.62
26:X:21:PRO:HG2	26:X:24:LYS:HD3	1.79	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
7:D:172:VAL:HG12	7:D:173:GLU:N	2.14	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
5:B:329:TYR:CE2	23:U:15:PRO:HG2	2.35	0.62
25:W:13:MET:HE3	25:W:17:ILE:HG22	1.79	0.62
25:W:88:THR:HG22	25:W:89:ASP:H	1.64	0.62
1:0:2878:U:H2'	1:0:2879:A:O4'	1.99	0.62
1:0:282:C:H1'	1:0:368:C:N4	2.14	0.62
1:0:960:G:H4'	40:0:7877:HOH:O	1.99	0.62
4:A:194:MET:HE1	4:A:199:HIS:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3069:U:OP1	16:N:4:PRO:HG3	2.00	0.62
4:A:131:HIS:O	4:A:132:ASP:HB2	2.00	0.62
1:0:1118:A:H8	1:0:1119:G:H5''	1.65	0.62
1:0:656:G:H5'	17:O:3:THR:CG2	2.28	0.62
1:0:120:A:H5'	29:1:20:ARG:HH21	1.64	0.62
7:D:58:VAL:CG1	7:D:60:GLU:HG2	2.30	0.62
15:M:69:LYS:O	15:M:73:ARG:NH2	2.32	0.62
20:R:106:GLY:HA2	20:R:109:MET:HE3	1.80	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
8:E:31:ARG:HH12	8:E:68:HIS:CD2	2.18	0.62
20:R:99:ALA:HB1	20:R:109:MET:CE	2.30	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
1:0:797:A:C4'	28:Z:10:ARG:N	2.63	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
18:P:115:SER:N	18:P:118:GLN:HE21	1.92	0.62
1:0:2533:C:H5'	1:0:2533:C:H6	1.65	0.61
1:0:2769:C:C2'	1:0:2770:G:H5'	2.30	0.61
1:0:960:G:H3'	1:0:960:G:N3	2.15	0.61
5:B:58:PRO:HA	5:B:63:GLU:OE2	1.99	0.61
16:N:139:TRP:HA	16:N:139:TRP:HE3	1.65	0.61
25:W:84:VAL:HG12	40:W:6679:HOH:O	1.99	0.61
1:0:545:G:C8	1:0:545:G:H5'	2.31	0.61
11:H:63:GLU:HA	40:H:9545:HOH:O	2.00	0.61
13:K:75:ARG:HD3	13:K:112:PRO:O	2.00	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
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
9:F:50:VAL:CG1	9:F:60:VAL:HG11	2.30	0.61
25:W:137:GLN:NE2	25:W:141:HIS:HE1	1.91	0.61
1:0:625:U:H5''	1:0:1044:C:N4	2.15	0.61
1:0:1119:G:H22	1:0:1246:A:H2	1.43	0.61
1:0:1882:C:OP1	4:A:192:VAL:HG23	2.01	0.61
1:0:542:A:H5'	1:0:542:A:C8	2.28	0.61
1:0:164:G:H4'	14:L:30:ARG:HD3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:316:A:N3	1:0:336:G:O2'	2.32	0.61
4:A:88:ILE:HD13	4:A:100:PRO:HD3	1.81	0.61
8:E:68:HIS:O	8:E:72:MET:HG3	1.99	0.61
17:O:32:ARG:HB2	40:O:4656:HOH:O	2.01	0.61
5:B:72:THR:HB	40:B:9599:HOH:O	1.99	0.61
7:D:149:ARG:HH12	16:N:15:GLU:HA	1.65	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
1:0:1189:A:O2'	1:0:1208:C:H2'	2.00	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
40:O:6053:HOH:O	5:B:298:LYS:HG2	2.00	0.61
8:E:101:GLU:HB2	8:E:116:THR:O	2.00	0.61
20:R:9:ASP:O	20:R:13:THR:HB	2.00	0.61
21:S:57:THR:HG22	21:S:58:MET:N	2.15	0.61
1:0:1058:A:H2'	1:0:1060:C:H5''	1.82	0.61
5:B:154:VAL:HG12	5:B:156:LYS:HG2	1.83	0.61
7:D:51:ARG:HH11	7:D:68:PRO:HB3	1.65	0.61
13:K:34:VAL:CG2	13:K:47:ALA:HB2	2.30	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
30:2:22:PRO:HG2	30:2:25:VAL:HG23	1.82	0.61
7:D:23:VAL:HG22	7:D:73:VAL:HB	1.81	0.61
9:F:37:THR:O	9:F:41:GLU:HG3	2.01	0.61
30:2:22:PRO:HG2	30:2:25:VAL:CG2	2.31	0.60
5:B:190:MET:HE2	5:B:194:PHE:CD1	2.36	0.60
12:J:19:MET:CE	12:J:132:LEU:HD11	2.31	0.60
5:B:71:VAL:HG11	5:B:296:LEU:HD22	1.82	0.60
7:D:22:VAL:HG22	7:D:74:THR:HG22	1.82	0.60
1:0:656:G:C5'	17:O:3:THR:HG22	2.29	0.60
1:0:2426:G:H1'	40:O:6602:HOH:O	1.99	0.60
9:F:1:PRO:H3	9:F:4:VAL:HG23	1.66	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
1:0:553:G:P	27:Y:204:ARG:HH22	2.24	0.60
1:0:1946:C:H2'	1:0:1971:G:C8	2.36	0.60
1:0:2270:G:H4'	4:A:223:ARG:NH1	2.17	0.60
4:A:194:MET:CE	4:A:199:HIS:HB2	2.32	0.60
16:N:86:LEU:HD12	16:N:125:ALA:HB2	1.83	0.60
26:X:9:VAL:HG22	26:X:88:GLU:OE2	2.01	0.60
2:9:3020:G:O2'	2:9:3021:G:H5'	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
29:1:10:LYS:HG3	40:1:9489:HOH:O	2.00	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
21:S:73:ASP:OD1	21:S:76:GLU:HG3	2.01	0.60
25:W:139:GLY:O	25:W:141:HIS:HD2	1.85	0.60
1:0:1159:G:H1	1:0:1208:C:H42	1.50	0.60
4:A:88:ILE:HG22	4:A:88:ILE:O	2.02	0.60
5:B:275:GLY:O	5:B:291:ASP:HA	2.01	0.60
5:B:8:LYS:HG3	5:B:220:VAL:HG12	1.84	0.60
12:J:75:PRO:HG2	12:J:105:LEU:CD2	2.31	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
13:K:34:VAL:HG22	13:K:47:ALA:HB2	1.83	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
26:X:72:VAL:HG13	26:X:85:VAL:CG1	2.32	0.60
1:0:1205:U:H2'	1:0:1206:U:C5'	2.32	0.60
2:9:3040:C:N4	7:D:53:LYS:HE3	2.17	0.60
9:F:99:THR:O	9:F:100:ASP:HB2	2.01	0.60
27:Y:144:ARG:HH11	27:Y:144:ARG:HG3	1.67	0.60
1:0:2064:U:H5'	1:0:2652:U:H4'	1.83	0.59
1:0:2524:G:H21	1:0:2526:C:H41	1.48	0.59
1:0:2896:A:N3	1:0:2896:A:H2'	2.17	0.59
1:0:396:U:O2'	1:0:418:C:H4'	2.02	0.59
4:A:179:MET:HG2	4:A:186:TRP:CB	2.32	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
1:0:2820:A:OP1	5:B:98:THR:HG22	2.03	0.59
9:F:2:VAL:HG22	9:F:57:GLU:OE1	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
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
7:D:170:TYR:O	7:D:171:ASP:HB3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:67:ARG:O	14:L:71:GLU:HG3	2.03	0.59
1:0:1766:U:O2	1:0:1778:A:H5'	2.03	0.59
2:9:3029:C:C2'	2:9:3030:C:H5'	2.33	0.59
9:F:12:LEU:HD21	9:F:111:ILE:HG23	1.83	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
17:O:39:THR:O	17:O:115:ARG:NH2	2.33	0.59
1:0:2726:U:O2'	26:X:22:ASN:ND2	2.35	0.59
26:X:12:ILE:HD12	26:X:36:HIS:ND1	2.17	0.59
1:0:391:U:OP2	15:M:84:LYS:NZ	2.35	0.59
5:B:145:HIS:HD2	5:B:146:THR:O	1.86	0.59
5:B:141:ARG:HG2	5:B:165:ARG:HA	1.84	0.59
32:I:92:PRO:C	32:I:94:GLU:H	2.06	0.59
14:L:36:ASP:HB2	40:L:9437:HOH:O	2.02	0.59
1:0:2644:C:O2'	1:0:2645:U:H5'	2.03	0.59
12:J:74:ARG:HH12	12:J:76:ASP:HB2	1.64	0.59
1:0:2291:A:C8	1:0:2309:C:H5'	2.38	0.59
1:0:2338:G:H2'	7:D:129:ASP:OD1	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
1:0:516: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
29:1:56:GLU:HG2	29:1:56:GLU:OXT	2.03	0.58
8:E:23:GLU:HG2	8:E:28:SER:HB3	1.85	0.58
40:0:9737:HOH:O	15:M:82:ARG:HD2	2.01	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
32:I:102:VAL:O	32:I:106:LYS:HG3	2.03	0.58
25:W:88:THR:HG23	25:W:110:GLN:HE21	1.65	0.58
25:W:88:THR:HG22	25:W:90:TYR:HD1	1.68	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
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
16:N:162:ASP:HA	40:N:9327:HOH:O	2.02	0.58
1:0:138:U:H5''	1:0:139:C:OP2	2.03	0.58
1:0:2524:G:H21	1:0:2526:C:H5	1.49	0.58
7:D:49:PRO:HB3	7:D:73:VAL:HG22	1.84	0.58
16:N:143:ARG:HH21	16:N:169:PRO:HB2	1.69	0.58
18:P:135:ALA:HB1	18:P:139:ARG:HH12	1.67	0.58
1:0:2420:G:O2'	1:0:2421:G:H5'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:305:ASP:O	5:B:306:LYS:HB2	2.04	0.58
32:I:78:LEU:HD12	32:I:112:LYS:HZ2	1.66	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
26:X:76:ARG:HH11	26:X:76:ARG:HG3	1.67	0.58
1:O:263:U:O4'	9:F:59:ILE:HD13	2.03	0.58
2:9:3039:U:H1'	2:9:3044:A:H61	1.68	0.58
32:I:110:GLU:HA	32:I:113:HIS:NE2	2.18	0.58
16:N:69:TYR:HE2	16:N:184:ILE:HG13	1.68	0.58
31:3:65:THR:HG22	31:3:67:LEU:HG	1.85	0.58
2:9:3051:A:H5'	16:N:160:SER:CB	2.34	0.58
24:V:39:ALA:N	24:V:40:PRO:CD	2.66	0.58
1:O:621:C:H5'	27:Y:132:ASP:OD2	2.03	0.58
31:3:70:ARG:HB3	40:3:9510:HOH:O	2.04	0.58
4:A:121:ALA:O	4:A:124:VAL:HG22	2.03	0.58
6:C:78:ARG:HG3	6:C:78:ARG:NH1	2.19	0.58
8:E:116:THR:HG22	8:E:151:LEU:HD22	1.85	0.58
32:I:113:HIS:N	32:I:114:PRO:HD2	2.18	0.58
13:K:4:LEU:CD2	13:K:116:GLU:HB3	2.32	0.58
14:L:57:VAL:HG12	14:L:57:VAL:O	2.04	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
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:797:A:C5'	28:Z:10:ARG:N	2.67	0.58
1:O:441:A:H1'	1:O:442:A:N7	2.19	0.58
1:O:657:G:OP1	6:C:27:ARG:NH2	2.29	0.58
7:D:136:ARG:NH1	7:D:157:LEU:HA	2.16	0.58
1:O:1730:G:H5''	1:O:1731:C:H6	1.69	0.57
27:Y:189:ASN:HD22	27:Y:189:ASN:C	2.07	0.57
1:O:121:U:OP2	30:2:10:ARG:NH2	2.33	0.57
1:O:2795:C:O2'	1:O:2796:U:H5'	2.04	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
1:O:2237:G:H1'	1:O:2238:A:C8	2.40	0.57
1:O:2769:C:O2'	1:O:2770:G:H5'	2.04	0.57
1:O:506:G:H22	1:O:509:A:H5'	1.69	0.57
2:9:3018:U:H2'	2:9:3019:G:H8	1.70	0.57
1:O:1943:C:H4'	4:A:211:LYS:O	2.05	0.57
5:B:162:MET:HE2	5:B:310:ARG:CD	2.28	0.57
5:B:175:LEU:O	5:B:175:LEU:HD23	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:62:ARG:HA	5:B:65:MET:CE	2.34	0.57
9:F:48:VAL:HG12	9:F:97:ALA:CB	2.33	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
2:9:3014:G:H5'	2:9:3014:G:C8	2.39	0.57
6:C:79:ARG:O	6:C:87:ARG:HG2	2.04	0.57
9:F:13:GLU:OE1	9:F:77:VAL:HG13	2.05	0.57
16:N:23:ARG:HH11	16:N:23:ARG:HG2	1.69	0.57
23:U:47:ARG:HG3	40:U:4381:HOH:O	2.03	0.57
5:B:102:THR:HG21	5:B:182:VAL:O	2.04	0.57
11:H:40:ALA:HB1	11:H:137:TYR:CE2	2.40	0.57
32:I:139:ILE:HG22	32:I:140:GLU:N	2.20	0.57
25:W:26:ILE:HB	40:W:5420:HOH:O	2.03	0.57
26:X:43:VAL:HG12	26:X:44:ASP:N	2.19	0.57
1:0:1634:G:H3'	40:0:4466:HOH:O	2.04	0.57
4:A:95:PRO:HG2	4:A:98:GLU:HG2	1.86	0.57
6:C:127:ARG:HD3	6:C:129:HIS:HE1	1.68	0.57
6:C:129:HIS:HD2	6:C:165:ASP:OD2	1.88	0.57
1:0:2694:A:H4'	8:E:91:PHE:HE1	1.69	0.57
1:0:20: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
10:G:64:ASN:N	10:G:64:ASN:HD22	2.01	0.57
1:0:2676:C:H4'	12:J:70:PHE:CD1	2.39	0.57
1:0:1189:A:H1'	1:0:1209:C:O4'	2.04	0.57
5:B:17:LYS:O	5:B:260:HIS:HD2	1.86	0.57
6:C:140:VAL:HB	40:C:9252:HOH:O	2.04	0.57
1:0:1180:U:O2'	32:I:92:PRO:HD2	2.05	0.57
15:M:24:GLN:NE2	15:M:27:ARG:HH11	2.03	0.57
22:T:41:ARG:NH1	22:T:41:ARG:HG2	2.19	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
16:N:61:ALA:HB3	16:N:88:ALA:HB2	1.87	0.57
20:R:39:THR:HG22	20:R:107:GLU:O	2.05	0.57
21:S:77:VAL:O	21:S:80:ARG:HG2	2.05	0.57
27:Y:154:ARG:HH11	27:Y:154:ARG:HB3	1.69	0.57
11:H:170:ASN:N	11:H:170:ASN:HD22	2.01	0.57
40:0:4931:HOH:O	15:M:83:SER:HB3	2.04	0.57
28:Z:19:GLY:O	28:Z:23:ARG:HG2	2.05	0.57
1:0:256:C:H2'	1:0:257:G:O4'	2.05	0.56
6:C:242:GLU:HB2	40:C:9186:HOH:O	2.05	0.56
2:9:3041:C:O4'	7:D:50:VAL:HG13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
7:D:59:GLY:O	7:D:61:PHE:N	2.38	0.56
25:W:5:VAL:O	25:W:52:VAL:HG23	2.04	0.56
25:W:4:LEU:O	25:W:32:CYS:HA	2.05	0.56
1:O:1730:G:C5'	1:O:1731:C:C6	2.87	0.56
1:O:2524:G:N2	1:O:2526:C:H41	2.03	0.56
1:O:2717:C:O2'	1:O:2718:C:H5''	2.05	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
15:M:107:ARG:NH1	40:M:9378:HOH:O	2.38	0.56
16:N:115:VAL:HG22	40:N:9354:HOH:O	2.05	0.56
24:V:64:GLY:O	24:V:65:ASP:HB2	2.03	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
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
1:O:1681:G:H5''	1:O:1682:A:H5'	1.87	0.56
1:O:2105:C:H5'	40:4:7933:HOH:O	2.05	0.56
1:O:871:G:H8	1:O:871:G:H5''	1.70	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
20:R:18:LEU:HG	20:R:91:LEU:HD13	1.87	0.56
25:W:4:LEU:HD11	25:W:45:VAL:HG12	1.88	0.56
1:O:737:A:H2'	1:O:738:G:O4'	2.05	0.56
4:A:206:ARG:HD3	4:A:206:ARG:H	1.71	0.56
9:F:50:VAL:HG21	9:F:63:ILE:HG21	1.88	0.56
12:J:74:ARG:NH1	12:J:105:LEU:HD11	2.21	0.56
13:K:55:VAL:HG12	13:K:56:SER:N	2.20	0.56
22:T:48:VAL:HG22	22:T:96:VAL:HG22	1.87	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
1:O:1595:G:O2'	1:O:1596:U:H5'	2.06	0.56
1:O:2563:U:H2'	1:O:2565:C:O5'	2.05	0.56
30:2:48:ASP:O	30:2:49:GLU:HB2	2.05	0.56
5:B:40:GLY:HA3	40:B:9637:HOH:O	2.04	0.56
7:D:57:THR:HG23	7:D:63:ILE:HA	1.88	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
25:W:52:VAL:HG22	25:W:53:ALA:N	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:126:PRO:HG2	27:Y:128:PHE:CE1	2.41	0.56
27:Y:154:ARG:NH1	27:Y:155:ARG:HG2	2.19	0.56
1:0:1592:G:O2'	1:0:1593:C:O4'	2.24	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
1:0:1878:G:O2'	1:0:1879:U:OP2	2.24	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:135:VAL:HG21	4:A:147:ARG:NH1	2.20	0.55
4:A:123:GLY:HA3	4:A:162:GLY:HA2	1.86	0.55
1:0:2320:U:H4'	1:0:2321:A:O4'	2.06	0.55
8:E:34:TRP:O	12:J:127:ILE:HD11	2.06	0.55
1:0:2721:U:H4'	13:K:87:ARG:HG3	1.88	0.55
16:N:149:GLU:O	16:N:152:GLU:HB3	2.05	0.55
1:0:2453:G:H5''	40:L:9442:HOH:O	2.04	0.55
16:N:154:LEU:O	16:N:155:GLU:HB2	2.06	0.55
40:0:6753:HOH:O	23:U:56:ARG:HB3	2.05	0.55
24:V:11:MET:HB3	24:V:15:GLU:HB2	1.88	0.55
1:0:248:A:H5'	1:0:249:G:OP2	2.07	0.55
2:9:3076:G:C3'	2:9:3077:A:H5''	2.27	0.55
6:C:236:THR:HG21	40:C:9178:HOH:O	2.05	0.55
2:9:3041:C:H4'	7:D:48:MET:HB3	1.88	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
28:Z:10:ARG:HA	40:Z:9215:HOH:O	2.06	0.55
5:B:120:ASP:OD2	5:B:123:ALA:HB2	2.07	0.55
10:G:12:ILE:N	10:G:13:PRO:CD	2.69	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
22:T:40:VAL:HG22	22:T:41:ARG:N	2.22	0.55
24:V:56:ILE:O	24:V:60:GLN:HG3	2.05	0.55
1:0:1200:A:H4'	40:0:7793:HOH:O	2.07	0.55
1:0:1209:C:H2'	1:0:1210:G:H8	1.71	0.55
1:0:558:C:O2'	1:0:559:U:H5''	2.06	0.55
5:B:112:THR:HG23	5:B:158:LYS:HZ1	1.71	0.55
5:B:84:LEU:HB2	5:B:182:VAL:HG21	1.89	0.55
7:D:44:ILE:HG12	7:D:83:PHE:HE1	1.72	0.55
2:9:3014:G:O2'	16:N:1:ALA:HB2	2.05	0.55
18:P:111:GLU:HG2	18:P:111:GLU:O	2.06	0.55
19:Q:32:GLU:HA	19:Q:71:TYR:OH	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:64:THR:O	25:W:68:THR:HG22	2.06	0.55
1:0:2072:G:C6	1:0:2533:C:H1'	2.42	0.55
1:0:870:G:C2'	1:0:871:G:H5''	2.35	0.55
11:H:171:ALA:HA	40:H:9535:HOH:O	2.06	0.55
14:L:136:ALA:HB3	40:L:9475:HOH:O	2.06	0.55
16:N:89:GLY:O	16:N:92:ALA:HB3	2.07	0.55
1:0:2645:U:OP2	1:0:2645:U:C6	2.59	0.55
1:0:272:A:H5'	1:0:273:G:OP2	2.07	0.55
5:B:185:GLY:HA2	40:B:9625:HOH:O	2.05	0.55
1:0:2521:A:OP2	11:H:3:ALA:HB3	2.07	0.55
12:J:75:PRO:HB3	12:J:132:LEU:HB3	1.89	0.55
14:L:91:VAL:HG13	14:L:120:LEU:HD23	1.88	0.55
25:W:13:MET:HE1	25:W:18:GLN:HA	1.89	0.55
1:0:1236:A:C8	12:J:63:ILE:HD11	2.41	0.55
30:2:36:ASN:HB3	30:2:39:ARG:HG3	1.89	0.55
2:9:3057:A:H8	7:D:141:VAL:HG21	1.72	0.55
5:B:62:ARG:HA	5:B:65:MET:HE2	1.88	0.55
6:C:214:THR:HG23	40:C:9237:HOH:O	2.06	0.55
22:T:49:GLU:OE2	22:T:97:ARG:HD2	2.07	0.55
24:V:1:THR:HG23	24:V:2:VAL:N	2.22	0.55
1:0:2365:G:H5''	40:Q:6597:HOH:O	2.06	0.55
1:0:2502:C:C2'	1:0:2503:A:H5'	2.36	0.55
40:0:9698:HOH:O	5:B:214:PRO:HD2	2.06	0.55
15:M:79:ALA:HB3	15:M:81:ARG:NH1	2.22	0.55
40:0:3147:HOH:O	18:P:81:LYS:HG2	2.06	0.55
24:V:42:ASN:HB3	40:V:7247:HOH:O	2.06	0.55
1:0:1406:A:H4'	1:0:1407:A:H5''	1.88	0.54
1:0:1528:A:H2'	1:0:1529:G:O4'	2.07	0.54
1:0:2524:G:H21	1:0:2526:C:N4	2.04	0.54
9:F:13:GLU:OE2	9:F:78:GLU:HG2	2.07	0.54
15:M:68:ARG:HD3	15:M:68:ARG:O	2.08	0.54
1:0:2416:G:O2'	16:N:25:ARG:HG2	2.06	0.54
1:0:485:A:N3	1:0:487:G:H5''	2.22	0.54
5:B:5:ARG:HH11	5:B:8:LYS:HE2	1.72	0.54
5:B:97:LEU:O	5:B:98:THR:HG23	2.06	0.54
8:E:22:VAL:HG12	8:E:76:VAL:HG11	1.89	0.54
17:O:59:VAL:CG2	17:O:111:VAL:HG21	2.37	0.54
1:0:949:U:C4'	19:Q:95:GLU:HA	2.37	0.54
4:A:107:ASN:OD1	4:A:120:ARG:HD2	2.07	0.54
5:B:321:PRO:HA	40:B:9646:HOH:O	2.07	0.54
8:E:31:ARG:HH12	8:E:68:HIS:CG	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:O:1067:A:H5'	40:O:4901:HOH:O	2.06	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:2670:G:O2'	1:O:2671:U:H5'	2.07	0.54
4:A:101:GLU:OE2	4:A:131:HIS:HB2	2.08	0.54
1:O:2717:C:OP1	5:B:207:LYS:HG3	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
24:V:56:ILE:HG22	24:V:60:GLN:HE21	1.72	0.54
25:W:65:VAL:HG12	25:W:116:LEU:HD13	1.89	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
1:O:2866:U:H4'	1:O:2867:G:H5'	1.89	0.54
2:9:3029:C:O3'	7:D:138:GLY:HA2	2.07	0.54
1:O:1667:A:H2'	1:O:1668:U:C6	2.43	0.54
1:O:656:G:OP2	17:O:37:ARG:HD2	2.08	0.54
40:O:3309:HOH:O	5:B:254:GLN:HG3	2.08	0.54
5:B:321:PRO:HG3	40:B:9595:HOH:O	2.08	0.54
11:H:169:GLY:C	11:H:170:ASN:HD22	2.11	0.54
12:J:93:ARG:HH11	12:J:93:ARG:CB	2.13	0.54
15:M:66:SER:HB3	15:M:128:TRP:CD1	2.43	0.54
1:O:12:U:H2'	1:O:13:G:H5'	1.90	0.54
2:9:3114:G:O6	16:N:11:ARG:HD3	2.07	0.54
1:O:1853:C:OP1	4:A:231:LYS:HG3	2.08	0.54
1:O:151:A:H2'	1:O:152:A:O4'	2.07	0.54
1:O:2894:C:O2'	1:O:2895:C:H5'	2.07	0.54
1:O:834:G:H4'	1:O:835:U:OP2	2.08	0.54
1:O:1641:A:H2'	1:O:1642:A:H5'	1.90	0.53
1:O:1902:G:H2'	1:O:1903:U:O4'	2.08	0.53
1:O:286:U:H2'	1:O:287:C:C6	2.43	0.53
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:O:757:C:OP1	14:L:27:ARG:HD2	2.07	0.53
8:E:154:ILE:HD11	8:E:157:LYS:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:1335:C:OP2	27:Y:207:SER:HB3	2.08	0.53
1:O:1189:A:H1'	1:O:1209:C:C1'	2.38	0.53
1:O:156:C:H5''	15:M:171:ARG:CD	2.27	0.53
4:A:94:LEU:N	4:A:94:LEU:HD23	2.24	0.53
5:B:139:ASP:HB3	40:B:9552:HOH:O	2.08	0.53
6:C:236:THR:HA	40:C:9252:HOH:O	2.07	0.53
9:F:60:VAL:HG12	9:F:60:VAL:O	2.09	0.53
14:L:150:GLN:HB3	40:L:9471:HOH:O	2.08	0.53
16:N:86:LEU:HD21	16:N:180:LEU:CD1	2.38	0.53
1:O:1819:G:H2'	1:O:1820:G:H4'	1.89	0.53
1:O:558:C:H2'	1:O:559:U:C5'	2.38	0.53
6:C:194:PHE:HA	6:C:234:VAL:HG13	1.91	0.53
8:E:145:ALA:HB1	8:E:168:ILE:CD1	2.38	0.53
1:O:709:G:O2'	17:O:25:VAL:CG1	2.56	0.53
22:T:47:THR:HB	22:T:100:ASP:HB3	1.90	0.53
1:O:2711:U:H1'	40:O:4024:HOH:O	2.08	0.53
1:O:40:C:H4'	40:O:7476:HOH:O	2.08	0.53
4:A:165:THR:HG22	40:A:9604:HOH:O	2.09	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
10:G:20:VAL:O	10:G:24:VAL:HG23	2.08	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
23:U:5:GLU:HG2	23:U:10:GLY:O	2.07	0.53
6:C:20:ASP:O	6:C:23:GLU:HB2	2.08	0.53
15:M:77:HIS:HD2	15:M:79:ALA:O	1.91	0.53
25:W:88:THR:HG23	25:W:110:GLN:HB3	1.91	0.53
1:O:1555:G:H4'	1:O:1630:A:H2	1.73	0.53
15:M:60:VAL:C	15:M:61:ILE:HD12	2.28	0.53
1:O: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
31:3:70:ARG:HG2	31:3:70:ARG:HH11	1.74	0.53
4:A:164:ARG:CZ	40:A:9572:HOH:O	2.56	0.53
1:O:1363:G:OP1	6:C:76:ARG:NH2	2.42	0.53
13:K:58:THR:HG22	13:K:59:LYS:HG3	1.90	0.53
15:M:167:GLY:O	15:M:171:ARG:HG3	2.09	0.53
1:O:1476:A:O2'	1:O:1477:C:H5'	2.08	0.53
1:O:538:C:OP2	27:Y:134:HIS:HE1	1.91	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
22:T:9:LYS:CE	22:T:13:ARG:NH1	2.65	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1118:A:C8	1:0:1119:G:H5'	2.44	0.53
1:0:2812:A:C2	1:0:2814:A:N6	2.65	0.53
5:B:264:GLU:CG	5:B:267:LYS:HE2	2.29	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
1:0:1626:A:H2'	1:0:1627:G:O4'	2.08	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
1:0:2541:U:H5'	1:0:2541:U:H6	1.74	0.52
2:9:3049:G:O2'	2:9:3050:G:H5'	2.10	0.52
32:I:99:ASP:O	32:I:100:LEU:HD23	2.09	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
1:0:1268:C:O2'	27:Y:169:ARG:HB2	2.09	0.52
1:0:1352:A:O2'	1:0:1353:C:OP1	2.24	0.52
1:0:288:A:H2'	1:0:289:G:C8	2.43	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
32:I:105:VAL:HG11	32:I:129:VAL:CG2	2.39	0.52
17:O:87:THR:O	17:O:91:GLN:HG3	2.08	0.52
18:P:98:ILE:HD12	18:P:102:ARG:NE	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
1:0:949:U:O2'	19:Q:40:HIS:HE1	1.93	0.52
5:B:232:TRP:HD1	5:B:235:ARG:HD2	1.74	0.52
5:B:232:TRP:CD1	5:B:235:ARG:HD2	2.44	0.52
14:L:134:GLU:HG3	40:L:9458:HOH:O	2.10	0.52
2:9:3008:G:O6	16:N:11:ARG:NH1	2.42	0.52
19:Q:75:ILE:HD13	19:Q:84:ILE:HD11	1.91	0.52
1:0:1878:G:O2'	1:0:1879:U:P	2.68	0.52
1:0:2032:U:H2'	1:0:2033:G:C5'	2.40	0.52
12:J:19:MET:HE3	12:J:132:LEU:HD11	1.91	0.52
6:C:233:THR:HG22	6:C:234:VAL:N	2.25	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
22:T:32:ARG:NH1	22:T:38:ARG:NH1	2.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2626:C:H2'	1:O:2627:G:C8	2.45	0.52
1:O:750:A:O3'	6:C:101:ASP:HB2	2.09	0.52
4:A:217:ARG:CG	4:A:217:ARG:HH11	2.23	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
27:Y:117:LEU:HA	27:Y:174:VAL:HG11	1.92	0.52
1:O:1187:U:O2'	1:O:1189:A:H2	1.91	0.52
1:O:2346:C:O5'	1:O:2346:C:H6	1.93	0.52
1:O:364:C:H2'	1:O:365:G:O4'	2.10	0.52
1:O:848:C:H5'	40:O:7728:HOH:O	2.09	0.52
32:I:114:PRO:HG2	32:I:115:ASP:H	1.75	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
1:O:1738:C:H1'	40:O:7770:HOH:O	2.10	0.51
1:O:2415:A:N3	16:N:26:LEU:HD13	2.25	0.51
15:M:98:GLN:O	15:M:102:GLU:HG3	2.10	0.51
40:O:7093:HOH:O	27:Y:155:ARG:HD2	2.08	0.51
1:O:1060:C:H6	1:O:1060:C:H5'	1.76	0.51
1:O:1328:A:OP1	27:Y:169:ARG:HD2	2.10	0.51
2:9:3042:C:O2	7:D:76:ARG:NH1	2.43	0.51
4:A:128:LEU:HD21	4:A:131:HIS:HE1	1.75	0.51
8:E:35:TYR:HA	12:J:127:ILE:CD1	2.41	0.51
1:O:2081:A:H4'	12:J:69:TYR:CE1	2.45	0.51
14:L:92:ASP:HA	14:L:121:ILE:HB	1.92	0.51
1:O:962:C:H1'	16:N:5:ARG:HH12	1.75	0.51
25:W:149:LEU:HG	25:W:153:MET:CE	2.40	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
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
1:O:1181:A:N1	1:O:1192:A:O2'	2.40	0.51
1:O:2064:U:H5'	1:O:2652:U:O3'	2.10	0.51
1:O:920:C:H5''	1:O:921:G:O5'	2.10	0.51
2:9:3049:G:C2'	2:9:3050:G:H5'	2.41	0.51
5:B:258:GLY:H	5:B:260:HIS:CE1	2.28	0.51
8:E:11:VAL:HG12	8:E:12:ASP:N	2.24	0.51
8:E:154:ILE:HG13	8:E:156:ASP:OD1	2.10	0.51
1:O:1242:A:C5'	12:J:82:THR:HG23	2.31	0.51
27:Y:112:GLU:OE1	27:Y:112:GLU:HA	2.10	0.51
28:Z:42:CYS:SG	28:Z:44:GLU:HB2	2.51	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:O:2769:C:H2'	1:O:2770:G:C5'	2.40	0.51
6:C:154:VAL:O	6:C:158:GLU:HG3	2.11	0.51
8:E:23:GLU:HG2	8:E:28:SER:CB	2.41	0.51
9:F:28:ALA:CB	9:F:99:THR:HG23	2.41	0.51
11:H:170:ASN:N	11:H:170:ASN:ND2	2.59	0.51
32:I:113:HIS:N	32:I:114:PRO:CD	2.73	0.51
24:V:25:THR:HG22	24:V:29:ASN:HD21	1.75	0.51
1:O:1234:U:N3	5:B:244:PRO:HB3	2.26	0.51
1:O:2505:G:C2'	1:O:2506:A:H5'	2.41	0.51
6:C:136:VAL:HG22	6:C:137:PRO:HA	1.93	0.51
7:D:128:LEU:HB2	40:D:6007:HOH:O	2.11	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:O:1594:C:OP2	18:P:120:ARG:HD2	2.10	0.51
28:Z:26:VAL:O	28:Z:30:GLU:HG3	2.10	0.51
1:O:1730:G:C5'	1:O:1731:C:H6	2.23	0.51
1:O:2712:G:H5'	40:K:4183:HOH:O	2.11	0.51
9:F:91:VAL:CG1	9:F:92:GLY:H	2.14	0.51
11:H:56:GLN:NE2	11:H:126:ARG:HE	2.09	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
27:Y:99:ALA:HB2	27:Y:233:TYR:CZ	2.46	0.51
1:O:1351:G:OP1	6:C:96:LYS:NZ	2.39	0.51
1:O:1701:A:H5''	1:O:1702:U:H3'	1.93	0.51
1:O:299:U:H5'	40:O:7789:HOH:O	2.11	0.51
5:B:215:VAL:HB	5:B:234:ARG:HH12	1.76	0.51
5:B:254:GLN:HG2	5:B:255:GLY:H	1.76	0.51
1:O:475:G:OP1	6:C:73:LEU:CD2	2.58	0.51
20:R:82:GLU:O	20:R:86:LYS:HG3	2.11	0.51
25:W:38:THR:O	25:W:42:ARG:HB2	2.10	0.51
25:W:5:VAL:O	25:W:52:VAL:CG2	2.59	0.51
1:O:1400:C:H4'	26:X:56:GLU:HG2	1.92	0.51
1:O:134:U:H6	1:O:134:U:H5''	1.75	0.51
1:O:2456:A:H2'	1:O:2457:U:C6	2.46	0.51
1:O:328:U:O4'	6:C:202:THR:CG2	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3002:U:OP2	2:9:3003:A:H5'	2.10	0.51
8:E:35:TYR:HA	12:J:127:ILE:HD12	1.93	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
14:L:145:LEU:O	14:L:145:LEU:HD23	2.10	0.51
1:0:1218:U:H2'	1:0:1219:U:C6	2.46	0.50
1:0:2718:C:H5'	1:0:2718:C:C6	2.44	0.50
1:0:776:A:OP1	29:1:28:HIS:HE1	1.95	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
15:M:72:ALA:HB2	15:M:93:ARG:HG2	1.93	0.50
23:U:9:CYS:HA	23:U:52:THR:HG23	1.93	0.50
25:W:139:GLY:O	25:W:141:HIS:CD2	2.63	0.50
27:Y:112:GLU:CD	27:Y:115:ARG:NH1	2.64	0.50
1:0:1462:C:H2'	1:0:1463:A:C8	2.47	0.50
1:0:2896:A:H5''	40:X:5399:HOH:O	2.10	0.50
1:0:588:G:O6	25:W:154:ARG:NH1	2.45	0.50
5:B:41:PHE:CD2	5:B:190:MET:HE3	2.47	0.50
32:I:101:SER:H	32:I:104:GLN:NE2	2.09	0.50
40:9:1361:HOH:O	16:N:41:LYS:HE3	2.10	0.50
17:O:42:GLU:HB2	40:O:2176:HOH:O	2.10	0.50
1:0:2661:U:H3	1:0:2812:A:H62	1.60	0.50
1:0:945:U:H2'	1:0:946:C:C6	2.46	0.50
2:9:3057:A:C8	7:D:141:VAL:HG21	2.46	0.50
4:A:36:ASP:C	4:A:38:ILE:H	2.15	0.50
1:0:870:G:OP2	4:A:3:ARG:HD3	2.12	0.50
32:I:105:VAL:HG11	32:I:129:VAL:HG22	1.92	0.50
23:U:9:CYS:O	23:U:52:THR:HG23	2.11	0.50
1:0:2414:A:H2'	1:0:2415:A:C8	2.47	0.50
1:0:2487:C:H1'	40:0:5938:HOH:O	2.10	0.50
1:0:241:A:C2	1:0:378:A:H4'	2.47	0.50
1:0:407:A:H2'	1:0:408:A:C8	2.47	0.50
4:A:192:VAL:HG11	4:A:207:GLN:HB3	1.93	0.50
14:L:104:ASP:O	14:L:105:TYR:HB3	2.11	0.50
14:L:143:THR:O	14:L:147:GLU:HG3	2.10	0.50
17:O:53:GLN:HE21	17:O:56:GLU:CD	2.15	0.50
1:0:2726:U:O2	1:0:2749:U:O5'	2.30	0.50
1:0:447:A:OP2	22:T:1:SER:HB2	2.11	0.50
5:B:307:ARG:HB3	40:B:9642:HOH:O	2.11	0.50
6:C:236:THR:HG22	6:C:239:ALA:CB	2.41	0.50
7:D:25:MET:HE1	7:D:37:ALA:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:38:LYS:HE2	11:H:42:ASP:HB2	1.93	0.50
32:I:138:THR:HG22	32:I:139:ILE:N	2.26	0.50
15:M:164:THR:CG2	15:M:165:GLY:N	2.74	0.50
20:R:119:VAL:O	20:R:119:VAL:HG12	2.11	0.50
22:T:71:VAL:CG1	22:T:72:ILE:N	2.74	0.50
1:O:1350:U:H2'	1:O:1351:G:O4'	2.11	0.50
4:A:39:ALA:HB3	4:A:61:GLU:OE2	2.11	0.50
5:B:16:ARG:NH2	40:B:9557:HOH:O	2.39	0.50
5:B:162:MET:CE	5:B:308:LEU:HD21	2.36	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
1:O:119:A:H2'	1:O:120:A:H5''	1.93	0.50
1:O:2265:U:H2'	1:O:2266:A:C8	2.47	0.50
1:O:2507:G:H2'	1:O:2510:C:N4	2.27	0.50
31:3:35:TRP:HB2	40:3:9493:HOH:O	2.12	0.50
9:F:50:VAL:CG2	9:F:63:ILE:HG21	2.41	0.50
12:J:47:THR:HG22	12:J:48:GLY:N	2.26	0.50
13:K:28:GLU:HB3	13:K:59:LYS:HB2	1.93	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
1:O:1477:C:H5'	1:O:1868:G:C5'	2.41	0.50
1:O:2524:G:N2	1:O:2526:C:H5	2.10	0.50
1:O:292:G:H2'	1:O:358:G:N2	2.27	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
11:H:158:THR:HB	11:H:159:PRO:HD3	1.94	0.50
12:J:13:ASP:OD1	12:J:15:ARG:HB3	2.12	0.50
16:N:36:ALA:O	16:N:37:ARG:HD2	2.12	0.50
40:O:3164:HOH:O	25:W:119:HIS:HE1	1.95	0.50
1:O:65:C:O2'	1:O:66:G:H5'	2.12	0.50
6:C:104:ASP:O	6:C:108:GLN:HG3	2.12	0.50
7:D:25:MET:CE	7:D:41:LEU:HG	2.38	0.50
8:E:20:ILE:HD11	8:E:40:VAL:CG1	2.39	0.50
10:G:12:ILE:HD12	40:G:692:HOH:O	2.11	0.50
2:9:3023:U:O2'	2:9:3024:U:H4'	2.12	0.49
40:O:5157:HOH:O	4:A:206:ARG:HD3	2.11	0.49
8:E:166:VAL:HG12	40:E:3134:HOH:O	2.12	0.49
8:E:7:ILE:HG22	8:E:45:ASP:O	2.11	0.49
17:O:97:SER:OG	17:O:100:GLN:HG3	2.12	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:29:ASP:OD1	21:S:31:ARG:NH1	2.45	0.49
27:Y:115:ARG:NE	40:Y:9356:HOH:O	2.45	0.49
1:O:1279:U:O2	1:O:1279:U:H2'	2.12	0.49
1:O:2072:G:H3'	1:O:2073:G:C5'	2.42	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
16:N:114:LYS:O	16:N:118:ILE:HG13	2.12	0.49
24:V:39:ALA:O	24:V:41:GLU:N	2.44	0.49
1:O:2541:U:C2	1:O:2619:UR3:H3U2	2.47	0.49
1:O:2911:C:O2'	1:O:2912:C:H5'	2.12	0.49
11:H:27:LYS:H	11:H:59:HIS:CD2	2.20	0.49
20:R:104:PHE:HB3	20:R:109:MET:HE1	1.94	0.49
22:T:38:ARG:HG3	22:T:38:ARG:HH11	1.77	0.49
1:O: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
28:Z:30:GLU:HG2	28:Z:33:MET:HE3	1.95	0.49
1:O:2889:U:H4'	1:O:2890:A:H5'	1.95	0.49
4:A:232:ARG:NH2	4:A:236:GLY:O	2.37	0.49
6:C:236:THR:H	6:C:239:ALA:HB3	1.77	0.49
11:H:58:ARG:HG3	11:H:58:ARG:NH1	2.27	0.49
20:R:29:LYS:NZ	40:R:9451:HOH:O	2.45	0.49
1:O:1200:A:H3'	40:O:6281:HOH:O	2.11	0.49
1:O:2502:C:H2'	1:O:2503:A:H5'	1.95	0.49
1:O:926:A:O2'	14:L:41:HIS:HD2	1.96	0.49
29:1:25:LYS:O	29:1:25:LYS:HG2	2.12	0.49
6:C:118:THR:O	6:C:136:VAL:HG13	2.11	0.49
11:H:45:VAL:HA	11:H:167:PRO:O	2.12	0.49
16:N:179:LEU:HD23	16:N:184:ILE:HD12	1.94	0.49
1:O:1592:G:H2'	1:O:1593:C:C6	2.48	0.49
1:O:2100:A:H4'	6:C:64:GLY:O	2.12	0.49
1:O:309:C:OP1	22:T:97:ARG:NH2	2.39	0.49
4:A:217:ARG:HH11	4:A:217:ARG:HG3	1.76	0.49
5:B:320:GLN:HE21	5:B:321:PRO:HD2	1.77	0.49
1:O:678:G:OP2	6:C:107:ARG:NH2	2.45	0.49
1:O:2346:C:H4'	7:D:52:THR:CG2	2.42	0.49
7:D:24:HIS:HB2	7:D:72:LYS:CB	2.43	0.49
12:J:142:ASN:O	12:J:144:THR:N	2.46	0.49
14:L:144:ASP:HA	14:L:147:GLU:OE1	2.11	0.49
21:S:8:PRO:HD2	24:V:32:ALA:HA	1.95	0.49
1:O:1118:A:C8	1:O:1118:A:C3'	2.90	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:820:G:O2'	1:0:856:G:H4'	2.13	0.49
2:9:3052:A:O2'	2:9:3053:G:H5'	2.13	0.49
6:C:27:ARG:O	6:C:31:ILE:HG13	2.13	0.49
8:E:81:GLU:HG2	8:E:134:SER:CB	2.42	0.49
11:H:46:GLN:NE2	11:H:137:TYR:HE2	2.08	0.49
12:J:45:VAL:HG22	12:J:46:ILE:N	2.27	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
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
16:N:110:THR:HB	16:N:113:SER:HG	1.75	0.49
1:0:542:A:H2'	1:0:543:G:O4'	2.12	0.49
7:D:50:VAL:O	7:D:71:ALA:HA	2.13	0.49
9:F:111:ILE:O	9:F:115:VAL:HG23	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
22:T:112:LEU:HD23	22:T:119:ALA:HB3	1.93	0.49
1:0:1506:U:H6	1:0:1506:U:H5'	1.78	0.49
1:0:2090:G:H2'	1:0:2091:G:C8	2.47	0.49
1:0:2846:C:H4'	40:0:5619:HOH:O	2.11	0.49
1:0:775:G:OP1	29:1:16:HIS:HE1	1.96	0.49
1:0:797:A:H4'	28:Z:10:ARG:N	2.28	0.49
30:2:35:ARG:HB2	40:2:2691:HOH:O	2.11	0.49
5:B:265:LEU:HD21	5:B:316:ARG:HD3	1.95	0.49
6:C:246:ARG:NH1	40:C:9174:HOH:O	2.45	0.48
8:E:69:ILE:HA	8:E:72:MET:CE	2.43	0.48
16:N:167:ASP:C	16:N:168:LEU:HG	2.34	0.48
16:N:36:ALA:C	16:N:37:ARG:HD2	2.34	0.48
18:P:10:ALA:HA	18:P:13:VAL:HG12	1.94	0.48
22:T:89:ARG:HG3	22:T:89:ARG:O	2.13	0.48
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
24:V:64:GLY:O	24:V:65:ASP:CB	2.60	0.48
1:0:1119:G:N2	1:0:1246:A:N1	2.61	0.48
1:0:920:C:H4'	1:0:921:G:C2	2.49	0.48
1:0:999:C:H2'	1:0:1000:C:O4'	2.12	0.48
17:O:14:LEU:CG	17:O:102:ILE:HD11	2.43	0.48
1:0:475:G:OP1	6:C:73:LEU:HD22	2.12	0.48
1:0:2408:A:H4'	31:3:15:ASN:O	2.13	0.48
4:A:52:SER:HB2	4:A:164:ARG:HH11	1.78	0.48
5:B:190:MET:CE	5:B:194:PHE:CD1	2.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:104:ASP:HA	6:C:107:ARG:NH1	2.27	0.48
7:D:25:MET:CE	7:D:37:ALA:HB1	2.42	0.48
27:Y:126:PRO:HG2	27:Y:128:PHE:CZ	2.49	0.48
28:Z:36:ASP:HB3	28:Z:45:ASP:O	2.13	0.48
1:0:1183:C:H5	1:0:1192:A:OP1	1.96	0.48
1:0:1527:A:H1'	1:0:1528:A:C8	2.48	0.48
1:0:2508:C:H2'	40:0:7232:HOH:O	2.12	0.48
1:0:2102:G:H5''	1:0:2538:A:C2	2.48	0.48
1:0:319:A:H4'	1:0:338:C:C5	2.48	0.48
26:X:34:ARG:NH1	26:X:48:VAL:O	2.46	0.48
6:C:157:LEU:HD22	6:C:162:VAL:CG1	2.43	0.48
16:N:36:ALA:HB1	16:N:118:ILE:HD12	1.96	0.48
22:T:38:ARG:HG3	22:T:38:ARG:NH1	2.29	0.48
24:V:39:ALA:C	24:V:41:GLU:N	2.65	0.48
1:0:1921:A:O2'	1:0:1922:A:H5'	2.14	0.48
1:0:2509:A:H2'	1:0:2510:C:O4'	2.13	0.48
1:0:2472:C:O2'	1:0:2634:G:H4'	2.13	0.48
11:H:34:GLY:HA3	11:H:84:LYS:HA	1.95	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
17:O:80:ASP:OD1	17:O:81:PHE:N	2.45	0.48
1:0:2032:U:H2'	1:0:2033:G:H5'	1.94	0.48
1:0:666:A:H2'	1:0:667:C:O4'	2.14	0.48
4:A:72:GLU:HG3	28:Z:66:GLY:HA2	1.95	0.48
5:B:56:ASP:HB3	5:B:322:ARG:HE	1.79	0.48
12:J:131:THR:HB	12:J:134:GLU:OE1	2.14	0.48
13:K:27:ARG:HD2	40:K:4747:HOH:O	2.14	0.48
14:L:10:SER:O	14:L:11:ARG:HB3	2.14	0.48
15:M:24:GLN:HA	15:M:24:GLN:NE2	2.28	0.48
15:M:59:GLY:HA3	15:M:141:ILE:HD12	1.95	0.48
26:X:7:GLU:HA	26:X:74:ALA:O	2.14	0.48
1:0:1724:U:H5''	40:0:4309:HOH:O	2.12	0.48
1:0:2883:A:H2'	1:0:2884:G:O4'	2.14	0.48
1:0:969:G:H1	1:0:999:C:H42	1.62	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
14:L:123:ASP:O	14:L:146:GLY:HA2	2.13	0.48
14:L:97:VAL:HG12	14:L:98:GLU:O	2.13	0.48
15:M:184:ARG:HG3	15:M:185:PRO:HA	1.96	0.48
18:P:98:ILE:HD12	18:P:102:ARG:CZ	2.43	0.48
25:W:65:VAL:CG1	25:W:116:LEU:HD13	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2587:OMU:H6	1:0:2587:OMU:O5'	2.13	0.48
1:0:653:C:H2'	1:0:654:A:C8	2.48	0.48
6:C:84:VAL:O	6:C:85:LYS:HB2	2.14	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
21:S:56:ASN:O	30:2:8:LYS:NZ	2.42	0.48
1:0:1789:G:O6	18:P:73:HIS:HE1	1.97	0.48
1:0:1739:G:H1'	1:0:2726:U:O4	2.13	0.48
1:0:2769:C:H2'	1:0:2770:G:H5'	1.95	0.48
1:0:558:C:C2'	1:0:559:U:H5''	2.44	0.48
8:E:5:LEU:HD21	8:E:66:GLN:HG3	1.95	0.48
11:H:3:ALA:HA	11:H:58:ARG:NH1	2.28	0.48
14:L:91:VAL:CG1	14:L:120:LEU:HD23	2.43	0.48
16:N:64:SER:C	16:N:66:LEU:H	2.17	0.48
17:O:96:VAL:HG13	17:O:100:GLN:HB2	1.96	0.48
24:V:1:THR:CG2	24:V:2:VAL:H	2.20	0.48
24:V:8:ILE:HG21	24:V:59:ILE:HG13	1.96	0.48
40:0:5826:HOH:O	25:W:122:ARG:NH2	2.41	0.48
25:W:142:ASP:HB2	40:W:2729:HOH:O	2.14	0.48
1:0:1044:C:H5''	40:0:9649:HOH:O	2.13	0.47
1:0:1603:A:H5''	1:0:1605:G:H5'	1.96	0.47
1:0:1736:A:H1'	40:0:8086:HOH:O	2.14	0.47
1:0:2852:A:H5''	40:0:5770: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
15:M:43:PRO:HG3	15:M:62:VAL:HG21	1.95	0.47
15:M:79:ALA:HB3	15:M:81:ARG:HH12	1.79	0.47
1:0:2112:A:H2'	1:0:2113:G:C8	2.49	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
5:B:267:LYS:HD2	40:B:9530:HOH:O	2.13	0.47
13:K:14:LYS:HG3	13:K:32:ILE:O	2.13	0.47
14:L:35:ARG:HD3	14:L:35:ARG:C	2.35	0.47
20:R:106:GLY:HA2	20:R:109:MET:CE	2.44	0.47
1:0:1730:G:H5''	1:0:1731:C:C6	2.49	0.47
1:0:2749:U:H5'	40:0:8433:HOH:O	2.13	0.47
1:0:2812:A:N7	40:0:7959:HOH:O	2.35	0.47
4:A:149:ASP:OD1	4:A:151:GLN:HB2	2.14	0.47
5:B:58:PRO:HA	5:B:63:GLU:CD	2.34	0.47
13:K:55:VAL:CG1	13:K:56:SER:N	2.77	0.47
22:T:81:LYS:HD2	22:T:87:VAL:HG11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:154:ARG:HH12	27:Y:155:ARG:CG	2.21	0.47
1:O:1972:U:H2'	1:O:1973:A:C5'	2.44	0.47
1:O:2611:G:H5'	1:O:2613:G:C8	2.49	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
26:X:74:ALA:CB	26:X:85:VAL:HG22	2.44	0.47
1:O:558:C:C2'	1:O:559:U:C5'	2.93	0.47
5:B:53:LEU:HD21	5:B:270:ILE:HD12	1.97	0.47
6:C:133:ARG:HG3	6:C:133:ARG:HH11	1.79	0.47
32:I:106:LYS:O	32:I:110:GLU:HG3	2.14	0.47
12:J:130:VAL:HG12	12:J:131:THR:N	2.30	0.47
40:O:7351:HOH:O	15:M:178:LYS:HB2	2.14	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
1:O:317:A:OP1	22:T:52:ARG:O	2.33	0.47
23:U:11:THR:HG22	23:U:53:ASP:OD2	2.15	0.47
1:O:1979:G:O2'	1:O:1980:U:OP1	2.27	0.47
1:O:2681:A:H4'	1:O:2682:C:H5'	1.97	0.47
1:O:2717:C:H2'	1:O:2718:C:C5'	2.40	0.47
1:O:2906:A:H5'	1:O:2907:C:O4'	2.15	0.47
2:9:3018:U:H2'	2:9:3019:G:C8	2.50	0.47
1:O:2545:U:OP2	5:B:2:GLN:NE2	2.47	0.47
5:B:5:ARG:NH1	5:B:8:LYS:HE2	2.30	0.47
6:C:25:PRO:HG2	40:C:9125:HOH:O	2.14	0.47
11:H:29:ALA:HB3	11:H:66:ARG:HH12	1.80	0.47
16:N:166:ALA:O	16:N:167:ASP:O	2.33	0.47
1:O:1185:U:H2'	1:O:1186:C:C6	2.48	0.47
1:O:185:G:H4'	1:O:186:A:H4'	1.96	0.47
1:O:2421:G:H4'	40:O:5324:HOH:O	2.13	0.47
1:O:2443:C:H1'	14:L:56:LYS:HE3	1.97	0.47
1:O:1881:A:OP1	4:A:199:HIS:HE1	1.97	0.47
6:C:218:VAL:N	40:C:9225:HOH:O	2.48	0.47
40:O:3822:HOH:O	32:I:92:PRO:HD3	2.13	0.47
23:U:52:THR:HG22	23:U:54:THR:H	1.77	0.47
24:V:5:VAL:CG1	24:V:9:ARG:NH1	2.78	0.47
1:O:1406:A:H4'	1:O:1407:A:C5'	2.45	0.47
1:O:29:C:C2'	1:O:30:U:H5'	2.44	0.47
2:9:3059:C:H2'	2:9:3060:C:C6	2.50	0.47
7:D:84:LEU:HA	7:D:87:ALA:HB3	1.97	0.47
8:E:106:ASN:ND2	8:E:109:GLY:HA2	2.30	0.47
11:H:56:GLN:HE21	11:H:126:ARG:HE	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:98:VAL:HG22	13:K:102:GLU:C	2.35	0.47
14:L:80:ASP:HB2	14:L:90:ARG:HB3	1.96	0.47
14:L:98:GLU:O	14:L:99:GLU:HB2	2.15	0.47
7:D:146:LYS:NZ	16:N:107:ASN:HD21	2.13	0.47
26:X:25:ARG:HD2	40:X:5356:HOH:O	2.15	0.47
27:Y:184:GLU:OE1	27:Y:204:ARG:NH1	2.48	0.47
1:O:2503:A:P	11:H:151:ARG:HH22	2.38	0.47
1:O:710:G:H5'	17:O:25:VAL:HG13	1.97	0.47
1:O:932:U:H2'	1:O:933:C:C6	2.50	0.47
5:B:41:PHE:HB3	5:B:190:MET:HE1	1.97	0.47
6:C:133:ARG:NE	6:C:138:VAL:HG22	2.29	0.47
9:F:118:LEU:O	9:F:119:ARG:HB3	2.15	0.47
32:I:131:THR:O	32:I:135:LEU:HG	2.15	0.47
1:O:1992:U:OP2	13:K:66:ARG:HD2	2.14	0.47
14:L:53:ARG:HH22	14:L:57:VAL:HG12	1.80	0.47
1:O:1066:U:H2'	1:O:1067:A:C8	2.49	0.47
31:3:55:VAL:HG22	40:3:9444:HOH:O	2.15	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
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
27:Y:187:VAL:HG23	27:Y:192:ASP:HB3	1.96	0.47
27:Y:99:ALA:HB2	27:Y:233:TYR:CE2	2.50	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
2:9:3091:C:H2'	2:9:3092:G:O4'	2.15	0.47
1:O:475:G:C5'	6:C:73:LEU:HD23	2.45	0.47
12:J:43:ARG:HG2	40:J:5361:HOH:O	2.15	0.47
16:N:37:ARG:NE	40:N:9330:HOH:O	2.47	0.47
1:O:1667:A:C8	1:O:1667:A:H5'	2.41	0.46
31:3:42:ARG:HH11	31:3:42:ARG:HG3	1.80	0.46
4:A:36:ASP:HB2	4:A:85:SER:H	1.79	0.46
5:B:87:TYR:O	5:B:138:GLY:N	2.34	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
8:E:1:PRO:HG2	8:E:59:MET:SD	2.56	0.46
16:N:119:GLN:O	16:N:123:ILE:HG13	2.15	0.46
40:O:5274:HOH:O	16:N:21:HIS:HD2	1.97	0.46
17:O:47:ARG:HG3	17:O:47:ARG:HH11	1.80	0.46
18:P:89:ASN:HB3	18:P:92:GLU:HB2	1.96	0.46
20:R:104:PHE:CB	20:R:109:MET:HE1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1333:U:H2'	1:0:1334:C:H6	1.80	0.46
1:0:447:A:OP1	22:T:2:LYS:HG2	2.15	0.46
2:9:3001:U:H5'	2:9:3121:C:O2	2.15	0.46
40:0:3549:HOH:O	6:C:78:ARG:HD3	2.15	0.46
10:G:64:ASN:N	10:G:64:ASN:ND2	2.63	0.46
11:H:30:GLN:H	11:H:66:ARG:HH11	1.63	0.46
32:I:139:ILE:CG2	32:I:140:GLU:N	2.78	0.46
16:N:78:MET:HB2	16:N:79:PRO:HD3	1.97	0.46
25:W:88:THR:CG2	25:W:89:ASP:H	2.28	0.46
26:X:85:VAL:HG12	26:X:86:GLU:N	2.30	0.46
1:0:57:C:H5'	24:V:46:ILE:HG21	1.98	0.46
30:2:5:LYS:O	30:2:9:LYS:HG3	2.15	0.46
31:3:60:LYS:HG3	31:3:61:PRO:HD2	1.96	0.46
2:9:3039:U:H1'	2:9:3044:A:N6	2.30	0.46
7:D:154:LYS:H	7:D:154:LYS:CD	2.24	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
1:0:1211:G:O2'	1:0:1212:C:H5'	2.16	0.46
4:A:71:PRO:HD2	4:A:74:VAL:HG21	1.98	0.46
5:B:243:ASN:HA	5:B:244:PRO:C	2.36	0.46
5:B:305:ASP:O	5:B:306:LYS:CB	2.63	0.46
15:M:68:ARG:NH2	15:M:73:ARG:HD3	2.31	0.46
17:O:88:LYS:HD3	40:O:7061:HOH:O	2.15	0.46
20:R:119:VAL:O	20:R:119:VAL:CG1	2.63	0.46
1:0:500:G:O2'	20:R:94:ASN:ND2	2.48	0.46
23:U:20:MET:CE	23:U:30:HIS:NE2	2.79	0.46
1:0:399:C:H5'	15:M:179:GLY:O	2.15	0.46
29:1:8:GLN:HE22	29:1:11:LYS:HZ1	1.62	0.46
3:4:76:DA:H5''	38:4:9701:SPS:C6	2.45	0.46
2:9:3029:C:H2'	2:9:3030:C:C5'	2.42	0.46
4:A:132:ASP:OD1	4:A:133:ARG:N	2.49	0.46
4:A:58:VAL:HG21	4:A:68:ILE:HD12	1.98	0.46
4:A:70:ALA:HA	4:A:71:PRO:HD3	1.76	0.46
9:F:21:GLU:O	9:F:24:ARG:HG3	2.15	0.46
17:O:14:LEU:CD2	17:O:102:ILE:HD11	2.46	0.46
20:R:33:ARG:NH1	40:R:9454:HOH:O	2.40	0.46
22:T:40:VAL:HG22	22:T:41:ARG:H	1.81	0.46
1:0:1717:A:H5''	18:P:54:LYS:HB2	1.97	0.46
1:0:2019:A:H5'	40:0:5087:HOH:O	2.16	0.46
1:0:462:A:H2'	40:0:5427:HOH:O	2.15	0.46
14:L:120:LEU:HD12	14:L:133:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:143:THR:CG2	14:L:144:ASP:N	2.78	0.46
17:O:26:TRP:HA	17:O:26:TRP:CE3	2.50	0.46
1:O:1299:G:H5'	40:O:4642:HOH:O	2.15	0.46
1:O:622:G:P	27:Y:148:GLY:HA3	2.55	0.46
31:3:18:GLN:OE1	31:3:73:GLU:HB3	2.15	0.46
4:A:96:LEU:HG	4:A:152:CYS:O	2.16	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
13:K:114:ALA:HB3	13:K:117:VAL:HG23	1.96	0.46
15:M:90:ARG:HB2	31:3:46:ILE:HD11	1.98	0.46
23:U:17:THR:CG2	23:U:18:GLY:H	2.27	0.46
25:W:29:VAL:O	25:W:30:ASN:HB2	2.16	0.46
26:X:9:VAL:HG13	26:X:88:GLU:OE2	2.15	0.46
1:O:2837:U:H2'	40:O:7315:HOH:O	2.14	0.46
1:O:951:A:O2'	1:O:952:G:H5'	2.16	0.46
31:3:69:TYR:O	31:3:77:ALA:HA	2.16	0.46
4:A:66:ARG:HH11	4:A:66:ARG:HB2	1.80	0.46
11:H:18:GLU:HG3	11:H:19:TYR:CE1	2.51	0.46
15:M:95:LYS:HA	15:M:170:ASN:HD21	1.81	0.46
1:O:57:C:H5'	24:V:46:ILE:CG2	2.46	0.46
25:W:88:THR:CG2	25:W:90:TYR:HD1	2.27	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
1:O:432:G:O2'	1:O:433:C:H5'	2.16	0.46
1:O:451:C:O2'	1:O:452:G:H5'	2.15	0.46
1:O:834:G:H3'	1:O:835:U:H4'	1.98	0.46
4:A:126:ALA:HB1	4:A:138:VAL:CG1	2.46	0.46
4:A:125:ASN:HB3	4:A:158:VAL:HG12	1.98	0.46
5:B:140:LEU:HD23	40:B:9578:HOH:O	2.16	0.46
2:9:3006:C:H4'	16:N:35:VAL:HG11	1.98	0.46
17:O:25:VAL:HG23	40:O:3062:HOH:O	2.16	0.46
22:T:41:ARG:NH1	22:T:42:VAL:O	2.49	0.46
26:X:25:ARG:NH2	40:X:5740:HOH:O	2.48	0.46
27:Y:144:ARG:NH1	40:Y:9377:HOH:O	2.49	0.46
1:O:1202:A:H2'	1:O:1203:G:O4'	2.16	0.46
38:4:9701:SPS:O1	38:4:9701:SPS:H91	2.16	0.46
2:9:3028:U:H2'	2:9:3029:C:C6	2.51	0.46
11:H:73:LEU:HD21	11:H:146:VAL:HA	1.98	0.46
14:L:144:ASP:O	14:L:147:GLU:HB2	2.16	0.46
17:O:26:TRP:HA	17:O:26:TRP:HE3	1.80	0.46
27:Y:151:SER:HB3	27:Y:154:ARG:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1167:G:H2'	1:0:1168:C:O4'	2.16	0.45
1:0:1419:U:H2'	1:0:1685:A:C2	2.52	0.45
1:0:1730:G:H5'	1:0:1731:C:C6	2.50	0.45
1:0:2531:U:O2'	1:0:2532:A:H5'	2.16	0.45
1:0:2679:G:H2'	1:0:2681:A:OP2	2.15	0.45
1:0:664:U:O4	1:0:681:G:H5''	2.16	0.45
5:B:138:GLY:O	5:B:139:ASP:O	2.34	0.45
5:B:71:VAL:CG1	5:B:296:LEU:HD22	2.46	0.45
5:B:41:PHE:CG	5:B:79:MET:HE2	2.51	0.45
7:D:159:PRO:O	7:D:163:VAL:HG23	2.17	0.45
8:E:81:GLU:O	8:E:172:PRO:HD3	2.16	0.45
8:E:81:GLU:HG2	8:E:134:SER:HB3	1.97	0.45
15:M:66:SER:HB3	15:M:128:TRP:NE1	2.31	0.45
18:P:135:ALA:HB1	18:P:139:ARG:NH1	2.31	0.45
20:R:82:GLU:OE1	20:R:86:LYS:HE3	2.16	0.45
23:U:52:THR:CG2	23:U:54:THR:HB	2.46	0.45
1:0:1086:A:C6	25:W:11:VAL:HG11	2.51	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
1:0:2825:C:H4'	1:0:2826:G:O5'	2.15	0.45
1:0:415:A:O2'	1:0:416:G:H5'	2.17	0.45
4:A:36:ASP:O	4:A:36:ASP:CG	2.54	0.45
9:F:26:THR:HG21	9:F:103:GLU:HG3	1.97	0.45
18:P:16:VAL:HG13	18:P:20:ARG:NH1	2.31	0.45
26:X:76:ARG:O	26:X:77:PHE:HB3	2.16	0.45
1:0:1135:G:H5'	40:0:6446:HOH:O	2.16	0.45
1:0:1829:A:H2'	1:0:1830:C:H5'	1.99	0.45
1:0:1847:A:OP1	4:A:175:LYS:HG3	2.16	0.45
1:0:249:G:O2'	1:0:250:C:H5'	2.17	0.45
9:F:20:LEU:HB2	9:F:49:PHE:CZ	2.51	0.45
14:L:89:PHE:CD1	14:L:89:PHE:N	2.85	0.45
16:N:33:ARG:NH2	40:N:9350:HOH:O	2.50	0.45
23:U:14:GLU:OE1	23:U:15:PRO:HD2	2.17	0.45
25:W:88:THR:CG2	25:W:89:ASP:N	2.78	0.45
27:Y:106:THR:CG2	27:Y:107:PRO:HD2	2.47	0.45
1:0:2619:UR3:H2'	1:0:2620:U:C6	2.51	0.45
1:0:289:G:H5'	40:0:5159:HOH:O	2.17	0.45
2:9:3005:G:OP1	16:N:17:ARG:NH2	2.50	0.45
6:C:124:VAL:HA	6:C:230:GLY:O	2.16	0.45
8:E:101:GLU:HA	8:E:118:ILE:HG13	1.97	0.45
8:E:16:ASP:O	8:E:17:HIS:HB2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:54:VAL:HG11	12:J:138:THR:HG21	1.99	0.45
15:M:107:ARG:CG	15:M:107:ARG:NH1	2.78	0.45
22:T:12:ARG:NH1	40:T:3035:HOH:O	2.49	0.45
23:U:20:MET:CG	23:U:28:THR:HG23	2.47	0.45
1:O:734:U:H1'	1:O:737:A:N6	2.32	0.45
40:O:9834:HOH:O	4:A:11:ARG:HD3	2.17	0.45
7:D:51:ARG:HD3	40:D:7636:HOH:O	2.16	0.45
9:F:102:GLY:O	9:F:103:GLU:HB2	2.16	0.45
12:J:103:VAL:HG12	40:J:5907:HOH:O	2.16	0.45
13:K:109:LEU:CD1	13:K:113:ILE:HD11	2.46	0.45
15:M:164:THR:CG2	15:M:166:ALA:H	2.27	0.45
17:O:59:VAL:CG2	17:O:111:VAL:CG2	2.95	0.45
23:U:6:CYS:C	23:U:8:TYR:H	2.19	0.45
24:V:25:THR:HG22	24:V:29:ASN:ND2	2.32	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
1:O:2697:A:H2'	1:O:2698:G:O4'	2.17	0.45
1:O:371:U:H2'	1:O:372:A:H8	1.80	0.45
5:B:217:ARG:HG3	5:B:257:THR:CG2	2.47	0.45
6:C:168:ARG:NH2	6:C:190:ALA:O	2.50	0.45
7:D:167:GLU:C	7:D:169:THR:H	2.20	0.45
14:L:66:VAL:HG23	14:L:67:ARG:N	2.31	0.45
16:N:86:LEU:O	16:N:90:LEU:HG	2.15	0.45
20:R:25:PHE:CZ	20:R:29:LYS:HE2	2.50	0.45
26:X:43:VAL:CG1	26:X:47:ALA:HB3	2.45	0.45
1:O:1149:U:H5''	1:O:1151:G:O4'	2.17	0.45
1:O:1745:G:H22	1:O:2033:G:H5'	1.82	0.45
1:O:2289:G:H21	1:O:2291:A:H2	1.62	0.45
1:O:2356:A:H2'	1:O:2357:G:O4'	2.16	0.45
1:O:2506:A:O2'	1:O:2507:G:O5'	2.35	0.45
1:O:968:G:O2'	1:O:969:G:H5'	2.17	0.45
4:A:122:SER:O	4:A:124:VAL:HG13	2.17	0.45
9:F:68:ASP:C	9:F:70:LYS:H	2.20	0.45
40:O:5514:HOH:O	11:H:58:ARG:HG3	2.16	0.45
15:M:81:ARG:HG2	15:M:85:ARG:O	2.16	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
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
1:O:1741:U:H3'	40:O:3369:HOH:O	2.16	0.45
1:O:497:A:H2'	1:O:498:A:C5'	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:59:A:H5'	40:0:4886:HOH:O	2.15	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
6:C:233:THR:HG22	6:C:234:VAL:H	1.82	0.45
6:C:236:THR:O	6:C:237:GLU:C	2.54	0.45
8:E:69:ILE:HA	8:E:72:MET:HE3	1.97	0.45
23:U:9:CYS:CA	23:U:52:THR:HG23	2.47	0.45
24:V:38:GLY:C	24:V:40:PRO:HD2	2.36	0.45
1:0:1151:G:OP1	10:G:63:ARG:NH1	2.50	0.45
1:0:1180:U:H1'	40:0:3822:HOH:O	2.17	0.45
30:2:20:ARG:HG3	30:2:21:VAL:N	2.31	0.45
31:3:75:GLY:HA2	40:3:9510:HOH:O	2.16	0.45
1:0:1654:U:H2'	4:A:47:HIS:HD2	1.82	0.45
4:A:66:ARG:HH11	4:A:66:ARG:CB	2.29	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
7:D:60:GLU:O	7:D:61:PHE:C	2.55	0.45
13:K:119:GLN:HG2	13:K:119:GLN:O	2.17	0.45
1:0:120:A:H2'	1:0:120:A:N3	2.32	0.45
1:0:2073:G:H5''	40:0:4398:HOH:O	2.16	0.45
1:0:2329:C:O2'	1:0:2330:U:H5'	2.17	0.45
1:0:968:G:H1'	11:H:32:LYS:HD2	1.98	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
7:D:10:PHE:CD1	7:D:11:HIS:N	2.85	0.45
7:D:170:TYR:O	7:D:171:ASP:CB	2.65	0.45
1:0:1056:U:H2'	1:0:1057:A:O4'	2.16	0.44
1:0:1603:A:C5'	1:0:1605:G:H5'	2.47	0.44
1:0:1942:A:H3'	40:0:7797:HOH:O	2.17	0.44
1:0:2415:A:H2'	1:0:2416:G:H5'	1.98	0.44
1:0:2591:C:H2'	1:0:2592:G:O4'	2.17	0.44
6:C:157:LEU:HD22	6:C:162:VAL:HG11	1.98	0.44
9:F:109:GLU:HG2	9:F:113:ASP:OD2	2.17	0.44
11:H:29:ALA:C	11:H:30:GLN:HG3	2.38	0.44
12:J:19:MET:HE2	12:J:132:LEU:HD11	1.98	0.44
13:K:87:ARG:NH1	40:K:4066:HOH:O	2.49	0.44
16:N:74:PRO:HG2	16:N:159:TYR:CE1	2.52	0.44
18:P:13:VAL:HG11	18:P:40:VAL:CG1	2.47	0.44
18:P:18:LYS:O	18:P:21:VAL:HG13	2.17	0.44
26:X:25:ARG:HD3	26:X:64:ALA:O	2.17	0.44
1:0:1250:C:O2'	1:0:1251:C:H5'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1435:U:H5'	40:0:3201:HOH:O	2.16	0.44
1:0:1835:U:C5	1:0:1840:A:N7	2.69	0.44
2:9:3052:A:H2'	2:9:3053:G:O4'	2.17	0.44
2:9:3064:C:C2'	2:9:3065:A:H5'	2.48	0.44
5:B:168:GLY:O	5:B:169:GLY:O	2.36	0.44
5:B:277:GLU:N	5:B:278:PRO:HD2	2.32	0.44
5:B:60:SER:HA	5:B:61:PRO:HD3	1.86	0.44
6:C:142:ASP:OD1	6:C:236:THR:HG23	2.16	0.44
6:C:49:ASP:HB3	6:C:52:ALA:HB2	1.99	0.44
7:D:91:ALA:HB2	7:D:106:PHE:CD2	2.52	0.44
7:D:154:LYS:HD2	7:D:154:LYS:N	2.26	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
2:9:3051:A:H5'	16:N:160:SER:HB2	1.99	0.44
22:T:53:GLY:HA3	40:T:6384:HOH:O	2.17	0.44
26:X:12:ILE:HD12	26:X:36:HIS:CG	2.52	0.44
1:0:1166:A:N6	1:0:1180:U:H3	2.00	0.44
1:0:1768:C:H2'	1:0:1769:C:O4'	2.17	0.44
1:0:1972:U:H2'	1:0:1973:A:H5''	1.98	0.44
1:0:2456:A:H2'	1:0:2457:U:H6	1.83	0.44
1:0:1684:A:H1'	30:2:43:ARG:HH22	1.83	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
6:C:246:ARG:NH1	6:C:246:ARG:HB3	2.32	0.44
8:E:116:THR:CG2	8:E:151:LEU:HD22	2.47	0.44
10:G:68:GLU:O	10:G:72:ASP:HB2	2.18	0.44
16:N:108:SER:HA	16:N:109:PRO:HD3	1.82	0.44
27:Y:107:PRO:HD3	27:Y:182:PHE:CE1	2.52	0.44
1:0:177:A:H2'	1:0:178:U:O4'	2.16	0.44
1:0:2073:G:H3'	40:0:4398:HOH:O	2.18	0.44
1:0:2361:A:H2'	1:0:2362:A:C8	2.51	0.44
4:A:164:ARG:NE	40:A:9572:HOH:O	2.50	0.44
4:A:99:ILE:O	4:A:131:HIS:CE1	2.70	0.44
7:D:173:GLU:OE1	7:D:174:VAL:HG23	2.18	0.44
7:D:66:GLY:O	7:D:67:ASP:HB3	2.17	0.44
12:J:63:ILE:CG2	12:J:64:GLY:N	2.79	0.44
15:M:95:LYS:HD2	15:M:99:ARG:HG2	1.98	0.44
17:O:38:ARG:NH1	40:O:7674:HOH:O	2.50	0.44
18:P:115:SER:HG	18:P:118:GLN:HG3	1.81	0.44
1:0:447:A:OP1	22:T:1:SER:HB2	2.17	0.44
1:0:794:U:H3	1:0:819:A:H61	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:101:GLU:HB3	8:E:117:THR:HA	2.00	0.44
40:O:9644:HOH:O	14:L:30:ARG:HD2	2.16	0.44
15:M:86:GLN:O	15:M:88:VAL:HG23	2.16	0.44
16:N:112:GLY:HA2	16:N:137:ALA:N	2.32	0.44
1:O:2364:A:H5''	19:Q:15:LYS:HD3	2.00	0.44
19:Q:25:PRO:HA	19:Q:26:PRO:HD3	1.83	0.44
1:O:602:A:O2'	1:O:605:C:H4'	2.17	0.44
2:9:3092:G:H2'	2:9:3093:A:C8	2.53	0.44
5:B:36:PRO:HB3	5:B:174:ARG:CB	2.47	0.44
5:B:24:PRO:CG	5:B:204:GLY:HA2	2.48	0.44
5:B:74:ILE:HD13	5:B:309:VAL:HG21	2.00	0.44
6:C:7:ASP:OD1	6:C:11:ASN:N	2.50	0.44
11:H:76:GLU:O	11:H:77:LEU:HD23	2.16	0.44
32:I:93:GLN:HA	32:I:96:PHE:HE2	1.83	0.44
14:L:145:LEU:C	14:L:145:LEU:HD23	2.37	0.44
16:N:168:LEU:HA	16:N:169:PRO:HD3	1.77	0.44
23:U:4:ARG:NH1	23:U:4:ARG:HG2	2.31	0.44
25:W:119:HIS:HD2	25:W:120:PRO:O	2.00	0.44
27:Y:178:HIS:CG	27:Y:179:PRO:HD2	2.53	0.44
1:O:1098:A:O3'	25:W:129:LYS:HE2	2.18	0.44
1:O:1120:U:H5''	1:O:1120:U:C6	2.53	0.44
1:O:220:C:H1'	40:O:6282:HOH:O	2.17	0.44
1:O:236:A:H8	1:O:236:A:OP1	2.01	0.44
1:O:2791:U:H1'	1:O:2792:A:H5''	1.99	0.44
5:B:14:GLY:HA2	5:B:15:PRO:C	2.37	0.44
5:B:225:GLY:HA3	40:B:9567:HOH:O	2.18	0.44
11:H:66:ARG:HD3	40:H:9545:HOH:O	2.18	0.44
18:P:63:ARG:NH2	40:P:190:HOH:O	2.51	0.44
20:R:39:THR:CG2	20:R:107:GLU:O	2.66	0.44
21:S:57:THR:HG22	21:S:59:ASP:H	1.81	0.44
24:V:20:LEU:HD11	24:V:53:ILE:HG23	2.00	0.44
1:O:1025:C:H5'	25:W:23:MET:O	2.17	0.44
28:Z:30:GLU:HA	28:Z:33:MET:HE3	1.99	0.44
1:O:1182:C:H1'	1:O:1192:A:C8	2.50	0.44
1:O:1751:G:C2'	1:O:1752:G:H5''	2.42	0.44
1:O:1476:A:O2'	1:O:1868:G:H5'	2.18	0.44
1:O:111:C:HO2'	29:1:20:ARG:HG2	1.76	0.44
4:A:135:VAL:HG13	4:A:135:VAL:O	2.17	0.44
8:E:101:GLU:OE2	8:E:115:ARG:HD3	2.17	0.44
1:O:1852:A:H5''	4:A:232:ARG:O	2.18	0.44
1:O:1926:G:H2'	1:O:1927:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2506:A:O2'	1:0:2507:G:P	2.76	0.44
1:0:407:A:H5'	40:0:6540:HOH:O	2.17	0.44
1:0:90:A:H2'	1:0:91:G:O4'	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
1:0:926:A:O2'	14:L:41:HIS:CD2	2.71	0.44
19:Q:75:ILE:HD13	19:Q:84:ILE:CD1	2.48	0.44
21:S:57:THR:HG23	40:S:9487:HOH:O	2.17	0.44
1:0:335:U:H4'	22:T:92:ASP:OD2	2.18	0.44
40:0:5826:HOH:O	25:W:119:HIS:CG	2.71	0.44
27:Y:209:VAL:HG12	27:Y:214:ARG:HG3	1.99	0.44
1:0:1203:G:O2'	1:0:1204:C:H5'	2.17	0.43
1:0:1252:A:H2'	1:0:1253:C:O4'	2.17	0.43
1:0:2254:G:O2'	1:0:2255:A:H5'	2.18	0.43
40:0:5006:HOH:O	30:2:39:ARG:HG2	2.18	0.43
30:2:48:ASP:O	30:2:49:GLU:CB	2.65	0.43
4:A:26:ASP:O	4:A:26:ASP:OD1	2.36	0.43
5:B:162:MET:HG3	5:B:310:ARG:HD3	2.00	0.43
9:F:11:ASP:O	9:F:14:ASP:HB2	2.17	0.43
11:H:99:LYS:HD3	11:H:119:LYS:HD3	1.98	0.43
15:M:36:ALA:HB1	40:M:9353:HOH:O	2.17	0.43
20:R:18:LEU:HB2	20:R:143:VAL:HG13	1.98	0.43
20:R:95:ALA:HB2	20:R:145:LEU:HD23	2.00	0.43
24:V:12:THR:HG23	24:V:14:ALA:H	1.82	0.43
1:0:1163:G:H2'	1:0:1164:U:C5	2.52	0.43
1:0:1306:U:OP1	6:C:184:ARG:HD2	2.18	0.43
1:0:2491:G:H1'	40:0:7345:HOH:O	2.17	0.43
1:0:263:U:C2	9:F:59:ILE:HD12	2.53	0.43
6:C:46:TYR:CE2	6:C:98:ARG:NH1	2.86	0.43
7:D:51:ARG:NH1	7:D:68:PRO:HB3	2.32	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
40:9:3472:HOH:O	16:N:41:LYS:HD3	2.17	0.43
20:R:96:VAL:HG13	20:R:106:GLY:HA3	2.00	0.43
25:W:141:HIS:HB2	25:W:146:ILE:HG12	2.00	0.43
26:X:43:VAL:CG1	26:X:44:ASP:N	2.81	0.43
1:0:137:U:H2'	1:0:139:C:C5	2.53	0.43
1:0:196:G:H1'	1:0:198:A:N7	2.34	0.43
1:0:1972:U:C2'	1:0:1973:A:H5''	2.48	0.43
1:0:449:A:N7	6:C:43:LYS:HG2	2.33	0.43
1:0:699:C:H2'	1:0:744:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:205:VAL:O	5:B:307:ARG:NE	2.49	0.43
9:F:32:GLY:N	40:F:3111:HOH:O	2.50	0.43
9:F:49:PHE:HE1	9:F:98:VAL:HG23	1.84	0.43
1:0:1015:C:H2'	1:0:1016:U:C6	2.53	0.43
1:0:1218:U:H2'	1:0:1219:U:H6	1.82	0.43
1:0:1132:A:N6	1:0:1229:C:H2'	2.33	0.43
1:0:1342:C:O2'	1:0:1343:C:H5'	2.18	0.43
1:0:1406:A:H5'	1:0:1407:A:C8	2.54	0.43
1:0:2649:A:O4'	1:0:2650:U:H5	2.01	0.43
1:0:371:U:H2'	1:0:372:A:C8	2.53	0.43
1:0:921:G:H4'	1:0:924:G:N1	2.33	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
1:0:1206:U:C6	1:0:1206:U:H5'	2.33	0.43
1:0:1211:G:H2'	1:0:1212:C:H6	1.83	0.43
1:0:1503:U:H2'	1:0:1504:A:O4'	2.19	0.43
1:0:1838:U:H1'	1:0:2644:C:O4'	2.18	0.43
1:0:2372:A:H2'	1:0:2373:U:C6	2.54	0.43
1:0:2515:C:C2'	1:0:2516:G:H5'	2.48	0.43
1:0:308:U:C2	22:T:52:ARG:NH2	2.87	0.43
1:0:830:G:O2'	1:0:831:U:H5'	2.18	0.43
1:0:93:C:H5''	24:V:1:THR:CB	2.43	0.43
4:A:201:PHE:HB3	40:A:9617:HOH:O	2.18	0.43
4:A:65:ARG:HH11	4:A:65:ARG:HG2	1.83	0.43
12:J:54:VAL:O	12:J:58:GLU:HG3	2.18	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
1:0:1268:C:O2'	1:0:1269:G:H5'	2.18	0.43
1:0:2676:C:H4'	12:J:70:PHE:HD1	1.83	0.43
1:0:544:G:C3'	1:0:545:G:H5''	2.49	0.43
1:0:945:U:H2'	1:0:946:C:H6	1.83	0.43
6:C:120:ASP:C	6:C:120:ASP:OD1	2.57	0.43
6:C:184:ARG:HB3	40:C:9167:HOH:O	2.18	0.43
11:H:56:GLN:NE2	11:H:93:GLN:HG2	2.31	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
25:W:106:THR:OG1	25:W:109:GLU:HB2	2.19	0.43
1:0:1201:C:C2'	1:0:1202:A:H5'	2.44	0.43
1:0:1189:A:H1'	1:0:1209:C:H1'	1.99	0.43
1:0:1439:C:OP1	30:2:41:HIS:HE1	2.02	0.43
1:0:1482:A:O2'	1:0:1483:C:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:9:3044:A:H2'	2:9:3045:A:O4'	2.19	0.43
5:B:132:HIS:CE1	5:B:171:VAL:HG21	2.54	0.43
5:B:248:ARG:NH2	40:B:9527:HOH:O	2.44	0.43
5:B:51:VAL:HG21	5:B:327:VAL:HG13	1.99	0.43
8:E:18:LEU:HD13	8:E:34:TRP:CG	2.53	0.43
12:J:43:ARG:NH1	40:J:5361:HOH:O	2.52	0.43
21:S:38:ALA:O	21:S:42:GLU:HG3	2.18	0.43
25:W:11:VAL:O	25:W:12:ASN:HB2	2.18	0.43
1:0:10:U:O4	1:0:532:A:OP2	2.37	0.43
1:0:1213:C:O2'	1:0:1214:G:H5'	2.19	0.43
1:0:271:C:H41	1:0:378:A:H2	1.62	0.43
1:0:559:U:H5'	1:0:559:U:C6	2.44	0.43
29:1:28:HIS:CD2	29:1:31:LYS:HG3	2.53	0.43
1:0:2250:G:OP1	4:A:31:LYS:HD3	2.19	0.43
6:C:45:ASP:OD2	6:C:98:ARG:HD2	2.19	0.43
1:0:2346:C:O3'	7:D:52:THR:HG23	2.19	0.43
11:H:83:TYR:C	11:H:83:TYR:CD1	2.92	0.43
13:K:125:ALA:O	13:K:127:ALA:N	2.47	0.43
16:N:143:ARG:HE	16:N:143:ARG:HB3	1.65	0.43
40:0:7250:HOH:O	16:N:4:PRO:HD2	2.18	0.43
19:Q:30:VAL:O	19:Q:30:VAL:HG12	2.18	0.43
24:V:8:ILE:CG2	24:V:59:ILE:HG13	2.49	0.43
25:W:26:ILE:O	25:W:26:ILE:HG12	2.17	0.43
1:0:1175:G:H2'	1:0:1176:C:O4'	2.19	0.43
1:0:1206:U:C5'	1:0:1206:U:H6	2.21	0.43
1:0:2032:U:C2'	1:0:2033:G:H5''	2.49	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
2:9:3006:C:OP1	16:N:37:ARG:CZ	2.67	0.43
40:0:4961:HOH:O	4:A:11:ARG:CZ	2.66	0.43
4:A:66:ARG:NH1	4:A:66:ARG:CB	2.81	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
22:T:78:THR:HB	22:T:87:VAL:O	2.19	0.43
22:T:88:PRO:HB3	40:T:6320:HOH:O	2.19	0.43
1:0:1044:C:H3'	1:0:1045:G:H5''	2.01	0.43
1:0:1755:A:H2'	1:0:1756:G:O4'	2.19	0.43
30:2:19:SER:O	30:2:36:ASN:ND2	2.43	0.43
4:A:217:ARG:NH1	4:A:217:ARG:CG	2.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:98:ARG:NH1	40:C:9161:HOH:O	2.51	0.43
8:E:105:GLU:HG2	8:E:113:PRO:HB3	2.01	0.43
12:J:39:VAL:CG1	12:J:40:ASN:N	2.82	0.43
13:K:13:GLU:OE1	13:K:44:LEU:HD12	2.19	0.43
14:L:92:ASP:OD1	14:L:94:ARG:HB2	2.18	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
22:T:49:GLU:HB3	22:T:59:GLU:CG	2.44	0.43
27:Y:151:SER:HB3	27:Y:154:ARG:CB	2.49	0.43
1:O:1196:C:H2'	1:O:1197:G:O4'	2.18	0.42
1:O:1377:C:H1'	40:O:7728:HOH:O	2.18	0.42
1:O:2435:U:H1'	40:O:5968:HOH:O	2.19	0.42
1:O:603:A:H5''	1:O:604:G:OP1	2.18	0.42
1:O:793:A:C5'	18:P:83:LYS:HG2	2.49	0.42
31:3:65:THR:HG23	31:3:88:LEU:HD22	2.00	0.42
2:9:3001:U:O3'	2:9:3003:A:H5''	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
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
13:K:63:GLU:HB2	40:K:6344:HOH:O	2.19	0.42
22:T:75:GLU:O	22:T:76:ASP:HB2	2.19	0.42
28:Z:75:GLY:O	28:Z:78:THR:HB	2.18	0.42
1:O:1189:A:HO2'	1:O:1208:C:H2'	1.82	0.42
1:O:1226:G:H5'	40:O:5079:HOH:O	2.19	0.42
1:O:2428:G:N7	31:3:60:LYS:NZ	2.65	0.42
1:O:565:A:OP2	1:O:592:G:N1	2.49	0.42
31:3:70:ARG:HG3	31:3:77:ALA:HB2	2.01	0.42
7:D:62:ASP:HA	40:D:4233:HOH:O	2.17	0.42
9:F:28:ALA:HB3	9:F:99:THR:O	2.19	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:O:1186:C:H5''	32:I:119:TYR:CE1	2.54	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:O:1174:A:C5	1:O:1201:C:H4'	2.54	0.42
1:O:2015:A:H2'	1:O:2016:U:O4'	2.19	0.42
1:O:2251:G:H2'	1:O:2252:A:C8	2.54	0.42
1:O:2353:A:H4'	1:O:2354:A:O5'	2.17	0.42
4:A:192:VAL:HG12	4:A:207:GLN:CB	2.41	0.42
7:D:23:VAL:O	7:D:23:VAL:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:5:ASP:O	9:F:119:ARG:NH1	2.52	0.42
13:K:49:LEU:HD12	13:K:80:ILE:HD13	2.01	0.42
15:M:46:LEU:HD22	15:M:50:ARG:HG3	2.02	0.42
19:Q:75:ILE:CD1	19:Q:84:ILE:HD11	2.50	0.42
40:O:7872:HOH:O	22:T:9:LYS:HB2	2.18	0.42
25:W:73:LEU:HA	25:W:73:LEU:HD12	1.89	0.42
26:X:7:GLU:HA	26:X:75:ALA:HA	2.01	0.42
27:Y:107:PRO:HB3	27:Y:182:PHE:CE2	2.54	0.42
1:O:1925:G:O2'	1:O:1926:G:H5'	2.20	0.42
1:O:2478:U:O2'	1:O:2479:A:H5'	2.20	0.42
1:O:362:G:H2'	1:O:363:A:C8	2.54	0.42
4:A:88:ILE:CD1	4:A:100:PRO:HD3	2.45	0.42
4:A:94:LEU:HG	4:A:99:ILE:HD11	2.00	0.42
14:L:143:THR:CG2	14:L:144:ASP:H	2.32	0.42
16:N:35:VAL:HG12	16:N:37:ARG:HD3	2.01	0.42
22:T:115:GLU:CG	22:T:116:ASP:N	2.79	0.42
25:W:48:VAL:O	25:W:48:VAL:CG1	2.67	0.42
26:X:74:ALA:HB2	26:X:85:VAL:HG22	2.02	0.42
1:O:137:U:OP1	1:O:259:G:O2'	2.37	0.42
1:O:1476:A:H1'	1:O:1867:G:O2'	2.19	0.42
1:O:2587:OMU:H2'	1:O:2589:U:H5''	2.01	0.42
30:2:19:SER:HB3	40:2:4479:HOH:O	2.20	0.42
31:3:20:HIS:HA	31:3:70:ARG:O	2.20	0.42
7:D:52:THR:HB	7:D:70:GLY:C	2.39	0.42
7:D:67:ASP:O	7:D:69:ILE:HG13	2.20	0.42
32:I:113:HIS:HE1	32:I:121:LEU:HD22	1.82	0.42
12:J:45:VAL:CG2	12:J:129:PHE:CD1	3.03	0.42
14:L:12:THR:HG21	14:L:16:GLY:O	2.18	0.42
16:N:182:GLY:O	16:N:183:ASP:C	2.57	0.42
24:V:1:THR:OG1	24:V:2:VAL:N	2.52	0.42
24:V:16:ARG:NH2	24:V:63:GLU:HG3	2.35	0.42
30:2:49:GLU:HB2	40:2:131:HOH:O	2.20	0.42
2:9:3107:C:H5	40:9:3167:HOH:O	2.02	0.42
7:D:10:PHE:CG	7:D:11:HIS:N	2.87	0.42
9:F:106:ALA:HB3	40:F:6617:HOH:O	2.18	0.42
17:O:18:ALA:HB2	17:O:26:TRP:HB2	2.01	0.42
17:O:49:GLU:OE1	17:O:70:LEU:HD12	2.19	0.42
20:R:114:VAL:HA	20:R:144:GLU:O	2.19	0.42
21:S:6:LYS:O	21:S:7:HIS:HB3	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:34:LEU:HD12	25:W:107:LEU:HD11	2.01	0.42
1:0:1159:G:H1	1:0:1208:C:N4	2.16	0.42
1:0:1588:G:C6	1:0:1589:G:N1	2.88	0.42
1:0:204:A:H2'	1:0:205:U:H5'	2.01	0.42
1:0:2577:A:H5'	40:0:8264:HOH:O	2.18	0.42
1:0:2667:G:H1'	1:0:2914:A:N3	2.34	0.42
1:0:2809:G:H2'	1:0:2810:G:O4'	2.19	0.42
1:0:646:G:H2'	1:0:647:U:C6	2.55	0.42
1:0:87:C:C2	30:2:30:ASP:OD2	2.73	0.42
1:0:1654:U:H2'	4:A:47:HIS:CD2	2.55	0.42
5:B:16:ARG:NE	40:B:9557:HOH:O	2.28	0.42
8:E:22:VAL:O	8:E:28:SER:HA	2.20	0.42
1:0:1185:U:H4'	32:I:123:ASN:HB3	2.01	0.42
18:P:55:LYS:HG2	18:P:56:GLY:N	2.34	0.42
25:W:38:THR:HG22	25:W:39:ASP:H	1.84	0.42
1:0:1185:U:H5'	40:0:7910:HOH:O	2.20	0.42
1:0:1603:A:H5''	1:0:1604:G:H3'	2.02	0.42
1:0:2324:G:N2	1:0:2377:U:H1'	2.35	0.42
30:2:18:ASN:ND2	30:2:40:ARG:H	2.17	0.42
31:3:6:ARG:HA	31:3:20:HIS:O	2.20	0.42
4:A:81:GLN:N	4:A:92:ASN:OD1	2.42	0.42
5:B:234:ARG:NH1	40:B:9612:HOH:O	2.52	0.42
1:0:2780:C:C1'	8:E:143:GLN:HE21	2.25	0.42
40:0:6241:HOH:O	13:K:87:ARG:CZ	2.68	0.42
15:M:164:THR:HG22	15:M:167:GLY:H	1.85	0.42
15:M:76:ARG:HG3	15:M:88:VAL:HG21	2.02	0.42
1:0:171:C:OP2	15:M:84:LYS:HG3	2.19	0.42
18:P:89:ASN:OD1	18:P:92:GLU:HB2	2.19	0.42
26:X:43:VAL:HG12	26:X:47:ALA:HB3	2.00	0.42
27:Y:122:ARG:NH2	40:Y:9336:HOH:O	2.52	0.42
1:0:1573:A:H2'	1:0:1574:C:O4'	2.19	0.42
1:0:1759:A:N3	1:0:1818:C:H2'	2.35	0.42
1:0:2011:A:H4'	1:0:2012:U:O5'	2.20	0.42
2:9:3039:U:H3'	2:9:3040:C:H5''	2.01	0.42
40:0:3426:HOH:O	5:B:252:PRO:HD3	2.20	0.42
11:H:88:ARG:HG2	11:H:133:LEU:O	2.20	0.42
13:K:118:ALA:HB1	13:K:125:ALA:CB	2.50	0.42
13:K:74:VAL:HG12	13:K:74:VAL:O	2.18	0.42
22:T:3:GLN:HA	22:T:4:PRO:HD3	1.85	0.42
23:U:20:MET:HE3	23:U:30:HIS:NE2	2.35	0.42
26:X:30:MET:CE	26:X:58:ALA:HB3	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2034:U:H4'	40:0:6439:HOH:O	2.20	0.42
1:0:295:C:H2'	1:0:296:G:O4'	2.19	0.42
1:0:737:A:H3'	1:0:737:A:C8	2.55	0.42
1:0:879:C:H5	40:0:3763:HOH:O	2.03	0.42
29:1:28:HIS:O	29:1:32:LYS:N	2.45	0.42
4:A:207:GLN:O	4:A:208:HIS:HB3	2.20	0.42
4:A:223:ARG:NE	40:A:9559:HOH:O	2.52	0.42
4:A:95:PRO:HA	4:A:153:ARG:HA	2.02	0.42
7:D:99:ASP:HB3	7:D:103:ASN:H	1.85	0.42
9:F:70:LYS:C	9:F:72:VAL:H	2.23	0.42
11:H:28:ILE:HA	11:H:63:GLU:OE1	2.20	0.42
16:N:154:LEU:CG	16:N:155:GLU:H	2.25	0.42
23:U:44:ARG:HB3	40:U:3805:HOH:O	2.19	0.42
27:Y:133:HIS:HD2	40:Y:9384:HOH:O	2.03	0.42
1:0:1174:A:C6	1:0:1201:C:H4'	2.55	0.41
1:0:2089:A:O2'	1:0:2090:G:H5'	2.20	0.41
1:0:2523:U:O2'	1:0:2524:G:H5'	2.20	0.41
5:B:1:PRO:O	5:B:2:GLN:HB2	2.20	0.41
7:D:15:GLU:HA	7:D:16:PRO:HD3	1.83	0.41
11:H:146:VAL:HG22	40:H:9542:HOH:O	2.20	0.41
15:M:120:VAL:HG11	15:M:130:GLU:HG3	2.01	0.41
21:S:11:THR:H	21:S:14:ALA:HB3	1.83	0.41
22:T:102:ASP:OD1	22:T:104:GLU:HG3	2.20	0.41
1:0:1257:C:H2'	1:0:1258:G:O4'	2.20	0.41
1:0:1507:C:H4'	40:0:4185:HOH:O	2.20	0.41
1:0:1748:U:H4'	40:0:7963:HOH:O	2.19	0.41
1:0:2768:A:O2'	1:0:2769:C:O4'	2.33	0.41
1:0:2869:G:H2'	1:0:2870:C:O4'	2.20	0.41
1:0:304:G:H1'	1:0:347:A:N6	2.34	0.41
1:0:941:G:C5	1:0:942:U:C4	3.09	0.41
4:A:112:PRO:HD3	4:A:152:CYS:SG	2.60	0.41
8:E:20:ILE:O	8:E:30:THR:HA	2.20	0.41
40:0:4417:HOH:O	11:H:11:LYS:HE2	2.20	0.41
12:J:143:LYS:HG3	12:J:145:TRP:CE2	2.55	0.41
16:N:152:GLU:C	16:N:154:LEU:N	2.74	0.41
18:P:14:LEU:O	18:P:16:VAL:HG23	2.20	0.41
20:R:114:VAL:HG13	20:R:114:VAL:O	2.20	0.41
20:R:61:GLN:NE2	40:R:9451:HOH:O	2.53	0.41
24:V:59:ILE:O	24:V:63:GLU:HG2	2.20	0.41
1:0:2363:G:O2'	19:Q:11:ARG:HG3	2.20	0.41
1:0:2637:A:H5''	38:4:9701:SPS:O3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:271:C:O2	1:0:273:G:H5''	2.19	0.41
1:0:380:A:H2'	40:0:7686:HOH:O	2.19	0.41
29:1:28:HIS:HD2	29:1:30:LYS:H	1.68	0.41
2:9:3056:A:C3'	2:9:3057:A:H5''	2.50	0.41
4:A:43:VAL:O	4:A:44:ASP:HB2	2.20	0.41
7:D:167:GLU:OE2	7:D:173:GLU:HB3	2.20	0.41
8:E:1:PRO:HD2	8:E:53:GLU:O	2.20	0.41
11:H:51:VAL:CG1	11:H:53:GLU:O	2.68	0.41
2:9:3004:G:O2'	16:N:44:ARG:NH2	2.53	0.41
6:C:27:ARG:HD2	17:O:5:PRO:HD2	2.02	0.41
18:P:55:LYS:CG	18:P:56:GLY:N	2.82	0.41
22:T:79:LEU:HG	22:T:89:ARG:HB2	2.02	0.41
23:U:19:THR:HG22	23:U:20:MET:N	2.35	0.41
26:X:72:VAL:CG1	26:X:85:VAL:CG1	2.98	0.41
1:0:1236:A:H2'	1:0:1237:U:O4'	2.20	0.41
1:0:1524:U:HO2'	1:0:1525:G:P	2.44	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
1:0:2769:C:C2'	1:0:2770:G:C5'	2.98	0.41
1:0:2784:A:H1'	8:E:60:SER:OG	2.20	0.41
1:0:447:A:O2'	1:0:448:G:H5'	2.20	0.41
1:0:522:U:O2'	1:0:1366:C:H5'	2.19	0.41
7:D:27:ILE:HB	40:D:5858:HOH:O	2.19	0.41
1:0:2338:G:OP1	7:D:97:GLN:HG2	2.20	0.41
8:E:81:GLU:HA	8:E:133:VAL:O	2.20	0.41
1:0:2453:G:H4'	14:L:50:GLY:C	2.40	0.41
15:M:183:THR:CG2	15:M:194:ALA:HB1	2.46	0.41
16:N:62:HIS:HB3	16:N:65:ASP:OD1	2.20	0.41
16:N:67:ALA:C	16:N:69:TYR:H	2.23	0.41
18:P:98:ILE:CD1	18:P:102:ARG:NE	2.84	0.41
18:P:15:ASP:O	18:P:15:ASP:OD1	2.39	0.41
1:0:1020:A:H2'	1:0:1021:G:C8	2.56	0.41
1:0:162:C:H2'	1:0:163:U:H5'	2.02	0.41
1:0:1657:A:H2'	1:0:1658:A:C8	2.55	0.41
1:0:1666:C:C2'	1:0:1667:A:H5''	2.50	0.41
1:0:1675:C:H5''	30:2:5:LYS:HD2	2.03	0.41
1:0:1565:C:O4'	1:0:2738:G:H1'	2.20	0.41
1:0:697:G:H4'	1:0:730:G:O3'	2.21	0.41
1:0:899:C:H5'	40:0:3789:HOH:O	2.21	0.41
4:A:30:ARG:HB3	4:A:30:ARG:HE	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:43:VAL:HG21	4:A:59:GLU:HG3	2.01	0.41
5:B:154:VAL:HA	5:B:155:PRO:HD3	1.88	0.41
10:G:12:ILE:HG22	10:G:17:GLN:NE2	2.36	0.41
11:H:140:VAL:HG12	11:H:140:VAL:O	2.21	0.41
12:J:39:VAL:HG11	12:J:107:ASN:CG	2.41	0.41
15:M:74:LYS:HE3	15:M:75:ARG:O	2.20	0.41
21:S:10:VAL:HG11	24:V:36:ALA:CA	2.49	0.41
26:X:76:ARG:NH1	26:X:76:ARG:HG3	2.35	0.41
28:Z:10:ARG:C	28:Z:12:GLY:H	2.23	0.41
1:0:1773:G:C8	28:Z:16:ALA:HA	2.56	0.41
1:0:1318:A:H4'	1:0:1343:C:H4'	2.02	0.41
1:0:2253:G:O2'	1:0:2254:G:H5'	2.21	0.41
1:0:2351:C:H2'	1:0:2352:G:O4'	2.20	0.41
1:0:2428:G:H5'	40:0:7132:HOH:O	2.21	0.41
1:0:290:C:O2'	1:0:291:C:H5'	2.20	0.41
1:0:625:U:H5''	1:0:1044:C:H41	1.86	0.41
31:3:7:PHE:CE1	31:3:9:THR:HB	2.56	0.41
12:J:42:GLU:O	12:J:131:THR:HG23	2.20	0.41
16:N:24:LEU:HD13	19:Q:26:PRO:HB3	2.03	0.41
22:T:115:GLU:HG3	22:T:116:ASP:H	1.81	0.41
40:0:6789:HOH:O	27:Y:158:LYS:HD3	2.19	0.41
27:Y:213:LYS:HE3	27:Y:213:LYS:HB2	1.85	0.41
27:Y:102:LEU:HD11	27:Y:225:GLY:HA2	2.02	0.41
1:0:1299:G:N2	40:0:5231:HOH:O	2.53	0.41
1:0:2388:C:H2'	1:0:2389:U:O4'	2.21	0.41
1:0:2517:A:H2'	1:0:2518:C:O4'	2.21	0.41
1:0:695:C:H2'	1:0:696:C:C6	2.55	0.41
40:0:9728:HOH:O	5:B:229:ARG:HD2	2.20	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
7:D:135:VAL:HG22	7:D:136:ARG:H	1.86	0.41
7:D:166:ILE:O	7:D:169:THR:N	2.54	0.41
7:D:60:GLU:O	7:D:60:GLU:HG3	2.21	0.41
9:F:48:VAL:CG2	9:F:74:PHE:HB3	2.51	0.41
11:H:17:ARG:HD3	11:H:23:ILE:HD12	2.03	0.41
11:H:36:LYS:HA	11:H:84:LYS:NZ	2.36	0.41
15:M:82:ARG:O	15:M:84:LYS:N	2.53	0.41
1:0:2299:G:O6	19:Q:1:PRO:HA	2.21	0.41
19:Q:22:GLY:O	19:Q:23:THR:C	2.58	0.41
23:U:39:ASN:ND2	23:U:44:ARG:HH11	2.18	0.41
24:V:1:THR:O	24:V:2:VAL:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:O:5826:HOH:O	25:W:69:ARG:NH2	2.54	0.41
26:X:73:ARG:NH1	26:X:73:ARG:HB2	2.35	0.41
1:O:1173:A:H4'	1:O:1174:A:C8	2.56	0.41
1:O:1505:U:H1'	40:O:8100:HOH:O	2.20	0.41
1:O:1556:G:O2'	1:O:1557:G:H5'	2.21	0.41
1:O:1636:G:O2'	1:O:1637:A:H5'	2.20	0.41
1:O:2515:C:H2'	1:O:2516:G:C5'	2.51	0.41
1:O:359:U:H3'	40:O:6290:HOH:O	2.20	0.41
31:3:38:ARG:HB3	31:3:42:ARG:NH1	2.31	0.41
4:A:223:ARG:CZ	40:A:9559:HOH:O	2.69	0.41
5:B:146:THR:C	5:B:148:PRO:HD3	2.41	0.41
8:E:20:ILE:HD12	8:E:33:LEU:CD1	2.49	0.41
12:J:95:ARG:HG2	12:J:99:GLU:OE2	2.21	0.41
13:K:82:ARG:NH2	13:K:115:ARG:HG2	2.36	0.41
13:K:7:ASP:OD2	13:K:81:ARG:NH2	2.54	0.41
14:L:80:ASP:HB3	14:L:90:ARG:HB3	2.02	0.41
15:M:82:ARG:O	15:M:83:SER:C	2.59	0.41
16:N:71:TRP:HB2	40:N:9335:HOH:O	2.19	0.41
21:S:57:THR:HG22	21:S:59:ASP:N	2.34	0.41
27:Y:148:GLY:O	27:Y:154:ARG:HD3	2.21	0.41
28:Z:49:ARG:HB2	28:Z:55:TRP:CZ3	2.56	0.41
30:2:11:LEU:HA	30:2:11:LEU:HD23	1.90	0.41
4:A:104:PRO:HG3	4:A:127:GLN:OE1	2.21	0.41
5:B:141:ARG:HD2	5:B:163:GLU:OE2	2.21	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
6:C:133:ARG:NH1	40:C:9214:HOH:O	2.53	0.41
6:C:162:VAL:HG13	6:C:192:ILE:HD11	2.02	0.41
9:F:57:GLU:O	9:F:61:MET:HG3	2.21	0.41
11:H:167:PRO:O	11:H:168:ALA:HB2	2.21	0.41
13:K:118:ALA:HB1	13:K:125:ALA:HB2	2.03	0.41
16:N:38:LYS:HD3	16:N:107:ASN:ND2	2.36	0.41
1:O:721:A:H4'	17:O:51:TYR:CD1	2.55	0.41
1:O:1095:U:O2	25:W:120:PRO:HG2	2.21	0.41
1:O:2281:C:C2'	1:O:2282:U:H5'	2.50	0.41
1:O:255:A:H2'	1:O:256:C:C6	2.56	0.41
3:4:76:DA:H8	38:4:9701:SPS:H81	1.85	0.41
2:9:3118:C:H4'	16:N:56:ASP:OD1	2.21	0.41
5:B:62:ARG:HA	5:B:65:MET:HE3	2.03	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:I:118:SER:CB	32:I:123:ASN:HB2	2.50	0.41
14:L:59:GLU:HB3	40:L:9465:HOH:O	2.20	0.41
19:Q:66:LYS:HB2	19:Q:70:ALA:O	2.21	0.41
22:T:32:ARG:HH12	22:T:38:ARG:HH12	1.66	0.41
28:Z:39:CYS:HA	28:Z:40:PRO:HD3	1.95	0.41
1:O:2016:U:H2'	1:O:2017:U:C6	2.55	0.41
1:O:2553:A:H2'	1:O:2553:A:N3	2.35	0.41
5:B:84:LEU:O	5:B:99:GLU:HA	2.21	0.41
7:D:88:LEU:N	7:D:89:PRO:CD	2.84	0.41
32:I:72:VAL:CG1	32:I:73:PRO:HD2	2.51	0.41
12:J:71:TYR:CD1	12:J:72:PRO:HD2	2.56	0.41
2:9:3011:A:P	19:Q:19:ARG:HH21	2.43	0.41
22:T:81:LYS:HD2	22:T:87:VAL:CG1	2.52	0.41
25:W:6:GLN:CB	25:W:26:ILE:HD11	2.27	0.41
1:O:1132:A:N3	1:O:2521:A:O2'	2.49	0.40
1:O:1163:G:H5'	32:I:115:ASP:O	2.21	0.40
1:O:2094:G:O6	1:O:2649:A:H2	2.04	0.40
1:O:526:U:H2'	1:O:527:U:C6	2.56	0.40
1:O:819:A:H5''	40:Z:9220:HOH:O	2.20	0.40
31:3:70:ARG:CG	31:3:77:ALA:HB2	2.51	0.40
5:B:320:GLN:HA	5:B:321:PRO:HD3	1.95	0.40
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
32:I:78:LEU:CD1	32:I:112:LYS:HZ2	2.32	0.40
17:O:15:LYS:HD3	17:O:19:ARG:NH2	2.36	0.40
27:Y:144:ARG:NH2	40:Y:9411:HOH:O	2.51	0.40
28:Z:39:CYS:O	28:Z:42:CYS:O	2.40	0.40
1:O:1176:C:H3'	40:O:5396:HOH:O	2.22	0.40
1:O:1797:A:H2'	1:O:1799:G:O5'	2.22	0.40
1:O:2421:G:H2'	40:O:4646:HOH:O	2.20	0.40
1:O:2515:C:H2'	1:O:2516:G:H5'	2.03	0.40
1:O:27:U:H2'	1:O:28:G:O4'	2.21	0.40
1:O:2821:C:H4'	5:B:116:PRO:HG3	2.03	0.40
1:O:2908:A:H2'	1:O:2909:G:C4'	2.51	0.40
2:9:3044:A:O4'	7:D:76:ARG:NE	2.55	0.40
5:B:24:PRO:HG3	5:B:204:GLY:HA2	2.03	0.40
11:H:54:THR:O	11:H:55:VAL:HG13	2.21	0.40
32:I:108:ILE:C	32:I:110:GLU:H	2.24	0.40
12:J:90:LYS:HB2	36:J:9302:CL:CL	2.57	0.40
16:N:23:ARG:NH1	16:N:23:ARG:HG2	2.34	0.40
17:O:23:GLY:C	40:O:3062:HOH:O	2.59	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:81:PHE:N	17:O:81:PHE:CD1	2.89	0.40
18:P:94:TRP:CZ2	18:P:98:ILE:HG13	2.56	0.40
1:O:1077:G:H2'	1:O:1080:C:H42	1.86	0.40
1:O:1342:C:C2'	1:O:1343:C:H5'	2.51	0.40
1:O:2070:G:H2'	1:O:2072:G:OP1	2.22	0.40
1:O:2612:A:H4'	40:O:4260:HOH:O	2.21	0.40
1:O:338:C:H4'	6:C:174:ILE:HD11	2.02	0.40
1:O:432:G:H2'	1:O:433:C:H6	1.86	0.40
5:B:149:ASP:HB2	40:B:9579:HOH:O	2.21	0.40
6:C:123:LEU:HD23	6:C:123:LEU:HA	1.84	0.40
7:D:165:PHE:O	7:D:168:SER:HB3	2.22	0.40
11:H:165:SER:OG	11:H:168:ALA:HB3	2.21	0.40
12:J:107:ASN:ND2	12:J:107:ASN:C	2.73	0.40
2:9:3028:U:P	16:N:39:SER:OG	2.80	0.40
24:V:12:THR:OG1	24:V:13:PRO:HD2	2.20	0.40
27:Y:170:SER:OG	27:Y:175:ARG:HG3	2.21	0.40
1:O:2326:U:H4'	1:O:2412:G:H4'	2.04	0.40
1:O:920:C:H5'	1:O:921:G:C4	2.56	0.40
1:O:956:G:H2'	1:O:957:A:O4'	2.21	0.40
31:3:17:HIS:O	31:3:18:GLN:HG3	2.22	0.40
2:9:3095:C:O2'	2:9:3096:C:H5'	2.22	0.40
4:A:36:ASP:O	4:A:38:ILE:N	2.48	0.40
5:B:102:THR:CG2	5:B:182:VAL:HG12	2.51	0.40
8:E:7:ILE:HA	8:E:8:PRO:HD3	1.95	0.40
1:O:1242:A:O3'	12:J:20:GLY:HA3	2.22	0.40
14:L:73:VAL:HG21	14:L:116:HIS:CD2	2.57	0.40
24:V:12:THR:HG23	24:V:14:ALA:N	2.36	0.40
25:W:126:ASP:HB3	25:W:135:GLY:O	2.21	0.40
1:O:1380:U:O4	1:O:2748:G:H1'	2.22	0.40
1:O:1504:A:H5'	40:O:4966:HOH:O	2.20	0.40
1:O:2896:A:N3	1:O:2896:A:C2'	2.84	0.40
1:O:401:C:O2'	15:M:92:THR:HB	2.22	0.40
1:O:559:U:H2'	1:O:560:C:O4'	2.22	0.40
1:O:816:G:C6	1:O:817:G:N1	2.90	0.40
31:3:48:ASN:ND2	31:3:50:GLY:H	2.20	0.40
4:A:32:VAL:HG12	4:A:34:ASP:N	2.36	0.40
40:O:4664:HOH:O	5:B:216:LYS:HE2	2.20	0.40
6:C:194:PHE:CE2	6:C:234:VAL:HG11	2.56	0.40
7:D:96:SER:C	7:D:98:PHE:H	2.24	0.40
11:H:70:ASN:O	11:H:74:ILE:HG13	2.21	0.40
19:Q:91:LEU:C	19:Q:92:ARG:HG2	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:U:52:THR:HG21	23:U:54:THR:HB	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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%)	11	7
5	B	335/338 (99%)	312 (93%)	19 (6%)	4 (1%)	15	12
6	C	244/246 (99%)	226 (93%)	18 (7%)	0	100	100
7	D	134/177 (76%)	103 (77%)	23 (17%)	8 (6%)	2	0
8	E	170/178 (96%)	163 (96%)	7 (4%)	0	100	100
9	F	117/120 (98%)	102 (87%)	13 (11%)	2 (2%)	11	7
10	G	25/348 (7%)	25 (100%)	0	0	100	100
11	H	156/171 (91%)	140 (90%)	13 (8%)	3 (2%)	9	6
12	J	140/145 (97%)	132 (94%)	6 (4%)	2 (1%)	13	10
13	K	130/132 (98%)	121 (93%)	8 (6%)	1 (1%)	22	21
14	L	141/165 (86%)	118 (84%)	21 (15%)	2 (1%)	13	10
15	M	192/194 (99%)	181 (94%)	9 (5%)	2 (1%)	18	16
16	N	184/187 (98%)	161 (88%)	13 (7%)	10 (5%)	2	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%)	20	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	U	51/66 (77%)	48 (94%)	3 (6%)	0	100	100
24	V	63/71 (89%)	57 (90%)	3 (5%)	3 (5%)	2	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%)	3	1
29	1	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
30	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
31	3	90/92 (98%)	87 (97%)	2 (2%)	1 (1%)	17	13
32	I	68/162 (42%)	54 (79%)	11 (16%)	3 (4%)	3	1
All	All	3705/4430 (84%)	3410 (92%)	246 (7%)	49 (1%)	14	11

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

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Mol	Chain	Res	Type
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
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%)	16	17
5	B	282/283 (100%)	268 (95%)	14 (5%)	28	34
6	C	193/193 (100%)	176 (91%)	17 (9%)	12	11
7	D	117/148 (79%)	111 (95%)	6 (5%)	28	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	E	152/156 (97%)	148 (97%)	4 (3%)	51	64
9	F	93/94 (99%)	89 (96%)	4 (4%)	33	41
10	G	27/283 (10%)	26 (96%)	1 (4%)	39	49
11	H	132/138 (96%)	127 (96%)	5 (4%)	38	47
12	J	118/121 (98%)	111 (94%)	7 (6%)	23	26
13	K	106/106 (100%)	100 (94%)	6 (6%)	24	28
14	L	113/127 (89%)	111 (98%)	2 (2%)	64	77
15	M	158/158 (100%)	153 (97%)	5 (3%)	44	56
16	N	149/150 (99%)	142 (95%)	7 (5%)	30	37
17	O	93/94 (99%)	89 (96%)	4 (4%)	33	41
18	P	113/117 (97%)	112 (99%)	1 (1%)	82	91
19	Q	79/80 (99%)	77 (98%)	2 (2%)	53	65
20	R	117/122 (96%)	116 (99%)	1 (1%)	82	91
21	S	71/74 (96%)	71 (100%)	0	100	100
22	T	105/106 (99%)	100 (95%)	5 (5%)	30	36
23	U	44/52 (85%)	44 (100%)	0	100	100
24	V	51/57 (90%)	50 (98%)	1 (2%)	60	74
25	W	130/130 (100%)	126 (97%)	4 (3%)	45	57
26	X	66/74 (89%)	59 (89%)	7 (11%)	8	7
27	Y	120/196 (61%)	108 (90%)	12 (10%)	9	8
28	Z	60/68 (88%)	59 (98%)	1 (2%)	66	79
29	1	46/47 (98%)	46 (100%)	0	100	100
30	2	42/46 (91%)	40 (95%)	2 (5%)	30	36
31	3	79/79 (100%)	76 (96%)	3 (4%)	38	47
32	I	58/130 (45%)	58 (100%)	0	100	100
All	All	3093/3611 (86%)	2959 (96%)	134 (4%)	33	41

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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%)	0
2	9	121/122 (99%)	16 (13%)	0
3	4	1/5 (20%)	0	0
All	All	2867/3049 (94%)	253 (8%)	0

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U
1	0	840	U
1	0	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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

There are no RNA pucker outliers to report.

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

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	14,22,23	1.04	1 (7%)	18,31,34	3.66	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	OMG	0	2588	1	18,26,27	1.03	1 (5%)	22,38,41	2.47	5 (22%)
1	UR3	0	2619	1	14,22,23	0.86	0	16,32,35	0.70	0
1	PSU	0	2621	1	16,21,22	1.61	3 (18%)	20,30,33	6.13	4 (20%)
1	1MA	0	628	1,35	16,25,26	1.02	1 (6%)	13,37,40	1.18	1 (7%)

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	-	0/5/27/28	0/2/2/2
1	OMG	0	2588	1	-	0/5/27/28	0/3/3/3
1	UR3	0	2619	1	-	0/3/25/26	0/2/2/2
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	1MA	0	628	1,35	-	0/3/25/26	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C5-C1'	-4.67	1.48	1.52
1	0	2621	PSU	C2-N1	2.60	1.43	1.38
1	0	2587	OMU	C4-N3	2.83	1.38	1.33
1	0	2621	PSU	C4-N3	2.85	1.38	1.33
1	0	628	1MA	C6-N6	2.98	1.34	1.27
1	0	2588	OMG	C6-N1	3.34	1.39	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	N1-C2-N3	-19.15	114.63	128.40
1	0	2621	PSU	C5-C4-N3	-13.01	114.76	125.43
1	0	2588	OMG	C5-C6-N1	-8.34	111.61	123.48
1	0	628	1MA	C2-N3-C4	-3.67	110.78	116.41
1	0	2587	OMU	C5-C4-N3	-3.56	114.62	123.12
1	0	2588	OMG	C2-N3-C4	-2.73	111.97	115.16
1	0	2588	OMG	N3-C2-N1	-2.42	123.93	127.46
1	0	2588	OMG	C6-C5-C4	-2.13	118.73	120.84
1	0	2621	PSU	C6-N1-C2	2.68	119.65	115.36
1	0	2588	OMG	C6-N1-C2	6.33	125.17	116.06
1	0	2621	PSU	C4-N3-C2	13.95	127.36	115.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2587	OMU	C4-N3-C2	14.92	126.95	114.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2587	OMU	2	0
1	0	2619	UR3	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	20,23,23	1.68	5 (25%)	18,30,30	2.78	3 (16%)

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	-	0/15/18/18	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	4	9701	SPS	C9-C10	-3.36	1.41	1.48
38	4	9701	SPS	O15-S15	-2.28	1.43	1.50
38	4	9701	SPS	C1-N2	2.33	1.37	1.33
38	4	9701	SPS	C5-N4	2.80	1.38	1.34
38	4	9701	SPS	C1-C6	4.16	1.53	1.44

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	4	9701	SPS	C6-C1-N2	-8.42	118.51	124.45
38	4	9701	SPS	C6-C5-N4	-2.21	119.52	121.92
38	4	9701	SPS	C1-N2-C3	7.07	121.34	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	4	9701	SPS	4	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	0	2749/2922 (94%)	-0.23	91 (3%) 47 44	19, 43, 76, 127	0
2	9	122/122 (100%)	0.03	6 (4%) 30 29	39, 58, 76, 127	0
3	4	4/5 (80%)	0.90	1 (25%) 1 1	52, 54, 55, 58	0
4	A	237/240 (98%)	0.43	14 (5%) 23 22	26, 45, 70, 85	0
5	B	337/338 (99%)	0.24	10 (2%) 51 48	27, 47, 65, 73	0
6	C	246/246 (100%)	-0.08	2 (0%) 86 85	26, 44, 61, 69	0
7	D	140/177 (79%)	2.07	61 (43%) 0 0	51, 74, 102, 109	0
8	E	172/178 (96%)	0.70	20 (11%) 5 5	40, 57, 69, 74	0
9	F	119/120 (99%)	1.00	31 (26%) 1 1	45, 62, 82, 87	0
10	G	29/348 (8%)	2.66	17 (58%) 0 0	59, 77, 83, 86	0
11	H	160/171 (93%)	0.72	27 (16%) 2 2	41, 54, 79, 83	0
12	J	142/145 (97%)	-0.03	3 (2%) 64 61	36, 45, 58, 71	0
13	K	132/132 (100%)	-0.10	2 (1%) 74 72	32, 43, 59, 64	0
14	L	145/165 (87%)	0.66	22 (15%) 2 2	26, 56, 90, 100	0
15	M	194/194 (100%)	0.50	19 (9%) 8 7	32, 42, 65, 70	0
16	N	186/187 (99%)	0.93	34 (18%) 1 1	42, 56, 89, 94	0
17	O	115/116 (99%)	0.07	3 (2%) 56 54	37, 50, 60, 65	0
18	P	143/149 (95%)	0.05	2 (1%) 75 73	35, 47, 57, 66	0
19	Q	95/96 (98%)	0.15	3 (3%) 48 46	39, 45, 56, 67	0
20	R	150/155 (96%)	-0.07	0 100 100	29, 41, 56, 64	0
21	S	81/85 (95%)	0.24	5 (6%) 21 20	39, 52, 66, 79	0
22	T	119/120 (99%)	0.55	7 (5%) 23 22	38, 50, 70, 92	0
23	U	53/66 (80%)	0.23	5 (9%) 9 8	38, 47, 61, 69	0
24	V	65/71 (91%)	1.77	18 (27%) 1 0	46, 64, 93, 97	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	W	154/154 (100%)	0.01	1 (0%) 89 88	36, 47, 60, 68	0
26	X	82/92 (89%)	0.50	10 (12%) 5 4	39, 50, 69, 85	0
27	Y	142/241 (58%)	0.22	9 (6%) 21 19	28, 41, 59, 73	0
28	Z	73/83 (87%)	0.49	9 (12%) 5 4	43, 58, 70, 76	0
29	1	56/57 (98%)	-0.37	0 100 100	25, 32, 39, 48	0
30	2	46/50 (92%)	0.36	3 (6%) 20 18	31, 49, 62, 71	0
31	3	92/92 (100%)	0.26	4 (4%) 36 34	34, 51, 60, 70	0
32	I	70/162 (43%)	6.02	67 (95%) 0 0	90, 102, 117, 118	0
All	All	6650/7479 (88%)	0.21	506 (7%) 15 13	19, 47, 79, 127	0

All (506) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
32	I	71	GLY	18.3
7	D	63	ILE	17.5
16	N	166	ALA	15.7
24	V	1	THR	15.5
32	I	133	THR	14.1
32	I	79	ILE	12.6
32	I	76	ALA	11.9
32	I	118	SER	11.2
32	I	75	THR	10.8
32	I	85	PHE	10.3
7	D	57	THR	10.1
32	I	137	VAL	9.6
32	I	116	LEU	9.5
32	I	77	GLU	9.2
32	I	105	VAL	9.1
24	V	40	PRO	9.0
4	A	237	GLY	8.9
32	I	96	PHE	8.9
7	D	61	PHE	8.7
32	I	81	ASP	8.6
22	T	119	ALA	8.3
32	I	121	LEU	8.3
24	V	39	ALA	8.1
32	I	113	HIS	8.1
32	I	109	ALA	8.1
16	N	165	ALA	8.0

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Mol	Chain	Res	Type	RSRZ
32	I	91	GLU	7.9
2	9	3001	U	7.5
7	D	10	PHE	7.5
32	I	88	GLY	7.3
32	I	132	CYS	7.2
32	I	78	LEU	7.2
32	I	125	ALA	7.2
32	I	107	GLN	7.1
1	0	282	C	7.1
32	I	126	LYS	7.0
1	0	1951	G	7.0
32	I	87	THR	7.0
32	I	102	VAL	6.9
32	I	108	ILE	6.9
7	D	90	LEU	6.7
10	G	26	MET	6.6
15	M	70	GLY	6.6
32	I	104	GLN	6.6
10	G	23	ILE	6.4
4	A	37	VAL	6.3
32	I	86	GLU	6.3
32	I	93	GLN	6.2
32	I	129	VAL	6.2
32	I	114	PRO	6.1
22	T	118	SER	5.9
26	X	80	GLU	5.9
7	D	170	TYR	5.9
1	0	497	A	5.9
32	I	136	GLY	5.9
24	V	38	GLY	5.9
32	I	111	GLN	5.8
26	X	88	GLU	5.8
1	0	1199	A	5.8
32	I	138	THR	5.8
21	S	81	ILE	5.6
32	I	98	ALA	5.6
32	I	97	VAL	5.5
7	D	44	ILE	5.5
1	0	1202	A	5.4
2	9	3002	U	5.4
32	I	119	TYR	5.4
2	9	3024	U	5.3

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Mol	Chain	Res	Type	RSRZ
32	I	89	SER	5.3
32	I	117	LEU	5.3
32	I	122	THR	5.3
30	2	49	GLU	5.3
16	N	180	LEU	5.2
16	N	68	GLU	5.2
7	D	93	LEU	5.2
1	0	1177	A	5.2
1	0	1173	A	5.1
8	E	45	ASP	5.0
32	I	74	PRO	5.0
10	G	27	ILE	4.9
32	I	134	SER	4.9
32	I	83	ALA	4.8
14	L	91	VAL	4.8
32	I	72	VAL	4.7
7	D	166	ILE	4.7
22	T	117	ASP	4.7
1	0	1172	G	4.7
24	V	37	GLY	4.6
22	T	116	ASP	4.6
1	0	1965	C	4.6
30	2	35	ARG	4.6
1	0	970	U	4.6
13	K	132	VAL	4.6
7	D	92	GLU	4.5
12	J	70	PHE	4.5
7	D	88	LEU	4.5
7	D	134	LEU	4.5
1	0	514	G	4.5
2	9	3023	U	4.5
4	A	36	ASP	4.5
7	D	11	HIS	4.5
10	G	71	LEU	4.5
1	0	280	C	4.4
32	I	84	GLY	4.4
7	D	66	GLY	4.4
13	K	118	ALA	4.4
17	O	22	GLY	4.4
9	F	22	VAL	4.3
1	0	1200	A	4.3
32	I	80	LYS	4.3

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Mol	Chain	Res	Type	RSRZ
1	0	2508	C	4.3
11	H	171	ALA	4.2
4	A	133	ARG	4.2
15	M	86	GLN	4.2
10	G	69	ARG	4.2
7	D	107	GLY	4.2
1	0	284	C	4.2
8	E	100	ASP	4.2
14	L	81	VAL	4.2
24	V	36	ALA	4.2
27	Y	235	GLU	4.1
16	N	160	SER	4.1
32	I	99	ASP	4.1
11	H	146	VAL	4.1
1	0	1948	G	4.1
7	D	135	VAL	4.1
16	N	175	LEU	4.0
32	I	103	ASP	4.0
1	0	1171	A	4.0
15	M	74	LYS	4.0
14	L	80	ASP	4.0
15	M	75	ARG	4.0
1	0	1192	A	4.0
1	0	735	C	4.0
27	Y	95	THR	4.0
7	D	62	ASP	3.9
1	0	1525	G	3.9
23	U	47	ARG	3.9
1	0	1950	G	3.9
16	N	163	PHE	3.9
7	D	91	ALA	3.9
9	F	99	THR	3.9
32	I	106	LYS	3.9
1	0	2237	G	3.9
28	Z	11	SER	3.9
1	0	2004	U	3.8
1	0	285	A	3.8
1	0	283	U	3.8
32	I	120	ASP	3.8
9	F	119	ARG	3.8
9	F	16	ALA	3.8
1	0	1168	C	3.8

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Mol	Chain	Res	Type	RSRZ
5	B	1	PRO	3.8
7	D	104	PHE	3.8
31	3	92	GLU	3.8
4	A	31	LYS	3.8
8	E	10	ASP	3.8
10	G	22	ALA	3.8
1	0	960	G	3.8
9	F	25	ASP	3.7
1	0	1198	U	3.7
7	D	64	ARG	3.7
9	F	28	ALA	3.7
8	E	6	GLU	3.7
7	D	69	ILE	3.7
11	H	73	LEU	3.7
14	L	75	LEU	3.7
27	Y	236	VAL	3.7
32	I	92	PRO	3.7
7	D	85	GLN	3.7
24	V	43	PRO	3.7
16	N	95	ALA	3.6
4	A	35	GLY	3.6
1	0	2769	C	3.6
22	T	82	THR	3.6
32	I	123	ASN	3.6
7	D	27	ILE	3.6
7	D	95	THR	3.6
32	I	110	GLU	3.6
28	Z	20	ARG	3.6
9	F	117	GLU	3.6
4	A	236	GLY	3.6
7	D	171	ASP	3.6
14	L	76	LEU	3.6
19	Q	95	GLU	3.5
7	D	106	PHE	3.5
16	N	184	ILE	3.5
32	I	124	ALA	3.5
2	9	3122	C	3.5
1	0	272	A	3.5
1	0	2511	A	3.5
11	H	168	ALA	3.5
1	0	10	U	3.5
7	D	81	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
32	I	90	GLY	3.5
1	0	1164	U	3.5
1	0	2238	A	3.5
1	0	1163	G	3.5
1	0	1966	U	3.5
7	D	172	VAL	3.4
7	D	40	ILE	3.4
1	0	1169	U	3.4
32	I	94	GLU	3.4
15	M	79	ALA	3.4
22	T	115	GLU	3.4
1	0	999	C	3.4
5	B	183	GLU	3.4
24	V	8	ILE	3.4
26	X	77	PHE	3.4
9	F	118	LEU	3.3
1	0	288	A	3.3
15	M	87	GLY	3.3
16	N	181	ASP	3.3
24	V	41	GLU	3.3
28	Z	22	SER	3.3
16	N	178	THR	3.3
14	L	97	VAL	3.3
1	0	2344	G	3.2
15	M	71	SER	3.2
7	D	51	ARG	3.2
11	H	35	ARG	3.2
1	0	369	G	3.2
7	D	173	GLU	3.2
11	H	111	ASP	3.2
10	G	66	LEU	3.2
26	X	85	VAL	3.2
32	I	112	LYS	3.2
7	D	89	PRO	3.2
26	X	71	ARG	3.2
16	N	147	ILE	3.2
7	D	56	ARG	3.2
1	0	1181	A	3.2
11	H	138	CYS	3.2
28	Z	21	VAL	3.2
8	E	87	PHE	3.2
10	G	24	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	0	138	U	3.2
24	V	59	ILE	3.1
15	M	76	ARG	3.1
32	I	100	LEU	3.1
1	0	1967	U	3.1
14	L	105	TYR	3.1
16	N	159	TYR	3.1
28	Z	24	ARG	3.1
1	0	281	U	3.1
8	E	154	ILE	3.1
32	I	115	ASP	3.1
9	F	12	LEU	3.1
26	X	10	VAL	3.1
16	N	134	ASP	3.1
7	D	41	LEU	3.0
14	L	62	ALA	3.0
4	A	85	SER	3.0
14	L	148	GLU	3.0
32	I	131	THR	3.0
9	F	101	ALA	3.0
18	P	18	LYS	3.0
12	J	4	ALA	3.0
14	L	100	ALA	3.0
1	0	370	G	3.0
8	E	43	ASP	3.0
9	F	105	ASP	3.0
15	M	88	VAL	3.0
10	G	12	ILE	2.9
7	D	73	VAL	2.9
14	L	145	LEU	2.9
16	N	161	GLY	2.9
16	N	155	GLU	2.9
6	C	61	PHE	2.9
11	H	83	TYR	2.9
9	F	100	ASP	2.9
9	F	106	ALA	2.9
9	F	107	ASP	2.9
14	L	147	GLU	2.9
14	L	79	ASP	2.9
8	E	126	ILE	2.9
7	D	130	VAL	2.9
32	I	130	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
5	B	2	GLN	2.9
32	I	135	LEU	2.9
16	N	185	GLU	2.8
1	0	358	G	2.8
11	H	149	ALA	2.8
16	N	158	LEU	2.8
1	0	1170	U	2.8
1	0	1174	A	2.8
9	F	26	THR	2.8
7	D	67	ASP	2.8
1	0	1162	G	2.8
28	Z	36	ASP	2.8
8	E	124	VAL	2.8
4	A	97	ALA	2.8
27	Y	96	GLU	2.8
15	M	80	GLY	2.8
9	F	110	ASP	2.8
8	E	88	TYR	2.8
27	Y	216	ARG	2.8
1	0	1180	U	2.8
24	V	2	VAL	2.8
10	G	67	LEU	2.8
1	0	362	G	2.8
11	H	78	GLY	2.8
1	0	279	C	2.8
21	S	20	PHE	2.8
14	L	106	VAL	2.8
19	Q	18	PRO	2.8
11	H	82	ASP	2.8
16	N	72	GLU	2.8
1	0	1165	G	2.8
10	G	15	TRP	2.8
7	D	154	LYS	2.8
7	D	18	ILE	2.7
11	H	47	ILE	2.7
10	G	73	ASP	2.7
16	N	183	ASP	2.7
1	0	361	C	2.7
15	M	84	LYS	2.7
16	N	2	THR	2.7
11	H	162	ARG	2.7
1	0	1190	G	2.7

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Mol	Chain	Res	Type	RSRZ
8	E	94	GLN	2.7
24	V	5	VAL	2.7
7	D	26	GLY	2.7
1	0	2345	A	2.7
1	0	1182	C	2.7
10	G	21	ASP	2.7
14	L	60	GLU	2.7
7	D	167	GLU	2.7
11	H	37	GLN	2.7
17	O	23	GLY	2.7
7	D	58	VAL	2.7
16	N	139	TRP	2.6
16	N	94	GLU	2.6
1	0	1203	G	2.6
5	B	123	ALA	2.6
15	M	77	HIS	2.6
25	W	86	GLU	2.6
11	H	39	ASP	2.6
1	0	1179	C	2.6
1	0	1184	C	2.6
7	D	68	PRO	2.6
7	D	157	LEU	2.6
9	F	98	VAL	2.6
11	H	141	GLU	2.6
1	0	441	A	2.6
1	0	969	G	2.6
5	B	57	GLU	2.6
5	B	117	GLU	2.6
30	2	39	ARG	2.6
1	0	1175	G	2.6
1	0	1947	G	2.6
32	I	73	PRO	2.5
24	V	10	ASP	2.5
1	0	295	C	2.5
9	F	19	ALA	2.5
9	F	23	ALA	2.5
11	H	139	ASN	2.5
10	G	65	THR	2.5
11	H	74	ILE	2.5
5	B	180	ASP	2.5
14	L	99	GLU	2.5
7	D	23	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
19	Q	76	VAL	2.5
27	Y	234	VAL	2.5
5	B	134	ALA	2.5
15	M	49	ALA	2.5
16	N	182	GLY	2.5
9	F	21	GLU	2.5
1	0	372	A	2.5
1	0	1527	A	2.5
1	0	1625	U	2.5
14	L	102	ASP	2.5
31	3	62	THR	2.5
31	3	56	PRO	2.5
24	V	3	LEU	2.5
1	0	2645	U	2.5
7	D	160	ALA	2.5
1	0	1161	A	2.5
4	A	65	ARG	2.5
11	H	67	LEU	2.5
1	0	736	A	2.5
1	0	1929	G	2.5
9	F	11	ASP	2.5
9	F	15	ASP	2.5
1	0	1526	A	2.4
1	0	2748	G	2.4
7	D	75	LEU	2.4
15	M	78	LYS	2.4
21	S	78	ALA	2.4
32	I	128	VAL	2.4
17	O	1	SER	2.4
14	L	149	ARG	2.4
9	F	103	GLU	2.4
7	D	74	THR	2.4
9	F	49	PHE	2.4
32	I	95	ASP	2.4
1	0	1000	C	2.4
11	H	79	GLU	2.4
7	D	84	LEU	2.4
1	0	1167	G	2.4
1	0	2747	C	2.4
26	X	7	GLU	2.4
11	H	137	TYR	2.4
24	V	46	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
11	H	142	ASP	2.4
23	U	53	ASP	2.4
11	H	166	SER	2.4
9	F	24	ARG	2.3
16	N	164	ASP	2.3
32	I	127	GLU	2.3
14	L	150	GLN	2.3
26	X	41	PHE	2.3
26	X	43	VAL	2.3
7	D	17	ARG	2.3
31	3	41	GLU	2.3
15	M	81	ARG	2.3
5	B	176	ASP	2.3
8	E	127	ASP	2.3
14	L	93	VAL	2.3
5	B	104	GLU	2.3
16	N	156	GLU	2.3
28	Z	25	ARG	2.3
7	D	77	ASP	2.3
14	L	104	ASP	2.3
32	I	82	GLU	2.3
1	0	1189	A	2.3
7	D	53	LYS	2.3
1	0	1208	C	2.3
2	9	3072	C	2.3
8	E	99	GLY	2.3
9	F	18	GLU	2.3
7	D	165	PHE	2.3
28	Z	45	ASP	2.3
24	V	14	ALA	2.3
23	U	54	THR	2.2
1	0	1964	U	2.2
9	F	109	GLU	2.2
10	G	25	GLU	2.2
16	N	138	ASP	2.2
8	E	86	VAL	2.2
9	F	108	VAL	2.2
12	J	5	GLU	2.2
24	V	63	GLU	2.2
23	U	55	ALA	2.2
1	0	365	G	2.2
1	0	716	G	2.2

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Mol	Chain	Res	Type	RSRZ
16	N	106	LEU	2.2
7	D	65	GLU	2.2
14	L	130	ARG	2.2
1	0	1279	U	2.2
16	N	172	PHE	2.2
27	Y	108	ASP	2.2
11	H	76	GLU	2.2
16	N	74	PRO	2.2
9	F	90	GLU	2.2
1	0	363	A	2.2
7	D	45	THR	2.2
7	D	86	THR	2.2
10	G	63	ARG	2.2
15	M	82	ARG	2.2
7	D	38	GLU	2.2
16	N	177	GLU	2.2
4	A	135	VAL	2.2
7	D	70	GLY	2.2
4	A	86	ALA	2.2
8	E	131	LEU	2.2
11	H	42	ASP	2.2
8	E	103	VAL	2.1
15	M	73	ARG	2.1
15	M	83	SER	2.1
9	F	115	VAL	2.1
10	G	68	GLU	2.1
21	S	70	GLU	2.1
4	A	38	ILE	2.1
28	Z	12	GLY	2.1
6	C	1	MET	2.1
16	N	69	TYR	2.1
1	0	1178	G	2.1
3	4	77	PHE	2.1
16	N	137	ALA	2.1
11	H	164	ASP	2.1
9	F	17	LEU	2.1
8	E	98	GLU	2.1
22	T	59	GLU	2.1
8	E	118	ILE	2.1
7	D	163	VAL	2.1
21	S	45	TYR	2.1
27	Y	98	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
23	U	45	GLU	2.1
1	0	1201	C	2.1
11	H	44	PRO	2.1
26	X	44	ASP	2.0
7	D	25	MET	2.0
8	E	129	GLU	2.0
24	V	45	ARG	2.0
18	P	141	ILE	2.0
1	0	1195	G	2.0
1	0	1183	C	2.0
16	N	152	GLU	2.0
8	E	169	THR	2.0
4	A	82	VAL	2.0
7	D	128	LEU	2.0
1	0	1913	C	2.0
27	Y	141	THR	2.0
1	0	293	A	2.0
15	M	194	ALA	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	1MA	0	628	23/24	0.98	0.13	-	28,32,33,34	0
1	OMU	0	2587	21/22	0.98	0.12	-	30,35,36,37	0
1	OMG	0	2588	24/25	0.97	0.12	-	30,34,36,38	0
1	UR3	0	2619	21/22	0.97	0.13	-	34,38,41,43	0
1	PSU	0	2621	20/21	0.97	0.13	-	31,33,38,38	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
37	SR	0	9500	1/1	0.89	1.90	97.52	197,197,197,197	0
35	NA	0	9125	1/1	0.96	0.80	64.35	93,93,93,93	0
35	NA	0	9173	1/1	0.86	0.24	26.07	59,59,59,59	0
35	NA	0	9178	1/1	0.90	0.52	25.47	52,52,52,52	0
37	SR	B	9521	1/1	0.19	0.88	24.03	185,185,185,185	0
35	NA	0	9169	1/1	0.83	0.64	19.58	90,90,90,90	0
35	NA	0	9185	1/1	0.71	0.41	19.54	52,52,52,52	0
35	NA	0	9172	1/1	0.66	0.46	18.11	76,76,76,76	0
37	SR	0	9406	1/1	1.00	0.22	17.72	43,43,43,43	0
35	NA	0	9168	1/1	0.88	0.17	17.34	66,66,66,66	0
35	NA	0	9164	1/1	0.64	0.32	17.19	60,60,60,60	0
35	NA	9	9183	1/1	0.62	0.34	16.89	77,77,77,77	0
33	MG	0	8008	1/1	0.99	0.23	15.40	16,16,16,16	0
35	NA	B	9161	1/1	0.81	0.27	14.47	62,62,62,62	0
33	MG	0	8013	1/1	0.98	0.39	13.41	14,14,14,14	0
35	NA	0	9177	1/1	0.94	0.40	12.70	71,71,71,71	0
33	MG	0	8001	1/1	0.98	0.21	12.61	23,23,23,23	0
37	SR	0	9410	1/1	0.99	0.20	12.46	45,45,45,45	0
33	MG	0	8038	1/1	0.99	0.26	12.25	18,18,18,18	0
37	SR	0	9482	1/1	0.89	0.19	11.22	115,115,115,115	0
35	NA	0	9118	1/1	0.95	0.22	8.83	49,49,49,49	0
33	MG	0	8012	1/1	0.98	0.24	8.53	37,37,37,37	0
33	MG	0	8065	1/1	0.63	0.52	8.39	93,93,93,93	0
33	MG	0	8021	1/1	0.93	0.24	7.72	56,56,56,56	0
33	MG	0	8017	1/1	0.98	0.15	7.33	23,23,23,23	0
37	SR	L	9409	1/1	0.99	0.21	7.32	49,49,49,49	0
33	MG	0	8052	1/1	0.83	0.20	5.86	74,74,74,74	0
37	SR	0	9407	1/1	0.99	0.17	5.61	46,46,46,46	0
36	CL	B	9319	1/1	0.97	0.25	5.45	53,53,53,53	0
33	MG	K	8069	1/1	1.00	0.23	5.03	24,24,24,24	0
33	MG	0	8080	1/1	0.95	0.20	4.94	46,46,46,46	0
33	MG	0	8060	1/1	0.91	0.23	4.94	76,76,76,76	0
35	NA	0	9156	1/1	0.99	0.16	4.65	55,55,55,55	0
35	NA	0	9150	1/1	0.87	0.19	4.58	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
33	MG	0	8056	1/1	0.90	0.21	4.26	54,54,54,54	0
33	MG	0	8110	1/1	0.97	0.20	4.12	44,44,44,44	0
35	NA	0	9159	1/1	0.97	0.18	3.47	46,46,46,46	0
35	NA	0	9171	1/1	0.95	0.14	3.00	66,66,66,66	0
35	NA	0	9127	1/1	0.85	0.16	2.77	57,57,57,57	0
37	SR	R	9418	1/1	0.99	0.16	2.62	54,54,54,54	0
37	SR	0	9416	1/1	1.00	0.16	2.47	47,47,47,47	0
35	NA	0	9120	1/1	0.78	0.15	2.36	55,55,55,55	0
36	CL	0	9316	1/1	0.87	0.21	2.23	69,69,69,69	0
37	SR	0	9424	1/1	1.00	0.17	2.17	46,46,46,46	0
33	MG	0	8097	1/1	0.96	0.16	1.97	57,57,57,57	0
37	SR	1	9419	1/1	0.99	0.15	1.97	43,43,43,43	0
35	NA	0	9174	1/1	0.90	0.13	1.94	61,61,61,61	0
33	MG	0	8020	1/1	0.98	0.17	1.65	36,36,36,36	0
33	MG	0	8058	1/1	0.92	0.20	1.57	39,39,39,39	0
37	SR	0	9457	1/1	0.99	0.12	1.48	49,49,49,49	0
35	NA	0	9162	1/1	0.95	0.14	1.44	49,49,49,49	0
33	MG	0	8074	1/1	0.99	0.22	1.28	20,20,20,20	0
35	NA	0	9182	1/1	0.93	0.13	1.23	63,63,63,63	0
35	NA	0	9114	1/1	0.86	0.15	1.03	56,56,56,56	0
35	NA	0	9124	1/1	0.95	0.16	0.92	53,53,53,53	0
37	SR	H	9486	1/1	0.97	0.14	0.90	107,107,107,107	0
37	SR	F	9595	1/1	0.99	0.16	0.82	92,92,92,92	0
33	MG	0	8107	1/1	0.88	0.14	0.80	70,70,70,70	0
35	NA	0	9132	1/1	0.89	0.14	0.75	54,54,54,54	0
35	NA	0	9117	1/1	0.93	0.15	0.75	32,32,32,32	0
35	NA	C	9104	1/1	0.95	0.19	0.74	31,31,31,31	0
37	SR	0	9475	1/1	0.96	0.11	0.54	76,76,76,76	0
35	NA	0	9186	1/1	0.88	0.13	0.48	67,67,67,67	0
36	CL	0	9315	1/1	0.94	0.11	0.47	53,53,53,53	0
36	CL	M	9318	1/1	0.96	0.18	0.45	40,40,40,40	0
35	NA	0	9165	1/1	0.95	0.17	0.35	44,44,44,44	0
37	SR	0	9451	1/1	0.98	0.12	0.32	64,64,64,64	0
38	SPS	4	9701	23/23	0.90	0.17	0.32	49,53,67,71	0
39	CD	U	9201	1/1	0.99	0.13	0.30	59,59,59,59	0
37	SR	0	9515	1/1	0.98	0.12	0.26	88,88,88,88	0
35	NA	0	9110	1/1	0.98	0.12	0.25	45,45,45,45	0
33	MG	0	8004	1/1	0.99	0.11	0.12	26,26,26,26	0
35	NA	0	9167	1/1	0.96	0.10	0.12	49,49,49,49	0
35	NA	0	9139	1/1	0.90	0.17	0.11	57,57,57,57	0
39	CD	Z	9203	1/1	0.98	0.14	0.01	59,59,59,59	0
33	MG	0	8054	1/1	0.79	0.12	-0.01	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
33	MG	0	8015	1/1	0.94	0.12	-0.08	29,29,29,29	0
35	NA	Q	9148	1/1	0.97	0.17	-0.25	51,51,51,51	0
36	CL	J	9321	1/1	0.96	0.15	-0.30	64,64,64,64	0
37	SR	0	9428	1/1	0.99	0.12	-0.35	49,49,49,49	0
35	NA	0	9166	1/1	0.86	0.10	-0.36	68,68,68,68	0
33	MG	0	8002	1/1	0.98	0.12	-0.48	29,29,29,29	0
33	MG	A	8066	1/1	0.88	0.12	-0.60	53,53,53,53	0
35	NA	M	9147	1/1	0.93	0.12	-0.63	43,43,43,43	0
35	NA	R	9137	1/1	0.92	0.11	-0.71	33,33,33,33	0
37	SR	0	9532	1/1	0.94	0.09	-0.96	115,115,115,115	0
39	CD	3	9204	1/1	0.98	0.08	-1.00	59,59,59,59	0
34	K	0	9002	1/1	0.87	0.09	-1.01	78,78,78,78	0
37	SR	0	9443	1/1	0.99	0.11	-1.02	54,54,54,54	0
33	MG	4	8118	1/1	0.90	0.12	-1.07	45,45,45,45	0
36	CL	O	9308	1/1	0.98	0.09	-1.10	59,59,59,59	0
33	MG	T	8073	1/1	0.96	0.15	-1.13	41,41,41,41	0
37	SR	0	9442	1/1	0.99	0.12	-1.13	59,59,59,59	0
35	NA	J	9146	1/1	0.94	0.09	-1.14	51,51,51,51	0
37	SR	0	9444	1/1	0.99	0.13	-1.14	50,50,50,50	0
35	NA	R	9138	1/1	0.97	0.08	-1.18	58,58,58,58	0
37	SR	0	9504	1/1	0.95	0.10	-1.26	88,88,88,88	0
37	SR	0	9509	1/1	0.96	0.11	-1.28	83,83,83,83	0
37	SR	0	9490	1/1	0.97	0.08	-1.37	101,101,101,101	0
33	MG	0	8096	1/1	0.95	0.10	-1.41	40,40,40,40	0
36	CL	0	9312	1/1	0.98	0.09	-1.62	47,47,47,47	0
33	MG	0	8028	1/1	0.99	0.12	-1.79	31,31,31,31	0
39	CD	1	9202	1/1	0.99	0.07	-1.89	55,55,55,55	0
37	SR	0	9534	1/1	0.99	0.09	-2.00	95,95,95,95	0
33	MG	0	8044	1/1	0.95	0.09	-2.04	35,35,35,35	0
37	SR	0	9468	1/1	0.70	0.07	-2.11	97,97,97,97	0
37	SR	0	9453	1/1	0.97	0.09	-2.21	68,68,68,68	0
37	SR	0	9483	1/1	0.95	0.08	-2.30	69,69,69,69	0
37	SR	3	9439	1/1	0.98	0.07	-2.32	64,64,64,64	0
33	MG	0	8067	1/1	0.97	0.10	-2.35	33,33,33,33	0
33	MG	0	8112	1/1	0.94	0.08	-2.44	45,45,45,45	0
35	NA	0	9143	1/1	0.97	0.07	-3.41	37,37,37,37	0
37	SR	0	9473	1/1	0.99	0.06	-3.53	69,69,69,69	0
37	SR	0	9455	1/1	0.99	0.10	-3.59	61,61,61,61	0
33	MG	0	8019	1/1	0.97	0.06	-3.64	47,47,47,47	0
37	SR	A	9436	1/1	0.98	0.03	-3.73	68,68,68,68	0
33	MG	0	8003	1/1	0.98	0.10	-3.83	26,26,26,26	0
36	CL	3	9304	1/1	0.96	0.04	-4.11	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
37	SR	0	9456	1/1	0.99	0.07	-4.18	64,64,64,64	0
33	MG	0	8032	1/1	0.98	0.09	-4.54	33,33,33,33	0
37	SR	0	9498	1/1	0.99	0.06	-4.64	61,61,61,61	0
35	NA	0	9131	1/1	0.98	0.07	-4.71	45,45,45,45	0
36	CL	0	9313	1/1	0.98	0.07	-4.93	47,47,47,47	0
36	CL	0	9305	1/1	0.98	0.06	-5.05	50,50,50,50	0
37	SR	0	9506	1/1	0.97	0.06	-5.68	74,74,74,74	0
35	NA	0	9135	1/1	0.98	0.09	-6.20	39,39,39,39	0
33	MG	Y	8109	1/1	0.99	0.04	-6.24	35,35,35,35	0
35	NA	0	9105	1/1	1.00	0.04	-7.06	33,33,33,33	0
35	NA	0	9123	1/1	0.99	0.08	-7.72	39,39,39,39	0
33	MG	0	8042	1/1	0.78	0.08	-	57,57,57,57	0
37	SR	0	9581	1/1	0.83	0.07	-	110,110,110,110	0
37	SR	0	9420	1/1	0.98	0.17	-	65,65,65,65	0
35	NA	0	9122	1/1	0.48	0.41	-	77,77,77,77	0
33	MG	0	8089	1/1	0.91	0.12	-	54,54,54,54	0
33	MG	0	8024	1/1	0.89	0.61	-	74,74,74,74	0
37	SR	0	9474	1/1	0.99	0.07	-	71,71,71,71	0
36	CL	0	9314	1/1	0.96	0.09	-	43,43,43,43	0
37	SR	0	9440	1/1	0.98	0.06	-	61,61,61,61	0
37	SR	0	9495	1/1	0.97	0.09	-	85,85,85,85	0
35	NA	0	9152	1/1	0.83	0.36	-	64,64,64,64	0
33	MG	0	8083	1/1	0.88	0.10	-	53,53,53,53	0
35	NA	0	9113	1/1	0.97	0.21	-	64,64,64,64	0
35	NA	0	9136	1/1	0.98	0.10	-	30,30,30,30	0
37	SR	0	9445	1/1	0.97	0.11	-	55,55,55,55	0
33	MG	0	8093	1/1	0.76	0.12	-	45,45,45,45	0
37	SR	0	9411	1/1	1.00	0.19	-	46,46,46,46	0
37	SR	0	9517	1/1	0.95	0.07	-	92,92,92,92	0
37	SR	0	9430	1/1	1.00	0.17	-	46,46,46,46	0
35	NA	0	9115	1/1	0.95	0.15	-	35,35,35,35	0
36	CL	0	9311	1/1	0.96	0.11	-	61,61,61,61	0
33	MG	0	8029	1/1	0.97	0.21	-	26,26,26,26	0
33	MG	0	8092	1/1	0.70	0.73	-	80,80,80,80	0
33	MG	0	8098	1/1	0.96	0.09	-	45,45,45,45	0
33	MG	0	8057	1/1	0.92	0.20	-	77,77,77,77	0
37	SR	0	9629	1/1	0.99	0.10	-	68,68,68,68	0
37	SR	0	9452	1/1	0.87	0.15	-	105,105,105,105	0
37	SR	A	9497	1/1	0.98	0.10	-	78,78,78,78	0
35	NA	0	9107	1/1	0.87	0.20	-	54,54,54,54	0
33	MG	0	8050	1/1	0.51	0.23	-	88,88,88,88	0
37	SR	0	9484	1/1	0.82	0.11	-	134,134,134,134	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
37	SR	0	9423	1/1	0.99	0.12	-	51,51,51,51	0
37	SR	0	9433	1/1	0.97	0.12	-	68,68,68,68	0
37	SR	0	9465	1/1	0.94	0.11	-	98,98,98,98	0
37	SR	0	9435	1/1	0.99	0.08	-	68,68,68,68	0
37	SR	0	9441	1/1	0.99	0.09	-	57,57,57,57	0
35	NA	0	9134	1/1	0.96	0.05	-	42,42,42,42	0
35	NA	0	9160	1/1	0.98	0.12	-	36,36,36,36	0
33	MG	0	8099	1/1	0.93	0.14	-	62,62,62,62	0
35	NA	0	9111	1/1	0.82	0.21	-	59,59,59,59	0
33	MG	0	8059	1/1	0.96	0.16	-	48,48,48,48	0
35	NA	0	9179	1/1	0.82	0.54	-	89,89,89,89	0
33	MG	0	8076	1/1	0.95	0.14	-	51,51,51,51	0
33	MG	0	8104	1/1	0.94	0.11	-	49,49,49,49	0
36	CL	0	9303	1/1	0.99	0.09	-	43,43,43,43	0
37	SR	0	9467	1/1	0.97	0.12	-	71,71,71,71	0
33	MG	0	8117	1/1	0.94	0.13	-	39,39,39,39	0
33	MG	0	8014	1/1	0.70	0.25	-	67,67,67,67	0
37	SR	9	9481	1/1	0.98	0.07	-	82,82,82,82	0
37	SR	9	9588	1/1	0.74	0.12	-	118,118,118,118	0
37	SR	0	9429	1/1	0.98	0.10	-	64,64,64,64	0
37	SR	0	9434	1/1	0.99	0.12	-	59,59,59,59	0
37	SR	0	9530	1/1	0.84	0.11	-	102,102,102,102	0
35	NA	0	9108	1/1	0.98	0.10	-	31,31,31,31	0
37	SR	0	9421	1/1	0.99	0.11	-	65,65,65,65	0
33	MG	0	8046	1/1	0.98	0.08	-	37,37,37,37	0
36	CL	A	9309	1/1	0.98	0.07	-	56,56,56,56	0
33	MG	0	8084	1/1	0.92	0.29	-	61,61,61,61	0
33	MG	0	8031	1/1	0.96	0.05	-	51,51,51,51	0
37	SR	0	9405	1/1	0.98	0.06	-	80,80,80,80	0
33	MG	0	8079	1/1	0.97	0.14	-	28,28,28,28	0
37	SR	0	9425	1/1	0.91	0.07	-	108,108,108,108	0
34	K	0	9001	1/1	0.90	0.31	-	84,84,84,84	0
36	CL	J	9302	1/1	0.95	0.07	-	54,54,54,54	0
37	SR	0	9529	1/1	0.90	0.11	-	136,136,136,136	0
35	NA	0	9175	1/1	0.90	0.18	-	47,47,47,47	0
33	MG	0	8101	1/1	0.85	0.11	-	59,59,59,59	0
33	MG	0	8102	1/1	0.90	0.08	-	66,66,66,66	0
33	MG	0	8026	1/1	0.97	0.14	-	28,28,28,28	0
37	SR	0	9566	1/1	0.91	0.05	-	92,92,92,92	0
33	MG	0	8036	1/1	0.91	0.09	-	56,56,56,56	0
37	SR	0	9585	1/1	0.97	0.10	-	83,83,83,83	0
33	MG	0	8009	1/1	0.97	0.05	-	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
36	CL	Y	9320	1/1	0.98	0.11	-	40,40,40,40	0
33	MG	0	8090	1/1	0.89	0.22	-	68,68,68,68	0
33	MG	0	8115	1/1	0.94	0.17	-	55,55,55,55	0
37	SR	0	9488	1/1	0.98	0.11	-	72,72,72,72	0
37	SR	0	9414	1/1	0.99	0.15	-	54,54,54,54	0
37	SR	0	9469	1/1	0.98	0.05	-	83,83,83,83	0
37	SR	0	9590	1/1	0.93	0.10	-	117,117,117,117	0
33	MG	0	8025	1/1	0.99	0.33	-	24,24,24,24	0
37	SR	0	9570	1/1	0.95	0.06	-	92,92,92,92	0
33	MG	0	8103	1/1	0.84	0.19	-	62,62,62,62	0
33	MG	0	8070	1/1	0.98	0.16	-	21,21,21,21	0
35	NA	0	9184	1/1	0.57	0.23	-	73,73,73,73	0
35	NA	0	9130	1/1	0.99	0.12	-	47,47,47,47	0
35	NA	0	9154	1/1	0.86	0.18	-	57,57,57,57	0
37	SR	0	9462	1/1	0.99	0.13	-	64,64,64,64	0
35	NA	0	9101	1/1	0.85	0.22	-	45,45,45,45	0
37	SR	0	9412	1/1	0.99	0.16	-	48,48,48,48	0
35	NA	0	9128	1/1	0.98	0.15	-	39,39,39,39	0
33	MG	0	8027	1/1	0.97	0.23	-	35,35,35,35	0
35	NA	S	9112	1/1	0.60	0.61	-	75,75,75,75	0
33	MG	0	8047	1/1	0.19	0.37	-	85,85,85,85	0
33	MG	0	8039	1/1	0.94	0.08	-	61,61,61,61	0
33	MG	0	8094	1/1	0.13	0.47	-	83,83,83,83	0
37	SR	0	9505	1/1	0.94	0.08	-	97,97,97,97	0
37	SR	0	9454	1/1	0.98	0.06	-	71,71,71,71	0
37	SR	0	9478	1/1	0.99	0.07	-	69,69,69,69	0
39	CD	O	9205	1/1	0.43	0.47	-	197,197,197,197	0
35	NA	0	9158	1/1	0.89	0.33	-	55,55,55,55	0
33	MG	0	8055	1/1	0.86	0.17	-	83,83,83,83	0
33	MG	0	8041	1/1	0.96	0.11	-	51,51,51,51	0
37	SR	0	9461	1/1	0.99	0.04	-	71,71,71,71	0
33	MG	0	8085	1/1	0.91	0.24	-	67,67,67,67	0
37	SR	0	9489	1/1	0.98	0.06	-	85,85,85,85	0
37	SR	0	9601	1/1	0.88	0.60	-	191,191,191,191	0
37	SR	0	9626	1/1	0.93	0.37	-	127,127,127,127	0
35	NA	0	9129	1/1	0.53	0.24	-	74,74,74,74	0
33	MG	0	8005	1/1	0.99	0.08	-	29,29,29,29	0
37	SR	9	9503	1/1	0.97	0.05	-	102,102,102,102	0
37	SR	A	9437	1/1	0.98	0.14	-	61,61,61,61	0
35	NA	0	9149	1/1	0.96	0.11	-	43,43,43,43	0
36	CL	R	9306	1/1	0.99	0.11	-	43,43,43,43	0
37	SR	S	9470	1/1	0.98	0.13	-	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
37	SR	0	9431	1/1	0.98	0.14	-	56,56,56,56	0
33	MG	0	8082	1/1	0.68	0.26	-	82,82,82,82	0
35	NA	0	9157	1/1	0.92	0.18	-	37,37,37,37	0
36	CL	J	9301	1/1	0.98	0.07	-	46,46,46,46	0
37	SR	0	9560	1/1	0.97	0.10	-	88,88,88,88	0
33	MG	0	8037	1/1	0.92	0.07	-	39,39,39,39	0
35	NA	0	9102	1/1	0.88	0.42	-	61,61,61,61	0
33	MG	0	8075	1/1	0.97	0.06	-	43,43,43,43	0
33	MG	0	8022	1/1	0.91	0.55	-	63,63,63,63	0
33	MG	0	8030	1/1	0.95	0.06	-	37,37,37,37	0
37	SR	B	9458	1/1	0.98	0.07	-	64,64,64,64	0
37	SR	0	9447	1/1	0.98	0.09	-	62,62,62,62	0
37	SR	0	9545	1/1	0.98	0.05	-	72,72,72,72	0
37	SR	0	9427	1/1	0.98	0.14	-	54,54,54,54	0
37	SR	0	9417	1/1	0.98	0.14	-	53,53,53,53	0
33	MG	9	8095	1/1	0.92	0.21	-	48,48,48,48	0
35	NA	0	9163	1/1	0.82	0.19	-	58,58,58,58	0
35	NA	0	9106	1/1	0.97	0.14	-	35,35,35,35	0
37	SR	0	9466	1/1	0.92	0.05	-	89,89,89,89	0
35	NA	0	9126	1/1	0.92	0.10	-	52,52,52,52	0
37	SR	0	9449	1/1	0.99	0.10	-	57,57,57,57	0
33	MG	0	8068	1/1	0.98	0.12	-	41,41,41,41	0
37	SR	0	9477	1/1	0.94	0.08	-	75,75,75,75	0
37	SR	0	9464	1/1	0.97	0.06	-	79,79,79,79	0
33	MG	0	8088	1/1	0.94	0.06	-	43,43,43,43	0
37	SR	1	9460	1/1	0.98	0.14	-	51,51,51,51	0
33	MG	0	8063	1/1	0.92	0.14	-	64,64,64,64	0
35	NA	D	9151	1/1	0.89	0.23	-	62,62,62,62	0
37	SR	0	9426	1/1	0.98	0.07	-	64,64,64,64	0
35	NA	0	9140	1/1	0.93	0.35	-	63,63,63,63	0
36	CL	0	9317	1/1	0.98	0.06	-	48,48,48,48	0
36	CL	L	9310	1/1	0.96	0.06	-	47,47,47,47	0
33	MG	0	8051	1/1	0.94	0.19	-	23,23,23,23	0
37	SR	0	9448	1/1	0.98	0.09	-	59,59,59,59	0
33	MG	0	8040	1/1	0.86	0.18	-	69,69,69,69	0
35	NA	0	9141	1/1	0.82	0.13	-	70,70,70,70	0
37	SR	0	9438	1/1	0.96	0.09	-	61,61,61,61	0
35	NA	0	9181	1/1	0.91	0.14	-	52,52,52,52	0
33	MG	0	8043	1/1	0.89	0.07	-	50,50,50,50	0
37	SR	0	9415	1/1	0.99	0.12	-	54,54,54,54	0
37	SR	0	9480	1/1	0.97	0.04	-	82,82,82,82	0
37	SR	0	9501	1/1	0.24	0.21	-	196,196,196,196	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
35	NA	0	9170	1/1	0.93	0.46	-	72,72,72,72	0
33	MG	0	8072	1/1	0.92	0.24	-	70,70,70,70	0
37	SR	0	9547	1/1	0.26	0.35	-	166,166,166,166	0
35	NA	0	9155	1/1	0.97	0.23	-	52,52,52,52	0
33	MG	0	8114	1/1	0.90	0.28	-	71,71,71,71	0
37	SR	0	9522	1/1	0.95	0.06	-	98,98,98,98	0
33	MG	0	8045	1/1	0.85	0.19	-	84,84,84,84	0
33	MG	0	8116	1/1	0.95	0.07	-	51,51,51,51	0
33	MG	0	8061	1/1	0.85	0.15	-	75,75,75,75	0
33	MG	0	8106	1/1	0.99	0.06	-	47,47,47,47	0
36	CL	N	9307	1/1	0.96	0.15	-	60,60,60,60	0
35	NA	0	9116	1/1	0.97	0.18	-	46,46,46,46	0
33	MG	0	8113	1/1	0.77	0.12	-	49,49,49,49	0
37	SR	0	9408	1/1	1.00	0.21	-	45,45,45,45	0
37	SR	0	9537	1/1	0.77	0.11	-	136,136,136,136	0
37	SR	0	9413	1/1	1.00	0.14	-	49,49,49,49	0
37	SR	0	9539	1/1	0.88	0.42	-	145,145,145,145	0
37	SR	0	9446	1/1	0.99	0.09	-	78,78,78,78	0
33	MG	0	8108	1/1	0.84	0.18	-	81,81,81,81	0
36	CL	0	9322	1/1	0.98	0.12	-	51,51,51,51	0
37	SR	0	9432	1/1	0.97	0.14	-	61,61,61,61	0
37	SR	0	9450	1/1	0.99	0.09	-	60,60,60,60	0
33	MG	0	8091	1/1	0.91	0.12	-	64,64,64,64	0
37	SR	0	9568	1/1	0.97	0.10	-	70,70,70,70	0
37	SR	0	9508	1/1	0.98	0.07	-	78,78,78,78	0
37	SR	0	9459	1/1	0.82	0.06	-	95,95,95,95	0
37	SR	0	9422	1/1	0.99	0.13	-	55,55,55,55	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.